

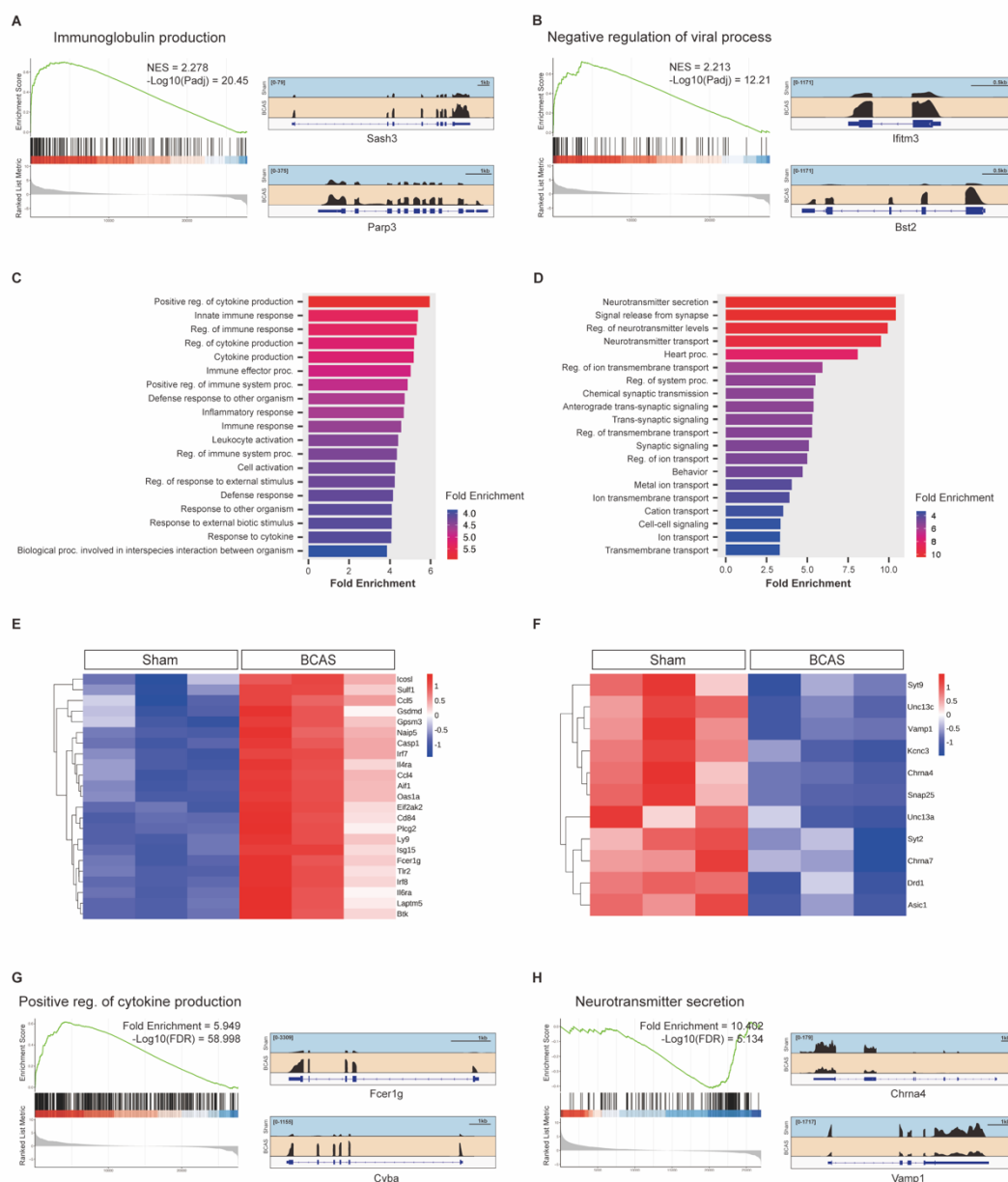


Figure S1. Striatum-specific pathway analysis of transcriptome changes.

