Supplementary Materials

Table S1: the Full List of CA-RGs

Gene Name									
ACTR2	ACTR3	AGO4	ALMS1	ANAPC1	ANAPC10	ANAPC11	ANAPC13	ANAPC15	ANAPC16
ANAPC2	ANAPC4	ANAPC5	ANAPC7	ANKLE1	ANKRD31	ARHGEF10	ARL2	ASPM	ASZ1
ATF5	ATM	ATRX	AURKA	AURKC	BAG6	BBS4	BCL2L11	BOLL	BRCA1
BRCA2	BRDT	BRIP1	BRME1	BRSK1	BTBD18	BUB1	BUB1B	BUB3	C10orf90
C11orf80	C14orf39	C1orf146	C2CD3	CALR	CATSPERZ	CCDC102B	CCDC57	CCNA1	CCNB1IP1
CCNB2	CCNB3	CCNE1	CCNE2	CCNF	CCNL1	CCNL2	CCP110	CDC16	CDC20
CDC23	CDC25A	CDC25B	CDC25C	CDC26	CDC27	CDK1	CDK2	CDK5RAP2	CENATAC
CENPC	CENPJ	CENPS	CENPX	CEP120	CEP131	CEP135	CEP152	CEP192	CEP250
CEP295	CEP295NL	CEP44	CEP63	CEP68	CEP72	CEP76	CEP85	CETN1	CETN2
CETN3	CHD3	CHEK1	CHFR	CHMP1A	CHMP1B	CHMP2A	CHMP2B	CHMP3	CHMP4B
CHMP4C	CHMP5	CHORDC1	CKAP5	CKS2	CNTD1	CNTLN	CNTROB	CORT	CROCC
CTNNB1	CYP26B1	DCTN1	DDX4	DEUP1	DMC1	DMRT1	DMRTC2	DNMT3L	DUSP1
DUSP13	EDN1	EDNRA	EHMT2	EME1	EME2	ERCC1	ERCC4	EREG	ESPL1
EXD1	EXO1	FAM9A	FAM9B	FAM9C	FANCA	FANCD2	FANCM	FBXO43	FBXO5
FBXW5	FES	FIGNL1	FKBP6	FMN2	FOXJ2	FOXJ3	FZR1	GADD45A	GEN1
GOLGA2	GPR3	H1-8	H2AX	HAUS1	HAUS2	HAUS3	HAUS4	HAUS5	HAUS6
HAUS7	HAUS8	HEPACAM2	HFM1	HORMAD1	HORMAD2	HSF2BP	HSPA2	HUS1	HUS1B
IHO1	INCENP	ING2	INSR	KASH5	KAT2A	KAT2B	KIAA0753	KIAA1614	KIF11
KIF18A	KIF25	KIF3A	KIF3B	KLHDC3	LFNG	LIF	M1AP	MAEL	MAJIN
MAP9	MAPK15	MARF1	MARK4	MASTL	MCMDC2	MCPH1	MDM1	MEI1	MEI4
MEIKIN	MEIOB	MEIOC	MEIOSIN	METTL3	MLH1	MLH3	MND1	MNS1	MOS
MOV10L1	MRE11	MSH4	MSH5	MSH6	MSX1	MSX2	MUS81	MYBL1	MYH9
NANOS2	NAT10	NBN	NCAPD2	NCAPD3	NCAPH	NCAPH2	NDC1	NDC80	NDE1
NDEL1	NEK2	NIN	NPM1	NPM2	NPPC	NPR2	NSFL1C	NSUN2	NUBP1
NUF2	NUMA1	NUP62	ODF2	OOEP	OSGIN2	OVOL1	P3H4	PARD6A	PARD6B
PARD6G	PCLAF	PCM1	PDCD6IP	PDE3A	PDE4DIP	PDIK1L	PIWIL1	PIWIL2	PIWIL3

PIWIL4	PKD2	PKHD1	PKMYT1	PLCB1	PLD6	PLK1	PLK2	PLK4	POC1B
PPP1R12A	PPP1R35	PPP2CA	PPP2R1A	PRDM7	PRDM9	PRR19	PSMA8	PSMC3IP	PSMD13
PTTG1	PTTG2	PTTG3P	RAB6C	RAD1	RAD21	RAD21L1	RAD50	RAD51	RAD51AP1
RAD51B	RAD51C	RAD51D	RAD54B	RAD54L	RANBP1	RBBP8	RBM14	RBM7	REC114
REC8	RMI1	RNF212	RNF212B	ROCK2	RPA1	RPL10L	RPS6KA2	RSPH1	RTTN
SAC3D1	SASS6	SDCCAG8	SGO1	SGO2	SHCBP1L	SHOC1	SIRT1	SIRT2	SIRT7
SLC16A1	SLC25A31	SLC26A8	SLC2A8	SLX4	SMC1A	SMC1B	SMC2	SMC3	SMC4
SPATA22	SPDYA	SPICE1	SPIN1	SPIRE1	SPIRE2	SPO11	SSX2IP	STAG1	STAG2
STAG3	STIL	STK35	STRA8	SUN1	SUN2	SYCE1	SYCE1L	SYCE2	SYCE3
SYCP1	SYCP2	SYCP2L	SYCP3	TAF1L	TDRD1	TDRD12	TDRD9	TDRKH	TERB1
TERB2	TERF1	TESMIN	TEX11	TEX12	TEX14	TEX15	TEX19	TMEM67	NPHP11
TOP2A	TOP2B	TOP3A	TRIM37	TRIM75	TRIP13	TTK	TUBB8	TUBE1	TUBG1
TUBG2	TUBGCP2	TUBGCP3	TUBGCP4	TUBGCP5	TUBGCP6	UBB	UBE2B	UBR2	UBXN2B
USP17L2	USP33	UTP14C	UVRAG	UXT	VPS4B	WASHC5	WBP2NL	WDR62	WEE2
WNT4	WNT5A	XPO1	XRCC2	XRCC3	YTHDC2	YTHDF2	ZCWPW1	ZFP42	ZNF318
ZSCAN21	ZW10	JBTS6	MECKELIN	MKS3	NPHP11	TNEM67	ACTR1A	ACTR1B	AGBL2
AGBL4	AJUBA	AKAP11	AKAP9	ALDOB	ARFGEF2	ARL2BP	ARL3	ATF4	AUNIP
BBS1	BBS2	BBS5	BBS7	BBS9	BCL2L1	BIRC6	BLOC1S2	BOD1	BOD1L2
BRSK2	C14orf166	C4orf47	C7orf31	CAMK2B	CC2D1A	CCDC113	CCDC116	CCDC124	CCDC13
CCDC14	CCDC141	CCDC146	CCDC151	CCDC28B	CCDC38	CCDC64	CCDC78	CCDC8	CCDC81
CCDC85B	CCDC92	CCDC96	CCNB1	CCSAP	CCT4	CCT5	CCT8	CDC14A	CDC42
CDK5RAP3	CDK6	CEP104	CEP112	CEP126	CEP128	CEP162	CEP164	CEP170	CEP19
CEP290	CEP350	CEP41	CEP55	CEP57	CEP57L1	CEP70	CEP78	CEP83	CEP85L
CEP89	CEP95	CEP97	CFAP20	CHD4	CIB1	CIR1	CLASP1	CLASP2	CLIC4
CLIC5	CNTRL	CRMP1	CSNK1A1	CSNK1D	CSPP1	CTDP1	CUL7	CYLD	DCAF12
DCLRE1B	DCTN2	DCTN3	DCTN4	DIAPH1	DISC1	DTL	DZIP1	ECM29	EFHC1
ERCC6L2	EVI5	FAM110A	FAM110B	FAM110C	FBF1	FBXL7	FEZ1	FGFR1OP	FIGN
FLII	FOPNL	FRY	FSD1	FTCD	GNAI1	GNAI2	GNAI3	HERC2	HOOK2
IFT140	IFT20	IFT88	IQCB1	IST1	JTB	KATNA1	KATNB1	KIAA058	KIF13A

								6	
KIF20B	KIF24	KIF2A	KIF2B	KIFC1	KIFC3	KIZ	KLHL22	LATS1	LATS2
LCA5	LRMP	LRRC45	LRRCC1	LRWD1	LZTS2	MAD1L1	MAK	MAP10	MAP2K1
MAP3K11	MAPK1	MAPRE1	MIB1	MKKS	MKS1	MLLT11	MPHOSPH9	MPLKIP	MTUS1
MVB12A	MZT1	MZT2A	MZT2B	NCKAP5L	NDRG1	NEDD1	NEIL1	NEK1	NEK6
NEK7	NEURL4	NINL	NPHP4	NR3C1	NUBP2	NUDCD2	OBSL1	OFD1	PAFAH1B1
PARP3	PCNT	PDE4D	PHF1	PIBF1	PLA2G3	PLEKHA7	PLK3	POC1A	POC5
PPP1R42	PPP4C	PPP4R2	PPP4R3A	PPP4R3B	PSKH1	PTK2	PTPN20	RAB11FIP3	RAB11FIP4
RAB8A	RABGAP1	RAD18	RASSF1	RASSF10	RASSF7	RBBP6	RELB	RGCC	RGS14
RILPL1	RILPL2	RITA1	RNF19A	ROCK1	RPGR	RPGRIP1L	RPS7	RUVBL1	SAXO1
SCLT1	SCYL1	2-Sep	SFI1	SLF1	SLMAP	SNCG	SNX10	SPAG5	SPAST
SPATC1	SPDL1	SSNA1	STARD9	STOX1	STX1B	TACC1	TACC2	TBCCD1	TCP1
TMUB1	TOPBP1	TPGS1	TRIOBP	TRIP4	TSKS	TSSK2	TTBK2	TTC19	TTC23L
TTC28	TTC8	TUBD1	TXNDC9	UBXN6	UNC119	USP20	WASH1	WASH2P	WASH3P
WDR35	WRAP73	YES1	ZFYVE19	ZFYVE26	ZMYND10	ZNF365			

Table S2: Clinical Information of Included Samples

Serial number	Gender (male/female)	Age (Years)	height (cm)	weight (kg)	Kellgren-Lawrence (K-L) Grade	disease course(Years)	enrollment time	specimen site	specimen size
OA1	Female	67	160	56	4	2	2024.5.23	femoral condyle	rice grain-sized
OA2	Female	58	159	61.5	4	1.5	2024.5.28	tibial condyle	rice grain-sized
OA3	Male	55	168	70	3	2	2024.5.28	femoral condyle	rice grain-sized
OA4	Male	51	168	72	4	1	2024.5.30	femoral condyle	rice grain-sized
OA5	Male	72	170	80	4	3	2024.5.30	femoral condyle	rice grain-sized
control1	Male	42	170	65	0	0	2024.9.14	femoral condyle	rice grain-sized

control 2	Male	42	168	47	0	0	2024.11.4	femoral condyle	rice grain-sized
control 3	Male	38	175	75	0	0	2025.3.14	femoral condyle	rice grain-sized
control 4	Male	44	153	65	0	0	2025.5.8	femoral condyle	rice grain-sized
control 5	Male	41	170	70	0	0	2025.5.29	femoral condyle	rice grain-sized

Table S3: Correlated primer sequence

Primer		Sequence
PLK2	F	GCGGACTATCACCTACCAGC
PLK2	R	CCCGAGTGCGAATGGTGG
SUN2	F	TGGAGGAACTGCATGGTGAC
SUN2	R	ATCCGAGTAGCCCACGTAGT
GAPDH	F	CGAAGGTGGAGTCAACGGATTT
GAPDH	R	

Table S4: Detailed results of GO functional enrichment analysis (landscape format, provided separately at the end of this file)

Table S5: F Statistics of Qualified IV SNPs for MR Analysis

SNP	F
rs116397662	29.79292102
rs34316188	274.0126728
rs344044	72.26183893
rs60204765	44.55425115
rs62274129	1562.234135
rs62276505	1549.322361
rs62278582	950.7997782
rs73013957	44.75334203
rs74694767	30.546576
rs7635194	241.8075408
rs76571345	33.33916031
rs79920523	64.74001158
rs1150347	80.21142472
rs12275999	25.82864455
rs17207890	944.7844474
rs500054	1149.374683
rs692806	181.4829037
rs7938725	328.6143459
rs1605740	42.87874206
rs34384235	33.50538091

rs62366403	54.8089122
rs76917228	25.29086975
rs4091703	387.457683
rs4680572	333.376137
rs55667203	31.44202654
rs55731730	419.9151415
rs62270444	30.13559058
rs6441324	344.0522617
rs1013339	2140.679743
rs11704021	1808.828921
rs1354034	41.77263578
rs138430	1845.917048
rs139307	28.45046434
rs17827494	451.2234718
rs35607824	79.87164824
rs4619721	112.4152961
rs5757333	252.0666452
rs79409900	31.85913613
rs10400322	42.00365068
rs10899150	155.805664
rs11236557	261.1840532
rs11236612	169.9163766
rs117143578	67.63564397
rs192134125	109.9648283
rs36016715	172.8991105
rs61895075	25.40281666
rs7130007	67.16464275
rs77845531	73.62820544
rs78131992	49.5602742
rs78757099	30.35574729

Table S6: GO Enrichment Analysis Results (landscape format, provided separately at the end of this file)

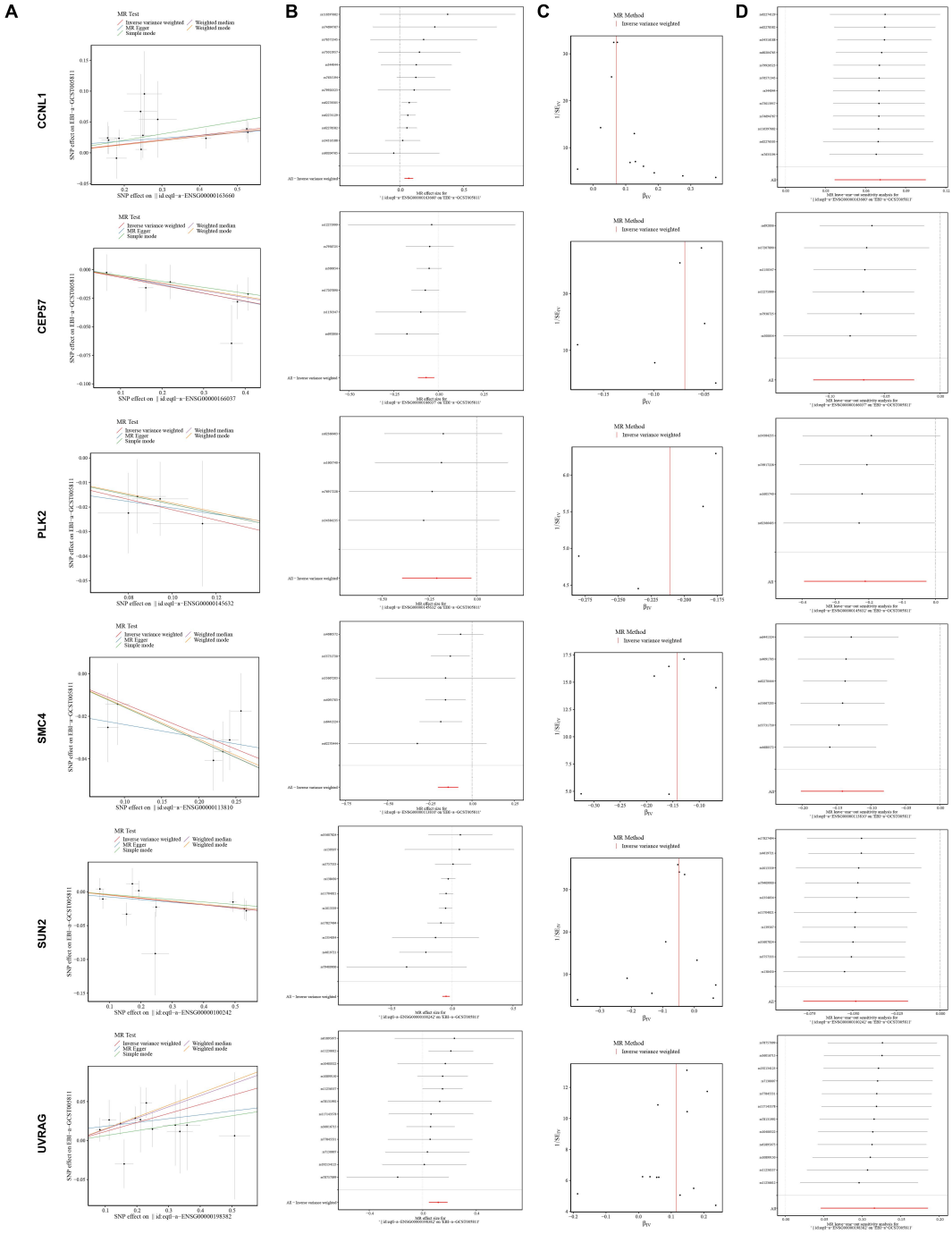

Figure S1: MR analysis results. (A) Scatter plots of exposure-outcome associations. (B) Forest plots of SNP effects. (C) Funnel plots for MR validity. (D) Leave-one-out sensitivity analysis.

