**Supplemental Table S1.** Summary statistics for sequencing and mapping data of five samples

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Number of cells | Mean reads per cell | Median genes per cell | Total genes detected | Median UMIs per cell | Total number of reads | Percent mapped reads | Remaining cells post filtering |
| Sample 1 | 2,779 | 71,256 | 3,662 | 20,356 | 17,769 | 198,022,303 | 62.6 | 2,426 |
| Sample 2 | 545 | 318,909 | 4,547 | 18,557 | 27,341 | 173,805,798 | 63.4 | 424 |
| Sample 3 | 3,103 | 56,459 | 2,944 | 19,261 | 11,214 | 175,193,813 | 71.8 | 2,906 |
| Sample 4 | 9,192 | 38,637 | 2,016 | 21,491 | 5,963 | 355,158,219 | 68.9 | 8,294 |
| Sample 5 | 4,863 | 26,471 | 2,804 | 20,235 | 10,150 | 128,728,889 | 67.2 | 4,737 |