

	Category	Term	Count	PValue	Genes
D1 D2-both-up-1	GO_MF	GO:0019904~protein domain specific binding	7	0.026	PRKCI, NDE1, ACTN1, STXBP1, MYH9, IQGAP1, GAB2
D1 D2-both-up-2	GO_BP	GO:0007015~actin filament organization	5	0.033	PRKCI, SRF, ACTN1, NCK2, EMP2
D1 D2-both-up-3	GO_BP	GO:0043065~positive regulation of apoptotic process	8	0.034	UNC13B, MTCH1, GADD45B, PRMT2, TNFRSF12A, ANKRD1, RARB, CYR61
D1 D2-both-up-4	GO_BP	GO:0030220~platelet formation	3	0.040	SRF, ACTN1, MYH9
D1 D2-both-up-5	GO_MF	GO:0032403~protein complex binding	7	0.050	MLKL, MAP1B, NCK2, RARB, ACTN4, IQGAP1, CD2AP
D1 D2-both-up-6	KEGG	mmu04530:Tight junction	5	0.056	PRKCI, ACTN1, MYH9, ACTN4, MYL12A
D1 D2-both-up-7	GO_BP	GO:0016477~cell migration	7	0.057	PRKCI, SPECC1L, FNDC3B, NCK2, EMP2, GAB2, CD2AP
D1 D2-both-up-8	KEGG	mmu04670:Leukocyte transendothelial migration	4	0.063	NCF2, ACTN1, ACTN4, MYL12A
D1 D2-both-up-9	GO_MF	GO:0019901~protein kinase binding	6	0.070	MLKL, STXBP1, CRY1, EMP2, IQGAP1, SASH1
D1 D2-both-up-10	GO_BP	GO:0071333~cellular response to glucose stimulus	3	0.073	UNC13B, SRF, UCP2
D1 D2-both-up-11	GO_MF	GO:0005543~phospholipid binding	5	0.079	PRKCI, HIP1, PLEKHA2, MAP1B, MYOF
D1-up-only-1	KEGG	mmu04144:Endocytosis	5	0.022	PAR6B, EHD4, H2-Q6, KIF5B, PSD3
D1-up-only-2	GO_BP	GO:0098609~cell-cell adhesion	4	0.045	TMEM47, EHD4, STAT1, ELMO2
D1-up-only-3	GO_MF	GO:0005525~GTP binding	5	0.061	EHD4, RAB13, IRGM2, UPRT, RAB6B
D1-up-only-4	KEGG	mmu04261:Adrenergic signaling in cardiomyocytes	3	0.078	CREB3L1, ATP1B2, CALM2
D1-up-only-5	KEGG	mmu04728:Dopaminergic synapse	3	0.100	CREB3L1, KIF5B, CALM2
D2-up-only-1	GO_BP	GO:0002062~chondrocyte differentiation	5	0.027	MUSTN1, ARID5A, SCX, FGFR1, BMPR1A
D2-up-only-2	GO_BP	GO:0045087~innate immune response	7	0.035	C1RA, ANXA1, IFITM2, ELF4, AXL, IL34, RELB
D2-up-only-3	GO_BP	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	20	0.046	JUN, ARID5A, IL18, LIF, SCX, TCF21, ARRB1, FOS, NPAS2, RELB, MLLT6, NR4A2, GDNF, ELF4, NDN, FOSB, NFE2L1, ZFP462, FGFR1, BMPR1A
D2-up-only-4	KEGG	mmu05132:Salmonella infection	5	0.052	JUN, IL18, FOS, KLC1, RAB7B
D2-up-only-5	GO_BP	GO:0034097~response to cytokine	6	0.054	JUN, SPARC, ALDH1A2, TIMP2, FOS, RELB
D2-up-only-6	GO_BP	GO:0015031~protein transport	10	0.056	RAB3B, ARHGAP33, SEC16B, AGAP1, APBA1, ARRB1, RAB7B, STX11, VAMP2, ARF6
