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(54) **COMPOUNDS AND METHODS FOR
TREATING, DETECTING, AND
IDENTIFYING COMPOUNDS TO TREAT
APICOMPLEXAN PARASITIC DISEASES**

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C07D 471/04 (2006.01)
C07D 487/04 (2006.01)

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CPC *C07D 215/233* (2013.01); *A61P 33/06* (2018.01); *C07D 401/12* (2013.01); *C07D 405/12* (2013.01); *C07D 471/04* (2013.01); *C07D 487/04* (2013.01)

(58) **Field of Classification Search**
CPC *C07D 215/213*
See application file for complete search history.

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(57) **ABSTRACT**

Disclosed herein; are novel compounds for treating apicomplexan parasite related disorders, methods for their use; cell line and non-human animal models of the dormant parasite phenotype and methods for their use in identifying new drugs to treat apicomplexan parasite related disorders, and biomarkers to identify disease due to the parasite and its response to treatment.

11 Claims, 147 Drawing Sheets
Specification includes a Sequence Listing.

(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 565 days.

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C07D 215/233 (2006.01)

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FIGURE 1A

Figure 1: Host transcriptomics data during EGS infections of human HFF, MM6 or NSC cells. Differential gene expression analysis of human fibroblasts infected with *T. gondii* EGS strain after 2 hs, 18 hs, and 48 hs, monomac 6 cells infected with *T. gondii* EGS for 18 hs or neuronal stem cells infected with *T. gondii* EGS strain for 18 hs.

gene_ID	logFC HFF (2h) (Uninf)	logFC HFF (18h) (Uninf)	logFC HFF (48h) (Uninf)	logFC MM6 (18h) (Uninf)	logFC NSC (18h) (Uninf)	Product Name
ENSG0000004846	-0.15	-4.24	-10.36	#N/A	#N/A	ATP-binding cassette, sub-family B (MDR/TAP), member 5
ENSG00000196616	-0.27	-5.58	-12.98	#N/A	#N/A	alcohol dehydrogenase 1B (class I), beta polypeptide
ENSG00000169607	0.88	4.90	5.69	#N/A	#N/A	cytoskeleton associated protein 2-like
ENSG00000089685	0.19	2.98	3.78	#N/A	#N/A	baculoviral (AP repeat containing 5
ENSG00000131747	0.64	4.97	4.31	#N/A	#N/A	topoisomerase (DNA) II alpha 170kDa
ENSG00000101057	-0.06	3.94	3.04	#N/A	#N/A	v-myb avian myeloblastosis viral oncogene homolog-like 2
ENSG00000148773	0.70	4.04	4.33	#N/A	#N/A	marker of proliferation Ki-67
ENSG00000170456	-0.54	-3.04	-5.04	2.15	#N/A	CD14 molecule
ENSG00000138347	1.33	3.91	3.54	#N/A	#N/A	myopalladin
ENSG00000138180	0.87	3.79	4.54	#N/A	#N/A	centrosomal protein 55kDa
ENSG00000078401	1.18	-2.53	-3.32	#N/A	#N/A	endothelin 1
ENSG00000154839	0.78	4.73	4.72	#N/A	#N/A	spindle and kinetochore associated complex subunit 1
ENSG00000096849	0.61	3.48	4.36	1.58	#N/A	proline rich 11
ENSG00000123356	2.02	-4.40	-4.52	#N/A	#N/A	nuclear receptor subfamily 4, group A, member 1
ENSG00000145386	0.51	4.28	4.94	#N/A	#N/A	cyclin A2
ENSG00000072571	0.67	4.37	4.79	#N/A	#N/A	hyaluronan-mediated motility receptor (RHAMM)
ENSG00000092853	0.39	3.85	3.52	#N/A	#N/A	claspain
ENSG00000093009	0.12	4.32	3.54	#N/A	#N/A	cell division cycle 45
ENSG00000142945	0.27	3.50	4.13	#N/A	#N/A	kinesin family member 2C
ENSG00000169679	0.24	4.10	4.82	#N/A	#N/A	BUB1 mitotic checkpoint serine/threonine kinase
ENSG00000112006	0.25	2.79	3.52	#N/A	#N/A	forkhead box M1
ENSG00000109805	0.10	4.51	4.61	#N/A	#N/A	non-SMC condensin I complex, subunit G
ENSG00000088325	0.04	2.95	3.84	#N/A	#N/A	TPX2, microtubule-associated
ENSG00000117724	0.48	3.94	4.54	#N/A	#N/A	centromere protein F, 350/400kDa
ENSG00000101447	1.24	3.43	4.52	#N/A	#N/A	family with sequence similarity 83, member D
ENSG00000168078	0.72	4.09	4.74	#N/A	#N/A	POZ binding kinase
ENSG00000161888	-0.25	3.20	3.54	#N/A	#N/A	SPC24, NDC80 kinetochore complex component
ENSG00000237649	0.72	3.39	3.39	#N/A	#N/A	kinesin family member C1
ENSG00000111665	0.23	3.06	3.69	#N/A	#N/A	cell division cycle associated 3
ENSG00000138778	0.68	3.81	3.86	#N/A	#N/A	centromere protein E, 312kDa
ENSG00000196611	0.45	4.45	4.97	#N/A	#N/A	matrix metalloproteinase 1
ENSG00000146670	0.67	3.86	3.37	#N/A	#N/A	cell division cycle associated 5
ENSG00000198901	0.27	2.81	3.41	#N/A	#N/A	protein regulator of cytokinesis 1
ENSG00000186871	-1.08	4.11	4.13	#N/A	#N/A	excision repair cross-complementation group 6-like
ENSG00000090889	0.17	3.53	3.88	#N/A	#N/A	kinesin family member 4A
ENSG00000112742	-0.24	4.17	4.79	#N/A	#N/A	TTK protein kinase
ENSG00000165486	0.58	4.30	4.54	#N/A	#N/A	spindle and kinetochore associated complex subunit 3
ENSG00000164109	0.51	3.73	4.53	#N/A	#N/A	MAD2 mitotic arrest deficient-like 1 (yeast)
ENSG000000976382	-0.05	3.24	3.58	#N/A	#N/A	sperm associated antigen 5
ENSG00000119508	1.48	-3.24	-4.26	#N/A	#N/A	nuclear receptor subfamily 4, group A, member 3
gene_ID	logFC HFF (2h) (Uninf)	logFC HFF (18h) (Uninf)	logFC HFF (48h) (Uninf)	logFC MM6 (18h) (Uninf)	logFC NSC (18h) (Uninf)	Product Name
ENSG00000100644	#N/A	#N/A	#N/A	1.07	#N/A	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
ENSG00000173486	#N/A	#N/A	#N/A	1.07	2.60	FK506 binding protein 2, 13kDa
ENSG00000169926	#N/A	#N/A	#N/A	1.07	#N/A	Kruppel-like factor 13
ENSG00000010404	#N/A	#N/A	#N/A	1.07	#N/A	iduronate 2-sulfatase
ENSG00000153132	#N/A	#N/A	#N/A	1.06	#N/A	calmeglin
ENSG00000282230	#N/A	#N/A	#N/A	1.06	#N/A	ADAM metalloproteinase domain 9
ENSG00000079739	#N/A	#N/A	#N/A	1.06	#N/A	phosphoglucomutase 1
ENSG00000143198	#N/A	#N/A	#N/A	1.06	1.23	microsomal glutathione S-transferase 3
ENSG00000143458	#N/A	#N/A	#N/A	1.06	#N/A	GA binding protein transcription factor, beta subunit 2
ENSG00000173221	#N/A	#N/A	#N/A	1.06	2.42	glutaredoxin (thioltransferase)
ENSG00000153048	#N/A	#N/A	#N/A	1.06	#N/A	calcium regulated heat stable protein 1, 24kDa
ENSG00000101363	#N/A	#N/A	#N/A	1.06	1.05	mannosidase, beta A, lysosomal-like
ENSG00000120727	#N/A	#N/A	#N/A	1.06	#N/A	poly(A) binding protein interacting protein 2
ENSG00000103335	#N/A	#N/A	#N/A	1.05	#N/A	piezo-type mechanosensitive ion channel component 1
ENSG00000112773	#N/A	#N/A	#N/A	1.05	#N/A	family with sequence similarity 46, member A
ENSG00000121067	#N/A	#N/A	#N/A	1.05	#N/A	speckle-type POZ protein
ENSG00000142002	#N/A	#N/A	#N/A	1.05	#N/A	dipeptidyl-peptidase 9
ENSG00000178567	#N/A	#N/A	#N/A	1.05	#N/A	EPM2A (leforin) interacting protein 1
ENSG00000103671	#N/A	#N/A	#N/A	1.05	#N/A	thyroid hormone receptor interactor 4
ENSG00000247558	#N/A	#N/A	#N/A	1.05	#N/A	OIP5 antisense RNA 1
ENSG00000256235	#N/A	#N/A	#N/A	1.05	#N/A	small integral membrane protein 3
ENSG00000119844	#N/A	#N/A	#N/A	1.05	#N/A	atp10a
ENSG00000119471	#N/A	#N/A	#N/A	1.04	#N/A	hydroxysteroid dehydrogenase like 2
ENSG00000102910	#N/A	#N/A	#N/A	1.04	#N/A	ion peptidase 2, peroxisomal
ENSG00000106261	#N/A	#N/A	#N/A	1.04	#N/A	zinc finger with KRAB and SCAN domains 1
ENSG00000138085	#N/A	#N/A	#N/A	1.04	#N/A	all-trans retinoic acid-induced differentiation factor
ENSG00000102908	#N/A	#N/A	#N/A	1.04	#N/A	nuclear factor of activated T-cells 5, tonically-responsive
ENSG00000161955	#N/A	#N/A	#N/A	1.04	#N/A	tumor necrosis factor (ligand) superfamily, member 13
ENSG00000189343	#N/A	#N/A	#N/A	1.04	#N/A	ribosomal protein S2 pseudogene 46
ENSG00000148908	#N/A	#N/A	#N/A	1.04	1.21	regulator of G-protein signaling 10
ENSG00000135090	#N/A	#N/A	#N/A	1.04	#N/A	TAO kinase 3
ENSG00000165118	#N/A	#N/A	#N/A	1.04	#N/A	chromosome 9 open reading frame 64
ENSG00000167193	#N/A	#N/A	#N/A	1.03	#N/A	γ-ork avian sarcoma virus CT10 oncogene homolog
ENSG00000172830	#N/A	#N/A	#N/A	1.03	#N/A	slingshot protein phosphatase 3
ENSG00000165927	#N/A	#N/A	#N/A	1.03	#N/A	membrane-spanning 4-domains, subfamily A, member 7
ENSG00000123975	#N/A	#N/A	#N/A	1.03	1.87	CDC2B protein kinase regulatory subunit 2
ENSG00000107819	#N/A	#N/A	#N/A	1.03	#N/A	sideroflexin 3
ENSG00000143369	#N/A	#N/A	#N/A	1.03	#N/A	extracellular matrix protein 1
ENSG000000038219	#N/A	#N/A	#N/A	1.02	#N/A	bioorientation of chromosomes in cell division 1 like 1
ENSG00000127507	#N/A	#N/A	#N/A	1.02	#N/A	adhesion G protein-coupled receptor E2

FIGURE 1B

ENSG00000143476	0.29	3.85	3.54	#N/A	#N/A	denticless E3 ubiquitin protein ligase homolog (Drosophila)
ENSG00000107966	1.88	-1.74	-1.01	#N/A	#N/A	mitogen-activated protein kinase kinase kinase 8
ENSG00000190826	0.20	3.21	4.14	#N/A	#N/A	Rho GTPase activating protein 11A
ENSG0000013810	-0.33	3.02	3.08	#N/A	#N/A	transforming, acidic coiled-coil containing protein 3
ENSG00000172548	0.61	-4.93	-4.60	#N/A	#N/A	NIPA-like domain containing 4
ENSG00000137331	2.18	-2.15	-2.31	#N/A	#N/A	immediate early response 3
ENSG00000024526	0.14	4.26	5.66	-1.12	#N/A	DEP domain containing 1
ENSG00000112984	0.64	3.00	4.41	#N/A	#N/A	kinesin family member 20A
ENSG00000166592	1.27	-5.02	-3.14	#N/A	#N/A	Ras-related associated with diabetes
ENSG00000158402	-0.76	3.59	4.21	#N/A	#N/A	cell division cycle 25C
ENSG00000108342	6.25	2.52	8.82	#N/A	#N/A	colony stimulating factor 3 (granulocyte)
ENSG00000171241	0.64	3.95	4.06	#N/A	#N/A	SHC SH2-domain binding protein 1
ENSG00000122952	-0.15	3.44	3.16	#N/A	1.03	ZW10 interacting kinetochore protein
ENSG00000163874	2.83	-2.49	-1.21	#N/A	#N/A	zinc finger CCHC-type containing 12A
ENSG00000131153	0.82	3.78	3.05	#N/A	#N/A	GINS complex subunit 2 (Psf2 homolog)
ENSG00000167900	0.10	2.57	3.19	#N/A	#N/A	thymidine kinase 1, soluble
ENSG00000143228	0.11	4.22	4.72	#N/A	#N/A	NUF2, NDC80 kinetochore complex component
ENSG00000149986	0.49	2.82	3.64	#N/A	#N/A	matrix metalloproteinase 3
ENSG000000241644	-0.77	-3.80	-4.78	#N/A	#N/A	endolethylamine N-methyltransferase
ENSG00000117399	-0.15	3.12	3.85	#N/A	#N/A	cell division cycle 20
ENSG00000175063	1.38	4.46	4.61	#N/A	1.74	ubiquitin-conjugating enzyme E2C
ENSG00000134690	-0.42	3.66	3.73	#N/A	#N/A	cell division cycle associated 8
ENSG00000154027	0.45	3.28	2.92	#N/A	#N/A	adenylate kinase 5
ENSG00000122877	1.33	-6.24	-5.00	#N/A	#N/A	early growth response 2
ENSG00000183856	-0.17	3.03	3.39	#N/A	#N/A	IQ motif containing GTPase activating protein 3
ENSG000000205835	-0.09	-2.62	-7.23	#N/A	#N/A	geminin coiled-coil domain containing
ENSG00000114226	0.40	3.53	4.15	#N/A	#N/A	anillin, actin binding protein
ENSG000000971539	0.62	3.37	3.86	#N/A	#N/A	thyroid hormone receptor interactor 13
ENSG00000080986	-0.06	3.45	3.76	#N/A	#N/A	NDC80 kinetochore complex component
ENSG00000090339	1.48	-2.27	-1.20	1.35	#N/A	intercellular adhesion molecule 1
ENSG00000087494	0.36	-3.14	-5.48	#N/A	#N/A	parathyroid hormone-like hormone
ENSG00000118193	0.70	4.18	5.11	#N/A	#N/A	kinesin family member 14
ENSG00000179386	1.29	-7.45	-6.06	#N/A	#N/A	early growth response 3
ENSG00000137193	1.29	-2.09	-1.63	#N/A	#N/A	Pim-1 proto-oncogene, serine/threonine kinase
ENSG00000163535	0.27	2.63	3.64	#N/A	#N/A	shugoshin-like 2 (S. pombe)
ENSG00000075702	1.30	4.35	4.16	-1.33	#N/A	WD repeat domain 62
ENSG00000151725	0.29	3.71	3.36	#N/A	#N/A	centromere protein U
ENSG00000163808	-0.26	3.65	3.69	#N/A	#N/A	kinesin family member 15
ENSG00000137310	0.62	3.71	3.13	#N/A	#N/A	transcription factor 19
ENSG00000065328	0.49	4.75	4.19	#N/A	#N/A	mitochondrion maintenance complex component 10
ENSG00000186185	0.82	4.86	4.16	#N/A	#N/A	kinesin family member 18B
ENSG00000122966	0.01	3.37	3.77	#N/A	#N/A	citron rho-interacting serine/threonine kinase
ENSG00000161800	0.23	3.00	3.46	#N/A	#N/A	Rac GTPase activating protein 1
ENSG00000087586	0.05	3.67	4.40	#N/A	#N/A	aurora kinase A
ENSG00000162063	-0.09	2.39	2.97	#N/A	#N/A	cyclin F
ENSG00000182667	-0.13	4.36	4.03	#N/A	#N/A	neurofilamin
ENSG00000113971	#N/A	#N/A	#N/A	1.02	#N/A	nephronophthisis 3 (adolescent)
ENSG00000182179	#N/A	#N/A	#N/A	1.02	#N/A	ubiquitin-like modifier activating enzyme 7
ENSG00000124357	#N/A	#N/A	#N/A	1.02	1.42	N-acetylglucosamine kinase
ENSG00000114423	#N/A	#N/A	#N/A	1.02	#N/A	Cbl proto-oncogene B, E3 ubiquitin protein ligase
ENSG00000135441	#N/A	#N/A	#N/A	1.02	#N/A	biogenesis of lysosomal organelles complex-1, subunit 1
ENSG00000129292	#N/A	#N/A	#N/A	1.02	#N/A	PHD finger protein 20-like 1
ENSG0000005024862	#N/A	#N/A	#N/A	1.02	#N/A	coiled-coil domain containing 28A
ENSG00000102893	#N/A	#N/A	#N/A	1.02	#N/A	phosphorylase kinase, beta
ENSG00000099860	#N/A	#N/A	#N/A	1.02	#N/A	growth arrest and DNA-damage-inducible, beta
ENSG00000124226	#N/A	#N/A	#N/A	1.02	1.05	ring finger protein 114
ENSG00000133639	#N/A	#N/A	#N/A	1.02	#N/A	B-cell translocation gene 1, anti-proliferative
ENSG00000162222	#N/A	#N/A	#N/A	1.02	1.13	tetratricopeptide repeat domain 9C
ENSG00000131408	#N/A	#N/A	#N/A	1.02	#N/A	nuclear receptor subfamily 1, group H, member 2
ENSG00000117407	#N/A	#N/A	#N/A	1.01	#N/A	artemin
ENSG000000282031	#N/A	#N/A	#N/A	1.01	1.59	transmembrane BAX inhibitor motif containing 4
ENSG00000170145	#N/A	#N/A	#N/A	1.01	#N/A	salt-inducible kinase 2
ENSG00000179152	#N/A	#N/A	#N/A	1.01	#N/A	T cell activation inhibitor, mitochondrial
ENSG00000122257	#N/A	#N/A	#N/A	1.01	#N/A	retinoblastoma binding protein 6
ENSG00000107798	#N/A	#N/A	#N/A	1.01	#N/A	lipase A, lysosomal acid, cholesterol esterase
ENSG00000106780	#N/A	#N/A	#N/A	1.01	#N/A	multiple EGF-like-domains 9
ENSG00000104976	#N/A	#N/A	#N/A	1.01	#N/A	small nuclear RNA activating complex, polypeptide 2, 45kDa
ENSG00000175550	#N/A	#N/A	#N/A	1.01	1.44	DR1-associated protein 1 (negative cofactor 2 alpha)
ENSG00000152244	#N/A	#N/A	#N/A	1.01	#N/A	ribosomal protein L29
ENSG00000161202	#N/A	#N/A	#N/A	1.00	#N/A	dishevelled segment polarity protein 3
ENSG00000125629	#N/A	#N/A	#N/A	1.00	#N/A	insulin induced gene 2
ENSG000000508513	#N/A	#N/A	#N/A	1.00	1.09	ST3 beta-galactoside alpha-2,3-sialyltransferase 1
ENSG000000206190	#N/A	#N/A	#N/A	1.00	#N/A	ATPase, class V, type 10A
ENSG00000035141	#N/A	#N/A	#N/A	-1.00	#N/A	family with sequence similarity 136, member A
ENSG00000140403	#N/A	#N/A	#N/A	-1.00	#N/A	DnaJ (Hsp40) homolog, subfamily A, member 4
ENSG00000197104	#N/A	#N/A	#N/A	-1.00	#N/A	KN motif and ankyrin repeat domains 1
ENSG00000114967	#N/A	#N/A	#N/A	-1.00	#N/A	eukaryotic translation initiation factor 4 gamma, 1
ENSG00000108883	#N/A	#N/A	#N/A	-1.00	#N/A	elongation factor Tu GTP binding domain containing 2
ENSG00000102900	#N/A	#N/A	#N/A	-1.00	#N/A	nucleoporin 93kDa
ENSG00000168936	#N/A	#N/A	#N/A	-1.00	#N/A	transmembrane protein 129, E3 ubiquitin protein ligase
ENSG00000163389	#N/A	#N/A	#N/A	-1.00	#N/A	protein O-glucosyltransferase 1
ENSG000000213639	#N/A	#N/A	#N/A	-1.01	#N/A	protein phosphatase 1, catalytic subunit, beta isozyme
ENSG00000057663	#N/A	#N/A	#N/A	-1.01	#N/A	autophagy related 5
ENSG00000109738	#N/A	#N/A	#N/A	-1.01	#N/A	major facilitator superfamily domain containing 10
ENSG00000025156	#N/A	#N/A	#N/A	-1.01	#N/A	heat shock transcription factor 2
ENSG00000138018	#N/A	#N/A	#N/A	-1.01	#N/A	ethanolaminephosphotransferase 1
ENSG00000166557	#N/A	#N/A	#N/A	-1.01	#N/A	transmembrane emp24 protein transport domain containing 3
ENSG00000185344	#N/A	#N/A	#N/A	-1.01	#N/A	ATPase, H+ transporting, lysosomal V0 subunit a2
ENSG00000160803	#N/A	#N/A	#N/A	-1.01	#N/A	ubiquitin 4
ENSG00000087365	#N/A	#N/A	#N/A	-1.01	#N/A	splicing factor 3b, subunit 2, 145kDa
ENSG00000188971	#N/A	#N/A	#N/A	-1.01	#N/A	RP11-427H3.3
ENSG000000258984	#N/A	#N/A	#N/A	-1.01	#N/A	UBE2F-SCLY readthrough (NMD candidate)

FIGURE 1C

ENSG00000171846	0.58	4.37	3.90	#N/A	1.32	ribonucleotide reductase M2
ENSG00000166396	1.78	4.16	5.43	#N/A	#N/A	serpin peptidase inhibitor, clade B (ovalbumin), member 7
ENSG00000136928	0.35	3.84	1.79	#N/A	#N/A	gamma-aminobutyric acid (GABA) B receptor, 2
ENSG00000178999	-0.69	3.44	3.23	#N/A	#N/A	aurora kinase B
ENSG00000126787	1.32	4.22	5.61	#N/A	#N/A	discs, large (Drosophila) homolog-associated protein 5
ENSG00000075218	0.49	3.75	4.04	#N/A	#N/A	G-2 and S-phase expressed 1
ENSG00000100297	-0.09	2.60	2.08	#N/A	#N/A	minichromosome maintenance complex component 5
ENSG00000138182	0.15	2.83	3.53	#N/A	#N/A	kinesin family member 20B
ENSG00000094804	0.36	3.73	2.48	#N/A	1.11	cell division cycle 6
ENSG00000113368	0.13	3.46	3.48	-1.30	#N/A	lamin B1
ENSG00000170312	-0.59	3.99	4.30	#N/A	#N/A	cyclin-dependent kinase 1
ENSG00000184557	1.62	-0.87	-0.62	4.68	1.34	suppressor of cytokine signaling 3
ENSG00000134057	0.68	2.53	3.88	#N/A	#N/A	cyclin B1
ENSG00000194738	-0.02	2.88	2.46	#N/A	#N/A	minichromosome maintenance complex component 4
ENSG00000166825	0.16	1.90	2.26	#N/A	#N/A	alanine (membrane) aminopeptidase
ENSG00000187955	-0.61	-1.71	-4.96	#N/A	#N/A	collagen, type XIV, alpha 1
ENSG00000119969	0.17	3.62	2.99	#N/A	#N/A	helicase, lymphoid-specific
ENSG00000198554	-0.12	2.80	2.38	#N/A	#N/A	WD repeat and HMG-box DNA binding protein 1
ENSG00000056556	1.83	-2.76	-2.64	2.34	#N/A	TNF receptor-associated factor 1
ENSG00000185215	1.70	-1.55	-0.76	#N/A	#N/A	tumor necrosis factor, alpha-induced protein 2
ENSG00000260549	1.01	4.18	4.77	#N/A	#N/A	metallothionein 1L (gene/psudogene)
ENSG00000166803	0.16	3.47	3.72	1.99	2.21	KIAA0101
ENSG00000166851	0.23	2.92	3.93	#N/A	#N/A	polo-like kinase 1
ENSG00000163710	-0.97	-2.13	-4.49	#N/A	#N/A	procollagen C-endopeptidase enhancer 2
ENSG00000163507	0.33	2.95	3.63	#N/A	#N/A	KIAA1524
ENSG00000105011	0.41	3.22	2.67	1.06	#N/A	anti-silencing function 18 histone chaperone
ENSG00000137804	0.33	3.32	3.40	#N/A	#N/A	nucleolar and spindle associated protein 1
ENSG00000124875	2.87	4.34	7.68	#N/A	#N/A	chemokine (C-X-C motif) ligand 6
ENSG00000144554	-0.26	2.88	2.71	#N/A	#N/A	Fanconi anemia, complementation group D2
ENSG00000085999	0.07	3.49	2.56	-1.23	#N/A	RAD54-like (S. cerevisiae)
ENSG00000140525	0.02	3.13	3.13	#N/A	#N/A	Fanconi anemia, complementation group 1
ENSG00000041982	0.99	4.02	3.66	#N/A	2.22	tenascin C
ENSG00000164611	0.00	2.28	3.42	#N/A	#N/A	pituitary tumor-transforming 1
ENSG00000125740	1.12	-6.58	-5.95	#N/A	#N/A	FBJ murine osteosarcoma viral oncogene homolog B
ENSG00000112312	0.18	2.89	2.87	#N/A	1.56	geminin, DNA replication inhibitor
ENSG00000184661	0.98	4.37	4.56	#N/A	#N/A	cell division cycle associated 2
ENSG00000117650	1.02	4.19	5.34	#N/A	#N/A	NIMA-related kinase 2
ENSG00000157456	0.32	2.54	3.65	#N/A	#N/A	cyclin B2
ENSG00000103489	0.95	2.97	3.00	#N/A	#N/A	xylosyltransferase 1
ENSG00000187741	-0.37	2.61	2.16	#N/A	#N/A	Fanconi anemia, complementation group A
ENSG00000123485	-0.04	3.68	3.36	#N/A	#N/A	Holliday junction recognition protein
ENSG00000134222	-0.49	2.64	2.62	#N/A	#N/A	proline/serine-rich coiled-coil 1
ENSG000000324265	0.30	3.02	4.24	#N/A	#N/A	paternally expressed 10
ENSG00000196355	1.28	-2.29	-1.39	#N/A	#N/A	Pim-3 proto-oncogene, serine/threonine kinase
ENSG00000101412	-0.25	2.76	2.08	#N/A	#N/A	E2F transcription factor 1
ENSG00000146918	0.23	2.81	2.91	#N/A	#N/A	non-SMC condensin II complex, subunit G2
ENSG00000113810	0.28	2.03	2.69	1.36	#N/A	structural maintenance of chromosomes 4
ENSG00000166508	-0.12	2.12	2.01	#N/A	#N/A	minichromosome maintenance complex component 7

ENSG00000175467	#N/A	#N/A	#N/A	-1.01	#N/A	squamous cell carcinoma antigen recognized by T cells 1
ENSG00000171497	#N/A	#N/A	#N/A	-1.01	#N/A	peptidylprolyl isomerase D
ENSG00000163444	#N/A	#N/A	#N/A	-1.01	#N/A	transmembrane protein 183A
ENSG00000112249	#N/A	#N/A	#N/A	-1.01	#N/A	activating signal cointegrator 1 complex subunit 3
ENSG00000170854	#N/A	#N/A	#N/A	-1.01	#N/A	MYC induced nuclear antigen
ENSG00000172053	#N/A	#N/A	#N/A	-1.01	#N/A	glutamine-IRNA synthetase
ENSG00000204946	#N/A	#N/A	#N/A	-1.01	#N/A	zinc finger family member 783
ENSG00000169045	#N/A	#N/A	#N/A	-1.02	#N/A	heterogeneous nuclear ribonucleoprotein H1 (H)
ENSG00000198799	#N/A	#N/A	#N/A	-1.02	#N/A	leucine-rich repeats and immunoglobulin-like domains 2
ENSG00000195676	#N/A	#N/A	#N/A	-1.02	#N/A	armadillo repeat containing 6
ENSG00000043514	#N/A	#N/A	#N/A	-1.02	#N/A	tRNA isopentenyltransferase 1
ENSG00000169689	#N/A	#N/A	#N/A	-1.02	#N/A	stimulated by retinoic acid 13
ENSG00000230257	#N/A	#N/A	#N/A	-1.02	#N/A	nuclear factor, erythroid 4
ENSG00000134186	#N/A	#N/A	#N/A	-1.02	#N/A	pre-mRNA processing factor 38B
ENSG00000161996	#N/A	#N/A	#N/A	-1.02	#N/A	WD repeat domain 80
ENSG00000132819	#N/A	#N/A	#N/A	-1.02	#N/A	RNA binding motif protein 38
ENSG00000273562	#N/A	#N/A	#N/A	-1.02	#N/A	nucleosome assembly protein 1-like 4
ENSG00000141522	#N/A	#N/A	#N/A	-1.02	#N/A	Rho GDP dissociation inhibitor (GDI) alpha
ENSG00000111144	#N/A	#N/A	#N/A	-1.02	#N/A	leukotriene A4 hydrolase
ENSG00000111667	#N/A	#N/A	#N/A	-1.02	#N/A	ubiquitin specific peptidase 5 (isopeptidase T)
ENSG00000103148	#N/A	#N/A	#N/A	-1.02	#N/A	NPR3-like, GATOR1 complex subunit
ENSG000000895289	#N/A	#N/A	#N/A	-1.02	#N/A	ependymin related 1
ENSG00000150949	#N/A	#N/A	#N/A	-1.02	#N/A	tsunoku-like, DNA repair protein
ENSG00000146463	#N/A	#N/A	#N/A	-1.02	#N/A	zinc finger, MYM-type 4
ENSG00000137288	#N/A	#N/A	#N/A	-1.02	#N/A	ubiquinol-cytochrome c reductase complex assembly factor 2
ENSG00000175634	#N/A	#N/A	#N/A	-1.03	#N/A	ribosomal protein S6 kinase, 70kDa, polypeptide 2
ENSG000000995319	#N/A	#N/A	#N/A	-1.03	#N/A	nucleoporin 188kDa
ENSG000000601497	#N/A	#N/A	#N/A	-1.03	#N/A	LAS1-like, ribosome biogenesis factor
ENSG00000113048	#N/A	#N/A	#N/A	-1.03	#N/A	mitochondrial ribosomal protein S27
ENSG00000106628	#N/A	#N/A	#N/A	-1.03	#N/A	polymerase (DNA directed), delta 2, accessory subunit
ENSG00000165792	#N/A	#N/A	#N/A	-1.03	#N/A	methyl-CpG binding domain protein 5
ENSG00000118900	#N/A	#N/A	#N/A	-1.03	#N/A	ubiquitin 1
ENSG00000008441	#N/A	#N/A	#N/A	-1.03	#N/A	nuclear factor IY (CCAAT-binding transcription factor)
ENSG00000152613	#N/A	#N/A	#N/A	-1.03	#N/A	far upstream element (FUSE) binding protein 1
ENSG00000128309	#N/A	#N/A	#N/A	-1.03	#N/A	mercaptopyruvate sulfurtransferase
ENSG00000166987	#N/A	#N/A	#N/A	-1.04	#N/A	methyl-CpG binding domain protein 5
ENSG00000158439	#N/A	#N/A	#N/A	-1.04	#N/A	stress-induced phosphoprotein 1
ENSG00000132323	#N/A	#N/A	#N/A	-1.04	#N/A	integrin-linked kinase-associated serine/threonine phosphatase
ENSG00000089280	#N/A	#N/A	#N/A	-1.04	#N/A	FUS RNA binding protein
ENSG00000198501	#N/A	#N/A	#N/A	-1.04	#N/A	transmembrane protein 222
ENSG00000160131	#N/A	#N/A	#N/A	-1.04	#N/A	VMA21 vacuolar H+-ATPase homolog (S. cerevisiae)
ENSG00000155688	#N/A	#N/A	#N/A	-1.04	#N/A	peptidase (mitochondrial processing) alpha
ENSG00000163349	#N/A	#N/A	#N/A	-1.04	#N/A	homeodomain interacting protein kinase 1
ENSG00000153574	#N/A	#N/A	#N/A	-1.04	#N/A	ribose 5-phosphate isomerase A
ENSG00000261739	#N/A	#N/A	#N/A	-1.04	#N/A	golgin A8 family, member 5
ENSG000000008853	#N/A	#N/A	#N/A	-1.04	#N/A	Rho-related BTB domain containing 2
ENSG00000013306	#N/A	#N/A	#N/A	-1.04	#N/A	solute carrier family 25, member 39
ENSG00000169914	#N/A	#N/A	#N/A	-1.04	#N/A	OTU deubiquitinase 3

FIGURE 1D

ENSG00000164283	1.64	6.40	7.66	#N/A	#N/A	endothelial cell-specific molecule 1
ENSG00000115163	-0.38	3.06	3.71	#N/A	#N/A	centromere protein A
ENSG00000143333	1.02	-2.95	-4.51	1.97	#N/A	regulator of G-protein signaling 16
ENSG00000187479	1.79	-4.03	-4.59	#N/A	#N/A	chromosome 11 open reading frame 96
ENSG00000132510	1.25	-2.92	-2.40	#N/A	#N/A	lysine (K)-specific demethylase 6B
ENSG00000177084	0.02	2.23	2.19	#N/A	#N/A	polymerase (DNA directed), epsilon, catalytic subunit
ENSG00000136982	0.99	4.46	4.19	#N/A	#N/A	DNA replication and sister chromatid cohesion 1
ENSG00000171320	-0.97	4.76	4.58	1.04	#N/A	establishment of sister chromatid cohesion N-acetyltransferase 2
ENSG00000169906	1.18	3.57	5.06	#N/A	#N/A	transmembrane 4 L six family member 1
ENSG00000156970	1.76	5.01	5.31	#N/A	#N/A	BUB1 mitotic checkpoint serine/threonine kinase B
ENSG00000165244	-0.04	2.80	2.23	#N/A	#N/A	zinc finger protein 367
ENSG00000167306	-0.97	-2.67	-4.75	#N/A	#N/A	myosin VB
ENSG00000138160	0.05	3.23	3.66	#N/A	#N/A	kinesin family member 11
ENSG00000189057	-0.19	3.88	3.37	1.31	#N/A	family with sequence similarity 111, member B
ENSG00000135451	-0.09	3.31	3.97	#N/A	#N/A	trophinin associated protein
ENSG00000276043	0.07	2.69	2.23	#N/A	#N/A	ubiquitin-like with PHD and ring finger domains 1
ENSG00000167676	0.01	2.41	2.16	#N/A	#N/A	chromatin assembly factor 1, subunit A (p150)
ENSG00000156802	0.33	3.25	2.89	#N/A	#N/A	ATPase family, AAA domain containing 2
ENSG00000051341	0.53	4.21	4.11	#N/A	#N/A	polymerase (DNA directed), theta
ENSG00000100906	1.67	-0.87	-0.23	#N/A	#N/A	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
ENSG00000137831	0.06	2.30	1.72	#N/A	#N/A	uveal autoantigen with coiled-coil domains and ankyrin repeats
ENSG00000117632	-0.91	1.81	2.57	#N/A	#N/A	statmin 1
ENSG00000162772	1.58	-3.01	-3.59	#N/A	1.66	activating transcription factor 3
ENSG00000147883	1.36	-1.47	-2.87	#N/A	#N/A	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)
ENSG00000178907	1.29	-1.74	-2.47	#N/A	#N/A	chromosome 6 open reading frame 4
ENSG00000107964	-0.15	2.07	1.52	#N/A	1.69	dickkopf WNT signaling pathway inhibitor 1
ENSG00000110031	-0.32	1.85	3.30	#N/A	#N/A	leupaxin
ENSG00000106462	0.62	3.33	2.81	#N/A	#N/A	enhancer of zeste 2 polycomb repressive complex 2 subunit
ENSG00000165304	-0.38	2.37	2.36	#N/A	#N/A	maternal embryonic leucine zipper kinase
ENSG00000163545	1.42	-1.57	-1.35	#N/A	#N/A	NUAK family, SNF1-like kinase, 2
ENSG00000138166	1.24	-1.95	-2.01	#N/A	#N/A	dual specificity phosphatase 5
ENSG00000139616	-0.03	3.58	3.86	#N/A	#N/A	breast cancer 2, early onset
ENSG00000092470	-0.09	3.01	2.74	#N/A	#N/A	WD repeat domain 76
ENSG000000973111	-0.05	2.29	1.86	#N/A	#N/A	minichromosome maintenance complex component 2
ENSG00000085846	-0.02	4.14	3.64	#N/A	#N/A	origin recognition complex, subunit 1
ENSG00000137033	0.95	4.43	2.76	#N/A	#N/A	interleukin 33
ENSG00000120446	0.13	2.99	2.48	#N/A	#N/A	breast cancer 1, early onset
ENSG00000269289	-0.64	-6.83	-3.25	#N/A	#N/A	CTB-92J24.3
ENSG00000176890	-0.07	2.76	2.67	#N/A	#N/A	thymidylate synthetase
ENSG00000137812	0.01	4.03	4.66	#N/A	#N/A	cancer susceptibility candidate 5
ENSG00000183763	-0.01	3.19	2.94	#N/A	#N/A	TRAF interacting protein
ENSG00000112118	-0.26	2.24	1.67	#N/A	#N/A	minichromosome maintenance complex component 3
ENSG00000171223	1.12	-3.19	-2.49	#N/A	#N/A	jun B proto-oncogene
ENSG00000077152	-0.51	2.30	2.47	1.06	#N/A	ubiquitin-conjugating enzyme E2T
ENSG00000168685	1.73	3.83	4.66	#N/A	#N/A	interleukin 7 receptor

ENSG00000280987	#N/A	#N/A	#N/A	-1.04	#N/A	matrin 3
ENSG00000007080	#N/A	#N/A	#N/A	-1.64	#N/A	coiled-coil domain containing 124
ENSG00000004455	#N/A	#N/A	#N/A	-1.05	#N/A	adenylate kinase 2
ENSG00000241945	#N/A	#N/A	#N/A	-1.05	#N/A	PWP2 periodic tryptophan protein homolog (yeast)
ENSG00000138363	#N/A	#N/A	#N/A	-1.05	#N/A	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase
ENSG00000167721	#N/A	#N/A	#N/A	-1.05	#N/A	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)
ENSG00000234495	#N/A	#N/A	#N/A	-1.05	#N/A	tripartite motif containing 27
ENSG00000170085	#N/A	#N/A	#N/A	-1.05	#N/A	SUMO-interacting motifs containing 1
ENSG00000178952	#N/A	#N/A	#N/A	-1.05	#N/A	Ta translation elongation factor, mitochondrial
ENSG00000163875	#N/A	#N/A	#N/A	-1.05	#N/A	MYST/Esa1-associated factor 6
ENSG00000146223	#N/A	#N/A	#N/A	-1.05	#N/A	ribosomal protein L7-like 1
ENSG00000134440	#N/A	#N/A	#N/A	-1.05	#N/A	asparaginyl-tRNA synthetase
ENSG00000110721	#N/A	#N/A	#N/A	-1.05	#N/A	cholesterol kinase alpha
ENSG000000696746	#N/A	#N/A	#N/A	-1.05	#N/A	heterogeneous nuclear ribonucleoprotein H3 (2H3)
ENSG00000198301	#N/A	#N/A	#N/A	-1.05	#N/A	SDA1 domain containing 1
ENSG00000171612	#N/A	#N/A	#N/A	-1.05	#N/A	solute carrier family 25 (pyrimidine nucleotide carrier), member 33
ENSG00000164024	#N/A	#N/A	#N/A	-1.05	#N/A	methionyl aminopeptidase 1
ENSG00000261221	#N/A	#N/A	#N/A	-1.05	#N/A	zinc finger protein 865
ENSG00000183306	#N/A	#N/A	#N/A	-1.05	#N/A	ribosomal RNA processing 7 homolog A
ENSG00000196790	#N/A	#N/A	#N/A	-1.05	#N/A	zinc finger protein 512B
ENSG00000118640	#N/A	#N/A	#N/A	-1.06	#N/A	vesicle-associated membrane protein 6
ENSG00000276187	#N/A	#N/A	#N/A	-1.06	#N/A	ER membrane-associated RNA degradation
ENSG00000071626	#N/A	#N/A	#N/A	-1.06	#N/A	DAZ associated protein 1
ENSG00000211460	#N/A	#N/A	#N/A	-1.06	#N/A	translin
ENSG0000025796	#N/A	#N/A	#N/A	-1.06	#N/A	SEC63 homolog (S. cerevisiae)
ENSG00000115306	#N/A	#N/A	#N/A	-1.06	#N/A	spectrin, beta, non-erythrocytic 1
ENSG00000169750	#N/A	#N/A	#N/A	-1.06	#N/A	res-related G3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)
ENSG00000118508	#N/A	#N/A	#N/A	-1.06	#N/A	RAB32, member RAS oncogene family
ENSG00000090376	#N/A	#N/A	#N/A	-1.07	#N/A	interleukin-1 receptor-associated kinase 3
ENSG00000105472	#N/A	#N/A	#N/A	-1.07	#N/A	C-type lectin domain family 11, member A
ENSG00000035115	#N/A	#N/A	#N/A	-1.07	#N/A	SH3 and SYLF domain containing 1
ENSG00000128050	#N/A	#N/A	#N/A	-1.07	#N/A	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase
ENSG00000039123	#N/A	#N/A	#N/A	-1.07	#N/A	superkiller viralicidal activity 2-like 2 (S. cerevisiae)
ENSG00000110075	#N/A	#N/A	#N/A	-1.07	#N/A	protein phosphatase 6, regulatory subunit 3
ENSG00000139437	#N/A	#N/A	#N/A	-1.07	#N/A	trichoplein, keratin filament binding
ENSG00000103319	#N/A	#N/A	#N/A	-1.07	#N/A	eukaryotic elongation factor 2 kinase
ENSG00000189660	#N/A	#N/A	#N/A	-1.07	#N/A	hexosaminidase (glycosyl hydrolase family 20, catalytic domain) containing
ENSG00000086504	#N/A	#N/A	#N/A	-1.07	#N/A	mitochondrial ribosomal protein L28
ENSG00000170608	#N/A	#N/A	#N/A	-1.07	#N/A	heat shock 70kDa protein 4
ENSG00000215440	#N/A	#N/A	#N/A	-1.07	#N/A	aminopeptidase-like 1
ENSG00000163528	#N/A	#N/A	#N/A	-1.07	#N/A	coiled-coil-helix-coiled-coil-helix domain containing 4
ENSG00000136463	#N/A	#N/A	#N/A	-1.07	#N/A	translational activator of mitochondrially encoded cytochrome c oxidase 1
ENSG00000230124	#N/A	#N/A	#N/A	-1.07	#N/A	acyl-CoA binding domain containing 6
ENSG00000184428	#N/A	#N/A	#N/A	-1.08	#N/A	topoisomerase (DNA) I, mitochondrial
ENSG00000156261	#N/A	#N/A	#N/A	-1.08	#N/A	chaperonin containing TCP1, subunit 6 (theta)

FIGURE 1E

ENSG00000152253	0.68	3.66	3.56	1.04	#N/A	SPC25, NDC80 kinetochore complex component
ENSG00000137563	0.32	1.70	3.07	#N/A	#N/A	gamma-glutamyl hydrolase (conjugase, folylpolyglutamylhydrolase)
ENSG00000110427	0.17	3.55	3.72	#N/A	#N/A	KIAA1549-like
ENSG00000142910	-1.22	-2.85	-4.45	#N/A	#N/A	tubulointerstitial nephritis antigen-like 1
ENSG00000144655	1.26	-2.21	-1.94	#N/A	#N/A	cysteine-serine-rich nuclear protein 1
ENSG00000112029	-0.08	3.25	2.94	#N/A	#N/A	F-box protein 5
ENSG00000128805	-0.08	1.32	2.28	#N/A	#N/A	Rho GTPase activating protein 22
ENSG00000179616	-0.33	1.96	2.04	#N/A	#N/A	kinesin family member 22
ENSG00000100162	-0.41	3.29	3.25	#N/A	#N/A	centromere protein M
ENSG00000163735	2.40	5.85	9.49	#N/A	#N/A	chemokine (C-X-C motif) ligand 5
ENSG00000167513	1.52	3.71	2.81	#N/A	#N/A	chromatin licensing and DNA replication factor 1
ENSG00000175605	1.32	-1.44	-2.26	#N/A	#N/A	cardiotrophin-like cytokine factor 1
ENSG00000121152	-0.49	3.34	3.02	#N/A	#N/A	non-SMC condensin I complex, subunit H
ENSG00000146232	1.13	-1.58	-1.06	#N/A	#N/A	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon
ENSG000001228716	0.45	2.25	2.64	#N/A	#N/A	dihydrofolate reductase
ENSG00000130816	0.13	1.85	1.79	#N/A	#N/A	DNA (cytosine-5-)-methyltransferase 1
ENSG00000109674	0.38	3.66	3.86	#N/A	#N/A	nei endonuclease VII-like 3 (E. coli)
ENSG00000111247	0.50	3.90	3.50	#N/A	#N/A	RAD51 associated protein 1
ENSG00000120129	1.10	-1.54	-1.58	#N/A	#N/A	dual specificity phosphatase 1
ENSG00000145356	-0.60	2.26	2.59	#N/A	#N/A	DNA-damage-inducible transcript 4-like
ENSG00000106003	0.71	-4.29	-5.56	#N/A	#N/A	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase
ENSG00000168369	1.63	-2.35	-1.35	#N/A	#N/A	major facilitator superfamily domain containing 2A
ENSG00000165349	-0.66	-2.65	-4.52	#N/A	#N/A	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3
ENSG00000125347	1.54	-0.69	-0.83	1.09	#N/A	interferon regulatory factor 1
ENSG00000168496	-0.62	2.10	1.92	#N/A	#N/A	flap structure-specific endonuclease 1
ENSG00000116717	1.30	-1.09	-1.49	#N/A	#N/A	growth arrest and DNA-damage-inducible, alpha
ENSG00000165891	0.23	3.49	3.93	#N/A	#N/A	E2F transcription factor 7
ENSG00000170961	2.39	3.39	6.89	#N/A	#N/A	hyaluronan synthase 2
ENSG00000111602	-0.12	1.96	1.76	#N/A	#N/A	timeless circadian clock
ENSG000001006210	1.06	-3.23	-2.64	#N/A	#N/A	chemokine (C-X3-C motif) ligand 1
ENSG00000139734	0.10	2.56	2.40	#N/A	#N/A	diaphanous-related formin 3
ENSG00000164087	0.58	2.04	2.68	-1.02	#N/A	POC1 centriolar protein A
ENSG00000149503	-0.73	1.66	1.91	#N/A	#N/A	inner centromere protein antigens 135/155kDa
ENSG00000167325	0.03	2.32	2.37	#N/A	#N/A	ribonucleotide reductase M1
ENSG00000102384	9.80	3.28	3.54	#N/A	#N/A	centromere protein 1
ENSG000001221829	-0.51	2.01	1.64	#N/A	#N/A	Fanconi anemia, complementation group G
ENSG00000164104	-1.11	1.50	1.59	#N/A	#N/A	high mobility group box 2
ENSG00000105486	-0.02	2.09	1.95	#N/A	#N/A	ligase I, DNA, ATP-dependent
ENSG00000197467	0.33	2.56	2.25	#N/A	#N/A	collagen, type XIII, alpha 1
ENSG00000118503	2.49	-0.89	0.22	#N/A	1.14	tumor necrosis factor, alpha-induced protein 3
ENSG00000164045	1.67	4.63	3.94	-1.24	#N/A	cell division cycle 25A
ENSG000001066279	0.02	3.73	4.53	#N/A	#N/A	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)
ENSG00000141138	-0.19	2.10	1.81	#N/A	#N/A	polymerase (DNA directed), alpha 2, accessory subunit
ENSG00000136106	-0.12	2.35	2.88	#N/A	#N/A	cytoskeleton associated protein 2
ENSG000001080839	9.06	2.60	2.52	#N/A	#N/A	retinoblastoma-like 1
ENSG000001241749	0.85	3.93	4.37	#N/A	#N/A	ribosomal protein S4 pseudogene 52
ENSG00000162267	-0.18	-3.94	-4.98	#N/A	#N/A	inter-alpha-trypsin inhibitor heavy chain 3
ENSG00000145191	#N/A	#N/A	#N/A	-1.06	#N/A	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa
ENSG00000106415	#N/A	#N/A	#N/A	-1.08	#N/A	glucocorticoid induced 1
ENSG00000108773	#N/A	#N/A	#N/A	-1.08	#N/A	L-lysine acetyltransferase 2A
ENSG00000114030	#N/A	#N/A	#N/A	-1.06	#N/A	karyopherin alpha 1 (importin alpha 5)
ENSG00000175471	#N/A	#N/A	#N/A	-1.08	#N/A	multiple C2 domains, transmembrane 1
ENSG00000198160	#N/A	#N/A	#N/A	-1.06	#N/A	mesoderm induction early response 1, transcriptional regulator
ENSG00000135776	#N/A	#N/A	#N/A	-1.06	#N/A	ATP-binding cassette, sub-family B (MDR/TAP), member 10
ENSG00000160221	#N/A	#N/A	#N/A	-1.08	#N/A	chromosome 21 open reading frame 33
ENSG00000105801	#N/A	#N/A	#N/A	-1.06	#N/A	zinc finger protein 195
ENSG00000104522	#N/A	#N/A	#N/A	-1.08	1.12	tissue specific transplantation antigen P35E
ENSG00000167961	#N/A	#N/A	#N/A	-1.06	#N/A	kelch-like family member 17
ENSG00000152234	#N/A	#N/A	#N/A	-1.08	#N/A	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle
ENSG00000184967	#N/A	#N/A	#N/A	-1.06	#N/A	nucleolar complex associated 4 homolog
ENSG00000196756	#N/A	#N/A	#N/A	-1.09	#N/A	small nucleolar RNA host gene 17
ENSG00000154174	#N/A	#N/A	#N/A	-1.09	#N/A	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)
ENSG00000109689	#N/A	#N/A	#N/A	-1.06	#N/A	stromal interaction molecule 2
ENSG00000101194	#N/A	#N/A	#N/A	-1.09	#N/A	solute carrier family 17 (vesicular nucleotide transporter), member 9
ENSG00000115489	#N/A	#N/A	#N/A	-1.09	#N/A	capping protein (actin filament) muscle Z-line, alpha 1
ENSG000001274523	#N/A	#N/A	#N/A	-1.09	#N/A	Williams-Beuren syndrome chromosome region 16
ENSG00000100220	#N/A	#N/A	#N/A	-1.06	#N/A	RNA 2',3'-cyclic phosphate and 5'-OH ligase
ENSG00000127278	#N/A	#N/A	#N/A	-1.09	#N/A	HECT and RLD domain containing E3 ubiquitin protein ligase 2
ENSG00000120685	#N/A	#N/A	#N/A	-1.09	#N/A	proline and serine rich 1
ENSG00000130731	#N/A	#N/A	#N/A	-1.09	#N/A	chromosome 15 open reading frame 13
ENSG00000130935	#N/A	#N/A	#N/A	-1.09	#N/A	nucleolar protein 11
ENSG00000147813	#N/A	#N/A	#N/A	-1.09	#N/A	nicotinate phosphoribosyltransferase
ENSG00000115419	#N/A	#N/A	#N/A	-1.09	#N/A	glutaminase
ENSG00000185699	#N/A	#N/A	#N/A	-1.09	#N/A	tuberous sclerosis 1
ENSG00000190216	#N/A	#N/A	#N/A	-1.09	#N/A	translocase of outer mitochondrial membrane 22 homolog (yeast)
ENSG00000173638	#N/A	#N/A	#N/A	-1.06	#N/A	solute carrier family 19 (folate transporter), member 1
ENSG00000110080	#N/A	#N/A	#N/A	-1.09	#N/A	ST3 beta-galactoside alpha-2,3-sialyltransferase 4
ENSG000001099604	#N/A	#N/A	#N/A	-1.09	#N/A	cell division cycle 34
ENSG000001275700	#N/A	#N/A	#N/A	-1.06	#N/A	apoptosis antagonizing transcription factor
ENSG00000134697	#N/A	#N/A	#N/A	-1.09	#N/A	guanine nucleotide binding protein-like 2 (nucleolar)
ENSG00000125912	#N/A	#N/A	#N/A	-1.10	#N/A	nicotin
ENSG0000010904487	#N/A	#N/A	#N/A	-1.10	#N/A	lysine (K)-specific demethylase 1A
ENSG00000115827	#N/A	#N/A	#N/A	-1.10	#N/A	DDB1 and CUL4 associated factor 17
ENSG00000165733	#N/A	#N/A	#N/A	-1.10	#N/A	BMS1 ribosome biogenesis factor
ENSG00000167969	#N/A	#N/A	#N/A	-1.10	#N/A	enoyl-CoA delta isomerase 1
ENSG000001975240	#N/A	#N/A	#N/A	-1.10	#N/A	GRAM domain containing 4
ENSG00000164654	#N/A	#N/A	#N/A	-1.10	#N/A	missing oocyte, meiosis regulator, homolog (Drosophila)
ENSG00000121210	#N/A	#N/A	#N/A	-1.10	#N/A	KIAA0522
ENSG00000124784	#N/A	#N/A	#N/A	-1.10	#N/A	RIO kinase 1
ENSG000001975856	#N/A	#N/A	#N/A	-1.10	#N/A	squamous cell carcinoma antigen recognized by T cells 3
ENSG00000151849	#N/A	#N/A	#N/A	-1.10	#N/A	centromere protein J
ENSG0000010967533	#N/A	#N/A	#N/A	-1.10	#N/A	ribosomal RNA processing 15 homolog
ENSG00000120694	#N/A	#N/A	#N/A	-1.10	#N/A	heat shock 105kDa/110kDa protein 1
ENSG00000136682	#N/A	#N/A	#N/A	-1.10	#N/A	COBW domain, containing 2

FIGURE 1F

ENSG00000136492	0.38	3.02	2.87	#N/A	#N/A	BRCA1 interacting protein C-terminal helixase 1
ENSG00000101003	-0.03	2.71	2.38	#N/A	#N/A	GIN5 complex subunit 1 (Psf1 homolog)
ENSG00000142731	0.53	3.67	3.96	#N/A	#N/A	polo-like kinase 4
ENSG00000181936	-0.35	3.06	2.86	#N/A	#N/A	GIN5 complex subunit 3 (Psf3 homolog)
ENSG00000124357	0.13	2.76	2.58	#N/A	#N/A	neuraminidase E3 ubiquitin protein ligase 1B
ENSG00000102992	-0.03	1.62	1.99	#N/A	#N/A	non-SMC condensin I complex, subunit D2
ENSG00000164619	0.94	4.34	3.77	#N/A	#N/A	BMP binding endothelial regulator
ENSG00000125536	1.38	1.67	4.66	#N/A	#N/A	interleukin 1, beta
ENSG00000136244	2.43	-2.45	0.13	#N/A	4.71	interleukin 6
ENSG00000138553	0.15	1.34	2.16	2.06	1.86	epithelial membrane protein 2
ENSG00000138658	-0.80	2.29	1.96	#N/A	#N/A	zinc finger, GRF-type containing 1
ENSG00000104099	-0.12	2.32	3.30	#N/A	#N/A	integrin, alpha 6
ENSG00000184992	-0.19	2.28	1.67	#N/A	#N/A	BR13 binding protein
ENSG00000117266	-0.57	-4.50	-1.79	#N/A	#N/A	cyclin-dependent kinase 18
ENSG00000104869	0.26	2.12	2.09	#N/A	#N/A	ribonuclease H2, subunit A
ENSG00000171033	0.73	3.21	6.54	#N/A	#N/A	protein kinase (cAMP-dependent, catalytic) inhibitor alpha
ENSG000001095303	-0.01	1.51	2.14	2.10	#N/A	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
ENSG00000133110	0.90	4.32	5.10	#N/A	#N/A	periostin, osteoblast specific factor
ENSG00000109685	-0.27	1.43	1.82	#N/A	#N/A	Wolf-Hirschhorn syndrome candidate 1
ENSG00000166845	-0.56	2.97	3.15	#N/A	#N/A	chromosome 18 open reading frame 54
ENSG00000128342	1.32	-5.64	-4.48	#N/A	#N/A	leukemia inhibitory factor
ENSG00000162607	-0.15	2.03	1.87	-1.09	#N/A	ubiquitin specific peptidase 1
ENSG00000127859	-0.23	1.78	1.40	#N/A	1.16	myosin XIX
ENSG00000114346	-0.30	2.06	2.61	#N/A	#N/A	epithelial cell transforming 2
ENSG00000109861	-0.13	0.98	2.65	3.98	3.78	coiled-coil domain containing 34
ENSG000001090466	-0.74	2.45	2.27	#N/A	#N/A	chromosome 1 open reading frame 112
ENSG00000101866	-0.19	1.58	1.48	#N/A	#N/A	polymerase (DNA directed), alpha 1, catalytic subunit
ENSG00000176619	-0.05	0.91	1.73	#N/A	#N/A	lamin B2
ENSG00000180875	-0.33	1.72	1.27	#N/A	#N/A	gremlin 2, DAN family BMP antagonist
ENSG00000186638	0.42	3.33	2.50	#N/A	#N/A	kinesin family member 24
ENSG00000144354	1.20	2.63	3.70	-1.35	#N/A	cell division cycle associated 7
ENSG00000123473	0.57	2.80	2.79	#N/A	#N/A	SCL/TAL1 interrupting locus
ENSG00000121621	1.08	3.32	4.23	#N/A	#N/A	kinesin family member 18A
ENSG00000121211	0.70	3.50	3.50	#N/A	#N/A	meiotic nuclear divisions 1 homolog (S. cerevisiae)
ENSG00000146263	0.09	2.71	2.21	#N/A	#N/A	MMS22-like, DNA repair protein
ENSG00000171208	0.82	3.06	3.01	#N/A	#N/A	neuropilin (NRP) and tolloid (TLL)-like 2
ENSG00000125885	-0.45	2.30	1.90	#N/A	#N/A	mitochondrial maintenance complex component 8
ENSG00000188486	0.30	1.98	1.79	#N/A	1.34	H2A histone family, member X
ENSG00000132436	0.45	2.20	2.28	-1.60	#N/A	fdgutin-like 1
ENSG00000179750	0.33	2.80	2.94	#N/A	#N/A	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B
ENSG00000127586	-0.53	2.54	2.57	-1.76	#N/A	CTF18, chromosome transmission fidelity factor 18 homolog (S. cerevisiae)
ENSG00000133392	1.31	-0.80	-2.68	#N/A	#N/A	myosin, heavy chain 11, smooth muscle
ENSG00000144810	0.61	1.79	1.93	#N/A	#N/A	collagen, type VIII, alpha 1
ENSG000001262406	1.10	2.84	2.79	#N/A	#N/A	matrix metalloproteinase 12
ENSG00000185697	0.63	3.47	3.45	#N/A	#N/A	v-myb avian myeloblastosis viral oncogene homolog-like 1
ENSG00000112298	#N/A	#N/A	#N/A	-1.11	#N/A	BCL2-associated athanogene 2
ENSG00000104809	#N/A	#N/A	#N/A	-1.11	#N/A	solute carrier family 22 (organic cation/carnitine transporter), member 16
ENSG00000164933	#N/A	#N/A	#N/A	-1.11	#N/A	solute carrier family 25 (mitochondrial folate carrier), member 32
ENSG00000118308	#N/A	#N/A	#N/A	-1.11	#N/A	lymphoid-restricted membrane protein
ENSG0000018597	#N/A	#N/A	#N/A	-1.11	#N/A	family with sequence similarity 50, member A
ENSG00000115459	#N/A	#N/A	#N/A	-1.11	#N/A	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit B1
ENSG00000116133	#N/A	#N/A	#N/A	-1.11	#N/A	24-dehydrocholesterol reductase
ENSG00000174579	#N/A	#N/A	#N/A	-1.11	#N/A	male-specific lethal 2 homolog (Drosophila)
ENSG00000128059	#N/A	#N/A	#N/A	-1.11	#N/A	phosphoribosyl pyrophosphate amidotransferase
ENSG00000164050	#N/A	#N/A	#N/A	-1.11	#N/A	plexin B1
ENSG00000138758	#N/A	#N/A	#N/A	-1.11	#N/A	septin 11
ENSG00000197774	#N/A	#N/A	#N/A	-1.11	#N/A	essential meiotic structure-specific endonuclease subunit 2
ENSG00000162384	#N/A	#N/A	#N/A	-1.11	#N/A	chromosome 1 open reading frame 123
ENSG00000103495	#N/A	#N/A	#N/A	-1.11	#N/A	MYC-associated zinc finger protein (purine-binding transcription factor)
ENSG00000173112	#N/A	#N/A	#N/A	-1.12	#N/A	small nuclear ribonucleoprotein polypeptide A
ENSG00000196547	#N/A	#N/A	#N/A	-1.12	#N/A	mannosidase, alpha, class 2A, member 2
ENSG000001098783	#N/A	#N/A	#N/A	-1.12	#N/A	heterogeneous nuclear ribonucleoprotein M
ENSG00000123734	#N/A	#N/A	#N/A	-1.12	#N/A	serine/threonine kinase receptor associated protein
ENSG00000106554	#N/A	#N/A	#N/A	-1.12	#N/A	coiled-coil-helix-coiled-coil-helix domain containing 3
ENSG00000115761	#N/A	#N/A	#N/A	-1.12	#N/A	nucleolar protein 10
ENSG00000164880	#N/A	#N/A	#N/A	-1.12	#N/A	integrator complex subunit 1
ENSG00000123505	#N/A	#N/A	#N/A	-1.12	#N/A	adenosylmethionine decarboxylase 1
ENSG00000130204	#N/A	#N/A	#N/A	-1.12	#N/A	translocase of outer mitochondrial membrane 40 homolog (yeast)
ENSG00000175376	#N/A	#N/A	#N/A	-1.12	#N/A	eukaryotic translation initiation factor 1A domain containing
ENSG000001097134	#N/A	#N/A	#N/A	-1.12	#N/A	THO complex 1
ENSG00000114770	#N/A	#N/A	#N/A	-1.12	#N/A	ATP-binding cassette, sub-family C (CFTR/MRP), member 5
ENSG00000157778	#N/A	#N/A	#N/A	-1.12	#N/A	proteasome (prosome, macropain) assembly chaperone 3
ENSG00000141456	#N/A	#N/A	#N/A	-1.13	#N/A	proline, glutamate and leucine rich protein 1
ENSG000001234032	#N/A	#N/A	#N/A	-1.13	#N/A	valyl-tRNA synthetase 2, mitochondrial
ENSG00000149115	#N/A	#N/A	#N/A	-1.13	#N/A	tankyrase 1 binding protein 1, 182kDa
ENSG00000106652	#N/A	#N/A	#N/A	-1.13	#N/A	interferon-related developmental regulator 1
ENSG00000155850	#N/A	#N/A	#N/A	-1.13	#N/A	solute carrier family 26 (anion exchanger), member 2
ENSG00000100359	#N/A	#N/A	#N/A	-1.13	#N/A	small G protein signaling modulator 3
ENSG00000187051	#N/A	#N/A	#N/A	-1.13	#N/A	ribosomal protein S19 binding protein 1
ENSG00000123465	#N/A	#N/A	#N/A	-1.13	#N/A	ADP-ribosylation factor-like 2
ENSG000001095415	#N/A	#N/A	#N/A	-1.13	#N/A	SEH1-like nucleoporin
ENSG00000168259	#N/A	#N/A	#N/A	-1.13	#N/A	DnaJ (Hsp40) homolog, subfamily C, member 7
ENSG00000148296	#N/A	#N/A	#N/A	-1.13	#N/A	surfeit 6
ENSG00000138698	#N/A	#N/A	#N/A	-1.13	#N/A	RAP1, GTP-GDP dissociation stimulator 1
ENSG00000184164	#N/A	#N/A	#N/A	-1.13	#N/A	cysteine-rich with EGF-like domains 2
ENSG00000176058	#N/A	#N/A	#N/A	-1.13	#N/A	taperin
ENSG000001065060	#N/A	#N/A	#N/A	-1.13	#N/A	UHRF1 binding protein 1
ENSG00000100722	#N/A	#N/A	#N/A	-1.13	#N/A	zinc finger CCH-type containing 14
ENSG00000163257	#N/A	#N/A	#N/A	-1.13	#N/A	DDI1 and CUL4 associated factor 16
ENSG000001275176	#N/A	#N/A	#N/A	-1.13	#N/A	acetyl-CoA carboxylase alpha

FIGURE 1G

ENSG0000013573	-0.24	2.45	2.13	#N/A	#N/A	DEAD/H (Asp-Glu-Ala-Asp/His) box helicase 11
ENSG00000137309	0.51	1.53	2.25	-1.64	#N/A	high mobility group AT-hook 1
ENSG00000153044	0.02	1.77	2.61	#N/A	#N/A	centromere protein H
ENSG00000075213	0.37	1.91	0.58	#N/A	#N/A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A
ENSG00000173207	-0.66	1.39	1.98	1.24	2.35	CDC28 protein kinase regulatory subunit 1B
ENSG00000130695	-1.34	1.72	1.43	#N/A	#N/A	centrosomal protein 85kDa
ENSG00000176206	1.29	4.01	3.88	#N/A	#N/A	ATPase family, AAA domain containing 5
ENSG00000147536	0.15	2.62	2.49	#N/A	#N/A	GIINS complex subunit 4 (Skf5 homolog)
ENSG00000005513	0.21	-5.82	-2.88	#N/A	#N/A	SRY (sex determining region Y)-box 8
ENSG00000132646	-0.03	2.19	1.74	#N/A	1.15	proliferating cell nuclear antigen
ENSG00000128578	-1.00	2.24	2.24	#N/A	#N/A	striatin interacting protein 2
ENSG00000159259	-0.03	2.61	1.83	#N/A	#N/A	chromatin assembly factor 1, subunit B (p60)
ENSG00000213551	-0.54	1.67	1.63	#N/A	1.23	DnaJ (Hsp40) homolog, subfamily C, member 9
ENSG00000129534	0.32	2.28	2.76	#N/A	#N/A	MIS18 binding protein 1
ENSG00000151503	-0.22	1.94	1.80	#N/A	#N/A	non-SMC condensin II complex, subunit D3
ENSG00000183814	-0.47	2.39	2.93	#N/A	#N/A	lin-9 DREAM MuvB core complex component
ENSG00000172061	0.04	1.30	2.10	#N/A	#N/A	leucine rich repeat containing 15
ENSG00000178966	-0.45	2.35	2.26	#N/A	#N/A	RecQ mediated genome instability 1
ENSG00000137807	0.44	2.28	2.42	#N/A	#N/A	kinesin family member 23
ENSG00000136824	-0.01	2.08	2.29	#N/A	#N/A	structural maintenance of chromosomes 2
ENSG00000139354	0.63	3.43	4.41	#N/A	#N/A	growth arrest-specific 2 like 3
ENSG00000120539	0.47	2.29	1.94	#N/A	#N/A	microtubule associated serine/threonine kinase-like
ENSG000000051180	-0.07	2.68	1.99	#N/A	#N/A	RAD51 recombinase
ENSG00000123416	0.44	2.01	1.99	#N/A	#N/A	tubulin, alpha 1b
ENSG00000169213	0.41	1.85	1.53	#N/A	#N/A	RAB3B, member RAS oncogene family
ENSG00000058804	0.03	1.87	2.15	-1.61	#N/A	NDC1 transmembrane nucleoporin
ENSG00000123374	-0.10	1.66	1.50	#N/A	1.09	cyclin-dependent kinase 2
ENSG00000198056	0.56	3.48	3.31	#N/A	#N/A	primase, DNA, polypeptide 1 (49kDa)
ENSG00000111331	-0.20	1.08	1.84	6.19	1.73	2'-5'-oligoadenylate synthetase 3, 100kDa
ENSG00000185361	0.80	0.68	2.66	#N/A	#N/A	tumor necrosis factor, alpha-induced protein 8 like 1
ENSG00000122861	0.52	2.38	2.71	#N/A	#N/A	plasminogen activator, urokinase
ENSG00000131979	1.36	-1.71	-1.31	#N/A	#N/A	GTP cyclohydrolase 1
ENSG00000136395	0.15	2.09	2.15	#N/A	#N/A	cyclin-dependent kinase 15
ENSG00000125146	1.19	2.84	3.25	3.39	#N/A	metallothionein 2A
ENSG00000144802	2.35	-0.28	0.47	1.41	#N/A	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta
ENSG00000152457	0.03	1.46	2.22	3.93	#N/A	DNA cross-link repair 1C
ENSG00000251562	0.54	-0.66	2.93	1.52	#N/A	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)
ENSG000000031691	-0.32	2.60	2.16	#N/A	#N/A	centromere protein Q
ENSG00000197299	-0.50	3.27	3.03	-1.16	#N/A	Bloom syndrome, RecQ helicase-like
ENSG000000057019	-0.08	1.90	2.12	#N/A	#N/A	discoidin, CUB and LCCL domain containing 2
ENSG000000062822	-0.14	1.94	1.66	#N/A	#N/A	polymerase (DNA directed), delta 1, catalytic subunit
ENSG00000135476	0.53	2.29	2.01	#N/A	#N/A	extra spindle pole bodies homolog 1 (S. cerevisiae)
ENSG00000163614	0.26	2.79	4.19	#N/A	1.22	CUB domain containing protein 1
ENSG00000101670	1.15	-1.59	-2.77	#N/A	#N/A	lipase, endothelial
ENSG00000138669	0.16	2.16	1.93	#N/A	#N/A	protein kinase, cGMP-dependent, type II
ENSG0000011201	-0.64	3.95	4.88	#N/A	#N/A	anosmin 1
ENSG00000006468	-1.14	1.02	2.50	#N/A	#N/A	ets variant 1

ENSG00000107262	#N/A	#N/A	#N/A	-1.13	#N/A	BCL2-associated athanogene
ENSG00000168906	#N/A	#N/A	#N/A	-1.13	#N/A	methionine adenosyltransferase II, alpha
ENSG00000185104	#N/A	#N/A	#N/A	-1.14	#N/A	Fas (TNFRSF6) associated factor 1
ENSG00000187954	#N/A	#N/A	#N/A	-1.14	#N/A	cysteine/histidine-rich 1
ENSG00000158882	#N/A	#N/A	#N/A	-1.14	#N/A	translocase of outer mitochondrial membrane 40 homolog (yeast)-like
ENSG00000141385	#N/A	#N/A	#N/A	-1.14	#N/A	AFC3-like AAA ATPase 2
ENSG00000168944	#N/A	#N/A	#N/A	-1.14	#N/A	centrosomal protein 120kDa
ENSG00000119929	#N/A	#N/A	#N/A	-1.14	#N/A	CuT copper transporter
ENSG00000132953	#N/A	#N/A	#N/A	-1.14	#N/A	exportin 4
ENSG00000115120	#N/A	#N/A	#N/A	-1.14	#N/A	phenylalanyl-tRNA synthetase, beta subunit
ENSG00000180198	#N/A	#N/A	#N/A	-1.14	#N/A	regulator of chromosome condensation 1
ENSG00000127837	#N/A	#N/A	#N/A	-1.14	#N/A	angio-associated, migratory cell protein
ENSG00000138399	#N/A	#N/A	#N/A	-1.14	#N/A	FAST kinase domains 1
ENSG00000130024	#N/A	#N/A	#N/A	-1.14	#N/A	PHD finger protein 10
ENSG000000987191	#N/A	#N/A	#N/A	-1.14	#N/A	proteasome (prosome, macropain) 26S subunit, ATPase, 5
ENSG00000115791	#N/A	#N/A	#N/A	-1.14	#N/A	crystallin, zeta (quinone reductase)
ENSG00000166988	#N/A	#N/A	#N/A	-1.14	#N/A	methionyl-tRNA synthetase
ENSG00000112640	#N/A	#N/A	#N/A	-1.14	#N/A	protein phosphatase 2, regulatory subunit B', delta
ENSG00000120948	#N/A	#N/A	#N/A	-1.15	#N/A	TAR DNA binding protein
ENSG00000146701	#N/A	#N/A	#N/A	-1.15	#N/A	malate dehydrogenase 2, NAD (mitochondrial)
ENSG00000130810	#N/A	#N/A	#N/A	-1.15	#N/A	peter pan homolog (Drosophila)
ENSG00000173457	#N/A	#N/A	#N/A	-1.15	#N/A	protein phosphatase 1, regulatory (inhibitor) subunit 14B
ENSG00000182162	#N/A	#N/A	#N/A	-1.15	#N/A	purinergic receptor P2Y, G-protein coupled, 8
ENSG00000008838	#N/A	#N/A	#N/A	-1.15	#N/A	mediator complex subunit 24
ENSG00000100029	#N/A	#N/A	#N/A	-1.15	#N/A	pesCADillo ribosomal biogenesis factor 1
ENSG00000162852	#N/A	#N/A	#N/A	-1.15	#N/A	connorin, connexin sorting protein
ENSG00000169718	#N/A	#N/A	#N/A	-1.15	#N/A	dihydropyrimidine synthase 1-like
ENSG00000116898	#N/A	#N/A	#N/A	-1.15	#N/A	mitochondrial ribosomal protein S15
ENSG000000983750	#N/A	#N/A	#N/A	-1.15	#N/A	Ras-related GTP binding B
ENSG00000145907	#N/A	#N/A	#N/A	-1.15	#N/A	GTPase activating protein (SH3 domain) binding protein 1
ENSG00000163539	#N/A	#N/A	#N/A	-1.15	#N/A	cytoplasmic linker associated protein 2
ENSG00000104164	#N/A	#N/A	#N/A	-1.15	#N/A	biogenesis of lysosomal organelles complex-1, subunit 6, pallidin
ENSG000000012983	#N/A	#N/A	#N/A	-1.15	#N/A	mitogen-activated protein kinase kinase kinase kinase 5
ENSG00000166411	#N/A	#N/A	#N/A	-1.15	#N/A	isocitrate dehydrogenase 3 (NAD+) alpha
ENSG00000128191	#N/A	#N/A	#N/A	-1.16	#N/A	DGCR8 microprocessor complex subunit
ENSG00000125247	#N/A	#N/A	#N/A	-1.16	#N/A	transmembrane and tetrahydropeptide repeat containing 4
ENSG00000138668	#N/A	#N/A	#N/A	-1.16	#N/A	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)
ENSG00000177830	#N/A	#N/A	#N/A	-1.16	#N/A	chitinase domain containing 1
ENSG00000129351	#N/A	#N/A	#N/A	-1.16	#N/A	interleukin enhancer binding factor 3, 90kDa
ENSG00000190410	#N/A	#N/A	#N/A	-1.16	#N/A	PHD finger protein 5A
ENSG00000138442	#N/A	#N/A	#N/A	-1.16	#N/A	WD repeat domain 12
ENSG00000124181	#N/A	#N/A	#N/A	-1.16	#N/A	phospholipase C, gamma 1
ENSG00000105063	#N/A	#N/A	#N/A	-1.16	#N/A	protein phosphatase 6, regulatory subunit 1
ENSG000000934090	#N/A	#N/A	#N/A	-1.16	#N/A	STAR-related lipid transfer (START) domain containing 7
ENSG00000150768	#N/A	#N/A	#N/A	-1.16	#N/A	dihydroipoamide S-acetyltransferase
ENSG00000152694	#N/A	#N/A	#N/A	-1.16	#N/A	excystosin-like glycosyltransferase 2
ENSG000000937474	#N/A	#N/A	#N/A	-1.16	#N/A	NOP2/Sun RNA methyltransferase family, member 2

FIGURE 1H

ENSG00000184445	0.18	2.29	2.20	#N/A	#N/A	kinetochore associated 1
ENSG00000198576	1.64	-4.85	-3.67	#N/A	#N/A	activity-regulated cytoskeleton-associated protein
ENSG00000119707	0.28	0.07	2.18	-1.07	#N/A	RNA binding motif protein 25
ENSG00000146410	-0.20	2.53	2.86	#N/A	#N/A	mitochondrial fission regulator 2
ENSG00000157661	-0.47	-1.71	1.61	6.39	#N/A	MX dynamin-like GTPase 1
ENSG00000177514	-0.28	1.94	1.10	#N/A	#N/A	polymerase (DNA-directed), delta 3, accessory subunit
ENSG00000149541	0.54	2.03	1.61	#N/A	#N/A	replication factor C (activator 1) 2, 40kDa
ENSG00000158050	2.41	-2.86	-2.01	#N/A	#N/A	dual specificity phosphatase 2
ENSG0000013297	0.15	1.26	1.73	#N/A	#N/A	claudin 11
ENSG00000178878	-0.34	2.06	1.50	1.01	#N/A	apolipoprotein L domain containing 1
ENSG00000100526	-0.12	2.40	3.38	#N/A	#N/A	cyclin-dependent kinase inhibitor 3
ENSG00000159388	1.01	-0.94	-0.93	2.26	#N/A	BTG family, member 2
ENSG00000166250	0.19	1.89	1.24	#N/A	#N/A	CXADR-like membrane protein
ENSG00000115687	-0.57	2.30	1.63	#N/A	#N/A	PAS domain containing serine/threonine kinase
ENSG00000123136	0.46	1.27	1.78	#N/A	1.08	DEAD (Asp-Glu-Ala-Asp) box polypeptide 35A
ENSG00000121957	-0.84	0.55	1.70	#N/A	#N/A	G-protein signaling modulator 2
ENSG00000133119	0.08	2.91	2.71	#N/A	#N/A	replication factor C (activator 1) 3, 38kDa
ENSG000001030419	-1.59	1.18	1.54	#N/A	#N/A	IKAROS family zinc finger 2 (Helios)
ENSG00000166004	-0.42	1.76	1.59	#N/A	#N/A	centrosomal protein 295kDa
ENSG00000108691	2.19	-2.42	-0.76	#N/A	1.98	chemokine (C-C motif) ligand 2
ENSG00000176974	-0.45	1.19	1.61	#N/A	#N/A	serine hydroxymethyltransferase 1 (soluble)
ENSG00000149948	0.97	2.68	3.27	#N/A	#N/A	high mobility group AT-hook 2
ENSG00000163739	4.12	0.05	4.15	#N/A	#N/A	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)
ENSG00000123496	0.92	4.12	3.29	#N/A	#N/A	interleukin 13 receptor, alpha 2
ENSG00000168393	-0.04	1.34	1.46	#N/A	#N/A	deoxythymidylate kinase (thymidylate kinase)
ENSG00000170779	0.50	2.28	2.05	#N/A	#N/A	cell division cycle associated 4
ENSG00000160957	-0.44	2.00	1.31	-1.45	#N/A	RecQ protein-like 4
ENSG000001072501	-0.16	1.27	1.22	#N/A	#N/A	structural maintenance of chromosomes 1A
ENSG00000105738	0.17	1.25	1.70	#N/A	#N/A	signal-induced proliferation-associated 1 like 3
ENSG000001023171	0.36	2.31	2.23	#N/A	#N/A	GRAM domain containing 1B
ENSG00000179156	0.05	1.74	1.90	#N/A	#N/A	oxysterol binding protein-like 6
ENSG00000100576	-0.27	1.19	1.71	#N/A	#N/A	KIAA0586
ENSG00000151014	2.03	-0.03	-0.27	#N/A	#N/A	CCR4 carbon catabolite repression 4-like (Saccharomyces)
ENSG00000122483	0.54	1.73	2.17	#N/A	#N/A	coiled-coil domain containing 18
ENSG0000010257219	1.21	2.82	2.13	#N/A	#N/A	RP11-54A9.1
ENSG000001097021	0.54	1.73	1.58	#N/A	#N/A	acyl-CoA thioesterase 7
ENSG00000103995	0.05	2.35	1.89	1.58	#N/A	centrosomal protein 152kDa
ENSG00000140534	0.38	2.44	1.72	#N/A	#N/A	TOPBP1-interacting checkpoint and replication regulator
ENSG00000149554	-0.21	1.56	1.66	#N/A	#N/A	checkpoint kinase 1
ENSG00000100714	0.26	1.51	1.34	-1.11	#N/A	methylene tetrahydrofolate dehydrogenase (NADP+ dependent) 1, methylene tetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase
ENSG00000156113	0.32	1.82	0.73	#N/A	#N/A	potassium channel, calcium activated large conductance subfamily M1 alpha, member 1
ENSG000001069399	1.07	-1.57	-0.63	2.30	#N/A	B-cell CLL/lymphoma 3
ENSG00000185883	#N/A	#N/A	#N/A	-1.17	#N/A	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c
ENSG00000100060	#N/A	#N/A	#N/A	-1.17	#N/A	MFNG O-fucosyltransferase 3-beta-N-acetylglucosaminyltransferase
ENSG00000135624	#N/A	#N/A	#N/A	-1.17	#N/A	chaperonin containing TCP1, subunit 7 (eta)
ENSG00000116560	#N/A	#N/A	#N/A	-1.17	#N/A	splicing factor proline/glutamine-rich
ENSG00000196591	#N/A	#N/A	#N/A	-1.17	#N/A	histone deacetylase 2
ENSG00000135372	#N/A	#N/A	#N/A	-1.17	#N/A	N-acetyltransferase 10 (GCN5-related)
ENSG00000169710	#N/A	#N/A	#N/A	-1.17	#N/A	fatty acid synthase
ENSG00000103202	#N/A	#N/A	#N/A	-1.17	#N/A	NME/NM23 nucleoside diphosphate kinase 4
ENSG00000183431	#N/A	#N/A	#N/A	-1.17	#N/A	splicing factor 3a, subunit 3, 66kDa
ENSG000001239285	#N/A	#N/A	#N/A	-1.17	#N/A	lymphocyte antigen 6 complex, locus G5B
ENSG0000010984073	#N/A	#N/A	#N/A	-1.17	#N/A	zinc metalloproteinase STE24
ENSG00000152117	#N/A	#N/A	#N/A	-1.17	#N/A	AC093838.4
ENSG00000109586	#N/A	#N/A	#N/A	-1.17	#N/A	polypeptide N-acetylglucosaminyltransferase 7
ENSG00000138709	#N/A	#N/A	#N/A	-1.16	#N/A	La ribonucleoprotein domain family, member 1B
ENSG000001085998	#N/A	#N/A	#N/A	-1.18	#N/A	protein O-linked mannose N-acetylglucosaminyltransferase 1 (beta 1,2-)
ENSG0000010884754	#N/A	#N/A	#N/A	-1.18	#N/A	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit
ENSG00000110200	#N/A	#N/A	#N/A	-1.18	#N/A	anaphase promoting complex subunit 15
ENSG00000145494	#N/A	#N/A	#N/A	-1.18	#N/A	NADH dehydrogenase (ubiquinone) F9-S protein 6, 13kDa (NADH-coenzyme Q reductase)
ENSG0000010274981	#N/A	#N/A	#N/A	-1.18	#N/A	poly-U binding splicing factor 60kDa
ENSG00000105176	#N/A	#N/A	#N/A	-1.18	#N/A	URI1, prefoldin-like chaperone
ENSG00000115241	#N/A	#N/A	#N/A	-1.18	#N/A	protein phosphatase, Mg2+/Mn2+ dependent, 1G
ENSG00000146731	#N/A	#N/A	#N/A	-1.18	#N/A	chaperonin containing TCP1, subunit 6A (zeta 1)
ENSG0000010232045	#N/A	#N/A	#N/A	-1.18	#N/A	euchromatic histone-lysine N-methyltransferase 2
ENSG000001077097	#N/A	#N/A	#N/A	-1.18	#N/A	topoisomerase (DNA) II beta 150kDa
ENSG00000163468	#N/A	#N/A	#N/A	-1.18	#N/A	chaperonin containing TCP1, subunit 3 (gamma)
ENSG00000128626	#N/A	#N/A	#N/A	-1.19	#N/A	mitochondrial ribosomal protein S12
ENSG00000137449	#N/A	#N/A	#N/A	-1.19	#N/A	cytoplasmic polyadenylation element binding protein 2
ENSG00000130764	#N/A	#N/A	#N/A	-1.19	#N/A	leucine rich repeat containing 47
ENSG000001231502	#N/A	#N/A	#N/A	-1.19	#N/A	LSM2 homolog, U6 small nuclear RNA and mRNA degradation associated
ENSG00000141577	#N/A	#N/A	#N/A	-1.19	#N/A	centrosomal protein 131kDa
ENSG000001075239	#N/A	#N/A	#N/A	-1.19	#N/A	acetyl-CoA acetyltransferase 1
ENSG00000104903	#N/A	#N/A	#N/A	-1.19	#N/A	lymphoblastic leukemia associated hematopoiesis regulator 1
ENSG00000163597	#N/A	#N/A	#N/A	-1.19	#N/A	small nuclear RNA host gene 16
ENSG00000108395	#N/A	#N/A	#N/A	-1.19	#N/A	tripartite motif containing 37
ENSG000001276681	#N/A	#N/A	#N/A	-1.19	#N/A	leukocyte receptor cluster (LRC) member 8
ENSG000001092529	#N/A	#N/A	#N/A	-1.19	#N/A	calpain 3
ENSG00000187630	#N/A	#N/A	#N/A	-1.19	#N/A	dehydrogenase/reductase (SDR family) member 4 like 2
ENSG00000114485	#N/A	#N/A	#N/A	-1.20	#N/A	protein phosphatase 5, catalytic subunit
ENSG00000185803	#N/A	#N/A	#N/A	-1.20	#N/A	solute carrier family 52 (riboflavin transporter), member 2
ENSG0000010204843	#N/A	#N/A	#N/A	-1.20	#N/A	dynactin 1
ENSG00000152990	#N/A	#N/A	#N/A	-1.20	#N/A	adhesion G protein-coupled receptor A3
ENSG00000107561	#N/A	#N/A	#N/A	-1.20	#N/A	eukaryotic translation initiation factor 3, subunit A

FIGURE 11

ENSG00000005189	-0.26	1.84	1.82	#N/A	#N/A	Putative RNA exonuclease NIEF-sp
ENSG00000157193	0.29	1.84	1.73	-1.04	#N/A	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor
ENSG00000181751	0.15	1.78	1.72	#N/A	#N/A	chromosome 5 open reading frame 30
ENSG00000117155	0.05	1.91	1.97	#N/A	#N/A	synovial sarcoma, X breakpoint 2 interacting protein
ENSG00000118655	0.14	2.36	1.83	#N/A	#N/A	DNA cross-link repair 1B
ENSG00000143493	-0.01	1.74	1.50	#N/A	#N/A	integrator complex subunit 7
ENSG00000101911	0.08	1.80	1.50	#N/A	#N/A	phosphoribosyl pyrophosphate synthetase 2
ENSG00000095002	0.28	1.85	1.48	#N/A	#N/A	mutS homolog 2
ENSG00000138376	0.40	2.59	2.69	#N/A	#N/A	BRCA1 associated RING domain 1
ENSG00000205206	-0.77	1.35	1.34	#N/A	#N/A	chromosome 4 open reading frame 46
ENSG00000187173	0.25	2.04	0.77	#N/A	#N/A	late committed envelope 2A
ENSG00000120802	0.09	1.82	2.28	#N/A	#N/A	thymopoietin
ENSG00000182481	-0.05	1.26	1.65	#N/A	#N/A	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
ENSG00000148848	0.59	1.59	1.54	#N/A	#N/A	ADAM metalloproteinase domain 12
ENSG00000145147	0.39	2.07	2.20	#N/A	#N/A	slit homolog 2 (Drosophila)
ENSG00000187257	-0.10	0.27	1.66	1.99	#N/A	round spermatid basic protein 1-like
ENSG00000120549	0.09	1.94	2.54	#N/A	#N/A	KIAA1217
ENSG00000138092	0.34	2.12	1.70	#N/A	#N/A	centromere protein O
ENSG00000050438	-0.12	1.49	2.19	#N/A	#N/A	solute carrier family 4, sodium bicarbonate cotransporter, member 8
ENSG00000164171	0.60	2.78	2.60	#N/A	2.08	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)
ENSG00000095752	1.30	-2.81	-2.40	#N/A	#N/A	interleukin 11
ENSG00000172167	-0.54	2.43	2.57	#N/A	#N/A	MDM2 binding protein
ENSG00000124207	0.08	1.83	1.90	#N/A	#N/A	CSE1 chromosome segregation 1-like (yeast)
ENSG00000177606	1.01	-0.56	-0.58	1.93	1.11	jun proto-oncogene
ENSG00000145779	1.43	-0.15	-0.02	#N/A	#N/A	tumor necrosis factor, alpha-induced protein 5
ENSG00000143401	0.05	0.98	1.62	#N/A	#N/A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
ENSG00000175166	0.18	1.22	1.28	#N/A	#N/A	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2
ENSG00000041353	0.38	2.34	2.66	#N/A	#N/A	RAB27B, member RAS oncogene family
ENSG00000171914	-0.17	1.30	0.95	#N/A	#N/A	tailin 2
ENSG00000099250	-0.13	1.32	1.21	#N/A	#N/A	neuropilin 1
ENSG00000164985	-0.09	0.95	1.38	#N/A	#N/A	PC4 and SFRS1 interacting protein 1
ENSG00000163781	-0.01	1.51	1.39	#N/A	#N/A	topoisomerase (DNA) II binding protein 1
ENSG00000117748	0.21	1.86	1.16	#N/A	#N/A	replication protein A2, 32kDa
ENSG00000137959	#N/A	#N/A	#N/A	8.67	#N/A	interferon-induced protein 44-like
ENSG00000185885	#N/A	#N/A	#N/A	8.20	#N/A	interferon induced transmembrane protein 1
ENSG00000088827	#N/A	#N/A	#N/A	8.06	#N/A	sialic acid binding Ig-like lectin 1, sialoadhesin
ENSG00000111335	#N/A	#N/A	#N/A	7.96	#N/A	2'-5'-oligoadenylate synthetase 2, 69/71kDa
ENSG00000213626	#N/A	#N/A	#N/A	7.25	1.15	limb bud and heart development
ENSG00000137965	#N/A	#N/A	#N/A	6.74	1.71	interferon-induced protein 44
ENSG00000100453	#N/A	#N/A	#N/A	6.72	#N/A	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)
ENSG00000133106	#N/A	#N/A	#N/A	6.54	#N/A	epithelial stromal interaction 1 (breast)
ENSG00000151555	#N/A	#N/A	#N/A	6.51	#N/A	otoferrin
ENSG00000137801	#N/A	#N/A	#N/A	6.42	#N/A	thrombospondin 1
ENSG00000198959	#N/A	#N/A	#N/A	6.36	1.96	transglutaminase 2
ENSG00000133316	#N/A	#N/A	#N/A	6.27	6.33	WD repeat domain 74
ENSG00000089127	#N/A	#N/A	#N/A	6.14	#N/A	2'-5'-oligoadenylate synthetase 1, 40/46kDa
ENSG00000235125	#N/A	#N/A	#N/A	-1.20	#N/A	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1
ENSG00000239960	#N/A	#N/A	#N/A	-1.20	#N/A	adenylosuccinate lyase
ENSG00000117448	#N/A	#N/A	#N/A	-1.20	#N/A	aldo-keto reductase family 1, member A1 (aldehyde reductase)
ENSG00000224531	#N/A	#N/A	#N/A	-1.21	#N/A	small integrin membrane protein 13
ENSG00000091527	#N/A	#N/A	#N/A	-1.21	#N/A	CDV3 homolog (mouse)
ENSG00000195642	#N/A	#N/A	#N/A	-1.21	#N/A	RAB, member RAS oncogene family-like 6
ENSG00000156669	#N/A	#N/A	#N/A	-1.21	#N/A	activating transcription factor 7 interacting protein 2
ENSG00000155189	#N/A	#N/A	#N/A	-1.21	#N/A	1-acylglycerol-3-phosphate O-acyltransferase 5
ENSG00000140474	#N/A	#N/A	#N/A	-1.21	#N/A	unc-51 like kinase 3
ENSG00000098684	#N/A	#N/A	#N/A	-1.21	#N/A	ALG8, alpha-1,2-mannosyltransferase
ENSG00000103448	#N/A	#N/A	#N/A	-1.21	2.60	cathepsin G
ENSG00000184465	#N/A	#N/A	#N/A	-1.21	#N/A	WD repeat domain 27
ENSG00000125445	#N/A	#N/A	#N/A	-1.21	#N/A	mitochondrial ribosomal protein S7
ENSG00000170632	#N/A	#N/A	#N/A	-1.21	#N/A	armadillo repeat containing 10
ENSG00000198888	#N/A	#N/A	#N/A	-1.21	#N/A	mitochondrially encoded NADH dehydrogenase 1
ENSG00000156876	#N/A	#N/A	#N/A	-1.21	#N/A	SAS-6 centriolar assembly protein
ENSG00000225903	#N/A	#N/A	#N/A	-1.22	#N/A	zinc finger protein 316
ENSG00000113360	#N/A	#N/A	#N/A	-1.22	#N/A	drossha, ribonuclease type III
ENSG00000112290	#N/A	#N/A	#N/A	-1.22	#N/A	WAS protein family, member 1
ENSG00000051128	#N/A	#N/A	#N/A	-1.22	#N/A	homer scaffolding protein 3
ENSG00000125630	#N/A	#N/A	#N/A	-1.22	#N/A	polymerase (RNA) I polypeptide B, 128kDa
ENSG00000179304	#N/A	#N/A	#N/A	-1.22	#N/A	family with sequence similarity 156, member B
ENSG00000148840	#N/A	#N/A	#N/A	-1.22	#N/A	peroxisome proliferator-activated receptor gamma, coactivator-related 1
ENSG00000247982	#N/A	#N/A	#N/A	-1.22	#N/A	long intergenic non-protein coding RNA 926
ENSG00000075415	#N/A	#N/A	#N/A	-1.22	#N/A	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3
ENSG00000256269	#N/A	#N/A	#N/A	-1.22	#N/A	hydroxymethylglutathione synthase
ENSG00000107833	#N/A	#N/A	#N/A	-1.22	1.45	nucleophosmin/nucleoplasm 3
ENSG00000167136	#N/A	#N/A	#N/A	-1.22	#N/A	endonuclease G
ENSG00000109534	#N/A	#N/A	#N/A	-1.22	1.88	GAR1 homolog, ribonucleoprotein
ENSG00000065809	#N/A	#N/A	#N/A	-1.22	#N/A	family with sequence similarity 107, member B
ENSG00000274811	#N/A	#N/A	#N/A	-1.22	#N/A	CLPTM1-like
ENSG00000153938	#N/A	#N/A	#N/A	-1.22	#N/A	guanine nucleotide binding protein-like 3 (nuclear)
ENSG00000169682	#N/A	#N/A	#N/A	-1.23	#N/A	spinster homolog 1 (Drosophila)
ENSG00000197451	#N/A	#N/A	#N/A	-1.23	#N/A	heterogeneous nuclear ribonucleoprotein A/B
ENSG00000185420	#N/A	#N/A	#N/A	-1.23	#N/A	SET and MYND domain containing 3
ENSG00000141858	#N/A	#N/A	#N/A	-1.23	#N/A	sterile alpha motif domain containing 1
ENSG00000281184	#N/A	#N/A	#N/A	-1.23	#N/A	proteasome (prosome, macropain) subunit, beta type, 1
ENSG00000198651	#N/A	#N/A	#N/A	-1.23	#N/A	UTP6, small subunit (SSU) processome component, homolog (yeast)
ENSG00000100726	#N/A	#N/A	#N/A	-1.23	#N/A	telomere maintenance 2
ENSG00000164151	#N/A	#N/A	#N/A	-1.23	#N/A	interactor of little elongation complex ELL subunit 1
ENSG00000212907	#N/A	#N/A	#N/A	-1.24	#N/A	mitochondrially encoded NADH dehydrogenase 4L
ENSG00000233369	#N/A	#N/A	#N/A	-1.24	#N/A	general transcription factor III, pseudogene 4
ENSG00000182568	#N/A	#N/A	#N/A	-1.24	#N/A	SATB homeobox 1
ENSG00000136950	#N/A	#N/A	#N/A	-1.24	#N/A	actin related protein 2/3 complex, subunit 5-like
ENSG00000158101	#N/A	#N/A	#N/A	-1.24	#N/A	nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1
ENSG00000152193	#N/A	#N/A	#N/A	-1.24	#N/A	ring finger protein 219

FIGURE 1J

ENSG00000169871	#N/A	#N/A	#N/A	6.10	3.97	tripartite motif containing 56
ENSG00000135114	#N/A	#N/A	#N/A	5.99	#N/A	Z'-5'-oligoadenylate synthetase-like
ENSG00000072694	#N/A	#N/A	#N/A	5.67	#N/A	Fc fragment of IgG, low affinity IIb, receptor (CD32)
ENSG00000196562	#N/A	#N/A	#N/A	5.78	#N/A	sulfatase 2
ENSG00000189221	#N/A	#N/A	#N/A	5.62	#N/A	monoamine oxidase A
ENSG00000269337	#N/A	#N/A	#N/A	5.61	#N/A	AL591479.1
ENSG00000181195	#N/A	#N/A	#N/A	5.60	#N/A	proenkephalin
ENSG00000225614	#N/A	#N/A	#N/A	5.52	#N/A	zinc finger protein 469
ENSG00000134369	#N/A	#N/A	#N/A	5.24	#N/A	neurin navigator 1
ENSG00000152404	#N/A	#N/A	#N/A	5.23	3.59	CWF19-like 2, cell cycle control (S. pombe)
ENSG00000142192	#N/A	#N/A	#N/A	5.11	#N/A	amyloid beta (A4) precursor protein
ENSG00000154153	#N/A	#N/A	#N/A	5.00	#N/A	family with sequence similarity 134, member B
ENSG00000134321	#N/A	#N/A	#N/A	4.99	#N/A	radical S-adenosyl methionine domain containing 2
ENSG00000126709	#N/A	#N/A	#N/A	4.96	3.67	interferon, alpha-inducible protein 6
ENSG00000187608	#N/A	#N/A	#N/A	4.89	2.10	ISG15 ubiquitin-like modifier
ENSG00000136960	#N/A	#N/A	#N/A	4.79	#N/A	endonuclease pyrophosphatase/phosphodiesterase 2
ENSG00000196141	#N/A	#N/A	#N/A	4.74	#N/A	spermatogenesis associated, serine-rich 2-like
ENSG00000136235	#N/A	#N/A	#N/A	4.71	2.66	glycoprotein (transmembrane) nmb
ENSG00000115414	#N/A	#N/A	#N/A	4.65	#N/A	fibronectin 1
ENSG00000152104	#N/A	#N/A	#N/A	4.50	#N/A	protein tyrosine phosphatase, non-receptor type 14
ENSG00000115977	#N/A	#N/A	#N/A	4.50	2.36	AP2 associated kinase 1
ENSG00000213918	#N/A	#N/A	#N/A	4.46	#N/A	deoxyribonuclease I
ENSG00000028277	#N/A	#N/A	#N/A	4.45	3.74	POU class 2 homeobox 2
ENSG00000130821	#N/A	#N/A	#N/A	4.44	#N/A	evolute carrier family 6 (neurotransmitter transporter), member 8
ENSG00000184979	#N/A	#N/A	#N/A	4.42	#N/A	ubiquitin specific peptidase 19
ENSG00000203812	#N/A	#N/A	#N/A	4.25	2.44	histone cluster 2, H2aa3
ENSG00000130586	#N/A	#N/A	#N/A	4.25	#N/A	helicase with zinc finger 2, transcriptional coactivator
ENSG00000181458	#N/A	#N/A	#N/A	4.21	#N/A	transmembrane protein 45A
ENSG00000247095	#N/A	#N/A	#N/A	4.19	#N/A	MIR210 host gene
ENSG00000135931	#N/A	#N/A	#N/A	4.16	1.76	armadillo repeat containing 9
ENSG00000180509	#N/A	#N/A	#N/A	4.04	#N/A	potassium channel, voltage gated subfamily E regulatory beta subunit 1
ENSG00000038427	#N/A	#N/A	#N/A	4.02	#N/A	versican
ENSG00000114013	#N/A	#N/A	#N/A	3.95	#N/A	CD86 molecule
ENSG00000204642	#N/A	#N/A	#N/A	3.94	#N/A	major histocompatibility complex, class I, F
ENSG00000203710	#N/A	#N/A	#N/A	3.88	#N/A	complement component (3b/4b) receptor 1 (Knops blood group)
ENSG00000244509	#N/A	#N/A	#N/A	3.86	2.18	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C
ENSG00000143190	#N/A	#N/A	#N/A	3.85	2.95	POU class 2 homeobox 1
ENSG00000185850	#N/A	#N/A	#N/A	3.85	#N/A	ZFP36 ring finger protein-like 1
ENSG00000179029	#N/A	#N/A	#N/A	3.85	#N/A	transmembrane protein 107
ENSG00000182578	#N/A	#N/A	#N/A	3.85	#N/A	colony stimulating factor 1 receptor
ENSG00000187193	#N/A	#N/A	#N/A	3.85	#N/A	metallothionein 1X
ENSG00000110324	#N/A	#N/A	#N/A	3.83	#N/A	interleukin 10 receptor, alpha
ENSG00000261064	#N/A	#N/A	#N/A	3.83	#N/A	RP11-1009B6.3
ENSG00000166750	#N/A	#N/A	#N/A	3.81	#N/A	echlafen family member 5
ENSG00000270647	#N/A	#N/A	#N/A	-1.24	#N/A	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa
ENSG00000140650	#N/A	#N/A	#N/A	-1.24	#N/A	phosphomannomutase 2
ENSG00000105263	#N/A	#N/A	#N/A	-1.24	#N/A	eukaryotic translation initiation factor 3, subunit B
ENSG00000304949	#N/A	#N/A	#N/A	-1.25	#N/A	reticulocalbin 1, EF-hand calcium binding domain
ENSG000005058044	#N/A	#N/A	#N/A	-1.25	#N/A	ELAV like RNA binding protein 1
ENSG00000165684	#N/A	#N/A	#N/A	-1.25	#N/A	small nuclear RNA activating complex, polypeptide 4, 19kDa
ENSG00000111641	#N/A	#N/A	#N/A	-1.25	#N/A	NOP2 nucleolar protein
ENSG00000143952	#N/A	#N/A	#N/A	-1.25	#N/A	vacuolar protein sorting 54 homolog (S. cerevisiae)
ENSG00000359600	#N/A	#N/A	#N/A	-1.25	#N/A	polymerase (RNA) III (DNA directed) polypeptide E (80kD)
ENSG00000167113	#N/A	#N/A	#N/A	-1.25	#N/A	coenzyme Q4
ENSG00000254364	#N/A	#N/A	#N/A	-1.25	#N/A	dynein, light chain, LC8-type 2
ENSG00000104529	#N/A	#N/A	#N/A	-1.25	#N/A	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
ENSG00000185874	#N/A	#N/A	#N/A	-1.25	#N/A	family with sequence similarity 35, member B, pseudogene
ENSG00000155271	#N/A	#N/A	#N/A	-1.26	#N/A	nuclear protein 6 (RNA-associated)
ENSG00000161618	#N/A	#N/A	#N/A	-1.26	#N/A	aldehyde dehydrogenase 16 family, member A1
ENSG00000134215	#N/A	#N/A	#N/A	-1.26	#N/A	vav 3 guanine nucleotide exchange factor
ENSG00000124571	#N/A	#N/A	#N/A	-1.26	#N/A	exportin 5
ENSG00000104907	#N/A	#N/A	#N/A	-1.26	#N/A	lRNA methyltransferase 1 homolog (S. cerevisiae)
ENSG00000165097	#N/A	#N/A	#N/A	-1.26	#N/A	lysine (K)-specific demethylase 1B
ENSG00000107949	#N/A	#N/A	#N/A	-1.26	#N/A	BRCA2 and CDKN1A interacting protein
ENSG00000116221	#N/A	#N/A	#N/A	-1.26	#N/A	mitochondrial ribosomal protein L37
ENSG00000141758	#N/A	#N/A	#N/A	-1.26	#N/A	thioredoxin-like 4A
ENSG00000309047	#N/A	#N/A	#N/A	-1.26	#N/A	transcription factor AP-4 (activating enhancer binding protein 4)
ENSG00000336549	#N/A	#N/A	#N/A	-1.26	#N/A	zinc finger, ZZ-type containing 3
ENSG00000213593	#N/A	#N/A	#N/A	-1.27	#N/A	thioredoxin-related transmembrane protein 2
ENSG00000204149	#N/A	#N/A	#N/A	-1.27	#N/A	ArfGAP with GTPase domain, ankyrin repeat and PH domain 6
ENSG000003031093	#N/A	#N/A	#N/A	-1.27	#N/A	family with sequence similarity 13, member B
ENSG00000109522	#N/A	#N/A	#N/A	-1.27	#N/A	glucosamine-phosphate N-acetyltransferase 1
ENSG00000167702	#N/A	#N/A	#N/A	-1.27	#N/A	kinesin family member C2
ENSG000003095906	#N/A	#N/A	#N/A	-1.27	#N/A	nucleotide binding protein 2
ENSG000003028310	#N/A	#N/A	#N/A	-1.27	#N/A	bromodomain containing 9
ENSG00000243725	#N/A	#N/A	#N/A	-1.27	#N/A	tetrapeptide repeat domain 4
ENSG00000156697	#N/A	#N/A	#N/A	-1.27	#N/A	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)
ENSG00000115232	#N/A	#N/A	#N/A	-1.27	#N/A	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)
ENSG000003087087	#N/A	#N/A	#N/A	-1.27	#N/A	serrate, RNA effector molecule
ENSG000003086200	#N/A	#N/A	#N/A	-1.27	#N/A	importin 11
ENSG00000188352	#N/A	#N/A	#N/A	-1.27	#N/A	locadhesin
ENSG00000184818	#N/A	#N/A	#N/A	-1.27	#N/A	dynein, axonemal, assembly factor 5
ENSG00000134748	#N/A	#N/A	#N/A	-1.27	#N/A	pre-mRNA processing factor 36A
ENSG00000138028	#N/A	#N/A	#N/A	-1.27	#N/A	cell growth regulator with EF-hand domain 1
ENSG00000255587	#N/A	#N/A	#N/A	-1.28	#N/A	RAB44, member RAS oncogene family
ENSG00000145725	#N/A	#N/A	#N/A	-1.28	#N/A	diphosphoinositol pentakisphosphate kinase 2
ENSG00000198824	#N/A	#N/A	#N/A	-1.28	#N/A	chromosome alignment maintaining phosphoprotein 1
ENSG00000125250	#N/A	#N/A	#N/A	-1.28	#N/A	PAN3 poly(A) specific ribonuclease subunit

FIGURE 1K

ENSG00000116741	#N/A	#N/A	#N/A	3.79	#N/A	regulator of G-protein signaling 2
ENSG0000020633	#N/A	#N/A	#N/A	3.79	#N/A	runx-related transcription factor 3
ENSG00000125726	#N/A	#N/A	#N/A	3.77	#N/A	CD70 molecule
ENSG00000243004	#N/A	#N/A	#N/A	3.71	2.82	AC005062.2
ENSG00000114268	#N/A	#N/A	#N/A	3.70	#N/A	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4
ENSG00000185507	#N/A	#N/A	#N/A	3.67	#N/A	interferon regulatory factor 7
ENSG00000153815	#N/A	#N/A	#N/A	3.63	#N/A	c-Maf inducing protein
ENSG00000204103	#N/A	#N/A	#N/A	3.59	#N/A	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog B
ENSG00000163633	#N/A	#N/A	#N/A	3.58	#N/A	chromosome 4 open reading frame 36
ENSG00000102524	#N/A	#N/A	#N/A	3.57	#N/A	tumor necrosis factor (ligand) superfamily, member 13b
ENSG00000196739	#N/A	#N/A	#N/A	3.57	#N/A	collagen, type XXVII, alpha 1
ENSG00000259112	#N/A	#N/A	#N/A	3.56	#N/A	NDUF02-KCTD14 readthrough
ENSG00000088826	#N/A	#N/A	#N/A	3.55	#N/A	spermine oxidase
ENSG00000108313	#N/A	#N/A	#N/A	3.54	#N/A	phospholipid scramblase 1
ENSG00000134326	#N/A	#N/A	#N/A	3.53	#N/A	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial
ENSG00000186918	#N/A	#N/A	#N/A	3.49	1.09	zinc finger protein 395
ENSG00000158768	#N/A	#N/A	#N/A	3.47	#N/A	F11 receptor
ENSG00000124762	#N/A	#N/A	#N/A	3.47	#N/A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
ENSG00000049323	#N/A	#N/A	#N/A	3.47	#N/A	latent transforming growth factor beta binding protein 1
ENSG00000138640	#N/A	#N/A	#N/A	3.46	#N/A	family with sequence similarity 13, member A
ENSG00000275585	#N/A	#N/A	#N/A	3.45	#N/A	arachidonate 5-lipoxygenase
ENSG00000213741	#N/A	#N/A	#N/A	3.42	2.02	ribosomal protein S29
ENSG00000130402	#N/A	#N/A	#N/A	3.42	1.80	actinin, alpha 4
ENSG00000251474	#N/A	#N/A	#N/A	3.39	#N/A	ribosomal protein L32 pseudogene 3
ENSG00000177410	#N/A	#N/A	#N/A	3.37	1.74	ZNFX1 antisense RNA 1
ENSG00000138433	#N/A	#N/A	#N/A	3.32	2.15	corepressor interacting with RBPJ, 1
ENSG00000267855	#N/A	#N/A	#N/A	3.28	2.60	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa
ENSG00000115165	#N/A	#N/A	#N/A	3.28	#N/A	cytohesin 1 interacting protein
ENSG00000109107	#N/A	#N/A	#N/A	3.25	#N/A	aldolase C, fructose-bisphosphate
ENSG00000307262	#N/A	#N/A	#N/A	3.21	#N/A	prolyl 4-hydroxylase, alpha polypeptide II
ENSG00000138496	#N/A	#N/A	#N/A	3.19	#N/A	poly (ADP-ribose) polymerase family, member 9
ENSG00000111674	#N/A	#N/A	#N/A	3.17	#N/A	enolase 2 (gamma, neuronal)
ENSG00000165029	#N/A	#N/A	#N/A	3.17	#N/A	ATP-binding cassette, sub-family A (ABC1), member 1
ENSG00000101745	#N/A	#N/A	#N/A	3.17	2.19	ankyrin repeat domain 12
ENSG00000259529	#N/A	#N/A	#N/A	3.15	#N/A	Uncharacterized protein
ENSG00000163823	#N/A	#N/A	#N/A	3.15	#N/A	chemokine (C-C motif) receptor 1
ENSG00000160593	#N/A	#N/A	#N/A	3.13	#N/A	adhesion molecule, interacts with CXADR antigen 1
ENSG00000166012	#N/A	#N/A	#N/A	3.10	2.17	TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa
ENSG00000119547	#N/A	#N/A	#N/A	3.06	#N/A	one cut homeobox 2
ENSG00000160932	#N/A	#N/A	#N/A	3.06	#N/A	lymphocyte antigen 6 complex, locus E
ENSG00000187837	#N/A	#N/A	#N/A	3.05	#N/A	histone cluster 1, H1c
ENSG00000186660	#N/A	#N/A	#N/A	3.04	#N/A	ZFP91 zinc finger protein
ENSG00000171856	#N/A	#N/A	#N/A	3.03	1.93	ribosomal protein S21
ENSG00000206053	#N/A	#N/A	#N/A	-1.28	#N/A	hematological and neurological expressed 1-like
ENSG00000007376	#N/A	#N/A	#N/A	-1.28	#N/A	RNA pseudouridylyl synthase domain containing 1
ENSG00000150401	#N/A	#N/A	#N/A	-1.28	#N/A	DDN1, defective in culin neddylation 1, domain containing 2
ENSG000000087435	#N/A	#N/A	#N/A	-1.26	#N/A	phosphatase and actin regulator 3
ENSG00000009899	#N/A	#N/A	#N/A	-1.26	#N/A	tRNA methyltransferase 2 homolog A (S. cerevisiae)
ENSG00000161036	#N/A	#N/A	#N/A	-1.28	#N/A	leucine-rich repeats and WD repeat domain containing 1
ENSG00000197906	#N/A	#N/A	#N/A	-1.26	#N/A	methyltransferase like 9
ENSG00000142864	#N/A	#N/A	#N/A	-1.26	#N/A	SERPINE1 mRNA binding protein 1
ENSG00000187796	#N/A	#N/A	#N/A	-1.29	#N/A	caspase recruitment domain family, member 9
ENSG00000169957	#N/A	#N/A	#N/A	-1.29	#N/A	zinc finger protein 758
ENSG00000198648	#N/A	#N/A	#N/A	-1.26	#N/A	serine threonine kinase 39
ENSG00000167790	#N/A	#N/A	#N/A	-1.29	#N/A	major facilitator superfamily domain containing 3
ENSG00000134684	#N/A	#N/A	#N/A	-1.29	#N/A	tyrosyl-tRNA synthetase
ENSG00000007923	#N/A	#N/A	#N/A	-1.26	#N/A	DnaJ (Hsp40) homolog, subfamily C, member 11
ENSG00000183137	#N/A	#N/A	#N/A	-1.29	#N/A	centrosomal protein 57kDa-like 1
ENSG00000153395	#N/A	#N/A	#N/A	-1.29	#N/A	lysophosphatidylcholine acyltransferase 1
ENSG00000151247	#N/A	#N/A	#N/A	-1.30	#N/A	eukaryotic translation initiation factor 4E
ENSG00000135379	#N/A	#N/A	#N/A	-1.30	#N/A	abhydrolase domain containing 17C
ENSG000000092820	#N/A	#N/A	#N/A	-1.30	#N/A	ezrin
ENSG00000151835	#N/A	#N/A	#N/A	-1.30	#N/A	sacsin molecular chaperone
ENSG000000048162	#N/A	#N/A	#N/A	-1.30	1.07	NOP16 nucleolar protein
ENSG00000162402	#N/A	#N/A	#N/A	-1.30	#N/A	ubiquitin specific peptidase 24
ENSG000000096475	#N/A	#N/A	#N/A	-1.30	#N/A	selenophosphate synthetase 1
ENSG00000188976	#N/A	#N/A	#N/A	-1.30	#N/A	NOO2-like nucleolar associated transcriptional repressor
ENSG00000167792	#N/A	#N/A	#N/A	-1.30	#N/A	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa
ENSG00000104884	#N/A	#N/A	#N/A	-1.30	#N/A	excision repair cross-complementation group 2
ENSG00000230903	#N/A	#N/A	#N/A	-1.30	#N/A	RPL9P8
ENSG00000100890	#N/A	#N/A	#N/A	-1.30	#N/A	KIAA0391
ENSG00000128452	#N/A	#N/A	#N/A	-1.31	#N/A	ceramide kinase-like
ENSG000000076248	#N/A	#N/A	#N/A	-1.31	#N/A	uracil DNA glycosylase
ENSG00000165661	#N/A	#N/A	#N/A	-1.31	#N/A	quiescins Q6 sulfhydryl oxidase 2
ENSG00000250067	#N/A	#N/A	#N/A	-1.31	#N/A	YjeF N-terminal domain containing 3
ENSG00000131323	#N/A	#N/A	#N/A	-1.31	#N/A	TNF receptor-associated factor 3
ENSG000000070785	#N/A	#N/A	#N/A	-1.31	#N/A	eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa
ENSG000000057757	#N/A	#N/A	#N/A	-1.31	#N/A	PITH (C-terminal proteasome-interacting domain of thioredoxin-like) domain containing 1
ENSG00000135316	#N/A	#N/A	#N/A	-1.31	#N/A	synaptotagmin binding, cytoplasmic RNA interacting protein
ENSG00000122965	#N/A	#N/A	#N/A	-1.31	#N/A	RNA binding motif protein 19
ENSG00000181472	#N/A	#N/A	#N/A	-1.31	#N/A	zinc finger and BTB domain containing 2
ENSG00000125485	#N/A	#N/A	#N/A	-1.31	#N/A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31
ENSG00000135598	#N/A	#N/A	#N/A	-1.32	#N/A	microtubule associated monooxygenase, calponin and LIM domain containing 1
ENSG00000135763	#N/A	#N/A	#N/A	-1.32	#N/A	URB2 ribosome biogenesis 2 homolog (S. cerevisiae)
ENSG00000228253	#N/A	#N/A	#N/A	-1.32	1.36	MT-ATP8
ENSG00000139842	#N/A	#N/A	#N/A	-1.32	#N/A	culin 4A

FIGURE 1L

ENSG00000169715	#N/A	#N/A	#N/A	3.01	1.39	metallothionein 1E
ENSG00000138642	#N/A	#N/A	#N/A	3.01	#N/A	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6
ENSG00000197555	#N/A	#N/A	#N/A	3.00	#N/A	signal-induced proliferation-associated 1 like 1
ENSG00000177409	#N/A	#N/A	#N/A	2.97	#N/A	sterile alpha motif domain containing 9-like
ENSG00000178726	#N/A	#N/A	#N/A	2.95	3.11	thrombospondin
ENSG00000133059	#N/A	#N/A	#N/A	2.95	#N/A	dual serine/threonine and tyrosine protein kinase
ENSG00000095086	#N/A	#N/A	#N/A	2.94	1.30	hook microtubule-tethering protein 2
ENSG00000176171	#N/A	#N/A	#N/A	2.92	#N/A	BCL2/adenovirus E1B 19kDa interacting protein 3
ENSG00000170412	#N/A	#N/A	#N/A	2.92	#N/A	G protein-coupled receptor, class C, group 5, member C
ENSG00000141905	#N/A	#N/A	#N/A	2.92	2.13	nuclear factor I/C (CCAAT-binding transcription factor)
ENSG00000134597	#N/A	#N/A	#N/A	2.91	2.28	RNA binding motif protein, X-linked 2
ENSG00000181890	#N/A	#N/A	#N/A	2.89	#N/A	pleomorphic adenoma gene 1
ENSG00000147872	#N/A	#N/A	#N/A	2.89	#N/A	perilipin 2
ENSG00000267121	#N/A	#N/A	#N/A	2.87	#N/A	CTD-2020K17.1
ENSG00000134955	#N/A	#N/A	#N/A	2.87	#N/A	solute carrier family 37 (glucose-6-phosphate transporter), member 2
ENSG00000173821	#N/A	#N/A	#N/A	2.86	#N/A	ring finger protein 213
ENSG00000153006	#N/A	#N/A	#N/A	2.85	2.34	SREK1-interacting protein 1
ENSG00000184675	#N/A	#N/A	#N/A	2.85	#N/A	histone cluster 2, H2be
ENSG00000203875	#N/A	#N/A	#N/A	2.84	1.98	small nucleolar RNA host gene 5
ENSG00000131944	#N/A	#N/A	#N/A	2.84	#N/A	Fanconi anemia core complex associated protein 24
ENSG00000122884	#N/A	#N/A	#N/A	2.84	#N/A	prolyl 4-hydroxylase, alpha polypeptide 1
ENSG00000055332	#N/A	#N/A	#N/A	2.84	#N/A	eukaryotic translation initiation factor 2-alpha kinase 2
ENSG00000270316	#N/A	#N/A	#N/A	2.82	#N/A	C10orf32-ASMT readthrough (NMD candidate)
ENSG00000197013	#N/A	#N/A	#N/A	2.81	#N/A	zinc finger protein 429
ENSG00000165071	#N/A	#N/A	#N/A	2.79	#N/A	transmembrane protein 71
ENSG00000270862	#N/A	#N/A	#N/A	2.78	#N/A	histone cluster 2, H4a
ENSG00000177954	#N/A	#N/A	#N/A	2.77	1.98	ribosomal protein S27
ENSG00000146192	#N/A	#N/A	#N/A	2.76	#N/A	FYVE, RhoGEF and PH domain containing 2
ENSG00000067082	#N/A	#N/A	#N/A	2.75	1.37	Kruppel-like factor 6
ENSG00000143315	#N/A	#N/A	#N/A	2.74	#N/A	phosphatidylinositol glycan anchor biosynthesis, class M
ENSG00000280755	#N/A	#N/A	#N/A	2.73	#N/A	SP110 nuclear body protein
ENSG00000171766	#N/A	#N/A	#N/A	2.73	#N/A	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
ENSG00000132274	#N/A	#N/A	#N/A	2.73	#N/A	tripartite motif containing 22
ENSG00000118515	#N/A	#N/A	#N/A	2.73	#N/A	serum/glucocorticoid regulated kinase 1
ENSG00000140941	#N/A	#N/A	#N/A	2.72	#N/A	microtubule-associated protein 1 light chain 3 beta
ENSG00000162956	#N/A	#N/A	#N/A	2.70	#N/A	mediator of cell motility 1
ENSG00000169403	#N/A	#N/A	#N/A	2.67	#N/A	platelet-activating factor receptor
ENSG00000205413	#N/A	#N/A	#N/A	2.67	#N/A	sterile alpha motif domain containing 9
ENSG00000098952	#N/A	#N/A	#N/A	2.66	2.15	SEC62 homolog (S. cerevisiae)
ENSG00000088886	#N/A	#N/A	#N/A	2.65	1.19	mitochondrial antiviral signaling protein
ENSG00000139626	#N/A	#N/A	#N/A	2.65	#N/A	integrin, beta 7
ENSG00000100592	#N/A	#N/A	#N/A	2.64	#N/A	dishevelled associated activator of morphogenesis 1
ENSG00000197358	#N/A	#N/A	#N/A	2.62	#N/A	BCL2/adenovirus E1B 19kDa interacting protein 3 pseudogene 1
ENSG00000113140	#N/A	#N/A	#N/A	2.61	#N/A	secreted protein, acidic, cysteine-rich (osteonectin)
ENSG00000104765	#N/A	#N/A	#N/A	2.58	#N/A	BCL2/adenovirus E1B 19kDa interacting protein 3-like
ENSG00000135916	#N/A	#N/A	#N/A	2.55	#N/A	integral membrane protein 2C

ENSG00000033011	#N/A	#N/A	#N/A	-1.32	#N/A	ALG1, chitobiosyl(diphosphochololol beta-mannosyltransferase
ENSG00000237550	#N/A	#N/A	#N/A	-1.32	#N/A	RPL3P9
ENSG00000148540	#N/A	#N/A	#N/A	-1.33	#N/A	chromosome 7 open reading frame 50
ENSG00000099901	#N/A	#N/A	#N/A	-1.33	#N/A	RAN binding protein 1
ENSG00000107815	#N/A	#N/A	#N/A	-1.33	#N/A	chromosome 10 open reading frame 2
ENSG00000101220	#N/A	#N/A	#N/A	-1.33	#N/A	chromosome 20 open reading frame 27
ENSG00000112787	#N/A	#N/A	#N/A	-1.33	#N/A	fibrosin-like 1
ENSG00000122566	#N/A	#N/A	#N/A	-1.33	#N/A	heterogeneous nuclear ribonucleoprotein A2/B1
ENSG00000072274	#N/A	#N/A	#N/A	-1.33	#N/A	transferrin receptor
ENSG00000148300	#N/A	#N/A	#N/A	-1.33	#N/A	REX4 homolog, 3'-5' exonuclease
ENSG00000099949	#N/A	#N/A	#N/A	-1.33	#N/A	leucine-zipper-like transcription regulator 1
ENSG00000174744	#N/A	#N/A	#N/A	-1.33	#N/A	breast cancer metastasis suppressor 1
ENSG00000154163	#N/A	#N/A	#N/A	-1.33	#N/A	ATP-binding cassette, sub-family E (ABP), member 1
ENSG00000110042	#N/A	#N/A	#N/A	-1.33	#N/A	deltex 4, E3 ubiquitin ligase
ENSG00000138074	#N/A	#N/A	#N/A	-1.33	#N/A	solute carrier family 5 (sodium/multivitamin and iodide cotransporter), member 6
ENSG00000165724	#N/A	#N/A	#N/A	-1.34	#N/A	zinc finger, MYND-type containing 19
ENSG00000136718	#N/A	#N/A	#N/A	-1.34	#N/A	IMP4, U3 small nucleolar ribonucleoprotein
ENSG00000197498	#N/A	#N/A	#N/A	-1.34	#N/A	ribosome production factor 2 homolog
ENSG00000154277	#N/A	#N/A	#N/A	-1.34	#N/A	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thioesterase)
ENSG00000172232	#N/A	#N/A	#N/A	-1.34	#N/A	azurocidin 1
ENSG00000177225	#N/A	#N/A	#N/A	-1.34	#N/A	Parkinson disease 7 domain containing 1
ENSG00000125910	#N/A	#N/A	#N/A	-1.34	#N/A	sphingosine-1-phosphate receptor 4
ENSG00000162408	#N/A	#N/A	#N/A	-1.34	#N/A	nucleolar protein 9
ENSG00000117450	#N/A	#N/A	#N/A	-1.34	#N/A	peroxiredoxin 1
ENSG000000933050	#N/A	#N/A	#N/A	-1.34	#N/A	ATP-binding cassette, sub-family F (GGN20), member 2
ENSG00000142875	#N/A	#N/A	#N/A	-1.34	#N/A	protein kinase, cAMP-dependent, catalytic, beta
ENSG00000133422	#N/A	#N/A	#N/A	-1.34	#N/A	MORC family CW-type zinc finger 2
ENSG000000565978	#N/A	#N/A	#N/A	-1.34	#N/A	Y box binding protein 1
ENSG00000158066	#N/A	#N/A	#N/A	-1.34	#N/A	splicing factor 1
ENSG00000048052	#N/A	#N/A	#N/A	-1.34	#N/A	histone deacetylase 9
ENSG00000142409	#N/A	#N/A	#N/A	-1.35	#N/A	zinc finger protein 737
ENSG00000148334	#N/A	#N/A	#N/A	-1.35	#N/A	prostaglandin E synthase 2
ENSG00000163291	#N/A	#N/A	#N/A	-1.35	#N/A	progesterin and adipoQ receptor family member III
ENSG00000155393	#N/A	#N/A	#N/A	-1.35	#N/A	HEAT repeat containing 3
ENSG00000158106	#N/A	#N/A	#N/A	-1.35	#N/A	ubiquitin-conjugating enzyme E2S
ENSG00000174547	#N/A	#N/A	#N/A	-1.35	#N/A	mitochondrial ribosomal protein L11
ENSG00000144867	#N/A	#N/A	#N/A	-1.35	#N/A	signal recognition particle receptor, B subunit
ENSG00000154207	#N/A	#N/A	#N/A	-1.35	#N/A	phosphoglycolate phosphatase
ENSG00000130638	#N/A	#N/A	#N/A	-1.35	#N/A	ataxin 10
ENSG00000091084	#N/A	#N/A	#N/A	-1.35	#N/A	glutamate-cysteine ligase, catalytic subunit
ENSG00000228875	#N/A	#N/A	#N/A	-1.35	#N/A	casein kinase 2, beta polypeptide
ENSG00000104341	#N/A	#N/A	#N/A	-1.35	#N/A	lysosomal protein transmembrane 4 beta
ENSG00000117419	#N/A	#N/A	#N/A	-1.35	#N/A	ERH1 exonuclease family member 3
ENSG00000184281	#N/A	#N/A	#N/A	-1.35	#N/A	tumor suppressing subtransferable candidate 4
ENSG00000173145	#N/A	#N/A	#N/A	-1.36	#N/A	NOC3-like DNA replication regulator
ENSG00000073960	#N/A	#N/A	#N/A	-1.36	#N/A	scavenger receptor class B, member 1

FIGURE 1M

ENSG00000171475	#N/A	#N/A	#N/A	2.55	#N/A	WAS/WASL interacting protein family, member 2
ENSG00000274233	#N/A	#N/A	#N/A	2.55	#N/A	chemokine (C-C motif) ligand 5
ENSG00000163565	#N/A	#N/A	#N/A	2.54	#N/A	interferon, gamma-inducible protein 16
ENSG00000155926	#N/A	#N/A	#N/A	2.54	#N/A	Src-like adaptor
ENSG00000138172	#N/A	#N/A	#N/A	2.53	#N/A	calcium homeostasis modulator 2
ENSG00000171724	#N/A	#N/A	#N/A	2.53	#N/A	vesicle amine transport 1-like
ENSG00000197063	#N/A	#N/A	#N/A	2.53	1.54	y-maf avian musculosarcomatous fibrosarcoma oncogene homolog G
ENSG00000171860	#N/A	#N/A	#N/A	2.52	#N/A	complement component 3a receptor 1
ENSG00000108771	#N/A	#N/A	#N/A	2.52	#N/A	DEXH (Asp-Glu-X-His) box polypeptide 58
ENSG00000137815	#N/A	#N/A	#N/A	2.52	1.82	RTF1 homolog, Pat1/RNA polymerase II complex component
ENSG00000103111	#N/A	#N/A	#N/A	2.52	#N/A	MON1 secretory trafficking family member B
ENSG00000217555	#N/A	#N/A	#N/A	2.51	#N/A	chemokine-like factor
ENSG00000189060	#N/A	#N/A	#N/A	2.49	1.05	H1 histone family, member 0
ENSG00000165233	#N/A	#N/A	#N/A	2.48	1.71	chromosome 9 open reading frame 89
ENSG00000278550	#N/A	#N/A	#N/A	2.48	#N/A	solute carrier family 43 (amino acid system L transporter), member 2
ENSG00000078053	#N/A	#N/A	#N/A	2.47	#N/A	RNA binding motif protein 7
ENSG00000138646	#N/A	#N/A	#N/A	2.47	#N/A	HECT and RLD domain containing E3 ubiquitin protein ligase 5
ENSG00000234545	#N/A	#N/A	#N/A	2.44	2.26	family with sequence similarity 133, member 8
ENSG00000135316	#N/A	#N/A	#N/A	2.44	#N/A	5'-nucleotidase, ecto (CD73)
ENSG00000141027	#N/A	#N/A	#N/A	2.44	#N/A	nuclear receptor corepressor 1
ENSG00000104081	#N/A	#N/A	#N/A	2.43	#N/A	Bcl2 modifying factor
ENSG00000139289	#N/A	#N/A	#N/A	2.42	#N/A	pleckstrin homology-like domain, family A, member 1
ENSG00000270898	#N/A	#N/A	#N/A	2.42	1.57	GPR75-ASB3 readthrough
ENSG00000138061	#N/A	#N/A	#N/A	2.42	3.33	cytochrome P450, family 1, subfamily B, polypeptide 1
ENSG000000007944	#N/A	#N/A	#N/A	2.41	#N/A	myosin regulatory light chain interacting protein
ENSG00000167851	#N/A	#N/A	#N/A	2.41	#N/A	CD300a molecule
ENSG00000173193	#N/A	#N/A	#N/A	2.41	#N/A	poly (ADP-ribose) polymerase family, member 14
ENSG00000107201	#N/A	#N/A	#N/A	2.40	#N/A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
ENSG00000090938	#N/A	#N/A	#N/A	2.39	#N/A	FGR proto-oncogene, Src family tyrosine kinase
ENSG00000125676	#N/A	#N/A	#N/A	2.39	1.85	THO complex 2
ENSG00000123354	#N/A	#N/A	#N/A	2.38	#N/A	low density lipoprotein receptor-related protein 1
ENSG00000132530	#N/A	#N/A	#N/A	2.38	#N/A	XIAP associated factor 1
ENSG00000142088	#N/A	#N/A	#N/A	2.36	#N/A	interferon induced transmembrane protein 3
ENSG00000158373	#N/A	#N/A	#N/A	2.36	#N/A	histone cluster 1, H2bd
ENSG00000111424	#N/A	#N/A	#N/A	2.36	#N/A	vitamin D (1,25-dihydroxyvitamin D3) receptor
ENSG00000188177	#N/A	#N/A	#N/A	2.35	#N/A	zinc finger CCHC-type containing 6
ENSG00000196968	#N/A	#N/A	#N/A	2.34	#N/A	fucosyltransferase 11 (alpha (1,3) fucosyltransferase)
ENSG00000139168	#N/A	#N/A	#N/A	2.33	1.71	zinc finger CCHC-type and RNA binding motif 1
ENSG00000272886	#N/A	#N/A	#N/A	2.33	#N/A	decapping mRNA 1A
ENSG00000258472	#N/A	#N/A	#N/A	2.33	#N/A	Uncharacterized protein
ENSG00000171992	#N/A	#N/A	#N/A	2.33	#N/A	synaptotagmin
ENSG00000162599	#N/A	#N/A	#N/A	2.33	#N/A	nuclear factor I/A
ENSG00000143847	#N/A	#N/A	#N/A	2.33	#N/A	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4
ENSG00000155502	#N/A	#N/A	#N/A	-1.36	#N/A	suppressor of var1, 3-like 1 (S. cerevisiae)
ENSG00000272325	#N/A	#N/A	#N/A	-1.36	#N/A	nucleoside diphosphate linked moiety X-type motif 3
ENSG00000098584	#N/A	#N/A	#N/A	-1.36	#N/A	heat shock protein 90kDa alpha (cytosolic), class B member 1
ENSG00000289713	#N/A	#N/A	#N/A	-1.36	#N/A	neuroblastoma breakpoint family, member 9
ENSG00000213339	#N/A	#N/A	#N/A	-1.36	#N/A	queuine tRNA-ribosyltransferase 1
ENSG00000145220	#N/A	#N/A	#N/A	-1.37	#N/A	Ly1 antibody reactive
ENSG00000006744	#N/A	#N/A	#N/A	-1.37	#N/A	elic ribonuclease Z 2
ENSG00000005844	#N/A	#N/A	#N/A	-1.37	#N/A	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)
ENSG00000050393	#N/A	#N/A	#N/A	-1.37	#N/A	mitochondrial calcium uniporter regulator 1
ENSG00000185138	#N/A	#N/A	#N/A	-1.37	#N/A	ankyrin repeat and sterile alpha motif domain containing 6
ENSG00000105447	#N/A	#N/A	#N/A	-1.37	#N/A	glutamate-rich WD repeat containing 1
ENSG00000185198	#N/A	#N/A	#N/A	-1.38	#N/A	protease, serine, 57
ENSG00000135002	#N/A	#N/A	#N/A	-1.38	#N/A	riboflavin kinase
ENSG00000068383	#N/A	#N/A	#N/A	-1.38	#N/A	inositol polyphosphate-5-phosphatase, 40kDa
ENSG00000149557	#N/A	#N/A	#N/A	-1.38	#N/A	fasciculation and elongation protein zeta 1 (zyglin 1)
ENSG00000235569	#N/A	#N/A	#N/A	-1.38	#N/A	mutS homolog 5
ENSG00000124587	#N/A	#N/A	#N/A	-1.38	#N/A	peroxisomal biogenesis factor 6
ENSG00000005379	#N/A	#N/A	#N/A	-1.38	#N/A	benzodiazepine receptor (peripheral) associated protein 1
ENSG00000144381	#N/A	#N/A	#N/A	-1.38	#N/A	heat shock 60kDa protein 1 (chaperonin)
ENSG00000110619	#N/A	#N/A	#N/A	-1.38	#N/A	cysteine tRNA synthetase
ENSG00000146433	#N/A	#N/A	#N/A	-1.38	#N/A	transmembrane protein 181
ENSG000000074071	#N/A	#N/A	#N/A	-1.39	#N/A	mitochondrial ribosomal protein S34
ENSG00000124562	#N/A	#N/A	#N/A	-1.39	#N/A	small nuclear ribonucleoprotein polypeptide C
ENSG00000100401	#N/A	#N/A	#N/A	-1.39	#N/A	Ran GTPase activating protein 1
ENSG00000114767	#N/A	#N/A	#N/A	-1.39	#N/A	ribosomal RNA processing 9, small subunit (SSU) processome component, homolog (yeast)
ENSG00000155229	#N/A	#N/A	#N/A	-1.39	#N/A	MRP19 homolog, cytosolic iron-sulfur assembly component
ENSG00000228300	#N/A	#N/A	#N/A	-1.39	#N/A	chromosome 19 open reading frame 24
ENSG00000122025	#N/A	#N/A	#N/A	-1.39	#N/A	fms-related tyrosine kinase 3
ENSG00000140750	#N/A	#N/A	#N/A	-1.39	#N/A	Rho GTPase activating protein 17
ENSG0000005047188	#N/A	#N/A	#N/A	-1.39	#N/A	YTH domain containing 2
ENSG00000175022	#N/A	#N/A	#N/A	-1.39	#N/A	UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptide 6
ENSG00000164164	#N/A	#N/A	#N/A	-1.40	#N/A	OTU deubiquitinase 4
ENSG00000121718	#N/A	#N/A	#N/A	-1.40	#N/A	paired immunoglobulin-like type 2 receptor beta
ENSG00000111066	#N/A	#N/A	#N/A	-1.40	#N/A	choline phosphotransferase 1
ENSG00000113013	#N/A	#N/A	#N/A	-1.40	#N/A	heat shock 70kDa protein 9 (mortalin)
ENSG00000136261	#N/A	#N/A	#N/A	-1.40	#N/A	basic leucine zipper and W2 domains 2
ENSG00000105211	#N/A	#N/A	#N/A	-1.40	#N/A	heat shock 27kDa protein 1
ENSG00000160208	#N/A	#N/A	#N/A	-1.40	#N/A	ribosomal RNA processing 1B
ENSG00000204839	#N/A	#N/A	#N/A	-1.40	#N/A	maestro heat-like repeat family member 6
ENSG00000179051	#N/A	#N/A	#N/A	-1.40	#N/A	regulator of chromosome condensation 2
ENSG00000153811	#N/A	#N/A	#N/A	-1.40	#N/A	WD repeat domain 43
ENSG000000577232	#N/A	#N/A	#N/A	-1.40	#N/A	DnaJ (Hsp40) homolog, subfamily C, member 10
ENSG00000163362	#N/A	#N/A	#N/A	-1.41	#N/A	chromosome 1 open reading frame 106

FIGURE 1N

ENSG00000216496	#N/A	#N/A	#N/A	2.32	1.20	interferon, gamma-inducible protein 30
ENSG00000147894	#N/A	#N/A	#N/A	2.32	#N/A	chromosome 9 open reading frame 72
ENSG00000116017	#N/A	#N/A	#N/A	2.31	#N/A	AT rich interactive domain 3A (RIGHT-like)
ENSG00000148247	#N/A	#N/A	#N/A	2.30	#N/A	pleckstrin homology domain interacting protein
ENSG00000151461	#N/A	#N/A	#N/A	2.30	1.58	UPF2 regulator of nonsense transcripts homolog (yeast)
ENSG00000145012	#N/A	#N/A	#N/A	2.29	#N/A	LIM domain containing preferred translocation partner in lipoma
ENSG00000237727	#N/A	#N/A	#N/A	2.29	#N/A	allograft inflammatory factor 1
ENSG00000180573	#N/A	#N/A	#N/A	2.28	1.45	histone cluster 1, H2ac
ENSG00000108825	#N/A	#N/A	#N/A	2.28	#N/A	long intergenic non-protein coding RNA 910
ENSG00000143546	#N/A	#N/A	#N/A	2.28	#N/A	S100 calcium binding protein A8
ENSG00000101384	#N/A	#N/A	#N/A	2.26	#N/A	jagged 1
ENSG00000271605	#N/A	#N/A	#N/A	2.26	#N/A	mast cell immunoglobulin-like receptor 1
ENSG00000127920	#N/A	#N/A	#N/A	2.27	#N/A	guanine nucleotide binding protein (G protein), gamma 11
ENSG00000183486	#N/A	#N/A	#N/A	2.27	#N/A	MX dynamin-like GTPase 2
ENSG00000135185	#N/A	#N/A	#N/A	2.26	1.53	transmembrane protein 243, mitochondrial
ENSG00000130208	#N/A	#N/A	#N/A	2.26	#N/A	apolipoprotein C-I
ENSG00000172831	#N/A	#N/A	#N/A	2.26	#N/A	carboxylesterase 2
ENSG00000159140	#N/A	#N/A	#N/A	2.25	#N/A	SON DNA binding protein
ENSG00000197323	#N/A	#N/A	#N/A	2.24	1.91	tripartite motif containing 33
ENSG00000183354	#N/A	#N/A	#N/A	2.22	#N/A	KIAA2026
ENSG00000145592	#N/A	#N/A	#N/A	2.22	#N/A	ribosomal protein L37
ENSG00000156603	#N/A	#N/A	#N/A	2.22	1.56	mediator complex subunit 19
ENSG00000169439	#N/A	#N/A	#N/A	2.21	#N/A	syndecan 2
ENSG00000165801	#N/A	#N/A	#N/A	2.21	#N/A	Rho guanine nucleotide exchange factor (GEF) 40
ENSG00000138266	#N/A	#N/A	#N/A	2.20	#N/A	membrane-associated ring finger (C3HC4) 9
ENSG00000182209	#N/A	#N/A	#N/A	2.20	1.64	ribosomal protein L35a
ENSG00000147443	#N/A	#N/A	#N/A	2.20	#N/A	docking protein 2, 56kDa
ENSG00000101966	#N/A	#N/A	#N/A	2.19	1.71	X-linked inhibitor of apoptosis, E3 ubiquitin protein ligase
ENSG00000168209	#N/A	#N/A	#N/A	2.19	#N/A	DNA-damage-inducible transcript 4
ENSG00000126759	#N/A	#N/A	#N/A	2.18	#N/A	complement factor properdin
ENSG00000196199	#N/A	#N/A	#N/A	2.18	1.60	M-phase phosphoprotein 8
ENSG00000164096	#N/A	#N/A	#N/A	2.18	#N/A	chromosome 4 open reading frame 3
ENSG00000165355	#N/A	#N/A	#N/A	2.17	#N/A	F-box protein 33
ENSG00000166482	#N/A	#N/A	#N/A	2.17	#N/A	microfibrillar-associated protein 4
ENSG00000188157	#N/A	#N/A	#N/A	2.16	#N/A	agrin
ENSG00000204130	#N/A	#N/A	#N/A	2.16	#N/A	RUN and FYVE domain containing 2
ENSG00000178951	#N/A	#N/A	#N/A	2.15	1.24	zinc finger and BTB domain containing 7A
ENSG00000205822	#N/A	#N/A	#N/A	2.15	#N/A	protein phosphatase 1, regulatory subunit 12A
ENSG00000275342	#N/A	#N/A	#N/A	2.15	1.14	Tyrosine-protein kinase SgK223
ENSG00000205756	#N/A	#N/A	#N/A	2.14	#N/A	crystallin, zeta (quinone reductase)-like 1
ENSG000002099337	#N/A	#N/A	#N/A	2.14	1.60	potassium channel, two pore domain subfamily K, member 6
ENSG00000160602	#N/A	#N/A	#N/A	2.13	#N/A	NIMA-related kinase 9
ENSG00000174936	#N/A	#N/A	#N/A	2.13	#N/A	seizure related 6 homolog (mouse)-like 2
ENSG00000104419	#N/A	#N/A	#N/A	2.13	#N/A	N-myc downstream regulated 1
ENSG00000229314	#N/A	#N/A	#N/A	2.13	#N/A	orosomucoid 1

ENSG00000184110	#N/A	#N/A	#N/A	-1.41	#N/A	eukaryotic translation initiation factor 3, subunit C
ENSG00000170144	#N/A	#N/A	#N/A	-1.41	#N/A	heterogeneous nuclear ribonucleoprotein A3
ENSG00000169714	#N/A	#N/A	#N/A	-1.41	#N/A	CCHC-type zinc finger, nucleic acid binding protein
ENSG00000169683	#N/A	#N/A	#N/A	-1.41	#N/A	leucine rich repeat containing 45
ENSG00000188807	#N/A	#N/A	#N/A	-1.41	#N/A	transmembrane protein 201
ENSG00000181666	#N/A	#N/A	#N/A	-1.41	#N/A	HKR1, GLI-Kruppel zinc finger family member
ENSG00000105281	#N/A	#N/A	#N/A	-1.41	#N/A	solute carrier family 1 (neutral amino acid transporter), member 5
ENSG00000184220	#N/A	#N/A	#N/A	-1.41	#N/A	oms1 ribosomal small subunit homolog (yeast)
ENSG00000148362	#N/A	#N/A	#N/A	-1.41	#N/A	chromosome 9 open reading frame 142
ENSG00000198786	#N/A	#N/A	#N/A	-1.42	#N/A	mitochondrially encoded NADH dehydrogenase 5
ENSG00000148824	#N/A	#N/A	#N/A	-1.42	#N/A	mitochondrial ribosome-associated GTPase 1
ENSG00000152620	#N/A	#N/A	#N/A	-1.42	#N/A	NAD kinase 2, mitochondrial
ENSG00000175857	#N/A	#N/A	#N/A	-1.42	#N/A	GRB2-binding adaptor protein, transmembrane
ENSG00000131778	#N/A	#N/A	#N/A	-1.42	#N/A	chromodomain helicase DNA binding protein 1-like
ENSG00000158715	#N/A	#N/A	#N/A	-1.43	#N/A	solute carrier family 45, member 3
ENSG00000140891	#N/A	#N/A	#N/A	-1.44	#N/A	amadiro repeat containing 5
ENSG00000205854	#N/A	#N/A	#N/A	-1.44	#N/A	polymerase (RNA) I polypeptide A, 194kDa
ENSG00000181029	#N/A	#N/A	#N/A	-1.44	#N/A	trafficking protein particle complex 5
ENSG000002074582	#N/A	#N/A	#N/A	-1.44	#N/A	BC1 (ubiquinol-cytochrome c reductase) synthesis-like
ENSG00000120053	#N/A	#N/A	#N/A	-1.44	#N/A	glutamic-oxaloacetic transaminase 1, soluble
ENSG00000101255	#N/A	#N/A	#N/A	-1.45	#N/A	hibbles pseudokinase 3
ENSG00000108963	#N/A	#N/A	#N/A	-1.45	#N/A	diphthamide biosynthesis 1
ENSG00000198868	#N/A	#N/A	#N/A	-1.45	#N/A	MT-ND4
ENSG00000101444	#N/A	#N/A	#N/A	-1.45	#N/A	adenosylhomocysteinase
ENSG00000140743	#N/A	#N/A	#N/A	-1.45	#N/A	cerebellar degeneration-related protein 2, 62kDa
ENSG00000142686	#N/A	#N/A	#N/A	-1.45	#N/A	chromosome 1 open reading frame 216
ENSG00000214753	#N/A	#N/A	#N/A	-1.45	#N/A	heterogeneous nuclear ribonucleoprotein U-like 2
ENSG00000104835	#N/A	#N/A	#N/A	-1.45	#N/A	seryl-tRNA synthetase 2, mitochondrial
ENSG00000167685	#N/A	#N/A	#N/A	-1.45	#N/A	zinc finger protein 444
ENSG00000198945	#N/A	#N/A	#N/A	-1.45	#N/A	33ymlt-like 3 (Drosophila)
ENSG00000130713	#N/A	#N/A	#N/A	-1.46	#N/A	exosome component 2
ENSG00000209830	#N/A	#N/A	#N/A	-1.46	#N/A	protein-O-mannosyltransferase 2
ENSG00000149150	#N/A	#N/A	#N/A	-1.46	#N/A	solute carrier family 43 (amino acid system L transporter), member 1
ENSG000002084774	#N/A	#N/A	#N/A	-1.48	#N/A	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase
ENSG00000270629	#N/A	#N/A	#N/A	-1.46	#N/A	neuroblastoma breakpoint family, member 14
ENSG00000205560	#N/A	#N/A	#N/A	-1.46	#N/A	carotene palmitoyltransferase 1B (muscle)
ENSG00000148843	#N/A	#N/A	#N/A	-1.46	#N/A	programmed cell death 11
ENSG00000178718	#N/A	#N/A	#N/A	-1.46	#N/A	ribonuclease P/MRP 25kDa subunit
ENSG00000130826	#N/A	#N/A	#N/A	-1.46	#N/A	dykeratosis congenita 1, dyskerin
ENSG00000132361	#N/A	#N/A	#N/A	-1.46	#N/A	clustered mitochondria (cluA/CLU1) homolog
ENSG00000214160	#N/A	#N/A	#N/A	-1.46	#N/A	ALG3, alpha-1,3- mannosyltransferase
ENSG00000128973	#N/A	#N/A	#N/A	-1.47	#N/A	steroid-lipofuscinosis, neuronal 6, late infantile, variant
ENSG00000214705	#N/A	#N/A	#N/A	-1.47	#N/A	interferon-related developmental regulator 2
ENSG00000137168	#N/A	#N/A	#N/A	-1.47	#N/A	peptidylprolyl isomerase (cyclophilin)-like 1
ENSG00000125257	#N/A	#N/A	#N/A	-1.47	#N/A	ATP-binding cassette, sub-family C (CFTR/MRP), member 4

FIGURE 10

ENSG0000059804	#N/A	#N/A	#N/A	2.12	#N/A	solute carrier family 2 (facilitated glucose transporter), member 3
ENSG00000139278	#N/A	#N/A	#N/A	2.11	#N/A	GLI pathogenesis-related 1
ENSG00000157350	#N/A	#N/A	#N/A	2.10	#N/A	ST3 beta-galactoside alpha-2,3-sialyltransferase 2
ENSG00000146275	#N/A	#N/A	#N/A	2.10	#N/A	proline-rich nuclear receptor coactivator 1
ENSG00000119004	#N/A	#N/A	#N/A	2.10	#N/A	cytochrome P450, family 20, subfamily A, polypeptide 1
ENSG00000121281	#N/A	#N/A	#N/A	2.09	#N/A	adenylate cyclase 7
ENSG00000245209	#N/A	#N/A	#N/A	2.06	#N/A	AP001007.1
ENSG00000204054	#N/A	#N/A	#N/A	2.08	3.38	long intergenic non-protein coding RNA 963
ENSG00000166595	#N/A	#N/A	#N/A	2.08	1.08	family with sequence similarity 96, member 8
ENSG00000160613	#N/A	#N/A	#N/A	2.07	#N/A	proprotein convertase subtilisin/kexin type 7
ENSG00000103248	#N/A	#N/A	#N/A	2.07	#N/A	methylenetetrahydrofolate synthetase domain containing
ENSG00000162645	#N/A	#N/A	#N/A	2.06	#N/A	guanylate binding protein 2, interferon-inducible
ENSG00000135216	#N/A	#N/A	#N/A	2.05	#N/A	CD38 molecule (thrombospondin receptor)
ENSG00000120688	#N/A	#N/A	#N/A	2.05	2.08	WW domain binding protein 4
ENSG00000059728	#N/A	#N/A	#N/A	2.05	#N/A	MAX dimerization protein 1
ENSG00000196227	#N/A	#N/A	#N/A	2.05	#N/A	family with sequence similarity 217, member 8
ENSG00000198863	#N/A	#N/A	#N/A	2.05	#N/A	RUN domain containing 1
ENSG00000136826	#N/A	#N/A	#N/A	2.05	#N/A	Kruppel-like factor 4 (gut)
ENSG00000233927	#N/A	#N/A	#N/A	2.04	#N/A	ribosomal protein S28
ENSG00000179085	#N/A	#N/A	#N/A	2.04	2.39	dolichyl-phosphate mannosyltransferase polypeptide 3
ENSG00000065089	#N/A	#N/A	#N/A	2.04	#N/A	phosphodiesterase 4A, cAMP-specific
ENSG00000129667	#N/A	#N/A	#N/A	2.03	#N/A	rhomboid 5 homolog 2 (Drosophila)
ENSG00000116977	#N/A	#N/A	#N/A	2.03	#N/A	lectin, galactoside-binding, soluble, 8
ENSG00000242711	#N/A	#N/A	#N/A	2.02	#N/A	proteasome (prosome, macropain) subunit, beta type, 9
ENSG00000135637	#N/A	#N/A	#N/A	2.01	2.03	coiled-coil domain containing 142
ENSG00000186162	#N/A	#N/A	#N/A	2.01	#N/A	cell death-inducing DFFA-like effector c pseudogene
ENSG00000197956	#N/A	#N/A	#N/A	2.00	1.50	S100 calcium binding protein A6
ENSG00000273686	#N/A	#N/A	#N/A	2.00	1.53	beta-2-microglobulin
ENSG00000163536	#N/A	#N/A	#N/A	2.00	#N/A	serpin peptidase inhibitor, clade 1 (neuroserpin), member 1
ENSG00000116667	#N/A	#N/A	#N/A	2.00	#N/A	chromosome 1 open reading frame 21
ENSG00000163221	#N/A	#N/A	#N/A	2.00	#N/A	S100 calcium binding protein A12
ENSG00000235308	#N/A	#N/A	#N/A	1.99	#N/A	major histocompatibility complex, class I, J (pseudogene)
ENSG00000163644	#N/A	#N/A	#N/A	1.99	1.18	protein phosphatase, Mg2+/Mn2+ dependent, 1K
ENSG00000101336	#N/A	#N/A	#N/A	1.98	#N/A	HCK proto-oncogene, Src family tyrosine kinase
ENSG00000130813	#N/A	#N/A	#N/A	1.95	#N/A	chromosome 19 open reading frame 66
ENSG00000110077	#N/A	#N/A	#N/A	1.96	#N/A	membrane-spanning 4-domains, subfamily A, member 6A
ENSG00000140948	#N/A	#N/A	#N/A	1.96	#N/A	zinc finger, CCHC domain containing 14
ENSG00000172809	#N/A	#N/A	#N/A	1.97	1.54	ribosomal protein L38
ENSG00000167207	#N/A	#N/A	#N/A	1.97	#N/A	nucleotide-binding oligomerization domain containing 2
ENSG00000131503	#N/A	#N/A	#N/A	1.97	#N/A	ankyrin repeat and KH domain containing 1
ENSG00000136770	#N/A	#N/A	#N/A	1.97	1.43	DnaJ (Hsp40) homolog, subfamily C, member 1
ENSG00000167604	#N/A	#N/A	#N/A	1.97	#N/A	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, delta
ENSG00000170801	#N/A	#N/A	#N/A	1.96	#N/A	HtrA serine peptidase 3
ENSG00000131067	#N/A	#N/A	#N/A	1.96	#N/A	gamma-glutamyltransferase 7
ENSG00000111981	#N/A	#N/A	#N/A	1.95	#N/A	UL16 binding protein 1
ENSG00000196576	#N/A	#N/A	#N/A	1.94	#N/A	plexin B2
ENSG00000082516	#N/A	#N/A	#N/A	-1.47	#N/A	gem (nuclear organelle) associated protein 5
ENSG00000130726	#N/A	#N/A	#N/A	-1.47	#N/A	tripartite motif containing 28
ENSG00000123545	#N/A	#N/A	#N/A	-1.48	#N/A	NADH dehydrogenase (ubiquinone) complex 1, assembly factor 4
ENSG00000135521	#N/A	#N/A	#N/A	-1.48	#N/A	LTV1 ribosome biogenesis factor
ENSG00000215041	#N/A	#N/A	#N/A	-1.48	#N/A	neuronal E3 ubiquitin protein ligase 4
ENSG000000985150	#N/A	#N/A	#N/A	-1.48	#N/A	importin 5
ENSG00000143643	#N/A	#N/A	#N/A	-1.48	#N/A	tetratricopeptide repeat domain 13
ENSG00000134905	#N/A	#N/A	#N/A	-1.48	#N/A	cysteine tRNA synthetase 2, mitochondrial (putative)
ENSG00000185504	#N/A	#N/A	#N/A	-1.48	#N/A	Fanconi anemia core complex associated protein 100
ENSG00000110090	#N/A	#N/A	#N/A	-1.48	#N/A	camphor palmitoyltransferase 1A (liver)
ENSG00000196535	#N/A	#N/A	#N/A	-1.49	#N/A	myosin XVIIIa
ENSG00000144138	#N/A	#N/A	#N/A	-1.49	1.19	solute carrier family 20 (phosphate transporter), member 1
ENSG00000124541	#N/A	#N/A	#N/A	-1.49	#N/A	ribosomal RNA processing 36
ENSG00000075407	#N/A	#N/A	#N/A	-1.49	#N/A	zinc finger protein 37A
ENSG00000241978	#N/A	#N/A	#N/A	-1.49	#N/A	A kinase (PRK) anchor protein 2
ENSG00000142185	#N/A	#N/A	#N/A	-1.49	#N/A	transient receptor potential cation channel, subfamily M, member 2
ENSG00000273645	#N/A	#N/A	#N/A	-1.50	#N/A	leucine repeat and BTB (POZ) domain containing 11
ENSG00000100219	#N/A	#N/A	#N/A	-1.50	#N/A	X-box binding protein 1
ENSG00000112159	#N/A	#N/A	#N/A	-1.50	#N/A	midasin AAA ATPase 1
ENSG00000178921	#N/A	#N/A	#N/A	-1.50	#N/A	phosphoribosylglycinamide synthase
ENSG00000108179	#N/A	#N/A	#N/A	-1.50	#N/A	peptidylprolyl isomerase F
ENSG00000197150	#N/A	#N/A	#N/A	-1.50	#N/A	ATP-binding cassette, sub-family E (MDR/TAP), member 8
ENSG00000106105	#N/A	#N/A	#N/A	-1.50	#N/A	glycyl-tRNA synthetase
ENSG00000185238	#N/A	#N/A	#N/A	-1.50	#N/A	protein arginine methyltransferase 3
ENSG00000098511	#N/A	#N/A	#N/A	-1.51	#N/A	mitogen-activated protein kinase kinase kinase 4
ENSG00000163393	#N/A	#N/A	#N/A	-1.51	#N/A	solute carrier family 22, member 15
ENSG00000149136	#N/A	#N/A	#N/A	-1.51	#N/A	structure specific recognition protein 1
ENSG00000112578	#N/A	#N/A	#N/A	-1.51	#N/A	bystin-like
ENSG00000274679	#N/A	#N/A	#N/A	-1.52	#N/A	spermatogenesis and centriole associated 1-like
ENSG00000132305	#N/A	#N/A	#N/A	-1.52	#N/A	inner membrane protein, mitochondrial
ENSG0000016922	#N/A	#N/A	#N/A	-1.52	#N/A	chromosome 1 open reading frame 109
ENSG00000164934	#N/A	#N/A	#N/A	-1.52	#N/A	DOB1 and CUL4 associated factor 13
ENSG000000971655	#N/A	#N/A	#N/A	-1.52	#N/A	methyl-CpG binding domain protein 3
ENSG00000165209	#N/A	#N/A	#N/A	-1.52	#N/A	spermatid perinuclear RNA binding protein
ENSG00000166123	#N/A	#N/A	#N/A	-1.52	#N/A	glutamic pyruvate transaminase (alanine aminotransferase) 2
ENSG00000167962	#N/A	#N/A	#N/A	-1.53	#N/A	zinc finger protein 598
ENSG00000179271	#N/A	#N/A	#N/A	-1.53	#N/A	growth arrest and DNA-damage-inducible, gamma interacting protein 1
ENSG00000268006	#N/A	#N/A	#N/A	-1.53	#N/A	PTCV1 antisense RNA 1
ENSG00000185760	#N/A	#N/A	#N/A	-1.54	#N/A	potassium channel, voltage gated KQT-like subfamily Q, member 5
ENSG00000230606	#N/A	#N/A	#N/A	-1.54	#N/A	AC159540.1
ENSG00000247077	#N/A	#N/A	#N/A	-1.54	#N/A	phosphoglycerate mutase family member 5
ENSG00000197728	#N/A	#N/A	#N/A	-1.54	#N/A	ribosomal protein S26
ENSG00000140263	#N/A	#N/A	#N/A	-1.54	#N/A	sorbitol dehydrogenase
ENSG00000171262	#N/A	#N/A	#N/A	-1.55	#N/A	family with sequence similarity 98, member B
ENSG00000277804	#N/A	#N/A	#N/A	-1.55	#N/A	proteinase 3
ENSG00000198727	#N/A	#N/A	#N/A	-1.55	#N/A	mitochondrially encoded cytochrome b

FIGURE 1P

ENSG00000085514	#N/A	#N/A	#N/A	1.93	#N/A	paired immunoglobulin-like type 2 receptor alpha
ENSG00000114023	#N/A	#N/A	#N/A	1.93	#N/A	family with sequence similarity 162, member A
ENSG00000197903	#N/A	#N/A	#N/A	1.92	1.45	histone cluster 1, H2bk
ENSG00000053254	#N/A	#N/A	#N/A	1.92	#N/A	forkhead box N3
ENSG00000106479	#N/A	#N/A	#N/A	1.92	#N/A	zinc finger protein 862
ENSG00000131469	#N/A	#N/A	#N/A	1.92	1.75	ribosomal protein L27
ENSG00000148186	#N/A	#N/A	#N/A	1.92	#N/A	gelectin
ENSG00000176788	#N/A	#N/A	#N/A	1.91	1.39	brain abundant, membrane attached signal protein 1
ENSG00000112343	#N/A	#N/A	#N/A	1.91	#N/A	tripartite motif containing 38
ENSG00000234741	#N/A	#N/A	#N/A	1.91	#N/A	growth arrest-specific 5 (non-protein coding)
ENSG00000125657	#N/A	#N/A	#N/A	1.91	#N/A	tumor necrosis factor (ligand) superfamily, member 9
ENSG00000051523	#N/A	#N/A	#N/A	1.90	#N/A	cytochrome b-245, alpha polypeptide
ENSG00000197879	#N/A	#N/A	#N/A	1.90	#N/A	myosin IC
ENSG00000257529	#N/A	#N/A	#N/A	1.89	#N/A	RPL36A-HNRNP2 readthrough
ENSG00000110828	#N/A	#N/A	#N/A	1.89	#N/A	solute carrier family 22, member 18
ENSG00000130303	#N/A	#N/A	#N/A	1.89	#N/A	bone marrow stromal cell antigen 2
ENSG00000196369	#N/A	#N/A	#N/A	1.88	#N/A	SLIT-ROBO Rho GTPase activating protein 2B
ENSG00000156482	#N/A	#N/A	#N/A	1.88	1.43	ribosomal protein L30
ENSG00000071082	#N/A	#N/A	#N/A	1.86	#N/A	ribosomal protein L31
ENSG00000089335	#N/A	#N/A	#N/A	1.87	#N/A	zinc finger protein 302
ENSG00000060339	#N/A	#N/A	#N/A	1.87	1.65	cell division cycle and apoptosis regulator 1
ENSG00000115415	#N/A	#N/A	#N/A	1.87	#N/A	signal transducer and activator of transcription 1, 91kDa
ENSG00000122694	#N/A	#N/A	#N/A	1.87	#N/A	GLI pathogenesis-related 2
ENSG00000090863	#N/A	#N/A	#N/A	1.87	#N/A	golgi glycoprotein 1
ENSG00000115267	#N/A	#N/A	#N/A	1.86	#N/A	interferon induced with helicase C domain 1
ENSG00000160445	#N/A	#N/A	#N/A	1.86	#N/A	zyg-11 related, cell cycle regulator
ENSG00000196209	#N/A	#N/A	#N/A	1.86	#N/A	signal-regulatory protein beta 2
ENSG00000073803	#N/A	#N/A	#N/A	1.86	#N/A	mitogen-activated protein kinase kinase kinase 13
ENSG00000125733	#N/A	#N/A	#N/A	1.85	1.21	thyroid hormone receptor interactor 10
ENSG00000166913	#N/A	#N/A	#N/A	1.85	#N/A	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta
ENSG00000204164	#N/A	#N/A	#N/A	1.85	#N/A	BMS1P5
ENSG00000114480	#N/A	#N/A	#N/A	1.85	#N/A	glucan (1,4-alpha-), branching enzyme 1
ENSG00000169925	#N/A	#N/A	#N/A	1.84	#N/A	bromodomain containing 3
ENSG00000152256	#N/A	#N/A	#N/A	1.84	#N/A	pyruvate dehydrogenase kinase, isozyme 1
ENSG00000100916	#N/A	#N/A	#N/A	1.84	#N/A	REC8 meiotic recombination protein
ENSG00000130775	#N/A	#N/A	#N/A	1.84	#N/A	thymocyte selection associated family member 2
ENSG00000106404	#N/A	#N/A	#N/A	1.84	#N/A	claudin 15
ENSG00000168461	#N/A	#N/A	#N/A	1.83	#N/A	RAB31, member RAS oncogene family
ENSG00000141506	#N/A	#N/A	#N/A	1.83	#N/A	phosphoinositide-3-kinase, regulatory subunit 5
ENSG00000034713	#N/A	#N/A	#N/A	1.83	#N/A	GABA(A) receptor-associated protein-like 2
ENSG00000002549	#N/A	#N/A	#N/A	1.83	#N/A	leucine aminopeptidase 3
ENSG00000120594	#N/A	#N/A	#N/A	1.83	#N/A	plexin domain containing 2
ENSG00000174720	#N/A	#N/A	#N/A	1.83	1.74	La ribonucleoprotein domain family, member 7
ENSG00000139182	#N/A	#N/A	#N/A	1.82	#N/A	calystrin 3
ENSG00000068697	#N/A	#N/A	#N/A	1.82	1.21	lysosomal protein transmembrane 4 alpha
ENSG00000183401	#N/A	#N/A	#N/A	1.82	#N/A	coiled-coil domain containing 159

ENSG00000109917	#N/A	#N/A	#N/A	-1.55	#N/A	ZPR1 zinc finger
ENSG00000007392	#N/A	#N/A	#N/A	-1.56	#N/A	LUC7-like
ENSG00000130725	#N/A	#N/A	#N/A	-1.58	#N/A	ubiquitin-conjugating enzyme E2M
ENSG00000112651	#N/A	#N/A	#N/A	-1.56	#N/A	mitochondrial ribosomal protein L2
ENSG00000166197	#N/A	#N/A	#N/A	-1.58	#N/A	nucleolar and coiled-body phosphoprotein 1
ENSG00000108561	#N/A	#N/A	#N/A	-1.56	#N/A	complement component 1, q subcomponent binding protein
ENSG00000103876	#N/A	#N/A	#N/A	-1.56	#N/A	fumarylacetoacetate hydrolase (fumarylacetoacetase)
ENSG00000178605	#N/A	#N/A	#N/A	-1.56	#N/A	GTP binding protein 6 (putative)
ENSG00000162129	#N/A	#N/A	#N/A	-1.58	#N/A	CtpB homolog, mitochondrial AAA ATPase chaperonin
ENSG00000224078	#N/A	#N/A	#N/A	-1.57	#N/A	small nuclear RNA host gene 14
ENSG00000204316	#N/A	#N/A	#N/A	-1.57	#N/A	mitochondrial ribosomal protein L38
ENSG00000146830	#N/A	#N/A	#N/A	-1.57	#N/A	GRB10 interacting GYF protein 1
ENSG00000255302	#N/A	#N/A	#N/A	-1.57	#N/A	EP300 interacting inhibitor of differentiation 1
ENSG00000226950	#N/A	#N/A	#N/A	-1.57	#N/A	differentiation antagonizing non-protein coding RNA
ENSG00000145703	#N/A	#N/A	#N/A	-1.58	#N/A	IQ motif containing GTPase activating protein 2
ENSG00000244165	#N/A	#N/A	#N/A	-1.56	#N/A	purinergic receptor P2Y, G-protein coupled, 11
ENSG00000132382	#N/A	#N/A	#N/A	-1.59	#N/A	MYB binding protein (P160) 1a
ENSG00000096063	#N/A	#N/A	#N/A	-1.59	#N/A	SRSF protein kinase 1
ENSG00000161547	#N/A	#N/A	#N/A	-1.56	#N/A	serine/arginine-rich splicing factor 2
ENSG00000131828	#N/A	#N/A	#N/A	-1.59	#N/A	pyruvate dehydrogenase (liponamide) alpha 1
ENSG00000142102	#N/A	#N/A	#N/A	-1.59	#N/A	ATH1, acid trehalase-like 1 (yeast)
ENSG00000196510	#N/A	#N/A	#N/A	-1.59	#N/A	anaphase promoting complex subunit 7
ENSG00000140006	#N/A	#N/A	#N/A	-1.59	#N/A	WD repeat domain 69
ENSG00000155526	#N/A	#N/A	#N/A	-1.60	#N/A	RNA pseudouridylation synthase domain containing 4
ENSG00000184575	#N/A	#N/A	#N/A	-1.60	#N/A	exportin, tRNA
ENSG00000183010	#N/A	#N/A	#N/A	-1.60	#N/A	pyrimidine-5-carboxylate reductase 1
ENSG00000117174	#N/A	#N/A	#N/A	-1.60	#N/A	zinc finger, HIT-type containing 6
ENSG00000143093	#N/A	#N/A	#N/A	-1.61	#N/A	shafin interacting protein 1
ENSG00000155848	#N/A	#N/A	#N/A	-1.62	#N/A	peroxisome proliferator-activated receptor gamma, coactivator 1 beta
ENSG00000138095	#N/A	#N/A	#N/A	-1.62	#N/A	leucine-rich pentapeptide repeat containing
ENSG00000133265	#N/A	#N/A	#N/A	-1.62	#N/A	HSPA (heat shock 70kDa) binding protein, cytoplasmic co-chaperone 1
ENSG00000223705	#N/A	#N/A	#N/A	-1.63	#N/A	NOP2/Sun domain family, member 5 pseudogene 1
ENSG00000126602	#N/A	#N/A	#N/A	-1.63	#N/A	TNF receptor-associated protein 1
ENSG00000123064	#N/A	#N/A	#N/A	-1.64	#N/A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54
ENSG000000070061	#N/A	#N/A	#N/A	-1.64	#N/A	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein
ENSG00000197785	#N/A	#N/A	#N/A	-1.64	#N/A	ATPase family, AAA domain containing 3A
ENSG00000106344	#N/A	#N/A	#N/A	-1.65	#N/A	RNA binding motif protein 28
ENSG00000254870	#N/A	#N/A	#N/A	-1.65	#N/A	ATP6V1G2-DDX39B readthrough (NMJ candidate)
ENSG00000118513	#N/A	#N/A	#N/A	-1.65	#N/A	v-myb avian myeloblastosis viral oncogene homolog
ENSG00000171163	#N/A	#N/A	#N/A	-1.65	#N/A	zinc finger protein 692
ENSG00000131368	#N/A	#N/A	#N/A	-1.65	#N/A	mitochondrial ribosomal protein S25
ENSG00000184232	#N/A	#N/A	#N/A	-1.66	#N/A	out of first homolog
ENSG000000917403	#N/A	#N/A	#N/A	-1.66	#N/A	solute carrier family 38, member 5
ENSG00000125901	#N/A	#N/A	#N/A	-1.67	#N/A	mitochondrial ribosomal protein S26
ENSG00000140044	#N/A	#N/A	#N/A	-1.67	#N/A	Jun dimerization protein 2
ENSG00000184787	#N/A	#N/A	#N/A	-1.67	#N/A	ubiquitin-conjugating enzyme E2G 2

FIGURE 1Q

ENSG00000069329	#N/A	#N/A	#N/A	1.81	#N/A	VPS35 retromer complex component
ENSG00000121858	#N/A	#N/A	#N/A	1.80	#N/A	tumor necrosis factor (ligand) superfamily, member 10
ENSG00000281490	#N/A	#N/A	#N/A	1.80	#N/A	capicua transcriptional repressor pseudogene 14
ENSG00000066933	#N/A	#N/A	#N/A	1.79	#N/A	myosin IXA
ENSG00000137628	#N/A	#N/A	#N/A	1.79	#N/A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60
ENSG00000105939	#N/A	#N/A	#N/A	1.79	#N/A	zinc finger CCH-type, antiviral 1
ENSG00000121310	#N/A	#N/A	#N/A	1.79	#N/A	enoyl CoA hydratase domain containing 2
ENSG000000085117	#N/A	#N/A	#N/A	1.78	#N/A	CD52 molecule
ENSG00000141096	#N/A	#N/A	#N/A	1.78	#N/A	dipeptidase 3
ENSG00000142156	#N/A	#N/A	#N/A	1.78	#N/A	collagen, type VI, alpha 1
ENSG00000197756	#N/A	#N/A	#N/A	1.77	#N/A	ribosomal protein L37a
ENSG00000160352	#N/A	#N/A	#N/A	1.77	#N/A	zinc finger protein 714
ENSG00000204138	#N/A	#N/A	#N/A	1.16	#N/A	phosphatase and actin regulator 4
ENSG00000136819	#N/A	#N/A	#N/A	1.76	1.55	chromosome 5 open reading frame 78
ENSG00000153029	#N/A	#N/A	#N/A	1.76	#N/A	major histocompatibility complex, class I-related
ENSG00000149187	#N/A	#N/A	#N/A	1.75	#N/A	CUGBP, Elav-like family member 1
ENSG00000166888	#N/A	#N/A	#N/A	1.74	#N/A	signal transducer and activator of transcription 6, interleukin-4 induced
ENSG00000214176	#N/A	#N/A	#N/A	1.74	#N/A	pleckstrin homology domain containing, family M (with RUN domain) member 1 pseudogene
ENSG00000175061	#N/A	#N/A	#N/A	1.74	#N/A	LRRCT5A antisense RNA 1
ENSG00000170525	#N/A	#N/A	#N/A	1.73	#N/A	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3
ENSG00000121289	#N/A	#N/A	#N/A	1.73	#N/A	centrosomal protein 89kDa
ENSG00000077380	#N/A	#N/A	#N/A	1.73	#N/A	dynein, cytoplasmic 1, intermediate chain 2
ENSG00000133112	#N/A	#N/A	#N/A	1.73	#N/A	tumor protein, translationally-controlled 1
ENSG00000178695	#N/A	#N/A	#N/A	1.72	#N/A	potassium channel tetramerization domain containing 12
ENSG00000131869	#N/A	#N/A	#N/A	1.72	#N/A	ninjurin 1
ENSG00000143771	#N/A	#N/A	#N/A	1.72	1.96	postrichon family AMPA receptor auxiliary protein 4
ENSG00000158270	#N/A	#N/A	#N/A	1.72	#N/A	collectin sub-family member 12
ENSG00000109390	#N/A	#N/A	#N/A	1.72	1.37	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa
ENSG000002276701	#N/A	#N/A	#N/A	1.71	#N/A	macrophage migration inhibitory factor (glycosylation-inhibiting factor)
ENSG00000105639	#N/A	#N/A	#N/A	1.71	#N/A	Janus kinase 3
ENSG00000185432	#N/A	#N/A	#N/A	1.71	#N/A	methyltransferase like 7A
ENSG00000160991	#N/A	#N/A	#N/A	1.70	1.04	ORAI calcium release-activated calcium modulator 2
ENSG00000128524	#N/A	#N/A	#N/A	1.70	1.96	ATPase, H ⁺ transporting, lysosomal 14kDa, V1 subunit F
ENSG00000110002	#N/A	#N/A	#N/A	1.70	#N/A	von Willebrand factor A domain containing 5A
ENSG00000163171	#N/A	#N/A	#N/A	1.69	#N/A	CDC42 effector protein (Rho GTPase binding) 3
ENSG00000143891	#N/A	#N/A	#N/A	1.66	#N/A	galactose mutarotase (aldose 1-epimerase)
ENSG00000008988	#N/A	#N/A	#N/A	1.68	1.26	ribosomal protein S20
ENSG00000162735	#N/A	#N/A	#N/A	1.66	#N/A	peroxisomal biogenesis factor 19
ENSG00000102921	#N/A	#N/A	#N/A	1.68	#N/A	NEDD4 binding protein 1
ENSG00000212338	#N/A	#N/A	#N/A	1.68	#N/A	Small nuclear RNA SNORA67
ENSG00000135046	#N/A	#N/A	#N/A	1.68	#N/A	annexin A1
ENSG00000070160	#N/A	#N/A	#N/A	1.68	#N/A	dual adaptor of phosphotyrosine and 3-phosphoinositides
ENSG00000083444	#N/A	#N/A	#N/A	1.67	#N/A	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1
ENSG00000232388	#N/A	#N/A	#N/A	1.67	1.34	long intergenic non-protein coding RNA 493
ENSG00000103066	#N/A	#N/A	#N/A	1.66	#N/A	phospholipase A2, group XV
ENSG00000112715	#N/A	#N/A	#N/A	1.66	1.02	vascular endothelial growth factor A
ENSG00000101040	#N/A	#N/A	#N/A	1.66	#N/A	zinc finger, MYND-type containing 8
ENSG00000175602	#N/A	#N/A	#N/A	-1.67	#N/A	coiled-coil domain containing 85B
ENSG00000139514	#N/A	#N/A	#N/A	-1.68	#N/A	solute carrier family 7 (anionic amino acid transporter, y ⁺ system), member 1
ENSG00000128272	#N/A	#N/A	#N/A	-1.69	#N/A	activating transcription factor 4
ENSG00000272752	#N/A	#N/A	#N/A	-1.70	#N/A	STAG3LSP-PVRIG2P-PILRB readthrough
ENSG00000107937	#N/A	#N/A	#N/A	-1.70	#N/A	GTP binding protein 4
ENSG00000180730	#N/A	#N/A	#N/A	-1.70	#N/A	shisa family member 2
ENSG00000065183	#N/A	#N/A	#N/A	-1.70	#N/A	WD repeat domain 3
ENSG00000177192	#N/A	#N/A	#N/A	-1.70	#N/A	pseudouridylyl synthase 1
ENSG000000930273	#N/A	#N/A	#N/A	-1.70	#N/A	nudC nuclear distribution protein
ENSG00000115053	#N/A	#N/A	#N/A	-1.71	#N/A	nucleosin
ENSG00000167635	#N/A	#N/A	#N/A	-1.71	#N/A	zinc finger protein 146
ENSG00000227686	#N/A	#N/A	#N/A	-1.71	#N/A	vaiyl-4RNA synthetase
ENSG00000115652	#N/A	#N/A	#N/A	-1.72	#N/A	UDP-glucuronate decarboxylase 1
ENSG00000104635	#N/A	#N/A	#N/A	-1.72	#N/A	solute carrier family 39 (zinc transporter), member 14
ENSG00000135972	#N/A	#N/A	#N/A	-1.72	#N/A	mitochondrial ribosomal protein S9
ENSG00000160256	#N/A	#N/A	#N/A	-1.72	#N/A	family with sequence similarity 207, member A
ENSG00000167114	#N/A	#N/A	#N/A	-1.72	#N/A	solute carrier family 27 (fatty acid transporter), member 4
ENSG00000251236	#N/A	#N/A	#N/A	-1.72	#N/A	block of proliferation 1
ENSG00000182168	#N/A	#N/A	#N/A	-1.73	#N/A	unc-5 netrin receptor C
ENSG00000183889	#N/A	#N/A	#N/A	-1.73	#N/A	Protein LOC102724993
ENSG00000171793	#N/A	#N/A	#N/A	-1.73	#N/A	GTP synthase 1
ENSG00000053372	#N/A	#N/A	#N/A	-1.73	#N/A	MRT4 homolog, ribosome maturation factor
ENSG00000140284	#N/A	#N/A	#N/A	-1.73	#N/A	solute carrier family 27 (fatty acid transporter), member 2
ENSG000000580608	#N/A	#N/A	#N/A	-1.73	#N/A	KIAA0020
ENSG00000091127	#N/A	#N/A	#N/A	-1.73	#N/A	pseudouridylyl synthase 7 (putative)
ENSG00000136444	#N/A	#N/A	#N/A	-1.74	#N/A	radical S-adenosyl methionine domain containing 1
ENSG00000165689	#N/A	#N/A	#N/A	-1.75	#N/A	serologically defined colon cancer antigen 3
ENSG00000108578	#N/A	#N/A	#N/A	-1.75	#N/A	bleomycin hydrolase
ENSG00000117528	#N/A	#N/A	#N/A	-1.76	#N/A	ATP-binding cassette, sub-family D (ALD), member 3
ENSG00000188933	#N/A	#N/A	#N/A	-1.76	#N/A	ubiquitin specific peptidase 32 pseudogene 1
ENSG00000160214	#N/A	#N/A	#N/A	-1.78	#N/A	ribosomal RNA processing 1
ENSG00000110104	#N/A	#N/A	#N/A	-1.76	#N/A	coiled-coil domain containing 86
ENSG000000907520	#N/A	#N/A	#N/A	-1.78	#N/A	TSR3, 20S rRNA accumulation, homolog (S. cerevisiae)
ENSG00000125459	#N/A	#N/A	#N/A	-1.79	#N/A	misato 1, mitochondrial distribution and morphology regulator
ENSG00000189007	#N/A	#N/A	#N/A	-1.79	#N/A	adenosine deaminase, tRNA-specific 2
ENSG000000503241	#N/A	#N/A	#N/A	-1.79	#N/A	isochorismatase domain containing 2
ENSG00000179041	#N/A	#N/A	#N/A	-1.80	1.29	ribosome biogenesis regulator homolog
ENSG00000189230	#N/A	#N/A	#N/A	-1.80	#N/A	PREL1 domain containing 1
ENSG00000180990	#N/A	#N/A	#N/A	-1.82	#N/A	scribbled planar cell polarity protein
ENSG00000213066	#N/A	#N/A	#N/A	-1.82	#N/A	FGFR1 oncogene partner
ENSG00000152642	#N/A	#N/A	#N/A	-1.82	#N/A	glycerol-3-phosphate dehydrogenase 1-like
ENSG00000134987	#N/A	#N/A	#N/A	-1.82	#N/A	WD repeat domain 36
ENSG00000167965	#N/A	#N/A	#N/A	-1.82	#N/A	MTOR associated protein, LST8 homolog
ENSG00000115758	#N/A	#N/A	#N/A	-1.82	#N/A	ornithine decarboxylase 1
ENSG00000071994	#N/A	#N/A	#N/A	-1.82	#N/A	programmed cell death 2
ENSG00000100427	#N/A	#N/A	#N/A	-1.82	#N/A	megaloencephalic leukoencephalopathy with subcortical cysts 1
ENSG00000182676	#N/A	#N/A	#N/A	-1.83	#N/A	protein phosphatase 1, regulatory subunit 27

FIGURE 1R

ENSG00000113811	#N/A	#N/A	#N/A	1.66	1.90	seienoprotein K
ENSG00000185068	#N/A	#N/A	#N/A	1.85	2.29	GTF2H5
ENSG00000186468	#N/A	#N/A	#N/A	1.65	#N/A	ribosomal protein S23
ENSG00000164733	#N/A	#N/A	#N/A	1.54	#N/A	cathepsin B
ENSG00000127663	#N/A	#N/A	#N/A	1.64	#N/A	lysine (K)-specific demethylase 4B
ENSG00000223960	#N/A	#N/A	#N/A	1.64	#N/A	AC009946.5
ENSG00000105647	#N/A	#N/A	#N/A	1.54	#N/A	phosphoinositide-3-kinase, regulatory subunit 2 (beta)
ENSG00000162909	#N/A	#N/A	#N/A	1.64	#N/A	calpain 2, (mu1) large subunit
ENSG00000164687	#N/A	#N/A	#N/A	1.63	#N/A	fatty acid binding protein 5 (psoriasis-associated)
ENSG00000254635	#N/A	#N/A	#N/A	1.63	#N/A	WAC antisense RNA 1 (head to head)
ENSG00000190918	#N/A	#N/A	#N/A	1.63	#N/A	ribosomal protein L39
ENSG00000174426	#N/A	#N/A	#N/A	1.63	#N/A	GTF2i repeat domain containing 2B
ENSG00000172530	#N/A	#N/A	#N/A	1.63	#N/A	BTG3 associated nuclear protein
ENSG00000137145	#N/A	#N/A	#N/A	1.63	#N/A	DENK/MADD domain containing 4C
ENSG00000100439	#N/A	#N/A	#N/A	1.63	#N/A	abhydrolase domain containing 4
ENSG00000132256	#N/A	#N/A	#N/A	1.63	#N/A	tripartite motif containing 5
ENSG00000265972	#N/A	#N/A	#N/A	1.62	#N/A	thioredoxin interacting protein
ENSG00000245910	#N/A	#N/A	#N/A	1.62	1.53	small nuclear RNA host gene 6
ENSG00000067066	#N/A	#N/A	#N/A	1.62	#N/A	SP100 nuclear antigen
ENSG00000166681	#N/A	#N/A	#N/A	1.62	#N/A	nerve growth factor receptor (TNFRSF18) associated protein 1
ENSG00000117475	#N/A	#N/A	#N/A	1.61	#N/A	basic leucine zipper nuclear factor 1
ENSG00000125691	#N/A	#N/A	#N/A	1.61	1.27	ribosomal protein L23
ENSG00000168172	#N/A	#N/A	#N/A	1.61	1.10	hook microtubule-anchoring protein 3
ENSG0000010276	#N/A	#N/A	#N/A	1.61	#N/A	CD8 molecule
ENSG00000173214	#N/A	#N/A	#N/A	1.61	#N/A	KIAA1919
ENSG00000126860	#N/A	#N/A	#N/A	1.60	#N/A	ecotropic viral integration site 2A
ENSG00000167419	#N/A	#N/A	#N/A	1.60	#N/A	lactoperoxidase
ENSG00000118263	#N/A	#N/A	#N/A	1.60	#N/A	Kruppel-like factor 7 (ubiquitous)
ENSG00000235623	#N/A	#N/A	#N/A	1.60	#N/A	oligodendrocyte maturation-associated long intergenic non-coding RNA
ENSG00000111859	#N/A	#N/A	#N/A	1.60	#N/A	neural precursor cell expressed, developmentally down-regulated 9
ENSG00000089041	#N/A	#N/A	#N/A	1.60	#N/A	purinergic receptor P2X, ligand gated ion channel, 7
ENSG00000125810	#N/A	#N/A	#N/A	1.60	#N/A	CD83 molecule
ENSG00000113494	#N/A	#N/A	#N/A	1.59	#N/A	prolactin receptor
ENSG00000163993	#N/A	#N/A	#N/A	1.59	#N/A	S100 calcium binding protein P
ENSG00000124831	#N/A	#N/A	#N/A	1.59	#N/A	leucine rich repeat (in FLII) interacting protein 1
ENSG00000170581	#N/A	#N/A	#N/A	1.59	#N/A	signal transducer and activator of transcription 2, 113kDa
ENSG00000050972	#N/A	#N/A	#N/A	1.59	#N/A	TRAF3 interacting protein 2
ENSG00000218739	#N/A	#N/A	#N/A	1.59	3.17	CEBPZ opposite strand
ENSG00000204272	#N/A	#N/A	#N/A	1.58	#N/A	RP11-622K12.1
ENSG00000178645	#N/A	#N/A	#N/A	1.58	#N/A	metecrin, glial cell differentiation regulator-like
ENSG00000185880	#N/A	#N/A	#N/A	1.58	#N/A	tripartite motif containing 69
ENSG00000158567	#N/A	#N/A	#N/A	1.58	#N/A	ubiquitin-conjugating enzyme E2L 6
ENSG00000101347	#N/A	#N/A	#N/A	1.58	#N/A	SAM domain and HD domain 1
ENSG00000159792	#N/A	#N/A	#N/A	1.56	#N/A	protein serine kinase H1

ENSG00000253729	#N/A	#N/A	#N/A	-1.83	#N/A	protein kinase, DNA-activated, catalytic polypeptide
ENSG00000106133	#N/A	#N/A	#N/A	-1.84	#N/A	NOP2/Sun domain family, member 5 pseudogene 2
ENSG00000232169	#N/A	#N/A	#N/A	-1.84	#N/A	ATP-binding cassette, sub-family F (GCN20), member 1
ENSG00000068831	#N/A	#N/A	#N/A	-1.84	#N/A	RAS guanyl releasing protein 2 (calcium and DAG-regulated)
ENSG00000168924	#N/A	#N/A	#N/A	-1.84	#N/A	leucine zipper-EF-hand containing transmembrane protein 1
ENSG00000162676	#N/A	#N/A	#N/A	-1.85	#N/A	growth factor independent 1 transcription repressor
ENSG00000195449	#N/A	#N/A	#N/A	-1.85	#N/A	yrdC N(6)-threonylcarbamoyltransferase domain containing
ENSG00000170571	#N/A	#N/A	#N/A	-1.85	#N/A	embigin
ENSG000000604478	#N/A	#N/A	#N/A	-1.85	#N/A	FK506 binding protein 4, 59kDa
ENSG00000141569	#N/A	#N/A	#N/A	-1.86	#N/A	tripartite motif containing 65
ENSG000000507541	#N/A	#N/A	#N/A	-1.86	#N/A	phosphatidylinositol glycan anchor biosynthesis, class C
ENSG00000188206	#N/A	#N/A	#N/A	-1.86	#N/A	HNRNPJ antisense RNA 1
ENSG00000123213	#N/A	#N/A	#N/A	-1.87	#N/A	neurolysin (metallopeptidase M3 family)
ENSG000000680982	#N/A	#N/A	#N/A	-1.87	#N/A	branched chain amino-acid transaminase 1, cytosolic
ENSG00000120254	#N/A	#N/A	#N/A	-1.87	#N/A	methyltetrahydrofolate dehydrogenase (NADP+ dependent) 1-like
ENSG00000196305	#N/A	#N/A	#N/A	-1.89	#N/A	isoleucyl-tRNA synthetase
ENSG00000103253	#N/A	#N/A	#N/A	-1.89	#N/A	hydroxyacylglutathione hydrolase-like
ENSG00000171791	#N/A	#N/A	#N/A	-1.89	#N/A	B-cell CLL/lymphoma 2
ENSG00000105677	#N/A	#N/A	#N/A	-1.90	#N/A	transmembrane protein 147
ENSG00000178105	#N/A	#N/A	#N/A	-1.90	#N/A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10
ENSG00000132768	#N/A	#N/A	#N/A	-1.91	#N/A	DPH2 homolog
ENSG00000133706	#N/A	#N/A	#N/A	-1.91	#N/A	leucyl-tRNA synthetase
ENSG00000116649	#N/A	#N/A	#N/A	-1.92	#N/A	spermidine synthase
ENSG00000171492	#N/A	#N/A	#N/A	-1.92	#N/A	leucine rich repeat containing 8 family, member D
ENSG00000120438	#N/A	#N/A	#N/A	-1.92	#N/A	t-complex 1
ENSG00000193426	#N/A	#N/A	#N/A	-1.94	#N/A	nuclear pore complex interacting protein family, member A1
ENSG00000172366	#N/A	#N/A	#N/A	-1.95	#N/A	family with sequence similarity 195, member A
ENSG00000183048	#N/A	#N/A	#N/A	-1.96	#N/A	solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10
ENSG00000144485	#N/A	#N/A	#N/A	-1.97	#N/A	hes family bHLH transcription factor 6
ENSG00000282283	#N/A	#N/A	#N/A	-1.97	#N/A	LPFR3
ENSG00000083097	#N/A	#N/A	#N/A	-1.97	#N/A	dopey family member 1
ENSG00000146457	#N/A	#N/A	#N/A	-1.97	#N/A	Wilms tumor 1 associated protein
ENSG00000132780	#N/A	#N/A	#N/A	-1.98	#N/A	nuclear autoantigenic sperm protein (histone-binding)
ENSG00000198744	#N/A	#N/A	#N/A	-1.98	#N/A	MT-CD3
ENSG00000114631	#N/A	#N/A	#N/A	-1.98	#N/A	podocalyxin-like 2
ENSG00000196497	#N/A	#N/A	#N/A	-1.99	#N/A	importin 4
ENSG00000172179	#N/A	#N/A	#N/A	-2.01	#N/A	prolactin
ENSG00000102241	#N/A	#N/A	#N/A	-2.03	#N/A	HIV-1 Tat specific factor 1
ENSG00000175416	#N/A	#N/A	#N/A	-2.03	#N/A	clathrin, light chain B
ENSG000000670081	#N/A	#N/A	#N/A	-2.03	#N/A	nucleobindin 2
ENSG00000198520	#N/A	#N/A	#N/A	-2.05	#N/A	chromosome 1 open reading frame 228
ENSG00000113575	#N/A	#N/A	#N/A	-2.08	#N/A	protein phosphatase 2, catalytic subunit, alpha isoform
ENSG00000135069	#N/A	#N/A	#N/A	-2.08	#N/A	phosphoserine aminotransferase 1
ENSG00000124802	#N/A	#N/A	#N/A	-2.09	#N/A	eukaryotic translation elongation factor 1 epsilon 1

FIGURE 1S

ENSG00000226710	#N/A	#N/A	#N/A	1.57	1.87	chromosome 6 open reading frame 48
ENSG0000025708	#N/A	#N/A	#N/A	1.57	#N/A	thymidine phosphorylase
ENSG00000115548	#N/A	#N/A	#N/A	1.57	#N/A	lysine (K)-specific demethylase 3A
ENSG00000070214	#N/A	#N/A	#N/A	1.57	#N/A	solute carrier family 44 (choline transporter), member 1
ENSG00000188243	#N/A	#N/A	#N/A	1.56	#N/A	COMM domain containing 6
ENSG00000132024	#N/A	#N/A	#N/A	1.56	#N/A	coiled-coil and G2 domain containing 1A
ENSG00000168056	#N/A	#N/A	#N/A	1.56	#N/A	latent transforming growth factor beta binding protein 3
ENSG00000125482	#N/A	#N/A	#N/A	1.56	#N/A	transcription termination factor, RNA polymerase I
ENSG00000109099	#N/A	#N/A	#N/A	1.56	2.11	peripheral myosin protein 22
ENSG00000130066	#N/A	#N/A	#N/A	1.55	1.38	spermidine/spermine N1-acetyltransferase 1
ENSG00000171617	#N/A	#N/A	#N/A	1.55	#N/A	ectodermal-neural cortex 1 (with BTB domain)
ENSG00000138814	#N/A	#N/A	#N/A	1.55	1.48	protein phosphatase 3, catalytic subunit, alpha isozyme
ENSG00000148660	#N/A	#N/A	#N/A	1.54	#N/A	calcium/calmodulin-dependent protein kinase II gamma
ENSG00000168528	#N/A	#N/A	#N/A	1.54	#N/A	serine incorporator 2
ENSG00000138396	#N/A	#N/A	#N/A	1.54	1.39	peptidylprolyl isomerase G (cyclophilin G)
ENSG00000111596	#N/A	#N/A	#N/A	1.53	1.45	CCR4-NOT transcription complex, subunit 2
ENSG00000135886	#N/A	#N/A	#N/A	1.53	#N/A	leish-like family member 36
ENSG00000081189	#N/A	#N/A	#N/A	1.53	#N/A	myocyte enhancer factor 2C
ENSG00000134419	#N/A	#N/A	#N/A	1.53	#N/A	ribosomal protein S15a
ENSG00000089159	#N/A	#N/A	#N/A	1.52	#N/A	pexidin
ENSG00000141012	#N/A	#N/A	#N/A	1.52	#N/A	galactosamine (N-acetyl)-6-sulfatase
ENSG00000104998	#N/A	#N/A	#N/A	1.52	#N/A	interleukin 27 receptor, alpha
ENSG00000164609	#N/A	#N/A	#N/A	1.52	#N/A	SLU7 splicing factor homolog (S. cerevisiae)
ENSG00000243749	#N/A	#N/A	#N/A	1.51	#N/A	ZMYM6 neighbor
ENSG00000187243	#N/A	#N/A	#N/A	1.51	#N/A	melanoma antigen family D4B
ENSG00000146425	#N/A	#N/A	#N/A	1.51	1.56	dynein, light chain, Tctex-type 1
ENSG00000103121	#N/A	#N/A	#N/A	1.51	1.81	C-x(9)-C motif containing 2
ENSG00000134138	#N/A	#N/A	#N/A	1.50	#N/A	Meis homeobox 2
ENSG00000265146	#N/A	#N/A	#N/A	1.50	#N/A	BZRAP1 antisense RNA 1
ENSG00000165030	#N/A	#N/A	#N/A	1.49	#N/A	nuclear factor, interleukin 3 regulated
ENSG00000121060	#N/A	#N/A	#N/A	1.49	#N/A	tripartite motif containing 25
ENSG00000103018	#N/A	#N/A	#N/A	1.49	#N/A	cytochrome b5 type B (outer mitochondrial membrane)
ENSG00000163840	#N/A	#N/A	#N/A	1.49	#N/A	doxif 3 like, E3 ubiquitin ligase
ENSG00000151366	#N/A	#N/A	#N/A	1.49	2.39	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa
ENSG00000132432	#N/A	#N/A	#N/A	1.49	2.10	Sec61 gamma subunit
ENSG00000106771	#N/A	#N/A	#N/A	1.49	#N/A	transmembrane protein 245
ENSG00000160691	#N/A	#N/A	#N/A	1.48	#N/A	SHC (Src homology 2 domain containing) transforming protein 1
ENSG00000099977	#N/A	#N/A	#N/A	1.48	1.09	D-dopa-chrome tautomerase
ENSG00000181523	#N/A	#N/A	#N/A	1.46	#N/A	N-sulfoglucosamine sulfohydrolase
ENSG00000114222	#N/A	#N/A	#N/A	1.46	#N/A	plasminogen activator, urokinase receptor
ENSG00000100055	#N/A	#N/A	#N/A	1.48	#N/A	cytohesin 4
ENSG00000164125	#N/A	#N/A	#N/A	1.46	#N/A	family with sequence similarity 198, member B
ENSG000000039523	#N/A	#N/A	#N/A	1.46	#N/A	family with sequence similarity 65, member A
ENSG00000142534	#N/A	#N/A	#N/A	1.48	#N/A	ribosomal protein S11
ENSG00000188021	#N/A	#N/A	#N/A	1.48	#N/A	ubiquitin 2
ENSG00000131446	#N/A	#N/A	#N/A	1.48	#N/A	mannosyl (alpha-1,3)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
ENSG00000134825	#N/A	#N/A	#N/A	1.47	2.06	transmembrane protein 258

ENSG00000009624	#N/A	#N/A	#N/A	-2.09	#N/A	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit
ENSG00000087269	#N/A	#N/A	#N/A	-2.09	#N/A	NOP14 nucleolar protein
ENSG00000185163	#N/A	#N/A	#N/A	-2.10	#N/A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51
ENSG00000221823	#N/A	#N/A	#N/A	-2.10	#N/A	protein phosphatase 3, regulatory subunit B, alpha
ENSG00000155380	#N/A	#N/A	#N/A	-2.11	#N/A	solute carrier family 16 (monocarboxylate transporter), member 1
ENSG000002235173	#N/A	#N/A	#N/A	-2.11	#N/A	HGH1 homolog
ENSG00000198763	#N/A	#N/A	#N/A	-2.11	#N/A	mitochondrially encoded NADH dehydrogenase 2
ENSG00000103266	#N/A	#N/A	#N/A	-2.11	#N/A	STIP1 homology and U-box containing protein 1, E3 ubiquitin protein ligase
ENSG00000282367	#N/A	#N/A	#N/A	-2.12	#N/A	phosphatidylserine synthase 2
ENSG00000116456	#N/A	#N/A	#N/A	-2.12	#N/A	WD repeat domain 77
ENSG00000179862	#N/A	#N/A	#N/A	-2.15	#N/A	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4
ENSG00000139675	#N/A	#N/A	#N/A	-2.17	#N/A	heterogeneous nuclear ribonucleoprotein A1-like 2
ENSG00000243716	#N/A	#N/A	#N/A	-2.18	#N/A	nuclear pore complex interacting protein family, member B5
ENSG00000183751	#N/A	#N/A	#N/A	-2.19	#N/A	transducin (beta)-like 3
ENSG00000114446	#N/A	#N/A	#N/A	-2.20	#N/A	intraflagellar transport 57
ENSG00000183605	#N/A	#N/A	#N/A	-2.21	#N/A	sideroflexin 4
ENSG00000103342	#N/A	#N/A	#N/A	-2.26	#N/A	G1 to S phase transition 1
ENSG00000198899	#N/A	#N/A	#N/A	-2.26	#N/A	mitochondrially encoded ATP synthase 6
ENSG00000120738	#N/A	#N/A	#N/A	-2.28	#N/A	early growth response 1
ENSG00000007264	#N/A	#N/A	#N/A	-2.29	#N/A	megakaryocyte-associated tyrosine kinase
ENSG00000226916	#N/A	#N/A	#N/A	-2.33	#N/A	WD repeat domain 46
ENSG00000174669	#N/A	#N/A	#N/A	-2.33	#N/A	solute carrier family 29 (equilibrative nucleoside transporter), member 2
ENSG00000183688	#N/A	#N/A	#N/A	-2.36	#N/A	family with sequence similarity 101, member B
ENSG00000116852	#N/A	#N/A	#N/A	-2.38	#N/A	kinesin family member 21B
ENSG00000074935	#N/A	#N/A	#N/A	-2.39	#N/A	tubulin, epsilon 1
ENSG00000160972	#N/A	#N/A	#N/A	-2.41	#N/A	ATPase family, AAA domain containing 38
ENSG00000224877	#N/A	#N/A	#N/A	-2.45	#N/A	chromosome 17 open reading frame 89
ENSG00000110660	#N/A	#N/A	#N/A	-2.45	#N/A	solute carrier family 35, member F2
ENSG00000011952	#N/A	#N/A	#N/A	-2.45	#N/A	NME/NM23 nucleoside diphosphate kinase 2
ENSG00000070669	#N/A	#N/A	#N/A	-2.45	#N/A	asparagine synthetase (glutamine-hydrolyzing)
ENSG00000277957	#N/A	#N/A	#N/A	-2.46	#N/A	SEN3-EIF4A1 readthrough (NMD candidate)
ENSG00000106070	#N/A	#N/A	#N/A	-2.46	#N/A	growth factor receptor-bound protein 10
ENSG00000262814	#N/A	#N/A	#N/A	-2.54	#N/A	mitochondrial ribosomal protein L12
ENSG00000175445	#N/A	#N/A	#N/A	-2.60	#N/A	lipoprotein lipase
ENSG00000160818	#N/A	#N/A	#N/A	-2.67	#N/A	G patch domain containing 4
ENSG00000154284	#N/A	#N/A	#N/A	-2.72	#N/A	GrpE-like 2, mitochondrial (E. coli)
ENSG000000052749	#N/A	#N/A	#N/A	2.74	#N/A	ribosomal RNA processing 12 homolog
ENSG00000106588	#N/A	#N/A	#N/A	-2.77	#N/A	proteasome (prosome, macropain) subunit, alpha type, 2
ENSG00000169246	#N/A	#N/A	#N/A	-3.18	#N/A	nuclear pore complex interacting protein family, member B3
ENSG00000169136	#N/A	#N/A	#N/A	-3.29	#N/A	activating transcription factor 5
ENSG00000176076	#N/A	#N/A	#N/A	-3.41	#N/A	potassium channel, voltage gated subfamily E regulatory beta subunit 5
ENSG000002239672	#N/A	#N/A	#N/A	-4.00	#N/A	NME/NM23 nucleoside diphosphate kinase 1
ENSG00000128965	#N/A	#N/A	#N/A	-4.85	#N/A	ChaC glutathione-specific gamma-glutamylcyclotransferase 1
ENSG00000263006	#N/A	#N/A	#N/A	7.14	#N/A	Rho-associated, coiled-coil containing protein kinase 1 pseudogene 1
ENSG00000240184	#N/A	#N/A	#N/A	5.51	#N/A	protocadherin gamma subfamily C, 3
ENSG000000099139	#N/A	#N/A	#N/A	4.94	#N/A	proprotein convertase subtilisin/kexin type 5
ENSG00000230453	#N/A	#N/A	#N/A	4.79	#N/A	ankyrin repeat domain 18B

