

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GO_BP	GO:0032835~glomerulus development	4	3.23	1.79E-05	WT1, PTPRO, TCF21, PLCE1	111	9	18082	72.4004004	0.012640745	0.01270329	0.01265
GO_BP	GO:0072015~glomerular visceral epithelial cell development	4	3.23	4.63E-05	NPFS1, PODXL, WT1, MAGI2	111	12	18082	54.3003003	0.032342694	0.01641511	0.016346
GO_MF	GO:0043565~sequence-specific DNA binding	13	10.48	3.85E-04	FOXC2, ZFP423, FOXD2, FOXD1, FOXL1, MAFA, NR4A1, NR4A3, MAFB, WT1, E2F1, LMX1B, HOXC8	105	633	17446	3.412292184	0.076633926	0.07971416	0.079714
GO_BP	GO:0007275~multicellular organism development	17	13.71	4.84E-04	ROBO2, NTNG2, FOXC2, ZFP423, PRM1, FZD2, FOXD1, WIPF3, SHISA3, SEMA3E, TDRD5, NPFS1, WIF1, LMX1B, HOXC8, NES, GAS7	111	1029	18082	2.691268528	0.290691134	0.11429917	0.113816
KEGG	mmu04360:Axon guidance	6	4.84	7.09E-04	ROBO2, NTNG2, ABLIM3, SEMA3G, SEMA3E, SRGAP1	44	129	7691	8.130021142	0.069816008	0.07305649	0.073056
GO_BP	GO:0072112~glomerular visceral epithelial cell differentiation	3	2.42	7.55E-04	FOXC2, WT1, PTPRO	111	7	18082	69.81467181	0.415039113	0.13381323	0.133247
GO_BP	GO:0019933~cAMP-mediated signaling	4	3.23	0.001046	KSR1, NPR3, ADM, ADCY1	111	33	18082	19.74556375	0.524478848	0.14072696	0.140132
GO_MF	GO:0001077~transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	8	6.45	0.001166	NR4A1, FOXC2, MAFB, NR4A3, FOXD1, WT1, TCF21, MAFA	105	270	17446	4.92303351	0.21451931	0.12065932	0.120659
GO_BP	GO:0001822~kidney development	6	4.84	0.001191	CDKN1C, ROBO2, FOXC2, FOXD1, WT1, TCF21	111	130	18082	7.518503119	0.570896268	0.14072696	0.140132
GO_BP	GO:0001657~ureteric bud development	4	3.23	0.003105	ROBO2, FOXC2, WT1, TCF21	111	48	18082	13.57507508	0.890084146	0.28197156	0.280778
GO_BP	GO:0071850~mitotic cell cycle arrest	3	2.42	0.003182	GADD45A, MAGI2, CDC14A	111	14	18082	34.90733591	0.895915821	0.28197156	0.280778
GO_BP	GO:0007399~nervous system development	8	6.45	0.008233	ROBO2, NTNG2, ZFP423, MAGI2, SEMA3E, GDPD5, NES, GAS7	111	377	18082	3.456783043	0.997176518	0.64859494	0.645851
GO_BP	GO:0008360~regulation of cell shape	5	4.03	0.010305	ANXA1, WIPF3, PLEKHO1, SEMA3E, GAS7	111	139	18082	5.859744637	0.999360279	0.73062145	0.72753
GO_MF	GO:0005515~protein binding	36	29.03	0.011556	RAB3B, CDKN1C, ZFP423, HSPB8, PTPRO, RASL11A, TCF21, ITPR3, RAVR2, E2F1, SRGAP1, ZBTB7C, NTNG2, KIRREL, FZD2, ANXA1, KSR1, GADD45A, APLP1, MAGI2, NGB, FNDC5, CLDN5, NR4A1, EHD2, MAFB, MYL7, NPFS1, WT1, NPFS2, PLEKHO1, VIM, NUPR1, ASTN2, SYNC, NES	105	4092	17446	1.461751152	0.909822559	0.44598654	0.445987
GO_BP	GO:0043010~camera-type eye development	4	3.23	0.011976	CDKN1C, FOXC2, WT1, LMX1B	111	78	18082	8.353892354	0.999807334	0.77193166	0.768665
KEGG	mmu04925:Aldosterone synthesis and secretion	4	3.23	0.012073	NR4A1, NPR1, ITPR3, ADCY1	44	86	7691	8.130021142	0.710293973	0.62173385	0.621734
GO_MF	GO:0017147~Wnt-protein binding	3	2.42	0.013734	FZD2, WIF1, PTPRO	105	30	17446	16.6152381	0.942878392	0.44598654	0.445987
GO_MF	GO:0003779~actin binding	7	5.65	0.015728	PLEKHH2, INF2, ABLIM3, NEBL, WIPF3, SYNPO, CORO2B	105	338	17446	3.441025641	0.962433676	0.44598654	0.445987
GO_MF	GO:0003700~transcription factor activity, sequence-specific DNA binding	12	9.68	0.016084	NR4A1, FOXC2, FOXD2, MAFB, NR4A3, FOXD1, WT1, E2F1, FOXL1, LMX1B, MAFA, HOXC8	105	883	17446	2.258016502	0.965138678	0.44598654	0.445987
GO_MF	GO:0030144~alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase activity	2	1.61	0.017778	MGAT5, MGAT5B	105	3	17446	110.768254	0.975601388	0.44598654	0.445987
GO_MF	GO:0016941~natriuretic peptide receptor activity	2	1.61	0.017778	NPR1, NPR3	105	3	17446	110.768254	0.975601388	0.44598654	0.445987
GO_BP	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	13	10.48	0.017819	FOXC2, FOXD1, TCF21, MAFA, DDN, NR4A1, NR4A3, MAFB, ABLIM3, WT1, E2F1, LMX1B, ZBTB7C	111	995	18082	2.128353479	0.999997142	0.90845757	0.904614
GO_BP	GO:0045103~intermediate filament-based process	2	1.61	0.01814	VIM, SYNC	111	3	18082	108.6006006	0.999997735	0.90845757	0.904614
GO_BP	GO:0006487~protein N-linked glycosylation	3	2.42	0.020194	MGAT5, MGAT5B, ST3GAL1	111	36	18082	13.57507508	0.999999488	0.90845757	0.904614
GO_BP	GO:0030513~positive regulation of BMP signaling pathway	3	2.42	0.020194	CRB2, ZFP423, FOXD1	111	36	18082	13.57507508	0.999999488	0.90845757	0.904614
GO_BP	GO:0001656~metanephros development	3	2.42	0.022358	ROBO2, FOXC2, WT1	111	38	18082	12.86059744	0.999999893	0.90845757	0.904614
GO_BP	GO:0030199~collagen fibril organization	3	2.42	0.023474	FOXC2, LMX1B, LOXL2	111	39	18082	12.53083853	0.999999953	0.90845757	0.904614
GO_MF	GO:0019834~phospholipase A2 inhibitor activity	2	1.61	0.023635	ANXA1, ANXA3	105	4	17446	83.07619048	0.99292448	0.44598654	0.445987
GO_MF	GO:0043533~inositol 1,3,4,5 tetrakisphosphate binding	2	1.61	0.023635	ITPR3, ASTN2	105	4	17446	83.07619048	0.99292448	0.44598654	0.445987
GO_MF	GO:0005509~calcium ion binding	10	8.06	0.0237	CRB2, EHD2, ANXA1, MYL7, ANXA3, PROS1, ITPR3, MCC, RHBDL3, ASTN2	105	699	17446	2.377001158	0.993021497	0.44598654	0.445987
GO_BP	GO:0071376~cellular response to corticotropin-releasing hormone stimulus	2	1.61	0.024114	NR4A1, NR4A3	111	4	18082	81.45045045	0.99999997	0.90845757	0.904614
GO_BP	GO:0045893~positive regulation of transcription, DNA-templated	9	7.26	0.024345	CDKN1C, NR4A1, FOXC2, ZFP423, FZD2, NR4A3, WT1, E2F1, MAFA	111	576	18082	2.545326577	0.999999975	0.90845757	0.904614
GO_MF	GO:0008467~[heparan sulfate]-glucosamine 3-sulfotransferase 1 activity	2	1.61	0.029456	HS3ST3A1, HS3ST6	105	5	17446	66.46095238	0.997948268	0.50812192	0.508122
KEGG	mmu04110:Cell cycle	4	3.23	0.031616	CDKN1C, GADD45A, E2F1, CDC14A	44	124	7691	5.63856305	0.962256487	0.92392082	0.923921
GO_BP	GO:0001658~branching involved in ureteric bud morphogenesis	3	2.42	0.034497	FOXD1, WT1, TCF21	111	48	18082	10.18130631	1	1	0.997175
GO_MF	GO:0004859~phospholipase inhibitor activity	2	1.61	0.035244	ANXA1, ANXA3	105	6	17446	55.38412698	0.999405089	0.53064375	0.530644
GO_MF	GO:0016757~transferase activity, transferring glycosyl groups	5	4.03	0.035889	MGAT5, MGAT5B, ST3GAL1, GALNT10, ST6GALNAC6	105	208	17446	3.994047619	0.999482034	0.53064375	0.530644
GO_BP	GO:0007096~regulation of exit from mitosis	2	1.61	0.035955	CDKN1C, CDC14A	111	6	18082	54.3003003	1	1	0.997175
GO_MF	GO:0008146~sulfotransferase activity	3	2.42	0.039832	HS3ST3A1, CHST1, HS3ST6	105	53	17446	9.404851752	0.999778221	0.54967501	0.549675
GO_BP	GO:0061469~regulation of type B pancreatic cell proliferation	2	1.61	0.041821	NR4A1, NR4A3	111	7	18082	46.54311454	1	1	0.997175
GO_BP	GO:0031100~organ regeneration	3	2.42	0.045651	NR4A3, ANXA3, ADM	111	56	18082	8.726833977	1	1	0.997175
GO_MF	GO:0046977~TAP binding	2	1.61	0.046716	H2-Q6, H2-Q7	105	8	17446	41.53809524	0.999949994	0.56883533	0.568835
GO_MF	GO:0038191~neuropilin binding	2	1.61	0.046716	SEMA3G, SEMA3E	105	8	17446	41.53809524	0.999949994	0.56883533	0.568835
GO_BP	GO:0030154~cell differentiation	10	8.06	0.048235	ROBO2, NTNG2, ZFP423, PRM1, WIPF3, SPEG, SEMA3E, THSD7A, TDRD5, GAS7	111	780	18082	2.088473088	1	1	0.997175
KEGG	mmu04921:Oxytocin signaling pathway	4	3.23	0.050896	NPR1, KCNJ12, ITPR3, ADCY1	44	150	7691	4.661212121	0.995146901	0.92392082	0.923921
GO_MF	GO:0005198~structural molecule activity	5	4.03	0.052727	CLDN5, ANXA1, VIM, SYNC, NES	105	236	17446	3.520177563	0.999986501	0.60636605	0.606366
GO_BP	GO:0060539~diaphragm development	2	1.61	0.053449	WT1, TCF21	111	9	18082	36.2002002	1	1	0.997175

GO_BP	GO:0060541~respiratory system development	2	1.61	0.053449	TCF21, SPEG	111	9	18082	36.2002002	1	1	0.997175
GO_BP	GO:0032836~glomerular basement membrane development	2	1.61	0.053449	NPHS1, WT1	111	9	18082	36.2002002	1	1	0.997175
GO_BP	GO:0043065~positive regulation of apoptotic process	6	4.84	0.053866	NR4A1, ANXA1, GADD45A, WT1, ADM, NUPR1	111	335	18082	2.917628076	1	1	0.997175
GO_BP	GO:0030036~actin cytoskeleton organization	4	3.23	0.055784	EHD2, INF2, ABLIM3, CORO2B	111	142	18082	4.588757772	1	1	0.997175
KEGG	mmu04514:Cell adhesion molecules (CAMs)	4	3.23	0.061348	NTNG2, CLDN5, H2-Q6, H2-Q7	44	162	7691	4.315937149	0.998431538	0.92392082	0.923921
GO_BP	GO:0007204~positive regulation of cytosolic calcium ion concentration	4	3.23	0.061613	FZD2, C1QTNF1, ITPR3, ADM	111	148	18082	4.402727051	1	1	0.997175
GO_BP	GO:0007411~axon guidance	4	3.23	0.062611	ROBO2, NR4A3, FOXD1, PTPRO	111	149	18082	4.373178548	1	1	0.997175
GO_BP	GO:0030855~epithelial cell differentiation	3	2.42	0.062804	FZD2, WT1, TCF21	111	67	18082	7.29407019	1	1	0.997175
GO_BP	GO:0006351~transcription, DNA-templated	18	14.52	0.063341	FOXC2, ZFP423, FOXD2, FOXD1, RASL11A, TCF21, FOXL1, MAFA, LOXL2, NR4A1, NR4A3, MAFB, ABLIM3, WT1, E2F1, LMX1B, NUPR1, HOXC8	111	1885	18082	1.555552369	1	1	0.997175
KEGG	mmu05202:Transcriptional misregulation in cancer	4	3.23	0.064108	NR4A3, WT1, PLAT, NUPR1	44	165	7691	4.237465565	0.998838474	0.92392082	0.923921
KEGG	mmu05166:HTLV-I infection	5	4.03	0.067124	FZD2, H2-Q6, H2-Q7, E2F1, ADCY1	44	276	7691	3.166584321	0.999164328	0.92392082	0.923921
GO_MF	GO:0030881~beta-2-microglobulin binding	2	1.61	0.074809	H2-Q6, H2-Q7	105	13	17446	25.56190476	0.999999898	0.791808	0.791808
GO_BP	GO:0007507~heart development	5	4.03	0.075143	ROBO2, FOXC2, WT1, ADM, FOXL1	111	261	18082	3.120706914	1	1	0.997175
GO_MF	GO:0042802~identical protein binding	8	6.45	0.07977	ROBO2, CLDN5, FOXC2, HSPB8, APLP1, VIM, SNCAIP, ACPP	105	625	17446	2.126750476	0.999999966	0.791808	0.791808
GO_MF	GO:0042608~T cell receptor binding	2	1.61	0.080328	H2-Q6, H2-Q7	105	14	17446	23.73605442	0.99999997	0.791808	0.791808
