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Journal of
Clinical Endocrinology and Metabolism

ISSN 2998-9213

Research Article

Single-Cell Sequencing Reveals A Regulatory Role Of WT1 In Mast Cell Proliferation In Endometrial Polyps.

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Abstract

Endometrial polyps are the predominant structural anomalies of the endometrial mucosa observed in unexplained infertility cases, potentially compromising endometrial receptivity and suggesting shared etiological characteristics. However, their comprehensive cell atlas and immune landscape remain inadequately defined. In this study, we employed single-cell RNA sequencing and bulk RNA-seq to systematically analyze ectopic endometrial polyps (EPs) alongside adjacent eutopic endometrial tissues (EUs). This enabled us to delineate alterations in cell composition and transcriptional dynamics across diverse cell types associated with endometrial polyps. Notably, we observed an increase and activation of mast cells, with significant transcriptional profile variations. Through transcription regulatory network analysis, WT1 was identified as a pivotal transcriptional regulator mediating mast cell proliferation in EPs, concomitant with the dysregulation of WT1 target genes involved in cell growth. These findings provide novel insights into the cellular heterogeneity and molecular mechanisms of endometrial polyps at single-cell resolution, presenting potential therapeutic targets for clinical intervention.

Keywords : Endometrial polyp; Single-cell RNA sequencing; Mast cells; WT1.

INTRODUCTION

Endometrial polyps (EPs) are localized, sessile, or pedunculated structural abnormality of the mucous membrane [1]. They are the most common structural abnormality of the mucous membrane of the endometrium detected in about 50% of cases of abnormal uterine bleeding and 35% of infertility[2,3]. The risk factors for endometrial polyps' development are tamoxifen usage[4], advanced age, hypertension, and obesity[5,6]. Though malignant transformation of EPs is rare[7,8], the endometrial polyp provides an unfavorable environment for the endometrium receptivity and other etiopathogeneses. However, the pathogenesis of EPs was not clear[9], and the exact cause of endometrial polyps is uncertain[10], One hypothesis suggests that the elevated levels of estrogen receptors (ERs) in the glandular cells of polyps are significantly higher than those found in normal endometrial tissue[11]. Studies also supposed it as endometrial localized chronic inflammation and mast cells might be essential to initiate and control the inflammation through cytokines and growth factors secretion. However, the cell landscape of endometrial polyps is still uncertain.

Evaluation of the endometrial cells and epithelial evolutionary trajectory in patients with EPs is an important line of investigation in the pathophysiology of the disease. Single-cell RNA sequencing (scRNA-seq) has become an essential technique for analyzing the complexity and diversity within tissues, offering insights into the cellular and molecular landscapes of complex tissues. By profiling both ectopic endometrial polyps and adjacent eutopic endometrium, this

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Received: 05-Jan-2025, Manuscript No. JOCEM-4404 **; Editor Assigned:** 06-Jan-2025 **; Reviewed:** 05-Feb-2025, QC No.JOCEM-4404 **; Published:** 07-Feb-2025, **DOI: 1**0.52338/jocem.2025.4404
Citation: Yu Lin. Single-Cell Sequencing Reveals a Regulatory Role of WT1 in Mast Cell Proliferation in Endometrial Polyps. Journal of Clinical Endocrinology and Metabolism. 2025 January; 9(1). doi: 10.52338/jocem.2025.4404.
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approach allows for a detailed comparison of the cellular dynamics and transcriptional alterations specific to EPs.

Mast cells serve a pivotal role in the pathobiology of type 2 (T2) allergic inflammatory airway diseases, such as asthma and chronic rhinosinusitis with nasal polyps[12]. These factors contribute to the advancement and intensity of type 2 inflammatory disorders through various mechanisms, such as the synthesis of eicosanoids, the production of cytokines, and the secretion of pre-existing mediators like proteases and histamine[13]. The expansion of Mast cells is a notable characteristic of both nasal and colonic polyps. Research suggests that the growth of these polyps is partially driven by the local proliferation of mast cells within the nasal polyp tissue[14]. Furthermore, a high density of activated Mast cells has been reported in endometrial polyps[15]. Therefore, identifying the factors that stimulate mast cells proliferation holds significant pathobiologic implications for endometrial polyps.

Given these insights, elucidating the transcriptional regulation and cellular interactions within endometrial polyps (EPs) is pivotal for understanding their pathophysiology. Here, we identify transcriptional regulators, notably WT1, as central to mast cell proliferation. This study seeks to delineate the role of WT1 in this proliferation process and its broader implications for EPs formation and progression. By dissecting transcriptional regulatory programs and cellular dynamics, we aim to uncover novel therapeutic targets for addressing EPs-associated symptoms and complications.

METHODS

Patients and samples

In this study, all samples were obtained from the international maternity and child health hospital of Medical school, Shanghai Jiaotong University, Shanghai, China. The detailed patients and sample information can be found in Table S1.Informed consent from patients were obtained before this work. All procedures involved were approved by the Institutional Review Board of international maternity and child health hospital.

Preparation of single cell suspensions

All endometrial tissue samples were processed independently using an identical protocol. In brief, the tissues were minced into small fragments, each measuring less than 1 mm in diameter. These fragments underwent enzymatic digestion with collagenase I (1 mg/ml; Thermo Fisher) and deoxyribonuclease I (0.2 mg/ml; Thermo Fisher) for 50 minutes on a rotator at 37 °C. The resulting digested mixture was filtered through a 70-μm cell strainer to isolate dissociated cells. Following this, the supernatant was discarded after centrifugation at 300g for 10 minutes, and the pellet was resuspended in 1 mL of red blood cell lysis buffer (Thermo Fisher) and incubated at 4 °C for 10 minutes to eliminate intact red blood cells. To further purify the single-cell suspension, a Dead Cell Removal Kit (Miltenyi) was employed to eliminate dead cells. The resultant pellet was then resuspended in 5 mL of calcium- and magnesium-free PBS containing 0.04% weight/volume BSA. Finally, 10 μl of this suspension was counted using a hemocytometer under an inverted microscope, with Trypan blue utilized to distinguish live cells. After confirming the quality of the single-cell suspensions, three samples from each group were selected for 10x Genomic sequencing, given the high costs associated with single-cell RNA sequencing.

Library construction for single cell gene expression

Six samples were processed using the 10x Genomics Chromium platform , as detailed in Table S1. The freshly prepared single-cell suspension was diluted to a concentration of 700-1200 cells per μl, following the guidelines provided in the 10x Genomics Chromium Next GEM Single Cell 3' Reagent Kits v3.1 (No. 1000268) for computational analysis and library construction. The resulting library was sequenced on the Illumina Nova 6000 PE150 platform.

Furthermore, eight samples were examined with the BD Rhapsody™ platform, as outlined in Table S1. In accordance with the manufacturer's guidelines, the single-cell suspension was modified to the correct volume for processing and capture using the BD Rhapsody™ Enhanced Cartridge Reagent Kit (Cat. No. 664887) along with the BD Rhapsody™ Cartridge Kit (Cat. No. 633733). Reverse transcription was carried out utilizing the BD Rhapsody™ cDNA kit (Cat. No. 633773), and the BD Rhapsody™ WTA Amplification Kit (Cat. No. 633801) was employed for constructing the DNA library. High-throughput sequencing was performed in PE-150 mode.

Processing Raw Data from scRNA-seq

The FASTQ files from 10xGenomics Chromium platform were initially analyzed using the 10xGenomics Chromium pipeline, employing the default parameters from the Cell Ranger single-cell software suite (v6.1.2) (10xGenomics) (accessible at https://www.10xgenomics.com/support/software/cell-ranger/latest). Following this, the FASTQ files from the BD Rhapsody™ platform were processed via the BD Rhapsody WTA analysis pipeline, utilizing the GRCh38 human genome as a reference (Seven Bridges, Charlestown, Mass). The resulting data were subsequently evaluated using SeqGeq 1.8.0 (BD Biosciences).

Single-cell gene expression quantification and determination of cell types

The single-cell RNA-seq data were analyzed using the Seurat R package (version 4.0.4). To exclude doublets, the R package DoubletFinder was employed. After conducting quality control, a total of 103,539 cells were retained for subsequent

bioinformatics analyses. To mitigate batch effects between samples and experiments, integration was performed using the fastMNN method. Dimensionality reduction was achieved with the "RunUMAP" function, allowing visualization through Uniform Manifold Approximation and Projection (UMAP). For subgroup clustering, cells of various types were separately extracted and clustered based on their first 22 clusters, using a resolution of 0.5. The Wilcoxon rank-sum test, executed with the "FindAllMarkers" function, identified markers for each cluster. Only genes with |avg_log2FC| > 0.25 and p_val_adj < 0.05 were considered significant marker genes. The marker genes for each cluster are detailed in Supplementary **Table S2**.

Bulk RNA sequencing and data analysis

To identify the genes responsible for endometrial polyps, we compare the expression profiles between 5 endometrial polyps and 5 eutopic endometrium. Adapter trimming and quality control were automated using Trim Galore (version 0.6.7). For genomic alignment, Hisat2 (version 2.1.0) was utilized to map sequences to the human reference genome (GRCh38). The read counts for each gene were calculated using featureCounts (version 1.6.3). Differentially expressed genes between the samples were determined using DEGseq2, applying thresholds of |Log2-fold change| > 1 and a p-value < 0.05.

Cellular Communication Networks in Single-Cell Sequencing Data

To explore enhanced cell-cell communication between mast cells and other cells, we utilized CellPhoneDB, a comprehensive tool designed to identify and visualize cell-type interactions based on signaling characteristics. we employed the METHOD 3: Retrieval of Differentially Expressed Interactions available in CellPhoneDB version 3[16], which leverages differentially expressed genes to extract and highlight enhanced cell communication.

WT1 knockdown with siRNAs

To investigate the role of WT1 in mast cell proliferation, we performed siRNA-mediated knockdown of WT1 in the HMC-1 mast cell line. The experiments were conducted in triplicate, with three samples undergoing WT1 knockdown and three control samples treated with a non-targeting siRNA. RNA sequencing was carried out to assess changes in gene expression 24 hours post-transfection. Following transfection, cell counts were measured at 0, 24, and 48 hours using CounterSTAR (ALIT Biotech, China).

Identification of DEGs between endometrial polyps and eutopic endometrial tissue

To identify differentially expressed genes (DEGs), we utilized the "FindMarkers" function in Seurat. The log fold change (Log2FC) and the adjusted p-values for each DEG were evaluated through ROC analysis. Only genes that met the criteria of |avg_logFC| > 0.25 and FDR (false discovery rate) indicated by p_val_adj < 0.05 were classified as DEGs.

Transcriptional Regulatory Network Analysis

The transcriptional regulatory network was examined using the GENIE3 (version 1.10.0) and RcisTarget (version 1.8.0) R packages as part of the SCENIC workflow (version 1.1.2.1), applying the default settings (28). Reference transcription factors (TFs) corresponding to hg19 were obtained via RcisTarget. The gene expression data from 31,503 cells were normalized using Seurat and served as input.Initially, co-expression modules were identified by analyzing the relationships between transcription factors and potential target genes based on the gene expression data through GENIE3. Following this, cis-regulatory motif enrichment analysis was conducted on all potential target genes within each co-expression module using RcisTarget. Only those target genes that were enriched with the specific motifs of their corresponding TFs were designated as direct target genes. Each transcription factor, along with its direct target genes, was categorized as a regulon. Finally, the gene regulatory interactions between fibroblast and epithelial cells were inferred using the Seurat FindAllMarkers function.

Pathway Enrichment Analysis and Visualization

It is was performed following a previous study[17], For pathway enrichment analysis and visualization of differentially expressed genes (DEGs), we followed a comprehensive protocol outlined by Reimand et al18. and utilized Metascape[19]. The initial step involved using g:Profiler to conduct pathway enrichment analysis on the DEG list. Subsequently, the results were visualized through EnrichmentMap (version 3.5.0) within Cytoscape (version 3.10.1). To facilitate the navigation and interpretation of the pathway enrichment outcomes, we employed AutoAnnotate (version 1.3.2) in Cytoscape. Metascape serves as an online platform that offers extensive resources for the annotation and analysis of gene lists.

Immunohistochemistry

Fresh human specimens were fixed in a 4% paraformaldehyde solution for 24 hours, subsequently embedded in paraffin, and sectioned into 5 μm slices. These sections underwent deparaffinization in xylene and rehydration in ethanol. Antigen retrieval was conducted using Tris-EDTA (pH 9.0) (Biosharp, Anhui, China) in a microwave. For the subsequent procedures, a staining kit from Absin (Shanghai, China) was utilized.In brief, the slides were treated with 3% H2O2 to inhibit endogenous peroxidase activity, followed by blocking with 5% BSA. The sections were then incubated overnight at 4 °C with primary antibodies targeting CD63 (1:200) and TPSB2 (1:200). This was followed by incubation with a secondary

antibody. Staining was carried out using DAB and hematoxylin. Observations and imaging of the slides were performed with a microscope (Leica, Germany).

Immunofluorescence

Paraffin sections with a thickness of 7 μm were prepared. Following dewaxing and rehydration, heat-mediated antigen retrieval was conducted using a citrate-based solution (pH 6.0). The sections were subsequently permeabilized in PBS supplemented with 0.4% Triton X-100 for 30 minutes at room temperature. After washing with PBS, the samples were then blocked with 5% bovine serum albumin (BSA) at room temperature for 1 hour. Following this, they were incubated overnight at 4 with primary antibodies against trytase (1:100, Abcam, ab8978, Cambridge, UK),. After washing with PBS, the samples were treated with 555-conjugated secondary antibodies (Invitrogen, California, A-31572, USA) for 1 hour in the dark at room temperature, then stained with 4,6-diamidino-2-phenylindole (DAPI). Immunofluorescence imaging was carried out using a confocal microscope (Leica, Germany).

Statistics

Cell distribution between the two groups was analyzed using unpaired two-tailed Wilcoxon rank-sum tests. For comparing gene expression or gene signatures between the two cell groups, unpaired two-tailed Student's t-tests were employed. All statistical analyses and visualizations were conducted using R. The specific statistical tests applied in the figures are detailed in the figure legends, with statistical significance defined as $p < 0.05$.

RESULTS

scRNA-seq profiling of endometrial polyps and eutopic endometrium tissues

We performed single-cell RNA sequencing to construct a global endometrial polyps (EPs) atlas, which profiled both ectopic endometrial and adjacent eutopic endometrium tissues (EU) from seven patients with endometrial polyps (**Fig.1A**). In sections stained with hematoxylin and eosin (H&E), we noted a twofold increase in the cross-sectional area of the glandular epithelium in the MP group compared to the EU group (Fig 1B), After rigorous quality control, a total of 103,539 cells were identified, including 52974 cells from eutopic endometrium and 50565 cells from the polyps, respectively. Average 2840 genes and 8914 unique molecular identifiers (UMIs) were obtained per cell, indicating sufficient coverage and transcripts representative(Fig. S1). Next, we performed unsupervised clustering analysis and genomic signature identification, 8 clusters were defined in the endometrium (**Fig.1C and D**), including epithelial cells (9.3 %), fibroblasts (67.1%), smooth muscle cells (SMCs) (2.5 %), endothelial cells (2.1 %), macrophages (3.8 %), NK cells (6.8 %), mast cells (1.1%), and CD8 T cells (7.2%). The number for each cell type in endometrial samples is shown in **Table1**. The correlation between these cell types confirms their identification (**Fig. S2**).

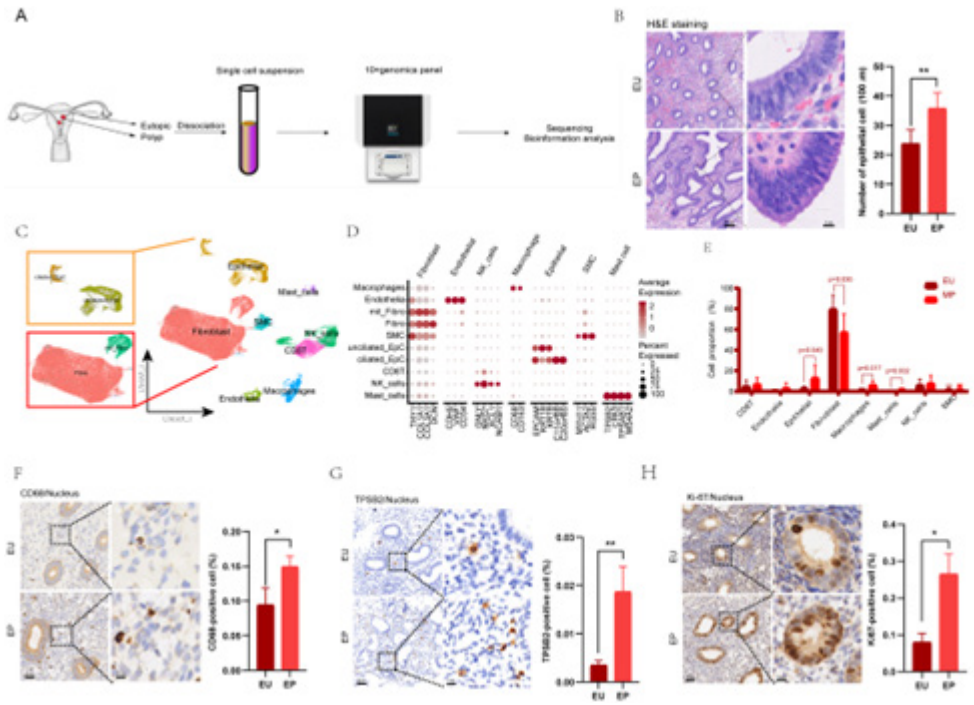
Table 1

Patients` Information												
Sample	**Patient ID**	**Age at Surgery (Years)**	**History of gestation**	**Phase of Cycle**	**The cycle days**	**Abnormal bleeding or not prior to Surgery (1=yes; 0=no)**	**Treatment received prior to Surgery (1=Surgery treatment; 2=drug treatment; 0=untreated)**	**Number of polyps**	**Polyps location in uterus**	**The diameter of the largest polyps(cm)**	**Experiment**	**No.cells analyzed**
EU1	1	47	1-1-0-0	proliferative	10/28	0	0	1	Right anterior	1.5	single cell RNAseq (BD Rhapsody)	5370
EP1												2519
EU2	2	41	5-2-3-0	proliferative	11/28	0	0	1	anterior	0.6	single cell RNAseq (BD Rhapsody)	4364
EP2												8526
EU3	3	29	0-0-0-0	proliferative	13/28	1	0	1	Right Lateral	1.2	single cell RNAseq (BD Rhapsody)	1091
EP3												1239

EU4	4	37	3-2-1-0	proliferative	11/30	0	0	1	anterior lateral	0.5	single cell RNAseq (BD Rhapsody)	6835
EP4												4592
EU5	5	42	1-1-0-0	proliferative	8/21	0	0	1	anterior	1.5	single cell RNAseq (10× Genomics)	12046
EP5												11254
EU6	6	27	0-0-0-0	proliferative	10/28-30	1	0	1	left horn	0.5	single cell RNAseq (10× Genomics)	13068
EP6												11407
EU7	7	28	0-0-0-0	proliferative	13/30	0	0	1	posterior fundus	1	single cell RNAseq (10× Genomics)	10200
EP7												11028
EU8	8	37	1-0-1-0	proliferative	11/30	0	1	2	anterior, fundus	1.5	Bulk RNAseq	
EP8												
EU9	9	35	1-0-0-1	proliferative	13/28	1	0	1	Right anterior	2.5	Bulk RNAseq	
EP9												
EU10	10	34	0-0-0-0	proliferative	9/28	0	0	1	anterior	0.5	Bulk RNAseq	
EP10												
EU11	11	28	1-0-1-0	proliferative	10/28-30	0	0	1	anterior	0.5	Bulk RNAseq	
EP11												
EU12	12	29	0-0-0-0	proliferative	11/30	1	0	1	fundus	1	Bulk RNAseq	
EP12												

Next, we examined the changes in cell composition associated with endometrial polyps and discovered a reduction in the proportion of fibroblasts within these polyps, while the proportions of epithelial cells (p=0.049), mast cells (p=0.002), and macrophages (p=0.017) increased (**Fig. 1E**). To validate these changes in cell composition within the polyps, we performed immunohistochemistry staining using cell-specific markers. Indeed, we observed that the numbers of CD68-positive macrophages and TPSB2-positive mast cells in the polyps were approximately twice as high as those in the eutopic endometrium (**Fig. 1F and G**), consistent with previous reports , . Moreover, the levels of Ki67 in the glandular epithelium of the polyps were elevated, corroborating the increase in epithelial cells we had observed (**Fig. 1H**). Collectively, these observations suggest glandular proliferation and immune cell infiltration, including macrophages and mast cells, in the polyps, likely contributing to the proliferative and inflammatory alterations observed.

Figure 1. Identification of Cell Types through scRNA-Seq Analysis of Endometrial Polyps.



(A) Schema: both ectopic endometrial polyps (EP) and adjacent eutopic endometrium tissues (EU) from seven patients with endometrial polyps were profiled with scRNA-seq.

(B) Hematoxylin and eosin staining of EP and adjacent EU. Scale bars, 60 μm and 5 μm (zoomed-in images). Left, representative images.

Right, quantitative analysis.

(C) Uniform manifold approximation and projection (UMAP) plot showing the eight cell types of endometrial polyps.

(D) Dot plot showing the expression of representative genes for each cell type.

(E) Bar graph showing cell proportions (%) of various cell types in EU (solid red) and EP (light red) groups, with significant differences indicated by p-values.

(F) Immunohistochemical staining for cell proliferation marker Ki67 in EU and EP. Scale bars, 60 μm and 5 μm (zoomed-in images). Left, representative images. Right, the proportion of Ki67 positive cells was quantiffed.

(G) Immunohistochemical staining for macrophage marker CD63 in EU and EP. Scale bars, 60 μm and 5 μm (zoomed-in images). Left, representative images. Right, the proportion of CD63 positive cells was quantified.

(H) Immunohistochemical staining for mast cell marker TPSB2 in EU and EP. Scale bars, 60 μm and 5 μm (zoomed-in images). Left, representative images. Right, the proportion of TPSB2 positive cells was quantiffed.

Aberrant gene expression in cell types from endometrial polyps' samples

To simultaneously define different gene expressions at the global and cellular levels, bulk RNA-seq was performed parallel for endometrial polyps and eutopic endometrium (**Fig.2A and 2B**). 94 upregulated and 16 downregulated genes were detected in endometrial polyps (log2FoldChange >1 & pvalue < 0.05 Supplemental **Table2**). Next, the GO analysis was performed. The results showed that regulation of inflammatory response, negative regulation of cell activation, and cellular lipid catabolic process associated signal pathway were activated in endometrial polyps. However, the genes involved in the proteoglycan metabolic process, neuron migration, and gas homeostasis were downregulated (**Fig.2C**).

We assessed alterations in the expression of inflammation-associated genes within the cellular layers of endometrial polyps to explore particular anomalies in molecular expression across various cell types. Notably, CD163, which was found to be upregulated in the bulk RNA-seq analysis, showed increased expression specifically in macrophages, while its expression remained unchanged in other cell types. Similarly, CST7, also upregulated in the bulk RNA-seq analysis, exhibited increased expression in mast cells, with no significant changes observed in other cells. Conversely, S100A9 and LPL, both upregulated in the bulk RNA-seq analysis, were found to be downregulated in macrophages and smooth muscle cells (SMCs) but remained unchanged in most other cell types (**Fig.2D and 2E**). These differences reflect the cellular heterogeneity in gene expression changes. Collectively, our findings highlight the complex and cell type-specific molecular landscape within endometrial polyps.

