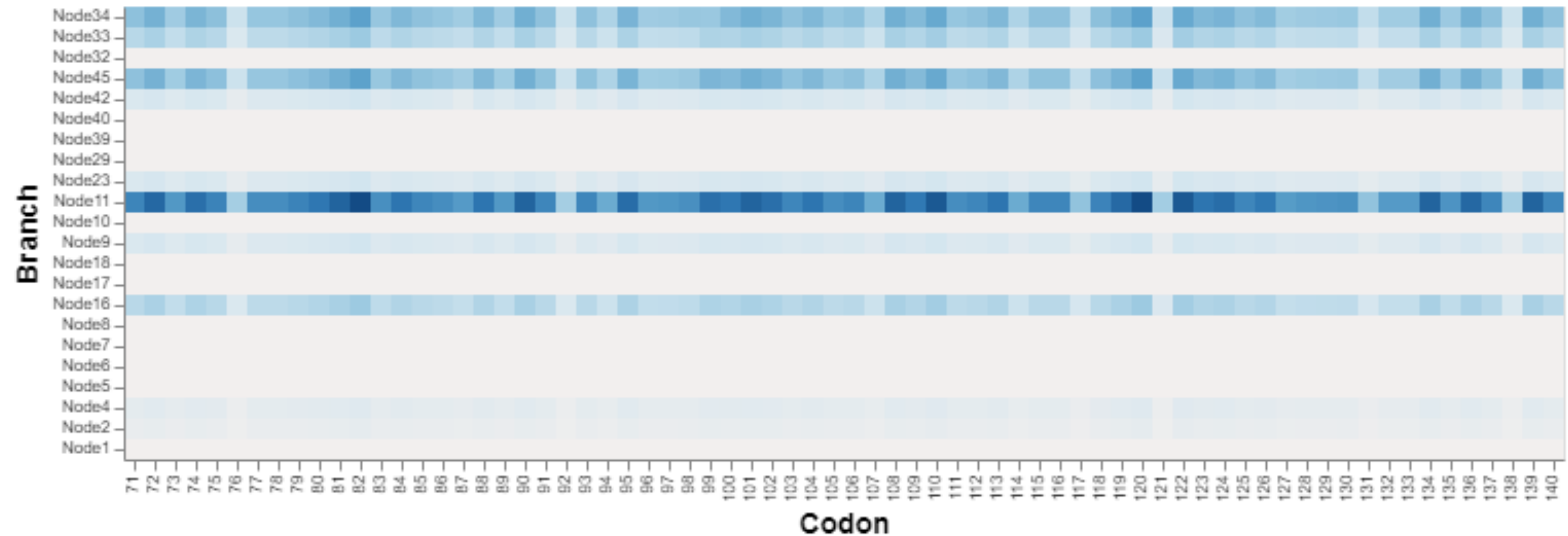
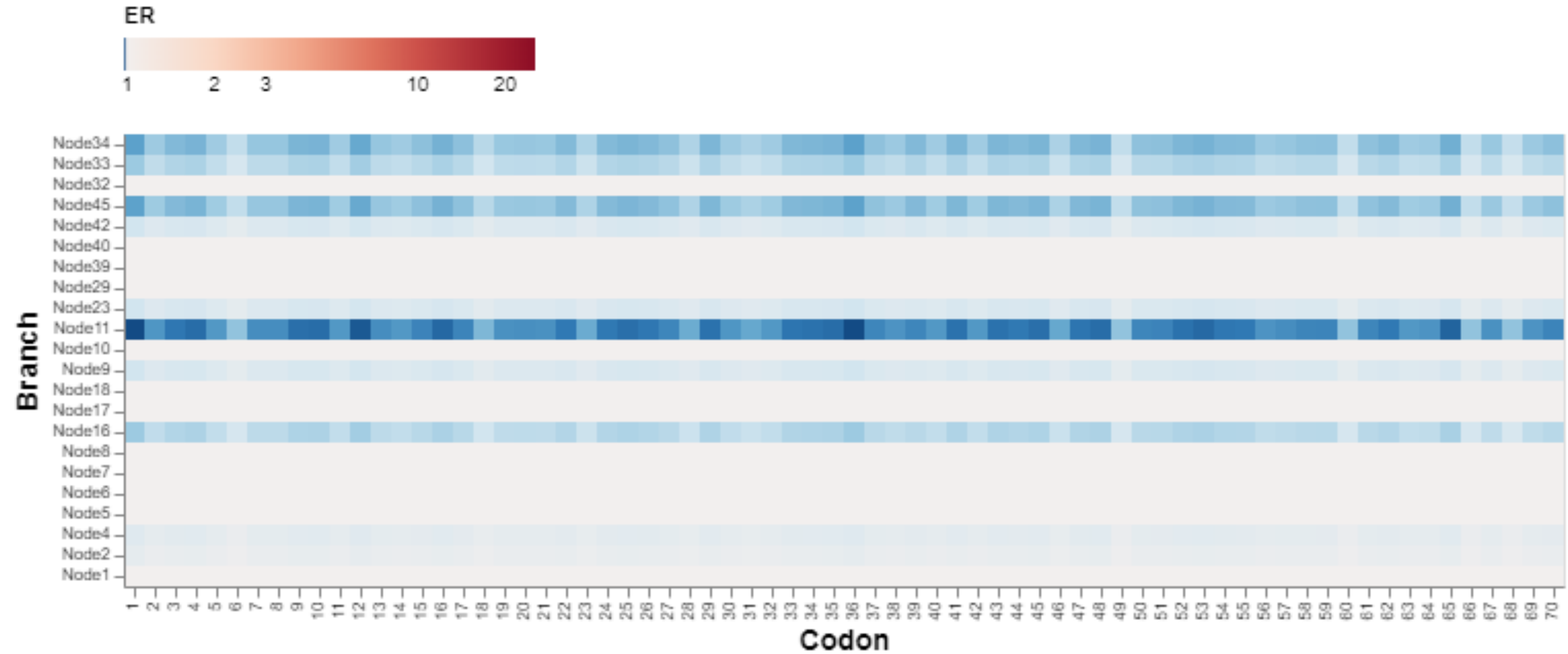


Plot type

Support for positive selection ▾

Figure 1. Empirical Bayes Factors for $\omega > 1$ at a particular branch and site (only tested branches are included).



FEL 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.

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

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	

FEL 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.

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

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	