

**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, <b>179, 264, 444</b>	<b>179, 264, 444, 548</b>
Crimean Congo hemm. fever NP	<b>195</b>	<b>9,195</b>
Hantaan G2	None	None
Human Parainfluenza (1) HN	37, <b>91, 358, 556</b>	<b>91, 358</b>
Influenza A (human H2N2) HA	<b>87, 166, 252, 358</b>	<b>87, 147,252, 358</b>
Influenza B NA	<b>42,106,345,436</b>	<b>42,106,345,436</b>
Mumps F	<b>57, 480</b>	<b>57, 480</b>
Mumps HN	399	None
Newcastle disease F	<b>1,4,5,7,16,18,108,516</b>	<b>1,5,7,16,108,493,505</b>
Newcastle disease HN	<b>2,54,58,228,262,284,306,471</b>	<b>2,58,228,262,284,306,471</b>
Newcastle disease N	<b>425, 430, 466</b>	<b>425, 430, 462, 466</b>
Newcastle disease P	12, <b>56,65,174,179,188,189, 204, 208, 213,217,218,239,306,332</b>	<b>56, 65, 146, 153, 174, 179, 189, 193, 204,208, 213, 218, 261,306,332</b>
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

