Table 1: The normalized mutation rate matrix and stationary distribution of base frequencies estimated with two out-groups, M. famulus and R. norvegicus, using the method described by Chan et al. (2012).

	A	C	G	T
A	0.48	0.09	0.32	0.11
C	0.19	0.00	0.12	0.69
G	0.69	0.12	0.00	0.19
T	0.11	0.32	0.08	0.48
Stationary Distribution	0.34	0.16	0.16	0.34