

Table 4. Effect of correcting for recombination when using fixed effects likelihood to detect positively selected sites.

Virus and gene	Positively Selected Codons	
	Uncorrected FEL	Corrected FEL
Cache Valley G	212,516,546,551	None
Canine Distemper H	158, 179, 264, 444	179, 264, 444, 548
Crimean Congo hemm. fever NP	195	9,195
Hantaan G2	None	None
Human Parainfluenza (1) HN	37, 91, 358, 556	91, 358
Influenza A (human H2N2) HA	87, 166, 252, 358	87, 147,252, 358
Influenza B NA	42,106,345,436	42,106,345,436
Mumps F	57, 480	57, 480
Mumps HN	399	None
Newcastle disease F	1,4, 5,7,16,18,108,516	1,5,7,16,108,493,505
Newcastle disease HN	2,54,58,228,262,284,306,471	2,58,228,262,284,306,471
Newcastle disease N	425, 430, 466	425, 430, 462, 466
Newcastle disease P	12, 56,65,174,179,188,189, 204, 208, 213,217,218,239,306,332	56, 65, 146, 153, 174, 179, 189, 193, 204,208, 213, 218, 261,306,332
Puumala NP	79	None

Test $p < 0.1$ was used to classify sites as selected. Codon sites found under selection by both methods are shown in bold.

Sites detected by FEL with and without dS variation

