The R package *Rsubread* is easier, faster, cheaper and better for alignment and quantification of RNA sequencing reads – Supplementary Materials

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Supplementary Figures

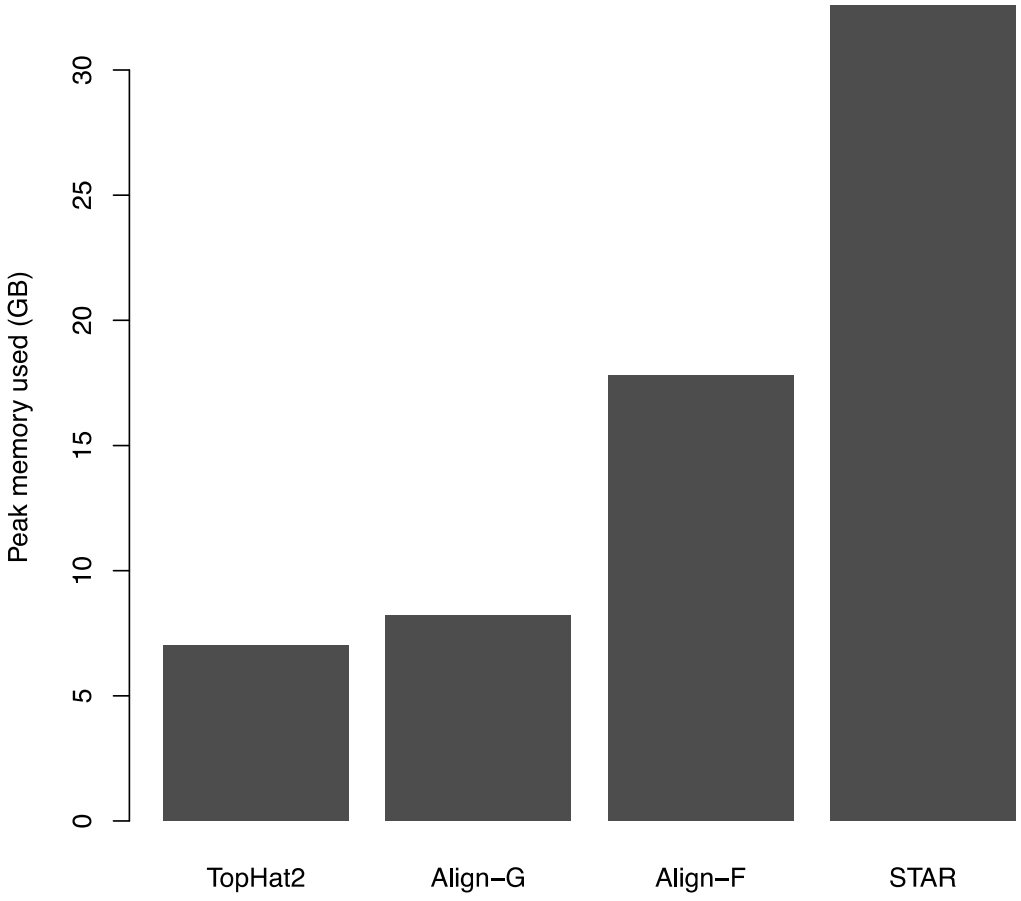

Fig. S1. Peak memory used by different read aligners. ~15 million pairs of 100bp reads generated from a SEQC UHRR sample were mapped to the human genome reference GRCh38.