FIGURE 1T

ENSG00000106948	#N/A	#N/A	#N/A	1.47	#N/A	AT-hook transcription factor
ENSG00000187098	#N/A	#N/A	#N/A	1.47	#N/A	microphthalmia-associated transcription factor
ENSG00000257923	#N/A	#N/A	#N/A	1.47	#N/A	cut-like homeobox 1
ENSG00000118181	#N/A	#N/A	#N/A	1.47	1.10	ribosomal protein S25
ENSG00000226474	#N/A	#N/A	#N/A	1.47	1.33	oligosaccharyltransferase complex subunit 4 (non-catalytic)
ENSG00000104731	#N/A	#N/A	#N/A	1.47	#N/A	keich domain containing 4
ENSG00000177961	#N/A	#N/A	#N/A	1.47	#N/A	ankyrin repeat and SOCS box containing 8
ENSG00000067057	#N/A	#N/A	#N/A	1.46	#N/A	phosphofructokinase, platelet
ENSG00000118267	#N/A	#N/A	#N/A	1.46	1.30	ZNF271
ENSG00000143226	#N/A	#N/A	#N/A	1.45	#N/A	Fc fragment of IgG, low affinity IIa, receptor (CD32)
ENSG00000172936	#N/A	#N/A	#N/A	1.45	#N/A	myeloid differentiation primary response 68
ENSG00000069966	#N/A	#N/A	#N/A	1.45	#N/A	guanine nucleotide binding protein (G protein), beta 5
ENSG0000014914	#N/A	#N/A	#N/A	1.45	#N/A	myotubularin related protein 11
ENSG00000078124	#N/A	#N/A	#N/A	1.44	1.52	alkaline ceramidase 3
ENSG00000132823	#N/A	#N/A	#N/A	1.44	#N/A	oxidative stress responsive serine-rich 1
ENSG00000123360	#N/A	#N/A	#N/A	1.44	#N/A	phosphodiesterase 1B, calmodulin-dependent
ENSG00000027697	#N/A	#N/A	#N/A	1.44	#N/A	interferon gamma receptor 1
ENSG00000119801	#N/A	#N/A	#N/A	1.44	#N/A	yippee-like 5
ENSG00000134107	#N/A	#N/A	#N/A	1.44	1.27	basic helix-loop-helix family, member e40
ENSG00000104921	#N/A	#N/A	#N/A	1.44	#N/A	Fc fragment of IgE, low affinity II, receptor for (CD23)
ENSG00000028137	#N/A	#N/A	#N/A	1.43	#N/A	tumor necrosis factor receptor superfamily, member 1B
ENSG00000105355	#N/A	#N/A	#N/A	1.43	#N/A	perlepin 3
ENSG00000109475	#N/A	#N/A	#N/A	1.43	#N/A	ribosomal protein L34
ENSG00000255439	#N/A	#N/A	#N/A	1.43	#N/A	Uncharacterized protein
ENSG00000137575	#N/A	#N/A	#N/A	1.43	#N/A	syndecan binding protein (syntenin)
ENSG00000168273	#N/A	#N/A	#N/A	1.43	#N/A	small integral membrane protein 4
ENSG00000086065	#N/A	#N/A	#N/A	1.43	#N/A	charged multivesicular body protein 5
ENSG00000205542	#N/A	#N/A	#N/A	1.43	#N/A	thymosin beta 4, X-linked
ENSG00000105193	#N/A	#N/A	#N/A	1.42	#N/A	ribosomal protein S16
ENSG00000163220	#N/A	#N/A	#N/A	1.42	#N/A	S100 calcium binding protein A8
ENSG00000166404	#N/A	#N/A	#N/A	1.42	#N/A	mixed lineage kinase domain-like
ENSG00000085719	#N/A	#N/A	#N/A	1.42	#N/A	ocspine R1
ENSG00000157895	#N/A	#N/A	#N/A	1.41	1.14	chromosome 12 open reading frame 43
ENSG00000140199	#N/A	#N/A	#N/A	1.41	#N/A	solute carrier family 12 (potassium/chloride transporter), member 6
ENSG00000137818	#N/A	#N/A	#N/A	1.41	#N/A	ribosomal protein, large, P1
ENSG00000272657	#N/A	#N/A	#N/A	1.41	#N/A	AP00320.7
ENSG00000164587	#N/A	#N/A	#N/A	1.41	#N/A	ribosomal protein S14
ENSG00000131981	#N/A	#N/A	#N/A	1.41	#N/A	lectin, galactoside-binding, soluble, 3
ENSG00000254995	#N/A	#N/A	#N/A	1.41	#N/A	STX16-NPEPL1 readthrough (NMD candidate)
ENSG00000098951	#N/A	#N/A	#N/A	1.41	#N/A	human immunodeficiency virus type 1 enhancer binding protein 1
ENSG00000133816	#N/A	#N/A	#N/A	1.41	#N/A	microtubule associated monooxygenase, coixinin and LIM domain containing 2
ENSG00000270106	#N/A	#N/A	#N/A	1.40	#N/A	TSNAX-DISC1 readthrough (NMD candidate)
ENSG00000196123	#N/A	#N/A	#N/A	1.40	#N/A	KIAA0695-like
ENSG00000115561	#N/A	#N/A	#N/A	1.40	#N/A	charged multivesicular body protein 3
ENSG00000266714	#N/A	#N/A	#N/A	1.40	#N/A	myosin XVb
ENSG00000101132	#N/A	#N/A	#N/A	1.30	1.29	prefoldin subunit 4
ENSG00000159251	#N/A	#N/A	#N/A	#N/A	4.02	actin, alpha, cardiac muscle 1
ENSG00000124212	#N/A	#N/A	#N/A	#N/A	3.55	prostaglandin I2 (prostaglyclin) synthase
ENSG00000188483	#N/A	#N/A	#N/A	#N/A	3.43	immediate early response 5-like
ENSG00000100292	#N/A	#N/A	#N/A	#N/A	3.33	heme oxygenase 1
ENSG00000115380	#N/A	#N/A	#N/A	#N/A	3.23	EGF containing fibulin-like extracellular matrix protein 1
ENSG00000098901	#N/A	#N/A	#N/A	#N/A	3.14	paired-like homeodomain 1
ENSG00000130513	#N/A	#N/A	#N/A	#N/A	2.72	growth differentiation factor 15
ENSG00000115541	#N/A	#N/A	#N/A	#N/A	2.68	heat shock 10kDa protein 1
ENSG00000115461	#N/A	#N/A	#N/A	#N/A	2.53	insulin-like growth factor binding protein 5
ENSG00000102802	#N/A	#N/A	#N/A	#N/A	2.53	mesenteric estrogen-dependent adipogenesis
ENSG00000139343	#N/A	#N/A	#N/A	#N/A	2.52	small nuclear ribonucleoprotein polypeptide F
ENSG00000197182	#N/A	#N/A	#N/A	#N/A	2.49	MIRLET7B host gene
ENSG00000104368	#N/A	#N/A	#N/A	#N/A	2.46	plasminogen activator, tissue
ENSG00000239927	#N/A	#N/A	#N/A	#N/A	2.43	ribonuclease P/MRP 21kDa subunit
ENSG00000111057	#N/A	#N/A	#N/A	#N/A	2.38	keratin 18, type I
ENSG00000145708	#N/A	#N/A	#N/A	#N/A	2.36	corticotropin releasing hormone binding protein
ENSG00000081870	#N/A	#N/A	#N/A	#N/A	2.36	heat shock protein family B (small), member 11
ENSG00000175768	#N/A	#N/A	#N/A	#N/A	2.36	translocase of outer mitochondrial membrane 5 homolog (yeast)
ENSG00000182004	#N/A	#N/A	#N/A	#N/A	2.26	small nuclear ribonucleoprotein polypeptide E
ENSG00000148671	#N/A	#N/A	#N/A	#N/A	2.22	adipogenesis regulatory factor
ENSG00000075826	#N/A	#N/A	#N/A	#N/A	2.22	SEC31 homolog B, COPII coating complex component
ENSG00000105591	#N/A	#N/A	#N/A	#N/A	2.13	mitochondrial ribosomal protein L32
ENSG00000143977	#N/A	#N/A	#N/A	#N/A	2.10	small nuclear ribonucleoprotein polypeptide G
ENSG00000154182	#N/A	#N/A	#N/A	#N/A	2.09	NADH dehydrogenase (ubiquinone) complex I, assembly factor 2
ENSG000000908394	#N/A	#N/A	#N/A	#N/A	2.05	microsomal glutathione S-transferase 1
ENSG00000152518	#N/A	#N/A	#N/A	#N/A	2.03	ZFP36 ring finger protein-like 2
ENSG00000262771	#N/A	#N/A	#N/A	#N/A	1.98	single-stranded DNA binding protein 1, mitochondrial
ENSG00000142396	#N/A	#N/A	#N/A	#N/A	1.98	endogenous retrovirus group K3, member 1
ENSG00000162385	#N/A	#N/A	#N/A	#N/A	1.98	mago homolog, exon junction complex core component
ENSG00000235365	#N/A	#N/A	#N/A	#N/A	1.95	GS1-600G8.5
ENSG00000179958	#N/A	#N/A	#N/A	#N/A	1.94	dCTP pyrophosphatase 1
ENSG00000158003	#N/A	#N/A	#N/A	#N/A	1.94	solute carrier family 3 (amino acid transporter heavy chain), member 2
ENSG00000173436	#N/A	#N/A	#N/A	#N/A	1.91	mitochondrial inner membrane organizing system 1
ENSG00000163156	#N/A	#N/A	#N/A	#N/A	1.91	sodium channel modifier 1
ENSG00000143256	#N/A	#N/A	#N/A	#N/A	1.91	prefoldin subunit 2
ENSG00000112769	#N/A	#N/A	#N/A	#N/A	1.91	tsmnin, alpha 4
ENSG00000082515	#N/A	#N/A	#N/A	#N/A	1.89	mitochondrial ribosomal protein L22
ENSG00000127922	#N/A	#N/A	#N/A	#N/A	1.88	split hand/foot malformation (ectrodactyly) type 1
ENSG00000198211	#N/A	#N/A	#N/A	#N/A	1.88	tubulin, beta 3 class II
ENSG00000090263	#N/A	#N/A	#N/A	#N/A	1.87	mitochondrial ribosomal protein S33
ENSG00000217930	#N/A	#N/A	#N/A	#N/A	1.87	presequence translocase-associated motor 16 homolog (S. cerevisiae)
ENSG00000104825	#N/A	#N/A	#N/A	#N/A	1.86	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta
ENSG00000229833	#N/A	#N/A	#N/A	#N/A	1.85	PET100 homolog
ENSG00000123353	#N/A	#N/A	#N/A	#N/A	1.85	ORMDL sphingolipid biosynthesis regulator 2
ENSG00000157779	#N/A	#N/A	#N/A	#N/A	1.85	insulin-like growth factor binding protein 5
ENSG00000147862	#N/A	#N/A	#N/A	#N/A	1.85	nuclear factor I/B

FIGURE 1U

ENSG00000124370	#N/A	#N/A	#N/A	1.40	#N/A	methylmalonyl CoA epimerase
ENSG00000156052	#N/A	#N/A	#N/A	1.40	#N/A	guanine nucleotide binding protein (G protein), q polypeptide
ENSG00000119950	#N/A	#N/A	#N/A	1.39	#N/A	MAX interactor 1, dimerization protein
ENSG00000163319	#N/A	#N/A	#N/A	1.39	2.47	mitochondrial ribosomal protein S18C
ENSG00000161970	#N/A	#N/A	#N/A	1.39	#N/A	ribosomal protein L26
ENSG00000197747	#N/A	#N/A	#N/A	1.39	#N/A	S100 calcium binding protein A10
ENSG00000106316	#N/A	#N/A	#N/A	1.39	#N/A	beta-site APP-cleaving enzyme 1
ENSG00000204364	#N/A	#N/A	#N/A	1.39	#N/A	complement component 2
ENSG00000158006	#N/A	#N/A	#N/A	1.39	#N/A	platelet-activating factor acetylhydrolase 2, 40kDa
ENSG00000208690	#N/A	#N/A	#N/A	1.39	#N/A	kizuna centrosomal protein
ENSG00000114737	#N/A	#N/A	#N/A	1.38	#N/A	cytokine inducible SH2-containing protein
ENSG00000115736	#N/A	#N/A	#N/A	1.38	#N/A	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
ENSG00000257341	#N/A	#N/A	#N/A	1.38	#N/A	cysteine-rich protein 1 (intestinal)
ENSG00000160710	#N/A	#N/A	#N/A	1.38	#N/A	adenosine deaminase, RNA-specific
ENSG00000142347	#N/A	#N/A	#N/A	1.38	#N/A	myosin IF
ENSG00000121552	#N/A	#N/A	#N/A	1.38	#N/A	cystatin A (steftin A)
ENSG00000198258	#N/A	#N/A	#N/A	1.38	1.92	ubiquitin-like 5
ENSG00000136816	#N/A	#N/A	#N/A	1.38	#N/A	torsin family 1, member B (torsin B)
ENSG000002043147	#N/A	#N/A	#N/A	1.37	2.14	mitochondrial ribosomal protein L33
ENSG00000119720	#N/A	#N/A	#N/A	1.37	#N/A	NRDE-2, necessary for RNA interference, domain containing
ENSG00000115886	#N/A	#N/A	#N/A	1.37	#N/A	aspartyl-tRNA synthetase
ENSG00000276276	#N/A	#N/A	#N/A	1.37	#N/A	ADP-ribosylation factor-like 17B
ENSG00000224152	#N/A	#N/A	#N/A	1.36	#N/A	AC009506.1
ENSG00000143553	#N/A	#N/A	#N/A	1.36	1.15	SNAP-associated protein
ENSG00000124172	#N/A	#N/A	#N/A	1.36	1.47	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit
ENSG00000105374	#N/A	#N/A	#N/A	1.36	#N/A	natural killer cell granule protein 7
ENSG00000186174	#N/A	#N/A	#N/A	1.36	#N/A	B-cell CLL/lymphoma 9-like
ENSG00000169860	#N/A	#N/A	#N/A	1.36	#N/A	purinergic receptor P2Y, G-protein coupled, 1
ENSG00000159399	#N/A	#N/A	#N/A	1.36	#N/A	hexokinase 2
ENSG00000122026	#N/A	#N/A	#N/A	1.36	1.09	ribosomal protein L21
ENSG00000189043	#N/A	#N/A	#N/A	1.36	1.46	NCUFA4, mitochondrial complex associated
ENSG00000143382	#N/A	#N/A	#N/A	1.36	#N/A	ADAMTS-like 4
ENSG00000167461	#N/A	#N/A	#N/A	1.36	#N/A	RAB8A, member RAS oncogene family
ENSG00000214022	#N/A	#N/A	#N/A	1.36	1.82	replication initiator 1
ENSG00000185722	#N/A	#N/A	#N/A	1.36	#N/A	ankyrin repeat and FYVE domain containing 1
ENSG00000166147	#N/A	#N/A	#N/A	1.35	#N/A	fibrillin 1
ENSG00000117523	#N/A	#N/A	#N/A	1.35	#N/A	proline-rich coiled-coil 2C
ENSG00000169756	#N/A	#N/A	#N/A	1.35	#N/A	LIM and senescent cell antigen-like domains 1
ENSG00000177917	#N/A	#N/A	#N/A	1.35	#N/A	ADP-ribosylation factor-like 6 interacting protein 6
ENSG00000143545	#N/A	#N/A	#N/A	1.35	#N/A	RAB13, member RAS oncogene family
ENSG00000100097	#N/A	#N/A	#N/A	1.35	#N/A	lectin, galactoside-binding, soluble, 1
ENSG00000237945	#N/A	#N/A	#N/A	1.35	#N/A	long intergenic non-protein coding RNA 549
ENSG00000111640	#N/A	#N/A	#N/A	1.35	#N/A	glyceraldehyde-3-phosphate dehydrogenase
ENSG00000186812	#N/A	#N/A	#N/A	1.34	#N/A	zinc finger protein 397
ENSG000002065518	#N/A	#N/A	#N/A	1.34	1.55	NADH dehydrogenase (ubiquinone): 1 beta subcomplex, 4, 15kDa
ENSG00000168275	#N/A	#N/A	#N/A	1.34	#N/A	cytochrome c oxidase assembly factor 6
ENSG00000177426	#N/A	#N/A	#N/A	#N/A	1.85	TGFB-induced factor homeobox 1
ENSG00000208023	#N/A	#N/A	#N/A	#N/A	1.85	MOK protein kinase
ENSG00000154723	#N/A	#N/A	#N/A	#N/A	1.81	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit F6
ENSG00000111832	#N/A	#N/A	#N/A	#N/A	1.79	RWD domain containing 1
ENSG00000176731	#N/A	#N/A	#N/A	#N/A	1.78	chromosome 8 open reading frame 56
ENSG00000198498	#N/A	#N/A	#N/A	#N/A	1.78	translation machinery associated 16 homolog (S. cerevisiae)
ENSG00000174917	#N/A	#N/A	#N/A	#N/A	1.75	chromosome 19 open reading frame 70
ENSG00000154582	#N/A	#N/A	#N/A	#N/A	1.74	transcription elongation factor B (SII), polypeptide 1 (15kDa, elongin C)
ENSG00000171303	#N/A	#N/A	#N/A	#N/A	1.73	potassium channel, two pore domain subfamily K, member 3
ENSG00000171246	#N/A	#N/A	#N/A	#N/A	1.72	neuronal pentraxin 1
ENSG00000105185	#N/A	#N/A	#N/A	#N/A	1.72	programmed cell death 5
ENSG00000148688	#N/A	#N/A	#N/A	#N/A	1.71	ribonuclease P/MRP 30kDa subunit
ENSG00000130770	#N/A	#N/A	#N/A	#N/A	1.71	ATPase inhibitory factor 1
ENSG00000161911	#N/A	#N/A	#N/A	#N/A	1.70	sequestosome 1
ENSG00000146066	#N/A	#N/A	#N/A	#N/A	1.69	HIG1 hypoxia inducible domain family, member 2A
ENSG00000165389	#N/A	#N/A	#N/A	#N/A	1.68	serine palmitoyltransferase, small subunit A
ENSG00000203805	#N/A	#N/A	#N/A	#N/A	1.67	phosphatidic acid phosphatase type 2 domain containing 1A
ENSG00000163827	#N/A	#N/A	#N/A	#N/A	1.66	leucine rich repeat containing 2
ENSG00000133169	#N/A	#N/A	#N/A	#N/A	1.65	brain expressed, X-linked 1
ENSG00000114784	#N/A	#N/A	#N/A	#N/A	1.65	eukaryotic translation initiation factor 1B
ENSG00000196352	#N/A	#N/A	#N/A	#N/A	1.65	CD55 molecule, decay accelerating factor for complement (Cromer blood group)
ENSG00000147669	#N/A	#N/A	#N/A	#N/A	1.64	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa
ENSG00000190902	#N/A	#N/A	#N/A	#N/A	1.64	proteasome (prosome, macropain) subunit, alpha type, 6
ENSG00000105825	#N/A	#N/A	#N/A	#N/A	1.63	tissue factor pathway inhibitor 2
ENSG00000185112	#N/A	#N/A	#N/A	#N/A	1.63	family with sequence similarity 43, member A
ENSG00000214046	#N/A	#N/A	#N/A	#N/A	1.62	small integral membrane protein 7
ENSG00000125743	#N/A	#N/A	#N/A	#N/A	1.62	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa
ENSG00000119705	#N/A	#N/A	#N/A	#N/A	1.61	SRA stem-loop interacting RNA binding protein
ENSG00000148690	#N/A	#N/A	#N/A	#N/A	1.61	fragile site, folio acid type, rare, fra(10)(q23.3) or fra(10)(q24.2) candidate 1
ENSG00000145354	#N/A	#N/A	#N/A	#N/A	1.61	CDGSH iron sulfur domain 2
ENSG00000104763	#N/A	#N/A	#N/A	#N/A	1.61	N-acylsphingosine amidohydrolase (acid ceramidase) 1
ENSG00000180799	#N/A	#N/A	#N/A	#N/A	1.61	coiled-coil domain containing 12
ENSG00000227051	#N/A	#N/A	#N/A	#N/A	1.61	chromosome 14 open reading frame 132
ENSG00000171453	#N/A	#N/A	#N/A	#N/A	1.61	polymerase (RNA) I polypeptide C, 30kDa
ENSG00000147535	#N/A	#N/A	#N/A	#N/A	1.61	phosphatidic acid phosphatase type 2 domain containing 1B
ENSG00000136897	#N/A	#N/A	#N/A	#N/A	1.60	mitochondrial ribosomal protein L50
ENSG00000130332	#N/A	#N/A	#N/A	#N/A	1.60	LSM7 homolog, U6 small nuclear RNA and mRNA degradation associated
ENSG00000173113	#N/A	#N/A	#N/A	#N/A	1.60	tRNA methyltransferase 11-2 homolog (S. cerevisiae)
ENSG00000273397	#N/A	#N/A	#N/A	#N/A	1.59	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa
ENSG00000143158	#N/A	#N/A	#N/A	#N/A	1.57	mitochondrial pyruvate carrier 2
ENSG00000166347	#N/A	#N/A	#N/A	#N/A	1.57	cytochrome b5 type A (microsomal)
ENSG00000161980	#N/A	#N/A	#N/A	#N/A	1.57	polymerase (RNA) II (DNA directed) polypeptide K, 12.3 kDa
ENSG00000167863	#N/A	#N/A	#N/A	#N/A	1.57	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d
ENSG00000101361	#N/A	#N/A	#N/A	#N/A	1.57	NOP56 ribonucleoprotein
ENSG00000120963	#N/A	#N/A	#N/A	#N/A	1.56	zinc finger protein 756
ENSG000002080762	#N/A	#N/A	#N/A	#N/A	1.56	mitochondrial pyruvate carrier 1

FIGURE 1V

ENSG00000125977	#N/A	#N/A	#N/A	1.34	1.64	eukaryotic translation initiation factor 2, subunit 2 beta, 36kDa
ENSG00000144791	#N/A	#N/A	#N/A	1.34	#N/A	LIM domains containing 1
ENSG00000206573	#N/A	#N/A	#N/A	1.34	#N/A	THUMP3 antisense RNA 1
ENSG00000240344	#N/A	#N/A	#N/A	1.33	#N/A	peptidylprolyl isomerase (cyclophilin)-like 3
ENSG00000188559	#N/A	#N/A	#N/A	1.33	#N/A	Ral GTPase activating protein, alpha subunit 2 (catalytic)
ENSG00000175482	#N/A	#N/A	#N/A	1.33	#N/A	polymerase (DNA-directed), delta 4, accessory subunit
ENSG00000134970	#N/A	#N/A	#N/A	1.33	#N/A	transmembrane emp24 protein transport domain containing 7
ENSG00000131507	#N/A	#N/A	#N/A	1.33	#N/A	Nedd4 family interacting protein 1
ENSG00000231500	#N/A	#N/A	#N/A	1.33	#N/A	ribosomal protein S18
ENSG00000101608	#N/A	#N/A	#N/A	1.33	#N/A	myosin, light chain 12A, regulatory, non-sarcomeric
ENSG00000167210	#N/A	#N/A	#N/A	1.33	#N/A	glucosaminyl (N-acetyl) transferase 1, core 2
ENSG00000180964	#N/A	#N/A	#N/A	1.33	#N/A	transcription elongation factor A (SII)-like B
ENSG00000118266	#N/A	#N/A	#N/A	1.32	#N/A	cAMP responsive element binding protein 1
ENSG00000105829	#N/A	#N/A	#N/A	1.32	1.29	Bel1 golgi vesicular membrane trafficking protein
ENSG00000163975	#N/A	#N/A	#N/A	1.32	#N/A	antigen p57 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5
ENSG00000169032	#N/A	#N/A	#N/A	1.32	#N/A	mitogen-activated protein kinase kinase 1
ENSG00000196663	#N/A	#N/A	#N/A	1.32	1.15	translocase of outer mitochondrial membrane 7 homolog (yeast)
ENSG00000070814	#N/A	#N/A	#N/A	1.32	2.22	Treacher Collins-Franceschetti syndrome 1
ENSG00000111275	#N/A	#N/A	#N/A	1.32	#N/A	aldehyde dehydrogenase 2 family (mitochondrial)
ENSG00000182634	#N/A	#N/A	#N/A	1.32	#N/A	matrix-remodelling associated 7
ENSG00000214413	#N/A	#N/A	#N/A	1.32	1.69	BBSome interacting protein 1
ENSG00000136448	#N/A	#N/A	#N/A	1.32	#N/A	N-myristoyltransferase 1
ENSG00000150991	#N/A	#N/A	#N/A	1.31	#N/A	ubiquitin C
ENSG00000119876	#N/A	#N/A	#N/A	1.31	1.58	cysteine-rich PDZ-binding protein
ENSG00000197256	#N/A	#N/A	#N/A	1.31	#N/A	KN motif and ankyrin repeat domains 2
ENSG00000280826	#N/A	#N/A	#N/A	1.31	#N/A	RP11-274B21.1
ENSG00000262418	#N/A	#N/A	#N/A	1.31	#N/A	protein tyrosine phosphatase, receptor type, C
ENSG00000120709	#N/A	#N/A	#N/A	1.31	#N/A	family with sequence similarity 53, member C
ENSG00000108560	#N/A	#N/A	#N/A	1.31	#N/A	GTPase, IMAP family member 2
ENSG00000177738	#N/A	#N/A	#N/A	1.31	#N/A	CTD-2201E18.3
ENSG00000155876	#N/A	#N/A	#N/A	1.30	#N/A	Ras-related GTP binding A
ENSG00000119820	#N/A	#N/A	#N/A	1.30	#N/A	Yip1 domain family, member 4
ENSG00000136238	#N/A	#N/A	#N/A	1.30	1.13	ras-related G3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
ENSG00000124201	#N/A	#N/A	#N/A	1.30	#N/A	zinc finger, NFX1-type containing 1
ENSG00000124614	#N/A	#N/A	#N/A	1.30	#N/A	ribosomal protein S10
ENSG00000111526	#N/A	#N/A	#N/A	1.30	#N/A	solute carrier family 16 (monocarboxylate transporter), member 3
ENSG00000198604	#N/A	#N/A	#N/A	1.30	#N/A	bromodomain adjacent to zinc finger domain, 1A
ENSG00000104814	#N/A	#N/A	#N/A	1.30	#N/A	mitogen-activated protein kinase kinase kinase kinase 1
ENSG00000110700	#N/A	#N/A	#N/A	1.30	#N/A	ribosomal protein S13
ENSG00000198682	#N/A	#N/A	#N/A	1.30	#N/A	3'-phosphoadenosine 5'-phosphosulfate synthase 2
ENSG00000167850	#N/A	#N/A	#N/A	1.29	#N/A	CD300c molecule

ENSG00000189403	#N/A	#N/A	#N/A	#N/A	1.55	high mobility group box 1
ENSG00000185043	#N/A	#N/A	#N/A	#N/A	1.55	calcium and integrin binding 1 (calmyrin)
ENSG00000133398	#N/A	#N/A	#N/A	#N/A	1.54	mediator complex subunit 10
ENSG00000104332	#N/A	#N/A	#N/A	#N/A	1.54	secreted frizzled-related protein 1
ENSG00000186577	#N/A	#N/A	#N/A	#N/A	1.54	chromosome 6 open reading frame 1
ENSG00000176953	#N/A	#N/A	#N/A	#N/A	1.54	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein
ENSG00000163170	#N/A	#N/A	#N/A	#N/A	1.53	boA family member 3
ENSG00000180992	#N/A	#N/A	#N/A	#N/A	1.53	mitochondrial ribosomal protein L14
ENSG00000120875	#N/A	#N/A	#N/A	#N/A	1.52	dual specificity phosphatase 4
ENSG00000116473	#N/A	#N/A	#N/A	#N/A	1.52	RAP1A, member of RAS oncogene family
ENSG00000205981	#N/A	#N/A	#N/A	#N/A	1.52	DnaJ (Hsp40) homolog, subfamily C, member 19
ENSG00000275724	#N/A	#N/A	#N/A	#N/A	1.51	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa, isoform CRA_e; NDUF43 protein; cDNA FLJ76508, highly similar to Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa (NDUF43), mRNA
ENSG00000172336	#N/A	#N/A	#N/A	#N/A	1.51	POP7 homolog, ribonuclease P/MRP subunit
ENSG00000139233	#N/A	#N/A	#N/A	#N/A	1.51	LLP homolog, long-term synaptic facilitation (Aplysia)
ENSG00000164258	#N/A	#N/A	#N/A	#N/A	1.50	NADH dehydrogenase (ubiquinone): Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)
ENSG00000141837	#N/A	#N/A	#N/A	#N/A	1.50	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
ENSG00000120533	#N/A	#N/A	#N/A	#N/A	1.49	enhancer of yellow 2 homolog (Drosophila)
ENSG000001190142	#N/A	#N/A	#N/A	#N/A	1.48	polymerase (RNA) II (DNA directed) polypeptide F
ENSG00000122641	#N/A	#N/A	#N/A	#N/A	1.48	inhibin, beta A
ENSG00000197070	#N/A	#N/A	#N/A	#N/A	1.48	arrestin domain containing 1
ENSG00000125356	#N/A	#N/A	#N/A	#N/A	1.47	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa
ENSG000002255717	#N/A	#N/A	#N/A	#N/A	1.47	small nuclear RNA host gene 1
ENSG00000225921	#N/A	#N/A	#N/A	#N/A	1.45	nuclear protein 7, 27kDa
ENSG00000171735	#N/A	#N/A	#N/A	#N/A	1.45	calmodulin binding transcription activator 1
ENSG00000124882	#N/A	#N/A	#N/A	#N/A	1.44	epiregulin
ENSG00000175606	#N/A	#N/A	#N/A	#N/A	1.43	transmembrane protein 70
ENSG00000167772	#N/A	#N/A	#N/A	#N/A	1.43	angiopoietin-like 4
ENSG00000164114	#N/A	#N/A	#N/A	#N/A	1.42	microtubule-associated protein 9
ENSG00000100836	#N/A	#N/A	#N/A	#N/A	1.42	poly(A) binding protein, nuclear 1
ENSG00000255044	#N/A	#N/A	#N/A	#N/A	1.42	NOP58 ribonucleoprotein
ENSG00000235162	#N/A	#N/A	#N/A	#N/A	1.42	chromosome 12 open reading frame 75
ENSG00000163463	#N/A	#N/A	#N/A	#N/A	1.39	keratinocyte associated protein 2
ENSG00000170088	#N/A	#N/A	#N/A	#N/A	1.38	transmembrane protein 192
ENSG00000178127	#N/A	#N/A	#N/A	#N/A	1.38	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa
ENSG00000105803	#N/A	#N/A	#N/A	#N/A	1.38	Sec61 beta subunit
ENSG00000178906	#N/A	#N/A	#N/A	#N/A	1.38	exosome component 4
ENSG00000136888	#N/A	#N/A	#N/A	#N/A	1.37	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1
ENSG00000271462	#N/A	#N/A	#N/A	#N/A	1.37	Williams Beuren syndrome chromosome region 22
ENSG00000183726	#N/A	#N/A	#N/A	#N/A	1.37	transmembrane protein 50A
ENSG0000011237	#N/A	#N/A	#N/A	#N/A	1.37	VPS29 retromer complex component
ENSG00000164405	#N/A	#N/A	#N/A	#N/A	1.37	ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa

FIGURE 1W

ENSG00000198265	#N/A	#N/A	#N/A	1.29	#N/A	helicase with zinc finger
ENSG00000113108	#N/A	#N/A	#N/A	1.29	#N/A	amyloid beta (A4) precursor protein-binding, family B, member 3
ENSG00000186470	#N/A	#N/A	#N/A	1.26	#N/A	butyrophilin, subfamily 3, member A2
ENSG00000109046	#N/A	#N/A	#N/A	1.28	#N/A	WD repeat and SOCS box containing 1
ENSG00000185808	#N/A	#N/A	#N/A	1.28	#N/A	phosphatidylinositol glycan anchor biosynthesis, class P
ENSG00000159055	#N/A	#N/A	#N/A	1.26	#N/A	MIS18 kinetochore protein A
ENSG00000164054	#N/A	#N/A	#N/A	1.26	#N/A	shisa family member 5
ENSG00000168961	#N/A	#N/A	#N/A	1.28	#N/A	lectin, galactoside-binding, soluble, 9
ENSG00000102265	#N/A	#N/A	#N/A	1.26	#N/A	TIMP metalloproteinase inhibitor 1
ENSG00000198951	#N/A	#N/A	#N/A	1.28	#N/A	N-acetylgalactosaminidase, alpha-
ENSG00000147439	#N/A	#N/A	#N/A	1.27	#N/A	bridging integrator 3
ENSG00000085224	#N/A	#N/A	#N/A	1.27	#N/A	alpha thalassemia/mental retardation syndrome X-linked
ENSG00000124067	#N/A	#N/A	#N/A	1.27	#N/A	solute carrier family 12 (potassium/chloride transporter), member 4
ENSG00000129610	#N/A	#N/A	#N/A	1.27	#N/A	shugoshin-like 1 (S. pombe)
ENSG00000145743	#N/A	#N/A	#N/A	1.27	#N/A	F-box and leucine-rich repeat protein 17
ENSG00000157349	#N/A	#N/A	#N/A	1.27	#N/A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 15B
ENSG000000281794	#N/A	#N/A	#N/A	1.26	#N/A	long intergenic non-protein coding RNA 969
ENSG00000253230	#N/A	#N/A	#N/A	1.26	#N/A	long intergenic non-protein coding RNA 599
ENSG00000100599	#N/A	#N/A	#N/A	1.26	#N/A	Ras and Rab interactor 3
ENSG00000105372	#N/A	#N/A	#N/A	1.26	#N/A	ribosomal protein S19
ENSG000000968137	#N/A	#N/A	#N/A	1.26	#N/A	pleckstrin homology domain containing, family H (with MYTH4 domain) member 3
ENSG00000248092	#N/A	#N/A	#N/A	1.26	#N/A	NNT antisense RNA 1
ENSG00000132963	#N/A	#N/A	#N/A	1.26	2.08	proteasome maturation protein
ENSG00000130164	#N/A	#N/A	#N/A	1.26	#N/A	low density lipoprotein receptor
ENSG00000144034	#N/A	#N/A	#N/A	1.25	2.52	TP53RK binding protein
ENSG00000102977	#N/A	#N/A	#N/A	1.25	#N/A	adrenocortical dysplasia homolog (mouse)
ENSG00000126016	#N/A	#N/A	#N/A	1.25	#N/A	ZFP36 ring finger protein
ENSG00000117394	#N/A	#N/A	#N/A	1.25	#N/A	solute carrier family 2 (facilitated glucose transporter), member 1
ENSG00000163125	#N/A	#N/A	#N/A	1.25	1.52	regulation of nuclear pre-mRNA domain containing 2
ENSG00000229117	#N/A	#N/A	#N/A	1.24	#N/A	ribosomal protein L41
ENSG00000169499	#N/A	#N/A	#N/A	1.24	#N/A	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2
ENSG00000117614	#N/A	#N/A	#N/A	1.24	1.50	SYF2 pre-mRNA-splicing factor
ENSG00000082074	#N/A	#N/A	#N/A	1.24	#N/A	FYN binding protein
ENSG00000099013	#N/A	#N/A	#N/A	1.24	#N/A	biliverdin reductase B
ENSG00000135974	#N/A	#N/A	#N/A	1.24	#N/A	chromosome 2 open reading frame 49
ENSG00000132950	#N/A	#N/A	#N/A	1.24	#N/A	zinc finger, MYM-type 5
ENSG00000205423	#N/A	#N/A	#N/A	1.23	#N/A	CTD nuclear envelope phosphatase 1 regulatory subunit 1
ENSG00000143353	#N/A	#N/A	#N/A	1.23	#N/A	lysophospholipase-like 1
ENSG00000172725	#N/A	#N/A	#N/A	1.23	#N/A	coronin, actin binding protein, 1B
ENSG000000254996	#N/A	#N/A	#N/A	1.23	1.59	BRICK1, SCAR/WAVE actin-nucleating complex subunit
ENSG00000175727	#N/A	#N/A	#N/A	1.23	1.32	MLX interacting protein
ENSG00000221963	#N/A	#N/A	#N/A	1.23	1.41	ubiquitin A-52 residue ribosomal protein fusion product 1
ENSG00000143507	#N/A	#N/A	#N/A	1.22	#N/A	dual specificity phosphatase 10
ENSG00000239382	#N/A	#N/A	#N/A	1.22	#N/A	aIkB homolog 6
ENSG00000118985	#N/A	#N/A	#N/A	1.22	#N/A	elongation factor, RNA polymerase II, 2

ENSG00000115363	#N/A	#N/A	#N/A	#N/A	1.37	eva-1 homolog A (C. elegans)
ENSG00000103889	#N/A	#N/A	#N/A	#N/A	1.37	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
ENSG00000104823	#N/A	#N/A	#N/A	#N/A	1.35	enoyl CoA hydratase 1, peroxisomal
ENSG00000100028	#N/A	#N/A	#N/A	#N/A	1.35	small nuclear ribonucleoprotein D3 polypeptide 1&kDa
ENSG00000112667	#N/A	#N/A	#N/A	#N/A	1.35	2'-deoxynucleoside 5'-phosphate N-hydrolase 1
ENSG00000146386	#N/A	#N/A	#N/A	#N/A	1.34	ABRA C-terminal like
ENSG00000131586	#N/A	#N/A	#N/A	#N/A	1.34	MRPL20
ENSG00000171813	#N/A	#N/A	#N/A	#N/A	1.34	PWWP domain containing 2B
ENSG00000111231	#N/A	#N/A	#N/A	#N/A	1.33	GPN-loop GTPase 3
ENSG00000136213	#N/A	#N/A	#N/A	#N/A	1.33	carbohydrate (chondroitin 4) sulfotransferase 12
ENSG00000171204	#N/A	#N/A	#N/A	#N/A	1.32	transmembrane protein 126E
ENSG00000138175	#N/A	#N/A	#N/A	#N/A	1.32	ADP-ribosylation factor-like 3
ENSG00000134049	#N/A	#N/A	#N/A	#N/A	1.32	immediate early response 3 interacting protein 1
ENSG00000195518	#N/A	#N/A	#N/A	#N/A	1.31	transmembrane protein 205
ENSG00000172465	#N/A	#N/A	#N/A	#N/A	1.31	transcription elongation factor A (SII)-like 1
ENSG00000108010	#N/A	#N/A	#N/A	#N/A	1.31	glutaredoxin 3
ENSG00000272835	#N/A	#N/A	#N/A	#N/A	1.31	single-pass membrane protein with aspartate-rich tail 1
ENSG00000162520	#N/A	#N/A	#N/A	#N/A	1.31	syncollin, intermediate filament protein
ENSG00000136810	#N/A	#N/A	#N/A	#N/A	1.31	thioredoxin
ENSG00000208408	#N/A	#N/A	#N/A	#N/A	1.31	G patch domain and ankyrin repeats 1
ENSG00000165502	#N/A	#N/A	#N/A	#N/A	1.30	ribosomal protein L36a-like
ENSG00000111364	#N/A	#N/A	#N/A	#N/A	1.30	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55
ENSG00000197019	#N/A	#N/A	#N/A	#N/A	1.30	SERTA domain containing 1
ENSG00000167747	#N/A	#N/A	#N/A	#N/A	1.30	chromosome 19 open reading frame 48
ENSG00000173915	#N/A	#N/A	#N/A	#N/A	1.30	up-regulated during skeletal muscle growth 5 homolog (mouse)
ENSG00000143106	#N/A	#N/A	#N/A	#N/A	1.30	proteasome (prosome, macropain) subunit, alpha type, 5
ENSG00000172977	#N/A	#N/A	#N/A	#N/A	1.29	K(lysine) acetyltransferase 5
ENSG00000108175	#N/A	#N/A	#N/A	#N/A	1.29	zinc finger, MIZ-type containing 1
ENSG00000172586	#N/A	#N/A	#N/A	#N/A	1.29	coiled-coil-helix-coiled-coil-helix domain containing 1
ENSG00000185782	#N/A	#N/A	#N/A	#N/A	1.28	transmembrane protein 558
ENSG000000970010	#N/A	#N/A	#N/A	#N/A	1.25	ubiquitin fusion degradation 1 like (yeast)
ENSG00000150551	#N/A	#N/A	#N/A	#N/A	1.28	LYG/PLAUR domain containing 1
ENSG00000162300	#N/A	#N/A	#N/A	#N/A	1.28	zinc finger protein-like 1
ENSG000000990266	#N/A	#N/A	#N/A	#N/A	1.28	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa
ENSG000000905075	#N/A	#N/A	#N/A	#N/A	1.28	polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa
ENSG00000183527	#N/A	#N/A	#N/A	#N/A	1.27	proteasome (prosome, macropain) assembly chaperone 1
ENSG00000168653	#N/A	#N/A	#N/A	#N/A	1.27	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)
ENSG00000170791	#N/A	#N/A	#N/A	#N/A	1.27	coiled-coil-helix-coiled-coil-helix domain containing 7
ENSG00000101182	#N/A	#N/A	#N/A	#N/A	1.26	proteasome (prosome, macropain) subunit, alpha type, 7
ENSG00000115350	#N/A	#N/A	#N/A	#N/A	1.26	polymerase (DNA-directed), epsilon 4, accessory subunit
ENSG00000171202	#N/A	#N/A	#N/A	#N/A	1.26	transmembrane protein 126A
ENSG00000148834	#N/A	#N/A	#N/A	#N/A	1.25	glutathione S-transferase omega 1
ENSG00000154032	#N/A	#N/A	#N/A	#N/A	1.25	H2A histone family, member Z
ENSG00000261740	#N/A	#N/A	#N/A	#N/A	1.25	Uncharacterized protein
ENSG00000143387	#N/A	#N/A	#N/A	#N/A	1.25	cathepsin K

FIGURE 1X

ENSG00000178802	#N/A	#N/A	#N/A	1.22	#N/A	mannose phosphate isomerase
ENSG00000135452	#N/A	#N/A	#N/A	1.22	#N/A	tetraspanin 31
ENSG00000227669	#N/A	#N/A	#N/A	1.22	#N/A	major histocompatibility complex, class I, H (pseudogene)
ENSG00000106617	#N/A	#N/A	#N/A	1.22	#N/A	protein kinase, AMP-activated, gamma 2 non-catalytic subunit
ENSG00000117697	#N/A	#N/A	#N/A	1.22	1.25	NSL1, MIS12 kinetochore complex component
ENSG00000168255	#N/A	#N/A	#N/A	1.21	#N/A	polymerase (RNA) II (DNA directed) polypeptide J3
ENSG00000168126	#N/A	#N/A	#N/A	1.21	#N/A	RAB8B, member RAS oncogene family
ENSG00000129696	#N/A	#N/A	#N/A	1.21	#N/A	TELO2 interacting protein 2
ENSG00000141971	#N/A	#N/A	#N/A	1.21	#N/A	multivesicular body subunit 12A
ENSG00000145247	#N/A	#N/A	#N/A	1.21	1.50	OCA1A domain containing 2
ENSG00000166341	#N/A	#N/A	#N/A	1.21	#N/A	dachshous cadherin-related 1
ENSG00000186010	#N/A	#N/A	#N/A	1.20	1.82	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13
ENSG00000125971	#N/A	#N/A	#N/A	1.20	1.45	dyxen, light chain, roadblock-type 1
ENSG00000160223	#N/A	#N/A	#N/A	1.20	#N/A	inducible T-cell co-stimulator ligand
ENSG00000165264	#N/A	#N/A	#N/A	1.20	1.14	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa
ENSG00000163131	#N/A	#N/A	#N/A	1.20	#N/A	cathepsin S
ENSG00000158869	#N/A	#N/A	#N/A	1.20	#N/A	Fc fragment of IgE, high affinity 1, receptor for, gamma polypeptide
ENSG00000154439	#N/A	#N/A	#N/A	1.20	#N/A	bobby sox homolog (Drosophila)
ENSG00000114062	#N/A	#N/A	#N/A	1.20	#N/A	ubiquitin protein ligase E3A
ENSG00000162704	#N/A	#N/A	#N/A	1.19	#N/A	actin related protein 2/3 complex, subunit 5, 16kDa
ENSG00000102316	#N/A	#N/A	#N/A	1.19	#N/A	melanoma antigen family D2
ENSG00000005238	#N/A	#N/A	#N/A	1.19	#N/A	family with sequence similarity 214, member B
ENSG00000149257	#N/A	#N/A	#N/A	1.19	#N/A	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)
ENSG00000084676	#N/A	#N/A	#N/A	1.18	#N/A	nuclear receptor coactivator 1
ENSG00000124766	#N/A	#N/A	#N/A	1.18	#N/A	SRY (sex determining region Y)-box 4
ENSG00000114391	#N/A	#N/A	#N/A	1.18	#N/A	ribosomal protein L24
ENSG00000159882	#N/A	#N/A	#N/A	1.18	#N/A	zinc finger protein 230
ENSG00000141426	#N/A	#N/A	#N/A	1.18	#N/A	chromosome 18 open reading frame 21
ENSG00000142687	#N/A	#N/A	#N/A	1.18	#N/A	KIAA319-like
ENSG00000127540	#N/A	#N/A	#N/A	1.18	1.82	ubiquinol-cytochrome c reductase, complex II subunit XI
ENSG00000160753	#N/A	#N/A	#N/A	1.18	#N/A	RUN and SH3 domain containing 1
ENSG00000114796	#N/A	#N/A	#N/A	1.17	#N/A	leish-like family member 24
ENSG00000196154	#N/A	#N/A	#N/A	1.17	#N/A	S100 calcium binding protein A4
ENSG00000177576	#N/A	#N/A	#N/A	1.17	#N/A	chromosome 18 open reading frame 32
ENSG00000164167	#N/A	#N/A	#N/A	1.17	#N/A	LSM6 homolog, U6 small nuclear RNA and mRNA degradation associated
ENSG00000278461	#N/A	#N/A	#N/A	1.17	1.50	mitochondrial ribosomal protein S36
ENSG00000096996	#N/A	#N/A	#N/A	1.17	#N/A	interleukin 12 receptor, beta 1
ENSG00000137606	#N/A	#N/A	#N/A	1.16	1.27	NADH dehydrogenase (ubiquinone) complex I, assembly factor 1
ENSG00000175305	#N/A	#N/A	#N/A	1.16	#N/A	cyclin E2
ENSG00000185088	#N/A	#N/A	#N/A	1.16	1.76	ribosomal protein S27-like
ENSG00000104812	#N/A	#N/A	#N/A	1.16	#N/A	glycogen synthase 1 (muscle)
ENSG00000160049	#N/A	#N/A	#N/A	1.16	1.27	DNA fragmentation factor, 45kDa, alpha polypeptide

ENSG00000102007	#N/A	#N/A	#N/A	#N/A	1.24	proteolipid protein 2 (colonic epithelium-enriched)
ENSG00000078668	#N/A	#N/A	#N/A	#N/A	1.23	voltage-dependent anion channel 3
ENSG00000173163	#N/A	#N/A	#N/A	#N/A	1.23	copper metabolism (Murr1) domain containing 1
ENSG00000106355	#N/A	#N/A	#N/A	#N/A	1.23	LSM5 homolog, U6 small nuclear RNA and mRNA degradation associated
ENSG00000183291	#N/A	#N/A	#N/A	#N/A	1.23	15 kDa selenoprotein
ENSG00000144681	#N/A	#N/A	#N/A	#N/A	1.22	SH3 and cysteine rich domain
ENSG00000135919	#N/A	#N/A	#N/A	#N/A	1.22	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2
ENSG000000990581	#N/A	#N/A	#N/A	#N/A	1.22	N-acetylglucosamine-1-phosphate transferase, gamma subunit
ENSG00000135047	#N/A	#N/A	#N/A	#N/A	1.22	cathepsin L
ENSG00000213024	#N/A	#N/A	#N/A	#N/A	1.22	nucleoporin 62kDa
ENSG00000154719	#N/A	#N/A	#N/A	#N/A	1.21	mitochondrial ribosomal protein L39
ENSG00000078140	#N/A	#N/A	#N/A	#N/A	1.21	ubiquitin-conjugating enzyme E2K
ENSG00000150779	#N/A	#N/A	#N/A	#N/A	1.21	translocase of inner mitochondrial membrane 8 homolog B (yeast)
ENSG00000155115	#N/A	#N/A	#N/A	#N/A	1.21	general transcription factor IIC, polypeptide 6, alpha 35kDa
ENSG00000102103	#N/A	#N/A	#N/A	#N/A	1.21	polyglutamine binding protein 1
ENSG00000206283	#N/A	#N/A	#N/A	#N/A	1.20	prefoldin subunit 6
ENSG00000103496	#N/A	#N/A	#N/A	#N/A	1.20	syntrophin 4
ENSG00000165596	#N/A	#N/A	#N/A	#N/A	1.19	3-hydroxyacyl-CoA dehydratase 1
ENSG00000187514	#N/A	#N/A	#N/A	#N/A	1.19	prothymosin, alpha
ENSG00000104131	#N/A	#N/A	#N/A	#N/A	1.19	eukaryotic translation initiation factor 3, subunit J
ENSG00000133997	#N/A	#N/A	#N/A	#N/A	1.19	mediator complex subunit 6
ENSG00000131876	#N/A	#N/A	#N/A	#N/A	1.19	small nuclear ribonucleoprotein polypeptide A'
ENSG00000256591	#N/A	#N/A	#N/A	#N/A	1.19	Uncharacterized protein
ENSG00000107404	#N/A	#N/A	#N/A	#N/A	1.18	dishevelled segment polarity protein 1
ENSG00000103152	#N/A	#N/A	#N/A	#N/A	1.19	N-methylputrescine DNA glycosylase
ENSG00000120656	#N/A	#N/A	#N/A	#N/A	1.19	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 20kDa
ENSG00000136003	#N/A	#N/A	#N/A	#N/A	1.18	iron-sulfur cluster assembly enzyme
ENSG00000273841	#N/A	#N/A	#N/A	#N/A	1.18	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa
ENSG00000111775	#N/A	#N/A	#N/A	#N/A	1.18	cytochrome c oxidase subunit VIa polypeptide 1
ENSG00000182154	#N/A	#N/A	#N/A	#N/A	1.18	mitochondrial ribosomal protein L41
ENSG00000090674	#N/A	#N/A	#N/A	#N/A	1.18	mucoilin 1
ENSG00000147684	#N/A	#N/A	#N/A	#N/A	1.17	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa
ENSG000000982020	#N/A	#N/A	#N/A	#N/A	1.17	protein phosphatase 2, regulatory subunit B'', gamma
ENSG00000140307	#N/A	#N/A	#N/A	#N/A	1.17	general transcription factor IIA, 2, 12kDa
ENSG00000161281	#N/A	#N/A	#N/A	#N/A	1.17	cytochrome c oxidase subunit VIa polypeptide 1 (muscle)
ENSG00000176340	#N/A	#N/A	#N/A	#N/A	1.17	cytochrome c oxidase subunit VIHa (ubiquitous)
ENSG00000155034	#N/A	#N/A	#N/A	#N/A	1.16	F-box and leucine-rich repeat protein 18
ENSG00000131732	#N/A	#N/A	#N/A	#N/A	1.16	zinc finger, CCHC domain containing 9
ENSG00000131462	#N/A	#N/A	#N/A	#N/A	1.18	tubulin, gamma 1
ENSG00000228907	#N/A	#N/A	#N/A	#N/A	1.15	ring finger protein 5, E3 ubiquitin protein ligase
ENSG00000171621	#N/A	#N/A	#N/A	#N/A	1.15	spA/ryanodine receptor domain and SOCS box containing 1
ENSG00000126653	#N/A	#N/A	#N/A	#N/A	1.15	nuclear speckle splicing regulatory protein 1

FIGURE 1Y

ENSG00000197324	#N/A	#N/A	#N/A	1.16	#N/A	low density lipoprotein receptor-related protein 10
ENSG00000196628	#N/A	#N/A	#N/A	1.16	#N/A	transcription factor 4
ENSG00000268858	#N/A	#N/A	#N/A	1.16	#N/A	egl-9 family hypoxia-inducible factor 2
ENSG00000134248	#N/A	#N/A	#N/A	1.16	1.73	late endosomal/lysosomal adaptor, MAPK and MTOR activator 5
ENSG00000223745	#N/A	#N/A	#N/A	1.16	#N/A	RP4-717I23.3
ENSG00000158417	#N/A	#N/A	#N/A	1.16	2.14	eukaryotic translation initiation factor 5B
ENSG00000185950	#N/A	#N/A	#N/A	1.15	#N/A	insulin receptor substrate 2
ENSG00000007047	#N/A	#N/A	#N/A	1.15	#N/A	MAP/microtubule affinity-regulating kinase 4
ENSG00000105220	#N/A	#N/A	#N/A	1.15	#N/A	glucose-6-phosphate isomerase
ENSG00000153113	#N/A	#N/A	#N/A	1.15	#N/A	calpastatin
ENSG00000135926	#N/A	#N/A	#N/A	1.15	#N/A	transmembrane BAX inhibitor motif containing 1
ENSG00000145050	#N/A	#N/A	#N/A	1.15	1.56	mesencephalic astrocyte-derived neurotrophic factor
ENSG00000183648	#N/A	#N/A	#N/A	1.14	1.45	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa
ENSG00000113732	#N/A	#N/A	#N/A	1.14	1.49	ATPase, H ⁺ transporting, lysosomal 9kDa, V0 subunit e 1
ENSG00000124006	#N/A	#N/A	#N/A	1.14	#N/A	obscurin-like 1
ENSG00000105856	#N/A	#N/A	#N/A	1.14	#N/A	HMG-box transcription factor 1
ENSG00000198507	#N/A	#N/A	#N/A	1.14	1.28	transcription elongation factor A (SII)-like 3
ENSG00000187118	#N/A	#N/A	#N/A	1.14	#N/A	C-x(9)-C motif containing 1
ENSG00000166928	#N/A	#N/A	#N/A	1.14	#N/A	membrane-spanning 4-domains, subfamily A, member 14
ENSG00000167625	#N/A	#N/A	#N/A	1.14	#N/A	zinc finger protein 526
ENSG00000102144	#N/A	#N/A	#N/A	1.13	#N/A	phosphoglycerate kinase 1
ENSG00000174282	#N/A	#N/A	#N/A	1.13	#N/A	zinc finger and BTB domain containing 4
ENSG00000156535	#N/A	#N/A	#N/A	1.13	#N/A	CD199 molecule
ENSG00000229252	#N/A	#N/A	#N/A	1.13	#N/A	major histocompatibility complex, class I, E
ENSG00000134954	#N/A	#N/A	#N/A	1.13	#N/A	γ-ets avian erythroblastosis virus E26 oncogene homolog 1
ENSG00000275199	#N/A	#N/A	#N/A	1.13	#N/A	γ-akt murine thymoma viral oncogene homolog 3
ENSG00000076850	#N/A	#N/A	#N/A	1.13	#N/A	G patch domain containing 1
ENSG00000117616	#N/A	#N/A	#N/A	1.13	#N/A	arginine/serine-rich protein 1
ENSG00000114544	#N/A	#N/A	#N/A	1.13	#N/A	solute carrier family 41, member 3
ENSG00000007571	#N/A	#N/A	#N/A	1.13	#N/A	discs, large homolog 1 (Drosophila)
ENSG00000005445	#N/A	#N/A	#N/A	1.13	#N/A	WD repeat domain 54
ENSG00000008854	#N/A	#N/A	#N/A	1.13	#N/A	chromosome 20 open reading frame 194
ENSG00000265681	#N/A	#N/A	#N/A	1.13	#N/A	ribosomal protein L17
ENSG00000168802	#N/A	#N/A	#N/A	1.12	#N/A	chromosome transmission fidelity factor 8
ENSG00000139684	#N/A	#N/A	#N/A	1.12	#N/A	esterase D
ENSG00000008324	#N/A	#N/A	#N/A	1.12	#N/A	synovial sarcoma translocation gene on chromosome 15-like 2
ENSG00000124098	#N/A	#N/A	#N/A	1.12	#N/A	family with sequence similarity 210, member 8
ENSG00000170315	#N/A	#N/A	#N/A	1.12	#N/A	ubiquitin B
ENSG000000064393	#N/A	#N/A	#N/A	1.12	#N/A	homeodomain interacting protein kinase 2
ENSG00000177200	#N/A	#N/A	#N/A	1.12	#N/A	chromodomain helicase DNA binding protein 9
ENSG00000105640	#N/A	#N/A	#N/A	1.12	#N/A	ribosomal protein L18a
ENSG00000006534	#N/A	#N/A	#N/A	1.12	#N/A	aldehyde dehydrogenase 3 family, member B1
ENSG00000276879	#N/A	#N/A	#N/A	1.12	#N/A	interferon, alpha-inducible protein 27-like 2
ENSG00000125870	#N/A	#N/A	#N/A	1.11	1.33	small nuclear ribonucleoprotein polypeptide 9
ENSG00000164074	#N/A	#N/A	#N/A	1.11	#N/A	chromosome 4 open reading frame 29

ENSG00000177889	#N/A	#N/A	#N/A	#N/A	1.15	ubiquitin-conjugating enzyme E2N
ENSG00000159199	#N/A	#N/A	#N/A	#N/A	1.15	ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit C1 (subunit 9)
ENSG00000128708	#N/A	#N/A	#N/A	#N/A	1.14	histone acetyltransferase 1
ENSG00000162961	#N/A	#N/A	#N/A	#N/A	1.14	dpy-30 histone methyltransferase complex regulatory subunit
ENSG00000189062	#N/A	#N/A	#N/A	#N/A	1.14	UPF3 regulator of nonsense transcripts homolog A (yeast)
ENSG00000105379	#N/A	#N/A	#N/A	#N/A	1.14	electron-transfer-flavoprotein, beta polypeptide
ENSG00000275145	#N/A	#N/A	#N/A	#N/A	1.14	F5HD region gene 1
ENSG00000163281	#N/A	#N/A	#N/A	#N/A	1.14	glucosamine-6-phosphate deaminase 2
ENSG00000143314	#N/A	#N/A	#N/A	#N/A	1.14	mitochondrial ribosomal protein L24
ENSG00000127184	#N/A	#N/A	#N/A	#N/A	1.14	cytochrome c oxidase subunit VIc
ENSG00000277359	#N/A	#N/A	#N/A	#N/A	1.13	40S ribosomal protein S9; Ribosomal protein S9, isoform CRA_c
ENSG00000105755	#N/A	#N/A	#N/A	#N/A	1.13	ethylmalonic encephalopathy 1
ENSG00000168734	#N/A	#N/A	#N/A	#N/A	1.13	protein kinase (cAMP-dependent, catalytic) inhibitor gamma
ENSG00000105364	#N/A	#N/A	#N/A	#N/A	1.12	mitochondrial ribosomal protein L4
ENSG00000159079	#N/A	#N/A	#N/A	#N/A	1.12	chromosome 21 open reading frame 59
ENSG00000105202	#N/A	#N/A	#N/A	#N/A	1.12	fibrinogen
ENSG00000136942	#N/A	#N/A	#N/A	#N/A	1.12	ribosomal protein L35
ENSG00000125835	#N/A	#N/A	#N/A	#N/A	1.12	small nuclear ribonucleoprotein polypeptides B and B1
ENSG00000198840	#N/A	#N/A	#N/A	#N/A	1.12	mitochondrially encoded NADH dehydrogenase 3
ENSG00000185222	#N/A	#N/A	#N/A	#N/A	1.11	WW domain binding protein 5
ENSG00000147533	#N/A	#N/A	#N/A	#N/A	1.11	golgin A7
ENSG00000190632	#N/A	#N/A	#N/A	#N/A	1.11	enhancer of rudimentary homolog (Drosophila)
ENSG00000104915	#N/A	#N/A	#N/A	#N/A	1.11	syntrophin 10
ENSG00000188643	#N/A	#N/A	#N/A	#N/A	1.11	S100 calcium binding protein A16
ENSG00000130766	#N/A	#N/A	#N/A	#N/A	1.11	sestrin 2
ENSG00000113068	#N/A	#N/A	#N/A	#N/A	1.11	prefoldin subunit 1
ENSG00000173141	#N/A	#N/A	#N/A	#N/A	1.10	mitochondrial ribosomal protein L57
ENSG00000095418	#N/A	#N/A	#N/A	#N/A	1.10	phosphohistidine phosphatase 1
ENSG00000147996	#N/A	#N/A	#N/A	#N/A	1.10	COBWW domain containing 5
ENSG000000983457	#N/A	#N/A	#N/A	#N/A	1.10	integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)
ENSG00000117280	#N/A	#N/A	#N/A	#N/A	1.10	RAB29, member RAS oncogene family
ENSG00000157613	#N/A	#N/A	#N/A	#N/A	1.10	cAMP responsive element binding protein 3-like 1
ENSG00000174021	#N/A	#N/A	#N/A	#N/A	1.10	guanine nucleotide binding protein (G protein); gamma 5
ENSG00000133641	#N/A	#N/A	#N/A	#N/A	1.10	chromosome 12 open reading frame 29
ENSG00000101843	#N/A	#N/A	#N/A	#N/A	1.09	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10
ENSG00000138785	#N/A	#N/A	#N/A	#N/A	1.09	integrator complex subunit 12
ENSG00000175334	#N/A	#N/A	#N/A	#N/A	1.09	barrier to autointegration factor 1
ENSG00000104979	#N/A	#N/A	#N/A	#N/A	1.09	chromosome 19 open reading frame 53
ENSG000000070423	#N/A	#N/A	#N/A	#N/A	1.09	ring finger protein 126
ENSG00000147586	#N/A	#N/A	#N/A	#N/A	1.08	mitochondrial ribosomal protein S28
ENSG00000186263	#N/A	#N/A	#N/A	#N/A	1.08	torin family 3, member A
ENSG00000162783	#N/A	#N/A	#N/A	#N/A	1.08	immediate early response 5
ENSG00000152407	#N/A	#N/A	#N/A	#N/A	1.08	phosphatidic acid phosphatase type 2B
ENSG00000160201	#N/A	#N/A	#N/A	#N/A	1.08	U2 small nuclear RNA auxiliary factor 1
ENSG00000257727	#N/A	#N/A	#N/A	#N/A	1.08	canopy FGF signaling regulator 2

FIGURE 12

ENSG00000163110	#N/A	#N/A	#N/A	1.11	#N/A	PDZ and LIM domain 5
ENSG00000164088	#N/A	#N/A	#N/A	1.11	#N/A	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1M
ENSG00000125354	#N/A	#N/A	#N/A	1.11	#N/A	sepin 6
ENSG00000130311	#N/A	#N/A	#N/A	1.10	1.42	DET1 and DDB1 associated 1
ENSG00000206503	#N/A	#N/A	#N/A	1.10	#N/A	major histocompatibility complex, class I, A
ENSG00000141296	#N/A	#N/A	#N/A	1.10	#N/A	slingshot protein phosphatase 2
ENSG00000116205	#N/A	#N/A	#N/A	1.10	#N/A	transcription elongation factor A (SII) N-terminal and central domain containing 2
ENSG00000237765	#N/A	#N/A	#N/A	1.10	1.23	family with sequence similarity 200, member B
ENSG00000107738	#N/A	#N/A	#N/A	1.09	#N/A	chromosome 10 open reading frame 54
ENSG00000380002	#N/A	#N/A	#N/A	1.09	#N/A	asparylglucosaminidase
ENSG00000153250	#N/A	#N/A	#N/A	1.09	#N/A	RNA binding motif, single stranded interacting protein 1
ENSG00000161203	#N/A	#N/A	#N/A	1.09	#N/A	adaptor-related protein complex 2, mu 1 subunit
ENSG00000132694	#N/A	#N/A	#N/A	1.09	#N/A	Rho guanine nucleotide exchange factor (GEF) 11
ENSG00000184752	#N/A	#N/A	#N/A	1.09	2.00	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12
ENSG00000133246	#N/A	#N/A	#N/A	1.09	#N/A	PML-RARA regulated adaptor molecule 1
ENSG00000125037	#N/A	#N/A	#N/A	1.09	#N/A	ER membrane protein complex subunit 3
ENSG00000241343	#N/A	#N/A	#N/A	1.09	1.18	ribosomal protein L36a
ENSG00000163960	#N/A	#N/A	#N/A	1.09	#N/A	UBX domain protein 7
ENSG00000108599	#N/A	#N/A	#N/A	1.09	#N/A	A kinase (PRKA) anchor protein 10
ENSG00000150540	#N/A	#N/A	#N/A	1.09	#N/A	histamine N-methyltransferase
ENSG00000082996	#N/A	#N/A	#N/A	1.06	#N/A	ring finger protein 13
ENSG00000110492	#N/A	#N/A	#N/A	1.08	#N/A	midkine (neurite growth-promoting factor 2)
ENSG00000105849	#N/A	#N/A	#N/A	1.06	1.33	TWIST neighbor
ENSG00000160058	#N/A	#N/A	#N/A	1.08	#N/A	BSD domain containing 1
ENSG00000105223	#N/A	#N/A	#N/A	1.06	#N/A	phospholipase D family, member 3
ENSG00000129636	#N/A	#N/A	#N/A	1.06	#N/A	integrin alpha FG-GAP repeat containing 1
ENSG000003034510	#N/A	#N/A	#N/A	1.08	#N/A	thymosin beta 10
ENSG00000143119	#N/A	#N/A	#N/A	1.06	#N/A	CD53 molecule
ENSG00000132581	#N/A	#N/A	#N/A	1.07	1.11	stromal cell-derived factor 2
ENSG00000105404	#N/A	#N/A	#N/A	1.07	#N/A	Rab acceptor 1 (prenylated)
ENSG00000205220	#N/A	#N/A	#N/A	1.07	#N/A	proteasome (prosome, macropain) subunit, beta type, 10
ENSG00000262349	#N/A	#N/A	#N/A	1.07	#N/A	RP11-620J15.3
ENSG00000143013	#N/A	#N/A	#N/A	1.07	#N/A	LIM domain only 4

ENSG00000136868	#N/A	#N/A	#N/A	#N/A	1.08	solute carrier family 31 (copper transporter), member 1
ENSG00000138495	#N/A	#N/A	#N/A	#N/A	1.08	COX17 cytochrome c oxidase copper chaperone
ENSG00000100442	#N/A	#N/A	#N/A	#N/A	1.07	FK506 binding protein 3, 25kDa
ENSG00000182117	#N/A	#N/A	#N/A	#N/A	1.07	NOP10 ribonucleoprotein
ENSG00000185022	#N/A	#N/A	#N/A	#N/A	1.07	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog F
ENSG00000156467	#N/A	#N/A	#N/A	#N/A	1.07	ubiquitin-cytochrome c reductase binding protein
ENSG00000115446	#N/A	#N/A	#N/A	#N/A	1.07	unc-50 homolog (C. elegans)
ENSG00000171421	#N/A	#N/A	#N/A	#N/A	1.06	mitochondrial ribosomal protein L36
ENSG00000188612	#N/A	#N/A	#N/A	#N/A	1.06	small ubiquitin-like modifier 2
ENSG00000157881	#N/A	#N/A	#N/A	#N/A	1.06	paraoxonase 4
ENSG00000131495	#N/A	#N/A	#N/A	#N/A	1.06	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa
ENSG00000152684	#N/A	#N/A	#N/A	#N/A	1.06	pelota homolog (Drosophila)
ENSG00000118363	#N/A	#N/A	#N/A	#N/A	1.06	signal peptidase complex subunit 2
ENSG00000113460	#N/A	#N/A	#N/A	#N/A	1.05	BRX1, biogenesis of ribosomes
ENSG00000167641	#N/A	#N/A	#N/A	#N/A	1.05	protein phosphatase 1, regulatory (inhibitor) subunit 14A
ENSG00000213619	#N/A	#N/A	#N/A	#N/A	1.05	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)
ENSG00000128463	#N/A	#N/A	#N/A	#N/A	1.05	ER membrane protein complex subunit 4
ENSG00000101665	#N/A	#N/A	#N/A	#N/A	1.05	methyltransferase like 13
ENSG00000117365	#N/A	#N/A	#N/A	#N/A	1.05	Sjogren syndrome/scleroderma autoantigen 1
ENSG00000117395	#N/A	#N/A	#N/A	#N/A	1.04	EBNA1 binding protein 2
ENSG00000150888	#N/A	#N/A	#N/A	#N/A	1.04	immediate early response 2
ENSG00000141560	#N/A	#N/A	#N/A	#N/A	1.04	fructosamine 3 kinase related protein
ENSG00000185651	#N/A	#N/A	#N/A	#N/A	1.04	ubiquitin-conjugating enzyme E2L 3
ENSG00000115539	#N/A	#N/A	#N/A	#N/A	1.03	phosducin-like 3
ENSG00000128609	#N/A	#N/A	#N/A	#N/A	1.03	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5
ENSG00000167283	#N/A	#N/A	#N/A	#N/A	1.02	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit G
ENSG00000118292	#N/A	#N/A	#N/A	#N/A	1.02	chromosome 1 open reading frame 54
ENSG00000237403	#N/A	#N/A	#N/A	#N/A	1.02	protein phosphatase 1, regulatory (inhibitor) subunit 11
ENSG00000183520	#N/A	#N/A	#N/A	#N/A	1.02	UTP11-like, U3 small nuclear ribonucleoprotein (yeast)
ENSG00000115750	#N/A	#N/A	#N/A	#N/A	1.02	ubiquitin carboxyl-terminal hydrolase L5
ENSG00000146574	#N/A	#N/A	#N/A	#N/A	1.02	CCZ1 homolog B, vacuolar protein trafficking and biogenesis associated
ENSG00000183011	#N/A	#N/A	#N/A	#N/A	1.01	N(alpha)-acetyltransferase 38, NatC auxiliary subunit
ENSG00000232112	#N/A	#N/A	#N/A	#N/A	1.01	translation machinery associated 7 homolog (S. cerevisiae)
ENSG00000112096	#N/A	#N/A	#N/A	#N/A	1.01	superoxide dismutase 2, mitochondrial

FIGURE 2A

Figure 2: Host miRNA transcriptomics data during EGS infections of MM6 or NSC cells. Differential expression analysis of human miRNA genes from MM6 or NSC cells infected with *T. gondii* EGS strain for 18 hours.

miRNA Gene	logFC (cont-inf) MM6	logFC (cont-inf) NSC
hsa-mir-708-5p	-11.46	-2.19
hsa-mir-708-3p	-10.28	-3.19
hsa-mir-29b-3p	-5.46	-1.23
ENST00000474173	-9.95	-10.14
hsa-mir-32-5p	-5.48	#N/A
hsa-mir-142-3p	-4.62	-3.24
ENST00000500868	-6.60	-8.05
ENST00000500633	-6.57	-9.22
hsa-mir-3656-3p	-9.66	-2.65
hsa-mir-19a-3p	-3.65	-1.59
ENST00000499697	-5.03	-6.24
ENST00000498989	-4.61	-9.27
hsa-mir-101-3p	-3.27	#N/A
ENST00000500011	-5.20	-4.72
hsa-mir-210-5p	-7.79	#N/A
hsa-mir-34c-5p	-7.76	#N/A
hsa-mir-218-5p	-5.28	#N/A
ENST00000501638	-4.61	-6.90
hsa-mir-212-3p	-5.02	#N/A
ENST00000500409	-5.57	-9.86
ENST00000501230	-4.65	#N/A
ENST00000500974	-4.29	-6.16
hsa-mir-132-5p	-4.09	#N/A
hsa-mir-10b-5p	-5.43	-2.77
hsa-mir-455-5p	-3.82	-1.03
hsa-mir-21-3p	-3.49	#N/A
hsa-mir-199a-5p	-4.21	1.41
ENST00000384148	3.83	#N/A
hsa-mir-132-3p	-3.23	#N/A
hsa-mir-142-5p	-3.27	-3.39
ENST00000500340	-4.55	-10.64
ENST00000487032	-4.88	-6.20
hsa-mir-381-3p	-4.26	#N/A
hsa-mir-374a-3p	-3.87	#N/A
hsa-mir-212-5p	-4.29	#N/A
hsa-mir-19b-3p	-2.65	-1.53

miRNA Gene	logFC (cont-inf) MM6	logFC (cont-inf) NSC
ENST00000384610	-2.08	#N/A
ENST00000384238	2.17	#N/A
hsa-mir-140-5p	-2.23	1.04
ENST00000500700	1.82	#N/A
ENST00000363657	-2.50	#N/A
hsa-mir-652-5p	-2.45	#N/A
ENST00000364950	2.12	#N/A
ENST00000452327	2.70	#N/A
hsa-mir-331-3p	-2.25	#N/A
ENST00000365663	3.48	#N/A
hsa-mir-4531-3p	-2.94	#N/A
ENST00000408175	2.02	#N/A
ENST00000384483	2.68	#N/A
ENST00000364596	2.10	#N/A
ENST00000365625	2.13	#N/A
hsa-mir-6087-5p	-2.30	#N/A
ENST00000384388	2.78	#N/A
hsa-mir-143-3p	-2.04	#N/A
ENST00000384240	2.13	-2.57
ENST00000384526	2.69	#N/A
ENST00000502243	2.40	#N/A
ENST00000490494	-3.34	#N/A
ENST00000365462	2.09	#N/A
ENST00000411366	2.08	-2.72
ENST00000383919	2.03	#N/A
ENST00000459329	2.14	#N/A
ENST00000408454	1.87	2.15
hsa-mir-1273h-5p	2.08	#N/A
ENST00000364273	-2.23	#N/A
ENST00000363894	2.14	#N/A
hsa-mir-92a-5p	1.99	#N/A
ENST00000501184	-3.02	#N/A
ENST00000365197	2.56	#N/A
ENST00000363640	2.02	#N/A
ENST00000486682	-2.38	-7.19
ENST00000365068	1.99	#N/A

miRNA Gene	logFC (cont-inf) MM6	logFC (cont-inf) NSC
ENST00000410312	1.93	#N/A
ENST00000461378	-1.57	#N/A
hsa-mir-1307-3p	1.45	#N/A
ENST00000458797	-1.36	#N/A
ENST00000500188	-1.77	#N/A
ENST00000362765	1.49	-1.54
ENST00000364829	1.74	#N/A
ENST00000492060	#N/A	-4.44
ENST00000461045	#N/A	-3.00
ENST00000501999	#N/A	-5.48
ENST00000501119	#N/A	-5.04
hsa-mir-155-5p	#N/A	3.53
ENST00000501823	#N/A	-5.54
hsa-mir-95-3p	#N/A	-4.08
ENST00000493956	#N/A	-1.90
ENST00000463737	#N/A	-1.84
ENST00000480364	#N/A	-2.93
ENST00000498894	#N/A	-4.31
hsa-mir-7974-3p	#N/A	2.69
ENST00000501120	#N/A	-4.02
ENST00000500692	#N/A	2.78
ENST00000500159	#N/A	-2.59
ENST00000499784	#N/A	-3.99
ENST00000491379	#N/A	-1.85
ENST00000500638	#N/A	-4.24
ENST00000479524	#N/A	-1.51
hsa-mir-486-5p	#N/A	-3.23
ENST00000458546	#N/A	2.69
ENST00000500895	#N/A	2.29
ENST00000468873	#N/A	4.77
ENST00000468972	#N/A	-2.69
ENST00000491707	#N/A	-2.21
hsa-mir-1268a-5p	#N/A	2.87
ENST00000501850	#N/A	-7.62
ENST00000489722	#N/A	-2.07
hsa-mir-181b-5p	#N/A	1.41

miRNA Gene	logFC (cont-inf) MM6	logFC (cont-inf) NSC
ENST00000363130	#N/A	-1.04
ENST00000365274	#N/A	-1.11
hsa-mir-410-3p	#N/A	1.07
ENST00000364699	#N/A	-1.12
hsa-mir-7976-5p	#N/A	1.47
ENST00000384335	#N/A	-1.21
ENST00000502222	#N/A	2.25
ENST00000364685	#N/A	-1.18
ENST00000401362	#N/A	1.91
ENST00000385578	#N/A	1.17

FIGURE 2B

hsa-mir-3179-3p	3.39	#N/A
ENST00000363443	-4.61	#N/A
ENST00000499746	-4.64	-9.78
hsa-mir-424-5p	-3.01	#N/A
ENST00000364915	4.86	#N/A
ENST00000410796	-3.51	-4.69
ENST00000471237	1.78	1.28
ENST00000489413	5.42	#N/A
hsa-mir-362-3p	-4.94	#N/A
ENST00000364931	3.72	3.90
ENST00000363549	4.96	#N/A
hsa-mir-4488-5p	-3.98	-3.11
ENST00000500066	-4.75	#N/A
ENST00000500656	3.30	#N/A
hsa-mir-151a-5p	-4.30	-1.88
hsa-mir-30a-5p	-2.87	#N/A
ENST00000500845	-4.48	#N/A
ENST00000499817	-3.61	#N/A
ENST00000363367	2.99	#N/A
hsa-mir-140-3p	-3.07	1.73
ENST00000501386	-4.68	-6.83
ENST00000498132	2.95	#N/A
hsa-mir-374a-5p	-2.73	#N/A
hsa-mir-20a-5p	-1.72	#N/A
hsa-mir-379-5p	-3.92	#N/A
hsa-mir-148a-3p	-2.11	#N/A
ENST00000499637	2.82	#N/A
hsa-mir-3065-5p	-3.45	#N/A
hsa-mir-301a-3p	-3.39	#N/A
hsa-mir-370-3p	-4.31	1.80
hsa-mir-590-3p	-2.63	#N/A
ENST00000458848	2.94	#N/A
ENST00000411281	-4.29	#N/A
hsa-mir-30e-5p	-2.60	#N/A
ENST00000481863	-3.29	#N/A
ENST00000502220	2.83	#N/A
ENST00000480442	-2.58	#N/A
hsa-mir-100-5p	-3.22	#N/A
ENST00000365477	-3.17	#N/A
hsa-mir-184-3p	-3.71	-1.45
ENST00000470561	2.84	1.31
hsa-mir-199b-5p	-2.79	#N/A
ENST00000408139	-2.57	#N/A
ENST00000459424	2.71	#N/A
ENST00000408564	2.78	#N/A

ENST00000362915	3.36	#N/A
ENST00000363651	1.99	#N/A
ENST00000384504	1.94	#N/A
hsa-mir-124-3p	-2.05	#N/A
ENST00000384312	3.77	#N/A
ENST00000474558	-5.43	#N/A
ENST00000498916	3.80	#N/A
ENST00000499645	-2.06	#N/A
ENST00000363674	2.04	-2.38
hsa-mir-152-5p	-2.07	#N/A
hsa-mir-1299-3p	-3.51	#N/A
ENST00000384254	2.62	#N/A
ENST00000499152	1.88	#N/A
ENST00000363985	1.92	-1.32
ENST00000500276	-2.45	#N/A
ENST00000500380	-2.84	#N/A
ENST00000365487	2.30	#N/A
hsa-mir-1273h-3p	1.87	#N/A
ENST00000363248	2.04	#N/A
ENST00000475825	-2.00	-1.77
hsa-mir-183-5p	1.81	-1.77
ENST00000499376	-5.79	#N/A
ENST00000487435	-2.38	#N/A
ENST00000384248	2.25	#N/A
ENST00000383994	2.09	#N/A
ENST00000499568	-2.94	-7.55
hsa-mir-660-5p	-1.94	#N/A
ENST00000384677	1.85	#N/A
ENST00000500705	-2.62	#N/A
ENST00000365046	2.74	#N/A
ENST00000500169	2.74	#N/A
ENST00000362412	2.38	#N/A
ENST00000465104	-1.89	#N/A
hsa-mir-494-3p	-2.78	#N/A
ENST00000384376	2.59	#N/A
ENST00000384762	2.44	#N/A
ENST00000487797	-1.74	#N/A
ENST00000501255	-2.32	#N/A
ENST00000364805	2.04	#N/A
ENST00000362918	2.03	#N/A
ENST00000384686	2.49	#N/A
ENST00000484473	-3.21	#N/A
ENST00000499929	-3.27	#N/A
ENST00000384373	2.13	#N/A
ENST00000384068	2.50	#N/A

ENST00000502135	#N/A	-3.51
hsa-mir-30a-3p	#N/A	1.42
hsa-mir-30c-3p	#N/A	1.70
ENST00000458878	#N/A	-2.06
ENST00000470405	#N/A	-4.22
ENST00000499710	#N/A	-2.31
ENST00000488123	#N/A	-1.31
ENST00000478633	#N/A	-1.91
ENST00000410413	#N/A	1.92
ENST00000501562	#N/A	-3.53
hsa-mir-574-5p	#N/A	1.49
ENST00000498924	#N/A	-7.09
ENST00000364315	#N/A	1.29
ENST00000363473	#N/A	1.25
ENST00000365651	#N/A	1.24
ENST00000362400	#N/A	1.25
ENST00000364485	#N/A	1.24
ENST00000496486	#N/A	-1.53
ENST00000365387	#N/A	1.24
ENST00000501284	#N/A	-4.74
ENST00000365055	#N/A	1.23
ENST00000363500	#N/A	1.24
ENST00000363511	#N/A	1.24
ENST00000362482	#N/A	1.24
ENST00000365656	#N/A	1.25
ENST00000491757	#N/A	-4.79
ENST00000410545	#N/A	1.79
ENST00000363040	#N/A	1.24
ENST00000364718	#N/A	1.24
ENST00000362464	#N/A	1.23
ENST00000363439	#N/A	-1.96
ENST00000363962	#N/A	-2.46
ENST00000410396	#N/A	1.26
ENST00000362526	#N/A	1.22
ENST00000500227	#N/A	-3.53
ENST00000362467	#N/A	1.23
ENST00000363754	#N/A	1.22
ENST00000500354	#N/A	-3.66
hsa-mir-93-5p	#N/A	1.22
hsa-mir-148b-3p	#N/A	1.16
ENST00000468070	#N/A	-3.51
ENST00000385582	#N/A	1.24
ENST00000363194	#N/A	-1.86
ENST00000483476	#N/A	-1.07
hsa-mir-3152-5p	#N/A	3.37

FIGURE 2C

ENST00000500754	-3.39	#N/A
ENST00000473313	-2.37	#N/A
hsa-mir-20a-3p	-2.55	#N/A
ENST00000489202	-2.70	-2.04
hsa-mir-30b-5p	-2.76	#N/A
hsa-mir-1307-5p	-2.59	#N/A
hsa-mir-29c-3p	-3.22	#N/A
ENST00000365574	2.88	2.02
ENST00000384314	2.96	#N/A
ENST00000500611	-3.82	-3.52
ENST00000364572	3.27	#N/A
ENST00000485443	-2.74	-1.38
hsa-mir-34a-5p	-3.03	#N/A
ENST00000384273	3.21	#N/A
ENST00000391230	-3.72	-5.34
hsa-mir-493-3p	-3.70	#N/A
ENST00000501131	5.23	#N/A
ENST00000499694	-3.29	#N/A
ENST00000499716	-3.34	#N/A
hsa-mir-1304-5p	2.62	#N/A
ENST00000500755	-3.42	-2.84
ENST00000365467	2.57	#N/A
ENST00000463508	1.59	1.35
ENST00000384084	2.72	#N/A
ENST00000364784	2.55	#N/A
ENST00000384106	3.24	#N/A
ENST00000493557	-2.78	#N/A
ENST00000362808	3.01	#N/A
ENST00000362881	3.14	#N/A
ENST00000363299	2.58	2.16
ENST00000383873	2.84	#N/A
ENST00000363250	3.36	#N/A
ENST00000384741	2.98	#N/A
ENST00000384743	2.92	#N/A
ENST00000364542	2.73	#N/A
hsa-mir-4301-5p	3.54	#N/A
hsa-mir-29c-5p	-3.39	#N/A
ENST00000365439	2.70	#N/A
ENST00000384650	2.72	#N/A
ENST00000384547	3.00	1.63
hsa-mir-134-5p	-4.20	#N/A
ENST00000501210	-2.79	#N/A
ENST00000362507	2.88	5.45
ENST00000384413	2.70	1.18
ENST00000491051	-2.69	#N/A

ENST00000364407	2.02	#N/A
ENST00000458898	2.05	#N/A
ENST00000500772	-2.10	#N/A
ENST00000470693	1.94	#N/A
ENST00000390872	1.95	#N/A
ENST00000501958	-2.27	#N/A
ENST00000363389	1.84	#N/A
ENST00000490522	-1.70	#N/A
ENST00000363880	1.92	#N/A
ENST00000501780	-2.66	#N/A
ENST00000499816	-3.21	-3.40
ENST00000502117	-1.94	#N/A
hsa-mir-191-3p	1.68	#N/A
ENST00000384627	2.16	#N/A
ENST00000410868	1.82	#N/A
hsa-mir-20b-5p	-1.72	#N/A
ENST00000384268	1.96	-1.66
ENST00000501629	-1.82	#N/A
ENST00000362512	2.63	#N/A
ENST00000410494	1.79	#N/A
ENST00000384753	1.94	#N/A
ENST00000501143	-3.31	#N/A
ENST00000384087	1.79	#N/A
ENST00000472430	-2.56	-2.83
ENST00000476501	-2.56	#N/A
ENST00000499786	-2.27	#N/A
ENST00000363963	1.78	#N/A
ENST00000384708	1.86	#N/A
ENST00000483314	3.27	#N/A
ENST00000384398	3.11	#N/A
ENST00000365370	2.73	#N/A
ENST00000363100	-5.71	#N/A
ENST00000362692	1.94	#N/A
ENST00000461728	3.29	#N/A
ENST00000458930	1.80	#N/A
ENST00000384586	2.64	#N/A
ENST00000363872	1.98	#N/A
ENST00000408082	1.82	#N/A
ENST00000499877	-1.87	#N/A
ENST00000364018	1.83	#N/A
ENST00000458932	1.93	#N/A
ENST00000363840	-1.60	#N/A
ENST00000390904	3.45	#N/A
ENST00000431050	-5.33	#N/A
ENST00000501637	-5.33	#N/A

hsa-mir-4485-3p	#N/A	-2.69
hsa-mir-222-3p	#N/A	1.16
ENST00000489326	#N/A	-1.66
ENST00000364768	#N/A	-1.78
ENST00000410569	#N/A	-6.76
ENST00000365559	#N/A	-6.80
ENST00000500404	#N/A	1.85
hsa-mir-15b-3p	#N/A	1.95
ENST00000363792	#N/A	-1.81
hsa-mir-1246-5p	#N/A	-1.38
ENST00000499345	#N/A	-3.03
ENST00000362455	#N/A	-6.76
ENST00000363450	#N/A	1.61
hsa-mir-99b-3p	#N/A	1.46
hsa-mir-548o-3p	#N/A	1.54
ENST00000493731	#N/A	-1.64
ENST00000481041	#N/A	-2.54
ENST00000465317	#N/A	2.21
ENST00000500146	#N/A	-2.62
ENST00000499533	#N/A	-3.94
ENST00000362704	#N/A	1.62
ENST00000365659	#N/A	1.55
ENST00000494556	#N/A	-1.85
ENST00000463081	#N/A	-1.15
ENST00000410731	#N/A	-6.71
ENST00000364361	#N/A	-6.71
ENST00000486381	#N/A	-4.22
ENST00000498581	#N/A	-1.11
ENST00000362344	#N/A	-1.81
ENST00000364588	#N/A	-4.02
ENST00000500497	#N/A	-3.11
ENST00000492114	#N/A	-1.69
ENST00000482200	#N/A	-1.75
hsa-mir-30b-3p	#N/A	3.48
ENST00000365328	#N/A	1.44
hsa-mir-345-5p	#N/A	1.46
hsa-mir-484-5p	#N/A	1.16
ENST00000410216	#N/A	-1.80
ENST00000498986	#N/A	-4.29
ENST00000481141	#N/A	1.58
ENST00000501686	#N/A	-3.37
ENST00000495906	#N/A	-1.98
ENST00000501339	#N/A	-3.39
ENST00000362928	#N/A	-1.68
ENST00000498933	#N/A	-3.58

FIGURE 2D

hsa-mir-493-5p	-3.37	1.10
hsa-mir-942-5p	2.48	2.00
ENST00000470848	-2.71	#N/A
ENST00000410183	-2.52	#N/A
ENST00000362423	2.25	#N/A
hsa-mir-33a-3p	-4.35	#N/A
ENST00000490401	-3.11	#N/A
ENST00000499204	-6.41	#N/A
hsa-mir-21-5p	-1.46	#N/A
ENST00000500894	2.54	#N/A
ENST00000499768	-6.36	#N/A
ENST00000499304	-2.84	#N/A
ENST00000384172	2.79	#N/A
ENST00000476850	3.02	#N/A
ENST00000501145	-2.90	#N/A
ENST00000364310	6.40	#N/A
hsa-mir-106b-5p	-2.59	#N/A
ENST00000501334	-3.08	#N/A
ENST00000362477	2.74	2.10
ENST00000384585	3.45	#N/A
ENST00000500576	-6.69	#N/A
ENST00000458981	3.08	#N/A
ENST00000408749	2.41	3.03
ENST00000384007	2.81	#N/A
ENST00000387943	2.38	2.74
ENST00000495608	-2.64	#N/A
ENST00000364234	2.39	#N/A
hsa-mir-124-5p	-2.48	#N/A
ENST00000365537	3.18	#N/A
hsa-mir-193a-3p	-3.42	#N/A
ENST00000363696	2.36	#N/A
ENST00000458922	-3.37	#N/A
ENST00000502038	-3.15	#N/A
hsa-mir-654-3p	-3.05	#N/A
ENST00000365037	-6.31	#N/A
ENST00000479561	-2.60	-5.15
ENST00000365606	3.07	#N/A
ENST00000365312	3.38	#N/A
ENST00000384637	2.86	#N/A
ENST00000365666	3.03	#N/A
ENST00000384178	2.34	#N/A
ENST00000485528	2.82	#N/A
ENST00000362698	2.30	1.92
ENST00000384245	2.57	#N/A
ENST00000363444	2.65	1.52

hsa-mir-224-5p	-5.43	#N/A
hsa-mir-4284-5p	-5.43	#N/A
ENST00000364632	-5.43	#N/A
hsa-mir-338-3p	-5.43	#N/A
ENST00000499616	-3.40	#N/A
ENST00000384416	1.69	#N/A
ENST00000478115	-1.97	-3.57
ENST00000363836	2.07	#N/A
hsa-mir-4791-5p	-1.94	#N/A
ENST00000363171	1.93	#N/A
ENST00000384078	1.98	#N/A
ENST00000384737	2.39	#N/A
ENST00000484776	2.17	#N/A
ENST00000468731	2.40	#N/A
ENST00000391033	1.73	#N/A
ENST00000471029	2.01	#N/A
ENST00000384297	1.86	#N/A
ENST00000501443	-2.80	#N/A
ENST00000364879	1.71	#N/A
ENST00000487144	-1.82	#N/A
ENST00000384653	1.89	#N/A
ENST00000362452	2.16	#N/A
ENST00000383874	2.41	#N/A
ENST00000365399	-1.88	#N/A
ENST00000363331	2.14	-1.85
hsa-mir-1537-3p	-5.77	#N/A
ENST00000384749	2.15	#N/A
ENST00000480363	2.28	#N/A
ENST00000501540	-2.26	#N/A
ENST00000384067	1.68	1.25
ENST00000501105	-1.93	#N/A
ENST00000384090	2.03	#N/A
hsa-mir-659-5p	-2.55	#N/A
ENST00000362721	2.02	#N/A
ENST00000363810	-2.17	#N/A
hsa-mir-6747-3p	1.66	#N/A
ENST00000461956	-3.20	#N/A
ENST00000384097	1.88	#N/A
ENST00000384136	1.75	#N/A
ENST00000383990	1.88	-1.81
ENST00000411192	1.82	#N/A
ENST00000383978	1.88	#N/A
ENST00000458975	1.80	#N/A
ENST00000410344	1.96	#N/A
ENST00000501171	-2.60	#N/A

ENST00000501370	#N/A	-2.90
hsa-mir-151b-3p	#N/A	-1.88
ENST00000472187	#N/A	-1.14
ENST00000476122	#N/A	-1.43
ENST00000498896	#N/A	-2.46
ENST00000363251	#N/A	-1.61
ENST00000499098	#N/A	-4.38
hsa-mir-618-5p	#N/A	1.42
ENST00000364533	#N/A	1.47
ENST00000410801	#N/A	-1.67
ENST00000500582	#N/A	-6.05
ENST00000410597	#N/A	-1.70
ENST00000363766	#N/A	-3.05
ENST00000500818	#N/A	-6.37
ENST00000410533	#N/A	1.42
ENST00000491227	#N/A	-1.54
hsa-mir-503-5p	#N/A	1.64
ENST00000502035	#N/A	-3.55
ENST00000364447	#N/A	-3.20
hsa-mir-1301-3p	#N/A	1.42
hsa-mir-541-5p	#N/A	3.11
ENST00000364774	#N/A	-1.53
ENST00000486026	#N/A	-3.74
ENST00000469345	#N/A	2.06
ENST00000478479	#N/A	-1.50
ENST00000364469	#N/A	-1.48
hsa-mir-23a-5p	#N/A	1.71
ENST00000499059	#N/A	1.73
hsa-mir-1468-5p	#N/A	1.63
hsa-mir-584-5p	#N/A	1.70
ENST00000500977	#N/A	-2.52
ENST00000499115	#N/A	-2.06
hsa-mir-324-3p	#N/A	1.36
hsa-mir-485-5p	#N/A	-1.27
ENST00000364009	#N/A	1.50
ENST00000463796	#N/A	1.03
ENST00000363301	#N/A	-1.39
ENST00000488256	#N/A	-1.63
ENST00000478663	#N/A	1.39
ENST00000459543	#N/A	2.60
ENST00000385575	#N/A	1.29
ENST00000471568	#N/A	-1.60
ENST00000410292	#N/A	-5.91
ENST00000502160	#N/A	-5.91
hsa-mir-193b-5p	#N/A	-1.67

FIGURE 2E

ENST00000363462	2.66	#N/A
ENST00000499246	-3.20	-4.41
ENST00000502018	-2.65	#N/A
hsa-mir-210-3p	-2.49	#N/A
ENST00000384205	2.59	#N/A
ENST00000501900	-2.87	-3.69
ENST00000463853	-3.34	#N/A
ENST00000499762	2.79	#N/A
ENST00000459194	2.52	#N/A
ENST00000383948	2.63	#N/A
ENST00000364628	2.67	#N/A
ENST00000384604	2.89	#N/A
ENST00000384302	2.97	#N/A
ENST00000491230	-2.55	#N/A
ENST00000364358	2.72	#N/A
ENST00000501607	-2.39	#N/A
hsa-mir-153-3p	-2.95	#N/A
ENST00000365484	2.58	#N/A
ENST00000501173	2.59	#N/A
hsa-mir-99a-3p	-3.27	#N/A
ENST00000384619	2.32	1.50
hsa-mir-19b-5p	-2.71	#N/A
hsa-mir-502-5p	-3.99	#N/A
ENST00000469579	-2.23	#N/A
ENST00000384530	3.09	#N/A
ENST00000481391	2.67	#N/A
ENST00000363977	3.09	#N/A
ENST00000501074	5.20	#N/A
ENST00000365153	-3.03	#N/A
ENST00000488304	-3.18	#N/A
ENST00000501998	3.08	#N/A
ENST00000365599	2.93	#N/A
ENST00000475810	3.68	#N/A
ENST00000466170	-2.19	#N/A
hsa-mir-3173-5p	2.67	#N/A
hsa-mir-190a-5p	-3.62	#N/A
ENST00000384026	2.70	#N/A
ENST00000384385	2.46	#N/A
ENST00000411404	2.64	#N/A
ENST00000364696	3.17	#N/A
ENST00000482377	-3.21	#N/A
hsa-mir-151a-3p	-2.41	#N/A
hsa-mir-146b-5p	2.01	#N/A
ENST00000500516	-2.63	#N/A
ENST00000384577	2.97	#N/A

ENST00000384210	2.41	#N/A
ENST00000500508	-2.50	#N/A
ENST00000476674	-1.80	-1.76
ENST00000474075	-1.97	-2.96
hsa-mir-369-3p	-2.71	#N/A
hsa-mir-548f-5p	-2.11	#N/A
ENST00000491516	-1.66	-1.97
ENST00000363750	2.33	#N/A
ENST00000384419	1.95	#N/A
ENST00000384656	1.84	#N/A
ENST00000384187	1.86	#N/A
hsa-mir-152-3p	-1.93	#N/A
ENST00000475628	1.83	#N/A
ENST00000419895	2.06	#N/A
ENST00000365571	1.36	#N/A
hsa-mir-27b-5p	-1.96	#N/A
ENST00000499014	-1.85	#N/A
ENST00000499438	-2.64	#N/A
ENST00000501856	-2.32	#N/A
ENST00000459135	-2.00	#N/A
ENST00000462879	-3.34	-5.22
ENST00000363548	1.86	#N/A
ENST00000363094	1.85	#N/A
ENST00000502161	-3.50	-4.95
ENST00000499095	-2.16	#N/A
hsa-mir-27a-3p	-1.49	#N/A
ENST00000500893	-2.21	-5.22
ENST00000363925	2.23	-1.34
ENST00000364208	-5.71	#N/A
ENST00000384119	1.82	-1.68
ENST00000384600	2.15	#N/A
ENST00000391196	1.71	#N/A
ENST00000501934	-2.08	#N/A
ENST00000501587	-2.08	#N/A
ENST00000500518	-1.76	#N/A
ENST00000365672	1.53	#N/A
ENST00000364916	1.68	-1.61
ENST00000493125	1.83	#N/A
ENST00000502192	1.72	#N/A
ENST00000364535	1.75	#N/A
ENST00000363660	1.56	#N/A
ENST00000363068	1.56	#N/A
ENST00000501338	2.54	#N/A
ENST00000365063	1.63	#N/A
ENST00000384344	2.21	#N/A

hsa-mir-4473-3p	#N/A	1.28
hsa-mir-887-3p	#N/A	3.11
ENST00000408376	#N/A	1.81
ENST00000502206	#N/A	-2.96
ENST00000362487	#N/A	-1.56
ENST00000362779	#N/A	1.38
hsa-mir-197-3p	#N/A	-1.31
ENST00000364393	#N/A	-1.81
ENST00000390997	#N/A	1.75
ENST00000408563	#N/A	-1.34
hsa-mir-3662-3p	#N/A	2.73
ENST00000501149	#N/A	-2.63
ENST00000468500	#N/A	-1.26
ENST00000500970	#N/A	2.56
ENST00000363046	#N/A	1.00
ENST00000363220	#N/A	-1.35
ENST00000499220	#N/A	3.74
ENST00000363257	#N/A	-1.42
ENST00000499917	#N/A	1.52
ENST00000365617	#N/A	-1.38
hsa-mir-375-3p	#N/A	1.58
ENST00000472473	#N/A	-3.52
hsa-mir-3182-5p	#N/A	-1.55
ENST00000467798	#N/A	-1.41
ENST00000499978	#N/A	-2.19
ENST00000500358	#N/A	-2.52
ENST00000487309	#N/A	1.92
ENST00000473668	#N/A	1.87
ENST00000363120	#N/A	1.26
ENST00000501042	#N/A	1.61
ENST00000411347	#N/A	-4.04
ENST00000410669	#N/A	-1.34
ENST00000465779	#N/A	-2.16
ENST00000365172	#N/A	1.21
ENST00000364377	#N/A	-1.54
ENST00000485927	#N/A	-1.23
hsa-mir-3613-5p	#N/A	-1.55
ENST00000365254	#N/A	-2.94
ENST00000363593	#N/A	1.31
ENST00000462216	#N/A	-1.95
ENST00000363849	#N/A	-5.65
ENST00000501275	#N/A	-2.99
ENST00000461333	#N/A	-1.47
ENST00000501646	#N/A	-2.42
ENST00000408481	#N/A	1.73

FIGURE 2F

ENST00000363723	-3.62	#N/A
ENST00000469253	-2.32	#N/A
hsa-mir-409-3p	-3.50	#N/A
hsa-mir-1254-5p	2.22	#N/A
hsa-mir-15a-5p	-2.13	#N/A
ENST00000410462	2.41	#N/A
ENST00000384161	2.31	#N/A
ENST00000492745	-2.14	#N/A
ENST00000383898	2.46	#N/A
ENST00000363435	2.44	#N/A
ENST00000500207	-2.96	-4.36
ENST00000363286	2.14	1.02
ENST00000501174	-2.70	#N/A
ENST00000482497	3.89	-1.08
ENST00000365604	2.82	2.51
ENST00000362591	2.21	#N/A
hsa-mir-651-5p	-2.18	#N/A
hsa-mir-31-5p	-6.76	#N/A
ENST00000471133	6.06	#N/A
ENST00000501075	-3.27	-2.95
ENST00000383895	5.35	#N/A
ENST00000365341	2.54	#N/A
hsa-mir-17-3p	-2.36	#N/A
ENST00000365532	2.51	#N/A
ENST00000387069	2.28	2.88
ENST00000499572	-2.57	-6.22
ENST00000410793	-2.41	#N/A
ENST00000362352	2.27	#N/A
hsa-mir-411-5p	-3.16	#N/A
ENST00000364102	2.41	1.38
ENST00000384606	3.07	#N/A
ENST00000471114	-2.28	-2.95
ENST00000384633	2.71	#N/A
ENST00000384630	2.71	#N/A
hsa-mir-455-3p	-2.29	#N/A
ENST00000500702	-2.46	-1.88
hsa-mir-127-3p	-2.61	#N/A
ENST00000384563	2.65	#N/A
ENST00000499656	-3.07	#N/A
ENST00000363636	2.17	#N/A
ENST00000362353	2.17	#N/A
ENST00000362562	2.16	#N/A
ENST00000487060	2.35	#N/A
ENST00000363624	2.11	#N/A
ENST00000384323	2.02	2.16

ENST00000499426	-5.21	#N/A
ENST00000501219	-5.21	#N/A
hsa-mir-889-3p	-5.21	#N/A
hsa-mir-6847-5p	3.41	#N/A
ENST00000470833	5.42	#N/A
hsa-mir-505-5p	5.42	#N/A
ENST00000365030	1.56	#N/A
ENST00000384567	1.61	#N/A
ENST00000459367	1.83	#N/A
ENST00000362695	2.27	#N/A
ENST00000364251	1.62	#N/A
ENST00000410290	1.57	#N/A
ENST00000384010	1.57	1.14
ENST00000491152	2.35	#N/A
ENST00000452527	-3.06	#N/A
ENST00000410694	1.88	#N/A
ENST00000384782	1.57	1.16
ENST00000383886	2.28	#N/A
ENST00000383861	1.56	1.13
ENST00000458811	1.82	1.67
ENST00000383925	1.57	1.13
ENST00000364228	1.40	#N/A
ENST00000485447	-2.38	#N/A
ENST00000501894	-1.70	#N/A
ENST00000483592	1.84	#N/A
hsa-mir-548aj-5p	-2.13	#N/A
ENST00000365208	1.66	#N/A
ENST00000384278	1.56	1.16
ENST00000501814	-1.82	-4.77
ENST00000362421	1.72	#N/A
ENST00000390910	1.79	#N/A
ENST00000363421	1.60	#N/A
ENST00000364558	-1.76	#N/A
ENST00000383869	1.55	1.15
ENST00000363271	1.68	#N/A
ENST00000410557	1.60	#N/A
ENST00000384659	1.55	1.11
ENST00000384135	1.62	#N/A
ENST00000499695	-1.69	-4.65
ENST00000411009	2.42	#N/A
ENST00000364348	1.67	#N/A
ENST00000459508	1.72	#N/A
ENST00000410794	1.78	#N/A
ENST00000383860	2.04	#N/A
ENST00000500662	-2.64	-4.95

ENST00000364948	#N/A	-1.08
ENST00000501116	#N/A	-2.39
ENST00000475601	#N/A	-1.47
hsa-mir-511-5p	#N/A	-2.75
ENST00000489070	#N/A	1.21
ENST00000363915	#N/A	-1.49
hsa-mir-107-3p	#N/A	1.17
ENST00000501853	#N/A	-3.57
hsa-mir-431-3p	#N/A	1.35
ENST00000362607	#N/A	1.25
ENST00000475473	#N/A	2.54
hsa-mir-215-5p	#N/A	-1.84
ENST00000499222	#N/A	-2.06
ENST00000363044	#N/A	-1.49
ENST00000501427	#N/A	-2.29
ENST00000401297	#N/A	1.69
ENST00000459083	#N/A	1.26
hsa-mir-1185-3p	#N/A	1.29
ENST00000434673	#N/A	-2.16
ENST00000501348	#N/A	-2.74
hsa-mir-5701-5p	#N/A	-1.19
hsa-mir-664a-3p	#N/A	-1.47
ENST00000499712	#N/A	-2.29
ENST00000364259	#N/A	1.67
ENST00000478832	#N/A	-1.23
ENST00000364819	#N/A	-1.28
ENST00000390833	#N/A	1.16
ENST00000485828	#N/A	-1.51
ENST00000466944	#N/A	-1.94
hsa-mir-451a-5p	#N/A	-2.74
ENST00000486576	#N/A	-2.65
ENST00000473410	#N/A	-1.18
ENST00000385607	#N/A	1.24
hsa-mir-16-3p	#N/A	1.08
ENST00000500979	#N/A	-2.22
hsa-mir-485-3p	#N/A	-1.15
ENST00000365138	#N/A	-1.59
ENST00000410482	#N/A	1.07
ENST00000408061	#N/A	1.10
hsa-mir-3620-5p	#N/A	5.55
ENST00000499775	#N/A	-5.34
ENST00000501399	#N/A	-5.34
hsa-mir-30d-3p	#N/A	2.00
hsa-mir-3591-3p	#N/A	-2.26
ENST00000501304	#N/A	-3.13

FIGURE 2G

ENST00000411187	2.82	#N/A	ENST00000363858	2.61	#N/A	hsa-mir-425-3p	#N/A	1.05
ENST00000499932	-3.00	#N/A	ENST00000362931	1.55	#N/A	ENST00000410856	#N/A	1.27
ENST00000493141	-3.03	-2.58	ENST00000501144	2.90	#N/A	ENST00000500809	#N/A	-2.58
ENST00000384589	2.61	#N/A	ENST00000391084	2.07	#N/A	ENST00000499055	#N/A	1.24
ENST00000365085	2.20	#N/A	ENST00000364308	1.47	#N/A	hsa-mir-625-3p	#N/A	-1.39
ENST00000364164	2.44	#N/A	ENST00000363552	1.87	#N/A	hsa-mir-874-3p	#N/A	1.03
hsa-mir-146b-3p	2.32	#N/A	ENST00000384436	1.56	#N/A	ENST00000384110	#N/A	-1.35
ENST00000384781	2.80	#N/A	ENST00000364113	1.50	#N/A	ENST00000362911	#N/A	-1.24
ENST00000501615	-2.78	#N/A	ENST00000390895	1.57	#N/A	ENST00000411012	#N/A	1.10
ENST00000500663	-2.61	-6.37	ENST00000383890	1.49	#N/A	ENST00000363091	#N/A	-1.23
ENST00000363190	2.86	#N/A	ENST00000502138	-2.01	#N/A	ENST00000496134	#N/A	1.70
ENST00000384744	2.04	#N/A	ENST00000408209	1.94	#N/A	hsa-mir-1287-5p	#N/A	1.22
ENST00000384776	2.49	#N/A	ENST00000485481	1.54	#N/A	ENST00000500202	#N/A	-2.26
hsa-mir-301b-3p	-2.98	#N/A	ENST00000384138	1.73	-1.65	ENST00000496828	#N/A	-1.78
ENST00000391154	2.11	#N/A	hsa-mir-4746-5p	1.54	#N/A	ENST00000458893	#N/A	1.13
ENST00000491579	-2.31	#N/A	ENST00000365096	-1.67	-1.24	ENST00000463779	#N/A	-2.71
ENST00000362862	2.23	#N/A	ENST00000384462	-1.63	#N/A	hsa-mir-431-5p	#N/A	1.24
ENST00000500553	-2.39	#N/A	ENST00000384541	1.49	#N/A	hsa-mir-1255a-5p	#N/A	1.62
ENST00000391172	2.23	#N/A	ENST00000363358	-2.69	#N/A	ENST00000363656	#N/A	-1.12
ENST00000383975	-2.28	#N/A	ENST00000424643	-2.29	#N/A	ENST00000365668	#N/A	-1.55
ENST00000365160	2.64	1.80	ENST00000365099	-2.29	#N/A	ENST00000365202	#N/A	-1.09
ENST00000459189	2.04	#N/A	hsa-mir-543-3p	-2.20	#N/A	ENST00000410717	#N/A	-1.22
ENST00000497848	1.92	#N/A	hsa-mir-145-5p	-1.67	#N/A	ENST00000499483	#N/A	1.45
ENST00000384527	2.48	#N/A	ENST00000362963	-2.01	#N/A	ENST00000500023	#N/A	-2.53
ENST00000499508	1.98	1.12	hsa-mir-744-5p	1.46	1.08	ENST00000480526	#N/A	1.41
ENST00000499850	-2.34	#N/A	hsa-mir-3912-3p	-1.60	#N/A	hsa-mir-584-3p	#N/A	2.78
ENST00000496399	1.70	#N/A	ENST00000364128	1.69	#N/A	ENST00000486970	#N/A	-3.04
hsa-mir-33a-5p	-3.67	#N/A	ENST00000384626	1.82	#N/A	ENST00000366303	#N/A	2.23
ENST00000362912	-2.49	#N/A	ENST00000500637	-1.66	#N/A	hsa-mir-671-3p	#N/A	-1.01
ENST00000498971	-3.72	#N/A	ENST00000411315	1.62	1.36	ENST00000386847	#N/A	1.06
ENST00000501356	-6.07	#N/A	ENST00000481967	1.56	#N/A	ENST00000460738	#N/A	1.51
hsa-mir-4690-3p	-6.07	#N/A	ENST00000364960	2.96	#N/A	ENST00000500043	#N/A	-2.87
ENST00000384281	2.15	#N/A	ENST00000474109	2.44	#N/A	ENST00000365598	#N/A	-5.22
ENST00000499378	-2.69	-5.46	hsa-mir-130a-3p	-5.53	#N/A	ENST00000408548	#N/A	2.03
hsa-mir-27b-3p	-1.84	#N/A	ENST00000499796	-5.53	#N/A	ENST00000363341	#N/A	-1.06
ENST00000364641	2.38	#N/A	hsa-mir-590-5p	-5.53	#N/A	ENST00000363964	#N/A	-1.37
hsa-mir-582-5p	-2.75	#N/A	ENST00000495498	1.74	#N/A	ENST00000364648	#N/A	-2.11
ENST00000384727	3.50	#N/A	ENST00000444141	1.56	#N/A	ENST00000478019	#N/A	-1.20
ENST00000384534	2.34	#N/A	hsa-mir-29a-3p	-1.49	#N/A	ENST00000363738	#N/A	-1.20
hsa-mir-582-3p	-2.27	#N/A	hsa-mir-323a-3p	-5.53	#N/A	ENST00000401270	#N/A	1.40
ENST00000501902	-2.25	-4.80	ENST00000502175	-5.53	#N/A	hsa-mir-7704-5p	#N/A	-1.27
hsa-mir-382-5p	-3.50	#N/A	hsa-mir-182-5p	1.53	#N/A	hsa-mir-671-5p	#N/A	1.11
ENST00000383934	2.58	#N/A	hsa-mir-449c-5p	-2.55	#N/A	ENST00000500738	#N/A	-2.64
ENST00000489347	-2.53	#N/A	ENST00000362680	1.62	#N/A	ENST00000362645	#N/A	-1.08
ENST00000362710	2.40	-1.20	hsa-mir-16-5p	-1.48	#N/A	ENST00000364914	#N/A	1.25

FIGURE 2H

ENST00000363455	2.11	#N/A
ENST00000384793	2.24	2.07
ENST00000467195	-2.39	-3.18
ENST00000459096	-2.15	#N/A
ENST00000501034	-2.70	#N/A
ENST00000501134	-2.43	#N/A
ENST00000363899	2.14	#N/A
ENST00000383924	1.91	#N/A
ENST00000362354	2.22	-3.09
ENST00000365075	2.18	#N/A
ENST00000499473	-2.86	#N/A
ENST00000364654	-2.86	#N/A
ENST00000384001	2.22	#N/A
ENST00000499305	-2.34	#N/A
ENST00000384127	2.63	#N/A
ENST00000410624	2.16	#N/A
ENST00000364337	2.57	#N/A
ENST00000411164	2.03	#N/A
ENST00000384716	2.18	#N/A
ENST00000383913	2.74	#N/A
ENST00000364432	3.07	#N/A
ENST00000459107	2.22	#N/A
hsa-mir-548x-5p	-2.59	#N/A
ENST00000500112	2.04	#N/A
hsa-mir-6516-3p	-2.92	#N/A
ENST00000384341	2.05	#N/A
ENST00000363372	2.21	#N/A
ENST00000471506	2.17	#N/A
hsa-mir-194-5p	-1.93	#N/A
ENST00000364937	3.92	#N/A
ENST00000501249	-2.33	#N/A
ENST00000362697	2.12	#N/A
ENST00000499758	-2.13	-2.44
ENST00000476606	-2.33	-3.13
hsa-mir-4521-5p	2.09	#N/A
ENST00000499909	-2.32	#N/A
ENST00000499925	-2.37	#N/A
ENST00000384750	2.11	#N/A
ENST00000486830	2.68	#N/A
ENST00000384378	3.29	#N/A
hsa-mir-4420-3p	1.97	#N/A
ENST00000365498	2.16	-1.88
hsa-mir-450b-5p	-2.32	#N/A
ENST00000501091	-2.24	#N/A
ENST00000363141	3.52	#N/A

ENST00000362667	-1.91	#N/A
ENST00000500049	-1.60	#N/A
ENST00000501843	-1.78	#N/A
ENST00000497631	1.71	#N/A
ENST00000363186	1.60	#N/A
ENST00000459124	1.41	#N/A
ENST00000499566	2.03	#N/A
ENST00000498910	-1.47	#N/A
hsa-mir-296-3p	1.40	2.08
ENST00000499061	-1.59	#N/A
ENST00000410129	1.49	#N/A
ENST00000364419	-1.64	#N/A
ENST00000496990	1.63	2.17
ENST00000386062	1.62	#N/A
hsa-mir-33b-3p	1.49	#N/A
hsa-mir-542-3p	-2.13	#N/A
ENST00000362540	1.50	-1.41
ENST00000459577	1.55	2.83
ENST00000459229	1.61	#N/A
ENST00000498878	1.50	#N/A
ENST00000500846	-1.66	#N/A
ENST00000364938	1.52	#N/A
ENST00000487367	2.35	#N/A
ENST00000502133	-2.91	#N/A
ENST00000447991	-2.91	#N/A
ENST00000501462	-2.99	#N/A
ENST00000500114	-2.99	#N/A
hsa-mir-450a-5p	-1.86	#N/A
ENST00000459041	1.54	#N/A
ENST00000501043	2.98	#N/A
ENST00000496481	-1.50	#N/A
ENST00000501125	-1.74	#N/A
ENST00000500444	-2.24	#N/A
ENST00000499480	-2.31	#N/A
ENST00000501658	-1.69	#N/A
ENST00000484771	1.90	#N/A
ENST00000501592	-2.99	#N/A
ENST00000499665	-1.84	#N/A
ENST00000502181	-1.71	#N/A
ENST00000475606	-5.09	#N/A
ENST00000480177	-5.09	#N/A
ENST00000499640	-5.09	#N/A
ENST00000410205	1.59	#N/A
ENST00000462564	-1.61	1.38
ENST00000362438	2.17	#N/A

ENST00000362750	#N/A	1.22
hsa-mir-1262-5p	#N/A	1.29
ENST00000484912	#N/A	-1.01
ENST00000499698	#N/A	2.70
ENST00000410980	#N/A	-2.34
hsa-mir-130b-3p	#N/A	1.16
ENST00000499543	#N/A	-1.44
ENST00000500134	#N/A	-1.93
hsa-mir-1268b-5p	#N/A	2.61
ENST00000384033	#N/A	1.48
ENST00000501159	#N/A	-2.84
ENST00000501903	#N/A	-2.84
ENST00000410818	#N/A	-2.95
ENST00000498954	#N/A	-2.95
ENST00000501206	#N/A	-1.79
ENST00000466665	#N/A	-1.06
ENST00000363788	#N/A	-2.10
hsa-mir-219a-3p	#N/A	1.68
hsa-mir-1180-3p	#N/A	1.06
hsa-mir-214-5p	#N/A	1.06
ENST00000481252	#N/A	-1.04
hsa-mir-548j-5p	#N/A	1.40
ENST00000410798	#N/A	-1.07
ENST00000502153	#N/A	5.20
hsa-mir-6720-5p	#N/A	5.20
ENST00000499262	#N/A	-5.08
ENST00000499793	#N/A	-5.08
ENST00000364448	#N/A	-1.53
hsa-mir-410-5p	#N/A	1.92
ENST00000499894	#N/A	-1.03
hsa-mir-3687-3p	#N/A	1.66
hsa-mir-3129-5p	#N/A	1.64
hsa-mir-937-3p	#N/A	-2.27
ENST00000408778	#N/A	2.00
ENST00000499388	#N/A	1.18
ENST00000501058	#N/A	-2.26
ENST00000499580	#N/A	1.87
ENST00000487740	#N/A	-1.47
ENST00000501092	#N/A	-1.63
hsa-mir-454-5p	#N/A	1.22
hsa-mir-489-3p	#N/A	-2.86
ENST00000444772	#N/A	-2.18
hsa-mir-122-5p	#N/A	-1.15
ENST00000384274	#N/A	-1.28
ENST00000410718	#N/A	-1.02

FIGURE 3A

Figure 3: EGS transcriptomics data during MM6 infections. Differential expression analysis of *T. gondii* genes from MM6 cells infected with *T. gondii* EGS strain for 18 hours compared to *T. gondii* gene expression from MM6 cells infected with GT1, ME49 or VEG strains for 18 hours.

gene ID	logFC (EGS/GT1)	logFC (EGS/ME49)	logFC (EGS/VEG)	Product Name
TGME49_232955	8.01	8.68	6.65	hypothetical protein
TGME49_323400	7.44	8.28	8.19	cytochrome c oxidase subunit iii subfamily protein
TGME49_322200	7.72	8.34	8.72	apocytochrome b, putative
TGME49_206550	4.89	2.98	6.27	hypothetical protein
TGME49_330000	8.23	9.02	7.63	cytochrome b
TGME49_237130	8.00	8.26	7.60	cytochrome b, putative
TGME49_255060	6.97	7.47	7.02	cytochrome b(N-terminal)/b6/petB subfamily protein
TGME49_252065	3.93	4.28	3.49	KRUF family protein
TGME49_305460	2.60	2.65	1.90	methionine aminopeptidase 2, putative
TGME49_301222	2.58	2.86	2.73	DNA repair protein Rad4 domain-containing protein
TGME49_252220	2.24	#N/A	1.54	tetratricopeptide repeat domain containing protein
TGME49_250670	3.64	#N/A	1.06	hypothetical protein
TGME49_302055	8.07	10.62	8.51	ribosomal protein RPS12
TGME49_279340	2.25	2.37	1.48	hypothetical protein
TGME49_252070	3.61	3.75	6.63	KRUF family protein
TGME49_225555	1.93	1.82	1.58	hypothetical protein
TGME49_275860	2.23	2.29	2.17	hypothetical protein
TGME49_217530	3.58	3.78	2.37	hypothetical protein
TGME49_254030	1.93	2.07	2.13	zinc finger CDGSH-type domain-containing protein
TGME49_253790	2.72	#N/A	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_249230	3.23	#N/A	#N/A	hypothetical protein
TGME49_260250	-2.90	-2.61	-1.90	cyclin domain protein, cyclin H family protein
TGME49_294400	-3.34	-2.54	-3.73	hypothetical protein
TGME49_226310	-2.88	-3.64	-2.13	zinc finger (CCCH type) motif-containing protein
TGME49_233925	10.75	10.32	10.59	hypothetical protein

gene ID	logFC (EGS/GT1)	logFC (EGS/ME49)	logFC (EGS/VEG)	Product Name
TGME49_319860	-1.01	#N/A	#N/A	DNA polymerase family B protein
TGME49_216750	-1.10	-1.10	#N/A	Paf1/RNA polymerase II complex component LEO1
TGME49_202510	1.65	#N/A	#N/A	multi-pass transmembrane protein
TGME49_261720	-0.98	-1.16	-0.99	metal cation transporter, ZIP family protein
TGME49_262860	-1.51	-1.63	-2.20	ADP-ribosylation factor family protein 1, putative
TGME49_207990	0.97	#N/A	#N/A	ribosomal RNA large subunit methyltransferase J protein
TGME49_320650	-1.52	-1.43	#N/A	ankyrin repeat-containing protein
TGME49_221160	1.68	#N/A	#N/A	acetyltransferase, GNAT family protein
TGME49_309090	-1.20	-1.08	#N/A	hypothetical protein
TGME49_237550	1.76	1.49	#N/A	hypothetical protein
TGME49_244680	1.39	#N/A	#N/A	hypothetical protein
TGME49_231870	-1.74	-1.89	-1.86	tetratricopeptide repeat-containing protein
TGME49_308020	-0.87	#N/A	#N/A	SAG-related sequence SRS57
TGME49_251470	-1.01	#N/A	#N/A	hypothetical protein
TGME49_253960	1.10	2.02	1.85	oxidoreductase, short chain dehydrogenase/reductase family protein
TGME49_232750	0.95	#N/A	#N/A	23S rRNA (adenine(1618)-N(6))-methyltransferase, putative
TGME49_254000	0.92	1.26	1.63	hypothetical protein
TGME49_237190	1.43	#N/A	#N/A	hypothetical protein
TGME49_269730	-0.92	#N/A	#N/A	myosin-light-chain kinase
TGME49_202430	-1.36	#N/A	-1.38	hypothetical protein
TGME49_225080	1.55	#N/A	1.56	ribosomal protein RPS18
TGME49_231200	1.47	#N/A	#N/A	hypothetical protein
TGME49_262690	2.92	#N/A	3.11	ribosomal protein RPL27
TGME49_272910	0.85	#N/A	#N/A	T-complex protein 1 delta subunit
TGME49_311625	-1.37	-1.42	-1.49	WD domain, G-beta repeat-containing protein

FIGURE 3B

TGME49_223660	1.91	2.65	2.39	50S ribosomal protein L4, putative
TGME49_235630	1.82	1.28	1.89	hypothetical protein
TGME49_286928	-3.71	-3.10	-3.90	hypothetical protein
TGME49_294980	4.14	1.48	#N/A	hypothetical protein
TGME49_273870	-2.06	-1.83	-1.97	SWI2/SNF2 ISWI-like (AT hook)
TGME49_260430	3.50	2.69	4.09	hypothetical protein
TGME49_251180	2.60	3.13	2.36	KRUF family protein
TGME49_301250	7.47	8.53	8.01	hypothetical protein
TGME49_299030	1.91	2.12	1.79	RNA recognition motif 2 protein
TGME49_285710	2.51	1.31	1.39	hypothetical protein
TGME49_290150	-2.45	-2.18	-1.42	hypothetical protein
TGME49_260480	2.83	2.05	#N/A	leucine rich repeat-containing protein
TGME49_277270	2.73	3.04	1.95	NTPase II
TGME49_322000	-2.57	-2.38	-3.55	myosin-light-chain kinase
TGME49_258390	2.65	1.39	#N/A	DnaJ protein, putative
TGME49_266740	3.44	#N/A	#N/A	RNA recognition motif-containing protein
TGME49_300010	-4.97	-4.45	-4.50	hypothetical protein
TGME49_242240	-3.22	-2.54	-3.68	rhodopy kinase family protein ROP19A
TGME49_207430	-2.44	-1.84	-2.11	ATP-dependent RNA helicase DDX1, putative
TGME49_253900	2.85	1.57	1.38	parasite porphobilinogen synthase PBGS
TGME49_212940	-8.20	-10.97	-7.44	hypothetical protein
TGME49_315885	5.95	5.94	6.02	glycosyltransferase, putative
TGME49_251170	2.42	2.24	1.98	KRUF family protein
TGME49_234460	2.14	2.80	#N/A	hypothetical protein
TGME49_259950	2.03	0.86	#N/A	carbonate dehydratase, eukaryotic-type domain-containing protein
TGME49_213067	1.80	1.98	#N/A	hypothetical protein
TGME49_221320	2.55	2.37	1.65	acetyl-CoA carboxylase ACC1
TGME49_257350	1.55	1.40	1.05	eukaryotic translation initiation factor, putative
TGME49_313100	-3.03	-2.51	-2.94	signal recognition particle SRP54 protein
TGME49_241155	3.09	1.88	#N/A	hypothetical protein
TGME49_215430	4.78	4.60	4.46	hypothetical protein
TGME49_200310	1.68	1.64	1.55	hypothetical protein
TGME49_236270	-3.59	-3.34	-2.80	hypothetical protein
TGME49_231180	-2.31	-2.97	-3.51	hypothetical protein
TGME49_259570	-1.51	#N/A	#N/A	CMP/dCMP deaminase, zinc-binding, putative
TGME49_212310	0.98	1.04	0.97	vacuolar ATP synthetase
TGME49_237280	-0.92	#N/A	#N/A	TLD protein
TGME49_276220	0.97	1.35	#N/A	hypothetical protein
TGME49_268680	0.90	#N/A	#N/A	hypothetical protein
TGME49_275420	-1.14	-1.19	#N/A	histone lysine-specific demethylase LSD1/BHC110/KDMA1A
TGME49_235140	-0.88	#N/A	-0.86	hypothetical protein
TGME49_219750	0.84	#N/A	#N/A	cytochrome c, putative
TGME49_227830	-1.02	#N/A	#N/A	mitochondrial inner membrane translocase TIM44, putative
TGME49_318650	0.85	0.90	1.08	transhydrogenase
TGME49_291620	-0.92	#N/A	#N/A	hypothetical protein
TGME49_227570	0.90	1.08	#N/A	transmembrane amino acid transporter protein
TGME49_316660	-1.10	#N/A	-1.20	cullin family protein
TGME49_207665	-2.56	#N/A	#N/A	kinesin motor domain-containing protein
TGME49_207120	-1.46	#N/A	#N/A	Sad1/UNC family protein
TGME49_273595	1.50	#N/A	#N/A	hypothetical protein
TGME49_210360	1.17	1.08	#N/A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41 family protein
TGME49_311160	-0.88	#N/A	#N/A	PWI domain-containing protein
TGME49_286580	0.92	#N/A	#N/A	hypothetical protein
TGME49_280770	1.02	#N/A	#N/A	regulator of chromosome condensation (RCC1) repeat-containing protein
TGME49_217820	-0.96	-0.93	#N/A	PCI domain-containing protein
TGME49_226020	0.95	1.25	#N/A	transporter, major facilitator family protein
TGME49_216230	-0.92	#N/A	#N/A	hypothetical protein
TGME49_253410	0.98	#N/A	#N/A	hypothetical protein
TGME49_255660	-1.12	-1.26	#N/A	EF hand domain-containing protein
TGME49_270120	-1.15	#N/A	#N/A	thioredoxin-like protein TLP1
TGME49_205130	-0.83	#N/A	#N/A	hypothetical protein
TGME49_249410	1.07	#N/A	#N/A	hypothetical protein
TGME49_209090	-1.16	-1.32	-1.65	proteasome maturation factor ump1 protein
TGME49_277760	-0.91	#N/A	#N/A	adenylosuccinate lyase, putative
TGME49_211630	-0.80	#N/A	#N/A	hypothetical protein
TGME49_310950	-0.80	#N/A	#N/A	AP2 domain transcription factor AP2XI-3

FIGURE 3C

TGME49_275640	1.79	1.61	1.67	hypothetical protein
TGME49_299080	1.66	1.84	1.66	VTC domain-containing protein
TGME49_232600	2.23	1.57	#N/A	phospholipase, patatin family protein
TGME49_312140	-4.04	-4.67	#N/A	hypothetical protein
TGME49_215930	-8.19	-7.79	-6.94	mediator complex subunit MED21
TGME49_299000	2.45	#N/A	#N/A	hypothetical protein
TGME49_254710	1.72	1.44	1.05	serine esterase (DUF676) protein
TGME49_247410	1.50	1.28	1.36	hypothetical protein
TGME49_233130	3.15	2.06	#N/A	nucleoside transporter protein
TGME49_267020	-2.38	-4.42	#N/A	hypothetical protein
TGME49_253750	1.73	1.65	1.53	PLU-1 family protein
TGME49_227810	1.57	1.65	#N/A	rhoGTPase family protein ROP11 (incomplete catalytic triad)
TGME49_207960	-2.40	-2.30	-2.73	hypothetical protein
TGME49_272410	3.57	3.54	3.71	phosphogluconate dehydrogenase (decarboxylating), NAD binding domain-containing protein
TGME49_215940	-2.46	-2.34	-1.97	Acetyl-coenzyme A transporter, putative
TGME49_233870	1.95	1.82	0.98	hypothetical protein
TGME49_254690	1.57	1.25	#N/A	phospholipase/carboxylesterase
TGME49_217555	1.35	1.38	0.89	hypothetical protein
TGME49_240700	-2.10	-1.71	-1.63	ubiquitin family protein
TGME49_260310	2.97	1.84	1.52	ATP-binding cassette transporter ABC.B1
TGME49_258720	1.64	1.93	1.99	Ubiquitin family protein, putative
TGME49_301280	-3.03	-2.29	#N/A	hypothetical protein
TGME49_254660	1.60	1.43	1.25	ankyrin repeat-containing protein
TGME49_247930	-3.26	-2.87	-2.90	SNARE domain-containing protein
TGME49_268225	-8.90	-9.99	-9.10	hypothetical protein
TGME49_206695	3.11	1.95	#N/A	hypothetical protein
TGME49_231370	2.43	1.26	#N/A	phospholipase, patatin family protein
TGME49_214380	-2.49	-1.99	#N/A	hypothetical protein
TGME49_259010	-1.97	-1.82	-1.66	vacuolar ATP synthase subunit d, putative
TGME49_306020	2.01	1.21	1.32	hypothetical protein
TGME49_254080	1.47	1.48	1.13	metal cation transporter, ZIP family protein
TGME49_240250	-1.53	-1.40	-1.39	macro domain-containing protein
TGME49_283790	3.32	#N/A	#N/A	protein kinase, putative
TGME49_293820	-1.59	-1.22	-1.01	calpain family cysteine protease domain-containing protein

TGME49_225240	0.91	1.15	#N/A	50S ribosomal protein L13, putative
TGME49_213010	-1.19	-2.88	#N/A	hypothetical protein
TGME49_204060	-1.35	-1.44	#N/A	SNARE domain-containing protein
TGME49_227780	1.46	1.55	#N/A	hypothetical protein
TGME49_238230	0.96	0.85	#N/A	Ser/Thr phosphatase family protein
TGME49_211030	-0.85	-1.10	#N/A	hypothetical protein
TGME49_228330	-1.61	#N/A	#N/A	NLI interacting factor family phosphatase
TGME49_310802	-1.21	#N/A	#N/A	CRAL/TRIO domain-containing protein
TGME49_219590	-1.13	#N/A	#N/A	RuvB family 1 protein
TGME49_319600	-1.15	#N/A	#N/A	alpha-tubulin N-acetyltransferase, putative
TGME49_280410	-0.91	#N/A	#N/A	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_301170	-6.07	-9.48	-7.08	SAG-related sequence SRS19D
TGME49_235560	1.73	#N/A	#N/A	hypothetical protein
TGME49_280750	-0.98	#N/A	#N/A	rudimentary enhancer, putative
TGME49_254380	-1.33	#N/A	#N/A	ribosomal protein L11, putative
TGME49_252280	1.08	#N/A	1.54	hypothetical protein
TGME49_230850	-0.86	#N/A	#N/A	hypothetical protein
TGME49_248690	-1.36	-1.32	#N/A	hypothetical protein
TGME49_278205	-0.80	#N/A	#N/A	hypothetical protein
TGME49_215640	-0.99	-1.04	#N/A	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_202390	-0.93	#N/A	#N/A	S15 sporozoite-expressed protein
TGME49_257685	0.90	#N/A	#N/A	hypothetical protein
TGME49_228010	-1.60	-1.70	#N/A	hypothetical protein
TGME49_278060	-1.66	-3.05	-1.76	Mre11 DNA-binding domain-containing protein
TGME49_313200	-1.67	-1.66	-2.23	leucine rich repeat-containing protein
TGME49_257300	-0.97	#N/A	#N/A	hypothetical protein
TGME49_219190	-1.06	#N/A	#N/A	nuclear movement protein domain containing protein
TGME49_246178	-1.17	#N/A	#N/A	hypothetical protein
TGME49_248870	-0.98	#N/A	#N/A	SNARE associated Golgi protein
TGME49_213930	-1.48	#N/A	#N/A	3' exonuclease family, domain 1 domain-containing protein
TGME49_287515	-1.69	#N/A	#N/A	hypothetical protein
TGME49_297720	-1.02	-1.24	-1.14	trehalose-phosphatase
TGME49_251730	-1.16	-1.40	#N/A	hypothetical protein
TGME49_205200	0.92	1.04	1.15	hypothetical protein

FIGURE 3D

TGME49_258790	-1.72	-2.03	-1.35	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_220240	1.59	2.02	1.45	hypothetical protein
TGME49_295935	1.50	1.37	1.08	KRUF family protein
TGME49_246490	-1.55	-1.02	-0.91	hypothetical protein
TGME49_225930	1.29	1.14	0.78	triose-phosphate isomerase TPI-I
TGME49_297495	-7.98	-9.14	#N/A	hypothetical protein
TGME49_240510	2.77	1.44	#N/A	hypothetical protein
TGME49_299210	1.86	1.80	#N/A	CTP synthase
TGME49_306895	1.69	1.61	1.38	hypothetical protein
TGME49_321540	-1.74	-1.49	-1.18	hypothetical protein
TGME49_254770	1.45	1.66	1.67	Ser/Thr phosphatase family protein
TGME49_290580	-2.49	-3.63	-2.61	ATP-binding cassette G family transporter ABCG89
TGME49_234640	-1.84	-1.52	-1.24	hypothetical protein
TGME49_208440	1.33	1.46	1.59	hypothetical protein
TGME49_252310	1.63	#N/A	1.02	hypothetical protein
TGME49_252360	1.57	1.05	1.78	rhoGTPase family protein ROP24 (incomplete catalytic triad)
TGME49_254620	1.89	1.10	1.56	ribosomal protein RPL39
TGME49_243410	-2.01	-1.79	-1.36	tetratricopeptide repeat-containing protein
TGME49_279350	2.28	2.79	1.20	hypothetical protein
TGME49_293280	2.37	#N/A	#N/A	cyclin protein
TGME49_224220	-1.94	-1.73	-1.35	serine/threonine-protein phosphatase PP2A catalytic subunit
TGME49_253470	1.39	1.48	1.02	alveolin domain containing intermediate filament IMC13
TGME49_239270	-1.71	-2.30	-1.67	hypothetical protein
TGME49_203540	1.80	1.51	#N/A	RNA binding protein, putative
TGME49_293430	1.38	1.33	1.13	hypothetical protein
TGME49_244370	6.17	6.57	6.32	TDC1, putative
TGME49_219520	-1.51	-1.34	-1.38	histone arginine methyltransferase PRMT1
TGME49_261750	-1.75	-1.87	-1.64	rhoGTPase neck protein RON10
TGME49_242340	1.66	#N/A	0.96	ribosomal protein RPS29
TGME49_285190	-1.73	-1.76	-1.68	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_319540	-2.36	-2.49	-1.62	hypothetical protein
TGME49_278050	-1.45	-1.03	#N/A	proteasome subunit alpha type 1, putative

TGME49_213388	-1.46	-1.41	#N/A	hypothetical protein
TGME49_254480	1.45	#N/A	1.42	WD domain, G-beta repeat-containing protein
TGME49_238180	-0.95	#N/A	#N/A	26S proteasome regulatory complex subunit, putative
TGME49_220470	-1.04	#N/A	#N/A	hypothetical protein
TGME49_218740	1.54	#N/A	#N/A	membrane protein, putative
TGME49_222110	-1.24	#N/A	#N/A	PUB domain-containing protein
TGME49_236250	-1.28	#N/A	#N/A	regulator of chromosome condensation (RCC1) repeat-containing protein
TGME49_310230	-1.14	-1.13	#N/A	hypothetical protein
TGME49_256060	-1.00	-1.24	#N/A	nucleosome assembly protein (nap) protein
TGME49_205250	0.96	1.32	7.91	rhoGTPase protein ROP18
TGME49_240570	1.00	#N/A	#N/A	hypothetical protein
TGME49_312160	0.89	1.26	#N/A	hypothetical protein
TGME49_315280	-1.30	-1.86	#N/A	hypothetical protein
TGME49_256760	-0.93	#N/A	#N/A	pyruvate kinase PyK1
TGME49_217400	1.51	-1.37	-1.32	hypothetical protein
TGME49_254470	0.87	1.02	0.95	hypothetical protein
TGME49_217770	0.82	1.14	#N/A	hypothetical protein
TGME49_252210	1.25	#N/A	#N/A	pentatricopeptide repeat domain-containing protein
TGME49_306610	-1.56	-1.45	#N/A	3' exonuclease family, domain 1 domain-containing protein
TGME49_308093	0.79	#N/A	1.75	rhoGTPase family protein (incomplete catalytic triad)
TGME49_261460	-1.01	-1.01	#N/A	transcriptional elongation factor FACT80
TGME49_240910	-1.09	#N/A	-1.21	hypothetical protein
TGME49_294180	-1.26	#N/A	#N/A	tRNA-methyltransferase family protein
TGME49_234900	-0.85	-0.99	#N/A	PHD-finger domain-containing protein
TGME49_214470	-1.19	#N/A	#N/A	Ulp1 protease family, C-terminal catalytic domain-containing protein
TGME49_224070	-1.28	-1.32	#N/A	hypothetical protein
TGME49_221670	-0.81	#N/A	#N/A	transcriptional elongation factor FACT140
TGME49_242010	1.26	#N/A	#N/A	glucose inhibited division protein A subfamily protein
TGME49_254090	1.09	0.96	#N/A	hypothetical protein
TGME49_216910	-1.01	#N/A	#N/A	hypothetical protein
TGME49_269438	1.09	#N/A	#N/A	hypothetical protein
TGME49_279430	1.00	#N/A	#N/A	cwf18 pre-mRNA splicing factor protein

FIGURE 3E

TGME49_247340	2.08	#N/A	4.66	hypothetical protein
TGME49_320005	-2.72	-2.78	-2.39	hypothetical protein
TGME49_305160	3.60	3.04	2.59	histone H2Ba
TGME49_289050	2.13	1.75	#N/A	FIKK kinase, putative
TGME49_252290	1.89	#N/A	1.16	importin alpha, putative
TGME49_262010	1.74	1.18	#N/A	calmodulin CAM2
TGME49_249770	2.68	1.95	#N/A	Nmda1 protein
TGME49_228750	2.50	#N/A	#N/A	TGME49_228750 CAM kinase, RAD family
TGME49_277700	2.31	1.39	#N/A	ribosomal protein S14 precursor, putative
TGME49_233500	1.50	#N/A	0.89	triose-phosphate isomerase TPI-II
TGME49_311440	1.65	1.24	1.31	SAG-related sequence SRS50
TGME49_308840	1.66	#N/A	1.87	SAG-related sequence SRS51
TGME49_277710	-1.81	-1.81	-1.61	hypothetical protein
TGME49_215390	2.51	1.69	2.46	TIM10 family protein, putative
TGME49_215895	1.71	0.96	0.98	AP2 domain-containing protein
TGME49_260520	1.96	1.94	#N/A	hypothetical protein
TGME49_278510	-1.51	-1.43	-1.62	protein phosphatase 2C domain-containing protein
TGME49_252390	1.30	0.73	1.81	hypothetical protein
TGME49_312310	-2.52	-2.41	-2.24	ATPase, AAA family protein
TGME49_254050	1.39	1.59	1.30	optic atrophy 3 protein (opa3) protein
TGME49_213280	1.45	2.31	1.97	SAG-related sequence SRS25
TGME49_260210	-2.94	-2.82	-2.52	DnaJ domain-containing protein
TGME49_246978	-2.87	-2.84	-2.90	hypothetical protein
TGME49_279450	-7.76	-8.01	-7.66	adenylosuccinate synthetase, putative
TGME49_233030	-1.36	-1.03	-1.20	gliding-associated protein GAP70
TGME49_270530	-1.63	-1.14	-1.26	ubiquitin fusion degradation protein UFD1CY
TGME49_308090	2.51	#N/A	2.58	rhoptry protein ROP5
TGME49_205680	1.65	1.88	1.48	hypothetical protein
TGME49_268570	-1.42	-1.14	#N/A	zinc finger (CCH type) motif-containing protein
TGME49_263270	-1.53	#N/A	#N/A	glycerophosphodiester phosphodiesterase family protein
TGME49_262910	2.83	1.44	#N/A	NADH-cytochrome b5 reductase 1, putative
TGME49_219832	-2.70	-2.64	-2.42	cyclin-dependent kinase regulatory subunit protein
TGME49_217010	-1.86	-1.53	-1.33	hypothetical protein
TGME49_312600	1.17	1.81	1.23	heat shock protein HSP21

TGME49_275650	1.13	#N/A	1.27	hypothetical protein
TGME49_225170	-1.22	#N/A	#N/A	hypothetical protein
TGME49_286790	-1.12	-1.22	#N/A	nuclear factor NF2
TGME49_295960	-1.27	#N/A	#N/A	hypothetical protein
TGME49_233430	1.41	#N/A	#N/A	hypothetical protein
TGME49_253070	1.36	#N/A	#N/A	hydrolase, TatD family protein
TGME49_249900	1.17	#N/A	#N/A	adenine nucleotide translocator, putative
TGME49_273140	-1.37	-1.45	#N/A	radical SAM methyltransferase, MiaB/RimO family protein
TGME49_231480	0.94	#N/A	#N/A	GCN1, putative
TGME49_321650	-0.82	-0.79	#N/A	hypothetical protein
TGME49_319740	-1.41	-1.51	#N/A	transporter, major facilitator family protein
TGME49_201880	0.73	0.72	0.87	hypothetical protein
TGME49_204040	1.61	#N/A	#N/A	hypothetical protein
TGME49_266750	0.85	#N/A	#N/A	transporter/permease protein, putative
TGME49_227150	0.87	#N/A	1.22	glutaredoxin, putative
TGME49_291120	-1.11	-1.11	#N/A	trafficking protein mon1 subfamily protein
TGME49_285950	-1.50	#N/A	#N/A	hypothetical protein
TGME49_239680	0.97	#N/A	#N/A	hypothetical protein
TGME49_213790	-1.09	-1.09	-1.10	hypothetical protein
TGME49_318690	1.29	1.35	1.49	RNA recognition motif-containing protein
TGME49_254290	1.08	1.01	#N/A	hypothetical protein
TGME49_280570	#N/A	5.19	5.07	SAG-related sequence SRS35A
TGME49_291040	#N/A	5.96	4.68	lactate dehydrogenase LDH2
TGME49_259020	#N/A	5.33	6.15	bradyzoite antigen BAG1
TGME49_216140	#N/A	3.66	1.19	tetratricopeptide repeat-containing protein
TGME49_299010	#N/A	4.46	#N/A	hypothetical protein
TGME49_202970	#N/A	-5.95	#N/A	hypothetical protein
TGME49_264240	#N/A	-10.43	-6.12	hypothetical protein
TGME49_312905	#N/A	-3.09	#N/A	hypothetical protein
TGME49_244700	#N/A	-2.91	#N/A	NAD(+)/NADH kinase domain-containing protein
TGME49_280400	#N/A	-3.11	#N/A	hypothetical protein
TGME49_233000	#N/A	-2.52	#N/A	KOW motif domain-containing protein
TGME49_266950	#N/A	-2.61	#N/A	protein kinase, putative
TGME49_203720	#N/A	2.05	1.19	vitamin k epoxide reductase family protein

FIGURE 3F

TGME49_249860	-1.63	-1.42	-1.57	hypothetical protein
TGME49_223040	1.52	1.48	0.97	hypothetical protein
TGME49_275320	-1.56	-1.34	-1.50	penicillin amidase
TGME49_255650	-1.54	#N/A	-1.18	DHHC zinc finger domain-containing protein
TGME49_242110	-2.88	#N/A	-3.56	rhoptyr kinase family protein ROP38
TGME49_254520	1.33	1.57	1.45	mediator complex subunit MED11
TGME49_266100	1.48	1.33	1.51	rhoptyr kinase family protein ROP41
TGME49_247770	1.21	1.09	#N/A	hypothetical protein
TGME49_215540	-8.74	-8.70	#N/A	hypothetical protein
TGME49_254910	2.11	#N/A	#N/A	hypothetical protein
TGME49_287470	2.41	2.95	#N/A	hypothetical protein
TGME49_252250	2.15	#N/A	1.30	ATPase, AAA family protein
TGME49_240520	2.21	#N/A	#N/A	hypothetical protein
TGME49_220400	2.00	1.70	1.45	actin depolymerizing factor ADF
TGME49_262500	-1.75	-1.50	-1.13	hypothetical protein
TGME49_207630	-3.63	-3.31	-3.45	peptidyl-tRNA hydrolase domain-containing protein
TGME49_210430	-1.34	-1.23	-0.93	DnaJ domain-containing protein
TGME49_290600	6.12	6.38	6.31	succinyl-CoA-synthetase alpha SCSA
TGME49_211220	-1.89	-1.98	#N/A	hypothetical protein
TGME49_286140	-1.99	-1.63	-1.40	hypothetical protein
TGME49_268730	2.02	1.22	#N/A	glutaredoxin-related protein
TGME49_311210	-1.66	-1.38	-1.53	hypothetical protein
TGME49_284190	1.69	#N/A	#N/A	pyruvate carboxylase
TGME49_200595	-9.05	-7.22	#N/A	hypothetical protein
TGME49_271935	1.72	2.09	2.02	hypothetical protein
TGME49_261000	-1.86	-1.73	#N/A	MutS domain V domain-containing protein
TGME49_280518	-1.51	-1.09	#N/A	hypothetical protein
TGME49_320110	2.87	2.51	3.01	proliferating cell nuclear antigen PCNA2
TGME49_209755	-1.64	3.95	3.84	hypothetical protein
TGME49_286720	1.48	0.86	#N/A	heat shock protein HSP28
TGME49_321360	1.18	1.69	1.55	clustered-asparagine-rich protein
TGME49_202540	-1.37	-0.98	#N/A	3'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_230490	-1.72	-1.20	-1.58	phosphatidylinositol 4-phosphate 5-kinase
TGME49_297420	-2.07	-1.75	-1.64	beta-tubulin cofactor D, putative
TGME49_253290	1.20	1.29	1.10	valyl-tRNA synthetase
TGME49_217951	-1.96	-2.00	4.96	hypothetical protein

TGME49_235680	#N/A	-2.63	#N/A	peptidase M16 inactive domain-containing protein
TGME49_289350	#N/A	-3.12	#N/A	ATP-binding cassette G family transporter ABCG84
TGME49_307770	#N/A	-2.38	#N/A	fumble protein
TGME49_207210	#N/A	3.26	4.66	hypothetical protein
TGME49_311460	#N/A	-2.95	#N/A	hypothetical protein
TGME49_209940	#N/A	-2.26	#N/A	transporter/permease protein
TGME49_283540	#N/A	1.98	1.10	hypothetical protein
TGME49_210210	#N/A	-9.04	#N/A	hypothetical protein
TGME49_213255	#N/A	-2.66	#N/A	hypothetical protein
TGME49_264260	#N/A	-4.82	#N/A	hypothetical protein
TGME49_280490	#N/A	-1.99	#N/A	U-box domain-containing protein
TGME49_221840	#N/A	3.66	4.30	hypothetical protein
TGME49_306688	#N/A	-3.91	#N/A	hypothetical protein
TGME49_238140	#N/A	-2.18	-1.15	hypothetical protein
TGME49_263820	#N/A	-2.10	#N/A	DEAD/DEAH box helicase domain-containing protein
TGME49_240220	#N/A	-2.27	#N/A	hypothetical protein
TGME49_216680	#N/A	-2.19	#N/A	ankyrin repeat-containing protein
TGME49_214410	#N/A	1.67	1.11	hypothetical protein
TGME49_253690	#N/A	1.66	1.79	hypothetical protein
TGME49_306338	#N/A	-2.76	#N/A	dynein gamma chain, flagellar outer arm, putative
TGME49_297840	#N/A	-1.92	#N/A	DNA primase, large subunit
TGME49_204050	#N/A	2.64	#N/A	subtilisin SUB1
TGME49_298060	#N/A	-2.83	#N/A	Toxoplasma gondii family C protein
TGME49_202020	#N/A	2.74	2.69	DnAK-TPR
TGME49_275460	#N/A	2.53	1.38	hypothetical protein
TGME49_240880	#N/A	-2.58	#N/A	hypothetical protein
TGME49_205210	#N/A	-5.32	#N/A	hypothetical protein
TGME49_251540	#N/A	1.64	#N/A	dense granule protein GRA9
TGME49_236670	#N/A	2.12	2.81	hypothetical protein
TGME49_316470	#N/A	-2.66	#N/A	hypothetical protein
TGME49_217020	#N/A	-2.26	#N/A	ATPase, AFG1 family protein
TGME49_218750	#N/A	-2.82	#N/A	hypothetical protein
TGME49_312520	#N/A	-2.75	#N/A	tRNA dimethylallyltransferase
TGME49_234530	#N/A	1.69	1.33	hypothetical protein
TGME49_316250	#N/A	1.44	1.00	hypothetical protein
TGME49_315130	#N/A	1.51	0.93	L-isoadipate protein carboxyl methyltransferase family protein

FIGURE 3G

TGME49_259530	-1.67	-1.62	-1.69	GalNac
TGME49_268620	-3.08	-2.80	-2.80	blood stage antigen 41-3 precursor, putative
TGME49_223150	-2.63	-2.38	-2.36	START domain-containing protein
TGME49_223640	1.73	#N/A	#N/A	ATP-citrate lyase, putative
TGME49_201790	-1.60	-1.12	#N/A	FHA domain-containing protein
TGME49_237195	-2.18	-1.66	#N/A	hypothetical protein
TGME49_252270	1.93	#N/A	#N/A	L1P family of ribosomal protein
TGME49_253990	1.44	1.02	0.91	hypothetical protein
TGME49_293550	-1.38	-1.09	#N/A	hypothetical protein
TGME49_254610	1.75	1.37	#N/A	Tim10/DDP family zinc finger superfamily protein
TGME49_254900	1.33	0.89	#N/A	proteasome subunit beta type 2, putative
TGME49_306730	-3.20	#N/A	-2.45	hypothetical protein
TGME49_248630	-1.60	-1.11	#N/A	actin-related protein ARP1
TGME49_252500	1.20	1.38	1.53	polo kinase
TGME49_238073	-2.22	#N/A	#N/A	hypothetical protein
TGME49_227330	1.71	1.13	#N/A	hypothetical protein
TGME49_222900	1.37	#N/A	#N/A	phosphoserine phosphatase
TGME49_205510	-1.20	#N/A	#N/A	nucleolar protein 5, putative
TGME49_255635	-4.70	-3.83	-5.53	hypothetical protein
TGME49_204110	-2.91	-2.23	#N/A	eIF2 kinase IF2K-C
TGME49_259115	-2.00	-5.11	-1.48	ABC1 family protein
TGME49_321550	1.54	1.11	#N/A	hypothetical protein
TGME49_213800	-1.29	-0.89	#N/A	protein phosphatase 2b regulatory subunit, putative
TGME49_258030	-2.43	-2.70	#N/A	DNA polymerase
TGME49_252190	2.13	2.25	1.41	KRUF family protein
TGME49_292200	-1.23	-0.93	#N/A	RNA recognition motif-containing protein
TGME49_247530	1.25	1.99	1.67	hypothetical protein
TGME49_298990	1.50	0.89	#N/A	ferredoxin NADP+ oxidoreductase FNR
TGME49_229440	-1.85	-1.88	-2.19	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_293480	1.93	#N/A	2.09	MoeA N-terminal region (domain I and II) domain-containing protein
TGME49_239410	-1.36	-1.12	#N/A	hypothetical protein
TGME49_237410	-1.64	-1.14	-1.13	protein phosphatase 2C domain-containing protein
TGME49_257180	-1.98	-2.08	-1.89	RecF/RecN/SMC N terminal domain-containing protein
TGME49_217350	-2.50	-2.31	-2.26	methyltransferase MTA70, putative

TGME49_240650	#N/A	-1.59	-1.13	coatamer protein complex, subunit alpha, putative
TGME49_297910	#N/A	-3.38	#N/A	hypothetical protein
TGME49_262050	#N/A	2.31	1.98	rhoGTPase family protein ROP39
TGME49_239250	#N/A	-1.47	#N/A	diacylglycerol kinase, putative
TGME49_268860	#N/A	4.31	4.11	enolase 1
TGME49_240840	#N/A	-2.01	#N/A	histone lysine demethylase JmjC NO66
TGME49_202780	#N/A	1.32	1.04	rhoGTPase family protein ROP25
TGME49_262590	#N/A	-3.61	#N/A	hypothetical protein
TGME49_312330	#N/A	1.73	#N/A	hypothetical protein
TGME49_301160	#N/A	-3.93	#N/A	SAG-related sequence SRS19C
TGME49_293740	#N/A	1.33	0.99	hypothetical protein
TGME49_244120	#N/A	-2.11	-1.84	hypothetical protein
TGME49_288860	#N/A	-1.61	#N/A	RuvB family 2 protein
TGME49_292975	#N/A	-1.81	#N/A	hypothetical protein
TGME49_253180	#N/A	2.53	2.00	hypothetical protein
TGME49_297492	#N/A	-4.59	-3.43	hypothetical protein
TGME49_277510	#N/A	-1.70	-1.09	cytoplasmic dynein intermediate chain
TGME49_246200	#N/A	-2.81	-2.46	zinc finger (CCCH type) motif-containing protein
TGME49_258230	#N/A	2.52	#N/A	rhoGTPase family protein ROP20
TGME49_217420	#N/A	-2.47	-1.59	hypothetical protein
TGME49_215700	#N/A	-1.84	#N/A	phosphatidylinositol 3- and 4-kinase
TGME49_225290	#N/A	2.97	#N/A	GDA1/CD39 (nucleoside phosphatase) family protein
TGME49_307650	#N/A	-1.81	#N/A	uracil-DNA glycosylase
TGME49_263730	#N/A	-1.66	#N/A	FAD-dependent glycerol-3-phosphate dehydrogenase
TGME49_263100	#N/A	-2.14	#N/A	hypothetical protein
TGME49_248990	#N/A	1.22	#N/A	hypothetical protein
TGME49_269690	#N/A	1.16	#N/A	hypothetical protein
TGME49_310970	#N/A	-1.43	#N/A	hypothetical protein
TGME49_323100	#N/A	1.64	#N/A	hypothetical protein
TGME49_316710	#N/A	1.24	#N/A	hypothetical protein
TGME49_290700	#N/A	1.27	#N/A	hypothetical protein
TGME49_239810	#N/A	1.60	#N/A	hypothetical protein
TGME49_269180	#N/A	-1.20	-1.22	MIF4G domain-containing protein
TGME49_285870	#N/A	1.32	#N/A	SAG-related sequence SRS20A

FIGURE 3H

TGME49_230140	2.10	#N/A	#N/A	vacuolar sorting protein 9 (vps9) domain-containing protein
TGME49_319580	-2.55	-2.72	-2.59	hypothetical protein
TGME49_281450	-1.99	-1.50	#N/A	cell-cycle-associated protein kinase, putative
TGME49_203390	-1.39	-1.16	#N/A	CRAL/TRIO domain-containing protein
TGME49_295950	1.65	2.39	1.36	KRUF family protein
TGME49_270580	2.21	#N/A	3.82	HECT-domain (ubiquitin-transferase) domain-containing protein
TGME49_243465	3.08	#N/A	#N/A	hypothetical protein
TGME49_253860	1.32	1.25	1.04	Tyrosine kinase-like (TKL) protein
TGME49_251460	-1.84	-1.36	-1.56	hypothetical protein
TGME49_253100	1.15	1.26	1.15	hypothetical protein
TGME49_222040	-2.70	-2.83	-3.28	Ran-interacting Mog1 protein
TGME49_289310	-1.53	-1.26	-1.11	cullin family protein
TGME49_228360	1.39	0.88	1.31	peptidyl-prolyl isomerase FKBP12, putative
TGME49_201260	-1.25	-1.14	-1.27	sugar transporter ST3
TGME49_228630	-1.29	-1.09	#N/A	hypothetical protein
TGME49_232960	-1.48	-1.21	-1.32	oxidoreductase, 2OG-Fe(II) oxygenase family protein
TGME49_262625	2.05	1.47	#N/A	peptidase family c50 protein
TGME49_263060	1.64	1.13	#N/A	Proteasome/cyclosome repeat-containing protein
TGME49_240950	-3.19	-3.14	-2.61	hypothetical protein
TGME49_240440	1.45	1.19	1.01	hypothetical protein
TGME49_316270	1.43	1.40	1.61	Rab geranylgeranyl transferase type II beta subunit, putative
TGME49_289720	-1.72	-1.60	#N/A	hypothetical protein
TGME49_273400	-2.22	-1.55	#N/A	hypothetical protein
TGME49_288580	2.50	1.40	#N/A	RNA methylase, putative
TGME49_287160	-1.25	-1.19	#N/A	internal kinesin motor domain protein
TGME49_213635	2.50	2.45	#N/A	hypothetical protein
TGME49_298610	-1.15	-1.02	#N/A	GYF domain-containing protein
TGME49_203730	-2.06	-2.40	-2.44	hypothetical protein
TGME49_313230	2.39	2.44	2.45	eukaryotic initiation factor-2, alpha subunit
TGME49_226755	1.53	1.60	1.13	3'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_253600	1.77	2.31	1.45	hypothetical protein
TGME49_254630	1.34	1.08	#N/A	CMGC kinase

TGME49_289540	#N/A	1.20	#N/A	hypothetical protein
TGME49_246130	#N/A	1.27	#N/A	serpin (serine proteinase inhibitor) superfamily protein
TGME49_263740	#N/A	-1.88	#N/A	ABC transporter transmembrane region domain-containing protein
TGME49_260190	#N/A	-1.57	#N/A	microneme protein MIC13
TGME49_276920	#N/A	-1.63	-1.73	protein phosphatase 2C domain-containing protein
TGME49_253700	#N/A	1.05	#N/A	transporter, major facilitator family protein
TGME49_254150	#N/A	1.91	1.62	hypothetical protein
TGME49_237015	#N/A	1.37	0.96	hypothetical protein
TGME49_264870	#N/A	1.39	1.20	Sodium neurotransmitter symporter family protein
TGME49_226580	#N/A	1.12	#N/A	hypothetical protein
TGME49_202620	#N/A	1.18	#N/A	hypothetical protein
TGME49_213680	#N/A	-2.26	-2.37	MmgE/PrpD family protein
TGME49_245530	#N/A	3.38	#N/A	hypothetical protein
TGME49_296015	#N/A	1.22	1.16	hypothetical protein
TGME49_272600	#N/A	-1.29	#N/A	adaptin c-terminal domain-containing protein
TGME49_285830	#N/A	-1.60	-1.21	hypothetical protein
TGME49_226260	#N/A	1.23	#N/A	hypothetical protein
TGME49_310210	#N/A	1.73	#N/A	hypothetical protein
TGME49_255960	#N/A	-1.75	-1.38	hypothetical protein
TGME49_240580	#N/A	-1.94	#N/A	hypothetical protein
TGME49_297180	#N/A	-1.25	#N/A	hypothetical protein
TGME49_311660	#N/A	-1.65	#N/A	histone lysine methyltransferase, SET, putative
TGME49_253490	#N/A	1.38	1.22	hypothetical protein
TGME49_257910	#N/A	4.40	#N/A	hypothetical protein
TGME49_269930	#N/A	-2.18	#N/A	calcium binding egf domain-containing protein
TGME49_201380	#N/A	1.04	#N/A	chorismate synthase, putative
TGME49_253170	#N/A	1.97	1.79	zinc carboxypeptidase, putative
TGME49_307570	#N/A	-1.64	-1.35	glycerol-3-phosphate dehydrogenase (gpdh), putative
TGME49_310100	#N/A	-2.01	#N/A	mannosyltransferase (pig-m) protein
TGME49_299060	#N/A	1.37	#N/A	sodium/hydrogen exchanger NHE2
TGME49_203290	#N/A	1.61	#N/A	hypothetical protein
TGME49_247250	#N/A	-1.28	#N/A	RbAp46

FIGURE 3i

TGME49_309070	-2.16	-1.93	-1.67	hypothetical protein
TGME49_233680	-2.80	-2.92	-2.65	nuclear movement family protein
TGME49_229470	-1.47	-1.06	-1.37	hypothetical protein
TGME49_207180	2.21	#N/A	#N/A	indole-3-glycerol phosphate synthase domain-containing protein
TGME49_290740	-2.43	-2.09	#N/A	hypothetical protein
TGME49_230430	-2.22	-1.88	-2.06	vesicle-associated membrane protein, putative
TGME49_294060	1.52	0.97	#N/A	hypothetical protein
TGME49_300980	2.31	#N/A	#N/A	hypothetical protein
TGME49_286510	1.70	1.27	1.10	hypothetical protein
TGME49_248130	-2.53	-2.03	-2.01	hypothetical protein
TGME49_285470	2.15	1.63	#N/A	patched family protein
TGME49_283550	1.34	1.04	0.97	hypothetical protein
TGME49_300055	-1.16	#N/A	#N/A	hypothetical protein
TGME49_297780	-1.71	-2.60	-1.53	ATPase/histidine kinase/DNA gyrase B/HSP90 domain-containing protein
TGME49_293040	-1.91	-1.63	#N/A	hypothetical protein
TGME49_258590	-2.37	-2.06	-2.53	hypothetical protein
TGME49_215785	2.21	1.79	#N/A	rhoGTP protein ROP2A
TGME49_214400	1.75	1.71	1.40	hypothetical protein
TGME49_237290	-1.50	-1.34	-1.25	hypothetical protein
TGME49_268810	-1.75	-1.47	-1.52	ck2 beta subunit
TGME49_237830	-1.92	-1.66	-1.95	DNA polymerase I domain-containing protein
TGME49_226380	1.18	1.80	1.34	hypothetical protein
TGME49_227335	2.40	1.44	#N/A	hypothetical protein
TGME49_274070	-2.79	-3.35	-2.85	ThiF family protein
TGME49_215400	-2.20	-1.61	-1.74	RNA recognition motif-containing protein
TGME49_241300	1.80	#N/A	#N/A	hypothetical protein
TGME49_253140	1.54	1.52	1.47	hypothetical protein
TGME49_305990	3.44	2.44	#N/A	hypothetical protein
TGME49_288400	-1.71	-1.81	-1.67	LETM1 family protein
TGME49_273530	-2.31	-1.77	#N/A	flagellar associated protein
TGME49_277540	2.13	1.89	#N/A	hypothetical protein
TGME49_220500	-1.33	#N/A	#N/A	UBX domain-containing protein
TGME49_225440	-4.18	-4.09	-3.61	hypothetical protein
TGME49_293840	1.98	#N/A	#N/A	hypothetical protein
TGME49_212090	1.14	1.15	1.15	hypothetical protein

TGME49_264780	#N/A	-1.66	#N/A	UTP-glucose-1-phosphate uridylyltransferase subfamily protein
TGME49_268790	#N/A	1.04	#N/A	hypothetical protein
TGME49_259700	#N/A	1.16	0.83	hypothetical protein
TGME49_205150	#N/A	-1.81	#N/A	ACR, YagE family COG1723 domain-containing protein
TGME49_248830	#N/A	-1.43	#N/A	phosphoinositide phospholipase PIPLC
TGME49_254580	#N/A	1.29	#N/A	UDP-galactose transporter family protein
TGME49_278270	#N/A	-2.06	-1.58	nucleolar protein, structural component of H/ACA snoRNPs, putative
TGME49_264660	#N/A	1.41	#N/A	SAG-related sequence SRS44
TGME49_229650	#N/A	-1.58	-1.29	josephin protein
TGME49_214540	#N/A	1.16	1.33	hypothetical protein
TGME49_273030	#N/A	-1.68	#N/A	phosphoglycerate mutase family protein
TGME49_311780	#N/A	-1.47	#N/A	Zn-containing alcohol dehydrogenase
TGME49_215360	#N/A	1.53	#N/A	hypothetical protein
TGME49_262970	#N/A	1.54	#N/A	hypothetical protein
TGME49_241140	#N/A	-1.88	-1.55	DEAD/DEAH box helicase domain-containing protein
TGME49_219610	#N/A	1.77	1.62	hypothetical protein
TGME49_277260	#N/A	2.11	2.43	hypothetical protein
TGME49_315910	#N/A	1.44	#N/A	hypothetical protein
TGME49_240430	#N/A	-2.18	-2.23	glyoxalase family protein
TGME49_275755	#N/A	2.33	3.42	hypothetical protein
TGME49_307580	#N/A	-1.23	#N/A	CBS domain-containing protein
TGME49_257360	#N/A	1.87	#N/A	hypothetical protein
TGME49_202830	#N/A	1.10	#N/A	Elicitor-responsive protein, putative
TGME49_258940	#N/A	1.50	#N/A	acylphosphatase family protein
TGME49_279100	#N/A	1.08	1.35	hypothetical protein
TGME49_254880	#N/A	1.03	#N/A	Alpha-galactosidase
TGME49_271430	#N/A	-2.03	-1.77	hypothetical protein
TGME49_257290	#N/A	-1.92	#N/A	RNA 2'-phosphotransferase, Tpt1/KptA family protein
TGME49_253710	#N/A	1.14	#N/A	hypothetical protein
TGME49_245980	#N/A	2.76	#N/A	hypothetical protein
TGME49_227390	#N/A	-1.67	#N/A	hypothetical protein
TGME49_272650	#N/A	-1.50	-1.17	3'/5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_290970	#N/A	2.67	#N/A	8-amino-7-oxononanoate synthase
TGME49_227430	#N/A	-1.65	2.88	transmembrane amino acid transporter protein
TGME49_258670	#N/A	-1.66	#N/A	hypothetical protein

FIGURE 3J

TGME49_244230	-2.07	-1.85	#N/A	hypothetical protein
TGME49_258410	1.26	1.07	1.02	photosensitized INA-labeled protein PHIL1
TGME49_248160	-2.51	-2.29	-2.51	hypothetical protein
TGME49_261660	1.96	1.38	#N/A	hypothetical protein
TGME49_241610	1.80	#N/A	#N/A	hypothetical protein
TGME49_249390	-1.14	#N/A	#N/A	glutamate/leucine/phenylalanine/valine dehydrogenase family protein
TGME49_205330	1.10	1.39	1.01	hypothetical protein
TGME49_214970	-1.38	-1.28	-1.23	DNA replication licensing factor, putative
TGME49_291930	3.85	3.68	3.85	RNA recognition motif-containing protein
TGME49_309990	1.26	1.37	1.54	hypothetical protein
TGME49_210380	-1.30	-1.26	-1.15	hypothetical protein
TGME49_213570	4.50	4.95	4.84	hypothetical protein
TGME49_221675	1.12	1.51	#N/A	hypothetical protein
TGME49_246530	2.25	1.85	#N/A	phospholipase D active site domain-containing protein
TGME49_289620	1.19	0.81	#N/A	cathepsin CPC1
TGME49_294890	-1.47	-1.25	#N/A	hypothetical protein
TGME49_202580	2.00	1.59	#N/A	ATPase, AAA family protein
TGME49_266860	1.40	#N/A	#N/A	BTB/POZ domain-containing protein
TGME49_312270	1.16	1.48	1.37	rhoGTP protein ROP13
TGME49_266280	-1.44	-1.16	#N/A	HEAT repeat-containing protein
TGME49_218960	1.65	#N/A	#N/A	AP2 domain transcription factor AP2XII-1
TGME49_263860	-2.07	-1.85	#N/A	hypothetical protein
TGME49_310130	-1.62	-1.52	-1.58	Spc97 / Spc98 family protein
TGME49_316255	1.05	1.20	#N/A	hypothetical protein
TGME49_254720	1.69	2.04	1.44	dense granule protein GRA8
TGME49_271930	-1.06	-1.06	-0.99	hypothetical protein
TGME49_225130	-2.67	-3.12	-3.05	hypothetical protein
TGME49_301130	-2.25	-1.69	#N/A	hypothetical protein
TGME49_248400	1.31	1.09	#N/A	glyoxalase I, putative
TGME49_270830	1.20	1.18	#N/A	small nuclear ribonucleoprotein
TGME49_221330	-1.48	-1.02	-1.17	DNA gyrase/topoisomerase IV, A subunit domain-containing protein
TGME49_255510	-1.22	-1.31	-1.43	ankyrin repeat-containing protein
TGME49_253780	1.32	1.16	#N/A	GTP cyclohydrolase I, putative
TGME49_238240	4.88	5.33	5.25	bystin protein
TGME49_208910	-1.58	-1.60	-1.53	hypothetical protein
TGME49_225470	1.44	0.98	#N/A	peptide methionine sulfoxide reductase

TGME49_208010	#N/A	1.18	#N/A	hypothetical protein
TGME49_224830	#N/A	-2.46	#N/A	hypothetical protein
TGME49_293500	#N/A	-2.44	-2.99	hypothetical protein
TGME49_217640	#N/A	1.39	#N/A	hypothetical protein
TGME49_295400	#N/A	-2.03	-1.87	hypothetical protein
TGME49_267590	#N/A	-1.55	-1.36	hypothetical protein
TGME49_289340	#N/A	1.81	#N/A	hypothetical protein
TGME49_323110	#N/A	1.76	1.47	hypothetical protein
TGME49_280580	#N/A	1.79	3.89	SAG-related sequence SRS35B
TGME49_251520	#N/A	1.15	#N/A	hypothetical protein
TGME49_247360	#N/A	0.99	1.07	PAP2 superfamily protein
TGME49_244040	#N/A	-1.83	-1.68	HEAT repeat-containing protein
TGME49_295472	#N/A	-1.50	-1.45	C2 domain-containing protein
TGME49_318480	#N/A	-1.61	#N/A	SWI2/SNF2-containing protein RAD5
TGME49_224540	#N/A	-1.65	-1.52	hypothetical protein
TGME49_200320	#N/A	-1.13	-1.28	hypoxanthine-xanthine-guanine phosphoribosyl transferase HXGPRT
TGME49_300030	#N/A	-1.19	#N/A	hypothetical protein
TGME49_203790	#N/A	1.02	0.81	hypothetical protein
TGME49_206610	#N/A	-1.41	#N/A	pyruvate dehydrogenase complex subunit PDH-E2
TGME49_209050	#N/A	-1.38	-1.37	Tyrosine kinase-like (TKL) protein
TGME49_236890	#N/A	1.02	0.88	hypothetical protein
TGME49_313910	#N/A	1.57	#N/A	RNA recognition motif 2 protein
TGME49_254390	#N/A	1.58	#N/A	CRAL/TRIO domain-containing protein
TGME49_277490	#N/A	1.05	#N/A	hypothetical protein
TGME49_261022	#N/A	-2.98	#N/A	dynein heavy chain family protein
TGME49_273950	#N/A	-1.88	-1.68	replication factor C subunit 5, putative
TGME49_242570	#N/A	-1.04	#N/A	hypothetical protein
TGME49_207830	#N/A	1.05	#N/A	MORN repeat-containing protein
TGME49_212100	#N/A	-1.56	#N/A	ThiF family protein
TGME49_253940	#N/A	1.04	#N/A	CAM Kinase family, incomplete catalytic triad
TGME49_224170	#N/A	1.76	2.34	SAG-related sequence SRS60A
TGME49_220910	#N/A	-1.47	-1.62	HEAT repeat-containing protein
TGME49_249990	#N/A	1.43	#N/A	hypothetical protein
TGME49_224020	#N/A	1.06	1.06	hypothetical protein
TGME49_293470	#N/A	-1.12	-0.93	hypothetical protein
TGME49_208040	#N/A	-1.50	#N/A	aldo-keto reductase

FIGURE 3K

TGME49_310390	1.86	1.34	#N/A	hypothetical protein
TGME49_279410	1.27	0.99	#N/A	hypothetical protein
TGME49_270550	1.65	#N/A	#N/A	gamma-glutamyl phosphate reductase, putative
TGME49_247590	1.92	#N/A	#N/A	methyltransferase domain-containing protein
TGME49_262880	1.76	#N/A	#N/A	hypothetical protein
TGME49_293380	-2.19	-2.21	-1.76	histone lysine acetyltransferase HAT1
TGME49_224520	-1.10	-0.76	#N/A	alveolin domain containing intermediate filament IMC8
TGME49_259240	4.14	3.87	4.06	ribosomal protein RPS21
TGME49_319530	-1.18	-0.93	#N/A	splicing factor SF2
TGME49_312105	-2.30	-1.90	#N/A	hypothetical protein
TGME49_289940	1.77	#N/A	#N/A	uroporphyrinogen decarboxylase
TGME49_226240	1.50	1.06	1.60	bud site selection protein, putative
TGME49_244380	2.38	2.30	2.19	cactin
TGME49_283820	-2.80	-2.68	-2.83	glycine cleavage T-protein (aminomethyl transferase) domain-containing protein
TGME49_241305	1.59	#N/A	#N/A	hypothetical protein
TGME49_296121	1.39	1.48	#N/A	hypothetical protein
TGME49_288890	1.67	#N/A	#N/A	hypothetical protein
TGME49_299240	1.61	1.62	1.64	hypothetical protein
TGME49_255410	-1.45	-1.21	#N/A	hypothetical protein
TGME49_288000	1.31	#N/A	#N/A	hypothetical protein
TGME49_216020	-1.98	-1.83	-1.87	peptidase family c78 protein
TGME49_220640	-1.66	#N/A	#N/A	hypothetical protein
TGME49_320050	7.35	7.07	7.08	ribosomal protein RPL5
TGME49_278800	-1.23	-1.21	#N/A	zinc finger protein 36 family 3 protein
TGME49_298830	2.52	2.69	#N/A	hypothetical protein
TGME49_253330	1.55	3.85	1.57	Rhoptry kinase family protein, truncated (incomplete catalytic triad)
TGME49_265840	-1.35	-1.01	#N/A	hypothetical protein
TGME49_297730	-1.93	-1.75	-1.86	transcription elongation factor 1, putative
TGME49_239490	1.17	1.04	#N/A	dehydrogenase E1 component family protein
TGME49_226680	-1.19	-1.23	#N/A	hypothetical protein
TGME49_260790	-1.74	-1.54	#N/A	RAP domain-containing protein
TGME49_283710	-1.48	-1.50	-1.20	Longevity-assurance protein (LAG1) domain-containing protein
TGME49_266450	1.70	#N/A	#N/A	lysine decarboxylase family protein
TGME49_306890	2.64	#N/A	#N/A	hypothetical protein
TGME49_212300	#N/A	0.96	#N/A	hypothetical protein
TGME49_286180	#N/A	-2.39	#N/A	tRNA ligases class I (M) protein
TGME49_299015	#N/A	1.90	#N/A	hypothetical protein
TGME49_237860	#N/A	-2.24	#N/A	protein kinase domain-containing protein
TGME49_213730	#N/A	0.99	#N/A	lanthionine synthetase C family protein
TGME49_244670	#N/A	0.95	1.34	hypothetical protein
TGME49_225480	#N/A	-1.79	#N/A	hypothetical protein
TGME49_264970	#N/A	-1.82	-1.84	hypothetical protein
TGME49_253360	#N/A	0.97	0.86	hypothetical protein
TGME49_232780	#N/A	-1.39	#N/A	hypothetical protein
TGME49_220610	#N/A	-1.34	#N/A	protein phosphatase 2C domain-containing protein
TGME49_320610	#N/A	-1.67	-1.49	hypothetical protein
TGME49_208370	#N/A	1.17	#N/A	myosin heavy chain, putative
TGME49_234180	#N/A	1.08	1.00	hypothetical protein
TGME49_262600	#N/A	-2.01	#N/A	hypothetical protein
TGME49_207160	#N/A	1.90	2.16	SAG-related sequence SRS49D
TGME49_206640	#N/A	-1.11	#N/A	hypothetical protein
TGME49_214220	#N/A	1.16	#N/A	hypothetical protein
TGME49_286440	#N/A	1.01	0.97	malic enzyme
TGME49_294200	#N/A	1.35	#N/A	glucose-6-phosphate 1-dehydrogenase
TGME49_320430	#N/A	-1.26	#N/A	cell-cycle-control protein (translation regulation), putative
TGME49_284010	#N/A	-1.68	#N/A	5'-3' exonuclease, N-terminal resolvase family domain-containing protein
TGME49_293330	#N/A	1.37	#N/A	hypothetical protein
TGME49_243430	#N/A	1.04	#N/A	OTU family cysteine protease
TGME49_241130	#N/A	-2.00	#N/A	hypothetical protein
TGME49_261400	#N/A	-0.97	#N/A	hypothetical protein
TGME49_224210	#N/A	-1.35	#N/A	hypothetical protein
TGME49_209970	#N/A	-1.38	-1.33	Spc97 / Spc98 family protein
TGME49_213300	#N/A	-1.59	#N/A	hypothetical protein
TGME49_297940	#N/A	-1.28	#N/A	single-strand binding protein
TGME49_311770	#N/A	-1.18	#N/A	hypothetical protein
TGME49_318760	#N/A	1.10	#N/A	hypothetical protein
TGME49_245475	#N/A	1.52	#N/A	hypothetical protein
TGME49_260620	#N/A	0.84	#N/A	hypothetical protein

FIGURE 3L

TGME49_250100	1.44	1.23	1.71	hypothetical protein
TGME49_263710	-1.52	-1.68	-1.45	acyl-CoA:cholesterol acyltransferase alpha ACAT1-alpha
TGME49_236050	-3.84	-2.92	#N/A	fructose-bisphosphate aldolase, putative
TGME49_225250	1.27	0.88	1.03	LSU ribosomal protein L14P, putative
TGME49_311920	-1.24	-1.12	-1.17	GRAM domain-containing protein
TGME49_300240	-1.77	#N/A	-1.37	syntaxin 6, n-terminal protein
TGME49_203180	1.79	#N/A	#N/A	leucine rich repeat-containing protein
TGME49_267460	2.01	2.48	#N/A	AP2 domain transcription factor AP2IX-1
TGME49_209985	1.74	#N/A	2.85	cAMP-dependent protein kinase
TGME49_295990	1.16	1.11	1.00	ubiquitin conjugating enzyme E2, putative
TGME49_252630	1.14	1.10	0.91	hypothetical protein
TGME49_209440	1.71	#N/A	#N/A	hypothetical protein
TGME49_228160	1.14	1.73	1.84	acid phosphatase
TGME49_221410	-1.40	-1.15	-1.09	actin-like protein ALP4
TGME49_214270	2.82	2.72	2.98	translation initiation factor IF-2, putative
TGME49_280700	-1.43	#N/A	-1.78	arginine decarboxylase
TGME49_204055	-2.14	-1.67	#N/A	hypothetical protein
TGME49_290670	1.08	0.99	#N/A	leucyl aminopeptidase LAP
TGME49_315620	-1.29	-1.14	-1.02	vacuolar ATP synthase subunit C, putative
TGME49_271270	1.10	0.92	#N/A	hypothetical protein
TGME49_316230	-1.61	-1.42	-1.65	SAC1 phosphoinositide phosphatase, putative
TGME49_252430	1.05	1.30	1.46	hypothetical protein
TGME49_308010	-1.98	-1.86	#N/A	hypothetical protein
TGME49_295030	-1.06	#N/A	#N/A	hypothetical protein
TGME49_289650	1.03	0.98	0.97	PEP-carboxykinase I
TGME49_233160	-1.12	#N/A	#N/A	hypothetical protein
TGME49_208730	0.96	1.76	1.05	microneme protein, putative
TGME49_321410	2.80	2.79	2.86	hypothetical protein
TGME49_315300	-1.40	#N/A	-1.20	transcription factor IIB, putative
TGME49_262120	-1.16	-0.97	#N/A	IQ calmodulin-binding motif domain-containing protein
TGME49_289910	1.02	0.80	#N/A	hypothetical protein
TGME49_231960	-1.88	-3.35	-1.88	omega secalin, putative
TGME49_212210	1.36	#N/A	#N/A	hypothetical protein
TGME49_214100	-1.36	#N/A	#N/A	hypothetical protein
TGME49_314790	-1.76	-1.48	#N/A	small nuclear ribonucleoprotein G, putative
TGME49_293260	1.75	1.38	#N/A	ATPase/histidine kinase/DNA gyrase B/HSP90 domain-containing protein

TGME49_270510	#N/A	-1.37	-1.76	asparaginyl-tRNA synthetase (NOB+tRNA synthase)
TGME49_239740	#N/A	1.16	#N/A	dense granule protein GRA14
TGME49_308950	#N/A	1.04	1.08	histidine acid phosphatase superfamily protein
TGME49_254270	#N/A	1.10	1.33	hypothetical protein
TGME49_306190	#N/A	0.96	#N/A	hypothetical protein
TGME49_225990	#N/A	-1.34	#N/A	acyl transferase domain-containing protein
TGME49_247485	#N/A	-1.40	#N/A	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_225790	#N/A	1.61	#N/A	PDI family protein
TGME49_226520	#N/A	1.14	#N/A	hypothetical protein
TGME49_304750	#N/A	-1.89	#N/A	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_295015	#N/A	1.45	#N/A	patched family protein
TGME49_201840	#N/A	1.27	#N/A	aspartyl protease ASP1
TGME49_272380	#N/A	0.85	#N/A	hypothetical protein
TGME49_210370	#N/A	0.86	0.74	hypothetical protein
TGME49_222100	#N/A	1.01	#N/A	hypothetical protein
TGME49_291150	#N/A	-1.79	#N/A	hypothetical protein
TGME49_315600	#N/A	-1.37	#N/A	MCM2/3/5 family protein
TGME49_214600	#N/A	-1.21	#N/A	hypothetical protein
TGME49_205265	#N/A	1.64	#N/A	transporter, cation channel family protein
TGME49_218920	#N/A	0.86	0.76	proteasome subunit beta type, putative
TGME49_201780	#N/A	1.52	#N/A	microneme protein MIC2
TGME49_254070	#N/A	0.92	0.93	hypothetical protein
TGME49_273815	#N/A	-1.49	#N/A	hypothetical protein
TGME49_212270	#N/A	1.15	#N/A	hypothetical protein
TGME49_253640	#N/A	0.95	#N/A	hypothetical protein
TGME49_316260	#N/A	0.99	0.98	hypothetical protein
TGME49_316430	#N/A	-1.74	-1.77	target of rapamycin (TOR), putative
TGME49_217520	#N/A	0.98	0.87	hypothetical protein
TGME49_258050	#N/A	-1.98	#N/A	actin like protein ALP2a
TGME49_315580	#N/A	-0.97	#N/A	hypothetical protein
TGME49_320190	#N/A	-1.69	7.35	SAG-related sequence SRS16B
TGME49_257800	#N/A	-1.81	-1.66	polynucleotide adenyllyltransferase
TGME49_295658	#N/A	-1.27	#N/A	zinc finger in N-recognition protein
TGME49_220950	#N/A	1.49	1.44	hypothetical protein
TGME49_254510	#N/A	1.21	1.11	ankyrin repeat-containing protein
TGME49_242030	#N/A	-1.58	-1.71	hypothetical protein

FIGURE 3M

TGME49_269710	-1.40	-1.47	-1.49	hypothetical protein
TGME49_211440	-1.48	-1.86	-1.34	hypothetical protein
TGME49_251500	-1.24	-1.28	-1.23	eukaryotic initiation factor-3, subunit 3, putative
TGME49_254365	1.08	1.40	1.07	phosphatidate cytidylyltransferase
TGME49_246330	-1.24	-1.15	-1.14	CRAL/TRIO domain-containing protein
TGME49_214090	1.76	1.81	#N/A	signal peptidase
TGME49_288040	-1.30	-1.13	-1.09	hypothetical protein
TGME49_262935	2.22	#N/A	#N/A	hypothetical protein
TGME49_239710	-1.71	-1.61	#N/A	phosphomannomutase
TGME49_267420	0.99	1.43	0.95	mago nashi family protein 2, putative
TGME49_304520	-1.27	-0.94	#N/A	hypothetical protein
TGME49_202770	-1.12	#N/A	#N/A	RNA recognition motif-containing protein
TGME49_226710	0.97	#N/A	#N/A	hypothetical protein
TGME49_321630	-1.29	#N/A	-1.02	RNA recognition motif-containing protein
TGME49_207060	-1.46	#N/A	#N/A	ribonucleoside-diphosphate reductase small subunit
TGME49_300285	-1.55	#N/A	#N/A	hypothetical protein
TGME49_235740	-1.65	-1.69	-1.50	hypothetical protein
TGME49_249180	0.99	1.05	#N/A	bifunctional dihydrofolate reductase-thymidylate synthase
TGME49_258490	-1.76	-1.42	#N/A	hypothetical protein
TGME49_222952	2.17	#N/A	#N/A	phosphohistidine phosphatase
TGME49_285230	-1.63	-1.43	#N/A	PRP38 family protein
TGME49_290310	-2.41	#N/A	#N/A	hypothetical protein
TGME49_223600	-1.87	-1.69	#N/A	hypothetical protein
TGME49_213820	1.24	0.89	1.35	hypothetical protein
TGME49_204270	-1.57	-1.92	-1.63	hypothetical protein
TGME49_225050	1.08	#N/A	0.85	adenosylhomocysteinase, putative
TGME49_263480	1.83	#N/A	#N/A	sodium/hydrogen exchanger 3 protein
TGME49_265450	1.53	#N/A	#N/A	hexokinase
TGME49_275630	1.12	#N/A	#N/A	HECT-domain (ubiquitin-transferase) domain-containing protein
TGME49_237160	-1.53	-1.22	#N/A	hypothetical protein
TGME49_262780	-1.49	-1.80	-1.60	FHA domain-containing protein
TGME49_244130	1.91	#N/A	#N/A	hypothetical protein
TGME49_265650	-1.60	-1.18	#N/A	protein phosphatase 2C domain-containing protein

TGME49_312420	#N/A	0.88	#N/A	hypothetical protein
TGME49_208420	#N/A	1.49	#N/A	Sodium neurotransmitter symporter family protein
TGME49_313970	#N/A	-2.25	-2.61	Phytanoyl-CoA dioxygenase (PhyH) superfamily protein
TGME49_203050	#N/A	1.29	#N/A	AP2 domain transcription factor AP2Vila-6
TGME49_298070	#N/A	-2.10	#N/A	hypothetical protein
TGME49_216510	#N/A	-1.35	-1.55	thioredoxin, putative
TGME49_258826	#N/A	-1.97	#N/A	hypothetical protein
TGME49_290160	#N/A	-1.03	-1.13	sortilin, putative
TGME49_250220	#N/A	1.23	#N/A	hypothetical protein
TGME49_270330	#N/A	1.36	#N/A	cell-cycle-associated protein kinase, putative
TGME49_304955	#N/A	0.93	#N/A	serine/threonine specific protein phosphatase
TGME49_236870	#N/A	1.69	#N/A	hypothetical protein
TGME49_301290	#N/A	-1.43	#N/A	hypothetical protein
TGME49_266690	#N/A	-0.95	#N/A	hypothetical protein
TGME49_213480	#N/A	2.09	#N/A	hypothetical protein
TGME49_272370	#N/A	1.06	#N/A	hypothetical protein
TGME49_214980	#N/A	0.80	0.77	hypothetical protein
TGME49_279420	#N/A	1.17	#N/A	hypothetical protein
TGME49_255400	#N/A	1.35	#N/A	hypothetical protein
TGME49_318290	#N/A	-1.31	#N/A	hypothetical protein
TGME49_259990	#N/A	-1.01	#N/A	SAC3/GANP family protein
TGME49_220230	#N/A	-1.27	#N/A	leucine rich repeat-containing protein
TGME49_201710	#N/A	1.23	1.59	WD domain, G-beta repeat-containing protein
TGME49_310530	#N/A	-1.33	#N/A	SNF2 family N-terminal domain-containing protein
TGME49_285290	#N/A	1.07	#N/A	hypothetical protein
TGME49_232550	#N/A	0.93	#N/A	hypothetical protein
TGME49_278530	#N/A	0.76	#N/A	multiprotein bridging factor type 1 family transcriptional co-activator, putative
TGME49_210682	#N/A	1.85	#N/A	hypothetical protein
TGME49_218930	#N/A	3.26	#N/A	BTB/POZ domain-containing protein
TGME49_247330	#N/A	-0.87	#N/A	hypothetical protein
TGME49_299070	#N/A	0.88	#N/A	pyruvate kinase PyKII
TGME49_206680	#N/A	1.12	#N/A	hypothetical protein
TGME49_240590	#N/A	0.94	#N/A	DNA-directed RNA polymerase II RPB5

FIGURE 3N

TGME49_242640	1.08	1.10	#N/A	hypothetical protein
TGME49_208590	-1.26	-1.04	-1.08	vacuolar ATP synthase subunit 54kD, putative
TGME49_305340	-1.03	-0.97	-1.17	corepressor complex CRC230
TGME49_217780	1.70	1.47	#N/A	Sec20 protein
TGME49_299250	1.42	1.19	1.06	hypothetical protein
TGME49_314070	1.15	1.29	1.14	hypothetical protein
TGME49_258740	-1.51	-1.35	-1.35	eukaryotic initiation factor-2A, putative
TGME49_269425	-1.35	#N/A	#N/A	hypothetical protein
TGME49_231140	3.19	2.39	3.09	ribosomal protein RPS25
TGME49_305950	1.63	1.09	#N/A	tetratricopeptide repeat-containing protein
TGME49_285170	-3.11	-2.94	-2.95	methyltransferase small, putative
TGME49_245460	4.21	3.64	4.06	ribosomal protein RPS8
TGME49_320620	1.73	#N/A	#N/A	queuine tRNA ribosyl transferase
TGME49_309580	-1.39	-1.05	#N/A	transporter, major facilitator family protein
TGME49_254950	1.60	1.38	#N/A	RNA cap guanine-N2 methyltransferase
TGME49_305080	2.30	#N/A	#N/A	hypothetical protein
TGME49_275990	1.24	1.29	1.26	hypothetical protein
TGME49_268380	2.64	2.05	#N/A	RNA recognition motif-containing protein
TGME49_300060	1.24	1.00	1.01	signal peptidase subunit protein
TGME49_246080	-1.16	-0.95	#N/A	NAD dependent epimerase/dehydratase family protein
TGME49_275430	-1.69	-2.15	-1.69	hypothetical protein
TGME49_231100	1.16	0.90	#N/A	hypothetical protein
TGME49_237110	-1.34	-1.22	-1.16	replication factor C subunit 2, putative
TGME49_289680	1.16	0.82	#N/A	Ras-related protein Rab11
TGME49_249350	-1.19	#N/A	#N/A	esterase/lipase/thioesterase domain-containing protein
TGME49_248900	-1.98	-2.04	-1.61	hypothetical protein
TGME49_253950	1.35	1.22	#N/A	protein fam50a, putative
TGME49_224060	0.99	0.94	#N/A	thioredoxin, putative
TGME49_216375	-2.42	-2.35	#N/A	hypothetical protein
TGME49_318370	2.04	#N/A	#N/A	hypothetical protein
TGME49_218830	-2.05	-2.05	-1.83	hypothetical protein
TGME49_215010	-1.06	#N/A	#N/A	hypothetical protein
TGME49_217360	-1.96	-2.15	-2.11	hypothetical protein
TGME49_310360	-1.15	-1.20	-1.10	hypothetical protein

TGME49_214810	#N/A	1.18	1.24	hypothetical protein
TGME49_200450	#N/A	-1.67	-1.73	hypothetical protein
TGME49_253130	#N/A	0.85	#N/A	transporter, major facilitator family protein
TGME49_249670	#N/A	0.96	#N/A	cathepsin B
TGME49_229930	#N/A	0.93	#N/A	p25-alpha family protein
TGME49_231120	#N/A	1.02	1.05	ribosomal protein S11, putative
TGME49_221190	#N/A	1.32	#N/A	mRNA cleavage factor family protein, putative
TGME49_273380	#N/A	1.10	#N/A	ion channel protein
TGME49_218610	#N/A	-1.45	#N/A	ATPase (DUF699) protein
TGME49_244570	#N/A	-1.74	#N/A	hypothetical protein
TGME49_221590	#N/A	0.87	#N/A	dual specificity phosphatase, catalytic domain-containing protein
TGME49_233380	#N/A	1.13	#N/A	hypothetical protein
TGME49_319570	#N/A	-0.96	#N/A	WD domain, G-beta repeat-containing protein
TGME49_269940	#N/A	-1.72	#N/A	zinc finger motif, C2HC5-type protein
TGME49_289600	#N/A	0.79	#N/A	heat shock protein HSP29
TGME49_221440	#N/A	-1.36	#N/A	RPGR, putative
TGME49_242380	#N/A	-0.94	#N/A	fatty acid elongase
TGME49_250690	#N/A	-0.83	#N/A	zinc finger (CCH type) motif-containing protein
TGME49_244530	#N/A	1.03	#N/A	hypothetical protein
TGME49_315720	#N/A	-1.23	#N/A	Smg-4/UPF3 family protein
TGME49_313385	#N/A	1.23	1.64	hypothetical protein
TGME49_293900	#N/A	1.04	#N/A	sporozoite protein with an altered thrombospondin repeat SPATR
TGME49_247370	#N/A	-1.52	-1.54	hypothetical protein
TGME49_216490	#N/A	-1.65	#N/A	hypothetical protein
TGME49_308580	#N/A	-1.44	-1.64	Lon protease family protein
TGME49_246140	#N/A	-1.42	#N/A	hypothetical protein
TGME49_268220	#N/A	4.47	5.79	hypothetical protein
TGME49_316700	#N/A	1.40	#N/A	uridine kinase
TGME49_277840	#N/A	0.86	#N/A	Ras family protein
TGME49_214490	#N/A	-1.37	#N/A	peptidase M16 inactive domain-containing protein
TGME49_233450	#N/A	1.51	#N/A	SAG-related sequence SRS29A
TGME49_227580	#N/A	-1.02	-1.25	transmembrane amino acid transporter protein
TGME49_253320	#N/A	1.18	#N/A	hypothetical protein
TGME49_265790	#N/A	0.83	0.83	hypothetical protein

FIGURE 3o

TGME49_218730	-1.39	#N/A	#N/A	hypothetical protein
TGME49_209945	2.28	#N/A	#N/A	hypothetical protein
TGME49_272010	-1.63	-1.23	#N/A	Gar1 protein RNA binding region protein
TGME49_308060	1.48	1.36	#N/A	hypothetical protein
TGME49_260580	1.56	#N/A	#N/A	hypothetical protein
TGME49_265440	-1.26	-1.16	#N/A	hypothetical protein
TGME49_235980	-1.64	-1.58	#N/A	ARIADNE family protein
TGME49_214170	-1.70	-2.00	-1.82	hypothetical protein
TGME49_309400	-1.56	#N/A	#N/A	RecF/RecN/SMC N terminal domain-containing protein
TGME49_270140	-1.57	-1.27	#N/A	splicing factor DIM1, putative
TGME49_211250	-1.10	#N/A	#N/A	hypothetical protein
TGME49_312260	-1.42	-1.13	#N/A	hypothetical protein
TGME49_321560	-1.35	-1.47	-1.29	zinc knuckle domain-containing protein
TGME49_321640	-1.69	-2.03	#N/A	cell division protein CDC48AP
TGME49_268170	-1.89	-1.58	#N/A	hypothetical protein
TGME49_254915	3.02	2.78	2.20	hypothetical protein
TGME49_255290	-2.99	-3.89	-2.61	hypothetical protein
TGME49_222370	1.40	#N/A	#N/A	SAG-related sequence SRS13
TGME49_215347	-2.65	#N/A	#N/A	hypothetical protein
TGME49_286480	2.29	2.55	#N/A	hypothetical protein
TGME49_217220	-1.22	#N/A	-1.57	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_240060	1.23	2.18	0.98	hypothetical protein
TGME49_268200	1.63	#N/A	#N/A	RNA recognition motif-containing protein
TGME49_272640	-1.40	-1.31	#N/A	eukaryotic initiation factor-2B, epsilon subunit, putative
TGME49_321570	1.11	#N/A	#N/A	beta-hydroxyacyl-acyl carrier protein dehydratase (FABZ)
TGME49_216040	-2.01	-2.16	#N/A	30S ribosomal protein S15, putative
TGME49_232050	-1.13	-0.93	#N/A	DnaJ domain-containing protein
TGME49_228150	1.93	#N/A	#N/A	hypothetical protein
TGME49_250955	1.98	1.57	1.59	KRUF family protein
TGME49_228320	-3.53	-3.92	-4.10	hypothetical protein
TGME49_264820	1.40	#N/A	#N/A	RbAp48
TGME49_232130	-1.00	-0.77	-0.98	hypothetical protein
TGME49_290300	1.03	1.44	1.15	hypothetical protein
TGME49_255340	-1.52	-1.77	-1.29	tetratricopeptide repeat-containing protein

TGME49_246120	#N/A	0.98	#N/A	tetratricopeptide repeat-containing protein
TGME49_218570	#N/A	0.92	#N/A	Nin one binding (NOB1) Zn-ribbon family protein
TGME49_318525	#N/A	-1.15	-1.59	hypothetical protein
TGME49_319900	#N/A	-1.12	#N/A	hypothetical protein
TGME49_281910	#N/A	1.21	#N/A	hypothetical protein
TGME49_297230	#N/A	-1.25	-1.67	Vps53 family, N-terminal protein
TGME49_278815	#N/A	-0.92	#N/A	hypothetical protein
TGME49_306310	#N/A	-0.96	#N/A	RecF/RecN/SMC N terminal domain-containing protein
TGME49_255900	#N/A	0.75	#N/A	Bax inhibitor-1, putative
TGME49_218600	#N/A	-1.24	#N/A	RNA recognition motif-containing protein
TGME49_309360	#N/A	-1.21	#N/A	Nuf2
TGME49_200430	#N/A	-1.64	#N/A	cytidine and deoxycytidylate deaminase zinc-binding region domain-containing protein
TGME49_216435	#N/A	-1.06	#N/A	hypothetical protein
TGME49_301380	#N/A	-1.44	#N/A	elongation factor Tu GTP binding domain-containing protein
TGME49_213900	#N/A	-0.88	#N/A	regulator of chromosome condensation RCC1
TGME49_308075	#N/A	-0.99	#N/A	hypothetical protein
TGME49_268210	#N/A	-1.35	#N/A	AGC kinase
TGME49_268980	#N/A	0.81	0.80	hypothetical protein
TGME49_223540	#N/A	-1.08	#N/A	importin-beta N-terminal domain-containing protein
TGME49_228980	#N/A	-1.55	-1.68	hypothetical protein
TGME49_235398	#N/A	-1.20	#N/A	hypothetical protein
TGME49_209930	#N/A	-1.40	#N/A	hypothetical protein
TGME49_236010	#N/A	0.76	#N/A	prenylcysteine oxidase
TGME49_236630	#N/A	0.79	#N/A	hypothetical protein
TGME49_218520	#N/A	1.39	#N/A	microneme protein MIC6
TGME49_275610	#N/A	-1.03	#N/A	protein kinase, other
TGME49_278450	#N/A	0.78	#N/A	hypothetical protein
TGME49_222120	#N/A	-1.52	-1.66	hypothetical protein
TGME49_235880	#N/A	0.82	#N/A	brain protein 44 family protein
TGME49_213460	#N/A	-1.05	#N/A	hypothetical protein
TGME49_253300	#N/A	1.61	#N/A	hypothetical protein
TGME49_250950	#N/A	1.30	#N/A	KRUF family protein
TGME49_313480	#N/A	-2.19	-2.71	hypothetical protein
TGME49_285840	#N/A	-1.13	#N/A	RAP domain-containing protein

FIGURE 3P

TGME49_207230	1.10	1.16	0.90	hypothetical protein
TGME49_240740	-1.49	-1.43	#N/A	Sec1 family protein
TGME49_228300	-1.88	-1.74	-1.69	CCDC25 protein
TGME49_215040	-1.26	-1.33	#N/A	HEAT repeat-containing protein
TGME49_313590	-1.70	-1.47	-1.54	hypothetical protein
TGME49_294690	-1.04	#N/A	#N/A	rhomboid protease ROM5
TGME49_254730	1.74	#N/A	#N/A	POPLD (NUC188) domain-containing protein
TGME49_289150	-1.30	#N/A	#N/A	hypothetical protein
TGME49_300048	1.09	1.65	0.86	hypothetical protein
TGME49_281570	-1.64	-1.42	#N/A	hypothetical protein
TGME49_290840	-1.24	#N/A	#N/A	serine protease
TGME49_313180	-0.96	-0.87	-1.05	cell-cycle-associated protein kinase PRP4, putative
TGME49_289320	-1.06	#N/A	#N/A	casein kinase I, putative
TGME49_294730	-1.44	-1.42	-1.37	hypothetical protein
TGME49_251640	-1.48	-1.13	-1.29	ubiquitin-conjugating enzyme subfamily protein
TGME49_266990	-1.05	-1.22	-1.18	beta-COP
TGME49_288360	1.42	1.28	-1.24	tryptophanyl-tRNA synthetase (TrpRS2)
TGME49_263610	-1.62	-1.39	-1.84	hypothetical protein
TGME49_280560	-1.19	-1.50	-1.12	selenide, water dikinase
TGME49_251790	1.23	#N/A	#N/A	hypothetical protein
TGME49_316360	-1.34	#N/A	#N/A	hypothetical protein
TGME49_266900	1.15	1.04	1.65	cyclin, N-terminal domain-containing protein
TGME49_225800	1.18	0.91	#N/A	iron-sulfur assembly ATPase
TGME49_261850	2.02	#N/A	#N/A	helicase, putative
TGME49_288840	1.13	1.26	#N/A	hypothetical protein
TGME49_253000	1.04	1.22	1.28	ELMO/CED-12 family protein
TGME49_318320	-1.94	-2.05	-1.92	ATP-dependent Clp endopeptidase, proteolytic subunit ClpP domain-containing protein
TGME49_201200	-2.28	-1.97	#N/A	zinc finger (CCH type) motif-containing protein
TGME49_288700	-1.75	-1.76	-2.16	RecF/RecN/SMC N terminal domain-containing protein
TGME49_262430	1.49	#N/A	#N/A	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
TGME49_244260	-2.77	-3.96	#N/A	hypothetical protein
TGME49_254930	0.99	1.37	1.20	hypothetical protein
TGME49_214210	-1.23	#N/A	#N/A	rRNA pseudouridine synthase
TGME49_223950	1.07	#N/A	0.97	hypothetical protein
TGME49_202250	1.21	1.03	#N/A	hypothetical protein
TGME49_257530	#N/A	1.55	#N/A	transporter, major facilitator family protein
TGME49_232630	#N/A	0.73	#N/A	hypothetical protein
TGME49_285510	#N/A	0.78	#N/A	hypothetical protein
TGME49_269410	#N/A	1.18	#N/A	hypothetical protein
TGME49_231950	#N/A	0.82	#N/A	hypothetical protein
TGME49_205670	#N/A	0.79	#N/A	SF-assemblin/beta giardin protein
TGME49_248570	#N/A	-1.51	-1.74	hypothetical protein
TGME49_221580	#N/A	-0.96	-1.20	ribosomal RNA large subunit methyltransferase J protein
TGME49_249010	#N/A	0.83	#N/A	hypothetical protein
TGME49_237840	#N/A	-1.28	#N/A	hypothetical protein
TGME49_239087	#N/A	-1.40	#N/A	hypothetical protein
TGME49_253740	#N/A	-1.12	-1.22	hypothetical protein
TGME49_211330	#N/A	-1.87	#N/A	methionine aminopeptidase
TGME49_233838	#N/A	-1.99	#N/A	PET112 family, C terminal region domain-containing protein
TGME49_237500	#N/A	0.84	#N/A	protein phosphatase 2C domain-containing protein
TGME49_299270	#N/A	1.01	#N/A	hypothetical protein
TGME49_229340	#N/A	-1.63	#N/A	hypothetical protein
TGME49_258180	#N/A	-1.49	#N/A	hypothetical protein
TGME49_244220	#N/A	-1.97	#N/A	hypothetical protein
TGME49_276170	#N/A	0.73	#N/A	phosphatidylinositol 3- and 4-kinase
TGME49_202420	#N/A	1.43	#N/A	hypothetical protein
TGME49_208030	#N/A	1.24	#N/A	microneme protein MIC4
TGME49_312500	#N/A	-0.98	#N/A	hypothetical protein
TGME49_273770	#N/A	0.86	#N/A	hypothetical protein
TGME49_242260	#N/A	-1.23	-2.03	hypothetical protein
TGME49_245428	#N/A	1.44	2.67	hypothetical protein
TGME49_311250	#N/A	-1.11	-1.39	hypothetical protein
TGME49_318580	#N/A	-0.96	#N/A	glucosephosphate-mutase GPM2
TGME49_219070	#N/A	-0.99	#N/A	cyclic nucleotide-binding domain-containing protein
TGME49_213600	#N/A	1.73	#N/A	hypothetical protein
TGME49_206600	#N/A	-1.24	#N/A	sigma-70, region 3 protein
TGME49_266850	#N/A	1.02	1.27	3-demethylubiquinone-9 3-O-methyltransferase
TGME49_239600	#N/A	1.33	1.75	rhopty kinase family protein ROP23 (incomplete catalytic triad)
TGME49_211410	#N/A	-1.26	#N/A	translation initiation factor sui1 protein
TGME49_219820	#N/A	1.02	#N/A	polyubiquitin UbC, putative

