Allowing multi-nucleotide substitutions

- Some of the methods (e.g. BUSTED, aBSREL, RELAX) can extend substitution models to allow instantaneous double- and triple-"hits" (e.g. ACC to AGG)

- Sometimes multi-nucleotide changes along short branches at a single site can drive selection signal (possible false positives?)

- HyPhy includes a simple standard analysis for estimating alignment-wide multiple-hit rates.

Extra base hits: Widespread empirical support for instantaneous multiple-nucleotide changes

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See the preprint

Multi-Hit
results summary

INPUT DATA | **spike.fas** | **118** sequences | **1273** sites

⬇ Export ▾

Likelihood Test Results

▨ 3H vs ▪ 1H

LRT	2.307

p-value	0.511

▨ 3H vs. ▨ 2H

LRT	0.000

p-value	1.000

▨ 3H vs 🧭 3HSI

LRT	-0.000

p-value	1.000

▨ 2H vs ▪ 1H

LRT	2.307

p-value	0.129

🧭 3HSI vs ▨ 2H

LRT	0.000

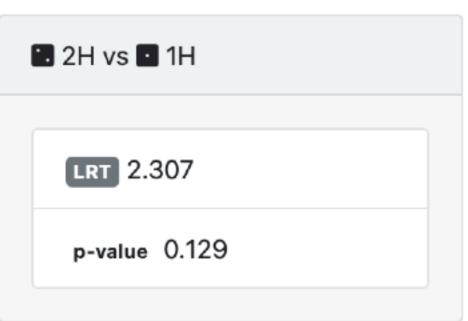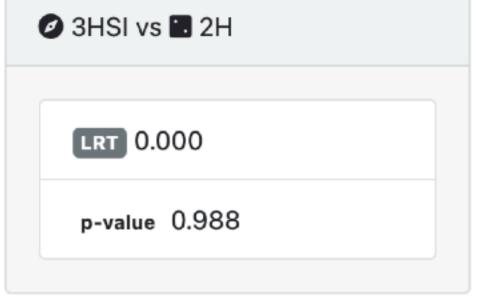| p-value	0.988

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
```