# CNVind - An open source cloud-based pipeline for rare CNVs detection in whole exome sequencing data based on the depth of coverage

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Supplementary Materials

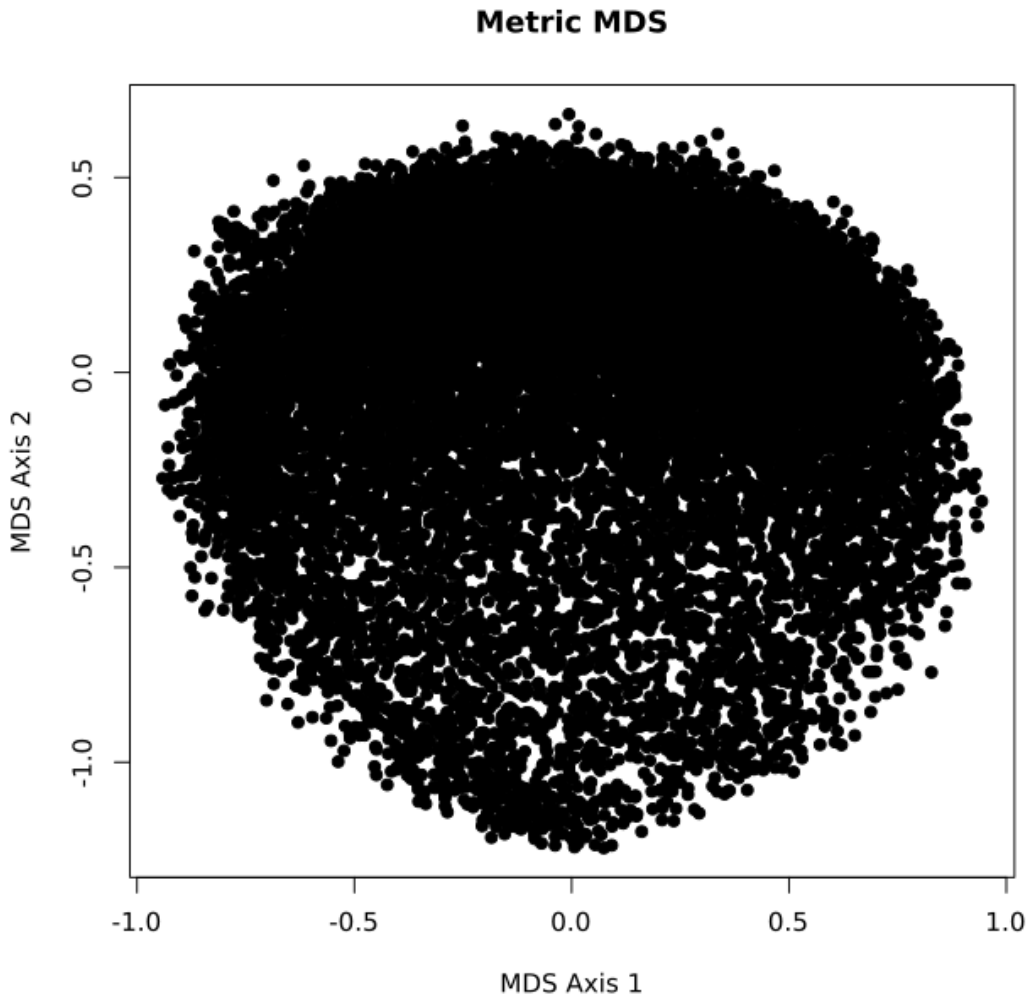


Figure S1: **Correlation between depth of coverage in sequencing regions of benchmark dataset (chromosome 1).**

