Systematic dissection of biases in whole-exome and whole-genome sequencing reveals major determinants of coding sequence coverage

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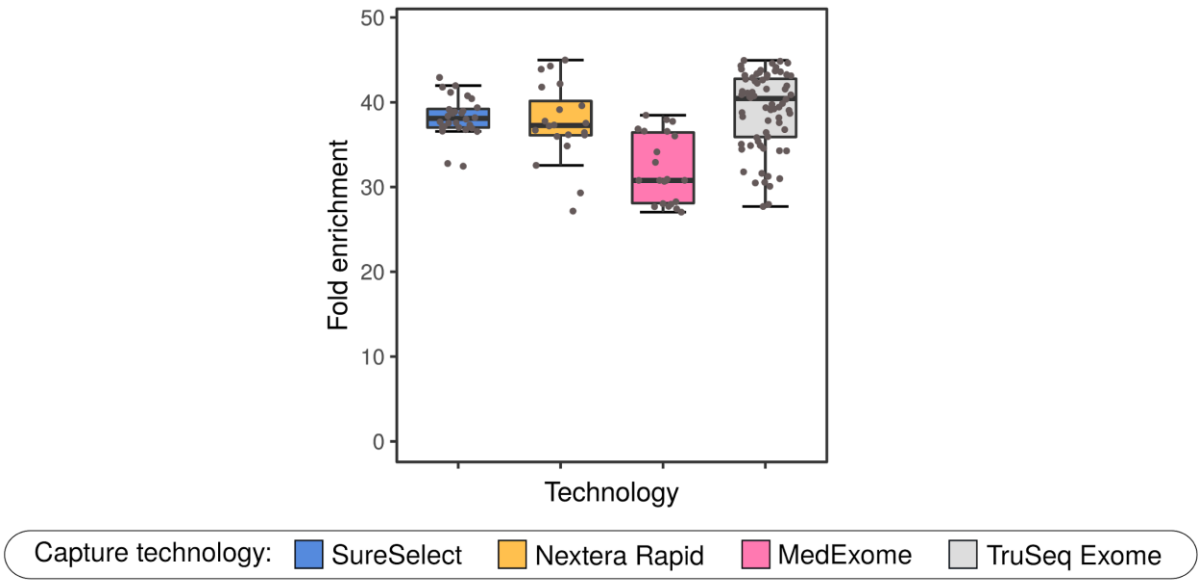
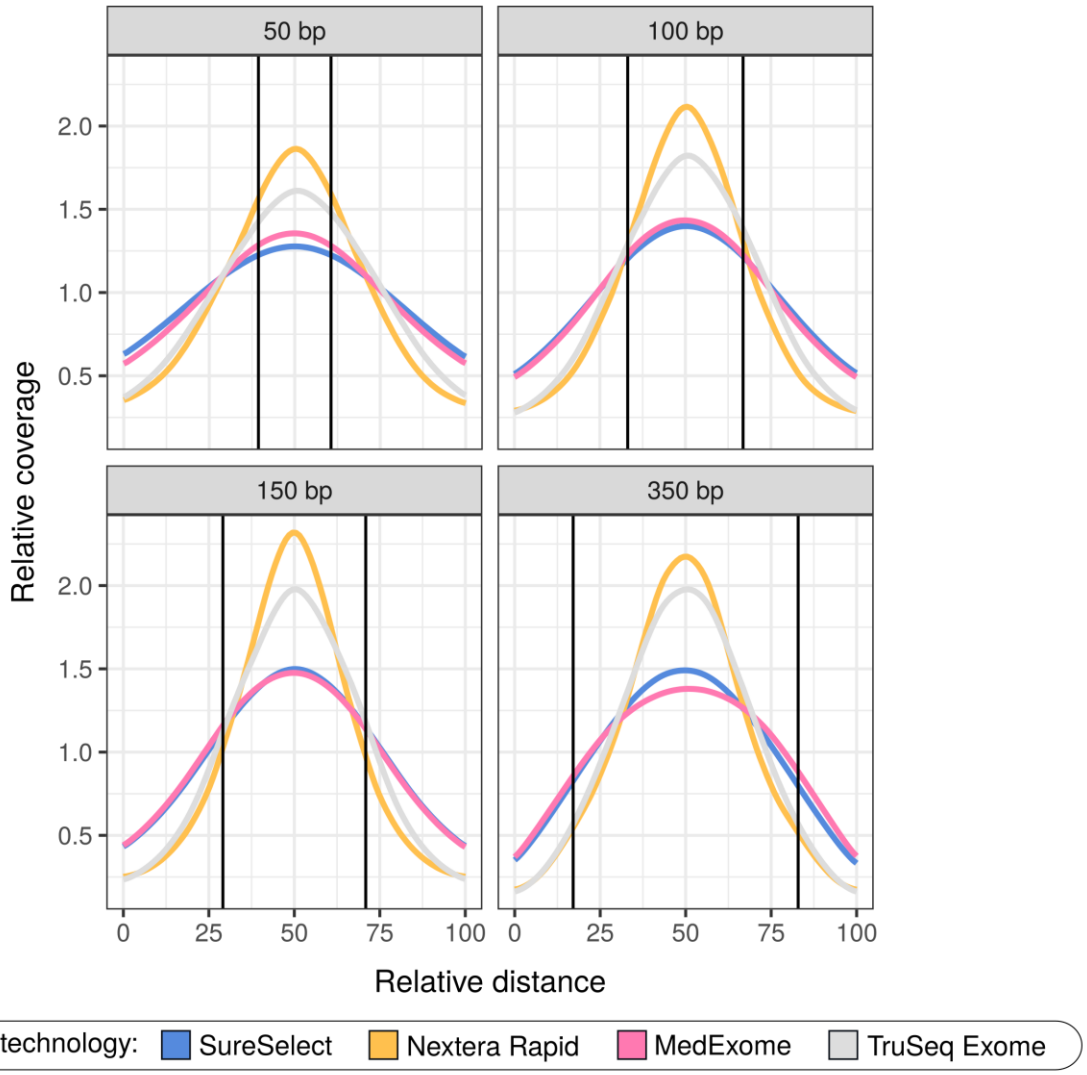
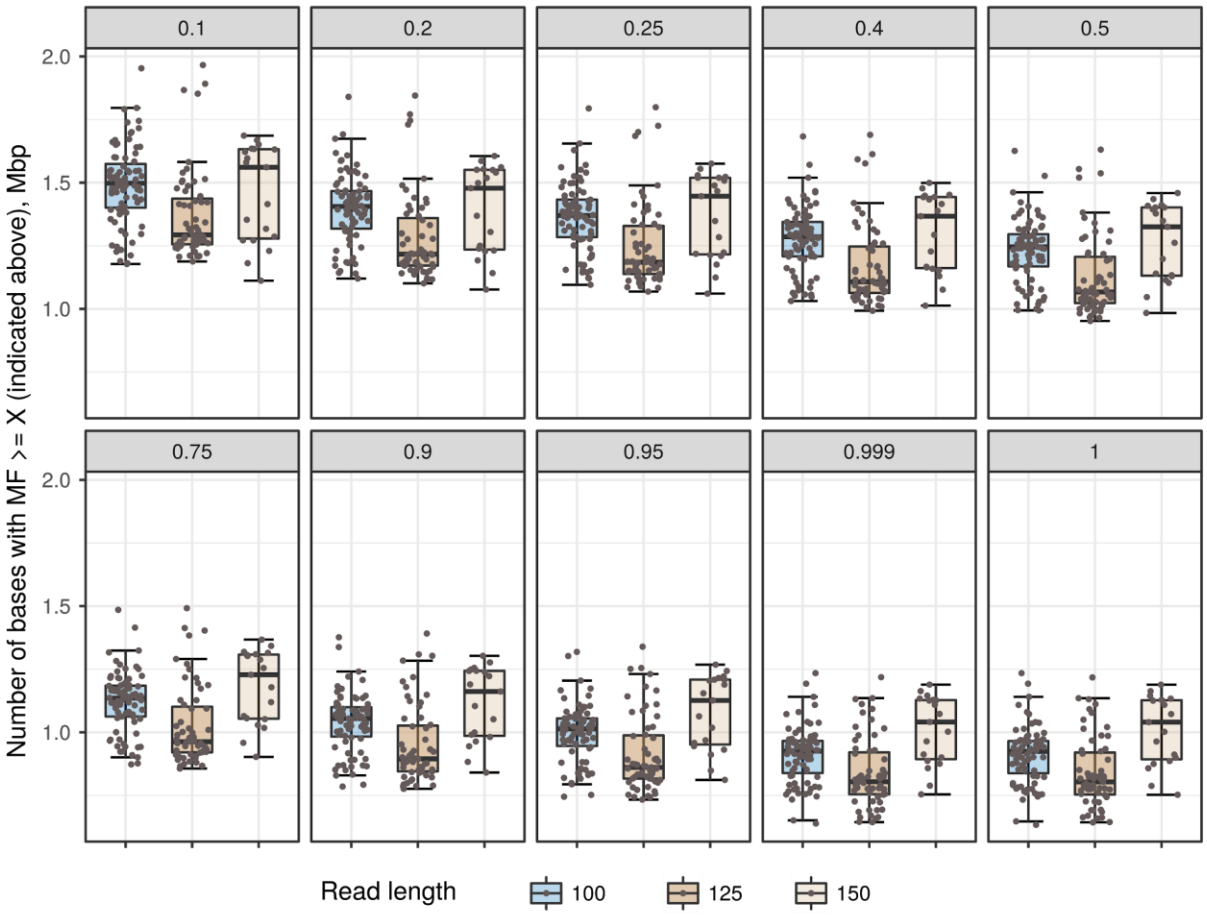
Supplementary Figures



