

Supplementary Table 6: ToppFun output for the DE genes in dc5Sc twins.

Category	ID	Name	p-value	Hit Count	Hit Count i	Hit in Query List
GO: Molecular Function	GO:0005509	calcium ion binding	3.15E-05	11	734	S100A10,VLDLR,COMP,SYT12,MATN2,PCDH19,EPDR1,PLN,PADI2,SCARA3,CDH8
GO: Molecular Function	GO:0005138	interleukin-6 receptor binding	2.33E-04	2	7	PYCARD,IL6
GO: Molecular Function	GO:0005201	extracellular matrix structural constituent	3.37E-04	5	178	COL4A3,COL11A1,COMP,MATN2,SCARA3
GO: Biological Process	GO:0035295	tube development	1.12E-08	19	1276	COL4A3, LIF, NRXN3, RAMP1, ALX1, SPINT2, MYLK, COMP, HOXD11, KLF5, UNC5B, ANGPT4, RGCC, CD24, MIR27B, LEP, IL6, TNS3, TBX5
GO: Biological Process	GO:0035239	tube morphogenesis	1.20E-08	17	1045	COL4A3,LIF,NRXN3,RAMP1,ALX1,SPINT2,MYLK,COMP,HOXD11,KLF5,UNC5B,ANGPT4,RGCC,MIR27B,LEP,IL6,TBX5
GO: Biological Process	GO:0051241	negative regulation of multicellular organismal process	2.66E-08	20	1500	COL4A3,LIF,ZBTB46,PDE4B,AVPR1A,KLF5,ANGPT4,PYCARD,RGCC,CD24,NAV3,IL1RL1,PLN,ZNF365,MIR27B,BANK1,LEP,IL6,CD200R1,TBX5
GO: Biological Process	GO:0048514	blood vessel morphogenesis	9.88E-08	14	755	COL4A3,LIF,NRXN3,RAMP1,MYLK,COMP,KLF5,UNC5B,ANGPT4,RGCC,MIR27B,LEP,IL6,TBX5
GO: Biological Process	GO:0001568	blood vessel development	4.12E-07	14	849	COL4A3,LIF,NRXN3,RAMP1,MYLK,COMP,KLF5,UNC5B,ANGPT4,RGCC,MIR27B,LEP,IL6,TBX5
GO: Biological Process	GO:0001944	vasculature development	6.69E-07	14	884	COL4A3,LIF,NRXN3,RAMP1,MYLK,COMP,KLF5,UNC5B,ANGPT4,RGCC,MIR27B,LEP,IL6,TBX5
GO: Biological Process	GO:0007155	cell adhesion	8.28E-07	18	1509	COL4A3, S100A10, NRXN3, SPINT2, COMP, NEGR1, PYCARD, PCDH19, RGCC, CD24, SORBS1, EPDR1, MIR27B, CDH8, LEP, IL6, CD200R1, JAM2
GO: Biological Process	GO:0022610	biological adhesion	8.86E-07	18	1516	COL4A3,S100A10,NRXN3,SPINT2,COMP,NEGR1,PYCARD,PCDH19,RGCC,CD24,SORBS1,EPDR1,MIR27B,CDH8,LEP,IL6,CD200R1,JAM2
GO: Biological Process	GO:0072359	circulatory system development	3.26E-06	16	1322	COL4A3,LIF,COL11A1,NRXN3,RAMP1,MYLK,COMP,KLF5,UNC5B,ANGPT4,RGCC,PLN,MIR27B,LEP,IL6,TBX5
GO: Biological Process	GO:0045597	positive regulation of cell differentiation	3.73E-06	15	1176	LIF,S100A10,VLDLR,ZBTB46,ALX1,HOXD11,NEGR1,KLF5,RGCC,CD24,RIMS1,ZNF365,LEP,IL6,TBX5
GO: Biological Process	GO:1903530	regulation of secretion by cell	4.79E-06	13	898	LIF,NRXN3,SYT12,AVPR1A,PYCARD,RGCC,ANO1,IL1RL1,RIMS1,BANK1,LEP,IL6,CD200R1
GO: Biological Process	GO:0048646	anatomical structure formation involved in morphogenesis	4.91E-06	16	1365	COL4A3,LIF,COL11A1,NRXN3,RAMP1,ALX1,SPINT2,HOXD11,KLF5,UNC5B,ANGPT4,RGCC,MIR27B,LEP,IL6,TBX5
GO: Biological Process	GO:0043062	extracellular structure organization	5.08E-06	10	510	COL4A3,VLDLR,COL11A1,SPINT2,COMP,RGCC,SCARA3,MIR27B,IL6,JAM2
GO: Biological Process	GO:0098609	cell-cell adhesion	5.60E-06	13	911	NRXN3,SPINT2,COMP,NEGR1,PYCARD,PCDH19,RGCC,CD24,CDH8,LEP,IL6,CD200R1,JAM2
GO: Biological Process	GO:0001525	angiogenesis	6.18E-06	11	645	COL4A3,LIF,NRXN3,RAMP1,KLF5,UNC5B,ANGPT4,RGCC,MIR27B,LEP,IL6
GO: Biological Process	GO:0001818	negative regulation of cytokine production	9.76E-06	8	326	PYCARD,RGCC,CD24,NAV3,IL1RL1,BANK1,IL6,CD200R1
GO: Biological Process	GO:0051216	cartilage development	9.95E-06	7	233	COL11A1,ALX1,COMP,HOXD11,MATN2,SCARA3,LEP
GO: Biological Process	GO:0051046	regulation of secretion	1.03E-05	13	964	LIF,NRXN3,SYT12,AVPR1A,PYCARD,RGCC,ANO1,IL1RL1,RIMS1,BANK1,LEP,IL6,CD200R1
GO: Biological Process	GO:0051094	positive regulation of developmental process	1.12E-05	17	1632	LIF,S100A10,VLDLR,ZBTB46,ALX1,HOXD11,NEGR1,KLF5,ANGPT4,RGCC,CD24,RIMS1,ZNF365,MIR27B,LEP,IL6,TBX5
GO: Biological Process	GO:0002063	chondrocyte development	1.87E-05	4	49	COL11A1,COMP,MATN2,SCARA3
GO: Biological Process	GO:0098868	bone growth	2.20E-05	4	51	COMP,MATN2,SCARA3,LEP
GO: Biological Process	GO:0048705	skeletal system morphogenesis	2.58E-05	7	270	COL11A1,ALX1,COMP,HOXD10,HOXD11,MATN2,SCARA3
GO: Biological Process	GO:0051674	localization of cell	2.65E-05	18	1932	PDE4B,ALX1,SPINT2,MYLK,ANGPT4,MATN2,PYCARD,RGCC,CD24,NAV3,PADI2,MIR27B,LEP,IL6,TNS3,CD200R1,JAM2,TBX5