KEGG	mmu00533:Glycosaminoglycan biosynthesis - keratan sulfate	2	1.61	0.080731	CHST1, ST3GAL1	44	15	7691	23.30606061	0.999813298	0.92392082	0.923921
KEGG	mmu00604:Glycosphingolipid biosynthesis - ganglio series	2	1.61	0.080731	ST3GAL1, ST6GALNAC6	44	15	7691	23.30606061	0.999813298	0.92392082	0.923921
GO_BP	GO:0042417~dopamine metabolic process	2	1.61	0.081909	NPR1, SNCAIP	111	14	18082	23.27155727	1	1	0.997175
GO_BP	GO:0007050~cell cycle arrest	3	2.42	0.087199	CDKN1C, GADD45A, VASH1	111	81	18082	6.0333667	1	1	0.997175
GO_BP	GO:0045197~establishment or maintenance of epithelial cell apical/basal polarity	2	1.61	0.087498	CRB2, MTCL1	111	15	18082	21.72012012	1	1	0.997175
GO_BP	GO:0007588~excretion	2	1.61	0.087498	KIRREL, NPHS2	111	15	18082	21.72012012	1	1	0.997175
GO_MF	GO:0030695~GTPase regulator activity	2	1.61	0.09127	RHPN1, GPSM3	105	16	17446	20.76904762	0.999999998	0.85876322	0.858763
GO_BP	GO:0006171~cAMP biosynthetic process	2	1.61	0.093054	ADM, ADCY1	111	16	18082	20.36261261	1	1	0.997175
GO_BP	GO:0014002~astrocyte development	2	1.61	0.098576	TSPAN2, VIM	111	17	18082	19.16481187	1	1	0.997175

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Id Enrichme	Bonferroni	Benjamini	FDR
GO_MF	GO:0005515~protein binding	213	29.38	5.40E-11	TDRKH, SPARC, SCX, RASSF2, ALCAM, DPYSL2, RAVR2, DAG1, SOX8, MYOZ1, EPHB1, SOX5, ANKS1B, CDON, PRKCI, RBFOX2, ACTN1, UNC5C, ACTN4, CD2AP, FNDC5, CLDN5, MYL6, MYL7, MAP1B, MAP1A, ASTN2, NBL1, OPTN, EPHA2, SPTBN5, NECAB3, STXBP1, IQGAP1, EPB41L5, FLRT2, MAP4, CHST14, PAG1, ZBTB7C, NTNG2, JUN, DTNA, FZD2, GADD45B, GADD45A, PBX2, PARVA, GDF5, VASN, EHD2, COL1A2, EHD4, FAT1, CDKN1C, BTG3, BTG2, HIP1, SLC44A2, SETD7, PTPRO, WFIKKN2, BHLHE41, OTUD7B, TCF21, STON2, SH3PXD2A, TMSB4X, PRX, ANKRD1, SH3BGRL2, RSPO1, LDLRAP1, TEAD4, ANXA1, ANXA2, PRMT2, TNFRSF12A, RRAS2, GAB2, CBFA2T3, SYN1, MDFIC, GAS1, PLEKHO1, TLR7, GLCCI1, MAPT, MYZAP, SYNC, MICU1, CRYAB, VAMP2, ARF6, PELI3, NKD1, ARNTL, RELB, ADCY5, PAK1, ARVCF, PLAGL1, DYNC1I1, GSN, SLC31A2, PLEKHA2, NDE1, WTIP, MPP5, VEGFA, TJP1, RIT1, WT1, APBA1, FRYL, RAB3B, STEAP3, NCF2, RASL11A, DACH1, KIF5B, SIRPA, DENND5A, LARGE1, BORCS6, NSF, CHRN1, KIRREL2, APLP1, MAGI2, ARMCX3, MYCL, FRMD6, ELMO1, FKBP7, AMPH, NUPR1, UTRN, AJUBA, HPCA, HTRA1, ITPR3, NREP, KLC1, AGER, NPAS2, SLC9A3R2, EFN1, NDN, SMYD1, KIF3C, ASIC2, SRGAP2, SRGAP1, PDZD7, WNT4, KIRREL, MLKL, ATP8B2, SYT9, SMAD6, TJAP1, ARHGAP33, NR4A2, GNAO1, NR4A1, MAFB, SERPINB6A, AMOTL2, PLXNB1, MAFK, NES, NFE2L1, FGFR2, FGFR1, BMPR1A, ITGB1, GPSM2, HSPB8, ARRB1, SYNE1, PPP1R9B, ADAMTS4, PDE4B, EFHD2, PMEPA1, LRRFIP1, PRKG1, ARHGEF12, KSR1, ITGA3, SGIP1, NGB, TGFBR3, CRY1, MYH9, ZFP423, NXN, SRF, NOD1, UACA, PARD6B, E2F1, FYN, NCAM1, LINGO1, NTRK3, PTPN12, MYO1D, TSPAN13, NPHS1, NPHS2, VIM	608	4092	17446	1.493607	3.86E-08	3.86E-08	3.76E-08
GO_BP	GO:0030036~actin cytoskeleton organization	24	3.31	1.06E-09	CTTNBP2, SRF, ARHGEF17, TMOD3, SHROOM3, ARHGEF18, PARVA, CORO2B, PPP1R9B, EHD2, ABR, EPB41L5, PAK1, INF2, FMNL2, ABLIM3, PALLD, DAAM2, MOB2, TMSB4X, DLC1, SPECC1L, ELMO1, TMSB10	642	142	18082	4.7603	2.86E-06	2.86E-06	2.83E-06
GO_MF	GO:0051015~actin filament binding	22	3.03	5.59E-09	SPTBN5, HIP1, ACTN1, WIPF3, TPM1, SHROOM3, ACTN4, RCS1D1, IQGAP2, CORO2B, SPTB, AIF1L, PPP1R9B, SYNE1, MYO1D, MYO1E, MYH9, UTRN, AJUBA, CTNNAL1, PKNOX2, GAS7	608	132	17446	4.782346	3.99E-06	2.00E-06	1.95E-06
GO_MF	GO:0003779~actin binding	36	4.97	8.94E-09	ITGB1, PLEKHH2, HIP1, WIPF3, HPCA, ABRA, MYLK, SYNE1, PPP1R9B, ABLIM3, MPRIP, TMSB4X, DAG1, MYOZ1, SYNPO, GSN, NEBL, ACTN1, TMOD3, TPM1, SHROOM3, PARVA, ACTN4, SPTB, CORO2B, AIF1L, MYO1D, MYO1E, INF2, FMNL2, PALLD, DAAM2, MAP1B, MAP1A, MYH9, UTRN	608	338	17446	3.056174	6.38E-06	2.13E-06	2.07E-06
KEGG	mmu04360:Axon guidance	21	2.90	1.71E-08	ROBO2, SEMA5A, ITGB1, NTNG2, SEMA6C, ARHGEF12, EPHA6, SEMA3G, UNC5C, SEMA3E, EFN1, PAK1, ABLIM3, DPYSL2, NCK2, FYN, PLXNB1, SRGAP2, SRGAP1, EPHB1, EPHA2	270	129	7691	4.637123	3.45E-06	3.47E-06	3.14E-06
GO_BP	GO:0016477~cell migration	24	3.31	3.13E-07	ITGB1, PRKCI, ENPEP, FOXC1, CD151, FNDC3B, EMP2, GAB2, VEGFA, PPP1R9B, CD2AP, PTK7, PODXL, BAMBI, PALLD, SPECC1L, ELMO1, NCK2, FAT1, ELMO2, SIRPA, SRGAP1, TNS3, EPHA2	642	191	18082	3.539071	8.48E-04	4.24E-04	4.20E-04
GO_BP	GO:0001657~ureteric bud development	12	1.66	6.97E-07	ROBO2, FOXC2, FOXC1, SDC4, GDNF, WT1, TCF21, RARB, NPNT, SMAD6, FGFR2, FGFR1	642	48	18082	7.041277	0.001886	6.29E-04	6.23E-04
GO_BP	GO:0072015~glomerular visceral epithelial cell development	7	0.97	1.49E-06	MYO1E, NPHS1, PODXL, WT1, MAGI2, IQGAP1, GLCCI1	642	12	18082	16.42965	0.004031	0.001009	0.001
GO_BP	GO:0007155~cell adhesion	39	5.38	4.59E-06	ITGB1, COL18A1, TENM3, ITGB5, AMIGO2, NEDD9, CYR61, DPP4, ARVCF, ALCAM, FLRT2, PODXL, EMILIN1, NCAM1, SVBP, CTNNAL1, EPHB1, CDON, CADM4, TNFRSF12A, LAMB2, ITGA3, ITGA2, APLP1, EMP2, PARVA, ATP1B2, NPNT, SULF1, BCAM, NPHS1, PTK7, SPECC1L, COL4A3, TYRO3, MYH9, NECTIN4, AJUBA, EPHA2	642	485	18082	2.264823	0.012353	0.002485	0.002462
GO_BP	GO:0008360~regulation of cell shape	18	2.48	8.73E-06	ANXA1, WIPF3, TPM1, SHROOM3, ARHGEF18, SEMA3E, PARVA, MYL12A, VEGFA, BAMBI, DLC1, S100A13, MYH9, PLEKHO1, FYN, PLXNB1, CDC42SE2, GAS7	642	139	18082	3.64728	0.023356	0.003937	0.003901
GO_MF	GO:0005543~phospholipid binding	14	1.93	1.05E-05	PRKCI, HIP1, ANXA1, SGIP1, PLEKHA2, MYOF, AGAP1, SPTB, PLA2G7, ARHGAP44, MAP1B, PSD3, AMPH, VAMP2	608	88	17446	4.564967	0.007492	0.00188	0.001833
GO_BP	GO:0007399~nervous system development	32	4.41	1.32E-05	SEMA5A, ROBO2, ZFP423, ZC4H2, SEMA3E, GDPD5, PPP1R9B, EFN1, DCDC2A, DPYSL2, ATOH8, SRGAP2, EPHB1, SEMA6C, NTNG2, SRRM4, NDE1, NTRK3, MAGI2, CABLES1, FOS, VEGFA, NR4A2, GDNF, MAP1B, KCTD11, MAFK, NES, NBL1, ARF6, BMPR1A, GAS7	642	377	18082	2.390672	0.035007	0.005089	0.005042
GO_BP	GO:0001666~response to hypoxia	21	2.90	1.67E-05	PRMT2, SRF, ITGA2, IL18, PLOD2, PLAT, ADM, ACTN4, WTIP, AGER, CBFA2T3, VEGFA, FOSL2, LOXL2, DPP4, NR4A2, TGFBR3, PAK1, UCP2, AJUBA, CRYAB	642	192	18082	3.080559	0.044242	0.005654	0.005602
GO_BP	GO:0030336~negative regulation of cell migration	15	2.07	2.24E-05	KANK1, SRF, MAGI2, TPM1, SULF1, AGER, ABR, DACH1, RRAS, DLC1, DAG1, SRGAP2, SRGAP1, RECK, WNT4	642	106	18082	3.985629	0.058834	0.006735	0.006672
GO_MF	GO:0030165~PDZ domain binding	15	2.07	5.06E-05	NSF, MPP3, DOCK4, FZD2, DTNA, KCNJ12, PLEKHA2, MAGI2, ARHGEF16, CRIM1, SYNJ2, NKD1, SLC9A3R2, TGFBR3, APBA1	608	116	17446	3.710441	0.035466	0.007222	0.00704
KEGG	mmu04810:Regulation of actin cytoskeleton	21	2.90	5.15E-05	ITGB1, ARHGEF12, GSN, ITGB5, ITGA3, ITGA2, ACTN1, F2R, RRAS2, ACTN4, IQGAP1, IQGAP2, MYL12A, MYLK3, MYLK, PAK1, MYL7, RRAS, TMSB4X, FGFR2, FGFR1	270	213	7691	2.808399	0.010345	0.005225	0.004736
GO_BP	GO:0007275~multicellular organism development	62	8.55	5.69E-05	SEMA5A, ROBO2, COL18A1, ZFP521, WIPF3, TCF23, TNFAIP2, SCX, PPP1R9B, DACH1, DPYSL2, CREB3L1, QK, ZFP37, SEMA6C, PRKCI, PRM1, FOXD1, TNFRSF12A, SHROOM3, UNC5C, SHISA3, NPNT, DISP1, SMO, KCTD11, LMX1B, KCTD15, GAS7, FOXC2, ZFP423, CASZ1, PKDCC, NXN, ZC4H2, SRF, SEMA3E, NKD1, EFN1, ARVCF, FLRT2, WIF1, ATOH8, HIVEP1, HOXC5, HOXC4, FYN, HIVEP2, HOXC8, WNT4, HOXC6, NTNG2, FZD2, GADD45B, NDE1, NTRK3, EYA4, TDRD5, ARHGAP24, VEGFA, NPHS1, NES	642	1029	18082	1.697023	0.142715	0.01415	0.014019
GO_BP	GO:0001822~kidney development	16	2.21	5.80E-05	CDKN1C, ROBO2, FOXC2, FOXC1, FOXD1, TCF21, SULF1, VEGFA, MYO1E, WT1, ALDH1A2, MMP17, NEK1, LZTS2, TNS2, WNT4	642	130	18082	3.466475	0.14526	0.01415	0.014019
GO_BP	GO:0007179~transforming growth factor beta receptor signaling pathway	12	1.66	6.35E-05	TGFBR3, ITGB1, CLDN5, JUN, COL1A2, ITGB5, GDNF, BAMBI, WFIKKN2, FOS, DUSP15, SMAD6	642	75	18082	4.506417	0.157875	0.01415	0.014019
GO_BP	GO:0090004~positive regulation of establishment of protein localization to plasma membrane	8	1.10	6.80E-05	ITGB1, PRKCI, ITGA3, KIF5B, ARHGEF16, ARF6, PPP1R9B, EPHA2	642	30	18082	7.510696	0.16808	0.01415	0.014019
GO_BP	GO:0007411~axon guidance	17	2.34	7.97E-05	ROBO2, SEMA5A, SEMA6C, FOXD1, LAMB2, PTPRO, UNC5C, EFN1, ALCAM, NR4A3, FLRT2, DPYSL2, KIF5B, GAS1, NCAM1, FYN, EPHB1	642	149	18082	3.213469	0.194024	0.015401	0.015259
GO_MF	GO:0004714~transmembrane receptor protein tyrosine kinase activity	10	1.38	9.24E-05	EPHA6, PTK7, AXL, NTRK3, TYRO3, MERTK, EPHB1, FGFR2, FGFR1, EPHA2	608	54	17446	5.313718	0.063824	0.010991	0.010714
KEGG	mmu04510:Focal adhesion	20	2.76	1.08E-04	ITGB1, JUN, ITGB5, LAMB2, ITGA3, ITGA2, ACTN1, PARVA, ACTN4, MYL12A, MYLK3, VEGFA, MYLK, PAK1, MYL7, COL1A2, COL4A3, COL4A6, COL4A5, FYN	270	207	7691	2.752192	0.021491	0.007277	0.006596
GO_BP	GO:0035914~skeletal muscle cell differentiation	10	1.38	1.24E-04	NR4A1, BTG2, PLAGL1, ANKRD1, SCX, SMYD1, SOX8, NUPR1, FOS, ATF3	642	55	18082	5.120929	0.284177	0.021124	0.020929
GO_BP	GO:0031175~neuron projection development	16	2.21	1.25E-04	ITGB1, LINGO1, BTG2, LAMB2, SRF, NGB, GDPD5, AGER, GNAO1, GDNF, PALLD, RAB13, NCAM1, MAP4, FRYL, FGFR1	642	139	18082	3.242027	0.286897	0.021124	0.020929
GO_BP	GO:0032836~glomerular basement membrane development	5	0.69	1.71E-04	MYO1E, NPHS1, WT1, COL4A3, SULF1	642	9	18082	15.64728	0.370425	0.025694	0.025457
GO_BP	GO:0032835~glomerulus development	5	0.69	1.71E-04	ENPEP, WT1, PTPRO, TCF21, PLCE1	642	9	18082	15.64728	0.370425	0.025694	0.025457

GO_MF	GO:0005178~integrin binding	13	1.79	1.82E-04	ITGB1, CD151, ITGB5, LAMB2, ITGA3, ITGA2, ACTN1, EMP2, NPNT, CYR61, COL4A3, TIMP2, UTRN	608	100	17446	3.73023	0.121602	0.015298	0.014913
GO_MF	GO:0015631~tubulin binding	9	1.24	1.94E-04	SGIP1, DAG1, FYN, MAPT, TPPP, MAP4, KLC1, EML1, EML2	608	47	17446	5.494611	0.129586	0.015298	0.014913
