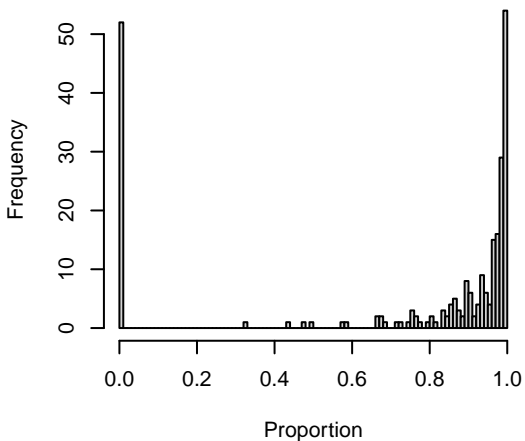
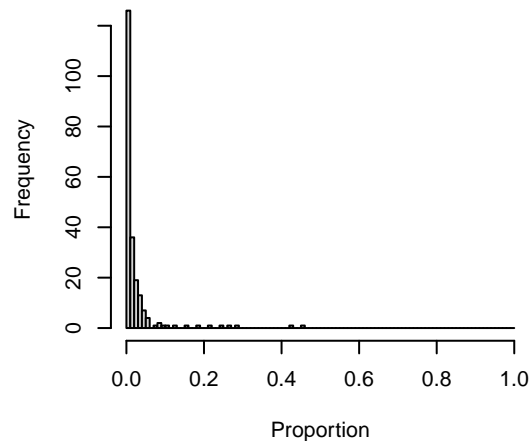


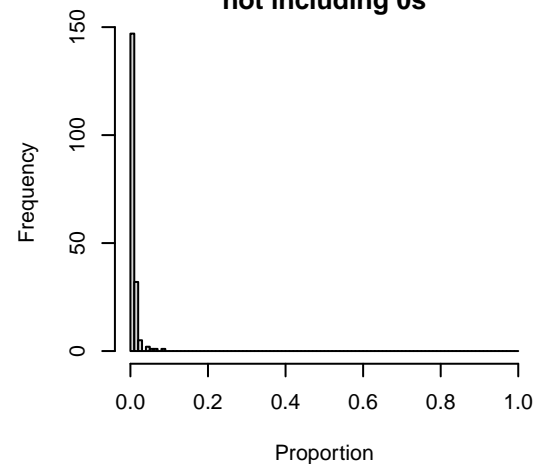
**Proportion of resamples agreeing
with consensus sequence,
not including 0s**



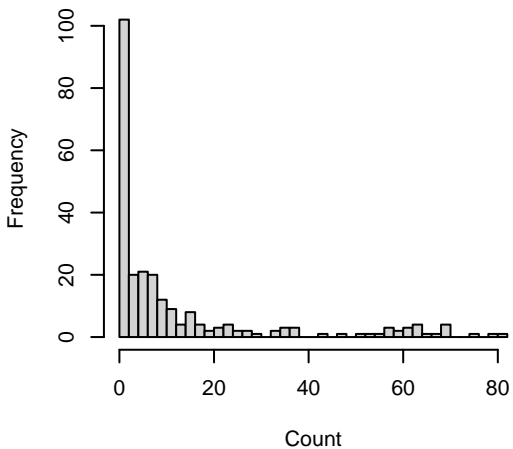
**Proportion of resamples agreeing
with second most common lineage
not including 0s**



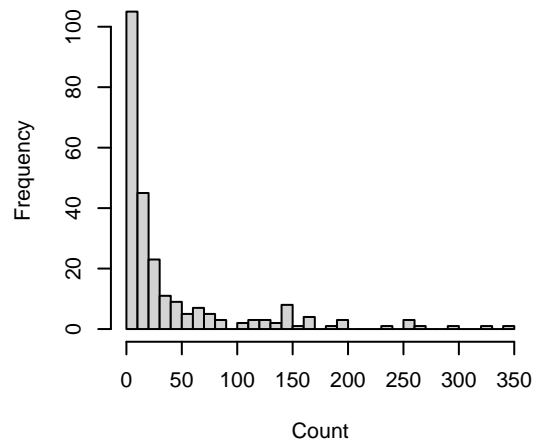
**Proportion of resamples agreeing
with third most common lineage
not including 0s**



Number of atoms



Number of unique lineages



**Ratio of most common versus
second most common lineage**

