Supplementary Materials for

Spatiotemporal reconstruction of the origin and assembly of smooth muscles in the intestinal villus

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Materials and methods

Sample preparation for single-cell RNA sequencing

Timed-pregnant C57BL/6J mice were purchased from Jackson's laboratory. We collected midguts - gut tubes extending from after the stomach to the end of the protruding midgut and the attached dorsal mesentery from E12.5 and E14.5 embryos. We collected 60 midguts at E12.5 and 35 midguts at E14.5. From E16.5, E18.5, and P1.5 stages, we dissected open the small intestine extending from after the stomach to the end of the ileum and flushed it with ice-cold PBS. The mesentery of the duodenum was disposed of to prevent sampling of the pancreas. We sampled small intestines from 2 animals each for stages E16.5, E18.5, and P1.5. Samples were stored in cold PBS on ice for not more than 30 minutes before processing. When enough samples of a particular stage were collected, the tissue was cut into ~1 mm pieces and transferred into a solution of Collagenase Type 1 (200 units/ml) and Hyaluronidase (100 units/ml) under mild agitation at 37°C. 5μl of the cell suspension was plated onto a hemocytometer every 5 minutes after 20 minutes of agitation and checked for the extent of dissociation. All samples reached a near single-cell suspension by the 35 - 40-minute mark and were passed through a 40 μm filter and centrifuged into a pellet. Following that, samples were resuspended in PBS containing 0.04% bovine serum albumin. Before loading the cells on 10x Chromium, Trypan Blue-stained cells from each sample were counted on an automated cell counter to determine their viability. The samples' cell viability ranged from 83-88% after adjusting for the cell size threshold. To obtain the appropriate number of transcriptomes from viable cells (10,000 cells each for E12.5 and E14.5 stages, and 5000 each for E16.5, E18.5, and P1.5 stages), we adjusted the number of cells loaded on 10x Chromium using these cell viabilities. Sequencing libraries were prepared according to the 10x Genomics 3' scRNA-seq library preparation protocol (v3) and were then sequenced on NextSeq550 75bp kit.

Single-cell RNA-seq data processing and visualization

Sequencing reads for scRNA-seq experiments were aligned to the mm10 mouse genome (assembly: GRCm38; release-93) to generate gene expression count matrices. The demultiplexing, barcode processing, gene counting, and aggregation were performed using the Cell Ranger software v3.1.0 (10x Genomics). Gene expression matrices were then read using Scanpy (v-1.8.1) package (*78*). Transcriptomes coming from more than one cell were then labeled and removed from individual scRNA-seq datasets using the scrublet (v-0.1) package (*79*). Cells with less than 200 unique genes and genes detected in less than 10 cells were excluded from the analysis. Cells with more than 30% mitochondrial transcripts were removed as stressed/ dying cells. After quality control filtering, we analyzed a total of 37,277 single-cell transcriptomes (E12.5: 10541 cells; E14.5: 11530; E16.5: 5227 cells; E18.5: 5271 cells; P1.5: 4708 cells) across five developmental stages. The scRNA-seq data was then normalized and highly variable genes were selected with min_disp=0.5 and max_mean=3 thresholds. We then performed mean centering and scaling while regressing out total UMI counts, percent mitochondrial UMIs, S score, and G2M score, followed by principal component analysis (PCA) to reduce the dimensions of the data to the top 30 principal components. Uniform Manifold Approximation and Projection (UMAP) and the Nearest Neighbor (NN) graph were initialized in this PCA space. The cells were then clustered using the Leiden method (resolution=0.5). Differential gene expression analysis (DGEA) was performed using the rank_gene_groups function in Scanpy with the two-sided Wilcoxon statistical method. Cell-type-specific canonical gene markers along with DGEA were used to assign cell-type labels. Trajectory inference on the cell type-labeled scRNA-seq data was performed using the Partition-based graph abstraction (PAGA) method (*80*). PAGA map was used to initialize UMAP reductions to preserve and visualize the global topology of data at the used clustering resolutions. PAGA map was then overlaid on UMAP using the Scanpy package for visualizing the global relationships between cell types. Normalized gene expression was visualized on DotPlots, UMAP plots, and Violin plots across cell type groups. RNA velocities for single cells were calculated and visualized with the scVelo (v-0.2.4) package (*16*, *81*). A few cell-type clusters representing cell states of the same cell type were grouped into broad cell-type groups using cell-type-specific genes and then used for downstream analysis.

Subclustering and analysis of intestinal mesenchymal cells and mesenchymal fibroblast cells

Normalized gene expression for all mesenchymal cell types was extracted from the combined scRNA-seq dataset. We used Scanpy to reselect the highly variable genes within that cell type group with min_disp = 0.5 and max_mean = 3 thresholds. We then performed mean centering and scaling while regressing out total UMI counts, percent mitochondrial transcripts, S score, and G2M score, followed by principal component analysis (PCA) to reduce the dimensions of the data to the top 30 principal components (PCs). Uniform Manifold Approximation and Projection (UMAP) and the Nearest Neighbor (NN) graph were initialized in this PCA space using the first 20 PCs. The cells were then reclustered using the Leiden method (resolution = 0.5) to get mesenchymal cell-type clusters. Clusters expressing colon-specific genes such as *Hoxd9*, *Hoxa9*, *Colec10*, and *Adamdec1* were excluded from the analysis. The remaining mesenchymal cells were reprocessed and clustered (resolution = 0.7) to update the mesenchymal cell type clusters. Cell-type-specific canonical gene markers along with DGEA were used to assign cell-type labels. Trajectory inference on the cell type-labeled mesenchymal scRNA-seq data was performed using the Partition-based graph abstraction (PAGA) method. PAGA graph was used to initialize UMAP reductions to preserve and visualize the global topology of data at the used clustering resolutions. PAGA map was then overlaid on UMAP using the Scanpy package for visualizing the global relationships between mesenchymal cell types. Normalized gene expression for differentially expressed genes and genes of interest was visualized on DotPlots and UMAP plots across cell-type subgroups. Normalized gene expression for the fibroblast clusters was extracted from the small intestinal mesenchymal scRNA-seq dataset. Fibroblast cells were then preprocessed and clustered (resolution = 0.4) to derive fibroblast subtype clusters. DGEA was used to assign fibroblast subtype labels.

Animal Models

Rosa26 CAG-tdTomato (JAX stock #007905) (*41*), Pdgfra CreERT2 (JAX stock #032770) (*40*), Tnc CreERT2 (a gift from C. M. Hao) (*55*), Hoxb6 Cre (JAX stock #017981) (*67*), Prox1 CreERT2 (JAX stock #022075) (*68*), Notch3 flox (a gift from J. Kitajewski and N. Adler) (*65*), Dll4 flox (*66*), Prox1-GFP (RRID:MMRRC_031006-UCD) (*64*) mice were previously described. All were maintained in Cornell university's pathogen-free barrier facility and were kept on a 12-hour light/dark cycle, with free access to standard chow pellets (Envigo) and water. All the mice used for mating were 2-6 months of age. Dams and studs were housed separately before timed mating. To track pregnancy progression, timed mated breeding pairs were checked every morning and separated upon finding a vaginal plug, staged as E 0.25. Post-natal stages are defined upon birth as P0. Sex was not taken into experimental consideration for embryonic stages and postnatal stages until P9. Only female mice were collected at stages beyond P9. Tail and toe snips collected from embryonic and postnatal mice respectively were used for genotyping by PCR amplification. For direct comparison, littermates of different genotypes were sorted into the same procedure. All animal experiments adhered to the guidelines of the Institutional Animal Care and Use Committee of Cornell University and were conducted within the scope of an approved animal protocol.

Cornell University operates its animal care and uses program under the Animal Welfare Assurance on file with the Office of Laboratory Animal Welfare.

Induction of Cre recombinase activity

Cre recombinase was activated to induce lineage tracing and gene knockout by intraperitoneal injection of tamoxifen (Sigma Aldrich, 45T5648) or 4-hydroxytamoxifen (4OHT) (Sigma Aldrich, H6278), the active metabolite of tamoxifen in peanut oil (Sigma, P2144), except for P0 pups where intragastric injections were performed (*82*). *Pdgfra CreERT2* and *Prox1 CreERT2* expressing strains were induced with a single dose of 30 mg/kg of 4OHT. This strategy was chosen as it resulted in visibly saturated reporter expression in crypt and villus mesenchymal cells and lacteals respectively and did not produce developmental defects in the WT and Cre+ mice induced in the prescribed intervals. 4OHT was suitable for this induction since *Pdgfra* and *Prox1* are genes constitutively expressed by villus fibroblast-like cells and lacteals respectively. *Tnc CreERT2* expressing strains were induced with a single dose of 100 mg/kg of tamoxifen. Tamoxifen was preferred to 4OHT since it allowed targeting of cells that express *Tnc* over a broader window to be labeled and did not produce developmental defects in the WT and Cre+ mice induced in the prescribed intervals. Using 4OHT to induce Tnc CreERT2 resulted in sparse reporter labeling and variability in labeling between replicate induction experiments.

Mouse tissue collection, staining procedures, and image acquisition

Whole-mount and section immunostaining of embryonic, perinatal, and adult intestinal tissue was adapted from previously described protocols (*24*, *83*, *84*). Briefly, the first jejunal loop was dissected from mice of specified stage and genotype in ice-cold 1X PBS, immediately followed by PBS washes and fixed overnight at 4°C in 4% paraformaldehyde (PFA)/PBS or into ice-cold

100% MeOH - suitable for detecting SMA^{low} cells and removing the fluorescence from endogenous reporters. Tissues fixed in PFA were washed into PBS and stored at 4°C up to a week before whole-mount immunostaining or processed for cryosectioning by dehydrating in a gradient of sucrose/PBS solutions, embedded in OCT Compound (Tissue-Tek), and stored in −80°C until sectioning. Tissues that were fixed in 100% MeOH were stored at −20°C and rehydrated into PBS with 0.1% Tween-20 before whole-mount immunostaining or being processed for cryosectioning as described above. All frozen sections were 15 μm thick. For immunostaining frozen sections, antigen retrieval was performed with a citrate-based antigen unmasking solution. Sections were then permeabilized with 0.1% Triton X-100 in PBS for 30 min, blocked in 3% BSA in PBS for 2 hours at room temperature, and incubated with primary antibodies diluted in blocking solution for 12-16 hours at 4°C. Sections were then washed and incubated with appropriate secondary antibodies (Invitrogen, 1:500) and DAPI (Invitrogen P36930, 1:1000, nuclear label) at room temperature for 1 hour. Samples were mounted in ProLong Gold Antifade Mountant (Thermo Fisher, P36930), and stored in the dark until imaging. For whole-mount immunostaining, tissues were blocked in 3% BSA, serum, and 0.3% Triton X-100 in PBS at 4°C for 12-16 hours, then incubated with primary antibodies 24-48 hours at 4°C. After washing for 6 hours in PBS with 0.3% Triton X-100 at room temperature, changing the wash every 30 mins, tissues were incubated in secondary antibody (1:500) for 12-16 hours at 4°C. Tissues were once again washed for 6 hours in PBS with 0.3% Triton X-100 at room temperature, changing the wash every 30 mins, and then post-fixed in 4% PFA for 12-16 hours at 4°C. Tissues were washed into PBS, sliced into 100-200 μm thick layers, and mounted with ProLong Gold Antifade Mountant. The following primary antibodies were used at a 1:100 dilution unless specified otherwise: SMA-FITC (Sigma, F3777), SMA-Cy3 (Sigma, C6198), PDGFRα (BD Biosciences, 558774), TNC (R&D, MAB2138), E-

CAD (Invitrogen, 14324980), FOXP2 (1:250, Abcam, ab16046), NOTCH3 (Abcam, ab23426), DLL4 (R&D, AF1389), LYVE1 (Abcam, ab14917), NRP2 (R&D, AF567), HEY2 (Proteintech, 10597), MCAM (Abcam, ab75769), RFP (Rockland, 600401379). Mounted samples were imaged on a Zeiss LSM 710 (Inverted Axio Observer.Z1) confocal microscope using 25x and 63x lenses. To capture the entire villi, multiple adjacent fields of view were stitched together on the Zeiss Zen platform before exporting images for further analysis. Image processing, confocal image stacking, and quantifications were performed using FIJI and Imaris 9.5.

Statistical quantification

We quantified the contribution of Pdgfra and Tnc lineage to villus SM formation from confocal z-stacks of villi taken at 1μm intervals, blinded to the genotype and stage of the images. Quantifications were made for ~15 villi from each biological replicate, with 3 biological replicates being analyzed for each lineage tracing induction interval (P0-P9, P9-P18, P18-P27). Individual villus SM fibers from each villus were analyzed for the presence of any tdTomato+ labeling colocalizing with $\mathrm{SMA}^{\mathrm{high}}$ expression. The contribution was calculated as the ratio of $\mathrm{SMA}^{\mathrm{high}}$ fibers with at least one tdTomato+ cell to the total number of $\mathrm{SMA}^{\mathrm{high}}$ fibers counted. Statistical analyses and graphical plotting were performed in GraphPad Prism 8 (La Jolla, CA). Comparison between different lineage tracing induction intervals was tested with one-way ANOVA and multiple comparisons with Tukey's correction. Data were expressed as the mean of the means from each biological replicate ± standard error of the mean (SEM).

We quantified the structural changes in the villus muscular-lacteal upon inducible knockout of *Notch3* and *Dll4* from maximum intensity projections of confocal z-stacks on FIJI, blinded to the genotype of the images. Quantifications were made for 25 villi from each biological replicate, with 3 biological replicates analyzed for each of the genotypes. Lacteal lengths were measured as to the highest LYVE+ cell, not considering any filopodia that might be projecting from it. Villus SM lengths were measured as the highest point reached by a SMA^{high} fiber in a particular villus, not considering the status of other fibers in the same villus. Lacteals, villus SM, and villus lengths were consistently measured for each villus and used for internal normalizations. Statistical analyses and graphical plotting were performed in GraphPad Prism 8 (La Jolla, CA). The spread of normalized measurements from each biological replicate was visualized as violin plots. Normalized values were sorted into bins and the data were plotted as the mean of the percentage fraction of values that fit into each bin on all the biological replicates. Cell protrusion longer than or equal to 6 µm was defined as lacteal filopodia for analysis. Comparison between genotypes was performed by two-way ANOVA with Šídák's correction or unpaired, two-tailed Student’s t-test. Data were expressed as the mean of the means from each biological replicate ± standard error of the mean (SEM).

Supplementary figure legends

Figure S1: **Single-cell RNA-seq analysis of developing mouse intestine at four embryonic and one postnatal stage of development. (A)** The number of unique genes detected per cell (left), number of unique transcripts per cell (center), and percentage of mitochondrial transcripts (right) in intestinal scRNA-seq datasets from five developmental stages. **(B)** Bar plot showing the number of viable intestinal cell transcriptomes captured in scRNA-seq experiments. **(C)** Dendrogram showing hierarchical clustering of single-cell transcriptomes from intestinal cell types across five developmental stages. **(D)** Pie chart showing the fraction of UMIs mapping to spliced and unspliced transcripts (left) and stacked bar plot showing changes in the fraction of spliced and unspliced molecules across mouse development stages (right). **(E)** Bar plot showing the proportion of cells from cell types in gut epithelium lineage across developmental stages. **(F)** Bar plot showing the proportion of cells from cell types in gut vasculature lineage across developmental stages.

Fig. S1

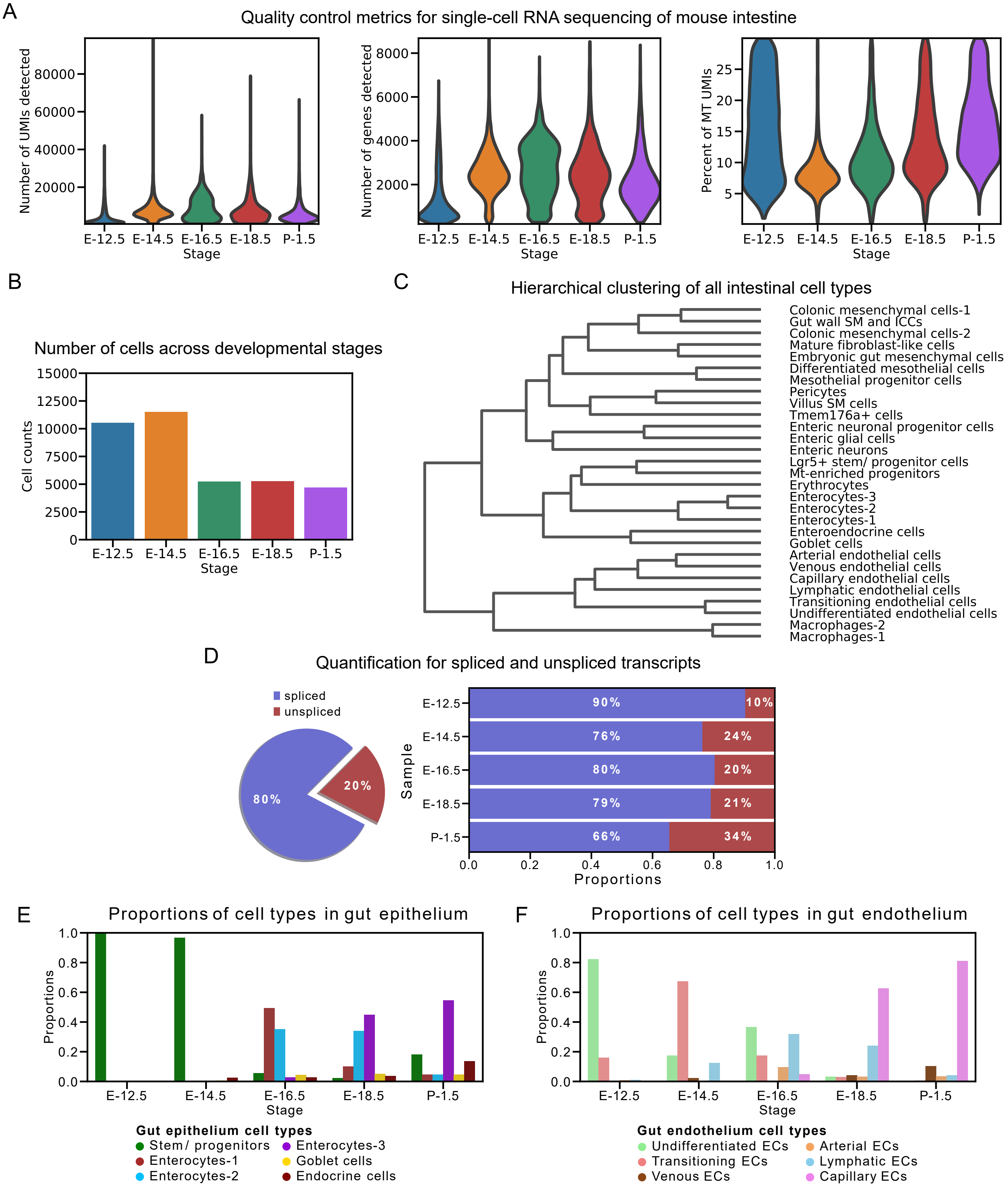

A
Quality control metrics for single-cell RNA sequencing of mouse intestine
Number of UMIs detected
80000
60000
40000
20000
Number of genes detected
8000
6000
4000
2000
Percent of MT UMIs
25
20
15
10
5
E-12.5
E-14.5
E-16.5
E-18.5
P-1.5
Stage
B
Number of cells across developmental stages
Cell counts
15000
12500
10000
7500
5000
2500
0
E-12.5
E-14.5
E-16.5
E-18.5
P-1.5
Stage
C
Hierarchical clustering of all intestinal cell types
Colonic mesenchymal cells-1
Gut wall SM and ICCs
Colonic mesenchymal cells-2
Mature fibroblast-like cells
Embryonic gut mesenchymal cells
Differentiated mesothelial cells
Mesothelial progenitor cells
Pericytes
Villus SM cells
Tmem176a+ cells
Enteric neuronal progenitor cells
Enteric glial cells
Enteric neurons
Lgr5+ stem/ progenitor cells
Mt-enriched progenitors
Erythrocytes
Enterocytes-3
Enterocytes-2
Enterocytes-1
Enteroendocrine cells
Goblet cells
Arterial endothelial cells
Venous endothelial cells
Capillary endothelial cells
Lymphatic endothelial cells
Transitioning endothelial cells
Undifferentiated endothelial cells
Macrophages-2
Macrophages-1
D
Quantification for spliced and unspliced transcripts
spliced
unspliced
80%
20%
Sample
E-12.5
90%
10%
E-14.5
76%
24%
E-16.5
80%
20%
E-18.5
79%
21%
P-1.5
66%
34%
0.0
0.2
0.4
0.6
0.8
1.0
Proportions
E
Proportions of cell types in gut epithelium
Proportions
1.0
0.8
0.6
0.4
0.2
0.0
E-12.5
E-14.5
E-16.5
E-18.5
P-1.5
Stage
Gut epithelium cell types
Stem/ progenitors
Enterocytes-1
Enterocytes-2
Enterocytes-3
Goblet cells
Endocrine cells
F
Proportions of cell types in gut endothelium
Proportions
1.0
0.8
0.6
0.4
0.2
0.0
E-12.5
E-14.5
E-16.5
E-18.5
P-1.5
Stage
Gut endothelium cell types
Undifferentiated ECs
Transitioning ECs
Venous ECs
Arterial ECs
Lymphatic ECs
Capillary ECs

Figure S2: **Single-cell RNA-seq analysis of mouse intestinal mesenchymal cells across development. (A)** UMAP plot of 9,445 single-cell transcriptomes from gut musculature at embryonic stages (E12.5, E14.5, E16.5, and E18.5) and one postnatal stage (P1.5), clustered by gene expression and colored by cluster labels. **(B)** UMAP plots showing mouse development stages for the gut musculature scRNA-seq data. **(C)** UMAP plot showing the expression of colon tissue-specific gene markers in the gut musculature scRNA-seq data. **(D)** Dot plot showing the differential gene expression analysis results for mesenchymal cell types in the small intestine. Cell type labels based on UMAP in Fig. 2A. **(E)** Heatmap showing the differential gene expression analysis results for three distinct smooth muscle clusters in the small intestinal scRNA-seq data.

Fig. S2

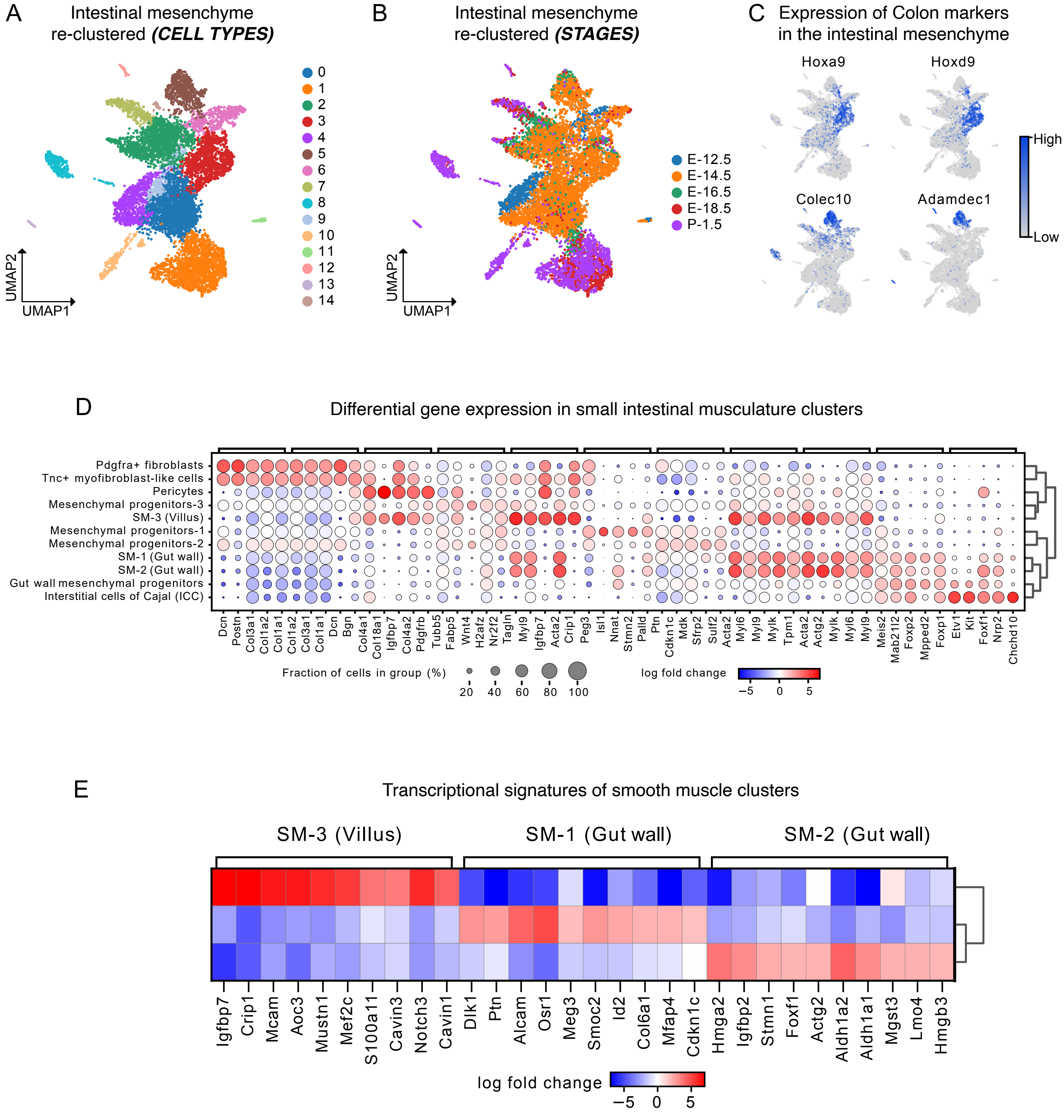

A
Intestinal mesenchyme
re-clustered (CELL TYPES)
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
UMAP2
UMAP1
B
Intestinal mesenchyme
re-clustered (STAGES)
E-12.5
E-14.5
E-16.5
E-18.5
P-1.5
UMAP2
UMAP1
C
Expression of Colon markers
in the intestinal mesenchyme
Hoxa9
Hoxd9
Colec10
Adamdec1
High
Low
D
Differential gene expression in small intestinal musculature clusters
Pdgfra+ fibroblasts
Tnc+ myofibroblast-like cells
Pericytes
Mesenchymal progenitors-3
SM-3 (Villus)
Mesenchymal progenitors-1
Mesenchymal progenitors-2
SM-1 (Gut wall)
SM-2 (Gut wall)
Gut wall mesenchymal progenitors
Interstitial cells of Cajal (ICC)
Dcn
Postn
Col3a1
Col1a2
Col1a1
Col1a2
Col3a1
Col1a1
Dcn
Bgn
Col4a1
Col18a1
Igfbp7
Col4a2
Pdgfrb
Tubb5
Fabp5
Wnt4
H2afz
Nr2f2
Tagln
Myl9
Igfbp7
Acta2
Crip1
Peg3
Isl1
Nnat
Stmn2
Palld
Ptn
Cdkn1c
Mdk
Sfrp2
Sulf2
Acta2
Myl6
Myl9
Mylk
Tpm1
Acta2
Actg2
Mylk
Myl6
Myl9
Meis2
Mab21l2
Foxp2
Mpped2
Foxp1
Etv1
Kit
Foxf1
Nrp2
Chchd10
Fraction of cells in group (%)
20
40
60
80
100
log fold change
−5
0
5
E
Transcriptional signatures of smooth muscle clusters
SM-3 (Villus)
SM-1 (Gut wall)
SM-2 (Gut wall)
Igfbp7
Crip1
Mcam
Aoc3
Mustn1
Mef2c
S100a11
Cavin3
Notch3
Cavin1
Dlk1
Ptn
Alcam
Osr1
Meg3
Smoc2
Id2
Col6a1
Mfap4
Cdkn1c
Hmga2
Igfbp2
Stmn1
Foxf1
Actg2
Aldh1a2
Aldh1a1
Mgst3
Lmo4
Hmgb3
log fold change
−5
0
5

Figure S3: **Expression of NRP2 and PDGFRα in the developing gut. (A)** UMAP showing *Nrp2* expression in the scRNA-seq trajectories of the small intestinal musculature and immunofluorescent staining jejunal villi sections. NRP2 expression (on cell membrane) is specific to the outer gut wall and mucosal lymphatic endothelium - colocalized with *Prox1*-GFP reporter (intracellular) and LYVE1 (on cell membrane). **(B)** The left image of both E18.5 and P9 panels shows wholemount immunostaining of jejunal villi epithelium with E-CAD (on cell membrane) and mesenchyme with PDGFRα (on cell membrane), whereas the rest of the images show a single 1μm section along the z stack. PDGFRα is expressed in the aggregated mesenchymal cells of the villus tip and a sub-epithelial lining of cells in the villus. **(C)** Scatter plots showing coexpression of *Pdgfra* with SM markers *Acta2* and *Myh11* in cells from the *muscularis mucosa*. Cell type labels are based on Fig. 2, A and B. **(D) and (E)** Immunofluorescent staining of tissue sections for PDGFRα and SMA (cytoplasmic). **(D)** PDGFRα is broadly expressed in the proximal midgut mesenchymal cells at E12.5. e - endoderm, m - gut tube mesenchyme **(E)** PDGFRα expression was detected in SMA- sub-epithelial cells and was lower or absent in SMA^{low} cells SM (yellow asterisks - *) at E18.5. Yellow boxes show substacks to only visualize specific DAPI+ nuclei from the areas of the magnified insets. All scale bars = 50μm.