GO_MF	GO:0017048~Rho GTPase binding	8	1.10	2.07E-04	DOCK11, FMNL2, INF2, DAAM2, ARHGEF16, IQGAP1, IQGAP2, SRGAP1	608	36	17446	6.376462	0.137134	0.015298	0.014913
GO_BP	GO:0016525~negative regulation of angiogenesis	11	1.52	2.16E-04	FOXC1, SPARC, CD59A, STAT1, PDE3B, COL4A3, LIF, SEMA3E, VASH1, SULF1, EPHA2	642	72	18082	4.303003	0.442389	0.030727	0.030443
GO_MF	GO:0043236~laminin binding	7	0.97	2.20E-04	ITGB1, BCAM, ITGA3, PLEKHA2, GPC1, ITGA2, DAG1	608	26	17446	7.725329	0.145194	0.015298	0.014913
KEGG	mmu04512:ECM-receptor interaction	12	1.66	2.29E-04	ITGB1, COL1A2, ITGB5, SDC4, ITGA3, LAMB2, ITGA2, COL4A3, DAG1, COL4A6, COL4A5, NPNT	270	88	7691	3.884343	0.04514	0.011604	0.010517
GO_MF	GO:0017124~SH3 domain binding	14	1.93	2.36E-04	DOCK4, CTTNBP2, SGIP1, WIPF3, SYNJ2, PTPN12, CD2AP, SH3BP5L, ELMO1, ELMO2, SH3BGRL2, SIRPA, QK, MAPT	608	118	17446	3.404382	0.154902	0.015298	0.014913
GO_BP	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	58	8.00	2.41E-04	GLP1R, CRTC1, TCF21, SCX, ARRB1, CYR61, ABRA, CREB3L1, NCK2, SOX8, SOX5, CDON, TEAD4, FOXD1, IL18, ARID5A, FOS, ARMCX3, SMO, ELF4, RARB, LMX1B, MAML3, ATF3, FOXC2, FOXC1, RNASEL, SRF, NPAS2, DDN, MLLT6, ARNTL, RELB, ABLIM3, PLAGL1, E2F1, NDN, ZBTB7C, ZFP462, JUN, STAT1, LIF, PBX2, MAFA, VEGFA, FOSL2, NR4A2, NR4A1, MAFB, NR4A3, GDNF, WT1, FOSB, LPIN2, NFE2L1, FGFR2, BMPR1A, FGFR1	642	995	18082	1.641785	0.478967	0.032581	0.03228
GO_BP	GO:0030154~cell differentiation	48	6.62	2.82E-04	SEMA5A, ROBO2, TDRKH, ZFP423, HIP1, PKDCC, TENM3, ZFP521, NXN, WIPF3, TCF23, TNFAIP2, SCX, ILDR2, SEMA3E, NKD1, PPP1R9B, EFN1, DPYSL2, ATOH8, SPEG, QK, THSD7A, ZFP37, WNT4, SEMA6C, NTNG2, SRRM4, PRM1, TNFRSF12A, GADD45B, NDE1, NTRK3, EYA4, NPNT, TDRD5, CBFA2T3, ARHGAP24, VEGFA, SYT17, ELF4, AXL, PMP22, KCTD11, ARF6, BMPR1A, EPHA2, GAS7	642	780	18082	1.733237	0.533762	0.036318	0.035982
GO_BP	GO:0007264~small GTPase mediated signal transduction	21	2.90	2.96E-04	RAB3B, BCAR3, GM266, DOCK5, DOCK4, RASL11A, RRAS2, AGAP1, ARHGEF18, ARHGAP33, ARL4C, DOCK11, ARL4D, RAB30, RIT1, RRAS, RAB13, PLCE1, RAB7B, RAB6B, ARF6	642	236	18082	2.506217	0.551359	0.036414	0.036078
GO_MF	GO:0098641~cadherin binding involved in cell-cell adhesion	23	3.17	3.19E-04	ITGB1, ANXA1, ANXA2, AHNAC, STAT1, TMOD3, ARHGEF16, PARVA, IQGAP1, VASN, CD2AP, FAM129B, SLC9A3R2, TJP1, FMNL2, EHD4, MPRIP, KIF5B, EFHD2, HIST2H3C2, MYH9, LRRFIP1, EPHA2	608	279	17446	2.365462	0.203792	0.018988	0.018509
GO_BP	GO:0001525~angiogenesis	21	2.90	3.49E-04	COL18A1, ENPEP, JUN, TNFRSF12A, ANXA2, PDE3B, TNFAIP2, IL18, TGFA, SEMA3E, PARVA, VASH1, ARHGAP24, VEGFA, CCDC80, MYH9, THSD7A, EPHB1, FGFR2, FGFR1, EPHA2	642	239	18082	2.474759	0.61141	0.041075	0.040695
GO_MF	GO:0005085~guanyl-nucleotide exchange factor activity	16	2.21	3.64E-04	BCAR3, DOCK5, ARHGEF10, DOCK4, ARHGEF12, PLEKHG2, ARHGEF17, ARHGEF16, ARHGEF18, DOCK11, ABR, PSD3, ELMO1, PLCE1, DENND5A, ARFGEF3	608	156	17446	2.942982	0.228691	0.01982	0.01932
GO_BP	GO:0030199~collagen fibril organization	8	1.10	3.90E-04	FOXC2, FOXC1, COL1A2, ANXA2, P3H1, SCX, LMX1B, LOXL2	642	39	18082	5.777458	0.65158	0.042955	0.042558
GO_BP	GO:0043065~positive regulation of apoptotic process	26	3.59	3.97E-04	ITGB1, MTCH1, STEAP3, ADM, AGER, UACA, CYR61, RASSF2, ADAMTSL4, ANKRD1, UNC13B, JUN, ANXA1, TNFRSF12A, GADD45B, PRMT2, GADD45A, NTRK3, IL18, UNC5C, NR4A1, LATS2, WT1, ALDH1A2, RARB, NUPR1	642	335	18082	2.185949	0.658529	0.042955	0.042558
GO_MF	GO:0005509~calcium ion binding	43	5.93	4.14E-04	CRB2, NECAB3, SPARC, PROS1, HPCA, ITPR3, MYL12A, NKD1, MAN1A2, EFHD2, DAG1, S100A13, SVEP1, RHBDL3, PAMR1, S100A11, C1RA, GSN, ANXA1, ANXA2, ANXA3, ACTN1, ACTN4, NPNT, SULF1, SYT9, MCC, DLK2, AIF1L, SYT17, NELL2, EHD2, MYL6, MYL7, EHD4, MMP17, MYL3, FAT1, FKBP7, MICU1, ASTN2, MEGF8, CALM2	608	699	17446	1.765158	0.255728	0.01982	0.01932
GO_MF	GO:0043565~sequence-specific DNA binding	40	5.52	4.16E-04	FOXC2, FOXC1, ZFP423, SRF, SCX, ARNTL, FOXS1, ZFP13, GBX1, CREB3L1, HOXC5, E2F1, HOXC4, SOX8, HIVEP2, HOXC8, HOXC6, PKNOX2, TEAD4, FOXD2, JUN, FOXD1, STAT1, PBX2, FOS, FOXL1, MAFA, FOSL2, NR4A2, NR4A1, NR4A3, MAFB, WT1, ELF4, FOSB, RARB, MAFK, LMX1B, ATF3, NFE2L1	608	633	17446	1.813212	0.257222	0.01982	0.01932
GO_MF	GO:0008373~sialyltransferase activity	6	0.83	5.03E-04	ST6GAL1, ST3GAL6, ST6GALNAC3, ST3GAL1, ST6GALNAC6, ST3GAL3	608	20	17446	8.608224	0.302018	0.022467	0.021901
KEGG	mmu04024:cAMP signaling pathway	18	2.48	5.13E-04	GLP1R, JUN, NPR1, F2R, PDE3B, RRAS2, FOS, ADCY1, ATP1B2, PLD1, ADCY5, PAK1, RRAS, CREB3L1, PDE4B, PDE3A, PLCE1, CALM2	270	197	7691	2.602707	0.098487	0.020834	0.018884
GO_BP	GO:0043524~negative regulation of neuron apoptotic process	16	2.21	5.80E-04	GLP1R, BTG2, PRKCI, JUN, STXB1P1, F2R, GDF5, VEGFA, NR4A2, NR4A3, GDNF, AXL, TYRO3, FYN, NES, OPTN	642	160	18082	2.816511	0.791742	0.060305	0.059748
KEGG	mmu04611:Platelet activation	14	1.93	6.37E-04	ITGB1, PRKCI, ARHGEF12, ITGA2, F2R, ITPR3, ADCY1, MYL12A, MYLK3, ADCY5, MYLK, COL1A2, FYN, PRKG1	270	131	7691	3.044218	0.120704	0.02092	0.018962
GO_BP	GO:0007015~actin filament organization	11	1.52	6.91E-04	PRKCI, SRF, TMSB4X, TMOD3, ACTN1, NCK2, FAT1, SIRPA, EMP2, TMSB10, PPP1R9B	642	83	18082	3.732725	0.845998	0.069239	0.068599
KEGG	mmu05205:Proteoglycans in cancer	18	2.48	7.21E-04	ITGB1, ARHGEF12, FZD2, ITGB5, SDC4, ITGA2, RRAS2, ITPR3, IQGAP1, VEGFA, PAK1, COL1A2, RRAS, SMO, GPC1, PLCE1, FGFR1, WNT4	270	203	7691	2.52578	0.135646	0.02092	0.018962
GO_BP	GO:0051271~negative regulation of cellular component movement	4	0.55	8.18E-04	TGFBR3, TMOD3, ACTN1, ACTN4	642	6	18082	18.77674	0.890929	0.079072	0.078342
GO_BP	GO:0019933~cAMP-mediated signaling	7	0.97	9.48E-04	GLP1R, KSR1, NPR3, PDE3A, ADM, ADCY1, ADCY5	642	33	18082	5.974417	0.923144	0.088402	0.087585
GO_MF	GO:0005518~collagen binding	9	1.24	9.51E-04	DPP4, ITGB1, MRC2, PAK1, SPARC, C1QTNF1, ITGA3, ITGA2, MAP1A	608	59	17446	4.377063	0.493025	0.039939	0.038933
GO_MF	GO:0005089~Rho guanyl-nucleotide exchange factor activity	10	1.38	0.001037	DOCK11, ARHGEF10, ABR, PLEKHG1, ARHGEF12, PLEKHG2, ARHGEF26, ARHGEF17, ARHGEF16, ARHGEF18	608	74	17446	3.877578	0.523199	0.041126	0.040089
GO_BP	GO:0045666~positive regulation of neuron differentiation	12	1.66	0.001058	SOCS2, ITGB1, MAP1B, TIMP2, RARB, BNIP2, KCTD11, GDPD5, GDF5, NBL1, CDON, FGFR1	642	103	18082	3.281372	0.943049	0.095433	0.094551
KEGG	mmu04530:Tight junction	11	1.52	0.001123	TJP1, CLDN5, PRKCI, PARD6B, ACTN1, RAB13, MYH9, ACTN4, MPP5, MYL12A, TJAP1	270	90	7691	3.481523	0.203056	0.028496	0.025829
KEGG	mmu05032:Morphine addiction	11	1.52	0.001447	GNAO1, GABRB1, PDE10A, GRK5, GABRA4, PDE3B, PDE4B, PDE3A, ARRB1, ADCY1, ADCY5	270	93	7691	3.369215	0.253591	0.032635	0.029581
GO_MF	GO:0005200~structural constituent of cytoskeleton	10	1.38	0.001513	EPB41L5, TUBB2B, TUBB2A, FRMD6, TUBA1A, TPM1, VIM, SPTB, MYOM2, LOR	608	78	17446	3.678728	0.660849	0.056868	0.055434
GO_BP	GO:0001764~neuron migration	13	1.79	0.00152	ITGA3, NDE1, NTRK3, SRF, NR4A2, TUBB2B, DCDC2A, AXL, NDN, FYN, MAPT, LMX1B, PRKG1	642	124	18082	2.952794	0.983689	0.123838	0.122693
GO_BP	GO:0030513~positive regulation of BMP signaling pathway	7	0.97	0.001523	TGFBR3, CRB2, ZFP423, FOXD1, SULF1, GDF5, CYR61	642	36	18082	5.476549	0.983837	0.123838	0.122693
GO_BP	GO:0016337~single organismal cell-cell adhesion	12	1.66	0.001562	CLDN5, ARVCF, KIRREL, KIRREL2, CCDC80, SRF, FAT1, MYH9, NECTIN4, CYR61, CDON, CD2AP	642	108	18082	3.129457	0.985449	0.123838	0.122693
GO_BP	GO:0035023~regulation of Rho protein signal transduction	10	1.38	0.001572	ARHGEF10, ABR, PLEKHG1, ARHGEF12, PLEKHG2, ARHGEF26, DLC1, ARHGEF17, ARHGEF16, ARHGEF18	642	77	18082	3.657806	0.985832	0.123838	0.122693
GO_BP	GO:0001755~neural crest cell migration	8	1.10	0.001602	SEMA5A, SEMA6C, EFN1, SMO, GDNF, SEMA3G, SOX8, SEMA3E	642	49	18082	4.598385	0.986956	0.123838	0.122693
GO_BP	GO:0002053~positive regulation of mesenchymal cell proliferation	7	0.97	0.001764	SMO, STAT1, GAS1, FGFR2, VEGFA, FGFR1, BMPR1A	642	37	18082	5.328534	0.991593	0.132576	0.13135
GO_MF	GO:0017134~fibroblast growth factor binding	6	0.83	0.001798	TGFBR3, FGFBP1, GPC1, S100A13, FGFR2, FGFR1	608	26	17446	6.621711	0.723257	0.064176	0.062558
GO_BP	GO:0008284~positive regulation of cell proliferation	34	4.69	0.001876	PTGER4, ITGB1, GLP1R, COL18A1, SCX, TGFA, IL6RA, ADM, DPP4, PAK1, GRK5, S100A13, TNS3, JUN, FGFBP1, STAT1, NTRK3, IL34, F2R, LIF, EMP2, GAB2, VEGFA, TGFBR3, SMO, GDNF, BAMBI, ALDH1A2, RARB, GAS1, ATF3, OPTN, FGFR2, FGFR1	642	542	18082	1.766815	0.993786	0.135411	0.134159

GO_BP	GO:0048675~axon extension	6	0.83	0.001952	SEMA5A, ITGB1, MAP1B, NDN, PLXNB1, MAPT	642	26	18082	6.499641	0.994949	0.135411	0.134159
GO_BP	GO:0032967~positive regulation of collagen biosynthetic process	6	0.83	0.001952	CREB3L1, ITGA2, F2R, IL18, SCX, WNT4	642	26	18082	6.499641	0.994949	0.135411	0.134159
GO_BP	GO:0007528~neuromuscular junction development	7	0.97	0.002033	UNC13B, PAK1, LAMB2, ZC4H2, COL4A5, UTRN, FGFR2	642	38	18082	5.18831	0.995946	0.135749	0.134495
GO_BP	GO:0048661~positive regulation of smooth muscle cell proliferation	10	1.38	0.002058	JUN, NR4A3, STAT1, ITGA2, IL18, IL6RA, SULF1, AGER, FGFR2, VEGFA	642	80	18082	3.520639	0.996203	0.135749	0.134495
GO_BP	GO:0034097~response to cytokine	10	1.38	0.002244	GNAO1, JUN, SPARC, STAT1, ALDH1A2, SRF, TIMP2, IL6RA, FOS, RELB	642	81	18082	3.477174	0.997708	0.143274	0.14195
GO_BP	GO:0006909~phagocytosis	8	1.10	0.002278	ANXA1, ANXA3, AXL, ELMO1, ELMO2, MERTK, GULP1, CDC42SE2	642	52	18082	4.333094	0.997909	0.143274	0.14195
