

# aBSREL analysis summary

- **West Nile Virus NS3 protein**

- 91% branches can be explained with simple (single  $dN/dS$ ) models
- 3 branches (9%, 60% of tree length) have evidence of multiple  $dN/dS$  rate classes over sites, but **none** with significant proportions of sites with  $dN/dS > 1$

- **HIV-1 transmission pair**

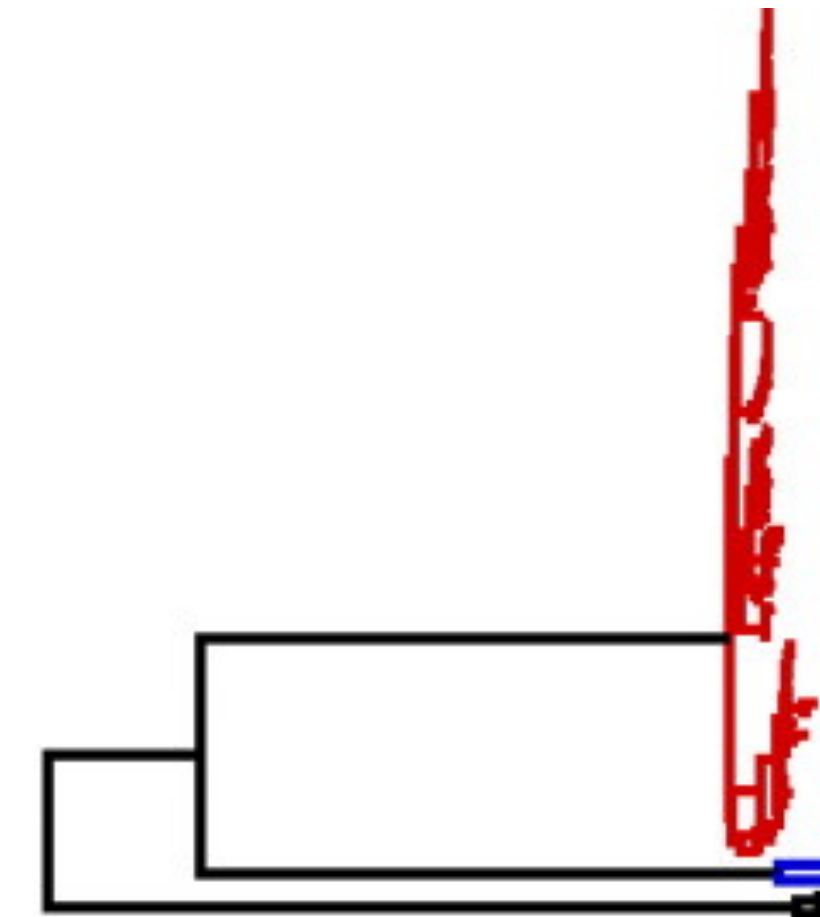
- 76% branches can be explained with simple (single  $dN/dS$ ) models
- 5 branches (24%, ~100% of tree length) have evidence of multiple  $dN/dS$  rate classes over sites
- 3 branches have small (1–7%), but statistically significant ( $p < 0.05$ , multiple testing corrected) proportions of sites with  $dN/dS > 1$ , including the **transmission** branch

- **SARS-CoV-2 spike**

- All but **one** branch can be explained with simple (single  $dN/dS$ ) models
- 1 long terminal branch (~34% of tree length) has evidence of multiple  $dN/dS$  rate classes over sites
- No evidence of branch level selection on internal branches.

- Using models that do not vary selection pressure across lineages yields a patently false “*too young*” estimate for the origin of **measles** (about 600 years ago)
- This estimate is refuted by clear historical records which suggest that measles is at least 1,500-5,000 years old
  - *This includes a treatise by a Persian physician Rhazes about **differential diagnosis of measles and smallpox** published circa 600 AD.*
- Same patterns found for corona-viruses, ebola, avian influenza and herpesvirus

A GTR +  $\Gamma_4$



B Lineage+Dual (two rate)