FIGURE 3Q

TGME49_270650	1.57	#N/A	2.02	deoxyribose-phosphate aldolase
TGME49_260610	-2.51	-2.50	-2.15	methyltransferase
TGME49_215710	-1.39	-1.38	-1.14	hypothetical protein
TGME49_318570	2.26	1.98	#N/A	SFT2 family protein
TGME49_202650	-1.59	-1.66	#N/A	hypothetical protein
TGME49_226830	-1.17	-0.98	#N/A	DnaK family protein
TGME49_312380	-1.95	-1.92	-2.37	tetralricopeptide repeat-containing protein
TGME49_218200	-2.13	-2.16	-2.74	UDP-sugar pyrophosphorylase
TGME49_260390	-1.48	#N/A	#N/A	hypothetical protein
TGME49_267450	-1.51	-1.25	-1.26	alpha-tubulin suppressor protein
TGME49_319930	-1.46	-1.27	#N/A	hypothetical protein
TGME49_253370	1.14	1.27	#N/A	hypothetical protein
TGME49_298840	1.20	1.36	1.64	hypothetical protein
TGME49_235490	-1.11	-0.90	-0.97	hypothetical protein
TGME49_300290	-1.47	#N/A	#N/A	SNARE domain-containing protein
TGME49_311310	-1.09	-1.08	#N/A	protein phosphatase 2B catalytic subunit, calcineurin family phosphatase superfamily protein
TGME49_225560	-1.13	-1.03	-1.11	hypothetical protein
TGME49_269430	-1.63	-1.43	#N/A	polyprenyl synthetase superfamily protein
TGME49_267620	1.08	#N/A	#N/A	multi-pass transmembrane protein
TGME49_268580	-1.25	-1.03	#N/A	hypothetical protein
TGME49_253560	1.29	0.99	#N/A	hypothetical protein
TGME49_319308	-1.95	#N/A	-3.01	hypothetical protein
TGME49_252230	1.47	#N/A	#N/A	hypothetical protein
TGME49_282170	1.22	#N/A	#N/A	hypothetical protein
TGME49_294820	1.18	#N/A	#N/A	type I fatty acid synthase, putative
TGME49_265390	-1.40	-1.28	#N/A	hypothetical protein
TGME49_233760	-1.53	-2.58	#N/A	hypothetical protein
TGME49_309280	-1.70	#N/A	#N/A	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_229250	1.53	#N/A	1.42	ribosomal protein RPL28
TGME49_313830	-1.30	-1.28	#N/A	AARP2CN (NUC121) domain-containing protein
TGME49_235020	-0.99	-0.87	-0.85	COPI protein, putative
TGME49_269420	2.18	2.15	#N/A	hypothetical protein
TGME49_211020	-1.69	#N/A	#N/A	RNA recognition motif-containing protein
TGME49_252260	1.73	#N/A	1.92	hypothetical protein
TGME49_254110	1.55	#N/A	#N/A	tryptophanyl-tRNA synthetase (TrpRS1)

TGME49_216760	#N/A	-1.38	-1.52	RNA pseudouridine synthase superfamily protein
TGME49_221200	#N/A	0.86	#N/A	CW-type Zinc Finger protein
TGME49_206415	#N/A	-0.99	#N/A	myosin K
TGME49_232640	#N/A	1.17	1.87	RNA 2'-phosphotransferase, Tpt1/KptA family protein
TGME49_243340	#N/A	-1.43	#N/A	atypical MEK-related kinase (incomplete catalytic triad)
TGME49_270450	#N/A	-1.71	#N/A	MCM2/3/5 family protein
TGME49_236240	#N/A	-0.96	#N/A	Tyrosine kinase-like (TKL) protein
TGME49_247680	#N/A	-1.68	-2.26	hypothetical protein
TGME49_313760	#N/A	0.81	#N/A	hypothetical protein
TGME49_262740	#N/A	-1.64	#N/A	hypothetical protein
TGME49_298970	#N/A	0.88	1.21	LSM3, U6 small nuclear RNA associated isoform 2 family protein
TGME49_313120	#N/A	-1.89	#N/A	DNA-directed RNA polymerase, alpha subunit
TGME49_229490	#N/A	-0.97	#N/A	tetralricopeptide repeat-containing protein
TGME49_219170	#N/A	-0.87	#N/A	hypothetical protein
TGME49_246090	#N/A	-1.11	#N/A	hypothetical protein
TGME49_278540	#N/A	0.93	#N/A	hypothetical protein
TGME49_307610	#N/A	-0.87	#N/A	elongation factor TS, putative
TGME49_249810	#N/A	-1.68	-1.84	activating signal cointegrator 1 complex subunit 3, putative
TGME49_299980	#N/A	0.75	#N/A	hypothetical protein
TGME49_223590	#N/A	0.69	#N/A	proteasome subunit
TGME49_277770	#N/A	-1.42	#N/A	hypothetical protein
TGME49_215530	#N/A	0.97	#N/A	hypothetical protein
TGME49_230410	#N/A	-1.11	#N/A	peroxiredoxin PRX3
TGME49_229620	#N/A	-1.21	#N/A	hypothetical protein
TGME49_315820	#N/A	-1.15	#N/A	hypothetical protein
TGME49_209020	#N/A	-1.85	-2.11	hypothetical protein
TGME49_216650	#N/A	0.72	#N/A	S15 sporozoite-expressed protein
TGME49_207420	#N/A	0.81	#N/A	hypothetical protein
TGME49_305120	#N/A	1.05	#N/A	transporter, solute:sodium symporter (SSS) family protein
TGME49_235920	#N/A	-1.00	-1.14	dynein, axonemal, heavy chain 2 family protein
TGME49_220330	#N/A	-1.48	#N/A	hypothetical protein
TGME49_259630	#N/A	0.85	#N/A	hypothetical protein
TGME49_227060	#N/A	-1.03	#N/A	hypothetical protein
TGME49_223410	#N/A	0.85	#N/A	eukaryotic initiation factor-4E, putative
TGME49_298050	#N/A	-1.10	#N/A	hypothetical protein

FIGURE 3R

TGME49_264840	-2.19	-2.86	#N/A	ATP-dependent DNA helicase, RecQ family protein
TGME49_263085	-1.79	#N/A	#N/A	hypothetical protein
TGME49_204420	-1.23	#N/A	#N/A	oocyst wall protein OWP1
TGME49_214180	-0.96	#N/A	#N/A	ENTH domain-containing protein
TGME49_222920	1.22	1.08	1.31	mbp-1 interacting protein-2a family protein
TGME49_212130	-1.33	-1.06	-1.20	phospholipase, patatin family protein
TGME49_316140	-1.10	#N/A	#N/A	hypothetical protein
TGME49_278770	-1.28	-1.27	-1.20	hypothetical protein
TGME49_270930	-1.14	-1.08	-0.99	hypothetical protein
TGME49_220940	1.41	1.51	1.84	ribosomal RNA methyltransferase (FtsJ) family protein
TGME49_253730	1.23	0.96	1.16	importin-beta N-terminal domain-containing protein
TGME49_225060	-1.19	-0.95	#N/A	nucleoredoxin family protein
TGME49_234360	-1.04	#N/A	#N/A	DNA topoisomerase I, putative
TGME49_249950	-1.55	#N/A	#N/A	Mak16 protein
TGME49_214530	-1.85	-2.24	#N/A	DnaJ domain-containing protein
TGME49_267580	2.00	1.62	#N/A	cyclin2 related protein
TGME49_204880	1.39	#N/A	#N/A	hypothetical protein
TGME49_311510	0.88	#N/A	#N/A	eIF2 kinase IF2K-B
TGME49_216920	-1.58	-1.49	-1.69	mediator complex subunit MED8
TGME49_310910	1.39	#N/A	#N/A	WD domain, G-beta repeat-containing protein
TGME49_231210	-1.13	#N/A	#N/A	sarcalumenin/eps15 family protein
TGME49_314660	-1.21	-0.96	-1.09	TPRX1 protein
TGME49_224730	-1.53	#N/A	#N/A	hypothetical protein
TGME49_301216	-2.44	-2.44	-2.21	endonuclease/exonuclease/phosphatase family protein
TGME49_244600	-1.52	-1.44	#N/A	hypothetical protein
TGME49_212220	0.94	#N/A	#N/A	hypothetical protein
TGME49_292110	1.45	1.84	#N/A	formate/nitrite transporter protein
TGME49_249620	-1.31	-1.53	#N/A	histone deacetylase HDAC2
TGME49_207680	-1.13	#N/A	#N/A	suppressor of kinetochore protein 1, putative
TGME49_289710	1.56	#N/A	#N/A	AP2 domain transcription factor AP2IX-5
TGME49_312050	-0.96	#N/A	#N/A	small GTPase Rab2, putative
TGME49_220290	-1.77	-1.84	#N/A	hypothetical protein
TGME49_313350	-1.35	-1.21	-1.19	hypothetical protein
TGME49_261540	1.31	#N/A	#N/A	DNA-directed RNA polymerase I RPAC2
TGME49_262980	-1.74	-1.73	-1.55	hypothetical protein
TGME49_220510	#N/A	1.22	#N/A	hypothetical protein
TGME49_233830	#N/A	-1.85	#N/A	hypothetical protein
TGME49_310470	#N/A	0.80	#N/A	cytochrome C oxidase subunit Iib, putative
TGME49_233480	#N/A	1.85	#N/A	SAG-related sequence SRS29C
TGME49_312670	#N/A	-1.43	#N/A	hypothetical protein
TGME49_258480	#N/A	-0.96	#N/A	hypothetical protein
TGME49_212200	#N/A	-1.40	#N/A	hypothetical protein
TGME49_214840	#N/A	0.81	#N/A	AP2 domain transcription factor AP2X7
TGME49_214150	#N/A	-1.32	#N/A	mitochondrial inner membrane translocase subunit TIM17, putative
TGME49_207800	#N/A	0.92	#N/A	hypothetical protein
TGME49_203700	#N/A	0.94	#N/A	SFT2 family protein
TGME49_209570	#N/A	0.97	#N/A	suppressor of mitotic defects protein
TGME49_225160	#N/A	0.81	0.88	hypothetical protein
TGME49_293760	#N/A	0.71	#N/A	EF hand domain-containing protein
TGME49_270770	#N/A	-0.99	#N/A	PWI domain-containing protein
TGME49_268280	#N/A	-0.76	#N/A	'chromo' (CHR)romatin Organization (MO)ifier) domain-containing protein
TGME49_310870	#N/A	-1.03	#N/A	integral membrane protein, putative
TGME49_320480	#N/A	-0.83	#N/A	Rab11b
TGME49_241150	#N/A	-1.02	#N/A	hypothetical protein
TGME49_218260	#N/A	1.31	#N/A	histone H3.3
TGME49_240500	#N/A	0.99	#N/A	hypothetical protein
TGME49_295410	#N/A	-0.98	#N/A	transcription initiation factor TFIIID complex subunit TAF6
TGME49_315660	#N/A	-1.25	#N/A	hypothetical protein
TGME49_290330	#N/A	-1.39	#N/A	chloride transporter, chloride channel (ClC) family protein
TGME49_269130	#N/A	-1.63	#N/A	hypothetical protein
TGME49_310730	#N/A	-0.94	-1.22	hypothetical protein
TGME49_293180	#N/A	0.77	#N/A	NADP-specific glutamate dehydrogenase
TGME49_297710	#N/A	-1.42	#N/A	hypothetical protein
TGME49_272400	#N/A	-1.45	-1.58	casein kinase II regulatory subunit protein
TGME49_232390	#N/A	-1.67	#N/A	18S rRNA biogenesis protein RCL1 protein
TGME49_267680	#N/A	-1.03	-1.21	microneme protein MIC12
TGME49_249560	#N/A	-1.17	#N/A	DNA-directed RNA polymerase alpha chain rpoA
TGME49_253540	#N/A	1.00	#N/A	hypothetical protein
TGME49_220460	#N/A	-1.73	-2.59	SNF7 family protein
TGME49_216460	#N/A	0.89	#N/A	hypothetical protein

FIGURE 3S

TGME49_229350	-1.31	#N/A	#N/A	HEAT repeat-containing protein
TGME49_299780	1.00	#N/A	0.89	hypothetical protein
TGME49_268900	-1.44	-1.22	#N/A	dense granular protein GRA10
TGME49_280710	-1.25	-1.05	#N/A	20S proteasome subunit beta 7, putative
TGME49_237260	-1.08	#N/A	#N/A	Coiled-coil domain containing 124 family protein
TGME49_263595	-1.57	-1.37	#N/A	RNA-binding protein
TGME49_246800	-1.24	-1.04	-1.47	acylaminoacyl-peptidase, putative
TGME49_205700	1.48	1.33	1.58	cyclophilin precursor
TGME49_268230	-2.84	-3.64	-3.86	hypothetical protein
TGME49_212800	-1.49	-1.48	#N/A	hypothetical protein
TGME49_273320	-0.86	#N/A	#N/A	hypothetical protein
TGME49_231230	-2.42	#N/A	#N/A	hypothetical protein
TGME49_214580	-3.68	-5.07	#N/A	tetralricopeptide repeat-containing protein
TGME49_209095	-1.13	#N/A	#N/A	hypothetical protein
TGME49_259600	1.52	#N/A	#N/A	hypothetical protein
TGME49_208820	1.15	1.40	#N/A	1-deoxy-D-xylulose-5-phosphate synthase
TGME49_224980	-1.23	#N/A	#N/A	hypothetical protein
TGME49_235610	-1.70	-1.73	#N/A	ATPase, AAA family protein
TGME49_294790	0.91	0.85	0.93	hypothetical protein
TGME49_248610	1.33	#N/A	#N/A	hypothetical protein
TGME49_292610	1.36	1.62	#N/A	Toxoplasma gondii family C protein
TGME49_253310	1.22	1.17	1.20	hypothetical protein
TGME49_275870	1.41	1.90	2.70	tubulin/FtsZ family, GTPase domain-containing protein
TGME49_292950	1.10	0.99	#N/A	hypothetical protein
TGME49_315100	2.60	5.72	#N/A	hypothetical protein
TGME49_200360	1.25	1.62	1.64	hypothetical protein
TGME49_207900	-1.23	-1.09	#N/A	transcription initiation factor TFIIIB
TGME49_314895	-1.50	#N/A	#N/A	hypothetical protein
TGME49_230705	1.26	1.20	1.07	hypothetical protein
TGME49_297510	-1.70	-1.54	-1.52	hypothetical protein
TGME49_228720	-1.65	#N/A	#N/A	hypothetical protein
TGME49_226100	-2.58	-3.82	#N/A	haloacid dehalogenase family hydrolase domain-containing protein
TGME49_270160	-1.39	#N/A	#N/A	hypothetical protein

TGME49_235500	#N/A	-1.48	#N/A	hypothetical protein
TGME49_294220	#N/A	0.93	#N/A	hypothetical protein
TGME49_209080	#N/A	2.34	#N/A	transport protein particle (trapp) component, bet3 protein
TGME49_209200	#N/A	0.83	#N/A	hypothetical protein
TGME49_312950	#N/A	0.82	#N/A	hypothetical protein
TGME49_295125	#N/A	1.05	#N/A	rhostry protein ROP4
TGME49_220350	#N/A	-1.05	#N/A	tRNA ligases class II (D, K and N) domain-containing protein
TGME49_289780	#N/A	0.98	#N/A	ATP-dependent hsl protease ATP-binding subunit hslU, putative
TGME49_289110	#N/A	-1.75	#N/A	hypothetical protein
TGME49_223530	#N/A	1.04	#N/A	hypothetical protein
TGME49_263130	#N/A	0.88	#N/A	citrate synthase, putative
TGME49_295050	#N/A	-0.97	#N/A	tRNA ligase class II core domain (G, H, P, S and T) domain-containing protein
TGME49_224350	#N/A	-0.82	#N/A	aminopeptidase N, putative
TGME49_230220	#N/A	-0.92	#N/A	hypothetical protein
TGME49_231750	#N/A	-1.19	#N/A	hypothetical protein
TGME49_291630	#N/A	-1.59	#N/A	hypothetical protein
TGME49_270690	#N/A	-0.96	-1.09	arginyl-tRNA synthetase
TGME49_282000	#N/A	1.40	#N/A	hypothetical protein
TGME49_236030	#N/A	-1.72	#N/A	hypothetical protein
TGME49_247960	#N/A	1.49	#N/A	hypothetical protein
TGME49_260670	#N/A	-1.26	#N/A	centrin, putative
TGME49_283860	#N/A	-1.48	-1.72	leucine rich repeat-containing protein
TGME49_301340	#N/A	-0.84	#N/A	DnaJ domain-containing protein
TGME49_254280	#N/A	1.24	#N/A	DNA-directed RNA polymerase III RPC9
TGME49_214080	#N/A	#N/A	7.75	toxofilin
TGME49_313440	#N/A	#N/A	4.65	hypothetical protein
TGME49_245432	#N/A	#N/A	2.70	hypothetical protein
TGME49_315802	#N/A	#N/A	-9.71	hypothetical protein
TGME49_320180	#N/A	#N/A	4.38	SAG-related sequence SRS16C
TGME49_254840	#N/A	#N/A	-2.21	tetralricopeptide repeat-containing protein
TGME49_241880	#N/A	#N/A	-1.64	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_221220	#N/A	#N/A	3.98	hypothetical protein
TGME49_218192	#N/A	#N/A	-2.95	hypothetical protein

FIGURE 3T

TGME49_278830	-0.99	-1.44	-1.19	glucose-6-phosphate 1-dehydrogenase
TGME49_249550	-1.45	-1.52	-1.70	hypothetical protein
TGME49_271030	1.84	1.47	#N/A	AP2 domain transcription factor AP2VIII-6
TGME49_246050	-2.03	-2.18	#N/A	hypothetical protein
TGME49_314700	1.42	#N/A	#N/A	hypothetical protein
TGME49_254800	1.27	2.05	1.68	hypothetical protein
TGME49_207065	1.19	1.20	1.08	hypothetical protein
TGME49_208740	1.29	2.17	#N/A	microneme protein, putative
TGME49_253820	0.94	1.05	1.08	hypothetical protein
TGME49_267660	-1.04	#N/A	#N/A	hypothetical protein
TGME49_267750	-1.15	-1.38	-1.06	hypothetical protein
TGME49_224310	-1.28	-1.12	#N/A	DHHC zinc finger domain-containing protein
TGME49_223910	-1.14	-1.53	#N/A	acyltransferase domain-containing protein
TGME49_258980	-1.74	#N/A	-1.61	hypothetical protein
TGME49_309010	-1.67	#N/A	#N/A	elongation factor P, putative
TGME49_238170	1.47	1.16	#N/A	hypothetical protein
TGME49_275450	0.85	1.04	1.16	hypothetical protein
TGME49_253650	0.84	1.02	1.12	DnaJ C terminal region domain-containing protein
TGME49_315250	1.10	1.11	#N/A	GAMM1 protein, putative
TGME49_221230	-1.20	#N/A	-1.10	hypothetical protein
TGME49_304670	-1.33	#N/A	-1.51	leucine rich repeat-containing protein
TGME49_284660	1.30	1.58	1.34	mitochondrial ribosomal protein s6-2, putative
TGME49_249380	-1.03	#N/A	#N/A	DHHC zinc finger domain-containing protein
TGME49_311905	-2.42	-2.49	-2.69	hypothetical protein
TGME49_263840	-1.19	-1.10	#N/A	hypothetical protein
TGME49_263785	-2.30	-3.00	-2.59	phosphatidate cytidyltransferase
TGME49_272030	-1.20	-1.05	#N/A	kelch repeat-containing protein
TGME49_268690	1.67	#N/A	#N/A	hypothetical protein
TGME49_244870	-1.26	-1.10	#N/A	quinone oxidoreductase, putative
TGME49_214320	1.13	1.16	#N/A	facilitative glucose transporter GT1
TGME49_229140	1.35	#N/A	#N/A	MaoC family domain-containing protein
TGME49_255240	-1.71	-1.95	-2.42	hypothetical protein
TGME49_247690	-1.07	#N/A	-1.05	phospholipid-translocating P-type ATPase, flippase subfamily protein

TGME49_297647	#N/A	#N/A	3.99	hypothetical protein
TGME49_257750	#N/A	#N/A	-2.35	homocysteine s-methyltransferase domain-containing protein
TGME49_212250	#N/A	#N/A	1.38	XPG N-terminal domain-containing protein
TGME49_319350	#N/A	#N/A	-1.82	SAG-related sequence SRS17B
TGME49_243298	#N/A	#N/A	-2.67	ICE family protease (caspase) p20 domain-containing protein
TGME49_223480	#N/A	#N/A	-2.62	sushi domain (scr repeat) domain-containing protein
TGME49_310060	#N/A	#N/A	1.91	small nuclease
TGME49_313870	#N/A	#N/A	-1.40	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_236990	#N/A	#N/A	2.33	beta-ketoacyl synthase, N-terminal domain-containing protein
TGME49_223020	#N/A	#N/A	-1.62	coproporphyrinogen III oxidase
TGME49_323320	#N/A	#N/A	-2.94	hypothetical protein
TGME49_229640	#N/A	#N/A	-1.65	hypothetical protein
TGME49_230630	#N/A	#N/A	2.06	ATPase family associated with various cellular activities (AAA) domain-containing protein
TGME49_267070	#N/A	#N/A	1.12	aquaporin 2
TGME49_314250	#N/A	#N/A	2.07	bradyzoite thoptry protein BRP1
TGME49_214575	#N/A	#N/A	1.71	hypothetical protein
TGME49_230080	#N/A	#N/A	-1.72	DEAD/DEAH box helicase domain-containing protein
TGME49_319312	#N/A	#N/A	-2.01	hypothetical protein
TGME49_207880	#N/A	#N/A	-1.59	hypothetical protein
TGME49_232060	#N/A	#N/A	1.73	hypothetical protein
TGME49_282190	#N/A	#N/A	-1.15	hydrolase, NUDIX family protein
TGME49_232270	#N/A	#N/A	-1.53	histidine acid phosphatase superfamily protein
TGME49_233300	#N/A	#N/A	-1.71	RhoGAP domain-containing protein
TGME49_242118	#N/A	#N/A	-3.74	myosin-light-chain kinase
TGME49_206430	#N/A	#N/A	-1.19	formin FRM1
TGME49_249730	#N/A	#N/A	-1.78	hypothetical protein
TGME49_243580	#N/A	#N/A	-1.07	Hit family protein involved in cell-cycle regulation, putative
TGME49_257340	#N/A	#N/A	-2.29	Ras family protein
TGME49_270595	#N/A	#N/A	2.39	UBA/TS-N domain-containing protein
TGME49_312560	#N/A	#N/A	-1.26	hypothetical protein
TGME49_277920	#N/A	#N/A	1.19	hypothetical protein
TGME49_315750	#N/A	#N/A	-1.33	hypothetical protein
TGME49_257120	#N/A	#N/A	-1.63	sugar transporter ST1

FIGURE 3U

TGME49_214750	-1.02	#N/A	-0.97	hypothetical protein
TGME49_263510	-1.86	-3.66	-2.31	Spc97 / Spc98 family protein
TGME49_308050	-1.10	#N/A	#N/A	thioredoxin domain-containing protein
TGME49_321170	1.39	1.06	1.75	Toxoplasma gondii family C protein
TGME49_222245	-1.08	#N/A	#N/A	hypothetical protein
TGME49_258070	-1.18	-1.50	-1.42	hypothetical protein
TGME49_289140	0.96	0.87	1.06	ribosomal protein l22/43, putative
TGME49_247460	0.85	#N/A	#N/A	proliferating cell nuclear antigen PCNA1
TGME49_251530	2.11	2.18	#N/A	hypothetical protein
TGME49_226270	1.09	0.91	#N/A	hypothetical protein
TGME49_204350	2.00	#N/A	#N/A	hypothetical protein
TGME49_228070	1.56	#N/A	#N/A	hypothetical protein
TGME49_280375	2.33	2.90	#N/A	hypothetical protein
TGME49_203080	1.05	1.07	#N/A	RNA recognition motif-containing protein
TGME49_301890	-1.68	-3.19	#N/A	Toxoplasma gondii family B protein
TGME49_235540	1.00	0.92	#N/A	eukaryotic initiation factor-2 beta, putative
TGME49_306260	1.02	1.17	#N/A	hypothetical protein
TGME49_299180	-1.97	#N/A	#N/A	prenylated protein, putative
TGME49_294310	1.42	#N/A	#N/A	hypothetical protein
TGME49_261670	1.33	#N/A	#N/A	ribonuclease H1/H2 small subunit protein
TGME49_208830	1.17	#N/A	1.16	hypothetical protein
TGME49_245540	-1.08	#N/A	#N/A	hypothetical protein
TGME49_216880	3.06	#N/A	2.88	guanine nucleotide-binding protein
TGME49_253615	1.30	1.46	#N/A	hypothetical protein
TGME49_295070	1.17	#N/A	#N/A	helicase associated domain (ha2) protein
TGME49_228110	-1.31	-1.12	#N/A	hypothetical protein
TGME49_285490	-1.46	-1.37	#N/A	helix-hairpin-helix motif domain-containing protein
TGME49_276930	0.80	1.44	1.04	hypothetical protein
TGME49_214780	-1.54	-1.33	#N/A	hydrolase, NUDIX family protein
TGME49_224480	-1.12	-1.03	#N/A	cell-cycle-associated protein kinase CLK, putative
TGME49_202280	-1.90	-3.15	-2.17	WD domain, G-beta repeat-containing protein
TGME49_210255	0.92	0.81	0.99	hypothetical protein
TGME49_265410	1.53	1.20	#N/A	G-protein beta WD-40 repeat containing protein

TGME49_262630	#N/A	#N/A	2.15	hypothetical protein
TGME49_221170	#N/A	#N/A	-1.28	CAAX metallo endopeptidase
TGME49_269290	#N/A	#N/A	-1.82	hypothetical protein
TGME49_213050	#N/A	#N/A	1.31	hypothetical protein
TGME49_229690	#N/A	#N/A	-1.13	autophagy-related protein 7 atg7, putative
TGME49_318750	#N/A	#N/A	1.30	deoxyribose-phosphate aldolase
TGME49_310460	#N/A	#N/A	-1.11	Rab6
TGME49_288245	#N/A	#N/A	1.31	hypothetical protein
TGME49_240710	#N/A	#N/A	-1.19	RNA recognition motif-containing protein
TGME49_314970	#N/A	#N/A	-1.05	root hair defective 3 gtp-binding protein (rhd3) protein
TGME49_204400	#N/A	#N/A	-0.97	ATPase synthase subunit alpha, putative
TGME49_243730	#N/A	#N/A	1.29	roptry protein ROP9
TGME49_298030	#N/A	#N/A	-1.96	Ubiquinol-cytochrome c chaperone, putative
TGME49_216810	#N/A	#N/A	1.13	5'-nucleotidase, C-terminal domain-containing protein
TGME49_238040	#N/A	#N/A	-1.31	protein disulfide-isomerase domain-containing protein
TGME49_314780	#N/A	#N/A	-1.05	myosin G
TGME49_306350	#N/A	#N/A	1.14	variable surface lipoprotein
TGME49_258090	#N/A	#N/A	-1.11	hypothetical protein
TGME49_240450	#N/A	#N/A	1.47	Maf family protein
TGME49_242870	#N/A	#N/A	-1.50	histone lysine methyltransferase, SET, putative
TGME49_298980	#N/A	#N/A	1.08	RNA pseudouridine synthase superfamily protein
TGME49_297320	#N/A	#N/A	-1.30	hypothetical protein
TGME49_310300	#N/A	#N/A	-1.53	hypothetical protein
TGME49_274160	#N/A	#N/A	-1.05	hypothetical protein
TGME49_290040	#N/A	#N/A	0.97	macrophage migration inhibitory factor, putative
TGME49_329800	#N/A	#N/A	-1.24	hypothetical protein
TGME49_218530	#N/A	#N/A	-1.09	proteasome-interacting thioredoxin domain-containing protein
TGME49_255215	#N/A	#N/A	1.78	hypothetical protein
TGME49_203600	#N/A	#N/A	-1.16	hypothetical protein
TGME49_270010	#N/A	#N/A	-1.50	hypothetical protein
TGME49_264760	#N/A	#N/A	-1.12	Oxysterol-binding protein
TGME49_297880	#N/A	#N/A	-1.54	dense granule protein DG32
TGME49_262070	#N/A	#N/A	-0.99	ribosomal ma assembly protein mis3, putative

FIGURE 3V

TGME49_245500	1.22	#N/A	#N/A	dipeptidyl peptidase iv (dpp iv) n-terminal region domain-containing protein
TGME49_245480	2.22	2.41	#N/A	hypothetical protein
TGME49_202980	-1.12	-1.34	-1.02	hypothetical protein
TGME49_209210	-1.10	-1.25	#N/A	hypothetical protein
TGME49_319710	-1.31	-1.20	#N/A	kinesin motor domain-containing protein
TGME49_220160	2.33	#N/A	#N/A	WD domain-containing protein
TGME49_263080	0.90	1.10	1.04	hypothetical protein
TGME49_306470	-1.14	-1.34	-1.10	isoprenylcysteine carboxyl methyltransferase (icmt) family protein
TGME49_313277	-2.03	#N/A	#N/A	hypothetical protein
TGME49_285540	-1.59	#N/A	#N/A	DNA-directed DNA polymerase
TGME49_201220	-1.50	-1.39	#N/A	zinc finger protein
TGME49_293190	-1.01	-0.97	-1.18	endonuclease/exonuclease/phosphatase family protein
TGME49_319500	-1.04	#N/A	#N/A	hypothetical protein
TGME49_238110	-1.50	-1.61	#N/A	replication factor a protein 3 protein
TGME49_246760	-2.21	-2.02	#N/A	hypothetical protein
TGME49_313600	-1.33	-1.36	-1.30	DDHD domain-containing protein
TGME49_265520	-0.89	#N/A	#N/A	hypothetical protein
TGME49_203350	1.48	#N/A	#N/A	hypothetical protein
TGME49_215060	-1.03	#N/A	#N/A	small GTP-binding protein sar1, putative
TGME49_211860	1.10	#N/A	1.16	hypothetical protein
TGME49_312940	0.97	#N/A	#N/A	hypothetical protein
TGME49_246970	-1.45	-1.31	#N/A	3'-5' exonuclease domain-containing protein
TGME49_320000	-1.41	-1.35	#N/A	SCY kinase (incomplete catalytic triad)
TGME49_294930	-1.08	-1.37	#N/A	leucine rich repeat-containing protein
TGME49_219720	1.24	#N/A	#N/A	Ras-related protein Rab-5C, putative
TGME49_254460	1.01	1.12	1.22	hypothetical protein
TGME49_266070	1.33	1.28	1.31	ribosomal protein RPL31
TGME49_305140	1.08	#N/A	#N/A	phospholipase, patatin family protein
TGME49_293790	1.08	5.43	4.52	hypothetical protein
TGME49_257595	-1.23	#N/A	#N/A	hypothetical protein
TGME49_254120	0.96	1.77	1.66	autophagy-related protein 8 atg8, putative
TGME49_221390	-1.24	-1.37	#N/A	hypothetical protein
TGME49_293220	1.44	#N/A	#N/A	DHHC zinc finger domain-containing protein
TGME49_311890	-0.94	-0.98	-0.86	hypothetical protein

TGME49_271760	#N/A	#N/A	-1.67	seryl-tRNA synthetase (SerRS2)
TGME49_216770	#N/A	#N/A	2.12	hypothetical protein
TGME49_235515	#N/A	#N/A	1.91	MORN repeat-containing protein
TGME49_306440	#N/A	#N/A	-1.34	hypothetical protein
TGME49_306280	#N/A	#N/A	0.99	mediator complex subunit MED7
TGME49_259860	#N/A	#N/A	-1.24	hypothetical protein
TGME49_224810	#N/A	#N/A	-1.98	hypothetical protein
TGME49_251620	#N/A	#N/A	-1.24	flap structure-specific endonuclease 1, putative
TGME49_262710	#N/A	#N/A	0.96	Ctr copper transporter family protein
TGME49_216730	#N/A	#N/A	-0.88	MCM2/3/5 family protein
TGME49_291940	#N/A	#N/A	-1.03	hypothetical protein
TGME49_248750	#N/A	#N/A	-1.52	hypothetical protein
TGME49_229790	#N/A	#N/A	-1.43	hypothetical protein
TGME49_239010	#N/A	#N/A	1.54	hypothetical protein
TGME49_223690	#N/A	#N/A	1.13	hypothetical protein
TGME49_222400	#N/A	#N/A	-0.85	hypothetical protein
TGME49_222380	#N/A	#N/A	-0.86	importin-beta N-terminal domain-containing protein
TGME49_247760	#N/A	#N/A	-1.29	AMP-binding enzyme domain-containing protein
TGME49_203170	#N/A	#N/A	-1.11	OB-fold nucleic acid binding domain-containing protein
TGME49_318430	#N/A	#N/A	-0.91	malate dehydrogenase MDH
TGME49_271300	#N/A	#N/A	1.38	DNA-directed RNA polymerase II RPB7
TGME49_274150	#N/A	#N/A	-1.72	hypothetical protein
TGME49_223490	#N/A	#N/A	1.15	hypothetical protein
TGME49_271960	#N/A	#N/A	0.83	hypothetical protein
TGME49_232450	#N/A	#N/A	-1.21	SWI2/SNF2-containing protein RAD54
TGME49_239560	#N/A	#N/A	-1.46	myosin E
TGME49_259190	#N/A	#N/A	-1.93	hypothetical protein
TGME49_217600	#N/A	#N/A	-0.98	calcium-dependent protein kinase CDPK9
TGME49_217670	#N/A	#N/A	-1.35	ribosomal protein RPS6
TGME49_250880	#N/A	#N/A	-0.81	kinase, p1kB family protein
TGME49_305900	#N/A	#N/A	1.13	hypothetical protein
TGME49_213030	#N/A	#N/A	0.78	hypothetical protein
TGME49_290940	#N/A	#N/A	-0.95	EMP/nonasparin domain family protein
TGME49_240890	#N/A	#N/A	-0.94	6-phosphofructokinase

FIGURE 3W

TGME49_278740	-1.25	#N/A	#N/A	diaminopimelate decarboxylase
TGME49_253880	0.81	0.86	0.81	GNS1/SUR4 family protein
TGME49_213910	-1.27	-1.12	#N/A	hypothetical protein
TGME49_304680	-1.43	-1.82	-1.73	ubiquitin family protein
TGME49_275810	1.45	#N/A	1.36	ribosomal protein RPS10
TGME49_221510	-1.15	#N/A	#N/A	hypothetical protein
TGME49_228370	-1.26	-1.53	-1.57	hypothetical protein
TGME49_315590	-1.38	-1.24	-1.80	macro domain-containing protein
TGME49_263290	1.46	#N/A	#N/A	rhomboid protease ROM2
TGME49_290270	-1.20	#N/A	#N/A	SPRY domain-containing protein
TGME49_202240	-2.36	-2.25	-2.68	RAP domain-containing protein
TGME49_248370	1.41	#N/A	#N/A	prefoldin subunit 6, putative
TGME49_290720	-0.83	#N/A	#N/A	vacuolar proton translocating ATPase subunit, putative
TGME49_263660	-2.33	-2.43	-2.37	hypothetical protein
TGME49_213710	-1.28	-1.86	-1.50	WD domain, G-beta repeat-containing protein
TGME49_283585	-1.30	#N/A	#N/A	hypothetical protein
TGME49_237480	-1.55	#N/A	#N/A	BRCA1 C Terminus (BRCT) domain-containing protein
TGME49_220530	-1.64	-1.91	-1.67	AP2 domain transcription factor AP2V1
TGME49_263720	-1.87	-2.18	-2.27	HMG (high mobility group) box domain-containing protein
TGME49_249240	1.13	1.22	1.10	calmodulin, putative
TGME49_225680	-1.74	-2.00	-1.74	hypothetical protein
TGME49_201400	-1.41	-2.11	-2.01	Sin3-associated polypeptide SAP18
TGME49_306410	-1.76	-2.03	-2.16	hypothetical protein
TGME49_249480	1.07	#N/A	#N/A	tetratricopeptide repeat-containing protein
TGME49_216260	-0.98	#N/A	#N/A	eukaryotic initiation factor-2B, gamma subunit, putative
TGME49_289180	-1.21	-1.13	#N/A	thioredoxin family redox-active protein, putative
TGME49_252640	1.57	5.22	5.49	P-type ATPase PMA1
TGME49_290950	-0.86	#N/A	#N/A	clathrin heavy chain, putative
TGME49_262700	-1.61	-1.71	-1.59	tetratricopeptide repeat-containing protein
TGME49_269075	1.68	#N/A	#N/A	hypothetical protein
TGME49_253380	0.83	#N/A	0.81	AP2 domain transcription factor AP2III-2
TGME49_258105	-2.15	-1.98	#N/A	hypothetical protein
TGME49_237230	1.11	1.49	1.16	hypothetical protein
TGME49_202300	-1.29	-1.24	-1.23	inosine triphosphate pyrophosphatase, putative
TGME49_215990	-1.57	-1.45	#N/A	helicase, putative

TGME49_297220	#N/A	#N/A	-1.93	AMP-binding enzyme domain-containing protein
TGME49_207400	#N/A	#N/A	0.91	hypothetical protein
TGME49_314460	#N/A	#N/A	-1.55	hypothetical protein
TGME49_216630	#N/A	#N/A	-1.53	trigger factor protein, putative
TGME49_297150	#N/A	#N/A	-1.26	MORN repeat-containing protein
TGME49_281480	#N/A	#N/A	1.05	WD domain, G-beta repeat-containing protein
TGME49_215370	#N/A	#N/A	1.03	hypothetical protein
TGME49_293780	#N/A	#N/A	1.38	hypothetical protein
TGME49_309752	#N/A	#N/A	0.75	succinate-Coenzyme A ligase, beta subunit, putative
TGME49_248950	#N/A	#N/A	-1.47	camer superfamily protein
TGME49_209610	#N/A	#N/A	1.07	oocyst wall protein OWP2
TGME49_310560	#N/A	#N/A	-1.83	hypothetical protein
TGME49_274010	#N/A	#N/A	-1.62	hypothetical protein
TGME49_221630	#N/A	#N/A	-1.23	hypothetical protein
TGME49_300130	#N/A	#N/A	1.58	apical membrane antigen 1 domain-containing protein
TGME49_243690	#N/A	#N/A	0.80	hypothetical protein
TGME49_268000	#N/A	#N/A	-1.45	hypothetical protein
TGME49_319590	#N/A	#N/A	1.20	hypothetical protein
TGME49_267350	#N/A	#N/A	0.91	LSM domain-containing protein
TGME49_220140	#N/A	#N/A	1.47	EF hand domain-containing protein
TGME49_235905	#N/A	#N/A	-1.99	ribonuclease Z, putative
TGME49_249300	#N/A	#N/A	-0.75	hypothetical protein
TGME49_314540	#N/A	#N/A	-1.32	hypothetical protein
TGME49_313410	#N/A	#N/A	-0.90	proteasome 26S regulatory subunit
TGME49_306460	#N/A	#N/A	-1.21	bromodomain-containing protein
TGME49_311140	#N/A	#N/A	-1.58	hypothetical protein
TGME49_237010	#N/A	#N/A	-0.94	hypothetical protein
TGME49_221470	#N/A	#N/A	-0.79	hypothetical protein
TGME49_307605	#N/A	#N/A	1.08	hypothetical protein
TGME49_254606	#N/A	#N/A	1.31	hypothetical protein
TGME49_307830	#N/A	#N/A	-0.80	hypothetical protein
TGME49_245710	#N/A	#N/A	-0.95	phosphatidylinositol-4-phosphate 5-kinase, putative
TGME49_306330	#N/A	#N/A	-1.00	phospholipase
TGME49_228690	#N/A	#N/A	-1.37	phosphatidylinositol 3- and 4-kinase
TGME49_235700	#N/A	#N/A	1.00	sedoheptulose-1,7-bisphosphatase

FIGURE 3X

TGME49_314840	-1.19	#N/A	#N/A	ubiquitin carboxyl-terminal hydrolase
TGME49_253440	0.81	1.17	1.15	cell-cycle-associated protein kinase SRPK, putative
TGME49_213950	-1.11	#N/A	#N/A	hypothetical protein
TGME49_308040	-1.22	#N/A	#N/A	ZPR1 zinc finger domain-containing protein
TGME49_207970	-3.06	#N/A	#N/A	HEAT repeat-containing protein
TGME49_208850	1.56	#N/A	2.52	SAG-related sequence SRS11
TGME49_210408	1.42	1.67	#N/A	HMG (high mobility group) box domain-containing protein
TGME49_254820	0.97	#N/A	#N/A	hypothetical protein
TGME49_293680	-1.30	-1.47	#N/A	hypothetical protein
TGME49_291690	-1.33	-1.27	#N/A	hypothetical protein
TGME49_260830	-2.20	-2.72	#N/A	hypothetical protein
TGME49_295420	-0.94	#N/A	#N/A	hypothetical protein
TGME49_226320	-1.05	-1.07	#N/A	hypothetical protein
TGME49_245730	2.35	#N/A	#N/A	phosphatidylinositol-4-phosphate 5-Kinase
TGME49_262730	0.88	1.38	1.45	rhoGTP protein ROP16
TGME49_312210	1.76	1.89	#N/A	hypothetical protein
TGME49_240600	0.97	#N/A	#N/A	chaperonin cpn60, putative
TGME49_301460	1.63	#N/A	#N/A	hypothetical protein
TGME49_297650	-1.02	#N/A	#N/A	Ser/Thr phosphatase family protein
TGME49_259720	-1.19	-1.18	#N/A	hypothetical protein
TGME49_305860	-0.87	-1.42	#N/A	calcium-dependent protein kinase CDPK3
TGME49_208580	-1.19	-1.26	-1.58	DNA ligase 1, putative
TGME49_291350	-1.66	#N/A	#N/A	hypothetical protein
TGME49_226080	-1.60	#N/A	#N/A	polyA polymerase
TGME49_215250	-1.94	-1.94	-2.07	thiamin pyrophosphokinase, catalytic domain-containing protein

TGME49_318510	#N/A	#N/A	-1.07	N-ethylmaleimide-sensitive fusion protein, putative
TGME49_297980	#N/A	#N/A	-1.38	hypothetical protein
TGME49_222960	#N/A	#N/A	-1.28	SCY kinase-related protein (incomplete catalytic triad)
TGME49_219860	#N/A	#N/A	-0.82	replication licensing factor, putative
TGME49_239480	#N/A	#N/A	-1.11	RNB family domain-containing protein
TGME49_273060	#N/A	#N/A	1.06	ribosomal protein S17, putative
TGME49_289640	#N/A	#N/A	1.30	hypothetical protein
TGME49_276120	#N/A	#N/A	1.32	histone lysine methyltransferase, SET, putative
TGME49_259550	#N/A	#N/A	-0.82	dihydropterolate synthase
TGME49_209270	#N/A	#N/A	-1.44	hypothetical protein
TGME49_249740	#N/A	#N/A	1.12	translation machinery associated tma7 protein
TGME49_232320	#N/A	#N/A	-1.70	hypothetical protein
TGME49_238880	#N/A	#N/A	1.11	hypothetical protein
TGME49_313160	#N/A	#N/A	-1.11	hypothetical protein
TGME49_310930	#N/A	#N/A	-0.95	hypothetical protein
TGME49_320588	#N/A	#N/A	-1.36	glycosyl hydrolases family 35 protein
TGME49_255330	#N/A	#N/A	-1.84	hypothetical protein
TGME49_297360	#N/A	#N/A	-1.00	hypothetical protein
TGME49_218910	#N/A	#N/A	1.76	hypothetical protein
TGME49_209070	#N/A	#N/A	0.99	hypothetical protein
TGME49_233220	#N/A	#N/A	-0.83	hypothetical protein
TGME49_267670	#N/A	#N/A	-2.57	hypothetical protein
TGME49_312360	#N/A	#N/A	-1.69	hypothetical protein
TGME49_249840	#N/A	#N/A	-1.64	dynein heavy chain 2, putative

FIGURE 4A

Figure 4: EGS expression during NSC infections. Differential expression analysis of *T. gondii* genes from neuronal stem cells infected with *T. gondii* EGS strain for 18 hours compared to *T. gondii* gene expression from neuronal stem cells infected with either GT1, ME49 or VEG strain for 18 hours.

Gene ID	LogFC(EGS/GT1)	LogFC(EGS/ME49)	LogFC(EGS/VEG)	Gene Name
TGME49_233925	6.94	7.05	9.00	hypothetical protein
TGME49_237130	7.84	8.63	10.14	cytochrome b, putative
TGME49_320050	4.19	4.45	4.35	ribosomal protein RPL5
TGME49_322200	12.41	10.27	12.41	apocytochrome b, putative
TGME49_330000	8.50	9.84	10.97	cytochrome b
TGME49_290600	3.14	3.32	2.50	succinyl-CoA-synthetase alpha SCSA
TGME49_323400	7.83	10.51	10.92	cytochrome c oxidase subunit iii subfamily protein
TGME49_322800	12.26	12.26	12.26	hypothetical protein
TGME49_301250	7.82	8.17	8.14	hypothetical protein
TGME49_255060	7.95	8.34	10.42	cytochrome b(N-terminal):b6/petB subfamily protein
TGME49_321360	3.31	3.10	2.94	clustered-asparagine-rich protein
TGME49_232955	11.47	11.71	13.87	hypothetical protein
TGME49_302055	11.93	11.93	11.93	ribosomal protein RPS12
TGME49_251180	4.23	3.68	2.68	KRUF family protein
TGME49_262690	1.96	1.87	1.88	ribosomal protein RPL27
TGME49_261240	7.55	8.23	5.94	histone H3
TGME49_238240	2.08	2.80	2.64	bystin protein
TGME49_250710	2.10	1.75	1.13	microneme protein MIC10
TGME49_244370	3.57	3.61	3.44	TDC1, putative
TGME49_213280	2.15	2.05	1.16	SAG-related sequence SRS25
TGME49_218520	1.84	1.97	1.22	microneme protein MIC6
TGME49_217530	4.13	4.39	4.18	hypothetical protein
TGME49_211695	4.77	3.87	3.16	hypothetical protein
TGME49_287040	3.80	2.26	1.45	hypothetical protein
TGME49_277230	3.85	4.50	3.76	hypothetical protein
TGME49_311230	1.78	1.55	1.23	hypothetical protein
TGME49_237230	1.90	1.74	1.26	hypothetical protein
TGME49_223660	3.08	2.72	3.20	50S ribosomal protein L4, putative
TGME49_293790	4.56	6.17	8.48	hypothetical protein
TGME49_219850	-1.44	-1.03	-1.48	prolyl-tRNA synthetase (ProRS)
TGME49_281910	1.12	1.57	1.35	hypothetical protein
TGME49_226540	1.29	#N/A	#N/A	protein kinase
TGME49_233310	-3.35	-3.28	-3.41	peptidase D, putative
TGME49_268280	-1.09	-1.00	#N/A	'chromo' (CHR)romatin Organization Modifier domain-containing protein
TGME49_231200	-2.31	-2.78	-2.96	hypothetical protein
TGME49_253020	-2.34	-2.98	-2.14	hypothetical protein
TGME49_297140	-2.67	-2.97	-2.91	U6 snRNA-associated sm family protein Lsm2, putative
TGME49_318300	-2.67	-2.49	-2.54	hypothetical protein
TGME49_309050	-8.03	-8.05	-8.38	hypothetical protein
TGME49_264030	-1.62	-1.66	-1.99	aminotransferase, putative
TGME49_203620	-3.35	-3.25	-3.12	hypothetical protein
TGME49_222840	1.50	1.67	1.21	Ser/Thr phosphatase family protein
TGME49_236780	-3.35	-3.23	-3.31	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_228230	1.08	1.22	1.30	hypothetical protein
TGME49_243410	-3.35	-3.39	-4.05	tetratricopeptide repeat-containing protein
TGME49_219300	1.39	1.38	1.11	ran binding protein
TGME49_313160	-2.67	-2.33	-3.20	hypothetical protein
TGME49_270150	-2.67	-2.79	-2.98	hypothetical protein
TGME49_253490	1.69	1.80	2.08	hypothetical protein
TGME49_300280	-2.36	-1.96	-2.41	LSM domain-containing protein
TGME49_206605	1.58	1.20	2.24	hypothetical protein
TGME49_204060	-2.67	-2.77	-2.62	SNARE domain-containing protein
TGME49_295850	-1.16	-1.35	-1.01	cyclic nucleotide-binding domain-containing protein
TGME49_278550	-1.98	-1.78	-1.52	elongation factor Tu GTP binding domain-containing protein
TGME49_215490	-1.27	#N/A	#N/A	transporter, major facilitator family protein
TGME49_200330	-1.65	-1.47	-1.42	hypothetical protein
TGME49_239320	-7.99	-7.58	-8.28	BoIA family protein
TGME49_275780	-7.99	-8.35	-7.94	hypothetical protein

FIGURE 4B

TGME49_293170	-5.98	-5.85	-5.65	hypothetical protein
TGME49_205680	3.65	2.99	2.15	hypothetical protein
TGME49_271935	2.89	2.66	1.85	hypothetical protein
TGME49_254710	2.29	2.02	1.52	serine esterase (DUF676) protein
TGME49_275860	2.82	2.43	2.23	hypothetical protein
TGME49_253690	1.70	1.87	1.24	hypothetical protein
TGME49_221840	4.60	4.42	6.21	hypothetical protein
TGME49_251400	3.32	2.83	3.02	hypothetical protein
TGME49_240060	2.01	1.66	#N/A	hypothetical protein
TGME49_224760	6.80	3.36	3.19	SAG-related sequence SRS40E
TGME49_236910	-4.99	-4.53	-4.60	U2 snRNP auxiliary factor, putative
TGME49_243615	4.37	3.28	3.29	hypothetical protein
TGME49_225790	2.95	1.70	#N/A	PDI family protein
TGME49_277080	1.51	#N/A	#N/A	microneme protein MIC5
TGME49_211030	-3.57	-3.84	-3.41	hypothetical protein
TGME49_259260	-2.69	-2.40	-2.61	membrane protein FtsH1
TGME49_261720	-5.75	-5.72	-6.53	metal cation transporter, ZIP family protein
TGME49_229010	-2.20	-2.17	-2.37	rhostry neck protein RON4
TGME49_273320	2.17	2.45	1.83	hypothetical protein
TGME49_233450	1.96	1.48	1.37	SAG-related sequence SRS29A
TGME49_239790	-10.72	-10.48	-10.51	BRCA1 C Terminus (BRCT) domain-containing protein
TGME49_275640	2.47	2.00	2.21	hypothetical protein
TGME49_290020	2.52	2.52	2.27	cyclin dependent kinase binding protein
TGME49_287170	-10.73	-10.57	-10.29	hypothetical protein
TGME49_269330	-10.62	-10.42	-10.60	hypothetical protein
TGME49_208370	1.60	1.75	1.58	myosin heavy chain, putative
TGME49_275870	4.13	2.54	4.24	tubulin/FtsZ family, GTPase domain-containing protein
TGME49_260430	5.02	3.90	4.88	hypothetical protein
TGME49_270700	2.17	1.73	1.62	hypothetical protein
TGME49_312140	-3.17	-3.53	#N/A	hypothetical protein
TGME49_228160	1.95	2.03	2.44	acid phosphatase
TGME49_214980	1.71	1.82	1.39	hypothetical protein
TGME49_201170	-2.54	-2.61	-2.77	hypothetical protein
TGME49_301222	3.12	3.03	3.48	DNA repair protein Rad4 domain-containing protein
TGME49_252430	1.96	1.68	2.15	hypothetical protein
TGME49_202080	-7.99	-8.07	-8.15	hypothetical protein
TGME49_203010	-1.15	-1.01	#N/A	aurora kinase
TGME49_216240	-1.77	-1.76	-1.96	hypothetical protein
TGME49_315590	-2.07	-1.95	-2.04	macro domain-containing protein
TGME49_228030	1.87	1.56	2.04	hypothetical protein
TGME49_297760	-7.99	-8.05	-8.91	hypothetical protein
TGME49_255160	-7.99	-8.88	-8.87	hypothetical protein
TGME49_260420	-1.77	-1.62	-1.69	HEC/Ndc80p family protein
TGME49_235420	-1.16	-1.30	-1.03	hypothetical protein
TGME49_268910	1.28	1.34	1.66	signal peptidase I protein
TGME49_215070	1.03	#N/A	1.23	ferroxidase FD
TGME49_228980	-8.00	-8.20	-8.67	hypothetical protein
TGME49_268750	-3.35	-3.38	-3.47	peptidyl-prolyl cis-trans isomerase E, putative
TGME49_224810	-3.54	-3.46	-3.76	hypothetical protein
TGME49_264420	4.88	2.95	3.44	lipoprotein, putative
TGME49_232960	-1.60	-1.60	-1.86	oxidoreductase, 2OG-Fe(II) oxygenase family protein
TGME49_218370	-2.06	-2.02	-2.20	hypothetical protein
TGME49_294020	-7.99	-8.74	-8.71	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_321550	1.09	1.04	#N/A	hypothetical protein
TGME49_249020	-2.07	-2.21	-2.17	kinesin motor domain-containing protein
TGME49_250500	-3.37	-3.58	-3.24	hypothetical protein
TGME49_226090	-3.34	-3.35	-2.55	DEAD/DEAH box helicase domain-containing protein
TGME49_234300	1.28	#N/A	1.07	hypothetical protein
TGME49_218800	-8.01	-8.20	-7.86	hypothetical protein
TGME49_305920	-3.30	-3.50	-3.62	endonuclease III family 1 protein
TGME49_211470	1.56	2.49	2.32	Fcf2 pre-rRNA processing protein
TGME49_299015	-8.24	-6.90	-8.68	hypothetical protein
TGME49_213445	-1.70	-1.43	#N/A	hypothetical protein
TGME49_265380	-2.07	-1.96	-1.86	tetratricopeptide repeat (TPR)-/U-box domain-containing protein
TGME49_319570	-1.68	-1.66	-1.90	WD domain, G-beta repeat-containing protein
TGME49_213590	-1.24	#N/A	-1.33	hypothetical protein
TGME49_289910	-1.33	-1.02	#N/A	hypothetical protein
TGME49_215520	-1.24	#N/A	#N/A	hypothetical protein
TGME49_257170	-3.30	-3.23	-2.95	hypothetical protein
TGME49_228630	-1.22	-1.14	-1.36	hypothetical protein

FIGURE 4C

TGME49_290700	2.40	2.22	1.76	hypothetical protein
TGME49_226310	-4.12	-4.25	-3.47	zinc finger (CCCH type) motif-containing protein
TGME49_251540	1.84	2.03	1.30	dense granule protein GRA9
TGME49_293570	-3.09	-3.03	-3.13	translocation protein sec62, putative
TGME49_290200	-2.13	-1.63	-2.00	NAD/NADP octopine/inopaline dehydrogenase, alpha-helical domain-containing protein
TGME49_261520	-5.37	-5.22	-5.14	nucleolar GTP-binding protein 1, putative
TGME49_306670	-3.53	-3.50	-3.72	hypothetical protein
TGME49_249990	2.26	2.33	1.69	hypothetical protein
TGME49_208450	1.90	1.40	#N/A	protease inhibitor PI2
TGME49_214220	1.64	1.87	1.37	hypothetical protein
TGME49_315885	2.12	2.57	2.61	glycosyltransferase, putative
TGME49_254620	1.38	#N/A	1.17	ribosomal protein RPL39
TGME49_219520	-2.77	-2.28	-2.64	histone arginine methyltransferase PRMT1
TGME49_269310	4.41	3.54	5.30	hypothetical protein
TGME49_239440	-10.43	-10.30	-10.36	protein kinase (incomplete catalytic triad)
TGME49_254120	2.06	2.28	1.94	autophagy-related protein 8 atg8, putative
TGME49_214350	-3.27	-2.91	-2.94	GTP-binding protein, putative
TGME49_206550	5.36	3.26	7.43	hypothetical protein
TGME49_245980	4.18	2.90	3.58	hypothetical protein
TGME49_222380	-2.54	-2.55	-2.57	importin-beta N-terminal domain-containing protein
TGME49_314500	-2.83	-3.17	-3.32	subtilisin SUB2
TGME49_266050	1.90	2.21	2.37	hypothetical protein
TGME49_223930	1.66	1.62	1.70	RNA recognition motif-containing protein
TGME49_319500	-10.40	-10.71	-10.47	hypothetical protein
TGME49_217820	-2.95	-2.54	-3.27	PCI domain-containing protein
TGME49_298620	-5.25	-5.08	-4.77	hypothetical protein
TGME49_265190	-4.42	-4.49	-4.37	Ulp1 protease family, C-terminal catalytic domain-containing protein
TGME49_245460	1.32	1.09	1.16	ribosomal protein RPS8
TGME49_315620	-5.25	-5.11	-5.42	vacuolar ATP synthase subunit C, putative
TGME49_282070	-2.08	-2.02	-1.87	hypothetical protein
TGME49_300220	-3.34	-3.20	-3.26	hypothetical protein
TGME49_290640	-1.34	-1.52	-1.13	DNA mismatch repair protein MSH6-1, putative
TGME49_238410	-2.63	-2.83	-3.02	hypothetical protein
TGME49_215060	-1.26	-1.16	-1.54	small GTP-binding protein sar1, putative
TGME49_320460	-3.30	-3.51	-3.20	ABC transporter transmembrane region domain-containing protein
TGME49_254200	-7.98	-8.32	-7.85	anticodon binding domain-containing protein
TGME49_203160	1.32	1.09	1.08	hypothetical protein
TGME49_247680	1.68	#N/A	#N/A	hypothetical protein
TGME49_282130	-2.28	-2.12	-2.19	hypothetical protein
TGME49_311150	-3.31	-3.61	-3.92	hypothetical protein
TGME49_222910	-1.50	-1.34	-1.38	phosphoglycerate mutase
TGME49_285272	-7.99	-8.13	-7.86	hypothetical protein
TGME49_281900	-1.14	-1.27	#N/A	SET domain containing lysine methyltransferase KMT6x
TGME49_288330	-3.30	-3.47	-3.41	histone lysine methyltransferase, SET, putative
TGME49_247930	-7.98	-7.69	-8.15	SNARE domain-containing protein
TGME49_226280	1.72	2.12	1.85	ribosomal protein L28, putative
TGME49_216750	1.04	#N/A	#N/A	Paf1/RNA polymerase II complex component LEO1
TGME49_271930	-1.16	-1.34	-1.52	hypothetical protein
TGME49_209210	-1.63	-2.20	-1.97	hypothetical protein
TGME49_301400	1.16	1.14	1.69	hypothetical protein
TGME49_312520	-3.33	-4.02	-2.69	tRNA dimethylallyltransferase
TGME49_305870	-2.64	-2.29	-2.08	DAD family protein
TGME49_226270	-2.66	-2.89	-3.07	hypothetical protein
TGME49_278230	-3.30	-3.04	-3.05	prenyltransferase and squalene oxidase repeat-containing protein
TGME49_243200	-1.25	-1.43	-1.33	hypothetical protein
TGME49_289720	-1.65	-1.42	-1.57	hypothetical protein
TGME49_222240	-1.28	-1.20	-1.27	hypothetical protein
TGME49_294250	-1.87	-1.84	-2.11	WD domain, G-beta repeat-containing protein
TGME49_311625	-2.04	-2.07	-1.97	WD domain, G-beta repeat-containing protein
TGME49_323110	1.18	1.44	1.42	hypothetical protein
TGME49_278160	-3.34	-3.38	-3.39	vesicle transport v-snare protein
TGME49_305540	-1.56	-1.62	-1.64	hypothetical protein

FIGURE 4D

TGME49_240650	-2.32	-2.36	-2.44	coatomer protein complex, subunit alpha, putative	TGME49_236630	-1.03	#N/A	-1.36	hypothetical protein
TGME49_292920	-2.40	-1.88	-2.22	heat shock protein 75, putative	TGME49_285810	-7.92	-8.37	-7.85	MYND finger domain-containing protein
TGME49_260500	-2.03	-1.98	-2.19	COP1 associated protein, putative	TGME49_290310	-2.04	-2.05	-1.79	hypothetical protein
TGME49_277000	-4.45	-4.39	-4.77	transport protein Sec24, putative	TGME49_232680	1.24	#N/A	1.15	hypothetical protein
TGME49_305160	3.42	3.64	2.96	histone H2Ba	TGME49_291590	-7.92	-8.34	-8.12	hypothetical protein
TGME49_278870	-1.83	-1.62	-1.81	myosin F	TGME49_295040	-1.04	#N/A	-1.24	HEAT repeat-containing protein
TGME49_212880	-2.79	-2.89	-2.83	surface antigen repeat-containing protein	TGME49_251710	1.67	2.12	1.15	hypothetical protein
TGME49_220930	-3.07	-2.68	-2.83	hypothetical protein	TGME49_278250	1.78	1.24	1.10	hypothetical protein
TGME49_250340	-2.65	-2.25	-2.60	centrin 2	TGME49_270190	-2.73	-2.74	-2.57	protein phosphatase 2C domain-containing protein
TGME49_287460	3.46	3.42	3.08	hypothetical protein	TGME49_246130	1.18	1.26	#N/A	serpin (serine proteinase inhibitor) superfamily protein
TGME49_209050	-10.21	-10.26	-10.25	Tyrosine kinase-like (TKL) protein	TGME49_211230	-1.40	-1.40	-1.32	eukaryotic initiation factor-2B, alpha subunit, putative
TGME49_261022	-2.70	-2.86	#N/A	dynein heavy chain family protein	TGME49_258450	-1.18	#N/A	#N/A	hypothetical protein
TGME49_253170	1.86	1.61	2.14	zinc carboxypeptidase, putative	TGME49_249890	1.63	1.64	1.71	hypothetical protein
TGME49_238895	-3.36	-3.03	-2.84	hypothetical protein	TGME49_211640	1.08	#N/A	1.34	hypothetical protein
TGME49_259240	1.55	1.36	1.03	ribosomal protein RPS21	TGME49_284540	-1.11	-1.03	-1.31	ATP synthase F1, delta subunit protein
TGME49_200300	6.27	6.44	3.36	hypothetical protein	TGME49_232750	-1.19	#N/A	#N/A	23S rRNA (adenine(1618)-N(6))-methyltransferase, putative
TGME49_239260	6.69	3.42	3.08	histone H4	TGME49_254660	1.09	1.21	1.48	ankyrin repeat-containing protein
TGME49_228690	-5.20	-5.43	-5.44	phosphatidylinositol 3- and 4-kinase	TGME49_311220	-1.93	-2.25	-1.94	hypothetical protein
TGME49_321530	1.55	1.44	#N/A	cathepsin CPL	TGME49_216510	-3.26	-3.95	-4.30	thioredoxin, putative
TGME49_244280	-1.60	-1.19	-2.12	hypothetical protein	TGME49_212940	-7.92	-10.38	-7.86	hypothetical protein
TGME49_247530	3.32	3.16	2.40	hypothetical protein	TGME49_201150	-1.56	-2.17	-1.77	heavy metal translocating P-type ATPase subfamily protein
TGME49_263870	-5.18	-5.03	-5.22	glutamate-tRNA ligase	TGME49_263440	-2.25	-1.71	-1.58	hypothetical protein
TGME49_270360	-5.16	-5.18	-5.33	hypothetical protein	TGME49_260830	-2.63	-3.12	#N/A	hypothetical protein
TGME49_257910	4.73	4.29	#N/A	hypothetical protein	TGME49_255960	-1.46	-1.45	-1.25	hypothetical protein
TGME49_251740	-3.48	-3.84	-3.65	AP2 domain transcription factor AP2XII-9	TGME49_210778	-1.73	-1.95	-1.97	hemimethylated DNA binding domain-containing protein
TGME49_240280	-2.57	-2.24	-2.45	S1/P1nuclease	TGME49_313960	-3.31	-2.93	-3.09	ribosomal protein L19 protein
TGME49_210300	-5.16	-5.29	-5.07	hypothetical protein	TGME49_208440	1.08	1.14	1.13	hypothetical protein
TGME49_249350	-10.14	-10.09	-10.39	esterase/lipase/thioesterase domain-containing protein	TGME49_267530	1.84	1.93	1.83	hypothetical protein
TGME49_242290	-2.55	-2.37	-2.68	proteasome subunit alpha1, putative	TGME49_246990	-2.60	-2.22	-2.24	hypothetical protein
TGME49_286120	-2.44	-2.26	-2.35	prolyl endopeptidase	TGME49_214380	1.51	1.31	1.30	hypothetical protein
TGME49_244880	-4.25	-4.05	-4.08	DNA-directed RNA polymerase I RPA1	TGME49_312660	-2.01	-1.51	-2.08	hypothetical protein
TGME49_294820	2.77	#N/A	#N/A	type I fatty acid synthase, putative	TGME49_269320	-7.92	-8.53	-8.43	hypothetical protein
TGME49_289710	-2.76	-2.62	-2.53	AP2 domain transcription factor AP2IX-5	TGME49_232000	1.02	1.15	#N/A	hypothetical protein
TGME49_261070	-4.20	-3.67	-3.15	apicoplast triosephosphate translocator APT1	TGME49_232970	-3.26	-3.14	-2.94	hypothetical protein
TGME49_294640	-1.70	-1.47	-1.55	ribonucleoside-diphosphate reductase large chain	TGME49_281980	-1.28	-1.49	-1.12	phosphatidate cytidyltransferase

FIGURE 4E

TGME49_290270	1.95	2.38	2.17	SPRY domain-containing protein
TGME49_202980	-2.87	-2.59	-2.28	hypothetical protein
TGME49_259010	-5.04	-4.48	-5.10	vacuolar ATP synthase subunit d, putative
TGME49_237210	-5.01	-4.90	-4.79	Tyrosine kinase-like (TKL) protein
TGME49_228280	2.80	2.37	2.53	hypothetical protein
TGME49_259550	-2.88	-2.93	-3.33	dihydropterate synthase
TGME49_231410	-2.46	-2.14	-2.50	hypothetical protein
TGME49_272370	1.86	#N/A	1.71	hypothetical protein
TGME49_294610	-1.60	-1.61	-1.38	histone lysine methyltransferase, SET, putative
TGME49_241830	2.46	2.13	2.35	peptidyl-prolyl cis-trans isomerase
TGME49_260800	2.39	1.71	1.69	hypothetical protein
TGME49_232650	2.05	2.25	2.06	hypothetical protein
TGME49_202420	2.21	2.25	1.97	hypothetical protein
TGME49_316280	-5.04	-5.04	-5.19	transporter, major facilitator family protein
TGME49_214410	2.79	2.96	3.26	hypothetical protein
TGME49_232560	-3.04	-2.22	-2.40	hypothetical protein
TGME49_253750	2.24	1.94	2.28	PLU-1 family protein
TGME49_214970	-1.94	-1.69	-1.90	DNA replication licensing factor, putative
TGME49_301270	1.53	1.26	1.33	Tyrosine kinase-like (TKL) protein
TGME49_274060	-2.24	-1.82	-2.10	2-oxoglutarate/malate translocase OMT
TGME49_291890	1.28	1.33	#N/A	microneme protein MIC1
TGME49_293480	2.74	#N/A	3.17	MoeA N-terminal region (domain I and II) domain-containing protein
TGME49_246330	-5.04	-5.33	-5.17	CRAL/TRIO domain-containing protein
TGME49_208530	-3.18	-3.01	-3.36	nicotinate phosphoribosyltransferase
TGME49_313870	2.00	1.67	#N/A	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_255650	-10.23	-10.24	-10.91	DHHC zinc finger domain-containing protein
TGME49_262380	-3.40	-3.08	-3.11	elongation factor Tu, putative
TGME49_207460	1.59	2.16	1.67	Rab5B protein
TGME49_221470	-2.08	-2.20	-2.15	hypothetical protein
TGME49_254080	1.41	1.64	1.59	metal cation transporter, ZIP family protein
TGME49_321650	-2.67	-2.84	-2.55	hypothetical protein
TGME49_267670	4.04	#N/A	1.90	hypothetical protein
TGME49_260440	1.42	1.37	1.21	nuclear factor NF3

TGME49_227050	-3.26	-3.36	-2.81	ATPase/histidine kinase/DNA gyrase B/HSP90 domain-containing protein
TGME49_320005	-3.26	-3.18	-3.28	hypothetical protein
TGME49_297230	-1.72	-1.95	-2.06	Vps53 family, N-terminal protein
TGME49_243790	-1.85	-1.82	-1.57	SAG-related sequence SRS33
TGME49_269720	1.99	1.63	#N/A	hypothetical protein
TGME49_207230	-1.74	#N/A	#N/A	hypothetical protein
TGME49_239700	-2.60	-3.30	-2.87	regulator of chromosome condensation (RCC1) repeat-containing protein
TGME49_219170	-1.55	-1.93	-1.51	hypothetical protein
TGME49_228170	1.28	1.04	#N/A	inner membrane complex protein IMC2A
TGME49_266810	-1.31	-1.25	-1.62	hypothetical protein
TGME49_305020	1.21	#N/A	#N/A	hypothetical protein
TGME49_309770	1.00	#N/A	#N/A	hypothetical protein
TGME49_271800	-1.50	#N/A	#N/A	serine esterase (DUF676) protein
TGME49_316240	-1.72	-1.51	-1.32	hypothetical protein
TGME49_202430	1.31	1.19	1.22	hypothetical protein
TGME49_214280	-7.97	-8.13	-7.97	phosphoadenosine phosphosulfate reductase family protein
TGME49_289640	1.47	1.86	2.07	hypothetical protein
TGME49_288900	1.61	1.26	1.82	Yos1 family protein
TGME49_270595	-1.69	-3.32	#N/A	UBA/TS-N domain-containing protein
TGME49_203290	1.35	1.50	1.69	hypothetical protein
TGME49_283800	-1.89	-1.99	-2.23	hypothetical protein
TGME49_248550	-3.34	-3.55	-3.59	SPX domain-containing protein
TGME49_228060	-3.35	-3.21	-2.94	hypothetical protein
TGME49_205050	2.54	#N/A	#N/A	hypothetical protein
TGME49_211680	-1.20	-1.12	-1.71	protein disulfide isomerase
TGME49_275750	-1.65	-1.31	-1.76	small nuclear ribonucleoprotein E, putative
TGME49_208050	-2.27	-2.54	-2.66	ABC transporter, putative
TGME49_240900	1.01	#N/A	1.11	AP2 domain transcription factor AP2V1-2
TGME49_204550	-2.60	-2.70	-2.74	hypothetical protein
TGME49_288620	1.02	1.03	#N/A	Erv1 / Alr family protein
TGME49_209880	-1.09	-1.19	#N/A	glutamic acid-rich protein, putative
TGME49_204410	-1.86	-2.01	-1.68	endonuclease/exonuclease/phosphatase family protein
TGME49_254900	-1.23	#N/A	-1.09	proteasome subunit beta type 2, putative

FIGURE 4F

TGME49_294770	-4.96	-4.97	-5.13	Armadillo/beta-catenin family repeat-containing protein
TGME49_218530	-9.93	-9.55	-10.01	proteasome-interacting thioredoxin domain-containing protein
TGME49_254720	1.30	1.02	#N/A	dense granule protein GRA8
TGME49_316600	1.58	1.38	#N/A	hypothetical protein
TGME49_219700	-1.98	-1.55	-1.94	DNA replication licensing factor MCM4, putative
TGME49_305590	-4.08	-4.24	-4.21	ABC transporter transmembrane region domain-containing protein
TGME49_213410	-2.26	-2.18	-1.97	small nuclear ribonucleoprotein f (snmp-f), putative
TGME49_323310	4.18	2.03	#N/A	hypothetical protein
TGME49_250820	-2.77	-2.93	-2.94	hypothetical protein
TGME49_297530	-9.90	-9.43	-9.68	DNA-directed RNA polymerase I RPA2
TGME49_299780	1.88	1.64	1.14	hypothetical protein
TGME49_226960	-1.42	-1.13	-1.58	phosphofructokinase PFKII
TGME49_228190	-2.01	-1.56	-1.90	eukaryotic initiation factor-3, subunit 5, putative
TGME49_207680	-4.07	-3.93	-4.57	suppressor of kinetochore protein 1, putative
TGME49_310750	-2.08	-1.99	-2.52	emp24/gp25L/p24 family protein
TGME49_218880	-2.55	-2.02	-2.54	SF-assemblin, putative
TGME49_253570	2.47	2.76	2.19	hypothetical protein
TGME49_235130	-3.68	-4.32	-3.97	transmembrane protein
TGME49_220250	1.74	1.86	1.84	Nucleotide-sensitive chloride conductance regulator (ICln) protein
TGME49_243430	2.37	2.08	1.86	OTU family cysteine protease
TGME49_217700	-9.90	-9.79	-9.87	AP2 domain transcription factor AP2XII-2
TGME49_254470	1.47	1.48	1.10	hypothetical protein
TGME49_211150	-4.87	-5.27	-4.82	hypothetical protein
TGME49_203300	2.63	2.78	2.96	hypothetical protein
TGME49_268960	1.73	1.49	1.13	hypothetical protein
TGME49_278510	-2.53	-2.72	-2.92	protein phosphatase 2C domain-containing protein
TGME49_227650	-3.07	-2.52	-2.35	microtubule-associated protein RP/EB family, putative
TGME49_318310	-2.15	-1.89	-2.07	transketolase
TGME49_239420	1.07	1.11	#N/A	protein kinase
TGME49_232500	-9.85	-9.78	-9.93	hypothetical protein
TGME49_273050	2.18	1.75	1.84	hypothetical protein
TGME49_228660	-3.57	-3.59	-3.53	Sec7 domain-containing protein
TGME49_219550	-1.08	#N/A	-1.13	dihydrodipicolyllysine-residue succinyltransferase component of oxoglutarate dehydrogenase
TGME49_233000	-1.28	-1.97	-1.07	KOW motif domain-containing protein
TGME49_202640	-7.85	-8.13	-8.04	RNA pseudouridine synthase superfamily protein
TGME49_220208	-7.86	-8.29	-7.90	hypothetical protein
TGME49_306950	-7.97	-7.84	-8.04	RAP domain-containing protein
TGME49_309390	-7.85	-7.64	-8.27	hypothetical protein
TGME49_277550	-7.86	-8.26	-8.19	UvrD/REP helicase domain-containing protein
TGME49_246780	-7.85	-8.42	-7.65	hypothetical protein
TGME49_299150	-7.85	-8.50	-8.75	AP2 domain transcription factor AP2III-3
TGME49_321640	-1.74	-1.84	#N/A	cell division protein CDC48AP
TGME49_298050	-1.82	-1.36	#N/A	hypothetical protein
TGME49_286740	2.43	2.15	3.41	microneme-like protein
TGME49_276990	-3.21	-3.32	-3.93	cytochrome b5 family heme/steroid binding domain-containing protein
TGME49_232320	-7.85	-8.04	-8.59	hypothetical protein
TGME49_216530	-7.86	-7.84	-8.54	ribosome recycling factor protein
TGME49_288210	1.38	1.11	1.19	PUL domain-containing protein
TGME49_215380	-3.24	-3.38	-3.25	hypothetical protein
TGME49_281675	1.77	1.68	1.83	protein kinase, putative
TGME49_209740	1.57	1.31	1.69	hypothetical protein
TGME49_243910	1.61	1.05	#N/A	Cof family hydrolase subfamily protein
TGME49_239250	1.05	#N/A	#N/A	diacylglycerol kinase, putative
TGME49_235402	-7.86	-8.39	-7.51	CorA family Mg2+ transporter protein
TGME49_269710	-1.12	#N/A	#N/A	hypothetical protein
TGME49_290960	-1.31	-1.20	-1.21	pyruvate phosphate dikinase, pep/pyruvate binding domain-containing protein
TGME49_247610	1.57	2.01	1.39	small nuclear ribonucleoprotein E, putative
TGME49_228000	1.14	#N/A	#N/A	splicing factor 3A subunit 2, putative
TGME49_321170	2.39	2.26	2.76	Toxoplasma gondii family C protein
TGME49_214190	1.61	#N/A	1.70	SAG-related sequence SRS46
TGME49_310730	-1.38	-1.10	-1.36	hypothetical protein
TGME49_323100	1.22	1.12	#N/A	hypothetical protein
TGME49_288045	-3.25	-3.53	-3.28	hypothetical protein
TGME49_224620	1.22	1.54	#N/A	hypothetical protein

FIGURE 4G

TGME49_250030	2.80	2.66	2.94	hypothetical protein
TGME49_239410	-2.31	-2.63	-2.59	hypothetical protein
TGME49_228100	-2.62	-1.89	-1.98	hypothetical protein
TGME49_204530	1.26	1.30	#N/A	microneme protein MIC11
TGME49_206610	-3.63	-3.26	-3.18	pyruvate dehydrogenase complex subunit PDH-E2
TGME49_306060	-1.39	-1.32	-1.59	rhostry neck protein RON8
TGME49_231430	-9.83	-9.75	-9.84	oligosaccharyl transferase sti3 protein, putative
TGME49_201860	1.08	1.09	#N/A	hypothetical protein
TGME49_223050	-1.44	-1.25	-1.58	ribosomal protein RPS20
TGME49_216730	-1.68	-1.23	-1.60	MCM2/3/5 family protein
TGME49_216820	1.42	1.54	#N/A	transporter, major facilitator family protein
TGME49_249540	1.55	1.86	1.71	hypothetical protein
TGME49_305180	-9.79	-9.86	-9.93	Na ⁺ /H ⁺ exchanger NHE3
TGME49_200360	2.53	2.31	1.90	hypothetical protein
TGME49_255410	-4.81	-4.73	-4.79	hypothetical protein
TGME49_316660	-9.79	-9.87	-10.13	culin family protein
TGME49_210682	5.42	2.68	3.05	hypothetical protein
TGME49_286450	1.08	1.00	#N/A	dense granule protein GRA5
TGME49_227810	1.36	1.34	#N/A	rhostry kinase family protein ROP11 (incomplete catalytic triad)
TGME49_278800	-2.27	-2.53	-1.89	zinc finger protein 36 family 3 protein
TGME49_268225	-5.13	-4.79	-5.03	hypothetical protein
TGME49_205580	1.68	1.39	1.37	nuclear factor NF4
TGME49_247460	-1.69	-1.50	-1.81	proliferating cell nuclear antigen PCNA1
TGME49_255180	-9.77	-10.08	-9.46	ubiquitin carboxyl-terminal hydrolase
TGME49_296010	-1.92	-1.76	-1.93	phosphatidylinositol 3- and 4-kinase
TGME49_293660	-3.96	-3.66	-3.81	hypothetical protein
TGME49_239540	-9.77	-9.86	-9.89	LEM3 (ligand-effect modulator 3) family / CDC50 family protein
TGME49_294630	-2.17	-2.14	-2.37	hypothetical protein
TGME49_207640	-2.14	-1.63	-2.13	isoleucyl-tRNA synthetase family protein
TGME49_318770	-4.78	-4.68	-4.35	aurora kinase(incomplete catalytic triad)
TGME49_314410	-2.66	-2.52	-2.67	aquarius, putative
TGME49_257360	2.37	1.80	1.01	hypothetical protein
TGME49_250840	-9.73	-9.60	-9.48	hypothetical protein
TGME49_297360	-1.55	-1.34	-1.42	hypothetical protein
TGME49_280590	-3.28	-2.85	#N/A	hypothetical protein
TGME49_242110	-7.85	-6.77	-8.92	rhostry kinase family protein ROP38
TGME49_268000	-2.56	-2.24	-2.63	hypothetical protein
TGME49_263130	1.16	1.21	#N/A	citrate synthase, putative
TGME49_284050	-1.53	-1.75	-1.41	DEAD/DEAH box helicase domain-containing protein
TGME49_275568	-1.53	-1.39	-1.11	GPI transamidase subunit PIG-U protein
TGME49_203390	-1.21	-1.15	-1.41	CRAL/TRIO domain-containing protein
TGME49_260310	1.50	1.61	1.21	ATP-binding cassette transporter ABC.B1
TGME49_244130	-1.50	-1.54	-1.39	hypothetical protein
TGME49_286640	-3.20	-2.84	-2.49	GTPase
TGME49_218960	-1.52	-1.28	-1.07	AP2 domain transcription factor AP2XII-1
TGME49_273500	-2.28	-1.78	#N/A	O-linked N-acetylglucosamine transferase
TGME49_210380	-1.33	-1.18	-1.26	hypothetical protein
TGME49_266110	1.48	1.30	1.44	DEAD/DEAH box helicase domain-containing protein
TGME49_235700	-1.43	-1.43	-1.05	sedoheptulose-1,7-bisphosphatase
TGME49_204400	-1.08	#N/A	-1.50	ATPase synthase subunit alpha, putative
TGME49_298020	-1.25	-1.19	-1.33	DEAD-family helicase
TGME49_262120	-1.20	-1.20	-1.51	IQ calmodulin-binding motif domain-containing protein
TGME49_310802	1.17	1.67	1.52	CRAL/TRIO domain-containing protein
TGME49_233680	-7.78	-8.49	-8.47	nuclear movement family protein
TGME49_223125	-1.80	-2.03	-1.82	ubiquitin family protein
TGME49_241840	1.44	1.36	#N/A	hypothetical protein
TGME49_269250	-1.11	#N/A	-1.29	Mov34/MPN/PAD-1 family protein
TGME49_211410	-3.17	-4.13	-3.86	translation initiation factor sui1 protein
TGME49_301300	-7.78	-8.35	-7.66	hypothetical protein
TGME49_314460	-7.78	-7.58	-8.49	hypothetical protein
TGME49_278770	-1.17	#N/A	-1.25	hypothetical protein
TGME49_307800	1.62	1.81	1.30	GDA1/CD39 (nucleoside phosphatase) family protein
TGME49_218280	-1.01	#N/A	-1.18	eukaryotic porin, putative
TGME49_259000	-7.78	-8.10	-8.11	hypothetical protein
TGME49_237110	-1.57	-1.68	-1.56	replication factor C subunit 2, putative
TGME49_261940	-7.78	-8.35	-8.16	hydrolase, alpha/beta fold family protein

FIGURE 4H

TGME49_293190	-2.94	-2.84	-3.24	endonuclease/exonuclease/phosphatase family protein
TGME49_253860	1.48	1.41	1.66	Tyrosine kinase-like (TKL) protein
TGME49_278050	-2.35	-2.32	-2.22	proteasome subunit alpha type 1, putative
TGME49_280490	-2.79	-3.83	-2.50	U-box domain-containing protein
TGME49_246580	-3.90	-3.68	-4.08	hypothetical protein
TGME49_232280	-9.84	-9.83	-9.89	hypothetical protein
TGME49_266070	1.16	1.25	#N/A	ribosomal protein RPL31
TGME49_271820	-9.72	-9.52	-8.87	lipoyltransferase and lipoate-protein ligase subfamily protein
TGME49_321690	-3.97	-3.66	-3.95	hypothetical protein
TGME49_227952	-2.77	-2.43	-2.49	14-3-3 superfamily protein
TGME49_293410	2.50	2.96	2.64	hypothetical protein
TGME49_212900	1.48	1.59	1.72	hypothetical protein
TGME49_313230	2.03	2.54	2.07	eukaryotic initiation factor-2, alpha subunit
TGME49_250330	-9.69	-9.74	-9.57	hypothetical protein
TGME49_294870	1.07	1.00	#N/A	universal stress family protein
TGME49_315530	-4.70	-4.61	-4.61	hypothetical protein
TGME49_267500	1.21	1.01	1.02	hypothetical protein
TGME49_205010	-2.30	-2.22	-2.55	U2 small nuclear ribonucleoprotein family protein, putative
TGME49_229020	-9.67	-9.96	-9.88	cell-cycle-associated protein kinase CDK, putative
TGME49_206690	-2.61	-2.42	-2.30	glideosome-associated protein with multiple-membrane spans GAPM2B
TGME49_268230	-9.94	-9.74	-10.16	hypothetical protein
TGME49_319370	-9.68	-9.43	-9.43	hypothetical protein
TGME49_293710	-2.10	-1.88	-1.65	Zn-finger in Ran binding protein and others domain-containing protein
TGME49_294690	1.74	1.96	1.64	rhomboid protease ROM5
TGME49_245510	-2.43	-2.58	-2.73	phospholipid-translocating P-type ATPase, flippase subfamily protein
TGME49_265390	-9.66	-9.76	-9.23	hypothetical protein
TGME49_213920	-3.43	-3.63	-3.03	hypothetical protein
TGME49_247360	2.42	2.39	2.19	PAP2 superfamily protein
TGME49_264830	-4.67	-4.61	-4.67	hypothetical protein
TGME49_202310	2.07	2.33	1.71	O-sialoglycoprotein endopeptidase
TGME49_234510	1.59	1.90	2.08	ankyrin repeat-containing protein
TGME49_290170	-2.49	-2.60	-2.51	kelch repeat domain containing/Serine/threonine protein phosphatase protein
TGME49_278940	1.78	1.80	1.40	HECT-domain (ubiquitin-transferase) domain-containing protein
TGME49_263230	-1.19	-1.17	#N/A	hypothetical protein
TGME49_223560	-2.58	-2.75	#N/A	hypothetical protein
TGME49_263210	-7.78	-8.59	-8.42	ubiquitin interaction motif domain-containing protein
TGME49_259650	-3.21	-2.79	#N/A	hypothetical protein
TGME49_252490	-1.96	-1.77	-2.36	vacuolar protein sorting 29, putative
TGME49_261780	1.11	1.08	#N/A	microneme protein MIC7
TGME49_254650	1.46	#N/A	#N/A	zinc finger protein
TGME49_256090	-7.77	-7.95	-8.16	glycerophosphodiester phosphodiesterase family protein
TGME49_228460	-1.69	-1.67	-1.50	hypothetical protein
TGME49_300130	1.76	1.92	3.11	apical membrane antigen 1 domain-containing protein
TGME49_271430	-3.16	-3.83	-3.18	hypothetical protein
TGME49_253800	-3.20	-3.15	-2.89	ribosomal protein L15, putative
TGME49_230150	1.31	#N/A	#N/A	ChAPs (Chs5p-Arf1p-binding proteins) protein
TGME49_277870	-1.80	-1.69	-2.06	hypothetical protein
TGME49_288930	-1.97	-2.41	-2.33	hypothetical protein
TGME49_222410	-1.36	-1.35	-1.18	hypothetical protein
TGME49_210960	-1.52	-1.20	-1.36	replication factor C subunit 4, putative
TGME49_225300	-1.58	-1.82	-1.76	hypothetical protein
TGME49_207160	-1.95	#N/A	4.41	SAG-related sequence SRS49D
TGME49_248445	-1.12	#N/A	#N/A	hypothetical protein
TGME49_236140	1.78	1.10	1.53	hypothetical protein
TGME49_290840	-1.41	-1.37	-1.05	serine protease
TGME49_230860	-1.96	-2.24	-2.33	hypothetical protein
TGME49_230050	1.49	1.74	1.85	50S ribosomal protein L3, putative
TGME49_248400	-1.77	-1.92	-1.92	glyoxalase I, putative
TGME49_254940	1.01	#N/A	#N/A	MIF4G domain-containing protein
TGME49_269800	-2.16	-1.93	-2.08	glutamine-dependent NAD(+) synthetase protein, putative
TGME49_205720	-7.77	-8.02	-7.98	Adenosine/AMP deaminase domain-containing protein
TGME49_221905	-1.03	#N/A	#N/A	hypothetical protein
TGME49_311380	-3.43	-3.97	#N/A	hypothetical protein
TGME49_218955	1.43	1.39	1.82	hypothetical protein
TGME49_225910	1.16	1.30	1.48	hypothetical protein
TGME49_283830	1.91	1.73	2.46	type I inorganic pyrophosphatase PPase

FIGURE 4i

TGME49_277720	-2.34	-2.24	-2.27	GDA1/CD39 (nucleoside phosphatase) family protein
TGME49_265110	-9.66	-9.30	-9.30	ribosome biogenesis protein, putative
TGME49_310030	-2.04	-2.06	-1.89	cyclase-associated protein, putative
TGME49_315100	4.95	3.08	#N/A	hypothetical protein
TGME49_254520	1.40	1.63	1.24	mediator complex subunit MED11
TGME49_212170	-9.63	-9.28	-9.18	GIY-YIG catalytic domain-containing protein
TGME49_265870	-3.46	-3.49	-3.80	pantoate-beta-alanine ligase
TGME49_213010	-4.86	-6.45	-4.64	hypothetical protein
TGME49_286460	3.16	2.96	5.01	hypothetical protein
TGME49_254410	1.95	1.74	1.12	protein phosphatase 2C, putative
TGME49_230410	-1.96	-2.13	-2.03	peroxiredoxin PRX3
TGME49_208020	2.18	3.67	4.25	AP2 domain transcription factor AP2lb-1
TGME49_313290	1.71	1.62	1.19	MORN repeat-containing protein
TGME49_309990	4.23	2.22	3.23	hypothetical protein
TGME49_315780	-3.14	-3.15	-3.31	myosin regulatory light chain, putative
TGME49_289370	1.70	#N/A	#N/A	hypothetical protein
TGME49_224880	-3.47	-4.06	-3.34	kinesin motor domain-containing protein
TGME49_240870	-2.71	-2.54	-2.88	beta adaptin protein, putative
TGME49_277940	-3.85	-4.02	-4.03	hypothetical protein
TGME49_252880	-2.57	-2.76	-2.78	hypothetical protein
TGME49_254050	1.64	1.81	1.82	optic atrophy 3 protein (opa3) protein
TGME49_239590	-4.66	-4.32	-4.54	WD domain, G-beta repeat-containing protein
TGME49_237550	2.81	2.61	2.49	hypothetical protein
TGME49_258150	-1.92	-1.69	-2.22	proteasome subunit alpha type 7, putative
TGME49_297745	-4.27	-4.28	-4.07	hypothetical protein
TGME49_239270	-2.16	-1.73	-1.16	hypothetical protein
TGME49_281400	-3.21	-2.67	-2.25	phosphofructokinase domain-containing protein
TGME49_318660	1.26	1.66	1.29	PP2C, putative
TGME49_305060	1.48	1.38	#N/A	CAP-Gly domain-containing protein
TGME49_262970	1.65	#N/A	#N/A	hypothetical protein
TGME49_229690	-9.57	-9.70	-10.43	autophagy-related protein 7 atg7, putative
TGME49_214575	2.05	1.73	2.55	hypothetical protein
TGME49_229470	-4.65	-4.34	-4.47	hypothetical protein
TGME49_251440	-9.71	-9.06	-8.69	ironinon c, isotype gamma, putative
TGME49_226705	-9.69	-9.73	-10.02	hypothetical protein

TGME49_213370	1.08	1.00	1.33	formin FRM3
TGME49_202230	-1.55	#N/A	-1.18	histone deacetylase HDAC5
TGME49_217560	1.08	1.18	#N/A	DNA-directed RNA polymerase II RPB10
TGME49_257755	1.96	2.33	#N/A	hypothetical protein
TGME49_266320	1.01	#N/A	#N/A	hypothetical protein
TGME49_309070	1.76	1.63	1.55	hypothetical protein
TGME49_234470	-1.77	-1.36	-1.48	hypothetical protein
TGME49_258380	-2.16	-2.01	-1.84	elongation factor p (ef-p) kow family domain-containing protein
TGME49_289510	1.23	1.20	1.58	hypothetical protein
TGME49_202350	-1.77	-1.53	-1.39	50S ribosomal protein L21, putative
TGME49_253540	1.43	1.51	1.31	hypothetical protein
TGME49_215030	-1.93	-2.16	-1.70	hypothetical protein
TGME49_212800	-1.42	-1.35	-1.48	hypothetical protein
TGME49_248630	-1.49	-1.39	-1.79	actin-related protein ARP1
TGME49_264450	-1.93	-1.93	-2.01	DNA topoisomerase III beta-1, putative
TGME49_217450	1.47	1.95	2.11	general transcription factor IIH polypeptide 5 GTF2H5
TGME49_213890	-7.79	-8.58	-8.36	Myb family DNA-binding domain-containing protein
TGME49_293060	-1.68	-1.75	-1.81	SPRY domain-containing protein
TGME49_276190	-2.20	-1.91	-2.20	hypothetical protein
TGME49_286180	-7.70	-8.73	-7.84	tRNA ligases class I (M) protein
TGME49_239300	-1.55	-1.58	-1.69	hypothetical protein
TGME49_273595	-1.66	-1.64	#N/A	hypothetical protein
TGME49_278170	-2.17	-1.69	-1.90	hypothetical protein
TGME49_294360	-1.32	#N/A	-1.28	ubiquitin specific protease 39 isoform 2, putative
TGME49_309920	-3.12	-3.37	-3.29	hypothetical protein
TGME49_311740	-2.16	-1.98	-1.75	hypothetical protein
TGME49_288710	1.43	1.75	1.81	hypothetical protein
TGME49_230830	1.48	#N/A	4.39	ATPase family associated with various cellular activities (AAA) domain-containing protein
TGME49_265070	-2.50	-2.53	-2.87	hypothetical protein
TGME49_227860	-7.70	-8.26	-8.00	hypothetical protein
TGME49_248110	1.24	1.41	#N/A	hypothetical protein
TGME49_297690	1.18	1.33	#N/A	hypothetical protein
TGME49_209950	-1.12	#N/A	-1.25	thioredoxin, putative
TGME49_244570	-7.71	-8.31	-8.04	hypothetical protein
TGME49_270760	-7.72	-8.29	-7.99	asparagine synthase

FIGURE 4J

TGME49_246490	-2.25	-2.01	-2.68	hypothetical protein
TGME49_220880	1.93	2.15	1.87	hypothetical protein
TGME49_225580	-9.55	-9.25	-9.25	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9, putative
TGME49_209060	-3.78	-3.86	-3.82	thrombospondin type 1 domain-containing protein
TGME49_265790	1.15	1.22	#N/A	hypothetical protein
TGME49_215590	-1.91	-1.78	-2.03	flavoprotein subunit of succinate dehydrogenase
TGME49_247960	2.06	2.01	1.46	hypothetical protein
TGME49_214140	1.26	1.33	1.35	hypothetical protein
TGME49_218560	-1.88	-1.73	-2.00	acetyl-coA carboxylase ACC2
TGME49_214230	1.64	1.80	1.24	Dopey, N-terminal domain-containing protein
TGME49_254370	-1.66	-1.59	-1.54	guanylyl cyclase
TGME49_260180	-1.99	-2.09	-2.13	hypothetical protein
TGME49_203830	-3.79	-3.78	-2.97	FHA domain-containing protein
TGME49_265500	-9.53	-9.38	-9.34	chloride transporter, chloride channel (ClC) family protein
TGME49_219730	1.55	1.51	1.33	hypothetical protein
TGME49_272010	-4.60	-3.93	-4.20	Gar1 protein RNA binding region protein
TGME49_254220	2.33	2.34	2.22	hypothetical protein
TGME49_237890	-4.58	-4.49	-3.76	calcium-dependent protein kinase CDPK4
TGME49_218362	-2.67	-2.55	-2.30	zinc finger protein ZFP1
TGME49_209440	-2.15	-2.34	-1.70	hypothetical protein
TGME49_232710	-1.08	#N/A	-1.01	ribosomal protein RPS3A
TGME49_222860	-1.58	-1.30	-1.33	eukaryotic translation initiation factor, putative
TGME49_274190	-4.63	-4.60	-4.96	eukaryotic initiation factor 2B epsilon subunit, putative
TGME49_248260	2.20	2.78	1.66	hypothetical protein
TGME49_254030	2.15	2.17	1.86	zinc finger CDGSH-type domain-containing protein
TGME49_295080	-9.53	-9.17	-8.87	hypothetical protein
TGME49_267620	-3.12	-2.52	-2.90	multi-pass transmembrane protein
TGME49_246570	2.72	2.11	1.56	hypothetical protein
TGME49_231150	2.64	3.03	2.83	hypothetical protein
TGME49_211250	-3.07	-2.84	-3.09	hypothetical protein
TGME49_231950	1.86	1.71	#N/A	hypothetical protein
TGME49_289300	-2.17	-1.85	-2.10	methionyl-tRNA synthetase
TGME49_205360	-2.51	-2.34	-2.57	hypothetical protein
TGME49_251170	2.93	2.39	2.43	KRUF family protein
TGME49_209120	1.31	1.35	#N/A	hypothetical protein
TGME49_309880	-1.33	-1.14	-1.04	hypothetical protein
TGME49_265460	1.09	1.37	1.18	hypothetical protein
TGME49_263505	-3.14	-3.18	-3.14	hypothetical protein
TGME49_294060	-1.05	-1.03	#N/A	hypothetical protein
TGME49_249870	-1.27	#N/A	#N/A	hypothetical protein
TGME49_271240	-2.48	-2.26	-1.91	hypothetical protein
TGME49_271990	1.28	#N/A	1.10	hypothetical protein
TGME49_242810	-3.14	-3.25	-3.27	hypothetical protein
TGME49_280450	-7.69	-8.54	-7.80	hypothetical protein
TGME49_288860	-2.73	-5.22	-2.93	RuvB family 2 protein
TGME49_214990	-1.75	-1.36	#N/A	hypothetical protein
TGME49_221390	-1.75	-1.78	-1.59	hypothetical protein
TGME49_305800	-1.75	-1.54	-1.83	6-pyruvoyl tetrahydrobiopterin synthase
TGME49_294730	-1.50	-1.46	-1.19	hypothetical protein
TGME49_263480	-1.46	#N/A	#N/A	sodium/hydrogen exchanger 3 protein
TGME49_201800	-1.16	-1.08	-1.91	hypothetical protein
TGME49_269770	-2.48	-2.73	-2.69	WD domain, G-beta repeat-containing protein
TGME49_213040	-1.54	-1.55	-1.45	hypothetical protein
TGME49_308090	1.09	#N/A	1.26	rhoGTP protein ROP5
TGME49_235880	1.02	1.06	#N/A	brain protein 44 family protein
TGME49_258970	1.01	#N/A	#N/A	hypothetical protein
TGME49_286270	-1.54	-2.25	-1.67	hypothetical protein
TGME49_263190	-3.12	-2.61	-2.46	adenylosuccinate lyase, putative
TGME49_227300	1.82	#N/A	1.91	hypothetical protein
TGME49_304750	-2.13	-2.09	#N/A	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_232630	-1.10	#N/A	#N/A	hypothetical protein
TGME49_301170	-7.68	-10.53	-7.53	SAG-related sequence SRS19D
TGME49_220440	-1.93	-2.04	-2.07	cyclin-dependent kinase regulatory subunit protein
TGME49_265650	-3.11	-3.43	-3.16	protein phosphatase 2C domain-containing protein
TGME49_234420	-1.37	#N/A	#N/A	ATPase, AAA family protein
TGME49_214400	-2.45	-2.07	-1.96	hypothetical protein
TGME49_272730	1.81	#N/A	3.75	hypothetical protein
TGME49_245710	-1.15	#N/A	-1.51	phosphatidylinositol-4-phosphate 5-kinase, putative

FIGURE 4K

TGME49_276970	-3.33	-3.38	-3.19	hypothetical protein
TGME49_269660	-2.64	-2.22	-2.16	TFIIH basal transcription factor complex helicase XPB subunit
TGME49_252390	1.43	#N/A	1.12	hypothetical protein
TGME49_266750	-1.78	-1.29	-1.53	transporter/permease protein, putative
TGME49_221675	1.34	1.45	1.46	hypothetical protein
TGME49_266990	-1.79	-1.44	-1.94	beta-COP
TGME49_312110	-2.50	-2.43	-2.32	apicoplast-associated thioredoxin family protein Atrx1
TGME49_268176	-2.82	-2.90	-3.25	hypothetical protein
TGME49_237170	-3.09	#N/A	-1.72	hypothetical protein
TGME49_238100	-2.33	-2.04	-2.61	transmembrane protein
TGME49_254730	1.89	2.31	2.50	POPLD (NUC188) domain-containing protein
TGME49_235020	-1.87	-1.55	-1.75	COP1 protein, putative
TGME49_262150	-9.48	-9.22	-9.42	kelch repeat and K+ channel tetramerisation domain containing protein
TGME49_295990	1.50	1.76	1.59	ubiquitin conjugating enzyme E2, putative
TGME49_249530	-1.80	-1.59	-1.77	exportin 1, putative
TGME49_319880	-4.52	-4.75	-4.00	MORN repeat-containing protein
TGME49_283540	1.64	2.10	1.14	hypothetical protein
TGME49_229420	-9.48	-9.23	-9.54	cytochrome c, putative
TGME49_310460	-2.85	-2.51	-3.13	Rab6
TGME49_204520	2.74	2.76	3.39	hypothetical protein
TGME49_222710	-2.82	-2.47	-2.64	IMP-specific 5'-nucleotidase 1, putative
TGME49_213660	-1.51	-1.12	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_202470	-9.48	-9.34	-8.80	rRNA metabolism protein, SBDS family protein
TGME49_290980	-2.82	-2.49	-2.32	glycine C-acetyltransferase, putative
TGME49_263550	1.66	1.82	1.76	39S ribosomal protein L47, mitochondrial precursor, putative
TGME49_219080	-9.48	-9.43	-9.29	edge expressed protein, putative
TGME49_293740	1.80	1.93	1.56	hypothetical protein
TGME49_263490	2.11	2.29	2.10	ubiquitin conjugating enzyme E2, putative
TGME49_219810	1.87	1.50	1.25	hypothetical protein
TGME49_205040	-1.79	-1.55	-1.73	PGAP1 family protein
TGME49_270770	-4.56	-4.45	-4.53	PWI domain-containing protein
TGME49_208722	-3.11	-3.32	-3.48	hypothetical protein
TGME49_217760	1.21	1.31	#N/A	GTP-binding protein
TGME49_231930	-3.15	-2.67	-2.46	hypothetical protein
TGME49_214530	-1.60	-2.02	#N/A	DnaJ domain-containing protein
TGME49_225110	1.03	1.07	#N/A	AP2 domain transcription factor AP2X-2
TGME49_216580	-1.64	-1.43	-1.57	hypothetical protein
TGME49_248370	1.14	1.74	1.12	prefoldin subunit 6, putative
TGME49_259600	-1.75	-1.56	#N/A	hypothetical protein
TGME49_254610	1.77	1.73	1.59	Tim10/DDP family zinc finger superfamily protein
TGME49_223480	-7.62	-8.02	-10.14	sushi domain (scr repeat) domain-containing protein
TGME49_319720	-3.13	-3.43	-2.96	hypothetical protein
TGME49_258930	-2.46	#N/A	#N/A	peptidylprolyl isomerase
TGME49_316520	-1.37	-1.13	-1.32	1,4-alpha-glucan-branching enzyme
TGME49_209170	-1.18	#N/A	-1.29	hypothetical protein
TGME49_329800	-1.37	-1.74	-2.18	hypothetical protein
TGME49_270370	-2.18	-2.01	-2.15	clathrin assembly protein AP19, putative
TGME49_218230	-1.72	#N/A	-1.33	histone lysine methyltransferase, SET, putative
TGME49_220330	-3.14	-4.05	-2.44	hypothetical protein
TGME49_212930	1.81	2.47	1.87	NifU family domain-containing protein
TGME49_291690	-3.07	-3.21	-3.09	hypothetical protein
TGME49_200430	-7.63	-8.32	-8.30	cytidine and deoxycytidylate deaminase zinc-binding region domain-containing protein
TGME49_208070	-1.14	#N/A	#N/A	inositol polyphosphate kinase
TGME49_301310	1.75	#N/A	#N/A	hypothetical protein
TGME49_266800	-1.61	-1.65	-1.94	integral membrane protein, putative
TGME49_224670	-1.87	-2.14	-1.89	DnaJ domain-containing protein
TGME49_245650	1.82	2.51	2.08	hypothetical protein
TGME49_294190	-3.07	-3.66	-2.87	enoyl-CoA hydratase/isomerase family protein
TGME49_225920	-2.09	-2.52	-2.30	hypothetical protein
TGME49_232210	-7.62	-8.23	-8.74	hypothetical protein
TGME49_247670	-2.15	#N/A	-2.02	ribulose-phosphate 3 epimerase family protein
TGME49_263730	-1.72	-2.70	-1.92	FAD-dependent glycerol-3-phosphate dehydrogenase

FIGURE 4L

TGME49_213067	1.34	1.18	#N/A	hypothetical protein
TGME49_237015	1.45	1.75	1.50	hypothetical protein
TGME49_280730	-9.46	-9.23	-8.90	cytosolic fe-s cluster assembling factor nbp35, putative
TGME49_227420	-9.48	-9.15	-9.24	4-hydroxy-3-methylbut-2-enyl diphosphate reductase
TGME49_310220	-4.57	-4.80	-4.55	hypothetical protein
TGME49_318400	-2.00	-1.56	-1.30	hypothetical protein
TGME49_257520	1.53	1.64	1.11	synaptobrevin protein
TGME49_226220	-2.77	-2.58	-2.89	alveolin domain containing intermediate filament IMC9
TGME49_244910	-3.71	-4.10	-4.11	MLZ/SP-RING zinc finger domain-containing protein
TGME49_309380	-3.25	-3.07	-3.21	Nur2
TGME49_274110	-9.43	-8.93	-8.80	glycoprotease family protein
TGME49_225250	2.04	1.74	1.93	LSU ribosomal protein L14P, putative
TGME49_223010	-3.26	-2.84	-3.05	hypothetical protein
TGME49_278720	-9.47	-9.16	-8.84	hypothetical protein
TGME49_320130	1.97	1.91	2.02	hypothetical protein
TGME49_267690	-4.49	-4.44	-3.85	hypothetical protein
TGME49_222930	-2.77	-2.69	-2.32	hypothetical protein
TGME49_297800	-3.02	-2.72	-2.56	RecF/RecN/SMC N terminal domain-containing protein
TGME49_203730	-9.41	-9.21	-9.23	hypothetical protein
TGME49_226910	-4.49	-4.89	-4.34	Amylo-alpha-1,6-glucosidase
TGME49_266410	1.84	1.99	1.53	hypothetical protein
TGME49_292130	-1.14	-1.30	-1.31	ribosomal protein RPL13A
TGME49_289730	-2.34	-2.12	-2.27	Pep3/Vps18/deep orange family protein
TGME49_201870	-2.79	-2.12	-2.21	tetratricopeptide repeat-containing protein
TGME49_216020	-9.41	-9.29	-9.61	peptidase family c78 protein
TGME49_313445	2.13	1.67	2.08	hypothetical protein
TGME49_225990	-3.24	-2.75	-2.62	acyl transferase domain-containing protein
TGME49_240860	-3.69	-3.68	-3.67	acyltransferase domain-containing protein
TGME49_285140	-9.42	-10.00	-9.49	hypothetical protein
TGME49_319580	-9.39	-9.39	-9.35	hypothetical protein
TGME49_247580	-9.41	-9.25	-9.15	glutaredoxin domain-containing protein
TGME49_253470	1.68	1.71	1.58	alveolin domain containing intermediate filament IMC13
TGME49_246100	-2.64	-2.24	-2.29	phosducin, putative
TGME49_232270	-7.62	-9.16	-9.76	histidine acid phosphatase superfamily protein
TGME49_315670	-1.18	#N/A	-1.26	HEAT repeat-containing protein
TGME49_262000	-3.11	-2.84	#N/A	AP2 domain transcription factor AP2Vlib-2
TGME49_273550	-3.06	-3.34	-3.42	hypothetical protein
TGME49_249600	-7.61	-7.86	-8.35	hypothetical protein
TGME49_232530	-2.09	-2.03	-1.66	hypothetical protein
TGME49_309780	-1.87	-1.66	#N/A	hypothetical protein
TGME49_286010	1.27	1.40	#N/A	hypothetical protein
TGME49_218830	1.45	#N/A	1.57	hypothetical protein
TGME49_281450	-2.45	-2.60	-2.46	cell-cycle-associated protein kinase, putative
TGME49_222160	-3.06	-3.52	#N/A	aldehyde dehydrogenase
TGME49_233540	-3.16	-3.25	-3.17	transporter, major facilitator family protein
TGME49_252400	2.27	2.06	2.94	HIT zinc finger protein
TGME49_221170	-1.08	#N/A	-1.40	CAAX metallo endopeptidase
TGME49_238940	1.86	2.31	1.18	GDP mannose 4,6-dehydratase, putative
TGME49_224490	-3.09	-3.25	-2.80	polyprenyl synthetase superfamily protein
TGME49_287980	-1.59	-1.59	-1.58	FHA domain-containing protein
TGME49_251920	1.40	1.67	2.09	hypothetical protein
TGME49_211650	-1.30	#N/A	#N/A	hypothetical protein
TGME49_251620	1.03	#N/A	#N/A	flap structure-specific endonuclease 1, putative
TGME49_221922	-3.06	-3.47	-3.32	NifU family domain-containing protein
TGME49_272550	-1.17	-1.18	#N/A	hypothetical protein
TGME49_271440	-2.41	-2.42	-2.60	NPL4 family protein
TGME49_272710	1.08	#N/A	#N/A	AP2 domain transcription factor AP2Vlib-4
TGME49_297330	1.28	1.06	1.08	hypothetical protein
TGME49_288460	-1.07	-1.02	#N/A	hypothetical protein
TGME49_293310	1.04	1.21	#N/A	ribosomal protein L20, putative
TGME49_258650	-2.41	-2.21	-1.90	protoheme ferro-lyase, putative
TGME49_252270	1.74	#N/A	1.90	L1P family of ribosomal protein
TGME49_314030	1.88	1.86	1.50	hypothetical protein
TGME49_206300	-2.41	-2.18	-1.99	hypothetical protein
TGME49_315360	-1.30	-1.25	-1.35	hypothetical protein
TGME49_258990	-2.40	-2.65	-2.61	bromodomain-containing protein

FIGURE 4M

TGME49_270930	-3.02	-3.19	-3.08	hypothetical protein
TGME49_241240	1.03	#N/A	#N/A	hypothetical protein
TGME49_294940	1.69	1.57	1.46	hypothetical protein
TGME49_226500	-4.54	-4.91	-4.82	hypothetical protein
TGME49_226430	-1.44	-1.36	-1.31	reticulin protein
TGME49_299250	2.72	2.76	2.79	hypothetical protein
TGME49_288820	1.59	1.34	1.67	hypothetical protein
TGME49_247760	-2.95	-2.70	-3.35	AMP-binding enzyme domain-containing protein
TGME49_311720	-1.01	#N/A	-1.30	chaperonin protein BiP
TGME49_306660	1.31	1.30	1.73	RNA pseudouridine synthase superfamily protein
TGME49_254000	1.44	1.26	1.37	hypothetical protein
TGME49_233140	-2.54	-2.06	-2.48	deoxyuridine 5'-triphosphate nucleotidohydrolase, putative
TGME49_280400	-9.41	-12.29	-9.61	hypothetical protein
TGME49_290160	-1.66	-1.61	-1.68	sortilin, putative
TGME49_271470	-4.41	-4.36	-3.99	hypothetical protein
TGME49_214960	1.60	1.61	1.13	AP2 domain transcription factor AP2X-8
TGME49_202920	-9.36	-9.54	-9.53	p-aminobenzoic acid synthase
TGME49_309590	1.01	#N/A	#N/A	rhopty protein ROP1
TGME49_270270	-3.68	-3.76	-4.08	hypothetical protein
TGME49_271810	-1.62	-1.16	-1.39	lanp, putative
TGME49_286260	-9.33	-9.40	-8.89	tetratricopeptide repeat-containing protein
TGME49_216770	-4.44	-4.35	-3.45	hypothetical protein
TGME49_205750	-2.90	-2.41	-2.43	histone deacetylase complex subunit Sin3
TGME49_201400	-4.43	-4.23	-4.47	Sin3-associated polypeptide SAP18
TGME49_273905	-4.39	-3.86	-4.37	hypothetical protein
TGME49_249360	-2.40	-2.22	-2.24	RED family protein
TGME49_310450	-2.42	-2.75	-2.34	myosin heavy chain, putative
TGME49_248860	2.36	1.77	1.66	hypothetical protein
TGME49_222400	1.21	1.64	1.08	hypothetical protein
TGME49_313880	-9.36	-8.94	-9.55	nuclear protein-like family protein
TGME49_247220	1.32	1.11	#N/A	nudix -type motif 9 isoform a family protein
TGME49_246930	-2.21	-2.30	-2.33	calmodulin CAM1
TGME49_259710	-2.95	-3.08	-3.61	protein kinase
TGME49_313380	-1.15	-1.15	-1.25	hypothetical protein
TGME49_249380	1.18	1.58	1.41	DHHC zinc finger domain-containing protein
TGME49_257990	-1.24	-1.50	-1.53	heat shock protein 101, putative
TGME49_269075	-7.64	-8.96	-8.49	hypothetical protein
TGME49_202730	-2.08	-1.96	-1.71	hypothetical protein
TGME49_246978	-3.01	-3.26	-2.93	hypothetical protein
TGME49_312220	-3.02	-3.23	-3.50	mitochondrial inner membrane translocase subunit TIM17, putative
TGME49_250090	1.08	#N/A	1.00	hypothetical protein
TGME49_221460	-1.18	#N/A	-1.54	phosphoglycerate mutase family protein
TGME49_243390	-2.40	-2.76	-2.56	hypothetical protein
TGME49_272720	-1.85	-1.84	#N/A	methyltransferase domain-containing protein
TGME49_288010	1.77	3.19	2.59	hypothetical protein
TGME49_246040	-1.56	-1.69	-1.87	MIF4G domain-containing protein
TGME49_240710	-1.49	-1.70	-1.71	RNA recognition motif-containing protein
TGME49_274000	-2.06	-2.41	-2.90	hypothetical protein
TGME49_240800	-1.41	-2.11	-2.22	MORN repeat-containing protein
TGME49_264820	1.31	#N/A	1.45	RbAp48
TGME49_243350	1.47	#N/A	#N/A	gamma-glutamyl hydrolase
TGME49_276130	1.13	#N/A	#N/A	cathepsin CPC2
TGME49_246690	-2.05	-1.83	-1.66	alpha amylase, catalytic domain-containing protein
TGME49_308940	-7.53	-8.29	-8.39	hypothetical protein
TGME49_209140	-1.16	-1.15	-1.18	anti-silencing protein, ASF1 family protein
TGME49_313300	1.14	1.35	1.28	YL1 nuclear protein C-terminal domain-containing protein
TGME49_263150	-7.53	-8.28	-8.57	tetratricopeptide repeat-containing protein
TGME49_227640	-1.39	#N/A	#N/A	hypothetical protein
TGME49_231940	-1.43	-1.13	-1.63	ThiF family protein
TGME49_300010	-7.54	-8.20	-8.38	hypothetical protein
TGME49_249850	-1.57	-1.52	-1.83	GAP40 protein
TGME49_266930	1.35	1.45	1.09	general transcription factor IIH polypeptide 3 GTF2H3
TGME49_253820	1.02	1.03	#N/A	hypothetical protein
TGME49_229720	-2.36	-3.02	#N/A	hypothetical protein
TGME49_270330	1.28	1.56	1.39	cell-cycle-associated protein kinase, putative
TGME49_312360	-3.00	-2.81	-2.92	hypothetical protein
TGME49_311260	-1.07	#N/A	#N/A	myosin light chain MLC1, putative
TGME49_277090	2.01	2.17	2.09	carrier superfamily protein

FIGURE 4N

TGME49_214200	-9.38	-9.55	-9.04	WD domain, G-beta repeat-containing protein
TGME49_243930	1.38	1.31	#N/A	hypothetical protein
TGME49_215420	-9.31	-8.88	-9.16	SNARE protein
TGME49_311680	-1.89	-1.73	-1.45	FUN14 family protein
TGME49_259200	-4.39	-4.23	-3.90	Na ⁺ /H ⁺ exchanger NHE1
TGME49_268580	-4.42	-3.87	-4.26	hypothetical protein
TGME49_269450	2.62	1.94	2.15	hypothetical protein
TGME49_266450	1.76	1.31	1.34	lysine decarboxylase family protein
TGME49_288360	-1.46	-1.31	-3.81	tryptophanyl-tRNA synthetase (TrpRS2)
TGME49_261480	1.77	1.95	1.76	phosphatidyl serine synthase
TGME49_210245	-9.40	-9.73	#N/A	hypothetical protein
TGME49_288400	-9.31	-9.50	-9.50	LETM1 family protein
TGME49_226810	-3.20	-3.51	-3.47	histone lysine methyltransferase SET1
TGME49_239800	-2.88	-3.25	-3.12	hypothetical protein
TGME49_270550	-9.37	-9.05	-9.15	gamma-glutamyl phosphate reductase, putative
TGME49_249250	1.28	1.13	1.14	ribosomal protein RPL35A
TGME49_207880	-9.44	-9.56	-10.92	hypothetical protein
TGME49_269920	-1.46	-1.18	-1.47	phosphatidylserine decarboxylase
TGME49_278815	-3.62	-3.98	-3.71	hypothetical protein
TGME49_207690	-4.37	-4.30	-4.73	programmed cell death 5 protein
TGME49_203720	2.55	3.14	1.89	vitamin k epoxide reductase family protein
TGME49_237500	1.34	1.01	#N/A	protein phosphatase 2C domain-containing protein
TGME49_320090	-3.11	-2.61	-2.20	hypothetical protein
TGME49_286630	-1.68	-1.41	-1.63	redoxin domain-containing protein
TGME49_257380	1.16	1.09	#N/A	hypothetical protein
TGME49_225050	-1.78	-1.53	-1.56	adenosylhomocysteinase, putative
TGME49_305980	-2.30	-2.23	-2.14	pyruvate dehydrogenase complex subunit PDH-E3I
TGME49_289600	1.41	#N/A	#N/A	heat shock protein HSP29
TGME49_223760	-9.25	-9.33	-9.63	hypothetical protein
TGME49_289050	1.24	1.02	#N/A	FIKK kinase, putative
TGME49_213060	1.66	1.34	1.91	WD domain, G-beta repeat-containing protein
TGME49_269690	1.26	1.49	#N/A	hypothetical protein

TGME49_277010	-7.53	-8.00	-8.62	Fe-S metabolism associated domain-containing protein
TGME49_260840	-3.00	-3.08	-2.63	hypothetical protein
TGME49_236580	-1.27	#N/A	-1.15	Prp31-15.5k-U4 SnRna Complex family protein
TGME49_256920	1.51	1.22	#N/A	phosphatidylinositol-4-phosphate 5-Kinase
TGME49_241170	-1.12	-1.21	#N/A	hypothetical protein
TGME49_248200	1.30	1.03	#N/A	ribosomal RNA (adenine(1779)-N(6)/adenine(1780)-N(6))-dimethyltransferase, putative
TGME49_226420	-1.21	-1.59	-1.98	peptidase family M3 protein
TGME49_221870	1.26	1.23	#N/A	hypothetical protein
TGME49_202480	-2.96	-3.07	-3.28	hypothetical protein
TGME49_228380	3.13	2.35	2.83	hypothetical protein
TGME49_305190	1.02	#N/A	#N/A	CorA family Mg2+ transporter protein
TGME49_213870	-1.14	-1.13	-1.72	UBA/TS-N domain-containing protein
TGME49_311750	1.96	#N/A	1.92	mago binding protein
TGME49_220160	-2.96	-3.23	-2.94	WD domain-containing protein
TGME49_235610	-2.96	-3.11	-3.19	ATPase, AAA family protein
TGME49_280522	-1.16	-1.27	-1.47	hypothetical protein
TGME49_244860	1.40	1.46	1.42	hypothetical protein
TGME49_315640	1.32	1.67	1.35	lipoyl(octanoyl) transferase
TGME49_294860	-1.54	-1.71	-1.68	hypothetical protein
TGME49_215480	-1.81	-1.74	-1.40	Adenosine/AMP deaminase domain-containing protein
TGME49_285880	1.58	1.31	#N/A	hypothetical protein
TGME49_260150	1.60	#N/A	1.15	tetratricopeptide repeat-containing protein
TGME49_314530	-3.00	-3.48	-2.77	RPAP1 family, C-terminal protein
TGME49_277820	-2.36	-2.43	-2.05	hypothetical protein
TGME49_310660	-2.96	-3.08	-3.40	Dillard family phosphatase domain-containing protein
TGME49_250060	1.45	1.17	#N/A	DNA-directed RNA polymerase I RPA12
TGME49_306020	-1.44	-1.68	-1.31	hypothetical protein
TGME49_319710	-1.38	-1.36	-1.07	kinesin motor domain-containing protein
TGME49_205240	-1.13	-1.20	#N/A	cleft lip and palate transmembrane protein 1 (clptm1) protein
TGME49_203710	-1.14	-1.16	#N/A	AP2 domain transcription factor AP2Vlla-4
TGME49_285700	-2.99	-2.83	#N/A	ubiquitin fusion degradation protein UFD1AP
TGME49_306510	1.91	1.82	3.54	hypothetical protein

FIGURE 4o

TGME49_228750	-3.59	-3.68	-3.53	TGME49_228750 CAM kinase, RAD family
TGME49_315250	-4.35	-3.92	-4.09	GAMM1 protein, putative
TGME49_320490	1.85	1.62	2.04	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D family protein
TGME49_312300	-1.87	-1.75	-1.71	Sec7 domain-containing protein
TGME49_260670	-9.26	-9.06	-9.55	centrin, putative
TGME49_273815	-9.34	-8.57	-8.62	hypothetical protein
TGME49_299200	1.77	1.45	1.21	Bet3 transport protein, putative
TGME49_236250	2.11	1.47	2.02	regulator of chromosome condensation (RCC1) repeat-containing protein
TGME49_204310	-1.40	-1.36	-1.56	hypothetical protein
TGME49_292160	1.77	1.89	1.97	hypothetical protein
TGME49_234980	1.96	1.83	1.94	hypothetical protein
TGME49_215390	2.45	2.61	3.43	TIM10 family protein, putative
TGME49_291940	-4.30	-4.60	-4.65	hypothetical protein
TGME49_234390	-9.29	-8.59	-8.45	hypothetical protein
TGME49_289580	-9.23	-9.72	-9.34	strictosidine synthase subfamily protein
TGME49_205510	-1.74	-1.43	-1.74	nucleolar protein 5, putative
TGME49_224540	-9.38	-9.79	-9.10	hypothetical protein
TGME49_284190	-3.70	-4.12	-3.49	pyruvate carboxylase
TGME49_227060	-9.25	-9.07	-9.03	hypothetical protein
TGME49_221720	-4.62	-4.67	-4.40	hypothetical protein
TGME49_238200	1.96	#N/A	#N/A	alpha/beta hydrolase fold domain-containing protein
TGME49_304460	-1.70	-1.44	-1.05	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_205540	-9.24	-9.08	-8.65	DEAD/DEAH box helicase domain-containing protein
TGME49_269650	-1.97	-1.61	-1.46	FFD and TFG box motifs protein
TGME49_320588	-9.23	-10.06	-9.75	glycosyl hydrolases family 35 protein
TGME49_320640	-9.26	-9.58	-9.58	peptidylprolyl isomerase domain-containing protein
TGME49_265010	-9.20	-8.94	-8.88	glutamate 5-kinase domain-containing protein
TGME49_314540	-9.20	-8.99	-9.02	hypothetical protein
TGME49_204420	3.59	3.11	2.28	oocyst wall protein OWP1
TGME49_263630	1.20	1.32	1.13	hypothetical protein
TGME49_288945	-2.45	-1.50	-1.45	hypothetical protein
TGME49_204100	-1.27	#N/A	-1.49	eIF2 kinase IIF2K-C
TGME49_271170	-2.95	-3.53	-3.28	dolichol kinase
TGME49_244140	-3.04	-3.04	#N/A	hypothetical protein
TGME49_319930	-1.25	-1.28	#N/A	hypothetical protein
TGME49_277490	1.04	1.26	#N/A	hypothetical protein
TGME49_219750	1.10	#N/A	#N/A	cytochrome c, putative
TGME49_315190	-1.06	-1.13	#N/A	CAM kinase, SNF1 family
TGME49_226060	1.15	1.40	1.29	transmembrane amino acid transporter protein
TGME49_311390	1.35	2.33	2.33	tRNA (guanine(9)-N(1))-methyltransferase
TGME49_235905	-2.32	-2.10	-2.00	ribonuclease z, putative
TGME49_319320	-1.38	-1.77	-1.36	hypothetical protein
TGME49_270670	1.17	2.08	3.19	hypothetical protein
TGME49_240430	1.18	1.11	1.39	glyoxalase family protein
TGME49_315920	-2.01	#N/A	-1.75	DNA-directed RNA polymerase II RPB11A
TGME49_310210	1.03	#N/A	1.01	hypothetical protein
TGME49_203050	1.92	1.88	1.66	AP2 domain transcription factor AP2Vila-6
TGME49_237195	1.68	#N/A	#N/A	hypothetical protein
TGME49_320690	-1.64	-1.29	-1.59	gamma-soluble NSF attachment protein, putative
TGME49_309940	-1.54	-1.30	-1.26	phospholipase D active site domain-containing protein
TGME49_246178	-1.78	-2.02	-1.91	hypothetical protein
TGME49_212100	-7.44	-9.12	-7.23	ThiF family protein
TGME49_203480	-2.97	-3.25	-3.09	hypothetical protein
TGME49_295460	1.07	#N/A	#N/A	Got1 family protein
TGME49_291350	-2.95	-3.01	-3.06	hypothetical protein
TGME49_240090	1.51	1.67	#N/A	rhoGTPase family protein ROP34, putative
TGME49_257960	-2.32	-2.82	-3.03	GDP-D-mannose pyrophosphorylase
TGME49_315910	1.03	1.65	1.00	hypothetical protein
TGME49_221518	-1.84	#N/A	#N/A	hypothetical protein
TGME49_242320	-1.23	-1.15	-1.31	B-box zinc finger domain-containing protein
TGME49_295980	-1.65	-1.62	-1.93	hypothetical protein
TGME49_215940	-1.29	-1.15	-1.37	Acetyl-coenzyme A transporter, putative

FIGURE 4P

TGME49_240570	-2.67	-2.74	-2.61	hypothetical protein
TGME49_249590	-1.74	-1.64	-1.85	proteasome subunit alpha type 5-2, putative
TGME49_216430	-1.75	-1.88	-1.58	TBC domain-containing protein
TGME49_282000	1.79	1.99	1.43	hypothetical protein
TGME49_242055	-9.20	-9.26	-8.91	DEAD/DEAH box helicase domain-containing protein
TGME49_318210	-9.22	-8.87	-8.65	hypothetical protein
TGME49_246970	-9.20	-8.84	-8.71	3'-5' exonuclease domain-containing protein
TGME49_280770	-1.52	-1.02	#N/A	regulator of chromosome condensation (RCC1) repeat-containing protein
TGME49_319910	1.82	1.73	1.90	WD domain, G-beta repeat-containing protein
TGME49_222960	-9.20	-9.40	-9.37	SCY kinase-related protein (incomplete catalytic triad)
TGME49_239740	1.01	#N/A	#N/A	dense granule protein GRA14
TGME49_310930	-3.09	-2.79	-3.22	hypothetical protein
TGME49_278630	-9.17	-9.11	-8.95	tetratricopeptide repeat-containing protein
TGME49_220950	1.20	1.59	1.57	hypothetical protein
TGME49_225745	-9.20	-9.66	-9.21	hypothetical protein
TGME49_207100	-9.17	-9.35	-8.99	hypothetical protein
TGME49_271460	2.14	1.54	2.34	protein c14orf29, putative
TGME49_239752	-1.50	-1.15	-1.35	hypothetical protein
TGME49_297870	-2.35	-2.13	-2.31	hypothetical protein
TGME49_226590	1.50	1.73	1.17	cytochrome C oxidase subunit IIa, putative
TGME49_236890	1.44	1.05	1.14	hypothetical protein
TGME49_241890	-9.17	-8.91	-9.04	hypothetical protein
TGME49_228770	-4.30	-3.81	-4.13	hypothetical protein
TGME49_222210	-9.17	-8.50	-8.80	SPFH domain / Band 7 family protein
TGME49_271060	-4.26	-4.00	-3.68	Sec1 family protein
TGME49_253180	2.52	1.98	1.95	hypothetical protein
TGME49_203740	-2.48	-1.93	-2.36	hypothetical protein
TGME49_205280	1.30	1.20	#N/A	hypothetical protein
TGME49_313400	-2.19	-1.86	-2.09	DnaJ domain-containing protein
TGME49_201680	-1.13	#N/A	-1.14	eukaryotic initiation factor-3 subunit 10, putative
TGME49_311070	-3.53	-3.69	-3.50	hypothetical protein
TGME49_249270	-1.19	#N/A	-1.22	protein disulfide isomerase-related protein (provisional), putative
TGME49_266280	-1.08	#N/A	#N/A	HEAT repeat-containing protein
TGME49_252065	1.65	2.13	1.94	KRUF family protein
TGME49_271010	1.80	#N/A	3.30	hypothetical protein
TGME49_226400	-1.41	-1.48	-1.44	lipoic acid synthase LIPA
TGME49_314890	-2.90	-3.63	-3.65	ThiF family protein
TGME49_222120	-2.90	-3.23	-3.12	hypothetical protein
TGME49_294750	-2.90	-2.84	-2.55	hypothetical protein
TGME49_251510	1.45	1.46	1.29	Ulp1 protease family, C-terminal catalytic domain-containing protein
TGME49_313690	-1.22	-1.22	-1.69	Sei1 repeat-containing protein
TGME49_267700	-2.92	-3.35	-2.87	hypothetical protein
TGME49_248340	-1.04	#N/A	#N/A	GTP-binding nuclear protein ran/tc4
TGME49_227260	-2.31	-2.26	-2.49	RIO1 family protein
TGME49_255300	-1.33	-1.61	-1.56	hypothetical protein
TGME49_259080	1.89	1.81	#N/A	hypothetical protein
TGME49_229030	-1.17	-1.13	-1.68	hypothetical protein
TGME49_233120	-1.37	-1.16	#N/A	AP2 domain transcription factor AP2V/III-2
TGME49_298980	-1.21	#N/A	#N/A	RNA pseudouridine synthase superfamily protein
TGME49_275770	-1.32	-1.31	-1.15	hypothetical protein
TGME49_267400	-1.04	-1.40	-1.28	ribosomal protein RPL32
TGME49_286130	1.59	#N/A	1.11	hypothetical protein
TGME49_316480	1.69	#N/A	#N/A	XRN 5'-3' exonuclease N-terminus protein
TGME49_208390	1.29	1.44	1.32	hypothetical protein
TGME49_259720	1.14	#N/A	#N/A	hypothetical protein
TGME49_225420	-2.28	-2.02	-2.04	histidine triad domain-containing protein
TGME49_281420	-2.28	-2.28	#N/A	histone deacetylase HDAC1
TGME49_270530	-2.02	-2.36	-2.87	ubiquitin fusion degradation protein UFD1CY
TGME49_246630	-1.49	#N/A	-1.70	DNA-directed RNA polymerase I RPA43
TGME49_253960	1.52	1.92	1.17	oxidoreductase, short chain dehydrogenase/reductase family protein
TGME49_274150	-2.90	-3.51	-3.79	hypothetical protein
TGME49_246010	2.82	#N/A	2.37	hypothetical protein

FIGURE 4Q

TGME49_205200	1.37	1.28	1.97	hypothetical protein
TGME49_250670	1.80	1.04	2.24	hypothetical protein
TGME49_212270	2.01	1.79	1.53	hypothetical protein
TGME49_219860	-1.38	#N/A	-1.53	replication licensing factor, putative
TGME49_248490	2.15	1.75	#N/A	hypothetical protein
TGME49_245730	-9.14	-9.31	-8.95	phosphatidylinositol-4-phosphate 5-Kinase
TGME49_203560	-9.21	-9.37	-9.40	hypothetical protein
TGME49_282150	-9.14	-9.14	-9.37	hypothetical protein
TGME49_239020	-9.22	-10.28	-8.90	ABC transporter transmembrane region domain-containing protein
TGME49_306440	-9.14	-9.17	-9.84	hypothetical protein
TGME49_305860	-1.98	-2.23	-2.36	calcium-dependent protein kinase CDPK3
TGME49_216070	-9.14	-9.09	-9.10	hypothetical protein
TGME49_209730	-9.14	-9.22	-9.53	hypothetical protein
TGME49_259090	1.54	1.29	#N/A	ubiquitin-conjugating enzyme subfamily protein
TGME49_209280	-4.24	-4.39	-4.08	hypothetical protein
TGME49_248530	-9.14	-9.02	-9.31	FATC domain-containing protein
TGME49_258470	1.18	1.46	#N/A	hypothetical protein
TGME49_249650	-9.14	-9.09	-9.59	apolipoprotein A-I binding protein, putative
TGME49_278975	-2.28	-2.23	-2.23	ICE family protease (caspase) p20 domain-containing protein
TGME49_204360	2.57	#N/A	#N/A	subtilisin SUB4
TGME49_202572	-9.14	-8.93	-8.95	ribophorin I protein
TGME49_210230	-9.18	-9.59	-9.02	hypothetical protein
TGME49_262040	-2.58	-2.27	-2.75	SAC3/GANP family protein
TGME49_223855	2.71	2.76	2.84	RNA recognition motif-containing protein
TGME49_240520	-9.14	-9.00	-8.80	hypothetical protein
TGME49_221350	-4.21	-3.63	-3.51	Ctr copper transporter family protein
TGME49_278700	-3.46	-3.04	-2.60	hypothetical protein
TGME49_280390	-2.58	-2.94	-2.68	HEAT repeat-containing protein
TGME49_294270	-9.11	-9.02	-8.83	histone arginine methyltransferase PRMT4/CARM1
TGME49_249470	-9.11	-8.94	-9.34	rhoptyr kinase family protein, truncated (incomplete catalytic triad)
TGME49_225800	-3.47	-3.24	-3.04	iron-sulfur assembly ATPase
TGME49_282220	1.49	1.53	1.93	AP2 domain transcription factor AP2Vlla-9
TGME49_297170	1.44	1.43	#N/A	50S ribosomal protein L17, putative
TGME49_290225	-2.90	-3.16	-3.01	hypothetical protein
TGME49_279390	-1.25	-1.07	-1.24	proliferation-associated protein 2G4, putative
TGME49_231040	-2.91	-2.69	-2.71	3' exoribonuclease family, domain 1 domain-containing protein
TGME49_263470	-1.17	#N/A	#N/A	ubiquitin carboxyl-terminal hydrolase UCHL3
TGME49_242625	-1.29	-1.28	#N/A	ATPase family associated with various cellular activities (AAA) subfamily protein
TGME49_267040	-2.28	-2.37	-2.52	hypothetical protein
TGME49_254606	1.64	2.48	2.32	hypothetical protein
TGME49_270975	-1.68	#N/A	-1.36	hypothetical protein
TGME49_284598	-7.35	-9.64	#N/A	haloacid dehalogenase family hydrolase domain-containing protein
TGME49_269705	1.40	2.18	2.25	hypothetical protein
TGME49_299030	1.22	1.06	1.19	RNA recognition motif 2 protein
TGME49_206415	-1.19	-1.34	-1.42	myosin K
TGME49_237840	-1.61	-1.42	#N/A	hypothetical protein
TGME49_307260	1.81	2.82	#N/A	Toxoplasma gondii family C protein
TGME49_226040	-1.13	-1.12	#N/A	EF hand domain-containing protein
TGME49_286190	-1.20	#N/A	#N/A	hypothetical protein
TGME49_222870	-1.34	-1.16	-1.41	hypothetical protein
TGME49_277540	-7.34	-8.33	-8.37	hypothetical protein
TGME49_254510	1.59	1.19	#N/A	ankyrin repeat-containing protein
TGME49_245770	2.70	#N/A	#N/A	hypothetical protein
TGME49_305820	-1.48	-1.53	#N/A	SGS domain-containing protein
TGME49_305620	-1.52	-1.42	-1.31	hypothetical protein
TGME49_278890	-1.97	-1.95	-1.74	hypothetical protein
TGME49_246050	-7.42	-7.93	-8.34	hypothetical protein
TGME49_260270	-1.44	-1.44	-1.34	HEAT repeat-containing protein
TGME49_213020	1.58	1.30	1.68	hypothetical protein
TGME49_220530	1.68	1.37	1.44	AP2 domain transcription factor AP2V-1
TGME49_209190	-1.16	#N/A	-1.05	ABC transporter transmembrane region domain-containing protein
TGME49_277850	-1.88	#N/A	-1.63	trypsin domain-containing protein
TGME49_294350	-1.06	#N/A	#N/A	DEAD/DEAH box helicase domain-containing protein
TGME49_202520	1.16	1.23	1.22	hypothetical protein

FIGURE 4R

TGME49_264600	-2.40	-2.43	-2.67	hypothetical protein
TGME49_297400	1.36	1.14	#N/A	hypothetical protein
TGME49_224960	1.35	1.34	1.40	hypothetical protein
TGME49_251410	-2.32	-1.71	-1.96	tetratricopeptide repeat-containing protein
TGME49_254870	1.36	1.24	1.70	hypothetical protein
TGME49_200320	-2.28	-2.54	-3.25	hypoxanthine-xanthine-guanine phosphoribosyl transferase HXGPRT
TGME49_294550	-1.62	-1.96	-2.09	dynein heavy chain
TGME49_318880	2.77	2.22	2.26	hypothetical protein
TGME49_305240	-3.04	-3.22	-3.24	XPA binding protein 2 family protein
TGME49_223800	-4.23	-4.26	-3.73	hypothetical protein
TGME49_286790	-4.19	-4.13	-4.49	nuclear factor NF2
TGME49_316200	1.65	1.42	1.12	phosphoglycerate mutase family protein
TGME49_266730	-9.08	-9.20	-8.85	leucyl-tRNA synthetase (LeuRS2)
TGME49_257700	2.48	3.12	3.22	hypothetical protein
TGME49_234460	1.47	2.22	#N/A	hypothetical protein
TGME49_236670	1.93	2.50	3.04	hypothetical protein
TGME49_270140	-9.11	-8.77	-8.70	splicing factor DIM1, putative
TGME49_268760	-1.32	#N/A	-1.21	hypothetical protein
TGME49_306960	-2.52	-2.15	-2.56	phenylalanine-tRNA ligase, beta subunit protein
TGME49_272770	-4.19	-3.81	-3.67	hypothetical protein
TGME49_314920	2.44	2.19	2.18	hypothetical protein
TGME49_251500	-1.41	-1.11	-1.61	eukaryotic initiation factor-3, subunit 3, putative
TGME49_244500	-1.77	-2.01	-1.75	Tubulin-tyrosine ligase family protein
TGME49_295658	-3.40	-3.61	-3.34	zinc finger in N-recognin protein
TGME49_294990	-9.08	-9.90	-9.75	hypothetical protein
TGME49_249460	-9.08	-8.57	-8.46	WD domain, G-beta repeat-containing protein
TGME49_314700	1.38	#N/A	1.31	hypothetical protein
TGME49_236860	-4.25	-4.69	-3.69	haloacid dehalogenase family hydrolase domain-containing protein
TGME49_291020	-2.13	-1.63	-2.06	myosin head (motor domain) domain-containing protein
TGME49_289700	-3.00	-2.49	-2.82	hypothetical protein
TGME49_200350	2.37	3.12	3.55	subtilisin SUB3
TGME49_257350	1.19	1.35	1.50	eukaryotic translation initiation factor, putative
TGME49_301380	-4.21	-4.18	-3.92	elongation factor Tu GTP binding domain-containing protein
TGME49_310140	-9.05	-8.97	-9.32	hypothetical protein
TGME49_277710	-1.12	-1.08	-1.23	hypothetical protein
TGME49_206700	-2.89	-2.96	-2.69	hypothetical protein
TGME49_238070	-2.84	-2.73	-3.39	glutaredoxin domain-containing protein
TGME49_242830	-1.39	-1.55	-1.77	XRN 5'-3' exonuclease N-terminus protein
TGME49_217780	1.28	#N/A	#N/A	Sec20 protein
TGME49_306195	2.13	2.36	2.44	hypothetical protein
TGME49_221410	-1.07	#N/A	-1.11	actin-like protein ALP4
TGME49_310330	-1.95	-2.05	-1.81	hypothetical protein
TGME49_244630	1.49	1.48	1.36	hypothetical protein
TGME49_215450	2.17	1.99	1.91	aquaporin 1
TGME49_261430	-1.58	-2.17	-1.36	hypothetical protein
TGME49_232090	-1.71	-1.63	-2.06	3-hydroxyacyl-CoA dehydrogenase, NAD binding domain-containing protein
TGME49_204080	-1.18	-1.55	-1.68	histidine acid phosphatase superfamily protein
TGME49_299060	-1.06	-1.08	-1.02	sodium/hydrogen exchanger NHE2
TGME49_312210	-2.23	-2.28	-2.95	hypothetical protein
TGME49_228070	1.21	#N/A	1.00	hypothetical protein
TGME49_229160	-2.87	-3.02	-2.82	DHHC zinc finger domain-containing protein
TGME49_318690	1.15	2.02	2.72	RNA recognition motif-containing protein
TGME49_301010	-1.14	-1.13	#N/A	serine/threonine protein phosphatase, putative
TGME49_263710	-1.18	-1.06	#N/A	acyl-CoA:cholesterol acyltransferase alpha ACAT1-alpha
TGME49_212735	-2.27	-2.65	-1.98	hypothetical protein
TGME49_221850	1.41	#N/A	#N/A	prohibitin family protein, putative
TGME49_307860	1.05	1.18	1.15	hypothetical protein
TGME49_227900	1.49	#N/A	1.54	AP2 domain transcription factor AP2X-1
TGME49_285930	-1.79	-1.89	-1.73	hypothetical protein
TGME49_268730	1.15	1.39	1.12	glutaredoxin-related protein
TGME49_229790	-1.71	-1.61	-1.96	hypothetical protein
TGME49_244010	-1.91	-2.04	-1.83	hypothetical protein
TGME49_272000	-1.91	-2.08	-1.96	hypothetical protein
TGME49_201770	1.67	#N/A	1.42	cullin 3, putative
TGME49_228780	1.20	1.11	1.08	Toxoplasma gondii family C protein
TGME49_309400	-1.94	-2.52	-2.53	RecF/RecN/SMC N terminal domain-containing protein
TGME49_320210	-1.21	#N/A	#N/A	WD domain, G-beta repeat domain containing protein
TGME49_292110	1.19	#N/A	#N/A	formate/nitrite transporter protein

FIGURE 4S

TGME49_213325	-9.08	-9.41	-9.45	TBC domain-containing protein
TGME49_221270	-1.90	-1.11	-1.47	oxidoreductase, 2OG-Fe(II) oxygenase family protein
TGME49_227030	-2.15	-1.78	-2.14	hypothetical protein
TGME49_215040	-2.38	-2.23	-2.05	HEAT repeat-containing protein
TGME49_299970	-1.47	-1.03	#N/A	tetratricopeptide repeat-containing protein
TGME49_274010	-4.16	-4.10	-4.26	hypothetical protein
TGME49_305470	-9.05	-9.47	-8.93	hypothetical protein
TGME49_231910	-1.73	-1.42	-1.74	ATP synthase F1 gamma subunit
TGME49_313830	-2.96	-2.78	-2.96	AARP2CN (NUC121) domain-containing protein
TGME49_228730	-9.05	-8.79	-8.45	hypothetical protein
TGME49_257050	-9.02	-8.85	-9.48	3-methyl-2-oxobutanoate hydroxymethyltransferase
TGME49_220430	-9.02	-9.22	-8.87	hypothetical protein
TGME49_240880	2.26	#N/A	3.30	hypothetical protein
TGME49_291680	-1.53	-1.47	-2.05	Sec23/Sec24 trunk domain-containing protein
TGME49_235398	-9.02	-9.26	-9.07	hypothetical protein
TGME49_271270	-1.73	-1.54	-1.79	hypothetical protein
TGME49_248450	-2.96	-2.70	-2.80	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_225480	-4.14	-4.30	-3.93	hypothetical protein
TGME49_287270	-2.97	-2.62	-2.49	hypothetical protein
TGME49_215570	-3.39	-3.51	-3.01	AP2 domain transcription factor AP2X-11
TGME49_279340	1.67	1.85	#N/A	hypothetical protein
TGME49_257490	-3.40	-3.88	-3.98	prefoldin subunit superfamily protein
TGME49_260390	-9.02	-8.88	-8.85	hypothetical protein
TGME49_272410	1.37	1.54	1.53	phosphogluconate dehydrogenase (decarboxylating), NAD binding domain-containing protein
TGME49_210760	-9.02	-8.72	-8.72	glutamine amidotransferase-related, putative
TGME49_264080	-1.51	-1.65	-1.60	acyl carrier protein ACP
TGME49_269970	1.29	1.73	1.32	hypothetical protein
TGME49_264130	1.98	1.68	1.50	hypothetical protein
TGME49_313780	-1.63	-1.52	-1.69	hypothetical protein
TGME49_214750	1.30	1.14	#N/A	hypothetical protein
TGME49_253090	1.71	2.14	2.21	DEAD/DEAH box helicase domain-containing protein
TGME49_306460	-9.02	-8.92	-9.19	bromodomain-containing protein
TGME49_313020	-3.36	-3.63	-4.21	STAS domain-containing protein
TGME49_234900	-1.02	-1.30	-1.13	PHD-finger domain-containing protein
TGME49_313660	1.36	1.32	3.66	hypothetical protein
TGME49_299190	1.15	#N/A	1.52	B-box zinc finger domain-containing protein
TGME49_258080	-1.59	-1.64	-1.75	hypothetical protein
TGME49_258100	-2.85	-2.95	-2.78	TPR repeat region protein
TGME49_315420	1.07	1.37	1.08	hypothetical protein
TGME49_213690	-1.55	-1.28	-1.36	ring box protein 1 family protein
TGME49_204350	-1.55	-1.93	-1.51	hypothetical protein
TGME49_272290	-1.21	-1.07	-1.01	pyruvate dehydrogenase complex subunit PD-HE1Beta
TGME49_245475	1.21	1.46	1.32	hypothetical protein
TGME49_268680	-1.07	#N/A	#N/A	hypothetical protein
TGME49_219530	-2.84	-2.83	-3.40	hypothetical protein
TGME49_240910	-1.36	-1.50	-1.84	hypothetical protein
TGME49_232380	-1.49	#N/A	#N/A	WD domain, G-beta repeat-containing protein
TGME49_226390	2.45	2.08	2.47	hypothetical protein
TGME49_225190	2.72	2.20	2.25	hypothetical protein
TGME49_298010	-1.23	-1.28	-1.13	hypothetical protein
TGME49_230230	1.31	1.08	#N/A	hypothetical protein
TGME49_202030	-1.05	-1.49	-1.60	hypothetical protein
TGME49_259700	-1.20	#N/A	-1.57	hypothetical protein
TGME49_217000	-1.43	-1.21	-1.36	hypothetical protein
TGME49_243590	-1.72	#N/A	-1.45	endonuclease/exonuclease/phosphatase family protein
TGME49_223040	1.07	1.49	1.13	hypothetical protein
TGME49_208040	-1.68	-1.85	-2.08	aldo-keto reductase
TGME49_297840	-1.11	-2.00	#N/A	DNA primase, large subunit
TGME49_255340	-1.12	-1.09	-1.08	tetratricopeptide repeat-containing protein
TGME49_314550	-2.19	#N/A	-2.38	hypothetical protein
TGME49_263840	-1.68	#N/A	-2.06	hypothetical protein
TGME49_316180	-1.68	#N/A	-2.10	hypothetical protein
TGME49_313280	1.19	#N/A	#N/A	WD domain, G-beta repeat-containing protein
TGME49_242845	-2.79	-3.08	-3.56	hypothetical protein
TGME49_200440	1.38	#N/A	1.32	hypothetical protein
TGME49_249702	-1.82	#N/A	-2.29	MC family transporter, putative

FIGURE 4T

TGME49_218740	3.24	1.73	1.68	membrane protein, putative
TGME49_291050	-1.84	-1.74	-1.43	histone kinase SNF1, putative
TGME49_219270	-1.01	#N/A	-1.21	multi-pass transmembrane protein
TGME49_310530	-4.14	-4.38	-4.26	SNF2 family N-terminal domain-containing protein
TGME49_227948	-1.31	-1.07	-1.37	peptidase M16 inactive domain-containing protein
TGME49_306520	1.91	1.87	1.58	tRNA pseudouridine synthase B, putative
TGME49_282040	-4.17	-4.28	-3.95	hypothetical protein
TGME49_225770	-8.99	-9.28	-8.97	Tyrosine kinase-like (TKL) protein
TGME49_205460	-8.99	-8.74	-8.77	AN1 family Zinc finger domain-containing protein
TGME49_214580	-4.14	-4.05	#N/A	tetratricopeptide repeat-containing protein
TGME49_268890	-1.88	-1.69	-1.90	citrate synthase I
TGME49_253600	2.37	1.71	1.18	hypothetical protein
TGME49_289750	-1.06	-1.04	-1.30	ribosomal-ubiquitin protein RPL40
TGME49_306310	-2.51	-2.68	-2.25	RecF/RecN/SMC N terminal domain-containing protein
TGME49_290970	-1.58	#N/A	2.51	8-amino-7-oxononanoate synthase
TGME49_320450	-3.41	-3.24	-3.22	ribosome biogenesis regulatory protein (rrs1) protein
TGME49_243210	1.30	1.03	#N/A	DUF862 domain-containing protein
TGME49_243250	-1.48	-1.35	-1.70	myosin H
TGME49_264220	-8.99	-8.61	-8.96	hypothetical protein
TGME49_234490	-2.94	-2.81	-2.36	kelch repeat-containing protein
TGME49_213400	-2.70	-2.62	-2.32	zinc finger (CCCH type) motif-containing protein
TGME49_273370	-3.09	-2.91	-2.82	coatomer gamma 2-subunit protein, putative
TGME49_205000	-8.99	-8.94	-8.94	phosphoglycerate mutase family protein
TGME49_215430	1.95	1.89	1.72	hypothetical protein
TGME49_306600	-8.99	-9.05	-9.22	RNA recognition motif-containing protein
TGME49_216380	-2.76	-2.49	-2.22	phospholipid-translocating P-type ATPase, flippase subfamily protein
TGME49_213600	-8.99	-8.29	-8.28	hypothetical protein
TGME49_203350	-9.03	-9.01	-9.18	hypothetical protein
TGME49_312622	-2.19	-2.27	-2.72	DUF803 domain-containing protein
TGME49_261750	-2.50	-2.87	-2.65	rhopty neck protein RON10
TGME49_307820	1.88	1.95	1.77	hypothetical protein
TGME49_221450	1.22	#N/A	#N/A	SPRY domain-containing protein
TGME49_251480	1.55	1.95	1.76	DEAD/DEAH box helicase domain-containing protein
TGME49_263360	-1.68	-1.96	-1.63	WD domain, G-beta repeat containing protein
TGME49_238870	1.12	#N/A	#N/A	hypothetical protein
TGME49_214470	-1.87	-2.20	-2.19	Ulp1 protease family, C-terminal catalytic domain-containing protein
TGME49_310770	-1.24	-1.15	-1.46	hypothetical protein
TGME49_264890	-2.19	-2.35	-2.25	hypothetical protein
TGME49_224890	1.01	#N/A	#N/A	hypothetical protein
TGME49_255195	1.40	1.92	1.10	hypothetical protein
TGME49_218200	-2.18	-2.17	-2.66	UDP-sugar pyrophosphorylase
TGME49_288990	-2.23	-2.21	-2.26	hypothetical protein
TGME49_205730	-2.18	-2.76	-2.44	hypothetical protein
TGME49_214500	1.19	1.12	1.38	ankyrin repeat-containing protein
TGME49_243240	1.56	1.37	1.26	WD domain, G-beta repeat-containing protein
TGME49_259230	-2.18	-2.42	-2.45	site-specific recombinase, phage integrase family protein
TGME49_267480	1.00	#N/A	1.07	tRNA (guanine(26)-N(2))-dimethyltransferase, putative
TGME49_320610	-2.21	-2.18	-1.92	hypothetical protein
TGME49_235450	1.19	#N/A	1.02	ubiquitin-conjugating enzyme subfamily protein
TGME49_255440	1.22	1.26	1.29	hypothetical protein
TGME49_207950	-1.54	-1.42	-1.58	hypothetical protein
TGME49_219832	-1.70	#N/A	#N/A	cyclin-dependent kinase regulatory subunit protein
TGME49_295590	1.30	1.36	1.89	hypothetical protein
TGME49_308930	-1.40	-1.24	-1.52	50S ribosomal protein L33, putative
TGME49_226620	-1.66	-1.65	#N/A	hypothetical protein
TGME49_202020	1.11	2.49	4.47	DnAK-TPR
TGME49_286510	-1.72	-1.62	#N/A	hypothetical protein
TGME49_319740	-1.53	#N/A	#N/A	transporter, major facilitator family protein
TGME49_304720	-1.57	-1.79	-1.72	hypothetical protein
TGME49_209090	-1.19	-1.13	-1.90	proteasome maturation factor ump1 protein
TGME49_203280	-2.18	-1.98	-2.28	hypothetical protein
TGME49_313570	-1.16	-1.31	-1.33	regulator of chromosome condensation (RCC1) repeat-containing protein

FIGURE 4U

TGME49_215460	-1.44	-1.16	-1.56	ribosomal protein RPS24
TGME49_221500	-8.98	-8.62	-8.71	dual specificity phosphatase, catalytic domain-containing protein
TGME49_319900	-2.01	-2.15	-1.86	hypothetical protein
TGME49_206600	-8.95	-8.94	-8.37	sigma-70, region 3 protein
TGME49_213635	4.91	2.19	-1.02	hypothetical protein
TGME49_294400	-2.02	-2.37	-2.42	hypothetical protein
TGME49_262060	-3.32	-2.90	-3.03	hypothetical protein
TGME49_306895	1.23	#N/A	1.09	hypothetical protein
TGME49_245670	-1.30	-1.06	#N/A	pyruvate dehydrogenase complex subunit PDH-E1Alpha
TGME49_214370	-8.95	-8.68	-8.91	hypothetical protein
TGME49_316350	-8.98	-8.75	-8.71	hypothetical protein
TGME49_297790	-2.45	-1.46	-2.08	hypothetical protein
TGME49_213620	2.19	1.68	3.04	ABC1 family protein
TGME49_277685	-9.05	-8.69	-7.38	hypothetical protein
TGME49_217740	-2.10	-1.89	-1.92	3-ketoacyl-(acyl-carrier-protein) reductase
TGME49_288290	2.38	1.85	#N/A	hypothetical protein
TGME49_280800	-1.79	-1.86	-1.91	SWI2/SNF2 SRCAP/Ino80
TGME49_306620	2.54	2.00	3.84	AP2 domain transcription factor AP2IX-9
TGME49_278850	-1.35	-1.38	-1.26	DHHC zinc finger domain-containing protein
TGME49_292235	-8.95	-9.04	-8.85	hypothetical protein
TGME49_271780	-2.90	-3.11	-2.75	Filamin/ABP280 repeat-containing protein
TGME49_309110	1.53	1.29	1.83	tRNA methyl transferase
TGME49_219485	1.57	1.26	2.11	hypothetical protein
TGME49_299000	1.46	1.03	#N/A	hypothetical protein
TGME49_267330	-2.42	-2.03	-2.30	fumarate hydratase
TGME49_284660	-8.95	-8.32	-8.53	mitochondrial ribosomal protein s6-2, putative
TGME49_205340	1.16	1.26	#N/A	ribosomal protein RPS12
TGME49_266470	-8.92	-8.81	-9.09	hypothetical protein
TGME49_227450	1.21	1.05	1.27	hydrolase, NUDIX family protein
TGME49_286650	-8.92	-9.00	-9.01	hypothetical protein
TGME49_290720	-1.63	-1.86	-1.87	vacuolar proton translocating ATPase subunit, putative
TGME49_278950	2.09	1.84	1.74	LSM domain-containing protein
TGME49_239340	-8.92	-8.79	-9.25	hypothetical protein
TGME49_262930	-8.92	-9.04	-9.47	hypothetical protein
TGME49_301120	-1.24	#N/A	-1.62	acetyl-CoA acetyltransferase
TGME49_311160	-1.15	-1.32	-1.53	PWI domain-containing protein
TGME49_238040	-1.13	-1.07	-1.90	protein disulfide-isomerase domain-containing protein
TGME49_262450	-1.10	-1.06	-1.15	hypothetical protein
TGME49_290630	1.03	#N/A	1.17	AP2 domain transcription factor AP2IX-7
TGME49_221630	-2.14	-3.28	-3.23	hypothetical protein
TGME49_215360	1.25	1.97	1.59	hypothetical protein
TGME49_273540	-1.52	#N/A	#N/A	phosphatidylserine synthase, putative
TGME49_207720	-1.30	-1.26	-1.20	hypothetical protein
TGME49_207960	-1.51	#N/A	-1.98	hypothetical protein
TGME49_288370	1.17	#N/A	1.28	hypothetical protein
TGME49_219710	1.08	#N/A	#N/A	hypothetical protein
TGME49_200375	-2.17	#N/A	-2.41	hypothetical protein
TGME49_292610	-7.12	-7.13	-8.91	Toxoplasma gondii family C protein
TGME49_224980	-1.09	#N/A	-1.23	hypothetical protein
TGME49_249690	-2.78	-2.89	-3.64	hypothetical protein
TGME49_273970	-2.72	-3.20	-3.09	CorA family Mg2+ transporter protein
TGME49_265470	1.29	#N/A	#N/A	hypothetical protein
TGME49_240730	-2.72	-2.99	-3.44	hypothetical protein
TGME49_293220	1.96	#N/A	1.85	DHHC zinc finger domain-containing protein
TGME49_305260	-2.72	-2.57	-2.89	hypothetical protein
TGME49_202800	-7.14	-8.37	-8.15	cytochrome c oxidase assembly protein COX11, putative
TGME49_266680	-1.66	#N/A	#N/A	hypothetical protein
TGME49_245530	2.61	2.09	#N/A	hypothetical protein
TGME49_278080	1.37	2.04	7.20	Toxoplasma gondii family A protein
TGME49_208430	1.29	1.13	#N/A	serine proteinase inhibitor PI-2, putative
TGME49_307575	-2.73	-3.79	-2.70	hypothetical protein
TGME49_320670	-1.11	-1.24	-1.24	vacuolar protein sorting 16, putative
TGME49_270350	-1.10	#N/A	-1.13	hypothetical protein
TGME49_255670	-2.72	-2.82	-3.09	methyltransferase domain-containing protein
TGME49_266380	-7.12	-7.15	-9.53	hypothetical protein
TGME49_213000	2.03	2.22	#N/A	replication factor C, subunit 5, putative
TGME49_240080	1.26	#N/A	#N/A	hypothetical protein
TGME49_244100	-1.12	#N/A	-1.43	snoRNA binding domain-containing protein

FIGURE 4V

TGME49_239780	-3.35	-3.53	-3.58	hypothetical protein
TGME49_309950	-8.92	-8.54	-8.45	NLE (NUC135) domain-containing protein
TGME49_285180	-1.64	-1.87	#N/A	hypothetical protein
TGME49_255250	-8.92	-8.70	-8.73	tRNA (cytosine(34)-C(5))-methyltransferase, putative
TGME49_250100	2.61	2.16	3.11	hypothetical protein
TGME49_231120	1.56	1.93	1.68	ribosomal protein S11, putative
TGME49_235630	1.16	1.36	1.72	hypothetical protein
TGME49_235740	-4.04	-3.29	-3.95	hypothetical protein
TGME49_222192	-8.92	-8.69	-8.27	hypothetical protein
TGME49_256880	-8.92	-8.93	-8.89	protein kinase domain-containing protein
TGME49_257720	2.71	#N/A	#N/A	proton ATPase, putative
TGME49_245580	2.05	1.12	1.03	hypothetical protein
TGME49_233500	1.39	1.19	1.23	triose-phosphate isomerase TPI-II
TGME49_214820	1.55	1.64	1.43	G-patch domain-containing protein
TGME49_288340	-8.89	-8.91	-9.30	UBX domain-containing protein
TGME49_254230	2.06	1.91	1.89	hypothetical protein
TGME49_285970	-8.88	-9.02	-8.90	30S ribosomal protein S5, putative
TGME49_222020	-2.64	-2.53	-2.29	phosphoglycerate kinase PGKII
TGME49_267340	2.10	1.75	2.16	hypothetical protein
TGME49_293440	-1.65	-1.84	-1.64	hypothetical protein
TGME49_266890	-1.81	-1.47	-1.43	hypothetical protein
TGME49_263540	2.06	2.32	2.39	hypothetical protein
TGME49_217688	-8.88	-8.98	-9.21	hypothetical protein
TGME49_293860	-8.88	-8.93	-9.03	hypothetical protein
TGME49_229380	-8.88	-8.60	-8.73	hypothetical protein
TGME49_265220	-4.07	-4.04	-3.83	co-chaperone GrpE protein
TGME49_209860	-8.89	-8.20	-8.38	SRP40, C-terminal domain-containing protein
TGME49_204280	1.22	1.27	1.28	cell-cycle-associated protein kinase DYRK, putative
TGME49_216335	2.20	1.13	3.61	hypothetical protein
TGME49_316680	1.23	1.10	#N/A	RNA pseudouridine synthase superfamily protein
TGME49_251680	-1.35	-1.19	-1.49	histamine-releasing factor, putative
TGME49_306930	-1.41	#N/A	-1.60	proteasome subunit beta type 7 precursor, putative
TGME49_266400	-8.92	-9.03	-8.79	hypothetical protein
TGME49_272570	1.42	1.57	2.02	dihydrouridine synthase (dus) protein
TGME49_247590	-1.83	-1.75	-1.86	methyltransferase domain-containing protein
TGME49_293050	-2.14	-2.81	-2.64	sybindin family protein
TGME49_214130	-1.12	#N/A	#N/A	hypothetical protein
TGME49_248750	2.15	#N/A	#N/A	hypothetical protein
TGME49_316750	-2.72	-2.93	-2.99	DEAD/DEAH box helicase domain-containing protein
TGME49_276100	-1.66	#N/A	-1.58	hypothetical protein
TGME49_227820	-1.22	-1.10	-1.19	hypothetical protein
TGME49_295430	-1.65	#N/A	#N/A	hypothetical protein
TGME49_232060	-1.54	#N/A	#N/A	hypothetical protein
TGME49_266860	1.15	#N/A	#N/A	BTB/POZ domain-containing protein
TGME49_258625	-7.11	-7.88	-8.44	peptidyl-prolyl cis-trans isomerase, FKBP type domain-containing protein
TGME49_276910	-1.07	-1.45	-1.02	endoplasmic reticulum lumen protein retaining receptor (ERD2) family protein
TGME49_223900	1.30	2.09	1.89	hypothetical protein
TGME49_244040	-1.40	#N/A	#N/A	HEAT repeat-containing protein
TGME49_216220	-1.06	-1.21	#N/A	AP2 domain transcription factor AP2XI-5
TGME49_248660	-1.64	#N/A	#N/A	hypothetical protein
TGME49_292960	1.35	#N/A	#N/A	hypothetical protein
TGME49_211480	-1.61	#N/A	-1.47	GTP-binding protein engA, putative
TGME49_207065	-1.61	-1.48	-1.77	hypothetical protein
TGME49_321600	-1.04	-1.13	#N/A	hypothetical protein
TGME49_203362	-2.71	-3.02	-3.06	hypothetical protein
TGME49_293700	-1.29	-1.37	-1.14	WD domain, G-beta repeat-containing protein
TGME49_218580	-1.61	-1.63	#N/A	RNA methyltransferase, TrmH family protein
TGME49_202190	1.08	1.29	1.15	hypothetical protein
TGME49_213388	1.10	#N/A	1.25	hypothetical protein
TGME49_263510	-1.16	-1.51	#N/A	Spc97 / Spc98 family protein
TGME49_314720	1.09	#N/A	#N/A	Sedlin, N-terminal region protein, putative
TGME49_219540	-1.52	#N/A	#N/A	cytosolic tRNA-Ala synthetase
TGME49_269700	1.37	1.67	1.75	NLI interacting factor family phosphatase
TGME49_322000	-1.27	#N/A	-2.58	myosin-light-chain kinase
TGME49_216055	-1.16	#N/A	#N/A	hypothetical protein
TGME49_257980	2.55	2.23	2.38	ribosome recycling factor protein

FIGURE 4W

TGME49_246460	-4.03	-4.13	-3.97	hypothetical protein
TGME49_290900	-8.89	-9.25	-9.44	hydrolase, NUDIX family protein
TGME49_221180	1.10	1.04	#N/A	hypothetical protein
TGME49_270620	2.33	2.77	2.90	DEAD/DEAH box helicase domain-containing protein
TGME49_320740	-1.78	-2.10	-1.72	hypothetical protein
TGME49_202580	1.81	2.05	#N/A	ATPase, AAA family protein
TGME49_260620	1.67	1.87	1.54	hypothetical protein
TGME49_226600	-2.24	-1.86	-1.80	syntaxin 5, putative
TGME49_304700	-3.99	-4.04	-3.83	hypothetical protein
TGME49_310860	-2.59	-2.48	-2.48	U5 snRNP-specific protein
TGME49_221590	1.01	1.58	#N/A	dual specificity phosphatase, catalytic domain-containing protein
TGME49_217730	2.08	1.06	1.00	hypothetical protein
TGME49_268170	-8.95	-8.41	-8.46	hypothetical protein
TGME49_213900	1.20	#N/A	1.12	regulator of chromosome condensation RCC1
TGME49_230580	-8.85	-8.56	-8.23	hypothetical protein
TGME49_304710	-1.30	#N/A	-1.16	eukaryotic peptide chain release factor, putative
TGME49_253000	1.29	1.21	1.17	ELMO/CED-12 family protein
TGME49_223450	-1.94	-1.97	-1.66	ubiquitin carboxyl-terminal hydrolase
TGME49_291980	-1.59	-1.53	-1.26	HECT-domain (ubiquitin-transferase) domain-containing protein
TGME49_212960	-8.89	-8.41	-8.61	hypothetical protein
TGME49_253100	1.20	#N/A	1.03	hypothetical protein
TGME49_264730	-8.85	-8.77	-8.53	hypothetical protein
TGME49_244530	1.01	1.56	#N/A	hypothetical protein
TGME49_231980	-8.85	-9.12	-9.49	hypothetical protein
TGME49_215260	-1.63	-1.22	-1.52	carbamoylphosphate synthetase
TGME49_253640	1.34	1.24	1.08	hypothetical protein
TGME49_268880	-3.23	-3.50	-2.91	hypothetical protein
TGME49_292375	3.37	#N/A	#N/A	KRUF family protein
TGME49_311870	-2.39	-2.50	-2.45	WD domain, G-beta repeat-containing protein
TGME49_253360	1.27	1.32	#N/A	hypothetical protein
TGME49_289150	1.52	1.83	1.12	hypothetical protein
TGME49_267600	-2.83	-3.08	-2.73	FHA domain-containing protein
TGME49_207665	-8.89	-7.99	-8.04	kinesin motor domain-containing protein
TGME49_308880	-8.85	-8.48	-8.45	ImpB/MucB/SamB family protein
TGME49_224090	-1.61	-1.72	-1.96	enoyl-CoA hydratase/isomerase family protein
TGME49_305030	-1.46	-1.51	-2.10	kinase, pfkB family protein
TGME49_307605	-1.00	-1.52	#N/A	hypothetical protein
TGME49_315710	1.43	#N/A	#N/A	hypothetical protein
TGME49_239310	-2.12	-2.79	-2.12	ribulose 5-phosphate isomerase
TGME49_215250	-1.79	-1.77	-1.72	thiamin pyrophosphokinase, catalytic domain-containing protein
TGME49_237160	-1.32	-1.25	#N/A	hypothetical protein
TGME49_218810	-1.29	#N/A	#N/A	histidyl-tRNA synthetase
TGME49_216960	1.10	1.04	#N/A	elongation factor Tu GTP binding domain-containing protein
TGME49_238080	1.27	#N/A	1.21	hypothetical protein
TGME49_293600	1.05	#N/A	#N/A	ribosomal protein RPL27
TGME49_289615	1.86	#N/A	#N/A	hypothetical protein
TGME49_267650	-1.48	-1.36	#N/A	hypothetical protein
TGME49_297270	-2.08	-2.35	-2.48	hypothetical protein
TGME49_239087	-1.78	#N/A	#N/A	hypothetical protein
TGME49_246730	1.03	1.38	#N/A	hypothetical protein
TGME49_243600	-1.04	-1.26	-1.08	acetyltransferase, GNAT family protein
TGME49_293680	-1.28	-1.52	-1.29	hypothetical protein
TGME49_264210	1.02	1.37	1.09	hypothetical protein
TGME49_249300	-1.63	#N/A	-1.97	hypothetical protein
TGME49_249310	-2.65	-2.82	-3.77	hypothetical protein
TGME49_210478	2.28	-1.44	5.25	hypothetical protein
TGME49_267855	-1.02	#N/A	-1.04	hypothetical protein
TGME49_255430	-1.48	#N/A	#N/A	Rae9 protein
TGME49_234280	-1.08	#N/A	#N/A	AMP deaminase
TGME49_238140	-1.15	-1.89	-1.19	hypothetical protein
TGME49_203750	-1.78	-1.89	-1.83	hypothetical protein
TGME49_246182	-1.29	#N/A	#N/A	hypothetical protein
TGME49_254480	1.43	#N/A	1.36	WD domain, G-beta repeat-containing protein
TGME49_262990	-2.67	-3.05	-3.00	hypothetical protein
TGME49_269417	-2.65	-2.99	#N/A	hypothetical protein
TGME49_258010	-1.62	-1.52	-1.64	calcium signaling protein kinase RAD53, putative
TGME49_211330	-2.18	#N/A	#N/A	methionine aminopeptidase
TGME49_219510	1.51	1.85	1.66	GTP binding protein 7 isoform 2 family protein, putative

FIGURE 4X

TGME49_263500	-4.01	-3.88	-4.19	vacuolar protein sorting-associated protein 26, putative
TGME49_219770	-8.91	-8.87	-8.54	30S ribosomal protein S12, putative
TGME49_310100	-8.85	-8.73	-8.67	mannosyltransferase (pig-m) protein
TGME49_211040	-1.31	-1.22	-1.61	Sec61beta family protein
TGME49_214830	-3.98	-3.85	-3.30	hypothetical protein
TGME49_285210	-8.90	-8.51	-8.47	hypothetical protein
TGME49_313330	-8.99	-9.05	-9.34	rhostry kinase family protein ROP27
TGME49_271760	-8.81	-8.98	-9.37	seryl-tRNA synthetase (SerRS2)
TGME49_309870	-8.81	-9.03	-9.48	hypothetical protein
TGME49_207480	-2.36	-2.40	-1.95	GCC2 and GCC3 domain-containing protein
TGME49_294290	-2.03	-1.98	-2.21	Der1ER1
TGME49_313760	1.01	#N/A	#N/A	hypothetical protein
TGME49_264690	-8.81	-8.55	-8.84	cyclin 4, putative
TGME49_272390	-8.82	-8.67	-7.80	hypothetical protein
TGME49_230190	-1.99	-1.94	-2.17	hypothetical protein
TGME49_209700	-3.96	-3.97	-4.13	hypothetical protein
TGME49_242800	-1.99	-1.79	-1.67	ribosome biogenesis protein NSA2, putative
TGME49_252380	1.97	1.24	1.82	hypothetical protein
TGME49_249610	-2.36	-2.58	-2.92	hypothetical protein
TGME49_257480	-2.96	-2.42	-2.41	NADP-dependent succinate-semialdehyde dehydrogenase
TGME49_259950	2.29	1.96	2.05	carbonate dehydratase, eukaryotic-type domain-containing protein
TGME49_250950	2.30	2.04	#N/A	KRUF family protein
TGME49_305090	1.60	1.86	2.15	kinase binding protein cgi-121 protein
TGME49_264780	-8.81	-9.08	-8.72	UTP-glucose-1-phosphate uridylyltransferase subfamily protein
TGME49_231030	-3.96	-3.65	-3.52	hypothetical protein
TGME49_221600	-8.81	-8.86	-8.12	hypothetical protein
TGME49_221200	1.50	1.24	1.15	CW-type Zinc Finger protein
TGME49_310130	-8.78	-9.44	-9.82	Spc97 / Spc98 family protein
TGME49_271200	-1.77	-1.34	-1.43	AP2 domain transcription factor AP2VIII-5
TGME49_217770	1.40	1.55	1.34	hypothetical protein
TGME49_202120	-1.56	-1.54	-1.59	hypothetical protein
TGME49_289100	-2.15	-1.72	-1.59	hypothetical protein
TGME49_261400	-1.51	-2.00	-1.02	hypothetical protein
TGME49_320550	-2.12	-1.90	-1.82	hypothetical protein
TGME49_231215	-8.78	-8.68	-8.75	hypothetical protein
TGME49_205380	-1.48	-1.55	-2.23	fructose-bisphosphatase I
TGME49_288560	-1.21	-1.61	-1.87	hypothetical protein
TGME49_248800	2.35	#N/A	#N/A	hypothetical protein
TGME49_289950	-1.08	-1.16	-1.01	hypothetical protein
TGME49_316150	-1.32	-1.76	#N/A	ULK kinase
TGME49_218192	-6.99	-7.38	-9.70	hypothetical protein
TGME49_232520	-1.24	#N/A	#N/A	brix domain-containing protein
TGME49_237100	1.27	#N/A	1.06	RAP domain-containing protein
TGME49_235660	-1.32	-1.29	#N/A	hypothetical protein
TGME49_311040	-1.12	#N/A	#N/A	hypothetical protein
TGME49_283900	-1.45	#N/A	-1.47	ATPase, AAA family protein
TGME49_226520	-1.12	#N/A	#N/A	hypothetical protein
TGME49_297980	1.38	#N/A	#N/A	hypothetical protein
TGME49_287480	1.04	#N/A	1.55	hypothetical protein
TGME49_204150	1.32	#N/A	#N/A	hypothetical protein
TGME49_264752	-2.63	-3.41	-3.52	HEAT repeat-containing protein
TGME49_203950	-1.04	#N/A	#N/A	Myb family DNA-binding domain-containing protein
TGME49_220150	-1.74	-1.79	-1.72	50S ribosomal protein L16, putative
TGME49_258050	-2.03	-2.05	-2.35	actin like protein ALP2a
TGME49_273885	-2.04	#N/A	-2.34	hypothetical protein
TGME49_246000	1.33	#N/A	1.66	large subunit ribosomal protein IMG2
TGME49_210310	-1.74	#N/A	-1.63	hypothetical protein
TGME49_312820	-1.43	#N/A	-1.86	hypothetical protein
TGME49_240480	-2.70	-2.92	#N/A	cpw-wpc domain-containing protein
TGME49_295090	1.07	1.32	#N/A	hypothetical protein
TGME49_255310	-1.27	-1.51	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_257070	-2.03	-2.02	-2.10	hypothetical protein
TGME49_293490	1.72	1.78	1.85	hypothetical protein
TGME49_251590	1.17	1.31	1.10	hypothetical protein
TGME49_273380	1.42	#N/A	#N/A	ion channel protein
TGME49_309960	-1.03	#N/A	#N/A	hypothetical protein
TGME49_262933	-1.61	-1.56	#N/A	hypothetical protein
TGME49_209530	1.26	#N/A	1.41	hypothetical protein
TGME49_262420	1.18	#N/A	#N/A	AP2 domain transcription factor APV1lb-1/ADA2-B
TGME49_271370	-1.82	#N/A	#N/A	hypothetical protein
TGME49_268640	2.40	#N/A	#N/A	BING4CT (NUC141) domain-containing protein
TGME49_212290	-1.10	#N/A	-1.20	ribosomal protein RPS19

FIGURE 4Y

TGME49_220100	-2.45	-2.35	-2.84	phosphoribosylpyrophosphate synthetase
TGME49_250690	-1.08	-1.30	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_318330	-8.77	-9.40	-9.40	histone lysine acetyltransferase MYST-A
TGME49_227930	1.20	1.43	1.31	hypothetical protein
TGME49_321440	-1.30	-1.15	-1.18	SWI2/SNF2 ISWI-like SANT
TGME49_202950	-1.45	-1.27	-1.07	hypothetical protein
TGME49_300290	-8.80	-8.49	-8.98	SNARE domain-containing protein
TGME49_249030	1.25	#N/A	#N/A	endonuclease/exonuclease/phosphatase family protein
TGME49_280380	1.22	#N/A	#N/A	poly(ADP-ribose) glycohydrolase
TGME49_311460	-2.88	-3.71	#N/A	hypothetical protein
TGME49_261620	1.56	2.13	1.94	hypothetical protein
TGME49_219070	1.18	#N/A	1.38	cyclic nucleotide-binding domain-containing protein
TGME49_310010	-1.27	-1.42	-1.26	rhoGTPase protein RON1
TGME49_237830	-8.77	-9.23	-9.48	DNA polymerase I domain-containing protein
TGME49_251800	1.68	2.31	2.19	hypothetical protein
TGME49_213790	-2.78	-3.06	-2.78	hypothetical protein
TGME49_219310	-1.41	-1.29	-1.31	DnaK family protein
TGME49_240300	-8.80	-8.47	-8.36	zinc finger domain, LSD1 subclass domain-containing protein
TGME49_298830	1.64	2.37	1.81	hypothetical protein
TGME49_236570	-1.26	-1.19	-1.58	lysine decarboxylase family protein
TGME49_289570	1.04	1.27	#N/A	phosphatidylinositol transfer protein
TGME49_266970	-3.21	-2.77	-3.02	hypothetical protein
TGME49_231130	-8.74	-9.12	-9.23	hypothetical protein
TGME49_252340	1.57	#N/A	1.23	hypothetical protein
TGME49_240540	-2.36	-2.20	-2.03	hypothetical protein
TGME49_209820	-8.77	-8.54	-8.59	syntaphin protein
TGME49_318410	-1.38	-1.14	-1.37	TCP-1 chaperonin, putative
TGME49_246800	-1.79	-1.35	-1.73	acylaminoacyl-peptidase, putative
TGME49_319640	1.06	1.11	1.26	hypothetical protein
TGME49_263040	-1.10	#N/A	-1.12	ribosomal protein RPS16
TGME49_297420	-3.92	-4.00	-3.85	beta-tubulin cofactor D, putative
TGME49_264840	-8.74	-9.06	-8.15	ATP-dependent DNA helicase, RecQ family protein
TGME49_237000	-3.90	-4.10	-4.26	polyphosphoinositide binding protein, putative
TGME49_237530	-8.74	-8.94	-8.75	hypothetical protein
TGME49_260640	-1.54	-2.13	-1.78	autophagy protein atg9 protein
TGME49_306890	-1.30	-1.42	#N/A	hypothetical protein
TGME49_233770	2.55	#N/A	-2.20	calcium-translocating P-type ATPase, PMCA-type protein
TGME49_310500	-1.12	#N/A	-1.17	hypothetical protein
TGME49_313090	-1.74	#N/A	-1.77	hypothetical protein
TGME49_278020	-2.58	-3.17	-2.94	hypothetical protein
TGME49_254420	2.12	#N/A	#N/A	phospholipase, patatin family protein
TGME49_292035	1.30	1.40	#N/A	hypothetical protein
TGME49_219130	-1.39	-1.87	-1.55	NADPH-glutathione reductase
TGME49_261960	1.21	1.52	1.20	hypothetical protein
TGME49_262890	-1.15	-1.50	-1.55	hypothetical protein
TGME49_288245	-1.00	#N/A	#N/A	hypothetical protein
TGME49_219100	-1.39	-1.60	-1.28	cyclin-dependent kinase regulatory subunit protein
TGME49_240700	-1.29	-1.21	-1.67	ubiquitin family protein
TGME49_316770	-1.39	-1.34	-1.37	undecaprenyl diphosphate synthase
TGME49_226350	1.16	#N/A	1.01	hypothetical protein
TGME49_289790	-2.58	-3.16	-2.92	hypothetical protein
TGME49_213752	-1.54	#N/A	-1.67	herpesviridae ul52/ul70 dna primase
TGME49_220460	-6.86	-8.40	-8.72	SNF7 family protein
TGME49_247280	-1.70	-2.16	-2.26	hypothetical protein
TGME49_278030	1.09	#N/A	#N/A	hypothetical protein
TGME49_211020	-1.39	-1.46	-1.86	RNA recognition motif-containing protein
TGME49_255270	1.98	#N/A	#N/A	hypothetical protein
TGME49_226080	1.13	#N/A	#N/A	polyA polymerase
TGME49_313630	2.69	#N/A	#N/A	hypothetical protein
TGME49_229200	-1.40	-1.32	#N/A	hypothetical protein
TGME49_242880	-1.70	-1.61	-1.76	flavoprotein
TGME49_286610	1.41	#N/A	#N/A	ribosomal protein RPS14, putative
TGME49_285660	-1.55	-2.12	-1.93	DEAD/DEAH box helicase domain-containing protein
TGME49_263560	1.13	1.29	#N/A	hypothetical protein
TGME49_257060	-1.70	-1.93	-2.12	translation initiation factor sui1 protein
TGME49_277260	#N/A	2.05	1.81	hypothetical protein
TGME49_202970	#N/A	-12.46	#N/A	hypothetical protein
TGME49_213570	#N/A	1.61	1.39	hypothetical protein

FIGURE 42

TGME49_280410	-1.95	-1.82	-1.69	3'/5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_290940	-1.57	-1.28	-1.48	EMP/nonaspanin domain family protein
TGME49_250115	1.14	#N/A	#N/A	hypothetical protein
TGME49_286750	-1.46	-1.50	-1.34	MA3 domain-containing protein
TGME49_270800	-3.97	-4.18	-4.23	GAF domain-containing protein
TGME49_223690	-8.74	-8.28	-8.14	hypothetical protein
TGME49_253320	-8.74	-8.05	-8.09	hypothetical protein
TGME49_217020	-3.37	-4.05	-2.23	ATPase, AFG1 family protein
TGME49_306470	-2.49	-2.47	-2.66	isoprenylcysteine carboxyl methyltransferase (icmt) family protein
TGME49_314280	2.69	2.21	2.47	AAR2 protein
TGME49_225690	-1.29	-1.43	-1.09	hypothetical protein
TGME49_292950	-1.21	#N/A	#N/A	hypothetical protein
TGME49_236550	-1.37	-1.20	-1.54	hypothetical protein
TGME49_226260	1.11	1.38	#N/A	hypothetical protein
TGME49_224600	-3.90	-3.70	-3.49	GTP binding protein
TGME49_216410	-8.82	-8.77	-8.55	hypothetical protein
TGME49_224310	-8.76	-8.90	-9.06	DHHC zinc finger domain-containing protein
TGME49_275755	2.14	3.25	3.34	hypothetical protein
TGME49_312330	-1.16	#N/A	#N/A	hypothetical protein
TGME49_219820	-1.23	#N/A	-1.03	polyubiquitin UbC, putative
TGME49_231180	1.62	#N/A	1.22	hypothetical protein
TGME49_261970	1.26	1.55	1.71	hypothetical protein
TGME49_212140	-4.01	-4.43	-4.21	hypothetical protein
TGME49_314730	-3.90	-3.97	-3.97	ALG6, ALG8 glycosyltransferase family protein
TGME49_297810	-1.39	-1.31	-1.71	hypothetical protein
TGME49_238950	-1.54	-1.75	-2.83	fatty acyl-CoA desaturase, putative
TGME49_294980	2.12	1.48	1.58	hypothetical protein
TGME49_292975	-3.16	-3.56	-2.70	hypothetical protein
TGME49_312860	-3.18	-2.92	-3.01	hypothetical protein
TGME49_268600	-3.13	-2.76	-2.96	DNA polymerase epsilon subunit B protein
TGME49_264860	-3.88	-3.77	-3.63	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_270900	-3.25	-3.24	-3.05	ATPase, AAA family protein
TGME49_269670	-3.14	-3.25	-2.67	hypothetical protein
TGME49_208740	#N/A	1.73	1.85	microneme protein, putative
TGME49_253430	#N/A	1.25	#N/A	asparagine synthetase, putative
TGME49_301890	#N/A	-3.97	#N/A	Toxoplasma gondii family B protein
TGME49_236040	#N/A	1.22	#N/A	fructose-1,6-bisphosphate aldolase
TGME49_267020	#N/A	-4.00	#N/A	hypothetical protein
TGME49_216140	#N/A	2.28	2.32	tetratricopeptide repeat-containing protein
TGME49_295440	#N/A	2.62	1.48	hypothetical protein
TGME49_210408	#N/A	1.13	#N/A	HMG (high mobility group) box domain-containing protein
TGME49_213255	#N/A	-5.17	#N/A	hypothetical protein
TGME49_286470	#N/A	1.35	1.18	AGC kinase
TGME49_269840	#N/A	1.41	#N/A	proteasome regulatory subunit
TGME49_242090	#N/A	1.04	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_205265	#N/A	2.34	#N/A	transporter, cation channel family protein
TGME49_217520	#N/A	1.29	1.16	hypothetical protein
TGME49_201390	#N/A	1.07	#N/A	hypothetical protein
TGME49_201785	#N/A	1.34	#N/A	hypothetical protein
TGME49_297940	#N/A	-2.13	#N/A	single-strand binding protein
TGME49_205170	#N/A	2.05	1.23	hypothetical protein
TGME49_217420	#N/A	-4.93	-4.14	hypothetical protein
TGME49_275610	#N/A	-1.70	#N/A	protein kinase, other
TGME49_295360	#N/A	1.14	#N/A	hypothetical protein
TGME49_275630	#N/A	-2.31	#N/A	HECT-domain (ubiquitin-transferase) domain-containing protein
TGME49_259115	#N/A	-3.62	#N/A	ABC1 family protein
TGME49_316470	#N/A	-3.66	#N/A	hypothetical protein
TGME49_297910	#N/A	-4.84	-2.63	hypothetical protein
TGME49_217400	#N/A	-3.18	-2.97	hypothetical protein
TGME49_213730	#N/A	1.28	#N/A	lanthionine synthetase C family protein
TGME49_306338	#N/A	-2.72	#N/A	dynein gamma chain, flagellar outer arm, putative
TGME49_291040	#N/A	4.27	8.36	lactate dehydrogenase LDH2
TGME49_249230	#N/A	-4.63	-4.83	hypothetical protein
TGME49_304740	#N/A	1.11	1.38	rhopty kinase family protein ROP35
TGME49_289540	#N/A	1.20	#N/A	hypothetical protein
TGME49_217550	#N/A	1.24	#N/A	hypothetical protein

FIGURE 4AA

TGME49_219800	-1.19	-1.05	-1.29	vacuolar ATP synthase subunit b, putative
TGME49_235490	-1.71	-1.64	-1.85	hypothetical protein
TGME49_312650	2.16	1.35	1.34	hypothetical protein
TGME49_244720	-3.87	-3.24	-3.58	hypothetical protein
TGME49_233410	1.71	2.08	1.48	Sof1 family domain-containing protein
TGME49_208200	-3.90	-3.86	-3.87	PHD-finger domain-containing protein
TGME49_205558	-1.08	#N/A	#N/A	NAC domain-containing protein
TGME49_256770	-1.33	-1.30	-1.47	eukaryotic translation initiation factor 4A, isoform 3, putative
TGME49_225160	1.17	#N/A	#N/A	hypothetical protein
TGME49_216120	-2.30	-2.20	-2.18	hypothetical protein
TGME49_272270	-8.70	-7.90	-7.71	radical SAM domain-containing protein
TGME49_264140	-1.79	-2.24	-1.45	hypothetical protein
TGME49_207770	-1.45	-1.29	-1.66	PCI domain-containing protein
TGME49_202280	-3.93	-4.40	-2.99	WD domain, G-beta repeat-containing protein
TGME49_310850	-8.75	-8.54	-8.68	MYND finger domain-containing protein
TGME49_223780	-1.90	-1.60	-1.76	hypothetical protein
TGME49_275350	-2.29	-1.94	-1.73	TBC domain-containing protein
TGME49_270580	-8.69	-10.08	#N/A	HECT-domain (ubiquitin-transferase) domain-containing protein
TGME49_253850	2.01	1.84	2.47	hypothetical protein
TGME49_252310	-2.02	-1.80	-1.27	hypothetical protein
TGME49_289310	-2.17	-2.16	-2.38	cullin family protein
TGME49_222060	-2.57	#N/A	-2.32	hypothetical protein
TGME49_310230	-8.70	-9.18	-9.01	hypothetical protein
TGME49_306530	-8.70	-8.20	-8.15	hypothetical protein
TGME49_276930	1.21	1.54	#N/A	hypothetical protein
TGME49_259520	-8.69	-8.72	-9.00	hypothetical protein
TGME49_210390	-8.74	-8.25	-8.60	WD domain, G-beta repeat-containing protein
TGME49_246230	-8.73	-8.45	-8.49	hypothetical protein
TGME49_307010	2.11	1.66	1.54	histone lysine demethylase JMJC1/KDM5D/JARID1D
TGME49_258670	-8.78	-9.80	-7.67	hypothetical protein
TGME49_294830	-2.83	-3.42	-2.72	methyltransferase domain-containing protein
TGME49_315600	-8.73	-9.28	-8.42	MCM2/3/5 family protein
TGME49_248820	#N/A	-9.38	#N/A	hypothetical protein
TGME49_244700	#N/A	-2.01	1.43	NAD(+)/NADH kinase domain-containing protein
TGME49_311100	#N/A	1.22	1.01	zinc finger (CCCH type) motif-containing protein
TGME49_218750	#N/A	-3.67	#N/A	hypothetical protein
TGME49_236540	#N/A	1.04	#N/A	RNA recognition motif-containing protein
TGME49_253930	#N/A	-2.02	-1.03	GCC2 and GCC3 domain-containing protein
TGME49_307770	#N/A	-2.20	#N/A	fumble protein
TGME49_254690	#N/A	1.06	#N/A	phospholipase/carboxylesterase
TGME49_294970	#N/A	1.33	#N/A	hypothetical protein
TGME49_245560	#N/A	1.10	1.35	hypothetical protein
TGME49_293900	#N/A	1.09	#N/A	sporozoite protein with an altered thrombospondin repeat SPATR
TGME49_318650	#N/A	1.15	#N/A	transhydrogenase
TGME49_239890	#N/A	1.15	#N/A	SCP family extracellular subfamily protein
TGME49_217410	#N/A	-9.14	-6.96	hypothetical protein
TGME49_269930	#N/A	-1.97	2.31	calcium binding egf domain-containing protein
TGME49_285870	#N/A	1.51	#N/A	SAG-related sequence SRS20A
TGME49_226580	#N/A	1.19	#N/A	hypothetical protein
TGME49_209940	#N/A	-2.39	#N/A	transporter/permease protein
TGME49_280500	#N/A	-4.11	#N/A	inorganic anion transporter, sulfate permease (SulP) family protein
TGME49_209985	#N/A	-2.18	1.72	cAMP-dependent protein kinase
TGME49_201780	#N/A	1.32	#N/A	microneme protein MIC2
TGME49_214100	#N/A	1.37	#N/A	hypothetical protein
TGME49_293760	#N/A	1.11	#N/A	EF hand domain-containing protein
TGME49_298070	#N/A	-9.23	-7.52	hypothetical protein
TGME49_269010	#N/A	1.25	1.36	AP2 domain transcription factor AP2VIII-7
TGME49_252500	#N/A	1.20	1.13	polo kinase
TGME49_299210	#N/A	1.03	#N/A	CTP synthase
TGME49_307570	#N/A	-1.29	#N/A	glycerol-3-phosphate dehydrogenase (gpdh), putative
TGME49_259020	#N/A	5.30	6.07	bradyzoite antigen BAG1
TGME49_301160	#N/A	-4.31	#N/A	SAG-related sequence SRS19C
TGME49_280370	#N/A	1.17	#N/A	hypothetical protein
TGME49_288530	#N/A	1.42	1.62	NOL1/NOP2/sun family protein

FIGURE 4BB

TGME49_315860	-2.13	-2.27	-2.21	EF hand domain-containing protein
TGME49_260320	-2.72	-2.93	-2.79	Noc2p family protein
TGME49_214770	-1.22	#N/A	-1.16	small GTP binding protein rab1a, putative
TGME49_294705	-8.71	-7.95	-8.35	hypothetical protein
TGME49_211630	1.02	1.20	#N/A	hypothetical protein
TGME49_255890	-3.11	-2.68	-2.76	pyridine nucleotide-disulfide oxidoreductase domain-containing protein
TGME49_292140	1.08	1.16	1.46	NIMA-related protein kinase NIMA1
TGME49_202620	1.02	1.00	#N/A	hypothetical protein
TGME49_290560	-3.84	-4.58	-3.90	ATP-binding cassette G family transporter ABCG89
TGME49_223150	-8.66	-8.53	-8.29	START domain-containing protein
TGME49_319312	2.20	2.19	#N/A	hypothetical protein
TGME49_243580	-2.65	-2.99	-4.10	Hit family protein involved in cell-cycle regulation, putative
TGME49_201900	-3.84	-3.84	-3.75	hypothetical protein
TGME49_243960	-1.04	#N/A	-1.09	nuclear transport factor 2 (ntf2) domain-containing protein
TGME49_255700	-1.94	-2.36	-2.42	hypothetical protein
TGME49_207180	-8.69	-8.79	-8.43	indole-3-glycerol phosphate synthase domain-containing protein
TGME49_292330	1.20	#N/A	1.16	hypothetical protein
TGME49_208970	-1.83	-1.94	-1.95	RNA recognition motif-containing protein
TGME49_264090	-3.12	-3.49	-3.20	hypothetical protein
TGME49_224020	1.43	1.50	1.43	hypothetical protein
TGME49_293380	-8.69	-8.48	-8.83	histone lysine acetyltransferase HAT1
TGME49_216390	-3.08	-3.12	-2.81	RNA methyltransferase, TrmH family protein
TGME49_249410	-2.51	-2.13	-1.73	hypothetical protein
TGME49_258230	-3.05	#N/A	-2.70	rhoGTPase family protein ROP20
TGME49_229370	-3.81	-4.00	-4.19	AP2 domain transcription factor AP2VIII-1
TGME49_278440	-1.90	-2.00	-2.07	SWI2/SNF2 Brahma-like putative
TGME49_278930	-2.03	-1.48	-1.65	Tubulin-tyrosine ligase family protein
TGME49_313270	-1.48	-1.51	-1.44	hypothetical protein
TGME49_203358	-3.84	-3.26	-3.49	hypothetical protein
TGME49_252190	2.27	1.94	1.56	KRUF family protein
TGME49_291140	-1.15	-1.02	-1.02	CCR4-Not complex component, Not1 protein
TGME49_305120	#N/A	1.18	#N/A	transporter, solute:sodium symporter (SSS) family protein
TGME49_264240	#N/A	-9.04	-7.39	hypothetical protein
TGME49_205700	#N/A	1.01	#N/A	cyclophilin precursor
TGME49_229630	#N/A	1.02	1.10	eIF2 kinase eIF2K-A (incomplete catalytic triad)
TGME49_278830	#N/A	-1.14	-1.79	glucose-6-phosphate 1-dehydrogenase
TGME49_207210	#N/A	2.74	6.79	hypothetical protein
TGME49_295960	#N/A	1.65	1.15	hypothetical protein
TGME49_301440	#N/A	-1.05	-1.17	calcium-dependent protein kinase CDPK1
TGME49_225000	#N/A	-1.48	#N/A	hypothetical protein
TGME49_295030	#N/A	1.07	#N/A	hypothetical protein
TGME49_260190	#N/A	-1.70	#N/A	microneme protein MIC13
TGME49_262050	#N/A	1.21	#N/A	rhoGTPase family protein ROP39
TGME49_307610	#N/A	-2.05	-1.42	elongation factor TS, putative
TGME49_264740	#N/A	1.01	#N/A	hypothetical protein
TGME49_267420	#N/A	1.12	#N/A	mago nashi family protein 2, putative
TGME49_263750	#N/A	-2.21	-1.31	hypothetical protein
TGME49_298840	#N/A	1.42	1.11	hypothetical protein
TGME49_314070	#N/A	1.40	1.30	hypothetical protein
TGME49_247250	#N/A	-1.57	#N/A	RbAp46
TGME49_306300	#N/A	-1.64	#N/A	hypothetical protein
TGME49_300055	#N/A	1.21	#N/A	hypothetical protein
TGME49_228200	#N/A	1.13	1.16	vacuolar (h+)-atpase g subunit protein
TGME49_263100	#N/A	-2.77	#N/A	hypothetical protein
TGME49_218910	#N/A	2.04	3.84	hypothetical protein
TGME49_215775	#N/A	-1.20	-1.13	rhoGTPase protein ROP8
TGME49_230350	#N/A	-1.13	-1.27	hypothetical protein
TGME49_257945	#N/A	2.51	4.42	3'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_233760	#N/A	-2.63	-2.10	hypothetical protein
TGME49_219738	#N/A	-1.76	-1.15	hypothetical protein
TGME49_312530	#N/A	1.09	1.08	splicing factor, CC1 family protein
TGME49_223570	#N/A	1.23	#N/A	hypothetical protein

FIGURE 4CC

TGME49_251885	-8.67	-7.96	-8.45	hypothetical protein
TGME49_296015	1.63	1.78	1.78	hypothetical protein
TGME49_310910	-8.67	-9.25	-8.88	WD domain, G-beta repeat-containing protein
TGME49_249790	-3.81	-3.89	-4.15	hypothetical protein
TGME49_269150	-8.65	-8.38	-8.45	DHHC zinc finger domain-containing protein
TGME49_300250	1.02	#N/A	#N/A	MN3/saliva family protein
TGME49_216630	-8.62	-8.21	-9.05	trigger factor protein, putative
TGME49_207800	-8.62	-8.11	-8.93	hypothetical protein
TGME49_218240	-1.16	#N/A	#N/A	hypothetical protein
TGME49_227320	-8.71	-8.68	-8.94	hypothetical protein
TGME49_222290	-3.81	-3.78	-4.11	LSM domain-containing protein
TGME49_225060	-2.43	-2.45	-2.83	nucleoredoxin family protein
TGME49_221295	-3.81	-4.08	-4.16	hypothetical protein
TGME49_285950	-8.68	-8.19	-8.09	hypothetical protein
TGME49_245590	2.04	1.89	1.27	rhomboid protease ROM6
TGME49_228130	1.71	1.67	1.68	hypothetical protein
TGME49_251850	-1.68	-1.52	-1.73	serine/threonine protein phosphatase
TGME49_215660	-8.62	-8.35	-8.11	hypothetical protein
TGME49_216170	-3.96	-3.81	-3.66	SufS subfamily cysteine desulfurase
TGME49_229490	-2.69	-2.71	-2.83	tetratricopeptide repeat-containing protein
TGME49_268900	-8.61	-8.63	-8.21	dense granular protein GRA10
TGME49_308060	-2.51	-2.21	-3.13	hypothetical protein
TGME49_305930	2.60	1.51	1.10	hypothetical protein
TGME49_293500	2.16	#N/A	1.06	hypothetical protein
TGME49_310270	-3.88	-4.08	-3.99	hypothetical protein
TGME49_277910	1.20	1.02	1.46	thrombospondin type 1 domain-containing protein
TGME49_289670	2.63	1.85	2.35	DNA repair metallo-beta-lactamase
TGME49_229500	-3.78	-3.82	-3.75	hypothetical protein
TGME49_212840	-8.67	-8.68	-8.08	HIT zinc finger protein
TGME49_294812	-3.81	-2.65	-3.12	RNA recognition motif-containing protein
TGME49_227010	-8.72	-8.64	-8.41	rhoGTPase family protein ROP30
TGME49_310670	-1.23	-1.17	-1.38	glycogen phosphorylase 1, putative
TGME49_231480	-1.54	-1.68	-1.60	GCN1, putative
TGME49_230950	-8.61	-9.15	-9.09	hypothetical protein
TGME49_225290	#N/A	2.09	3.12	GDA1/CD39 (nucleoside phosphatase) family protein
TGME49_315470	#N/A	-1.22	#N/A	hypothetical protein
TGME49_286090	#N/A	1.21	1.08	translation initiation factor eIF1, putative
TGME49_284780	#N/A	-1.22	-1.33	hypothetical protein
TGME49_308810	#N/A	-1.22	-1.91	rhoGTPase neck protein ROP9
TGME49_264190	#N/A	-2.85	-2.55	hypothetical protein
TGME49_219260	#N/A	-1.30	-1.05	cation-transporting ATPase, putative
TGME49_293780	#N/A	1.19	3.35	hypothetical protein
TGME49_280570	#N/A	2.08	6.96	SAG-related sequence SRS35A
TGME49_261570	#N/A	-1.05	-1.13	ribosomal protein RPL7A
TGME49_206320	#N/A	-1.23	#N/A	hypothetical protein
TGME49_255400	#N/A	1.34	1.27	hypothetical protein
TGME49_252640	#N/A	3.47	5.57	P-type ATPase PMA1
TGME49_315720	#N/A	-2.06	#N/A	Smg-4/UPF3 family protein
TGME49_289140	#N/A	1.35	1.10	ribosomal protein r22/r43, putative
TGME49_320750	#N/A	1.34	1.40	hypothetical protein
TGME49_232640	#N/A	1.84	2.93	RNA 2'-phosphotransferase, Tpt1/KptA family protein
TGME49_307650	#N/A	-1.55	#N/A	uracil-DNA glycosylase
TGME49_299010	#N/A	2.76	#N/A	hypothetical protein
TGME49_252280	#N/A	-1.75	#N/A	hypothetical protein
TGME49_240220	#N/A	-1.35	#N/A	hypothetical protein
TGME49_211720	#N/A	-1.07	#N/A	AP2 domain transcription factor AP2IV-5
TGME49_253615	#N/A	1.10	1.20	hypothetical protein
TGME49_246020	#N/A	-1.71	-1.58	SprT domain-containing protein
TGME49_253330	#N/A	2.26	#N/A	Rhoptry kinase family protein, truncated (incomplete catalytic triad)
TGME49_214900	#N/A	1.01	1.39	hypothetical protein
TGME49_248830	#N/A	-1.37	#N/A	phosphoinositide phospholipase PIPLC
TGME49_205690	#N/A	1.01	1.07	hypothetical protein
TGME49_318170	#N/A	1.25	1.50	hypothetical protein
TGME49_284645	#N/A	-2.12	-1.55	hypothetical protein
TGME49_218790	#N/A	-3.40	-3.03	elongation factor G C-terminus domain-containing protein
TGME49_293770	#N/A	1.29	#N/A	chitinase-like protein CLP1
TGME49_214520	#N/A	1.30	1.79	general transcription factor IIH polypeptide 4 GTF2H4
TGME49_263820	#N/A	-1.71	#N/A	DEAD/DEAH box helicase domain-containing protein

