




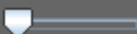
Site	Cover	Adenine	Thymine	Guanine	Cytosine	Deletion	Con.	HPS	Codons
0	100	1.0000	0.0000	0.0000	0.0000	0.0000	A	0	
1	101	0.0000	1.0000	0.0000	0.0000	0.0000	T	0	TGA:* (101), [1]
2	101	0.0000	0.0000	1.0000	0.0000	0.0000	G	0	
3	101	1.0000	0.0000	0.0000	0.0000	0.0000	A	0	
4	101	0.9802	0.0000	0.0198	0.0000	0.0000	A	1	AAG:K (99), GAG:E (2), [2]
5	101	1.0000	0.0000	0.0000	0.0000	0.0000	A	2	
6	101	0.0000	0.0000	1.0000	0.0000	0.0000	G	2	
7	101	0.0000	0.9802	0.0000	0.0198	0.0000	T	0	TGA:* (97), CGA:R (2), [2]
8	101	0.0000	0.0000	1.0000	0.0000	0.0000	G	0	
9	103	0.9806	0.0000	0.0194	0.0000	0.0000	A	0	
10	103	1.0000	0.0000	0.0000	0.0000	0.0000	A	1	AGG:R (103), [1]
11	103	0.0000	0.0000	1.0000	0.0000	0.0000	G	1	
12	104	0.0000	0.0000	1.0000	0.0000	0.0000	G	1	
13	104	0.0096	0.0000	0.9904	0.0000	0.0000	G	2	GGA:G (99), GGG:G (2), AGA:R (1), [3]
14	105	0.0000	0.0000	0.9810	0.0000	0.0190	G	3	
15	105	0.9810	0.0000	0.0190	0.0000	0.0000	A	3	
16	106	0.0000	0.0472	0.0000	0.9528	0.0000	C	0	CCA:P (98), TCA:S (5), CCG:P (2), CCC:P (1), [4]
17	106	0.0000	0.0000	0.0000	1.0000	0.0000	C	1	
18	106	0.9717	0.0000	0.0189	0.0094	0.0000	A	1	
19	106	0.7642	0.2358	0.0000	0.0000	0.0000	A	1	AGA:R (81), TGA:* (25), [2]
20	107	0.0000	0.0000	1.0000	0.0000	0.0000	G	1	
21	108	1.0000	0.0000	0.0000	0.0000	0.0000	A	0	
22	108	0.9537	0.0000	0.0463	0.0000	0.0000	A	1	AGA:R (103), GGA:G (5), [2]
23	108	0.0000	0.0000	1.0000	0.0000	0.0000	G	1	
24	108	1.0000	0.0000	0.0000	0.0000	0.0000	A	0	
25	108	0.9907	0.0000	0.0093	0.0000	0.0000	A	1	ATT:I (107), GTT:V (1), [2]
26	108	0.0000	1.0000	0.0000	0.0000	0.0000	T	1	
27	108	0.0000	1.0000	0.0000	0.0000	0.0000	T	1	
28	108	0.0000	0.0000	1.0000	0.0000	0.0000	G	1	GTC:V (108), [1]

Frame  1

Non Con. Freq.  0.00

Max. HPS  10

Save Selected Rows

Posterior  0.00

Apply Filter

CURRENT FILTER LEVEL: 0.00

