

| | CSC_432 | CSC_433 | CSC_478 | POP_92 | POP_160 |
|---|-------------|-------------|-------------|-------------|-------------|
| scMultiome QC metrics | | | | | |
| Estimated Number of Cells | 6,662 | 9,250 | 6,993 | 9,218 | 8,955 |
| ATAC Median Fragments per Cell | 14,722 | 13,866 | 22,841 | 14,158 | 10,876 |
| GEX Median Genes per Cell | 5,524 | 5,623 | 999 | 5,788 | 5,089 |
| Sequenced Read Pairs (ATAC) | 366,639,797 | 431,719,511 | 305,681,942 | 381,739,526 | 440,007,550 |
| Valid Barcodes | 96.2 | 96.6 | 97.7 | 97.3 | 96.4 |
| Q30 Bases in Barcode (ATAC) | 84.3 | 85.4 | 91.1 | 90.6 | 85.6 |
| Q30 Bases in Read 1 (ATAC) | 94.3 | 94.4 | 95.6 | 95.7 | 94 |
| Q30 Bases in Read 2 (ATAC) | 92 | 93.1 | 92.6 | 92.1 | 93.2 |
| Percent Duplicates (ATAC) | 25.2 | 21.7 | 17.4 | 35.9 | 25.6 |
| Number of Peaks (ATAC) | 121,403 | 112,768 | 154,393 | 184,828 | 144,236 |
| TSS Enrichment (ATAC) | 7.75 | 6.24 | 7.07 | 7.85 | 6.14 |
| Fraction of Fragments Overlapping Peaks | 52 | 27.6 | 32.9 | 37.7 | 30.8 |
| Fraction of Fragments Overlapping TSS | 34.6 | 47.6 | 56.3 | 61.2 | 47.5 |

Joint Metrics

| | | | | | |
|------------------------------------|---------|--------|--------|---------|--------|
| Metric | | | | | |
| Feature Linkages Detected | 129,064 | 16,160 | 10,021 | 101,078 | 21,841 |
| Linked Genes | 10,835 | 4,338 | 1,323 | 11,179 | 5,227 |
| Linked Peaks | 34,289 | 12,211 | 7,751 | 38,555 | 18,038 |
| Correlation Between ATAC and GEX | | | | | |
| Number of Distal Linkages | | | | | |
| Proportion of Significant Linkages | | | | | |

Addition Metrics

| | | | | | |
|--|--------|--------|--------|--------|--------|
| Sequencing Saturation (ATAC) | | | | | |
| Sequencing Saturation (GEX) | | | | | |
| Fraction of Reads in Peaks (ATAC) | | | | | |
| Fraction of Transcripts Mapped to Genome (GEX) | 97.5 | 97.4 | 25.4 | 97.5 | 97.9 |
| Median UMI Counts per Cell (GEX) | 21,034 | 23,252 | 2,341 | 19,994 | 17,162 |
| Median Fragments per Peak (ATAC) | 14,722 | 13,866 | 22,841 | 14,158 | 10,876 |

| | | | | | |
|---|------|------|------|------|------|
| Proportion of High-Quality Fragments (ATAC) | 65.6 | 55.3 | 87 | 89.6 | 55.2 |
| Proportion of Read Pairs Passing Filters (ATAC) | 88.3 | 89.2 | 90.3 | 91.1 | 88.7 |