GO: Biological Process	GO:0048870	cell motility	2.65E-05	18	1932	PDE4B,ALX1,SPINT2,MYLK,ANGPT4,MATN2,PYCARD,RGCC,CD24,NAV3,PADI2,MIR27B,LEP,IL6,TNS3,CD200R1,JAM2,TBX5
GO: Biological Process	GO:0050663	cytokine secretion	2.70E-05	7	272	PYCARD,RGCC,IL1RL1,BANK1,LEP,IL6,CD200R1
GO: Biological Process	GO:1903532	positive regulation of secretion by cell	2.77E-05	9	493	LIF,AVPR1A,PYCARD,RGCC,ANO1,IL1RL1,RIMS1,LEP,IL6
GO: Biological Process	GO:0032635	interleukin-6 production	2.82E-05	6	184	PYCARD,CD24,BANK1,LEP,IL6,CD200R1
GO: Biological Process	GO:0016477	cell migration	2.93E-05	17	1757	PDE4B,ALX1,MYLK,ANGPT4,MATN2,PYCARD,RGCC,CD24,NAV3,PADI2,MIR27B,LEP,IL6,TNS3,CD200R1,JAM2,TBX5
GO: Biological Process	GO:0060351	cartilage development involved in endochondral bone morphogenesis	2.97E-05	4	55	COMP,HOXD11,MATN2,SCARA3
GO: Biological Process	GO:0030198	extracellular matrix organization	4.15E-05	8	399	COL4A3,COL11A1,SPINT2,COMP,RGCC,SCARA3,IL6,JAM2
GO: Biological Process	GO:0051047	positive regulation of secretion	4.79E-05	9	529	LIF,AVPR1A,PYCARD,RGCC,ANO1,IL1RL1,RIMS1,LEP,IL6
GO: Biological Process	GO:0050900	leukocyte migration	5.15E-05	9	534	PDE4B,ANGPT4,PYCARD,CD24,PADI2,LEP,IL6,CD200R1,JAM2
GO: Biological Process	GO:0018108	peptidyl-tyrosine phosphorylation	5.96E-05	8	420	MST1R,LIF,CRIM1,ANGPT4,CD24,BANK1,LEP,IL6
GO: Biological Process	GO:0018212	peptidyl-tyrosine modification	6.26E-05	8	423	MST1R,LIF,CRIM1,ANGPT4,CD24,BANK1,LEP,IL6
GO: Biological Process	GO:0061448	connective tissue development	6.70E-05	7	314	COL11A1,ALX1,COMP,HOXD11,MATN2,SCARA3,LEP
GO: Biological Process	GO:0002062	chondrocyte differentiation	6.74E-05	5	132	COL11A1,COMP,HOXD11,MATN2,SCARA3
GO: Biological Process	GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	7.45E-05	6	219	LIF,ANGPT4,CD24,BANK1,LEP,IL6
GO: Biological Process	GO:0007267	cell-cell signaling	7.82E-05	17	1899	MST1R,LIF,LYPD6B,NRXN3,SYT12,HOXD11,AVPR1A,KLF5,CD24,ANO1,SORBS1,RIMS1,CDH8,LEP,IL6,CHRNE,TBX5
GO: Biological Process	GO:0042127	regulation of cell population proliferation	9.03E-05	17	1921	COL4A3,MST1R,LIF,EGLN3,SPINT2,COMP,AVPR1A,KLF5,PYCARD,RGCC,CD24,IL1RL1,MIR27B,LEP,IL6,TNS3,TBX5
GO: Biological Process	GO:0051093	negative regulation of developmental process	9.54E-05	13	1194	COL4A3,LIF,ZBTB46,KLF5,ANGPT4,RGCC,CD24,ZNF365,MIR27B,PRDM6,LEP,IL6,TBX5
GO: Biological Process	GO:0002791	regulation of peptide secretion	1.04E-04	9	585	LIF,PYCARD,RGCC,ANO1,IL1RL1,BANK1,LEP,IL6,CD200R1
GO: Biological Process	GO:0002790	peptide secretion	1.07E-04	10	729	LIF,COMP,PYCARD,RGCC,ANO1,IL1RL1,BANK1,LEP,IL6,CD200R1
GO: Biological Process	GO:0050707	regulation of cytokine secretion	1.15E-04	6	237	PYCARD,RGCC,IL1RL1,BANK1,IL6,CD200R1
GO: Biological Process	GO:0051270	regulation of cellular component movement	1.18E-04	13	1219	PDE4B,SPINT2,MYLK,ANGPT4,PYCARD,RGCC,NAV3,PLN,PADI2,MIR27B,IL6,CD200R1,TBX5
GO: Biological Process	GO:1901342	regulation of vasculature development	1.21E-04	8	465	COL4A3,LIF,KLF5,ANGPT4,RGCC,MIR27B,LEP,IL6
GO: Biological Process	GO:0060350	endochondral bone morphogenesis	1.43E-04	4	82	COMP,HOXD11,MATN2,SCARA3
GO: Biological Process	GO:0008284	positive regulation of cell population proliferation	1.75E-04	12	1096	MST1R,LIF,COMP,AVPR1A,KLF5,PYCARD,CD24,MIR27B,LEP,IL6,TNS3,TBX5
GO: Biological Process	GO:0050710	negative regulation of cytokine secretion	1.80E-04	4	87	RGCC,BANK1,IL6,CD200R1

GO: Biological Process	GO:0061061	muscle structure development	1.84E-04	10	779	LIF,COL11A1,MYLK,COMP,HOXD10,AVPR1A,KLF5,PRDM6,IL6,TBX5
GO: Biological Process	GO:1903531	negative regulation of secretion by cell	1.94E-04	6	261	LIF,RGCC,BANK1,LEP,IL6,CD200R1
GO: Biological Process	GO:0001817	regulation of cytokine production	2.04E-04	10	789	PDE4B,PYCARD,RGCC,CD24,NAV3,IL1RL1,BANK1,LEP,IL6,CD200R1
GO: Biological Process	GO:2000146	negative regulation of cell motility	2.11E-04	7	378	SPINT2,ANGPT4,RGCC,NAV3,PADI2,CD200R1,TBX5
