

Table S3: Partitions and nucleotide substitution models, used in the phylogenetic analysis, as optimized with PartitionFinder.

Partition	Best Model	Subset Partitions	Size
p1	K80+ Γ	CAD_pos3, EF1AF2_pos3	357
p2	K80+ Γ	CAD_pos1, LOP1_pos2, unc-4_pos2, TOP1_pos1	780
p3	HKY+ Γ	CAD_pos2, TOP1_pos2	417
p4	HKY+ Γ	CAD_introns, LOC15, LOP1_introns	2007
p5	HKY+ Γ	GRIK2	960
p6	SYM+ Γ	COX1_pos1	353
p7	TrN+ Γ	COX1_pos2	353
p8	GTR+ Γ	COX1_pos3	353
p9	TrN+ Γ	EF1AF2AF2_pos1, HIS3.3B_pos1, unc-4_pos1	433
p10	JC+ Γ	EF1AF2_pos2, HIS3.3B_pos2	349
p11	HKY+ Γ	EF1AF2_introns, unc-4_introns	1210
p12	GTR+ Γ	HIS3.3B_pos3	143
p13	GTR+ Γ	HIS3.3B_introns	213
p14	SYM+ Γ	LOP1_pos1	280
p15	GTR+ Γ	LOP1_pos3, UNC-4_pos3	363
p16	TrN+ Γ	TOP1_pos3	268