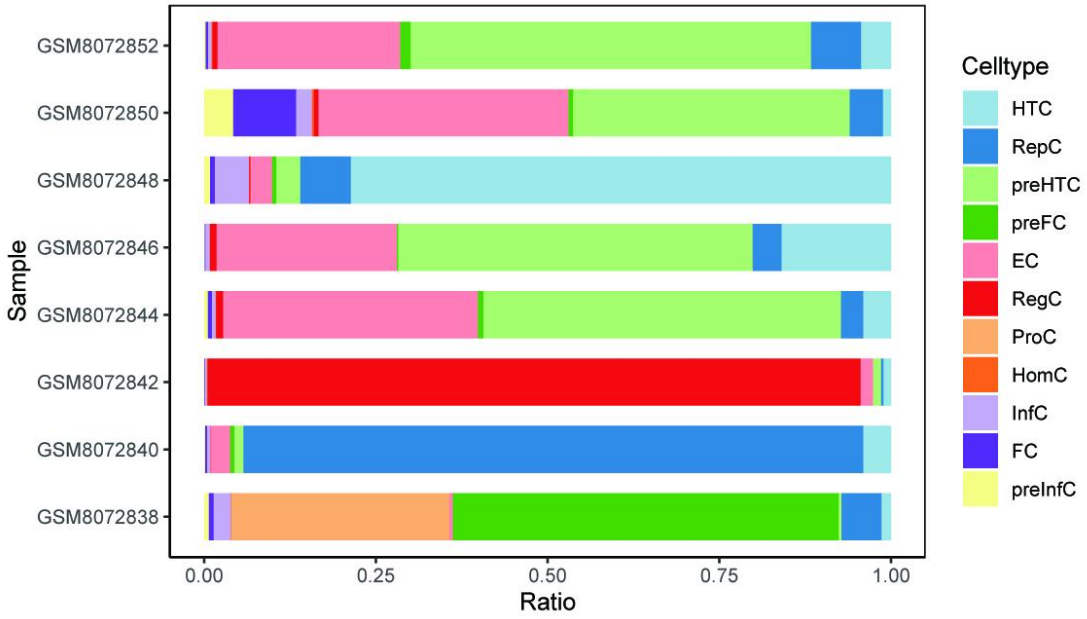

Figure S2: Proportion of cell types in individual samples from the scRNA-seq dataset.

Table S4	ONTOLOGY	ID	Descriptio	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count	richFactor
GO:0051321	BP	GO:0051321	meiotic cell cycle	17/42	285/18903	1.2093719632858e-20	2.0704448114529e-17	1.3659538069533e-17	SMC4/TOP2A/DUSP1/RBM7/INSR/SUN2/SHCBP1L/RMI1/MSX1/NDC80/CYP26B1/EDN1/CCNB1IP1/ASPM/ATM/RPA	17	0.596491228070175
GO:0031023	BP	GO:0031023	microtubule organizing center organization	14/42	150/18903	9.2321406186034e-20	7.9027123695245e-17	5.2137299388218e-17	GADD45A/CCNL1/CCDC102B/MARK4/PLK2/CEP72/UVRAG/KIF11/CLASP2/NDC80/SSX2IP/PAFAH1B1/CETN2/CDK	14	0.933333333333333
GO:0000280	BP	GO:0000280	nuclear division	18/42	481/18903	2.9407465482493e-18	1.6781860302009e-15	1.1071652793935e-15	SMC4/TOP2A/DUSP1/INSR/CUL7/SHCBP1L/RMI1/MSX1/KIF11/CLASP2/NDC80/SPDL1/CYP26B1/RGCC/EDN1/CCNB1IP1/ASP	18	0.374220374220374

GO:0007098	BP	GO:0007098	centrosome cycle	12/42	135/18903	9.85500317257915e-17	4.21794135786387e-14	2.78274168530985e-14	GADD45A/CCNL1/CCDC102B/MARK4/PLK2/CEP72/UVRAG/KIF11/NDC80/SSX2IP/CETN2	12	0.888888888888889
GO:1903046	BP	GO:1903046	meiotic cell cycle process	11/42	212/18903	8.59284252866617e-13	2.94218928181529e-10	1.94107790173869e-10	SMC4/TOP2A/SHCBP1L/RMI1/MSX1/NDC80/CYP26B1/EDN1/CCNB1IP1/ASP	11	0.518867924528302
GO:0140013	BP	GO:0140013	meiotic nuclear division	10/42	194/18903	1.1363810169263e-11	3.24247383496306e-09	2.13918742 30911e-09	SMC4/TOP2A/SHCBP1L/RMI1/MSX1/NDC80/CYP26B1/CCNB1IP1/ASPM/ATM	10	0.515463917525773
GO:0051783	BP	GO:0051783	regulation of nuclear division	9/42	145/18903	2.57322590169271e-11	6.29337534813989e-09	4.15198705641546e-09	DUSP1/INSR/CUL7/MSX1/NDC80/SPDL1/RGCC/EDN1/ATM	9	0.620689655172414
GO:0140014	BP	GO:0140014	mitotic nuclear division	11/42	325/18903	8.72643449831605e-11	1.86745698263963e-08	1.23203476535436e-08	SMC4/DUSP1/INSR/CUL7/KIF11/CLASP2/NDC80/SPDL1/RGCC/EDN1/ATM	11	0.338461538461538
GO:0007088	BP	GO:0007088	regulation of mitotic nuclear division	8/42	118/18903	1.79288349527689e-10	3.41046282657116e-08	2.25001636307849e-08	DUSP1/INSR/CUL7/NDC80/SPDL1/RGCC/EDN1/AT	8	0.677966101694915

GO:0033044	BP	GO:0033044	regulation of chromosome organization	9/42	252/18903	3.50323949125125e-09	5.99754600902215e-07	3.95681681485536e-07	SMC4/TOP2A/DUSP1/SHCBP1L/NDC80/MAPK1/SPDL1/ATM/CDK	9	0.357142857142857
GO:0007059	BP	GO:0007059	chromosome segregation	10/42	382/18903	8.35452730941653e-09	1.30026825033828e-06	8.57838067273104e-07	SMC4/TOP2A/DUSP1/RMI1/UVRAG/KIF11/NDC80/SPDL1/CCNB1IP1/ATM	10	0.261780104712042
GO:0007051	BP	GO:0007051	spindle organization	8/42	195/18903	9.7086692020632e-09	1.38510347282768e-06	9.13807197702966e-07	PLK2/SUN2/CEP72/UVRAG/KIF11/CLASP2/NDC80/ASPM	8	0.410256410256641
GO:0051304	BP	GO:0051304	chromosome separation	7/42	135/18903	1.77485665545613e-08	2.33734968780069e-06	1.54204145044893e-06	SMC4/TOP2A/DUSP1/RMI1/NDC80/SPDL1/ATM	7	0.518518518518518
GO:0022412	BP	GO:0022412	cellular process involved in reproduction in multicellu	10/42	430/18903	2.56568151135437e-08	3.1374619624562e-06	2.06990696367161e-06	TOP2A/SHCBP1L/CEP57/NDC80/PAFAH1B1/CYP26B1/EDN1/CCNB1IP1/ASPM/ATM	10	0.232558139534884
GO:0098813	BP	GO:0098813	nuclear chromosome segregation	9/42	321/18903	2.8606444559549e-08	3.26494887239653e-06	2.1540150885892e-06	SMC4/TOP2A/DUSP1/RMI1/KIF11/NDC80/SPDL1/CCNB1IP1/A	9	0.280373831775701

GO:1902850	BP	GO:1902850	microtubule cytoskeleton organization	7/42	163/18903	6.52101722446204e-08	6.97748843017438e-06	4.6033233433209e-06	PLK2/SUN2/KIF11/CLASP2/NDC80/SPDL1/PAFAH1B1	7	0.429447852760736
GO:0140694	BP	GO:0140694	non-membrane-bounded organelle assembly	9/42	386/18903	1.3824494965912e-07	1.3922079636259e-05	9.1849430949991e-06	PLK2/CEP72/KIF11/CLASP2/NDC80/EDN1/CETN2/ASPM/CDK2	9	0.233160621761658
GO:0051653	BP	GO:0051653	spindle localization	5/42	59/18903	1.9397642839442e-07	1.8449313633958e-05	1.2171737290481e-05	CLASP2/NDC80/SPDL1/PAFAH1B1/AS	5	0.847457627118644
GO:1901991	BP	GO:1901991	negative regulation of mitotic cell cycle phase transition	7/42	194/18903	2.1422290763036e-07	1.9302611466483e-05	1.2734691406503e-05	DUSP1/PLK2/NDC80/SPDL1/RGCC/ATM/CDK2	7	0.360824742268041
GO:0051298	BP	GO:0051298	centrosome duplication	5/42	74/18903	6.0904696009004e-07	5.2134419783707e-05	3.4395125693506e-05	PLK2/CEP72/NDC80/CETN2/CDK2	5	0.675675675675676
GO:0007093	BP	GO:0007093	mitotic cell cycle checkpoint signaling	6/42	141/18903	6.5100078868023e-07	5.3072064296217e-05	3.5013726629267e-05	DUSP1/PLK2/NDC80/SPDL1/ATM/CDK2	6	0.425531914893617
GO:0000819	BP	GO:0000819	sister chromatid segregation	7/42	239/18903	8.7546719528992e-07	6.8127265378925e-05	4.4946234475889e-05	SMC4/TOP2A/DUSP1/KIF11/NDC80/SPDL1/ATM	7	0.292887029288703

GO:0045930	BP	GO:0045930	negative regulation of mitotic cell cycle	7/42	246/18903	1.0620661512161e-06	7.9054663081824e-05	5.2155468203884e-05	DUSP1/PLK2/NDC80/SPDL1/RGCC/ATM/CDK2	7	0.284552845528455
GO:0045787	BP	GO:0045787	positive regulation of cell cycle	8/42	362/18903	1.1193419277526e-06	7.9846390846351e-05	5.2677802126251e-05	SMC4/INSR/MARK4/MSX1/NDC80/PAFAH1B1/RGCC/EDN1	8	0.220994475138122
GO:0040001	BP	GO:0040001	establishment of mitotic spindle localization	4/42	38/18903	1.4708062958999e-06	0.000100720815143226	6.6449480231604e-05	CLASP2/NDC80/SPDL1/PAFAH1B1	4	1.05263157894737
GO:0051657	BP	GO:0051657	maintenance of organelle location	3/42	11/18903	1.6621637834098e-06	0.000109447092199907	7.2206548161891e-05	UVRAG/PAFAH1B1/ASPM	3	2.72727272727273
GO:1901988	BP	GO:1901988	negative regulation of cell cycle phase	7/42	272/18903	2.0738856139486e-06	0.000131499710040002	8.6755526852509e-05	DUSP1/PLK2/NDC80/SPDL1/RGCC/ATM/CDK2	7	0.257352941176471
GO:0007099	BP	GO:0007099	centriole replicatio	4/42	42/18903	2.2159661450458e-06	0.000135490501439899	8.9388408783209e-05	PLK2/CEP72/CETN2/CDK	4	0.952380952380952
GO:2001251	BP	GO:2001251	negative regulation of chromosome organization	5/42	97/18903	2.3468048056563e-06	0.000138542407837366	9.1401871378193e-05	TOP2A/DUSP1/NDC80/SPDL1/ATM	5	0.515463917525773

GO:0042770	BP	GO:0042770	signal transduction in response to DNA	6/42	181/18903	2.79481246654701e-06	0.000155593644912313	0.000102651242616153	GADD45A/PLK2/MSX1/NDRG1/ATM/CDK2	6	0.331491712707182
GO:0045132	BP	GO:0045132	meiotic chromosome segregatio	5/42	101/18903	2.86561586251618e-06	0.000155593644912313	0.000102651242616153	SMC4/TOP2A/RMI1/CCNB1IP1/ATM	5	0.495049504950495
GO:0007094	BP	GO:0007094	mitotic spindle assembly checkpoint signaling	4/42	46/18903	3.20998414079503e-06	0.000155593644912313	0.000102651242616153	DUSP1/NDC80/SPDL1/ATM	4	0.869565217391304
GO:0071173	BP	GO:0071173	spindle assembly checkpoint signaling	4/42	46/18903	3.20998414079503e-06	0.000155593644912313	0.000102651242616153	DUSP1/NDC80/SPDL1/ATM	4	0.869565217391304
GO:0071174	BP	GO:0071174	mitotic spindle checkpoint signaling	4/42	46/18903	3.20998414079503e-06	0.000155593644912313	0.000102651242616153	DUSP1/NDC80/SPDL1/ATM	4	0.869565217391304
GO:0098534	BP	GO:0098534	centriole assembly	4/42	46/18903	3.20998414079503e-06	0.000155593644912313	0.000102651242616153	PLK2/CEP72/CETN2/CDK	4	0.869565217391304
GO:0000075	BP	GO:0000075	cell cycle checkpoint signaling	6/42	186/18903	3.27182898180097e-06	0.000155593644912313	0.000102651242616153	DUSP1/PLK2/NDC80/SPDL1/ATM/CDK	6	0.322580645161290
GO:0000910	BP	GO:0000910	cytokinesis	6/42	187/18903	3.37475687648499e-06	0.000156150912771413	0.000103018894124279	CEP55/CUL7/PLK2/SHCBP1L/UVRAG/CETN2	6	0.320855614973262
GO:0031577	BP	GO:0031577	spindle checkpoint signaling	4/42	47/18903	3.50294920855646e-06	0.000157817080132860	0.000104118130215542	DUSP1/NDC80/SPDL1/ATM	4	0.851063829787234

GO:2001252	BP	GO:2001252	positive regulation of chromosome organization	5/42	106/18903	3.6365080276076e-06	0.00015963378032416	0.00010531641332315 7	SMC4/SHCBP1L/MAPK1/ATM/CDK2	5	0.471698113207547
GO:0045841	BP	GO:0045841	negative regulation of mitotic metaphase/ anaphase transition	4/42	48/18903	3.8152585076478 2e-06	0.00016329306412732 7	0.00010773085207121 3	DUSP1/NDC80/SPDL1/ATM	4	0.833333333333333
GO:1902100	BP	GO:1902100	negative regulation of metaphase/ anaphase transition of cell cycle	4/42	50/18903	4.5011438910450 4e-06	0.00018551886608701 6	0.00012239408713192 8	DUSP1/NDC80/SPDL1/ATM	4	0.8
GO:1905818	BP	GO:1905818	regulation of chromosome separation	5/42	111/18903	4.5616658188453 9e-06	0.00018551886608701 6	0.00012239408713192 8	SMC4/DUSP1/NDC80/SPDL1/ATM	5	0.450450450450045
GO:0033046	BP	GO:0033046	negative regulation of sister chromatid segregatio	4/42	51/18903	4.8763720642031e-06	0.00018551886608701 6	0.00012239408713192 8	DUSP1/NDC80/SPDL1/ATM	4	0.784313725490196