GO: Biological Process	GO:0032940	secretion by cell	2.38E-04	15	1682	LIF,NRXN3,COMP,SYT12,AVPR1A,PYCARD,RGCC,ANO1,IL1RL1,RIMS1,PADI2,BANK1,LEP,IL6,CD200R1
GO: Biological Process	GO:0032675	regulation of interleukin-6 production	2.46E-04	5	174	PYCARD,CD24,BANK1,IL6,CD200R1
GO: Biological Process	GO:0003417	growth plate cartilage development	2.70E-04	3	39	COMP,MATN2,SCARA3
GO: Biological Process	GO:0035989	tendon development	2.83E-04	2	8	COL11A1,COMP
GO: Biological Process	GO:2000698	positive regulation of epithelial cell differentiation involved in kidney deve	2.83E-04	2	8	LIF,CD24
GO: Biological Process	GO:0010717	regulation of epithelial to mesenchymal transition	2.84E-04	4	98	ALX1,RGCC,IL6,TBX5
GO: Biological Process	GO:0051050	positive regulation of transport	2.89E-04	12	1157	LIF,MYLK,AVPR1A,PYCARD,RGCC,ANO1,SORBS1,IL1RL1,RIMS1,LEP,RHOU,IL6
GO: Biological Process	GO:0032642	regulation of chemokine production	2.95E-04	4	99	PYCARD,CD24,IL1RL1,IL6
GO: Biological Process	GO:0002792	negative regulation of peptide secretion	3.11E-04	5	183	RGCC,BANK1,LEP,IL6,CD200R1
GO: Biological Process	GO:0009306	protein secretion	3.18E-04	9	680	COMP,PYCARD,RGCC,ANO1,IL1RL1,BANK1,LEP,IL6,CD200R1
GO: Biological Process	GO:0003592	establishment of protein localization to extracellular region	3.22E-04	9	681	COMP,PYCARD,RGCC,ANO1,IL1RL1,BANK1,LEP,IL6,CD200R1
GO: Biological Process	GO:0140352	export from cell	3.23E-04	15	1730	LIF,NRXN3,COMP,SYT12,AVPR1A,PYCARD,RGCC,ANO1,IL1RL1,RIMS1,PADI2,BANK1,LEP,IL6,CD200R1
GO: Biological Process	GO:0010720	positive regulation of cell development	3.36E-04	9	685	LIF,S100A10,VLDLR,HOXD11,NEGR1,CD24,RIMS1,ZNF365,IL6
GO: Biological Process	GO:0000902	cell morphogenesis	3.40E-04	12	1178	S100A10,VLDLR,NRXN3,SPINT2,UNC5B,MATN2,RIMS1,SCARA3,ZNF365,CDH8,RHOU,IL6
GO: Biological Process	GO:0071692	protein localization to extracellular region	3.47E-04	9	688	COMP,PYCARD,RGCC,ANO1,IL1RL1,BANK1,LEP,IL6,CD200R1
GO: Biological Process	GO:0050708	regulation of protein secretion	3.55E-04	8	545	PYCARD,RGCC,ANO1,IL1RL1,BANK1,LEP,IL6,CD200R1
GO: Biological Process	GO:1901897	regulation of relaxation of cardiac muscle	3.64E-04	2	9	PDE4B,PLN
GO: Biological Process	GO:0048704	embryonic skeletal system morphogenesis	3.69E-04	4	105	COL11A1,ALX1,HOXD10,HOXD11
GO: Biological Process	GO:0051048	negative regulation of secretion	3.75E-04	6	295	LIF,RGCC,BANK1,LEP,IL6,CD200R1
GO: Biological Process	GO:0051271	negative regulation of cellular component movement	3.78E-04	7	416	SPINT2,ANGPT4,RGCC,NAV3,PADI2,CD200R1,TBX5
GO: Biological Process	GO:0050730	regulation of peptidyl-tyrosine phosphorylation	3.82E-04	6	296	LIF,ANGPT4,CD24,BANK1,LEP,IL6
GO: Biological Process	GO:0032602	chemokine production	3.83E-04	4	106	PYCARD,CD24,IL1RL1,IL6
GO: Biological Process	GO:0009628	response to abiotic stimulus	3.84E-04	13	1375	VLDLR,EGLN3,COL11A1,PDE4B,MYLK,AVPR1A,ANGPT4,RGCC,CD24,ANO1,SCARA3,CDH8,LEP
GO: Biological Process	GO:0048729	tissue morphogenesis	4.05E-04	10	860	LIF,COL11A1,ALX1,SPINT2,MYLK,HOXD11,MATN2,SCARA3,IL6,TBX5
GO: Biological Process	GO:0045765	regulation of angiogenesis	4.06E-04	7	421	COL4A3,LIF,ANGPT4,RGCC,MIR27B,LEP,IL6
GO: Biological Process	GO:0090087	regulation of peptide transport	4.32E-04	10	867	LIF,PYCARD,RGCC,ANO1,IL1RL1,BANK1,LEP,RHOU,IL6,CD200R1
GO: Biological Process	GO:0035136	forelimb morphogenesis	4.41E-04	3	46	HOXD10,HOXD11,TBX5
GO: Biological Process	GO:0001816	cytokine production	4.64E-04	10	875	PDE4B,PYCARD,RGCC,CD24,NAV3,IL1RL1,BANK1,LEP,IL6,CD200R1
GO: Biological Process	GO:0042102	positive regulation of T cell proliferation	4.72E-04	4	112	PYCARD,CD24,LEP,IL6
GO: Biological Process	GO:0040013	negative regulation of locomotion	4.73E-04	7	432	SPINT2,ANGPT4,RGCC,NAV3,PADI2,CD200R1,TBX5
GO: Biological Process	GO:0003416	endochondral bone growth	5.00E-04	3	48	COMP,MATN2,SCARA3
GO: Biological Process	GO:0060173	limb development	5.11E-04	5	204	ALX1,COMP,HOXD10,HOXD11,TBX5
GO: Biological Process	GO:0048736	appendage development	5.11E-04	5	204	ALX1,COMP,HOXD10,HOXD11,TBX5