Fig. S3

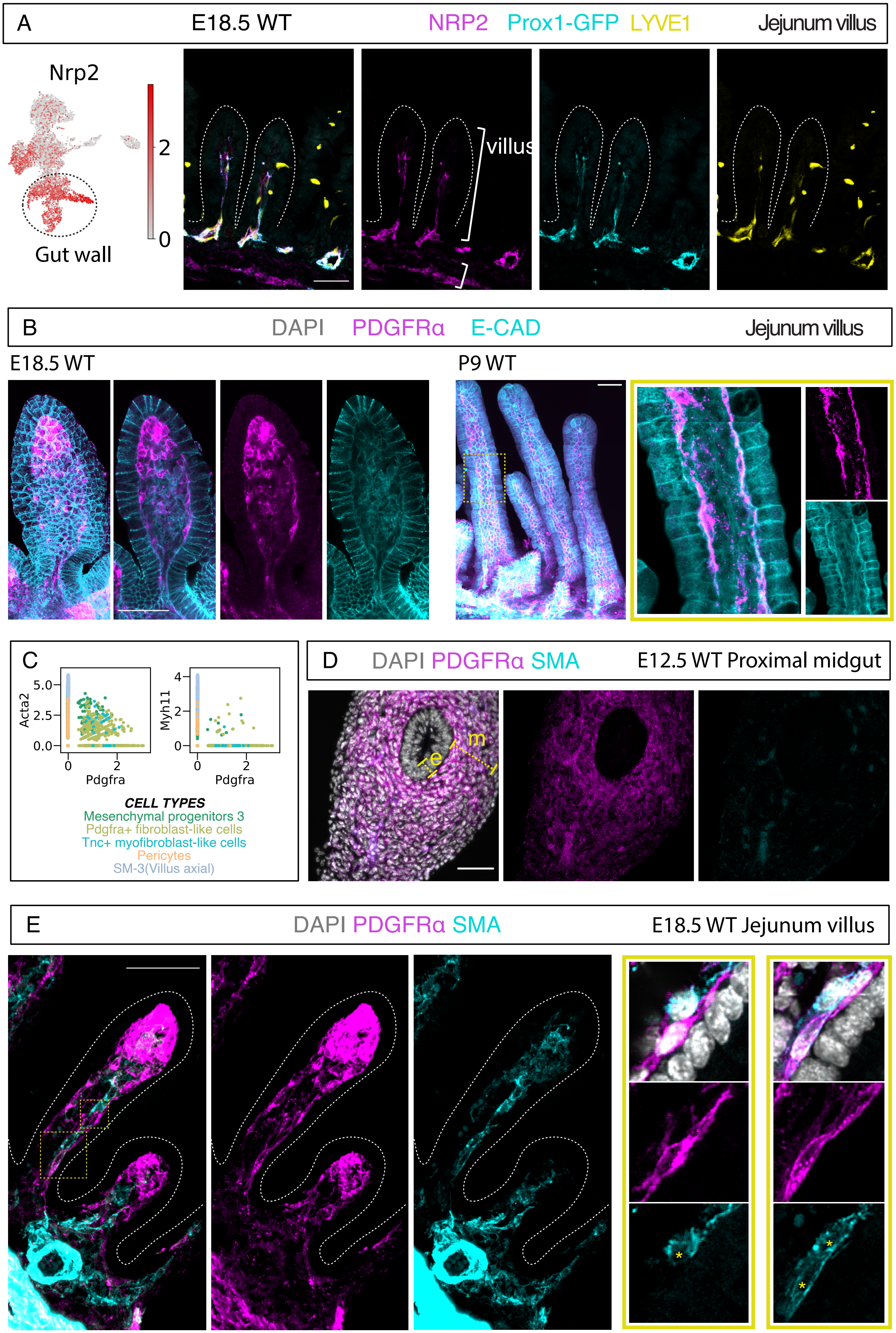
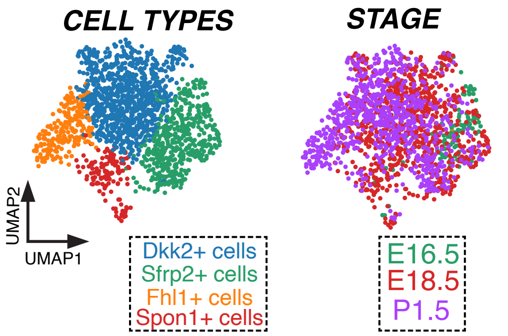

A
E18.5 WT
NRP2
Prox1-GFP
LYVE1
Jejunum villus
Nrp2
2
0
Gut wall
villus
B
DAPI
PDGFRα
E-CAD
Jejunum villus
E18.5 WT
P9 WT
C
Acta2
5.0
2.5
0.0
0
2
Pdgfra
Myh11
4
2
0
0
2
Pdgfra
CELL TYPES
Mesenchymal progenitors 3
Pdgfra+ fibroblast-like cells
Tnc+ myofibroblast-like cells
Pericytes
SM-3(Villus axial)
D
DAPI
PDGFRα
SMA
E12.5 WT Proximal midgut
m
e
E
DAPI
PDGFRα
SMA
E18.5 WT Jejunum villus
*
*
*

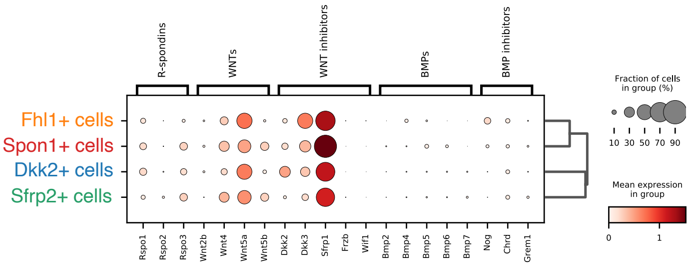
Figure S4. **Analyzing the heterogeneity of perinatal fibroblast-like cells from the small intestinal mesenchyme. (A)** UMAP plots of 1,708 single-cell transcriptomes from gut musculature fibroblast-like cells clustered by gene expression and colored by cluster labels and development stage. **(B)** Dot plot showing the expression of signaling ligands and inhibitors that define adult gut fibroblast heterogeneity in the fibroblast-like cell clusters. **(C)** Dot plot showing the differential gene expression analysis of perinatal fibroblast cell clusters. **(D)** Dot plot showing the expression of literature-derived genes defining adult gut fibroblast heterogeneity in the perinatal fibroblast cell clusters. **(E)** UMAP plots show the expression of genes associated with a myofibroblast-like cell phenotype. **(F)** Immunofluorescent staining of a jejunal villi section at P9 for TNC (intra/extracellular) and SMA. All scale bars = 50µm.

Fig. S4

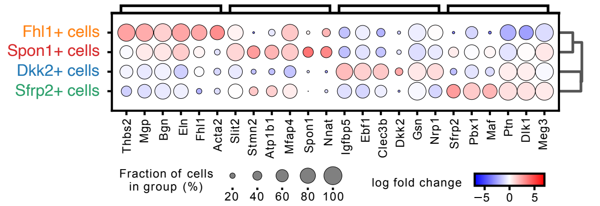
A Perinatal fibroblast-like cells



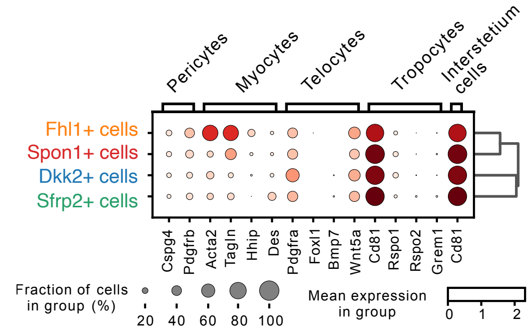
B Expression of signaling molecules in perinatal fibroblast-like clusters



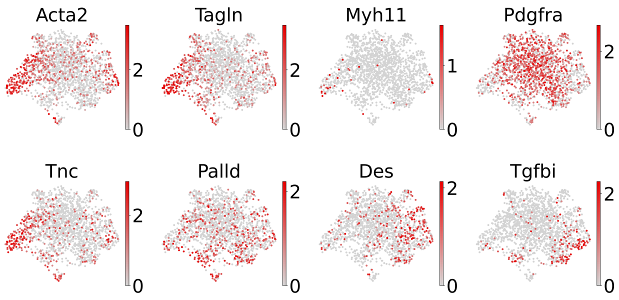
C Differentially expressed genes in perinatal fibroblast-like clusters



D Expression of adult fibroblast heterogeneity markers in perinatal fibroblast-like clusters



E Subset of perinatal fibroblasts display a myofibroblast-like transcriptional signature



F P9 WT TNC SMA Jejunum villus

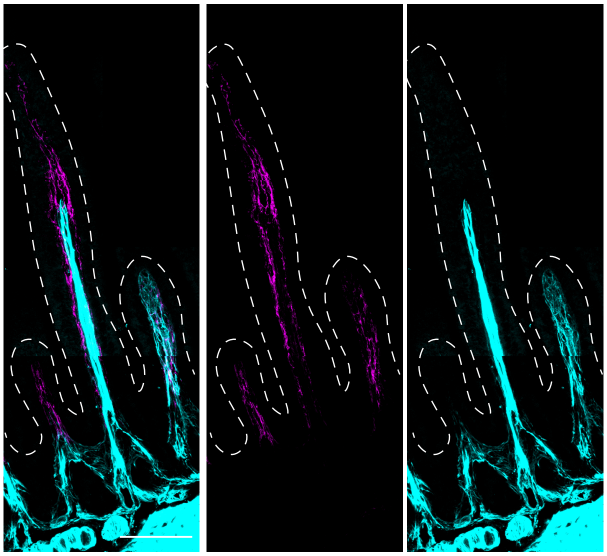


Figure S5. **NOTCH signaling regulates SM assembly in the villus and the mesentery. (A)** Immunofluorescent staining of jejunal villi section at P9 for HEY2 (intracellular) and SMA; magenta box shows a magnified inset. **(B)** Immunofluorescent staining of jejunal villi section at P9 for MCAM (extracellular/on cell membrane) and SMA; Cyan box shows a magnified inset. MCAM is expressed in villus SM fibers and the surrounding villus blood capillaries. **(C)** Immunofluorescent staining of *Prox1*-GFP (intracellular reporter) jejunal villi tissue sections at E18.5 for DLL4 (on cell membrane). A yellow dotted line outlines the lacteal with a DLL4+ tip. **(D)** Whole-mount immunofluorescent staining of jejunal villi for LYVE1 and SMA. Induced gene knockout of *Notch3* with *Hoxb6 Cre* results in a compromised assembly of villus SM around the lacteal (top panel). Binned quantification of the percentage of villi with given ratios of lacteal and villus SM lengths upon *Notch3* gene knockout using *Hoxb6 Cre* (bottom panel). Compared using two-way ANOVA followed by Šídák's multiple comparisons test (presented as mean ± SEM). iKO - inducibly knocked out. **(E)** Schematic for measurement of lacteal, SM, and villus lengths and filopodia presence. All scale bars = 50µm.

Fig. S5

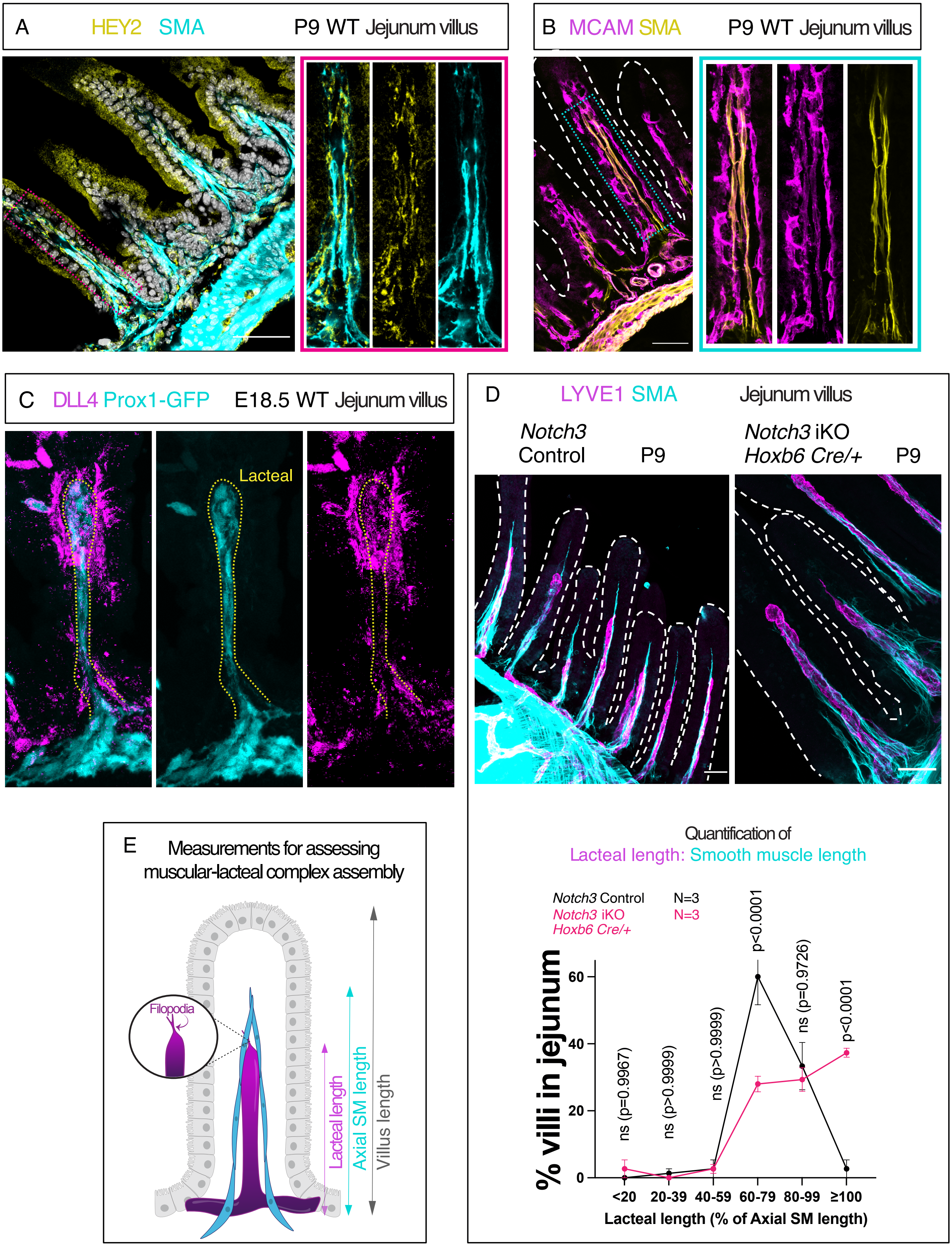

A
HEY2 SMA
P9 WT Jejunum villus
B
MCAM SMA
P9 WT Jejunum villus
C
DLL4 Prox1-GFP
E18.5 WT Jejunum villus
Lacteal
D
LYVE1 SMA
Jejunum villus
Notch3 Control
P9
Notch3 iKO Hoxb6 Cre/+
P9
Quantification of
Lacteal length: Smooth muscle length
Notch3 Control N=3
Notch3 iKO Hoxb6 Cre/+ N=3
% villi in jejunum
0
20
40
60
<20
20-39
40-59
60-79
80-99
≥100
Lacteal length (% of Axial SM length)
ns (p=0.9967)
ns (p>0.9999)
ns (p>0.9999)
p<0.0001
ns (p=0.9726)
p<0.0001
E
Measurements for assessing muscular-lacteal complex assembly
Filopodia
Lacteal length
Axial SM length
Villus length

Figure S6. Quantitative assessment of lacteal-villus SM structure upon induction of *Notch3* and *Dll4* knockout. (A-C) Binned quantification of the percentage of villi with a given villus SM length normalized to villus length upon inducing *Notch3* gene knockout using **(A)** *Pdgfra CreERT2* and **(B)** *Hoxb6 Cre* drivers and **(C)** inducing Dll4 gene knockout using *Prox1 CreERT2*. **(D-F)** Binned quantification of the percentage of villi with given lacteal length normalized to villus length upon inducing *Notch3* gene knockout using **(D)** *Pdgfra CreERT2* and **(E)** *Hoxb6 Cre* drivers and **(F)** inducing Dll4 gene knockout using *Prox1 CreERT2*. Length ratios in Fig. S6 A-F were compared by two-way ANOVA followed by Šídák's multiple comparisons test (presented as mean ± SEM). **(G-I)** Quantification of the percentage of lacteals counted with filopodia upon inducing *Notch3* gene knockout using **(G)** *Pdgfra CreERT2* and **(H)** *Hoxb6 Cre* drivers and **(I)** inducing Dll4 gene knockout using *Prox1 CreERT2*. The comparison was made using an unpaired t-test (presented as mean ± SEM). **(J)** Whole-mount immunofluorescent staining of jejunal mesentery for CD31 (on cell membrane) and SMA. *Notch3* iKO with *Hoxb6 Cre* results in loss of vascular SM coverage on mesenteric blood vessels. iKO - inducibly knocked out. All scale bars = 50µm.

Fig. S6

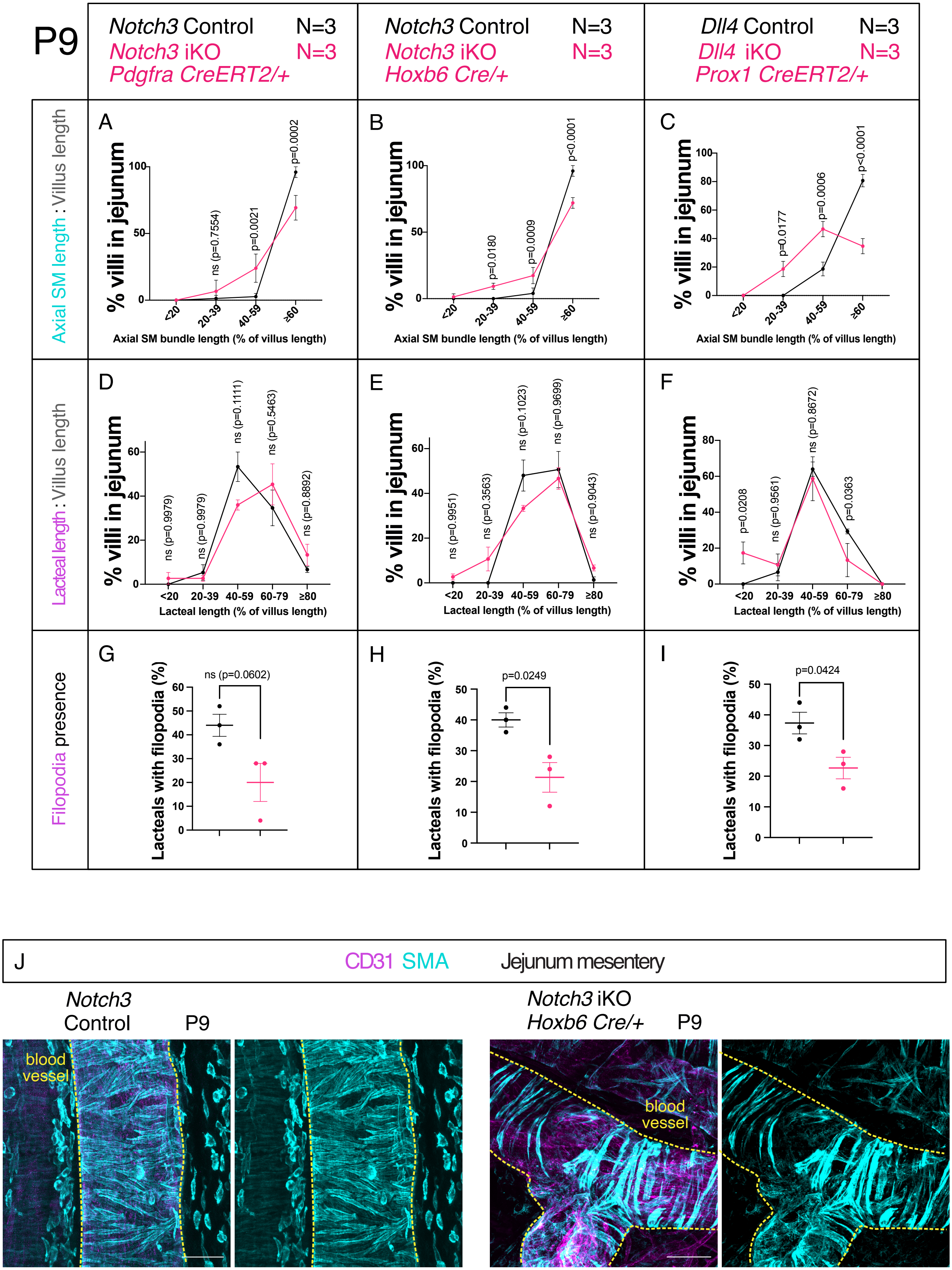

P9
Notch3 Control N=3
Notch3 iKO N=3
Pdgfra CreERT2/+
Notch3 Control N=3
Notch3 iKO N=3
Hoxb6 Cre/+
Dll4 Control N=3
Dll4 iKO N=3
Prox1 CreERT2/+
Axial SM length : Villus length
A
% villi in jejunum
Axial SM bundle length (% of villus length)
<20
20-39
40-59
≥60
0
50
100
ns (p=0.7554)
p=0.0021
p=0.0002
B
% villi in jejunum
Axial SM bundle length (% of villus length)
p=0.0180
p=0.0009
p<0.0001
C
% villi in jejunum
Axial SM bundle length (% of villus length)
0
20
40
60
80
100
p=0.0177
p=0.0006
p<0.0001
Lacteal length : Villus length
D
% villi in jejunum
Lacteal length (% of villus length)
<20
20-39
40-59
60-79
≥80
ns (p=0.9979)
ns (p=0.9979)
ns (p=0.1111)
ns (p=0.5463)
ns (p=0.8892)
E
% villi in jejunum
Lacteal length (% of villus length)
ns (p=0.9951)
ns (p=0.3563)
ns (p=0.1023)
ns (p=0.9699)
ns (p=0.9043)
F
% villi in jejunum
Lacteal length (% of villus length)
p=0.0208
ns (p=0.9561)
ns (p=0.8672)
p=0.0363
Filopodia presence
G
Lacteals with filopodia (%)
ns (p=0.0602)
H
Lacteals with filopodia (%)
p=0.0249
I
Lacteals with filopodia (%)
p=0.0424
J
CD31 SMA
Jejunum mesentery
Notch3 Control P9
blood vessel
Notch3 iKO Hoxb6 Cre/+ P9
blood vessel

Table S1. Differential gene expression analysis results for top 50 gene markers for all intestinal cell types in the intestinal scRNA-seq data.

Table S1:

Intestinal cell type markers					
names	**scores**	**logfoldchanges**	**pvals**	**pvals_adj**	**celltypes**
Gm42418	55.22175	2.050854	0	0	Mt-enriched progenitors
mt-Co3	44.62211	0.7420995	0	0	Mt-enriched progenitors
mt-Atp6	44.296143	0.7363998	0	0	Mt-enriched progenitors
mt-Nd2	43.04233	0.802821	0	0	Mt-enriched progenitors
mt-Nd4l	39.941357	1.9222971	0	0	Mt-enriched progenitors
mt-Nd4	38.96214	0.6512708	0	0	Mt-enriched progenitors
mt-Co2	38.181416	0.5975924	0	0	Mt-enriched progenitors
mt-Nd5	32.866264	0.7411984	6.67E-237	2.19E-234	Mt-enriched progenitors
Rps26	32.66595	0.49614283	4.76E-234	1.42E-231	Mt-enriched progenitors
mt-Cytb	31.926195	0.4850293	1.16E-223	2.64E-221	Mt-enriched progenitors
mt-Nd1	30.845373	0.52438986	6.46E-209	1.09E-206	Mt-enriched progenitors
Hbb-y	28.349735	2.60736	8.43E-177	7.93E-175	Mt-enriched progenitors
Npm1	21.928015	0.40209118	1.40E-106	2.85E-105	Mt-enriched progenitors
Rpl13	20.840704	0.29602665	1.85E-96	3.03E-95	Mt-enriched progenitors
Mdk	20.404648	1.1294323	1.52E-92	2.32E-91	Mt-enriched progenitors
H2afz	20.309578	0.4804583	1.06E-91	1.59E-90	Mt-enriched progenitors
Rpsa	19.5751	0.35181066	2.52E-85	3.34E-84	Mt-enriched progenitors
Rps8	19.542267	0.2248474	4.80E-85	6.32E-84	Mt-enriched progenitors
Rps3a1	19.32935	0.26723212	3.04E-83	3.90E-82	Mt-enriched progenitors
Ppia	19.3251	0.22645505	3.30E-83	4.22E-82	Mt-enriched progenitors
Ptma	19.214653	0.3820019	2.79E-82	3.50E-81	Mt-enriched progenitors
Rpl23a	18.162056	0.055260044	1.03E-73	1.09E-72	Mt-enriched progenitors
Eef1a1	18.09719	0.19793108	3.35E-73	3.50E-72	Mt-enriched progenitors
Rps5	18.013172	0.31193662	1.54E-72	1.59E-71	Mt-enriched progenitors
Tubb5	17.838688	0.44411156	3.54E-71	3.57E-70	Mt-enriched progenitors
Rpl10a	17.372416	0.099090315	1.33E-67	1.26E-66	Mt-enriched progenitors
Rps10	16.889242	0.16743271	5.40E-64	4.79E-63	Mt-enriched progenitors
Rps4x	16.18252	0.19260421	6.70E-59	5.44E-58	Mt-enriched progenitors
Rps24	16.122335	0.15790293	1.78E-58	1.43E-57	Mt-enriched progenitors
Rpl27a	15.935956	0.11532711	3.57E-57	2.82E-56	Mt-enriched progenitors
Hnrnpa1	15.865564	0.23972204	1.10E-56	8.59E-56	Mt-enriched progenitors
Rplp0	15.833658	0.2369266	1.82E-56	1.42E-55	Mt-enriched progenitors
Acta2	15.748067	1.8949043	7.08E-56	5.46E-55	Mt-enriched progenitors
Rpl5	15.647737	0.055734314	3.44E-55	2.62E-54	Mt-enriched progenitors
Ubb	15.4225855	0.010287929	1.15E-53	8.49E-53	Mt-enriched progenitors
Rpl11	15.354205	-0.014119527	3.32E-53	2.42E-52	Mt-enriched progenitors
Cdkn1c	14.320122	0.6634984	1.64E-46	1.04E-45	Mt-enriched progenitors
Rpl8	14.117662	0.10104622	2.96E-45	1.84E-44	Mt-enriched progenitors
Rack1	14.054337	0.09637018	7.25E-45	4.47E-44	Mt-enriched progenitors
Rps6	13.840042	0.009851726	1.46E-43	8.78E-43	Mt-enriched progenitors
Eef1b2	13.333687	0.03489094	1.47E-40	8.32E-40	Mt-enriched progenitors
Stmn1	13.162587	0.48860225	1.44E-39	7.98E-39	Mt-enriched progenitors
H3f3a	13.054708	-0.071771696	5.97E-39	3.27E-38	Mt-enriched progenitors
mt-Nd3	13.009311	0.117468014	1.08E-38	5.90E-38	Mt-enriched progenitors

Rpl3	12.914823	0.05243501	3.71E-38	2.00E-37	Mt-enriched progenitors
Rps9	12.892034	0.08725476	4.99E-38	2.68E-37	Mt-enriched progenitors
Rps20	12.694141	0.06722294	6.37E-37	3.35E-36	Mt-enriched progenitors
Rpl18	12.588078	0.08362859	2.46E-36	1.28E-35	Mt-enriched progenitors
Rps7	12.566561	-0.012194806	3.22E-36	1.67E-35	Mt-enriched progenitors
Rpl22	12.03908	-0.14896789	2.21E-33	1.08E-32	Mt-enriched progenitors
Ptn	78.945564	4.3167024	0	0	Embryonic gut mesenchymal cells
Dlk1	76.66971	4.229639	0	0	Embryonic gut mesenchymal cells
Cdkn1c	72.90695	2.9192133	0	0	Embryonic gut mesenchymal cells
Meg3	72.3049	3.9820652	0	0	Embryonic gut mesenchymal cells
Col3a1	72.09461	4.1242456	0	0	Embryonic gut mesenchymal cells
Itm2a	71.98131	3.6353319	0	0	Embryonic gut mesenchymal cells
Col1a1	71.31079	4.044361	0	0	Embryonic gut mesenchymal cells
Mdk	71.05593	3.0749211	0	0	Embryonic gut mesenchymal cells
Col1a2	70.7013	3.8208458	0	0	Embryonic gut mesenchymal cells
Cxcl12	69.6521	3.7261298	0	0	Embryonic gut mesenchymal cells
Peg3	68.161	3.3852537	0	0	Embryonic gut mesenchymal cells
Lgals1	66.76427	3.0294962	0	0	Embryonic gut mesenchymal cells
Mfap4	66.06227	3.4483144	0	0	Embryonic gut mesenchymal cells
Slit2	65.31612	3.8136482	0	0	Embryonic gut mesenchymal cells
Plagl1	63.713177	2.7603307	0	0	Embryonic gut mesenchymal cells
Mfap2	63.204384	2.627499	0	0	Embryonic gut mesenchymal cells
Sulf2	62.68722	3.0231998	0	0	Embryonic gut mesenchymal cells
Nr2f2	62.189785	2.9076881	0	0	Embryonic gut mesenchymal cells
Dcn	61.543835	3.569093	0	0	Embryonic gut mesenchymal cells
Gas1	59.423763	2.8051965	0	0	Embryonic gut mesenchymal cells
Gpc3	58.375153	2.4563487	0	0	Embryonic gut mesenchymal cells
Ifitm1	58.357662	2.9445179	0	0	Embryonic gut mesenchymal cells
Rcn3	57.854507	2.495613	0	0	Embryonic gut mesenchymal cells
Ccdc80	57.274128	3.131684	0	0	Embryonic gut mesenchymal cells
Lum	56.84273	3.3037667	0	0	Embryonic gut mesenchymal cells
Meis2	56.59872	2.5061584	0	0	Embryonic gut mesenchymal cells
Pbx1	55.71527	2.3287067	0	0	Embryonic gut mesenchymal cells
Grb10	55.54725	2.014409	0	0	Embryonic gut mesenchymal cells
Igf1	55.38201	3.2143197	0	0	Embryonic gut mesenchymal cells
Tpm2	55.00728	2.5270264	0	0	Embryonic gut mesenchymal cells
Col6a1	54.93239	2.552864	0	0	Embryonic gut mesenchymal cells
Sfr1	54.613293	1.7225825	0	0	Embryonic gut mesenchymal cells
Tshz2	54.599316	2.2937884	0	0	Embryonic gut mesenchymal cells
Col5a2	54.02136	2.3356779	0	0	Embryonic gut mesenchymal cells
Basp1	53.83214	2.2184188	0	0	Embryonic gut mesenchymal cells
Sfrp2	53.756813	3.527793	0	0	Embryonic gut mesenchymal cells
Kcnq1ot1	53.53762	2.1770139	0	0	Embryonic gut mesenchymal cells
Emp3	53.465992	2.249961	0	0	Embryonic gut mesenchymal cells
Serpinh1	53.411312	1.9481969	0	0	Embryonic gut mesenchymal cells
Igf2r	53.18072	2.1774852	0	0	Embryonic gut mesenchymal cells
Islr	52.799385	2.9895015	0	0	Embryonic gut mesenchymal cells