A-B Enrichment plots and IGV map tracks for representative genes of the top two up-regulated pathways analyzed by GSEA. **C-D** Bar plot showing enriched GO biological process terms of **(C)** up- and **(D)** down- regulated genes. **E** Heatmap, **G** Enrichment plots and IGV map tracks for representative genes of the top up-regulated pathway. **F** Heatmap, **H** Enrichment plots and IGV map tracks for representative genes of the top down-regulated pathway.

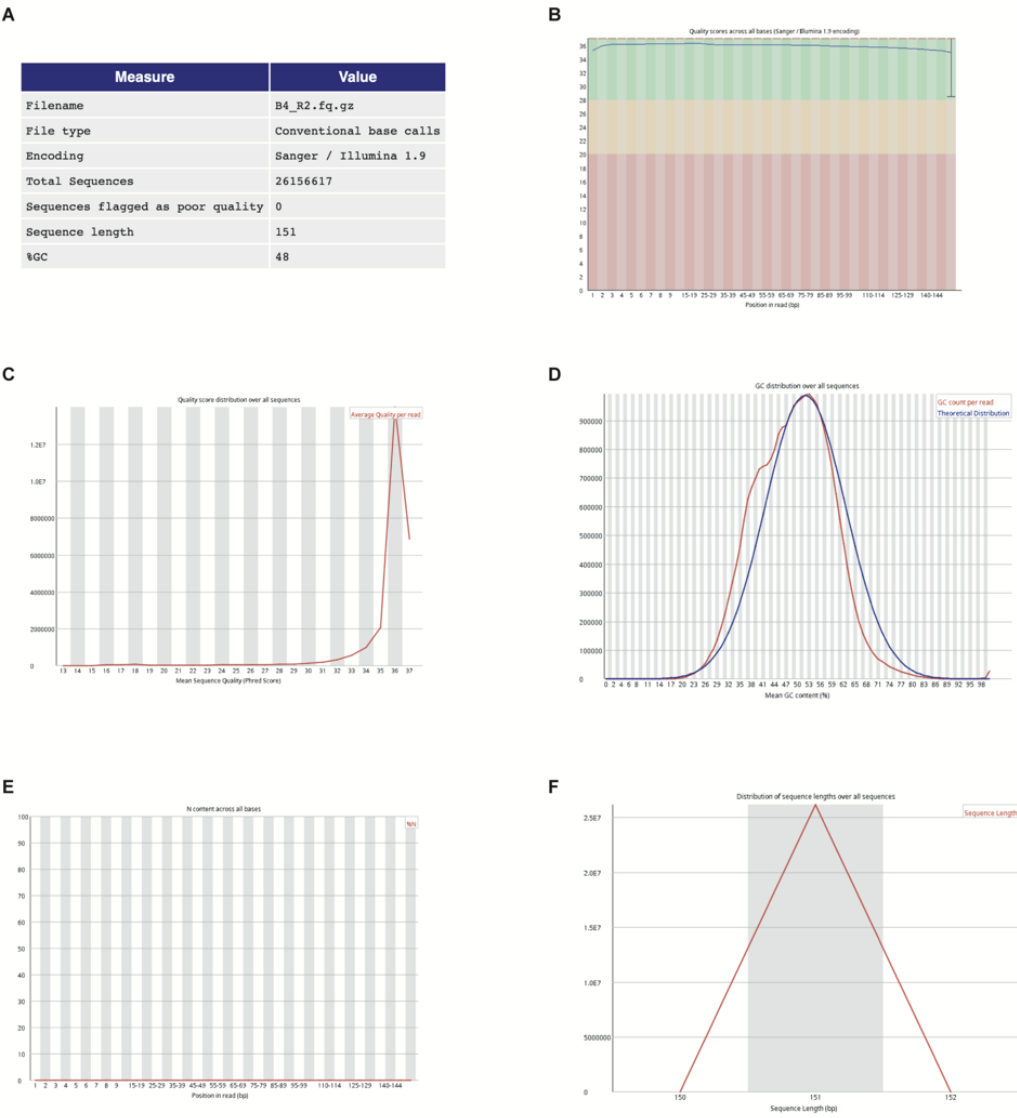


Figure S2. Representative images for FastQC data quality control in RNA-seq.