FIGURE 4DD

TGME49_243298	-8.61	-8.97	-8.88	ICE family protease (caspase) p20 domain-containing protein
TGME49_234190	-1.19	-1.10	-1.51	serine hydroxymethyltransferase 2, putative
TGME49_203060	1.16	1.09	#N/A	hypothetical protein
TGME49_295420	1.41	1.47	1.39	hypothetical protein
TGME49_233340	-2.45	-2.04	-2.23	hypothetical protein
TGME49_210980	1.49	1.58	1.67	alternative splicing type 3 and, putative
TGME49_270050	1.87	1.81	#N/A	hypothetical protein
TGME49_226900	1.66	1.23	1.11	hypothetical protein
TGME49_293730	-1.72	-1.95	-2.04	DHHC zinc finger domain-containing protein
TGME49_270090	-3.06	-3.16	-3.26	hypothetical protein
TGME49_318575	-8.61	-8.32	-8.69	hypothetical protein
TGME49_222940	3.27	1.75	4.65	hypothetical protein
TGME49_316900	-1.89	-1.47	-1.67	Sas10 C-terminal domain-containing protein
TGME49_239720	-8.57	-9.11	-8.71	50S ribosomal protein l24, putative
TGME49_299900	-8.57	-8.72	-8.45	hypothetical protein
TGME49_204380	-1.66	-1.72	-1.45	hypothetical protein
TGME49_263270	-1.32	#N/A	#N/A	glycerophosphodiester phosphodiesterase family protein
TGME49_290890	-2.41	-2.29	-2.85	carbonyl reductase 1, putative
TGME49_310570	-8.66	-8.60	-9.12	hypothetical protein
TGME49_217870	1.24	1.03	#N/A	DHHC zinc finger domain-containing protein
TGME49_306910	-2.21	-1.84	-2.37	hypothetical protein
TGME49_290740	-8.60	-8.14	-8.14	hypothetical protein
TGME49_309100	2.42	2.16	1.77	hypothetical protein
TGME49_223640	-8.67	-8.89	-7.99	hypothetical protein
TGME49_310300	-3.06	-2.61	-2.62	hypothetical protein
TGME49_291030	-3.82	-3.57	-3.67	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_244510	-8.57	-8.46	-7.58	AP2 domain transcription factor AP2V1-3
TGME49_310590	1.88	1.36	1.85	hypothetical protein
TGME49_262980	-8.57	-8.46	-8.65	hypothetical protein
TGME49_249950	-3.06	-2.20	-2.28	Mak16 protein
TGME49_219250	1.08	#N/A	1.12	acetyltransferase, GNAT family protein
TGME49_275310	-3.06	-3.07	-3.07	hypothetical protein
TGME49_285780	-8.61	-8.75	-8.59	hypothetical protein
TGME49_268430	-3.80	-3.45	-3.47	hypothetical protein
TGME49_306390	#N/A	-1.05	-1.62	hypothetical protein
TGME49_277220	#N/A	1.44	1.36	hypothetical protein
TGME49_239600	#N/A	-2.30	#N/A	rhoGTPase family protein ROP23 (incomplete catalytic triad)
TGME49_311080	#N/A	-1.92	-1.63	transporter, cation channel family protein
TGME49_271770	#N/A	-2.65	-2.03	hypothetical protein
TGME49_221260	#N/A	1.13	1.36	Class-II DAHP synthetase family protein
TGME49_209610	#N/A	1.15	#N/A	occyst wall protein OWP2
TGME49_311780	#N/A	-1.84	#N/A	Zn-containing alcohol dehydrogenase
TGME49_269885	#N/A	-1.06	-1.18	rhoGTPase metalloprotease toxolysin TLN1
TGME49_230080	#N/A	-2.25	-2.14	DEAD/DEAH box helicase domain-containing protein
TGME49_320480	#N/A	-1.14	#N/A	Rab11b
TGME49_315760	#N/A	-1.17	#N/A	AP2 domain transcription factor AP2X1-4
TGME49_231380	#N/A	1.20	#N/A	DNA-directed RNA polymerase II RPB4
TGME49_295610	#N/A	-1.14	-1.06	histone lysine methyltransferase, SET, putative
TGME49_222100	#N/A	-1.23	#N/A	hypothetical protein
TGME49_207830	#N/A	1.11	#N/A	MORN repeat-containing protein
TGME49_214940	#N/A	1.07	#N/A	MIC2-associated protein M2AP
TGME49_232980	#N/A	1.64	1.16	hypothetical protein
TGME49_240890	#N/A	-1.06	-1.27	6-phosphofructokinase
TGME49_225310	#N/A	-1.18	-1.30	ARF1-directed GTPase-activating protein, putative
TGME49_320100	#N/A	-1.06	#N/A	RNA recognition motif-containing protein
TGME49_262390	#N/A	-1.58	-1.70	TLD protein
TGME49_202410	#N/A	-1.62	-1.34	hypothetical protein
TGME49_281650	#N/A	-1.66	-1.49	hypothetical protein
TGME49_258350	#N/A	1.36	1.50	hypothetical protein
TGME49_311890	#N/A	-1.06	-1.36	hypothetical protein
TGME49_306540	#N/A	1.22	1.19	phosphotransferase enzyme family protein
TGME49_309190	#N/A	1.05	#N/A	hypothetical protein
TGME49_260520	#N/A	1.24	1.26	hypothetical protein
TGME49_223668	#N/A	1.55	1.96	LYAR-type C2HC zinc finger protein
TGME49_236510	#N/A	1.02	1.16	hypothetical protein
TGME49_241180	#N/A	-1.11	-1.49	hypothetical protein
TGME49_236070	#N/A	1.16	#N/A	pyrroline-5-carboxylate reductase
TGME49_306250	#N/A	1.53	1.16	hypothetical protein

FIGURE 4EE

TGME49_300020	-3.75	-3.85	-3.92	ATP-dependent metalloproteinase H1B subfamily protein
TGME49_313350	-3.75	-3.88	-3.92	hypothetical protein
TGME49_229290	-8.59	-7.86	-7.57	kelch repeat-containing protein
TGME49_258480	-1.88	-2.15	-1.69	hypothetical protein
TGME49_310710	-3.75	-3.67	-3.72	small ribosomal subunit Rsm22 protein
TGME49_230000	1.49	#N/A	#N/A	hypothetical protein
TGME49_295015	1.87	1.43	#N/A	patched family protein
TGME49_272640	-2.08	-1.99	-1.55	eukaryotic initiation factor-2B, epsilon subunit, putative
TGME49_208820	-3.81	-3.36	-4.32	1-deoxy-D-xylulose-5-phosphate synthase
TGME49_222920	-2.21	-1.66	-1.76	mbp-1 interacting protein-2a family protein
TGME49_232160	1.18	1.17	1.33	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_245485	1.89	2.07	2.12	microneme protein MIC9
TGME49_243490	-8.57	-8.38	-8.22	BCS1 family isoform 9, putative
TGME49_249560	-8.58	-8.94	-8.49	DNA-directed RNA polymerase alpha chain rpoA
TGME49_289290	-1.79	-1.62	-1.92	hypothetical protein
TGME49_244000	-8.57	-8.89	-8.53	DEAD/DEAH box helicase domain-containing protein
TGME49_285990	-3.82	-3.59	-3.77	Filamin/ABP280 repeat-containing protein
TGME49_260580	-2.07	-2.25	-2.15	hypothetical protein
TGME49_296340	3.34	4.60	3.29	hypothetical protein
TGME49_256030	-1.17	-1.04	#N/A	hypothetical protein
TGME49_263410	6.14	5.23	4.20	scavenger receptor cysteine-rich domain-containing protein
TGME49_249698	-8.60	-8.18	-8.20	hypothetical protein
TGME49_255740	-3.07	-2.80	-2.80	hypothetical protein
TGME49_235960	-8.56	-7.45	-8.01	hypothetical protein
TGME49_248570	-3.80	-3.88	-3.77	hypothetical protein
TGME49_268220	9.62	#N/A	6.66	hypothetical protein
TGME49_221440	-8.58	-9.14	-8.53	RPGR, putative
TGME49_259850	-8.53	-8.28	-8.38	hypothetical protein
TGME49_240370	6.91	8.07	8.58	Toxoplasma gondii family E protein
TGME49_248150	-3.75	-3.61	-3.97	hypothetical protein
TGME49_243340	-8.53	-8.47	-8.35	atypical MEK-related kinase (incomplete catalytic triad)
TGME49_209130	-8.53	-9.11	-9.35	regulator of chromosome condensation (RCC1) repeat-containing protein
TGME49_239830	-1.38	#N/A	#N/A	TBC domain-containing protein
TGME49_221585	-8.57	-8.19	-8.53	hypothetical protein
TGME49_212920	#N/A	1.27	1.53	hypothetical protein
TGME49_229450	#N/A	-1.79	-1.76	hypothetical protein
TGME49_301410	#N/A	-1.28	#N/A	hypothetical protein
TGME49_227270	#N/A	2.27	1.71	hypothetical protein
TGME49_308070	#N/A	-1.96	-2.16	hypothetical protein
TGME49_209070	#N/A	1.13	1.56	hypothetical protein
TGME49_255290	#N/A	-2.21	#N/A	hypothetical protein
TGME49_262170	#N/A	-2.13	-1.76	hypothetical protein
TGME49_240580	#N/A	-1.63	#N/A	hypothetical protein
TGME49_251790	#N/A	1.04	1.27	hypothetical protein
TGME49_242790	#N/A	-1.35	-1.81	trichothyalin, putative
TGME49_312480	#N/A	1.13	1.19	uracil phosphoribosyltransferase FUR1, putative
TGME49_226320	#N/A	1.14	1.17	hypothetical protein
TGME49_223130	#N/A	1.41	1.81	hypothetical protein
TGME49_272520	#N/A	-1.18	-1.36	hypothetical protein
TGME49_290000	#N/A	-7.76	-8.91	hypothetical protein
TGME49_264970	#N/A	-1.26	#N/A	hypothetical protein
TGME49_244290	#N/A	-1.20	#N/A	adapter-related protein
TGME49_273580	#N/A	-2.08	-1.81	hypothetical protein
TGME49_244250	#N/A	-1.02	-1.08	hypothetical protein
TGME49_265410	#N/A	1.14	#N/A	G-protein beta WD-40 repeat containing protein
TGME49_304490	#N/A	1.05	#N/A	hypothetical protein
TGME49_209755	#N/A	2.88	6.35	hypothetical protein
TGME49_316760	#N/A	1.37	1.08	hypothetical protein
TGME49_318730	#N/A	-1.21	-1.30	glycosyl transferase
TGME49_258700	#N/A	-1.09	-1.25	transporter, major facilitator family protein
TGME49_280580	#N/A	1.19	4.14	SAG-related sequence SRG35B
TGME49_267590	#N/A	-1.24	-1.10	hypothetical protein
TGME49_266690	#N/A	-1.12	-1.12	hypothetical protein
TGME49_233520	#N/A	-1.13	-1.09	ATP-dependent RNA helicase
TGME49_309610	#N/A	-3.07	-3.05	hypothetical protein
TGME49_237870	#N/A	-3.04	-3.13	FYVE zinc finger domain-containing protein
TGME49_244412	#N/A	-2.38	-1.85	hypothetical protein
TGME49_254915	#N/A	-2.51	#N/A	hypothetical protein

FIGURE 4FF

TGME49_242870	-8.53	-8.42	-9.02	histone lysine methyltransferase, SET, putative
TGME49_227115	-8.53	-8.32	-8.38	hypothetical protein
TGME49_304900	-1.22	#N/A	#N/A	hypothetical protein
TGME49_269130	-8.53	-7.92	-7.97	hypothetical protein
TGME49_228490	-2.63	-2.73	-2.64	hypothetical protein
TGME49_261650	-1.52	-1.11	#N/A	hypothetical protein
TGME49_304470	-3.00	-2.98	-2.80	oxidoreductase, putative
TGME49_283790	-1.57	-1.79	-1.31	protein kinase, putative
TGME49_280720	-8.53	-7.98	-8.46	hypothetical protein
TGME49_212860	1.22	1.11	1.90	hypothetical protein
TGME49_240460	-3.00	-2.50	-2.70	AP2 domain transcription factor AP2V1-1
TGME49_279430	-2.66	-2.90	-2.75	owf18 pre-mRNA splicing factor protein
TGME49_281510	-3.01	-3.35	-3.11	ribonuclease H1 large subunit, putative
TGME49_213460	2.47	#N/A	#N/A	hypothetical protein
TGME49_239560	-8.60	-8.57	-8.98	myosin E
TGME49_285260	2.21	2.73	2.87	hypothetical protein
TGME49_313360	1.44	1.10	1.20	hypothetical protein
TGME49_247300	1.01	1.39	#N/A	hypothetical protein
TGME49_256840	-3.72	-3.89	-4.47	hypothetical protein
TGME49_259530	-3.72	-3.93	-4.38	GalNac
TGME49_311500	-8.58	-8.99	-8.88	ThiF family protein
TGME49_251840	1.29	1.40	1.67	hypothetical protein
TGME49_250220	2.17	2.42	2.46	hypothetical protein
TGME49_216130	-1.94	-1.93	-2.29	ubiquitin conjugating enzyme E2, putative
TGME49_278130	-2.14	-1.77	-2.05	hypothetical protein
TGME49_293460	-3.75	-3.13	-2.94	ATP-dependent DNA ligase domain-containing protein
TGME49_308990	-3.72	-3.37	-2.98	transporter, solute:sodium symporter (SSS) family protein
TGME49_248790	2.18	2.11	1.96	hypothetical protein
TGME49_227140	2.65	2.29	3.00	hypothetical protein
TGME49_250830	-1.53	-1.24	-1.69	SAC3/GANP family protein
TGME49_305560	-3.72	-3.83	-4.05	Vps51/Vps67 protein
TGME49_300048	1.07	1.38	#N/A	hypothetical protein
TGME49_263290	2.97	2.59	2.69	rhomboid protease ROM2
TGME49_286560	-8.57	-8.68	-8.93	U6 snRNA-associated Sm family protein
TGME49_276900	-3.75	-3.60	-3.11	hypothetical protein
TGME49_300180	#N/A	-3.00	-2.69	hypothetical protein
TGME49_280750	#N/A	1.06	#N/A	rudimentary enhancer, putative
TGME49_222245	#N/A	1.08	#N/A	hypothetical protein
TGME49_293350	#N/A	-1.37	-1.06	mitochondrial carrier superfamily protein
TGME49_261990	#N/A	-1.08	#N/A	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_278260	#N/A	-2.99	-2.82	polynucleotide adenyllyltransferase
TGME49_231100	#N/A	-1.07	-1.00	hypothetical protein
TGME49_225330	#N/A	-1.14	-1.38	hypothetical protein
TGME49_220300	#N/A	-1.53	#N/A	ribosomal protein L15 protein
TGME49_232760	#N/A	1.05	#N/A	protein phosphatase inhibitor IPP2
TGME49_309010	#N/A	1.77	#N/A	elongation factor P, putative
TGME49_295950	#N/A	1.48	1.42	KRUF family protein
TGME49_267760	#N/A	-1.67	-1.87	hypothetical protein
TGME49_249320	#N/A	-1.99	-1.97	flavodoxin domain-containing protein
TGME49_313790	#N/A	1.11	#N/A	hypothetical protein
TGME49_261490	#N/A	-1.03	#N/A	hypothetical protein
TGME49_275420	#N/A	-1.37	-1.12	histone lysine-specific demethylase LSD1/BHC110/KDMA1A
TGME49_262860	#N/A	-2.30	-2.77	ADP-ribosylation factor family protein 1, putative
TGME49_221990	#N/A	-1.01	#N/A	hypothetical protein
TGME49_223600	#N/A	-1.99	-2.00	hypothetical protein
TGME49_262130	#N/A	-1.41	-1.55	hypothetical protein
TGME49_204880	#N/A	-1.82	#N/A	hypothetical protein
TGME49_320720	#N/A	-2.34	-2.05	hypothetical protein
TGME49_223270	#N/A	1.19	1.19	hypothetical protein
TGME49_236840	#N/A	-1.11	-1.26	zinc finger (C-x8-C-x5-C-x3-H)-2, putative
TGME49_240950	#N/A	-3.00	-2.50	hypothetical protein
TGME49_279370	#N/A	-1.05	#N/A	SNARE associated Golgi protein
TGME49_247640	#N/A	1.04	#N/A	hypothetical protein
TGME49_276120	#N/A	-2.46	#N/A	histone lysine methyltransferase, SET, putative
TGME49_231920	#N/A	1.38	1.51	oxidoreductase, short chain dehydrogenase/reductase family protein
TGME49_200250	#N/A	-1.00	#N/A	microneme protein MIC17A
TGME49_278780	#N/A	-1.37	-1.56	hypothetical protein
TGME49_285830	#N/A	-1.04	#N/A	hypothetical protein
TGME49_264460	#N/A	-2.02	#N/A	DNA-directed RNA polymerase III RPC5
TGME49_305230	#N/A	-2.30	#N/A	hypothetical protein

FIGURE 4GG

TGME49_286800	-8.52	-8.40	-8.64	hypothetical protein
TGME49_274130	-8.48	-8.65	-8.63	TBC domain-containing protein
TGME49_206695	1.84	2.04	2.63	hypothetical protein
TGME49_227350	-3.09	-3.12	-2.22	hypothetical protein
TGME49_209270	-8.57	-8.33	-8.29	hypothetical protein
TGME49_221710	-2.60	-2.51	-2.21	TBC domain-containing protein
TGME49_202750	-8.48	-8.29	-8.29	3' exoribonuclease family, domain 1 domain-containing protein
TGME49_320440	-2.35	-2.81	-1.56	hypothetical protein
TGME49_262550	-8.48	-8.21	-7.88	hypothetical protein
TGME49_268960	-2.98	-3.24	-3.38	5'-AMP-activated protein kinase subunit beta-1 family protein, putative
TGME49_218358	-8.52	-8.28	-8.17	zinc knuckle domain-containing protein
TGME49_262650	-3.77	-3.55	-3.54	WD domain, G-beta repeat-containing protein
TGME49_202010	-2.51	-3.08	-2.20	hypothetical protein
TGME49_319308	-2.63	-1.88	-4.12	hypothetical protein
TGME49_273920	-2.61	-2.42	-2.55	aldose reductase, putative
TGME49_249740	1.50	1.72	1.51	translation machinery associated tma7 protein
TGME49_309130	-8.48	-8.47	-8.17	hypothetical protein
TGME49_297900	1.40	1.69	1.37	hypothetical protein
TGME49_312960	1.26	1.72	1.67	hypothetical protein
TGME49_278240	-8.75	-8.54	#N/A	Zn-finger in Ran binding protein and others domain-containing protein
TGME49_295060	-8.49	-8.17	-7.75	exonuclease
TGME49_248870	1.36	1.25	#N/A	SNARE associated Golgi protein
TGME49_266390	-8.48	-8.00	-8.07	DNA mismatch repair protein, C-terminal domain-containing protein
TGME49_248140	3.21	#N/A	#N/A	hypothetical protein
TGME49_270230	-8.48	-8.80	-8.58	hypothetical protein
TGME49_248160	-8.48	-8.80	-9.03	hypothetical protein
TGME49_219660	3.07	#N/A	3.10	hypothetical protein
TGME49_279540	-8.54	-7.14	-8.72	hypothetical protein
TGME49_221280	-1.56	-1.31	-1.03	hypothetical protein
TGME49_318260	-3.69	-3.49	-3.67	transcription initiation factor TFIID subunit TAF5
TGME49_247700	1.31	1.14	1.32	AP2 domain transcription factor AP2XII-4
TGME49_253410	2.32	1.99	2.32	hypothetical protein
TGME49_250680	-2.58	-2.11	-2.09	TBC domain-containing kinase (incomplete catalytic triad)
TGME49_254390	1.06	#N/A	#N/A	CRAL/TRIO domain-containing protein
TGME49_208990	#N/A	1.21	1.48	hypothetical protein
TGME49_285680	#N/A	1.13	#N/A	dihydrolipoamide acyltransferase, putative
TGME49_214120	#N/A	-2.91	-2.85	hypothetical protein
TGME49_249450	#N/A	-2.89	-2.70	hypothetical protein
TGME49_255245	#N/A	1.40	#N/A	hypothetical protein
TGME49_252250	#N/A	-1.61	#N/A	ATPase, AAA family protein
TGME49_230920	#N/A	-2.86	-2.89	adaptor complexes medium subunit family protein
TGME49_214630	#N/A	-1.37	#N/A	hypothetical protein
TGME49_231815	#N/A	-1.98	#N/A	hypothetical protein
TGME49_315980	#N/A	-1.92	-2.11	EREBP-4 family protein
TGME49_287970	#N/A	-1.02	#N/A	hypothetical protein
TGME49_214170	#N/A	-1.58	-1.46	hypothetical protein
TGME49_270170	#N/A	-1.56	-1.44	hypothetical protein
TGME49_244150	#N/A	-1.93	#N/A	glycerate kinase
TGME49_201380	#N/A	1.15	#N/A	chorismate synthase, putative
TGME49_208360	#N/A	1.14	1.48	hypothetical protein
TGME49_285720	#N/A	-2.21	-1.90	ATP binding protein, putative
TGME49_249160	#N/A	-2.22	#N/A	UAA transporter family protein
TGME49_267440	#N/A	1.14	#N/A	RING zinc finger protein
TGME49_260480	#N/A	-2.84	-3.42	leucine rich repeat-containing protein
TGME49_227440	#N/A	1.02	1.14	WD domain, G-beta repeat-containing protein
TGME49_286030	#N/A	-1.08	#N/A	hypothetical protein
TGME49_278110	#N/A	-1.59	#N/A	1,3-beta-glucan synthase component protein
TGME49_305010	#N/A	-1.73	-1.71	pre-mRNA branch site protein p14, putative
TGME49_230890	#N/A	-1.40	#N/A	PHD-finger domain-containing protein
TGME49_252230	#N/A	-1.16	#N/A	hypothetical protein
TGME49_222300	#N/A	-1.18	#N/A	hypothetical protein
TGME49_234560	#N/A	-1.19	-1.08	hypothetical protein
TGME49_258940	#N/A	1.34	1.21	acylphosphatase family protein
TGME49_239690	#N/A	1.21	#N/A	hypothetical protein
TGME49_225120	#N/A	1.05	#N/A	hypothetical protein
TGME49_314710	#N/A	-1.22	-1.20	carrier superfamily protein
TGME49_209870	#N/A	-1.84	#N/A	HAD hydrolase, family IIA protein
TGME49_278060	#N/A	-1.62	#N/A	Mre11 DNA-binding domain-containing protein

FIGURE 4HH

TGME49_220175	2.95	2.52	2.87	hypothetical protein
TGME49_227910	-1.23	-1.06	-1.72	hypothetical protein
TGME49_203760	1.36	1.63	1.68	hypothetical protein
TGME49_297245	-1.46	-1.42	-1.09	transporter, major facilitator family protein
TGME49_271625	-8.49	-8.19	-8.07	serine--tRNA ligase
TGME49_205300	1.32	1.24	#N/A	hypothetical protein
TGME49_226030	-1.07	#N/A	-1.35	AGC kinase
TGME49_309890	-3.00	-3.19	-2.78	hypothetical protein
TGME49_260510	-2.95	-2.70	-2.86	ubiquitin thioesterase otubain-like family protein
TGME49_300285	-8.57	-8.51	-8.56	hypothetical protein
TGME49_229930	1.35	#N/A	#N/A	p25-alpha family protein
TGME49_248990	1.18	1.70	1.29	hypothetical protein
TGME49_209240	1.56	1.50	1.25	RNA methyltransferase
TGME49_289890	-3.06	-2.45	-2.64	hypothetical protein
TGME49_235478	-3.79	-4.09	-4.14	pantothenate kinase
TGME49_277840	1.13	#N/A	#N/A	Ras family protein
TGME49_270940	-8.50	-8.13	-8.10	hypothetical protein
TGME49_224580	-1.86	-1.73	-1.95	RNA recognition motif-containing protein
TGME49_242118	-8.44	-8.65	-9.98	myosin-light-chain kinase
TGME49_253510	2.42	2.70	2.46	transporter/permease protein
TGME49_220450	-8.43	-8.51	-7.24	ribonuclease HI protein
TGME49_262030	-8.43	-8.59	-7.63	ALG6, ALG8 glycosyltransferase family protein
TGME49_208500	-2.35	-2.69	-2.68	protein phosphatase 2C domain-containing protein
TGME49_243530	-8.44	-8.23	-7.39	pentatricopeptide repeat domain-containing protein
TGME49_316300	-8.44	-8.83	-8.15	ATP-dependent DNA helicase, RecQ family protein
TGME49_227310	-3.69	-3.45	-3.61	hypothetical protein
TGME49_230590	-8.44	-8.41	-8.73	chitobiosyldiphosphodolichol beta-mannosyltransferase
TGME49_309580	-2.95	-2.79	-2.64	transporter, major facilitator family protein
TGME49_213420	-8.43	-7.88	-7.90	RAP domain-containing protein
TGME49_270720	-8.55	-8.74	-8.70	hypothetical protein
TGME49_264870	1.73	1.57	1.55	Sodium:neurotransmitter symporter family protein
TGME49_275740	#N/A	-2.83	-2.66	hypothetical protein
TGME49_304650	#N/A	-1.23	#N/A	histidine acid phosphatase superfamily protein
TGME49_284040	#N/A	-1.33	-1.16	hypothetical protein
TGME49_313970	#N/A	-1.87	-2.25	Phytanoyl-CoA dioxygenase (PhyH) superfamily protein
TGME49_298060	#N/A	-2.00	#N/A	Toxoplasma gondii family C protein
TGME49_249190	#N/A	1.34	1.62	AP2 domain transcription factor AP2XII-6
TGME49_277895	#N/A	-1.39	#N/A	ubiquitin carboxyl-terminal hydrolase
TGME49_236130	#N/A	1.74	1.59	signal recognition particle (SRP9) domain-containing protein
TGME49_273310	#N/A	-1.30	-1.66	hypothetical protein
TGME49_211610	#N/A	1.00	#N/A	hypothetical protein
TGME49_215080	#N/A	-1.29	#N/A	hypothetical protein
TGME49_318320	#N/A	-2.16	-1.88	ATP-dependent Clp endopeptidase, proteolytic subunit ClpP domain-containing protein
TGME49_203030	#N/A	1.10	#N/A	N-methyl-D-aspartate receptor-associated protein
TGME49_234370	#N/A	-2.22	-2.11	SAG-related sequence SRS42
TGME49_240490	#N/A	-2.20	#N/A	hypothetical protein
TGME49_230990	#N/A	1.32	1.09	hypothetical protein
TGME49_204040	#N/A	-2.11	-2.00	hypothetical protein
TGME49_268010	#N/A	-1.26	-1.15	hypothetical protein
TGME49_308030	#N/A	-1.38	-1.36	hypothetical protein
TGME49_263580	#N/A	1.49	1.27	bromodomain-containing protein
TGME49_226980	#N/A	1.29	#N/A	hypothetical protein
TGME49_268560	#N/A	-1.60	#N/A	XPG N-terminal domain-containing protein
TGME49_218610	#N/A	-1.64	-1.51	ATPase (DUF699) protein
TGME49_265080	#N/A	-1.01	#N/A	Tubulin-tyrosine ligase family protein
TGME49_301450	#N/A	-1.00	#N/A	FG-GAP repeat-containing protein
TGME49_233300	#N/A	-2.07	-2.85	RhoGAP domain-containing protein
TGME49_318720	#N/A	1.15	#N/A	pyridoxal phosphate enzyme, YggS family protein
TGME49_320470	#N/A	1.90	1.79	hypothetical protein
TGME49_289010	#N/A	-1.78	#N/A	RNA recognition motif-containing protein
TGME49_225108	#N/A	-1.44	#N/A	SNF7 family protein
TGME49_257780	#N/A	-1.44	-1.56	hypothetical protein

FIGURE 4ii

TGME49_268210	-8.89	-9.53	-8.82	AGC kinase
TGME49_202180	-1.70	-1.32	#N/A	hypothetical protein
TGME49_318525	-1.80	-2.33	-1.61	hypothetical protein
TGME49_260160	3.22	2.71	2.93	hypothetical protein
TGME49_233220	1.38	1.04	#N/A	hypothetical protein
TGME49_285490	-8.43	-9.04	-9.07	helix-hairpin-helix motif domain-containing protein
TGME49_268590	1.07	1.10	#N/A	rhomboid protease ROM4
TGME49_259210	-8.43	-8.66	-8.38	jmjC domain-containing protein C2orf60
TGME49_215210	2.40	2.39	2.76	hypothetical protein
TGME49_234670	1.96	1.80	1.81	actin-like family protein
TGME49_263000	1.16	1.31	1.31	Beige/BEACH domain-containing protein
TGME49_229780	-3.65	-3.83	-4.23	GHMP kinase, N-terminal domain-containing protein
TGME49_316250	1.68	2.06	1.34	hypothetical protein
TGME49_261510	3.43	3.26	3.07	hypothetical protein
TGME49_289180	-8.44	-8.64	-8.35	thioredoxin family redox-active protein, putative
TGME49_213240	-8.45	-8.83	-8.59	hypothetical protein
TGME49_278470	-3.77	-3.38	-3.72	hypothetical protein
TGME49_254910	-2.58	-2.81	-2.61	hypothetical protein
TGME49_309250	-1.73	-1.54	-1.53	hypothetical protein
TGME49_278920	-2.97	-2.72	-3.20	hypothetical protein
TGME49_224660	1.13	1.12	1.20	transcription factor s-li (tfliis), central domain-containing protein
TGME49_254090	-1.68	-1.39	#N/A	hypothetical protein
TGME49_285650	-1.50	-1.41	#N/A	hypothetical protein
TGME49_285840	1.67	1.36	1.80	RAP domain-containing protein
TGME49_206480	1.17	1.40	#N/A	hypothetical protein
TGME49_232020	-1.94	-1.93	-1.92	hypothetical protein
TGME49_271870	-8.39	-8.47	-8.96	zinc carboxypeptidase superfamily protein
TGME49_317705	-2.02	-1.73	-1.59	enoyl-CoA hydratase/isomerase family protein
TGME49_271350	-8.39	-8.50	-9.10	bifunctional protein FcIC subfamily protein
TGME49_204050	1.54	3.19	#N/A	subtilisin SUB1
TGME49_231600	-2.33	-1.91	-2.49	HEAT repeat-containing protein
TGME49_203450	-2.15	-2.25	-2.19	DUF3228 domain-containing protein
TGME49_232730	#N/A	1.04	#N/A	acyl-CoA:diacylglycerol acyltransferase 1-related enzyme
TGME49_300330	#N/A	1.01	1.06	hypothetical protein
TGME49_294902	#N/A	-1.58	#N/A	hypothetical protein
TGME49_264200	#N/A	-1.76	#N/A	hypothetical protein
TGME49_245435	#N/A	1.27	#N/A	hypothetical protein
TGME49_301460	#N/A	1.13	1.27	hypothetical protein
TGME49_206500	#N/A	-2.71	-2.88	hypothetical protein
TGME49_240450	#N/A	1.35	1.81	Maf family protein
TGME49_239580	#N/A	-7.04	-9.11	hypothetical protein
TGME49_217500	#N/A	2.01	#N/A	HMG (high mobility group) box domain-containing protein
TGME49_257500	#N/A	1.30	1.33	hypothetical protein
TGME49_288640	#N/A	1.19	1.49	radical SAM domain-containing protein
TGME49_220260	#N/A	1.22	#N/A	hypothetical protein
TGME49_247240	#N/A	-1.21	-1.96	ubiquitin carboxyl-terminal hydrolase, family 1 protein
TGME49_242240	#N/A	-1.15	-1.32	roptry kinase family protein ROP19A
TGME49_227920	#N/A	-1.40	-1.66	hypothetical protein
TGME49_256910	#N/A	1.28	#N/A	hypothetical protein
TGME49_238130	#N/A	-1.23	-1.24	hypothetical protein
TGME49_243310	#N/A	1.37	#N/A	hypothetical protein
TGME49_258550	#N/A	-1.36	#N/A	SAG-related sequence SRS28
TGME49_247370	#N/A	-1.40	#N/A	hypothetical protein
TGME49_295680	#N/A	-1.29	-1.29	periodic tryptophan protein PWP2, putative
TGME49_269760	#N/A	1.16	1.29	'chromo' (CHR)romatin Organization MODifier) domain-containing protein
TGME49_289130	#N/A	-2.02	-1.94	hypothetical protein
TGME49_255320	#N/A	1.18	#N/A	mRNA turnover 4 (MRT4) family protein
TGME49_231625	#N/A	-1.76	#N/A	hypothetical protein
TGME49_206470	#N/A	1.11	#N/A	pyruvate dehydrogenase complex subunit PDH-E3II
TGME49_228010	#N/A	-1.53	#N/A	hypothetical protein
TGME49_256820	#N/A	-1.52	-1.65	zinc finger (CCCH type) motif-containing protein
TGME49_269630	#N/A	1.13	1.47	hypothetical protein
TGME49_243750	#N/A	2.11	2.44	tetrapeptide repeat-containing protein
TGME49_236990	#N/A	1.16	4.01	beta-ketoacyl synthase, N-terminal domain-containing protein

FIGURE 4JJ

TGME49_272680	-8.39	-8.53	-8.28	hypothetical protein
TGME49_224150	-8.39	-7.83	-8.15	hypothetical protein
TGME49_223510	-8.39	-8.72	-8.57	hypothetical protein
TGME49_311110	-3.62	-3.95	-4.24	Ubiquitin-fold modifier 1 precursor family protein, putative
TGME49_226970	1.16	1.03	#N/A	ribosomal protein RPS11
TGME49_264660	-1.28	#N/A	#N/A	SAG-related sequence SRS44
TGME49_263330	-8.48	-8.17	-8.20	Adaptin ear-binding coat-associated protein 2 (NECAP-2) isoform 2 family protein
TGME49_254290	1.41	1.44	1.66	hypothetical protein
TGME49_267560	2.04	1.64	1.89	folate-binding protein YgZ protein
TGME49_228320	-8.39	-7.69	-7.90	hypothetical protein
TGME49_246060	-8.46	-8.09	-8.64	DNA-dependent RNA polymerase
TGME49_284010	-3.62	-3.91	-3.01	5'-3' exonuclease, N-terminal resolvase family domain-containing protein
TGME49_270750	-2.18	-2.27	-1.69	hypothetical protein
TGME49_283850	-1.69	-1.75	-1.94	peptidyl-prolyl cis-trans isomerase
TGME49_209460	-8.39	-8.00	-7.97	hypothetical protein
TGME49_240960	2.32	2.00	1.75	AlG2 family protein
TGME49_234520	-2.31	-1.54	-2.17	U2 snRNP auxiliary factor, large subunit, splicing factor subfamily protein
TGME49_216850	-8.38	-7.64	-8.06	hypothetical protein
TGME49_261000	-1.53	-1.56	-1.53	MutS domain V domain-containing protein
TGME49_284170	-8.39	-8.22	-8.25	DHHC zinc finger domain-containing protein
TGME49_293840	1.34	1.05	#N/A	hypothetical protein
TGME49_221370	-3.61	-3.47	-3.01	hypothetical protein
TGME49_228340	-8.39	-8.49	-8.07	hypothetical protein
TGME49_275670	-1.17	-1.25	#N/A	alveolin domain containing intermediate filament IMC15
TGME49_318480	-2.29	-2.48	-2.01	SWI2/SNF2-containing protein RAD5
TGME49_246030	-8.38	-8.35	-8.28	mediator complex subunit MED17
TGME49_268870	-1.28	-1.11	-1.08	tetratricopeptide repeat-containing protein
TGME49_281990	1.60	1.70	1.70	Nicotinamidase
TGME49_264880	-2.29	-2.19	-2.05	NEDD8-activating enzyme E1 catalytic subunit
TGME49_288800	3.01	3.24	2.81	endonuclease/exonuclease/phosphatase family protein
TGME49_246190	-2.53	-2.68	-2.48	hypothetical protein
TGME49_312500	-1.52	-1.57	-1.71	hypothetical protein
TGME49_218000	#N/A	-1.71	-1.61	hypothetical protein
TGME49_305460	#N/A	1.60	#N/A	methionine aminopeptidase 2, putative
TGME49_217951	#N/A	-1.28	8.04	hypothetical protein
TGME49_267970	#N/A	-1.22	#N/A	DEAD/DEAH box helicase domain-containing protein
TGME49_215100	#N/A	-1.38	#N/A	PP-loop family protein
TGME49_219218	#N/A	-1.31	#N/A	hypothetical protein
TGME49_216440	#N/A	2.43	#N/A	OTU family cysteine protease
TGME49_238510	#N/A	-1.71	-2.21	hypothetical protein
TGME49_275840	#N/A	-1.96	#N/A	protein phosphatase 2C domain-containing protein
TGME49_267460	#N/A	-1.97	-2.04	AP2 domain transcription factor AP2IX-1
TGME49_222430	#N/A	-1.27	-1.21	HECT-domain (ubiquitin-transferase) domain-containing protein
TGME49_211730	#N/A	-1.55	#N/A	histone lysine methyltransferase SET8
TGME49_214740	#N/A	-1.09	#N/A	hypothetical protein
TGME49_253070	#N/A	-2.03	#N/A	hydrolase, TatD family protein
TGME49_289340	#N/A	1.80	#N/A	hypothetical protein
TGME49_233245	#N/A	-1.96	-2.09	hypothetical protein
TGME49_220480	#N/A	-2.53	-2.94	hypothetical protein
TGME49_297080	#N/A	-1.48	#N/A	pyridoxal kinase
TGME49_288700	#N/A	-1.11	-1.33	RecF/RecN/SMC N terminal domain-containing protein
TGME49_271610	#N/A	-1.05	#N/A	pyrroline-5-carboxylate reductase
TGME49_226240	#N/A	1.13	#N/A	bud site selection protein, putative
TGME49_231280	#N/A	1.09	#N/A	WD domain, G-beta repeat-containing protein
TGME49_267450	#N/A	-1.01	-1.07	alpha-tubulin suppressor protein
TGME49_268240	#N/A	1.24	1.64	hypothetical protein
TGME49_228110	#N/A	-1.24	#N/A	hypothetical protein
TGME49_226068	#N/A	-1.02	#N/A	DnaJ domain-containing protein
TGME49_217900	#N/A	-1.14	-1.50	hypothetical protein
TGME49_257390	#N/A	-1.97	#N/A	ribosome biogenesis GTP-binding protein YsxC protein
TGME49_248770	#N/A	-1.51	#N/A	hypothetical protein
TGME49_216700	#N/A	-2.50	-3.00	hypothetical protein
TGME49_273130	#N/A	1.43	1.66	SAG-related sequence SRS30A
TGME49_273720	#N/A	-1.15	#N/A	hypothetical protein

FIGURE 4KK

TGME49_208340	-1.20	#N/A	#N/A	hypothetical protein	TGME49_231220	#N/A	-1.93	-2.14	hypothetical protein
TGME49_262950	1.01	1.23	1.05	hypothetical protein	TGME49_218840	#N/A	-1.23	#N/A	mutS domain protein
TGME49_220870	1.62	1.88	1.59	hypothetical protein	TGME49_283585	#N/A	1.23	#N/A	hypothetical protein
TGME49_221610	-2.13	-2.20	-1.91	ubiquitin carboxyl-terminal hydrolase	TGME49_249770	#N/A	1.47	#N/A	Nmda1 protein
TGME49_211600	-2.28	-2.40	-2.09	hypothetical protein	TGME49_229350	#N/A	-1.24	-1.98	HEAT repeat-containing protein
TGME49_268720	-2.91	-2.96	-2.88	Hrf1 family protein	TGME49_291120	#N/A	-1.23	-1.24	trafficking protein mon1 subfamily protein
TGME49_312190	-1.68	-1.66	-2.11	hypothetical protein	TGME49_239070	#N/A	-1.47	-1.63	hypothetical protein
TGME49_300270	1.12	1.23	#N/A	hypothetical protein	TGME49_287220	#N/A	1.78	1.87	hypothetical protein
TGME49_248740	1.35	1.20	#N/A	hypothetical protein	TGME49_258826	#N/A	-1.74	#N/A	hypothetical protein
TGME49_275990	1.20	1.31	1.41	hypothetical protein	TGME49_268290	#N/A	-2.00	#N/A	DEAD/DEAH box helicase domain-containing protein
TGME49_217050	1.16	1.06	#N/A	ADA2-A transcriptional co-activator SAGA component	TGME49_219230	#N/A	-1.11	-1.11	AMP-binding enzyme domain-containing protein
TGME49_221690	-3.61	-3.74	-3.80	hypothetical protein	TGME49_255660	#N/A	-1.14	-1.64	EF hand domain-containing protein
TGME49_224950	-1.17	#N/A	#N/A	calcium-dependent protein kinase CDPK5	TGME49_232310	#N/A	-1.63	-1.73	endonuclease/exonuclease/phosphatase family protein
TGME49_321590	-1.34	#N/A	-1.41	hypothetical protein	TGME49_277680	#N/A	-1.13	-1.63	hypothetical protein
TGME49_316230	-2.26	-2.08	-2.47	SAC1 phosphoinositide phosphatase, putative	TGME49_270070	#N/A	2.20	#N/A	synaptobrevin family protein
TGME49_248640	-1.33	-1.23	-1.50	regulator of chromosome condensation (RCC1) repeat-containing protein	TGME49_210440	#N/A	1.04	1.04	polynucleotide adenylyltransferase
TGME49_243290	-2.10	-1.78	-2.13	hypothetical protein	TGME49_270300	#N/A	1.54	#N/A	hypothetical protein
TGME49_225470	1.25	1.29	1.35	peptide methionine sulfoxide reductase	TGME49_232590	#N/A	1.28	1.37	glutamate-cysteine ligase, catalytic subunit domain-containing protein
TGME49_275980	-3.58	-3.59	-3.79	coenzyme q (ubiquinone) biosynthesis protein coq4 protein	TGME49_230140	#N/A	-1.13	#N/A	vacuolar sorting protein 9 (vps9) domain-containing protein
TGME49_286140	-2.10	-1.35	-1.68	hypothetical protein	TGME49_294420	#N/A	-1.89	-1.86	programmed cell death protein 2, c-terminal domain-containing protein
TGME49_294390	-8.33	-8.18	-8.48	myosin light chain MLC4, putative	TGME49_249550	#N/A	-1.14	#N/A	hypothetical protein
TGME49_237480	-3.58	-3.84	-3.95	BRCA1 C Terminus (BRCT) domain-containing protein	TGME49_319600	#N/A	-1.17	#N/A	alpha-tubulin N-acetyltransferase, putative
TGME49_310520	-3.61	-3.49	#N/A	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein	TGME49_262700	#N/A	1.19	1.22	tetratricopeptide repeat-containing protein
TGME49_244670	-1.56	-1.63	-1.41	hypothetical protein	TGME49_306590	#N/A	1.35	1.47	hypothetical protein
TGME49_233860	-8.40	-8.46	-7.90	DALR anticodon binding domain-containing protein	TGME49_205550	#N/A	-1.43	-1.54	AGC kinase
TGME49_307020	-1.89	-1.40	-1.40	hypothetical protein	TGME49_217340	#N/A	-1.15	-1.32	hypothetical protein
TGME49_239620	-3.58	-3.81	-4.01	5'-nucleotidase, C-terminal domain-containing protein	TGME49_200460	#N/A	1.18	1.17	hypothetical protein
TGME49_310360	-1.39	-1.33	-1.82	hypothetical protein	TGME49_264670	#N/A	-1.01	-1.16	DNA polymerase family B protein
TGME49_278960	-1.75	-1.71	-1.55	hypothetical protein	TGME49_316490	#N/A	1.24	#N/A	hypothetical protein
TGME49_312340	-8.33	-8.15	-8.46	hypothetical protein	TGME49_313530	#N/A	-1.06	-1.22	transmembrane protein 167, putative
TGME49_209960	-1.70	-1.69	-2.20	glycosyltransferase	TGME49_231870	#N/A	-1.60	-1.59	tetratricopeptide repeat-containing protein
TGME49_310360	-8.34	-8.38	-8.50	brix domain containing protein	TGME49_208850	#N/A	-1.13	#N/A	SAG-related sequence SRS11
TGME49_318590	-8.37	-7.96	-8.02	MRP family domain-containing protein	TGME49_314390	#N/A	-1.19	-1.37	hypothetical protein

FIGURE 4LL

TGME49_201120	-1.68	-1.57	-1.34	ELMO/CED-12 family protein
TGME49_203840	1.45	1.53	1.84	DEAD/DEAH box helicase domain-containing protein
TGME49_264960	-8.34	-8.46	-8.59	hypothetical protein
TGME49_218820	-1.40	-1.39	-1.92	alba 2
TGME49_239080	-8.34	-8.07	-7.62	carrier superfamily protein
TGME49_239710	-8.33	-8.40	-8.73	phosphomannomutase
TGME49_244110	-1.27	-1.41	-1.59	nucleosome assembly protein (nap) protein
TGME49_258680	-2.07	-1.83	-2.11	TATA-box binding protein TBP2
TGME49_227390	-2.88	-2.55	-2.14	hypothetical protein
TGME49_240660	-8.35	-8.19	-8.05	hypothetical protein
TGME49_290340	-2.30	-1.97	-2.42	HEAT repeat-containing protein
TGME49_259830	1.56	1.66	1.49	diacylglycerol kinase catalytic domain-containing protein
TGME49_261600	1.04	1.15	1.08	creatine kinase domain-containing protein
TGME49_306330	-1.93	-2.15	-2.75	phospholipase
TGME49_224900	-1.16	#N/A	-1.32	adenylate kinase, putative
TGME49_246530	-3.69	-3.12	-3.15	phospholipase D active site domain-containing protein
TGME49_230010	-1.93	-1.43	-1.88	hypothetical protein
TGME49_203970	-2.86	-2.59	-2.35	dolichyl-diphosphooligosaccharide--protein glycosyltransferase
TGME49_283810	-3.59	-3.03	-3.72	hypothetical protein
TGME49_297890	1.20	1.72	1.19	hypothetical protein
TGME49_300260	-1.04	#N/A	-1.11	threonyl-tRNA synthetase family protein
TGME49_255940	1.68	1.79	2.44	hypothetical protein
TGME49_294720	-2.56	-2.34	-2.11	hypothetical protein
TGME49_260650	-3.58	-3.62	-3.12	glycosyltransferase, group 2 family protein
TGME49_257290	-8.36	-10.23	-8.16	RNA 2'-phosphotransferase, Tpt1/KptA family protein
TGME49_316570	1.04	1.05	#N/A	hypothetical protein
TGME49_238170	1.36	1.05	1.11	hypothetical protein
TGME49_224235	-8.28	-8.78	-8.25	translation initiation factor IF-3 protein
TGME49_224230	2.04	1.50	1.97	AP2 domain transcription factor AP2X-3
TGME49_242260	1.48	1.15	#N/A	hypothetical protein
TGME49_299050	1.17	1.05	#N/A	ribosomal protein RPL17
TGME49_315500	-1.60	-1.24	-1.57	hypothetical protein
TGME49_206390	-8.28	-8.38	-8.25	hypothetical protein

TGME49_205250	#N/A	#N/A	11.29	rhopty protein ROP18
TGME49_214080	#N/A	#N/A	6.66	toxofilin
TGME49_319350	#N/A	#N/A	-1.78	SAG-related sequence SRS17B
TGME49_226100	#N/A	#N/A	6.20	haloacid dehalogenase family hydrolase domain-containing protein
TGME49_320190	#N/A	#N/A	8.02	SAG-related sequence SRS16B
TGME49_270510	#N/A	#N/A	-1.78	asparaginyl-tRNA synthetase (NOB-tRNA synthase)
TGME49_245432	#N/A	#N/A	2.68	hypothetical protein
TGME49_289170	#N/A	#N/A	4.85	adenylate and guanylate cyclase catalytic domain-containing protein
TGME49_212250	#N/A	#N/A	2.42	XPG N-terminal domain-containing protein
TGME49_255210	#N/A	#N/A	3.10	ATPase, AAA family protein
TGME49_315320	#N/A	#N/A	-1.69	SAG-related sequence SRS52A
TGME49_253790	#N/A	#N/A	1.73	zinc finger (CCCH type) motif-containing protein
TGME49_320180	#N/A	#N/A	5.44	SAG-related sequence SRS16C
TGME49_279100	#N/A	#N/A	1.23	hypothetical protein
TGME49_203600	#N/A	#N/A	-1.53	hypothetical protein
TGME49_257530	#N/A	#N/A	-2.22	transporter, major facilitator family protein
TGME49_297880	#N/A	#N/A	-2.17	dense granule protein DG32
TGME49_217890	#N/A	#N/A	-1.40	alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen, putative
TGME49_237560	#N/A	#N/A	-1.20	iron-sulfur cluster protein ISCU
TGME49_307830	#N/A	#N/A	-1.52	hypothetical protein
TGME49_213050	#N/A	#N/A	2.16	hypothetical protein
TGME49_308950	#N/A	#N/A	1.10	histidine acid phosphatase superfamily protein
TGME49_224460	#N/A	#N/A	-2.12	aminopeptidase n, putative
TGME49_313440	#N/A	#N/A	4.64	hypothetical protein
TGME49_254840	#N/A	#N/A	-3.32	tetratricopeptide repeat-containing protein
TGME49_320630	#N/A	#N/A	-1.44	phosphotransferase enzyme family protein
TGME49_262630	#N/A	#N/A	3.44	hypothetical protein
TGME49_257750	#N/A	#N/A	-2.12	homocysteine s-methyltransferase domain-containing protein
TGME49_323320	#N/A	#N/A	-3.55	hypothetical protein
TGME49_315750	#N/A	#N/A	-1.69	hypothetical protein
TGME49_258580	#N/A	#N/A	-1.04	rhopty protein ROP17
TGME49_253880	#N/A	#N/A	1.18	GNS1/SUR4 family protein
TGME49_227380	#N/A	#N/A	1.17	hypothetical protein

FIGURE 4MM

TGME49_248880	-1.20	#N/A	-1.41	GTPase RAB7
TGME49_261710	-1.64	-1.46	-1.75	ankyrin repeat-containing protein
TGME49_294430	-3.54	-3.16	-3.04	hypothetical protein
TGME49_252070	1.65	2.10	10.19	KRUF family protein
TGME49_230500	-3.54	-3.42	-3.30	hypothetical protein
TGME49_293330	-8.28	-8.34	-8.42	hypothetical protein
TGME49_217350	-8.29	-8.53	-9.07	methyltransferase MTA70, putative
TGME49_216500	-3.54	-3.88	-4.05	tRNA synthetase, putative
TGME49_212725	-2.49	-2.24	-1.90	hypothetical protein
TGME49_238000	-3.58	-3.00	-3.04	peptidyl-prolyl isomerase
TGME49_236800	-8.29	-8.28	-8.45	hypothetical protein
TGME49_215550	-2.55	-1.97	-2.32	hypothetical protein
TGME49_294050	1.60	1.76	1.52	hypothetical protein
TGME49_258180	-8.34	-8.18	-7.91	hypothetical protein
TGME49_246160	2.25	2.31	2.70	hypothetical protein
TGME49_288260	-1.61	-1.37	-1.70	hypothetical protein
TGME49_254380	-8.29	-8.44	-8.45	ribosomal protein L11, putative
TGME49_221950	-1.47	-1.13	-1.25	spliceosome-associated protein, putative
TGME49_257370	2.21	1.96	2.16	hypothetical protein
TGME49_205160	1.94	1.40	1.90	hypothetical protein
TGME49_307980	2.27	1.51	1.94	GTP-binding protein lepA, putative
TGME49_216870	-2.22	-1.78	-1.78	DNA excision repair helicase
TGME49_235140	1.74	#N/A	#N/A	hypothetical protein
TGME49_216930	-1.60	-1.62	-1.54	cholinephosphate cytidylyltransferase
TGME49_313385	1.96	1.47	1.79	hypothetical protein
TGME49_264650	-8.32	-8.61	-7.56	phosphoacetylglucosamine mutase
TGME49_232780	-2.50	-3.16	-2.87	hypothetical protein
TGME49_297150	-1.30	-1.07	-1.20	MORN repeat-containing protein
TGME49_306030	-1.53	-1.69	-1.89	glutathione S-transferase, n-terminal domain containing protein
TGME49_216920	-2.52	-1.80	-1.94	mediator complex subunit MED8
TGME49_313418	-8.32	-8.06	-8.87	hypothetical protein
TGME49_226330	-8.28	-8.33	-7.92	hypothetical protein
TGME49_233890	-2.25	-1.95	-2.17	hypothetical protein
TGME49_312905	1.94	-1.52	2.29	hypothetical protein
TGME49_294380	-2.83	-2.19	-2.32	PP-loop domain-containing protein
TGME49_207370	#N/A	#N/A	1.01	hypothetical protein
TGME49_201820	#N/A	#N/A	1.51	hypothetical protein
TGME49_229480	#N/A	#N/A	-1.02	calcium binding protein precursor, putative
TGME49_231160	#N/A	#N/A	-1.01	hypothetical protein
TGME49_269980	#N/A	#N/A	-1.07	preprotein translocase Sec61, putative
TGME49_207620	#N/A	#N/A	-1.28	pyridine nucleotide-disulfide oxidoreductase domain-containing protein
TGME49_241880	#N/A	#N/A	-1.35	3'-5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_269420	#N/A	#N/A	1.21	hypothetical protein
TGME49_262640	#N/A	#N/A	-1.53	Cg8 family protein
TGME49_253440	#N/A	#N/A	1.08	cell-cycle-associated protein kinase SRPK, putative
TGME49_238970	#N/A	#N/A	-9.70	hypothetical protein
TGME49_282190	#N/A	#N/A	-1.51	hydrolase, NUDIX family protein
TGME49_290660	#N/A	#N/A	-1.01	RNA recognition motif-containing protein
TGME49_227580	#N/A	#N/A	-1.59	transmembrane amino acid transporter protein
TGME49_285510	#N/A	#N/A	-1.44	hypothetical protein
TGME49_249180	#N/A	#N/A	-1.22	bifunctional dihydrofolate reductase-thymidylate synthase
TGME49_268790	#N/A	#N/A	1.03	hypothetical protein
TGME49_309930	#N/A	#N/A	1.37	melibiase subfamily protein
TGME49_308010	#N/A	#N/A	1.53	hypothetical protein
TGME49_314400	#N/A	#N/A	-1.11	pyruvate dehydrogenase E1 component, beta subunit, putative
TGME49_286928	#N/A	#N/A	-2.53	hypothetical protein
TGME49_260260	#N/A	#N/A	-1.04	ribosomal protein RPP1
TGME49_214290	#N/A	#N/A	-1.17	DJ-1 family protein
TGME49_313180	#N/A	#N/A	-1.09	cell-cycle-associated protein kinase PRP4, putative
TGME49_308020	#N/A	#N/A	-1.24	SAG-related sequence SRS57
TGME49_233030	#N/A	#N/A	-1.11	gliding-associated protein GAP70
TGME49_216620	#N/A	#N/A	-1.15	EF hand domain-containing protein
TGME49_209260	#N/A	#N/A	-1.17	cytochrome c oxidase subunit, putative
TGME49_267070	#N/A	#N/A	1.24	aquaporin 2
TGME49_267680	#N/A	#N/A	-1.27	microneme protein MIC12
TGME49_271790	#N/A	#N/A	1.67	hypothetical protein
TGME49_247550	#N/A	#N/A	-1.04	heat shock protein HSP60
TGME49_215610	#N/A	#N/A	-1.93	hypothetical protein
TGME49_254160	#N/A	#N/A	-3.79	hypothetical protein
TGME49_278660	#N/A	#N/A	-1.24	P-type ATPase4, putative

FIGURE 4NN

TGME49_273030	-2.83	-3.34	-2.31	phosphoglycerate mutase family protein
TGME49_311090	-1.28	-1.25	-1.64	ubiquitin carboxyl-terminal hydrolase
TGME49_285980	1.02	1.15	#N/A	glucosephosphate-mutase GPM1
TGME49_271110	-3.54	-3.33	-2.96	hypothetical protein
TGME49_309800	-1.53	-1.21	-1.60	RNA recognition motif-containing protein
TGME49_264720	-3.51	-3.91	-3.61	hypothetical protein
TGME49_312430	1.36	1.71	1.25	hypothetical protein
TGME49_277070	1.47	1.30	1.37	SWI2/SNF2-containing protein
TGME49_271860	-8.31	-8.37	-7.92	tRNA (Uracil-5-)-methyltransferase
TGME49_226740	1.27	1.36	1.06	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_281570	-3.51	-3.93	-3.77	hypothetical protein
TGME49_203180	-3.51	-4.41	-3.69	leucine rich repeat-containing protein
TGME49_306410	-3.51	-3.96	-4.00	hypothetical protein
TGME49_221580	-1.28	-1.57	-1.50	ribosomal RNA large subunit methyltransferase J protein
TGME49_294740	-1.91	-2.10	-2.06	hypothetical protein
TGME49_257340	-8.23	-8.55	-8.65	Ras family protein
TGME49_305850	-1.04	#N/A	-1.10	RNA recognition motif-containing protein
TGME49_211090	-1.51	#N/A	-1.06	aminotransferase, class V superfamily protein
TGME49_266100	1.08	1.05	1.28	rhoGTPase family protein ROP41
TGME49_306560	-2.91	-2.99	-3.30	hypothetical protein
TGME49_217750	-3.51	-3.64	-3.69	hypothetical protein
TGME49_301130	-8.23	-8.11	-8.47	hypothetical protein
TGME49_226560	-3.51	-3.45	-3.67	zinc finger (CCCH type) motif-containing protein
TGME49_306210	-8.34	-8.28	-8.50	RNA polymerase II accessory factor CDC73
TGME49_202630	-1.21	-1.16	-1.38	ATP-dependent metalloprotease H8B subfamily protein
TGME49_289190	-8.23	-8.32	-7.82	tetratricopeptide repeat-containing protein
TGME49_313140	1.42	1.34	#N/A	isocitrate dehydrogenase
TGME49_213115	-8.23	-7.52	-8.68	hypothetical protein
TGME49_282140	1.28	#N/A	#N/A	cwf21 protein
TGME49_264040	-1.11	#N/A	-1.19	hypothetical protein
TGME49_208780	-2.45	-2.72	-3.00	ubiquitin-conjugating enzyme subfamily protein
TGME49_272670	-8.23	-8.33	-8.28	peptidase family M3 protein
TGME49_238180	-1.10	#N/A	-1.04	26S proteasome regulatory complex subunit, putative
TGME49_253160	#N/A	#N/A	1.30	hypothetical protein
TGME49_236210	#N/A	#N/A	-1.08	peptidase M16 family protein, putative
TGME49_235150	#N/A	#N/A	-1.01	transporter, major facilitator family protein
TGME49_310490	#N/A	#N/A	-1.20	ribosomal protein RPL27A
TGME49_266900	#N/A	#N/A	1.49	cyclin, N-terminal domain-containing protein
TGME49_305330	#N/A	#N/A	-1.02	cyclin, N-terminal domain-containing protein
TGME49_222370	#N/A	#N/A	1.49	SAG-related sequence SRS13
TGME49_209030	#N/A	#N/A	-1.03	actin ACT1
TGME49_226072	#N/A	#N/A	-1.13	Ser/Thr phosphatase family protein
TGME49_224935	#N/A	#N/A	1.43	hypothetical protein
TGME49_269390	#N/A	#N/A	1.20	CRAL/TRIO domain-containing protein
TGME49_311470	#N/A	#N/A	-1.07	rhoGTPase neck protein RON5
TGME49_289680	#N/A	#N/A	-1.06	Ras-related protein Rab11
TGME49_211340	#N/A	#N/A	1.29	hypothetical protein
TGME49_321410	#N/A	#N/A	1.14	hypothetical protein
TGME49_256000	#N/A	#N/A	-1.01	endoplasmic reticulum retention receptor
TGME49_224110	#N/A	#N/A	-1.33	adhesion regulating molecule region protein, putative
TGME49_308093	#N/A	#N/A	1.13	rhoGTPase kinase family protein (incomplete catalytic triad)
TGME49_314660	#N/A	#N/A	-1.38	TPRX1 protein
TGME49_213480	#N/A	#N/A	-2.18	hypothetical protein
TGME49_208710	#N/A	#N/A	1.64	DNA/RNA non-specific endonuclease
TGME49_250880	#N/A	#N/A	-1.64	kinase, p38 family protein
TGME49_231640	#N/A	#N/A	-1.24	alveolin domain containing intermediate filament IMC1
TGME49_233130	#N/A	#N/A	1.32	nucleoside transporter protein
TGME49_306430	#N/A	#N/A	-1.32	hypothetical protein
TGME49_248700	#N/A	#N/A	-1.40	alveolin domain containing intermediate filament IMC12
TGME49_277760	#N/A	#N/A	-1.28	adenylosuccinate lyase, putative
TGME49_255635	#N/A	#N/A	-3.63	hypothetical protein
TGME49_289920	#N/A	#N/A	1.18	hypothetical protein
TGME49_209160	#N/A	#N/A	-1.05	myristoyl CoA:protein N-myristoyltransferase
TGME49_306350	#N/A	#N/A	1.06	variable surface lipoprotein
TGME49_260400	#N/A	#N/A	1.33	hypothetical protein
TGME49_249780	#N/A	#N/A	-1.23	hypothetical protein

FIGURE 400

TGME49_233490	-8.29	-8.54	-8.38	hypothetical protein	TGME49_258060	#N/A	#N/A	-1.13	myosin heavy chain, putative
TGME49_233790	-8.22	-8.60	-8.77	serine/threonine protein kinase AktR, putative	TGME49_240810	#N/A	#N/A	-1.07	hypothetical protein
TGME49_293280	1.31	#N/A	2.97	cyclin protein	TGME49_234410	#N/A	#N/A	-1.04	transporter, small conductance mechanosensitive ion channel (MscS) family protein
TGME49_286230	1.29	#N/A	#N/A	hypothetical protein	TGME49_212970	#N/A	#N/A	3.81	protein kinase (incomplete catalytic triad)
TGME49_310320	-3.51	-3.68	-3.88	calreticulin family protein	TGME49_320260	#N/A	#N/A	1.68	hypothetical protein
TGME49_252870	1.95	1.89	2.35	hypothetical protein	TGME49_315930	#N/A	#N/A	-1.08	integral membrane protein, DUF56 family protein, putative
TGME49_237290	-1.40	-1.58	-1.30	hypothetical protein	TGME49_295340	#N/A	#N/A	-1.12	UV excision repair protein Rad23 protein
TGME49_268620	-8.23	-8.00	-7.69	blood stage antigen 41-3 precursor, putative	TGME49_201220	#N/A	#N/A	-1.90	zinc finger protein
TGME49_221640	2.25	1.86	1.56	hypothetical protein	TGME49_224170	#N/A	#N/A	1.95	SAG-related sequence SRS60A
TGME49_213880	2.50	2.67	2.68	hypothetical protein	TGME49_281500	#N/A	#N/A	1.89	hypothetical protein
TGME49_309160	-2.03	-1.94	-2.28	IgA-specific metalloendopeptidase	TGME49_235970	#N/A	#N/A	-1.02	eukaryotic initiation factor-2 gamma, putative
TGME49_260450	-8.23	-8.80	-8.14	DEAD/DEAH box helicase domain-containing protein	TGME49_206640	#N/A	#N/A	1.11	hypothetical protein
TGME49_248850	-8.24	-8.35	-8.91	methionine aminopeptidase	TGME49_304670	#N/A	#N/A	-1.33	leucine rich repeat-containing protein
TGME49_254800	1.72	1.78	1.43	hypothetical protein	TGME49_258980	#N/A	#N/A	-2.00	hypothetical protein
TGME49_300380	-2.80	-2.99	-2.52	endoplasmic reticulum oxidoreductin, putative	TGME49_288720	#N/A	#N/A	-1.43	ribosomal protein RPL10
TGME49_276170	1.39	1.53	1.24	phosphatidylinositol 3- and 4-kinase	TGME49_209150	#N/A	#N/A	-1.16	non-proton pumping type-II NADH dehydrogenase I
TGME49_307040	-1.48	-1.31	-1.59	shikimate dehydrogenase substrate binding domain-containing protein	TGME49_283820	#N/A	#N/A	1.31	glycine cleavage T-protein (aminomethyl transferase) domain-containing protein
TGME49_265850	1.90	1.76	1.78	hypothetical protein	TGME49_216910	#N/A	#N/A	1.30	hypothetical protein
TGME49_269290	-2.43	-2.87	-3.04	hypothetical protein	TGME49_286480	#N/A	#N/A	1.10	hypothetical protein
TGME49_318610	1.60	1.10	3.56	AP2 domain transcription factor AP2IV-3	TGME49_244440	#N/A	#N/A	-1.06	nucleoside transporter protein
TGME49_235460	1.27	1.27	1.19	hypothetical protein	TGME49_293650	#N/A	#N/A	1.82	hypothetical protein
TGME49_311250	-2.87	-3.38	-3.17	hypothetical protein	TGME49_314295	#N/A	#N/A	-3.23	ribosomal I25 family protein
TGME49_202680	-1.26	-1.16	-1.56	peptidase M16, alpha subunit, putative	TGME49_235730	#N/A	#N/A	1.57	hypothetical protein
TGME49_234220	-1.87	-2.06	-1.77	hypothetical protein	TGME49_281630	#N/A	#N/A	-1.30	hydroxyacylglutathione hydrolase
TGME49_215920	1.79	1.80	1.30	hypothetical protein	TGME49_290990	#N/A	#N/A	1.02	HEAT repeat-containing protein
TGME49_244470	-1.14	-1.10	#N/A	hypothetical protein	TGME49_212200	#N/A	#N/A	1.28	hypothetical protein
TGME49_244660	-3.51	-3.10	-3.40	hypothetical protein	TGME49_275470	#N/A	#N/A	1.49	dense granule protein GRA15
TGME49_252320	-8.22	-8.67	-7.92	Sas10/Utp3/C1D family protein	TGME49_254890	#N/A	#N/A	1.60	hypothetical protein
TGME49_270060	-2.22	-1.85	-1.61	hypothetical protein	TGME49_226790	#N/A	#N/A	1.95	ABC transporter, ATP-binding domain-containing protein
TGME49_262500	-1.42	-1.33	-1.65	hypothetical protein	TGME49_201670	#N/A	#N/A	1.33	DnaJ domain-containing protein
TGME49_315700	-2.80	-2.75	-3.13	hypothetical protein	TGME49_210840	#N/A	#N/A	-1.09	arginyl-tRNA synthetase family protein
TGME49_316540	-1.15	#N/A	#N/A	IMC sub-compartment protein ISP3	TGME49_220520	#N/A	#N/A	1.04	hypothetical protein
TGME49_214870	1.67	1.93	1.97	ribosomal protein L9, N-terminal domain-containing protein	TGME49_281920	#N/A	#N/A	-1.32	V-type ATPase, D subunit protein

FIGURE 4PP

TGME49_258030	-1.82	-1.31	#N/A	DNA polymerase
TGME49_253700	1.04	1.05	#N/A	transporter, major facilitator family protein
TGME49_251670	-3.47	-3.69	-3.72	werner helicase interacting protein 1, putative
TGME49_313860	1.80	1.64	1.64	regulator of chromosome condensation (RCC1) repeat-containing protein
TGME49_249840	-8.17	-8.94	-8.71	dynein heavy chain 2, putative
TGME49_272320	1.53	1.24	1.74	DHHC zinc finger domain-containing protein
TGME49_218270	-1.01	#N/A	#N/A	hypothetical protein
TGME49_263610	-1.59	-1.78	-1.78	hypothetical protein
TGME49_202460	-1.77	-1.92	-1.69	diacylglycerol kinase accessory domain (presumed) domain-containing protein
TGME49_271000	-2.27	-2.15	-1.88	hypothetical protein
TGME49_321300	-3.47	-3.61	-3.13	autophagy-related 12 variant 1, putative
TGME49_234950	1.64	2.07	1.59	protein kinase (incomplete catalytic triad)
TGME49_220920	-8.17	-8.04	-8.01	hypothetical protein
TGME49_235560	-8.18	-9.20	-8.05	hypothetical protein
TGME49_257595	-2.88	-2.54	-2.65	hypothetical protein
TGME49_305600	-8.17	-8.06	-8.12	hypothetical protein
TGME49_223672	1.66	#N/A	1.31	3'(2'),5'-bisphosphate nucleotidase
TGME49_229340	-8.17	-7.92	-8.33	hypothetical protein
TGME49_247380	-8.17	-8.91	-8.78	hypothetical protein
TGME49_239610	-3.47	-3.57	-3.56	hypothetical protein
TGME49_273850	-2.77	-2.77	-2.95	hypothetical protein
TGME49_312380	-8.17	-8.28	-8.34	tetratricopeptide repeat-containing protein
TGME49_230710	-3.53	-3.17	-2.93	cell division protein CDC48
TGME49_316360	-3.53	-3.41	-3.48	hypothetical protein
TGME49_229940	-2.40	-2.15	-2.14	cyclophilin, putative
TGME49_242850	-2.40	-2.07	-2.81	hypothetical protein
TGME49_216680	-2.15	-4.00	-2.46	ankyrin repeat-containing protein
TGME49_289000	-2.77	-3.04	-2.86	hypothetical protein
TGME49_228720	-8.17	-7.93	-7.96	hypothetical protein
TGME49_252360	1.02	#N/A	#N/A	rho GTPase family protein ROP24 (incomplete catalytic triad)
TGME49_312618	-1.89	#N/A	#N/A	hypothetical protein
TGME49_321610	-8.17	-8.43	-7.86	hypothetical protein
TGME49_235750	-8.17	-8.31	-8.43	ULK kinase

TGME49_218950	#N/A	#N/A	1.33	hypothetical protein
TGME49_310630	#N/A	#N/A	-1.27	hypothetical protein
TGME49_226000	#N/A	#N/A	-1.08	ATP synthase, putative
TGME49_216260	#N/A	#N/A	-1.03	eukaryotic initiation factor-2B, gamma subunit, putative
TGME49_287470	#N/A	#N/A	-1.60	hypothetical protein
TGME49_319920	#N/A	#N/A	-1.01	2-oxo acid dehydrogenases acyltransferase (catalytic domain) domain-containing protein
TGME49_254365	#N/A	#N/A	-1.17	phosphatidate cytidyltransferase
TGME49_255930	#N/A	#N/A	1.41	hypothetical protein
TGME49_261030	#N/A	#N/A	-3.23	pyridine nucleotide-disulfide oxidoreductase domain-containing protein
TGME49_224740	#N/A	#N/A	1.13	hypothetical protein
TGME49_217610	#N/A	#N/A	-1.83	hypothetical protein
TGME49_239050	#N/A	#N/A	1.05	hypothetical protein
TGME49_280790	#N/A	#N/A	1.23	phosphatidylinositol n-acetylglucosaminyltransferase
TGME49_231590	#N/A	#N/A	-1.57	SGS domain-containing protein
TGME49_230210	#N/A	#N/A	-1.10	alveolin domain containing intermediate filament IMC10
TGME49_208350	#N/A	#N/A	1.00	hypothetical protein
TGME49_216800	#N/A	#N/A	2.12	flagellar/basal body protein
TGME49_318430	#N/A	#N/A	-1.22	malate dehydrogenase MDH
TGME49_289120	#N/A	#N/A	1.08	hypothetical protein
TGME49_223020	#N/A	#N/A	-1.11	coproporphyrinogen III oxidase
TGME49_277970	#N/A	#N/A	1.14	dolichol-phosphate-mannose synthase family protein
TGME49_240050	#N/A	#N/A	1.14	hypothetical protein
TGME49_321540	#N/A	#N/A	-1.00	hypothetical protein
TGME49_243780	#N/A	#N/A	1.03	hypothetical protein
TGME49_207450	#N/A	#N/A	-1.41	DNA segment, Chr 10, Wayne State University 52, expressed family protein
TGME49_232035	#N/A	#N/A	-1.99	hypothetical protein
TGME49_288510	#N/A	#N/A	2.14	ubiquitin carboxyl-terminal hydrolase
TGME49_255215	#N/A	#N/A	2.48	hypothetical protein
TGME49_311320	#N/A	#N/A	-2.37	hypothetical protein
TGME49_207120	#N/A	#N/A	1.11	Sad1/UNC family protein
TGME49_221480	#N/A	#N/A	-1.20	hypothetical protein
TGME49_216190	#N/A	#N/A	1.35	hypothetical protein
TGME49_227630	#N/A	#N/A	2.27	hypothetical protein

FIGURE 4QQ

TGME49_216970	-1.15	-1.17	-1.81	coronin, putative	TGME49_258780	#N/A	#N/A	1.03	OTU family cysteine protease
TGME49_260370	-1.99	-2.21	-1.97	AtPH1 family protein	TGME49_249425	#N/A	#N/A	-1.13	hypothetical protein
TGME49_315690	-3.47	-3.51	-3.70	DnaJ domain-containing protein	TGME49_263070	#N/A	#N/A	-1.00	CMGC kinase, CK2 family
TGME49_270610	1.55	1.83	1.83	hypothetical protein	TGME49_257120	#N/A	#N/A	-1.20	sugar transporter ST1
TGME49_238110	-2.21	-2.31	-2.69	replication factor a protein 3 protein	TGME49_224470	#N/A	#N/A	1.05	hypothetical protein
TGME49_248890	-2.40	-2.11	-2.93	actin-like protein ALP3b	TGME49_222270	#N/A	#N/A	-1.25	hypothetical protein
TGME49_235680	-1.67	-2.96	-1.51	peptidase M16 inactive domain-containing protein	TGME49_265780	#N/A	#N/A	-1.16	flagellar/basal body protein
TGME49_319940	-8.17	-8.19	-8.17	hypothetical protein	TGME49_223420	#N/A	#N/A	1.31	DnaJ domain-containing protein
TGME49_312310	-2.81	-2.15	-2.50	ATPase, AAA family protein	TGME49_320620	#N/A	#N/A	-1.94	queuine tRNA ribosyl transferase
TGME49_239630	-3.49	-3.10	-3.39	cytidine and deoxycytidylate deaminase zinc-binding region domain-containing protein	TGME49_286050	#N/A	#N/A	1.09	hypothetical protein
TGME49_272475	-8.17	-8.78	-8.57	protein kinase domain-containing protein	TGME49_258462	#N/A	#N/A	-1.26	hypothetical protein
TGME49_212090	1.11	#N/A	1.09	hypothetical protein	TGME49_264980	#N/A	#N/A	1.18	hypothetical protein
TGME49_275330	-3.46	-4.05	-3.59	ribosomal protein RPL29	TGME49_219290	#N/A	#N/A	1.07	F-actin-capping protein subunit beta, putative
TGME49_201230	-2.76	-2.62	-2.70	kinesin motor domain-containing protein	TGME49_260790	#N/A	#N/A	-1.90	RAP domain-containing protein
TGME49_252220	-1.36	-2.92	-1.20	tetratricopeptide repeat domain containing protein	TGME49_310620	#N/A	#N/A	-1.02	starch binding domain-containing protein
TGME49_207940	-3.47	-3.27	-3.35	ribosomal protein S9, putative	TGME49_309370	#N/A	#N/A	-1.09	adaptin n terminal region domain-containing protein
TGME49_318460	-1.58	-1.48	-1.35	P-type ATPase of unknown pump specificity (type V) protein	TGME49_312700	#N/A	#N/A	1.71	hypothetical protein
TGME49_204270	-2.21	-2.35	-1.92	hypothetical protein	TGME49_309730	#N/A	#N/A	-1.23	thioredoxin reductase
TGME49_263590	-2.42	-1.94	-2.38	hypothetical protein	TGME49_289780	#N/A	#N/A	-1.42	ATP-dependent hsl protease ATP-binding subunit hslU, putative
TGME49_309220	-1.37	-1.77	-1.98	GTPase activating protein for Arf protein	TGME49_245540	#N/A	#N/A	-1.11	hypothetical protein
TGME49_210360	1.75	1.72	1.47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41 family protein	TGME49_250040	#N/A	#N/A	-1.57	hypothetical protein
TGME49_310350	-1.78	-1.49	-1.75	PGAP1 family protein	TGME49_263240	#N/A	#N/A	-1.31	hypothetical protein
TGME49_300990	1.85	#N/A	1.11	Toxoplasma gondii family C protein	TGME49_272210	#N/A	#N/A	-2.18	hypothetical protein
TGME49_263530	-1.60	-1.22	-1.36	chaperonin, putative	TGME49_255980	#N/A	#N/A	-1.31	hypothetical protein
TGME49_265400	-1.62	-1.73	-1.46	hypothetical protein	TGME49_305510	#N/A	#N/A	-1.13	hypothetical protein
TGME49_213670	-1.46	-1.10	-1.45	hypothetical protein	TGME49_251580	#N/A	#N/A	-1.03	hypothetical protein
TGME49_238230	-2.77	-2.62	-3.04	Ser/Thr phosphatase family protein	TGME49_291820	#N/A	#N/A	1.27	RNA helicase (UPF2 interacting domain) protein
TGME49_267390	-1.57	-1.02	-1.31	DNA-directed RNA polymerase I RPAC1	TGME49_270520	#N/A	#N/A	-1.26	hypothetical protein
TGME49_300060	-1.10	#N/A	#N/A	signal peptidase subunit protein	TGME49_240500	#N/A	#N/A	-1.31	hypothetical protein
TGME49_208590	-1.53	-1.79	-2.13	vacuolar ATP synthase subunit 54kD, putative	TGME49_311140	#N/A	#N/A	-2.15	hypothetical protein
TGME49_232360	-1.60	-1.87	-1.82	exonuclease	TGME49_259860	#N/A	#N/A	-1.21	hypothetical protein
TGME49_288570	-2.74	-2.66	-3.23	hypothetical protein	TGME49_314800	#N/A	#N/A	-1.12	hypothetical protein
TGME49_239130	1.45	1.07	1.43	Tyrosine kinase-like (TKL) protein	TGME49_223710	#N/A	#N/A	-1.04	tetratricopeptide repeat-containing protein

FIGURE 4RR

TGME49_318750	1.28	1.70	2.56	deoxyribose-phosphate aldolase
TGME49_226660	-1.30	-1.22	-1.34	hypothetical protein
TGME49_247330	-1.75	-2.74	-2.07	hypothetical protein
TGME49_269140	-1.79	-1.56	-1.49	transport protein particle component, Bet3 domain-containing protein
TGME49_219460	-2.74	-2.98	-2.53	hypothetical protein
TGME49_270160	-8.11	-8.21	-7.88	hypothetical protein
TGME49_311280	-8.12	-7.86	-7.97	hypothetical protein
TGME49_234610	-1.55	-1.14	-1.31	WD-40 repeat protein
TGME49_310810	-1.83	-1.85	-2.03	apyrase
TGME49_214800	-8.11	-8.10	-7.90	hypothetical protein
TGME49_301180	2.01	#N/A	3.30	SAG-related sequence SRS19F
TGME49_234440	-3.44	-4.26	#N/A	aminotransferase, putative
TGME49_240830	-8.11	-8.19	-7.68	hydrolase, alpha/beta fold family protein
TGME49_236280	2.04	1.77	1.75	hypothetical protein
TGME49_252510	1.49	1.41	#N/A	hypothetical protein
TGME49_297510	-8.12	-8.90	-8.74	hypothetical protein
TGME49_270650	1.77	1.20	2.01	deoxyribose-phosphate aldolase
TGME49_224330	-1.28	-1.03	#N/A	proteasome activator pa28 beta subunit protein
TGME49_310560	-3.42	-3.68	-3.74	hypothetical protein
TGME49_297720	-1.07	-1.26	-1.12	trehalose-phosphatase
TGME49_307810	-1.21	#N/A	-1.22	hypothetical protein
TGME49_258920	-8.13	-7.87	-8.20	hypothetical protein
TGME49_205570	-2.73	-2.75	-2.49	hypothetical protein
TGME49_255170	-3.43	-3.19	-2.43	hypothetical protein
TGME49_255690	-2.74	-2.81	-2.46	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase domain-containing protein
TGME49_227430	-1.72	-1.89	2.34	transmembrane amino acid transporter protein
TGME49_257150	-2.73	-2.37	-2.60	NOT2 / NOT3 / NOT5 family protein
TGME49_226840	-2.74	-2.20	-2.45	hypothetical protein
TGME49_267120	-2.74	-2.41	-2.50	hypothetical protein
TGME49_248130	-8.13	-8.09	-7.87	hypothetical protein
TGME49_253300	2.29	1.79	2.25	hypothetical protein
TGME49_306290	-1.87	-1.91	-2.04	DNA-directed RNA polymerase III RPC1
TGME49_297460	-8.12	-8.18	-8.51	hypothetical protein
TGME49_204140	-8.17	-8.24	-7.74	PHD-finger domain-containing protein
TGME49_209080	1.29	#N/A	#N/A	transport protein particle (trapp) component, bet3 protein
TGME49_318360	#N/A	#N/A	-1.64	hypothetical protein
TGME49_285480	#N/A	#N/A	1.45	hypothetical protein
TGME49_226690	#N/A	#N/A	-1.20	hypothetical protein
TGME49_267280	#N/A	#N/A	1.34	hypothetical protein
TGME49_309280	#N/A	#N/A	-2.10	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_307270	#N/A	#N/A	-1.37	hypothetical protein
TGME49_224160	#N/A	#N/A	1.03	hypothetical protein
TGME49_322010	#N/A	#N/A	-1.61	myosin-light-chain kinase
TGME49_233260	#N/A	#N/A	-1.52	GTP-binding protein, putative
TGME49_263785	#N/A	#N/A	1.23	phosphatidate cytidylyltransferase
TGME49_206710	#N/A	#N/A	2.02	hypothetical protein
TGME49_261370	#N/A	#N/A	1.03	hypothetical protein
TGME49_283730	#N/A	#N/A	-1.10	endomembrane protein 70 subfamily protein
TGME49_320070	#N/A	#N/A	-1.11	CDK-activating kinase assembly factor MAT1 protein
TGME49_262590	#N/A	#N/A	1.57	hypothetical protein
TGME49_267550	#N/A	#N/A	-1.06	leucine-rich repeat protein LRR1
TGME49_206490	#N/A	#N/A	-1.12	ICE family protease (caspase) p20 domain-containing protein
TGME49_225710	#N/A	#N/A	-2.09	mitochondrial inner membrane translocase subunit TIM17, putative
TGME49_289110	#N/A	#N/A	1.52	hypothetical protein
TGME49_221700	#N/A	#N/A	-1.11	hypothetical protein
TGME49_288730	#N/A	#N/A	1.41	hypothetical protein
TGME49_201810	#N/A	#N/A	1.07	hypothetical protein
TGME49_248180	#N/A	#N/A	2.57	hypothetical protein
TGME49_269050	#N/A	#N/A	-1.21	hypothetical protein
TGME49_257560	#N/A	#N/A	1.25	WD domain, G-beta repeat-containing protein
TGME49_300980	#N/A	#N/A	-1.20	hypothetical protein
TGME49_268250	#N/A	#N/A	-1.39	WD domain, G-beta repeat-containing protein
TGME49_219620	#N/A	#N/A	1.14	hypothetical protein
TGME49_305040	#N/A	#N/A	-1.59	HEAT repeat-containing protein
TGME49_213930	#N/A	#N/A	-1.72	3' exoribonuclease family, domain 1 domain-containing protein
TGME49_214310	#N/A	#N/A	1.60	hypothetical protein
TGME49_223725	#N/A	#N/A	2.08	hypothetical protein
TGME49_295000	#N/A	#N/A	-1.23	hypothetical protein
TGME49_246610	#N/A	#N/A	-2.04	hypothetical protein
TGME49_297060	#N/A	#N/A	-1.30	phosphoglycerate mutase PGMI

FIGURE 4SS

TGME49_273840	-2.40	-1.75	-2.09	brix domain-containing protein
TGME49_209930	-8.12	-9.20	-8.28	hypothetical protein
TGME49_308580	-2.37	-2.50	-2.51	Lon protease family protein
TGME49_313240	-2.78	-2.92	-3.07	ethylene-responsive RNA helicase, putative
TGME49_264440	-1.83	-1.58	-1.69	signal recognition particle receptor beta subunit protein
TGME49_231890	-1.86	-1.41	-1.25	beta-ketoacyl-acyl carrier protein synthase III, putative
TGME49_215290	-3.39	-3.84	-4.16	saccharopine dehydrogenase domain-containing protein
TGME49_299110	-1.95	-1.81	-2.10	cleft lip and palate transmembrane protein 1 (clptm1) protein
TGME49_223060	-1.76	-1.63	#N/A	MORN repeat-containing protein
TGME49_314840	-1.63	-1.71	-1.49	ubiquitin carboxyl-terminal hydrolase
TGME49_311510	-1.44	-1.14	-1.21	elF2 kinase IF2K-B
TGME49_304760	1.05	#N/A	1.04	RNA recognition motif-containing protein
TGME49_221490	-2.70	-2.37	-2.34	cell cycle regulator protein
TGME49_297780	-2.34	-2.98	-2.36	ATPase/histidine kinase/DNA gyrase B/HSP90 domain-containing protein
TGME49_257710	-3.39	-3.55	-3.82	actin-like protein ALP 5
TGME49_225680	-2.70	-2.84	-2.74	hypothetical protein
TGME49_227600	-1.12	-1.49	-1.37	ribosomal protein RPL34
TGME49_224350	-1.37	-1.10	-1.28	aminopeptidase N, putative
TGME49_233820	-8.05	-7.82	-8.59	DNA polymerase epsilon subunit B protein
TGME49_255390	-3.39	-3.61	-3.38	HEAT repeat-containing protein
TGME49_217360	-2.70	-2.95	-3.36	hypothetical protein
TGME49_273350	1.51	1.74	2.12	molybdopterin converting factor, subunit 2 protein
TGME49_230430	-8.05	-8.37	-9.16	vesicle-associated membrane protein, putative
TGME49_244230	-8.06	-8.91	-8.73	hypothetical protein
TGME49_242435	-3.39	-3.54	-3.49	hypothetical protein
TGME49_312280	-1.39	-1.31	-1.54	pre-mRNA-splicing factor ATP-dependent RNA helicase, putative
TGME49_295450	-1.22	#N/A	-1.26	sjoegren syndrome nuclear autoantigen 1 family protein
TGME49_212150	-8.06	-8.74	-8.79	hypothetical protein
TGME49_251890	-3.39	-4.36	-3.22	hypothetical protein
TGME49_318290	-8.05	-8.76	-8.23	hypothetical protein
TGME49_233090	-8.06	-8.10	-8.51	XPG N-terminal domain-containing protein
TGME49_216040	#N/A	#N/A	-1.19	30S ribosomal protein S15, putative
TGME49_203860	#N/A	#N/A	1.40	hypothetical protein
TGME49_263740	#N/A	#N/A	1.97	ABC transporter transmembrane region domain-containing protein
TGME49_309420	#N/A	#N/A	-1.37	ferlin family protein
TGME49_299040	#N/A	#N/A	-1.13	phosphatidylinositol n-acetylglucosaminyltransferase
TGME49_254810	#N/A	#N/A	1.22	hypothetical protein
TGME49_209290	#N/A	#N/A	-1.03	ribosomal protein RPS28
TGME49_290240	#N/A	#N/A	1.41	hypothetical protein
TGME49_313470	#N/A	#N/A	1.15	helix-hairpin-helix motif domain-containing protein
TGME49_201240	#N/A	#N/A	1.15	hypothetical protein
TGME49_205100	#N/A	#N/A	-1.46	hypothetical protein
TGME49_248840	#N/A	#N/A	-1.42	transporter, major facilitator family protein
TGME49_211300	#N/A	#N/A	-1.66	DUF74 family protein, putative
TGME49_308590	#N/A	#N/A	-1.13	Mov34/MPN/PAD-1 family protein
TGME49_249710	#N/A	#N/A	-1.46	Parkinson disease 7 domain containing 1 family protein
TGME49_210750	#N/A	#N/A	1.78	Ferredoxin-fold anticodon binding domain-containing protein
TGME49_320700	#N/A	#N/A	1.09	AP2 domain transcription factor AP2IV-1
TGME49_249490	#N/A	#N/A	-1.08	hypothetical protein
TGME49_277500	#N/A	#N/A	-1.47	26S proteasome regulatory subunit 7, putative
TGME49_270130	#N/A	#N/A	1.08	hypothetical protein
TGME49_298610	#N/A	#N/A	-1.04	GYF domain-containing protein
TGME49_250955	#N/A	#N/A	1.38	KRUF family protein
TGME49_258800	#N/A	#N/A	1.07	rhoptyr kinase family protein ROP31
TGME49_313070	#N/A	#N/A	-1.21	hypothetical protein
TGME49_265510	#N/A	#N/A	-1.01	hypothetical protein
TGME49_320680	#N/A	#N/A	1.44	AP2 domain transcription factor AP2IV-2
TGME49_269430	#N/A	#N/A	1.14	polyprenyl synthetase superfamily protein
TGME49_202220	#N/A	#N/A	1.47	hypothetical protein
TGME49_238190	#N/A	#N/A	-1.01	DNA-directed RNA polymerase II RPB3
TGME49_262460	#N/A	#N/A	-1.19	hypothetical protein
TGME49_239748	#N/A	#N/A	-1.39	hypothetical protein

FIGURE 4TT

TGME49_320015	-8.05	-8.10	-7.73	hypothetical protein
TGME49_218250	-2.13	-2.10	-2.35	TAP42 family protein
TGME49_203420	1.97	1.65	1.62	4'-phosphopantetheinyl transferase domain-containing protein
TGME49_221360	-2.13	-1.98	-1.89	hypothetical protein
TGME49_219140	-1.48	-1.50	-1.77	EF-1 guanine nucleotide exchange domain-containing protein
TGME49_312840	-1.82	-1.83	-2.14	hypothetical protein
TGME49_221830	1.87	3.37	3.34	subtilisin SUB12
TGME49_285470	1.99	1.28	1.85	patched family protein
TGME49_270450	-8.05	-8.04	-7.98	MCM2/3/5 family protein
TGME49_224190	-1.56	-1.33	-1.15	cation-transporting atpase family protein
TGME49_223070	-1.12	-1.16	-1.18	hypothetical protein
TGME49_313150	2.10	1.58	#N/A	DUF89/Fructose bisphosphatase
TGME49_226940	-3.41	-3.11	-2.78	ubiquitin carboxyl-terminal hydrolase
TGME49_291090	-8.07	-8.87	-8.45	SWI2/SNF2-containing protein
TGME49_297210	1.08	#N/A	#N/A	hypothetical protein
TGME49_217880	-8.05	-8.37	-7.75	RNA-binding protein Nova-1, putative
TGME49_290180	2.38	2.52	2.30	AP2 domain transcription factor AP2IX-6
TGME49_267140	-8.08	-7.60	-8.43	SAG-related sequence SRS38B
TGME49_230520	-1.22	-1.04	#N/A	cyclophilin 1, putative
TGME49_291010	2.02	1.83	2.29	hypothetical protein
TGME49_301350	-8.10	-8.70	-7.79	SNARE associated protein
TGME49_285520	-3.38	-3.05	-3.31	RNA cap guanine-N2 methyltransferase
TGME49_249820	-2.67	-2.97	-3.04	ATP-binding cassette sub-family B member 5
TGME49_208730	-1.15	#N/A	1.55	microneme protein, putative
TGME49_314000	1.22	1.47	#N/A	peptide methionine sulfoxide reductase msrB, putative
TGME49_216760	-8.06	-7.92	-8.19	RNA pseudouridine synthase superfamily protein
TGME49_314970	-1.21	-1.13	-1.54	root hair defective 3 gtp-binding protein (rhd3) protein
TGME49_258850	-8.04	-8.13	-8.11	hypothetical protein
TGME49_220110	1.72	1.56	2.05	hypothetical protein
TGME49_321660	-3.42	-3.15	#N/A	mannosyltransferase, putative
TGME49_319950	-1.79	#N/A	#N/A	rRNA-processing protein FCF1, putative
TGME49_244610	-3.34	-3.73	-3.43	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_288840	1.74	1.59	1.69	hypothetical protein
TGME49_205625	-3.38	-3.24	-2.80	hypothetical protein

TGME49_262760	#N/A	#N/A	-1.21	poly(ADP-ribose) glycohydrolase
TGME49_288240	#N/A	#N/A	1.21	hypothetical protein
TGME49_300320	#N/A	#N/A	2.19	dimethyladenosine transferase
TGME49_212770	#N/A	#N/A	-1.33	hypothetical protein
TGME49_269000	#N/A	#N/A	-1.62	ABC transporter family protein
TGME49_219682	#N/A	#N/A	-1.11	pyruvate dehydrogenase kinase, putative
TGME49_285670	#N/A	#N/A	1.81	hypothetical protein
TGME49_313710	#N/A	#N/A	-1.22	hypothetical protein

FIGURE 5A

Figure 5: EGS transcriptomics data during HFF infections. Differential *T. gondii* gene expression analysis of human HFF cells infected with *T. gondii* EGS strain for 2 hs, 18 hs or 48 hs compared to the average *T. gondii* gene expression of human MM6 and neuronal stem cells infected with either GT1, ME49 or VEG strains of *T. gondii* for 18 hours.

gene ID	logFC 2hs	logFC 18hs	logFC 48hs	Product name
TGME49_462910	1.31	12.08	11.89	large subunit ribosomal RNA
TGME49_457990	1.31	17.05	14.29	28S ribosomal RNA
TGME49_200010	11.50	9.86	10.81	hypothetical protein
TGME49_208370	4.76	1.14	#N/A	myosin heavy chain, putative
TGME49_280570	1.98	5.30	6.48	SAG-related sequence SRS35A
TGME49_251180	1.08	#N/A	1.09	KRUF family protein
TGME49_275860	1.98	1.13	1.07	hypothetical protein
TGME49_252430	1.08	#N/A	#N/A	hypothetical protein
TGME49_290700	1.98	1.34	1.15	hypothetical protein
TGME49_205250	11.50	3.92	4.15	rhoGTPase protein ROP18
TGME49_321480	1.31	5.25	4.55	SAG-related sequence SRS12B
TGME49_316250	1.31	#N/A	#N/A	hypothetical protein
TGME49_206550	4.76	4.04	3.33	hypothetical protein
TGME49_293790	1.98	4.41	3.95	hypothetical protein
TGME49_204050	11.50	#N/A	#N/A	subtilisin SUB1
TGME49_226380	1.56	#N/A	#N/A	hypothetical protein
TGME49_214980	2.42	#N/A	#N/A	hypothetical protein
TGME49_275460	1.98	#N/A	#N/A	hypothetical protein
TGME49_212300	2.42	#N/A	#N/A	hypothetical protein
TGME49_311100	1.31	1.01	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_214080	2.42	4.01	3.46	toxophilin
TGME49_289920	1.98	#N/A	#N/A	hypothetical protein
TGME49_312420	1.31	#N/A	#N/A	hypothetical protein
TGME49_270700	1.98	#N/A	#N/A	hypothetical protein
TGME49_215960	2.42	#N/A	1.03	hypothetical protein
TGME49_249990	1.08	#N/A	#N/A	hypothetical protein
TGME49_205680	11.50	#N/A	#N/A	hypothetical protein
TGME49_288475	1.98	3.36	3.34	hypothetical protein
TGME49_287040	1.98	1.24	1.15	hypothetical protein
TGME49_301250	1.31	3.87	3.67	hypothetical protein
TGME49_240060	1.08	#N/A	#N/A	hypothetical protein
TGME49_208450	4.76	#N/A	#N/A	protease inhibitor PI2
TGME49_233450	1.56	1.33	#N/A	SAG-related sequence SRS29A

gene ID	logFC 2hs	logFC 18hs	logFC 48hs	Product name
TGME49_270800	1.98	#N/A	1.35	GAF domain-containing protein
TGME49_220360	2.42	#N/A	#N/A	FAD binding domain-containing protein
TGME49_315310	1.31	#N/A	#N/A	hypothetical protein
TGME49_254220	1.08	#N/A	#N/A	hypothetical protein
TGME49_280375	1.98	#N/A	#N/A	hypothetical protein
TGME49_202620	11.50	#N/A	#N/A	hypothetical protein
TGME49_216770	2.42	#N/A	#N/A	hypothetical protein
TGME49_218910	2.42	#N/A	#N/A	hypothetical protein
TGME49_220470	2.42	#N/A	#N/A	hypothetical protein
TGME49_300020	1.31	#N/A	#N/A	ATP-dependent metalloprotease HflB subfamily protein
TGME49_278030	1.98	#N/A	#N/A	hypothetical protein
TGME49_206460	11.50	#N/A	#N/A	hypothetical protein
TGME49_255250	-4.38	#N/A	#N/A	tRNA (cytosine(34)-C(5))-methyltransferase, putative
TGME49_251840	1.08	#N/A	#N/A	hypothetical protein
TGME49_306630	1.31	#N/A	#N/A	tRNA methyltransferase complex GCD14 subunit protein
TGME49_246610	1.08	#N/A	#N/A	hypothetical protein
TGME49_282140	1.98	#N/A	#N/A	csf21 protein
TGME49_300052	1.31	#N/A	#N/A	hypothetical protein
TGME49_234350	1.56	#N/A	#N/A	hypothetical protein
TGME49_281440	1.98	#N/A	#N/A	hypothetical protein
TGME49_222070	1.56	#N/A	#N/A	elongation factor Tu GTP binding domain-containing protein
TGME49_233080	1.56	#N/A	#N/A	G-patch domain-containing protein
TGME49_202025	11.50	3.76	2.76	hypothetical protein
TGME49_269075	1.98	#N/A	#N/A	hypothetical protein
TGME49_232590	1.56	#N/A	#N/A	glutamate-cysteine ligase, catalytic subunit domain-containing protein
TGME49_288670	1.98	#N/A	#N/A	hypothetical protein
TGME49_275750	1.98	1.29	1.80	small nuclear ribonucleoprotein E, putative
TGME49_300990	1.31	#N/A	1.84	Toxoplasma gondii family C protein
TGME49_257755	2.35	#N/A	#N/A	hypothetical protein
TGME49_320640	1.31	#N/A	#N/A	peptidylprolyl isomerase domain-containing protein
TGME49_248660	1.08	1.70	#N/A	hypothetical protein
TGME49_236000	1.56	#N/A	#N/A	ferredoxin, putative
TGME49_208540	4.76	#N/A	#N/A	DEAD/DEAH box helicase domain-containing protein

FIGURE 5B

TGME49_213280	2.42	#N/A	#N/A	SAG-related sequence SRS25
TGME49_230830	1.56	1.42	#N/A	ATPase family associated with various cellular activities (AAA) domain-containing protein
TGME49_308020	1.31	#N/A	1.10	SAG-related sequence SRS57
TGME49_207400	4.76	#N/A	#N/A	hypothetical protein
TGME49_220380	2.42	#N/A	#N/A	hypothetical protein
TGME49_272370	1.98	1.03	#N/A	hypothetical protein
TGME49_320490	1.31	#N/A	#N/A	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D family protein
TGME49_207210	4.76	4.66	4.91	hypothetical protein
TGME49_249030	1.08	#N/A	#N/A	endonuclease/exonuclease/phosphatase family protein
TGME49_275870	1.98	2.37	1.43	tubulin/FtsZ family, GTPase domain-containing protein
TGME49_289050	1.98	#N/A	#N/A	FIKK kinase, putative
TGME49_214410	2.42	#N/A	#N/A	hypothetical protein
TGME49_289600	1.98	#N/A	#N/A	heat shock protein HSP29
TGME49_237230	1.08	#N/A	#N/A	hypothetical protein
TGME49_313440	1.31	1.91	1.66	hypothetical protein
TGME49_226540	1.56	#N/A	#N/A	protein kinase
TGME49_289630	1.98	#N/A	#N/A	microneme protein MIC16
TGME49_206510	11.50	#N/A	#N/A	toxolysin TLN4
TGME49_260310	2.35	1.66	3.09	ATP-binding cassette transporter ABC_B1
TGME49_294200	1.98	#N/A	#N/A	glucose-6-phosphate 1-dehydrogenase
TGME49_216820	2.42	#N/A	#N/A	transporter, major facilitator family protein
TGME49_321530	1.31	#N/A	#N/A	cathepsin CPL
TGME49_252390	1.08	#N/A	#N/A	hypothetical protein
TGME49_254460	1.08	1.68	1.98	hypothetical protein
TGME49_220950	2.42	#N/A	#N/A	hypothetical protein
TGME49_217680	2.42	#N/A	#N/A	hypothetical protein
TGME49_201785	11.50	#N/A	#N/A	hypothetical protein
TGME49_214575	2.42	#N/A	1.31	hypothetical protein
TGME49_283540	1.98	#N/A	#N/A	hypothetical protein
TGME49_323110	1.31	1.23	#N/A	hypothetical protein
TGME49_250115	1.08	#N/A	#N/A	hypothetical protein
TGME49_243930	1.08	#N/A	#N/A	hypothetical protein
TGME49_314970	1.31	#N/A	#N/A	root hair defective 3 gtp-binding protein (rh3) protein
TGME49_218520	2.42	#N/A	#N/A	microneme protein MIC6

TGME49_299000	1.31	#N/A	#N/A	hypothetical protein
TGME49_246010	1.08	#N/A	#N/A	hypothetical protein
TGME49_224160	1.56	#N/A	#N/A	hypothetical protein
TGME49_289170	1.98	#N/A	#N/A	adenylate and guanylate cyclase catalytic domain-containing protein
TGME49_221220	2.42	2.68	2.66	hypothetical protein
TGME49_273500	1.98	#N/A	#N/A	O-linked N-acetylglucosamine transferase
TGME49_313495	1.31	#N/A	#N/A	hypothetical protein
TGME49_217610	2.42	#N/A	#N/A	hypothetical protein
TGME49_217640	2.42	#N/A	#N/A	hypothetical protein
TGME49_293580	1.98	#N/A	#N/A	prefoldin subunit protein
TGME49_269705	1.98	#N/A	#N/A	hypothetical protein
TGME49_281910	1.98	#N/A	#N/A	hypothetical protein
TGME49_245730	1.08	#N/A	#N/A	phosphatidylinositol-4-phosphate 5-Kinase
TGME49_305090	1.31	#N/A	#N/A	kinase binding protein cgi-121 protein
TGME49_232640	1.56	1.73	1.57	RNA 2'-phosphotransferase, Tpt1/KptA family protein
TGME49_211695	4.76	-7.00	#N/A	hypothetical protein
TGME49_217010	2.42	#N/A	#N/A	hypothetical protein
TGME49_258720	2.35	#N/A	#N/A	Ubiquitin family protein, putative
TGME49_262060	2.35	#N/A	#N/A	hypothetical protein
TGME49_268320	1.47	#N/A	#N/A	hypothetical protein
TGME49_306520	1.31	#N/A	#N/A	tRNA pseudouridine synthase B, putative
TGME49_252510	1.08	#N/A	#N/A	hypothetical protein
TGME49_262970	2.35	#N/A	#N/A	hypothetical protein
TGME49_219250	2.42	#N/A	#N/A	acetyltransferase, GNAT family protein
TGME49_313060	1.31	#N/A	#N/A	eukaryotic translation initiation factor 2B, putative
TGME49_314070	1.31	#N/A	#N/A	hypothetical protein
TGME49_255270	2.35	#N/A	#N/A	hypothetical protein
TGME49_206500	11.50	#N/A	#N/A	hypothetical protein
TGME49_271320	1.98	2.97	3.07	hypothetical protein
TGME49_212090	4.76	#N/A	#N/A	hypothetical protein
TGME49_294750	1.98	#N/A	#N/A	hypothetical protein
TGME49_228780	1.56	#N/A	#N/A	Toxoplasma gondii family C protein
TGME49_202780	11.50	#N/A	#N/A	rhoGtry kinase family protein ROP25
TGME49_222245	1.56	#N/A	#N/A	hypothetical protein

FIGURE 5C

TGME49_257380	2.35	#N/A	#N/A	hypothetical protein
TGME49_251170	1.08	#N/A	#N/A	KRUF family protein
TGME49_276170	1.98	#N/A	#N/A	phosphatidylinositol 3- and 4-kinase
TGME49_219120	2.42	#N/A	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_236890	1.08	#N/A	#N/A	hypothetical protein
TGME49_277080	1.98	#N/A	#N/A	microneme protein MIC5
TGME49_228170	1.56	#N/A	#N/A	inner membrane complex protein IMC2A
TGME49_225540	1.56	#N/A	#N/A	hypothetical protein
TGME49_233140	1.56	#N/A	#N/A	deoxyuridine 5'-triphosphate nucleotidohydrolase, putative
TGME49_259950	2.35	#N/A	#N/A	carbonate dehydratase, eukaryotic-type domain-containing protein
TGME49_214940	2.42	#N/A	#N/A	MIC2-associated protein M2AP
TGME49_305980	1.31	#N/A	#N/A	pyruvate dehydrogenase complex subunit PDH-E3I
TGME49_243730	1.08	#N/A	#N/A	rhopty protein ROP9
TGME49_286470	1.98	#N/A	#N/A	AGC kinase
TGME49_202020	11.50	3.09	3.30	DnAK-TPR
TGME49_222130	1.56	#N/A	1.02	hypothetical protein
TGME49_321360	1.31	#N/A	#N/A	clustered-asparagine-rich protein
TGME49_206610	4.76	#N/A	#N/A	pyruvate dehydrogenase complex subunit PDH-E2
TGME49_226020	1.56	#N/A	#N/A	transporter, major facilitator family protein
TGME49_212900	2.42	#N/A	#N/A	hypothetical protein
TGME49_298980	1.31	#N/A	1.58	RNA pseudouridine synthase superfamily protein
TGME49_307820	1.31	#N/A	1.33	hypothetical protein
TGME49_270320	1.98	#N/A	1.34	protein phosphatase 2C domain-containing protein
TGME49_252190	1.08	#N/A	1.56	KRUF family protein
TGME49_246550	1.08	#N/A	#N/A	aspartyl protease ASP3
TGME49_289540	1.98	#N/A	#N/A	hypothetical protein
TGME49_268860	1.98	3.33	5.65	enolase 1
TGME49_217740	2.42	-9.88	#N/A	3-ketoacyl-(acyl-carrier-protein) reductase
TGME49_293260	1.98	1.17	#N/A	ATPase/histidine kinase/DNA gyrase B/HSP90 domain-containing protein
TGME49_227100	1.56	3.51	#N/A	hypothetical protein
TGME49_209060	4.76	#N/A	#N/A	thrombospondin type 1 domain-containing protein
TGME49_221320	2.42	#N/A	#N/A	acetyl-CoA carboxylase ACC1
TGME49_313910	1.31	#N/A	#N/A	RNA recognition motif 2 protein
TGME49_252070	1.08	3.55	4.63	KRUF family protein
TGME49_203310	11.50	#N/A	#N/A	dense granule protein GRA7
TGME49_232670	1.56	#N/A	#N/A	hypothetical protein
TGME49_200360	11.50	#N/A	#N/A	hypothetical protein

TGME49_277150	1.98	#N/A	#N/A	XPG N-terminal domain-containing protein
TGME49_232955	1.56	#N/A	-5.63	hypothetical protein
TGME49_217510	2.42	#N/A	#N/A	hypothetical protein
TGME49_313360	1.31	#N/A	#N/A	hypothetical protein
TGME49_234490	1.56	#N/A	#N/A	kelch repeat-containing protein
TGME49_202510	11.50	#N/A	#N/A	multi-pass transmembrane protein
TGME49_219240	2.42	#N/A	#N/A	Peptidyl-IRNA hydrolase PTH2 domain-containing protein
TGME49_229500	1.56	#N/A	1.54	hypothetical protein
TGME49_259830	2.35	#N/A	#N/A	diacylglycerol kinase catalytic domain-containing protein
TGME49_266940	2.35	#N/A	#N/A	DHHC zinc finger domain-containing protein
TGME49_202450	11.50	#N/A	#N/A	hypothetical protein
TGME49_300320	1.31	#N/A	#N/A	dimethyladenosine transferase
TGME49_215440	2.42	#N/A	#N/A	WWE domain-containing protein
TGME49_313110	1.31	#N/A	#N/A	hypothetical protein
TGME49_264650	2.35	#N/A	#N/A	phosphoacetylglucosamine mutase
TGME49_204320	11.50	#N/A	#N/A	hypothetical protein
TGME49_211480	4.76	#N/A	#N/A	GTP-binding protein engA, putative
TGME49_264030	2.35	#N/A	#N/A	aminotransferase, putative
TGME49_208570	4.76	#N/A	#N/A	ubiquitin conjugating enzyme E2, putative
TGME49_231020	1.56	#N/A	#N/A	hypothetical protein
TGME49_215540	2.42	#N/A	-6.53	hypothetical protein
TGME49_295950	1.31	#N/A	#N/A	KRUF family protein
TGME49_262680	2.35	-6.86	#N/A	hypothetical protein
TGME49_224990	1.56	#N/A	#N/A	hypothetical protein
TGME49_299780	1.31	#N/A	#N/A	hypothetical protein
TGME49_275755	1.98	2.12	1.72	hypothetical protein
TGME49_248540	1.08	#N/A	#N/A	hypothetical protein
TGME49_239795	1.08	#N/A	#N/A	hypothetical protein
TGME49_271935	1.98	#N/A	#N/A	hypothetical protein
TGME49_209680	4.76	#N/A	#N/A	hypothetical protein
TGME49_318880	1.31	-7.09	#N/A	hypothetical protein
TGME49_246160	1.08	#N/A	#N/A	hypothetical protein
TGME49_241175	1.08	1.89	#N/A	hypothetical protein
TGME49_316360	1.31	#N/A	#N/A	hypothetical protein
TGME49_209490	4.76	1.17	#N/A	hypothetical protein
TGME49_270805	1.98	#N/A	#N/A	hypothetical protein
TGME49_213020	2.42	#N/A	#N/A	hypothetical protein

FIGURE 5D

TGME49_221590	1.92	#N/A	#N/A	dual specificity phosphatase, catalytic domain-containing protein
TGME49_277230	1.98	#N/A	#N/A	hypothetical protein
TGME49_212270	4.76	#N/A	#N/A	hypothetical protein
TGME49_254470	1.08	#N/A	#N/A	hypothetical protein
TGME49_232000	1.56	#N/A	#N/A	hypothetical protein
TGME49_296340	1.31	2.61	2.84	hypothetical protein
TGME49_225170	1.56	#N/A	#N/A	hypothetical protein
TGME49_297400	1.31	#N/A	#N/A	hypothetical protein
TGME49_277260	1.98	1.36	1.08	hypothetical protein
TGME49_304500	1.31	#N/A	#N/A	hypothetical protein
TGME49_215360	2.42	#N/A	#N/A	hypothetical protein
TGME49_259020	2.35	4.75	5.87	bradyzoite antigen BAG1
TGME49_252640	1.08	6.04	5.81	P-type ATPase PMA1
TGME49_269690	1.98	#N/A	#N/A	hypothetical protein
TGME49_253690	1.08	1.30	#N/A	hypothetical protein
TGME49_247220	1.08	#N/A	#N/A	nudix -type motif 9 isoform a family protein
TGME49_247360	1.08	#N/A	#N/A	PAP2 superfamily protein
TGME49_262400	2.35	#N/A	#N/A	lipase
TGME49_254120	1.08	#N/A	#N/A	autophagy-related protein 8 atg8, putative
TGME49_280380	1.98	#N/A	#N/A	poly(ADP-ribose) glycohydrolase
TGME49_323400	1.31	3.56	4.59	cytochrome c oxidase subunit iii subfamily protein
TGME49_263550	2.35	1.57	#N/A	39S ribosomal protein L47, mitochondrial precursor, putative
TGME49_287460	1.98	2.09	3.13	hypothetical protein
TGME49_246130	1.08	#N/A	#N/A	serpin (serine proteinase inhibitor) superfamily protein
TGME49_264870	2.35	#N/A	#N/A	Sodium:neurotransmitter symporter family protein
TGME49_209100	4.76	#N/A	#N/A	PUB domain-containing protein
TGME49_240090	1.08	#N/A	#N/A	rhoptyr kinase family protein ROP34, putative
TGME49_304740	1.31	#N/A	#N/A	rhoptyr kinase family protein ROP35
TGME49_204520	11.50	2.00	1.45	hypothetical protein
TGME49_201780	11.50	#N/A	#N/A	microneme protein MIC2
TGME49_213050	2.42	#N/A	#N/A	hypothetical protein
TGME49_208020	4.76	#N/A	#N/A	AP2 domain transcription factor AP2lb-1
TGME49_319640	1.31	#N/A	#N/A	hypothetical protein
TGME49_250710	1.08	#N/A	#N/A	microneme protein MIC10

TGME49_260220	2.35	#N/A	#N/A	folate/biopterin transporter subfamily protein
TGME49_295020	1.62	-7.23	#N/A	Sterol-sensing domain of SREBP cleavage-activation domain-containing protein
TGME49_248830	1.08	#N/A	#N/A	phosphoinositide phospholipase PIPLC
TGME49_258850	2.35	#N/A	#N/A	hypothetical protein
TGME49_262600	2.35	#N/A	#N/A	hypothetical protein
TGME49_264730	2.35	#N/A	#N/A	hypothetical protein
TGME49_260470	2.35	#N/A	#N/A	heat shock protein DNAJ pfj4, putative
TGME49_222940	1.56	3.09	#N/A	hypothetical protein
TGME49_221640	1.56	#N/A	#N/A	hypothetical protein
TGME49_224090	1.56	#N/A	#N/A	enoyl-CoA hydratase/isomerase family protein
TGME49_316200	1.31	#N/A	#N/A	phosphoglycerate mutase family protein
TGME49_215380	2.42	#N/A	#N/A	hypothetical protein
TGME49_282170	1.98	#N/A	#N/A	hypothetical protein
TGME49_263220	2.35	#N/A	#N/A	rhoptyr kinase family protein ROP21
TGME49_254090	1.08	#N/A	1.06	hypothetical protein
TGME49_256090	2.35	#N/A	#N/A	glycerophosphodiester phosphodiesterase family protein
TGME49_309410	1.31	#N/A	#N/A	AP2 domain transcription factor AP2Xl-1
TGME49_219660	2.42	#N/A	2.21	hypothetical protein
TGME49_251450	1.08	#N/A	1.06	hypothetical protein
TGME49_310390	1.31	#N/A	#N/A	hypothetical protein
TGME49_301350	1.31	#N/A	#N/A	SNARE associated protein
TGME49_205200	11.50	#N/A	#N/A	hypothetical protein
TGME49_254950	1.08	#N/A	#N/A	RNA cap guanine-N2 methyltransferase
TGME49_206340	11.50	#N/A	#N/A	hypothetical protein
TGME49_286430	1.98	#N/A	#N/A	hypothetical protein
TGME49_243680	1.08	#N/A	#N/A	dihydrodipicolinate reductase
TGME49_250955	1.08	#N/A	#N/A	KRUF family protein
TGME49_251920	1.08	#N/A	#N/A	hypothetical protein
TGME49_277070	1.98	#N/A	#N/A	SWI2/SNF2-containing protein
TGME49_280470	1.98	#N/A	#N/A	AP2 domain transcription factor AP2VIIa-1
TGME49_254890	1.08	#N/A	1.83	hypothetical protein
TGME49_238970	1.08	#N/A	#N/A	hypothetical protein
TGME49_254280	1.08	2.32	#N/A	DNA-directed RNA polymerase III RPC9
TGME49_224890	1.56	#N/A	#N/A	hypothetical protein

FIGURE 5E

TGME49_232410	1.56	1.17	1.14	PDI family protein
TGME49_253440	1.08	#N/A	#N/A	cell-cycle-associated protein kinase SRPK, putative
TGME49_214440	2.42	#N/A	#N/A	4'-phosphopantetheinyl transferase superfamily protein
TGME49_313760	1.31	#N/A	#N/A	hypothetical protein
TGME49_314430	1.31	#N/A	#N/A	serine/threonine specific protein phosphatase
TGME49_291940	1.98	#N/A	#N/A	hypothetical protein
TGME49_260620	2.35	#N/A	#N/A	hypothetical protein
TGME49_297650	1.31	#N/A	#N/A	Ser/Thr phosphatase family protein
TGME49_225790	1.56	#N/A	#N/A	PDI family protein
TGME49_293252	1.98	3.40	4.86	hypothetical protein
TGME49_231430	1.56	#N/A	#N/A	oligosaccharyl transferase stt3 protein, putative
TGME49_233380	1.56	#N/A	#N/A	hypothetical protein
TGME49_314700	1.31	#N/A	#N/A	hypothetical protein
TGME49_310130	1.31	#N/A	#N/A	Spc97 / Spc98 family protein
TGME49_291040	1.98	4.24	5.12	lactate dehydrogenase LDH2
TGME49_315910	1.31	#N/A	#N/A	hypothetical protein
TGME49_310520	1.31	#N/A	1.52	3'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_209140	4.76	#N/A	#N/A	anti-silencing protein, ASF1 family protein
TGME49_220240	2.42	#N/A	#N/A	hypothetical protein
TGME49_215895	2.42	#N/A	#N/A	AP2 domain-containing protein
TGME49_216680	2.42	#N/A	#N/A	ankyrin repeat-containing protein
TGME49_244530	1.08	#N/A	#N/A	hypothetical protein
TGME49_254390	1.08	1.48	1.21	CRAL/TRIO domain-containing protein
TGME49_286460	1.98	#N/A	#N/A	hypothetical protein
TGME49_253560	1.08	#N/A	#N/A	hypothetical protein
TGME49_228160	1.56	#N/A	#N/A	acid phosphatase
TGME49_294980	1.98	#N/A	1.32	hypothetical protein
TGME49_222020	1.56	#N/A	#N/A	phosphoglycerate kinase PGKII
TGME49_225160	1.56	#N/A	#N/A	hypothetical protein
TGME49_276930	1.98	#N/A	#N/A	hypothetical protein
TGME49_209985	4.76	2.97	1.97	cAMP-dependent protein kinase
TGME49_229930	1.56	#N/A	#N/A	p25-alpha family protein
TGME49_247530	1.08	#N/A	#N/A	hypothetical protein
TGME49_218540	2.42	#N/A	#N/A	peptidase S15, putative

TGME49_218610	2.42	#N/A	#N/A	ATPase (DUF699) protein
TGME49_214960	2.42	#N/A	#N/A	AP2 domain transcription factor AP2X-8
TGME49_228150	1.56	#N/A	#N/A	hypothetical protein
TGME49_242730	1.08	#N/A	#N/A	guanylate kinase family protein
TGME49_233770	1.56	#N/A	#N/A	calcium-translocating P-type ATPase, PMCA-type protein
TGME49_215750	2.42	#N/A	2.18	cytidine and deoxycytidylate deaminase zinc-binding region domain-containing protein
TGME49_255350	2.35	2.40	#N/A	ATPase, putative
TGME49_320700	1.31	1.63	#N/A	AP2 domain transcription factor AP2IV-1
TGME49_225230	1.56	#N/A	#N/A	hypothetical protein
TGME49_278080	1.98	4.04	4.54	Toxoplasma gondii family A protein
TGME49_249410	1.08	#N/A	#N/A	hypothetical protein
TGME49_211610	4.76	#N/A	#N/A	hypothetical protein
TGME49_308965	1.31	#N/A	#N/A	hypothetical protein
TGME49_270595	1.98	#N/A	#N/A	UBA/T-S-N domain-containing protein
TGME49_220250	2.42	#N/A	#N/A	Nucleotide-sensitive chloride conductance regulator (ICln) protein
TGME49_218740	2.42	-8.05	#N/A	membrane protein, putative
TGME49_277090	1.98	#N/A	#N/A	carrier superfamily protein
TGME49_273640	1.98	#N/A	#N/A	hypothetical protein
TGME49_225470	1.56	#N/A	1.32	peptide methionine sulfoxide reductase
TGME49_288370	1.98	#N/A	#N/A	hypothetical protein
TGME49_268840	1.98	-8.64	#N/A	N6-adenosine-methyltransferase, putative
TGME49_270890	1.98	#N/A	#N/A	hypothetical protein
TGME49_200385	11.50	#N/A	#N/A	Myb family DNA-binding domain-containing protein
TGME49_253510	1.08	1.81	#N/A	transporter/permease protein
TGME49_289550	1.98	#N/A	#N/A	WD domain, G-beta repeat-containing protein
TGME49_297730	1.31	1.62	#N/A	transcription elongation factor 1, putative
TGME49_232960	1.56	#N/A	#N/A	oxidoreductase, 2OG-Fe(II) oxygenase family protein
TGME49_250940	1.08	#N/A	#N/A	hypothetical protein
TGME49_266880	2.35	#N/A	#N/A	dihydrouridine synthase, putative
TGME49_217560	2.42	#N/A	#N/A	DNA-directed RNA polymerase II RPB10
TGME49_226640	1.56	2.46	#N/A	zinc binding protein, putative
TGME49_319090	1.31	#N/A	#N/A	IgA-specific serine endopeptidase
TGME49_304490	1.31	#N/A	#N/A	hypothetical protein
TGME49_261590	2.35	#N/A	#N/A	ankyrin, putative

FIGURE 5F

TGME49_309580	1.31	#N/A	#N/A	transporter, major facilitator family protein
TGME49_266310	2.35	#N/A	#N/A	Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase
TGME49_293770	1.98	#N/A	#N/A	chitinase-like protein CLP1
TGME49_275640	1.98	1.46	#N/A	hypothetical protein
TGME49_239420	1.08	#N/A	#N/A	protein kinase
TGME49_254000	1.08	#N/A	1.21	hypothetical protein
TGME49_305460	1.31	2.07	2.50	methionine aminopeptidase 2, putative
TGME49_250220	1.08	1.94	1.36	hypothetical protein
TGME49_323100	1.31	#N/A	#N/A	hypothetical protein
TGME49_263560	2.35	#N/A	#N/A	hypothetical protein
TGME49_266760	2.35	#N/A	#N/A	isocitrate dehydrogenase
TGME49_210682	4.76	#N/A	#N/A	hypothetical protein
TGME49_312160	1.31	2.15	1.57	hypothetical protein
TGME49_255260	2.35	#N/A	#N/A	apical membrane antigen AMA1
TGME49_227390	1.56	#N/A	#N/A	hypothetical protein
TGME49_286000	1.98	#N/A	#N/A	hypothetical protein
TGME49_316710	1.31	#N/A	#N/A	hypothetical protein
TGME49_208590	4.76	#N/A	1.30	vacuolar ATP synthase subunit 54kD, putative
TGME49_288210	1.98	#N/A	#N/A	PUL domain-containing protein
TGME49_306620	1.31	1.44	#N/A	AP2 domain transcription factor AP2IX-9
TGME49_275420	1.98	#N/A	#N/A	histone lysine-specific demethylase LSD1/BHC110/KDMA1A
TGME49_209900	4.76	#N/A	#N/A	hypothetical protein
TGME49_253470	1.08	1.07	1.44	alveolin domain containing intermediate filament IMC13
TGME49_288650	1.98	#N/A	#N/A	dense granule protein GRA12
TGME49_300055	1.31	#N/A	#N/A	hypothetical protein
TGME49_217530	2.42	#N/A	#N/A	hypothetical protein
TGME49_255180	1.08	#N/A	#N/A	ubiquitin carboxyl-terminal hydrolase
TGME49_226310	1.56	#N/A	#N/A	zinc finger (CCH type) motif-containing protein
TGME49_259880	2.35	#N/A	#N/A	hypothetical protein
TGME49_212250	4.76	1.34	#N/A	XPG N-terminal domain-containing protein
TGME49_215550	2.42	#N/A	1.25	hypothetical protein
TGME49_213635	2.42	2.41	#N/A	hypothetical protein
TGME49_288840	1.98	#N/A	#N/A	hypothetical protein
TGME49_222948	1.56	-8.96	#N/A	hypothetical protein
TGME49_232750	1.56	#N/A	#N/A	23S rRNA (adenine(1618)-N(6))-methyltransferase, putative

TGME49_237015	1.08	#N/A	#N/A	hypothetical protein
TGME49_277870	1.98	#N/A	#N/A	hypothetical protein
TGME49_252880	1.08	#N/A	1.68	hypothetical protein
TGME49_250500	1.08	-7.08	#N/A	hypothetical protein
TGME49_222970	1.56	#N/A	#N/A	inositol(myo)-1(or 4)-monophosphatase 2, putative
TGME49_202310	11.50	#N/A	#N/A	O-sialoglycoprotein endopeptidase
TGME49_250670	1.08	#N/A	#N/A	hypothetical protein
TGME49_305080	1.31	#N/A	#N/A	hypothetical protein
TGME49_217430	2.42	#N/A	#N/A	protease inhibitor PI1
TGME49_225410	1.56	1.74	#N/A	histone H3 centromeric CENH3
TGME49_227860	1.56	#N/A	#N/A	hypothetical protein
TGME49_261220	2.35	#N/A	#N/A	transcription elongation factor SPT4
TGME49_270300	1.98	#N/A	#N/A	hypothetical protein
TGME49_270610	1.98	#N/A	#N/A	hypothetical protein
TGME49_252670	1.08	#N/A	1.32	hypothetical protein
TGME49_319620	1.31	#N/A	#N/A	hypothetical protein
TGME49_301180	1.31	#N/A	#N/A	SAG-related sequence SRS19F
TGME49_268980	1.98	#N/A	#N/A	hypothetical protein
TGME49_218950	2.42	#N/A	#N/A	hypothetical protein
TGME49_267970	2.35	-8.22	#N/A	DEAD/DEAH box helicase domain-containing protein
TGME49_285470	1.98	#N/A	1.70	patched family protein
TGME49_240300	1.08	#N/A	#N/A	zinc finger domain, LSD1 subclass domain-containing protein
TGME49_289250	1.98	#N/A	#N/A	cydophilin, putative
TGME49_220208	2.42	#N/A	#N/A	hypothetical protein
TGME49_257020	2.35	#N/A	#N/A	hypothetical protein
TGME49_230150	1.56	#N/A	#N/A	ChAPs (Chs5p-Arf1p-binding proteins) protein
TGME49_294990	1.98	#N/A	#N/A	hypothetical protein
TGME49_236670	-4.91	#N/A	#N/A	hypothetical protein
TGME49_309190	1.31	#N/A	#N/A	hypothetical protein
TGME49_312280	1.31	#N/A	#N/A	pre-mRNA-splicing factor ATP-dependent RNA helicase, putative
TGME49_208722	4.76	#N/A	#N/A	hypothetical protein
TGME49_256880	2.35	-8.61	#N/A	protein kinase domain-containing protein
TGME49_222850	1.56	#N/A	#N/A	stress responsive a/b barrel domain-containing protein
TGME49_219150	2.42	#N/A	#N/A	zinc finger, zz type domain-containing protein
TGME49_216030	2.42	#N/A	#N/A	hypothetical protein

FIGURE 5G

TGME49_270260	1.98	#N/A	2.03	hypothetical protein
TGME49_253750	1.08	#N/A	#N/A	PLU-1 family protein
TGME49_295420	1.31	#N/A	#N/A	hypothetical protein
TGME49_315680	1.31	#N/A	#N/A	vacuolar protein sorting-associated protein vps4, putative
TGME49_321630	1.31	#N/A	#N/A	RNA recognition motif-containing protein
TGME49_284010	1.98	#N/A	#N/A	5'-3' exonuclease, N-terminal resolvase family domain-containing protein
TGME49_269310	1.98	#N/A	#N/A	hypothetical protein
TGME49_222240	1.56	#N/A	#N/A	hypothetical protein
TGME49_217750	2.42	#N/A	-4.62	hypothetical protein
TGME49_288000	1.98	#N/A	#N/A	hypothetical protein
TGME49_251540	1.08	#N/A	#N/A	dense granule protein GRA9
TGME49_209755	4.76	4.10	5.58	hypothetical protein
TGME49_219590	2.42	#N/A	#N/A	RuvB family 1 protein
TGME49_290190	1.98	#N/A	#N/A	hypothetical protein
TGME49_220440	2.42	#N/A	#N/A	cyclin-dependent kinase regulatory subunit protein
TGME49_260540	2.35	#N/A	#N/A	alveolin domain containing intermediate filament IMC14
TGME49_220890	2.42	#N/A	#N/A	hypothetical protein
TGME49_232160	1.56	1.08	#N/A	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_216500	2.42	#N/A	#N/A	tRNA synthetase, putative
TGME49_261790	2.35	#N/A	#N/A	hypothetical protein
TGME49_245490	1.08	#N/A	#N/A	microneme protein MIC8
TGME49_202580	11.50	#N/A	1.20	ATPase, AAA family protein
TGME49_243470	1.08	4.58	4.67	hypothetical protein
TGME49_244450	1.08	#N/A	#N/A	protein phosphatase 2C domain-containing protein
TGME49_249230	1.08	#N/A	#N/A	hypothetical protein
TGME49_268010	2.35	#N/A	#N/A	hypothetical protein
TGME49_299030	1.31	1.42	1.73	RNA recognition motif 2 protein
TGME49_265400	2.35	#N/A	#N/A	hypothetical protein
TGME49_226520	1.56	#N/A	#N/A	hypothetical protein
TGME49_293280	1.98	#N/A	#N/A	cyclin protein
TGME49_312105	1.31	-8.91	-5.44	hypothetical protein
TGME49_222050	1.56	#N/A	#N/A	hypothetical protein
TGME49_274150	1.98	#N/A	#N/A	hypothetical protein
TGME49_254710	1.08	#N/A	#N/A	serine esterase (DUF676) protein
TGME49_215210	2.42	#N/A	#N/A	hypothetical protein
TGME49_221350	2.42	#N/A	#N/A	Ctr copper transporter family protein

TGME49_222180	1.56	#N/A	#N/A	hypothetical protein
TGME49_227430	1.56	#N/A	2.76	transmembrane amino acid transporter protein
TGME49_221500	2.42	#N/A	#N/A	dual specificity phosphatase, catalytic domain-containing protein
TGME49_220260	2.42	#N/A	#N/A	hypothetical protein
TGME49_310970	1.31	-4.58	#N/A	hypothetical protein
TGME49_239530	1.08	-6.09	#N/A	alanine-glyoxylate aminotransferase
TGME49_207160	4.76	3.72	4.66	SAG-related sequence SRS49D
TGME49_244700	1.08	-4.99	#N/A	NAD(+)/NADH kinase domain-containing protein
TGME49_253330	1.08	2.37	2.64	Rhoptry kinase family protein, truncated (incomplete catalytic triad)
TGME49_249260	1.08	-9.86	#N/A	cell-cycle-associated protein kinase CDK, putative
TGME49_313270	1.31	-4.80	#N/A	hypothetical protein
TGME49_208730	4.76	1.74	1.06	microneme protein, putative
TGME49_290970	1.98	2.59	2.50	8-amino-7-oxononanoate synthase
TGME49_312660	1.31	-9.00	#N/A	hypothetical protein
TGME49_209970	4.76	-9.27	#N/A	Spc97 / Spc98 family protein
TGME49_243210	1.08	-10.07	#N/A	DUF862 domain-containing protein
TGME49_319730	1.31	-8.83	#N/A	YOU2 family C2C2 zinc finger protein
TGME49_310530	1.31	-9.05	#N/A	SNF2 family N-terminal domain-containing protein
TGME49_299990	1.31	1.99	1.46	archaease family protein
TGME49_208740	4.76	1.28	#N/A	microneme protein, putative
TGME49_291810	1.98	-4.40	#N/A	thioredoxin domain-containing protein
TGME49_269438	1.98	-9.21	#N/A	hypothetical protein
TGME49_241305	1.08	-8.92	#N/A	hypothetical protein
TGME49_312430	1.31	-8.70	#N/A	hypothetical protein
TGME49_209070	4.76	-9.94	#N/A	hypothetical protein
TGME49_228180	1.56	-8.92	#N/A	cytochrome C oxidase assembly factor COX15, putative
TGME49_286928	1.98	-8.89	#N/A	hypothetical protein
TGME49_318575	1.31	-8.67	#N/A	hypothetical protein
TGME49_264670	2.35	-8.85	#N/A	DNA polymerase family B protein
TGME49_229200	1.56	-8.72	#N/A	hypothetical protein
TGME49_273840	1.98	-8.66	#N/A	brix domain-containing protein
TGME49_298990	1.31	1.79	#N/A	ferredoxin NADP+ oxidoreductase FNR
TGME49_312140	1.31	-4.37	#N/A	hypothetical protein
TGME49_224600	1.56	-8.73	#N/A	GTP binding protein
TGME49_216930	2.42	1.78	#N/A	cholinesphosphate cytidyltransferase
TGME49_220370	2.42	-5.05	#N/A	hypothetical protein

FIGURE 5H

TGME49_221840	1.56	4.17	4.38	hypothetical protein
TGME49_268225	2.35	-9.66	-7.05	hypothetical protein
TGME49_265480	2.35	#N/A	#N/A	hypothetical protein
TGME49_249540	1.08	#N/A	#N/A	hypothetical protein
TGME49_266920	2.35	#N/A	#N/A	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_268230	2.35	-9.26	-9.26	hypothetical protein
TGME49_226580	1.56	#N/A	#N/A	hypothetical protein
TGME49_234530	1.56	#N/A	#N/A	hypothetical protein
TGME49_248110	1.08	#N/A	#N/A	hypothetical protein
TGME49_202572	11.50	#N/A	#N/A	ribophorin i protein
TGME49_220390	2.42	#N/A	#N/A	hypothetical protein
TGME49_315440	1.31	#N/A	#N/A	hypothetical protein
TGME49_223750	1.56	#N/A	#N/A	hypothetical protein
TGME49_244300	1.08	#N/A	#N/A	hypothetical protein
TGME49_258710	2.35	#N/A	#N/A	T-complex protein 10 C-terminus protein
TGME49_202770	11.50	#N/A	#N/A	RNA recognition motif-containing protein
TGME49_232035	1.56	-8.62	-4.53	hypothetical protein
TGME49_254690	1.08	1.06	1.20	phospholipase/carboxylesterase
TGME49_280370	1.98	#N/A	#N/A	hypothetical protein
TGME49_242845	1.08	-8.83	#N/A	hypothetical protein
TGME49_226990	1.56	#N/A	#N/A	hypothetical protein
TGME49_207100	4.76	#N/A	#N/A	hypothetical protein
TGME49_219810	2.42	#N/A	#N/A	hypothetical protein
TGME49_280522	1.98	#N/A	#N/A	hypothetical protein
TGME49_315950	1.31	#N/A	#N/A	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_212940	2.42	-8.65	#N/A	hypothetical protein
TGME49_203060	11.50	#N/A	#N/A	hypothetical protein
TGME49_269130	1.98	#N/A	#N/A	hypothetical protein
TGME49_258030	2.35	#N/A	#N/A	DNA polymerase
TGME49_224970	1.56	#N/A	#N/A	nucleolar protein,nop52 protein
TGME49_221180	2.42	#N/A	#N/A	hypothetical protein
TGME49_311230	1.31	#N/A	1.03	hypothetical protein
TGME49_247300	1.08	#N/A	#N/A	hypothetical protein
TGME49_319590	1.31	#N/A	#N/A	hypothetical protein
TGME49_240780	1.08	#N/A	#N/A	hypothetical protein
TGME49_208310	4.76	#N/A	#N/A	hypothetical protein
TGME49_254920	1.08	2.59	2.48	hypothetical protein

TGME49_272000	1.98	-8.53	#N/A	hypothetical protein
TGME49_232550	1.56	1.62	1.18	hypothetical protein
TGME49_245580	1.08	-8.59	#N/A	hypothetical protein
TGME49_278500	1.98	-8.69	#N/A	ribosomal RNA large subunit methyltransferase J protein
TGME49_309950	1.31	-8.44	#N/A	NLE (NUC135) domain-containing protein
TGME49_221900	1.56	-8.31	#N/A	hypothetical protein
TGME49_249560	1.08	-8.51	#N/A	DNA-directed RNA polymerase alpha chain rpoA
TGME49_264660	2.35	1.56	1.29	SAG-related sequence SRS44
TGME49_238020	1.08	-8.56	#N/A	hypothetical protein
TGME49_240970	1.08	-8.94	#N/A	hypothetical protein
TGME49_301430	1.31	-8.67	#N/A	septum formation protein maf, putative
TGME49_214340	2.42	-4.76	#N/A	hypothetical protein
TGME49_230000	1.56	-8.74	#N/A	hypothetical protein
TGME49_246060	1.08	-8.27	#N/A	DNA-dependent RNA polymerase
TGME49_263710	2.35	-5.14	#N/A	acyl-CoA:cholesterol acyltransferase alpha ACAT1-alpha
TGME49_261740	2.35	1.22	1.29	hypothetical protein
TGME49_305050	1.31	1.88	#N/A	calmodulin, putative
TGME49_246590	1.08	-8.29	#N/A	hypothetical protein
TGME49_235460	1.56	-8.56	#N/A	hypothetical protein
TGME49_266950	2.35	-9.24	#N/A	protein kinase, putative
TGME49_219290	2.42	-8.61	#N/A	F-actin-capping protein subunit beta, putative
TGME49_203760	11.50	-8.87	#N/A	hypothetical protein
TGME49_246200	1.08	-8.46	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_313960	1.31	-8.02	#N/A	ribosomal protein L19 protein
TGME49_249480	1.08	1.62	1.21	tetratricopeptide repeat-containing protein
TGME49_254080	1.08	1.09	1.41	metal cation transporter, ZIP family protein
TGME49_230110	1.56	-8.60	#N/A	hypothetical protein
TGME49_268770	1.98	-8.36	#N/A	dual specificity phosphatase, catalytic domain-containing protein
TGME49_240660	1.08	-8.25	#N/A	hypothetical protein
TGME49_244160	1.08	-8.35	#N/A	transcription initiation factor TFIID complex subunit TAF12
TGME49_271145	1.98	-8.12	#N/A	hypothetical protein
TGME49_319940	1.31	-8.14	#N/A	hypothetical protein
TGME49_243298	1.08	-8.28	#N/A	ICE family protease (caspase) p20 domain-containing protein
TGME49_297320	1.31	-9.10	#N/A	hypothetical protein
TGME49_268170	2.35	-8.39	-4.39	hypothetical protein
TGME49_221585	2.42	-8.87	#N/A	hypothetical protein
TGME49_270620	1.98	-8.01	#N/A	DEAD/DEAH box helicase domain-containing protein

FIGURE 5i

TGME49_221480	2.42	#N/A	#N/A	hypothetical protein
TGME49_204530	11.50	#N/A	#N/A	microneme protein MIC11
TGME49_213730	2.42	#N/A	#N/A	lanthionine synthetase C family protein
TGME49_293270	1.98	#N/A	#N/A	hypothetical protein
TGME49_304880	1.31	#N/A	#N/A	hypothetical protein
TGME49_252420	1.08	2.16	#N/A	histone arginine methyltransferase PRMT3
TGME49_265790	2.35	#N/A	#N/A	hypothetical protein
TGME49_270865	1.98	#N/A	#N/A	adenylate cyclase, putative
TGME49_269950	1.98	#N/A	#N/A	hypothetical protein
TGME49_245630	1.08	#N/A	#N/A	hypothetical protein
TGME49_220330	2.42	#N/A	#N/A	hypothetical protein
TGME49_215160	2.42	#N/A	#N/A	hypothetical protein
TGME49_231890	1.56	#N/A	#N/A	beta-ketoacyl-acyl carrier protein synthase III, putative
TGME49_310210	1.31	#N/A	#N/A	hypothetical protein
TGME49_225680	1.56	-8.69	#N/A	hypothetical protein
TGME49_242640	1.08	#N/A	#N/A	hypothetical protein
TGME49_255690	2.35	#N/A	#N/A	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase domain-containing protein
TGME49_253640	1.08	#N/A	#N/A	hypothetical protein
TGME49_237500	1.08	#N/A	#N/A	protein phosphatase 2C domain-containing protein
TGME49_308040	1.31	#N/A	#N/A	ZPR1 zinc finger domain-containing protein
TGME49_211460	4.76	#N/A	#N/A	hypothetical protein
TGME49_300048	1.31	#N/A	#N/A	hypothetical protein
TGME49_250730	1.08	#N/A	#N/A	60S ribosomal protein L7-B, putative
TGME49_306040	1.31	#N/A	#N/A	CHY zinc finger protein
TGME49_315100	1.31	3.51	3.91	hypothetical protein
TGME49_250950	1.08	#N/A	#N/A	KRUF family protein
TGME49_202520	11.50	#N/A	#N/A	hypothetical protein
TGME49_257080	2.35	#N/A	#N/A	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_205180	11.50	#N/A	#N/A	RNA recognition motif-containing protein
TGME49_266450	2.35	#N/A	#N/A	lysine decarboxylase family protein
TGME49_315280	1.31	-8.97	#N/A	hypothetical protein

TGME49_278270	1.98	-8.09	#N/A	nucleolar protein, structural component of H/ACA snoRNPs, putative
TGME49_254630	1.08	1.35	1.64	CMGC kinase
TGME49_298060	1.31	-8.32	#N/A	Toxoplasma gondii family C protein
TGME49_297510	1.31	-8.78	#N/A	hypothetical protein
TGME49_285850	1.98	-8.30	#N/A	peptidyl-prolyl cis-trans isomerase, FKBP-type domain-containing protein
TGME49_313480	1.31	-8.44	#N/A	hypothetical protein
TGME49_257290	2.35	-8.13	#N/A	RNA 2'-phosphotransferase, Tpt1/KptA family protein
TGME49_313200	1.31	-8.34	#N/A	leucine rich repeat-containing protein
TGME49_252440	1.08	2.33	2.11	peptidase c13 family protein
TGME49_254365	1.08	1.24	1.44	phosphatidate cytidylyltransferase
TGME49_238190	1.08	1.55	#N/A	DNA-directed RNA polymerase II RPB3
TGME49_267340	2.35	1.84	#N/A	hypothetical protein
TGME49_262050	2.35	1.14	1.18	rhoGTPase family protein ROP39
TGME49_204490	11.50	-7.99	#N/A	hypothetical protein
TGME49_232510	1.56	-8.65	#N/A	hypothetical protein
TGME49_283585	1.98	-8.28	#N/A	hypothetical protein
TGME49_247610	1.08	-8.03	#N/A	small nuclear ribonucleoprotein E, putative
TGME49_240480	1.08	-8.00	#N/A	cpw-wpc domain-containing protein
TGME49_244200	1.08	1.00	#N/A	2-oxoglutarate dehydrogenase e1 component, mitochondrial precursor, putative
TGME49_258940	2.35	-7.94	#N/A	acylphosphatase family protein
TGME49_317705	1.31	-5.13	#N/A	enoyl-CoA hydratase/isomerase family protein
TGME49_280580	1.98	1.89	2.66	SAG-related sequence SRS35B
TGME49_293500	1.98	-8.17	#N/A	hypothetical protein
TGME49_227115	1.56	-8.32	#N/A	hypothetical protein
TGME49_316090	1.31	-7.84	#N/A	RNAse P Rpr2/Rpp21 subunit domain-containing protein
TGME49_253790	1.08	1.16	1.53	zinc finger (CCH type) motif-containing protein
TGME49_258780	2.35	-8.93	#N/A	OTU family cysteine protease
TGME49_275780	1.98	-7.96	#N/A	hypothetical protein
TGME49_220230	2.42	-4.57	#N/A	leucine rich repeat-containing protein
TGME49_255215	1.08	-8.40	#N/A	hypothetical protein
TGME49_205010	11.50	1.08	#N/A	U2 small nuclear ribonucleoprotein family protein, putative

FIGURE 5J

TGME49_330000	1.31	3.95	4.62	cytochrome b
TGME49_207065	4.76	#N/A	#N/A	hypothetical protein
TGME49_209095	4.76	#N/A	#N/A	hypothetical protein
TGME49_238510	1.08	#N/A	#N/A	hypothetical protein
TGME49_232340	1.56	#N/A	#N/A	protein phosphatase 2C domain-containing protein
TGME49_250100	1.08	#N/A	#N/A	hypothetical protein
TGME49_228980	1.56	-8.09	-4.97	hypothetical protein
TGME49_321450	1.31	#N/A	#N/A	Myb family DNA-binding domain-containing protein
TGME49_260410	2.35	#N/A	#N/A	hypothetical protein
TGME49_225990	1.56	#N/A	#N/A	acyl transferase domain-containing protein
TGME49_205490	11.50	#N/A	#N/A	integral membrane protein, putative
TGME49_236800	1.08	#N/A	#N/A	hypothetical protein
TGME49_257350	2.35	#N/A	1.09	eukaryotic translation initiation factor, putative
TGME49_223660	1.56	#N/A	#N/A	50S ribosomal protein L4, putative
TGME49_306890	1.31	#N/A	#N/A	hypothetical protein
TGME49_230180	1.56	#N/A	#N/A	hypothetical protein
TGME49_203280	11.50	#N/A	#N/A	hypothetical protein
TGME49_268680	1.98	#N/A	#N/A	hypothetical protein
TGME49_223390	1.56	#N/A	#N/A	activating signal cointegrator 1 complex subunit 3 family 1 ASCC3L1, putative
TGME49_206450	11.50	#N/A	#N/A	autophagy-related cysteine peptidase atg4, putative
TGME49_273970	1.98	#N/A	#N/A	CorA family Mg ²⁺ transporter protein
TGME49_277270	1.98	#N/A	#N/A	NTPase II
TGME49_263420	2.35	#N/A	#N/A	ubiquitin-specific protease USP4
TGME49_239710	1.08	-8.73	#N/A	phosphomannomutase
TGME49_286480	1.98	#N/A	#N/A	hypothetical protein
TGME49_278230	1.98	#N/A	#N/A	prenyltransferase and squalene oxidase repeat-containing protein
TGME49_207930	4.76	#N/A	#N/A	phosphatidylethanolamine-binding protein
TGME49_219820	2.42	#N/A	#N/A	polyubiquitin UbC, putative
TGME49_258870	2.35	#N/A	#N/A	hypothetical protein
TGME49_243430	1.08	#N/A	#N/A	OTU family cysteine protease
TGME49_215910	2.42	#N/A	#N/A	hypothetical protein
TGME49_259200	2.35	#N/A	#N/A	Na ⁺ /H ⁺ exchanger NHE1
TGME49_225900	1.56	#N/A	#N/A	hypothetical protein
TGME49_251400	1.08	#N/A	1.27	hypothetical protein

TGME49_279540	1.98	-8.17	#N/A	hypothetical protein
TGME49_244645	1.08	-7.70	1.38	hypothetical protein
TGME49_250900	1.08	-7.59	#N/A	hypothetical protein
TGME49_301310	1.31	-4.46	#N/A	hypothetical protein
TGME49_248670	1.08	1.02	#N/A	V-type H ⁽⁺⁾ -translocating pyrophosphatase VP1
TGME49_223150	1.56	-8.54	#N/A	START domain-containing protein
TGME49_230080	1.56	-8.52	#N/A	DEAD/DEAH box helicase domain-containing protein
TGME49_226700	1.56	-7.84	#N/A	nuclease, putative
TGME49_235478	1.56	-4.89	#N/A	pantothenate kinase
TGME49_248440	1.08	-8.41	#N/A	hypothetical protein
TGME49_255930	2.35	-8.12	#N/A	hypothetical protein
TGME49_226280	1.56	-7.80	#N/A	ribosomal protein L28, putative
TGME49_221370	2.42	-8.41	#N/A	hypothetical protein
TGME49_310290	1.31	-7.56	#N/A	regulator of chromosome condensation (RCC1) repeat-containing protein
TGME49_264752	2.35	-7.90	#N/A	HEAT repeat-containing protein
TGME49_309390	1.31	2.01	#N/A	hypothetical protein
TGME49_314790	1.31	-5.50	#N/A	small nuclear ribonucleoprotein G, putative
TGME49_309080	1.31	-7.56	#N/A	hypothetical protein
TGME49_239087	1.08	-8.18	#N/A	hypothetical protein
TGME49_269430	1.98	-8.29	#N/A	polyprenyl synthetase superfamily protein
TGME49_289000	1.98	-8.54	#N/A	hypothetical protein
TGME49_217450	2.42	-8.05	#N/A	general transcription factor IIH polypeptide 5 GTF2H5
TGME49_277700	1.98	-7.85	#N/A	ribosomal protein S14 precursor, putative
TGME49_281950	1.98	-8.54	#N/A	membrane protein, putative
TGME49_209930	4.76	-8.42	#N/A	hypothetical protein
TGME49_316470	1.31	-8.45	#N/A	hypothetical protein
TGME49_323010	1.31	-7.77	#N/A	hypothetical protein
TGME49_289010	1.98	-8.16	#N/A	RNA recognition motif-containing protein
TGME49_243760	1.08	-8.49	#N/A	hypothetical protein
TGME49_263215	2.35	-7.63	4.51	hypothetical protein
TGME49_306338	1.31	-8.39	#N/A	dynein gamma chain, flagellar outer arm, putative
TGME49_254930	1.08	1.13	#N/A	hypothetical protein
TGME49_293860	1.98	-4.63	#N/A	hypothetical protein
TGME49_236990	1.08	1.82	1.74	beta-ketoacyl synthase, N-terminal domain-containing protein

FIGURE 5K

TGME49_200450	11.50	#N/A	#N/A	hypothetical protein
TGME49_242810	1.08	#N/A	#N/A	hypothetical protein
TGME49_302055	1.31	#N/A	#N/A	ribosomal protein RPS12
TGME49_259040	2.35	#N/A	#N/A	hypothetical protein
TGME49_314500	1.31	#N/A	#N/A	subtilisin SUB2
TGME49_295430	1.31	#N/A	#N/A	hypothetical protein
TGME49_250870	1.08	#N/A	#N/A	DHHC zinc finger domain-containing protein
TGME49_287515	1.98	-7.54	#N/A	hypothetical protein
TGME49_260430	2.35	3.55	2.41	hypothetical protein
TGME49_279350	1.98	#N/A	#N/A	hypothetical protein
TGME49_248850	1.08	#N/A	#N/A	methionine aminopeptidase
TGME49_285700	1.98	#N/A	#N/A	ubiquitin fusion degradation protein UFD1AP
TGME49_253950	1.08	#N/A	#N/A	protein fam50a, putative
TGME49_318440	1.31	#N/A	#N/A	helicase associated domain (ha2) protein
TGME49_200430	11.50	#N/A	#N/A	cytidine and deoxycytidylate deaminase zinc-binding region domain-containing protein
TGME49_283702	1.98	#N/A	#N/A	FATC domain-containing protein
TGME49_262080	2.35	#N/A	#N/A	hypothetical protein
TGME49_293000	1.98	#N/A	#N/A	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_261480	2.35	#N/A	#N/A	phosphatidyl serine synthase
TGME49_204360	11.50	#N/A	#N/A	subtilisin SUB4
TGME49_318170	1.31	#N/A	#N/A	hypothetical protein
TGME49_224620	1.56	#N/A	#N/A	hypothetical protein
TGME49_301170	1.31	-7.88	#N/A	SAG-related sequence SRS19D
TGME49_225550	1.56	#N/A	#N/A	phosphatidylserine decarboxylase
TGME49_213460	2.42	1.08	1.36	hypothetical protein
TGME49_201710	11.50	#N/A	#N/A	WD domain, G-beta repeat-containing protein
TGME49_291890	1.98	#N/A	#N/A	microneme protein MIC1
TGME49_253700	1.08	#N/A	#N/A	transporter, major facilitator family protein
TGME49_252065	1.08	#N/A	1.68	KRUF family protein
TGME49_278940	1.98	#N/A	#N/A	HECT-domain (ubiquitin-transferase) domain-containing protein
TGME49_209770	4.76	#N/A	#N/A	helicase, putative
TGME49_285950	1.98	#N/A	#N/A	hypothetical protein
TGME49_217160	2.42	#N/A	2.35	Der1 family protein
TGME49_286010	1.98	#N/A	#N/A	hypothetical protein
TGME49_286050	1.98	#N/A	#N/A	hypothetical protein

TGME49_220150	2.42	-8.31	#N/A	50S ribosomal protein L16, putative
TGME49_236130	1.56	-8.58	#N/A	signal recognition particle (SRP9) domain-containing protein
TGME49_284170	1.98	-7.74	#N/A	DHHC zinc finger domain-containing protein
TGME49_321170	1.31	1.91	2.39	Toxoplasma gondii family C protein
TGME49_218790	2.42	-7.73	#N/A	elongation factor G C-terminus domain-containing protein
TGME49_310200	1.31	-8.08	#N/A	hypothetical protein
TGME49_290240	1.98	-8.41	#N/A	hypothetical protein
TGME49_288290	1.98	-8.19	#N/A	hypothetical protein
TGME49_244680	1.08	-7.56	#N/A	hypothetical protein
TGME49_242118	1.08	-8.30	-4.57	myosin-light-chain kinase
TGME49_224200	1.56	-7.93	#N/A	tRNA pseudouridine synthase
TGME49_220480	2.42	-7.77	#N/A	hypothetical protein
TGME49_229290	1.56	-7.60	#N/A	kelch repeat-containing protein
TGME49_295320	1.31	-8.26	#N/A	embryo sac development arrest EDA7, putative
TGME49_243265	1.08	-7.82	#N/A	protamine P1 protein
TGME49_229720	1.56	-8.10	#N/A	hypothetical protein
TGME49_220530	2.42	-8.48	#N/A	AP2 domain transcription factor AP2V-1
TGME49_226090	1.56	-7.82	#N/A	DEAD/DEAH box helicase domain-containing protein
TGME49_270050	1.98	1.95	#N/A	hypothetical protein
TGME49_270960	1.98	-8.11	#N/A	hypothetical protein
TGME49_269830	1.98	2.93	#N/A	RAP domain-containing protein
TGME49_288845	1.98	-8.19	#N/A	hypothetical protein
TGME49_257160	2.35	1.16	1.02	hypothetical protein
TGME49_243615	1.08	-7.78	#N/A	hypothetical protein
TGME49_297460	1.31	-8.44	#N/A	hypothetical protein
TGME49_254200	1.08	1.84	#N/A	anticodon binding domain-containing protein
TGME49_248800	1.08	-7.78	#N/A	hypothetical protein
TGME49_205050	11.50	-8.15	-5.06	hypothetical protein
TGME49_254135	1.08	-7.46	#N/A	hypothetical protein
TGME49_311790	1.31	1.99	#N/A	hypothetical protein
TGME49_233838	1.56	-7.66	#N/A	PET112 family, C terminal region domain-containing protein
TGME49_227270	1.56	-8.24	#N/A	hypothetical protein
TGME49_254840	1.08	-7.96	#N/A	tetratricopeptide repeat-containing protein
TGME49_288240	1.98	-7.71	#N/A	hypothetical protein
TGME49_242110	1.08	-7.95	#N/A	rhoGTPase family protein ROP38

FIGURE 5L

TGME49_269010	1.98	#N/A	#N/A	AP2 domain transcription factor AP2VIII-7
TGME49_248990	1.08	#N/A	#N/A	hypothetical protein
TGME49_217410	2.42	#N/A	#N/A	hypothetical protein
TGME49_253180	1.08	#N/A	1.08	hypothetical protein
TGME49_232360	1.56	#N/A	#N/A	exonuclease
TGME49_301400	1.31	#N/A	#N/A	hypothetical protein
TGME49_211330	4.76	#N/A	#N/A	methionine aminopeptidase
TGME49_205265	11.50	#N/A	#N/A	transporter, cation channel family protein
TGME49_277490	1.98	#N/A	#N/A	hypothetical protein
TGME49_279100	1.98	#N/A	#N/A	hypothetical protein
TGME49_216140	2.42	2.20	2.49	tetratricopeptide repeat-containing protein
TGME49_263190	2.35	#N/A	#N/A	adenylosuccinate lyase, putative
TGME49_230820	1.56	#N/A	#N/A	hypothetical protein
TGME49_239748	1.08	#N/A	#N/A	hypothetical protein
TGME49_293650	1.98	#N/A	#N/A	hypothetical protein
TGME49_256840	2.35	#N/A	#N/A	hypothetical protein
TGME49_305990	1.31	1.86	1.67	hypothetical protein
TGME49_251770	1.08	#N/A	1.01	hypothetical protein
TGME49_305930	1.31	#N/A	#N/A	hypothetical protein
TGME49_264220	2.35	#N/A	#N/A	hypothetical protein
TGME49_217790	2.42	#N/A	#N/A	S1 RNA binding domain-containing protein
TGME49_310410	1.31	-7.42	#N/A	WD domain, G-beta repeat-containing protein
TGME49_266480	2.35	#N/A	#N/A	hypothetical protein
TGME49_247030	1.08	#N/A	#N/A	hypothetical protein
TGME49_216810	2.42	#N/A	#N/A	5'-nucleotidase, C-terminal domain-containing protein
TGME49_312600	1.31	#N/A	1.07	heat shock protein HSP21
TGME49_254150	1.08	#N/A	#N/A	hypothetical protein
TGME49_202730	11.50	#N/A	#N/A	hypothetical protein
TGME49_319580	1.31	#N/A	#N/A	hypothetical protein
TGME49_255980	2.35	#N/A	#N/A	hypothetical protein
TGME49_213300	2.42	#N/A	#N/A	hypothetical protein
TGME49_242870	1.08	#N/A	#N/A	histone lysine methyltransferase, SET, putative
TGME49_270720	1.98	#N/A	#N/A	hypothetical protein
TGME49_274130	1.98	#N/A	#N/A	TBC domain-containing protein
TGME49_293900	1.98	#N/A	#N/A	sporozoite protein with an altered thrombospondin repeat SPATR

TGME49_285510	1.98	1.03	1.03	hypothetical protein
TGME49_204140	11.50	-7.83	#N/A	PHD-finger domain-containing protein
TGME49_269940	1.98	-7.77	#N/A	zinc finger motif, C2HC5-type protein
TGME49_300130	1.31	2.35	#N/A	apical membrane antigen 1 domain-containing protein
TGME49_201180	11.50	-8.19	#N/A	hypothetical protein
TGME49_226670	1.56	-7.51	#N/A	hypothetical protein
TGME49_316480	1.31	-7.54	#N/A	XRN 5'-3' exonuclease N-terminus protein
TGME49_314530	1.31	-7.84	#N/A	RPAP1 family, C-terminal protein
TGME49_300360	1.31	-8.03	#N/A	ADP/ATP translocase
TGME49_215400	2.42	-8.32	#N/A	RNA recognition motif-containing protein
TGME49_210310	4.76	-7.90	#N/A	hypothetical protein
TGME49_238070	1.08	-8.06	#N/A	glutaredoxin domain-containing protein
TGME49_209460	4.76	-7.93	#N/A	hypothetical protein
TGME49_202240	11.50	-7.95	#N/A	RAP domain-containing protein
TGME49_301280	1.31	-7.38	#N/A	hypothetical protein
TGME49_207180	4.76	-7.87	#N/A	indole-3-glycerol phosphate synthase domain-containing protein
TGME49_224150	1.56	-7.63	#N/A	hypothetical protein
TGME49_268740	1.98	-7.62	#N/A	hypothetical protein
TGME49_216370	2.42	-7.59	#N/A	hypothetical protein
TGME49_246930	1.08	1.17	1.29	calmodulin CAM1
TGME49_222210	1.56	-4.48	#N/A	SPFH domain / Band 7 family protein
TGME49_309610	1.31	-7.99	#N/A	hypothetical protein
TGME49_251590	1.08	-4.36	#N/A	hypothetical protein
TGME49_316490	1.31	-7.84	#N/A	hypothetical protein
TGME49_221980	1.56	-7.78	#N/A	U1 zinc finger protein
TGME49_223530	1.56	1.30	#N/A	hypothetical protein
TGME49_318380	1.31	-8.30	#N/A	hypothetical protein
TGME49_246690	1.08	-7.90	#N/A	alpha amylase, catalytic domain-containing protein
TGME49_247290	1.08	-8.11	#N/A	hypothetical protein
TGME49_262000	2.35	-7.73	#N/A	AP2 domain transcription factor AP2VIIb-2
TGME49_277770	1.98	-8.16	#N/A	hypothetical protein
TGME49_285540	1.98	-7.78	#N/A	DNA-directed DNA polymerase
TGME49_232220	1.56	-7.38	#N/A	SWIB/MDM2 domain-containing protein
TGME49_258826	2.35	-8.03	#N/A	hypothetical protein
TGME49_228040	1.56	-7.48	#N/A	PPIC-type PPIASE domain-containing protein

FIGURE 5M

TGME49_211470	4.76	#N/A	#N/A	Fcf2 pre-rRNA processing protein
TGME49_301300	1.31	-8.04	#N/A	hypothetical protein
TGME49_291600	1.98	#N/A	#N/A	gamma interferon inducible lysosomal thiol reductase (GILT) protein
TGME49_272380	1.98	#N/A	#N/A	hypothetical protein
TGME49_242670	1.08	-7.47	#N/A	hypothetical protein
TGME49_207040	4.76	#N/A	#N/A	hypothetical protein
TGME49_313340	1.31	#N/A	#N/A	hypothetical protein
TGME49_236620	2.44	#N/A	#N/A	protein kinase (incomplete catalytic triad)
TGME49_262590	2.35	-7.98	-5.38	hypothetical protein
TGME49_226060	1.56	#N/A	#N/A	transmembrane amino acid transporter protein
TGME49_273050	1.98	#N/A	#N/A	hypothetical protein
TGME49_308590	1.31	#N/A	#N/A	Mov34/MPN/PAD-1 family protein
TGME49_313418	1.31	#N/A	#N/A	hypothetical protein
TGME49_200590	11.50	#N/A	#N/A	Toxoplasma gondii family C protein
TGME49_237130	1.08	4.00	4.35	cytochrome b, putative
TGME49_273280	1.98	#N/A	#N/A	hypothetical protein
TGME49_269700	1.98	#N/A	#N/A	NLI interacting factor family phosphatase
TGME49_312380	1.31	-8.23	#N/A	tetratricopeptide repeat-containing protein
TGME49_297900	1.31	#N/A	#N/A	hypothetical protein
TGME49_213480	2.42	#N/A	#N/A	hypothetical protein
TGME49_237530	1.08	#N/A	#N/A	hypothetical protein
TGME49_200350	11.50	#N/A	#N/A	subtilisin SUB3
TGME49_254380	1.08	#N/A	1.62	ribosomal protein L11, putative
TGME49_202610	11.50	#N/A	#N/A	protein phosphatase 2C domain-containing protein
TGME49_240240	1.08	#N/A	#N/A	subtilisin SUB5
TGME49_255060	1.08	3.16	3.30	cytochrome b(N-terminal)/b6/petB subfamily protein
TGME49_309600	1.31	#N/A	#N/A	hypothetical protein
TGME49_271840	1.98	#N/A	#N/A	hypothetical protein
TGME49_320620	1.31	#N/A	#N/A	queuine tRNA ribosyl transferase
TGME49_289620	1.98	#N/A	#N/A	cathepsin CPC1
TGME49_226260	1.56	#N/A	#N/A	hypothetical protein
TGME49_255190	1.08	#N/A	#N/A	myosin C
TGME49_218850	2.42	-7.60	#N/A	ribosomal protein RPS9
TGME49_277560	1.98	-8.40	#N/A	hypothetical protein
TGME49_254555	1.08	#N/A	#N/A	histone lysine acetyltransferase GCN5-A
TGME49_225510	1.56	#N/A	#N/A	RAP domain-containing protein

TGME49_311060	1.31	-7.75	#N/A	metal-dependent phosphohydrolase HD domain-containing protein
TGME49_210478	4.76	2.80	#N/A	hypothetical protein
TGME49_309000	1.31	-7.64	#N/A	hypothetical protein
TGME49_305610	1.31	-7.34	#N/A	hypothetical protein
TGME49_273530	1.98	-7.78	#N/A	flagellar associated protein
TGME49_246560	1.08	1.01	#N/A	vacuolar ATP synthase subunit g, putative
TGME49_249450	1.08	-7.65	#N/A	hypothetical protein
TGME49_258820	2.35	1.08	1.48	hypothetical protein
TGME49_310910	1.31	1.39	#N/A	WD domain, G-beta repeat-containing protein
TGME49_264070	2.35	-7.41	#N/A	F5/8 type C domain-containing protein
TGME49_310250	1.31	-7.69	#N/A	hypothetical protein
TGME49_217470	2.42	-7.70	#N/A	hypothetical protein
TGME49_224170	1.56	2.43	2.22	SAG-related sequence SRS60A
TGME49_219640	2.42	-7.67	#N/A	hypothetical protein
TGME49_271280	1.98	-7.40	#N/A	60S ribosome subunit biogenesis protein NIP7, putative
TGME49_262810	2.35	-7.54	#N/A	iron donor protein CyaY protein
TGME49_305455	1.31	-7.11	#N/A	hypothetical protein
TGME49_241860	1.08	-7.70	#N/A	N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein Piga, family GT4 protein
TGME49_270940	1.98	-7.74	#N/A	hypothetical protein
TGME49_232240	1.56	-7.27	#N/A	hypothetical protein
TGME49_304640	1.31	-7.64	#N/A	hypothetical protein
TGME49_255160	1.08	-7.75	#N/A	hypothetical protein
TGME49_299270	1.31	1.55	#N/A	hypothetical protein
TGME49_273550	1.98	-8.07	#N/A	hypothetical protein
TGME49_251530	1.08	-7.49	#N/A	hypothetical protein
TGME49_299070	1.31	1.18	1.47	pyruvate kinase PyKII
TGME49_205625	11.50	-7.77	#N/A	hypothetical protein
TGME49_283740	1.98	-7.60	#N/A	RNA recognition motif-containing protein
TGME49_262630	2.35	-7.33	#N/A	hypothetical protein
TGME49_268350	1.98	-7.61	#N/A	hypothetical protein
TGME49_218192	2.42	-7.59	#N/A	hypothetical protein
TGME49_297925	1.31	-7.46	#N/A	HesB-like domain-containing protein
TGME49_221880	1.56	-8.02	#N/A	hypothetical protein
TGME49_215347	2.42	-7.36	#N/A	hypothetical protein
TGME49_246140	1.08	-8.20	#N/A	hypothetical protein
TGME49_318490	1.31	-7.78	#N/A	hypothetical protein

FIGURE 5N

TGME49_229020	1.56	#N/A	#N/A	cell-cycle-associated protein kinase CDK, putative
TGME49_221490	2.42	#N/A	#N/A	cell cycle regulator protein
TGME49_253960	1.08	#N/A	1.29	oxidoreductase, short chain dehydrogenase/reductase family protein
TGME49_260520	2.35	#N/A	1.01	hypothetical protein
TGME49_288800	1.98	#N/A	#N/A	endonuclease/exonuclease/phosphatase family protein
TGME49_222370	1.56	1.35	1.97	SAG-related sequence SRS13
TGME49_313160	1.31	#N/A	#N/A	hypothetical protein
TGME49_299980	1.31	#N/A	1.08	hypothetical protein
TGME49_216335	2.42	2.91	1.84	hypothetical protein
TGME49_288820	1.98	#N/A	1.04	hypothetical protein
TGME49_244540	1.08	#N/A	#N/A	mitochondrial carrier superfamily protein
TGME49_310310	1.31	#N/A	#N/A	WD domain, G-beta repeat-containing protein
TGME49_227780	1.56	#N/A	#N/A	hypothetical protein
TGME49_234670	1.56	#N/A	#N/A	actin-like family protein
TGME49_299240	1.31	#N/A	#N/A	hypothetical protein
TGME49_244510	1.08	-7.66	#N/A	AP2 domain transcription factor AP2V1-3
TGME49_253570	1.08	#N/A	#N/A	hypothetical protein
TGME49_225500	1.56	#N/A	#N/A	hypothetical protein
TGME49_249698	1.08	#N/A	#N/A	hypothetical protein
TGME49_239290	1.08	#N/A	#N/A	hypothetical protein
TGME49_240960	1.08	#N/A	#N/A	AIG2 family protein
TGME49_275980	1.98	#N/A	#N/A	coenzyme q (ubiquinone) biosynthesis protein coq4 protein
TGME49_233220	1.56	#N/A	#N/A	hypothetical protein
TGME49_259650	2.35	#N/A	#N/A	hypothetical protein
TGME49_209820	4.76	#N/A	#N/A	syntaxin protein
TGME49_206700	4.76	#N/A	#N/A	hypothetical protein
TGME49_286740	1.98	#N/A	#N/A	microneme-like protein
TGME49_263580	2.35	#N/A	#N/A	bromodomain-containing protein
TGME49_273310	1.98	#N/A	#N/A	hypothetical protein
TGME49_205190	11.50	#N/A	#N/A	hypothetical protein
TGME49_204130	11.50	#N/A	#N/A	perforin-like protein PLP1
TGME49_203050	11.50	#N/A	#N/A	AP2 domain transcription factor AP2V1a-6
TGME49_313680	1.31	#N/A	#N/A	hypothetical protein
TGME49_201390	11.50	#N/A	#N/A	hypothetical protein
TGME49_223480	1.56	#N/A	#N/A	sushi domain (scr repeat) domain-containing protein

TGME49_241310	1.08	-7.57	#N/A	hypothetical protein
TGME49_230920	1.56	-7.70	#N/A	adaptor complexes medium subunit family protein
TGME49_242580	1.08	-7.80	#N/A	iron only hydrogenase large subunit, C-terminal domain-containing protein
TGME49_253530	1.08	-7.47	#N/A	hypothetical protein
TGME49_314680	1.31	-7.00	#N/A	hypothetical protein
TGME49_235640	1.56	-7.65	#N/A	formyl transferase domain-containing protein
TGME49_244140	1.08	-7.17	#N/A	hypothetical protein
TGME49_243610	1.08	-7.67	#N/A	C-5 cytosine-specific DNA methylase superfamily protein
TGME49_209530	4.76	-7.62	#N/A	hypothetical protein
TGME49_269750	1.98	-7.63	#N/A	CrcB family protein
TGME49_211400	4.76	-7.61	#N/A	DEAD/DEAH box helicase domain-containing protein
TGME49_222160	1.56	1.75	#N/A	aldehyde dehydrogenase
TGME49_314295	1.31	2.11	#N/A	ribosomal l25 family protein
TGME49_268340	1.98	2.13	#N/A	glycosyltransferase family 28 C-terminal domain-containing protein
TGME49_314920	1.31	-7.87	#N/A	hypothetical protein
TGME49_266870	2.35	-7.38	#N/A	transporter, major facilitator family protein
TGME49_313273	1.31	-7.84	#N/A	hypothetical protein
TGME49_277050	1.98	-7.26	#N/A	hypothetical protein
TGME49_291010	1.98	-7.55	#N/A	hypothetical protein
TGME49_204055	11.50	-7.60	#N/A	hypothetical protein
TGME49_297495	1.31	-6.99	#N/A	hypothetical protein
TGME49_262510	2.35	-7.33	#N/A	GTP-binding protein engB, putative
TGME49_223580	1.56	-7.81	#N/A	mediator complex subunit MED4
TGME49_249930	1.08	-7.03	#N/A	hypothetical protein
TGME49_286550	1.98	1.37	#N/A	hypothetical protein
TGME49_261410	2.35	-7.58	#N/A	protein-tyrosine-phosphatase
TGME49_301160	1.31	-7.44	#N/A	SAG-related sequence SRS19C
TGME49_261030	2.35	-7.65	#N/A	pyridine nucleotide-disulfide oxidoreductase domain-containing protein
TGME49_274120	1.98	1.07	#N/A	hypothetical protein
TGME49_323320	1.31	-7.24	#N/A	hypothetical protein
TGME49_216840	2.42	-7.25	#N/A	hypothetical protein
TGME49_257980	2.35	-7.57	#N/A	ribosome recycling factor protein
TGME49_271190	1.98	-7.37	#N/A	bicoid-interacting protein BIN3
TGME49_291330	1.98	1.08	#N/A	RNA recognition motif-containing protein
TGME49_258420	2.35	-4.66	#N/A	hypothetical protein

FIGURE 5o

TGME49_245428	1.08	#N/A	#N/A	hypothetical protein
TGME49_265260	2.35	#N/A	#N/A	hypothetical protein
TGME49_316220	1.31	#N/A	#N/A	mediator complex subunit MED6
TGME49_263390	2.35	#N/A	1.37	hypothetical protein
TGME49_313710	1.31	#N/A	#N/A	hypothetical protein
TGME49_237650	1.08	#N/A	#N/A	hypothetical protein
TGME49_285710	1.98	1.37	1.72	hypothetical protein
TGME49_208550	4.76	#N/A	#N/A	hypothetical protein
TGME49_233830	1.56	-7.61	#N/A	hypothetical protein
TGME49_260150	2.35	-7.18	1.72	tetratricopeptide repeat-containing protein
TGME49_231800	1.56	#N/A	#N/A	helicase, putative
TGME49_269420	1.98	#N/A	1.15	hypothetical protein
TGME49_262900	2.35	#N/A	#N/A	hypothetical protein
TGME49_207980	4.76	#N/A	#N/A	PIG-P protein
TGME49_253600	1.08	#N/A	#N/A	hypothetical protein
TGME49_249680	1.08	#N/A	#N/A	RNA polymerase II associated Paf1 complex component PAF1
TGME49_212735	2.42	#N/A	#N/A	hypothetical protein
TGME49_217692	2.42	-7.66	#N/A	hypothetical protein
TGME49_253940	1.08	#N/A	1.02	CAM Kinase family, incomplete catalytic triad
TGME49_221190	2.42	#N/A	#N/A	mma cleavage factor family protein, putative
TGME49_257700	2.35	#N/A	#N/A	hypothetical protein
TGME49_218720	2.42	#N/A	#N/A	calcium-dependent protein kinase CDPK6
TGME49_249840	1.08	#N/A	#N/A	dynein heavy chain 2, putative
TGME49_318610	1.31	#N/A	#N/A	AP2 domain transcription factor AP2IV-3
TGME49_235360	1.56	#N/A	#N/A	hypothetical protein
TGME49_267775	2.35	-7.80	#N/A	hypothetical protein
TGME49_233540	1.56	#N/A	#N/A	transporter, major facilitator family protein
TGME49_291590	1.98	-7.62	#N/A	hypothetical protein
TGME49_286240	1.98	#N/A	#N/A	kelch repeat protein, putative
TGME49_266930	2.35	#N/A	#N/A	general transcription factor IIH polypeptide 3 GTF2H3
TGME49_236870	1.08	#N/A	#N/A	hypothetical protein
TGME49_234230	1.56	#N/A	#N/A	hypothetical protein
TGME49_225490	1.56	#N/A	#N/A	calcium-dependent protein kinase CDPK2
TGME49_280410	1.98	#N/A	#N/A	3'5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_258100	2.35	-7.80	#N/A	TPR repeat region protein
TGME49_276210	1.98	#N/A	1.17	phosphoglycerate mutase family protein

TGME49_270630	1.98	-7.29	#N/A	hypothetical protein
TGME49_219720	2.42	1.15	#N/A	Ras-related protein Rab-5C, putative
TGME49_308930	1.31	1.34	1.46	50S ribosomal protein L33, putative
TGME49_329100	1.31	-7.28	#N/A	Toxoplasma gondii family C protein
TGME49_244580	1.08	-7.43	#N/A	L1P family of ribosomal protein
TGME49_255870	2.35	-7.37	#N/A	WD domain, G-beta repeat-containing protein
TGME49_216190	2.42	-7.43	#N/A	hypothetical protein
TGME49_254140	1.08	-6.57	#N/A	DNA-directed RNA polymerase II RPABC4
TGME49_313090	1.31	-7.45	#N/A	hypothetical protein
TGME49_210770	4.76	-7.39	#N/A	hypothetical protein
TGME49_271290	1.98	-7.33	#N/A	hypothetical protein
TGME49_273540	1.98	-7.60	#N/A	phosphatidylserine synthase, putative
TGME49_320580	1.31	-7.38	#N/A	hypothetical protein
TGME49_268985	1.98	-7.07	#N/A	hypothetical protein
TGME49_262430	2.35	1.19	1.17	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
TGME49_239310	1.08	1.33	#N/A	ribulose 5-phosphate isomerase
TGME49_253680	1.08	-7.15	#N/A	hypothetical protein
TGME49_225360	1.56	-7.78	#N/A	hypothetical protein
TGME49_244430	1.08	-7.77	#N/A	pseudouridylate synthase, putative
TGME49_263323	2.35	-7.32	#N/A	tetratricopeptide repeat protein 11, putative
TGME49_264420	2.35	-7.53	#N/A	lipoprotein, putative
TGME49_275470	1.98	-7.33	#N/A	dense granule protein GRA15
TGME49_220212	2.42	-7.25	#N/A	pseudouridine synthase
TGME49_263430	2.35	-7.50	#N/A	3-hydroxyisobutyrate dehydrogenase
TGME49_207970	4.76	-7.09	-5.26	HEAT repeat-containing protein
TGME49_254260	1.08	1.66	#N/A	COX19 cytochrome c oxidase assembly family protein
TGME49_289900	1.98	-7.04	#N/A	n-acetyltransferase family protein
TGME49_316610	1.31	-7.62	#N/A	hypothetical protein
TGME49_271250	1.98	-7.50	#N/A	hypothetical protein
TGME49_201840	11.50	1.04	#N/A	aspartyl protease ASP1
TGME49_312680	1.31	1.54	#N/A	60S ribosomal protein L27, putative
TGME49_233930	1.56	-7.30	#N/A	CAF1 family ribonuclease
TGME49_306455	1.31	2.46	#N/A	hypothetical protein
TGME49_223725	1.56	-7.40	#N/A	hypothetical protein
TGME49_258900	2.35	1.36	#N/A	hypothetical protein
TGME49_222155	1.56	-6.92	#N/A	hypothetical protein

FIGURE 5P

TGME49_253100	1.08	1.49	1.81	hypothetical protein
TGME49_234510	1.56	1.01	#N/A	ankyrin repeat-containing protein
TGME49_294690	1.98	#N/A	#N/A	rhomboid protease ROM5
TGME49_285480	1.98	#N/A	#N/A	hypothetical protein
TGME49_227560	1.56	#N/A	#N/A	IWS1 transcription factor, putative
TGME49_234980	1.56	-4.80	#N/A	hypothetical protein
TGME49_255330	2.35	#N/A	#N/A	hypothetical protein
TGME49_285170	1.98	-7.62	#N/A	methyltransferase small, putative
TGME49_232760	1.56	#N/A	#N/A	protein phosphatase inhibitor IPP2
TGME49_232630	1.56	#N/A	#N/A	hypothetical protein
TGME49_216700	2.42	#N/A	#N/A	hypothetical protein
TGME49_314250	1.31	3.09	2.65	bradyzoite rhoptry protein BRP1
TGME49_283550	1.98	#N/A	#N/A	hypothetical protein
TGME49_267580	2.35	1.04	#N/A	cyclin2 related protein
TGME49_203160	11.50	#N/A	#N/A	hypothetical protein
TGME49_263490	2.35	#N/A	#N/A	ubiquitin conjugating enzyme E2, putative
TGME49_293780	1.98	1.77	1.90	hypothetical protein
TGME49_299250	1.31	#N/A	#N/A	hypothetical protein
TGME49_261075	2.35	#N/A	1.60	hypothetical protein
TGME49_306510	1.31	#N/A	#N/A	hypothetical protein
TGME49_234460	1.56	1.01	#N/A	hypothetical protein
TGME49_254770	1.08	1.21	#N/A	Ser/Thr phosphatase family protein
TGME49_297647	1.31	#N/A	#N/A	hypothetical protein
TGME49_237425	1.08	#N/A	#N/A	AP2 domain transcription factor AP2X-6
TGME49_207665	4.76	#N/A	#N/A	kinesin motor domain-containing protein
TGME49_205110	11.50	-7.19	#N/A	hypothetical protein
TGME49_246120	1.08	#N/A	#N/A	tetratricopeptide repeat-containing protein
TGME49_245432	1.08	#N/A	#N/A	hypothetical protein
TGME49_268560	1.98	#N/A	#N/A	XPG N-terminal domain-containing protein
TGME49_311450	1.31	#N/A	#N/A	zinc finger, c2h2 type domain-containing protein
TGME49_268000	2.35	#N/A	#N/A	hypothetical protein
TGME49_305950	1.31	#N/A	#N/A	tetratricopeptide repeat-containing protein
TGME49_265170	2.35	#N/A	#N/A	hypothetical protein
TGME49_220510	2.42	#N/A	#N/A	hypothetical protein
TGME49_246990	1.08	#N/A	#N/A	hypothetical protein
TGME49_310560	1.31	#N/A	#N/A	hypothetical protein

TGME49_290630	1.98	1.29	#N/A	AP2 domain transcription factor AP2IX-7
TGME49_269417	1.98	-7.03	#N/A	hypothetical protein
TGME49_207470	4.76	-7.26	#N/A	hypothetical protein
TGME49_210800	4.76	1.23	#N/A	activator of hsp90 ATPase, putative
TGME49_233130	1.56	1.30	1.18	nucleoside transporter protein
TGME49_207070	4.76	2.47	#N/A	glycosyl transferase, putative
TGME49_257740	2.35	1.11	#N/A	UMP-CMP kinase
TGME49_263410	2.35	2.78	#N/A	scavenger receptor cysteine-rich domain-containing protein
TGME49_244260	1.08	-7.47	#N/A	hypothetical protein
TGME49_254520	1.08	#N/A	1.88	mediator complex subunit MED11
TGME49_253880	1.08	#N/A	1.45	GNS1/SUR4 family protein
TGME49_276940	1.98	#N/A	1.41	ribosome associated membrane protein RAMP4, putative
TGME49_293840	1.98	#N/A	2.10	hypothetical protein
TGME49_248740	1.08	#N/A	1.82	hypothetical protein
TGME49_313900	1.31	#N/A	2.08	non-specific serine/threonine protein kinase
TGME49_229990	1.56	#N/A	1.15	T-complex protein 1 subunit alpha, putative
TGME49_315220	1.31	#N/A	1.15	rhoptry protein ROP14
TGME49_310060	1.31	#N/A	1.98	small nuclease
TGME49_264240	2.35	#N/A	-4.81	hypothetical protein
TGME49_299200	1.31	#N/A	1.55	Bet3 transport protein, putative
TGME49_247770	1.08	#N/A	1.08	hypothetical protein
TGME49_223900	1.56	#N/A	2.97	hypothetical protein
TGME49_276140	1.98	#N/A	1.13	ADP ribosylation factor ARF1
TGME49_207830	4.76	#N/A	1.54	MORN repeat-containing protein
TGME49_315250	1.31	#N/A	1.54	GAMM1 protein, putative
TGME49_254400	1.08	#N/A	2.00	LSU ribosomal protein L2P, putative
TGME49_239500	1.08	#N/A	1.30	proteasome subunit alpha type, putative
TGME49_319550	1.31	#N/A	1.10	membrane protein C17G8.08c, putative
TGME49_253000	1.08	#N/A	1.20	ELMO/CED-12 family protein
TGME49_260870	2.35	#N/A	2.09	zinc finger cdgsh type protein
TGME49_226755	1.56	#N/A	1.30	3'/5'-cyclic nucleotide phosphodiesterase domain-containing protein
TGME49_218270	2.42	#N/A	1.22	hypothetical protein
TGME49_239490	1.08	#N/A	1.14	dehydrogenase E1 component family protein
TGME49_209850	4.76	#N/A	1.51	RNA recognition motif-containing protein
TGME49_249780	1.08	#N/A	1.09	hypothetical protein
TGME49_254570	1.08	#N/A	1.21	hypothetical protein

FIGURE 5Q

TGME49_297770	1.31	#N/A	#N/A	hypothetical protein
TGME49_206540	11.50	#N/A	#N/A	hypothetical protein
TGME49_236140	1.56	-7.22	#N/A	hypothetical protein
TGME49_279330	1.98	#N/A	1.31	DEAD/DEAH box helicase family protein
TGME49_254730	1.08	#N/A	#N/A	POPLD (NUC188) domain-containing protein
TGME49_319360	1.31	#N/A	#N/A	SAG-related sequence SRS17A
TGME49_319720	1.31	#N/A	#N/A	hypothetical protein
TGME49_243510	1.08	#N/A	#N/A	OTU family cysteine protease
TGME49_226850	1.56	#N/A	#N/A	TBC domain-containing protein
TGME49_298830	1.31	#N/A	#N/A	hypothetical protein
TGME49_271800	1.98	#N/A	#N/A	serine esterase (DUF676) protein
TGME49_264120	2.35	-7.79	#N/A	Myb family DNA-binding domain-containing protein
TGME49_320680	1.31	-7.24	#N/A	AP2 domain transcription factor AP2IV-2
TGME49_207900	4.76	#N/A	#N/A	transcription initiation factor TFIIB
TGME49_270580	1.98	-7.35	#N/A	HECT-domain (ubiquitin-transferase) domain-containing protein
TGME49_266740	2.35	2.00	1.93	RNA recognition motif-containing protein
TGME49_239810	1.08	#N/A	#N/A	hypothetical protein
TGME49_253490	1.08	#N/A	#N/A	hypothetical protein
TGME49_255245	1.08	#N/A	#N/A	hypothetical protein
TGME49_230170	1.56	#N/A	#N/A	hypothetical protein
TGME49_311280	1.31	#N/A	#N/A	hypothetical protein
TGME49_288860	1.98	#N/A	#N/A	RuvB family 2 protein
TGME49_239910	1.08	#N/A	#N/A	cyclin-dependent kinase
TGME49_231215	1.56	#N/A	#N/A	hypothetical protein
TGME49_292055	1.98	#N/A	#N/A	calcium dependent protein kinase CDPK8
TGME49_226100	1.56	-7.32	-7.32	haloacid dehalogenase family hydrolase domain-containing protein
TGME49_310500	1.31	#N/A	#N/A	hypothetical protein
TGME49_237020	1.08	#N/A	#N/A	exonuclease
TGME49_205540	11.50	#N/A	#N/A	DEAD/DEAH box helicase domain-containing protein
TGME49_296121	1.31	#N/A	#N/A	hypothetical protein
TGME49_293480	1.98	#N/A	#N/A	MoeA N-terminal region (domain I and II) domain-containing protein
TGME49_213060	2.42	-4.64	#N/A	WD domain, G-beta repeat-containing protein
TGME49_254720	1.08	#N/A	#N/A	dense granule protein GRA8
TGME49_219230	2.42	#N/A	#N/A	AMP-binding enzyme domain-containing protein
TGME49_280700	1.98	#N/A	#N/A	arginine decarboxylase
TGME49_214580	2.42	#N/A	#N/A	tetratricopeptide repeat-containing protein
TGME49_289140	1.98	#N/A	#N/A	ribosomal protein L22/43, putative

TGME49_208850	4.76	#N/A	2.67	SAG-related sequence SRS11
TGME49_211010	4.76	#N/A	1.79	hypothetical protein
TGME49_278020	1.98	#N/A	1.86	hypothetical protein
TGME49_225050	1.56	#N/A	1.06	adenosylhomocysteinase, putative
TGME49_283790	1.98	#N/A	1.50	protein kinase, putative
TGME49_292260	1.98	#N/A	3.28	SAG-related sequence SRS36B
TGME49_254410	1.08	#N/A	1.30	protein phosphatase 2C, putative
TGME49_276220	1.98	#N/A	1.53	hypothetical protein
TGME49_320515	1.31	#N/A	1.15	hypothetical protein
TGME49_290678	1.98	#N/A	1.70	hypothetical protein
TGME49_213820	2.42	#N/A	1.16	hypothetical protein
TGME49_258550	2.35	#N/A	1.79	SAG-related sequence SRS28
TGME49_259700	2.35	#N/A	1.14	hypothetical protein
TGME49_288880	1.98	#N/A	2.14	hypothetical protein
TGME49_260480	2.35	#N/A	1.80	leucine rich repeat-containing protein
TGME49_311490	1.31	#N/A	2.49	hypothetical protein
TGME49_285720	1.98	#N/A	1.70	ATP binding protein, putative
TGME49_288870	1.98	#N/A	1.95	hypothetical protein
TGME49_289090	1.98	#N/A	2.52	hypothetical protein
TGME49_253970	1.08	#N/A	1.91	hypothetical protein
TGME49_223095	1.56	#N/A	2.42	hypothetical protein
TGME49_245475	1.08	#N/A	1.73	hypothetical protein
TGME49_270560	1.98	#N/A	1.90	peptidyl-prolyl cis-trans isomerase family 1
TGME49_257685	2.35	#N/A	1.16	hypothetical protein
TGME49_275770	1.98	#N/A	1.18	hypothetical protein
TGME49_315260	1.31	#N/A	-4.45	alanine dehydrogenase
TGME49_298970	1.31	#N/A	1.05	LSM3, U6 small nuclear RNA associated isoform 2 family protein
TGME49_309130	1.31	#N/A	2.10	hypothetical protein
TGME49_306640	1.31	#N/A	1.55	hypothetical protein
TGME49_252290	1.08	#N/A	1.33	importin alpha, putative
TGME49_286560	1.98	#N/A	1.58	U6 snRNA-associated Sm family protein
TGME49_226068	1.56	#N/A	1.08	DnaJ domain-containing protein
TGME49_233695	1.56	#N/A	1.09	hypothetical protein
TGME49_230100	1.56	#N/A	1.63	membrane protein, putative
TGME49_231000	1.56	#N/A	1.28	START domain-containing protein
TGME49_223610	1.56	#N/A	1.63	hypothetical protein
TGME49_218810	2.42	#N/A	1.22	histidyl-tRNA synthetase

FIGURE 5R

TGME49_219630	2.42	#N/A	#N/A	flavodoxin domain-containing protein
TGME49_278250	1.98	#N/A	#N/A	hypothetical protein
TGME49_257370	2.35	#N/A	#N/A	hypothetical protein
TGME49_295960	1.31	#N/A	#N/A	hypothetical protein
TGME49_278720	1.98	#N/A	#N/A	hypothetical protein
TGME49_224270	1.56	#N/A	#N/A	hypothetical protein
TGME49_284590	1.98	#N/A	#N/A	hypothetical protein
TGME49_267670	2.35	-7.58	#N/A	hypothetical protein
TGME49_245980	1.08	-8.63	#N/A	hypothetical protein
TGME49_275310	1.98	#N/A	#N/A	hypothetical protein
TGME49_250090	1.08	#N/A	#N/A	hypothetical protein
TGME49_210360	4.76	#N/A	#N/A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41 family protein
TGME49_226560	1.56	#N/A	#N/A	zinc finger (CCCH type) motif-containing protein
TGME49_262480	2.35	#N/A	1.16	dynein light chain roadblock-type 2, putative
TGME49_229390	1.56	#N/A	#N/A	hypothetical protein
TGME49_268650	1.98	#N/A	#N/A	chaperone clpB protein, putative
TGME49_287430	1.98	#N/A	#N/A	hypothetical protein
TGME49_242270	1.08	#N/A	#N/A	hypothetical protein
TGME49_284598	1.98	#N/A	#N/A	haloacid dehalogenase family hydrolase domain-containing protein
TGME49_312210	1.31	1.63	1.28	hypothetical protein
TGME49_268730	1.98	#N/A	1.94	glutaredoxin-related protein
TGME49_224470	1.56	#N/A	#N/A	hypothetical protein
TGME49_225290	1.56	2.64	3.06	GDA1/CD39 (nucleoside phosphatase) family protein
TGME49_273660	1.98	#N/A	#N/A	AP2 domain transcription factor AP2VIII-3
TGME49_305120	1.31	1.15	#N/A	transporter, solute:sodium symporter (SSS) family protein
TGME49_266890	2.35	#N/A	#N/A	hypothetical protein
TGME49_269200	1.98	#N/A	#N/A	crooked neck family 1 protein isoform 2, putative
TGME49_309990	1.31	#N/A	#N/A	hypothetical protein
TGME49_220880	2.42	#N/A	#N/A	hypothetical protein
TGME49_271600	1.98	#N/A	#N/A	hypothetical protein
TGME49_248450	1.08	#N/A	1.22	zinc finger, C3HC4 type (RING finger) domain-containing protein
TGME49_267370	2.35	#N/A	#N/A	kinesin motor domain-containing protein
TGME49_220870	2.42	#N/A	#N/A	hypothetical protein
TGME49_216800	2.42	#N/A	#N/A	flagellar/basal body protein

TGME49_276130	1.98	#N/A	1.13	cathepsin CPC2
TGME49_271090	1.98	#N/A	1.87	hypothetical protein
TGME49_249890	1.08	#N/A	1.73	hypothetical protein
TGME49_243980	1.08	#N/A	1.48	hypothetical protein
TGME49_238420	1.08	#N/A	1.45	hypothetical protein
TGME49_313040	1.31	#N/A	1.23	hypothetical protein
TGME49_294040	1.98	#N/A	1.03	KDEL endoplasmic reticulum protein retention receptor 2 (KDEL2), putative
TGME49_212960	2.42	#N/A	1.39	hypothetical protein
TGME49_233100	1.56	#N/A	1.21	SPFH domain / Band 7 family protein
TGME49_310070	1.31	#N/A	1.00	methyltransferase, putative
TGME49_238880	1.08	#N/A	1.82	hypothetical protein
TGME49_309380	1.31	#N/A	1.09	Nuf2
TGME49_213746	2.42	#N/A	1.98	hypothetical protein
TGME49_308090	1.31	#N/A	1.04	rhoGTP protein ROP5
TGME49_258490	2.35	#N/A	1.73	hypothetical protein
TGME49_299080	1.31	#N/A	1.04	VTC domain-containing protein
TGME49_239610	1.08	#N/A	1.28	hypothetical protein
TGME49_253730	1.08	#N/A	1.12	importin-beta N-terminal domain-containing protein
TGME49_310220	1.31	#N/A	1.17	hypothetical protein
TGME49_243480	1.08	#N/A	1.88	50S ribosomal protein L3, putative
TGME49_253900	1.08	#N/A	1.26	parasite porphobilinogen synthase PBGS
TGME49_204060	11.50	#N/A	1.41	SNARE domain-containing protein
TGME49_217400	2.42	#N/A	1.19	hypothetical protein
TGME49_260660	2.35	#N/A	1.25	50S ribosomal protein L23, putative
TGME49_252630	1.08	#N/A	1.05	hypothetical protein
TGME49_211860	4.76	#N/A	1.05	hypothetical protein
TGME49_301222	1.31	#N/A	1.27	DNA repair protein Rad4 domain-containing protein
TGME49_228710	1.56	#N/A	1.91	hypothetical protein
TGME49_271240	1.98	#N/A	1.25	hypothetical protein
TGME49_218530	2.42	#N/A	1.09	proteasome-interacting thioredoxin domain-containing protein
TGME49_256100	2.35	#N/A	1.60	tetratricopeptide repeat-containing protein
TGME49_262910	2.35	#N/A	1.72	NADH-cytochrome b5 reductase 1, putative
TGME49_255890	2.35	#N/A	1.19	pyridine nucleotide-disulfide oxidoreductase domain-containing protein
TGME49_231940	1.56	#N/A	1.10	ThiF family protein

FIGURE 5S

TGME49_258010	2.35	#N/A	#N/A	calcium signaling protein kinase RAD53, putative
TGME49_202568	11.50	#N/A	#N/A	hypothetical protein
TGME49_257560	2.35	-7.70	#N/A	WD domain, G-beta repeat-containing protein
TGME49_247340	1.08	2.56	#N/A	hypothetical protein
TGME49_258458	2.35	#N/A	#N/A	hypothetical protein
TGME49_236790	-4.71	#N/A	#N/A	hypothetical protein

TGME49_251570	1.08	#N/A	2.16	CAAX amino terminal protease family protein
TGME49_310840	1.31	#N/A	1.42	hypothetical protein
TGME49_313700	1.31	#N/A	1.58	hypothetical protein
TGME49_262040	2.35	#N/A	1.01	SAC3/GANP family protein
TGME49_234300	1.56	#N/A	1.29	hypothetical protein
TGME49_285810	1.98	#N/A	1.46	MYND finger domain-containing protein

