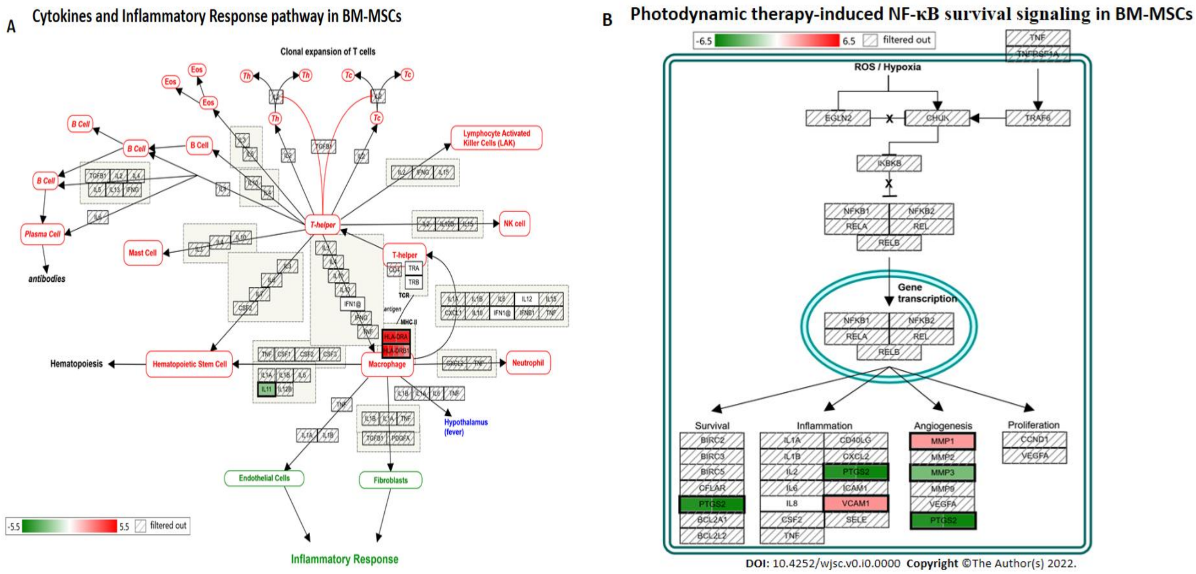
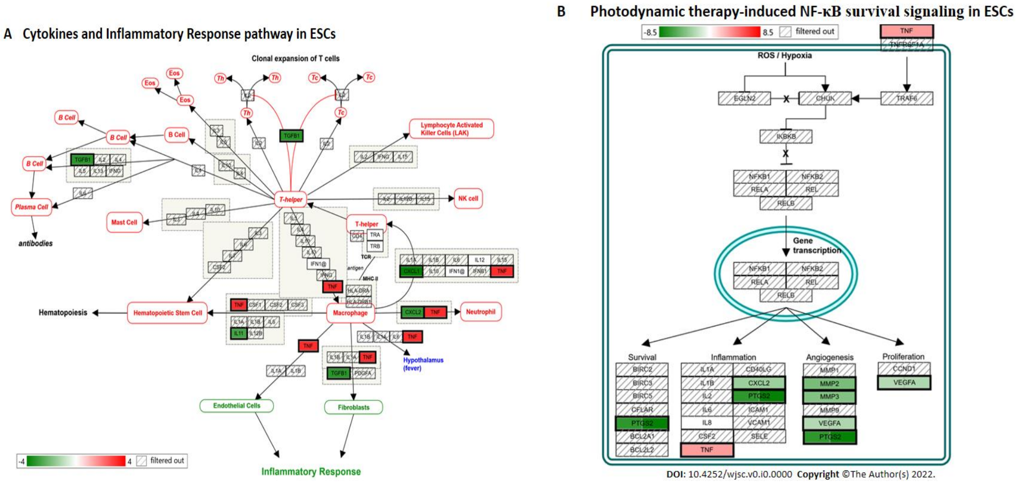

A Cytokines and Inflammatory Response pathway in BM-MSCs

B Photodynamic therapy-induced NF-κB survival signaling in BM-MSCs

DOI: 10.4252/wjsc.v0.i0.0000

Supplementary Figure 1 Differentially expressed genes. A: Cytokines and inflammatory response pathway in BM-MSCs; B: Photodynamic induced NF-kB survival pathway.



DOI: 10.4252/wjsc.v0.i0.0000

Supplementary Figure 2 Differentially expressed genes. A: Cytokines and inflammatory response pathway; B: Photodynamic induced NF-kB survival pathway.

Supplementary Table 1 List of the unique genes that are differentially expressed in Wharton's jelly-derived mesenchymal stromal/stem cells as compared with Bone marrow **mesenchymal stromal/stem cells or ESCs or fibroblasts.**

ID	**Gene symbol**	**Description**
202274_at	ACTG2	Actin, gamma 2, smooth muscle, enteric
229004_at	ADAMTS15	ADAM metallopeptidase with thrombospondin type 1 motif 15
209869_at	ADRA2A	Adrenoceptor alpha 2A
229070_at	ADTRP	Androgen-dependent TFPI-regulating protein
204348_s_at	AK4	Adenylate kinase 4
203180_at	ALDH1A3	Aldehyde dehydrogenase 1 family, member A3
202203_s_at	AMFR	Autocrine motility factor receptor, E3 ubiquitin protein ligase
207992_s_at	AMPD3	Adenosine monophosphate deaminase 3
241869_at	APOL6	Apolipoprotein L, 6
205239_at	AREG	Amphiregulin
225166_at	ARHGAP18	Rho GTPase activating protein 18
232994_s_at	ARHGEF28	Rho guanine nucleotide exchange factor 28
228890_at	ATOH8	Atonal bHLH transcription factor 8
209281_s_at	ATP2B1	ATPase, Ca++ transporting, plasma membrane 1
210818_s_at	BACH1; GRIK1-AS2	BTB and CNC homology 1, basic leucine zipper transcription factor 1; GRIK1 antisense RNA 2
221530_s_at	BHLHE41	Basic helix-loop-helix family, member e41
210538_s_at	BIRC3	Baculoviral IAP repeat containing 3
228570_at	BTBD11	BTB (POZ) domain containing 11
220975_s_at	C1QTNF1	C1q and tumor necrosis factor related protein 1
224197_s_at	C1QTNF1	C1q and tumor necrosis factor related protein 1
209970_x_at	CASP1	Caspase 1
216598_s_at	CCL2	Chemokine (C-C motif) ligand 2

205476_at	CCL20	Chemokine (C-C motif) ligand 20
209582_s_at	CD200	CD200 molecule
218451_at	CDCP1	CUB domain containing protein 1
204726_at	CDH13	Cadherin 13
205532_s_at	CDH6	Cadherin 6, type 2, K-cadherin (fetal kidney)
218182_s_at	CLDN1	Claudin 1
214841_at	CNIH3	Cornichon family AMPA receptor auxiliary protein 3
223796_at	CNTNAP3; CNTNAP3B; CNTNAP3P2; LOC100289279; LOC105369234	Contactin associated protein-like 3; contactin associated protein-like 3B; contactin associated protein-like 3 pseudogene 2; contactin associated protein-like 3-like; contactin-associated protein-like 3B
203477_at	COL15A1	Collagen, type XV, alpha 1
212940_at	COL6A1	Collagen, type VI, alpha 1
228728_at	CPED1	Cadherin-like and PC-esterase domain containing 1
202575_at	CRABP2	Cellular retinoic acid binding protein 2
208978_at	CRIP2	Cysteine-rich protein 2
210229_s_at	CSF2	Colony stimulating factor 2 (granulocyte-macrophage)
207442_at	CSF3	Colony stimulating factor 3
202902_s_at	CTSS	Cathepsin S
203666_at	CXCL12	Chemokine (C-X-C motif) ligand 12
207850_at	CXCL3	Chemokine (C-X-C motif) ligand 3
215101_s_at	CXCL5	Chemokine (C-X-C motif) ligand 5
207147_at	DLX2	Distal-less homeobox 2
205003_at	DOCK4	Dedicator of cytokinesis 4
203716_s_at	DPP4	Dipeptidyl-peptidase 4
244107_at	DSC3	Desmocollin 3