GO:0033048	BP	GO:0033048	negative regulation of mitotic sister chromatid segregatio	4/42	51/18903	4.8763720642031e-06	0.000185518866087016	0.000122394087131928	DUSP1/NDC80/SPDL1/ATM	4	0.784313725490196
GO:2000816	BP	GO:2000816	negative regulation of mitotic sister chromatid separation	4/42	51/18903	4.8763720642031e-06	0.000185518866087016	0.000122394087131928	DUSP1/NDC80/SPDL1/ATM	4	0.784313725490196
GO:0000070	BP	GO:0000070	mitotic sister chromatid segregatio	6/42	204/18903	5.5698344392176e-06	0.000202970983289068	0.000133907934744 94	SMC4/DUSP1/KIF11/NDC80/SPDL1/ATM	6	0.294117647058824
GO:0051985	BP	GO:0051985	negative regulation of chromosome segregatio	4/42	53/18903	5.6956333202657e-06	0.000202970983289068	0.000133907934744 94	DUSP1/NDC80/SPDL1/ATM	4	0.754716981132075
GO:1905819	BP	GO:1905819	negative regulation of chromosome separation	4/42	53/18903	5.6956333202657e-06	0.000202970983289068	0.000133907934744 94	DUSP1/NDC80/SPDL1/ATM	4	0.754716981132075
GO:0010948	BP	GO:0010948	negative regulation of cell cycle process	7/42	318/18903	5.8093330497455 2e-06	0.000202970983289068	0.000133907934744 94	DUSP1/PLK2/NDC80/SPDL1/RGCC/ATM/CDK2	7	0.220125786163522

GO:0051293	BP	GO:0051293	establishment of spindle localization	4/42	54/18903	6.14140091364182e-06	0.000210281567283096	0.000138731014322898	CLASP2/NDC80/SPDL1/PAFAH1B1	4	0.740740740740741
GO:0033047	BP	GO:0033047	regulation of mitotic sister chromatid segregation	4/42	56/18903	7.10964705430283e-06	0.000234071456864739	0.000154426139458845	DUSP1/NDC80/SPDL1/ATM	4	0.714285714285714
GO:0045839	BP	GO:0045839	negative regulation of mitotic nuclear division	4/42	56/18903	7.10964705430283e-06	0.000234071456864739	0.000154426139458845	DUSP1/NDC80/SPDL1/ATM	4	0.714285714285714
GO:0044772	BP	GO:0044772	mitotic cell cycle phase transition	8/42	473/18903	8.09405326590515e-06	0.000254815473732932	0.000168111782658286	DUSP1/PLK2/CLASP2/NDC80/SPDL1/RGCC/ATM/C	8	0.169133192389006
GO:0007131	BP	GO:0007131	reciprocal meiotic recombination	4/42	58/18903	8.18624477529865e-06	0.000254815473732932	0.000168111782658286	TOP2A/RMI1/CCNB1IP1/ATM	4	0.689655172413793
GO:0140527	BP	GO:0140527	reciprocal homologous recombination	4/42	58/18903	8.18624477529865e-06	0.000254815473732932	0.000168111782658286	TOP2A/RMI1/CCNB1IP1/ATM	4	0.689655172413793
GO:0051785	BP	GO:0051785	positive regulation of nuclear division	4/42	59/18903	8.76750065050735e-06	0.000268035020026533	0.000176833236896501	INSR/MSX1/RGCC/EDN1	4	0.677966101694915
GO:0007127	BP	GO:0007127	meiosis I	5/42	131/18903	1.02521036666504e-05	0.000307922832935182	0.000203148794724207	TOP2A/RMI1/NDC80/CCNB1IP1/ATM	5	0.381679389312977

GO:0051983	BP	GO:0051983	regulation of chromosome segregatio	5/42	132/18903	1.06383503332038e-05	0.00031401 4754662842	0.00020716 7874909757	SMC4/DUSP1 /NDC80/SPD L1/ATM	5	0.37878787 8787879
GO:0007052	BP	GO:0007052	mitotic spindle organizati on	5/42	133/18903	1.10358820 75469e-05	0.00032022 7629037339	0.00021126 675231005	PLK2/SUN2/ KIF11/CLAS P2/NDC80	5	0.37593984 962406
GO:0051784	BP	GO:0051784	negative regulation of nuclear division	4/42	63/18903	1.14012758 279057e-05	0.00032531 640362291	0.00021462 4016900752	DUSP1/NDC8 0/SPDL1/AT M	4	0.63492063 4920635
GO:1901990	BP	GO:1901990	regulation of mitotic cell cycle phase transition	7/42	354/18903	1.16839773 956547e-05	0.00032791 7529530507	0.00021634 0081890208	DUSP1/PLK2 /NDC80/SPD L1/RGCC/AT M/CDK2	7	0.19774011 299435
GO:0051445	BP	GO:0051445	regulation of meiotic cell cycle	4/42	64/18903	1.21418264 85761e-05	0.00033527 1079735852	0.00022119 150796641	DUSP1/INSR /MSX1/ASPM	4	0.625
GO:0061982	BP	GO:0061982	meiosis I cell cycle process	5/42	137/18903	1.27435727 248166e-05	0.00034553 5914410717	0.00022796 3622825073	TOP2A/RMI1 /NDC80/CCN B1IP1/ATM	5	0.36496350 3649635
GO:0035825	BP	GO:0035825	homologous recombinat ion	4/42	65/18903	1.29172304 452604e-05	0.00034553 5914410717	0.00022796 3622825073	TOP2A/RMI1 /CCNB1IP1/ ATM	4	0.61538461 5384615
GO:0048762	BP	GO:0048762	mesenchyma l cell differenti ation	6/42	252/18903	1.85566861 303676e-05	0.00048875 4563925989	0.00032245 059462161	CUL7/MSX1/ CLASP2/MAP K1/RGCC/ED N1	6	0.23809523 8095238

GO:0030330	BP	GO:0030330	DNA damage response, signal transduction by p53 class mediator	4/42	74/18903	2.16374875266673e-05	0.000561263312812945	0.00037028746596673	PLK2/MSX1/NDRG1/ATM	4	0.540540540540541
GO:0090068	BP	GO:0090068	positive regulation of cell cycle process	6/42	260/18903	2.21335791471388e-05	0.000565562499998531	0.00037312808717673	SMC4/INSR/MSX1/NDC80/RGCC/EDN1	6	0.230769230769231
GO:0071900	BP	GO:0071900	regulation of protein serine/threonine kinase activity	7/42	395/18903	2.36790984379244e-05	0.000596156125378333	0.00039330762575685 7	GADD45A/CCNL1/DUSP1/INSR/UVRAG/RGCC/EDN1	7	0.177215189873418
GO:0007292	BP	GO:0007292	female gamete generation	5/42	159/18903	2.61551238365806e-05	0.000648950318959797	0.00042813803015485 8	TOP2A/NDC80/EDN1/ASPM/ATM	5	0.314465408805031
GO:0045786	BP	GO:0045786	negative regulation of cell cycle	7/42	405/18903	2.77874868204899e-05	0.000679602534809695	0.00044836050162985 9	DUSP1/PLK2/NDC80/SPDL1/RGCC/ATM/CDK2	7	0.172839506172839
GO:0001837	BP	GO:0001837	epithelial to mesenchymal	5/42	169/18903	3.5039916681465e-05	0.000844906159981 24	0.00055741779984005 8	CUL7/MSX1/CLASP2/RGCC/EDN1	5	0.295857988165680 8
GO:0031571	BP	GO:0031571	mitotic G1 DNA damage checkpoint signaling	3/42	29/18903	3.57983601054998e-05	0.000851205451397 44	0.00056157368995908 3	PLK2/ATM/CDK2	3	1.034482758620 69

GO:0044819	BP	GO:0044819	mitotic G1/S transition checkpoint signaling	3/42	30/18903	3.97144963964963e-05	0.00093138654562742	0.00061447 2309061868	PLK2/ATM/CDK2	3	1
GO:0051642	BP	GO:0051642	centrosome localization	3/42	32/18903	4.83683978941881e-05	0.00110408929593133	0.00072841 1100918791	SUN2/PAFAH1B1/ASPM	3	0.9375
GO:0071539	BP	GO:0071539	protein localization to centrosome	3/42	32/18903	4.83683978941881e-05	0.00110408929593133	0.00072841 1100918791	MARK4/CEP72/SNX10	3	0.9375
GO:0030071	BP	GO:0030071	regulation of mitotic metaphase/anaphase transition	4/42	92/18903	5.1046106768137e-05	0.00114988072088224	0.00075862 1503631732	DUSP1/NDC80/SPDL1/ATM	4	0.43478260 8695652
GO:0000132	BP	GO:0000132	establishment of mitotic spindle orientatio	3/42	33/18903	5.3123043769829e-05	0.00115122342954364	0.00075950 734130615	NDC80/SPDL1/PAFAH1B1	3	0.90909090 9090909
GO:0007143	BP	GO:0007143	female meiotic nuclear division	3/42	33/18903	5.3123043769829e-05	0.00115122342954364	0.00075950 734130615	TOP2A/NDC80/ATM	3	0.90909090 9090909
GO:0061842	BP	GO:0061842	microtubule organizing center localizati	3/42	33/18903	5.3123043769829e-05	0.00115122342954364	0.00075950 734130615	SUN2/PAFAH1B1/ASPM	3	0.90909090 9090909

GO:1901987	BP	GO:1901987	regulation of cell cycle phase	7/42	453/18903	5.65817474723909e-05	0.00119992595376103	0.00079163 8310615831	DUSP1/PLK2/NDC80/SPDL1/RGCC/ATM/CDK2	7	0.15452538 6313466
GO:0007091	BP	GO:0007091	metaphase/anaphase transition of mitotic cell cycle	4/42	95/18903	5.78802336483229e-05	0.00119992595376103	0.00079163 8310615831	DUSP1/NDC80/SPDL1/ATM	4	0.42105263 1578947
GO:1902099	BP	GO:1902099	regulation of metaphase/anaphase transition of cell cycle	4/42	95/18903	5.78802336483229e-05	0.00119992595376103	0.00079163 8310615831	DUSP1/NDC80/SPDL1/ATM	4	0.42105263 1578947
GO:1905508	BP	GO:1905508	protein localization to microtubule	3/42	34/18903	5.81739802349098e-05	0.00119992595376103	0.00079163 8310615831	MARK4/CEP72/SNX10	3	0.88235294 1176471
GO:0060485	BP	GO:0060485	organizing mesenchyme development	6/42	313/18903	6.23810989071452e-05	0.00127138620629801	0.00083878 3447711363	CUL7/MSX1/CLASP2/MAPK1/RGCC/ED	6	0.19169329 0734824
GO:0010965	BP	GO:0010965	regulation of mitotic sister chromatid separation	4/42	98/18903	6.53593924013455e-05	0.00129407133239186	0.00085374 9716955527	DUSP1/NDC80/SPDL1/ATM	4	0.40816326 5306122

GO:0044784	BP	GO:0044784	metaphase/anaphase transition of cell cycle	4/42	98/18903	6.53593924013455e-05	0.00129407133239186	0.00085374 9716955527	DUSP1/NDC80/SPDL1/ATM	4	0.40816326 5306122
GO:0007281	BP	GO:0007281	germ cell developmen t	6/42	316/18903	6.57618025222501e-05	0.00129407133239186	0.00085374 9716955527	CEP57/PAFAH1B1/EDN1/CCNB1IP1/ASPM/ATM	6	0.18987341 7721519
GO:0051306	BP	GO:0051306	mitotic sister chromatid separation	4/42	101/18903	7.35199977205174e-05	0.00143029813747188	0.00094362 3894187981	DUSP1/NDC80/SPDL1/ATM	4	0.39603960 3960396
GO:0033045	BP	GO:0033045	regulation of sister chromatid segregatio	4/42	107/18903	9.20344853242857e-05	0.00177037 12233166	0.00116798 347431057	DUSP1/NDC80/SPDL1/ATM	4	0.37383177 5700935
GO:0051294	BP	GO:0051294	establishm ent of spindle orientatio	3/42	40/18903	9.51626783010865e-05	0.00181020561390511	0.00119426 37873341	NDC80/SPDL1/PAFAH1B1	3	0.75
GO:0045840	BP	GO:0045840	positive regulation of mitotic nuclear division	3/42	44/18903	0.00012677 8247231018	0.00238510284900553	0.00157354 608766781	INSR/RGCC/EDN1	3	0.68181818 1818182
GO:0010639	BP	GO:0010639	negative regulation of organelle organizati on	6/42	366/18903	0.00014722 5515352609	0.00273967480743117	0.00180747 114385984	TOP2A/DUSP1/CLASP2/NDC80/SPDL1/ATM	6	0.16393442 6229508

GO:0007163	BP	GO:0007163	establishment or maintenance of cell polarity	5/42	234/18903	0.00016307 8053956924	0.00300203 901477692	0.00198056 312275924	CLASP2/NDC80/SPDL1/PAFAH1B1/CYP26B1	5	0.21367521 3675214
GO:0002688	BP	GO:0002688	regulation of leukocyte chemotaxis	4/42	127/18903	0.00017848 4580296053	0.00325069 788794513	0.00214461 315406119	DUSP1/MAPK1/EDN1/MTUS1	4	0.31496062 992126
GO:0051225	BP	GO:0051225	spindle assembly	4/42	128/18903	0.00018394 670288727	0.00331491 321413691	0.00218697 852851015	KIF11/CLASP2/NDC80/ASPM	4	0.3125
GO:0097529	BP	GO:0097529	myeloid leukocyte migration	5/42	242/18903	0.00019069 8159311496	0.00340078 3841055	0.00224363 075593459	DUSP1/MAPK1/PAFAH1B1/EDN1/MTUS	5	0.20661157 0247934
GO:1901203	BP	GO:1901203	positive regulation of extracellular matrix assembly	2/42	10/18903	0.00021443 9226597935	0.00374612 199934352	0.00247146 391127373	CLASP2/RGCC	2	2
GO:1904779	BP	GO:1904779	regulation of protein localization to centrosome	2/42	10/18903	0.00021443 9226597935	0.00374612 199934352	0.00247146 391127373	MARK4/CEP72	2	2
GO:0007140	BP	GO:0007140	male meiotic nuclear division	3/42	53/18903	0.00022114 9970118703	0.00382433 079639615	0.00252306 132841433	SHCBP1L/CYP26B1/ATM	3	0.56603773 5849057

GO:0032886	BP	GO:0032886	regulation of microtubule-based process	5/42	252/18903	0.000230095858058208	0.003924131142337833	0.002588903538937833	CCNL1/MARK4/PLK2/CLASP2/PAFAH1B1	5	0.198412698412698
GO:0046605	BP	GO:0046605	regulation of centrosome cycle	3/42	54/18903	0.000233797533013118	0.003924131142337833	0.002588903538937833	CCNL1/MARK4/PLK2	3	0.555555555555556
GO:0072698	BP	GO:0072698	protein localization to microtubule cytoskeleton	3/42	54/18903	0.000233797533013118	0.003924131142337833	0.002588903538937833	MARK4/CEP72/SNX10	3	0.555555555555556
GO:0044380	BP	GO:0044380	protein localization to cytoskeleton	3/42	58/18903	0.000289052066681891	0.004804438234557250	0.003169676725086040	MARK4/CEP72/SNX10	3	0.517241379310345
GO:0090596	BP	GO:0090596	sensory organ morphogenesis	5/42	272/18903	0.000327239035929609	0.005386857976072020	0.003553921918547270	ATF4/MSX1/MAPK1/CYP26B1/EDN1	5	0.183823529411765
GO:0030010	BP	GO:0030010	establishment of cell	4/42	150/18903	0.000337229606710385	0.005498448444649330	0.003627542536343290	NDC80/SPDL1/PAFAH1B1/CYP26B1	4	0.266666666666667
GO:0051656	BP	GO:0051656	establishment of organelle localization	6/42	437/18903	0.000382234748156135	0.006173451781540590	0.004072868766350870	SUN2/CLASP2/NDC80/SPDL1/PAFAH1B1/ATM	6	0.137299771167048

