

BRANCH-SITE RANDOM EFFECTS dN/dS METHOD

Original (no selection, p = 0.50)

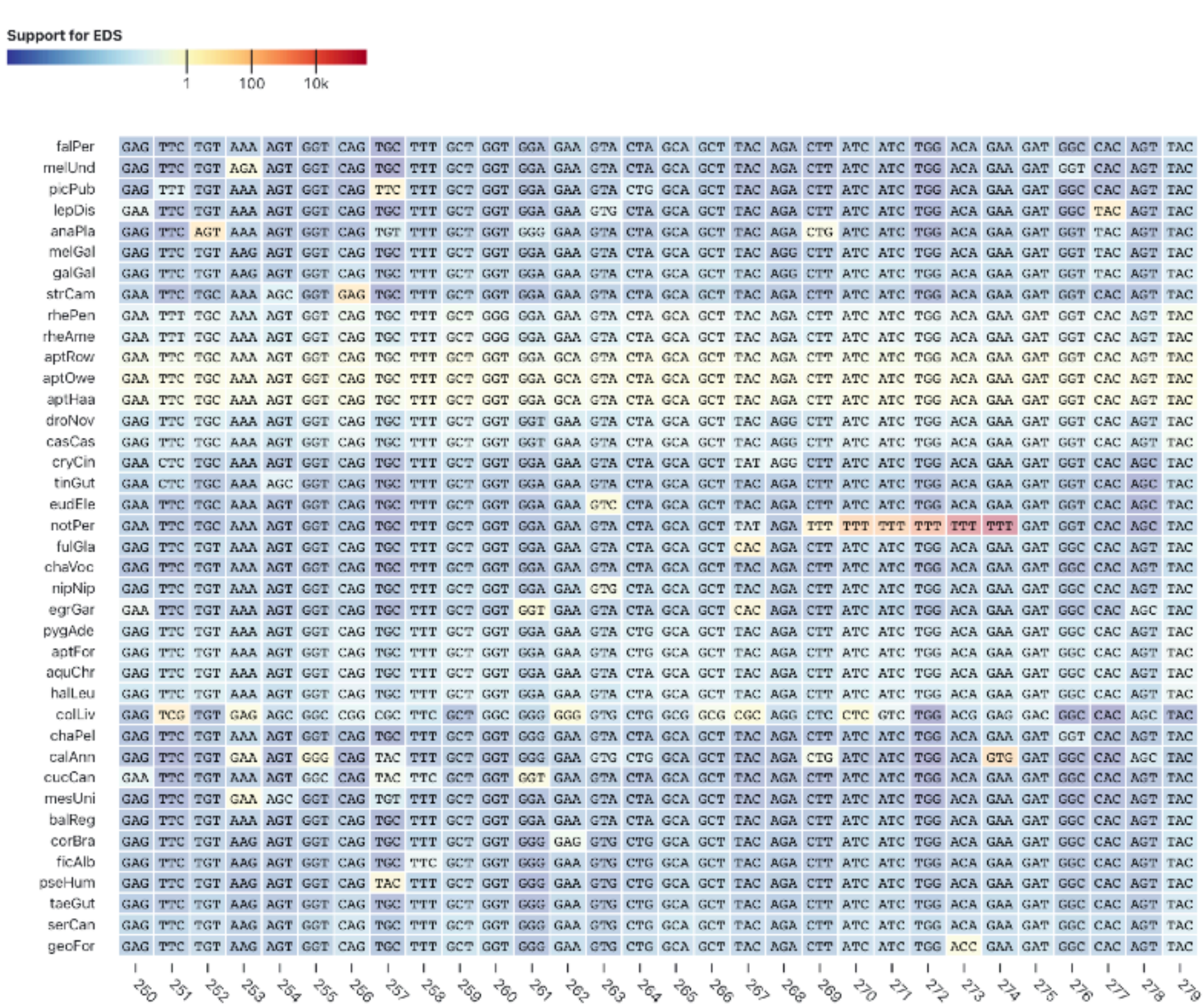
ω distribution

0.1333 (44.644%)
0.3708 (48.792%)
1.118 (6.5581%)

+error (selection, p = 0.0026)

ω distribution

0.02043 (28.451%)
0.4251 (71.522%)
127.8 (0.026700%)



JOURNAL ARTICLE

Gene-Wide Identification of Episodic Selection FREE

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- Sensitive dN/dS (ω) models can “zoom-in” on small fractions of alignments
- Those could (should*) be real biological features indicative of accelerated evolutionary rates
- But they can (and often appear to be) artifacts due to MSA/sequence quality issues
- These apparent issues remain even after applying current state-of-the-art

MSA/filtering tools (e.g. PRANK, PREQUAL) in this space

- Need a method to separate the signal from the noise
- What are some obvious evolutionary features of the noise?
- We developed this method out of necessity, because the signal was being overwhelmed by the noise in high-throughput screens for selection.