Nrk	52.575447	3.1605518	0	0	Embryonic gut mesenchymal cells
Col5a1	51.479637	2.4922316	0	0	Embryonic gut mesenchymal cells
6330403K07Rik	51.477936	2.542841	0	0	Embryonic gut mesenchymal cells
Fbn2	51.056614	2.4368393	0	0	Embryonic gut mesenchymal cells
Col6a2	50.477882	2.5414813	0	0	Embryonic gut mesenchymal cells
Maged2	50.13233	1.928196	0	0	Embryonic gut mesenchymal cells
Nenf	49.704247	1.7338778	0	0	Embryonic gut mesenchymal cells
Zeb2	49.486893	2.3481064	0	0	Embryonic gut mesenchymal cells
Tpm1	49.39089	1.8290464	0	0	Embryonic gut mesenchymal cells
Meis2	63.716145	3.4395528	0	0	Gut wall SM and ICCs
Mab21l2	58.512177	3.70486	0	0	Gut wall SM and ICCs
Foxp2	56.907925	4.7088127	0	0	Gut wall SM and ICCs
Myl9	54.55882	3.7660847	0	0	Gut wall SM and ICCs
Psd	52.931683	3.9433517	0	0	Gut wall SM and ICCs
Tpm2	52.75127	3.3411193	0	0	Gut wall SM and ICCs
Meg3	52.10823	3.3097026	0	0	Gut wall SM and ICCs
Lsp1	51.878147	3.250352	0	0	Gut wall SM and ICCs
Foxf1	51.529892	3.7153242	0	0	Gut wall SM and ICCs
Mfap4	50.597324	2.9257329	0	0	Gut wall SM and ICCs
Cald1	50.060814	2.5104866	0	0	Gut wall SM and ICCs
Tshz2	49.409145	2.479462	0	0	Gut wall SM and ICCs
Tpm1	49.30804	2.383468	0	0	Gut wall SM and ICCs
Acta2	49.0889	4.2892942	0	0	Gut wall SM and ICCs
Tcf21	48.647305	3.240261	0	0	Gut wall SM and ICCs
Smoc2	48.490566	3.307185	0	0	Gut wall SM and ICCs
Ptn	48.459465	2.9119325	0	0	Gut wall SM and ICCs
Cpe	48.200287	2.904587	0	0	Gut wall SM and ICCs
Mylk	47.61521	3.9271388	0	0	Gut wall SM and ICCs
Foxp1	46.914715	2.2720158	0	0	Gut wall SM and ICCs
Pbx1	46.24322	2.2745633	0	0	Gut wall SM and ICCs
Mfap2	45.40918	2.1915116	0	0	Gut wall SM and ICCs
Mdk	44.0885	2.2835927	0	0	Gut wall SM and ICCs
Ldhb	43.674755	2.499247	0	0	Gut wall SM and ICCs
Plagl1	43.476494	2.1811397	0	0	Gut wall SM and ICCs
Dlk1	41.24301	2.4088	0	0	Gut wall SM and ICCs
Col6a1	41.05064	2.228946	0	0	Gut wall SM and ICCs
Col23a1	39.669605	3.8224094	0	0	Gut wall SM and ICCs
Emp3	39.583996	1.9637014	0	0	Gut wall SM and ICCs
Osr1	39.52665	3.1534233	0	0	Gut wall SM and ICCs
Rbpms	39.38933	1.8872286	0	0	Gut wall SM and ICCs
Mpped2	38.868988	2.9437077	0	0	Gut wall SM and ICCs
Tgfb1i1	38.48308	2.4228466	0	0	Gut wall SM and ICCs
Lgals1	38.21143	2.0379891	0	0	Gut wall SM and ICCs
Actg2	38.136803	4.157855	0	0	Gut wall SM and ICCs
Emilin1	38.008755	2.109987	0	0	Gut wall SM and ICCs
Cdkn1c	37.897293	1.8348536	0	0	Gut wall SM and ICCs
Col3a1	37.718838	2.0780044	0	0	Gut wall SM and ICCs

Gas1	37.56372	2.096485	0.00E+00	3.76E-306	Gut wall SM and ICCs
Col1a1	37.550762	2.0287337	0.00E+00	5.98E-306	Gut wall SM and ICCs
Atxn7l3b	37.125557	1.4094803	1.09E-301	4.65E-299	Gut wall SM and ICCs
Pde5a	37.123493	3.1115856	1.17E-301	4.91E-299	Gut wall SM and ICCs
Actn1	36.753937	2.0262244	1.01E-295	4.12E-293	Gut wall SM and ICCs
Meis1	36.453568	2.0733795	6.04E-291	2.42E-288	Gut wall SM and ICCs
Cnn2	36.385433	1.8550379	7.24E-290	2.84E-287	Gut wall SM and ICCs
Ifitm1	36.380787	2.1855395	8.57E-290	3.30E-287	Gut wall SM and ICCs
Tgfbi	36.117195	2.3868785	1.22E-285	4.60E-283	Gut wall SM and ICCs
Sfr1	36.043858	1.3433397	1.72E-284	6.38E-282	Gut wall SM and ICCs
Fbn2	35.9414	2.1014433	6.90E-283	2.51E-280	Gut wall SM and ICCs
Ppp1r14a	35.676136	3.040072	9.27E-279	3.31E-276	Gut wall SM and ICCs
Myl9	23.24291	6.357422	1.68E-119	3.30E-115	Villus SM cells
Cald1	23.056437	4.5162992	1.27E-117	1.25E-113	Villus SM cells
Tagln	22.927877	7.4723625	2.45E-116	1.60E-112	Villus SM cells
Tpm1	22.841188	4.3872786	1.79E-115	8.78E-112	Villus SM cells
Acta2	22.77456	7.1621795	8.20E-115	3.22E-111	Villus SM cells
Myh11	22.753717	7.4150047	1.32E-114	4.32E-111	Villus SM cells
Notch3	22.59172	6.2829595	5.23E-113	1.47E-109	Villus SM cells
Crip1	22.493162	4.898636	4.84E-112	1.19E-108	Villus SM cells
Itga1	22.37222	5.414259	7.34E-111	1.60E-107	Villus SM cells
Tpm2	22.264046	5.107404	8.25E-110	1.62E-106	Villus SM cells
Aoc3	22.204529	7.175294	3.11E-109	5.55E-106	Villus SM cells
Mustn1	22.068495	7.309997	6.35E-108	1.04E-104	Villus SM cells
Mcam	21.995644	4.8955116	3.17E-107	4.79E-104	Villus SM cells
Jag1	21.963966	5.5547223	6.37E-107	8.94E-104	Villus SM cells
Flna	21.660809	3.970021	4.81E-104	6.30E-101	Villus SM cells
Pde3a	21.494814	4.829668	1.74E-102	2.14E-99	Villus SM cells
Eln	21.076513	6.763937	1.31E-98	1.51E-95	Villus SM cells
Actn1	21.029022	4.067434	3.56E-98	3.89E-95	Villus SM cells
Ndufa4l2	21.008862	5.765369	5.44E-98	5.63E-95	Villus SM cells
Gm13889	20.832863	5.149148	2.18E-96	2.14E-93	Villus SM cells
7-Sep	20.803616	2.7574422	4.01E-96	3.76E-93	Villus SM cells
Tinagl1	20.646194	4.727289	1.06E-94	9.43E-92	Villus SM cells
Actg2	20.493322	5.446238	2.47E-93	2.11E-90	Villus SM cells
Lmod1	20.35727	6.896699	4.00E-92	3.28E-89	Villus SM cells
Ebf1	20.06908	4.0201297	1.38E-89	1.08E-86	Villus SM cells
Des	20.018885	4.5562387	3.77E-89	2.85E-86	Villus SM cells
Mylk	19.769741	4.18334	5.43E-87	3.95E-84	Villus SM cells
Parm1	19.559113	4.83483	3.45E-85	2.42E-82	Villus SM cells
Il13ra1	19.550528	5.552531	4.08E-85	2.77E-82	Villus SM cells
Igfbp7	19.534924	4.681866	5.54E-85	3.63E-82	Villus SM cells
Mprip	19.509851	3.2659945	9.05E-85	5.74E-82	Villus SM cells
Cryab	19.462425	4.615676	2.29E-84	1.40E-81	Villus SM cells
Zeb2	19.333712	3.658651	2.80E-83	1.66E-80	Villus SM cells
Pdgfa	19.321325	4.092767	3.55E-83	2.05E-80	Villus SM cells
Axl	19.04588	4.1110225	7.11E-81	3.99E-78	Villus SM cells

Mef2c	18.95127	3.5805366	4.31E-80	2.35E-77	Villus SM cells
Cavin3	18.936806	3.1132085	5.67E-80	3.01E-77	Villus SM cells
S100a11	18.912397	2.790459	9.02E-80	4.66E-77	Villus SM cells
Lgals1	18.909836	3.2879026	9.47E-80	4.77E-77	Villus SM cells
Map3k20	18.808157	4.8804893	6.47E-79	3.18E-76	Villus SM cells
Gucy1a1	18.795109	4.4054832	8.28E-79	3.97E-76	Villus SM cells
Lgalsl	18.746939	4.652959	2.05E-78	9.59E-76	Villus SM cells
Inpp4b	18.700426	6.1014977	4.91E-78	2.24E-75	Villus SM cells
Itgb1	18.662842	2.4812727	9.93E-78	4.44E-75	Villus SM cells
Mfge8	18.537836	3.4495654	1.02E-76	4.47E-74	Villus SM cells
Cavin1	18.38893	3.311995	1.61E-75	6.88E-73	Villus SM cells
Rbpms	18.286673	2.8694232	1.06E-74	4.42E-72	Villus SM cells
Carmn	18.2492	4.9774036	2.10E-74	8.60E-72	Villus SM cells
Col4a1	18.246147	3.5404775	2.22E-74	8.90E-72	Villus SM cells
Vcl	18.239594	3.7320158	2.50E-74	9.84E-72	Villus SM cells
Col3a1	68.81824	6.070898	0	0	Mature fibroblast-like cells
Col1a2	68.807434	6.0038905	0	0	Mature fibroblast-like cells
Dcn	68.53309	6.660593	0	0	Mature fibroblast-like cells
Col1a1	68.48009	6.0437093	0	0	Mature fibroblast-like cells
Postn	68.0536	6.666659	0	0	Mature fibroblast-like cells
Gsn	67.52638	5.1995945	0	0	Mature fibroblast-like cells
Col6a1	66.84064	5.0187817	0	0	Mature fibroblast-like cells
Lum	66.35979	5.6463695	0	0	Mature fibroblast-like cells
Col6a2	64.16716	4.8444805	0	0	Mature fibroblast-like cells
Itm2a	63.068893	4.799483	0	0	Mature fibroblast-like cells
Gpc3	62.030563	3.8312948	0	0	Mature fibroblast-like cells
Col5a1	61.68618	4.3954663	0	0	Mature fibroblast-like cells
Col6a3	60.95909	4.696173	0	0	Mature fibroblast-like cells
Dlk1	60.932144	4.662213	0	0	Mature fibroblast-like cells
Col14a1	60.518948	5.3290095	0	0	Mature fibroblast-like cells
Meg3	59.72622	4.3124638	0	0	Mature fibroblast-like cells
Col5a2	58.368027	3.6140187	0	0	Mature fibroblast-like cells
Peg3	58.31231	3.7968574	0	0	Mature fibroblast-like cells
S100a6	57.86392	4.127279	0	0	Mature fibroblast-like cells
Vcan	57.325916	4.598796	0	0	Mature fibroblast-like cells
Mfap5	57.164886	7.180412	0	0	Mature fibroblast-like cells
Fstl1	56.814976	3.2235727	0	0	Mature fibroblast-like cells
Bgn	56.01776	3.9652283	0	0	Mature fibroblast-like cells
Itih5	55.356552	6.297062	0	0	Mature fibroblast-like cells
Sparc	54.93775	3.0283134	0	0	Mature fibroblast-like cells
Fbn1	54.697178	3.8747296	0	0	Mature fibroblast-like cells
Ptn	54.100525	3.8641572	0	0	Mature fibroblast-like cells
Zim1	52.07769	5.4143896	0	0	Mature fibroblast-like cells
Ebf1	51.806595	4.0701723	0	0	Mature fibroblast-like cells
Ltbp4	51.66096	3.4199617	0	0	Mature fibroblast-like cells
Nid1	51.435665	3.2807417	0	0	Mature fibroblast-like cells
Akap12	51.163757	3.4093466	0	0	Mature fibroblast-like cells

Fbln1	50.824837	3.3421545	0	0	Mature fibroblast-like cells
Cpe	50.642223	3.5481462	0	0	Mature fibroblast-like cells
Serping1	50.34927	4.5167985	0	0	Mature fibroblast-like cells
Zeb2	50.229095	3.3153687	0	0	Mature fibroblast-like cells
Pcolce	49.87349	4.1551776	0	0	Mature fibroblast-like cells
Cxcl12	49.821507	3.8162963	0	0	Mature fibroblast-like cells
Nfix	49.43688	3.6513908	0	0	Mature fibroblast-like cells
Ahnak	49.36701	2.9047375	0	0	Mature fibroblast-like cells
Mfap2	48.62343	2.738882	0	0	Mature fibroblast-like cells
Sparcl1	48.449398	3.0240214	0	0	Mature fibroblast-like cells
Laptm4a	48.375343	2.0287054	0	0	Mature fibroblast-like cells
Igfbp4	48.259552	2.3000944	0	0	Mature fibroblast-like cells
Matn2	47.93846	5.0470047	0	0	Mature fibroblast-like cells
Nrk	47.77457	3.9105058	0	0	Mature fibroblast-like cells
Malat1	47.45972	2.4746706	0	0	Mature fibroblast-like cells
Eln	47.42231	3.8588972	0	0	Mature fibroblast-like cells
Mgp	47.33506	4.0952606	0	0	Mature fibroblast-like cells
Tnxb	47.033676	5.9110074	0	0	Mature fibroblast-like cells
Pdgfrb	26.57167	6.7837596	1.44E-155	2.84E-151	Pericytes
Rgs5	26.138807	8.287025	1.32E-150	1.30E-146	Pericytes
Col18a1	26.102139	5.225403	3.45E-150	2.26E-146	Pericytes
Ebf1	25.772293	5.34448	1.81E-146	8.91E-143	Pericytes
Myh9	24.907974	4.1194277	6.10E-137	2.40E-133	Pericytes
Cygb	24.681223	6.2386165	1.70E-134	5.57E-131	Pericytes
Col4a1	24.483109	4.640808	2.24E-132	6.28E-129	Pericytes
Gm13889	24.203682	5.70721	2.03E-129	5.00E-126	Pericytes
Rarres2	23.866814	4.7903886	6.78E-126	1.48E-122	Pericytes
4-Sep	23.407127	5.54353	3.62E-121	7.11E-118	Pericytes
Col4a2	23.121704	3.977938	2.80E-118	5.00E-115	Pericytes
Cald1	22.985682	3.393512	6.48E-117	1.06E-113	Pericytes
Mcam	22.893688	4.45857	5.37E-116	8.12E-113	Pericytes
Notch3	22.76777	5.6506968	9.57E-115	1.34E-111	Pericytes
Rasgrp2	22.438423	4.614568	1.66E-111	2.18E-108	Pericytes
Itga1	22.27364	4.617569	6.66E-110	8.18E-107	Pericytes
Igfbp7	22.244413	4.595246	1.28E-109	1.48E-106	Pericytes
Ndufa4l2	22.206507	5.678251	2.97E-109	3.24E-106	Pericytes
Lamb1	22.181274	3.5580478	5.21E-109	5.39E-106	Pericytes
Ifitm3	21.685986	3.2405834	2.78E-104	2.73E-101	Pericytes
Abcc9	21.519659	4.930246	1.02E-102	9.54E-100	Pericytes
Nid2	21.447367	3.754792	4.83E-102	4.32E-99	Pericytes
Gjc1	21.33381	3.738762	5.51E-101	4.71E-98	Pericytes
Gcnt2	21.190289	5.2124085	1.17E-99	9.61E-97	Pericytes
Art3	20.99857	7.546938	6.76E-98	5.31E-95	Pericytes
Phlda1	20.779444	4.731678	6.64E-96	5.02E-93	Pericytes
Gucy1a1	20.611944	4.6607337	2.14E-94	1.56E-91	Pericytes
Epas1	20.470669	4.07041	3.93E-93	2.76E-90	Pericytes
Cbfa2t3	20.423689	4.465081	1.03E-92	6.98E-90	Pericytes

Ifitm1	20.38058	3.4828548	2.49E-92	1.63E-89	Pericytes
Tns1	20.37263	4.09165	2.93E-92	1.85E-89	Pericytes
Nid1	20.159008	3.3489168	2.24E-90	1.38E-87	Pericytes
Fabp7	19.742086	4.656515	9.38E-87	5.59E-84	Pericytes
Cspg4	19.540178	5.5744104	5.00E-85	2.89E-82	Pericytes
Lhfp	19.288683	4.540321	6.69E-83	3.75E-80	Pericytes
Bgn	19.246437	3.3075037	1.51E-82	8.25E-80	Pericytes
Ggt5	19.139992	6.2746315	1.17E-81	6.23E-79	Pericytes
Tgfb2	19.11884	4.070555	1.76E-81	9.10E-79	Pericytes
Fn1	19.114653	3.4335558	1.91E-81	9.61E-79	Pericytes
Mfge8	19.0359	3.3545012	8.60E-81	4.23E-78	Pericytes
Zeb2	19.012377	3.3456268	1.35E-80	6.46E-78	Pericytes
Axl	18.839672	3.8952353	3.57E-79	1.63E-76	Pericytes
Id3	18.827648	2.6355486	4.48E-79	2.00E-76	Pericytes
Foxf1	18.824963	3.5625083	4.72E-79	2.06E-76	Pericytes
Ednra	18.748598	5.130908	1.99E-78	8.49E-76	Pericytes
Tmem176a	18.136272	2.5699399	1.65E-73	6.89E-71	Pericytes
Slc12a2	18.012678	3.7717693	1.55E-72	6.21E-70	Pericytes
Spon2	17.635916	5.6547647	1.31E-69	5.13E-67	Pericytes
Kcnj8	17.492441	4.162304	1.64E-68	6.30E-66	Pericytes
Des	17.491371	3.5170844	1.67E-68	6.30E-66	Pericytes
Meis2	49.51553	3.6113727	0	0	Colonic mesenchymal cells-1
Mdk	42.37892	2.8566587	0	0	Colonic mesenchymal cells-1
Fbn2	42.292976	3.2173364	0	0	Colonic mesenchymal cells-1
Mab21l2	42.01252	3.4253073	0	0	Colonic mesenchymal cells-1
Tshz2	41.736526	2.7828603	0	0	Colonic mesenchymal cells-1
Atxn7l3b	40.46149	2.060923	0	0	Colonic mesenchymal cells-1
Tcf21	40.279915	3.448098	0	0	Colonic mesenchymal cells-1
Fst	40.24272	5.7438073	0	0	Colonic mesenchymal cells-1
Tgfbi	40.096043	3.3845325	0	0	Colonic mesenchymal cells-1
Igfbp5	39.35987	3.3307352	0	0	Colonic mesenchymal cells-1
Ptn	38.75091	3.189411	0	0	Colonic mesenchymal cells-1
Isoc1	38.10058	3.0061903	0	0	Colonic mesenchymal cells-1
Igfbp2	37.78928	3.2576354	0	0	Colonic mesenchymal cells-1
Nnat	37.53502	2.8263543	2.47E-308	3.47E-305	Colonic mesenchymal cells-1
Basp1	37.047348	2.3811445	1.98E-300	2.60E-297	Colonic mesenchymal cells-1
Sox11	36.83415	2.6913192	5.25E-297	6.44E-294	Colonic mesenchymal cells-1
6330403K07Rik	36.33355	2.7758453	4.78E-289	5.53E-286	Colonic mesenchymal cells-1
Hoxd9	35.720924	5.6485133	1.87E-279	2.04E-276	Colonic mesenchymal cells-1
Nfib	35.492996	2.2245293	6.30E-276	6.52E-273	Colonic mesenchymal cells-1
Meg3	35.332664	3.0499315	1.85E-273	1.82E-270	Colonic mesenchymal cells-1
Mfap2	35.048496	2.256027	4.11E-269	3.85E-266	Colonic mesenchymal cells-1
Gas1	34.920128	2.6008823	3.68E-267	3.29E-264	Colonic mesenchymal cells-1
Meis1	34.624065	2.4966612	1.10E-262	9.38E-260	Colonic mesenchymal cells-1
Hoxa10	34.002167	5.6286407	2.07E-253	1.69E-250	Colonic mesenchymal cells-1
Pbx1	33.779434	2.2181537	3.95E-250	3.11E-247	Colonic mesenchymal cells-1
Gpc3	31.730356	2.075876	5.93E-221	4.48E-218	Colonic mesenchymal cells-1

Smoc2	31.084194	2.8581443	3.94E-212	2.87E-209	Colonic mesenchymal cells-1
Lgals1	31.004183	2.2127454	4.73E-211	3.32E-208	Colonic mesenchymal cells-1
Cdkn1c	30.94993	2.0207891	2.55E-210	1.73E-207	Colonic mesenchymal cells-1
Hoxd10	30.93751	6.6146946	3.74E-210	2.45E-207	Colonic mesenchymal cells-1
Col3a1	30.746174	2.4121797	1.38E-207	8.45E-205	Colonic mesenchymal cells-1
Mfap4	30.640007	2.2830148	3.59E-206	2.14E-203	Colonic mesenchymal cells-1
Zfhx3	30.26783	2.1814907	3.04E-201	1.76E-198	Colonic mesenchymal cells-1
Lsp1	29.838255	2.3974082	1.25E-195	7.00E-193	Colonic mesenchymal cells-1
Chd3	29.566975	1.9532949	3.97E-192	2.17E-189	Colonic mesenchymal cells-1
Zfhx4	28.936089	2.589001	4.20E-184	2.23E-181	Colonic mesenchymal cells-1
Clmp	28.77396	2.843177	4.54E-182	2.35E-179	Colonic mesenchymal cells-1
Tpm1	28.363766	1.6563262	5.66E-177	2.85E-174	Colonic mesenchymal cells-1
H2afy2	28.315477	2.0045216	2.23E-176	1.09E-173	Colonic mesenchymal cells-1
H2afv	27.949804	1.4803782	6.63E-172	3.18E-169	Colonic mesenchymal cells-1
Cdh11	27.80729	2.220307	3.54E-170	1.66E-167	Colonic mesenchymal cells-1
Hmgn1	27.636677	1.2910414	4.04E-168	1.84E-165	Colonic mesenchymal cells-1
Hoxd11	27.60816	6.6915894	8.88E-168	3.97E-165	Colonic mesenchymal cells-1
Ldhb	27.550432	2.06493	4.37E-167	1.91E-164	Colonic mesenchymal cells-1
Rnd3	27.429487	2.6180859	1.22E-165	5.21E-163	Colonic mesenchymal cells-1
Tceal9	27.237625	1.3037452	2.33E-163	9.74E-161	Colonic mesenchymal cells-1
H3f3b	27.075947	0.89768666	1.89E-161	7.74E-159	Colonic mesenchymal cells-1
Myl9	26.967001	2.1291196	3.60E-160	1.45E-157	Colonic mesenchymal cells-1
Foxf1	26.960402	2.6459544	4.31E-160	1.69E-157	Colonic mesenchymal cells-1
Col1a1	26.77577	1.9178876	6.19E-158	2.39E-155	Colonic mesenchymal cells-1
Col14a1	30.992035	4.1594977	6.90E-211	1.36E-206	Colonic mesenchymal cells-2
Lum	30.690897	4.0102706	7.53E-207	7.40E-203	Colonic mesenchymal cells-2
Mfap4	29.977705	3.470011	1.92E-197	1.26E-193	Colonic mesenchymal cells-2
Tcf21	29.959522	3.615165	3.31E-197	1.62E-193	Colonic mesenchymal cells-2
Ifitm1	29.445429	3.347466	1.44E-190	5.66E-187	Colonic mesenchymal cells-2
Lgals1	28.8175	2.9759526	1.29E-182	4.24E-179	Colonic mesenchymal cells-2
Col1a1	28.618546	3.653225	3.95E-180	1.11E-176	Colonic mesenchymal cells-2
Col3a1	28.601568	3.709616	6.42E-180	1.58E-176	Colonic mesenchymal cells-2
Sfrp1	28.2453	3.5576887	1.63E-175	3.55E-172	Colonic mesenchymal cells-2
Snai2	28.028715	4.0403705	7.26E-173	1.43E-169	Colonic mesenchymal cells-2
Cd63	27.622112	2.202051	6.04E-168	1.08E-164	Colonic mesenchymal cells-2
Cald1	27.516214	2.6087236	1.12E-166	1.84E-163	Colonic mesenchymal cells-2
Colec10	27.45542	6.326544	5.99E-166	9.05E-163	Colonic mesenchymal cells-2
Mab21l2	27.27662	3.1595187	8.03E-164	1.13E-160	Colonic mesenchymal cells-2
Col6a1	26.595074	2.8454726	7.74E-156	1.01E-152	Colonic mesenchymal cells-2
Col1a2	26.320919	3.0806375	1.11E-152	1.36E-149	Colonic mesenchymal cells-2
Adamdec1	25.41016	5.4823866	1.95E-142	2.25E-139	Colonic mesenchymal cells-2
Rgs5	25.401716	4.672331	2.41E-142	2.53E-139	Colonic mesenchymal cells-2
Tgfbi	25.40125	2.9395535	2.44E-142	2.53E-139	Colonic mesenchymal cells-2
Mdk	25.366533	2.5595465	5.90E-142	5.80E-139	Colonic mesenchymal cells-2
Lsp1	24.800112	2.7874513	8.94E-136	8.37E-133	Colonic mesenchymal cells-2
Foxf1	24.713959	3.08812	7.57E-135	6.76E-132	Colonic mesenchymal cells-2
Zeb2	24.435768	2.6210082	7.13E-132	6.09E-129	Colonic mesenchymal cells-2

Gpc3	24.332596	2.333367	8.86E-131	7.26E-128	Colonic mesenchymal cells-2
Ccnd2	24.322754	2.3558576	1.13E-130	8.85E-128	Colonic mesenchymal cells-2
Gpc6	24.293583	3.6837223	2.29E-130	1.73E-127	Colonic mesenchymal cells-2
Ppp1r14a	24.2547	3.3945017	5.90E-130	4.29E-127	Colonic mesenchymal cells-2
Atxn7l3b	24.225775	1.8018101	1.19E-129	8.36E-127	Colonic mesenchymal cells-2
Col6a2	24.159847	2.686757	5.88E-129	3.99E-126	Colonic mesenchymal cells-2
Pdgfra	23.741455	3.6719182	1.35E-124	8.82E-122	Colonic mesenchymal cells-2
Pkdcc	23.641726	3.0054967	1.44E-123	9.10E-121	Colonic mesenchymal cells-2
Olfml3	23.539682	2.737628	1.60E-122	9.83E-120	Colonic mesenchymal cells-2
Gucy1b1	23.419348	3.3960054	2.71E-121	1.62E-118	Colonic mesenchymal cells-2
Fibin	23.176735	4.542821	7.82E-119	4.52E-116	Colonic mesenchymal cells-2
Rcn3	22.99613	2.233363	5.10E-117	2.86E-114	Colonic mesenchymal cells-2
H2afy2	22.906551	2.2829313	4.00E-116	2.18E-113	Colonic mesenchymal cells-2
Dcn	22.864828	2.8346004	1.04E-115	5.53E-113	Colonic mesenchymal cells-2
Ogn	22.657442	3.4887078	1.18E-113	6.09E-111	Colonic mesenchymal cells-2
Vcan	22.543646	2.668179	1.55E-112	7.81E-110	Colonic mesenchymal cells-2
Fn1	22.477034	2.4174552	6.96E-112	3.42E-109	Colonic mesenchymal cells-2
Serpinh1	22.294899	1.8565792	4.14E-110	1.98E-107	Colonic mesenchymal cells-2
Gucy1a1	22.191479	3.2779431	4.15E-109	1.94E-106	Colonic mesenchymal cells-2
Meis2	22.01022	2.189643	2.30E-107	1.05E-104	Colonic mesenchymal cells-2
Acta2	21.50567	2.4031699	1.38E-102	6.15E-100	Colonic mesenchymal cells-2
Cdh11	21.496775	2.3703198	1.67E-102	7.29E-100	Colonic mesenchymal cells-2
Fbln1	21.327356	2.0838077	6.33E-101	2.70E-98	Colonic mesenchymal cells-2
Rcn1	21.08531	2.0300753	1.09E-98	4.44E-96	Colonic mesenchymal cells-2
Nkx2-3	20.983782	2.202569	9.23E-98	3.70E-95	Colonic mesenchymal cells-2
Mfap2	20.96568	1.962706	1.35E-97	5.31E-95	Colonic mesenchymal cells-2
Hmgn1	20.630596	1.3940287	1.46E-94	5.62E-92	Colonic mesenchymal cells-2
Adamdec1	14.214449	8.369211	7.45E-46	1.46E-41	Tmem176a+ cells
Tmem176a	14.163879	5.040193	1.53E-45	1.51E-41	Tmem176a+ cells
Tmem176b	13.8991375	4.396839	6.41E-44	4.20E-40	Tmem176a+ cells
Col6a4	13.74352	9.505418	5.57E-43	2.74E-39	Tmem176a+ cells
Gm13889	13.52374	5.934609	1.13E-41	4.05E-38	Tmem176a+ cells
Col6a1	13.517305	4.775067	1.24E-41	4.05E-38	Tmem176a+ cells
Malat1	13.166081	3.3361597	1.38E-39	3.86E-36	Tmem176a+ cells
Plpp3	12.876387	5.0059085	6.11E-38	1.50E-34	Tmem176a+ cells
Ptch1	12.614443	5.0776424	1.76E-36	3.84E-33	Tmem176a+ cells
Lamb1	12.199491	3.479922	3.13E-34	5.80E-31	Tmem176a+ cells
Lama5	12.196527	6.0181413	3.24E-34	5.80E-31	Tmem176a+ cells
Col6a2	11.927069	4.104745	8.55E-33	1.40E-29	Tmem176a+ cells
Ifitm3	11.720597	3.2346668	1.00E-31	1.51E-28	Tmem176a+ cells
AW112010	11.630608	6.2180257	2.88E-31	4.04E-28	Tmem176a+ cells
Aldh1a3	11.51101	8.747937	1.16E-30	1.52E-27	Tmem176a+ cells
Foxf1	11.273899	4.31611	1.77E-29	2.17E-26	Tmem176a+ cells
Col18a1	10.986155	3.69019	4.46E-28	5.15E-25	Tmem176a+ cells
Tgfbi	10.964802	4.470023	5.64E-28	6.16E-25	Tmem176a+ cells
Pten	10.830628	3.408931	2.46E-27	2.31E-24	Tmem176a+ cells
Nkx2-3	10.759071	3.4067073	5.37E-27	4.80E-24	Tmem176a+ cells

