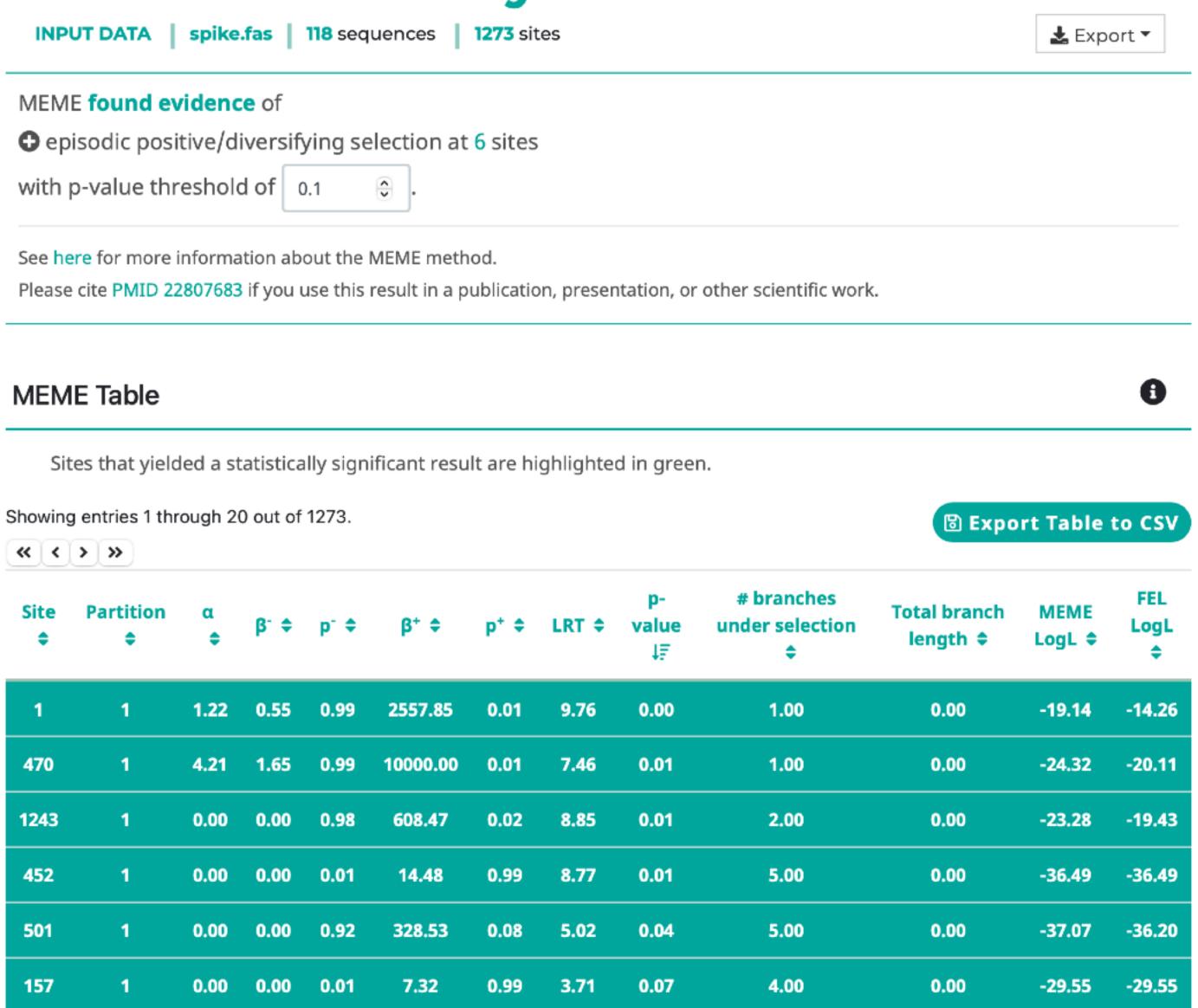
Mixed Effects Model of Evolution results summary



hyphy meme --alignment spike.fas --tree spike.tree

Interpreting dN/dS for intra-host and intra-species pathogen

- dN/dS can be estimated for all sorts of sequence data (e.g., it has been done for cancer SNP data)
- Traditional interpretation of dN/dS is based on the assumption that substitution ~ fixation
- Not the same for intra-species / intra-host pathogens

- Much of variation is due to polymorphism, or even dead-end mutations
- This is because selection has not had a chance to "filter" mutations (except for patently deleterious ones)
- This often manifests as differences in selective "regimes" between tips and internal branches