GO:0036294	BP	GO:0036294	cellular response to decreased oxygen	4/42	159/18903	0.000420609920319503	0.006729758725112040	0.004439886320736120	ATF4/RGCC/EDN1/NDRG1	4	0.251572327044025
GO:0010632	BP	GO:0010632	regulation of epithelial cell migration	5/42	292/18903	0.000452767242150791	0.007177199245945870	0.004735080417424940	GADD45A/PLK2/CLASP2/RGCC/EDN1	5	0.171232876712329
GO:0007004	BP	GO:0007004	telomere maintenance via telomerase	3/42	69/18903	0.000482554932170083	0.007579211411698920	0.005000303642863350	MAPK1/ATM/RPA1	3	0.434782608695652
GO:0000212	BP	GO:0000212	meiotic spindle organization	2/42	15/18903	0.000496843283754310	0.007594604480244450	0.005010459055153890	NDC80/ASPM	2	1.333333333333333
GO:0061307	BP	GO:0061307	cardiac neural crest cell differentiation involved in heart developmen	2/42	15/18903	0.000496843283754310	0.007594604480244450	0.005010459055153890	MAPK1/EDN1	2	1.333333333333333
GO:0061308	BP	GO:0061308	cardiac neural crest cell developmen t involved in heart developmen	2/42	15/18903	0.000496843283754310	0.007594604480244450	0.005010459055153890	MAPK1/EDN1	2	1.333333333333333

GO:0043517	BP	GO:0043517	positive regulation of DNA damage response, signal transduction by p53 class mediator	2/42	16/18903	0.000567021211169682	0.008515265908092 06	0.005617855582502 94	MSX1/ATM	2	1.25
GO:1901201	BP	GO:1901201	regulation of extracellular matrix assembly	2/42	16/18903	0.000567021211169682	0.008515265908092 06	0.005617855582502 94	CLASP2/RGCC	2	1.25
GO:0072331	BP	GO:0072331	signal transduction by p53 class mediator	4/42	173/18903	0.000578193925796033	0.008607547834459 2	0.005678737596147 76	PLK2/MSX1/NDRG1/ATM	4	0.23121387283237
GO:0036293	BP	GO:0036293	response to decreased oxygen	5/42	309/18903	0.000585519064845863	0.008641453784621 71	0.005701106684025 51	ATF4/RGCC/EDN1/NDRG1/ATM	5	0.16181229773462 8
GO:2000573	BP	GO:2000573	positive regulation of DNA biosynthetic process	3/42	74/18903	0.000592450671617029	0.008669021793233 79	0.005719294382771 68	MAPK1/RGCC/ATM	3	0.40540540540540 5
GO:0071453	BP	GO:0071453	cellular response to oxygen levels	4/42	175/18903	0.000603703467142558	0.008758816404644 57	0.005778535416984 52	ATF4/RGCC/EDN1/NDRG1	4	0.22857142857142 9

GO:0006278	BP	GO:0006278	RNA-templated DNA biosynthetic process	3/42	75/18903	0.00061618 5291372587	0.00885404 752146653	0.00584136 312748007	MAPK1/ATM/ RPA1	3	0.4
GO:0018105	BP	GO:0018105	peptidyl-serine phosphorylation	5/42	313/18903	0.00062061 080757943	0.00885404 752146653	0.00584136 312748007	GADD45A/PLK2/MAPK1/ATM/CDK2	5	0.15974440 8945687
GO:0070192	BP	GO:0070192	chromosome organization involved in meiotic	3/42	76/18903	0.00064051 966424921	0.00895604 836264848	0.00590865 70911964	SMC4/CCNB1IP1/ATM	3	0.39473684 2105263
GO:0042481	BP	GO:0042481	regulation of odontogenesis	2/42	17/18903	0.00064171 9131672179	0.00895604 836264848	0.00590865 70911964	MSX1/EDN1	2	1.17647058 823529
GO:0031503	BP	GO:0031503	protein-containing complex localization	4/42	178/18903	0.00064345 4409232338	0.00895604 836264848	0.00590865 70911964	RPGR/CEP72/SSX2IP/ATM	4	0.22471910 1123595
GO:0001667	BP	GO:0001667	ameboidal-type cell migration	6/42	492/18903	0.00071403 9426381156	0.00964227 258135598	0.00636138 617793591	GADD45A/PLK2/CLASP2/PAFAH1B1/RGCC/EDN1	6	0.12195121 9512195
GO:0000712	BP	GO:0000712	resolution of meiotic recombination intermediates	2/42	18/18903	0.00072091 7576176148	0.00964227 258135598	0.00636138 617793591	TOP2A/RMI1	2	1.11111111 111111

GO:0006977	BP	GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	2/42	18/18903	0.000720917576176148	0.009642272581355980	0.006361386177935910	PLK2/ATM	2	1.111111111111111
GO:0034501	BP	GO:0034501	protein localization to kinetochor	2/42	18/18903	0.000720917576176148	0.009642272581355980	0.006361386177935910	NDC80/SPDL1	2	1.111111111111111
GO:1903083	BP	GO:1903083	protein localization to condensed chromosome	2/42	18/18903	0.000720917576176148	0.009642272581355980	0.006361386177935910	NDC80/SPDL1	2	1.111111111111111
GO:2000045	BP	GO:2000045	regulation of G1/S transition of mitotic cell cycle	4/42	185/18903	0.000743386174327865	0.009865714189529490	0.006508799388443890	PLK2/RGCC/ATM/CDK2	4	0.216216216216216
GO:0010833	BP	GO:0010833	telomere maintenance via telomere lengthenin	3/42	81/18903	0.000771401865651782	0.010081221328212600	0.006650977917592300	MAPK1/ATM/RPA1	3	0.370370370370370
GO:0044773	BP	GO:0044773	mitotic DNA damage checkpoint signaling	3/42	81/18903	0.000771401865651782	0.010081221328212600	0.006650977917592300	PLK2/ATM/CDK2	3	0.370370370370370

GO:0051303	BP	GO:0051303	establishment of chromosome localization	3/42	82/18903	0.000799462535643474	0.010340373328568	0.00682195067729555	NDC80/SPDL1/ATM	3	0.365853658536585
GO:0006310	BP	GO:0006310	DNA recombination	5/42	332/18903	0.000809351650717356	0.010340373328568	0.00682195067729555	TOP2A/RMI1/CCNB1IP1/ATM/RPA1	5	0.150602409638554
GO:0018209	BP	GO:0018209	peptidyl-serine modification	5/42	332/18903	0.000809351650717356	0.010340373328568	0.00682195067729555	GADD45A/PLK2/MAPK1/ATM/CDK2	5	0.150602409638554
GO:0051302	BP	GO:0051302	regulation of cell division	4/42	190/18903	0.000821180065438504	0.010413779792820 1	0.00687037980674865	PLK2/UVRAG/CETN2/ASPM	4	0.210526315789474
GO:0070482	BP	GO:0070482	response to oxygen levels	5/42	337/18903	0.000865470925654818	0.010894751652360 7	0.00718769584541502	ATF4/RGCC/EDN1/NDRG1/ATM	5	0.148367952522255
GO:0044774	BP	GO:0044774	mitotic DNA integrity checkpoint	3/42	85/18903	0.000887519366338784	0.011075132247742 7	0.00730670001342102	PLK2/ATM/CDK2	3	0.352941176470588
GO:0042474	BP	GO:0042474	middle ear morphogenesis	2/42	20/18903	0.000892738463895 15	0.011075132247742 7	0.00730670001342102	MSX1/EDN1	2	1
GO:0032872	BP	GO:0032872	regulation of stress-activated MAPK cascade	4/42	195/18903	0.000904565505324297	0.011141123346152 5	0.00735023693459273	GADD45A/DUSP1/MAPK1/PAFAH1B1	4	0.205128205128205

GO:2000134	BP	GO:2000134	negative regulation of G1/S transition of mitotic cell cycle	3/42	87/18903	0.000949510783439577	0.011542393416072 2	0.007614970570244 37	PLK2/ATM/CDK2	3	0.344827586206897
GO:0070302	BP	GO:0070302	regulation of stress-activated protein kinase signaling cascade	4/42	198/18903	0.000957371416520005	0.011542393416072 2	0.007614970570244 37	GADD45A/DUSP1/MAPK1/PAFAH1B1	4	0.202020202020202
GO:0071897	BP	GO:0071897	DNA biosynthetic process	4/42	198/18903	0.000957371416520005	0.011542393416072 2	0.007614970570244 37	MAPK1/RGCC/ATM/RPA1	4	0.202020202020202
GO:0036092	BP	GO:0036092	phosphatidylinositol-3-phosphate biosynthet	2/42	21/18903	0.000985322271499081	0.011553915950729	0.007622572439210 63	UVRAG/ATM	2	0.952380952380952
GO:0090231	BP	GO:0090231	regulation of spindle checkpoint	2/42	21/18903	0.000985322271499081	0.011553915950729	0.007622572439210 63	DUSP1/NDC80	2	0.952380952380952
GO:0090266	BP	GO:0090266	regulation of mitotic cell cycle spindle assembly checkpoint	2/42	21/18903	0.000985322271499081	0.011553915950729	0.007622572439210 63	DUSP1/NDC80	2	0.952380952380952
GO:1903504	BP	GO:1903504	regulation of mitotic spindle checkpoint	2/42	21/18903	0.000985322271499081	0.011553915950729	0.007622572439210 63	DUSP1/NDC80	2	0.952380952380952

GO:0050000	BP	GO:0050000	chromosome localization	3/42	89/18903	0.001014184611502	0.011811458880879	0.007792483636816 47	NDC80/SPDL1/ATM	3	0.337078651685393
GO:0045995	BP	GO:0045995	regulation of embryonic developmen	3/42	90/18903	0.001047541885623 08	0.012117511541802 1	0.007994398600807 69	INSR/CLASP2/PAFAH1B1	3	0.333333333333333
GO:2000241	BP	GO:2000241	regulation of reproductive process	4/42	206/18903	0.001108770873316 96	0.012739702920259 3	0.008404882706245 87	DUSP1/INSR/MSX1/ASPM	4	0.194174757281553
GO:0030705	BP	GO:0030705	cytoskeleton-dependent intracellular	4/42	208/18903	0.001149101883321 39	0.013115082828308 2	0.008652535584588 44	RPGR/SUN2/SSX2IP/PAFAH1B1	4	0.192307692307692
GO:0051383	BP	GO:0051383	kinetochore organizati	2/42	23/18903	0.001183740476568 66	0.013412439205371 2	0.008848713273095 98	SMC4/NDC80	2	0.869565217391304
GO:0060271	BP	GO:0060271	cilium assembly	5/42	362/18903	0.001190824041598 38	0.013412439205371 2	0.008848713273095 98	RPGR/MARK4/SNX10/SSX2IP/CCDC28	5	0.138121546961326
GO:0032465	BP	GO:0032465	regulation of cytokinesi	3/42	95/18903	0.001224747034847 24	0.013704358978160 4	0.009041304220096 92	PLK2/UVRAG/CETN2	3	0.315789473684211
GO:0010631	BP	GO:0010631	epithelial cell migration	5/42	366/18903	0.001250291934037 97	0.013853041407100 4	0.009139395861915 09	GADD45A/PLK2/CLASP2/RGCC/EDN1	5	0.136612021857923
GO:1902806	BP	GO:1902806	regulation of cell cycle G1/S phase transition	4/42	213/18903	0.001254424399796 96	0.013853041407100 4	0.009139395861915 09	PLK2/RGCC/ATM/CDK2	4	0.187793427230047

GO:0051153	BP	GO:0051153	regulation of striated muscle cell	3/42	96/18903	0.00126230984784326	0.0138530414071004	0.00913939586191509	MSX1/CYP26B1/EDN1	3	0.3125
GO:0007097	BP	GO:0007097	nuclear migration	2/42	24/18903	0.00128953659886349	0.0140461932612655	0.00926682573127019	SUN2/PAFAH1B1	2	0.833333333333333
GO:0090132	BP	GO:0090132	epithelium migration	5/42	369/18903	0.00129631923789716	0.0140461932612655	0.00926682573127019	GADD45A/PLK2/CLASP2/RGCC/EDN1	5	0.13550135501355
GO:1902807	BP	GO:1902807	negative regulation of cell cycle G1/S phase transition	3/42	98/18903	0.00133959967401632	0.0144238656724272	0.00951599106401527	PLK2/ATM/CDK2	3	0.306122448979592
GO:0090130	BP	GO:0090130	tissue migration	5/42	374/18903	0.00137580969523 67	0.0147211637390327	0.00971213028282225	GADD45A/PLK2/CLASP2/RGCC/EDN1	5	0.133689839572193
GO:0051446	BP	GO:0051446	positive regulation of meiotic cell cycle	2/42	25/18903	0.00139969865044114	0.0148837521090387	0.00981939622048604	INSR/MSX1	2	0.8
GO:0043583	BP	GO:0043583	ear development	4/42	221/18903	0.00143675117606498	0.0151834445273039	0.0100171150871847	MSX1/MAPK1/PAFAH1B1/EDN1	4	0.180995475113122
GO:0034453	BP	GO:0034453	microtubule	2/42	26/18903	0.00151420764280989	0.0157110514211547	0.0103651980908135	CEP57/CLASP2	2	0.769230769230769
GO:0051307	BP	GO:0051307	meiotic chromosome separation	2/42	26/18903	0.00151420764280989	0.0157110514211547	0.0103651980908135	TOP2A/RMI1	2	0.769230769230769
GO:1904353	BP	GO:1904353	regulation of telomere	2/42	26/18903	0.00151420764280989	0.0157110514211547	0.0103651980908135	MAPK1/ATM	2	0.769230769230769

GO:0048477	BP	GO:0048477	oogenesis	3/42	103/18903	0.00154568972429901	0.0159410892048187	0.0105169630575323	EDN1/ASPM/ATM	3	0.29126213592233
GO:0051651	BP	GO:0051651	maintenance of location	4/42	226/18903	0.00155967725246504	0.0159890266683953	0.0105485892965332	SUN2/UVRAG/PAFAH1B1/ASPM	4	0.17699115 0442478
GO:0110020	BP	GO:0110020	regulation of actomyosin structure organization	3/42	104/18903	0.00158915380150696	0.0161942339772614	0.0106839726128883	CLASP2/RGCC/EDN1	3	0.28846153 8461538
GO:1903055	BP	GO:1903055	positive regulation of extracellular matrix organization	2/42	27/18903	0.00163304464682643	0.0164841123324508	0.0108752167564681	CLASP2/RGCC	2	0.74074074 0740741
GO:0071241	BP	GO:0071241	cellular response to inorganic	4/42	229/18903	0.00163685 69488999	0.0164841123324508	0.0108752167564681	ATF4/MAPK1/EDN1/CDK2	4	0.17467248 9082969
GO:0010594	BP	GO:0010594	regulation of endothelial cell migration	4/42	230/18903	0.00166316460541772	0.0165542895560902	0.0109215154321494	GADD45A/PLK2/RGCC/EDN1	4	0.17391304 3478261
GO:0050920	BP	GO:0050920	regulation of chemotaxis	4/42	230/18903	0.00166316460541772	0.0165542895560902	0.0109215154321494	DUSP1/MAPK1/EDN1/MTUS1	4	0.17391304 3478261
GO:0044782	BP	GO:0044782	cilium organization	5/42	391/18903	0.00167326149618338	0.0165585183899766	0.0109243053568894	RPGR/MARK4/SNX10/SSX2IP/CCDC28	5	0.12787723 7851662

