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Single-cell RNA-sequencing data processing

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Protocol status: Working
We use this protocol and it's working

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Abstract

This protocol describes the steps used for processing our single cell RNA-sequencing data set.

Troubleshooting

Single-cell RNA-sequencing data processing

1 Align reads (.bcl files) to the mouse reference genome (mm10)

2 Analyze data using Seurat's standard workflow

3 Include only cells containing between 200 and 5000 genes and less than 20% mitochondrial RNA

4 Using default parameters of Seurat, log normalize data across cells and identify the 1500 most highly variable genes

5 Identify cell types by clustering the data using the first 13 principal components and a clustering resolution of 0.3