All branches

FEL

Fixed Effects Likelihood

FEL analysis was performed on the alignment from /home/datamonkey/datamonkey-js-server/production/app/fel/output/668162d9ab6e044dbc7ffe34. Statistical significance is evaluated based on 50 site-level parametric bootstrap replicates. This analysis **includes** site to site synonymous rate variation. Profile approximate confidence intervals for site-level dN/dS ratios have been computed.

Export ▾

Suggested citation: Not So Different After All: A Comparison of Methods for Detecting Amino Acid Sites Under Selection (2005). Mol Biol Evol 22 (5): 1208-1222

p-value threshold [0.1] Update

25 sequences in the alignment	**567** codon sites in the alignment	**1** partitions
35 median branches/partition used for testing	**55** non-invariant sites tested	**50** parametric bootstrap replicates
0 Sites under diversifying positive selection at p≤0.1	**24** Sites under purifying selection at p≤0.1	

Internal branches

FEL

Fixed Effects Likelihood

FEL analysis was performed on the alignment from /home/datamonkey/datamonkey-js-server/production/app/fel/output/66816b85ab6e044dbc7ffe5a. Statistical significance is evaluated based on 50 site-level parametric bootstrap replicates. This analysis **includes** site to site synonymous rate variation. Profile approximate confidence intervals for site-level dN/dS ratios have been computed.

Export ▾

Suggested citation: Not So Different After All: A Comparison of Methods for Detecting Amino Acid Sites Under Selection (2005). Mol Biol Evol 22 (5): 1208-1222

p-value threshold [0.1] Update

25 sequences in the alignment	**567** codon sites in the alignment	**1** partitions
35 median branches/partition used for testing	**46** non-invariant sites tested	**50** parametric bootstrap replicates
0 Sites under diversifying positive selection at p≤0.1	**3** Sites under purifying selection at p≤0.1	

