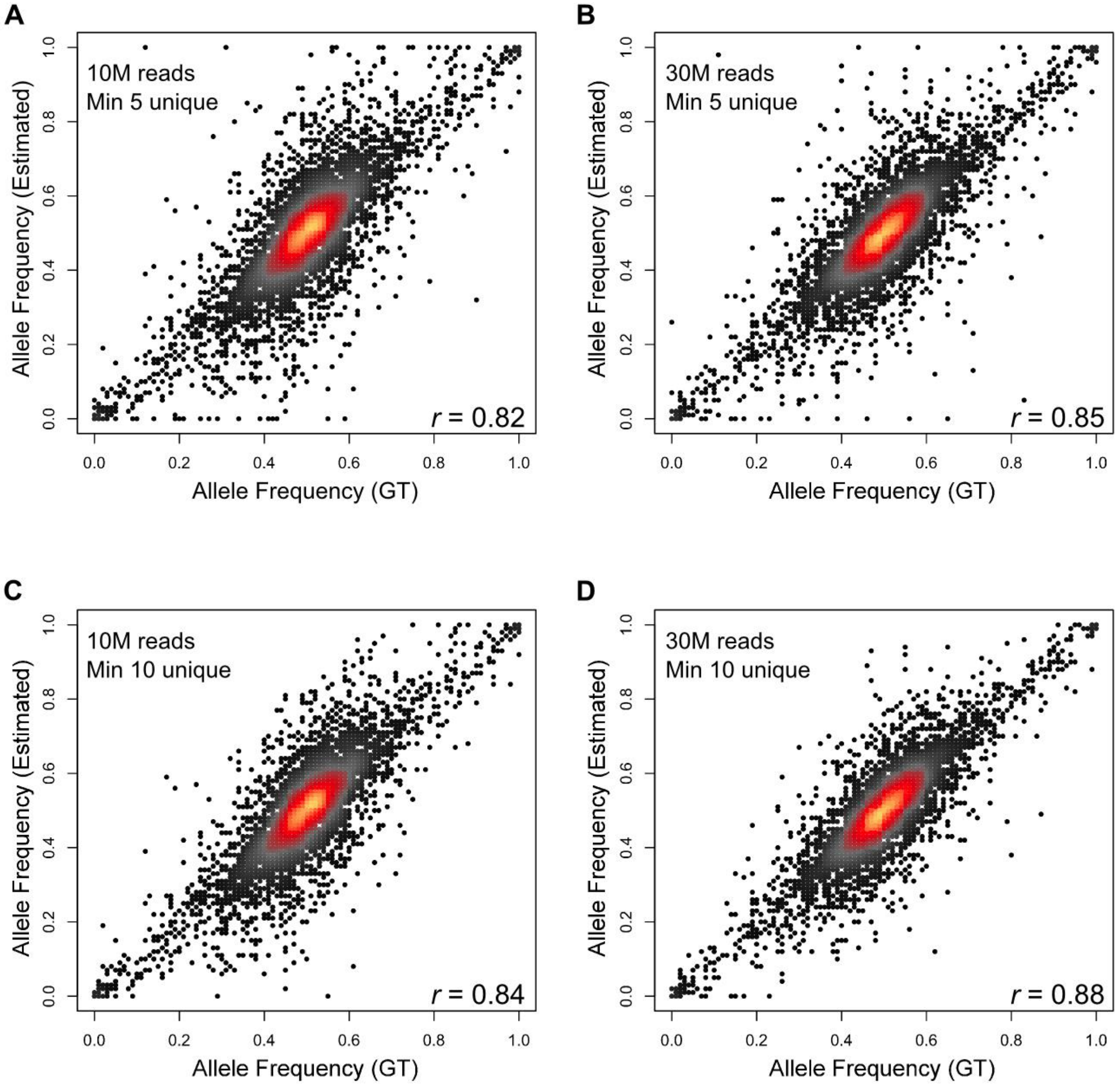

Figure S1 Characterization of sequencing depth and unique read threshold on estimation of allele-specific expression. Estimated allele frequency (y-axis) is plotted in panels A-D against the ground truth allele frequency (x-axis) for robustly expressed genes (sum of allele counts ≥ 100) in the simulated DO dataset. Allele frequency estimates are improved by increasing the read depth from 10 million (panels A and C) to 30 million reads (panels B and D) and by increasing the gene inclusion stringency to require ten (panels C and D) rather than five (panels A and B) reads with unique allele alignments.