10x multiome (scRNA-seq+scATAC-seq) analysis pipeline v3

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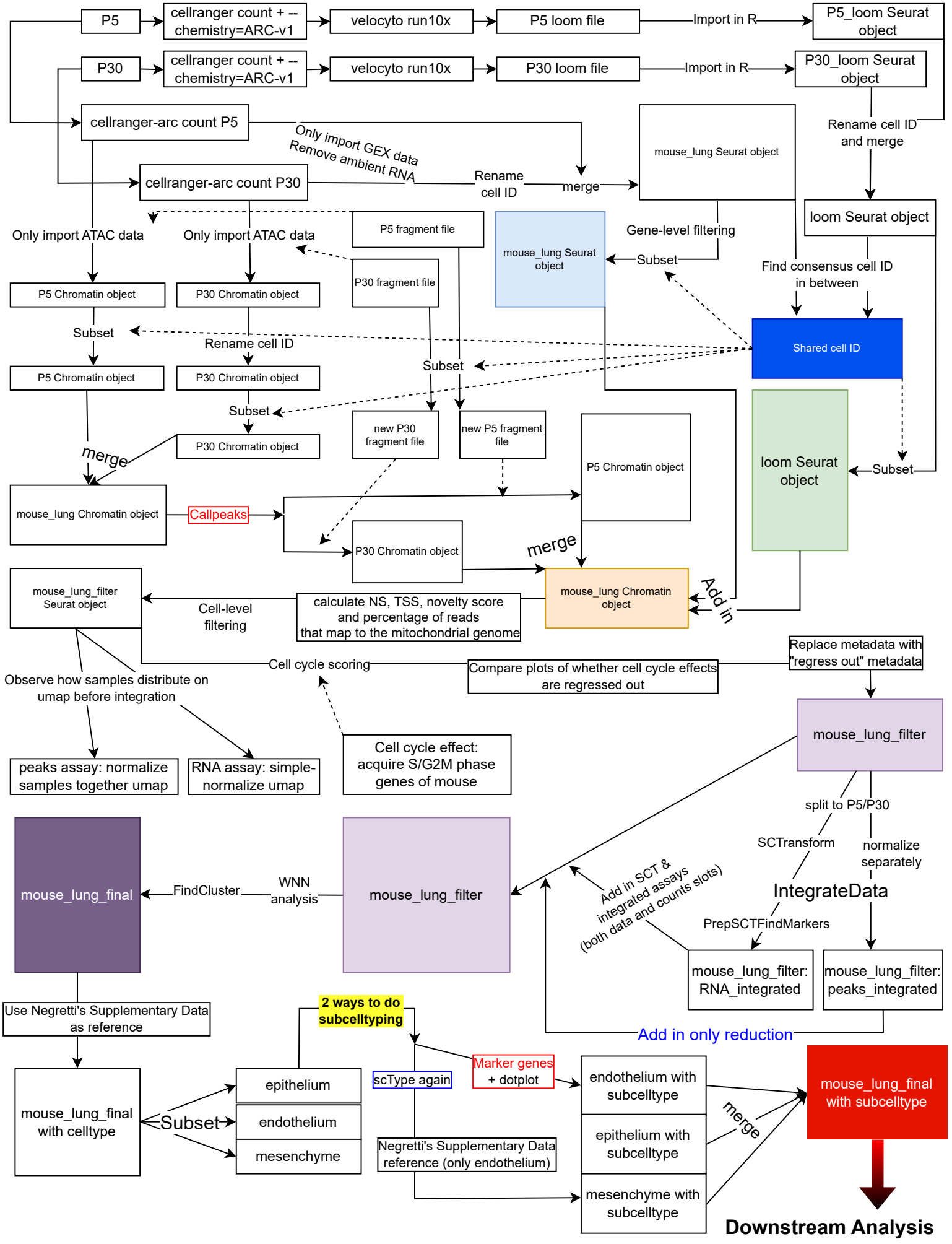
This is the v3-version workflow that the result of `cellranger-arc count` function are used as raw data, and the "Seurat::IntegrateData" pipeline is performed to correct the batch effect. Other versions can be found in Notion.

Here we have 2 samples: lung cells from P5 and P30 mouse.