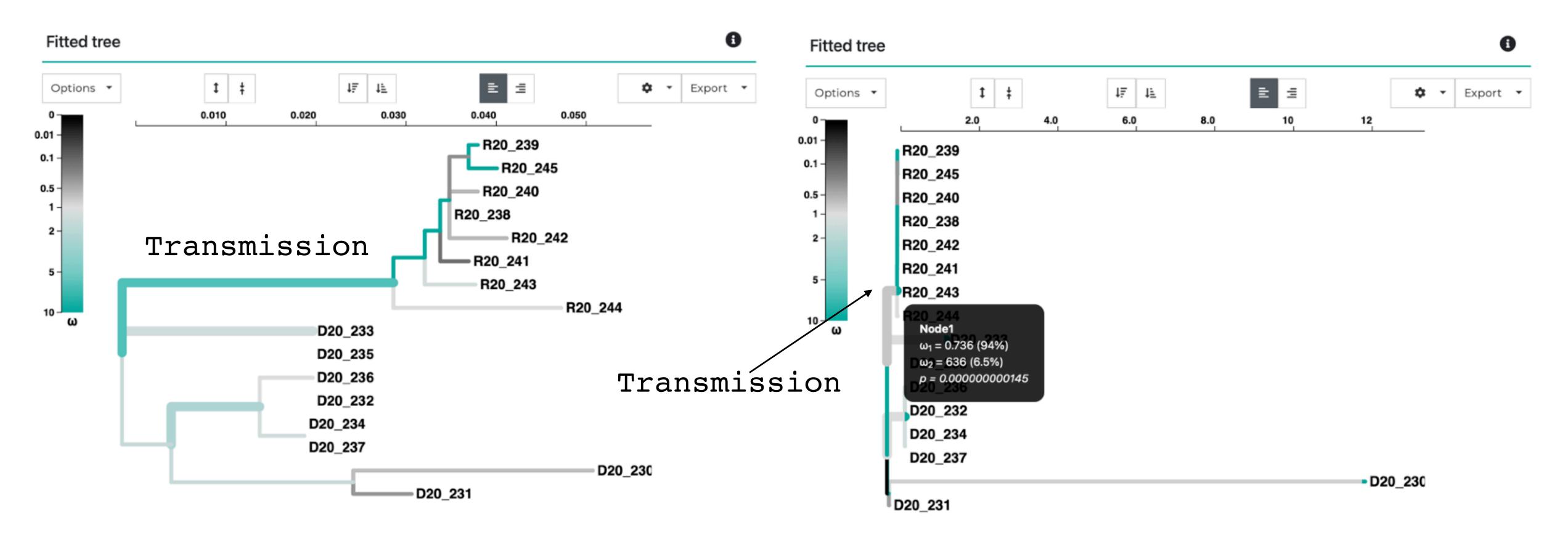
HIV-1 env



One dN/dS per branch

Adaptive dN/dS per branch

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.