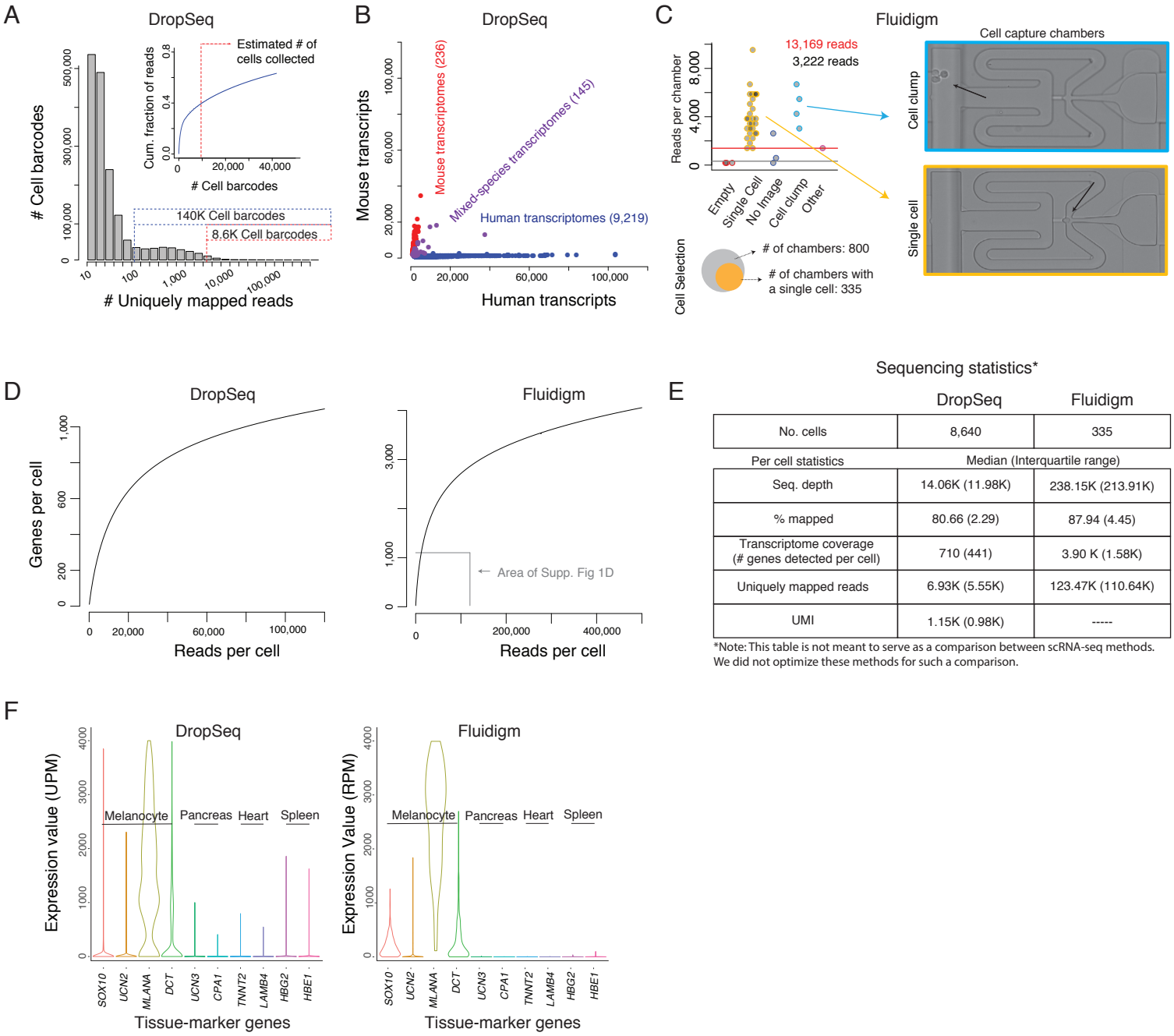
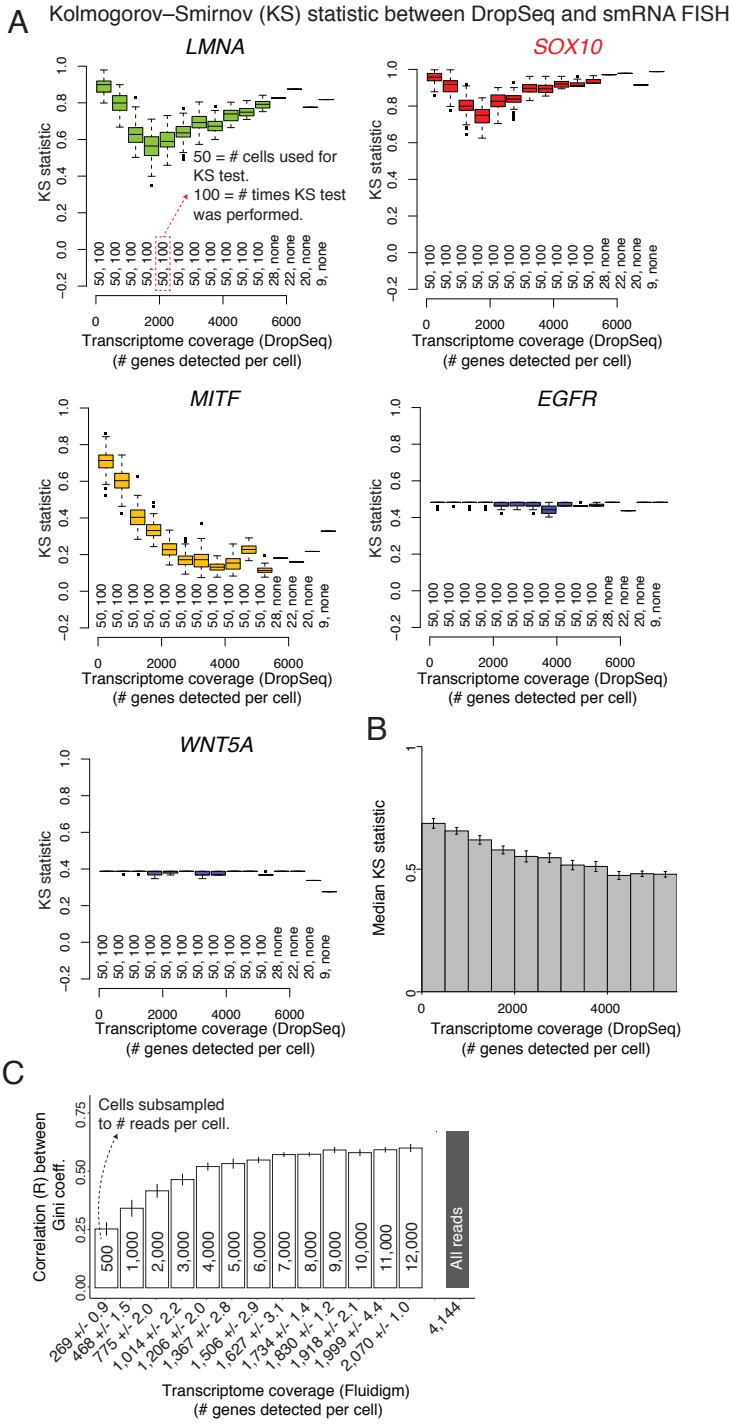