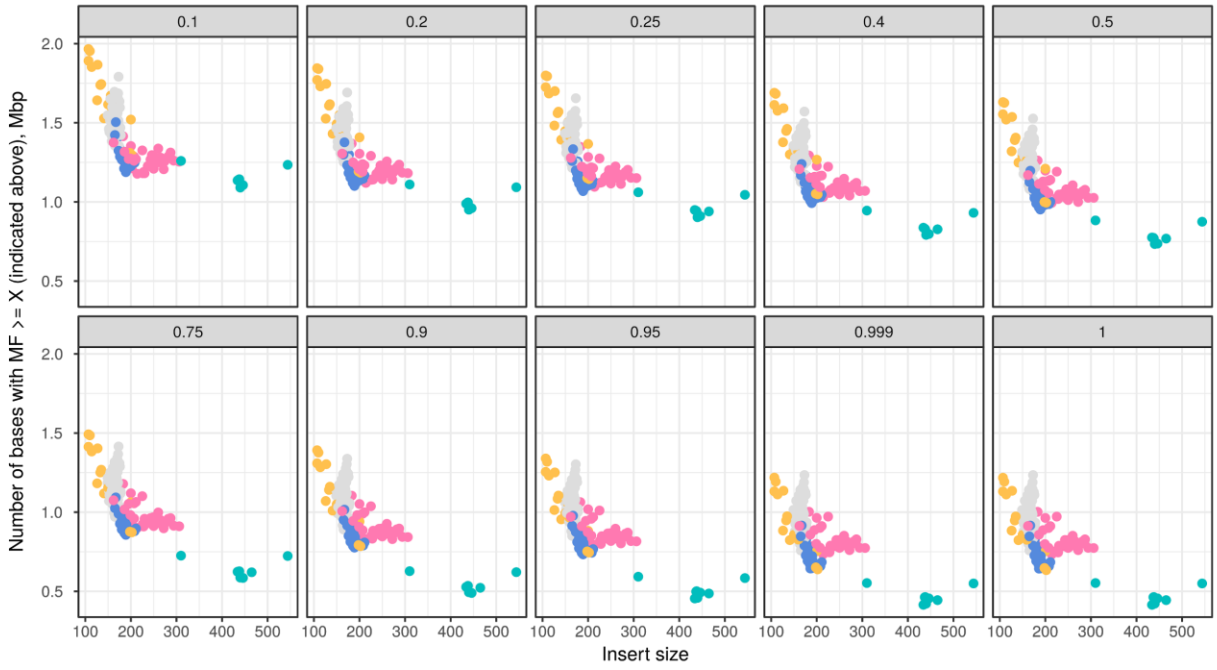
Supplementary Figure 1. Fold enrichment of CDS regions for WES samples included in the study.



Supplementary Figure 2. Profiles of relative coverage within exons divided into 4 quartiles according to the length of an interval. 100 bp of flanking bases are included; solid lines delineate CDS margins.



Supplementary Figure 3. The number of bases having an MF >= X (indicated above each plot) for WES and WGS samples having indicated paired end read lengths.



Supplementary Figure 4. The number of bases having an MF = X (indicated above each plot) for all samples plotted against the library mean insert size.