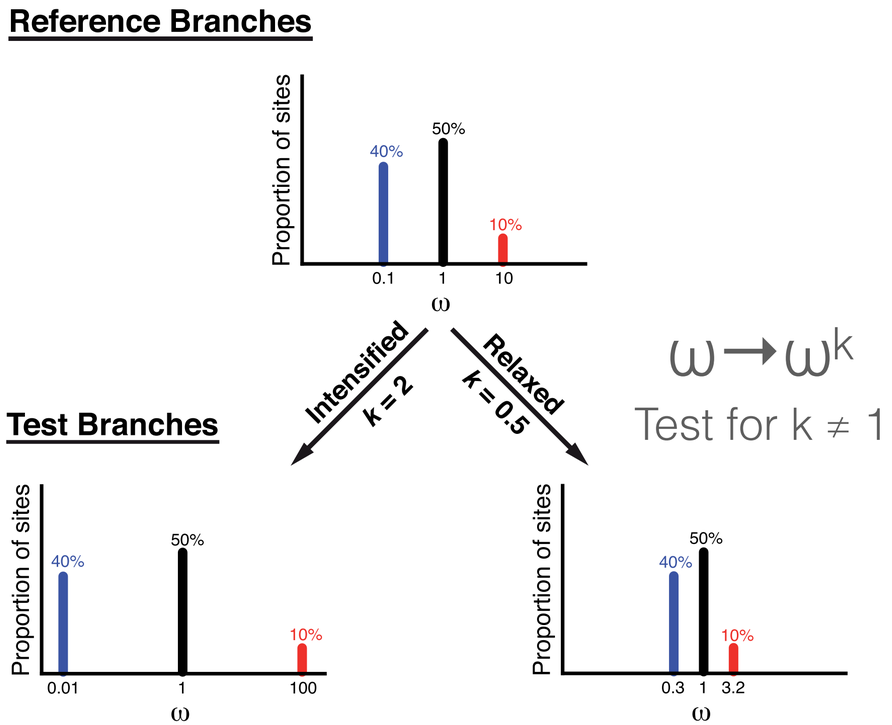

Table 1. Test for Relaxed Selection Using RELAX in Various Taxonomic Groups.

Taxa	Gene/Genes	Test Branches	Reference Branches	k[a]	*P*-Value
γ-proteobacteria	Single-copy orthologs	Primary/secondary endosymbionts	Free-living γ-proteobacteria	0.30	< 0.0001
		Primary endosymbionts	Free-living γ-proteobacteria	0.28	< 0.0001
		Secondary endosymbionts	Free-living γ-proteobacteria	0.61	< 0.0001
		Primary endosymbionts	Secondary endosymbionts	0.56	< 0.0001
Bats	*SWS1*	HDC echolocating and cave roosting (pseudogenes)	LDC echolocating and tree roosting (functional genes)	0.16	< 0.0001
		LDC echolocating	Tree roosting	1.07	0.577
	M/LWS1	HDC echolocating and cave roosting	LDC echolocating and tree roosting	0.70	0.495
		Echolocating species	Tree- and cave-roosting species	0.21	0.0005
		HDC echolocating	LDC echolocating	0.84	0.427
Bornavirus	Nucleoprotein	Endogenous viral elements	Exogenous virus	0.02	< 0.0001
Daphnia pulex	Mitochondrial protein-coding genes	Asexual	Sexual	0.63	< 0.0001

[a]Estimated selection intensity.

Comparing alpha vs delta clades in SARS-CoV-2

- Are selective pressures on the Delta SARS-CoV-2 clade relaxed or intensified compared to the Alpha clade?
- Partition the tree into corresponding clades.
- See http://www.hyphy.org/tutorials/CL-prompt-tutorial/#preparing-labeled-phylogenies for how to label phylogenies