**Supplemental Table S2.** Summary of the cell and gene filtering process

|  |  |
| --- | --- |
| Procedure | Count |
| Cells removed by library size (outside 3 x MAD range)a | 0 |
| Cells removed by number detected genes (outside 3 x MAD range) | 77 |
| Cells removed by reads mapped to mitochondrial genes (outside 3 x MAD range) | 1,559 |
| Cells removed by reads mapped to ribosomal genes (outside 3 x MAD range) | 102 |
| Cells removed by reads mapped to mitochondrial genes (> 20 % total reads)b | 0 |
| Cells removed by reads mapped to ribosomal genes (> 50 % total reads) | 0 |
| Genes removed by number of expressed cells (< 1 % total cells)c | 16,674 |
| Remaining cells post filtering | 18,787 |
| Remaining genes post filtering | 16,064 |

aMAD stands for median absolute deviation. A cell that had library size, or total genes, or mapped reads for mitochondrial genes or ribosomal genes outside the 3xMAD range was removed.

bA second round filtering using hard cut-offs for mitochondrial or ribosomal genes

cA gene that was detected in fewer than 1% of the total cells was removed