

Supplementary Table S9: Unique Gene Ontologies enriched in Mild / Moderate Severity group.

Unique Gene Ontologies identified from comparison between control and Mild / Moderate genes (n = 228 genes).

Control/Mild	PValue	Genes
regulation_of_microtubule_polymerization_or_depolymerization	0.004674856	STMN1, SKA1, SKA2
negative_regulation_of_immune_response	0.002675584	COL3A1, L2RA, FDXP3
negative_regulation_of_inflammatory_response	0.003802817	IL2RA, ACOD1, FDXP3, PPARD
chromosome_segregation	0.06735181	NEK2, BUB1, SKA1, SKA2
cellular_response_to_interferon_beta	0.048967231	ACOD1, FIT1, GMI2185
digestive_tract_development	0.07193068	COL3A1, CCNB1, KIT
cellular_response_to_hypoxia	0.094551368	CCNB1, BNIP3, SLC29A1, PPARD
response_to_mechanical_stimulus	0.141879727	COL3A1, JUN, CCNB1
positive_regulation_of_fibroblast_proliferation	0.14921515	JUN, CCNB1, SPH1
negative_regulation_of_NF-kappaB_transcription_factor_activity	0.152781901	PRMT2, ACOD1, FDXP3
cellular_response_to_organic_cyclic_compound	0.186354871	CCNB1, PAK3, KIF5
cell-matrix_adhesion	0.197770231	COL3A1, ITGA1, EPR3
embryo_development	0.201594568	CCK2, BUB1, EPOR
positive_regulation_of_cell_growth	0.244102541	EXOSC4, SPH1, TA99B
hematopoietic_progenitor_cell_differentiation	0.27525283	RPL1, GPR144, APOB30PDBR1
positive_regulation_of_MAPK_cascade	0.298596927	PEL1, KIT, NENF
response_to_hypoxia	0.327175049	PAK1, PRMT2, BNIP3, SOD4
positive_regulation_of_cell_migration	0.35402183	PAK1, MINK1, SPH1, KIT
cytokine-mediated_signaling_pathway	0.454888918	CISH, RTNARL1, KIT
cilium_morphogenesis	0.535033048	ARL3, FUZ, CELSR3
RNA_splicing	0.72296497	LSM10, CIOBP, NITEK4

Supplementary Table S9: Unique Gene Ontologies enriched in Severe group.

Unique Gene Ontologies identified from comparison between control and Severe genes (n = 383 genes).

Control/Severe	PValue	Genes
adipose_tissue_development	0.070333091	LRPS, SPG20, PPARD
positive_regulation_of_fat_cell_differentiation	0.13044735	KLF3, ZBTB16, LRPS
learning_or_memory	0.19161396	BHLHE40, POU5F1, EBI
embryonic_dig_t_morphogenesis	0.20745744	ZBTB16, LRPS, FUZ
protein_homotetramerization	0.245479557	CHC1, SHMT1, ACAD5
mitochondrion_organization	0.27879455	CAIY, CHC1D10, MAPK13
endocytosis	0.41151207	MRC1, LRPS, LDUK, RIN2
anterior/posterior_pattern_specification	0.429291256	ZBTB16, LRPS, FUZ
defense_response	0.43988847	NG2, ACOD1, CAMP
positive_regulation_of_angiogenesis	0.461356273	ANKK3, SPH1, CAMP
peptidyl-serine_phosphorylation	0.510966169	RPS6KA2, STK39, MAPK13
regulation_of_cell_shape	0.544628943	EPSC, CDC42EP2, RHOU
positive_regulation_of_ERK1_and_ERK2_cascade	0.6977464	JUN, EPOR, HAVCR2

Supplementary Table S9: Unique Gene Ontologies enriched in Severe-specific group.

Unique Gene Ontologies identified from comparison between Mild / Moderate and Severe genes (n = 352 genes).

Mild/Severe	PValue	Genes
covalent_chromatin_modification	0.023964686	CBX8, TSPY12, HIRA, PRDM9, HDAC10, SS18L1, DPY30, DNAAF1, HDAC6
RNA_processing	0.025183059	DUS2, TSEN1, ZBTB80, LAGE1, GTPBP3
intracellular_protein_transport	0.02958175	ACD, GNK3, NPH3AL, COG7, RUNC1, EVI1, SEC24C, HDAC6
cellular_amo_acid_biosynthetic_process	0.04191359	PSAT1, ASL, ENDPH1
negative_regulation_of_peptidase_activity	0.04721579	ITIH6, SERPINC1, NGP, SPINT2, STFA2
microtubule_cytoskeleton_organization	0.130632253	UXT, MAP1S, MARK4, TTL
cellular_calcium_ion_homeostasis	0.142561883	SLC24A1, SLC37A4, NUCB2, CHERP
G1/S_transition_of_mitotic_cell_cycle	0.19393284	PLK3, RCC1, RHOU
cholesterol_metabolic_process	0.323966939	PMVK, LRPS, LDUK
ubiquitin-dependent_protein_catabolic_process	0.326025928	FBXW8, USP11, FBXO4, HDAC6
protein_polyubiquitination	0.38919217	LRSAM1, FBXO4, HDAC6

Supplementary Table S9: Common Gene Ontologies in Mild / Moderate and Severe group.

Common Gene Ontologies identified from comparison between Mild / Moderate (n = 328 genes) and Severe (n = 383 genes).

Control/Mild & Control/Severe	NM_pvalue	NM_Genes	NS_pvalue	NS_Genes
methylation	0.002088567	PRMT6, METTL2, CARM1	0.33032971	PRDM9, CARM1, SMYD3, NBP2
protein_homodimerization	0.615612922	TMEM120A, KCTD11, KCTD7	0.46492144	RIPK3, TMEM120A, IGHMBP2, KCTD7
negative_regulation_of_protein_kinase_activity	0.07851251	PKB, CSH, HTNARL1, GADD3	0.34489287	PKB, CSH, GADD45G
fatty_acid_biosynthetic_process	0.02571083	HACD1, OXSM, ACSL3	0.24547956	PTGES2, OXSM, MCAT
small_GTPase_mediated_signal_transduction	0.452466087	ARHGAP31, RAB20, ARL3, R8	0.80884775	RAB20, RHOU, RND1
RNA_processing	0.044014038	EXOSC4, GPM9493, NOP2, MT	0.21993726	GPM9493, NOP2, MTERF4, RRP1
cell_differentiation	0.83333737	EOHES, HIK, STMN1, KIT, CC	0.09114339	EOHES, HIK, STMN1, PIP40, GADD45G
regulation_of_cell_proliferation	0.214444117	RNF126, TNFRSF18, KCTD11	0.55973661	RNF126, TNFRSF18, FOXM1, PIP40
regulation_of_cell_cycle	0.00523021	JUN, PSMA2, E2F5, PRK11, G	0.17417436	JUN, PSMA2, PRK11, GADD45G
phospholipid_biosynthetic_process	0.02425744	GPAM, GPT1, LCAT1, CR1	0.00092368	GPAM, LDUK, LCAT1, CR1, SFRP1, PPARD
response_to_radiation	0.089140463	COL3A1, JUN, RT	0.05636621	PLK3, COL3A1, JUN
mitotic_metaphase_plate_congression	0.00537955	CCNB1, PSRC1, RRS3, SPD1	0.07033309	PSRC1, KIF5B, RRS1
actin_cytoskeleton_organization	0.181797868	PAK1, PHLN1, CDC42EP2, H	0.11004577	FMN1, CDC42EP2, PHL3, RHOU, POU1M4

Supplementary Table S9: Common Gene Ontologies in Severe and Severe-specific Group.

