

**Supplementary Table 1 List of significant DEGs containing 86 up-regulated genes and 114**

down-regulated genes					
ID	logFC	adj.P.Val	ID	logFC	adj.P.Val
PITX2	2.317023077	3.06E-22	ODC1	0.566215385	0.000320017
ZIC2	2.542992308	5.92E-21	PI3	1.550819231	0.000433323
HOXD11	1.981573077	1.26E-20	ASPN	0.627121154	0.000559366
HOXD10	1.393120577	5.59E-18	AFAP1L2	0.519846154	0.000605678
HOXD8	1.430192308	5.86E-16	HSD17B2	0.765623077	0.00074201
PLAG1	1.027534615	1.23E-12	ADM	0.774903846	0.001020833
HOXB7	0.948083346	1.91E-10	DSC2	0.557450962	0.001046279
SLC1A3	0.619634615	8.22E-10	KRT15	0.993065385	0.001388729
SBF2-AS1	0.586296154	1.58E-09	DLX2	0.522557692	0.00150002
HOXD-AS2	0.831319231	2.03E-09	NRN1	0.694111538	0.00150448
PCDH7	0.728637692	9.34E-09	STK39	0.567923077	0.001642042
FOXF2	0.846011538	1.23E-08	LRMP	0.635244231	0.001732497
COL4A6	0.733255115	2.43E-08	SRPX	0.541469231	0.001886103
PAX6	1.613711538	2.65E-08	PTX3	0.933173077	0.00217769
BPGM	0.884373077	3.79E-08	NGFR	0.643134615	0.00312671
KCNJ2	0.658961538	1.29E-07	ARL14	0.509192308	0.003264903
GHR	0.663988462	1.76E-07	PLA2G2A	1.109030769	0.004082487
PMAIP1	0.690930769	3.30E-07	P2RY2	0.512496154	0.004701358
HENMT1	0.718292308	4.33E-07	MAT1A	0.504515385	0.005120616
THBS2	0.801453846	7.48E-07	S100A2	0.510046154	0.005465285
ISL2	1.006907692	8.25E-07	FMO1	0.564188462	0.006062777
STARD3NL	0.586546154	1.60E-06	LGR6	0.578703846	0.006193931
MTCL1	0.795280769	2.17E-06	HMCN1	0.518076923	0.006472828
FLJ32255	0.622665385	2.71E-06	BMP2	0.500851923	0.009563274
DEPDC7	0.927546154	3.81E-06	LOC100506388	0.531238462	0.010315475
PYGL	0.534553846	6.71E-06	SFRP4	0.697253846	0.01090746
LOC100506563	0.565676923	7.66E-06	ANXA3	0.635034615	0.014680863
KCNS1	0.771611538	9.81E-06	TRBC1	0.509006308	0.017331195
EN2	0.805680769	1.02E-05	ST6GAL2	0.580944231	0.017534324
ABHD3	0.518396154	1.36E-05	C15orf48	0.921615385	0.017572789
LTBP2	0.506526923	1.81E-05	CLIC2	0.556861538	0.019516762
IGFL2	0.746946154	1.88E-05	AOX1	0.517161538	0.019870454
LMO1	0.595692308	2.15E-05	ABCG2	0.589846154	0.020933733
PITX1	0.615236538	3.76E-05	PNLIPRP3	0.513084615	0.020950553
DLX1	0.633880769	4.15E-05	CCL27	0.588473077	0.022816633
FABP7	1.397984615	4.91E-05	APOBEC3B	0.66535	0.023865117
CXCR2	0.595980769	6.55E-05	LYZ	0.569403846	0.025803664
PAPLN	0.500167308	7.83E-05	CCL19	0.976530769	0.034827192
DRAM1	0.546369231	0.000115904	CCL18	0.733838462	0.035375442
PLAU	0.544475	0.000123438	KRT31	0.877830769	0.041032148
GEM	0.755976923	0.000225965	RSPO3	0.704542308	0.044028743
IGFBP3	1.099946154	0.000263091	CCL2	0.547142308	0.049143589
ACOT4	0.511746154	0.000274383	MT1M	0.648934615	0.049681699

WBP5	-0.916723077	8.43E-15	TMEM99	-0.794884615	0.000199914
BEX2	-1.091684615	5.40E-12	RNASE7	-0.906807615	0.000202275
NMNAT3	-0.640173077	2.61E-11	LOC286189	-0.525465385	0.000203751
NGFRAP1	-0.832123077	4.13E-11	HS3ST6	-0.5592	0.000224368
TRAM1L1	-1.252238462	1.83E-10	LOC100288860	-0.606284615	0.000240304
CYP39A1	-1.671424423	1.91E-10	IL18R1	-0.511988462	0.000268311
PON2	-0.512871731	4.05E-10	NFE2	-1.032288462	0.000285746
KIF21A	-0.865709615	6.35E-09	CCDC178	-1.087176923	0.000285746
INSIG2	-0.606419231	9.34E-09	SLC6A14	-0.653388462	0.000291884
MOXD1	-0.6907025	1.28E-08	TNNT1	-0.752180769	0.00034603
AMDHD1	-1.427884615	1.69E-08	UPK1B	-0.542790385	0.000367508
SP8	-0.880744231	3.19E-08	FLRT3	-0.765413462	0.000384499
HOXA1	-0.547434615	3.44E-08	CARD18	-0.870080769	0.000534406
WFDC21P	-0.631169231	3.61E-08	CPM	-0.502757	0.000700716
UBASH3B	-0.573484615	4.61E-08	MLF1	-0.642523077	0.000846819
HPGD	-0.5623	4.61E-08	XKRX	-0.513526923	0.000873353
SIMC1	-0.54565	6.03E-08	PLS1	-0.515123077	0.000879046
SLC1A6	-1.527528192	6.31E-08	ALOX12B	-0.599342308	0.000885182
PLOD2	-0.841865385	6.96E-08	AQP9	-0.511315385	0.000889097
ASGR1	-0.601661538	9.30E-08	IL37	-0.680011538	0.000929785
TMEM231	-0.507626923	2.49E-07	ACER1	-0.522261538	0.000966447
GGH	-0.992638462	2.49E-07	HRASLS	-1.042728846	0.001147163
CHMP4C	-0.628796154	2.95E-07	AZGP1	-0.530753846	0.001173538
CDH12	-0.8949	3.09E-07	LOC100130476	-0.602892308	0.00135444
AF131215.8	-0.798965385	3.29E-07	C2CD2	-0.510438462	0.001529431
ANKFN1	-0.549236538	3.30E-07	BTC	-1.054619231	0.001551762
MDFIC	-0.612607731	3.40E-07	GDA	-0.984751923	0.001836922
TRPS1	-0.623153846	3.59E-07	C10orf99	-1.067301923	0.001947407
PABPC4L	-0.657103846	4.53E-07	PCP4L1	-0.510342308	0.001991569
SLC35G1	-0.663450038	4.72E-07	RNF180	-0.503633308	0.002016851
LRP12	-0.568455269	5.06E-07	CDHR1	-0.700338462	0.002187563
GATA3	-0.517738385	5.78E-07	NDRG4	-0.616176923	0.002247356
PON3	-1.124953846	5.78E-07	WFDC12	-0.892069231	0.002574636
KCNMB4	-0.661492154	8.25E-07	CYP7B1	-0.549569231	0.002586907
CACNA2D1	-0.522401923	9.42E-07	AGPAT9	-0.511034615	0.003051924
UBE2E2	-0.686615385	1.10E-06	SLC45A4	-0.629257692	0.004017593
MUC15	-0.606540385	1.44E-06	CSRP2	-0.681638462	0.004542298
RUNDC3B	-1.60605	1.52E-06	TMEM170B	-0.563288462	0.004617748
TUSC3	-0.519043846	1.60E-06	E2F8	-0.690342308	0.004838269
CHL1	-0.94865	1.92E-06	PSG7	-0.737892308	0.005021057
ACADL	-0.762480769	2.17E-06	GBP6	-0.510623077	0.005473216
ROBO1	-0.522988462	2.39E-06	C5orf46	-0.736042308	0.005730979
CES4A	-0.547680769	2.46E-06	RASGRP1	-0.611976923	0.006386657
DLX5	-0.643638462	2.71E-06	HSD11B1	-0.726153846	0.006759472
SLC47A2	-1.540965385	2.74E-06	SLC16A14	-0.695242308	0.007352273
SLURP1	-0.539007692	3.82E-06	RP11-999E24.3	-0.682384615	0.007527342