GO:0002685	BP	GO:0002685	regulation of leukocyte migration	4/42	231/18903	0.00168976569597396	0.0166257406408473	0.0109686545177257	DUSP1/MAPK1/EDN1/MTUS1	4	0.173160173160173
GO:0060348	BP	GO:0060348	bone development	4/42	233/18903	0.00174385510281795	0.0168910035776484	0.0111436589023713	MSX1/SNX10/PAFAH1B1/CYP26B1	4	0.171673819742489
GO:0010758	BP	GO:0010758	regulation of macrophage chemotaxis	2/42	28/18903	0.00175619079253587	0.0168910035776484	0.0111436589023713	MAPK1/MTUS1	2	0.714285714285714
GO:0030878	BP	GO:0030878	thyroid gland development	2/42	28/18903	0.00175619079253587	0.0168910035776484	0.0111436589023713	MAPK1/EDN1	2	0.714285714285714
GO:0051647	BP	GO:0051647	nucleus localization	2/42	28/18903	0.00175619079253587	0.0168910035776484	0.0111436589023713	SUN2/PAFAH1B1	2	0.714285714285714
GO:0090398	BP	GO:0090398	cellular senescence	3/42	108/18903	0.00177066182926431	0.0169350449815 67	0.0111727147474308	PLK2/ATM/CDK2	3	0.277777777777778
GO:0050900	BP	GO:0050900	leukocyte migration	5/42	398/18903	0.00180858817427848	0.0172016830798042	0.0113486263801217	DUSP1/MAPK1/PAFAH1B1/EDN1/MTUS	5	0.125628140703518
GO:0010458	BP	GO:0010458	exit from mitosis	2/42	29/18903	0.00188362726901219	0.0178164082019275	0.0117541847028211	CLASP2/RGCC	2	0.689655172413793
GO:0051403	BP	GO:0051403	stress-activated MAPK cascade	4/42	239/18903	0.00191334550634182	0.0179980632244901	0.011874029660525	GADD45A/DUSP1/MAPK1/PAFAH1B1	4	0.167364016736402
GO:0030595	BP	GO:0030595	leukocyte chemotaxis	4/42	240/18903	0.00194266524158259	0.0181740048830022	0.0119901052874209	DUSP1/MAPK1/EDN1/MTU	4	0.166666666666667
GO:0061640	BP	GO:0061640	cytoskeleton-dependent	3/42	113/18903	0.00201512258928415	0.0186500220271824	0.0123041525056362	CEP55/CUL7/SHCBP1L	3	0.265486725663717

GO:1901798	BP	GO:1901798	positive regulation of signal transduction by p53 class mediator	2/42	30/18903	0.00201533532419903	0.0186500220271824	0.0123041525056362	MSX1/ATM	2	0.666666666666667
GO:0034502	BP	GO:0034502	protein localization to chromosome	3/42	115/18903	0.00211849477369235	0.0194560832728744	0.0128359427888553	NDC80/SPDL1/RPA1	3	0.260869565217391
GO:0031098	BP	GO:0031098	stress-activated protein kinase signaling cascade	4/42	246/18903	0.00212516797431514	0.0194560832728744	0.0128359427888553	GADD45A/DUSP1/MAPK1/PAFAH1B1	4	0.162601626601626
GO:0000079	BP	GO:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity	3/42	117/18903	0.00222511452657256	0.0202627450504905	0.0133681292665865	GADD45A/CCNL1/RGCC	3	0.256410256410256
GO:0000082	BP	GO:0000082	G1/S transition of mitotic cell cycle	4/42	250/18903	0.00225323265958493	0.0204102344614254	0.0134654338275 39	PLK2/RGCC/ATM/CDK2	4	0.16
GO:0034390	BP	GO:0034390	smooth muscle cell apoptotic	2/42	32/18903	0.00229149145587465	0.0205394417406146	0.0135506769476632	ATF4/EDN1	2	0.625

GO:0034391	BP	GO:0034391	regulation of smooth muscle cell apoptotic	2/42	32/18903	0.00229149145587465	0.0205394417406146	0.0135506769476632	ATF4/EDN1	2	0.625
GO:0010927	BP	GO:0010927	cellular component assembly involved in morphogene	3/42	119/18903	0.00233501731309865	0.0208205710417963	0.0137361488996463	CLASP2/PAFAH1B1/EDN1	3	0.252100840336134
GO:1904029	BP	GO:1904029	regulation of cyclin-dependent protein kinase activity	3/42	120/18903	0.00239121075682864	0.0212111544854437	0.0139938322447621	GADD45A/CCNL1/RGCC	3	0.25
GO:0000077	BP	GO:0000077	DNA damage checkpoint signaling	3/42	121/18903	0.00244823797722041	0.0214942739333402	0.0141806172715655	PLK2/ATM/CDK2	3	0.247933884297521
GO:2000278	BP	GO:2000278	regulation of DNA biosynthetic process	3/42	121/18903	0.00244823797722041	0.0214942739333402	0.0141806172715655	MAPK1/RGCC/ATM	3	0.247933884297521
GO:0032212	BP	GO:0032212	positive regulation of telomere maintenance via	2/42	34/18903	0.00258451034248028	0.0225749066649298	0.0148935531551092	MAPK1/ATM	2	0.588235294117647
GO:0042471	BP	GO:0042471	ear morphogenesis	3/42	124/18903	0.00262436470116954	0.0228066617685394	0.0150464511052894	MSX1/MAPK1/EDN1	3	0.241935483870968

GO:0043244	BP	GO:0043244	regulation of protein-containing complex	3/42	126/18903	0.0027460284744641	0.0237434381226391	0.0156644792828282	INSR/UVRAG/CLASP2	3	0.238095238095238
GO:0048732	BP	GO:0048732	gland development	5/42	441/18903	0.0028234153846319	0.0242898851180396	0.0160249991841894	INSR/MSX1/MAPK1/EDN1/ATM	5	0.113378684807256
GO:0043243	BP	GO:0043243	positive regulation of protein-containing complex	2/42	36/18903	0.0028942440707072531	0.0246514718859788	0.0162635448436149	INSR/UVRAG	2	0.555555555555556
GO:0050775	BP	GO:0050775	positive regulation of dendrite morphogene	2/42	36/18903	0.0028942440707072531	0.0246514718859788	0.0162635448436149	CUL7/PAFAH1B1	2	0.555555555555556
GO:0031570	BP	GO:0031570	DNA integrity checkpoint signaling	3/42	129/18903	0.0029349748537511 1	0.0248746383644649	0.0164107765540255	PLK2/ATM/CDK2	3	0.232558139534884
GO:1904358	BP	GO:1904358	positive regulation of telomere maintenance via telomere	2/42	37/18903	0.0030553330311088 1	0.0257671435924054	0.0169995973159438	MAPK1/ATM	2	0.540540540540541
GO:0007611	BP	GO:0007611	learning or memory	4/42	273/18903	0.0030946860345569	0.0259710906429481	0.0171341492006169	INSR/PLK2/MAPK1/PAFAH1B1	4	0.146520146520147

GO:0043516	BP	GO:0043516	regulation of DNA damage response, signal transduction by p53 class mediator	2/42	38/18903	0.003220545654085253	0.026895483706312	0.017744007634575	MSX1/ATM	2	0.526315789473684
GO:0035270	BP	GO:0035270	endocrine system development	3/42	135/18903	0.003336482165249033	0.027594480516455733	0.018205163301867333	INSR/MAPK1/EDN1	3	0.222222222222222
GO:0042476	BP	GO:0042476	odontogenesis	3/42	135/18903	0.003336482165249033	0.027594480516455733	0.018205163301867333	MSX1/SNX10/EDN1	3	0.222222222222222
GO:0044843	BP	GO:0044843	cell cycle G1/S phase transition	4/42	280/18903	0.003388300760260083	0.027888321642140733	0.018399021840886	PLK2/RGCC/ATM/CDK2	4	0.142857142857143
GO:0043542	BP	GO:0043542	endothelial cell migration	4/42	281/18903	0.003431743051443323	0.028110737340052433	0.018545758218074433	GADD45A/PLK2/RGCC/EDN1	4	0.142348754448399
GO:0016233	BP	GO:0016233	telomere capping	2/42	40/18903	0.003563269027800823	0.028911452964905233	0.019074021785134833	MAPK1/ATM	2	0.5
GO:0048246	BP	GO:0048246	macrophage chemotaxis	2/42	40/18903	0.003563269027800823	0.028911452964905233	0.019074021785134833	MAPK1/MTUS1	2	0.5
GO:0045429	BP	GO:0045429	positive regulation of nitric oxide biosynthetic process	2/42	42/18903	0.003922269043901473	0.031674172656411933	0.020896696544718333	INSR/EDN1	2	0.476190476190476
GO:0014065	BP	GO:0014065	phosphatidylinositol 3-kinase signaling	3/42	145/18903	0.004077539426840743	0.032773462435452433	0.021621941215715933	CEP55/INSR/EDN1	3	0.206896551724138

GO:0071459	BP	GO:0071459	protein localization to chromosome, centromeri	2/42	43/18903	0.004107827683570720	0.032862621468565700	0.021680762933946800	NDC80/SPDL1	2	0.465116279069767
GO:0001666	BP	GO:0001666	response to hypoxia	4/42	296/18903	0.004129778661017460	0.032884563105404200	0.021695238694108900	RGCC/EDN1/NDRG1/ATM	4	0.135135135135135
GO:0022411	BP	GO:0022411	cellular component disassembl	5/42	483/18903	0.004163783009668970	0.033001835706265100	0.021772608037888900	TOP2A/INSR/UVRAG/CLASP2/PAFAH1	5	0.103519668737060
GO:1904407	BP	GO:1904407	positive regulation of nitric oxide metabolic process	2/42	44/18903	0.004297401466253560	0.033748400505624300	0.022265146177161100	INSR/EDN1	2	0.454545454545455
GO:1905521	BP	GO:1905521	regulation of macrophage migration	2/42	44/18903	0.004297401466253560	0.033748400505624300	0.022265146177161100	MAPK1/MTUS1	2	0.454545454545455
GO:0006302	BP	GO:0006302	double-strand break repair	4/42	300/18903	0.004331017429207820	0.033857086021935100	0.022336850283777900	RMI1/UVRAG/ATM/RPA1	4	0.133333333333333
GO:0051054	BP	GO:0051054	positive regulation of DNA metabolic process	4/42	301/18903	0.004382346431354670	0.034083403137659300	0.022486160579628900	MAPK1/RGCC/ATM/CDK2	4	0.132890365448505

GO:0016525	BP	GO:0016525	negative regulation of angiogenesis	3/42	149/18903	0.0043997851012983	0.0340834031376593	0.0224861605796289	GADD45A/PLK2/RGCC	3	0.201342281879195
GO:0043535	BP	GO:0043535	regulation of blood vessel endothelial cell migration	3/42	150/18903	0.0044826943971062 1	0.0344777799417853	0.0227463464569206	GADD45A/PLK2/RGCC	3	0.2
GO:1900744	BP	GO:1900744	regulation of p38MAPK cascade	2/42	45/18903	0.0044909725040993 7	0.0344777799417853	0.0227463464569206	GADD45A/DUSP1	2	0.444444444444444
GO:0071456	BP	GO:0071456	cellular response to hypoxia	3/42	151/18903	0.0045665493350053	0.0347463664956848	0.0229235435623892	RGCC/EDN1/NDRG1	3	0.198675496688742
GO:2000181	BP	GO:2000181	negative regulation of blood vessel morphogenesis	3/42	151/18903	0.0045665493350053	0.0347463664956848	0.0229235435623892	GADD45A/PLK2/RGCC	3	0.198675496688742
GO:1901343	BP	GO:1901343	negative regulation of vasculature	3/42	152/18903	0.0046513531019372 9	0.0352350288075958	0.0232459332947309	GADD45A/PLK2/RGCC	3	0.197368421052632
GO:0085029	BP	GO:0085029	extracellular matrix assembly	2/42	46/18903	0.0046885229656327 1	0.0353601379610714	0.0233284727202592	CLASP2/RGCC	2	0.434782608695652

GO:0044089	BP	GO:0044089	positive regulation of cellular component	5/42	498/18903	0.00473774403438135	0.0355746394160565	0.0234699877603471	MARK4/CLASP2/RGCC/ATM/CDK2	5	0.100401606425703
GO:0000723	BP	GO:0000723	telomere maintenanc	3/42	154/18903	0.00482381970444008	0.0360627918515346	0.0237920411071671	MAPK1/ATM/RPA1	3	0.194805194805195
GO:0042073	BP	GO:0042073	intraciliary	2/42	47/18903	0.00489003507560067	0.0363988697801232	0.0240137649250321	RPGR/SSX2IP	2	0.425531914893617
GO:0050890	BP	GO:0050890	cognition	4/42	314/18903	0.00508756669580747	0.0371211948449905	0.0244903111588015	INSR/PLK2/MAPK1/PAFAH1B1	4	0.127388535031847
GO:0044839	BP	GO:0044839	cell cycle G2/M phase transition	3/42	157/18903	0.00508971359430957	0.0371211948449905	0.0244903111588015	NDC80/ATM/CDK2	3	0.191082802547771
GO:0010171	BP	GO:0010171	body morphogenesis	2/42	48/18903	0.00509549111482054	0.0371211948449905	0.0244903111588015	MSX1/CLASP2	2	0.416666666666667
GO:0048538	BP	GO:0048538	thymus developmen	2/42	48/18903	0.00509549111482054	0.0371211948449905	0.0244903111588015	MAPK1/ATM	2	0.416666666666667
GO:1901976	BP	GO:1901976	regulation of cell cycle checkpoint	2/42	48/18903	0.00509549111482054	0.0371211948449905	0.0244903111588015	DUSP1/NDC80	2	0.416666666666667
GO:0030261	BP	GO:0030261	chromosome condensation	2/42	49/18903	0.00530487342002797	0.0381594256096613	0.0251752727982752	SMC4/TOP2A	2	0.408163265306122
GO:0034198	BP	GO:0034198	cellular response to amino acid	2/42	49/18903	0.00530487342002797	0.0381594256096613	0.0251752727982752	ATF4/MAPK1	2	0.408163265306122
GO:0035094	BP	GO:0035094	response to	2/42	49/18903	0.00530487342002797	0.0381594256096613	0.0251752727982752	MAPK1/EDN1	2	0.408163265306122

GO:0051147	BP	GO:0051147	regulation of muscle cell differentiation	3/42	160/18903	0.005364312605166460	0.038363071757708400	0.025309626165777800	MSX1/CYP26B1/EDN1	3	0.1875
GO:0060326	BP	GO:0060326	cell chemotaxis	4/42	319/18903	0.005378000713697440	0.038363071757708400	0.025309626165777800	DUSP1/MAPK1/EDN1/MTU	4	0.125391849529781
GO:0032873	BP	GO:0032873	negative regulation of stress-activated MAPK cascade	2/42	51/18903	0.005735346454030880	0.040077196446126000	0.026440501590440900	DUSP1/PAFAH1B1	2	0.392156862745098
GO:0060324	BP	GO:0060324	face development	2/42	51/18903	0.005735346454030880	0.040077196446126000	0.026440501590440900	MSX1/MAPK1	2	0.392156862745098
GO:0070303	BP	GO:0070303	negative regulation of stress-activated protein kinase signaling cascade	2/42	51/18903	0.005735346454030880	0.040077196446126000	0.026440501590440900	DUSP1/PAFAH1B1	2	0.392156862745098
GO:1903793	BP	GO:1903793	positive regulation of anion transport	2/42	51/18903	0.005735346454030880	0.040077196446126000	0.026440501590440900	ATF4/EDN1	2	0.392156862745098
GO:1990928	BP	GO:1990928	response to amino acid	2/42	51/18903	0.005735346454030880	0.040077196446126000	0.026440501590440900	ATF4/MAPK1	2	0.392156862745098
GO:0007030	BP	GO:0007030	Golgi organization	3/42	165/18903	0.005841535676411260	0.040653288935024700	0.026820572446680700	CUL7/CLASP2/MAPK1	3	0.181818181818182

GO:0010970	BP	GO:0010970	transport along microtubul positive	3/42	168/18903	0.006139727458434460	0.042160994186452700	0.027815264856163200	RPGR/SSX2IP/PAFAH1B1	3	0.178571428571429
GO:0048639	BP	GO:0048639	regulation of developmental growth	3/42	168/18903	0.006139727458434460	0.042160994186452700	0.027815264856163200	INSR/PAFAH1B1/EDN1	3	0.178571428571429
GO:0032210	BP	GO:0032210	regulation of telomere maintenance via	2/42	53/18903	0.006181313984111930	0.042160994186452700	0.027815264856163200	MAPK1/ATM	2	0.377358490566038
GO:0051155	BP	GO:0051155	positive regulation of striated muscle cell	2/42	53/18903	0.006181313984111930	0.042160994186452700	0.027815264856163200	CYP26B1/EDN1	2	0.377358490566038
GO:0071622	BP	GO:0071622	regulation of granulocyte	2/42	53/18903	0.006181313984111930	0.042160994186452700	0.027815264856163200	MAPK1/EDN1	2	0.377358490566038
GO:0000724	BP	GO:0000724	double-strand break repair via homologous recombination	3/42	169/18903	0.006241117265357450	0.042399971263063300	0.027972927425766700	RMI1/ATM/RPA1	3	0.177514792899408

