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>	179, 264, 444, 548
Crimean Congo hemm. fever NP	195	$9,\! 195$
Hantaan G2	None	None
Human Parainfluenza (1) HN	37, <b>91, 358</b> , 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	<b>57</b> , <b>480</b>	<b>57</b> , 480
Mumps HN	399	None
Newcastle disease F	<b>1</b> , 4, <b>5</b> , <b>7</b> , <b>16</b> , 18, <b>108</b> , 516	<b>1,5,7,16,108</b> ,493,505
Newcastle disease HN	<b>2</b> , 54, <b>58</b> , <b>228</b> , <b>262</b> , <b>284</b> , <b>306</b> , <b>471</b>	$2,\!58,\!228,\!262,\!284,\!306,\!471$
Newcastle disease N	$425,\ 430,\ 466$	<b>425, 430</b> , 462, <b>466</b>
Newcastle disease P	12, <b>56,65,174,179</b> ,188, <b>189, 204</b> ,	<b>56, 65</b> , 146, 153, <b>174, 179, 189</b> ,
	<b>208</b> , <b>213</b> ,217, <b>218</b> ,239, <b>306</b> , <b>332</b>	193, <b>204,208, 213, 218</b> , 261, <b>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