Common Gene Ontologies identified from comparison between Severe (n = 383 genes) and Severe-specific (n = 352 genes).

Mild/Severe & Control/Severe	MS_pvalue	MS_Genes	NS_pvalue	NS_Genes
cholesterol_metabolic_process	0.323966939	PMVK, LRPS, LDUK	0.31673023	PMVK, LRPS, LDUK
protein_polyubiquitination	0.38919217	LRSAM1, FBXO4, HDAC6	0.38183024	LRSAM1, FBXO4, HDAC6
microtubule_cytoskeleton_organization	0.130632253	UXT, MAP1S, MARK4, TTL	0.34955235	UXT, MARK4, TTL
RNA_processing	0.025183059	DUS2, TSEN1, ZBTB80, LAGE1, GTPBP3	0.04721579	ITIH6, SERPINC1, NGP, SPINT2, STFA2
cellular_calcium_ion_homeostasis	0.142561883	SLC24A1, SLC37A4, NUCB2, CHERP	0.34807395	SLC24A1, NUCB2, CHERP
covalent_chromatin_modification	0.023964686	CBX8, TSPY12, HIRA, PRDM9	0.25773298	ING4, CBX8, HIRA, PRDM9, DPY30, HDAC6
ubiquitin-dependent_protein_catabolic_process	0.326025928	FBXW8, USP11, FBXO4, HDAC6	0.59042395	RANBP1, FBXO4, HDAC6
cellular_amo_acid_biosynthetic_process	0.04191359	PSAT1, ASL, ENDPH1	0.04051884	PSAT1, ASL, ENDPH1
G1/S_transition_of_mitotic_cell_cycle	0.19393284	PLK3, RCC1, RHOU	0.04538723	RANBP1, PLK3, RCC1, RHOU
intracellular_protein_transport	0.02958175	ACD, GNK3, NPH3AL, COG7	0.57439996	ACD, ARPI1, SEC24C, HDAC6
negative_regulation_of_peptidase_activity	0.04721579	ITIH6, SERPINC1, NGP, SPN	0.44417943	CSTF, NGP, STFA2

Supplementary Table S9: Common Gene Ontologies in Mild / Moderate, Severe and Severe-specific Groups.

Common Gene Ontologies identified from comparison between Mild / Moderate (n = 328 genes), Severe (n = 383 genes) and Severe-specific (n = 352 genes).

Common_all	CM_pvalue	CM_genes	CS_pvalue	CS_genes	MS_pvalue	MS_genes
cell_cycle	0.000270109	ZBTB49, ARL3, FOXM1, SKA1	0.26503138	ING4, CDT1, 1	0.55233066	TSPY12, CDT1, PLK3, CHAF1B, KLHL22, RCC1, MARK4, PDCD11, MAPK13
apoptotic_process	0.001092327	REK3, DFBP, BNIP3, TNFRSF1	0.01158806	DHPL, PLK3, 1	0.06807289	PLK3, CSMNP2, MAP1S, IAT1K, ERCC2, NAF1, EMCA, GZMB, BMP, DEDD, MFSO10
cell_division	0.00206798	CCNB1, CDC6, PRCL1, ARL3	0.52897933	CDC6, FHL2, RCL1, MARK4	0.80884775	RAB20, RHOU, RND1
metabolic_process	0.01021093	ACAD8, PAK1, GPAM, NAT2, 2	0.3741E-06	ACAD8, ARS8	0.00040206	ARS8, FAL1, CRTCL1, GTP1, PGAM1, MCAT, HX2, GALNS, ALDH3A1, BDH1, ALPL, DNA2, NEIL1, DIPDC, ACAD8, GLA, ENDPH1
positive_regulation_of_cell_proliferation	0.05060447	JUN, PAK1, KIF5, HIK, SPH1	0.047073073	CBX8, JMY, S1	0.83953278	CBX8, ALDH3A1, NTR1, LRPS, MARK4, CAMP
fatty_acid_metabolic_process	0.089140463	COL3A1, GPAM, OXSM, ACSL3	0.14125059	GPAM, PTGE2	0.66666041	PTGES2, ACAD8, MCAT
lipid_metabolic_process	0.111665352	HACD1, GPAM, OXSM, ACSL3	0.07261979	GPAM, PTGE2	0.21854857	ARV1, PLCB3, PTGES2, PMVK, PLD1, ACAD8, LDUK, MCAT, PLD2
response_to_glucocorticoid	0.18934872	GPR83, ACSL1, HMMT	0.07292124	ALDH3A1, 1	0.23638842	ALDH3A1, ANKRD1, ALPL
positive_regulation_of_gene_expression	0.24339782	PLSCR1, PLAG1, RPS6KA2, F1	0.04074694	PLSCR1, PLAG1	0.89059794	RASL1, TAD3, KIF4, LDUK
inflammatory_response	0.283095189	MAMP25, TUSC2, TNFRSF18, 1	0.07641609	MAMP25, TUS	0.66004747	RPS6KA4, LTBAR1, STAB1, TNFRSF4, HAVCR2
regulation_of_transcription,_DNA-templated	0.357634774	GMI4326, ZFP872, PLAG1, 2	0.13954373	CSNP2, PRD	0.01279333	HDH9B, CSNP2, PRDM9, HDAC10, CRTCL1, IGHMBP2, DPY30, ZBTB42, TTF2, HDAC6, E, RPT, RPS6KA4, HIRA, 1931001902ZNRK, MNT, CHAF1B, SERTAD3, ALKBH3, TAF1C, ZFP560, NRRP2, DNAAF1, DEDD, BCL9, TSPY12, CBX8, PIAS3, GMI5446, SS18L1, ZBTB16, ZFP619, AXIN2, KIF4, POU2F2, HOPX, ZFP90, MAPK13, ZFP69, MAFB, TADA3, ERCC2, FIR, PPE
immune_system_process	0.40882843	DACH1, CSK2, BUB1, PIP40	0.77659098	GMEB10, DM	0.54411361	GMEB10, FBXW8, ERCC2, AXIN2
intracellular_signal_transduction	0.409061399	SPS81, CSH1, RPS6KA2, GPR1	0.39876304	SPS81, CSH1, 1	0.70963224	RPS6KA4, PLCB3, CDC42BP2, DEFB, MAPK13
cellular_response_to_DNA_damage_stimulus	0.453463799	PRMT6, RPL1, FBXW8, CHAF1	0.17294921	PLK3, CHAF1	0.10156167	USP4M1, COG1, RPL2, VPS18, TRAM1, PK26
immune_response	0.542973999	PLSCR1, TNFRSF18, IL2RA, T1	0.2692638	PLSCR1, TNF	0.69227156	COLEC12, CTLA4, OAS1C, TNFRSF4
positive_regulation_of_protein_phosphorylation	0.577818217	PAK1, SPH1, PEL12	0.6864247	SPH1, PEL12	0.69543911	GRK3, AXIN2, CAMP
transcription	0.59230623	RAB20, NTR1, ARL3, FUZ, PRD	0.80804691	LRSAM1, RAE	0.800717	USP4M1, COG1, RPL2, VPS18, TRAM1, PK26
innate_immune_response	0.608824163	CLEC4N, CIOBP, OAS1A, ACE	0.58578601	CLEC4N, ACE	0.8961255	CFH, ECSIT, CAMP, HAVCR2
response_to_lipopolysaccharide	0.615612922	JUN, TNFRSF18, ACOD1	0.24713697	JUN, TNFRSF	0.73070878	ACE, ALPL, TNFRSF4
regulation_of_apoptotic_process	0.61113918	TNFRSF18, BCL2, FBXO10	0.47448208	TNFRSF18, B	0.75811748	LRPS, TNFRSF4, DEDD
cell_surface_receptor_signaling_pathway	0.672820963	ADGRG3, GPR83, CELSR3	0.54084031	ADGRG3, AD	0.87250554	UPK18, ADGRG1, TSPAN3
multicellular_organism_development	0.760001005	EOHES, HAD31, DACH1, TNF	0.77466239	EOHES, DACH1	0.99944825	OLFML3, FNTR, LRPS, TNFRSF4, HOPX