Table 2.

	p_val	avg_log2FC	pct.1	pct.2	p_val_adj	cluster	gene	change
MT1X	3.95E-62	0.567729335	0.358	0.213	2.07E-57	CD8T	MT1X	up
SCGB2A1	3.52E-201	0.542504173	0.354	0.059	1.84E-196	CD8T	SCGB2A1	up
WFDC2	8.42E-171	0.516935289	0.425	0.132	4.41E-166	CD8T	WFDC2	up
MT2A	2.74E-37	0.471645707	0.509	0.43	1.44E-32	CD8T	MT2A	up
MT1E	3.64E-32	0.40759225	0.216	0.121	1.91E-27	CD8T	MT1E	up
SCGB1D2	4.25E-81	0.281832434	0.173	0.033	2.22E-76	CD8T	SCGB1D2	up
RBP1	1.60E-68	-0.251456109	0.068	0.203	8.39E-64	CD8T	RBP1	down
DIO2	9.59E-63	-0.251718214	0.07	0.198	5.02E-58	CD8T	DIO2	down
COL3A1	4.60E-47	-0.259477593	0.397	0.56	2.41E-42	CD8T	COL3A1	down
ECM1	1.07E-90	-0.268129557	0.042	0.187	5.58E-86	CD8T	ECM1	down
LGALS1	3.17E-85	-0.291988872	0.622	0.786	1.66E-80	CD8T	LGALS1	down
MGP	6.24E-78	-0.303603062	0.095	0.254	3.27E-73	CD8T	MGP	down
SFRP4	6.15E-76	-0.311830861	0.485	0.653	3.22E-71	CD8T	SFRP4	down
GNLY	6.23E-48	-0.327327307	0.179	0.335	3.26E-43	CD8T	GNLY	down
SCGB1D21	3.92E-37	1.004224648	0.829	0.42	2.05E-32	ciliated_EpC	SCGB1D2	up
SCGB1D4	1.51E-28	0.876886452	0.777	0.401	7.92E-24	ciliated_EpC	SCGB1D4	up
TFF3	6.75E-27	0.850530063	0.739	0.408	3.54E-22	ciliated_EpC	TFF3	up
CHGA	2.89E-14	0.642833135	0.535	0.236	1.51E-09	ciliated_EpC	CHGA	up
SCGB2A11	1.43E-37	0.508104213	0.988	0.885	7.51E-33	ciliated_EpC	SCGB2A1	up
WFDC21	3.55E-25	0.496883184	0.978	0.79	1.86E-20	ciliated_EpC	WFDC2	up
PAEP	1.59E-13	0.464580968	0.409	0.089	8.33E-09	ciliated_EpC	PAEP	up
SOD3	1.87E-16	0.447220389	0.616	0.261	9.77E-12	ciliated_EpC	SOD3	up
SPP1	1.15E-14	0.44264295	0.355	0.045	6.01E-10	ciliated_EpC	SPP1	up

CFAP70	1.87E-15	0.424399087	0.732	0.465	9.80E-11	ciliated_EpC	CFAP70	up
LINC01480	1.20E-13	0.411553809	0.88	0.675	6.29E-09	ciliated_EpC	LINC01480	up
FXYD3	2.30E-10	0.403404512	0.559	0.287	1.21E-05	ciliated_EpC	FXYD3	up
EPHX1	3.15E-15	0.40190866	0.852	0.605	1.65E-10	ciliated_EpC	EPHX1	up
CLU	1.46E-13	0.39861419	0.8	0.605	7.64E-09	ciliated_EpC	CLU	up
PIGR	3.33E-13	0.395426635	0.651	0.363	1.74E-08	ciliated_EpC	PIGR	up
EPPIN	2.24E-14	0.387416063	0.62	0.28	1.17E-09	ciliated_EpC	EPPIN	up
CD59	1.25E-14	0.386671247	0.764	0.478	6.52E-10	ciliated_EpC	CD59	up
BX890604.2	9.87E-12	0.369878311	0.601	0.376	5.17E-07	ciliated_EpC	BX890604.2	up
METRN	1.64E-14	0.3693577	0.863	0.713	8.56E-10	ciliated_EpC	METRN	up
GALNT4	1.59E-13	0.367983813	0.438	0.146	8.32E-09	ciliated_EpC	GALNT4	up
GSTA3	3.83E-15	0.366017046	0.715	0.439	2.00E-10	ciliated_EpC	GSTA3	up
BMPR1B	6.37E-15	0.365954987	0.622	0.293	3.33E-10	ciliated_EpC	BMPR1B	up
SYNE1	1.88E-12	0.363573242	0.728	0.465	9.84E-08	ciliated_EpC	SYNE1	up
MS4A8	4.32E-12	0.359314708	0.899	0.707	2.26E-07	ciliated_EpC	MS4A8	up
NDUFC2	1.54E-11	0.354029994	0.736	0.529	8.06E-07	ciliated_EpC	NDUFC2	up
POU2AF1	4.06E-14	0.353123814	0.491	0.185	2.13E-09	ciliated_EpC	POU2AF1	up
SRGAP3	1.70E-12	0.346248474	0.676	0.382	8.89E-08	ciliated_EpC	SRGAP3	up
WFDC6	1.40E-15	0.345344851	0.383	0.07	7.34E-11	ciliated_EpC	WFDC6	up
NT5E	2.22E-11	0.343168726	0.517	0.255	1.16E-06	ciliated_EpC	NT5E	up
TMBIM4	1.89E-11	0.336422324	0.627	0.369	9.91E-07	ciliated_EpC	TMBIM4	up
CSRP2	7.02E-13	0.330425353	0.754	0.503	3.68E-08	ciliated_EpC	CSRP2	up
IFI27	1.17E-14	0.32942119	0.947	0.854	6.15E-10	ciliated_EpC	IFI27	up
PLPP2	6.79E-10	0.329262364	0.643	0.433	3.56E-05	ciliated_EpC	PLPP2	up
HOMER2	3.89E-11	0.328636327	0.781	0.497	2.04E-06	ciliated_EpC	HOMER2	up
ANKUB1	6.28E-11	0.325484649	0.677	0.452	3.29E-06	ciliated_EpC	ANKUB1	up
KCNN3	2.16E-12	0.323300188	0.616	0.338	1.13E-07	ciliated_EpC	KCNN3	up
ASRGL1	6.81E-13	0.314241989	0.924	0.758	3.57E-08	ciliated_EpC	ASRGL1	up
CD9	7.94E-11	0.3136687	0.771	0.529	4.16E-06	ciliated_EpC	CD9	up
NFIA	1.00E-11	0.313181006	0.742	0.471	5.24E-07	ciliated_EpC	NFIA	up
C4orf48	2.63E-07	0.31153119	0.678	0.478	0.013787146	ciliated_EpC	C4orf48	up
GADD45G	7.97E-08	0.311328377	0.526	0.306	0.004172822	ciliated_EpC	GADD45G	up
CP	1.68E-07	0.309994233	0.463	0.248	0.00878835	ciliated_EpC	CP	up
AL365259.1	1.02E-11	0.309780351	0.496	0.236	5.34E-07	ciliated_EpC	AL365259.1	up
FABP6	4.15E-10	0.308634013	0.754	0.548	2.17E-05	ciliated_EpC	FABP6	up
PGR	7.59E-12	0.307362385	0.874	0.701	3.97E-07	ciliated_EpC	PGR	up
HLA-DRA	5.66E-09	0.30592408	0.535	0.312	0.000296387	ciliated_EpC	HLA-DRA	up
HLA-C	1.11E-08	0.305480166	0.714	0.541	0.000578906	ciliated_EpC	HLA-C	up
GTF2I	1.43E-08	0.304650343	0.681	0.497	0.000749873	ciliated_EpC	GTF2I	up
PAX8	9.81E-11	0.304380068	0.773	0.561	5.14E-06	ciliated_EpC	PAX8	up
CATSPERD	4.42E-10	0.302855809	0.604	0.369	2.31E-05	ciliated_EpC	CATSPERD	up
ATOX1	1.46E-10	0.302577301	0.632	0.369	7.67E-06	ciliated_EpC	ATOX1	up
ENPP2	1.23E-10	0.301208676	0.506	0.242	6.43E-06	ciliated_EpC	ENPP2	up
FUCA1	2.21E-10	0.297786923	0.581	0.363	1.16E-05	ciliated_EpC	FUCA1	up
HYDIN	1.60E-09	0.295845261	0.771	0.554	8.37E-05	ciliated_EpC	HYDIN	up
MICOS13	9.64E-10	0.29323782	0.733	0.51	5.05E-05	ciliated_EpC	MICOS13	up
UGT2B7	2.46E-11	0.292405926	0.553	0.261	1.29E-06	ciliated_EpC	UGT2B7	up
LINC00240	1.78E-10	0.291099255	0.614	0.376	9.31E-06	ciliated_EpC	LINC00240	up
SSPN	1.61E-10	0.289860913	0.613	0.357	8.42E-06	ciliated_EpC	SSPN	up
BHLHE41	3.17E-10	0.289554162	0.716	0.459	1.66E-05	ciliated_EpC	BHLHE41	up
SCPEP1	4.20E-11	0.289424065	0.597	0.344	2.20E-06	ciliated_EpC	SCPEP1	up

SLC23A1	1.67E-08	0.288275825	0.693	0.497	0.00087406	ciliated_EpC	SLC23A1	up
C16orf89	7.89E-13	0.287977412	0.376	0.089	4.13E-08	ciliated_EpC	C16orf89	up
RNASEK	8.28E-06	0.286794411	0.63	0.42	0.43329628	ciliated_EpC	RNASEK	up
KIAA1324	7.65E-10	0.285814107	0.641	0.369	4.00E-05	ciliated_EpC	KIAA1324	up
SYNE2	2.82E-09	0.283737064	0.773	0.618	0.000147506	ciliated_EpC	SYNE2	up
AC084866.1	6.16E-10	0.283123117	0.725	0.503	3.22E-05	ciliated_EpC	AC084866.1	up
ATP6V0C	2.60E-08	0.282169742	0.547	0.293	0.001362647	ciliated_EpC	ATP6V0C	up
CATIP	4.41E-10	0.281889054	0.507	0.248	2.31E-05	ciliated_EpC	CATIP	up
FBLN1	4.23E-07	0.281162874	0.728	0.503	0.022128103	ciliated_EpC	FBLN1	up
CFAP47	1.15E-09	0.28115668	0.656	0.42	6.02E-05	ciliated_EpC	CFAP47	up
PKHD1L1	6.77E-08	0.280380707	0.459	0.242	0.003544584	ciliated_EpC	PKHD1L1	up
MT-ATP6	1.51E-15	0.280233863	0.98	0.866	7.92E-11	ciliated_EpC	MT-ATP6	up
DNAH11	1.33E-08	0.278965344	0.729	0.535	0.000694931	ciliated_EpC	DNAH11	up
AKAP9	8.74E-09	0.277885063	0.877	0.662	0.000457778	ciliated_EpC	AKAP9	up
ALG1L	3.51E-10	0.274320309	0.528	0.261	1.84E-05	ciliated_EpC	ALG1L	up
CCDC88A	1.39E-08	0.273844692	0.662	0.401	0.000725692	ciliated_EpC	CCDC88A	up
SMIM19	1.66E-10	0.272050895	0.756	0.541	8.71E-06	ciliated_EpC	SMIM19	up
C11orf54	6.32E-10	0.27100599	0.479	0.248	3.31E-05	ciliated_EpC	C11orf54	up
C2orf88	1.10E-07	0.2694555	0.774	0.503	0.005766478	ciliated_EpC	C2orf88	up
MT-ND3	8.10E-08	0.268640092	0.957	0.777	0.004242497	ciliated_EpC	MT-ND3	up
UACA	8.13E-09	0.267747805	0.766	0.599	0.000425535	ciliated_EpC	UACA	up
TXNIP	2.46E-08	0.264443619	0.801	0.611	0.001289795	ciliated_EpC	TXNIP	up
AL022068.1	6.40E-09	0.263874727	0.609	0.401	0.000334925	ciliated_EpC	AL022068.1	up
TMED6	2.66E-10	0.263271327	0.425	0.166	1.39E-05	ciliated_EpC	TMED6	up
IRX3	7.02E-09	0.263097091	0.7	0.439	0.000367338	ciliated_EpC	IRX3	up
DTHD1	2.44E-09	0.262677116	0.723	0.522	0.000127895	ciliated_EpC	DTHD1	up
ZNF486	4.50E-11	0.261081528	0.379	0.115	2.36E-06	ciliated_EpC	ZNF486	up
HLA-DRB1	1.97E-08	0.260618881	0.436	0.197	0.00103403	ciliated_EpC	HLA-DRB1	up
LSM7	7.97E-09	0.259347751	0.593	0.363	0.000417354	ciliated_EpC	LSM7	up
DNAJB13	2.24E-09	0.258670633	0.86	0.669	0.00011748	ciliated_EpC	DNAJB13	up
MT-CYB	1.27E-07	0.256746001	0.966	0.815	0.006626209	ciliated_EpC	MT-CYB	up
NME2	1.65E-05	0.254958603	0.612	0.369	0.862828266	ciliated_EpC	NME2	up
RBBP7	2.28E-09	0.25444989	0.76	0.535	0.000119415	ciliated_EpC	RBBP7	up
NDUFA7	4.56E-07	0.254001605	0.582	0.344	0.023870433	ciliated_EpC	NDUFA7	up
ALDH1L1	1.70E-07	0.253719924	0.581	0.35	0.008877	ciliated_EpC	ALDH1L1	up
RESF1	1.42E-07	0.25321668	0.594	0.389	0.007419111	ciliated_EpC	RESF1	up
RARRES2	2.01E-08	-0.250115067	0.133	0.28	0.001054227	ciliated_EpC	RARRES2	down
MTATP6P1	0.004266311	-0.251699025	0.333	0.471	1	ciliated_EpC	MTATP6P1	down
TGFBI	2.88E-09	-0.255350676	0.092	0.236	0.00015105	ciliated_EpC	TGFBI	down
SRGAP3-AS2	1.59E-09	-0.255925063	0.126	0.299	8.35E-05	ciliated_EpC	SRGAP3-AS2	down
SERPINH1	2.24E-07	-0.264627707	0.239	0.401	0.011742388	ciliated_EpC	SERPINH1	down
CNN3	6.45E-08	-0.265067355	0.214	0.382	0.00337836	ciliated_EpC	CNN3	down
IGF1	0.319987036	-0.265409812	0.36	0.344	1	ciliated_EpC	IGF1	down
GHITM	7.14E-08	-0.26881676	0.426	0.592	0.003738235	ciliated_EpC	GHITM	down
ECM11	5.65E-08	-0.269619781	0.143	0.299	0.002956943	ciliated_EpC	ECM1	down
SPARC	0.07739704	-0.272868522	0.357	0.382	1	ciliated_EpC	SPARC	down
DCN	1.21E-09	-0.272939081	0.11	0.268	6.35E-05	ciliated_EpC	DCN	down
AC023300.2	1.72E-07	-0.282550052	0.603	0.682	0.00902502	ciliated_EpC	AC023300.2	down
COL6A1	2.67E-05	-0.283304034	0.255	0.376	1	ciliated_EpC	COL6A1	down
NREP	6.84E-06	-0.287553517	0.188	0.318	0.358311647	ciliated_EpC	NREP	down
IGFBP2	9.85E-09	-0.291617428	0.205	0.376	0.000515481	ciliated_EpC	IGFBP2	down

VCAN	4.41E-05	-0.293311489	0.385	0.49	1	ciliated_EpC	VCAN	down
MTND1P23	2.89E-06	-0.293355656	0.204	0.35	0.151284552	ciliated_EpC	MTND1P23	down
SMIM6	3.92E-08	-0.298711593	0.77	0.822	0.002053121	ciliated_EpC	SMIM6	down
NAPSB	1.42E-05	-0.305591431	0.095	0.204	0.74480578	ciliated_EpC	NAPSB	down
ZNF295-AS1	2.35E-05	-0.323105309	0.573	0.605	1	ciliated_EpC	ZNF295-AS1	down
TAGLN2	6.66E-14	-0.338958633	0.811	0.854	3.49E-09	ciliated_EpC	TAGLN2	down
SFRP41	0.000250639	-0.339930509	0.714	0.707	1	ciliated_EpC	SFRP4	down
AC007906.2	2.93E-13	-0.344233792	0.82	0.873	1.54E-08	ciliated_EpC	AC007906.2	down
MT-RNR1	7.67E-06	-0.344288023	0.332	0.497	0.401646505	ciliated_EpC	MT-RNR1	down
LGALS11	0.000242185	-0.352766779	0.535	0.554	1	ciliated_EpC	LGALS1	down
MT-RNR2	0.000344453	-0.353107361	0.333	0.503	1	ciliated_EpC	MT-RNR2	down
COL1A1	1.31E-07	-0.372261919	0.749	0.803	0.006843584	ciliated_EpC	COL1A1	down
COL3A11	2.61E-07	-0.454589786	0.645	0.713	0.013649621	ciliated_EpC	COL3A1	down
MT-RNR21	6.64E-29	0.712782364	0.487	0.231	3.48E-24	Endothelia	MT-RNR2	up
MTATP6P11	1.22E-34	0.614257063	0.483	0.228	6.37E-30	Endothelia	MTATP6P1	up
MT-RNR11	9.88E-27	0.601966686	0.486	0.23	5.17E-22	Endothelia	MT-RNR1	up
CCL21	5.74E-21	0.598695576	0.176	0.03	3.01E-16	Endothelia	CCL21	up
CDKN1A	2.03E-43	0.571499244	0.619	0.357	1.07E-38	Endothelia	CDKN1A	up
CLU1	1.62E-37	0.502550767	0.582	0.324	8.48E-33	Endothelia	CLU	up
FOSB	3.13E-40	0.473071525	0.778	0.567	1.64E-35	Endothelia	FOSB	up
ZFP36	6.87E-29	0.437483105	0.769	0.625	3.60E-24	Endothelia	ZFP36	up
NR4A1	3.54E-28	0.43477702	0.566	0.364	1.85E-23	Endothelia	NR4A1	up
SOCS3	2.64E-29	0.430143675	0.75	0.631	1.38E-24	Endothelia	SOCS3	up
BHLHE40	5.67E-23	0.413576294	0.628	0.488	2.97E-18	Endothelia	BHLHE40	up
KLF6	2.88E-32	0.409395492	0.792	0.627	1.51E-27	Endothelia	KLF6	up
EGR1	3.28E-25	0.392776331	0.726	0.601	1.72E-20	Endothelia	EGR1	up
PRSS23	1.09E-31	0.3902255	0.69	0.475	5.71E-27	Endothelia	PRSS23	up
KLF4	1.03E-25	0.383381228	0.617	0.409	5.38E-21	Endothelia	KLF4	up
GSN	9.45E-34	0.383259309	0.719	0.573	4.95E-29	Endothelia	GSN	up
TFF31	7.08E-24	0.362721658	0.166	0.015	3.70E-19	Endothelia	TFF3	up
ATF3	7.44E-24	0.362453293	0.451	0.246	3.90E-19	Endothelia	ATF3	up
C2CD4B	4.57E-18	0.360461885	0.593	0.451	2.39E-13	Endothelia	C2CD4B	up
FABP5	0.000194679	0.350649914	0.254	0.206	1	Endothelia	FABP5	up
HSPA1B	4.68E-16	0.349969768	0.639	0.522	2.45E-11	Endothelia	HSPA1B	up
BTG2	6.95E-24	0.349785972	0.573	0.399	3.64E-19	Endothelia	BTG2	up
NRP2	5.88E-17	0.347953202	0.361	0.2	3.08E-12	Endothelia	NRP2	up
PDPN	2.81E-19	0.347533116	0.189	0.045	1.47E-14	Endothelia	PDPN	up
RHOB	6.09E-23	0.346463552	0.731	0.567	3.19E-18	Endothelia	RHOB	up
MT-ATP8	3.00E-18	0.337565352	0.702	0.596	1.57E-13	Endothelia	MT-ATP8	up
SLC2A3	3.51E-19	0.336456495	0.674	0.557	1.84E-14	Endothelia	SLC2A3	up
FABP4	1.23E-16	0.335509629	0.115	0.009	6.42E-12	Endothelia	FABP4	up
IGFBP5	6.12E-12	0.334759824	0.405	0.273	3.21E-07	Endothelia	IGFBP5	up
GDF15	1.26E-16	0.330820268	0.383	0.221	6.60E-12	Endothelia	GDF15	up
MAFF	7.92E-22	0.325277362	0.59	0.427	4.15E-17	Endothelia	MAFF	up
CCL2	9.11E-13	0.322963937	0.442	0.31	4.77E-08	Endothelia	CCL2	up
IFI6	2.55E-20	0.322896547	0.733	0.627	1.34E-15	Endothelia	IFI6	up
LGALS3	3.47E-26	0.318605688	0.632	0.464	1.82E-21	Endothelia	LGALS3	up
IRF1	2.61E-18	0.313133481	0.721	0.636	1.37E-13	Endothelia	IRF1	up
SCGB2A12	1.07E-29	0.310676432	0.351	0.116	5.59E-25	Endothelia	SCGB2A1	up
TMEM70	2.77E-15	0.306044393	0.568	0.452	1.45E-10	Endothelia	TMEM70	up
DUSP5	1.64E-17	0.305266838	0.527	0.364	8.59E-13	Endothelia	DUSP5	up

TSPAN7	2.44E-19	0.302206557	0.501	0.345	1.28E-14	Endothelia	TSPAN7	up
TIMP3	4.03E-20	0.302155791	0.673	0.525	2.11E-15	Endothelia	TIMP3	up
ADIRF	5.92E-17	0.302149208	0.418	0.252	3.10E-12	Endothelia	ADIRF	up
ICAM1	2.17E-13	0.294180582	0.53	0.397	1.14E-08	Endothelia	ICAM1	up
PROX1	2.54E-09	0.286447238	0.414	0.319	0.000132992	Endothelia	PROX1	up
SNHG5	1.38E-21	0.284714958	0.704	0.593	7.23E-17	Endothelia	SNHG5	up
SOCS2	2.83E-15	0.274425575	0.505	0.366	1.48E-10	Endothelia	SOCS2	up
JUND	1.02E-28	0.274309678	0.893	0.848	5.36E-24	Endothelia	JUND	up
THBD	6.72E-14	0.269345569	0.57	0.43	3.52E-09	Endothelia	THBD	up
GADD45B	5.56E-17	0.265845192	0.749	0.64	2.91E-12	Endothelia	GADD45B	up
PGM5	8.04E-19	0.262333631	0.326	0.155	4.21E-14	Endothelia	PGM5	up
SLC25A25	5.75E-12	0.261774883	0.501	0.393	3.01E-07	Endothelia	SLC25A25	up
HSPA1A	4.70E-13	0.261362317	0.8	0.743	2.46E-08	Endothelia	HSPA1A	up
BCL3	1.68E-11	0.260401412	0.521	0.412	8.79E-07	Endothelia	BCL3	up
MCL1	1.08E-19	0.259577074	0.782	0.701	5.66E-15	Endothelia	MCL1	up
PPP1R15A	1.67E-20	0.258468738	0.786	0.709	8.73E-16	Endothelia	PPP1R15A	up
RPL26P19	4.15E-15	0.25450281	0.304	0.149	2.17E-10	Endothelia	RPL26P19	up
KLF2	6.14E-14	0.254229992	0.741	0.625	3.22E-09	Endothelia	KLF2	up
FOS	1.58E-17	0.252713848	0.871	0.8	8.27E-13	Endothelia	FOS	up
WFDC22	2.94E-16	0.252603326	0.408	0.243	1.54E-11	Endothelia	WFDC2	up
SELENOP	3.72E-18	0.25246542	0.664	0.543	1.95E-13	Endothelia	SELENOP	up
MSX1	5.17E-17	0.252113534	0.361	0.187	2.70E-12	Endothelia	MSX1	up
MATR3	6.63E-15	0.250775437	0.328	0.164	3.47E-10	Endothelia	MATR3	up
JUNB	3.63E-21	0.250192971	0.872	0.804	1.90E-16	Endothelia	JUNB	up
MEIS2	8.77E-18	-0.252891831	0.521	0.691	4.59E-13	Endothelia	MEIS2	down
S100A13	9.87E-19	-0.253746508	0.511	0.691	5.17E-14	Endothelia	S100A13	down
ARL6IP4	1.22E-18	-0.256682546	0.386	0.6	6.36E-14	Endothelia	ARL6IP4	down
EDIL3	5.82E-26	-0.257122005	0.227	0.445	3.05E-21	Endothelia	EDIL3	down
CITED4	1.07E-17	-0.25894364	0.62	0.755	5.59E-13	Endothelia	CITED4	down
STARD4	1.06E-23	-0.262449887	0.257	0.475	5.54E-19	Endothelia	STARD4	down
RPS10	3.75E-14	-0.262567909	0.552	0.715	1.97E-09	Endothelia	RPS10	down
FN1	5.46E-21	-0.26368575	0.719	0.818	2.86E-16	Endothelia	FN1	down
HIST1H4C	8.20E-19	-0.265662583	0.389	0.564	4.30E-14	Endothelia	HIST1H4C	down
VWA1	1.23E-22	-0.272872632	0.602	0.781	6.43E-18	Endothelia	VWA1	down
NEAT1	5.90E-18	-0.273520539	0.732	0.806	3.09E-13	Endothelia	NEAT1	down
COL4A1	1.38E-36	-0.273526035	0.851	0.913	7.21E-32	Endothelia	COL4A1	down
ARHGAP18	1.01E-20	-0.274127712	0.579	0.719	5.30E-16	Endothelia	ARHGAP18	down
GTF2I1	1.31E-22	-0.283690911	0.475	0.675	6.85E-18	Endothelia	GTF2I	down
CASC15	1.31E-20	-0.286733097	0.336	0.512	6.86E-16	Endothelia	CASC15	down
MLEC	7.62E-28	-0.29709997	0.65	0.799	3.99E-23	Endothelia	MLEC	down
SLC39A10	6.11E-24	-0.301243554	0.583	0.746	3.20E-19	Endothelia	SLC39A10	down
NME21	1.60E-18	-0.30240219	0.471	0.676	8.40E-14	Endothelia	NME2	down
NFAT5	1.91E-23	-0.305341257	0.558	0.713	1.00E-18	Endothelia	NFAT5	down
FAM167B	2.60E-27	-0.326613556	0.282	0.5	1.36E-22	Endothelia	FAM167B	down
MIF	4.44E-21	-0.326791867	0.492	0.724	2.33E-16	Endothelia	MIF	down
APCDD1	1.01E-35	-0.333608017	0.676	0.843	5.31E-31	Endothelia	APCDD1	down
EIF4A1	2.85E-25	-0.340953261	0.465	0.697	1.49E-20	Endothelia	EIF4A1	down
IGFBP21	1.14E-32	-0.341656465	0.584	0.77	5.96E-28	Endothelia	IGFBP2	down
EEF1G	3.06E-22	-0.342897308	0.468	0.701	1.60E-17	Endothelia	EEF1G	down
CCDC85B	2.10E-34	-0.350542775	0.538	0.772	1.10E-29	Endothelia	CCDC85B	down
RPS17	2.42E-27	-0.353560357	0.451	0.688	1.27E-22	Endothelia	RPS17	down