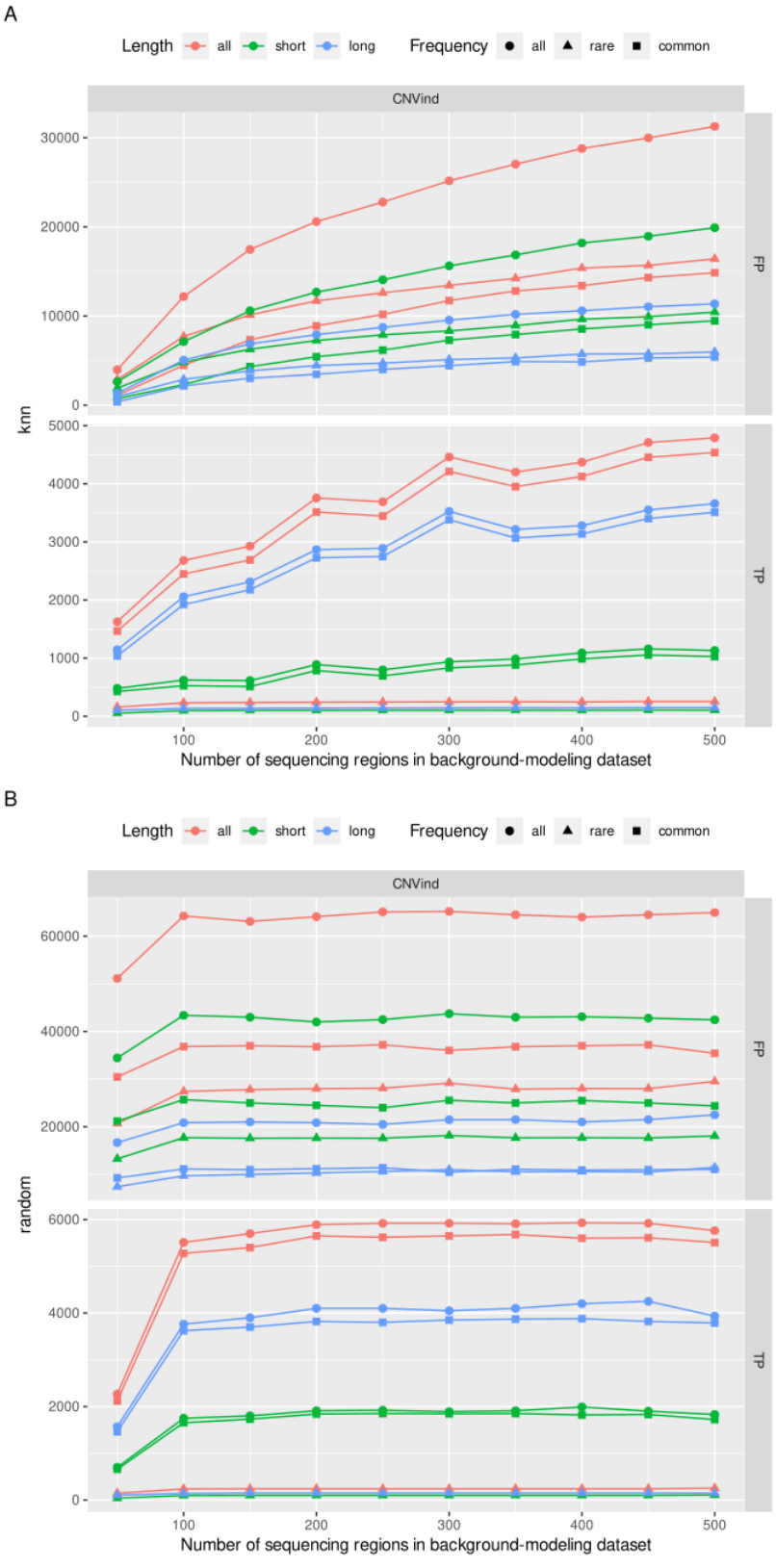


Figure S2: **Effect of the size of the set of sequencing regions which models background on the number of CNVs detected by the CNVind tool (chromosome 1).**