negative_regulation_of_gene_expression	0.770148354	CCNB1, PLAG1, FOXP3	0.85690979	PLAG1, LDLR	0.67526697	ACE, KLFA, LDLR, HAVERK2
translocation	0.786236574	CAMPE1, MTF3, MRP14L, N	0.58880701	GAB2J2, GW	0.15549519	GAB2J2, NHP2, IGHMBP2, MRP13B, RPS27L, MNP15B, MRP13G, GRS1, MTRF1L
oxidation-reduction_process	0.842754884	ACAD8, SQLE, TMLHE, PFRD	0.86948056	ACAD8, ALDH	0.17526991	DNNA1D, RETSAT, NDUF2C, HMGD1A, DHODH, DUS2, ALDH3A1, AKR7A5, ALKBH4, BDN1, PIR, D2HGDH, ACADS
protein_ubiquitination	0.896565614	CISH, PELI2, KCTD11	0.8888054	FBOX40, CSH	0.62866597	FBOX40, FBXW8, FBXD4, KLHL22, FBXL22
proteolysis	0.946592806	MMP25, AGA, LAP3, OTUD3	0.98118488	MMP25, GCF	0.94828028	ACE, GEA, USP11, CTNMB, PRR52J
signal_transduction	0.957323221	ADGRG1, ANKRD431, RGS1	0.93421335	ADGRG1, AD	0.99926983	GRK3, PLCB3, GNG17, ADGRF1, GRK4, IMPA2, ITB4R1
cell_adhesion	0.96505084	CXADR, ITGA1, CELSR3	0.95045178	PTPR8, CXAD	0.9542912	PTPR8, AMIGO3, STAB1, EMLIN1
G-protein_coupled_receptor_signaling_pathway	0.999800659	ADGRG1, OLFRA57, RGS1, GF	0.99996747	ADGRG1, AD	0.99999998	PLCB3, GNG17, ADGRF1, ITB4R1

Supplementary Table S9. Total Gene Ontologies enriched in Mild / Moderate Group.

Gene ontologies were identified by DAVID pathway analyses of n = 328 unique genes in Mild / Moderate group compared with Control group.