	DropSeq	Fluidigm
No. cells	8,640	335
Per cell statistics	Median (Interquartile range)	
Seq. depth	14.06K (11.98K)	238.15K (213.91K)
% mapped	80.66 (2.29)	87.94 (4.45)
Transcriptome coverage (# genes detected per cell)	710 (441)	3.90 K (1.58K)
Uniquely mapped reads	6.93K (5.55K)	123.47K (110.64K)
UMI	1.15K (0.98K)	-----

*Note: This table is not meant to serve as a comparison between scRNA-seq methods. We did not optimize these methods for such a comparison.

Supplemental Figure 1. Related to Figure 2. (A) Distribution of reads across all barcodes sequenced in DropSeq represented as the number of cell barcodes containing a given number of uniquely mapped reads (main figure), and the cumulative fraction of reads as a function of the number of barcodes (inset). (B) Scatterplot representing the number of human and mouse transcripts associated with each cell barcode in the DropSeq dataset. (C) Distribution of reads across a capture chamber in Fluidigm's platform (top left), example of a single cell (yellow) as well as a cell clump (blue) inside the cell capture chambers (right), and proportion of cell capture chambers containing a single cell (bottom left). (D) Sequencing coverage assessed as the number of genes detected per cell as a function of the number of reads obtained for each cell for DropSeq (left) and Fluidigm (right). (E) Sequencing statistics for libraries built with DropSeq (n = 1 biological replicate) and Fluidigm (n = 1 biological replicate). This table is not meant to serve as a comparison between single cell RNA sequencing methods. We did not optimize either platform for such a comparison. (F) Gene expression estimates of tissue-marker genes for DropSeq (left) and Fluidigm (right).



Supplemental Figure 2. Related to Figure 3. (A) Comparison of the gene expression distribution (Kolmogorov-Smirnov statistic) for five genes (LMNA, SOX10, MITF, EGFR, and WNT5A) measured by DropSeq and single molecule RNA FISH (smRNA FISH). We measured the KS statistic across different levels of transcriptome coverage (# genes detected per cell). Unless otherwise indicated, at each level of transcriptome coverage the KS test was repeated 100 times, each time randomly sampling 50 cells from the population. The distribution of KS values across bootstrap replicates is depicted as a boxplot. (B) Median KS statistic between DropSeq and single molecule RNA FISH of 26 genes across varying degrees of transcriptome coverage. Bar height indicates the average across bootstrap replicates. Error bars represent ± 1 standard deviation across bootstrap replicates. (C) Correlation between Gini coefficient estimates measured by Fluidigm and single molecule RNA FISH after subsampling cells with high transcriptome coverage to different degrees of reads depth. The numbers inside the bars represent the number of reads subsampled. The average number of genes detected across all cells at a given subsample depth is reported in the x-axis. Error bars represent ± 1 standard deviation across bootstrap replicates.