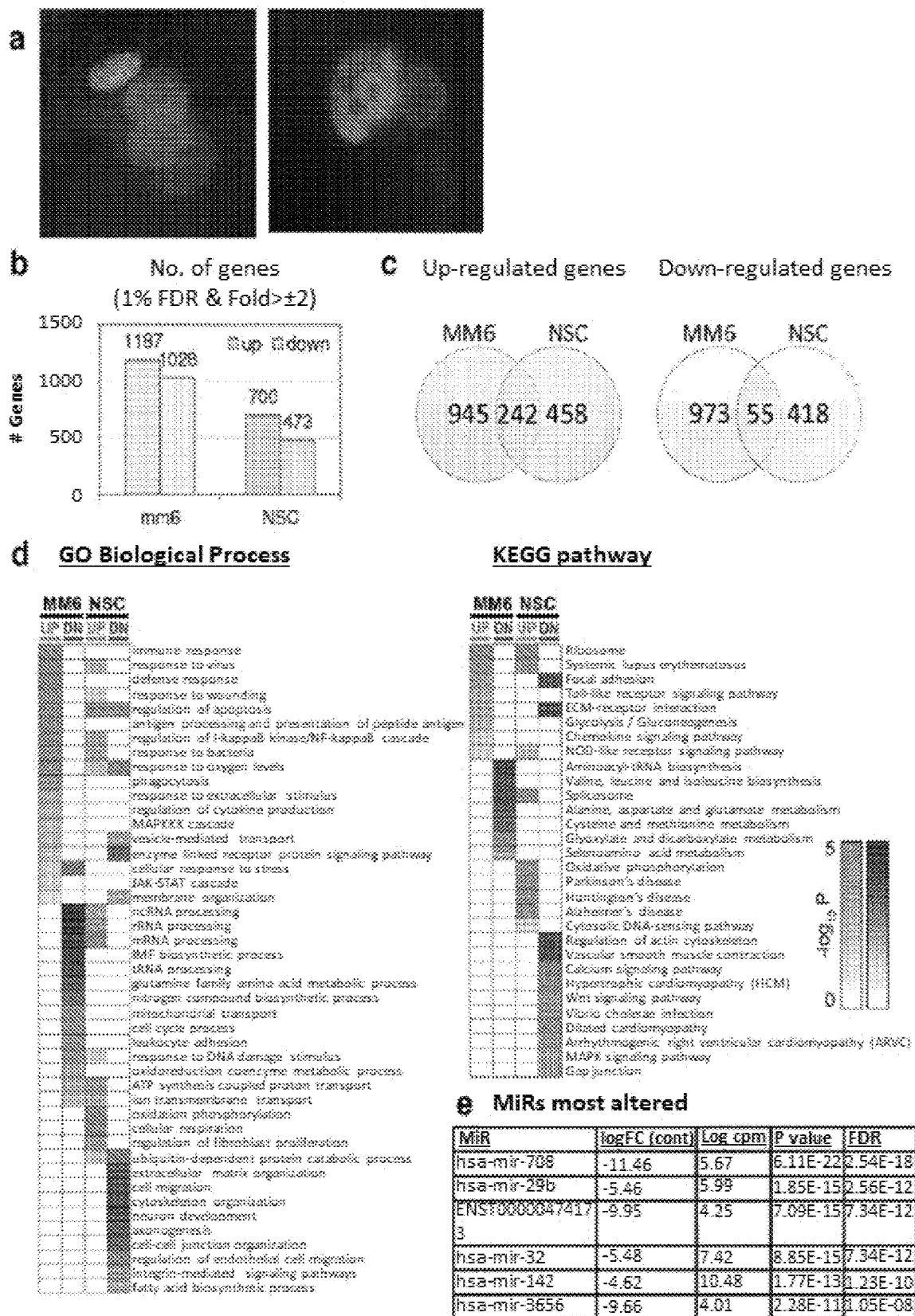


Figure 6

FIGURE 7

a

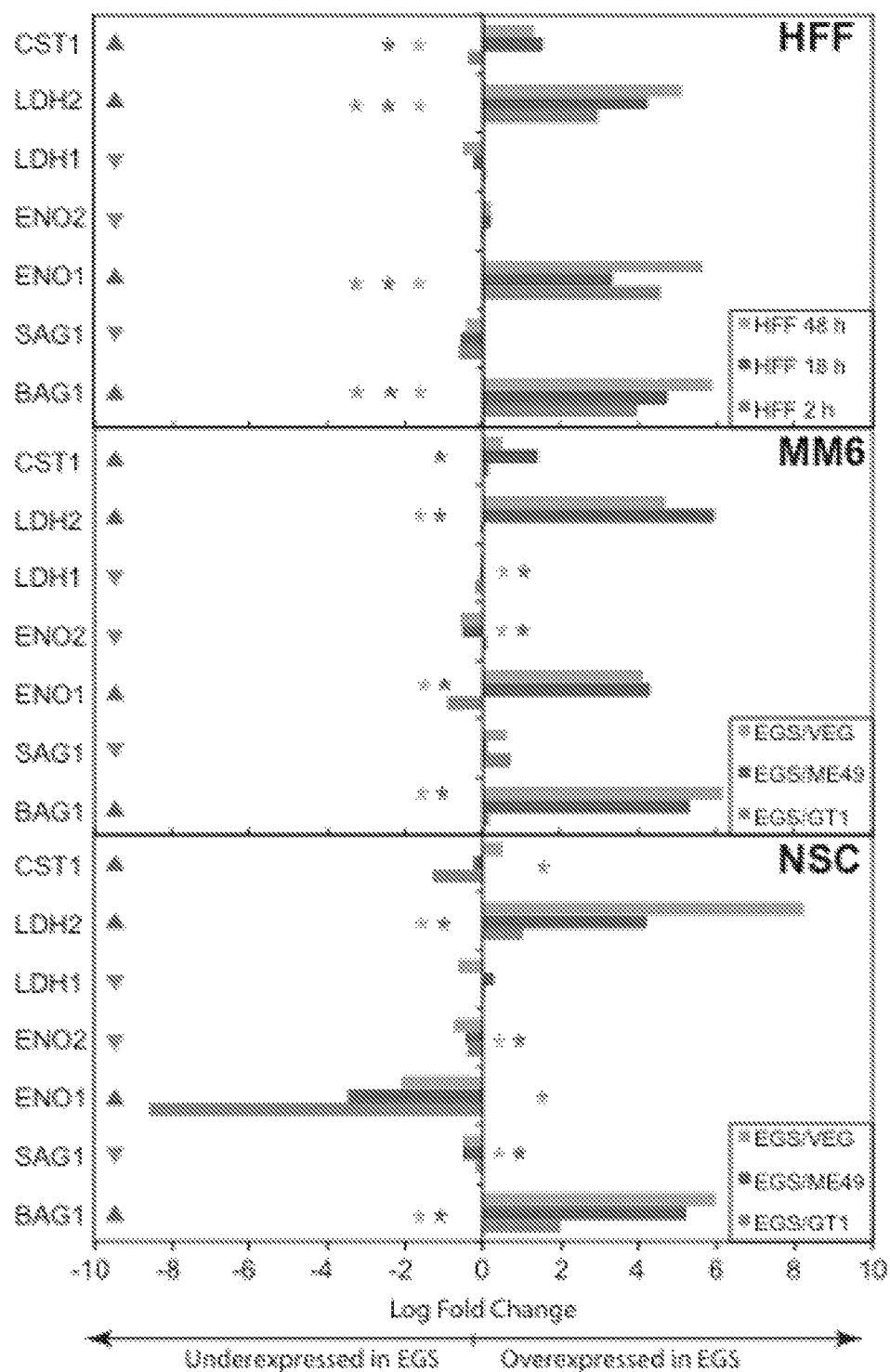


FIGURE 7

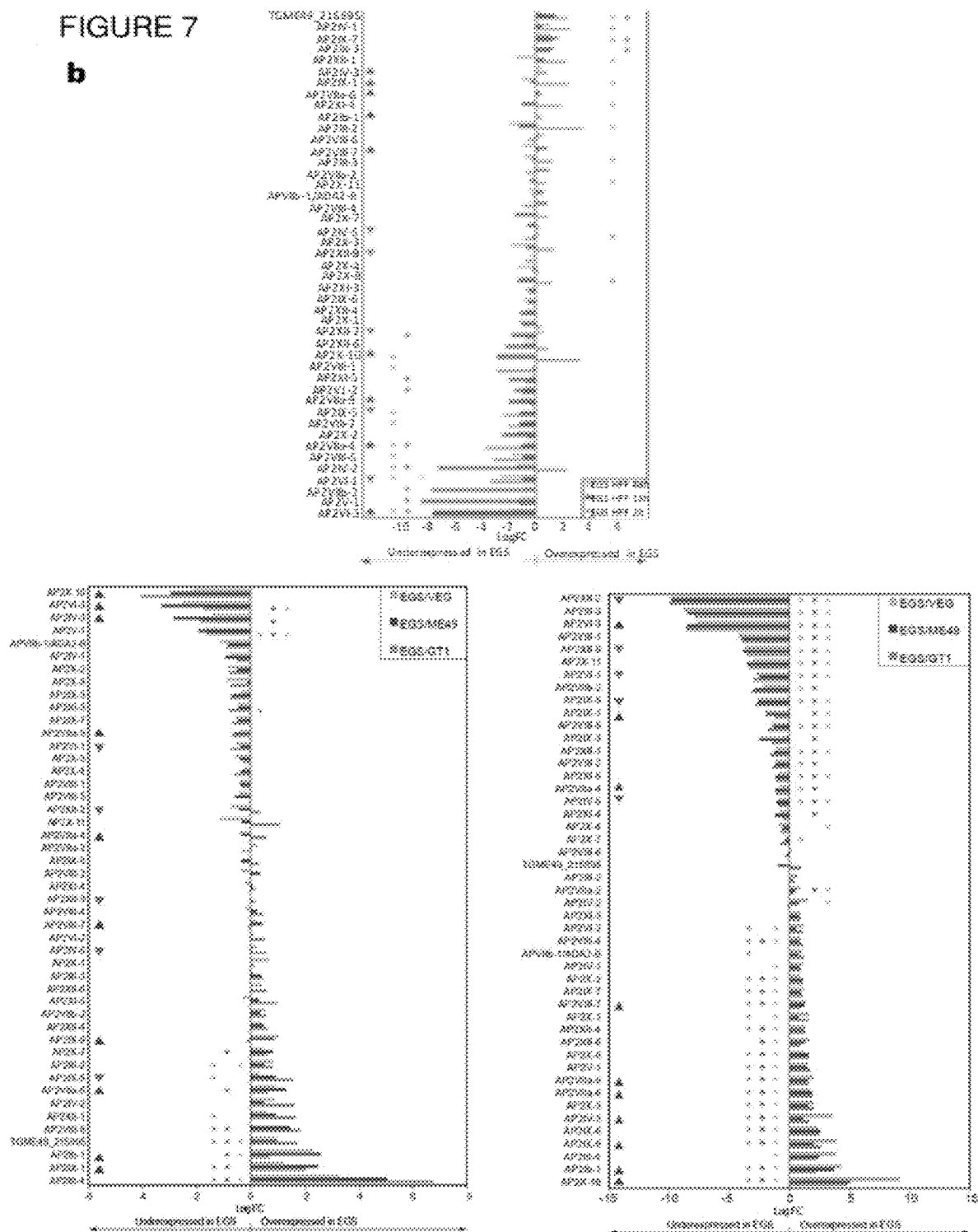
b

FIGURE 7

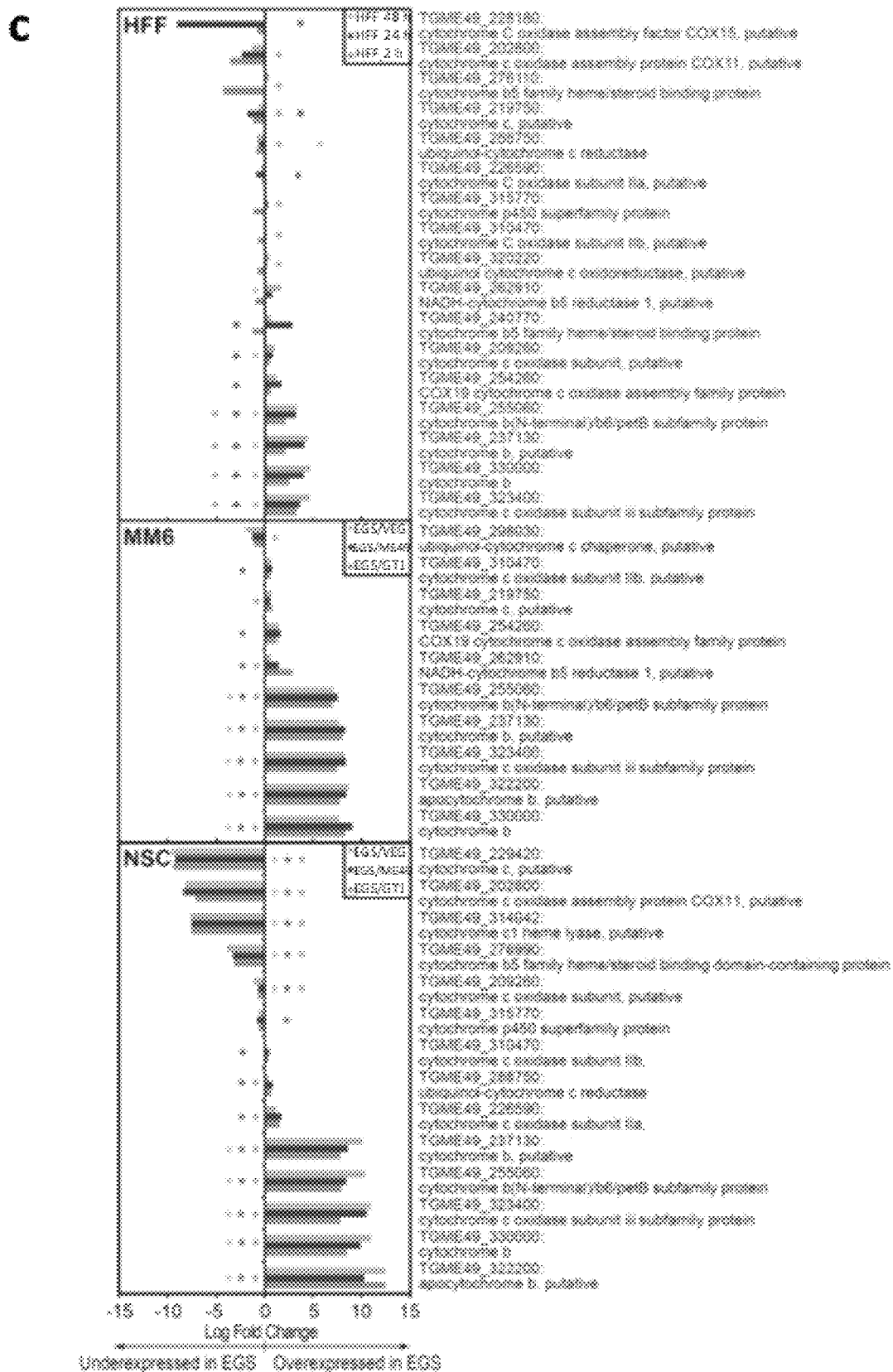
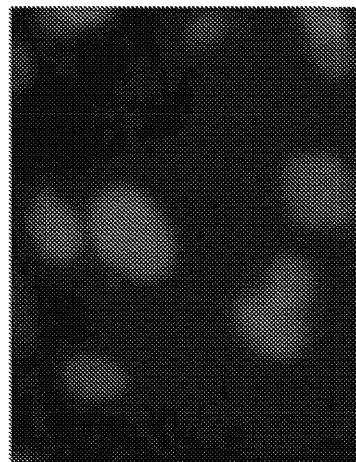
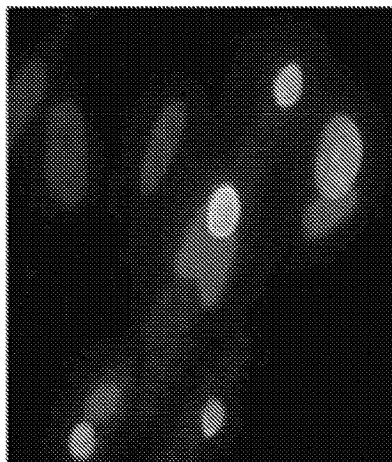
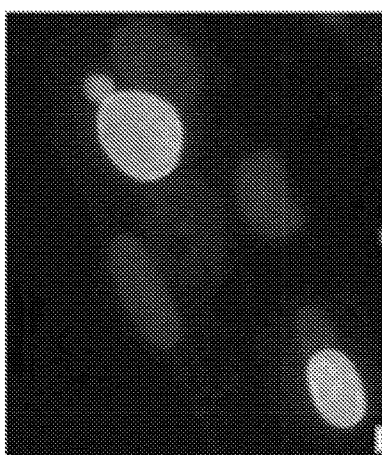
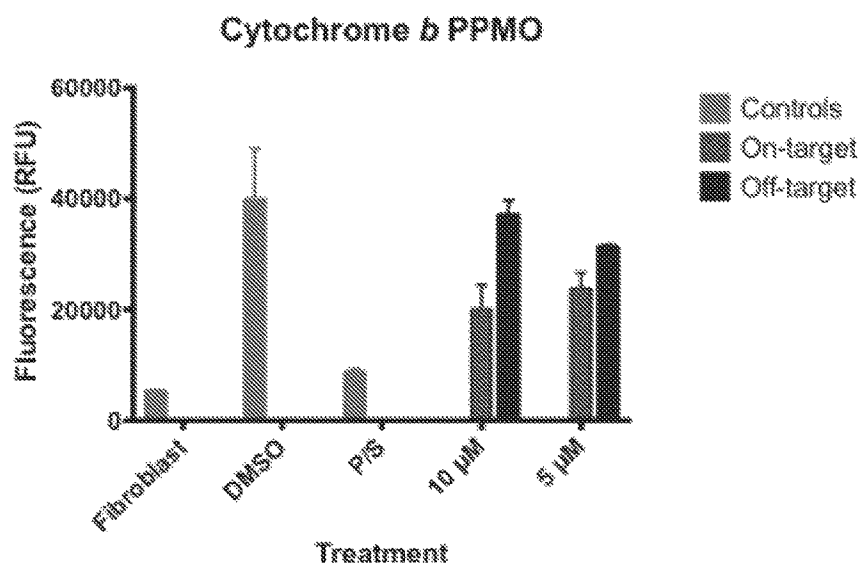


FIGURE 7

d



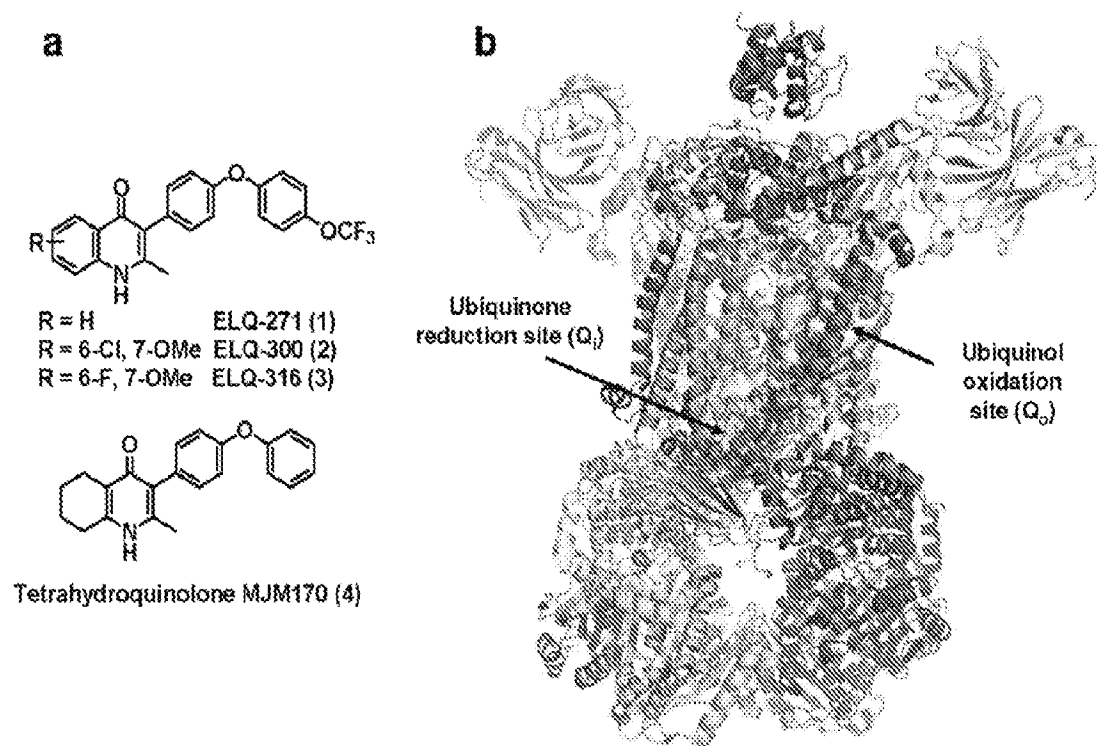


Figure 8

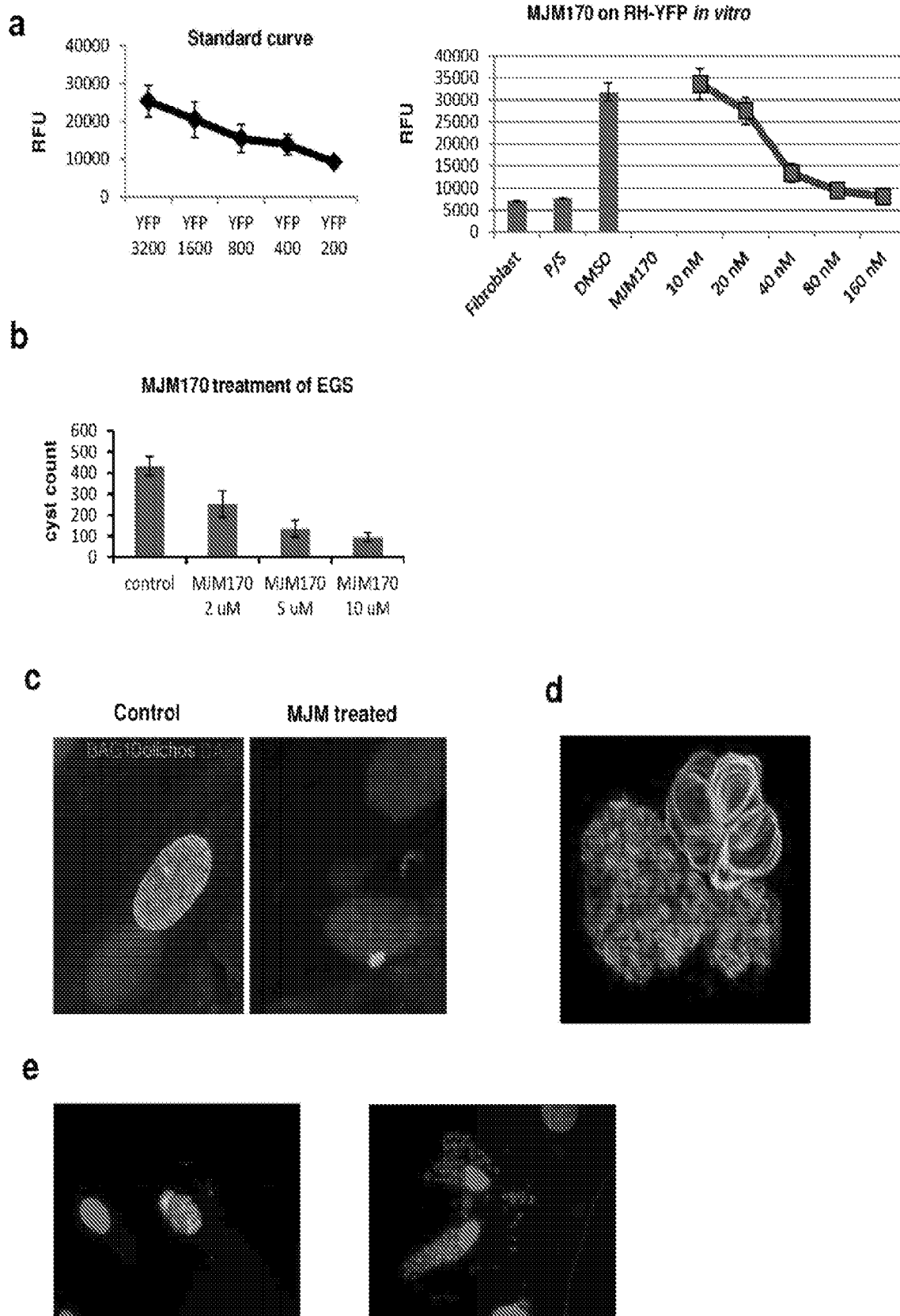


Figure 9

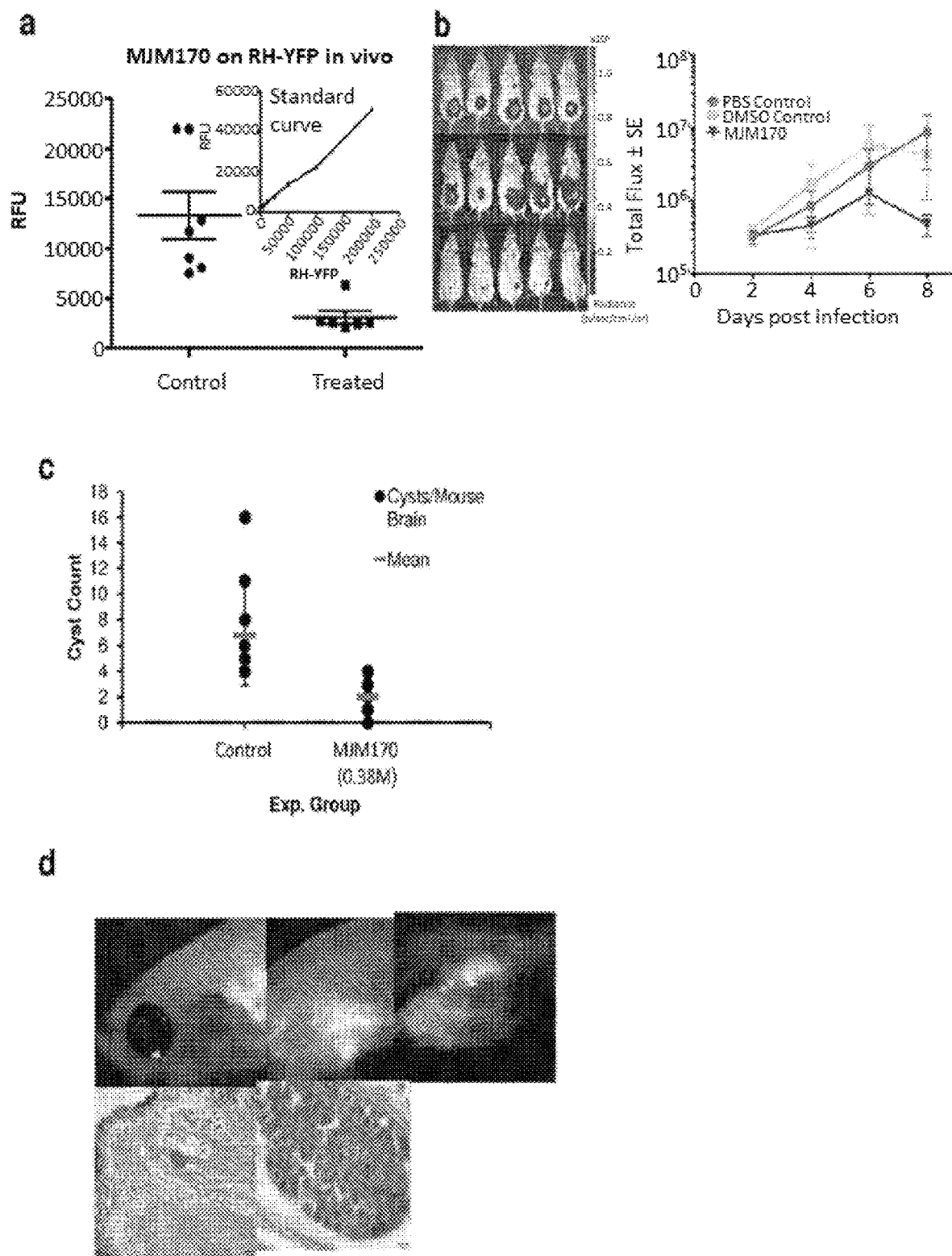


Figure 10

Figure 11

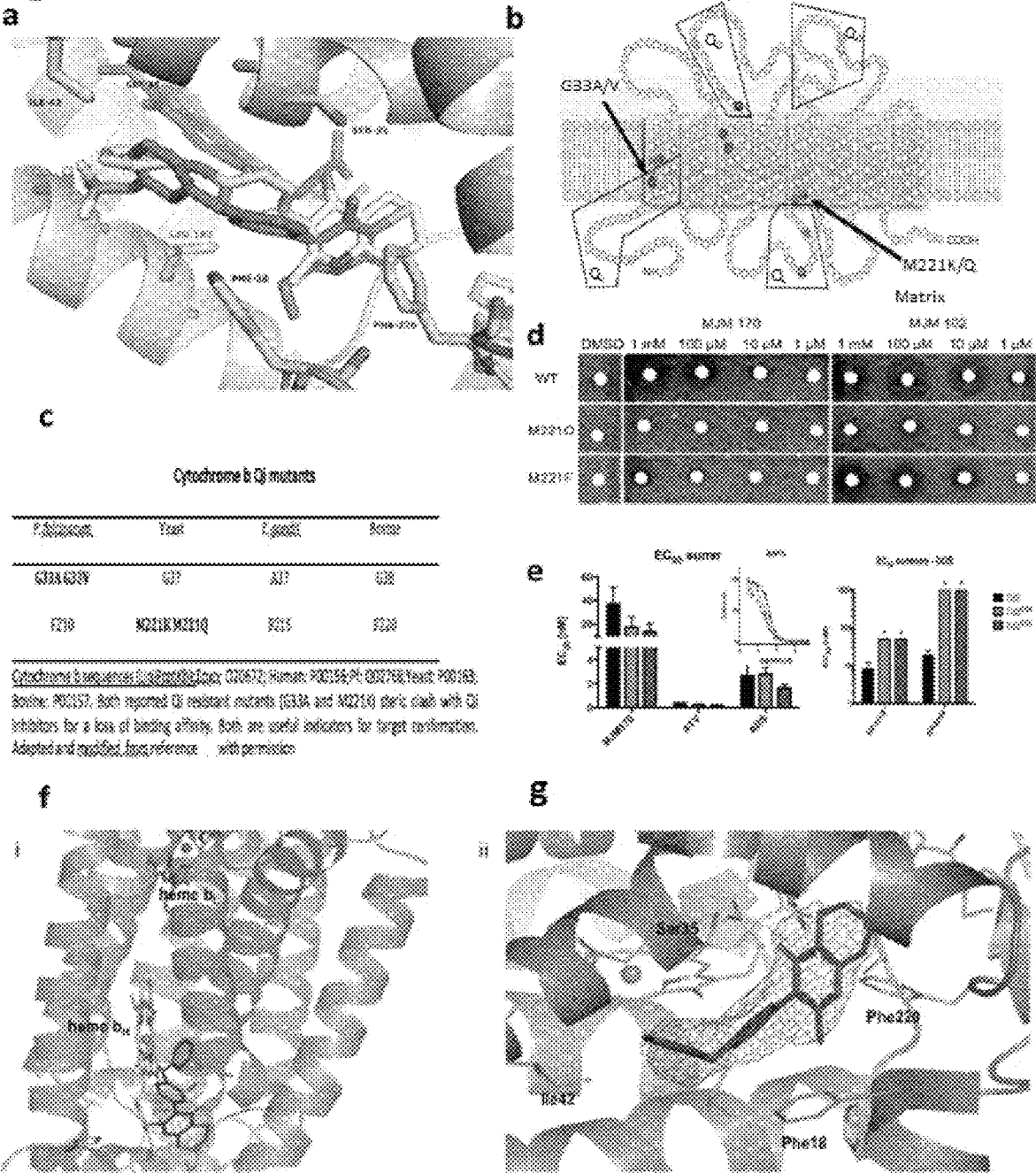


Figure 12

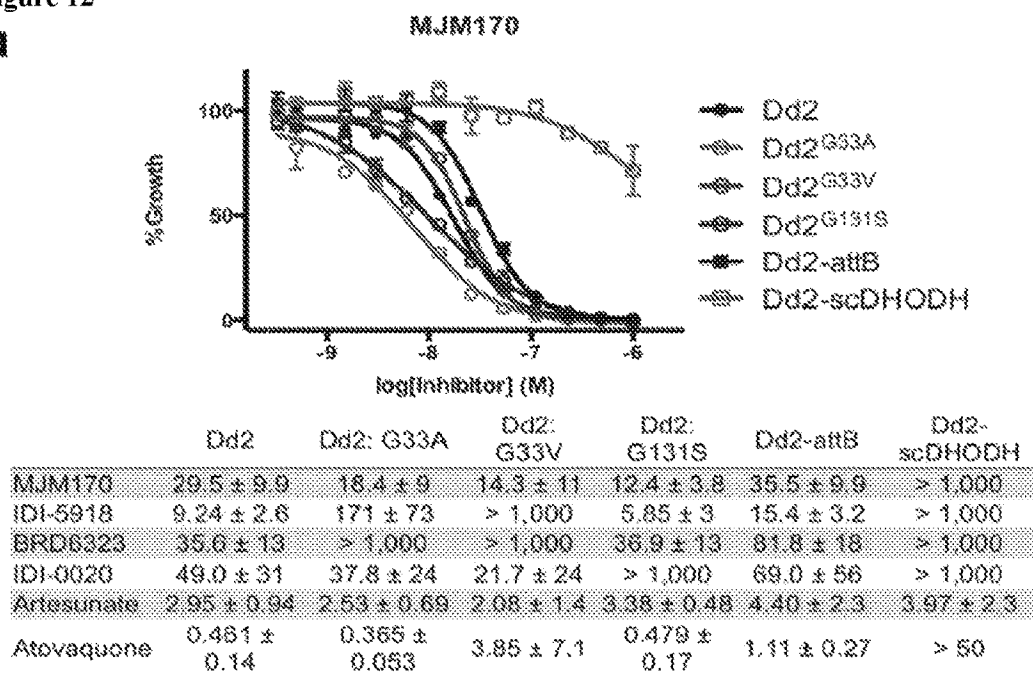
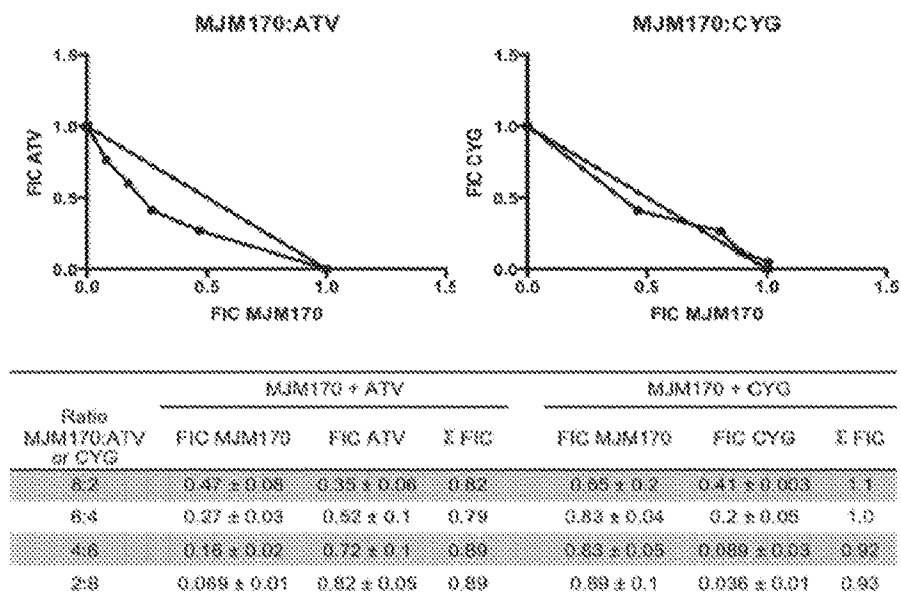
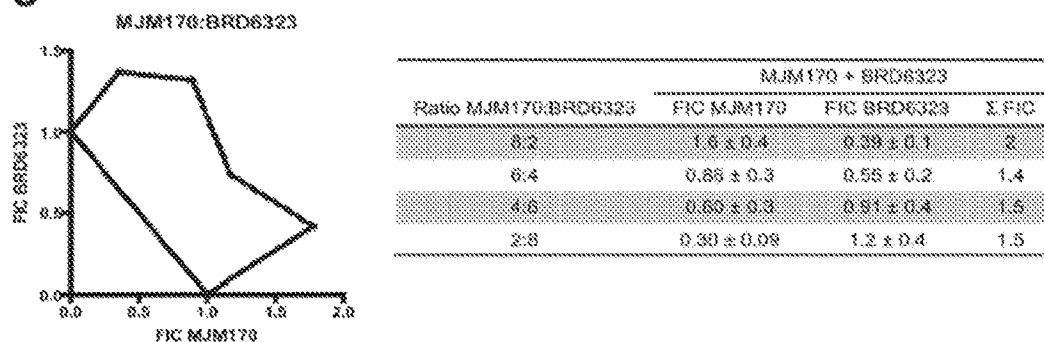
a**b****c**

Figure 13

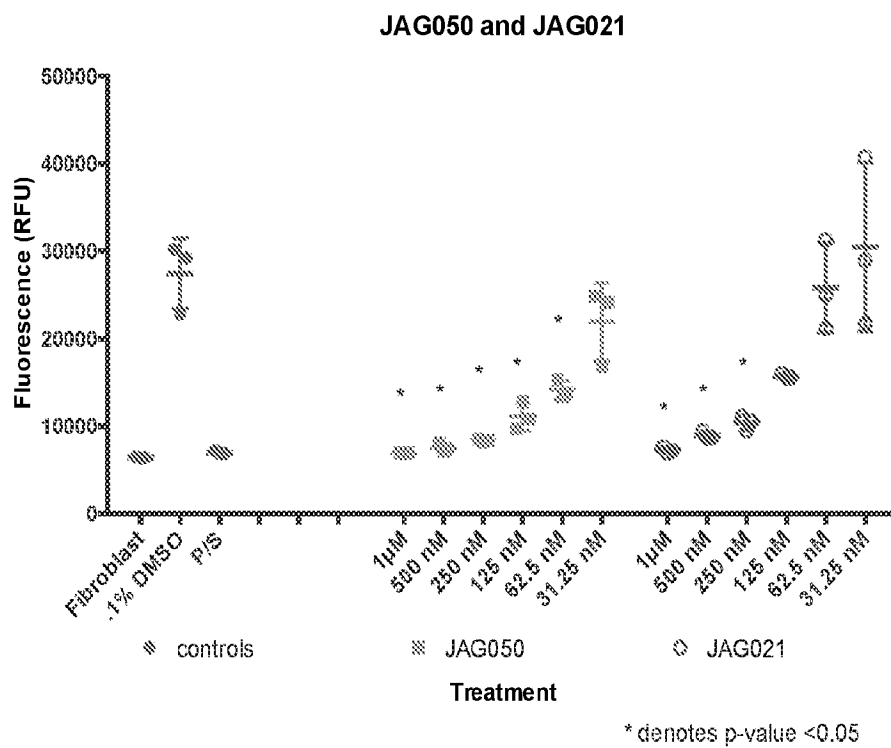


Figure 14

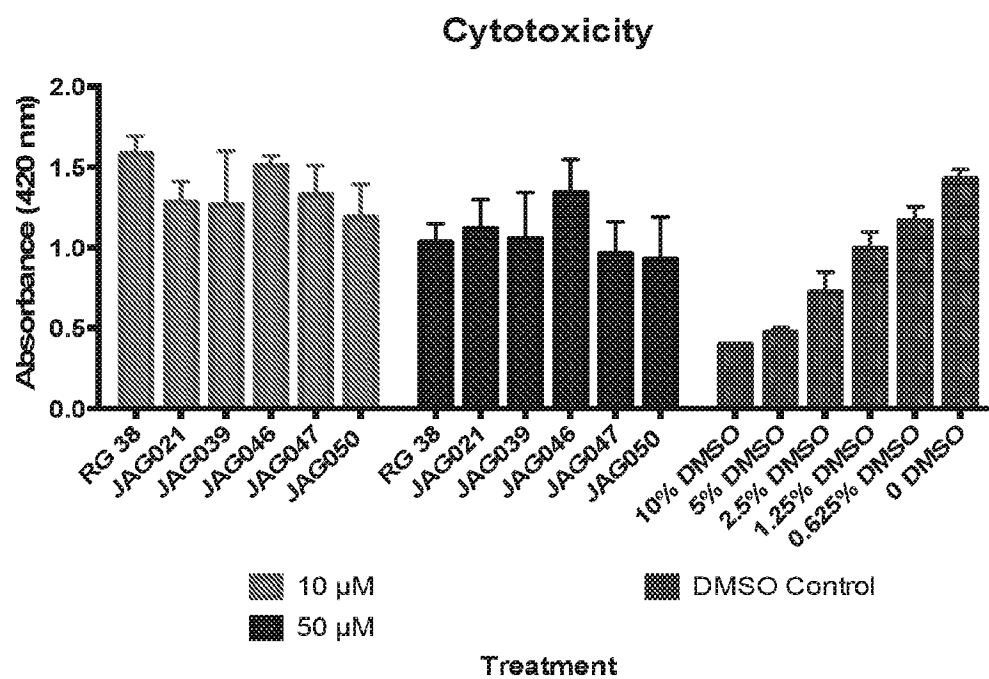


Figure 15

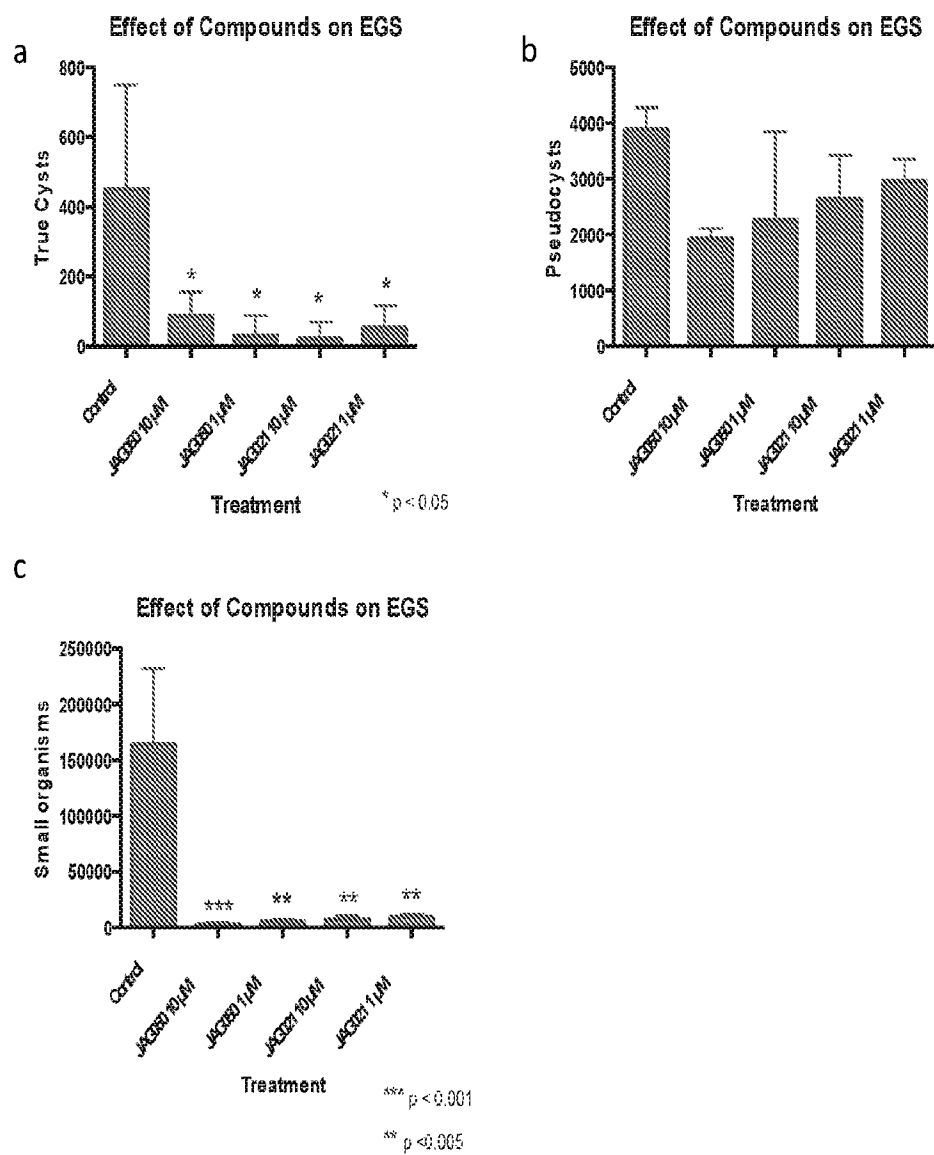


Figure 16. Binding assays of JAG 21 to bovine cytochrome bc (Kansa Sveta

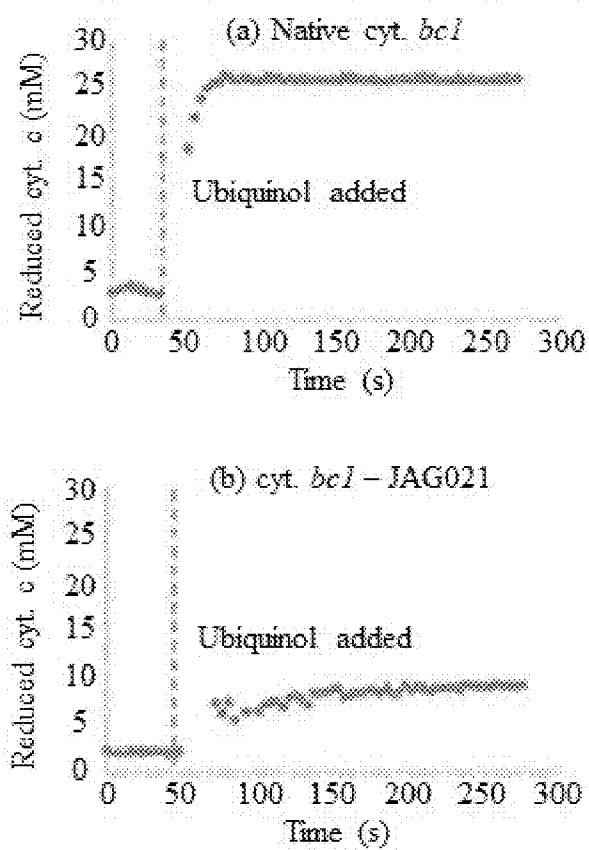


Figure 17.

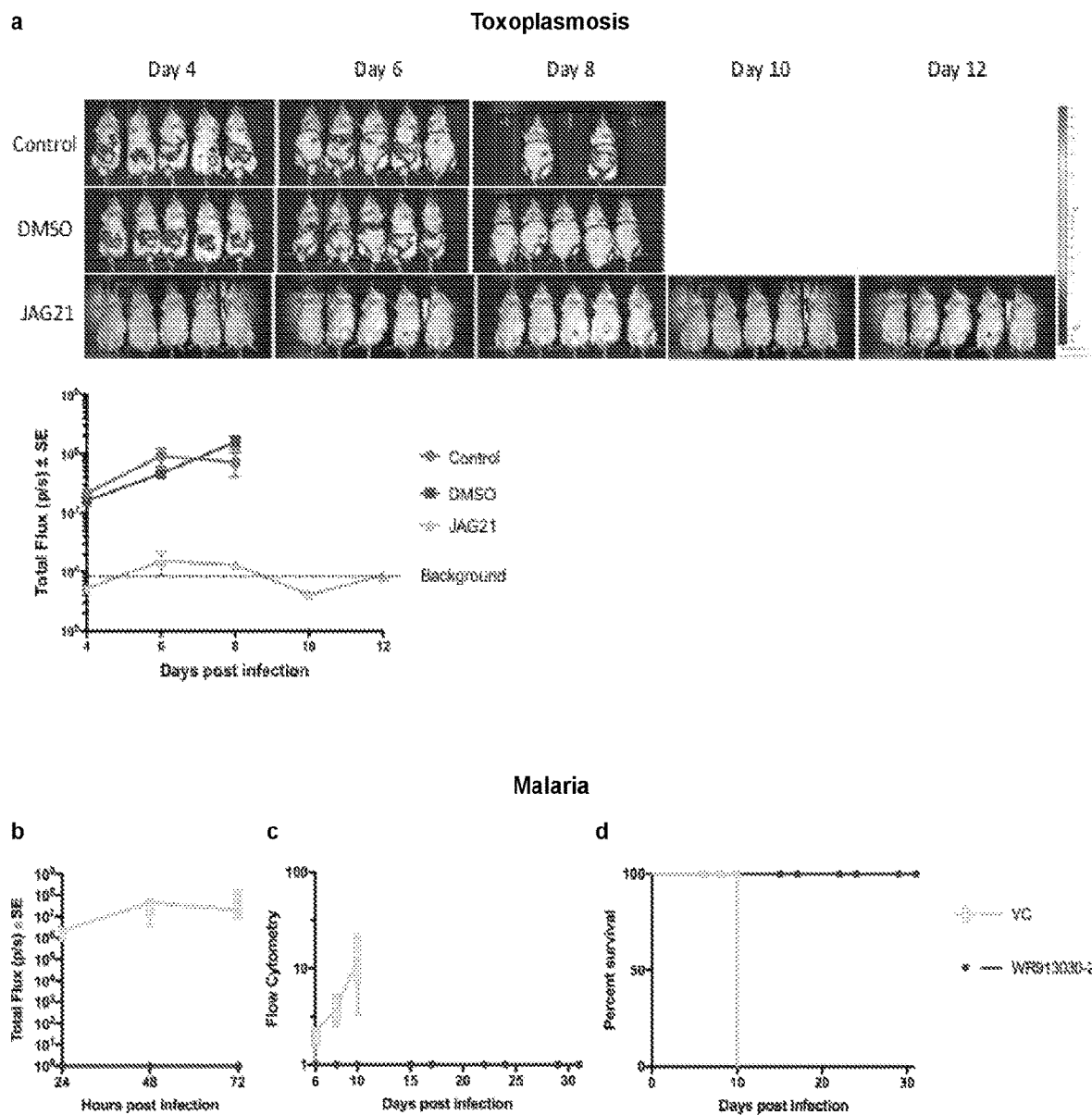


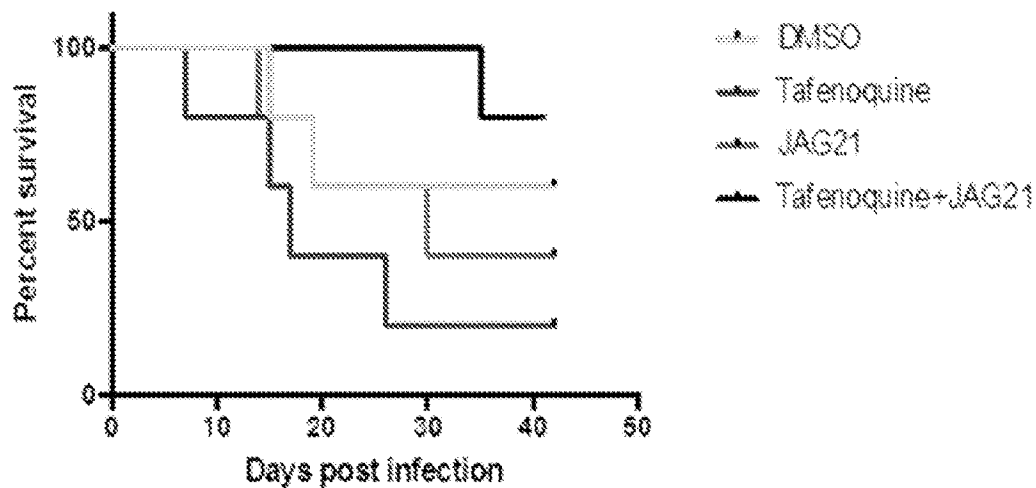
Figure 18.

Goal: To test if JAG21 and/or Tafenoquine be able to kill the dormant stage of *T. gondii*: rps13

Experiment design:

	-1	0	0-13	14-on	
	s	s	s		
	*	*	*	↓	
	Taf	quine	rps13	JAG21/DMSO daily	Tet in water
4 groups: 5/group		D-1:	D0	D0-D13 daily	D0-D13 daily
		Inject Tafenoquine	Inject rps13	Inject JAG21	Inject DMSO
Control			x		x
Tafenoquine		x	x		x
JAG21			x	x	
T+J		x	x	x	
4 groups: 5/group		D14			
		Give tet water			
Control		x	Monitor the mice		
Tafenoquine		x	Take out the spleen once the		
JAG21		x	mouse is really sick for histopath		
T+J		x			

Run 1



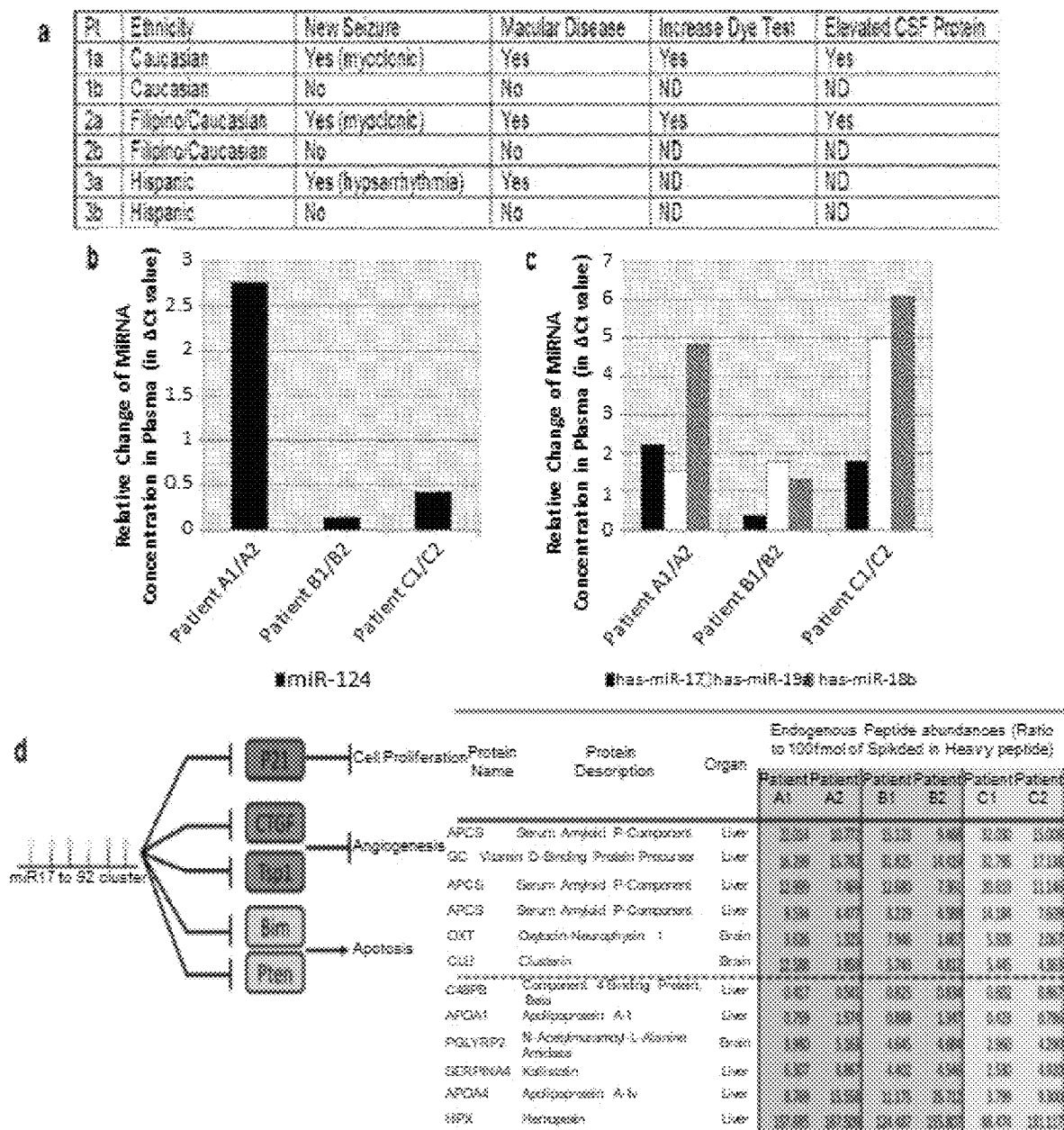


Figure 19

IPA pathway analysis for alternative spliced genes

Alternatively spliced genes

☒ **GT1(63)**: RPS24, NDUFA4C2, EXOC7, TIMM8B, SNRNP70, MAX, RPLP0, NEK7, SRSF6, SLC4A7, SRSF11, PPAN, FMO3, RTN3, FSTL1, WNK1, SEC11A, DCUN1D4, TIA1, RNF220, FUBP1, COL12A1, COUGA2, IEF1A1, RPS27A, FN1, CAPN2, DDIX5, MAP1LC3A, APEX1, MAGED2, SLC25A3, CD46, NDUFA10, ANAPC5, ECI2, RASGF4, SRRM1, COPS5, BAX, RBM39, FAOS3, CUC42SE1, IDI1, MAP3K7, CAPRIN2, MRPS22, DDIX208, PFON5, COG4, L3MBTL2, HMGN1, PIPRM, AQR, NDUFS2, TSPAN4, RPS21, NIT2, UOX39A, HSD17B4, CACNB3, LPCAT4, ACAOV1

☐ **ME49(3)**: NOC2L, PKMYT1, CPSF31

☒ **VEG(29)**: LOXL3, MYL6, CALD1, EIF4A2, FLNA, RPS9, MAP4, UBE2I, ISOC2, DMPK, RARGE1, ACO1153D, RPL12, FKBP10, FAM211A-AS1, PSME2, CSNK1D, CFH, CDC157, ADAMTS1, TSPAN17, ARMCK6, SLC25A39, TMEM259, NME4, NDUFS7, TNFRSF14, BRAT1, TINAGL1

Top 5 Ingenuity Canonical Pathways enriched by alternative spliced genes in GT1

Pathways	P-value	# Genes	Molecules
Toll-like Receptor Signaling	1.26E-02	6	MAP3K7, Ubb, UBB, TAB1, TAB2, UBC
p38 MAPK Signaling	6.37E-02	5	MAP3K7, TAB1, TAB2, HMGN1, MAX
Wnt/β-catenin Signaling	1.08E-01	5	MAP3K7, Ubb, UBB, TAB1, UBC
EIF2 Signaling	1.24E-01	5	UBA52, RPLP0, RPS24, RPS27A, RPS21
Huntington's Disease Signaling	1.66E-01	5	Ubb, UBB, BAX, UBC, CAPN2

Top 5 Ingenuity Canonical Pathways enriched by alternative spliced genes in VEG

Pathways	P-value	# Genes	Molecules
Axonal Guidance Signaling	2.02E-01	4	MYL6, ADAMTS5, MYL6B, ADAMTS1
Salvage Pathways of Pyrimidine Ribonucleotides	1.11E-01	3	CSNK1D, DMPK, NME4
ILK Signaling	1.77E-01	3	MYL6, FLNA, MYL6B
EIF2 Signaling	1.77E-01	3	RPL12, RPS9, EIF4A2
mTOR Signaling	1.81E-01	3	RPS9, EIF4B, EIF4A2

Immune response or neurodegenerative signal?
No pathways enriched by ME 49 due to small number of genes.

Figure 19E

FIGURE 20A

GOBP	GO id	GO term	inn6 up	inn6 down	NGC up	NGC down
GO:0006955		immune response	CD8A, IL27RA, BNIIP, TNFSF15, IRF4L, APOBEC3G, STM, CFP, NO22, MYO88, NFIL5, APN, ICAM1, HLA-F, SP100, HLA-E, B5-2, NEF2, LY96, HLA-A, CDCE12, CT55, HLA-E, HLA-F, CD8, DCLEC1, CD8E, TNFSF13B, UBE1P, VEGFA, C3DSE1, ICOSL3, PTPRN, GARP, HLA-DRA, MAVS, PSM830, GPR183, IRH1, CCL2, HLA-DRA1, EMPD3, HRTM3, CCR1, OAS2, BP665, RSAD2, HFE, OAS1, CD70, OAS2, CCL5, MIF, SLIC1A1, TMED7, TNFSF18, POU2F2, FCER1G, BCL3, MRL1, C2, THBS1, DHX58, P38, PTPRC, CR1, IL8, SAMHD1, MYO1F, CD300C, TNFSF9, TRIM22, AIM2, PSM89, DVX58, TNFAIP2, CYBA, GPI, TNFSF10, OASL, S18, SCG2B, CD300A, CT51, BNIIP, POMP, TGFBR3, CCL5, IL6	None	None	None
GO:0008515		response to virus	MAVS, TIRH, FGR, ZC3H4V1, RSAD2, BNIIP, RPS15A, APOBEC3G, CCL5, TRIM5, S4415, BCL3, MX1, MX2, IRVOR1, PTPRC, BST2, SAMHD1, IR44, IR18, STAT1, TRIM22, STAT2, DDX58, IR39, PLSCH1, IRF7, BNIIP3, EIR2A2	None	MAVS, PLSCH1, IL6, BST2, ISG15, IRF7, IR44, MX1, CCL5, SAMHD1	None
GO:0006952		defense response	IL10A8, IL27RA, AIF1, S100A9, BNIIP3, APOBEC3G, MAMP25, CFP, NLKCA, NO22, MYO88, HISTH2B, HMOX1, ADAM, HISTH2B, HCF5, MX1, MX2, S100A9, SP100, NO22, LY96, P3, COLCE1, NLRP1, S100E1, HIF1A, HISTH2B, ICOSL3, PTPRN, HLA-DRA, ACVR1, MAVS, CSAR1, IFH1, CCL2, PSM89, FGR, CCR1, RSAD2, CCL5, MIF, TMED7, SLIC1A1, TNFSF18, LGALS3BP, MERV, RAC1, BCL3, C2, THBS1, DHX58, SPPI, FNN1, PTPRC, HISTH2B, CR1, LIPA, IL8, HCK, ANKRA1, SAMHD1, MPO15, CD300C, TP73, S100A12, DDX58, ORM1, CYBA, P2RX7, NLRP1, POK1, IRF7, BNP3, ALOX5, IGFBP4, CD14	None	None	None
GO:0006911		response to wounding	PPARA, S100A8, AIF1, S100A9, MAMP25, CFP, NLKCA, MYO88, GNA, HMOX1, ADAM, KERP15, S100E1, GATM, LY96, P3, STXBP1, PLAIN, S100E1, CD36, THBD, HIF1A, GNAQ, YCAN, C1S, PKO1, PTPRN, ACVR1, CSAR1, CCL2, PSM89, CCR1, COL3A1, NIN1, CCL5, MDK, TGM1, MIF, C2B, TMED7, SLIC1A1, TNFSF18, MERV, P2RY1, YAC1, C2, THBS1, PAPS2, SPPI, FNN1, KLF6, CR1, LIPA, MAP2K1, IL8, ANKRA1, TP73, S100A12, ORM1, CYBA, PLSCH1, P2RX7, NLRP1, CD36, IRF7, ALOX5, IGFBP4, CD14	None	CCL2, TNF, C1R, CCL5, CASP6, S1PR3, HMOX1, RAC1, TP73, RAB27A, SCG2, PLAT, KLF6, IL6, LY96, LY7, ITGA2, SOD2, PLSCH1, CD55, THBD, EREG, F3, RIF, NGF	None
GO:0042881		regulation of apoptosis	MYO2C, PIGA5, MIF, BNIIP, TNFSF15, P2RY1, CD40, TP73, NLKCA, PTPRC, APP, NO22, MYO88, HMOX1, TP71, NGRAP1, MX1, NAZK6, ADAM9, NOL3, RANG, ACTH4, DFFA, SOCS3, NDUFA13, IFI16, PRKCE, VLRP1, ARHGEF11, BTG2, TNFSF18, BTG1, JUN, HIPK2, VEGFA, UBC, UBE1, CT55, UBA52, ACVR1, RAF1, FG02, INH1, CCL2, XIAP, PAPA2, ADAMTSL4, SO4A, CD70, MIF, VDR, DDX198, RAC1, TMG2, BCL3, BCL2, THBS1, PHLCD2, DMF, KUNIS, PHILAD, TDRP, PTPRC, LGALS1, CRES1, ANKRA1, WIF4B, STAT1, BIRC5, TP73, TRADD, CDKN1A, SON, TNFSF10, P2RX7, PHL3, NLRP1, CT51, BNIIP1, NLRP12, MAP3K1, IRF6	None	None	None
GO:0048002		antigen processing and presentation of peptide antigen	HLA-H, SLIC1A1, HLA-A, HFE, HFE, FCER1G, MRL1, HLA-E, HLA-DRA, STM, HLA-F	None	None	None
GO:0043122		regulation of t-h-leptin-induced TNF-kappa-B cascade	MAVS, BST2, CDKN1B, LGALS1, HCF1P, CCL1, LGALS3, TRADD, TRAF3P2, TRIM38, TMED7, C18ORF2, TNFSF13, NO22, MYO88, HMOX1, SHSAS, NLRP12, TMG2, OTU7D8, C2D1A	None	MAVS, UBE2N, TRAF3P2, BST2, NLRP2, SLIC1A1, SOSTM1, CDKN1B, HMOX1, TMG2, TNFAIP3	None
GO:0006917		response to bacterium	MAVS, CCL2, FGR, IL27RA, PTSS2, CCL5, B2M, CFP, SLIC1A1, NO22, NLKCA, MYO88, HISTH2B, HISTH2B, BCL3, H5-TP28B, LY96, SOCS3, HCK, MYO16, STAT1, S100A12, P2RX7, THBD, HISTH2B, JUN, CD14, PTPRN	None	MAVS, IL6, HISTH2B, CCL2, SOCS3, LY96, LY7, S100A12, CCL5, CCL2, HISTH2B, JUN, MBS1, CT55, NF	None
GO:0070482		response to oxygen levels	PPARA, CAV1, SLC1A1, CCL2, R1T1, NOL3, ACTN4, SOCS3, ALDO3, APOD1, ERL2, BNIIP3, CAPN2, DDT4, CDKN1A, HIF1A, FLOD1, CAS, PLOD2, HMOX1, VEGFA, ALDH2, THBS1, CCL1A1, P2RX7, CD36, IRP1, CD39, HCK, FCER1G, COLCE1, ARCA1, THBS1, CD14	None	PLAT, CCL2, ACTN4, SOCS3, HMOX1, VEGFA, NHA2, ITGA2, SFRP4, SOD2, ANGPT14	None
GO:0006908		phagocytosis	PPARA, CAV1, CCL2, PTG2, UBE1, HFE, VDR, P2RX7, GSN, HMOX1, SPPI, SLC8A1, SP100, RANG, GATM, SOCS3, AXI, STAT1, CDKN1A, P2RX7, RPS19, JUN, COL1A1, A, OX5, S18	None	None	None
GO:0006991		response to extracellular stimulus	PPARA, CAV1, CCL2, PTG2, UBE1, HFE, VDR, P2RX7, GSN, HMOX1, SPPI, SLC8A1, SP100, RANG, GATM, SOCS3, AXI, STAT1, CDKN1A, P2RX7, RPS19, JUN, COL1A1, A, OX5, S18	None	None	None
GO:0018117		regulation of cytokine production	MAVS, IL27RA, H5T, CRB1, NLRP1, DDX58, TMED7, SLIC1A1, NO22, CCR6, P2RX7, MYO88, HIF1A, HMOX1, NLRP12, IRF1, BCL3, FCER1G, BCL3, THBS1, CD14	None	None	None
GO:0006165		MAPK cascade	PTPRC, HGR1, CAV1, R1T1, MAP3K1, TACKS, DUSP10, MAPK4, PDE6G, JUSP4, SH2D3C, P2RX7, GAB1, SHC1, MAP3K1, MAPK7, THBS1, GADD45B, MAP3K13, MAP2K6, A3APM9	None	None	None
GO:0016192		vesicle-mediated transport	DIA, CHMP5, C18ORF7, HMOX1, HMOX2, R1P1, APP, CD39, GSN, CDLX3, STXBP1, COLCE1, CDKN1, LR10, R1N2, RAB1, CUL1, VAMP1, PCL1, NAB, CAV1, R1T1, HFE, ABCA1, CCL5, SLIC1A1, PUNE, RAC1, BCL3, F1C1, V5S3, STX11, TRP10, THBS1, NPA25, AP2M1, GABARAP2, RAB8A, HCK, INH8, WIF15, SNAPIN, WIP1, P2RX7, LR17B, LRPI, NDUO4, CPM3, MAP3K1, CD34	None	None	None
GO:0007167		enzyme-linked receptor protein signaling pathway	HGR1, CCL2, CD3A, TP73, UBE1, COL3A1, PKN, PIP, RASBP1, GAB1, SHC1, AGPR, SH2, ADAM9, CSF1R, TNFR1, R32, R1T1, SRAIP2, ARS5B, CRB1, AXI, DOK2, PRLR, JUN, CSRP1, F1P2, VEGFA, COL4A2, TGFBR3, JAK3, ACVR1	None	None	None
GO:0035554		cellular response to stress	NG4, CAV1, XIAP, PAM175A, DUSP10, HFE, MAPK4, RPS27, TPW1, PKN, ACD, INH8B, HMOX1, GAB1, RASBP1, BCL3, R1N2, HIF1A, PHOXA3, CDKN1A, MAP2K6, LK2, SP100, TACKS, IFI16, GTF2S3, E1P01, FOXP3, ESO2, TP73, ATRK, DCLEC1, SH2D3C, POLD4, CDKN1A, HIF1A, NLRP1, BTG2, NDUO4, JUN, IRF7, HIPK2, BXC01, VCAN, MAP3K1, HIF2A2, MAP3K13	None	None	None
GO:0007260		JAK-STAT cascade	DSM, CCL2, PRLR, SOCS3, UBE1, STAT1, STAT2	None	None	None
GO:0016044		membrane organization	CAV1, LDKR, HFE, BNIIP3, ABCA1, HMOX2, SLIC1A1, CD9, APP, CD39, BLOC1S1, RAC1, C18ORF1, AGPR, THBS1, TRP10, STX11, RAB8A, HCK, STXBP1, COLCE1, PLSCH1, P2RX7, CD36, LRPI, LRPI0, NDUO4, OTOF, R1N2, CD14, R1N3	None	None	None
GO:0034470		mRNA processing	None	None	None	None
GO:0006304		mRNA processing	None	None	None	None
GO:0006397		mRNA processing	None	None	None	None
GO:0006185		IMP biosynthetic process	None	None	None	None
GO:0008033		mRNA processing	None	None	None	None
GO:0008064		glutamine family amino acid metabolic process	None	None	None	None
GO:0044271		nitrogen compound biosynthetic process	None	None	None	None
GO:0006393		mitochondrial transport	None	None	None	None
GO:0024242		cell cycle process	None	None	None	None
GO:0007150		leukocyte adhesion	None	None	None	None
GO:0006974		response to DNA damage stimulus	None	None	None	None
GO:0006733		oxidoreduction coenzyme metabolic process	None	None	None	None
GO:0015986		ATP synthase coupled proton transport	None	None	None	None
GO:0044220		ion transmembrane transport	None	None	None	None
GO:0006119		oxidative phosphorylation	None	None	None	None

[illegible]

List of candidate genes as targets for the developments of antiparasitic compounds that inhibit bradyzoite development and/or survival in the host.

[illegible]

[illegible]

[illegible]

FIGURE 21D

TGME49_22490	edcun-dependent protein kinase CDK4	MFUKTSNHCSCNATFFGDLNVAQHSDRYGNVFNQKSVLSTDASSPPTVRSQEVCFDEGGFVRLKLIWRASGEIYWEPTNRVYLTANTSSMENWVGLATCSITFFLPQIPSPSPYKHAERTKVEASSVHLHSASISDQSGS DTGTCSQVDESRTRQKVRGQPASVGTGKATAAERQKGVVMPYHQCSTQRRHSISTQADEAAGGGRHYSPKBSAFLANTGPTNYTYVTKTCRCGTWGEVLYIDNGTGARRAKVPCYVEDADPRGGEIEHUKSDHPHRLY ETFEEDMTDFYLVMEYCTDGLFORLVHGQVTEALACRMRGILAAVAYCHAHRYAHRDCKENFLFHDNPESPKLQFGLAARFISGCPMRTAGTPYYVSPQVLEORYGPECQVWSAGVMMVILQSYPPFNAPSDRMANKVRA GHYTFPQSEWSRVSIGAKLISRLDRHPRTRISAEQALRHANFAMHAPGDHFEPLGLDLSNFRFPQGLSRUKKALTVACHLEDSEIEGLKNLFTOLDTEGGOVLVEERKGIERSQVHLPTDMVLEDYLVREVDATGTSIDYTEFAA CLHGSHYRBEACRAAFRLVDNGDGLYSAGELPQVFNMGDLETDAAASLEADADGQHTTFDEPQGLMRKVPSLALVTEHTVSMNRPTCSRTNISEASLTYPRAIG (SEQ ID NO: 22)	TGME49_chrx.2,207,266..2,214,584(+)
TGME49_30000	cyclochrome b	WHSRTLSLSMSLFRALVYFRCALNUNSYHFGFLVAMTFVLQITGLAFRYTSEASCASFASVQHLVREVAAGWEFRMLHATTASVFLGLHMTPLGLYNWSYSYLTAYMSGLVLYLTATAPLCYVLPWGQNSPKGATVITNLSPI PYLVPWLLGGYVVSQVTLKPRFLVHLFPLIGQIRVLMFVHLHNGSSNPAGDITLVNAPYPRMLTDAGQLSYUGLFLQAFGLMELSHPKNSPYARFYTLRYFEWFLAYYAVLVNPSKTGGLLVFNSSUNLGLLSERALKTRMLR QGFMTFNVAAGVWVYVMMFLIKSAPQATYLYGRLATLYLTGLVALCY (SEQ ID NO: 23)	KE138188:213..1,319(-)
TGME49_32220	apocytochrome b, putative	RLCKYHRLCSLTSQLSYUGLFLQAFGLMELSHPKNSPYARFYTLRYFEWFLAYYAVLVNPSKTGGLLVFNSSUNLGLLSERALKTRMLR (SEQ ID NO: 24)	KE138872:1..398(+)
TGME49_32340	cyclochrome c oxidase subunit II, subfamily protein	MSVHHNFTGLLKANSVGFQYPTTLRLFKGYVLGVYGLJLSLVLTAREWYSDASMSSTVYGVISETQLFSFFWGVYTTSTWTLQGLQGLDLPDPSRLFMTIMLSALSVSSVYLVKQHLYTSCNMFLLVSRMLVCTEYGLSY INDNGFDNGLFLTGHSFHYVGAIGFFNQGMYSLLYTYLPVNCITLSKCKGLKFSEFTLYLVHFEAVWMMHVTLYL (SEQ ID NO: 25)	KE139158:358..1,245(+)
TGME49_227130	cyclochrome b, putative	MSLFRALVYFRCALNUNSYHFGFLVAMTFVLQITGLAFRYTSEASCASFASVQHLVREVAAGWEFRMLHATTASVFLGLHMTPLGLYNWSYSYLTAYMSGLVLYLTATAPLCYVLPWGQNSPKGATVITNLSPI (SEQ ID NO: 26)	TGME49_chrx.5,732,558..5,734,754(+)
TGME49_22060	cyclochrome b1/6mer/oligopeptide subfamily protein	WVHSHHMTVGLQVTRAVFSAMTMAFTGTQKRNWLTVMASHNTRTRDVAALCFLLFTLGGTTOVMQWAGMDVALNDTYVVAHSPVLSGLAATKGFVYSKDMFGDTLPRNWTGSSPYLVNAPVFLASMLFLPMRLGF WMMPRRFGTVDYLCNTWCSNQLVYVTPQKXLRNPFYSEMTPTSTMYLASEYYSYLTAYMSGLVLYLTATAPLCYVLPWGQNSPKGATVITNLSPIPLVPLALGGYYSQVTLKPRFLVHLFPLIGQIRVLMFVHLNGLSHPA DITLVNAPYPRMLTDAGQLSYUGLFLQAFGLMELSHPKNSPYARFYTLRYFEWFLAYYAVLVNPSKTGGLLVFNSSUNLGLLSERALKTRMLR (SEQ ID NO: 27)	KE139167:91..1,594(-)

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COMPOUNDS AND METHODS FOR TREATING, DETECTING, AND IDENTIFYING COMPOUNDS TO TREAT APICOMPLEXAN PARASITIC DISEASES

CROSS REFERENCE

This application is a U.S. national phase application of International Patent Application no. PCT/US2016/067795, filed on Dec. 20, 2016, which claims the benefit of U.S. Provisional Patent Application No. 62/270,264, filed Dec. 21, 2015, and U.S. Provisional Application No. 62/306,385, filed Mar. 10, 2016, each incorporated by reference herein in their entirety.

STATEMENT OF GOVERNMENT RIGHTS

This invention was made with government support under National Institutes of Health (NIH) contract number HHNS272200900007C, NIH, National Institute of Allergy and Infectious Diseases of the National Institutes of Health (NIAID) award numbers R01AI071319 (NIAID) and R01AI027530 (NIAID); NIAID contract Number HHNS272200900007C; NIAID award number U19AI110819; NIAID award numbers U01 AI077887 (NIAID) and U01AI082180 (NIAID); National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK) Grant #5T35DK062719-28; Defense Threat Reduction Agency award number 13-C-0055, and Department of Defense award numbers W911NF-09-D0001 and W911SR-07-C0101. The government has certain rights in the invention.

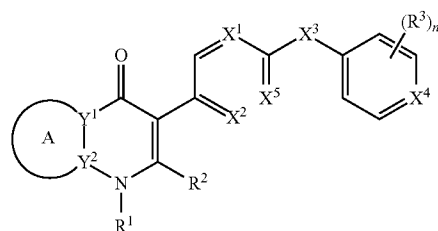
BACKGROUND

Apicomplexan parasitic infections, such as *Toxoplasma gondii* infections, can cause systemic symptoms, damage and destroy tissues, especially eye and brain and cause fatalities. Primary infections may be asymptomatic, or cause fever, headache, malaise, lymphadenopathy, and rarely meningoencephalitis, myocarditis, or pericarditis. Retinochoroiditis and retinal scars develop in up to 30% of infected persons, and epilepsy may occur. In immunocompromised and congenitally infected persons, active infection frequently is harmful. Recrudescence arises from incurable, dormant cysts throughout life. Current treatments against active *T. gondii* tachyzoites can have side effects such as hypersensitivity, kidney stones, and bone marrow suppression, limiting their use. Latent bradyzoites are not significantly affected by any medicines. Atovaquone partially, and transiently, limits cyst burden in mice, but resistance develops with clinical use. Thus, *T. gondii* infection is incurable with recrudescence from latent parasites posing a continual threat. Estimates of costs for available, suboptimal medicines to treat active, primary ocular, gestational and congenital infections, in just the U.S. and Brazil, exceed \$5 billion per year. Improved medicines are needed urgently. Molecular targets shared by *T. gondii* and *Plasmodia* make re-purposing compounds a productive strategy.

SUMMARY OF THE INVENTION

In one aspect, the invention provides compounds of the structure of Formula (I), pharmaceutical compositions thereof, and methods for their use in treating apicomplexan parasite related disorders):

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(I)

or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof,

wherein

ring A combines with Y¹ and Y₂ to form a C₃₋₇cycloalkenyl or heteroaryl ring,

wherein the C₃₋₇cycloalkenyl or heteroaryl is optionally substituted by halogen, C₁₋₃alkyl, C₁₋₃alkoxy, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR, cyano or phenyl;

Y¹ is C or N;

Y² is C or N;

X¹ is C(R^{x1}) or N,

wherein R^{x1} is hydrogen, halogen, C₁₋₃alkyl, C₁₋₃alkoxy or C₁₋₃haloalkyl;

X² is C(R^{x2}) or N,

wherein R^{x2} is hydrogen, halogen, C₁₋₃alkyl, C₁₋₃alkoxy or C₁₋₃haloalkyl;

X³ is O, N(R), S or C₁₋₃alkyl;

X⁴ is C or N;

X⁵ is C or N;

R¹ is hydrogen or C₁₋₃alkyl;

R² is hydrogen, C₁₋₃alkyl, C₁₋₃haloalkyl, —CH₂OH, —CH₂OR or —C(O)OR;

n is 0, 1, 2, 3 or 4;

each R³ is independently halogen, C₁₋₃alkyl, C₁₋₃alkoxy, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR or SF₅;

or two R³ groups, together with the carbons to which they are attached, form a 1,3-dioxolane; and

each R is independently hydrogen or C₁₋₃alkyl.

In another aspect, the invention provides cell lines infected with an apicomplexan parasite, wherein the apicomplexan parasite genome comprises a gene encoding an Apetela 2 IV-4 protein with an M=>I modification at residue 570 ("AP2 IV-4 M570I") compared to its orthologous gene on the reference *T. gondii* ME49 strain (gene ID: TGME49_318470), non-human animal models comprising cell lines of the invention, and methods for use of each in identifying compounds for treating an apicomplexan parasitic infection.

In another aspect, the invention provides methods for treating an apicomplexan parasite infection (such as a *T. gondii* infection), comprising administering to a subject in need thereof an amount effective to treat the infection of an inhibitor (of up-regulated genes) or an activator (of down-regulated genes) of 1 or more of the up-regulated genes listed in FIG. 1 or FIG. 2.

In a further aspect, the invention provides methods for identifying test compounds for apicomplexan parasite therapy, comprising identifying test compounds that reduce expression (for up-regulated genes), or increase expression (for down-regulated genes) of 1 or more of the apicomplexan parasite genes in FIGS. 3-5.

In one aspect, the invention provides a plurality of isolated probes that in total selectively bind to at least 2, 3, 4,

5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 500, or all of the markers listed in FIGS. 3-5, complements thereof, or their expression products, or functional equivalents thereof wherein at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or all of the probes in total are selective for markers that are upregulated in the EGS strain of *T. gondii* after infection of human fibroblasts, neuronal stem cells or monocytic lineage cells.

In another aspect, the invention provides a plurality of isolated probes that in total selectively bind to at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 500, or all of the markers listed in FIG. 1-2, complements thereof, or their expression products, or functional equivalents thereof, wherein at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or all of the probes in total are selective for markers that are upregulated in human fibroblasts, neuronal stem cells or monocytic lineage cells after infection with *T. gondii*, including but not limited to infection with the EGS strain of *T. gondii*.

In another aspect, the invention provides methods for monitoring *T. gondii* infection in a subject, comprising monitoring levels in a blood sample from the subject of one or more markers selected from the group consisting of clusterin, oxytocin, PGLYRP2 (N-acetylmuramoyl-L-alanine amidase), Apolipoprotein A1 (apoA1), miR-17-92, and miR-124, wherein a change in levels of the one or more circulating markers compared to control correlates with *T. gondii* infection in the subject.

In another aspect, the invention provides methods for treating a *T. gondii* infection, comprising administering to a subject with a *T. gondii* infection an amount effective to treat the infection of ApoA1.

DESCRIPTION OF THE FIGURES

FIG. 1. Host transcriptomics data during EGS infections of human HFF, MM6 or NSC cells. Differential gene expression analysis of human fibroblasts infected with *T. gondii* EGS strain after 2 hs, 18 hs, and 48 hs, monomac 6 cells infected with *T. gondii* EGS for 18 hs or neuronal stem cells infected with *T. gondii* EGS strain for 18 hours.

FIG. 2. Host miRNA transcriptomics data during EGS infections of MM6 or NSC cells. Differential expression analysis of human miRNA genes from MM6 or NSC cells infected with *T. gondii* EGS strain for 18 hours.

FIG. 3. EGS transcriptomics data during MM6 infections. Differential expression analysis of *T. gondii* genes from MM6 cells infected with *T. gondii* EGS strain for 18 hours compared to *T. gondii* gene expression from MM6 cells infected with GT1, ME49 or VEG strains for 18 hours.

FIG. 4. EGS expression during NSC infections. Differential expression analysis of *T. gondii* genes from neuronal stem cells infected with *T. gondii* EGS strain for 18 hours compared to *T. gondii* gene expression from neuronal stem cells infected with either GT1, ME49 or VEG strain for 18 hours.

FIG. 5. EGS transcriptomics data during HFF infections. Differential *T. gondii* gene expressing analysis of human HFF cells infected with *T. gondii* EGS strain for 2 hs, 18 hs or 48 hs compared to the average *T. gondii* gene expression of human MM6 and neuronal stem cells infected with either GT1, ME49 or VEG strains of *T. gondii* for 18 hours.

FIG. 6. EGS morphology and effect on host cell transcriptomes a. EGS in human MM6 cells and NSC form cysts. Left NSC with EGS. Right MM6 with EGS. Note green dolichos cyst walls and BAG1 (red) in NSC. DAPI stained nuclei (blue). b, c, d. Effects of EGS infection on

MM6 and NSC transcriptomes: EGS transcripts in MM6 compared with NSC shows overlap of, as well as unique patterns of, transcripts. Differentially expressed genes in MM6 and NSC cells infected with EGS parasite were identified based on criteria of 1% FDR and absolute fold-change ≥ 2 . Number of DEGs in each cell line are presented with bar graph (b) and Venn diagram are used to show general comparison of DEGs identified between the two cell lines (c). There is both communality, overlap in genes modulated and independence in others between cell types indicating cell type also influences cell type. Red and green colors were used to represent up- and down-regulated genes, cell line used is indicated on bottom (b-d). Functional enrichment analysis was performed for gene ontology (GO) biological process and KEGG pathways (d). P-values derived from analysis were $-\log 10$ transformed and presented as a heat map. Pink and blue colors indicate GO terms or KEGG pathways enriched by up- and down-regulated genes, respectively. Enriched pathways or biological processes are listed on right of panels and cell lines are indicated on top. e. Host cell miR-seq analysis reveals that EGS regulates host cell miRNAs critical in pathogenesis and latency. An especially interesting down-modulated miRNA is hsa-miR-708-5p which is expressed particularly in brain and retina cells causing apoptosis⁶⁵. When *T. gondii* down-modulates this as an encysted bradyzoite in neuronal cells, it would prevent hosts from initiating apoptosis to eliminate chronically infected neurons. f Parasite genetics and human host cell type have a profound influence on *T. gondii* gene expression. MDS plot comparing *T. gondii* gene expression profiles from MM6 and NSC cells infected with EGS, GT1, ME49 and VEG strains for 18 hours and HFF cell cultures infected with EGS strain for 2, 18 and 48 hours.

FIG. 7. Differential Gene Expression (DGE) analyses and effects of inhibition of cytochrome bc1. a. DGE analysis of bradyzoite- and tachyzoite-specific markers during EGS infections of HFF cultures at 2, 18 and 48 hours (top panel), MM6 cells at 18 hours (middle panel) or NSC cultures at 18 hours (bottom panel) versus infections of same host cells with canonical strains GT1, ME49 or VEG at 18 hours (averaged across the three canonical strains for HFF infections). Genes reported as being over- or under-expressed during bradyzoite differentiation is indicated with red or green arrows respectively. “*”, q-value ≤ 0.05 ; Log FC, logarithm of the fold change in gene expression. CST1, SAG-related sequence SRS44^{S114}; LDH2, lactate dehydrogenase 2^{S115}; LDH1, lactate dehydrogenase 1^{S115}; ENO2, enolase 2; ENO1, enolase 1^{S116}; SAG1, SAG-related sequence SRS29B; BAG1, bradyzoite antigen BAG1^{S115}. b. DGE analysis of genes encoding AP2 family of transcription factor during the same infection experiments as described in (m). Red and green arrows denote AP2 genes found to be over- or under-expressed during bradyzoite development^{S117}. “*”, q-value ≤ 0.05 . c. *T. gondii* cytochrome family genes differentially expressed during same experimental infections as described in (m). “*”, q-value ≤ 0.05 . d. Effect of known cytochrome b inhibitors on EGS. Morpholino conjugated to a Vivoporter (called PPMO) designed to knock down cytochrome b compared with off target control has a significant effect in reducing replication of YFP RH strain tachyzoites at 5 and 10 μM ($p < 0.05$) but only a very small effect on size and number of EGS cysts in HFF. As a poorly soluble inhibitor of cytochrome b, ELQ271 was reported to partially reduce cyst numbers in mice²⁷ and is shown herein also to reduce the EGS cysts in vitro at 10 μM in this novel model. This demonstrates the utility of this novel in vitro model by indicating that inhibition of

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cytochrome b Qi is associated with reduction of cysts in vivo in a mouse model, even when there are serious limitations caused by insolubility of this inhibitory compound. This poor solubility significantly limits ELQ271 as a candidate for progression to a medicine. Increasing selectivity for the parasite enzyme with our new scaffold is another critical challenge.

FIG. 8. a. Structures of the ELQ class (1-3) and the tetrahydroquinolone scaffold (4).^{27,45,49,53} Low solubility of the ELQs has been a serious concern going into preclinical evaluation for treatment of malaria.²⁷ b. *Saccharomyces cerevisiae* cytochrome bc₁ X-ray structure (PDB ID: 1KB9)⁵ The complex contains 11 subunits and 3 respiratory subunits (cytochrome b, cytochrome c1 and Rieske protein). The cytochrome b subunit provides both quinone binding sites (Q_o and Q_i) highlighted as grey and pink surfaces respectively.

FIG. 9. ELQ inhibitors provide a new scaffold and approach yielding compounds that are potent inhibitors of tachyzoites and cysts in vitro. a-e. Study of Inhibitors in vitro is summarized in Table 2 and led to selection of MJM170 as a promising novel scaffold for both tachyzoites and bradyzoites. a. MJM170 markedly reduces RH YFP tachyzoites in tissue culture robustly at low nanoM levels. (Standard curve left and effect on RH YFP, right panel). b,c. MJM170 markedly reduces EGS bradyzoites in cysts in vitro. Inhibition of cytochrome b Qi eliminates cysts in HFF infected with EGS. Without inhibitory compound in HFF (note, oval cyst with green border staining dolichos) and adjacent panel with inhibitory MJM170 compound (note absence of cysts with small amount of amorphous residual dolichos). MJM170 eliminated tachyzoites followed to 10 days of culture and bradyzoites in cysts in vitro. Summary comparison of each of the compounds tested in vitro and their ADMET is in Table 2. Note improvement in solubility, properties amenable for compounds to cross blood brain barrier with new scaffold. d. EGS transfected with stage specific reporters for fluors, red tachyzoite SAG1, Green bradyzoite LDH2.

FIG. 10. MJM170 is also effective against RH and Prugneaud tachyzoites and Me49 bradyzoites, in vivo with translucent zebrafish providing a novel model with potential for scalable in vivo assays in which tachyzoites with fluorescent reporters and bradyzoites in cysts can be visualized efficiently. a: 25 mg/kg daily MJM170 administered intraperitoneally eliminates active infection due to RH tachyzoites stably transfected with YFP in mice (RFU control vs rx with MJM 170, p<0.004). For the standard curve in the inset, RFU increase with increasing concentrations of fluorescent tachyzoites (R²=0.99). b. MJM 170 25 mg/kg daily reduces Type 2 parasites. c. MJM 170 reduces cysts in mice infected 2.5 months earlier and treated for 17 days with 12.5 mg/kg daily then without compound for 3 days:cyst count of wet prep of brain homogenate. d. Zebra fish can be used to visualize fluorescent tachyzoites and cysts in more chronic infections.

FIG. 11. MJM170 targets apicomplexan cytochrome bc₁ Qi: modelling, yeast surrogate assays, target validation, co-crystallography and nanoM inhibition of *P. falciparum* and *T. gondii* a. Modeling: MJM170 (yellow) modelled within cytochrome b Q_i site (grey) highlighting residues (green) involved in binding. b. Mutations for yeast, *P. falciparum*, predicted for *T. gondii* and bovine enzyme. Relevant mutations are indicated by colored dots in Q_i domains on the bottom of the image of mitochondrion membrane for *S. cerevisiae* and *P. falciparum*, and where those amino acids are in *T. gondii*, human and bovine

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enzymes. Red dot marks G33A/V in Q_i domain of *P. falciparum*. c. Cytochrome b mutants and sequence accession numbers. d. MJM 170 inhibits wild-type but not mutant yeast. Compounds MJM 170 and ELQ 271 with wild type and mutant yeast validate predictions that M221 K/Q would create a steric clash and resistance. e. MJM170 is a potent low nM inhibitor of *Plasmodium falciparum*. In Table 2, wild type *P. falciparum* also are tested and is inhibited at <50 nM by this scaffold. D6 is a drug sensitive strain from Sierra Leone, C235 is a multi-drug resistant strain from Thailand, W2 is a chloroquine resistant strain from Thailand, and C2B has resistance to a variety of drugs including atovaquone. Mutant G33V did not confirm prediction of a steric clash. f. MJM170 binds within Q_i site of bovine cytochrome bc₁ as shown by X-ray crystallography. f(i). An omit Fo-Fc electron density map (green) at 5σ allows unambiguous positioning of MJM170 (magenta) within the Q_i site with the tetrahydroquinolone group near heme b_H (white) and diphenyl ether directed out of the channel. f(ii)-MJM 170 molecule is included into the structure, the 2Fo-Fc electron density map at 1σ (grey) allows placement of the planar head between heme b_H and Phe220 with the carbonyl group positioned in a polar region surrounded by Ser35 and Asp228. g. A stereo picture of the 2Fo-Fc electron density map. Electron density at 1σ level around cytochrome b α-helices 118-128 and 183-199 close to MJM180 compound in X-ray structure of cytochrome bc₁. Inset: Crystal of mammalian cytochrome bc₁ complex.

FIG. 12. MJM170 potently inhibits *P. falciparum* mitochondrial electron transport important for synthesis of pyrimidines, is modestly synergistic with atovaquone, additive with cycloguanil and antagonistic with Q_i inhibitor. a. MJM170 is highly potent (Dd2, black curve, EC₅₀=29.5 nM) without cross-resistance in previously reported cytochrome b drug-resistant mutant parasite lines including ubiquinone reduction site mutants (Dd2^{G33A} and Dd2^{G33V}, light blue and dark blue curves, respectively). Dose-response curve from representative assay. MJM170 cannot inhibit a parasite supplemented with a yeast cytosolic DHODH (scDHODH, green curve) demonstrating that its primary activity in *P. falciparum* is to inhibit electron transport necessary for pyrimidine biosynthesis. Inset Table. Dose-response phenotypes of a panel of *P. falciparum* cytochrome b mutant parasite lines. EC₅₀ values were calculated using whole-cell SYBR Green assay and listed as mean±standard deviation of three biological replicates, each with triplicate measurements. b., c. Isobolograms with MJM170 plus atovaquone or cycloguanil or Q_i inhibitor BRD6323: b. Combinations were with atovaquone (ATV) or cycloguanil (CYG) at multiple fixed volumetric ratios (10:0, 8:2, 6:4, 4:6, 2:8, and 0:10) in Dd2 parasites. Slight synergy observed with combinations of MJM170 and atovaquone while MJM170 and cycloguanil dosed in combination showed additive effect. Fractional inhibitory concentrations (FIC) for each drug were calculated and plotted. Shown is a representative isobologram for each combination of compounds. Table below lists FICs for each compound and ratio tested (values are mean from three independent assays±standard deviation). Synergy was defined as a combined FIC <1.0, additivity as FIC=1.0, and antagonism as FIC >1.0. c. Isobologram Figure: MJM170 was tested in combination with previously reported reduction site inhibitor BRD6323 at multiple fixed volumetric ratios (10:0, 8:2, 6:4, 4:6, 2:8, and 0:10) in Dd2 parasites. Antagonism was observed with combinations of MJM170 and BRD6323, another bulky inhibitor of cytochrome bc, as opposed to synergy observed with oxidation site inhibitor atovaquone.

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Fractional inhibitory concentrations (FIC) for each drug were calculated and plotted. Representative isobologram of three independent assays is shown. Table below lists FICs for each compound and ratio tested (values are means from three independent assays $\pm$ standard deviation). Definitions as in b.

FIG. 13. Effects of compounds against RH-YFP. Graph is a representative example of an experiment testing two of the compounds against tachyzoites (RH-YFP). On the vertical axis is fluorescence in relative fluorescence units, where decrease in fluorescence compared to the DMSO control indicates parasite inhibition. On the horizontal axis are the different treatment conditions.

FIG. 14. The results of a cytotoxicity assay. 10 μ M solution of compound was compared to the DMSO control closest to 0.1% DMSO (0% DMSO) and the 50 μ M solution was compared to the DMSO control closest to 0.5% DMSO (0.625% DMSO). The differences were not found to be statistically significant.

FIG. 15. Effects of compounds against EGS. a-c) Graphs comparing the effects of JAG050 and JAG021 on EGS.

FIG. 16. Binding assays show selectivity with binding to the bovine enzyme which is not as robust as has been seen with other cytb inhibitors

FIG. 17. JAG21 is a mature lead that protects against *Toxoplasma gondii* tachyzoites and cures *Plasmodium berghei* sporozoites, blood and liver stages with oral administration of single dose 2.5 mg/kg and 3 doses protect at 0.5 mg/kg. Single dose causal prophylaxis in 5 C57BL/6 albino mice at 2.5 mpk dosed on day 0, 1 hour after intravenous administration of 10,000 *P. berghei* sporozoites. 3 dose causal prophylaxis treatment in 5 C57BL/6 albino mice at 0.6 mpk dosed on days -1, 0, and +1. A representative figure for higher dose (5 mg/kg) is shown, but all experiments with the amounts mentioned above had efficacy measured as cure measured as survival, luminescence and parasitemia quantitated by flow cytometry are similar to these.

FIG. 18. Tafenoquine and JAG21 are both needed to contain RPS 13A. One additional mouse in the tafenoquine and JAG21 died outside the time on this graph others remained healthy.

FIG. 19. Serum biomarkers from boys with active brain disease due to *Toxoplasma* reflect infection and neurodegeneration. a. Tabular clinical summary: Three pairs of children, matched demographically; one in each pair had severe disease and one mild or no manifestations. One pair dizygotic, discordant twins. Each ill child had new myoclonic or hypsarrhythmic seizures. Two children had T2 weighted abnormalities on brain MRIs similar to active inflammatory and parasitic disease in murine model⁸ b-e. Protein and miR serum biomarkers: Panel of nanoproteomics and miR sequencing performed on serum obtained at time of new illness. MiRNA concentration measured and difference in concentration graphed. Abundance of peptides measured. Note: Presence of markers of neurodegeneration, inflammation, and protein misfolding include clusterin, diminished ApoJ, serum amyloid, and oxytocin in ill children compared with their healthy controls.

FIG. 20. List of up-regulated or down-regulated genes involved in specific host cell pathways or indications.

FIG. 21. List of exemplary proteins important for apicomplexan parasite bradyzoite development and/or survival in the host.

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stated, the techniques utilized may be found in any of several well-known references such as: *Molecular Cloning: A Laboratory Manual* (Sambrook, et al., 1989, Cold Spring Harbor Laboratory Press), *Gene Expression Technology* (Methods in Enzymology, Vol. 185, edited by D. Goeddel, 1991. Academic Press, San Diego, Calif.), "Guide to Protein Purification" in *Methods in Enzymology* (M. P. Deutscher, ed., (1990) Academic Press, Inc.); *PCR Protocols: A Guide to Methods and Applications* (Innis, et al. 1990. Academic Press, San Diego, Calif.), *Culture of Animal Cells: A Manual of Basic Technique, 2nd Ed.* (R. I. Freshney. 1987. Liss, Inc. New York, N.Y.), *Gene Transfer and Expression Protocols*, pp. 109-128, ed. E. J. Murray, The Humana Press Inc., Clifton, N.J.), and the Ambion 1998 Catalog (Ambion, Austin, Tex.).

As used herein, the singular forms "a", "an" and "the" include plural referents unless the context clearly dictates otherwise. "And" as used herein is interchangeably used with "or" unless expressly stated otherwise.

As used herein, the amino acid residues are abbreviated as follows: alanine (Ala; A), asparagine (Asn; N), aspartic acid (Asp; D), arginine (Arg; R), cysteine (Cys; C), glutamic acid (Glu; E), glutamine (Gln; Q), glycine (Gly; G), histidine (His; H), isoleucine (Ile; I), leucine (Leu; L), lysine (Lys; K), methionine (Met; M), phenylalanine (Phe; F), proline (Pro; P), serine (Ser; S), threonine (Thr; T), tryptophan (Trp; W), tyrosine (Tyr; Y), and valine (Val; V).

All embodiments of any aspect of the invention can be used in combination, unless the context clearly dictates otherwise.

In one aspect, the invention provides cell lines infected with an apicomplexan parasite, wherein the apicomplexan parasite genome comprises a gene encoding an Apetela 2 IV-4 protein with an M $\Rightarrow$ I modification at residue 570 ("AP2 IV-4 M570I") compared to its orthologous gene on the reference *T. gondii* ME49 strain (gene ID: TGME49_318470). As described in the examples that follow, Apetela 2 (AP2) IV-iv is known to be a bradyzoite gene expression repressor⁵⁶, and the AP2 IV-4 M570I mutant results in an apicomplexan parasite that remains as a bradyzoite in tissue cultures passaged extensively, capable of producing oocysts when administered to cats definitively proving its true bradyzoite phenotype.

As further described in the examples that follow, critical flaws and limitations of available methods and models for developing medicines to cure apicomplexan infections, such as *T. gondii* infections, include lack of in vitro culture systems for cysts and scalable, easy to use animal models for screening compounds. The cell lines of this aspect of the invention unexpectedly possess a true, dormant parasite phenotype in tissue culture and can be used, for example, to screen for drugs that can be used to treat apicomplexan parasitic infections, as well as a research tool for studying apicomplexan parasites in the dormant phenotype. The cell lines can be used, for example, as a model of bradyzoite infection. A generalized apicomplexan life cycle comprises a rapidly growing tachyzoite and slow-growing, latent bradyzoite that forms tissue cysts (i.e.: dormant phenotype). Such dormant parasites are present in the brains of 2 billion persons worldwide across their lifetimes and are incurable. Quite remarkably, the inventors have discovered that in human cells this encysted parasite turns on host cell pathways important for altering ribosomal function, mis-splicing of transcripts, oxidative pathways, and, those pathways found to be altered in Alzheimer's and Parkinson's diseases. Extensive details on the model are described in the examples that follow.

DETAILED DESCRIPTION OF THE INVENTION

All references cited are herein incorporated by reference in their entirety. Within this application, unless otherwise

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In one embodiment, the apicomplexan parasite genome comprises a gene encoding AP2 IV-4 M570I that further differs from its orthologous gene on the reference *T. gondii* ME49 strain (gene ID: TGME49_318470) in encoding the amino acid sequence GGNRPHYH-
VAKQEWVRVRYMNGKRMRTYSAKFYGYETAHT-
MAEDFAHYVDKH E (SEQ ID NO: 1) beginning at residue 821. In a further embodiment, the gene encoding AP2 IV-4 M570I encodes the following amino acid sequence, or functional equivalents thereof:

(SEQ ID NO: 2)
MAAPAPSAEAPAKRRCPFLPRETPVSSSEDETRKTLQHDTLGCCLPRSS
SGQPELAASAASQVGHLSAALLQLVQTSAGGVPQAVLRNLFSSIH
RNPKPLPANALAAPNSSLYASLTSLSSAAALPGAGPAYSQAPSPASA
DLLQSEQFGSAAKNPSPNEASPIALALLGEAARAATTPTVPALSAVCP
AASSGVSLPSASDTLALAQSSLSSTGCASDVKASRPEEHPAFASGTA
NRQSLQLQALLLSTAPLAFSGPLSSASTTLPASSGAVSSRNAGAYQFE
RLQLQAEAAKVALLPNATSKMSQSSVPQRDLTRKTSLFDPGRGLSAD
DASRRYNTRGANS GGAGLRGTGVHATTEQSGALDAGERTRPFGAGED
ESAQKGPDSRGRQRPALDASNILGLLAAFQPSQAPAIRDLSPASHLS
AAATGALPLTASFTASALASSQCLPAGTPASSASPPFSEVLSTTEES
STTKETDASASTLLAFLOKYSASVSLGGASDFLGQLQKGSLLPPLSLA
EPSSALPSSFLGSDGGTIDTRNGNGEKTTPPIHLFQSAFRIPSPSQQ
NLLDALLASSCTTATSRSDGSGNLGCPVVDERNAKLAGPAHLPCSF
QISSSSGEPGRKTGGRVHRQGTSSQSGRVRSGKNGGSAAPRQSSSEN
VPSTPTVSSHEAPHRAGFPSTPYELASPSHQLDLLRLGAFLLGGAGK
QDASVHSDGTGLSGEPSHRSCSLSRGLTQESVLQLSDTTSTSRGEP
NEPSQGCNVAAASLPAGFPQPSGGAAKAREGRGAGGAGAAPVPLRA
DVTLLGGNRPHYHVAKQEWVRVRYMNGKRMRTYSAKFYGYETAHTMAE
DFAHYVDKHEALPDMMMTAMMLQAQANSAASSGQTVPLARGIRASSA
SAGAGGHVSKSATKGSVAASSEGSTSMGSDATRSQEGEAELCPLAAG
LSRPLASMHSAAGNAVAQGRQESKEEAPGGQAWFGEPGKFRASSEAL
CGSGSSAEGRDGHSEVLWATLGKVHDASQGGKIKPEKPLTVARGRLA
LGAEDKSNQLGVDLDGSGGAQGLPGVRQPRQMKNSEECSLRSDSKGMA
LSKRFGFLPSQTPSCDSMTLPFPGGFDALSLSALSSCASLPVAHEGN
NFQKGHTGDIVALASQSGTQRPASVVLSDANVSGSSPSHPTWQREGA
AVSGRADEFSSLSVTPSTVPLSSFTMEDIKGEEGDPSRRFALVGESMK
NVSAPFVQALFPTSSIANAELLPVDFLHNSCSDAKLESSIPRGLAGN
NPSMTATAVAATAVSHQIFDITTLFGEFLREFAKEKVNFEFHEYGLEAS
PLTVEASPEVSLFGKATPGRCVPAGGSTPAGISKMSGETLSGLSASEL
SLVSARTNTTTTGEQFALARGLFPGDSEGRDEKPKQLSQQELLVLSSH
ALVNLTSSSTYVLMHTLKASLSKSTEAVQLHQPLLEAASEAKATDEAKT
REEQESSECDHEYPGSSLEATTGALPRLSPALSASSKDLPLSLSASA
SLESVTPFAGLPLEEGTLSASVGLASSDDEHDTSLLFKTEAAKKRSLF

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-continued

STAADGDESRTYNDGLGQPMEEIIRSCVSTSCGEAVATTTLSAIGPGT
GASGALLDSESRESLGEKPGAALRAGAHTPAPSRAPTPSRTFSSTSS
5 TATSALLCDSNVVHEKLSAQKGDSEAGERKGDSEKEEVEEMWKEEDE
EVQRCCTGSAETDSTEATRGEAWRRGKQSEKKPSVITLNLLETHRH
LALTISQLKRPVAQQLRFILPIAAPQLLPCILPPASFQGTGESGDGKA
10 EAEAKGSSSLGQVLETALGHGTRLAPSASAMVPPRKDEAASAVPEAKT
LTGLANAGVTREASRTLEAEQVSRKRSREEVVDSETAGDEGDMENVP
ETRDGTTTRPGSRQYDTSPSNDGTPKATAKSRVIRDQAALERLLLP
15 QDTPCSCCTDRPCPCDRQQVADMIYLFYAVPARQQAESSKEGSTQRLQ
FAARDTNERKDARTGEETQGGETEAKVIRDPEERGVCESGSSQNAHT
QFDAETASSMSSDPRADKESNAQDAHMADKTSFVSDLPQPSGEFAPS
LLSETSLDVAMADSRGTPSEIHGFFTRSDQKRASFSSSSLLAAGHAV
20 ASFSSSLAGVVSGAGERRECAGPSLGDLSLIGLLSLSYPAMLAFILPL
QSLHHTVSGMILTLLHKKLIHRFICAHRLRLVLDMMRRPAGGALKSRGA
HGDTEAAEAQVERRRREHEREETNLAIYGREGNAEAANTFPLVDTVS
25 SLLSPGSLRQENSEVERRDNDDEERLELITGIARESPKPKSKDSVSPFL
STAPCPGTEAESSDCSASSACSGTPTGTEGETGDIASFLSPSGEVK
QTIMLA
30

The mutations at residue 570 and beginning at residue 821 compared to the Apetela 2 IV-4 orthologous protein encoded by the reference *T. gondii* ME49 strain (gene ID: TGME49_318470) are presented in bold font and underlining in the above sequence. A “functional equivalent” is a gene encoding an Apetela 2 IV-4 protein that is at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence provided above, includes the noted mutations at residue 570 and beginning residues 821-874, and that does not represses bradyzoite gene expression in a tachyzoite in an apicomplexan parasite.

As used here, “apicomplexan parasites” are a phylum of the kingdom Protista (formerly a division of protozoa called Sporozoa); named for a complex of cell organelles (apical microtubule complex) at the apex of the sporozoite form that can penetrate host cells. It includes, but is not limited to, the medically important genera *Plasmodium*, *Toxoplasma*, *Cryptosporidium*, and *Isospora*. Thus, in one embodiment, the apicomplexan parasite is selected from the group consisting of *Plasmodium*, *Toxoplasma*, *Cryptosporidium*, and *Isospora*. In a specific embodiment, the apicomplexan is a wild type, mutant, or recombinant *Toxoplasma gondii* strain. In various further embodiments, the apicomplexan parasite is *Toxoplasma gondii* of clade B.

In another embodiment, the apicomplexan parasite is a G0 arrested parasite, including but not limited to a *Toxoplasma gondii* strain RPS 13 delta (Hutson et al., PLoS One. Nov. 22, 2010; dx.doi.org/10.1371/journal.pone.0014057). This cell line can be used, for example, to identify companion compounds for THQ that eliminate the G0 arrested stage of *T. gondii* along with the active and the slowly growing bradyzoite stage.

In another embodiment, the apicomplexan parasite is *Toxoplasma gondii* strain EGS (ATCC® Number:PRA-396™). As described in the examples that follow, the EGS

strain was extensively characterized in vitro to show that true cysts develop, making the EGS strain especially useful for drug development.

In all embodiments of this aspect of the invention, the cell line can be any suitable cell line capable of supporting apicomplexan parasitic infection, including but not limited to mammalian cells (mouse, rat, human, etc.), zebrafish cells, etc. In one specific embodiment, the cell line is a human cell line; exemplary human cell lines for use in this aspect of the invention include, but are not limited to fibroblasts, stem cells, neurons, monocytes, and ocular cells 9 including primary human cells). As described in the examples that follow, the apicomplexan parasites form cysts in the host cell lines that enlarge over time and then destroy host cell monolayers as single cell organisms. As such, the cell lines of the invention are extremely useful as in vitro models of apicomplexan parasite infection. Such models can be used, for example, to test for candidate compounds that inhibit cyst formation and/or destruction of host cell monolayers; such candidate compounds would be useful in treating apicomplexan parasite infection.

In another embodiment, the apicomplexan parasite genome is recombinantly engineered to express a reporter polypeptide, including but not limited to fluorescent or luminescent proteins. This embodiment permits ready visualization of the parasite and facilitates automated quantitative analysis. In one embodiment, the reporter polypeptide is operatively linked to a promoter that is activated in the bradyzoite stage or a promoter that is activated in the merozoite stage. Any suitable promoter that is activated in the bradyzoite stage or merozoite stage may be used. In one embodiment the promoter that is activated in the bradyzoite stage is the *T. gondii* BAG1 encoding gene promoter or a functional equivalent thereof. The BAG1 promoter sequence can be obtained as disclosed in Bohne et al., Molecular and Biochemical Parasitology 85 (1997) 89-98. In one embodiment, the BAG promoter comprises SEQ ID NO:3, or functional equivalent thereof, from the *T. gondii* VEG strain.

A "functional equivalent" of the BAG1 promoter is a promoter from any strain of *T. gondii* that promotes expression of BAG1 in the VEG strain, as well as an promoter nucleic acid sequence that is 50%, 60%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:3 and drives expression of a BAG1 gene in a *T. gondii* strain.

As described in the examples that follow, the cell lines of the invention can be administered to/ingested by non-human animal models to provide an in vivo model of apicomplexan parasitic infection that develop the classic, gold standard bradyzoite phenotype of producing oocysts. This, in another aspect, the invention provides non-human animal models of apicomplexan parasitic infection, comprising a non-human animal that has ingested or otherwise comprises the cell line of any embodiment or combination of embodiments of the invention. In one embodiment, the non-human animal produces oocysts. Any suitable non-human animal model that produces oocysts can be used, including but not limited to cats.

In another aspect, the invention provides non-human animal models of apicomplexan parasitic infection, comprising a non-human animal that has ingested or otherwise comprises oocysts produced by the non-human animal model that has ingested or otherwise comprises the cell line of any embodiment or combination of embodiments of the invention. As described in detail in the examples that follow, oocysts given to non-human animal models such as mice created an illness and histopathology phenotypically char-

acteristic for typical, virulent parasites causing dose related proliferation of the parasite (exemplified by *T. gondii*) with necrosis in terminal ileum, pneumonia at 9-10 days, with brain parasites by 17 days and dose-related mortality. Thus, the non-human animal models of this aspect of the invention are particularly useful in screening for drugs to treat the effects of apicomplexan parasite infection.

As will be understood by those of skill in the art, the oocysts do not need to be isolated prior to ingestion; they may be present, for example, in tissue (including but not limited to brain tissue) taken from the non-human animals that have ingested or otherwise comprise the cell lines of the invention, which then produce oocysts. Any suitable non-human animal model can be used, including but not limited to mice, rats, cats, zebrafish, non-human primates, cattle, sheep, and pigs. In one specific embodiment, the non-human animal is a mouse.

In another aspect the present invention provides methods of identifying compounds for treating an apicomplexan parasitic infection, comprising contacting one or more test compounds to the cell line of any embodiment or combination of embodiments of the invention, wherein those positive test compounds that reduce bradyzoite cyst amounts in the cell line are candidates to treat an apicomplexan parasitic infection. As disclosed above, the cell lines of the invention unexpectedly possess a true, dormant parasite phenotype in tissue culture and can be used to screen for drugs that can be used to treat apicomplexan parasitic infections. Any reduction in bradyzoite cyst amounts in the cell line indicates that the test compound may be useful for treating an apicomplexan parasitic infection. In various embodiments, positive test compounds are those that reduce bradyzoite cyst amounts by at least 5%, 10%, 15%, 20%, 25%, 50%, 75%, 90%, or more.

In another aspect the present invention provides methods of identifying compounds for treating an apicomplexan parasitic infection, comprising administering one or more test compounds to the animal model of any aspect or embodiment of the invention, wherein those positive test compounds that reduce one or more symptoms of the infection and/or reduce parasitic titer in the animal model are candidates to treat an apicomplexan parasitic infection. In one embodiment, those positive test compounds that reduce oocyst production and/or reduce bradyzoite cyst amounts in the animal model are candidates to treat an apicomplexan parasitic infection. Any reduction in oocysts production and/or bradyzoite cyst amounts indicate that the test compound may be useful for treating an apicomplexan parasitic infection. In various embodiments, positive test compounds are those that reduce oocysts production and/or bradyzoite cyst amounts by at least 5%, 10%, 15%, 20%, 25%, 50%, 75%, 90%, or more.

In one embodiment of any of the methods of identifying compounds for treating an apicomplexan parasitic infection of the invention, positive test compounds are candidates for treating *Toxoplasma gondii* or *Plasmodium falciparum* infection, including drug resistant strains and or other plasmodial infections. The methods can be used to test any suitable type of candidate compound, including but not limited to polypeptides, antibodies, nucleic acids, organic compounds, etc. Treatment effects of the test compounds may be assessed relative to a suitable control, such as the cell lines or non-human animal models of the invention that are not treated with the test compound. It is well within the level of those of skill in the art to determine a suitable control in light of the teachings herein.

In one specific embodiment, the cell line, or non-human animal model that has ingested or otherwise comprises the cell line, comprises a G0 arrested parasite (such as RPS 13 delta) and is used to identify companion compounds for tetrahydroquinolones (THQ) that eliminate the G0 arrested stage of an apicomplexan parasite, such as *T. gondii*, along with the active and the slowly growing bradyzoite stage.

RPS 13 Δ is a genetically engineered conditional knockout parasite that has a unique transcriptome documenting its G0 state, G1 arrest in the absence of tetracycline but grows normally in the presence of tetracycline which removes the repressor from the promoter. The method may utilize, for example, a system that when there is no anhydrotetracycline to remove the engineered tetracycline responsive repressor from the 4 tetracycline response elements engineered in tandem in the promoter; these parasites persist in tissue culture for long times (months). This embodiment is based on the observation that this conditional knockout RPS13 delta parasite when it is in its arrested in G1 state is not susceptible to the effect of any inhibitors that effect processes essential to the tachyzoite or bradyzoite form including those tested in vitro so far. In this embodiment the conditional knockout RPS13 delta parasite is amenable to testing inhibitors of hypnozoite like organisms by culturing them without tetracycline in the presence of the compound and determining whether any parasites can be rescued by adding tetracycline to determine whether they are still capable of persisting and becoming tachyzoites that grow rapidly in the presence of tetracycline. Furthermore, the methods may comprise testing RPS13 delta in mice, and involves the observations that when RPS13 delta is administered to wild type mice without tetracycline the RPS13 delta parasite induces a protective immune response as a vaccine dependent on interferon gamma and has no adverse effect on the mice, nor can it be rescued with tetracycline or inhibitors of iNOS (intracellular nitrogen oxide synthase) such as LNAME (L-N^G-Nitroarginine methyl ester) which abrogate effects of interferon gamma after 7 days. For example, that in interferon gamma knock out mice or mice treated with antibody to interferon, RPS13 delta is lethal for the mice, where the attenuated organism persists, can be observed, until mice succumb slowly. Another example may be a SCID mouse or a steroid treated mouse that is more susceptible due to immune compromise.

In another embodiment, RPS13 delta can be used to test compounds in vitro against this G0 truly dormant stage, and against compounds that can target the hypnozoite state but that must be metabolized in the liver to produce toxic electron containing compounds in vivo.

In all these embodiments, the methods can be used to determine if compounds have parasitocidal effects on hypnozoite forms and be used in conjunction with THQ compounds, such as tafenoquine, known in primate models and in humans as the only compound besides primaquine which has a lethal effect on the malaria hypnozoite in primates or in humans. However, tafenoquine is not active against actively proliferating organisms and requires a compound that is effective against more rapidly and slowly growing forms to produce radical cure of malaria.

In another embodiment, the THQ compound may be primaquine, a compound that has a similar effect when metabolized and is ineffective against *T. gondii* tachyzoites in tissue culture and can therefore be utilized in the same manner as tafenoquine to inhibit the hypnozoite form of apicomplexan parasites to produce radical cure.

Compounds identified using the methods of these various embodiment of the invention can be used together the THQ

compound(s) to treat/cure the active tachyzoite, the slowly growing bradyzoite, and the G0 arrested hypnozoite-like phase of the apicomplexan infections the active tachyzoite, the slowly growing bradyzoite, and the G0 arrested hypnozoite-like phase of the apicomplexan infections

As described in detail in the examples that follow, the inventors carried out transcriptome analysis of both the apicomplexan parasite and the host cells after parasite infection of the host cells. The resulting transcriptomes provide a signature for apicomplexan parasites (such as *T. gondii* strains EGS), which helps in identification of targets for drug development, as well as a signature for infected host cells (such as human foreskin fibroblasts (HFF) human monocytic cells (ex: MM6), and human primary neuronal stem cells (NSC)), which helps in identification of targets for treating apicomplexan infection. As shown in the examples, EGS transcription was influenced by host cell type (FIG. 6). Transcriptomics using host mRNA and miR profiling of EGS cultures in MM6, and NSC cells for 18 hours demonstrated that this parasite modulates host transcripts involved in protein misfolding, neurodegeneration, endoplasmic reticulum stress, spliceosome alteration, ribosome biogenesis, cell cycle, epilepsy, and brain cancer among others (FIG. 6). The number of genes significantly up or down regulated in MM6 and NSC cells compared to uninfected controls are depicted in FIG. 6. Overexpressed genes differ from those of GT1, ME49 and VEG tachyzoite-infected human NSC cells, but modify the same or connected pathways. Hsa-miR-708-5p was the most affected miRNA (down-modulated) by EGS (FIG. 6e. miR-708-5p is a regulator that promotes apoptosis in neuronal and retinal cells, which could maintain a niche for EGS-like encysted bradyzoites to persist.

The genes identified in the host transcriptome study are thus targets for anti-parasite therapy, as well as markers of apicomplexan parasite infection (such as *T. gondii* infection). In various embodiments, the invention may thus comprise methods for treating an apicomplexan parasite infection (such as a *T. gondii* infection), comprising administering to a subject in need thereof an amount effective to treat the infection of an inhibitor (of up-regulated genes) or an activator (of down-regulated genes) of 1 or more (i.e.: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) of the up-regulated genes listed in FIG. 1 (protein encoding genes) or FIG. 2 (miRNA). In various non-limiting embodiments, the inhibitor is selected from the group consisting of a target-specific inhibitory antibody, aptamer, siRNA, shRNA, antisense oligonucleotide, or small molecule.

In one embodiment, the target is miR-708-5p. In various further embodiments the targets are one or more of the genes listed in Table 1 below, or from FIGS. 20-21, which provide a more complete list of up-regulated or down-regulated genes involved in specific host cell pathways or indications. The table shows up-regulated or down-regulated genes involved in specific host cell pathways or indications ("KEGG pathway"), such as systemic lupus erythematosus, (SLE), Parkinson's disease, etc. In an exemplary embodiment, the methods comprise administering to the subject in need thereof an inhibitor (of up-regulated genes) or an activator (of down-regulated genes) of one or more (1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or all 13) of genes HIST2H2AA3, HIST1H2AC, HIST1H2BC, ACTN4, SNRPD3, ELANE, CIR, HIST1H2BK, H2AFZ, SNRPB, H2AFX, CTSG, and HIST1H4H, to treat apicomplexan parasite infection-associated SLE. One of skill in the art will understand from the table that the methods may be used to treat apicomplexan parasite infection-associated Parkinson's, Huntington's dis-

ease, Alzheimer's disease, etc. using an inhibitor (of up-regulated genes) or an activator (of down-regulated genes) against 1 or more (i.e., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or more, such as all) of the target genes listed for the specific indication. Similarly, one of skill in the art will understand from the table that the methods may be used to treat apicomplexan parasite infection-associated disorders relating to ribosomal assembly, spliceosome assembly, oxidative phosphorylation, etc. using an inhibitor (of up-regulated genes) or an activator (of down-regulated genes) against 1 or more (i.e., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or more, such as all) of the target genes listed for the specific indication.

TABLE 1

KEGG id	KEGG pathway	P-value	Genes
hsa03010	Ribosome	4.6E-07	RPL35A, RPL36A, RPL35, RPS9, RPL27, RPS27L, RPL38, RPS25, RPS27, RPL30, RPL23, RPS29, RPL21, RPS20, RPS21, UBA52, RPL36AL
hsa05322	Systemic lupus erythematosus	0.00082	HIST2H2AA3, HIST1H2AC, HIST1H2BC, ACTN4, SNRPD3, ELANE, C1R, HIST1H2BK, H2AFZ, SNRPB, H2AFX, CTSG, HIST1H4H
hsa04621	NOD-like receptor signalling pathway	0.01458	IL6, CCL2, XIAP, NFKBIB, NFKBIA, TNFAIP3, BIRC3, CCL5
hsa03040	Spliceosome	4.1E-06	SNRPA1, CCDC12, MAGOH, SNRPD3, LSM6, LSM7, SNRPB2, SNRPD2, PPIH, SNRPB, PQBP1, SYF2, LSM5, U2AF1, MAGOHB, THOC2, SNRPF, SNRPE, SNRPG
hsa00190	Oxidative phosphorylation	6.4E-16	ATP5E, NDUFB4, ATP6V0E1, NDUFB6, NDUFB9, COX7C, ATP6V1G1, ATP5G1, UQCQRQ, NDUFB1, NDUFB2, NDUFSS, NDUFSS4, ATP5L, NDUFSS3, COX17, ATP5H, ATP5J, NDUF4A, NDUF45, NDUF42, NDUF43, COX7A1, NDUF46, COX8A, NDUF42, NDUF41, NDUF41, ATP6V1F, NDUFV2, COX6A1, UQCRB
hsa05012	Parkinson's disease	2.4E-14	ATP5E, NDUFB4, NDUFB6, NDUFB9, COX7C, ATP5G1, UQCQRQ, NDUFB1, NDUFB2, NDUFSS, NDUFSS4, HTRA2, NDUFSS3, ATP5H, ATP5J, NDUF4A, NDUF45, NDUF42, NDUF43, COX7A1, NDUF46, COX8A, NDUF42, NDUF41, UBE2L3, NDUF41, VDAC3, NDUFV2, COX6A1, UQCRB
hsa05016	Huntington's disease	2.2E-13	ATP5E, NDUFB4, POLR2F, NDUFB6, POLR2K, NDUFB9, POLR2J, COX7C, ATP5G1, UQCQRQ, NDUFB1, NDUFB2, NDUFSS, NDUFSS4, TGM2, CREB3L1, NDUFSS3, ATP5H, ATP5J, NDUF4A, NDUF45, NDUF42, NDUF43, COX7A1, NDUF46, COX8A, NDUF42, NDUF41, NDUF41, VDAC3, SOD2, NDUFV2, COX6A1, UQCRB
hsa05010	Alzheimer's disease	9E-11	ATP5E, NDUFB4, NDUFB6, NDUFB9, COX7C, ATP5G1, UQCQRQ, NDUFB1, NDUFB2, NDUFSS, NDUFSS4, PPP3CA, NDUFSS3, ATP5H, ATP5J, NDUF4A, NDUF45, NDUF42, NDUF43, COX7A1, NDUF46, COX8A, NDUF42, NDUF41, ITPR3, NDUF41, NDUFV2, COX6A1, UQCRB
hsa04623	Cytosolic DNA-sensing pathway	0.0077	MAVS, IL6, POLR3K, NFKBIB, IRF7, NFKBIA, POLR1C, CCL5

In one embodiment, the invention provides methods for treating an apicomplexan parasite infection, comprising treating a subject with an apicomplexan parasite infection an amount effective to inhibit activity or expression from the apicomplexan parasite of one or more proteins listed in FIG. 21.

In another embodiment, the invention provides methods for identifying a compound to treat an apicomplexan infection, comprising identifying a compound that inhibits activity or expression of one or more proteins listed in FIG. 21

from an apicomplexan parasite present in an infected host cell.

The proteins listed in FIG. 21 are believed to be particularly important for apicomplexan parasite bradyzoite development and/or survival in the host. Thus, targeting expression and/or activity of these proteins from the apicomplexan parasite will be effective to inhibit bradyzoite development and/or survival in the host.

EGS transcripts in HHF, MM6, and NSC cells were enriched for genes transcribed in bradyzoites, including known bradyzoite transcripts, certain Apetela 2s and cytochrome b and other cytochromes (FIG. 7b-c). Among

transcripts with the most increased fold change in EGS across all three cell lines were: cytochrome b; cytochrome c oxidase subunit III subfamily protein; apocytochrome b; cytochrome b, putative; and cytochrome b (N-terminal)/b6/petB subfamily protein. Other over-expressed genes include bradyzoite transcription factor AP2IX-9 and plant-like heat-shock protein BAG1 (FIG. 7 a-c). The up- or down-regulated genes identified in the parasite transcriptome study are thus targets against which to identify drugs for anti-apicomplexan parasite (such as *T. gondii*) therapy, by identifying test compounds that reduce expression of over-expressed

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genes, or promote expression of down-regulated genes. In various embodiments, positive test compounds are those that reduce expression (for up-regulated genes), or decrease expression (for down-regulated genes) of 1 or more (i.e.: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 50, 100, or more) of the up-regulated apicomplexan parasite genes in FIGS. 3-5 after host cell infection by at least 5%, 10%, 15%, 20%, 25%, 50%, 75%, 90%, or more. The drug screening assays may employ the cell lines and non-human animal models of the present invention. In one embodiment, the methods comprise identifying test compounds that reduce expression from the apicomplexan parasite after cell infection of 1 or more of cytochrome b; cytochrome c oxidase subunit III subfamily protein; apocytochrome b, cytochrome b, putative, cytochrome b (N-terminal)/b6/petB subfamily protein, bradyzoite transcription factor AP2IX-9 and plant-like heat-shock protein BAG1.

In another aspect, the invention provides compositions comprising a plurality of isolated probes that in total selectively bind to at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 500, or all of the markers listed in FIGS. 3-5, complements thereof, or their expression products, or functional equivalents thereof wherein at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or all of the probes in total are selective for markers that are upregulated in the EGS strain of *T. gondii* after infection of human fibroblasts, neuronal stem cells or monocytic lineage cells.

Functional equivalents are allelic variants of the recited marker from other *T. gondii* strains. In one embodiment, the markers include two or more of apetela 2 transcription factors, cytochrome b, cytochrome oxidase, or functional equivalents thereof. The markers may further comprise one or more of enolase 1, lactate dehydrogenase 2, bradyzoite antigen 1 and cyst wall protein, or functional equivalents thereof. In another embodiment,

In a further aspect, the invention provides a plurality of isolated probes that in total selectively bind to at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 250, 500, or all of the markers listed in FIG. 1-2, complements thereof, or their expression products, or functional equivalents thereof, wherein at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or all of the probes in total are selective for markers that are upregulated in human fibroblasts, neuronal stem cells or monocytic lineage cells after infection with *T. gondii*, including but not limited to infection with the EGS strain of *T. gondii*.

In one embodiment of each of these aspects, the plurality of isolated probes comprises polynucleotide probes. In another embodiment, the plurality of isolated probes comprises antibody probes. In all of the above embodiments, the isolated probes can be labelled with a detectable label. Methods for detecting the label include, but are not limited to spectroscopic, photochemical, biochemical, immunochemical, physical or chemical techniques. Any suitable detectable label can be used.

The compositions can be stored frozen, in lyophilized form, or as a solution. In one embodiment, the compositions can be placed on a solid support, such as in a microarray or microplate format; this embodiment facilitates use of the compositions in various detection assays.

The compositions of the invention can be used, for example, to test patient samples for up-regulation or down-regulation of the one or more markers disclosed in the figures, to assist in diagnosing a subject as having an apicomplexan parasite infection (such as *T. gondii*) or to monitor treatment of a subject receiving therapy for an

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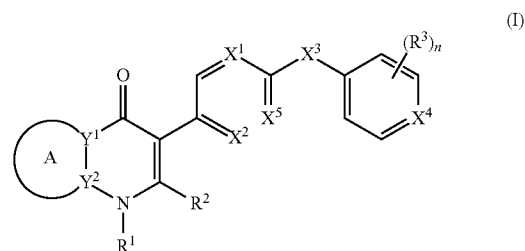
apicomplexan-associated disorder. In one embodiment, such methods comprise testing the patient samples for increased expression of at least 1, 2, 3, 4, 5, 6, or all 7 of apetela 2 transcription factors, cytochrome b, cytochrome oxidase, enolase 1, lactate dehydrogenase 2, bradyzoite antigen 1 and cyst wall protein, or functional equivalents thereof.

In one embodiment, the transcriptome provides the signature of cytochrome b as an important part of the bradyzoite transcriptional pathways and a signature that demonstrates effective inhibition of cytochrome b with abrogation of the signature when treatment is with an inhibitor of cytochrome b, which when used early after infection can confirm selectivity of compound. Cytochrome b functions for pyrimidine synthesis in *Plasmodium falciparum* so that it will be synergistic or additive in effect with inhibitors of DHODH.

The invention thus also provides pathway to improved inhibitors of cytochrome b through co-crystallography that defines the chemical space and pi stacking which facilitates design of improved medicines and their delivery into tachyzoites and bradyzoites using molecular transporters such as octaarginine, or carbonate, and also improves their solubility and access to encysted bradyzoites.

In various embodiments, the methods for monitoring treatment of an apicomplexan parasitic infection (such as a *T. gondii* infection), comprising monitoring expression, protein in serum or plasma, and/or activity of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or all of the markers listed in FIGS. 1-5 (such as a human subject) being treated for an apicomplexan parasitic infection, wherein a decrease or increase in expression and/or presence and/or activity of the one or more markers indicates that the treatment is effective. In one exemplary embodiment, infection is in the subject's brain or other neurologic tissue.

In another aspect, the present disclosure provides compounds having the structure of Formula (I):



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof,

wherein

ring A combines with Y¹ and Y₂ to form a C₃₋₇-cycloalkenyl or heteroaryl ring,

wherein the C₃₋₇-cycloalkenyl or heteroaryl is optionally substituted by halogen, C₁₋₃alkyl, C₁₋₃alkoxy, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR, cyano or phenyl;

Y¹ is C or N;

Y² is C or N;

X¹ is C(R^{x1}) or N,

wherein R^{x1} is hydrogen, halogen, C₁₋₃alkyl, C₁₋₃alkoxy or C₁₋₃haloalkyl;

X² is C(R^{x2}) or N,

wherein R^{x2} is hydrogen, halogen, C₁₋₃alkyl, C₁₋₃alkoxy or C₁₋₃haloalkyl;

X³ is O, N(R), S or C₁₋₃alkyl;

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X^4 is C or N;

X^5 is C or N;

R^1 is hydrogen or C_{1-3} alkyl;

R^2 is hydrogen, C_{1-3} alkyl, C_{1-3} haloalkyl, $-\text{CH}_2\text{OH}$, $-\text{CH}_2\text{OR}$ or $-\text{C(O)OR}$;

n is 0, 1, 2, 3 or 4;

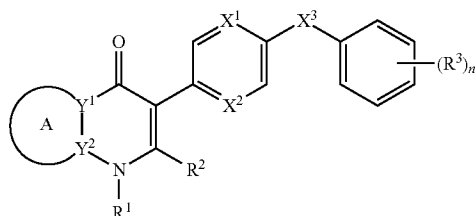
each R^3 is independently halogen, C_{1-3} alkyl, C_{1-3} alkoxy, C_{1-3} haloalkyl, $-\text{O}-C_{1-3}$ haloalkyl, $-\text{S}-C_{1-3}$ haloalkyl, $-\text{C(O)OR}$ or SF_5 ;

or two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane; and

each R is independently hydrogen or C_{1-3} alkyl.

The compounds of the invention have been demonstrated in the examples herein as useful, for example, in treating diseases associated with apicomplexan parasite infection.

In some embodiments, the compounds are of Formula (Ia):



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof,

wherein

ring A combines with Y^1 and Y^2 to form a C_{3-7} cycloalkenyl or heteroaryl ring,

wherein the C_{3-7} cycloalkenyl or heteroaryl is optionally substituted by halogen, C_{1-3} alkyl, C_{1-3} alkoxy, C_{1-3} haloalkyl, $-\text{O}-C_{1-3}$ haloalkyl, $-\text{S}-C_{1-3}$ haloalkyl, $-\text{C(O)OR}$, cyano or phenyl;

Y^1 is C or N;

Y^2 is C or N;

X^1 is $C(R^{x1})$ or N,

wherein R^{x1} is hydrogen, halogen, C_{1-3} alkyl, C_{1-3} alkoxy or C_{1-3} haloalkyl;

X^2 is $C(R^{x2})$ or N,

wherein R^{x2} is hydrogen, halogen, C_{1-3} alkyl, C_{1-3} alkoxy or C_{1-3} haloalkyl;

X^3 is O, N(R), S or C_{1-3} alkyl;

R^1 is hydrogen or C_{1-3} alkyl;

R^2 is hydrogen, C_{1-3} alkyl or $-\text{C(O)OR}$;

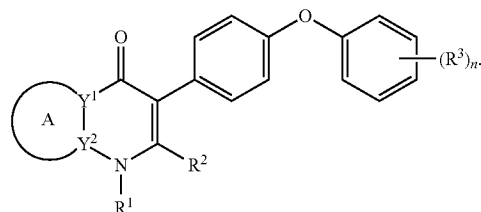
n is 0, 1, 2, 3 or 4;

each R^3 is independently halogen, C_{1-3} alkyl, C_{1-3} alkoxy, C_{1-3} haloalkyl, $-\text{O}-C_{1-3}$ haloalkyl, $-\text{S}-C_{1-3}$ haloalkyl, $-\text{C(O)OR}$ or SF_5 ; and

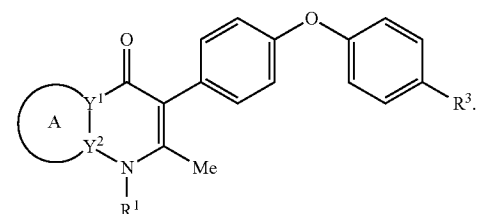
each R is independently hydrogen or C_{1-3} alkyl.

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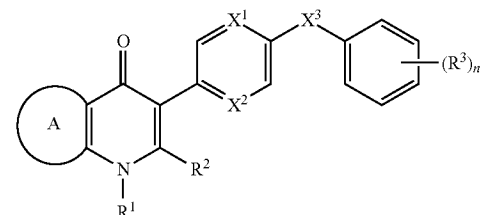
In some embodiments, the compounds are of Formula (Ib):



In some embodiments, the compounds are of Formula (Ic):



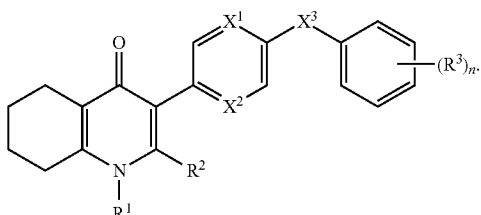
In some embodiments, the compounds are of Formula (II):



wherein

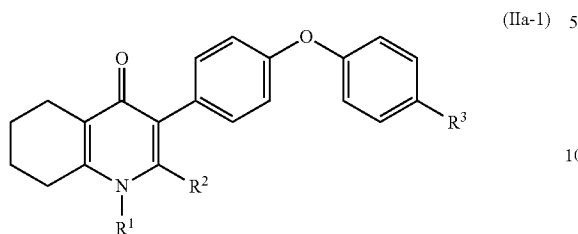
ring A combines with the carbon atoms with which it is attached to form a C_{3-7} cycloalkenyl.

In some embodiments, the compounds are of Formula (IIa):



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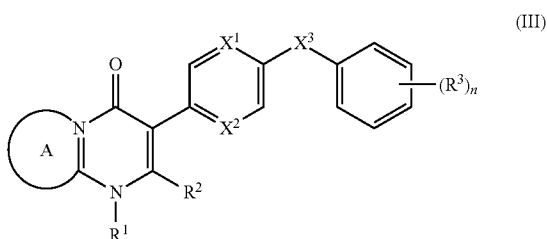
In some embodiments, the compounds are of Formula (IIa-1):



wherein

R³ is hydrogen, halogen, C₁₋₃alkyl or C₁₋₃haloalkyl.

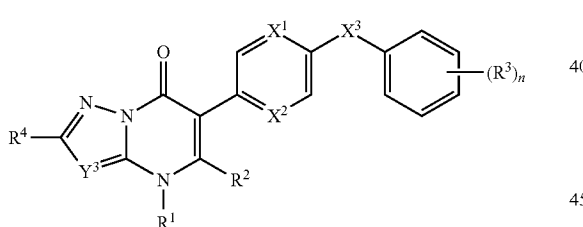
In some embodiments, the compounds are of Formula (III):



wherein

ring A combines with the nitrogen atom and carbon atom with which it is attached to form a heteroaryl ring.

In some embodiments, the compounds are of Formula (IIIa):

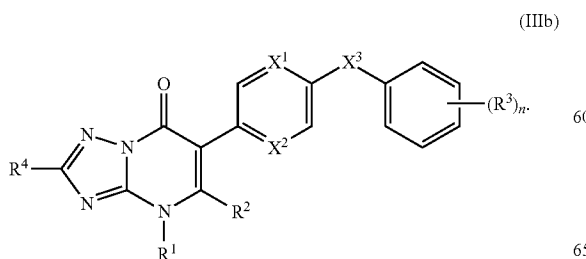


wherein

Y³ is C(R⁵) or N; and

R⁴ and R⁵ are independently hydrogen, halogen, C₁₋₃alkyl, C₁₋₃alkoxy, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR, cyano or phenyl.

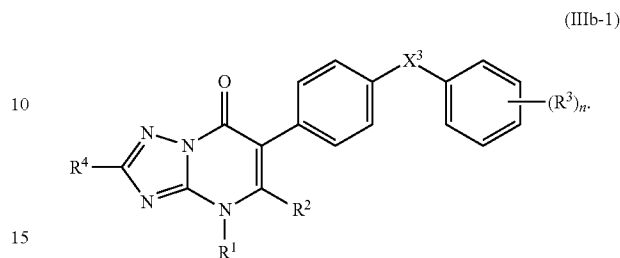
In some embodiments, the compounds are of Formula (IIIb):



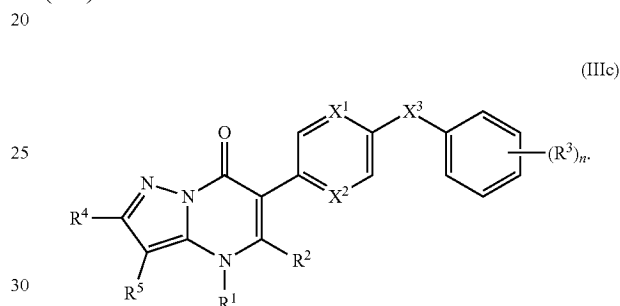
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In some embodiments, the compounds are of R⁴ is hydrogen or C₁₋₃alkyl.

In some embodiments, the compounds are of Formula (IIIb-1):



In some embodiments, the compounds are of Formula (IIIc):

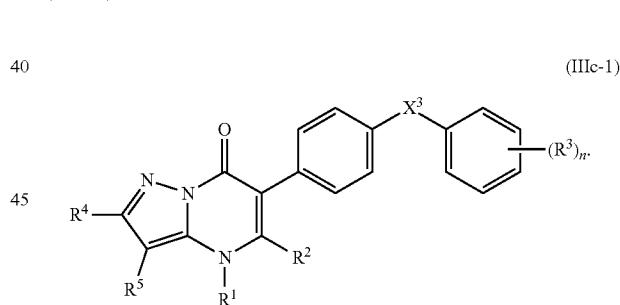


In some embodiments,

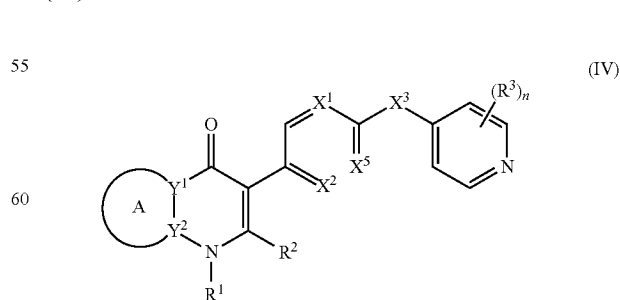
R⁴ is hydrogen or C₁₋₃alkyl or phenyl; and

R⁵ is hydrogen or cyano.

In some embodiments, the compounds are of Formula (IIIc-1):



In some embodiments, the compounds are of Formula (IV):



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof,

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wherein

ring A combines with Y¹ and Y₂ to form a C₃₋₇cycloalkenyl or heteroaryl ring,

wherein the C₃₋₇cycloalkenyl or heteroaryl is optionally substituted by halogen, C₁₋₃alkyl, C₁₋₃alkoxy, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR, cyano or phenyl;

Y¹ is C or N;

Y² is C or N;

X¹ is C(R^{x1}) or N,

wherein R^{x1} is hydrogen, halogen, C₁₋₃alkyl, C₁₋₃alkoxy or C₁₋₃haloalkyl;

X² is C(R^{x2}) or N,

wherein R^{x2} is hydrogen, halogen, C₁₋₃alkyl, C₁₋₃alkoxy or C₁₋₃haloalkyl;

X³ is O, N(R), S or C₁₋₃alkyl;

X⁵ is C or N;

R¹ is hydrogen or C₁₋₃alkyl;

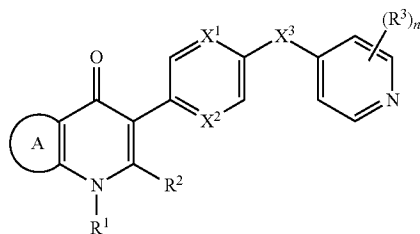
R² is hydrogen, C₁₋₃alkyl, C₁₋₃haloalkyl, —CH₂OH, —CH₂OR or —C(O)OR;

n is 0, 1, 2, 3 or 4;

each R³ is independently halogen, C₁₋₃alkyl, C₁₋₃alkoxy, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR or SF₅; and

each R is independently hydrogen or C₁₋₃alkyl.

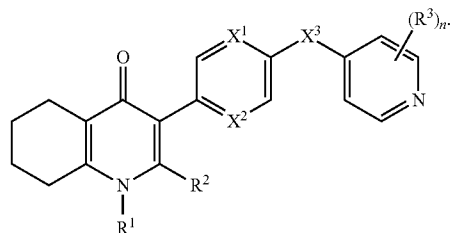
In some embodiments, the compounds are of Formula (IVa):



wherein

ring A combines with the carbon atoms with which it is attached to form a C₃₋₇cycloalkenyl.

In some embodiments, the compounds are of Formula (IVb):



In some embodiments, Y¹ is C. In other embodiments, Y¹ is N.

In some embodiments, Y² is C. In other embodiments, Y² is N.

In some embodiments, Y¹ is C. In other embodiments, Y¹ is N.

In some embodiments, X¹ is C(R^{x1}) wherein R^{x1} is hydrogen, halogen, C₁₋₃alkyl, C₁₋₃alkoxy or C₁₋₃haloalkyl. In other embodiments, X¹ is N.

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In some embodiments, X¹ is C(R^{x1}) wherein R^{x1} is selected from any of groups (1a)-(1x):

(1a) hydrogen, halogen, C₁₋₃alkyl, C₁₋₃alkoxy or C₁₋₃haloalkyl;

(1b) halogen, C₁₋₃alkyl, C₁₋₃alkoxy or C₁₋₃haloalkyl;

(1c) hydrogen;

(1d) halogen or C₁₋₃haloalkyl;

(1e) halogen or C₁₋₃alkyl;

(1f) C₁₋₃alkyl;

(1g) hydrogen, methyl or ethyl;

(1h) methyl or ethyl;

(1i) methyl;

(1j) ethyl;

(1k) propyl;

(1l) hydrogen, methyl or propyl;

(1m) methyl or propyl;

(1n) hydrogen, ethyl or propyl;

(1o) ethyl or propyl;

(1p) C₁₋₃haloalkyl;

(1q) C₁₋₃fluoroalkyl;

(1r) fluoromethyl

(1s) difluoromethyl

(1t) trifluoromethyl

(1u) fluoromethyl

(1v) fluoropropyl

(1w) —CH₂OH;

(1x) —CH₂OR;

In some embodiments, X² is C(R^{x2}) wherein R^{x2} is hydrogen, halogen, C₁₋₃alkyl, C₁₋₃alkoxy or C₁₋₃haloalkyl. In other embodiments, X² is N.

In some embodiments, X² is C(R^{x2}) wherein R^{x2} is selected from any of groups (2a)-(2x):

(2a) hydrogen, halogen, C₁₋₃alkyl, C₁₋₃alkoxy or C₁₋₃haloalkyl;

(2b) halogen, C₁₋₃alkyl, C₁₋₃alkoxy or C₁₋₃haloalkyl;

(2c) hydrogen;

(2d) halogen or C₁₋₃haloalkyl;

(2e) halogen or C₁₋₃alkyl;

(2f) C₁₋₃alkyl;

(2g) hydrogen, methyl or ethyl;

(2h) methyl or ethyl;

(2i) methyl;

(2j) ethyl;

(2k) propyl;

(2l) hydrogen, methyl or propyl;

(2m) methyl or propyl;

(2n) hydrogen, ethyl or propyl;

(2o) ethyl or propyl;

(2p) C₁₋₃haloalkyl;

(2q) C₁₋₃fluoroalkyl;

(2r) fluoromethyl

(2s) difluoromethyl

(2t) trifluoromethyl

(2u) fluoromethyl

(2v) fluoropropyl

(2w) —CH₂OH;

(2x) —CH₂OR;

In some embodiments, X³ is selected from any of groups (3a)-(3p):

(3a) O, N(R), S or C₁₋₃alkyl;

(3b) O, N(R) or S;

(3c) O or N(R);

(3d) 0;

(3e) N(R);

(3f) S or C₁₋₃alkyl;

(3g) O, N(R), or C₁₋₃alkyl;

(3h) O or C₁₋₃alkyl;

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- (3i) N(R), S or C₁₋₃alkyl;
 (3j) N(R) or C₁₋₃alkyl;
 (3k) O or C₁₋₃alkyl;
 (3l) C₁₋₃alkyl;
 (3m) methylene
 (3n) ethylene;
 (3o) propylene;
 (3p) NH.
 In some embodiments, X⁴ is C. In other embodiments, X⁴ is N.
 In some embodiments, X⁵ is C. In other embodiments, X⁵ is N.
 In some embodiments, R¹ is selected from any of groups (4a)-(4l):
 (4a) hydrogen or C₁₋₃alkyl;
 (4b) hydrogen;
 (4c) C₁₋₃alkyl;
 (4d) hydrogen, methyl or ethyl;
 (4e) methyl or ethyl;
 (4f) methyl;
 (4g) ethyl;
 (4h) propyl;
 (4i) hydrogen, methyl or propyl;
 (4j) methyl or propyl;
 (4k) hydrogen, ethyl or propyl;
 (4l) ethyl or propyl;
 In some embodiments, R² is selected from any of groups (5a)-(5gg):
 (5a) hydrogen, C₁₋₃alkyl, C₁₋₃haloalkyl, —CH₂OH, —CH₂OR or —C(O)OR;
 (5b) C₁₋₃alkyl, C₁₋₃haloalkyl, —CH₂OH, —CH₂OR or —C(O)OR;
 (5c) hydrogen, C₁₋₃haloalkyl, —CH₂OH, —CH₂OR or —C(O)OR;
 (5d) hydrogen, C₁₋₃alkyl, —CH₂OH, —CH₂OR or —C(O)OR;
 (5e) hydrogen, C₁₋₃alkyl, C₁₋₃haloalkyl, —CH₂OR or —C(O)OR;
 (5f) hydrogen, C₁₋₃alkyl, C₁₋₃haloalkyl, —CH₂OH, or —C(O)OR;
 (5g) hydrogen, C₁₋₃alkyl, C₁₋₃haloalkyl, —CH₂OH, or —CH₂OR;
 (5h) hydrogen or C₁₋₃alkyl;
 (5i) hydrogen;
 (5j) C₁₋₃alkyl;
 (5k) hydrogen, methyl or ethyl;
 (5l) methyl or ethyl;
 (5m) methyl;
 (5n) ethyl;
 (5o) propyl;
 (5p) hydrogen, methyl or propyl;
 (5q) methyl or propyl;
 (5r) hydrogen, ethyl or propyl;
 (5s) ethyl or propyl;
 (5t) C₁₋₃haloalkyl, —CH₂OH, —CH₂OR or —C(O)OR;
 (5u) C₁₋₃haloalkyl;
 (5v) C₁₋₃fluoralkyl;
 (5w) fluoromethyl
 (5x) difluoromethyl
 (5y) trifluoromethyl
 (5z) fluoromethyl
 (5aa) fluoropropyl
 (5bb) —CH₂OH;
 (5cc) —CH₂OR;
 (5dd) —C(O)OR;
 (5ee) —C(O)OH;
 (5ff) —C(O)OMe;
 (5gg) —C(O)OEt

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- In some embodiments, n is selected from any of groups (6a)-(6k):
 (6a) n is 1, 2, 3, or 4.
 (6b) n is 0, 1, 2, or 3.
 (6c) n is 0, 1, or 2.
 (6d) n is 0 or 1.
 (6e) n is 1 or 2.
 (6f) n is 2 or 3.
 (6g) n is 1.
 (6h) n is 2.
 (6i) n is 3.
 (6j) n is 4.
 (6k) n is 0.
 In some embodiments, R³ is selected from any of groups (7a)-(7cc):
 (7a) each R³ is independently halogen, C₁₋₃alkyl, C₁₋₃alkoxy, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR, SF₅, or two R³ groups, together with the carbons to which they are attached, form a 1,3-dioxolane;
 (7b) each R³ is independently C₁₋₃alkyl, C₁₋₃alkoxy, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR or SF₅;
 (7c) each R³ is independently halogen, C₁₋₃alkoxy, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR or SF₅;
 (7d) each R³ is independently halogen, C₁₋₃alkyl, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR or SF₅;
 (7e) each R³ is independently halogen, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR or SF₅;
 (7f) each R³ is independently halogen, C₁₋₃alkyl, C₁₋₃alkoxy, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR or SF₅;
 (7g) each R³ is independently C₁₋₃alkyl, C₁₋₃alkoxy, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR or SF₅;
 (7h) each R³ is independently —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR or SF₅;
 (7i) each R³ is independently halogen, C₁₋₃alkyl, C₁₋₃alkoxy, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR or SF₅;
 (7j) each R³ is independently halogen, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —C(O)OR, or two R³ groups, together with the carbons to which they are attached, form a 1,3-dioxolane;
 (7k) each R³ is independently halogen, C₁haloalkyl, —O—C₁haloalkyl, —C(O)OR, or two R³ groups, together with the carbons to which they are attached, form a 1,3-dioxolane;
 (7l) each R³ is independently fluoro, chloro, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —C(O)OR, or two R³ groups, together with the carbons to which they are attached, form a 1,3-dioxolane;
 (7m) each R³ is independently fluoro, chloro, trifluoromethyl, —O—C₁₋₃haloalkyl, —C(O)OR, or two R³ groups, together with the carbons to which they are attached, form a 1,3-dioxolane;
 (7n) each R³ is independently fluoro, chloro, trifluoromethyl, —OCF₃, —C(O)OR, or two R³ groups, together with the carbons to which they are attached, form a 1,3-dioxolane;

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- (7o) each R^3 is independently fluoro, chloro, trifluoromethyl, $-\text{OCF}_3$, $-\text{C}(\text{O})\text{OH}$, or two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane;
- (7p) each R^3 is independently trifluoromethyl, $-\text{OCF}_3$, $-\text{C}(\text{O})\text{OH}$, or two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane;
- (7q) each R^3 is independently fluoro, chloro, $-\text{OCF}_3$, $-\text{C}(\text{O})\text{OH}$, or two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane;
- (7r) each R^3 is independently fluoro, chloro, trifluoromethyl, $-\text{OCF}_3$, or two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane;
- (7s) each R^3 is independently fluoro, chloro, trifluoromethyl or $-\text{OCF}_3$;
- (7t) each R^3 is independently fluoro, chloro, trifluoromethyl, $-\text{OCF}_3$ or $-\text{C}(\text{O})\text{OH}$;
- (7u) each R^3 is independently fluoro, chloro, trifluoromethyl or $-\text{OCF}_3$;
- (7v) each R^3 is independently fluoro, chloro or trifluoromethyl;
- (7w) each R^3 is independently fluoro or chloro;
- (7x) each R^3 is independently fluoro;
- (7y) each R^3 is independently chloro;
- (7z) each R^3 is trifluoromethyl;
- (7aa) each R^3 is $-\text{OCF}_3$;
- (7bb) each R^3 is $-\text{C}(\text{O})\text{OH}$;

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- (7cc) two R^3 groups, together with the carbons to which they are attached, form a 1,3-dioxolane;
- In some embodiments, R is selected from any of groups (8a)-(8l):

- (8a) hydrogen or C_{1-3} alkyl;
- (8b) hydrogen;
- (8c) C_{1-3} alkyl;
- (8d) hydrogen, methyl or ethyl;
- (8e) methyl or ethyl;
- (8f) methyl;
- (8g) ethyl;
- (8h) propyl;
- (8i) hydrogen, methyl or propyl;
- (8j) methyl or propyl;
- (8k) hydrogen, ethyl or propyl;
- (8l) ethyl or propyl;

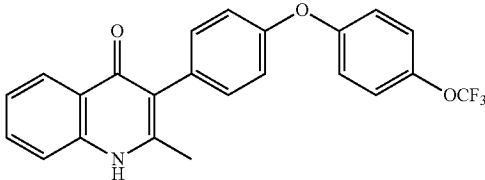
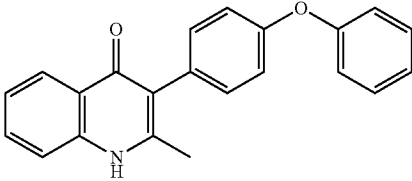
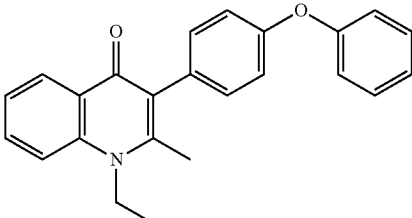
In some embodiments, the compound is of Formula (I), (Ia), (Ib) or (Ic), and X^1 , X^2 , X^3 , R^1 , R^2 , R^3 and n are selected from any combination of groups (1a)-(8l).

In some embodiments, the compound is of Formula (II), (IIa) or (IIa-1), and X^1 , X^2 , X^3 , R^1 , R^2 , R^3 and n are selected from any combination of groups (1a)-(8l).

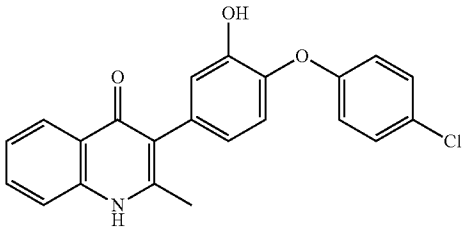
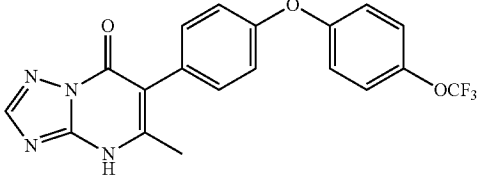
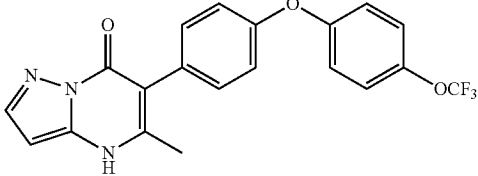
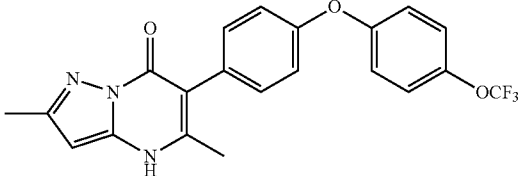
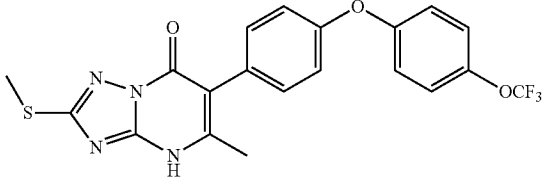
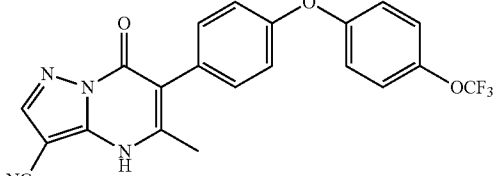
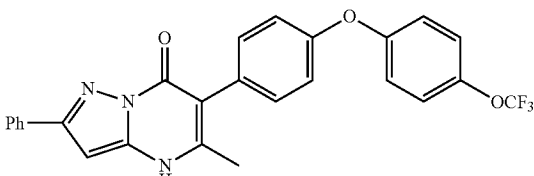
In some embodiments, the compound is of Formula (III), (IIIa), (IIIb), (IIIb-1), (IIIc) or (IIIc-1), and X^1 , X^2 , X^3 , R^1 , R^2 , R^3 and n are selected from any combination of groups (1a)-(8l).

In some embodiments, the compound is of Formula (IV), (IVa) or (IVb) and X^1 , X^2 , X^3 , R^1 , R^2 , R^3 and n are selected from any combination of groups (1a)-(8l).

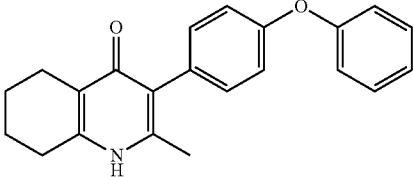
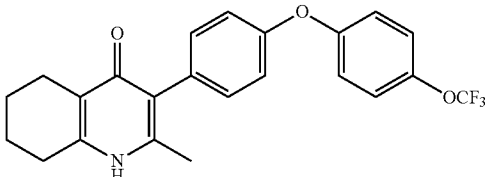
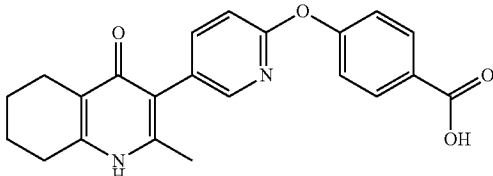
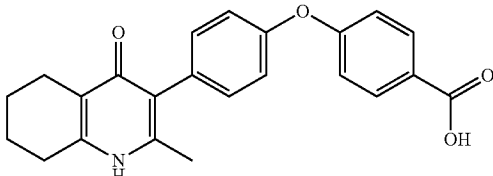
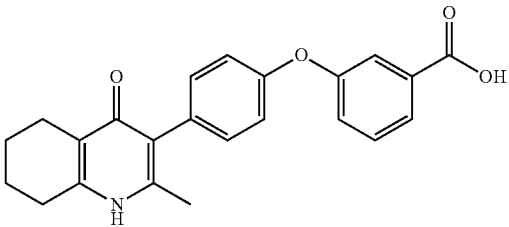
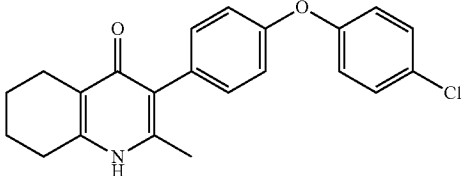
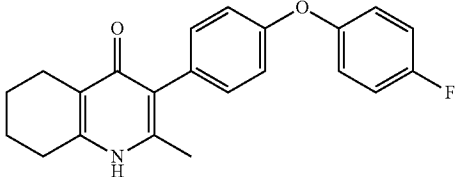
In some embodiments, the compound is:

No.	ID	Structure	Name
ELQ-type systems			
PA1	MJM102/ MJM113 (ELQ- 271)		2-methyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)quinolin-4(1H)-one
PA2	MJM 129		2-methyl-3-(4-phenoxyphenyl)quinolin-4(1H)-one
PA3	JM10		1-ethyl-2-methyl-3-(4-phenoxyphenyl)quinolin-4(1H)-one

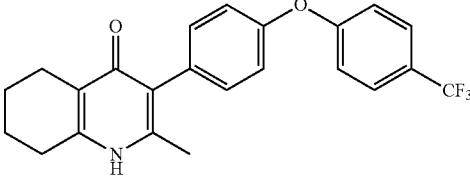
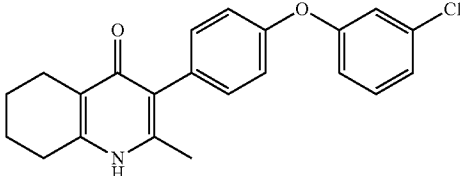
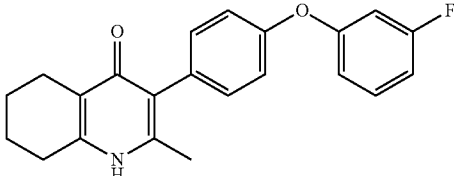
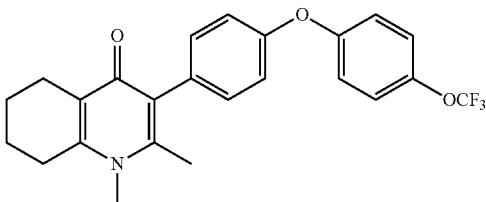
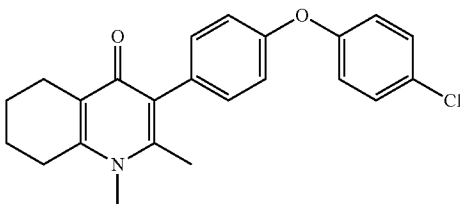
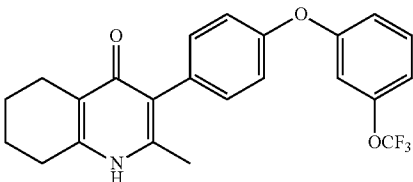
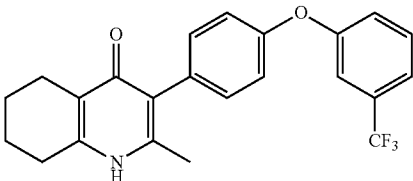
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No.	ID	Structure	Name
PA4	RG38		3-(4-(4-chlorophenoxy)-3-hydroxyphenyl)-2-methylquinolin-4(1H)-one
5,6-fused pyridone systems			
1	MJM136		5-methyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-[1,2,4]triazolo[1,5-a]pyrimidin-7(4H)-one
2	MJM141		5-methyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one
3	JAG006		2,5-dimethyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one
4	JAG013		5-methyl-2-(methylthio)-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-[1,2,4]triazolo[1,5-a]pyrimidin-7(4H)-one
5	JAG014		5-methyl-7-oxo-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-4,7-dihydropyrazolo[1,5-a]pyrimidine-3-carbonitrile
6	JAG015		5-methyl-2-phenyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one

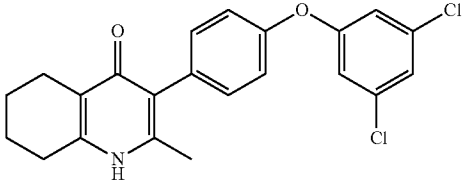
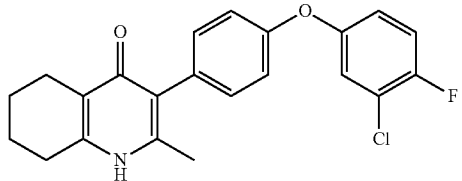
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No.	ID	Structure	Name
Tetrahydroquinolones (THQ)			
7	MJM170		2-methyl-3-(4-phenoxyphenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
8	JAG21		2-methyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
9	JAG039		4-((5-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)pyridin-2-yl)oxy)benzoic acid
10	JAG046		4-(4-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)phenoxy)benzoic acid
11	JAG047		3-(4-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)phenoxy)benzoic acid
12	JAG50		3-(4-(4-chlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
13	JAG58		3-(4-(4-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

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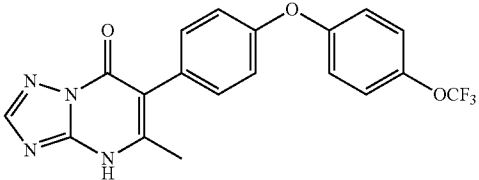
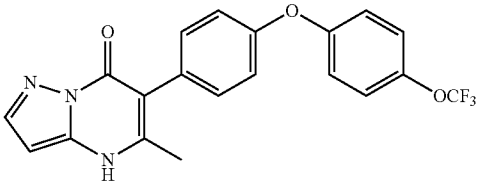
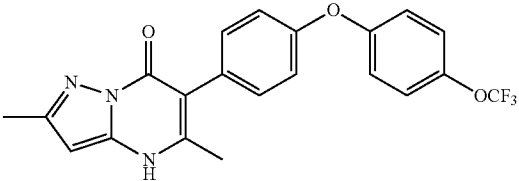
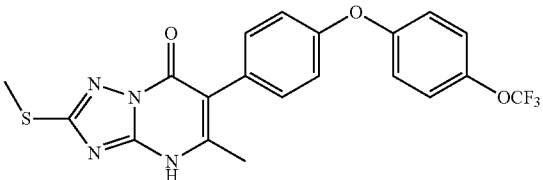
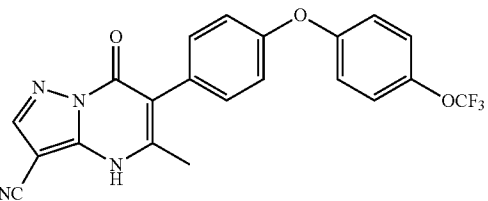
No.	ID	Structure	Name
14	JAG63		2-methyl-3-(4-(4-(trifluoromethyl)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
15	JAG062		3-(4-(3-chlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
16	JAG067		3-(4-(3-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
17	JAG023		1,2-dimethyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
18	JAG077		3-(4-(4-chlorophenoxy)phenyl)-1,2-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
19	AS006		2-methyl-3-(4-(3-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
20	AS0012		2-methyl-3-(4-(3-(trifluoromethyl)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one

-continued

No.	ID	Structure	Name
21	AS021		3-(4-(3,5-dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
22	AS022		3-(4-(3-chloro-4-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof.

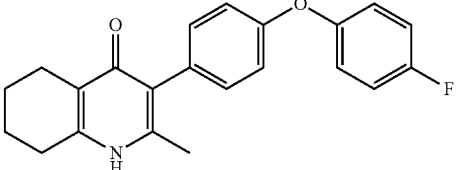
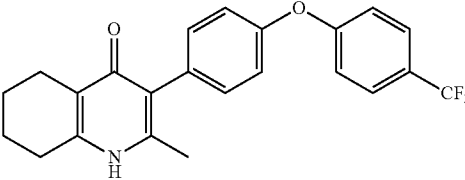
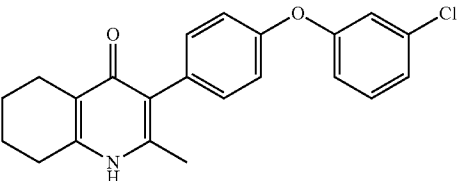
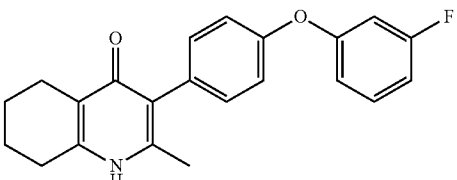
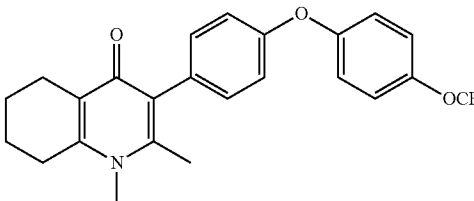
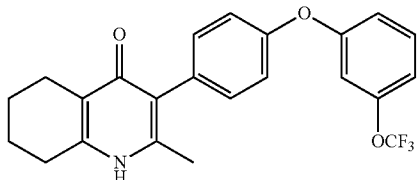
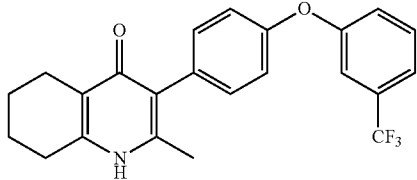
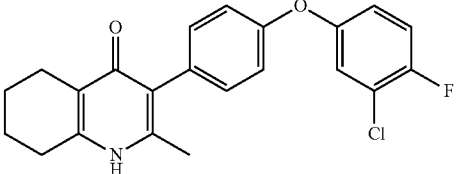
In some embodiments, the compound is:

ID	Structure	Name
MJM136		5-methyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-[1,2,4]triazolo[1,5-a]pyrimidin-7(4H)-one
MJM141		5-methyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one
JAG006		2,5-dimethyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one
JAG013		5-methyl-2-(methylthio)-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-[1,2,4]triazolo[1,5-a]pyrimidin-7(4H)-one
JAG014		5-methyl-7-oxo-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-4,7-dihydropyrazolo[1,5-a]pyrimidine-3-carbonitrile

-continued

ID	Structure	Name
JAG015		5-methyl-2-phenyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one.
MJM170		2-methyl-3-(4-phenoxyphenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG21		2-methyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG039		methyl 3-((5-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)pyridin-2-yl)oxy)benzoate
JAG046		4-(4-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)phenoxy)benzoic acid
JAG047		3-(4-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)phenoxy)benzoic acid
JAG50		3-(4-(4-chlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

-continued

ID	Structure	Name
JAG58		3-(4-(4-Fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG63		2-Methyl-3-(4-(4-(trifluoromethyl)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG062		3-(4-(3-Chlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG069		3-(4-(3-Fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG023		1,2-dimethyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4-one
AS006/ JAG143		3-(4-(3,4-Dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
AS012/ JAG144		3-(4-(3,4-Dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
AS021/ JAG145		3-[4-(3-chloro-4-fluorophenoxy)phenyl]-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4-one

-continued

ID	Structure	Name
AS034/ JAG148		3-{4-[(2,6-dichloropyridin-4-yl)oxy]phenyl}-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4-one
AS022		3-[4-(3,5-dichlorophenoxy)phenyl]-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4(1H)-one
JAG084		3-(4-(3,4-Dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG091		3(4-(4-Trifluoromethoxyphenoxy)phenyl)-2-(carboxylate)-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG092		3-(6-(4-Trifluoromethoxyphenoxy)pyridin-3-yl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG095		3-(4-Phenoxypheyl)-1,2,3,4,5,6,7,8-octahydroquinazoline-2,4,dione
JAG099		3(4-(4-Trifluoromethoxyphenoxy)phenyl)-2-(methylhydroxy)-5,6,7,8-tetrahydroquinolin-4(1H)-one

-continued

ID	Structure	Name
AS032		3-[4-(2H-1,3-benzodioxo1-5-yloxy)phenyl]-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4-one
JAG100		6-Ethyl-3-(4-(4-trifluoromethoxyphenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG106		3(4-(4-Trifluoromethoxyphenoxy)phenyl)-2,6-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG107		3(4-(4-Trifluoromethoxyphenoxy)phenyl)-2,7-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
JAG121		7-Ethyl-2-methyl-3(4-(4-trifluoromethoxyphenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
JA129		3(4-(4-trifluoromethoxyphenoxy)phenyl)-2-methyl-1,7-naphthyrid-4(1H)-one
JAG162		7-Trifluoromethyl-2-methyl-3(4-(4-trifluoromethoxyphenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one

or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof.

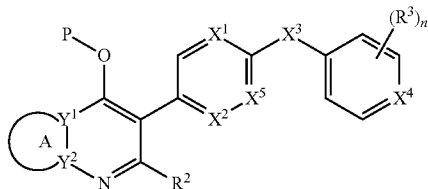
In another aspect, the invention provides prodrugs of a compound of Formula (I). The term “prodrug” is intended to represent covalently bonded carriers, which are capable of releasing the active ingredient when the prodrug is administered to a mammalian subject. Release of the active ingredient occurs in vivo. Prodrugs can be prepared by

techniques known to one skilled in the art. These techniques generally modify appropriate functional groups in a given compound. These modified functional groups however regenerate original functional groups by routine manipulation or in vivo. Prodrugs of compounds of the invention include compounds wherein an amino, hydroxy, carboxylic or a similar group is modified. Examples of prodrugs include, but are not limited to esters (e.g., acetate, formate,

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and benzoate), carbamates (e.g., N,N-dimethylaminocarbo-
nyl), amides (e.g., trifluoroacetyl amino, acetyl amino, and
the like), and the like. A complete discussion of prodrugs is
found in Huttunen, K. M. and Rautio J. *Current Topics in*
Medicinal Chemistry, 2011, 11, 2265-2287 and Stella, V. J.
et al. (2007). *Prodrugs: Challenges and Awards Part 1*. New
York: Springer. The disclosure of both references is herein
incorporated by reference in its entirety.

In some embodiments, the prodrug of a compound of
Formula (I) has the structure of Formula (I-p):



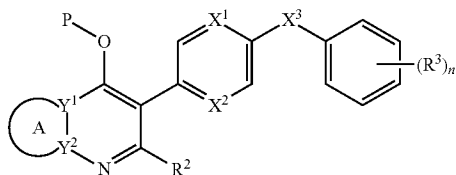
or a stereoisomer thereof, or a pharmaceutically acceptable
salt thereof, wherein

ring A, Y¹, Y², X¹, X², X³, X⁴, X⁵, R, R³ and n are as
described above;

R² is hydrogen, C₁₋₃alkyl, C₁₋₃haloalkyl, —CH₂OH,
—CH₂OR, —C(O)OR or —CH₂OP; and

P is —C(O)OR', —C(O)R', —C(O)NR'₂ or —OP(O)
(OR')OR', wherein each R' is independently hydrogen
or C₁₋₃alkyl.

In some embodiments, the prodrug is a compound of
Formula (Ia-p):



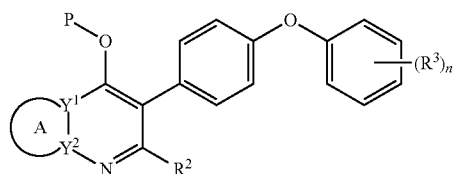
or a stereoisomer thereof, or a pharmaceutically acceptable
salt thereof, wherein

ring A, Y¹, Y², X¹, X², X³, R, R², R³ and n are as
described above;

R² is hydrogen, C₁₋₃alkyl, C₁₋₃haloalkyl, —CH₂OH,
—CH₂OR, —C(O)OR or —CH₂OP; and

P is —C(O)OR', —C(O)R', —C(O)NR'₂ or —OP(O)
(OR')OR', wherein each R' is independently hydrogen
or C₁₋₃alkyl.

In some embodiments, the prodrug is a compound of
Formula (Ib-p):



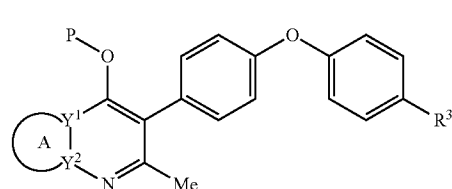
or a stereoisomer thereof, or a pharmaceutically acceptable
salt thereof, wherein

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ring A, Y¹, Y², R, R², R³ and n are as described above;
R² is hydrogen, C₁₋₃alkyl, C₁₋₃haloalkyl, —CH₂OH,
—CH₂OR, —C(O)OR or —CH₂OP; and

P is —C(O)OR', —C(O)R', —C(O)NR'₂ or —OP(O)
(OR')OR', wherein each R' is independently hydrogen
or C₁₋₃alkyl.

In some embodiments, the prodrug is a compound of
Formula (Ic-p):

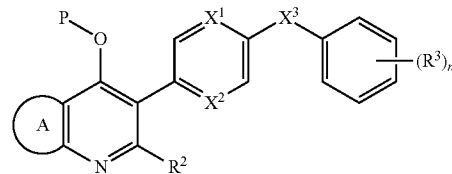


or a stereoisomer thereof, or a pharmaceutically acceptable
salt thereof, wherein

ring A, Y¹, Y², R and R³ are as described above; and

P is —C(O)OR', —C(O)R', —C(O)NR'₂ or —OP(O)
(OR')OR', wherein each R' is independently hydrogen
or C₁₋₃alkyl.

In some embodiments, the prodrug is a compound of
Formula (II-p):

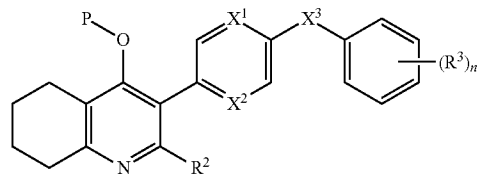


or a stereoisomer thereof, or a pharmaceutically acceptable
salt thereof, wherein

ring A, X¹, X², X³, R, R², R³ and n are as described above;
R² is hydrogen, C₁₋₃alkyl, C₁₋₃haloalkyl, —CH₂OH,
—CH₂OR, —C(O)OR or —CH₂OP; and

P is —C(O)OR', —C(O)R', —C(O)NR'₂ or —OP(O)
(OR')OR', wherein each R' is independently hydrogen
or C₁₋₃alkyl.

In some embodiments, the prodrug is a compound of
Formula (IIa-p):



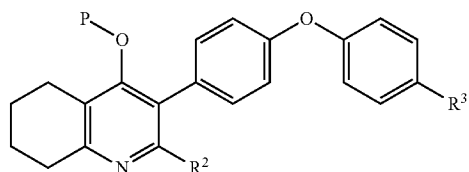
or a stereoisomer thereof, or a pharmaceutically acceptable
salt thereof, wherein

X¹, X², X³, R, R², R³ and n are as described above;
R² is hydrogen, C₁₋₃alkyl, C₁₋₃haloalkyl, —CH₂OH,
—CH₂OR, —C(O)OR or —CH₂OP; and

P is —C(O)OR', —C(O)R', —C(O)NR'₂ or —OP(O)
(OR')OR', wherein each R' is independently hydrogen
or C₁₋₃alkyl.

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In some embodiments, the prodrug is a compound of Formula (IIa-1-p):



(IIa-1-p) 5

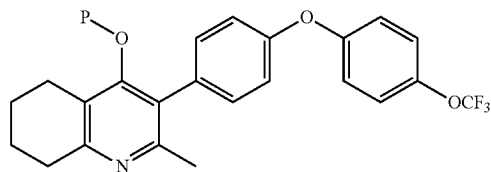
or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

R, R², R³ and n are as described above;

R² is hydrogen, C₁₋₃alkyl, C₁₋₃haloalkyl, —CH₂OH, —CH₂OR, —C(O)OR or —CH₂OP; and

P is —C(O)OR', —C(O)R', —C(O)NR'₂ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C₁₋₃alkyl.

In some embodiments, the prodrug is a compound of Formula (IIa-2-p):

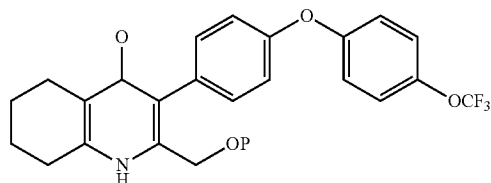


(IIa-2-p) 30

or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

P is —C(O)OR', —C(O)R', —C(O)NR'₂ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C₁₋₃alkyl.

In some embodiments, the prodrug is a compound of Formula (IIa-3-p):



(IIa-3-p) 50

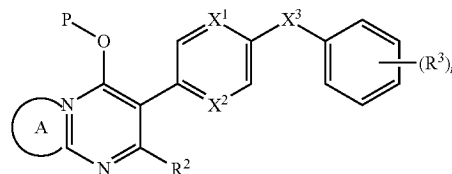
or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

P is —C(O)OR', —C(O)R', —C(O)NR'₂ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C₁₋₃alkyl.

In some embodiments, the prodrug is a compound of Formula (III-p):

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(III-p)



10

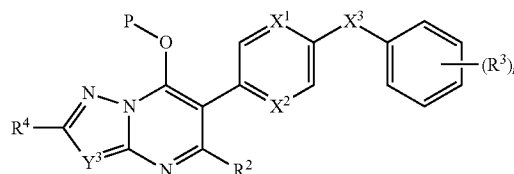
or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

ring A, X¹, X², X³, R, R², R³ and n are as described above;

R² is hydrogen, C₁₋₃alkyl, C₁₋₃haloalkyl, —CH₂OH, —CH₂OR, —C(O)OR or —CH₂OP; and

P is —C(O)OR', —C(O)R', —C(O)NR'₂ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C₁₋₃alkyl.

In some embodiments, the prodrug is a compound of Formula (IIIa-p):



30

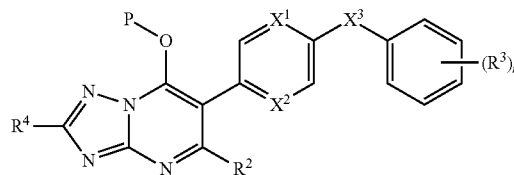
or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

Y³, X¹, X², X³, R, R², R³, R⁴ and n are as described above;

R² is hydrogen, C₁₋₃alkyl, C₁₋₃haloalkyl, —CH₂OH, —CH₂OR, —C(O)OR or —CH₂OP; and

P is —C(O)OR', —C(O)R', —C(O)NR'₂ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C₁₋₃alkyl.

In some embodiments, the prodrug is a compound of Formula (IIIb-p):



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or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

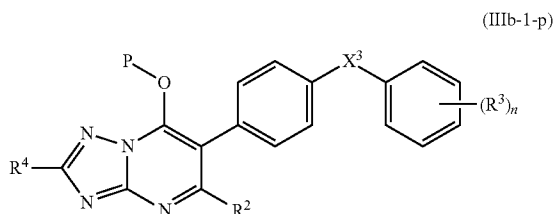
X¹, X², X³, R, R², R³, R⁴ and n are as described above;

R² is hydrogen, C₁₋₃alkyl, C₁₋₃haloalkyl, —CH₂OH, —CH₂OR, —C(O)OR or —CH₂OP; and

P is —C(O)OR', —C(O)R', —C(O)NR'₂ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C₁₋₃alkyl.

In some embodiments, the prodrug is a compound of Formula (IIIb-1-p):

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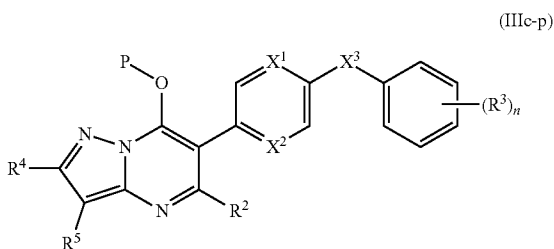
or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

X^3 , R , R^2 , R^3 , R^4 and n are as described above;

R^2 is hydrogen, C_{1-3} alkyl, C_{1-3} haloalkyl, $-CH_2OR$, $-C(O)OR$ or $-CH_2OP$; and

P is $-C(O)OR'$, $-C(O)R'$, $-C(O)NR'_2$ or $-OP(O)(OR')OR'$, wherein each R' is independently hydrogen or C_{1-3} alkyl.

In some embodiments, the prodrug is a compound of Formula (IIIc-p):



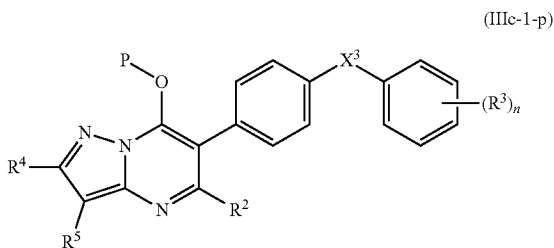
or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

X^1 , X^2 , X^3 , R , R^2 , R^3 , R^4 , R^5 and n are as described above;

R^2 is hydrogen, C_{1-3} alkyl, C_{1-3} haloalkyl, $-CH_2OH$, $-CH_2OR$, $-C(O)OR$ or $-CH_2OP$; and

P is $-C(O)OR'$, $-C(O)R'$, $-C(O)NR'_2$ or $-OP(O)(OR')OR'$, wherein each R' is independently hydrogen or C_{1-3} alkyl.

In some embodiments, the prodrug is a compound of Formula (IIIc-1-p):



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

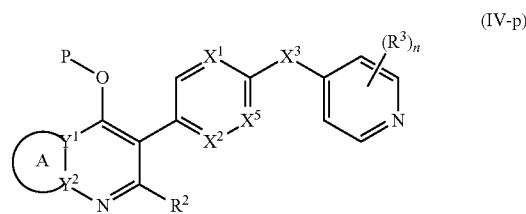
X^3 , R , R^2 , R^3 , R^4 , R^5 and n are as described above;

R^2 is hydrogen, C_{1-3} alkyl, C_{1-3} haloalkyl, $-CH_2OH$, $-CH_2OR$, $-C(O)OR$ or $-CH_2OP$; and

P is $-C(O)OR'$, $-C(O)R'$, $-C(O)NR'_2$ or $-OP(O)(OR')OR'$, wherein each R' is independently hydrogen or C_{1-3} alkyl.

In some embodiments, the prodrug is a compound of Formula (IV-p):

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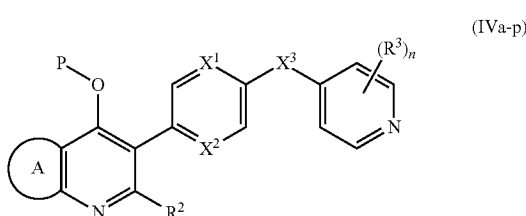
or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

ring A, Y^1 , Y^2 , X^1 , X^2 , X^3 , X^5 , R , R^2 , R^3 and n are as described above;

R^2 is hydrogen, C_{1-3} alkyl, C_{1-3} haloalkyl, $-CH_2OH$, $-CH_2OR$, $-C(O)OR$ or $-CH_2OP$; and

P is $-C(O)OR'$, $-C(O)R'$, $-C(O)NR'_2$ or $-OP(O)(OR')OR'$, wherein each R' is independently hydrogen or C_{1-3} alkyl.

In some embodiments, the prodrug is a compound of Formula (IVa-p):



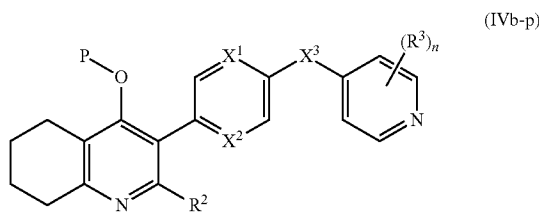
or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

ring A, X^1 , X^2 , R , R^2 , R^3 and n are as described above;

R^2 is hydrogen, C_{1-3} alkyl, C_{1-3} haloalkyl, $-CH_2OH$, $-CH_2OR$, $-C(O)OR$ or $-CH_2OP$; and

P is $-C(O)OR'$, $-C(O)R'$, $-C(O)NR'_2$ or $-OP(O)(OR')OR'$, wherein each R' is independently hydrogen or C_{1-3} alkyl.

In some embodiments, the prodrug is a compound of Formula (IVb-p):



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

X^1 , X^2 , X^3 , R , R^2 , R^3 and n are as described above;

R^2 is hydrogen, C_{1-3} alkyl, C_{1-3} haloalkyl, $-CH_2OH$, $-CH_2OR$, $-C(O)OR$ or $-CH_2OP$; and

P is $-C(O)OR'$, $-C(O)R'$, $-C(O)NR'_2$ or $-OP(O)(OR')OR'$, wherein each R' is independently hydrogen or C_{1-3} alkyl.

In some embodiments, the compound is of any of Formulae (I-p), (Ia-p), (Ib-p), (Ic-p), (II-p), (Ia-1-p), (IIa-2-p), (IIa-3-p), (III-p), (IIIa-p), (IIIb-p), (IIIb-1-p), (IIIc-p), (IIIc-1-p), (IV-p), (Iva-p) or (IVb-p), and X^1 , X^2 , X^3 , R^1 , R^2 , R^3 and n are selected from any combination of groups (1a)-(81).

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In some embodiments, the compound is of Formulae (I-p), (Ia-p), (Ib-p), (Ic-p), (II-p), (Ia-1-p), (IIa-2-p), (IIa-3-p), (III-p), (IIIA-p), (IIIB-p), (IIIB-1-p), (IIIC-p), (IIIC-1-p), (IV-p), (Iva-p) or (IVb-p), X^1 , X^2 , X^3 , R^1 , R^2 , R^3 and n are selected from any combination of groups (1a)-(8l), and P is $-\text{C}(\text{O})_2\text{R}'$.

In some embodiments, the compound is of Formulae (I-p), (Ia-p), (Ib-p), (Ic-p), (II-p), (Ia-1-p), (IIa-2-p), (IIa-3-p), (III-p), (IIIA-p), (IIIB-p), (IIIB-1-p), (IIIC-p), (IIIC-1-p), (IV-p), (Iva-p) or (IVb-p), X^1 , X^2 , X^3 , R , R^2 , R^3 and n are selected from any combination of groups (1a)-(8l), and P is $-\text{C}(\text{O})\text{R}'$.

In some embodiments, the compound is of Formulae (I-p), (Ia-p), (Ib-p), (Ic-p), (II-p), (Ia-1-p), (IIa-2-p), (IIa-3-p), (III-p), (IIIA-p), (IIIB-p), (IIIB-1-p), (IIIC-p), (IIIC-1-p), (IV-p), (Iva-p) or (IVb-p), X^1 , X^2 , X^3 , R , R^2 , R^3 and n are selected from any combination of groups (1a)-(8l), and P is $-\text{C}(\text{O})\text{NR}'_2$.

In some embodiments, the compound is of Formulae (I-p), (Ia-p), (Ib-p), (Ic-p), (II-p), (Ia-1-p), (IIa-2-p), (IIa-3-p), (III-p), (IIIA-p), (IIIB-p), (IIIB-1-p), (IIIC-p), (IIIC-1-p), (IV-p), (Iva-p) or (IVb-p), X^1 , X^2 , X^3 , R , R^2 , R^3 and n are selected from any combination of groups (1a)-(8l), and P is $-\text{OP}(\text{O})(\text{OR}')\text{OR}'$.

In another aspect, the invention provides a pharmaceutical composition comprising a compound of Formula (I-p) and a pharmaceutically acceptable diluent, excipient, or carrier.

In some embodiments, the pharmaceutical composition is a combination comprising a compound of Formula (I), an 8-Aminoquinoline drug and a pharmaceutically acceptable diluent, excipient, or carrier.

In some embodiments, the pharmaceutical composition is a combination comprising a compound of Formula (I), tafenoquine and a pharmaceutically acceptable diluent, excipient, or carrier.

In some embodiments, the pharmaceutical composition is a combination comprising a compound of Formula (I-p), an 8-Aminoquinoline drug and a pharmaceutically acceptable diluent, excipient, or carrier.

In some embodiments, the pharmaceutical composition is a combination comprising a compound of Formula (I-p), tafenoquine and a pharmaceutically acceptable diluent, excipient, or carrier.

In another aspect, the invention provides a pharmaceutical composition comprising a compound of claim Formula (I) and a pharmaceutically acceptable diluent, excipient, or carrier. In another aspect, the invention provides a method for treating an apicomplexan parasitic infection, comprising administering to a subject (such as a human subject) in need thereof an amount effective to treat the infection of the compound of Formula (I) or a pharmaceutical composition comprising a compound of Formula (I). In some embodiments of the method, the infection comprises a *Toxoplasma gondii* infection and/or a *Plasmodium falciparum* infection. In some embodiments of the method, the infection comprises an infection in the subject's brain and/or the subject's eye. In some embodiments of the method, the compound is a prodrug of Formula (I-p).

In another aspect, the invention provides a method for treating an apicomplexan parasitic infection, comprising administering to a subject (such as a human subject) in need thereof an amount effective to treat the infection of a combination comprising a compound of Formula (I) and a 8-Aminoquinoline drug or a pharmaceutical composition comprising a compound of Formula (I) and a 8-Aminoquinoline drug. In some embodiments of the method, the infection comprises a *Toxoplasma gondii* infection and/or a

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Plasmodium falciparum infection. In some embodiments of the method, the infection comprises an infection in the subject's brain and/or the subject's eye. In some embodiments of the method, the compound is a prodrug of Formula (I-p). In some embodiments of the method, the 8-Aminoquinoline drug is tafenoquine.

In some embodiments of the method, the subject is immune compromised. In some embodiments of the method, the subject is immune compromised due to cancer/cancer treatment, autoimmune disease, and/or AIDS. In some embodiments of the method, the subject has malaria, and the treating comprises reducing severity of one or more symptoms of malaria, and/or reducing recurrence of symptoms of malaria. In some embodiments of the method, the subject has toxoplasmosis, and the treating comprises reducing severity of one or more symptoms of toxoplasmosis, and/or reducing recurrence of symptoms of toxoplasmosis. In some embodiments of the method, the treating comprises reducing parasitic load in the subject. In some embodiments of the method, the treating comprises reducing the bradyzoite form and/or the tachyzoite form of the parasite in the subject. In some embodiments of the method, the method further comprises administering to the subject one or more additional compounds in an amount effective to treat the infection. In some embodiments of the method, the one or more additional compounds are selected from the group consisting of pyrimethamine, sulfadiazine, cycloguanil, inhibitors of calcium kinases or dense granules or vacuolar ATPases, atovaquone, and bulky cytochrome Qi inhibitors, itraconazole and other inhibitors of *T. gondii*.

In another aspect, the invention provides a method for monitoring treatment of an apicomplexan parasitic infection (including but not limited to any of the treatments of claims 23-33), comprising monitoring expression, protein in serum or plasma, and/or activity of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or all of the markers listed in Table and figures in Example 8/FIG. 8 in the Appendix in a subject (such as a human subject) being treated for an apicomplexan parasitic infection, wherein a decrease or increase in expression and/or presence and/or activity of the one or more markers indicates that the treatment is effective.

In some embodiments of the method, the infection is a *T. gondii* infection. In some embodiments of the method, the infection is in the subject's brain or other neurologic tissue.

Definitions

Terms used herein may be preceded and/or followed by a single dash, “—”, or a double dash, “=”, to indicate the bond order of the bond between the named substituent and its parent moiety; a single dash indicates a single bond and a double dash indicates a double bond or a pair of single bonds in the case of a spiro-substituent. In the absence of a single or double dash it is understood that a single bond is formed between the substituent and its parent moiety; further, substituents are intended to be read “left to right” unless a dash indicates otherwise. For example, alkyl, alkyl-, and -alkyl indicate the same functionality.

Further, certain terms herein may be used as both monovalent and divalent linking radicals as would be familiar to those skilled in the art, and by their presentation linking between two other moieties. For example, an alkyl group can be both a monovalent radical or divalent radical; in the latter case, it would be apparent to one skilled in the art that an additional hydrogen atom is removed from a monovalent alkyl radical to provide a suitable divalent moiety.

The term "alkoxy" as used herein, means an alkyl group, as defined herein, appended to the parent molecular moiety through an oxygen atom. Representative examples of alkoxy include, but are not limited to, methoxy, ethoxy, propoxy, 2-propoxy, butoxy, tert-butoxy, pentyloxy, and hexyloxy.

The term "alkyl" as used herein, means a straight or branched chain hydrocarbon containing from 1 to 10 carbon atoms, unless otherwise specified. Representative examples of alkyl include, but are not limited to, methyl, ethyl, n-propyl, iso-propyl, n-butyl, sec-butyl, iso-butyl, tert-butyl, n-pentyl, isopentyl, neopentyl, n-hexyl, 3-methylhexyl, 2,2-dimethylpentyl, 2,3-dimethylpentyl, n-heptyl, n-octyl, n-nonyl, and n-decyl. When an "alkyl" group is a linking group between two other moieties, then it may also be a straight or branched chain; examples include, but are not limited to $-\text{CH}_2-$, $-\text{CH}_2\text{CH}_2-$, $-\text{CH}_2\text{CH}_2\text{CH}(\text{CH}_3)-$, $-\text{CH}_2\text{CH}(\text{CH}_2\text{CH}_3)\text{CH}_2-$. The terms "cyano" and "nitrile" as used herein, mean a $-\text{CN}$ group.

"Cycloalkenyl" as used herein refers to a monocyclic or a bicyclic cycloalkenyl ring system. Monocyclic ring systems are cyclic hydrocarbon groups containing from 3 to 8 carbon atoms, where such groups are unsaturated (i.e., containing at least one annular carbon-carbon double bond), but not aromatic. Examples of monocyclic ring systems include cyclopentenyl and cyclohexenyl. Bicyclic cycloalkenyl rings are bridged monocyclic rings or a fused bicyclic rings. Bridged monocyclic rings contain a monocyclic cycloalkenyl ring where two non-adjacent carbon atoms of the monocyclic ring are linked by an alkylene bridge of between one and three additional carbon atoms (i.e., a bridging group of the form $-(\text{CH}_2)_w-$, where w is 1, 2, or 3). Representative examples of bicyclic cycloalkenyls include, but are not limited to, norbornenyl and bicyclo [2.2.2]oct-2-enyl. Fused bicyclic cycloalkenyl ring systems contain a monocyclic cycloalkenyl ring fused to either a phenyl, a monocyclic cycloalkyl, a monocyclic cycloalkenyl, a monocyclic heterocyclyl, or a monocyclic heteroaryl. The bridged or fused bicyclic cycloalkenyl is attached to the parent molecular moiety through any carbon atom contained within the monocyclic cycloalkenyl ring. Cycloalkenyl groups are optionally substituted with one or two groups which are independently oxo or thia.

The term "halo" or "halogen" as used herein, means $-\text{Cl}$, $-\text{Br}$, $-\text{I}$ or $-\text{F}$.

The term "haloalkyl" as used herein, means at least one halogen, as defined herein, appended to the parent molecular moiety through an alkyl group, as defined herein. Representative examples of haloalkyl include, but are not limited to, chloromethyl, 2-fluoroethyl, trifluoromethyl, pentafluoroethyl, and 2-chloro-3-fluoropentyl.

The term "heteroaryl," as used herein, means a monocyclic heteroaryl or a bicyclic ring system containing at least one heteroaromatic ring. The monocyclic heteroaryl can be a 5 or 6 membered ring. The 5 membered ring consists of two double bonds and one, two, three or four nitrogen atoms and optionally one oxygen or sulfur atom. The 6 membered ring consists of three double bonds and one, two, three or four nitrogen atoms. The 5 or 6 membered heteroaryl is connected to the parent molecular moiety through any carbon atom or any nitrogen atom contained within the heteroaryl. Representative examples of monocyclic heteroaryl include, but are not limited to, furyl, imidazolyl, isoxazolyl, isothiazolyl, oxadiazolyl, oxazolyl, pyridinyl, pyridazinyl, pyrimidinyl, pyrazinyl, pyrazolyl, pyrrolyl, tetrazolyl, thiadiazolyl, thiazolyl, thienyl, triazolyl, and triazinyl. The bicyclic heteroaryl consists of a monocyclic het-

eroaryl fused to a phenyl, a monocyclic cycloalkyl, a monocyclic cycloalkenyl, a monocyclic heterocyclyl, or a monocyclic heteroaryl. The fused cycloalkyl or heterocyclyl portion of the bicyclic heteroaryl group is optionally substituted with one or two groups which are independently oxo or thia. When the bicyclic heteroaryl contains a fused cycloalkyl, cycloalkenyl, or heterocyclyl ring, then the bicyclic heteroaryl group is connected to the parent molecular moiety through any carbon or nitrogen atom contained within the monocyclic heteroaryl portion of the bicyclic ring system. When the bicyclic heteroaryl is a monocyclic heteroaryl fused to a phenyl ring or a monocyclic heteroaryl, then the bicyclic heteroaryl group is connected to the parent molecular moiety through any carbon atom or nitrogen atom within the bicyclic ring system. Representative examples of bicyclic heteroaryl include, but are not limited to, benzimidazolyl, benzofuranyl, benzothienyl, benzoxadiazolyl, benzoxathiadiazolyl, benzothiazolyl, cinnolinyl, 5,6-dihydroquinolin-2-yl, 5,6-dihydroisoquinolin-1-yl, furopyridinyl, indazolyl, indolyl, isoquinolinyl, naphthyridinyl, quinolinyl, purinyl, 5,6,7,8-tetrahydroquinolin-2-yl, 5,6,7,8-tetrahydroquinolin-3-yl, 5,6,7,8-tetrahydroquinolin-4-yl, 5,6,7,8-tetrahydroisoquinolin-1-yl, thienopyridinyl, 4,5,6,7-tetrahydrobenzo[c][1,2,5]oxadiazolyl, and 6,7-dihydrobenzo[c][1,2,5]oxadiazol-4(5H)-onyl. In certain embodiments, the fused bicyclic heteroaryl is a 5 or 6 membered monocyclic heteroaryl ring fused to either a phenyl ring, a 5 or 6 membered monocyclic cycloalkyl, a 5 or 6 membered monocyclic cycloalkenyl, a 5 or 6 membered monocyclic heterocyclyl, or a 5 or 6 membered monocyclic heteroaryl, wherein the fused cycloalkyl, cycloalkenyl, and heterocyclyl groups are optionally substituted with one or two groups which are independently oxo or thia.

The term "hydroxy" as used herein, means an $-\text{OH}$ group.

The term "nitro" as used herein, means a $-\text{NO}_2$ group.

The term "oxo" as used herein means a $=\text{O}$ group.

The term "saturated" as used herein means the referenced chemical structure does not contain any multiple carbon-carbon bonds. For example, a saturated cycloalkyl group as defined herein includes cyclohexyl, cyclopropyl, and the like.

The term "thia" as used herein means a $=\text{S}$ group.

The term "unsaturated" as used herein means the referenced chemical structure contains at least one multiple carbon-carbon bond, but is not aromatic. For example, a unsaturated cycloalkyl group as defined herein includes cyclohexenyl, cyclopentenyl, cyclohexadienyl, and the like.

As used herein, the term "cell" is meant to refer to a cell that is in vitro, ex vivo or in vivo. In some embodiments, an ex vivo cell can be part of a tissue sample excised from an organism such as a mammal. In some embodiments, an in vitro cell can be a cell in a cell culture. In some embodiments, an in vivo cell is a cell living in an organism such as a mammal.

As used herein, the term "contacting" refers to the bringing together of indicated moieties in an in vitro system or an in vivo system. For example, "contacting" a parasite with a compound includes the administration of a compound described herein to an individual or patient, such as a human, infected with the parasite, as well as, for example, introducing a compound into a sample containing a cellular or purified preparation containing the parasite.

In another aspect, the invention provides methods for monitoring *T. gondii* infection in a subject, comprising monitoring levels in a blood sample from the subject of one or more markers selected from the group consisting of

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clusterin, oxytocin, PGLYRP2 (N-acetylmuramoyl-L-alanine amidase), Apolipoprotein A1 (apoA1), miR-17-92, and miR-124, wherein a change in levels of the one or more circulating markers compared to control correlates with *T. gondii* infection in the subject. The inventors have discovered these specific markers of active *T. gondii* infection, as described in the examples that follow.

The blood sample can be whole blood, serum, blood plasma, or any other suitable blood sample in which circulating IgG from a person with toxoplasmosis may be present. For example, the blood sample may be a plasma sample. As used herein, a "plasma sample" means blood plasma, the liquid component of blood, and is prepared, for example, by centrifugation of whole blood to remove blood cells. As used herein, a plasma sample also includes a blood serum sample, in which blood clotting factors have been removed.

Any suitable control can be used, including but not limited to a reference value obtained from one or more subjects that either do not have a *T. gondii* infection, or that are known to have a *T. gondii* infection, a previous blood sample obtained from the same subject, or any other suitable control. It is well within the level of those of skill in the art to determine an appropriate control for an intended use in light of the teachings herein. The change in level from control that correlates with *T. gondii* infection in the subject may be a difference of 10%, 25%, 50%, 100%, or more. In one embodiment, the difference is a statistically significant increase as judged by standard statistical analysis.

The level (e.g., quantity or amount) of a particular biomarker can be measured in the blood sample using a variety of methods known to those of skill in the art. Such methods include, but are not limited to, flow cytometry, ELISA using red blood cell, platelet, or white blood cell lysates (e.g., lymphocyte lysates), and radioimmunoassay.

In one embodiment, the method is used to monitor effect on the subject of a therapy for *T. gondii* infection. In this embodiment, the subject is receiving therapy for a *T. gondii* infection, and the methods permit attending medical personnel to assess efficacy of the therapy. In this embodiment, the blood sample test may, for example, be carried out periodically over time during the course of therapy. In another embodiment, the method is used to diagnose whether the subject is suffering from a *T. gondii* infection. In this embodiment, the subject is suspected of suffering from a *T. gondii* infection based on the presence of one or more symptoms, and the methods can be used to assist in providing a more definitive diagnostic, along with all other factors to be considered by an attending physician.

In various embodiments of these methods:

(a) an increase in level of one or more of clusterin, oxytocin, miR-17-92, or miR-124 compared to control correlates with active *T. gondii* infection; and/or

(b) a decrease in level of one or more of PGLYRP2 or ApoA1 compared to control correlates with active *T. gondii* infection.

In further embodiments of these methods:

(a) a decrease in level of one or more of clusterin, oxytocin, miR-17-92, or miR-124 compared to a level of the one or more markers in a serum sample obtained from the subject at an earlier time point correlates with a positive effect of the therapy in treating active *T. gondii* infection; and/or

(b) an increase in level of one or more of PGLYRP2 or ApoA1 compared to a level of the one or more markers in a serum sample obtained from the subject at an earlier time point correlates with a positive effect of the therapy in treating correlates with active *T. gondii* infection.

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In one embodiment, the *T. gondii* infection involves neuronal damage and/or retinal damage in the subject. For example, the *T. gondii* infection may involve neuronal damage selected from the group consisting of neurodegeneration and/or seizures.

In another aspect, the invention provides methods for treating a *T. gondii* infection, comprising administering to a subject with a *T. gondii* infection an amount effective to treat the infection of ApoA1. As shown in the examples that follow, a reduction in apoA1 closely correlates with active *T. gondii* infection. The apoA1 may be administered as a protein therapeutic, or may be administered in an expression construct (such as a recombinant viral vector, etc.) that expresses apoA1 (i.e.: gene therapy).

