

	Category	Term	Count	PValue	Genes
D2-3m-up-1	GO_BP	GO:0051384~response to glucocorticoid	5	0.008	SPARC, ANXA3, IGFBP2, ADM, PTGDS
D2-3m-up-2	GO_BP	GO:0009611~response to wounding	4	0.031	GDNF, F2R, ADM, VASH1
D2-3m-up-3	GO_BP	GO:0015031~protein transport	10	0.034	RAB3B, ARHGAP33, SEC16B, STXB1, S100A13, APBA1, RAB7B, STX11, VAMP2, ARF6
D2-3m-up-4	GO_BP	GO:0043065~positive regulation of apoptotic process	11	0.038	MTCH1, ANXA1, PRMT2, TNFRSF12A, ADAMTSL4, ALDH1A2, ANKRD1, IL18, RARB, ADM, CYR61
D2-3m-up-5	GO_MF	GO:0048306~calcium-dependent protein binding	5	0.062	ANXA1, ANXA2, ANXA3, S100A11, VAMP2
D2-3m-up-6	GO_BP	GO:0002376~immune system process	7	0.072	GSDMD, C1RA, ANXA1, IFITM2, AXL, IL34, OTUD7B
D2-3m-up-7	KEGG	mmu00310:Lysine degradation	3	0.078	COLGALT2, SETD7, PLOD2
D2-3m-up-8	GO_MF	GO:0005509~calcium ion binding	14	0.083	C1RA, NECAB3, SPARC, ANXA1, ANXA2, ANXA3, ACTN1, MYL12A, AIF1L, NELL2, S100A13, EFHD2, PAMR1, S100A11
D2-3m-up-9	GO_BP	GO:0045087~innate immune response	6	0.084	GSDMD, C1RA, ANXA1, IFITM2, AXL, IL34
D2-3m-up-10	GO_BP	GO:0006954~inflammatory response	7	0.096	GSDMD, ANXA1, AXL, IL34, F2R, IL18, TSPAN2
D2-6m-up-1	KEGG	mmu04010:MAPK signaling pathway	11	0.003	JUN, GADD45B, RRAS, GADD45A, SRF, RRAS2, ARRB1, FOS, DUSP8, RELB, FGFR1
D2-6m-up-2	KEGG	mmu04380:Osteoclast differentiation	8	0.005	JUN, NCF2, IFNGR1, FOSB, GAB2, FOS, RELB, FOSL2
D2-6m-up-3	GO_BP	GO:0006366~transcription from RNA polymerase II promoter	6	0.009	JUN, SRF, FOSB, ARRB1, FOS, FOSL2
D2-6m-up-4	GO_BP	GO:0032870~cellular response to hormone stimulus	6	0.009	SOCS2, JUN, NCF2, IGFBP2, FOSB, FOS
D2-6m-up-5	GO_MF	GO:0070412~R-SMAD binding	5	0.011	JUN, ANKRD1, PMEPA1, FOS, SMAD6
D2-6m-up-6	GO_BP	GO:0007568~aging	8	0.016	JUN, CNP, UCP2, IGFBP2, TIMP2, NCAM1, FOS, PPP1R9B
D2-6m-up-7	GO_BP	GO:0006355~regulation of transcription, DNA-templated	31	0.017	KANK2, BTG2, HIP1, ZBTB46, SRF, SCX, ZBTB42, ARRB1, NPAS2, ARNTL, RELB, FOXS1, HOXC5, PTRF, SAMD4, JUN, ARID5A, FOS, WTIP, SMAD6, FOSL2, MDFIC, ELF4, CRY1, FOSB, VOPP1, MAFK, NUPR1, ATF3, NFE2L1, VGLL3
D2-6m-up-8	GO_MF	GO:0032403~protein complex binding	11	0.021	ITGB1, RRAS, MLKL, MAP1B, NCK2, APBA1, IQGAP1, ACTN4, FGFR1, PPP1R9B, CD2AP
D2-6m-up-9	GO_BP	GO:0007015~actin filament organization	7	0.024	PRKCI, SRF, ACTN1, NCK2, EMP2, TMSB10, PPP1R9B
D2-6m-up-10	GO_MF	GO:0001047~core promoter binding	5	0.027	GADD45A, CRY1, NPAS2, RELB, ARNTL