All branches

Figure 1. Maximum likelihood estimates of dN/dS at each site, together with estimated profile condifence intervals (if available). dN/dS = 1 (neutrality) is depicted as a horizontal gray line. Boundaries between partitions (if present) are shown as vertibal dashed lines.
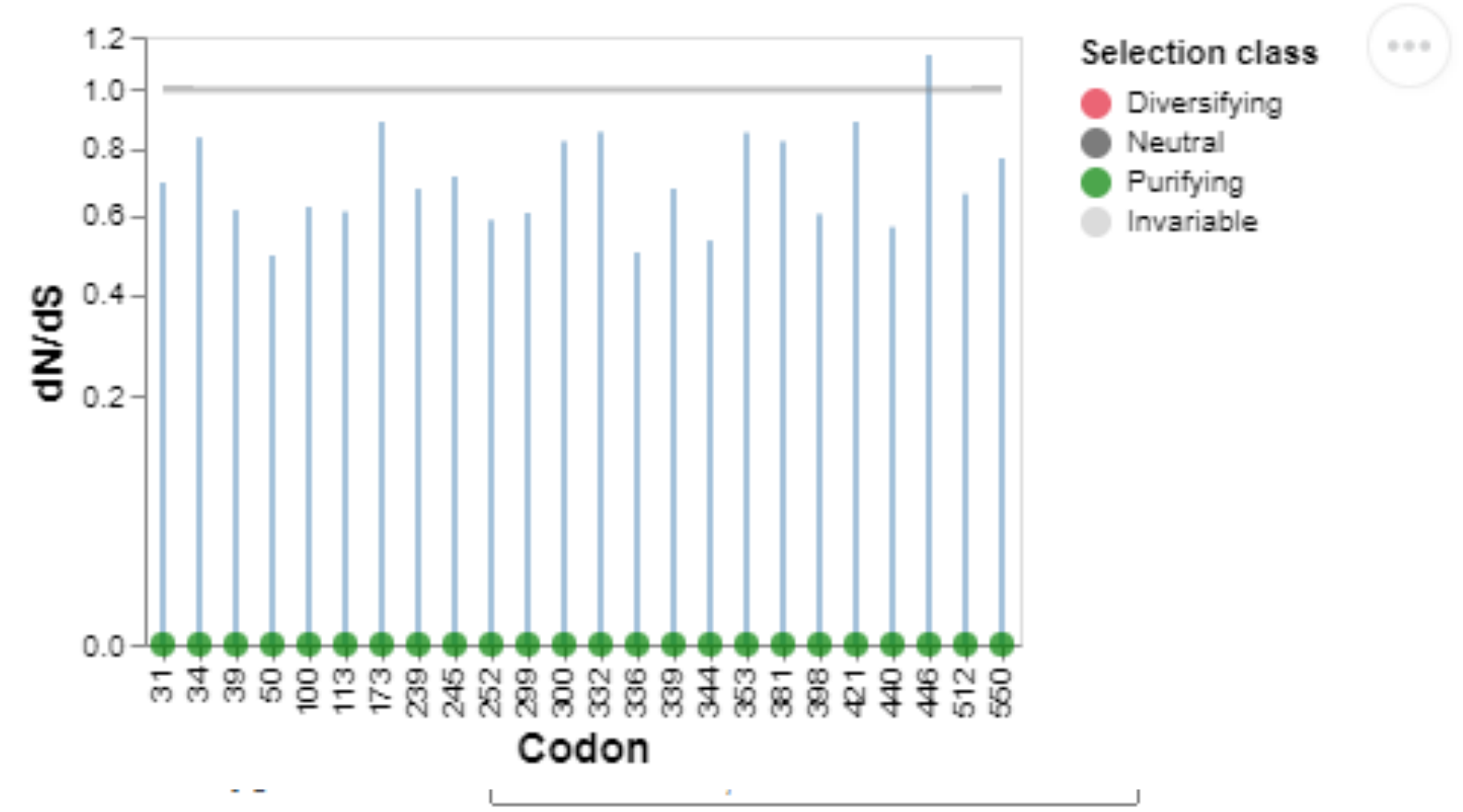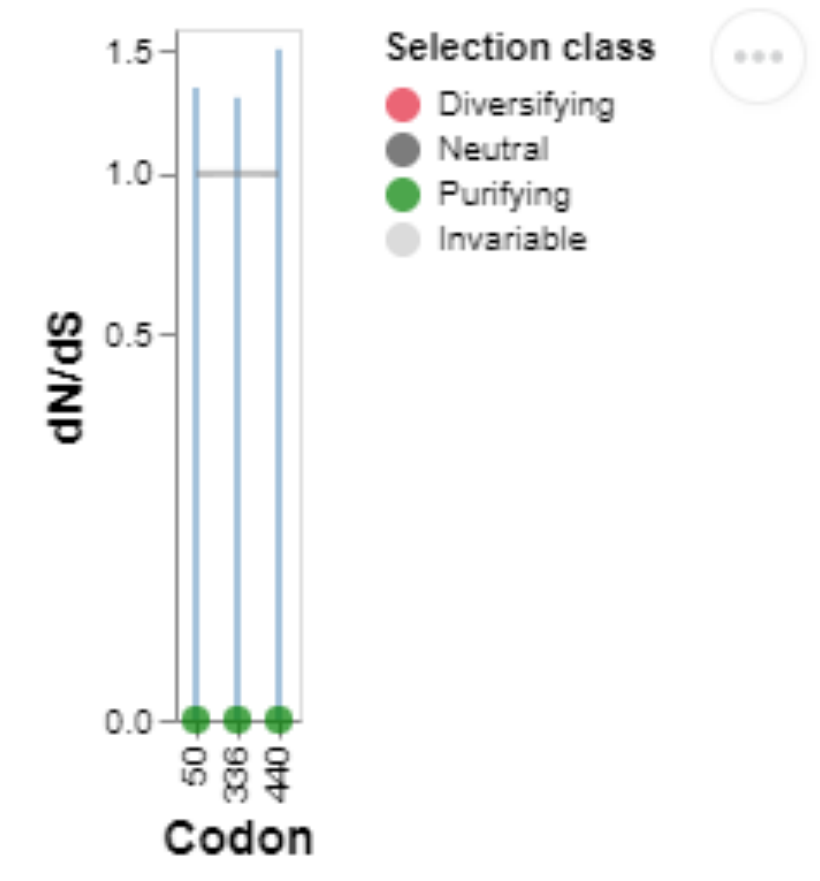
Internal nodes only

Figure 1. Maximum likelihood estimates of dN/dS at each site, together with estimated profile condifence intervals (if available). dN/dS = 1 (neutrality) is depicted as a horizontal gray line. Boundaries between partitions (if present) are shown as vertibal dashed lines.

Sites 50, 336 and 440 are found in both results

234