ControlVsMild	PValue	Genes
cell_cycle	2.70E-04	ZBTB49, ARL3, FOXM1, SKA1, SKA2, ING4, CCNB1, CDC45, PSRC1, NUF2, CKS2, NEK2, KCTD11, PIM3, SPD11, BUB1, E2F7, LIN28
apoptotic_process	0.001039237	BEX3, DFFB, BNIPI3, TNFRSF18, PDCD5, G0S2, FBXO10, GADD45G, ING4, PAK1, PLSRC1, MIEN1, C1QBP, PIM3, BUB1, PPARD
cell_division	0.002068768	CCNB1, CDC45, PSRC1, ARL3, NUF2, CKS2, NEK2, SPD11, BUB1, SKA1, SPG20, SKA2
methylation	0.002088567	PRMT6, METTL25, CARNMT1, PRMT2, SMYD5, NOP2, HNMT, TRMT61A
phospholipid_biosynthetic_process	0.003425744	GPAM, CHPT1, LCLAT1, CRLS1, PPARD
regulation_of_microtubule_polymerization_or_depolymerization	0.004675856	STMN1, SKA1, SKA2
mitotic_metaphase_plate_congression	0.005377955	CCNB1, PSRC1, RRS1, SPD11
negative_regulation_of_immune_response	0.005675584	COL3A1, IL2RA, FOXP3
negative_regulation_of_cell_proliferation	0.007552869	ING4, JUN, RPS6KA2, ZBTB49, ITGA1, PDCD5, FUZ, FOXP3, SOX4, IFIT3, E2F7
defense_response_to_virus	0.008492176	PLSCR1, EXOSC4, GPAM, BNIPI3, IFIT3B, OAS1A, IFIT3
positive_regulation_of_apoptotic_process	0.009114764	ING4, PLSRC1, JUN, PRMT2, RPS6KA2, BNIPI3, C1QBP, PDCD5, SOX4, GADD45G
DNA_replication	0.00968336	ING4, CDC45, ORC6, RFC4, MCMDC2, DTD1
metabolic_process	0.010021031	ACAD8, PAK1, GPAM, NAT2, OXSM, EOGT, ACOD1, ACSBG1, ACSL3, UMP5, LCLAT1, ACAT2
response_to_virus	0.011865461	BCL3, STMN1, OAS1A, FOXP3, IFIT3
cellular_process	0.026048354	JUN, PSRC1, PPARD
brain_development	0.026740033	EOMES, SPHK1, STMN1, CTNS, ACSL3, HNMT, EPOR
mitotic_nuclear_division	0.027390632	CCNB1, PSRC1, NUF2, NEK2, SPD11, BUB1, SKA1, SKA2
regulation_of_cell_cycle	0.030523021	JUN, PSMG2, E2F5, PRR11, GADD45G
response_to_radiation	0.039410461	COL3A1, JUN, KIT
rRNA_processing	0.044014038	EXOSC4, GM9493, NOP2, MTERF4, RRP9
heart_development	0.057830088	COL3A1, CXADR, RPS6KA2, MTERF4, EPOR, SOX4, PPARD
positive_regulation_of_cell_proliferation	0.06060447	JUN, PAK1, KLF5, HLX, SPHK1, NOP2, KIT, FOXM1, EPOR, SOX4, PPARD
negative_regulation_of_inflammatory_response	0.063805817	IL2RA, ACOD1, FOXP3, PPARD
chromosome_segregation	0.06735181	NEK2, BUB1, SKA1, SKA2
cellular_response_to_interferon-beta	0.068967231	ACOD1, IFIT3, GM12185
digestive_tract_development	0.071930368	COL3A1, CCNB1, KIT
negative_regulation_of_apoptotic_process	0.076024403	JUN, MIEN1, BNIPI3, TNFRSF18, SPHK1, BCL3, PIM3, PSMG2, TAF9B, IFIT3, PPARD
negative_regulation_of_protein_kinase_activity	0.078512511	PKIB, CISH, RTN4RL1, GADD45G
fatty_acid_metabolic_process	0.08239829	HACD1, GPAM, OXSM, ACSBG1, ACSL3
positive_regulation_of_transcription_DNA-templated	0.083114547	EOMES, JUN, KLF5, PSRC1, PRMT2, BCL3, CKS2, FOXM1, FOXP3, SOX4, PPARD
cellular_response_to_hypoxia	0.094551368	CCNB1, BNIPI3, SLC29A1, PPARD
actin_cytoskeleton_reorganization	0.103610151	PAK1, CXADR, KIT
lipid_metabolic_process	0.111665352	HACD1, GPAM, OXSM, ACSBG1, CHPT1, ACSL3, LCLAT1, CRLS1, PPARD
protein_autophosphorylation	0.126814458	PAK1, KIT, STK39, NEK2, PIM3
response_to_mechanical_stimulus	0.141879272	COL3A1, JUN, CCNB1
positive_regulation_of_fibroblast_proliferation	0.149129155	JUN, CCNB1, SPHK1
negative_regulation_of_NF-kappaB_transcription_factor_activity	0.152781901	PRMT2, ACOD1, FOXP3
fatty_acid_biosynthetic_process	0.182571082	HACD1, OXSM, ACSL3
cellular_response_to_organic_cyclic_compound	0.186354871	CCNB1, PAK1, KLF5
response_to_glucocorticoid	0.186354871	GPR83, ACSBG1, HNMT
actin_cytoskeleton_organization	0.187978658	PAK1, FMNL2, CD42EP2, FHL3
cell-matrix_adhesion	0.197770231	COL3A1, ITGA1, EPDR1
embryo_development	0.201594568	CKS2, BUB1, EPOR
regulation_of_cell_proliferation	0.214444117	RNF126, TNFRSF18, KCTD11, FOXM1, PPARD
negative_regulation_of_transcription_from_RNA_polymerase_II_promoter	0.238027278	PRMT6, EOMES, JUN, KLF5, DACH1, C1QBP, FOXM1, TAF9B, FOXP3, E2F7, PPARD
positive_regulation_of_gene_expression	0.243397082	PLSCR1, PLAG1, RPS6KA2, PDCD5, KIT, FOXP3, PPARD
positive_regulation_of_cell_growth	0.244102541	EXOSC4, SPHK1, TAF9B
wound_healing	0.259674433	COL3A1, PAK1, PPARD
liver_development	0.263570388	JUN, HLX, FOXM1
negative_regulation_of_transcription_DNA-templated	0.264837728	PRMT6, ING4, JUN, DACH1, PRMT2, BASP1, BCL3, FOXM1, FOXP3
hematopoietic_progenitor_cell_differentiation	0.275258283	RRS1, GPATCH4, 4930430F08RIK
inflammatory_response	0.293095189	MMP25, TUSC2, TNFRSF18, SPHK1, KIT, ACOD1
positive_regulation_of_MAPK_cascade	0.298596927	PEL12, KIT, NENF
response_to_hypoxia	0.327175049	PAK1, PRMT2, BNIPI3, SOX4
positive_regulation_of_transcription_from_RNA_polymerase_II_promoter	0.353729997	EOMES, JUN, PLAG1, ZBTB49, FOXM1, FOXP3, PLSRC1, KLF5, JPX, BCL3, TAF9B, SOX4, E2F7
regulation_of_transcription_DNA-templated	0.357634774	GM14326, ZFP825, PLAG1, ZBTB49, ZBTB48, ZFP948, FOXM1, IKZF5, DACH1, HLX, C1QBP, TAF9B, E2F5, SOX4, E2F7, PRMT6, EOMES, JUN, ZFP994, MTERF4, FOXP3, KLF5, ZFP40, BCL3, TFEC, ZFP27, PPARD
positive_regulation_of_cell_migration	0.359402181	PAK1, MIEN1, SPHK1, KIT
immune_system_process	0.375487094	EOMES, CLEC4N, C1QBP, IL2RA, ACOD1, IFIT3
cellular_response_to_lipopolysaccharide	0.376732744	PLSCR1, MRC1, ACOD1, PPARD
protein_phosphorylation	0.402257556	CCNB1, PAK1, RPS6KA2, KIT, STK39, NEK2, PIM3, BUB1
cell_proliferation	0.408828343	DACH1, CKS2, BUB1, PPARD
intracellular_signal_transduction	0.409061339	SPSB1, CISH, RPS6KA2, GPR182, KIT, STK39
transcription_DNA-templated	0.422558508	PRMT6, EOMES, JUN, PLAG1, ZBTB49, ZBTB48, FOXM1, FOXP3, IKZF5, KLF5, DACH1, HLX, C1QBP, TFEC, BCL3, ZFP27, TAF9B, E2F5, SOX4, E2F7, PPARD, LIN28
positive_regulation_of_neuron_projection_development	0.426707343	RANBP1, SPHK1, EPOR
adaptive_immune_response	0.430307702	EOMES, CLEC4N, C1QBP
cellular_response_to_DNA_damage_stimulus	0.452403799	PRMT6, BCL3, FBXO6, FOXM1, AP5S1, E2F7
small_GTPase_mediated_signal_transduction	0.452646087	ARHGAP31, RAB20, ARL3, RND1
cytokine-mediated_signaling_pathway	0.454888918	CISH, RTN4RL1, KIT
phosphorylation	0.464041547	PAK1, RPS6KA2, SPHK1, KIT, STK39, NEK2, PIM3, BUB1
negative_regulation_of_neuron_apoptotic_process	0.502623886	JUN, BHLHB9, EPOR
cilium_morphogenesis	0.535033048	ARL3, FUZ, CELSR3
immune_response	0.542973399	PLSCR1, TNFRSF18, IL2RA, TNFSF13B
positive_regulation_of_protein_phosphorylation	0.577818217	PAK1, SPHK1, PELI2
protein_transport	0.593190633	RAB20, NXT1, ARL3, FUZ, PEX12, AP5S1, GPM6B
innate_immune_response	0.608824163	CLEC4N, C1QBP, OAS1A, ACOD1, IFIT3
response_to_lipopolysaccharide	0.615612922	JUN, TNFRSF18, ACOD1
protein_homoooligomerization	0.615612922	TMEM120A, KCTD11, KCTD7
regulation_of_apoptotic_process	0.621113918	TNFRSF18, BCL3, FBXO10
DNA_repair	0.652572006	PRMT6, FBXO6, FOXM1, AP5S1
cell_surface_receptor_signaling_pathway	0.672820961	ADGRG3, GPR83, CELSR3
RNA_splicing	0.72296497	LSM10, C1QBP, MTERF4
multicellular_organism_development	0.760001005	EOMES, HACD1, DACH1, TNFRSF18, STMN1, KCTD11, FUZ, LCLAT1, CELSR3, GADD45G
negative_regulation_of_gene_expression	0.770148354	CCNB1, PLAG1, FOXP3
regulation_of_transcription_from_RNA_polymerase_II_promoter	0.790727688	EOMES, KLF5, CKS2, FOXP3
translation	0.796326874	GM9493, MTIF3, MRP143, WARS2

Supplementary Table S9. Total Gene Ontologies enriched in Severe Group.

