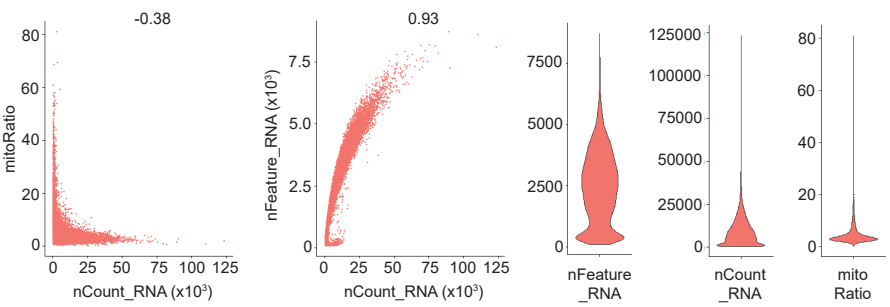


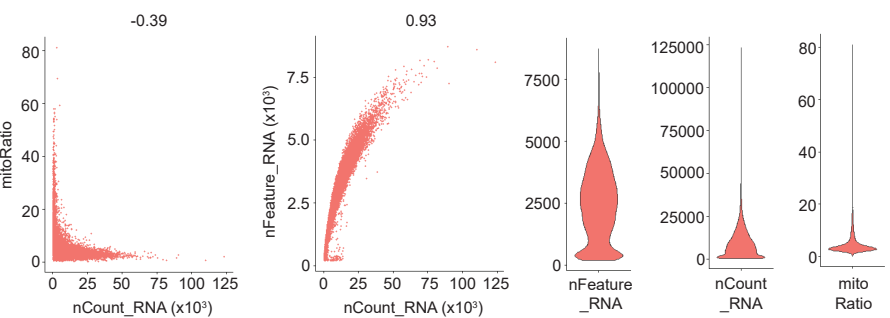
C scRNA-seq quality control and filtering

| Step | Number of cells | % cells remaining |
|---|-----------------|-------------------|
| Step 0: Starting number of cells in pre-processed data | 28,277 | 100 |
| Step 1: Load pre-processed data into Seurat min.features = 100 | 28,023 | 99.1 |
| Step 2: Removal of cells with nFeatures < 200 | 27,743 | 98.11 |
| Step 3: Removal of cells with over 5% of genes mitochondrial-derived percent.mt > 0.05 | 20,664 | 73.07 |
| Step 4: Removal of cells with nFeatures > 6000 | 20,422 | 72.22 |

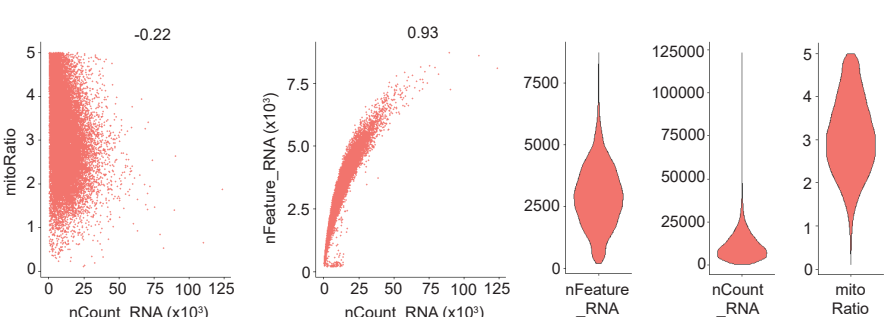
Step 1
Load pre-processed data into Seurat min.features = 100



Step 2
Removal of cells with nFeatures < 200



Step 3
Removal of cells with over 5% of genes derived from mitochondria percent.mt > 0.05



Step 4
Removal of cells with nFeatures > 6000

