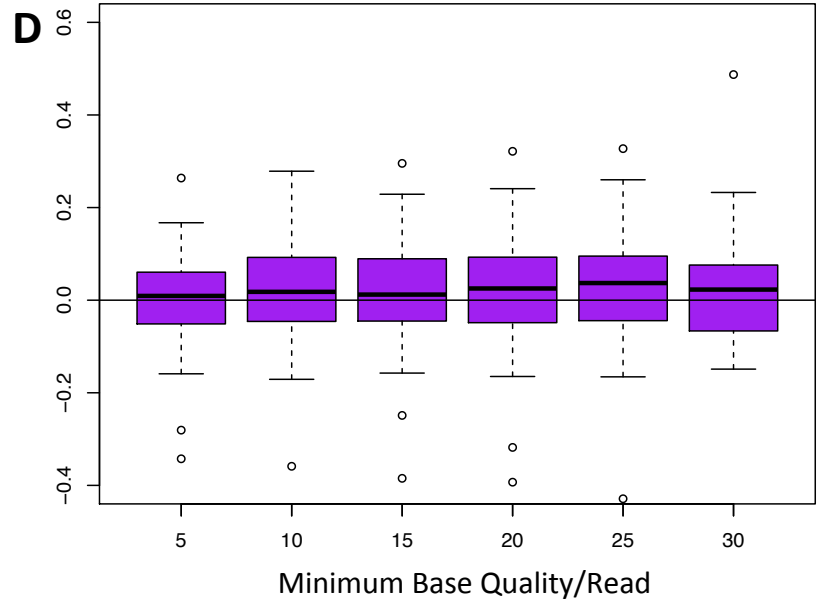
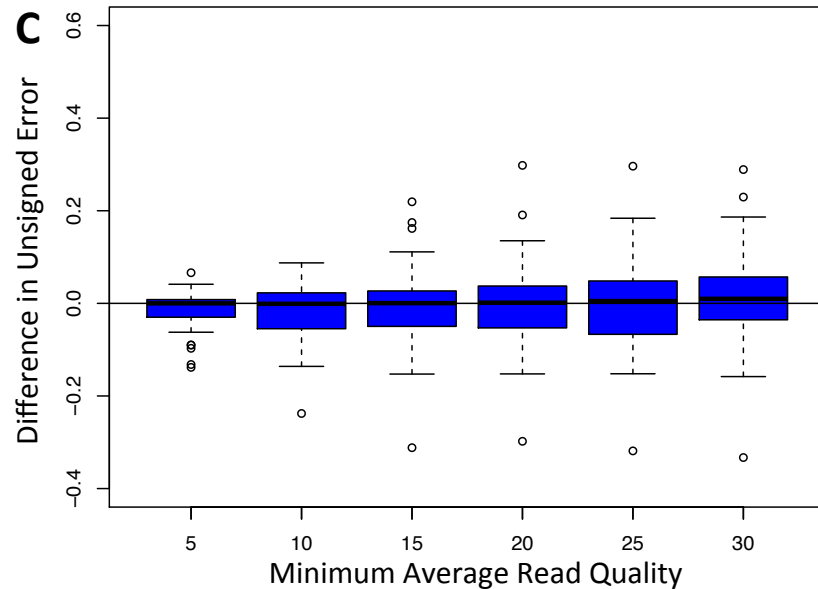
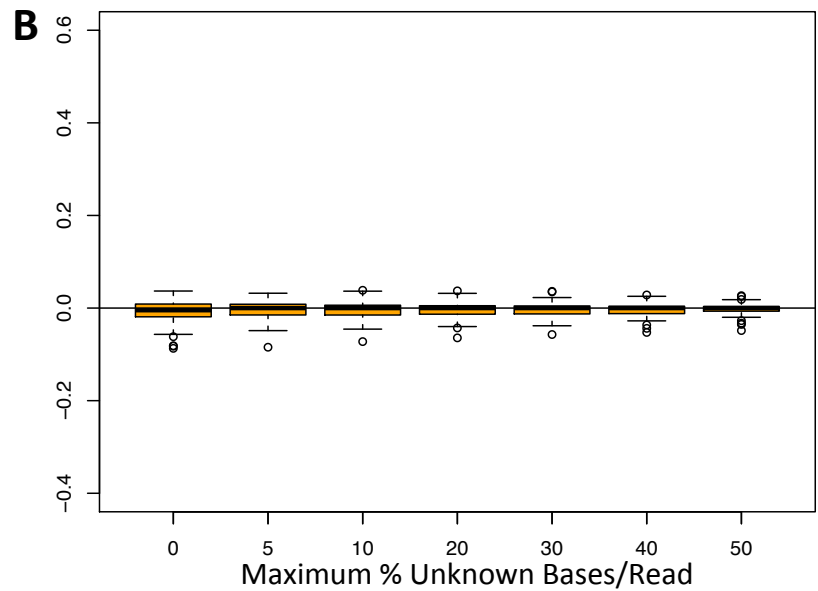
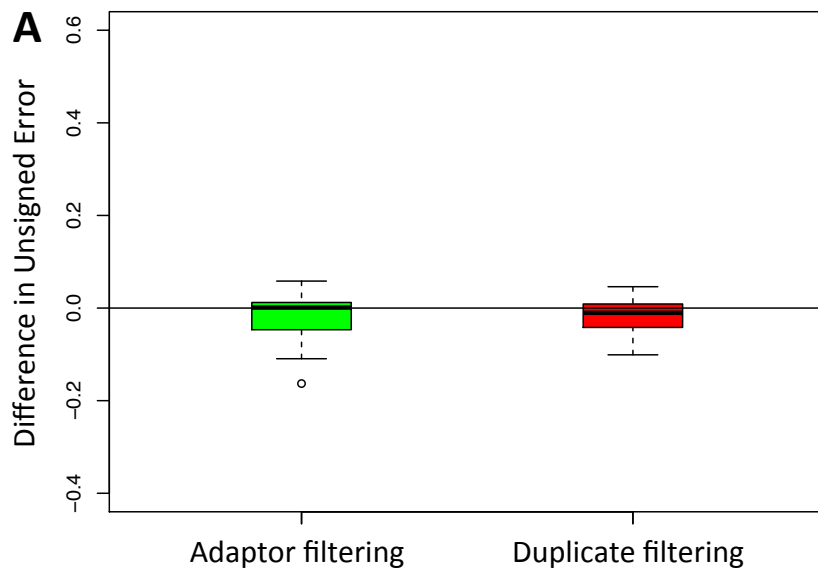




Effect of quality control filters on accurate estimation of AGS. We used MicrobeCensus to estimate genome size for 42 short-read Illumina genome projects using various quality control filters. Plotted are the differences in error with and without using the quality filter. **(a-b)** There is a consistent, but small reduction in error when removing adaptor contamination, filtering duplicate reads, and filtering reads that contain unknown base calls. **(c)** There is a small reduction in error when filtering the lowest quality reads (minimum average quality < 5). **(d)** When filtering reads by their minimum quality score, there is an overall increase in prediction error.