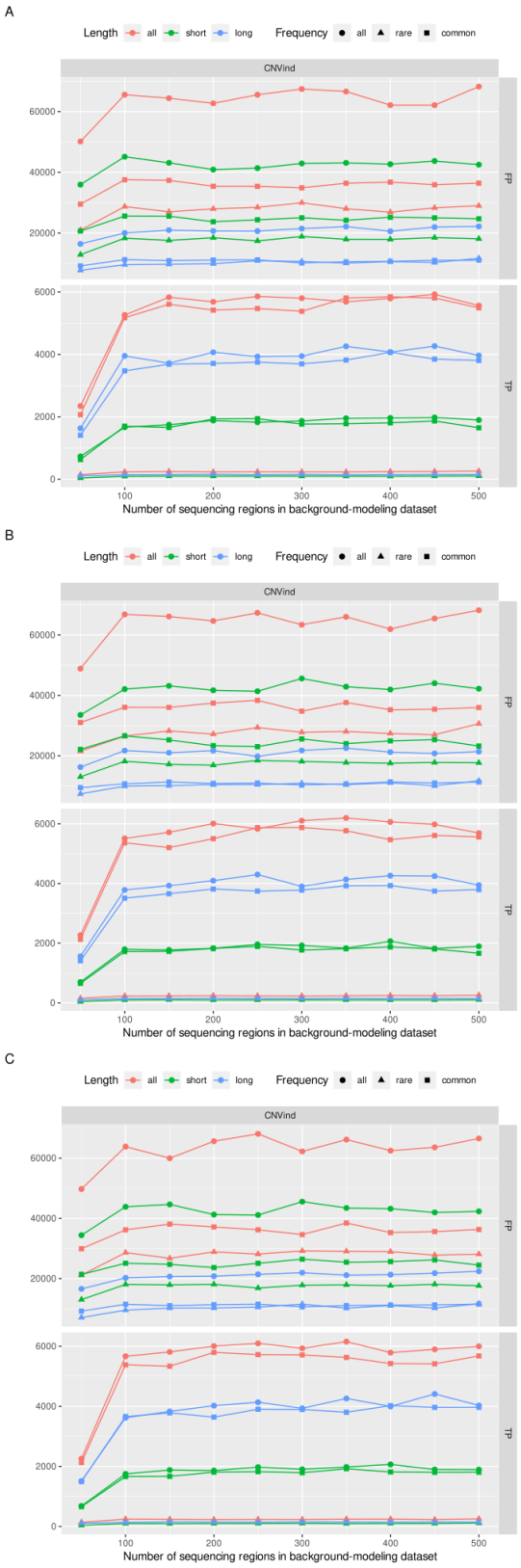


Figure S3: **Effect of using other metrics when selecting the k most similar sequencing regions: (A) GC content, (B) sequencing region length, (C) mean depth of coverage in the sequencing region (chromosome 1).**