GO: Biological Process	GO:1901343	negative regulation of vasculature development	5.46E-04	5	207	COL4A3,LIF,KLF5,ANGPT4,RGCC
GO: Biological Process	GO:0001501	skeletal system development	5.48E-04	8	582	COL11A1,ALX1,COMP,HOXD10,HOXD11,MATN2,SCARA3,LEP
GO: Biological Process	GO:0060290	transdifferentiation	5.53E-04	2	11	LIF,TBX5
GO: Biological Process	GO:0071864	positive regulation of cell proliferation in bone marrow	5.53E-04	2	11	MIR27B,IL6
GO: Biological Process	GO:0046903	secretion	6.01E-04	15	1834	LIF,NRXN3,COMP,SYT12,AVPR1A,PYCARD,RGCC,ANO1,IL1RL1,RIMS1,PADI2,BANK1,LEP,IL6,CD200R1
GO: Biological Process	GO:0010718	positive regulation of epithelial to mesenchymal transition	6.33E-04	3	52	ALX1,RGCC,IL6
GO: Biological Process	GO:0099536	synaptic signaling	6.46E-04	10	913	LYPD6B,NRXN3,SYT12,AVPR1A,CD24,SORBS1,RIMS1,CDH8,IL6,CHRNE
GO: Biological Process	GO:0086023	adenylate cyclase-activating adrenergic receptor signaling pathway involv	6.62E-04	2	12	PDE4B,PLN
GO: Biological Process	GO:0043410	positive regulation of MAPK cascade	7.21E-04	8	607	MST1R,LIF,PYCARD,CD24,MIR27B,BANK1,LEP,IL6
GO: Biological Process	GO:0022603	regulation of anatomical structure morphogenesis	7.57E-04	12	1288	COL4A3,LIF,S100A10,HOXD11,ANGPT4,RGCC,RIMS1,MIR27B,LEP,RHOU,IL6,TBX5
GO: Biological Process	GO:0060349	bone morphogenesis	7.57E-04	4	127	COMP,HOXD11,MATN2,SCARA3
GO: Biological Process	GO:0072182	regulation of nephron tubule epithelial cell differentiation	7.81E-04	2	13	LIF,CD24
GO: Biological Process	GO:0070091	glucagon secretion	7.81E-04	2	13	LEP,IL6
GO: Biological Process	GO:0032989	cellular component morphogenesis	7.99E-04	12	1296	S100A10,VLDLR,NRXN3,SPINT2,UNC5B,MATN2,RIMS1,SCARA3,ZNF365,CDH8,RHOU,IL6
GO: Biological Process	GO:0048666	neuron development	8.05E-04	12	1297	LIF,VLDLR,NRXN3,HOXD10,NEGR1,UNC5B,MATN2,CD24,RIMS1,ZNF365,LEP,IL6
GO: Biological Process	GO:0030155	regulation of cell adhesion	8.32E-04	9	777	S100A10,SPINT2,PYCARD,RGCC,CD24,MIR27B,LEP,IL6,JAM2
GO: Biological Process	GO:2000145	regulation of cell motility	8.40E-04	11	1120	SPINT2,MYLK,ANGPT4,PYCARD,RGCC,NAV3,PADI2,MIR27B,IL6,CD200R1,TBX5
GO: Biological Process	GO:0002793	positive regulation of peptide secretion	8.52E-04	6	345	LIF,PYCARD,RGCC,ANO1,IL1RL1,IL6

GO: Biological Process	GO:0007517	muscle organ development	8.70E-04	7	479	LIF,COL11A1,MYLK,HOXD10,KLF5,IL6,TBX5
GO: Biological Process	GO:0031346	positive regulation of cell projection organization	8.70E-04	7	479	LIF,VLDLR,NEGR1,CD24,NAV3,RIMS1,IL6
GO: Biological Process	GO:0071863	regulation of cell proliferation in bone marrow	9.10E-04	2	14	MIR27B,IL6
GO: Biological Process	GO:0051222	positive regulation of protein transport	9.13E-04	7	483	PYCARD,RGCC,ANO1,IL1RL1,LEP,RHOJ,IL6
GO: Biological Process	GO:0051051	negative regulation of transport	9.37E-04	8	632	LIF,RGCC,PLN,MIR27B,BANK1,LEP,IL6,CD200R1
GO: Biological Process	GO:0001934	positive regulation of protein phosphorylation	9.71E-04	11	1140	MST1R,LIF,VLDLR,ANGPT4,PYCARD,RGCC,CD24,MIR27B,BANK1,LEP,IL6
GO: Biological Process	GO:0032715	negative regulation of interleukin-6 production	1.01E-03	3	61	CD24,BANK1,CD200R1
GO: Biological Process	GO:0072160	nephron tubule epithelial cell differentiation	1.05E-03	2	15	LIF,CD24
GO: Biological Process	GO:0090197	positive regulation of chemokine secretion	1.05E-03	2	15	PYCARD,IL1RL1
GO: Biological Process	GO:0071838	cell proliferation in bone marrow	1.05E-03	2	15	MIR27B,IL6
GO: Biological Process	GO:2000402	negative regulation of lymphocyte migration	1.05E-03	2	15	PADI2,CD200R1
GO: Biological Process	GO:0048706	embryonic skeletal system development	1.09E-03	4	140	COL11A1,ALX1,HOXD10,HOXD11
GO: Biological Process	GO:0030336	negative regulation of cell migration	1.09E-03	6	362	ANGPT4,RGCC,NAV3,PADI2,CD200R1,TBX5
GO: Biological Process	GO:0035265	organ growth	1.10E-03	5	242	COMP,MATN2,SCARA3,LEP,TBX5
GO: Biological Process	GO:0019221	cytokine-mediated signaling pathway	1.15E-03	9	814	MST1R,LIF,PYCARD,CD24,IL1RL1,PADI2,LEP,RHOJ,IL6
