A  Co-expression validation of transcription units

Number of gene pairs predicted to be part of the same TU

B  Summary statistics of Nanopore native RNA-seq data

Total reads 466,393 (sample 1) + 556,850 (sample 2)
Median quality 9.3 (88% base calling accuracy)
Median length 358 nucleotides
Total alignments 382,290 + 392,743
Genome mappability 77 + 67%
Median counts/gene 30