HAPLN1	3.17E-35	-0.370596557	0.123	0.348	1.66E-30	Endothelia	HAPLN1	down
RPL17	3.35E-22	-0.372417783	0.504	0.755	1.75E-17	Endothelia	RPL17	down
RPL36A	9.10E-29	-0.384275795	0.498	0.74	4.76E-24	Endothelia	RPL36A	down
VCAN1	1.90E-22	-0.397996047	0.424	0.591	9.97E-18	Endothelia	VCAN	down
DPEP1	1.11E-54	-0.472558932	0.193	0.494	5.83E-50	Endothelia	DPEP1	down
CCND1	0	0.72224076	0.526	0.113	0	Fibro	CCND1	up
HSPB6	0	0.609489377	0.753	0.443	0	Fibro	HSPB6	up
IGFBP6	0	0.588384908	0.509	0.249	0	Fibro	IGFBP6	up
HMGA1	0	0.574310998	0.359	0.071	0	Fibro	HMGA1	up
CDKN1A1	0	0.535796883	0.499	0.189	0	Fibro	CDKN1A	up
PLAC9	0	0.527456845	0.48	0.229	0	Fibro	PLAC9	up
GDF151	0	0.515856767	0.355	0.085	0	Fibro	GDF15	up
TIMP31	0	0.477999935	0.717	0.4	0	Fibro	TIMP3	up
SOCS31	0	0.471885836	0.66	0.525	0	Fibro	SOCS3	up
S100A4	0	0.425199005	0.508	0.249	0	Fibro	S100A4	up
GPNMB	0	0.401776149	0.565	0.305	0	Fibro	GPNMB	up
NKAIN4	0	0.398727113	0.306	0.015	0	Fibro	NKAIN4	up
CFD	0	0.391043815	0.299	0.078	0	Fibro	CFD	up
ZMAT3	0	0.388106488	0.455	0.201	0	Fibro	ZMAT3	up
FXYD6	0	0.370193132	0.467	0.196	0	Fibro	FXYD6	up
CKB	0	0.365190431	0.876	0.762	0	Fibro	CKB	up
APOE	0	0.349651052	0.794	0.693	0	Fibro	APOE	up
PTN	0	0.343137589	0.671	0.513	0	Fibro	PTN	up
SCGB2A13	0	0.342294552	0.369	0.075	0	Fibro	SCGB2A1	up
COL18A1	0	0.33394017	0.538	0.317	0	Fibro	COL18A1	up
HSPA1B1	0	0.333319151	0.611	0.487	0	Fibro	HSPA1B	up
TGM2	0	0.331436126	0.729	0.56	0	Fibro	TGM2	up
CLU2	0	0.325715571	0.504	0.295	0	Fibro	CLU	up
DNAJB1	0	0.324166235	0.785	0.676	0	Fibro	DNAJB1	up
EMP3	0	0.32330593	0.76	0.64	0	Fibro	EMP3	up
GSN1	0	0.316255528	0.826	0.704	0	Fibro	GSN	up
FBLN2	0	0.315782486	0.518	0.261	0	Fibro	FBLN2	up
ZFP361	0	0.310341886	0.742	0.643	0	Fibro	ZFP36	up
NFIX	0	0.296543414	0.637	0.46	0	Fibro	NFIX	up
LMNA	0	0.295878997	0.836	0.716	0	Fibro	LMNA	up
PAPPA	0	0.294783107	0.45	0.244	0	Fibro	PAPPA	up
PGF	0	0.293796842	0.249	0.05	0	Fibro	PGF	up
AEBP1	0	0.285901997	0.612	0.464	0	Fibro	AEBP1	up
HSPA1A1	0	0.283955225	0.783	0.699	0	Fibro	HSPA1A	up
DUSP1	0	0.281946785	0.779	0.688	0	Fibro	DUSP1	up
PLAG1	0	0.28183485	0.258	0.022	0	Fibro	PLAG1	up
WFDC23	0	0.280872098	0.393	0.183	0	Fibro	WFDC2	up
ATF31	0	0.277934728	0.537	0.399	0	Fibro	ATF3	up
FAM171A2	0	0.272030112	0.347	0.138	0	Fibro	FAM171A2	up
BTG21	0	0.26581098	0.672	0.548	0	Fibro	BTG2	up
C11orf96	0	0.260995148	0.715	0.565	0	Fibro	C11orf96	up
EFEMP1	0	0.260317056	0.356	0.215	0	Fibro	EFEMP1	up
MSX11	0	0.259588502	0.392	0.186	0	Fibro	MSX1	up
KLF21	0	0.257394477	0.39	0.23	0	Fibro	KLF2	up
DES	0	0.255971667	0.206	0.017	0	Fibro	DES	up
METTL7A	0	0.253923511	0.461	0.273	0	Fibro	METTL7A	up

KCTD12	0	0.253873022	0.455	0.28	0	Fibro	KCTD12	up
PPP1R1B	0	0.25251945	0.177	0.009	0	Fibro	PPP1R1B	up
COL4A5	0	0.251430389	0.399	0.214	0	Fibro	COL4A5	up
SLC16A1	0	-0.253881461	0.266	0.481	0	Fibro	SLC16A1	down
WNT5A	0	-0.266862149	0.453	0.667	0	Fibro	WNT5A	down
P2RY14	0	-0.266894672	0.363	0.566	0	Fibro	P2RY14	down
VWC2	0	-0.268171107	0.287	0.51	0	Fibro	VWC2	down
PRSS12	0	-0.274907831	0.153	0.396	0	Fibro	PRSS12	down
CD24	0	-0.280144167	0.689	0.854	0	Fibro	CD24	down
MMP11	0	-0.281070552	0.727	0.903	0	Fibro	MMP11	down
ANKRD29	0	-0.281934736	0.259	0.48	0	Fibro	ANKRD29	down
SLC5A3	0	-0.282979941	0.486	0.682	0	Fibro	SLC5A3	down
APCDD11	0	-0.283992676	0.569	0.774	0	Fibro	APCDD1	down
TNC	0	-0.286641049	0.274	0.472	0	Fibro	TNC	down
S100A131	0	-0.287165276	0.62	0.747	0	Fibro	S100A13	down
SDK1	0	-0.289562228	0.434	0.661	0	Fibro	SDK1	down
LHFPL6	0	-0.307284843	0.276	0.514	0	Fibro	LHFPL6	down
OGN	0	-0.310055811	0.656	0.836	0	Fibro	OGN	down
MGP1	0	-0.315710409	0.684	0.81	0	Fibro	MGP	down
MARCKS	0	-0.317034423	0.766	0.907	0	Fibro	MARCKS	down
LEF1	0	-0.318081475	0.252	0.519	0	Fibro	LEF1	down
TUNAR	0	-0.319898153	0.197	0.439	0	Fibro	TUNAR	down
RBP7	0	-0.341655542	0.275	0.519	0	Fibro	RBP7	down
CFI	0	-0.345066959	0.233	0.5	0	Fibro	CFI	down
NREP1	0	-0.355782307	0.738	0.926	0	Fibro	NREP	down
VCAN2	0	-0.35939554	0.744	0.914	0	Fibro	VCAN	down
ADAM12	0	-0.362118285	0.454	0.721	0	Fibro	ADAM12	down
RBP11	0	-0.37699359	0.684	0.86	0	Fibro	RBP1	down
DIO21	0	-0.3820085	0.729	0.911	0	Fibro	DIO2	down
PCSK5	0	-0.391757243	0.447	0.712	0	Fibro	PCSK5	down
GLIPR1	0	-0.401001424	0.425	0.654	0	Fibro	GLIPR1	down
IL32	0	-0.445618448	0.207	0.52	0	Fibro	IL32	down
TGFBI1	0	-0.459833685	0.553	0.814	0	Fibro	TGFBI	down
ADAMTS9	0	-0.46849397	0.43	0.73	0	Fibro	ADAMTS9	down
F13A1	0	-0.573862967	0.181	0.575	0	Fibro	F13A1	down
ECM12	0	-0.622991688	0.654	0.938	0	Fibro	ECM1	down
SCGB2A14	4.07E-61	0.386437874	0.371	0.11	2.13E-56	Macrophages	SCGB2A1	up
WFDC24	2.95E-44	0.342779205	0.416	0.192	1.54E-39	Macrophages	WFDC2	up
HLA-DRB5	2.52E-15	0.317092636	0.345	0.23	1.32E-10	Macrophages	HLA-DRB5	up
KLF41	1.37E-38	0.29101541	0.842	0.729	7.20E-34	Macrophages	KLF4	up
SELENOP1	3.97E-11	0.266876374	0.501	0.416	2.08E-06	Macrophages	SELENOP	up
LGALS12	9.64E-39	-0.264005014	0.762	0.894	5.05E-34	Macrophages	LGALS1	down
DIO22	5.04E-31	-0.267370301	0.195	0.372	2.64E-26	Macrophages	DIO2	down
ECM13	1.59E-42	-0.278004993	0.144	0.338	8.30E-38	Macrophages	ECM1	down
COL3A12	1.74E-21	-0.28207872	0.668	0.807	9.09E-17	Macrophages	COL3A1	down
MGP2	1.13E-40	-0.319907923	0.214	0.419	5.91E-36	Macrophages	MGP	down
SFRP42	4.21E-43	-0.370587732	0.62	0.785	2.20E-38	Macrophages	SFRP4	down
RPL171	1.52E-13	0.900876443	0.674	0.193	7.97E-09	Mast_cells	RPL17	up
RPL36A1	2.06E-13	0.827926297	0.679	0.205	1.08E-08	Mast_cells	RPL36A	up
RPS101	3.63E-14	0.817718054	0.681	0.261	1.90E-09	Mast_cells	RPS10	up
LTC4S	8.46E-14	0.744113675	0.672	0.239	4.43E-09	Mast_cells	LTC4S	up

CTSG	1.60E-09	0.703938123	0.567	0.25	8.37E-05	Mast_cells	CTSG	up
EEF1G1	4.18E-11	0.702077019	0.604	0.182	2.19E-06	Mast_cells	EEF1G	up
HSPE1	8.76E-13	0.701099114	0.658	0.341	4.59E-08	Mast_cells	HSPE1	up
GABARAP	3.29E-12	0.69498763	0.592	0.182	1.72E-07	Mast_cells	GABARAP	up
NME22	3.47E-12	0.691885646	0.596	0.182	1.82E-07	Mast_cells	NME2	up
ATP6V0C1	3.37E-12	0.682749403	0.527	0.136	1.77E-07	Mast_cells	ATP6V0C	up
RNASEK1	8.03E-12	0.678982451	0.618	0.193	4.21E-07	Mast_cells	RNASEK	up
RPS171	3.99E-12	0.678232058	0.539	0.148	2.09E-07	Mast_cells	RPS17	up
EIF4A11	8.04E-11	0.659280029	0.565	0.227	4.21E-06	Mast_cells	EIF4A1	up
MIF1	2.75E-11	0.65694838	0.568	0.159	1.44E-06	Mast_cells	MIF	up
SELENOK	3.81E-16	0.648060583	0.8	0.511	1.99E-11	Mast_cells	SELENOK	up
NDUFA13	2.92E-11	0.613751558	0.575	0.216	1.53E-06	Mast_cells	NDUFA13	up
WDR83OS	2.22E-10	0.599880454	0.48	0.125	1.16E-05	Mast_cells	WDR83OS	up
CKLF	3.04E-10	0.571521344	0.628	0.318	1.59E-05	Mast_cells	CKLF	up
RPL18A	8.52E-12	0.54478006	0.824	0.659	4.46E-07	Mast_cells	RPL18A	up
C4orf481	2.21E-09	0.537969931	0.484	0.159	0.000115505	Mast_cells	C4orf48	up
ARL6IP41	2.10E-09	0.535951837	0.458	0.125	0.000110083	Mast_cells	ARL6IP4	up
HPGDS	3.05E-13	0.524692158	0.836	0.614	1.60E-08	Mast_cells	HPGDS	up
KRTCAP2	6.06E-09	0.516767484	0.452	0.125	0.000317067	Mast_cells	KRTCAP2	up
LAT	1.24E-08	0.512868794	0.453	0.125	0.000646922	Mast_cells	LAT	up
ARPC3	1.77E-11	0.494554066	0.78	0.5	9.26E-07	Mast_cells	ARPC3	up
DUSP2	5.21E-05	0.494523258	0.389	0.205	1	Mast_cells	DUSP2	up
TIMP1	9.13E-10	0.492155499	0.684	0.477	4.78E-05	Mast_cells	TIMP1	up
BST2	1.38E-08	0.481312892	0.585	0.33	0.000720702	Mast_cells	BST2	up
NEAT11	1.18E-09	0.480738876	0.795	0.602	6.18E-05	Mast_cells	NEAT1	up
CYBA	1.03E-07	0.480146951	0.583	0.295	0.00537711	Mast_cells	CYBA	up
TOMM6	3.02E-08	0.479471768	0.407	0.091	0.001579764	Mast_cells	TOMM6	up
DDT	7.05E-08	0.475782571	0.362	0.091	0.003690036	Mast_cells	DDT	up
NDUFC21	1.32E-07	0.469218942	0.455	0.193	0.00688898	Mast_cells	NDUFC2	up
SCGB2A15	8.36E-07	0.467657867	0.285	0.045	0.043764132	Mast_cells	SCGB2A1	up
MICOS10	7.02E-08	0.465896953	0.461	0.193	0.003674014	Mast_cells	MICOS10	up
UBE2S	3.06E-07	0.463022731	0.554	0.364	0.016030402	Mast_cells	UBE2S	up
TSPO	2.15E-08	0.462580926	0.571	0.33	0.001127703	Mast_cells	TSPO	up
HIST1H4C1	9.12E-07	0.455501321	0.503	0.261	0.047739361	Mast_cells	HIST1H4C	up
ARPC1B	4.24E-07	0.455212904	0.471	0.205	0.022222924	Mast_cells	ARPC1B	up
ATP5F1D	2.08E-07	0.443301448	0.532	0.273	0.010914375	Mast_cells	ATP5F1D	up
S100A10	4.38E-07	0.442135056	0.541	0.307	0.022911217	Mast_cells	S100A10	up
SERTAD1	2.18E-06	0.439785582	0.546	0.307	0.114209886	Mast_cells	SERTAD1	up
S100A6	3.76E-20	0.437214604	0.955	0.932	1.97E-15	Mast_cells	S100A6	up
SELENOH	4.87E-07	0.434597192	0.444	0.17	0.025510246	Mast_cells	SELENOH	up
WFDC25	2.59E-05	0.428194213	0.3	0.102	1	Mast_cells	WFDC2	up
MT2A1	0.000354175	0.419645192	0.451	0.273	1	Mast_cells	MT2A	up
GNG5	7.83E-07	0.418074957	0.457	0.159	0.041014357	Mast_cells	GNG5	up
RPL36AL	9.43E-12	0.416121384	0.845	0.705	4.94E-07	Mast_cells	RPL36AL	up
ARHGAP181	1.52E-07	0.415848838	0.624	0.398	0.007968874	Mast_cells	ARHGAP18	up
POLD4	2.58E-06	0.415317369	0.362	0.125	0.134974271	Mast_cells	POLD4	up
C9orf16	1.75E-06	0.412284092	0.482	0.239	0.091378566	Mast_cells	C9orf16	up
FAU	2.92E-15	0.407268982	0.952	0.864	1.53E-10	Mast_cells	FAU	up
CD69	6.25E-06	0.406797007	0.756	0.534	0.327201961	Mast_cells	CD69	up
PHLDA2	2.00E-05	0.406340667	0.328	0.114	1	Mast_cells	PHLDA2	up
CLIC1	8.42E-13	0.405431988	0.874	0.75	4.41E-08	Mast_cells	CLIC1	up

HPGD	5.94E-11	0.402748846	0.917	0.841	3.11E-06	Mast_cells	HPGD	up
IDS	1.15E-05	0.398853865	0.48	0.239	0.60305759	Mast_cells	IDS	up
CD37	2.60E-09	0.39768828	0.8	0.591	0.000136267	Mast_cells	CD37	up
UQCR11	4.95E-06	0.397458283	0.533	0.307	0.259262097	Mast_cells	UQCR11	up
SAMSN1	1.41E-08	0.395084434	0.822	0.602	0.000740377	Mast_cells	SAMSN1	up
UBXN1	3.83E-06	0.389530927	0.494	0.273	0.200376201	Mast_cells	UBXN1	up
VPS28	9.21E-07	0.386207349	0.603	0.375	0.048245314	Mast_cells	VPS28	up
NDUFA11	1.01E-05	0.383642816	0.482	0.261	0.529524217	Mast_cells	NDUFA11	up
TYROBP	2.94E-08	0.381233581	0.791	0.625	0.001538353	Mast_cells	TYROBP	up
VAMP8	2.01E-06	0.380465922	0.6	0.386	0.10539572	Mast_cells	VAMP8	up
UXT	6.74E-06	0.378333985	0.449	0.239	0.352766071	Mast_cells	UXT	up
GPX4	5.30E-08	0.377657276	0.735	0.58	0.002774177	Mast_cells	GPX4	up
RPL10	6.48E-16	0.375770386	0.959	0.977	3.39E-11	Mast_cells	RPL10	up
HLA-C1	4.59E-08	0.375116441	0.781	0.625	0.002401597	Mast_cells	HLA-C	up
LDHB	2.11E-06	0.372285476	0.633	0.443	0.110342974	Mast_cells	LDHB	up
BCL2A1	0.000155948	0.371342716	0.329	0.136	1	Mast_cells	BCL2A1	up
FCER1G	7.93E-11	0.369944693	0.912	0.795	4.15E-06	Mast_cells	FCER1G	up
FXYD5	3.29E-07	0.368822419	0.84	0.614	0.017251545	Mast_cells	FXYD5	up
RABAC1	2.59E-05	0.367800652	0.467	0.261	1	Mast_cells	RABAC1	up
COX4I1	1.69E-09	0.366966772	0.82	0.659	8.83E-05	Mast_cells	COX4I1	up
CRIP1	8.89E-05	0.36585427	0.305	0.114	1	Mast_cells	CRIP1	up
CD83	8.86E-07	0.36262733	0.732	0.614	0.046375704	Mast_cells	CD83	up
ATP6V1G1	3.86E-06	0.361571452	0.601	0.409	0.2023308	Mast_cells	ATP6V1G1	up
ABRACL	2.92E-05	0.360812091	0.389	0.182	1	Mast_cells	ABRACL	up
TMEM176B	1.99E-05	0.360330839	0.563	0.409	1	Mast_cells	TMEM176B	up
RGS10	2.04E-06	0.358909754	0.679	0.534	0.107029508	Mast_cells	RGS10	up
C17orf49	9.84E-06	0.358574817	0.301	0.08	0.515324412	Mast_cells	C17orf49	up
AC020916.1	3.66E-05	0.356853421	0.61	0.432	1	Mast_cells	AC020916.1	up
THUMPD3-AS1	2.09E-05	0.356149357	0.338	0.125	1	Mast_cells	THUMPD3-AS1	up
COX17	5.61E-05	0.353406594	0.462	0.284	1	Mast_cells	COX17	up
IL18	7.06E-05	0.352697603	0.402	0.216	1	Mast_cells	IL18	up
C18orf32	1.41E-05	0.351663469	0.316	0.102	0.740669802	Mast_cells	C18orf32	up
SCAND1	2.09E-05	0.349769571	0.304	0.102	1	Mast_cells	SCAND1	up
TRAPPC5	1.25E-05	0.348480914	0.312	0.091	0.656892713	Mast_cells	TRAPPC5	up
S100A41	3.17E-11	0.347089274	0.939	0.841	1.66E-06	Mast_cells	S100A4	up
BIRC3	0.000193657	0.344336921	0.566	0.443	1	Mast_cells	BIRC3	up
SRP14	3.03E-09	0.34402443	0.831	0.727	0.000158499	Mast_cells	SRP14	up
NDUFV2	1.22E-05	0.343390073	0.297	0.08	0.636231689	Mast_cells	NDUFV2	up
CIAO2B	5.75E-05	0.341373455	0.44	0.261	1	Mast_cells	CIAO2B	up
SPNS1	2.00E-05	0.341230933	0.249	0.057	1	Mast_cells	SPNS1	up
GABARAPL2	3.28E-05	0.341147088	0.488	0.307	1	Mast_cells	GABARAPL2	up
NACA	1.63E-15	0.339587878	0.954	0.864	8.56E-11	Mast_cells	NACA	up
RPL22	2.87E-10	0.339441847	0.866	0.795	1.50E-05	Mast_cells	RPL22	up
GTF2B	0.00015292	0.339258055	0.373	0.193	1	Mast_cells	GTF2B	up
DNAJB6	4.60E-05	0.336670505	0.612	0.5	1	Mast_cells	DNAJB6	up
COX5B	1.53E-05	0.334743099	0.599	0.398	0.80369622	Mast_cells	COX5B	up
SKP1	7.69E-08	0.333268243	0.728	0.636	0.004028912	Mast_cells	SKP1	up
RPS15	7.13E-13	0.329974608	0.913	0.92	3.73E-08	Mast_cells	RPS15	up
RPL22L1	0.000111277	0.32960816	0.482	0.295	1	Mast_cells	RPL22L1	up
RPL24	7.61E-13	0.325108484	0.929	0.898	3.98E-08	Mast_cells	RPL24	up

EDF1	1.03E-05	0.322107007	0.667	0.534	0.536796435	Mast_cells	EDF1	up
ZFAS1	7.58E-06	0.322084558	0.685	0.58	0.39696074	Mast_cells	ZFAS1	up
PSME1	9.17E-05	0.32192201	0.53	0.364	1	Mast_cells	PSME1	up
IER2	8.53E-08	0.321873318	0.876	0.841	0.004468597	Mast_cells	IER2	up
RHEX	7.08E-07	0.321558937	0.817	0.682	0.037075004	Mast_cells	RHEX	up
RBM4	9.95E-05	0.321223481	0.356	0.159	1	Mast_cells	RBM4	up
MT1X1	0.008945435	0.320823969	0.208	0.102	1	Mast_cells	MT1X	up
DYNLL1	5.06E-07	0.31704905	0.784	0.67	0.026497738	Mast_cells	DYNLL1	up
IGFLR1	0.000104977	0.316625356	0.269	0.091	1	Mast_cells	IGFLR1	up
CKS2	0.000818282	0.316546282	0.438	0.284	1	Mast_cells	CKS2	up
FTL	1.14E-17	0.314372979	0.972	0.989	5.96E-13	Mast_cells	FTL	up
TMBIM41	0.000134593	0.312536437	0.443	0.239	1	Mast_cells	TMBIM4	up
CAPG	2.73E-07	0.311226648	0.875	0.773	0.014309866	Mast_cells	CAPG	up
RPL26	2.64E-13	0.31021697	0.959	0.955	1.38E-08	Mast_cells	RPL26	up
MRPS24	2.55E-05	0.308583666	0.234	0.045	1	Mast_cells	MRPS24	up
RPL7A	1.18E-12	0.307166183	0.933	0.92	6.19E-08	Mast_cells	RPL7A	up
SNHG8	2.86E-05	0.305447863	0.627	0.5	1	Mast_cells	SNHG8	up
PSMB10	5.01E-05	0.304505957	0.259	0.068	1	Mast_cells	PSMB10	up
TNF	0.004527583	0.304103235	0.29	0.159	1	Mast_cells	TNF	up
NDUFB8	0.000241547	0.303948331	0.427	0.261	1	Mast_cells	NDUFB8	up
COX6A1	5.01E-05	0.303737126	0.592	0.443	1	Mast_cells	COX6A1	up
GIHCG	0.000231305	0.303173396	0.26	0.091	1	Mast_cells	GIHCG	up
PRG2	0.000989647	0.302913215	0.184	0.045	1	Mast_cells	PRG2	up
NEDD8	0.0001628	0.302452884	0.535	0.409	1	Mast_cells	NEDD8	up
RPS26	1.07E-07	0.301712438	0.798	0.705	0.005586528	Mast_cells	RPS26	up
DNAJB11	6.89E-07	0.301024361	0.837	0.795	0.036094734	Mast_cells	DNAJB1	up
PRDX1	1.41E-06	0.299616377	0.784	0.727	0.073696864	Mast_cells	PRDX1	up
FTH1	1.39E-21	0.296043119	0.998	1	7.29E-17	Mast_cells	FTH1	up
TOMM5	0.000131379	0.295970645	0.239	0.068	1	Mast_cells	TOMM5	up
UBB	2.92E-16	0.295868623	0.973	0.989	1.53E-11	Mast_cells	UBB	up
BTG1	2.02E-07	0.294780663	0.845	0.761	0.01057497	Mast_cells	BTG1	up
TMEM176A	0.000654189	0.292187098	0.365	0.205	1	Mast_cells	TMEM176A	up
ANXA4	0.000462931	0.292053537	0.511	0.352	1	Mast_cells	ANXA4	up
ELOB	4.37E-05	0.291914456	0.644	0.489	1	Mast_cells	ELOB	up
MRPL18	0.001574517	0.286476983	0.361	0.227	1	Mast_cells	MRPL18	up
FAM133B	0.001348083	0.286304697	0.37	0.227	1	Mast_cells	FAM133B	up
PDCD6	0.000192158	0.286241521	0.274	0.091	1	Mast_cells	PDCD6	up
FIS1	0.000368837	0.286227157	0.482	0.33	1	Mast_cells	FIS1	up
ATP5MG	1.09E-05	0.285238721	0.697	0.614	0.568638773	Mast_cells	ATP5MG	up
TSTD1	0.001066893	0.283641788	0.364	0.216	1	Mast_cells	TSTD1	up
MALAT1	1.91E-15	0.283384386	0.999	1	1.00E-10	Mast_cells	MALAT1	up
BEX4	0.0003394	0.283331397	0.509	0.341	1	Mast_cells	BEX4	up
LYL1	0.000666826	0.283217847	0.363	0.182	1	Mast_cells	LYL1	up
DRAP1	0.000234717	0.283107104	0.549	0.409	1	Mast_cells	DRAP1	up
PET100	0.000423021	0.282044091	0.323	0.148	1	Mast_cells	PET100	up
SUPT4H1	0.000225787	0.281645766	0.25	0.08	1	Mast_cells	SUPT4H1	up
NDUFB7	0.00056874	0.281365539	0.37	0.205	1	Mast_cells	NDUFB7	up
SAT1	6.01E-09	0.27943347	0.911	0.886	0.000314551	Mast_cells	SAT1	up
NDUFA4	1.39E-06	0.279128123	0.786	0.705	0.072763047	Mast_cells	NDUFA4	up
MPG	0.00028019	0.279120649	0.304	0.125	1	Mast_cells	MPG	up
ANKRD28	0.001831529	0.278329292	0.452	0.318	1	Mast_cells	ANKRD28	up