PLAGL1	-0.640276885	3.97E-06	SLC46A2	-0.688107692	0.007801763
NUDT11	-0.562288462	5.40E-06	CRNN	-0.554373077	0.008082634
NELL2	-1.269253846	1.99E-05	ALDH3A1	-0.70595	0.013969591
ENTPD3	-0.525259615	2.24E-05	CHRNA9	-0.770234615	0.01607223
CHP2	-0.545011538	4.43E-05	LOC338667	-0.949038462	0.016574411
BCHE	-1.194723077	5.82E-05	BLMH	-0.703180769	0.023341202
CLCA4	-0.880823077	8.26E-05	CASP14	-0.500496154	0.027651475
NPY1R	-0.879276923	0.000102104	ADAMTS3	-0.515073077	0.028933103
SLITRK6	-0.782489692	0.000139114	LCE1E	-0.650344231	0.030478217
CYP2J2	-0.639	0.000148773	PSG4	-0.661123077	0.046280861
GPT2	-0.574084615	0.000181479	MAP7D2	-0.539146154	0.047143025

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Supplementary Table 2 GSEA results based on Gene Ontology gene sets

Category	Description	enrichmentScore	NES	p.adjust	qvalue
GOMF	GOMF_TUBULIN_BINDING	-0.331920513	-1.378067543	0.047829533	0.040959023
GOMF	GOMF_SULFUR_COMPOUND_BINDING	0.404948656	1.525006134	0.035700308	0.03057211
GOMF	GOMF_SIGNALING_RECEPTOR_REGULATOR_ACTIVITY	0.379844784	1.508916802	0.006173531	0.005286729
GOMF	GOMF_SERINE_HYDROLASE_ACTIVITY	0.435169978	1.570412885	0.044435086	0.038052175
GOMF	GOMF_R_SMAD_BINDING	0.743683521	1.931440345	0.009090459	0.007784653
GOMF	GOMF_PROTEOGLYCAN_BINDING	0.647667059	1.800287885	0.037457761	0.032077112
GOMF	GOMF_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPORATION_OR_REDUCTION_OF_MOLECULAR_OXYGEN_REDUCED_FLAVIN_OR_FLAVOPROTEIN_AS_ONE_DONOR_AND_INCORPORATION_OF_ONE_ATOM_OF_OXYGEN	-0.655607465	-1.95405367	0.01466115	0.012555138
GOMF	GOMF_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPORATION_OR_REDUCTION_OF_MOLECULAR_OXYGEN	-0.416218659	-1.58852113	0.041290593	0.035359374
GOMF	GOMF_MONOOXYGENASE_ACTIVITY	-0.464307572	-1.646183935	0.045014213	0.038548113
GOMF	GOMF_MICROTUBULE_BINDING	-0.377185986	-1.513353861	0.026920393	0.023053393
GOMF	GOMF_MHC_PROTEIN_COMPLEX_BINDING	0.682859537	1.835403296	0.031101076	0.026633539
GOMF	GOMF_MHC_CLASS_II_PROTEIN_COMPLEX_BINDING	0.737058008	1.882338899	0.023806676	0.020386948
GOMF	GOMF_INTEGRIN_BINDING	0.561732242	1.995020475	0.000179698	0.000153885
GOMF	GOMF_INSULIN_LIKE_GROWTH_FACTOR_I_BINDING	0.880636266	2.039489789	0.004356058	0.003730329
GOMF	GOMF_INSULIN_LIKE_GROWTH_FACTOR_BINDING	0.815840126	2.093163792	0.002208085	0.001890903
GOMF	GOMF_IMMUNE_RECEPTOR_ACTIVITY	0.502654196	1.76318218	0.007154211	0.006126539
GOMF	GOMF_HEPARIN_BINDING	0.473858802	1.688839744	0.020653793	0.017686963
GOMF	GOMF_GROWTH_FACTOR_BINDING	0.487666186	1.69227963	0.017240666	0.014764117
GOMF	GOMF_GLYCOSAMINOGLYCAN_BINDING	0.432129993	1.601874304	0.01685455	0.014433466
GOMF	GOMF_G_PROTEIN_COUPLED_RECEPTOR_BINDING	0.46503134	1.760035173	0.002208085	0.001890903
GOMF	GOMF_FRIZZLED_BINDING	0.658581334	1.841652002	0.024015333	0.020565632
GOMF	GOMF_FIBRONECTIN_BINDING	0.726894794	1.966547881	0.013562982	0.011614717
GOMF	GOMF_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT	0.607506264	2.185356611	2.92E-07	2.50E-07
GOMF	GOMF_EXTRACELLULAR_MATRIX_BINDING	0.633627451	1.90846265	0.018135403	0.015530329
GOMF	GOMF_ENDOPEPTIDASE_ACTIVITY	0.377483756	1.478484648	0.027989324	0.023968776
GOMF	GOMF_DNA_BINDING_TRANSCRIPTION_ACTIVATOR_ACTIVITY	0.373838548	1.47953182	0.018371357	0.01573239
GOMF	GOMF_CYTOSKELETAL_MOTOR_ACTIVITY	-0.455873438	-1.655769995	0.039202749	0.033571441
GOMF	GOMF_CYTOKINE_BINDING	0.496170734	1.749550554	0.006695818	0.005733992
GOMF	GOMF_CYTOKINE_ACTIVITY	0.457120924	1.696846003	0.005977518	0.005118873
GOMF	GOMF_CORECEPTOR_ACTIVITY	0.621949784	1.817526155	0.031639951	0.027095006
GOMF	GOMF_COLLAGEN_BINDING	0.713451851	2.244158574	4.26E-05	3.65E-05
GOMF	GOMF_CHEMOKINE_RECEPTOR_BINDING	0.617888469	1.884605445	0.016160375	0.013839006
GOMF	GOMF_CHEMOKINE_BINDING	0.683449969	1.879853503	0.026889721	0.023027127
GOMF	GOMF_CHEMOKINE_ACTIVITY	0.65456481	1.902992123	0.01685455	0.014433466
GOMF	GOMF_CCR_CHEMOKINE_RECEPTOR_BINDING	0.765085975	2.069870654	0.003070741	0.002629642
GOMF	GOMF_C_C_CHEMOKINE_BINDING	0.69259827	1.798765473	0.038613879	0.033067159
GOMF	GOMF_ANTIGEN_BINDING	0.631984057	1.99785175	0.006472144	0.005542448
GOCC	GOCC_VESICLE_LUMEN	0.425603957	1.644854989	0.003723695	0.003188802
GOCC	GOCC_PROTEIN_COMPLEX_INVOLVED_IN_CELL_ADHESION	0.711492935	2.059038983	0.00155929	0.001335305
GOCC	GOCC_PLATELET_ALPHA_GRANULE_LUMEN	0.627904072	1.967235796	0.003286043	0.002814017
GOCC	GOCC_PLATELET_ALPHA_GRANULE	0.617687631	2.038726826	0.000712006	0.000609729
GOCC	GOCC_MICROTUBULE	-0.353209669	-1.481455771	0.007865622	0.006735758

