

**S8 Table.** Enriched pathways in the differentially expressed genes of absolute log<sub>2</sub> fold change of FPKM > 4 ordered by statistical significance

ID	Name	Q-value	Count	Genes
M5889	Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins	2.27E-11	54	SERPINA3, ANXA8L1, S100A8, S100A12, PI3, SERPINA4, CCL28, LOXL4, MMP1, CCL20, MMP7, MMP10, COL4A1, COL4A2, COL5A1, SFTPBP, GDF15, BCAN, MUC13, IL23A, CSF2, IGFBP3, IGFBP5, PRG2, SCUBE3, WNT10A, IL1A, FAM20A, CTSE, MEGF11, SERPINB7, PRSS1, IL15, IL18, TNFSF10, SPOCK1, IL17C, COL25A1, CCL27, NELL1, FREM2, CRISPLD1, FGF19, FGFBP1, INHBE, MUC5B, EDIL3, CXCL3, LGALS7, FSTL1, VWA5A, LOX, LTB, SERPINA5
M5885	Ensemble of genes encoding ECM-associated proteins including ECM-affiliated proteins, ECM regulators, and secreted factors	1.10E-08	41	SERPINA3, ANXA8L1, S100A8, S100A12, PI3, SERPINA4, CCL28, LOXL4, MMP1, CCL20, MMP7, MMP10, SFTPBP, GDF15, MUC13, IL23A, CSF2, SCUBE3, WNT10A, IL1A, FAM20A, CTSE, MEGF11, SERPINB7, PRSS1, IL15, IL18, TNFSF10, IL17C, CCL27, FREM2, FGF19, FGFBP1, INHBE, MUC5B, CXCL3, LGALS7, FSTL1, LOX, LTB, SERPINA5
M5883	Genes encoding secreted soluble factors	3.60E-05	22	S100A8, S100A12, CCL28, CCL20, GDF15, IL23A, CSF2, SCUBE3, WNT10A, IL1A, MEGF11, IL15, IL18, TNFSF10, IL17C, CCL27, FGF19, FGFBP1, INHBE, CXCL3, FSTL1, LTB
200309	Rheumatoid arthritis	8.07E-03	9	ATP6V1C2, MMP1, CCL20, IL23A, CSF2, IL1A, IL15, IL18, LTB
83051	Cytokine-cytokine receptor interaction	1.10E-02	15	CCL28, CCL20, IL23A, CSF2, IL1A, IL7R, IL15, TNFRSF9, IL18, TNFSF10, CCL27, INHBE, CXCL3, LTB, TNFRSF1B
M3468	Genes encoding enzymes and their regulators involved in the remodeling of the extracellular matrix	4.17E-02	13	SERPINA3, PI3, SERPINA4, LOXL4, MMP1, MMP7, MMP10, FAM20A, CTSE, SERPINB7, PRSS1, LOX, SERPINA5
730306	Assembly of collagen fibrils and other multimeric structures	4.80E-02	6	LOXL4, MMP7, COL4A1, COL4A2, COL5A1, LOX

Q values were estimated by Benjamini and Hochberg procedure to control the false discovery rate. FPKM, fragments per kilobase of transcript per million fragments mapped.