Bgn	10.731783	3.7262146	7.22E-27	6.17E-24	Tmem176a+ cells
Tpm1	10.645919	2.8900406	1.82E-26	1.38E-23	Tmem176a+ cells
Ifitm1	10.599764	3.6264734	2.99E-26	2.17E-23	Tmem176a+ cells
Pdgfra	10.553733	5.5359735	4.88E-26	3.41E-23	Tmem176a+ cells
Nid1	10.542481	3.2425482	5.50E-26	3.60E-23	Tmem176a+ cells
Bmp4	10.516327	5.314901	7.27E-26	4.61E-23	Tmem176a+ cells
Foxf2	10.399313	6.58673	2.50E-25	1.49E-22	Tmem176a+ cells
mt-Cytb	10.393878	1.0272892	2.64E-25	1.53E-22	Tmem176a+ cells
Lgmn	10.353432	3.3604872	4.04E-25	2.27E-22	Tmem176a+ cells
Col1a2	10.327357	3.3793235	5.30E-25	2.89E-22	Tmem176a+ cells
Igfbp7	10.303835	3.2004547	6.77E-25	3.50E-22	Tmem176a+ cells
Hhip	10.088512	7.624265	6.21E-24	2.98E-21	Tmem176a+ cells
Pla2g4a	10.080806	4.7744503	6.72E-24	3.14E-21	Tmem176a+ cells
4-Sep	10.060891	4.689889	8.23E-24	3.76E-21	Tmem176a+ cells
Cebpd	10.044651	4.1808815	9.70E-24	4.33E-21	Tmem176a+ cells
Npnt	9.878523	5.83122	5.16E-23	2.16E-20	Tmem176a+ cells
Txnip	9.77443	2.623941	1.45E-22	5.81E-20	Tmem176a+ cells
Col6a3	9.644387	3.8420525	5.19E-22	2.00E-19	Tmem176a+ cells
Meg3	9.603405	3.2581747	7.73E-22	2.92E-19	Tmem176a+ cells
Myh9	9.49659	2.644387	2.17E-21	7.61E-19	Tmem176a+ cells
Itgb1	9.442357	2.0090888	3.64E-21	1.19E-18	Tmem176a+ cells
Lhfp	9.239886	4.068866	2.47E-20	7.58E-18	Tmem176a+ cells
Pros1	9.145848	4.993562	5.92E-20	1.74E-17	Tmem176a+ cells
Tnc	9.128705	5.3123045	6.93E-20	2.00E-17	Tmem176a+ cells
Ghr	9.09464	3.0651472	9.49E-20	2.70E-17	Tmem176a+ cells
Gpx3	8.912282	3.1340992	5.00E-19	1.29E-16	Tmem176a+ cells
Col5a1	8.857502	2.7933683	8.18E-19	2.09E-16	Tmem176a+ cells
Bmp5	8.824468	6.6443024	1.10E-18	2.77E-16	Tmem176a+ cells
Plac8	8.745874	3.0855193	2.21E-18	5.50E-16	Tmem176a+ cells
Cebpb	8.68175	2.8032296	3.90E-18	9.15E-16	Tmem176a+ cells
mt-Nd4l	82.83756	2.6259253	0	0	Undifferentiated endothelial cells
Tmsb10	78.873764	1.4938555	0	0	Undifferentiated endothelial cells
Gm42418	75.4467	1.9576218	0	0	Undifferentiated endothelial cells
Tmsb4x	73.941925	1.2967736	0	0	Undifferentiated endothelial cells
Gnas	73.56396	1.483446	0	0	Undifferentiated endothelial cells
Mest	67.66803	2.3645527	0	0	Undifferentiated endothelial cells
Actb	65.2704	1.0742474	0	0	Undifferentiated endothelial cells
mt-Nd2	63.90755	0.8753704	0	0	Undifferentiated endothelial cells
Fabp5	62.57754	2.2761815	0	0	Undifferentiated endothelial cells
Fkbp1a	61.861866	1.5665957	0	0	Undifferentiated endothelial cells
Ppia	60.914215	0.71327484	0	0	Undifferentiated endothelial cells
Actg1	58.29407	0.8549969	0	0	Undifferentiated endothelial cells
Vim	58.13862	1.739398	0	0	Undifferentiated endothelial cells
mt-Atp6	57.590267	0.6965734	0	0	Undifferentiated endothelial cells
Pfn1	57.19869	0.95856416	0	0	Undifferentiated endothelial cells
mt-Nd5	51.870167	0.9219526	0	0	Undifferentiated endothelial cells
Gng11	51.751644	2.2497587	0	0	Undifferentiated endothelial cells

Gnai2	51.51373	1.2380847	0	0	Undifferentiated endothelial cells
Cfl1	51.18317	0.7789835	0	0	Undifferentiated endothelial cells
Tagln2	49.27014	1.6057245	0	0	Undifferentiated endothelial cells
mt-Nd4	49.21613	0.6376001	0	0	Undifferentiated endothelial cells
Hbb-y	47.992954	2.8816113	0	0	Undifferentiated endothelial cells
mt-Co3	47.03551	0.56097454	0	0	Undifferentiated endothelial cells
S100a16	46.18638	2.220543	0	0	Undifferentiated endothelial cells
Crip2	45.541252	2.0035799	0	0	Undifferentiated endothelial cells
Ptma	44.502876	0.64303625	0	0	Undifferentiated endothelial cells
Ran	43.338406	0.91955477	0	0	Undifferentiated endothelial cells
Fabp4	43.214073	2.3756166	0	0	Undifferentiated endothelial cells
Calm1	43.084953	0.7526446	0	0	Undifferentiated endothelial cells
mt-Nd1	42.5368	0.56760716	0	0	Undifferentiated endothelial cells
Dynll1	42.394352	0.76259303	0	0	Undifferentiated endothelial cells
mt-Co2	40.25813	0.46933395	0	0	Undifferentiated endothelial cells
Gng5	39.38165	0.44480553	0	0	Undifferentiated endothelial cells
H2afz	38.197598	0.79098094	0	0	Undifferentiated endothelial cells
Tubb5	37.960922	0.8538713	0	0	Undifferentiated endothelial cells
Eif5a	37.62533	0.7472813	8.2845677179555e-310	9.63E-308	Undifferentiated endothelial cells
Hspa8	37.295937	0.44171816	1.91E-304	2.14E-302	Undifferentiated endothelial cells
Tcf15	36.854313	2.9452744	2.49E-297	2.57E-295	Undifferentiated endothelial cells
Hsp90ab1	34.607334	0.5474333	1.96E-262	1.42E-260	Undifferentiated endothelial cells
Tpm4	34.570026	1.0931448	7.13E-262	5.11E-260	Undifferentiated endothelial cells
Ramp2	34.12096	1.5973027	3.61E-255	2.39E-253	Undifferentiated endothelial cells
mt-Cytb	33.40779	0.39525375	1.06E-244	6.20E-243	Undifferentiated endothelial cells
Rps6	32.807667	0.33575132	4.58E-236	2.43E-234	Undifferentiated endothelial cells
Plvap	32.326283	1.5622653	2.99E-229	1.47E-227	Undifferentiated endothelial cells
Prdx1	32.306095	0.39639595	5.74E-229	2.80E-227	Undifferentiated endothelial cells
Nes	31.804855	2.3313777	5.55E-222	2.51E-220	Undifferentiated endothelial cells
Icam2	31.396496	2.2078125	2.26E-216	9.57E-215	Undifferentiated endothelial cells
Rbp1	31.189423	1.1635487	1.48E-213	6.07E-212	Undifferentiated endothelial cells
Rps2	30.66677	0.39054313	1.58E-206	6.06E-205	Undifferentiated endothelial cells
Eif4a1	29.760569	0.34567103	1.27E-194	4.32E-193	Undifferentiated endothelial cells
Cdh5	54.905457	3.900877	0	0	Transitioning endothelial cells
Icam2	53.713192	3.765203	0	0	Transitioning endothelial cells
Egfl7	53.553642	3.7762299	0	0	Transitioning endothelial cells
Cldn5	53.43777	4.0260377	0	0	Transitioning endothelial cells
Ecscr	51.89413	3.424478	0	0	Transitioning endothelial cells
Mest	51.51567	2.8511584	0	0	Transitioning endothelial cells
Emcn	50.444893	3.5495138	0	0	Transitioning endothelial cells
Esam	50.277508	3.3551679	0	0	Transitioning endothelial cells
Col18a1	50.058765	3.2571363	0	0	Transitioning endothelial cells
S100a16	49.530006	2.929165	0	0	Transitioning endothelial cells
Plxnd1	49.361626	3.1228356	0	0	Transitioning endothelial cells
Pecam1	49.18656	3.270362	0	0	Transitioning endothelial cells
Ramp2	49.041542	3.0285213	0	0	Transitioning endothelial cells
Fkbp1a	48.95607	1.9730138	0	0	Transitioning endothelial cells

Cd93	47.739307	3.2172563	0	0	Transitioning endothelial cells
Gnas	47.6722	1.7099848	0	0	Transitioning endothelial cells
Kdr	46.79413	2.946396	0	0	Transitioning endothelial cells
Tcf15	46.464916	3.4374392	0	0	Transitioning endothelial cells
Gng11	46.383247	2.7484345	0	0	Transitioning endothelial cells
Lmo2	45.832577	3.0024333	0	0	Transitioning endothelial cells
Gnai2	45.760315	1.8273051	0	0	Transitioning endothelial cells
Plvap	45.454247	2.9033084	0	0	Transitioning endothelial cells
Crip2	45.002583	2.671287	0	0	Transitioning endothelial cells
Ccdc85b	44.109524	2.6499732	0	0	Transitioning endothelial cells
Col4a1	43.76719	2.6705616	0	0	Transitioning endothelial cells
Vamp5	43.6589	2.8657465	0	0	Transitioning endothelial cells
Cav1	43.600666	2.6968277	0	0	Transitioning endothelial cells
Rasip1	42.978172	2.780279	0	0	Transitioning endothelial cells
Flt1	42.937153	2.6838582	0	0	Transitioning endothelial cells
Tmsb10	42.53384	1.3315324	0	0	Transitioning endothelial cells
Gimap6	42.360344	2.8313203	0	0	Transitioning endothelial cells
Aplnr	41.982147	3.3775086	0	0	Transitioning endothelial cells
Col4a2	41.663963	2.4137697	0	0	Transitioning endothelial cells
Col15a1	41.589764	2.809881	0	0	Transitioning endothelial cells
Gimap1	41.52706	3.0529172	0	0	Transitioning endothelial cells
Ctla2a	41.355106	2.7966852	0	0	Transitioning endothelial cells
Tmsb4x	41.036835	1.195654	0	0	Transitioning endothelial cells
Vim	40.796055	2.0341368	0	0	Transitioning endothelial cells
Abhd17a	40.30944	1.9595733	0	0	Transitioning endothelial cells
Tmem255a	40.272327	3.3455956	0	0	Transitioning endothelial cells
Actg1	39.700592	0.98435223	0	0	Transitioning endothelial cells
Cd34	39.699265	2.5248199	0	0	Transitioning endothelial cells
Plk2	39.37609	2.6757329	0	0	Transitioning endothelial cells
Elk3	39.374786	2.4025235	0	0	Transitioning endothelial cells
Bst2	39.318867	2.3693094	0	0	Transitioning endothelial cells
Tie1	39.27626	2.706325	0	0	Transitioning endothelial cells
Cavin3	39.266666	2.1709368	0	0	Transitioning endothelial cells
Ralb	38.658554	1.9976398	0	0	Transitioning endothelial cells
Eng	38.48788	2.2237732	0	0	Transitioning endothelial cells
Tspan6	38.38377	2.1969264	0	0	Transitioning endothelial cells
Vwf	31.569065	6.7315025	9.82E-219	1.93E-214	Venous endothelial cells
Cavin2	30.976673	5.0471425	1.11E-210	1.09E-206	Venous endothelial cells
Fabp4	30.851273	6.2342343	5.39E-209	3.53E-205	Venous endothelial cells
Ptprb	30.131538	5.2873454	1.87E-199	9.20E-196	Venous endothelial cells
Fbln2	29.88902	5.8806653	2.73E-196	1.07E-192	Venous endothelial cells
Eln	29.812563	6.211465	2.69E-195	8.80E-192	Venous endothelial cells
Cav1	29.792004	4.5716853	4.96E-195	1.39E-191	Venous endothelial cells
Calcrl	29.256126	5.2392254	3.75E-188	9.22E-185	Venous endothelial cells
Cldn5	29.250225	5.2254634	4.46E-188	9.74E-185	Venous endothelial cells
Ackr3	29.0636	5.7757154	1.04E-185	2.04E-182	Venous endothelial cells
Fbln5	28.926275	5.527806	5.58E-184	9.97E-181	Venous endothelial cells

Aplnr	28.766838	4.726275	5.58E-182	9.13E-179	Venous endothelial cells
S100a10	28.617424	3.1448176	4.08E-180	6.17E-177	Venous endothelial cells
Cd9	27.864332	3.4708986	7.22E-171	1.01E-167	Venous endothelial cells
Cd36	27.496967	4.8059354	1.91E-166	2.50E-163	Venous endothelial cells
Ramp2	27.08062	3.627333	1.67E-161	2.05E-158	Venous endothelial cells
Fbn1	26.347012	3.8390353	5.55E-153	6.42E-150	Venous endothelial cells
Slc6a6	26.295628	3.7166717	2.15E-152	2.35E-149	Venous endothelial cells
Clec14a	26.215826	4.222568	1.75E-151	1.81E-148	Venous endothelial cells
Pecam1	26.188631	3.8331292	3.58E-151	3.52E-148	Venous endothelial cells
Procr	26.058512	5.19969	1.08E-149	1.01E-146	Venous endothelial cells
Iqgap1	26.036507	3.101217	1.91E-149	1.71E-146	Venous endothelial cells
Aqp1	25.992214	6.41198	6.06E-149	5.18E-146	Venous endothelial cells
Cavin1	25.885763	3.3406467	9.63E-148	7.89E-145	Venous endothelial cells
Aplp2	25.869457	2.7910938	1.47E-147	1.16E-144	Venous endothelial cells
Lbp	25.701311	5.0348177	1.13E-145	8.54E-143	Venous endothelial cells
Entpd1	25.647678	4.8109846	4.49E-145	3.27E-142	Venous endothelial cells
Ehd4	25.34424	3.7111263	1.04E-141	7.30E-139	Venous endothelial cells
Plvap	25.273867	3.986584	6.19E-141	4.20E-138	Venous endothelial cells
Egfl7	25.240908	3.6699665	1.43E-140	9.34E-138	Venous endothelial cells
Tie1	25.10752	3.675476	4.12E-139	2.61E-136	Venous endothelial cells
Foxp1	24.970613	2.9114444	1.28E-137	7.83E-135	Venous endothelial cells
Cdh5	24.938961	3.6013315	2.81E-137	1.68E-134	Venous endothelial cells
Ifitm3	24.870472	3.0374687	1.55E-136	8.72E-134	Venous endothelial cells
Txnip	24.870457	2.8345299	1.55E-136	8.72E-134	Venous endothelial cells
Palmd	24.869287	5.388723	1.60E-136	8.73E-134	Venous endothelial cells
Emcn	24.766588	3.7505097	2.05E-135	1.09E-132	Venous endothelial cells
Fstl1	24.510572	2.8577206	1.14E-132	5.89E-130	Venous endothelial cells
Klf2	24.44059	3.9600923	6.34E-132	3.19E-129	Venous endothelial cells
Rapgef5	24.436926	3.9926984	6.93E-132	3.41E-129	Venous endothelial cells
Itgb1	24.3569	2.405584	4.90E-131	2.35E-128	Venous endothelial cells
Crip2	24.109278	3.0246398	2.00E-128	9.35E-126	Venous endothelial cells
Utrn	24.02505	3.2488005	1.52E-127	6.96E-125	Venous endothelial cells
AU021092	23.918499	4.688472	1.97E-126	8.78E-124	Venous endothelial cells
Plxnd1	23.857826	3.1921856	8.40E-126	3.67E-123	Venous endothelial cells
H2-D1	23.80119	3.0926073	3.25E-125	1.39E-122	Venous endothelial cells
Ece1	23.707102	3.2333605	3.05E-124	1.25E-121	Venous endothelial cells
Jam2	23.70693	4.7859387	3.06E-124	1.25E-121	Venous endothelial cells
Lmo2	23.562134	3.2846014	9.43E-123	3.78E-120	Venous endothelial cells
S100a16	23.531479	2.9140692	1.94E-122	7.64E-120	Venous endothelial cells
Fbln5	23.534048	7.3221703	1.83E-122	3.59E-118	Arterial endothelial cells
Fn1	22.699717	5.5665154	4.51E-114	4.43E-110	Arterial endothelial cells
Tm4sf1	22.470411	5.443712	8.08E-112	5.30E-108	Arterial endothelial cells
Ptprb	22.426718	5.2873693	2.16E-111	1.06E-107	Arterial endothelial cells
Eln	21.736912	6.825557	9.19E-105	3.61E-101	Arterial endothelial cells
Fstl1	21.533268	3.5279408	7.60E-103	2.49E-99	Arterial endothelial cells
Sox17	20.890144	5.4899206	6.58E-97	1.85E-93	Arterial endothelial cells
Gja5	20.790735	8.107904	5.25E-96	1.29E-92	Arterial endothelial cells

Cldn5	20.59594	4.918551	2.98E-94	6.52E-91	Arterial endothelial cells
Pecam1	20.418386	4.1724944	1.15E-92	2.26E-89	Arterial endothelial cells
Fbln2	20.3857	5.588142	2.24E-92	4.00E-89	Arterial endothelial cells
Ltbp4	20.328836	4.197796	7.15E-92	1.17E-88	Arterial endothelial cells
Epas1	20.296648	4.6423335	1.38E-91	2.08E-88	Arterial endothelial cells
Gja4	20.11792	5.4978547	5.14E-90	7.22E-87	Arterial endothelial cells
Jag1	20.102028	5.130797	7.08E-90	9.28E-87	Arterial endothelial cells
Mmrn2	19.527096	4.356726	6.46E-85	7.94E-82	Arterial endothelial cells
Ramp2	19.424377	3.6259181	4.80E-84	5.55E-81	Arterial endothelial cells
Vim	19.385536	2.8302274	1.02E-83	1.12E-80	Arterial endothelial cells
Cdh5	19.20068	3.81259	3.65E-82	3.78E-79	Arterial endothelial cells
Clec14a	19.169867	4.3822846	6.61E-82	6.49E-79	Arterial endothelial cells
Vwf	19.067535	5.2421627	4.70E-81	4.40E-78	Arterial endothelial cells
Lmo2	18.947865	3.944684	4.60E-80	4.11E-77	Arterial endothelial cells
Edn1	18.659678	5.8344164	1.05E-77	9.00E-75	Arterial endothelial cells
Stmn2	18.518902	4.2592115	1.45E-76	1.19E-73	Arterial endothelial cells
Crip2	18.26731	3.1324344	1.51E-74	1.18E-71	Arterial endothelial cells
Cav1	18.261986	3.7627573	1.66E-74	1.26E-71	Arterial endothelial cells
Heg1	18.2091	3.8939555	4.37E-74	3.18E-71	Arterial endothelial cells
Trim47	17.911953	4.257567	9.51E-72	6.68E-69	Arterial endothelial cells
Cd93	17.907404	3.62426	1.03E-71	7.00E-69	Arterial endothelial cells
Klf2	17.8528	3.929023	2.75E-71	1.80E-68	Arterial endothelial cells
Itgb1	17.750233	2.3442461	1.72E-70	1.09E-67	Arterial endothelial cells
Mgp	17.674643	5.2323575	6.58E-70	4.04E-67	Arterial endothelial cells
Htra1	17.472239	6.207558	2.33E-68	1.39E-65	Arterial endothelial cells
Tie1	17.45735	3.7540443	3.03E-68	1.75E-65	Arterial endothelial cells
Mecom	17.450497	4.6320167	3.41E-68	1.92E-65	Arterial endothelial cells
Col18a1	17.435303	3.4182372	4.45E-68	2.43E-65	Arterial endothelial cells
Cavin2	17.411953	3.4433882	6.70E-68	3.56E-65	Arterial endothelial cells
Tek	17.284752	4.1877365	6.13E-67	3.17E-64	Arterial endothelial cells
Cavin1	17.068075	3.1563928	2.57E-65	1.29E-62	Arterial endothelial cells
Vegfc	17.036768	5.0733323	4.38E-65	2.15E-62	Arterial endothelial cells
Azin1	17.032894	3.5366488	4.68E-65	2.24E-62	Arterial endothelial cells
Iqgap1	16.959286	2.9364154	1.64E-64	7.69E-62	Arterial endothelial cells
Ehd2	16.951971	3.5234473	1.86E-64	8.51E-62	Arterial endothelial cells
Efnb2	16.935125	3.722077	2.48E-64	1.11E-61	Arterial endothelial cells
Icam2	16.790934	3.4831698	2.84E-63	1.24E-60	Arterial endothelial cells
Sox18	16.78344	3.4344432	3.23E-63	1.38E-60	Arterial endothelial cells
Ehd4	16.643688	3.3976142	3.36E-62	1.41E-59	Arterial endothelial cells
Sema3g	16.642004	6.427812	3.46E-62	1.42E-59	Arterial endothelial cells
Sparcl1	16.610897	3.0225127	5.81E-62	2.33E-59	Arterial endothelial cells
Ecscr	16.355072	3.1447413	4.00E-60	1.57E-57	Arterial endothelial cells
Mmrn1	38.78331	7.8837867	0	0	Lymphatic endothelial cells
Cldn5	37.1719	5.0639377	1.94E-302	1.91E-298	Lymphatic endothelial cells
Gnas	36.580715	2.256054	5.79E-293	3.80E-289	Lymphatic endothelial cells
Klhl4	36.516953	5.4034023	5.97E-292	2.93E-288	Lymphatic endothelial cells
Prox1	35.319645	7.473259	2.93E-273	1.15E-269	Lymphatic endothelial cells

Cavin2	35.190308	4.363723	2.81E-271	9.21E-268	Lymphatic endothelial cells
Stab1	34.179245	4.2996764	4.92E-256	1.38E-252	Lymphatic endothelial cells
Flt4	33.62374	4.81937	7.55E-248	1.85E-244	Lymphatic endothelial cells
Col18a1	33.198704	3.554133	1.12E-241	2.45E-238	Lymphatic endothelial cells
Gng11	32.876705	3.2402847	4.73E-237	9.30E-234	Lymphatic endothelial cells
Thy1	32.873657	7.8902574	5.23E-237	9.35E-234	Lymphatic endothelial cells
Ecscr	32.074493	3.5213256	1.00E-225	1.64E-222	Lymphatic endothelial cells
Vim	31.345053	2.4815824	1.14E-215	1.72E-212	Lymphatic endothelial cells
Egfl7	30.850811	3.4863691	5.46E-209	7.67E-206	Lymphatic endothelial cells
Lyve1	30.788923	6.7086444	3.69E-208	4.83E-205	Lymphatic endothelial cells
Ccl21a	30.68589	9.522429	8.78E-207	1.08E-203	Lymphatic endothelial cells
Lbp	30.360197	5.698302	1.84E-202	2.13E-199	Lymphatic endothelial cells
Gja1	30.267927	4.0149555	3.03E-201	3.31E-198	Lymphatic endothelial cells
Elk3	30.21613	3.2161028	1.45E-200	1.50E-197	Lymphatic endothelial cells
Tbx1	30.021204	8.034812	5.19E-198	5.10E-195	Lymphatic endothelial cells
Ramp2	29.272015	2.9828246	2.36E-188	2.20E-185	Lymphatic endothelial cells
Fn1	29.247368	3.4075615	4.85E-188	4.33E-185	Lymphatic endothelial cells
Nrp2	29.166826	3.2818708	5.11E-187	4.37E-184	Lymphatic endothelial cells
Aplp2	29.144375	2.6141026	9.84E-187	8.06E-184	Lymphatic endothelial cells
Cav1	29.000765	3.434704	6.43E-185	5.06E-182	Lymphatic endothelial cells
Lmo2	28.60823	3.0692952	5.31E-180	4.01E-177	Lymphatic endothelial cells
Fgl2	28.532103	6.383753	4.68E-179	3.41E-176	Lymphatic endothelial cells
Rab11a	28.49634	2.322308	1.30E-178	9.13E-176	Lymphatic endothelial cells
Arl4a	28.371708	3.074432	4.52E-177	3.06E-174	Lymphatic endothelial cells
Prss23	28.17334	3.3687022	1.24E-174	8.13E-172	Lymphatic endothelial cells
Lims1	28.075243	2.6532032	1.97E-173	1.25E-170	Lymphatic endothelial cells
Sox18	28.03484	3.0498683	6.11E-173	3.75E-170	Lymphatic endothelial cells
Reln	28.02443	6.6844077	8.19E-173	4.88E-170	Lymphatic endothelial cells
Wnk1	27.993216	2.5421727	1.97E-172	1.14E-169	Lymphatic endothelial cells
Tie1	27.733736	3.1865647	2.74E-169	1.54E-166	Lymphatic endothelial cells
Ptpn18	27.668797	3.0457802	1.66E-168	9.05E-166	Lymphatic endothelial cells
Sgk3	27.23474	3.8429868	2.52E-163	1.34E-160	Lymphatic endothelial cells
Cd47	27.198198	2.4234693	6.82E-163	3.53E-160	Lymphatic endothelial cells
S100a16	26.903913	2.620688	1.98E-159	9.96E-157	Lymphatic endothelial cells
Degs1	26.762302	2.703449	8.88E-158	4.36E-155	Lymphatic endothelial cells
Ppfibp1	26.734922	2.86167	1.85E-157	8.86E-155	Lymphatic endothelial cells
Timp3	26.219368	2.8151748	1.60E-151	7.48E-149	Lymphatic endothelial cells
Myzap	25.909925	3.8740509	5.15E-148	2.35E-145	Lymphatic endothelial cells
Cdh5	25.894245	2.707567	7.73E-148	3.45E-145	Lymphatic endothelial cells
Myct1	25.852747	2.9372723	2.27E-147	9.90E-145	Lymphatic endothelial cells
Pard6g	25.664934	4.0107536	2.88E-145	1.23E-142	Lymphatic endothelial cells
Tmsb10	25.557108	1.3057114	4.58E-144	1.91E-141	Lymphatic endothelial cells
Slc45a3	25.502012	8.409014	1.87E-143	7.67E-141	Lymphatic endothelial cells
Sptssa	24.883963	1.9145975	1.11E-136	4.45E-134	Lymphatic endothelial cells
Nudt4	24.773153	2.7191508	1.75E-135	6.86E-133	Lymphatic endothelial cells
Igfbp7	89.78948	7.615959	0	0	Capillary endothelial cells
Plvap	88.494316	6.4106455	0	0	Capillary endothelial cells

Col4a1	86.826614	5.1916265	0	0	Capillary endothelial cells
Kdr	84.18997	5.656364	0	0	Capillary endothelial cells
Flt1	84.16475	6.309623	0	0	Capillary endothelial cells
Col4a2	83.84393	4.8045063	0	0	Capillary endothelial cells
Rgcc	82.400894	6.249624	0	0	Capillary endothelial cells
Fabp4	79.200775	5.3882804	0	0	Capillary endothelial cells
Sparcl1	78.923775	4.267553	0	0	Capillary endothelial cells
Plpp3	78.118065	4.8120294	0	0	Capillary endothelial cells
Eng	78.01707	4.6008716	0	0	Capillary endothelial cells
Emcn	77.949104	4.8969836	0	0	Capillary endothelial cells
Hspg2	77.80623	4.3845534	0	0	Capillary endothelial cells
Pecam1	77.20558	4.506887	0	0	Capillary endothelial cells
Col15a1	77.195435	5.1079273	0	0	Capillary endothelial cells
Egfl7	76.83877	4.411851	0	0	Capillary endothelial cells
Itm2b	75.01674	2.5420551	0	0	Capillary endothelial cells
Ly6a	74.057915	6.610785	0	0	Capillary endothelial cells
Ctla2a	73.80668	5.136814	0	0	Capillary endothelial cells
Adgrf5	73.59198	4.8342695	0	0	Capillary endothelial cells
Slco2a1	73.55666	6.242526	0	0	Capillary endothelial cells
Ptprb	73.13749	5.304671	0	0	Capillary endothelial cells
Cdh5	73.004326	4.3133926	0	0	Capillary endothelial cells
Ifitm3	72.90854	3.2934346	0	0	Capillary endothelial cells
Tcim	71.96361	4.407952	0	0	Capillary endothelial cells
Mcam	71.86014	4.507082	0	0	Capillary endothelial cells
Tm4sf1	71.83103	4.5313907	0	0	Capillary endothelial cells
Esam	71.30216	4.2655807	0	0	Capillary endothelial cells
Nid1	71.224754	3.7596745	0	0	Capillary endothelial cells
Sox18	70.8572	4.3729167	0	0	Capillary endothelial cells
Ly6c1	70.84272	6.9642467	0	0	Capillary endothelial cells
Cd34	70.540146	3.8187659	0	0	Capillary endothelial cells
Tcf4	70.470665	3.1852684	0	0	Capillary endothelial cells
Ets1	70.30005	3.8154159	0	0	Capillary endothelial cells
Vwa1	70.02036	5.4885607	0	0	Capillary endothelial cells
Sparc	69.2066	2.9715197	0	0	Capillary endothelial cells
Msn	69.079765	3.312232	0	0	Capillary endothelial cells
Cd93	69.00599	4.2622275	0	0	Capillary endothelial cells
Pcdh17	68.817894	4.6590676	0	0	Capillary endothelial cells
Epas1	68.797356	4.6742935	0	0	Capillary endothelial cells
Mgll	68.4712	4.6326466	0	0	Capillary endothelial cells
Thbs1	68.238716	5.146039	0	0	Capillary endothelial cells
Myct1	67.927376	4.4942694	0	0	Capillary endothelial cells
Cd300lg	67.784645	8.077618	0	0	Capillary endothelial cells
Ramp2	67.59119	3.3666542	0	0	Capillary endothelial cells
Robo4	66.526344	4.933957	0	0	Capillary endothelial cells
Plpp1	66.4924	3.9864419	0	0	Capillary endothelial cells
Rflnb	66.48284	4.0470586	0	0	Capillary endothelial cells
Gimap6	66.2773	4.0190077	0	0	Capillary endothelial cells