Gene ontologies were identified by DAVID pathway analyses of n = 383 unique genes in Severe group compared with Control group.

ControlVsSevere	PValue	Genes
metabolic_process	2.37E-06	ACAD8, ARSA, FAHD1, CRTCL1, OXSM, PGAM1, ACOD1, MCAT, LCLAT1, ACAT2, GALNS, ALDH3A1, GPAM, EOGT, ALPL, NEIL1, UMPS, DIP2C, ACADS, GLA, ENOPH1
phospholipid_biosynthetic_process	0.006923676	GPAM, PLD1, LCLAT1, CRLS1, PPARD
apoptotic_process	0.01538806	DFFB, PLK3, CSRN2, TNFRSF18, PDCD5, NAIF1, G0S2, GZMB, MFS10, GADD45G, ING4, PLSR1, EMC4, BMF, PPARD
DNA_replication	0.021237432	ING4, CDT1, CHAF1B, CDC45, MCMDC2, DTD1
cellular_process	0.037588764	JUN, PSRC1, PPARD
regulation_of_reactive_oxygen_species_metabolic_process	0.040518842	RIPK3, TUSC2, FOXM1
cellular_amino_acid_biosynthetic_process	0.040518842	PSAT1, ASL, ENOPH1
neuromuscular_process	0.043532113	POMK, IGHMBP2, SPG20
G1/S_transition_of_mitotic_cell_cycle	0.045367227	RANBP1, PLK3, RCC1, RHOU
positive_regulation_of_cell_proliferation	0.047508729	CBX8, JUN, SPHK1, NOP2, LRP5, FOXM1, EPOR, ALDH3A1, KLF5, HLX, MARK4, CAMP, PPARD
positive_regulation_of_telomerase_activity	0.049797998	PKIB, ACD, WRAP53
heart_development	0.051664945	NEK8, COL3A1, CXADR, RPS6KA2, MTERF4, EPOR, HOPX, PPARD
cellular_response_to_lipoplysaccharide	0.053025125	PLSCR1, TNIP3, MRC1, ACOD1, CAMP, PPARD, HAVCR2
response_to_radiation	0.056366214	PLK3, COL3A1, JUN
positive_regulation_of_telomere_maintenance_via_telomerase	0.063217432	PKIB, ACD, WRAP53
positive_regulation_of_apoptotic_process	0.06784274	ING4, PLSR1, JUN, RPS6KA2, ZBTB16, PDCD5, CTAA4, BMF, GADD45G
mitotic_metaphase_plate_congression	0.070333091	PSRC1, KIFC5B, RRS1
adipose_tissue_development	0.070333091	LRP5, SPG20, PPARD
response_to_glucocorticoid	0.071921398	ALDH3A1, ANXA3, ALPL, GPR83
lipid_metabolic_process	0.072619793	GPAM, PTGES2, OXSM, PMVK, PLD1, ACADS, LCLAT1, LDLR, MCAT, CRLS1, PPARD
inflammatory_response	0.07641609	MMP25, TUSC2, TNFRSF18, SPHK1, LTB4R1, STAB1, ACOD1, TNFRSF4, HAVCR2
phosphorylation	0.096393027	NEK8, PLK3, RIPK3, SPHK1, CDC42BPG, STK39, MAPK13, NAGK, GRK4, RPS6KA2, PMVK, POMK, MARK4
protein_tetramerization	0.097069794	SHMT1, ASL, SBF2
actin_cytoskeleton_organization	0.11024577	FMNL2, CDC42EP2, FHL3, RHOU, PDLIM4
positive_regulation_of_transcription_DNA-templated	0.122978897	EOMES, SERTAD3, JUN, KLF5, PSRC1, PTGES2, ZBTB16, BCL3, TADA3, LRP5, FOXM1, PPARD
liver_development	0.12306059	JUN, HLX, ASL, FOXM1
positive_regulation_of_fat_cell_differentiation	0.13044735	KLF5, ZBTB16, LRP5
learning_or_memory	0.139161396	BHLHB9, POMK, DBI
fatty_acid_metabolic_process	0.1412509	GPAM, PTGES2, OXSM, ACADS, MCAT
actin_cytoskeleton_reorganization	0.143565029	EPS8, CXADR, CDC42BPG
brain_development	0.145415798	EOMES, SPHK1, STMN1, POMK, CTNS, EPOR
cellular_response_to_DNA_damage_stimulus	0.17329092	PLK3, CHAF1B, BCL3, EXOS, CTAA4, FBXO6, NEIL1, FOXM1, AP5S1
regulation_of_cell_cycle	0.174174359	JUN, PSMG2, PRR11, GADD45G
embryonic_digit_morphogenesis	0.207645744	ZBTB16, LRP5, FUZ
negative_regulation_of_cell_growth	0.216586548	SERTAD3, PSRC1, NAIF1, PPARD
rRNA_processing	0.219937657	GM9493, NOP2, MTERF4, RRP9
negative_regulation_of_cell_proliferation	0.224585613	ING4, JUN, RPS6KA2, ZBTB49, ZBTB16, PDCD5, FUZ, CHERP
negative_regulation_of_transcription_from_RNA_polymerase_II_promoter	0.229900591	CBX8, EOMES, PLK3, JUN, ZBTB16, IGHMBP2, ZBTB42, FOXM1, HOPX, UXT, KLF5, DACH1, PPARD
defense_response_to_bacterium	0.230926304	ANXA3, BCL3, STAB1, MUC5B, CAMP
transcription_DNA-templated	0.232573012	CSRN2, PRDM9, PLAG1, CRTCL1, ZBTB49, IGHMBP2, DPY30, ZBTB42, FOXM1, HDAC6, UXT, HIRA, CHAF1B, SERTAD3, DACH1, HLX, POLR2J, CBX8, EOMES, JUN, HOPX, MAPK13, KLF5, MAFB, BCL3, TADA3, TFEC, ZFP27, PPARD
protein_homotetramerization	0.245479557	CRTCL1, SHMT1, ACADS
fatty_acid_biosynthetic_process	0.245479557	PTGES2, OXSM, MCAT
response_to_lipoplysaccharide	0.247136969	JUN, TNFRSF18, ACOD1, ALPL, TNFRSF4
covalent_chromatin_modification	0.257732979	ING4, CBX8, HIRA, PRDM9, DPY30, HDAC6
adaptive_immune_response	0.264327305	EOMES, CLEC4N, CTAA4, HAVCR2
cell_cycle	0.265031384	ING4, CDT1, PLK3, CHAF1B, CDC45, PSRC1, ZBTB49, RCC1, MARK4, FOXM1, MAPK13
immune_response	0.269263804	PLSCR1, TNFRSF18, CTAA4, OAS1C, TNFRSF4, TNFSF13B
mitochondrion_organization	0.278792455	CXADR, CHCHD10, MAPK13
response_to_virus	0.293053854	BCL3, STMN1, OAS1A
tRNA_processing	0.297800171	TSEN34, LAGE3, GTPBP3
cholesterol_metabolic_process	0.316730229	PMVK, LRP5, LDLR
protein_phosphorylation	0.319177215	NEK8, PLK3, RIPK3, GRK4, RPS6KA2, CDC42BPG, STK39, POMK, MARK4, MAPK13
regulation_of_transcription_DNA-templated	0.319543727	CSRN2, PRDM9, PLAG1, CRTCL1, ZBTB49, IGHMBP2, DPY30, ZBTB42, FOXM1, HDAC6, UXT, HIRA, CHAF1B, SERTAD3, DACH1, HLX, ZFP560, CBX8, EOMES, JUN, ZBTB16, MTERF4, ZFP619, HOPX, MAPK13, ZFP69, KLF5, MAFB, BCL3, TADA3, TFEC, ZFP27, PPARD
defense_response_to_Gram-positive_bacterium	0.3355424	PLD1, CAMP, HAVCR2
negative_regulation_of_protein_kinase_activity	0.344892868	PKIB, CISH, GADD45G
microtubule_cytoskeleton_organization	0.349552351	UXT, MARK4, TTL
defense_response_to_virus	0.362350864	PLSCR1, GPAM, OAS1A, OAS1C
cellular_calcium_ion_homeostasis	0.368073914	SLC24A1, NUCB2, CHERP
methylation	0.369297096	PRDM9, CARNMT1, SMYD5, NOP2
protein_polyubiquitination	0.381830236	LRSAM1, FBXO4, HDAC6
aging	0.383270539	ALDH3A1, COL3A1, JUN, FBXO4
DNA_repair	0.387818211	CHAF1B, EXOS, FBXO6, NEIL1, FOXM1, AP5S1
intracellular_signal_transduction	0.398763044	SPS81, CISH, RPS6KA2, CDC42BPG, GPR182, STK39, MAPK13
skeletal_system_development	0.399971014	ACD, COL3A1, ZBTB16
positive_regulation_of_gene_expression	0.404766943	PLSCR1, PLAG1, RPS6KA2, TADA3, PDCD5, LDLR, PPARD
endocytosis	0.411511207	MRC1, LRP5, LDLR, RIN2
anterior/posterior_pattern_specification	0.422291256	ZBTB16, LRP5, FUZ
defense_response	0.439838047	NGP, ACOD1, CAMP
negative_regulation_of_peptidase_activity	0.444179427	CSTB, NGP, STFA2
positive_regulation_of_angiogenesis	0.461356273	ANXA3, SPHK1, CAMP
protein_homoooligomerization	0.464921439	RIPK3, TMEM120A, IGHMBP2, KCTD7
regulation_of_apoptotic_process	0.471482083	TNFRSF18, BCL3, LRP5, TNFRSF4
peptidyl-serine_phosphorylation	0.510966169	RPS6KA2, STK39, MAPK13
positive_regulation_of_transcription_from_RNA_polymerase_II_promoter	0.513940621	EOMES, CSRN2, JUN, PRDM9, PLAG1, CRTCL1, ZBTB49, LRP5, FOXM1, PLSR1, KLF5, JPK, MAFB, BCL3
cell_division	0.528979235	CDC45, PSRC1, KIFC5B, RCC1, MARK4, SPG20
positive_regulation_of_neuron_projection_development	0.530739709	RANBP1, SPHK1, EPOR
regulation_of_cell_shape	0.534628941	EPS8, CDC42EP2, RHOU