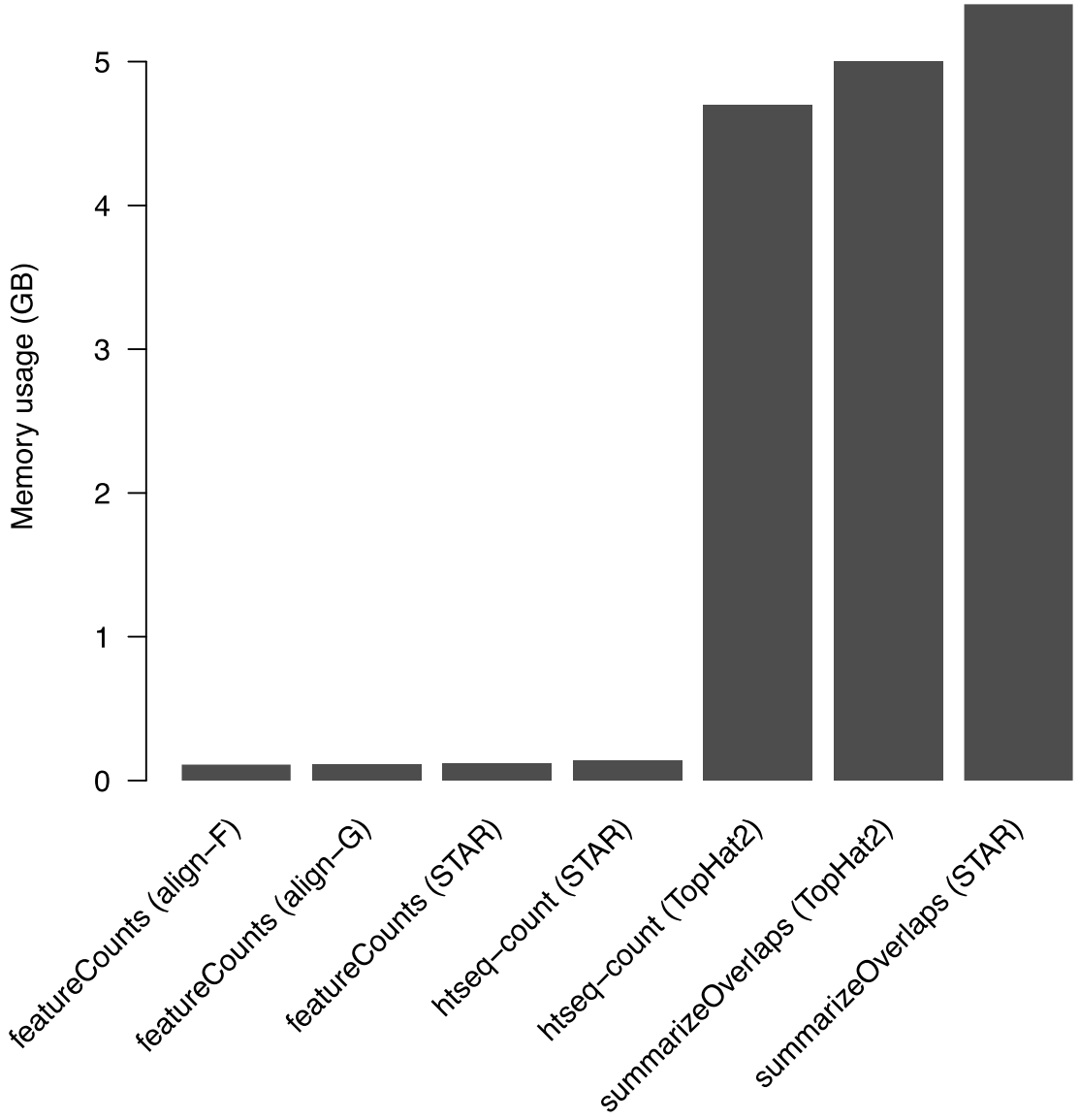

Fig. S2. Peak memory used by different quantification tools. A SEQC UHRR dataset was used in this comparison. Reads aligned by different aligners were assigned to NCBI RefSeq human genes by different quantification tools.