GO_BP	GO:0030335~positive regulation of cell migration	17	2.34	0.002437	ITGB1, SEMA6C, COL18A1, NTRK3, F2R, SEMA3G, RRAS2, SEMA3E, ACTN4, PLD1, AGER, CYR61, VEGFA, MYLK, PAK1, PODXL, MYADM	642	203	18082	2.358654	0.998643	0.149812	0.148427
GO_BP	GO:0055010~ventricular cardiac muscle tissue morphogenesis	6	0.83	0.002751	TGFBR3, FOXC2, FOXC1, TPM1, MYL3, FGFR2	642	28	18082	6.035381	0.999422	0.165395	0.163866
GO_MF	GO:0001968~fibronectin binding	6	0.83	0.002978	ITGB1, CCDC80, SDC4, ITGA3, PLEKHA2, VEGFA	608	29	17446	5.936706	0.881119	0.10126	0.098707
GO_BP	GO:0009311~oligosaccharide metabolic process	5	0.69	0.003219	ST6GAL1, ST3GAL6, ST6GALNAC3, ST3GAL1, ST3GAL3	642	18	18082	7.823641	0.999838	0.181418	0.179741
GO_BP	GO:0021954~central nervous system neuron development	5	0.69	0.003219	LINGO1, GABRB1, BTG2, LMX1B, FGFR1	642	18	18082	7.823641	0.999838	0.181418	0.179741
GO_BP	GO:0001574~ganglioside biosynthetic process	5	0.69	0.003219	ST3GAL6, ST6GALNAC3, ST3GAL1, ST6GALNAC6, ST3GAL3	642	18	18082	7.823641	0.999838	0.181418	0.179741
KEGG	mmu04015:Rap1 signaling pathway	17	2.34	0.003308	ITGB1, PRKCI, DOCK4, MAGI2, F2R, ADCY1, SIPA1L2, ADCY5, VEGFA, GNAO1, PARD6B, RRAS, PLCE1, CALM2, FGFR2, FGFR1, EPHA2	270	214	7691	2.262842	0.487905	0.067144	0.06086
GO_MF	GO:0004713~protein tyrosine kinase activity	12	1.66	0.003323	EPHA6, PKDCC, AXL, NTRK3, TYRO3, NEK1, FYN, MERTK, EPHB1, FGFR2, FGFR1, EPHA2	608	121	17446	2.845694	0.90714	0.10785	0.105131
GO_BP	GO:0030900~forebrain development	10	1.38	0.003385	GNAO1, CNP, DLC1, NDE1, ALDH1A2, SRF, APLP1, E2F1, FYN, PRKG1	642	86	18082	3.275013	0.999896	0.186844	0.185117
GO_BP	GO:0051250~negative regulation of lymphocyte activation	3	0.41	0.003676	AXL, TYRO3, MERTK	642	3	18082	28.16511	0.999953	0.192097	0.190322
GO_BP	GO:0032387~negative regulation of intracellular transport	3	0.41	0.003676	MAP1B, MAPT, CRYAB	642	3	18082	28.16511	0.999953	0.192097	0.190322
GO_BP	GO:0010976~positive regulation of neuron projection development	13	1.79	0.003721	ITGB1, PRKCI, TENM3, ITGA3, MAGI2, LIF, PTK7, MOB2, ANKRD1, QK, FYN, KIF3C, FGFR1	642	138	18082	2.653235	0.999958	0.192097	0.190322
GO_BP	GO:0001937~negative regulation of endothelial cell proliferation	6	0.83	0.003764	SPARC, STAT1, ATOH8, VASH1, SULF1, AGER	642	30	18082	5.633022	0.999963	0.192097	0.190322
GO_MF	GO:0046982~protein heterodimerization activity	31	4.28	0.004109	ITGB1, SPTBN5, ZFP423, HIP1, TENM3, H2-Q6, H2-Q7, BHLHE41, H2-Q4, SCX, ADCY5, ARNTL, SOX8, PDZD7, SOX5, JUN, FZD2, ITGA3, ITGA2, INHBB, FOS, SPTB, VEGFA, DLK2, NR4A2, NR4A1, AXL, TYRO3, AMPH, MICU1, ATF3	608	514	17446	1.730577	0.947136	0.127565	0.124349
GO_BP	GO:0018279~protein N-linked glycosylation via asparagine	6	0.83	0.004359	ST6GAL1, ST3GAL6, ST6GALNAC3, ST3GAL1, ST6GALNAC6, ST3GAL3	642	31	18082	5.451311	0.999993	0.21327	0.211299
GO_BP	GO:0070372~regulation of ERK1 and ERK2 cascade	6	0.83	0.004359	TGFBR3, RRAS, EPHB1, CYR61, FGFR2, EPHA2	642	31	18082	5.451311	0.999993	0.21327	0.211299
GO_BP	GO:0032963~collagen metabolic process	4	0.55	0.004415	TGFBR3, P3H2, P3H1, TNS2	642	10	18082	11.26604	0.999994	0.21327	0.211299
GO_BP	GO:0016311~dephosphorylation	11	1.52	0.005348	DUSP10, DUSP3, PTPRO, PTPN21, PTPN12, SYNJ2, DUSP15, DUSP8, ACPP, PTPN14, CDC14A	642	109	18082	2.84235	1	0.253784	0.251439
GO_BP	GO:0051894~positive regulation of focal adhesion assembly	5	0.69	0.005788	EPB41L5, SDC4, IQGAP1, WNT4, VEGFA	642	21	18082	6.705978	1	0.257945	0.255561
GO_BP	GO:0032060~bleb assembly	4	0.55	0.005912	PMP22, EMP2, EMP3, MYLK	642	11	18082	10.24186	1	0.257945	0.255561
GO_BP	GO:0009100~glycoprotein metabolic process	4	0.55	0.005912	MAN1A2, PCSK6, ST6GALNAC3, ST6GALNAC6	642	11	18082	10.24186	1	0.257945	0.255561
GO_BP	GO:0048333~mesodermal cell differentiation	4	0.55	0.005912	ITGB1, ITGA3, ITGA2, FGFR2	642	11	18082	10.24186	1	0.257945	0.255561
GO_BP	GO:0032940~secretion by cell	4	0.55	0.005912	AXL, TYRO3, PCSK6, MERTK	642	11	18082	10.24186	1	0.257945	0.255561
GO_BP	GO:0032870~cellular response to hormone stimulus	7	0.97	0.006047	ROBO2, SOCS2, JUN, NCF2, IGF2BP2, FOSB, FOS	642	47	18082	4.194803	1	0.259643	0.257243
GO_MF	GO:0019904~protein domain specific binding	20	2.76	0.006156	ITGB1, PRKCI, GSN, ZFP521, ITGA3, NDE1, ACTN1, STXBP1, IQGAP1, GAB2, MPP5, TJP1, MYO1D, EHD2, EPB41L5, TUBA1A, NPHS1, MYH9, MAPT, CALM2	608	289	17446	1.985749	0.987831	0.159949	0.155916
GO_MF	GO:0004672~protein kinase activity	31	4.28	0.006502	RNASEL, PKDCC, MAST4, NPR1, MYLK3, MYLK, PPP1R9B, PAK1, RASSF2, GRK5, SPEG, NEK1, FYN, EPHB1, PRKG1, PRKCI, EPHA6, KSR1, MLKL, NTRK3, MERTK, LATS2, PTK7, AXL, STK26, TYRO3, TRIB2, FGFR2, BMPR1A, EPHA2, FGFR1	608	531	17446	1.675172	0.990513	0.159949	0.155916
KEGG	mmu04390:Hippo signaling pathway	13	1.79	0.006523	TEAD4, CRB2, PRKCI, FZD2, WTIP, MPP5, GDF5, PARD6B, FRMD6, LATS2, AJUBA, BMPR1A, WNT4	270	151	7691	2.452367	0.733369	0.115427	0.104624
GO_MF	GO:0008022~protein C-terminus binding	16	2.21	0.006541	NSF, SPTBN5, KSR1, NCF2, EML2, PPP1R9B, CD2AP, SLC9A3R2, TJP1, BCAM, AMPH, VIM, OPTN, VAMP2, SASH1, VGLL3	608	209	17446	2.196676	0.990773	0.159949	0.155916
GO_MF	GO:0008201~heparin binding	13	1.79	0.006567	APLP1, PCSK6, AGER, CYR61, VEGFA, NELL2, TGFBR3, CCDC80, ADAMTSL5, NCAM1, RSPO1, FGFR2, FGFR1	608	151	17446	2.470351	0.990943	0.159949	0.155916
GO_MF	GO:0001077~transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	19	2.62	0.006567	TEAD4, FOXC2, JUN, FOXD1, SRF, TCF21, FOS, MAFA, RELB, ARNTL, NR4A2, NR4A1, NR4A3, MAFB, ELF4, WT1, CREB3L1, NDN, FOSB	608	270	17446	2.019213	0.990945	0.159949	0.155916

GO_MF	GO:0004725~protein tyrosine phosphatase activity	10	1.38	0.006643	DUSP10, DUSP3, EYA4, PTPRO, PTPN21, PTPN12, DUSP15, DUSP8, PTPN14, CDC14A	608	97	17446	2.958152	0.991424	0.159949	0.155916
GO_BP	GO:0048286~lung alveolus development	7	0.97	0.006709	PKDCC, MAN1A2, LIF, TCF21, TNS3, FGFR2, VEGFA	642	48	18082	4.107412	1	0.273643	0.271114
GO_BP	GO:0045444~fat cell differentiation	9	1.24	0.006822	NR4A2, NR4A1, RNASEL, NR4A3, GRK5, INHBB, SOX8, SMAD6, METRNL	642	79	18082	3.208683	1	0.273643	0.271114
KEGG	mmu04145:Phagosome	14	1.93	0.006823	COLEC12, ITGB1, C1RA, ITGB5, NCF2, ITGA2, H2-Q6, H2-Q7, MRC2, TUBB2B, TUBB2A, TUBA1A, RAB7B, DYNC111	270	171	7691	2.33212	0.749182	0.115427	0.104624
GO_BP	GO:0032332~positive regulation of chondrocyte differentiation	5	0.69	0.006879	PKDCC, MUSTN1, GDF5, LOXL2, SOX5	642	22	18082	6.401161	1	0.273643	0.271114
GO_BP	GO:1902895~positive regulation of pri-miRNA transcription from RNA polymerase II promoter	5	0.69	0.006879	JUN, SRF, FOS, SMAD6, BMPR1A	642	22	18082	6.401161	1	0.273643	0.271114
GO_BP	GO:0035329~hippo signaling	5	0.69	0.006879	TEAD4, LATS2, AMOTL2, WTIP, AJUBA	642	22	18082	6.401161	1	0.273643	0.271114
GO_MF	GO:0019834~phospholipase A2 inhibitor activity	3	0.41	0.006921	ANXA1, ANXA2, ANXA3	608	4	17446	21.52056	0.992977	0.159949	0.155916
GO_BP	GO:1901491~negative regulation of lymphangiogenesis	3	0.41	0.007179	FOXC1, VASH1, EPHA2	642	4	18082	21.12383	1	0.277402	0.274839
GO_BP	GO:0071376~cellular response to corticotropin-releasing hormone stimulus	3	0.41	0.007179	NR4A2, NR4A1, NR4A3	642	4	18082	21.12383	1	0.277402	0.274839
GO_MF	GO:0044548~S100 protein binding	4	0.55	0.00729	ANXA2, AHNAK, IQGAP1, AGER	608	12	17446	9.564693	0.994614	0.159949	0.155916
GO_MF	GO:0017166~vinculin binding	4	0.55	0.00729	DLC1, ACTN1, DAG1, UTRN	608	12	17446	9.564693	0.994614	0.159949	0.155916
GO_BP	GO:0003007~heart morphogenesis	8	1.10	0.00735	FOXC2, FOXC1, FLRT2, SMO, DLC1, ALDH1A2, VEGFA, BMPR1A	642	64	18082	3.520639	1	0.278599	0.276024
GO_MF	GO:0032403~protein complex binding	23	3.17	0.007393	NSF, ITGB1, MLKL, ITGA2, PROS1, MAGI2, ACTN4, IQGAP1, PPP1R9B, CD2AP, GNAO1, MYO1E, RRAS, MAP1B, NCK2, RARB, APBA1, AMPH, FYN, MAPT, EPHB1, VAMP2, FGFR1	608	358	17446	1.843474	0.994998	0.159949	0.155916
GO_BP	GO:0048589~developmental growth	6	0.83	0.007416	SMO, SRF, GAS1, IL6RA, ADM, BMPR1A	642	35	18082	4.828304	1	0.278599	0.276024
GO_BP	GO:0098609~cell-cell adhesion	15	2.07	0.00757	STAT1, ARHGEF16, PARVA, VASN, FAM129B, SLC9A3R2, TJP1, TMEM47, FMNL2, EHD4, MPRIP, EFHD2, ELMO2, HIST2H3C2, LRRFIP1	642	189	18082	2.235326	1	0.280492	0.2779
GO_BP	GO:1904754~positive regulation of vascular associated smooth muscle cell migration	4	0.55	0.007677	DOCK5, DOCK4, PAK1, IQGAP1	642	12	18082	9.38837	1	0.280639	0.278045
KEGG	mmu05146:Amoebiasis	11	1.52	0.007686	COL1A2, SERPINB6A, SERPINB6B, LAMB2, ACTN1, COL4A3, COL4A6, COL4A5, ACTN4, ADCY1, RAB7B	270	117	7691	2.678094	0.789548	0.119436	0.108257
GO_BP	GO:0060045~positive regulation of cardiac muscle cell proliferation	5	0.69	0.008098	TGFBR3, NCAM1, FGFR2, FGFR1, BMPR1A	642	23	18082	6.12285	1	0.292057	0.289357
GO_MF	GO:0005525~GTP binding	24	3.31	0.008101	RAB3B, GM266, NPR1, RASL11A, IRGM2, RRAS2, AGAP1, ARL4C, GNAO1, EHD2, ARL4D, TUBB2B, RAB30, RIT1, TUBB2A, TUBA1A, EHD4, RRAS, RRAGB, RAB13, UPRT, RAB7B, RAB6B, ARF6	608	383	17446	1.798062	0.996996	0.170125	0.165836
KEGG	mmu05414:Dilated cardiomyopathy	9	1.24	0.008237	ITGB1, ITGB5, ITGA3, ITGA2, TPM1, MYL3, DAG1, ADCY1, ADCY5	270	83	7691	3.088755	0.811895	0.119436	0.108257
GO_BP	GO:0010634~positive regulation of epithelial cell migration	6	0.83	0.008366	EPB41L5, DOCK5, JUN, ITGA3, ITGA2, GAB2	642	36	18082	4.694185	1	0.297761	0.29501
GO_MF	GO:0008134~transcription factor binding	22	3.03	0.008757	FOXC1, JUN, RFXO2, SRF, NAB1, NAB2, ARID5A, PBX2, ARRB1, FOS, MED12L, ARNTL, NR4A1, MAFB, MDFIC, CSDC2, ATOH8, E2F1, ANKRD1, CRY1, SOX8, TRIB2	608	342	17446	1.845818	0.998127	0.17569	0.171261
GO_BP	GO:0035556~intracellular signal transduction	25	3.45	0.008766	MAST4, NPR1, NOD1, ADCY1, ASB15, ADCY5, SOCS2, ABR, DCDC2A, PLCE1, TNS3, PAG1, TNS2, PEA15A, UNC13B, PRKCI, ARHGEF12, KSR1, WSB2, GAB2, TGFBR3, DOK1, SH3BP5L, LATS2, MYZAP	642	400	18082	1.760319	1	0.307944	0.305098