D2-6m-up-11	GO_BP	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	21	0.031	RNASEL, JUN, SRF, ARID5A, LIF, SCX, ARRB1, FOS, CYR61, NPAS2, FOSL2, RELB, MLLT6, ARNTL, ELF4, NCK2, FOSB, ATF3, NFE2L1, ZFP462, FGFR1
D2-6m-up-12	KEGG	mmu05140:Leishmaniasis	5	0.032	ITGB1, JUN, NCF2, IFNGR1, FOS
D2-6m-up-13	GO_BP	GO:0006351~transcription, DNA-templated	27	0.037	KANK2, BTG2, HIP1, ZBTB46, SRF, SCX, ZBTB42, ARRB1, NPAS2, ARNTL, RELB, FOXS1, HOXC5, PTRF, JUN, ARID5A, WTIP, SMAD6, FOSL2, MDFIC, ELF4, CRY1, VOPP1, MAFK, NUPR1, ATF3, VGLL3
D2-6m-up-14	GO_BP	GO:0045666~positive regulation of neuron differentiation	7	0.039	SOCS2, ITGB1, MAP1B, TIMP2, BNIP2, NBL1, FGFR1
D2-6m-up-15	GO_MF	GO:0008134~transcription factor binding	10	0.043	JUN, RFXO2, MDFIC, SRF, ARID5A, ANKRD1, CRY1, ARRB1, FOS, ARNTL
D2-6m-up-16	GO_MF	GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding	9	0.047	JUN, ELF4, SRF, FOSB, FOS, SMAD6, ATF3, RELB, FOSL2
D2-6m-up-17	GO_MF	GO:0003690~double-stranded DNA binding	5	0.052	JUN, CRY1, FOSB, FOS, FOSL2
D2-6m-up-18	GO_MF	GO:0019900~kinase binding	5	0.052	ITGB1, CRY1, EMP2, VIM, PPP1R9B
D2-6m-up-19	GO_MF	GO:0005200~structural constituent of cytoskeleton	6	0.055	TUBB2B, TUBB2A, TUBA1A, TPM1, VIM, SPTB
D2-6m-up-20	GO_BP	GO:0009612~response to mechanical stimulus	5	0.056	BTG2, JUN, IGFBP2, FOSB, INHBB
D2-6m-up-21	GO_BP	GO:0006357~regulation of transcription from RNA polymerase II promoter	8	0.057	ANKRD1, FOSB, MAFK, NUPR1, FOS, ATF3, RELB, FOSL2
D2-6m-up-22	GO_BP	GO:0034097~response to cytokine	6	0.060	JUN, SPARC, SRF, TIMP2, FOS, RELB
D2-6m-up-23	GO_BP	GO:0035914~skeletal muscle cell differentiation	6	0.060	BTG2, ANKRD1, SCX, NUPR1, FOS, ATF3
D2-6m-up-24	GO_MF	GO:0003682~chromatin binding	8	0.070	JUN, SRF, ARID5A, NUPR1, FOS, SMAD6, RELB, FOSL2
D2-6m-up-25	GO_BP	GO:0043065~positive regulation of apoptotic process	11	0.075	UNC13B, ITGB1, MTCH1, JUN, GADD45B, TNFRSF12A, ADAMTSL4, GADD45A, ANKRD1, NUPR1, CYR61
D2-6m-up-26	GO_MF	GO:0005515~protein binding	58	0.077	ITGB1, BTG2, HIP1, SPARC, NCF2, SCX, ARRB1, PPP1R9B, ADAMTS4, SH3PXD2A, EFHD2, ANKRD1, PMEPA1, DENND5A, LDLRAP1, PRKCI, RFXO2, TNFRSF12A, ACTN1, RRAS2, ACTN4, GAB2, CD2AP, MDFIC, MAP1B, CRY1, MYH9, NUPR1, UTRN, NBL1, ARF6, SRF, NREP, IQGAP1, KLC1, NKD1, NPAS2, ARNTL, RELB, NCAM1, KIF3C, MAP4, JUN, ATP8B2, MLKL, GADD45B, GADD45A, PLEKHA2, PTPN12, WTIP, SMAD6, SERPINB6A, AMOTL2, APBA1, MAFK, VIM, NFE2L1, FGFR1
D2-6m-up-27	GO_MF	GO:0044212~transcription regulatory region DNA binding	7	0.077	JUN, ARID5A, ARRB1, FOS, SMAD6, ATF3, FOSL2