cell_surface_receptor_signaling_pathway	0.540840308 ADGRG3, ADGRF1, GPR83, CELSR3
immune_system_process	0.54612887 EOMES, CLEC4N, CTLA4, ACOD1, ECSIT, HAVCR2
regulation_of_cell_proliferation	0.559736606 RNF126, TNFRSF18, FOXM1, PPARD
intracellular_protein_transport	0.574399964 ACD, ARFIP1, SEC24D, HDAC6
regulation_of_transcription_from_RNA_polymerase_II_promoter	0.579084886 EOMES, KLF5, MAFB, TADA3, IGHMBP2, ECSIT
innate_immune_response	0.585786013 CLEC4N, OAS1A, ACOD1, ECSIT, CAMP, HAVCR2
translation	0.588007006 GMR210, GM9493, IGHMBP2, MRPL39, MTIF3, WARS2
ubiquitin-dependent_protein_catabolic_process	0.590423947 RANBP1, FBXO4, HDAC6
negative_regulation_of_neuron_apoptotic_process	0.611132364 JUN, BHLHB9, EPOR
negative_regulation_of_transcription,_DNA-templated	0.616546879 ING4, JUN, DACH1, BASP1, ZBTB16, BCL3, FOXM1, TNFRSF4
protein_ubiquitination	0.685880539 FBXO40, CISH, PELI2, FBXO4, FBXL22
positive_regulation_of_protein_phosphorylation	0.686424777 SPHK1, PELI2, CAMP
mitotic_nuclear_division	0.693002835 PSRC1, TADA3, RCC1, MARK4
positive_regulation_of_ERK1_and_ERK2_cascade	0.6977464 JUN, EPOR, HAVCR2
negative_regulation_of_apoptotic_process	0.737463569 PLK3, JUN, TNFRSF18, SPHK1, BCL3, PSMG2, PPARD
multicellular_organism_development	0.774662388 EOMES, DACH1, OLFML3, TNFRSF18, STMN1, LRP5, FUZ, LCLAT1, TNFRSF4, HOPX, CELSR3, GADD45G
cell_proliferation	0.776590976 GMR210, DACH1, PPARD
small_GTPase_mediated_signal_transduction	0.808847745 RAB20, RHOU, RND1
negative_regulation_of_gene_expression	0.856909789 PLAG1, LDLR, HAVCR2
oxidation-reduction_process	0.869480562 ACAD8, ALDH3A1, AKR7A5, TMLHE, RETSAT, NDUFC2, ACADS
protein_transport	0.880486911 LRSAM1, RAB20, FUZ, PEX12, AP551, PEX26
response_to_drug	0.933877148 ALDH3A1, JUN, ABCB1B
signal_transduction	0.934253352 ADGRG3, ADGRF1, GRK4, IMPA2, RGS1, GPR182, LTBR1, GPR83, TAS2R135, RIN2, EPOR, CELSR3
transmembrane_transport	0.949498893 SCN4A, ABCB1B, MFSD10
cell_adhesion	0.95045278 PTPRS, CXADR, STAB1, CELSR3
transport	0.963954675 LRSAM1, NDUFC2, CTNS, DBI, FUZ, PEX12, ABCA13, MFSD10, PEX26, CACNB1, RAB20, CPTP, SCN4A, SLC29A1, LDLR, ABCB1B, AP551
proteolysis	0.98114848 MMP25, GCA, GZMB, OTUD3
cell_differentiation	0.99114339 EOMES, HLX, STMN1, PPARD, GADD45G
G-protein_coupled_receptor_signaling_pathway	0.999967465 ADGRG3, ADGRF1, RGS1, GPR182, LTBR1, GPR83, TAS2R135, CELSR3

Supplementary Table S9. Total Gene Ontologies enriched in Severe-specific Group.

