

Predictor	π_0	Model probabilities (conditional on effect)			
		GC-only	control-only	unequal	No interaction
Cis SNPs (eQTL mapping)	0.207 (0.181,0.232)	0.031 (0.021,0.042)	0.026 (0.016,0.038)	0.001 (0.000,0.003)	0.942 (0.927,0.955)
Population differences	0.5834 (0.569,0.597)	0.090 (0.076,0.105)	0.089 (0.075,0.104)	0.009 (0.002,0.019)	0.812 (0.793,0.830)
Growth rate	0.6339 (0.623,0.645)	0.001 (0,0.004)	0.022 (0.016,0.029)	0.000 (0.000,0.001)	0.977 (0.970,0.983)
Mitochondrial genome copy number	0.7874 (0.777,0.796)	0.007 (0.003,0.014)	0.01 (0.005,0.017)	0.000 (0.000,0.001)	0.983 (0.974,0.990)
EBV genome copy number	0.8725 (0.865,0.881)	0.004 (0,0.013)	0.006 (0,0.013)	0.000 (0.000,0.003)	0.991 (0.980,0.998)

Confidence intervals for each point estimates are shown in parentheses.