ANAPC16	0.00084276	0.277919585	0.447	0.307	1	Mast_cells	ANAPC16	up
DBI	0.00017639	0.276477517	0.617	0.534	1	Mast_cells	DBI	up
PYCARD	0.000279825	0.276218284	0.433	0.239	1	Mast_cells	PYCARD	up
HIGD2A	0.001409671	0.274778879	0.403	0.273	1	Mast_cells	HIGD2A	up
GPR65	0.003152197	0.274104393	0.452	0.318	1	Mast_cells	GPR65	up
ATP5F1C	0.000328326	0.273421245	0.555	0.443	1	Mast_cells	ATP5F1C	up
DNAJA1	2.71E-09	0.272627033	0.915	0.875	0.000141714	Mast_cells	DNAJA1	up
PSMA7	0.000165573	0.271742604	0.632	0.534	1	Mast_cells	PSMA7	up
PPP1R2	0.002596617	0.269849032	0.369	0.25	1	Mast_cells	PPP1R2	up
A1BG	7.08E-05	0.269193355	0.192	0.023	1	Mast_cells	A1BG	up
ATP6V0B	0.000439277	0.26908942	0.578	0.455	1	Mast_cells	ATP6V0B	up
CCDC59	0.002196176	0.26853506	0.421	0.295	1	Mast_cells	CCDC59	up
NXT1	0.00147742	0.267127146	0.364	0.216	1	Mast_cells	NXT1	up
SPINT2	0.001070765	0.266769506	0.444	0.284	1	Mast_cells	SPINT2	up
COX7A2	0.00035358	0.264940659	0.597	0.5	1	Mast_cells	COX7A2	up
ANAPC11	0.001597411	0.264450649	0.363	0.227	1	Mast_cells	ANAPC11	up
OSTF1	0.000883194	0.264400298	0.326	0.159	1	Mast_cells	OSTF1	up
LGALS31	5.40E-05	0.264366812	0.732	0.682	1	Mast_cells	LGALS3	up
UBE2V1	0.000659631	0.261381282	0.274	0.114	1	Mast_cells	UBE2V1	up
CST7	0.002395214	0.260968956	0.344	0.193	1	Mast_cells	CST7	up
CST3	2.06E-05	0.26073065	0.727	0.659	1	Mast_cells	CST3	up
NDST2	0.002145999	0.260586708	0.259	0.125	1	Mast_cells	NDST2	up
PSMA2	0.001809194	0.260342258	0.365	0.227	1	Mast_cells	PSMA2	up
GPS2	0.000427366	0.259696482	0.224	0.068	1	Mast_cells	GPS2	up
SNX6	0.002821064	0.258378088	0.36	0.239	1	Mast_cells	SNX6	up
NDUFB10	0.00113105	0.258181558	0.463	0.307	1	Mast_cells	NDUFB10	up
CHMP4A	0.000428414	0.257213045	0.244	0.08	1	Mast_cells	CHMP4A	up
PSMA1	0.00179737	0.256420047	0.336	0.193	1	Mast_cells	PSMA1	up
G3BP2	0.001394803	0.255595653	0.568	0.443	1	Mast_cells	G3BP2	up
RPL28	3.40E-12	0.255547816	0.961	0.955	1.78E-07	Mast_cells	RPL28	up
AGTRAP	0.001225202	0.255335743	0.356	0.182	1	Mast_cells	AGTRAP	up
ATP6V1F	0.000229056	0.255234452	0.698	0.58	1	Mast_cells	ATP6V1F	up
SUB1	6.18E-06	0.254886855	0.791	0.716	0.323329968	Mast_cells	SUB1	up
CD91	2.71E-06	0.254758409	0.824	0.773	0.142034076	Mast_cells	CD9	up
COX16	0.000321342	0.251398441	0.198	0.045	1	Mast_cells	COX16	up
NUTM2A-AS1	0.001418012	0.250900581	0.285	0.136	1	Mast_cells	NUTM2A-AS1	up
NDUFA71	0.000200322	0.250866518	0.209	0.045	1	Mast_cells	NDUFA7	up
NFKBIA	7.55E-12	0.250861623	0.965	0.943	3.95E-07	Mast_cells	NFKBIA	up
AL157895.1	0.000500763	0.250387471	0.643	0.568	1	Mast_cells	AL157895.1	up
NME3	0.001478136	0.250185793	0.318	0.17	1	Mast_cells	NME3	up
PAPSS2	1.65E-12	-0.250095673	0.057	0.261	8.66E-08	Mast_cells	PAPSS2	down
FOXL2NB	6.82E-13	-0.250167051	0.056	0.261	3.57E-08	Mast_cells	FOXL2NB	down
IFITM2	9.49E-07	-0.250202117	0.765	0.909	0.049677547	Mast_cells	IFITM2	down
RAI1	3.24E-06	-0.250824524	0.113	0.284	0.169570873	Mast_cells	RAI1	down
ZBTB38	6.68E-05	-0.25086274	0.266	0.477	1	Mast_cells	ZBTB38	down
CTTN	2.22E-08	-0.250865864	0.114	0.318	0.001164256	Mast_cells	CTTN	down
CAPZA1	0.000175077	-0.251072473	0.353	0.545	1	Mast_cells	CAPZA1	down
ACTN1	8.72E-07	-0.251075046	0.117	0.295	0.045658513	Mast_cells	ACTN1	down
RERE	0.000120046	-0.251091841	0.295	0.489	1	Mast_cells	RERE	down
FADS2	1.71E-07	-0.251149527	0.106	0.295	0.00894561	Mast_cells	FADS2	down
TOB2	1.36E-05	-0.251281672	0.24	0.466	0.711016982	Mast_cells	TOB2	down

SMARCC1	5.28E-06	-0.251666435	0.233	0.466	0.276360516	Mast_cells	SMARCC1	down
DDX42	6.10E-05	-0.251823062	0.2	0.375	1	Mast_cells	DDX42	down
NORAD	0.000113105	-0.251877239	0.481	0.682	1	Mast_cells	NORAD	down
SP1	1.07E-07	-0.251882016	0.108	0.307	0.005612604	Mast_cells	SP1	down
JAZF1	3.66E-07	-0.25196512	0.165	0.398	0.019181209	Mast_cells	JAZF1	down
TBC1D5	3.64E-10	-0.252019023	0.123	0.375	1.90E-05	Mast_cells	TBC1D5	down
VEGFA	0.000467551	-0.252658513	0.45	0.67	1	Mast_cells	VEGFA	down
PABPC1	3.33E-09	-0.253096835	0.874	0.977	0.000174507	Mast_cells	PABPC1	down
TPM2	6.08E-07	-0.253500677	0.174	0.409	0.031829192	Mast_cells	TPM2	down
NONO	0.000211669	-0.253876093	0.387	0.602	1	Mast_cells	NONO	down
ARHGAP1	5.01E-06	-0.253945311	0.122	0.295	0.262392258	Mast_cells	ARHGAP1	down
MACF1	0.000161703	-0.254000658	0.317	0.511	1	Mast_cells	MACF1	down
BTBD3	2.60E-11	-0.254254871	0.064	0.261	1.36E-06	Mast_cells	BTBD3	down
SCAP	4.74E-07	-0.25434558	0.075	0.227	0.024813149	Mast_cells	SCAP	down
C16orf72	4.97E-06	-0.254470349	0.187	0.398	0.260414643	Mast_cells	C16orf72	down
EGR11	7.23E-07	-0.254587174	0.855	0.932	0.037837379	Mast_cells	EGR1	down
LSM14A	1.36E-05	-0.254635456	0.295	0.534	0.713521574	Mast_cells	LSM14A	down
ADGRA2	2.05E-09	-0.254663394	0.096	0.307	0.000107418	Mast_cells	ADGRA2	down
MT-TF	1.73E-11	-0.254763173	0.073	0.295	9.05E-07	Mast_cells	MT-TF	down
LCOR	4.13E-08	-0.254843213	0.101	0.295	0.00216201	Mast_cells	LCOR	down
LRRC58	1.34E-05	-0.254956319	0.11	0.261	0.703950679	Mast_cells	LRRC58	down
RAB1A	0.000207835	-0.254976672	0.358	0.545	1	Mast_cells	RAB1A	down
PHLDB1	2.26E-08	-0.255686875	0.1	0.295	0.001182298	Mast_cells	PHLDB1	down
MT-ND2	1.62E-16	-0.255738085	0.994	1	8.47E-12	Mast_cells	MT-ND2	down
CYB5R3	3.92E-05	-0.255799683	0.304	0.534	1	Mast_cells	CYB5R3	down
PCYOX1	1.81E-06	-0.256334284	0.155	0.352	0.094928965	Mast_cells	PCYOX1	down
PDLIM1	3.34E-07	-0.256386788	0.091	0.261	0.017492455	Mast_cells	PDLIM1	down
RPS13P2	1.32E-10	-0.256523012	0.047	0.216	6.89E-06	Mast_cells	RPS13P2	down
AR	1.38E-05	-0.256807574	0.139	0.307	0.723167569	Mast_cells	AR	down
VASN	6.02E-09	-0.256811207	0.078	0.261	0.000315062	Mast_cells	VASN	down
DUSP8	4.49E-08	-0.257082216	0.094	0.284	0.002350064	Mast_cells	DUSP8	down
SNX1	2.57E-06	-0.258110415	0.163	0.364	0.134456427	Mast_cells	SNX1	down
MT-ND1	1.81E-20	-0.258386097	0.99	1	9.49E-16	Mast_cells	MT-ND1	down
ADAM33	1.91E-08	-0.258514322	0.087	0.273	0.000998312	Mast_cells	ADAM33	down
CDK16	9.36E-10	-0.258639317	0.077	0.273	4.90E-05	Mast_cells	CDK16	down
HNRNPM	0.000109997	-0.259182442	0.545	0.773	1	Mast_cells	HNRNPM	down
GNLY1	3.91E-09	-0.259299734	0.03	0.159	0.000204959	Mast_cells	GNLY	down
CCN1	6.19E-06	-0.259351465	0.156	0.352	0.323938804	Mast_cells	CCN1	down
MFGE8	1.46E-06	-0.259409016	0.145	0.341	0.07666062	Mast_cells	MFGE8	down
MAP7D1	5.88E-06	-0.259451057	0.208	0.42	0.307688447	Mast_cells	MAP7D1	down
GALNT1	7.63E-06	-0.260017246	0.194	0.398	0.399315348	Mast_cells	GALNT1	down
SLC25A37	1.39E-07	-0.26003813	0.125	0.33	0.007257633	Mast_cells	SLC25A37	down
SPTAN1	4.50E-06	-0.260116288	0.23	0.455	0.235526403	Mast_cells	SPTAN1	down
C14orf132	2.49E-08	-0.260155681	0.094	0.284	0.00130588	Mast_cells	C14orf132	down
EMC10	6.16E-06	-0.260224379	0.275	0.511	0.322690437	Mast_cells	EMC10	down
MAGT1	5.25E-06	-0.260234164	0.177	0.375	0.274832681	Mast_cells	MAGT1	down
TWSG1	1.31E-08	-0.260256878	0.111	0.318	0.000683392	Mast_cells	TWSG1	down
PTEN	6.67E-06	-0.260351741	0.248	0.477	0.349242139	Mast_cells	PTEN	down
RELA	5.64E-06	-0.260461171	0.248	0.489	0.295089099	Mast_cells	RELA	down
MAP1B	4.11E-08	-0.26073283	0.124	0.341	0.002153747	Mast_cells	MAP1B	down
PDS5B	5.38E-06	-0.260911502	0.177	0.375	0.281641647	Mast_cells	PDS5B	down

ABL1	5.33E-07	-0.261047427	0.121	0.307	0.027926451	Mast_cells	ABL1	down
GPX1	1.60E-08	-0.261068729	0.099	0.307	0.00083707	Mast_cells	GPX1	down
CTSK	2.02E-06	-0.261353797	0.146	0.341	0.105715002	Mast_cells	CTSK	down
TAF6	2.93E-09	-0.261861178	0.104	0.318	0.000153456	Mast_cells	TAF6	down
EP300	1.28E-05	-0.262175172	0.252	0.466	0.66997559	Mast_cells	EP300	down
ACTR2	0.000190835	-0.262500284	0.443	0.67	1	Mast_cells	ACTR2	down
TRAM1	3.33E-05	-0.262643868	0.312	0.534	1	Mast_cells	TRAM1	down
FAM120A	1.02E-05	-0.262821271	0.262	0.5	0.533627437	Mast_cells	FAM120A	down
SNORD3A	1.24E-09	-0.262966591	0.065	0.25	6.50E-05	Mast_cells	SNORD3A	down
CLIP3	2.48E-14	-0.263054584	0.055	0.273	1.30E-09	Mast_cells	CLIP3	down
SBNO1	7.14E-06	-0.263809484	0.144	0.318	0.373627367	Mast_cells	SBNO1	down
SEC13	8.52E-07	-0.264143356	0.186	0.409	0.04459087	Mast_cells	SEC13	down
RANBP2	5.85E-05	-0.26465348	0.269	0.466	1	Mast_cells	RANBP2	down
HNRNPR	5.38E-05	-0.264780384	0.436	0.659	1	Mast_cells	HNRNPR	down
DYNC1H1	1.89E-05	-0.264993171	0.256	0.466	0.990218061	Mast_cells	DYNC1H1	down
KDM5C	1.21E-06	-0.265099547	0.173	0.386	0.063189576	Mast_cells	KDM5C	down
TMEM214	7.47E-07	-0.265178151	0.128	0.318	0.03910244	Mast_cells	TMEM214	down
NUTF2	1.69E-05	-0.265269083	0.227	0.432	0.884212148	Mast_cells	NUTF2	down
NXF1	1.52E-07	-0.265294769	0.182	0.432	0.007980174	Mast_cells	NXF1	down
EMX2	1.01E-06	-0.265444879	0.145	0.341	0.052680226	Mast_cells	EMX2	down
CCBE1	9.22E-08	-0.265452257	0.094	0.273	0.004825815	Mast_cells	CCBE1	down
JMJD1C	0.000265188	-0.26557288	0.399	0.602	1	Mast_cells	JMJD1C	down
WLS	1.56E-06	-0.265611489	0.123	0.295	0.081907529	Mast_cells	WLS	down
CLSTN1	7.25E-07	-0.265649423	0.16	0.364	0.037982774	Mast_cells	CLSTN1	down
EFEMP2	8.36E-08	-0.265965803	0.137	0.352	0.004376173	Mast_cells	EFEMP2	down
EI24	1.64E-06	-0.26613224	0.178	0.386	0.085969078	Mast_cells	EI24	down
WBP11	4.31E-05	-0.266286373	0.346	0.58	1	Mast_cells	WBP11	down
DAXX	5.39E-08	-0.266357657	0.109	0.307	0.002822906	Mast_cells	DAXX	down
ZC3HAV1	5.13E-06	-0.266371999	0.252	0.489	0.268627636	Mast_cells	ZC3HAV1	down
EIF4A1P10	1.45E-11	-0.266698571	0.074	0.295	7.61E-07	Mast_cells	EIF4A1P10	down
NT5DC2	1.78E-05	-0.268127014	0.221	0.42	0.933657918	Mast_cells	NT5DC2	down
NCOR2	0.000161608	-0.268165019	0.293	0.477	1	Mast_cells	NCOR2	down
CARM1	6.04E-10	-0.268678489	0.098	0.318	3.16E-05	Mast_cells	CARM1	down
RHOQ	1.54E-07	-0.26871449	0.171	0.409	0.008056	Mast_cells	RHOQ	down
STIM1	7.88E-09	-0.268733949	0.13	0.364	0.000412329	Mast_cells	STIM1	down
ANK2	5.51E-11	-0.268969457	0.047	0.216	2.89E-06	Mast_cells	ANK2	down
COPB2	6.95E-06	-0.26939141	0.274	0.511	0.363700344	Mast_cells	COPB2	down
RAD23B	2.82E-05	-0.269646678	0.304	0.523	1	Mast_cells	RAD23B	down
PITPNA	3.89E-09	-0.269763648	0.117	0.341	0.000203444	Mast_cells	PITPNA	down
TRIP6	7.20E-10	-0.269824001	0.106	0.33	3.77E-05	Mast_cells	TRIP6	down
AGO2	1.58E-07	-0.270011594	0.115	0.307	0.008270053	Mast_cells	AGO2	down
GABARAPL1	4.87E-06	-0.270475429	0.199	0.409	0.25484613	Mast_cells	GABARAPL1	down
RPN1	2.77E-05	-0.270499594	0.217	0.409	1	Mast_cells	RPN1	down
RBM25	3.69E-05	-0.271150633	0.515	0.727	1	Mast_cells	RBM25	down
IPO7	1.11E-07	-0.271202219	0.184	0.432	0.005789525	Mast_cells	IPO7	down
TRIM56	2.08E-08	-0.271370572	0.137	0.364	0.001088138	Mast_cells	TRIM56	down
PTPN14	1.29E-19	-0.271480177	0.04	0.273	6.74E-15	Mast_cells	PTPN14	down
MEIS1	6.50E-09	-0.271700281	0.097	0.295	0.000340344	Mast_cells	MEIS1	down
STAT6	1.86E-08	-0.271730661	0.109	0.318	0.000971993	Mast_cells	STAT6	down
TPBG	1.69E-09	-0.272081168	0.121	0.352	8.87E-05	Mast_cells	TPBG	down
CLTC	1.01E-05	-0.272867524	0.26	0.489	0.527534419	Mast_cells	CLTC	down

COPG1	5.32E-08	-0.272908006	0.143	0.364	0.002785853	Mast_cells	COPG1	down
APOD	3.76E-10	-0.273554177	0.1	0.33	1.97E-05	Mast_cells	APOD	down
KANK2	3.69E-06	-0.274265029	0.237	0.477	0.193299164	Mast_cells	KANK2	down
MED1	2.14E-08	-0.274557696	0.106	0.307	0.00112183	Mast_cells	MED1	down
PEA15	7.25E-08	-0.274576132	0.156	0.386	0.003798149	Mast_cells	PEA15	down
TUNAR1	2.96E-12	-0.274625051	0.05	0.239	1.55E-07	Mast_cells	TUNAR	down
BRD2	7.55E-05	-0.274776697	0.553	0.761	1	Mast_cells	BRD2	down
MARVELD1	8.54E-08	-0.275348016	0.114	0.307	0.004469968	Mast_cells	MARVELD1	down
NFE2L1	2.76E-08	-0.276117683	0.18	0.443	0.001446277	Mast_cells	NFE2L1	down
SEPTIN9	4.14E-06	-0.276141605	0.358	0.648	0.217021865	Mast_cells	SEPTIN9	down
RAP2B	1.40E-07	-0.276240073	0.163	0.398	0.007304849	Mast_cells	RAP2B	down
PRKCSH	3.77E-06	-0.276293064	0.252	0.489	0.19724617	Mast_cells	PRKCSH	down
TNC1	4.35E-10	-0.276807666	0.074	0.273	2.28E-05	Mast_cells	TNC	down
TCEAL9	7.04E-08	-0.276862742	0.156	0.386	0.003686565	Mast_cells	TCEAL9	down
PRXL2A	1.64E-05	-0.276974879	0.183	0.364	0.857937972	Mast_cells	PRXL2A	down
EIF4G1	1.69E-06	-0.277421899	0.209	0.432	0.088335217	Mast_cells	EIF4G1	down
TIAL1	3.15E-06	-0.277496638	0.237	0.466	0.16485676	Mast_cells	TIAL1	down
PSME3	1.12E-08	-0.277667658	0.146	0.386	0.000588844	Mast_cells	PSME3	down
ARHGEF40	1.25E-06	-0.279078239	0.215	0.455	0.065218898	Mast_cells	ARHGEF40	down
UBXN7	5.60E-07	-0.279745769	0.107	0.284	0.029316979	Mast_cells	UBXN7	down
MAFF1	0.000136436	-0.279863294	0.275	0.466	1	Mast_cells	MAFF	down
MAN1A2	5.11E-07	-0.280700176	0.189	0.42	0.026772442	Mast_cells	MAN1A2	down
RAB1B	3.76E-07	-0.280895977	0.206	0.455	0.019677002	Mast_cells	RAB1B	down
TEAD2	4.95E-10	-0.281091703	0.082	0.284	2.59E-05	Mast_cells	TEAD2	down
CREB3L2	1.52E-05	-0.281129049	0.259	0.477	0.79572524	Mast_cells	CREB3L2	down
WDR82	7.79E-06	-0.281284158	0.226	0.432	0.407917534	Mast_cells	WDR82	down
EIF2S3	3.08E-05	-0.281323875	0.493	0.727	1	Mast_cells	EIF2S3	down
SPN	1.25E-05	-0.281421468	0.144	0.318	0.652797059	Mast_cells	SPN	down
APOBEC3C	7.54E-06	-0.281604138	0.261	0.5	0.394672505	Mast_cells	APOBEC3C	down
ACTN4	4.31E-05	-0.281671693	0.476	0.682	1	Mast_cells	ACTN4	down
CLEC11A	1.08E-07	-0.281760266	0.158	0.386	0.005664674	Mast_cells	CLEC11A	down
CTSB	4.72E-05	-0.282389756	0.529	0.773	1	Mast_cells	CTSB	down
RNF10	3.21E-07	-0.282577221	0.207	0.455	0.016792872	Mast_cells	RNF10	down
EPN1	5.18E-07	-0.282660192	0.16	0.364	0.02712304	Mast_cells	EPN1	down
CERS2	3.57E-06	-0.282917575	0.26	0.5	0.186736108	Mast_cells	CERS2	down
SDC3	1.18E-10	-0.283086538	0.1	0.33	6.16E-06	Mast_cells	SDC3	down
PRICKLE2	9.84E-12	-0.283103066	0.077	0.295	5.15E-07	Mast_cells	PRICKLE2	down
ABCG1	4.32E-12	-0.283584801	0.053	0.25	2.26E-07	Mast_cells	ABCG1	down
ITGA5	4.76E-13	-0.283609736	0.083	0.33	2.49E-08	Mast_cells	ITGA5	down
ARF1	9.11E-07	-0.283823447	0.668	0.875	0.047705006	Mast_cells	ARF1	down
MTSS2	1.36E-15	-0.283908438	0.043	0.25	7.13E-11	Mast_cells	MTSS2	down
TEAD1	1.16E-10	-0.284005397	0.101	0.33	6.08E-06	Mast_cells	TEAD1	down
FKBP10	3.62E-07	-0.284019097	0.146	0.352	0.018957551	Mast_cells	FKBP10	down
TCF7L2	2.37E-08	-0.284044773	0.108	0.307	0.001238937	Mast_cells	TCF7L2	down
RCC2	6.68E-08	-0.284472718	0.175	0.42	0.003497464	Mast_cells	RCC2	down
AL355309.1	8.11E-13	-0.284654531	0.062	0.284	4.24E-08	Mast_cells	AL355309.1	down
ELMSAN1	2.03E-07	-0.284797724	0.164	0.386	0.01060782	Mast_cells	ELMSAN1	down
MAVS	1.57E-09	-0.285028658	0.103	0.318	8.23E-05	Mast_cells	MAVS	down
FJX1	1.51E-09	-0.285116213	0.095	0.307	7.88E-05	Mast_cells	FJX1	down
COPA	2.86E-05	-0.285440322	0.31	0.511	1	Mast_cells	COPA	down
ERN1	1.45E-07	-0.285580735	0.157	0.375	0.007598147	Mast_cells	ERN1	down

