

Supp Table 2

UP	Cluster 3 12 genes		KEGG: Cytokine-cytokine receptor interaction (IL1B, CXCL8, CXCL1, IL1A, CXCL5) q=1.16E-9	KEGG: TNF signaling pathway (IL1B, CXCL1, CXCL5, MMP3) q=0.00003247	Wikipathways: Senescence and autophagy in cancer (CXCL8, CXCL1, IL1B, IL1A, IL24) q=1.393E-7	Reactome: Signaling by qPCR (CXCL5, CXCL1, CXCL8, C3, CCL7, MMP3) q=0.000037	Biocarta: NFKB signaling (IL1A) q=0.01	Jensen compartments: Extracellular space (IL1A, CXCL1, IL1B, MMP3, IL24, CCL7, C3, IL13RA2, CXCL5) q=0.000001063				
	Cluster 11 19 genes		KEGG: Cytokine-cytokine receptor interaction (IL6, IL11, CXCL10, CCL20, CXCL3, TNFSF15) q=0.0000054	KEGG: TNF signaling pathway (IL6, CXCL10, CCL20, CXCL3) q=0.00007088	Wikipathways: Senescence and autophagy in cancer (IL6, TNFSF15, SERPINB2) q=0.003268	Reactome: G alpha signaling events (CXCL10, CCL20, CXCL3, RGS1B) q=0.004354						
	Cluster 12 8 genes		GO Cellular component: ER-Golgi (AREG) q=0.03	Wikipathways: Matrix metalloproteinases (MMP1) q=0.02	Reactome: Collagen degradation (MMP1) q=0.05							
	Cluster 16 7 genes		KEGG: ECM-receptor interaction (TGA10) q=0.05	GO Molecular function: Protein binding involved in cell-matrix adhesion (TGA10) q=0.01	KEGG: Notch signaling pathway (DLL4) q=0.05	Wikipathways: Notch regulation of human endothelial cell calcification (DLL4) q=0.05						
	Cluster 17 12 genes		Wikipathways: Senescence and autophagy in cancer (PLAT, BMP2) q=0.01698	Wikipathways: Quercetin and NFkBAP-1 induced cell apoptosis (PTGS2) q=0.04	Reactome: Signaling by BMP (GREM2, BMP2) q=0.002653	Reactome: Dissolution of fibrin clot (PLAT) q=0.033						
	Cluster 18 31 genes		GO Biological process: Mesodermal cell differentiation (ITGA2, HMGA2) q=0.002965	Biocarta: Platelet amyloid precursor protein pathway (PLAU) q=0.03	Biocarta: Fibrinolysis pathway (PLAU) q=0.03	KEGG: Mineral absorption (MT2A, MT1E, MT1L) q=0.001	GO Biological process: Cellular response to ions (MTL1, MT1E, MT2A) q=0.00057					
	Cluster 13 16 genes		Biocarta: CD40L signaling pathway (TNFAIP3) q=0.01									
	Cluster 10 7 genes		GO Molecular function: BMP binding (GREM1) q=0.01	Reactome: Amino acid transport across the plasma membrane (SLC7A2) q=0.04								
	Cluster 6 13 genes		KEGG: Apoptosis (CTSK, ERN1) q=0.01	GO Biological process: Positive regulation of ECM disassembly (PDFN) q=0.05	Wikipathways: Osteoclast signaling (TNFRSF11B, CTSK) q=0.00062	Wikipathways: TGFB signaling pathway (TGIF1) q=0.1	Kinase perturbations: TGFB2 knockout (perturbations) (TNFRSF11B, CTSK, NIAK2, PDE7B) q=0.0018	Reactome: Metal ion transporters (SLC39A14, SLC11A2) q=0.0049	KEGG: Lysosome (CTSK, SLC11A2, ARSG) q=0.0008			
	Cluster 14 24 genes		Biocarta: IL6 signaling pathway (CEBFB) q=0.05	Panther: Apoptosis signaling pathway (MCL1, RELB) q=0.04	GO Biological process: Positive regulation of myoblast differentiation (RIPOR2, BTG1) q=0.04	Wikipathways: Myometrial relaxation and contraction pathways (MAFF, ETS2, GJA1) q=0.02						
	Cluster 15 29 genes		KEGG: TNF signaling pathway (NFKBIA, CCL2, ICAM1, LIF) q=0.0001	Reactome: Anchoring fibril formation (LAMB3, COL7A1) q=0.01	GO Biological process: Positive regulation of cellular extravasation (RIPOR2, ICAM1) q=0.01	Wikipathways: Complement and coagulation cascades (PLAUR, BDKRB1) q=0.05						
	Cluster 19 30 genes		KEGG: TNF signaling pathway (MAPK13, IKBKB, VEGFC) q=0.01	Wikipathways: Heart development (VEGFC, SMAD1) q=0.05	Biocarta: Keratinocyte differentiation (MAPK13, IKBKB) q=0.03	Panther: TGFB signaling pathway (MAPK13, SMAD1) q=0.09						
	Cluster 20 19 genes		Reactome: Integrin cell surface interactions (ITGA6, COL13A1) q=0.08	Reactome: Collagen formation (ITGA6, COL13A1) q=0.08								