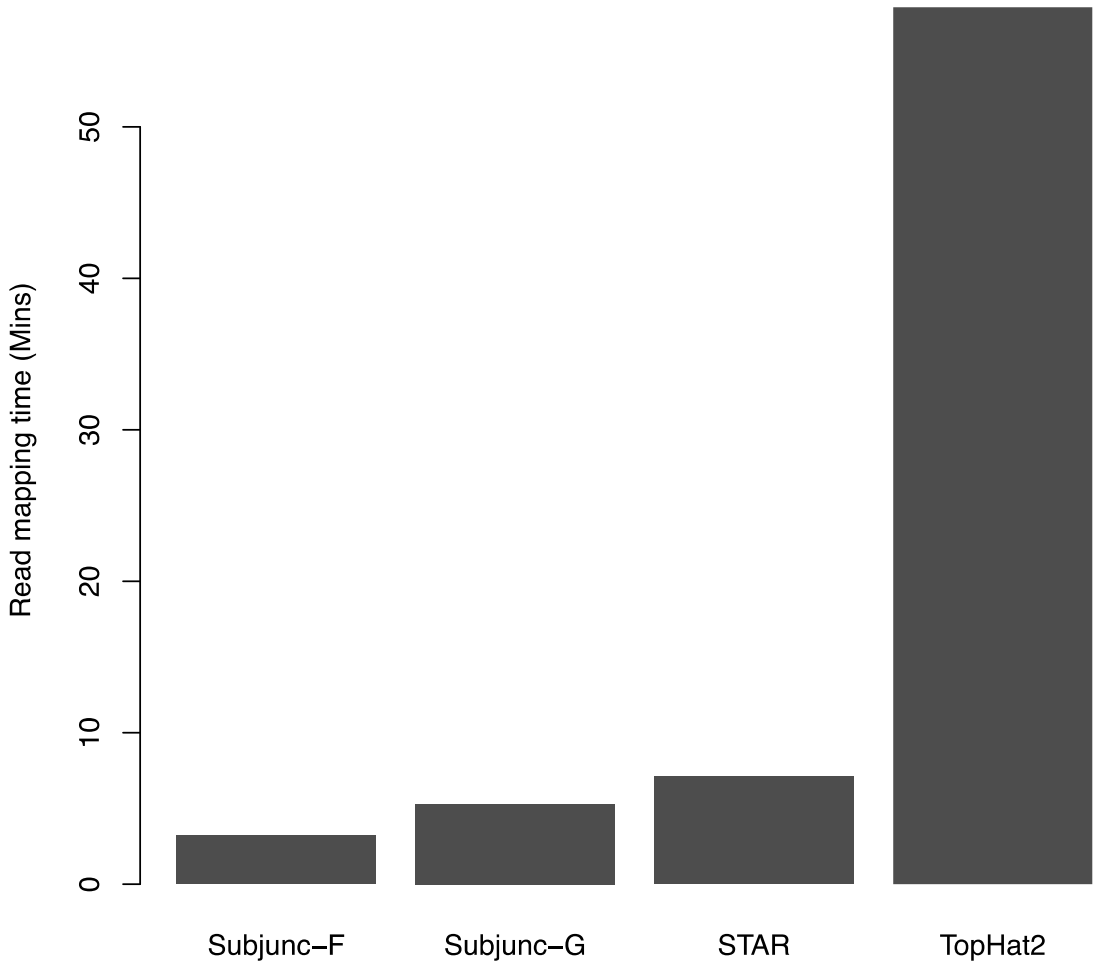

Fig. S3. Running time of read aligners for exon-level RNA-seq analysis. ~15 million pairs of reads generated from a SEQC UHRR sample were mapped to human genome reference GRCh38 by each aligner.