PGBD5	9.86E-08	-0.285903485	0.138	0.352	0.005162554	Mast_cells	PGBD5	down
TSKU	6.62E-10	-0.286387997	0.094	0.307	3.47E-05	Mast_cells	TSKU	down
RND3	7.51E-07	-0.286515437	0.128	0.318	0.039325495	Mast_cells	RND3	down
PUM1	1.51E-06	-0.286584101	0.239	0.477	0.078892719	Mast_cells	PUM1	down
MTND2P28	6.82E-09	-0.286850561	0.114	0.341	0.000356852	Mast_cells	MTND2P28	down
SELENOP2	5.87E-07	-0.287143134	0.178	0.398	0.030734074	Mast_cells	SELENOP	down
SMOC2	6.69E-11	-0.287157407	0.067	0.261	3.50E-06	Mast_cells	SMOC2	down
EIF4A2	5.38E-06	-0.287189338	0.666	0.886	0.281702783	Mast_cells	EIF4A2	down
RPL13AP5	2.08E-17	-0.288153495	0.03	0.227	1.09E-12	Mast_cells	RPL13AP5	down
RBPMS	3.61E-08	-0.288624849	0.122	0.33	0.001888666	Mast_cells	RBPMS	down
ADD1	2.67E-06	-0.288787849	0.289	0.545	0.139891903	Mast_cells	ADD1	down
ABHD2	3.61E-06	-0.28984042	0.221	0.443	0.188822102	Mast_cells	ABHD2	down
BMP1	1.65E-09	-0.290034473	0.123	0.352	8.63E-05	Mast_cells	BMP1	down
EIF2AK2	3.23E-07	-0.290272617	0.216	0.466	0.016893928	Mast_cells	EIF2AK2	down
CD164	4.27E-06	-0.290487729	0.343	0.614	0.223611532	Mast_cells	CD164	down
TUBB	5.82E-06	-0.290968994	0.536	0.784	0.304621052	Mast_cells	TUBB	down
EEF2	1.11E-07	-0.291050746	0.737	0.943	0.005809769	Mast_cells	EEF2	down
CFAP20	4.45E-08	-0.291091226	0.159	0.398	0.002329947	Mast_cells	CFAP20	down
CLPTM1	1.08E-07	-0.292069697	0.17	0.398	0.005678294	Mast_cells	CLPTM1	down
ARF6	5.20E-06	-0.292305824	0.485	0.761	0.272033911	Mast_cells	ARF6	down
CEBPB	5.23E-05	-0.292656664	0.391	0.591	1	Mast_cells	CEBPB	down
BCL9L	1.26E-11	-0.292836757	0.077	0.295	6.61E-07	Mast_cells	BCL9L	down
GPI	2.11E-05	-0.292943566	0.197	0.375	1	Mast_cells	GPI	down
PGD	4.61E-07	-0.29311203	0.201	0.432	0.024130481	Mast_cells	PGD	down
AC024293.1	7.55E-10	-0.293360212	0.097	0.318	3.95E-05	Mast_cells	AC024293.1	down
PTMAP5	1.15E-09	-0.293431046	0.107	0.341	6.00E-05	Mast_cells	PTMAP5	down
TGM21	2.07E-06	-0.293820797	0.128	0.307	0.108299839	Mast_cells	TGM2	down
PTBP3	3.56E-06	-0.294423653	0.265	0.511	0.186378678	Mast_cells	PTBP3	down
ZCCHC24	4.09E-07	-0.294729217	0.122	0.307	0.021440817	Mast_cells	ZCCHC24	down
BSDC1	4.80E-09	-0.294776395	0.168	0.432	0.000251336	Mast_cells	BSDC1	down
GRINA	8.57E-08	-0.295009151	0.205	0.466	0.004487259	Mast_cells	GRINA	down
KLF9	7.39E-08	-0.296013229	0.118	0.318	0.003871314	Mast_cells	KLF9	down
COL15A1	7.62E-11	-0.296093885	0.075	0.284	3.99E-06	Mast_cells	COL15A1	down
QSOX1	9.61E-11	-0.296260701	0.104	0.341	5.03E-06	Mast_cells	QSOX1	down
ARID1A	4.88E-06	-0.296300505	0.288	0.523	0.255442553	Mast_cells	ARID1A	down
HNRNPL	5.91E-06	-0.296376743	0.305	0.545	0.309651448	Mast_cells	HNRNPL	down
EIF4G3	1.05E-06	-0.296447044	0.199	0.42	0.055169487	Mast_cells	EIF4G3	down
CD248	2.87E-07	-0.296485116	0.14	0.341	0.015040392	Mast_cells	CD248	down
IRF2BPL	1.92E-06	-0.296486141	0.233	0.477	0.100433416	Mast_cells	IRF2BPL	down
LPP	2.34E-07	-0.297013024	0.133	0.33	0.012243936	Mast_cells	LPP	down
MLLT1	4.03E-07	-0.297214299	0.182	0.409	0.021112197	Mast_cells	MLLT1	down
LAMC1	1.13E-08	-0.297512902	0.093	0.284	0.000593135	Mast_cells	LAMC1	down
QPRT	5.36E-08	-0.298597807	0.193	0.443	0.002804128	Mast_cells	QPRT	down
SSR1	4.68E-07	-0.298671736	0.24	0.489	0.024515354	Mast_cells	SSR1	down
PPP2R2C	6.71E-10	-0.298865104	0.078	0.273	3.51E-05	Mast_cells	PPP2R2C	down
SLC16A11	3.65E-10	-0.29932708	0.081	0.284	1.91E-05	Mast_cells	SLC16A1	down
EHD2	8.09E-11	-0.299376621	0.095	0.318	4.24E-06	Mast_cells	EHD2	down
TIPARP	2.24E-05	-0.2995186	0.421	0.648	1	Mast_cells	TIPARP	down
MYADM	1.52E-06	-0.29963569	0.74	0.909	0.07954045	Mast_cells	MYADM	down
CRISPLD2	3.88E-10	-0.300706236	0.086	0.295	2.03E-05	Mast_cells	CRISPLD2	down
DPY19L1	9.13E-09	-0.300725466	0.116	0.33	0.00047783	Mast_cells	DPY19L1	down

LAPTM4B	2.35E-07	-0.300822143	0.202	0.443	0.012307668	Mast_cells	LAPTM4B	down
CANX	5.62E-06	-0.300844045	0.602	0.773	0.294265253	Mast_cells	CANX	down
EIF3A	1.63E-05	-0.301666811	0.425	0.659	0.855413698	Mast_cells	EIF3A	down
RBM5	4.75E-07	-0.301925338	0.22	0.466	0.024854566	Mast_cells	RBM5	down
NRP1	1.63E-08	-0.302012395	0.143	0.364	0.000851261	Mast_cells	NRP1	down
LTBP3	1.64E-07	-0.302476773	0.139	0.341	0.008566349	Mast_cells	LTBP3	down
YWHAG	1.36E-07	-0.303268901	0.248	0.523	0.007114918	Mast_cells	YWHAG	down
ZYG11B	3.96E-12	-0.30328535	0.096	0.341	2.07E-07	Mast_cells	ZYG11B	down
SPON1	1.07E-09	-0.303309377	0.133	0.375	5.61E-05	Mast_cells	SPON1	down
PLXNB2	6.70E-11	-0.303591254	0.101	0.33	3.51E-06	Mast_cells	PLXNB2	down
CCNL2	5.44E-07	-0.303963614	0.204	0.432	0.028474145	Mast_cells	CCNL2	down
PABPN1	3.96E-07	-0.30398641	0.243	0.489	0.020739879	Mast_cells	PABPN1	down
DDB1	3.78E-07	-0.3041004	0.209	0.443	0.019767958	Mast_cells	DDB1	down
ADAMTS91	6.28E-12	-0.304221521	0.096	0.341	3.29E-07	Mast_cells	ADAMTS9	down
CNP	9.52E-12	-0.30480416	0.113	0.375	4.98E-07	Mast_cells	CNP	down
MT-ND5	2.81E-15	-0.30508639	0.971	1	1.47E-10	Mast_cells	MT-ND5	down
GREB1	1.24E-14	-0.305542227	0.065	0.295	6.47E-10	Mast_cells	GREB1	down
RPS3AP47	3.56E-14	-0.305711589	0.049	0.261	1.86E-09	Mast_cells	RPS3AP47	down
MT-TD	1.31E-14	-0.305826725	0.06	0.295	6.84E-10	Mast_cells	MT-TD	down
TIA1	1.41E-08	-0.305901685	0.196	0.466	0.000738515	Mast_cells	TIA1	down
BASP1	1.57E-05	-0.306171915	0.355	0.58	0.824045884	Mast_cells	BASP1	down
RBBP6	8.33E-06	-0.3067374	0.375	0.602	0.436054251	Mast_cells	RBBP6	down
MSL1	5.80E-07	-0.307298748	0.154	0.352	0.030373003	Mast_cells	MSL1	down
EIF4H	3.82E-06	-0.308895516	0.458	0.716	0.200135614	Mast_cells	EIF4H	down
DST	1.36E-05	-0.309012285	0.227	0.42	0.713623646	Mast_cells	DST	down
SREK1	1.19E-06	-0.309708398	0.254	0.489	0.062550505	Mast_cells	SREK1	down
TLE5	4.31E-06	-0.309829919	0.444	0.682	0.225713942	Mast_cells	TLE5	down
SNHG16	4.32E-08	-0.310705137	0.182	0.42	0.002262096	Mast_cells	SNHG16	down
MEST	5.74E-09	-0.310747713	0.096	0.295	0.000300611	Mast_cells	MEST	down
SERPINE1	2.19E-09	-0.311312565	0.059	0.227	0.000114508	Mast_cells	SERPINE1	down
PARVA	5.85E-11	-0.311633952	0.117	0.364	3.06E-06	Mast_cells	PARVA	down
WT1	1.64E-10	-0.311902409	0.102	0.33	8.60E-06	Mast_cells	WT1	down
BCAS1	2.95E-15	-0.312488362	0.052	0.273	1.55E-10	Mast_cells	BCAS1	down
RAB11B	1.56E-06	-0.313225223	0.304	0.557	0.081923297	Mast_cells	RAB11B	down
ZEB1	7.85E-13	-0.313262517	0.082	0.318	4.11E-08	Mast_cells	ZEB1	down
IGFBP22	6.95E-05	-0.313581169	0.182	0.352	1	Mast_cells	IGFBP2	down
COL12A1	2.23E-12	-0.313757098	0.06	0.261	1.17E-07	Mast_cells	COL12A1	down
TMEM98	7.98E-10	-0.314541633	0.137	0.386	4.18E-05	Mast_cells	TMEM98	down
REV3L	5.42E-06	-0.315081559	0.284	0.511	0.28359626	Mast_cells	REV3L	down
BMPR2	1.13E-08	-0.31537767	0.159	0.398	0.000593228	Mast_cells	BMPR2	down
HPSE2	2.18E-19	-0.315822222	0.044	0.284	1.14E-14	Mast_cells	HPSE2	down
PRDM1	1.58E-12	-0.315825659	0.089	0.33	8.25E-08	Mast_cells	PRDM1	down
TSHZ3	1.23E-14	-0.316324352	0.078	0.33	6.45E-10	Mast_cells	TSHZ3	down
HSPB61	1.88E-06	-0.316517841	0.154	0.352	0.098610842	Mast_cells	HSPB6	down
CS	1.90E-09	-0.317132466	0.144	0.398	9.95E-05	Mast_cells	CS	down
RAB7A	1.25E-06	-0.317272436	0.524	0.773	0.065272664	Mast_cells	RAB7A	down
UBE3A	1.05E-06	-0.31729648	0.275	0.523	0.054953707	Mast_cells	UBE3A	down
SURF4	1.02E-08	-0.318232837	0.246	0.545	0.000536138	Mast_cells	SURF4	down
SHISA5	1.92E-09	-0.319131247	0.166	0.432	0.000100467	Mast_cells	SHISA5	down
UBE2R2	1.93E-07	-0.319879723	0.319	0.602	0.010120226	Mast_cells	UBE2R2	down
KLF10	1.34E-05	-0.320406664	0.452	0.693	0.701922848	Mast_cells	KLF10	down

ANGPTL2	4.79E-13	-0.320411337	0.071	0.295	2.51E-08	Mast_cells	ANGPTL2	down
LRP1	7.41E-09	-0.320450579	0.154	0.386	0.000387841	Mast_cells	LRP1	down
ADAR	2.75E-07	-0.320980293	0.226	0.455	0.014415373	Mast_cells	ADAR	down
ANXA5	1.52E-05	-0.321675612	0.508	0.67	0.79708094	Mast_cells	ANXA5	down
BRD4	1.17E-07	-0.321824954	0.345	0.659	0.006132349	Mast_cells	BRD4	down
G6PC3	1.31E-09	-0.322469127	0.138	0.375	6.84E-05	Mast_cells	G6PC3	down
FLRT2	8.53E-14	-0.322644508	0.083	0.33	4.46E-09	Mast_cells	FLRT2	down
MLXIP	7.24E-12	-0.323901743	0.131	0.409	3.79E-07	Mast_cells	MLXIP	down
RORB	1.31E-07	-0.324386348	0.15	0.375	0.006847811	Mast_cells	RORB	down
ZKSCAN1	6.21E-08	-0.324774239	0.199	0.443	0.003248929	Mast_cells	ZKSCAN1	down
NUCKS1	1.34E-07	-0.324843503	0.567	0.83	0.007036	Mast_cells	NUCKS1	down
PBX1	2.51E-06	-0.325233577	0.491	0.727	0.131296537	Mast_cells	PBX1	down
DBN1	3.09E-08	-0.325281254	0.165	0.398	0.001618307	Mast_cells	DBN1	down
LEF11	4.06E-18	-0.325298243	0.062	0.33	2.13E-13	Mast_cells	LEF1	down
SEMA5A	1.62E-11	-0.325535626	0.078	0.295	8.50E-07	Mast_cells	SEMA5A	down
RBFOX2	1.27E-10	-0.327279936	0.155	0.432	6.64E-06	Mast_cells	RBFOX2	down
STT3B	1.66E-08	-0.327467646	0.205	0.466	0.000868755	Mast_cells	STT3B	down
GLG1	1.31E-10	-0.328476016	0.137	0.398	6.84E-06	Mast_cells	GLG1	down
PTBP1	1.47E-06	-0.32853557	0.34	0.602	0.0767664	Mast_cells	PTBP1	down
CLMP	3.73E-12	-0.329712325	0.114	0.375	1.96E-07	Mast_cells	CLMP	down
GALNT2	6.85E-10	-0.329940615	0.12	0.352	3.58E-05	Mast_cells	GALNT2	down
CHMP4B	2.90E-07	-0.330170831	0.31	0.591	0.01520107	Mast_cells	CHMP4B	down
NDN	1.91E-07	-0.33063235	0.176	0.398	0.009997697	Mast_cells	NDN	down
IL6ST	1.75E-08	-0.332311924	0.217	0.477	0.000918718	Mast_cells	IL6ST	down
ATF4	2.88E-07	-0.333281503	0.437	0.727	0.01509647	Mast_cells	ATF4	down
RNF130	6.83E-07	-0.33366062	0.404	0.67	0.035769676	Mast_cells	RNF130	down
TAB2	4.42E-09	-0.334767505	0.177	0.443	0.00023167	Mast_cells	TAB2	down
TMED10	7.49E-07	-0.33504948	0.447	0.625	0.039227126	Mast_cells	TMED10	down
EMP1	3.70E-12	-0.335363342	0.069	0.284	1.94E-07	Mast_cells	EMP1	down
CHST14	5.31E-14	-0.336014757	0.09	0.352	2.78E-09	Mast_cells	CHST14	down
IGFBP7	1.74E-05	-0.336127208	0.343	0.568	0.910910803	Mast_cells	IGFBP7	down
ERGIC1	2.93E-10	-0.336348353	0.212	0.523	1.53E-05	Mast_cells	ERGIC1	down
AKT2	3.94E-09	-0.336995025	0.149	0.386	0.000206433	Mast_cells	AKT2	down
LENG8	1.39E-08	-0.338490499	0.225	0.511	0.00072914	Mast_cells	LENG8	down
RPL34P27	3.78E-14	-0.340402735	0.095	0.375	1.98E-09	Mast_cells	RPL34P27	down
TPP1	4.94E-07	-0.340501377	0.301	0.568	0.025845475	Mast_cells	TPP1	down
SND1	7.94E-09	-0.340591503	0.219	0.489	0.000415533	Mast_cells	SND1	down
ACO2	2.05E-09	-0.340963396	0.179	0.443	0.000107222	Mast_cells	ACO2	down
SCARB2	2.99E-09	-0.342531627	0.171	0.42	0.000156474	Mast_cells	SCARB2	down
LOXL2	1.27E-12	-0.344067264	0.073	0.295	6.66E-08	Mast_cells	LOXL2	down
YWHAE	1.54E-09	-0.344789478	0.649	0.875	8.06E-05	Mast_cells	YWHAE	down
DDR2	8.54E-10	-0.345692819	0.135	0.375	4.47E-05	Mast_cells	DDR2	down
RPL7P9	1.41E-12	-0.345886099	0.106	0.375	7.40E-08	Mast_cells	RPL7P9	down
ZBTB7A	1.27E-07	-0.346497946	0.303	0.568	0.006661604	Mast_cells	ZBTB7A	down
AL590867.2	6.65E-14	-0.346554542	0.084	0.341	3.48E-09	Mast_cells	AL590867.2	down
AMOTL2	5.50E-16	-0.346732472	0.064	0.307	2.88E-11	Mast_cells	AMOTL2	down
GANAB	2.83E-08	-0.346842979	0.201	0.443	0.001481643	Mast_cells	GANAB	down
SHFL	9.62E-09	-0.34685627	0.176	0.42	0.000503588	Mast_cells	SHFL	down
PDGFRA	2.51E-13	-0.347088835	0.112	0.386	1.32E-08	Mast_cells	PDGFRA	down
HDAC7	5.67E-13	-0.34736614	0.107	0.375	2.97E-08	Mast_cells	HDAC7	down
SPTLC2	1.00E-10	-0.347910173	0.138	0.398	5.25E-06	Mast_cells	SPTLC2	down

ATXN1	1.96E-08	-0.348995006	0.26	0.557	0.001023623	Mast_cells	ATXN1	down
PCBP2	8.54E-08	-0.349089684	0.535	0.761	0.004473202	Mast_cells	PCBP2	down
CALU	8.93E-07	-0.349203475	0.355	0.602	0.046751726	Mast_cells	CALU	down
SRF	1.16E-10	-0.349825829	0.113	0.352	6.09E-06	Mast_cells	SRF	down
ADAM121	1.60E-06	-0.350055035	0.245	0.455	0.08401966	Mast_cells	ADAM12	down
OLFM1	7.74E-12	-0.350296998	0.101	0.341	4.05E-07	Mast_cells	OLFM1	down
SSBP3	6.62E-07	-0.351121598	0.289	0.534	0.034642468	Mast_cells	SSBP3	down
SMARCA2	6.74E-08	-0.351482822	0.246	0.511	0.003527851	Mast_cells	SMARCA2	down
ZFP362	4.49E-08	-0.35335048	0.76	0.898	0.002350554	Mast_cells	ZFP36	down
GPX8	1.92E-12	-0.354057752	0.125	0.398	1.00E-07	Mast_cells	GPX8	down
MT-ND4L	1.93E-13	-0.354275161	0.855	0.977	1.01E-08	Mast_cells	MT-ND4L	down
ATXN2L	2.42E-08	-0.354329928	0.238	0.511	0.001268824	Mast_cells	ATXN2L	down
RPL31	1.57E-16	-0.354575224	0.894	0.989	8.24E-12	Mast_cells	RPL31	down
IL321	1.21E-12	-0.354875433	0.096	0.352	6.36E-08	Mast_cells	IL32	down
SULF2	3.29E-10	-0.356338363	0.151	0.409	1.72E-05	Mast_cells	SULF2	down
ATN1	2.07E-08	-0.357224301	0.239	0.523	0.001081385	Mast_cells	ATN1	down
PRRX1	2.56E-11	-0.358676922	0.148	0.432	1.34E-06	Mast_cells	PRRX1	down
PRRC2B	1.15E-09	-0.358845823	0.215	0.5	6.04E-05	Mast_cells	PRRC2B	down
HAND2-AS1	5.39E-15	-0.359568632	0.111	0.409	2.82E-10	Mast_cells	HAND2-AS1	down
ESR1	8.57E-10	-0.359618558	0.188	0.466	4.49E-05	Mast_cells	ESR1	down
WNT2	3.12E-13	-0.360176262	0.104	0.364	1.63E-08	Mast_cells	WNT2	down
KDELR1	1.37E-07	-0.360465202	0.443	0.716	0.007187458	Mast_cells	KDELR1	down
RBP12	9.45E-07	-0.36103698	0.189	0.398	0.049460953	Mast_cells	RBP1	down
MXRA7	1.60E-11	-0.361105303	0.152	0.432	8.39E-07	Mast_cells	MXRA7	down
RAB5B	1.36E-12	-0.361235756	0.166	0.489	7.15E-08	Mast_cells	RAB5B	down
PLOD1	8.02E-12	-0.363081378	0.138	0.409	4.20E-07	Mast_cells	PLOD1	down
FOXL2	1.91E-13	-0.364403977	0.097	0.352	1.00E-08	Mast_cells	FOXL2	down
PPIC	1.49E-12	-0.365013646	0.12	0.386	7.80E-08	Mast_cells	PPIC	down
ERRFI1	1.54E-13	-0.365151905	0.074	0.307	8.05E-09	Mast_cells	ERRFI1	down
LAMB1	3.36E-10	-0.368215587	0.106	0.33	1.76E-05	Mast_cells	LAMB1	down
MTRNR2L12	1.39E-14	-0.369403664	0.118	0.432	7.28E-10	Mast_cells	MTRNR2L12	down
AL031727.1	2.28E-16	-0.370555462	0.067	0.33	1.20E-11	Mast_cells	AL031727.1	down
MAP4	1.34E-08	-0.370627619	0.251	0.511	0.000701682	Mast_cells	MAP4	down
HIC1	1.00E-09	-0.370694469	0.162	0.42	5.26E-05	Mast_cells	HIC1	down
CAPNS1	3.73E-08	-0.372256936	0.433	0.705	0.001951432	Mast_cells	CAPNS1	down
PENK	1.59E-13	-0.372992575	0.049	0.25	8.34E-09	Mast_cells	PENK	down
TRIB1	1.25E-10	-0.373354409	0.103	0.33	6.56E-06	Mast_cells	TRIB1	down
SYNCRIP	3.90E-09	-0.373372491	0.335	0.648	0.000204076	Mast_cells	SYNCRIP	down
PMEPA1	1.08E-06	-0.373507637	0.392	0.614	0.056604476	Mast_cells	PMEPA1	down
MTCO1P12	2.20E-18	-0.373571169	0.076	0.375	1.15E-13	Mast_cells	MTCO1P12	down
ZNF516	8.85E-12	-0.373696057	0.134	0.398	4.63E-07	Mast_cells	ZNF516	down
CRTAP	2.45E-07	-0.373750622	0.379	0.625	0.012847767	Mast_cells	CRTAP	down
PAMR1	6.20E-10	-0.373759184	0.126	0.364	3.25E-05	Mast_cells	PAMR1	down
MFAP2	3.71E-11	-0.374351619	0.147	0.42	1.94E-06	Mast_cells	MFAP2	down
COL27A1	7.99E-10	-0.374422147	0.137	0.375	4.19E-05	Mast_cells	COL27A1	down
BTBD2	5.45E-15	-0.374711084	0.113	0.409	2.86E-10	Mast_cells	BTBD2	down
RCN1	5.41E-09	-0.375096373	0.209	0.466	0.000283401	Mast_cells	RCN1	down
SSR3	1.13E-07	-0.375312384	0.449	0.716	0.005940912	Mast_cells	SSR3	down
BEX3	1.59E-08	-0.375326439	0.244	0.523	0.000832733	Mast_cells	BEX3	down
H1F0	7.20E-10	-0.375558086	0.214	0.511	3.77E-05	Mast_cells	H1F0	down
AC116533.1	3.16E-13	-0.37850405	0.14	0.455	1.66E-08	Mast_cells	AC116533.1	down