GOCC	GOCC_MHC_PROTEIN_COMPLEX	0.720917984	1.82631232	0.046838097	0.040110003
GOCC	GOCC_MHC_CLASS_II_PROTEIN_COMPLEX	0.819408176	1.897689967	0.038613879	0.033067159
GOCC	GOCC_MEMBRANE_MICRODOMAIN	0.406496304	1.573368885	0.015897523	0.013613911
GOCC	GOCC_LAMELLAR_BODY	-0.794124693	-1.936680128	0.019300075	0.016528279
GOCC	GOCC_KINESIN_COMPLEX	-0.585325891	-1.851898676	0.017843563	0.015280411
GOCC	GOCC KERATIN FILAMENT	0.811625681	2.525412315	9.56E-08	8.19E-08
GOCC	GOCC_INTERMEDIATE_FILAMENT_CYTOSKELETON	0.678375014	2.439849603	9.56E-08	8.19E-08
GOCC	GOCC_INTERMEDIATE_FILAMENT	0.74874529	2.62293617	9.56E-08	8.19E-08
GOCC	GOCC_EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	0.504828287	1.963143453	1.08E-07	9.24E-08
GOCC	GOCC_ENDOPLASMIC_RETICULUM_LUMEN	0.484789064	1.864144209	5.11E-05	4.38E-05
GOCC	GOCC_COLLAGEN_TRIMER	0.570032789	1.851652954	0.013260009	0.011355265
GOCC	GOCC_COLLAGEN_CONTAINING_EXTRACELLULAR_MATRIX	0.565677344	2.226674307	9.56E-08	8.19E-08
GOCC	GOCC_CELL_SUBSTRATE_JUNCTION	0.396828919	1.561571189	0.006472144	0.005542448
GOCC	GOCC_BASEMENT_MEMBRANE	0.620320686	2.066055526	0.000720891	0.000617338
GOCC	GOCC_AUTOPHAGOSOME_MEMBRANE	-0.573978377	-1.815996546	0.025650833	0.0219662
GOBP	GOBP_ZINC_ION_HOMEOSTASIS	0.635199368	1.789878765	0.041469614	0.03551268
GOBP	GOBP_WOUND_HEALING	0.393201321	1.548280841	0.010127277	0.008672536
GOBP	GOBP_WNT_SIGNALING_PATHWAY_INVOLVED_IN_HEART_DEVELOPMENT	0.837458511	1.79622861	0.024130432	0.020664198
GOBP	GOBP_VIRAL_LIFE_CYCLE	0.409849459	1.576075608	0.015167819	0.012989026
GOBP	GOBP_VIRAL_GENOME_REPLICATION	0.535863637	1.847287289	0.005011482	0.004291604
GOBP	GOBP_VENTRAL_SPINAL_CORD_DEVELOPMENT	0.660532868	1.934751737	0.01033363	0.008849248
GOBP	GOBP_UROGENITAL_SYSTEM_DEVELOPMENT	0.436410813	1.692033255	0.000932503	0.000798553
GOBP	GOBP_UMP_BIOSYNTHETIC_PROCESS	0.81243362	1.7425538	0.047720045	0.040865263
GOBP	GOBP_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	0.409706304	1.585821215	0.005778587	0.004948518
GOBP	GOBP_TRANSITION_METAL_ION_HOMEOSTASIS	0.490741829	1.699846398	0.022204517	0.019014932
GOBP	GOBP_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_SIGNALING_PATHWAY	0.427364954	1.553588794	0.028995505	0.024830424
GOBP	GOBP_TRANSFORMING_GROWTH_FACTOR_BETA_PRODUCTION	0.675327193	1.95437642	0.006472144	0.005542448
GOBP	GOBP_TISSUE_MIGRATION	0.432711755	1.662321125	0.002681949	0.002296698
GOBP	GOBP_TELENCEPHALON_REGIONALIZATION	0.844797481	1.913865453	0.020871514	0.01787341
GOBP	GOBP_T_CELL_ACTIVATION	0.404176564	1.605239347	0.000713347	0.000610877
GOBP	GOBP_SYNAPSE_PRUNING	0.825759424	1.813368545	0.047017588	0.040263711
GOBP	GOBP_STEROL_METABOLIC_PROCESS	-0.43873722	-1.648778706	0.019151823	0.016400745
GOBP	GOBP_STEROID_METABOLIC_PROCESS	-0.352918161	-1.436056222	0.040129438	0.034365014
GOBP	GOBP_SPHINGOLIPID_METABOLIC_PROCESS	-0.478499736	-1.798206626	0.004356058	0.003730329
GOBP	GOBP_SPHINGOLIPID_BIOSYNTHETIC_PROCESS	-0.49855033	-1.767590265	0.013562982	0.011614717
GOBP	GOBP_SMOOTH_MUSCLE_CELL_MIGRATION	0.614544479	1.942721103	0.013260009	0.011355265
GOBP	GOBP_SMALL_MOLECULE_CATABOLIC_PROCESS	-0.343728147	-1.430667147	0.029514302	0.025274697
GOBP	GOBP_SKELETAL_SYSTEM_MORPHOGENESIS	0.454439935	1.686894096	0.006347957	0.0054361
GOBP	GOBP_SKELETAL_SYSTEM_DEVELOPMENT	0.432431217	1.726261978	4.16E-05	3.56E-05
GOBP	GOBP_SENSORY_SYSTEM_DEVELOPMENT	0.378745895	1.4845847	0.013795007	0.011813413
GOBP	GOBP_SECONDARY_ALCOHOL_METABOLIC_PROCESS	-0.449705822	-1.695192134	0.016620965	0.014233434
GOBP	GOBP_SALIVARY_GLAND_DEVELOPMENT	0.643083852	1.787548172	0.040129438	0.034365014
GOBP	GOBP_RESPONSE_TO_VIRUS	0.483828287	1.875878247	7.55E-06	6.46E-06
GOBP	GOBP_RESPONSE_TO_TYPE_I_INTERFERON	0.556625461	1.724587896	0.040129438	0.034365014
GOBP	GOBP_RESPONSE_TO_TUMOR_NECROSIS_FACTOR	0.447102777	1.657787812	0.009496041	0.008131975
GOBP	GOBP_RESPONSE_TO_TRANSFORMING_GROWTH_FACTOR_BETA	0.457335608	1.720443322	0.003070741	0.002629642