GO: Biological Process	GO:0018193	peptidyl-amino acid modification	1.16E-03	12	1352	MST1R,LIF,EGLN3,CRIM1,ANGPT4,H1-2,CD24,PADI2,PRDM6,BANK1,LEP,IL6
GO: Biological Process	GO:0060348	bone development	1.19E-03	5	246	COMP,HOXD11,MATN2,SCARA3,LEP
GO: Biological Process	GO:0010976	positive regulation of neuron projection development	1.22E-03	6	370	LIF,VLDLR,NEGR1,CD24,RIMS1,IL6
GO: Biological Process	GO:0120035	regulation of plasma membrane bounded cell projection organization	1.22E-03	9	821	LIF,VLDLR,NEGR1,KLF5,CD24,NAV3,RIMS1,ZNF365,IL6
GO: Biological Process	GO:0051223	regulation of protein transport	1.27E-03	9	825	PYCARD,RGCC,ANO1,IL1RL1,BANK1,LEP,RHOJ,IL6,CD200R1
GO: Biological Process	GO:0030326	embryonic limb morphogenesis	1.27E-03	4	146	ALX1,HOXD10,HOXD11,TBX5
GO: Biological Process	GO:0035113	embryonic appendage morphogenesis	1.27E-03	4	146	ALX1,HOXD10,HOXD11,TBX5
GO: Biological Process	GO:1905953	negative regulation of lipid localization	1.33E-03	3	67	MIR27B,LEP,IL6
GO: Biological Process	GO:0031344	regulation of cell projection organization	1.33E-03	9	831	LIF,VLDLR,NEGR1,KLF5,CD24,NAV3,RIMS1,ZNF365,IL6
GO: Biological Process	GO:0045598	regulation of fat cell differentiation	1.34E-03	4	148	KLF5,MIR27B,LEP,IL6
GO: Biological Process	GO:0032270	positive regulation of cellular protein metabolic process	1.34E-03	14	1774	COL4A3,MST1R,LIF,VLDLR,EGLN3,RAMP1,ANGPT4,PYCARD,RGCC,CD24,MIR27B,BANK1,LEP,IL6
GO: Biological Process	GO:0072537	fibroblast activation	1.35E-03	2	17	RGCC,LEP
GO: Biological Process	GO:1901077	regulation of relaxation of muscle	1.35E-03	2	17	PDE4B,PLN
GO: Biological Process	GO:0086103	G protein-coupled receptor signaling pathway involved in heart process	1.35E-03	2	17	PDE4B,PLN
GO: Biological Process	GO:0042391	regulation of membrane potential	1.35E-03	7	517	NALCN,AVPR1A,ANO1,RIMS1,PLN,IL6,CHRNE
GO: Biological Process	GO:0071345	cellular response to cytokine stimulus	1.36E-03	11	1188	MST1R,LIF,EGLN3,KLF5,PYCARD,CD24,IL1RL1,PADI2,LEP,RHOJ,IL6
GO: Biological Process	GO:0032880	regulation of protein localization	1.36E-03	11	1188	LIF,PYCARD,RGCC,ANO1,SORBS1,IL1RL1,BANK1,LEP,RHOJ,IL6,CD200R1
GO: Biological Process	GO:0031401	positive regulation of protein modification process	1.37E-03	12	1379	MST1R,LIF,VLDLR,RAMP1,ANGPT4,PYCARD,RGCC,CD24,MIR27B,BANK1,LEP,IL6
GO: Biological Process	GO:2000401	regulation of lymphocyte migration	1.38E-03	3	68	PYCARD,PADI2,CD200R1
GO: Biological Process	GO:0050671	positive regulation of lymphocyte proliferation	1.41E-03	4	150	PYCARD,CD24,LEP,IL6
GO: Biological Process	GO:1904951	positive regulation of establishment of protein localization	1.42E-03	7	521	PYCARD,RGCC,ANO1,IL1RL1,LEP,RHOJ,IL6
GO: Biological Process	GO:0042327	positive regulation of phosphorylation	1.44E-03	11	1197	MST1R,LIF,VLDLR,ANGPT4,PYCARD,RGCC,CD24,MIR27B,BANK1,LEP,IL6
GO: Biological Process	GO:0003012	muscle system process	1.45E-03	7	523	PDE4B,MYLK,COMP,SORBS1,PLN,LEP,CHRNE
GO: Biological Process	GO:0032946	positive regulation of mononuclear cell proliferation	1.48E-03	4	152	PYCARD,CD24,LEP,IL6
GO: Biological Process	GO:0040012	regulation of locomotion	1.50E-03	11	1203	SPINT2,MYLK,ANGPT4,PYCARD,RGCC,NAV3,PADI2,MIR27B,IL6,CD200R1,TBX5
GO: Biological Process	GO:0032722	positive regulation of chemokine production	1.50E-03	3	70	PYCARD,IL1RL1,IL6
GO: Biological Process	GO:0090196	regulation of chemokine secretion	1.52E-03	2	18	PYCARD,IL1RL1
GO: Biological Process	GO:0090171	chondrocyte morphogenesis	1.52E-03	2	18	MATN2,SCARA3
GO: Biological Process	GO:0003429	growth plate cartilage chondrocyte morphogenesis	1.52E-03	2	18	MATN2,SCARA3
GO: Biological Process	GO:0003414	chondrocyte morphogenesis involved in endochondral bone morphogenesis	1.52E-03	2	18	MATN2,SCARA3
GO: Biological Process	GO:0006936	muscle contraction	1.56E-03	6	388	PDE4B,MYLK,COMP,SORBS1,PLN,CHRNE
GO: Biological Process	GO:0001666	response to hypoxia	1.56E-03	6	388	VLDLR,EGLN3,ANGPT4,RGCC,CD24,LEP
GO: Biological Process	GO:0001837	epithelial to mesenchymal transition	1.66E-03	4	157	ALX1,RGCC,IL6,TBX5