GO:0043525	BP	GO:0043525	positive regulation of neuron apoptotic process	2/42	55/18903	0.006642636701807360	0.044867264601999400	0.029600697809853300	ATF4/ATM	2	0.363636363636364
GO:0000725	BP	GO:0000725	recombinational	3/42	173/18903	0.006656708650062990	0.044867264601999400	0.029600697809853300	RMI1/ATM/RPA1	3	0.173410404624277
GO:0051235	BP	GO:0051235	maintenance of location	4/42	342/18903	0.006857838505179530	0.046041645179872000	0.030375482832023300	SUN2/UVRAG/PAFAH1B1/ASPM	4	0.116959064327485
GO:0010634	BP	GO:0010634	positive regulation of epithelial cell migration	3/42	176/18903	0.006979006508083720	0.046672106022809900	0.030791422628181900	PLK2/CLASP2/EDN1	3	0.170454545454545
GO:0062197	BP	GO:0062197	cellular response to chemical	4/42	345/18903	0.007068857774208840	0.046697431487594300	0.030808130832629500	ATF4/MAPK1/EDN1/ATM	4	0.115942028985507
GO:0043534	BP	GO:0043534	blood vessel endothelial cell migration	3/42	177/18903	0.007088472075849100	0.046697431487594300	0.030808130832629500	GADD45A/PLK2/RGCC	3	0.169491525423729
GO:0007080	BP	GO:0007080	mitotic metaphase plate congressio	2/42	57/18903	0.007119176178891420	0.046697431487594300	0.030808130832629500	NDC80/SPDL1	2	0.350877192982456
GO:0038066	BP	GO:0038066	p38MAPK cascade	2/42	57/18903	0.007119176178891420	0.046697431487594300	0.030808130832629500	GADD45A/DUSP1	2	0.350877192982456

GO:1903053	BP	GO:1903053	regulation of extracellular matrix organization	2/42	57/18903	0.00711917617889142	0.0466974314875943	0.0308081308326295	CLASP2/RGCC	2	0.350877192982456
GO:0048015	BP	GO:0048015	phosphatidylinositol-mediated signaling	3/42	178/18903	0.0071989580929911	0.0470405200580182	0.0310344798464422	CEP55/INSR/EDN1	3	0.168539325842697
GO:0001961	BP	GO:0001961	positive regulation of cytokine-mediated signaling pathway	2/42	58/18903	0.00736310918289891	0.0477486474284959	0.0315016593032318	PAFAH1B1/EDN1	2	0.344827586206897
GO:0048599	BP	GO:0048599	oocyte developmen	2/42	58/18903	0.00736310918289891	0.0477486474284959	0.0315016593032318	EDN1/ATM	2	0.344827586206897
GO:0048017	BP	GO:0048017	inositol lipid-mediated signaling	3/42	182/18903	0.0076511530330781	0.0494293358212442	0.0326104754895444	CEP55/INSR/EDN1	3	0.164835164835165
GO:0006998	BP	GO:0006998	nuclear envelope organization	2/42	60/18903	0.00786221615992568	0.0504124122314336	0.0332590496337483	SUN2/PAFAH1B1	2	0.333333333333333
GO:1905517	BP	GO:1905517	macrophage migration	2/42	60/18903	0.00786221615992568	0.0504124122314336	0.0332590496337483	MAPK1/MTUS1	2	0.333333333333333
GO:0032200	BP	GO:0032200	telomere organization	3/42	185/18903	0.00800112574929579	0.0511116689656507	0.0337203767831673	MAPK1/ATM/RPA1	3	0.162162162162162

GO:0030865	BP	GO:0030865	cortical cytoskeleton organization	2/42	61/18903	0.008117356070904490	0.0512959243662875	0.0338419373124856	PAFAH1B1/AKAP11	2	0.327868852459016
GO:1904356	BP	GO:1904356	regulation of telomere maintenance via telomere	2/42	61/18903	0.008117356070904490	0.0512959243662875	0.0338419373124856	MAPK1/ATM	2	0.327868852459016
GO:0043405	BP	GO:0043405	regulation of MAP kinase activity	3/42	186/18903	0.008119857186485940	0.0512959243662875	0.0338419373124856	DUSP1/INSR/EDN1	3	0.161290322580645
GO:0003002	BP	GO:0003002	regionalization	4/42	360/18903	0.008188789240185700	0.0513524072498092	0.0338792012906083	MSX1/CYP26B1/EDN1/AT	4	0.111111111111111
GO:0010038	BP	GO:0010038	response to metal	4/42	360/18903	0.008188789240185700	0.0513524072498092	0.0338792012906083	ATF4/MAPK1/EDN1/NDRG	4	0.111111111111111
GO:0009994	BP	GO:0009994	oocyte differentiation	2/42	62/18903	0.008376197645560080	0.0521456377061777	0.0344025265978410	EDN1/ATM	2	0.322580645161290
GO:0045428	BP	GO:0045428	regulation of nitric oxide biosynthetic process	2/42	62/18903	0.008376197645560080	0.0521456377061777	0.0344025265978410	INSR/EDN1	2	0.322580645161290
GO:0007286	BP	GO:0007286	spermatid development	3/42	189/18903	0.008482302637091470	0.0524249173815906	0.0345867783758281	CEP57/PAFAH1B1/CCNB1IP1	3	0.158730158730159
GO:0071478	BP	GO:0071478	cellular response to	3/42	189/18903	0.008482302637091470	0.0524249173815906	0.0345867783758281	GADD45A/ATF4/ATM	3	0.158730158730159

GO:0030336	BP	GO:0030336	negative regulation of cell migration	4/42	368/18903	0.008831321137017755	0.054385689879764	0.035880377054222 1	GADD45A/DUSP1/CLASP2/RGCC	4	0.108695652173913
GO:0045143	BP	GO:0045143	homologous chromosome segregatio	2/42	64/18903	0.008904918254984485	0.054447214473333 37	0.035920967246610 3	CCNB1IP1/ATM	2	0.3125
GO:0050891	BP	GO:0050891	multicellular organismal water homeostasi	2/42	64/18903	0.008904918254984485	0.054447214473333 37	0.035920967246610 3	CYP26B1/AKAP11	2	0.3125
GO:0060760	BP	GO:0060760	positive regulation of response to	2/42	65/18903	0.009174763658359 01	0.055699274408193 7	0.036747000393502 1	PAFAH1B1/EDN1	2	0.307692307692308
GO:0080164	BP	GO:0080164	regulation of nitric oxide metabolic process	2/42	65/18903	0.009174763658359 01	0.055699274408193 7	0.036747000393502 1	INSR/EDN1	2	0.307692307692308
GO:0048515	BP	GO:0048515	spermatid differentiation	3/42	196/18903	0.009364731908538 28	0.056651664407835 8	0.037375329506645 2	CEP57/PAFAH1B1/CCNB1IP1	3	0.153061224489796
GO:0048814	BP	GO:0048814	regulation of dendrite morphogene	2/42	66/18903	0.009448243462330 06	0.056755764236873 9	0.037444008255143 7	CUL7/PAFAH1B1	2	0.303030303030303
GO:0071300	BP	GO:0071300	cellular response to retinoic	2/42	66/18903	0.009448243462330 06	0.056755764236873 9	0.037444008255143 7	CYP26B1/ATM	2	0.303030303030303

GO:0071248	BP	GO:0071248	cellular response to metal	3/42	198/18903	0.009626366888803399	0.057611708531663 8	0.038008708346332 5	ATF4/MAPK1/EDN1	3	0.151515151515152
GO:0006303	BP	GO:0006303	double-strand break repair via nonhomologous end joining	2/42	67/18903	0.009725340984609 13	0.057611708531663 8	0.038008708346332 5	UVRAG/ATM	2	0.298507462686567
GO:0007405	BP	GO:0007405	neuroblast proliferation	2/42	67/18903	0.009725340984609 13	0.057611708531663 8	0.038008708346332 5	PAFAH1B1/ASPM	2	0.298507462686567
GO:0032206	BP	GO:0032206	positive regulation of telomere	2/42	67/18903	0.009725340984609 13	0.057611708531663 8	0.038008708346332 5	MAPK1/ATM	2	0.298507462686567
GO:0046854	BP	GO:0046854	phosphatidylinositol phosphate biosynthetic process	2/42	68/18903	0.010006039596009 9	0.059070137201272 1	0.038970891058143 7	UVRAG/ATM	2	0.294117647058824
GO:2000146	BP	GO:2000146	negative regulation of cell motility	4/42	383/18903	0.010123656042497 6	0.059559103590226 3	0.039293481402061 5	GADD45A/DUSP1/CLASP2/RGCC	4	0.104438642297650
GO:0030104	BP	GO:0030104	water homeostasis	2/42	69/18903	0.010290322720303 6	0.060126390775289 3	0.039667743053299	CYP26B1/AKAP11	2	0.289855072463768
GO:0061180	BP	GO:0061180	mammary gland epithelium developmen	2/42	69/18903	0.010290322720303 6	0.060126390775289 3	0.039667743053299	MSX1/MAPK1	2	0.289855072463768

GO:0031032	BP	GO:0031032	actomyosin structure organization	3/42	204/18903	0.0104368541502599	0.0607751506981124	0.0400957554716396	CLASP2/RGCC/EDN1	3	0.147058823529412
GO:0048167	BP	GO:0048167	regulation of synaptic	3/42	207/18903	0.0108565710777611	0.0628672801039928	0.0414760154645747	ATF4/PLK2/MAPK1	3	0.144927536231884
GO:0051310	BP	GO:0051310	metaphase plate congressio	2/42	71/18903	0.0108695764665782	0.0628672801039928	0.0414760154645747	NDC80/SPDL1	2	0.28169014084507
GO:0001701	BP	GO:0001701	in utero embryonic developmen	4/42	393/18903	0.0110503438201311	0.0636976047813619	0.0420238132872261	MSX1/MAPK1/EDN1/CCNB1IP1	4	0.101781170483461
GO:0099111	BP	GO:0099111	microtubule-based transport	3/42	209/18903	0.0111417721233154	0.0640091069634763	0.0422293235193126	RPGR/SSX2IP/PAFAH1B1	3	0.143540669856459
GO:0090307	BP	GO:0090307	mitotic spindle assembly	2/42	74/18903	0.0117649295560523	0.0673630749162594	0.0444420679938185	KIF11/CLASP2	2	0.27027027027027
GO:0071479	BP	GO:0071479	cellular response to ionizing	2/42	75/18903	0.0120703746043997	0.0688816044091075	0.0454439015807749	GADD45A/ATM	2	0.266666666666667
GO:0006809	BP	GO:0006809	nitric oxide biosynthetic process	2/42	76/18903	0.0123792896027821	0.0704097800663224	0.0464520991214731	INSR/EDN1	2	0.263157894736842
GO:0010827	BP	GO:0010827	regulation of glucose transmembrane transport	2/42	77/18903	0.0126916583934696	0.0719474144689402	0.0474665369682568	INSR/EDN1	2	0.259740259740260

GO:0043537	BP	GO:0043537	negative regulation of blood vessel endothelial cell migration	2/42	78/18903	0.0130074648704043	0.0732525653228033	0.04832759 6280969	GADD45A/RGCC	2	0.25641025 6410256
GO:0061045	BP	GO:0061045	negative regulation of wound healing	2/42	78/18903	0.0130074648704043	0.0732525653228033	0.04832759 6280969	CLASP2/EDN1	2	0.25641025 6410256
GO:0007018	BP	GO:0007018	microtubule-based movement	4/42	415/18903	0.0132787419 31492	0.0745351022515221	0.04917373 62985018	RPGR/KIF11/SSX2IP/PAFAH1B1	4	0.09638554 21686747
GO:0040013	BP	GO:0040013	negative regulation of locomotion	4/42	419/18903	0.0137125952646254	0.0767188336373811	0.05061442 97177262	GADD45A/DUSP1/CLASP2/RGCC	4	0.09546539 37947494
GO:0097061	BP	GO:0097061	dendritic spine organization	2/42	81/18903	0.0139753501302413	0.0779342000748309	0.05141625 47222661	INSR/PAFAH1B1	2	0.24691358 0246914
GO:0071902	BP	GO:0071902	positive regulation of protein serine/threonine kinase activity	3/42	229/18903	0.0142335025 33867	0.0787451042187198	0.05195124 0055759	INSR/RGCC/EDN1	3	0.13100436 6812227

GO:0010770	BP	GO:0010770	positive regulation of cell morphogenesis involved in differenti	2/42	82/18903	0.0143047473201062	0.0787451042187198	0.0519512400055759	CUL7/PAFAH1B1	2	0.24390243902439
GO:0046209	BP	GO:0046209	nitric oxide metabolic process	2/42	82/18903	0.0143047473201062	0.0787451042187198	0.0519512400055759	INSR/EDN1	2	0.24390243902439
GO:0051149	BP	GO:0051149	positive regulation of muscle cell differentiation	2/42	82/18903	0.0143047473201062	0.0787451042187198	0.0519512400055759	CYP26B1/EDN1	2	0.24390243902439
GO:0050769	BP	GO:0050769	positive regulation of neurogenesis	3/42	231/18903	0.0145668654091089	0.0798070196515537	0.0526518274016952	CUL7/PAFAH1B1/ASPM	3	0.12987012987013
GO:0014032	BP	GO:0014032	neural crest cell developmen	2/42	83/18903	0.0146375002436091	0.0798070196515537	0.0526518274016952	MAPK1/EDN1	2	0.24096385542168
GO:2001057	BP	GO:2001057	reactive nitrogen species metabolic process	2/42	83/18903	0.0146375002436091	0.0798070196515537	0.0526518274016952	INSR/EDN1	2	0.24096385542168

GO:0031331	BP	GO:0031331	positive regulation of cellular catabolic	4/42	429/18903	0.0148366980840513	0.0806362765710978	0.0531989207825799	INSR/PLK2/UVRAG/ATM	4	0.0932400932400932
GO:0008406	BP	GO:0008406	gonad developmen	3/42	233/18903	0.0149046611238817	0.0807493033040677	0.0532734889604431	INSR/ASPM/ATM	3	0.128755364806867
GO:0006289	BP	GO:0006289	nucleotide-excision repair	2/42	84/18903	0.0149735996792225	0.0808668853338452	0.0533510624466404	CETN2/RPA1	2	0.238095238095238
GO:0000281	BP	GO:0000281	mitotic cytokinesi	2/42	85/18903	0.0153130233012197	0.0824399241876985	0.0543888578001353	CEP55/CUL7	2	0.235294117647059
GO:0032102	BP	GO:0032102	negative regulation of response to developmen	4/42	436/18903	0.0156575156017349	0.0840303031666775	0.0554380935181044	DUSP1/PLK2/CLASP2/EDN1	4	0.0917431192660551
GO:0045137	BP	GO:0045137	t of primary sexual characteri	3/42	238/18903	0.0157685922710641	0.0843619686501927	0.0556569062725386	INSR/ASPM/ATM	3	0.126050420168067
GO:0010660	BP	GO:0010660	regulation of muscle cell apoptotic process	2/42	87/18903	0.0160017869413182	0.0850778237376919	0.0561291840079583	ATF4/EDN1	2	0.229885057471264
GO:2000243	BP	GO:2000243	positive regulation of reproducti ve process	2/42	87/18903	0.0160017869413182	0.0850778237376919	0.0561291840079583	INSR/MSX1	2	0.229885057471264

