

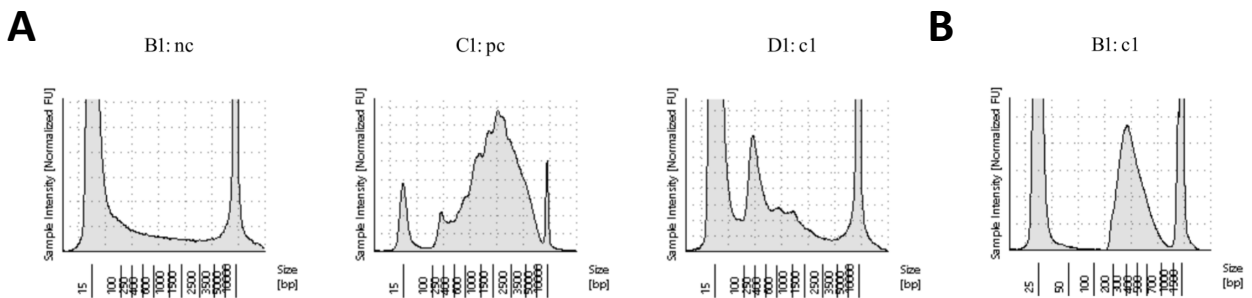
Title: Concurrent analysis of genome and transcriptome in one single cell

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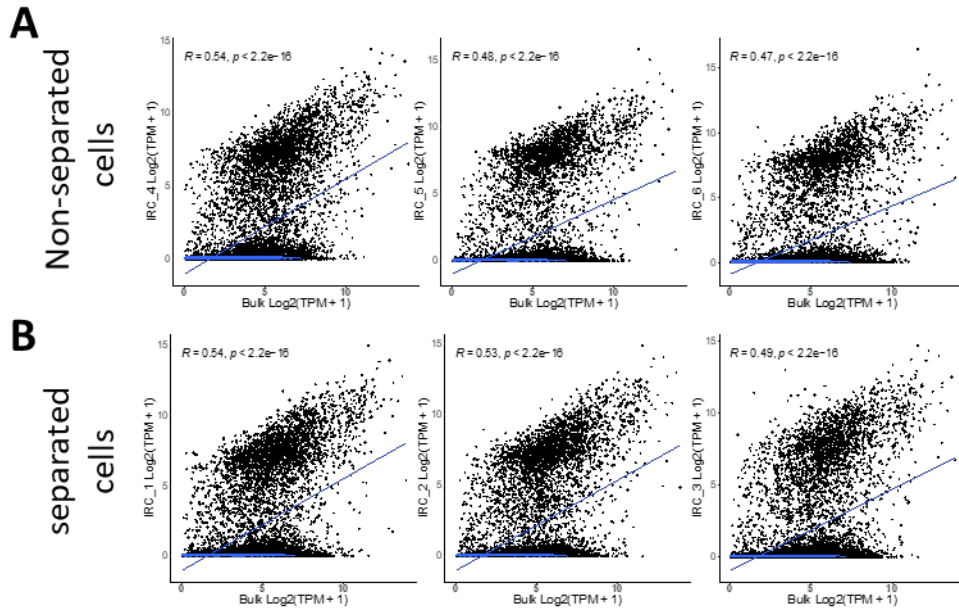
Supplementary tables and figures

Table 1: LDO results of separated and non-separated single cells. $\Delta\Delta CT$ values greater than 0.2 mark the passing of the particular genomic loci (highlighted in green).

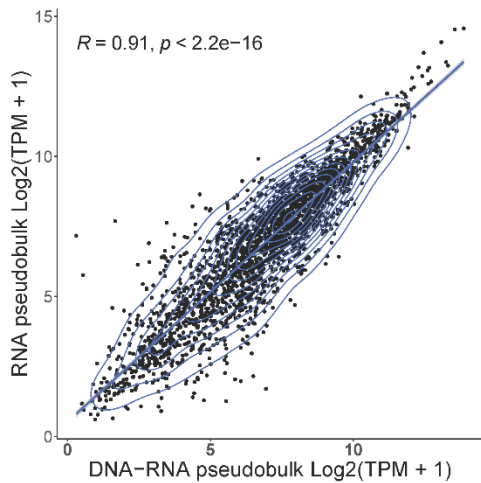
	sep_1	sep_2	sep_3	non-sep1	non-sep2	non-sep3
target 1	1.562419	1.16816	0.757456	0.20583	0.462665	0.516902
target 2	0.378329	0.924101	0.385863	0.309555	0.255154	0.138418
target 3	1.040357	0.244198	0.002706	0.463318	0.129319	0.959483
target 4	0.073058	2.03288	0.715105	0.515424	0.310383	0.23392
target 5	1.015064	0.16847	0.328062	0.629856	3.384569	0.695215
target 6	0.69544	4.320695	0.187688	0.512731	1.674983	0.411174
target 7	1.462495	0.36903	0.308607	0.828195	0.915885	0.453706
target 8	1.792035	0.791462	2.27111	0.239909	0.466191	0.295373



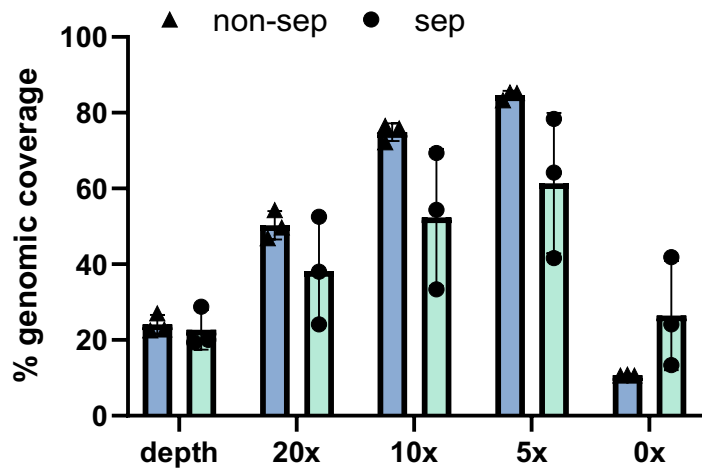
Supplementary Figure 1: Samples were run on a Tape Station device for quality control purposes. A) cDNA from separated samples. C1 represents sample selected for library preparation. B1 negative control and C1 positive control (1ng RNA as input). B) Final library of separated samples after amplification.



Supplementary Figure 2: Single cell gene expression correlates with mRNA expression of bulk. A) Overlapping genes in pseudo bulk consisting of three non-separated single cells and bulk. D) Overlapping genes of pseudo bulk from three separated single cells and bulk.



Supplementary Figure 3: The pseudo bulks from mRNA of separated and non-separated cells correlate well.



Supplementary Figure 4: Genomic coverage across single cells.