KEGG	mmu05222:Small cell lung cancer	9	1.24	0.008837	ITGB1, ITGA3, LAMB2, ITGA2, COL4A3, E2F1, COL4A6, RARB, COL4A5	270	84	7691	3.051984	0.833528	0.119589	0.108396
GO_MF	GO:0070412~R-SMAD binding	5	0.69	0.008858	JUN, ANKRD1, PMEPA1, FOS, SMAD6	608	24	17446	5.977933	0.998259	0.17569	0.171261
GO_BP	GO:0003148~outflow tract septum morphogenesis	5	0.69	0.00945	RARB, PARVA, SMAD6, FGFR2, BMPR1A	642	24	18082	5.867731	1	0.327712	0.324683
GO_MF	GO:0005102~receptor binding	25	3.45	0.009879	ITGB1, ITGB5, NXPB3, H2-Q6, H2-Q7, H2-Q4, PLAT, VTCN1, SYNE1, DPP4, SLC9A3R2, ENSA, TAC4, FYN, RSP01, LDLRAP1, TNS2, WNT4, CADM4, F2R, LIF, GDF5, EML2, VEGFA, NECTIN4	608	412	17446	1.741146	0.999166	0.187286	0.182564
GO_MF	GO:0048306~calcium-dependent protein binding	8	1.10	0.009968	MYO1D, ANXA1, ANXA2, ANXA3, CALM2, S100A11, SYN1, VAMP2	608	69	17446	3.32685	0.999217	0.187286	0.182564
KEGG	mmu04925:Aldosterone synthesis and secretion	9	1.24	0.010133	NR4A2, NR4A1, DAGLA, NPR1, CREB3L1, ITPR3, ADCY1, CALM2, ADCY5	270	86	7691	2.981008	0.872205	0.122154	0.110721
GO_BP	GO:0008285~negative regulation of cell proliferation	24	3.31	0.010326	KANK2, ITGB1, BTG2, JUN, SRF, MAGI2, F2R, P3H2, LIF, ADM, SMAD6, CBFA2T3, PTPN14, WT1, DLC1, ALDH1A2, TIMP2, PMP22, NDN, SH3BP4, RARB, LZTS2, FGFR2, TNS2	642	384	18082	1.760319	1	0.353571	0.350304
GO_MF	GO:0008017~microtubule binding	15	2.07	0.010387	SGIP1, MTCL1, NDE1, EML1, EML2, DPYSL2, MAP1B, KIF5B, MAP1A, MAPT, TPPP, KIF3C, MAP4, CRYAB, DYNC111	608	200	17446	2.152056	0.999422	0.190165	0.185371
GO_MF	GO:0003700~transcription factor activity, sequence-specific DNA binding	45	6.21	0.010699	FOXC2, FOXC1, SRF, NPAS2, ARNTL, RELB, FOXS1, DACH1, ZFP13, CREB3L1, ATOH8, HOXC5, E2F1, HOXC4, SOX8, HIVEP2, HOXC8, HOXC6, SOX5, TEAD4, FOXD2, JUN, FOXD1, STAT1, PBX2, FOS, FOXL1, MAFA, SMAD6, CBFA2T3, FOSL2, NR4A2, NR4A1, MYCL, NR4A3, MAFB, WT1, ELF4, FOSB, RARB, MAFK, LMX1B, ZFP772, ATF3, NFE2L1	608	883	17446	1.462326	0.999538	0.190982	0.186168
KEGG	mmu04918:Thyroid hormone synthesis	8	1.10	0.010834	CREB3L1, GPX8, GPX7, ITPR3, ADCY1, ATP1B2, TSHB, ADCY5	270	70	7691	3.25545	0.88924	0.122154	0.110721
KEGG	mmu05200:Pathways in cancer	24	3.31	0.010978	PTGER4, ITGB1, JUN, ARHGEF12, FZD2, LAMB2, STAT1, ITGA3, ITGA2, F2R, TGFA, FOS, ADCY1, ADCY5, VEGFA, SMO, COL4A3, COL4A6, E2F1, RARB, COL4A5, FGFR2, FGFR1, WNT4	270	395	7691	1.730745	0.892455	0.122154	0.110721
GO_MF	GO:0008467~[heparan sulfate]-glucosamine 3-sulfotransferase 1 activity	3	0.41	0.011127	HS3ST3B1, HS3ST3A1, HS3ST6	608	5	17446	17.21645	0.999694	0.194703	0.189794
GO_MF	GO:0042608~T cell receptor binding	4	0.55	0.011453	H2-Q6, H2-Q7, H2-Q4, FYN	608	14	17446	8.198308	0.999732	0.194703	0.189794
GO_BP	GO:0043410~positive regulation of MAPK cascade	10	1.38	0.011579	ITGB1, C1QTNF1, KSR1, F2R, TIMP2, LIF, BNIP2, FGFR2, CDON, FGFR1	642	104	18082	2.708184	1	0.386494	0.382922

GO_BP	GO:0072162~metanephric mesenchymal cell differentiation	3	0.41	0.011684	STAT1, TCF21, WNT4	642	5	18082	16.89907	1	0.386494	0.382922
KEGG	mmu04022:cGMP-PKG signaling pathway	13	1.79	0.011686	NPR1, SRF, PDE3B, ITPR3, ADCY1, ATP1B2, MYLK3, ADCY5, MYLK, CREB3L1, PDE3A, CALM2, PRKG1	270	163	7691	2.271825	0.906941	0.122154	0.110721
GO_BP	GO:0014911~positive regulation of smooth muscle cell migration	6	0.83	0.011716	PTGER4, P2RY6, TMSB4X, ITGA2, IL18, AGER	642	39	18082	4.333094	1	0.386494	0.382922
GO_BP	GO:0006915~apoptotic process	32	4.41	0.012489	KANK2, MTCH1, STEAP3, HIP1, NOD1, PAK1, GRK5, ZFP385B, ADAMTSL4, E2F1, BNIP2, PEA15A, GSN, TNFRSF12A, GADD45B, SIVA1, STAT1, APLP1, NGB, UNC5C, SULF1, GULP1, NR4A1, WT1, STK26, DLC1, ELMO1, ELMO2, MAPT, FGFR2, FAIM, EPHA2	642	570	18082	1.581199	1	0.404493	0.400754
KEGG	mmu04971:Gastric acid secretion	8	1.10	0.012554	HRH2, ITPR3, ADCY1, ATP1B2, CALM2, MYLK3, ADCY5, MYLK	270	72	7691	3.165021	0.922069	0.122154	0.110721
GO_BP	GO:0001954~positive regulation of cell-matrix adhesion	5	0.69	0.012575	EPB41L5, PLEKHA2, DAG1, EMP2, UTRN	642	26	18082	5.416367	1	0.404493	0.400754
KEGG	mmu04380:Osteoclast differentiation	11	1.52	0.012637	JUN, NCF2, IFNGR1, STAT1, FOSB, SIRPA, FYN, GAB2, FOS, RELB, FOSL2	270	126	7691	2.486802	0.923378	0.122154	0.110721
GO_BP	GO:0001568~blood vessel development	8	1.10	0.012742	TGFBR3, FOXC2, FOXC1, FOXS1, COL1A2, ALDH1A2, VEGFA, EPHA2	642	71	18082	3.173533	1	0.404493	0.400754
GO_BP	GO:0034613~cellular protein localization	7	0.97	0.012882	ARMCX3, PRKCI, FRMD6, LATS2, RRAGB, AJUBA, OPTN	642	55	18082	3.58465	1	0.404493	0.400754
GO_BP	GO:0034446~substrate adhesion-dependent cell spreading	6	0.83	0.01301	AXL, FNDC3B, TYRO3, PARVA, MERTK, SRGAP2	642	40	18082	4.224766	1	0.404493	0.400754
GO_MF	GO:0042803~protein homodimerization activity	41	5.66	0.013153	ZFP423, HIP1, TENM3, MTCL1, SRF, PTPRO, NPR3, BHLHE41, IL6RA, NOD1, SYNE1, DPP4, S100A13, LRRFIP1, SRGAP2, PRKG1, PDZD7, JUN, CADM4, ANXA1, PRMT2, STAT1, ACTN1, TPM1, INHBB, ACTN4, VEGFA, DLK2, NR4A1, NR4A3, GDNF, STK26, MYH9, NECTIN4, ACP, CRYAB, NBL1, ATF3, FGFR2, BMPR1A, FGFR1	608	798	17446	1.474257	0.999922	0.213869	0.208477
GO_MF	GO:0048365~Rac GTPase binding	6	0.83	0.013363	DOCK4, NCF2, IQGAP1, IQGAP2, SRGAP2, SRGAP1	608	41	17446	4.199134	0.999933	0.213869	0.208477
GO_MF	GO:0045499~chemorepellent activity	5	0.69	0.013479	SEMA5A, SEMA6C, FLRT2, SEMA3G, SEMA3E	608	27	17446	5.313718	0.999938	0.213869	0.208477
GO_BP	GO:0007409~axonogenesis	10	1.38	0.013776	NTNG2, LINGO1, PAK1, CNP, LRTM2, MAP1B, NDN, MAPT, ADCY1, FGFR2	642	107	18082	2.632253	1	0.41871	0.414841
GO_BP	GO:0001501~skeletal system development	10	1.38	0.013776	CDKN1C, FOXC2, FOXC1, RASSF2, PKDCC, COL1A2, NPR3, WFIKKN2, HOXC4, EPHA2	642	107	18082	2.632253	1	0.41871	0.414841
GO_BP	GO:0045893~positive regulation of transcription, DNA-templated	32	4.41	0.014275	CDKN1C, FOXC2, FOXC1, ZFP423, SRF, SETD7, SCX, ABRA, NPAS2, ARNTL, TMSB4X, ATOH8, E2F1, SOX8, WNT4, JUN, FZD2, PRMT2, STAT1, F2R, FOS, MAFA, FOSL2, NR4A2, NR4A1, NR4A3, SMO, MDFIC, WT1, BAMBI, ELF4, BMPR1A	642	576	18082	1.564728	1	0.423271	0.419359
GO_BP	GO:0070830~bicellular tight junction assembly	5	0.69	0.014357	ITGB1, SRF, RAB13, ACTN4, MPP5	642	27	18082	5.215761	1	0.423271	0.419359
GO_BP	GO:0010595~positive regulation of endothelial cell migration	6	0.83	0.014396	FOXC2, SPARC, ANXA3, ATOH8, SASH1, VEGFA	642	41	18082	4.121723	1	0.423271	0.419359
KEGG	mmu04010:MAPK signaling pathway	17	2.34	0.014596	JUN, DUSP3, GADD45B, GADD45A, SRF, RRAS2, ARR1, FOS, DUSP8, RELB, NR4A1, PAK1, DUSP10, RRAS, MAPT, FGFR2, FGFR1	270	251	7691	1.929275	0.948705	0.134683	0.122077
GO_BP	GO:0043149~stress fiber assembly	4	0.55	0.014672	ITGB1, ITGB5, SRF, ARR1	642	15	18082	7.510696	1	0.426758	0.422814
GO_BP	GO:0010628~positive regulation of gene expression	24	3.31	0.015741	PTGER4, SEC16B, FOXC1, GSN, FOXD1, ITGA3, NTRK3, IL18, LIF, SCX, VASH1, AGER, VEGFA, RELB, C1QTNF1, SMO, MUSTN1, ALDH1A2, E2F1, SOX8, QK, VIM, ATF3, FGFR2	642	399	18082	1.694142	1	0.452105	0.447926
KEGG	mmu04921:Oxytocin signaling pathway	12	1.66	0.015863	GNAO1, MYL6, JUN, NPR1, KCNJ12, ITPR3, ADCY1, FOS, CALM2, MYLK3, ADCY5, MYLK	270	150	7691	2.278815	0.960441	0.140005	0.126902
GO_BP	GO:0010811~positive regulation of cell-substrate adhesion	6	0.83	0.015878	ITGB1, CCDC80, ITGA3, EMILIN1, NPNT, CYR61	642	42	18082	4.023587	1	0.452105	0.447926
GO_BP	GO:0042542~response to hydrogen peroxide	7	0.97	0.016463	GNAO1, JUN, NR4A3, GJA3, STAT1, STK26, CRYAB	642	58	18082	3.399237	1	0.463874	0.459587
GO_MF	GO:0004859~phospholipase inhibitor activity	3	0.41	0.016517	ANXA1, ANXA2, ANXA3	608	6	17446	14.34704	0.999993	0.256371	0.249908
GO_BP	GO:0097350~neutrophil clearance	3	0.41	0.017117	ANXA1, AXL, MERTK	642	6	18082	14.08255	1	0.471118	0.466764
GO_BP	GO:0001974~blood vessel remodeling	6	0.83	0.017458	TGFBR3, FOXC2, FOXC1, AXL, LIF, VEGFA	642	43	18082	3.930015	1	0.471118	0.466764
GO_BP	GO:0048013~ephrin receptor signaling pathway	6	0.83	0.017458	EFNB1, EPHA6, NCK2, FYN, EPHB1, EPHA2	642	43	18082	3.930015	1	0.471118	0.466764
GO_BP	GO:0090303~positive regulation of wound healing	4	0.55	0.017591	PTGER4, KANK1, ANXA1, MYLK	642	16	18082	7.041277	1	0.471118	0.466764
GO_BP	GO:0006198~cAMP catabolic process	4	0.55	0.017591	PDE10A, PDE3B, PDE4B, PDE3A	642	16	18082	7.041277	1	0.471118	0.466764
GO_MF	GO:0005096~GTPase activator activity	16	2.21	0.017798	DOCK4, JUN, ARHGAP12, ARHGAP19, AGAP1, ARHGAP28, ARR1, SIPA1L2, ARHGAP24, ARHGAP23, ARHGAP33, ARHGAP44, ABR, DLC1, SRGAP2, SRGAP1	608	235	17446	1.953639	0.999997	0.270382	0.263566
GO_BP	GO:0050679~positive regulation of epithelial cell proliferation	8	1.10	0.018028	NR4A3, SMO, HTRA1, GAS1, TGFA, FGFR2, VEGFA, BMPR1A	642	76	18082	2.964748	1	0.478107	0.473688
GO_BP	GO:0043392~negative regulation of DNA binding	5	0.69	0.018381	JUN, SMO, WFIKKN2, E2F1, ZFP462	642	29	18082	4.856053	1	0.479081	0.474654
GO_BP	GO:0042060~wound healing	9	1.24	0.018419	PAK1, SPARC, SDC4, PTK7, MUSTN1, ITGA2, TPM1, TGFA, DCBLD2	642	94	18082	2.696659	1	0.479081	0.474654
KEGG	mmu05132:Salmonella infection	8	1.10	0.018886	TJP1, JUN, IFNGR1, IL18, FOS, KLC1, RAB7B, DYNC1I1	270	78	7691	2.921557	0.97875	0.159741	0.14479
GO_BP	GO:0042552~myelination	7	0.97	0.019199	CLDN5, NAB1, NAB2, PMP22, QK, FYN, TSPAN2	642	60	18082	3.285929	1	0.481081	0.476635
GO_BP	GO:0030198~extracellular matrix organization	10	1.38	0.020084	COL18A1, CCDC80, ADAMTSL4, LAMB2, APLP1, COL4A6, EMILIN1, NPNT, RECK, CYR61	642	114	18082	2.470624	1	0.481081	0.476635