219850_s_at	EHF	Ets homologous factor
1554273_a_at	ERAP2	Endoplasmic reticulum aminopeptidase 2
205767_at	EREG	Epiregulin
231944_at	ERO1B	Endoplasmic reticulum oxidoreductase beta
203980_at	FABP4	Fatty acid binding protein 4, adipocyte
227320_at	FAM101A; ZNF664-FAM101A	Family with sequence similarity 101, member A; filamin-interacting protein FAM101A
226804_at	FAM20A	Family with sequence similarity 20, member A
210287_s_at	FLT1	Fms-related tyrosine kinase 1
203705_s_at	FZD7	Frizzled class receptor 7
213524_s_at	G0S2	G0/G1 switch 2
222773_s_at	GALNT12	Polypeptide N-acetylgalactosaminyltransferase 12
221577_x_at	GDF15	Growth differentiation factor 15
238681_at	GDPD1	Glycerophosphodiester phosphodiesterase domain containing 1
205100_at	GFPT2	Glutamine-fructose-6-phosphate transaminase 2
229105_at	GPR39	G protein-coupled receptor 39
213142_x_at	GSAP	Gamma-secretase activating protein
203821_at	HBEGF	Heparin-binding EGF-like growth factor
202957_at	HCLS1	Hematopoietic cell-specific Lyn substrate 1
204689_at	HHEX	Hematopoietically expressed homeobox
228697_at	HINT3	Histidine triad nucleotide binding protein 3
208025_s_at	HMGA2	High mobility group AT-hook 2
239153_at	HOTAIR	HOX transcript antisense RNA
208493_at	HOXA11	Homeobox A11
229400_at	HOXD10	Homeobox D10
202637_s_at	ICAM1	Intercellular adhesion molecule 1
208937_s_at	ID1	Inhibitor of DNA binding 1, dominant negative helix-

		loop-helix protein
201565_s_at	ID2	Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
209291_at	ID4	Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
206172_at	IL13RA2	Interleukin 13 receptor, alpha 2
210118_s_at	IL1A	Interleukin 1 alpha
205067_at	IL1B	Interleukin 1 beta
203828_s_at	IL32	Interleukin 32
209821_at	IL33	Interleukin 33
205207_at	IL6	Interleukin 6
231779_at	IRAK2	Interleukin 1 receptor associated kinase 2
204627_s_at	ITGB3	Integrin beta 3
203710_at	ITPR1	Inositol 1,4,5-trisphosphate receptor, type 1
210078_s_at	KCNAB1	Potassium channel, voltage gated subfamily A regulatory beta subunit 1
214595_at	KCNG1	Potassium channel, voltage gated modifier subfamily G, member 1
210119_at	KCNJ15	Potassium channel, inwardly rectifying subfamily J, member 15
239787_at	KCTD4	Potassium channel tetramerization domain containing 4
227875_at	KLHL13	Kelch-like family member 13
228937_at	LACC1	Laccase (multicopper oxidoreductase) domain containing 1
205569_at	LAMP3	Lysosomal-associated membrane protein 3
221011_s_at	LBH	Limb bud and heart development
206481_s_at	LDB2	LIM domain binding 2

200923_at	LGALS3BP	Lectin, galactoside-binding, soluble, 3 binding protein
218326_s_at	LGR4	Leucine-rich repeat containing G protein-coupled receptor 4
205266_at	LIF	Leukemia inhibitory factor
227929_at	LIN7A	Lin-7 homolog A (C. elegans)
215223_s_at	LOC100129518; SOD2	Uncharacterized LOC100129518; superoxide dismutase 2, mitochondrial
243961_at	LOC100505622	Uncharacterized LOC100505622
232504_at	LOC285628	MIR146A host gene
218559_s_at	MAFB	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog B
36711_at	MAFF	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog F
207761_s_at	METTL7A	Methyltransferase like 7A
205680_at	MMP10	Matrix metallopeptidase 10
231688_at	MMP8	Matrix metallopeptidase 8
219959_at	MOCOS	Molybdenum cofactor sulfurase
203037_s_at	MTSS1	Metastasis suppressor 1
217738_at	NAMPT	Nicotinamide phosphoribosyltransferase
204749_at	NAP1L3	Nucleosome assembly protein 1-like 3
212843_at	NCAM1	Neural cell adhesion molecule 1
207535_s_at	NFKB2	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)
201502_s_at	NFKBIA	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
205893_at	NLGN1	Neuroligin 1
39549_at	NPAS2	Neuronal PAS domain protein 2

222020_s_at	NTM	Neurotrimin
220911_s_at	NYNRIN	NYN domain and retroviral integrase containing
238469_at	OGFRL1	Opioid growth factor receptor-like 1
1554503_a_at	OSCAR	Osteoclast associated, immunoglobulin-like receptor
242871_at	PAQR5	Progestin and adipoQ receptor family member V
225975_at	PCDH18	Protocadherin 18
219295_s_at	PCOLCE2	Procollagen C-endopeptidase enhancer 2
205501_at	PDE10A	Phosphodiesterase 10A
209621_s_at	PDLIM3	PDZ and LIM domain 3
208502_s_at	PITX1	Paired-like homeodomain 1
209529_at	PLPP2	Phospholipid phosphatase 2
209355_s_at	PLPP3	Phospholipid phosphatase 3
210910_s_at	POMZP3	POM121 and ZP3 fusion
227749_at	POU2F2	POU class 2 homeobox 2
226069_at	PRICKLE1	Prickle homolog 1
230708_at	PRICKLE1	Prickle homolog 1
215707_s_at	PRNP	Prion protein
209465_x_at	PTN	Pleiotrophin
1560425_s_at	PTPRD-AS1	PTPRD antisense RNA 1
204802_at	RRAD	Ras-related associated with diabetes
1560477_a_at	SAMD11	Sterile alpha motif domain containing 11
236782_at	SAMD3	Sterile alpha motif domain containing 3
202376_at	SERPINA3	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3
200986_at	SERPING1	Serpin peptidase inhibitor, clade G (C1 inhibitor), member 1
202035_s_at	SFRP1	Secreted frizzled-related protein 1
225548_at	SHROOM3	Shroom family member 3

213664_at	SLC1A1	Solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1
205421_at	SLC22A3	Solute carrier family 22 (organic cation transporter), member 3
206376_at	SLC6A15	Solute carrier family 6 (neutral amino acid transporter), member 15
1558920_at	SLC8A1-AS1	SLC8A1 antisense RNA 1
232636_at	SLITRK4	SLIT and NTRK-like family, member 4
1566342_at	SOD2	Superoxide dismutase 2, mitochondrial
219993_at	SOX17	SRY box 17
229778_at	SPX	Spexin hormone
204595_s_at	STC1	Stanniocalcin 1
203001_s_at	STMN2	Stathmin 2
232914_s_at	SYTL2	Synaptotagmin-like 2
230438_at	TBX15	T-box 15
203887_s_at	THBD	Thrombomodulin
219892_at	TM6SF1	Transmembrane 6 superfamily member 1
223557_s_at	TMEFF2	Transmembrane protein with EGF-like and two follistatin-like domains 2
213338_at	TMEM158	Transmembrane protein 158 (gene/pseudogene)
202643_s_at	TNFAIP3	Tumor necrosis factor, alpha-induced protein 3
221085_at	TNFSF15	Tumor necrosis factor (ligand) superfamily, member 15
204485_s_at	TOM1L1	Target of myb1 like 1 membrane trafficking protein
235737_at	TSLP	Thymic stromal lymphopoietin
210513_s_at	VEGFA	Vascular endothelial growth factor A
218810_at	ZC3H12A	Zinc finger CCCH-type containing 12A

206373_at	ZIC1	Zic family member 1
219877_at	ZMAT4	Zinc finger, matrin-type 4

Supplementary Table 2 Gene Ontology and different pathways associated with unique genes of WJ-MSCs

Source	Term name	Term ID	Adjusted_p_value	Negative_log10_of_adjusted_p_value	Intersections
Gene Ontology: Biological Process (for Negative log10 > 6.0)					
GO:BP	Regulation of multicellular organismal process	GO:0051239	3.73E-10	9.428835828	ADRA2A,ADTRP,AREG,ATOH8,ATP2B1,BHLHE41,BIRC3,C1QTNF1,CASP1,CD200,CRABP2,CSF2,CSF3,CXCL12,DLX2,DOCK4,EREG,FABP4,FLT1,FZD7,G0S2,GDF15,HBEGF,HCLS1,HHEX,HMGA2,HOXA11,ICAM1,ID1,ID2,ID4,IL1A,IL1B,IL33,IL6,ITGB3,ITPR1,LBH,LGR4,LIF,MAFB,MAFF,MMP8,NFKB2,NFKBIA,NLGN1,NPAS2,OSCAR,PLPP3,PRICKLE1,PRNP,PTN,SERPING1,SFRP1,SLC1A1,SLITRK4,SOX17,SPX,STC1,STMN2,SYTL2,THBD,TNFAIP3,TSLP,VEGFA,ZC3H12A
GO:BP	Positive regulation of	GO:0051240	5.66E-10	9.24713796	ADRA2A,ATOH8,ATP2B1,BIRC3,C1QTNF1,CASP1,CD200,CRABP2,CSF2,CSF3,C

	multicellular organismal process				XCL12,DLX2,EREG,FABP4,FLT1,G0S2,HBEGF,HCLS1,HMGA2,HOXA11,ICAM1,ID2,IL1A,IL1B,IL33,IL6,ITGB3,LBH,LGR4,LIF,MMP8,NFKB2,NLGN1,NPAS2,OSCAR,PLPP3,PTN,SLC1A1,SLITRK4,SPX,STMN2,SYTL2,THBD,TNFAIP3,TSLP,VEGFA,ZC3H12A
GO:BP	Positive regulation of macromolecule metabolic process	GO:0010604	5.37E-09	8.270384475	ACTG2,ADRA2A,ADTRP,AREG,ATOH8,BIRC3,C1QTNF1,CASP1,CCL2,CCL20,CDH13,CSF2,CSF3,DLX2,EHF,EREG,FAM20A,FLT1,FZD7,GDF15,GSAP,HBEGF,HCLS1,HHEX,HMGA2,HOXA11,HOXD10,ICAM1,ID1,ID2,ID4,IL1A,IL1B,IL33,IL6,IRAK2,ITGB3,LAMP3,LBH,LDB2,LGR4,LIF,MAFB,MAFF,MMP8,NAMPT,NFKB2,NFKBIA,NPAS2,PCOLCE2,PITX1,POU2F2,PRICKLE1,PRNP,SFRP1,SOX17,TBX15,TNFAIP3,TNFSF15,TOM1L1,TSLP,VEGFA,ZC3H12A,ZIC1

