

Table - 6: Substitution models selected by IQ-TREE for partitions in the phylogeny of Carnivora. The table shows the partition ID and the corresponding evolutionary model, with adjustments for variation in substitution rates across sites. Models like TIM3+F+I+G4 and GTR+F+I+G4 are the most frequent.

Carnivora	
ID	Model
1	ND5_1st: TIM2+F+I+G4
2	ND5_2st: GTR+F+I+G4
3	ND5_3st: TIM3+F+R3
4	Cytb_1st: GTR+F+I+G4
5	Cytb_2st: K3Pu+F+R2
6	Cytb_3st: TPM3+F+R3
7	ATP6_1st: TIM3+F+I+G4
8	ATP6_2st: TN+F+R2
9	ATP6_3st: TIM3+F+I+G4
10	ATP8_1st: TN+F+I+G4
11	ATP8_2st: K3Pu+F+I+G4
12	ATP8_3st: TIM3+F+I+G4
13	ND4L_1st: TIM2e+I+G4
14	ND4L_2st: TPM3+F+R2
15	ND4L_3st: K3Pu+F+I+G4
16	ND4_1st: GTR+F+I+G4
17	ND4_2st: TVM+F+I+G4
18	ND4_3st: K3Pu+F+R3
19	ND3_1st: GTR+F+I+G4
20	ND3_2st: TIM3+F+I+G4
21	ND3_3st: K3Pu+F+R2
22	ND2_1st: GTR+F+I+G4
23	ND2_2st: TPM3+F+I+G4
24	ND2_3st: HKY+F+G4
25	ND1_1st: GTR+F+I+G4
26	ND1_2st: TIM+F+I
27	ND1_3st: TPM3+F+R3
28	COX3_1st: TIM3e+G4
29	COX3_2st: TIM2+F+R2
30	COX3_3st: TIM3+F+I+G4
31	COX2_1st: TIM3+F+G4
32	COX2_2st: TPM3+F+R2
33	COX2_3st: TIM3+F+R3
34	COX1_1st: TIM3e+I+G4
35	COX1_2st: TIM2+F+I
36	COX1_3st: TN+F+I+G4
37	ND6_1st: TN+F+G4
38	ND6_2st: TPM3+F+G4
39	ND6_3st: K3Pu+F+I+G4

Table - 7: Substitution models selected by IQ-TREE for partitions in the phylogeny of Artiodactyla. The table lists the partition ID and the corresponding evolutionary model, accounting for variations in substitution rates across sites. Models like TIM2+F+I+G4 and TN+F+I+G4 are frequently used, reflecting the diversity of evolutionary patterns in the dataset.

Artiodactyla	
ID	Model
1	ND5_1st: TIM2+F+I+G4
2	ND5_2st: TVM+F+I+G4
3	ND5_3st: TN+F+R2
4	Cytb_1st: TIM3e+I
5	Cytb_2st: HKY+F+I
6	Cytb_3st: TN+F+I+G4
7	ATP6_1st: TIM3+F+G4
8	ATP6_2st: TIM3+F+I
9	ATP6_3st: TN+F+I+G4
10	ATP8_1st: TN+F+R3
11	ATP8_2st: TN+F+G4
12	ATP8_3st: TPM3+F+R2
13	ND4L_1st: TIM3e+G4
14	ND4L_2st: HKY+F+I
15	ND4L_3st: TPM3+F+I
16	ND4_1st: GTR+F+G4
17	ND4_2st: TIM2+F+I
18	ND4_3st: TN+F+I+G4
19	ND3_1st: TIM2e+R3
20	ND3_2st: TPM3+F+R2
21	ND3_3st: HKY+F+G4
22	ND2_1st: GTR+F+G4
23	ND2_2st: TPM3+F+I
24	ND2_3st: TIM2+F+R2
25	ND1_1st: TIM2+F+G4
26	ND1_2st: HKY+F+I
27	ND1_3st: TN+F+I+G4
28	COX3_1st: TIM2+F+G4
29	COX3_2st: TIM3+F+I
30	COX3_3st: HKY+F+R3
31	COX2_1st: TIme+I+G4
32	COX2_2st: TIM3+F+I
33	COX2_3st: TIM+F+I+G4
34	COX1_1st: TIM3e+G4
35	COX1_2st: TPM3+F+I
36	COX1_3st: TN+F+I+G4
37	ND6_1st: GTR+F+R3
38	ND6_2st: HKY+F+G4
39	ND6_3st: HKY+F+R2

Table - 8: Substitution models selected by IQ-TREE for partitions in the phylogeny of Chiroptera. The table lists the partition ID and the respective evolutionary model, considering rate variation across sites. Common models like GTR+F+I+G4 and TIM3+F+R3 highlight the range of evolutionary dynamics across different gene regions.

Chiroptera	
ID	Model
1	ND5_1st: TIM3+F+R5
2	ND5_2st: GTR+F+I+G4
3	ND5_3st: TVM+F+I+G4
4	Cytb_1st: GTR+F+I+G4
5	Cytb_2st: TVM+F+I+G4
6	Cytb_3st: HKY+F+R5
7	ATP6_1st: TIM3+F+R3
8	ATP6_2st: GTR+F+R3
9	ATP6_3st: TPM3+F+R4
10	ATP8_1st: TIM2+F+I+G4
11	ATP8_2st: HKY+F+R3
12	ATP8_3st: TIM+F+I+G4
13	ND4L_1st: GTR+F+R3
14	ND4L_2st: TIM3+F+I+G4
15	ND4L_3st: TPM3+F+I+G4
16	ND4_1st: GTR+F+R4
17	ND4_2st: TVM+F+I+G4
18	ND4_3st: TIM2+F+R4
19	ND3_1st: SYM+R3
20	ND3_2st: TPM3+F+I+G4
21	ND3_3st: TPM3+F+R4
22	ND2_1st: GTR+F+I+G4
23	ND2_2st: GTR+F+R3
24	ND2_3st: TIM3+F+R3
25	ND1_1st: GTR+F+I+G4
26	ND1_2st: K3Pu+F+R3
27	ND1_3st: HKY+F+R5
28	COX3_1st: SYM+R3
29	COX3_2st: TVM+F+R2
30	COX3_3st: TPM3+F+R4
31	COX2_1st: SYM+I+G4
32	COX2_2st: TIM3+F+I+G4
33	COX2_3st: HKY+F+R4
34	COX1_1st: SYM+I+G4
35	COX1_2st: K3Pu+F+I+G4
36	COX1_3st: TPM2+F+R5
37	ND6_1st: TIM3+F+R3
38	ND6_2st: GTR+F+I+G4
39	ND6_3st: HKY+F+R4