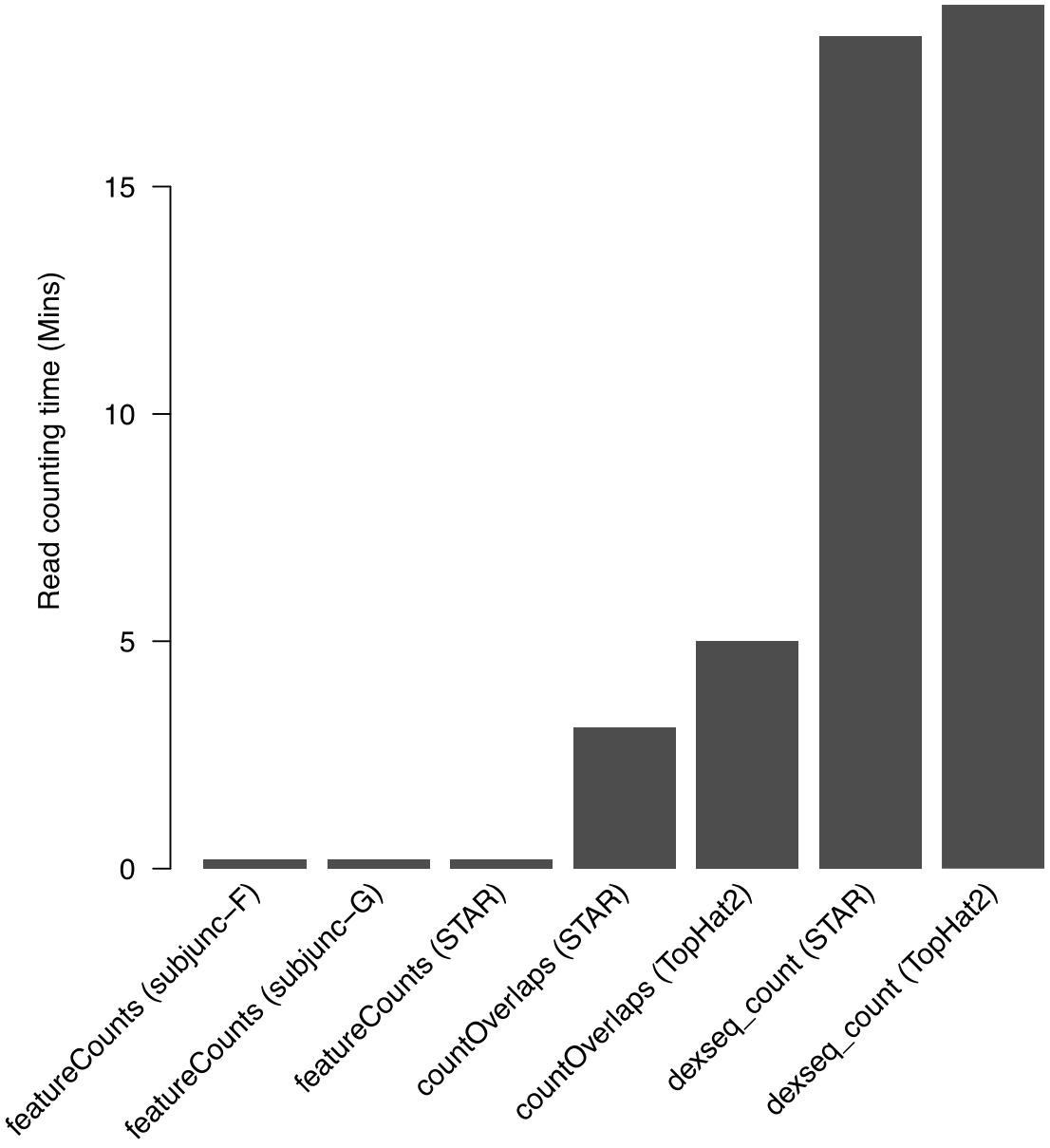

Fig. S4. Running time of quantification tools for exon-level RNA-seq analysis. A SEQC UHRR dataset was used in this comparison. Mapped reads were assigned to NCBI RefSeq human exons by each quantification tool. Labels under each bar indicate the quantification tool and the aligner (in parenthesis) used for producing the mapped reads that were fed to the quantification tool.

