Supplemental Materials

Estimating the size of long tandem repeat expansions from short reads with ScatTR

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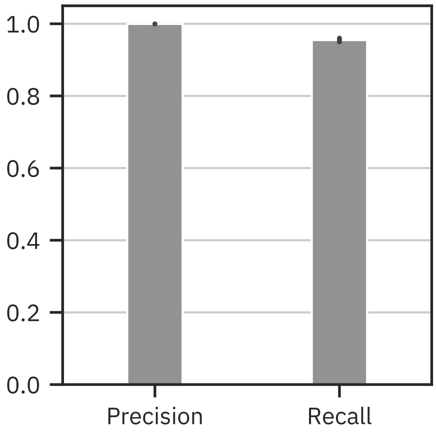
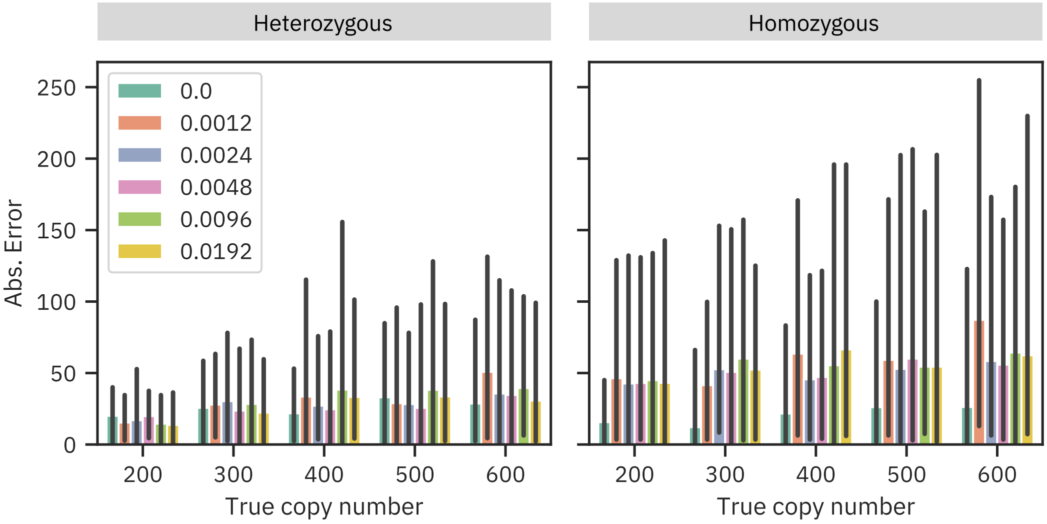
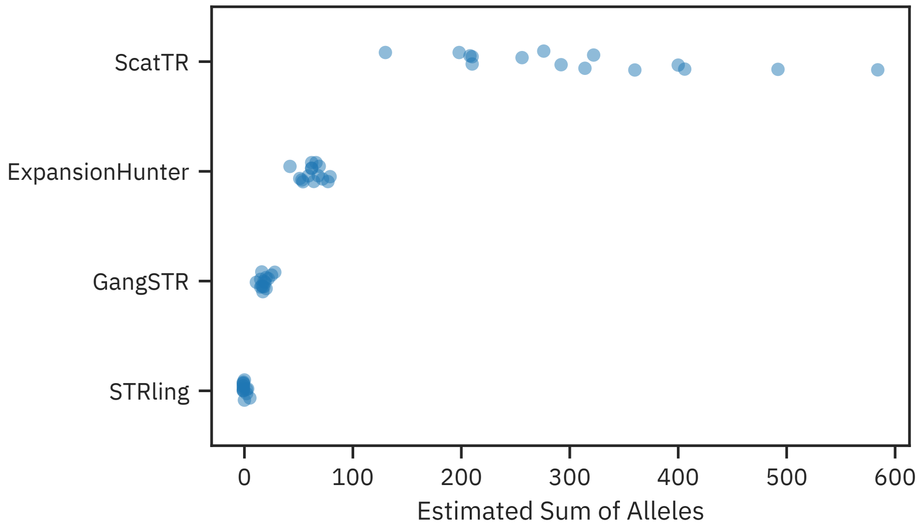


Supplemental Figure S1. Precision and recall of IRR extraction from 540 simulated WGS samples.



Supplemental Figure S2. Absolute error of ScatTR across varying sequencing error rates in simulated WGS samples. Error bars represent 95% confidence intervals across 30 TR loci.



Supplemental Figure S3. Comparison of the estimated sum of alleles for the *C9orf72* repeat expansion by ScatTR, ExpansionHunter, GangSTR, and STRling. The analysis was performed on short-read WGS data from 15 ALS patients with confirmed expansions.