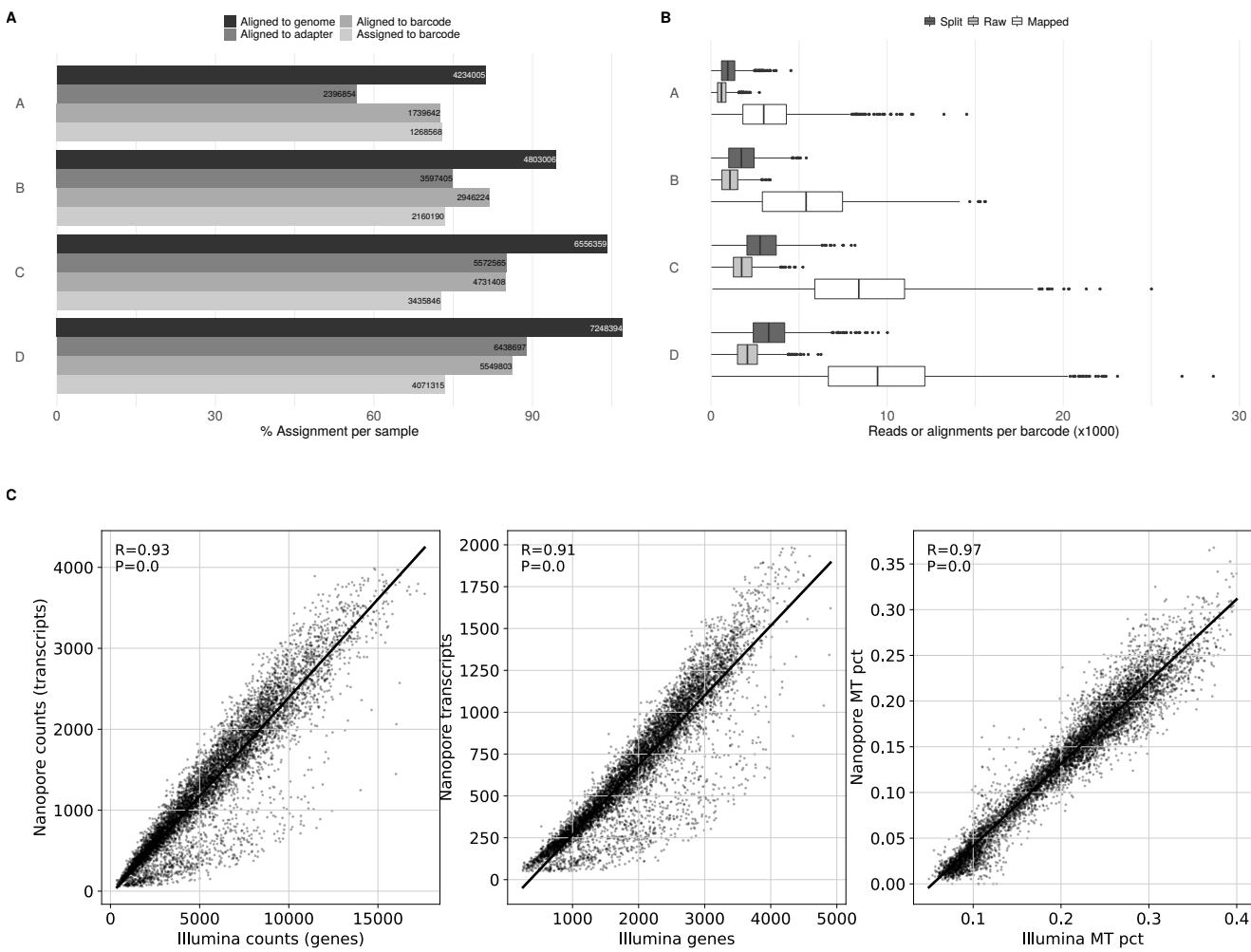
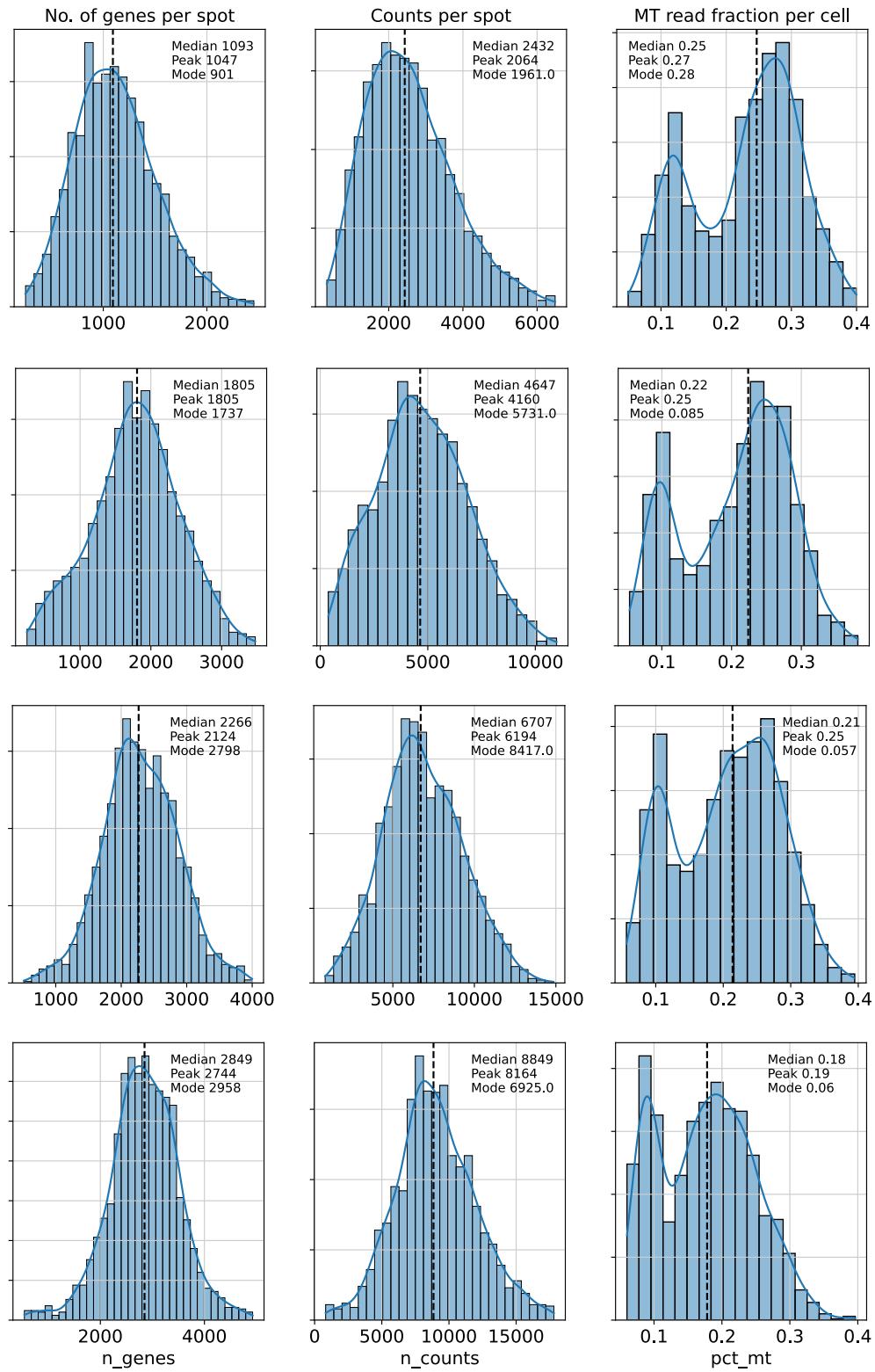


## Supplementary Material

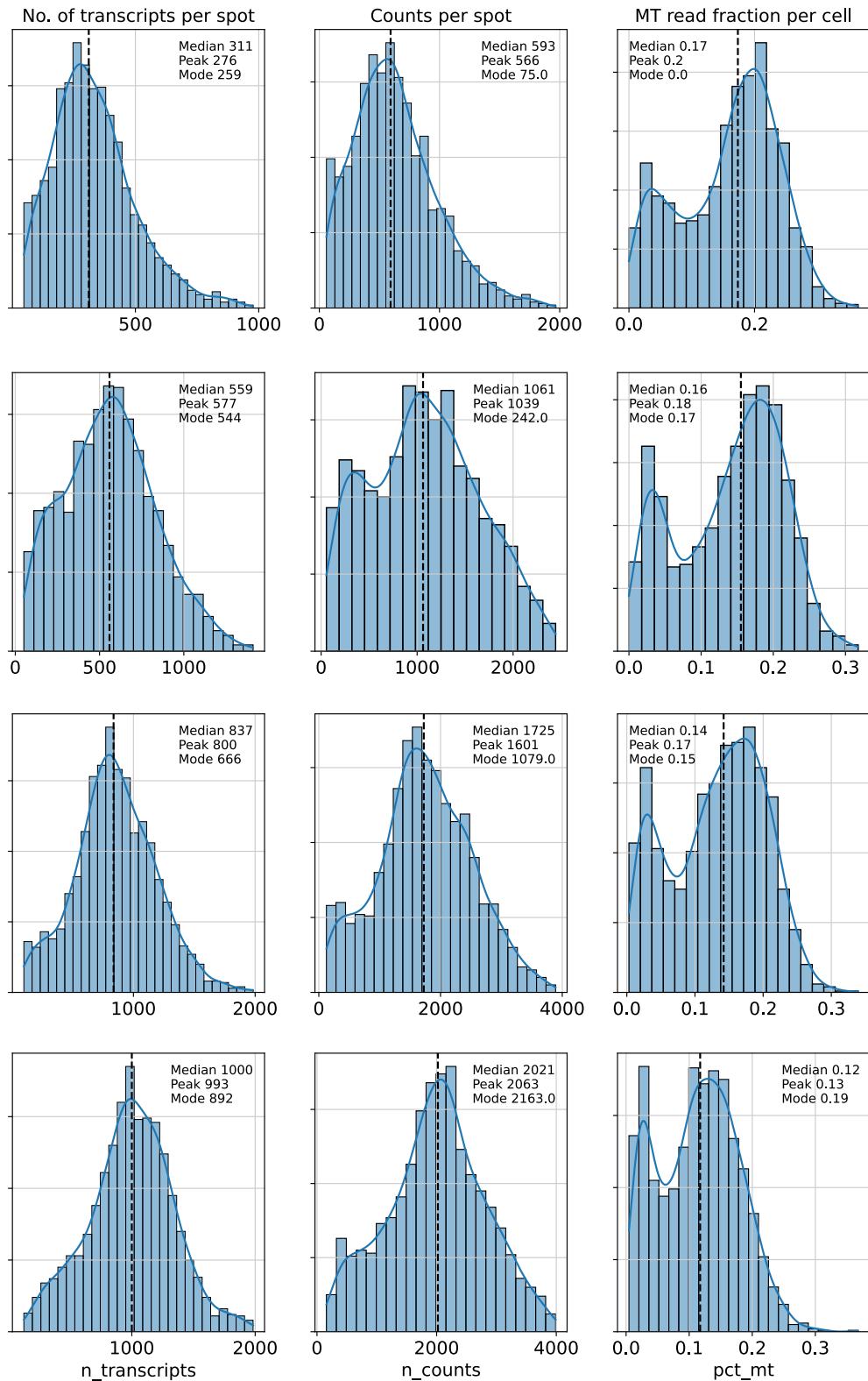
### 1 SUPPLEMENTARY TABLES AND FIGURES



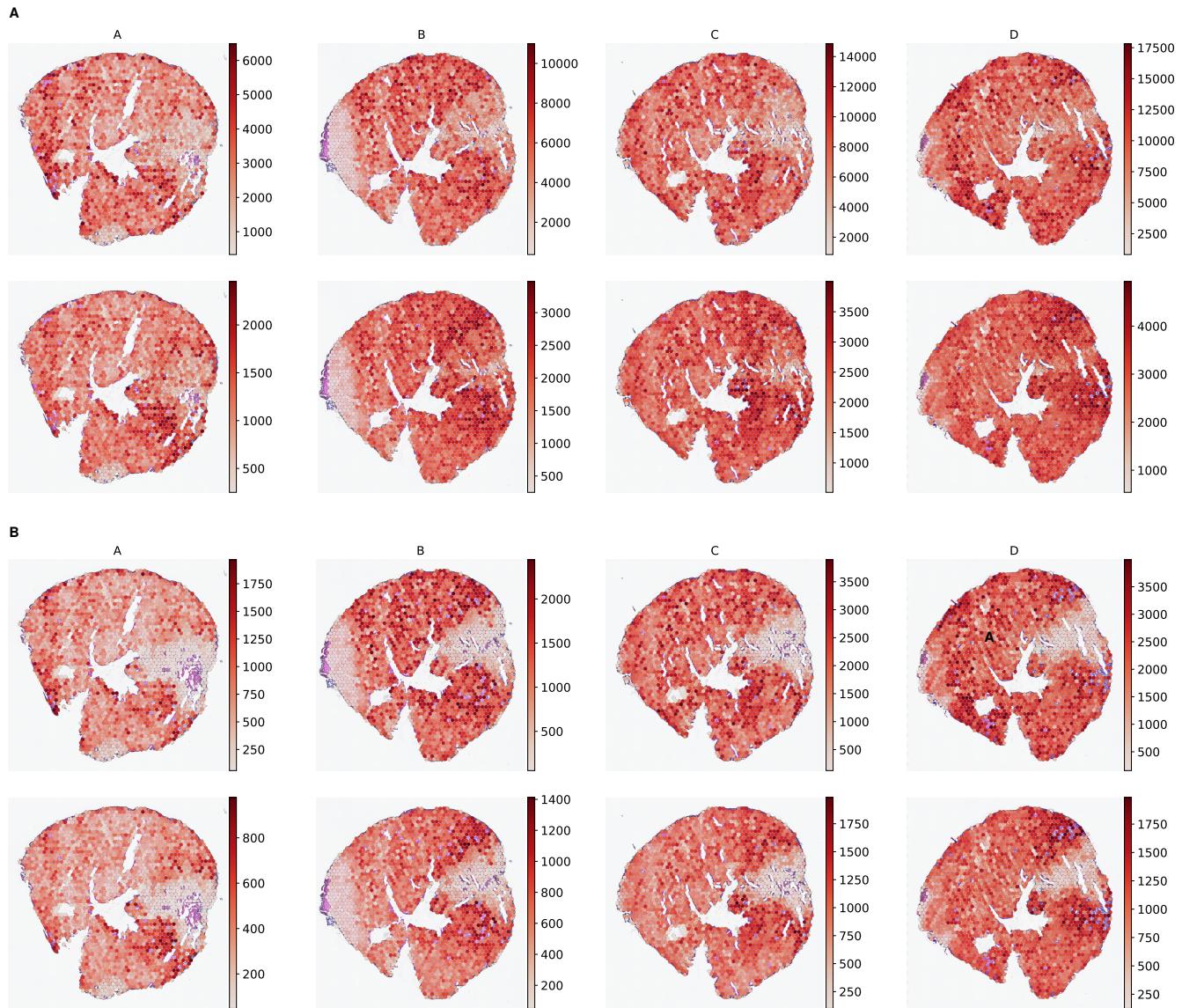
**Figure S1.** scNAST methodology. A Percentage of assignment by SCNAPBAR at each step of the workflow for each heart slice (reads shown in bars). Reads aligned to genome are shown as a percentage of total reads. B Number of reads (or alignments) for each heart slice per spatial barcode. Split alignments are obtained from the genome mapped reads in SCNAPBAR. Raw reads correspond to primary alignments converted to FASTQ format. Mapped are alignments to the transcriptome used for transcript abundance quantification. C Scatter plots showing the correlation between read counts, genes or transcripts, and the percentage of mitochondrial reads between Illumina and Nanopore libraries for all four samples, using the intersection of common spatial barcodes after quality filtering.



