Additional file 6: Sequence divergence between Asia II 3 and MED transcriptomes

	% CpG	% GC	Loci	% Differences		Compared kb	ts/tv[e]
				mean	SE		
5' UTRs[a]	7.48	37.44	102				
All				3.57	0.27	10.92	1.25
No CpG				3.14	0.25	10.11	1.10
CpG				9.84	1.50	0.82	2.29
CDS[b]	7.53	43.93	2529				
All				1.84	0.03	1072.12	2.70
No CpG				1.38	0.03	991.42	2.36
CpG				8.06	0.14	80.70	3.69
nd sites[c]	6.60	44.42	2529				
All				0.49	0.02	628.75	1.31
No CpG				0.44	0.02	587.25	1.17
CpG				1.26	0.08	41.50	2.34
4d sites[d]	12.93	39.29	2529				
All				5.58	0.09	152.04	2.00
No CpG				3.64	0.08	132.38	1.48
CpG				20.83	0.43	19.66	3.06
3' UTRs	4.62	36.27	102				
All				3.13	0.29	15.54	1.61
No CpG				2.74	0.27	14.82	1.34
CpG				13.66	1.85	0.72	4.30

[a] UTRs: untranslated regions.

[b] CDS: coding sequence.

[c] nd sites: non-degenerative sites.

[d] 4d sites: fourfold-degenerate sites where no changes cause any amino acid replacement.

[e] ts/tv: ration of transitions (ts) over transversions (tv).