GO:0032984	BP	GO:0032984	protein-containing complex disassembl	3/42	242/18903	0.0164797903575896	0.087347990997503	0.0576269025702907	INSR/UVRAG/CLASP2	3	0.12396694214876
GO:0048864	BP	GO:0048864	stem cell developmen	2/42	89/18903	0.0167036683787 28	0.0882613588406862	0.0582294872331876	MAPK1/EDN1	2	0.22471910 1123595
GO:0050804	BP	GO:0050804	modulation of chemical synaptic transmissi	4/42	448/18903	0.0171306694962269	0.0902390959308935	0.0595342781196807	ATF4/PLK2/MAPK1/EDN1	4	0.08928571 42857143
GO:0048568	BP	GO:0048568	embryonic organ developmen	4/42	449/18903	0.0172572351889455	0.0903498006249158	0.0596073180677242	ATF4/MSX1/MAPK1/EDN1	4	0.08908685 9688196
GO:0099177	BP	GO:0099177	regulation of trans-synaptic signaling	4/42	449/18903	0.0172572351889455	0.0903498006249158	0.0596073180677242	ATF4/PLK2/MAPK1/EDN1	4	0.08908685 9688196
GO:0106027	BP	GO:0106027	neuron projection organizati on	2/42	91/18903	0.0174185434380326	0.0903652920179145	0.0596175346379872	INSR/PAFAH1B1	2	0.21978021 978022
GO:1901216	BP	GO:1901216	positive regulation of neuron death	2/42	91/18903	0.0174185434380326	0.0903652920179145	0.0596175346379872	ATF4/ATM	2	0.21978021 978022
GO:1903351	BP	GO:1903351	cellular response to	2/42	91/18903	0.0174185434380326	0.0903652920179145	0.0596175346379872	ATF4/MAPK1	2	0.21978021 978022
GO:0048863	BP	GO:0048863	stem cell differenti ation	3/42	248/18903	0.0175801224668376	0.0909280050248516	0.0599887785241428	MSX1/MAPK1/EDN1	3	0.12096774 1935484

GO:0010657	BP	GO:0010657	muscle cell apoptotic	2/42	92/18903	0.0177808149893619	0.0914136794648237	0.0603091970399387	ATF4/EDN1	2	0.217391304347826
GO:1903350	BP	GO:1903350	response to	2/42	92/18903	0.0177808149893619	0.0914136794648237	0.0603091970399387	ATF4/MAPK1	2	0.217391304347826
GO:0032508	BP	GO:0032508	DNA duplex unwinding	2/42	93/18903	0.0181462887416714	0.0927356606738552	0.0611813599994138	TOP2A/RPA1	2	0.215053763344086
GO:0044070	BP	GO:0044070	regulation of anion transport	2/42	93/18903	0.0181462887416714	0.0927356606738552	0.0611813599994138	ATF4/EDN1	2	0.215053763344086
GO:0051492	BP	GO:0051492	regulation of stress fiber assembly	2/42	94/18903	0.0185149493967176	0.0940581405550432	0.0620538519527659	CLASP2/RGCC	2	0.212765957446809
GO:1903035	BP	GO:1903035	negative regulation of response	2/42	94/18903	0.0185149493967176	0.0940581405550432	0.0620538519527659	CLASP2/EDN1	2	0.212765957446809
GO:0014033	BP	GO:0014033	neural crest cell differentiation	2/42	96/18903	0.0192617704685055	0.0975625770475781	0.0643658664363326	MAPK1/EDN1	2	0.208333333333333
GO:0003007	BP	GO:0003007	heart morphogenesis	3/42	258/18903	0.0195037674117538	0.0984969020912168	0.0649822773880199	INSR/MSX1/EDN1	3	0.116279069767442
GO:0002690	BP	GO:0002690	positive regulation of leukocyte chemotaxis	2/42	97/18903	0.0196399005348223	0.0986026677877297	0.0650520551747626	MAPK1/EDN1	2	0.206185567010309

GO:0010596	BP	GO:0010596	negative regulation of endothelial cell migration	2/42	97/18903	0.0196399005348223	0.0986026677877297	0.0650520551747626	GADD45A/RGCC	2	0.206185567010309
GO:0060349	BP	GO:0060349	bone morphogenesis	2/42	98/18903	0.0200211568027558	0.0996401757160403	0.0657365399307128	MSX1/CYP26B1	2	0.204081632653061
GO:1990868	BP	GO:1990868	response to	2/42	98/18903	0.0200211568027558	0.0996401757160403	0.0657365399307128	DUSP1/EDN1	2	0.204081632653061
GO:1990869	BP	GO:1990869	cellular response to	2/42	98/18903	0.0200211568027558	0.0996401757160403	0.0657365399307128	DUSP1/EDN1	2	0.204081632653061
GO:0045927	BP	GO:0045927	positive regulation of growth	3/42	261/18903	0.0201028001625369	0.0997565112540048	0.0658132901057272	INSR/PAFAH1B1/EDN1	3	0.114942528735632
GO:0007389	BP	GO:0007389	pattern specification	4/42	472/18903	0.0203323956370 8	0.1000981589211 29	0.0660386894505481	MSX1/CYP26B1/EDN1/ATM	4	0.084745762711864 4
GO:0006885	BP	GO:0006885	regulation of pH	2/42	99/18903	0.0204055242193189	0.1000981589211 29	0.0660386894505481	MAPK1/EDN1	2	0.202020202020202
GO:0010389	BP	GO:0010389	regulation of G2/M transition of mitotic cell cycle	2/42	99/18903	0.0204055242193189	0.1000981589211 29	0.0660386894505481	ATM/CDK2	2	0.202020202020202
GO:0032392	BP	GO:0032392	DNA geometric change	2/42	99/18903	0.0204055242193189	0.1000981589211 29	0.0660386894505481	TOP2A/RPA1	2	0.202020202020202
GO:0031667	BP	GO:0031667	response to nutrient	4/42	474/18903	0.020614833	0.1008359838260 11	0.0665254615379427	ATF4/RMI1/MAPK1/CYP26B1	4	0.084388185654008 4

GO:0010769	BP	GO:0010769	regulation of cell morphogenesis involved in differenti	2/42	100/18903	0.0207929877801737	0.1009898294445	0.0666269595388274	CUL7/PAFAH1B1	2	0.2
GO:0030316	BP	GO:0030316	osteoclast differentiation	2/42	100/18903	0.0207929877801737	0.1009898294445	0.0666269595388274	SNX10/PAFAH1B1	2	0.2
GO:0032204	BP	GO:0032204	regulation of telomere	2/42	101/18903	0.0211835325294974	0.1009898294445	0.0666269595388274	MAPK1/ATM	2	0.19801980198019
GO:0050773	BP	GO:0050773	regulation of dendrite	2/42	103/18903	0.0219738060120386	0.1009898294445	0.0666269595388274	CUL7/PAFAH1B1	2	0.19417475728155
GO:0001821	BP	GO:0001821	histamine secretion	1/42	10/18903	0.0220030411114478	0.1009898294445	0.0666269595388274	EDN1	1	1
GO:0003253	BP	GO:0003253	cardiac neural crest cell migration involved in outflow tract morphogenesis	1/42	10/18903	0.0220030411114478	0.1009898294445	0.0666269595388274	EDN1	1	1
GO:0003330	BP	GO:0003330	regulation of extracellular matrix constituent	1/42	10/18903	0.0220030411114478	0.1009898294445	0.0666269595388274	RGCC	1	1

GO:0014824	BP	GO:0014824	artery smooth muscle contractio	1/42	10/18903	0.02200304 11114478	0.10098982 94445	0.06662695 95388274	EDN1	1	1
GO:0034397	BP	GO:0034397	telomere localizati on	1/42	10/18903	0.02200304 11114478	0.10098982 94445	0.06662695 95388274	ATM	1	1
GO:0035878	BP	GO:0035878	nail developmen	1/42	10/18903	0.02200304 11114478	0.10098982 94445	0.06662695 95388274	MSX1	1	1
GO:0042045	BP	GO:0042045	epithelial fluid transport	1/42	10/18903	0.02200304 11114478	0.10098982 94445	0.06662695 95388274	EDN1	1	1
GO:0043587	BP	GO:0043587	tongue morphogene sis	1/42	10/18903	0.02200304 11114478	0.10098982 94445	0.06662695 95388274	CYP26B1	1	1
GO:0044341	BP	GO:0044341	sodium- dependent phosphate transport	1/42	10/18903	0.02200304 11114478	0.10098982 94445	0.06662695 95388274	ATF4	1	1
GO:0048865	BP	GO:0048865	stem cell fate commitment	1/42	10/18903	0.02200304 11114478	0.10098982 94445	0.06662695 95388274	EDN1	1	1
GO:0051409	BP	GO:0051409	response to nitrosativ	1/42	10/18903	0.02200304 11114478	0.10098982 94445	0.06662695 95388274	ATM	1	1
GO:0051660	BP	GO:0051660	establishm ent of centrosome localizati on	1/42	10/18903	0.02200304 11114478	0.10098982 94445	0.06662695 95388274	PAFAH1B1	1	1
GO:0060536	BP	GO:0060536	cartilage morphogene sis	1/42	10/18903	0.02200304 11114478	0.10098982 94445	0.06662695 95388274	MSX1	1	1

GO:0061626	BP	GO:0061626	pharyngeal arch artery morphogene regulation of	1/42	10/18903	0.02200304 11114478	0.10098982 94445	0.06662695 95388274	EDN1	1	1
GO:0070099	BP	GO:0070099	chemokine-mediated signaling pathway	1/42	10/18903	0.02200304 11114478	0.10098982 94445	0.06662695 95388274	EDN1	1	1
GO:0070294	BP	GO:0070294	renal sodium ion absorption	1/42	10/18903	0.02200304 11114478	0.10098982 94445	0.06662695 95388274	EDN1	1	1
GO:0090220	BP	GO:0090220	chromosome localizati on to nuclear envelope involved in homologous chromosome	1/42	10/18903	0.02200304 11114478	0.10098982 94445	0.06662695 95388274	ATM	1	1
GO:1905461	BP	GO:1905461	positive regulation of vascular associated smooth muscle cell	1/42	10/18903	0.02200304 11114478	0.10098982 94445	0.06662695 95388274	ATF4	1	1

GO:2000048	BP	GO:2000048	negative regulation of cell-cell adhesion mediated by	1/42	10/18903	0.02200304 11114478	0.10098982 94445	0.06662695 95388274	RGCC	1	1
GO:0060291	BP	GO:0060291	long-term synaptic potentiati on	2/42	104/18903	0.02237350 50749902	0.10241561 6813859	0.06756760 75020109	PLK2/MAPK1	2	0.19230769 2307692
GO:0008585	BP	GO:0008585	female gonad developmen	2/42	105/18903	0.02277622 59856142	0.10296348 2687414	0.06792905 61507592	INSR/ATM	2	0.19047619 047619
GO:0071868	BP	GO:0071868	cellular response to monoamine	2/42	105/18903	0.02277622 59856142	0.10296348 2687414	0.06792905 61507592	ATF4/MAPK1	2	0.19047619 047619
GO:0071870	BP	GO:0071870	cellular response to catecholam	2/42	105/18903	0.02277622 59856142	0.10296348 2687414	0.06792905 61507592	ATF4/MAPK1	2	0.19047619 047619
GO:1901796	BP	GO:1901796	regulation of signal transducti on by p53 class mediator	2/42	105/18903	0.02277622 59856142	0.10296348 2687414	0.06792905 61507592	MSX1/ATM	2	0.19047619 047619
GO:0071103	BP	GO:0071103	DNA conformati on change	2/42	106/18903	0.02318195 40286732	0.10296348 2687414	0.06792905 61507592	TOP2A/RPA1	2	0.18867924 5283019

GO:0010717	BP	GO:0010717	regulation of epithelial to mesenchymal	2/42	107/18903	0.0235906745366507	0.102963482687414	0.0679290561507592	CLASP2/RGCC	2	0.186915887850467
GO:1903532	BP	GO:1903532	positive regulation of secretion by cell	3/42	278/18903	0.0236891622876141	0.102963482687414	0.0679290561507592	CLASP2/RGCC/EDN1	3	0.107913669064748
GO:0051962	BP	GO:0051962	positive regulation of nervous system developmen	3/42	279/18903	0.0239102919206404	0.102963482687414	0.0679290561507592	CUL7/PAFAH1B1/ASPM	3	0.107526882172043
GO:0032231	BP	GO:0032231	regulation of actin filament bundle assembly	2/42	108/18903	0.0240023728896203	0.102963482687414	0.0679290561507592	CLASP2/RGCC	2	0.185185185185185
GO:0032526	BP	GO:0032526	response to retinoic	2/42	108/18903	0.0240023728896203	0.102963482687414	0.0679290561507592	CYP26B1/ATM	2	0.185185185185185
GO:0071867	BP	GO:0071867	response to	2/42	108/18903	0.0240023728896203	0.102963482687414	0.0679290561507592	ATF4/MAPK1	2	0.185185185185185
GO:0071869	BP	GO:0071869	response to catecholam	2/42	108/18903	0.0240023728896203	0.102963482687414	0.0679290561507592	ATF4/MAPK1	2	0.185185185185185
GO:0003357	BP	GO:0003357	noradrener gic neuron differenti ation	1/42	11/18903	0.0241771729207595	0.102963482687414	0.0679290561507592	EDN1	1	0.909090909090909

GO:0008300	BP	GO:0008300	isoprenoid catabolic process	1/42	11/18903	0.0241771729207595	0.1029634826874140	0.0679290561507592	CYP26B1	1	0.9090909090909090
GO:0010172	BP	GO:0010172	embryonic body morphogenesis	1/42	11/18903	0.0241771729207595	0.1029634826874140	0.0679290561507592	CLASP2	1	0.9090909090909090
GO:0014820	BP	GO:0014820	tonic smooth muscle contractio	1/42	11/18903	0.0241771729207595	0.1029634826874140	0.0679290561507592	EDN1	1	0.9090909090909090
GO:0044771	BP	GO:0044771	meiotic cell cycle phase transition	1/42	11/18903	0.0241771729207595	0.1029634826874140	0.0679290561507592	NDC80	1	0.9090909090909090
GO:0045793	BP	GO:0045793	positive regulation of cell size	1/42	11/18903	0.0241771729207595	0.1029634826874140	0.0679290561507592	EDN1	1	0.9090909090909090
GO:0051081	BP	GO:0051081	nuclear membrane disassembl	1/42	11/18903	0.0241771729207595	0.1029634826874140	0.0679290561507592	PAFAH1B1	1	0.9090909090909090
GO:0060020	BP	GO:0060020	Bergmann glial cell differentiation	1/42	11/18903	0.0241771729207595	0.1029634826874140	0.0679290561507592	MAPK1	1	0.9090909090909090
GO:0060439	BP	GO:0060439	trachea morphogenesis	1/42	11/18903	0.0241771729207595	0.1029634826874140	0.0679290561507592	MAPK1	1	0.9090909090909090
GO:0060623	BP	GO:0060623	regulation of chromosome condensation	1/42	11/18903	0.0241771729207595	0.1029634826874140	0.0679290561507592	SMC4	1	0.9090909090909090

GO:0071044	BP	GO:0071044	histone mRNA catabolic process	1/42	11/18903	0.0241771729207595	0.1029634826874140	0.0679290561507592	ATM	1	0.9090909090909090
GO:0072584	BP	GO:0072584	caveolin-mediated endocytosi	1/42	11/18903	0.0241771729207595	0.1029634826874140	0.0679290561507592	MAPK1	1	0.9090909090909090
GO:0086100	BP	GO:0086100	endothelin receptor signaling pathway	1/42	11/18903	0.0241771729207595	0.1029634826874140	0.0679290561507592	EDN1	1	0.9090909090909090
GO:0110011	BP	GO:0110011	regulation of basement membrane organizati	1/42	11/18903	0.0241771729207595	0.1029634826874140	0.0679290561507592	CLASP2	1	0.9090909090909090
GO:1990440	BP	GO:1990440	positive regulation of transcription from RNA polymerase II promoter in response to	1/42	11/18903	0.0241771729207595	0.1029634826874140	0.0679290561507592	ATF4	1	0.9090909090909090
GO:1990535	BP	GO:1990535	neuron projection maintenanc	1/42	11/18903	0.0241771729207595	0.1029634826874140	0.0679290561507592	INSR	1	0.9090909090909090