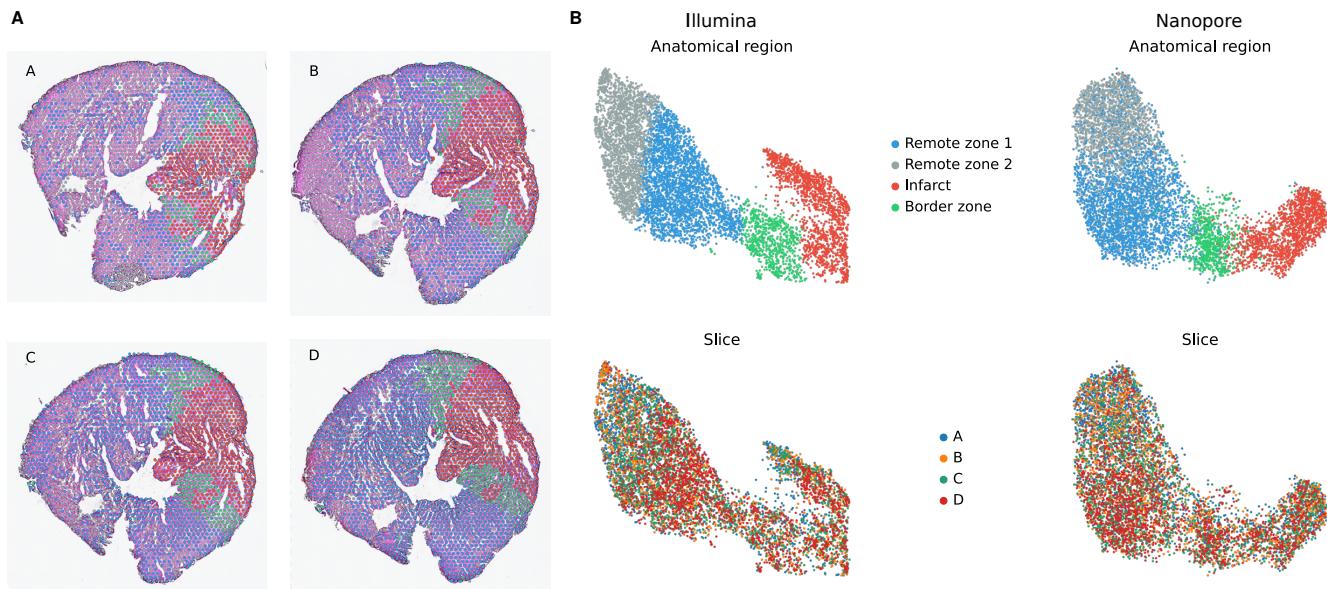
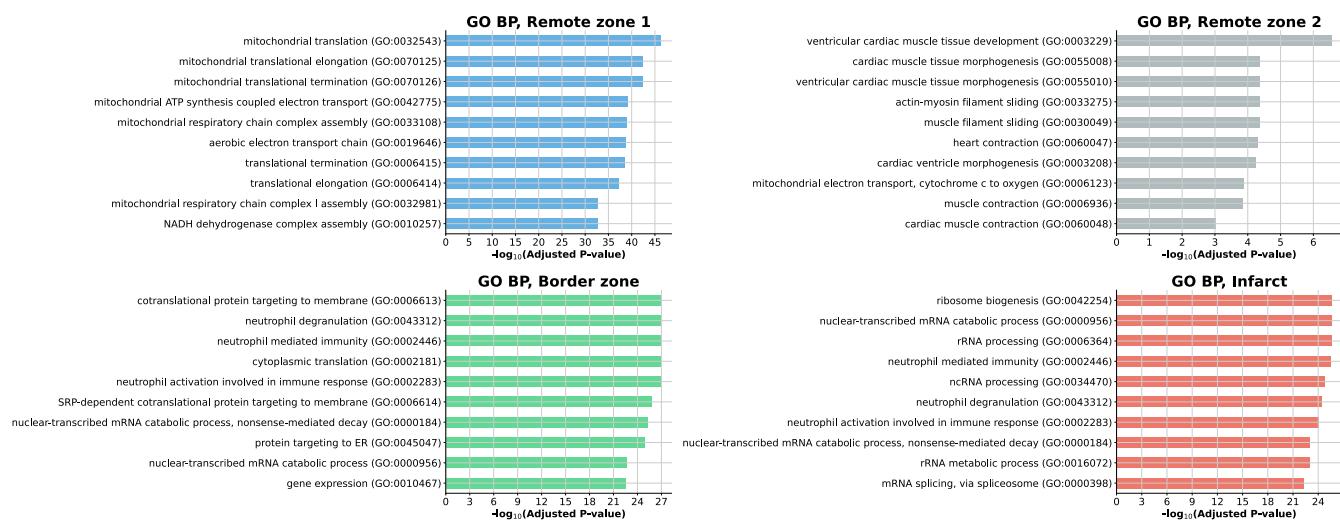
**Figure S2.** Quality control (Illumina). Distribution of number of genes, UMIs, and mitochondrial fraction per spatial spot after quality filtering, for each heart slice. From top to bottom: A, B, C, and D.