GO: Biological Process	GO:0055119	relaxation of cardiac muscle	1.69E-03	2	19	PDE4B,PLN
GO: Biological Process	GO:0010888	negative regulation of lipid storage	1.69E-03	2	19	LEP,IL6
GO: Biological Process	GO:0003422	growth plate cartilage morphogenesis	1.69E-03	2	19	MATN2,SCARA3
GO: Biological Process	GO:0030030	cell projection organization	1.77E-03	14	1827	LIF,VLDLR,NRXN3,MYLK,NEGR1,KLF5,UNC5B,MATN2,CD24,NAV3,RIMS1,ZNF365,RHOJ,IL6
GO: Biological Process	GO:0036293	response to decreased oxygen levels	1.82E-03	6	400	VLDLR,EGLN3,ANGPT4,RGCC,CD24,LEP
GO: Biological Process	GO:0042531	positive regulation of tyrosine phosphorylation of STAT protein	1.83E-03	3	75	LIF,LEP,IL6
GO: Biological Process	GO:0072006	nephron development	1.86E-03	4	162	COL4A3,LIF,HOXD11,CD24

GO: Biological Process	GO:0070665	positive regulation of leukocyte proliferation	1.86E-03	4	162	PYCARD,CD24,LEP,IL6
GO: Biological Process	GO:2000696	regulation of epithelial cell differentiation involved in kidney development	1.88E-03	2	20	LIF,CD24
GO: Biological Process	GO:0090195	chemokine secretion	1.88E-03	2	20	PYCARD,IL1RL1
GO: Biological Process	GO:0070201	regulation of establishment of protein localization	1.89E-03	9	874	PYCARD,RGCC,ANO1,IL1RL1,BANK1,LEP,RHOU,IL6,CD200R1
GO: Biological Process	GO:0030334	regulation of cell migration	1.89E-03	10	1052	MYLK,ANGPT4,PYCARD,RGCC,NAV3,PADI2,MIR27B,IL6,CD200R1,TBX5
GO: Biological Process	GO:0009887	animal organ morphogenesis	1.91E-03	11	1240	LIF,COL11A1,ALX1,MYLK,COMP,HOXD10,HOXD11,MATN2,SCARA3,IL6,TBX5
GO: Biological Process	GO:0007338	single fertilization	1.99E-03	4	165	MST1R,HOXD10,HOXD11,RIMS1
GO: Biological Process	GO:0060341	regulation of cellular localization	2.00E-03	10	1060	LIF,NRXN3,SYT12,ANO1,SORBS1,RIMS1,PLN,MIR27B,LEP,RHOU
GO: Biological Process	GO:0098916	anterograde trans-synaptic signaling	2.15E-03	9	891	LYPD6B,NRXN3,SYT12,AVPR1A,CD24,RIMS1,CDH8,IL6,CHRNE
GO: Biological Process	GO:0007268	chemical synaptic transmission	2.15E-03	9	891	LYPD6B,NRXN3,SYT12,AVPR1A,CD24,RIMS1,CDH8,IL6,CHRNE
GO: Biological Process	GO:0022008	neurogenesis	2.16E-03	14	1866	LIF,VLDLR,NRXN3,HOXD10,NEGR1,UNC5B,MATN2,CD24,NAV3,RIMS1,ZNF365,PRDM6,LEP,IL6
GO: Biological Process	GO:0023061	signal release	2.18E-03	7	562	LIF,NRXN3,SYT12,ANO1,RIMS1,LEP,IL6
GO: Biological Process	GO:0050727	regulation of inflammatory response	2.21E-03	6	416	PYCARD,CD24,IL1RL1,LEP,IL6,CD200R1
GO: Biological Process	GO:0046628	positive regulation of insulin receptor signaling pathway	2.27E-03	2	22	SORBS1,LEP
GO: Biological Process	GO:0001780	neutrophil homeostasis	2.27E-03	2	22	PDE4B,IL6
GO: Biological Process	GO:0001502	cartilage condensation	2.27E-03	2	22	COL11A1,ALX1
GO: Biological Process	GO:009537	trans-synaptic signaling	2.30E-03	9	900	LYPD6B,NRXN3,SYT12,AVPR1A,CD24,RIMS1,CDH8,IL6,CHRNE
GO: Biological Process	GO:0097435	supramolecular fiber organization	2.31E-03	8	729	S100A10,COL11A1,COMP,PYCARD,RGCC,NAV3,SORBS1,RHOU
GO: Biological Process	GO:0051247	positive regulation of protein metabolic process	2.34E-03	14	1882	COL4A3,MST1R,LIF,VLDLR,EGLN3,RAMP1,ANGPT4,PYCARD,RGCC,CD24,MIR27B,BANK1,LEP,IL6
GO: Biological Process	GO:0050709	negative regulation of protein secretion	2.37E-03	4	173	RGCC,BANK1,IL6,CD200R1
GO: Biological Process	GO:0045937	positive regulation of phosphate metabolic process	2.40E-03	11	1277	MST1R,LIF,VLDLR,ANGPT4,PYCARD,RGCC,CD24,MIR27B,BANK1,LEP,IL6
GO: Biological Process	GO:0010562	positive regulation of phosphorus metabolic process	2.40E-03	11	1277	MST1R,LIF,VLDLR,ANGPT4,PYCARD,RGCC,CD24,MIR27B,BANK1,LEP,IL6
GO: Biological Process	GO:0070482	response to oxygen levels	2.46E-03	6	425	VLDLR,EGLN3,ANGPT4,RGCC,CD24,LEP
GO: Biological Process	GO:0035107	appendage morphogenesis	2.47E-03	4	175	ALX1,HOXD10,HOXD11,TBX5
GO: Biological Process	GO:0035108	limb morphogenesis	2.47E-03	4	175	ALX1,HOXD10,HOXD11,TBX5
GO: Biological Process	GO:0098743	cell aggregation	2.48E-03	2	23	COL11A1,ALX1
GO: Biological Process	GO:0017121	plasma membrane phospholipid scrambling	2.48E-03	2	23	ANO4,ANO1
