

Sup Table S5, scRNA-seq (PBMC)

seq_id		Number of Reads	Reads Mapped Confidently to Transcriptome	Reads mapped confidently to intronic regions	Sequencing Saturation	Q30 bases in RNA read	number of cell after cut-off
gc_003	s_029	127,837,255	51.90%	31.60%	79.40%	91.00%	2,671
gc_005	s_040	140,135,847	63.40%	20.60%	73.70%	86.70%	5,320
gc_007	s_045	138,436,653	63.10%	23.60%	92.20%	90.50%	1,515
gc_009	s_067	120,096,634	64.90%	21.70%	85.60%	84.90%	3,418
gc_010	s_075	43,860,040	58.30%	27.00%	85.80%	89.90%	941