FSCN1	2.36E-10	-0.378979637	0.171	0.443	1.24E-05	Mast_cells	FSCN1	down
DAB2	8.70E-09	-0.380337304	0.205	0.455	0.000455503	Mast_cells	DAB2	down
SLC38A2	8.44E-08	-0.3816798	0.323	0.58	0.004418513	Mast_cells	SLC38A2	down
GJA1	8.88E-09	-0.38239662	0.157	0.386	0.000465186	Mast_cells	GJA1	down
CLIC4	4.51E-13	-0.382659419	0.148	0.443	2.36E-08	Mast_cells	CLIC4	down
CDC42EP4	8.52E-10	-0.384169086	0.161	0.409	4.46E-05	Mast_cells	CDC42EP4	down
LTBP1	4.38E-13	-0.384284826	0.137	0.432	2.29E-08	Mast_cells	LTBP1	down
MYL9	6.05E-09	-0.384653845	0.186	0.443	0.00031672	Mast_cells	MYL9	down
U2AF2	7.00E-11	-0.385824961	0.249	0.591	3.66E-06	Mast_cells	U2AF2	down
SPIN1	1.13E-10	-0.386182764	0.232	0.545	5.93E-06	Mast_cells	SPIN1	down
CREB3L1	3.12E-13	-0.386940659	0.104	0.364	1.63E-08	Mast_cells	CREB3L1	down
CHSY1	6.30E-13	-0.38712777	0.144	0.443	3.30E-08	Mast_cells	CHSY1	down
OSR2	2.61E-09	-0.391110431	0.168	0.42	0.000136433	Mast_cells	OSR2	down
IMPAD1	2.39E-12	-0.391306669	0.14	0.42	1.25E-07	Mast_cells	IMPAD1	down
AC243919.1	1.18E-19	-0.39147637	0.056	0.33	6.16E-15	Mast_cells	AC243919.1	down
CNN2	1.19E-10	-0.393593975	0.296	0.67	6.22E-06	Mast_cells	CNN2	down
ITGB1	6.90E-08	-0.394800538	0.404	0.659	0.003615075	Mast_cells	ITGB1	down
OS9	2.38E-09	-0.39625149	0.352	0.659	0.000124479	Mast_cells	OS9	down
TPM4	4.44E-10	-0.397052776	0.612	0.795	2.33E-05	Mast_cells	TPM4	down
KPNB1	2.21E-09	-0.397570333	0.3	0.591	0.000115586	Mast_cells	KPNB1	down
GASK1B	8.82E-13	-0.398302534	0.124	0.398	4.62E-08	Mast_cells	GASK1B	down
SH3PXD2A	9.74E-12	-0.399436532	0.187	0.5	5.10E-07	Mast_cells	SH3PXD2A	down
ITGA6	1.05E-12	-0.399798474	0.108	0.364	5.51E-08	Mast_cells	ITGA6	down
RAB31	1.33E-12	-0.400817124	0.119	0.386	6.99E-08	Mast_cells	RAB31	down
PTCH1	2.87E-11	-0.404380698	0.168	0.455	1.50E-06	Mast_cells	PTCH1	down
C1S	2.58E-11	-0.404495871	0.168	0.455	1.35E-06	Mast_cells	C1S	down
RAI14	1.56E-13	-0.404989708	0.141	0.443	8.17E-09	Mast_cells	RAI14	down
SDK11	4.84E-17	-0.407884572	0.091	0.386	2.53E-12	Mast_cells	SDK1	down
WNT5A1	6.35E-15	-0.408623349	0.094	0.364	3.32E-10	Mast_cells	WNT5A	down
FLNA	3.10E-10	-0.410831007	0.283	0.602	1.62E-05	Mast_cells	FLNA	down
MME	9.41E-16	-0.411974366	0.094	0.375	4.93E-11	Mast_cells	MME	down
PLPP1	4.30E-09	-0.412456521	0.294	0.591	0.000225403	Mast_cells	PLPP1	down
IFI61	5.53E-10	-0.412668985	0.246	0.557	2.90E-05	Mast_cells	IFI6	down
APCDD12	9.89E-12	-0.412889267	0.116	0.364	5.18E-07	Mast_cells	APCDD1	down
CKAP4	2.65E-10	-0.413201109	0.184	0.455	1.39E-05	Mast_cells	CKAP4	down
HNRNPUL1	4.43E-11	-0.41320559	0.289	0.648	2.32E-06	Mast_cells	HNRNPUL1	down
TCF12	5.09E-13	-0.413912844	0.162	0.466	2.67E-08	Mast_cells	TCF12	down
TBX3	1.08E-14	-0.414275321	0.145	0.466	5.64E-10	Mast_cells	TBX3	down
RPL6P27	3.08E-17	-0.414984229	0.087	0.386	1.61E-12	Mast_cells	RPL6P27	down
ANXA2	3.07E-10	-0.416724411	0.244	0.534	1.61E-05	Mast_cells	ANXA2	down
CALD1	5.87E-10	-0.419429411	0.234	0.534	3.07E-05	Mast_cells	CALD1	down
EIF4G2	9.80E-13	-0.420170415	0.597	0.875	5.13E-08	Mast_cells	EIF4G2	down
EWSR1	1.16E-10	-0.42045889	0.306	0.636	6.10E-06	Mast_cells	EWSR1	down
RYBP	8.78E-10	-0.42075844	0.377	0.716	4.60E-05	Mast_cells	RYBP	down
RPL37P6	5.57E-25	-0.421546105	0.05	0.352	2.92E-20	Mast_cells	RPL37P6	down
KLF42	2.24E-08	-0.421612196	0.403	0.693	0.001172165	Mast_cells	KLF4	down
MARCKSL1	3.38E-08	-0.422074904	0.356	0.614	0.001770014	Mast_cells	MARCKSL1	down
HDLBP	1.01E-09	-0.422773776	0.383	0.67	5.31E-05	Mast_cells	HDLBP	down
PRSS231	2.74E-10	-0.422855285	0.192	0.477	1.43E-05	Mast_cells	PRSS23	down
FBLN11	6.97E-07	-0.423471564	0.332	0.557	0.036509022	Mast_cells	FBLN1	down
PSAP	5.26E-14	-0.423503977	0.714	0.955	2.75E-09	Mast_cells	PSAP	down

MYH9	7.07E-10	-0.4251328	0.326	0.625	3.70E-05	Mast_cells	MYH9	down
ATP2A2	5.15E-11	-0.426758232	0.282	0.625	2.69E-06	Mast_cells	ATP2A2	down
COL7A1	5.74E-12	-0.427602002	0.13	0.398	3.01E-07	Mast_cells	COL7A1	down
CDK2AP1	1.45E-10	-0.427930668	0.272	0.58	7.59E-06	Mast_cells	CDK2AP1	down
TUG1	1.16E-12	-0.430135499	0.213	0.545	6.08E-08	Mast_cells	TUG1	down
VCL	3.92E-13	-0.431433868	0.19	0.511	2.05E-08	Mast_cells	VCL	down
PTMS	2.62E-09	-0.435906189	0.493	0.693	0.000137425	Mast_cells	PTMS	down
GLIPR11	4.09E-14	-0.439354137	0.098	0.364	2.14E-09	Mast_cells	GLIPR1	down
TTC3	5.07E-10	-0.442967483	0.345	0.648	2.66E-05	Mast_cells	TTC3	down
ZNF704	3.73E-11	-0.446403249	0.188	0.466	1.95E-06	Mast_cells	ZNF704	down
SOCS32	2.80E-09	-0.447068775	0.217	0.5	0.000146771	Mast_cells	SOCS3	down
LUM	3.69E-10	-0.451819808	0.215	0.511	1.93E-05	Mast_cells	LUM	down
CCND2	6.21E-11	-0.452794497	0.295	0.625	3.25E-06	Mast_cells	CCND2	down
RPL3P4	1.63E-19	-0.45331721	0.107	0.455	8.52E-15	Mast_cells	RPL3P4	down
MAGED1	1.52E-12	-0.454141795	0.181	0.489	7.94E-08	Mast_cells	MAGED1	down
RPL26P191	1.61E-16	-0.454212882	0.143	0.5	8.44E-12	Mast_cells	RPL26P19	down
GNB1	3.26E-11	-0.45588357	0.422	0.773	1.71E-06	Mast_cells	GNB1	down
MIR1244-2	6.79E-15	-0.456071731	0.171	0.534	3.56E-10	Mast_cells	MIR1244-2	down
ANTXR1	4.00E-17	-0.456361731	0.106	0.409	2.10E-12	Mast_cells	ANTXR1	down
PCSK51	7.29E-16	-0.456984653	0.111	0.409	3.82E-11	Mast_cells	PCSK5	down
F13A11	2.27E-18	-0.457918671	0.06	0.318	1.19E-13	Mast_cells	F13A1	down
CALR	3.21E-14	-0.460081843	0.634	0.898	1.68E-09	Mast_cells	CALR	down
CTDSP2	2.86E-15	-0.460581735	0.165	0.5	1.50E-10	Mast_cells	CTDSP2	down
MAP3K20	6.23E-12	-0.460756581	0.176	0.466	3.26E-07	Mast_cells	MAP3K20	down
TCF4	4.89E-11	-0.462113148	0.211	0.511	2.56E-06	Mast_cells	TCF4	down
TWIST2	8.37E-14	-0.463067401	0.137	0.432	4.38E-09	Mast_cells	TWIST2	down
SEC31A	2.49E-12	-0.466461782	0.341	0.705	1.31E-07	Mast_cells	SEC31A	down
NID1	1.19E-17	-0.471191323	0.123	0.455	6.24E-13	Mast_cells	NID1	down
HOXA10	5.23E-15	-0.471925409	0.197	0.568	2.74E-10	Mast_cells	HOXA10	down
RPL15P3	8.71E-20	-0.472945706	0.081	0.398	4.56E-15	Mast_cells	RPL15P3	down
MARCKS1	5.13E-11	-0.474755159	0.216	0.511	2.69E-06	Mast_cells	MARCKS	down
CAVIN1	2.76E-11	-0.480110495	0.381	0.682	1.44E-06	Mast_cells	CAVIN1	down
FBN1	1.43E-17	-0.480715421	0.137	0.477	7.50E-13	Mast_cells	FBN1	down
IGFBP4	5.36E-09	-0.481978028	0.253	0.511	0.00028074	Mast_cells	IGFBP4	down
UBA1	7.58E-16	-0.482341846	0.237	0.648	3.97E-11	Mast_cells	UBA1	down
NFIC	4.12E-11	-0.483249205	0.321	0.636	2.15E-06	Mast_cells	NFIC	down
AC007969.1	2.28E-23	-0.484167766	0.08	0.432	1.19E-18	Mast_cells	AC007969.1	down
PGR1	3.09E-13	-0.484317096	0.202	0.523	1.62E-08	Mast_cells	PGR	down
HDGF	2.36E-14	-0.485448057	0.234	0.591	1.24E-09	Mast_cells	HDGF	down
GDF7	1.54E-15	-0.485570594	0.138	0.455	8.08E-11	Mast_cells	GDF7	down
ZFP36L1	1.80E-10	-0.485747347	0.527	0.795	9.44E-06	Mast_cells	ZFP36L1	down
PXDN	1.59E-18	-0.488633271	0.111	0.432	8.31E-14	Mast_cells	PXDN	down
PIM1	4.58E-10	-0.490331074	0.203	0.466	2.40E-05	Mast_cells	PIM1	down
PALLD	3.58E-11	-0.492113715	0.301	0.625	1.88E-06	Mast_cells	PALLD	down
MMP14	3.57E-14	-0.492133751	0.162	0.489	1.87E-09	Mast_cells	MMP14	down
LGALS3BP	1.39E-11	-0.492746362	0.203	0.489	7.26E-07	Mast_cells	LGALS3BP	down
FN11	1.06E-15	-0.496490959	0.156	0.5	5.55E-11	Mast_cells	FN1	down
KHSRP	2.08E-14	-0.500966221	0.207	0.557	1.09E-09	Mast_cells	KHSRP	down
AL022718.1	1.58E-26	-0.501600698	0.063	0.409	8.26E-22	Mast_cells	AL022718.1	down
MATR31	1.58E-15	-0.502042549	0.193	0.591	8.29E-11	Mast_cells	MATR3	down
SIGLEC17P	2.08E-14	-0.504760421	0.237	0.659	1.09E-09	Mast_cells	SIGLEC17P	down

APP	6.24E-13	-0.506488117	0.194	0.5	3.27E-08	Mast_cells	APP	down
COL4A2	1.58E-15	-0.506999148	0.185	0.534	8.27E-11	Mast_cells	COL4A2	down
MGP3	1.12E-07	-0.509942039	0.227	0.455	0.005883726	Mast_cells	MGP	down
SDC2	8.22E-18	-0.517253838	0.121	0.443	4.30E-13	Mast_cells	SDC2	down
SPARCL1	3.57E-10	-0.523477532	0.268	0.568	1.87E-05	Mast_cells	SPARCL1	down
USP22	2.09E-15	-0.530823006	0.26	0.636	1.09E-10	Mast_cells	USP22	down
RTL8C	1.59E-16	-0.532589912	0.232	0.625	8.31E-12	Mast_cells	RTL8C	down
VCAN3	2.71E-14	-0.537710535	0.182	0.523	1.42E-09	Mast_cells	VCAN	down
C11orf961	3.72E-10	-0.54005638	0.219	0.5	1.95E-05	Mast_cells	C11orf96	down
H19	1.15E-11	-0.543136334	0.19	0.477	6.01E-07	Mast_cells	H19	down
C1R	7.09E-17	-0.544896424	0.177	0.534	3.71E-12	Mast_cells	C1R	down
CDH11	5.38E-16	-0.545938183	0.187	0.534	2.82E-11	Mast_cells	CDH11	down
EDNRA	1.32E-14	-0.547365225	0.163	0.477	6.91E-10	Mast_cells	EDNRA	down
COL14A1	3.41E-15	-0.550272961	0.174	0.511	1.79E-10	Mast_cells	COL14A1	down
OLFML3	3.08E-17	-0.55031253	0.172	0.534	1.61E-12	Mast_cells	OLFML3	down
CNN31	1.61E-15	-0.553082636	0.182	0.523	8.44E-11	Mast_cells	CNN3	down
PCOLCE	1.28E-13	-0.554112516	0.231	0.568	6.73E-09	Mast_cells	PCOLCE	down
COL6A2	6.85E-14	-0.556188384	0.248	0.591	3.58E-09	Mast_cells	COL6A2	down
RHOB1	3.82E-10	-0.557721653	0.384	0.659	2.00E-05	Mast_cells	RHOB	down
OAF	8.57E-15	-0.558228242	0.279	0.636	4.48E-10	Mast_cells	OAF	down
MDK	3.57E-10	-0.563285726	0.345	0.614	1.87E-05	Mast_cells	MDK	down
ZYX	3.00E-13	-0.566670296	0.272	0.58	1.57E-08	Mast_cells	ZYX	down
IRF2BP2	1.28E-14	-0.56723429	0.43	0.784	6.70E-10	Mast_cells	IRF2BP2	down
PGRMC1	3.37E-13	-0.576261851	0.288	0.625	1.77E-08	Mast_cells	PGRMC1	down
TGFBI2	2.07E-22	-0.589986194	0.136	0.534	1.09E-17	Mast_cells	TGFBI	down
THY1	2.31E-13	-0.590183305	0.22	0.545	1.21E-08	Mast_cells	THY1	down
IGFBP51	2.87E-08	-0.595356569	0.301	0.545	0.001502045	Mast_cells	IGFBP5	down
FSTL1	3.78E-18	-0.599326619	0.193	0.568	1.98E-13	Mast_cells	FSTL1	down
MMP2	1.88E-17	-0.606538957	0.205	0.602	9.85E-13	Mast_cells	MMP2	down
DCN1	4.60E-16	-0.606896297	0.206	0.557	2.41E-11	Mast_cells	DCN	down
COL6A3	5.81E-19	-0.608836447	0.18	0.568	3.04E-14	Mast_cells	COL6A3	down
ALDH1A2	5.82E-17	-0.61504784	0.164	0.5	3.05E-12	Mast_cells	ALDH1A2	down
AP001324.1	4.66E-34	-0.617194159	0.069	0.477	2.44E-29	Mast_cells	AP001324.1	down
CPXM1	1.71E-18	-0.629520731	0.199	0.58	8.94E-14	Mast_cells	CPXM1	down
MTND1P231	4.84E-20	-0.639203871	0.163	0.568	2.53E-15	Mast_cells	MTND1P23	down
SPON2	3.16E-19	-0.640974581	0.187	0.568	1.66E-14	Mast_cells	SPON2	down
CD241	1.01E-16	-0.647022843	0.202	0.557	5.28E-12	Mast_cells	CD24	down
SFRP1	4.10E-13	-0.658303825	0.26	0.591	2.15E-08	Mast_cells	SFRP1	down
TIMP2	4.28E-19	-0.669105286	0.212	0.602	2.24E-14	Mast_cells	TIMP2	down
NR2F2	6.36E-16	-0.671889043	0.259	0.625	3.33E-11	Mast_cells	NR2F2	down
CRABP2	9.85E-21	-0.674472549	0.165	0.557	5.15E-16	Mast_cells	CRABP2	down
SERPINH11	1.04E-17	-0.675029777	0.21	0.58	5.45E-13	Mast_cells	SERPINH1	down
ISLR	1.11E-18	-0.698169855	0.196	0.58	5.80E-14	Mast_cells	ISLR	down
COL5A1	1.13E-15	-0.703550909	0.239	0.58	5.90E-11	Mast_cells	COL5A1	down
ECM14	4.04E-21	-0.703863952	0.181	0.591	2.11E-16	Mast_cells	ECM1	down
COL5A2	1.22E-22	-0.705125465	0.167	0.58	6.40E-18	Mast_cells	COL5A2	down
OGN1	1.09E-21	-0.736951553	0.153	0.534	5.68E-17	Mast_cells	OGN	down
DIO23	2.00E-17	-0.737543797	0.187	0.557	1.05E-12	Mast_cells	DIO2	down
MT-ATP81	5.13E-20	-0.74156612	0.391	0.807	2.68E-15	Mast_cells	MT-ATP8	down
COL6A11	2.22E-18	-0.748873874	0.26	0.648	1.16E-13	Mast_cells	COL6A1	down
MMP111	2.12E-15	-0.760899733	0.239	0.58	1.11E-10	Mast_cells	MMP11	down

SFRP43	3.36E-12	-0.763150146	0.501	0.739	1.76E-07	Mast_cells	SFRP4	down
NREP2	1.24E-23	-0.788150734	0.223	0.659	6.49E-19	Mast_cells	NREP	down
COL1A2	5.84E-17	-0.802074847	0.432	0.784	3.06E-12	Mast_cells	COL1A2	down
SPARC1	8.06E-16	-0.823842149	0.334	0.67	4.22E-11	Mast_cells	SPARC	down
IGF11	5.98E-18	-0.829965275	0.268	0.648	3.13E-13	Mast_cells	IGF1	down
MTATP6P12	4.32E-20	-0.834021712	0.304	0.795	2.26E-15	Mast_cells	MTATP6P1	down
MT-RNR12	1.95E-19	-0.87648487	0.315	0.807	1.02E-14	Mast_cells	MT-RNR1	down
COL1A11	3.53E-19	-0.904405832	0.514	0.864	1.85E-14	Mast_cells	COL1A1	down
COL3A13	1.51E-24	-0.962218181	0.485	0.92	7.93E-20	Mast_cells	COL3A1	down
MT-RNR22	4.01E-17	-0.966083104	0.315	0.807	2.10E-12	Mast_cells	MT-RNR2	down
CCND11	1.90E-271	0.640852415	0.548	0.111	9.96E-267	mit_Fibro	CCND1	up
IGFBP61	2.93E-126	0.585931727	0.46	0.181	1.53E-121	mit_Fibro	IGFBP6	up
PLAC91	1.03E-110	0.442078187	0.439	0.182	5.40E-106	mit_Fibro	PLAC9	up
CDKN1A2	3.39E-86	0.387207999	0.6	0.327	1.78E-81	mit_Fibro	CDKN1A	up
SCGB2A16	9.26E-187	0.378774039	0.465	0.106	4.85E-182	mit_Fibro	SCGB2A1	up
GDF152	1.79E-99	0.353809496	0.367	0.12	9.38E-95	mit_Fibro	GDF15	up
WFDC26	6.44E-81	0.317228785	0.461	0.227	3.37E-76	mit_Fibro	WFDC2	up
ANXA1	1.30E-67	0.317085663	0.662	0.433	6.79E-63	mit_Fibro	ANXA1	up
BGN	1.19E-65	0.310270399	0.615	0.43	6.25E-61	mit_Fibro	BGN	up
HSPB62	1.99E-57	0.300658956	0.753	0.586	1.04E-52	mit_Fibro	HSPB6	up
SOCS33	2.26E-29	0.298793306	0.673	0.549	1.18E-24	mit_Fibro	SOCS3	up
APOE1	4.10E-40	0.292414269	0.741	0.642	2.14E-35	mit_Fibro	APOE	up
HMGA11	1.01E-52	0.287781674	0.267	0.108	5.30E-48	mit_Fibro	HMGA1	up
GPNMB1	5.36E-72	0.274568625	0.549	0.309	2.81E-67	mit_Fibro	GPNMB	up
NKAIN41	9.38E-190	0.271485544	0.263	0.009	4.91E-185	mit_Fibro	NKAIN4	up
COL18A11	5.16E-67	0.266274288	0.506	0.277	2.70E-62	mit_Fibro	COL18A1	up
ZMAT31	3.20E-66	0.265299376	0.507	0.273	1.68E-61	mit_Fibro	ZMAT3	up
LOXL1	5.76E-72	0.262089667	0.523	0.29	3.02E-67	mit_Fibro	LOXL1	up
RPS27L	2.74E-68	0.259614738	0.814	0.703	1.44E-63	mit_Fibro	RPS27L	up
TIMP32	5.27E-54	0.258515729	0.711	0.512	2.76E-49	mit_Fibro	TIMP3	up
FXYD61	1.76E-65	0.257862426	0.54	0.318	9.22E-61	mit_Fibro	FXYD6	up
S100A42	1.65E-58	0.25407323	0.424	0.222	8.65E-54	mit_Fibro	S100A4	up
CLU3	7.18E-46	0.250544984	0.57	0.407	3.76E-41	mit_Fibro	CLU	up
S100A61	5.77E-61	0.250057249	0.865	0.796	3.02E-56	mit_Fibro	S100A6	up
OGN2	2.08E-45	-0.261412445	0.594	0.762	1.09E-40	mit_Fibro	OGN	down
IL322	7.99E-44	-0.27052503	0.389	0.565	4.19E-39	mit_Fibro	IL32	down
F13A12	3.30E-52	-0.277377718	0.509	0.698	1.73E-47	mit_Fibro	F13A1	down
TNC2	6.29E-49	-0.289040527	0.501	0.665	3.29E-44	mit_Fibro	TNC	down
SCGB2A17	8.30E-269	0.662104335	0.413	0.058	4.35E-264	NK_cells	SCGB2A1	up
WFDC27	4.52E-210	0.648777682	0.468	0.142	2.37E-205	NK_cells	WFDC2	up
MT2A2	2.40E-31	0.432363158	0.412	0.315	1.26E-26	NK_cells	MT2A	up
MT1X2	6.21E-39	0.421247452	0.274	0.161	3.25E-34	NK_cells	MT1X	up
CXCR4	1.42E-109	0.414073179	0.723	0.504	7.43E-105	NK_cells	CXCR4	up
SCGB1D22	4.58E-126	0.350011596	0.225	0.033	2.40E-121	NK_cells	SCGB1D2	up
IGFBP52	1.79E-42	0.345443534	0.361	0.227	9.35E-38	NK_cells	IGFBP5	up
ITM2C	1.96E-65	0.333252465	0.493	0.311	1.03E-60	NK_cells	ITM2C	up
CLU4	1.94E-77	0.324685996	0.256	0.095	1.02E-72	NK_cells	CLU	up
LMNA1	3.86E-48	0.284757955	0.488	0.353	2.02E-43	NK_cells	LMNA	up
GNG2	3.70E-50	0.273219457	0.351	0.202	1.94E-45	NK_cells	GNG2	up
CAPS	2.62E-74	0.271154674	0.245	0.086	1.37E-69	NK_cells	CAPS	up
FBLN12	5.33E-31	0.265329371	0.413	0.31	2.79E-26	NK_cells	FBLN1	up

