

Table S6. Nonsynonymous to synonymous nucleotide substitution frequency ratios (dN/dS) for Carnivora UGT genes obtained using 3 different input tree topologies.

Input tree	Order (sub-order)	Family	UGT1A6			UGT1A1		
			Taxa (n) ¹	Seq. (n) ¹	dN/dS	Taxa (n) ¹	Seq. (n) ¹	dN/dS
Maximum likelihood		All species (average value)	49	50	0.3926	47	38	0.3811
	Carnivora (Feliformia)	Felidae	18	16	0.6785	18	15	0.4476
		Hyenidae	4	4	0.508	4	3	0.5258
		Herpestidae	1	1	0.2533	1	1	0.2171
		Viverridae	2	2	0.4815	2	2	0.3556
	Carnivora (Caniformia)	Ursidae	2	2	0.2148	2	1	0.9952
		Procyonidae	1	1	0.4983	1	1	0.2866
		Ailuridae	1	1	0.2102	0	0	-
		Mustelidae	2	2	0.3215	2	2	0.2832
		Otariidae	0	0	-	3	1	>999
		Phocidae	2	2	1.1708	2	2	0.7129
		Canidae	4	4	0.1826	4	3	0.1211
	Non-Carnivora	Cattle, sheep, pig, horse	4	6	0.3945	1	1	0.4166
		Mouse, rat, rabbit	3	4	0.3659	2	2	0.4112
		Primates	5	5	0.3969	5	4	0.4127
Bayesian		All species (average value)	49	50	0.3922	47	38	0.3826
	Carnivora (Feliformia)	Felidae	18	16	0.6332	18	15	0.4325
		Hyenidae	4	4	0.5043	4	3	0.5148
		Herpestidae	1	1	0.2546	1	1	0.216
		Viverridae	2	2	0.4843	2	2	0.3454
	Carnivora (Caniformia)	Ursidae	2	2	0.2056	2	1	1.3389
		Procyonidae	1	1	0.5168	1	1	0.2928
		Ailuridae	1	1	0.1952	0	0	-
		Mustelidae	2	2	0.328	2	2	0.2761
		Otariidae	0	0	-	3	1	>999
		Phocidae	2	2	1.1337	2	2	0.6003
		Canidae	4	4	0.1778	4	3	0.1215
	Non-Carnivora	Cattle, sheep, pig, horse	4	6	0.3954	1	1	0.4133
		Mouse, rat, rabbit	3	4	0.3719	2	2	0.4137
		Primates	5	5	0.3925	5	4	0.3543
Maximum parsimony		All species (average value)	49	50	0.3889	47	38	0.384
	Carnivora (Feliformia)	Felidae	18	16	0.6512	18	15	0.4378
		Hyenidae	4	4	0.5064	4	3	0.5142
		Herpestidae	1	1	0.2523	1	1	0.2159
		Viverridae	2	2	0.4805	2	2	0.3453
	Carnivora (Caniformia)	Ursidae	2	2	0.1992	2	1	1.3439
		Procyonidae	1	1	0.6332	1	1	0.2926
		Ailuridae	1	1	0.1262	0	0	-
		Mustelidae	2	2	0.1672	2	2	0.276
		Otariidae	0	0	-	3	1	>999
		Phocidae	2	2	1.1193	2	2	0.6192
		Canidae	4	4	0.1819	4	3	0.1214
	Non-Carnivora	Cattle, sheep, pig, horse	4	6	0.3937	1	1	0.4133
		Mouse, rat, rabbit	3	4	0.4412	2	2	0.3294
		Primates	5	5	0.3621	5	4	0.4688

¹ Number of sampled taxa and unique translated sequences (seq.) used in each analysis. Differences between the numbers of taxa and sequences within each group arise from the presence of multiple UGT1A6 genes in mouse (2) and horse (3) (see Tables S1 for details), as well as exclusion of any sequences found to be identical to any other sequence after cropping. Sequences that were excluded from the final analysis (and the identical sequence included in the analysis) were as follows: PanTro_A1 (HomSap_A1), CanRuf_A1 (CanFam_A1), HyaHya_A1 (ParBru_A1), PumCo2_A1 (PumCon_A1), LeoGeo_A1 (LeoTig_A1), PanPar_A1 (PanUnc_A1), PhoHoo_A1 (CalUrs_A1), UrsThi_A1 (UrsMar_A1), LeoGeo_A6 (LeoTig_A6), PriBen_A6 (FelCat_A6).