KEGG	mmu04144:Endocytosis	17	2.34	0.020389	PRKCI, H2-Q6, H2-Q7, AGAP1, ARR1, PLD1, EPN3, EHD2, PARD6B, EHD4, GRK5, KIF5B, PSD3, AMPH, LDLRAP1, FGFR2, ARF6	270	261	7691	1.855357	0.98441	0.165558	0.150062
GO_BP	GO:0043010~camera-type eye development	8	1.10	0.020521	CDKN1C, FOXC2, FOXC1, WT1, ALDH1A2, GAS1, LMX1B, CRYAB	642	78	18082	2.888729	1	0.481081	0.476635
GO_BP	GO:0007160~cell-matrix adhesion	8	1.10	0.020521	ITGB1, BCAM, ITGB5, SRF, ITGA2, SIRPA, EMP2, NPNT	642	78	18082	2.888729	1	0.481081	0.476635

GO_BP	GO:0007568~aging	13	1.79	0.020546	CDKN1C, JUN, GSN, CNP, IGFBP2, ADM, FOS, PPP1R9B, GNAO1, UCP2, TIMP2, NCAM1, CRYAB	642	173	18082	2.116453	1	0.481081	0.476635
GO_BP	GO:0001701~in utero embryonic development	19	2.62	0.020617	TEAD4, ITGB1, FOXC1, DUSP3, SRF, TPM1, VEGFA, TGFB3, EPB41L5, MYO1E, SMO, SPEG, MYH9, SOX8, APBA1, FGFR2, SOX5, FGFR1, BMPR1A	642	299	18082	1.789756	1	0.481081	0.476635
GO_BP	GO:0071560~cellular response to transforming growth factor beta stimulus	7	0.97	0.020677	EPB41L5, PDE3A, ANKRD1, SCX, FYN, WNT4, SOX5	642	61	18082	3.232062	1	0.481081	0.476635
GO_BP	GO:0002042~cell migration involved in sprouting angiogenesis	4	0.55	0.020808	ITGB1, NR4A1, SRF, VEGFA	642	17	18082	6.627084	1	0.481081	0.476635
GO_BP	GO:0035024~negative regulation of Rho protein signal transduction	4	0.55	0.020808	ITGB1, KANK1, ITGA3, DLC1	642	17	18082	6.627084	1	0.481081	0.476635
GO_BP	GO:1900745~positive regulation of p38MAPK cascade	4	0.55	0.020808	GADD45B, GADD45A, SASH1, VEGFA	642	17	18082	6.627084	1	0.481081	0.476635
GO_BP	GO:0014032~neural crest cell development	4	0.55	0.020808	FOXC2, FOXC1, ALDH1A2, BMPR1A	642	17	18082	6.627084	1	0.481081	0.476635
GO_BP	GO:0014002~astrocyte development	4	0.55	0.020808	LAMB2, TSPAN2, VIM, AGER	642	17	18082	6.627084	1	0.481081	0.476635
GO_BP	GO:0042692~muscle cell differentiation	4	0.55	0.020808	ANKRD1, SPEG, QK, SYNE1	642	17	18082	6.627084	1	0.481081	0.476635
GO_MF	GO:0016791~phosphatase activity	10	1.38	0.022033	DUSP10, DUSP3, PTPRO, PTPN21, PTPN12, DUSP15, DUSP8, ACPP, PTPN14, CDC14A	608	118	17446	2.431702	1	0.327734	0.319472
GO_MF	GO:0003836~beta-galactoside (CMP) alpha-2,3-sialyltransferase activity	3	0.41	0.022595	ST3GAL6, ST3GAL1, ST3GAL3	608	7	17446	12.29746	1	0.328749	0.320461
GO_BP	GO:0002062~chondrocyte differentiation	6	0.83	0.022812	MUSTN1, ARID5A, SCX, GDF5, FGFR1, BMPR1A	642	46	18082	3.67371	1	0.500786	0.496158
GO_BP	GO:0001837~epithelial to mesenchymal transition	5	0.69	0.02304	TGFB3, EPB41L5, FGFR2, LOXL2, WNT4	642	31	18082	4.54276	1	0.500786	0.496158
GO_MF	GO:0051393~alpha-actinin binding	4	0.55	0.023165	ITGB1, PDLIM2, NPHS1, DAG1	608	18	17446	6.376462	1	0.328749	0.320461
GO_BP	GO:0072112~glomerular visceral epithelial cell differentiation	3	0.41	0.023406	FOXC2, WT1, PTPRO	642	7	18082	12.07076	1	0.500786	0.496158
GO_BP	GO:0002043~blood vessel endothelial cell proliferation involved in sprouting angiogenesis	3	0.41	0.023406	SEMA5A, VEGFA, EPHA2	642	7	18082	12.07076	1	0.500786	0.496158
GO_BP	GO:0014037~Schwann cell differentiation	3	0.41	0.023406	NAB1, GPC1, NAB2	642	7	18082	12.07076	1	0.500786	0.496158
GO_BP	GO:0032288~myelin assembly	3	0.41	0.023406	GPC1, PMP22, MPP5	642	7	18082	12.07076	1	0.500786	0.496158
GO_BP	GO:0032534~regulation of microvillus assembly	3	0.41	0.023406	PODXL, ATP8B1, PLD1	642	7	18082	12.07076	1	0.500786	0.496158
GO_BP	GO:0048842~positive regulation of axon extension involved in axon guidance	3	0.41	0.023406	SEMA5A, MEGF8, VEGFA	642	7	18082	12.07076	1	0.500786	0.496158
GO_MF	GO:0004721~phosphoprotein phosphatase activity	11	1.52	0.023482	DUSP10, DUSP3, EYA4, PTPRO, PTPN21, PTPN12, DUSP15, DUSP8, PTPN14, CDC14A, TNS2	608	139	17446	2.270754	1	0.328749	0.320461
GO_BP	GO:0009612~response to mechanical stimulus	7	0.97	0.02386	BTG2, JUN, STAT1, IGFBP2, FOSB, INHBB, ASIC2	642	63	18082	3.129457	1	0.500786	0.496158
GO_BP	GO:0030326~embryonic limb morphogenesis	7	0.97	0.02386	MUSTN1, ALDH1A2, PBX2, LMX1B, MEGF8, GDF5, FGFR1	642	63	18082	3.129457	1	0.500786	0.496158
GO_BP	GO:0030111~regulation of Wnt signaling pathway	4	0.55	0.024326	DCDC2A, MDFIC, ITGA3, FOXL1	642	18	18082	6.258913	1	0.500786	0.496158
GO_BP	GO:0060996~dendritic spine development	4	0.55	0.024326	PAK1, NCK2, SRGAP2, EPHB1	642	18	18082	6.258913	1	0.500786	0.496158
GO_BP	GO:0051693~actin filament capping	4	0.55	0.024326	GSN, TPM1, MYH9, SPTB	642	18	18082	6.258913	1	0.500786	0.496158
GO_BP	GO:0007166~cell surface receptor signaling pathway	15	2.07	0.024598	GLP1R, FZD2, ANXA1, CD151, NPR1, VASN, TSPAN15, CD59B, TSPAN13, SMO, TSPAN17, COL4A3, NCAM1, FYN, TSPAN2	642	219	18082	1.929117	1	0.500786	0.496158
GO_BP	GO:0007565~female pregnancy	8	1.10	0.024693	ENDOU, ITGA2, UCP2, IGFBP2, FOSB, UPRT, ADM, FOS	642	81	18082	2.781739	1	0.500786	0.496158
GO_BP	GO:0007265~Ras protein signal transduction	6	0.83	0.024808	DOK1, RIT1, JUN, KSR1, PLCE1, RRAS2	642	47	18082	3.595546	1	0.500786	0.496158
GO_BP	GO:0050796~regulation of insulin secretion	6	0.83	0.024808	STXBP1, PDE3B, ENSA, SYT9, VAMP2, ARNTL	642	47	18082	3.595546	1	0.500786	0.496158
GO_BP	GO:0007605~sensory perception of sound	11	1.52	0.025168	TJP1, SLC9A3R2, CLIC5, SRRM4, DCDC2A, SERPINB6A, ATP8B1, EYA4, MAP1A, ASIC2, FGFR1	642	138	18082	2.245045	1	0.504297	0.499636
GO_BP	GO:0001658~branching involved in ureteric bud morphogenesis	6	0.83	0.026912	FOXD1, GDNF, WT1, TCF21, NPNT, WNT4	642	48	18082	3.520639	1	0.535281	0.530333
KEGG	mmu00510:N-Glycan biosynthesis	6	0.83	0.027439	ST6GAL1, MAN1A2, MGAT5, MGAT4A, MGAT5B, ALG14	270	49	7691	3.487982	0.996376	0.214234	0.194183
GO_BP	GO:0006897~endocytosis	13	1.79	0.027995	HIP1, SGIP1, WIPF3, APLP1, STON1, ARRB1, STON2, MRC2, EHD2, MYO1E, DPYSL2, SH3BP4, LDLRAP1	642	181	18082	2.022908	1	0.536121	0.531166
GO_BP	GO:0048255~mRNA stabilization	4	0.55	0.028144	GDNF, E2F1, QK, VEGFA	642	19	18082	5.929497	1	0.536121	0.531166
GO_BP	GO:0048598~embryonic morphogenesis	4	0.55	0.028144	GAS1, AI597479, CDON, BMPR1A	642	19	18082	5.929497	1	0.536121	0.531166
GO_BP	GO:0031589~cell-substrate adhesion	4	0.55	0.028144	ITGB1, ITGA2, SMAD6, EPHB1	642	19	18082	5.929497	1	0.536121	0.531166
GO_BP	GO:0010951~negative regulation of endopeptidase activity	4	0.55	0.028144	CRB2, SERPINB6A, SERPINB6B, TIMP2	642	19	18082	5.929497	1	0.536121	0.531166
GO_BP	GO:0050880~regulation of blood vessel size	4	0.55	0.028144	TGFB3, FOXC2, FOXC1, NPR1	642	19	18082	5.929497	1	0.536121	0.531166

GO_MF	GO:0008046~axon guidance receptor activity	3	0.41	0.029441	ROBO2, SEMA5A, EPHB1	608	8	17446	10.76028	1	0.389484	0.379666
GO_MF	GO:0046977~TAP binding	3	0.41	0.029441	H2-Q6, H2-Q7, H2-Q4	608	8	17446	10.76028	1	0.389484	0.379666
GO_MF	GO:0070888~E-box binding	5	0.69	0.029457	ATOH8, BHLHE41, SCX, TCF21, ARNTL	608	34	17446	4.219717	1	0.389484	0.379666
GO_MF	GO:0016757~transferase activity, transferring glycosyl groups	14	1.93	0.030364	COLGALT2, ST6GAL1, GALNT10, EXTL1, MGAT5, MGAT4A, MGAT5B, B3GALT2, ST3GAL6, LARGE1, ST6GALNAC3, ST3GAL1, ST6GALNAC6, ST3GAL3	608	208	17446	1.931332	1	0.393952	0.384021
KEGG	mmu04540:Gap junction	8	1.10	0.030419	TJP1, TUBB2B, TUBB2A, TUBA1A, ITPR3, ADCY1, PRKG1, ADCY5	270	86	7691	2.649785	0.99805	0.228704	0.207298
GO_BP	GO:0032287~peripheral nervous system myelin maintenance	3	0.41	0.030484	FA2H, PRX, MPP5	642	8	18082	10.56192	1	0.568676	0.563421
GO_BP	GO:0010518~positive regulation of phospholipase activity	3	0.41	0.030484	HPCA, CYR61, FGFR2	642	8	18082	10.56192	1	0.568676	0.563421
GO_BP	GO:0038063~collagen-activated tyrosine kinase receptor signaling pathway	3	0.41	0.030484	COL4A3, COL4A6, COL4A5	642	8	18082	10.56192	1	0.568676	0.563421
GO_MF	GO:0042802~identical protein binding	32	4.41	0.030898	ROBO2, GPSM2, FOXC2, STXBP1, HSPB8, NOD1, AGER, DPP4, GJA3, BNIP2, SH3BP4, EMILIN1, JUN, STAT1, NDE1, APLP1, SNCAIP, SMAD6, GDF5, VEGFA, NELL2, CLDN5, COL1A2, STK26, AMOTL2, VIM, MICU1, ACPP, CRYAB, ATF3, OPTN, FGFR1	608	625	17446	1.469137	1	0.393952	0.384021
GO_BP	GO:0006919~activation of cysteine-type endopeptidase activity involved in apoptotic process	7	0.97	0.031174	MTCH1, HIP1, STAT1, DLC1, COL4A3, F2R, NOD1	642	67	18082	2.942623	1	0.571029	0.565751
GO_BP	GO:0048709~oligodendrocyte differentiation	5	0.69	0.031264	DUSP10, CNP, SOX8, TSPAN2, SOX5	642	34	18082	4.141928	1	0.571029	0.565751
GO_BP	GO:0071526~semaphorin-plexin signaling pathway	5	0.69	0.031264	SEMA5A, SEMA6C, SEMA3G, PLXNB1, SEMA3E	642	34	18082	4.141928	1	0.571029	0.565751
GO_BP	GO:0006936~muscle contraction	6	0.83	0.031454	CHRN1, MYL6, ANXA1, ANXA2, TMOD3, MYOM2	642	50	18082	3.379813	1	0.571029	0.565751
GO_BP	GO:0007520~myoblast fusion	4	0.55	0.03226	NPHS1, MYH9, PLEKHO1, CDON	642	20	18082	5.633022	1	0.581757	0.57638
GO_BP	GO:0001570~vasculogenesis	7	0.97	0.033207	TGFBR3, MYO1E, SMO, WT1, QK, ADM, EPHA2	642	68	18082	2.899349	1	0.594859	0.589361
KEGG	mmu04270:Vascular smooth muscle contraction	10	1.38	0.033605	MYL6, ARHGEF12, NPR1, ITPR3, ADCY1, CALM2, PRKG1, MYLK3, ADCY5, MYLK	270	127	7691	2.242928	0.998997	0.243633	0.22083
GO_BP	GO:0051591~response to cAMP	6	0.83	0.033894	JUN, SPARC, STAT1, PDE3A, FOSB, FOS	642	51	18082	3.313542	1	0.603178	0.597604
GO_BP	GO:0001707~mesoderm formation	5	0.69	0.034341	CRB2, NR4A3, SRF, SCX, BMPR1A	642	35	18082	4.023587	1	0.607137	0.601526
GO_MF	GO:0030215~semaphorin receptor binding	4	0.55	0.034972	SEMA5A, SEMA6C, SEMA3G, SEMA3E	608	21	17446	5.465539	1	0.435777	0.424791
GO_MF	GO:0035091~phosphatidylinositol binding	8	1.10	0.035399	ARHGAP33, MYO1E, HIP1, SH3PXD2A, ITPR3, PXDC1, PLD1, SNX31	608	89	17446	2.579243	1	0.435777	0.424791
GO_BP	GO:0031532~actin cytoskeleton reorganization	6	0.83	0.036448	PAK1, ANXA1, PTK7, NPHS2, MYH9, PARVA	642	52	18082	3.24982	1	0.635366	0.629494
