**Supplementary Table S1**

Additional information of scRNA-seq data: maximum number of counts per gene and maximum fraction

of mitochondrial reads.

| Sample ID | Maximum RNA counts per gene | Maximum percentage of mitochondrial reads |
|---|---|---|
| **100PO** | 80000 | 10 |
| **100CAF** | 60000 | 15 |
| **100PO/CAF** | 90000 | 10 |
| **107PO** | 70000 | 10 |
| **107CAF** | 60000 | 10 |
| **107PO/CAF** | 90000 | 10 |
| **112PO** | 100000 | 10 |
| **112CAF** | 30000 | 15 |
| **112PO/CAF** | 100000 | 10 |