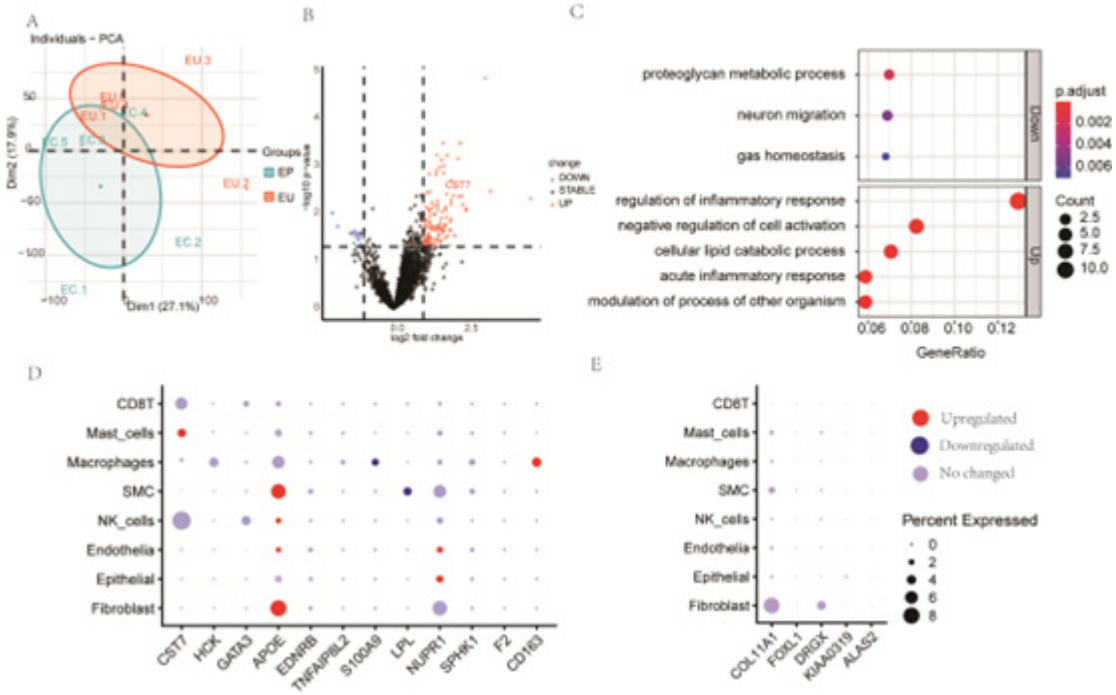
EZR	1.34E-69	0.264204238	0.788	0.671	7.04E-65	NK_cells	EZR	up
PAEP1	3.63E-91	0.251920764	0.124	0.004	1.90E-86	NK_cells	PAEP	up
SYTL3	7.88E-47	-0.250320936	0.307	0.474	4.13E-42	NK_cells	SYTL3	down
RBP13	4.61E-39	-0.251522089	0.214	0.342	2.41E-34	NK_cells	RBP1	down
TMIGD2	3.93E-49	-0.253194603	0.316	0.485	2.06E-44	NK_cells	TMIGD2	down
DAPK2	7.36E-65	-0.254983767	0.122	0.289	3.85E-60	NK_cells	DAPK2	down
CD38	1.30E-56	-0.263410087	0.283	0.475	6.81E-52	NK_cells	CD38	down
RNF1301	1.26E-65	-0.268117873	0.246	0.428	6.61E-61	NK_cells	RNF130	down
LINC00996	1.23E-74	-0.276035438	0.116	0.294	6.42E-70	NK_cells	LINC00996	down
CMC1	3.23E-58	-0.281631464	0.514	0.678	1.69E-53	NK_cells	CMC1	down
FCER1G1	8.36E-83	-0.289587848	0.623	0.783	4.38E-78	NK_cells	FCER1G	down
TRDC	4.99E-79	-0.292019339	0.607	0.759	2.61E-74	NK_cells	TRDC	down
NCAM1	1.93E-65	-0.293767781	0.345	0.559	1.01E-60	NK_cells	NCAM1	down
KIR2DL3	2.32E-83	-0.293875704	0.079	0.249	1.22E-78	NK_cells	KIR2DL3	down
CCL3	2.67E-38	-0.295896978	0.427	0.552	1.40E-33	NK_cells	CCL3	down
EPAS1	3.20E-67	-0.300311821	0.276	0.471	1.67E-62	NK_cells	EPAS1	down
KIR2DL4	1.99E-79	-0.3199576	0.153	0.345	1.04E-74	NK_cells	KIR2DL4	down
ECM15	1.28E-56	-0.339918195	0.19	0.339	6.69E-52	NK_cells	ECM1	down
ITGAX	5.10E-83	-0.348461095	0.246	0.481	2.67E-78	NK_cells	ITGAX	down
COTL1	3.70E-114	-0.379873696	0.603	0.803	1.94E-109	NK_cells	COTL1	down
GZMB	4.28E-118	-0.499115035	0.344	0.607	2.24E-113	NK_cells	GZMB	down
GNLY2	2.28E-152	-0.62962152	0.463	0.713	1.19E-147	NK_cells	GNLY	down
ADIRF1	6.84E-80	0.571275386	0.711	0.336	3.58E-75	SMC	ADIRF	up
PTGDS	1.35E-44	0.563886143	0.532	0.303	7.09E-40	SMC	PTGDS	up
MT2A3	3.36E-72	0.540267635	0.846	0.634	1.76E-67	SMC	MT2A	up
BTG22	4.16E-85	0.522278884	0.799	0.514	2.18E-80	SMC	BTG2	up
ATF32	2.95E-77	0.510354775	0.834	0.639	1.54E-72	SMC	ATF3	up
CKB1	9.11E-82	0.509568703	0.803	0.535	4.77E-77	SMC	CKB	up
MT1E1	9.02E-60	0.48769541	0.473	0.191	4.72E-55	SMC	MT1E	up
COL14A11	2.07E-74	0.478870208	0.766	0.463	1.08E-69	SMC	COL14A1	up
SOCS34	2.52E-72	0.477925822	0.835	0.603	1.32E-67	SMC	SOCS3	up
CDKN1A3	1.81E-66	0.457471854	0.603	0.282	9.47E-62	SMC	CDKN1A	up
CFD1	4.49E-71	0.447770979	0.353	0.061	2.35E-66	SMC	CFD	up
FXYD1	8.51E-69	0.441094846	0.615	0.291	4.46E-64	SMC	FXYD1	up
EPHA7	5.17E-64	0.438708269	0.35	0.077	2.71E-59	SMC	EPHA7	up
PTN1	7.07E-52	0.428351124	0.657	0.403	3.70E-47	SMC	PTN	up
KLF22	1.43E-59	0.426711316	0.659	0.384	7.50E-55	SMC	KLF2	up
S100A62	1.10E-51	0.416189173	0.799	0.632	5.75E-47	SMC	S100A6	up
S100A43	5.96E-44	0.415643354	0.68	0.442	3.12E-39	SMC	S100A4	up
CCL22	3.15E-34	0.410835218	0.436	0.217	1.65E-29	SMC	CCL2	up
NR4A11	2.64E-50	0.406349503	0.782	0.578	1.38E-45	SMC	NR4A1	up
SCGB2A18	2.17E-82	0.401415315	0.453	0.108	1.14E-77	SMC	SCGB2A1	up
HSPA1B2	1.38E-49	0.398991715	0.771	0.521	7.23E-45	SMC	HSPA1B	up
TGM22	8.56E-44	0.392587256	0.532	0.299	4.48E-39	SMC	TGM2	up
DNAJB12	2.91E-65	0.392244079	0.879	0.758	1.52E-60	SMC	DNAJB1	up
WFDC28	1.75E-59	0.376394405	0.532	0.229	9.18E-55	SMC	WFDC2	up
PLAC92	5.20E-45	0.372885903	0.655	0.436	2.72E-40	SMC	PLAC9	up
MFAP4	1.37E-66	0.365309358	0.372	0.083	7.16E-62	SMC	MFAP4	up
HSPA1A2	7.78E-53	0.358084568	0.906	0.788	4.07E-48	SMC	HSPA1A	up
GADD45B1	1.36E-38	0.357106328	0.799	0.66	7.12E-34	SMC	GADD45B	up
MYC	6.47E-41	0.353428142	0.681	0.459	3.39E-36	SMC	MYC	up

EPAS11	6.26E-51	0.352881861	0.734	0.483	3.28E-46	SMC	EPAS1	up
CEBPD	2.25E-45	0.348218621	0.814	0.697	1.18E-40	SMC	CEBPD	up
IRF11	4.71E-43	0.346183013	0.811	0.665	2.47E-38	SMC	IRF1	up
MAFF2	2.36E-45	0.341293016	0.73	0.527	1.24E-40	SMC	MAFF	up
GAS6	1.51E-54	0.340789747	0.774	0.562	7.89E-50	SMC	GAS6	up
MSX12	2.83E-50	0.335525216	0.465	0.19	1.48E-45	SMC	MSX1	up
ZFP363	2.04E-44	0.334752191	0.865	0.749	1.07E-39	SMC	ZFP36	up
FOSB1	1.85E-55	0.334169298	0.93	0.817	9.70E-51	SMC	FOSB	up
MUSTN1	2.82E-30	0.332145954	0.314	0.127	1.47E-25	SMC	MUSTN1	up
TIPARP1	3.62E-35	0.331450163	0.584	0.376	1.90E-30	SMC	TIPARP	up
SLIT3	5.25E-43	0.328996973	0.689	0.409	2.75E-38	SMC	SLIT3	up
DUSP11	2.58E-43	0.324989653	0.796	0.665	1.35E-38	SMC	DUSP1	up
CLU5	2.52E-67	0.324493586	0.358	0.072	1.32E-62	SMC	CLU	up
HSPB63	3.83E-38	0.315996751	0.53	0.292	2.01E-33	SMC	HSPB6	up
RGS16	8.48E-29	0.314252735	0.727	0.553	4.44E-24	SMC	RGS16	up
CRISPLD21	1.42E-36	0.312899056	0.703	0.507	7.45E-32	SMC	CRISPLD2	up
LITAF	7.69E-45	0.309429412	0.751	0.572	4.02E-40	SMC	LITAF	up
KLF43	2.44E-40	0.305510094	0.447	0.205	1.28E-35	SMC	KLF4	up
CD92	5.74E-41	0.305397315	0.316	0.102	3.00E-36	SMC	CD9	up
SERTAD11	4.73E-40	0.301567618	0.739	0.604	2.48E-35	SMC	SERTAD1	up
MT1X3	3.57E-26	0.292013719	0.322	0.152	1.87E-21	SMC	MT1X	up
SPARCL11	4.54E-49	0.291434337	0.914	0.838	2.37E-44	SMC	SPARCL1	up
PGF1	2.56E-32	0.290668328	0.608	0.397	1.34E-27	SMC	PGF	up
ECRG4	1.43E-53	0.288828694	0.307	0.065	7.47E-49	SMC	ECRG4	up
ADAMTS1	6.37E-27	0.284391249	0.661	0.491	3.34E-22	SMC	ADAMTS1	up
ANXA11	4.76E-36	0.281738941	0.419	0.197	2.49E-31	SMC	ANXA1	up
EFEMP11	5.32E-43	0.277039345	0.277	0.068	2.79E-38	SMC	EFEMP1	up
TOB1	3.24E-29	0.275678125	0.561	0.373	1.69E-24	SMC	TOB1	up
ID3	3.55E-27	0.275432948	0.761	0.609	1.86E-22	SMC	ID3	up
RARRES21	1.35E-31	0.274324736	0.735	0.598	7.07E-27	SMC	RARRES2	up
JUNB1	2.99E-59	0.274272944	0.934	0.895	1.57E-54	SMC	JUNB	up
DPEP11	1.67E-45	0.273460817	0.328	0.095	8.74E-41	SMC	DPEP1	up
MYH11	3.86E-18	0.27283983	0.515	0.346	2.02E-13	SMC	MYH11	up
C11orf962	5.28E-49	0.267469206	0.96	0.901	2.76E-44	SMC	C11orf96	up
ID2	1.10E-26	0.267082339	0.5	0.31	5.76E-22	SMC	ID2	up
MIR99AHG	4.38E-28	0.262978661	0.581	0.379	2.29E-23	SMC	MIR99AHG	up
NFIL3	1.76E-27	0.262692149	0.575	0.397	9.21E-23	SMC	NFIL3	up
NR4A3	1.36E-39	0.261609887	0.325	0.111	7.13E-35	SMC	NR4A3	up
TIMP33	5.88E-35	0.252353569	0.905	0.802	3.08E-30	SMC	TIMP3	up
EGR12	2.54E-35	0.251643984	0.919	0.845	1.33E-30	SMC	EGR1	up
TWIST1	2.16E-27	-0.250166284	0.266	0.442	1.13E-22	SMC	TWIST1	down
SOX4	2.65E-67	-0.250453397	0.92	0.979	1.39E-62	SMC	SOX4	down
ANGPT2	1.87E-21	-0.252332065	0.514	0.685	9.82E-17	SMC	ANGPT2	down
MIR4435-2HG	4.80E-26	-0.252834904	0.572	0.726	2.51E-21	SMC	MIR4435-2HG	down
SPON21	4.74E-30	-0.254186389	0.725	0.832	2.48E-25	SMC	SPON2	down
EGFL6	1.03E-25	-0.254235791	0.289	0.462	5.39E-21	SMC	EGFL6	down
LINGO1	1.67E-30	-0.255892648	0.333	0.548	8.74E-26	SMC	LINGO1	down
FN12	7.39E-33	-0.257010664	0.746	0.862	3.87E-28	SMC	FN1	down
MARCKSL11	9.66E-45	-0.258128485	0.77	0.886	5.06E-40	SMC	MARCKSL1	down
GLIPR12	1.35E-28	-0.259295226	0.246	0.424	7.08E-24	SMC	GLIPR1	down

STMN1	2.22E-27	-0.261117263	0.503	0.666	1.16E-22	SMC	STMN1	down
TBX31	1.32E-30	-0.261534547	0.581	0.721	6.92E-26	SMC	TBX3	down
C4orf482	3.93E-33	-0.262657413	0.424	0.606	2.06E-28	SMC	C4orf48	down
HOPX	1.79E-16	-0.262824982	0.439	0.554	9.36E-12	SMC	HOPX	down
ENC1	6.85E-26	-0.263299807	0.407	0.581	3.59E-21	SMC	ENC1	down
FARP1	2.05E-36	-0.264612171	0.575	0.752	1.08E-31	SMC	FARP1	down
COL4A11	2.96E-65	-0.264676098	0.932	0.988	1.55E-60	SMC	COL4A1	down
FAP	2.35E-29	-0.269423762	0.259	0.434	1.23E-24	SMC	FAP	down
PXDN1	9.30E-40	-0.271495837	0.631	0.809	4.87E-35	SMC	PXDN	down
TSHZ2	6.00E-32	-0.274145657	0.359	0.593	3.14E-27	SMC	TSHZ2	down
AGPAT5	2.21E-36	-0.276446062	0.309	0.518	1.16E-31	SMC	AGPAT5	down
WNT5A2	1.25E-30	-0.27815796	0.167	0.344	6.53E-26	SMC	WNT5A	down
FBLIM1	3.99E-43	-0.280640845	0.639	0.821	2.09E-38	SMC	FBLIM1	down
FAM162B	3.19E-24	-0.281238077	0.326	0.491	1.67E-19	SMC	FAM162B	down
PLAT	1.08E-31	-0.281650056	0.543	0.699	5.67E-27	SMC	PLAT	down
LOXL21	1.40E-25	-0.283139491	0.405	0.56	7.32E-21	SMC	LOXL2	down
NES	5.90E-36	-0.283265546	0.681	0.797	3.09E-31	SMC	NES	down
ADAM122	7.18E-42	-0.285015484	0.232	0.481	3.76E-37	SMC	ADAM12	down
PELI1	2.19E-34	-0.287195023	0.415	0.606	1.15E-29	SMC	PELI1	down
CASC151	1.08E-38	-0.289169378	0.309	0.531	5.66E-34	SMC	CASC15	down
BMP11	8.05E-46	-0.293007801	0.533	0.733	4.21E-41	SMC	BMP1	down
HTRA3	3.97E-27	-0.295043426	0.185	0.347	2.08E-22	SMC	HTRA3	down
DIO24	1.02E-28	-0.295696596	0.538	0.708	5.35E-24	SMC	DIO2	down
RGS4	3.72E-29	-0.296395403	0.243	0.432	1.95E-24	SMC	RGS4	down
LAMB11	1.58E-41	-0.298404395	0.634	0.821	8.26E-37	SMC	LAMB1	down
A2M	2.89E-46	-0.302951106	0.707	0.85	1.51E-41	SMC	A2M	down
COL5A21	1.28E-60	-0.303766932	0.804	0.932	6.68E-56	SMC	COL5A2	down
CD2481	1.69E-53	-0.305016477	0.727	0.868	8.84E-49	SMC	CD248	down
RARRES1	2.43E-42	-0.313734068	0.143	0.359	1.27E-37	SMC	RARRES1	down
CYTOR	1.69E-52	-0.355140932	0.687	0.85	8.85E-48	SMC	CYTOR	down
MARCKS2	1.50E-87	-0.355863421	0.816	0.939	7.87E-83	SMC	MARCKS	down
SULF1	6.96E-49	-0.375054107	0.423	0.661	3.64E-44	SMC	SULF1	down
FJX11	4.31E-52	-0.380900567	0.504	0.742	2.25E-47	SMC	FJX1	down
MXRA5	1.50E-73	-0.433106589	0.258	0.577	7.83E-69	SMC	MXRA5	down
MMP112	2.01E-83	-0.436462422	0.765	0.926	1.05E-78	SMC	MMP11	down
ECM16	4.47E-83	-0.470454782	0.525	0.807	2.34E-78	SMC	ECM1	down
APCDD13	1.75E-75	-0.473679016	0.441	0.735	9.15E-71	SMC	APCDD1	down
NREP3	1.60E-118	-0.494715598	0.707	0.944	8.36E-114	SMC	NREP	down
RBP14	2.84E-117	-0.529063378	0.61	0.886	1.49E-112	SMC	RBP1	down
PAEP2	5.44E-265	1.1623452	0.62	0.159	2.85E-260	unciliated_EpC	PAEP	up
CLU6	2.70E-231	0.983878697	0.696	0.352	1.41E-226	unciliated_EpC	CLU	up
SOD31	5.80E-167	0.688610558	0.549	0.225	3.04E-162	unciliated_EpC	SOD3	up
SLPI	2.26E-177	0.650635762	0.821	0.606	1.19E-172	unciliated_EpC	SLPI	up
PIGR1	6.43E-149	0.641209842	0.617	0.34	3.37E-144	unciliated_EpC	PIGR	up
SCGB1D23	9.21E-140	0.611770699	0.808	0.62	4.82E-135	unciliated_EpC	SCGB1D2	up
CCDC146	3.27E-166	0.607075352	0.666	0.377	1.71E-161	unciliated_EpC	CCDC146	up
SCGB2A19	1.56E-285	0.571232212	0.972	0.846	8.16E-281	unciliated_EpC	SCGB2A1	up
SCGB3A1	1.28E-107	0.519548912	0.43	0.155	6.73E-103	unciliated_EpC	SCGB3A1	up
KLK11	9.28E-122	0.510322135	0.495	0.221	4.86E-117	unciliated_EpC	KLK11	up
HLA-DRB11	8.32E-66	0.44446909	0.413	0.231	4.35E-61	unciliated_EpC	HLA-DRB1	up
SRARP	9.29E-111	0.437326736	0.403	0.128	4.86E-106	unciliated_EpC	SRARP	up

CP1	1.15E-81	0.41324638	0.327	0.104	6.04E-77	unciliated_EpC	CP	up
HLA-DRA1	2.95E-62	0.405326558	0.486	0.317	1.54E-57	unciliated_EpC	HLA-DRA	up
TFF32	4.36E-91	0.388112355	0.341	0.098	2.28E-86	unciliated_EpC	TFF3	up
FBLN13	1.27E-122	0.375490301	0.835	0.79	6.65E-118	unciliated_EpC	FBLN1	up
CST1	9.27E-53	0.35628316	0.232	0.073	4.86E-48	unciliated_EpC	CST1	up
IL1R1	1.60E-70	0.335352832	0.615	0.457	8.38E-66	unciliated_EpC	IL1R1	up
IGFBP71	4.95E-56	0.333531545	0.691	0.599	2.59E-51	unciliated_EpC	IGFBP7	up
CST4	6.63E-73	0.330990252	0.197	0.019	3.47E-68	unciliated_EpC	CST4	up
IFI62	5.46E-55	0.326903828	0.655	0.529	2.86E-50	unciliated_EpC	IFI6	up
CREB3L11	3.43E-56	0.309080962	0.564	0.359	1.80E-51	unciliated_EpC	CREB3L1	up
EHF	2.47E-68	0.307712225	0.717	0.591	1.29E-63	unciliated_EpC	EHF	up
GNG11	3.31E-63	0.307017183	0.672	0.542	1.73E-58	unciliated_EpC	GNG11	up
SERPINA5	2.94E-53	0.302573283	0.688	0.593	1.54E-48	unciliated_EpC	SERPINA5	up
NUPR1	4.31E-49	0.302144161	0.418	0.248	2.26E-44	unciliated_EpC	NUPR1	up
PALMD	3.09E-50	0.302033406	0.404	0.239	1.62E-45	unciliated_EpC	PALMD	up
SERPING1	4.59E-51	0.299544156	0.492	0.353	2.40E-46	unciliated_EpC	SERPING1	up
CKB2	8.17E-48	0.292096787	0.683	0.56	4.28E-43	unciliated_EpC	CKB	up
TCEA3	8.43E-63	0.284903249	0.418	0.215	4.41E-58	unciliated_EpC	TCEA3	up
IGFBP62	5.76E-36	0.284298298	0.218	0.094	3.01E-31	unciliated_EpC	IGFBP6	up
TXNIP1	6.67E-87	0.276058784	0.886	0.793	3.49E-82	unciliated_EpC	TXNIP	up
MPC2	2.22E-47	0.269947773	0.586	0.505	1.16E-42	unciliated_EpC	MPC2	up
CD74	3.24E-43	0.265365212	0.706	0.676	1.70E-38	unciliated_EpC	CD74	up
CFH	1.20E-39	0.263708202	0.271	0.134	6.31E-35	unciliated_EpC	CFH	up
PHLDA3	3.95E-47	0.257367761	0.345	0.188	2.07E-42	unciliated_EpC	PHLDA3	up
ACSL5	1.07E-27	0.255155907	0.565	0.494	5.59E-23	unciliated_EpC	ACSL5	up
RXFP1	1.38E-48	0.254568254	0.374	0.205	7.22E-44	unciliated_EpC	RXFP1	up
HLA-DMA	3.50E-29	0.252405565	0.416	0.323	1.83E-24	unciliated_EpC	HLA-DMA	up
PKHD1L11	1.39E-40	0.251097817	0.448	0.284	7.26E-36	unciliated_EpC	PKHD1L1	up
SFRP44	9.24E-35	-0.250606461	0.662	0.809	4.84E-30	unciliated_EpC	SFRP4	down
CCN2	2.56E-39	-0.260096957	0.388	0.547	1.34E-34	unciliated_EpC	CCN2	down
AC246817.1	2.68E-157	-0.26609397	0.068	0.303	1.41E-152	unciliated_EpC	AC246817.1	down
EMID1	2.73E-63	-0.268517634	0.384	0.582	1.43E-58	unciliated_EpC	EMID1	down
TRMT9B	3.01E-75	-0.26930473	0.235	0.45	1.58E-70	unciliated_EpC	TRMT9B	down
NSG1	4.46E-113	-0.270043691	0.111	0.329	2.33E-108	unciliated_EpC	NSG1	down
COL3A14	1.25E-39	-0.278328584	0.618	0.797	6.52E-35	unciliated_EpC	COL3A1	down
C4orf483	4.35E-57	-0.285959093	0.436	0.594	2.28E-52	unciliated_EpC	C4orf48	down
MSX2	2.90E-82	-0.290349308	0.341	0.604	1.52E-77	unciliated_EpC	MSX2	down
ECM17	1.00E-57	-0.292500053	0.196	0.376	5.24E-53	unciliated_EpC	ECM1	down
VCAN4	1.02E-66	-0.304145317	0.347	0.576	5.34E-62	unciliated_EpC	VCAN	down
NREP4	1.37E-79	-0.315798204	0.276	0.508	7.18E-75	unciliated_EpC	NREP	down
GLA	3.21E-83	-0.324268946	0.196	0.403	1.68E-78	unciliated_EpC	GLA	down
GCLC	2.56E-81	-0.3335096	0.399	0.606	1.34E-76	unciliated_EpC	GCLC	down
MGP4	5.62E-78	-0.336425559	0.263	0.498	2.94E-73	unciliated_EpC	MGP	down
LGALS13	6.24E-82	-0.353952597	0.571	0.809	3.26E-77	unciliated_EpC	LGALS1	down
CPM	7.77E-97	-0.36113717	0.695	0.856	4.07E-92	unciliated_EpC	CPM	down
RBP15	1.84E-103	-0.38041321	0.329	0.598	9.63E-99	unciliated_EpC	RBP1	down
PDLIM11	4.27E-134	-0.41185447	0.591	0.791	2.23E-129	unciliated_EpC	PDLIM1	down
IGFBP23	2.14E-139	-0.435023616	0.338	0.664	1.12E-134	unciliated_EpC	IGFBP2	down

Figure 2. Bulk RNA-seq Profiles in EP versus EU, Aberrant Gene Expression in Cell Types from Endometrial Polyps' samples.



(A) The PCA plot displays the distribution of individuals along the first two principal components (Dim1 and Dim2). Individuals are color-coded by group: EP (blue circles) and EU (orange triangles).

(B) The volcano plot displays gene expression changes from EP to EU of bulk RNA-seq (EU, n = 5; EP, n = 5), highlighting significant genes (green) versus non-significant ones (red) based on log2 fold change and adjusted p-values.

(C) Bar plots illustrating the gene ontology (GO) enrichment analysis of genes that are either upregulated or downregulated between EU and EP. Fisher's exact tests (two-sided) were conducted, with a p.adjust of less than 0.05 considered statistically significant.

(D-E) Dot plots showing the relative expression changes of specific genes from bulk RNA-seq data across various cell types in single-cell analyses. The size of the dots indicates the percentage of expression.

Endometrial polyps exhibit cell type-specific changes in their transcriptional regulatory programs

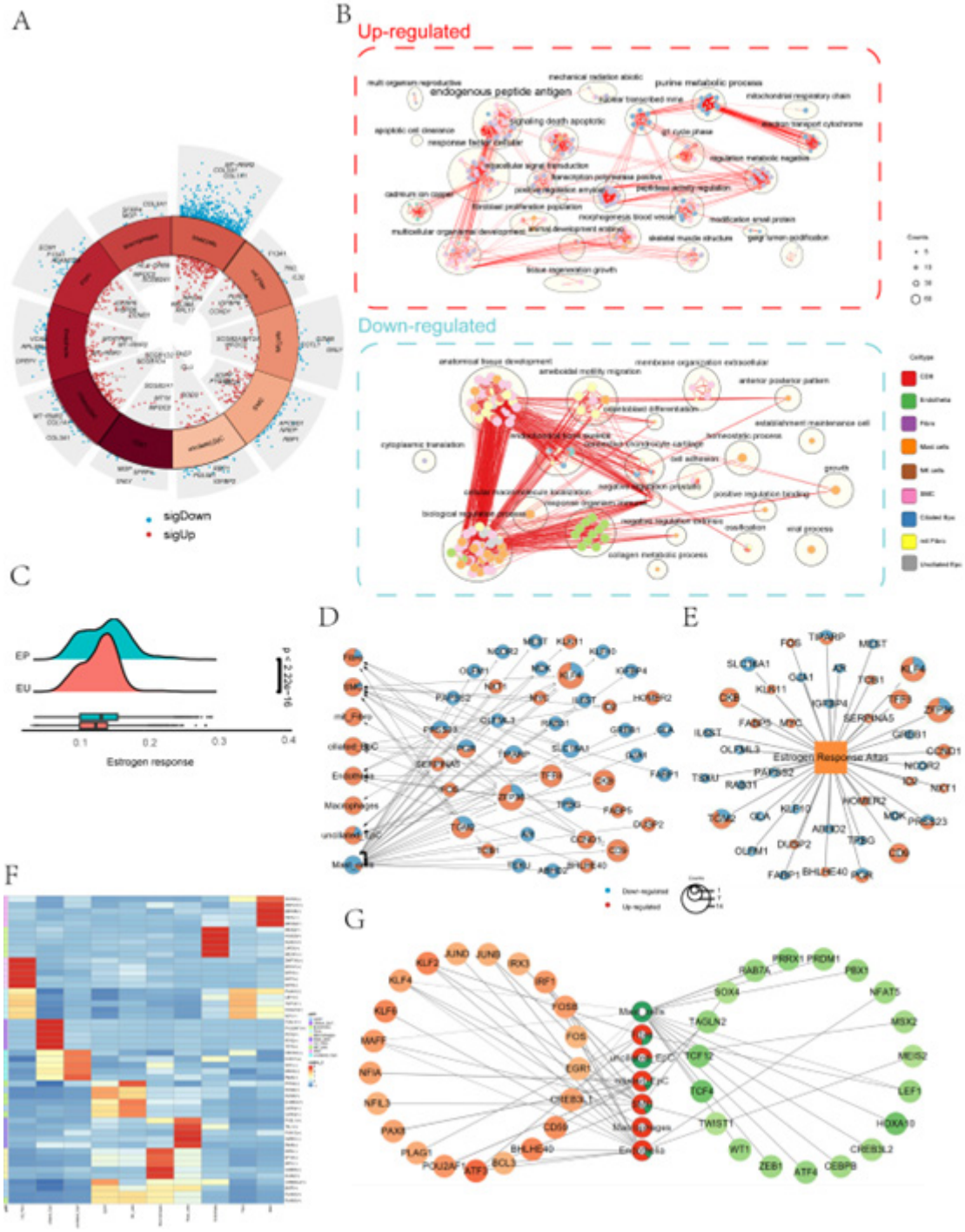
To distinguish between the shared and distinct gene expression alterations linked to endometrial polyps within each cell type, we examined the differentially expressed genes (DEGs) across the major cell types found in both endometrial (EU) and polyp samples. A total of 1,534 DEGs associated with polyps (with |log2FoldChange| > 0.25 and adjusted P value < 0.05) were identified, exhibiting differential expression in at least one cell type across both EU and MP samples (**Fig. 3A**), Major cell types in endometrium, included Mast cell, SMC, ciliated-epithelia and unciliated-epithelia, were most affected by polpys, as manifested by high DEG counts of 727, 236, 124 and 120 respectively (**Fig 4B** and **Table S2**), While there was significant variability in the differentially expressed genes (DEGs) among various cell types, certain Gene Ontology (GO) term annotations were common across the primary cell types. For example, the downregulated DEGs were enriched in biological regulation process (ADAM12, APCDD1, BMP1, and COL3A1) and Upregulated DEGs were associated with inflammatory response and antigen processing (MSX1, ATF3, CLU, and IRF1), metabolic process (NME2, NDUFA7, and, LDHB), and response factor cellular such as: response to hormone (AR, JAK1/3, CRY1, STAT3, FOS) (**Fig 3B**).