Gene ontologies were identified by DAVID pathway analyses of n = 352 unique genes in Severe group compared with Mild / Moderate group.

GO Term	P-Value	Genes
Mild/Severe		
metabolic_process	4.02E-04	ARSA, FAHD1, CRTCL, GSTP1, PGAM1, MCAT, HK2, GALNS, ALDH3A1, BDH1, ALPL, DNA2, NEILL, DIP2C, ACADS, GLA, ENOPH1
tol-like_receptor_3_signaling_pathway	0.00574487	COLEC12, CD86, HAVCR2
protein_import_into_peroxisome_matrix	0.00712405	PEX16, PEX10, PEX26
regulation_of_transcription_DNA-templated	0.01273933	INO80B, CSRN2P, PRDM9, HDAC10, CRTCL, IGHMBP2, DYP30, ZBTB42, TTF2, HDAC6, UXT, RPS6KA4, HIRA, 91300190Z2RIK, MNT, CHAF1B, SERTAD3, ALKBH4, TAF1C, ZFP560, NRBF2, DMAP1, DEDD, BCL9L, TSPYL2, CBX8, PIAS3, GM15446, SS18L1, ZBTB16, ZFP619, AXIN2, KLF4, POU2F2, HOPX, ZFP90, MAPK13, ZFP69, MAFB, TADA3, ERCC2, PIR, PPIE
phosphorylation	0.0147479	NEK8, PLK3, RPK3, CDC42BP5, PASK, HK2, MAPK13, RPS6KA4, GRK3, NAGK, GRK4, FASTK, PMVK, POMK, CDC8A, MARK4
transcription_DNA-templated	0.02059491	INO80B, CSRN2P, PRDM9, HDAC10, CRTCL, IGHMBP2, DYP30, ZBTB42, TTF2, HDAC6, UXT, HIRA, MNT, CHAF1B, SERTAD3, ALKBH4, TAF1C, NRBF2, DMAP1, POLR2J, DEDD, BCL9L, TSPYL2, CBX8, PIAS3, SS18L1, KLF4, POU2F2, HOPX, ZFP90, MAPK13, MAFB, TADA3, ERCC2, PIR, ZSCAN25
covalent_chromatin_modification	0.02396460	CBX8, TSPYL2, HIRA, PRDM9, HDAC10, SS18L1, DYP30, DMAP1, HDAC6
tRNA_processing	0.02518366	DUS2, TSEN34, ZBTB80S, LAGE3, GTPBP3
intracellular_protein_transport	0.03295818	ACD, GRK3, RPH3AL, COG7, RUNC1D, EVISL, SEC24D, HDAC6
cellular_amino_acid_biosynthetic_process	0.04179136	PSAT1, ASL, ENOPH1
positive_regulation_of_telomerase_activity	0.05134023	ACD, KLF4, WRAP53
histone_deacetylation	0.05468067	HDAC10, HDAC6, HOPX
DNA_repair	0.0577022	INO80B, CHAF1B, ERCC2, RPS27L, EXOS, DNA2, DMAP1, NEIL1, FAAP100
negative_regulation_of_peptidase_activity	0.06721558	ITH5, SERPINB10, NGP, SPINT2, STFA2
bone_mineralization	0.07620147	ERCC2, AXIN2, GLA
mitochondrial_translation	0.08001253	MRPS25, MRPS18A, QRSL1
telomere_maintenance	0.08780568	ACD, FBXO4, DNA2
cellular_response_to_DNA_damage_stimulus	0.10158417	INO80B, PLK3, CHAF1B, ERCC2, RPS27L, EXOS, CTLA4, DNA2, NEIL1, FAAP100
canonical_Wnt_signaling_pathway	0.11067925	BCL9, LRPS, KLF4, BCL9L
somatic_stem_cell_population_maintenance	0.12097643	BCL9, LRPS, BCL9L
histone_H3_acetylation	0.1253152	TAF6L, TADA3, MBIP
lung_alveolus_development	0.12963078	ERH1F1, ACE, HOPX
microtubule_cytoskeleton_organization	0.13053225	UXT, MAP1S, MARK4, TTL
protein_phosphorylation	0.13424432	RPS6KA4, NEK8, PLK3, GRK3, RPK3, GRK4, FASTK, CDC42BP5, POMK, MARK4, PASK, MAPK13
cellular_calcium_ion_homeostasis	0.14256188	SLC24A1, SLC37A4, NUCB2, CHERP
translation	0.15549519	GM8210, NHP2, IGHMBP2, MRPL39, RPS27L, MRPS18A, MRPL36, QRSL1, MTRF11
organ_regeneration	0.16582538	ACE, ANXA3, GSTP1
cellular_response_to_hydrogen_peroxide	0.17040555	CBX8, KLF4, HDAC6
oxidation-reduction_process	0.17526092	OXNAD1, RETSAT, NDUFC2, HIGD1A, DHODH, DUS2, ALDH3A1, AKR7A5, ALKBH4, BDH1, PIR, D2HGDH, ACADS
G1/S_transition_of_mitotic_cell_cycle	0.19393284	PLK3, RCC1, RHOU
cholesterol_homeostasis	0.19867761	LRPS, SLC37A4, LDLR
apoptotic_process	0.20807038	PLK3, CSRN2P, MAP1S, FASTK, ERCC2, NAI1, EMC4, GZMB, BMF, DEDD, MFSD10
negative_regulation_of_ERK1_and_ERK2_cascade	0.21299709	ERRH1, GSTP1, KLF4
positive_regulation_of_transcription_DNA-templated	0.2214475	SERTAD3, PTGES2, SS18L1, ZBTB16, TADA3, FNTB, ERCC2, LRPS, KLF4, POU2F2, ZFP90
regulation_of_protein_stability	0.23221737	TADA3, QRSL1, HDAC6
response_to_nutrient	0.24670748	ALDH3A1, ARSA, SLC37A4
lipid_metabolic_process	0.25188457	ARV1, PLCB3, PTGES2, PMVK, PLD1, ACADS, LDLR, MCAT, PLBD2
response_to_glucocorticoid	0.25638642	ALDH3A1, ANXA3, ALPL
response_to_organic_cyclic_compound	0.28058811	ALDH3A1, FNTB, SLC37A4
autophagy	0.28326278	ARSA, LRSAML, NRBF2, WDR24
cellular_response_to_lipopolysaccharide	0.29116896	CD86, TNIP3, GSTP1, CAMP, HAVCR2
steroid_metabolic_process	0.2999287	PMVK, SLC37A4, LDLR
ribosome_biogenesis	0.32396694	NHP2, MRPL36, ERALL1
cholesterol_metabolic_process	0.32966694	PMVK, LRPS, LDLR
ubiquitin-dependent_protein_catabolic_process	0.33023593	FBXW8, UBR1, FBXO4, HDAC6
transmembrane_transport	0.33952195	ABCD4, SLC12A4, SCN4A, SLC37A4, SLC8B1, ABCB1B, MFSD10
defense_response_to_Gram-positive_bacterium	0.34304728	PLD1, CAMP, HAVCR2