**Figure S3.** Quality control (Nanopore). Distribution of number of transcripts, counts, and mitochondrial fraction per spatial spot after assignment and quality filtering, for each heart slice. From top to bottom: A, B, C, and D.



**Figure S4.** Spatial distribution of UMIs or counts (top) and genes or transcripts (bottom), for each A Illumina and B Nanopore libraries, for each heart slice (from left to right).

**Figure S5.****Figure S6.**

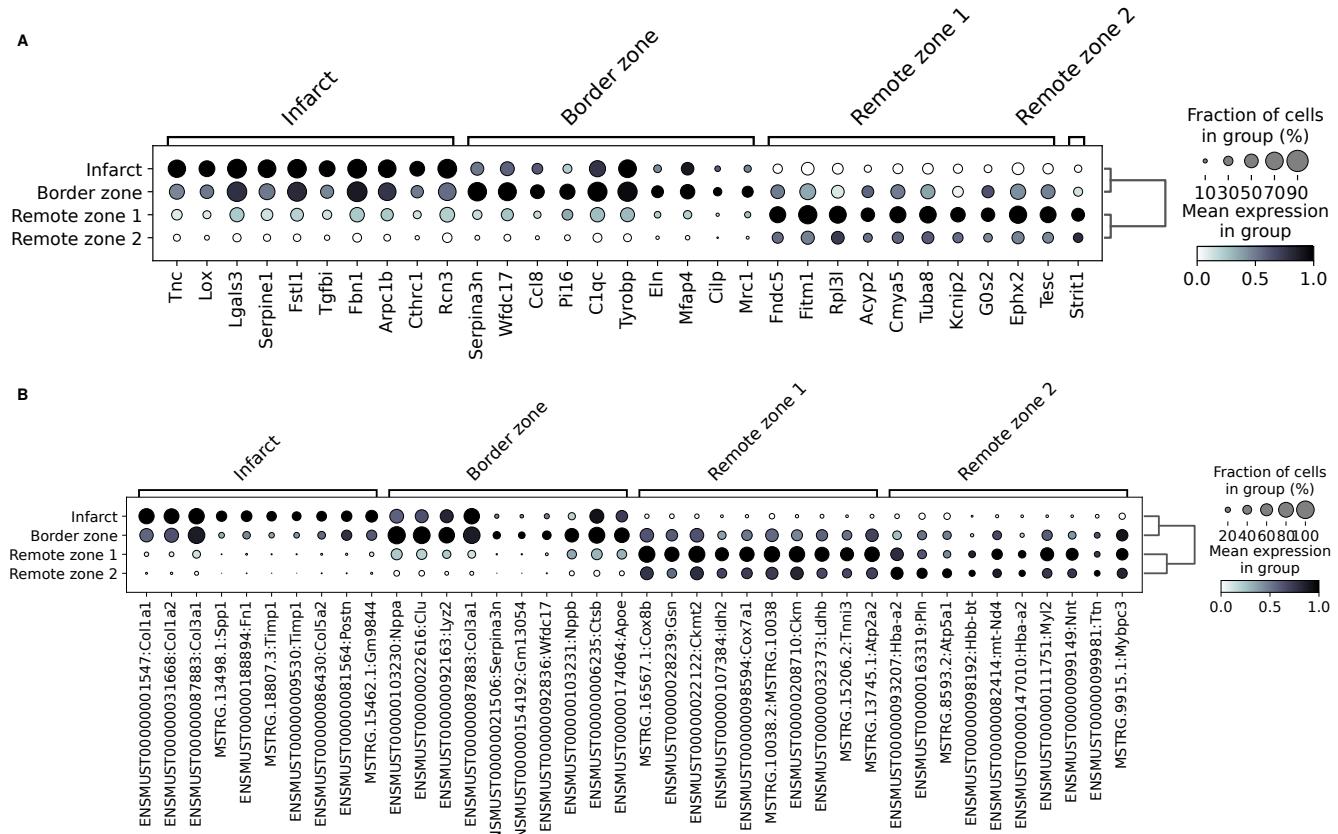


Figure S7.