

Console

Terminal ×

Background Jobs ×

R 4.4.1 · ~/git-repos/Hayford\_Melanoma\_2024/scRNA/code/ ↗

Using method 'umap'

0% 10 20 30 40 50 60 70 80 90 100%

[-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

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16:28:06 Optimization finished

Found 2 SCT models. Recorrecting SCT counts using minimum median counts: 22907

|+++++| 100% elapsed=08s

To continue, you must manually enter the Seurat cluster indices for the small (fast-dividing) and large (slow-dividing) idling and untreated clusters in the UMAP space. You can do this by inspecting the plots in the file 'scRNA/code/UMAP\_combined\_SKMEL5\_hg38\_qcCCReg\_allPlots.pdf'.

Open the file and press [enter] when you're ready to continue.