GO_MF	GO:0008146~sulfotransferase activity	6	0.83	0.036539	HS3ST3B1, HS3ST3A1, UST, CHST1, CHST14, HS3ST6	608	53	17446	3.248386	1	0.440212	0.429114
GO_BP	GO:0032869~cellular response to insulin stimulus	8	1.10	0.036604	PRKCI, PAK1, STAT1, PDE3B, UCP2, RAB13, INHBB, VAMP2	642	88	18082	2.560464	1	0.635366	0.629494
GO_BP	GO:0051412~response to corticosterone	4	0.55	0.036672	NTRK3, FOSB, FOS, CALM2	642	21	18082	5.364783	1	0.635366	0.629494
GO_MF	GO:0035612~AP-2 adaptor complex binding	3	0.41	0.036993	HIP1, ARRB1, LDLRAP1	608	9	17446	9.564693	1	0.440212	0.429114
KEGG	mmu04924:Renin secretion	7	0.97	0.037251	PTGER4, NPR1, PDE3B, PDE3A, ITPR3, CALM2, ADCY5	270	71	7691	2.808399	0.999533	0.260757	0.236351
GO_BP	GO:0006468~protein phosphorylation	30	4.14	0.037431	RNASEL, PKDCC, MAST4, NPR1, MYLK3, MYLK, PAK1, GRK5, SPEG, NEK1, FYN, ST3GAL1, EPHB1, PRKG1, PRKCI, EPHA6, KSR1, MLKL, NTRK3, MERTK, LATS2, PTK7, AXL, STK26, TYRO3, TRIB2, FGFR2, BMPR1A, EPHA2, FGFR1	642	576	18082	1.466933	1	0.635366	0.629494
GO_BP	GO:0051965~positive regulation of synapse assembly	7	0.97	0.037525	LINGO2, FLRT2, LRTM2, NTRK3, AMIGO2, ASIC2, EPHB1	642	70	18082	2.816511	1	0.635366	0.629494
GO_BP	GO:0042088~T-helper 1 type immune response	3	0.41	0.038286	IL18, RELB, VEGFA	642	9	18082	9.38837	1	0.635366	0.629494
GO_BP	GO:0031340~positive regulation of vesicle fusion	3	0.41	0.038286	ANXA1, ANXA2, KIF5B	642	9	18082	9.38837	1	0.635366	0.629494
GO_BP	GO:0060426~lung vasculature development	3	0.41	0.038286	LIF, TCF21, VEGFA	642	9	18082	9.38837	1	0.635366	0.629494
GO_BP	GO:0060539~diaphragm development	3	0.41	0.038286	WT1, TCF21, DISP1	642	9	18082	9.38837	1	0.635366	0.629494
GO_BP	GO:0016043~cellular component organization	3	0.41	0.038286	FMNL2, INF2, DAAM2	642	9	18082	9.38837	1	0.635366	0.629494
GO_BP	GO:0071277~cellular response to calcium ion	6	0.83	0.039117	JUN, FOSB, IQGAP1, ADCY1, FOS, MYLK	642	53	18082	3.188503	1	0.645199	0.639236
KEGG	mmu04520:Adherens junction	7	0.97	0.039496	TJP1, ACTN1, FYN, ACTN4, IQGAP1, NECTIN4, FGFR1	270	72	7691	2.769393	0.999708	0.267258	0.242244
GO_BP	GO:0060976~coronary vasculature development	5	0.69	0.041005	TGFBR3, PTK7, WT1, MEGF8, SMAD6	642	37	18082	3.806096	1	0.666207	0.66005
GO_BP	GO:0008219~cell death	5	0.69	0.041005	PARP4, PMP22, EMP2, EMP3, SNCAIP	642	37	18082	3.806096	1	0.666207	0.66005
GO_BP	GO:0031668~cellular response to extracellular stimulus	4	0.55	0.041376	NR4A2, GSDMD, AXL, FOS	642	22	18082	5.120929	1	0.666207	0.66005

GO_BP	GO:0048260~positive regulation of receptor-mediated endocytosis	4	0.55	0.041376	HIP1, SGIP1, LDLRAP1, SYNE1	642	22	18082	5.120929	1	0.666207	0.66005
GO_BP	GO:0030512~negative regulation of transforming growth factor beta receptor signaling pathway	6	0.83	0.041903	TGFBR3, BAMBI, HTRA1, PMEPA1, SMAD6, VASN	642	54	18082	3.129457	1	0.670693	0.664494
GO_MF	GO:0005520~insulin-like growth factor binding	4	0.55	0.044261	IGFBP2, HTRA1, CRIM1, CYR61	608	23	17446	4.990275	1	0.509712	0.496862
GO_MF	GO:0017075~syntaxin-1 binding	4	0.55	0.044261	NSF, UNC13B, STXBP1, VAMP2	608	23	17446	4.990275	1	0.509712	0.496862
GO_BP	GO:0043491~protein kinase B signaling	5	0.69	0.044592	LINGO1, AXL, TYRO3, MERTK, EPHA2	642	38	18082	3.705935	1	0.70218	0.69569
GO_BP	GO:0001656~metanephros development	5	0.69	0.044592	ROBO2, FOXC2, GDNF, WT1, WNT4	642	38	18082	3.705935	1	0.70218	0.69569
GO_BP	GO:0043434~response to peptide hormone	7	0.97	0.044649	BTG2, PRKCI, SPARC, ANXA1, STAT1, DAG1, PLD1	642	73	18082	2.700764	1	0.70218	0.69569
GO_BP	GO:0009952~anterior/posterior pattern specification	9	1.24	0.045693	BTG2, SMO, ALDH1A2, HOXC5, HOXC4, HOXC8, HOXC6, CDON, BMPR1A	642	112	18082	2.263268	1	0.702612	0.696118
GO_BP	GO:0014850~response to muscle activity	4	0.55	0.046368	FNDC5, ITGA2, METRNL, TNS2	642	23	18082	4.89828	1	0.702612	0.696118
GO_BP	GO:0001708~cell fate specification	4	0.55	0.046368	ITGB1, TEAD4, SMO, CDON	642	23	18082	4.89828	1	0.702612	0.696118
GO_BP	GO:0090190~positive regulation of branching involved in ureteric bud morphogenesis	4	0.55	0.046368	SMO, GDNF, SOX8, VEGFA	642	23	18082	4.89828	1	0.702612	0.696118
GO_BP	GO:0048041~focal adhesion assembly	4	0.55	0.046368	DLC1, ITGA2, ACTN1, AJUBA	642	23	18082	4.89828	1	0.702612	0.696118
GO_BP	GO:0035767~endothelial cell chemotaxis	3	0.41	0.046754	NR4A1, RAB13, VEGFA	642	10	18082	8.449533	1	0.702612	0.696118
GO_BP	GO:0046620~regulation of organ growth	3	0.41	0.046754	FOXC2, FOXC1, LATS2	642	10	18082	8.449533	1	0.702612	0.696118
GO_BP	GO:0042698~ovulation cycle	3	0.41	0.046754	GABRB1, AXL, TYRO3	642	10	18082	8.449533	1	0.702612	0.696118
GO_BP	GO:0001649~osteoblast differentiation	9	1.24	0.047721	TGFBR3, MRC2, SMO, TMSB4X, CREB3L1, RRAS2, SOX8, CYR61, EPHA2	642	113	18082	2.243239	1	0.70691	0.700377
GO_BP	GO:0060348~bone development	6	0.83	0.047824	PTGER4, SPARC, P3H1, RARB, SULF1, FGFR2	642	56	18082	3.01769	1	0.70691	0.700377
GO_BP	GO:0031100~organ regeneration	6	0.83	0.047824	TGFBR3, NR4A3, ANXA3, AXL, LIF, ADM	642	56	18082	3.01769	1	0.70691	0.700377
KEGG	mmu04923:Regulation of lipolysis in adipocytes	6	0.83	0.048225	NPR1, PDE3B, ADCY1, PRKG1, TSHB, ADCY5	270	57	7691	2.998441	0.999954	0.312913	0.283625
GO_BP	GO:0030168~platelet activation	5	0.69	0.048349	AXL, SRF, F2R, TYRO3, MERTK	642	39	18082	3.610911	1	0.708241	0.701695
GO_BP	GO:0051260~protein homooligomerization	13	1.79	0.048438	GSDMD, KCNF1, KCNG2, SPTBN5, ITPR3, C1QTNF1, EHD4, C1QTNF7, KCTD11, MICU1, CRYAB, OPTN, KCTD15	642	197	18082	1.858611	1	0.708241	0.701695
GO_MF	GO:0000982~transcription factor activity, RNA polymerase II core promoter proximal region sequence-specific binding	4	0.55	0.049318	JUN, ARNTL, FOSL2, DDN	608	24	17446	4.782346	1	0.542654	0.528974
GO_MF	GO:0003785~actin monomer binding	4	0.55	0.049318	TMSB4X, MYL3, TMSB10, PKNOX2	608	24	17446	4.782346	1	0.542654	0.528974
KEGG	mmu04610:Complement and coagulation cascades	7	0.97	0.049326	C1RA, CD59B, CD59A, PROS1, F2R, PLAT, CD55	270	76	7691	2.623635	0.999963	0.312913	0.283625
GO_MF	GO:0008138~protein tyrosine/serine/threonine phosphatase activity	5	0.69	0.049401	DUSP10, DUSP3, DUSP15, DUSP8, CDC14A	608	40	17446	3.58676	1	0.542654	0.528974
GO_BP	GO:0045987~positive regulation of smooth muscle contraction	4	0.55	0.051642	SRF, ITGA2, F2R, NPNT	642	24	18082	4.694185	1	0.740216	0.733375
GO_BP	GO:0030866~cortical actin cytoskeleton organization	4	0.55	0.051642	EHD2, FMNL2, RAB13, ARF6	642	24	18082	4.694185	1	0.740216	0.733375
GO_BP	GO:0009987~cellular process	4	0.55	0.051642	GNAO1, JUN, MAP1B, RRAS2	642	24	18082	4.694185	1	0.740216	0.733375
KEGG	mmu04970:Salivary secretion	7	0.97	0.051999	ITPR3, ADCY1, ATP1B2, CALM2, PRKG1, VAMP2, ADCY5	270	77	7691	2.589562	0.999979	0.319871	0.289932
GO_BP	GO:0001569~patterning of blood vessels	5	0.69	0.052276	SEMA5A, FOXC2, SRF, SEMA3E, VEGFA	642	40	18082	3.520639	1	0.740216	0.733375
GO_BP	GO:0045773~positive regulation of axon extension	5	0.69	0.052276	PAK1, TNFRSF12A, SRF, MAP1B, MAPT	642	40	18082	3.520639	1	0.740216	0.733375
GO_BP	GO:0006486~protein glycosylation	9	1.24	0.054153	ST6GAL1, EXTL1, B3GALT2, ST3GAL6, ST6GALNAC3, ST3GAL1, GALNT10, ST6GALNAC6, ST3GAL3	642	116	18082	2.185224	1	0.740216	0.733375
GO_BP	GO:0050885~neuromuscular process controlling balance	6	0.83	0.054216	ABR, CLIC5, FOXS1, RBFOX2, NR4A3, ADCY5	642	58	18082	2.913632	1	0.740216	0.733375
GO_MF	GO:0005086~ARF guanyl-nucleotide exchange factor activity	4	0.55	0.054644	PSD3, NCK2, AMPH, ARFGEF3	608	25	17446	4.591053	1	0.59115	0.576247
KEGG	mmu04915:Estrogen signaling pathway	8	1.10	0.05533	GNAO1, JUN, CREB3L1, ITPR3, ADCY1, FOS, CALM2, ADCY5	270	98	7691	2.325321	0.99999	0.330352	0.299432
GO_BP	GO:0060395~SMAD protein signal transduction	7	0.97	0.055377	JUN, ATOH8, MAGI2, INHBB, VIM, FOS, GDF5	642	77	18082	2.560464	1	0.740216	0.733375
GO_BP	GO:0035413~positive regulation of catenin import into nucleus	3	0.41	0.05583	SEMA5A, KANK1, BAMBI	642	11	18082	7.681393	1	0.740216	0.733375
GO_BP	GO:0043589~skin morphogenesis	3	0.41	0.05583	COL1A2, SRF, ITGA2	642	11	18082	7.681393	1	0.740216	0.733375
GO_BP	GO:0000904~cell morphogenesis involved in differentiation	3	0.41	0.05583	EPB41L5, LAMB2, MYH9	642	11	18082	7.681393	1	0.740216	0.733375

GO_BP	GO:0060068~vagina development	3	0.41	0.05583	AXL, TYRO3, MERTK	642	11	18082	7.681393	1	0.740216	0.733375
GO_BP	GO:0048762~mesenchymal cell differentiation	3	0.41	0.05583	FOXC1, FGFR2, FGFR1	642	11	18082	7.681393	1	0.740216	0.733375
GO_BP	GO:0060484~lung-associated mesenchyme development	3	0.41	0.05583	PTK7, FGFR2, FGFR1	642	11	18082	7.681393	1	0.740216	0.733375
GO_BP	GO:0048339~paraxial mesoderm development	3	0.41	0.05583	EPB41L5, FGFR1, BMPR1A	642	11	18082	7.681393	1	0.740216	0.733375
GO_BP	GO:2000772~regulation of cellular senescence	3	0.41	0.05583	VASH1, BMPR1A, ARNTL	642	11	18082	7.681393	1	0.740216	0.733375
GO_BP	GO:0007017~microtubule-based process	5	0.69	0.056371	TUBB2B, TUBB2A, TUBA1A, MAP1B, KIF5B	642	41	18082	3.434769	1	0.740216	0.733375
GO_BP	GO:0031397~negative regulation of protein ubiquitination	5	0.69	0.056371	NXN, PELI3, CRY1, FYN, ARRB1	642	41	18082	3.434769	1	0.740216	0.733375
GO_MF	GO:0001948~glycoprotein binding	7	0.97	0.056967	ITGB1, ITGA3, TGFA, FYN, VIM, FGFR1, BMPR1A	608	79	17446	2.542513	1	0.597306	0.582248
GO_BP	GO:0032456~endocytic recycling	4	0.55	0.057192	ARL4C, EHD2, EHD4, RAB13	642	25	18082	4.506417	1	0.740216	0.733375
GO_BP	GO:0007585~respiratory gaseous exchange	4	0.55	0.057192	MAFB, DACH1, MAN1A2, NDN	642	25	18082	4.506417	1	0.740216	0.733375
GO_BP	GO:0003382~epithelial cell morphogenesis	4	0.55	0.057192	EPB41L5, HRH2, PALLD, FAT1	642	25	18082	4.506417	1	0.740216	0.733375