D2-6m-up-28	GO_MF	GO:0005543~phospholipid binding	7	0.077	PRKCI, HIP1, PLEKHA2, MAP1B, MYOF, AGAP1, SPTB
D2-6m-up-29	GO_MF	GO:0051015~actin filament binding	9	0.083	HIP1, ACTN1, TPM1, MYH9, ACTN4, UTRN, SPTB, AIF1L, PPP1R9B
D2-6m-up-30	GO_MF	GO:0002020~protease binding	5	0.086	ADAMTS4, ITGB1, SERPINB6A, ADAMTSL4, TIMP2
D2-6m-up-31	GO_BP	GO:1902895~positive regulation of pri-miRNA transcription from RNA polymerase II promoter	4	0.087	JUN, SRF, FOS, SMAD6
D2-6m-up-32	GO_BP	GO:0006469~negative regulation of protein kinase activity	4	0.087	SOCS2, DBNDD2, GADD45B, GADD45A
D2-6m-up-33	GO_BP	GO:0007017~microtubule-based process	4	0.087	TUBB2B, TUBB2A, TUBA1A, MAP1B
D2-6m-up-34	GO_BP	GO:0032922~circadian regulation of gene expression	4	0.087	CRY1, NPAS2, RELB, ARNTL
D2-6m-up-35	GO_BP	GO:0051726~regulation of cell cycle	5	0.092	ITGB1, JUN, GADD45B, GADD45A, ARNTL
D2-6m-up-36	KEGG	mmu04668:TNF signaling pathway	4	0.093	JUN, MLKL, LIF, FOS
D2-6m-up-37	GO_MF	GO:0003779~actin binding	13	0.096	ITGB1, HIP1, ACTN1, TPM1, ACTN4, SPTB, AIF1L, PPP1R9B, MPRIP, DAAM2, MAP1B, MYH9, UTRN
D2-6m-up-38	KEGG	mmu05168:Herpes simplex infection	5	0.100	JUN, RNASEL, IFNGR1, FOS, ARNTL
D2-6m-up-39	KEGG	mmu05132:Salmonella infection	5	0.100	JUN, IFNGR1, FOS, KLC1, RAB7B
D2-3m6m-up-both-1	GO_BP	GO:0042060~wound healing	4	0.044	SPARC, SDC4, MUSTN1, TPM1

D2-3m6m-up-both-2	GO_BP	GO:0045765~regulation of angiogenesis	3	0.046	TNFRSF12A, EMP2, VASH1
D2-3m6m-up-both-3	KEGG	mmu04014:Ras signaling pathway	4	0.052	RRAS, RRAS2, GAB2, ARF6
D2-3m6m-up-both-4	GO_BP	GO:0001558~regulation of cell growth	3	0.072	SOCS2, IGFBP2, CYR61
D2-3m6m-up-both-5	GO_BP	GO:0045860~positive regulation of protein kinase activity	3	0.072	SDC4, IQGAP1, CYR61
D2-3m6m-up-both-6	GO_MF	GO:0005525~GTP binding	6	0.089	ARL4C, TUBA1A, RRAS, RRAS2, RAB7B, ARF6
D2-3m6m-up-both-7	GO_BP	GO:0045666~positive regulation of neuron differentiation	4	0.095	SOCS2, MAP1B, TIMP2, BNIP2
D2-3m-up-only-1	KEGG	mmu00310:Lysine degradation	3	0.027	COLGALT2, SETD7, PLOD2
D2-3m-up-only-2	GO_MF	GO:0004859~phospholipase inhibitor activity	3	0.036	ANXA1, ANXA2, ANXA3
D2-3m-up-only-3	GO_MF	GO:0019834~phospholipase A2 inhibitor activity	3	0.036	ANXA1, ANXA2, ANXA3
D2-3m-up-only-4	GO_MF	GO:0048306~calcium-dependent protein binding	4	0.052	ANXA1, ANXA2, ANXA3, VAMP2
D2-3m-up-only-5	GO_BP	GO:0009611~response to wounding	3	0.066	GNDF, F2R, ADM
D2-3m-up-only-6	GO_BP	GO:0030182~neuron differentiation	4	0.072	NR4A2, GDNF, ALDH1A2, HOXC8
