

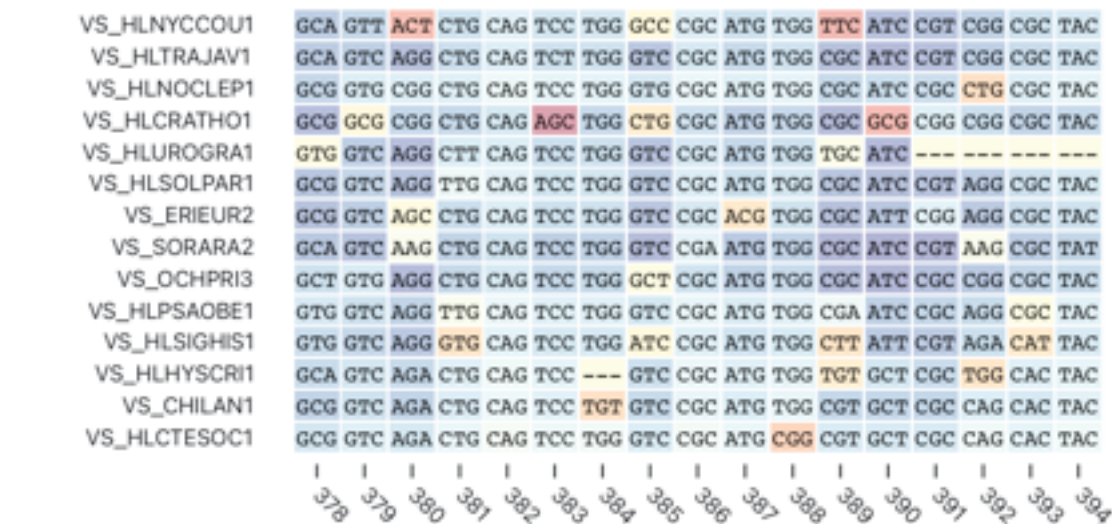
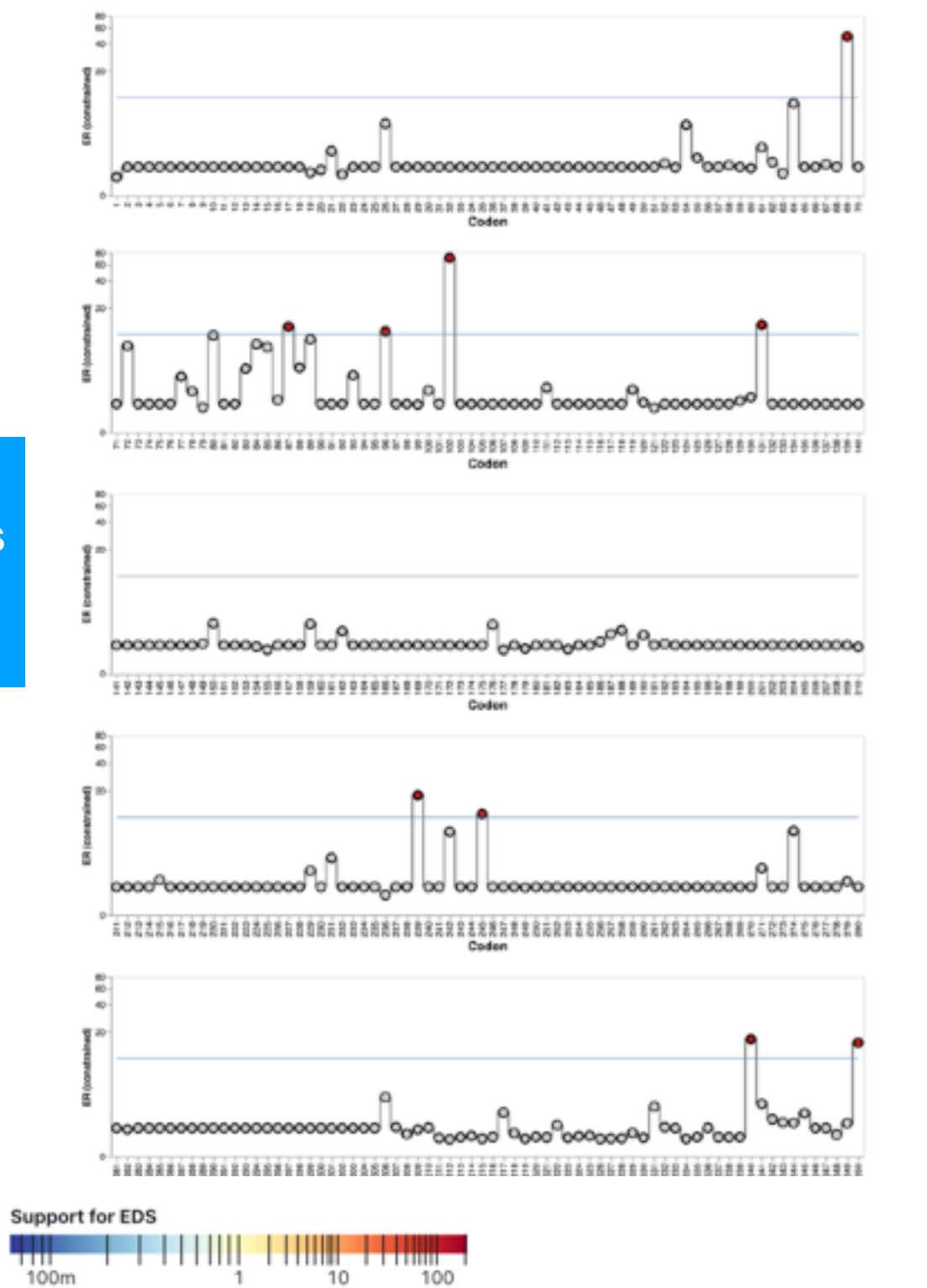
REAL