D2-up-only-7	GO_BP	GO:0006355~regulation of transcription, DNA-templated	28	0.064	ZBTB46, RASL11A, SETD7, SCX, TCF21, ZBTB42, ARRB1, NPAS2, RELB, FOXS1, HOXC5, NDN, LRRFIP1, HOXC8, PTRF, JUN, ARID5A, FOS, WTIP, SMAD6, NR4A2, MYCL, ELF4, FOSB, VOPP1, MAFK, NUPR1, NFE2L1
D2-up-only-8	GO_BP	GO:0010628~positive regulation of gene expression	10	0.072	PTGER4, SEC16B, MUSTN1, ALDH1A2, IL18, LIF, SCX, VIM, VASH1, RELB
D2-up-only-9	GO_MF	GO:0070412~R-SMAD binding	4	0.075	JUN, PMEPA1, FOS, SMAD6
D2-up-only-10	GO_BP	GO:1902895~positive regulation of pri-miRNA transcription from RNA polymerase II promoter	4	0.081	JUN, FOS, SMAD6, BMPR1A
D2-up-only-11	KEGG	mmu04350:TGF-beta signaling pathway	4	0.094	INHBB, SMAD6, NBL1, BMPR1A
D2-up-only-12	KEGG	mmu05133:Pertussis	4	0.094	ITGB1, JUN, C1RA, FOS
D1up-D2down-1	GO_BP	GO:0035458~cellular response to interferon-beta	2	0.031	STAT1, IRGM2
D1up-D2down-2	GO_BP	GO:0002474~antigen processing and presentation of peptide antigen via MHC class I	2	0.046	H2-Q6, H2-Q4
D1up-D2down-3	GO_MF	GO:0030881~beta-2-microglobulin binding	2	0.048	H2-Q6, H2-Q4
D1up-D2down-4	GO_MF	GO:0042605~peptide antigen binding	2	0.048	H2-Q6, H2-Q4
D1up-D2down-5	GO_MF	GO:0046977~TAP binding	2	0.048	H2-Q6, H2-Q4
D1up-D2down-6	GO_MF	GO:0042608~T cell receptor binding	2	0.064	H2-Q6, H2-Q4
D1up-D2down-7	KEGG	mmu04919:Thyroid hormone signaling pathway	2	0.089	STAT1, ATP1B2
D1 D2-both-down-1	GO_BP	GO:0032836~glomerular basement membrane development	4	0.007	NPHS1, WT1, COL4A3, SULF1
D1 D2-both-down-2	GO_MF	GO:0000981~RNA polymerase II transcription factor activity, sequence-specific DNA binding	5	0.016	FOXD2, BHLHE41, SOX8, FOXL1, SOX5
D1 D2-both-down-3	GO_BP	GO:0072112~glomerular visceral epithelial cell differentiation	3	0.025	FOXC2, WT1, PTPRO
D1 D2-both-down-4	GO_BP	GO:0043010~camera-type eye development	4	0.033	FOXC2, WT1, GAS1, LMX1B
D1 D2-both-down-5	GO_MF	GO:0004252~serine-type endopeptidase activity	4	0.035	HTRA1, PLAT, PCSK6, RHBDL3
D1 D2-both-down-6	GO_BP	GO:0048010~vascular endothelial growth factor receptor signaling pathway	3	0.048	FOXC2, SULF1, VEGFA
D1 D2-both-down-7	GO_BP	GO:0001822~kidney development	5	0.058	FOXC2, WT1, SULF1, TNS2, VEGFA
D1 D2-both-down-8	GO_MF	GO:0008017~microtubule binding	5	0.061	SGIP1, MTCL1, DPYSL2, MAPT, DYNC111
D1 D2-both-down-9	GO_BP	GO:0007409~axonogenesis	4	0.062	NTNG2, LINGO1, PAK1, MAPT
D1 D2-both-down-10	GO_MF	GO:0003677~DNA binding	12	0.071	FOXC2, ZBTB8A, FOXD2, ZFP423, WT1, TOP1MT, BHLHE41, SOX8, FOXL1, LMX1B, MAFA, SOX5
D1 D2-both-down-11	GO_BP	GO:0010506~regulation of autophagy	3	0.075	MTCL1, MAPT, LMX1B