GOBP	GOBP_RESPONSE_TO_STEROID_HORMONE	0.39587218	1.531181725	0.027557743	0.02359919
GOBP	GOBP_RESPONSE_TO_PROSTAGLANDIN_E	0.720171394	1.84771089	0.049034621	0.041991006
GOBP	GOBP_RESPONSE_TO_OXYGEN_LEVELS	0.422270948	1.625455842	0.006792196	0.005816526
GOBP	GOBP_RESPONSE_TO_MOLECULE_OF_BACTERIAL_ORIGIN	0.381814223	1.477914542	0.044478196	0.038089092
GOBP	GOBP_RESPONSE_TO_KETONE	0.450384317	1.63242073	0.01930075	0.016528279
GOBP	GOBP_RESPONSE_TO_INTERLEUKIN_1	0.520272923	1.798082396	0.00521506	0.004465939
GOBP	GOBP_RESPONSE_TO_INTERFERON_GAMMA	0.573982346	1.987833278	0.000509518	0.000436328
GOBP	GOBP_RESPONSE_TO_CHEMOKINE	0.666693579	2.216872972	2.17E-05	1.86E-05
GOBP	GOBP_RESPONSE_TO_BMP	0.452629014	1.61293178	0.038613879	0.033067159
GOBP	GOBP_RESPIRATORY_ELECTRON_TRANSPORT_CHAIN	0.587711212	1.949968052	0.006075722	0.005202971
GOBP	GOBP_REGULATION_OF_WNT_SIGNALING_PATHWAY_PLANAR_CELL_POLARITY_PATHWAY	0.793709817	1.896265238	0.025216395	0.021594167
GOBP	GOBP_REGULATION_OF_WATER_LOSS_VIA_SKIN	-0.691070386	-1.902944399	0.027656749	0.023683974
GOBP	GOBP_REGULATION_OF_VIRAL_GENOME_REPLICATION	0.537875793	1.750793139	0.026669504	0.022838543
GOBP	GOBP_REGULATION_OF_VASCULATURE_DEVELOPMENT	0.443035697	1.684856271	0.005867476	0.005024638
GOBP	GOBP_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	0.435247644	1.639109842	0.008372598	0.00716991
GOBP	GOBP_REGULATION_OF_TAU_PROTEIN_KINASE_ACTIVITY	0.824365174	1.81030677	0.047187271	0.04040902
GOBP	GOBP_REGULATION_OF_T_CELL_PROLIFERATION	0.453967903	1.625494804	0.031906663	0.027323406
GOBP	GOBP_REGULATION_OF_T_CELL_ACTIVATION	0.420069344	1.625904169	0.007610648	0.006517411
GOBP	GOBP_REGULATION_OF_PEPTIDASE_ACTIVITY	0.369632457	1.455134625	0.033583503	0.028759375
GOBP	GOBP_REGULATION_OF_OSTEOBLAST_PROLIFERATION	0.758938577	1.971059659	0.005987966	0.00512782
GOBP	GOBP_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	0.500239731	1.709497964	0.013562982	0.011614717
GOBP	GOBP_REGULATION_OF_NON_CANONICAL_WNT_SIGNALING_PATHWAY	0.752198799	1.95889187	0.008319361	0.00712432
GOBP	GOBP_REGULATION_OF_NEUROTRANSMITTER_LEVELS	-0.376860193	-1.486513175	0.044677041	0.038259373
GOBP	GOBP_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	0.489564227	1.671192543	0.047692236	0.040841448
GOBP	GOBP_REGULATION_OF_MORPHOGENESIS_OF_A_BRANCHING_STRUCTURE	0.627972298	1.917078071	0.013562982	0.011614717
GOBP	GOBP_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	0.500992552	1.710204648	0.031472689	0.026951771
GOBP	GOBP_REGULATION_OF_MACROPHAGE_MIGRATION	0.724809107	2.042383059	0.002031115	0.001739354
GOBP	GOBP_REGULATION_OF_MACROPHAGE_CHEMOTAXIS	0.720619024	1.894991188	0.01930075	0.016528279
GOBP	GOBP_REGULATION_OF_LYMPHOCYTE_ACTIVATION	0.426122032	1.68680988	0.000444793	0.0003809
GOBP	GOBP_REGULATION_OF_LEUKOCYTE_PROLIFERATION	0.485144585	1.820474078	0.000509518	0.000436328
GOBP	GOBP_REGULATION_OF_LEUKOCYTE_MIGRATION	0.511843861	1.881698403	0.000472806	0.00040489
GOBP	GOBP_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	0.405450526	1.548113808	0.02668864	0.02285493
GOBP	GOBP_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	0.577133621	1.985508729	0.000712006	0.000609729
GOBP	GOBP_REGULATION_OF_INSULIN_LIKE_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	0.810377274	2.052940878	0.003639945	0.003117082
GOBP	GOBP_REGULATION_OF_HORMONE_BIOSYNTHETIC_PROCESS	0.737982367	1.869541778	0.031363765	0.026858494
GOBP	GOBP_REGULATION_OF_HEMOPOIESIS	0.372128404	1.437636078	0.048275428	0.041340868
GOBP	GOBP_REGULATION_OF GRANULOCYTE DIFFERENTIATION	0.823137379	1.921130781	0.012792756	0.010955131
GOBP	GOBP_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	0.499626093	1.772946451	0.006840268	0.005857693
GOBP	GOBP_REGULATION_OF_ESTABLISHMENT_OF_PLANAR_POLARITY	0.601670561	1.860695632	0.017240666	0.014764117
GOBP	GOBP_REGULATION_OF_COMPLEMENT_ACTIVATION	0.742805397	1.851353165	0.039916314	0.034182504
GOBP	GOBP_REGULATION_OF_CHEMOTAXIS	0.496239803	1.826782618	0.000808997	0.000692788
GOBP	GOBP_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_FACTOR	0.41133878	1.570536378	0.020871514	0.01787341

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GOBP	GOBP_REGULATION_OF_CELLULAR_EXTRAVASATION	0.647787954	1.842648502	0.024132505	0.020665973
GOBP	GOBP_REGULATION_OF_CELL_SUBSTRATE_ADHESION	0.450261807	1.656214162	0.013562982	0.011614717
GOBP	GOBP_REGULATION_OF_CELL_MATRIX_ADHESION	0.503862085	1.733433182	0.020385955	0.017457599
GOBP	GOBP_REGULATION_OF_CELL_CELL_ADHESION	0.428644909	1.691578589	0.000459146	0.000393191
GOBP	GOBP_REGULATION_OF_CELL_ADHESION_MEDIATED_BY_INTEGRIN	0.61553785	1.830749329	0.032509079	0.027839287
GOBP	GOBP_REGULATION_OF_BMP_SIGNALING_PATHWAY	0.504012479	1.69043283	0.046838097	0.040110003
GOBP	GOBP_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	0.414068651	1.599495433	0.00776294	0.006647827
GOBP	GOBP_REGULATION_OF_ANIMAL_ORGAN_MORPHOGENESIS	0.525160655	1.818612569	0.004356058	0.003730329
GOBP	GOBP_REGIONALIZATION	0.443264054	1.712273627	0.000712006	0.000609729
GOBP	GOBP_RECEPTOR_METABOLIC_PROCESS	0.449314361	1.605445235	0.030171403	0.025837409
GOBP	GOBP_RECEPTOR_MEDIATED_ENDOCYTOSIS	0.422759527	1.58860505	0.01382422	0.011838429
GOBP	GOBP_PROTEIN_TRANSPORT_ALONG_MICROTUBULE	-0.833091053	-1.991924178	0.026463149	0.02266183
GOBP	GOBP_PROTEIN_MONO_ADP_RIBOSYLATION	0.803918022	1.821254163	0.047720045	0.040865263
GOBP	GOBP_PROTEIN_KINASE_B_SIGNALING	0.448059694	1.625749181	0.016550745	0.0141733
GOBP	GOBP_POSITIVE_REGULATION_OF_T_CELL_PROLIFERATION	0.502676823	1.697179495	0.038613879	0.033067159
GOBP	GOBP_POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	0.752485703	1.991893052	0.00948406	0.008121715
GOBP	GOBP_POSITIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	0.393219265	1.547828006	0.007970088	0.006825219
GOBP	GOBP_POSITIVE_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	0.587812461	1.794477848	0.041247433	0.035322415
GOBP	GOBP_POSITIVE_REGULATION_OF_NON_CANONICAL_WNT_SIGNALING_PATHWAY	0.774912853	1.808578947	0.045065036	0.038591635
GOBP	GOBP_POSITIVE_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	0.555898046	1.748574011	0.037847404	0.032410785
GOBP	GOBP_POSITIVE_REGULATION_OF_MAPK_CASCADE	0.392593419	1.55512854	0.003286043	0.002814017
GOBP	GOBP_POSITIVE_REGULATION_OF_MACROPHAGE_MIGRATION	0.755506032	1.962144903	0.006472144	0.005542448
GOBP	GOBP_POSITIVE_REGULATION_OF_MACROPHAGE_CHEMOTAXIS	0.767332049	1.861015338	0.029353998	0.025137421
GOBP	GOBP_POSITIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	0.501319894	1.786711483	0.006173531	0.005286729
GOBP	GOBP_POSITIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	0.590957071	2.067484937	3.13E-05	2.68E-05
GOBP	GOBP_POSITIVE_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	0.574441609	1.913249531	0.00822631	0.007044635
GOBP	GOBP_POSITIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	0.458368949	1.714518937	0.005982588	0.005123215
GOBP	GOBP_POSITIVE_REGULATION_OF_INFLAMMATORY_RESPONSE_TO_O_ANTIGENIC_STIMULUS	0.815636522	1.749423567	0.044651048	0.038237115
GOBP	GOBP_POSITIVE_REGULATION_OF_IMMUNE_RESPONSE	0.410566433	1.635997587	0.000509518	0.000436328
GOBP	GOBP_POSITIVE_REGULATION_OF_FOCAL_ADHESION_ASSEMBLY	0.68407435	1.798890707	0.049174336	0.042110651
GOBP	GOBP_POSITIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	0.613473834	1.836209692	0.017801745	0.0152446
GOBP	GOBP_POSITIVE_REGULATION_OF_ERK1_AND_ERK2_CASCADE	0.465692819	1.699575852	0.006695818	0.005733992
GOBP	GOBP_POSITIVE_REGULATION_OF_DNA_BINDING_TRANSCRIPTION_FACTOR_ACTIVITY	0.398564529	1.510984818	0.036682758	0.031413435
GOBP	GOBP_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	0.376414465	1.491708674	0.013260009	0.011355265
GOBP	GOBP_POSITIVE_REGULATION_OF_CHEMOTAXIS	0.586393708	2.052331895	5.11E-05	4.38E-05
GOBP	GOBP_POSITIVE_REGULATION_OF_CELL_SUBSTRATE_JUNCTION_ORGANIZATION	0.651458431	1.771348859	0.040129438	0.034365014
GOBP	GOBP_POSITIVE_REGULATION_OF_CELL_MATRIX_ADHESION	0.588770106	1.802688955	0.027911095	0.023901785