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



Standard BUSTED method results, $p \leq 0.001$ for both

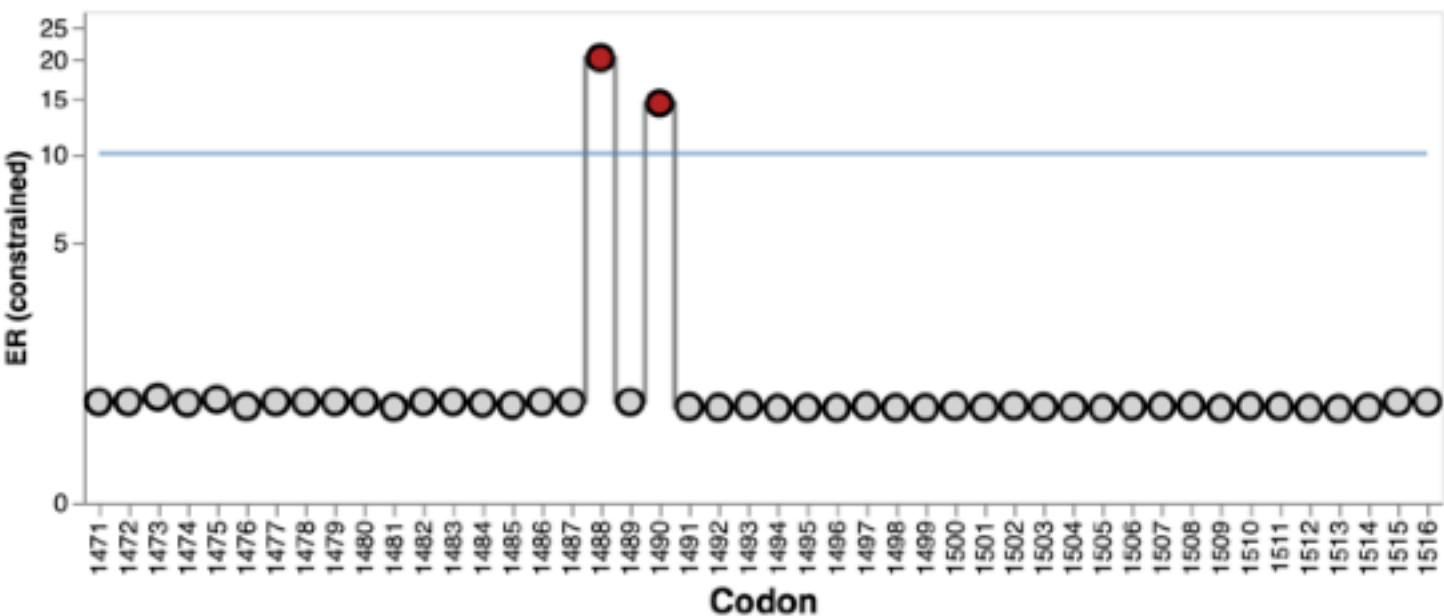
NOT REAL

KRT8

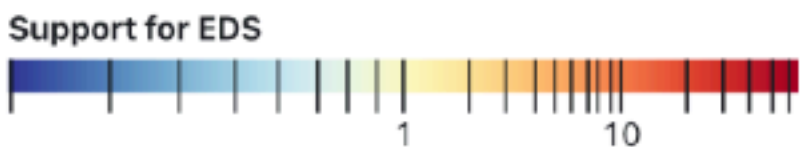
$\omega_1=0.02107$ (80.763%)
 $\omega_2=0.6961$ (18.533%)
 $\omega_3=136.3$ (0.70395%)

A large ω value with
narrow support

Evidence of
selection is
a localized
clump



Obvious alignment/
homology issues,
here in one sequence



VS_TUPBEL1	---/-	---/-	---/-	---/-	---/-	---/-	---/-	---/-	---/-	---/-	---/-	---/-	---/-	---/-	---/-	---/-	---/-	---/-	---/-
VS_OCHPRI3	---/-	---/-	AGC/S	TCC/S	TCC/S	AGC/S	---/-	---/-	TCC/S	CGA/R	---/-	---/-	GGC/G	AGC/S	AGC/S	AGC/S	AGC/S	AGC/S	AGC/S
VS_HLPERLONPAC1	---/-	---/-	AGC/S	TCC/S	TCA/S	AGC/S	---/-	---/-	TCT/S	AGG/R	GTG/V	GGC/G	AGT/S	GGC/G	AGC/S	AGC/S	AGC/S	AGC/S	AGC/S
VS_HLHYSCRI1	---/-	---/-	AGC/S	TCC/S	TCC/S	AGT/S	---/-	---/-	TCC/S	CGA/R	---/-	---/-	GGC/G	AGC/S	AGC/S	AGC/S	AGC/S	AGC/S	AGC/S
VS_HLCTESOC1	---/-	---/-	AGC/S	TCT/S	TCC/S	AGC/S	---/-	---/-	TCC/S	AGA/R	---/-	---/-	GGC/G	AGC/S	AGC/S	AGC/S	AGC/S	AGC/S	AGC/S
VS_HLTRAJAV1	---/-	---/-	AGC/S	TCC/S	TCG/S	ACC/T	---/-	---/-	ACC/T	CGA/R	---/-	---/-	GGC/G	AGC/S	GGC/G	AGC/S	AGC/S	AGC/S	AGC/S