D2-3m-up-only-7	GO_BP	GO:0007204~positive regulation of cytosolic calcium ion concentration	4	0.095	PTGER4, F2R, ADM, PRKG1
D2-6m-up-only-1	GO_BP	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	20	0.000	RNASEL, JUN, SRF, ARID5A, LIF, SCX, ARRB1, FOS, NPAS2, FOSL2, RELB, MLLT6, ARNTL, ELF4, NCK2, FOSB, ATF3, NFE2L1, ZFP462, FGFR1
D2-6m-up-only-2	GO_BP	GO:0006355~regulation of transcription, DNA-templated	25	0.000	BTG2, HIP1, ZBTB46, SRF, SCX, ARRB1, NPAS2, ARNTL, RELB, FOXS1, HOXC5, JUN, ARID5A, FOS, WTIP, SMAD6, FOSL2, MDFIC, ELF4, FOSB, MAFK, NUPR1, ATF3, NFE2L1, VGLL3
D2-6m-up-only-3	GO_BP	GO:0006366~transcription from RNA polymerase II promoter	6	0.001	JUN, SRF, FOSB, ARRB1, FOS, FOSL2
D2-6m-up-only-4	GO_MF	GO:0003700~transcription factor activity, sequence-specific DNA binding	15	0.001	JUN, SRF, FOS, SMAD6, NPAS2, FOSL2, RELB, ARNTL, FOXS1, ELF4, HOXC5, FOSB, MAFK, ATF3, NFE2L1
D2-6m-up-only-5	GO_BP	GO:0006351~transcription, DNA-templated	22	0.001	BTG2, JUN, HIP1, ZBTB46, SRF, ARID5A, SCX, ARRB1, WTIP, SMAD6, NPAS2, FOSL2, RELB, ARNTL, FOXS1, MDFIC, ELF4, HOXC5, MAFK, NUPR1, ATF3, VGLL3
D2-6m-up-only-6	GO_MF	GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding	9	0.002	JUN, ELF4, SRF, FOSB, FOS, SMAD6, ATF3, RELB, FOSL2
D2-6m-up-only-7	KEGG	mmu04380:Osteoclast differentiation	7	0.004	JUN, NCF2, IFNGR1, FOSB, FOS, RELB, FOSL2
D2-6m-up-only-8	KEGG	mmu04010:MAPK signaling pathway	9	0.004	JUN, GADD45B, GADD45A, SRF, ARRB1, FOS, DUSP8, RELB, FGFR1
D2-6m-up-only-9	GO_MF	GO:0043565~sequence-specific DNA binding	13	0.004	JUN, SRF, SCX, FOS, FOSL2, ARNTL, FOXS1, ELF4, HOXC5, FOSB, MAFK, ATF3, NFE2L1
D2-6m-up-only-10	GO_MF	GO:0003682~chromatin binding	8	0.004	JUN, SRF, ARID5A, NUPR1, FOS, SMAD6, RELB, FOSL2
D2-6m-up-only-11	GO_MF	GO:0044212~transcription regulatory region DNA binding	7	0.007	JUN, ARID5A, ARRB1, FOS, SMAD6, ATF3, FOSL2
D2-6m-up-only-12	KEGG	mmu05140:Leishmaniasis	5	0.008	ITGB1, JUN, NCF2, IFNGR1, FOS
D2-6m-up-only-13	GO_MF	GO:0003677~DNA binding	18	0.009	JUN, SRF, ARID5A, SCX, FOS, SMAD6, NPAS2, FOSL2, RELB, ARNTL, FOXS1, ELF4, HOXC5, FOSB, MAFK, NUPR1, ATF3, NFE2L1
D2-6m-up-only-14	GO_MF	GO:0005515~protein binding	40	0.014	ITGB1, BTG2, HIP1, NCF2, SRF, SCX, ARRB1, KLC1, NKD1, NPAS2, ARNTL, PPP1R9B, RELB, ADAMTS4, SH3PXD2A, DENND5A, NCAM1, MAP4, KIF3C, LDLRAP1, PRKCI, JUN, MLKL, ATP8B2, GADD45B, GADD45A, PLEKHA2, ACTN4, WTIP, SMAD6, CD2AP, MDFIC, MYH9, AMOTL2, MAFK, NUPR1, UTRN, NBL1, NFE2L1, FGFR1