In one embodiment, the subject to be treated has a decreased level of serum ApoA1 compared to control.

```
UniProtKB-P02647 (APOA1_HUMAN) (SEQ ID NO: 4)
MKAAVLT LAV LFLTGSQARH FWQQDEPPQS PWDRVKDLAT
VYVDVLKDSG RDYVSQFEQS ALGKQLNLKL LDNWDVSTST
FSKLRQLGVP VTQEFWDNLE KETEGRLQEM SKDLEEVKAK
VQPYLDDFQK KWQEEMEL YR QKVEPLRAEL QEGARQKLHE
LQEKLSPLGE EMRDRARAHV DALRTHLAPY SDELQRQLAA
RLEALKENG G ARLAEYHAKA TEHLSTLSEK AKPALEDLRQ
GLLPVLESFK VSFLSALEEY TKKLNTQ.
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As used herein, the term "individual" or "patient," or "subject" used interchangeably, refers to any animal, including mammals, preferably mice, rats, other rodents, rabbits, dogs, cats, swine, cattle, sheep, horses, or primates, and most preferably humans.

As used herein, the phrase "amount effective", "therapeutically effective amount" or "effective to treat" refers to the amount of active compound or pharmaceutical agent that elicits the biological or medicinal response that is being sought in a tissue, system, animal, individual or human by a researcher, veterinarian, medical doctor or other clinician.

In certain embodiments, a therapeutically effective amount can be an amount suitable for (1) preventing the disease; for example, preventing a disease, condition or disorder in an individual who may be predisposed to the disease, condition or disorder but does not yet experience or display the pathology or symptomatology of the disease; (2) inhibiting the disease; for example, inhibiting a disease, condition or disorder in an individual who is experiencing or displaying the pathology or symptomatology of the disease, condition or disorder; or (3) ameliorating the disease; for example, ameliorating a disease, condition or disorder in an individual who is experiencing or displaying the pathology or symptomatology of the disease, condition or disorder (i.e., reversing the pathology and/or symptomatology) such as decreasing the severity of disease.

As used here, the terms "treatment" and "treating" means (i) ameliorating the referenced disease state, for example, ameliorating a disease, condition or disorder in an individual who is experiencing or displaying the pathology or symptomatology of the disease, condition or disorder (i.e., reversing or improving the pathology and/or symptomatology) such as decreasing the severity of disease; or (ii) eliciting the

referenced biological effect (e.g., reducing parasitic load or adverse effects the parasite is causing in the human it infects).

As used herein, the phrase “pharmaceutically acceptable salt” refers to both pharmaceutically acceptable acid and base addition salts and solvates. Such pharmaceutically acceptable salts include salts of acids such as hydrochloric, phosphoric, hydrobromic, sulfuric, sulfinic, formic, toluene-sulfonic, methanesulfonic, nitric, benzoic, citric, tartaric, maleic, hydroiodic, alkanolic such as acetic, HOOC—(CH₂)_n—COOH where n is 0-4, and the like. Non-toxic pharmaceutical base addition salts include salts of bases such as sodium, potassium, calcium, ammonium, and the like. Those skilled in the art will recognize a wide variety of non-toxic pharmaceutically acceptable addition salts.

Example 1. New Paradigms for Understanding and Step Changes in Treating Active and Chronic, Persistent Apicomplexan Infections

Abstract

Toxoplasma gondii, the most common parasitic infection of human brain and eye, persists across lifetimes, can progressively damage sight, and is currently incurable. New, curative medicines are needed urgently. Herein, we develop novel models to facilitate drug development: EGS strain *T. gondii* forms cysts in vitro that induce oocysts in cats, the gold standard criterion for cysts. These cysts highly express cytochrome b. Using these models, we envisioned, and then created, novel 4-(1H)-quinolone scaffolds that target the cytochrome bc₁ complex Q_i site, of which, a substituted 5,6,7,8-tetrahydroquinolin-4-one inhibits active infection (IC₅₀, 30 nM) and cysts (IC₅₀, 4 μM) in vitro, and in vivo (25 mg/kg), and drug resistant *Plasmodium falciparum* (IC₅₀, <30 nM), with clinically relevant synergy. Mutant yeast and co-crystallographic studies demonstrate binding to the bc₁ complex Q_i site. Our results have direct impact on improving outcomes for those with toxoplasmosis, malaria, and ~2 billion persons chronically infected with encysted bradyzoites.

Toxoplasma gondii infections can cause systemic symptoms, damage and destroy tissues¹⁻¹⁰, especially eye and brain¹⁻¹⁰ and cause fatalities⁵¹⁻²⁰. Primary infections may be asymptomatic, or cause fever, headache, malaise, lymphadenopathy, and rarely meningoencephalitis, myocarditis, or pericarditis^{9,11,12}. Retinochoroiditis and retinal scars develop in up to 30% of infected persons^{1,7,13}, and epilepsy may occur^{6,14}. In immune-compromised and congenitally infected persons, active infection frequently is harmful¹⁻¹⁰. Recrudescence arises from incurable, dormant cysts throughout life^{6,7,9,10}. In rodents, chronic infection alters fear, smell, reward pathways, neurotransmitters such as GABA and dopamine, and causes abnormal neurologic functions¹⁵. Although this parasite is present in the brains of 2-3 billion persons worldwide, consequences are unknown. Neurobehavioral abnormalities and differences in serum cytokines, chemokines, and growth factors were associated with seropositivity in humans^{16, 17}.

Current treatments against active *T. gondii* tachyzoites can have side effects such as hypersensitivity, kidney stones, and bone marrow suppression, limiting their use¹⁰. Latent bradyzoites are not significantly affected by any medicines⁶. Atovaquone partially, and transiently, limits cyst burden in mice¹⁸, but resistance develops with clinical use¹⁹⁻²⁴. Thus, *T. gondii* infection is incurable with recrudescence from latent parasites posing a continual threat. Estimates of costs for available, suboptimal medicines to treat active, primary

ocular, gestational and congenital infections, in just the U.S. and Brazil, exceed \$5 billion per year. Improved medicines are needed urgently. Molecular targets shared by *T. gondii* and *Plasmodia* make re-purposing compounds a productive strategy.

Critical flaws and limitations of available methods and models for developing medicines to cure *T. gondii* infections include lack of in vitro culture systems for cysts and scalable, easy to use animal models for screening compounds. To address these challenges, we characterized the EGS parasite, isolated in 1994 from amniotic fluid of a congenitally infected Brazilian fetus^{24a}, that form cyst-like structures in vitro²⁵. In our characterization of EGS in vitro, herein, we discovered that true cysts develop, making EGS especially useful for drug development. EGS parasites can infect zebrafish, and we have characterized this, as well as a fluorescent tachyzoite and cyst assay in this new model²⁶. Further, cytochrome bc₁ expression is markedly increased in encysted EGS bradyzoites suggesting cytochrome bc₁ might be a viable drug target for this life stage. This mitochondrial membrane bound protein complex cytochrome bc₁, part of the electron transport chain responsible for generating ubiquinone for pyrimidine biosynthesis in *Plasmodium*, is the molecular target of the naphthoquinone, atovaquone²⁷⁻⁵². Partial efficacy, rapid emergence of drug resistance in malaria and toxoplasmosis limit clinical usefulness of atovaquone. We present new 4-(1H)-quinolone scaffolds that target the Q_i site of cytochrome bc₁ in apicomplexan parasites. Our lead 5,6,7,8-tetrahydroquinolin-4-one compound, MJM170, is highly effective against apicomplexan parasites and has substantially enhanced solubility compared with other reported quinolones due to its' new scaffold. Direct visualisation in the crystallographic structure opens the way to design a new generation of compounds for both parasites.

Results

Characterization of EGS Strain Develops Novel In Vitro Models to Test Compounds.

Genotyping and Phylogenetic Analysis of EGS:

We isolated and sequenced genomic DNA from the EGS²⁵ (25) parasite, which formed cysts when grown in human foreskin fibroblasts (HFF) in culture. Phylogenetic analysis based on 796,168 SNPs across 62 *T. gondii* genomes revealed that EGS is closely related to other Brazilian strains including TgCatBr1, TgCatBr18 and TgCatBr25 and ancient South American MAS. All these grouped to clade B, haplogroup 4 and 8. Full genome sequence analysis of EGS compared with canonical and geographically closely related parasite genomic sequences reveal a non-synonymous mutation and disordered c terminal sequence in Apetela 2 (AP2) IV-iv, a bradyzoite repressor. EGS differs from other isolates by non-synonymous SNPs in Apetela 2 IV-iv, M=>I (570) and a disordered area beginning at 821, GGNRPYHVAKQEWVRVRYMNGKRKMRTYSAKFY GYETAHTMAEDFAHYVDKHE (SEQ ID NO: 1). AP2 IV-iv is a member of the plant-like transcription factor family unique to apicomplexan parasites. This AP2 represses tachyzoite to bradyzoite conversion,⁵⁶ among other differences. Because AP2 IV-iv is a bradyzoite gene expression repressor⁵⁶, a mutation could create a parasite like EGS that remains as an encysted bradyzoite.

Phenotypes of EGS in Human Cells In Vitro, and in Cats and Mice:

EGS in Human Foreskin Fibroblasts (HFF).

In vitro, these EGS parasites form cysts that enlarge over ~48-96 hours and then destroy monolayers as single cell organisms. This created novel, useful in vitro models. Cyst

walls are thick in electron micrographs (data not shown). Cyst-like structures' perimeters demonstrate dolichos, with bradyzoites within them staining with BAG1 and nuclei with Dapi. Kinetic analysis of EGS in HFF cultures, 2, 18, and 72 hours after infection, RNA-seq and MiR-seq results demonstrated varied expression signatures over time in culture (FIG. 5) with expression of bradyzoite markers by 18 hours and Apetela 2 signatures by 2 hours.

Cats Fed EGS in HFF Cultures or Mouse Brain Produce Oocysts.

When HFF tissue cultures with these cyst structures were fed to cats, they developed the classic, gold standard bradyzoite phenotype of producing oocysts in two replicate experiments. All other *T. gondii* strains cultured for more than 30 passages, as EGS was since the 1990s, lose the ability to produce oocysts when fed to cats (JP Dubey, personal observations.). This experiment established that these were true bradyzoites in cysts formed in vitro under standard culture conditions. Oocysts also formed 10 days after feeding cats mouse brains infected with EGS stably transfected with tachyzoite SAG1 promoter-driven mcherry, and bradyzoite BAG1 promoter-driven green fluorescent protein (GFP), and merozoite promoter-driven blue fluorescent protein, engineered to facilitate creation of automated, scalable in vitro and in vivo assays. In vitro, these promoters did not provide a fluorescence signal robust enough to detect differences between 2×10^5 and 650 parasites useful in scalable assays (data not shown).

EGS is Virulent in Mice.

When these EGS oocysts were fed to mice they produced disease indistinguishable from other virulent Brazilian strains. Oocysts given to mice per-orally created an illness and histopathology phenotypically characteristic for typical, virulent parasites causing dose related proliferation of *T. gondii* with necrosis in terminal ileum, pneumonia at 9-10 days, with brain parasites by 17 days and dose-related mortality.

EGS has a Bradyzoite/Cyst Morphology and Alters the Transcriptomes of the Biologically Relevant Human Monocytic Cell Line MM6 and Human Primary Neuronal Stem Cells (NSC).

Human cells particularly relevant to human toxoplasmosis were infected with different strains of *T. gondii* to better characterize EGS parasites. Immunofluorescence staining of EGS-infected MM6 and NSC cultures revealed the development of cysts (FIG. 6a) and accordingly, EGS gene expression resembled that of bradyzoites when compared to equivalent infections done with GT1, ME49 or VEG strains. Interestingly, EGS transcription was influenced by host cell type (FIG. 6). Transcriptomics using host mRNA and miR profiling of EGS cultures in MM6, and NSC cells for 18 hours demonstrated that this parasite modulates host transcripts involved in protein misfolding, neurodegeneration, endoplasmic reticulum stress, spliceosome alteration, ribosome biogenesis, cell cycle, epilepsy, and brain cancer among others (FIG. 6). The number of genes significantly up or down regulated in MM6 and NSC cells compared to uninfected controls are depicted in FIG. 6. Overexpressed genes differ from those of GT1, ME49 and VEG tachyzoite-infected human NSC cells (FIG. 7a), but modify the same or connected pathways (McLeod et al, unpublished observations). Hsa-miR-708-5p was the most affected miRNA (down-modulated) by EGS (FIG. 6e; FIG. 2). miR-708-5p is a regulator that promotes apoptosis in neuronal and retinal cells, which could maintain a niche for EGS-like encysted bradyzoites to persist.

EGS Transcripts Demonstrate Importance of Cytochromes and Key Apetela 2 Transcription Factors in this Life Cycle Stage.

EGS transcripts in HHF, MM6, and NSC cells were enriched for genes transcribed in bradyzoites, including known bradyzoite transcripts, certain Apetela 2s and cytochrome b and other cytochromes (FIG. 7b-c). Among transcripts with the most increased fold change in EGS across all three cell lines were: cytochrome b; cytochrome c oxidase subunit III subfamily protein; apocytochrome b; cytochrome b, putative; and cytochrome b (N-terminal)/b6/petB subfamily protein. Other over-expressed genes include bradyzoite transcription factor AP2IX-9 and plant-like heat-shock protein BAG1 (FIG. 7 a-c).

Identifying Novel and Efficacious Compounds Against *T. gondii* Cytochrome bc₁.

Increased expression of cytochromes in EGS (FIG. 7c) made it pertinent to synthesize and test an endochin-like quinolone (ELQ) 271, which was previously reported to inhibit *T. gondii* cytochrome bc₁ Q_i site and reduce, but not eliminate, brain cyst numbers in mice²⁷. ELQ271 also inhibited EGS in vitro (FIG. 7d bottom) demonstrating that our in vitro model correlates with previously reported partial activity of ELQ271 against bradyzoites in cysts in mouse brain. Vivoporter-PMOs inhibiting cytochrome bc₁ had a modest effect on tachyzoite replication and a small effect on size and number of EGS cysts (FIG. 7d top). Minimal effect might be related to limited entry of vivoporter into cysts or mitochondria.

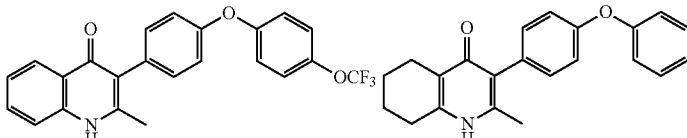
ELQs have been a focus for drug development for malaria (ELQ 300) and toxoplasmosis (ELQ 271 and 316) as they were reported to be potent and selective (versus human cytochrome bc₁) inhibitors of *P. falciparum* cytochrome bc₁ at nanomolar concentrations²⁷. ELQs are part of the 4-(1H)-quinolone class of cytochrome bc₁ inhibitor^{36,42,40,45,49,52,53,54,56-62} and (Doggett et al, 13th International Toxoplasmosis Meeting Abstract, Gettysburg Pa., June 2015), a scaffold that suffers from limited aqueous solubility. Another aspect of inhibitor design for this system is minimizing the inhibition of mammalian cytochrome bc₁, which shares ~40% sequence identity to the *T. gondii* ortholog within the Q substrate sites. Thus, we set out to design potent and selective inhibitors of *T. gondii* cytochrome bc₁ with improved solubility (FIG. 8) compared to known quinolone-based inhibitors. Noting the previous work of GSK on the preclinical development of Clodipol derivatives which led to terminating studies secondary to toxicity in the rat models, as another serious deficiency⁶³ and the incorporation of the diphenyl ether group onto the central 4-(1H)-quinolone core as reported by Riscoe et al.²⁷, we focused on the central core ring system. Doggett, Riscoe et al's²⁷ ELQ 271 (FIG. 8) was reported to be ineffective against yeast with a mutation in the Q_i site. Nonetheless, it recently was shown that ELQs can bind both Q_i and Q_o depending on subtle chemical changes⁶¹⁻³. As a result of our initial efforts, a 5,6,7,8-tetrahydroquinolone (MJM170, 2) displayed promising results. (FIG. 8; Table 2). We chose ELQ271 for comparison because it had the greatest activity at the lowest dose (5 mg/kg) in the mouse model of Doggett despite the higher cytotoxicity toward human fibroblasts in the in vitro toxicity studies.²⁷

MJM170 is a potent inhibitor of *T. gondii* tachyzoites (RH-YFP strain, IC₅₀ 0.03 μ M) and bradyzoites (EGS strain, IC₅₀ 4 μ M), equipotent to ELQ271 (Table 2, FIG. 9). MJM170 showed 10-fold improved aqueous kinetic solubility (pH 7.4) over ELQ 271 (Table 2), 3-fold improved FaSSIF/FeSSIF (pH 6.5) solubility, with similar human

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microsomal stability profiles (146 vs 172 minutes). A different method from that in reference⁴⁹ was used. MJM170 has a significantly decreased mouse microsomal stability compared to ELQ 271 (20 vs >200 minutes). MJM170 was further evaluated with MDCK-MDR1 cells (a measure of blood-brain barrier permeability) and results suggest that MJM170 could cross the blood brain barrier and not suffer from P-glycoprotein efflux. These data highlight the potential of the 5,6,7,8-tetrahydroquinolin-4-one scaffold for further hit-to-lead development.

TABLE 2

Comparison of ELQ 271 and MJM170 in our biological assays: inhibition of apicomplexan parasites and ADME/Tox. ELQ 271 was synthesised in-house.		
Compound	ELQ 271	MJM170
Structure		
Mol. Wt.	411.4	331.4
<i>T. gondii</i> Tachyzoite IC ₅₀ μM	0.03	0.03
<i>T. gondii</i> Bradyzoite IC ₅₀ μM	1	4
<i>P. falciparum</i> IC ₅₀ μM ^a	0.03 (D6) 0.09 (TM91C235) 0.10 (W2) 0.13 (C2B)	0.01 (D6) 0.03 (TM91C235) 0.03 (W2) 0.01 (C2B)
HFF Toxicity CC ₅₀ μM	20	20
Kinetic Solubility PBS pH 7.4 μM ^b	0.15	1.97
FaSSIF Solubility pH 6.5 μM ^b	3.4	9.8
Human microsomal stability T _{1/2} mins ^b	171.9	146.3
Mouse microsomal stability T _{1/2} mins ^b	>200	21.0
MDCK-MDR1 P _{app} A-B × 10 ⁶ cm/s ^b	N.D.	32.1
MDCK-MDR1 Efflux Ratio ^b	N. D.	1.23

^aThe D6 strain (Sierra Leone) is drug sensitive, the TM91C235 (Thailand) is multi-drug resistant, the W2 strain (Thailand) is chloroquine resistant, and the C2B strain is multi-drug resistant with pronounced resistance to atovaquone.

^bADME carried out by ChemPartner Shanghai Ltd. N.D. not determined. Human and mouse microsomal stability differs as is known to occur for other compounds such as TMP/SMX.

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resistance of yeast and *P. falciparum* with known cytochrome b Q_i mutations predicted to cause a steric clash with MJM170 (FIG. 11). Recently, we reported co-crystal structures of GSK's cytochrome bc₁ inhibitors bound to bovine cytochrome bc₁ at the Q_i site⁵² demonstrating that these pyridone inhibitors and other structurally related inhibitors bind to an alternative site to atovaquone on cytochrome bc₁. This structure allowed us to model MJM170 within the Q_i site using the Maestro Suite from Schrödinger. This molecular modelling predicted steric

MJM 170 is Effective In Vivo Against Tachyzoites, and Modestly Against Bradyzoites in Cysts of Mice, and Development of a Scalable Zebrafish Assay.

MJM170 was highly efficacious against RH (FIG. 10a) and Prugniald (FIG. 10b) strain tachyzoites in mice at 25 mg/kg without toxicity for 5 days (p<0.00), and modestly reduced numbers of Me49 strain cysts established >2 months earlier when treated with 12.5-25 mg mg/kg for 17 days (p<0.002) (FIG. 10c). In analysis of parallel histopathology, there was a similar trend (data not shown). Translucent zebra fish can be infected with EGS, other *T. gondii* that make cysts, and RH YFP preparing for a novel model for scalable screening (FIG. 10d).

Cytochrome bc₁ Q_i is the Binding Site of MJM170 which is Potent Against *Plasmodium falciparum* and Yeast. Tetrahydroquinolone Binds to the Q_i Site of Cytochrome bc₁:

Studies to determine whether cytochrome bc₁ Q_i is the molecular target of MJM170 initially included studies of

clashes in mutant yeast and *P. falciparum* cytochrome bc₁ with MJM170 (FIG. 11a).

Co-Crystallization of MJM170 with Bovine Cytochrome bc₁ and Modelling of the *T. gondii* Enzyme Confirm the Target.

Co-crystallization validates predictions made with modelling and confirmed using assays with *S. cerevisiae* mutants (FIG. 11d). There was no steric clash for *P. falciparum*-model based upon this crystal structure, consistent with in vitro assays (FIGS. 11 e,f). MJM170 was co-crystallized with bovine cytochrome bc₁ and the resulting good quality electron density maps allowed for unambiguous placement of MJM170 within the Q_i site (FIG. 11f). The planar region of the quinolone group is held between heme b_H and Phe220 and the additional ring further extends into the hydrophobic cavity at the apex of the binding site towards Pro24 and

Ile27. The carbonyl group of the compound is surrounded by Ser35, Asp228 and the carbonyl of Trp31, while its amine moiety lies between His201 and Ser205. The diphenyl ether group extends outwards towards the hydrophobic residues Ile39 and Ile42 and forms a stacking interaction with Phe18 (FIG. 11f). An example of a stereo electron density involving Ile118-Met129 and Phe183-Phe199 is shown in FIG. 11g).

Surrogate Assays Demonstrate Efficacy of Compounds, Providing Target Validation and Added Value as MJM170 is Effective Against Wild Type but not M221Q(F) Mutant Yeast.

Mutants of *S. cerevisiae* were used to further confirm the molecular target of MJM170 (FIG. 11d), and documented that the Q_i domain in cytochrome b is essential for its efficacy. This approach provided insight into binding of compounds to the enzyme. Crystallographic structure of bovine cytochrome bc₁ with GSK932121⁵² indicates that certain amino acids are critical in tetrahydroquinolone binding and explains why there is inhibition by certain compounds. Previous studies reported that no cross-resistance is observed between ELQs and atovaquone in *P. falciparum*. This is rationalised as atovaquone binds the Q_o site on cytochrome bc₁. A yeast M221Q substitution within the Q_i site displayed resistance to ELQ inhibition further confirming that this to be the target site²⁷. MJM170 and ELQ271 were effective against *S. cerevisiae* wild type parental AD1-9 strain at 1 mM, 100, 5 and 1 μ M when grown on non-fermentable, glycerol medium forcing reliance on ATP production for respiration. Yeast strains with point mutations in the cytochrome b gene that substitute methionine by glutamine (M221Q) or phenylalanine (M221F) at position 221 in the Q_i site predicted to yield a steric clash upon inhibitor binding were resistant to MJM170 (FIG. 11d).

Tetrahydroquinolones are Potent Against Wild Type *P. falciparum*, and *P. falciparum* G33A/V and Other Drug Resistant Mutants but not DHODH Mutant.

MJM170 is highly effective against *P. falciparum* (Table 2) including multiple strains resistant to available antimicrobials and a cytochrome bc₁ Q_i mutant (FIG. 12). Resistance against transgenic *P. falciparum* yeast DHODH mutant strain indicates MJM170 affects mitochondria suggesting that the mode of action against *P. falciparum* is through inhibition of electron transport (FIG. 12a).

Potentially Clinically Useful Combinations with Tetrahydroquinolone Demonstrated in Synergy Studies.

To determine whether there might be clinically relevant synergies and additive effects, combinations of MJM170 with other clinically available and useful compounds also were tested. Earlier, we had found cycloguanil and related biguanide triazines⁶⁴ were active against *T. gondii* tachyzoites and *P. falciparum* making it relevant to test them in combination with MJM170. We observed modest synergy in vitro for atovaquone, additive effect with cycloguanil, and antagonism with BRD6323, a Q_i inhibitor for *P. falciparum* (FIG. 12b). Combining atovaquone with proguanil (active component cycloguanil) as Malarone^R for malaria provides an approach to reduce selection of drug resistant *plasmodium* mutants.

Discussion

The results presented here offer a molecular understanding and therapeutic strategies for one of the most common parasitic infections of human brain and eye, and that persists across lifetimes in around 2 billion people worldwide. We have developed new models to facilitate discovery of curative treatments for toxoplasmosis. We have characterized the Brazilian *T. gondii* isolate called EGS that was known to be morphologically similar to encysted bradyzoites in tissue

culture. We further validate the cystic nature of these EGS infected cultures, since they are able to induce the intra-intestinal life cycle when fed to cats ultimately resulting in oocyst secretion. This is the first such description of this phenotype and provides definitive proof that this unique parasite has a true cyst phenotype when maintained in vitro. Our data also provide a number of other major conceptual advances on EGS by demonstrating the following: (i) Genome sequencing of this EGS isolate demonstrates that EGS has a typical Brazilian virulent genotype and phylogeny, (ii) EGS is a haplogroup 4 *T. gondii*. Consistent with a genotype that is known to be pathogenic and virulent for mice, we demonstrate that EGS oocyst induced infection is similar to that of other virulent Brazilian parasites. For example, mice fed EGS oocysts demonstrated ileal parasites causing necrosis, as well as pneumonitis, encephalitis and systemic infection leading to death. This indicates that the ability to form cysts in culture does not alter the pathogenicity of EGS in mice. However, potentially relevant to its in vitro bradyzoite phenotype, full genome sequencing revealed that it has nonsynonymous single nucleotide repeat sequence differences from other Brazilian and canonical U.S. and European parasites which do not share its in vitro bradyzoite phenotype. EGS has a non-synonymous mutation in a bradyzoite repressor, Apetela 2 (AP2) IV-iv, plant like transcription factor. AP2s interact with HATs and HDACs to modulate transcriptional signatures in apicomplexan parasites⁵⁵. This Apetela 2, plant-like transcription factor gene, AP2IV-4, represses bradyzoite genes during the tachyzoite cell cycle, thereby preventing commitment to the bradyzoite developmental pathway⁵⁶. If the observed substitution or disordered N terminus results in a defective or non-functional molecule, this could provide an explanation for the observed bradyzoite phenotype of EGS parasites. This is consistent with our findings that EGS in HFF forms cysts by 24 hours, characterized by BAG1, and Dolichos staining at 24, 48, and 96 hours after infection. These cysts gradually enlarge until 48-96 hrs in culture, when single *T. gondii* begin to destroy HFF monolayers. These are the cultures of bradyzoites in cysts that when fed to cats ~48 hours after infection form oocysts which are virulent in mice, providing definitive proof of an in vitro bradyzoite phenotype for the EGS strain of *T. gondii*.

The transcriptomic studies with this EGS isolate have provided critical insights into host cell mechanisms that are a prominent part of the ability of the encysted parasite to persist in this untreatable life cycle stage, and biologic consequences of such persistent infection. RNAseq and miR seq of EGS infected human host cells included human fibroblasts, monocytic and neuronal stem cells with this encysted EGS strain parasite. These provide an understanding of the types of perturbations of biologically relevant host cells this bradyzoite life cycle stage can cause, providing insights into unique aspects of pathogenesis of this infection with untreatable cysts and its consequences. We found that EGS modifies critical host cell pathways. For example we find in vitro modulations of host cell pathways in human, primary neuronal stem cells are the same as those associated with modulation of host cell replication as seen with malignancies, and in neurodegenerative diseases. Further, it is noteworthy that the level of a microRNA that specifies apoptosis in eye and brain cells is markedly down modulated by this EGS bradyzoite which would inhibit host protective apoptotic mechanisms allowing parasites to persist in brain and eye without a critical protective mechanism. EGS, as an encysted bradyzoite, clearly alters biologic processes including cell cycle, cell death, alternative splicing, protein syn-

thesis, protein folding and ubiquitination and down regulates hsa-miR-708-5p that specifies apoptosis in neuronal and retinal cells⁶⁵.

RNA and MiR sequencing and transcriptomic analyses of the EGS parasites also identified molecular targets that are critical for the bradyzoite life cycle stage in the parasite as well. These molecular targets include cytochrome b, as critically increased in dormant, encysted parasites. Cytochrome b was increased along with known cyst constituents like enolase 1, Cyst wall protein, Lactate dehydrogenase 2, bradyzoite antigen 1, Apetela 2 plant like transcription factors not present in animals, such as AP2 IX-ix, and cytochrome oxidase. Our work provides a new means to identify stage specific molecular targets, and emphasizes that cytochrome bc₁ complex is a critical target. The transcriptome of EGS parasites in HFF over time are similar to those of in vivo bradyzoites in terms of known critical genes modified. Finally, EGS presents a much-needed assay for identifying novel molecular targets present in bradyzoites in vitro. EGS was also useful to evaluate the effect of inhibitors on encysted bradyzoites in vitro.

Recent crystallographic studies with the bovine cytochrome bc₁ complex allowed us to rationally design a novel compound to target the Q_i site of cytochrome b. Our novel compound was designed to address issues with poor solubility of existing quinolone/pyridone Q_i inhibitors. One of these compounds MJM170, a substituted 5,6,7,8-tetrahydroquinolin-4-one inhibits active infection (IC₅₀ 30 nM) and cysts (IC₅₀ 4 μM) in vitro, and in vivo (25 mg/kg). It is predicted to cross the blood brain barrier with no efflux as demonstrated in an in vitro MDR1-MDCK permeability assay (Table 2), indicating this class of compounds have promise for treatment of central nervous system infections. When we tested MJM170 against wild type and multi-drug resistant *P. falciparum*, we found it was also potent (IC₅₀ <30 nM against all strains). In combination studies, MJM170 was identified as additive with cycloguanil and modestly synergistic with atovaquone. Studies of yeast and malaria mutants, as surrogate assays, and co-crystallography studies with bovine cytochrome bc₁ confirm the mechanism of action/target for MJM170. The co-crystal structure of MJM170 in complex with bovine cytochrome bc₁ reveals a clear binding mode within the Q_i site. Using homology models of the apicomplexan Q_i sites, there are clear differences between the binding sites of the apicomplexan and mammalian orthologs which can be used to fine-tune the selectivity of our scaffold towards apicomplexan bc₁. The larger binding pocket of the apicomplexan versus the mammalian bc₁ may provide a way forward to increase selectivity. Our work provides a conceptual and a practical step change forward that provides a foundation for further testing and improvements to efficacy, toxicity, solubility, oral absorption, large animal toxicology that will be needed to reach the clinic. Our work reported herein not only provides new and important insights into the biology of *T. gondii*, especially the bradyzoite life cycle stage and the remarkable effects of this parasite on its human host's cells, but also provides critical molecular targets and new methods to identify others. Armed with this information, a novel scaffold with intrinsically higher solubility than the equivalent quinolone has been designed with holds promise towards developing a much-needed curative medicine for those with toxoplasmosis, malaria, and ~2 billion persons chronically infected with presently incurable, encysted bradyzoites which persist and can recrudescence lifelong.

Methods

All methods were carried out in accordance with approved guidelines set at the University of Leeds by the Education & Training Resources office and all experimental protocols were approved by the IRB committees; University of Chicago Institutional Animal Care and Use Committee (IACUC) and all experimental protocols were approved by the IRB committee; United States Department of Agriculture IACUC and all experimental protocols were approved by the IRB committees; J Craig Venter Institute Research ethics committee; University of Liverpool UK Office for Research Integrity (UKRIO) and all experimental protocols were approved by the IRB committees; Harvard School of Public Health HMS IACUC and all experimental protocols were approved by the IRB committees; The Broad Institute IACUC and all experimental protocols were approved by the IRB committees; Walter Reed Army Institute of Research Division of Human Subjects Protection (DHSP) and all experimental protocols were approved by the IRB committees; Oregon State University IACUC and all experimental protocols were approved by the IRB committees; Institute for Systems Biology ethics committee; Albert Einstein College of Medicine IACUC and all experimental protocols were approved by the IRB committees; Strathclyde University Ethics Committee (UEC) and all experimental protocols were approved by the IRB committees; Institute for Integrative Biology of the Cell IACUC and all experimental protocols were approved by the IRB committees, and the Centre national de la recherche scientifique IACUC and all experimental protocols were approved by the IRB committees.

Cells and Parasites for Work with *T. gondii*

Cells:

The cells utilized for *T. gondii* assays included human foreskin fibroblasts (HFF), Human MonoMac 6 cells (MM6), and Neuronal Stem cells (NSC) from a temporal lobe biopsy.

Toxoplasma gondii.

The strains of *T. gondii* utilized in this work were: RH-YFP Tachyzoites of the RH-YFP strain were passaged in human foreskin fibroblasts (HFF cells); EGS-Bradyzoite assays use the EGS strain, isolated from amniotic fluid of human with congenital toxoplasmosis; Other strains used are: Me49; Prugnau; Beverly; Veg; GT1. All other than EGS are *T. gondii* tachyzoites. These parasites are passaged in HFF.

Isolation of DNA and RNA.

EGS single celled organisms were grown in Human Foreskin Fibroblasts, filtered free of host cells. gDNA was isolated and processed for sequencing as described. For isolation of RNA RIN scores were >8.

Gene Sequencing, Genomics, RNA and MiR Sequencing, Systems Analysis, Metabolomics

Genome Sequencing of *T. gondii* EGS Strain.

A single Illumina paired-end barcoded library was prepared from tachyzoite gDNA with Illumina TrueSeq library preparation kit. The library was then sequenced using 100 bp paired-end reads in one ninth of a lane of an Illumina HiSeq 2000 machine to generate ~2 Gbp of genome sequence.

Single Nucleotide Polymorphism (SNP) Identification and Annotation.

Illumina genome sequencing reads from EGS or downloaded from GenBank SRA database for GT1 (SRR516419), VEG (SRR516406) and TgCatBr1 (SRR350737) were aligned to the *T. gondii* ME49 reference genome assembly (ABPA02000000, ToxoDB release 13.0) with Bowtie2 and realigned around gaps using the GATK toolkit. SNP calls were done simultaneously across all four strains with sam-

tools utility mpileup, requiring a minimum SNP coverage of 5 reads and an alternative allele frequency of 0.8 or higher, given the haploid nature of these genomes. Thereafter, SnpEff and a gff3 file containing the annotation of *T. gondii* ME49 downloaded from ToxoDB v13.0 were used to classify the different types of mutations identified in each strain. Allelic variants that were different between EGS and the rest of the strain were considered EGS-specific.

Phylogenetic Network Analysis.

A total of 790,168 single nucleotide polymorphisms spanning the entire *T. gondii* genome from 62 different strains representing all major haplogroups were downloaded from ToxoDB, combined with SNP data from the same sites from the EGS strain and directly incorporated as a FASTA file into SplitsTree v4.13.1 to generate unrooted phylogenetic networks using a neighbor-net method.

Differential Gene Expression (DGE) Analysis.

Total RNA extracted from human cell cultures infected (or not) with a number of *T. gondii* strains for 2 h, 18 h or 48 h was treated with miRNeasy Mini Kit columns (Qiagen) following manufacturer instructions to separate mRNA and miRNA fractions. Afterwards, Illumina barcoded sequencing libraries were constructed with TruSeq RNA Sample Preparation Kits v2 (Illumina) for mRNA and miRNA TruSeq Small RNA Library Preparation Kit (Illumina) for miRNA. Libraries were sequenced as 100 bp single reads with Illumina HiSeq 2000 apparatus in pulls of 6 or 9 samples per lane for mRNA (yield ~3 Gbp per sample) and miRNA (yield ~2 Gbp per sample) libraries respectively. For protein coding genes, reads were mapped to the human (release GRCh38) and *T. gondii* ME49 strain (ToxoDB release 13.0) reference genome assemblies and annotations with CLC Genomic Workbench software (CLC Bio-Qiagen, Aarhus, Denmark) and raw read counts per gene were then analyzed with the R package EdgeR using a generalized linear model likelihood ratio test to identify genes that are differentially expressed among samples.

For miRNA DGE analysis, reads were depleted of adaptor and primer sequences and mapped to the human reference genome assembly (GRCh38) and the miRNA annotation from miRBase v21 (see the mirbase web site) with CLC Genomic Workbench software. Identification of human miRNA genes that are differentially expressed across treatments was carried out with EdgeR from raw read counts per miRNA gene using a generalized linear model likelihood ratio test.

For both mRNA and miRNA DGE analyses p-values were adjusted for multiple hypotheses testing using the False Discovery Rate method. MDS plots and heat maps were generated with the plotMDS tool from EdgeR and the R tool heatmap. Differentially expressed genes (DEGs) in MM6 and NSC cell lines infected with EGS parasites were identified under the criteria of 1% FDR and absolute log 2-fold-change >1.5 (i.e. fold-change >2 and <0.5 for up- and down-regulated genes, respectively).

Functional Enrichment Analysis

GO enrichment analyses were performed for up- or down-regulated genes, by using the Database for Annotation, Visualization and Integrated Discovery (DAVID) v6.7. GO slim enrichment analysis was performed for genes carrying potential change-of-function mutations in EGS that were absent in strains ME49, VAND or TgCatBr1. GO slim database was downloaded from QuickGO provided by EMBL-EBI. Using taxonomy id "508771" for the ME49 strain, relevant GO slim terms were retrieved. GO slim enrichment analysis was performed with Fisher's exact test based on the GO slim terms.

Assay for Oocyst Development in Cats.

Oocysts were collected from feces of *Toxoplasma*-free cats 3-14 days after feeding infected cell cultures or infected mouse brains. Oocysts were separated from feces by sugar floatation, sporulated in 2% sulfuric acid by aeration at room temperature for 1 week. After removing sulfuric acid oocysts were inoculated orally in to Swiss Webster albino mice. All tissues of mice that died or euthanized were studied histologically after staining with hematoxylin and eosin and by BAG1 antibodies to *T. gondii* as described. (Dubey J P, Ferreira L R, Martins J, McLeod R. Oral oocyst-induced mouse model of toxoplasmosis: effect of infection with *Toxoplasma gondii* strains of different genotypes, dose, and mouse strains (transgenic, out-bred, inbred) on pathogenesis and mortality. Parasitology 139:1-13, Epub 2011. PMID: 22078010; also referred t herein as S39)

Chemical Synthesis.

Final compounds had >95% purity determined by high performance liquid chromatography (HPLC) and 300 and/or 500 MHz NMR spectrometers. Liquid chromatography-mass spectrometry (LC-MS) and high resolution mass spectrometers (HRMS) analytical systems were used to determine integrity and purity of all intermediates and final compounds.

Synthesis of

2-methyl-5,6,7,8-tetrahydroquinolin-4-one (6)

Platinum oxide (100 mg, 10 mol %) was added to a solution of 4-hydroxy-2-methylquinoline (5, 1.00 g, 6.28 mmol, 1.00 eq) in glacial acetic acid (10.0 ml). The heterogeneous mixture was catalytically hydrogenated under a balloon of hydrogen. After 22 hrs, TLC (10% MeOH-DCM) confirmed complete reaction. The mixture was filtered through celite under vacuum, washing thoroughly with EtOAc. The filtrate was concentrated and the resulting residue purified by column chromatography (10% MeOH-DCM) to give the desired product as a pale yellow oil (917 mg, 5.65 mmol, 89%); R_f 0.14 (10% MeOH-DCM); δ_H (300 MHz, CDCl₃) 1.74-1.76 (4H, m, CH₂), 2.29 (3H, s, Me), 2.49-2.52 (2H, m, CH₂), 2.67-2.70 (2H, m, CH₂), 6.16 (1H, s, Ar—H); δ_C (125 MHz, CDCl₃) 19.0 (Me), 21.8 (CH₂), 22.1 (CH₂), 27.1 (CH₂), 112.5 (CH), 122.4 (Cq), 146.4 (Cq), 147.0 (Cq), 178.3 (Cq); Spectroscopic data consistent with literature values (JMC, 1993, 36, 1245-54).

Synthesis of

2-methyl-3-iodo-5,6,7,8-tetrahydroquinolin-4-one (7)

Butylamine (6.20 ml, 62.8 mmol, 10.0 eq) was added to a suspension of 2-methyl-5,6,7,8-tetrahydroquinolin-4-one (6, 1.02 g, 6.28 mmol, 1.00 eq) in DMF (10.0 ml). To this heterogeneous mixture was added I₂ (1.60 g, 6.28 mmol, 1.00 eq) in a saturated solution of KI (6.00 ml). After 20 hrs stirring at R.T., a precipitate formed in the orange solution. Excess iodine was quenched with 0.1 M sodium thiosulfate solution. The precipitate was filtered by vacuum filtration, washed with distilled H₂O and dried (Na₂SO₄) to give the desired product as a colourless solid (1.76 g, 6.09 mmol, quantitative yield); δ_H (300 MHz, DMSO-d₆) 1.61-1.70 (4H, m, CH₂), 2.29 (2H, t, J 6.0, CH₂), 2.43 (2H, s, CH₂), CH₃ under DMSO peak.

Synthesis of 2-methyl-3-iodo-4-ethoxy-5,6,7,8-tetrahydroquinoline (8)

Potassium carbonate (1.53 g, 11.1 mmol, 2.00 eq) was added to a heterogeneous mixture of 2-methyl-3-iodo-5,6,

7,8-tetrahydroquinolin-4-one (7, 1.60 g, 5.56 mmol, 1.00 eq) in DMF (15.0 ml), and the reaction heated to 50° C. for 30 mins. The R.B. flask was removed from the heating mantle and ethyl iodide was added dropwise. The reaction was then heated at 50° C. for 18 hrs. The reaction was cooled to R.T., quenched with water (40 ml). The resulting emulsion formed which was extracted with EtOAc (50 ml). EtOAc layer were washed with water (3×30 ml), brine (3×30 ml), dried (Na₂SO₄) and concentrated to give a pale yellow oil (1.09 g, 3.44 mmol, 61%); R_f 0.88 (1:1 Pet-EtOAc); HPLC (RT=1.67 mins); LCMS (Method A), (RT=1.6 min, m/z (ES) Found MH⁺ 318.0); δ_H (500 MHz, CDCl₃) 1.49 (3H, t, J 7.0, ethoxy CH₃), 1.73-1.78 (2H, m, CH₂), 1.84-1.88 (2H, m, CH₂), 2.78-2.69 (51H, m, CH₂ & CH₃), 2.84 (2H, t, J 6.5, CH₂), 3.97 (2H, q, J 7.0, OCH₂); δ_C (125 MHz, CDCl₃) 15.6 (CH₃), 22.3 (CH₂), 22.8 (CH₂), 23.6 (CH₂), 29.3 (CH₃), 32.0 (CH₂), 68.4 (OCH₂), 90.9 (Cq), 124.5 (Cq), 158.3 (Cq), 158.9 (Cq), 163.9 (Cq).

Synthesis of 2-methyl-3-(4-phenoxyphenyl)-4-ethoxy-5,6,7,8-tetrahydroquinoline (10)

2-Methyl-3-iodo-4-ethoxy-5,6,7,8-tetrahydroquinoline (8, 0.266 g, 0.839 mmol, 1.00 eq), Pd(PPh₃)₄ (0.048 mg, 0.0419 mmol, 5 mol %) and 4-phenoxyphenylboronic acid (9, 0.270 mg, 1.26 mmol, 1.50 eq) were charged to a R.B. flask under N₂(g)⁴⁹. Degassed DMF (10.0 ml) was added to the flask followed by 2M K₂CO₃ (1.60 ml). The flask was heated to 85° C. under N₂(g). After 15 mins, TLC (4:1 Pet-EtOAc) confirmed reaction was complete. The reaction was cooled and diluted with EtOAc (15 ml), filtered through celite and partitioned between EtOAc (10 ml) and H₂O (25 ml). Combined organics were washed with H₂O (3×30 ml), then brine (3×30 ml), dried (Na₂SO₄) and concentrated to give a red oil which was purified by column chromatography (3:1 Pet-EtOAc), to give the desired product as a pale yellow oil (0.235 mg, 0.655 mmol, 78%); R_f 0.31 (3:1 Pet-EtOAc); HPLC (RT=3.08 mins); δ_H (300 MHz, CDCl₃) 1.04 (3H, t, J 7.0, ethoxy CH₃), 1.76-1.93 (4H, m, 2×CH₂), 2.32 (3H, s, CH₃), 2.72 (2H, t, J 6.0, CH₂), 2.91 (2H, t, J 6.5, CH₂), 3.50 (2H, q, J 7.0, OCH₂), 7.05-7.16 (5H, m, Ar—H), 7.20-7.29 (2H, m, Ar—H), 7.31-7.43 (2H, m, Ar—H); δ_C (125 MHz, CDCl₃) 15.7 (CH₃), 22.5 (CH₂), 23.0 (CH₃), 23.3 (CH₂), 23.4 (CH₂), 32.7 (CH₂), 68.2 (OCH₂), 118.6 (CH), 118.9 (CH), 123.4 (CH), 126.8 (Cq), 129.8 (CH), 131.5 (CH), 154.9 (Cq), 156.5 (Cq), 157.1 (Cq), 157.3 (Cq); m/z (ES) (Found: MH⁺, 360.1973. C₂₄H₂₆NO₂ requires MH, 360.1964).

Synthesis of 2-methyl-3-(4-phenoxyphenyl)-4-ethoxy-5,6,7,8-tetrahydroquinoline (MJM170, 4)⁴⁹

Aqueous hydrobromic acid (>48%) (1.00 ml) was added to a solution of 2-methyl-3-(4-phenoxyphenyl)-4-ethoxy-5,6,7,8-tetrahydroquinoline (10, 0.226 mg, 0.630 mmol, 1.00 eq) in glacial acetic acid (2 ml). The reaction was stirred at 90° C. for 5 days, monitoring by LCMS. The reaction was cooled to R.T. and the pH adjusted to pH5 with 2M NaOH. The precipitate was collected by vacuum filtration and recrystallized from MeOH:H₂O to give the desired product as an off-white solid (0.155 g, 0.467 mmol, 74%); HPLC (RT=2.56 mins); δ_H (500 MHz, DMSO-d₆) 1.66-1.72 (4H, m, 2×CH₂), 2.08 (3H, s, CH₃), 2.31 (2H, t, J 6.0, CH₂), 2.56 (2H, t, J 6.0, CH₂), 6.99 (2H, d, J 8.5, Ar—H), 7.06 (2H, d, J 7.5, Ar—H), 7.14-7.18 (3H, m, Ar—H), 7.40-7.43 (2H, m, Ar—H), 11.0 (1H, s, NH); δ_C (125 MHz, DMSO-d₆) 17.7 (CH₃), 21.5 (CH₂), 21.8 (CH₂), 21.9 (CH₂), 26.2 (CH₂),

117.8 (CH), 118.6 (CH), 121.2 (Cq), 123.3 (CH), 123.7 (Cq), 130.0 (CH), 131.4 (Cq), 132.3 (CH), 142.3 (Cq), 143.2 (Cq), 155.0 (Cq), 156.8 (Cq), 175.4 (Cq); m/z (ES) (Found: MH⁺, 332.1654. C₂₂H₂₂NO₂ requires MH, 332.1645).

ADME Studies of Inhibitors:

Compounds that were highly effective in vitro (IC₅₀<1 μM) were tested for ADME profiling⁵⁴³⁻⁵⁸ by Shanghai ChemPartner Ltd. Initial studies focused on aqueous kinetic solubility pH 7.4, microsomal metabolic stability (human and mouse) and Blood-Brain Barrier (BBB) permeability (performed with MDCK-MDR1 cells as described).

In Vitro Assays

Cytotoxicity Assay

Toxicity Analysis.

Lack of toxicity for mammalian host cells was demonstrated first by visual inspection of monolayers following giemsa staining, in separate methods by incorporation of a mitochondrial cell death reagent called WST we used successfully for this purpose and in separate experiments.

Toxicity assays were conducted using WST-1 cell proliferation reagent (Roche). HFF were grown on a flat, clear-bottomed, black 96-well plate. Confluent HFF were treated with inhibitory compounds at concentrations equal to those being tested in challenge assays. Compounds were diluted in IMDM-C, and 20 μl were added to each designated well, with triplicates for each condition. A gradient of 2 fold-decreasing concentrations of DMSO in clear IMDM-C was used as a control. The plate was incubated for 72 hours at 37° C. 10 μl of WST-1 reagent (Roche) were added to each well and the cells were incubated for 30 to 60 minutes. Absorbance was read using a fluorometer at 420 nm. A higher degree of color change (and absorbance) indicated mitochondrial activity and cell viability.

In Vitro Cellular Assays for Effects on *T. gondii*

Vivo PMO:

Vivo-PMO (Vivo porter linked to morpholinos) to knock down cytochrome b and an off-target PPMO (Vivo porter) were utilized at concentrations of 5 and 10 μM as previously described with both cultures of RH-YFP tachyzoites and EGS. Morpholino sequence for cytochrome b/c knockdown is 5' AGTGTTCCTCGAAACCATGCTAACAC 3' (SEQ ID NO: 5), and for unrelated sequence, off target, is 5' CCTCT-TACCTCAGTTACAATTTATA 3' (SEQ ID NO: 6).

Tetrahydroquinolone Compounds:

Compounds synthesized at the University of Leeds were initially prepared in 10 mM Stock solutions made with 100% Dimethyl Sulfoxide (DMSO) [Sigma Aldrich], and working concentrations were made with IMDM-C (1×, [+], glutamine, [+], 25 mM HEPES, [−], Phenol red, 10% FBS) [Gibco, Denmark].

Tachyzoite Assays:

Type 1 Parasites.

Human foreskin fibroblasts (HFF) were cultured on a flat, clear-bottomed, black 96-well plate to 90% to 100% confluence. IMDM (1×, [+], glutamine, [+], 25 mM HEPES, [+], Phenol red, 10% FBS [gibco, Denmark]) was removed from each well and replaced with IMDM-C (1×, [+], glutamine, [+], 25 mM HEPES, [−], Phenol red, 10% FBS)[Gibco, Denmark]. Type I RH parasites expressing Yellow Fluorescent Protein (RH-YFP) were lysed from host cells by double passage through a 27-gauge needle. Parasites were counted and diluted to 32,000/mL in IMDM-C. Fibroblast cultures were infected with 3200 tachyzoites of the Type I RH-YFP strain and returned to incubator at 37° C. for 1-2 hours to allow for infection. Diluted solutions of the compounds were made using IMDM-C, and 20 μl were added to each designated well, with triplicates for each condition. Controls

included pyrimethamine/sulfadiazine (current standard of treatment), DMSO only, fibroblast only, and an untreated YFP gradient with 2 fold dilutions of the parasite. Cells were incubated at 37° C. for 72 hours. The plates were read using a fluorimeter (Synergy H4 Hybrid Reader, BioTek) To ascertain the amount of yellow fluorescent protein, in relative fluorescence units (RFU), as a measure of parasite burden after treatment. Compounds were not considered effective or pursued for further analysis if there were no signs of inhibition at 1 μ M. Data was collected using Gen5 software and analyzed with Excel.

Type II Parasites.

To test type II parasites, *T. gondii* ME49 and Prugneaud parasites expressing luciferase or GFP. We tested them in vitro and in vivo as we have described.

EGS Strain Bradyzoite Assay.

HFF cells were grown in IMDM (1 $\times$, [+] glutamine, [+] 25 mM HEPES, [+] Phenol red, 10% FBS, [Gibco, Denmark]) on removable, sterile glass disks in the bottom of a clear, flat-bottomed 24-well plate. Cultures were infected with 3 $\times$ 10⁴ parasites (EGS strain) per well, in 0.5 mL media and plate was returned to incubator at 37° C. overnight. The following day, the media was removed and clear IMDM and compounds were added to making various concentrations of the drug, to a total volume of 0.5 mL. Two wells were filled with media only, as a control. Plates were returned to the 37° C. incubator for 72 hours.

Efficacy was determined following fixation. Staining was used to determine the numbers of cysts in cultures without and with treatment with the test compounds. Cells were fixed using 4% paraformaldehyde and stained with Fluorescein-labeled Dolichos Biflorus Agglutinin, DAPI, and anti-BAG1, and anti-SAG1. Disks were removed and mounted onto glass slides and visualized using microscopy (Nikon T17). Slides were also scanned using a CRI Panoramic Scan Whole Slide Scanner and viewed using Panoramic Viewer Software.

When cysts that had dolichos in their cyst wall were eliminated or markedly reduced in size and number, a compound was considered efficacious against bradyzoites in cysts.

Statistical Analyses.

Significance of differences were determined using Student's t-test. P<0.05 was considered significant. Every experiment was replicated at least twice. A Pearson test was used to confirm a correlation between increasing dose and increasing inhibition. An ANOVA and subsequent pair wise comparison with Dunnett correction was used to determine whether or not inhibition or toxicity at a given concentration was statistically significant. Stata/SE 12.1 was used for this analysis. This study was approved by the University of Chicago IRB, IBC, and IACUC.

In Vivo Analysis (Mice and Zebra Fish):

Initial Screening with Tachyzoites Using IVIS, Fluorescence, and Histopathology:

Ability of compounds to abrogate tachyzoites multiplication was assessed using an in vivo imaging system (IVIS). To facilitate this we have *T. gondii* strains from each of the 3 major lineages expressing the luciferase gene. In these studies mice are injected intraperitoneally with tachyzoites and parasite proliferation followed up to 30 days post infection. Removal of brains at 30 days allows parasite quantitation by bioluminescence ex vivo using the IVIS. As an alternative method to improve screening efficiency and scalability it is possible for initial screening to use zebrafish with histopathology and visualization as shown in FIG. 6. Quantitation also was performed using QT PCR as described

for mice or in translucent Casper zebrafish with parasites with fluors or luciferase to screen rapidly. Tachyzoites and bradyzoites in cysts were used for IP infection and compounds given intraperitoneally.

Type II Parasites.

To test type II parasites, we used *T. gondii* Me49 and Prugneaud parasites^{S39}.

Encephalitis:

The ability of compounds to reduce cyst burden and prevent encephalitis induced by the Type II strain of *T. gondii* were tested. Encephalitis was assessed by histological analyses and parasite burdens evaluated by quantitation of cysts.

Oocyst Induced Disease:

The oocyst challenge model is ideal for this study because oocysts can be diluted at one time and stored at 4° C. for 12 months without loss of infectivity titer. For treatment of chronic infection there were 5 to 10 mice per group treated 2 months after infection was established by compound in DMSO for parenteral administration administered once per day. Treatment was for 17 days.

Zebrafish

Zebrafish were acclimatized to 37 degrees a degree a day and then infected with tachyzoites or cysts of RH YFP, Me49, Veg *T. gondii* as described. The use of RH YFP was performed for the first time herein in order to develop a rapidly scalable assay for drug development. This is the initial demonstration of cyst formation by 10 days in Zebrafish.

Tissue Processing and Histopathology:

All organs including eyes and brains were fixed in 0.1M phosphate buffer (pH 7.4) containing 4% formaldehyde. Sections were cut from paraffin-embedded tissues and stained with Hematoxylin and Eosin (H&E) or immunoperoxidase stained. All sections were examined and assessed without knowledge of the group from which they originated^{S39}.

Testing of Cytochrome b Qi Mutant Yeast

Target Validation with Mutant *S. cerevisiae* (Growth Inhibition):

Three *S. cerevisiae* strains were used: M221Q and M221F cytochrome b mutants and wild type. They share the same nuclear genetic background deriving from AD1-9 (kindly given by M. Ghislain, UCL, Belgium). AD1-9 harbors multiple deletions in the ABC transporter genes that render the strain more sensitive to drugs than standard yeast strains^{S65}.

Cytochrome b mutant M221F was generated by mitochondrial transformation as described. M221 Q was selected as suppressor from a respiratory deficient mutant. Analysis of revertants from respiratory deficient mutants within the center N of cytochrome b in *Saccharomyces cerevisiae*.

Protocol: Yeast strains were grown over 48 hours at 33° C. in liquid YPG medium [1% yeast extract, 2% (wt/vol) peptone, and 3% (vol/vol) glycerol]. Cultures were diluted to an OD₆₀₀ of 0.05 and grown for 2 hrs. Cultures were then combined with YPG containing 6% melted agar for a total volume of 15-20 mL and poured onto OmniTray single-well rectangular plates that measured 86 mm by 128 mm (ThermoScientific). Filter paper disks (7 mm diameter, 3 μ m thick) were placed onto the cooled agar plates. Compounds were dissolved in DMSO in diluted concentrations (1 mM, 500 μ M, 100 μ M, and 10 μ M) and 10 microliters were applied to a disk. A single disk with DMSO on each plate was used as a control. Plates were incubated at 33° C. Images were obtained after 4 days using GelDoc XR Imag-

ing System (BioRad) and Quantity One software. Drug effect was assessed by the presence and size of a zone of inhibition around the disks.

Testing of *P. falciparum*: D6 is a drug sensitive strain from Sierra Leone, C235 is a multi-drug resistant strain from Thailand, W2 is a chloroquine resistant strain from Thailand, and C2B has resistance to a variety of drugs including atovaquone.

Testing of *P. falciparum* Cytochrome b Qi and DHODH Mutants and Drug Combinations for *P. falciparum*

Parasite Strains and Culture Maintenance.

We used the following parasite line from the MR4 repository of the American Type Culture Collection (ATCC): Dd2 (MRA-156). Mutant Dd2 parasites harboring a G33A or G33V substitution in cytochrome b were as reported. Dd2 parasites with a G131 S mutation in cytochrome b and transgenic lines expressing a chromosomally integrated copy of the *S. cerevisiae* DHODH were utilized as previously described. Parasites were cultured by standard methods in RPMI media supplemented with 5% human O⁺ serum and 0.25% AlbuMAX® II (Life Technologies 11021-045). In Vitro Drug Sensitivity and EC₅₀ Determinations

Drug susceptibility was measured using the SYBR Green method. Twelve point curves based on 2-fold dilutions of the test compound were carried out in triplicate each day and replicated on at least three different days. EC₅₀ values were calculated using a nonlinear regression curve fit in Prism 6.0 for Mac (GraphPad Software, Inc.).

Studies of Compound, Drug Combinations In Vitro.

Isobologram experiments were performed in similar fashion utilizing the modified fixed ratio methodology. Briefly, MJM170 and either atovaquone or cycloguanil or BRD6323 were mixed at multiple fixed volumetric ratios (10:0, 8:2, 6:4, 4:6, 2:8, and 0:10) and then serially diluted in 12-point 2-fold dilutions and dispensed in triplicate to 384-well assay plates and replicated on three different days. EC₅₀ values were calculated as above, and FICs were calculated for each drug combination as described^{S76}. Synergy was defined as an FIC <1.0, additivity as FIC=1.0, and antagonism as FIC >1.0.

Molecular Modelling/Chemogenomics.

X-ray structures of the cytochrome bc₁ complex are available from the Protein DataBanks^{S80}. An Homology model of the *T. gondii* cytochrome bc₁ complex was generated using the Phyre webserver. Molecular modelling and docking was performed on high performance Linux clusters at the University of Leeds, using specialist software: SPROUT^{S82} & eHiTS^{S83} (SymBioSis), Maestro & Glides^{S84} (Schrodinger), AutoDock (Scripps Institute), ROCS/EON^{S85} & VIDA^{S86} (OpenEye) and the Marvin/JChem suites (ChemAxon).

X-Ray Crystallography:

Cytochrome bc₁ was purified using standard techniques. Crude bovine mitochondria were isolated from fresh cow heart and solubilised in DDM. The solution was clarified by ultracentrifugation at 200,000 g for 1 hour at 4° C. and the supernatant applied to a DEAE CL-6B sepharose column ca. 50 ml pre-equilibrated in 50 mM KPi (pH 7.5), 250 mM NaCl, 3 mM NaN₃, 0.1 g/L DDM, washed with two CV and eluted along a gradient from 250 mM to 500 mM NaCl. Cyt. bc₁ containing fractions were pooled and concentrated before loading on a Sepharose S300 column ca. 120 ml equilibrated with 20 mM KMOPS (pH 7.2), 100 mM NaCl, 0.5 mM EDTA, 0.1 g/L DDM at 0.5 ml/min. 10 mM MJM170 stock in DMSO was added to the eluted protein in a two-fold molar excess and allowed to incubate at 4° C. for 1 hour. Increasing amounts of PEG4000 were then added to

precipitate cyt. bc₁ and separate remaining contaminants. The cyt. bc₁ was then resuspended before buffer exchange into a final buffer (25 mM KPi (pH 7.5), 3 mM NaN₃, 0.015% DDM) and concentrated to 40 mg/ml. 1.6% HECAMEG was added to the protein solution prior to crystals growing by the hanging drop vapour diffusion method against a reservoir of 50 mM KPi (pH 6.8), 100 mM NaCl, 3 mM NaN₃, 9% PEG4000, 0.16% HECMAEG. Crystals were flash frozen in 23% glycerol in reservoir solution as a cryoprotectant. Multiple wedges of data were collected at 100K from different points on the same crystal at 124 Diamond Light Source using 0.9686 Å X-rays with a Pilatus3 6M detector.

Datasets were processed in iMosflm and combined using Blend to produce a complete merged dataset. Refinement was carried out with Refmac using ProSMART to generate secondary structure restraints to assist in the low-resolution refinement. The ligand MJM170 was produced using JLi-gand^{S92} and modelled in the Q_i site of cyt. bc₁ using Coot. Cycles of alternating Refmac5 and manual modelling resulted in a completed model. Data collection and refinement statistics are summarised in table 1A. For 3715 residues 95.2% are Ramachandran favored, 4.6% allowed and 0.3% outliers.

Interpretation of Data and Statistical Analyses

(1) Sample Size and Number of Experiments.

There were 3 replicate samples per group for in vitro experiments. All experiments were performed with sufficient sample sizes to have an 80% power to detect differences at the 5% level of significance.

(2) Statistics.

Groups included untreated or mock treated controls. Results were compared using students T test, Chi square analysis or Fisher's exact test as appropriate for the data set. When there were more than two groups, pairwise comparisons were made only when F-test for the ANOVA was significant at the 5% levels using protected least significant difference (LSD) test approach.

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Example 2. Potent Anti-Apicomplexan Tetrahydroquinolone

Summary:

Apicomplexan infections cause substantial morbidity and mortality. Herein, we created a next generation tetrahydroquinolone that we found to be an anti-apicomplexan, mature, lead compound. We utilized sphere-like 3D space and predicted flexibility conferred by eliminating double bonds in this lead compound. This was to optimize ADMET and create a compound, JAG21, that is potent against *Toxoplasma gondii* tachyzoites (IC 90 <125 nM) and bradyzoites (IC 90 500 nM), and drug resistant *Plasmodium falciparum* in vitro (IC 90 <50 nM), not toxic to human HepG cells (>17 μM). Further, we demonstrate metabolic stability with assays for human and mouse liver microsomal activity and logs improved aqueous solubility at pH 7.4. This compound displays a balanced set of physicochemical and pharmacologic properties, including clean hERG, CYP profile, and a long (days in humans), predicted half-life and predicted ability to cross blood brain barrier. This allowed progression towards in vivo studies. In vivo *Toxoplasma* tachyzoites were cleared from mice at a dose of 5 mg/kg/day (IP). JAG21 acted in conjunction with tafenoquine (3 mg/kg single dose) to protect against a G0 arrested parasite that could persist in interferon Y knockout mice similar to the effect of tafenoquine for malaria hypnozoites. There was cure with oral dosing, 0.625 mg/kg, 3 oral doses of JAG21, and cure with a single dose of 2.5 mg/kg, of *P. berghei* sporozoite, blood and liver stages in mice. There was no parasitemia and 100% survival at 30 days. This mature lead compound has improved solubility and diminished toxicity relative to other cytochrome b Qi inhibitors, without formulation as a pro-drug. Selectivity for apicomplexan enzyme relative to mammalian enzymes was demonstrated with co-crystallography, binding and enzyme assays. This compound has real promise as a mature, lead compound.

Malaria results in death of one child every eleven seconds and 1 million children a year, with drug resistance eliminating usefulness of successive generations of new medicines each decade. The related apicomplexan parasite, *Toxoplasma gondii*, is the most frequent parasitic infection of humans, in the world. It is the second most frequent, single

cause of food born associated death in the United States; It is the most frequent infectious cause of destruction of the back of the human eye; It is a cause of death and illness from recrudescence disease from its latent form in those who are immune compromised or immunologically immature; It has been estimated that in a ten year period, there are 1.9 million new cases of this congenital infection globally, causing 12 million disability adjusted life years from damage to the fetal brain and eye. This is neglected, rarely diagnosed, and thus often untreated or mistreated disease. There are approximately 2 billion people throughout the world who have this parasite in their brain lifelong. No medicine eliminates this chronic encysted form of the parasite which causes epilepsy and may contribute to neurodegenerative disease. Certainly, new and improved medicines are greatly needed for both these diseases. These two apicomplexan parasites, *Plasmodia* and *Toxoplasma*, often share molecular targets inhibited by the same inhibitory compounds.

Herein we identify a mature lead compound that is highly efficacious against *T. gondii* tachyzoites and bradyzoites in vitro, tachyzoites in vivo, likely to be active against cysts in vivo with experiments ongoing, all drug resistant forms of *Plasmodium falciparum*, *Plasmodium berghei* in mouse model in single or three doses at low amounts against the sporozoite, blood and liver stages of *plasmodium* when administered orally at 2.5 mg/kg and at 1.25 mg kg for 100% of mice with three doses. It was found to add to protection in conjunction with tafenoquine in immune compromised mice infected with a G0/tachyzoite form of *T. gondii* which resembles the malaria hypnozoite when treated with tafenoquine in conjunction with anti-blood stage parasite compounds. The data which follow present the creation and characterization of this broad spectrum anti-apicomplexan lead compound.

Materials and Methods

Toxoplasma gondii

Tachyzoites of the RH-YFP strain were passaged in human foreskin fibroblasts (HFF cells)(15). Bradyzoite assays use the EGS strain, isolated from a human with congenital toxoplasmosis (16,17). These parasites are also passaged in human foreskin fibroblasts. RPS13 delta was prepared and utilized as described (Hutson, McLeod et al 2010)

Tetrahydroquinolone (THQ) Compounds

The THQ compounds were synthesized at the University of Leeds as described in Example 3. 10 mM stock solutions were made with 100% Dimethyl Sulfoxide (DMSO) [Sigma Aldrich] and working concentrations were made with IMDM-C (1x, [+], glutamine, [+], 25 mM HEPES, [-], Phenol red, 10% FBS)[Gibco, Denmark]). Compounds are shown herein.

In Vitro Challenge Assay for *Toxoplasma* Tachyzoites

Protocol adapted from Fomovska, et. al. (18,19). Human foreskin fibroblasts (HFF) were cultured on a flat, clear-bottomed, black 96-well plate to 90% to 100% confluence. IMDM (1x, [+], glutamine, [+], 25 mM HEPES, [+], Phenol red, 10% FBS [gibco, Denmark]) was removed from each well and replaced with IMDM-C (1x, [+], glutamine, [+], 25 mM HEPES, [-], Phenol red, 10% FBS)[gibco, Denmark]). Type I RH parasites expressing Yellow Fluorescent Protein (RH-YFP) were lysed from host cells by double passage through a 27-gauge needle. Parasites were counted and diluted to 32,000/mL in IMDM-C. Fibroblast cultures were infected with 3200 tachyzoites of the Type I RH strain expressing Yellow Fluorescent Protein (RH-YFP) and returned to incubator at 37° C. for 1-2 hours to allow for infection (15). Various concentrations of the compounds

were made using IMDM-C, and 20 µl were added to each designated well, with triplicates for each condition. Controls included pyrimethamine/sulfadiazine (current standard of treatment), 0.1% DMSO only, fibroblast only, and an untreated YFP gradient with 2 fold dilutions of the parasite. Cells were incubated at 37° C. for 72 hours. Plates were read using a fluorimeter (Synergy H4 Hybrid Reader, BioTek) to ascertain the amount of yellow fluorescent protein, in relative fluorescence units (RFU), as a measure of parasite burden after treatment. Data was collected using Gen5 software. IC₅₀ was calculated by graphical analysis in Excel.

An initial screening assay of 10 µM, 1 µM, 100 nM, and 10 nM was performed. Compounds were not considered effective or pursued for further analysis if there were no signs of inhibition of tachyzoites at 1 µM. If compounds did appear to be effective at 1 µM, another experiment was conducted to assess effect at 1 µM, 500 nM, 250 nM, 125 nM, 62.5 nM, and 31.25 nM.

Cytotoxicity Assay

Toxicity assays were conducted using WST-1 cell proliferation reagent (Roche) as described in Fomovska, et. al. (18,19). HFF were grown on a flat, clear-bottomed, black 96-well plate. Confluent HFF were treated with inhibitory compounds at concentrations of 10 µM and 50 µM. Compounds were diluted in IMDM-C, and 20 µl were added to each designated well, with triplicates for each condition. A gradient of 2 fold-decreasing concentrations of DMSO from 10% to 0% in clear IMDM-C was used as a control. The plate was incubated for 72 hours at 37° C. 10 µl of WST-1 reagent (Roche) were added to each well and the cells were incubated for 30 to 60 minutes. Absorbance was read using a fluorimeter at 420 nm. A higher degree of color change (and absorbance) indicated mitochondrial activity and cell viability.

In Vitro Challenge Assay for Bradyzoites

HFF cells were grown in IMDM (1x, [+], glutamine, [+], 25 mM HEPES, [+], Phenol red, 10% FBS, [gibco, Denmark]) on removable, sterile glass disks in the bottom of a clear, flat-bottomed 24-well plate. Cultures were infected with 3x10⁴ parasites (EGS strain) per well, in 0.5 mL media and plate was returned to incubator at 37° C. overnight. The following day, the media was removed and clear IMDM and compounds were added to making various concentrations of the drug, to a total volume of 0.5 mL. 2 wells were filled with media only, as a control. Plates were returned to the 37° C. incubator for 72 hours, and checked once every 24 hours. If tachyzoites were visible in the control before 72 hours, the cells were fixed and stained.

Cells were fixed using 4% paraformaldehyde and stained with Fluorescein-labeled Dolichos Biflorus Agglutinin, DAPI, and BAG1. Disks were removed and mounted onto glass slides and visualized using microscopy (Nikon TI7). Slides were scanned using a CRI Panoramic Scan Whole Slide Scanner and viewed using Panoramic Viewer Software. Effects of the compounds were quantified by counting cysts in the controls and treated cells. Cysts and persisting organisms were counted in a representative field of view and then multiplied by a factor determined by the total area of the disk in order to estimate the number of cysts and organisms in each condition.

Assessment of Compound Degradation and Microbicidal Effect on *Toxoplasma*

HFF were cultured in a 96-well plate and infected with RH-YFP as described above on Day 0, 20 µL of compound was added to 9 wells for each compound and concentration (3 conditions, 3 wells per condition). In condition I, media was removed and replaced with fresh media on Day 3. In

condition II, media was removed and replaced with fresh media and more compound on Day 3. In condition III, media was not replaced on Day 3, nor was the compound refreshed. On Day 6, media was removed and replaced with clean media in all wells. On Day 3, 6, and 9 plate was read in the fluorimeter and analyzed graphically in Prism (GraphPad Software).

Toxoplasma In Vivo

IVIS. Mice were infected intraperitoneally with 20×10^3 *Toxoplasma gondii* (Pru strain expressing luciferase) tachyzoites. Treatment commenced 2 hours later with JAG21 (5 mg/kg) which was dissolved in DMSO and administered intraperitoneally in a total volume of 0.05 ml. Mice were imaged every second day starting on day 4 post infection using a IVIS Spectrum (Caliper Life Sciences) for a 1 minute exposures, with medium binning, 20 minutes post injection with 150 mg/kg of D-luciferin potassium salt solution.

Brain cysts: Mice were infected intraperitoneally with 20×10^3 . Treatment commenced 2 hours later with JAG21 (5 mg/kg) which was dissolved in DMSO and administered intraperitoneally in a total volume of 0.05 ml. After 30 days, treatment with JAG21 was begun each day for 14 days intraperitoneally. In experiments when tafenoquine was administered alone or with JAG21 in some groups 3 mg/kg tafenoquine was administered once on day -1. Cysts in brain were quantitated after concluding treatment.

RPS13 Δ . This G0 arrested parasite persists in tissue culture for prolonged times in the absence of tetracycline. The design of this experiment is shown in FIG. 18. The parasite (x) was used to infect interferon gamma knockout mice. For the first y days no tetracycline was administered. After that time tetracycline was administered. Mice were observed and at the time they appeared ill or at the termination of the experiment they were euthanized and tissues fixed in formalin and stained with hematoxylin and eosin or immunoperoxidase stained and parasite burden was assessed.

Malaria Assays

Methods for enzyme assays²¹⁻³: Professor Giancarlo A. Biagini, Dr Richard S. Priestley, Department of Parasitology, Liverpool School of Tropical Medicine, Pembroke Place, Liverpool, L3 5QA, UK.

Materials

Plasmodium falciparum: 3D7 strain was obtained from the Liverpool School of Tropical Medicine. Protease cocktail inhibitor was obtained from Roche. Bradford protein assay dye reagent was obtained from Bio-Rad. All other reagents were obtained from Sigma-Aldrich. Decylubiquinol was produced as per Fisher et al. (Fisher et al. 2004)²¹. In brief, 25 mg of decylubiquinol were dissolved in 400 μ l of nitrogen-saturated hexane. An equal volume of aqueous 1 M sodium dithionite was added, and the mixture vortexed until colorless. The organic phase containing the decylubiquinol was collected, the solvent was evaporated under N_2 and the decylubiquinol finally dissolved in 100 μ l of 96% ethanol (acidified with 10 mM HCl). Concentrations of decylubiquinol was determined spectrophotometrically on a Cary 300 Bio UV/visible spectrophotometer (Varian, UK) from absolute spectra, using $\epsilon_{288-320}=8.1 \text{ mM}^{-1}\text{cm}^{-1}$. Decylubiquinol was stored at -80°C . and used within two weeks.

Plasmodium falciparum: Culture and Extract Preparation

Plasmodium falciparum: strain 3D7 blood-stage cultures were maintained by the method of Trager and Jensen (Trager & Jensen 2005)²³. Cultures contained a 2% suspension of O+ human erythrocytes in RPMI 1640 medium containing

L-glutamine and sodium carbonate, and supplemented with 10% pooled human AB+ serum, 25 mM HEPES (pH 7.4) and 20 μ M gentamicin sulphate. Cultures were grown under a gaseous headspace of 4% O_2 and 3% CO_2 in N_2 at 37°C . Cultures were grown to a parasitaemia of 5% before use.

The protocol for the preparation of parasite extract was adapted from Fisher et al. (Fisher et al. 2009)²². Free parasites were prepared from infected erythrocytes pooled from five T75 flasks, by adding 5 volumes of 0.15% (w/v) saponin in phosphate-buffered saline (137 mM NaCl, 2.7 mM KCl, 1.76 mM K_2HPO_4 , 8.0 mM Na_2HPO_4 , 5.5 mM D-glucose, pH 7.4) for 5 min, followed by three washes by centrifugation in RPMI containing HEPES (25 mM), and a final resuspension in potassium phosphate buffer (50 mM K_2HPO_4 , 50 mM KH_2PO_4 , 2 mM EDTA, pH7.4) containing a protease inhibitor cocktail (Complete Mini; Roche). Parasite extract was then prepared by disruption with a sonicating probe for 5 s, followed by a 1 min rest period on ice to prevent the sample overheating. This process was performed three times. The parasite extract was used immediately. The protein concentration of the parasite extract was determined by Bradford protein assay (Bio-Rad).

Pfbc₁ Native Assay

Plasmodium falciparum bc₁ complex cytochrome c reductase (Pfbc₁) activity was measured by monitoring cytochrome c reduction at 550 versus 542 nm using a Cary 300 Bio UV-Visible Spectrophotometer (Varian, UK), using a protocol adapted from Fisher et al. (Fisher et al. 2009)²¹⁻²³. The assay was performed in potassium phosphate buffer in a quartz cuvette and in a final volume of 700 μ L. Potassium cyanide (10 μ M), oxidised cytochrome c (30 μ M), parasite extract (100 μ g protein) and compound/DMSO were added sequentially to the cuvette, with mixing between each addition. Test compounds were added to a final concentration of 1 μ M. DMSO (0.1% v/v) and atovaquone (1 μ M), a known malarial cytochrome bc₁ complex inhibitor, were used as negative and positive controls respectively. The reaction was initiated by the addition of 50 μ M decylubiquinol and allowed to proceed for 3 min.

Data Analysis

Malaria

In Vitro Studies:

D6 is a drug sensitive strain from Sierra Leone, C235 is a multi-drug resistant strain from Thailand, W2 is a chloroquine resistant strain from Thailand, and C2B has resistance to a variety of drugs including atovaquone. These assays were performed as described.

Compound Activity Against *Plasmodium falciparum*:

Compound activity against *P. falciparum*, a causative agent of malaria, was tested using the Malaria SYBR Green I—Based Fluorescence (MSF) Assay. This; microtiter plate drug sensitivity assay uses the presence of malarial DNA as a measure of parasitic proliferation in the presence of antimalarial drugs or experimental compounds based on modifications of previously described methods by Plouffe et al (20) and Johnson et al. As the intercalation of SYBR Green I dye and its resulting fluorescence is relative to parasite growth, a test compound that inhibits the growth of the parasite will result in a lower fluorescence.

Selected compounds were examined for activity against four strains of *P. falciparum*: D6 (CDC/Sierra Leone), a drug-sensitive strain readily killed by chloroquine, TM91-C235, a multi-drug resistant strain resistant to chloroquine,

W2, a chloroquine resistant strain from Thailand, and C2B has resistance to a variety of drugs including atovaquone. *P. berghei* Model Sporozoite, Blood Stage, and Liver Stage Model.

P. berghei sporozoites. The methods that follow are taken directly from^{24,25}. From laboratory-reared female *Anopheles stephensi*, isolation, inoculation and viability check *Plasmodium berghei* sporozoites (luciferase expressing) were obtained and maintained at 18° C. for 17 to 22 days after feeding on malaria-infected Swiss CD-1/ICR mice. From malaria-infected mosquitoes, salivary glands were extracted and sporozoites obtained. Briefly, mosquitoes were separated into head/thorax and abdomen. Thoraxes and heads were triturated with a mortar and pestle and suspended in medium RPMI 1640 containing 1% C57BL/6 mouse serum (Rockland Co, Gilbertsville, Pa., USA). 50-80 heads with glands total were placed into a 0.5 ml Osaki tube on top of glass wool with enough dissection media to cover the heads. Until all mosquitoes had been dissected, the Osaki tube was kept on ice. Sporozoites that were isolated from the same batch of mosquitoes were inoculated into C57BL/6, 2D knock-out and 2D knock-out/2D6 knock-in C57BL/6 mice on the same day to control for biological variability in sporozoite preparations. On day 0, each mouse was inoculated intravenously in the tail vein with approximately 10,000 sporozoites suspended in 0.1 ml volume. They were stained with a vital dye containing fluorescein diacetate (50 mg/ml in acetone) and ethidium bromide (20 µg/ml in phosphate buffered saline; Sigma Chemical Co, St. Louis, Mo., USA) and counted in a haemocytometer to ensure that inoculated sporozoites were viable following the isolation procedure. Viability of the sporozoites ranged from 90 to 100%.

Animals

The mice used in these experiments were Swiss Webster females. The animals were acclimated for seven days (quarantine) on arrival. The animals were housed in a cage maintained in a room with 34-68% relative humidity, a temperature range of 64-79° F., and a 12-hr light/dark cycles. Water and food were provided during quarantine and throughout the study. The mice were fed a standard rodent maintenance diet. All animal studies were performed under protocols that are IACUC-approved. All animal care, handling, and use was performed in accordance with the current Guide for the Care and Use of Laboratory Animals (1996). Test Compounds and Administration

At the time of preparation of the suspension solution, compounds tested in these experiments were dosed based on the body weight. The suspension solution of oral agents, using homogenizer (PRO Scientific Inc, Monroe, Conn., USA) with 10 ml open-slotted generator to homogenize drug powder mixture at 20,000-22,000 rpm for 5 min in ice bath, were prepared in 0.5% (w/v) hydroxyethyl cellulose and 0.2% (0.5% HECT, v/v) Tween-80 in distilled water.

A three consecutive day-treatment regimen (-1, 0, 1 day) or a once-a-day, one dose on day 0 was used in assessments. Drug suspensions were transferred to a 20-ml bottle, drawn into a 1-ml syringe, and delivered to the designated recipient via intragastric feeder (18 gauge).

1 hour after intravenous administration of 10,000 *P. berghei* sporozoites, single dose causal prophylaxis in 5 C57BL/6 albino mice at 2.5 mpk dosed on day 0. In 5 C57BL/6 albino mice, 3 dose causal prophylaxis treatment at 0.6 mpk dosed on days -1, 0, and +1.

In Vivo Imaging System Spectrum

All of the in vivo imaging system (IVIS) methods utilized have been described previously [6]. Briefly TQ and NPC-

1161B were administered orally on days -1, 0 and 1 with respect to sporozoite inoculation. All inoculated mice were tested using the Xenogen IVIS-200 Spectrum (Caliper Life Sciences, Hopkinton, Mass., USA) IVIS instrument at 24, 48 and 72 hr post-sporozoite infection. Additionally, using a flow cytometry system (FC500 MPL, Beckman Coulter, Miami, Fla., USA), blood-stage infections were measured. For the IVIS calibration in each test, positive and negative controls were used. D-Luciferin potassium salt, (Xenogen, California and Goldbio, St Louis, Mo., USA), the luciferase substrate, was inoculated intraperitoneally into mice at a concentration of 200 mg/kg 15 min before luminescence analysis. Three min post-luciferin administration the mice were anesthetized using isoflurane. The mice, in the IVIS on the 37° C. platform, were then positioned ventral side up. Through nose cone delivery, the mice continued to receive isoflurane. The exposure time of the camera was 5 min for the 24, 48 and 72 hr time points with f-stop=1 and large binning setting. Using Living Image® 3.0 software, photons emitted from specific regions were quantified.

Parasitemia was measured after days of IVIS imaging. During a total of 30 days, mice were observed and parasitemia level determined using FACs analysis. (Pybus et al. Malaria Journal 2013, 12:212; Marcsisin et al. Malaria Journal 2014, 13:2).

Bovine Cytochrome bc1 Purification Protocol

Preparation of Crude Mitochondria:

Whole bovine heart was collected directly from slaughter and transported on ice to the cold room. All work was carried out at 4° C. Fat and other tissues were removed leaving only lean muscle that was then cut into small cubes. The cubes were then transferred to a waring blender and homogenisation buffer (250 mM sucrose; 20 mM K₂HPO₄; 2 mM succinic acid; 0.5 mM EDTA) was added at a ration of 2.6 L buffer per 1 L of muscle tissue. The solution was then homogenised. The resulting homogenate was adjusted to pH 7.8 using 2 M Tris and PMSF was added to a concentration of 0.1 mM. The homogenate was then centrifuged in a Sorvall GS-3 rotor at 3000 rpm for 20 mins. The resulting supernatant was then transferred to a Sorvall GSA rotor and centrifuged at 12,000 rpm for 20 mins. The pellet was then re-suspended and washed in buffer 1 (50 mM KPi (pH 7.5); 0.1 mM PMSF) before centrifugation under the same conditions again. The pellet was collected and frozen at -80° C. for use later.

Solubilisation of Membrane Proteins:

The frozen mitochondria were thawed and re-suspended in buffer 2 (50 mM KPi (pH 7.5); 150 mM NaCl; 3 mM NaN₃; 0.1 mM PMSF) and a sample taken for a BCA assay. The remaining sample was centrifuged at 42,000 rpm in a Beckman Ti70 rotor for 60 mins. The pellet was re-suspended in the same wash buffer to a volume of 70 ml with the addition 0.1 mg DDM per 1 mg of protein and centrifuged at 42,000 rpm in a Beckman Ti70 rotor for 60 mins. The pellet was then re-suspended in the same wash buffer to a final volume of 215 ml with the addition of 0.9 mg DDM per 1 mg of protein and centrifuged for a final time at 42,000 rpm in a Beckman Ti70 rotor for 60 mins. The supernatant was collected.

Purification of Cytochrome bc1:

Whilst being purified, the presence of protein was determined using 280 nm absorbance and the presence of haem was determined using 415 nm soret band peak and 462 nm absorbance. The solubilised protein solution was first applied to a DEAE-Sepharose CL-6B column (ca. 50 ml) pre-equilibrated in buffer A (50 mM KPi (pH 7.5); 150 mM NaCl; 0.03% DDM; 3 mM NaN₃) washed with 2 CV buffer

A and eluted along a gradient with buffer B (50 mM KPi (pH 7.5); 350 mM NaCl; 0.03% DDM; 3 mM NaN₃). The collected protein was pooled and diluted twofold with buffer C (50 mM KPi (pH 7.5); 0.03% DDM; 3 mM NaN₃) before application to a hydroxyapatite column (ca. 15 ml) pre-equilibrated with buffer C. The column was washed with 10 CV of buffer C before elution along a gradient with Buffer C* (1000 mM KPi (pH 7.5); 0.03% DDM; 3 mM NaN₃). Fractions containing cytochrome bc₁, as identified by 415 nm absorbance, were then collected, pooled and concentrated to 1.5 ml using an Amicon Ultra-15 (Amicon, MWCO 100,000). The sample was then applied to a Sephacryl-S300 column (ca. 120 ml) pre-equilibrated in buffer D (25 mM KPi (pH 7.5); 100 mM NaCl; 0.015% DDM; 3 mM NaN₃) and ran at a flow rate of 0.5 ml/min. Purified cytochrome bc₁ fractions were then collected and concentrated to 30 mg/m.

Bovine Enzyme Crystallography:

Compounds designed using structure-based analyses of cytochrome b co-crystallized with JAG21 as described in

Cytotoxicity Assay Using HFF and WST-1 and IC50 with HEP G Cells:

Because *T. gondii* grows inside cells, if a compound was toxic to host Human Foreskin Fibroblast Cells (HFF), then it would make the compound appear to be spuriously effective; in actuality only toxicity for the host cell would be measured. Cytotoxicity to human foreskin fibroblasts was therefore assessed for all compounds at 10 μ M and 50 μ M. Results of this experiment are in FIG. 14 and Table 3. A two-way ANOVA and subsequent pairwise comparison found none of the differences in absorbance, compared to the controls, to be statistically significant ($p > 0.05$). This suggests that these compounds are not toxic at 10 μ M or 50 μ M and that toxicity to cells is attributed to DMSO in the solution, not the compound. IC50 with HEP G cells was performed as described and toxicity was: HEP G2 IC50 17.70 microM ($r^2=0.97$) JAG 21; JAG 50 7.1 microM $r^2=0.98$.

TABLE 3

Cytotoxicity to human foreskin fibroblasts was therefore assessed for all compounds at 10 μ M and 50 μ M. Graph is representative of replicate experiment.					
Observation	Control	JAG050 10 μ M	JAG050 1 μ M	JAG021 10 μ M	JAG021 1 μ M
a					
True Cysts	4.67 $\pm$ 3.06 [2-8]	1 $\pm$ 0.82 [0-2]	0.25 $\pm$ 0.5 [0-1]	0.25 $\pm$ 0.5 [0-1]	0.5 $\pm$ 0.6 [0-1]
Pseudocysts	40.3 $\pm$ 11.4 [31-53]	20.5 $\pm$ 2.9 [17-24]	23.25 $\pm$ 10.31 [14-38]	25.5 $\pm$ 5.1 [19-30]	29 $\pm$ 6 [21-34]
Small organisms	1600 $\pm$ 436 [1100-1900]	31 $\pm$ 16 [8-43]	58 $\pm$ 24 [27-85]	73.25 $\pm$ 30.9 [30-101]	90.5 $\pm$ 33.5 [63-137]
b					
True Cysts	452	88	29	22	54
Pseudocysts	3884	1921	2269	2638	2955
Small organisms	16404	3018	5086	7309	9734

Example 1²⁶. This was done to optimize medicine-like properties using structure activity principles and analyses. Compounds synthesized as above were used in these assays as follows: 10 mM stock solutions were made with 100% Dimethyl Sulfoxide (DMSO) [Sigma Aldrich] and working concentrations were made with IMDM-C (1 $\times$, [+], glutamine, [+], 25 mM HEPES, [-], Phenol red, 10% FBS)[gibco, Denmark]).

Statistical Analysis:

A Pearson test was used to confirm a correlation between increasing dose and increasing inhibition. An ANOVA and subsequent pairwise comparison with Dunnett correction was used to determine whether or not inhibition or toxicity at a given concentration was statistically significant. Stata/SE 12.1 was used for this analysis.

Results

Tetrahydroquinolone Compounds:

In Vitro Challenge Assay for Tachyzoites:

Seven compounds (Table 1) were tested and each compound was tested at least twice. JAG021 and JAG050 demonstrated effect below 1 μ M, and were tested at lower concentrations. A representative graph of this data is shown in FIG. 13. JAG050 and JAG021 were identified as lead compounds because the IC₅₀ values were 55 and 188 nM respectively. Correlation between concentration of compound and inhibition of parasite growth and activity (as measured by fluorescence) was observed for all compounds except JAG046.

In Vitro Challenge Assay for Bradyzoites

Lead compounds JAG050 and JAG021 were tested against EGS because of their effects on tachyzoites (RH-YFP). Under immunofluorescence microscopy, the following forms were observed: "true cysts" with a dolichostaining wall, "pseudocysts" or tight clusters of parasites, and small organisms. If there were fewer than four parasites visible in a cluster, the organisms were counted individually (as "small organisms"). A statistically significant reduction in the number of true cysts and small organisms was observed at 1 μ M and 10 μ M for both compounds ($p < 0.05$, $p < 0.005$, FIG. 15a-c).

ADME properties of THQs.

In vitro ADME analyse of the THQ compounds were outsourced to ChemPartner Shanghai Ltd. ELQ-271 was tested as a comparison. THQs which were potent inhibitors of *T. gondii* tachyzoites were assessed for their kinetic solubility, metabolic stability in human and mouse liver microsomes, and their ability to permeate across MDCK-MDK1 cell membranes (in vitro measure of blood-brain barrier (BBB) permeability). Solubility, half-life and BBB permeability/efflux results are shown in Table 4. The kinetic solubility (PBS, pH 7.4) of compounds JAG021 and JAG050, 7 and 16 μ M respectively, were higher than MJM170 (2 μ M) and ELQ-271 (0.2 μ M). JAG021 was the most metabolically stable compound in human liver microsomes (>99% remaining after 45 mins) compared with

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other THQs and ELQ-271, although it displayed a much shorter half-life of 101 mins in mouse liver microsomes. All THQs tested in the MDK1 (MJM170, JAG021 and JAG050) MDCK-MDK1 system exhibit high permeability ($P_{app} > 10 \times 10^6$ cm/s) and low efflux (efflux ratio < 1.5).

TABLE 4

Chart compares properties of solubility and half-life of JAG050 and JAG021 to parent compounds ELQ 271 and MJM170. The test system was 100 mM Phosphate Buffer (pH 7.4).: $< 10 \mu\text{M}$ is low solubility, $10\text{--}80 \mu\text{M}$ is moderate solubility and $> 80 \mu\text{M}$ is high solubility. A $T_{1/2} < 30$ minutes indicates susceptibility to metabolism, between 30 and 120 minutes indicates moderate metabolism and > 120 minutes indicates stability in the liver.			
Compound	Solubility (pH 7.4)*	Human liver microsomes [#]	Mouse liver microsomes [#]
ELQ271	0.15 μM	171.93 min	448.13 min
MJM170	1.97 μM	146.33 min	20.97 min
JAG021	7.07 μM	∞	101.09 min
JAG050	16.41 μM	99.04 min	68.55 min

Enzyme Assays:

Enzyme reduction of cytochrome c by the parasite extract is mediated by *P. falciparum* bc₁ complex cytochrome c reductase (Pfbc₁). All three compounds (1 μM) significantly inhibited the reduction of cytochrome c by the parasite extract, (JAG021=86.4 $\pm$ 3.2; JAG099=81.3 $\pm$ 6.0; MJM170=69.7 $\pm$ 11.3% atovaquone response). This clearly demonstrates the compounds are inhibitors of Pfbc₁. Additional data demonstrating effect on bovine and *Plasmodium falciparum* enzyme are shown in Table 5. There is selectivity for the malaria enzyme.

TABLE 5

Inhibition of Pfbc ₁ by compounds.	
Compound (1 μM)	Inhibition of cytochrome c reduction (% atovaquone response)
JAG021	86.4 $\pm$ 3.2
JAG099	81.3 $\pm$ 6.0
MJM170	69.7 $\pm$ 11.3

Data shown are mean $\pm$ s.e.m. of 4 independent experiments performed in triplicate.

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Binding Assays and Co Crystallography.

JAG021 has lower binding affinity to bovine cytochrome bc in comparison with previous compounds that we have tested. JAG 21 'inhibits' Cytbc1 but not fully, indicating that it will be less toxic for bovine/human cyt bc (FIG. 16)

Assessment of Compound Degradation and Microbicidal Effect on *Toxoplasma gondii*

Compounds JAG050 and JAG021 were observed for degradation and microbicidal effect. Neither compound was found to be microbicidal; when media was replaced with clean media, the parasites appeared to resume activity and replication. In comparing the 6-day exposure with no addition of compound to the 6-day exposure with the addition of compound, it did not appear that the compound was being degraded over time. In condition II, in which the compound is refreshed, there appears to be a rise in fluorescence on day 6 in the 1 μM treatment group for both compounds. However, these differences were not found to be statistically significant ($p > 0.05$).

Effective of JAG21 on *Toxoplasma gondii*.

JAG21 at 5 mg/kg eliminates *T. gondii* tachyzoites seen in luminescence studies (FIG. 17).

JAG21 Against G0 Arrested and Normal (No Tet Repressor) *Toxoplasma* RPS13 Delta in Interferon Gamma Knock-out Mice Plus and Minus Tetracycline.

Our data show that the combination of JAG21 and tafenoquine treatment is superior to either alone against RPS 13 Δ minus tetracycline (FIG. 18). The data indicates that this appears to be a dormant parasite that is less susceptible to JAG21 than either the slowly growing EGS bradyzoites or the rapidly proliferating tachyzoites.

Malaria:

In Vitro.

Results are shown in Table 6. JAG 21 is a 40-65 nM inhibitor of *Plasmodium falciparum* including effect against all drug resistant strains. The effects of the other compounds are also shown in this table and are in the range of 50-200 nM.

TABLE 6

Inhibition of <i>P. falciparum</i> in vitro including drug resistant isolates								
Compound ID	SYBR Green D6		SYBR Green C235		SYBR Green W2		SYBR Green C2B	
	IC50 (uM)	SYBR D6 R ²	IC50 (uM)	TM91C235 R ²	IC50 (uM)	SYBR W2 R ²	IC50 (uM)	SYBR C2B R ²
JAG006	0.29	0.90	0.88	0.92	2.46	0.92	1.66	0.94
JAG021	0.01435	0.9572	0.06164	0.9706	0.05518	0.9727	0.04042	0.9847
JAG050	0.04664	0.9138	0.06913	0.9562	0.03136	0.9693	0.03635	0.9427
JAG047	3.746	0.9738	12.56	0.9218	9.072	0.9358	7.781	0.9575
JAG039	9.595	0.9532	>20	N/A	>20	N/A	>20	N/A
JAG046	6.716	0.9844	>20	N/A	>20	N/A	>20	N/A
RG38	2.84	0.8936	13.66	0.8338	9.245	0.7954	>20	N/A

In Vivo.

Single dose causal prophylaxis in 5 C57BL/6 albino mice at 2.5 mpk dosed on day 0, 1 hour after intravenous administration of 10,000 *P. berghei* sporozoites. 3 dose causal prophylaxis treatment in 5 C57BL/6 albino mice at 0.6 mpk dosed on days -1, 0, and +1. A representative figure for higher dose (5 mg/kg) is shown, but all experiments with the amounts mentioned above had efficacy measured as cure measured as survival, luminescence and parasitemia quantitated by flow cytometry are similar to these. (FIG. 17)

Discussion

JAG050 and JAG021 were identified as lead compounds, demonstrating potent inhibition of tachyzoites and bradyzoites and no toxicity to human foreskin fibroblasts in our in vitro model. While compounds inhibited parasite replication and activity, there did not appear to be a microbicidal effect.

Toxoplasmosis is highly prevalent and the impact of this disease can be devastatingly severe. Current treatments have toxic side effects and are not curative. JAG050 and JAG021 are lead compounds in the search for a new curative medicine because they demonstrate effect on both life stages and were not toxic to the human cells in our in vitro model.

Experiments testing the compounds against the EGS strain had some surprising findings. While true cysts in vitro appeared to be completely eliminated by treatment, or their number significantly reduced, parasites did persist in tight, clustered, cyst-like structures, or pseudo-cysts, and small punctate life forms that resemble tachyzoites. One possible explanation is that the dolichos-staining organisms that remain 48 hours after treatment are in a separate, hypnozoite-like life stage that is not affected by the compounds.

JAG050 and JAG021 do not appear to have a microbicidal effect on the RH-YFP parasites. However, in comparing the two conditions in which cells and parasites were exposed to the drug for 6 days, it does not appear that the parasites or host cells are degrading the compounds. In order to cure toxoplasmosis, a companion drug that can work synergistically with the compounds of the present invention may be helpful. Primaquine and tafenoquine, which are the only medicines that can treat the hypnozoite stage of *Plasmodium vivax* and *P. ovale*, may be potential candidates. We had demonstrated synergy with an earlier generation compound with atovaquone and additive effect with cycloguanil.²⁶

JAG21 demonstrated high efficacy against *Toxoplasma* tachyzoites in our vitro and in vivo models, low nanoM efficacy against drug resistant *P. falciparum*, and single dose causal prophylaxis in a mouse model of *P. berghei* sporozoites infection

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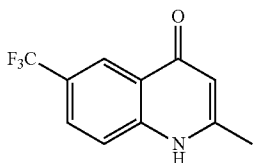
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General Method A

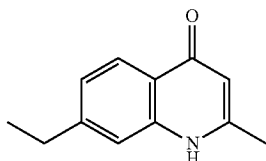
2,2-Dimethyl-1,3-dioxane-4,6-dione (1.5 equiv.) was dissolved in trimethylorthoacetate (2 equiv.) and heated to 115° C. for 2 hrs. The reaction was cooled to allow the addition of the aniline (1 equiv.) before being heated to 115° C. for a further 2 hrs. The reaction mixture was then allowed to cool and was concentrated in vacuo, remaining solvent was washed off with cold methanol. The precipitate was then dissolved in minimum volume of Dowtherm A and refluxed at 250° C. for 1.5 hours. The reaction mixture was allowed to cool and the precipitate filtered followed by washing with hexane to afford the title compound.

2-Methyl-6-(trifluoromethyl)quinolin-4(1H)-one



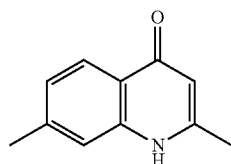
The title compound was synthesised by general method A using 4-trifluoromethyl aniline (2.00 g, 12.4 mmol) to yield the title compound as a white amorphous solid (466 mg, 2.05 mmol, 17%). ¹H NMR (300 MHz, MeOD) δ 8.42 (s, 1H), 7.81 (dd, J=8.8 Hz, 2.1 Hz, 1H), 7.60 (d, J=8.8 Hz, 1H), 6.16 (s, 1H), 2.40 (s, 3H); M/Z (ESI+); 228.06 (Found MH⁺ 228.0634, C₁₁H₈F₃NO requires 228.0630).

7-ethyl-2-methylquinolin-4(1H)-one



The title compound was synthesised following general procedure A from 3-ethylaniline (1.4 mL, 11.1 mmol). The title compound was isolated as a colourless solid (210 mg, 1.12 mmol, 10%). ¹H NMR (500 MHz, CDCl₃) δ 9.72 (s, 1H), 8.17 (d, J=8.3 Hz, 1H), 7.16 (s, 1H), 7.10 (d, J=8.3 Hz, 1H), 6.07 (s, 1H), 2.66 (q, J=7.6 Hz, 2H), 2.33 (s, 3H), 1.18 (t, J=7.6 Hz, 3H);

2,7-Dimethylquinolin-4(1H)-one

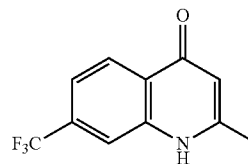


The title compound was synthesised following general procedure A from 3-methylaniline (7.5 mL, 42 mmol). The

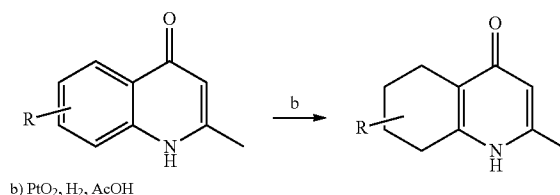
94

title compound was isolated as a colourless solid (370 mg, 2.13 mmol, 5%). ¹H NMR (400 MHz, CDCl₃) δ 9.58 (s, 1H), 8.24 (d, J=8.3 Hz, 1H), 7.22 (s, 1H), 7.16 (d, J=8.3 Hz, 1H), 6.15 (s, 1H), 2.46 (s, 3H), 2.41 (s, 3H).

7-trifluoromethyl-2-methylquinolin-4(1H)-one



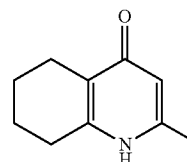
The title compound was synthesised following general procedure A from 3-trifluoromethyl-aniline (3 mL, 24 mmol). The title compound was isolated with its regiomers and separation was not achieved and so was carried forwards as a mixture (1.5 g).



General Method B

The 4-hydroxyquinolone (1 equiv.) was dissolved in acetic acid (10.0 mL) under inert conditions. platinum dioxide (5% weight equiv.) was added and a hydrogen balloon was attached. The reaction was left to proceed for 12 hours. The resulting suspension was filtered through a pad of Celite and washed with ethyl acetate (10.0 mL). The filtrate was concentrated in vacuo to afford a yellow/brown oil. Purification by column chromatography (10% methanol in chloroform) afforded the title compound.

2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

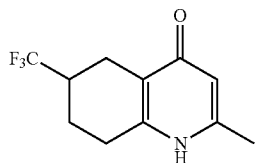


A solution of 4-hydroxy-2-methyl-quinilone (1.00 g, 6.28 mmol) in acetic acid (10.0 mL) was catalytically hydrogenated over platinum dioxide (0.10 g, 0.44 mmol) for 12 hours. The resulting suspension was filtered through a pad of Celite and washed with ethyl acetate (10.0 mL). The filtrate was concentrated in vacuo to afford a yellow/brown oil. Purification by column chromatography (10% methanol in chloroform) afforded the title compound as a colourless amorphous solid. (1.02 g, 6.25 mmol, 99%). ¹H NMR; (500

95

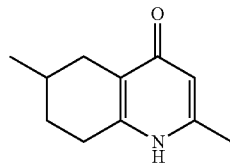
MHz, Chloroform-d); δ 6.29 (s, 1H), 2.71 (t, J=6.1 Hz, 2H), 2.48 (t, J=6.1 Hz, 2H), 2.32 (s, 3H), 1.78-1.69 (m, 4H); M/Z (ESI+); 164.1122 (Found MH⁺, 164.11 C₁₀H₁₃NO requires 164.1075).

2-Methyl-6-(trifluoromethyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one



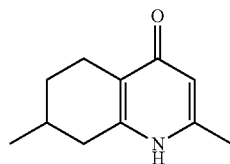
The title compound was synthesised following general procedure B from 2-methyl-6-(trifluoromethyl)quinolin-4(1H)-one (466 mg, 2.0 mmol). The title compound was isolated as colourless solid (230 mg, 0.99 mmol, 49%). ¹H NMR (500 MHz, MeOD) δ 6.32 (s, 1H), 2.94 (dd, J=16.7, 5.1 Hz, 1H), 2.86 (dd, J=8.4, 4.1 Hz, 2H), 2.65-2.52 (m, 1H), 2.41 (dd, J=22.8, 11.5 Hz, 1H), 2.36 (s, 3H), 2.28-2.15 (m, 1H), 1.75 (tt, J=12.8, 9.1 Hz); M/Z (ESI+); 232.10 (Found MH⁺; 232.0955, C₁₁H₁₂F₃NO requires 232.0949).

2,6-Dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one



The title compound was synthesised following general procedure B from 2,6-dimethyl-quinolin-4(1H)-one (1.0 g, 5.78 mmol). The title compound was isolated as a colourless solid (780 mg, 4.30 mmol, 76%). ¹H NMR (400 MHz, CDCl₃) δ 12.26 (s, 1H), 6.09 (s, 1H), 2.88-2.64 (m, 3H), 2.30 (s, 3H), 1.98 (dd, J=16.9, 10.1 Hz, 1H), 1.87 (d, J=12.4 Hz, 1H), 1.77 (m, 1H), 1.39 (ddd, J=23.9, 11.1, 6.0 Hz, 1H), 1.08 (d, J=6.5 Hz, 3H); M/Z (ESI+); 178.13 (Found MH⁺; 178.1280, C₁₁H₁₅NO requires 177.1154).

2,7-Dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

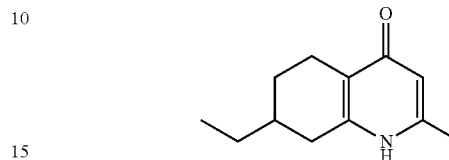


The title compound was synthesised following general procedure B from 2,7-Dimethyl-quinolin-4(1H)-one (350 mg, 2.0 mmol). The title compound was isolated as a colourless solid (311 mg, 1.75 mmol, 88%). ¹H NMR (500 MHz, MeOD) δ 6.31 (s, 1H), 2.78 (dd, J=17.0, 5.1 Hz), 2.73 (ddd, J=17.7, 5.2, 2.7 Hz), 2.45-2.31 (m, 2H), 2.00-1.87 (m,

96

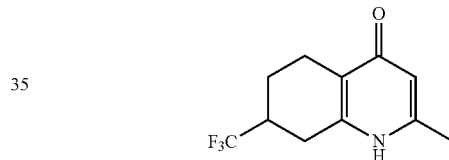
2H), 2.37 (s, Me), 1.37 (m, 2H), 1.13 (d, J=6.6 Hz, 3H); M/Z (ESI+); 178.13 (Found MH⁺; 178.1278, C₁₁H₁₅NO requires 177.1154).

5 7-ethyl-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

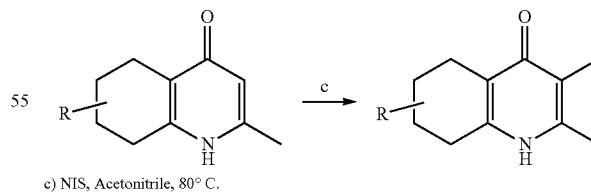


The title compound was synthesised following general procedure B from 7-ethyl-2-methylquinolin-4(1H)-one (420 mg, 1.78 mmol). The title compound was isolated as a colourless solid (360 mg, 1.5 mmol, 84%). ¹H NMR (400 MHz, CDCl₃) δ 12.20 (s, 1H), 6.09 (s, 1H), 2.88-2.66 (m, 2H), 2.46-2.19 (m, 5H, 2-Me), 1.95 (d, J=13.0 Hz, 1H), 1.63 (s, 1H), 1.38 (td, J=13.9, 6.9 Hz, 2H), 1.33-1.22 (m, 1H) 0.94 (t, J=7.4, 3H); M/Z (ESI+); 192.14 (Found MH⁺; 192.1378 C₁₂H₁₇NO requires 192.1383).

7-trifluoromethyl-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one



The title compound was synthesised following general procedure B from a mixture of 7-trifluoromethyl-2-methylquinolin-4(1H)-one & 5-trifluoromethyl-2-methylquinolin-4(1H)-one (1.5 g). The title compound was isolated as a colourless solid (495 mg, 2.14 mmol). ¹H NMR (500 MHz, CDCl₃/MeOD, 1:1) δ 5.99 (s, 1H), 2.73-2.60 (m, 2H), 2.53 (dd, J=16.3, 12.0 Hz, 1H), 2.35 (s, 1H), 2.20 (ddd, J=17.7, 11.4, 5.9 Hz, 1H), 2.11 (s, 3H), 2.09-2.01 (m, 1H), 1.42 (ddd, J=25.0, 12.1, 5.7 Hz, 1H); M/Z (ESI+); 232.10 (Found MH⁺; 232.0953, C₁₁H₁₂F₃NO requires 232.0949).



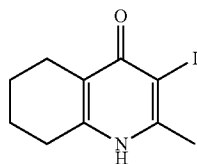
General Method C

Potassium iodide solution (sat aq, 5.60 mL mmol⁻¹) and n-butylamine (10 equiv.) were added to a solution of the tetrahydroquinolin-4(1H)-one (1 equiv.) and iodine (1 equiv.) in DMF (10.0 mL). The reaction mixture was stirred

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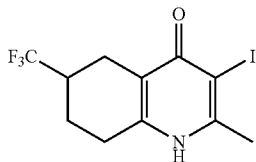
at room temperature for 16 hours. Observed colour change from dark purple to orange. Sodium thiosulphate (250 mg in 10.0 mL water) was then added causing precipitation of a colourless solid. Filtration (washed 2×10 mL water) afforded the title compound.

4(1H), 3-iodo-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one



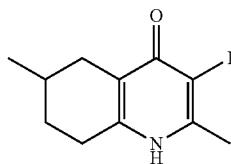
Saturated potassium iodide solution (sat aq, 5.60 mL) and n-butylamine (5.80 mL, 58.3 mmol) was added to a solution of 2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one (0.95 g, 5.83 mmol) and iodine (1.48 g, 5.83 mmol) in DMF (10.0 mL). The reaction mixture was stirred at room temperature for 16 hours. Observed colour change from dark purple to orange. Sodium thiosulphate (250 mg in 10.0 mL water) was then added followed by filtration (washed 2×10 mL water) to afford the title compound (39) as colourless microcrystals (1.45 g, 5.02 mmol, 86%). ¹H NMR (500 MHz, methanol-d₄): δ 2.53 (t, J=6.1 Hz, 2H), 2.44 (s, 3H), 2.30 (t, J=6.1 Hz, 2H), 1.73-1.67 (m, 2H), 1.67-1.61 (m, 2H); M/Z (ESI+); 290.00 (Found MH⁺, 290.0037 C₁₀H₁₂INO requires 290.0036).

3-iodo-2-methyl-6-(trifluoromethyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one



The title compound was synthesised following general procedure C from 2-methyl-6-(trifluoromethyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one (230 mg, 1.0 mmol). The title compound was isolated as colourless solid (300 mg, 0.84 mmol, 84%). ¹H NMR (400 MHz, DMSO) δ 11.58 (s, 1H), 2.75 (d, J=5.6 Hz, 1H), 2.72-2.67 (m, 2H), 2.62 (dd, J=7.4, 5.8 Hz, 1H), 2.46 (s, 3H), 2.31 (d, J=22.7 Hz, 1H), 2.15 (dd, J=16.4, 11.1 Hz, 1H), 2.07 (dd, J=6.6, 5.4 Hz, 1H), 1.68-1.51 (m, 1H); M/Z (ESI+); 357.99 (Found MH⁺, 357.9914, C₁₁H₁₁F₃INO requires 357.9910).

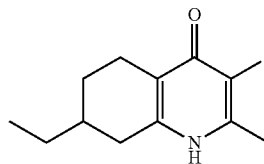
3-iodo-2,6-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one



98

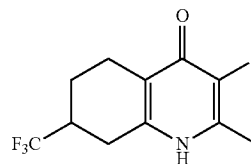
The title compound was synthesised following general procedure C from 2,6-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one (750 mg, 4.24 mmol). The title compound was isolated as colourless solid (740 mg, 2.44 mmol, 58%). ¹H NMR (500 MHz, CDCl₃/MeOD) δ 2.36 (dd, J=17.3, 4.8 Hz), 2.25 (d, J=4.8 Hz, 2H), 2.15 (s, 3H), 1.57 (dd, J=17.3, 10.4 Hz, 1H), 1.51 (d, J=10.9 Hz, 1H), 1.36 (s, 1H), 1.09-0.94 (m, 1H), 0.69 (d, J=6.6 Hz, 3H); M/Z (ESI+); 304.02 (Found MH⁺, 304.0190, C₁₁H₁₄INO requires 304.0193).

3-iodo-7-ethyl-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

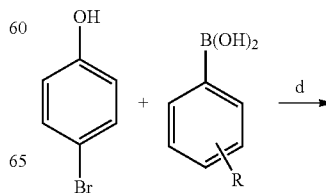


The title compound was synthesised following general procedure C from 7-ethyl-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one (110 mg, 0.57 mmol). The title compound was isolated as colourless solid (180 mg, 0.57 mmol, 99%). ¹H NMR (400 MHz, MeOD) δ 2.62 (dd, J=17.2, 4.4 Hz, 2H), 2.47 (s, 3H), 2.34-2.22 (m, 1H), 2.18 (dd, J=17.8, 9.6 Hz, 1H), 1.92-1.81 (m, 1H), 1.64-1.50 (m, 1H), 1.34 (dtd, J=14.1, 7.2, 2.2 Hz, 2H), 1.21 (ddd, J=24.1, 10.9, 5.6 Hz, 1H), 0.91 (t, J=7.4 Hz, 3H); M/Z (ESI+); 318.03 (Found MH⁺, 318.0261, C₁₂H₁₆INO requires 318.0349).

3-iodo-7-trifluoromethyl-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

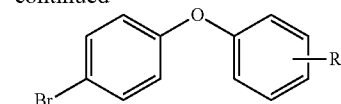


The title compound was synthesised following general procedure C from 7-trifluoromethyl-2-methylquinolin-4(1H)-one (480 mg, 2.10 mmol). The title compound was isolated as a colourless solid (688 mg, 1.92 mmol, 91%). ¹H NMR (500 MHz, CDCl₃/MeOD, 1:1) δ 2.40 (dd, J=16.0, 4.9 Hz, 2H), 2.24 (dd, J=17.9, 8.3 Hz, 1H), 2.20-2.12 (m, 1H), 2.12 (s, 2H), 2.00-1.86 (m, 1H), 1.94 (s, 1H), 1.75 (s, 1H), 1.74 (dd, J=13.5, 5.9 Hz, 1H), 1.13 (ddd, J=19.4, 12.1, 5.8 Hz, 1H). M/Z (ESI+); 357.99 (Found MH⁺, 357.9915, C₁₁H₁₁F₃INO requires 357.9910).



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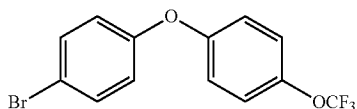
-continued

d) Cu(OAc)₂, Pyridine, TEA, DCM,

General Procedure d

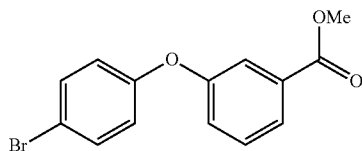
Copper (II) acetate (1 equiv.), triethylamine (5 equiv.), and pyridine (5 equiv.) was added to a solution of the boronic acid (1.5 equiv.) and phenol (1 equiv.) in dichloromethane (10 mL mmol⁻¹) over heat-activated 4 Å molecular sieves. The reaction mixture was stirred over 16 hours at room temperature. The reaction mixture was quenched with HCl (0.5 M, 20 mL mmol⁻¹) and filtered through a pad of Celite, followed by repeated washing with water (10 mL mmol⁻¹). The organic layer was extracted with brine, dried over magnesium sulphate, and concentrated in vacuo. Purification by silica gel chromatography (ethyl acetate/hexane) afforded the title compound.

1-Bromo-4-(4-(trifluoromethoxy)phenoxy)benzene



The title compound was synthesised, from 4-bromophenol (0.42 g, 2.43 mmol) and 4-trifluoromethoxy benzene boronic acid (1.00 g, 4.68 mmol), according to general procedure d as a colourless oil (70%, 0.53 g, 1.63 mmol). ¹H NMR (500 MHz, Chloroform-d) δ 7.37 (d, J=9.0 Hz, 2H), 7.10 (d, J=9.1 Hz, 2H), 6.91 (d, J=9.1 Hz, 2H), 6.80 (d, J=9.0 Hz, 2H);

Methyl 3-(4-bromophenoxy)benzoate

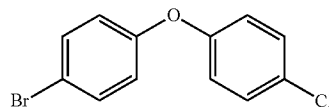


The title compound was synthesised, from 4-bromophenol (0.42 g, 2.43 mmol) and 3-methoxycarbonyl phenyl boronic acid (0.43 g, 2.43 mmol), according to general procedure D. The title compound (43) was isolated as colourless glassy solid (0.21 g, 0.69 mmol, 28%). ¹H NMR (500 MHz, CDCl₃) δ 7.73 (dt, J=7.7, 1.2 Hz, 1H), 7.59-7.53 (m, 1H), 7.38 (d, J=9.0 Hz, 2H), 7.34 (t, J=8.4 Hz, 2H), 7.13 (ddd, J=8.4, 2.5, 0.9 Hz, 1H), 6.82 (d, J=9.0 Hz, 2H), 3.83

100

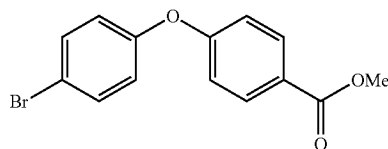
(s, 3H); M/Z (ESI+); 307.00 (Found MH⁺, 306.9962 C₁₄H₁₁BrO₃ requires; 306.9964).

1-bromo-4-(4-chlorophenoxy)benzene



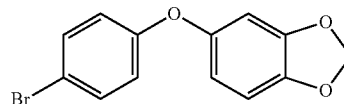
The title compound was synthesised, from 4-bromophenol (0.5 g, 2.80 mmol) and 4-trifluoromethoxy benzene boronic acid (0.6 g, 4.20 mmol), according to general procedure D. The title compound was isolated as a colourless needles (160 mg, 0.56 mmol, 20%). ¹H NMR (500 MHz, CDCl₃) δ 7.43 (d, J=9.0 Hz, 2H), 7.30 (d, J=9.0 Hz, 2H), 6.93 (d, J=9.0 Hz, 2H), 6.86 (d, J=9.0 Hz, 2H).

Methyl 4-(4-bromophenoxy)benzoate



The title compound was synthesised, from 4-bromophenol (0.42 g, 2.43 mmol) and 4-methoxycarbonyl phenyl boronic acid (0.43 g, 2.43 mmol), according to general procedure D. The title compound was isolated as colourless plate crystals (0.25 g, 0.81 mmol, 33%). ¹H NMR (500 MHz, CDCl₃) δ 7.94 (d, J=8.9 Hz, 2H), 7.41 (d, J=8.9 Hz, 2H), 6.91 (d, J=8.8 Hz, 2H), 6.87 (d, J=8.9 Hz, 2H), 3.83 (s, 3H); M/Z (ESI+); 307.00 (Found MH⁺, 306.9961 C₁₄H₁₁BrO₃ requires 306.9964).

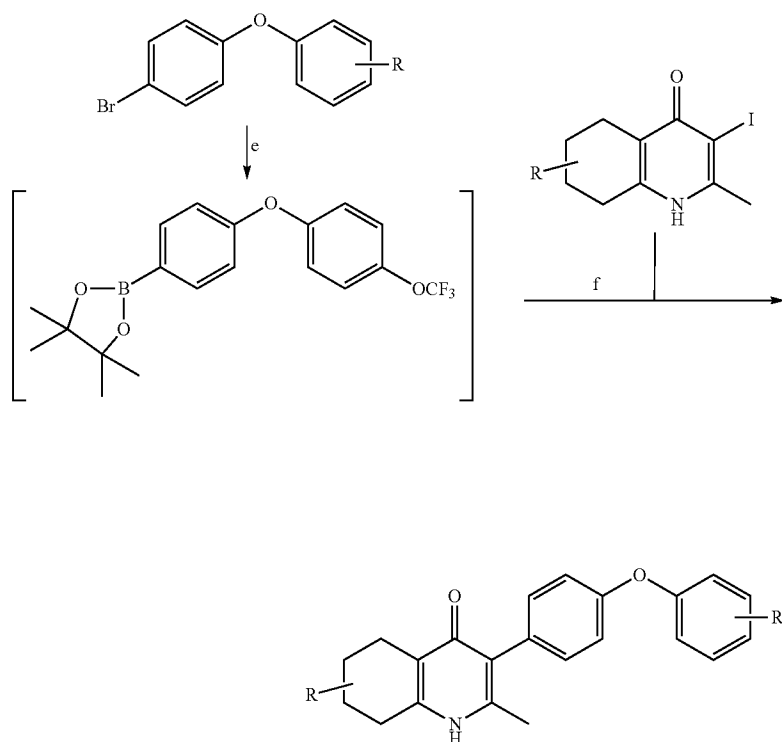
5-(4-bromophenoxy)-2H-1,3-benzodioxole



The title compound was synthesised, from 4-bromophenol (500 mg, 2.89 mmol) and 3,4-methyleneoxy-phenyl boronic acid (719 mg, 4.34 mmol) according to general procedure D. The title compound was isolated as a pale yellow oil (196 mg, 0.67 mmol, 23%). ¹H NMR (500 MHz, Chloroform-d) δ 7.43 (d, J 8.5 Hz, 2H), 6.86 (d, J 8.5 Hz, 2H), 6.79 (d, J 8.5 Hz, 1H), 6.59 (d, J 2.5 Hz, 1H), 6.51 (dd, J 8.5 & 2.5 Hz, 1H), 6.00 (s, 2H);

101

102

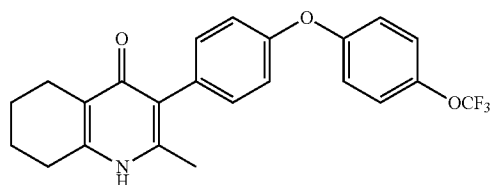


e) Pd(dppf)Cl₂, Bispinocolatodiborane, KOAc, DMF, 80° C. f) Pd(dppf)Cl₂, Na₂CO₃, DMF, 80° C.

1.1 General Method E & F

A flask charged with the 4-bromo-diarylether (1 equiv.), bispinocolatodiborane (1.1 equiv.), KOAc (3 equiv.) and Pd(dppf)Cl₂ (3 mol %) was flushed with nitrogen. DMF (2.00 mL) was added and the reaction was stirred at 80° C. for 18 hours. After cooling the solution to room temperature, 3-iodotetrahydroquinoline (2 equiv.), PdCl₂(dppf) (3 mol %) and Na₂CO₃ (2M, 5 equiv.) were added and the mixture was stirred at 80° C. under nitrogen for a further 24 hours. The solution was cooled to room temperature, the product was extracted with Et₂O (15.0 mL). The organic layers were combined and washed with H₂O (15.0 mL), brine and dried over MgSO₄ and concentrated in vacuo. This was followed by purification by silica gel chromatography (ethyl acetate/petroleum ether).

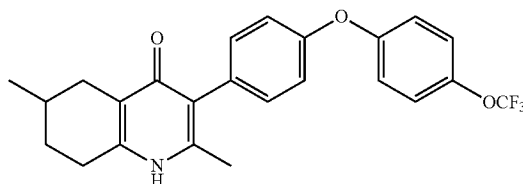
2-methyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one



The title compound was synthesised following general procedure E&F from 3-iodo-5,6,7,8-tetrahydroquinolin-4(1H)-one (260 mg, 0.9 mmol) and 4-bromo(4-trifluoromethoxy)phenyl (200 mg, 0.6 mmol). The title compound was isolated as colourless solid (38 mg, 0.09

mmol, 15%). ¹H NMR (500 MHz, DMSO) δ 11.07 (s, 1H), 7.40 (d, J=8.5 Hz, 2H), 7.19 (d, J=8.6 Hz, 2H), 7.13 (d, J=9.0 Hz, 2H), 7.02 (d, J=8.5 Hz, 2H), 2.54 (t, J=6.0 Hz, 2H, H-8), 2.28 (t, J=5.9 Hz, 2H), 2.07 (s, 3H), 1.71 (m, 2H), 1.65 (m, 2H); M/Z (ESI+); 416.15 (Found MH⁺, 416.1492 C₂₃H₂₀F₃NO₃ requires 416.1473).

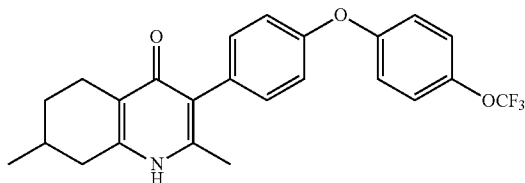
3(4-(4-trifluoromethoxyphenoxy)phenyl)-2,6-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one



The title compound was synthesised following general procedure E&F from 3-iodo-2,6-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one (270 mg, 0.9 mmol) and 4-bromo(4-trifluoromethoxy)phenyl (200 mg, 0.6 mmol). The title compound was isolated as colourless solid (40 mg, 0.09 mmol, 15%). ¹H NMR (500 MHz, CDCl₃/MeOD) δ 6.86 (d, J=8.3 Hz, 4H), 6.79-6.64 (m, 4H), 2.43 (dd, J=17.5, 4.9 Hz, 1H), 2.37 (s, 2H), 1.81 (s, 3H), 1.70-1.54 (m, 2H), 1.45 (m, 1H), 1.09 (dt, J=20.7, 10.5 Hz, 1H), 0.76 (d, J=6.6 Hz, 3H); M/Z (ESI+); 452.14 (Found MNa⁺, 452.1446 C₂₄H₂₂F₃NO₃ requires 452.1444).

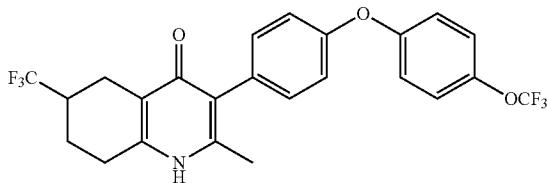
103

3(4-(4-trifluoromethoxyphenoxy)phenyl)-2,7-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one



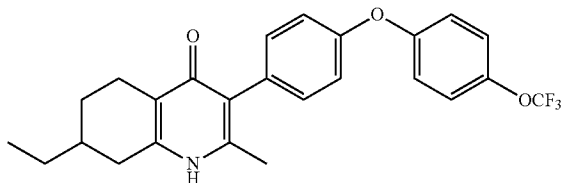
The title compound was synthesised following general procedure E&F from 3-iodo-2,7-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one (120 mg, 0.4 mmol) and 4-bromo(4-trifluoromethoxyphenoxy)phenyl (87 mg, 0.27 mmol). The title compound was isolated as colourless solid (30 mg, 0.07 mmol, 26%). ¹H NMR (400 MHz, DMSO) δ 10.90 (s, 1H), 7.41 (d, J=8.5 Hz, 2H), 7.20 (d, J=7.9 Hz, 2H), 7.14 (d, J=8.5 Hz, 2H), 7.03 (d, J=7.9 Hz, 2H), 2.61 (m, 2H), 2.20 (dd, J=16.4, 9.6 Hz, 2H), 2.08 (s, 3H), 1.81 (m, 2H), 1.24 (s, 1H), 1.04 (d, J=5.9 Hz, 3H); M/Z (ESI+); 452.14 (Found MNa⁺; 452.1446 C₂₄H₂₂F₃NO₃ requires 452.1444).

6-Ethyl-3-(4-(4-trifluoromethoxyphenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one



The title compound was synthesised following general procedure E&F from 3-iodo-2-methyl-6-(trifluoromethyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one (300 mg, 0.84 mmol) and 4-bromo-(4-trifluoromethoxyphenoxy)phenyl (185 mg, 0.56 mmol). The title compound was afforded as a colourless solid. (20 mg, 0.04 mmol, 7%). ¹H NMR (500 MHz, TFA) δ 7.39 (d, J=7.7 Hz, 4H), 7.34 (d, J=7.1 Hz, 2H), 7.24 (d, J=8.5 Hz, 2H), 3.32 (d, J=14.9 Hz, 2H), 3.21 (dd, J=13.8, 5.6 Hz, 1H), 2.89 (dd, J=18.0, 9.6 Hz, 1H), 2.73 (dd, J=15.3, 6.9 Hz, 1H), 2.57 (s, 3H), 2.52 (d, J=13.5 Hz, 1H), 2.07 (d, J=16.0 Hz, 1H, H-7b); M/Z (ESI+); 484.14 (Found MH⁺ 484.1358, C₂₄H₁₉F₆NO₃ requires 484.1342).

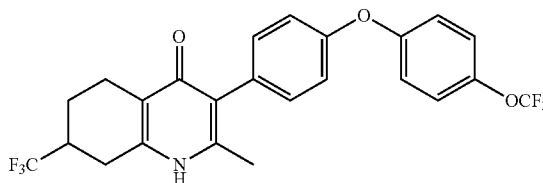
7-Ethyl-2-methyl-3(4-(4-trifluoromethoxyphenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one



104

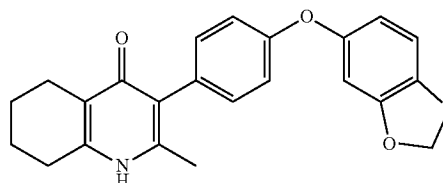
The title compound was synthesised following general procedure E&F from 7-ethyl-2-methylquinolin-4(1H)-one (170 mg, 0.54 mmol) and 4-bromo-(4-trifluoromethoxyphenoxy)phenyl (120 mg, 0.36 mmol). The title compound was isolated as a colourless solid (17 mg, 0.04 mmol, 11%). ¹H NMR (500 MHz, CDCl₃) δ 11.50 (s, 1H), 7.16 (dd, J=15.3, 8.2 Hz, 4H), 6.94 (dd, J=16.6, 8.3 Hz, 4H), 2.78 (d, J=16.1 Hz, 1H), 2.60 (d, J=21.4 Hz, 1H), 2.39 (s, 1H), 2.13 (dd, J=15.8, 10.8 Hz, 1H), 1.96 (s, 3H), 1.59 (s, 1H), 1.43-1.32 (m, 2H), 1.32-1.18 (m, 2H), 0.94 (t, J=7.2 Hz, 3H); M/Z (ESI+); 444.18 (Found MH⁺; 444.1784, C₂₅H₂₄F₃NO₃ requires 444.1781).

7-trifluoromethyl-2-methyl-3(4-(4-trifluoromethoxyphenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one



The title compound was synthesised following general procedure x from 7-trifluoromethyl-2-methylquinolin-4(1H)-one (360 mg, 0.99 mmol) and 4-bromo-(4-trifluoromethoxyphenoxy)phenyl (220 mg, 0.66 mmol). The title compound was isolated as a colourless solid (95 mg, 0.20 mmol, 30%). M/Z (ESI+); 484.14 (Found MH⁺ 484.1358, C₂₄H₁₉F₆NO₃ requires 484.1342).

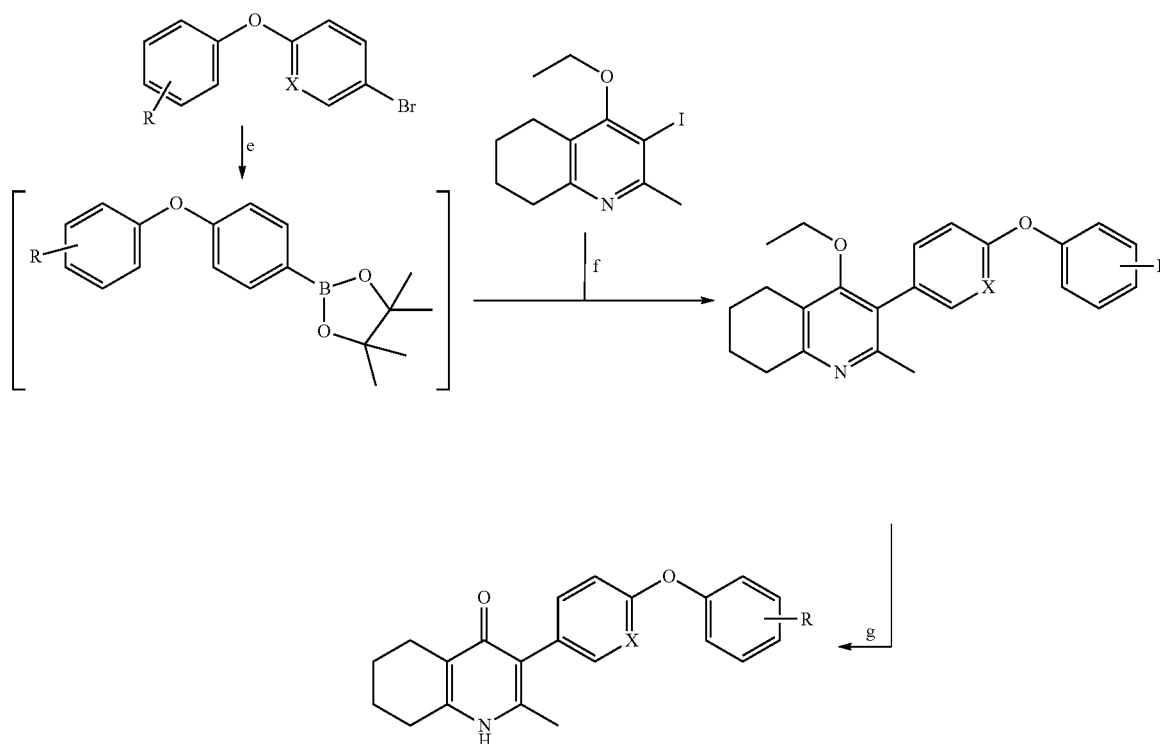
3-[4-(2H-1,3-benzodioxol-5-yloxy)phenyl]-2-methyl-5,6,7,8-tetrahydroquinolin-4-one



The title compound was synthesised from 5-(4-bromophenoxy)-2H-1,3-benzodioxole (200 mg, 0.68 mmol) and 3-iodo-5,6,7,8-tetrahydroquinolin-4(1H)-one (288 mg, 1.02 mmol). The title compound was isolated as a pale grey solid (40 mg, 0.11 mmol, 16%). HPLC; 3.28 min (86%); δ ¹H NMR (500 MHz, TFA) δ 7.35 (d, J 8.5 Hz, 2H), 7.31-7.29 (m, 3H), 6.98 (s, 1H), 6.79 (s, 1H), 6.10 (s, 2H), 3.09 (t, J 5.0 Hz, 2H), 2.90 (t, J 5.0 Hz, 2H), 2.52 (s, 3H), 2.11-2.05 (m, 4H); M/Z (ESI); 375.1563, (C₂₃H₂₁NO₄ requires 375.1471).

105

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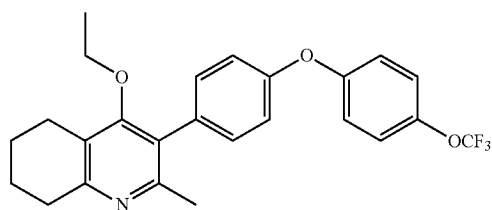


e) Pd(dppf)Cl₂, Bispinocolatodiborane, KOAc, DMF, 80° C. f) Pd(dppf)Cl₂, Na₂CO₃, DMF, 80° C., g) HBr, AcOH 120° C.

1.2 General Method E & F

A flask charged with the 4-bromo-diarylether (1 equiv.), bispinocolatodiborane (1.1 equiv.), KOAc (3 equiv.) and Pd(dppf)Cl₂ (3 mol %) was flushed with nitrogen. DMF (2.00 mL) was added and the reaction was stirred at 80° C. for 18 hours. After cooling the solution to room temperature, 3-iodo-2-methyl-5,6,7,8-tetrahydroquinoline (2 equiv.), PdCl₂(dppf) (3 mol %) and Na₂CO₃ (2M, 5 equiv.) were added and the mixture was stirred at 80° C. under nitrogen for a further 24 hours. The solution was cooled to room temperature, the product was extracted with Et₂O (15.0 mL). The organic layers were combined and washed with H₂O (15.0 mL), brine and dried over MgSO₄ and concentrated in vacuo. This was followed by purification by silica gel chromatography (ethyl acetate/petroleum ether).

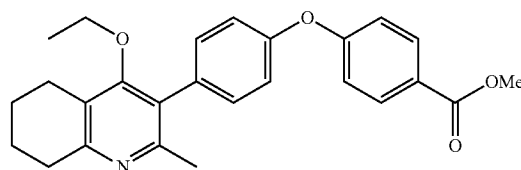
4-ethoxy-2-methyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydro quinoline



The title compound was synthesised from 1-Bromo-4-(4-(trifluoromethoxy)phenoxy)benzene (100 mg, 0.30 mmol) according to general procedure E&F, to afford the title compound as a colourless gum/viscous oil (30 mg, 0.07

mmol, 23%). ¹H NMR (500 MHz, Acetone) δ 7.28 (d, J=8.7 Hz, 2H), 7.26 (d, J=9.1 Hz, 2H), 7.09 (d, J=9.1 Hz, 2H), 7.07 (d, J=8.7 Hz, 2H), 3.52 (q, J=7.0 Hz, 2H), 2.85 (t, J=6.5 Hz, 2H), 2.78 (t, J=6.2 Hz, 2H), 2.26 (s, 3H), 1.89-1.81 (m, 2H), 1.81-1.72 (m, 2H), 0.93 (t, J=7.0 Hz, 3H); M/Z (ESI+); 444.18 (Found MH⁺, 444.1792 C₂₅H₂₄F₃NO₃ requires 444.1781).

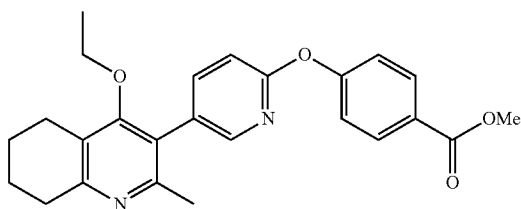
Methyl 4-(4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenoxy)benzoate



The title compound was synthesised from methyl 4-(4-bromophenoxy)benzoate (150 mg, 0.49 mmol) according to general procedure E&F. The title compound was isolated as colourless microcrystals (56 mg, 0.13 mmol, 27%). ¹H NMR (500 MHz, CDCl₃) δ 8.03 (d, J=8.7 Hz, 2H), 7.29 (d, J=8.4 Hz, 2H), 7.11 (d, J=8.4 Hz, 2H), 7.03 (d, J=8.7 Hz, 2H), 3.90 (s, 3H), 3.51 (q, J=7.0 Hz, 2H), 2.91 (t, J=6.2 Hz, 2H), 2.72 (t, J=6.0 Hz, 2H), 2.32 (s, 3H), 1.91-1.84 (m, 2H), 1.83-1.76 (m, 2H), 1.04 (t, J=7.0 Hz, 3H); M/Z; 418.20 (ESI+); 418.20 (Found MH⁺, 418.2037 C₂₆H₂₇NO₄ requires 418.2018).

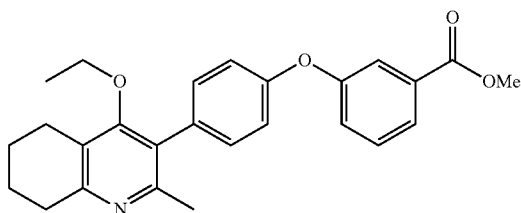
107

Methyl 4-((5-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)pyridin-2-yl)oxy) benzoate



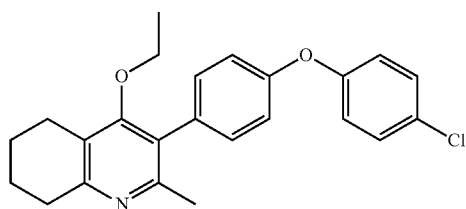
The title compound was synthesised from methyl 3-((5-bromopyridin-2-yl)oxy)benzoate (100 mg, 0.33 mmol) according to general procedure E&F. The title compound was isolated as a colourless gum/semisolid (30 mg, 0.07 mmol, 21%). ¹H NMR (500 MHz, CDCl₃) δ 8.13 (d, J=2.3 Hz, 1H, H-6'), 8.10 (d, J=8.7 Hz, 2H), 7.67 (dd, J=8.4, 2.4 Hz, 1H, H-4'), 7.24 (d, J=8.7 Hz, 2H), 7.05 (d, J=8.4 Hz, 1H), 3.91 (s, 3H), 3.53 (q, J=7.0 Hz, 2H), 2.92 (t, J=6.3 Hz, 2H), 2.71 (t, J=6.2 Hz, 2H), 1.06 (t, J=7.0 Hz, 3H); M/Z (ESI+); 419.20 (Found MH⁺, 419.1993 C₂₅H₂₆N₂O₄ requires 419.1970).

Methyl 3-(4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenoxy)benzoate



The title compound was synthesised from methyl 3-(4-bromophenoxy)benzoate (150 mg, 0.49 mmol) according to general procedure E&F. The title compound was isolated as colourless crystals (50 mg, 0.12 mmol, 25%). ¹H NMR (500 MHz, CDCl₃) δ 7.73 (d, J=7.7 Hz, 1H), 7.65-7.60 (m, 1H), 7.37 (t, J=7.9 Hz, 1H), 7.19 (m, 3H), 7.00 (d, J=8.6 Hz, 2H), 3.83 (s, J=, 3H), 3.45 (q, J=7.0 Hz, 2H), 2.85 (t, J=6.3 Hz, 2H), 2.65 (t, J=6.2 Hz, 2H), 2.26 (s, 3H), 1.88-1.78 (m, 2H), 1.76-1.67 (m, 2H), 0.99 (t, J=7.0 Hz, 3H); M/Z (ESI+); 418.20 (Found MH⁺ 418.2030, C₂₆H₂₇NO₄ requires 418.2018).

Formation of: 3-(4-(4-chlorophenoxy)phenyl)-4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinoline



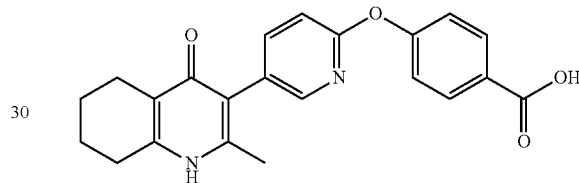
108

The title compound was synthesised from 1-bromo-4-(4-chlorophenoxy)benzene (70 mg, 0.24 mmol) according to general procedure E&F. The title compound was isolated as colourless oil (20 mg, 0.05 mmol, 27%). ¹H NMR (500 MHz, CDCl₃) δ 7.25 (d, J=8.9 Hz, 2H), 7.17 (d, J=8.7 Hz, 2H), 6.98 (d, J=8.7 Hz, 2H), 6.93 (d, J=8.9 Hz, 2H), 3.45 (q, J=7.0 Hz, 2H), 2.89 (t, J=6.3 Hz, 2H), 2.65 (t, J=6.1 Hz, 2H), 2.28 (s, 3H), 1.90-1.61 (m, 4H), 0.98 (t, J=7.0 Hz, 3H); M/Z (ESI+); 394.16 (Found MH⁺394.1575, C₂₄H₂₄ClNO₂ requires 394.1568).

1.3 General Method G

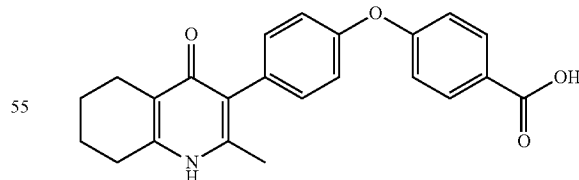
To a solution of the 4-ethoxy-3-(diaryl ether)-hydroxyquinolone (1 equiv.) in acetic acid (2 mL mmol⁻¹) was added hydrogen bromide (>48% w/v (aq)) (1 mL mmol⁻¹). The reaction mixture was then heated to 90° C. and left to reflux for 72 hours. The reaction mixture was neutralised with sodium hydroxide (2 M, 30.0 mL) and precipitate formed. The reaction mixture was then filtered to afford the title compound and purified.

Methyl 3-((5-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)pyridin-2-yl)oxy) benzoate



The title compound was synthesised from methyl 4-((5-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)pyridin-2-yl)oxy) benzoate (30 mg, 0.07 mmol) according to general procedure G. The title compound was isolated as colourless semi solid (13 mg, 0.03 mmol, 45%). ¹H NMR (500 MHz, DMSO) δ 12.83 (s, 1H, NH), 11.03 (s, 1H, CO₂H), 8.00 (d, J=8.7 Hz, 2H), 7.99 (s, 1H), 7.73 (dd, J=8.4, 2.4 Hz, 1H), 7.24 (d, J=8.7 Hz, 2H), 7.12 (d, J=8.4 Hz, 1H), 2.56 (t, J=5.8 Hz, 2H), 2.30 (t, J=5.8 Hz, 2H), 2.11 (s, 3H), 1.82-1.51 (m, 4H); M/Z (ESI+); 377.15 (Found MH⁺, 377.1497 C₂₂H₂₀N₂O₄ requires 377.1496).

4-(4-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)phenoxy)benzoic Acid

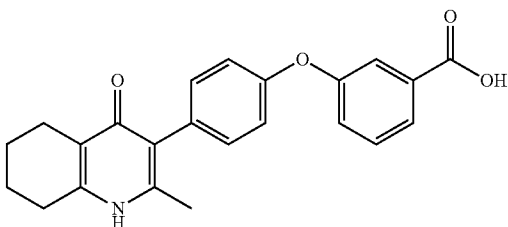


The title compound was synthesised from methyl 4-(4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenoxy)benzoate (50 mg, 0.17 mmol) according to general procedure G. The title compound was isolated as colourless crystals (33 mg, 0.09 mmol, 48%). ¹H NMR (500 MHz, DMSO) δ 13.79 (s, 1H), 12.80 (s (b), 1H), 7.99 (d, J=8.8 Hz, 2H), 7.36 (d, J=8.7 Hz, 2H), 7.24 (d, J=8.7 Hz, 2H), 7.14 (d, J=8.8 Hz, 2H), 2.92 (t, J=5.1 Hz, 2H), 2.62 (t, J=5.0 Hz, 2H),

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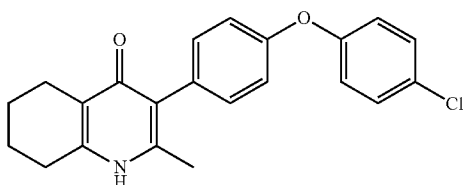
2.31 (s, 3H), 1.90-1.76 (m, 4H); M/Z (ESI+); 376.16 (Found MH⁺, 376.1550, C₂₃H₂₁NO₄ requires 376.1543).

3-(4-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)phenoxy)benzoic acid

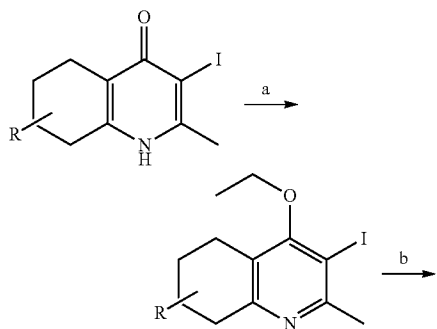


The title compound was synthesised from 3-methyl 3-(4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenoxy)benzoate (50 mg, 0.17 mmol) according to general procedure G. The title compound was isolated as colourless crystals (7 mg, 0.02 mmol, 12%). ¹H NMR (500 MHz, DMSO) δ 13.00 (s, 1H), 11.31 (s, 1H), 7.70 (d, J=7.9 Hz, 1H), 7.52 (t, J=7.9 Hz, 1H), 7.48 (dd, J=2.2, 1.6 Hz, 1H), 7.31 (dd, J=7.9, 1.6 Hz, 1H), 7.21 (d, J=8.6 Hz, 2H), 7.04 (d, J=8.6 Hz, 2H), 2.58 (t, J=5.8 Hz, 2H), 2.32 (t, J=5.8 Hz, 2H), 2.09 (s, 3H), 1.76-1.59 (m, 4H); M/Z (ESI+); 376.15 (Found MH⁺ 376.1547, C₂₃H₂₁NO₄ requires 376.1543).

3-(4-(4-chlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

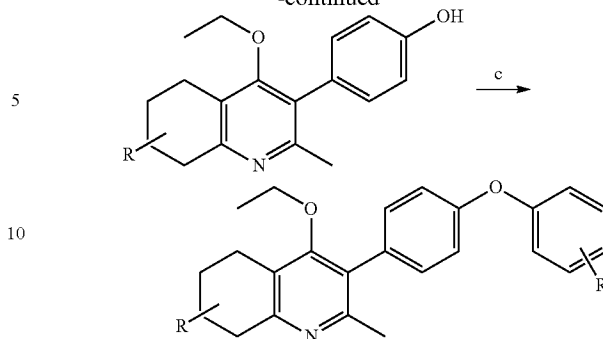


The title compound was synthesised from 3-(4-(4-chlorophenoxy)phenyl)-4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinoline (20 mg, 0.5 mmol) according to general procedure G. The title compound was isolated as colourless solid (18 mg, 0.05 mmol, 95%). ¹H NMR (500 MHz, DMSO) δ 10.99 (s, 1H), 7.44 (d, J=8.9 Hz, 2H), 7.18 (d, J=8.6 Hz, 2H), 7.05 (d, J=8.9 Hz, 2H), 7.04 (d, J=8.6 Hz, 2H), 2.56 (t, J=5.3 Hz, 2H), 2.29 (t, J=5.3 Hz, 2H), 2.07 (s, 3H), 1.78-1.55 (m, 4H); M/Z (ESI+); 366.13 (Found MH⁺ 366.1262, C₂₂H₂₁ClNO₂ requires 366.1253).

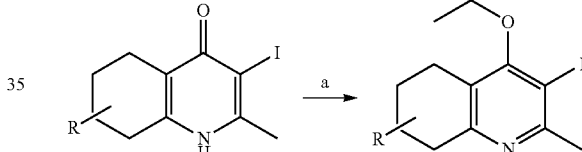
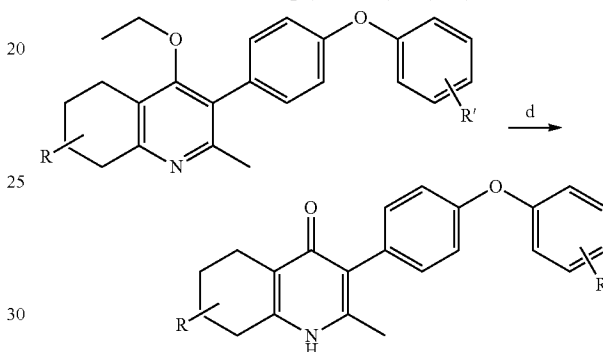


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-continued



R = H, 5-Me, 6-Me, 7-Me, 6-CF₃, 7-CF₃, 7-Et R' = 3-F, 3-Cl, 3-CF₃, 3-CO₂H, 4-F, 4-Cl, 4-CF₃, 4-OCF₃, 4-CO₂H, 3 & 4-Cl, 3-Cl, 4-F, 3 & 5-Cl

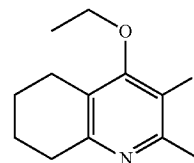


a) EtI, K₂CO₃, DMF, 80° C.

40 a) EtI, K₂CO₃, DMF, 80° C., b) 4-Hydroxyphenyl boronic acid, Pd(PPh₃)₄, Na₂CO₃, DMF, 80° C., c) Phenyl boronic acid, Cu(OAc)₂, Pyridine, TEA, DCM, d) HBr (40% aq), Acetic acid, 120° C.

4-ethoxy-3-iodo-2-methyl-5,6,7,8-tetrahydroquinoline

50



55

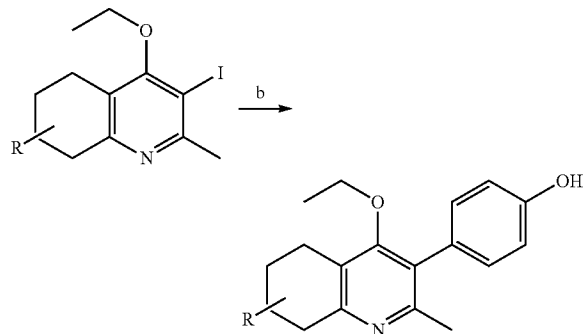
A suspension of 4(1H), 3-iodo-2-methyl, 5,6,7,8-tetrahydroquinolinone (2.20 g, 7.61 mmol) and Potassium carbonate (2.10 g, 15.2 mmol) in DMF (20.0 mL) was heated to 50° C. and stirred for 45 minutes. The reaction mixture was removed from the heat and ethyl iodide (0.89 mL, 11.4 mmol) was added dropwise. The reaction mixture was then heated to 50° C. and stirred for a further 18 hours. Formation of a yellow emulsion was observed. The reaction mixture was then quenched with water (40.0 mL). The organic phase was extracted using the polar extraction technique (ethyl

60

65

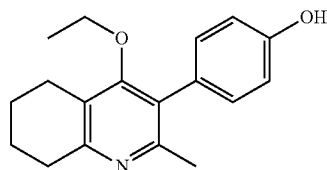
111

acetate, 3×40.0 mL), and the resulting organic layers were combined and dried over MgSO_4 and concentrated in vacuo to afford the title compound as an orange oil. (2.00 g, 6.32 mmol, 83%). δ H NMR (500 MHz, Chloroform- d); δ 3.96 (q, $J=7.0$ Hz, 2H), 2.84 (t, $J=6.3$ Hz, 2H), 2.74 (t, $J=6.3$ Hz, 2H), 2.71 (s, 3H), 1.89-1.82 (m, 2H), 1.78-1.72 (m, 2H), 1.49 (t, $J=7.0$ Hz, 3H); M/Z (ESI+); 318.04 (Found MH^+ , 318.0350, $\text{C}_{12}\text{H}_{17}\text{INO}$ requires 318.0349).



b) 4-Hydroxyphenyl boronic acid, $\text{Pd}(\text{PPh}_3)_4$, Na_2CO_3 , DMF, 80°C .

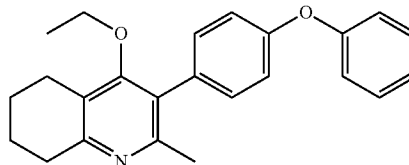
4-(4-Ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenol



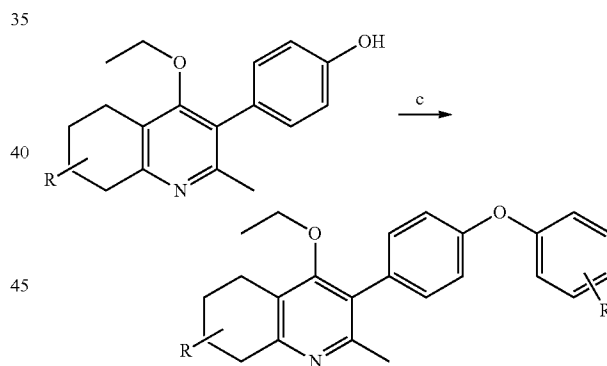
To a nitrogen flushed flask charged with 4-ethoxy-3-iodo-2-methyl-5,6,7,8-tetrahydroquinoline (400 mg, 1.26 mmol), 4 hydroxybenzene boronic acid (260 mg, 1.89 mmol) and palladium tetra(triphenylphosphine) (73 mg, 0.06 mmol) was added degassed DMF (10 mL). Potassium carbonate (aq) (3 mL, 2 M) was added and the reaction mixture brought up to 80°C and stirred for 3 hours. The reaction mixture was then cooled to room temperature and diluted with water (10 mL). The organic phase was then extracted using ethyl acetate (3×20 mL). The organic phases were combined and washed with water (3×20 mL) and then dried with brine (1×10 mL) and MgSO_4 , before concentration in vacuo. The resulting redish brown solid was then recrystallized in ethyl acetate. To yield the title compound as a colourless solid (220 mg, 0.78 mmol, 61%). ^1H NMR (500 MHz, MeOD) δ 7.07 (d, $J=8.6$ Hz, 2H), 6.86 (d, $J=8.6$ Hz, 2H), 3.51 (q, $J=7.0$ Hz, 2H), 2.83 (t, $J=6.3$ Hz, 2H), 2.72 (t, $J=6.1$ Hz, 2H), 2.23 (s, 3H), 1.95-1.72 (m, 4H), 1.00 (t, $J=7.0$ Hz, 3H); M/Z (ESI+); 284.17 (Found MH^+ 284.1664, $\text{C}_{18}\text{H}_{21}\text{NO}_2$ requires 284.1651).

112

4-ethoxy-2-methyl-3-(4-phenoxyphenyl)-5,6,7,8-tetrahydroquinoline



A solution of 4-ethoxy, 3-iodo, 2-methyl, 5,6,7,8-tetrahydro, quinolone (1.00 g, 3.16 mmol), 4-phenoxy phenyl boronic acid (1.01 g, 4.73 mmol), Palladium (II) tetra(triphenyl-phosphine) (0.18 g, 0.16 mmol) and dipotassium carbonate (2.00 M, 6.40 mL) dissolved in degassed DMF (20.0 mL) was heated to 85°C and stirred for 12 hours. Observed colour change from yellow to black. The reaction mixture was allowed to cool to room temperature before dilution with ethyl acetate (15.0 mL). The organic layer was extracted using polar extraction technique, before being collected and dried over MgSO_4 . The solution was then concentration in vacuo to afford the title compound as colourless fine needles (0.45 g, 1.25 mmol, 40%). δ H NMR (126 MHz, Chloroform- d); δ 7.35 (t, $J=7.6$ Hz, 2H), 7.23 (d, $J=8.5$ Hz, 2H), 7.11 (t, $J=7.6$ Hz, 1H), 7.05 (d, 4H) 3.42 (q, $J=7.0$ Hz, 2H), 2.82 (t, $J=6.4$ Hz, 2H), 2.62 (t, $J=6.3$ Hz, 2H), 2.23 (s, 3H), 1.80-1.74 (m, 2H), 1.73-1.67 (m, 2H), 1.49 (t, $J=7.0$ Hz, 3H); M/Z (ESI+); 360.20 (Found MH^+ , 360.1963, $\text{C}_{24}\text{H}_{26}\text{NO}_2$ requires 360.1958).



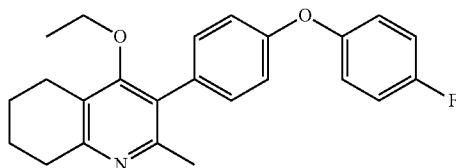
c) Phenyl boronic acid, $\text{Cu}(\text{OAc})_2$, Pyridine, TEA, DCM

General Method C

Copper (II) acetate (1 equiv.), triethylamine (5 equiv.), and pyridine (5 equiv.) was added to a solution of the boronic acid (1.5 equiv.) and phenol (1 equiv.) in dichloromethane (10 mL mmol^{-1}) over heat-activated 4 Å molecular sieves. The reaction mixture was stirred over 16 hours at room temperature. The reaction mixture was quenched with HCl (0.5 M, 20 mL mmol^{-1}) and filtered through a pad of Celite, followed by repeated washing with water (10 mL mmol^{-1}). The organic layer was extracted with brine, dried over magnesium sulphate, and concentrated in vacuo. Purification by silica gel chromatography (ethyl acetate/hexane) afforded the title compound.

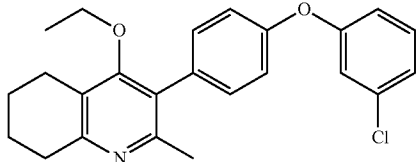
113

4-Ethoxy-3-(4-(4-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline



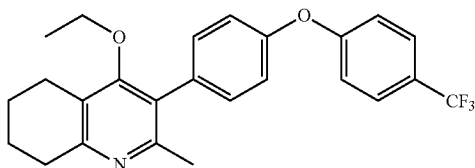
The title compound was synthesised from 4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenol (60 mg, 0.21 mmol) and 4-fluorobenzene boronic acid (45 mg, 0.31 mmol), according to general procedure C as pink micro crystals (70%, 55 mg, 0.15 mmol). ¹H NMR (500 MHz, Chloroform-d) δ 7.14 (d, J=8.6 Hz, 2H), 6.97 (m, 6H), 3.44 (q, J=7.0 Hz, 2H), 2.87 (t, J=6.2 Hz, 2H), 2.64 (t, J=6.1 Hz, 2H), 2.26 (s, 3H), 1.78 (m, 4H), 0.97 (t, J=7.0 Hz, 3H); M/Z (ESI+); 378.19 (Found MH⁺ 378.1877, C₂₄H₂₄FNO₂ requires).

3-(4-(3-Chlorophenoxy)phenyl)-4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinoline



The title compound was synthesised from 4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenol (250 mg, 0.88 mmol) and 3-chlorobenzene boronic acid (205 mg, 1.32 mmol), according to general procedure C as a viscous orange oil (78%, 270 mg, 0.68 mmol). ¹H NMR (500 MHz, CDCl₃) δ 7.28-7.22 (m, 1H), 7.20 (d, J=8.3 Hz, 2H), 7.02 (d, J=8.3 Hz, 2H), 6.81-6.72 (m, 2H), 6.67 (dd, J=10.2, 2.1 Hz, 1H), 3.44 (q, J=7.0 Hz, 2H), 2.86 (t, J=6.2 Hz, 2H), 2.65 (t, J=6.1 Hz, 2H), 2.26 (s, 3H), 1.82 (m, 2H), 1.77-1.69 (m, 2H), 0.98 (t, J=7.0 Hz, 3H); M/Z (ESI+); 394.16 (Found MH⁺; 394.1588, C₂₄H₂₄ClNO₂ requires 394.1574).

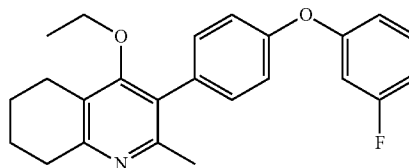
4-Ethoxy-2-methyl-3-(4-(4-(trifluoromethyl)phenoxy)phenyl)-5,6,7,8-tetrahydroquinoline



114

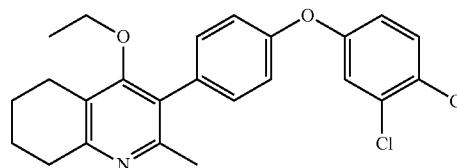
The title compound was synthesised from 4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenol (60 mg, 0.21 mmol) and 4-trifluoromethylbenzene boronic acid (62 mg, 0.29 mmol), according to general procedure C as a viscous orange oil (55%, 47 mg, 0.11 mmol). ¹H NMR (500 MHz, CDCl₃) δ 7.61 (d, J=8.7 Hz, 2H), 7.28 (d, J=8.5 Hz, 2H), 7.15-7.06 (m, 5H), 3.54 (q, J=7.0 Hz, 2H), 2.98 (t, J=6.3 Hz, 2H), 2.72 (t, J=6.2 Hz, 2H), 2.37 (s, 3H), 1.94-1.85 (m, 2H), 1.84-1.77 (m, 2H), 1.06 (t, J=7.0 Hz, 3H), M/Z (ESI+); 428.18 (Found MH⁺ 428.1842, C₂₅H₂₄F₃NO₂ requires 428.1832).

4-Ethoxy-3-(4-(3-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline



The title compound was synthesised from 4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenol (250 mg, 0.88 mmol) and 3-fluorobenzene boronic acid (184 mg, 1.32 mmol), according to general procedure G as a yellow oil (57%, 190 mg, 0.50 mmol). ¹H NMR (500 MHz, CDCl₃) δ 7.25 (dd, J=15.0, 8.2 Hz, 1H), 7.18 (d, J=8.6 Hz, 2H), 7.04 (d, J=8.6 Hz, 2H), 6.81-6.75 (m, 2H), 6.69 (dt, J=10.1, 2.3 Hz, 1H), 3.49 (q, J=7.0 Hz, 2H), 3.04 (m, 2H), 2.65 (t, J=6.2 Hz, 2H), 2.39 (s, 3H), 1.87-1.79 (m, 2H), 1.79-1.70 (m, 2H), 1.02 (t, J=7.0 Hz, 3H); M/Z (ESI+); 378.19 (Found MH⁺ 378.1877, C₂₄H₂₄FNO₂ requires).

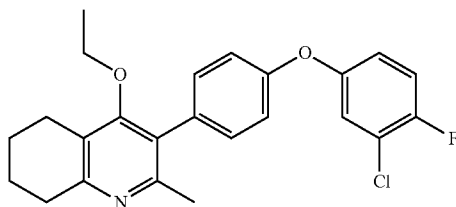
4-Ethoxy-3-(4-(3,4-dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline



The title compound was synthesised from 4-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenol (100 mg, 0.34 mmol) and 3,4-dichlorobenzene boronic acid (93 mg, 0.51 mmol), according to general procedure C as an orange oil (49%, 70 mg, 0.16 mmol). ¹H NMR (300 MHz, CDCl₃) δ 7.34 (d, J=8.8 Hz, 1H), 7.20 (dd, J=7.1, 1.6 Hz, 2H), 7.06 (d, J=2.8 Hz, 1H), 7.03-6.97 (m, 2H), 6.85 (dd, J=8.8, 2.8 Hz, 1H), 3.46 (q, J=7.0 Hz, 2H), 2.91 (t, J=6.2 Hz, 2H), 2.65 (t, J=6.1 Hz, 2H), 2.29 (s, 3H), 1.90-1.62 (m, 4H), 0.99 (t, J=7.0 Hz, 3H); M/Z (ESI+); 428.12 (Found MH⁺; 428.1202, C₂₄H₂₃Cl₂NO₂ requires 428.1184).

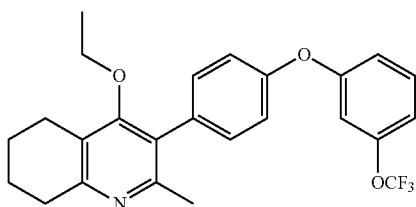
115

4-Ethoxy-3-(4-(3-chloro-4-fluorophenoxy)phenyl)-
2-methyl-5,6,7,8-tetrahydroquinoline



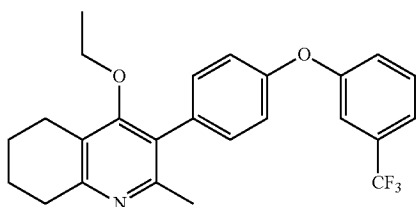
The title compound was synthesised from 4-(4-ethoxy-2-
methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenol (250 mg, 0.88 mmol) and 3-chloro-4-fluorophenylboronic acid (230 mg, 1.32 mmol), according to general procedure C. The title compound was collected as a pale orange solid (104 mg, 0.25 mmol, 29%). ¹H NMR (400 MHz, CDCl₃) δ 7.26 (d, J=8.2 Hz, 2H), 7.17-7.11 (t, J=8.7 Hz, 1H), 7.09 (dd, J=6.1, 2.9 Hz, 1H), 7.04 (d, J=8.3 Hz, 2H), 6.97-6.91 (m, 1H), 3.50 (dd, J=14.0, 7.0 Hz, 1H), 2.91 (t, J=6.2 Hz, 2H), 2.72 (t, J=5.9 Hz, 2H), 2.31 (s, 3H), 1.95-1.84 (m, 2H), 1.81 (m, 2H), 1.04 (t, J=7.0 Hz, 3H); M/Z (ESI); 412.1489, C₂₄H₂₃ClFNO₂ requires 411.1401.

4-Ethoxy-3-(4-(3-trifluoromethoxyphenoxy)phenyl)-
2-methyl-5,6,7,8-tetrahydroquinoline



The title compound was synthesised from 4-(4-ethoxy-2-
methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenol (200 mg, 0.71 mmol) and 3-trifluoromethoxyphenylboronic acid (218 mg, 1.06 mmol) according to general procedure C. The title compound was collected as a purple/brown oil (132 mg, 0.32 mmol, 42%); ¹H NMR (400 MHz, CDCl₃) δ 7.29 (t, J=8.3 Hz, 1H), 7.21 (d, J=8.3 Hz, 2H), 7.03 (d, J=8.2 Hz, 2H), 6.90 (d, J=8.2 Hz, 2H), 6.81 (s, 1H), 3.44 (dd, J=14.0, 7.0 Hz, 2H), 2.84 (t, J=6.2 Hz, 2H), 2.65 (t, J=6.0 Hz, 2H), 2.25 (s, 3H), 1.86-1.78 (m, 2H), 1.74 (dd, J=10.2, 4.6 Hz, 2H), 0.97 (t, J=7.0 Hz, 3H); M/Z (ESI); 444.1786, C₂₅H₂₅F₃NO₃ requires 444.1781.

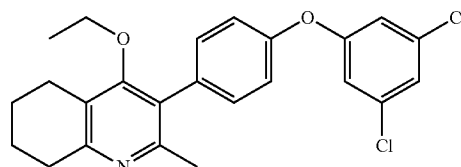
4-Ethoxy-3-(4-(3-trifluoromethylphenoxy)phenyl)-2-
methyl-5,6,7,8-tetrahydroquinoline



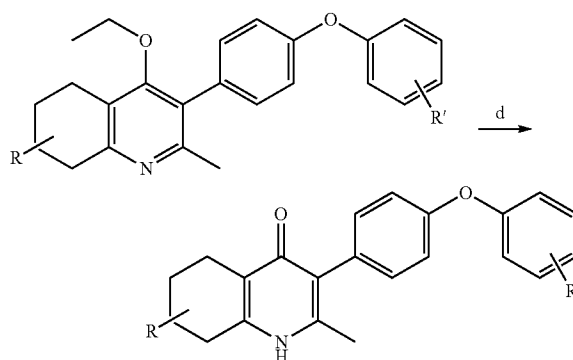
116

The title compound was synthesised from 4-(4-ethoxy-2-
methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenol (300 mg, 1.06 mmol) and 3-trifluoromethylphenyl boronic acid (302 mg, 1.59 mmol) according to general procedure C. The title compound was collected as a yellow oil (198 mg, 0.46 mmol, 44%). ¹H NMR (400 MHz, CDCl₃) δ 7.44-7.38 (m, 1H), 7.32 (d, J=7.8 Hz, 1H), 7.17 (s, 2H), 7.12 (d, J=8.3 Hz, 2H), 7.01 (d, J=8.4 Hz, 2H), 3.45 (q, J=7.0 Hz, 2H), 2.85 (t, J=6.0 Hz, 2H), 2.62 (t, J=5.7 Hz, 2H), 2.25 (s, 3H), 1.73 (m, 4H), 1.00 (t, J=7.0 Hz, 3H); M/Z (ESI); 427.1852, C₂₅H₂₄F₃NO₂ requires 427.1759.

3-[4-(3,5-dichlorophenoxy)phenyl]-4-ethoxy-2-
methyl-5,6,7,8-tetrahydroquinoline



The title compound was synthesised from 4-(4-ethoxy-2-
methyl-5,6,7,8-tetrahydroquinolin-3-yl)phenol (250 mg, 0.88 mmol) and 3,5-dichlorophenylboronic acid (278 mg, 1.32 mmol) according to general procedure C. The title compound was collected as a yellow solid (50 mg, 0.12 mmol, 13%). ¹H NMR (500 MHz, Chloroform-d) δ 7.34-7.32 (m, 2H), 7.13-7.11 (m, 3H), 6.93 (d, J=1.8 Hz, 2H), 3.54 (q, J=7.0 Hz, 2H), 2.94 (t, J=6.1 Hz, 2H), 2.75 (t, J=6.3 Hz, 2H), 2.39 (s, 3H), 1.95-1.81 (m, 4H), 1.08 (t, J=7.0 Hz, 3H); M/Z (ESI); 428.1194, C₂₄H₂₄Cl₂NO₂ requires 428.1179.



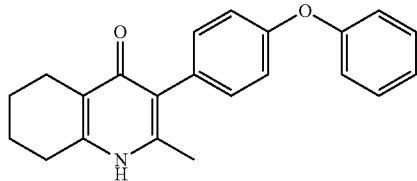
d) HBr (40% aq), Acetic acid, 120° C.

1.4 General Method D

To a solution of the 4-ethoxy-3-(diaryl ether)-hydroxyquinolone (1 equiv.) in acetic acid (2 mL mmol⁻¹) was added hydrogen bromide (>48% w/v (aq)) (1 mL mmol⁻¹). The reaction mixture was then heated to 90° C. and left to reflux for 72 hours. The reaction mixture was neutralised with sodium hydroxide (2 M, 30.0 mL) and precipitate formed. The reaction mixture was then filtered to afford the title compound and purified.

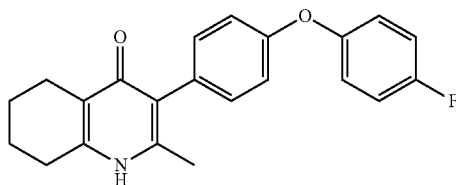
117

Formation of: 2-methyl-3-(4-phenoxyphenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one



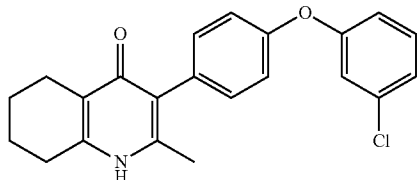
The title compound was synthesised from 4-ethoxy-3-(4-phenoxy, benzene),2-methyl-5,6,7,8-hydroquinolone (0.43 g, 1.20 mmol) following general procedure D to afford the title compound as colourless microcrystals (0.39 g, 1.20 mmol, 99%). ¹H NMR (500 MHz, DMSO-d₆) δ 7.38 (t, J=7.9 Hz, 2H, H-3" & 5"), 7.17 (d, J=8.5 Hz, 2H), 7.14 (t, J=7.4 Hz, 1H), 7.05 (d, J=7.9 Hz, 2H), 6.98 (d, J=8.5 Hz, 2H), 2.56 (t, J=5.9 Hz, 2H), 2.30 (t, J=6.1 Hz, 2H), 2.08 (s, 3H), 1.75-1.68 (m, 2H), 1.68-1.62 (m, 2H); M/Z (ESI+); 332.17 (Found MH⁺, 332.1673, C₂₂H₂₁NO₂ requires 332.1650).

3-(4-(4-Fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one



The title compound was synthesised from 4-ethoxy-3-(4-(4-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline (45 mg, 0.12 mmol) according to general procedure D. The title compound was isolated as colourless solid (25 mg, 0.07 mmol, 60%). ¹H NMR (500 MHz, DMSO) δ 7.25 (t, J=8.7 Hz, 2H), 7.17 (d, J=8.5 Hz, 2H), 7.11 (dd, J=8.9, 4.5 Hz, 2H), 6.96 (d, J=8.5 Hz, 2H), 2.59-2.53 (m, 2H), 2.30 (t, J=5.2 Hz, 2H), 2.08 (s, 3H), 1.72 (m, 2H), 1.66 (m, 2H); M/Z (ESI+); 350.16 (Found MH⁺ 350.1562, C₂₂H₂₀FNO₂ requires 350.1550).

3-(4-(3-Chlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

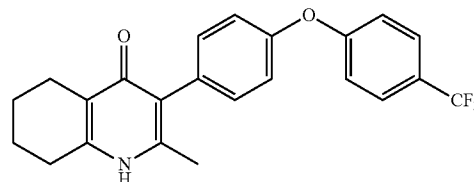


The title compound was synthesised from 3-(4-(3-chlorophenoxy)phenyl)-4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinoline (200 mg, 0.51 mmol) according to general procedure D. The title compound was isolated as colourless solid (120 mg, 0.33 mmol, 66%). ¹H NMR (500 MHz, DMSO) δ

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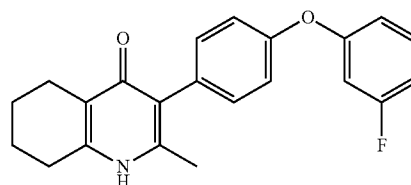
11.71 (s, 1H), 7.44 (t, J=8.2 Hz, 1H), 7.25 (d, J=8.6 Hz, 2H), 7.22 (ddd, J=8.0, 1.9, 0.8 Hz, 1H), 7.10 (t, J=2.0 Hz, 1H), 7.09 (d, J=8.6 Hz, 2H), 7.03 (ddd, J=8.2, 2.3, 0.6, 1H), 2.65 (t, J=5.9 Hz, 2H), 2.39 (t, J=5.2 Hz, 2H), 2.14 (s, 3H), 1.84-1.59 (m, 4H); M/Z (ESI+); 366.13 (Found MH⁺ 366.1262, C₂₂H₂₀ClNO₂ requires 366.1255).

2-Methyl-3-(4-(4-(trifluoromethyl)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one



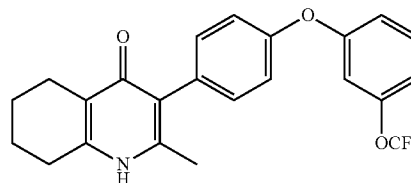
The title compound was synthesised from 4-ethoxy-2-methyl-3-(4-(4-(trifluoromethyl)phenoxy)phenyl)-5,6,7,8-tetrahydroquinoline (47 mg, 0.12 mmol) according to general procedure D. The title compound was isolated as colourless solid (25 mg, 0.07 mmol, 60%). ¹H NMR (500 MHz, DMSO) δ 11.14 (s, 1H), 7.77 (d, J=8.6 Hz, 2H), 7.26 (d, J=8.6 Hz, 2H), 7.19 (d, J=8.6 Hz, 2H), 7.12 (d, J=8.6 Hz, 2H), 2.59 (t, J=5.8 Hz, 2H), 2.33 (t, J=6.4 Hz, 2H), 2.12 (s, 3H), 1.73 (m, 2H), 1.70-1.64 (m, 2H); M/Z (ESI+); 400.15 (Found MH⁺; 400.1528, C₂₃H₂₀F₃NO₂ requires 400.1519).

3-(4-(3-Fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one



The title compound was synthesised from 4-ethoxy-3-(4-(3-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline (170 mg, 0.45 mmol) according to general procedure D. The title compound was isolated as colourless solid (110 mg, 0.31 mmol, 70%). ¹H NMR (500 MHz, DMSO) δ 7.47 (dt, J=8.6, 7.1 Hz, 1H), 7.31 (d, J=8.7 Hz, 2H), 7.17 (d, J=8.7 Hz, 2H), 7.02 (tdd, J=8.5, 2.3, 0.7 Hz, 1H), 6.97-6.88 (m, 2H), 2.83 (t, J=6.1 Hz, 2H), 2.54 (t, J=5.8 Hz, 2H), 2.25 (s, 3H), 1.87-1.69 (m, 4H); M/Z (ESI+); 350.16 (Found MH⁺; 350.1569, C₂₂H₂₁FNO₂ requires 350.1556).

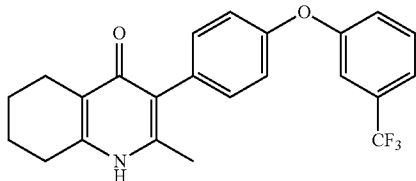
3-(4-(3,4-Dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one



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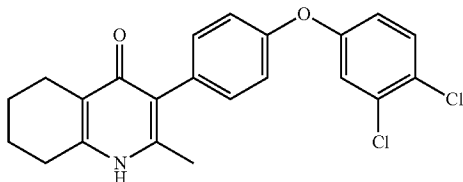
The title compound was synthesised from 4-Ethoxy-3-(4-(3-trifluoromethoxyphenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline (100 mg, 0.23 mmol) according to general procedure D. The title compound was isolated as colourless solid (72 mg, 0.16 mmol, 76%). ¹H NMR (501 MHz, DMSO) δ 11.27 (s, 1H, NH), 7.51 (t, J=8.3 Hz, 1H), 7.22 (d, J=8.5 Hz, 2H), 7.12 (d, J=7.6 Hz, 1H), 7.07 (d, J=8.5 Hz, 2H), 7.03 (dd, J=8.6, 1.7 Hz, 1H), 7.00 (s, 1H), 2.58 (t, J=5.2 Hz, 2H), 2.32 (t, J=6.2 Hz, 2H), 2.09 (s, 3H), 1.76-1.69 (m, 2H), 1.69-1.61 (m, 2H); M/Z (ESI+); 416.15 (Found MH⁺; 416.1469, C₂₃H₂₁F₃NO₃ requires 416.1468).

3-(4-(3,4-Dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one



The title compound was synthesised from 4-Ethoxy-3-(4-(3-trifluoromethylphenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline (193 mg, 0.45 mmol) according to general procedure D. The title compound was isolated as colourless solid (174 mg, 0.44 mmol, 96%). ¹H NMR (501 MHz, DMSO) δ 11.15 (s, 1H), 7.63 (t, J=8.6 Hz, 1H), 7.48 (d, J=8.2 Hz, 1H), 7.30 (s, 2H), 7.22 (d, J=8.4 Hz, 2H), 7.07 (d, J=8.4 Hz, 2H), 2.56 (t, J=3.3 Hz, 2H), 2.30 (t, J=5.3 Hz, 2H), 2.08 (s, 3H), 1.71 (dd, J=6.0, 4.6 Hz, 2H), 1.68-1.60 (m, 2H); M/Z (ESI+); 400.15 (Found MH⁺; 400.1519 requires C₂₃H₂₁F₃NO₂ requires 400.1519).

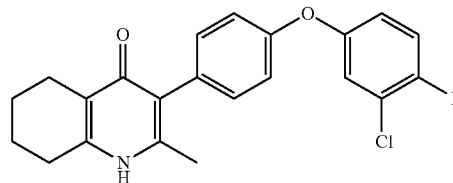
3-(4-(3,4-Dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one



The title compound was synthesised from 4-ethoxy-3-(4-(3,4-dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline (60 mg, 0.15 mmol) according to general procedure D. The title compound was isolated as colourless solid (35 mg, 0.08 mmol, 59%). ¹H NMR (500 MHz, DMSO) δ 10.95 (s, 1H), 7.66 (d, J=8.5 Hz, 1H), 7.31 (s, 1H), 7.23 (d, J=8.2 Hz, 2H), 7.08 (d, J=7.6 Hz, 2H), 7.04 (d, J=8.9 Hz, 1H), 2.55 (m, 2H), 2.30 (m, 2H), 2.09 (s, 3H), 1.72 (m, 2H), 1.66 (m, 2H); M/Z (ESI+); 400.09 (Found MH⁺; 400.0881, C₂₂H₂₀Cl₂NO₂ requires 400.0866).

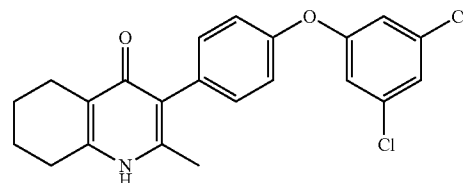
120

3-[4-(3-chloro-4-fluorophenoxy)phenyl]-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4-one

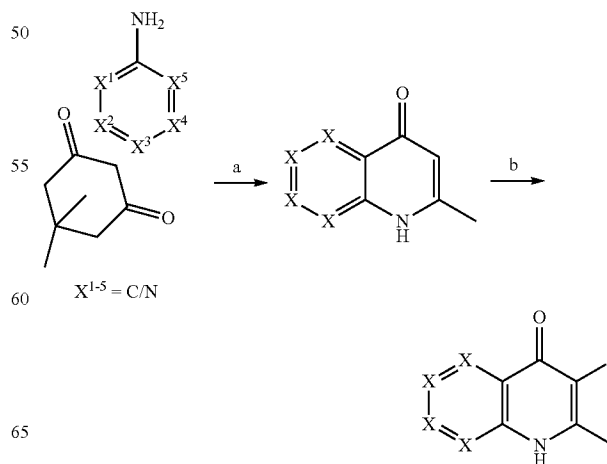


The title compound was synthesised from 4-Ethoxy-3-(4-(3-chloro-4-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinoline (90 mg, 2.18 mmol) The title compound was isolated as a pale grey precipitate (55 mg, 0.14 mmol, 66%). ¹H NMR (500 MHz, TFA) δ 7.39 (d, J 8.6 Hz, 2H), 7.32 (d, J 8.5 Hz, 2H), 7.27-7.24 (m, 2H), 7.12-7.09 (m, 1H), 3.10 (t, J 5.8 Hz, 2H), 2.91 (t, J 5.9 Hz, 2H), 2.54 (s, 3H), 2.15-2.03 (m, 4H); M/Z (ESI); 384.1167, (C₂₂H₂₀ClFNO₂ requires 384.1161).

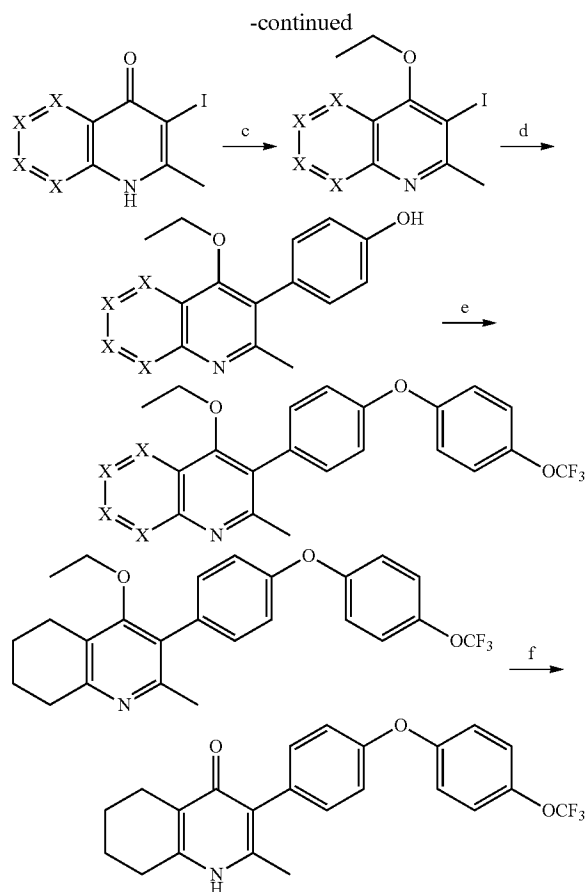
3-[4-(3,5-dichlorophenoxy)phenyl]-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4(1H)-one



The title compound was synthesised from 3-[4-(3,5-dichlorophenoxy)phenyl]-4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinoline (40 mg, 0.93 mmol) according to general procedure D. The title compound was isolated as colourless solid (31 mg, 0.08 mmol, 83%). ¹H NMR (500 MHz, TFA) δ 7.44 (d, J=8.5 Hz, 2H), 7.39 (d, J=8.0 Hz, 2H), 7.30 (s, 1H), 7.10 (s, 2H), 3.12 (t, J=5.5 Hz, 2H), 2.93 (t, J=5.5 Hz, 2H), 2.57 (s, 3H), 2.09-2.00 (m, 4H); M/Z (ESI); 400.0874, C₂₂H₂₀Cl₂NO₂ requires 400.0866.



121

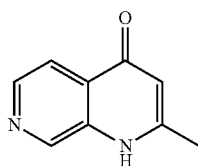


a) i) Meldrums acid, triethylorthoacetate, 110° C., ii) Aniline, 110° C., iii) Dowtherm A, 250° C., b) NIS, Acetonitrile, 80° C., c) EtI, K₂CO₃, DMF, 80° C., d) 4-Hydroxyphenyl boronic acid, Pd(PPh₃)₄, Na₂CO₃, DMF, 80° C., e) Phenyl boronic acid, Cu(OAc)₂, Pyridine, TEA, DCM, f) HBr (40% aq), Acetic acid, 120° C.

General Method A

2,2-Dimethyl-1,3-dioxane-4,6-dione (1.5 equiv.) was dissolved in trimethylorthoacetate (2 equiv.) and heated to 115° C. for 2 hrs. The reaction was cooled to allow the addition of the aniline (1 equiv.) before being heated to 115° C. for a further 2 hrs. The reaction mixture was then allowed to cool and was concentrated in vacuo, remaining solvent was washed off with cold methanol. The precipitate was then dissolved in minimum volume of Dowtherm A and refluxed at 250° C. for 1.5 hours. The reaction mixture was allowed to cool and the precipitate filtered followed by washing with hexane to afford the title compound.

2-Methyl-1,7-naphthyrid-4(1H)-one



The title compound was synthesised using 3-amino pyridine (3.0 g, 32 mmol) following general procedure A. To

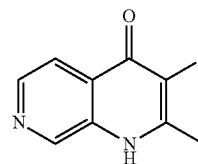
122

give the title compound as colourless solid (489 mg, 3.1 mmol, 10%). ¹H NMR (500 MHz, CDCl₃) 8.52 (s, 1H, H-8), 7.72 (d, J=8.0 Hz, J=8.0 Hz, 1H, H-5), 7.59-7.31 (m, 1H, H-6), 6.18 (s, 1H, H-3), 2.28 (s, 3H, Me). M/Z (ESI+); (Found MH⁺; requires).

General Method B

2-Methyl-naphthyrid-4(1H)-one (1 equiv.) and N-Iodosuccinamide (1.2 equiv.) were dissolved in acetonitrile (5 mL mmol⁻¹) and stirred and heated at 80° C. for 3 hours. The reaction mixture was then allowed to cool and the mixture filtered, the precipitate was then washed with water (15 mL) to afford the title compound as a colourless solid.

3-Iodo-2-methyl-1,7-naphthyrid-4(1H)-one

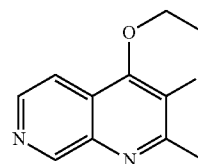


The title compound was synthesised using 2-Methyl-1,7-naphthyrid-4(1H)-one (480 mg, 3.0 mmol) following general procedure B. To give the title compound as colourless solid (740 mg, 2.6 mmol, 86%). ¹H NMR (500 MHz, CDCl₃) δ 8.36-7.91 (m, 1H), 7.49 (dd, J=8.4, 1.1 Hz, 1H), 7.18 (dd, J=8.6, 4.2 Hz, 1H), 2.27 (s, 3H). M/Z (ESI+); (Found MH⁺; requires).

General Method C

A suspension of the 4(1H), 3-Iodo-2-methyl-naphthyrid-4(1H)-one (1 equiv.) and potassium carbonate (2 equiv.) in DMF (20.0 mL) was heated to 50° C. and stirred for 45 minutes. The reaction mixture was removed from the heat and ethyl iodide (1.5 equiv.) was added dropwise. The reaction mixture was then heated and kept at 50° C. with stirring for a further 18 hrs. Formation of a yellow emulsion was observed. The reaction mixture was then quenched with water (40.0 mL). The organic phase was extracted using the polar extraction technique (ethyl acetate, 3×40.0 mL), and the resulting organic layers were combined and dried over MgSO₄ and concentrated in vacuo to afford the title compound.

4-Ethoxy-3-iodo-2-methyl-1,7-naphthyridine



The title compound was synthesised using, 3-Iodo-2-methyl-naphthyrid-4(1H)-one (720 mg, 2.5 mmol) following general procedure C. To give the title compound as brown gum (244 mg, 0.8 mmol, 33%). ¹H NMR (500 MHz, CDCl₃) δ 8.87 (dd, J=4.0, 1.5 Hz, 1H), 8.31 (dd, J=8.5, 1.6 Hz, 1H),

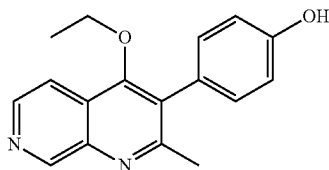
123

7.63 (dd, J=8.5, 4.1 Hz, 1H), 4.84 (q, J=7.0 Hz, 2H), 3.00 (s, 3H), 1.59 (t, J=7.0 Hz, 3); M/Z (ESI+); (Found MH⁺; requires).

General Method F

To a nitrogen flushed flask charged with the 4-Ethoxy-3-iodo-2-methyl-naphthyridine (400 mg, 1.26 mmol), 4-hydroxybenzene boronic acid (260 mg, 1.89 mmol) and palladium tetra(triphenylphosphine) (73 mg, 0.06 mmol) was added degassed DMF (10 mL). Potassium carbonate (3 mL, 2 M_(aq)) was added and the reaction mixture brought up to 80° C. and stirred for 3 hours. The reaction mixture was then cooled to room temperature and diluted with water (10 mL). The organic phase was then extracted using ethyl acetate (3×20 mL). The organic phases were combined and washed with water (3×20 mL) and then dried with brine (1×10 mL) and MgSO₄, before concentration in vacuo. The resulting solid was then recrystallized in ethyl acetate to afford the title compound.

4-Ethoxy-3-phenol-2-methyl-1,7-naphthyridine

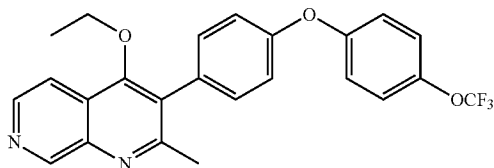


The title compound was synthesised using, 4-Ethoxy-3-iodo-2-methyl-1,7-naphthyridine (230 mg, 0.73 mmol) following general procedure F. To give the title compound an orange powder (80 mg, 0.8 mmol, 28%). ¹H NMR (400 MHz, MeOD) δ 8.78 (dd, J=4.1, 1.4 Hz, 1H), 8.24 (dd, J=8.6, 1.4 Hz, 1H), 7.64 (dd, J=8.6, 4.2 Hz, 1H), 7.08 (d, J=8.5 Hz, 2H), 6.84 (d, J=8.5 Hz, 2H), 4.12 (q, J=7.0 Hz, 2H), 2.39 (s, 3H), 1.05 (t, J=7.0 Hz, 3H); M/Z (ESI+); (Found MH⁺; requires).

General Method G

Copper (II) acetate (1 equiv.), triethylamine (5 equiv.), and pyridine (5 equiv.) was added to a solution of the boronic acid (1.5 equiv.) and phenol (1 equiv.) in dichloromethane (10 mL mmol⁻¹) over heat-activated 4 Å molecular sieves. The reaction mixture was stirred over 16 hours at room temperature. The reaction mixture was quenched with HCl (0.5 M, 20 mL mmol⁻¹) and filtered through a pad of Celite, followed by repeated washing with water (10 mL mmol⁻¹). The organic layer was extracted with brine, dried over magnesium sulphate, and concentrated in vacuo. Purification by silica gel chromatography (ethyl acetate/hexane) afforded the title compound.

4-Ethyl-3 (4-(4-trifluoromethoxyphenoxy)phenyl)-2-methyl-1,7-naphthyridone



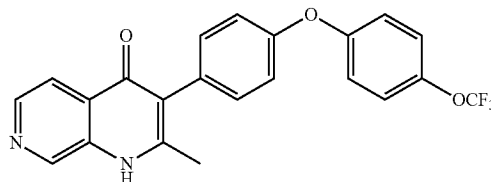
124

The title compound was synthesised using 4-Ethoxy-3-iodo-2-methyl-1,7-naphthyridine (70 mg, 0.25 mmol) and 4-trifluoromethoxybenzenboronic acid (79 mg, 0.38 mmol) following general procedure G. To give the title compound as a red crystalline solid (34 mg, 0.08 mmol, 20%). ¹H NMR (400 MHz, CDCl₃) δ 8.90 (dd, J=4.0, 1.3 Hz, 1H), 8.33 (dd, J=8.5, 1.3 Hz, 1H), 7.61 (dd, J=8.5, 4.1 Hz, 1H), 7.31 (d, J=8.5 Hz, 2H), 7.24 (d, J=8.7 Hz, 2H), 7.13 (d, J=8.7 Hz, 2H), 7.10 (d, J=9.1 Hz, 2H), 4.43 (q, J=7.0 Hz, 2H), 2.54 (s, 3H), 1.19 (t, J=7.0 Hz, 3H); M/Z (ESI+); (Found MH⁺; requires).

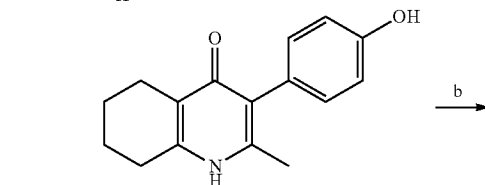
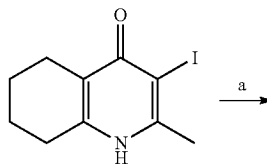
General Method J

To a solution of the 4-Ethyl-3(4-(4-trifluoromethoxyphenoxy)phenyl)-2-methylnaphthyridone (1 equiv.) in acetic acid (2 mL mmol⁻¹) was added hydrogen bromide (>48% w/v (aq)) (1 mL mmol⁻¹). The reaction mixture was then heated to 90° C. and left to reflux for 72 hours. The reaction mixture was neutralised with sodium hydroxide (2 M, 30.0 mL) and precipitate formed. The reaction mixture was then filtered to afford the title compound.

3(4-(4-trifluoromethoxyphenoxy)phenyl)-2-methyl-1,7-naphthyrid-4(1H)-one

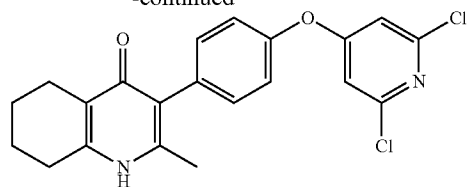


The title compound was synthesised from 4-Ethyl-3(4-(4-trifluoromethoxyphenoxy)phenyl)-2-methyl-1,7-naphthyridone (31 mg, 0.07 mmol). To give the title compound as a colourless solid (13 mg, 0.03 mmol, 45%). ¹H NMR (400 MHz, CDCl₃) δ 8.44 (d, J=3.6 Hz, 1H), 7.75 (d, J=8.2 Hz, 1H), 7.36 (dd, J=8.3, 4.1 Hz, 1H), 7.02 (d, J=8.6 Hz, 2H), 6.96 (d, J=8.5 Hz, 2H), 6.83 (d, J=9.2 Hz, 4H), 2.09 (s, 3H); M/Z (ESI+); 413.11 (Found MH⁺; 413.1104 C₂₂H₁₅F₃N₂O₃ requires 413.1107).



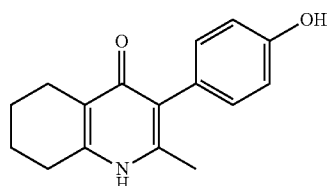
125

-continued



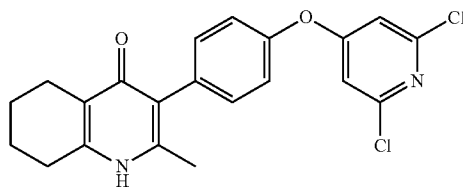
a) 4-Hydroxybenzene boronic acid, Pd(PPh₃)₄, Na₂CO₃ (aq), DMF 80° C., b) 2,4,6 trichloropyridine, K₂CO₃, DMF, 100° C.

3-phenol-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one



The title compound was synthesised from 4(1H)-3-iodo-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one (500 mg, 1.73 mmol) and 4-hydroxyphenylboronic acid (318 mg, 2.30 mmol) and palladium tetra(triphenylphosphine) (73 mg, 0.06 mmol) was added degassed DMF (10 mL). Potassium carbonate (aq) (3 mL, 2 M) was added and the reaction mixture brought up to 80° C. and stirred for 3 hours. The reaction mixture was then cooled to room temperature and diluted with water (10 mL). Organics were extracted with ethyl acetate (3×10 mL). The aqueous layer was neutralised using hydrochloric acid (2 M), causing the title compound, a grey precipitate to crash out which was collected by vacuum filtration (150 mg, 0.58 mmol, 44%). ¹H NMR (400 MHz, MeOD) δ 6.91 (d, J=8.6 Hz, 2H), 6.71 (d, J=8.6 Hz, 2H), 2.57 (t, J=6.0 Hz), 2.39 (t, J=5.6 Hz, 2H), 2.03 (s, 3H), 1.77-1.61 (m, 4H); M/Z (ESI); 255.1341 (C₁₆H₁₇NO₂ requires 255.1259).

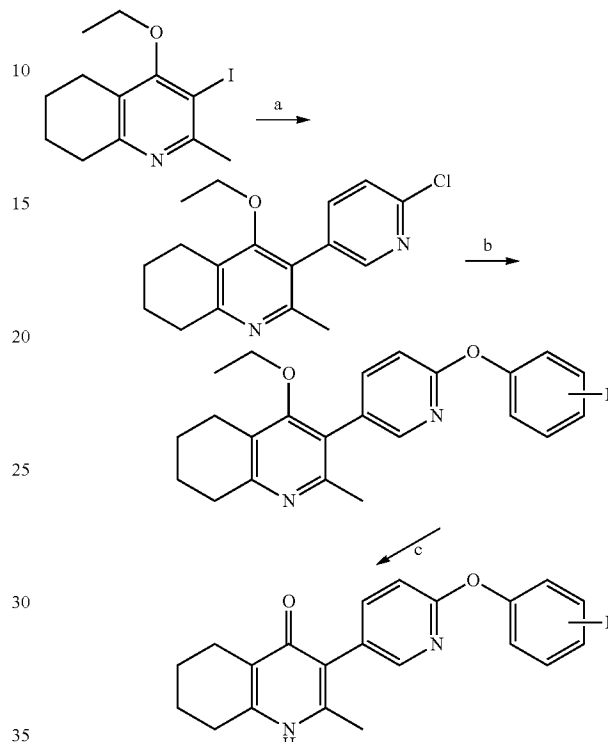
3-{4-[(2,6-dichloropyridin-4-yl)oxy]phenyl}-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4-one



3-phenol-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one (120 mg, 0.47 mmol) and potassium carbonate (78 mg, 0.56 mmol) were dissolved in DMF (3 mL) and the reaction mixture was stirred for 15 mins. Following this, 2,4,6-Trichloropyridine (86 mg, 0.47 mmol) was added and the mixture was heated to 100° C. and stirred for 18 hours under an inert atmosphere. The reaction mixture was allowed to cool to room temperature and was diluted with water (5 mL). The resulting pale grey precipitate was collected by vacuum filtration, washed with water (5 mL) and dried (118 mg, 0.29

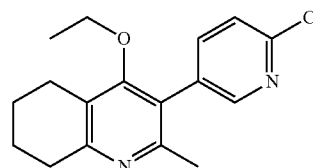
126

mmol, 63%). δ ¹H NMR (500 MHz, TFA) δ 7.66 (d, J 8.5 Hz, 2H), 7.56 (d, J 8.5 Hz, 2H), 7.44 (s, 2H), 3.10 (t, J 5.0 Hz, 2H), 2.90 (t, J 5.0 Hz, 2H), 2.55 (s, 3H), 2.10-2.08 (m, 4H); M/Z (ESI); 400.0826, (C₂₁H₁₈Cl₂N₂O₂ requires 400.0745).



a) 2-Chloropyridine-5-boronic acid, Pd(PPh₃)₄, Na₂CO₃ (aq), DMF 80° C., b) Phenol, K₂CO₃, DMF, 100° C.

4-Ethoxy-3-(6-chloropyridin-3-yl)-2-methyl-5,6,7,8-tetrahydroquinoline

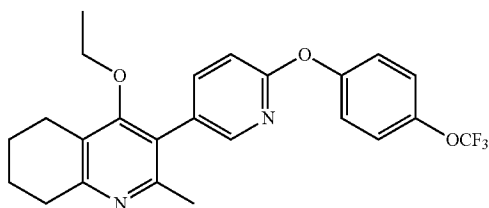


To a nitrogen flushed flask charged with 4-ethoxy-3-iodo-2-methyl-5,6,7,8-tetrahydroquinoline (1.5 g, 4.7 mmol), 2-chloropyridine-5-boronic acid (1.12 g, 7.1 mmol) and palladium tetra(triphenylphosphine) (271 mg, 0.24 mmol) was added degassed DMF (20 mL). Potassium carbonate (3 mL, 2 M_(aq)) was added and the reaction mixture brought up to 80° C. and stirred for 3 hours. The reaction mixture was then cooled to room temperature and diluted with water (10 mL). The organic phase was then extracted using ethyl acetate (3×20 mL). The organic phases were combined and washed with water (3×20 mL) and then dried with brine (1×10 mL) and MgSO₄, before concentration in vacuo. The resulting residue was purified by column chromatography (Pet:EtOAc), to yield the title compound as a yellow plate-

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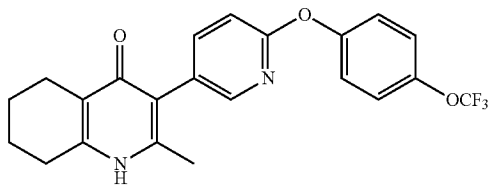
lets (330 mg, 1.09 mmol, 23%). HPLC; 2.17 min (100% ref area); ^1H NMR (500 MHz, CDCl_3) δ 8.33 (d, $J=2.4$ Hz, 1H), 7.60 (dd, $J=8.2, 2.4$ Hz, 1H), 7.44-7.42 (d, $J=8.2$, 1H), 3.53 (q, $J=7.0$ Hz, 2H), 2.98 (t, $J=6.2$ Hz, 2H), 2.72 (t, $J=6.2$ Hz, 2H), 2.35 (s, 3H), 1.93-1.85 (m, 2H), 1.84-1.76 (m, 2H), 1.06 (t, $J=7.0$ Hz, 3H); M/Z (ESI+); 303.13 (Found MH^+ ; 303.1266, $\text{C}_{17}\text{H}_{19}\text{ClN}_2\text{O}$ requires 303.1259).

4-Ethoxy-3-(6-(4-trifluoromethoxyphenoxy)pyridin-3-yl)-2-methyl-5,6,7,8-tetrahydroquinoline



4-Ethoxy-3-(6-chloropyridin-3-yl)-2-methyl-5,6,7,8-tetrahydroquinoline (250 mg, 0.82 mmol), 4-trifluoromethoxyphenol (178 mg, 1.0 mmol) and potassium carbonate (276 mg, 1.7 mmol) were dissolved in DMF and refluxed at 110°C for 24 hrs. The reaction mixture was then cooled to room temperature and diluted with water (10 mL). The organic phase was then extracted using ethyl acetate (3×20 mL). The organic phases were combined and washed with water (3×20 mL) and then dried with brine (1×10 mL) and MgSO_4 , before concentration in vacuo. The resulting residue was purified by reverse phase column chromatography (H_2O : acetonitrile), to yield the title compound as a yellow oil (75 mg, 0.17 mmol, 20%). ^1H NMR (400 MHz, CDCl_3) δ 8.03 (d, $J=2.2$ Hz, 1H), 7.58 (dd, $J=8.4, 2.2$ Hz, 1H), 7.29-7.07 (m, 4H), 6.95 (d, $J=8.4$ Hz, 1H), 3.46 (q, $J=7.0$ Hz, 2H), 2.85 (t, $J=6.3$ Hz, 2H), 2.64 (t, $J=6.1$ Hz, 2H), 2.25 (s, 3H), 1.81 (dt, $J=12.2, 6.3$ Hz, 2H), 1.77-1.68 (m, 2H), 0.99 (t, $J=7.0$ Hz, 3H); M/Z (ESI+); 445.18 (Found MH^+ ; 445.1759, $\text{C}_{24}\text{H}_{23}\text{F}_3\text{N}_2\text{O}_3$ requires 445.1739).

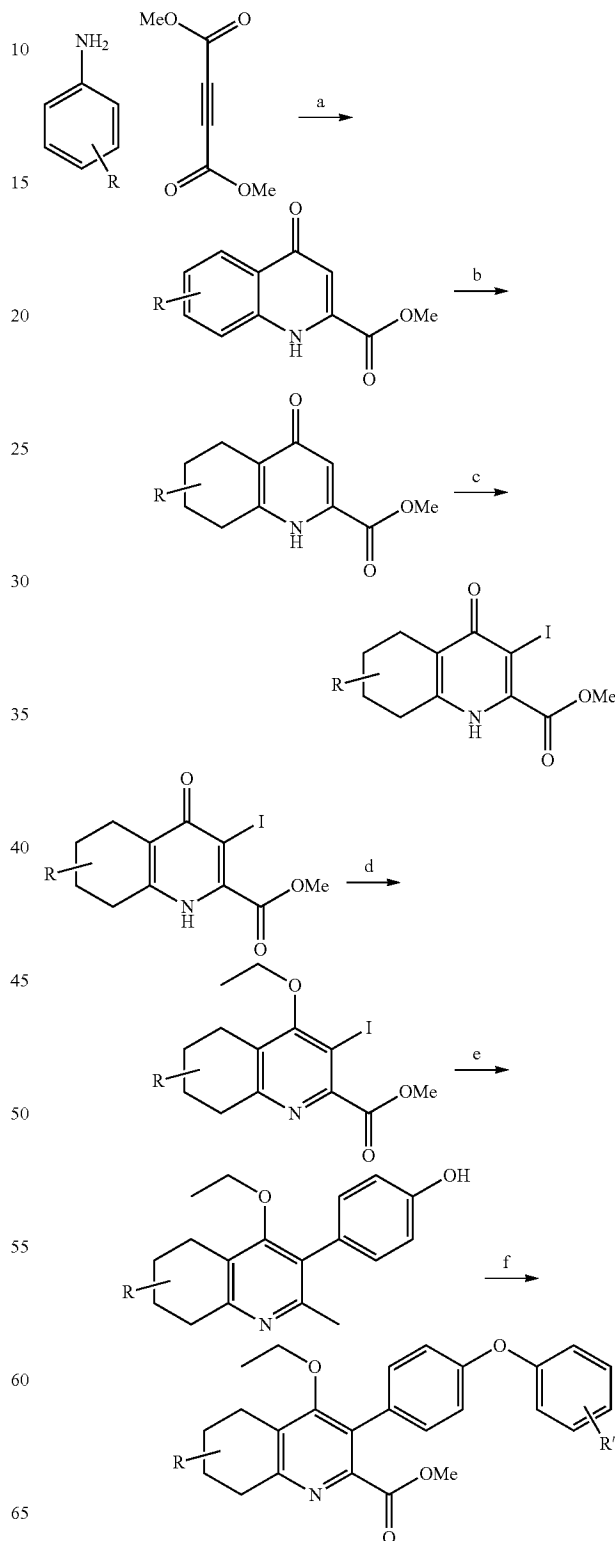
3-(6-(4-Trifluoromethoxyphenoxy)pyridin-3-yl)-2-methyl-5,6,7,8-tetrahydroquinolin-(4)-one



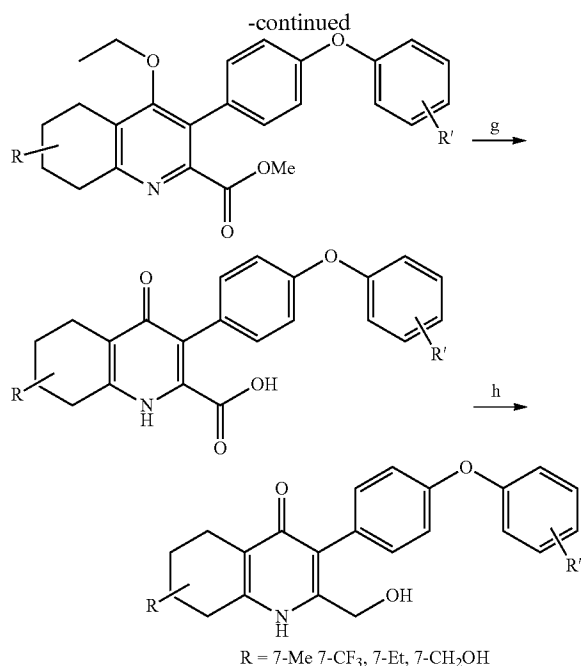
The title compound was synthesised from 4-ethoxy-3-(6-(4-trifluoromethoxyphenoxy)pyridin-3-yl)-2-methyl-5,6,7,8-tetrahydroquinoline (70 mg, 0.15 mmol) according to general procedure J. The title compound was isolated as colourless solid (13 mg, 0.03 mmol, 20%). ^1H NMR (400 MHz, DMSO) δ 11.07 (s, 1H), 7.94 (d, $J=2.2$ Hz, 1H), 7.70

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(dd, $J=8.4, 2.4$ Hz, 1H), 7.43 (d, $J=8.7$ Hz, 2H), 7.29 (d, $J=9.0$ Hz, 2H), 7.09 (d, $J=8.4$ Hz, 1H), 2.56 (t, $J=5.1$ Hz, 2H), 2.30 (t, $J=5.9$ Hz, 2H), 2.10 (s, 3H), 1.79-1.57 (m, 4H); M/Z (ESI+); 417.14 (Found MH^+ ; 417.1432, $\text{C}_{22}\text{H}_{19}\text{F}_3\text{N}_2\text{O}_3$ requires 417.1421).



129

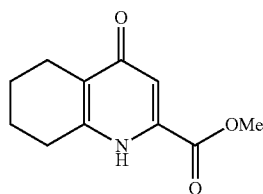


a) i) Ethanol, ii) Dowtherm A, 250° C., b) PtO₂, H₂, AcOH, c) NIS, Acetonitrile, 80° C., d) EtI, K₂CO₃, DMF, 80° C., e) 4-Hydroxyphenyl boronic acid, Pd(PPh₃)₄, DMF, 80° C., f) Phenyl boronic acid, Cu(OAc)₂, Pyridine, TEA, DCM, g) HBr (40% aq), Acetic acid, 120° C., h) i) MeOH, ii) DiBAL.

General Method B

The 4-hydroxyquinolinone (1 equiv.) was dissolved in acetic acid (10.0 mL) under inert conditions. platinum dioxide (5% weight equiv.) was added and a hydrogen balloon was attached. The reaction was left to proceed for 12 hours. The resulting suspension was filtered through a pad of Celite and washed with ethyl acetate (10.0 mL). The filtrate was concentrated in vacuo to afford a yellow/brown oil. Purification by column chromatography (10% methanol in chloroform) afforded the title compound.

2-(Methoxycarboxylate)-5,6,7,8-tetrahydroquinolin-4(1H)-one



The title compound was synthesised following general procedure B from 2-(methoxycarboxylate)quinolin-4(1H)-one (500 mg, 2.5 mmol). The title compound was isolated as colourless solid (470 mg, 2.4 mmol, %). ¹H NMR (500 MHz, CDCl₃) δ 8.89 (s, 1H), 7.07 (s, 1H), 3.95 (s, 3H), 2.74 (t, J=6.1 Hz, 2H), 2.56 (t, J=6.2 Hz, 2H), 1.82 (dt, J=8.0, 6.1 Hz, 1H), 1.79-1.69 (m, 1H); M/Z (ESI+); 208.10 (Found MH⁺; 208.0977, C₁₁H₁₃NO₃ requires 208.0974).

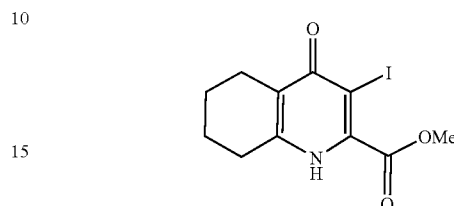
1.5 General Method C

The tetrahydroquinolin-4(1H)-one (1 equiv.) and N-Iodo-succinamide (1.2 equiv.) were dissolved in acetonitrile (5

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mL mmol⁻¹) and stirred and heated at 80° C. for 3 hours. The reaction mixture was then allowed to cool and the mixture filtered, the precipitate was then washed with water (15 mL) to afford the title compound as a colourless solid

3-Iodo-2-(methoxycarboxylate)-5,6,7,8-tetrahydroquinolin-4(1H)-one

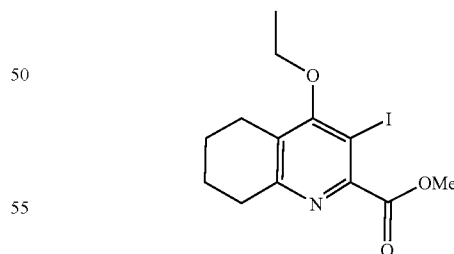


The title compound was synthesised following general procedure C from 2-(methoxycarboxylate)-5,6,7,8-tetrahydroquinolin-4(1H)-one (450 mg, 2.20 mmol). The title compound was isolated as colourless solid (612 mg, 1.8 mmol, 84%). ¹H NMR (400 MHz, DMSO) δ 11.93 (s, 1H), 3.91 (s, 3H), 2.58 (s, 2H), 2.34 (t, 2H), 1.90-1.45 (m, 4H); M/Z (ESI+); 333.99 (Found MH⁺; 333.9935, C₁₁H₁₂INO₃ requires; 333.9935).

General Method D

A suspension of the 4(1H), 3-iodo-tetrahydroquinolinone (1 equiv.) and potassium carbonate (2 equiv.) in DMF (20.0 mL) was heated to 50° C. and stirred for 45 minutes. The reaction mixture was removed from the heat and ethyl iodide (1.5 equiv.) was added dropwise. The reaction mixture was then heated and kept at 50° C. with stirring for a further 18 hrs. Formation of a yellow emulsion was observed. The reaction mixture was then quenched with water (40.0 mL). The organic phase was extracted using the polar extraction technique (ethyl acetate, 3x40.0 mL), and the resulting organic layers were combined and dried over MgSO₄ and concentrated in vacuo to afford the title compound.

4-Ethoxy-3-iodo-2-(methoxycarboxylate)-5,6,7,8-tetrahydroquinoline



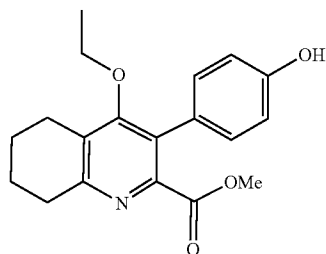
The title compound was synthesised following general procedure D from 3-iodo-2-(methoxycarboxylate)-5,6,7,8-tetrahydroquinolin-4(1H)-one (500 mg, 1.5 mmol). The title compound was isolated as colourless crystals (450 mg, 1.25 mmol, 83%). ¹H NMR (300 MHz, CDCl₃) δ 3.94 (q, J=7.0 Hz, 2H), 3.90 (s, 3H), 2.84 (t, J=6.4 Hz, 2H), 2.73 (t, J=6.2 Hz, 2H), 1.87-1.64 (m, 4H), 1.43 (t, J=7.0 Hz, 3H); M/Z (ESI+); 362.03 (Found MH⁺; 362.0256, C₁₃H₁₆INO₃ requires 362.0248).

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1.6 General Method E

To a nitrogen flushed flask charged with the 4-ethoxy-3-iodo-tetrahydroquinoline (400 mg, 1.26 mmol), 4-hydroxybenzene boronic acid (260 mg, 1.89 mmol) and palladium tetra(triphenylphosphine) (73 mg, 0.06 mmol) was added degassed DMF (10 mL). Potassium carbonate (3 mL, 2 M_(aq)) was added and the reaction mixture brought up to 80° C. and stirred for 3 hours. The reaction mixture was then cooled to room temperature and diluted with water (10 mL). The organic phase was then extracted using ethyl acetate (3×20 mL). The organic phases were combined and washed with water (3×20 mL) and then dried with brine (1×10 mL) and MgSO₄, before concentration in vacuo. The resulting solid was then recrystallized in ethyl acetate to afford the title compound.

4-(4-Ethoxy-(methoxycarboxylate)-5,6,7,8-tetrahydroquinolin-3-yl)phenol



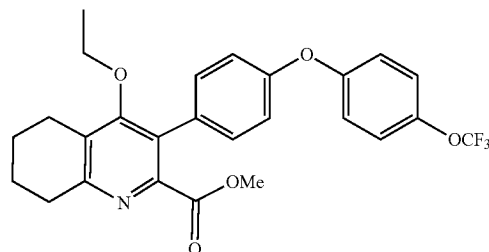
The title compound was synthesised following general procedure E from 4-ethoxy-3-iodo-2-(methoxycarboxylate)-5,6,7,8-tetrahydroquinoline (400 mg, 1.11 mmol). The title compound was isolated as a solid (200 mg, 0.61 mmol, 55%). ¹H NMR (500 MHz, CDCl₃) δ 7.11 (d, J=8.6 Hz, 2H), 6.77 (d, J=8.6 Hz, 2H), 3.60 (s, 3H), 3.43 (q, J=7.0 Hz, 2H), 2.91 (t, J=6.4 Hz, 2H), 2.71 (t, J=6.3 Hz, 2H), 1.82 (m, 2H), 1.78-1.69 (m, 2H), 0.98 (t, J=7.0 Hz, 3H); M/Z (ESI+); 328.16 (Found MH⁺; 328.1551, C₁₉H₂₁NO₄ requires; 328.1543).

General Method F

Copper (II) acetate (1 equiv.), triethylamine (5 equiv.), and pyridine (5 equiv.) was added to a solution of the boronic acid (1.5 equiv.) and phenol (1 equiv.) in dichloromethane (10 mL mmol⁻¹) over heat-activated 4 Å molecular sieves. The reaction mixture was stirred over 16 hours at room temperature. The reaction mixture was quenched with HCl (0.5 M, 20 mL mmol⁻¹) and filtered through a pad of Celite, followed by repeated washing with water (10 mL mmol⁻¹). The organic layer was extracted with brine, dried over magnesium sulphate, and concentrated in vacuo. Purification by silica gel chromatography (ethyl acetate/hexane) afforded the title compound.

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4-Ethoxy-3(4-(4-trifluoromethoxyphenoxy)phenyl)-2-(methoxycarboxylate)-5,6,7,8-tetrahydroquinoline

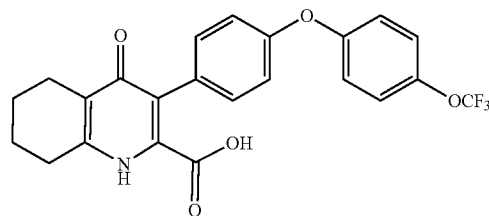


The title compound was synthesised following general procedure F from 4-(4-ethoxy-(methoxycarboxylate)-5,6,7,8-tetrahydroquinolin-3-yl)phenol (180 mg, 0.55 mmol). The title compound was isolated as a yellow oil (210 mg, 0.43 mmol, 78%). ¹H NMR (500 MHz, CDCl₃) δ 7.32 (d, J=8.6 Hz, 2H), 7.22 (d, J=8.6 Hz, 2H), 7.05 (dd, J=8.8, 3.0 Hz, 4H), 3.73 (s, 3H), 3.55 (q, J=7.0 Hz, 2H), 3.05 (t, J=4.7 Hz, 2H), 2.80 (t, J=6.2 Hz, 2H), 1.99-1.88 (m, 2H), 1.88-1.79 (m, 2H), 1.09 (t, J=7.0 Hz, 3H).

General Method G

To a solution of the 4-ethoxy-3-(diaryl ether)-hydroxyquinolone (1 equiv.) in acetic acid (2 mL mmol⁻¹) was added hydrogen bromide (>48% w/v (aq)) (1 mL mmol⁻¹). The reaction mixture was then heated to 90° C. and left to reflux for 72 hours. The reaction mixture was neutralised with sodium hydroxide (2 M, 30.0 mL) and precipitate formed. The reaction mixture was then filtered to afford the title compound.

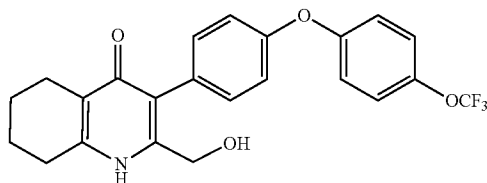
3(4-(4-Trifluoromethoxyphenoxy)phenyl)-2-(carboxylate)-5,6,7,8-tetrahydroquinolin-4(1H)-one



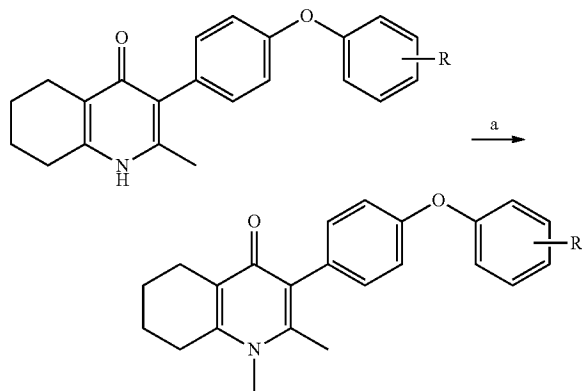
The title compound was synthesised following general procedure G from 4-ethoxy-3(4-(4-trifluoromethoxyphenoxy)phenyl)-2-(methoxycarboxylate)-5,6,7,8-tetrahydroquinoline (200 mg, 0.42 mmol). The title compound was isolated as a colourless solid (80 mg, 0.18 mmol, 43%). ¹H NMR (400 MHz, DMSO) δ 7.41 (d, J=8.8 Hz, 2H), 7.21 (d, J=8.3 Hz, 2H), 7.12 (d, J=8.8 Hz, 2H), 7.01 (d, J=8.3 Hz, 2H), 2.64 (t, J=5.6 Hz, 2H), 2.35 (t, J=5.6 Hz, 2H), 1.94-1.33 (m, 4H); M/Z (ESI+); 446.12 (Found MH⁺; 446.1207, C₂₃H₁₈F₃NO₅ requires 446.1210).

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3(4-(4-Trifluoromethoxyphenoxy)phenyl)-2-(meth-
ylhydroxy)-5,6,7,8-tetrahydroquinolin-4(1H)-one

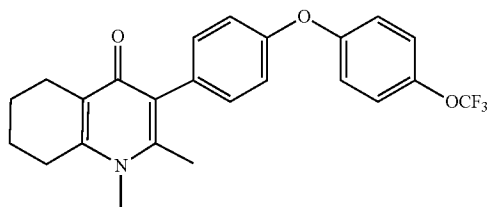


3(4-(4-trifluoromethoxyphenoxy)phenyl)-2-(carboxy-
late)-5,6,7,8-tetrahydroquinolin-4(1H)-one (80 mg, 0.17
mmol) was dissolved in methanol (5 mL) with the addition
of HCl (1 mL, conc.) heated to 80° C. for 24 hours. The
reaction mixture was diluted with water (10 mL) and the
organics extracted with EtOAc (3x10 mL) before being
dried and concentrated in vacuo. The crude material was
then dissolved in dry THF under inert atmosphere and
cooled to 0° C. Diisobutylaluminium hydride was then
added slowly with stirring. After two hours the reaction pH
was lowered to 3 through addition of HCl (2M). Dilution
of the solution with water caused precipitation. The title com-
pound was isolated as via filtration as a pale yellow solid (38
mg, 0.09 mmol, 55%). ¹H NMR (400 MHz, DMSO) δ 11.06
(s, 1H), 7.41 (d, J=8.8 Hz, 2H), 7.25 (d, J=8.6 Hz, 2H), 7.15
(d, J=9.1 Hz, 2H), 7.05 (d, J=8.6 Hz, 2H), 5.53 (s, 1H), 4.25
(s, 2H), 2.67 (t, J=5.6 Hz, 2H), 2.35 (t, J=6.2 Hz, 2H),
1.82-1.56 (m, 4H); M/Z (ESI+); 432.14 (Found MH+;
432.1445, C₂₃H₂₀F₃NO₄ requires 432.1423).



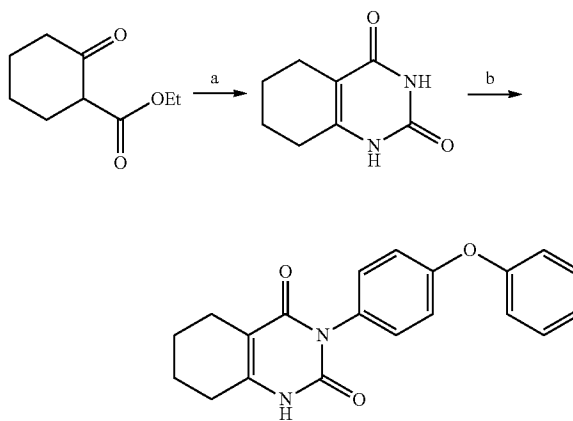
a) MeI, NaH, DMF, 90° C.

1,2-dimethyl-3-(4-(4-(trifluoromethoxy)phenoxy)
phenyl)-5,6,7,8-tetrahydroquinolin-4-one



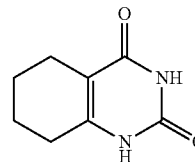
134

2-methyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,
6,7,8-tetrahydroquinolin-4(1H)-one (60 mg, 0.14 mmol)
was dissolved in DMF (0.1 mL) under Nitrogen. Sodium
Hydride (4 mg, 0.17 mmol) was added and the reaction
heated to 90° C. for 30 minutes. Methyl iodide (80 mg, 0.56
mmol) was added and the reaction continued for a further 2
hours. Reaction mixture was allowed to cool and organics
extracted with ethyl acetate, followed by drying with brine
and magnesium sulphate. Organics were concentrated in
vacuo and purified by column chromatography (DCM). To
give the title compound as a colourless solid (20 mg, 0.04
mmol, 35%). ¹H NMR (400 MHz, DMSO) δ 7.41 (d, J=8.6
Hz, 2H), 7.19-7.08 (m, 4H), 7.06 (d, J=8.5 Hz, 2H), 3.53 (s,
3H), 2.71 (t, J=6.2 Hz, 2H), 2.38 (t, J=6.0 Hz, 2H), 2.19 (s,
3H), 1.75 (d, J=5.7 Hz, 2H), 1.66-1.56 (m, 2H).



a) Urea, NaOMe, Ethanol, 80° C., b) 4-phenoxyphenyl boronic acid, CuOAc₂,
Pyridine, triethylamine, Ethanol

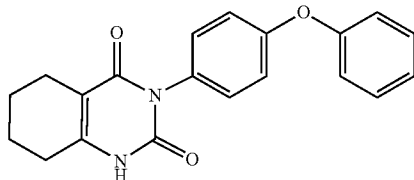
1,2,3,4,5,6,7,8-Octahydroquinazoline-2,4,dione



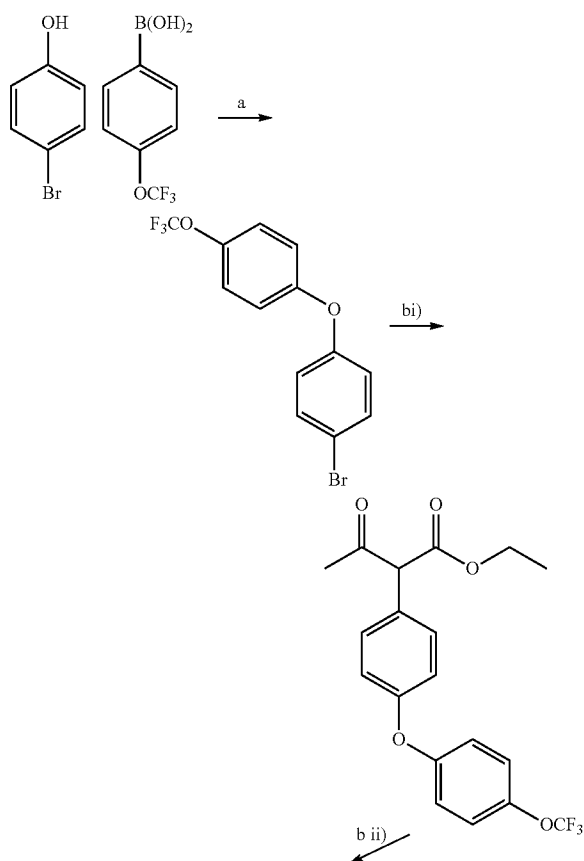
Urea (0.48 g, 8.0 mmol) and ethyl-2-oxocyclohexancar-
boxylate (1.0 g, 6.0 mmol) were dissolved in ethanol (10
mL). Sodium methoxide (3 mL, 12.0 mmol) was added and
the reaction mixture refluxed at 80° C. for 15 hours. The
reaction mixture was allowed to cool and the resulting
precipitate was washed with diethyl ether (2x10 mL) to
afford the title compound as a white solid. (526 mg 3.17
mmol, 53%). ¹H NMR (501 MHz, DMSO) δ 10.72 (s, 1H),
8.50 (s, 1H), 2.28 (t, J=6.2 Hz, 2H), 2.12 (t, J=6.2 Hz, 2H),
1.69-1.60 (m, 2H), 1.59-1.51 (m, 2H); M/Z (ESI+); 167.08
(Found MH+; 167.0815, C₈H₁₀N₂O₂ requires 167.0815).

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3-(4-Phenoxyphenyl)-1,2,3,4,5,6,7,8-octahydroquinazoline-2,4-dione

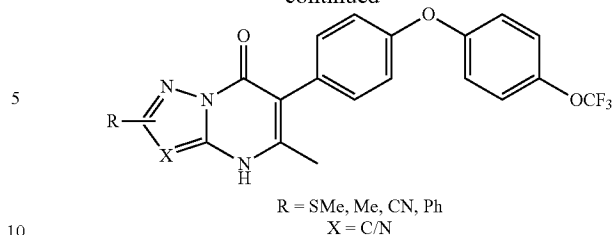


1,2,3,4,5,6,7,8-Octahydroquinazoline-2,4-dione (300 mg, 1.8 mmol), 4phenoxyphenyl boronic acid (600 mg, 2.7 mmol) and copper acetate (330 mg, 1.8 mmol) were dissolved in ethanol (20 mL). Triethylamine (1.2 mL, 9.0 mmol), and pyridine (0.66 mL, 9.0 mmol) were added immediately and the reaction stirred overnight. The reaction was filtered through celite neutralised with HCl (0.5 M, 60 mL) to give crude solid, this was then recrystallized in DCM to afford product as colourless needles (60 mg, 0.18 mmol, 10%). ¹H NMR (500 MHz, DMSO) δ 11.04 (s, 1H), 7.45 (t, J=7.1 Hz, 2H), 7.20 (d, J=7.5 Hz, 3H), 7.09 (d, J=7.8 Hz, 2H), 7.04 (d, J=7.9 Hz, 2H), 2.39 (s, 2H), 2.22 (s, 2H), 1.68 (m, 4H); M/Z (ESI+); 335.14 (Found MH⁺; 335.1394, C₂₀H₁₈N₂O₃ requires 335.1390).



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-continued

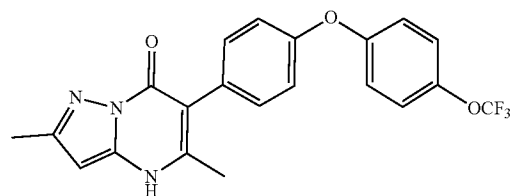


a) Cu(OAc)₂, Pyridine, TEA, DCM, b) i) Ethylacetoacetate, Pd(OAc)₂, JohnPhos, K₃PO₄, Tol, 90° C., b) ii) pyrazole/triazole, AcOH, 120° C.

General Procedure B

Toluene (2.00 mL) was added to a flask flushed with nitrogen and charged with 1-Bromo-4-(4-(trifluoromethoxy)phenoxy)benzene (0.30 g, 0.90 mmol), ethyl acetoacetate (0.252 mL, 0.99 mmol), palladium acetate (10.1 mg, 0.045 mmol), (2-Biphenyl)di-tert-butylphosphine (26.8 mg, 0.09 mmol) and potassium phosphate (0.252 g, 1.2 mmol). The reaction mixture was then heated to 90° C. for 16 hours. The reaction mixture was cooled to room temperature followed by dilution in DCM (15.0 mL) and filtration through a pad of Celite. The reaction mixture was then concentrated in vacuo and passed through a silica plug. The resulting oil containing crude ethyl 3-oxo-2-4-(4-(trifluoromethoxy)phenoxy)phenylbutanoate (1 equiv.) was dissolved in acetic acid (2.00 mL). 3-amino-tria-/pyrazole (1 equiv.) was added to the solution. The solution was heated to 120° C. and refluxed for 16 hours. The reaction mixture was then allowed to cool to room temperature. Addition of H₂O (2.00 mL) caused precipitation of a white solid. Precipitate was filtered and washed with H₂O (2×10.0 mL). The solid was then recrystallized in appropriate solvent to give the title compound.

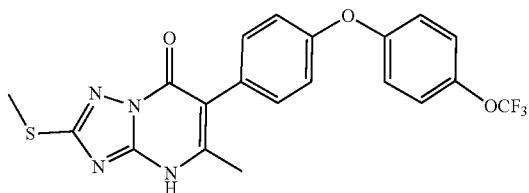
2,5-dimethyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one



The title compound was synthesised from 3-amino-5-methyl-pyrazole (30.0 mg, 0.31 mmol) according to general procedure B (recrystallized in EtOAc) to afford the title compound as colourless platelets (47.0 mg, 0.11 mmol, 36%). ¹H NMR (500 MHz, Chloroform-d) δ 7.27 (d, J=8.6 Hz, 2H), 7.16 (d, J=8.7 Hz, 2H), 6.99 (d, J=8.9 Hz, 2H), 6.95 (d, J=8.6 Hz, 2H), 5.80 (s, 1H), 2.34 (s, 3H), 2.21 (s, 3H) M/Z (ESI); 419.12 (Found MH⁺ 416.1221, C₂₁H₁₆F₃N₃O₃ requires 416.1217).

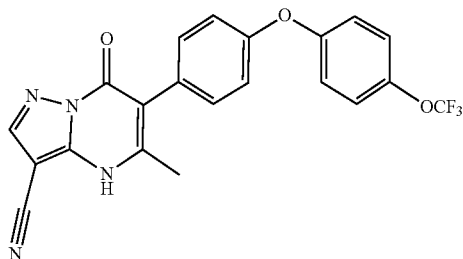
137

5-methyl-2-(methylthio)-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-[1,2,4]triazolo [1,5-a]pyrimidin-7(4H)-one



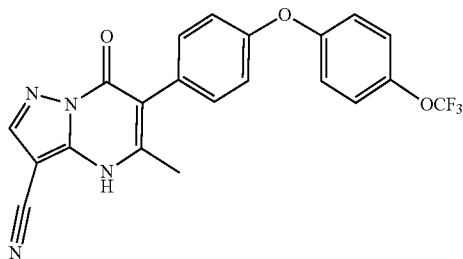
The title compound was synthesised from 3-amino-5-methio-1,2,4triazole (30.0 mg, 0.31 mmol) according to general procedure B to afford the title compound as colourless flake crystals (recrystallized EtOAc) (54.0 mg, 0.12 mmol, 39%). δ H NMR (500 MHz, Chloroform-d); δ 7.30 (d, J=8.6 Hz, 2H), 7.22 (d, J=8.7 Hz, 2H), 7.09 (d, J=8.7 Hz, 2H), 7.07 (d, J=8.6 Hz, 2H), 2.74 (s, 3H), 2.49 (s, 2H); M/Z (ESI); 449.09 (Found MH^+ 449.0893, $C_{20}H_{15}F_3N_4O_3S$ requires 449.0893).

5-methyl-7-oxo-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-4,7-dihydropyrazolo[1,5-a]pyrimidine-3-carbonitrile



The title compound was synthesised from 3-amino-4-carbonitrile-1,2,pyrazole (45 mg, 0.42 mmol) according to general procedure B to afford the title compound as white flake crystals (recrystallized EtOAc), (43 mg, 0.10 mmol, 23%); δ H NMR (500 MHz, DMSO) δ 8.49 (s, 1H), 7.51 (d, J=8.9 Hz, 2H), 7.44 (d, J=8.6 Hz, 2H), 7.28 (d, J=8.9 Hz, 2H), 7.20 (d, J=8.6 Hz, 2H), 2.32 (s, 3H). M/Z (ESI+); 427.10 (Found MH^+ 427.1018, $C_{21}H_{13}F_3N_4O_3$ requires 427.1012).

5-methyl-2-phenyl-6-(4-(4-(trifluoromethoxy)phenoxy)phenyl)pyrazolo[1,5-a]pyrimidin-7(4H)-one



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The title compound was synthesised from 3-amino-4-carbonitrile-1,2,pyrazole (0.067 g, 0.42 mmol) according to general procedure B (recrystallized in DMSO) to afford the title compound as a grey micro crystals (0.15 g, 0.31 mmol, 74%). δ H NMR (500 MHz, DMSO) δ 12.47 (s, 1H, NH), 8.01 (d, J=6.8 Hz, 2H, H-2' & 6'), 7.53-7.40 (m, 5H, H-3', 4', 5', 2' & 6'), 7.38 (d, J=8.7 Hz, 2H, H-2'' & 6''), 7.20 (d, J=9.1 Hz, 2H, H-3' & 5'), 7.11 (d, J=8.7 Hz, 2H, H-3'' & 5''), 6.62 (s, 1H, H-3), 2.22 (s, 3H, Me); M/Z (ESI+); 478.1378 (Found MH^+ , $C_{26}H_{18}F_3N_3O_3$ requires 478.1373).

In Vitro Challenge Assay for *Toxoplasma* Tachyzoites

Protocol adapted from Fomovska, et. al. (Fomovska A, Huang Q, El Bissati K, Mui E J, Witola W H, Cheng G, et al. Novel N-Benzoyl-2-Hydroxybenzamide Disrupts Unique Parasite Secretory Pathway. Antimicrob Agents Chemother [Internet]. 2012 May [cited 2015 Jul. 8]; 56(5):2666-82; Fomovska A, Wood R D, Mui E, Dubey J P, Ferreira L R, Hickman M R, et al. Salicylanilide inhibitors of *Toxoplasma gondii*. J Med Chem. 2012 Oct. 11; 55(19):8375-91.). Human foreskin fibroblasts (HFF) were cultured on a flat, clear-bottomed, black 96-well plate to 90% to 100% confluence. IMDM (1 $\times$, [+] glutamine, [+] 25 mM HEPES, [+] Phenol red, 10% FBS [gibco, Denmark]) was removed from each well and replaced with IMDM-C (1 $\times$, [+] glutamine, [+] 25 mM HEPES, [-] Phenol red, 10% FBS)[gibco, Denmark]. Type I RH parasites expressing Yellow Fluorescent Protein (RH-YFP) were lysed from host cells by double passage through a 27-gauge needle. Parasites were counted and diluted to 32,000/mL in IMDM-C. Fibroblast cultures were infected with 3200 tachyzoites of the Type I RH strain expressing Yellow Fluorescent Protein (RH-YFP) and returned to incubator at 37 $^{\circ}$ C. for 1-2 hours to allow for infection (Gubbels M-J, Li C. Striepen B. High-Throughput Growth Assay for *Toxoplasma gondii* Using Yellow Fluorescent Protein. Antimicrob Agents Chemother [Internet]. 2003 January [cited 2015 Jul. 8]; 47(1):309-16.). Various concentrations of the compounds were made using IMDM-C, and 20 μ l were added to each designated well, with triplicates for each condition. Controls included pyrimethamine/sulfadiazine (current standard of treatment), 0.1% DMSO only, fibroblast only, and an untreated YFP gradient with 2 fold dilutions of the parasite. Cells were incubated at 37 $^{\circ}$ C. for 72 hours. Plates were read using a fluorimeter (Synergy H4 Hybrid Reader, BioTek) to ascertain the amount of yellow fluorescent protein, in relative fluorescence units (RFU), as a measure of parasite burden after treatment. Data was collected using Gen5 software. IC50 was calculated by graphical analysis in Excel.

In Vitro Challenge Assay for Bradyzoites

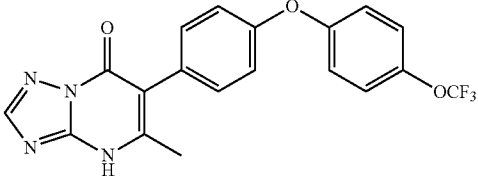
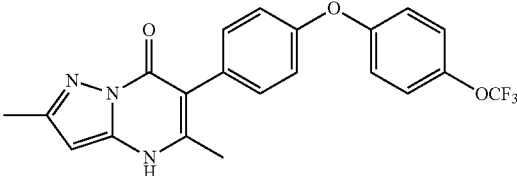
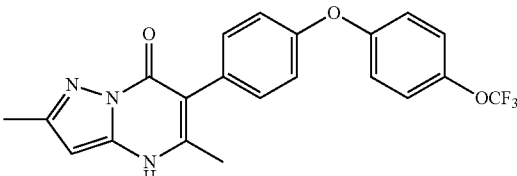
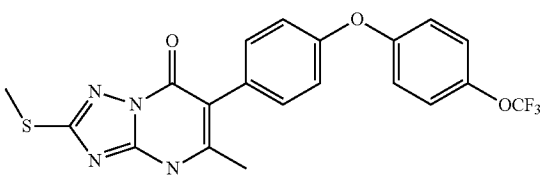
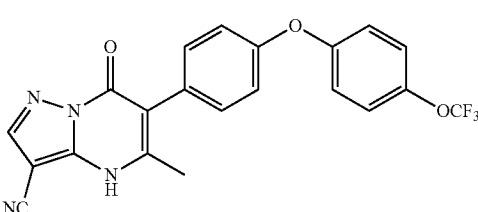
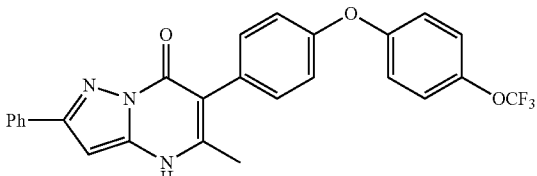
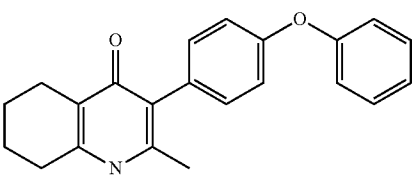
HFF cells were grown in IMDM (1 $\times$, [+] glutamine, [+] 25 mM HEPES, [+] Phenol red, 10% FBS, [gibco, Denmark]) on removable, sterile glass disks in the bottom of a clear, flat-bottomed 24-well plate. Cultures were infected with 3 $\times$ 10⁴ parasites (EGS strain) per well, in 0.5 mL media and plate was returned to incubator at 37 $^{\circ}$ C. overnight. The following day, the media was removed and clear IMDM and compounds were added to making various concentrations of the drug, to a total volume of 0.5 mL. 2 wells were filled with media only, as a control. Plates were returned to the 37 $^{\circ}$ C. incubator for 72 hours, and checked once every 24 hours. If tachyzoites were visible in the control before 72 hours, the cells were fixed and stained. Cells were fixed using 4% paraformaldehyde and stained with Fluorescein-labeled Dolichos Biflorus Agglutinin, DAPI, and BAG1. Disks were removed and mounted onto glass slides and visualized using microscopy (Nikon T17). Slides were scanned using a CRI Panoramic Scan Whole Slide Scanner and viewed using

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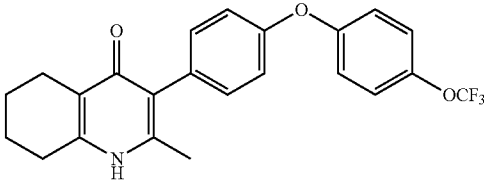
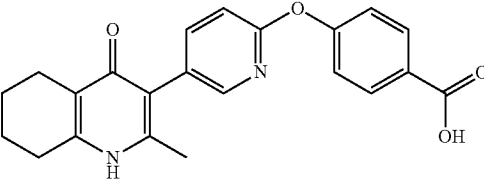
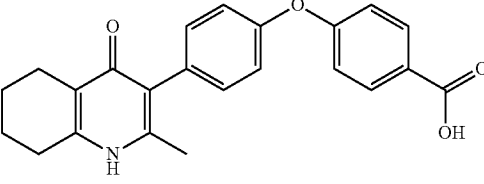
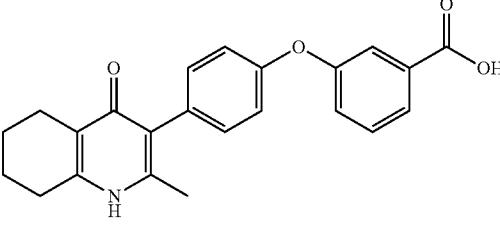
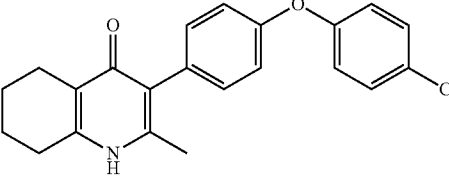
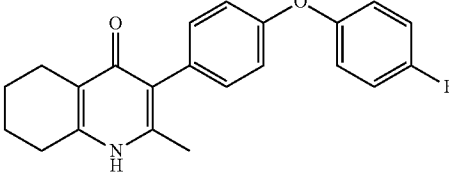
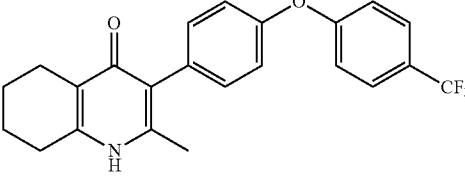
Panoramic Viewer Software. Effects of the compounds were quantified by counting cysts in the controls and treated cells. Cysts and persisting organisms were counted in a representative field of view and then multiplied by a factor deter-

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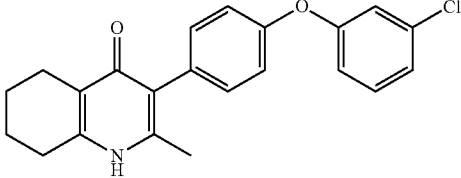
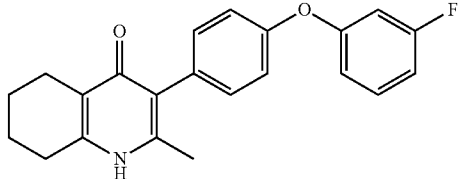
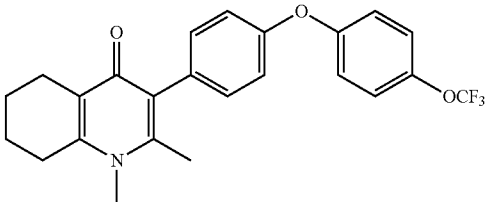
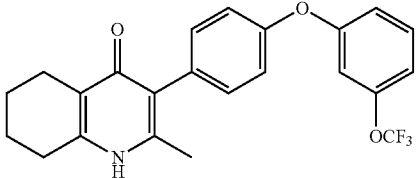
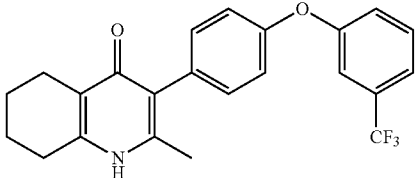
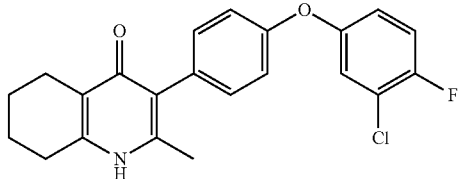
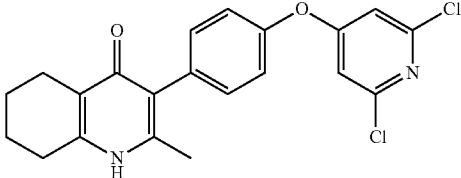
mined by the total area of the disk in order to estimate the number of cysts and organisms in each condition. Data was collected using Gen5 software. IC₅₀ was calculated by graphical analysis in Excel.

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MJM136		1.0-10.0	>10	0.2
MJM141		1.0-10.0	1.0-10.0	0.16
JAG006		>1	N.D.	0.29
JAG013		>1	N.D.	1.31
JAG014		>1	N.D.	0.71
JAG015		>1	N.D.	>20
MJM170		0.03	1.0-10.0	0.01

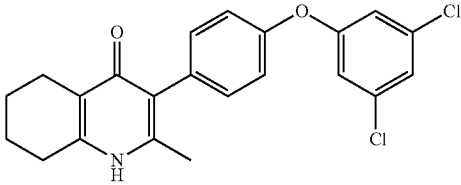
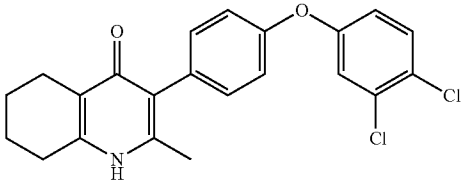
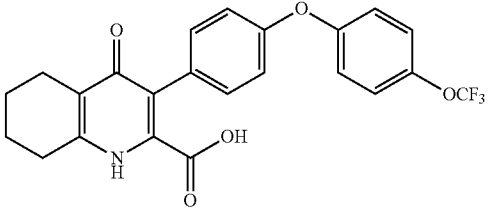
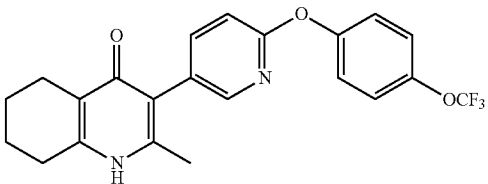
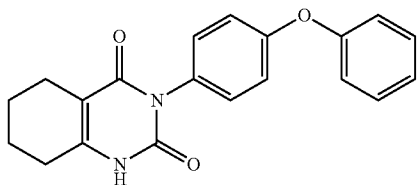
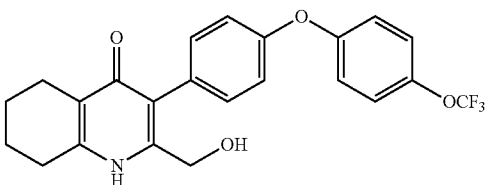
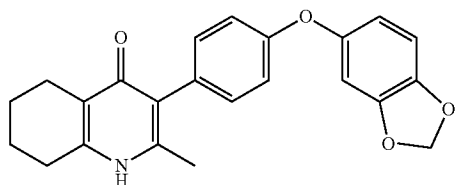
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		Tachy IC ₅₀ μM	IC ₅₀ μM	IC ₅₀ μM
JAG21		0.09	N.D.	0.01435
JAG039		7.6	N.D.	9.595
JAG046		>10	N.D.	6.716
JAG047		>10	N.D.	3.746
JAG50		0.055	N.D.	0.04664
JAG58		0.04-0.08	N.D.	Awaiting Testing
JAG63		0.1-0.3	N.D.	Awaiting Testing

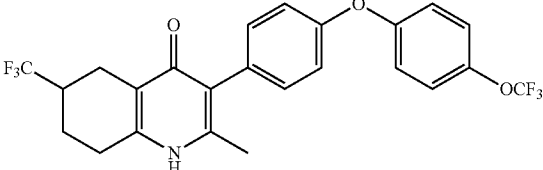
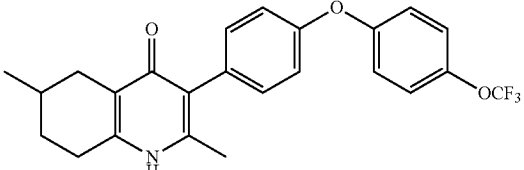
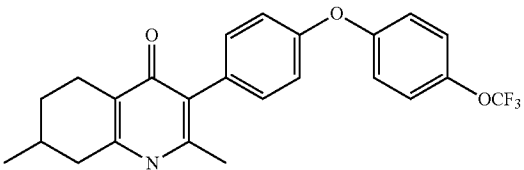
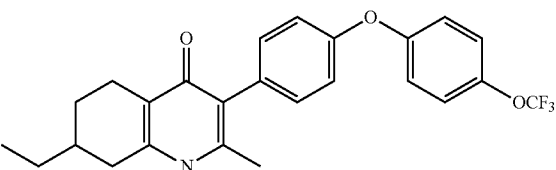
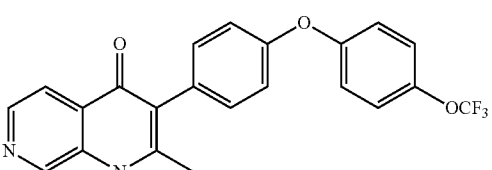
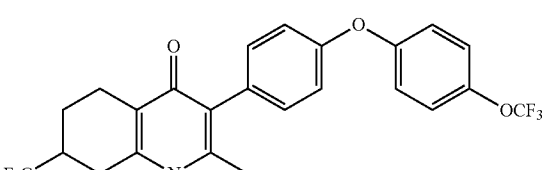
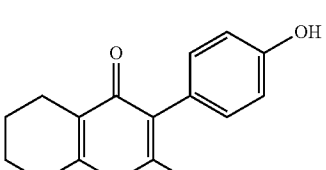
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ID	Structure	Brady		
		Tachy IC ₅₀ μ M	IC ₅₀ μ M	Pf D6 IC ₅₀ μ M
JAG062		0.016	N.D.	N.D.
JAG069		0.02	N.D.	N.D.
JAG023		1	N.D.	N.D.
AS006/ JAG143		0.06- 0.08	N.D.	N.D.
AS012/ JAG144		0.3	N.D.	N.D.
AS021/ JAG145		0.08	N.D.	N.D.
AS034/ JAG148		0.1- 0.5	N.D.	N.D.

-continued

ID	Structure	Brady		Pf D6
		Tachy IC ₅₀ μM	IC ₅₀ μM	
AS022		0.02-0.04	N.D.	N.D.
JAG084		0.04-0.08	N.D.	N.D.
JAG091		>1	N.D.	N.D.
JAG092		1	N.D.	N.D.
JAG095		>10	N.D.	N.D.
JAG099		0.32	N.D.	N.D.
AS032		0.1-0.3	N.D.	N.D.

-continued

ID	Structure	Tachy IC ₅₀ μ M	Brady IC ₅₀ μ M	Pf D6 IC ₅₀ μ M
JAG100		>10	N.D.	N.D.
JAG106		~1	N.D.	N.D.
JAG107		1	N.D.	N.D.
JAG121		0.1	N.D.	N.D.
JAG129		0.1	N.D.	N.D.
JAG162		0.5	N.D.	N.D.
JAG094		1	N.D.	N.D.

Biological Activity Studies

Malaria In Vitro Studies:

D6 is a drug sensitive strain from Sierra Leone, C235 is a multi-drug resistant strain from Thailand, W2 is a chloroquine resistant strain from Thailand, and C2B has resistance to a variety of drugs including atovaquone. These assays were performed using standard protocols.

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Compound Activity Against *Plasmodium falciparum*:

Compound activity against *P. falciparum*, a causative agent of malaria, was tested using the Malaria SYBR Green I—Based Fluorescence (MSF) Assay. This; microtiter plate drug sensitivity assay uses the presence of malarial DNA as a measure of parasitic proliferation in the presence of antimalarial drugs or experimental compounds based on

modifications of previously described methods known in the art. As the intercalation of SYBR Green I dye and its resulting fluorescence is relative to parasite growth, a test compound that inhibits the growth of the parasite will result in a lower fluorescence. Selected compounds were examined for activity against four strains of *P. falciparum*: D6 (CDC/Sierra Leone), a drugsensitive strain readily killed by chloroquine, TM91-C235, a multi-drug resistant strain resistant to chloroquine, W2, a chloroquine resistant strain from Thailand, and C2B has resistance to a variety of drugs including atovaquone.

ID	Parasite strains	SYBR Green D6 IC50 (uM)	SYBR D6 R ²	SYBR Green C235 IC50 (uM)	SYBR TM91C235 R ²
MJM129	D6, C235, W2, C2B	0.03	0.94	0.07	0.94
MJM136	D6, C235, W2, C2B	0.20	0.99	0.58	0.98
MJM141	D6, C235, W2, C2B	0.16	0.96	0.57	0.95
MJM170	D6, C235, W2, C2B	0.01	0.98	0.03	0.99
JAG006	D6, C235, W2, C2B	0.29	0.90	0.88	0.92
JAG013	D6, C235, W2, C2B	1.31	0.98	2.60	0.96
JAG014	D6, C235, W2, C2B	0.71	0.94	1.35	0.99
JAG015	D6, C235, W2, C2B	>20	N/A	>20	N/A
JM10	D6, C235, W2, C2B	0.88	0.94	4.48	0.97
JAG021	D6, C235, W2, C2B	0.01435	0.9572	0.06164	0.9706
JAG047	D6, C235, W2, C2B	3.746	0.9738	12.56	0.9218
JAG046	D6, C235, W2, C2B	6.716	0.9844	>20	N/A
JAG039	D6, C235, W2, C2B	9.595	0.9532	>20	N/A
JAG050	D6, C235, W2, C2B	0.04664	0.9138	0.06913	0.9562
RG38	D6, C235, W2, C2B	2.884	0.8936	13.66	0.8338

ID	Parasite strains	SYBR Green W2 IC50 (uM)	SYBR W2 R ²	SYBR Green C2B IC50 (uM)	SYBR C2B R ²
MJM129	D6, C235, W2, C2B	0.08	0.93	0.01	0.94
MJM136	D6, C235, W2, C2B	0.55	0.98	0.38	0.99
MJM141	D6, C235, W2, C2B	0.63	0.88	0.48	0.95
MJM170	D6, C235, W2, C2B	0.03	0.99	0.01	0.99
JAG006	D6, C235, W2, C2B	2.46	0.92	1.66	0.94
JAG013	D6, C235, W2, C2B	2.35	0.96	1.39	0.94
JAG014	D6, C235, W2, C2B	1.27	0.99	0.92	0.98
JAG015	D6, C235, W2, C2B	>20	N/A	>20	N/A
JM10	D6, C235, W2, C2B	5.36	0.90	6.75	0.81
JAG021	D6, C235, W2, C2B	0.05518	0.9727	0.04042	0.9847
JAG047	D6, C235, W2, C2B	9.072	0.9358	7.781	0.9575
JAG046	D6, C235, W2, C2B	>20	N/A	>20	N/A
JAG039	D6, C235, W2, C2B	>20	N/A	>20	N/A
JAG050	D6, C235, W2, C2B	0.03136	0.9693	0.03635	0.9427
RG38	D6, C235, W2, C2B	9.245	0.7954	>20	N/A

Example 5: Effect of Active Forms of *T. gondii* on Transcriptomes, Proteomes and Mechanisms Whereby this Occurs and Reflection of the Same Type of Damage to Neuronal Cells in Circulating Biomarkers from Children

Since we found signature pathways reflecting influence of the bradyzoite stage (characteristic of the chronic *Toxoplasma gondii* infection) in primary human neuronal stem cells in tissue culture on pathways of neurodevelopment, neuroplasticity, and neurotoxicity, we asked whether the active form of the parasite would also affect those pathways. It did. We found alterations in pathways similar to those shown with EGS bradyzoites in transcriptomics and proteomics (FIG. 19 with explanatory figure legends and methods). These abnormalities suggested that there might be

circulating biomarkers reflecting such damage to neuronal cells in patients. In that context we then asked whether serum biomarkers from ill children would reflect neuronal damage and neurodegeneration.

5 Methods.

Biomarkers: Serum collection was from children in the National Collaborative Congenital Toxoplasmosis Study (NCCCTS). Children have serum drawn at each visit. Sera characterized were obtained at a visit when new seizures were noted for ill children. These sera were analyzed with nano proteomic and miR analyses as described earlier by

Hood, Wang et al. This was done using a panel of markers known to be abnormal in patients with Alzheimer's and other neurodegenerative diseases. This was done to determine whether the same biomarkers present in serum or plasma from persons with these neurodegenerative disease might be present in sera from the ill children. The children are described more fully in the figure legend.

Murine Study of Apolipoprotein A1:

Wildtype mice on a C57Bl6/J background, mice in which the Apolipoprotein A1 gene was knocked out (Apo A1^{-/-}) were utilized in this experiment. They were immunized with an attenuated strain of the RH strain of *Toxoplasma* in which ribosomal proteins small subunit 13 was placed under the control of a tetracycline repressor by placing 4 tet O elements in the promoter and a tetracycline regulatable repressor with YFP was stably transfected. This immunized the mice and

subsequently the mice were challenged with the Me49 strain *T. gondii* and cysts were counted or luminescence in brain measured.

EGS and Canonical Type 1,2,3 Transcriptomics Details and Type 1, 2, 3 Proteomics, Analysis of Alternatively Spliced Genes, and Immunofluorescence Studies:

Details of the specific genes with altered transcription caused by EGS in Example 1 are discussed above. Transcriptomics were carried out as described in Example 1.

iTRAQ data from *T. gondii* infected cell cultures. Protein quantified, extracted, subjected to mass spectroscopy, and sequence analysis from each flask, ~180-190 ug proteins were extracted and 50 ug were used for 8-plex iTRAQ. A raw table listing relative ratios for all peptide identified in 8 samples was created. The ratio should be 0.125 (1.000/8) if one peptide/protein evenly distributes in 8 samples. Ratios of peptides from the same proteins are then calculated to protein ratios. A "Ratio to Channel 0" then included a total of 4,367 proteins identified with iTRAQ ratio. The protein ratios crossed 8 samples (4 conditions in duplicates) and were raw data from mass spec and converted to ratios against Channel 0, i.e. Control sample. They are then normalized and ratios made. "Prot with high score" has 3,359 proteins identified by more than 1 peptide and with ProteinProphet probability >0.8 (=FDR<1%). Among these 3,3359 proteins with high confidence, 10 proteins up >2-fold in either of the 3 infected cells vs. controls, while 28 proteins down >2-fold were identified. Occurrence of differences in alternative splicing between infected and uninfected cells was done with rMATS. Method for IFA are as described in Example 1. The antibodies are to SAG1, P50-NFkB.

Results:

Human serum biomarkers in ill congenitally infected children reflect *T. gondii* infection and neuronal damage. Three pairs of children were studied. In each demographically-matched pair, one child had severe disease and the other had mild or no clinical illness. Each child had serum stored from evaluations at the same ages. The second pair are dizygotic, discordant twins. Each of the three ill children had new myoclonic-"infantile" spasms, or hypsarrhythmic seizures. For two, this was associated with a rise in or high *T. gondii* specific IgG antibody titers (FIG. 19a). IgG was not measured for the third ill child. A panel of nanoproteomics and miR sequencing was performed on serum obtained at the time of this new illness. The two ill children diagnosed more recently had T2 weighted abnormalities on brain MRIs similar to active inflammatory and parasitic caused brain disease seen in a murine model. Ill children compared with their paired healthy controls had alterations in miRs and increases in serum proteins associated with neurodegeneration, inflammation, a misfolded protein response and protein misfolding. Elevated proteins included clusterin, and oxytocin (FIG. 19 b-d). PGLYRP2 (N-acetylmuramoyl-L-alanine amidase) and Apolipoprotein B1 were depressed. miR-17-92, which *T. gondii* RH strain markedly increases in HFF cultures, also was increased in sera of the ill children, as was miR-124 (FIG. 19b,c). miR-124 is associated with neurodegeneration. This indicates active brain destruction by the parasite or the response to it. These circulating proteins and miRs are clinically useful biomarkers to identify active toxoplasmic brain (and possibly retinal) disease.

To determine whether the presence of one of these biomarkers could be confirmed, a murine model was used. In this example of biomarkers in a murine experiment recapitulating the data of biomarkers in the serum of the ill children, APOA1 knockout and wild type mice were

infected with *Toxoplasma*. The wild type and uninfected mice had less radiance from luciferase parasites and fewer cysts, and less immunologic reaction to the lower parasite burden in brain (data not shown). This demonstrates that the circulating ApoA1 diminishing in the boys who were ill as a biomarker. This provides evidence that these biomarkers that were abnormal in the children had counterparts in murine models.

To determine whether similar pathways as were abnormal in EGS Example 1 were perturbed by the canonical U.S./European types of parasites and mechanisms whereby this might occur, transcriptomics, proteomics, analysis of alternatively spliced genes and immunofluorescence were also performed. Experimental data showed similar perturbation of pathways by canonical U.S./European type parasites that infected the children with the biomarkers through similar transcriptomics analyses demonstrating biological effect of Type I, II, III parasites on localization of NFkB, STAT 3 and STAT 6 in primary human neuronal stem cells. These abnormalities are caused by the canonical U.S. and European types of parasites growing as tachyzoites in the human primary neuronal stem cells and monocytic cells. These finding along with those demonstrated by the Omic studies of EGS (Example 1) suggest a mechanism whereby circulating biomarkers reflecting damage to neuronal cells in patients can occur. Placed in this context, we hypothesize that serum biomarkers from ill children reflect neuronal damage and neurodegeneration, as confirmed by our murine models, and findings seen in tissue culture and/or in patients.

DISCUSSION

The signature pathways we noted in studies of human primary neuronal stem cells which reflected abnormalities and gene products associated with neurodegenerative disease and the mechanisms whereby *T. gondii* can cause such pathology prompted study of biomarkers in a small number of ill versus well children. Biomarkers of active brain *T. gondii* infection in humans were found. The serum biomarkers shown in FIG. 19 are increased (e.g., clusterin, oxytocin, amyloid, and mir 17-92 and mir 124) or diminished, including PGLYRP2 (N-acetylmuramoyl-L-alanine amidase) and Apolipoprotein-A1 which are indicative of infection. These are consistent with the transcriptome demonstrating signature pathways in GO slim and KEGG analyses with effect on ribosomes, alternative splicing and neurodegenerative diseases, including Alzheimer's disease, Huntingtons disease, and Parkinson's disease by encysted EGS, and for example pathways of response to oxidative stress, regulation of apoptosis, and alternative splicing of toll receptors that were abnormal in the same cells infected by the canonical US/European parasites (active tachyzoites) that the children had. Other manifestations of active disease in the brain diminished with treatment and are not abnormal in the dizygotic healthy twin of one child or demographically matched well children. This is consistent with these biomarkers being selected to be assayed with MiR sequencing and proteomics based on their differences in diseases of neurodegeneration. These ill children had developed new seizures, elevations in antibody titer, elevated cerebrospinal fluid protein in one child, and abnormal T2 weighted alterations in T2 weighted brain magnetic resonance imaging. The biomarkers that were characteristic of neurodegeneration in the ill children and when diminished were associated with greater severity of disease in a murine model will be useful to monitor disease and response to treatment of disease due to this parasite. Restoration to normal values being indicative of favorable response to treatment and presence may also mark recrudescence of disease. ApoA1 may also be a useful treatment.

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 35 40 45
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 50 55 60
 His Leu Ser Ser Ala Ala Leu Leu Gln Leu Val Gln Thr Gln Ser Ala
 65 70 75 80
 Gly Gly Val Pro Gln Ala Val Leu Arg Asn Leu Phe Ser Ser Ile His
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 Pro Asn Glu Ala Ser Pro Ile Leu Ala Leu Leu Gly Glu Ala Ala Arg
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Ser	Ser	Gly	Ala	Val	Ser	Ser	Arg	Asn	Ala	Gly	Ala	Tyr	Gln	Phe	Glu
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Arg	Leu	Leu	Gln	Ala	Glu	Ala	Ala	Lys	Val	Lys	Ala	Leu	Leu	Pro	Asn
		290				295					300				
Ala	Thr	Ser	Lys	Ser	Met	Ser	Gln	Ser	Ser	Val	Pro	Gln	Arg	Asp	Leu
		305			310					315					320
Thr	Arg	Lys	Thr	Ser	Leu	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Ser	Ala	Asp
				325					330					335	
Asp	Ala	Ser	Arg	Arg	Tyr	Asn	Thr	Arg	Gly	Ala	Asn	Ser	Gly	Gly	Ala
			340					345					350		
Gly	Leu	Arg	Arg	Gly	Thr	Gly	Val	His	Ala	Thr	Thr	Glu	Gln	Ser	Gly
		355					360					365			
Ala	Leu	Asp	Ala	Gly	Glu	Arg	Thr	Arg	Pro	Phe	Gly	Ala	Gly	Glu	Asp
		370				375					380				
Glu	Ser	Ala	Gln	Gly	Lys	Pro	Asp	Ser	Arg	Gly	Arg	Gln	Arg	Pro	Gly
		385			390					395					400
Ala	Leu	Asp	Ala	Ser	Asn	Ile	Leu	Gly	Leu	Leu	Ala	Ala	Phe	Gln	Pro
			405					410						415	
Ser	Gln	Ala	Pro	Ala	Ile	Arg	Asp	Leu	Ser	Ala	Pro	Ser	His	Leu	Ser
			420					425					430		
Ala	Ala	Ala	Thr	Gly	Ala	Leu	Pro	Leu	Thr	Ala	Ser	Phe	Thr	Ala	Ser
		435					440					445			
Ala	Leu	Ala	Ser	Ser	Gln	Cys	Leu	Pro	Ala	Gly	Thr	Pro	Ala	Ser	Ser
		450				455					460				
Ser	Ala	Ser	Pro	Pro	Phe	Ser	Glu	Val	Leu	Ser	Thr	Thr	Glu	Glu	Ser
					470					475					480
Ser	Thr	Thr	Lys	Glu	Thr	Asp	Ala	Ser	Ala	Ser	Thr	Leu	Leu	Ala	Phe
			485						490					495	
Leu	Gln	Lys	Tyr	Ser	Ala	Val	Ser	Gly	Leu	Gly	Gly	Ala	Ser	Asp	Phe
			500					505					510		
Leu	Gly	Gln	Leu	Gln	Gly	Lys	Ser	Ser	Leu	Pro	Pro	Leu	Ser	Leu	Ala
		515				520						525			
Glu	Pro	Ser	Ser	Ala	Leu	Pro	Ser	Ser	Phe	Leu	Gly	Gly	Ser	Asp	Gly
		530				535					540				
Gly	Thr	Ile	Asp	Thr	Arg	Asn	Gly	Asn	Gly	Glu	Lys	Thr	Thr	Pro	Pro
					550					555					560
Ile	His	Leu	Phe	Gln	Ser	Ala	Phe	Arg	Ile	Pro	Ser	Pro	Ser	Gln	Gln
			565					570						575	
Asn	Leu	Leu	Asp	Ala	Leu	Leu	Ala	Ser	Ser	Cys	Thr	Thr	Ala	Thr	Ser
			580					585					590		
Arg	Ser	Asp	Gly	Ser	Gly	Asn	Leu	Gly	Cys	Pro	Val	Val	Asp	Glu	Arg
		595				600						605			
Asn	Ala	Lys	Leu	Ala	Gly	Pro	Ala	His	Pro	Leu	Pro	Cys	Ser	Phe	Pro
		610				615					620				
Gln	Ile	Ser	Ser	Ser	Ser	Gly	Glu	Pro	Gly	Arg	Lys	Thr	Gly	Gly	Arg
					630					635					640
Val	His	Arg	Gln	Gly	Thr	Ser	Gln	Ser	Gly	Gly	Arg	Val	Arg	Ser	Gly
			645						650					655	
Lys	Asn	Gly	Gly	Ser	Ala	Ala	Pro	Pro	Arg	Gln	Ser	Ser	Ser	Glu	Asn
			660					665					670		
Val	Pro	Ser	Thr	Pro	Thr	Val	Ser	Ser	His	Glu	Ala	Pro	His	Arg	Ala
		675					680					685			

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Gly	Phe	Pro	Ser	Gln	Thr	Pro	Tyr	Glu	Leu	Ser	Ala	Ser	Pro	Ser	His
690						695					700				
Gln	Leu	Asp	Leu	Leu	Arg	Leu	Gly	Ala	Phe	Leu	Gly	Gly	Ala	Gly	Lys
705					710					715					720
Gln	Asp	Ala	Ser	Val	His	Ser	Asp	Glu	Thr	Gly	Thr	Leu	Ser	Gly	Glu
				725					730					735	
Pro	Ser	His	Arg	Ser	Cys	Ser	Leu	Ser	Arg	Gly	Leu	Thr	Gln	Glu	Ser
			740					745					750		
Val	Leu	Gln	Leu	Ser	Asp	Thr	Thr	Ser	Thr	Ser	Arg	Glu	Gly	Glu	Pro
	755						760					765			
Asn	Glu	Pro	Ser	Gln	Gly	Cys	Val	Asn	Val	Ala	Ala	Ser	Leu	Pro	Ala
770						775				780					
Phe	Gly	Pro	Gln	Pro	Ser	Ser	Gly	Ala	Ala	Lys	Ala	Arg	Glu	Gly	Arg
785					790					795					800
Arg	Gly	Ala	Gly	Gly	Ala	Gly	Ala	Ala	Pro	Pro	Val	Pro	Leu	Arg	Ala
			805						810					815	
Asp	Val	Thr	Leu	Gly	Gly	Asn	Arg	Pro	His	Tyr	His	Val	Ala	Lys	Gln
			820				825						830		
Glu	Trp	Arg	Val	Arg	Tyr	Tyr	Met	Asn	Gly	Lys	Arg	Lys	Met	Arg	Thr
	835						840					845			
Tyr	Ser	Ala	Lys	Phe	Tyr	Gly	Tyr	Glu	Thr	Ala	His	Thr	Met	Ala	Glu
850						855					860				
Asp	Phe	Ala	His	Tyr	Val	Asp	Lys	His	Glu	Ala	Leu	Pro	Asp	Ser	Met
865					870					875					880
Met	Met	Thr	Ala	Met	Met	Leu	Gln	Ala	Gln	Ala	Asn	Ser	Ala	Ala	Ser
			885						890					895	
Ser	Gly	Gln	Thr	Val	Pro	Leu	Ala	Arg	Gly	Ile	Arg	Ala	Ser	Ser	Ala
			900					905					910		
Ser	Ala	Gly	Ala	Gly	Gly	His	Val	Ser	Lys	Ser	Ala	Thr	Lys	Gly	Ser
	915						920					925			
Val	Ala	Ala	Ser	Ser	Glu	Gly	Ser	Thr	Ser	Met	Gly	Ser	Asp	Ala	Thr
	930					935					940				
Arg	Ser	Gln	Glu	Gly	Glu	Ala	Ala	Glu	Leu	Cys	Pro	Leu	Ala	Ala	Gly
945					950					955					960
Leu	Ser	Arg	Pro	Leu	Ala	Ser	Met	His	Ser	Ala	Ala	Gly	Asn	Ala	Val
			965					970					975		
Ala	Gln	Gly	Arg	Gln	Glu	Ser	Lys	Glu	Glu	Ala	Pro	Gly	Gly	Gln	Ala
			980					985					990		
Trp	Phe	Gly	Glu	Pro	Gly	Lys	Phe	Arg	Ala	Ser	Ser	Glu	Ala	Ala	Leu
	995						1000						1005		
Cys	Gly	Ser	Gly	Ser	Ser	Ala	Glu	Gly	Arg	Asp	Gly	His	Glu	Ser	
1010						1015						1020			
Glu	Val	Leu	Trp	Ala	Thr	Leu	Gly	Lys	Val	His	Asp	Ala	Ser	Gln	
1025						1030						1035			
Gly	Lys	Lys	Ile	Lys	Pro	Glu	Lys	Pro	Leu	Thr	Val	Ala	Arg	Gly	
1040						1045						1050			
Arg	Leu	Ala	Leu	Gly	Ala	Glu	Asp	Lys	Ser	Gln	Asn	Leu	Gly	Val	
1055						1060						1065			
Asp	Leu	Gly	Asp	Ser	Gly	Gly	Ala	Gln	Gly	Leu	Pro	Gly	Val	Arg	
1070						1075						1080			
Gln	Pro	Arg	Gln	Met	Lys	Asn	Ser	Glu	Glu	Cys	Ser	Leu	Arg	Asp	
1085						1090							1095		

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Ser Asp 1100	Lys Gly Met Ala Leu 1105	Ser Lys Arg Phe Gly 1110	Phe Leu Pro
Ser Gln 1115	Thr Pro Ser Cys Asp 1120	Ser Met Thr Leu Pro 1125	Phe Pro Gly
Gly Phe 1130	Asp Ala Leu Ser Leu 1135	Ser Ser Ala Leu Ser 1140	Ser Cys Ala
Ser Leu 1145	Pro Val Ala His Glu 1150	Gly Asn Asn Phe Gln 1155	Lys Gly His
Thr Gly 1160	Asp Ile Val Ala Leu 1165	Ala Ser Gln Ser Gly 1170	Thr Gln Arg
Pro Ala 1175	Ser Val Val Leu Ser 1180	Arg Asp Ala Asn Val 1185	Ser Gly Ser
Ser Pro 1190	Ser His Pro Thr Trp 1195	Gln Arg Glu Gly Ala 1200	Ala Val Ser
Gly Arg 1205	Ala Asp Glu Phe Ser 1210	Ser Leu Ser Val Thr 1215	Pro Ser Thr
Val Pro 1220	Leu Ser Ser Phe Thr 1225	Met Glu Asp Ile Lys 1230	Gly Glu Glu
Gly Asp 1235	Pro Ser Arg Arg Phe 1240	Ala Leu Val Gly Glu 1245	Ser Met Lys
Asn Val 1250	Ser Ala Pro Glu Val 1255	Gln Ala Leu Phe Pro 1260	Thr Ser Ser
Ile Ala 1265	Asn Ala Glu Leu Leu 1270	Pro Val Asp Phe Leu 1275	His Ser Asn
Ser Cys 1280	Ser Ala Asp Lys Leu 1285	Glu Ser Ser Ile Pro 1290	Arg Gly Leu
Ala Gly 1295	Asn Asn Pro Ser Met 1300	Thr Ala Thr Ala Val 1305	Ala Ala Thr
Ala Val 1310	Ser His Gln Ile Phe 1315	Asp Thr Ile Thr Leu 1320	Phe Gly Glu
Phe Leu 1325	Arg Glu Phe Ala Lys 1330	Glu Lys Val Asn Glu 1335	Phe His Glu
Tyr Gly 1340	Leu Glu Ala Ser Pro 1345	Leu Thr Val Glu Ala 1350	Ser Pro Glu
Val Ser 1355	Leu Phe Gly Lys Ala 1360	Thr Phe Gly Arg Cys 1365	Pro Val Ala
Gly Gly 1370	Ser Thr Pro Ala Gly 1375	Ile Ser Lys Met Ser 1380	Gly Glu Thr
Leu Ser 1385	Gly Leu Ser Ala Ser 1390	Glu Leu Ser Leu Val 1395	Ser Ala Arg
Thr Asn 1400	Thr Thr Thr Gly Glu 1405	Glu Gln Phe Ala Leu 1410	Ala Arg Gly
Leu Phe 1415	Pro Gly Asp Ser Glu 1420	Gly Asp Arg Asp Glu 1425	Lys Lys Pro
Gln Leu 1430	Ser Gln Gln Glu Leu 1435	Leu Val Leu Ser His 1440	Ala Leu Val
Asn Leu 1445	Thr Ser Ser Thr Tyr 1450	Val Leu Met His Thr 1455	Leu Lys Ala
Ser Leu 1460	Ser Lys Ser Thr Glu 1465	Ala Val Gln Leu His 1470	Gln Pro Leu
Leu Glu 1475	Ala Ala Ser Glu Ala 1480	Lys Ala Thr Asp Glu 1485	Ala Lys Thr
Arg Glu	Glu Gln Glu Ser Ser	Glu Cys Asp His Glu	Tyr Pro Pro

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1490	1495	1500
Gly Ser Ser Leu Glu Ala Thr Thr Gly Ala Leu Pro Phe Arg Leu		
1505	1510	1515
Ser Pro Ala Leu Ser Ala Ser Ser Lys Asp Leu Pro Ser Leu Ser		
1520	1525	1530
Ala Ser Ala Ser Leu Glu Ser Val Thr Pro Phe Ala Gly Leu Pro		
1535	1540	1545
Leu Glu Glu Gly Thr Leu Ser Ala Ser Val Gly Leu Ala Ser Ser		
1550	1555	1560
Asp Asp Glu His Asp Thr Ser Leu Leu Phe Lys Thr Glu Ala Ala		
1565	1570	1575
Lys Lys Arg Ser Leu Phe Ser Thr Ala Ala Asp Gly Asp Glu Ser		
1580	1585	1590
Arg Thr Tyr Asn Asp Gly Leu Gly Gln Pro Met Glu Glu Glu Ile		
1595	1600	1605
Arg Ser Cys Val Ser Thr Ser Cys Gly Glu Ala Val Ala Thr Thr		
1610	1615	1620
Thr Leu Ser Ala Ile Gly Pro Gly Thr Gly Ala Ser Gly Ala Leu		
1625	1630	1635
Leu Asp Ser Glu Ser Arg Glu Ser Leu Gly Glu Lys Pro Gly Ala		
1640	1645	1650
Ala Leu Arg Ala Gly Ala His Thr Pro Ala Pro Ser Arg Ala Pro		
1655	1660	1665
Thr Pro Ser Arg Thr Phe Ser Phe Thr Ser Ser Ser Thr Ala Thr		
1670	1675	1680
Ser Ala Ala Leu Leu Cys Asp Ser Asn Val Val His Glu Lys Leu		
1685	1690	1695
Ser Ala Gln Gly Lys Asp Ser Glu Ala Gly Glu Arg Lys Gly Asp		
1700	1705	1710
Ser Glu Lys Glu Glu Glu Val Glu Met Trp Lys Glu Glu Asp Glu		
1715	1720	1725
Glu Val Gln Arg Cys Thr Gly Ser Ala Glu Thr Asp Ser Thr Glu		
1730	1735	1740
Ala Thr Arg Gly Glu Glu Ala Trp Arg Arg Gly Lys Gln Ser Glu		
1745	1750	1755
Lys Lys Pro Ser Val Ile Thr Thr Ala Leu Asn Leu Leu Glu Thr		
1760	1765	1770
His Arg His Leu Ala Leu Thr Ile Ser Gln Leu Lys Arg Pro Val		
1775	1780	1785
Ala Gln Gln Leu Arg Phe Ile Leu Pro Ile Ala Ala Pro Gln Leu		
1790	1795	1800
Leu Pro Cys Ile Leu Pro Pro Ala Ser Phe Gln Gly Thr Gly Glu		
1805	1810	1815
Ser Gly Asp Gly Lys Ala Glu Ala Glu Ala Lys Gly Ser Ser Ser		
1820	1825	1830
Leu Gly Gln Val Leu Glu Thr Ala Leu Gly His Gly Thr Arg Leu		
1835	1840	1845
Ala Pro Ser Ala Ser Ala Met Val Pro Pro Arg Lys Asp Glu Ala		
1850	1855	1860
Ala Ser Ala Val Pro Glu Ala Lys Thr Leu Thr Gly Leu Ala Asn		
1865	1870	1875
Ala Gly Val Thr Arg Glu Ala Ala Ser Arg Thr Leu Glu Ala Glu		
1880	1885	1890

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Gln Val 1895	Ser Arg Lys Arg 1900	Ser Arg Glu Glu Val 1905	Val Asp Ser Glu
Thr Ala 1910	Gly Asp Glu Gly Asp 1915	Met Glu Asn Val 1920	Pro Glu Thr Arg
Asp Gly 1925	Thr Thr Arg Pro Gly 1930	Ser Arg Gln Tyr 1935	Asp Thr Ser Pro
Ser Asn 1940	Asp Gly Thr Lys Pro 1945	Pro Ala Thr Ala 1950	Lys Ser Arg Val
Ile Arg 1955	Asp Gln Ala Ala Leu 1960	Glu Arg Leu Leu Leu 1965	Ala Pro Phe
Gln Asp 1970	Thr Pro Thr Cys Ser 1975	Cys Thr Asp Arg 1980	Pro Cys Pro Cys
Asp Arg 1985	Gln Gln Val Ala Asp 1990	Met Ile Tyr Leu Phe 1995	Tyr Ala Val
Pro Ala 2000	Arg Gln Gln Ala Glu 2005	Ser Ser Lys Glu Gly 2010	Ser Thr Gln
Arg Leu 2015	Gln Phe Ala Ala Arg 2020	Asp Thr Asn Glu Arg 2025	Lys Asp Ala
Arg Thr 2030	Gly Glu Glu Thr Gln 2035	Gly Gly Glu Thr Glu 2040	Ala Lys Glu
Val Ile 2045	Arg Asp Pro Glu Glu 2050	Arg Gly Val Cys Glu 2055	Gly Ser Ser
Ser Gln 2060	Asn Ala His Thr Gln 2065	Phe Asp Ala Glu Thr 2070	Ala Ser Ser
Ser Met 2075	Ser Ser Asp Pro Arg 2080	Ala Asp Lys Glu Ser 2085	Asn Ala Gln
Asp Ala 2090	His Met Ala Asp Lys 2095	Thr Ser Phe Val Ser 2100	Asp Leu Pro
Gln Pro 2105	Ser Gly Glu Phe Ala 2110	Pro Ser Leu Leu Ser 2115	Glu Thr Ser
Leu Asp 2120	Val Ala Met Ala Asp 2125	Ser Arg Gly Thr Pro 2130	Ser Glu Ile
His Gly 2135	Phe Phe Thr Arg Ser 2140	Asp Glu Gln Lys Arg 2145	Ala Ser Phe
Ser Ser 2150	Ser Ser Leu Leu Ala 2155	Ala Gly His Ala Val 2160	Ala Ser Phe
Ser Ser 2165	Ser Leu Ala Gly Val 2170	Val Ser Gly Ala Gly 2175	Glu Arg Arg
Glu Cys 2180	Ala Gly Pro Ser Leu 2185	Gly Asp Leu Ser Thr 2190	Ile Gly Leu
Leu Ser 2195	Leu Ser Tyr Pro Ala 2200	Met Leu Ala Phe Ile 2205	Leu Pro Leu
Gln Ser 2210	Leu Leu His Thr Val 2215	Ser Gly Met Ile Leu 2220	Thr Leu His
Lys Lys 2225	Leu Ile His Arg Phe 2230	Ile Cys Ala His Leu 2235	Arg Leu Val
Leu Asp 2240	Asp Asp Met Arg Arg 2245	Pro Ala Gly Gly Ala 2250	Leu Lys Ser
Arg Gly 2255	Ala His Gly Asp Thr 2260	Glu Ala Ala Glu Ala 2265	Gln Val Glu
Arg Arg 2270	Arg Arg Glu His Glu 2275	Arg Glu Glu Thr Thr 2280	Asn Leu Ala

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Ile Gly Tyr Arg Glu Gly Asn Ala Glu Ala Ala Asn Thr Phe Pro	
2285 2290 2295	
Leu Val Asp Thr Val Ser Ser Leu Leu Ser Pro Gly Ser Leu Arg	
2300 2305 2310	
Gln Glu Asn Ser Glu Val Glu Arg Arg Asp Asn Asp Glu Glu Arg	
2315 2320 2325	
Leu Glu Leu Ile Thr Gly Ile Ala Arg Glu Ser Pro Lys Pro Ser	
2330 2335 2340	
Glu Lys Asp Ser Val Ser Pro Phe Leu Ser Thr Ala Pro Cys Pro	
2345 2350 2355	
Gly Thr Glu Ala Glu Ser Ser Asp Cys Ser Ala Ser Ser Ala Cys	
2360 2365 2370	
Ser Gly Thr Pro Thr Glu Gly Thr Glu Gly Gly Glu Thr Gly Asp	
2375 2380 2385	
Ile Ala Ser Phe Leu Ser Pro Ser Gly Glu Val Lys Gln Thr Ile	
2390 2395 2400	
Met Leu Ala	
2405	

<210> SEQ ID NO 3
 <211> LENGTH: 1217
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

tatccagttg cccggtctct tctacattct tctcgatgta gcggcggcgt tctgtgttcc	60
ttagagcgag tccacgcacc agcctcgtgg agtcgaacag ttttcgccag agcggggaca	120
gccggtggaa gacagaacag gagggattca ccgtcacctc gtttgcttcc ttctggtgat	180
ggagggaata agccgacaga ctcaattctt aacagttcat ggagagggg caacgacgtc	240
accatccagc tttccattca cttaaccgca caagcgttct gctcgttagt caagcctcac	300
tcgccagtcg aaagccatta aaagttcgcg tttctggctc tcgtttgtgc cggaagtctg	360
ccaaagcaaa caaaggatct gaaaccgagt agcagtgaac gcgtgacagt gcagaggggt	420
gccccgctcg gcgtcctctc tgtccacgaa cagccacaat tctcatcacg agaagtcctc	480
ctccccgga tcttctctca gttccccatg actgcctccg gttctcgcac ggaaggcgat	540
ccgccttcac gctccccggc ctttgccagt tttgtgcaag aaggtcgccc gtcttattct	600
tgtcacgttc cctgtatcta ctcggttcac tgcgtctac agaagctctt cttegccttc	660
tactgatcag tgcactctac gagatgcact atcatcagtc ctgaactcca tgtttggtg	720
gaaacctggg cgtgctgtgt cgcagcgagt cgcgagattg ccggcctgtc gacgagttcc	780
cgtttttctt gcaactggcta cagcgtagcg gcttcgcctg ctcaactggc acggtactgg	840
ccgcacgggt tcacgatcct gaggtcggcg agatgccct gtctggcgag gccttttgtc	900
tacgcagcga cctctgtcta ctagagaaag gcagaaggcc ggagcgtttt ctcatatgtg	960
ctactctttg tcttctcgga tcttcctgtc gttcagctgt gctttttcca aaggagacct	1020
gtgtgcagag gacttcgctg ctaaaaagca gaagagtgcg cggcgtgtgt agctcagtgg	1080
catttcggga ctcggtcttg cgtcgttcgc gactggacgt cgtcgtctgt gagagcgtca	1140
aactagggag aagggggcgg ccagagcggt cggaataa tctgcaaagc ccaggtcccg	1200
tatgatattc aaaaaag	1217

<210> SEQ ID NO 4

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<211> LENGTH: 267
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

Met Lys Ala Ala Val Leu Thr Leu Ala Val Leu Phe Leu Thr Gly Ser
1          5          10          15

Gln Ala Arg His Phe Trp Gln Gln Asp Glu Pro Pro Gln Ser Pro Trp
20          25          30

Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val Leu Lys Asp
35          40          45

Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu Gly Lys
50          55          60

Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr Ser Thr
65          70          75          80

Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp
85          90          95

Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys
100         105         110

Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe
115         120         125

Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu
130         135         140

Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu
145         150         155         160

Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala
165         170         175

Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp
180         185         190

Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn
195         200         205

Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu
210         215         220

Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln
225         230         235         240

Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala
245         250         255

Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln
260         265

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<210> SEQ ID NO 5
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 5

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agtggttctcg aaaccatgct aacac

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25

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<210> SEQ ID NO 6
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 6

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cctcttacct cagttacaat ttata

