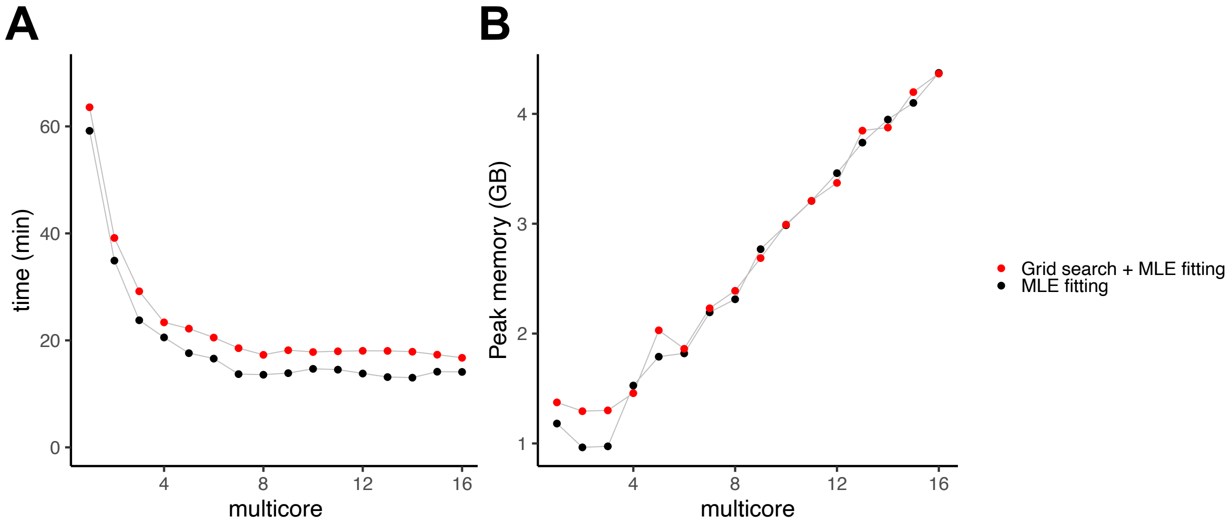

Supplemental Figure S7. Computational performance of TrioMix. Performance was demonstrated in two examples. When the sequence from NA19662 (offspring) is used, MLE optimization initially fails to converge, which then uses additional grid search methods to re-estimate the initial guesses for likelihood optimization (red circle). When the offspring's sequences were in silico contaminated with its sibling (NA19685) with 25%, optimization converges with initial guesses (black circle). (A) The total runtime of TrioMix is shown with a varying number of cores. Compute time is slightly increased for samples that do not converge initially (red circle). (B) Peak memory consumptions of TrioMix are shown with a varying number of cores. Performance evaluation was conducted on an AWS instance with a dockerized TrioMix on Ubuntu 20.04 LTS operating system with Intel(R) Xeon(R) CPU E5-2666 v3 @ 2.90GHz (max 16 CPU) processor. In this case, 1,907,413 common SNPs identified from gnomAD v3.0 for GRCh38 were used.