GO_BP	GO:0043001~Golgi to plasma membrane protein transport	4	0.55	0.057192	NSF, VAMP4, OPTN, VAMP2	642	25	18082	4.506417	1	0.740216	0.733375
GO_BP	GO:0048010~vascular endothelial growth factor receptor signaling pathway	4	0.55	0.057192	FOXC2, FOXC1, SULF1, VEGFA	642	25	18082	4.506417	1	0.740216	0.733375
GO_BP	GO:0048593~camera-type eye morphogenesis	4	0.55	0.057192	TENM3, FAT1, EPHB1, VEGFA	642	25	18082	4.506417	1	0.740216	0.733375
GO_MF	GO:0019838~growth factor binding	5	0.69	0.057355	FGFBP1, IGFBP2, HTRA1, CYR61, VEGFA	608	42	17446	3.415962	1	0.597306	0.582248
KEGG	mmu05410:Hypertrophic cardiomyopathy (HCM)	7	0.97	0.057605	ITGB1, ITGB5, ITGA3, ITGA2, TPM1, MYL3, DAG1	270	79	7691	2.524004	0.999994	0.334107	0.302836
GO_MF	GO:0044325~ion channel binding	9	1.24	0.058244	ACTN1, PDE4B, FYN, ARRB1, ACTN4, CALM2, VAMP2, CBARP, PPP1R9B	608	120	17446	2.152056	1	0.597306	0.582248
GO_BP	GO:0060326~cell chemotaxis	7	0.97	0.058282	SEMA5A, DOCK4, ARHGEF16, ELMO2, EPHB1, VEGFA, EPHA2	642	78	18082	2.527638	1	0.743646	0.736773
GO_BP	GO:0071260~cellular response to mechanical stimulus	7	0.97	0.058282	PTGER4, GADD45A, ITGA2, DAG1, ANKRD1, SCX, TLR7	642	78	18082	2.527638	1	0.743646	0.736773
GO_BP	GO:0009749~response to glucose	7	0.97	0.058282	GLP1R, NCF2, COL4A3, ENSA, ILDR2, MAFA, VAMP2	642	78	18082	2.527638	1	0.743646	0.736773
GO_MF	GO:0019905~syntaxin binding	7	0.97	0.059865	NSF, UNC13B, TXLNB, STXBP1, SYT9, VAMP2, SYT17	608	80	17446	2.510732	1	0.597306	0.582248
GO_MF	GO:0030552~cAMP binding	4	0.55	0.060233	PDE10A, PDE3B, PDE4B, PDE3A	608	26	17446	4.414474	1	0.597306	0.582248
GO_MF	GO:0043425~bHLH transcription factor binding	4	0.55	0.060233	BHLHE41, SCX, TCF21, ARNTL	608	26	17446	4.414474	1	0.597306	0.582248
GO_BP	GO:0007162~negative regulation of cell adhesion	5	0.69	0.060633	SEMA5A, PODXL, PDE3B, PLXNB1, AGER	642	42	18082	3.352989	1	0.767886	0.760789
GO_BP	GO:0045892~negative regulation of transcription, DNA-templated	29	4.00	0.06075	ZFP423, NAB1, NAB2, BHLHE41, SCX, LOXL2, ARNTL, RELB, FOXS1, DACH1, ATOH8, E2F1, HIVEP1, SMYD1, SOX8, SOX5, WNT4, JUN, RBFOX2, FOXD1, PRMT2, ATP8B1, CBFA2T3, SMO, MDFIC, WT1, CRY1, NFKBIE, ATF3	642	579	18082	1.410688	1	0.767886	0.760789
GO_BP	GO:0007030~Golgi organization	7	0.97	0.061276	RAB30, SPTBN5, ATP8B2, ATP8B1, OPTN, TJAP1, SYNE1	642	79	18082	2.495643	1	0.770941	0.763816
GO_BP	GO:0022604~regulation of cell morphogenesis	4	0.55	0.063012	FMNL2, SPARC, AGO4, WTIP	642	26	18082	4.333094	1	0.78005	0.772841
GO_BP	GO:0048843~negative regulation of axon extension involved in axon guidance	4	0.55	0.063012	SEMA5A, SEMA6C, SEMA3G, SEMA3E	642	26	18082	4.333094	1	0.78005	0.772841
GO_BP	GO:0001934~positive regulation of protein phosphorylation	12	1.66	0.063598	PTGER4, PAK1, ANXA2, MPRIP, MOB2, IL34, ARRB1, RSP01, AGER, CYR61, CDON, VEGFA	642	184	18082	1.836855	1	0.78005	0.772841
GO_BP	GO:0006351~transcription, DNA-templated	80	11.03	0.063953	BTG2, ZFP521, HIP1, CRTCL1, NAB1, NAB2, RASL11A, SETD7, BHLHE41, TCF21, SCX, ARRB1, ABRA, LOXL2, DACH1, CREB3L1, SOX8, LRRFIP1, ZFP37, SOX5, TEAD4, FOXD2, FOXD1, ARID5A, FOXL1, CBFA2T3, MDFIC, ELF4, CRY1, RARB, VOPP1, LMX1B, NUPR1, AJUBA, ATF3, VGLL3, KANK2, ZFP667, FOXC2, FOXC1, ZBTB8A, ZFP423, CASZ1, ZBTB46, SRF, ZBTB42, AEBP1, MED12L, NPAS2, ARNTL, RELB, FOXS1, ABLIM3, GBX1, ATOH8, HIVEP1, HOXC5, E2F1, SMYD1, HOXC4, NDN, HIVEP2, HOXC8, HOXC6, JUN, STAT1, EYA4, PBX2, WTIP, MAFA, SMAD6, PTPN14, FOSL2, NR4A2, NR4A1, MAFB, NR4A3, WT1, MAFK, LPIN2	642	1885	18082	1.195336	1	0.78005	0.772841
GO_MF	GO:0044212~transcription regulatory region DNA binding	14	1.93	0.064548	FOXC2, FOXC1, JUN, ARID5A, ARRB1, FOS, SMAD6, FOSL2, WT1, CREB3L1, E2F1, HIVEP2, ATF3, SOX5	608	233	17446	1.724108	1	0.631335	0.615419
GO_BP	GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	8	1.10	0.064751	DOK1, EPHA6, GDNF, NTRK3, FYN, EPHB1, PAG1, EPHA2	642	100	18082	2.253209	1	0.78005	0.772841
GO_BP	GO:0090002~establishment of protein localization to plasma membrane	5	0.69	0.065062	TSPAN15, TSPAN17, RAB13, MPP5, WNT4	642	43	18082	3.275013	1	0.78005	0.772841
GO_BP	GO:0050927~positive regulation of positive chemotaxis	3	0.41	0.065461	NTRK3, ITGA2, VEGFA	642	12	18082	7.041277	1	0.78005	0.772841
GO_BP	GO:0001818~negative regulation of cytokine production	3	0.41	0.065461	AXL, MERTK, EPHA2	642	12	18082	7.041277	1	0.78005	0.772841

GO_BP	GO:0042989~sequestering of actin monomers	3	0.41	0.065461	GSN, TMSB4X, TMSB10	642	12	18082	7.041277	1	0.78005	0.772841
GO_BP	GO:0002011~morphogenesis of an epithelial sheet	3	0.41	0.065461	SRF, DAG1, MPP5	642	12	18082	7.041277	1	0.78005	0.772841
GO_BP	GO:0043116~negative regulation of vascular permeability	3	0.41	0.065461	TJP1, PDE3A, ADM	642	12	18082	7.041277	1	0.78005	0.772841
GO_BP	GO:0021953~central nervous system neuron differentiation	3	0.41	0.065461	NR4A2, SMO, SOX5	642	12	18082	7.041277	1	0.78005	0.772841
GO_MF	GO:0043548~phosphatidylinositol 3-kinase binding	4	0.55	0.066077	AXL, TYRO3, FYN, CALM2	608	27	17446	4.250975	1	0.637551	0.621478
GO_MF	GO:0033549~MAP kinase phosphatase activity	2	0.28	0.068378	DUSP10, DUSP3	608	2	17446	28.69408	1	0.642389	0.626194
GO_MF	GO:0004119~cGMP-inhibited cyclic-nucleotide phosphodiesterase activity	2	0.28	0.068378	PDE3B, PDE3A	608	2	17446	28.69408	1	0.642389	0.626194
GO_BP	GO:0006931~substrate-dependent cell migration, cell attachment to substrate	2	0.28	0.069644	EPB41L5, TNFRSF12A	642	2	18082	28.16511	1	0.78834	0.781054
GO_BP	GO:0001971~negative regulation of activation of membrane attack complex	2	0.28	0.069644	CD59B, CD59A	642	2	18082	28.16511	1	0.78834	0.781054
GO_BP	GO:0006677~glycosylceramide metabolic process	2	0.28	0.069644	ST6GALNAC3, ST6GALNAC6	642	2	18082	28.16511	1	0.78834	0.781054
GO_BP	GO:0048378~regulation of lateral mesodermal cell fate specification	2	0.28	0.069644	FGFR1, BMPR1A	642	2	18082	28.16511	1	0.78834	0.781054
GO_BP	GO:1902257~negative regulation of apoptotic process involved in outflow tract morphogenesis	2	0.28	0.069644	FOXC2, FOXC1	642	2	18082	28.16511	1	0.78834	0.781054
GO_BP	GO:1903923~positive regulation of protein processing in phagocytic vesicle	2	0.28	0.069644	GSN, MYH9	642	2	18082	28.16511	1	0.78834	0.781054
GO_BP	GO:0035607~fibroblast growth factor receptor signaling pathway involved in orbitofrontal cortex development	2	0.28	0.069644	FGFR2, FGFR1	642	2	18082	28.16511	1	0.78834	0.781054
GO_BP	GO:0072249~metanephric glomerular visceral epithelial cell development	2	0.28	0.069644	NPHS2, LAMB2	642	2	18082	28.16511	1	0.78834	0.781054
GO_BP	GO:0035617~stress granule disassembly	2	0.28	0.069644	KIF5B, KLC1	642	2	18082	28.16511	1	0.78834	0.781054
GO_BP	GO:0001941~postsynaptic membrane organization	2	0.28	0.069644	CHRN1, GDNF	642	2	18082	28.16511	1	0.78834	0.781054
GO_BP	GO:0048706~embryonic skeletal system development	5	0.69	0.069654	HOXC5, SCX, GAS1, SULF1, HOXC6	642	44	18082	3.200581	1	0.78834	0.781054
GO_BP	GO:0051496~positive regulation of stress fiber assembly	5	0.69	0.069654	ARHGEF10, PAK1, SDC4, TPM1, WNT4	642	44	18082	3.200581	1	0.78834	0.781054
GO_MF	GO:0000149~SNARE binding	6	0.83	0.071577	STXBP1, TNFAIP2, VAMP4, SYT9, STX11, VAMP2	608	64	17446	2.69007	1	0.644941	0.628682
KEGG	mmu05140:Leishmaniasis	6	0.83	0.072388	ITGB1, JUN, NCF2, IFNGR1, STAT1, FOS	270	64	7691	2.670486	1	0.408185	0.369981
GO_MF	GO:0008191~metalloendopeptidase inhibitor activity	3	0.41	0.073166	WFIKK2, TIMP2, RECK	608	13	17446	6.621711	1	0.644941	0.628682
GO_MF	GO:0004115~3',5'-cyclic-AMP phosphodiesterase activity	3	0.41	0.073166	PDE3B, PDE4B, PDE3A	608	13	17446	6.621711	1	0.644941	0.628682
GO_MF	GO:0030898~actin-dependent ATPase activity	3	0.41	0.073166	MYO1D, MYL6, MYH9	608	13	17446	6.621711	1	0.644941	0.628682
GO_MF	GO:0030881~beta-2-microglobulin binding	3	0.41	0.073166	H2-Q6, H2-Q7, H2-Q4	608	13	17446	6.621711	1	0.644941	0.628682
GO_BP	GO:0030324~lung development	9	1.24	0.073913	SPARC, ITGA3, ALDH1A2, LIF, AARD, FGFR2, VEGFA, FGFR1, BMPR1A	642	124	18082	2.044242	1	0.831241	0.823559
GO_BP	GO:0006911~phagocytosis, engulfment	5	0.69	0.074408	GSN, ELMO1, SIRPA, MYH9, GULP1	642	45	18082	3.129457	1	0.831241	0.823559
GO_BP	GO:0045765~regulation of angiogenesis	4	0.55	0.07543	TNFRSF12A, EMP2, VASH1, EPHA2	642	28	18082	4.023587	1	0.831241	0.823559
GO_BP	GO:0043117~positive regulation of vascular permeability	3	0.41	0.075595	PDE3A, IL18, VEGFA	642	13	18082	6.499641	1	0.831241	0.823559
GO_BP	GO:0008406~gonad development	3	0.41	0.075595	SERPINB6A, SERPINB6B, WT1	642	13	18082	6.499641	1	0.831241	0.823559
GO_BP	GO:0001946~lymphangiogenesis	3	0.41	0.075595	FOXC2, PTPN14, VEGFA	642	13	18082	6.499641	1	0.831241	0.823559
GO_BP	GO:0040037~negative regulation of fibroblast growth factor receptor signaling pathway	3	0.41	0.075595	GPC1, SULF1, WNT4	642	13	18082	6.499641	1	0.831241	0.823559
GO_BP	GO:0007010~cytoskeleton organization	8	1.10	0.076413	FMNL2, ABLIM3, DLC1, DPYSL2, ELMO2, SIRPA, WTIP, AJUBA	642	104	18082	2.166547	1	0.836834	0.8291
GO_MF	GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding	19	2.62	0.077636	TEAD4, JUN, FOXD1, STAT1, SRF, BHLHE41, FOS, MAFA, SMAD6, FOSL2, DDN, RELB, NR4A2, NR4A3, MAFB, ELF4, NDN, FOSB, ATF3	608	359	17446	1.518628	1	0.675999	0.658957

GO_BP	GO:0000188~inactivation of MAPK activity	3	0.41	0.097188	DUSP10, DUSP3, DUSP8	642	15	18082	5.633022	1	0.959468	0.9506
GO_BP	GO:0040008~regulation of growth	6	0.83	0.097686	NELL2, SOCS2, IGFBP2, NDN, NEDD9, KCTD11	642	69	18082	2.44914	1	0.96088	0.951999
GO_MF	GO:0003714~transcription corepressor activity	10	1.38	0.097771	RBFOX2, BHLHE41, ANKRD1, SMYD1, AEBP1, WTIP, AJUBA, CBFA2T3, LOXL2, WNT4	608	157	17446	1.827648	1	0.761455	0.742259