GO:BP	Positive regulation of nitrogen compound metabolic process	GO:0051173	1.02E-08	7.992533632	ADRA2A,ADTRP,AREG,ATOH8,BIRC3,C1QTNF1,CASP1,CCL2,CCL20,CDH13,CSF2,CSF3,DLX2,EHF,EREG,FAM20A,FLT1,FZD7,GDF15,GSAP,HBEGF,HCLS1,HHEX,HMGA2,HOXA11,HOXD10,ICAM1,ID2,ID4,IL1A,IL1B,IL33,IL6,IRAK2,ITGB3,LBH,LDB2,LGR4,LIF,MAFB,MAFF,MMP8,NAMPT,NFKB2,NFKBIA,NPAS2,PCOLCE2,PITX1,POU2F2,PRICKLE1,PRNP,SFRP1,SOX17,TBX15,TNFAIP3,TNFSF15,TOM1L1,TSLP,VEGFA,ZC3H12A,ZIC1
GO:BP	Positive regulation of biological process	GO:0048518	1.02E-08	7.992533632	ACTG2,ADRA2A,ADTRP,ALDH1A3,AREG,ATOH8,ATP2B1,BIRC3,C1QTNF1,CASP1,CCL2,CCL20,CD200,CDH13,CLDN1,CRABP2,CRIP2,CSF2,CSF3,CTSS,CXCL12,CXCL5,DLX2,DOCK4,DPP4,EHF,EREG,FABP4,FAM20A,FLT1,FZD7,G0S2,GDF15,GSAP,HBEGF,HCLS1,HHEX,HMGA2,HOXA11,H

					OXD10,ICAM1,ID1,ID2,ID4,IL13RA2,IL1A,IL1B,IL33,IL6,IRAK2,ITGB3,LAMP3,LBH,LDB2,LGR4,LIF,MAFB,MAFF,MMP8,NAMPT,NFKB2,NFKBIA,NLGN1,NPAS2,OSCAR,PCOLCE2,PITX1,PLPP3,POMZP3,POU2F2,PRICKLE1,PRNP,PTN,SERPING1,SFRP1,SLC1A1,SLITRK4,SOX17,SPX,STC1,STMN2,SYTL2,TBX15,THBD,TNFAIP3,TNFSF15,TOM1L1,TSLP,VEGFA,ZC3H12A,ZIC1
GO:BP	Positive regulation of metabolic process	GO:0009893	1.13E-08	7.947579826	ACTG2,ADRA2A,ADTRP,AREG,ATOH8,BIRC3,C1QTNF1,CASP1,CCL2,CCL20,CDH13,CSF2,CSF3,DLX2,EHF,EREG,FABP4,FAM20A,FLT1,FZD7,G0S2,GDF15,GSAP,HBEGF,HCLS1,HHEX,HMGA2,HOXA11,HOXD10,ICAM1,ID1,ID2,ID4,IL1A,IL1B,IL33,IL6,IRAK2,ITGB3,LAMP3,LBH,LDB2,LGR4,LIF,MAFB,MAFF,MMP8,NAMPT,NFKB2,NFKBIA,NPAS2,PCOLCE2,PITX1,POU2F2,P

					RICKLE1,PRNP,SFRP1,SOX17,TBX15,TNFAIP3,TNFSF15,TOM1L1,TSLP,VEGFA,ZC3H12A,ZIC1
GO:BP	Response to cytokine	GO:0034097	1.65E-08	7.782451203	BIRC3,CASP1,CCL2,CCL20,CLDN1,CSF2,CSF3,CXCL12,CXCL3,CXCL5,EREG,FABP4,GFPT2,HCLS1,ICAM1,IL13RA2,IL1A,IL1B,IL32,IL33,IL6,IRAK2,LAMP3,LIF,NCAM1,NFKB2,NFKBIA,PCOLCE2,SFRP1,SOX17,TNFAIP3,TNFSF15,TSLP,VEGFA,ZC3H12A
GO:BP	Anatomical structure morphogenesis	GO:0009653	2.58E-08	7.587756439	ACTG2,ADTRP,ALDH1A3,AREG,ARHGAP18,ATOH8,CCL2,CDH13,CDH6,COL15A1,COL6A1,CRABP2,CXCL12,DLX2,EREG,FAM20A,FLT1,FZD7,GDF15,HBEGF,HCLS1,HHEX,HMGA2,HOXA11,HOXD10,ICAM1,ID1,ID2,ID4,IL1A,IL1B,IL6,ITGB3,LGR4,LIF,MAFB,MMP8,MTSS1,NCAM1,NFKB2,NLGN1,PITX1,PRICKLE1,PTN,SFRP1,SHROOM3,SLITRK4,SOX17,STC1,TBX15,TMEF

					F2,TNFAIP3,VEGFA,ZC3H12A,ZIC1
GO:BP	Multicellular organismal process	GO:0032501	2.58E-08	7.587756439	ACTG2,ADRA2A,ADTRP,AK4,ALDH1A3,AMFR,AMPD3,AREG,ATOH8,ATP2B1,BHLHE41,BIRC3,C1QTNF1,CASP1,CCL2,CD200,CDH13,CDH6,CLDN1,COL15A1,COL6A1,CRABP2,CRIP2,CSF2,CSF3,CXCL12,DLX2,DOCK4,DPP4,DSC3,EHF,ERAP2,EREG,FABP4,FAM20A,FLT1,FZD7,G0S2,GDF15,HBEGF,HCLS1,HHEX,HMGA2,HOXA11,HOXD10,ICAM1,ID1,ID2,ID4,IL1A,IL1B,IL33,IL6,ITGB3,ITPR1,KCNAB1,LBH,LDB2,LGR4,LIF,LIN7A,MAFB,MAFF,MMP8,MTSS1,NAMPT,NCAM1,NFKB2,NFKBIA,NLGN1,NPAS2,NTM,OSCAR,PAQR5,PCDH18,PDLIM3,PITX1,PLPP3,POMZP3,POU2F2,PRICKLE1,PRNP,PTN,SERPINA3,SERPING1,SFRP1,SHROOM3,SLC1A1,SLITRK4,SOX17,SPX,STC1,STMN2,SYTL2,T

					BX15,THBD,TMEFF2,TNFAIP3,TSLP,VEGFA,ZC3H12A,ZIC1
GO:BP	Cellular response to cytokine stimulus	GO:0071345	2.74E-08	7.561656406	BIRC3,CASP1,CCL2,CCL20,CLDN1,CSF2,CSF3,CXCL12,CXCL3,CXCL5,EREG,FABP4,GFPT2,HCLS1,ICAM1,IL13RA2,IL1A,IL1B,IL32,IL33,IL6,IRAK2,LIF,NCAM1,NFKBIA,PCOLCE2,SFRP1,SOX17,TNFAIP3,TNFSF15,TSLP,VEGFA,ZC3H12A
GO:BP	Positive regulation of cellular metabolic process	GO:0031325	3.79E-08	7.420823005	ADRA2A,ADTRP,AREG,ATOH8,BIRC3,C1QTNF1,CASP1,CCL2,CCL20,CDH13,CSF2,CSF3,DLX2,EHF,EREG,FAM20A,FLT1,FZD7,GDF15,GSAP,HBEGF,HCLS1,HHEX,HMGA2,HOXA11,HOXD10,ICAM1,ID2,ID4,IL1A,IL1B,IL33,IL6,IRAK2,ITGB3,LBH,LDB2,LGR4,LIF,MAFB,MAFF,MMP8,NAMPT,NFKB2,NFKBIA,NPAS2,PCOLCE2,PITX1,POU2F2,PRICKLE1,PRNP,SFRP1,SOX17,TBX15,TNFAIP3,TNFSF15,TO