DOWN	Cluster 4 9 genes		GO Biological Process: Muscle hypertrophy (HTR2B) q=0.04	GO Biological Process: Blood vessel diameter (HTR2B) q=0.04	Mammalian phenotype: Cardiovascular system physiology (TNNT2, HTR2B) q=0.04	Mammalian phenotype: Abnormal heart development (TNNT2, HTR2B) q=0.03					
	Cluster 8 41 genes		KEGG: Vascular smooth muscle contraction (GUCY1B3, ADRA1B, ACTA2) q=0.07	KEGG: Myometrial relaxation and contraction (OXR, CORIN, ACTA2, IGFBP3) q=0.005	KEGG: Focal adhesion-P13K-AKT/TOR (PDGFR, COL11A1, FGF9) q=0.14	GO Molecular function: Type II transforming growth factor b receptor binding (BAMBI) q=0.09	Panther: TGFB signaling (GDFS, BAMBI) q=0.13				
	Cluster 7 59 genes		Reactome: Smooth muscle contraction (ACTG2, TPM2) q=0.8	Reactome: Extracellular matrix organization (SDC2, NTN4, COL8A2, BMP4) q=0.6	GO Biological Process: Cell differentiation involved in metanephros development (DSR1, BMP4) q=0.04	GO Biological Process: Cell migration involved in heart development (PDGFRB, SNAI2) q=0.03	GO Biological Process: Cardiac muscle cell differentiation (BMP4, EFNB2) q=0.04	Reactome: TGFB signaling (ID2, BMP4) q=0.8			
	Cluster 9 30 genes		GO Biological Process: Positive regulation of smooth muscle cell proliferation (STAT1, IL6R, HMOX1) q=0.00579	Reactome: Extracellular matrix organization (MFAP4, FBN2, TGFB2, COL14A1, ADAMTS5, ADAMTS1, ADAMTS8, VCAM1) q=1.1E-6	GO Biological Process: Extracellular matrix organization (TGFB2, COL14A1, ADAMTS5, FBN2, VCAM1) q=0.005	GO Biological Process: Embryo development ending in birth or egg hatching (TGFB2, STOX2) q=0.02	Wikipathways: Endochondral ossification (TGFB2, STAT2, ADAMTS5, ADAMTS1) q=0.00009818				
	Cluster 2 44 genes		GO Cellular component: Cytoskeleton (CNN2, CNN1, MARCKS, CNN3, CDC42EP3, MTCL1, LIMOD1) q=0.002	GO Cellular component: Focal adhesion (CNN2, CNN1, MARCKS, CNN3, LIMS2, FHL2, TES) q=0.0005	GO Cellular component: Rough endoplasmic reticulum (TRAM2, TRAM1) q=0.02						

SASP	ECM	NOTCH	TGFBeta	Coagulation	Differentiation, development	Muscle	Metals	Other
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