

TABLE S2

Divergence between duplicated *MT+* genes and their autosomal counterparts

<i>MT+</i> Gene	Autosomal Paralog	Alignment Region	Alignment Length	Gaps	Total Gap Length	Substitutions	Divergence		Codon Substitution Rate				
							Score	SE	dN	SE	dS	SE	dN/dS
MTP0428 Region													
MTP0428	294656	Intergenic	788	7	462	33	0.1100	0.0188	0.0443	0.0045	0.065	0.0091	0.682
		CDS	3213	17	99	150	0.0501	0.0045					
		Intron	703	8	43	33	0.0519	0.0084					
MTA Region													
MTA5	396153	CDS	1494	1	1500	39	0.0268	0.0039	0.0123	0.0033	0.0766	0.016	0.161
		Intron	984	11	37	75	0.0844	0.0093					
MTA4	185335	Intergenic	468	5	54	24	0.0605	0.0117	0.0058	0.0024	0.0991	0.0243	0.059
		CDS	2643	5	32	49	0.0191	0.0026					
		Intron	5220	38	564	343	0.0780	0.0046					
psMTA2	195673	Intergenic	1724	7	174	58	0.0385	0.0054	0.0186	0.0058	0.0302	0.0089	0.616
		CDS	1011	1	7	22	0.0223	0.0048					
		Intron	169	1	8	5	0.0318	0.0149					
MTA3	185334	Intergenic	3672	20	1923	102	0.0609	0.0061	0.0055	0.0039	0.0267	0.0155	0.206
		CDS	501	1	15	5	0.0104	0.0047					
		Intron	358	4	41	14	0.0456	0.0116					
294708	152340	Intergenic	9628	22	7834	93	0.0540	0.0059	0.0131	0.0093	0	0	ND
		CDS	185	0	0	3	0.0165	0.0091					
		Intron	164	0	0	3	0.0186	0.0106					
SRL Region													
SRLc	168182	CDS	720	1	6	22	0.0316	0.0068	0.0261	0.0073	0.0361	0.0139	0.723
		Intron	481	5	44	26	0.0625	0.0117					
SRLb	168182	CDS	1049	2	4	35	0.0344	0.0057	0.0167	0.0068	0.0438	0.0182	0.381
		Intron	1398	3	11	79	0.0596	0.0066					
SRLa	168182	CDS	1528	1	18	43	0.0292	0.0045	0.0173	0.0039	0.0588	0.0119	0.294
		Intron	327	4	8	27	0.0908	0.0185					

Alignments of cDNAs and genomic DNAs were used to define the intergenic and intronic DNA sequences. CDS: coding sequence. Intron: non-coding sequence between the start and stop codons of the CDS. Intergenic: Non-coding sequence outside of the CDS. Divergence scores determined as per[77]. Codon substitution rates were determined as per[71]. SE is the Standard Error. ND: Not determined