					M1L1,TSLP,VEGFA,ZC3H12A,ZIC1
GO:BP	Positive regulation of cell population proliferation	GO:0008284	4.96E-08	7.304390816	ADRA2A,AREG,CDH13,CLDN1,CRIP2,CSF2,CSF3,CXCL12,CXCL5,DPP4,EREG,FLT1,FZD7,HBEGF,HCLS1,HMGA2,ID1,ID2,ID4,IL1B,IL6,ITGB3,LBH,LIF,NAMPT,PTN,SFRP1,TNFAIP3,TSLP,VEGFA
GO:BP	Positive regulation of peptidyl-tyrosine phosphorylation	GO:0050731	1.68E-07	6.774574709	ADRA2A,AREG,CSF2,CSF3,EREG,HBEGF,HCLS1,ICAM1,IL6,ITGB3,LIF,PRNP,TSLP,VEGFA
GO:BP	Cellular response to chemical stimulus	GO:0070887	3.00E-07	6.523542896	ADRA2A,ADTRP,AK4,AMFR,ATP2B1,BIRC3,CASP1,CCL2,CCL20,CLDN1,COL6A1,CSF2,CSF3,CTSS,CXCL12,CXCL3,CXCL5,DOCK4,DPP4,EREG,FABP4,FLT1,FZD7,GDF15,GFPT2,HBEGF,HCLS1,HHEX,HMGA2,ICAM1,ID1,ID2,IL13RA2,IL1A,IL1B,IL32,IL33,IL6,IRAK2,ITGB3,LBH,LGR4,LIF,NAMPT,N

					CAM1,NFKBIA,NLGN1,PCOLCE2,PRNP,PTN,SFRP1,SOX17,STC1,STMN2,TNFAIP3,TNFSF15,TSLP,VEGFA,ZC3H12A
GO:BP	Regulation of response to stimulus	GO:0048583	3.37E-07	6.472437548	ADRA2A,ADTRP,AMFR,AREG,ARHGAP18,ARHGEF28,ATP2B1,BIRC3,C1QTNF1,CASP1,CCL2,CCL20,CD200,CDH13,CLDN1,CNIH3,CRABP2,CSF2,CSF3,CTSS,CXCL12,DLX2,DPP4,EREG,FABP4,FLT1,FZD7,G0S2,GDF15,HBEGF,HCLS1,HHEX,HMGA2,ICAM1,ID1,IL13RA2,IL1A,IL1B,IL33,IL6,IRAK2,ITGB3,ITPR1,LBH,LGR4,LIF,MMP8,NAMPT,NCAM1,NFKBIA,NLGN1,NPAS2,OSCAR,PDE10A,PLPP3,PRICKLE1,PRNP,PTN,SERPING1,SFRP1,SOX17,SPX,THBD,TNFAIP3,TNFSF15,TSLP,VEGFA,ZC3H12A,ZIC1
GO:BP	Cellular developmental process	GO:0048869	3.40E-07	6.469074258	AREG,ARHGAP18,ARHGEF28,ATOH8,BHLHE41,CCL2,CDH13,CDH6,CLDN1,COL15A1,COL6A1,CRABP2,C

					SF2,CSF3,CXCL12,DLX2,DSC3,EHF,EREG,FABP4,FLT1,FZD7,GDF15,HCLS1,HHEX,HMGA2,HOXA11,HOXD10,ICAM1,ID1,ID2,ID4,IL1A,IL1B,IL33,IL6,ITGB3,KCNAB1,LBH,LGR4,LIF,MAFB,MAFF,MMP8,MTSS1,NAMPT,NCAM1,NFKB2,NFKBIA,NLGN1,NTM,OSCAR,PAQR5,PITX1,POMZP3,POU2F2,PRICKLE1,PRNP,PTN,SFRP1,SHROOM3,SLITRK4,SOX17,STC1,STMN2,TBX15,TMEFF2,VEGFA,ZC3H12A,ZIC1
GO:BP	Cell population proliferation	GO:0008283	3.49E-07	6.457059179	ADRA2A,AREG,ATOH8,CCL2,CD200,CDH13,CLDN1,CRIP2,CSF2,CSF3,CXCL12,CXCL5,DPP4,EHF,EREG,FLT1,FZD7,HBEGF,HCLS1,HHEX,HMGA2,ID1,ID2,ID4,IL1A,IL1B,IL33,IL6,ITGB3,LBH,LGR4,LIF,MTSS1,NAMPT,NFKBIA,PRNP,PTN,SFRP1,SOX17,STC1,TNFAIP3,TSLP,VEGFA
GO:B	Regulation	GO:000	3.49E-07	6.45705917	ADRA2A,ADTRP,AREG,C1

P	of protein phosphorylation	1932		9	QTNF1,CCL2,CCL20,CSF2,CSF3,EREG,FABP4,FAM20A,FLT1,FZD7,GDF15,HBEGF,HCLS1,HHEX,HMGA2,ICAM1,ID1,IL1B,IL6,IRAK2,ITGB3,LBH,LIF,MMP8,PLPP3,PRNP,SFRP1,TNFAIP3,TNFSF15,TOM1L1,TSLP,VEGFA,ZC3H12A
GO:BP	Cellular response to organic substance	GO:0071310	3.57E-07	6.447501735	ADRA2A,ADTRP,AMFR,ATP2B1,BIRC3,CASP1,CCL2,CCL20,CLDN1,COL6A1,CSF2,CSF3,CTSS,CXCL12,CXCL3,CXCL5,EREG,FABP4,FLT1,FZD7,GDF15,GFPT2,HCLS1,HHEX,ICAM1,ID1,IL13RA2,IL1A,IL1B,IL32,IL33,IL6,IRAK2,ITGB3,LBH,LGR4,LIF,NAMPT,NCAM1,NFKBIA,PCOLCE2,PRNP,PTN,SFRP1,SOX17,STC1,STMN2,TNFAIP3,TNFSF15,TSLP,VEGFA,ZC3H12A
GO:BP	Response to external stimulus	GO:0009605	3.90E-07	6.409344832	ADTRP,ALDH1A3,ATP2B1,BIRC3,C1QTNF1,CASP1,CCL2,CCL20,CD200,CDH13,CLDN1,CSF2,CSF3,CTSS,CXCL12,CXCL3,CXCL5,DOC

					K4,DPP4,EREG,FABP4,FAM20A,FLT1,GDF15,HBEGF,HMGA2,ICAM1,ID2,IL1A,IL1B,IL33,IL6,IRAK2,ITGB3,LGR4,MMP8,NAMPT,NCAM1,NFKB2,NFKBIA,PTN,SERPING1,SFRP1,SHROOM3,SLC22A3,SPX,STC1,THBD,TMEFF2,TNFAIP3,TSLP,VEGFA,ZC3H12A
GO:BP	Cellular response to lipopolysaccharide	GO:0071222	3.90E-07	6.409344832	CASP1,CCL2,CSF2,CSF3,CXCL3,CXCL5,ICAM1,IL1A,IL1B,IL6,IRAK2,NFKBIA,TNFAIP3,ZC3H12A
GO:BP	Cell surface receptor signaling pathway	GO:0007166	3.90E-07	6.409344832	ADRA2A,AMFR,AREG,ARHGEF28,ATOH8,BIRC3,BTBD11,CASP1,CCL2,CCL20,CDH13,CDH6,CNIH3,CSF2,CSF3,CXCL12,CXCL3,CXCL5,DLX2,EREG,FLT1,FZD7,G0S2,GDF15,HBEGF,HCLS1,HHEX,ICAM1,ID1,IL13RA2,IL1A,IL1B,IL32,IL33,IL6,IRAK2,ITGB3,LGR4,LIF,MTSS1,NCAM1,NFKBIA,NLGN1,OSCAR,PLPP3,PRICKLE1,PRNP,PTN,SFRP1,SOX17,TNFAIP3,TNFSF15,TSLP,

					VEGFA,ZC3H12A,ZIC1
GO:BP	Regulation of phosphorylation	GO:0042325	3.90E-07	6.409344832	ADRA2A,ADTRP,AK4,AREG,C1QTNF1,CCL2,CCL20,CSF2,CSF3,EREG,FABP4,FAM20A,FLT1,FZD7,GDF15,HBEGF,HCLS1,HHEX,HMGA2,ICAM1,ID1,IL1B,IL6,IRAK2,ITGB3,LBH,LDB2,LIF,MMP8,PLPP3,PRNP,SFRP1,TNFAIP3,TNFSF15,TOM1L1,TSLP,VEGFA,ZC3H12A
GO:BP	Positive regulation of protein metabolic process	GO:0051247	4.15E-07	6.382159433	ADRA2A,ADTRP,AREG,BIRC3,C1QTNF1,CASP1,CCL2,CCL20,CSF2,CSF3,EREG,FAM20A,FLT1,FZD7,GDF15,GSAP,HBEGF,HCLS1,HMGA2,ICAM1,IL1A,IL1B,IL33,IL6,IRAK2,ITGB3,LIF,MMP8,NFKBIA,PCOLCE2,PRICKLE1,PRNP,SOX17,TNFAIP3,TNFSF15,TOM1L1,TSLP,VEGFA,ZC3H12A
GO:BP	Regulation of cell population proliferation	GO:0042127	4.15E-07	6.382159433	ADRA2A,AREG,ATOH8,CCL2,CD200,CDH13,CLDN1,CRIP2,CSF2,CSF3,CXCL12,CXCL5,DPP4,EREG,FLT1,FZD7,HBEGF,HCLS1,HHEX,

