

Table S12. Models of nucleotide substitution for maximum likelihood phylogenetic analyses of combined and partitioned data in Fig. 2, Supplemental Figures 1-5. NOTE: Y genes only 127 individuals (males).

Data Partition	Model	Rate Matrix (AC,AG,AT,CG,CT,GT)	Gamma Shape Parameter	Nucleotide Frequency (A,G,C,T)	P-Invariant
Combined	TVM+I+G	1.0492 3.9254 0.6220 1.2887 3.9254 1.0000	0.8892	0.2901 0.2101 0.2137 0.2861	0.2359
X	TVM+I+G	1.3458 5.8210 0.6388 1.3717 5.8210 1.0000	0.8714	0.2744 0.2048 0.2215 0.2993	0.1833
Y	TVM+I+G	0.9110 3.4368 0.7433 1.7805 3.4368	1.3424	0.2984 0.1968 0.2389	0.1486
Autosome	TVM+I+G	1.0332 4.0131 0.5804 1.2855 4.0131 1.0000	0.8870	0.2892 0.2130 0.2126 0.2852	0.2024
Intron	TVM+I+G	1.0416 3.6909 0.5346 1.4049 3.6909 1.0000	1.0071	0.3016 0.1881 0.2006 0.3097	0.1103
Exon	TrN+I+G	1.0000 4.7679 1.0000 1.0000 5.3084 1.0000	0.8558	0.2653 0.2504 0.2463 0.2380	0.3289
UTR	TVM+I+G	1.0085 3.3907 0.5332 1.0395 3.3907 1.0000	0.8742	0.2998 0.2011 0.1997 0.2994	0.1079