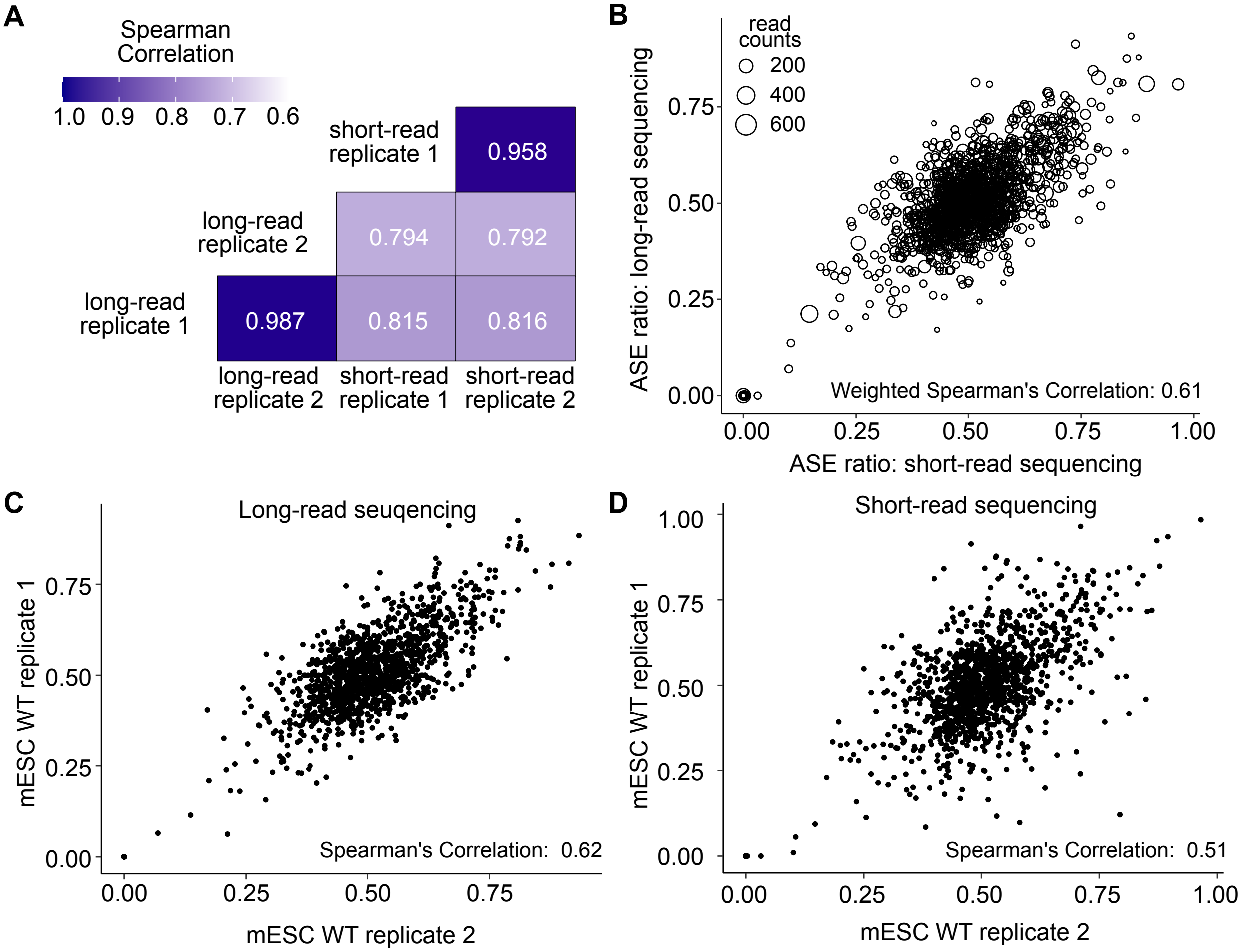

Supplemental Figure. 2 | ASE ratio correlation between long-read and short-read sequencing.

A Per transcript RNA expression was calculated by counts per million normalization and compared. B) Transcript-level Allele-Specific Expression (ASE) ratios were calculated and plotted using CAST allele ratio (CAST read counts) / (CAST read counts + B6 read counts). The correlation between estimated ASE ratio was calculated between long-read and short-read sequencing using the mean of the replicates weighted by read counts from long-read sequencing (depicted with the size of the circles). The correlation between replicates from each method exhibited similar correlation levels (C, D).