					HMGA2,ID1,ID2,ID4,IL1A,IL1B,IL6,ITGB3,LBH,LIF,MTSS1,NAMPT,NFKBIA,PRNP,PTN,SFRP1,SOX17,TNFAIP3,TSLP,VEGFA
GO:BP	Response to lipopolysaccharide	GO:0032496	4.38E-07	6.358698545	CASP1,CCL2,CLDN1,CSF2,CSF3,CXCL3,CXCL5,ICAM1,IL1A,IL1B,IL6,IRAK2,NFKB2,NFKBIA,THBD,TNFAIP3,ZC3H12A
GO:BP	Regulation of peptidyl-tyrosine phosphorylation	GO:0050730	4.38E-07	6.358698545	ADRA2A,AREG,CSF2,CSF3,EREG,HBEGF,HCLS1,ICAM1,IL6,ITGB3,LIF,PRNP,SFRP1,TSLP,VEGFA
GO:BP	Positive regulation of protein phosphorylation	GO:0001934	4.38E-07	6.358698545	ADRA2A,ADTRP,AREG,C1QTNF1,CCL2,CCL20,CSF2,CSF3,EREG,FAM20A,FLT1,FZD7,GDF15,HBEGF,HCLS1,HMGA2,ICAM1,IL1B,IL6,IRAK2,ITGB3,LIF,MMP8,PRNP,TNFSF15,TOM1L1,TSLP,VEGFA,ZC3H12A
GO:BP	Developmental process	GO:0032502	5.07E-07	6.294757758	ACTG2,ADTRP,AK4,ALDH1A3,AMFR,AREG,ARHGAP18,ARHGEF28,ATOH8,ATP2B1,BHLHE41,BIRC3,CCL

					2,CDH13,CDH6,CLDN1,COL15A1,COL6A1,CRABP2,CRIP2,CSF2,CSF3,CXCL12,DLX2,DSC3,EHF,EREG,FABP4,FAM20A,FLT1,FZD7,GDF15,HBEGF,HCLS1,HHEX,HMGA2,HOXA11,HOXD10,ICAM1,ID1,ID2,ID4,IL1A,IL1B,IL33,IL6,ITGB3,ITPR1,KCNAB1,LBH,LDB2,LGR4,LIF,LIN7A,MAFB,MAFF,MMP8,MTSS1,NAMPT,NCAM1,NFKB2,NFKBIA,NLGN1,NPAS2,NTM,OSCAR,PAQR5,PCDH18,PDLIM3,PITX1,POMZP3,POU2F2,PRICKLE1,PRNP,PTN,SERPING1,SFRP1,SHROOM3,SLITRK4,SOX17,STC1,STMN2,TBX15,TMEFF2,TNFAIP3,VEGFA,ZC3H12A,ZIC1
GO:BP	Regulation of phosphate metabolic process	GO:0019220	5.38E-07	6.269342633	ADRA2A,ADTRP,AK4,AREG,C1QTNF1,CCL2,CCL20,CSF2,CSF3,EREG,FABP4,FAM20A,FLT1,FZD7,GDF15,HBEGF,HCLS1,HHEX,HMGA2,ICAM1,ID1,IL1B,IL6,IRAK2,ITGB3,LBH,LDB2,LIF,

					MMP8,PLPP3,PRNP,PTN,SFRP1,SYTL2,TNFAIP3,TNFSF15,TOM1L1,TSLP,VEGFA,ZC3H12A
GO:BP	Epithelial cell proliferation	GO:0050673	5.38E-07	6.269342633	AREG,ATOH8,CCL2,CDH13,CLDN1,CXCL12,EHF,EREG,FLT1,FZD7,ID1,ID2,ITGB3,LGR4,MTSS1,PTN,SFRP1,TNFAIP3,VEGFA
GO:BP	Regulation of phosphorus metabolic process	GO:0051174	5.38E-07	6.269342633	ADRA2A,ADTRP,AK4,AREG,C1QTNF1,CCL2,CCL20,CSF2,CSF3,EREG,FABP4,FAM20A,FLT1,FZD7,GDF15,HBEGF,HCLS1,HHEX,HMGA2,ICAM1,ID1,IL1B,IL6,IRAK2,ITGB3,LBH,LDB2,LIF,MMP8,PLPP3,PRNP,PTN,SFRP1,SYTL2,TNFAIP3,TNFSF15,TOM1L1,TSLP,VEGFA,ZC3H12A
GO:BP	Cellular response to molecule of bacterial origin	GO:0071219	5.48E-07	6.261376104	CASP1,CCL2,CSF2,CSF3,CXCL3,CXCL5,ICAM1,IL1A,IL1B,IL6,IRAK2,NFKBIA,TNFAIP3,ZC3H12A
GO:BP	Tissue development	GO:0009888	6.00E-07	6.22206808	ACTG2,ALDH1A3,AREG,ATOH8,ATP2B1,CLDN1,COL6A1,CRABP2,DLX2,DSC3,

					EHF,EREG,FAM20A,FZD7,HBEGF,HMGA2,HOXA11,HOXD10,ICAM1,ID1,ID2,ID4,IL1B,IL6,ITGB3,KCNAB1,LBH,LDB2,LGR4,LIF,MAFF,MMP8,MTSS1,PITX1,PRICKLE1,PRNP,PTN,SFRP1,SHROOM3,SOX17,STC1,TMEFF2,VEGFA
GO:BP	Cytokine-mediated signaling pathway	GO:0019221	6.00E-07	6.22206808	BIRC3,CASP1,CCL2,CCL20,CSF2,CSF3,CXCL12,CXCL3,CXCL5,EREG,ICAM1,IL13RA2,IL1A,IL1B,IL32,IL33,IL6,IRAK2,LIF,NCAM1,NFKBIA,TNFAIP3,TNFSF15,TSLP,VEGFA
GO:BP	Cellular response to lipid	GO:0071396	6.45E-07	6.190659234	ADTRP,ATP2B1,CASP1,CCL2,CLDN1,CSF2,CSF3,CXCL3,CXCL5,FZD7,ICAM1,IL1A,IL1B,IL6,IRAK2,LBH,NFKBIA,PTN,SFRP1,STC1,TNFAIP3,ZC3H12A
GO:BP	Positive regulation of gene expression	GO:0010628	6.63E-07	6.178503303	ACTG2,ADTRP,ATOH8,C1QTNF1,CDH13,CSF2,CSF3,DLX2,EHF,FZD7,HCLS1,HHEX,HMGA2,HOXA11,HOXD10,ID1,ID2,ID4,IL1A,IL1B,IL33,IL6,LAMP3,LBH,LD

					B2,LGR4,LIF,MAFB,MAFF,MMP8,NAMPT,NFKB2,NFKBIA,NPAS2,PITX1,POU2F2,SFRP1,SOX17,TBX15,VEGFA,ZC3H12A,ZIC1
GO:BP	Anatomical structure formation involved in morphogenesis	GO:0048646	6.69E-07	6.174551039	ADTRP,ALDH1A3,ATOH8,CCL2,CDH13,COL15A1,COL6A1,EREG,FAM20A,FLT1,FZD7,GDF15,HHEX,HMGA2,HOXA11,ID1,IL1A,IL1B,IL6,ITGB3,MAFB,MMP8,NFKB2,PRICKLE1,PTN,SFRP1,SHROOM3,SOX17,TNFAIP3,VEGFA,ZC3H12A
GO:BP	Negative regulation of response to stimulus	GO:0048585	6.78E-07	6.168608287	ADRA2A,ADTRP,AMFR,AREG,C1QTNF1,CCL2,CD200,CSF2,CXCL12,DLX2,DPP4,EREG,GDF15,HBEGF,HHEX,HMGA2,ICAM1,IL13RA2,IL1A,IL1B,IL33,IL6,ITPR1,LBH,LGR4,LIF,NAMPT,NFKBIA,PDE10A,PRICKLE1,PRNP,SERPING1,SFRP1,SOX17,SPX,THBD,TNFAIP3,ZC3H12A
GO:BP	Response to molecule	GO:0002237	7.06E-07	6.151221178	CASP1,CCL2,CLDN1,CSF2,CSF3,CXCL3,CXCL5,ICAM1,IL1A,IL1B,IL6,IRAK2,NF