D2-6m-up-only-15	GO_BP	GO:0006357~regulation of transcription from RNA polymerase II promoter	7	0.015	FOSB, MAFK, NUPR1, FOS, ATF3, RELB, FOSL2
D2-6m-up-only-16	GO_BP	GO:0051726~regulation of cell cycle	5	0.016	ITGB1, JUN, GADD45B, GADD45A, ARNTL
D2-6m-up-only-17	GO_BP	GO:1902895~positive regulation of pri-miRNA transcription from RNA polymerase II promoter	4	0.021	JUN, SRF, FOS, SMAD6
D2-6m-up-only-18	KEGG	mmu05168:Herpes simplex infection	5	0.030	JUN, RNASEL, IFNGR1, FOS, ARNTL
D2-6m-up-only-19	GO_MF	GO:0001077~transcriptional activator activity, RNA polymerase II core promoter proximal region sequen	7	0.034	JUN, ELF4, SRF, FOSB, FOS, RELB, ARNTL
D2-6m-up-only-20	KEGG	mmu04668:TNF signaling pathway	4	0.035	JUN, MLKL, LIF, FOS
D2-6m-up-only-21	GO_MF	GO:0001047~core promoter binding	4	0.036	GADD45A, NPAS2, RELB, ARNTL
D2-6m-up-only-22	GO_BP	GO:0035914~skeletal muscle cell differentiation	5	0.038	BTG2, SCX, NUPR1, FOS, ATF3
D2-6m-up-only-23	GO_MF	GO:0046982~protein heterodimerization activity	9	0.040	ITGB1, JUN, HIP1, SCX, INHBB, FOS, SPTB, ATF3, ARNTL
D2-6m-up-only-24	GO_MF	GO:0035612~AP-2 adaptor complex binding	3	0.051	HIP1, ARRB1, LDLRAP1
D2-6m-up-only-25	GO_MF	GO:0000976~transcription regulatory region sequence-specific DNA binding	3	0.051	MAFK, ATF3, ARNTL
D2-6m-up-only-26	GO_BP	GO:0043161~proteasome-mediated ubiquitin-dependent protein catabolic process	3	0.052	ARRB1, CD2AP, ARNTL
D2-6m-up-only-27	GO_MF	GO:0003690~double-stranded DNA binding	4	0.057	JUN, FOSB, FOS, FOSL2
D2-6m-up-only-28	GO_BP	GO:0009612~response to mechanical stimulus	4	0.060	BTG2, JUN, FOSB, INHBB
D2-6m-up-only-29	GO_BP	GO:0032870~cellular response to hormone stimulus	4	0.060	JUN, NCF2, FOSB, FOS
D2-6m-up-only-30	GO_BP	GO:0045893~positive regulation of transcription, DNA-templated	9	0.062	JUN, MDFIC, ELF4, SRF, SCX, FOS, NPAS2, ARNTL, FOSL2
D2-6m-up-only-31	KEGG	mmu04660:T cell receptor signaling pathway	4	0.062	JUN, NCK2, FOS, NFKBIE
D2-6m-up-only-32	GO_MF	GO:0008134~transcription factor binding	7	0.066	JUN, MDFIC, SRF, ARID5A, ARRB1, FOS, ARNTL
D2-6m-up-only-33	GO_BP	GO:0031175~neuron projection development	6	0.073	ITGB1, BTG2, SRF, NCAM1, MAP4, FGFR1
D2-6m-up-only-34	KEGG	mmu04662:B cell receptor signaling pathway	3	0.075	JUN, FOS, NFKBIE
D2-6m-up-only-35	GO_MF	GO:0032403~protein complex binding	7	0.080	ITGB1, MLKL, NCK2, ACTN4, FGFR1, PPP1R9B, CD2AP
D2-6m-up-only-36	GO_MF	GO:0000982~transcription factor activity, RNA polymerase II core promoter proximal region sequence-s	3	0.092	JUN, ARNTL, FOSL2