A Basic statistics. **B** Per base sequence quality. **C** Per sequence quality scores. **D** Per sequence GC content. **E** Per base N content. **F** Sequence Length Distribution.

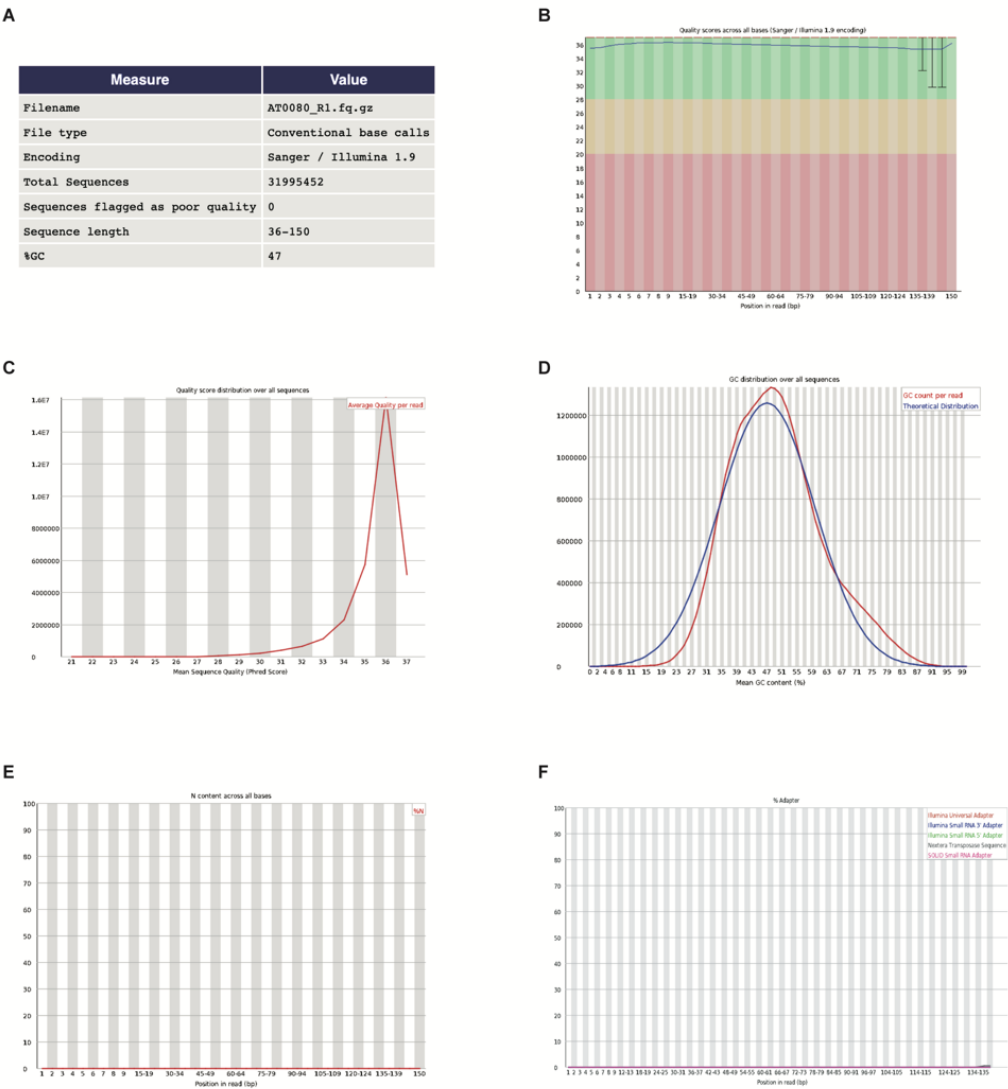


Figure S3. Representative images for FastQC data quality control in ATAC-seq.

A Basic statistics. **B** Per base sequence quality. **C** Per sequence quality scores. **D** Per sequence GC content. **E** Per base N content. **F** Adapter content.