**Supplementary File 2. Cell subpopulations are identified in multiple biological replicates**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  | Cell number from each biological replicate | P-value (before Holm-Bonferroni correction) |
| mclust cluster | Number of cells in cluster | Biological replicate 1 | Biological replicate 2 | Biological replicate 3 | Biological replicate 1 | Biological replicate 2 | Biological replicate 3 |
| 1 | 61  | 23 | 21 | 17 |  0.46  | 0.13  |  0.94 |
| 2 | 9 | 3 | 3 | 3 |  0.69  | 0.46  |  0.69 |
| 3 | 18 | 7 | 9 | 2 |  0.50  | 0.034  |  1.00 |
| 4 | 13 | 3 | 7 | 3 |  0.90  | 0.038  |  0.90 |
| 5 | 22 | 10 | 4 | 8 |  0.25  | 0.89  |  0.58 |
| 6 | 16 | 3 | 2 | 11 |  0.96 | 0.96  |  0.0086 |
| 7 | 20 | 5 | 3 | 12 |  0.90  | 0.94 |  0.027 |
| 8 | 5 | 1 | 0 | 4 |  0.90  | 1.00 |  0.062 |
| 9 | 16 | 3 | 0 | 13 |  0.96  | 1.00 |  0.0003\* |
| 10 | 6 | 4 | 1 | 1 |  0.13 | 0.85 |  0.93 |
| 11 | 35 | 17 | 11 | 7 |  0.094  | 0.35 |  0.99 |

\*Significant after Holm-Bonferroni correction.

The number of cells in each mclust cluster from Figure 4 is shown along with the number of those cells from each of three biological replicates. P-values from binomial probability tests (see Methods) are shown and those significant after Holm-Bonferroni correction (namely Cluster 9 which was enriched for cells from replicate 3) are indicated with an asterisk.