**S1 Table. Model quality as assessed by AIC.**

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| **ID** | **Model** | **Δ AIC** |
| A |  | 0 |
| B |  | 1,123.24 |
| C |  | 1,820.08 |
| D |  | 2,059.26 |
| E |  | 2,298.44 |
| F |  | 3,487.73 |
| G |  | 4,082.94 |
| H |  | 4,641.86 |
| I |  | 31,610.46 |
| J |  | 34,525.13 |
| K |  | 40,814.98 |
| L |  | 33,265.94 |
| M |  | 26,957.81 |

Models are shown alongside their Δ AIC, the improvement in AIC relative to a null, intercept model (model A). Model terms are consistent with notation used in Equations 1-7 and are described in full in S2 Table. Models A-H include every combination of base terms introduced in Equation 1. Relative AIC scores led to H being strongly preferred and other combinations were therefore discounted. Models I and J contain 62 branch terms identified using Equation 2. Model J also includes terms for seven substitutions identified using Equation 3. Model K generates a fitted value for every observed combination of reference virus and test virus and corresponds to Equation 7. Models L and M include only substitution terms to explain antigenic differences and no branch terms. Model L includes all 18 identified substitutions (7 identified using Equation 3 and 11 identified using Equation 4). Model M contains terms for the substitutions of highest antigenic impact (K141E and ΔK130) only.