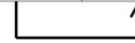


B

	Mid-secretory (LH+8)		Late-secretory		<i>In vitro</i>
	Epithelial	Stromal	Epithelial	Stromal	Stroma
Raw reads per cell	3 804 806	3 996 306	3 046 911	2 868 949	3 224 877
Low quality read rate (%)	10.14	13.60	11.37	12.69	13.01
Improper STRT read rate (%)	10.86	9.43	9.70	9.69	8.80
PCR redundancy	144.48	81.43	57.27	41.16	38.82
Qualified reads per cell	20 854	36 868	38 840	53 326	63 590
Mapped rate (%)	56.85	73.68	60.93	77.14	82.52
Mapped reads per cell (median)	6 330	21 486	7 223	37 298	55 974
Spike-in reads per cell	1 897	1 268	540	305	151
5'-end capture rate (spike-in, %)	97.69	99.18	97.23	96.36	96.65
5'-end capture rate (mRNA, %)	57.02	40.53	72.84	70.69	86.36



Supplementary Figure S2 Single-cell quality control on agarose gel and by RNA-seq. **(A)** Pooled single-cell cDNAs are amplified by PCR and loaded on 2% agarose TAE gel for QC. Equal cDNA broad smear is expected from 0.2–5 Kb range. **(B)** Epithelial and stromal cells from two biopsies were sequenced on one Illumina HiSeq2000 lane. Stromal cells from late secretory biopsy were cultivated and analysed in parallel (pointed by arrow). The description of all measured RNA-seq QC parameters are described in <https://github.com/shka/STRTprep>.