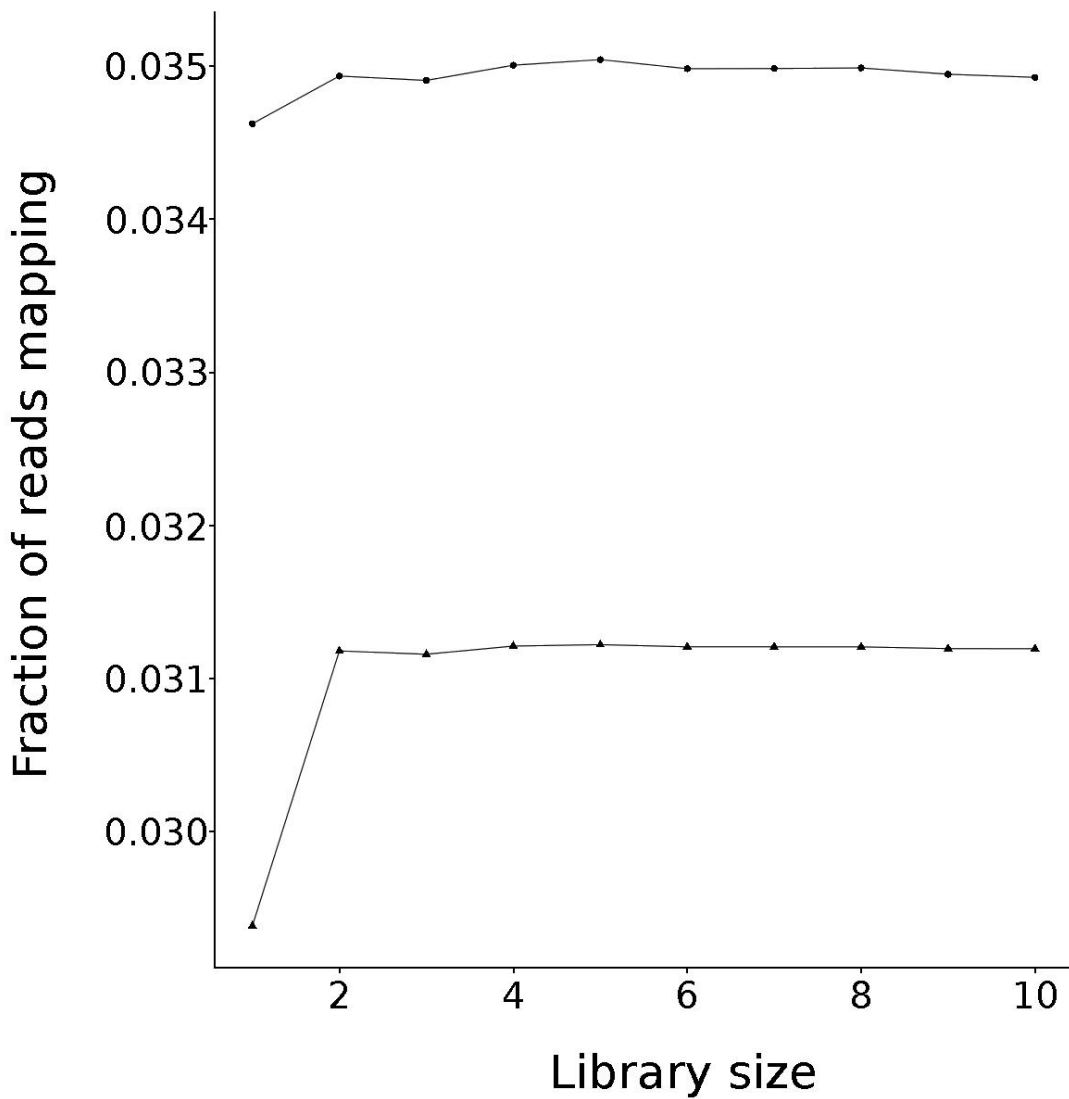


Additional file 3.



Effect of the number of sequences in the reference library on the number of reads mapped. Reference libraries were created with between one and 10 sequences per major allelic type (3 to 30 sequences total). Dummy reads created from 964 long read sequences and were aligned to the sequence libraries using BWA-MEM. The fraction of all reads that were mapped to the reference library is shown for read lengths of 100 bp (circles) and 75 bp (triangles).