

# All branches

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

# Internal branches

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

All  
branches

Internal  
nodes only

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

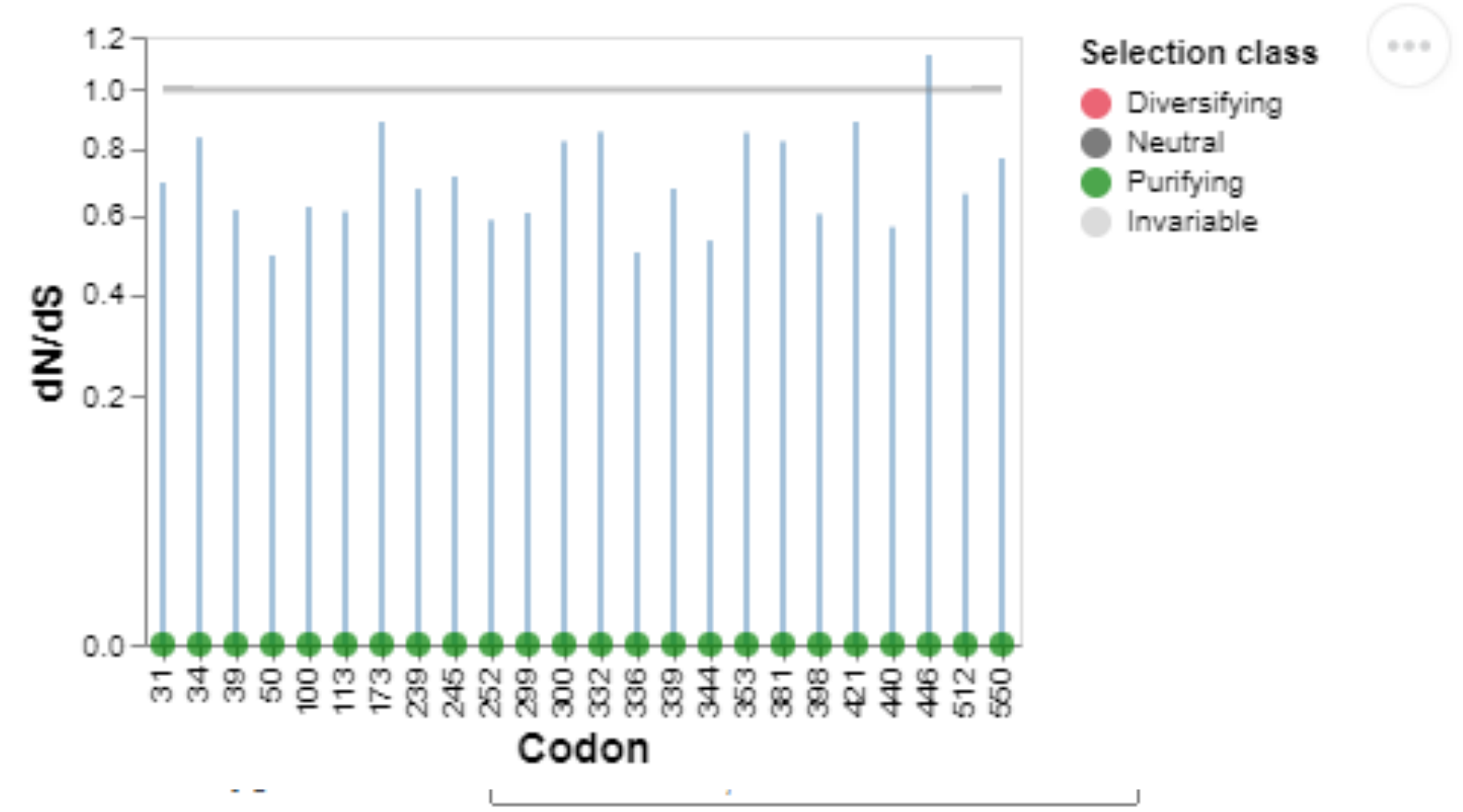
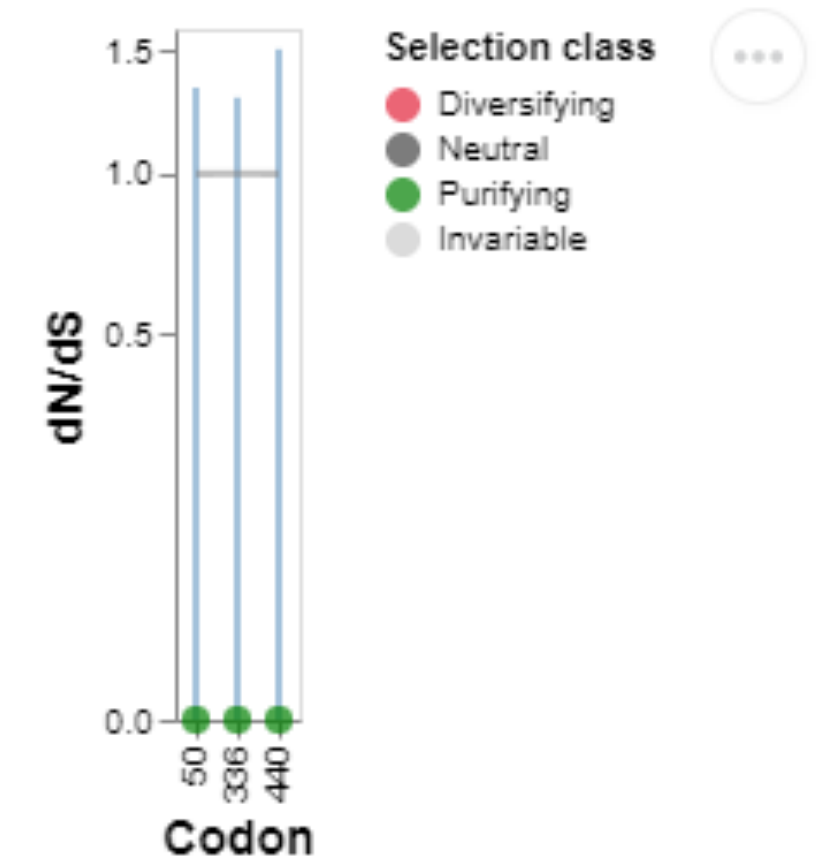


Figure 1. Maximum likelihood estimates of dN/dS at each site, together with estimated profile confidence intervals (if available). dN/dS = 1 (neutrality) is depicted as a horizontal gray line. Boundaries between partitions (if present) are shown as vertical dashed lines.



Sites 50,  
336 and  
440 are  
found in  
both  
results