

Sample identification	HILO	wHILO	HISLETS
Estimated Number of Cells	4,078	4,840	3,245
Fraction Reads in Cells	88.90%	89.20%	79.70%
Mean Reads per Cell	16,482	13,496	22,195
Median Genes per Cell	1,582	1,455	1,486
Total Genes Detected	22,003	22,076	21,007
Median UMI Counts per Cell	4,754	4,220	5,618
Number of Reads	67,216,051	65,324,121	72,025,806
Valid Barcodes	98.50%	98.50%	98.60%
Reads Mapped Confidently to Transcriptome	58.30%	58.10%	64.40%
Reads Mapped Confidently to Exonic Reagions	62.20%	62.00%	68.10%
Reads Mapped Confidently to Intergenic Reagions	24%	23.70%	19.00%
Reads Mapped Confidently to Intergenic Reagions	4.70%	4.70%	4.20%
Reads Mapped Antisense to Gene	4.10%	4.00%	4.40%
Sequencing Saturation	32.30%	27.00%	38.60%
Q30 Bases in Barcode	96.80%	96.80%	96.80%
Q30 Bases in RNA Read	80.50%	79.40%	80.40%
Q30 Bases in UMI	96.40%	96.40%	96.40%
Genomic Modification	CRISPR-InsulinGFP Reporter		None
Transcriptome	GRCh38		
Chemistry	Single Cell 3' v2		
Cell Ranger Version	2.0.2		