

	Category	Term	Count	PValue
D1-3w-up-1	KEGG	mmu04530:Tight junction	7	0.001
D1-3w-up-2	GO_MF	GO:0019904~protein domain specific binding	8	0.002
D1-3w-up-3	GO_MF	GO:0044822~poly(A) RNA binding	7	0.018
D1-3w-up-4	GO_BP	GO:0014070~response to organic cyclic compound	3	0.029
D1-3w-up-5	GO_BP	GO:0032869~cellular response to insulin stimulus	4	0.039
D1-3w-up-6	GO_MF	GO:0005543~phospholipid binding	5	0.046
D1-3w-up-7	GO_MF	GO:0005525~GTP binding	7	0.048
D1-3w-up-8	GO_BP	GO:0072659~protein localization to plasma membrane	3	0.054
D1-3w-up-9	KEGG	mmu04670:Leukocyte transendothelial migration	4	0.059
D1-3w-up-10	GO_MF	GO:0005509~calcium ion binding	9	0.061
D1-3w-up-11	GO_MF	GO:0032403~protein complex binding	6	0.076
D1-3w-up-12	GO_BP	GO:0070830~bicellular tight junction assembly	3	0.083
D1-3w-up-13	GO_MF	GO:0047485~protein N-terminus binding	3	0.085
D1-3w-up-14	GO_BP	GO:0007155~cell adhesion	8	0.090
D1-3w-up-15	KEGG	mmu04910:Insulin signaling pathway	3	0.094
D1-24w-up-1	KEGG	mmu05168:Herpes simplex infection	4	0.046
D1-24w-up-2	GO_BP	GO:0007017~microtubule-based process	3	0.086
D1-24w-up-3	GO_BP	GO:0045773~positive regulation of axon extension	3	0.086
D1-24w-up-4	GO_MF	GO:0042826~histone deacetylase binding	3	0.087
D1-3w-up-only-1	KEGG	mmu04530:Tight junction	7	0.000
D1-3w-up-only-2	GO_MF	GO:0019904~protein domain specific binding	7	0.002
D1-3w-up-only-3	GO_MF	GO:0005543~phospholipid binding	5	0.016
D1-3w-up-only-4	KEGG	mmu04670:Leukocyte transendothelial migration	4	0.026
D1-3w-up-only-5	GO_BP	GO:0072659~protein localization to plasma membrane	3	0.028
D1-3w-up-only-6	GO_BP	GO:0070830~bicellular tight junction assembly	3	0.045
D1-3w-up-only-7	GO_MF	GO:0047485~protein N-terminus binding	3	0.047
D1-3w-up-only-8	GO_MF	GO:0051015~actin filament binding	5	0.064
D1-3w-up-only-9	GO_MF	GO:0048365~Rac GTPase binding	3	0.068
D1-3w-up-only-10	GO_MF	GO:0044822~poly(A) RNA binding	5	0.074
D1-3w-up-only-11	GO_BP	GO:0015031~protein transport	5	0.077
D1-3w-up-only-12	GO_MF	GO:0042803~protein homodimerization activity	7	0.084
D1-3w-up-only-13	GO_MF	GO:0032403~protein complex binding	5	0.085
D1-3w-up-only-14	GO_BP	GO:0043434~response to peptide hormone	3	0.086
D1-3w-up-only-15	GO_BP	GO:0050821~protein stabilization	3	0.086
D1-3w-up-only-16	GO_MF	GO:0005509~calcium ion binding	7	0.092
D1-24w-up-only-1	GO_MF	GO:0044212~transcription regulatory region DNA binding	4	0.076
D1-24w-up-only-2	GO_BP	GO:0006366~transcription from RNA polymerase II promoter	3	0.082
D1-24w-up-only-3	KEGG	mmu04728:Dopaminergic synapse	3	0.100