GO: Biological Process	GO:0051969	regulation of transmission of nerve impulse	2.48E-03	2	23	AVPR1A,IL6
GO: Biological Process	GO:0045649	regulation of macrophage differentiation	2.48E-03	2	23	LIF,ZBTB46
GO: Biological Process	GO:1903055	positive regulation of extracellular matrix organization	2.48E-03	2	23	RGCC,IL6
GO: Biological Process	GO:0032970	regulation of actin filament-based process	2.55E-03	6	428	S100A10,PDE4B,PYCARD,RGCC,PLN,RHOU
GO: Biological Process	GO:0034097	response to cytokine	2.56E-03	11	1287	MST1R,LIF,EGLN3,KLF5,PYCARD,CD24,IL1RL1,PADI2,LEP,RHOU,IL6
GO: Biological Process	GO:0003433	chondrocyte development involved in endochondral bone morphogenesis	2.70E-03	2	24	MATN2,SCARA3
GO: Biological Process	GO:0051151	negative regulation of smooth muscle cell differentiation	2.70E-03	2	24	KLF5,PRDM6
GO: Biological Process	GO:0003418	growth plate cartilage chondrocyte differentiation	2.70E-03	2	24	MATN2,SCARA3
GO: Biological Process	GO:0001959	regulation of cytokine-mediated signaling pathway	2.78E-03	4	181	PYCARD,CD24,PADI2,IL6
GO: Biological Process	GO:0050769	positive regulation of neurogenesis	2.88E-03	7	591	LIF,VLDLR,NEGR1,CD24,RIMS1,ZNF365,IL6
GO: Biological Process	GO:0042129	regulation of T cell proliferation	2.90E-03	4	183	PYCARD,CD24,LEP,IL6
GO: Biological Process	GO:0032682	negative regulation of chemokine production	2.93E-03	2	25	CD24,IL6
GO: Biological Process	GO:1900078	positive regulation of cellular response to insulin stimulus	2.93E-03	2	25	SORBS1,LEP
GO: Biological Process	GO:0046888	negative regulation of hormone secretion	2.99E-03	3	89	LIF,LEP,IL6
GO: Biological Process	GO:0051145	smooth muscle cell differentiation	2.99E-03	3	89	COMP,KLF5,PRDM6
GO: Biological Process	GO:0002819	regulation of adaptive immune response	3.13E-03	4	187	PYCARD,CD24,IL1RL1,IL6
GO: Biological Process	GO:0034104	negative regulation of tissue remodeling	3.17E-03	2	26	CD24,IL6
GO: Biological Process	GO:0014015	positive regulation of gliogenesis	3.18E-03	3	91	LIF,ZNF365,IL6
GO: Biological Process	GO:0010876	lipid localization	3.19E-03	6	448	ANO4,VLDLR,ANO1,MIR27B,LEP,IL6
GO: Biological Process	GO:1901676	positive regulation of histone H3-K27 acetylation	3.24E-03	1	1	LIF
GO: Biological Process	GO:0032913	negative regulation of transforming growth factor beta3 production	3.24E-03	1	1	CD24
GO: Biological Process	GO:0106090	positive regulation of cell adhesion involved in sprouting angiogenesis	3.24E-03	1	1	MIR27B
GO: Biological Process	GO:0071298	cellular response to L-ascorbic acid	3.24E-03	1	1	LEP
GO: Biological Process	GO:0099156	cell-cell signaling via exosome	3.24E-03	1	1	KLF5
GO: Biological Process	GO:2000486	negative regulation of glutamine transport	3.24E-03	1	1	LEP
GO: Biological Process	GO:0061586	positive regulation of transcription by transcription factor localization	3.24E-03	1	1	KLF5
GO: Biological Process	GO:1905929	positive regulation of invadopodium disassembly	3.24E-03	1	1	NAV3
GO: Biological Process	GO:1905927	regulation of invadopodium disassembly	3.24E-03	1	1	NAV3

GO: Biological Process	GO:0032600	chemokine receptor transport out of membrane raft	3.24E-03	1	1	CD24
GO: Biological Process	GO:1904651	positive regulation of fat cell apoptotic process	3.24E-03	1	1	LEP
GO: Biological Process	GO:0110026	regulation of DNA strand resection involved in replication fork processing	3.24E-03	1	1	ZNF365
GO: Biological Process	GO:0032597	B cell receptor transport into membrane raft	3.24E-03	1	1	CD24
GO: Biological Process	GO:0032595	B cell receptor transport within lipid bilayer	3.24E-03	1	1	CD24
GO: Biological Process	GO:0032599	protein transport out of membrane raft	3.24E-03	1	1	CD24
GO: Biological Process	GO:1905878	invadopodium disassembly	3.24E-03	1	1	NAV3
GO: Biological Process	GO:0033606	chemokine receptor transport within lipid bilayer	3.24E-03	1	1	CD24
GO: Biological Process	GO:0046014	negative regulation of T cell homeostatic proliferation	3.24E-03	1	1	CD24
GO: Biological Process	GO:0001100	negative regulation of exit from mitosis	3.24E-03	1	1	RGCC