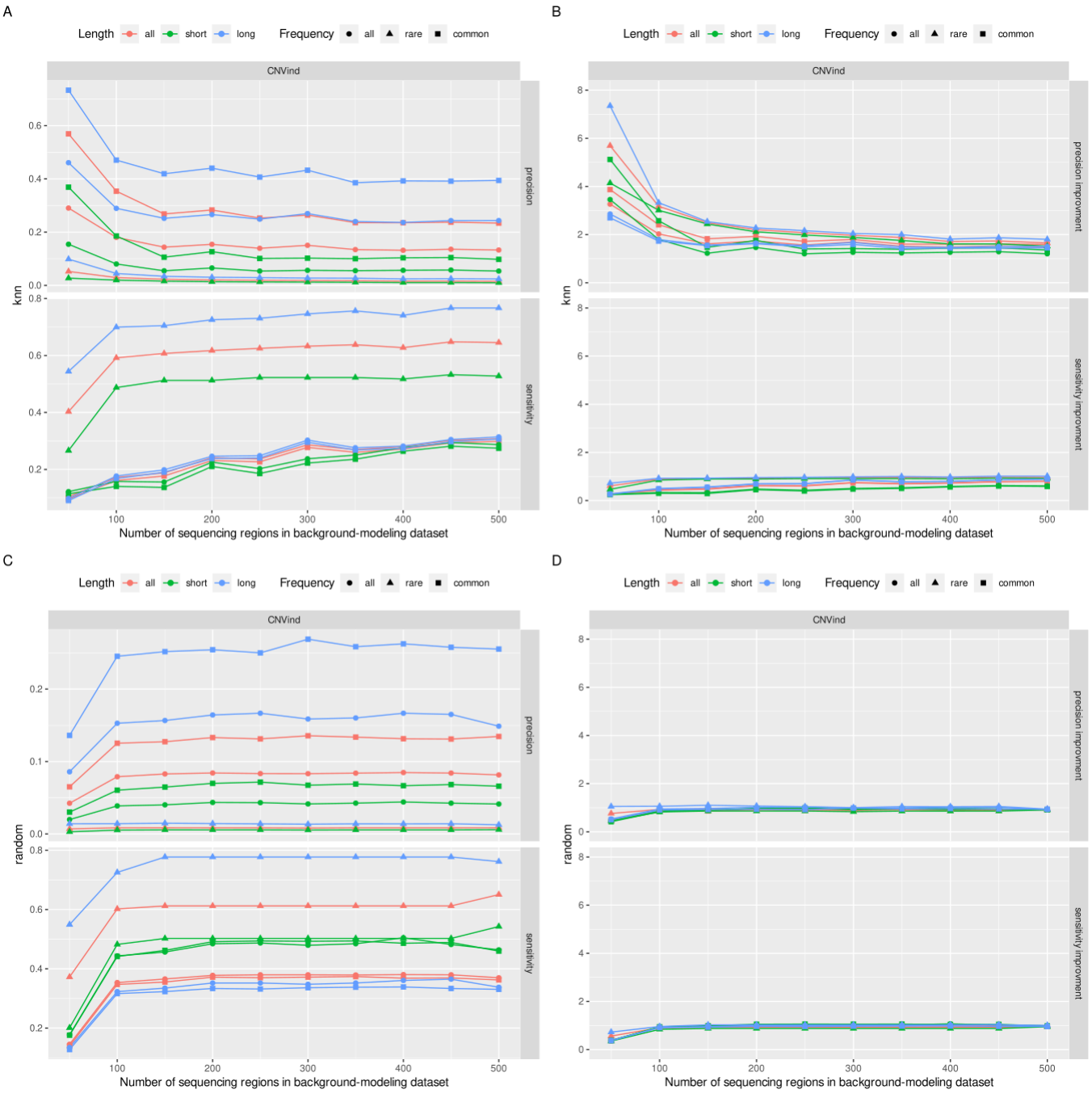


Figure S4: **Effect of the size of the set of sequencing regions which models background on the results' sensitivity and precision. (chromosome 1).**

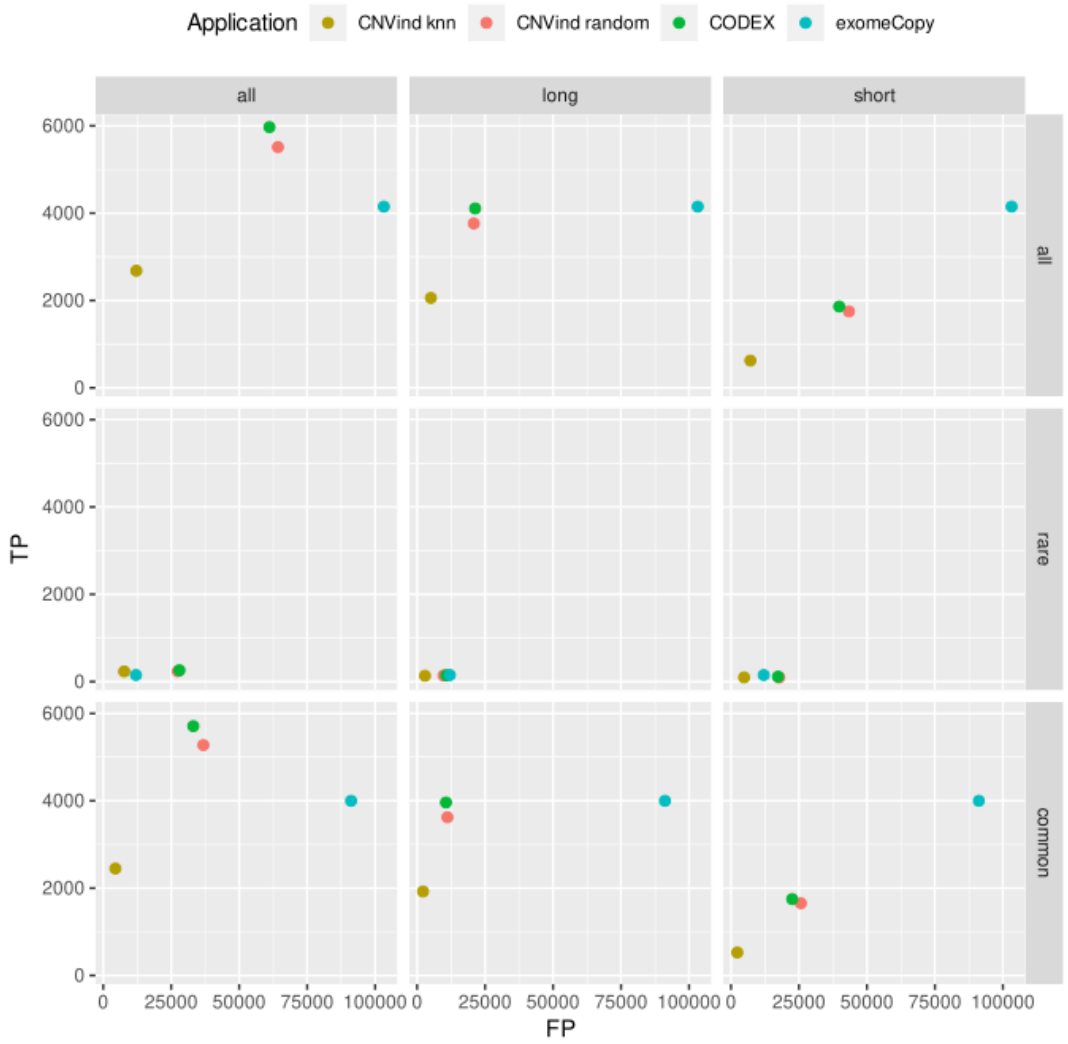


Figure S5: **Comparison of the results obtained by the CODEX, exomeCopy, and CNVind applications in knn and random modes (chromosome 1).**