negative_regulation_of_transcription_from_RNA_polymerase	0.35828938	UXT, CBX8, PLK3, MNT, HDAC10, ZBTB16, IGHMBP2, ZBTB42, DMAP1, KLF4, HOPX, ZFP90
protein_polyubiquitination	0.3899211	LRSAML, FBXO4, HDAC6
aging	0.39391981	CD86, ALDH3A1, ERCC2, FBXO4
nucleosome_assembly	0.39453067	TSPYL2, TSPYL3, CHAF1B
dephosphorylation	0.41733334	PTPRB, PTPRO, ALPL
lipid_catabolic_process	0.41733334	PLCB3, PLD1, PLBD2
response_to_ethanol	0.45288985	ARSA, GSTP1, DMAP1
DNA_replication	0.47873499	CDT1, CHAF1B, DNA2
negative_regulation_of_cell_growth	0.48713394	TSPYL2, SERTAD3, NAI1
glucose_homeostasis	0.52011294	RPH3AL, SLC37A4, SLC8B1
regulation_of_ion_transmembrane_transport	0.52812307	CACNB1, CLIC3, SCNA4
transcription_from_RNA_polymerase_II_promoter	0.53996814	ERCC2, KLF4, POLR2J
sensory_perception_of_sound	0.53996814	CLIC3, TMIE, ESPN
protein_dephosphorylation	0.53996814	PTPRB, PTPRO, PTPRO
adaptive_immune_response	0.54387077	CD86, CTLA4, HAVCR2
cell_proliferation	0.54411361	GM8210, FBXW8, ERCC2, AXIN2
cell_cycle	0.55231066	TSPYL2, CDT1, PLK3, CHAF1B, KLHL22, RCC1, MARK4, PDCCD2L, MAPK13
negative_regulation_of_cell_proliferation	0.56463611	PPP2R3D, ZBTB16, FNTB, AXIN2, KLF4, CHERP
regulation_of_transcription_from_RNA_polymerase_II_pr	0.59427377	MAFB, TADA3, IGHMBP2, NRBF2, KLF4, ECSIT
fatty_acid_metabolic_process	0.60666041	PTGES2, ACADS, MCAT
positive_regulation_of_apoptotic_process	0.63953837	ACE, ZBTB16, CTLA4, BMF, DHODH
response_to_drug	0.64875116	CD86, ALDH3A1, RPH3AL, ABCB1B, DHODH
chemical_synaptic_transmission	0.65958927	CACNB1, SLC12A4, PLCB3
inflammatory_response	0.66004747	RPS6KA4, LTBR1, STAB1, TNFRSF4, HAVCR2
negative_regulation_of_gene_expression	0.67526697	ACE, KLF4, LDLR, HAVCR2
immune_response	0.69227156	COLEC12, CTLA4, CAS1C, TNFRSF4
positive_regulation_of_protein_phosphorylation	0.69543911	GRK3, AXIN2, CAMP
protein_ubiquitination	0.69866597	FBXO40, FBXW8, FBXO4, KLHL22, FBXL22
mitotic_nuclear_division	0.70400407	TADA3, KLHL22, RCC1, MARK4
defense_response_to_bacterium	0.71488016	ANXA3, STAB1, CAMP
response_to_lipopolysaccharide	0.73070878	ACE, ALPL, TNFRSF4
regulation_of_apoptotic_process	0.73581748	LRPS, TNFRSF4, DEDD
immune_system_process	0.73964125	CD86, CFH, CTLA4, ECSIT, HAVCR2
Wnt_signaling_pathway	0.76931695	BCL9, LRPS, AXIN2
intracellular_signal_transduction	0.76963124	RPS6KA4, PLCB3, CDC42BP5, DEF8, MAPK13
cell_surface_receptor_signaling_pathway	0.78250954	UPK1B, ADGRF1, TSPAN3
mRNA_processing	0.79461861	TSEN34, PPIE, TTF2, CTR1
positive_regulation_of_cell_proliferation	0.83953178	CBX8, ALDH3A1, FNTB, LRPS, MARK4, CAMP
positive_regulation_of_transcription_from_RNA_polymerase	0.8424354	RPS6KA4, BCL9, CSRN2P, MAFB, PRDM9, CRTCL, ERCC2, LRPS, KLF4, POU2F2, BCL9L
heart_development	0.85762892	NEK8, PKD1L1, HOPX
cell_division	0.86938787	KIF5B, KLHL22, RCC1, MARK4
transport	0.87714036	ABCD4, CLIC3, SLC12A4, LRSAML, COG7, SLC35C1, PKD1L1, NDUFC2, VPS37B, HIGD1A, SLC8B1, TRAM2, MFSD10, PEX26, CACNB1, RILPL2, CPTP, SCNA4, LDLR, ABCB1B
negative_regulation_of_transcription_DNA-templated	0.8777437	HDAC10, ZBTB16, DMAP1, KLF4, TNFRSF4, ZFP90
protein_transport	0.88920717	LRSAML, COG7, RILPL2, VPS37B, TRAM2, PEX26
positive_regulation_of_gene_expression	0.89595794	PIAS3, TADA3, KLF4, LDLR
innate_immune_response	0.89691255	CFH, ECSIT, CAMP, HAVCR2
proteolysis	0.94826928	ACE, GCA, USP11, GZMB, PRSS22
cell_adhesion	0.9542912	PTPRB, AMIGO3, STAB1, EMILIN1
nervous_system_development	0.95916932	AMIGO3, MAP1S, MARK4
spermatogenesis	0.9708523	ACE, PRDM9, DEDD
negative_regulation_of_apoptotic_process	0.99543161	PLK3, GSTP1, HIGD1A
signal_transduction	0.99926083	GRK3, PLCB3, GNGT2, ADGRF1, GRK4, IMPA2, LTBR1

multicellular_organism_development	0.99944825 OLFML3, FNTB, LRP5, TNFRSF4, HOPX
G-protein_coupled_receptor_signaling_pathway	0.99999998 PLCB3, GNGT2, ADGRF1, LTBR1
mitophagy_in_response_to_mitochondrial_depolarization	0.0295736 SERPINB10, CHAF1B, SLC35C1, SLC37A4, HDAC6, HK2
xenophagy	0.15173832 SERPINB10, CHAF1B, SLC35C1, SLC37A4
positive_regulation_of_defense_response_to_virus_by_host_cell	0.21358567 SERPINB10, CHAF1B, SLC35C1, SLC37A4
calcium_ion_transmembrane_transport	0.10793219 CACNB1, SLC24A1, PKD1L1, SLC8B1
calcium_ion_transport	0.55160703 CACNB1, PKD1L1, SLC8B1
ion_transport	0.88226645 CACNB1, CLIC5, SLC12A4, PKD1L1, SCN4A, SLC8B1