Accounting for recombination

- First screen the alignment to find putative non-recombinant fragments (e.g. using GARD)

- Apply a model-based test (MEME, FUBAR) using multiple phylogenies (one per fragment), but inferring other parameters (e.g. nucleotide substitution biases and base frequencies) from the entire alignment

- This has been shown to work very well on simulated and empirical data

- This is the approach does not work for analyses assuming a single tree (BUSTED, aBSREL).

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,**	**56, 65**, 146, 153, **174, 179, 189**,
	208, 213,217,**218**,239,**306,332**	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.