

Table 4. Best-fitting models of evolution and parameters selected for each codon position with hierarchical likelihood methods. Codon positions with similar model and model parameters were regrouped into the same partition³. Symbols and abbreviations represent: Π , frequency of base; *Tratio*, transition / transversion ratio; *rmat*, rate matrix; *PInvar*, proportion of invariable sites; *alpha*, shape of gamma distribution.

Gene	Codon position	Length	π A	π C	π G	Best model	Tratio or Rmat	alpha	Pinvar	Partition number
POMC	1	160	0.30	0.23	0.34	TVM+G	(2.9 2.1 0.9 0.8 2.1)	0.64	0	1
	2	160	0.40	0.17	0.27	GTR+G	(2.4 2.9 1.6 3.5 6.9)	0.50	0	2
	3	160	0.30	0.22	0.34	TVM+G	(3.4 2.4 1.1 0.9 2.4)	0.63	0	1
BDNF	1	235	0.29	0.20	0.31	GTR+G	(4.7 3.2 1.9 0.9 13.8)	0.32	0	3
	2	236	0.25	0.25	0.25	TrNef+I	(1.0 4.2 1.0 1.0 1.3)	0.02	0.75	4
	3	236	0.25	0.25	0.25	SYM+G	2.95	0.93	0	5
RAG1	1	485	0.32	0.21	0.27	GTR+I+G	(2.3 1.8 0.9 0.8 3.8)	0.94	0.39	6
	2	485	0.35	0.20	0.16	GTR+I+G	(2.1 8.9 1.5 5.6 3.5)	0.64	0.57	7
	3	486	0.27	0.24	0.22	TrN+I+G	(1.0 4.8 1.0 1.0 5.6)	3.72	0.02	8

Primers developed for this study: BDNF_DRV_F1: 5'-ACCATCCTTTTCCTKACTATGG-3'; BDNF_DRV_R1: 5'-CTATCTCCCCTTTTAATGGTC-3'; POMC_DRV_F1: 5'-ATATGTCATGASCCAYTTYCGCTGGAA-3'; POMC_DRV_R1: 5'-GGCRTTYTTGAAWAGATCATTAGWGG-3'; RAG_DRV_PIF: 5'-ACAACTGGACGRCAGATTTTCCAGCC-3'; RAG_DRV_PIR: 5'-GTGATGCTTCAGCACATCCTC-3'.