Cd81	66.1666	2.1054316	0	0	Capillary endothelial cells
Bex1	55.212868	4.493469	0	0	Lgr5+ stem/ progenitor cells
Epcam	52.03011	4.4348702	0	0	Lgr5+ stem/ progenitor cells
Bex4	51.338818	3.6084425	0	0	Lgr5+ stem/ progenitor cells
Mif	50.97397	2.0410118	0	0	Lgr5+ stem/ progenitor cells
Spint2	46.232044	3.0994074	0	0	Lgr5+ stem/ progenitor cells
Krt19	45.972622	3.562554	0	0	Lgr5+ stem/ progenitor cells
Cldn7	45.97086	3.6116402	0	0	Lgr5+ stem/ progenitor cells
Krt8	45.7374	3.3636153	0	0	Lgr5+ stem/ progenitor cells
Stard10	45.402912	3.3991072	0	0	Lgr5+ stem/ progenitor cells
Rpl14	45.20539	1.0248518	0	0	Lgr5+ stem/ progenitor cells
Tspan8	45.134136	3.7707462	0	0	Lgr5+ stem/ progenitor cells
Rpl32	44.15847	0.8756179	0	0	Lgr5+ stem/ progenitor cells
Wfdc2	43.670288	4.0757623	0	0	Lgr5+ stem/ progenitor cells
Krt18	43.629726	3.2087321	0	0	Lgr5+ stem/ progenitor cells
Cldn3	42.84976	4.1248055	0	0	Lgr5+ stem/ progenitor cells
Rpl12	42.305195	1.0096365	0	0	Lgr5+ stem/ progenitor cells
Eef1b2	41.797752	1.1307305	0	0	Lgr5+ stem/ progenitor cells
Pcbd1	41.37513	2.9050703	0	0	Lgr5+ stem/ progenitor cells
Rps3	41.357502	0.88101584	0	0	Lgr5+ stem/ progenitor cells
Fkbp4	40.866737	2.0343304	0	0	Lgr5+ stem/ progenitor cells
Rpl27a	40.853367	0.7510251	0	0	Lgr5+ stem/ progenitor cells
Rps23	40.829536	0.8988371	0	0	Lgr5+ stem/ progenitor cells
Lgals2	39.92297	3.4978187	0	0	Lgr5+ stem/ progenitor cells
Rpl10a	39.55256	0.8755326	0	0	Lgr5+ stem/ progenitor cells
Rps13	39.503296	0.7800775	0	0	Lgr5+ stem/ progenitor cells
Cystm1	39.47718	2.7224216	0	0	Lgr5+ stem/ progenitor cells
Rps5	39.41215	0.92026067	0	0	Lgr5+ stem/ progenitor cells
Hspe1	39.403725	1.5181063	0	0	Lgr5+ stem/ progenitor cells
Cdx2	39.148636	3.4054902	0	0	Lgr5+ stem/ progenitor cells
Cldn6	39.111134	6.964539	0	0	Lgr5+ stem/ progenitor cells
Rps10	38.978947	0.704051	0	0	Lgr5+ stem/ progenitor cells
Tpi1	38.9767	1.7053907	0	0	Lgr5+ stem/ progenitor cells
Ttr	38.630722	3.136799	0	0	Lgr5+ stem/ progenitor cells
Rpl28	38.599464	0.6745202	0	0	Lgr5+ stem/ progenitor cells
Rpl3	38.324097	0.9446244	0	0	Lgr5+ stem/ progenitor cells
Rps20	38.180603	0.6704649	0	0	Lgr5+ stem/ progenitor cells
Rpsa	38.13921	0.92531383	0	0	Lgr5+ stem/ progenitor cells
Ldha	38.105495	1.6245693	0	0	Lgr5+ stem/ progenitor cells
Akr1c19	37.71008	2.571044	0	0	Lgr5+ stem/ progenitor cells
Rbp4	37.566673	4.984028	0.00E+00	3.70E-306	Lgr5+ stem/ progenitor cells
Crb3	37.424297	3.2746747	1.57E-306	7.54E-304	Lgr5+ stem/ progenitor cells
Rpl19	37.3731	0.7121402	1.07E-305	5.00E-303	Lgr5+ stem/ progenitor cells
Hsp90aa1	37.338875	1.444746	3.84E-305	1.76E-302	Lgr5+ stem/ progenitor cells
Rps19	37.318245	0.75811595	8.30E-305	3.71E-302	Lgr5+ stem/ progenitor cells
Rpl26	37.178204	0.6898636	1.54E-302	6.71E-300	Lgr5+ stem/ progenitor cells
Rpl13	37.110344	0.6428809	1.91E-301	8.17E-299	Lgr5+ stem/ progenitor cells

Rpl8	36.98361	0.8192285	2.10E-299	8.78E-297	Lgr5+ stem/ progenitor cells
Rack1	36.904358	0.84744966	3.93E-298	1.61E-295	Lgr5+ stem/ progenitor cells
Npm1	36.74171	1.0982567	1.58E-295	6.20E-293	Lgr5+ stem/ progenitor cells
Rps3a1	36.534424	0.6900639	3.15E-292	1.21E-289	Lgr5+ stem/ progenitor cells
Epcam	69.46512	5.6213465	0	0	Enterocytes-1
Cldn7	68.3597	5.2297873	0	0	Enterocytes-1
Pycard	67.70125	4.5776653	0	0	Enterocytes-1
Lypd8	66.69021	5.9060364	0	0	Enterocytes-1
Krt8	66.58098	4.8837533	0	0	Enterocytes-1
Lgals4	65.615036	5.997247	0	0	Enterocytes-1
Oat	65.538246	4.195455	0	0	Enterocytes-1
Mt1	65.23722	5.044687	0	0	Enterocytes-1
Krt19	64.73143	4.8128166	0	0	Enterocytes-1
Atp1b1	64.71045	4.3440685	0	0	Enterocytes-1
Aldh1b1	64.15497	4.5572443	0	0	Enterocytes-1
Ndrg1	64.01326	4.346907	0	0	Enterocytes-1
Tspan8	62.998215	4.517108	0	0	Enterocytes-1
Lgals2	62.67992	4.9912395	0	0	Enterocytes-1
Spint2	62.40842	3.754218	0	0	Enterocytes-1
Mgst1	61.98809	3.820584	0	0	Enterocytes-1
Hspd1	61.780025	2.7867846	0	0	Enterocytes-1
Ociad2	61.51047	4.1710668	0	0	Enterocytes-1
Cdh17	61.468063	4.552955	0	0	Enterocytes-1
Cps1	60.417057	5.1351633	0	0	Enterocytes-1
S100g	60.077213	4.3066545	0	0	Enterocytes-1
Cystm1	59.95376	3.902756	0	0	Enterocytes-1
Tm4sf20	59.7715	4.3316574	0	0	Enterocytes-1
Fbp2	59.473614	4.067253	0	0	Enterocytes-1
Mgst3	59.212452	3.3627238	0	0	Enterocytes-1
Akr1c19	58.80441	4.124409	0	0	Enterocytes-1
Tm4sf5	58.74384	4.1211853	0	0	Enterocytes-1
Anxa4	58.734932	3.733457	0	0	Enterocytes-1
Chchd10	58.501213	3.6208506	0	0	Enterocytes-1
Chpt1	58.301926	3.6771474	0	0	Enterocytes-1
Fabp2	58.084366	4.0516405	0	0	Enterocytes-1
Hspe1	57.613728	2.0128727	0	0	Enterocytes-1
Plac8	57.44593	3.6576338	0	0	Enterocytes-1
Aldob	57.389545	4.0296454	0	0	Enterocytes-1
Spink1	56.726414	3.7064116	0	0	Enterocytes-1
Klf5	56.71239	3.9855962	0	0	Enterocytes-1
Ckmt1	56.61256	3.8344567	0	0	Enterocytes-1
Vil1	56.53001	3.975547	0	0	Enterocytes-1
Prap1	56.505943	4.4648714	0	0	Enterocytes-1
Eps8l3	56.294838	3.9942153	0	0	Enterocytes-1
Ugt2b34	56.202347	4.381238	0	0	Enterocytes-1
Gna11	56.009106	2.8744059	0	0	Enterocytes-1
Otc	55.96696	4.4270372	0	0	Enterocytes-1

Gipc2	55.839676	3.7838352	0	0	Enterocytes-1
Akr1c13	55.822517	3.8173056	0	0	Enterocytes-1
Hadh	55.593224	2.8282561	0	0	Enterocytes-1
Amn	55.438744	4.1145315	0	0	Enterocytes-1
Calml4	55.329063	3.3484585	0	0	Enterocytes-1
Dbi	55.229755	2.3655093	0	0	Enterocytes-1
Gsto1	54.945267	2.929926	0	0	Enterocytes-1
Apoa4	69.51632	8.33324	0	0	Enterocytes-2
Apoa1	69.469604	8.330999	0	0	Enterocytes-2
Mttp	69.09272	6.509332	0	0	Enterocytes-2
Mamdc4	68.824455	6.678704	0	0	Enterocytes-2
Acsl5	68.27702	5.592249	0	0	Enterocytes-2
Apoc3	68.14572	7.3966002	0	0	Enterocytes-2
Apob	68.09869	6.406065	0	0	Enterocytes-2
Prap1	68.05809	6.600485	0	0	Enterocytes-2
Fabp2	67.87579	8.0084	0	0	Enterocytes-2
Chpt1	67.684944	5.326595	0	0	Enterocytes-2
Ace2	67.34102	6.558198	0	0	Enterocytes-2
Spink1	67.136444	6.035091	0	0	Enterocytes-2
Ckmt1	66.89047	5.812171	0	0	Enterocytes-2
Glb1	66.78754	5.0050826	0	0	Enterocytes-2
Aldob	66.74444	5.847734	0	0	Enterocytes-2
Muc13	66.69614	5.605587	0	0	Enterocytes-2
Dgat2	66.540184	6.232572	0	0	Enterocytes-2
Naga	66.48544	5.185841	0	0	Enterocytes-2
Amn	66.3892	5.7010984	0	0	Enterocytes-2
Smim24	66.38537	5.2385583	0	0	Enterocytes-2
Scd2	66.19795	3.9184225	0	0	Enterocytes-2
Dbi	66.161125	3.5436497	0	0	Enterocytes-2
Rbp2	66.11607	7.3933277	0	0	Enterocytes-2
Alpi	65.97057	6.444012	0	0	Enterocytes-2
Akr1c13	65.95002	5.3099375	0	0	Enterocytes-2
Fabp1	65.861206	8.5372305	0	0	Enterocytes-2
Fbp2	65.81629	5.299619	0	0	Enterocytes-2
Hmgcs2	65.81629	5.594484	0	0	Enterocytes-2
Akr1c19	65.78804	5.483113	0	0	Enterocytes-2
Cdhr5	65.776596	6.0516386	0	0	Enterocytes-2
Reep6	65.76117	5.3981586	0	0	Enterocytes-2
Lgals4	65.710976	6.3273883	0	0	Enterocytes-2
Cdh17	65.70879	5.1672797	0	0	Enterocytes-2
Maob	65.673294	6.0777955	0	0	Enterocytes-2
Creb3l3	65.66364	6.877013	0	0	Enterocytes-2
Myo15b	65.64842	5.362803	0	0	Enterocytes-2
Bpnt1	65.53623	4.923611	0	0	Enterocytes-2
Sult1b1	65.489006	5.793227	0	0	Enterocytes-2
Neu1	65.233345	4.8126397	0	0	Enterocytes-2
Eps8l3	65.057014	5.239022	0	0	Enterocytes-2

Calml4	64.688805	4.382403	0	0	Enterocytes-2
Mogat2	64.6357	5.526076	0	0	Enterocytes-2
Renbp	64.51815	4.857888	0	0	Enterocytes-2
Ctsa	64.4281	3.9748895	0	0	Enterocytes-2
Sult1d1	64.40586	5.3288336	0	0	Enterocytes-2
Tm4sf5	64.25322	4.8657846	0	0	Enterocytes-2
Tm4sf20	64.195595	4.9949813	0	0	Enterocytes-2
Cystm1	64.1361	4.634478	0	0	Enterocytes-2
Pdzk1ip1	64.131035	5.3359413	0	0	Enterocytes-2
Clec2h	64.12034	5.9149485	0	0	Enterocytes-2
Fabp2	44.78577	8.853637	0	0	Enterocytes-3
Rbp2	42.87948	7.8003387	0	0	Enterocytes-3
Ftl1	41.585514	2.4964297	0	0	Enterocytes-3
Lgals4	41.37771	6.0211177	0	0	Enterocytes-3
Npl	40.58744	6.8058333	0	0	Enterocytes-3
Oat	39.82526	4.6176033	0	0	Enterocytes-3
Aldob	39.561672	5.7658024	0	0	Enterocytes-3
Apoc3	39.223156	6.4400516	0	0	Enterocytes-3
Fth1	39.165154	2.277027	0	0	Enterocytes-3
Fabp1	38.691578	7.5830593	0	0	Enterocytes-3
Dbi	38.531815	3.2856104	0	0	Enterocytes-3
Ckmt1	37.977478	5.5462837	0	0	Enterocytes-3
Spink1	37.900898	5.652116	0	0	Enterocytes-3
Ass1	37.680786	5.7713547	0	0	Enterocytes-3
Apoa1	37.221603	5.8886476	3.05E-303	3.33E-300	Enterocytes-3
Cystm1	35.33457	4.7121625	1.73E-273	1.70E-270	Enterocytes-3
Gpx3	34.56928	5.5815716	7.32E-262	5.99E-259	Enterocytes-3
Apoa4	33.364265	5.1421547	4.52E-244	2.96E-241	Enterocytes-3
S100a1	33.14358	5.0822673	7.01E-241	4.17E-238	Enterocytes-3
Scp2	33.08306	3.2146556	5.21E-240	2.92E-237	Enterocytes-3
Renbp	32.86903	4.9469466	6.09E-237	3.24E-234	Enterocytes-3
Akr1c19	32.62035	4.727818	2.11E-233	1.06E-230	Enterocytes-3
Acaa2	32.469833	3.6922102	2.84E-231	1.40E-228	Enterocytes-3
Hadh	32.40953	3.5071406	2.01E-230	9.43E-228	Enterocytes-3
Mdh1	32.177635	2.7692502	3.63E-227	1.62E-224	Enterocytes-3
Slc9a3r1	32.09364	3.992081	5.41E-226	2.36E-223	Enterocytes-3
Fbp2	31.177828	4.5339007	2.13E-213	7.75E-211	Enterocytes-3
Slc25a3	30.876242	1.7490197	2.49E-209	8.59E-207	Enterocytes-3
Serpinb6a	30.775576	3.2982292	5.56E-208	1.88E-205	Enterocytes-3
Clec2h	30.602535	5.54745	1.13E-205	3.77E-203	Enterocytes-3
Cox7c	30.588535	1.7053123	1.74E-205	5.70E-203	Enterocytes-3
Uqcrq	30.259296	2.3485224	3.94E-201	1.25E-198	Enterocytes-3
Rab11a	30.25155	3.0066457	4.98E-201	1.55E-198	Enterocytes-3
Chchd2	30.243286	1.3236135	6.39E-201	1.96E-198	Enterocytes-3
Sult1b1	30.188652	4.990303	3.34E-200	1.01E-197	Enterocytes-3
Hmgcs2	29.882477	4.4140153	3.32E-196	9.20E-194	Enterocytes-3
Bex4	29.533588	3.8996942	1.07E-191	2.80E-189	Enterocytes-3

Chpt1	29.468513	3.9233603	7.29E-191	1.89E-188	Enterocytes-3
Slc25a5	29.399866	2.0475473	5.51E-190	1.41E-187	Enterocytes-3
Selenop	29.284079	3.235975	1.65E-188	4.12E-186	Enterocytes-3
Akr1c13	29.204453	4.443906	1.70E-187	4.13E-185	Enterocytes-3
Anxa4	29.073183	4.1338677	7.84E-186	1.88E-183	Enterocytes-3
Guca2b	28.48784	5.4173393	1.66E-178	3.66E-176	Enterocytes-3
Cox5a	28.271202	1.7266595	7.81E-176	1.71E-173	Enterocytes-3
Prap1	28.057447	4.2904954	3.24E-173	6.70E-171	Enterocytes-3
Eps8l3	27.692621	4.30864	8.57E-169	1.65E-166	Enterocytes-3
Calml4	27.58537	3.723878	1.67E-167	3.12E-165	Enterocytes-3
Plin3	27.578121	3.4743812	2.04E-167	3.78E-165	Enterocytes-3
Txndc17	27.295898	2.2049901	4.74E-164	8.55E-162	Enterocytes-3
Cstb	27.223059	3.143755	3.46E-163	6.13E-161	Enterocytes-3
Agr2	26.170574	12.01832	5.75E-151	1.13E-146	Goblet cells
Tff3	26.13607	11.303531	1.42E-150	1.39E-146	Goblet cells
Fcgbp	25.362043	11.448082	6.62E-142	4.34E-138	Goblet cells
Krt18	25.297665	5.189072	3.39E-141	1.67E-137	Goblet cells
Spint2	25.118046	4.7269545	3.16E-139	1.15E-135	Goblet cells
Fxyd3	25.11368	6.8455043	3.53E-139	1.15E-135	Goblet cells
Tpd52	25.032125	4.9243765	2.73E-138	7.67E-135	Goblet cells
Stard10	25.012339	5.0668173	4.49E-138	1.10E-134	Goblet cells
Krt8	24.662064	5.1448417	2.73E-134	5.97E-131	Goblet cells
Sct	24.485462	8.440702	2.11E-132	4.15E-129	Goblet cells
Tspan8	24.349716	4.9222507	5.84E-131	9.72E-128	Goblet cells
Serpina1b	24.349043	7.5299854	5.93E-131	9.72E-128	Goblet cells
Guca2a	24.227701	7.827113	1.14E-129	1.72E-126	Goblet cells
Cldn3	23.931479	5.3756065	1.44E-126	2.02E-123	Goblet cells
Hepacam2	23.694794	8.698347	4.08E-124	5.35E-121	Goblet cells
Gmds	23.582987	4.513719	5.76E-123	7.08E-120	Goblet cells
Lgals4	23.449144	5.77365	1.35E-121	1.56E-118	Goblet cells
Tpsg1	23.364502	11.724909	9.82E-121	1.07E-117	Goblet cells
Galnt7	23.260845	4.66685	1.10E-119	1.14E-116	Goblet cells
Spink4	23.07405	11.165083	8.44E-118	8.29E-115	Goblet cells
Phgr1	23.059866	5.5644603	1.17E-117	1.10E-114	Goblet cells
Gm1123	22.961842	9.103927	1.12E-116	1.00E-113	Goblet cells
Gcnt3	22.882614	9.788913	6.92E-116	5.91E-113	Goblet cells
Txndc5	22.849693	3.79769	1.47E-115	1.21E-112	Goblet cells
Clca1	22.689018	12.697485	5.75E-114	4.52E-111	Goblet cells
Smim6	22.573038	6.254271	7.98E-113	6.03E-110	Goblet cells
Car8	22.245104	4.3573365	1.26E-109	9.16E-107	Goblet cells
Muc2	22.231771	11.614806	1.69E-109	1.19E-106	Goblet cells
Qsox1	22.13536	4.83937	1.44E-108	9.78E-106	Goblet cells
Krt19	22.103333	4.303239	2.94E-108	1.92E-105	Goblet cells
Epcam	22.079948	4.7040653	4.93E-108	3.12E-105	Goblet cells
Lypd8	22.076317	5.13634	5.34E-108	3.28E-105	Goblet cells
Cldn7	21.96367	4.325219	6.41E-107	3.82E-104	Goblet cells
Tspan1	21.955776	6.746655	7.63E-107	4.41E-104	Goblet cells

Galnt12	21.903168	5.8995943	2.42E-106	1.36E-103	Goblet cells
Tspan13	21.69169	3.3592787	2.46E-104	1.34E-101	Goblet cells
Fut2	21.609804	8.784787	1.45E-103	7.72E-101	Goblet cells
Selenom	21.601505	3.4389093	1.74E-103	8.99E-101	Goblet cells
Smim14	21.524435	3.379475	9.19E-103	4.63E-100	Goblet cells
Ramp1	21.438421	4.890588	5.86E-102	2.88E-99	Goblet cells
Scin	21.432629	6.4196644	6.63E-102	3.18E-99	Goblet cells
Foxa3	21.284227	6.715504	1.59E-100	7.44E-98	Goblet cells
Krt7	21.156345	3.945099	2.41E-99	1.10E-96	Goblet cells
Gfpt1	21.145916	3.8581061	3.01E-99	1.34E-96	Goblet cells
S100a6	21.142157	3.906018	3.26E-99	1.42E-96	Goblet cells
Lsr	21.058619	4.05281	1.91E-98	8.15E-96	Goblet cells
Ehf	20.884733	6.589454	7.37E-97	3.02E-94	Goblet cells
Ccl9	20.884718	6.8904014	7.37E-97	3.02E-94	Goblet cells
Ms4a8a	20.875826	5.6180573	8.88E-97	3.56E-94	Goblet cells
Spdef	20.868128	9.959942	1.04E-96	4.10E-94	Goblet cells
Fxyd3	21.3488	6.9097476	4.00E-101	7.86E-97	Enteroendocrine cells
Tm4sf4	21.17511	8.253503	1.62E-99	1.59E-95	Enteroendocrine cells
Krt8	21.089972	4.9037886	9.83E-99	6.44E-95	Enteroendocrine cells
Aplp1	20.439259	5.9563384	7.49E-93	3.67E-89	Enteroendocrine cells
Spint2	20.428493	4.127133	9.33E-93	3.67E-89	Enteroendocrine cells
Cck	20.390823	10.108879	2.02E-92	6.61E-89	Enteroendocrine cells
Chgb	20.337658	10.224763	5.97E-92	1.68E-88	Enteroendocrine cells
Insm1	20.205956	6.897596	8.68E-91	2.13E-87	Enteroendocrine cells
Cpe	19.841843	4.282301	1.30E-87	2.83E-84	Enteroendocrine cells
Sct	19.809828	10.678531	2.45E-87	4.81E-84	Enteroendocrine cells
Tff3	19.61663	7.9072237	1.12E-85	1.99E-82	Enteroendocrine cells
Neurod1	19.26183	13.68912	1.12E-82	1.84E-79	Enteroendocrine cells
Hepacam2	19.125175	8.248772	1.56E-81	2.36E-78	Enteroendocrine cells
Cacna1a	19.114258	5.0770793	1.92E-81	2.70E-78	Enteroendocrine cells
Ttr	18.966846	5.254751	3.21E-80	4.20E-77	Enteroendocrine cells
Stard10	18.767925	3.9595811	1.38E-78	1.70E-75	Enteroendocrine cells
Bex2	18.712849	3.7542238	3.89E-78	4.50E-75	Enteroendocrine cells
Cystm1	18.683567	3.9009464	6.74E-78	7.35E-75	Enteroendocrine cells
Krt18	18.665873	3.8642366	9.38E-78	9.71E-75	Enteroendocrine cells
Vwa5b2	18.269276	8.2923565	1.45E-74	1.43E-71	Enteroendocrine cells
Fam183b	18.214827	6.9462113	3.94E-74	3.68E-71	Enteroendocrine cells
Krt7	18.122068	4.188857	2.13E-73	1.91E-70	Enteroendocrine cells
Chga	17.902206	7.6646953	1.13E-71	9.68E-69	Enteroendocrine cells
Epcam	17.503271	4.0063276	1.35E-68	1.06E-65	Enteroendocrine cells
Pcsk1	17.424538	9.266074	5.37E-68	4.06E-65	Enteroendocrine cells
Tpd52	17.313593	3.1495795	3.71E-67	2.70E-64	Enteroendocrine cells
Ddc	17.249117	5.4503455	1.14E-66	7.97E-64	Enteroendocrine cells
Pax6	17.201801	11.911305	2.57E-66	1.74E-63	Enteroendocrine cells
Clps	17.10995	9.05349	1.25E-65	8.20E-63	Enteroendocrine cells
Serpina1c	16.971493	7.38226	1.33E-64	8.46E-62	Enteroendocrine cells
Bsg	16.88407	2.1067972	5.89E-64	3.62E-61	Enteroendocrine cells

Selenom	16.852163	2.9006822	1.01E-63	6.02E-61	Enteroendocrine cells
Lgals2	16.763992	4.3269334	4.48E-63	2.59E-60	Enteroendocrine cells
Gfra3	16.630909	7.2968197	4.16E-62	2.34E-59	Enteroendocrine cells
Scgn	16.554739	11.09793	1.48E-61	8.08E-59	Enteroendocrine cells
Isl1	16.51819	5.618051	2.71E-61	1.44E-58	Enteroendocrine cells
Anxa4	16.361963	3.2743394	3.57E-60	1.85E-57	Enteroendocrine cells
Cldn7	16.331867	3.467253	5.86E-60	2.95E-57	Enteroendocrine cells
Scg3	16.228907	5.8903184	3.15E-59	1.55E-56	Enteroendocrine cells
Cdkn1a	16.14333	4.860263	1.27E-58	6.06E-56	Enteroendocrine cells
Rimbp2	16.023457	9.625607	8.76E-58	4.01E-55	Enteroendocrine cells
Prnp	15.933997	3.0386984	3.68E-57	1.64E-54	Enteroendocrine cells
Hmgn3	15.615635	3.2476897	5.70E-55	2.43E-52	Enteroendocrine cells
Serpinb1a	15.526969	3.601449	2.28E-54	9.53E-52	Enteroendocrine cells
Rbp4	15.514488	5.8718786	2.77E-54	1.13E-51	Enteroendocrine cells
Rph3al	15.400054	5.4144654	1.64E-53	6.56E-51	Enteroendocrine cells
Cldn4	15.372856	4.6927905	2.49E-53	9.78E-51	Enteroendocrine cells
Lsr	15.340988	3.529568	4.07E-53	1.57E-50	Enteroendocrine cells
Gch1	14.983499	4.455547	9.41E-51	3.43E-48	Enteroendocrine cells
Smim22	14.960397	3.5693083	1.33E-50	4.76E-48	Enteroendocrine cells
Tubb3	59.8455	8.330788	0	0	Enteric neurons
Dpysl3	59.33426	5.7338777	0	0	Enteric neurons
Tuba1a	59.12858	4.0613966	0	0	Enteric neurons
Phox2b	58.307087	6.664038	0	0	Enteric neurons
Elavl4	57.35558	8.39197	0	0	Enteric neurons
Uchl1	57.208286	5.724713	0	0	Enteric neurons
Map1b	56.00317	4.8099036	0	0	Enteric neurons
Cadm1	55.708374	6.2641296	0	0	Enteric neurons
Tlx2	53.917294	6.55518	0	0	Enteric neurons
Stmn1	52.786316	2.8626635	0	0	Enteric neurons
Tubb2b	52.567627	4.4543867	0	0	Enteric neurons
Bex2	52.024452	4.1393185	0	0	Enteric neurons
Prdx2	51.743057	1.9445248	0	0	Enteric neurons
Tagln3	51.46556	7.1810217	0	0	Enteric neurons
Stmn3	51.31881	8.023682	0	0	Enteric neurons
Sox11	50.85533	3.7254374	0	0	Enteric neurons
Elavl3	50.53903	8.302963	0	0	Enteric neurons
Celf3	50.359505	6.849462	0	0	Enteric neurons
Phox2a	49.192116	8.708404	0	0	Enteric neurons
Hand2	48.807415	3.7163837	0	0	Enteric neurons
Gap43	48.792713	5.6510835	0	0	Enteric neurons
Mllt11	48.66334	5.7110972	0	0	Enteric neurons
Crmp1	48.583736	5.3863134	0	0	Enteric neurons
Nnat	48.205067	3.6103685	0	0	Enteric neurons
Eml5	48.17918	7.127553	0	0	Enteric neurons
Syt11	47.874172	5.1314926	0	0	Enteric neurons
Hoxa5	47.402637	4.76242	0	0	Enteric neurons
Rtn1	47.262177	7.3763504	0	0	Enteric neurons

Basp1	46.16643	2.8681867	0	0	Enteric neurons
Hoxb5	45.844234	5.0007477	0	0	Enteric neurons
Syt1	45.600765	7.9778805	0	0	Enteric neurons
Hist3h2ba	45.036175	4.1974792	0	0	Enteric neurons
Sox4	45.020832	2.7132025	0	0	Enteric neurons
Kif5c	44.832897	6.7103686	0	0	Enteric neurons
Scg5	44.642483	5.825138	0	0	Enteric neurons
Pcsk1n	44.607605	7.0079083	0	0	Enteric neurons
Jpt1	44.448177	2.309086	0	0	Enteric neurons
Chrna3	44.011814	7.3566976	0	0	Enteric neurons
Ppp1r14b	43.881874	2.2574308	0	0	Enteric neurons
Hoxb4	43.784386	3.5491917	0	0	Enteric neurons
Ptma	43.245663	1.1219649	0	0	Enteric neurons
Hsp90aa1	43.215984	1.8867742	0	0	Enteric neurons
Mxra7	43.153572	3.0628061	0	0	Enteric neurons
H3f3a	42.87432	1.0327502	0	0	Enteric neurons
Tubb5	42.411755	1.8562682	0	0	Enteric neurons
Stmn2	42.388763	5.107012	0	0	Enteric neurons
2010111I01Rik	41.821262	3.1561828	0	0	Enteric neurons
Ttc3	41.684284	2.1937275	0	0	Enteric neurons
Nsg1	41.354656	3.8168347	0	0	Enteric neurons
Miat	41.10949	6.0150037	0	0	Enteric neurons
Mpz	27.283978	11.103612	6.57E-164	1.29E-159	Enteric glial cells
Plp1	27.101595	7.685401	9.43E-162	9.27E-158	Enteric glial cells
Marcks	26.885048	3.162971	3.29E-159	2.15E-155	Enteric glial cells
Mal	26.721539	10.317742	2.65E-157	1.30E-153	Enteric glial cells
Col14a1	26.44525	5.8683157	4.14E-154	1.63E-150	Enteric glial cells
Sparc	26.162613	3.833173	7.08E-151	2.32E-147	Enteric glial cells
Dst	26.13424	4.8996787	1.49E-150	4.18E-147	Enteric glial cells
Dbi	26.108698	3.7195125	2.90E-150	7.13E-147	Enteric glial cells
Fam198b	26.099724	5.3876143	3.67E-150	8.02E-147	Enteric glial cells
Egfl8	25.856987	8.2407875	2.03E-147	3.99E-144	Enteric glial cells
Epb41l3	25.66215	4.8945436	3.09E-145	5.53E-142	Enteric glial cells
Cryab	25.603708	5.8107605	1.39E-144	2.27E-141	Enteric glial cells
Aatk	25.554478	8.062706	4.90E-144	7.40E-141	Enteric glial cells
Postn	25.318724	5.434991	1.99E-141	2.79E-138	Enteric glial cells
Arpc1b	25.268038	3.2100618	7.18E-141	9.40E-138	Enteric glial cells
Zeb2	24.999977	4.2499356	6.12E-138	7.51E-135	Enteric glial cells
Serpine2	24.986685	4.824242	8.53E-138	9.86E-135	Enteric glial cells
Matn2	24.924223	5.704742	4.07E-137	4.44E-134	Enteric glial cells
Sostdc1	24.91303	8.5320215	5.38E-137	5.56E-134	Enteric glial cells
Olfml2a	24.80466	7.489607	7.98E-136	7.85E-133	Enteric glial cells
Ctnnal1	24.692747	5.731118	1.28E-134	1.20E-131	Enteric glial cells
Vim	24.62094	3.0046082	7.54E-134	6.73E-131	Enteric glial cells
Pmp22	24.55491	4.2806535	3.83E-133	3.28E-130	Enteric glial cells
Ednrb	24.4572	4.9414783	4.22E-132	3.45E-129	Enteric glial cells
Abca8a	24.268917	7.257539	4.18E-130	3.28E-127	Enteric glial cells