D1-3w24w-up-both-1	GO_MF	GO:0005525~GTP binding	4	0.029
D1-3w24w-up-both-2	GO_BP	GO:0007599~hemostasis	2	0.055
D1-3w24w-up-both-3	GO_MF	GO:0042605~peptide antigen binding	2	0.076
D1-3w24w-up-both-4	GO_MF	GO:0030881~beta-2-microglobulin binding	2	0.076
D1-3w24w-up-both-5	GO_MF	GO:0046977~TAP binding	2	0.076
D1-3w24w-up-both-6	GO_BP	GO:0030335~positive regulation of cell migration	3	0.077
D1-3w24w-up-both-7	GO_BP	GO:0002474~antigen processing and presentation of peptide antigen	2	0.081
D1-3w24w-up-both-8	GO_BP	GO:0007155~cell adhesion	4	0.088
D1-3w-down-1	GO_BP	GO:0072358~cardiovascular system development	3	0.032
D1-3w-down-2	GO_MF	GO:0004252~serine-type endopeptidase activity	4	0.040
D1-3w-down-3	GO_MF	GO:0005201~extracellular matrix structural constituent	3	0.054
D1-3w-down-4	GO_BP	GO:0048010~vascular endothelial growth factor receptor signaling pathway	3	0.060
D1-3w-down-5	KEGG	mmu00510:N-Glycan biosynthesis	3	0.089
D1-3w-down-6	GO_BP	GO:0010506~regulation of autophagy	3	0.093
D1-3w-down-7	GO_BP	GO:0032836~glomerular basement membrane development	3	0.093
D1-24w-down-1	GO_MF	GO:0043565~sequence-specific DNA binding	9	0.014
D1-24w-down-2	GO_BP	GO:0072112~glomerular visceral epithelial cell differentiation	3	0.017
D1-24w-down-3	GO_BP	GO:0045893~positive regulation of transcription, DNA-templated	7	0.030
D1-24w-down-4	KEGG	mmu04024:cAMP signaling pathway	5	0.046
D1-24w-down-5	GO_BP	GO:0051260~protein homooligomerization	4	0.058
D1-24w-down-6	GO_MF	GO:0003677~DNA binding	11	0.063
D1-24w-down-7	GO_BP	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	9	0.067
D1-24w-down-8	GO_MF	GO:0008146~sulfotransferase activity	3	0.085
D1-24w-down-9	GO_BP	GO:0019933~cAMP-mediated signaling	3	0.095
D1-3w-down-only-1	GO_MF	GO:0005201~extracellular matrix structural constituent	3	0.029
D1-3w-down-only-2	GO_BP	GO:0048010~vascular endothelial growth factor receptor signaling pathway	3	0.033
D1-3w-down-only-3	GO_BP	GO:0016525~negative regulation of angiogenesis	4	0.048
D1-3w-down-only-4	KEGG	mmu04974:Protein digestion and absorption	3	0.071
D1-3w-down-only-5	KEGG	mmu04151:PI3K-Akt signaling pathway	4	0.091
D1-24w-down-only-1	GO_BP	GO:0072112~glomerular visceral epithelial cell differentiation	3	0.007
D1-24w-down-only-2	GO_BP	GO:0045893~positive regulation of transcription, DNA-templated	6	0.019
D1-24w-down-only-3	GO_BP	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	7	0.065
D1-24w-down-only-4	GO_BP	GO:0006468~protein phosphorylation	5	0.066
D1-24w-down-only-5	GO_MF	GO:0043565~sequence-specific DNA binding	6	0.076
D1-24w-down-only-6	GO_MF	GO:0005524~ATP binding	7	0.080