	of bacterial origin				KB2,NFKBIA,THBD,TNFAIP3,ZC3H12A
GO:BP	Negative regulation of multicellular organismal process	GO:0051241	7.06E-07	6.151221178	ADTRP,AREG,ATP2B1,C1QTNF1,CD200,DLX2,DOCK4,FZD7,GDF15,HHEX,ID1,ID2,ID4,IL1B,IL33,IL6,LGR4,MAFB,MMP8,NFKBIA,NLGN1,PRICKLE1,PRNP,PTN,SERPING1,SFRP1,SOX17,SPX,STC1,STMN2,THBD,TNFAIP3,ZC3H12A
GO:BP	System development	GO:0048731	7.06E-07	6.151221178	ACTG2,ADTRP,AK4,ALDH1A3,AREG,ATOH8,ATP2B1,BHLHE41,CCL2,CDH13,CLDN1,COL15A1,COL6A1,CRABP2,CRIP2,CSF2,CSF3,CXCL12,DLX2,DSC3,EREG,FAM20A,FLT1,FZD7,HBEGF,HCLS1,HHEX,HMGA2,HOXA11,HOXD10,ICAM1,ID1,ID2,ID4,IL1A,IL1B,IL33,IL6,ITGB3,KCNAB1,LBH,LDB2,LGR4,LIF,LIN7A,MAFB,MAFF,MTSS1,NCAM1,NFKB2,NFKBIA,NLGN1,NPAS2,NTM,OSCAR,PCDH18,PDLIM3,PITX1,POU2F2,PRICKLE1,PTN,SFRP1,SHROOM3

					,SLITRK4,SOX17,STC1,STMN2,TBX15,TMEFF2,TNFAIP3,VEGFA,ZC3H12A,ZIC1
GO:BP	Tube morphogenesis	GO:0035239	7.38E-07	6.132140516	ADTRP,AREG,ATOH8,CCL2,CDH13,COL15A1,EREG,FLT1,HHEX,HMGA2,HOXA11,ID1,ID2,IL1A,IL1B,IL6,ITGB3,LGR4,MTSS1,PRICKLE1,PTN,SFRP1,SHROOM3,SOX17,TNFAIP3,VEGFA,ZC3H12A
GO:BP	Regulation of localization	GO:0032879	7.53E-07	6.123452316	ADRA2A,ADTRP,ARHGAP18,ATOH8,ATP2B1,C1QTNF1,CASP1,CCL2,CCL20,CD200,CDH13,CLDN1,CNIH3,CTSS,CXCL12,DOCK4,DPP4,EREG,FLT1,HBEGF,HCLS1,ICAM1,IL13RA2,IL1A,IL1B,IL33,IL6,ITGB3,ITPR1,KCNAB1,KCNG1,KCNJ15,LDB2,LGR4,LIF,MMP8,NFKBIA,NLGN1,PLPP3,PRNP,PTN,RRAD,SFRP1,SPX,STC1,SYTL2,TMEFF2,TNFAIP3,TSLP,VEGFA,ZC3H12A,ZIC1

GO:BP	Response to organic substance	GO:0010033	8.33E-07	6.079591018	ADRA2A,ADTRP,AMFR,AREG,ATP2B1,BIRC3,CASP1,CCL2,CCL20,CDH13,CLDN1,COL6A1,CSF2,CSF3,CTSS,CXCL12,CXCL3,CXCL5,EREG,FABP4,FLT1,FZD7,GDF15,GFPT2,HCLS1,HHEX,ICAM1,ID1,IL13RA2,IL1A,IL1B,IL32,IL33,IL6,IRAK2,ITGB3,LAMP3,LBH,LGR4,LIF,NAMPT,NCAM1,NFKB2,NFKBIA,PCOLCE2,PRNP,PTN,SFRP1,SOX17,STC1,STMN2,THBD,TNFAIP3,TNFSF15,TSLP,VEGFA,ZC3H12A
GO:BP	Immune system process	GO:0002376	8.50E-07	6.070612837	ADTRP,AMPD3,BIRC3,CASP1,CCL2,CCL20,CD200,CLDN1,CRIP2,CSF2,CSF3,CTSS,CXCL12,CXCL3,CXCL5,DPP4,ERAP2,EREG,FLT1,FZD7,HCLS1,HHEX,ICAM1,ID2,IL13RA2,IL1A,IL1B,IL32,IL33,IL6,IRAK2,ITGB3,LAMP3,LGR4,LIF,MAFB,METTL7A,MMP8,NAMPT,NCAM1,NFKB2,NFKBIA,OSCAR,POU2F2,PRNP,PTN,SERP

					INA3,SERPING1,SFRP1,THBD,TNFAIP3,TNFSF15,TSLP,VEGFA,ZC3H12A
GO:BP	Multicellular organism development	GO:0007275	8.75E-07	6.058137497	ACTG2,ADTRP,AK4,ALDH1A3,AREG,ATOH8,ATP2B1,BHLHE41,CCL2,CDH13,CDH6,CLDN1,COL15A1,COL6A1,CRABP2,CRIP2,CSF2,CSF3,CXCL12,DLX2,DSC3,EHF,EREG,FAM20A,FLT1,FZD7,HBEGF,HCLS1,HHEX,HMGA2,HOXA11,HOXD10,ICAM1,ID1,ID2,ID4,IL1A,IL1B,IL33,IL6,ITGB3,ITPR1,KCNAB1,LBH,LDB2,LGR4,LIF,LIN7A,MAFB,MAFF,MMP8,MTSS1,NCAM1,NFKB2,NFKBIA,NLGN1,NPAS2,NTM,OSCAR,PAQR5,PCDH18,PDLIM3,PITX1,POU2F2,PRICKLE1,PTN,SFRP1,SHROOM3,SLITRK4,SOX17,STC1,STMN2,TBX15,TMEFF2,TNFAIP3,VEGFA,ZC3H12A,ZIC1
GO:BP	Cell differentiation	GO:0030154	9.73E-07	6.012029938	AREG,ARHGEF28,ATOH8,BHLHE41,CCL2,CLDN1,COL15A1,COL6A1,CRABP2,

					CSF2,CSF3,CXCL12,DLX2,DSC3,EHF,EREG,FABP4,FLT1,FZD7,GDF15,HCLS1,HHEX,HMGA2,HOXA11,HOXD10,ICAM1,ID1,ID2,ID4,IL1A,IL1B,IL33,IL6,ITGB3,KCNAB1,LBH,LGR4,LIF,MAFB,MAFF,MMP8,MTSS1,NCAM1,NFKB2,NFKBIA,NLGN1,NTM,OSCAR,PAQR5,PITX1,POMZP3,POU2F2,PRICKLE1,PRNP,PTN,SFRP1,SHROOM3,SLITRK4,SOX17,STC1,STMN2,TBX15,TMEFF2,VEGFA,ZC3H12A,ZIC1

Gene Ontology: Molecular function (for Negative log10 > 2.0)

Source	**Term Name**	**Term ID**	**Adjusted_p_value**	**Negative_log10_of_adjusted_p_value**	**Intersections**
GO:MF	Cytokine activity	GO:0005125	9.08E-12	11.04179769	AREG,CCL2,CCL20,CSF2,CSF3,CXCL12,CXCL3,CXCL5,GDF15,IL1A,IL1B,IL32,IL33,IL6,LIF,NAMPT,TNFSF15,TSLP,VEGFA
GO:MF	Signaling receptor activator	GO:0030546	4.34E-11	10.36297331	AREG,CCL2,CCL20,CSF2,CSF3,CXCL12,CXCL3,CXCL5,DPP4,EREG,GDF15,HBEG

	activity				F,IL1A,IL1B,IL32,IL33,IL6,LIF,NAMPT,PTN,SPX,STC1,TNFSF15,TSLP,VEGFA
GO:MF	Receptor ligand activity	GO:0048018	4.34E-11	10.36297331	AREG,CCL2,CCL20,CSF2,CSF3,CXCL12,CXCL3,CXCL5,DPP4,EREG,GDF15,HBEGF,IL1A,IL1B,IL32,IL33,IL6,LIF,NAMPT,PTN,SPX,STC1,TNFSF15,TSLP,VEGFA
GO:MF	Receptor regulator activity	GO:0030545	2.08E-10	9.681189258	AREG,CCL2,CCL20,CSF2,CSF3,CXCL12,CXCL3,CXCL5,DPP4,EREG,GDF15,HBEGF,IL1A,IL1B,IL32,IL33,IL6,LIF,NAMPT,PTN,SPX,STC1,TNFSF15,TSLP,VEGFA
GO:MF	Cytokine receptor binding	GO:0005126	5.69E-08	7.244962003	CCL2,CCL20,CSF2,CSF3,CXCL12,CXCL3,CXCL5,IL1A,IL1B,IL33,IL6,ITGB3,LIF,TNFSF15,TSLP,VEGFA
GO:MF	Molecular function regulator	GO:0098772	4.34E-07	6.363007642	AREG,ARHGAP18,ARHGEF28,BIRC3,CASP1,CCL2,CCL20,CNIH3,CSF2,CSF3,CXCL12,CXCL3,CXCL5,DOCK4,DPP4,EREG,FAM20A,GDF15,HBEGF,IL1A,IL1B,IL32,IL33,IL6,ITPR1,KCNAB1,LIF,NAMPT,PCOLCE2,PRNP,PTN,RRAD,SERPINA3,SERP