Apoe	24.239447	5.4269185	8.54E-130	6.46E-127	Enteric glial cells
Gpm6b	24.180456	5.5417027	3.57E-129	2.60E-126	Enteric glial cells
Mbp	24.110035	6.448651	1.96E-128	1.38E-125	Enteric glial cells
Plekha4	23.978676	7.6246886	4.64E-127	3.15E-124	Enteric glial cells
Cadm4	23.804249	6.8149347	3.02E-125	1.98E-122	Enteric glial cells
Qk	23.50397	3.2519693	3.71E-122	2.35E-119	Enteric glial cells
Col11a1	23.344978	6.7577424	1.55E-120	9.52E-118	Enteric glial cells
Metrn	23.270779	4.573564	8.77E-120	5.22E-117	Enteric glial cells
Sorbs1	22.989223	4.9358325	5.97E-117	3.45E-114	Enteric glial cells
Sema3b	22.868118	5.853512	9.65E-116	5.42E-113	Enteric glial cells
Timp3	22.808004	3.8692262	3.82E-115	2.08E-112	Enteric glial cells
Sfrp1	22.800774	4.1710753	4.50E-115	2.39E-112	Enteric glial cells
Ank3	22.696379	4.871057	4.86E-114	2.52E-111	Enteric glial cells
Cnp	22.69439	4.757909	5.09E-114	2.56E-111	Enteric glial cells
Gas7	22.576315	5.128048	7.41E-113	3.64E-110	Enteric glial cells
Col18a1	22.469873	3.7687933	8.18E-112	3.92E-109	Enteric glial cells
Adam23	22.40515	7.1119976	3.51E-111	1.64E-108	Enteric glial cells
Nid1	22.390432	3.4950027	4.88E-111	2.23E-108	Enteric glial cells
Ttyh1	22.385963	6.2373543	5.39E-111	2.41E-108	Enteric glial cells
Gfra3	22.35109	8.66082	1.18E-110	5.15E-108	Enteric glial cells
Itga6	22.313175	3.694224	2.75E-110	1.18E-107	Enteric glial cells
Lamb1	22.079218	3.4140563	5.01E-108	2.08E-105	Enteric glial cells
Lpar1	22.078588	4.3204384	5.08E-108	2.08E-105	Enteric glial cells
Lama2	22.044815	6.530158	1.07E-107	4.30E-105	Enteric glial cells
Col1a2	21.912014	4.290551	2.00E-106	7.84E-104	Enteric glial cells
Ednrb	59.622982	5.325398	0	0	Enteric neuronal progenitor cells
Fabp7	57.62774	6.900466	0	0	Enteric neuronal progenitor cells
Tgfb2	55.26723	4.887304	0	0	Enteric neuronal progenitor cells
Rbp1	55.06415	3.5095766	0	0	Enteric neuronal progenitor cells
Metrn	53.553406	4.845452	0	0	Enteric neuronal progenitor cells
Phox2b	52.43191	5.069202	0	0	Enteric neuronal progenitor cells
Ckb	48.679134	3.2287755	0	0	Enteric neuronal progenitor cells
Lmo4	48.67387	3.3970656	0	0	Enteric neuronal progenitor cells
Gfra1	48.536484	4.8297215	0	0	Enteric neuronal progenitor cells
Sox10	48.154617	6.7656217	0	0	Enteric neuronal progenitor cells
Cdh2	47.44174	4.0954185	0	0	Enteric neuronal progenitor cells
Tpt1	47.284634	0.79696316	0	0	Enteric neuronal progenitor cells
Foxd3	47.2772	6.6782517	0	0	Enteric neuronal progenitor cells
Ccnd1	46.887184	3.3229575	0	0	Enteric neuronal progenitor cells
Ppp1r14b	45.999126	2.2684503	0	0	Enteric neuronal progenitor cells
Ascl1	45.686516	5.528994	0	0	Enteric neuronal progenitor cells
Slitrk6	45.360466	5.3593397	0	0	Enteric neuronal progenitor cells
Cacng4	44.53552	4.7372756	0	0	Enteric neuronal progenitor cells
Cthrc1	44.216553	3.9713883	0	0	Enteric neuronal progenitor cells
Hand2	44.01606	3.138335	0	0	Enteric neuronal progenitor cells
Erbb3	43.83706	4.463894	0	0	Enteric neuronal progenitor cells
Celf2	42.34074	2.788005	0	0	Enteric neuronal progenitor cells

Pcbp4	42.04178	3.0212636	0	0	Enteric neuronal progenitor cells
Cnp	41.914314	4.0177636	0	0	Enteric neuronal progenitor cells
Tuba1a	40.93534	2.2729743	0	0	Enteric neuronal progenitor cells
Chd7	40.84152	3.1459112	0	0	Enteric neuronal progenitor cells
Nell2	40.47814	5.697067	0	0	Enteric neuronal progenitor cells
Zeb2	39.50572	2.6162581	0	0	Enteric neuronal progenitor cells
Wwtr1	39.112957	2.6017377	0	0	Enteric neuronal progenitor cells
Gsta4	38.87383	3.4551632	0	0	Enteric neuronal progenitor cells
Ldhb	38.694412	2.5089033	0	0	Enteric neuronal progenitor cells
Kif21a	38.67227	3.6072853	0	0	Enteric neuronal progenitor cells
Syt11	38.60189	3.8164191	0	0	Enteric neuronal progenitor cells
Gm12688	38.056065	6.565499	0	0	Enteric neuronal progenitor cells
Serpine2	37.56713	3.2317383	0.00E+00	4.16E-306	Enteric neuronal progenitor cells
Dnajc1	37.50709	2.6486366	7.06E-308	3.85E-305	Enteric neuronal progenitor cells
Ptprz1	37.421543	5.8486342	1.74E-306	9.26E-304	Enteric neuronal progenitor cells
Ncam1	37.162663	2.672295	2.74E-302	1.42E-299	Enteric neuronal progenitor cells
Tshz1	36.98831	2.8211102	1.77E-299	8.89E-297	Enteric neuronal progenitor cells
Marcks	36.89556	1.6931293	5.44E-298	2.67E-295	Enteric neuronal progenitor cells
Gpm6b	36.82437	3.7830915	7.52E-297	3.61E-294	Enteric neuronal progenitor cells
Sox4	36.58367	2.0558121	5.20E-293	2.43E-290	Enteric neuronal progenitor cells
Plp1	36.419346	5.197176	2.10E-290	9.61E-288	Enteric neuronal progenitor cells
Tbx3	36.367283	3.3106582	1.40E-289	6.26E-287	Enteric neuronal progenitor cells
H2afz	35.740765	1.5850068	9.21E-280	4.02E-277	Enteric neuronal progenitor cells
Stmn1	35.65634	1.876343	1.88E-278	8.03E-276	Enteric neuronal progenitor cells
Jpt1	34.75116	1.7584643	1.33E-264	5.57E-262	Enteric neuronal progenitor cells
E130114P18Rik	34.476414	5.9622893	1.81E-260	7.41E-258	Enteric neuronal progenitor cells
Pmepa1	34.264606	2.379778	2.64E-257	1.06E-254	Enteric neuronal progenitor cells
Zfp536	34.22188	5.0314007	1.14E-256	4.49E-254	Enteric neuronal progenitor cells
Upk3b	48.758854	6.214994	0	0	Mesothelial progenitor cells
Igfbp2	42.967884	4.0254207	0	0	Mesothelial progenitor cells
Igfbp5	40.86034	3.809444	0	0	Mesothelial progenitor cells
Upk1b	39.471436	5.928985	0	0	Mesothelial progenitor cells
Wt1	39.162865	4.573309	0	0	Mesothelial progenitor cells
Cryab	38.87915	4.153923	0	0	Mesothelial progenitor cells
Tmem108	38.51766	4.839414	0	0	Mesothelial progenitor cells
Bcam	38.26458	3.9196124	0	0	Mesothelial progenitor cells
Fbln2	37.93017	3.654816	0	0	Mesothelial progenitor cells
Krt19	37.16882	3.5746374	2.18E-302	4.28E-299	Mesothelial progenitor cells
Podxl	37.144054	3.2161431	5.47E-302	9.77E-299	Mesothelial progenitor cells
Nnat	36.625175	2.9835184	1.14E-293	1.86E-290	Mesothelial progenitor cells
Dcn	36.51134	3.5034578	7.33E-292	1.11E-288	Mesothelial progenitor cells
Smim1	36.05521	3.1238525	1.14E-284	1.60E-281	Mesothelial progenitor cells
Pmp22	34.910694	2.856222	5.12E-267	6.70E-264	Mesothelial progenitor cells
Npnt	34.74867	4.3935766	1.45E-264	1.78E-261	Mesothelial progenitor cells
Itm2a	34.67071	2.8370762	2.18E-263	2.52E-260	Mesothelial progenitor cells
Gas1	34.6315	2.6717925	8.48E-263	9.26E-260	Mesothelial progenitor cells
Krt7	34.300285	3.342193	7.77E-258	8.04E-255	Mesothelial progenitor cells

P3h4	33.97815	3.0559278	4.68E-253	4.60E-250	Mesothelial progenitor cells
Myrf	33.65168	4.621739	2.95E-248	2.76E-245	Mesothelial progenitor cells
Alad	33.592587	2.6925788	2.15E-247	1.92E-244	Mesothelial progenitor cells
Slc9a3r1	33.478203	2.5318992	1.00E-245	8.55E-243	Mesothelial progenitor cells
Aprt	33.17624	1.8714306	2.37E-241	1.94E-238	Mesothelial progenitor cells
S100a6	33.17156	2.7491786	2.77E-241	2.18E-238	Mesothelial progenitor cells
Frem2	32.80059	4.941621	5.78E-236	4.37E-233	Mesothelial progenitor cells
Hspb1	32.59621	3.3329093	4.64E-233	3.38E-230	Mesothelial progenitor cells
Gpc3	32.269943	2.2718372	1.85E-228	1.30E-225	Mesothelial progenitor cells
Aldh1a2	32.19536	4.52092	2.05E-227	1.39E-224	Mesothelial progenitor cells
Aebp1	31.6777	3.1781247	3.15E-220	2.06E-217	Mesothelial progenitor cells
Tgm2	31.525095	3.6196566	3.94E-218	2.50E-215	Mesothelial progenitor cells
Tceal9	31.251982	1.5381082	2.10E-214	1.29E-211	Mesothelial progenitor cells
Ezr	31.098583	2.3740067	2.52E-212	1.50E-209	Mesothelial progenitor cells
Tmem151a	31.067532	5.0934653	6.61E-212	3.82E-209	Mesothelial progenitor cells
Dlk1	30.972569	2.6743052	1.26E-210	7.09E-208	Mesothelial progenitor cells
Col3a1	30.909296	2.7078376	8.96E-210	4.89E-207	Mesothelial progenitor cells
Muc16	30.887045	5.9058266	1.78E-209	9.47E-207	Mesothelial progenitor cells
Rcn3	30.750904	2.1699183	1.19E-207	6.15E-205	Mesothelial progenitor cells
C1qtnf4	30.58136	3.3161764	2.17E-205	1.09E-202	Mesothelial progenitor cells
Npm1	30.531334	1.1789416	1.00E-204	4.92E-202	Mesothelial progenitor cells
Cdh3	30.16033	3.795653	7.85E-200	3.76E-197	Mesothelial progenitor cells
Lrrn4	30.02374	5.295676	4.81E-198	2.25E-195	Mesothelial progenitor cells
Col1a2	29.910555	2.366577	1.43E-196	6.56E-194	Mesothelial progenitor cells
Mdk	29.811302	2.2307448	2.79E-195	1.25E-192	Mesothelial progenitor cells
1810058I24Rik	29.766428	1.5852524	1.06E-194	4.64E-192	Mesothelial progenitor cells
Cavin3	29.686422	2.046383	1.15E-193	4.91E-191	Mesothelial progenitor cells
Wfdc2	29.685123	3.7081885	1.19E-193	5.00E-191	Mesothelial progenitor cells
Cnpy2	29.561604	1.615269	4.66E-192	1.91E-189	Mesothelial progenitor cells
Tmem176b	29.235659	1.652337	6.83E-188	2.74E-185	Mesothelial progenitor cells
Col1a1	29.174486	2.476033	4.09E-187	1.61E-184	Mesothelial progenitor cells
Msln	38.749584	9.953745	0	0	Differentiated mesothelial cells
S100a6	38.449112	5.640334	0	0	Differentiated mesothelial cells
Igfbp6	37.976128	7.5929823	0	0	Differentiated mesothelial cells
Crip1	37.80899	5.5031486	0	0	Differentiated mesothelial cells
Upk3b	37.75611	6.6443644	0	0	Differentiated mesothelial cells
Rarres2	37.45369	6.086227	5.23E-307	1.71E-303	Differentiated mesothelial cells
Dcn	37.03181	6.1704516	3.52E-300	9.89E-297	Differentiated mesothelial cells
Krt19	36.943176	5.317848	9.37E-299	2.30E-295	Differentiated mesothelial cells
Col6a1	36.364307	4.73578	1.56E-289	3.41E-286	Differentiated mesothelial cells
Fbln2	36.282036	5.4059014	3.11E-288	6.11E-285	Differentiated mesothelial cells
Sparc	36.13917	3.5951467	5.50E-286	9.83E-283	Differentiated mesothelial cells
Col3a1	35.959774	5.4670696	3.56E-283	5.83E-280	Differentiated mesothelial cells
Aebp1	35.923763	5.197392	1.30E-282	1.97E-279	Differentiated mesothelial cells
Col1a1	35.805954	5.411652	8.92E-281	1.25E-277	Differentiated mesothelial cells
Cav1	35.641113	4.5115485	3.24E-278	4.24E-275	Differentiated mesothelial cells
Efemp1	35.0804	7.2912116	1.34E-269	1.65E-266	Differentiated mesothelial cells

Col1a2	35.002644	5.002118	2.05E-268	2.37E-265	Differentiated mesothelial cells
Igfbp5	34.82245	4.9740996	1.11E-265	1.21E-262	Differentiated mesothelial cells
C3	34.262028	9.324508	2.89E-257	2.99E-254	Differentiated mesothelial cells
Krt7	34.202164	4.7298603	2.25E-256	2.21E-253	Differentiated mesothelial cells
Cavin1	33.745846	3.6592662	1.23E-249	1.15E-246	Differentiated mesothelial cells
Col6a2	33.638966	4.1056223	4.52E-248	4.04E-245	Differentiated mesothelial cells
Eln	33.595097	4.281467	1.98E-247	1.69E-244	Differentiated mesothelial cells
Anxa1	33.51692	4.78238	2.73E-246	2.24E-243	Differentiated mesothelial cells
Lrrn4	33.446056	7.185182	2.94E-245	2.31E-242	Differentiated mesothelial cells
Upk1b	33.417538	6.638736	7.63E-245	5.76E-242	Differentiated mesothelial cells
Gpc3	33.215824	3.42816	6.36E-242	4.63E-239	Differentiated mesothelial cells
Wt1	33.194447	5.0969844	1.29E-241	9.09E-239	Differentiated mesothelial cells
Laptm4a	31.661554	2.3247797	5.26E-220	3.56E-217	Differentiated mesothelial cells
Arhgap29	31.622486	3.6337223	1.81E-219	1.19E-216	Differentiated mesothelial cells
Mgp	31.540314	4.1007986	2.43E-218	1.54E-215	Differentiated mesothelial cells
Sulf1	31.316593	4.2705135	2.77E-215	1.70E-212	Differentiated mesothelial cells
Hspb1	31.243008	4.4389205	2.78E-214	1.65E-211	Differentiated mesothelial cells
S100a11	30.905134	2.6998682	1.02E-209	5.89E-207	Differentiated mesothelial cells
Gas6	30.9014	4.0326295	1.14E-209	6.42E-207	Differentiated mesothelial cells
Col5a2	30.77845	3.1943707	5.09E-208	2.78E-205	Differentiated mesothelial cells
Col14a1	30.488092	4.2691255	3.75E-204	1.99E-201	Differentiated mesothelial cells
Loxl1	30.402378	4.0777106	5.11E-203	2.64E-200	Differentiated mesothelial cells
Ezr	30.197239	3.268922	2.57E-200	1.30E-197	Differentiated mesothelial cells
S100a10	30.083515	2.5677702	7.96E-199	3.91E-196	Differentiated mesothelial cells
Cdh11	29.985939	3.4599223	1.50E-197	7.17E-195	Differentiated mesothelial cells
Lgals3	29.973919	5.0313272	2.15E-197	1.00E-194	Differentiated mesothelial cells
Rspo1	29.973299	5.9444685	2.19E-197	1.00E-194	Differentiated mesothelial cells
Gpm6a	29.796614	6.5987644	4.32E-195	1.93E-192	Differentiated mesothelial cells
Nbl1	29.750818	4.4064536	1.69E-194	7.39E-192	Differentiated mesothelial cells
P3h4	29.413889	3.7422614	3.65E-190	1.56E-187	Differentiated mesothelial cells
Dlk1	29.335226	3.6755493	3.69E-189	1.54E-186	Differentiated mesothelial cells
Aldh1a2	29.072218	5.1150913	8.06E-186	3.30E-183	Differentiated mesothelial cells
Col5a1	29.02385	3.2124689	3.29E-185	1.32E-182	Differentiated mesothelial cells
Ahnak	28.854944	2.888742	4.39E-183	1.73E-180	Differentiated mesothelial cells
Tmsb4x	77.4404	2.7611694	0	0	Macrophages-1
Fcer1g	76.10649	8.235345	0	0	Macrophages-1
Tyrobp	75.112755	8.098489	0	0	Macrophages-1
Apoe	68.94213	6.752044	0	0	Macrophages-1
Coro1a	67.83591	6.782404	0	0	Macrophages-1
Cst3	67.01098	3.156911	0	0	Macrophages-1
Cyba	66.126595	3.3167388	0	0	Macrophages-1
Ctss	63.977787	6.4094663	0	0	Macrophages-1
Rac2	63.5765	7.3107696	0	0	Macrophages-1
Cd52	62.354317	6.943082	0	0	Macrophages-1
Lst1	61.942978	6.654906	0	0	Macrophages-1
Arhgdib	61.38649	4.7557435	0	0	Macrophages-1
Laptm5	61.140102	6.44515	0	0	Macrophages-1

C1qb	61.08476	7.3101907	0	0	Macrophages-1
Ctsc	60.837868	5.23919	0	0	Macrophages-1
Aif1	60.268826	6.708236	0	0	Macrophages-1
Ly86	59.88904	6.9793825	0	0	Macrophages-1
B2m	59.551434	2.8958833	0	0	Macrophages-1
Fth1	59.333523	1.7365551	0	0	Macrophages-1
C1qc	58.89426	7.1607995	0	0	Macrophages-1
Spi1	58.837257	6.8099194	0	0	Macrophages-1
Fcgr3	58.69424	6.854046	0	0	Macrophages-1
Ftl1	57.346676	1.6298988	0	0	Macrophages-1
Ptpn18	56.46074	4.072212	0	0	Macrophages-1
Ms4a6c	56.284958	6.722319	0	0	Macrophages-1
Lyz2	56.219357	6.452283	0	0	Macrophages-1
Csf1r	55.88633	5.3697114	0	0	Macrophages-1
Clta	55.674263	1.8920282	0	0	Macrophages-1
Psap	55.57336	3.0413165	0	0	Macrophages-1
C1qa	55.513226	6.9790397	0	0	Macrophages-1
Gmfg	54.86484	4.1827483	0	0	Macrophages-1
Actb	54.012596	1.2676115	0	0	Macrophages-1
Ctsb	54.010014	2.953879	0	0	Macrophages-1
Lgmn	53.859512	4.375999	0	0	Macrophages-1
Sh3bgrl3	53.827415	2.04106	0	0	Macrophages-1
Unc93b1	53.603565	4.8725743	0	0	Macrophages-1
Arpc1b	52.811974	2.1753645	0	0	Macrophages-1
Fau	52.51823	0.95210224	0	0	Macrophages-1
Ms4a6b	51.680187	6.420207	0	0	Macrophages-1
Itm2b	51.106293	1.9658134	0	0	Macrophages-1
Rgs10	50.67765	3.7026494	0	0	Macrophages-1
Ctsh	50.14758	4.060067	0	0	Macrophages-1
Cd68	49.9106	6.16043	0	0	Macrophages-1
Lcp1	49.861725	3.4182224	0	0	Macrophages-1
Pld4	49.76825	6.6382613	0	0	Macrophages-1
Cotl1	49.429775	2.3590887	0	0	Macrophages-1
Fyb	48.806244	5.770856	0	0	Macrophages-1
Cd53	48.700306	6.5143495	0	0	Macrophages-1
Pf4	47.628403	7.0783167	0	0	Macrophages-1
Psmb8	46.956417	4.452586	0	0	Macrophages-1
Ctss	34.6019	7.585671	2.37E-262	4.65E-258	Macrophages-2
Cd74	34.49518	10.031071	9.47E-261	9.31E-257	Macrophages-2
Psap	34.300953	4.9357224	7.60E-258	4.98E-254	Macrophages-2
C1qc	34.220596	7.630758	1.19E-256	5.87E-253	Macrophages-2
Apoe	34.0742	7.8429947	1.78E-254	6.99E-251	Macrophages-2
C1qb	33.971947	7.5637603	5.78E-253	1.89E-249	Macrophages-2
C1qa	33.910557	7.617849	4.66E-252	1.31E-248	Macrophages-2
Ctsc	33.630558	5.9113193	6.00E-248	1.47E-244	Macrophages-2
H2-Ab1	33.46984	9.090098	1.32E-245	2.89E-242	Macrophages-2
H2-Aa	33.223198	9.560768	4.98E-242	9.78E-239	Macrophages-2

Aif1	33.14279	6.441567	7.19E-241	1.29E-237	Macrophages-2
Cd52	33.12272	6.661426	1.40E-240	2.29E-237	Macrophages-2
Tyrobp	33.063034	6.6371627	1.01E-239	1.53E-236	Macrophages-2
Csf1r	32.711105	5.9867425	1.09E-234	1.52E-231	Macrophages-2
H2-Eb1	32.70291	9.081044	1.42E-234	1.86E-231	Macrophages-2
Lgmn	32.626312	5.5331955	1.74E-233	2.13E-230	Macrophages-2
Pla2g7	32.32107	7.282564	3.54E-229	4.09E-226	Macrophages-2
Fcer1g	32.29009	6.4554167	9.64E-229	1.05E-225	Macrophages-2
Tmsb4x	32.238052	2.6960335	5.17E-228	5.35E-225	Macrophages-2
Unc93b1	31.856625	5.4557266	1.07E-222	1.05E-219	Macrophages-2
Ctsh	31.7263	5.2454886	6.74E-221	6.31E-218	Macrophages-2
H2-DMa	31.513723	7.0913157	5.63E-218	5.03E-215	Macrophages-2
Adamdec1	31.504217	7.616871	7.60E-218	6.50E-215	Macrophages-2
Ccl24	31.253445	7.810197	2.00E-214	1.64E-211	Macrophages-2
Coro1a	31.023195	5.357899	2.62E-211	2.06E-208	Macrophages-2
B2m	31.011305	3.4567804	3.80E-211	2.87E-208	Macrophages-2
Fcgr3	30.981724	5.7641735	9.50E-211	6.92E-208	Macrophages-2
Man2b1	30.833279	4.2396226	9.39E-209	6.59E-206	Macrophages-2
Tspan13	30.676609	3.766786	1.17E-206	7.91E-204	Macrophages-2
Ms4a6c	30.671333	6.043811	1.37E-206	8.99E-204	Macrophages-2
AW112010	30.577806	7.17225	2.41E-205	1.53E-202	Macrophages-2
Mpeg1	30.494146	6.5635624	3.12E-204	1.91E-201	Macrophages-2
Lyz2	30.390863	5.423932	7.25E-203	4.32E-200	Macrophages-2
Ms4a6b	30.379358	5.8341184	1.03E-202	5.95E-200	Macrophages-2
Gm2a	30.335781	5.223245	3.87E-202	2.17E-199	Macrophages-2
Ly6e	30.315226	4.0799294	7.22E-202	3.94E-199	Macrophages-2
Ly86	30.125246	5.703745	2.26E-199	1.20E-196	Macrophages-2
Prdx5	29.954975	3.1876502	3.79E-197	1.96E-194	Macrophages-2
Ctsb	29.92919	3.3401105	8.21E-197	4.14E-194	Macrophages-2
Mafb	29.905724	5.09575	1.66E-196	8.15E-194	Macrophages-2
Sat1	29.809916	3.6450655	2.91E-195	1.39E-192	Macrophages-2
Gatm	29.775366	5.019974	8.14E-195	3.81E-192	Macrophages-2
Spi1	29.74259	5.4348254	2.16E-194	9.88E-192	Macrophages-2
Lst1	29.55362	5.27855	5.90E-192	2.64E-189	Macrophages-2
Ptprc	29.465433	6.1264563	7.99E-191	3.49E-188	Macrophages-2
Npc2	29.289637	2.695033	1.41E-188	6.00E-186	Macrophages-2
Fth1	29.272675	2.0264626	2.31E-188	9.66E-186	Macrophages-2
Ms4a6d	29.239248	6.022433	6.15E-188	2.52E-185	Macrophages-2
Cyba	29.173658	3.0309594	4.19E-187	1.68E-184	Macrophages-2
Lpcat2	29.07049	5.9942017	8.48E-186	3.33E-183	Macrophages-2
Hba-a1	29.42806	12.496491	2.40E-190	2.51E-186	Erythrocytes
Hba-a2	29.42599	12.359651	2.55E-190	2.51E-186	Erythrocytes
Hbb-bt	29.204794	12.01571	1.69E-187	1.10E-183	Erythrocytes
Hbb-bs	28.465912	10.69772	3.10E-178	1.52E-174	Erythrocytes
Fth1	26.281044	2.9835837	3.16E-152	1.24E-148	Erythrocytes
Alas2	23.13419	11.091679	2.10E-118	1.72E-115	Erythrocytes
Ftl1	21.960766	1.6956807	6.83E-107	3.53E-104	Erythrocytes

Hbb-y	20.733438	9.706763	1.73E-95	6.18E-93	Erythrocytes
Bpgm	20.397833	4.8840203	1.75E-92	5.20E-90	Erythrocytes
Hba-x	20.291992	10.382186	1.51E-91	4.19E-89	Erythrocytes
Blvrb	19.848158	3.5787628	1.14E-87	2.96E-85	Erythrocytes
Gpx1	18.41803	2.9854677	9.42E-76	1.65E-73	Erythrocytes
Prdx2	18.027212	1.6910319	1.19E-72	1.87E-70	Erythrocytes
Car2	17.924929	6.2123623	7.53E-72	1.13E-69	Erythrocytes
Hbb-bh1	17.856838	10.456967	2.56E-71	3.75E-69	Erythrocytes
Nudt4	17.29021	3.8088634	5.57E-67	7.45E-65	Erythrocytes
Slc4a1	17.277695	11.046378	6.93E-67	9.13E-65	Erythrocytes
Fam210b	16.514507	4.765595	2.89E-61	3.03E-59	Erythrocytes
Creg1	16.076473	3.2699144	3.73E-58	3.44E-56	Erythrocytes
Fech	15.780026	4.11633	4.27E-56	3.53E-54	Erythrocytes
Snca	15.584298	6.7965684	9.31E-55	7.06E-53	Erythrocytes
Fam46c	15.450652	6.504288	7.47E-54	5.48E-52	Erythrocytes
Slc25a37	14.740357	4.9791512	3.55E-49	2.09E-47	Erythrocytes
Gclm	14.1354685	2.846137	2.30E-45	1.16E-43	Erythrocytes
Ube2l6	14.062289	4.802167	6.48E-45	3.21E-43	Erythrocytes
Mkrn1	13.627349	3.7558036	2.75E-42	1.22E-40	Erythrocytes
Epb41	13.506338	3.3828459	1.43E-41	6.22E-40	Erythrocytes
Gypa	11.286525	9.756786	1.53E-29	3.97E-28	Erythrocytes
Gm42418	11.173034	1.1150085	5.53E-29	1.39E-27	Erythrocytes
Pdzk1ip1	10.9555855	3.1418173	6.25E-28	1.50E-26	Erythrocytes
Rhd	10.702056	9.9813385	9.95E-27	2.25E-25	Erythrocytes
Hsd3b6	10.610274	11.048098	2.67E-26	5.93E-25	Erythrocytes
2-Mar	10.4626665	2.679516	1.28E-25	2.73E-24	Erythrocytes
Bnip3l	10.023657	1.4121541	1.20E-23	2.34E-22	Erythrocytes
Ermap	9.768	8.744655	1.54E-22	2.83E-21	Erythrocytes
Kel	9.601904	11.12177	7.85E-22	1.37E-20	Erythrocytes
Oaz1	9.292808	0.69919336	1.50E-20	2.44E-19	Erythrocytes
Tmcc2	9.153021	4.447661	5.54E-20	8.69E-19	Erythrocytes
Trim10	8.996066	11.539749	2.34E-19	3.54E-18	Erythrocytes
Pim1	8.247742	2.7787302	1.61E-16	2.06E-15	Erythrocytes
Glrx5	8.191169	1.2982198	2.59E-16	3.24E-15	Erythrocytes
Ppp1r15a	8.113387	3.20106	4.92E-16	6.04E-15	Erythrocytes
Pabpc1	7.970064	0.7166131	1.59E-15	1.87E-14	Erythrocytes
Hmbs	7.767945	2.066567	7.98E-15	8.94E-14	Erythrocytes
Ube2o	7.5791807	3.1037362	3.48E-14	3.76E-13	Erythrocytes
Cd59a	7.5112133	2.8937314	5.86E-14	6.23E-13	Erythrocytes
Fam220a	7.355246	2.5990536	1.91E-13	1.95E-12	Erythrocytes
Nt5c3	7.251903	2.308122	4.11E-13	4.11E-12	Erythrocytes
Tspo2	7.027985	8.459726	2.10E-12	1.98E-11	Erythrocytes
Rbm38	6.604775	3.0701199	3.98E-11	3.34E-10	Erythrocytes

Table S2: Differential gene expression analysis results for top 50 gene markers for all mesenchymal cell types in the small intestinal musculature scRNA-seq data.