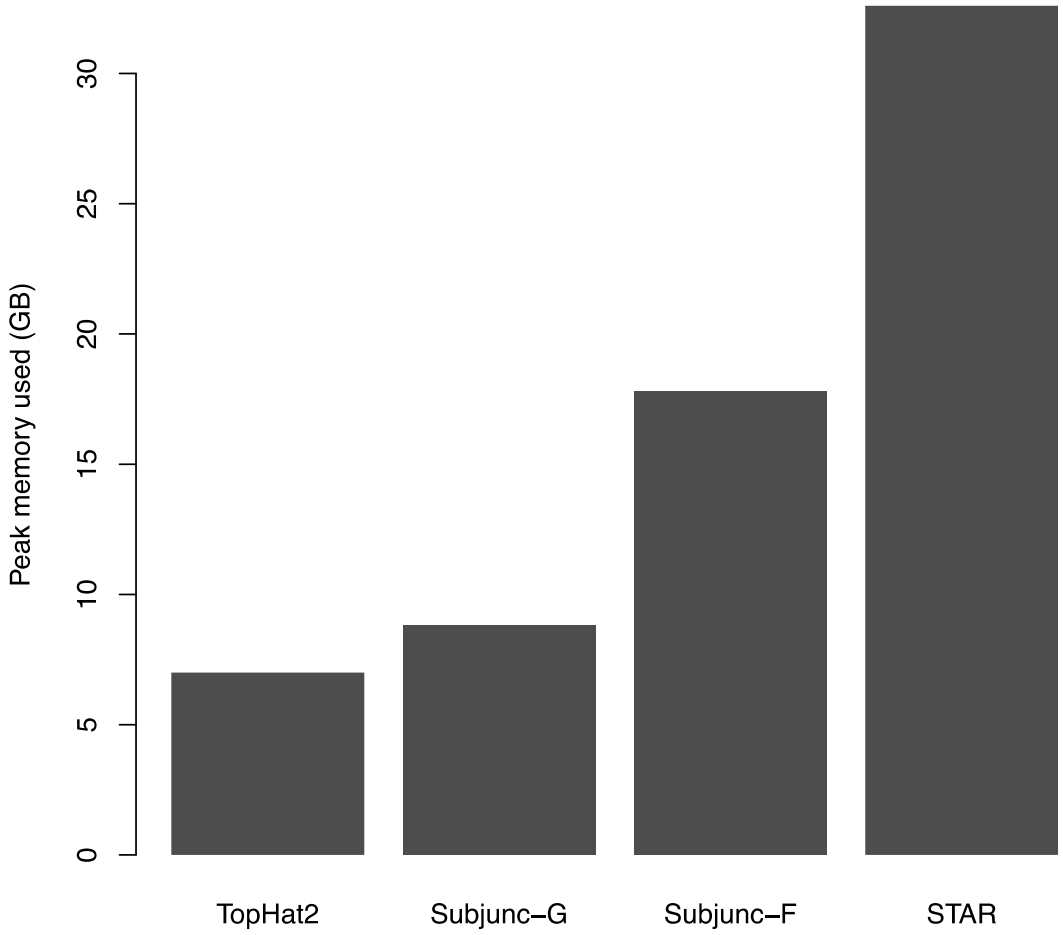

Fig. S5. Amount of peak memory used by read aligners in exon-level analysis of RNA-seq data. ~15 million pairs of reads generated from a SEQC UHRR sample were mapped to human genome reference GRCh38 by each aligner.

