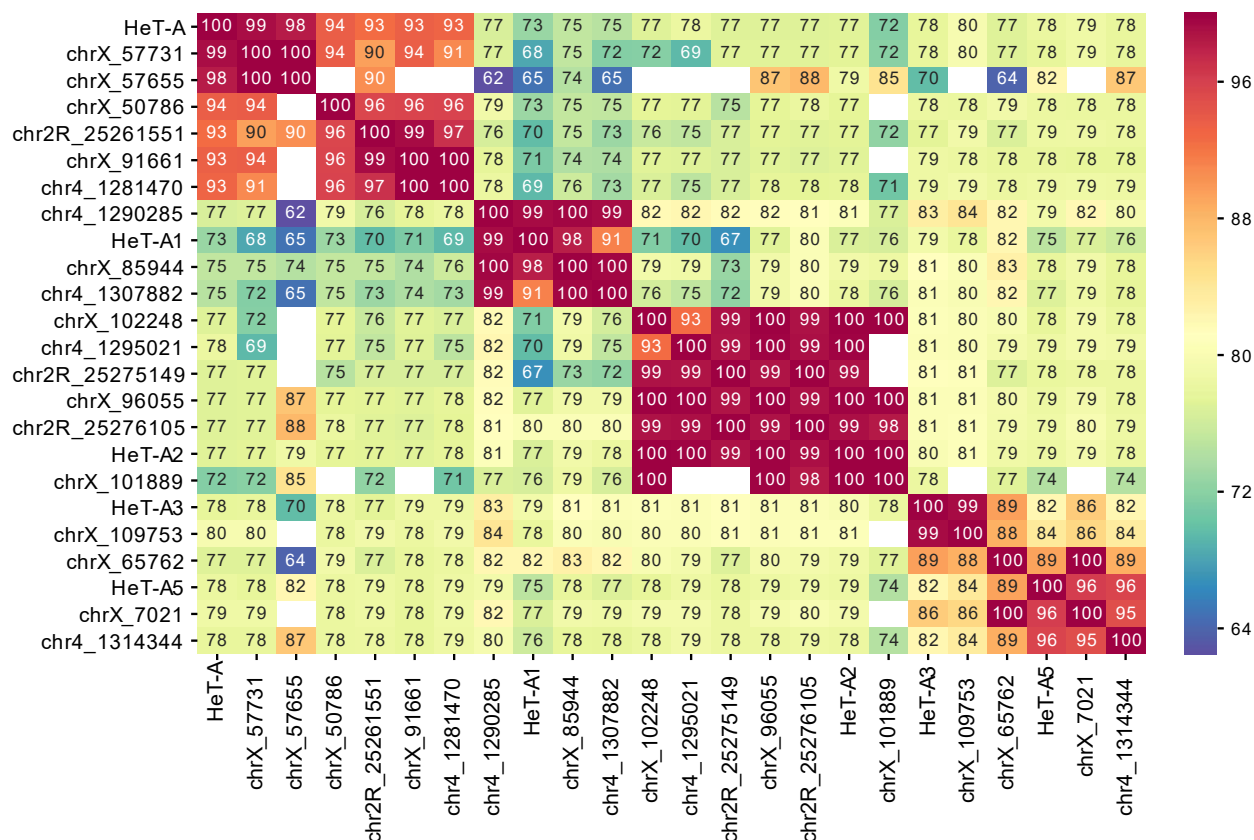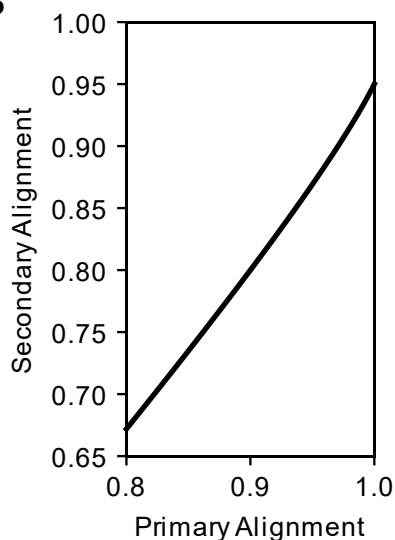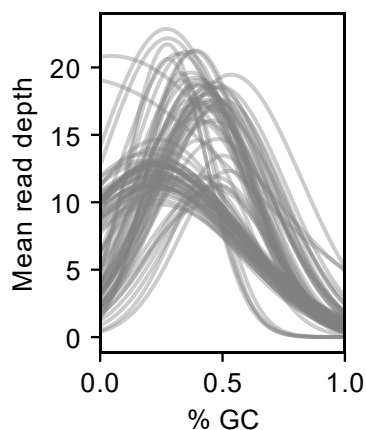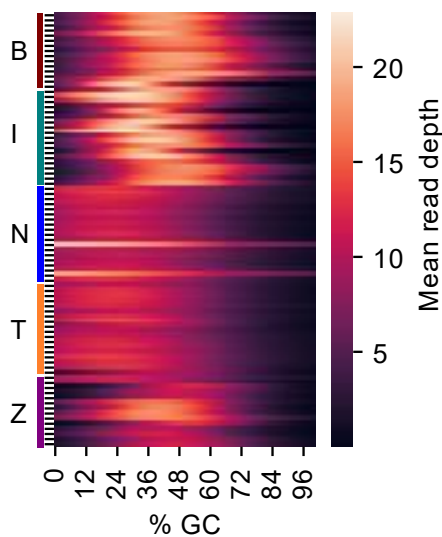A

B

C

D

Figure S3. Details on interpreting alignments to telomeric transposable elements (A) Percent identities of all >300 bp insertions annotated as *HeT-A* in the UCSC genome browser repeat-masker track of the Release 6 reference-genome telomeres. Percent identities are based on a ClustalOmega multiple sequence alignment with default parameters. The Repbase consensus sequence and the representatives we chose for each *HeT-A* subfamily in our repeat index are indicated as such. The white cells indicate no alignment between a pair of sequences, all involving alignments with the two shortest *HeT-A* fragments. (B) A depiction of how we define ambiguous alignments. The black line indicates how diverged the second best alignment must be for a primary alignment with a given percent identity to be considered unambiguous. (C) The expected relationship between read depth and %GC for each of the GDL strains. The variability of this relationship across strains is what necessitated controlling for %GC when estimating copy number. (D) A heatmap of the expected relationship between read depth and %GC, sorted by population.