D2-6m-up-only-37	GO_MF	GO:0000980~RNA polymerase II distal enhancer sequence-specific DNA binding	3	0.092	JUN, SCX, NFE2L1
D2-6m-up-only-38	GO_BP	GO:0007568~aging	5	0.092	JUN, CNP, NCAM1, FOS, PPP1R9B
D2-6m-up-only-39	GO_BP	GO:0010976~positive regulation of neuron projection development	5	0.092	ITGB1, PRKCI, LIF, KIF3C, FGFR1

D2-6m-up-only-40	GO_BP	GO:0045892~negative regulation of transcription, DNA-templated	8	0.093	JUN, FOXS1, MDFIC, SCX, NFKBIE, ATF3, RELB, ARNTL
D2-6m-up-only-41	GO_BP	GO:0070373~negative regulation of ERK1 and ERK2 cascade	3	0.095	LIF, ARRB1, ATF3
D2-6m-up-only-42	GO_BP	GO:1900745~positive regulation of p38MAPK cascade	3	0.095	GADD45B, GADD45A, SASH1
D2-6m-up-only-43	GO_BP	GO:0043149~stress fiber assembly	3	0.095	ITGB1, SRF, ARRB1
D2-3m-down-1	KEGG	mmu04514:Cell adhesion molecules (CAMs)	6	0.018	NTNG2, CLDN5, ALCAM, H2-Q6, H2-Q7, NCAM1
D2-3m-down-2	GO_MF	GO:0005215~transporter activity	5	0.040	ABCA2, SLC37A2, ABCA5, SLCO2A1, ABCA9
D2-3m-down-3	GO_MF	GO:0016787~hydrolase activity	17	0.042	GGT5, ENPEP, ATP8B1, PTPRO, HTRA1, PTPN21, PLAT, DUSP15, GPPD5, SULF1, PTPN14, PLA2G7, MMP23, ARSJ, DPYSL2, MMP17, PLCE1
D2-3m-down-4	GO_BP	GO:0007155~cell adhesion	14	0.045	COL18A1, ITGB5, LAMB2, ITGA3, SULF1, ARVCF, ALCAM, NPHS1, PODXL, COL4A3, NCAM1, SVEP1, EPHB1, CDON
D2-3m-down-5	GO_BP	GO:0007411~axon guidance	8	0.045	ROBO2, SEMA6C, ALCAM, LAMB2, DPYSL2, PTPRO, NCAM1, EPHB1
D2-3m-down-6	GO_BP	GO:0008217~regulation of blood pressure	4	0.065	ENPEP, NPR1, NPR3, TAC4
D2-3m-down-7	KEGG	mmu04510:Focal adhesion	8	0.081	PAK1, ITGB5, ITGA3, LAMB2, COL4A3, COL4A5, MYLK3, MYLK
D2-6m-down-1	GO_BP	GO:0007411~axon guidance	10	0.008	ROBO2, SEMA5A, ALCAM, NR4A3, FLRT2, LAMB2, PTPRO, GAS1, UNC5C, EPHB1
D2-6m-down-2	GO_BP	GO:0072015~glomerular visceral epithelial cell development	6	0.010	MYO1E, NPHS1, PODXL, WT1, MAGI2, GLCCI1
D2-6m-down-3	GO_BP	GO:0032836~glomerular basement membrane development	5	0.012	MYO1E, NPHS1, WT1, COL4A3, SULF1
D2-6m-down-4	GO_BP	GO:0043010~camera-type eye development	6	0.021	CDKN1C, FOXC2, WT1, GAS1, LMX1B, CRYAB
D2-6m-down-5	GO_MF	GO:0005244~voltage-gated ion channel activity	4	0.042	KCNF1, CLIC5, CLIC3, KCNJ12
D2-6m-down-6	GO_BP	GO:0006813~potassium ion transport	4	0.043	NSF, KCNF1, KCNJ12, ATP1B2
D2-6m-down-7	GO_BP	GO:0007155~cell adhesion	15	0.052	ITGB5, LAMB2, AMIGO2, APLP1, ATP1B2, NPNT, SULF1, DPP4, ARVCF, ALCAM, FLRT2, NPHS1, PODXL, COL4A3, EPHB1