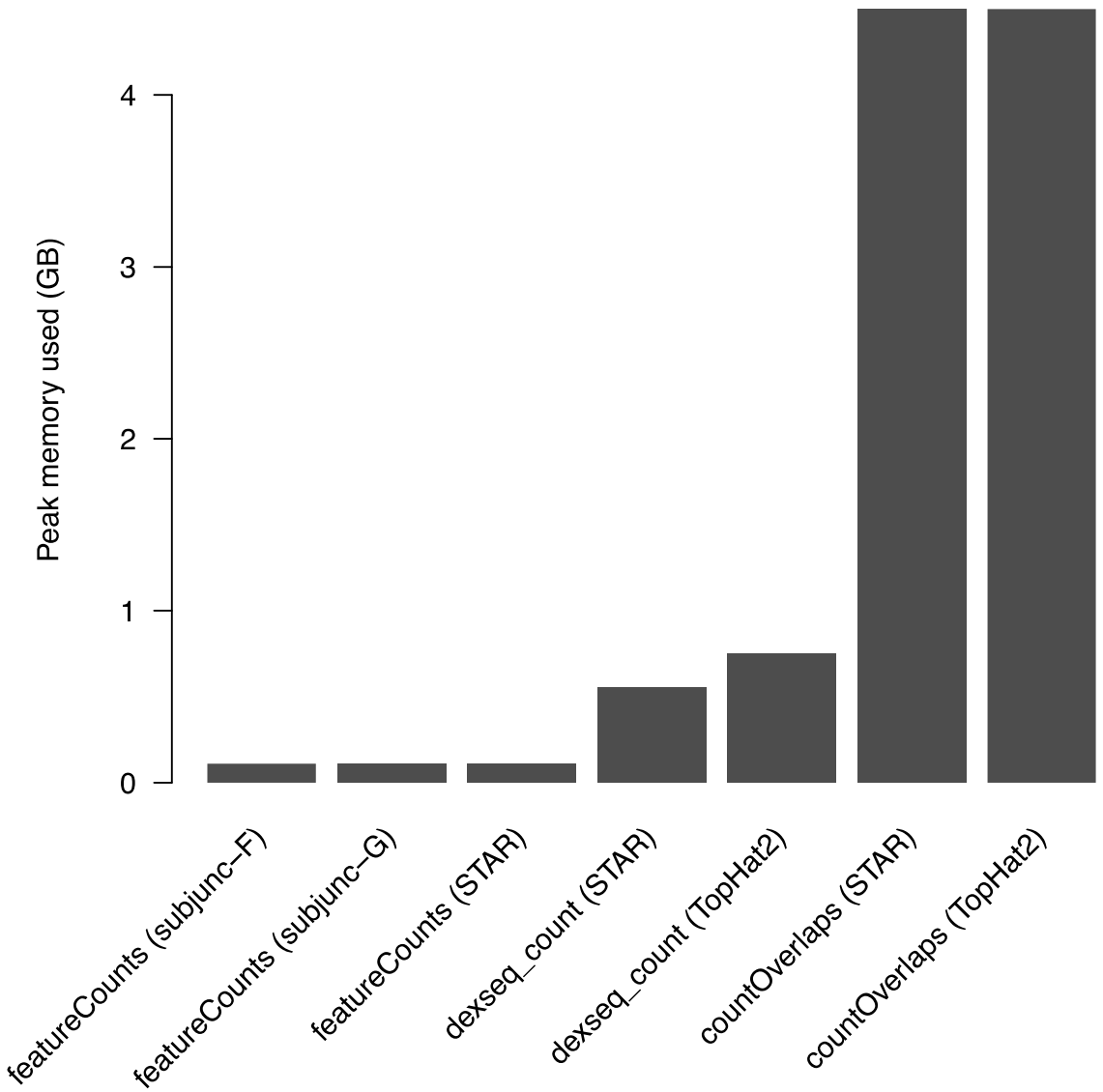

Fig. S6. Amount of peak memory used by quantification tools in exon-level analysis of RNA-seq data. A SEQC UHRR dataset was used in this comparison. Mapped reads were assigned to NCBI RefSeq human exons by each quantification tool. Labels under each bar indicate the quantification tool and the aligner (in parenthesis) used for producing the mapped reads that were fed to the quantification tool.