- Let’s examine another example (from Zoonomia), where we downsample the genes down to 16 species (using **treemer**)

- Two genes that show evidence of episodic positive diversifying selection

  - One likely “real”

  - One likely “not real”

  - How can we tell?

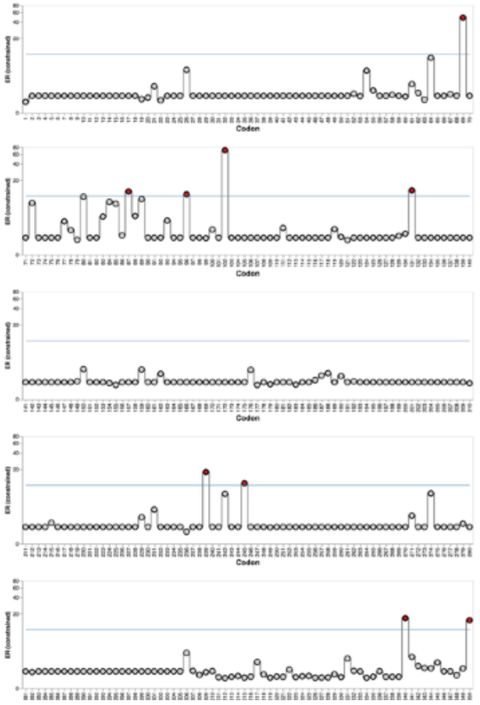
Standard BUSTED method results, p ≤ 0.001 for both

REAL

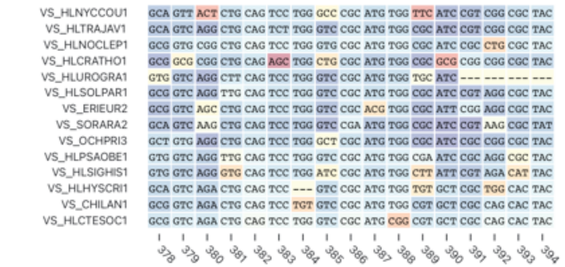
## IQCF1

$\omega_1$=0.4085 (79.597%)
$\omega_2$=0.4078 (15.784%)
$\omega_3$=11.16 (4.6197%)

Reasonable ω value with broad support




Nicely dispersed sites with evidence of selection



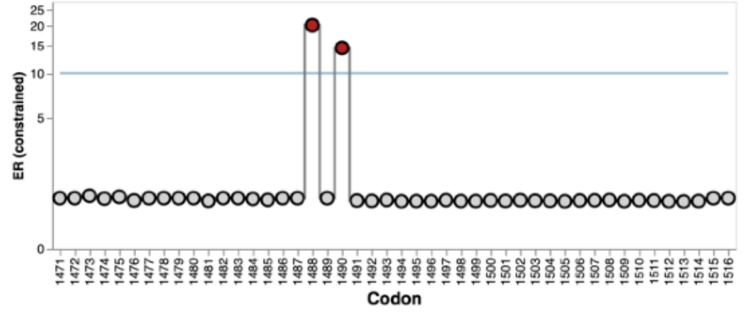

No clear issues with an area of the alignment where there's support for selection

NOT REAL

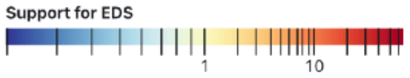
## KRT8

$\omega_1$=0.02107 (80.763%)
$\omega_2$=0.6961 (18.533%)
$\omega_3$=136.3 (0.70395%)

A large ω value with narrow support




Evidence of selection is a localized clump




Obvious alignment/ homology issues, here in one sequence