

# aBSREL analysis

- **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.

# Correlates of evolutionary complexity

An analysis of ~9,000 curated gene alignments from *selectome.unil.ch*

