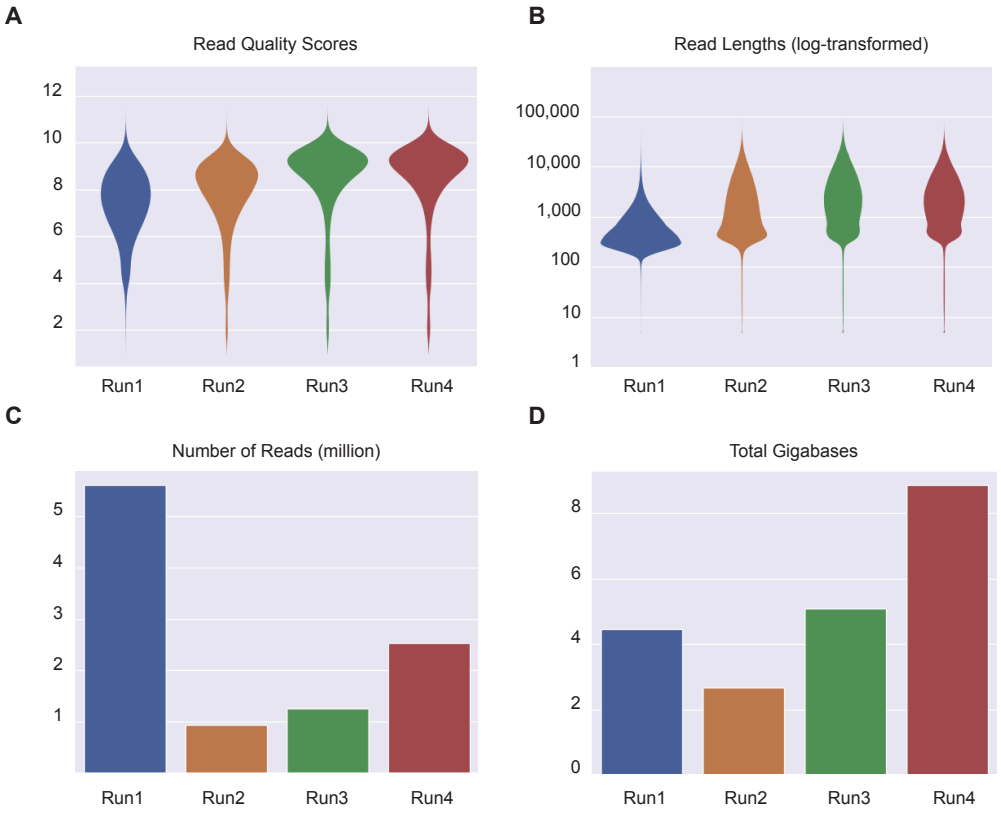
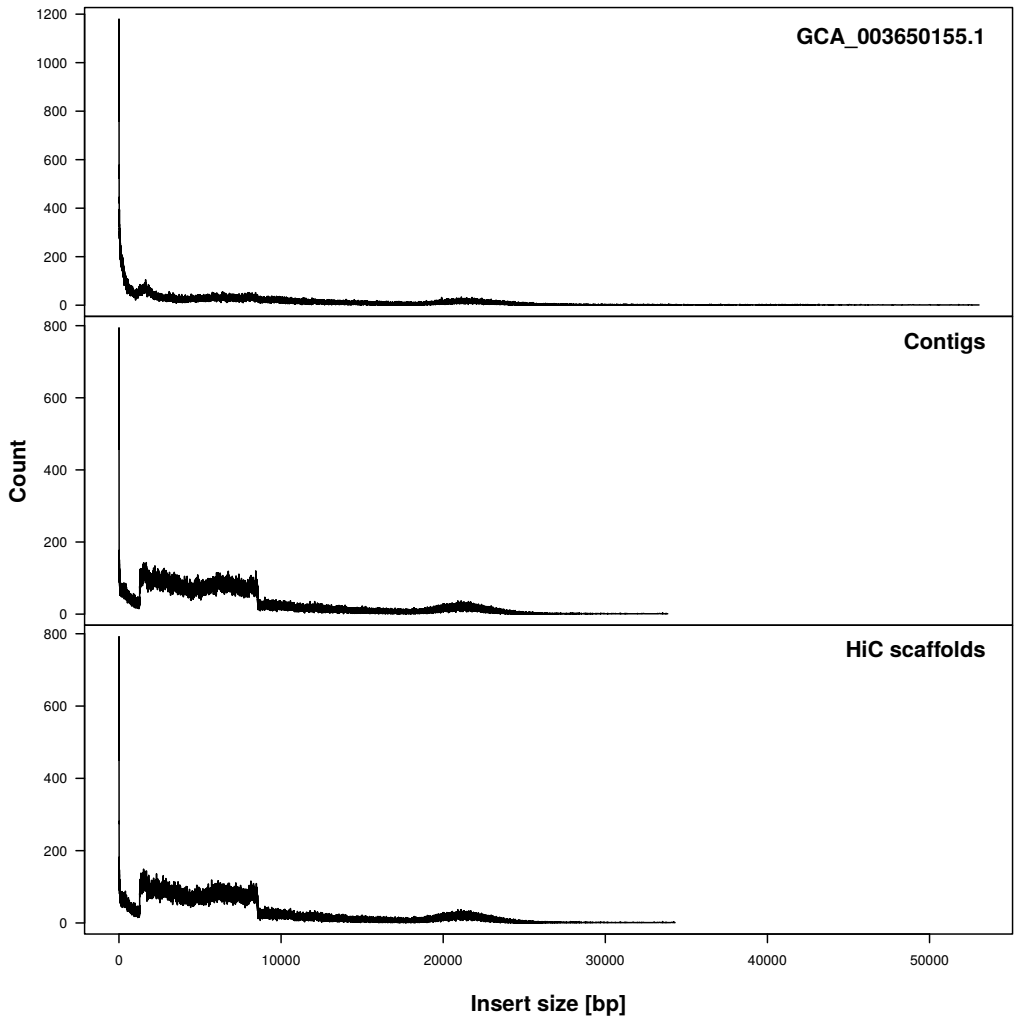
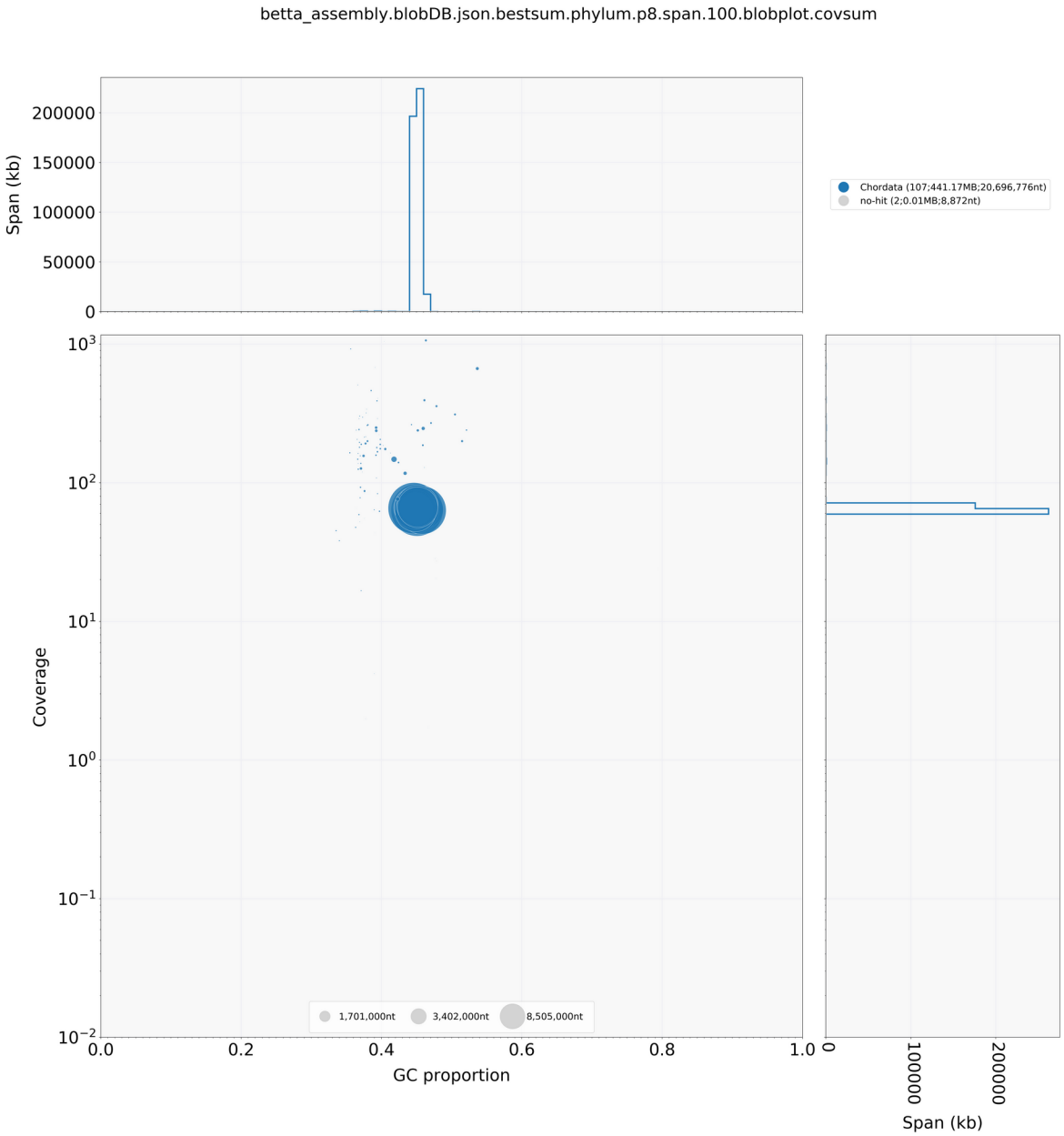
Supplementary Figures



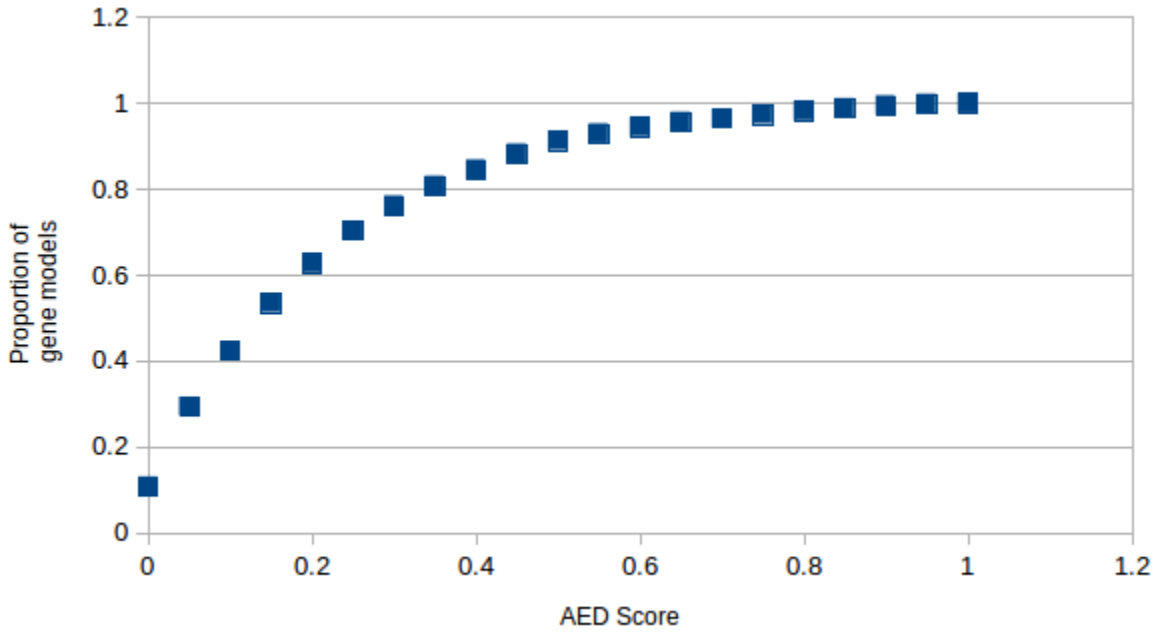
Supplementary Figure 1: Comparison of the data output and read lengths between all four MinION sequencing runs. Run 1: Oxford Nanopore Technologies (ONT) 1D sequencing kit (SQK–LSK109) and Run 2-4: ONT Rapid sequencing kit (SQK-RAD004). A) Read quality scores of the four different runs, B) bog-transformed read lengths, C) numbers of reads, and D) the total amount of sequencing data generated.



Supplementary Figure 2: Insert sizes of the 5 kbp mate pair read library of Fan et al. (2018), mapped against the chromosome-level assembly of Fan et al. (2018) (GCA_003650155.1; top panel), our nanopore-based baseline assembly (middle panel) and our chromosome-level assembly (bottom panel).



Supplementary Figure 3: Blobtools plot showing the taxonomic assignments (blue colour for Chordata, and gray for "no hits") of the different scaffolds, and scaffold-wide coverage and GC contents. The scaffolds were blasted against the NCBI nucleotide database.



Supplementary Figure 4. Distribution of Annotation Edit Distance (AED) scores. About 90% of all gene models show AED scores of < 0.5 indicating a high quality of our gene models.