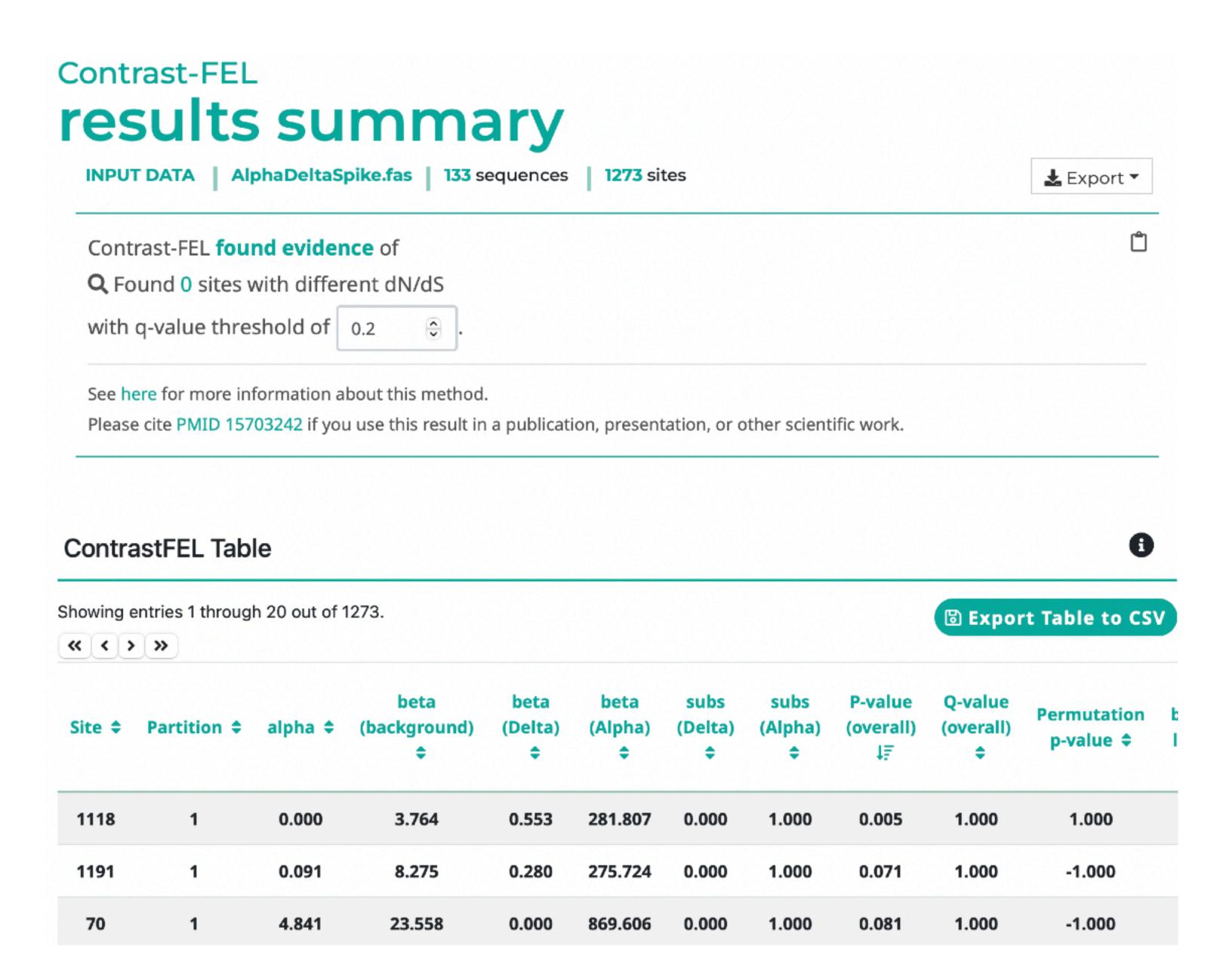# Which sites are evolving differentially?

- We have established that in the HIV example, donor, recipient, and transmission branches evolve differently.

- Can we identify specific sites where this may be occurring?

    - Why is this of interest?

- More generally, given a tree with N sets of branches, we fish to find sites where evolution is different between these N sets, with a degree of statistical significance.

- Solution: use a fixed effects method (Contrast-FEL)

    - For each branch set **i**, estimate a dN/dS ration (**N** total ratios)

    - Test whether or not any of the ratios are different (group test)

    - For each pair of ratios, test if they are different [up to N (N-1) / 2 tests]

- Can identify subtle differences among selective pressures.

Contrast-FEL
results summary

INPUT DATA | **AlphaDeltaSpike.fas** | **133** sequences | **1273** sites

⬇ Export ▾

Contrast-FEL **found evidence** of

🔍 Found **0** sites with different dN/dS

with q-value threshold of [0.2 ⇅] .

See here for more information about this method.
Please cite PMID 15703242 if you use this result in a publication, presentation, or other scientific work.

ContrastFEL Table ⓘ

Showing entries 1 through 20 out of 1273.

🔲 **Export Table to CSV**

« ‹ › »

Site ⇅	Partition ⇅	alpha ⇅	beta (background) ⇅	beta (Delta) ⇅	beta (Alpha) ⇅	subs (Delta) ⇅	subs (Alpha) ⇅	P-value (overall) ⬇	Q-value (overall) ⇅	Permutation p-value ⇅	
1118	1	0.000	3.764	0.553	281.807	0.000	1.000	0.005	1.000	1.000	
1191	1	0.091	8.275	0.280	275.724	0.000	1.000	0.071	1.000	-1.000	
70	1	4.841	23.558	0.000	869.606	0.000	1.000	0.081	1.000	-1.000	

`hyphy contrast-fel --alignment data/AlphaDeltaSpike.fas --tree data/AlphaDeltaSpike.tree --branch-set Alpha --branch-set Delta`