Strategy 1: Seurat analysis with default analysis setup

Filtering criteria ::

1. Remove lowly expressed genes :: min.cells == Expression of a gene must be detected in 1 out of 500 cells

2. Remove low-quality cells & cells with high total read count ::

- If expression of at least 200 genes have not been detected a cell, the cell has been removed

- Cells with a total read count more than 110000 have been removed

- Cells with read count from mitochondrial genes equal or more than 5% and read count from chloroplast genes more than 10% have been removed

Normalization method :: Log-Normalization

Selection of highly variable genes :: 2000 highly variable genes have been selected for each replicate

Integration feature : Anchor features selected by Seurat

Dimension reduction :: 50 PCs have been used to compute UMAP and TSNE

Cell clusters identification :: 50 PCs have been used to identify cell clusters with a range of resolution parameters, 0.1 – 1.2 with 0.1 increment