					ING1,SPX,STC1,TNFSF15,TOM1L1,TSLP,VEGFA
GO:MF	Growth factor receptor binding	GO:0070851	1.19477E-06	5.922716634	AREG,CSF2,CSF3,EREG,HBEGF,IL1A,IL1B,IL6,ITGB3,TSLP,VEGFA
GO:MF	Signaling receptor binding	GO:0005102	1.87038E-06	5.72806973	ADRA2A,AREG,CCL2,CCL20,CSF2,CSF3,CXCL12,CXCL3,CXCL5,DOCK4,DPP4,EREG,FABP4,FZD7,GDF15,HBEGF,ICAM1,IL1A,IL1B,IL32,IL33,IL6,ITGB3,LIF,MTSS1,NAMPT,NLGN1,PRNP,PTN,SFRP1,SPX,STC1,SYTL2,TNFSF15,TSLP,VEGFA
GO:MF	Growth factor activity	GO:0008083	6.05709E-06	5.217735818	AREG,CSF2,CSF3,CXCL12,EREG,GDF15,HBEGF,IL6,LIF,PTN,VEGFA
GO:MF	Protein binding	GO:0005515	0.001086466	2.96398387	ADRA2A,AK4,ALDH1A3,AMFR,AMPD3,APOL6,AREG,ARHGAP18,ARHGEF28,ATOH8,ATP2B1,BHLHE41,BIRC3,BTBD11,C1QTNF1,CASP1,CCL2,CCL20,CD200,CDCP1,CDH13,CDH6,CLDN1,COL6A1,CRABP2,CRIP2,CSF2,CSF3,CTSS,CXCL12,CXCL3,CXCL5,DLX2,DOC

					K4,DPP4,DSC3,EREG,ERO1B,FABP4,FAM20A,FLT1,FZD7,G0S2,GDF15,GFPT2,GPR39,GSAP,HBEGF,HCLS1,HHEX,HINT3,HMGA2,ICAM1,ID1,ID2,ID4,IL13RA2,IL1A,IL1B,IL32,IL33,IL6,IRAK2,ITGB3,ITPR1,KCNAB1,KCNG1,KCNJ15,KCTD4,KLHL13,LACC1,LBH,LDB2,LGALS3BP,LGR4,LIF,LIN7A,MAFB,MAFF,MOCOS,MTSS1,NAMPT,NCAM1,NFKB2,NFKBIA,NLGN1,NPAS2,NTM,PAQR5,PCOLCE2,PDE10A,PDLIM3,PITX1,PLPP2,PLPP3,POMZP3,POU2F2,PRICKLE1,PRNP,PTN,RRAD,SAMD11,SAMD3,SERPINA3,SERPING1,SFRP1,SHROOM3,SLC1A1,SLC22A3,SLITRK4,SOX17,SPX,STC1,STMN2,SYTL2,TBX15,THBD,TM6SF1,TMEFF2,TNFAIP3,TNFSF15,TOM1L1,TSLP,VEGFA,ZC3H12A,ZMAT4
GO:MF	Chemokine activity	GO:0008009	0.002447468	2.611282939	CCL2,CCL20,CXCL12,CXCL3,CXCL5

GO:MF	RNA polymerase II transcription factor binding	GO:0001085	0.006470362	2.189071418	HCLS1,ID1,ID2,ID4,PITX1
GO:MF	Chemokine receptor binding	GO:0042379	0.009928934	2.003097358	CCL2,CCL20,CXCL12,CXCL3,CXCL5
GO:MF	DNA-binding transcription activator activity	GO:0001216	0.009928934	2.003097358	DLX2,EHF,HMGA2,HOXD10,MAFB,MAFF,NFKB2,PITX1,POU2F2,SOX17,TBX15,ZIC1
GO:MF	DNA-binding transcription activator activity, RNA polymerase II-specific	GO:0001228	0.009928934	2.003097358	DLX2,EHF,HMGA2,HOXD10,MAFB,MAFF,NFKB2,PITX1,POU2F2,SOX17,TBX15,ZIC1

Gene Ontology: Cellular Compartment (for Negative log10 > 2.0)

Source	**Term Name**	**Term ID**	**Adjusted_p_value**	**Negative_log10_of_adjusted_p_**	**Intersections**

				value	
GO:CC	Extracellular matrix	GO:0031012	1.4475E-05	4.839380264	ADAMTS15,CDH13,COL15A1,COL6A1,CTSS,CXCL12,GDF15,ICAM1,LGALS3BP,MMP10,MMP8,NCAM1,POMZP3,PTN,SERPINA3,SERPING1,SFRP1,TMEFF2,VEGFA
GO:CC	Collagen-containing extracellular matrix	GO:0062023	1.60591E-05	4.79427757	ADAMTS15,CDH13,COL15A1,COL6A1,CTSS,CXCL12,GDF15,ICAM1,LGALS3BP,MMP8,NCAM1,PTN,SERPINA3,SERPING1,SFRP1,TMEFF2
GO:CC	Extracellular region	GO:0005576	1.60591E-05	4.79427757	ACTG2,ADAMTS15,ALDH1A3,AMPD3,APOL6,AREG,ATP2B1,C1QTNF1,CCL2,CCL20,CDCP1,CDH13,COL15A1,COL6A1,CRABP2,CSF2,CSF3,CTSS,CXCL12,CXCL3,CXCL5,DPP4,DSC3,EREG,FABP4,FAM20A,FLT1,GDF15,HBEGF,ICAM1,IL13RA2,IL1A,IL1B,IL32,IL33,IL6,ITGB3,LGALS3BP,LIF,LIN7A,METTL7A,MMP10,MMP8,NAMPT,NCAM1,NLGN1,

					NTM,OSCAR,PCOLCE2,POMZP3,PRNP,PTN,SERPINA3,SERPING1,SFRP1,SLC1A1,SPX,STC1,THBD,TMEFF2,TNFAIP3,TNFSF15,TOM1L1,TSLP,VEGFA
GO:CC	Extracellular space	GO:0005615	2.61083E-05	4.583221563	ACTG2,ADAMTS15,ALDH1A3,AREG,ATP2B1,C1QTNF1,CCL2,CCL20,CDH13,COL15A1,COL6A1,CRABP2,CSF2,CSF3,CTSS,CXCL12,CXCL3,CXCL5,DPP4,EREG,FABP4,FAM20A,FLT1,GDF15,HBEGF,ICAM1,IL13RA2,IL1A,IL1B,IL32,IL33,IL6,ITGB3,LGALS3BP,LIF,LIN7A,MMP10,MMP8,NAMPT,OSCAR,PRNP,PTN,SERPINA3,SERPING1,SFRP1,SLC1A1,SPX,STC1,THBD,TNFAIP3,TNFSF15,TOM1L1,TSLP,VEGFA
GO:CC	cell surface	GO:0009986	0.002411727	2.617671768	ADAMTS15,ADTRP,AREG,CD200,CDH13,CDH6,CXCL12,DPP4,HBEGF,ICAM1,IL13RA2,ITGB3,NCAM1,NLGN1,OSCAR,PRNP,PTN,SFRP1,THBD,VEGFA

KEGG (for Negative log10 > 2.0)

Source	**Term Name**	**Term ID**	**Adjusted_p_value**	**Negative_log10_of_adjusted_p_value**	**Intersections**
KEGG	Rheumatoid arthritis	KEGG:05323	1.96E-08	7.706719219	CCL2,CCL20,CSF2,CXCL12,CXCL3,CXCL5,FLT1,ICAM1,IL1A,IL1B,IL6,VEGFA
KEGG	TNF signaling pathway	KEGG:04668	1.72E-07	6.763905159	BIRC3,CCL2,CCL20,CSF2,CXCL3,CXCL5,ICAM1,IL1B,IL6,LIF,NFKBIA,TNFAIP3
KEGG	Cytokine-cytokine receptor interaction	KEGG:04060	5.06E-07	6.296036939	CCL2,CCL20,CSF2,CSF3,CXCL12,CXCL3,CXCL5,GDF15,IL13RA2,IL1A,IL1B,IL32,IL33,IL6,LIF,TNFSF15,TSLP
KEGG	IL-17 signaling pathway	KEGG:04657	1.87096E-06	5.727935787	CCL2,CCL20,CSF2,CSF3,CXCL3,CXCL5,IL1B,IL6,NFKBIA,TNFAIP3
KEGG	NF-kappa B signaling pathway	KEGG:04064	0.000385765	3.413676681	BIRC3,CXCL12,CXCL3,ICAM1,IL1B,NFKB2,NFKBIA,TNFAIP3
KEGG	NOD-like receptor signaling pathway	KEGG:04621	0.000534174	3.272317134	BIRC3,CASP1,CCL2,CXCL3,IL1B,IL6,ITPR1,NAMPT,NFKBIA,TNFAIP3
KEGG	Legionellosis	KEGG:05134	0.000745716	3.127426822	CASP1,CXCL3,IL1B,IL6,NFKB2,NFKBIA
KEG	Prion	KEGG:	0.0007457	3.12742682	IL1A,IL1B,IL6,NCAM1,PR

