HIV-1 *env*

Fitted tree
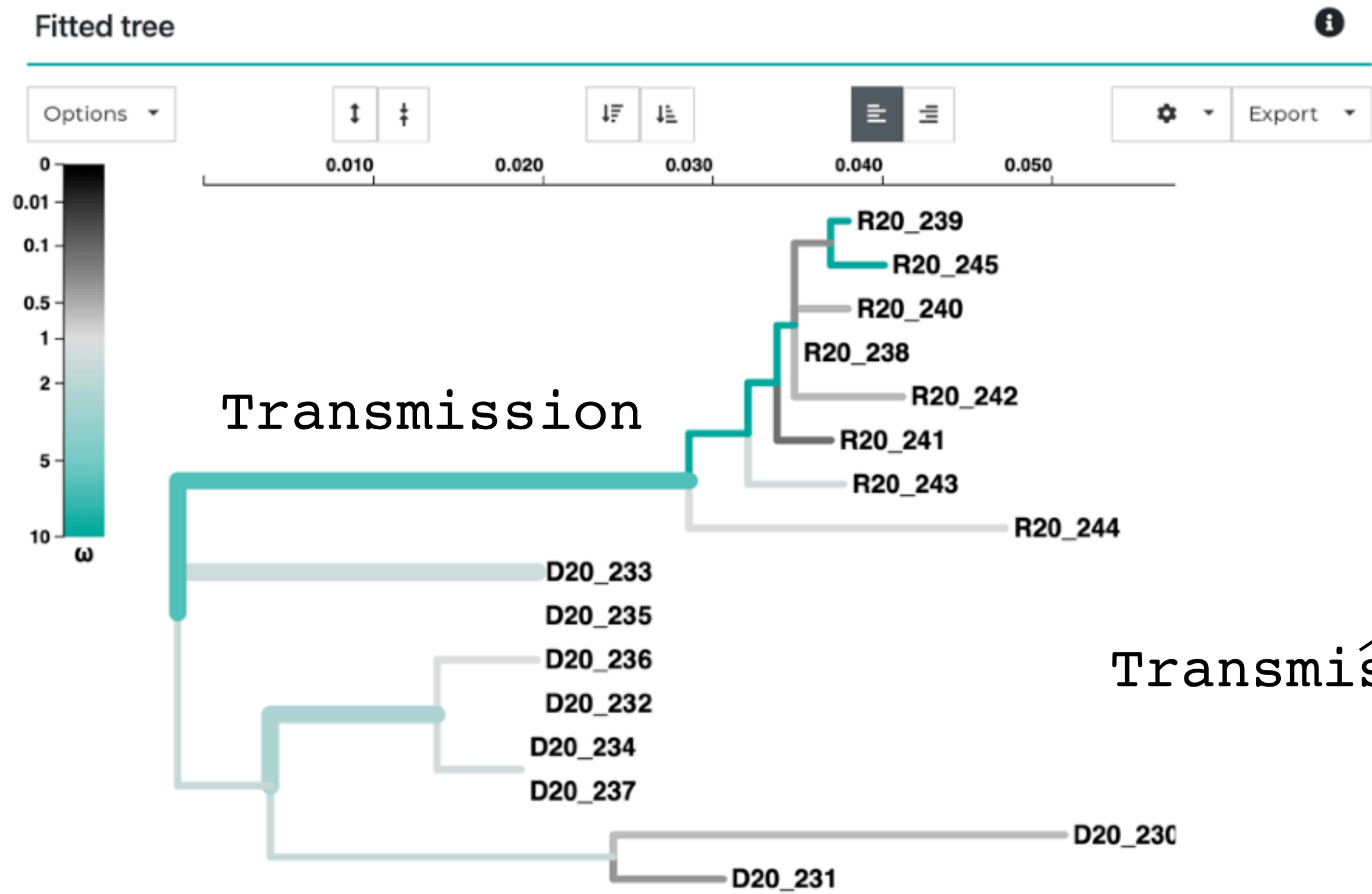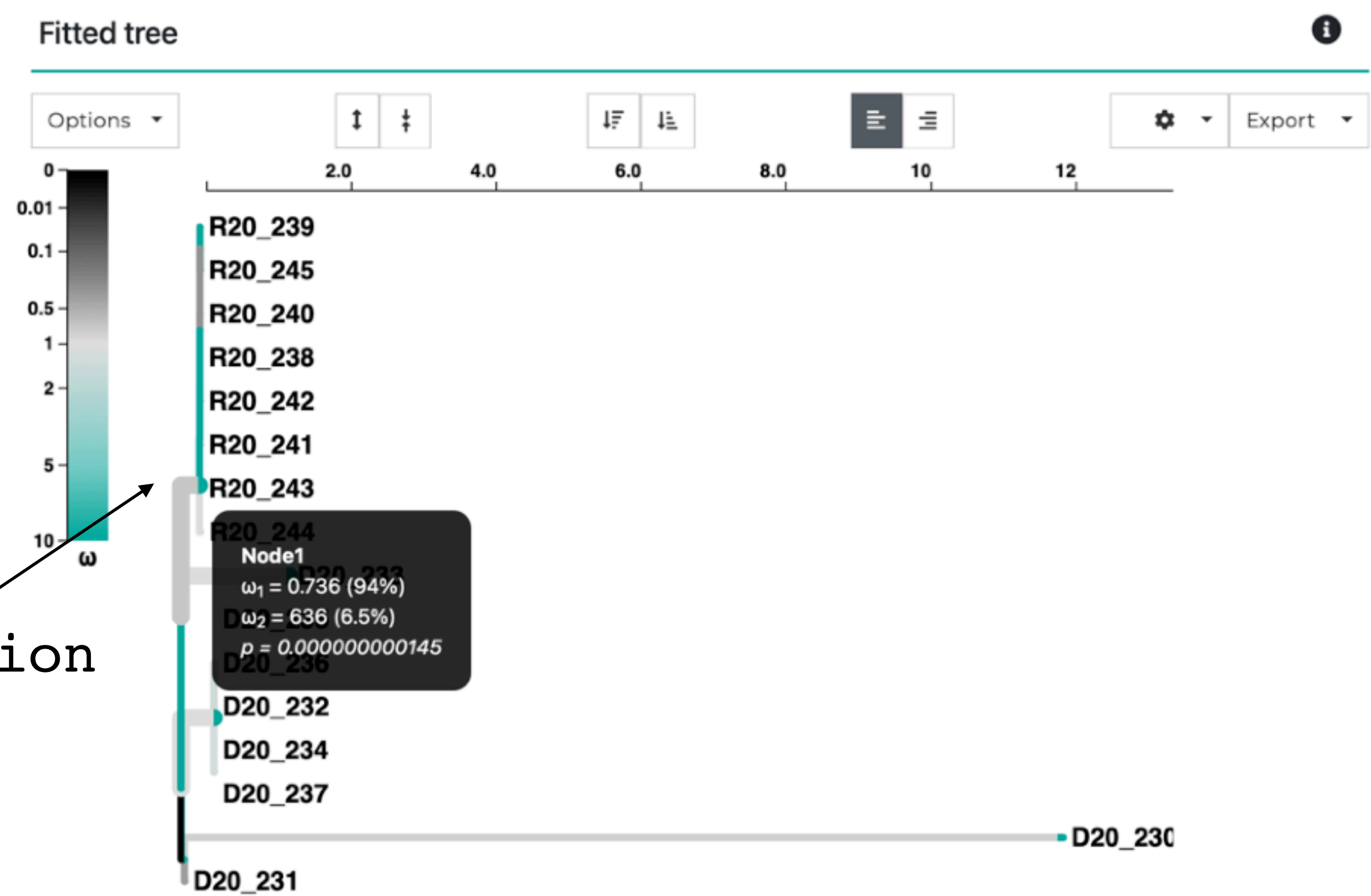
One dN/dS per branch

Adaptive dN/dS per branch

44

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.