

Table S2. Annotation of the repetitive sequences in the two assembled genomes

Library	Rebase				RepeatModuler				Combined library			
Species	QH		SP		QH		SP		QH		SP	
Category	Length (Mb)	% in assembly	Length (Mb)	% in assembly	Length (Mb)	% in assembly	Length (Mb)	% in assembly	Length (Mb)	% in assembly	Length (Mb)	% in assembly
SINEs	0.08	0.04%	0.08	0.04%	0.00	0	0.00	0	0.02	0.01%	0.02	0.01%
LINEs	2.48	1.37%	2.46	1.41%	2.82	1.56%	3.17	1.82%	3.45	1.91%	3.78	2.17%
LTRs	17.59	9.72%	16.82	9.65%	12.88	7.11%	12.82	7.35%	16.74	9.24%	16.07	9.22%
DNAs	8.12	4.48%	7.88	4.52%	3.41	1.88%	3.76	2.16%	6.41	3.54%	6.60	3.79%
Unclassified	0.98	0.54%	0.94	0.54%	38.84	21.45%	35.59	20.42%	35.62	19.67%	33.23	19.07%
Total	29.25	16.16%	28.18	16.17%	57.94	32.00%	55.33	31.75%	62.23	34.37%	59.69	34.25%
Simple repeats	2.67	1.47%	2.64	1.52%	2.23	1.23%	2.15	1.23%	1.99	1.10%	1.99	1.14%
Low complexity	0.81	0.45%	0.80	0.46%	0.54	0.30%	0.53	0.30%	0.51	0.28%	0.51	0.29%
Total		18.13%		18.19%		33.39%		33.21%		35.57%		35.55%