```

25

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<210> SEQ ID NO 7

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<211> LENGTH: 968

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 7

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Met Leu Ser Arg Arg Cys Lys Arg Ser Ser Ala Glu Asp Ser Gly Ala
 1             5             10             15

Asn Glu Val Gly Ala Asn Ala Asp Gln Ser Lys Arg Leu Arg His Ser
 20             25             30

Leu Asp Ser Ile Ile Glu Lys Gly Gly Asp Pro Val Asn His Asp Ser
 35             40             45

Ala Met Leu Leu Asp Cys Ala Pro Thr Gln Thr Gly Arg Ala Phe Ala
 50             55             60

Phe Leu Ser Met Pro Ala Pro Ile Glu Pro Ser Gly Asn Glu Glu Ser
 65             70             75             80

Ala Pro Ala Val His Arg Asp Ser Gly Val Gly Gly Ile Asp Tyr Pro
 85             90             95

Arg Pro Val Ala Ser Ile Ser Val Glu Ser Ser Ser Gln Val Val Ala
100            105            110

Pro Arg Asp Glu Asn Pro Ser Ala Ser Tyr Gln Arg Arg Gly Asp Ser
115            120            125

Pro Pro Ser Leu Arg Asn Gly Gly Asp Arg Gln Glu Arg Lys Arg Thr
130            135            140

Ala Val Ala Pro Glu Ala Asn Glu Pro Gln Asp Asn Glu Thr Lys Asn
145            150            155            160

Glu Glu Trp Leu Gln Leu Ala Arg Leu Lys Pro Lys Val Glu Gly Val
165            170            175

Cys Phe Asp Arg Phe Phe Arg Arg Trp Val Ala Lys Arg Ala Gly Leu
180            185            190

Lys Lys Val Tyr Phe Pro Val Tyr Lys Tyr Gly Phe Asp Arg Ala Tyr
195            200            205

Glu Leu Ala Val Ala Thr Arg Arg Gly Leu Glu Asn Asp Ala Ala Ala
210            215            220

Gly Ile Arg Ala Val Gly Ala Leu Arg Pro Arg Ile Ser Glu Ala Ala
225            230            235            240

Gly Cys Thr Ser Ser Pro Gly Met Leu Ser Glu Asp Ala Cys Pro Glu
245            250            255

Lys Pro Pro Val Pro Val Gln Pro Pro Arg Thr Leu Ser Thr Arg Ala
260            265            270

Thr Ala Ala Gln Ala Glu Val Lys Ser Gly Asp Ser Ala Glu Ser Thr
275            280            285

Lys Asn Asp Ser Glu Gly Ala His Val Leu Glu Gly Ala Glu Leu Gln
290            295            300

Thr Pro Glu Arg Ser Thr Ser Asn Thr Ile Cys Trp Ala Thr Ala Ala
305            310            315            320

Glu Gly Ser Ile Ser Lys Thr Asp Gly Phe Gln Asn Arg Ser Ser Pro
325            330            335

Ser Gly Phe Gly His Gly Ser Arg Asn Lys Pro Glu Leu Ser Gln Gln
340            345            350

Lys Val Glu Thr Thr Ser Arg Gly Ile Arg Ser Ala Ser Ala Ser Cys
355            360            365

Asn Arg Glu Lys Asp Gln Gly Gly Ser Ala Cys Ser Val Leu Ser Ile
370            375            380

Ala Ser Phe Ser Leu Ser Gln Ile Asp Glu Glu Leu Glu Gly Ile Asn

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385	390	395	400
Asp Glu Ala Tyr Glu Ala Glu Arg Leu Gln Ala Asp Glu Asp Arg Ser	405	410	415
His Ala Pro Ala Ala Ser His Gly Glu Gly Gly Thr Ser Ala Gly Glu	420	425	430
Ser Thr Ala Ala Ser Thr Thr Gly Ser Glu Asp Ser Gly Pro Leu Arg	435	440	445
Ala Ala Thr Ser Pro Leu Met Phe Pro Gln Gly Ser Glu Gly Ser Ala	450	455	460
Ser Ser Ala Ser Thr Glu Ile Met Val Leu Asp Asp Glu Ser Met Gln	465	470	475
Gln Ala Leu Val Thr Ala Ser Ala Glu Thr Leu Asn Lys Leu Arg Ser	485	490	495
Thr Leu Pro Ala Gly Val His Phe Asp Phe Ala Ser Lys Arg Trp Phe	500	505	510
Ala Val Tyr Ser Ser His Glu Ser Pro Glu Ala Thr Gln Arg Asp Pro	515	520	525
Val Arg Pro Lys Glu Arg Val Arg Ile Phe Asp Pro Thr Gln Tyr Glu	530	535	540
Gly Ser Met Leu Lys Ala Phe His Ala Cys Arg Ser Phe Cys Gly Ser	545	550	555
Val Glu Ala Gly Ala Ser Asp Trp Asp Ser Val Pro Gln Leu Val Pro	565	570	575
Glu Gln Arg Lys Gln Gly Glu Cys Gln Asp Thr Ser Gly Ser Ser Asp	580	585	590
Gln Gly Ala Asn Arg Leu Ser Pro Thr Glu Thr Glu Asn Pro Pro Thr	595	600	605
Ala Asp His Pro Arg Ser Leu Ser Ala Thr Thr Arg Pro Glu Gly Ser	610	615	620
Leu Glu Gln Thr Gln His Pro Gln Arg Asn Arg Gly Ile Leu Gly Ile	625	630	635
Gln Pro Gly Glu Thr Glu Gly Leu Gln Val Pro Ser Asn Gly His Gly	645	650	655
Val Asn Ala Gly Asp Ile Glu Thr Asn Leu Leu Asp Ala Glu Phe Gly	660	665	670
Ser Glu Thr Arg Ala Arg Thr Thr Ala Leu Pro His Leu Arg Arg Ser	675	680	685
Gln Arg Arg Ala Asp Pro Ala Arg Ser Val His Ser Asn Thr Phe Ala	690	695	700
Gly Gln Glu Leu His Gln Ser Pro Lys Pro Gly Asn Gln Thr Ser Arg	705	710	715
Gly Glu Ser Gly Arg Ser Ser Leu Arg Arg Lys Asn Gln Val Ser Thr	725	730	735
Asn Glu Lys Gly Leu Pro Gly Glu Gly Gly Cys Arg Thr Asp Glu Lys	740	745	750
Ser Lys Gln Val Ser Tyr Val Ser Phe Ser Glu Pro Ile Thr Val Arg	755	760	765
Tyr Gln Gln Val Pro Thr Glu Ser Ala Ser Thr Arg Gly Cys Ser Gln	770	775	780
Arg Arg Pro Gln Asn Ala Glu Glu Leu Glu Asp Arg Arg Ser Pro Leu	785	790	795
Thr Arg Gln Glu Glu Arg Thr Glu Ser Asp Pro Arg Thr Thr Ala Gly	805	810	815

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Leu Cys Gln Glu Asn Pro His Pro Ser Tyr Arg Phe Leu Arg Gln Gln
 820 825 830
 Ser Arg Glu Leu Ala Val Arg Cys Leu Leu Val Ile Phe Gly Asn Leu
 835 840 845
 Ala Asp Val Cys Thr Pro Ala Leu Phe Arg Leu Phe Pro Gln Asp Arg
 850 855 860
 Cys Arg Arg Val Arg Ala Val Leu Gln His Arg Asp Leu Leu Gln Ser
 865 870 875 880
 Gly Lys His Thr Arg Val Leu Leu Ser Ala Tyr Phe Gln Leu Phe Trp
 885 890 895
 Pro Leu Leu Glu Thr Arg Thr Leu Pro Gln His Tyr Ser Ala Asp Tyr
 900 905 910
 Ile Arg Arg Leu Leu Asn Gly Met His Asn Val Ala Ala Met His Lys
 915 920 925
 Ser Leu Phe Pro Glu Tyr Pro Leu Arg Gly Glu Leu Asp Asn Arg Glu
 930 935 940
 Gly Pro Tyr Ala Phe Leu Asp Asp Thr Ala Ala Glu Gly Ile Asn Phe
 945 950 955 960
 Phe Glu Thr Asp Phe Asp Glu Pro
 965

<210> SEQ ID NO 8
 <211> LENGTH: 425
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 8

Met Ala Tyr Gln Arg Arg Arg Ala Ala Ala Cys Thr Ile Glu Val Ser
 1 5 10 15
 Arg Asp Leu Phe Ser Pro Glu Arg Asn Leu His Asp Asn Phe Ser Ser
 20 25 30
 Leu Ala Ile Thr Met Ala Phe Arg Thr Val Ser Lys Val Leu Pro Thr
 35 40 45
 Leu Ser His Cys Phe Pro Gly Pro Leu Ser Val Ala Ala Ser Ser Ser
 50 55 60
 Leu Pro Gly His Ser Lys Gly Glu Glu Ser Val Pro Cys Arg Val His
 65 70 75 80
 Arg Ser Phe Arg Leu Ser Pro Val Ala Asp His Glu Ala Glu Ala Leu
 85 90 95
 Ser Gly Ser Gly Asn Asp Thr Ser Gly Cys Ser Gln Arg Asp Arg Phe
 100 105 110
 Cys Ala Gly Asn Gly Ser Asp Cys Lys Ala Arg Arg Thr Ser Asp Gly
 115 120 125
 Asn Gly Ser Pro Pro Thr Asn Ala Arg Met Ser Glu Lys Leu Ser Leu
 130 135 140
 Phe Lys Asn His Ala Tyr Ser Cys Leu Glu Gln Arg Ala Cys Pro Ala
 145 150 155 160
 Ser Asn Arg Asn Leu Gly Asp Thr Ala Ala Cys Pro Leu Ser Ala Phe
 165 170 175
 Cys Arg Ser Leu Val Arg Arg Thr Pro Ser Arg Leu Trp Leu Pro Pro
 180 185 190
 Gln Cys Ser Leu Leu Ser Gly Cys Ser Ala Arg Ser Cys Pro Pro Lys
 195 200 205
 Ile Ser Val Arg Ala Thr Asn Gly Ala Ser Glu Gln Ala Ser Trp Gln

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210	215	220
Asp Phe His Pro Ala Leu Gly Arg Ala Val Val Pro Leu Ser Leu Ser		
225	230	235 240
Gly Arg Gly Thr Ala Gly Thr His Leu Val Arg Lys Phe Gly Thr Gln		
	245	250 255
Arg Val Val Gln Lys Arg Arg His Gln Met Arg Ile Leu His Pro Ala		
	260	265 270
Gln Thr Ala Tyr Val Pro Val Glu Gln Arg Pro Pro Pro Ile Pro His		
	275	280 285
Ser Leu Thr Ala Ser Ser Thr Val Lys Arg Leu Leu Asn Asn Asn Thr		
	290	295 300
Val Ala Ala Lys Glu Ala Ala Lys Arg Ile Asn Trp Gly Ala Tyr Ile		
305	310	315 320
Ser His Gln Arg Gly Val Arg Trp His Pro Gln Gly Ala Trp Arg Val		
	325	330 335
Gln Phe Ser Arg Arg Asn His Glu Arg Asn Phe Phe Val Arg Cys Glu		
	340	345 350
Cys Tyr Phe Arg Val Gly Thr Tyr Gly Phe Gln Met Ala Lys Asp Leu		
	355	360 365
Ala Ile Arg Tyr Arg Gln Arg Leu Glu Lys Glu Trp Glu Glu Leu Gln		
	370	375 380
Glu Gln Trp Thr Lys Leu Asp Ile Leu Glu Ala Glu Gln Arg Ala Lys		
385	390	395 400
Tyr Lys Glu Lys Arg Glu Glu His Leu Leu Leu Gly Ala Gly Glu Glu		
	405	410 415
Pro Glu Leu His Ser Arg Arg Ser Lys		
	420	425
<210> SEQ ID NO 9		
<211> LENGTH: 2674		
<212> TYPE: PRT		
<213> ORGANISM: Homo sapiens		
<400> SEQUENCE: 9		
Met Asp Gly Ser Gly Glu Ser Ser Gly His Leu Phe Lys Pro Gly His		
1	5	10 15
Gly Glu Ala Arg Val Ser Val His Arg Gly Ser Leu Thr Asp Ser Gly		
	20	25 30
Ser Leu Pro Ala Ala Ser Arg Cys His Ser Gln Asp Asn Lys Leu Ser		
	35	40 45
Leu Pro Cys Ala Gly Ser Met Leu Pro Ala Ser Ser Gly Arg Phe Ser		
	50	55 60
Cys Asp Ser Ala Leu Phe Gly Gly Pro Val Asp Ser Ala Cys Ser Ser		
65	70	75 80
Asp Trp Thr Pro Val Val Ser Pro Ser Arg Asp Leu Ser Ala Asp Gly		
	85	90 95
Thr Asp Ser Ser Ser Val Ser Gly Ser Arg Gly Ser Ser Leu Pro Phe		
	100	105 110
Gly Ser Pro Thr Ser Ala Leu Leu Arg Pro Ser Ser Glu Ala Ser Ala		
	115	120 125
Asn Phe Pro Arg Leu His Lys Ser Val His Ala Leu Asp Asp Lys Met		
	130	135 140
Arg Gly Leu Asp Ala Gln Leu Tyr Val Arg Pro His Gln Thr Leu Pro		
145	150	155 160

Leu 165	Gln	Pro	Arg	Leu 180	Arg	Glu	Thr	Asp	Leu 170	Cys	Arg	Asn	Gly	Glu 175	Asp
Gly	Arg	Pro	Gly 180	Lys	Phe	Asp	Ser	Pro 185	His	Leu	Gly	Ser	Ser 190	Ala	Gly
Pro	Tyr	Gly 195	His	Ser	Phe	Leu	Ala 200	Asn	Pro	Gln	Leu	Thr 205	Pro	Phe	Val
Pro	Gln	His	Leu	Ser	Ser	Ser 215	Pro	Pro	Gln	Pro	Val 220	Leu	Ser	Pro	Pro
Gly 225	Glu	Glu	Gly	Arg	Asn 230	Ser	Ala	Ala	Phe	Gly 235	Lys	Thr	Val	Ser	Arg 240
Leu	Asn	Thr	Gly 245	Gly	Gly	Glu	Arg	Gln	Asp 250	Ser	Ser	Glu	Asp	Gln 255	Val
Gly	Gly	Thr	Gly 260	Arg	Gln	Ser	Asp	Gln 265	Ala	Thr	Lys	Ala	Asn 270	Ser	Gly
Ser	Thr	Pro 275	Ala	Gly	Cys	Ala	Gln 280	Thr	Ala	Gly	Leu	Leu 285	Thr	Asp	Val
Gln	Ser 290	Ser	Gly	Thr	Asn 295	Val	Glu	His	Gly	Arg	Glu 300	His	Phe	Ser	Thr
Pro 305	Gln	Lys	Pro	Ala	Asp 310	Gly	Ser	Ala	Arg	Thr 315	Cys	Gly	Phe	Arg	Glu 320
Thr	Arg	Val	Ser 325	Pro	Ser	Asn	Ser	Ser	Leu 330	Pro	Arg	Thr	Ala	Cys 335	Arg
Ser	Arg	Leu 340	Asp	Ala	Phe	Leu	Pro	Gln 345	Lys	Ser	Val	Ser	Pro 350	Asp	His
Glu	His	Val 355	Arg	Gly	Thr	Gly	Gly 360	Ala	Arg	Ala	Phe	Val 365	Gly	Gly	Asp
Ser	Pro 370	Phe	Pro	Glu	Lys	Pro 375	Asp	Thr	Leu	Pro	Ala 380	Thr	Val	Thr	Ala
Glu 385	Leu	Ala	Thr	Glu	Ala 390	Pro	Pro	Ala	Ser	Arg 395	Asp	Pro	Pro	Val	Glu 400
Glu	Phe	Pro	Gly 405	Ala	His	Glu	Leu	Glu	Ser 410	Leu	Pro	Pro	Pro	His 415	Val
Asn	Ser	Gly 420	Arg	Pro	Pro	Ile	Gly	Glu 425	Lys	Asp	Gly	Ala 430	Ala	Ala	Ser
Pro	Gly 435	Val	Ser	Arg	Leu	Pro	Ser 440	Gln	Glu	Arg	Val	His 445	Thr	Leu	Leu
Tyr	Pro 450	Asn	Glu	Lys	Asp 455	Ala	Ser	Ser	Leu	Ser	Arg 460	Cys	Cys	Pro	Ser
Ser 465	Met	Gln	Pro	Pro	Pro 470	Ala	Gly	Pro	Arg	Gln 475	Glu	Glu	Ala	Arg	Ser 480
Phe	Ser	Val	Ser 485	Ala	Ala	Ser	Ala	Pro	Gly 490	Ala	Pro	Pro	Gly	Ile 495	Val
Tyr	Gln	Ala	Ser 500	Ala	Cys	Ala	Ser	Pro 505	Ala	Thr	Val	Ala	Ser 510	Phe	Ala
Thr	Pro	Leu 515	Thr	Thr	Pro	Val	Gly 520	Ala	Ser	Ala	Gln	Ser 525	Glu	Pro	Ala
Ala 530	Leu	His	Ala	His	Ser	Arg 535	Ser	Arg	Thr	Gly 540	Ala	His	Pro	Glu	Ala
Leu 545	Pro	Pro	Gly	Val	Pro 550	Gly	Val	Thr	Ser	Gln 555	Leu	Gly	Arg	Gly	Ala 560
Arg	Gly	Asp	Arg 565	Glu	Thr	Leu	Ala	Gly	Gly 570	Ala	Arg	Pro	Gly	Gln 575	Asp
Gly	Val	Cys	Glu	Arg	Arg	Gly	Asp	Val	Ala	Arg	Gly	Arg	Leu	Gly	Glu

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580						585						590					
Val	Ser	Val	Ala	Gly	Asp	Glu	Ala	Ala	Glu	Gly	Thr	Ser	His	Lys	Ala		
		595					600					605					
Ala	Leu	Glu	Gly	Ala	Tyr	Val	Gln	Asp	Gly	Cys	Ser	Pro	Gln	Pro	Leu		
		610					615					620					
Asn	Pro	His	Ala	Pro	Ser	Gly	Ile	Ser	Ala	Pro	Thr	Asn	Gly	Ser	Ser		
		625					630					635			640		
Glu	Leu	Ala	Ser	Ser	Ala	Ile	Pro	Ala	Ser	Thr	Cys	His	Asp	Ala	Phe		
															655		
Val	Arg	Ser	Pro	Val	Ser	Gly	Ser	Asp	Cys	Met	Ser	Val	Ala	Asn	Pro		
															670		
Gly	Gly	Pro	Pro	Gly	Ala	Leu	Gly	Gly	Leu	Phe	Pro	Ser	Pro	Arg	Gly		
		675					680					685					
Pro	Ser	Gly	Pro	Arg	Pro	Thr	Pro	His	Pro	Ala	Gln	Met	Ala	Phe	Ala		
		690					695					700					
Phe	Val	Gly	Gln	Gln	Pro	Val	Phe	Pro	Gly	Phe	Asp	Ala	Ser	Gln	Pro		
		705					710					715			720		
Ala	Gly	Ser	Thr	Phe	Gln	Tyr	Pro	Pro	Ile	Arg	Gly	Ala	Val	Ser	Gly		
															735		
Val	Ser	Pro	Pro	Pro	Pro	Met	His	Pro	Ser	Ser	Phe	Ala	Gln	Pro	Val		
															750		
Trp	Ser	Pro	Thr	Ser	Val	Pro	Ser	Ser	Ser	Val	Ser	Ser	Ser	Val	Ser		
		755					760					765					
Ser	Ser	Gly	Val	Ser	Ser	Ser	Ala	Pro	Pro	Pro	Leu	Ala	Val	Gly	Phe		
		770					775					780					
Gln	Asn	Pro	Cys	Pro	Trp	Arg	Pro	Thr	Ala	Pro	Arg	Asp	Arg	Ser	Glu		
		785					790					795			800		
Gly	Gly	Ala	Gly	Ser	Pro	Gly	Val	Ser	Cys	Gly	Ser	Ala	Pro	Pro	Ala		
							805								815		
Pro	Thr	His	Pro	Thr	Gly	Lys	Gly	Gly	Ala	Ala	Gly	Arg	Ala	Gly	Lys		
							820								830		
Gln	Leu	Gly	Gln	Ala	Thr	Arg	Phe	Leu	Ser	Ser	Val	Ser	Gly	Val	Val		
							835					845					
Tyr	Asp	Lys	Gly	Gly	Glu	Lys	Trp	Ile	Ala	Arg	Trp	Ser	Glu	Asn	Gly		
		850					855					860					
Lys	Pro	Phe	Lys	Lys	Thr	Phe	Ala	Val	Gly	Lys	His	Gly	Phe	Asp	Ala		
		865					870					875			880		
Ala	Arg	Lys	Met	Ala	Glu	Asp	Cys	Arg	Leu	Gln	Ala	Leu	Tyr	Ala	Lys		
							885					890			895		
Arg	Trp	Asn	Ser	Ala	Ser	Gly	Leu	Pro	Ala	Ser	Phe	Ser	Lys	Ser	Asn		
							900								910		
Ser	Leu	Gly	Arg	Ser	Thr	Pro	Gly	Asp	Arg	Gly	Lys	Thr	Glu	Ser	Thr		
							915					925					
Asn	Ser	Ala	Lys	Cys	Lys	Arg	Asp	Thr	Ser	Gly	Glu	Ser	Gly	Cys	Thr		
		930					935					940					
Asp	Thr	Gly	Leu	Arg	Ser	Leu	His	Met	Gly	Gly	Ala	Gly	Asp	Leu	Ser		
		945					950					955			960		
Ser	Leu	Gly	His	Pro	Gly	Thr	Pro	Pro	Arg	Asp	Gln	Glu	Gly	Ala	Pro		
							965								975		
Ala	Ser	Phe	Leu	Leu	Glu	Gly	Thr	Gly	Val	Val	Arg	Ser	Ser	Gln	Val		
							980								990		
Gln	Thr	Pro	Phe	Arg	Leu	Tyr	Asp	Ser	Val	Pro	Ser	Pro	Leu	Arg	Ser		
		995					1000					1005					

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Gly Asp 1010	Ala Leu Gly Ala Gln 1015	Arg Gly Leu Val Pro 1020	Gln Leu Leu
Asn Asn 1025	Ala Leu Val Gly Val 1030	Pro Phe Ala Pro Pro 1035	Pro Gly Ala
Ser His 1040	Ser Gly Cys Ser Ala 1045	Ala Leu Pro Pro Gly 1050	Pro Gly Ala
Pro Val 1055	Gln Val Ser Ser Pro 1060	His Thr Gly Phe Val 1065	Ala Pro Ala
Asp Val 1070	Asp Ala Pro Pro Arg 1075	Asp Gly Leu Glu Gly 1080	Leu Gly Gly
Ala Ala 1085	Glu Val Ser Pro Gln 1090	Ile Ala Val Gln Asp 1095	Gly Gly Lys
Lys Gly 1100	Glu Gly Leu Leu Gly 1105	Ser Ala Ser Leu Ser 1110	Val Arg Arg
Arg Arg 1115	Lys Arg Glu Pro Asp 1120	Glu Lys Phe Ser Pro 1125	Gly Glu Ser
Asn Ala 1130	Ala Val Lys Lys Thr 1135	Pro Arg Pro Gly Ser 1140	Phe His Pro
His Ser 1145	Cys Pro Gly Ser Glu 1150	Gly Phe Arg Ser His 1155	Asp Gly Pro
Gly Asp 1160	Ser Thr Glu Ala Arg 1165	Cys Ala Gly Leu Pro 1170	Ala Phe Gln
His Ala 1175	Thr Ala Pro Ser Ser 1180	Val Cys Trp Pro Ser 1185	Thr Ala Ser
Leu Pro 1190	Ser Leu Asp Lys Ala 1195	Gly Gln Arg Ala Glu 1200	His Ala Gly
Pro Ser 1205	Ala Phe Ser Ser Phe 1210	Ser Ser Val Gln Gln 1215	Ser Pro Gly
Ser Val 1220	Glu Thr Trp Arg Pro 1225	Glu Gly Asp Gly Gly 1230	Pro Ala Ser
Pro Ala 1235	Arg Asp Ala Gly Arg 1240	Arg Gly Ala Glu Ser 1245	Glu Glu Arg
Glu Thr 1250	Gly Glu Leu Ala Gly 1255	Pro Phe Ala Gly Val 1260	Ser Ala Ser
Ala Gly 1265	Ser Ala Ser Arg Lys 1270	Gly Gln Gln Lys Gln 1275	Leu Thr Arg
Gln Ile 1280	Gln Arg Gln Gln Gln 1285	Leu Tyr Arg Gln Gln 1290	Glu Ala Leu
Leu Gln 1295	Asn Gln Glu Glu Leu 1300	Phe Ser Arg Leu Leu 1305	Arg Arg Arg
Ser Arg 1310	Gln Glu Arg Ser Asp 1315	Val Arg Arg Arg Met 1320	Gln Arg Asp
Val Ser 1325	Ser Leu Arg Arg Leu 1330	Pro Ala Met Leu Leu 1335	Ser Pro Leu
Arg Asp 1340	Thr Leu Val Ala Ser 1345	Ala Ala Arg Leu Pro 1350	Leu Ala Thr
Arg Gly 1355	Thr Lys Arg Glu Ser 1360	Gln Lys Glu Arg Arg 1365	Asp Cys Gly
Ala Gly 1370	Ile Gly Gly Glu Thr 1375	Ala Ser Glu Lys Lys 1380	Glu Met Ala
Glu Pro 1385	Val Arg Val His Arg 1390	Arg Asp Arg Gly Gly 1395	Ala Arg Asp

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Glu	Glu	Lys	Pro	Ser	Thr	Glu	Gly	Val	Arg	Gln	Ala	Asp	Pro	Lys	
1400						1405					1410				
Gly	Arg	Lys	Ala	Glu	Gly	Phe	Pro	Thr	Trp	Val	Ile	Pro	Pro	Asn	
1415						1420					1425				
Glu	Glu	Leu	Lys	Ala	Ala	Gln	Val	Leu	Arg	Ala	Leu	Arg	Val	Gln	
1430						1435					1440				
Arg	Arg	Ala	Ala	Ala	Arg	Glu	Gly	Lys	Leu	Leu	Glu	Ser	Leu	Leu	
1445						1450					1455				
Val	His	Arg	Gly	Glu	Gly	Glu	Gly	Thr	Phe	Ser	Glu	Glu	Thr	Glu	
1460						1465					1470				
Gly	Asn	Thr	Gly	Ile	Glu	Asp	Ala	Gly	Thr	Glu	Ser	Asp	Ala	Thr	
1475						1480					1485				
Val	Thr	Gln	Glu	Thr	Ala	Glu	Lys	Val	Val	Glu	Asn	Val	Gln	Lys	
1490						1495					1500				
Met	Glu	Glu	Leu	Glu	Ser	Lys	Val	Glu	Lys	Glu	Asn	Glu	Arg	Arg	
1505						1510					1515				
Arg	Glu	Ala	Glu	Asp	Glu	Thr	Pro	Lys	Gln	Ser	Ser	Glu	Glu	Ala	
1520						1525					1530				
Pro	Gly	Val	Gln	Gln	Ser	Pro	His	Lys	Leu	Ser	Thr	Asn	Asn	Glu	
1535						1540					1545				
Asn	Asp	Ala	Ser	Pro	Gln	Lys	Leu	Thr	Lys	Ser	Val	Arg	Phe	Ala	
1550						1555					1560				
Glu	Ser	Val	Ala	Gly	Ser	Ser	Ser	Ala	Val	Gln	Thr	Ala	Gly	Ala	
1565						1570					1575				
Ala	Asp	Glu	Glu	Pro	Leu	Ala	Thr	Glu	Thr	Leu	Glu	Gly	Arg	Arg	
1580						1585					1590				
Val	Gly	Gly	Ile	Pro	Val	Pro	Ala	Thr	Ser	Ser	Pro	Ala	Pro	Val	
1595						1600					1605				
Phe	Pro	Cys	Thr	Ala	Ala	Gln	Leu	Gly	Asp	Leu	Cys	Met	Asp	Thr	
1610						1615					1620				
Leu	Tyr	Ala	Leu	Gly	Thr	Val	Arg	Pro	Gln	Trp	Arg	Arg	Gln	Asp	
1625						1630					1635				
His	Arg	Arg	Ala	Phe	Gly	Trp	His	Leu	Ser	Gln	Ile	Lys	Pro	Asp	
1640						1645					1650				
Leu	Ile	Leu	Pro	Ser	Leu	His	Ala	Ser	Arg	Val	Leu	Arg	Arg	Leu	
1655						1660					1665				
Ser	Pro	Arg	Pro	Ser	Asn	Ala	Val	Glu	Phe	Pro	Arg	Glu	Glu	Leu	
1670						1675					1680				
Ala	Ala	Ala	Ser	Ser	Ala	Ala	Gly	Leu	Val	Tyr	Gly	Glu	Gly	Leu	
1685						1690					1695				
Ser	Ser	His	His	Thr	Leu	Arg	Ser	Tyr	Val	Asp	Ala	Phe	Arg	Pro	
1700						1705					1710				
Leu	Phe	Ser	Ser	Pro	Ser	Ser	Pro	Pro	Leu	Glu	Phe	Leu	His	Leu	
1715						1720					1725				
Ser	Ser	Gly	Asp	Leu	Leu	Met	Ser	Leu	Trp	Gln	Leu	Glu	Glu	Gly	
1730						1735					1740				
Gly	Arg	Ala	Ala	Val	Ile	Asp	Asn	Val	Leu	Leu	Ala	Leu	Asp	Ala	
1745						1750					1755				
Leu	Tyr	Glu	Arg	His	Thr	Gly	Arg	Arg	Leu	Arg	Gly	Thr	Ala	Pro	
1760						1765					1770				
Pro	Pro	Phe	Ala	Val	Ser	Ser	Pro	Ser	Ser	Ala	Pro	Ser	Ser	Leu	
1775						1780					1785				
Phe	Ala	Leu	Ala	His	Leu	Gln	Gly	Gly	Ala	Thr	Ser	Thr	Thr	Pro	

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1790	1795	1800
Leu Pro Ala Thr Ala Leu Pro Ser Pro Pro Phe Pro Arg Val Ser		
1805	1810	1815
Ser Ala Pro Asp Ser Pro Val Phe Ala Pro Asp Ala Ser His Gly		
1820	1825	1830
Pro Ser Gln Arg Arg Gln Val Ser Pro His Val Thr Phe Glu Thr		
1835	1840	1845
Pro Pro Thr His Pro Arg Asp Arg Asp Ser Glu Thr Ser Val Glu		
1850	1855	1860
Arg Asn Ala Ser Pro Glu Ala Ser Pro Gln Ala Ala Thr Leu Ala		
1865	1870	1875
Ala Pro Ala Pro Cys Asp Gly Asp Arg Glu Glu Asn Phe Val Leu		
1880	1885	1890
Ala Tyr Asn Pro Glu Ala Lys Ala Leu Arg Gln Val Asn Phe Leu		
1895	1900	1905
Ala Val Gly Val Arg Val Phe Leu His Leu Glu Val Val Glu Glu		
1910	1915	1920
Met Leu His Leu Gln Ala Lys Met Gln Arg Thr Pro Gly Arg Asp		
1925	1930	1935
Asp Arg Ala Thr Ala Ser Ser Gly Pro Ser Val Asp Asp Gly Ser		
1940	1945	1950
Gly Leu Met Thr Ser Leu Pro Ser Thr Cys Ser Gly Val Ser Gly		
1955	1960	1965
Lys Lys Asp Pro Met His Trp Ser Ala Leu Phe Val Thr Val Pro		
1970	1975	1980
Ala Pro Ser Val Ser Thr Ala Ala Ser Lys Pro Leu Phe Val Val		
1985	1990	1995
Ala Glu Met Val Asp Arg Arg Leu Gln Val Pro Cys Gly Glu Gln		
2000	2005	2010
Leu Leu Phe Arg Pro Leu Pro Leu Ser Pro Ala Ala Pro Ser Ala		
2015	2020	2025
Leu Leu Ala Phe Ala Pro Ala Arg Val Cys Gln Leu Leu Arg Ala		
2030	2035	2040
Gly Ala Met Cys Leu Thr Arg Phe Thr Glu Lys Glu Gly Gly Lys		
2045	2050	2055
Arg Pro Arg Gly Ser Ala Gln Arg Cys Ser Ala Ala Ser Ser Phe		
2060	2065	2070
Phe Tyr Ser Pro Pro Pro Leu Asp Leu Ser His Leu Ala Ser Phe		
2075	2080	2085
Ala Pro Ala Ala Ser Thr Leu Thr Pro Pro Ser Ser Pro Ala Ser		
2090	2095	2100
Ser Pro Ser Ala Ser Ala Ser Gln Thr Gly Pro Gly Arg Ala Lys		
2105	2110	2115
Ser Arg Gly Thr Ser Pro Val Gly Pro Glu Ser Pro Glu Ala Ala		
2120	2125	2130
Ser Thr Thr Ser Asp Gly Leu Ala Val Pro Gly Ser Ala Ser Ala		
2135	2140	2145
Val Ser Thr Pro Gly Val Pro Ala Gly Ala Ser Gly Ala Ser Leu		
2150	2155	2160
Gly Ala Pro Ala Pro Ser Pro Met Ala Ser Pro Gly Gly Ser Pro		
2165	2170	2175
Gly Arg Pro Pro Lys Pro Val Cys Cys Pro Ala Ala Pro Gly Ile		
2180	2185	2190

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Glu Thr	Ala Trp Arg Cys Lys	Cys Ser His Arg Arg	His Glu Leu
2195	2200	2205	
Gln Leu	Glu Ile Lys Gln Lys	Leu Arg Gln Asp Lys	Lys Arg Cys
2210	2215	2220	
Leu Ala	Leu Ile Arg Glu Tyr	Pro Asp Leu Ser Leu	Leu Val Gly
2225	2230	2235	
Ala Pro	Pro Ala Thr Pro Arg	Glu Lys Glu Thr Gly	Ala Lys Arg
2240	2245	2250	
Gln Ala	Pro Glu Gly Arg Arg	Thr Ala Thr Pro Ser	Gly Ser Gly
2255	2260	2265	
Thr Leu	Thr Ala Lys Gly Gly	Asp Leu Gln Gly Ser	Thr Pro Ser
2270	2275	2280	
Gly Ala	Gly Leu Leu Ser Leu	Ala Arg Thr Ser Gln	Leu Glu Met
2285	2290	2295	
Leu Ala	Tyr Leu Val Glu Val	Asp Pro Trp Lys Tyr	Ala Lys Asn
2300	2305	2310	
Arg Gln	Asp Ala Pro Lys Pro	Glu Glu Ile Pro Gly	Leu Leu Ala
2315	2320	2325	
Lys Tyr	Lys Ala Ala Val Arg	Thr Ala Glu Tyr Gly	Arg Met Leu
2330	2335	2340	
Gln Lys	Trp Arg Ala Gly Gln	Ser Arg Glu Asp Glu	Gly Arg Gly
2345	2350	2355	
Gly Ala	Asp Gly Arg Lys Glu	Gly Asp Gly Leu Leu	Ser Pro Thr
2360	2365	2370	
Ala Ser	Pro Pro Ser Arg Arg	Lys Gln Gly Lys Asp	Ser Ser Pro
2375	2380	2385	
Asn Ser	Ala Ser Ser Gln Ala	Ser Gly Pro Ala Pro	Ser Pro Ser
2390	2395	2400	
Leu Ser	Pro Gly Ala Gly Ala	Ala Ala Val Leu Glu	Ala Glu Lys
2405	2410	2415	
Pro Glu	Pro Gln Ser Pro Gln	Glu Ser Pro Cys Pro	Leu Glu Pro
2420	2425	2430	
Ala Ala	Gly Gln Glu Pro Arg	Ala Thr Ser Ser Ala	Leu Pro Ala
2435	2440	2445	
Gly Ser	Pro Pro Trp Ala Leu	Pro Leu Val Pro Pro	Gly Gly Ser
2450	2455	2460	
Pro Arg	Ala Ser Val Ser Pro	Ser Val Leu Glu Glu	Leu Leu Arg
2465	2470	2475	
Ile Gln	Thr Ala Met Ser Gln	Leu Ala Ile Gly Thr	Ala Ile Cys
2480	2485	2490	
Val Arg	Val Lys Ala Leu Leu	Gly Leu Pro Ala Gly	Ala Glu Gln
2495	2500	2505	
His Ile	Arg Gly Val Val Thr	Arg Asn Ala Leu Lys	Phe Pro Trp
2510	2515	2520	
Glu Lys	Pro Ala Ala Pro Gln	Val Gln Ala Ala Gly	Pro Ser Val
2525	2530	2535	
Gly Ala	Ser Arg Thr Ser Pro	Ser Arg Arg Leu Ser	Gly Gly Val
2540	2545	2550	
Leu Pro	Gly Asp Glu Ala Gly	Glu Arg Arg Glu Lys	Gly Gly Ala
2555	2560	2565	
Arg Arg	Gly Val Ala Glu Gly	Asp Thr Glu Lys Lys	Glu Asp Glu
2570	2575	2580	

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Gly Thr	Ala Leu Cys Ala Gly	Ser Arg Glu Thr Glu	Ala Asp Gly
2585	2590	2595	
Ala Gly	Tyr Leu Thr Leu Ser	Leu Asn Asn Arg Lys	Glu Glu Phe
2600	2605	2610	
Ile Leu	Ser Phe Arg Glu Val	Gln Cys Leu Val Ala	Gln Asp Asp
2615	2620	2625	
Leu Arg	Leu Val Arg Thr Arg	Ala Arg Gln Trp Val	Ser Ser Phe
2630	2635	2640	
Gly Pro	Gln Pro Ser Ala Asp	Arg Lys Gly Glu Arg	Glu Glu Glu
2645	2650	2655	
Lys Glu	Thr Gly Gly Arg Thr	Arg Lys Phe Val Val	Asp Glu Asp
2660	2665	2670	

Phe

<210> SEQ ID NO 10
 <211> LENGTH: 2282
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 10

Met Asp Ser Gly Arg Asp Val Lys Asp Gly Thr Ala Gly Ser Arg Pro	
1 5 10 15	
Lys Asp Gly Gly Asp Gly Val Gly Glu Thr Arg Ala Ser Gly Arg Glu	
20 25 30	
Ser Glu Glu Arg Ser Leu Gln Leu Glu Ala Asn Glu Cys Pro Gly Ala	
35 40 45	
Val Met Ser Arg Arg Glu Asp Glu Ala Glu Pro Gln Ser Ser Pro Ser	
50 55 60	
Ser Ser Pro Pro Arg Glu Glu Gly Pro Gln Asn Val Asp Asp Ala Asp	
65 70 75 80	
Thr Ala Asn Gly Ser Gly Glu Ala Gly Leu Gln Arg Pro Pro Gln Lys	
85 90 95	
Arg Arg Leu Glu Gln Gly Leu Glu Ala Glu Ala Gly Val Gly Ser Ser	
100 105 110	
Arg Val Glu Glu Val Glu Ala Val Cys Arg Lys Arg Pro Ala Phe Ser	
115 120 125	
Gly Val Ala Asp Ala Phe Leu Glu Arg Pro Val Thr Leu Lys Asn Ser	
130 135 140	
Ser Glu Glu Asp Ala Ala Arg Leu Ser Gly Asp Asp Ala Ala Gly Ala	
145 150 155 160	
Ser Leu Leu Ser Val Arg Ser Ala Gly Ala Leu Thr Gly Asp Phe Pro	
165 170 175	
Ser Ser Ser Ser Arg Leu Pro Ala Met Leu Ser Gly Ala Arg Gly Glu	
180 185 190	
Asn Ala Glu Glu Ser Val Arg Asp Ala His Thr Pro Ala Gln Asp Ser	
195 200 205	
Arg Asp Ser Ala Leu Ala Ser Phe Ala Pro Thr Leu Ala Pro Gly Gln	
210 215 220	
Glu Ser Glu Tyr Thr Arg Ala Lys Leu Trp Ser Ile Glu Lys Ala Phe	
225 230 235 240	
Asp Ala Phe Leu Ala Asp Gln Lys Ala Asn Gly Arg Arg Gln Gly Ser	
245 250 255	
Arg Ser Met Arg Glu Pro Ser His Ala His Pro Gly Leu Ser Ala Glu	
260 265 270	

Arg	Glu	Thr	Ser	Ser	Gly	Ala	Ser	Ala	Ala	Thr	Ser	Asp	Leu	Ser	Arg
		275					280					285			
Glu	Asp	Val	Glu	Glu	Leu	Phe	Arg	Gln	His	Gly	Val	Ser	Pro	Arg	Glu
	290					295				300					
Leu	Val	Arg	Met	Leu	Ser	Gly	Arg	Arg	Asp	Gly	Pro	Gly	Thr	Ser	Pro
305					310					315					320
Glu	Glu	Leu	Arg	Ala	Ala	Val	Ala	Trp	Ala	Arg	Gln	Leu	Phe	Pro	Ala
				325					330					335	
Ala	Pro	Arg	Ser	Pro	Ser	Glu	Leu	Arg	Met	Tyr	Leu	Gln	Arg	Ala	Val
			340					345					350		
Leu	Asp	Arg	Gln	Lys	Arg	Leu	Arg	Glu	Arg	Trp	Gly	Ala	Glu	Ala	Asn
	355						360					365			
Pro	Cys	Gly	Asp	Ala	Ser	Val	Tyr	Gly	Asp	Glu	Lys	Leu	Arg	Glu	His
	370					375					380				
Leu	Ser	Asp	Leu	Ser	Ala	Phe	Met	Pro	His	Leu	Asp	Ala	Gly	Arg	Glu
385					390					395					400
Val	Tyr	Met	Gln	Trp	Gln	Arg	Ser	Arg	Gly	Arg	Arg	Asp	Phe	Asp	Ala
			405						410					415	
Phe	Val	Arg	Pro	Pro	Gly	Leu	Thr	Pro	Phe	Arg	Asp	Ser	Ser	Ser	Arg
			420					425					430		
Gln	Gly	Asp	Phe	Ala	Ala	Ser	Pro	Leu	Tyr	Ser	Phe	Ser	Ser	Arg	Thr
		435					440					445			
Pro	Trp	Ala	Ser	Ala	Cys	Lys	Glu	Ala	Ser	Thr	Pro	Pro	Ala	Ala	Lys
	450					455					460				
Gln	Gln	Ala	Pro	Pro	Pro	Ser	Leu	Trp	Asn	Leu	Pro	Asn	Arg	Pro	Gln
465					470					475					480
Pro	Tyr	Thr	Leu	Ala	Asp	Val	Gln	Glu	Ala	Met	Glu	Gly	Pro	Glu	Gly
			485						490					495	
Val	Leu	Arg	Val	Ala	Arg	Pro	Leu	Thr	Gly	Phe	Gly	Glu	Asp	Ala	Glu
			500					505					510		
Ser	Leu	Ser	Phe	Ala	Ser	Leu	Pro	Lys	Gly	Ala	Glu	Thr	Leu	Phe	Trp
		515					520					525			
Ser	Ser	Gly	Arg	Gly	Leu	Tyr	Phe	Leu	Arg	His	Leu	Glu	Arg	Thr	Lys
	530					535					540				
Ala	Gly	Glu	His	Asp	Val	Val	Gly	Glu	Ala	Gly	Val	Trp	Val	Ala	Ala
545					550					555					560
Ser	Glu	Glu	Glu	Phe	Gly	Gly	Phe	Ile	Ile	His	Arg	Lys	Phe	Ser	Val
				565					570					575	
Ala	Lys	Phe	Gly	Phe	Glu	Arg	Ala	Lys	Met	Leu	Ala	Cys	Arg	Trp	Tyr
		580						585					590		
Asn	Asp	Arg	Gln	Glu	Ala	Arg	Arg	Gly	Gln	His	Ala	Leu	Pro	His	Arg
		595					600					605			
Glu	Lys	Pro	Lys	Gly	Ile	Met	Ser	Ser	Asp	Arg	Pro	Leu	Ser	Arg	Glu
	610					615					620				
Ala	Ala	Pro</													

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690	695	700
Lys Tyr Gly Phe Ala Lys Ala Lys Glu Cys Ala Ile Arg Met Lys Met 705 710 715 720		
Ser Leu Val Gly Gln Pro Gly Val Ser Gln Ser Gly Arg Gln Ala Pro 725 730 735		
Phe Pro Val Arg Pro Phe Thr Ser Arg Ala Cys Ser Pro Leu Gln Asp 740 745 750		
Phe Phe Arg Glu Gly Asp Arg Arg Val Ala Ala Ser Ser Phe Ser Leu 755 760 765		
Leu Pro Ser Gly Arg Gly Glu Pro Arg Gly Ser Leu Gly Ser Ser Gln 770 775 780		
Gly Ala Asp Asp Glu Arg Ser Lys Pro Gln Ser Cys Arg Gly Leu Val 785 790 795 800		
Glu Gln Leu Leu Ala Arg Phe Gln Asp Ser Glu Gly Phe Thr Arg Gly 805 810 815		
Leu Pro Gly Asp Asp Glu Asn Arg Gly Lys Arg Leu Ser Lys Gln Ala 820 825 830		
Gln Asp Asp Phe Gln Ser Trp Arg Pro Pro Pro Gly Ala Arg Phe Gly 835 840 845		
Ser Ala Ala Gln Ala Ser Arg His Ser Thr Asp Glu Val Gly Gly Phe 850 855 860		
Ala Gly Phe Pro Gly Phe Ala Ala Ser His Cys Gly Glu Lys Pro Gly 865 870 875 880		
Gly Glu Gly Pro Ser Phe Leu Gln Lys Ser Gly Phe Val Gln Glu Asn 885 890 895		
Ala Phe Ser Pro Pro Ser Glu Arg Phe Glu Thr Gly Val His Arg Arg 900 905 910		
Val Pro Ser Leu Ser Ser Glu Leu Ala Asn Pro Gln Val Thr Glu Glu 915 920 925		
Val Glu Glu Phe Leu Phe Ser Leu Ser Thr Arg Ala Arg Gln Ser Leu 930 935 940		
Leu Ala Ser Leu Arg Arg Gly Ala Glu Asp Ser Arg Arg Ser Ala Trp 945 950 955 960		
Pro Gly Ala Ser Arg Asp Cys His Thr Gly Ala Gly Thr Pro Gly Gly 965 970 975		
Thr Asp Val Ala Asp Arg Arg Ala Thr Arg Glu Thr Arg Arg Asp Arg 980 985 990		
Glu Gly Glu Glu Ser Thr Ser Glu Asp Gly Thr Val Arg Arg Glu Thr 995 1000 1005		
Asp Ala Gly Ala Val Ser Pro Asp Glu Val Ser Arg Ala Asn Ala 1010 1015 1020		
Glu Glu Arg Ala Ala Gly Glu Lys Thr Arg Ser Ser Glu Arg Ile 1025 1030 1035		
Trp Thr Gly Glu Gly Glu Arg Ser Ala Gly Asp Arg Asp Asp Lys 1040 1045 1050		
Gly Glu Gly Glu Gly Gly Gly Val Val Glu Gly Arg Thr Glu 1055 1060 1065		
Lys Gly Gly Asp Asp Asp Lys Lys Pro Gly Glu Glu Glu Ser Ala 1070 1075 1080		
Glu Arg Glu Glu Glu Leu Lys Asn Asp Ala Tyr Ala Tyr Phe Thr 1085 1090 1095		
His Leu Thr Asn Arg Glu Trp Asp Leu Leu Asp Tyr Leu Asp Thr 1100 1105 1110		

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Leu Asp 1115	Phe Glu Thr Val Asp 1120	Leu Asp Ala Val Met 1125	Pro Phe Ile
Asn Gln 1130	Val Pro Lys Val Arg 1135	Gly Val Cys Phe Asp 1140	Arg Lys Gly
Leu Tyr 1145	Trp Ile Ser Gln Trp 1150	His Ser Gln Gln Lys 1155	Lys His Arg
Glu Trp 1160	Phe Gly Val Lys Arg 1165	Leu Gly Phe Arg Lys 1170	Ala Trp Ala
Leu Ala 1175	Val Cys Val Arg Arg 1180	Asp Ala Glu Lys Val 1185	Glu Asp Glu
Pro Val 1190	Asp Tyr Pro Lys Leu 1195	Pro Asp Tyr Glu Glu 1200	Val Leu Gly
Val Thr 1205	Tyr Ala Arg Phe Ala 1210	Ser Gly Arg Tyr Trp 1215	Val Ala His
Tyr Met 1220	Arg Pro Ala Ala Pro 1225	Ser Ser Gly Cys Leu 1230	Gly Ser Val
Gly Arg 1235	Lys Leu Phe Pro Val 1240	Ser Glu Ser Ser Phe 1245	Glu Glu Ala
Arg Ser 1250	Gln Ala Val Ala Val 1255	Ala Thr Ala Phe Pro 1260	Leu Pro Leu
Ala Phe 1265	Phe Val Asp Pro Glu 1270	Arg Arg Ala Thr Ser 1275	Ala Phe Glu
Ser Ala 1280	Arg Ala Glu Asn Leu 1285	Gln Gly Asp Lys Gln 1290	Val Leu Leu
Ser Lys 1295	Asn Cys Leu Phe Asn 1300	Val Phe Thr Trp Leu 1305	Asn Gly Gly
Ala Ser 1310	Trp Thr Asn Val Arg 1315	Arg Trp Ala His Ala 1320	Lys Arg Met
Gln Leu 1325	Ala Glu Asp Asp Trp 1330	Pro Gln Gln Phe Phe 1335	Ser Leu Pro
Ser Pro 1340	Ala Lys Gly Asp Ser 1345	Phe Ala Glu Ala Glu 1350	Lys Glu Arg
Ala Glu 1355	Glu Arg Thr Gly Gly 1360	Glu Glu Val Lys Ala 1365	Asn Ser Ala
Ser Arg 1370	Ala Ala Ala Lys Ser 1375	Glu Trp Pro Val Ala 1380	Ser Thr Thr
Ser Pro 1385	Ala Glu Asp Leu Ala 1390	Ser Ser Gly Ser Pro 1395	Arg Asp Leu
Gln Lys 1400	Leu Ser Pro Leu Leu 1405	Ala Asp Ser Ser Leu 1410	Thr Lys Glu
Leu Leu 1415	Gly Gly Asp Arg Glu 1420	Leu Gly Asn Ala Met 1425	Asp Gly Ala
Arg Gly 1430	Pro Arg Gly Leu Asp 1435	Thr Ala Lys Gly Arg 1440	Ala Lys Asp
Glu Glu 1445	Arg Leu Thr Ala Lys 1450	Asp Ala Glu Ser Arg 1455	Gln Ala Thr
Leu Pro 1460	Gly Gly Arg Ala Ala 1465	His Gly Gly Gly Val 1470	Gly Gly Ser
Leu Gly 1475	Thr Ala Cys Glu Glu 1480	Glu Leu Asp Glu Pro 1485	Leu Ser Pro
Leu Asp 1490	Ile Glu Ser Ile Val 1495	Ala Asp Ala Tyr Glu 1500	Ser Phe Ser

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Asp	Glu	Asp	Ala	Glu	Gly	Glu	Gly	Asp	Gly	Gly	Lys	Pro	Gly	Lys
1505						1510					1515			
Arg	Ile	Arg	Leu	Pro	Lys	Ile	Gly	Gly	Val	Tyr	Tyr	Lys	Arg	Asp
1520						1525					1530			
Gly	Asn	Tyr	Lys	Ala	Trp	Ala	Ala	Ser	Trp	His	Ile	Gln	Gly	Lys
1535						1540					1545			
Arg	Thr	Arg	Arg	Tyr	Phe	Thr	Val	Lys	Lys	His	Gly	Phe	Arg	Asn
1550						1555					1560			
Ala	Tyr	Leu	Lys	Ala	Val	Arg	Ala	Arg	Arg	Glu	Ala	Glu	Arg	His
1565						1570					1575			
Glu	Gly	Ile	Ser	Val	Lys	His	Arg	His	His	Ala	Leu	Val	Pro	Gly
1580						1585					1590			
His	Pro	Gly	Asn	Met	Leu	Gly	Ala	Ser	Lys	Val	Cys	Ala	Glu	Ser
1595						1600					1605			
His	Glu	Val	Ser	Gly	Phe	Pro	His	Gly	Asp	Glu	Asp	Ser	Arg	Leu
1610						1615					1620			
Thr	Arg	Gly	Gly	Ala	Ser	His	Ala	Ala	Val	Ala	Pro	Gly	Arg	Val
1625						1630					1635			
Asn	Arg	Glu	Arg	Ser	Val	Ala	Leu	Val	Asp	Arg	Ala	Thr	Lys	Asp
1640						1645					1650			
Asp	Glu	Asp	Asp	Glu	Arg	Asp	Leu	Gln	Arg	Glu	Lys	Thr	Gly	Ala
1655						1660					1665			
Gly	Gly	Gly	Glu	Ala	Cys	Ser	Gly	Glu	Ser	Val	Lys	Val	Ala	Leu
1670						1675					1680			
Gly	Thr	Arg	His	Asp	Ser	Phe	Ser	Asp	Gly	Ser	Cys	Arg	Thr	Leu
1685						1690					1695			
Asp	Lys	Leu	Ser	Thr	Gln	Phe	Glu	Gln	Lys	Pro	Arg	Gly	Gly	Ala
1700						1705					1710			
Gly	Glu	Glu	Ala	Glu	His	Pro	Thr	Arg	Lys	Gln	Gly	Gln	Glu	Thr
1715						1720					1725			
Gly	Gly	Val	Asp	Glu	Pro	Leu	Ser	Arg	Ala	Ala	Ser	Ile	Val	Gly
1730						1735					1740			
Gly	Arg	Glu	Val	Arg	Leu	Thr	Ser	Gly	Val	Ser	Val	His	Leu	Thr
1745						1750					1755			
Pro	Leu	Glu	Arg	Val	Ala	Lys	Ala	Val	Asp	Val	Asp	Leu	Lys	Glu
1760						1765					1770			
Leu	Thr	Asp	Arg	Val	Ser	Arg	Ala	Ala	Phe	Arg	Gly	Gly	Asp	Ser
1775						1780					1785			
Arg	Leu	Phe	His	Arg	Thr	Val	Asp	Asn	Cys	Glu	Gly	Glu	Ala	Asp
1790						1795					1800			
Glu	Val	Ala	Gln	Gly	Leu	Asp	Thr	His	Arg	Glu	Asp	Val	Asp	Val
1805						1810					1815			
Thr	Arg	Asn	Leu	Glu	Phe	Ala	Met	Ala	Arg	Glu	Thr	Leu	Asp	Val
1820						1825					1830			
Leu	Leu	Ser	Asp	Leu	Tyr	Ser	Val	Val	Ala	Lys	Leu	Ser	Gly	Ala
1835						1840					1845			
Gly	Arg	Trp	Thr	Ser	Leu	Val	Ser	Pro	Thr	Ala	Ala	Glu	Ala	Glu
1850						1855					1860			
Pro	Leu	Val	Ser	Ala	Trp	Asp	Arg	Ser	Ala	Arg	Glu	Glu	Arg	Arg
1865						1870					1875			
Glu	Lys	Phe	Glu	Asp	Thr	Asn	Ala	Ala	Ser	Asp	Glu	Pro	Gly	Tyr
1880						1885					1890			
Pro	Thr	Ser	Ser	Ala	Gln	Ile	His	Val	Ala	Ile	Gln	Leu	Val	Val

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1895	1900	1905
Ile Lys His Tyr Leu Ala Thr 1910	Val Arg Thr Ala Asn Arg Val Glu 1915	1920
Gln Ile Ala Pro Leu Leu Ala 1925	Leu Phe Glu Pro Cys Ile Lys Gln 1930	1935
Gly Met Leu Pro His Glu Cys 1940	Ala Leu Pro Arg Leu Arg Trp Leu 1945	1950
Val Cys Gln Leu Cys Arg Ala 1955	Ser Leu Pro Trp Leu Asp Glu Ser 1960	1965
Asp Val Leu Thr Asp Ala Leu 1970	Leu Tyr Arg His Leu Glu Glu Leu 1975	1980
Val Glu Thr Glu Glu Ala Glu 1985	Ala Pro Gln Glu Gly Val Pro Pro 1990	1995
Gly Gly Gln Ile Val Phe Ser 2000	Ala Gly Phe Ala Glu Gly Asn Ser 2005	2010
Thr Val Ala Ser Arg Asn Val 2015	Phe Thr Gly Glu Ser Arg Val Ala 2020	2025
Gly Gly Phe Arg Thr Asp Ser 2030	Glu Lys Glu Ser Gly Ile Asp Asp 2035	2040
Arg Asp Glu Ala Ser Leu Ala 2045	Ala Leu Ile Cys Leu Pro Gly Lys 2050	2055
Gly Lys Lys Leu Arg Glu Glu 2060	Ala Asp Val Glu Lys Asp Asp Thr 2065	2070
Ser Ala Ser Leu Asn Cys Glu 2075	Ser Gly Lys Lys Thr Glu Ala Glu 2080	2085
Ser Gln His Ser Arg Ser Pro 2090	Thr Glu Val Ala Ala Ser Ser Val 2095	2100
Ser Gly Ser Glu Gly Lys Asp 2105	Gly Ser Ser Asp Asn Glu Arg Ser 2110	2115
Gly Asp Ala Asp Asp Ala Thr 2120	Glu Gly Ser Glu Lys Cys Glu Lys 2125	2130
Thr Arg Gly Gly Asp Gln Arg 2135	Arg Ala Ala Pro Arg Thr Ser Ser 2140	2145
Ala Ser Thr Ala Ser Gly Glu 2150	Thr Pro Glu Lys Ser Lys Asn Arg 2155	2160
Gly Ser Asp Ala Leu Lys Gly 2165	Lys Asn Glu Gly Gly Ala Thr Gly 2170	2175
Thr Ser Gly Glu Gln Arg Asp 2180	Asp Glu Asp Arg Asp Leu Glu Asn 2185	2190
Val Glu Ile Ser Lys Asp Thr 2195	Arg Ala Gly Ser Gly Gly Arg Arg 2200	2205
Arg Thr Gly Glu Arg Arg Gly 2210	Gln Arg Phe Cys Ala Ser Gly Gly 2215	2220
Glu Leu Arg Val Ser Glu Glu 2225	Ser Pro Asp Arg Ala Lys Thr Glu 2230	2235
Lys Ser Lys Gly Glu Pro Val 2240	Arg Asp Ser Leu Ser Pro Asp Ala 2245	2250
Ser Ser Arg Leu Pro Ser Arg 2255	Cys Gly Thr Pro Pro Pro Ala Ala 2260	2265
Ala Thr Gly Ser Cys Ala Thr 2270	Val Glu Ser Asp Val Pro Ala 2275	2280

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<211> LENGTH: 3236

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 11

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Met Thr Thr Val Ser Arg Ala His Ala Ser Arg Ser Arg Arg Lys Ser
 1          5          10          15

Arg Asp Glu Asp Ser Glu Gly Ser Ser Leu Pro Ala Val Gly Ile His
      20          25          30

Glu Thr Gln Ser Pro Val Phe Ser Arg Glu Gly His Glu Gly Asp Arg
      35          40          45

Ala Ala Gln Pro Glu Asp Val Val Ala Ala Glu Ser His Ser Asn Pro
      50          55          60

Gln Trp Pro Thr Pro Leu Asp Thr Gly Phe Asp Lys Gly Ala Pro Pro
      65          70          75          80

Leu Gly Cys Ser Arg Ser Glu Glu Leu Arg Ser Pro Pro Met Ala Ser
      85          90          95

Gly Ser Phe His Gly Ser Gly Thr Gly Gly Asp Gly Gly Cys Leu Leu
      100          105          110

Ser Leu Glu Ala His Ala Val Ser Lys Asp Ser Glu Arg Gln Val Asn
      115          120          125

Ser Gly Leu Pro Gly Gly Gly Asp Glu Ile Ser Gly Arg Leu Ser Pro
      130          135          140

Ser Cys Ala Ser Leu Pro Leu Val Ala Ala Ala Leu Ser Pro Val Glu
      145          150          155          160

Asp Thr Arg Leu Glu Arg Asp Ser Ser Ile Pro Val Leu Lys Pro Ser
      165          170          175

Leu Ser Ile Pro Asn Leu Leu Val Thr Ser Pro Ser Leu Thr Ser Val
      180          185          190

Ser Tyr Val Cys Glu Ala Asp Arg Ser Ala Glu Gly Lys Ala Pro Ser
      195          200          205

Met Asp Ala Leu Pro Pro Ser His Ser Ala Ala Pro Glu Ser Gly Leu
      210          215          220

Trp Arg Glu Cys Asp Glu Arg Gly Lys Asn Ser Phe Phe Ser Ser Gly
      225          230          235          240

Leu Pro Ala His Pro Glu Gly Asn Gly Glu Arg Ala Gly Glu Gly Gln
      245          250          255

Asp Pro Arg Ser Gly Asp Phe Glu Thr Pro Glu Glu Ala Ala Phe Ser
      260          265          270

Val Gln Arg Ile Leu Gln Glu Ser Glu Glu Leu Phe Leu Leu Ser Gly
      275          280          285

Cys Ala Arg Glu Asp Arg Gly Gly Glu Ser Asp Ala Ala Phe Lys Thr
      290          295          300

Met Thr Arg Ser Glu Gly Ala Phe Ser Arg Glu Pro Ala His Arg His
      305          310          315          320

Ala Phe Ala Lys Pro Gly Asn Gly Gly Glu Ser Glu Pro Phe Met Ser
      325          330          335

Ile Asp Glu Glu Arg Ala Ala Ser Pro Ser Ala Ser Gly Pro Ser Ser
      340          345          350

Tyr Ala Phe Leu Ser Phe Glu Glu Thr Ser Ala Gly Ser Arg Arg Ser
      355          360          365

Pro Asp Ala Gln Ser Pro Pro Leu Ser Gly His Leu Ser Asp Gly Asp
      370          375          380

Arg Thr Gln Arg Lys Ala Gly Glu Arg Phe Leu Glu Asp Pro Arg Gly

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385	390	395	400
Asn Leu Lys Arg Ser Arg Ser Pro Leu Ile Ala Arg Asp Cys Asn Arg			
	405	410	415
Ser Leu Gly Thr Cys Asp Ser Ser Leu Thr Thr Arg Gly Pro Val Ala			
	420	425	430
Ser Asp Thr Ser Pro Arg Arg Gly Tyr Thr Asp Gln Trp His Ser His			
	435	440	445
Arg Lys Ala Gln Ser Pro Gly Arg Phe Arg Arg Thr Asn Thr Glu Gly			
	450	455	460
Asn Ala Thr Pro Val Asp Ser Gln Ser Ser Pro Pro Ser Lys Lys Arg			
	465	470	475
Cys Cys Leu Ala Glu Arg Phe Ala Phe Glu Arg Arg Arg Gln Pro Pro			
	485	490	495
Val Pro Leu Pro Ser Val Ala Ser Ala Val Ala Ala Ala Leu Ala Gln			
	500	505	510
Phe Pro Pro Gly Ala Cys Thr Ala Ala Val Glu Arg Ala Asp Asp Val			
	515	520	525
Pro Pro Glu Gly Ser Gly Asn Gly Val Leu Pro Gly Gly Glu Val Ser			
	530	535	540
Asp Leu Ser Leu Ser Asp Arg Lys Ser Gly Ala Ser Pro Arg Gln Thr			
	545	550	555
Leu Asp Thr Phe Leu Pro Ala Lys Gly Ala Ser Ala Ala Leu Lys Gln			
	565	570	575
Glu Gly Ser Ser Ser Glu Ile Gly Glu Gly Cys Pro Ala Ser Asp Asp			
	580	585	590
Ala Ala Val Ala Ala Thr Leu Ser Gly Trp Lys Arg Gly Arg Gly Pro			
	595	600	605
Arg Ser Gly Cys Val Ser Gly Ser Ser Arg Ala Ser Ser Leu Glu His			
	610	615	620
Ala Gly Ala Arg Arg Arg Ser Gly Val Glu Arg Lys Arg Arg Glu Lys			
	625	630	635
Arg Lys Ala Ala Leu Ala Thr Ala Ala Val Val Ser Ala Ser Val Arg			
	645	650	655
Arg Leu Ala Leu Val Ala Ala Pro Cys Leu Val Glu Asn Thr Leu Arg			
	660	665	670
Gln Trp Trp Arg Leu Gln Glu Gln Val Gly Asp Glu Leu Asp Asn Gly			
	675	680	685
Gly Val Ser Glu Glu Gln Thr Thr Gly Arg Ser Gly Arg Arg Thr Gly			
	690	695	700
Lys Asn Pro Ile Val Gly Gly Arg Val Lys Glu Gly Glu Gln Ser Val			
	705	710	715
Arg Leu Glu Ile Glu Arg Ser Gly Asp Ser Pro Arg Asn Thr Ala Lys			
	725	730	735
Thr Glu Pro Gly Asp Gln Gly Ala Ala Gln Gly Gln Gly Gly Pro Glu			
	740	745	750
Gln Ile Ala Glu Asn Glu Ser Gly Thr Glu Arg Met Glu Thr Ser Gln			
	755	760	765
Thr Lys Gln Glu Ala Gln Asp Leu Pro Leu His Arg Glu Ala Ala Ser			
	770	775	780
Ala Ser Ala Thr Pro Phe Ile Pro Glu Gly Arg Thr Gln Glu Arg Asp			
	785	790	795
Ser Tyr Leu Arg Val Thr Leu Phe Ala Ala Ser Gln Val Leu Asn Ser			
	805	810	815

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Gly Gln Phe Arg Gln Ala Ile Arg Met Phe Pro Gly Ala Asp Ser Pro
 820 825 830
 Arg Gly Asp Gln Arg Ser Arg Cys Val Val Arg Val Tyr Lys Gln Ser
 835 840 845
 Leu Arg Lys Arg Arg Leu Ser Gly Asp Arg Asn Arg Arg Val Gly Glu
 850 855 860
 Asp Gly Asn Leu Val Ser Val Ser Leu Arg Asp Leu Leu Ala Asn Ser
 865 870 875 880
 Gly Glu Asp Trp Glu Pro Ser Ser Pro Ser Ala Ala Thr Arg Pro Leu
 885 890 895
 Pro Leu Ala Pro Ser Ala Leu Ser Ala His Gln Ala Arg Ser Ser Phe
 900 905 910
 Gly Ser Phe Ser Arg Arg Ser Ala Glu Gly Val Pro Gly Pro Ser Pro
 915 920 925
 Trp Gly Gly Asp Cys Ser Pro Thr Ala Ala Arg Ser Pro Leu Pro Leu
 930 935 940
 Ser Thr Ser His Asp Leu Arg Arg Arg Arg Val Cys Pro Pro Arg Arg
 945 950 955 960
 Arg Tyr Ser Pro Ser Glu Ser Val His Ser Ser Asp Gly Arg Gly Gly
 965 970 975
 Ala Cys Ala Ile Ala Ala Lys Lys Pro Lys Gly Arg Arg Ser Arg Gly
 980 985 990
 Arg Glu Glu Gln Thr Arg Glu Glu Val Ser Glu Ser Arg Cys Ser Thr
 995 1000 1005
 Pro Arg Ser Cys Ser Ser Val Arg Tyr Ala Val Ser Asp Gly Ser
 1010 1015 1020
 Pro Ala Ser Ser Arg Ala His Leu Gly Arg Pro Asp Asp Glu Gly
 1025 1030 1035
 Asp Glu Arg Met Thr Gly Gly Gln Arg Thr Pro Arg Gly Thr Pro
 1040 1045 1050
 Gln Glu Gly Glu Asp Ser Asp Phe Leu Pro Ala Gly Met Ser Gly
 1055 1060 1065
 Leu Arg Gly Gly Thr Leu Pro Leu Asp Gln Leu Gly Glu Arg Ser
 1070 1075 1080
 Arg Ser Ala Glu Arg Trp Met Pro Ala Pro Ser Val Ala Val Val
 1085 1090 1095
 Pro Phe Ala Pro Asn Ile Leu Ala Lys Lys His Ala Glu Asp Val
 1100 1105 1110
 Glu Asn Gln Leu Asp Gly Gly Lys Met Ser Leu Asp Gly Val Gly
 1115 1120 1125
 Gln Lys Glu Cys Gly Leu Val Glu Thr Gly Asp Thr Gly Glu Gln
 1130 1135 1140
 Glu Ala Ala Val Ala Ala Ser Glu Lys Arg Arg Pro Leu Glu Ala
 1145 1150 1155
 Gln Thr Pro Gly Arg His Gly Thr Thr Val Leu Met Lys Gly Glu
 1160 1165 1170
 Gly Leu Leu Ala Gly Arg Thr Ser Glu Val Asp Gly Asp Arg Thr
 1175 1180 1185
 Gly Glu Lys Thr Thr Gln Ile Ser Pro Phe Ser Glu Ala Thr Gly
 1190 1195 1200
 Ile Cys Ile Leu Arg Arg Ser Pro Arg Arg Val Gln Ser Asn Ser
 1205 1210 1215

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Ser	Glu	Ala	Ser	Arg	Thr	Ala	Val	Arg	Ser	Thr	Glu	Gly	Leu	Glu
1220						1225					1230			
Thr	Ser	Asp	Lys	Leu	Gly	Val	Asp	Val	Gly	Thr	Thr	Asn	Lys	Glu
1235						1240					1245			
Ala	Asp	Ser	Phe	Ser	Ala	Ser	Cys	Asp	Ser	Pro	Arg	Asp	Ser	Leu
1250						1255					1260			
Glu	Arg	Asn	Val	Gly	Glu	Ile	Val	Ala	Ile	Trp	Ala	Arg	Ala	Arg
1265						1270					1275			
Asp	Ala	Lys	Gln	Gly	Gly	Arg	Ile	Arg	Arg	Arg	Val	Trp	Leu	Pro
1280						1285					1290			
Pro	Gly	Met	Ala	Thr	His	Gly	Gly	His	Glu	Gly	Asn	Glu	Gln	Asn
1295						1300					1305			
Asn	Glu	Ala	Ile	Cys	Gly	Gly	Gly	Ala	Thr	Pro	Met	Met	Lys	Thr
1310						1315					1320			
Glu	Arg	Ala	Met	Glu	Glu	Gly	Arg	Gly	Asp	Ala	Lys	Thr	His	Pro
1325						1330					1335			
Val	Gly	Gly	Thr	Tyr	Ala	Glu	Thr	Glu	Lys	Lys	Val	Val	Asp	Glu
1340						1345					1350			
Met	Lys	Ala	Trp	Trp	Ser	Lys	Leu	Thr	Cys	Ala	Ser	Val	Glu	Ala
1355						1360					1365			
Val	Pro	Val	Gln	Thr	Leu	Thr	Leu	Asp	Asp	Phe	Ala	Arg	Ala	Phe
1370						1375					1380			
Ser	Thr	Val	Ala	Asn	Arg	Ala	Val	Asp	Leu	Leu	Cys	Leu	Ala	Phe
1385						1390					1395			
Arg	Ala	Arg	Gly	Ala	Gly	Pro	Val	Phe	Arg	Pro	Val	Leu	Ser	Ser
1400						1405					1410			
Ser	Pro	Lys	Gln	Gln	Gly	Asn	Ser	Pro	Gln	Pro	Glu	Ser	Glu	Asp
1415						1420					1425			
Val	Glu	Thr	Arg	Ile	Glu	Thr	Tyr	Arg	Gln	Gln	Val	Arg	Arg	Leu
1430						1435					1440			
Tyr	Arg	Arg	Arg	Gln	Gln	Leu	His	Glu	Ala	Thr	Gly	Asn	Ser	Pro
1445						1450					1455			
Phe	Ser	Ser	Ser	Arg	Val	Gly	Gly	Ala	Leu	Gln	Arg	Arg	Ile	Gly
1460						1465					1470			
Glu	Leu	Gln	Arg	Leu	Arg	Glu	Ala	His	Gly	Arg	Val	Asp	Ile	Pro
1475						1480					1485			
Asn	Glu	Gly	Pro	Arg	Arg	Glu	Glu	Asp	Ser	Glu	Lys	Cys	Pro	Ala
1490						1495					1500			
Ser	Leu	Trp	Asp	Val	Pro	Leu	Arg	Gln	Arg	Lys	Gln	Gly	Arg	Lys
1505						1510					1515			
Arg	Val	Ser	Pro	Trp	Tyr	Ser	Val	Gly	Val	Arg	Trp	Leu	Ala	Asp
1520						1525					1530			
Phe	Ser	Ala	Phe	Glu	Tyr	Phe	Val	Val	Lys	Asn	Tyr	Arg	Lys	Glu
1535						1540					1545			
Asp	Leu	Gly	Ala	Thr	Val	Ser	Leu	Ser	Asn	Arg	Gly	Glu	Ala	Ser
1550						1555					1560			
Asp	Thr	Thr	Trp	Ser	Val	Asp	Gly	Thr	Gly	Ser	Gln	Arg	Ala	Pro
1565						1570					1575			
Val	Pro	Cys	Leu	Ser	Arg	Ala	Gly	Thr	Pro	Arg	Thr	Val	Ser	Pro
1580						1585					1590			
Ser	Pro	Pro	Ser	Ala	Asp	Ala	Met	Asn	Leu	Trp	Ala	Gln	Ala	Tyr
1595						1600					1605			
Ala	Pro	Ser	Leu	Asn	Gln	Pro	Arg	Gly	Met	Ser	Pro	Ala	Thr	Thr

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1610	1615	1620
Pro Pro Leu Ser Glu Ser Ala Thr Pro Arg Gly Asn Val Ser Pro		
1625	1630	1635
Pro Phe Ser Glu Ala Ser Ser Ser Gly Gln Arg Gly Lys Lys Val		
1640	1645	1650
Ala Pro Gly Pro Ser Ala Asp Glu Lys Lys Asp Glu Asp Tyr Gln		
1655	1660	1665
Ser Ala Gly Ser Leu Arg Trp Glu Val Asp Gly Gly Gln Arg Arg		
1670	1675	1680
Gln Val Gln Val Arg Ser Arg Leu Leu Leu His Glu Leu Leu Gln		
1685	1690	1695
Pro Pro Ser Leu Asp Ala Thr Gly Leu Arg Thr Ala Leu Val Leu		
1700	1705	1710
Ile Val Leu Arg Leu Gln Arg Phe Leu Arg Leu Lys Glu Gly Gly		
1715	1720	1725
Val Asn Asn Arg Gly Arg Gly Gln Arg Ser Glu Arg Lys Arg Arg		
1730	1735	1740
Cys Arg Ala Met Pro Pro Ile Phe Ile Phe Arg Asp Asp Ser Asn		
1745	1750	1755
Ala Phe Gln Glu Ala Leu Leu Ala Lys Lys Leu Asp Ile Arg Leu		
1760	1765	1770
Asp Ser Asp Ser Pro His Thr Asp Val Pro Ser Arg Arg Ser Leu		
1775	1780	1785
Asp Gly Glu Val Gly Asp Glu Arg Arg Arg Leu Arg Ser Val Lys		
1790	1795	1800
Pro Thr Asn Ser Asn Asp Leu Ser Asp Glu Arg Gly Pro Pro Pro		
1805	1810	1815
Pro Ser Thr Met Ser Pro His Ser Leu Gly Ser Gly Pro Cys Asp		
1820	1825	1830
Thr Gln Glu Gly Val Gln Asn Leu Gln Gln Asp Ala Ser Leu Phe		
1835	1840	1845
Ser Pro Ala Leu Ala Gln Gly Gln Ala His Ala His Thr Asp Ala		
1850	1855	1860
Val Pro Gly Ala Arg His Asp Asp Val Leu Pro Arg Ser Pro Arg		
1865	1870	1875
Phe Pro Val Val Asp Ala Gly Pro Glu Glu Thr Pro Arg Pro Glu		
1880	1885	1890
Val Glu Ser Met Leu Asp Ser Glu Ser Gly Asp Pro Thr Gly Leu		
1895	1900	1905
Gly Gln Ala Ser Arg Arg Arg Trp Arg Gly Arg Gly Ser Arg Thr		
1910	1915	1920
Ser Val Gln Arg Thr Val Ser Thr Cys Leu His Glu Asp His Ser		
1925	1930	1935
Gly Asp Lys Thr Pro Arg Glu Glu Thr Phe Gly Gly Asp Ala Ala		
1940	1945	1950
Ser Leu Leu Arg Val Ala Ser Ser Val Pro Pro Ser Thr Cys Ser		
1955	1960	1965
Ser Pro Gln Ser Ser Ser Gly Gly Arg Arg Glu Arg Gly Arg Arg		
1970	1975	1980
Gly Val Arg Gly Arg Arg Gly Arg Gly Arg Leu Ile Ser Gln Gln		
1985	1990	1995
Gly Ser Ser Leu Leu Gly Gln Thr Val Ser Ala Gly Ala Leu Ser		
2000	2005	2010

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Ser Gly 2015	Asp Thr Ala Gly 2020	Ile Ser Thr Glu Gly 2025	Glu Asn Arg
Arg Asn 2030	Ala Val Arg Pro Gly 2035	Ala Leu Glu His Ser 2040	Asp Glu Asp
Lys Glu 2045	Asp Leu Ser Ala Ser 2050	Ser Pro Pro Ser Asp 2055	Asp Gly Ile
Ser Gln 2060	Arg Ser Ser Gly Ser 2065	Gln Gly Asp Ser Ser 2070	Ser Ser Gly
Gly Pro 2075	Ser Ser Glu Ala Cys 2080	Arg Lys Thr Thr Ser 2085	His Val Ala
Ala Lys 2090	Ala Asp Ser Ala Ser 2095	Pro Arg Ala Leu His 2100	Pro Ser Ala
Arg Pro 2105	Gln Pro Arg Gly Thr 2110	Ala Ser Trp Thr Pro 2115	Gly Gly Glu
Pro Ala 2120	Val Ser Gly Val Gln 2125	His Pro Ser Ala Leu 2130	Thr Pro Ser
Pro Ser 2135	Arg Gly Arg Phe Ser 2140	Glu Asp Asn Val Ala 2145	Ser Arg Val
Ser Arg 2150	Val Ser Ser Val Gly 2155	Ala Leu Leu Arg Ser 2160	Arg Cys Val
Val Gly 2165	Glu Glu Gln Lys Glu 2170	Thr Gln Asn Ser Cys 2175	Ser Leu Trp
Val Val 2180	Glu Lys Gly Ala Leu 2185	Glu Pro Phe Trp Trp 2190	Arg Thr Ala
Ser Ala 2195	Val Gly Cys Val Ser 2200	Ala Gly Arg Arg Asp 2205	His Ser Asp
Lys Asp 2210	Ala Asn Arg Leu Phe 2215	Leu Ala Asp Lys Glu 2220	Ala Gly Thr
Gly Pro 2225	Leu Gln Asp Phe Val 2230	Leu Pro Asp Phe Ser 2235	Gly Ser Ala
Arg Glu 2240	Ile His Gly Asp Glu 2245	Arg Gly Ser Asp Ser 2250	Asp Ala Ser
Cys Lys 2255	Ser Ala Ala Leu Ser 2260	Thr Thr Ser Asp Ser 2265	Ser Gly Ile
Ser Glu 2270	Val Ser Leu Asp Leu 2275	Glu Ser Thr Val Gln 2280	Glu Val Ala
Leu Gly 2285	Thr Ile Leu Ser Ser 2290	Ala Leu Ser Ala Leu 2295	His Gly Lys
Thr Gly 2300	Asp Gly Asp Thr Gln 2305	Glu Ser Asp Ala Glu 2310	Arg Glu Ala
Asn Ala 2315	Asp Asp Gly Ser Ala 2320	Thr Gly Val Asn Glu 2325	Lys Asp Leu
Arg Gly 2330	Glu Ser Arg Pro Glu 2335	Leu Pro Ser Pro Ile 2340	Pro Gly Lys
Asp Glu 2345	Leu Gly Ser Gln Glu 2350	Glu Gly Lys Thr Ala 2355	Ser Ser Leu
Pro Ser 2360	Val Lys Ala Glu Gln 2365	Gly Gly Ser Glu Arg 2370	Gly Gly Ala
Asp Glu 2375	Ile Val Lys Lys Ala 2380	Thr Ser Val Leu Arg 2385	Ala Cys Lys
Asp Pro 2390	Asp Glu Ala Thr Ser 2395	Thr Ser Leu Val Pro 2400	Glu Gly Glu

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Asp	Glu	Asn	Asp	Ala	Cys	Gly	Ala	Leu	Glu	Pro	Asp	Ser	Leu	Val
2405						2410					2415			
Ser	Val	Ser	Ala	Leu	Gly	Glu	Ser	Ser	Glu	Glu	Leu	Phe	Thr	Glu
2420						2425					2430			
Val	Pro	Gln	Asn	Glu	Lys	Glu	Leu	Lys	Lys	Thr	Leu	Gln	His	Val
2435						2440					2445			
Asp	Pro	Arg	Leu	Cys	Gln	Gln	Met	Leu	His	Gly	Gly	Leu	Cys	Phe
2450						2455					2460			
Ile	Arg	Thr	Tyr	Val	Asp	Leu	Glu	Thr	Lys	Lys	Glu	Ser	Leu	Gln
2465						2470					2475			
Ala	Gly	Pro	Phe	Ala	Ala	Lys	Arg	Arg	Arg	Val	Ala	Gln	Leu	Leu
2480						2485					2490			
Arg	Gly	Leu	Gln	Gly	Leu	Phe	Asp	Ala	Leu	Glu	Ser	Val	Arg	Glu
2495						2500					2505			
Arg	Glu	Gly	Asp	Asp	Leu	Ser	Gly	Glu	His	Glu	Gly	Asp	Ser	Ala
2510						2515					2520			
Ser	Gly	Gly	Leu	Phe	Thr	Ala	Glu	Gln	Glu	Lys	Glu	Gly	Ala	Asp
2525						2530					2535			
Lys	Val	Ser	Gly	Asp	Arg	Glu	Asn	Ala	Gly	Glu	Arg	Gly	Gln	Lys
2540						2545					2550			
Thr	Ala	Ala	Glu	Thr	Gly	Asp	Gln	Lys	Ala	Ser	Ile	Glu	Asp	Ala
2555						2560					2565			
Val	Ala	Ala	Ala	Phe	Cys	Arg	Arg	Val	Gly	Ala	Ala	Ile	Ala	Thr
2570						2575					2580			
Glu	Thr	Cys	Gly	Ser	Ile	Gln	Thr	Val	Phe	Pro	Glu	Ile	Gly	Glu
2585						2590					2595			
Ala	Tyr	Asp	Val	Glu	Asp	Ser	Val	Ala	Arg	Leu	Gly	Ala	Pro	Pro
2600						2605					2610			
Arg	Ala	Pro	Val	Arg	Thr	Arg	Arg	Glu	Cys	Thr	Gly	Thr	Gly	Phe
2615						2620					2625			
Thr	Ser	Thr	Ala	Ala	Leu	Pro	Glu	Pro	Arg	Gly	Glu	Asp	Gly	Arg
2630						2635					2640			
Lys	Gln	Glu	Thr	Ser	Glu	Pro	Leu	Gly	Val	Glu	Ala	Ala	Asp	Lys
2645						2650					2655			
Thr	Asp	Ile	Gln	Gly	Glu	Tyr	Ala	Gln	Glu	Ser	Glu	His	Thr	Trp
2660						2665					2670			
Thr	Gln	Glu	Met	Gly	Arg	Lys	Ala	Ser	Leu	Phe	Leu	Ser	Gly	Thr
2675						2680					2685			
Leu	Glu	Leu	Ala	Gln	Leu	Lys	Glu	Glu	Gln	Gln	Val	Glu	Glu	Leu
2690						2695					2700			
Gln	Gly	Glu	Gly	Asp	Pro	Leu	Thr	Ser	Phe	Leu	Leu	Pro	Ser	Asp
2705						2710					2715			
Gln	Ser	Asp	Ser	Thr	Lys	Lys	Ala	Asn	Glu	Glu	Cys	Met	Gly	Gly
2720						2725					2730			
Arg	Thr	Ala	Arg	Glu	Leu	Tyr	Ala	Glu	Arg	Glu	Glu	Asp	Val	Lys
2735						2740					2745			
Thr	Leu	Gly	Arg	Arg	Arg	Glu	Ala	Gln	Thr	Glu	Ser	Arg	Ala	Arg
2750						2755					2760			
Gly	Pro	His	Val	Asp	Ser	Ser	Ala	Glu	Ala	Ala	Ser	Val	Ala	Gln
2765						2770					2775			
Gly	Asp	Glu	Gly	Gly	Glu	Glu	Ala	Arg	Lys	Arg	Lys	Lys	Asp	Glu
2780						2785					2790			
Lys	Arg	Glu	Lys	Arg	Ser	Gly	Asn	Ala	Phe	Leu	Asp	Ala	Leu	Leu

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2795	2800	2805
Glu Pro Ala Leu Arg Glu Asp Val Gly Arg Ala Phe Leu Thr Asp 2810 2815 2820		
Phe Gly Ser Gln Ala Pro Gln Asn Ser Thr Asp Ala Gly Lys Pro 2825 2830 2835		
Ile Phe Leu Ser Pro Cys Val Phe Gly Val Arg Gly Gly Ala Arg 2840 2845 2850		
Trp Lys Lys Leu Gly Leu Phe Asn Asp Glu Ala Gln Arg Glu Gly 2855 2860 2865		
Thr Glu Ser Ser Pro Trp Arg Asn Asp Cys Ser Asp Pro Met Ser 2870 2875 2880		
Tyr Arg Ala Asp Ala Pro His Thr Trp Arg Arg His Glu Gly Leu 2885 2890 2895		
Leu Trp Gly Gly Ser Arg His Ala Ala Ser Ala Leu Arg His His 2900 2905 2910		
Gly Arg Lys Ser Pro Ala Phe Leu Ser Pro Gln Trp Glu Asp Asp 2915 2920 2925		
Glu Arg Leu Ser Leu Ser Ser Ser Ala Asp Glu Arg Gly Tyr Thr 2930 2935 2940		
Ser Ser Gly Ser Glu Arg Phe Leu Ser Ile Pro Thr Arg Arg Lys 2945 2950 2955		
Tyr Gly Leu Arg Phe Gln Arg Arg Ser Thr Lys Thr Gly Arg Ala 2960 2965 2970		
Pro Ser Pro Thr Ala Gly Arg Ser Ser Val Asn Arg Ser Gly Trp 2975 2980 2985		
Arg Glu Thr Leu Arg Pro Ser Ser Gly Phe Ser Gly Glu Glu Thr 2990 2995 3000		
Pro Arg Ser Leu Ser Ser Arg Arg Arg Arg Gly Gly Leu Gly Gly 3005 3010 3015		
Ser Ser Pro Thr Ala Phe Arg Pro Pro Met Thr Arg Ala Ala Thr 3020 3025 3030		
Gly Lys Ala Ala Ala Cys Val Arg His Gly Asp Gly Asp Glu Cys 3035 3040 3045		
Ala Glu Pro Asp Ser Gln Phe Gly Ala Phe Gly Ser Ala Asp Leu 3050 3055 3060		
Gly Leu Ser Asp Arg Arg Gly Glu Ala Gly Glu Ala Asp Thr Arg 3065 3070 3075		
Glu Glu Lys Ala Gly Gly Ser Ala Arg His Gly Lys Arg Gly Ser 3080 3085 3090		
Gly Val Arg Ser Gly Gly Ala Arg Glu Ala Gly Ser Asp Ala Gly 3095 3100 3105		
Thr Asp Thr Leu Trp Val Ala Pro Gly Ser Gly Pro Asn Thr Cys 3110 3115 3120		
Arg Ser Gly Arg Lys Ser Pro Ala Ala Ala Ala Leu Ser Ser Leu 3125 3130 3135		
Pro Thr Gly Val Tyr Phe Asp Ala Ser Arg Lys Leu Trp Arg Cys 3140 3145 3150		
Gln Trp Arg Glu Asn Gly Arg Phe Lys Thr Lys Gly Phe Ser Leu 3155 3160 3165		
Asn Val Tyr Lys Thr Leu Lys Glu Ala Arg Arg Ala Cys Val Val 3170 3175 3180		
Tyr Arg Cys Leu Met Gly Gly Trp Glu Val Asp Pro Arg Trp Leu 3185 3190 3195		

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Gly Pro Asp Asp Asp Glu Gln Asp Asn Ser Gly Gly Ala Asp Glu
3200 3205 3210

Val Gly Arg Pro Val Pro Ser Asp Gly Ile Ser Asp Val Val Gly
3215 3220 3225

Glu Ala Arg Arg Lys Gly Glu Tyr
3230 3235

<210> SEQ ID NO 12

<211> LENGTH: 1670

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 12

Met Ile Asn Leu His Gln Leu Phe Arg Val Phe Ser Arg Val Ser Ser
1 5 10 15

Ser Ala Ser Asp Pro Ser Ala Ser Asn Pro Ser Pro Ala Ser Leu Val
20 25 30

Ser Val Pro Ala Leu Gln Thr Leu Ser Phe Pro Ala Leu Gln Gln Gln
35 40 45

Asp Leu Leu Ala Ser Leu Ala Ala Ala Ser Leu Pro Gly Pro Asp Ser
50 55 60

Val Thr Met Ser Ser Ser Pro Thr Ser Val Leu Asn Ser Ser Phe Cys
65 70 75 80

Ser Leu Pro Ser Ser Arg Lys Pro Ala Ala Leu Pro Phe Pro Ala Thr
85 90 95

Ser Pro Lys Thr Pro His Leu Ser Asp Ser Phe Pro Ala Ser Ala Ile
100 105 110

Ser Gly Pro Ser Ser Pro Gly Leu Gln Glu Leu Leu Ala Ser Pro Glu
115 120 125

Leu Ala Ala Ala Ala Leu Ala Ser Leu Gln Lys Gln Gln Leu Arg Leu
130 135 140

Ala Leu Gly Thr Glu Arg Gly Gly Cys Gly Ala Arg Gly Asp Glu His
145 150 155 160

Leu His Ser Ile Leu Leu Gln His Lys Ala Thr Ser Glu Asn Ala Met
165 170 175

Arg Trp Ser Trp His Ala Gly Arg Asp Gly Ala Gln Glu Leu Asp Thr
180 185 190

Val Pro Glu Thr Phe Asp Leu Pro Leu Ser Leu Ser Ser Phe Leu Gly
195 200 205

Val Ala Pro Gln Gln Pro Ser Ser Leu Pro Arg Ser Ser Leu Leu Pro
210 215 220

Pro Thr Asp Phe Ser Leu Thr Asp Gly Thr Leu Arg Val Ser Ser Ser
225 230 235 240

Met Leu Pro Ala Leu Ala Thr Gly Ser Glu Ser Gly Ser Ser Arg Gly
245 250 255

Leu Asn Ser Ala Gln Ala Ser Pro Ser Phe Ser Ser Leu Arg Gly Pro
260 265 270

Pro Val Ser Val Pro Glu Glu Glu Val Ser Gly Ser Leu Glu Gly Ser
275 280 285

Pro Gly Pro Phe Ser Ser Gly His Pro Pro Ala Ala Pro Ser His Pro
290 295 300

Cys Ser Thr Val Ser Gly Ala Asp Thr Gln Glu Ala Glu Pro Pro Leu
305 310 315 320

Leu Thr Leu Val Ala Val Asn Thr Pro Asp Ala Gln Asp Pro Ala Val

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325								330					335				
Asp	Gly	Ala	Ser	Leu	Cys	Ala	Ser	Lys	Glu	Gly	Met	Arg	Thr	Ser	Ser		
			340					345					350				
Ala	Asp	Leu	Gly	Asp	Ser	Leu	Leu	Ala	Pro	Pro	Gly	His	Gly	Ser	Ala		
		355					360					365					
Ala	Pro	Leu	Pro	Gly	Arg	His	Leu	Gly	Ser	Asp	Ala	Thr	Arg	Thr	Thr		
	370					375					380						
Thr	Thr	Thr	Gly	Ser	Gly	Ala	Pro	Glu	Ser	Pro	Ser	Leu	Pro	Leu	Ala		
385					390					395					400		
Arg	Gly	Asp	Cys	Glu	Gly	Ala	Glu	Arg	Gly	Leu	Ala	Leu	Leu	Glu	Ala		
			405						410					415			
Pro	Val	Asn	Gly	Phe	Asn	Leu	Ala	Ala	Ser	Gln	Ser	Val	Leu	Gly	Gly		
		420						425					430				
Phe	Ala	Ala	Asp	Thr	Arg	Gly	Glu	Ala	Gly	Glu	Lys	Gly	Ile	Ala	Pro		
	435						440					445					
Gln	Ser	Arg	Lys	Ala	Arg	Lys	Pro	Gly	Thr	Ala	Val	Glu	Thr	Ala	Gly		
	450					455					460						
Ala	Pro	Glu	Ala	Val	Arg	Arg	Gly	Arg	Ala	Ala	Cys	Asn	Gly	Glu	Ala		
	465				470					475					480		
Glu	Thr	Thr	Gly	Leu	Glu	Thr	Ala	Pro	Gln	Gln	Val	Ser	Thr	Ser	Glu		
			485						490					495			
Glu	Thr	Ala	Lys	Ser	Gly	Arg	Glu	Leu	Ala	Cys	Ala	Arg	Ala	Gly	Met		
		500					505						510				
Asp	Glu	Glu	Glu	Asp	Ala	Ala	Phe	Pro	Ser	His	Val	Val	Ser	Glu	Phe		
	515						520					525					
Arg	Gly	Pro	Pro	Glu	Ile	Ser	Asn	Val	Phe	Asn	Asp	Leu	Asp	Cys	Ser		
	530					535					540						
Ser	Ala	Val	Glu	Arg	Pro	Gln	Gly	Cys	Leu	Gln	His	Ala	Ala	Val	Gln		
545					550					555					560		
Pro	Phe	Leu	Pro	Ala	Val	Ala	Pro	Glu	Val	Arg	Pro	Ser	Ala	Thr	Thr		
		565						570						575			
Ala	Gly	Arg	Thr	Pro	Met	Gly	Leu	Trp	Ser	Glu	Ala	Gly	Arg	Val	Ser		
		580					585						590				
Ser	Leu	Glu	Thr	Asp	Thr	Ala	Glu	Ile	Gly	Arg	Arg	Leu	Asp	Gly	Glu		
	595					600						605					
Ser	Ser	Gly	Ser	Pro	Asp	Arg	Trp	Gly	Asp	Ala	Arg	Leu	Ser	Ser	Pro		
	610					615				620							
Asp	Ser	Val	Pro	Ser	Ser	Ala	Asp	Val	Pro	Val	Pro	Ser	Arg	Pro	Gln		
625					630					635					640		
Cys	Gln	Glu	Gln	Val	Pro	Gln	Val	Asp	Pro	Asp	Ser	Ser	His	Pro	Leu		
		645						650						655			
Phe	Ala	Ser	Cys	Ser	Ala	Gly	Ser	Ser	Ser	Thr	Ala	Gly	Ser	Ala	Ser		
		660					665						670				
Ala	Leu	Ala	Gly	Leu	Ala	Ser	Pro	Phe	Pro	Pro	Pro	Lys	Ser	Pro	Lys		
	675						680					685					
Thr	Gly	Ala	Asn	Asp	Pro	Arg	Met	Thr	Pro	Ser	Glu	Gly	Glu	Met	Arg		
	690					695					700						
Ala	Val	Ser	Gly	Ala	Pro	Pro	Ser	Leu	His	Met	Ser	Pro	Pro	Ile	Pro		
705					710					715					720		
Pro	Leu	Ala	Leu	Gln	Asp	Ser	Phe	Gly	Glu	Cys	Thr	Ala	Ser	Ser	Leu		
		725						730						735			
Ala	Gly	Val	Asp	Ala	Pro	Glu	Ala	Thr	Ala	Gly	Gly	Leu	Ala	Glu	Gly		
		740					745					750					

Val	Ala	Thr	Gly	Gly	Gly	Ser	Asp	Ser	Val	Gly	Glu	Gly	Arg	Leu	Pro	
	755						760					765				
Gly	Ala	Ala	Ser	Leu	Glu	Val	Pro	Ser	Ser	Pro	Ser	Ala	Leu	Leu	Ser	
	770					775					780					
Gly	Ala	Pro	Ala	Ser	Leu	Leu	Leu	Leu	Leu	Arg	Asn	Gly	Gln	Ser	Gly	
	785				790					795					800	
Ala	Ala	Ala	Leu	Val	Ala	Ala	Met	Gln	Gln	His	Gln	Ala	Leu	Ser	Gly	
			805						810					815		
Asp	Ala	Glu	Glu	Ala	Leu	Glu	Ala	Val	Leu	Ala	Gly	Gly	Ser	Asn	Val	
			820					825					830			
Gly	Asp	Met	Ala	Asn	Ser	Ser	Arg	Gly	Leu	Glu	Thr	Val	Gly	Asp	Gly	
	835						840					845				
Thr	Arg	Gly	Ser	Ala	His	Thr	Thr	His	Ala	Ala	His	Ser	Ser	Gly	Arg	
	850					855					860					
Asn	Ala	Val	Gly	Ala	Cys	Pro	Ala	Pro	Asp	Arg	Glu	Gly	Glu	Thr	Val	
	865				870					875					880	
Ala	Val	Pro	Thr	Ser	Val	Leu	Thr	Asn	Asn	Pro	Ala	Ser	Thr	Ser	Lys	
			885						890					895		
Thr	Met	Pro	Ser	Val	Tyr	Ser	Thr	Pro	Ala	Ser	Ala	Gly	Leu	Ser	Leu	
			900					905					910			
Thr	Ser	Ser	Ser	Thr	Pro	Pro	Val	Leu	Pro	Thr	Pro	Asn	Pro	Gly	Ala	
	915						920					925				
Gly	Met	Pro	Pro	Leu	Ala	Ser	Ala	His	Ala	Ala	Ser	Pro	Ala	Val	Pro	
	930					935					940					
Gly	Asp	Ala	Asn	Leu	Gln	Ser	Leu	Phe	Phe	Trp	Ala	Pro	Gln	Ala	Cys	
	945				950					955					960	
Pro	Leu	Gln	Pro	Gly	Ala	Leu	Ala	Val	Asp	Ala	Ser	Ala	Ser	Ser	Cys	
			965						970					975		
Gly	Gly	Val	Gly	Ser	Cys	Asn	Gly	Gly	Pro	Ala	Pro	Pro	Gly	Pro	Ser	
			980					985					990			
Pro	Val	Ala	Glu	Leu	Leu	Asp	Ala	Ser	Gly	Ser	Gly	Pro	Phe	Gly	Ala	
	995					1000						1005				
Ala	Gly	Ser	Gly	Ala	Gln	Leu	Ala	Ala	Gly	Pro	Phe	Gly	Ala	Ala		
	1010					1015					1020					
Thr	Pro	Ala	Ser	Ala	Thr	Phe	Gln	Gln	Gln	Leu	Leu	Leu	Leu	Ser		
	1025					1030					1035					
Ala	Ala	Phe	Asp	Gln	Ile	Gly	Ser	Ser	Ser	Phe	Pro	Val	Val	Gly		
	1040					1045					1050					
Gly	Glu	Asn	Phe	Ile	Gly	Tyr	Ser	Ala	Leu	Ser	Ala	Ala	Arg	Pro		
	1055				1060						1065					
Asp	Ala	Ser	Asp	Leu	Ser	Ala	Ser	Gly	Gly	Pro	Pro	Ala	Ser	Leu		
	1070					1075					1080					
Pro	Val</															

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Pro	Glu	Glu	Asn	Thr	Gln	Gly	Pro	Gly	Arg	Ser	Ala	Ala	Val	Val
1160						1165					1170			
Gly	Arg	Ala	Thr	Lys	Lys	Gln	Arg	Arg	Gly	Pro	Pro	His	Ser	Gly
1175						1180					1185			
Ala	Ala	Val	Ser	Ser	Gly	Ala	Pro	Ser	Gly	Val	Leu	Ala	Val	Pro
1190						1195					1200			
Gly	Cys	Leu	Gly	Pro	Pro	Ser	Val	Ala	Lys	Gly	Pro	Gly	Ser	Asp
1205						1210					1215			
Glu	Phe	Asn	Leu	Gln	Gln	Leu	Gln	Gln	Ser	Arg	Asp	Ser	Arg	His
1220						1225					1230			
Ser	Ala	Asp	Asn	Ala	Ser	Gly	Ile	Pro	Asn	Trp	Pro	Pro	Val	Phe
1235						1240					1245			
Ser	Asn	Gly	Asn	His	Thr	Leu	Gly	Val	Gly	Thr	Arg	Ser	Pro	Ser
1250						1255					1260			
Pro	Ser	Val	Cys	Ser	Ile	Ser	His	Asp	Ala	Gly	Phe	Phe	Gly	Ala
1265						1270					1275			
Ser	Gly	Ser	Asn	His	Ala	Gly	Ser	Leu	Ser	Thr	Pro	Val	Cys	Leu
1280						1285					1290			
Pro	Gln	Leu	Pro	Gly	Ala	Ala	Ser	Ala	Ser	Glu	Gly	Pro	Cys	Glu
1295						1300					1305			
Ala	Gln	Gln	Thr	Pro	Pro	Gly	Ser	Ile	Pro	Glu	Ala	Thr	Thr	Leu
1310						1315					1320			
Gly	Gly	Leu	Ser	Ala	Ala	Ser	Gly	Asn	Pro	Asn	Ser	Thr	Phe	Ser
1325						1330					1335			
Val	Ser	Ala	Gly	Gly	Gly	Val	Ala	Pro	Ala	Ile	Leu	Asn	Leu	Ser
1340						1345					1350			
Ser	Ala	Ser	Arg	Thr	Ser	Ser	Gln	Thr	Ser	Pro	Cys	Cys	Pro	Thr
1355						1360					1365			
Ala	Pro	Gly	Ser	Leu	Leu	Ser	Gly	Gly	Ser	Gly	Pro	Ala	Leu	Phe
1370						1375					1380			
Phe	Ala	Gly	Pro	Pro	Ser	Pro	Leu	Gln	Lys	Ala	Pro	Val	Tyr	Ala
1385						1390					1395			
Gly	Gly	Ser	Gly	Ser	Val	Cys	Ala	Ser	Ser	Gly	Asp	Ala	Ile	Ala
1400						1405					1410			
Ala	Ala	Ala	Leu	Leu	His	Leu	Arg	Thr	Leu	Gln	Gln	Leu	Gln	Glu
1415						1420					1425			
Leu	Gln	Arg	His	Phe	Gln	Arg	Pro	Gly	Ser	Leu	Pro	Pro	Ala	Val
1430						1435					1440			
Thr	Pro	Ala	Cys	Leu	Pro	Ser	Gly	Val	Ala	Gly	Cys	Ser	Pro	Ala
1445						1450					1455			
Gly	Leu	Gly	Ala	Ser	Thr	Pro	Gly	Thr	His	Ser	Val	Val	Cys	Asn
1460						1465					1470			
Ser	Ser	Ala	Ser	Pro	Val	Pro	Gly	Ala	Ser	Arg	Val	Pro	Arg	Arg
1475						1480					1485			
Pro	Asp	Gly	Arg	Gly	Thr	Gly	Gly	Ala	Gly	Gly	Asp	Pro	Gly	Pro
1490						1495					1500			
Ser	Lys	Arg	Gly	Ser	Val	Ser	Val	Ser	Pro	Ser	Ala	Gln	Gln	Phe
1505						1510					1515			
Val	Leu	Leu	Gln	Leu	Lys	Gln	Gln	Gln	Pro	Gly	Ser	His	Gly	Asn
1520						1525					1530			
Ala	Leu	Ser	Leu	Gly	Thr	Gln	Gly	Asn	Ser	Ser	Asn	Pro	Ala	Pro
1535						1540					1545			
Ala	Gly	Gly	Ala	Gly	Ala	Pro	Gln	Gln	His	His	Pro	Gly	Val	Cys

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1550	1555	1560
Tyr Ser Pro Pro Lys Asp Val Trp Arg Ala Arg Ile Thr Val Asp		
1565	1570	1575
Gly Arg Gln His Glu Gln Gln Phe Ser Val Lys Arg His Gly Phe		
1580	1585	1590
Glu Glu Ala Arg Leu Leu Ala Val Gln Trp Arg Ala His Met Glu		
1595	1600	1605
Asn Leu Arg Leu Gly Gly Ala Ala Lys Gly Lys Gly Asn Ala Ser		
1610	1615	1620
Ala Ser Ser Ala Ser Ala Ala Thr Ala Thr Ser Gln Gly Ser Ser		
1625	1630	1635
Gln Ser Ser His Gln Pro Pro Leu Gly Ser Leu Met Val Ser Gly		
1640	1645	1650
Asn Ser Gly Met Ser Gly Pro Gly Ala Gly Pro Leu Ala Asn Arg		
1655	1660	1665
Gly Leu		
1670		

<210> SEQ ID NO 13

<211> LENGTH: 2330

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 13

Met Ser Asp Tyr Ala Pro Ser Arg Phe Ala Ser Pro Pro Gly Asn Ala		
1	5	10
His Pro Lys Ser Pro Leu Phe Ala Arg Pro His Ser Cys Arg Glu Met		
20	25	30
Glu Thr Arg Ala Ser Val Gly Thr Ser Arg Gly Ser Arg Gln Pro Leu		
35	40	45
Cys Leu Arg Gly Ser Pro His Gly Cys Leu Ser Pro Gln Lys Gly Gln		
50	55	60
Asp Arg Leu Pro Ser Phe Ser Pro Leu Arg Thr Gln Pro Thr Leu Leu		
65	70	75
Ser Pro Pro Phe Pro Ser Lys Gly Cys Phe Ser Ser Cys Leu Pro Ser		
85	90	95
Ser Gln Ala Phe Thr Ser His Arg Ala Arg Gly Pro Ser Pro Glu Val		
100	105	110
His Ala Val Ser Ala Asp Ala Ser Thr Ser Ser Ser Pro Ile Ser Pro		
115	120	125
Ala Ser Arg Ser Ala Ser Glu Gln Gln Pro Arg Arg Glu Met Cys Ser		
130	135	140
Pro Pro Gly Ala Ser Ser Asp Ser Thr Ser Pro Thr Gly Ser Ser Ser		
145	150	155
Cys Ser Ala Glu Gln Asp Asp Val Leu Cys Phe Arg Gln Arg Phe His		
165	170	175
Leu Pro Pro Leu Leu His Leu Ser Thr Ser Arg Lys Arg Leu Arg Glu		
180	185	190
Glu Asp Ala Ser Ala Ser Ala Cys Ile Ser Ser Leu Gly Asn Leu Pro		
195	200	205
Leu Asp Val Asp Thr Lys Arg Arg Arg Gln Glu Tyr Asp Arg Leu Ser		
210	215	220
Thr Ala Ser Leu Ser Ser Phe Arg Ser Pro Lys Thr Pro Arg Leu Pro		
225	230	235
		240

Ser 300	Cys 301	Leu 302	Ala 303	Arg 245	Arg 304	Asp 305	Pro 306	Glu 250	Glu 250	Ser 307	His 308	Ala 309	Asp 254	Leu 255	Ser 310
Glu 260	Ser 261	Arg 262	Thr 260	Phe 261	Leu 262	Gln 263	Arg 264	Leu 265	Glu 266	Ala 267	Ala 268	Gly 269	Gln 270	Ser 271	Arg 272
Lys 273	Gly 274	Asp 275	Thr 276	Ser 277	Arg 278	Glu 279	Thr 280	Ile 281	Glu 282	Ala 283	Asp 284	Glu 285	Lys 286	Lys 287	Val 288
Leu 290	Ser 291	Thr 292	His 293	Ser 294	Thr 295	Asp 296	Thr 297	Ser 298	Val 299	Gln 300	Arg 301	Ser 302	Pro 303	Ser 304	Glu 305
Ser 305	Ala 306	Glu 307	Arg 308	Arg 309	Ser 310	Phe 311	Gly 312	Lys 313	Arg 314	Ser 315	Asp 316	Pro 317	Asn 318	Asn 319	Gly 320
Leu 321	Pro 322	Met 323	Ala 324	His 325	Ser 326	Pro 327	Thr 328	Pro 329	Phe 330	Thr 331	Ser 332	Lys 333	Arg 334	Thr 335	Asp 336
Leu 337	Gly 338	His 339	Ala 340	Leu 341	Asp 342	Asn 343	Ala 344	Leu 345	Ser 346	Met 347	Arg 348	Ala 349	Ala 350	Ser 351	Arg 352
Cys 353	Gly 354	Phe 355	Pro 356	Gly 357	Pro 358	Ala 359	Glu 360	Ala 361	Thr 362	Val 363	Ala 364	Pro 365	Ala 366	Ala 367	Ser 368
Gly 369	Ala 370	Ser 371	Arg 372	Thr 373	Ala 374	Ser 375	Pro 376	Leu 377	Pro 378	Phe 379	Thr 380	Val 381	Pro 382	Val 383	Val 384
Leu 385	Ala 386	Ala 387	Ser 388	Pro 389	Pro 390	Thr 391	Met 392	Pro 393	Ser 394	Ala 395	Cys 396	Ser 397	Pro 398	Asp 399	Leu 400
Cys 401	Arg 402	Ala 403	Ser 404	Thr 405	Ser 406	Pro 407	Leu 408	Ser 409	Cys 410	Ala 411	Gly 412	Val 413	Ser 414	Ser 415	Leu 416
Asp 417	Ala 418	Pro 419	Gln 420	Ala 421	Val 422	Gly 423	Arg 424	Arg 425	Ser 426	Glu 427	Val 428	Ala 429	Ala 430	Cys 431	Val 432
Ser 433	Pro 434	Ala 435	Ala 436	Ser 437	Glu 438	Glu 439	Thr 440	Val 441	Gly 442	Asp 443	Thr 444	Arg 445	Glu 446	His 447	Ala 448
Asp 449	Leu 450	Ser 451	Ser 452	Pro 453	Val 454	Ala 455	Trp 456	Pro 457	Val 458	Ala 459	Cys 460	Leu 461	Ala 462	Ser 463	Ser 464
Pro 465	Gly 466	Val 467	Ala 468	Lys 469	Lys 470	Pro 471	Leu 472	Asp 473	Leu 474	Gln 475	Ile 476	Asp 477	Pro 478	Glu 479	Gln 480
Pro 481	Arg 482	Gly 483	Asn 484	Asp 485	Lys 486	Leu 487	Val 488	Glu 489	Pro 490	Glu 491	Phe 492	Pro 493	Gly 494	Gly 495	Thr 496
Ala 497	Ala 498	Val 499	Ser 500	Glu 501	Ser 502	Ala 503	Pro 504	Val 505	Ala 506	Gly 507	Ala 508	Asp 509	Ala 510	Pro 511	Arg 512
Leu 513	Cys 514	Asp 515	Tyr 516	Gly 517	Leu 518	Ser 519	Glu 520	Ala 521	Gly 522	Val 523	Leu 524	Pro 525	Ala 526	Ser 527	Gly 528
Pro 529	Trp 530	Leu 531	Arg 532	Lys 533	Pro 534	Asn 535	Pro 536	Met 537	Leu 538	Thr 539	Pro 540	Asp 541	Thr 542	Glu 543	Trp 544
Ala 545	Ala 546	Pro 547	Ser 548	Ser 549	Gln 550	Glu 551	Asp 552	Arg 553	Ala 554	Cys 555	Thr 556	Gln 557	Lys 558	Glu 559	Thr 560
Ser 561	Ala 562	Ala 563	Arg 564	Leu 565	Ala 566	Pro 567	Asn 568	Leu 569	Leu 570	Tyr 571	Arg 572	Gln 573	Ala 574	Asp 575	Ala 576
Ala 577	Ala 578	Asp 579	Asn 580	Val 581	Thr 582	Lys 583	Gly 584	His 585	Glu 586	Asp 587	Asp 588	Ser 589	Gln 590	Phe 591	Pro 592
Leu 593	Arg 594	Ser 595	Gly 596	Ser 597	Phe 598	Thr 599	Ser 600	Ser 601	Ala 602	Val 603	Ala 604	Cys 605	Pro 606	Ser 607	Pro 608
Pro 609	Asp 610	Val 611	Gln 612	Ala 613	Asp 614	Ser 615	Glu 616	Ala 617	Ala 618	Cys 619	Thr 620	Trp 621	Gly 622	Thr 623	Pro 624
Gly 625	Asn 626	Gly 627	Asp												

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660	665	670
Pro Ser Met Arg Pro Val His Phe Gly Gly Phe Glu Ala Trp Gly Gly		
675	680	685
Asn Ser Glu Ala Ser Gln Gly Asp Ala Gln Gly Leu Gln Phe Pro Arg		
690	695	700
Val Glu Arg Phe Ser Ser Arg Arg Thr Glu His Gly Ser Glu Gly Gly		
705	710	715
Phe Cys Gly Gln Leu Ala Gly Glu Leu Leu Pro Thr Ser Thr Ser Gly		
725	730	735
Gln Pro His Ser Gln His Val Ala Asp Leu Glu Ser His Thr Gly Ala		
740	745	750
Val Phe Ala Ser Cys Asp Pro Ala Met His Ala His Ala Ser Leu Tyr		
755	760	765
Gly Tyr Pro Gly Ala Phe Tyr Asn Ser Phe Gly Thr Ala Ser Ser Ile		
770	775	780
Phe Asp Leu Thr Gln Pro Pro Gln Ala Phe Leu Tyr Gly Gly Thr Tyr		
785	790	795
Gly Asn Asn Gly Pro Asp Asp Tyr Cys Val His Arg Thr Asn Ser Thr		
805	810	815
Ser Cys Gln Gly Phe Thr Ala Pro Asp Asn Ile Ser Thr Gly Thr Leu		
820	825	830
Asn Thr Ala Asp Ala Gln Gln Glu Trp Thr Thr Pro Ala Pro Val Ser		
835	840	845
Asp Ala Ala Val Gly His Trp Glu Thr Ser Asp Phe Gly Pro Gln His		
850	855	860
Leu Asn Gly Arg Ala Ser Ser Ser Val Pro Asp His Gly Gly Gly Leu		
865	870	875
Pro Phe Gly Gly Asn Gly Asn Ser Trp Gly Thr Ser Gly Asn Gly Asp		
885	890	895
Ala Trp Gly Thr Pro Gly Asn Gly Asp Thr Cys Glu Ser Thr Gly Gly		
900	905	910
Trp Arg Gly Thr Thr Asn Val Glu Gly His Thr Cys Leu Thr Gly Glu		
915	920	925
Asp Gly Ser Arg Tyr Gly Leu Gln Ala Pro Leu Ser Gln Asp Ser Pro		
930	935	940
Tyr Gln Pro Pro Leu Pro Pro Met Gln Pro Val His Phe Ala Asn Phe		
945	950	955
Tyr Ser Ala Cys Phe Pro Pro Leu Pro Pro Pro Val Phe Pro Gly		
965	970	975
Ile Gly Cys Val Ser Ala Ser Tyr Pro Asp Ile Leu Leu Pro Gln Ala		
980	985	990
Arg Phe Leu Ser Gln Ser Cys Pro Gly Pro Pro Ser Val Leu Arg Cys		
995	1000	1005
Pro Pro Pro Ala Ala Leu Leu Arg Gly Ser Ser Pro Leu Asp Cys		
1010	1015	1020
Trp Ser Leu Pro Ala Leu Pro Ser Leu Pro Arg Ile Pro Ser Asp		
1025	1030	1035
Phe Ala Ser Asp Pro Ala Ser Val Pro Leu Pro Ala Ala Val Gln		
1040	1045	1050
Asn Leu Pro Glu Asp Ser Pro Arg Leu Arg Leu Pro Cys Gln Gly		
1055	1060	1065
Ala Ser Thr Arg Asp Gln Ser Pro Leu Gln Tyr Glu Gly Asn Phe		
1070	1075	1080