Table S2:

Small intestine musculature cell type markers					
names	**scores**	**logfoldchanges**	**pvals**	**pvals_adj**	**celltypes**
Isl1	26.858887	4.905148	6.64E-159	6.53E-155	Mesenchymal progenitors-1
Peg3	25.508183	1.8861797	1.60E-143	1.05E-139	Mesenchymal progenitors-1
Nnat	23.692251	1.9364665	4.33E-124	1.70E-120	Mesenchymal progenitors-1
Stmn2	23.56522	3.3697066	8.77E-123	2.87E-119	Mesenchymal progenitors-1
Palld	23.25425	1.9439565	1.29E-119	3.62E-116	Mesenchymal progenitors-1
Sfrp1	22.56248	1.6866161	1.01E-112	2.49E-109	Mesenchymal progenitors-1
Nr2f2	21.943539	1.4336491	9.98E-107	2.18E-103	Mesenchymal progenitors-1
Capn6	21.929276	2.1726575	1.37E-106	2.68E-103	Mesenchymal progenitors-1
Pitx2	20.617445	3.2603903	1.91E-94	3.42E-91	Mesenchymal progenitors-1
Hsp90ab1	20.107424	0.686816	6.35E-90	9.61E-87	Mesenchymal progenitors-1
Tac2	19.576954	3.6341603	2.43E-85	3.19E-82	Mesenchymal progenitors-1
Igf1	19.38159	1.596314	1.10E-83	1.36E-80	Mesenchymal progenitors-1
Ncam1	19.192003	1.4705824	4.32E-82	4.99E-79	Mesenchymal progenitors-1
Unc5c	19.019835	1.9966387	1.17E-80	1.28E-77	Mesenchymal progenitors-1
Zfhx4	18.590439	1.4768733	3.84E-77	3.97E-74	Mesenchymal progenitors-1
Abcg2	18.379238	1.9944003	1.93E-75	1.89E-72	Mesenchymal progenitors-1
mt-Nd4l	18.355783	1.3428615	2.97E-75	2.78E-72	Mesenchymal progenitors-1
Prnp	18.343693	1.5215296	3.71E-75	3.31E-72	Mesenchymal progenitors-1
Mif	18.326105	1.046231	5.12E-75	4.38E-72	Mesenchymal progenitors-1
6330403K07Rik	18.149532	1.251263	1.29E-73	1.06E-70	Mesenchymal progenitors-1
Csrp2	18.14384	1.2091146	1.44E-73	1.13E-70	Mesenchymal progenitors-1
Mtch1	17.755987	0.9795887	1.55E-70	1.17E-67	Mesenchymal progenitors-1
Scrn1	17.589123	3.3199053	2.98E-69	2.17E-66	Mesenchymal progenitors-1
Cxcl13	17.126991	3.0622718	9.34E-66	6.33E-63	Mesenchymal progenitors-1
Tnfaip8	16.988089	1.3921928	1.01E-64	6.59E-62	Mesenchymal progenitors-1
Mdk	16.7902	0.84231925	2.88E-63	1.77E-60	Mesenchymal progenitors-1
Igfbp5	16.540018	1.3059584	1.89E-61	1.13E-58	Mesenchymal progenitors-1
Adamtsl1	16.512463	1.9370743	2.98E-61	1.73E-58	Mesenchymal progenitors-1
Tnc	16.312477	2.526372	8.05E-60	4.52E-57	Mesenchymal progenitors-1
Mmp16	16.004185	1.8206564	1.19E-57	6.35E-55	Mesenchymal progenitors-1
Cux2	15.93571	2.158107	3.58E-57	1.85E-54	Mesenchymal progenitors-1
Rps7	15.3624935	0.505355	2.92E-53	1.40E-50	Mesenchymal progenitors-1
Adgrl3	15.049983	1.8204485	3.45E-51	1.54E-48	Mesenchymal progenitors-1
Hmga2	14.998642	1.67256	7.49E-51	3.27E-48	Mesenchymal progenitors-1
Cxcl12	14.98065	1.0651245	9.83E-51	4.20E-48	Mesenchymal progenitors-1
Bex3	14.972045	0.7934023	1.12E-50	4.68E-48	Mesenchymal progenitors-1
Ntm	14.765787	2.2876954	2.43E-49	9.97E-47	Mesenchymal progenitors-1
Fam198b	14.675321	2.640863	9.28E-49	3.65E-46	Mesenchymal progenitors-1
Set	14.665883	0.68690073	1.07E-48	4.11E-46	Mesenchymal progenitors-1
Sulf2	14.590967	1.0031513	3.21E-48	1.21E-45	Mesenchymal progenitors-1
Gata6	14.588172	1.386048	3.34E-48	1.24E-45	Mesenchymal progenitors-1
Kif26b	14.554781	2.5649695	5.45E-48	1.98E-45	Mesenchymal progenitors-1
Npm1	14.529127	0.56530786	7.92E-48	2.83E-45	Mesenchymal progenitors-1
Prdx2	14.459044	0.63339627	2.20E-47	7.71E-45	Mesenchymal progenitors-1

Anp32a	14.333595	0.9578102	1.35E-46	4.65E-44	Mesenchymal progenitors-1
Runx1t1	14.224085	1.2054642	6.49E-46	2.13E-43	Mesenchymal progenitors-1
Hnrnpc	14.101229	0.82769376	3.73E-45	1.16E-42	Mesenchymal progenitors-1
Rps11	14.051917	0.32404253	7.50E-45	2.30E-42	Mesenchymal progenitors-1
Rpl7a	13.914193	0.7332692	5.19E-44	1.55E-41	Mesenchymal progenitors-1
Angpt1	13.913132	2.0563998	5.27E-44	1.55E-41	Mesenchymal progenitors-1
Mdk	35.873814	1.218615	7.82E-282	1.54E-277	Mesenchymal progenitors-2
Ptn	35.34815	1.3921417	1.07E-273	1.05E-269	Mesenchymal progenitors-2
Cdkn1c	35.126724	1.3007306	2.64E-270	1.73E-266	Mesenchymal progenitors-2
Sfrp2	29.608776	1.9731007	1.15E-192	5.66E-189	Mesenchymal progenitors-2
Calr	27.89462	1.0373204	3.10E-171	1.22E-167	Mesenchymal progenitors-2
Rpl12	27.105158	0.5815119	8.56E-162	2.80E-158	Mesenchymal progenitors-2
Rpl14	26.73997	0.5361936	1.62E-157	4.53E-154	Mesenchymal progenitors-2
Rps19	26.60864	0.5836611	5.39E-156	1.32E-152	Mesenchymal progenitors-2
Sulf2	26.306936	1.3790835	1.60E-152	3.49E-149	Mesenchymal progenitors-2
Rps23	26.120115	0.61122495	2.15E-150	4.23E-147	Mesenchymal progenitors-2
Rpl27a	25.654322	0.45712432	3.78E-145	6.20E-142	Mesenchymal progenitors-2
Rpl13	25.208975	0.4056025	3.19E-140	4.83E-137	Mesenchymal progenitors-2
Rpl32	24.834528	0.48112136	3.80E-136	5.33E-133	Mesenchymal progenitors-2
Rps10	24.814005	0.45879033	6.33E-136	8.29E-133	Mesenchymal progenitors-2
Rpl19	24.75366	0.5570034	2.83E-135	3.48E-132	Mesenchymal progenitors-2
Rps18	24.592133	0.6695748	1.53E-133	1.77E-130	Mesenchymal progenitors-2
Rps17	24.455431	0.57831687	4.41E-132	4.81E-129	Mesenchymal progenitors-2
Lgals1	24.22944	0.73610336	1.09E-129	1.07E-126	Mesenchymal progenitors-2
Rps13	24.070684	0.49189126	5.07E-128	4.75E-125	Mesenchymal progenitors-2
Rps15a	24.051119	0.45233122	8.13E-128	7.26E-125	Mesenchymal progenitors-2
Rpl28	23.971905	0.43181145	5.46E-127	4.67E-124	Mesenchymal progenitors-2
Rps20	23.872688	0.3939113	5.89E-126	4.82E-123	Mesenchymal progenitors-2
Slit2	23.812807	1.3568157	2.46E-125	1.93E-122	Mesenchymal progenitors-2
Rpl11	23.475216	0.60496306	7.31E-122	5.32E-119	Mesenchymal progenitors-2
Eef1b2	23.215904	0.733394	3.15E-119	2.21E-116	Mesenchymal progenitors-2
Rpl18	23.147524	0.620622	1.54E-118	1.04E-115	Mesenchymal progenitors-2
Rpl26	22.9614	0.43589354	1.13E-116	7.43E-114	Mesenchymal progenitors-2
Tmsb10	22.792862	0.68991345	5.40E-115	3.42E-112	Mesenchymal progenitors-2
Rps14	22.57606	0.62598956	7.45E-113	4.58E-110	Mesenchymal progenitors-2
Rps27a	22.530386	0.41040206	2.09E-112	1.25E-109	Mesenchymal progenitors-2
Pdia6	22.284115	0.8967081	5.27E-110	3.05E-107	Mesenchymal progenitors-2
Csrp2	22.125822	1.1419438	1.78E-108	1.00E-105	Mesenchymal progenitors-2
Eef1g	22.02815	0.850932	1.55E-107	8.45E-105	Mesenchymal progenitors-2
Rps15	21.893759	0.5011342	2.98E-106	1.58E-103	Mesenchymal progenitors-2
Rps11	21.724335	0.40908927	1.21E-104	6.09E-102	Mesenchymal progenitors-2
Rps24	21.518728	0.3204036	1.04E-102	5.11E-100	Mesenchymal progenitors-2
Rps25	21.414408	0.45857945	9.81E-102	4.70E-99	Mesenchymal progenitors-2
Rps8	21.06925	0.36857876	1.52E-98	6.65E-96	Mesenchymal progenitors-2
Rpl22l1	20.980295	0.5913727	9.93E-98	4.24E-95	Mesenchymal progenitors-2
Ppib	20.915401	0.66077036	3.88E-97	1.59E-94	Mesenchymal progenitors-2
Rps16	20.762815	0.48329863	9.39E-96	3.69E-93	Mesenchymal progenitors-2

Rpl23	20.544868	0.36890954	8.55E-94	3.30E-91	Mesenchymal progenitors-2
Marcks	20.54283	0.76938057	8.92E-94	3.37E-91	Mesenchymal progenitors-2
Dad1	20.500282	0.7805883	2.14E-93	7.94E-91	Mesenchymal progenitors-2
Dlk1	20.380707	0.98953474	2.48E-92	9.03E-90	Mesenchymal progenitors-2
Id3	20.305168	1.1276157	1.16E-91	4.14E-89	Mesenchymal progenitors-2
Rplp1	20.159838	0.4146724	2.21E-90	7.61E-88	Mesenchymal progenitors-2
Rpl18a	20.133692	0.51141804	3.74E-90	1.27E-87	Mesenchymal progenitors-2
Rpl41	20.126467	0.46229905	4.33E-90	1.44E-87	Mesenchymal progenitors-2
Mif	19.921263	0.9039041	2.66E-88	8.72E-86	Mesenchymal progenitors-2
Wnt4	17.47528	2.4254398	2.21E-68	4.34E-64	Mesenchymal progenitors-3
Tubb5	16.889206	1.0259817	5.40E-64	5.31E-60	Mesenchymal progenitors-3
Fabp5	16.837751	1.5860473	1.29E-63	8.45E-60	Mesenchymal progenitors-3
Ptma	15.768492	0.54897654	5.13E-56	2.52E-52	Mesenchymal progenitors-3
Cdc7	15.746746	1.9709287	7.23E-56	2.84E-52	Mesenchymal progenitors-3
Ppia	15.145021	0.5131448	8.17E-52	2.68E-48	Mesenchymal progenitors-3
Ybx1	15.005781	0.6988501	6.73E-51	1.89E-47	Mesenchymal progenitors-3
H2afz	14.551476	1.1007379	5.72E-48	1.12E-44	Mesenchymal progenitors-3
Ran	14.495257	0.94101727	1.30E-47	2.32E-44	Mesenchymal progenitors-3
Rpsa	14.209553	0.5347843	7.99E-46	1.21E-42	Mesenchymal progenitors-3
Ccl11	14.104558	2.4102883	3.56E-45	4.66E-42	Mesenchymal progenitors-3
Pclaf	14.00606	2.0962923	1.43E-44	1.76E-41	Mesenchymal progenitors-3
Jag1	13.891552	1.6165274	7.13E-44	8.24E-41	Mesenchymal progenitors-3
Hsp90aa1	13.827956	0.825944	1.73E-43	1.89E-40	Mesenchymal progenitors-3
Eif5a	13.552082	0.83299357	7.70E-42	7.97E-39	Mesenchymal progenitors-3
Ranbp1	13.503243	0.9531882	1.50E-41	1.47E-38	Mesenchymal progenitors-3
Rbm3	13.41821	0.6524041	4.73E-41	4.43E-38	Mesenchymal progenitors-3
7-Sep	13.405351	0.9021831	5.63E-41	4.81E-38	Mesenchymal progenitors-3
Heyl	13.180256	2.210717	1.14E-39	9.34E-37	Mesenchymal progenitors-3
Stmn1	12.9887905	1.1522387	1.42E-38	1.11E-35	Mesenchymal progenitors-3
Nr2f2	12.960137	1.0638602	2.06E-38	1.56E-35	Mesenchymal progenitors-3
Gnas	12.884535	0.3828071	5.50E-38	4.00E-35	Mesenchymal progenitors-3
Rpl41	12.6763315	0.43125272	8.00E-37	5.42E-34	Mesenchymal progenitors-3
Tagln	12.560654	1.4210595	3.47E-36	2.28E-33	Mesenchymal progenitors-3
Hmgb2	12.399411	1.2634095	2.63E-35	1.67E-32	Mesenchymal progenitors-3
Acta2	12.383945	1.367347	3.19E-35	1.96E-32	Mesenchymal progenitors-3
Top2a	12.318841	2.061647	7.17E-35	4.27E-32	Mesenchymal progenitors-3
Ndufa4l2	12.209259	1.9008229	2.77E-34	1.60E-31	Mesenchymal progenitors-3
Tyms	12.132065	1.5985794	7.14E-34	4.01E-31	Mesenchymal progenitors-3
Tmsb10	12.001671	0.5884809	3.48E-33	1.85E-30	Mesenchymal progenitors-3
Spc24	11.981578	1.7588466	4.44E-33	2.30E-30	Mesenchymal progenitors-3
Cdk1	11.927413	1.5894871	8.52E-33	4.18E-30	Mesenchymal progenitors-3
Snrpd1	11.914461	0.7643332	9.95E-33	4.77E-30	Mesenchymal progenitors-3
Tubb4b	11.905338	1.1817101	1.11E-32	5.19E-30	Mesenchymal progenitors-3
Tuba1a	11.768622	0.9503621	5.66E-32	2.59E-29	Mesenchymal progenitors-3
Mfge8	11.720615	1.2883848	9.99E-32	4.46E-29	Mesenchymal progenitors-3
Mif	11.690772	0.7933306	1.42E-31	6.21E-29	Mesenchymal progenitors-3
Tuba1b	11.681423	1.0062397	1.59E-31	6.78E-29	Mesenchymal progenitors-3

Rnaseh2c	11.601612	1.0857564	4.04E-31	1.66E-28	Mesenchymal progenitors-3
Dut	11.525445	1.0873984	9.82E-31	3.94E-28	Mesenchymal progenitors-3
Hist1h1b	11.519483	2.4869208	1.05E-30	4.06E-28	Mesenchymal progenitors-3
Cd63	11.507465	0.64808613	1.21E-30	4.57E-28	Mesenchymal progenitors-3
Nasp	11.484375	0.99702394	1.58E-30	5.86E-28	Mesenchymal progenitors-3
Zeb2	11.465051	1.060508	1.98E-30	7.19E-28	Mesenchymal progenitors-3
Hspa8	11.452798	0.52371716	2.28E-30	8.14E-28	Mesenchymal progenitors-3
Prdx4	11.414949	0.9025896	3.52E-30	1.24E-27	Mesenchymal progenitors-3
Selenoh	11.1753645	0.9282549	5.38E-29	1.86E-26	Mesenchymal progenitors-3
Pdgfrb	11.140287	1.1069546	7.99E-29	2.69E-26	Mesenchymal progenitors-3
Atad2	11.139148	1.4712259	8.09E-29	2.69E-26	Mesenchymal progenitors-3
Itga1	11.1181	1.8830605	1.02E-28	3.35E-26	Mesenchymal progenitors-3
Mab21l2	33.330154	2.3240654	1.41E-243	2.78E-240	Gut wall mesenchymal progenitors
Meis2	32.752075	1.5972643	2.84E-235	5.07E-232	Gut wall mesenchymal progenitors
Foxp2	29.323433	2.4806557	5.21E-189	6.83E-186	Gut wall mesenchymal progenitors
Rps14	28.90197	0.8387376	1.13E-183	1.39E-180	Gut wall mesenchymal progenitors
Mpped2	27.495504	2.4582653	1.99E-166	2.30E-163	Gut wall mesenchymal progenitors
Rps16	27.16772	0.6598157	1.56E-162	1.71E-159	Gut wall mesenchymal progenitors
Foxp1	26.102072	1.7862933	3.45E-150	2.95E-147	Gut wall mesenchymal progenitors
Col23a1	24.62663	2.4244103	6.55E-134	4.29E-131	Gut wall mesenchymal progenitors
Tgfbi	24.39047	1.9835577	2.16E-131	1.37E-128	Gut wall mesenchymal progenitors
Ldhb	24.159233	1.6388464	5.97E-129	3.35E-126	Gut wall mesenchymal progenitors
Rpl18a	23.639986	0.6296829	1.50E-123	7.95E-121	Gut wall mesenchymal progenitors
Npm1	23.598022	0.7372546	4.04E-123	2.09E-120	Gut wall mesenchymal progenitors
Rgs10	22.793818	2.0858512	5.28E-115	2.41E-112	Gut wall mesenchymal progenitors
Rps19	22.776077	0.55848384	7.92E-115	3.54E-112	Gut wall mesenchymal progenitors
Rpl15	22.64336	0.6277398	1.62E-113	6.78E-111	Gut wall mesenchymal progenitors
Foxf1	22.61781	1.906878	2.89E-113	1.19E-110	Gut wall mesenchymal progenitors
Sub1	22.370314	0.8438424	7.66E-111	3.01E-108	Gut wall mesenchymal progenitors
Hsp90ab1	22.146479	0.66970646	1.13E-108	4.18E-106	Gut wall mesenchymal progenitors
Rps23	22.02176	0.58822364	1.78E-107	6.25E-105	Gut wall mesenchymal progenitors
Atp5g2	21.947935	0.92239374	9.06E-107	3.12E-104	Gut wall mesenchymal progenitors
Rpl5	21.910261	0.5928985	2.07E-106	6.91E-104	Gut wall mesenchymal progenitors
Tpt1	21.640617	0.35949427	7.45E-104	2.40E-101	Gut wall mesenchymal progenitors
Cox7a2l	21.608438	0.9552674	1.50E-103	4.74E-101	Gut wall mesenchymal progenitors
Rps13	21.191492	0.50249386	1.14E-99	3.51E-97	Gut wall mesenchymal progenitors
Tcf21	21.08024	1.3328248	1.21E-98	3.65E-96	Gut wall mesenchymal progenitors
Rps27a	20.983974	0.433137	9.19E-98	2.74E-95	Gut wall mesenchymal progenitors
Rpl30	20.598389	0.45330924	2.84E-94	7.97E-92	Gut wall mesenchymal progenitors
Etv1	20.546724	2.3169777	8.23E-94	2.28E-91	Gut wall mesenchymal progenitors
Nnat	20.430973	1.5137366	8.87E-93	2.39E-90	Gut wall mesenchymal progenitors
Cox4i1	20.221975	0.62443626	6.27E-91	1.64E-88	Gut wall mesenchymal progenitors
Rpl23	19.67536	0.39007637	3.51E-86	8.72E-84	Gut wall mesenchymal progenitors
Rps5	19.563734	0.6646863	3.15E-85	7.55E-83	Gut wall mesenchymal progenitors
Rpl17	19.51226	0.50629544	8.64E-85	2.05E-82	Gut wall mesenchymal progenitors
Lsp1	19.419302	1.2702795	5.30E-84	1.23E-81	Gut wall mesenchymal progenitors
Atxn7l3b	19.396885	0.8369448	8.20E-84	1.87E-81	Gut wall mesenchymal progenitors

Rps24	19.337269	0.34140328	2.61E-83	5.76E-81	Gut wall mesenchymal progenitors
Rpl18	19.13799	0.5792315	1.22E-81	2.58E-79	Gut wall mesenchymal progenitors
Rps7	19.11829	0.5382085	1.78E-81	3.72E-79	Gut wall mesenchymal progenitors
Rnd3	19.081095	1.4400035	3.63E-81	7.50E-79	Gut wall mesenchymal progenitors
Tceal9	18.987627	0.69197726	2.16E-80	4.42E-78	Gut wall mesenchymal progenitors
Tshz2	18.849098	0.82720375	2.99E-79	5.82E-77	Gut wall mesenchymal progenitors
Btg1	18.613476	1.2073365	2.50E-77	4.77E-75	Gut wall mesenchymal progenitors
Smoc2	18.586365	1.1692034	4.14E-77	7.83E-75	Gut wall mesenchymal progenitors
Rpl34	18.573303	0.5825076	5.28E-77	9.89E-75	Gut wall mesenchymal progenitors
Rps4x	18.568588	0.4489223	5.77E-77	1.07E-74	Gut wall mesenchymal progenitors
Fgfr2	18.003754	2.6498208	1.82E-72	3.19E-70	Gut wall mesenchymal progenitors
Kit	17.917227	2.339064	8.65E-72	1.49E-69	Gut wall mesenchymal progenitors
Rpl7	17.811392	0.4082594	5.77E-71	9.85E-69	Gut wall mesenchymal progenitors
Gm266	17.791574	1.4630076	8.21E-71	1.39E-68	Gut wall mesenchymal progenitors
Iqgap2	17.757391	2.0305507	1.51E-70	2.54E-68	Gut wall mesenchymal progenitors
Myl6	29.365566	1.7925792	1.51E-189	2.97E-185	SM-1 (Gut wall)
Mylk	28.951904	3.700022	2.66E-184	2.61E-180	SM-1 (Gut wall)
Acta2	28.823053	4.0383463	1.10E-182	7.23E-179	SM-1 (Gut wall)
Myl9	27.981304	2.917007	2.74E-172	1.35E-168	SM-1 (Gut wall)
Tpm1	26.200666	2.0111089	2.61E-151	1.03E-147	SM-1 (Gut wall)
Tagln	25.174133	3.2636192	7.69E-140	2.52E-136	SM-1 (Gut wall)
Tpm2	23.630833	2.0106785	1.86E-123	5.22E-120	SM-1 (Gut wall)
Cnn2	23.592638	2.0617948	4.59E-123	1.13E-119	SM-1 (Gut wall)
Psd	22.819832	2.3352578	2.91E-115	6.36E-112	SM-1 (Gut wall)
Myh11	22.26487	3.5030818	8.10E-110	1.59E-106	SM-1 (Gut wall)
Id2	21.868464	2.177464	5.19E-106	9.27E-103	SM-1 (Gut wall)
Alcam	20.636417	2.260035	1.29E-94	1.95E-91	SM-1 (Gut wall)
Ckb	20.217667	2.508817	6.84E-91	9.61E-88	SM-1 (Gut wall)
Foxp2	19.549559	2.3421092	4.16E-85	5.45E-82	SM-1 (Gut wall)
Actg2	19.504871	2.6528316	9.98E-85	1.23E-81	SM-1 (Gut wall)
Cnn1	19.48547	3.3776443	1.46E-84	1.69E-81	SM-1 (Gut wall)
Lsp1	19.007517	1.8311113	1.48E-80	1.61E-77	SM-1 (Gut wall)
Pde5a	18.608177	2.377091	2.76E-77	2.71E-74	SM-1 (Gut wall)
Dstn	18.525509	1.5457859	1.29E-76	1.20E-73	SM-1 (Gut wall)
Csrp1	17.613907	2.04056	1.93E-69	1.46E-66	SM-1 (Gut wall)
Meis2	16.816757	1.2358439	1.84E-63	1.34E-60	SM-1 (Gut wall)
Foxp1	16.488764	1.6624762	4.42E-61	3.10E-58	SM-1 (Gut wall)
Actg1	15.965099	0.73953605	2.24E-57	1.42E-54	SM-1 (Gut wall)
Actb	15.9387	0.6823814	3.41E-57	2.10E-54	SM-1 (Gut wall)
Tgfb1i1	15.850874	1.4370635	1.39E-56	8.01E-54	SM-1 (Gut wall)
Mab21l2	15.812432	1.6525301	2.55E-56	1.43E-53	SM-1 (Gut wall)
Mpped2	15.549988	2.037179	1.59E-54	8.69E-52	SM-1 (Gut wall)
Lmod1	15.395253	3.059047	1.76E-53	9.36E-51	SM-1 (Gut wall)
Cdc42ep3	15.05187	2.399394	3.36E-51	1.65E-48	SM-1 (Gut wall)
Rbpms	14.996408	1.3706721	7.75E-51	3.71E-48	SM-1 (Gut wall)
Bend5	14.950721	2.480825	1.54E-50	7.21E-48	SM-1 (Gut wall)
Flna	14.930747	1.3077612	2.08E-50	9.50E-48	SM-1 (Gut wall)

Pfn1	14.736863	0.81632525	3.74E-49	1.67E-46	SM-1 (Gut wall)
Map1b	14.450501	1.5099825	2.49E-47	1.04E-44	SM-1 (Gut wall)
Myocd	14.396389	2.877125	5.45E-47	2.19E-44	SM-1 (Gut wall)
Cox8a	14.130979	0.75173545	2.45E-45	9.43E-43	SM-1 (Gut wall)
Smoc2	14.043636	1.3060979	8.43E-45	3.18E-42	SM-1 (Gut wall)
Nexn	13.847269	2.1441479	1.32E-43	4.90E-41	SM-1 (Gut wall)
Cox4i1	13.776282	0.63335353	3.54E-43	1.27E-40	SM-1 (Gut wall)
Fermt2	13.587285	1.2274176	4.76E-42	1.67E-39	SM-1 (Gut wall)
Ppp1r12b	13.545967	1.835356	8.37E-42	2.89E-39	SM-1 (Gut wall)
Synpo2	13.460748	2.447975	2.66E-41	9.02E-39	SM-1 (Gut wall)
Rgmb	13.27612	2.2656412	3.18E-40	1.03E-37	SM-1 (Gut wall)
Uqcrh	13.1166115	0.6260795	2.65E-39	8.25E-37	SM-1 (Gut wall)
Id1	12.956664	1.5953032	2.15E-38	6.61E-36	SM-1 (Gut wall)
Pdlim7	12.528747	1.1888081	5.20E-36	1.50E-33	SM-1 (Gut wall)
Ccdc107	12.409522	1.6082335	2.32E-35	6.51E-33	SM-1 (Gut wall)
Tmsb4x	12.106928	0.48516512	9.71E-34	2.69E-31	SM-1 (Gut wall)
Abracl	12.052793	1.0890341	1.87E-33	5.12E-31	SM-1 (Gut wall)
Ppia	12.04175	0.4934402	2.14E-33	5.77E-31	SM-1 (Gut wall)
Actg2	32.368217	5.4703603	7.69E-230	1.51E-225	SM-2 (Gut wall)
Acta2	31.732866	4.8293247	5.47E-221	5.38E-217	SM-2 (Gut wall)
Mylk	30.234638	4.2434764	8.31E-201	5.44E-197	SM-2 (Gut wall)
Myl6	28.669262	1.8817941	9.22E-181	3.63E-177	SM-2 (Gut wall)
Myl9	28.09378	3.233155	1.17E-173	3.82E-170	SM-2 (Gut wall)
Dstn	27.657328	2.540293	2.28E-168	6.40E-165	SM-2 (Gut wall)
Cnn1	27.523314	4.8816113	9.24E-167	2.27E-163	SM-2 (Gut wall)
Myh11	27.447113	4.651604	7.52E-166	1.64E-162	SM-2 (Gut wall)
Ckb	27.314167	3.579085	2.88E-164	5.66E-161	SM-2 (Gut wall)
Cald1	26.727957	2.0083055	2.23E-157	3.98E-154	SM-2 (Gut wall)
Tpm1	26.339376	2.1395364	6.79E-153	1.11E-149	SM-2 (Gut wall)
Hmga2	25.713661	3.4595747	8.22E-146	1.15E-142	SM-2 (Gut wall)
Foxf1	25.428349	2.9918125	1.23E-142	1.61E-139	SM-2 (Gut wall)
Tagln	24.614618	3.499669	8.81E-134	9.62E-131	SM-2 (Gut wall)
Igfbp2	24.515003	3.3141804	1.02E-132	1.06E-129	SM-2 (Gut wall)
Tpm2	24.440805	2.3683035	6.30E-132	6.19E-129	SM-2 (Gut wall)
Actb	23.624207	1.0078144	2.17E-123	1.86E-120	SM-2 (Gut wall)
Mgst3	23.006216	2.897808	4.04E-117	2.94E-114	SM-2 (Gut wall)
Abracl	22.667263	2.0124457	9.43E-114	6.62E-111	SM-2 (Gut wall)
Cfl1	22.535948	1.144291	1.84E-112	1.21E-109	SM-2 (Gut wall)
Fermt2	22.343649	1.9949713	1.39E-110	8.82E-108	SM-2 (Gut wall)
Pdlim7	22.088036	2.1052816	4.12E-108	2.53E-105	SM-2 (Gut wall)
Rbpms	21.693575	1.9420911	2.36E-104	1.40E-101	SM-2 (Gut wall)
Flna	21.068363	1.7491508	1.55E-98	8.71E-96	SM-2 (Gut wall)
Cnn2	20.993334	1.8287827	7.55E-98	4.01E-95	SM-2 (Gut wall)
Psd	20.916435	2.0914907	3.79E-97	1.91E-94	SM-2 (Gut wall)
Synpo2	20.522549	3.238311	1.35E-93	6.65E-91	SM-2 (Gut wall)
Myocd	20.457087	3.6844559	5.20E-93	2.49E-90	SM-2 (Gut wall)
Mab21l2	20.121744	2.0438914	4.76E-90	2.18E-87	SM-2 (Gut wall)