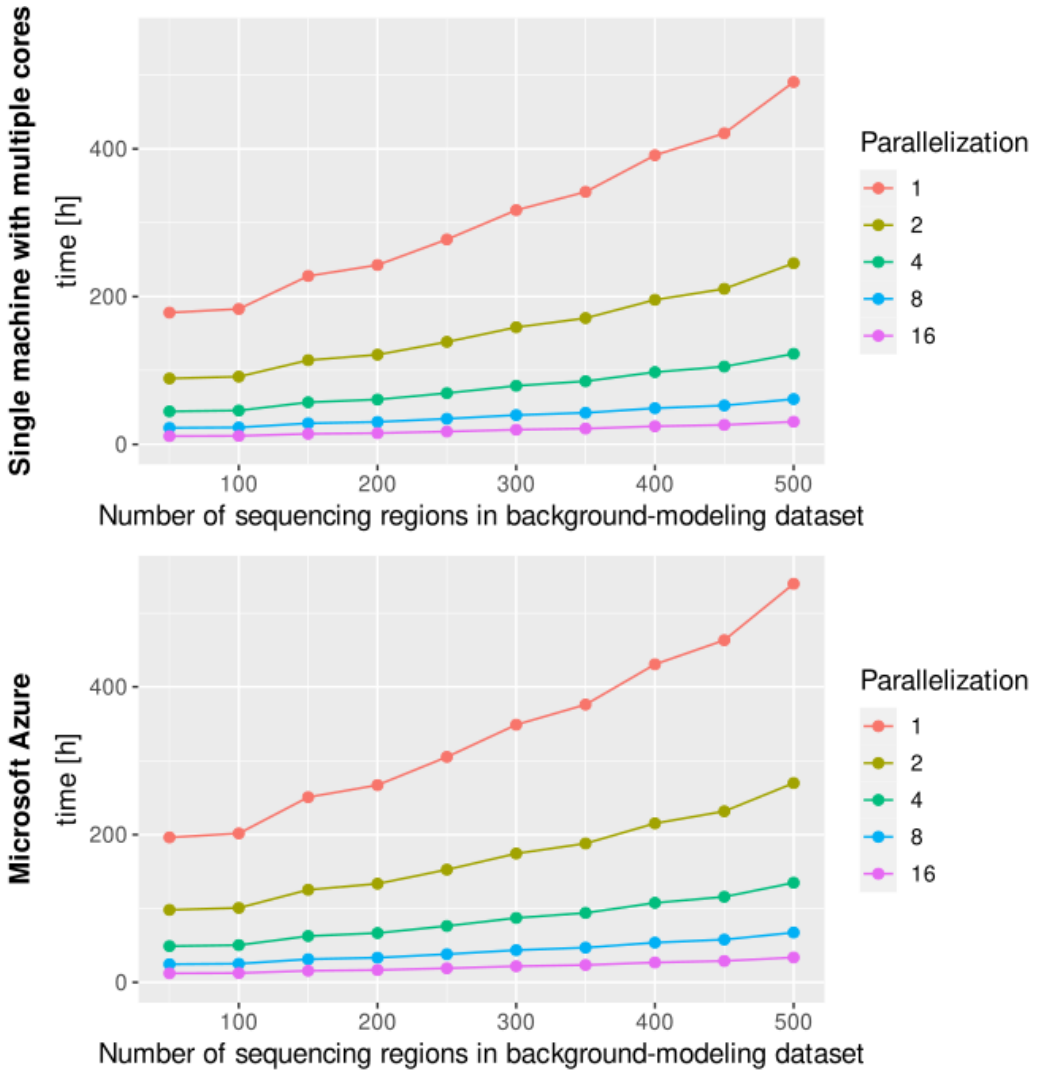


Figure S6: **Comparison of the depth of coverage normalization computation times for the CNVind application on a single machine with multiple cores and in Microsoft Azure cloud (chromosome 1).**