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Gly Gly	Ser Asp	Glu Val	Leu	Arg Pro	Gln Val	Glu	Val Ala	Glu
1085			1090			1095		
Asn Arg	Gly Thr	Pro Asn	Phe	Leu Ala	Ala Ser	Tyr	Ser Leu	Leu
1100			1105			1110		
Gly Ala	Phe Ser	Cys Glu	Gly	Asp Asn	Arg Asp	Asn	Glu Tyr	Glu
1115			1120			1125		
Thr Gln	Leu Trp	Gln Gln	Leu	Asn Glu	Ser Gly	Glu	Leu Gly	Val
1130			1135			1140		
Ser Gly	Leu Pro	Gln Pro	Tyr	Ser Val	Glu Glu	Gly	Arg Arg	Gln
1145			1150			1155		
Glu Leu	Gln Ser	Pro Tyr	Pro	Ala Pro	Tyr Glu	Asn	Ile Pro	Tyr
1160			1165			1170		
Ser Thr	Pro Ser	Tyr Asn	Ser	Val Ser	Tyr Thr	Ala	Ala Ser	Lys
1175			1180			1185		
Asp Arg	Leu Val	Gly Asp	Asn	Thr Ala	Tyr Asn	Gly	Ala Ala	Tyr
1190			1195			1200		
Cys Pro	Phe Tyr	Gly Gly	Ser	Gly Met	Tyr Glu	Thr	Pro Gln	Arg
1205			1210			1215		
Ser Glu	Glu Asn	Ser Leu	Tyr	Ser Ala	Asp Pro	Gln	Val His	Phe
1220			1225			1230		
Ser Glu	Ser Glu	Lys Thr	Gly	Ser Ser	Asp Ser	Phe	Pro Tyr	Ser
1235			1240			1245		
Phe Phe	Ser Leu	Gly Thr	Pro	Ala Leu	Tyr Pro	Gly	Gly Ser	Leu
1250			1255			1260		
Gln Thr	Gly Ala	His Leu	Glu	Glu Val	Pro Gly	Ser	Gly Asp	Ala
1265			1270			1275		
Glu Gly	Ser Ala	Trp Ser	Pro	Ser Leu	Glu Ser	Arg	Arg Leu	Arg
1280			1285			1290		
Gly Arg	Thr Arg	Ser Pro	His	Ala Gln	Ser Pro	Asn	Ser Asn	Arg
1295			1300			1305		
Ser Arg	Gly Ala	Ala Trp	Thr	Phe Ser	Pro Ala	Ser	Leu Pro	Phe
1310			1315			1320		
Glu Val	Pro Ala	Ala Ala	Lys	Ala Ser	Gly Arg	Lys	Arg Arg	Ala
1325			1330			1335		
Pro Gly	Ser Leu	Pro Ala	Gln	Thr Asp	Arg Gly	His	Lys Asp	Phe
1340			1345			1350		
Leu Leu	Glu Leu	Leu Ala	Ser	Arg Leu	Glu Pro	Val	Lys Gly	Val
1355			1360			1365		
His Met	Asp Arg	Leu Arg	Lys	Thr Trp	Val Ala	Ser	Trp Leu	Val
1370			1375			1380		
Gly Lys	Arg Arg	Ile Thr	Arg	Ile Phe	Ser Phe	Gln	Lys Phe	Gly
1385			1390			1395		
Phe Phe	Gly Ala	Arg Glu	Gln	Ala Ile	Arg His	Arg	Arg Glu	Ala
1400			1405			1410		
Leu Leu	Asn Pro	Glu Leu	Asp	Asn Ser	Glu Arg	Arg	Glu Ala	Leu
1415			1420			1425		
Ala Asn	Val Glu	Arg Ala	Thr	Asp Asp	Glu Leu	Gln	Gln Ala	Ala
1430			1435			1440		
Asp Ala	Leu Pro	Phe Val	Val	Gly Val	Thr Tyr	His	Arg Ala	Ser
1445			1450			1455		
Arg Cys	Trp Val	Ala Asn	His	Arg Lys	Pro Met	Gly	Lys Ile	Val
1460			1465			1470		

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Gln Arg	Lys Lys	Phe Ala	Val	Ala Glu	Leu Gly	Phe	Leu Glu	Ala	
1475			1480			1485			
Arg Tyr	His Ala	Ala Val	Met	Met Phe	Cys Trp	Asn	Lys Gln	Gly	
1490			1495			1500			
Arg Thr	Gln Glu	Pro Glu	Asp	Tyr Asp	Gln Gly	Ala	Thr Glu	Ala	
1505			1510			1515			
Phe Asn	Ser Arg	Gln Val	Pro	Gln Arg	Pro Gly	Asp	Asp Arg	Ala	
1520			1525			1530			
Phe Glu	Phe Ser	His Pro	Thr	Cys Ser	Glu Asn	Glu	Pro Leu	Tyr	
1535			1540			1545			
Thr Leu	Lys Ala	Leu Asp	Ser	Gly Thr	Cys Asp	Asp	Ala Met	Val	
1550			1555			1560			
Leu Leu	Ala Phe	Ile Cys	Gly	Ser Pro	Trp Arg	Lys	Ile Cys	Arg	
1565			1570			1575			
Gly Gln	Gln Cys	Gly Asp	Asp	Pro Thr	Leu Leu	Glu	Ala Ala	Ser	
1580			1585			1590			
Thr Ile	Gln Thr	Glu Lys	Ser	Leu Trp	Arg Thr	Arg	Val Lys	Ser	
1595			1600			1605			
Ala Ala	Asp Glu	Val Arg	Glu	Gly Pro	Gln Arg	Arg	Leu Glu	Gly	
1610			1615			1620			
Thr Asp	Ala Gly	Asp Ser	Gly	Ala Phe	Pro Arg	Gly	Gln Ser	Pro	
1625			1630			1635			
Glu Lys	Gly Arg	Pro Arg	Arg	Arg Arg	Lys Thr	Ala	Thr Leu	Arg	
1640			1645			1650			
Glu Gln	Glu Asp	Val Thr	Glu	Asp Lys	Thr Glu	Asp	Gly Arg	Glu	
1655			1660			1665			
Asp Lys	Thr Glu	Asp Gly	Gly	Glu Asp	Lys Thr	Glu	Asp Gly	Gly	
1670			1675			1680			
Glu Asp	Gly Arg	Glu Asp	Glu	Gly Glu	Asp Glu	Gly	Glu Asp	Pro	
1685			1690			1695			
Gly His	Gly Trp	Gly Glu	Arg	Arg Arg	Cys Arg	Lys	Ser Asp	Arg	
1700			1705			1710			
Glu Asn	Ala Gly	Glu Ala	Glu	Arg Gly	Gln Lys	Arg	Glu Lys	Arg	
1715			1720			1725			
Gln Gln	Ser Glu	Gly Arg	Cys	Val Val	Ala Glu	Val	Asp Leu	Arg	
1730			1735			1740			
Asp Ala	Lys Asp	Thr Val	Val	Arg Arg	Asn Arg	Val	Ala Arg	Arg	
1745			1750			1755			
Glu Gly	Leu Glu	Thr Gly	Phe	Gly Lys	Lys Asn	Ala	Lys Ser	Gly	
1760			1765			1770			
Ala Glu	Ser Cys	Leu Ser	Gln	Thr Pro	Ala Leu	Gly	Pro Ser	Ser	
1775			1780			1785			
Pro Pro	Phe Pro	Val Ser	Phe	Lys Lys	Arg Arg	Lys	Ser Ser	Ser	
1790			1795			1800			
Arg Glu	Ala Asp	Leu Arg	Gln	Ser Arg	Pro Arg	Arg	His Arg	Asn	
1805			1810			1815			
Asp Thr	Glu Glu	Ala Arg	Ser	Ile Cys	Glu Asp	Ser	Pro Ser	Ser	
1820			1825			1830			
Glu Val	Ala Pro	Thr Pro	Ala	Ser Ser	Ser Phe	Ser	Pro Ala	Ala	
1835			1840			1845			
Ser Leu	Ser Ser	Asp Gly	Ser	Arg Leu	Gly Ser	His	Asn His	Asp	
1850			1855			1860			
Leu Thr	Asp Ser	Gly Arg	Ser	Ala Ser	Val Ser	Arg	Gly Arg	Ser	

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1865	1870	1875
Thr Asp Phe Ser Met Phe Ala Gly Leu Pro Tyr Leu Lys Ser Leu 1880 1885 1890		
Glu Ser Asn Thr Arg Phe Val Pro Pro Ser Arg Pro Gly Glu Ser 1895 1900 1905		
Gly Leu Pro Asn Val Tyr Ala Ser Tyr Asn Ser Gly Leu Ala Phe 1910 1915 1920		
Glu Ala Asn Arg Pro Cys Pro Leu Ala Phe Asp Ser Arg Ala Asp 1925 1930 1935		
Pro Thr Gly Trp Pro His Thr Phe Pro His Pro Ala Glu Ala Tyr 1940 1945 1950		
Gly Ser Gly Ile Ala Ser Trp Thr Pro Asn Ala Asn Gly Phe Phe 1955 1960 1965		
Glu Ser Leu Ala Tyr Thr Gly Asn Leu Glu Glu Leu Arg Asp Leu 1970 1975 1980		
Cys Gly Arg Thr Pro Asp Ala Arg Asp Ser Ser Asp His Trp Gln 1985 1990 1995		
Glu Ala Ala Ala Ala Ser Ser Arg Leu Pro Leu Arg Pro Pro 2000 2005 2010		
Ala Val His Ser Trp Gln Asp Ala Pro Cys Ala Lys Asp Pro Ala 2015 2020 2025		
Pro Cys Val Glu Leu Ala Arg Asp Glu Cys Leu Ala Gly Gly Asp 2030 2035 2040		
Arg Gln Thr Cys Arg Phe His Ser Ala Phe Asp Ser Ala Asp Ala 2045 2050 2055		
Gly Asp Tyr Lys Phe Asn Thr Asp Ala Arg Cys Leu Arg Gly Pro 2060 2065 2070		
Thr Phe Asn Pro His Ser Asn Ala Val Ala Thr Leu Arg Arg Glu 2075 2080 2085		
Gln Glu Ala Ala Arg Gly Ala Ser Gly Gln Thr Pro Ser Phe Phe 2090 2095 2100		
Phe Pro Arg Leu Val Pro Val Ala Gln Thr Asp Trp Glu Ala Asp 2105 2110 2115		
Pro Gly Arg Gly Ser Gly Asp Ser Leu Ser Ala Pro His Glu Ala 2120 2125 2130		
Gly Glu Ala Val Gly Val Glu Gly Ser Glu Gly Ala Pro Cys Glu 2135 2140 2145		
Trp Asn Phe Glu Arg Asp Ala His Pro Val Ile Leu Pro Thr Ser 2150 2155 2160		
Asn Cys Ser His Gly His Glu Arg Leu Ala Ser Ser Asn Ala Phe 2165 2170 2175		
Thr Glu Ala Lys Gln Arg Asn Ala Leu Arg Cys Thr Pro Gln Glu 2180 2185 2190		
Thr Val Gly Gly Val Asn Glu Asn Gly Ser Pro Leu Phe Ser Thr 2195 2200 2205		
His Arg Asp Ala Pro Glu Ala Met Ser Ala Leu Thr Glu Val Ser 2210 2215 2220		
Asp Arg Glu Thr Gln Arg Gly Pro Ala Val Leu Gln Ser Gly Asn 2225 2230 2235		
Thr Glu Ala Leu Leu Gln Asp Ser Thr Ser Asn Ser Ala Ser Pro 2240 2245 2250		
Thr Gln Arg Arg Ala His Gly Leu Asp Pro Glu Pro Asp Glu Ser 2255 2260 2265		

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Lys Ala Arg Gly Glu Arg Ser Lys Glu Glu Asp Arg Glu Thr Leu
 2270 2275 2280
 Arg Thr Glu Ala Pro Ser Lys Gly Arg Lys Gln Ile Leu Ser Pro
 2285 2290 2295
 Pro Thr Glu Arg Asn Ser Met Tyr Gly Glu Ala Met Ser Ile Asp
 2300 2305 2310
 Arg Gln Val Ser Ala Leu Pro Thr Leu Leu Ser His Gly Thr Ala
 2315 2320 2325
 Phe Pro
 2330

<210> SEQ ID NO 14
 <211> LENGTH: 1438
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 14

Met Ala Ala Ala Ser Pro Pro Ala Gln Pro Leu Gly Ala Thr Ser Pro
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 Cys Thr Phe Ser Pro Pro Cys Ser Phe Ser Pro Ser Asp Thr Cys Ser
 20 25 30
 Val Phe Phe Ala Thr Pro Ser Arg Ala Val Ser Ala Val Pro Glu Leu
 35 40 45
 Pro Ala Thr Ser Ser Ala Gln Leu Pro Glu Arg Thr Arg Leu Arg Asn
 50 55 60
 Arg Ser Ile Gln Ser Ala Ser Thr Thr Glu Ala Ser Pro Phe Val Asp
 65 70 75 80
 Ser Ala Ser Leu Phe Pro Glu Ser Leu Ser Glu Ala Pro Lys Ala Val
 85 90 95
 Ser Val Asp Gly Glu Ser Arg Arg Thr Arg Glu Arg Arg Arg Lys Ser
 100 105 110
 Arg Ser Leu Leu Ala Ala Ala Glu Glu Thr Pro Glu Ala Thr Ala Ala
 115 120 125
 Ser Pro Asn Gly Ser Ser Ser Glu Ile Ser Asp Glu Ala Ser Thr Phe
 130 135 140
 Val Leu Thr Pro Ala Thr Ala Ser Leu Ala Pro Ala Ala Leu Pro Pro
 145 150 155 160
 Phe Met Thr Glu Arg Ser Asp Pro Thr Glu Lys Lys Tyr Glu Ala Gln
 165 170 175
 Asn Met Gln Val Thr Ala Val Glu Pro Val Gly Leu Ala Pro Arg Ser
 180 185 190
 Ala Ser Arg Ser Glu Leu Gly Asp Ala Glu Ser Leu Ser Ala Gly Lys
 195 200 205
 Ser Gly Leu Gln Gly Glu Ser Ala Ala Pro Thr Ala Ala Leu Glu Ala
 210 215 220
 Asp Ala Gly Glu Thr Arg Leu Glu Thr Gly Leu Ala Gly Glu Pro Val
 225 230 235 240
 Asn Ser Ser Ser Glu Gly Val Gly Tyr Gly Gly Asp Glu Gln Thr Val
 245 250 255
 Ala Gly Glu Thr Arg Glu Pro Gly Thr Ala Glu Glu Lys Leu Gly Asp
 260 265 270
 Leu Lys Pro Glu Val Arg Pro Arg Phe His Ala Tyr Ala Glu Gln Asp
 275 280 285
 Val Cys Ala Trp Ala Thr Ser Met Leu Ala Arg Lys Glu Leu Arg Lys

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290	295	300
Leu Lys Ala Ala Ala Val	Lys Leu Glu Gly Asp	Arg Met Pro Arg Ser
305	310	315 320
Asp Val Val Gly Leu Tyr Phe	Lys Lys His Arg	Pro Cys Trp Ser Val
	325 330	335
Asp Tyr His Thr Arg Gln Gly	Lys Arg Lys Thr	Val Glu Phe Phe Val
	340 345	350
Pro Asp Leu Ser Arg Glu Thr	Ile Glu Leu Val	Leu Val His Ala Ile
	355 360	365
Glu Cys Arg Lys Tyr Met	Pro Arg Arg Phe Asp	Gln Ala Pro Ala Phe
370	375	380
Val Pro Glu Pro Asp Asp	Thr Thr Ser Gly Met	Pro Tyr Arg Tyr Gly
385	390	395 400
Ala Arg Leu Leu Ser Pro	Lys Val Leu Ala Trp	Ile Val Glu Asn Thr
	405 410	415
Asn Gly Ser Gly Arg Thr	Ser Gln His Gly His	Gly Gln Ser Arg Arg
	420 425	430
Leu Glu Gly Asp Lys Val Gly	Glu Gly Asp Ala Gly	Ala Gln Leu Leu
	435 440	445
Ser Gly Pro Ala Gly Ile	Asp Ala Phe Gly Ser	Arg Ser Pro Arg Ala
450	455	460
Gly Phe Ala Arg Gln Arg	Asp Asn Asn Ser Arg	Arg Gln Gly Lys Ala
465	470	475 480
Ser Gly Cys Arg Pro Gly	Ala Asp Leu Ala Thr	Ser Ser Glu Glu Lys
	485 490	495
Ala Thr Arg Glu Gly Glu Thr	Glu Leu Pro Gly Gly	Ser Ala Gly Pro
	500 505	510
Gly Ser Val Pro Ala Gly Thr	Ala Tyr Gly Asp Tyr	Ala Arg Gln Leu
	515 520	525
Pro Ser Glu Gly Tyr Gln Thr	Pro Pro Thr Met Glu	Gly Arg Met Thr
530	535	540
Pro Ala Gly Leu Leu Ser	Gly Gln Glu Phe Gly	His Gly Gln Gly Met
545	550	555 560
Gln Gly Ala Gly Val Met	Trp Arg Asp Asp	Pro Arg Gln Ala Leu Gln
	565 570	575
Ala Met Pro Gln Pro Leu Asn	Leu Ala Pro His Ala	Thr Pro Phe Met
	580 585	590
Ser Arg Ala Gly Gly Leu Tyr	Asp Gln Arg Glu Ala	Ser Val Glu Pro
595	600	605
Gly Arg Asp Val Tyr Pro	Val His Tyr Pro Thr	Pro Tyr Ala Tyr Gly
610	615	620
Pro Gly Ile Pro Ala Asp	Ala Gly Ala Pro Ser	Ala Gly Pro Gly Pro
625	630	635 640
Tyr Pro His Gln Phe Pro	Ser Gly Gly Ala Gly	Tyr Val Val Asn Gly
	645 650	655
Arg Val Pro Asp Ser Ala Asp	His Glu Ala His Ser	Pro Arg Ser Pro
	660 665	670
Glu Ser Tyr Trp Gly Pro	Gln Ala Gly Ser Gln	Gly Ala Glu Asp Lys
	675 680	685
Asp Cys Gln Val Val Gly	Cys Met Leu Pro Asn	Gly Ser Glu Met Ala
690	695	700
Met Arg Arg Met Glu Ser	Tyr Val Gly Asp Arg	Asp Asn Leu Arg Gly
705	710	715 720

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Ser Ala Ala Phe Ala Gly Asp Gly Arg Thr Gln Ala Glu Gly Leu Ser
 725 730 735
 Pro Gln Cys Glu Pro Asn Ala Lys Arg Arg Arg Leu Gln Ala Gly Gly
 740 745 750
 Asp Gly Ser Asn Gly Gly Leu Glu Ala Ser Gly Pro Glu Arg Pro Phe
 755 760 765
 Pro Gly Ser Gln Met Leu Gln Pro Ser Asp Glu Trp Ala Arg Asn Gly
 770 775 780
 Gln Arg Ala Phe Ala Val Gln Pro Gly Thr Gly Gly Arg Thr Phe Met
 785 790 795 800
 Asn Gly Gly Phe Arg Gln Pro Gly Pro Glu Asp Ala Arg Gln Pro Leu
 805 810 815
 Leu Leu Ser Ser Ala Pro Tyr Ser Pro Pro Ser Val Phe Pro Ala Ala
 820 825 830
 Pro Pro His Leu Ser His Ala Val Arg Leu Pro Pro Gly Ser Ser Asp
 835 840 845
 Ala Ala His Arg Thr Pro Met Ser Gly Ala Ala Gly Cys Ala Ser Pro
 850 855 860
 Val Ala Ser Ala Phe Arg Lys Glu Ala Glu Ala Ser Glu Trp Pro Ser
 865 870 875 880
 Asn Glu Val Tyr Gly Ser Pro Gln Ala Phe Pro Asp Lys Ala Asn Ala
 885 890 895
 Phe Ala Lys Gly Val Thr Leu Pro Arg Arg Gln Ser Phe Ala Phe Ser
 900 905 910
 Asp Ala Gly Leu Pro Thr Pro Thr Thr Ser Pro His His Gly Ser Tyr
 915 920 925
 Cys Ala Ser Thr Ile Ala Ser Ser Ser Pro Lys Ser Ala Ser Pro Val
 930 935 940
 Ser Gln Ser Gly Cys Phe Pro Cys Asp Phe Tyr Pro Ala Thr Ala His
 945 950 955 960
 Tyr Ser Gly Pro Gly Val Glu Thr Pro Ser Asp Val Ser Ser Phe Val
 965 970 975
 Pro Ala Pro Ala Glu Thr Ala Glu Gln Gln Ile His Gly Ala Gly Gln
 980 985 990
 Ala Ala Val Lys Thr Pro Glu Ser Gly Leu His Met Pro Ser Ser Gly
 995 1000 1005
 Trp Pro Gln Gln Ala Ser Val Pro Gly Ala His Gly Ala Glu Phe
 1010 1015 1020
 Tyr Ala Ser Arg Ala Phe Ala Asn Gly Ala His Ala Pro Ser Leu
 1025 1030 1035
 Ser Leu Arg Pro Ser Trp Arg Tyr Pro Gly Gly Glu Arg Ser Glu
 1040 1045 1050
 Gly Asp Leu Thr Thr Gln Glu Gln Asn Ala Pro Ala Gly Ala Ser
 1055 1060 1065
 Pro Ser Ser Pro Val Trp Ser Gly Asn Thr Gly Val Cys Thr Thr
 1070 1075 1080
 Glu Gly Cys Gly Val Trp Leu Glu Asn Arg Gln Ala Ala Gly Ser
 1085 1090 1095
 Val Glu Gly Ala Ala Asp Pro Gly Val Gln Gly Ser Ala Cys Met
 1100 1105 1110
 Gln Gly Lys Pro Gln Glu Gly Gly Arg Cys Ser Pro Glu Pro Ala
 1115 1120 1125

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Leu Gly	Val Arg	Arg Pro	Ala	Glu Phe	Ala Gly	Ala	Pro Val	Gly
1130			1135			1140		
Ala Cys	Arg Ala	Val Glu	Asp	Arg Thr	Met Thr	Gly	Glu Arg	Gly
1145			1150			1155		
Ala Trp	Gly Asn	Glu Ala	Arg	Arg Glu	Thr Val	Thr	Gly Asp	Gln
1160			1165			1170		
Glu Cys	Cys Gly	Asp Gln	Ala	Arg Asp	Pro Met	Val	Phe Ser	His
1175			1180			1185		
Met Gly	Ser Arg	Ala Glu	Leu	Ser Gly	Phe Asp	Asp	Gly Ser	Glu
1190			1195			1200		
Leu Pro	Pro Ala	Ser Pro	Leu	Asn Glu	Cys Met	His	Pro Leu	Gly
1205			1210			1215		
Lys Pro	Gly Ser	Arg Ile	Phe	Pro Glu	Phe Gly	Ala	Trp Pro	Gly
1220			1225			1230		
Ser Pro	Pro His	Glu Gly	Ser	Phe Val	Gln Glu	Phe	Asp Ile	Phe
1235			1240			1245		
Lys Glu	Asn Gly	Glu Gly	Ala	Ala Gly	Ala Val	Asp	Asp Ala	Met
1250			1255			1260		
Ala Leu	Trp Pro	Asn Gly	Gly	Ala Phe	Gly Gln	Arg	Thr Asp	Pro
1265			1270			1275		
Leu Ala	His Glu	Glu Glu	Lys	Glu Gly	Glu Leu	Trp	Lys Gly	Gln
1280			1285			1290		
Pro Thr	Pro Phe	Cys Ser	Ser	Pro Ala	Leu Trp	Cys	Val Cys	Pro
1295			1300			1305		
Val Glu	His Thr	Arg Glu	Phe	Asp Val	Met Asp	Met	Val Thr	Leu
1310			1315			1320		
Pro Asp	Leu Ser	His Thr	Ala	Gly Pro	Val Ser	Arg	Pro Leu	Pro
1325			1330			1335		
Asn Ala	Pro Leu	Cys Gly	Gly	Cys Val	Val Ala	Gly	Val Gly	Glu
1340			1345			1350		
Ala Gln	Ala Gly	Asp Gly	Glu	Ser Lys	Gln Gly	Ala	Lys Leu	Ala
1355			1360			1365		
Pro Asp	Ser Gln	His Leu	His	Gly Gly	Ala Ala	Asn	Pro Gly	Ala
1370			1375			1380		
Val Gly	Lys Leu	Val Thr	Asp	Glu Thr	Ala Gln	Thr	Ser Gly	Arg
1385			1390			1395		
Glu Gln	His Pro	Gly Glu	Gly	Asp Ser	Thr Glu	Gln	Arg Leu	Ser
1400			1405			1410		
Gly Leu	Ala Ala	Arg Ala	Thr	Pro Gln	Arg Glu	Thr	Lys Arg	Pro
1415			1420			1425		
Gly Pro	Ser Arg	Arg Thr	Glu	Gly Glu	Leu			
1430			1435					

<210> SEQ ID NO 15

<211> LENGTH: 3817

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 15

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1		5		10		15	

Ala Phe	Leu His	His Thr	Glu Lys	Leu Glu	Arg Leu	Pro Gly	Thr Gly
	20		25			30	

Glu Thr	Thr Ile	Arg Gly	Met Ser	Phe Thr	Pro Pro	Tyr Ile	Cys Met
	35		40			45	

Glu 50	Pro	Pro	Arg	Ala	Asn 55	Cys	Glu	Ala	Leu	Arg 60	Leu	Lys	Ser	Pro	
Pro 65	Glu	Asn	Arg	Ala 70	Phe	Ser	Ser	Arg	Ser	Glu 75	Ser	Pro	Ser	Pro	Thr 80
Pro	Phe	Ala	Arg	Glu 85	Cys	Ala	Ser	Leu	Gly 90	Leu	Val	Trp	Gly	Asp 95	Glu
Gly	Thr	Arg	Ala 100	Gly	Leu	Leu	Arg	Thr 105	Arg	Leu	Phe	Thr	Pro 110	Pro	Asp
His	Thr	Pro 115	His	Leu	Leu	Ala	Glu 120	Thr	Gly	Ala	Ser	Cys 125	Leu	Glu	Asp
Leu	Phe 130	Pro	Gly	Thr	Val	Pro 135	Gln	Leu	Leu	Ser	His 140	Leu	Pro	Ser	Pro
Pro 145	Pro	Val	Pro	Gly 150	Val	Ala	Arg	Ala	Ser	Arg 155	Ser	Ser	Ser	Pro	Leu 160
Ala	Gly	Gly	Ser	Ser 165	Leu	Ala	Cys	Ala	Ser	Pro 170	Trp	Pro	Arg	Ser	Ala 175
Thr	Pro	Phe	Phe 180	Ala	Ala	Asn	Met	Pro 185	Ala	Leu	Leu	Pro	Gly 190	Arg	Gly
Pro	Met	Arg 195	Val	Thr	Lys	Trp	Leu 200	Asp	Gly	Gln	Val	Ser 205	Asp	Pro	Gln
Ser	Asp 210	Ser	Cys	Leu	Arg	Gly 215	Gly	Ala	Ser	Arg 220	Val	Glu	Arg	Ala	Ala
Ala 225	Leu	Leu	Cys	Gly	Arg 230	Ser	Glu	Glu	Glu	Gln 235	Glu	Arg	Glu	Arg	Ser 240
Val	Asp	Glu	Arg	Arg 245	Leu	Arg	Lys	Ala	Ile 250	Gly	Val	Thr	Asp	Glu	Asp 255
Glu	Ser	Glu	Arg 260	Glu	Arg	Glu	Thr	Glu 265	Gly	Gly	Val	His 270	Glu	Arg	Leu
Ser	Arg 275	Cys	Ala	Ala	Ala	Thr	Ala 280	Ala	Asp	Arg	Ala	Asn 285	Asn	Leu	Leu
Gly 290	Leu	Gly	Val	Glu	Arg	Gly 295	Pro	Glu	Val	Ala	Gly 300	Gly	Arg	Leu	Gly
Gly 305	Tyr	Trp	Thr	Thr	Glu 310	Ser	Glu	Val	Tyr	Pro 315	Gln	Arg	Ile	Gly	Glu 320
Leu	Glu	Gly	Glu 325	Gly	Leu	Gly	Ser	Pro	Asp 330	Pro	Val	Ala	Ala	Ser	Ala 335
Leu	Val	Thr	Ala 340	Val	Gln	Asp	Ser	Arg 345	Glu	Asn	Leu	Asn 350	Cys	Leu	Thr
Gly	Val 355	Leu	Thr	Thr	Leu	Arg	Leu 360	Ser	Ser	Arg	Asp 365	Ser	Glu	Gly	Asp
Phe 370	Asp	Leu	Pro	Leu	Phe	Val 375	Gln	Ser	Arg	Lys 380	Trp	Arg	Ala	Lys	Tyr
Asn 385	Arg	Arg	Ser	Leu	Asp 390	Leu	Lys	Gly	Thr	Val 395	Ala	Arg	Ser	Lys	Ala 400
Leu	Gly	Tyr	Pro	Ala 405	Gly	Leu	Gln	Ile	Pro 410	Glu	Thr	Tyr	Arg	Asp	Leu 415
Lys	Asn	Cys 420	Met	Gln	Arg	Pro	Pro	Ser 425	Ile	Asp	Ala	Ala	Asp 430	Ser	Arg
Ala	Trp 435	Arg	Ser	Ala	Glu	Ala	Pro 440	Arg	Ala	Ala	Lys	Lys 445	Val	Phe	Ser
Glu 450	Gly	Arg	Arg	Ala	Thr	Asp 455	Arg	Asp	Glu	Gln 460	Val	Ala	Phe	Val	Glu

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Asp	Glu	Val	Thr	Glu	Gln	Leu	Leu	Phe	Asn	Ala	Asn	Ala	Ala	Val	Glu	465	470	475	480
Gly	Thr	Thr	Leu	Tyr	Asn	Asn	Leu	Leu	Cys	Lys	Tyr	Gly	Leu	Glu	Thr	485	490	495	
Arg	Cys	Phe	Ser	Thr	Ser	Ser	Ala	Pro	Gly	Asn	Thr	Ala	Phe	Glu	Ser	500	505	510	
Arg	Leu	Ala	Arg	Ser	Asp	Ala	Asp	Pro	Thr	Ala	Ser	Ser	Gln	Ser	Ala	515	520	525	
Ser	Ala	Leu	Ser	His	Ala	Ala	Val	Ser	Pro	Ser	Leu	Ala	Ser	Ala	Leu	530	535	540	
Pro	Val	Ser	Ser	Leu	Leu	Leu	Glu	Asp	Ala	Ala	Asp	Ala	Val	Gly	Asp	545	550	555	560
Arg	Ser	Glu	Leu	Glu	Thr	Gly	Ser	Gln	Ala	Glu	Ala	Ala	Ile	Pro	Thr	565	570	575	
Ser	Glu	Ala	Ser	Cys	Met	Arg	Arg	Glu	Lys	His	Val	Gly	Glu	Glu	Ser	580	585	590	
Arg	Ala	Asp	Lys	Gly	Ala	Phe	Leu	Arg	Ser	Ala	Ser	Asp	Ser	Thr	His	595	600	605	
Ala	Glu	Glu	Asp	Gly	Leu	Ser	Gly	Gly	Lys	Asp	Ala	Ser	Ser	Arg	Glu	610	615	620	
Gly	Gly	Ser	Glu	Glu	Arg	Glu	Glu	Ala	Ala	His	Glu	Ala	Ala	Asp	Ser	625	630	635	640
Leu	Trp	Ser	Leu	Val	Leu	Asn	Arg	Asn	Ile	Ala	Ala	Leu	Pro	Gly	Phe	645	650	655	
Met	Thr	Val	Gly	Arg	Tyr	Glu	Cys	Asp	Leu	Leu	Pro	Lys	Arg	Ser	Ala	660	665	670	
Phe	Ser	Arg	Lys	Gln	Leu	Ala	Gly	Leu	Val	Ala	Gly	Ser	Arg	Pro	Leu	675	680	685	
Pro	Val	Leu	Pro	Ser	Ser	Ser	Asp	Thr	Pro	Gly	Ser	Ala	Ser	Thr	Glu	690	695	700	
Leu	Leu	Ala	Glu	Arg	Val	Ala	Cys	Ala	Leu	Thr	Leu	Asp	Glu	Gly	Glu	705	710	715	720
Ala	Trp	Asn	Pro	Ser	Asp	Ala	Ser	Asp	Leu	Asp	Asp	Phe	Leu	Glu	Ser	725	730	735	
Ser	Cys	Ala	Pro	Asn	Ala	Leu	Arg	Arg	Gly	Arg	Gln	Ala	Val	Val	Pro	740	745	750	
Val	Arg	Gly	Ala	Arg	Arg	Arg	Arg	Gly	Ala	Asp	Leu	Gly	Leu	Ser	Pro	755	760	765	
Pro	Pro	Ser	Ser	Pro	Ala	Val	Arg	Cys	Arg	Ser	Leu	Val	Arg	Trp	Ser	770	775	780	
Gln	Gln	Arg	Pro	Phe	Phe	Ser	Asn	Val	Ser	Ala	Cys	Ala	Gly	Ala	Ala	785	790	795	800
Asp	Ser	Arg	Arg	Glu	Glu	Trp	Lys	Asp	Ala	Gly	Lys	Val	Ala	Lys	Pro	805	810	815	
Gly	Ser	Glu	Ser	Ala	Leu	Thr	Ser	Arg	Asp	Leu	His	Ala	Ser	Thr	Gly	820	825	830	
Leu	Val	Asn	Ala	Ala	Leu	Asp	Ser	Ser	Glu	Gln	Lys	Ser	Gly	Glu	Arg	835	840	845	
Glu	Ser	Ser	Leu	Ser	Pro	Gln	Glu	Arg	Ile	Leu	Thr	Gln	Val	Lys	Lys	850	855	860	
Glu	Leu	Glu	Asp	Glu	Arg	Val	Arg	Glu	Lys	Gln	Thr	Ile	Arg	Asp	Lys	865	870	875	880
Asp	Ser	Glu	Lys	Gly	Gln	Gly	Gly	Glu	Ser	Asn	His	His	Met	Pro	Gly				

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885						890						895				
Thr	Ala	Asn	Gly	Gln	Arg	Thr	Pro	Asn	Glu	Gly	Glu	Ala	Pro	Met	Glu	
			900						905				910			
Thr	Glu	Glu	Ala	Pro	Thr	Leu	Glu	Pro	Ser	Asn	Gly	Met	His	Arg	Asp	
		915					920					925				
Gly	Gln	Asp	Ala	Gly	Ala	Arg	Met	His	Ser	Ser	Ser	Thr	Arg	Ala	Leu	
		930					935					940				
Glu	Gly	Ala	Val	Glu	Asp	Glu	Pro	Lys	Val	Thr	Leu	Pro	Asp	Lys	Asp	
945					950					955					960	
Glu	Pro	His	Ala	Ser	Ala	Leu	Cys	Gly	Glu	Arg	Glu	Lys	Gln	Arg	Gln	
			965						970					975		
Ser	Phe	Phe	Ser	Ser	Val	Ser	Ser	Arg	Glu	Asp	Ala	Gln	Asp	Glu	Asp	
		980						985					990			
Ser	Arg	Trp	Cys	Val	Ala	Gly	Gly	Met	Tyr	Asn	Gly	Trp	Lys	Gly	Thr	
		995					1000						1005			
Tyr	Asp	Val	Trp	Ile	Tyr	Arg	Arg	Val	Ser	Ala	Ala	Leu	Arg	Glu		
	1010					1015						1020				
Gly	Lys	Gly	Glu	Glu	Glu	Lys	Arg	Arg	Glu	Gly	Glu	Lys	Arg	Lys		
	1025					1030						1035				
Thr	Gly	Lys	Gly	Lys	Gln	Ser	Val	His	Thr	Ala	Ser	Leu	Gly	Ala		
	1040					1045						1050				
Gly	Gly	Ala	Gln	Gly	Leu	Ser	Pro	Gly	Glu	Thr	Gln	Ala	Ser	Gly		
	1055					1060						1065				
Leu	Ala	Pro	Gly	Ser	Thr	Pro	Leu	Gly	Ser	Ala	Gly	Thr	Leu	Ser		
	1070					1075						1080				
Ala	Gly	Arg	Asn	Gly	Glu	Glu	Thr	Arg	Glu	Ser	Thr	Gly	Ser	Pro		
	1085					1090						1095				
Ala	Gly	Ala	Phe	Ala	Ser	Ser	Ser	Ser	Leu	Ala	Ala	Lys	Gly	Gln		
	1100					1105						1110				
Asn	Gly	His	Ala	Ser	Val	Glu	Asp	Leu	Lys	Thr	Gln	Lys	Glu	Glu		
	1115					1120						1125				
Ser	Leu	Gly	Cys	Val	Leu	Ser	Ala	Ser	Ala	Leu	Pro	Leu	Asn	Pro		
	1130					1135						1140				
His	Ser	Gly	Glu	Thr	Arg	Glu	Asp	Ser	Ala	Gly	Arg	Asp	Glu	Glu		
	1145					1150						1155				
Lys	Gly	Glu	Glu	Arg	Glu	Arg	Asp	Glu	Asn	Glu	Pro	Pro	Leu	Tyr		
	1160					1165						1170				
Glu	Trp	Arg	Val	Lys	Arg	Phe	Ser	Ala	Leu	Ile	His	Gly	His	Glu		
	1175					1180						1185				
Lys	Ala	Ser	Arg	Leu	Ala	Cys	Lys	Tyr	Cys	Val	Tyr	Leu	Glu	Arg		
	1190					1195						1200				
Phe	Gly	Arg	Ile	Arg	Gly	Arg	Leu	Ser	Ile	Cys	Ser	Thr	Cys	Cys		
	1205					1210						1215				
Arg	Asp	Ala	Cys	Ser	Gly	Cys	Met	Pro	Ser	Lys	Lys	Arg	Ala	Ala		
	1220					1225						1230				
Gly	Ala	Asp	Phe	Ser	Pro	His	Cys	Arg	Asn	Gly	Arg	Asp	Ala	Gly		
	1235					1240						1245				
Val	Gly	Gly	Ala	Gly	Arg	Ala	Pro	Lys	Arg	Arg	Val	Gln	Ala	Lys		
	1250					1255						1260				
Lys	Gly	Ala	Ala	Gly	Ala	Ala	Gly	Val	Cys	Gly	Asp	Arg	Ala	Arg		
	1265					1270						1275				
Lys	Gly	Lys	Gly	Glu	Asp	Glu	Pro	Glu	Arg	Asp	Gly	Leu	Asp	Arg		
	1280					1285						1290				

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Arg Glu	Glu Gly Gly Thr	Pro	Ser Ser Lys Gln Thr	Ala Glu Arg
1295		1300		1305
Arg Gly	Ala Ala Lys Lys	Glu	Gly Arg Glu Glu Asp	Asp Arg Val
1310		1315		1320
Asp Gly	Lys Gly Thr Ser	Leu	Ser Leu Glu Asn Asn	Ser Phe Glu
1325		1330		1335
Ser Ser	Cys Pro Ala Met	Arg	Ser Ser Leu Arg Ala	Ser Phe Glu
1340		1345		1350
Val Lys	Gly Pro Leu Ser	Pro	Ser Ser Ala Asp Asp	Arg Pro Asn
1355		1360		1365
Glu Gly	Ala Ala Gly Arg	Gly	Ala Pro Pro Gly Ser	Glu Gly Pro
1370		1375		1380
Ser Arg	Asp Leu Ala Leu	Arg	Ser His Ser Phe Ser	Ser Ala Ser
1385		1390		1395
Ser Ser	Arg Lys Ser Ala	Lys	Asn Ala Ala Glu Ser	Leu Arg Arg
1400		1405		1410
Ile Ala	Gly Pro Leu Phe	Arg	Ser Ser Gly Asp Leu	Thr Ala Ser
1415		1420		1425
Gln Leu	Gly Ala Glu Thr	Glu	Glu Ser Asp Val Leu	Gln Asp Val
1430		1435		1440
Phe Glu	Leu Tyr Ser Glu	Ala	Gly Glu Ala Trp Glu	Thr Cys Thr
1445		1450		1455
Thr Pro	Val Ser Phe Ser	Pro	Ser Leu Ser Val Ala	Ser Arg Asp
1460		1465		1470
Thr Leu	Val Val Leu Gly	Gly	Ser Gln Thr Thr Ala	Val Ala Arg
1475		1480		1485
Leu Asp	Ser Gly Lys Met	Ser	Glu Ala Val Arg Arg	Ser Ser Asn
1490		1495		1500
Ala Leu	Ser Ala Ala Ala	Ser	Ser Phe Pro Lys Gly	Lys Gly Phe
1505		1510		1515
Gly Gly	Ala Ser Lys Lys	Thr	Asp Ser Val Thr Leu	Ser Phe Leu
1520		1525		1530
Ala Arg	Val Cys Arg Asn	Leu	Arg Met Phe Leu Leu	Leu Cys Gln
1535		1540		1545
His Asn	Thr Val Ala Gly	Gly	Leu Pro Gly Asp Ser	Lys Cys Val
1550		1555		1560
Cys Arg	Ala Gln Ser Gly	Pro	Gly Gly Ala Gly Leu	Ala Gly Ala
1565		1570		1575
Asp Gly	Arg Ala Pro Gly	Asp	Leu Gly Asp Ser Lys	Gly Thr Ala
1580		1585		1590
Ile Ala	Arg Gly Pro Gly	Gly	Ala Ala Gly Arg Ala	His Gly Ser
1595		1600		1605
Glu Pro	Trp Ala Ser Pro	Asn	Tyr Thr Gly Gly Pro	Phe Phe Pro
1610		1615		1620
Pro Ala	Gly Ser Ala Pro	Ser	Gly Trp Pro Pro Val	Ala Gln Ala
1625		1630		1635
Asn Ser	Arg Pro Glu Val	Leu	Ser Ala Ile Gln Gly	Ala Gln Gly
1640		1645		1650
Gln Gly	Pro His Val Ala	His	Ser Leu Arg Leu Ala	Ala Ser Leu
1655		1660		1665
Ser Pro	Ala Gln Thr Thr	Ser	Glu Ser Phe Leu Ala	Pro Glu Ser
1670		1675		1680

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Phe 1685	Ala	Ala	Gly	Val	Arg	Pro 1690	Leu	Leu	Glu	Gly	Ser 1695	Leu	Ser	Val
Leu 1700	Ile	Pro	Glu	Glu	Pro	Gln 1705	Val	Gly	Leu	Gly	Pro 1710	Ser	Ala	Gly
Gln 1715	Gln	Leu	Ala	Ser	Ser	Ser 1720	Leu	Ser	Pro	Gly	Val 1725	Ser	Val	Lys
Ala 1730	Glu	Pro	Ser	Ser	Tyr	Phe 1735	Gln	Ser	Ala	Gln	Gly 1740	Thr	Cys	Arg
Asp 1745	Val	Ser	Ala	Gly	Ala	Arg 1750	Thr	Ala	Met	Pro	Ser 1755	Ser	Phe	Leu
Glu 1760	Gln	Gly	Arg	Pro	Gly	Ala 1765	Ala	Pro	Gly	His	Ala 1770	Pro	Ser	Gly
Val 1775	Gly	Arg	Cys	Pro	Pro	Gln 1780	Gly	Arg	Asp	Ala	Ser 1785	Pro	Gly	Cys
Pro 1790	Gly	Phe	Arg	Thr	Pro	Pro 1795	Ala	Gly	Phe	Asp	Gly 1800	Pro	Ser	Ser
Ser 1805	Gly	Ala	Gly	Tyr	Ser	Leu 1810	Ser	Pro	Tyr	Gly	Tyr 1815	Pro	Gly	Thr
Glu 1820	Ile	Ser	Pro	His	Leu	Ala 1825	Pro	Phe	Phe	Pro	Glu 1830	Pro	Tyr	Arg
Arg 1835	Phe	Arg	Glu	Ser	Arg	Gly 1840	Gly	Pro	Ala	Trp	Ile 1845	His	Ser	Pro
Gly 1850	Ser	Val	Asp	Val	Pro	Ser 1855	Ser	Gly	Leu	Gln	Ser 1860	Pro	Phe	Thr
Gly 1865	Phe	His	Ala	Thr	Ser	Gly 1870	Ser	Ser	Pro	Pro	Arg 1875	Leu	Gly	Pro
Ser 1880	Glu	Gly	Ala	Ser	Phe	Ala 1885	Glu	Ala	Ser	Pro	Arg 1890	Ala	Leu	Ala
Gly 1895	Asp	Leu	Gly	Pro	Ala	Gly 1900	Phe	Leu	Gly	Ala	Ser 1905	Ala	Gly	Ala
Pro 1910	Ala	Ala	Glu	Gly	Arg	Gly 1915	Pro	Leu	Phe	Asp	Pro 1920	Ser	Ala	Glu
Gly 1925	Glu	Gly	Lys	Phe	Ala	Pro 1930	Asp	Ala	Gly	Ala	Leu 1935	Gly	Thr	Val
Glu 1940	Gly	Pro	Ala	Asp	Cys	Arg 1945	Thr	Gln	Gly	Glu	Thr 1950	Gly	Arg	Thr
Ala 1955	Asp	Glu	Asp	Glu	Lys	Lys 1960	Lys	Ala	Lys	Lys	Ala 1965	Lys	Lys	His
Gly 1970	Arg	Ile	Thr	Asp	Ile	Glu 1975	Glu	Arg	Leu	Ala	Arg 1980	Glu	Glu	Pro
Tyr 1985	Asp	Val	Val	Glu	Glu	Gly 1990	Asp	Asp	Pro	Glu	Pro 1995	Thr	Arg	Gln
Leu 2000	Gly	Leu	Glu	Ala	Thr	Glu 2005	Lys	Glu	Gln	Asp	Val 2010	Pro	Arg	Ser
Gly 2015	Asp	Ser	Lys	Ser	Pro	Asp 2020	Gln	Asp	Ser	Pro	Gly 2025	Gln	Pro	Ala
Asp 2030	Ile	Met	His	Gly	Tyr	Phe 2035	Lys	Ala	Arg	Val	Arg 2040	Asn	Arg	Arg
Val 2045	Lys	Asp	Gly	Leu	Leu	Leu 2050	Arg	Met	Thr	Ala	Val 2055	Leu	Val	Gly
Lys 2060	Gly	Phe	Tyr	Asp	Leu	Glu 2065	Thr	Val	Glu	Pro	Gly 2070	Ala	Pro	Arg
Arg	Arg	Gly	Gly	Trp	Gly	Glu	Ser	Gly	Glu	Glu	Glu	Glu	Glu	Ser

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2075	2080	2085
Glu Thr Lys Tyr Leu Phe Ser Asn Pro Ala Ser Gln Lys Pro Cys		
2090	2095	2100
Asp Phe Ile Leu Tyr Phe Asp Thr Arg Glu Asn Arg Asp Ala Ser		
2105	2110	2115
Val Ala Ile Leu Asn Gln Ala Leu Pro Ala Pro Pro Pro Arg Leu		
2120	2125	2130
Pro Pro Lys Asn Gly Glu Ser Gln Ala Arg Arg Thr Leu Arg Gln		
2135	2140	2145
Leu Tyr Asp His Phe Leu Glu Pro Lys Cys Gln Cys Leu Glu Asp		
2150	2155	2160
Lys Thr Leu Lys Val Lys His Gly Val Ile Asn Leu Leu Gly Phe		
2165	2170	2175
Pro Arg Leu Tyr Val Lys Leu His Cys Ser Met Ser Trp Asp Glu		
2180	2185	2190
Arg Leu Ser Leu Phe Ser Ser Phe Leu His Trp Leu Cys Arg Glu		
2195	2200	2205
Asp Asp Ser Gln Pro Pro Pro Trp Ser Ser Pro Glu Leu His Pro		
2210	2215	2220
Glu Leu Leu Ala Tyr Leu Val Asp Leu Gly Arg Lys Gly Phe Ala		
2225	2230	2235
Ser Gly Gly Ala Ala Thr Thr Ala Val Val Asn Ala Pro Asp Leu		
2240	2245	2250
Pro Leu Asp Asp Ser Ala Leu Ser Lys Lys Asn Ala Ala Leu Ile		
2255	2260	2265
Arg Ala Tyr Met Gln Gln Asp Thr Gly Ala Ser Gly Pro Ser Gly		
2270	2275	2280
Ser Val Gly Ala Thr Ser Ser Asp Pro Glu Ala Pro Arg Lys Asp		
2285	2290	2295
Asp Glu Ala Glu Glu Gly Glu Lys Asp Asp Ser Asn Ala Ala Leu		
2300	2305	2310
Val Glu Gly Pro Ala Pro Glu Thr Ser Gly Asp Ser Thr Gly Ala		
2315	2320	2325
Ala Gln Pro Cys Gly Lys Gly Arg Glu Glu Arg Glu Ala Gly Asp		
2330	2335	2340
Lys Arg Gly Pro Gly Asn Glu Gly Cys Gly Lys Gly Asp Gly Phe		
2345	2350	2355
Gly Ser Pro Val Ala Val Ala Gly Thr Thr Ala Ala Pro Gly Glu		
2360	2365	2370
Thr Glu Ser Val Ser Cys Pro Ser Ser Thr Ser Gly Gly Gly Ala		
2375	2380	2385
Ser Ser Ala Leu Ser Ser Gly Pro Ser Asp Ser Ala Ala Ala Pro		
2390	2395	2400
Asp Gly Cys Glu Ser Ser Pro Val Ala Leu Glu Ser Ala Ser Leu		
2405	2410	2415
Leu Ser Phe Ser Pro Ser Ala Ala Arg Ala Glu Val Leu Thr Val		
2420	2425	2430
Pro Gly Val Gly Leu Val Asn Phe Ser Leu Pro Asp Gly Val Lys		
2435	2440	2445
Phe Asp Lys Ser Lys Leu Ala Phe Arg Cys Tyr Trp Arg Glu Gly		
2450	2455	2460
His Ala Gly Val Val Thr Val Gly Ala Gly Ala Ala Val Ser Pro		
2465	2470	2475

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Ser	Ser	Gly	Ala	Gly	Thr	Phe	Val	Pro	Ser	Arg	Pro	Thr	Val	Cys
2480						2485					2490			
Thr	Ala	Gln	Asn	Lys	Ser	Arg	Thr	Phe	Ser	Cys	Arg	Lys	Tyr	Gly
2495						2500					2505			
Leu	Tyr	Gln	Ser	Arg	Val	Leu	Ala	Leu	Gln	Ala	Arg	Leu	Leu	Ser
2510						2515					2520			
Glu	Leu	Leu	Trp	Pro	Gln	Pro	Pro	Ser	Pro	Ala	Arg	Leu	Arg	Val
2525						2530					2535			
Ser	Ala	Met	Ala	Ala	Val	Val	Tyr	Gly	Leu	Ile	Ala	Ala	Pro	Met
2540						2545					2550			
Pro	Phe	Thr	Asp	Pro	Trp	Gln	Ala	Val	Cys	Gly	Val	Ser	Val	Ala
2555						2560					2565			
Glu	Asp	Ala	Leu	Arg	Gln	Arg	Arg	Glu	Val	Trp	Lys	Asn	Leu	Leu
2570						2575					2580			
Asp	Pro	Arg	Gln	Arg	Arg	Pro	Ala	Pro	Ala	Pro	Ile	Ser	Gln	Leu
2585						2590					2595			
Ser	Leu	Pro	Pro	Val	Ser	Gly	Pro	Pro	His	Ala	Ser	Ser	Ala	Thr
2600						2605					2610			
Gln	Glu	Leu	Pro	Asn	Arg	Pro	Gly	Thr	Pro	Trp	Pro	Gly	Gln	Glu
2615						2620					2625			
Thr	Val	Cys	Gly	Ala	Arg	Gly	Pro	Ala	Pro	Gly	Leu	Ala	Ser	Ala
2630						2635					2640			
Trp	Ala	Thr	Tyr	Gly	Asn	Pro	Gly	Asp	Arg	Asp	Ala	Ala	Glu	Pro
2645						2650					2655			
Gln	Ser	Thr	Tyr	Val	Gly	Arg	Gly	Pro	Ala	Gly	Ala	Glu	Gly	Pro
2660						2665					2670			
Gly	Gly	Gly	Ile	Ala	Val	His	Arg	Glu	Trp	Ala	Arg	Asn	Ser	Gly
2675						2680					2685			
Ser	Glu	Ala	Ala	Gln	Pro	Cys	Gln	Phe	Gly	Arg	Ala	Val	Glu	Arg
2690						2695					2700			
Pro	Val	Pro	Gly	Pro	Gln	Ser	Ser	Leu	Gly	Pro	Gly	Gly	Asp	Asn
2705						2710					2715			
Arg	Gly	Asp	His	Met	Ala	Tyr	Asp	Gln	Ser	Pro	Ala	Gly	Pro	Ala
2720						2725					2730			
Ser	Asn	Ala	Pro	Gly	Pro	Thr	Pro	Pro	Phe	Val	Gly	Pro	Phe	Ser
2735						2740					2745			
Pro	Gly	Leu	Val	Leu	Arg	His	Gly	Pro	Pro	Ala	Phe	Ser	Gln	Asp
2750						2755					2760			
Pro	Ser	Leu	His	Arg	Pro	Pro	Phe	Ala	Ala	Gly	Thr	Gly	Pro	Ala
2765						2770					2775			
Gly	Gln	Arg	Leu	Ala	Ser	Asp	Ser	Pro	Tyr	Pro	Leu	Lys	Asn	Glu
2780						2785					2790			
Ala	Ser	Pro	Gln	Leu	Ala	Met	Ala	His	Ala	Pro	Gly	Phe	Glu	Asn
2795						2800					2805			
Ser	Asp	Gly	Phe	Gln	Gly	Glu	Gln	Pro	Leu	Ala	Lys	Gln	Arg	Lys
2810						2815					2820			
Ile	Glu	Gly	Ala	Ser	Asp	Arg	Pro	Val	Pro	Asp	Glu	Gly	Gln	Val
2825						2830					2835			
Leu	Gly	Thr	Ile	Ser	His	Gly	Lys	Ser	Pro	Ala	Ala	Arg	Pro	Val
2840						2845					2850			
Asp	Gly	Asp	Phe	Ala	Pro	Asp	Gly	Arg	Ser	Pro	Leu	Phe	Ser	Gln
2855						2860					2865			

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Asp	Ala	Ser	Gly	Val	Gly	Gly	Gly	Arg	Pro	Ser	Gly	Val	Gly	Gly
2870						2875					2880			
Gln	Leu	Ala	Ala	Gly	Gly	Lys	Gly	His	Phe	Ala	Thr	Ala	Pro	Phe
2885						2890					2895			
Gly	Ser	Gly	Thr	Leu	Pro	Thr	Thr	Arg	Gly	Pro	Ser	Gln	Pro	Gly
2900						2905					2910			
Gly	Asp	Gly	Leu	Ser	His	Arg	Ser	Gly	Thr	Glu	Pro	Ala	Ala	Ala
2915						2920					2925			
Tyr	Ser	Ser	Pro	Ala	Gly	Ala	Ala	Tyr	Pro	Ser	Ala	Ser	Asn	Ala
2930						2935					2940			
Ser	Pro	Ile	Tyr	Gly	Ala	Ala	Pro	Lys	Arg	Glu	Gly	Asp	Ser	Pro
2945						2950					2955			
Phe	Gly	Pro	Ala	Pro	Pro	Ser	Gly	Tyr	Cys	Arg	Pro	Gly	Ser	Pro
2960						2965					2970			
Ala	Val	Asp	Pro	Lys	Leu	Pro	Gly	Ser	Val	Pro	Ser	Ser	Gly	Asn
2975						2980					2985			
Leu	Asp	Ser	Val	Asn	Tyr	Gly	Ser	Phe	Phe	Pro	Gly	Gln	Gln	Ala
2990						2995					3000			
Pro	Gln	Gly	Asp	Gly	Arg	Ile	Ala	Pro	Trp	Gly	Ser	Gly	His	Val
3005						3010					3015			
Gly	Ala	Pro	Arg	Gly	Glu	Ala	Arg	Gly	Ser	Glu	Arg	Val	Gly	His
3020						3025					3030			
Ala	Gly	Ala	Ser	Arg	Gly	Leu	Thr	Gly	His	Glu	Leu	Glu	Glu	Gly
3035						3040					3045			
Gln	Gly	Gly	Pro	Gly	Glu	Glu	Gly	Ala	Gly	Arg	Glu	Arg	Gln	Arg
3050						3055					3060			
Lys	Arg	Arg	Lys	Ser	Ala	Met	Ser	Met	Ser	Ser	Gln	Gly	Glu	Asn
3065						3070					3075			
Thr	Pro	Leu	Phe	Ala	Pro	Thr	Ser	Leu	Pro	Pro	Val	Pro	Phe	Ala
3080						3085					3090			
Ser	Gly	Asp	Ser	Leu	Ala	Asp	Gly	Ser	Gly	Ser	Asp	Phe	Gly	Gln
3095						3100					3105			
Gln	Leu	Gly	Pro	Pro	Phe	Ser	His	Gly	Ser	His	Ala	Pro	Pro	Phe
3110						3115					3120			
Pro	Glu	Ala	Asn	Ala	Val	Gly	Ser	Gln	His	Phe	Thr	Ala	Asp	Asn
3125						3130					3135			
Leu	Glu	Thr	Pro	Gly	Leu	Pro	Ala	Glu	Leu	Gly	Gly	Gly	Asp	Gly
3140						3145					3150			
Arg	Arg	Gln	Ser	Gly	Ser	Thr	His	Glu	Glu	Val	Ser	Gly	Pro	Arg
3155						3160					3165			
Ala	Gly	Gly	Glu	Lys	Gly	Glu	Phe	Ser	Leu	Glu	Gly	Ala	Pro	Gln
3170						3175					3180			
Ala	Ala	Ala	Gln	Gln	Leu	Ser	Ala	Glu	Thr	Leu	Thr	Phe	Leu	Leu
3185						3190					3195			
Gly	Thr	Asn	Val	Val	Trp	Glu	Glu	Asn	Glu	Lys	Arg	Trp	Arg	Val
3200						3205					3210			
Gln	Val	Arg	Pro	Pro	Ser	Pro	Arg	Gly	Cys	Asp	Gly	Glu	Gly	Ala
3215						3220					3225			
Asp	Gly	Lys	Leu	Gly	Gly	Glu	Lys	Lys	Lys	Arg	Lys	Arg	Asp	Gly
3230						3235					3240			
Phe	Ser	Ala	Gly	Gly	Glu	Arg	Arg	Arg	Ser	Ser	Thr	Gly	Asn	Glu
3245						3250					3255			
Pro	Asp	Asp	Gln	His	Lys	Ala	Gly	Thr	Leu	Glu	Trp	Val	Ser	Met

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3260	3265	3270
Ala Gln Leu His Gln Ala Gln Lys Leu Gln Asn Gln Leu Val Gly		
3275	3280	3285
Lys Met Glu Arg Gly Lys Gly Glu Gly Gly Asp Glu Glu Arg Leu		
3290	3295	3300
Gly Gly Asp Gly Arg Gly Asn Ile Phe Phe Asp Ala Asn Gly Ser		
3305	3310	3315
Asp Glu Asn Ala Lys Lys Ala Ala Leu Leu Lys Ala Arg Arg Trp		
3320	3325	3330
Leu Arg Arg Arg Ile Val Gln Gly Gln Ile Leu Val Thr Gly Leu		
3335	3340	3345
Ser Arg Asp Gly Leu Phe Ser Ser Arg Pro Asp Glu Pro Glu Arg		
3350	3355	3360
Ser Ser Ser Val Ser Thr Gly Ala Phe Thr Gly Ser Ser Pro Asn		
3365	3370	3375
Asp Lys Pro Thr Asp Leu Asn Ala Ala Val Pro Pro Leu Ser Pro		
3380	3385	3390
Phe Phe Ser Pro Ile Pro Phe Gly Ala Thr Thr Ala Pro His Arg		
3395	3400	3405
Pro Ser Pro Gly Phe Tyr Pro Pro Ala Pro Ala His Pro Thr Glu		
3410	3415	3420
Asp Gly Cys Arg Pro Pro Met Pro Ala Pro Val Pro Met His Ala		
3425	3430	3435
Pro Gln Gly Pro Val Asp Ser Arg Thr Tyr Arg Gly Ala Arg Pro		
3440	3445	3450
Val Tyr Pro Gly Ser Asp Val Thr Pro Gln Thr Cys His Gly Val		
3455	3460	3465
Arg Pro Glu Ser Met Gln Glu Glu Gly Arg Ala Ala Leu Leu Ala		
3470	3475	3480
Glu Gln Gly Ser Ala Phe Phe Val Ser Gly Asp Gly Lys Gly Asp		
3485	3490	3495
Asn Arg Gly Ala Thr Val Gly Gln Ile Arg Gln Gly Thr Val Arg		
3500	3505	3510
Val Met Gln Ser Gln Thr Ala Ser Gln Ser Leu Asp Gln Gly Phe		
3515	3520	3525
Asp Leu Pro His Pro Pro Ala Pro Gly Pro Ala Tyr Arg Gly Val		
3530	3535	3540
Pro Val Gly His Gly Pro Ser Gly Pro Tyr Tyr Leu Asn Gly Gly		
3545	3550	3555
Cys Val Ala Gln Arg Pro Tyr Ala Thr Phe Ser Asn Leu Ala Gly		
3560	3565	3570
Pro Val Gln Gly Ser Phe Pro Pro Leu Glu Phe Ser Asn Gly Gly		
3575	3580	3585
Leu Pro Thr Thr Ala Leu Gly Arg Arg Gly Ser Asp Ser Gly Pro		
3590	3595	3600
Gln Gly Ala Gly Arg Asn Ala Ser Gln Met Gln Pro Gly Phe Ala		
3605	3610	3615
Ser Arg Pro His Gly Pro Glu Arg Leu Gly Arg Glu Ser Ala Pro		
3620	3625	3630
Gln Ser Gly Ala Pro Pro Gly Phe Ser Pro His Ala His Gly Arg		
3635	3640	3645
Gly Glu Arg Asp Arg Pro Ser Phe Ser Gly Ala Thr Thr Met Pro		
3650	3655	3660

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Leu Ala Ser Leu Thr Ala Phe Ser His Pro Ala Ala Gly Pro Met
 3665 3670 3675
 Phe Val Gly Thr Glu Gly Arg Gly Gln Gln Gly Asp Ile His Pro
 3680 3685 3690
 Asn Leu Cys Gly Val Ala Pro Val Gly Gly Pro Arg Gly Pro Ala
 3695 3700 3705
 His Ala Pro Met Pro Ala Tyr Gly Pro Gly Gly Ala Ala Gly Pro
 3710 3715 3720
 Pro Arg Asp Asp Arg Arg Ala Glu Gly Gly Ala Pro Gly Val Ser
 3725 3730 3735
 His Ser Asp Ile Phe Leu Ala Asn Asp Arg Arg Leu His Pro Glu
 3740 3745 3750
 Met Cys Leu His Ser Ala Pro Ser Trp Gly Pro Ala Gly Thr Phe
 3755 3760 3765
 Ala Ser Pro Asp Asn Arg Gln Asn Ala Glu Pro Trp Pro Ala Ala
 3770 3775 3780
 His Ala Ser Ser Asn Asn Phe Phe Asp Tyr Thr Gly Val Asn Met
 3785 3790 3795
 Pro Ala Ala Gly Pro Pro Ile Gln Leu Asp Trp Ser Lys Val Arg
 3800 3805 3810
 Gly Ala Gly Gly
 3815

<210> SEQ ID NO 16

<211> LENGTH: 432

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 16

Met Asp Arg Ala Gly Leu Leu Phe Leu Arg Gly Ala Ala Gly Pro Gly
 1 5 10 15
 Pro Leu Lys Cys Phe Gly Pro Arg Val Glu Ala Phe Ser Gly Ser Ile
 20 25 30
 Ser Leu Leu Ser Leu Asp Ser Arg Gly Pro Thr Pro Phe Arg Thr Pro
 35 40 45
 Phe His Thr Thr Ser Ala Leu Ser Lys Ser Arg Gln Pro Pro Lys Glu
 50 55 60
 Ser Pro Glu Ser Ala Ala Ala Cys Thr Phe Ser Pro Leu Phe Pro Ser
 65 70 75 80
 Pro Val Arg Ala Ser Pro His Arg Asn Leu Leu Gly Ala Arg Val Ser
 85 90 95
 Val Pro Cys Lys Pro Leu Ala Cys Val Gly Ala Pro Lys Arg Arg His
 100 105 110
 Gly Glu Thr Ser Asp Gly Phe Ser Ser Arg Ala Ala Val Ala Ala Glu
 115 120 125
 Ala Leu Pro Pro Trp Pro Ser Asp Phe Leu Gln Ser Glu Glu Ile Ala
 130 135 140
 Val Asp Ser Pro Gln Lys Pro Thr Gly Phe Ser Arg Pro Ser Asn Ala
 145 150 155 160
 Arg Val Ser Pro Ala Pro Asn Ala Trp Glu Ala Ala Ala Val Phe Arg
 165 170 175
 Arg Leu His Ala Phe Asp Ser Gly Leu Arg Gly Asp Ala Ser Gly Ala
 180 185 190
 Phe Ala Ala Ser Ala Thr Cys Gly Cys Leu Ala Ala Ala Ser Arg Arg

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195	200	205
Asn Pro Cys Leu Pro Ala Tyr Gln Leu Ser Trp Asn Leu Leu Gln Ala 210 215 220		
Arg Met Phe Gly Gly Arg Ala Gly Gly Leu Lys Arg Arg Lys Pro Arg 225 230 235 240		
Arg Asp Pro Gly Arg Val Ile Gln Ser Gly Met Gly Arg Arg Gln Glu 245 250 255		
Phe Phe Trp Pro Glu Lys Ala Arg Arg Thr Arg Val Pro Leu Tyr Gln 260 265 270		
Asn Ser Arg Pro Asn Leu Val Tyr Asp Gln Arg Phe Arg Arg Phe Met 275 280 285		
Cys Met Trp Tyr Ala Asn Gly Val Gln Val Phe Arg Pro Phe Ser Cys 290 295 300		
Arg Gly Arg Arg Gly Gly Arg Gly Lys Glu Gly Leu Pro Asp Gly Leu 305 310 315 320		
Gly Ile Gly Arg Gly Ser Gly Thr Trp Glu Arg Ala Arg Ala Lys Ala 325 330 335		
Val Val Leu Leu Lys Gln Leu Gln Arg Gln Gly His Leu Asp Arg Leu 340 345 350		
Ala Lys Pro Asp Val Thr Arg Ser Gly Val Arg Gly Val Tyr Phe Asp 355 360 365		
Thr Glu Glu Lys Leu Trp Val Ala Thr Trp Asn Glu His Gly Leu Arg 370 375 380		
Arg Phe Lys Ala Phe Pro Thr Met Glu Met Gly Phe Asp Ala Ala Tyr 385 390 395 400		
Gln Ala Ala Val Ala Val Arg Arg Gln Lys Leu Arg Glu Asn Tyr Ile 405 410 415		
Phe Ser Met Gln Arg Asn Arg Lys Lys Ser Gly Arg Pro Pro Phe Lys 420 425 430		
<210> SEQ ID NO 17		
<211> LENGTH: 1919		
<212> TYPE: PRT		
<213> ORGANISM: Homo sapiens		
<400> SEQUENCE: 17		
Met Glu Leu Pro Asp Gln Ala Ala Tyr Gly Arg Gln Leu Ala Lys Arg 1 5 10 15		
Arg Arg Leu Ser Ala Ser Glu Glu Glu Ala Thr Leu Ala Ser Lys Asn 20 25 30		
Asp Gly Lys Glu Gly Leu Gln Glu Pro Ala Gly Ala Thr Ala Gly His 35 40 45		
Leu Leu Pro Ala Glu Glu Pro Gly Gln Tyr Thr Pro Glu His Thr Glu 50 55 60		
Gly Arg Arg Glu Phe Arg Arg His Pro Val Val Leu Pro Gly Gly Gly 65 70 75 80		
Arg Lys Ala Ala Ser Tyr Gly Leu Ile Ala Val Gly Gly Gly Asp Ser 85 90 95		
Leu Arg Ala Ser Arg Arg Thr Arg Ser Ser Ala Ser Ile Glu Thr Ser 100 105 110		
Ala Glu Glu Lys Glu Thr Tyr Thr Ser Pro Glu Leu Gly Pro Gly Ala 115 120 125		
Ser Trp Ser Val Ser Thr Val Lys Gly Ser Lys Gly Arg Ser Asp Glu 130 135 140		

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Glu	Gly	Arg	Ala	Gly	Lys	Arg	Ala	Gly	Ala	Cys	Ala	Ala	Arg	Asp	Ser	145	150	155	160
Ala	Ala	Gly	Ser	Arg	Thr	Leu	Ala	Gln	Ala	His	Arg	Gly	Ala	Asp	Glu	165	170	175	
Glu	Arg	Met	Pro	Pro	His	Ser	Pro	Ala	Arg	Asp	Gly	Ser	His	Gln	Val	180	185	190	
Cys	Trp	Asp	Ser	Asp	Ala	Leu	Pro	Ser	Pro	Tyr	Asp	Leu	Gly	Leu	Ser	195	200	205	
Glu	Ala	Asp	Asp	Glu	Glu	Val	Ser	Pro	Gln	Lys	Glu	Ala	Leu	Ala	Glu	210	215	220	
Lys	Asn	Gly	Leu	Val	Leu	Phe	Ala	Glu	Gln	Ser	Leu	Gln	Gly	Val	Gly	225	230	235	240
Leu	Ala	Thr	Leu	Thr	Val	Pro	Ser	Gly	Ala	Thr	Ser	Ser	Lys	Gly	Ala	245	250	255	
Phe	Ser	Ala	Gly	Ser	Pro	Phe	Leu	Pro	Gly	Ser	Gly	Thr	Thr	Ala	Ser	260	265	270	
Pro	Arg	Ser	Pro	Val	Pro	Arg	Gly	Asp	Lys	Ser	Leu	Gly	Asp	Gly	Ser	275	280	285	
Val	Gly	Ser	Asp	Asp	Val	Ser	Ala	Lys	Ala	Ser	Pro	His	Ala	His	His	290	295	300	
Asn	Val	Thr	Ala	Gly	Ala	Asp	Ala	Ser	Gln	Ser	Ser	Glu	Asp	Ala	Phe	305	310	315	320
Phe	Pro	Ala	Ala	Pro	Pro	Gly	Gly	Val	Pro	Gly	Thr	Leu	Thr	Val	Glu	325	330	335	
Asp	Leu	Leu	Thr	Met	Pro	Glu	Arg	Arg	Gln	Asp	Pro	Glu	Ala	Glu	Lys	340	345	350	
Ala	Ala	Lys	Thr	Asp	Phe	Asp	Cys	Leu	Ala	Ala	Leu	Ile	Gln	Asp	Ala	355	360	365	
Leu	Gly	Glu	Ala	Gly	Gly	Ala	Ala	Gly	Arg	Val	Ala	Pro	Lys	Arg	Arg	370	375	380	
Cys	Arg	Thr	Leu	Gly	Ala	Gly	Phe	Asn	Pro	Thr	His	Ser	Ala	Arg	Pro	385	390	395	400
Gly	Ser	Gly	Ser	Val	Ala	Gly	Leu	Glu	Ala	Pro	Gly	Ala	Leu	Gly	Arg	405	410	415	
Glu	Leu	Asp	Ala	Leu	Val	Ala	Gly	Gly	Ser	Pro	Glu	Glu	Ser	Arg	Ala	420	425	430	
Asp	Leu	Glu	Pro	Asp	Gly	Gln	Ala	Ala	Gly	Ala	Ser	Trp	Gln	Glu	Ser	435	440	445	
Leu	His	Leu	Gln	Tyr	Asp	Thr	Arg	Asn	Gly	Gly	Thr	Tyr	Glu	Glu	Asp	450	455	460	
Leu	Asp	Ser	Ala	Ser	Leu	Ser	Phe	Leu	Leu	Gly	His	Ser	Glu	Gly	Ser	465	470	475	480
Glu	Lys	Gly	Pro	Ala	Leu	Ser	Ala	Ser	Ala	Gly	Ala	Ser	Thr	Ala	Ala	485	490	495	
Ser	Val	Ser	Ser	Phe	Phe	Pro	Ser	Glu	Ala	Ala	Cys	Gly	Val	Tyr	Ala	500	505	510	
Pro	Gly	Gln	His	Gly	Arg	Pro	Thr	Gln	Ser	Gln	Asp	Pro	Ala	Lys	Glu	515	520	525	
Arg	Gln	Arg	Arg	Leu	Ala	Arg	Asp	Arg	Glu	Thr	Leu	Asn	Leu	Ser	Ala	530	535	540	
Gln	Ile	Ala	Ala	Arg	Phe	Lys	Ser	Cys	Arg	Thr	Glu	Asp	Val	Met	Arg	545	550	555	560
Leu	Phe	Arg	Arg	Tyr	Leu	Ala	Val	Ser	Ser	Arg	Gln	Val	Arg	Asp	Pro				

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565							570					575				
Ala	Thr	Leu	Glu	Arg	Val	Val	Ala	Ala	Cys	Cys	Tyr	Ile	Ser	Ser	Arg	
			580					585					590			
Gln	Ala	Met	Asp	Gly	Leu	Ser	Leu	Ser	Asp	Ile	Cys	His	Glu	Met	Asp	
			595				600					605				
Ala	Ser	Asn	Gly	Gln	Asp	Leu	Phe	Ala	Ala	Gly	Cys	Glu	Ala	Arg	Gly	
			610			615					620					
Lys	Lys	Leu	Ala	Asp	Gly	Glu	Gly	Met	Gly	Arg	Gly	Glu	Ser	Asp	Arg	
					630					635					640	
Glu	Arg	Ala	Gly	Gly	Ala	His	Ala	Ser	Met	Arg	Cys	Lys	Ser	Leu	Gly	
				645					650					655		
Lys	Trp	Val	Val	Arg	Ile	Cys	Arg	Lys	Leu	Gln	Leu	Gln	Ala	Leu	Pro	
			660					665					670			
Asp	Lys	Asp	Asp	Asp	Pro	Glu	Glu	Arg	Ala	Asn	Arg	Val	Leu	Ala	Arg	
			675				680					685				
Val	Lys	Gln	Leu	Leu	Ile	Ala	Lys	Met	Glu	Glu	Glu	Glu	Gln	Arg	Arg	
			690			695					700					
Pro	Gln	Leu	Val	Asn	Ala	Phe	Val	Arg	Ala	Thr	Gln	Ser	Ala	Val	Glu	
					710					715					720	
Lys	Gln	Arg	Leu	Lys	Ala	Glu	Gly	Asp	Arg	Ser	Glu	Ala	Asp	Ser	Leu	
				725					730					735		
Ala	Ser	Leu	Glu	Ser	Leu	Leu	Gly	Asp	Glu	Ala	Arg	Arg	Ala	Asp	Ala	
			740					745					750			
Arg	Ala	Asp	Ala	Glu	Ala	Arg	Arg	Gln	Thr	Pro	Ala	Glu	Ala	Gln	Leu	
		755					760					765				
Gly	Asp	Phe	Leu	Asp	Gly	His	Gln	Gly	Gly	Glu	Lys	Thr	Gly	Arg	Val	
		770				775					780					
Ser	Ser	Ala	Arg	Ile	Asn	Gly	Arg	Ala	Ala	Glu	Ala	Ser	Pro	Ala	Pro	
					790					795					800	
Pro	Ala	Pro	Gln	Gly	Ser	Thr	Ala	Pro	Ala	Asp	Ser	Thr	Pro	Ala	Ala	
				805					810					815		
Gly	Ser	Glu	Glu	Arg	Gln	Ala	Leu	Asn	Ala	Ile	Glu	Glu	Leu	Leu	Ala	
			820					825					830			
Gln	Val	Thr	Gly	Gly	Ser	Asn	Leu	Asp	Cys	Phe	Gly	Ser	Ala	Thr	Leu	
			835				840					845				
Ala	Ala	Val	Asp	Ser	Asp	Leu	Ala	Ser	Gly	Thr	Ser	His	Val	Asp	Arg	
			850			855					860					
Glu	Ser	Cys	Ala	Arg	Leu	Arg	Arg	Leu	Asp	Lys	Ser	Gly	Arg	Asp	Ala	
					870					875					880	
Phe	Ala	Ala	Asp	Ala	Asp	Gly	Pro	Glu	Arg	Pro	Thr	Glu	Asn	Glu	Val	
				885					890					895		
Glu	Pro	Glu	Ala	Arg	Pro	Gly	Ala	Ala	Gly	Val	Leu	Ala	Glu	Asp	Val	
			900				905						910			
Asp	Glu	Ala	Ser	Met	Ala	Leu	Thr	Pro	Asn	Pro	Asp	Asp	Arg	Ser	Ser	
			915				920					925				
Ser	Ala	Ser	Gly	Asp	Ala	Ala	Glu	Pro	Val	Ala	Ser	Ile	Arg	Leu	Glu	
						935					940					
Gln	Arg	Glu	Glu	Lys	Asn	Gly	Asp	Ala	Ser	Gly	Leu	Ser	Leu	Asp	Ile	
					950					955					960	
Cys	Pro	Ser	Leu	Phe	Asp	Pro	Val	Asp	Met	Pro	Ala	Leu	Ser	Ala	Ser	
				965					970					975		
Ser	Glu	Gly	Asp	Ser	Gly	Asp	Ser	Ser	Pro	Phe	Ser	Pro	Ile	Leu	Thr	
			980					985					990			

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Ser	Leu	Leu	Ser	Ala	Ser	Leu	Pro	Pro	Ser	Glu	Thr	Leu	Ala	Gln	Ala
	995						1000					1005			
Lys	Asp	Met	Gln	Pro	Ala	Ala	Arg	Leu	Gln	Leu	Gln	Arg	Phe	Thr	
	1010					1015					1020				
Trp	Leu	Gln	Lys	Met	Arg	Ala	Glu	Ala	Leu	Glu	Lys	Leu	Lys	Lys	
	1025					1030					1035				
Glu	Lys	Glu	Ala	Val	Phe	Arg	Gly	Leu	Val	Leu	Leu	Gln	Arg	Ile	
	1040					1045					1050				
Leu	Gln	Leu	Phe	Tyr	Asp	Val	Lys	Gln	Gly	Glu	Ser	Asp	Gly	Glu	
	1055					1060					1065				
Arg	Glu	Asp	Gly	Glu	Asp	Gly	Glu	Gly	Lys	Lys	Arg	Gln	Lys	Gly	
	1070					1075					1080				
Trp	Thr	Glu	Glu	Asp	Pro	Leu	Asp	Lys	Arg	Trp	Arg	Ala	Arg	Gly	
	1085					1090					1095				
Arg	Cys	Asp	Ala	Val	Ser	Leu	Ala	Ser	Leu	Ile	Ile	Ile	Val	Phe	
	1100					1105					1110				
Lys	Trp	Met	Gln	Ile	Pro	Ile	Pro	Gln	Arg	Ile	Ala	Leu	Asp	Ala	
	1115					1120					1125				
Leu	His	Val	Asp	Arg	Lys	Ser	Val	Tyr	Lys	Arg	Arg	Leu	Glu	Gln	
	1130					1135					1140				
Met	His	Ile	Leu	Lys	Thr	Leu	Phe	Gly	His	Leu	Arg	Gly	Met	Val	
	1145					1150					1155				
Glu	Lys	Lys	Asp	Gly	Ser	Ser	Ser	Ser	Ala	Leu	Ala	Glu	Glu	Leu	
	1160					1165					1170				
Lys	Ala	Ser	Leu	Pro	Pro	His	Leu	Ala	Ser	Leu	Leu	Gln	Gln	Val	
	1175					1180					1185				
Val	Gly	Asn	Pro	Ala	Thr	Met	Gln	Arg	Leu	Leu	Ala	Leu	Ala	Asp	
	1190					1195					1200				
Glu	Glu	Glu	Glu	Leu	Gly	Asn	Phe	Ile	Ser	Ser	Gln	Ser	Leu	Gly	
	1205					1210					1215				
Ser	Asp	Gly	Glu	Ser	Gly	Lys	Ala	Ser	Ala	Gly	Leu	Gly	Gly	Val	
	1220					1225					1230				
Pro	Pro	Pro	Ala	Ala	Ala	Ala	Ser	Pro	Thr	Pro	Val	Lys	Thr	Ser	
	1235					1240					1245				
Gln	Ala	Ser	Phe	His	Pro	Gln	Ala	Pro	Ala	Ala	Ser	Ser	Pro	Glu	
	1250					1255					1260				
Ser	Ser	Ala	Pro	Ser	Val	Ala	Val	Glu	Pro	Glu	Gln	Asp	Ala	Ala	
	1265					1270					1275				
Ser	Ser	Ser	Phe	Leu	Ala	Ala	Ile	Leu	Ala	Glu	Val	Ala	Ala	Glu	
	1280					1285					1290				
Arg	Glu	Val	Gly	Ala	Val	Lys	Thr	Arg	Gly	Pro	Gly	Asp	Ala	Glu	
	1295					1300					1305				
Arg	Thr	Ala	Ala	Glu	Leu	Gly	Phe	Gln	Thr	Arg	Lys	Lys	Arg	Arg	
	1310					1315					1320				
Val	Ser	Glu	Leu	Asn	Ala	Gln	Arg	Ser	Pro	Asp	Asn	Gly	Leu	Gly	
	1325					1330					1335				
Ser	Asp	Leu	Tyr	Asp	Glu	Asp	Arg	Glu	Ala	Ser	Ser	Ala	Val	Pro	
	1340					1345					1350				
Val	Ala	Ser	Pro	Leu	Ala	Asn	Leu	Cys	Ser	Ser	Leu	Ser	Ser	Ser	
	1355					1360					1365				
Ser	His	Arg	Asn	Pro	Ser	Glu	Met	Ala	Ala	Val	Ala	Ser	Val	Ala	
	1370					1375					1380				

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Pro	Ser	Pro	Arg	Ala	Ala	Arg	His	Pro	Arg	Ala	Pro	Asp	Glu	Met
1385						1390					1395			
Thr	Leu	Gln	Gly	Leu	Ala	Val	Gly	Lys	Asp	Ala	Gly	Thr	Pro	Arg
1400						1405					1410			
Gln	Ala	Gly	Gly	Tyr	Ala	Gly	Thr	Phe	Leu	Pro	Gly	Asp	Gly	Asp
1415						1420					1425			
Arg	Val	Ser	Glu	Gly	Glu	Asp	Gly	Arg	Ser	Glu	Arg	Val	Arg	Ala
1430						1435					1440			
Arg	Phe	Leu	Ala	Glu	Arg	Gly	Ser	Met	Asp	Ala	Ser	Ser	Ser	Phe
1445						1450					1455			
Ala	Leu	Gly	Phe	Ser	Leu	Ala	Glu	Ala	Leu	Leu	Arg	His	Gly	Phe
1460						1465					1470			
Cys	Leu	Pro	Ser	Pro	Ser	Asp	Pro	Pro	Ala	Gly	Leu	Ala	Asp	Ala
1475						1480					1485			
Gln	Phe	Ala	Thr	Gly	Asp	Leu	Leu	Arg	Asp	Gly	Gly	Ser	Ser	Ser
1490						1495					1500			
Gly	Glu	Arg	Ala	Leu	Arg	Met	Gln	Pro	Glu	Gly	Phe	Ser	Ala	Thr
1505						1510					1515			
Arg	Gly	Ser	Arg	Pro	Ala	Val	Ala	Pro	Gly	Pro	Ala	Gly	Phe	Gly
1520						1525					1530			
Ile	Gln	Ala	Glu	Ala	Glu	His	Glu	Gly	Arg	Gly	Asp	Val	Asn	Ser
1535						1540					1545			
Thr	Asp	Val	Ile	Phe	Ser	Asn	Arg	Ala	Thr	Arg	Asp	Ile	Ile	Ala
1550						1555					1560			
Ser	Phe	Leu	Ala	Ser	Ala	Ser	Thr	Glu	Gly	His	Pro	Gly	Thr	Ala
1565						1570					1575			
Ser	Leu	Thr	Gly	Arg	Gly	Leu	Glu	Asp	Gly	Arg	Ser	Pro	Arg	Leu
1580						1585					1590			
Arg	Gly	Pro	Leu	Ala	Ala	Val	Pro	Lys	Ala	Val	Ser	Gln	Ala	Asp
1595						1600					1605			
Arg	Gly	Pro	Gly	Arg	Phe	Asn	Arg	Gly	Ala	Ser	Gly	Ser	Cys	Arg
1610						1615					1620			
Gln	Pro	Ser	Ser	Arg	Ser	Pro	Pro	Leu	Pro	Val	Ser	Pro	Tyr	Arg
1625						1630					1635			
Gly	Arg	Thr	Gly	Asp	Ser	Ser	Arg	Gln	Arg	Pro	Leu	Ser	Pro	Ser
1640						1645					1650			
Ser	Leu	Phe	Ala	Ala	Ala	Ala	Ser	Met	Ala	Gly	Val	Leu	Pro	Gly
1655						1660					1665			
Pro	Leu	Pro	Ser	Ser	Arg	Ser	Ala	Gly	Ser	Ser	Ala	Leu	Ser	Pro
1670						1675					1680			
Gly	Val	Glu	Arg	Ser	Pro	Arg	Glu	Arg	Val	Ala	Ala	Gln	Ala	Leu
1685						1690					1695			
Glu	Ala	Thr	Arg	Arg	Gly	Asp	Val	Asp	Asp	Arg	Ser	Leu	His	Pro
1700						1705					1710			
Ser	Ser	Ser	Val	Ser	Ala	Val	Arg	Ser	Leu	Leu	Pro	Ala	Glu	Pro
1715						1720					1725			
Ala	Leu	Gly	Gly	Ala	Ser	Pro	Phe	Ala	Ser	Ser	Ala	Leu	Ala	Met
1730						1735					1740			
Gly	Leu	Pro	Glu	Ala	Gly	Ala	Ser	Gln	Ala	Gly	Ala	Asp	Ala	Pro
1745						1750					1755			
Leu	Ala	Ser	Pro	Ser	Ile	Ala	Leu	Ala	Thr	Val	Ala	His	Leu	Lys
1760						1765					1770			
Ala	Ala	Glu	Lys	Ala	Leu	Leu	Asp	Ser	Val	Pro	Asp	Ser	Ala	Arg

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1775	1780	1785
Val Val Ser Leu Gln Phe Glu Arg Thr Gln Gln Arg Trp Val Cys		
1790	1795	1800
Lys Trp Gln Arg His Lys Pro Ala Gly Ala Pro Ala Asn Arg Lys		
1805	1810	1815
Glu Pro Trp His Arg Arg Cys Phe Ser Val Ile Lys Tyr Gly Tyr		
1820	1825	1830
Glu Gly Ala His Ala Leu Ala Ala Ala Val Ala Lys Lys Leu Arg		
1835	1840	1845
Asp Gly Arg Arg Ala Leu Leu Gln Lys Gln Arg Arg Leu Glu Glu		
1850	1855	1860
Glu Gly Leu Ala Glu Ala Glu Glu Ala Pro Arg Asp Glu Glu Glu		
1865	1870	1875
Val Gly Asp Ala Glu Asp Glu Glu Pro Leu Gly Ala Ala Glu Glu		
1880	1885	1890
Ala Glu Glu Thr Val Ser Pro Arg Val Asp Ala Gly Gly Asp Arg		
1895	1900	1905
Ser Ala Ser Gly Ser Ala Glu Ala Gly Lys Gln		
1910	1915	

<210> SEQ ID NO 18

<211> LENGTH: 485

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 18

Met Cys Val Lys Lys Glu Gly Gly Asp Gly Lys Arg Gly Asn Glu Lys		
1	5	10 15
Asn Gln Val Asn Asp Lys Gly Val Lys Arg Thr Gly Arg Asp Val Glu		
20	25	30
Ser Arg His Ala Pro Ser Val Pro His Leu Glu Lys Leu Val Asp Met		
35	40	45
Ala Met Val Tyr Ser Ser Cys Leu Pro Pro Cys Asp Ser Ser Gln Gly		
50	55	60
Gly Asp Gly Glu Arg Val Lys Arg Asn Ala Gly Ala Lys Arg Lys Gln		
65	70	75 80
Gly Gln Gly Glu Ser Gln Asp Arg Leu Lys Ala Leu His Asp Ser His		
85	90	95
Pro Leu Gln Cys Val Trp Tyr Leu Glu Ser Ser Pro Ala Thr Asn Ile		
100	105	110
Thr Leu Pro Ser Glu Ser Gly Ser Leu Lys Ser Pro Ser Ser Pro Ser		
115	120	125
Lys Arg Ala Ser Pro Asp Arg Val Met Glu Val Ser Ala Ser Leu Cys		
130	135	140
Lys Glu Glu Gln Lys Arg Arg Glu Gly Pro Arg Glu Gly Gln Trp Cys		
145	150	155 160
Cys Ser Trp Ser Phe Pro Arg Gly Arg Pro Thr Gly Thr Lys Phe Ser		
165	170	175
Val Lys Leu Phe Gly Tyr Glu Glu Ala Lys Arg Leu Ala Leu Tyr Thr		
180	185	190
Ala Leu Tyr Ala Tyr Ser Pro Glu Glu Arg Cys Asp Val Leu Gln Glu		
195	200	205
Leu Ile Asp Glu Val Leu Ala Thr Ala Ser Ser Ala Ser Leu Ser Ala		
210	215	220

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Ser His Leu Pro Asn Pro Glu Arg Phe Pro Ala Ile Leu Glu Leu Gln
225                230                235                240

Pro Gln Pro Leu Ser Leu Ser Ser Ser Leu Ser Pro Ser Leu Cys Val
                245                250                255

Arg Leu Asp Ala Cys Ala Phe Pro Ser Pro Val Leu Ser Gly Ser Pro
                260                265                270

Leu Cys Ser Ser Pro Gly Leu Ser Ser Arg Gly Arg Asn Gly Ser Lys
                275                280                285

Ala Ala Arg Glu Thr Leu Ser Ile Asp Arg Gly Ile Arg Leu Ser Ser
290                295                300

Gln Ser Ser Ala Ser Ser Asn Ala Met Pro Ser Gln Phe Pro Gln Arg
305                310                315                320

Trp Gln Ala Thr Glu Val Arg Met Ser Leu Leu Cys Arg Ser Ser Phe
                325                330                335

Arg Ala Ser Arg Arg Arg Glu Gly Gly Asn His Gly Glu Ala Glu Ala
                340                345                350

Glu Ala Lys Arg Ala Gly Gln Thr Arg Glu Lys Thr Gly Arg Arg Asp
                355                360                365

Lys Gly Asn His Pro His Asp Leu Ser Val Asn Asn Arg Lys Glu Pro
370                375                380

Asn Lys Leu Glu Lys Ser His Ser Ser Cys Ser Pro Arg Arg Ser Leu
385                390                395                400

Phe Ser Ser Ile Gln Val Gln Gln Asp Glu Arg Ser Gly Gly Arg Leu
                405                410                415

Leu His Gly Phe Arg Gly Asp Met Glu Glu Gly Lys Arg Ala Ser Arg
                420                425                430

Ala Asn Lys His Val Glu Ala Lys Lys Gly Glu Val Thr Gly Arg Arg
                435                440                445

Lys Gly Val Cys Gly Gly Ala Leu Phe Gly Cys Phe Pro Ala Arg Arg
450                455                460

Gly Arg Glu Arg Gly Glu Asp Glu Gly Glu Arg Glu Lys Ala Gly Gln
465                470                475                480

Val Asn Ala Gln His
                485

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<210> SEQ ID NO 19

<211> LENGTH: 3837

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 19

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Met Ala Phe Ala Pro Arg Thr Ser Pro Arg Leu Ser Ala Gly Ala Gly
1          5          10          15

Gly Pro Ser Glu Ala Ser Arg Gly Gly Thr Ala Ala Gly Ala Pro Leu
20         25         30

Gly Pro Val Glu Thr Pro Thr Gly Arg Glu Pro Ser Ser Pro Phe Leu
35         40         45

Arg Ser Ala Ser Ala Lys Arg Val Thr Arg Ala Arg Ala Gly Phe Leu
50         55         60

Ala Ser Ser Pro Asp Asn Gln Ser Arg Ser Thr Ser Pro Leu Arg Pro
65         70         75         80

Ala Asp Ala Leu Arg Ile Ser Glu Ala Ser Ser Ala Ser Ala Pro Gly
85         90         95

Val Arg Arg Ser Leu Arg Ala Ser Asn Ala Arg Pro Pro Val Ser Ala
100        105        110

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Ser	Arg	Gly	Leu	Met	Gly	Lys	Ala	Gly	Glu	Glu	Gly	Glu	Gly	Ala	Ser
		115					120					125			
Gly	Gly	Gly	Arg	Pro	Gly	Gly	Ala	Arg	Arg	Thr	Ser	Gly	Gly	Gly	Glu
		130				135					140				
Asp	Val	Cys	Ala	Ser	Pro	Arg	Asp	Ile	Ser	Tyr	Arg	Asp	Lys	Gly	Ala
					150					155					160
Gly	Gly	Asp	Ala	Thr	Ala	Ser	Ser	Asn	Ser	Gln	Ser	Pro	Ser	Ser	Val
				165						170				175	
Asp	Ala	Ala	Val	Ser	Ser	Ser	Tyr	Ser	Val	Ala	Ser	Ser	Val	Ser	Ser
			180					185					190		
Pro	Pro	Ala	Ser	Ser	Leu	Ser	Ser	Ala	Leu	Ser	Ser	Ser	Phe	Ser	Ser
		195					200					205			
Ser	Thr	Leu	Ser	Arg	Ser	Gly	Ser	Ser	Val	Cys	Pro	Arg	Ala	Thr	Ser
		210				215					220				
Ala	Val	Ser	Ala	Thr	Leu	Gln	Gln	Gly	Glu	Arg	Ser	Gln	Glu	Ser	Ser
					230					235					240
Leu	Leu	Ala	Gly	Glu	Arg	Glu	Thr	Asp	Arg	Asp	Ala	Asn	Arg	Pro	Gln
				245						250				255	
Arg	Glu	Thr	Asp	Glu	Gly	Gln	Gly	Ala	Lys	Ser	Glu	Thr	Asp	Arg	Ala
			260					265					270		
Pro	Glu	Asp	Asp	Arg	Gly	Arg	Ser	Arg	Arg	Gly	Ser	Ala	Ser	Pro	Val
		275					280					285			
Gln	Gly	Pro	Phe	Ser	Pro	Arg	Gly	Phe	Phe	Ser	Asn	Ala	Val	Thr	Lys
		290				295					300				
Glu	Asn	Ser	Ala	Tyr	Pro	Ala	Thr	Ser	Gly	Gln	Ser	Gly	Gln	Glu	Val
					310					315					320
Gly	Cys	Arg	Pro	Asn	Ser	Thr	Leu	Ser	Ser	Val	Ser	Val	Cys	Ser	Leu
				325						330				335	
Ser	Ser	Arg	Pro	Pro	Ser	Thr	Leu	Ala	Ser	Asp	Gln	Leu	Leu	Ser	Val
			340					345					350		
Pro	Asn	Gly	Asp	Ala	Ser	Thr	Val	Ser	Thr	Ser	Ser	Pro	Ser	Leu	Ser
		355					360					365			
Cys	Ser	Cys	Ser	Ser	Phe	Ser	Ser	Ser	Ser	Ser	Ser	Leu	Ser	Ser	Ser
		370				375					380				
Ser	Leu	Leu	Ser	Ser	Ser	Pro	Leu	Ser	Ser	Thr	Pro	Ser	Ser	Phe	Phe
					390					395					400
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ala	Ser	Val	Ala	Pro	Pro	Gly
				405					410					415	
Glu	Gly	Lys	Gly	Arg	Pro	Pro	Val	Arg	Ser	Gly	Arg	Gly	Ala	Cys	Pro
				420				425					430		
Arg	Lys	Pro	Ala	Gly	Pro	Pro	Pro	Arg	Leu	Cys	Val	Pro	Tyr	Gln	Cys
		435					440					445			
Gln	Phe	Asn	Val	Glu	Lys	Arg	Glu	Trp	Arg	Ala	Arg	Tyr	Leu	Phe	Arg
		450				455					460				
Gly	Gln	Lys	Lys	Met	Arg	Val	Phe	Ser	Leu						

Asn	Leu		Gly	Pro	Gly	Ala	Ser	Glu	Glu	Glu	Thr	Val	Gly	Gly	Glu
530					535						540				
Gly	Gly	Glu	Asp	Ala	Glu	Ser	Arg	Ala	Ala	Glu	Lys	Glu	Arg	Glu	Glu
545					550					555					560
Glu	Gly	Lys	Ala	Ser	Ser	Ser	Ser	Gly	Ser	Ser	Asp	Gln	Asn	Ile	Thr
				565					570					575	
Arg	Val	Glu	Ser	Ser	Glu	Ala	Lys	Glu	Asp	Gly	Glu	Glu	Asn	Ser	Ala
			580					585					590		
Ser	Ser	Lys	Pro	Pro	Gly	Ala	Ala	Ser	Ala	Ala	Thr	Glu	Pro	Ala	Gly
		595					600					605			
Gly	Asp	Ala	Asp	Gly	Arg	Pro	Gly	Arg	Ala	Ala	Ser	Gly	Pro	Gly	Asp
	610					615					620				
Ala	Cys	Arg	Ser	Val	Thr	Ser	Thr	Glu	Thr	Glu	Ala	Ala	Val	Ala	Val
625					630					635					640
Ala	Pro	Glu	Ala	Lys	Gly	Gly	Pro	Ser	Ser	Asp	Val	Ser	Cys	Thr	Leu
				645					650					655	
Asp	Lys	Ser	Arg	Glu	Ser	Arg	Gly	Asn	Gly	Val	Ala	Gly	Lys	Arg	Glu
			660					665					670		
Asn	Pro	Ala	Trp	Ala	Val	Ser	Pro	Ser	Ser	Phe	Ala	Ala	Phe	Val	Glu
		675					680					685			
Thr	Ala	Lys	Ala	Arg	Gln	Trp	Val	Thr	Glu	Ala	Ser	Arg	Leu	Gln	Ala
	690				695							700			
Ala	Ser	Leu	Pro	Pro	Leu	Ala	Pro	Ala	Glu	Arg	Pro	Ala	Arg	Pro	Pro
705					710					715					720
Ile	Leu	Pro	Thr	Leu	Ala	Ser	Ser	Arg	Ala	Arg	Arg	Cys	Thr	Ser	His
				725					730					735	
Ser	Leu	Ile	Ser	Gly	Leu	Ser	Ala	Arg	Glu	Gly	Ser	Gln	Arg	Thr	Val
			740					745					750		
Ser	Gln	Gly	Asp	Ser	Leu	Ser	Pro	Ala	Ser	Gly	Leu	Ala	Gly	Glu	Pro
		755					760					765			
Gly	Ala	Val	Arg	Glu	Ala	Glu	Gly	Arg	Glu	Ala	Ile	Ala	Val	Asp	Asp
	770					775					780				
Glu	Thr	Gly	Gly	Glu	His	Arg	Asp	Phe	Pro	His	Ser	Gln	Gly	Pro	Ala
785					790					795					800
Gly	Arg	Gly	Arg	Leu	Ala	Gly	Ala	Arg	Pro	Ser	Ser	Ser	Asp	Met	Arg
				805					810					815	
Gly	Glu	Lys	Arg	Gly	Arg	Arg	Ala	Leu	Arg	Glu	Gly	Glu	Ser	Lys	Arg
			820					825					830		
Pro	Cys	Arg	Arg	Arg	Glu	Asp	Leu	Lys	Ser	Glu	Glu	Gly	Gln	Arg	Glu
		835					840					845			
Arg	Arg	Arg	Arg	Asp	Thr	Ala	Trp	Pro	Ala	Gly	Arg	Arg	Glu	Ala	Ser
	850					855					860				
His	Gly	Arg	Gln	Asp	Ser	Arg	Val	Lys	Glu	Glu	Thr	Pro	Ala	Pro	Asp
865					870					875					880
Ala	Gly	Ala	Ala												

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945	950	955	960
Ser Leu Ala Ser Pro Ser Ala Ser Trp His Ala Ala Gln Gly Glu Ala	965	970	975
Glu Ile Pro Gly Ala Ser Thr Gly Phe Val Asp Ser Pro Cys Ser Ala	980	985	990
Asn Gly Ser Leu Asp Asp Ser Gly Leu Gly Gly Pro Ala Ala Ala Leu	995	1000	1005
Gln Lys Ser Trp Arg Asp Arg Lys Arg Asn Arg Lys Lys Leu Ser	1010	1015	1020
Lys Ser Met His Arg Lys Ser Leu Ala Ser Leu Gly Met Arg Ala	1025	1030	1035
Pro Pro Gln Asn Ala Cys Leu Ala Asp Pro Ser Asp Val Gly Leu	1040	1045	1050
Gly Val Gln Met Pro Ser Asp Ala Gly Thr Val Pro Gly Ile Ser	1055	1060	1065
Pro Pro Ser Phe Gly Ala Ser Glu Gln Lys Ala Ser Ser Ser Ala	1070	1075	1080
Leu Gly Leu Ala Phe Arg Ala Ser Ser Ser Phe Ser Pro Lys Asn	1085	1090	1095
Gly Asp Val Glu Pro Ala Gly Arg Asn Pro Pro Gln Phe Leu Pro	1100	1105	1110
Thr Ala Ser Val Gln Arg Ala Asp Pro Pro Gly Thr Gly Ala Pro	1115	1120	1125
Pro Ser Gln Gln Val Val Ser Ser Ala Ser Pro Cys Ser Pro Ser	1130	1135	1140
Ala Leu Ala Ala Thr Ala Ser Pro Gly Ala Cys Arg Gly Gly Ala	1145	1150	1155
Ser Arg Asn Gly Asp Pro Gln Gly Glu Arg Phe Ser Phe Pro Ala	1160	1165	1170
Ser Pro Thr Ser Gln Tyr Arg Trp Tyr Ala His Pro Asp Gly Gly	1175	1180	1185
Ala Thr Gly Pro Ser Cys Cys Arg Gln His Val Gly Gly Ser Gly	1190	1195	1200
Gly Gly Gly Trp Pro Val Val Trp Leu Lys Gln Leu Glu Met Ala	1205	1210	1215
Val Asn Gly Pro Pro Lys Phe Cys Ser Tyr Val Glu Ala Val Asp	1220	1225	1230
Lys His Leu Arg Leu Gly Gly Leu Arg Arg Pro Val Ala Phe Leu	1235	1240	1245
Pro Leu Ala Ser Arg Pro Ala Ser Pro Thr Gly Leu Gly Gly Gly	1250	1255	1260
Leu Gly Ala Pro Gly Pro Ala Leu Arg Gln Ala Ser Glu Lys Ala	1265	1270	1275
Leu Ala Ala Glu Gly Arg Gln Gly Gln Asn Glu Glu Lys Gln Val	1280	1285	1290
Gly Trp Lys Ser Ala Thr Gly Ser Lys Ala Gly Met Phe Gln Gly	1295	1300	1305
Asp Ser Gly Glu Thr Thr Ser Glu Arg Gly Ala Glu Glu Ala Glu	1310	1315	1320
Gly Thr Gly Gly Gly Arg Arg Gly Ile Leu Gly Lys Glu Glu Glu	1325	1330	1335
Asp Arg Asn Gly Gly Glu Gly Glu Lys Ala Ala Thr Pro Thr Met	1340	1345	1350

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Gly	Gly	Ala	Ser	Pro	Ala	Ala	Ser	Asp	Asp	Ala	Leu	Ser	Pro	Met
1355						1360					1365			
Lys	Ala	Asp	Arg	Pro	Ala	Glu	Ala	Leu	Gly	Thr	Gly	Gly	Ser	Ala
1370						1375					1380			
Pro	Thr	His	Ala	Asp	Ser	Arg	Arg	Ala	Pro	Gly	Met	Pro	Glu	Gly
1385						1390					1395			
Glu	Lys	Met	Thr	Gly	Pro	Ser	Lys	Glu	Gln	Glu	Met	Ala	Glu	Ala
1400						1405					1410			
Gly	Glu	Arg	Asp	Arg	Cys	Glu	Arg	Ser	Leu	Glu	Arg	Asn	Ala	Glu
1415						1420					1425			
Leu	Val	Leu	Lys	Glu	Asn	Val	Ser	Met	Thr	Ser	Ala	Ser	Asp	Val
1430						1435					1440			
Ser	Glu	Ala	Ala	Glu	Glu	Lys	Gly	Ala	Pro	Lys	Lys	Leu	Ala	Ser
1445						1450					1455			
Ser	Pro	His	Ser	Val	Glu	Ser	Pro	Cys	Gly	Arg	Thr	Ala	Glu	Lys
1460						1465					1470			
Thr	Gly	Thr	Leu	Asn	Thr	Ser	Glu	Lys	Gly	Glu	Asn	Thr	Arg	Thr
1475						1480					1485			
Ala	Glu	Gly	Asp	Asp	Pro	Gly	Thr	Thr	Ile	Val	Lys	Glu	Glu	Phe
1490						1495					1500			
Pro	Leu	Leu	Pro	Ala	Pro	Glu	Thr	Pro	Val	Thr	Val	Thr	Ala	Gln
1505						1510					1515			
Asp	Leu	Leu	Ser	Pro	Thr	Val	Tyr	Thr	Pro	Arg	Trp	Gln	Ala	Thr
1520						1525					1530			
Val	Gly	Lys	Ser	Leu	Glu	Leu	Gly	Ser	Leu	Asn	Cys	Glu	Lys	Ser
1535						1540					1545			
Cys	Glu	Arg	Gly	His	Trp	Ala	Asp	Ala	Ser	Ala	Cys	Asp	Leu	Glu
1550						1555					1560			
Thr	Lys	Asp	Leu	Arg	Leu	Pro	Glu	Asp	Asn	Lys	Ser	Glu	Glu	Leu
1565						1570					1575			
Lys	Lys	Glu	Thr	Gly	Met	Phe	Leu	Gly	Val	Glu	Gly	Glu	Gln	Val
1580						1585					1590			
Glu	Glu	Ala	Lys	Ser	Ser	Lys	Glu	Ala	Phe	Ser	Pro	Glu	Glu	Arg
1595						1600					1605			
Glu	Arg	Glu	Glu	Gln	Lys	Glu	Ser	Ser	Lys	Ala	Ala	Gly	Gly	Gly
1610						1615					1620			
Asp	Ser	Cys	Arg	Thr	Pro	Arg	Gln	Gln	Glu	Ala	Thr	Pro	Arg	Ala
1625						1630					1635			
Ser	Glu	Glu	Cys	Gln	Pro	Glu	Ser	Arg	Ile	Asp	Met	Lys	Val	Ser
1640						1645					1650			
Pro	Asn	Thr	Glu	Met	Met	Val	Glu	Lys	Leu	Glu	Glu	Thr	Arg	Val
1655						1660					1665			
Gln	Asn	Thr	Glu	Glu	Pro	Glu	Lys	Val	Glu	Glu	Lys	Glu	Glu	Gly
1670						1675					1680			
Gly	Ser	Val	Cys	Arg	Asp	Val	Ser	Val	Ala	Ser	Pro	Leu	Glu	Ser
1685						1690					1695			
Pro	Asn	Ser	Arg	Leu	Ser	Glu	Lys	Gly	Asp	Gln	Ser	Glu	Thr	Pro
1700						1705					1710			
Ala	Gly	Val	Ala	Pro	Pro	Ser	Ser	Ser	Ala	Leu	Glu	Ala	Arg	Ala
1715						1720					1725			
Gly	Arg	Asp	Ser	Ala	Leu	Leu	Ser	Ala	Ser	Leu	Pro	Leu	Ser	Pro
1730						1735					1740			

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Arg	Ala	Ser	Cys	Pro	Pro	Thr	Gln	Ser	Ala	Ser	Pro	Ala	Ser	Arg
1745						1750					1755			
Asp	Pro	Thr	Pro	Ala	Ser	Leu	Arg	Val	Ser	Ser	Val	Ala	Ser	Gly
1760						1765					1770			
Asp	Arg	Asn	Gly	Pro	Thr	Gly	Ile	Leu	Phe	Arg	Pro	Leu	Ser	Ser
1775						1780					1785			
Pro	His	Lys	Arg	Val	Ser	Phe	Cys	Leu	Arg	Gly	Gly	Ala	Glu	Pro
1790						1795					1800			
Pro	Gln	Arg	Pro	Leu	Ser	Glu	Ala	Val	Pro	Tyr	Pro	Leu	Asn	Ala
1805						1810					1815			
Arg	Leu	Gln	Glu	Ile	Val	Ser	Arg	Phe	Arg	Leu	Leu	Gln	Gly	Val
1820						1825					1830			
Ser	Ala	Ala	Arg	Val	Ser	Ser	His	Gly	Lys	Gly	Glu	Thr	Ser	Ser
1835						1840					1845			
Gln	Ala	Thr	Pro	Lys	Ala	Val	Gln	Gly	Glu	Ala	Thr	Val	Lys	Glu
1850						1855					1860			
Lys	Ala	Thr	Val	Thr	Pro	Thr	Glu	Ser	Ala	Lys	Ser	Leu	Ala	Gly
1865						1870					1875			
Gly	Gln	Ala	Glu	Thr	Glu	Lys	Gly	Glu	Ser	Pro	Ser	Gly	Ala	Glu
1880						1885					1890			
Ala	Ala	Thr	Gln	Lys	Ala	Asp	Glu	Lys	Glu	Lys	Thr	Pro	Asp	Thr
1895						1900					1905			
Asp	Ala	Thr	Gln	Ser	Arg	Ser	Thr	Ser	Ser	Gly	Phe	Glu	Thr	Gln
1910						1915					1920			
Glu	Ala	Lys	Thr	Ala	Pro	Ala	Ser	Ile	Leu	Pro	Ala	Ser	Ser	Leu
1925						1930					1935			
Pro	Ser	Ser	Asp	Arg	Pro	Ser	Ala	Ser	Cys	Ser	Asp	Thr	His	Ala
1940						1945					1950			
Ser	Arg	Asp	Ala	Val	Pro	Leu	Ala	Ser	Ser	Pro	Ser	Ser	Ser	Ser
1955						1960					1965			
Ser	Pro	Ala	Leu	Arg	Arg	Cys	Ser	Val	Arg	Gly	Lys	Asp	Leu	Val
1970						1975					1980			
Ser	Ala	Pro	Val	Asp	Ser	Phe	Ser	Glu	Gly	Asp	Ser	Ser	Asp	Ala
1985						1990					1995			
Arg	Pro	Phe	Val	Ser	Val	Arg	Asp	Leu	Ala	Val	Lys	Leu	Tyr	Arg
2000						2005					2010			
Trp	Leu	Glu	Gln	Gly	Glu	Gly	Leu	Pro	Ala	Ala	Ala	Gly	Glu	Pro
2015						2020					2025			
Gln	Gly	Ala	Cys	Gly	Val	Gly	Ala	Lys	Ala	Gln	Ala	Arg	Glu	Ala
2030						2035					2040			
Leu	Arg	Ile	Asp	Thr	Val	Pro	Phe	Ile	Ser	Arg	Trp	Arg	Gln	Met
2045						2050					2055			
Leu	Glu	Arg	Ser	Leu	Ser	Ile	Ala	Ser	Asp	Leu	Arg	Lys	Leu	Asp
2060						2065					2070			
Leu	Gln	Val	Val	His	Leu	Val	Glu	Leu	Thr	Glu	Ala	Leu	His	Ile
2075						2080					2085			
Ala	Val	Tyr	Ile	Cys	Gly	Gln	Leu	Arg	Arg	Arg	Leu	Arg	Glu	Gly
2090						2095					2100			
Ala	Ala	Pro	Asp	Ala	Gly	Ala	Ala	Glu	Asp	Leu	Ala	Pro	Val	Asp
2105						2110					2115			
Val	Asp	Asp	Pro	Arg	Gly	Cys	Ser	Gln	Gln	Ser	Gly	Asp	Thr	Arg
2120						2125					2130			
Asp	Ser	Ser	Ser	Pro	Ala	Thr	Pro	Gly	Gly	Arg	Leu	Ala	Gly	Gly

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2135	2140	2145
Ala Gly Gly Ala Ala Thr Ser Pro Lys Gly Gln Ala Phe Ala Pro		
2150	2155	2160
Arg Gly Gly Glu Gly Glu Ile Lys Pro Gln Glu Thr Gly Asn Ser		
2165	2170	2175
Gly Asp Ser Lys Ala Glu Gly Lys Glu Ala Ser Gly Asp Ala Asn		
2180	2185	2190
Thr Ser Glu Gly Lys Arg Leu Ser Gly Glu Val Asp Lys Thr Ala		
2195	2200	2205
Glu Val Glu Thr Ala Gly Ser Glu Asp Ile Asn Val Glu Arg Gly		
2210	2215	2220
Val Pro Gly Ala Gln Ala Glu Thr Ala Arg Thr Glu Met Asn Gly		
2225	2230	2235
Gly Val Val Lys Gly Gln Glu Thr Ser Gly Asp Ile Leu Ser Val		
2240	2245	2250
Gly Ser Ser Gln Val Leu Ser Leu Ser Ser Pro Ser Leu Ser His		
2255	2260	2265
Leu Ala Ser Ser Ser Gly Lys Gly Pro Leu Lys Pro Thr Ser Ser		
2270	2275	2280
Pro Ser Ser Ser Leu Tyr Ala Leu Ser Pro Ser Ser Ser Ala Ala		
2285	2290	2295
Ser Pro Phe Ser Ala Gln Leu Ala Ser Pro Ser Ser His Ala Pro		
2300	2305	2310
Leu Ser Leu Ser Phe Arg Ser Ser Ser Ser Pro Thr Ser Leu Ser		
2315	2320	2325
Ser Pro Leu Ala Ser Tyr Pro Phe Pro Gln Thr Leu Gln Gln Thr		
2330	2335	2340
Ser Ala Ser Pro Ser Ser Ser Ala Ser Ala Arg Pro Ser Cys Ala		
2345	2350	2355
Ser Val Lys Pro Leu Arg Glu Ala Gly Asp Leu Val Arg Ala Ala		
2360	2365	2370
Ala Arg Ala Ala Leu Glu Gln Ala Gln Val Phe Gly Val Gly Gly		
2375	2380	2385
Lys Leu Ser Asp Ala Thr His Gln Leu Ala Ala Arg Val Thr Val		
2390	2395	2400
Ala Val Arg Ala Ala Met Leu Ala Lys Gly Glu Gly Gly Leu Thr		
2405	2410	2415
Arg Gly Asp Val Asp Leu Leu Val Glu Glu Thr Glu Arg Phe Val		
2420	2425	2430
Arg Glu Ala Arg Phe Lys Ala Gln Glu Thr Ala Ala Glu Thr Thr		
2435	2440	2445
Ala Leu Pro Asp Gly Val Ala Glu Val Val Ser Ser Glu Ala Gly		
2450	2455	2460
Leu Gly Leu Gln Thr Thr Asn His Ala Pro Val Ser Pro Ala Ala		
2465	2470	2475
Ala Pro Ser Ala Gly Gly Ala Phe Ala Gly Leu Thr Glu Ala Val		
2480	2485	2490
Glu Val Glu Ala Arg Gln Leu Pro Glu Ala Ser Glu Arg Val Gly		
2495	2500	2505
Arg Val Ser Ser Pro Arg Gly Ser Leu Gly Phe Glu Ala Met Asp		
2510	2515	2520
Leu Ala Gly Glu Leu His Leu Val Lys Val Leu Asn Ala Phe His		
2525	2530	2535

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Arg His	Thr Glu Cys Leu Met	Asn Glu Arg Glu Arg	Leu Ile Gln
2540	2545	2550	
Ala Thr	Asn Glu Asp Leu Ser	Phe Leu Leu His	Ala Met Glu Leu
2555	2560	2565	
Ala Leu	Pro Ser Gly Leu Asp	Thr Pro Leu Leu Ser	Ile Leu Glu
2570	2575	2580	
Gly Asp	Val Asp Ile Leu Pro	Pro Leu Pro Pro	Pro Asn Val Glu
2585	2590	2595	
Ala Leu	Ile Tyr Leu His Ala	Val Ser Leu Ala Gln	Ala Asp Ala
2600	2605	2610	
Ser Ala	Ser Pro Ser Ser Pro	Ser Ala Val Ala Pro	Cys Leu Leu
2615	2620	2625	
Ser Pro	Ser Ala Arg Leu Leu	Leu Ala His Phe	Ala Gly Ala Ser
2630	2635	2640	
Pro Thr	Ala Gly Gly Leu Gly	Gly Asp Ser Ala Lys	Gly Arg Thr
2645	2650	2655	
Met Ser	Ser Phe Pro Gly Arg	Pro Gly Glu Glu Arg	His Arg Ala
2660	2665	2670	
Asp Glu	Arg Lys Gly Ser Val	Leu Pro Val Arg Arg	Gly Arg Pro
2675	2680	2685	
Pro Ser	Ser Ala Arg Leu Asn	Ala Leu Arg Arg Leu	His Ala Val
2690	2695	2700	
Gly Glu	Pro Ala Ala Asp Ala	Gly Leu Asp Thr Val	Asn Gly Arg
2705	2710	2715	
Phe Arg	Ser Lys Arg Leu Arg	Ala Met Ser Gln Glu	Glu Glu Ala
2720	2725	2730	
Arg Arg	Ala Ala Thr His Ala	Ser Pro Thr Ile Pro	Tyr Pro Leu
2735	2740	2745	
Ser Arg	Tyr Leu His Arg Pro	Pro Arg Leu Leu Ser	Pro Thr Asp
2750	2755	2760	
Ala Gly	His Phe Ala Ser Ser	Tyr Ser Ser Pro Leu	Ser His Pro
2765	2770	2775	
Leu Ser	Lys Gly Ser Ser Leu	Thr Ser Pro Lys Arg	Gln Arg Arg
2780	2785	2790	
Ser Val	Cys Ser Glu Ala Pro	Glu His Glu Arg Lys	Asn Leu Arg
2795	2800	2805	
Ser Leu	Phe Lys Ser Pro Ser	Ala Gln Arg Glu Glu	Ala Pro Arg
2810	2815	2820	
Ser Leu	Thr Arg Pro Phe Gly	Pro Leu Lys Gly Glu	Gly Phe Ser
2825	2830	2835	
Pro Ala	Ser Leu Gly Thr Leu	Gly Ser Arg Arg Gln	Ser Glu Leu
2840	2845	2850	
Gly Ile	Arg Arg Arg Asp Ala	Leu Val Ala Phe Pro	Pro Ala Gly
2855	2860	2865	
Met Pro	Cys His Pro Ala Ser	Pro Gly Arg Arg Leu	Glu Arg Pro
2870	2875	2880	
Arg Val	Asp Gly Ala Asp Met	Asp Gly Glu Arg Arg	Arg Arg Thr
2885	2890	2895	
Arg Cys	Ala Gly Asp Arg Leu	Glu Glu Arg Arg Arg	Pro Leu Gly
2900	2905	2910	
Pro Val	Tyr Ile Pro Thr Lys	Val Arg Asp Pro Ala	Thr Gly Arg
2915	2920	2925	

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Val	Ala	Val	Cys	Ala	Cys	Asp	Thr	Glu	Arg	Gly	Glu	Arg	Val	Arg
2930						2935					2940			
Lys	Val	Gln	Leu	Phe	Glu	Lys	Pro	His	Val	Gly	Ala	Phe	Trp	Cys
2945						2950					2955			
Ala	Arg	Tyr	Gly	Pro	Asn	Asp	Glu	Phe	Val	Arg	Cys	Phe	Ser	Ile
2960						2965					2970			
Glu	Lys	Val	Gly	Ser	Leu	Lys	Ala	Leu	Val	Ser	Ala	Val	Arg	Phe
2975						2980					2985			
Arg	Gln	Tyr	Val	Thr	Gly	His	Ser	Leu	Gly	Tyr	Gly	Val	Gly	Asn
2990						2995					3000			
Cys	Val	Pro	Val	Glu	Thr	Ile	Arg	Ser	Ala	Gly	Arg	Arg	Asp	Arg
3005						3010					3015			
Asn	Gly	Asp	Val	Ala	Pro	Asp	Arg	Pro	Leu	Lys	Gln	Ala	Ala	Ala
3020						3025					3030			
Ser	Pro	Pro	Pro	Ala	Gly	Val	Ala	Gly	Ala	Leu	Gly	Arg	Gly	Glu
3035						3040					3045			
Val	Gly	Gln	Ala	Gln	Asp	Glu	Ser	Gly	Glu	Thr	Arg	Asp	Ala	Val
3050						3055					3060			
Glu	Glu	Glu	Gly	Arg	Gly	Gln	Glu	Pro	Leu	Gly	Ser	Gly	Glu	Gly
3065						3070					3075			
Ala	Ser	Gly	Val	Ala	Ala	Lys	Glu	Gly	His	Gly	Ser	Ser	Arg	Gly
3080						3085					3090			
Glu	Gly	Glu	Gly	Ala	Glu	Gly	Arg	Thr	Asp	Ser	Ala	Ala	Gly	Ser
3095						3100					3105			
Thr	Ala	Gly	Asp	Arg	Ser	Thr	Glu	Asp	Ser	Ser	Arg	Leu	Leu	Ser
3110						3115					3120			
Glu	Gly	Arg	Asp	Ala	Lys	His	Gly	Ser	Ser	Pro	Ala	Gly	Gly	Ser
3125						3130					3135			
Glu	Ala	Leu	Ala	Pro	Gly	Gly	Glu	His	Ala	Leu	Ala	Glu	Gly	Ser
3140						3145					3150			
Glu	Lys	Val	Gly	Arg	Ala	Gln	Glu	Thr	Glu	Ala	Arg	Lys	Glu	Asp
3155						3160					3165			
Leu	Arg	Thr	Ser	Gln	Asn	Glu	Thr	His	Ser	Gly	Glu	Asp	Val	Ser
3170						3175					3180			
Ser	Leu	Asn	Glu	Lys	Ala	Leu	Asp	Ser	Pro	Arg	Ser	Ser	Ala	Pro
3185						3190					3195			
Gln	Gly	Lys	Ser	Asp	Gln	Gly	Arg	Glu	Pro	Ile	Ala	Leu	Arg	Ile
3200						3205					3210			
Arg	Ser	Thr	Leu	Pro	Pro	Ser	Glu	Val	Asp	Lys	Gln	Glu	Ala	Ala
3215						3220					3225			
Gly	Gln	Gly	Gly	Ser	Ala	Ser	Glu	Leu	Ala	Phe	Pro	Thr	Gly	Val
3230						3235					3240			
Ser	Leu	Ala	Ser	Pro	Val	Ser	Pro	Phe	Ser	Ala	Leu	Ala	Arg	Ser
3245						3250					3255			
Pro	Ile	Ser	Ala	Arg	Ala	Ser	Ser	Val	Ser	Pro	Gly	Ala	Cys	Asp
3260						3265					3270			
Arg	Pro	Asp	Val	Ser	Arg	Arg	His	Ser	Gly	Ser	Ser	Asp	Glu	Ala
3275						3280					3285			
Ser	Glu	Ala	Leu	Trp	Asp	Leu	Gly	Glu	Asp	Leu	Gly	Phe	Ala	Gly
3290						3295					3300			
Asp	Asp	Ala	Asn	Phe	Pro	Phe	Leu	Asp	Ser	Glu	Asn	Ser	Ala	Leu
3305						3310					3315			
Leu	Phe	Ala	Pro	Pro	Arg	His	Leu	Met	Ser	Pro	Gly	Ser	Ala	Ser

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3320	3325	3330
Pro Thr Gly Gly Gly Leu Gly Ile His Tyr Asp Lys Thr Lys His		
3335	3340	3345
Arg Trp Lys Ala Thr Trp Thr Thr Leu Asp Gly Gln Arg Ala Ser		
3350	3355	3360
Thr Ser Phe Ser Val Lys Val Leu Gly Met Glu Arg Ala Arg Glu		
3365	3370	3375
Leu Ala Leu Glu Ala Arg Gln Arg Ala Leu Ala Gly Leu Asp Pro		
3380	3385	3390
Arg Glu Val Arg Asp Glu Met Val Ala Gly Gly Ala Ala Ala Arg		
3395	3400	3405
Asp Arg Glu Arg Glu Arg Gly Arg Gln Asp Gly Arg Arg Glu Gly		
3410	3415	3420
Ser Glu Arg Arg Val Gly Phe Glu Ala Glu Ala Glu Gly Thr Glu		
3425	3430	3435
Ala Ala Ser Glu Arg Leu Arg Arg Arg Gly Glu Arg Glu Asp Gly		
3440	3445	3450
Asp Glu Glu Arg Arg Arg Lys Lys Thr Arg Gly Asp Glu Leu Arg		
3455	3460	3465
Gly Ala Glu Gly Asp Arg Glu Glu Arg Glu Leu Arg Arg Arg Lys		
3470	3475	3480
Thr Ser Glu Glu Arg Arg Lys Gly Lys Asn Glu Ala Ala Lys Asn		
3485	3490	3495
Glu Ala Ala Lys Asn Glu Ala Ala Lys Asn Glu Gly Gly Lys Gly		
3500	3505	3510
Glu Thr Trp Lys Val Arg Glu Gly Gly Lys Thr Pro Leu Gly Val		
3515	3520	3525
Lys Ser His Arg Ala Lys Val Val Gly Gln Thr Val Glu Arg Arg		
3530	3535	3540
Gly Glu Glu Arg Arg Arg Asp Leu Arg Gly Ser Arg Arg Glu Glu		
3545	3550	3555
Gly Lys Thr Val Trp Gly Gln Glu Gln Asp Ala Glu His Gln Val		
3560	3565	3570
Phe Glu Gly Val Lys Glu Asp Asp Asn Glu Arg Gly Arg Arg Arg		
3575	3580	3585
Glu Arg Arg Arg Phe Glu Glu Arg Asp Ser Leu Arg Gly Ser His		
3590	3595	3600
Gly Ala Thr Pro Ser Asp Glu Gln Arg Gln Met Arg Arg Gln Thr		
3605	3610	3615
Ile Leu Gly Ser Arg Glu Val Asp Gly Lys Pro Leu Ser Phe Asp		
3620	3625	3630
Asp Thr His Arg Val Asp Ala Gln Leu Gly Ile Gln Asn Glu Val		
3635	3640	3645
Ala Phe Pro Gly Pro Gln Gly Val Gly Gly Ala Gly Asn Ser Leu		
3650	3655	3660
Gln Phe Gly Arg Glu Gly Glu Arg Phe Ala Ser Ser Ser Pro Val		
3665	3670	3675
Ala Phe Leu Arg Thr Lys Glu Glu Asp Glu Glu Ile Val Glu Val		
3680	3685	3690
Phe Leu Thr Pro Glu Gly Ser Gly Ser Glu Arg Asp Lys Ala Ser		
3695	3700	3705
Ser Val Ser Ala Ser Ser Ala Pro Arg Asp Ser Arg Pro Ala Ser		
3710	3715	3720

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Pro Arg  Leu Arg Ala Ser Arg  Leu Arg Glu Ser Ala  Arg Leu Gln
3725                      3730                      3735

Arg Arg  Leu Glu Glu Ala Glu  Val His Asp Arg Gly  Ser Arg Pro
3740                      3745                      3750

Leu Arg  Pro Glu Glu Arg Arg  Val Ala Lys Arg His  Val Ala Glu
3755                      3760                      3765

Glu Asn  Val Asp Ala Thr Phe  Ser Ala Gly Ala Gly  Gly Thr Lys
3770                      3775                      3780

Lys Ile  Arg Pro His Ser Ser  His Asp Phe Ser Ala  Glu Gly Leu
3785                      3790                      3795

Ser Lys  Phe Gln Glu Leu Leu  Thr Trp Asp Cys Glu  Val Glu Ile
3800                      3805                      3810

Asp Gly  Thr Asp Ala His Val  Trp Arg Ala Val Ala  Ala Leu Pro
3815                      3820                      3825

Gly Pro  Arg Pro Arg Pro Arg  Tyr Val
3830                      3835

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<210> SEQ ID NO 20
<211> LENGTH: 1292
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 20

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Met Cys Gln Glu Arg Lys Pro Arg Glu Leu Ser Leu Arg Asn Asn Ser
1              5              10              15

Arg Ala Arg Glu Arg Arg Gly Ser Lys Leu Glu Pro Gly Val Ser Cys
20              25              30

Leu Ser Leu Ser Ala Cys Pro Ser Val Ala Pro Asn Asp Arg Gly Gly
35              40              45

Val Thr Thr Pro Arg Ser Leu His Ala Trp Thr Arg Glu Val Ser Ala
50              55              60

Cys Arg Leu Pro Arg Gln Gln Val Ser Arg Pro Leu Pro Arg Arg Ser
65              70              75              80

Leu Ser Arg Pro Arg Ser Glu Pro Asp Ala Ser Pro Val Lys Gly Pro
85              90              95

Gly Gln Arg Val Glu Ala Ser Ala Val Glu Gly Gly Pro Ser Ala Ser
100             105             110

Ser Ala Glu Arg Leu Gln Val Asp Asp Gly Leu Ala Ala Met Arg Lys
115             120             125

Thr Lys Lys Gly Lys Gly Glu Glu Gly Gly Glu Glu Thr Glu Arg Trp
130             135             140

Ala Thr Gln Ala Val Glu Gln Gln Gly Thr Leu Lys Pro Ala Gly Glu
145             150             155             160

Glu Thr Ala Val Pro Gly Ala Ser Glu Arg Ser Ala Ser Pro Gln Gln
165             170             175

Ala Met Glu Gly Ser Cys Gly Val Glu Thr Pro Glu Thr Phe Phe Gly
180             185             190

Val Ser Thr Gly Asn Ser Gln Gly Ser Pro Ser Pro Glu Ser Val Ala
195             200             205

Gly Glu Glu Ala Arg Pro Glu Arg Glu Asn Ala Glu Lys Ser Ala Thr
210             215             220

Gly Gly Ser Ala Ser Lys Ala Lys Lys Pro Ser Arg Glu Ser Ala Arg
225             230             235             240

Arg Pro Asp Thr Ala Leu Ile Asp Arg His Leu Ile Ala Ala Ser Pro

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245							250					255				
Ser	Pro	Ser	Ser	Ala	Arg	Arg	Ser	Ser	Thr	Cys	Ser	Pro	Ser	Pro	His	
			260					265					270			
Ser	Arg	Glu	Gly	Glu	Asp	Lys	Pro	Gly	Ser	Gly	Ala	Pro	Pro	Ala	Ser	
		275					280					285				
Ser	Pro	Ser	Ala	Asn	Ala	Gly	Ala	Leu	Glu	Pro	Ala	Glu	Lys	Gly	Thr	
		290				295					300					
Leu	Gly	Ser	Pro	Pro	Gln	Asp	Val	Leu	Pro	Ala	Leu	Pro	Ala	Ser	Ser	
305					310					315					320	
Ser	Ser	Pro	Ser	Thr	Gly	Gly	Gly	Ser	Pro	Leu	Ser	Pro	Pro	Pro	Gly	
				325					330					335		
Gln	Ala	Pro	Arg	Ala	Glu	Ser	Gly	Ala	Pro	Gly	Ser	Gly	Ala	Leu	Ser	
			340					345					350			
Leu	Arg	Arg	Ser	Leu	Arg	His	Arg	Gln	Pro	Val	Arg	Pro	Ala	Ala	Ile	
		355					360					365				
Ala	Val	Ser	Pro	Leu	Gly	Gly	Pro	Gly	Ser	Ser	Leu	Ser	Ser	Arg	Ser	
		370				375					380					
Ala	Ser	Pro	Thr	Arg	Arg	Gly	Gly	Val	Ser	Pro	Cys	Gly	Pro	Ala	Thr	
385					390					395					400	
Ala	Val	Gly	Lys	Gly	Ala	Gly	Ala	Ala	Ser	Gly	Ala	Ala	Ala	Leu	Pro	
				405					410					415		
Gly	Val	Gly	Ala	Lys	Ala	Pro	Pro	Ser	Ala	Thr	Pro	Leu	Ala	Gly	Leu	
			420					425					430			
Ser	Gly	Arg	Ser	Leu	Leu	Ala	Ser	Val	Ser	Pro	Ser	Ala	Ala	Ala	Leu	
		435					440					445				
Gly	Pro	Gly	Ala	Pro	Gly	Lys	Lys	Lys	Ala	Gly	Gln	Val	Gln	Gly	Ala	
		450				455					460					
Ala	Lys	Ala	Arg	Gly	Ala	Pro	Pro	Phe	Val	Leu	Ala	Glu	Tyr	Trp	Pro	
465					470					475					480	
Gly	Val	Thr	Leu	Asp	Glu	Met	Glu	Lys	Gly	Glu	Leu	Ser	Trp	Ala	Arg	
			485						490					495		
Ala	Ala	Ala	Gly	Leu	Pro	Leu	Pro	Ala	Ser	Pro	His	Lys	Val	Pro	Gly	
			500					505					510			
Gly	Pro	Ala	Pro	Pro	Val	Gly	Gly	Pro	Pro	Ala	Arg	Asp	Glu	Asp	Ser	
		515					520					525				
Val	Ala	Ala	Cys	Ala	Gly	Glu	Lys	Gly	Lys	Glu	Lys	Ala	Phe	Leu	Gly	
		530				535					540					
Ser	Gly	Arg	Ser	Gln	Ala	Ala	Gln	Gly	Leu	Pro	Gly	Ile	Asp	Ala	Val	
545					550					555					560	
Ala	Ala	Ala	Cys	Trp	Gly	Gly	Ala	Gly	Val	Asp	Ser	Arg	Val	Leu	Ala	
				565					570					575		
Pro	Ala	Glu	Gly	Glu	Ala	Ser	Gly	Ala	Phe	Gly	Pro	Gly	Gly	Glu	Lys	
			580					585					590			
Lys	Lys	Val	His	Ala	Ser	Ser	Asp	Ser	Ser	Gly	Gly	Ser	Arg	Ala	Ala	
		595					600					605				
Leu	Gly	Gly	Arg	Ala	Ser	Val	Gln	Gly	Lys	Ala	Arg	Lys	Pro	Ala	Gly	
		610				615					620					
Trp	Glu	Glu	Glu	Arg	Gly	Arg	Arg	Asp	Asp	Arg	Ser	Arg	Gly	Arg	Arg	
625					630					635					640	
Asp	Glu	Thr	Asp	Gly	Pro	Arg	Phe	Asp	Val	Thr	Trp	Phe	Val	Asp	Asp	
				645					650					655		
Ser	Pro	Leu	Ala	His	Thr	Arg	Lys	Arg	Thr	Arg	Trp	Asp	Ser	Leu	Trp	
			660					665					670			

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Val Arg Pro Ala Ser Pro	Val Arg Val Val Gly Asp Ser Ala Pro Glu
675	680 685
Glu Ser Pro Glu Arg Arg	Glu Gly Gly Gly Arg Ala Pro Asp Leu Gln
690	695 700
Ala Ser Met Ala Lys Arg Arg Thr Ala Asp Ser Gly Leu Glu Glu Glu	
705	710 715 720
Ala Gln Val Glu Arg Gly Phe Ser Ser Ser Asp Ser Asp Asp Cys Asp	
	725 730 735
Trp His Leu Pro Thr Arg Thr Val Ser Ser Ser Leu Ala Pro Phe Ala	
	740 745 750
Ala Ser Lys Ala His Leu Val Pro Arg Cys Cys Tyr Cys Leu Leu Pro	
	755 760 765
Arg Arg Leu Pro Gly Arg His Thr Glu Ala Gly Gly Pro Pro Arg Asp	
	770 775 780
Leu Leu Gly Trp Ser Thr Ser Val Glu Ser Glu Glu Thr Arg Gly Arg	
	785 790 795 800
Tyr Leu Gln Leu Tyr Cys Ala Cys Thr Lys Arg Pro Phe Gly Glu Ser	
	805 810 815
Val Leu Gln Gly Ala Ala Gly Arg Arg Gly Leu Leu Leu Pro Val Ala	
	820 825 830
Thr Asn Ala Leu Leu Tyr Ser Val Arg Arg Val Ala Leu Asp Gly Ala	
	835 840 845
Ala Ser Glu Gln Lys Ser Glu Ala Leu Pro Thr Ser Ala Val Ser Arg	
	850 855 860
Pro Ser Ser Ala Val Arg Ala Arg Ser Ser Cys Ala Ser Ser Gly Cys	
	865 870 875 880
Asp Asp Gly Arg Ala Glu Val Ala Pro Gly Ala Pro Ala Glu Thr Ile	
	885 890 895
Tyr Arg Trp Arg Asp Pro Cys Thr Leu Gln Thr Phe Ser Ser Ser Leu	
	900 905 910
Asp Arg Ile Gln Gly Ser Leu Ala Ala Thr Ala Ala Val Ala Ala Ala	
	915 920 925
Ala Glu Ser Ala Gly Lys Pro Val Ala Phe Leu Pro Arg Leu Tyr Trp	
	930 935 940
Asp Ser Gln Ala Asp Cys Tyr Ile Ala Ser Cys Leu Arg Trp Glu Glu	
	945 950 955 960
Glu Ala Gln Pro Thr Pro Ala Ala Glu Arg Gly Glu Lys Arg Asn Gly	
	965 970 975
Val Glu Arg Pro Ala Glu Ala Arg Glu Arg Gly Arg Asp Glu Lys Lys	
	980 985 990
Pro Glu Asp Pro Ser Val Pro Gly Leu Arg Arg Arg Ser Leu Lys Leu	
	995 1000 1005
Leu Gln Lys Lys Phe Ser Val Ala Phe Leu Gly Asp Ala Lys Ala	
	1010 1015 1020
His Phe Tyr Ala Ser Glu Trp Leu Lys Trp Gln His Lys Gly Gln	
	1025 1030 1035
Arg Met Met Asp Glu Glu Asp Arg Arg Gln Glu Val Ala Arg Gln	
	1040 1045 1050
Met Leu Leu Val Ser Pro Leu Leu Ala Gly Arg Lys Ala Pro Ala	
	1055 1060 1065
Lys Ala Pro Gly Gly Cys Ser Lys Lys Ala Ser Ser Leu Ser Ala	
	1070 1075 1080

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Ala Gln Leu Ala Leu Ala Ser	Gly Arg Pro Leu Thr	Pro Glu Glu
1085	1090	1095
Glu Ala Glu Leu Lys Arg Gln	Leu Glu Asn Lys Glu	Arg Gln Lys
1100	1105	1110
Lys Gln Lys Leu Leu Arg Gln	Gln Trp Arg Arg Gln	Gln Ala Arg
1115	1120	1125
Glu Ala Lys Leu Arg Leu Arg	Glu Ala Glu Ala Ala	Ala Ala Ala
1130	1135	1140
Ala Ala Ala Ala Gly Ala Pro	Ser Ala Pro Gly Thr	Thr Gly Ala
1145	1150	1155
Ser Gln Thr Arg Ser Pro Gln	Ser Gln Gln Lys Ser	Glu Ser Leu
1160	1165	1170
Pro Val Leu Arg Ser Lys Thr	Glu Val Leu Gln Pro	Ser Pro Gly
1175	1180	1185
Ala Ser Phe Ala Pro Ala Ser	Ser Arg Ser Thr Leu	Pro Ala Gly
1190	1195	1200
Glu Ser Gly Ala Ala Pro Cys	Glu Gly Val Gly Thr	Arg Arg Ser
1205	1210	1215
Ala Ala Ser Ala Thr Ser Val	Ala Pro Glu Lys Val	Thr Gly Arg
1220	1225	1230
Lys Ser Glu Thr Ala Arg Asp	Ala Ala Ser Ala Ser	Leu Glu Ala
1235	1240	1245
Ala Lys Ser Thr Met Val Thr	Arg Gly Gly Gly Arg	Gly Ser Ser
1250	1255	1260
Val Val Ala Val Thr Arg Ser	Thr Ser Ser Pro Ser	Gly Arg Ala
1265	1270	1275
Ala Ser Val Ala Ser Ser Thr	Leu Gly Gly Phe Gly	Ala Arg
1280	1285	1290

<210> SEQ ID NO 21

<211> LENGTH: 2406

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 21

Met Ala Ala Pro Ala Pro Ser Ala Glu Ala Arg Pro Ala Lys Arg Arg
1 5 10 15
Cys Phe Pro Leu Pro Arg Glu Thr Pro Val Ser Ser Glu Asp Glu Thr
20 25 30
Arg Lys Thr Leu Gln His Asp Thr Leu Gly Cys Leu Pro Arg Ser Ser
35 40 45
Ser Gly Gln Pro Glu Leu Ala Ala Ser Ala Ala Ser Gln Val Gly
50 55 60
His Leu Ser Ser Ala Ala Leu Leu Gln Leu Val Gln Thr Gln Ser Ala
65 70 75 80
Gly Gly Val Pro Gln Ala Val Leu Arg Asn Leu Phe Ser Ser Ile His
85 90 95
Arg Asn Pro Lys Pro Leu Pro Ala Asn Ala Leu Ala Ala Thr Pro Asn
100 105 110
Ser Ser Leu Tyr Ala Ser Leu Thr Ser Leu Ser Ser Ala Ala Ala Leu
115 120 125
Pro Gly Ala Gly Pro Ala Tyr Ser Gln Ala Pro Ser Pro Ala Ser Ala
130 135 140
Asp Leu Leu Gln Ser Glu Gln Phe Arg Ser Ala Ala Lys Asn Pro Ser
145 150 155 160

Pro 165	Asn	Glu	Ala	Ser	Pro	Ile	Leu	Ala	Leu	Leu	Gly	Glu	Ala	Ala	Arg
Ala 180	Ala	Thr	Thr	Pro	Arg	Thr	Val	Pro	Ala	Leu	Ser	Ala	Val	Cys	Pro
Ala 195	Ala	Ser	Ser	Gly	Val	Ser	Leu	Pro	Pro	Ala	Ser	Asp	Thr	Leu	Ala
Leu 210	Ala	Gln	Ser	Ser	Leu	Ser	Ser	Ser	Thr	Gly	Cys	Ala	Ser	Asp	Val
Lys 225	Ala	Ser	Arg	Pro	Glu	Glu	His	Pro	Ala	Phe	Ala	Ser	Gly	Thr	Ala
Asn	Arg	Gln	Ser	Leu	Leu	Gln	Ala	Leu	Leu	Leu	Ser	Thr	Ala	Pro	Leu
Ala 260	Phe	Ser	Gly	Pro	Ser	Leu	Ser	Ser	Ala	Ser	Thr	Thr	Leu	Pro	Ala
Ser 275	Ser	Gly	Ala	Val	Ser	Ser	Arg	Asn	Ala	Gly	Ala	Tyr	Gln	Phe	Glu
Arg 290	Leu	Leu	Gln	Ala	Glu	Ala	Ala	Lys	Val	Lys	Ala	Leu	Leu	Pro	Asn
Thr 305	Thr	Ser	Lys	Ser	Met	Ser	Gln	Ser	Ser	Val	Pro	Gln	Arg	Asp	Leu
Thr	Arg	Lys	Thr	Ser	Leu	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Ser	Ala	Asp
Asp	Ala	Ser	Arg	Arg	Tyr	Asn	Thr	Arg	Gly	Ala	Asn	Ser	Gly	Gly	Ala
Gly 355	Leu	Arg	Arg	Gly	Thr	Gly	Val	His	Ala	Thr	Thr	Glu	Gln	Ser	Gly
Ala 370	Leu	Asp	Ala	Gly	Glu	Arg	Thr	Arg	Pro	Phe	Gly	Ala	Gly	Glu	Asp
Glu 385	Ser	Ala	Gln	Gly	Lys	Pro	Asp	Ser	Arg	Gly	Arg	Gln	Arg	Pro	Gly
Ala	Leu	Asp	Ala	Ser	Asn	Ile	Leu	Gly	Leu	Leu	Ala	Ala	Phe	Gln	Pro
Ser	Gln	Ala	Pro	Ala	Ile	Arg	Asp	Leu	Ser	Ala	Pro	Ser	His	Leu	Ser
Ala 435	Ala	Ala	Thr	Gly	Ala	Leu	Pro	Leu	Thr	Ala	Ser	Phe	Thr	Ala	Ser
Ala 450	Leu	Ala	Ser	Ser	Gln	Cys	Leu	Pro	Ala	Gly	Thr	Pro	Ala	Ser	Ser
Ser 465	Ala	Ser	Pro	Pro	Phe	Ser	Glu	Val	Leu	Ser	Thr	Thr	Glu	Glu	Ser
Ser	Thr	Thr	Lys	Glu	Thr	Asp	Ala	Ser	Ala	Ser	Thr	Leu	Leu	Ala	Phe
Leu	Gln	Lys	Tyr	Ser	Ala	Val	Ser	Gly	Leu	Gly	Gly	Ala	Ser	Asp	Phe
Leu	Gly	Gln	Leu	Gln	Gly	Lys	Thr	Ser	Leu	Pro	Pro	Leu	Ser	Leu	Ala
Glu 530	Pro	Ser	Ser	Ala	Leu	Pro	Ser	Ser	Phe	Leu	Gly	Gly	Ser	Asp	Gly
Gly 545	Thr	Ile	Asp	Thr	Arg	Asn	Gly	Asn	Gly	Glu	Lys	Thr	Thr	Pro	Pro
Ile	His	Leu	Phe	Gln	Ser	Ala	Phe	Arg	Met	Pro	Ser	Pro	Ser	Gln	Gln

Asn	Leu	Leu	Asp	Ala	Leu	Leu	Ala	Ser	Ser	Cys	Thr	Thr	Ala	Thr	Ser
			580					585					590		
Arg	Ser	Asp	Gly	Ser	Gly	Asn	Leu	Gly	Cys	Pro	Val	Val	Asp	Glu	Arg
		595					600					605			
Asn	Ala	Lys	Leu	Ala	Gly	Pro	Ala	His	Pro	Leu	Pro	Cys	Ser	Phe	Pro
		610				615					620				
Gln	Ile	Ser	Ser	Ser	Ser	Gly	Glu	Pro	Gly	Arg	Lys	Thr	Gly	Gly	Arg
625					630					635					640
Val	His	Arg	Gln	Gly	Thr	Ser	Gln	Ser	Gly	Gly	Arg	Val	Arg	Ser	Gly
				645					650					655	
Lys	Asn	Gly	Gly	Ser	Ala	Ala	Pro	Pro	Arg	Gln	Ser	Ser	Ser	Asp	Asn
			660					665					670		
Val	Pro	Ser	Thr	Pro	Thr	Val	Ser	Ser	His	Glu	Ala	Pro	His	Arg	Ala
			675				680					685			
Gly	Phe	Pro	Ser	Gln	Thr	Pro	Tyr	Glu	Leu	Ser	Ala	Ser	Pro	Ser	His
						695					700				
Gln	Leu	Asp	Leu	Leu	Arg	Leu	Gly	Ala	Phe	Leu	Gly	Gly	Ala	Gly	Lys
705					710					715					720
Gln	Asp	Ala	Ser	Val	His	Ser	Asp	Glu	Thr	Gly	Thr	Leu	Ser	Gly	Glu
				725					730					735	
Pro	Ser	His	Arg	Ser	Cys	Ser	Leu	Ser	Arg	Gly	Leu	Thr	Gln	Glu	Ser
			740					745					750		
Val	Leu	Gln	Leu	Ser	Asp	Thr	Thr	Ser	Thr	Ser	Arg	Glu	Gly	Glu	Pro
			755				760					765			
Asn	Glu	Pro	Ser	Gln	Gly	Cys	Val	Asn	Val	Ala	Ala	Ser	Leu	Pro	Ala
						775					780				
Phe	Gly	Pro	Gln	Pro	Ser	Ser	Gly	Ala	Ala	Lys	Ala	Arg	Glu	Gly	Arg
785					790					795					800
Arg	Gly	Ala	Gly	Gly	Ala	Gly	Ala	Ala	Pro	Pro	Val	Pro	Leu	Arg	Ala
				805					810					815	
Asp	Val	Thr	Leu	Gly	Gly	Asn	Arg	Pro	His	Tyr	His	Val	Ala	Lys	Gln
			820					825					830		
Glu	Trp	Arg	Val	Arg	Tyr	Tyr	Met	Asn	Gly	Lys	Arg	Lys	Met	Arg	Thr
		835					840					845			
Tyr	Ser	Ala	Lys	Phe	Tyr	Gly	Tyr	Glu	Thr	Ala	His	Thr	Met	Ala	Glu
						855					860				
Asp	Phe	Ala	His	Tyr	Val	Asp	Lys	His	Glu	Ala	Leu	Pro	Asp	Ser	Met
865					870					875					880
Met	Met	Thr	Ala	Met	Met	Leu	Gln	Ala	Gln	Ala	Asn	Ser	Ala	Ala	Ser
				885					890					895	
Ser	Gly	Gln	Thr	Val	Pro	Leu	Ala	Arg	Gly	Ile	Arg	Ala	Ser	Ser	Ala
			900					905					910		
Ser	Thr	Gly	Ala	Gly	Gly	His	Val	Ser	Lys	Ser	Ala	Thr	Lys	Gly	Ser
		915					920					925			
Val	Ala	Ala	Ser	Ser	Glu	G									

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995				1000				1005			
Cys Gly	Ser Gly	Ser Ser	Ala	Glu Gly	Arg Asp	Gly	His Glu	Ser			
1010			1015			1020					
Glu Val	Leu Trp	Ala Thr	Leu	Gly Lys	Val His	Asp	Ala Ser	Gln			
1025			1030			1035					
Gly Lys	Lys Ile	Lys Pro	Glu	Lys Pro	Leu Thr	Val	Ala Arg	Gly			
1040			1045			1050					
Arg Leu	Ala Leu	Gly Ala	Glu	Asp Lys	Ser Gln	Asn	Leu Gly	Val			
1055			1060			1065					
Asp Leu	Val Asp	Ser Gly	Glu	Ala Gln	Gly Leu	Pro	Gly Val	Arg			
1070			1075			1080					
Gln Pro	Arg Gln	Met Lys	Asn	Ser Glu	Glu Cys	Ser	Leu Arg	Asp			
1085			1090			1095					
Ser Asp	Lys Gly	Met Ala	Leu	Ser Lys	Arg Phe	Gly	Phe Leu	Pro			
1100			1105			1110					
Ser Gln	Thr Pro	Ser Cys	Asp	Ser Met	Thr Leu	Pro	Phe Pro	Gly			
1115			1120			1125					
Gly Phe	Asp Ala	Leu Ser	Leu	Ser Ser	Ala Leu	Ser	Ser Cys	Ala			
1130			1135			1140					
Ser Leu	Pro Val	Ala His	Glu	Gly Asn	Asn Phe	Gln	Lys Gly	His			
1145			1150			1155					
Thr Gly	Asp Ile	Val Ala	Leu	Ala Ser	Gln Ser	Gly	Thr Gln	Arg			
1160			1165			1170					
Pro Ala	Ser Val	Val Leu	Ser	Arg Asp	Ala Asn	Val	Ser Gly	Ser			
1175			1180			1185					
Ser Pro	Ser His	Pro Thr	Trp	Gln Arg	Glu Gly	Ala	Ala Val	Ser			
1190			1195			1200					
Gly Arg	Ala Asp	Glu Phe	Ser	Ser Leu	Ser Val	Thr	Pro Ser	Thr			
1205			1210			1215					
Val Pro	Leu Ser	Ser Phe	Thr	Met Glu	Asp Ile	Lys	Gly Glu	Lys			
1220			1225			1230					
Gly Asp	Pro Ser	Arg Arg	Phe	Ala Leu	Val Gly	Glu	Ser Met	Lys			
1235			1240			1245					
Asn Val	Ser Ala	Pro Glu	Val	Gln Ala	Leu Phe	Pro	Thr Ser	Ser			
1250			1255			1260					
Ile Ala	Asn Ala	Glu Leu	Leu	Pro Val	Asp Phe	Leu	His Ser	Asn			
1265			1270			1275					
Ser Cys	Ser Ala	Asp Lys	Leu	Glu Ser	Ser Ile	Pro	Arg Gly	Leu			
1280			1285			1290					
Ala Gly	Asn Asn	Pro Ser	Met	Thr Ala	Thr Ala	Val	Ala Ala	Thr			
1295			1300			1305					
Ala Val	Ser His	Gln Ile	Phe	Asp Thr	Ile Thr	Leu	Phe Gly	Glu			
1310			1315			1320					
Phe Leu	Arg Glu	Phe Ala	Lys	Glu Lys	Val Asn	Glu	Phe His	Glu			
1325			1330			1335					
Tyr Gly	Leu Glu	Ala Ser	Pro	Leu Thr	Val Glu	Ala	Ser Ser	Glu			
1340			1345			1350					
Val Ser	Leu Phe	Gly Lys	Ala	Thr Phe	Gly Arg	Cys	Pro Val	Ala			
1355			1360			1365					
Gly Gly	Ser Thr	Pro Ala	Gly	Ile Ser	Lys Met	Ser	Gly Glu	Thr			
1370			1375			1380					
Leu Ser	Gly Leu	Ser Ala	Ser	Glu Leu	Ser Leu	Val	Ser Ala	Arg			
1385			1390			1395					

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Thr Asn	Thr Thr Thr Gly Glu	Glu Gln Phe Ala Leu	Ala Arg Gly
1400	1405	1410	
Leu Phe	Pro Gly Asp Ser Glu	Gly Asp Arg Asp Glu	Lys Lys Pro
1415	1420	1425	
Gln Leu	Ser Gln Gln Glu Leu	Leu Val Leu Ser His	Ala Leu Val
1430	1435	1440	
Asn Leu	Thr Ser Ser Thr Tyr	Val Leu Met His Thr	Leu Lys Ala
1445	1450	1455	
Ser Leu	Ser Lys Ser Thr Glu	Ala Val Gln Leu His	Gln Pro Leu
1460	1465	1470	
Leu Glu	Ala Ala Ser Glu Ala	Lys Ala Thr Asp Glu	Ala Lys Thr
1475	1480	1485	
Arg Glu	Glu Gln Glu Ser Ser	Glu Cys Asp His Glu	Tyr Pro Pro
1490	1495	1500	
Arg Ser	Ser Leu Glu Ala Thr	Thr Gly Ala Leu Pro	Phe Arg Leu
1505	1510	1515	
Ser Pro	Ala Leu Ser Ala Ser	Ser Lys Asp Leu Pro	Ser Leu Ser
1520	1525	1530	
Ala Ser	Ala Ser Leu Glu Ser	Val Thr Pro Phe Ala	Gly Leu Pro
1535	1540	1545	
Leu Glu	Glu Gly Thr Leu Ser	Ala Ser Val Gly Leu	Ala Ser Ser
1550	1555	1560	
Asp Asp	Glu His Asp Thr Ser	Leu Leu Phe Lys Thr	Glu Ala Ala
1565	1570	1575	
Lys Lys	Arg Ser Leu Phe Ser	Thr Ala Ala Asp Gly	Asp Glu Ser
1580	1585	1590	
Arg Thr	Tyr Asn Asp Gly Leu	Gly Gln Pro Met Glu	Glu Glu Ile
1595	1600	1605	
Arg Ser	Cys Val Ser Thr Ser	Cys Gly Glu Ala Val	Ala Thr Thr
1610	1615	1620	
Thr Leu	Ser Ala Ile Gly Pro	Gly Thr Gly Ala Ser	Gly Ala Leu
1625	1630	1635	
Leu Asp	Ser Glu Ser Arg Glu	Ser Leu Gly Glu Lys	Pro Gly Ala
1640	1645	1650	
Ala Leu	Arg Ala Gly Ala His	Thr Pro Ala Pro Ser	Arg Ala Pro
1655	1660	1665	
Thr Pro	Ser Arg Thr Phe Ser	Phe Thr Ser Ser Ser	Thr Ala Thr
1670	1675	1680	
Ser Ala	Ala Leu Leu Cys Asp	Ser Asn Val Val His	Glu Lys Leu
1685	1690	1695	
Arg Ala	Gln Gly Lys Asp Ser	Glu Ala Gly Glu Arg	Lys Gly Asp
1700	1705	1710	
Ser Glu	Lys Glu Glu Glu Val	Glu Met Trp Lys Glu	Glu Asp Glu
1715	1720	1725	
Glu Val	Gln Arg Cys Thr Gly	Ser Ala Glu Thr Asp	Ser Thr Glu
1730	1735	1740	
Ala Thr	Arg Gly Glu Glu Ala	Trp Arg Arg Gly Lys	Gln Ser Glu
1745	1750	1755	
Lys Lys	Pro Ser Val Ile Thr	Thr Ala Leu Asn Leu	Leu Glu Thr
1760	1765	1770	
His Arg	His Leu Ala Leu Thr	Ile Ser Gln Leu Lys	Arg Pro Val
1775	1780	1785	

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Ala	Gln	Gln	Leu	Arg	Phe	Ile	Leu	Pro	Ile	Ala	Ala	Pro	Gln	Leu
1790						1795					1800			
Leu	Pro	Cys	Ile	Leu	Pro	Pro	Ala	Ser	Phe	Gln	Gly	Pro	Gly	Glu
1805						1810					1815			
Ser	Gly	Asp	Gly	Lys	Ala	Glu	Ala	Glu	Ala	Lys	Gly	Ser	Ser	Ser
1820						1825					1830			
Leu	Gly	Gln	Val	Leu	Glu	Thr	Ala	Leu	Gly	His	Gly	Thr	Arg	Leu
1835						1840					1845			
Ala	Pro	Ser	Ala	Ser	Ala	Met	Val	Pro	Pro	Arg	Lys	Asp	Glu	Ala
1850						1855					1860			
Ala	Ser	Ala	Val	Pro	Glu	Ala	Lys	Thr	Phe	Thr	Gly	Leu	Ala	Asn
1865						1870					1875			
Ala	Gly	Val	Met	Arg	Glu	Ala	Ala	Ser	Arg	Thr	Leu	Glu	Ala	Glu
1880						1885					1890			
Gln	Val	Ser	Arg	Lys	Arg	Ser	Arg	Glu	Glu	Val	Val	Asp	Ser	Glu
1895						1900					1905			
Thr	Ala	Gly	Asp	Glu	Gly	Asp	Met	Glu	Asn	Val	Pro	Glu	Thr	Leu
1910						1915					1920			
Asp	Ala	Thr	Thr	Ser	Pro	Gly	Ser	Arg	Gln	Tyr	Asp	Lys	Ser	Pro
1925						1930					1935			
Ser	Asn	Gly	Gly	Thr	Lys	Pro	Pro	Ala	Thr	Ala	Lys	Ser	Arg	Val
1940						1945					1950			
Ile	Arg	Asp	Gln	Ala	Ala	Leu	Glu	Arg	Leu	Leu	Leu	Ala	Pro	Phe
1955						1960					1965			
Gln	Asp	Thr	Pro	Thr	Cys	Ser	Cys	Thr	Asp	Arg	Pro	Cys	Pro	Cys
1970						1975					1980			
Asp	Arg	Gln	Gln	Val	Ala	Asp	Met	Ile	Tyr	Leu	Phe	Tyr	Ala	Val
1985						1990					1995			
Pro	Ala	Arg	Gln	Gln	Ala	Glu	Ser	Ser	Lys	Glu	Gly	Ser	Thr	Gln
2000						2005					2010			
Arg	Leu	Gln	Phe	Ala	Ala	Arg	Asp	Thr	Asn	Glu	Arg	Lys	Asp	Ala
2015						2020					2025			
Arg	Thr	Gly	Glu	Glu	Thr	Gln	Gly	Gly	Glu	Thr	Glu	Ala	Lys	Glu
2030						2035					2040			
Val	Ile	Arg	Asp	Pro	Glu	Glu	Arg	Gly	Val	Cys	Glu	Gly	Ser	Ser
2045						2050					2055			
Ser	Gln	Asn	Ala	His	Thr	Gln	Phe	Asp	Ala	Glu	Thr	Ala	Ser	Ser
2060						2065					2070			
Ser	Met	Ser	Ser	Asp	Pro	Arg	Ala	Asp	Lys	Glu	Ser	Asn	Ala	Gln
2075						2080					2085			
Asp	Ala	His	Met	Ala	Asp	Lys	Thr	Ser	Phe	Val	Ser	Asp	Leu	Pro
2090						2095					2100			
Gln	Pro	Ser	Gly	Glu	Phe	Ala	Pro	Ser	Leu	Leu	Ser	Glu	Thr	Ser
2105						2110					2115			
Leu	Asp	Val	Ala	Met	Ala	Asp	Ser	Arg	Gly	Thr	Thr	Ser	Glu	Ile
2120						2125					2130			
His	Gly	Phe	Phe	Thr	Arg	Ser	Asp	Glu	Gln	Lys	Arg	Ala	Ser	Phe
2135						2140					2145			
Ser	Ser	Ser	Ser	Leu	Leu	Ala	Ala	Gly	His	Ala	Val	Ala	Ser	Phe
2150						2155					2160			
Ser	Ser	Ser	Leu	Ala	Gly	Val	Val	Ser	Gly	Ala	Gly	Glu	Arg	Arg
2165						2170					2175			
Glu	Cys	Ala	Gly	Pro	Ser	Leu	Gly	Asp	Leu	Ser	Thr	Ile	Gly	Leu

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2180	2185	2190
Leu Ser Leu Ser Tyr Pro Ala Met Leu Ala Phe Ile Leu Pro Leu		
2195	2200	2205
Gln Ser Leu Leu His Met Val Ser Gly Met Ile Leu Thr Leu His		
2210	2215	2220
Lys Lys Leu Ile His Arg Phe Ile Cys Ala His Leu Arg Leu Val		
2225	2230	2235
Leu Asp Asp Asp Met Arg Arg Pro Ala Gly Gly Ala Leu Lys Ser		
2240	2245	2250
Arg Gly Ala His Gly Asp Thr Glu Ala Ala Glu Ala Gln Val Glu		
2255	2260	2265
Arg Arg Arg Arg Glu His Glu Arg Glu Glu Thr Thr Asn Leu Ala		
2270	2275	2280
Ile Gly Tyr Arg Glu Gly Asn Ala Glu Ala Ser Asn Thr Phe Pro		
2285	2290	2295
Leu Val Asp Thr Val Ser Ser Leu Leu Ser Pro Gly Ser Leu Arg		
2300	2305	2310
Gln Glu Asn Ser Glu Val Glu Arg Arg Asp Asn Asp Glu Glu Arg		
2315	2320	2325
Leu Glu Leu Ile Thr Gly Ile Ala Arg Glu Ser Pro Lys Pro Ser		
2330	2335	2340
Glu Lys Asp Ser Val Ser Pro Phe Leu Ser Thr Ala Pro Cys Pro		
2345	2350	2355
Gly Thr Glu Ala Glu Ser Ser Asp Cys Ser Ala Ser Ser Ala Cys		
2360	2365	2370
Ser Gly Thr Pro Thr Glu Gly Thr Glu Gly Gly Glu Thr Gly Asp		
2375	2380	2385
Ile Ala Ser Phe Leu Ser Pro Ser Gly Asp Val Lys Gln Thr Ile		
2390	2395	2400
Met Leu Ala		
2405		

<210> SEQ ID NO 22

<211> LENGTH: 711

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 22

Met Pro Leu Lys Thr Ser Trp His Cys Ser Cys Asn Ala Thr Phe Pro			
1	5	10	15
Gly Asp Leu Leu Met Val Val Ala Asn His Asp Arg Val Gly Asn Trp			
20	25	30	
Asn Pro Gln Asn Ser Val Val Leu Ser Thr Asp Ala Ser Ser Phe Pro			
35	40	45	
Thr Trp Arg Ser Gly Glu Val Cys Phe Asp Glu Gln Gln Pro Val Arg			
50	55	60	
Leu Glu Tyr Lys Leu Ile Ile Arg Arg Ala Ser Gly Glu Ile Tyr Trp			
65	70	75	80
Glu Pro Ile Pro Thr Asn Arg Val Val Thr Leu Thr Ala Asn Thr Ser			
85	90	95	
Ser Val Ile Glu Asn Val Trp Gly Ser Leu Ala Thr Cys Ser Ile Thr			
100	105	110	
Phe Phe Pro Leu Gln Pro Ile Pro Ser Pro Ser Phe Tyr Lys His Ala			
115	120	125	

Glu 130	Arg	Thr	Lys	Lys	Glu	Ala 135	Ser	Ser	Ser	Val	His	Leu 140	His	Ser	Ala	Ser
Ile 145	Ser	Asp	Asp	Ser	Gly 150	Ser	Asp	Thr	Gly	Thr	Cys	Ser	Gln	Val	Asp 160	
Glu	Ser	Arg	Thr	Gln 165	Arg	Asn	Val	Arg	Gly	Gln	Pro	Ala	Ser	Val	Gly 175	
Thr	Gly	Lys	Ala 180	Thr	Ala	Ala	Glu	Arg	Gly	Gly	Lys	Gly	Tyr	Val	Met	
Pro	His	His 195	Gln	Cys	Ser	Thr	Ser 200	Gln	Arg	Arg	His	Ser 205	Ile	Ser	Thr	
Gln	Ala 210	Ala	Asp	Glu	Ala	Ala 215	Gly	Gly	Gly	Asn	Arg	Val	Ser	Phe	Lys	
Arg 225	Ser	Ala	Phe	Ile	Leu 230	Ala	Asn	Thr	Gly	Pro	Ile	Thr	Asn	Tyr	Tyr 240	
Thr	Val	Ser	Lys	Thr 245	Ile	Gly	Arg	Gly	Thr	Trp	Gly	Glu	Val	Lys	Leu 255	
Val	Ile	Asp	Asn 260	Gly	Thr	Gly	Ala	Arg	Arg	Ala	Ala	Lys	Lys	Ile	Pro	
Lys	Cys	Tyr 275	Val	Glu	Asp	Ala	Asp 280	Arg	Phe	Arg	Gln	Glu	Ile	Glu	Ile	
Met	Lys 290	Ser	Leu	Asp	His	Pro 295	Asn	Ile	Val	Arg	Leu	Tyr	Glu	Thr	Phe	
Glu 305	Asp	Met	Thr	Asp	Phe 310	Tyr	Leu	Val	Met	Glu	Tyr	Cys	Thr	Gly	Gly 320	
Glu	Leu	Phe	Asp	Arg 325	Leu	Val	His	Gln	Gly	Val	Phe	Thr	Glu	Ala	Leu 335	
Ala	Cys	Arg	Ile 340	Met	Arg	Gln	Ile	Leu 345	Ala	Ala	Val	Ala	Tyr	Cys	His	
Ala	His	Arg 355	Val	Ala	His	Arg	Asp 360	Leu	Lys	Pro	Glu	Asn	Phe	Leu	Phe	
Leu	His 370	Asp	Asn	Pro	Glu	Ser 375	Pro	Ile	Lys	Leu	Ile	Asp	Phe	Gly	Leu	
Ala 385	Ala	Arg	Phe	Lys	Ser 390	Gly	Gln	Pro	Met	Arg 395	Thr	Arg	Ala	Gly	Thr 400	
Pro	Tyr	Tyr	Val	Ser 405	Pro	Gln	Val	Leu	Glu	Gly	Arg	Tyr	Gly	Pro	Glu 415	
Cys	Asp	Val	Trp 420	Ser	Ala	Gly	Val	Met 425	Met	Tyr	Ile	Leu	Leu	Cys	Gly	
Tyr	Pro	Pro 435	Phe	Asn	Ala	Pro	Ser 440	Asp	Arg	Ala	Ile	Met	Asn	Lys	Val	
Arg 450	Ala	Gly	His	Tyr	Thr	Phe 455	Pro	Asp	Ser	Glu	Trp	Ser	Arg	Val	Ser	
Leu 465	Gln	Ala	Lys	Asp	Leu 470	Ile	Ser	Arg	Leu	Leu 475	Asp	Arg	His	Pro	Arg 480	
Thr	Arg	Ile	Ser	Ala 485	Glu	Gln	Ala	Leu	Arg	His	Ala	Trp	Phe	Ala	Met 495	
His	Ala	Pro	Gly 500	Asp	His	Phe	Glu	Pro 505	Leu	Gly	Leu	Asp	Ile	Leu	Ser	
Lys	Phe	Arg	Arg	Phe	Gln	Gly	Leu 520	Ser	Arg	Leu	Lys	Lys	Leu	Ala	Leu	
Thr 530	Val	Ile	Ala	Gln	His	Leu 535	Glu	Asp	Ser	Glu	Ile	Glu	Gly	Leu	Lys	
Asn	Leu	Phe	Thr	Gln	Leu	Asp	Thr	Glu	Gly	Asp	Gly	Val	Leu	Thr	Val	

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545	550	555	560
Glu Glu Ile Arg Lys Gly Ile Glu Arg Ser Gly Val His Leu Pro Pro			
	565	570	575
Asp Met Val Leu Glu Asp Val Leu Arg Glu Val Asp Thr Ala Gly Thr			
	580	585	590
Gly Ser Ile Asp Tyr Thr Glu Phe Ile Ala Ala Cys Leu His Gln Ser			
	595	600	605
His Tyr Ile Arg Glu Glu Ala Cys Arg Ala Ala Phe Arg Val Leu Asp			
	610	615	620
Ile Asn Gly Asp Gly Leu Val Ser Ala Gln Glu Leu Arg Gln Val Phe			
	625	630	635
His Met Ala Gly Asp Leu Glu Thr Asp Ala Ala Ala Glu Leu Leu Glu			
	645	650	655
Ala Asp Ala Asp Gly Asp Gly His Ile Thr Phe Asp Glu Phe Cys Gly			
	660	665	670
Leu Met Arg Lys Val Pro Ser Leu Ala Leu Val Thr Glu His Thr Val			
	675	680	685
Ser Met Met Arg Arg Thr Cys Ser Arg Thr Asn Ile Ser Glu Ala Ser			
	690	695	700
Leu Thr Pro Arg Ala Thr Gly			
	705	710	

<210> SEQ ID NO 23
 <211> LENGTH: 368
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 23

Met Val Ser Arg Thr Leu Ser Leu Ser Met Ser Leu Phe Arg Ala His			
1	5	10	15
Leu Val Phe Tyr Arg Cys Ala Leu Asn Leu Asn Ser Ser Tyr Asn Phe			
	20	25	30
Gly Phe Leu Val Ala Met Thr Phe Val Leu Gln Ile Ile Thr Gly Ile			
	35	40	45
Thr Leu Ala Phe Arg Tyr Thr Ser Glu Ala Ser Cys Ala Phe Ala Ser			
	50	55	60
Val Gln His Leu Val Arg Glu Val Ala Ala Gly Trp Glu Phe Arg Met			
	65	70	75
Leu His Ala Thr Thr Ala Ser Phe Val Phe Leu Cys Ile Leu Ile His			
	85	90	95
Met Thr Arg Gly Leu Tyr Asn Trp Ser Tyr Ser Tyr Leu Thr Thr Ala			
	100	105	110
Trp Met Ser Gly Leu Val Leu Tyr Leu Leu Thr Ile Ala Thr Ala Phe			
	115	120	125
Leu Gly Tyr Val Leu Pro Trp Gly Gln Met Ser Phe Trp Gly Ala Thr			
	130	135	140
Val Ile Thr Asn Leu Leu Ser Pro Ile Pro Tyr Leu Val Pro Trp Leu			
	145	150	155
Leu Gly Gly Tyr Tyr Val Ser Asp Val Thr Leu Lys Arg Phe Phe Val			
	165	170	175
Leu His Phe Ile Leu Pro Phe Ile Gly Cys Ile Ile Ile Val Leu His			
	180	185	190
Ile Phe Tyr Leu His Leu Asn Gly Ser Ser Asn Pro Ala Gly Ile Asp			
	195	200	205

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Thr Ala Leu Lys Val Ala Phe Tyr Pro His Met Leu Met Thr Asp Ala
 210 215 220
 Lys Cys Leu Ser Tyr Leu Ile Gly Leu Ile Phe Leu Gln Ala Ala Phe
 225 230 235 240
 Gly Leu Met Glu Leu Ser His Pro Asp Asn Ser Ile Pro Val Asn Arg
 245 250 255
 Phe Val Thr Pro Leu His Ile Val Pro Glu Trp Tyr Phe Leu Ala Tyr
 260 265 270
 Tyr Ala Val Leu Lys Val Ile Pro Ser Lys Thr Gly Gly Leu Leu Val
 275 280 285
 Phe Met Ser Ser Leu Ile Asn Leu Gly Leu Leu Ser Glu Ile Arg Ala
 290 295 300
 Leu Asn Thr Arg Met Leu Ile Arg Gln Gln Phe Met Thr Arg Asn Val
 305 310 315 320
 Val Ser Gly Trp Val Ile Ile Trp Val Tyr Ser Met Ile Phe Leu Ile
 325 330 335
 Ile Ile Gly Ser Ala Ile Pro Gln Ala Thr Tyr Ile Leu Tyr Gly Arg
 340 345 350
 Leu Ala Thr Ile Leu Tyr Leu Thr Thr Gly Leu Val Leu Cys Leu Tyr
 355 360 365

<210> SEQ ID NO 24
 <211> LENGTH: 84
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 24

Lys Leu Cys Lys Tyr His His Phe Leu Cys Ser Leu Thr Ser Gln Leu
 1 5 10 15
 Ser Tyr Leu Ile Gly Leu Ile Phe Leu Gln Ala Ala Phe Gly Leu Met
 20 25 30
 Glu Leu Ser His Pro Asp Asn Ser Ile Pro Val Asn Arg Phe Val Thr
 35 40 45
 Pro Leu His Ile Val Pro Glu Trp Tyr Phe Leu Ala Tyr Tyr Ala Val
 50 55 60
 Leu Lys Val Ile Pro Ser Lys Thr Gly Gly Leu Leu Val Phe Met Ser
 65 70 75 80
 Ser Thr Cys Gln

<210> SEQ ID NO 25
 <211> LENGTH: 244
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 25

Met Ile Ala Val His His His Pro Thr Gly Leu Leu Lys Thr Ala Lys
 1 5 10 15
 Ser Val Gly Phe Gln Tyr Pro Thr Thr Leu Arg Leu Phe His Ile Gly
 20 25 30
 Tyr Val Leu Gly Val Ile Tyr Gly Leu Leu Leu Ser Leu Val Leu Thr
 35 40 45
 Ala Arg Glu Asn Tyr Tyr Ser Asp Ala Ser Met Ile Ser Thr Ile Val
 50 55 60
 Leu Gly Val Ile Ile Ser Glu Thr Gly Leu Phe Ile Ser Phe Phe Trp
 65 70 75 80
 Gly Val Tyr Thr Thr Ser Trp Thr Thr Gly Leu Asp Leu Glu Gly Leu

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85	90	95
Cys Leu Pro Asp Pro Ser Ser Ile Val Leu Phe Met Thr Ile Met Leu		
100	105	110
Ser Ala Leu Ser Ile Val Val Ser Ser Val Tyr Leu Lys Asn Gln His		
115	120	125
Leu Tyr Thr Ser Cys Thr Asn Ile Met Ile Phe Thr Leu Val Val Ser		
130	135	140
Phe Leu Met Leu Val Cys Thr Glu Tyr Leu Gly Leu Ser Ile Tyr Ile		
145	150	155
Asn Asp Asn Gly Phe Gly Asn Gly Leu Phe Ile Leu Thr Gly Ile His		
165	170	175
Phe Ser His Val Ile Val Gly Ala Ile Leu Gly Phe Phe Asn Gln Gly		
180	185	190
Met Tyr Ser Ser Leu Val Thr Tyr Leu Pro Val Asn Cys Ile Thr Leu		
195	200	205
Ser Lys Cys Lys Gly Thr Leu Cys Lys Ile Phe Ser Glu Pro Phe Thr		
210	215	220
Ile Leu Tyr Leu His Phe Val Glu Ala Val Trp Ile Met Ile His Val		
225	230	235
240		
Thr Phe Tyr Leu		

<210> SEQ ID NO 26
 <211> LENGTH: 156
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 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 26

Met Ser Leu Phe Arg Ala His Leu Val Phe Tyr Arg Cys Ala Leu Asn		
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Leu Asn Ser Ser Tyr Asn Phe Gly Phe Leu Val Ala Met Thr Phe Val		
20	25	30
Leu Gln Ile Ile Thr Gly Ile Thr Leu Ala Phe Arg Tyr Thr Ser Glu		
35	40	45
Ala Ser Cys Ala Phe Ala Ser Val Gln His Leu Val Arg Glu Val Ala		
50	55	60
Ala Gly Trp Glu Phe Arg Met Leu His Ala Thr Thr Ala Ser Phe Val		
65	70	75
Phe Leu Cys Ile Leu Ile His Met Thr Arg Gly Leu Tyr Asn Trp Ser		
85	90	95
Tyr Ser Tyr Leu Thr Thr Ala Trp Met Ser Gly Leu Val Leu Tyr Leu		
100	105	110
Leu Thr Ile Ala Thr Ala Phe Leu Gly Tyr Ala Thr Ser Asn Tyr Thr		
115	120	125
Thr Leu Cys Gln Glu Gly Ser Gln Ile Thr Leu Ile Ile Phe Val Ile		
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Leu Ile His Gly Val Gln Leu Val Leu Phe Leu Gln		
145	150	155

<210> SEQ ID NO 27
 <211> LENGTH: 403
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 27

Trp Ala His His Met Met Thr Val Gly Leu Glu Val Asp Thr Arg Ala		
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15		

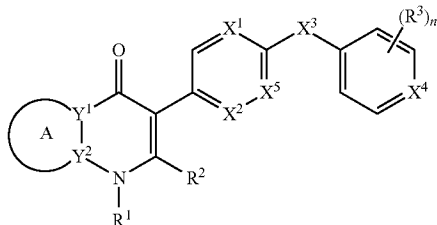
Tyr	Phe	Ser	Ala	Met	Thr	Ile	Met	Ile	Ala	Ile	Pro	Thr	Gly	Thr	Lys
		20						25				30			
Ile	Phe	Asn	Trp	Leu	Gly	Thr	Tyr	Met	Ala	Ser	His	Asn	Thr	Thr	Arg
		35				40						45			
Thr	Ile	Asp	Leu	Trp	Ala	Ala	Leu	Cys	Phe	Ile	Leu	Leu	Phe	Thr	Leu
		50				55				60					
Gly	Gly	Thr	Thr	Gly	Val	Val	Met	Gly	Asn	Ala	Gly	Met	Asp	Ile	Ala
65				70						75				80	
Leu	His	Asp	Thr	Tyr	Tyr	Ile	Val	Ala	His	Phe	His	Phe	Val	Leu	Ser
		85						90						95	
Leu	Gly	Ala	Ile	Leu	Ala	Thr	Ile	Cys	Gly	Phe	Val	Phe	Tyr	Ser	Lys
		100						105				110			
Asp	Met	Phe	Gly	Asp	Thr	Leu	Asn	Leu	Phe	His	Val	Asn	Thr	Gly	Ser
		115				120						125			
Ser	Pro	Tyr	Leu	Asn	Ile	Trp	Phe	Val	Val	Phe	Leu	Ala	Ser	Ile	Met
130						135						140			
Leu	Ile	Phe	Leu	Pro	Met	His	Ile	Leu	Gly	Phe	Asn	Val	Met	Pro	Arg
145				150						155				160	
Arg	Ile	Pro	Asp	Tyr	Pro	Asp	Tyr	Leu	Cys	Tyr	Ile	Asn	Thr	Trp	Cys
		165						170						175	
Ser	Ile	Val	Gln	Leu	Val	Val	Tyr	Thr	Pro	Gln	Lys	Lys	Leu	Ile	Asn
		180						185				190			
Asn	Pro	Val	Ser	Glu	Met	Ile	Thr	Pro	Ser	Thr	Met	Val	Leu	Ile	Ile
195						200						205			
Leu	Ala	Ser	Glu	Tyr	Tyr	Ser	Tyr	Leu	Thr	Thr	Ala	Trp	Met	Ser	Gly
210						215				220					
Leu	Val	Leu	Tyr	Leu	Leu	Thr	Ile	Ala	Thr	Ala	Phe	Leu	Gly	Tyr	Val
225				230						235				240	
Leu	Pro	Trp	Gly	Gln	Met	Ser	Phe	Trp	Gly	Ala	Thr	Val	Ile	Thr	Asn
		245						250						255	
Leu	Leu	Ser	Pro	Ile	Pro	Tyr	Leu	Val	Pro	Trp	Leu	Leu	Gly	Gly	Tyr
		260						265				270			
Tyr	Val	Ser	Asp	Val	Thr	Leu	Lys	Arg	Phe	Phe	Val	Leu	His	Phe	Ile
275						280						285			
Leu	Pro	Phe	Ile	Gly	Cys	Ile	Ile	Ile	Val	Leu	His	Ile	Phe	Tyr	Leu
290				295						300					
His	Leu	Asn	Gly	Ser	Ser	Asn	Pro	Ala	Gly	Ile	Asp	Thr	Ala	Leu	Lys
305				310						315				320	
Val	Ala	Phe	Tyr	Pro	His	Met	Leu	Met	Thr	Asp	Ala	Lys	Cys	Leu	Ser
		325						330						335	
Tyr	Leu	Ile	Gly	Leu	Ile	Phe	Leu	Gln	Ala	Ala	Phe	Gly	Leu	Met	Glu
		340						345				350			
Leu	Ser	His	Pro	Asp	Asn	Ser	Ile	Pro	Val	Asn	Arg	Phe	Val	Thr	Pro
355						360						365			
Leu	His	Ile	Val	Pro	Glu	Trp	Tyr	Phe	Leu	Ala	Tyr	Tyr	Ala	Val	Leu
370						375				380					
Lys	Val	Ile	Pro	S											

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We claim:

1. A compound of the structure of

(a) Formula (I):



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

ring A combines with Y¹ and Y₂ to form a C₃₋₇cycloalkenyl or heteroaryl ring, wherein the C₃₋₇cycloalkenyl or heteroaryl is optionally substituted by halogen, C₁₋₃alkyl, C₁₋₃alkoxy, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR, cyano or phenyl;

Y¹ is C;Y₂ is C or N;X¹ is C(R^{x1}) or N,

wherein R^{x1} is hydrogen, halogen, C₁₋₃alkyl, C₁₋₃alkoxy or C₁₋₃haloalkyl;

X² is C(R^{x2}) or N,

wherein R^{x2} is hydrogen, halogen, C₁₋₃alkyl, C₁₋₃alkoxy or C₁₋₃haloalkyl;

X³ is O, N(R), S or C₁₋₃alkyl;X⁴ is C or N;X⁵ is C or N;R¹ is hydrogen or C₁₋₃alkyl;

R² is hydrogen, C₁₋₃alkyl, C₁₋₃haloalkyl, —CH₂OH, —CH₂OR or —C(O)OR;

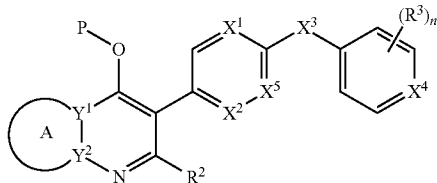
n is 0, 1, 2, 3 or 4;

each R³ is independently halogen, C₁₋₃alkyl, C₁₋₃alkoxy, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR or SF₅;

or two R³ groups, together with the carbons to which they are attached, form a 1,3-dioxolane; and

each R is independently hydrogen or C₁₋₃alkyl; or

(b) compound of the structure of Formula (I-p):



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

ring A combines with Y¹ and Y₂ to form a C₃₋₇cycloalkenyl or heteroaryl ring,

wherein the C₃₋₇cycloalkenyl or heteroaryl is optionally substituted by halogen, C₁₋₃alkyl, C₁₋₃alkoxy, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR, cyano or phenyl;

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Y¹ is C;Y₂ is C or N;X¹ is C(R^{x1}) or N,

wherein R^{x1} is hydrogen, halogen, C₁₋₃alkyl, C₁₋₃alkoxy or C₁₋₃haloalkyl;

X² is C(R^{x2}) or N,

wherein R^{x2} is hydrogen, halogen, C₁₋₃alkyl, C₁₋₃alkoxy or C₁₋₃haloalkyl;

X³ is O, N(R), S or C₁₋₃alkyl;X⁵ is C or N;

P is —C(O)OR', —C(O)R', —C(O)NR'₂, wherein R' is hydrogen, C₁₋₃alkyl or —CH₂OR;

R² is hydrogen, C₁₋₃alkyl, C₁₋₃haloalkyl, —CH₂OH, —CH₂OR, —C(O)OR or —CH₂OP;

P is —C(O)OR', —C(O)R', —C(O)NR'₂ or —OP(O)(OR')OR', wherein each R' is independently hydrogen or C₁₋₃alkyl;

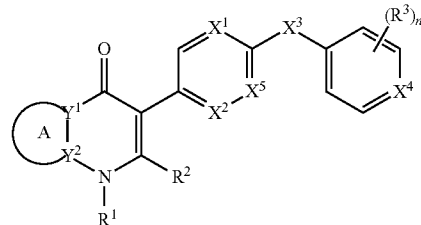
n is 0, 1, 2, 3 or 4;

each R³ is independently halogen, C₁₋₃alkyl, C₁₋₃alkoxy, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR or SF₅;

or two R³ groups, together with the carbons to which they are attached, form a 1,3-dioxolane; and

each R is independently hydrogen or C₁₋₃alkyl.

2. The compound of claim 1, having the structure of (I):



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof,

wherein

ring A combines with Y¹ and Y₂ to form a C₃₋₇cycloalkenyl or heteroaryl ring,

wherein the C₃₋₇cycloalkenyl or heteroaryl is optionally substituted by halogen, C₁₋₃alkyl, C₁₋₃alkoxy, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR, cyano or phenyl;

Y¹ is C;Y₂ is C or N;X¹ is C(R^{x1}) or N,

wherein R^{x1} is hydrogen, halogen, C₁₋₃alkyl, C₁₋₃alkoxy or C₁₋₃haloalkyl;

X² is C(R^{x2}) or N,

wherein R^{x2} is hydrogen, halogen, C₁₋₃alkyl, C₁₋₃alkoxy or C₁₋₃haloalkyl;

X³ is O, N(R), S or C₁₋₃alkyl;X⁴ is C or N;X⁵ is C or N;R¹ is hydrogen or C₁₋₃alkyl;

R² is hydrogen, C₁₋₃alkyl, C₁₋₃haloalkyl, —CH₂OH, —CH₂OR or —C(O)OR;

n is 0, 1, 2, 3 or 4;

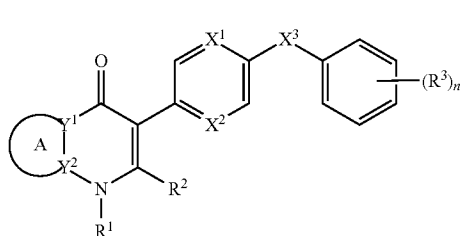
each R³ is independently halogen, C₁₋₃alkyl, C₁₋₃alkoxy, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR or SF₅;

or two R³ groups, together with the carbons to which they are attached, form a 1,3-dioxolane; and

each R is independently hydrogen or C₁₋₃alkyl.

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3. The compound of claim 1, having the structure of (Ia):



or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

ring A combines with Y¹ and Y₂ to form a C₃₋₇cycloalkenyl or heteroaryl ring,

wherein the C₃₋₇cycloalkenyl or heteroaryl is optionally substituted by halogen, C₁₋₃alkyl, C₁₋₃alkoxy, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR, cyano or phenyl;

Y¹ is C;

Y₂ is C or N;

X¹ is C(R^{x1}) or N,

wherein R^{x1} is hydrogen, halogen, C₁₋₃alkyl, C₁₋₃alkoxy or C₁₋₃haloalkyl;

X² is C(R^{x2}) or N,

wherein R^{x2} is hydrogen, halogen, C₁₋₃alkyl, C₁₋₃alkoxy or C₁₋₃haloalkyl;

X³ is O, N(R), S or C₁₋₃alkyl;

R¹ is hydrogen or C₁₋₃alkyl;

R² is hydrogen, C₁₋₃alkyl or —C(O)OR;

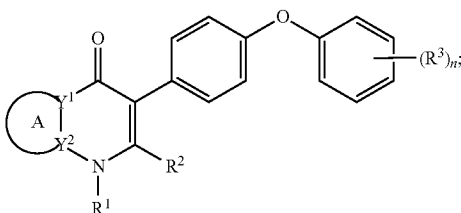
n is 0, 1, 2, 3 or 4;

each R³ is independently halogen, C₁₋₃alkyl, C₁₋₃alkoxy, C₁₋₃haloalkyl, —O—C₁₋₃haloalkyl, —S—C₁₋₃haloalkyl, —C(O)OR or SF₅; and

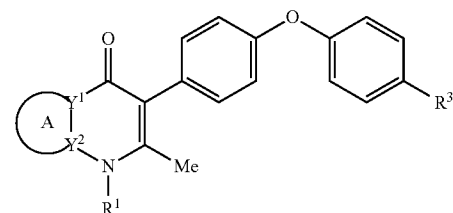
each R is independently hydrogen or C₁₋₃alkyl.

4. The compound of claim 3, having

(a) the structure of Formula (Ib):

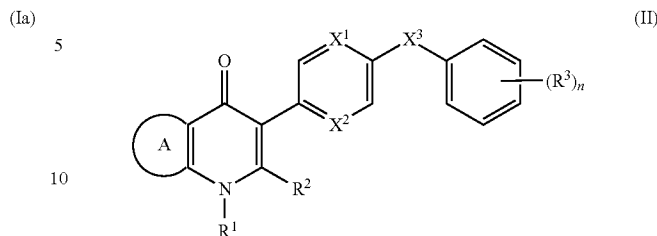


(b) the structure of Formula (Ic):



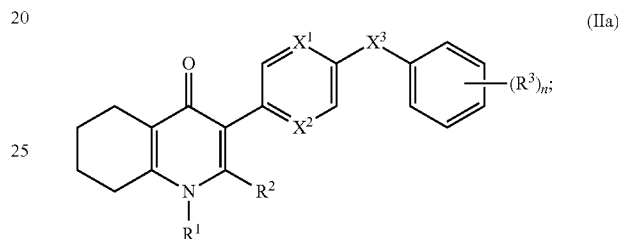
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(c) the structure of Formula (II):



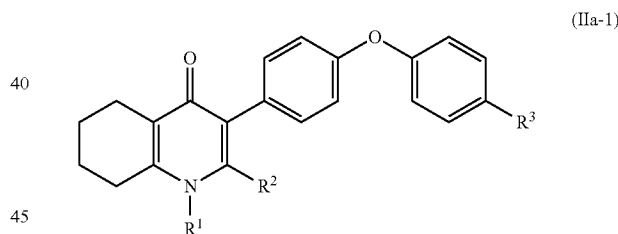
wherein ring A combines with the carbon atoms with which it is attached to form a C₃₋₇ cycloalkenyl;

(d) the structure of Formula (IIa):



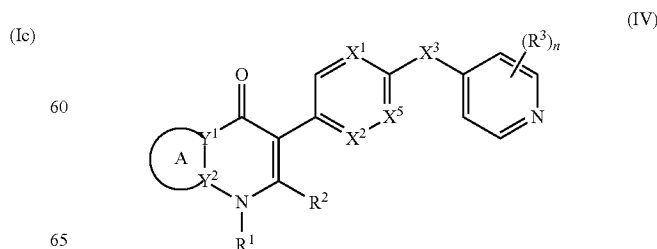
or

(e) the structure of Formula (IIa-1):



wherein R³ is hydrogen, halogen, C₁₋₃alkyl or C₁₋₃ haloalkyl.

5. The compound of claim 1, having the structure of Formula (IV):



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or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof, wherein

ring A combines with Y^1 and Y_2 to form a C_{3-7} cycloalkenyl or heteroaryl ring,

wherein the C_{3-7} cycloalkenyl or heteroaryl is optionally substituted by halogen, C_{1-3} alkyl, C_{1-3} alkoxy, C_{1-3} haloalkyl, $-O-C_{1-3}$ haloalkyl, $-S-C_{1-3}$ haloalkyl, $-C(O)OR$, cyano or phenyl;

Y^1 is C;

Y^2 is C or N;

X^1 is $C(R^{x1})$ or N,

wherein R^{x1} is hydrogen, halogen, C_{1-3} alkyl, C_{1-3} alkoxy or C_{1-3} haloalkyl;

X^2 is $C(R^{x2})$ or N,

wherein R^{x2} is hydrogen, halogen, C_{1-3} alkyl, C_{1-3} alkoxy or C_{1-3} haloalkyl;

X^3 is O, N(R), S or C_{1-3} alkyl;

X^3 is C or N;

X^5 is C or N;

R^1 is hydrogen or C_{1-3} alkyl;

R^2 is hydrogen, C_{1-3} alkyl, C_{1-3} haloalkyl, $-CH_2OH$, $-CH_2OR$ or $-C(O)OR$;

n is 0, 1, 2, 3 or 4;

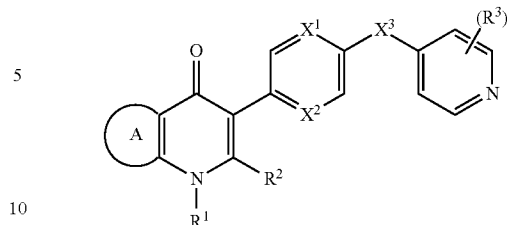
each R^3 is independently halogen, C_{1-3} alkyl, C_{1-3} alkoxy, C_{1-3} haloalkyl, $-O-C_{1-3}$ haloalkyl, $-S-C_{1-3}$ haloalkyl, $-C(O)OR$ or SF_5 ; and

each R is independently hydrogen or C_{1-3} alkyl.

6. The compound of claim 5, having the structure of Formula (IVa):

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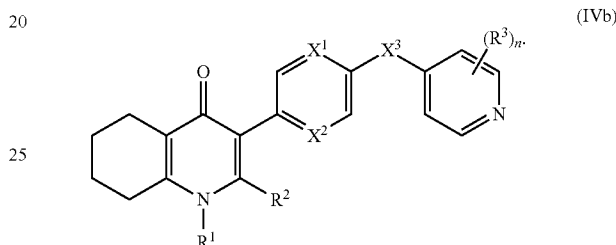
(IVa)



wherein

ring A combines with the carbon atoms with which it is attached to form a C_{3-7} cycloalkenyl.

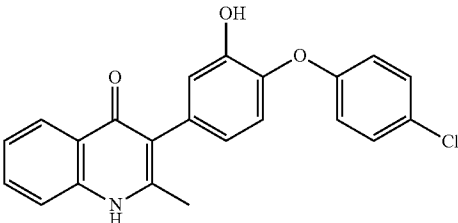
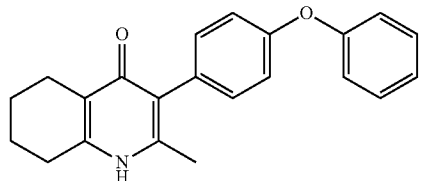
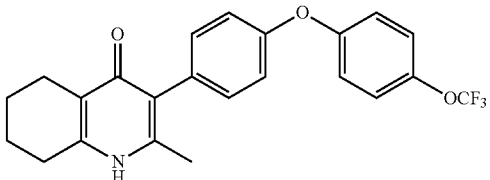
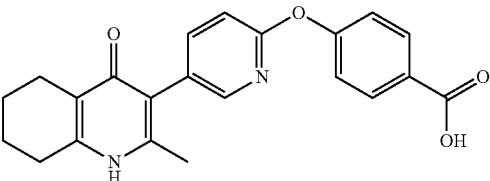
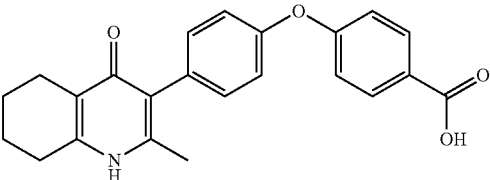
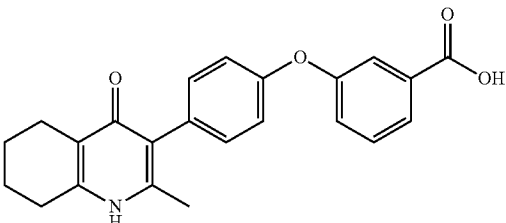
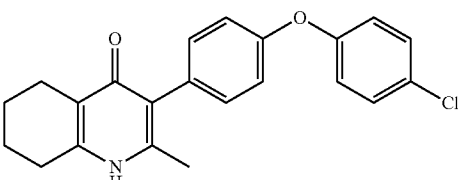
7. The compound of claim 5, having the structure of Formula (IVb):



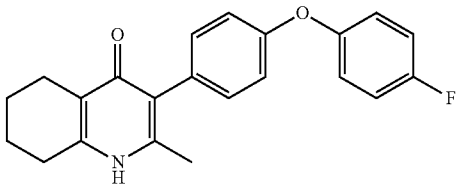
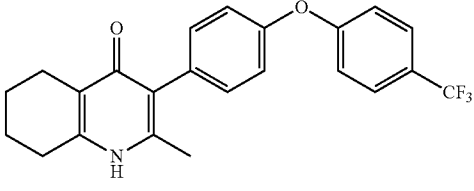
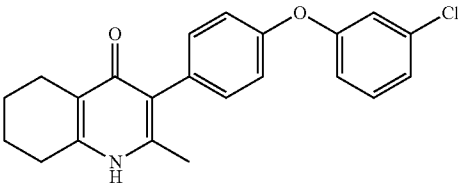
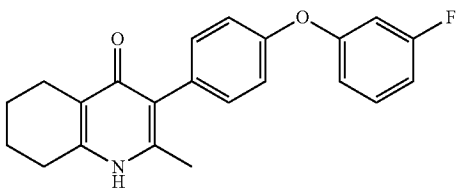
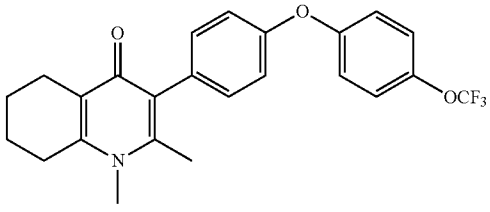
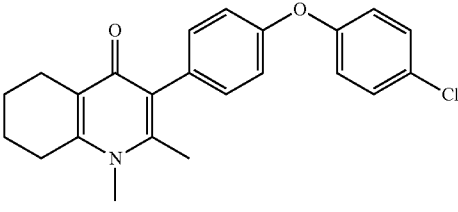
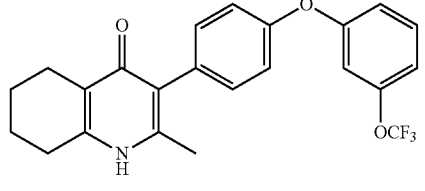
8. A compound that is:

Structure	Name
	2-methyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)quinolin-4(1H)-one
	2-methyl-3-(4-phenoxyphenyl)quinolin-4(1H)-one
	1-ethyl-2-methyl-3-(4-phenoxyphenyl)quinolin-4(1H)-one

-continued

Structure	Name
	3-(4-(4-chlorophenoxy)-3-hydroxyphenyl)-2-methylquinolin-4(1H)-one
	2-methyl-3-(4-phenoxyphenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
	2-methyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
	4-((5-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)pyridin-2-yl)oxy)benzoic acid
	4-(4-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)phenoxy)benzoic acid
	3-(4-(2-methyl-4-oxo-1,4,5,6,7,8-hexahydroquinolin-3-yl)phenoxy)benzoic acid
	3-(4-(4-chlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

-continued

Structure	Name
	3-(4-(4-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
	2-methyl-3-(4-(4-(trifluoromethyl)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
	3-(4-(3-chlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
	3-(4-(3-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
	1,2-dimethyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
	3-(4-(4-chlorophenoxy)phenyl)-1,2-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
	2-methyl-3-(4-(3-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one

-continued

Structure	Name
	2-methyl-3-(4-(3-(trifluoromethyl)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
	3-(4-(3,5-dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
	3-(4-(3-chloro-4-fluorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

methyl 3-((5-(4-ethoxy-2-methyl-5,6,7,8-tetrahydroquinolin-3-yl)pyridin-2-yl)oxy) benzoate
 1,2-dimethyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4-one
 3-(4-(3,4-Dichlorophenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
 3-[4-(3-chloro-4-fluorophenoxy)phenyl]-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4-one
 3-{4-[(2,6-dichloropyridin-4-yl)oxy]phenyl}-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4-one
 3-[4-(3,5-dichlorophenoxy)phenyl]-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4(1H)-one
 3-(4-(4-Trifluoromethoxyphenoxy)phenyl)-2-(carboxylate)-5,6,7,8-tetrahydroquinolin-4(1H)-one
 3-(6-(4-Trifluoromethoxyphenoxy)pyridin-3-yl)-2-methyl-5,6,7,8-tetrahydroquinolin-4-one
 3-(4-Phenoxyphe-nyl)-1,2,3,4,5,6,7,8-octahydroquinazoline-2,4,dione
 3-(4-(4-Trifluoromethoxyphenoxy)phenyl)-2-(methylhydroxy)-5,6,7,8-tetrahydroquinolin-4(1H)-one
 3-[4-(2H-1,3-benzodioxol-5-yloxy)phenyl]-2-methyl-5,6,7,8-tetrahydro-1H-quinolin-4-one
 6-Ethyl-3-(4-(4-trifluoromethoxyphenoxy)phenyl)-2-methyl-5,6,7,8-tetrahydroquinolin-4(1H)-one

30 3-(4-(4-Trifluoromethoxyphenoxy)phenyl)-2,6-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
 3-(4-(4-Trifluoromethoxyphenoxy)phenyl)-2,7-dimethyl-5,6,7,8-tetrahydroquinolin-4(1H)-one
 7-Ethyl-2-methyl-3(4-(4-trifluoromethoxyphenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
 35 3-(4-(4-trifluoromethoxyphenoxy)phenyl)-2-methyl-1,7-naphthyrid-4(1H)-one
 7-Trifluoromethyl-2-methyl-3(4-(4-trifluoromethoxyphenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one
 or a stereoisomer thereof, or a pharmaceutically acceptable salt thereof.
 40 **9.** The compound of claim 1 that is 2-methyl-3-(4-(4-(trifluoromethoxy)phenoxy)phenyl)-5,6,7,8-tetrahydroquinolin-4(1H)-one, or a pharmaceutically acceptable salt thereof.
10. A pharmaceutical composition comprising a compound of claim 1 and a pharmaceutically acceptable diluent, excipient, or carrier.
11. A method for treating an apicomplexan parasitic infection, comprising administering to a subject in need thereof an amount effective to treat the infection of the compound or pharmaceutical composition of claim 1.
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