Decemb	er 2019	November 2020	May 2021	

- Prioritizing a mutation as "adaptive" or "conserved" based on a simple combination of factors
 - Selective past and present of the site (positive, negative, neither)
 - Evolutionary credibility
 - Does this mutation appear in a large fraction of genomic contexts (haplotypes)?

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Continued evolution, complex selection dynamics, transition to endemic?

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Coord	Gene/site	Recent	Туре	Periods	Freq	Codon	AA	Predicted	HRank	AScore
28687	N/139	+	Alternating	14	0.0022	TTG→TTT	L→F	0	0.002	4.645
23398	S/613	+	Alternating	13	0.0039	CAG→CAT	Q→H	0	0	4.615
28687	N/139	+	Alternating	14	0.0018	TTG→TTC	L→F	0	0.006	4.613
17685	helicase/484	+	Alternating	8	0.0002	$GTT \rightarrow TTT$	V→F	0	0.006	4.32
28678	N/136	+	Alternating	8	0.0008	GAG→GAT	E→D	0	0.006	4.319
26175	ORF3a/262	+	Alternating	7	0.0006	CCA→TCA	P→S	0	0.004	4.293
18969	exonuclease	+	Alternating	8	0.0004	$AAG \rightarrow AAT$	$K \rightarrow N$	0	0.01	4.289
11740	nsp6/257	+	Alternating	8	0.0002	CAG→CAT	Q→H	0	0.011	4.277
25632	ORF3a/81	+	Alternating	8	0.0002	TGC→TTC	C→F	0	0.012	4.269
28678	N/136	+	Alternating	8	0.0001	GAG→CAG	E→Q	0	0.013	4.255
29299	N/343	+	Alternating	7	0.0003	GAT→CAT	D→H	0	0.008	4.253
26175	ORF3a/262	+	Alternating	7	0.0003	CCA→CTA	P→L	0	0.009	4.244
29347	N/359	+	Alternating	6	0.0008	GCA→TCA	A→S	0	0.005	4.24
29299	N/343	+	Alternating	7	0.0001	GAT→TAT	D→Y	0	0.01	4.235
24871	S/1104	+	Alternating	5	0.0041	GTA→TTA	V→L	0	0	4.235