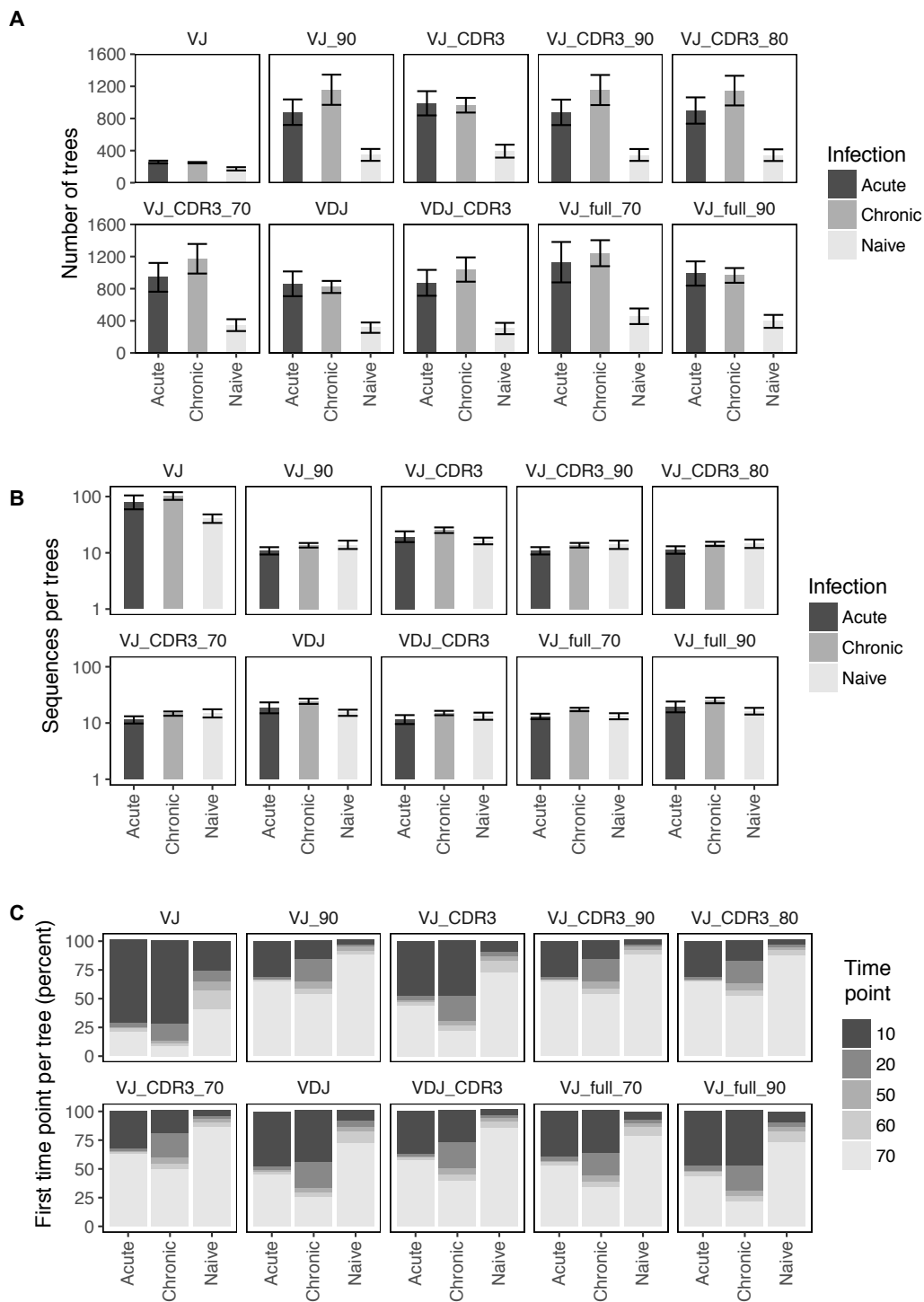


Supplementary material for “The influence of the phylogenetic inference pipeline on murine antibody repertoires sequencing data following viral infection”, Yermanos et al.