GOBP	GOBP_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	0.46884814	1.790113392	0.000540691	0.000463023
GOBP	GOBP_POSITIVE_REGULATION_OF_CELL_ADHESION	0.445393194	1.757622052	3.95E-05	3.38E-05
GOBP	GOBP_POSITIVE_REGULATION_OF_CELL_ACTIVATION	0.451573862	1.74293299	0.000563004	0.000482131
GOBP	GOBP_POSITIVE_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	0.473886416	1.619439265	0.034493283	0.029538469
GOBP	GOBP_PLASMINOGEN_ACTIVATION	0.713983576	1.823410157	0.044651048	0.038237115
GOBP	GOBP_PITUITARY_GLAND_DEVELOPMENT	0.71210803	2.060819049	0.001479119	0.00126665
GOBP	GOBP_PHAGOCYTOSIS	0.441841615	1.645875886	0.011496205	0.009844824
GOBP	GOBP_PERIPHERAL_NERVOUS_SYSTEM_NEURON_DIFFERENTIATION	0.812204318	1.84002654	0.040129438	0.034365014
GOBP	GOBP_PEPTIDE_ANTIGEN_ASSEMBLY_WITH_MHC_CLASS_II_PROTEIN_COMPLEX	0.857846404	1.94342743	0.013795007	0.011813413
GOBP	GOBP_PATTERN_SPECIFICATION_PROCESS	0.405700309	1.601115823	0.002461716	0.002108101
GOBP	GOBP_PATHWAY_RESTRICTED_SMAD_PROTEIN_PHOSPHORYLATION	0.60716515	1.881174581	0.011244138	0.009628965
GOBP	GOBP_OSTEOBLAST_PROLIFERATION	0.730798546	1.977109125	0.010959273	0.00938502
GOBP	GOBP_OSTEOBLAST_DIFFERENTIATION	0.413846195	1.529023843	0.047720045	0.040865263
GOBP	GOBP_OSSIFICATION	0.411219373	1.61187223	0.001774476	0.00151958
GOBP	GOBP_ORGANIC_HYDROXY_COMPOUND_CATABOLIC_PROCESS	-0.583268063	-1.97589202	0.002945728	0.002522586
GOBP	GOBP_ORGANIC_HYDROXY_COMPOUND_BIOSYNTHETIC_PROCESS	-0.381255014	-1.515487147	0.029353998	0.025137421
GOBP	GOBP_ODONTOGENESIS	0.538471598	1.864851368	0.00279392	0.002392585
GOBP	GOBP_NOREPINEPHRINE_METABOLIC_PROCESS	-0.818058304	-1.955980811	0.043057617	0.036872573
GOBP	GOBP_NON_CANONICAL_WNT_SIGNALING_PATHWAY	0.620909921	1.992974501	0.003639945	0.003117082
GOBP	GOBP_NEUTROPHIL_MIGRATION	0.616255637	2.107621242	5.11E-05	4.38E-05
GOBP	GOBP_NEUTROPHIL_CHEMOTAXIS	0.64450376	2.161633612	6.75E-05	5.78E-05
GOBP	GOBP_NEURON_REMODELING	0.809167289	1.873972815	0.045320712	0.038810584
GOBP	GOBP_NEURON_FATE_COMMITMENT	0.642732611	2.0027726	0.00210247	0.00180046
GOBP	GOBP_NEURON_DEATH	0.401594073	1.549440482	0.014967295	0.012817306
GOBP	GOBP_NEURAL_CREST_CELL_MIGRATION	0.555862957	1.732084355	0.043057617	0.036872573
GOBP	GOBP_NEURAL_CREST_CELL_DIFFERENTIATION	0.4959066	1.665147165	0.043057617	0.036872573
GOBP	GOBP_NEPHRON_DEVELOPMENT	0.46823029	1.661845885	0.022719048	0.019455554
GOBP	GOBP_NEGATIVE_REGULATION_OF_WNT_SIGNALING_PATHWAY	0.460366756	1.648406781	0.024780963	0.021221283
GOBP	GOBP_NEGATIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION	0.616125233	1.870061904	0.01466115	0.012555138
GOBP	GOBP_NEGATIVE_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	0.502827223	1.719691102	0.024015333	0.020565632
GOBP	GOBP_NEGATIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	0.398050793	1.551910464	0.014408348	0.01233865
GOBP	GOBP_NEGATIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	0.51474511	1.750541832	0.018371357	0.01573239
GOBP	GOBP_NEGATIVE_REGULATION_OF_PEPTIDASE_ACTIVITY	0.419455191	1.56866841	0.034635675	0.029660407
GOBP	GOBP_NEGATIVE_REGULATION_OF_PATHWAY_RESTRICTED_SMAD_PROTEIN_PHOSPHORYLATION	0.824233407	1.81001741	0.047187271	0.04040902
GOBP	GOBP_NEGATIVE_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	0.613626028	1.793201613	0.036179231	0.030982238
GOBP	GOBP_NEGATIVE_REGULATION_OF_LYMPHOCYTE_ACTIVATION	0.453597382	1.609910674	0.040129438	0.034365014
GOBP	GOBP_NEGATIVE_REGULATION_OF_LOCOMOTION	0.417784137	1.608184674	0.009090459	0.007784653
GOBP	GOBP_NEGATIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	0.647524433	1.892263047	0.01685455	0.014433466
GOBP	GOBP_NEGATIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	0.475359132	1.645988919	0.03347091	0.028662956