Ncam1	19.555471	1.8695769	3.71E-85	1.62E-82	SM-2 (Gut wall)
Fbxl22	19.448042	4.6152735	3.03E-84	1.27E-81	SM-2 (Gut wall)
Rpl7	19.306967	0.6592516	4.69E-83	1.92E-80	SM-2 (Gut wall)
Ccnd2	19.228235	1.655463	2.15E-82	8.44E-80	SM-2 (Gut wall)
Aldh1a1	19.00672	3.1492658	1.50E-80	5.67E-78	SM-2 (Gut wall)
Nexn	18.823496	2.7524896	4.85E-79	1.73E-76	SM-2 (Gut wall)
Hacd1	18.781618	2.5175133	1.07E-78	3.75E-76	SM-2 (Gut wall)
Csrp1	18.160748	2.095492	1.06E-73	3.52E-71	SM-2 (Gut wall)
Pdlim3	18.151606	4.2232003	1.25E-73	4.08E-71	SM-2 (Gut wall)
Pfn1	17.99265	0.95018035	2.22E-72	7.17E-70	SM-2 (Gut wall)
Aldh1a2	17.966671	3.8221672	3.55E-72	1.13E-69	SM-2 (Gut wall)
Lpp	17.91691	1.8304708	8.70E-72	2.67E-69	SM-2 (Gut wall)
Foxp1	17.399197	1.695838	8.37E-68	2.42E-65	SM-2 (Gut wall)
Cavin2	17.110971	2.1026309	1.23E-65	3.40E-63	SM-2 (Gut wall)
Mgll	17.040113	2.9764671	4.14E-65	1.13E-62	SM-2 (Gut wall)
Carmn	17.0214	2.204779	5.70E-65	1.53E-62	SM-2 (Gut wall)
Ppia	17.014069	0.627659	6.46E-65	1.72E-62	SM-2 (Gut wall)
Nrp2	17.006601	1.9985754	7.34E-65	1.92E-62	SM-2 (Gut wall)
Ccdc107	16.806856	2.066406	2.17E-63	5.55E-61	SM-2 (Gut wall)
Slc25a3	16.678028	0.9839158	1.89E-62	4.71E-60	SM-2 (Gut wall)
Tgfb1i1	16.520905	1.4702163	2.59E-61	6.30E-59	SM-2 (Gut wall)
Etv1	25.943613	5.0950403	2.15E-148	4.22E-144	Interstetial cells of Cajal (ICC)
Kit	24.41064	4.9320855	1.32E-131	1.30E-127	Interstetial cells of Cajal (ICC)
Chchd10	23.020771	5.7466364	2.89E-117	1.89E-113	Interstetial cells of Cajal (ICC)
Foxf1	22.60268	3.3619392	4.08E-113	2.00E-109	Interstetial cells of Cajal (ICC)
Nrp2	22.123743	3.3182485	1.87E-108	7.34E-105	Interstetial cells of Cajal (ICC)
Ap1s2	20.801422	3.4855437	4.20E-96	6.35E-93	Interstetial cells of Cajal (ICC)
Enpep	20.465628	5.2724814	4.36E-93	4.51E-90	Interstetial cells of Cajal (ICC)
mt-Cytb	19.903658	0.8565883	3.78E-88	3.23E-85	Interstetial cells of Cajal (ICC)
Cpe	19.565535	2.0356038	3.04E-85	2.39E-82	Interstetial cells of Cajal (ICC)
mt-Nd4	19.504019	0.8134009	1.01E-84	7.12E-82	Interstetial cells of Cajal (ICC)
Pcdh17	19.472065	4.7613006	1.89E-84	1.24E-81	Interstetial cells of Cajal (ICC)
Tmem158	19.042852	3.2533882	7.53E-81	4.48E-78	Interstetial cells of Cajal (ICC)
Rgs10	18.681164	2.845442	7.05E-78	3.64E-75	Interstetial cells of Cajal (ICC)
Cox8a	18.419783	1.1914186	9.12E-76	4.37E-73	Interstetial cells of Cajal (ICC)
Btg1	18.383265	2.0980535	1.79E-75	8.17E-73	Interstetial cells of Cajal (ICC)
Foxp2	18.310055	2.6231787	6.88E-75	2.94E-72	Interstetial cells of Cajal (ICC)
Ppargc1a	18.302588	4.5644584	7.89E-75	3.30E-72	Interstetial cells of Cajal (ICC)
mt-Nd2	17.85487	0.76456505	2.65E-71	1.00E-68	Interstetial cells of Cajal (ICC)
Spry1	17.818432	3.1218667	5.08E-71	1.89E-68	Interstetial cells of Cajal (ICC)
Edn3	17.796125	3.5221226	7.57E-71	2.76E-68	Interstetial cells of Cajal (ICC)
Atp2b1	17.666378	1.7861906	7.61E-70	2.61E-67	Interstetial cells of Cajal (ICC)
Thbs4	17.665722	3.7923837	7.70E-70	2.61E-67	Interstetial cells of Cajal (ICC)
Ldhb	17.621752	2.225136	1.68E-69	5.49E-67	Interstetial cells of Cajal (ICC)
Elovl6	17.432724	2.8543735	4.66E-68	1.48E-65	Interstetial cells of Cajal (ICC)
mt-Nd1	17.190653	0.7767325	3.12E-66	9.29E-64	Interstetial cells of Cajal (ICC)
Atp2a3	17.161842	4.30058	5.13E-66	1.50E-63	Interstetial cells of Cajal (ICC)

Pde3a	16.90477	2.6734402	4.15E-64	1.20E-61	Interstetial cells of Cajal (ICC)
Dkk2	16.798588	2.9416158	2.50E-63	6.92E-61	Interstetial cells of Cajal (ICC)
mt-Co3	16.76088	0.56051064	4.72E-63	1.29E-60	Interstetial cells of Cajal (ICC)
Ano1	16.647177	3.7945626	3.17E-62	8.54E-60	Interstetial cells of Cajal (ICC)
Itpk1	16.411863	3.7845078	1.57E-60	4.07E-58	Interstetial cells of Cajal (ICC)
Foxp1	16.278208	1.9633447	1.41E-59	3.53E-57	Interstetial cells of Cajal (ICC)
Osr1	16.06725	1.8147062	4.33E-58	1.04E-55	Interstetial cells of Cajal (ICC)
Atp5b	15.994735	1.159727	1.39E-57	3.29E-55	Interstetial cells of Cajal (ICC)
Slc12a2	15.848769	2.6828299	1.43E-56	3.28E-54	Interstetial cells of Cajal (ICC)
Atp1a1	15.426984	2.1654	1.08E-53	2.30E-51	Interstetial cells of Cajal (ICC)
Ppp1r14a	15.230865	2.3440852	2.21E-52	4.61E-50	Interstetial cells of Cajal (ICC)
Aldoa	15.098896	1.5368929	1.65E-51	3.24E-49	Interstetial cells of Cajal (ICC)
Prkcq	14.882437	5.6278887	4.29E-50	8.26E-48	Interstetial cells of Cajal (ICC)
mt-Co2	14.605012	0.50883216	2.61E-48	4.84E-46	Interstetial cells of Cajal (ICC)
C2cd4a	14.532364	5.492038	7.56E-48	1.36E-45	Interstetial cells of Cajal (ICC)
Timp3	14.460291	2.2214167	2.16E-47	3.86E-45	Interstetial cells of Cajal (ICC)
Rbpms	14.385435	1.559861	6.39E-47	1.11E-44	Interstetial cells of Cajal (ICC)
H19	14.036057	1.0206126	9.38E-45	1.54E-42	Interstetial cells of Cajal (ICC)
Uqcr10	14.011864	1.313422	1.32E-44	2.14E-42	Interstetial cells of Cajal (ICC)
Atp1b3	13.996274	2.1374762	1.64E-44	2.65E-42	Interstetial cells of Cajal (ICC)
Atp2a2	13.893143	1.9307842	6.97E-44	1.08E-41	Interstetial cells of Cajal (ICC)
Aldh1b1	13.704129	3.4368577	9.59E-43	1.44E-40	Interstetial cells of Cajal (ICC)
Slc38a1	13.647338	2.5747325	2.09E-42	3.12E-40	Interstetial cells of Cajal (ICC)
2010107E04Rik	13.43607	1.2406986	3.72E-41	5.37E-39	Interstetial cells of Cajal (ICC)
Dcn	58.4214	4.4921694	0	0	Pdgfra+ fibroblast-like cells
Postn	57.662373	5.0452905	0	0	Pdgfra+ fibroblast-like cells
Col3a1	57.481396	2.7412927	0	0	Pdgfra+ fibroblast-like cells
Gsn	56.237007	3.322065	0	0	Pdgfra+ fibroblast-like cells
Col1a2	56.024487	3.246254	0	0	Pdgfra+ fibroblast-like cells
Col1a1	55.797672	2.754864	0	0	Pdgfra+ fibroblast-like cells
S100a6	53.34749	3.997101	0	0	Pdgfra+ fibroblast-like cells
Col6a1	52.901024	2.4502263	0	0	Pdgfra+ fibroblast-like cells
Lum	51.081955	3.0453007	0	0	Pdgfra+ fibroblast-like cells
Mfap5	50.882915	6.067314	0	0	Pdgfra+ fibroblast-like cells
Col14a1	49.866238	4.042242	0	0	Pdgfra+ fibroblast-like cells
Itih5	49.743477	5.1414413	0	0	Pdgfra+ fibroblast-like cells
Col6a2	49.549107	2.517978	0	0	Pdgfra+ fibroblast-like cells
Sparc	48.768295	1.8460482	0	0	Pdgfra+ fibroblast-like cells
S100a10	48.59025	3.0719876	0	0	Pdgfra+ fibroblast-like cells
Itm2a	47.888084	2.2380567	0	0	Pdgfra+ fibroblast-like cells
Gpc3	47.637432	1.9877486	0	0	Pdgfra+ fibroblast-like cells
Cd34	44.728333	4.403257	0	0	Pdgfra+ fibroblast-like cells
Col5a1	44.62751	2.2283921	0	0	Pdgfra+ fibroblast-like cells
Dlk1	43.98017	1.8000433	0	0	Pdgfra+ fibroblast-like cells
Clec3b	43.348377	9.025129	0	0	Pdgfra+ fibroblast-like cells
Vim	42.85277	1.3433007	0	0	Pdgfra+ fibroblast-like cells
Col6a3	42.772522	2.2620316	0	0	Pdgfra+ fibroblast-like cells

Nid1	42.63602	2.6310709	0	0	Pdgfra+ fibroblast-like cells
Ebf1	41.128963	3.1147728	0	0	Pdgfra+ fibroblast-like cells
Fstl1	41.12784	1.5886719	0	0	Pdgfra+ fibroblast-like cells
Col5a2	40.913696	1.6960328	0	0	Pdgfra+ fibroblast-like cells
Igfbp7	40.506027	3.1548657	0	0	Pdgfra+ fibroblast-like cells
Zim1	40.038944	3.235103	0	0	Pdgfra+ fibroblast-like cells
Vcan	39.814625	2.5752034	0	0	Pdgfra+ fibroblast-like cells
Serping1	39.098633	2.982793	0	0	Pdgfra+ fibroblast-like cells
Igfbp4	39.05853	1.4080992	0	0	Pdgfra+ fibroblast-like cells
Fbln1	39.022877	2.3417127	0	0	Pdgfra+ fibroblast-like cells
Akap12	38.73043	2.1283462	0	0	Pdgfra+ fibroblast-like cells
Tnxb	38.64362	4.1143627	0	0	Pdgfra+ fibroblast-like cells
Ahnak	38.57577	1.9836315	0	0	Pdgfra+ fibroblast-like cells
Col5a3	38.45757	4.848876	0	0	Pdgfra+ fibroblast-like cells
Pcolce	38.356598	2.8340878	0	0	Pdgfra+ fibroblast-like cells
Sparcl1	37.40638	1.8692746	3.08E-306	1.23E-303	Pdgfra+ fibroblast-like cells
Matn2	36.999092	3.2932703	1.18E-299	4.48E-297	Pdgfra+ fibroblast-like cells
Ltbp4	36.150963	1.9566725	3.59E-286	1.24E-283	Pdgfra+ fibroblast-like cells
Bgn	35.812428	1.8907233	7.08E-281	2.32E-278	Pdgfra+ fibroblast-like cells
Crip1	35.10319	3.0133147	6.03E-270	1.79E-267	Pdgfra+ fibroblast-like cells
Fndc1	34.937813	5.1029835	1.98E-267	5.82E-265	Pdgfra+ fibroblast-like cells
Fbn1	34.698925	1.7362343	8.18E-264	2.36E-261	Pdgfra+ fibroblast-like cells
Fmo1	34.60709	3.4842885	1.98E-262	5.55E-260	Pdgfra+ fibroblast-like cells
Laptm4a	34.508305	1.083589	6.02E-261	1.67E-258	Pdgfra+ fibroblast-like cells
Peg3	34.320324	2.0074563	3.91E-258	1.07E-255	Pdgfra+ fibroblast-like cells
Rpl39	33.949524	0.6536679	1.24E-252	3.25E-250	Pdgfra+ fibroblast-like cells
Ogn	33.709435	2.6838143	4.21E-249	1.05E-246	Pdgfra+ fibroblast-like cells
Bgn	15.995763	2.9893765	1.37E-57	1.44E-53	Tnc+ Acta-low myofibroblast-like cells
Eln	15.991424	4.857492	1.47E-57	1.44E-53	Tnc+ Acta-low myofibroblast-like cells
Thbs2	15.830831	4.122994	1.91E-56	1.25E-52	Tnc+ Acta-low myofibroblast-like cells
Mgp	15.707175	4.123225	1.35E-55	6.64E-52	Tnc+ Acta-low myofibroblast-like cells
Col1a2	15.501913	3.0601203	3.37E-54	1.32E-50	Tnc+ Acta-low myofibroblast-like cells
Col1a1	14.483223	2.469776	1.55E-47	5.07E-44	Tnc+ Acta-low myofibroblast-like cells
Fhl1	14.159526	4.2423396	1.63E-45	4.58E-42	Tnc+ Acta-low myofibroblast-like cells
Igfbp7	14.010166	3.5356836	1.35E-44	3.32E-41	Tnc+ Acta-low myofibroblast-like cells
Col14a1	13.934968	3.408484	3.88E-44	8.48E-41	Tnc+ Acta-low myofibroblast-like cells
Col3a1	13.763715	2.2284214	4.21E-43	7.53E-40	Tnc+ Acta-low myofibroblast-like cells
Crip1	13.37645	3.6422386	8.30E-41	1.25E-37	Tnc+ Acta-low myofibroblast-like cells
Vcan	13.324292	2.7942693	1.67E-40	2.19E-37	Tnc+ Acta-low myofibroblast-like cells
Postn	13.312839	3.5489023	1.95E-40	2.39E-37	Tnc+ Acta-low myofibroblast-like cells
Col16a1	12.812887	2.7699258	1.39E-37	1.09E-34	Tnc+ Acta-low myofibroblast-like cells
Adamts2	12.763438	3.6108527	2.62E-37	1.98E-34	Tnc+ Acta-low myofibroblast-like cells
Nid1	12.388156	2.5296078	3.03E-35	1.75E-32	Tnc+ Acta-low myofibroblast-like cells
Tnc	12.068644	4.1860723	1.55E-33	7.79E-31	Tnc+ Acta-low myofibroblast-like cells
Cdh11	12.058776	2.0610626	1.74E-33	8.57E-31	Tnc+ Acta-low myofibroblast-like cells
mt-Co1	11.971597	0.8587143	5.01E-33	2.34E-30	Tnc+ Acta-low myofibroblast-like cells
Col5a1	11.950187	1.9864753	6.48E-33	2.83E-30	Tnc+ Acta-low myofibroblast-like cells

Prss35	11.929967	4.2074833	8.26E-33	3.53E-30	Tnc+ Acta-low myofibroblast-like cells
Mfap4	11.8951435	1.8793751	1.25E-32	5.24E-30	Tnc+ Acta-low myofibroblast-like cells
Fbn1	11.857787	1.9432724	1.96E-32	8.03E-30	Tnc+ Acta-low myofibroblast-like cells
mt-Nd1	11.794946	0.8888106	4.14E-32	1.60E-29	Tnc+ Acta-low myofibroblast-like cells
Col4a1	11.791092	2.2074451	4.34E-32	1.64E-29	Tnc+ Acta-low myofibroblast-like cells
Matn2	11.71455	2.912099	1.07E-31	3.77E-29	Tnc+ Acta-low myofibroblast-like cells
mt-Cytb	11.705652	0.84591615	1.19E-31	4.11E-29	Tnc+ Acta-low myofibroblast-like cells
Hsp90b1	11.686445	1.7253615	1.50E-31	5.07E-29	Tnc+ Acta-low myofibroblast-like cells
Sparc	11.655961	1.4854481	2.14E-31	7.01E-29	Tnc+ Acta-low myofibroblast-like cells
Dcn	11.625521	3.0187216	3.06E-31	9.85E-29	Tnc+ Acta-low myofibroblast-like cells
mt-Nd4	11.431315	0.777661	2.92E-30	8.19E-28	Tnc+ Acta-low myofibroblast-like cells
Fhl2	11.389752	3.3557909	4.70E-30	1.28E-27	Tnc+ Acta-low myofibroblast-like cells
Igfbp3	11.352109	4.0783405	7.24E-30	1.95E-27	Tnc+ Acta-low myofibroblast-like cells
mt-Atp6	11.243146	0.71512395	2.50E-29	6.31E-27	Tnc+ Acta-low myofibroblast-like cells
Col4a2	11.061187	2.23107	1.94E-28	4.70E-26	Tnc+ Acta-low myofibroblast-like cells
S100a6	10.977774	2.5263157	4.89E-28	1.16E-25	Tnc+ Acta-low myofibroblast-like cells
mt-Co2	10.924955	0.69815457	8.76E-28	2.05E-25	Tnc+ Acta-low myofibroblast-like cells
Col6a3	10.910924	1.8700353	1.02E-27	2.36E-25	Tnc+ Acta-low myofibroblast-like cells
Nov	10.805969	4.2848387	3.23E-27	7.29E-25	Tnc+ Acta-low myofibroblast-like cells
Malat1	10.707688	1.0095245	9.37E-27	2.07E-24	Tnc+ Acta-low myofibroblast-like cells
Col6a1	10.704979	1.6252376	9.65E-27	2.11E-24	Tnc+ Acta-low myofibroblast-like cells
Ntrk3	10.665707	3.4437175	1.47E-26	3.18E-24	Tnc+ Acta-low myofibroblast-like cells
Pls3	10.54595	2.5575383	5.30E-26	1.11E-23	Tnc+ Acta-low myofibroblast-like cells
Loxl1	10.5300255	2.3189363	6.28E-26	1.29E-23	Tnc+ Acta-low myofibroblast-like cells
Pam	10.493087	2.7068543	9.29E-26	1.86E-23	Tnc+ Acta-low myofibroblast-like cells
mt-Co3	10.396481	0.62230235	2.57E-25	5.01E-23	Tnc+ Acta-low myofibroblast-like cells
Cst3	10.382669	1.6805627	2.97E-25	5.73E-23	Tnc+ Acta-low myofibroblast-like cells
Epha3	10.3741455	2.9040303	3.25E-25	6.20E-23	Tnc+ Acta-low myofibroblast-like cells
Lhfp	10.356723	2.5660331	3.90E-25	7.37E-23	Tnc+ Acta-low myofibroblast-like cells
mt-Nd2	10.308067	0.7211153	6.48E-25	1.21E-22	Tnc+ Acta-low myofibroblast-like cells
Mustn1	20.52483	6.398448	1.29E-93	2.54E-89	SM-3 (Villus)
Tagln	20.431337	5.856213	8.81E-93	8.65E-89	SM-3 (Villus)
Mcam	20.221539	5.86431	6.33E-91	4.15E-87	SM-3 (Villus)
Crip1	20.1853	5.2411427	1.32E-90	6.48E-87	SM-3 (Villus)
Myl9	20.159714	4.440641	2.21E-90	8.69E-87	SM-3 (Villus)
Mef2c	20.143057	4.903547	3.10E-90	1.01E-86	SM-3 (Villus)
Aoc3	20.03507	5.3929815	2.72E-89	7.65E-86	SM-3 (Villus)
Cav1	19.889505	5.684899	5.02E-88	1.23E-84	SM-3 (Villus)
Myh11	19.773561	5.705443	5.03E-87	1.10E-83	SM-3 (Villus)
Cald1	19.764402	2.770548	6.03E-87	1.19E-83	SM-3 (Villus)
Igfbp7	19.673204	4.682124	3.66E-86	6.54E-83	SM-3 (Villus)
Tinagl1	19.65783	6.8869596	4.95E-86	8.11E-83	SM-3 (Villus)
Itga1	19.631382	5.2637486	8.34E-86	1.26E-82	SM-3 (Villus)
Acta2	19.511976	5.223098	8.69E-85	1.22E-81	SM-3 (Villus)
Tpm1	19.489986	2.9697218	1.34E-84	1.75E-81	SM-3 (Villus)
Eln	19.460575	5.5974407	2.37E-84	2.91E-81	SM-3 (Villus)
Flna	19.441757	3.113771	3.42E-84	3.96E-81	SM-3 (Villus)

Tm4sf1	19.283438	5.603838	7.40E-83	7.65E-80	SM-3 (Villus)
Jag1	19.230103	4.204888	2.07E-82	2.04E-79	SM-3 (Villus)
Il13ra1	19.1992	6.419101	3.76E-82	3.52E-79	SM-3 (Villus)
Esam	19.163095	5.9778275	7.53E-82	6.72E-79	SM-3 (Villus)
Cavin3	19.009155	3.065477	1.43E-80	1.22E-77	SM-3 (Villus)
Pdgfa	18.957657	4.2810426	3.82E-80	3.13E-77	SM-3 (Villus)
Notch3	18.822992	4.1887817	4.89E-79	3.85E-76	SM-3 (Villus)
Cav2	18.494095	6.7613964	2.30E-76	1.62E-73	SM-3 (Villus)
Uba2	18.459137	3.4032235	4.40E-76	2.98E-73	SM-3 (Villus)
Bcam	18.333843	5.584166	4.44E-75	2.82E-72	SM-3 (Villus)
Cavin1	18.252016	3.2497687	1.99E-74	1.22E-71	SM-3 (Villus)
Actn1	18.223846	3.2251806	3.34E-74	1.99E-71	SM-3 (Villus)
Lgalsl	18.195965	4.377082	5.56E-74	3.21E-71	SM-3 (Villus)
Tpm2	18.188145	2.9687235	6.41E-74	3.60E-71	SM-3 (Villus)
Gm13889	18.140223	5.149919	1.53E-73	8.37E-71	SM-3 (Villus)
Inpp4b	18.062143	6.368537	6.33E-73	3.36E-70	SM-3 (Villus)
Lmod1	18.008503	4.9412885	1.67E-72	8.64E-70	SM-3 (Villus)
Rgs7bp	17.946276	4.6663857	5.13E-72	2.59E-69	SM-3 (Villus)
Col4a1	17.593493	2.930351	2.76E-69	1.36E-66	SM-3 (Villus)
Dstn	17.544193	2.6952748	6.59E-69	3.16E-66	SM-3 (Villus)
Parm1	17.499388	3.8028615	1.45E-68	6.78E-66	SM-3 (Villus)
Crip2	17.450434	3.8212454	3.42E-68	1.56E-65	SM-3 (Villus)
Map3k20	17.427467	4.542068	5.11E-68	2.28E-65	SM-3 (Villus)
Pde3a	17.254097	3.4037647	1.04E-66	4.55E-64	SM-3 (Villus)
Wtip	17.096083	3.3565717	1.59E-65	6.64E-63	SM-3 (Villus)
Cryab	17.053783	4.171619	3.28E-65	1.34E-62	SM-3 (Villus)
Mfge8	16.99911	3.361401	8.34E-65	3.34E-62	SM-3 (Villus)
7-Sep	16.830502	1.9385679	1.46E-63	5.62E-61	SM-3 (Villus)
Ndufa4l2	16.746647	4.056599	5.99E-63	2.26E-60	SM-3 (Villus)
Actn4	16.734217	2.721576	7.38E-63	2.74E-60	SM-3 (Villus)
Actg2	16.615961	3.778279	5.34E-62	1.94E-59	SM-3 (Villus)
Procr	16.416985	5.9100966	1.45E-60	5.07E-58	SM-3 (Villus)
Zfhx3	16.402012	2.5723062	1.85E-60	6.38E-58	SM-3 (Villus)
Col18a1	26.236198	7.0498924	1.03E-151	2.02E-147	Pericytes
Col4a1	26.044394	4.321435	1.56E-149	1.53E-145	Pericytes
Pdgfrb	25.45854	4.705067	5.68E-143	3.72E-139	Pericytes
Rgs5	25.248634	6.8217325	1.17E-140	5.76E-137	Pericytes
Col4a2	25.05333	3.9045007	1.61E-138	6.31E-135	Pericytes
Myh9	25.042831	4.501427	2.09E-138	6.84E-135	Pericytes
Igfbp7	24.393513	4.5150485	2.00E-131	4.38E-128	Pericytes
Gm13889	23.63744	5.964197	1.59E-123	3.12E-120	Pericytes
Mcam	23.326578	5.424364	2.38E-120	3.60E-117	Pericytes
4-Sep	23.273073	6.351825	8.31E-120	1.17E-116	Pericytes
Ebf1	23.044256	3.8746367	1.68E-117	2.20E-114	Pericytes
Cygb	22.61001	4.2592506	3.45E-113	3.99E-110	Pericytes
Epas1	21.919008	6.292048	1.71E-106	1.77E-103	Pericytes
Rarres2	21.751703	3.0938501	6.66E-105	6.54E-102	Pericytes

Rasgrp2	21.65907	4.283235	4.99E-104	4.67E-101	Pericytes
Lamb1	21.585014	3.0144823	2.48E-103	2.22E-100	Pericytes
Ifitm3	21.553246	2.2356727	4.94E-103	4.22E-100	Pericytes
Itga1	21.548573	4.5623546	5.46E-103	4.47E-100	Pericytes
Nid2	21.205221	3.6211898	8.55E-100	6.46E-97	Pericytes
Gcnt2	21.178709	6.9073825	1.50E-99	1.09E-96	Pericytes
Crip2	21.166977	3.9145317	1.93E-99	1.35E-96	Pericytes
Cbfa2t3	20.428207	5.3083463	9.39E-93	6.15E-90	Pericytes
Art3	20.412916	7.782628	1.28E-92	8.14E-90	Pericytes
Fabp7	20.39438	5.5588684	1.88E-92	1.15E-89	Pericytes
Notch3	20.297976	3.6590533	1.34E-91	7.98E-89	Pericytes
Ndufa4l2	20.096212	4.0404286	7.96E-90	4.35E-87	Pericytes
Phlda1	20.070345	4.2805786	1.34E-89	7.12E-87	Pericytes
Tagln2	19.305065	3.2430224	4.87E-83	2.33E-80	Pericytes
mt-Cytb	19.064531	0.96496373	4.98E-81	2.33E-78	Pericytes
Tgfb2	18.851683	4.06647	2.85E-79	1.24E-76	Pericytes
Gjc1	18.673065	2.6221154	8.20E-78	3.43E-75	Pericytes
Abcc9	18.632103	3.1366665	1.76E-77	6.94E-75	Pericytes
Igfbp3	18.484596	4.2006626	2.75E-76	1.06E-73	Pericytes
Mfge8	18.328901	3.1374207	4.87E-75	1.80E-72	Pericytes
Myo1b	18.19981	3.6366415	5.18E-74	1.85E-71	Pericytes
Tns1	18.164825	3.0429611	9.80E-74	3.44E-71	Pericytes
Tmem176a	18.161282	2.6232257	1.05E-73	3.60E-71	Pericytes
Thbd	18.13528	4.9650655	1.68E-73	5.69E-71	Pericytes
Ggt5	17.987276	5.162026	2.45E-72	8.16E-70	Pericytes
Gucy1a1	17.738016	3.1058128	2.13E-70	6.87E-68	Pericytes
Tpm4	17.678562	1.9609044	6.13E-70	1.94E-67	Pericytes
Tmsb4x	17.649542	1.0184737	1.03E-69	3.20E-67	Pericytes
Cspg4	17.387798	3.6634243	1.02E-67	3.09E-65	Pericytes
Nid1	17.356855	2.357471	1.75E-67	5.21E-65	Pericytes
Lama4	17.350592	3.1673887	1.95E-67	5.64E-65	Pericytes
Id3	17.23514	2.0788634	1.45E-66	4.12E-64	Pericytes
Serpinb1a	17.217113	4.829537	1.98E-66	5.55E-64	Pericytes
Lgmn	17.16792	3.7983334	4.62E-66	1.28E-63	Pericytes
Gng11	17.040451	2.6999054	4.12E-65	1.09E-62	Pericytes
mt-Nd4	16.860243	0.79953	8.82E-64	2.25E-61	Pericytes