D2-6m-down-8	GO_BP	GO:0051965~positive regulation of synapse assembly	5	0.057	LINGO2, FLRT2, NTRK3, AMIGO2, EPHB1
D2-6m-down-9	GO_BP	GO:0001822~kidney development	8	0.058	CDKN1C, ROBO2, MYO1E, FOXC2, WT1, SULF1, TNS2, VEGFA
D2-6m-down-10	KEGG	mmu04514:Cell adhesion molecules (CAMs)	6	0.064	NTNG2, CLDN5, ALCAM, H2-Q6, H2-Q7, VTCN1
D2-6m-down-11	GO_MF	GO:0016740~transferase activity	19	0.077	HS3ST3B1, HS3ST3A1, ZAK, NTRK3, MERTK, GALNT10, MYLK3, MYLK, PAK1, LATS2, EXTL1, STK26, MGAT5, MGAT5B, CHST1, ST3GAL6, ST6GALNAC3, EPHB1, ST6GALNAC6
D2-6m-down-12	GO_MF	GO:0016757~transferase activity, transferring glycosyl groups	7	0.084	EXTL1, MGAT5, MGAT5B, ST3GAL6, ST6GALNAC3, GALNT10, ST6GALNAC6
D2-6m-down-13	GO_MF	GO:0045499~chemorepellent activity	4	0.087	SEMA5A, FLRT2, SEMA3G, SEMA3E
D2-6m-down-14	GO_BP	GO:0032835~glomerulus development	4	0.089	ENPEP, WT1, PTPRO, PLCE1
D2-6m-down-15	GO_BP	GO:0001569~patterning of blood vessels	4	0.089	SEMA5A, FOXC2, SEMA3E, VEGFA
D2-6m-down-16	GO_BP	GO:0034765~regulation of ion transmembrane transport	4	0.089	KCNF1, CLIC5, CLIC3, KCNJ12
D2-6m-down-17	GO_MF	GO:0000981~RNA polymerase II transcription factor activity, sequence-specific DNA binding	6	0.089	FOXO2, PLAGL1, BHLHE41, SOX8, FOXL1, SOX5
D2-6m-down-18	GO_MF	GO:0004252~serine-type endopeptidase activity	5	0.092	DPP4, HTRA1, PLAT, PCSK6, RHBDL3
D2-6m-down-19	GO_BP	GO:0050679~positive regulation of epithelial cell proliferation	5	0.094	NR4A3, HTRA1, GAS1, TGFA, VEGFA
D2-3m-down-only-1	GO_MF	GO:0005201~extracellular matrix structural constituent	3	0.029	COL1A2, COL4A3, COL4A5
D2-3m-down-only-2	GO_BP	GO:0048010~vascular endothelial growth factor receptor signaling pathway	3	0.033	FOXC1, SULF1, VEGFA
D2-3m-down-only-3	GO_BP	GO:0016525~negative regulation of angiogenesis	4	0.048	FOXC1, COL4A3, VASH1, SULF1
D2-3m-down-only-4	KEGG	mmu04974:Protein digestion and absorption	3	0.071	COL1A2, COL4A3, COL4A5
D2-3m-down-only-5	KEGG	mmu04151:PI3K-Akt signaling pathway	4	0.091	COL1A2, COL4A3, COL4A5, VEGFA
D2-6m-down-only-1	GO_BP	GO:0043010~camera-type eye development	5	0.008	CDKN1C, FOXC2, WT1, GAS1, CRYAB
D2-6m-down-only-2	GO_BP	GO:0001569~patterning of blood vessels	4	0.013	SEMA5A, FOXC2, SEMA3E, VEGFA
D2-6m-down-only-3	GO_BP	GO:0001822~kidney development	6	0.030	CDKN1C, MYO1E, FOXC2, WT1, TNS2, VEGFA
D2-6m-down-only-4	GO_MF	GO:0000981~RNA polymerase II transcription factor activity, sequence-specific DNA binding	5	0.032	FOXO2, PLAGL1, BHLHE41, FOXL1, SOX5
