Multi-Hit results summary

INPUT DATA

spike.fas

118 sequences

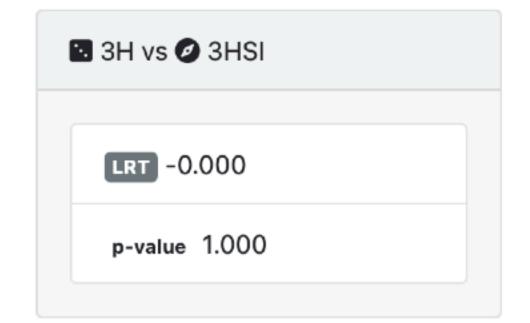
1273 sites

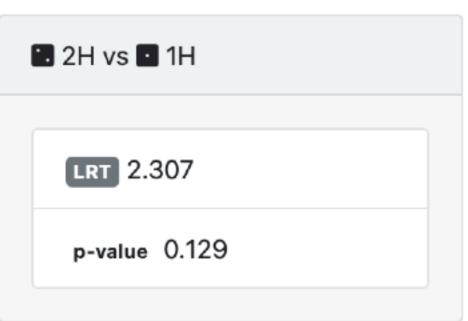


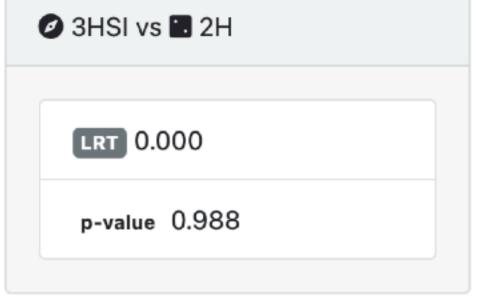
Likelihood Test Results











See here for more information about this method.

Please cite biorxv if you use this result in a publication, presentation, or other scientific work.

hyphy fmm --alignment spike fas --tree spike tree --triple-islands Yes

WNV NS3

results summary

INPUT DATA

WestNileVirus_NS3.fas | 19 sequences

619 sites

≛ Export ▼

Likelihood Test Results



3H vs. 🗀 2H

■ 2H vs ■ 1H

LRT 7.400

p-value 0.007

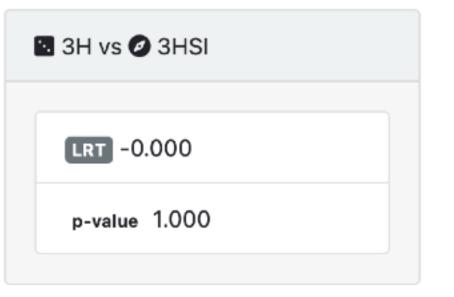
3HSI vs 3 2H

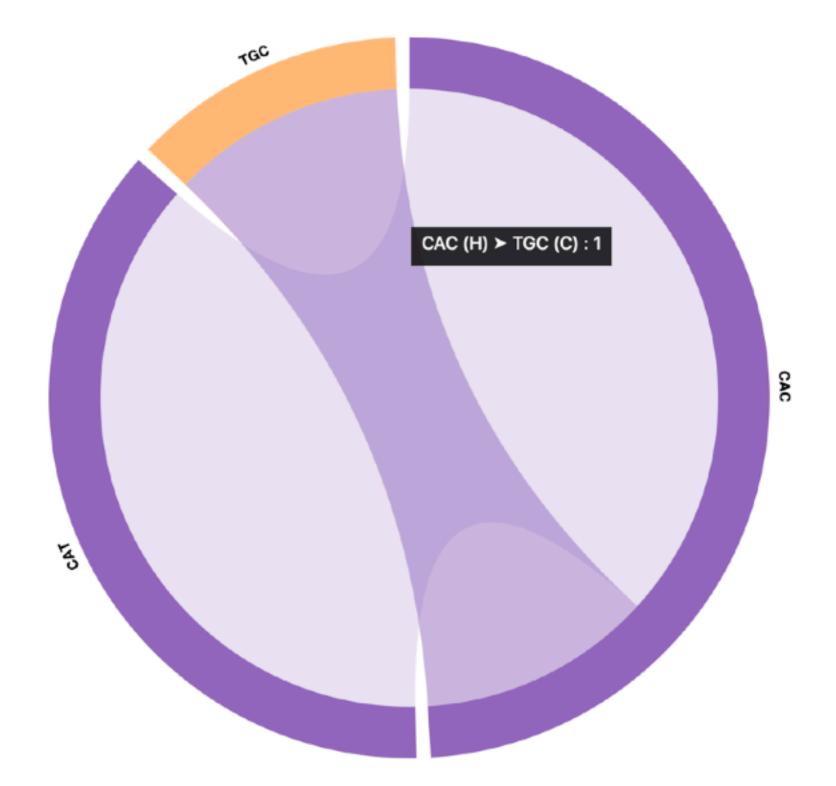
LRT 0.006

LRT 0.006

p-value 0.997

p-value 0.936





See here for more information about this method.

Please cite biorxv if you use this result in a publication, presentation, or other scientific work.

1 individual site which showed sufficiently strong preference for multiple-hit models

Site	ER (2 vs 1)	ER (3 vs 2)	ER (3-island vs 2)	ER (3-island vs 3)	Substitutions
::	::	::	::	::	::
87	54.0092	1.0065	1.0020	1.0045	CAC->CAT(3)TGC(1)