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GOBP	GOBP_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	0.476185692	1.865068956	4.16E-06	3.56E-06
GOBP	GOBP_NEGATIVE_REGULATION_OF_HYDROLASE_ACTIVITY	0.404353228	1.557541897	0.014408348	0.01233865
GOBP	GOBP_NEGATIVE_REGULATION_OF_GROWTH	0.421492953	1.577081307	0.018371357	0.01573239
GOBP	GOBP_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	0.64586444	1.837177022	0.026358236	0.022571987
GOBP	GOBP_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_FACTOR_STIMULUS	0.523568622	1.746901149	0.043884661	0.037580815
GOBP	GOBP_NEGATIVE_REGULATION_OF_CELL_DIVISION	-0.79465349	-1.994866802	0.008391048	0.007185709
GOBP	GOBP_NEGATIVE_REGULATION_OF_CELL_CELL_ADHESION	0.433971199	1.564129558	0.030990705	0.026539021
GOBP	GOBP_NEGATIVE_REGULATION_OF_CELL_ADHESION	0.433875174	1.652096088	0.005565359	0.004765919
GOBP	GOBP_NEGATIVE_REGULATION_OF_CELL_ACTIVATION	0.435495186	1.592652988	0.034383662	0.029444595
GOBP	GOBP_NEGATIVE_REGULATION_OF_CANONICAL_WNT_SIGNALING_PATHWAY	0.458656918	1.591612833	0.047549951	0.040719602
GOBP	GOBP_NEGATIVE_REGULATION_OF_BMP_SIGNALING_PATHWAY	0.574339546	1.743234082	0.041858618	0.035845805
GOBP	GOBP_MYELOID_LEUKOCYTE_MIGRATION	0.586242393	2.164206072	9.56E-08	8.19E-08
GOBP	GOBP_MYELOID_LEUKOCYTE_DIFFERENTIATION	0.432254758	1.593069982	0.034577683	0.029610746
GOBP	GOBP_MYELOID_LEUKOCYTE_ACTIVATION	0.458582527	1.702440795	0.006294377	0.005390216
GOBP	GOBP_MYELOID_CELL_DIFFERENTIATION	0.374186765	1.455978869	0.041874084	0.03585905
GOBP	GOBP_MUSCLE_CELL_MIGRATION	0.606097415	1.975305491	0.003284878	0.002813019
GOBP	GOBP_MORPHOGENESIS_OF_AN_EPITHELIUM	0.424521754	1.695553545	0.000111717	9.57E-05
GOBP	GOBP_MORPHOGENESIS_OF_A_BRANCHING_STRUCTURE	0.486109799	1.777756101	0.002461716	0.002108101
GOBP	GOBP_MONONUCLEAR_CELL_MIGRATION	0.527305616	1.911222451	0.000409542	0.000350713
GOBP	GOBP_MONOCYTE_CHEMOTAXIS	0.65473314	2.028554074	0.00213662	0.001829704
GOBP	GOBP_MOLTING_CYCLE	0.560186271	1.916744	0.002978783	0.002550893
GOBP	GOBP_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY	0.528996154	1.724028152	0.043363216	0.037134274
GOBP	GOBP_MESONEPHROS_DEVELOPMENT	0.532767436	1.798773936	0.014408348	0.01233865
GOBP	GOBP_MESENCHYME_DEVELOPMENT	0.405174727	1.554320978	0.016948299	0.014513748
GOBP	GOBP_MESENCHYMAL_CELL_DIFFERENTIATION	0.429871154	1.607923562	0.018599533	0.015927789
GOBP	GOBP_MEMBRANE_LIPID_METABOLIC_PROCESS	-0.449203506	-1.754803474	0.003610783	0.003092109
GOBP	GOBP_MEMBRANE_LIPID_BIOSYNTHETIC_PROCESS	-0.46324577	-1.738417808	0.016406054	0.014049394
GOBP	GOBP_MACROPHAGE_MIGRATION	0.664752364	2.002402384	0.00593883	0.005085742
GOBP	GOBP_MACROPHAGE_CHEMOTAXIS	0.655476704	1.81488579	0.035354948	0.030276359
GOBP	GOBP_MACROAUTOPHAGY	-0.368084655	-1.499282223	0.024015333	0.020565632
GOBP	GOBP_LYMPHOCYTE_MIGRATION	0.50073729	1.699398862	0.032394299	0.027740995
GOBP	GOBP_LYMPHOCYTE_MEDIATED_IMMUNITY	0.44246676	1.688852488	0.005867476	0.005024638
GOBP	GOBP_LYMPHOCYTE_COSTIMULATION	0.59958434	1.775001703	0.040690319	0.034845328
GOBP	GOBP_LYMPHOCYTE_CHEMOTAXIS	0.600687927	1.833784159	0.029353998	0.025137421
GOBP	GOBP_LIPOPOLYSACCHARIDE_MEDIATED_SIGNALING_PATHWAY	0.547800535	1.6972457	0.047720045	0.040865263
GOBP	GOBP_LEUKOCYTE_TETHERING_OR_ROLLING	0.657275378	1.807859356	0.046380297	0.039717964
GOBP	GOBP_LEUKOCYTE_PROLIFERATION	0.449492864	1.73692827	0.000871319	0.000746158
GOBP	GOBP_LEUKOCYTE_MIGRATION	0.516892453	2.009472568	9.56E-08	8.19E-08
GOBP	GOBP_LEUKOCYTE_MEDIATED_IMMUNITY	0.417076594	1.626087781	0.003639945	0.003117082
GOBP	GOBP_LEUKOCYTE_CHEMOTAXIS	0.562994048	2.086325084	1.99E-06	1.70E-06
GOBP	GOBP_LEUKOCYTE_CELL_CELL_ADHESION	0.451529139	1.75367751	0.000323593	0.00027711
GOBP	GOBP_KIDNEY_EPITHELIUM_DEVELOPMENT	0.451418084	1.591747972	0.036977984	0.031666254
GOBP	GOBP_INTERMEDIATE_FILAMENT_ORGANIZATION	0.733942764	2.087717945	0.000720891	0.000617338
GOBP	GOBP_INTERMEDIATE_FILAMENT_BASED_PROCESS	0.63246212	1.989405853	0.003284878	0.002813019