D1-24w-down-only-7	KEGG	mmu04024:cAMP signaling pathway	4	0.091
D1-24w-down-only-8	GO_MF	GO:0019901~protein kinase binding	4	0.094
D1-24w-down-only-9	GO_BP	GO:0060009~Sertoli cell development	2	0.099
D1-3w24w-down-both-1	GO_BP	GO:0007626~locomotory behavior	2	0.095

Genes
PRKCI, ACTN1, RAB13, MYH9, ACTN4, MPP5, MYL12A
PRKCI, NDE1, ACTN1, STXBP1, MYH9, IQGAP1, MPP5, CALM2
H2-Q6, STXBP1, FNDC3B, H2-Q4, MYH9, ACTN4, PARP12
BTG2, NCF2, EPHX1
PRKCI, STAT1, PDE3B, RAB13
PRKCI, HIP1, PSD3, MYOF, PLA2G7
TUBB2B, TUBB2A, EHD4, RAB13, IRGM2, RRAS2, UPRT
STXBP1, RAB13, EMP2
NCF2, ACTN1, ACTN4, MYL12A
EHD4, ANXA3, PROS1, ACTN1, S100A13, SVEP1, ACTN4, CALM2, MYL12A
MLKL, PROS1, RARB, ACTN4, IQGAP1, CD2AP
RAB13, ACTN4, MPP5
STXBP1, ACTN4, CALM2
TNFRSF12A, SPECC1L, MYH9, SVEP1, EMP2, EMILIN1, ATP1B2, CYR61
PRKCI, PDE3B, CALM2
RNASEL, IFNGR1, H2-Q6, ARNTL
TUBB2B, MAP1B, KIF5B
TNFRSF12A, SRF, MAP1B
SRF, ANKRD1, CRY1
PRKCI, ACTN1, RAB13, MYH9, ACTN4, MPP5, MYL12A
PRKCI, ACTN1, STXBP1, MYH9, IQGAP1, MPP5, CALM2
PRKCI, HIP1, PSD3, MYOF, PLA2G7
NCF2, ACTN1, ACTN4, MYL12A
STXBP1, RAB13, EMP2
RAB13, ACTN4, MPP5
STXBP1, ACTN4, CALM2
HIP1, ACTN1, MYH9, ACTN4, PKNOX2
DOCK4, NCF2, IQGAP1
STXBP1, FNDC3B, MYH9, ACTN4, PARP12
STXBP1, RAB13, S100A13, MYH9, ACTN4
HIP1, PRMT2, STAT1, ACTN1, S100A13, MYH9, ACTN4
MLKL, RARB, ACTN4, IQGAP1, CD2AP
BTG2, PRKCI, STAT1
HIP1, STXBP1, ATP1B2
ANXA3, ACTN1, S100A13, SVEP1, ACTN4, CALM2, MYL12A
CREB3L1, HIVEP2, ATF3, FOSL2
SRF, HIVEP2, FOSL2
CREB3L1, KIF5B, ARNTL
TUBB2B, EHD4, IRGM2, RRAS2
PROS1, F2R
H2-Q6, H2-Q4
H2-Q6, H2-Q4
H2-Q6, H2-Q4
F2R, RRAS2, CYR61
H2-Q6, H2-Q4
TNFRSF12A, SPECC1L, EMILIN1, CYR61
CRB2, NXN, SPEG
HTRA1, PLAT, PCSK6, RHBDL3
COL1A2, COL4A3, COL4A5
FOXC1, SULF1, VEGFA
MAN1A2, MGAT5, MGAT5B
MTCL1, MAPT, LMX1B
NPHS1, COL4A3, SULF1
FOXC2, ZFP423, GBX1, WT1, E2F1, SOX8, FOXL1, LMX1B, MAFA
FOXC2, WT1, PTPRO
FOXC2, ZFP423, BAMBI, WT1, E2F1, SOX8, MAFA
GLP1R, PAK1, NPR1, PDE4B, ADCY5
KCNF1, KCNG2, C1QTNF7, KCTD11
FOXC2, ZFP423, GBX1, WT1, TOP1MT, BHLHE41, E2F1, SOX8, FOXL1, LMX1B, MAFA
GLP1R, FOXC2, WT1, E2F1, SOX8, LMX1B, MAFA, ZBTB7C, DDN
HS3ST3A1, CHST1, HS3ST6
GLP1R, KSR1, ADCY5
COL1A2, COL4A3, COL4A5
FOXC1, SULF1, VEGFA
FOXC1, COL4A3, VASH1, SULF1
COL1A2, COL4A3, COL4A5
COL1A2, COL4A3, COL4A5, VEGFA
FOXC2, WT1, PTPRO
FOXC2, BAMBI, WT1, E2F1, SOX8, MAFA
GLP1R, FOXC2, WT1, E2F1, SOX8, MAFA, ZBTB7C
PAK1, KSR1, NPR1, TRIB2, MYLK3
FOXC2, GBX1, WT1, E2F1, SOX8, MAFA
PAK1, KSR1, NPR1, UBE2QL1, NOD1, TRIB2, MYLK3

GLP1R, PAK1, NPR1, PDE4B
PAK1, NPR1, E2F1, TNS2
WT1, SOX8
LMX1B, ADCY5