

A

Site in HA

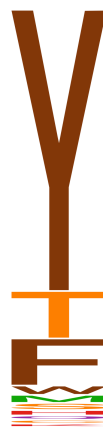
90



51



23



490



81

Implied dN/dS (ω_r)

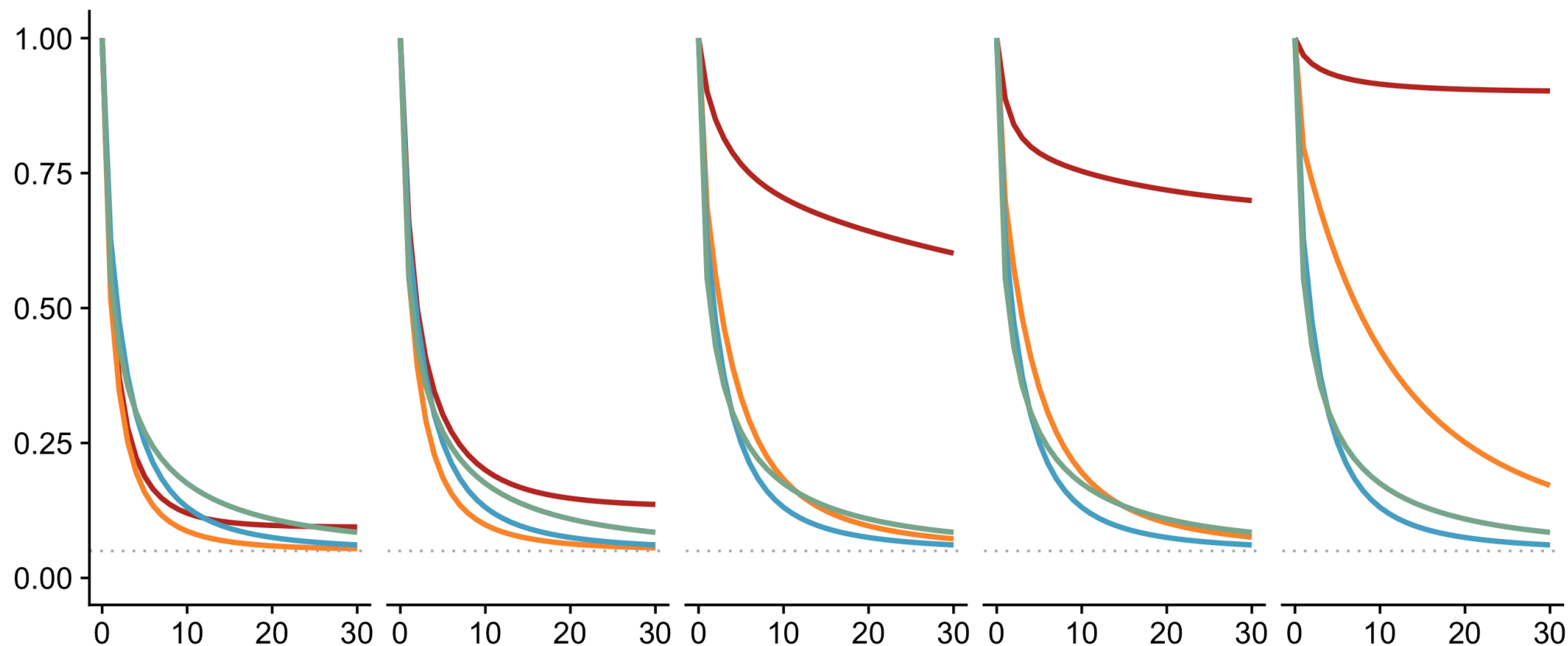
0.80

0.61

0.27

0.18

0.06

Expected pairwise amino-acid
identity at a site

Branch length (codon substitutions per site)

Model ■ ExpCM ■ GY94 ■ GY94 + $\Gamma\omega$ ■ GY94 + implied dN/dS (ω_r)

B

Time to identity

95% 75% 50%

0.00	0.50	1.75	ExpCM
0.00	0.25	1.75	GY94
0.00	0.25	1.25	GY94 + $\Gamma\omega$
0.00	0.00	1.25	GY94 + ω_r
0.25	5.75	74.75	ExpCM
0.00	0.25	1.75	GY94
0.00	0.00	2.50	GY94 + $\Gamma\omega$
0.00	0.50	1.25	GY94 + ω_r
0.25	10.5	∞	ExpCM
0.00	0.25	1.75	GY94
0.00	0.00	2.50	GY94 + $\Gamma\omega$
0.00	0.50	2.74	GY94 + ω_r

Site 51

Site 23

Site 490