GOBP	GOBP_INTEGRIN_MEDIATED_SIGNALING_PATHWAY	0.547263413	1.862023761	0.005350461	0.00458189
GOBP	GOBP_INSULIN_LIKE_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	0.769399516	2.1303156	0.000540691	0.000463023
GOBP	GOBP_INNER_EAR_MORPHOGENESIS	-0.467138177	-1.660818179	0.036254387	0.031046598
GOBP	GOBP_IMMUNOGLOBULIN_PRODUCTION	0.493356795	1.696977221	0.042652752	0.036525866
GOBP	GOBP_IMMUNE_RESPONSE_REGULATING_SIGNALING_PATHWAY	0.367014206	1.441831069	0.038630356	0.033081269
GOBP	GOBP_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CIRCULATING_IMMUNOGLOBULIN	0.678098963	2.057843704	0.001796129	0.001538123
GOBP	GOBP_HUMORAL_IMMUNE_RESPONSE	0.470192069	1.755874716	0.001700387	0.001456133
GOBP	GOBP_HETEROTYPIC_CELL_CELL_ADHESION	0.633837733	1.975055915	0.003070741	0.002629642
GOBP	GOBP_HEMOSTASIS	0.410888778	1.523511918	0.043946482	0.037633756
GOBP	GOBP_HEART_MORPHOGENESIS	0.407450601	1.531078643	0.031101076	0.026633539
GOBP	GOBP GRANULOCYTE MIGRATION	0.608409982	2.15236236	2.64E-06	2.26E-06
GOBP	GOBP GRANULOCYTE CHEMOTAXIS	0.637053629	2.182692781	1.49E-05	1.27E-05
GOBP	GOBP GRANULOCYTE ACTIVATION	0.617142225	1.807657195	0.036001335	0.030829896
GOBP	GOBP GLYCOPROTEIN METABOLIC PROCESS	0.38939487	1.509812815	0.016351122	0.014002353
GOBP	GOBP_GLIOGENESIS	0.42861509	1.642302106	0.009930124	0.008503704
GOBP	GOBP_GLIAL_CELL_FATE_COMMITMENT	0.826970392	1.873478673	0.030990705	0.026539021
GOBP	GOBP_GLIAL_CELL_DIFFERENTIATION	0.417032793	1.539542199	0.036001335	0.030829896
GOBP	GOBP_GASTRULATION	0.472288852	1.699300178	0.009090459	0.007784653
GOBP	GOBP_GABAERGIC_NEURON_DIFFERENTIATION	0.823559075	1.865750428	0.031639951	0.027095006
GOBP	GOBP_FORMATION_OF_PRIMARY_GERM_LAYER	0.502302555	1.726163312	0.030990705	0.026539021
GOBP	GOBP_EYE_MORPHOGENESIS	0.461687104	1.645459634	0.029357196	0.025140159
GOBP	GOBP_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	0.444249414	1.640016639	0.009501727	0.008136845
GOBP	GOBP_EXTRACELLULAR_MATRIX_DISASSEMBLY	0.576199027	1.787764162	0.042690012	0.036557773
GOBP	GOBP_EXTERNAL_ENCAPSULATING_STRUCTURE_ORGANIZATION	0.544513356	2.09380016	9.56E-08	8.19E-08
GOBP	GOBP_EXOCRINE_SYSTEM_DEVELOPMENT	0.641696981	1.89967142	0.01466115	0.012555138
GOBP	GOBP_ESTABLISHMENT_OF_TISSUE_POLARITY	0.596236352	1.921198289	0.00776294	0.006647827
GOBP	GOBP_EPIDERMIS_DEVELOPMENT	0.386075817	1.483938486	0.030990705	0.026539021
GOBP	GOBP_EOSINOPHIL_MIGRATION	0.825764598	2.091921816	0.001845475	0.001580381
GOBP	GOBP_EOSINOPHIL_CHEMOTAXIS	0.865355999	2.092418033	0.000563004	0.000482131
GOBP	GOBP_ENTRY_INTO_HOST	0.456373265	1.619461777	0.032394299	0.027740995
GOBP	GOBP_ENDOTHELIAL_CELL_MIGRATION	0.427187159	1.570258083	0.023203461	0.019870382
GOBP	GOBP_ENDOMEMBRANE_SYSTEM_ORGANIZATION	-0.319772223	-1.368450467	0.036682758	0.031413435
GOBP	GOBP_ENDODERMAL_CELL_DIFFERENTIATION	0.658374496	1.923970227	0.013562982	0.011614717
GOBP	GOBP_ENDODERM_FORMATION	0.578563361	1.75578055	0.040129438	0.034365014
GOBP	GOBP_ENDODERM_DEVELOPMENT	0.552396525	1.794364598	0.01930075	0.016528279
GOBP	GOBP_ENDOCRINE_SYSTEM_DEVELOPMENT	0.474620912	1.647010445	0.026861021	0.023002549
GOBP	GOBP_EMBRYONIC_SKELETAL_SYSTEM_DEVELOPMENT	0.494990455	1.712726408	0.018081518	0.015484185
GOBP	GOBP_EMBRYONIC_ORGAN_DEVELOPMENT	0.375686937	1.486681311	0.01030618	0.008825741
GOBP	GOBP_EMBRYONIC_EYE_MORPHOGENESIS	0.659030197	1.824724712	0.031472689	0.026951771
GOBP	GOBP_DIVALENT_INORGANIC_CATION_HOMEOSTASIS	0.370087527	1.469504117	0.014408348	0.01233865
GOBP	GOBP_DIENCEPHALON_DEVELOPMENT	0.646337801	2.097414588	0.000696327	0.000596303
GOBP	GOBP_DENDRITIC_CELL_MIGRATION	0.729450305	2.006379066	0.006976342	0.00597422
GOBP	GOBP_DENDRITIC_CELL_CHEMOTAXIS	0.761112518	2.001475768	0.00442183	0.003786652
GOBP	GOBP_DENDRITIC_CELL_ANTIGEN_PROCESSING_AND_PRESENTATION	0.805611343	1.825090336	0.046149197	0.03952006
GOBP	GOBP_DEFENSE_RESPONSE_TO_SYMBIONT	0.462157575	1.754703062	0.001732518	0.001483649
GOBP	GOBP_CYTOLYSIS	0.720563787	1.871395466	0.01685455	0.014433466

GOBP	GOBP_CYTOKINE_MEDIATED_SIGNALING_PATHWAY	0.429876788	1.704006833	0.00010469	8.97E-05
GOBP	GOBP_CONNECTIVE_TISSUE_DEVELOPMENT	0.437101322	1.642497268	0.006173531	0.005286729
GOBP	GOBP_COMPLEMENT_ACTIVATION_ALTERNATIVE_PATHWAY	0.799308023	1.909640004	0.021211338	0.018164419
GOBP	GOBP_COMPLEMENT_ACTIVATION	0.704296027	2.206573293	5.11E-05	4.38E-05
GOBP	GOBP_COLLAGEN_METABOLIC_PROCESS	0.517138525	1.703692527	0.03677105	0.031489045
GOBP	GOBP_CHRONIC_INFLAMMATORY_RESPONSE	0.810945827	1.96085504	0.008507796	0.007285687
GOBP	GOBP_CEREBRAL_CORTEX_GABAERGIC_INTERNEURON_DIFFERENTIATION	0.8507732	1.82478671	0.015412273	0.013198365
GOBP	GOBP_CELLULAR_RESPONSE_TO_INTERLEUKIN_1	0.526337652	1.76972025	0.024955753	0.021370965
GOBP	GOBP_CELLULAR_RESPONSE_TO_INTERFERON_GAMMA	0.569849164	1.935058061	0.00210247	0.00180046
GOBP	GOBP_CELLULAR_EXTRAVASATION	0.629334213	2.032734876	0.001700387	0.001456133
GOBP	GOBP_CELL_SUBSTRATE_JUNCTION_ORGANIZATION	0.536809902	1.805162135	0.013562982	0.011614717
GOBP	GOBP_CELL_SUBSTRATE_ADHESION	0.474416214	1.832802486	3.13E-05	2.68E-05
GOBP	GOBP_CELL_RECOGNITION	0.475084816	1.696646893	0.013576746	0.011626504
GOBP	GOBP_CELL_MATRIX_ADHESION	0.516696706	1.918510691	0.000114867	9.84E-05
GOBP	GOBP_CELL_GROWTH	0.365355398	1.448420126	0.02668864	0.02285493
GOBP	GOBP_CELL_FATE_SPECIFICATION	0.566066577	1.888696749	0.011675346	0.009998232
GOBP	GOBP_CELL_FATE_COMMITMENT	0.460870219	1.74551741	0.002086808	0.001787047
GOBP	GOBP_CELL_CHEMOTAXIS	0.53499782	2.051572443	1.64E-07	1.40E-07
GOBP	GOBP_CELL_ADHESION_MEDIATED_BY_INTEGRIN	0.629773842	2.059206364	0.000928868	0.00079544
GOBP	GOBP_CARTILAGE_DEVELOPMENT	0.470558196	1.698119568	0.01021893	0.008751024
GOBP	GOBP_CARDIOCYTE_DIFFERENTIATION	0.46218534	1.617213969	0.045398035	0.0388768
GOBP	GOBP_CARDIAC_NEURAL_CREST_CELL_MIGRATION_INVOLVED_IN_OUTFLOW_TRACT_MORPHOGENESIS	0.862951767	1.895042969	0.021147353	0.018109625
GOBP	GOBP_CARDIAC_NEURAL_CREST_CELL_DEVELOPMENT_INVOLVED_IN_OUTFLOW_TRACT_MORPHOGENESIS	0.841072651	1.947863323	0.021450315	0.018369068
GOBP	GOBP_CAMERA_TYPE_EYE_MORPHOGENESIS	0.484249464	1.661255113	0.029522433	0.025281661
GOBP	GOBP_CALCIIUM_ION_EXPORT	-0.842789701	-1.895447544	0.019359195	0.016578329
GOBP	GOBP_BRANCHING_MORPHOGENESIS_OF_AN_EPITHELIAL_TUBE	0.484374591	1.723766322	0.008516923	0.007293503
GOBP	GOBP_BONE_DEVELOPMENT	0.460336593	1.692341546	0.009930124	0.008503704
GOBP	GOBP_BILE_ACID_METABOLIC_PROCESS	-0.649104415	-2.015118358	0.004356058	0.003730329
GOBP	GOBP_BILE_ACID_BIOSYNTHETIC_PROCESS	-0.670381382	-1.970440885	0.019151823	0.016400745
GOBP	GOBP_BASEMENT_MEMBRANE_ORGANIZATION	0.746621732	2.01991732	0.006173531	0.005286729
GOBP	GOBP_B_CELL_MEDIATED_IMMUNITY	0.585079397	2.047731912	5.28E-05	4.52E-05
GOBP	GOBP_ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT	0.574191957	1.827515636	0.021947629	0.018794945
GOBP	GOBP_APOPTOTIC_CELL_CLEARANCE	0.606036379	1.794102239	0.035700308	0.03057211
GOBP	GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_II	0.69100334	1.799525374	0.045065036	0.038591635
GOBP	GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_ANTIGEN	0.611472518	1.777711491	0.047017588	0.040263711
GOBP	GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION	0.506468164	1.698669075	0.043057617	0.036872573
GOBP	GOBP_ANTERIOR_POSTERIOR_PATTERN_SPECIFICATION	0.442054306	1.627268452	0.019359195	0.016578329
GOBP	GOBP_AMMONIUM_ION_METABOLIC_PROCESS	-0.709857407	-1.923874885	0.047187271	0.04040902
GOBP	GOBP_AMEBOIDAL_TYPE_CELL_MIGRATION	0.426785905	1.679956285	0.000509518	0.000436328
GOBP	GOBP_ALCOHOL_METABOLIC_PROCESS	-0.371527907	-1.547214612	0.005982588	0.005123215
GOBP	GOBP_ALCOHOL_CATABOLIC_PROCESS	-0.581056029	-1.849021844	0.023351546	0.019997196
GOBP	GOBP_AGING	0.462738243	1.778337256	0.000509518	0.000436328
GOBP	GOBP_ADENOHYPOPHYSIS_DEVELOPMENT	0.777244317	1.814020379	0.043057617	0.036872573
GOBP	GOBP_ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECOGNITION	0.441924925	1.694662974	0.002256712	0.001932545

