Supplemental Table 1. Cell Capture and Sequencing Metrics for scRNAseq of C57BL/6J mouse pituitary gland fed either Control (Ctrl) or High Fat Diet (HFD)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Ctrl 1 | Ctrl 2 | HFD 1 | HFD 2 |
| Number of cells | 7,463 | 8,173 | 10,921 | 8,180 |
| Total sequence reads | 770,377,703 | 676,466,100 | 617,667,548 | 718,862,907 |
| Sequencing saturation | 79.7% | 75.7% | 78.6% | 78.8% |
| Fraction of reads in cells | 86.0% | 90.1% | 86.3% | 90.7% |
| Total genes detected | 23,199 | 23,216 | 22,759 | 23,265 |
| Mean reads per cell | 103,226 | 82,768 | 56,558 | 87,881 |
| Median genes detected per cell | 3,004 | 3,468 | 1,707 | 3,139 |
| Median UMI per cell | 9,9433 | 11,771 | 4,822 | 10,490 |
| Reads mapped to genome | 94.5% | 94.2% | 93.1% | 95.3% |
| Reads mapped uniquely to transcriptome | 73.9% | 72.6% | 70.6% | 74.3% |