GO: Biological Process	GO:0042103	positive regulation of T cell homeostatic proliferation	3.24E-03	1	1	CD24
GO: Biological Process	GO:0034102	erythrocyte clearance	3.24E-03	1	1	CD24
GO: Biological Process	GO:0034107	negative regulation of erythrocyte clearance	3.24E-03	1	1	CD24
GO: Biological Process	GO:0034106	regulation of erythrocyte clearance	3.24E-03	1	1	CD24
GO: Biological Process	GO:0048792	spontaneous exocytosis of neurotransmitter	3.24E-03	1	1	SYT12
GO: Biological Process	GO:0034119	negative regulation of erythrocyte aggregation	3.24E-03	1	1	CD24
GO: Biological Process	GO:0016525	negative regulation of angiogenesis	3.25E-03	4	189	COL4A3,LIF,ANGPT4,RGCC
GO: Biological Process	GO:0022407	regulation of cell-cell adhesion	3.26E-03	6	450	SPINT2,PYCARD,RGCC,CD24,LEP,IL6
GO: Biological Process	GO:0042509	regulation of tyrosine phosphorylation of STAT protein	3.28E-03	3	92	LIF,LEP,IL6
GO: Biological Process	GO:0043065	positive regulation of apoptotic process	3.29E-03	8	772	COL4A3,EGLN3,UNC5B,PYCARD,RGCC,CD24,LEP,IL6
GO: Biological Process	GO:0052548	regulation of endopeptidase activity	3.30E-03	6	451	COL4A3,EGLN3,SPINT2,CRIM1,PYCARD,IL6
GO: Biological Process	GO:0045685	regulation of glial cell differentiation	3.38E-03	3	93	LIF,ZNF365,IL6
GO: Biological Process	GO:0050714	positive regulation of protein secretion	3.47E-03	5	315	PYCARD,RGCC,ANO1,IL1RL1,IL6
GO: Biological Process	GO:2000181	negative regulation of blood vessel morphogenesis	3.50E-03	4	193	COL4A3,LIF,ANGPT4,RGCC
GO: Biological Process	GO:0043068	positive regulation of programmed cell death	3.52E-03	8	781	COL4A3,EGLN3,UNC5B,PYCARD,RGCC,CD24,LEP,IL6
GO: Biological Process	GO:0010975	regulation of neuron projection development	3.52E-03	7	613	LIF,VLDLR,NEGR1,CD24,RIMS1,ZNF365,IL6
GO: Biological Process	GO:0060759	regulation of response to cytokine stimulus	3.57E-03	4	194	PYCARD,CD24,PADI2,IL6
GO: Biological Process	GO:0006919	activation of cysteine-type endopeptidase activity involved in apoptotic pr	3.59E-03	3	95	COL4A3,EGLN3,PYCARD
GO: Biological Process	GO:0031175	neuron projection development	3.60E-03	10	1150	LIF,VLDLR,NRXN3,NEGR1,UNC5B,MATN2,CD24,RIMS1,ZNF365,IL6
GO: Biological Process	GO:2000178	negative regulation of neural precursor cell proliferation	3.67E-03	2	28	SPINT2,CD24
GO: Biological Process	GO:0051130	positive regulation of cellular component organization	3.69E-03	11	1350	LIF,S100A10,VLDLR,NEGR1,PYCARD,RGCC,CD24,NAV3,RIMS1,RHOU,IL6
GO: Biological Process	GO:0007260	tyrosine phosphorylation of STAT protein	3.70E-03	3	96	LIF,LEP,IL6
GO: Biological Process	GO:0046427	positive regulation of receptor signaling pathway via JAK-STAT	3.81E-03	3	97	LIF,LEP,IL6
GO: Biological Process	GO:0045785	positive regulation of cell adhesion	3.83E-03	6	465	S100A10,PYCARD,CD24,MIR27B,LEP,IL6
GO: Biological Process	GO:0002682	regulation of immune system process	3.93E-03	13	1775	LIF,ZBTB46,PDE4B,PYCARD,RGCC,CD24,IL1RL1,PADI2,SCARA3,BANK1,LEP,IL6,CD200R1
GO: Biological Process	GO:0060536	cartilage morphogenesis	3.93E-03	2	29	MATN2,SCARA3
GO: Biological Process	GO:0048644	muscle organ morphogenesis	4.03E-03	3	99	LIF,COL11A1,MYLK
GO: Biological Process	GO:0120036	plasma membrane bounded cell projection organization	4.20E-03	13	1789	LIF,VLDLR,NRXN3,MYLK,NEGR1,KLF5,UNC5B,MATN2,CD24,NAV3,RIMS1,ZNF365,IL6
GO: Biological Process	GO:0030182	neuron differentiation	4.20E-03	12	1578	LIF,VLDLR,NRXN3,HOXD10,NEGR1,UNC5B,MATN2,CD24,RIMS1,ZNF365,LEP,IL6
GO: Biological Process	GO:0045666	positive regulation of neuron differentiation	4.20E-03	6	474	LIF,VLDLR,NEGR1,CD24,RIMS1,IL6
GO: Biological Process	GO:0060706	cell differentiation involved in embryonic placenta development	4.21E-03	2	30	LIF,SPINT2
GO: Biological Process	GO:1904894	positive regulation of receptor signaling pathway via STAT	4.26E-03	3	101	LIF,LEP,IL6
GO: Biological Process	GO:0050886	endocrine process	4.38E-03	3	102	LIF,AVPR1A,LEP
GO: Biological Process	GO:0003413	chondrocyte differentiation involved in endochondral bone morphogenesis	4.49E-03	2	31	MATN2,SCARA3