OMBINATION\_OF\_IMMUNE\_RECEPTORS\_BUILT\_FROM\_IMMUNOGL

OBULIN\_SUPERFAMILY\_DOMAINS

GOBP	GOBP_ADAPTIVE_IMMUNE_RESPONSE	0.417806101	1.64901019	0.000509518	0.000436328
GOBP	GOBP_ACTIVATION_OF_IMMUNE_RESPONSE	0.453781173	1.747335323	0.001153151	0.000987506

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**Supplementary Table 3 GSEA results based on KEGG pathway gene sets**

ID	enrichmentScore	NES	p.adjust	qvalue
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	0.521744781	1.968418821	4.65E-06	3.78E-06
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	0.762576227	2.206015889	1.98E-05	1.61E-05
KEGG_FOCAL_ADHESION	0.534724135	1.969654011	1.98E-05	1.61E-05
KEGG_CHEMOKINE_SIGNALING_PATHWAY	0.519461279	1.8920852	9.68E-05	7.86E-05
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	0.696330296	2.055146103	0.000105409	8.56E-05
KEGG_CELL_ADHESION_MOLECULES_CAMS	0.562730589	1.935737794	0.00015256	0.000123933
KEGG_PATHWAYS_IN_CANCER	0.425399753	1.642194258	0.000669387	0.000543781
KEGG_ECM_RECEPTOR_INTERACTION	0.602705959	1.946666098	0.000811504	0.000659231
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	0.643182979	2.030468345	0.001070432	0.000869573
KEGG_LEISHMANIA_INFECTION	0.62036107	1.95842172	0.003353335	0.002724105
KEGG_HEMATOPOIETIC_CELL_LINEAGE	0.55889503	1.81400437	0.003353335	0.002724105
KEGG_ASTHMA	0.737312133	1.940058126	0.00551249	0.00447811
KEGG_TGF_BETA_SIGNALING_PATHWAY	0.562233447	1.815944861	0.005835911	0.004740843
KEGG_SMALL_CELL_LUNG_CANCER	0.549150629	1.783526253	0.007383855	0.005998326
KEGG_HEDGEHOG_SIGNALING_PATHWAY	0.599598933	1.778595257	0.011893146	0.00966148
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.522827493	1.74081779	0.01360693	0.011053684
KEGG_ALLOGRAFT_REJECTION	0.673703742	1.82363843	0.017044038	0.013845843
KEGG_HISTIDINE_METABOLISM	-0.657846191	-1.851004218	0.02089219	0.016971917
KEGG_DNA_REPLICATION	0.640149707	1.770535695	0.02089219	0.016971917
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	0.473823455	1.617449584	0.022523315	0.018296972
KEGG_PRIMARY_BILE_ACID_BIOSYNTHESIS	-0.744548264	-1.849881615	0.025365815	0.020606097
KEGG_SPHINGOLIPID_METABOLISM	-0.636474696	-1.830264539	0.027782345	0.022569182
KEGG_P53_SIGNALING_PATHWAY	0.53550295	1.67811785	0.030012429	0.024380806
KEGG_APOPTOSIS	0.496610026	1.615407091	0.032308455	0.026245999
KEGG_TYPE_I_DIABETES_MELLITUS	0.601546415	1.700881195	0.043621993	0.03543663
KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	0.683874799	1.760882983	0.047167716	0.038317023
KEGG_AUTOIMMUNE_THYROID_DISEASE	0.563702328	1.645277192	0.04964249	0.040327423

**Supplementary Table 4 List of hub genes in the ME pink module**

No.	gene names	No.	gene names
1	ATP2C2	19	CHMP4C
2	TCEAL8	20	PCDH7
3	THRB	21	PLAGL1
4	GGT6	22	UBE2E2
5	FAM171B	23	NGFRAP1
6	ATP13A4	24	WBP5
7	C5orf30	25	HOXB7
8	PON2	26	BPGM
9	PTGER3	27	BEX2
10	CACNA2D1	28	HOXD10
11	HPGD	29	TRAM1L1
12	UBASH3B	30	PON3
13	NMNAT3	31	HOXD8
14	SLC1A3	32	SLC1A6
15	INSIG2	33	CYP39A1
16	SLURP1	34	HOXD11
17	LRP12	35	PITX2
18	WFDC21P	36	ZIC2

**Supplementary Table 5 KEGG pathway analysis for 9 feature genes**

ID	Pathway	Q-value	geneID
hsa00260	Glycine, serine and threonine metabolism	0.043934637558643	BPGM
hsa00010	Glycolysis / Gluconeogenesis	0.043934637558643	BPGM
hsa04721	Synaptic vesicle cycle	0.043934637558643	SLC1A3
hsa04350	TGF-beta signaling pathway	0.043934637558643	PITX2