D2-6m-down-only-5	GO_BP	GO:0035924~cellular response to vascular endothelial growth factor stimulus	3	0.038	NR4A1, GAS1, VEGFA
D2-6m-down-only-6	GO_BP	GO:1902476~chloride transmembrane transport	3	0.038	CLIC5, GABRB1, CLIC3
D2-6m-down-only-7	GO_BP	GO:0042542~response to hydrogen peroxide	4	0.038	GNAO1, NR4A3, STK26, CRYAB
D2-6m-down-only-8	GO_BP	GO:0051965~positive regulation of synapse assembly	4	0.038	LINGO2, FLRT2, NTRK3, AMIGO2
D2-6m-down-only-9	GO_BP	GO:0050679~positive regulation of epithelial cell proliferation	4	0.056	NR4A3, GAS1, TGFA, VEGFA
D2-6m-down-only-10	KEGG	mmu00534:Glycosaminoglycan biosynthesis - heparan sulfate / heparin	3	0.057	HS3ST3B1, HS3ST3A1, EXTL1
D2-6m-down-only-11	GO_BP	GO:0043066~negative regulation of apoptotic process	7	0.061	NR4A3, WT1, AMIGO2, GAS1, TGFA, CRYAB, VEGFA
D2-6m-down-only-12	GO_BP	GO:0006813~potassium ion transport	3	0.070	NSF, KCNF1, ATP1B2
D2-6m-down-only-13	GO_BP	GO:0043154~negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	3	0.070	NR4A1, CRYAB, VEGFA
D2-6m-down-only-14	GO_BP	GO:0006821~chloride transport	3	0.070	CLIC5, GABRB1, CLIC3
D2-6m-down-only-15	GO_BP	GO:0001938~positive regulation of endothelial cell proliferation	3	0.070	SEMA5A, NR4A1, VEGFA
D2-6m-down-only-16	GO_BP	GO:0007507~heart development	5	0.070	FOXC2, WT1, NTRK3, ADM, FOXL1
D2-6m-down-only-17	GO_MF	GO:0005244~voltage-gated ion channel activity	3	0.071	KCNF1, CLIC5, CLIC3
D2-6m-down-only-18	GO_MF	GO:0005254~chloride channel activity	3	0.071	CLIC5, GABRB1, CLIC3
D2-6m-down-only-19	GO_MF	GO:0042802~identical protein binding	8	0.073	DPP4, FOXC2, STK26, APLP1, SNCAIP, ACP, CRYAB, VEGFA
D2-6m-down-only-20	GO_BP	GO:0007275~multicellular organism development	12	0.094	SEMA5A, FOXC2, FLRT2, WIF1, NTRK3, WIPF3, UNC5C, SEMA3E, NPNT, ARHGAP24, HOXC6, VEGFA

D2-3m6m-down-both-1	KEGG	mmu04514:Cell adhesion molecules (CAMs)	5	0.015	NTNG2, CLDN5, ALCAM, H2-Q6, H2-Q7
D2-3m6m-down-both-2	KEGG	mmu04510:Focal adhesion	7	0.022	PAK1, ITGB5, LAMB2, COL4A3, COL4A5, MYLK3, MYLK
D2-3m6m-down-both-3	GO_BP	GO:0031290~retinal ganglion cell axon guidance	3	0.038	ROBO2, ALCAM, EPHB1
D2-3m6m-down-both-4	GO_BP	GO:0072015~glomerular visceral epithelial cell development	4	0.038	NPHS1, PODXL, MAGI2, GLCCI1
D2-3m6m-down-both-5	GO_MF	GO:0005524~ATP binding	11	0.065	MYO1D, PAK1, ABCA5, NPR1, ZAK, ATP8B1, ABCA9, HSPA12A, EPHB1, MYLK3, MYLK
D2-3m6m-down-both-6	GO_BP	GO:0007155~cell adhesion	9	0.073	ARVCF, ALCAM, ITGB5, NPHS1, PODXL, LAMB2, COL4A3, SULF1, EPHB1