G	diseases	05020	16	2	NP
KEGG	AGE-RAGE signaling pathway in diabetic complications	KEGG:04933	0.001877503	2.72641936	CCL2,ICAM1,IL1A,IL1B,IL6,THBD,VEGFA
KEGG	Malaria	KEGG:05144	0.002834483	2.547526078	CCL2,CSF3,ICAM1,IL1B,IL6
KEGG	Pertussis	KEGG:05133	0.002834483	2.547526078	CASP1,CXCL5,IL1A,IL1B,IL6,SERPING1
KEGG	Influenza A	KEGG:05164	0.006143896	2.21155612	CASP1,CCL2,ICAM1,IL1A,IL1B,IL33,IL6,NFKBIA
KEGG	Cytosolic DNA-sensing pathway	KEGG:04623	0.006904382	2.160875211	CASP1,IL1B,IL33,IL6,NFKBIA
KEGG	Hematopoietic cell lineage	KEGG:04640	0.006904382	2.160875211	CSF2,CSF3,IL1A,IL1B,IL6,ITGB3
KEGG	Fluid shear stress and atherosclerosis	KEGG:05418	0.007396238	2.130989138	CCL2,ICAM1,IL1A,IL1B,ITGB3,THBD,VEGFA
KEGG	Viral protein interaction	KEGG:04061	0.007396238	2.130989138	CCL2,CCL20,CXCL12,CXCL3,CXCL5,IL6

	with cytokine and cytokine receptor				
KEGG	Transcriptional misregulation in cancer	KEGG:05202	0.008569489	2.067045091	BIRC3,CSF2,FLT1,HHEX,HMGA2,HOXA11,ID2,IL6
KEGG	C-type lectin receptor signaling pathway	KEGG:04625	0.008689023	2.061029078	CASP1,IL1B,IL6,ITPR1,NFKB2,NFKBIA

Reactome (for Negative log10 > 2.0)

Source	**Term Name**	**Term ID**	**Adjusted_p_value**	**Negative_log10_of_adjusted_p_value**	**Intersections**
REAC	Interleukin-10 signaling	REAC:R-HSA-6783783	1.08E-07	6.966799909	CCL2,CCL20,CSF2,CSF3,ICAM1,IL1A,IL1B,IL6,LIF
REAC	Cytokine Signaling in Immune system	REAC:R-HSA-1280215	2.6134E-05	4.582794532	AREG,BIRC3,CASP1,CCL2,CCL20,CSF2,CSF3,EREG,HBEGF,ICAM1,IL13RA2,IL1A,IL1B,IL32,IL33,IL6,IRAK2,ITGB3,LIF,NCAM1,NFKB2,

					NFKBIA,TNFSF15,TSLP,VEGFA
REAC	Signaling by Interleukins	REAC:R-HSA-449147	3.08896E-05	4.51018771	CASP1,CCL2,CCL20,CSF2,CSF3,ICAM1,IL13RA2,IL1A,IL1B,IL32,IL33,IL6,IRAK2,LIF,NFKB2,NFKBIA,TSLP,VEGFA
REAC	Interleukin-1 processing	REAC:R-HSA-448706	4.96837E-05	4.303785899	CASP1,IL1A,IL1B,NFKB2
REAC	Interleukin-4 and Interleukin-13 signaling	REAC:R-HSA-6785807	0.000689221	3.16164169	CCL2,ICAM1,IL13RA2,IL1A,IL1B,IL6,LIF,VEGFA
REAC	Inhibition of Signaling by Overexpressed EGFR	REAC:R-HSA-5638303	0.002466694	2.607884681	AREG,EREG,HBEGF
REAC	Signaling by Overexpressed Wild-Type EGFR in Cancer	REAC:R-HSA-5638302	0.002466694	2.607884681	AREG,EREG,HBEGF
REAC	EGFR	REAC:	0.0032153	2.49277302	AREG,EREG,HBEGF

	interacts with phospholipase C-gamma	R-HSA-212718	41	8	
REAC	Immune System	REAC:R-HSA-168256	0.003309175	2.480280206	AMPD3,AREG,BIRC3,CASP1,CCL2,CCL20,CD200,CSF2,CSF3,CTSS,ERAP2,EREG,HBEGF,ICAM1,IL13RA2,IL1A,IL1B,IL32,IL33,IL6,IRAK2,ITGB3,ITPR1,KLHL13,LIF,METTL7A,MMP8,NCAM1,NFKB2,NFKBIA,OSCAR,SERPINA3,SERPING1,TNFAIP3,TNFSF15,TSLP,VEGFA
REAC	GRB2 events in EGFR signaling	REAC:R-HSA-179812	0.004983676	2.302450184	AREG,EREG,HBEGF
REAC	Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling	REAC:R-HSA-168643	0.005280502	2.277324769	BIRC3,CASP1,IRAK2,NFKB2,TNFAIP3

	pathways				
REAC	SHC1 events in EGFR signaling	REAC:R-HSA-180336	0.0054995	2.25967683	AREG,EREG,HBEGF
REAC	Chemokine receptors bind chemokines	REAC:R-HSA-380108	0.005784957	2.237699836	CCL2,CCL20,CXCL12,CXCL3,CXCL5
REAC	NOD1/2 Signaling Pathway	REAC:R-HSA-168638	0.008322589	2.079741565	BIRC3,CASP1,IRAK2,TNFAIP3
REAC	Interleukin-1 family signaling	REAC:R-HSA-446652	0.008322589	2.079741565	CASP1,IL1A,IL1B,IL33,IRAK2,NFKB2,NFKBIA

Wikipathway (for Negative log10 > 2.0)

Source	**Term Name**	**Term ID**	**Adjusted_p_value**	**Negative_log10_of_adjusted_p_value**	**Intersections**
WP	Photodynamic therapy-induced NF-kB survival	WP:WP3617	1.66185E-06	5.779408894	BIRC3,CSF2,ICAM1,IL1A,IL1B,IL6,NFKB2,VEGFA

	signaling				
WP	Development and heterogeneity of the ILC family	WP:WP3893	0.000244178	3.612292579	AREG,ID2,IL1B,IL33,IL6,TSLP
WP	Cytokines and Inflammatory Response	WP:WP530	0.0010608	2.974251754	CSF2,CSF3,IL1A,IL1B,IL6
WP	Vitamin B12 Metabolism	WP:WP1533	0.001590552	2.798452159	CCL2,ICAM1,IL1B,IL6,NFKB2,SERPINA3
WP	Signal transduction through IL1R	WP:WP4496	0.002144788	2.668615646	IL1A,IL1B,IL6,IRAK2,NFKBIA
WP	Hematopoietic Stem Cell Differentiation	WP:WP2849	0.002806347	2.551858613	CSF2,CSF3,IL1A,IL1B,IL6,ITGB3
WP	Folate Metabolism	WP:WP176	0.004878841	2.311683331	CCL2,ICAM1,IL1B,IL6,NFKB2,SERPINA3
WP	TNF	WP:WP	0.0048788	2.31168333	BIRC3,CCL2,IL6,NFKB2,NF

	related weak inducer of apoptosis (TWEAK) Signaling Pathway	2036	41	1	KBIA
WP	IL1 and megakaryocytes in obesity	WP:WP2865	0.004878841	2.311683331	CCL2,HBEGF,ICAM1,IL1B
WP	miRNAs involvement in the immune response in sepsis	WP:WP4329	0.009752879	2.010867152	ICAM1,IL1A,IL6,NFKB2,NFKBIA
miRNA (for Negative log10 > 2.0)					
MIRNA	hsa-miR-335-5p	MIRNA:hsa-miR-335-5p	0.000169292	3.771363233	AMPD3,AREG,ARHGEF28,BHLHE41,C1QTNF1,CCL20,CDCP1,CLDN1,CNIH3,COL15A1,COL6A1,CRIP2,CXCL3,EHF,EREG,ERO1B,FABP4,GALNT12,GDF15,GDPD1,HOXA11,ICAM1,ID4,IL1A,IL33,IL6,IRAK2,ITPR1,LIF,LIN7A,MAFB,MAFF,MOCOS,NFKBIA,NPAS2,PLPP3,R

	RAD,SERPINA3,SERPING1,SFRP1,SHROOM3,SLC1A1,SOX17,TBX15,THBD,TMEFF2,TSLP,VEGFA,ZC3H12A