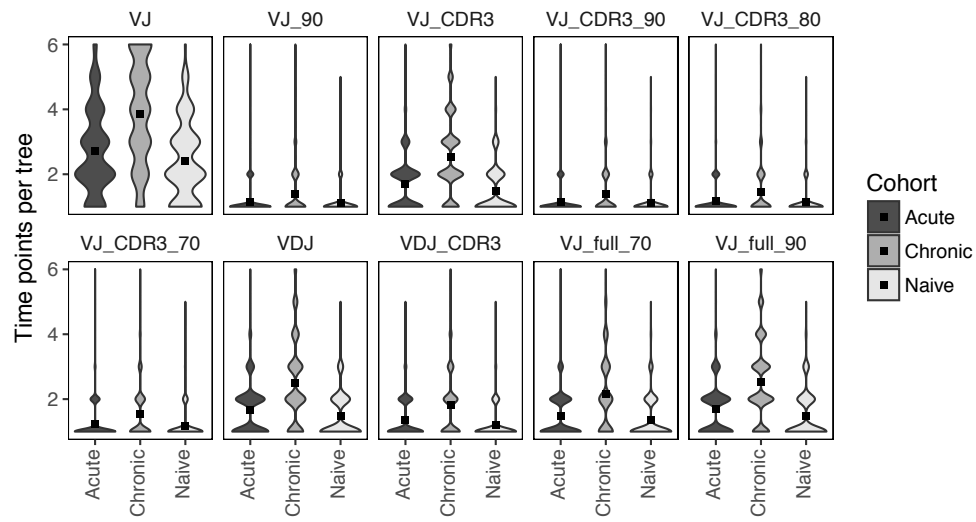


Figure S2. Distribution of time points found within each clonal lineage. For each rooting strategy, all clonal lineages from a given cohort were grouped and the number of distinct time points for each tree was calculated. Box indicates the average number of time points sampled across all clonal lineages of the indicated cohort.

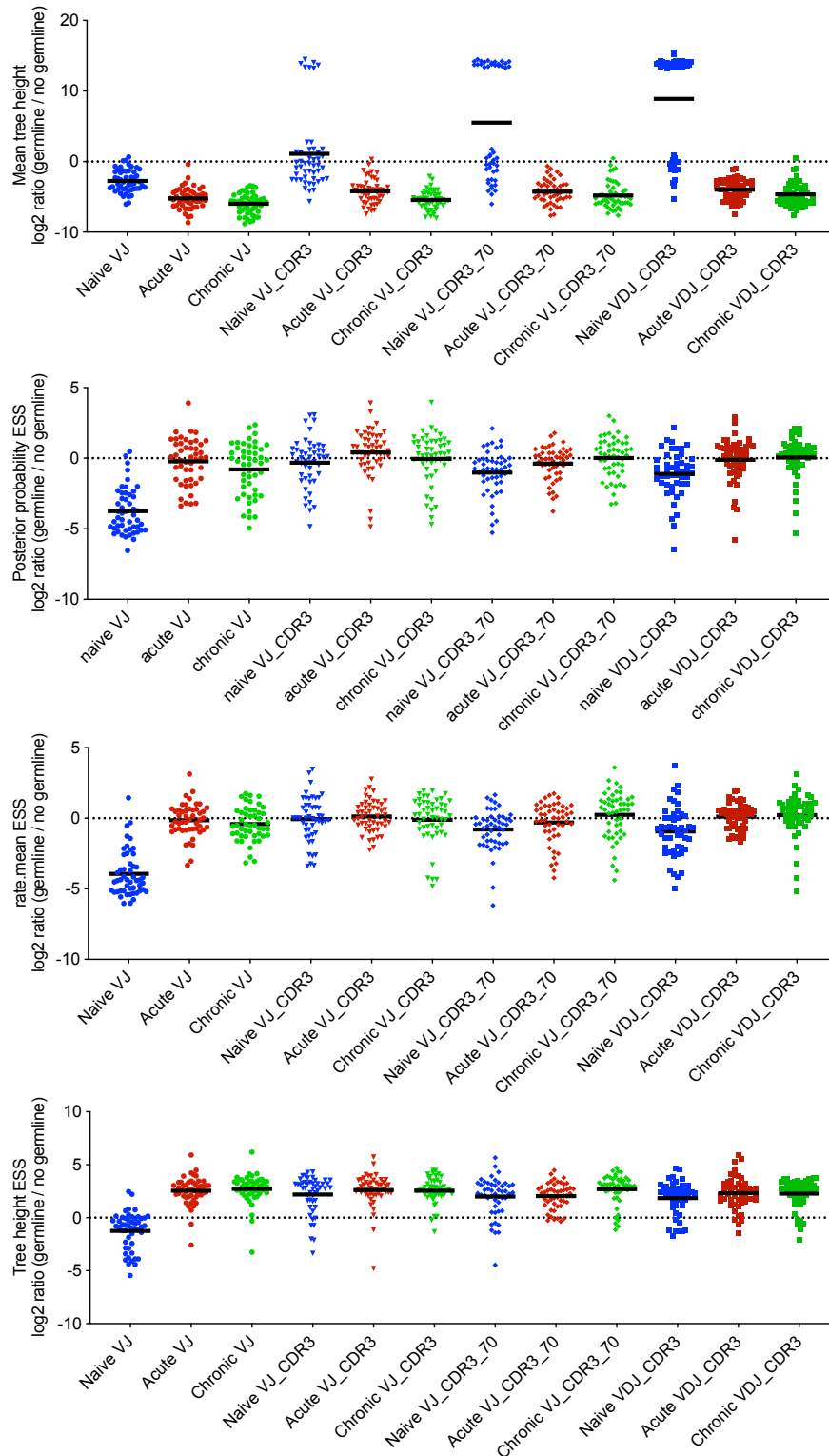


Figure S3. Inclusion of reference germline segments impacts on tree height and effective size sampling (ESS) values after phylogenetic inference with BEAST. The log₂ ratios of various output parameters from BEAST were compared for clonal lineages containing identical sequences either with or without the inclusion of the reference germline.

