

Sequence and transcriptome Reference



ImmGen is currently using the GRCm38 - mm10 genome assembly to map RNAseq data.

For single-cell RNAseq, BCL files are demultiplexed into FASTQ files using the Cell Ranger function `cellranger mkfastq`. Count matrices for GEX and FBC data are generated using the function `cellranger count`, and TCR data is generated using the function `cellranger vdj` (if applicable). Output data is further cleaned and analyzed using R software. ImmGen is currently using GRCm38 release M25, and the following versions of software: Cell Ranger 7.0.0 & R 4.2.1

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