D1 D2-both-down-12	GO_BP	GO:0008283~cell proliferation	4	0.079	FOXC2, COL4A3, LMX1B, VEGFA
D1 D2-both-down-13	GO_MF	GO:0043565~sequence-specific DNA binding	8	0.084	FOXC2, FOXD2, ZFP423, WT1, SOX8, FOXL1, LMX1B, MAFA
D1-down-only-1	GO_BP	GO:0016567~protein ubiquitination	4	0.011	KLHL29, WSB2, UBE2QL1, KCTD11
D1-down-only-2	GO_MF	GO:0005524~ATP binding	8	0.042	EPHA6, KSR1, TYRO3, UBE2QL1, SPEG, NOD1, TRIB2, ADCY5
D1-down-only-3	GO_MF	GO:0008134~transcription factor binding	5	0.044	FOXC1, E2F1, CRY1, PBX2, TRIB2
D1-down-only-4	GO_BP	GO:0019933~cAMP-mediated signaling	3	0.067	GLP1R, KSR1, ADCY5
D1-down-only-5	GO_BP	GO:0007049~cell cycle	5	0.093	MARVELD1, E2F1, PMP22, KCTD11, VASH1
D2-down-only-1	GO_BP	GO:0007155~cell adhesion	16	0.020	COL18A1, ITGB5, LAMB2, ITGA3, AMIGO2, ATP1B2, NPNT, DPP4, ARVCF, ALCAM, FLRT2, PODXL, NCAM1, SVEP1, EPHB1, CDON
D2-down-only-2	GO_BP	GO:0007411~axon guidance	9	0.024	ROBO2, SEMA5A, ALCAM, NR4A3, FLRT2, LAMB2, UNC5C, NCAM1, EPHB1
D2-down-only-3	GO_BP	GO:0000187~activation of MAPK activity	4	0.041	NTRK3, PLCE1, TGFA, ARRB1
D2-down-only-4	GO_BP	GO:0006811~ion transport	9	0.049	CLIC5, GABRB1, STEAP3, CLIC3, KCNJ12, SLCO2A1, ITPR3, ATP1B2, SLC38A4
D2-down-only-5	GO_BP	GO:0042542~response to hydrogen peroxide	5	0.054	GNAO1, NR4A3, STAT1, STK26, CRYAB
D2-down-only-6	GO_BP	GO:0051965~positive regulation of synapse assembly	5	0.054	LINGO2, FLRT2, NTRK3, AMIGO2, EPHB1
D2-down-only-7	GO_MF	GO:0042277~peptide binding	5	0.055	DPP4, ENPEP, H2-Q6, H2-Q7, H2-Q4
D2-down-only-8	GO_BP	GO:0001574~ganglioside biosynthetic process	4	0.084	ST3GAL6, ST6GALNAC3, ST6GALNAC6, ST3GAL3
D2-down-only-9	GO_BP	GO:0019221~cytokine-mediated signaling pathway	4	0.084	FLRT2, IFNGR1, STAT1, IL6RA
D2-down-only-10	GO_MF	GO:0045499~chemorepellent activity	4	0.085	SEMA5A, FLRT2, SEMA3G, SEMA3E
d1-up d2-down-1	GO_BP	GO:0035458~cellular response to interferon-beta	2	0.031	STAT1, IRGM2
d1-up d2-down-2	GO_BP	GO:0002474~antigen processing and presentation of peptide antigen via MHC class I	2	0.046	H2-Q6, H2-Q4
d1-up d2-down-3	GO_MF	GO:0030881~beta-2-microglobulin binding	2	0.048	H2-Q6, H2-Q4
d1-up d2-down-4	GO_MF	GO:0042605~peptide antigen binding	2	0.048	H2-Q6, H2-Q4
d1-up d2-down-5	GO_MF	GO:0046977~TAP binding	2	0.048	H2-Q6, H2-Q4
d1-up d2-down-6	GO_MF	GO:0042608~T cell receptor binding	2	0.064	H2-Q6, H2-Q4
d1-up d2-down-7	KEGG	mmu04919:Thyroid hormone signaling pathway	2	0.089	STAT1, ATP1B2