VS_HLCRATHO1	---/-	---/-	AGC/S	TCC/S	TCG/S	TCC/S	---/-	---/-	TCC/S	CGG/R	---/-	---/-	GGC/G	AGC/S	AGC/S	AGC/S	AGC/S	AGC/S	AGC/S
VS_HLUROGRA1	---/-	AAC/N	CGC/R	ATC/I	AGC/S	TCC/S	---/-	TCG/S	TCC/S	TTC/F	---/-	GGC/G	CGA/R	GTG/V	GGA/G	AGC/S	AGC/S	AGC/S	AGC/S
VS_HLSOLPAR1	---/-	---/-	AGC/S	TCC/S	TCC/S	TCC/S	---/-	---/-	TCC/S	CGG/R	---/-	---/-	GGC/G	AGC/S	AGC/S	AGC/S	AGC/S	AGC/S	AGC/S
VS_ERIEUR2	---/-	---/-	AGC/S	CCC/P	TCC/S	GCC/A	---/-	---/-	TCC/S	CGG/R	---/-	---/-	GGC/G	AGC/S	AGC/S	AGC/S	AGC/S	AGC/S	AGC/S
VS_SORARA2	---/-	---/-	AGC/S	TCC/S	TCC/S	ACC/T	---/-	---/-	ACC/T	CGG/R	---/-	---/-	GGC/G	AGC/S	ACC/T	AGC/S	AGC/S	AGC/S	AGC/S

- The simple fix here is to include an **explicit error component** in the model
- We simply allow a small fraction of the alignment (e.g. $\leq 1\%$) to evolve with abiologically high rates (e.g. $dN/dS \geq 100$)
- This is in addition to the standard model which allows negative,

neutral, and positive selection regimes.

- The primary goal of this analysis is to classify the selective regime on a gene (in the presence of specific types of errors)
- So error detection (and filtering) is a byproduct of an already useful analysis