Furthermore, Estrogen is implicated in the development of endometrial polyps, and a detailed analysis indicated an increased expression of genes associated with the estrogen response, as identified in the Molecular Signatures Database (MSigDB) (**Fig.3C**), In a joint analysis of differentially expressed genes (DEGs) within the estrogen response database, the gene set score (AUCell) of whole tissue and multiple cell types demonstrated an activation of genes related to estrogen response, except for mast cells and unciliated epithelia (**Fig.3C and Fig.S3**). Consistently, we identified that the majority of genes involved in the estrogen response were upregulated across multiple cell types, except for mast cells (Fig.3D). Notably, TGM2, a gene associated with extracellular matrix remodeling and apoptosis[16], exhibited elevated expression levels in fibroblasts and smooth muscle cells (SMCs). Additionally, TFF3, which possesses anti-apoptotic properties[17], and CKB, involved in cellular energy homeostasis[18], were both found to be increased in the epithelial cells of endometrial polyps. Conversely, the hormone receptors AR (Androgen Receptor) and PGR (Progesterone Receptor) were downregulated in mast cells within endometrial polyps (**Fig.3E**).

Next, we performed SCENIC analysis to identify key transcription factors (TFs) present in various cell types within endometrial polyps. (**Fig. 3F and 3G**). The identified core TFs include FOSB, FOS, JUNB, and JUND, which are components of the AP-1

complex that showed upregulation in epithelial cells, macrophages, endothelial cells, and SMCs. These factors are associated with cell proliferation, apoptosis, and stress responses, and their expression changes have also been observed in colorectal polyps[19]. Furthermore, KLF6, KLF2, and KLF4, members of the KLF family, were found to be upregulated in fibroblasts, endothelial cells, and SMCs. These factors are crucial for cell proliferation, with KLF4 notably promoting the formation of intestinal polyps[20]. EGR1, which has been noted for altered expression in patients with nasal polyps, was also upregulated in the endothelial cells and SMCs of endometrial polyps. Additionally, we observed the downregulation of HOXA10, a gene implicated in endometrial polyps [21], particularly in mast cells, suggesting a distinctive transcriptional network within these cells (**Fig.3G**). Notably, the analysis of transcription factors (TFs) that were co-downregulated across different cell types indicated that mast cell transcription factors were the most significantly downregulated. Taken together, these results shed light on the transcriptional regulatory mechanisms underlying endometrial polyps, identifying crucial factors that drive their development and progression.

Figure 3. Transcriptional changes in various cell types between EU and EP.



(A) Circular diagram displays gene expression changes in endometrial polyps across various cell types. significant downregulated genes

are shown in blue (sigDown), while upregulated genes are in red (sigUp). The placement of dots represent expression levels, offering insights into differential gene expression among cell populations.

(B) Network illustrates the representative Gene Ontology (GO) terms and pathways associated with differentially expressed genes (DEGs) between endometrial uterine (EU) and endometrial polyp (EP) samples. Nodes are depicted as pie charts, with the size of each pie reflecting the total number of genes associated with that term. The pie charts are color-coded by cell types, and the size of each slice indicates the proportion of genes from the specific gene list contributing to that term. Connections between two terms are drawn if their similarity exceeds 0.3.

(C) Ridge plot showing the AUC score of estrogen response gene set in EP.

(D) Network visualization highlights differentially expressed genes (DEGs) that are upregulated (in red) and downregulated (on the right) between endometrial uterine (EU) and endometrial polyp samples, specifically those that overlap with genes associated with estrogen response gene sets. The pie charts on the left depict various cell types, with red indicating upregulated genes and blue representing downregulated ones. The size of each node reflects the number of target genes linked to a particular cell type. Red nodes signify upregulated DEGs, while the blue nodes on the right denote downregulated DEGs.

(E) Network plot illustrates the upregulated and downregulated differentially expressed genes (DEGs) across all cell types that intersect with genes annotated in the estrogen response gene sets. The size of each node reflects the occurrence of DEGs across various cell types. The red sections of the nodes represent upregulated genes, while the blue sections indicate downregulated genes.

(F) Heatmap displaying the SCENIC analysis of cell type-specific core regulatory transcription factors (TFs) in polyps.

(G) Network visualization depicts the core regulatory transcription factors (TFs) that are upregulated (on the left) and downregulated (on the right) in endometrial polyps. The pie charts in the center illustrate various cell types, with red indicating upregulated TFs and green indicating downregulated ones. The left side showcases red nodes representing upregulated TFs, while the right side features blue nodes for downregulated TFs.

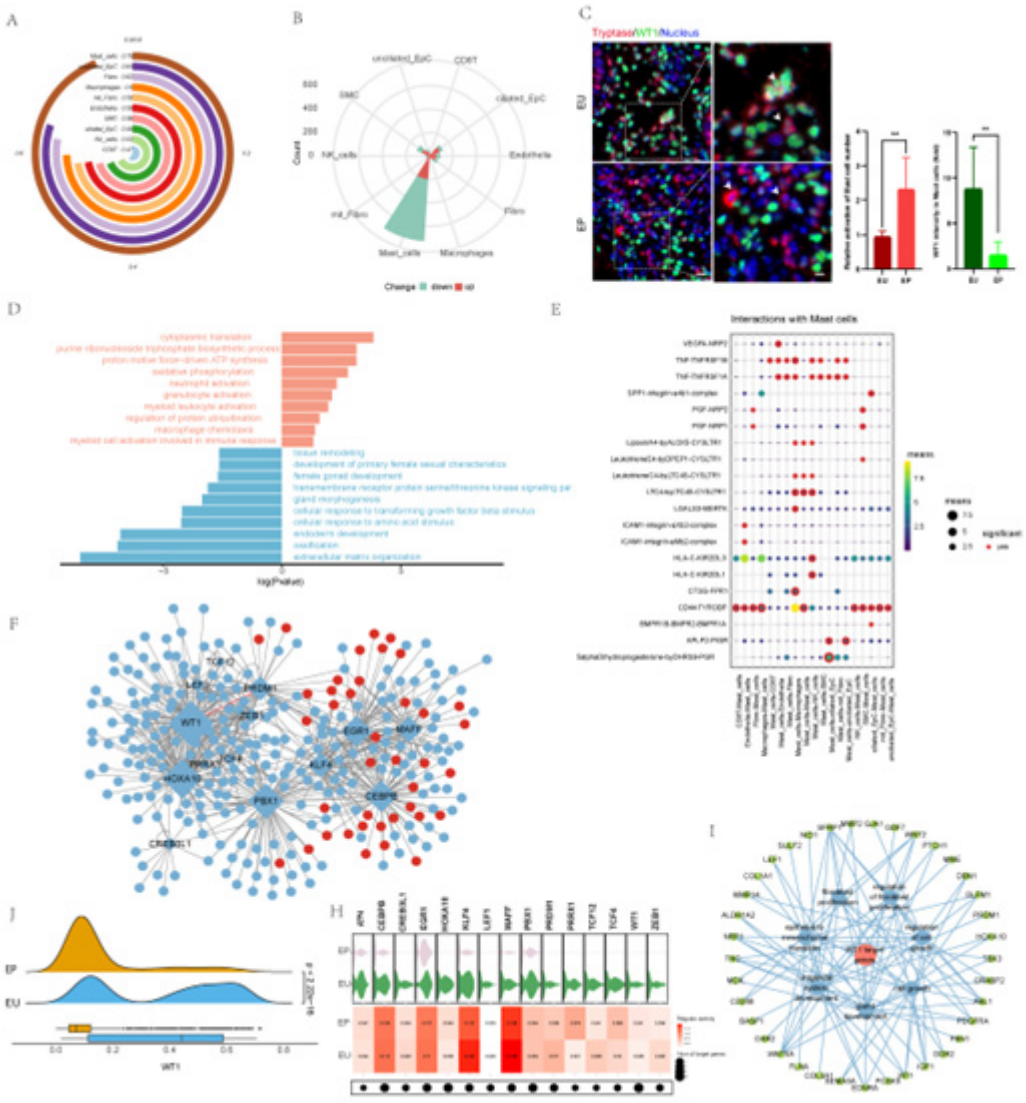
Increase in Mast Cell Number and Activation Associated with Susceptibility to Endometrial Polyp Development

To gain a deeper understanding of the transcriptomic landscape of endometrial polyps, we utilized augur analysis. This method identifies cell types that are most responsive to biological perturbations in single-cell data[22]. Our findings indicated that mast cells were the most significantly affected cell type in endometrial polyps (**Fig.4A**). The changes in cell proportions and transcriptional profiles suggested that mast cells play a pivotal role in the development of endometrial polyps (**Fig.1H and 4B**). Mast cells contribute to inflammation and tissue remodeling within polyps by releasing cytokines and growth factors, thereby affecting the growth and persistence of these polyps[23-25]. The tryptase serves as a marker of mast-cell activation[26], and our analysis revealed significant activation of mast cells within endometrial polyps (**Fig.4C**). To investigate this, we performed gene enrichment analysis of DEGs in mast cells. The results showed significant enrichment of upregulated genes also associated with granulocyte activation (CTSG, TYROBP, IL18) and proton motive force-driven ATP synthesis (ATP6V0C, NDUFA13, ATP5F1D). Conversely, downregulated genes were enriched in pathways related to gland morphogenesis (MMP2, IGFBP5, MDK) and female gonad development (NR2F2, SFRP1, PGR) (**Fig.4D**).

Next, we explored whether cellular communications between mast cells and other cell types in the EPs were altered. Utilizing the bioinformatic tool CellphoneDB, we assessed enhanced cell-cell communications in the EPs based on upregulated differentially expressed genes. Our analysis revealed that steroid-related signaling, specifically the interaction of 5alphaDihydroprogesterone facilitated by DHRS9 with the progesterone receptor (PGR), and tumor necrosis factor signaling through TNF-TNFRSF1B interactions, were enhanced between mast cells and epithelial/fibroblast cells in the EPs. This finding aligns with previous studies showing significantly higher levels of PGR in glandular epithelium in EPs[27]. Furthermore, angiogenesis signaling, particularly the VEGFA-NRP2 interaction, demonstrated increased activity between mast cells and endothelial cells (**Fig.4E**). These findings suggest that the increase and activation of mast cells in the EPs are closely correlated with a heightened susceptibility to the development of endometrial polyps.

Transcription factor (TF) network analysis identified 15 specific regulators with significant differences between EPs and EU. Notably, the WT1 regulon was found to be downregulated in endometrial polyps and central to a gene network that influences mast cell function (**Fig.4F**). Both the transcription level and regulon activity of WT1 were decreased in endometrial polyps and verified downregulation of WT1 in EPs mast cells by immunofluorescence (**Fig.4H and 4C**). Sequencing data indicated that WT1 broadly regulates 37 differentially expressed genes (DEGs) in mast cells, with these target genes showing disturbances in endometrial polyps as WT1 expression decreases (**Fig.4Jand 4H**). Specifically, the DEGs targeted by WT1 were linked to cell growth (WT1, IGF1, and WNT2) and epithelial to mesenchymal transition (SFRP1, WNT2, WNT5A) (**Fig 4I**). These findings imply that the repression of WT1 and the disruption of its downstream transcriptional network likely contribute to the proliferation of mast cells in endometrial polyps.

Figure 4. Profiling of mast cell changes in endometrial polyps.

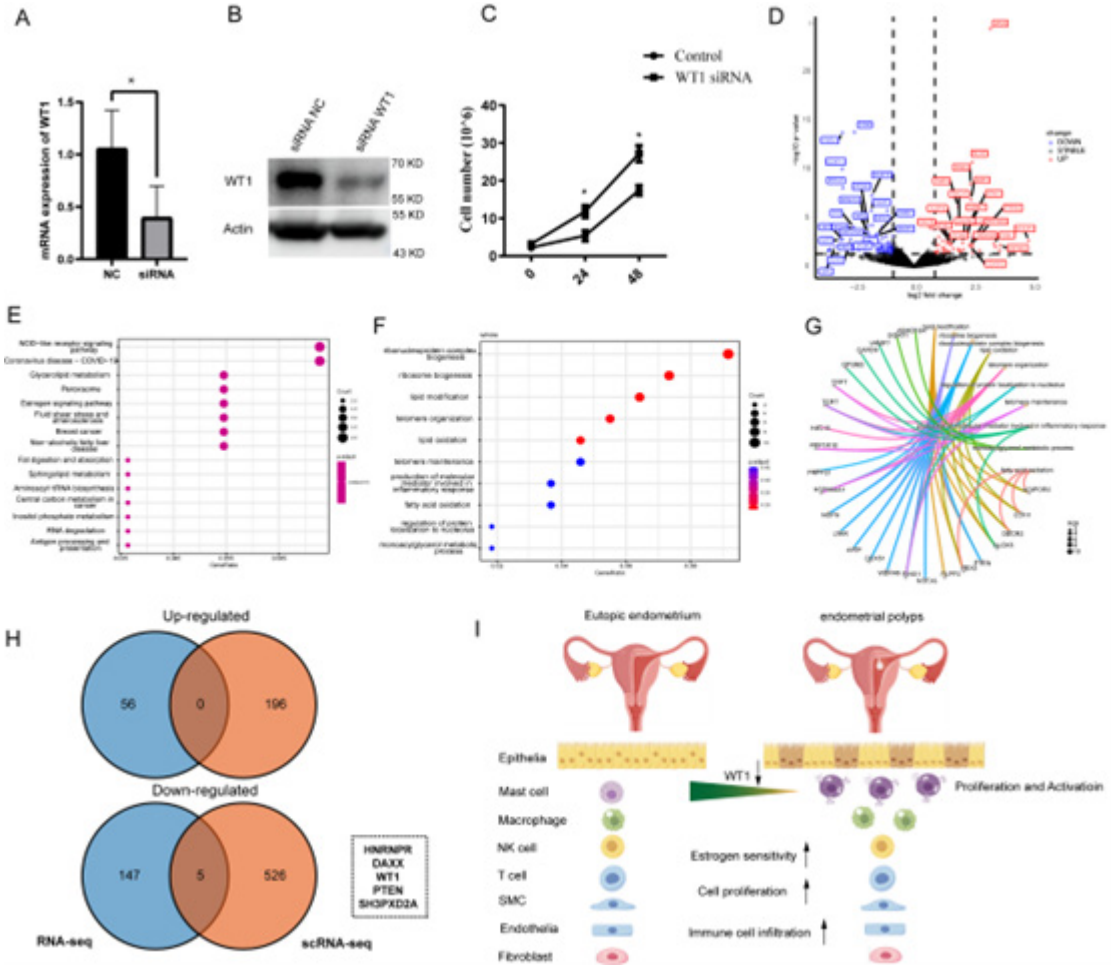


(A) Circular plot illustrates the prioritization of cell types that are most reactive to biological changes during the formation of endometrial polyps. This analysis was conducted using Augur, a technique designed to identify cell types exhibiting the most significant responses in single-cell data.
(B) Rose diagram illustrates the counts of differentially expressed genes (DEGs) in various cell types from endometrial polyp formation. Upregulated DEGs are represented in red, while downregulated DEGs are shown in green
(C) Co-staining of Tryptase and WT1 in EU and EP. Left, representative image of Tryptase and WT1 in EU and EP. Middle, the relative Tryptase positive cells was quantiffed. Right, quantitative data of WT1 expression in Mast cells. Scale bars, 10μm and 5μm (zoomed-in images). **P < 0.01.
(D) Bar plot displays the significance of biological processes (BP) associated with differentially expressed genes, Upregulated DEGs are represented in red, while downregulated DEGs are shown in blue. The x-axis represents the negative logarithm of the p-values.
(E) Visualization of cell-cell communication interactions identified using CellPhoneDB. The dot plot displays the mean interaction scores between various cell types, specifically focusing on interactions involving mast cells and other cell populations. The size of each dot corresponds to the mean interaction score. The color gradient represents the mean scores, with purple denoting lower values and green indicating higher values. A red dot indicates statistically significant interactions. Interactions are listed on the y-axis, while the different cell types are represented on the x-axis.
(E) Regulatory network illustrates potential key transcriptional regulators in mast cells. In this visualization, larger nodes signify transcription factors (TFs), while smaller nodes represent target genes. The size of the TF nodes is directly proportional to the number of genes they regulate. Nodes colored in red indicate upregulation, whereas blue nodes denote downregulation.
(F) Figure presents the expression of various transcription factors (TFs) in mast cell across EP and EU. The upper section displays violin plots showing the expression of each TF in mast cell across EP and EU. The lower section features a heatmap representing the regulation activity of each TF in mast cell across EP and EU. the size of the black circles below indicates the number of target genes associated with each TF.
(G) A ridge plot displays the AUC scores of WT1-regulated gene sets in polyps.
(I) Network plot illustrates the enrichment of representative terms associated with WT1 target genes. The genes linked to these terms are displayed on the outer edge of the diagram.

Knockdown of WT1 promote Mast cell proliferation in endometrial polyps

To explore the functional role of WT1 in endometrial polyps, WT1 was knocked down in the human mast cell line HMC-1 using siRNA. Post-transfection, WT1 reduction was confirmed at both RNA and protein levels via RT-qPCR and western blot analyses (**Fig.5A and 5B**). Following WT1 knockdown, HMC-1 cell proliferation was significantly enhanced (**Fig.5C**). RNA sequencing was subsequently conducted to evaluate gene expression changes. Volcano plot analysis revealed significant upregulation and downregulation of various genes after WT1 knockdown (**Fig.5D**), indicating its regulatory role in mast cell function.KEGG pathway analysis highlighted modifications in crucial signaling pathways, such as the estrogen signaling pathway and central carbon metabolism, relevant to cell growth and proliferation (**Fig 5E**). Furthermore, Gene Ontology (GO) enrichment analysis showed that knocking down WT1 affected pathways involved in lipid metabolism (e.g., PLPP2, ALOX5, and ECH1), ribosome biogenesis (e.g., NOP9, LYAR, WDR46), and telomere maintenance (e.g., TERT, PPP1R10, PINX1) (**Fig.5F and 5G**). Notably, several differentially expressed genes (DEGs) were found to overlap between WT1-knockdown HMC-1 cells and EPs mast cells. This overlap included no upregulated genes but featured five downregulated genes that are significantly associated with the proliferation and apoptosis of HMC-1 (**Fig.5H**). Collectively, these findings provide a molecular overview of how WT1 deficiency enhances mast cell proliferation. This underscores WT1's essential role in managing pathways linked to cellular growth and metabolism, suggesting that its disruption may disturb cellular equilibrium and contribute to conditions like endometrial polyps.

Figure 5. Knockdown of WT1 induced Mast cell proliferation in endometrial polyps.



(A) qPCR results show the efficiency of WT1 knockdown. *P < 0.05, **P < 0.01.
(B)Westernblot show the efficiency of WT1 knockdown.
(C) Cell number demonstrate cell proliferation after WT1 knockdown.
(D) Volcano plot showing differentially expressed genes in HMC-1 mast cells following WT1 knockdown. Genes with significant upregulation are marked in red, while those with significant downregulation are marked in blue.
(E) KEGG pathway analysis identifying altered signaling pathways, including the estrogen signaling pathway and central carbon metabolism.
(F-G) GO enrichment analysis of biological processes affected by WT1 knockdown
(H) Venn diagram illustrates the genes that are common between the differentially expressed genes (DEGs) identified in HMC-1 cells following WT1 silencing and those found in mast cells through snRNA-seq analysis.

(I) Schematic (produced using Figdraw) illustrates the pathological alterations observed in endometrial polyps.

DISCUSSION

In this study, we performed single-cell RNA sequencing (scRNA-seq) to construct a comprehensive cellular and molecular atlas of endometrial polyps and adjacent eutopic endometrium (EU) tissues. Our findings provide significant insights into the cellular composition changes, gene expression profiles, and transcriptional regulatory mechanisms associated with EPs, with a particular emphasis on the role of mast cells and the transcription factor WT1. The scRNA-seq analysis revealed substantial shifts in cell populations within EPs compared to EU tissues. Specifically, there was an increase in the proportions of epithelial cells, mast cells, and macrophages, along with a decrease in fibroblasts. Immunohistochemistry staining confirmed these observations, showing elevated numbers of CD68-positive macrophages and TPSB2-positive mast cells in the polyps. These findings suggest that glandular proliferation and immune cell infiltration are key features of EPs, contributing to their proliferative and inflammatory characteristics (**Fig.5I**).

Transcription factor analysis revealed crucial regulatory elements, including the AP-1 complex (FOSB, FOS, JUNB, and JUND) and KLF family members (KLF6, KLF2, and KLF4), which were upregulated in various cell types within EPs. These transcription factors are associated with key processes such as cell proliferation, apoptosis, and stress responses, aligning with the pathological features of EPs. Additionally, the downregulation of HOXA10 and other transcription factors in mast cells indicated a unique transcriptional network in these cells, underscoring their significance in EPs biology.

Mast cell proliferation is a key factor in nasal polyp hyperplasia during type II inflammation14. Similarly, we observed a high density of activated mast cells in endometrial polyps, aligning with previous studies15. This suggests a strong connection between mast cell proliferation and endometrial polyps. WT1, initially identified as a tumor suppressor in Wilms' Tumor, influences various cancers and developmental processes through target genes like IGF1R, PDGFA, EGF, and TGF-β. Our research indicates a significant reduction of WT1 expression in mast cells within endometrial polyps. Experiments with WT1 knockdown in the HMC-1 mast cell line showed that decreased WT1 levels lead to increased mast cell proliferation and activity, highlighting WT1's suppressive role. This aligns with prior findings linking c-KIT (CD117) receptor mutations to mast cell proliferation, contributing to conditions such as systemic mastocytosis. Previously, the mechanisms behind mast cell proliferation in uterine polyps were unclear. Our study addresses this by demonstrating that WT1 downregulation disrupts its regulatory network, resulting in abnormal mast cell growth in endometrial polyps.

In conclusion, our research indicates that the downregulation of WT1 in mast cells is a crucial factor driving their proliferation and the inflammatory milieu in endometrial polyps. Targeting WT1 and its related regulatory networks could provide new therapeutic avenues for treating endometrial polyps.

Limitations of the study

Despite the significant findings regarding the cellular and molecular landscape of endometrial polyps presented in this study, the sample size, although sufficient for exploratory analyses, was limited to seven patients, which may affect the generalizability of the results. Larger, more diverse cohorts are needed to validate the findings and assess potential variations in different populations. Additionally, the functional assays performed, such as the WT1 knockdown in the HMC-1 mast cell line, may not completely replicate the in vivo conditions present in endometrial polyps. It is crucial to conduct further experiments in primary human mast cells or relevant animal models to confirm the functional relevance of the identified transcriptional changes.

Resource availability

Lead contact

Information and requests for resources should be directed to the lead contact, Hong Xu (xuhong1558@sjtu.edu.cn) or Xiaoying He (hexiaoying@51mch.com)

Materials availability

This study did not generate new unique reagents.

Data and code availability

The accession number for the single-cell sequencing data reported in this paper is deposited in the China National Center for Bioinformation under the accession number PRJCA032064.

Methods

All methods can be found in the accompanying transparent methods supplemental file.

Acknowledgments

We would like to express our sincere gratitude to Professor Lihui Lin for providing the HMC-1 cell line, which significantly contributed to the success of this study. This work was supported by the National Natural Science Foundation of China [NO. 8247168, 82271679, 82071622, XH].

Author contributions

H.X.Y and H.X. ,Y.L. conceptualized the study and supervised the project; Y.Y., Y.W.Q., W.Z.S., H.T, and L.C conducted the experiments; Y.L performed the bioinformatic analyses of scRNA-seq and RNA-seq; T.H., and C.L., collected clinical samples; Y.L., H.X.Y and H.X wrote the manuscript, with all the authors contributing to writing and providing feedback.

Declaration of interests

The authors declare no competing interests.

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