GO:0030038	BP	GO:0030038	contractile actin filament bundle assembly	2/42	109/18903	0.0244170345151142	0.1032147236787 05	0.0680948097068682	CLASP2/RGCC	2	0.1834862385321 1
GO:0043149	BP	GO:0043149	stress fiber assembly	2/42	109/18903	0.0244170345151142	0.1032147236787 05	0.0680948097068682	CLASP2/RGCC	2	0.1834862385321 1
GO:0046545	BP	GO:0046545	development of primary female sexual characteri	2/42	109/18903	0.0244170345151142	0.1032147236787 05	0.0680948097068682	INSR/ATM	2	0.1834862385321 1
GO:1902749	BP	GO:1902749	regulation of cell cycle G2/M phase transition	2/42	110/18903	0.0248346448879932	0.1047214582469 07	0.0690888617184774	ATM/CDK2	2	0.1818181818181 82
GO:0014066	BP	GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	2/42	111/18903	0.0252551895303161	0.1062331313904 21	0.0700861719023128	CEP55/INSR	2	0.1801801801801 8
GO:0006260	BP	GO:0006260	DNA replicatio	3/42	286/18903	0.0254898432013768	0.1069573812763 65	0.0705639880161953	RMI1/RPA1/CDK2	3	0.1048951048951 05
GO:0007548	BP	GO:0007548	sex differentiation	3/42	288/18903	0.0259513128509665	0.1073937044100 82	0.0708518475356724	INSR/ASPM/ATM	3	0.1041666666666 67
GO:0034599	BP	GO:0034599	cellular response to oxidative	3/42	288/18903	0.0259513128509665	0.1073937044100 82	0.0708518475356724	ATF4/MAPK1/EDN1	3	0.1041666666666 67

GO:0010633	BP	GO:0010633	negative regulation of epithelial cell migration	2/42	113/18903	0.0261050239467401	0.107393704410082	0.0708518475356724	GADD45A/RGCC	2	0.176991150442478
GO:1904659	BP	GO:1904659	glucose transmembrane transport	2/42	113/18903	0.0261050239467401	0.107393704410082	0.0708518475356724	INSR/EDN1	2	0.176991150442478
GO:0002327	BP	GO:0002327	immature B cell differentiation	1/42	12/18903	0.0263465863622864	0.107393704410082	0.0708518475356724	ATM	1	0.833333333333333
GO:0030397	BP	GO:0030397	membrane disassembl	1/42	12/18903	0.0263465863622864	0.107393704410082	0.0708518475356724	PAFAH1B1	1	0.833333333333333
GO:0035815	BP	GO:0035815	positive regulation of renal sodium excretion	1/42	12/18903	0.0263465863622864	0.107393704410082	0.0708518475356724	EDN1	1	0.833333333333333
GO:0061309	BP	GO:0061309	cardiac neural crest cell development involved in outflow tract morphogenesis	1/42	12/18903	0.0263465863622864	0.107393704410082	0.0708518475356724	EDN1	1	0.833333333333333
GO:0061517	BP	GO:0061517	macrophage proliferation	1/42	12/18903	0.0263465863622864	0.107393704410082	0.0708518475356724	MAPK1	1	0.833333333333333

GO:0071372	BP	GO:0071372	cellular response to follicle-stimulating hormone	1/42	12/18903	0.0263465863622864	0.107393704410082	0.0708518475356724	EDN1	1	0.833333333333333
GO:0090232	BP	GO:0090232	positive regulation of spindle checkpoint	1/42	12/18903	0.0263465863622864	0.107393704410082	0.0708518475356724	NDC80	1	0.833333333333333
GO:0090267	BP	GO:0090267	positive regulation of mitotic cell cycle spindle assembly checkpoint	1/42	12/18903	0.0263465863622864	0.107393704410082	0.0708518475356724	NDC80	1	0.833333333333333
GO:0051146	BP	GO:0051146	striated muscle cell differenti	3/42	293/18903	0.0271247500798357	0.110303021702325	0.0727712384939709	MSX1/CYP26B1/EDN1	3	0.102389078498294
GO:0048562	BP	GO:0048562	embryonic organ morphogenesis	3/42	294/18903	0.0273628239588843	0.110683290073915	0.0730221164838358	MSX1/MAPK1/EDN1	3	0.102040816326531
GO:0008645	BP	GO:0008645	hexose transmembrane transport	2/42	116/18903	0.0274014233431703	0.110683290073915	0.0730221164838358	INSR/EDN1	2	0.172413793103448
GO:0021987	BP	GO:0021987	cerebral cortex developmen	2/42	117/18903	0.0278392721921546	0.110683290073915	0.0730221164838358	PAFAH1B1/ASPM	2	0.170940170940171

GO:0043406	BP	GO:0043406	positive regulation of MAP kinase activity	2/42	117/18903	0.0278392721921546	0.110683290073915	0.0730221164838358	INSR/EDN1	2	0.170940170940171
GO:0030326	BP	GO:0030326	embryonic limb morphogenesis	2/42	118/18903	0.0282799552756678	0.110683290073915	0.0730221164838358	MSX1/CYP26B1	2	0.169491525423729
GO:0035113	BP	GO:0035113	embryonic appendage morphogenesis	2/42	118/18903	0.0282799552756678	0.110683290073915	0.0730221164838358	MSX1/CYP26B1	2	0.169491525423729
GO:0097193	BP	GO:0097193	intrinsic apoptotic signaling pathway	3/42	298/18903	0.0283263995938652	0.110683290073915	0.0730221164838358	ATF4/MSX1/ATM	3	0.100671140939597
GO:0003096	BP	GO:0003096	renal sodium ion transport	1/42	13/18903	0.0285112914267502	0.110683290073915	0.0730221164838358	EDN1	1	0.769230769230769
GO:0007144	BP	GO:0007144	female meiosis I	1/42	13/18903	0.0285112914267502	0.110683290073915	0.0730221164838358	NDC80	1	0.769230769230769
GO:0035810	BP	GO:0035810	positive regulation of urine volume	1/42	13/18903	0.0285112914267502	0.110683290073915	0.0730221164838358	EDN1	1	0.769230769230769
GO:0042363	BP	GO:0042363	fat-soluble vitamin catabolic	1/42	13/18903	0.0285112914267502	0.110683290073915	0.0730221164838358	CYP26B1	1	0.769230769230769
GO:0051608	BP	GO:0051608	histamine transport	1/42	13/18903	0.0285112914267502	0.110683290073915	0.0730221164838358	EDN1	1	0.769230769230769

GO:0071287	BP	GO:0071287	cellular response to manganese	1/42	13/18903	0.028511291426750 2	0.110683290073915	0.073022116483583 58	ATF4	1	0.769230769230769
GO:0071389	BP	GO:0071389	cellular response to mineralocorticoid	1/42	13/18903	0.028511291426750 2	0.110683290073915	0.073022116483583 58	EDN1	1	0.769230769230769
GO:0071481	BP	GO:0071481	cellular response to X-ray	1/42	13/18903	0.028511291426750 2	0.110683290073915	0.073022116483583 58	ATM	1	0.769230769230769
GO:0072537	BP	GO:0072537	fibroblast activation	1/42	13/18903	0.028511291426750 2	0.110683290073915	0.073022116483583 58	RGCC	1	0.769230769230769
GO:1903624	BP	GO:1903624	regulation of DNA catabolic process	1/42	13/18903	0.028511291426750 2	0.110683290073915	0.073022116483583 58	ATM	1	0.769230769230769
GO:1905939	BP	GO:1905939	regulation of gonad developmen	1/42	13/18903	0.028511291426750 2	0.110683290073915	0.073022116483583 58	INSR	1	0.769230769230769
GO:1990253	BP	GO:1990253	cellular response to leucine starvation	1/42	13/18903	0.028511291426750 2	0.110683290073915	0.073022116483583 58	ATF4	1	0.769230769230769
GO:2001053	BP	GO:2001053	regulation of mesenchymal cell apoptotic process	1/42	13/18903	0.028511291426750 2	0.110683290073915	0.073022116483583 58	MSX1	1	0.769230769230769

GO:0015749	BP	GO:0015749	monosaccharide transmembrane transport	2/42	119/18903	0.0287234584887032	0.111254662743574	0.0733990734898274	INSR/EDN1	2	0.167067226890756
GO:0007613	BP	GO:0007613	memory	2/42	120/18903	0.0291697677722942	0.112728312474419	0.0743712981339473	INSR/PLK2	2	0.166666666666667
GO:0051047	BP	GO:0051047	positive regulation of secretion	3/42	304/18903	0.0298055700134846	0.112923144774683	0.0744998366596377	CLASP2/RGCC/EDN1	3	0.098684210526316
GO:0048675	BP	GO:0048675	axon extension	2/42	122/18903	0.0300707485447176	0.112923144774683	0.0744998366596377	PAFAH1B1/EDN1	2	0.163934426229508
GO:0071901	BP	GO:0071901	negative regulation of protein serine/threonine kinase activity	2/42	122/18903	0.0300707485447176	0.112923144774683	0.0744998366596377	GADD45A/DUSP1	2	0.163934426229508
GO:0048608	BP	GO:0048608	reproductive structure	3/42	306/18903	0.0303076306737096	0.112923144774683	0.0744998366596377	INSR/ASPM/ATM	3	0.098039215686275
GO:0030282	BP	GO:0030282	bone mineralization	2/42	123/18903	0.0305253921446769	0.112923144774683	0.0744998366596377	ATF4/SNX10	2	0.162601626016260
GO:0071675	BP	GO:0071675	regulation of mononuclear cell migration	2/42	123/18903	0.0305253921446769	0.112923144774683	0.0744998366596377	DUSP1/MAPK1	2	0.162601626016260

GO:0010720	BP	GO:0010720	positive regulation of cell developmen	3/42	307/18903	0.03056034 74072761	0.11292314 4774683	0.07449983 66596377	CUL7/PAFAH 1B1/ASPM	3	0.09771986 97068404
GO:0007100	BP	GO:0007100	mitotic centrosome separation	1/42	14/18903	0.03067129 80842451	0.11292314 4774683	0.07449983 66596377	KIF11	1	0.71428571 4285714
GO:0021819	BP	GO:0021819	layer formation in cerebral	1/42	14/18903	0.03067129 80842451	0.11292314 4774683	0.07449983 66596377	PAFAH1B1	1	0.71428571 4285714
GO:0022038	BP	GO:0022038	corpus callosum developmen	1/42	14/18903	0.03067129 80842451	0.11292314 4774683	0.07449983 66596377	PAFAH1B1	1	0.71428571 4285714
GO:0030238	BP	GO:0030238	male sex determinat ion	1/42	14/18903	0.03067129 80842451	0.11292314 4774683	0.07449983 66596377	INSR	1	0.71428571 4285714
GO:0032306	BP	GO:0032306	regulation of prostaglan din secretion	1/42	14/18903	0.03067129 80842451	0.11292314 4774683	0.07449983 66596377	EDN1	1	0.71428571 4285714
GO:0032308	BP	GO:0032308	positive regulation of prostaglan din secretion	1/42	14/18903	0.03067129 80842451	0.11292314 4774683	0.07449983 66596377	EDN1	1	0.71428571 4285714
GO:0032486	BP	GO:0032486	Rap protein signal transducti	1/42	14/18903	0.03067129 80842451	0.11292314 4774683	0.07449983 66596377	PLK2	1	0.71428571 4285714

GO:0035630	BP	GO:0035630	bone mineralization involved in bone maturation	1/42	14/18903	0.0306712980842451	0.1129231447746836	0.0744998366596377	SNX10	1	0.7142857142857142
GO:0051231	BP	GO:0051231	spindle elongation	1/42	14/18903	0.0306712980842451	0.1129231447746836	0.0744998366596377	KIF11	1	0.7142857142857142
GO:0051645	BP	GO:0051645	Golgi localization	1/42	14/18903	0.0306712980842451	0.1129231447746836	0.0744998366596377	UVRAG	1	0.7142857142857142
GO:0055057	BP	GO:0055057	neuroblast division	1/42	14/18903	0.0306712980842451	0.1129231447746836	0.0744998366596377	ASPM	1	0.7142857142857142
GO:0070278	BP	GO:0070278	extracellular matrix constituent	1/42	14/18903	0.0306712980842451	0.1129231447746836	0.0744998366596377	RGCC	1	0.7142857142857142
GO:0070307	BP	GO:0070307	lens fiber cell development	1/42	14/18903	0.0306712980842451	0.1129231447746836	0.0744998366596377	ATF4	1	0.7142857142857142
GO:1902287	BP	GO:1902287	semaphorin-plexin signaling pathway involved in axon guidance	1/42	14/18903	0.0306712980842451	0.1129231447746836	0.0744998366596377	EDN1	1	0.7142857142857142
GO:2000105	BP	GO:2000105	positive regulation of DNA-templated DNA replicatio	1/42	14/18903	0.0306712980842451	0.1129231447746836	0.0744998366596377	CDK2	1	0.7142857142857142

GO:0007162	BP	GO:0007162	negative regulation of cell adhesion	3/42	308/18903	0.0308141878204113	0.1132057715634	0.0746862966598178	DUSP1/CLASP2/RGCC	3	0.0974025974025974
GO:0046660	BP	GO:0046660	female sex differentiation	2/42	124/18903	0.0309827860371934	0.1135814340378 48	0.0749341359583197	INSR/ATM	2	0.1612903225 80645
GO:0055074	BP	GO:0055074	calcium ion	3/42	309/18903	0.0310691514524035	0.1136546736891 34	0.0749824550347031	ATF4/SNX10/EDN1	3	0.0970873786407767
GO:0042063	BP	GO:0042063	gliogenesis	3/42	310/18903	0.0313252378277166	0.1141038450235 12	0.0752787910171106	MAPK1/PAFAH1B1/NDRG1	3	0.0967741935483871
GO:0061458	BP	GO:0061458	reproductive system development	3/42	310/18903	0.0313252378277166	0.1141038450235 12	0.0752787910171106	INSR/ASPM/ATM	3	0.0967741935483871
GO:0003014	BP	GO:0003014	renal system process	2/42	125/18903	0.0314429163916031	0.1142893266718 14	0.0754011605502069	EDN1/AKAP11	2	0.16
GO:0006650	BP	GO:0006650	glycerophospholipid metabolic process	3/42	311/18903	0.0315824464560 76	0.1145532803661 06	0.0755753011761141	UVRAG/PAFAH1B1/ATM	3	0.0964630225080386
GO:0001768	BP	GO:0001768	establishment of T cell polarity	1/42	15/18903	0.0328266162842801	0.1146921777116 07	0.0756669372138185	CYP26B1	1	0.6666666666666667
GO:0006206	BP	GO:0006206	pyrimidine nucleobase metabolic process	1/42	15/18903	0.0328266162842801	0.1146921777116 07	0.0756669372138185	MAPK1	1	0.6666666666666667
GO:0007567	BP	GO:0007567	parturition	1/42	15/18903	0.0328266162842801	0.1146921777116 07	0.0756669372138185	EDN1	1	0.6666666666666667
GO:0009111	BP	GO:0009111	vitamin catabolic process	1/42	15/18903	0.0328266162842801	0.1146921777116 07	0.0756669372138185	CYP26B1	1	0.6666666666666667

GO:0010457	BP	GO:0010457	centriole-centriole cohesion	1/42	15/18903	0.0328266162842801	0.1146921777111607	0.0756669372138185	CCDC102B	1	0.6666666666666667
GO:0014029	BP	GO:0014029	neural crest formation	1/42	15/18903	0.0328266162842801	0.1146921777111607	0.0756669372138185	EDN1	1	0.6666666666666667
GO:0030174	BP	GO:0030174	regulation of DNA-templated DNA replication	1/42	15/18903	0.0328266162842801	0.1146921777111607	0.0756669372138185	CDK2	1	0.6666666666666667
GO:0031453	BP	GO:0031453	positive regulation of heterochromatin formation	1/42	15/18903	0.0328266162842801	0.1146921777111607	0.0756669372138185	CDK2	1	0.6666666666666667
GO:0034392	BP	GO:0034392	negative regulation of smooth muscle cell apoptotic	1/42	15/18903	0.0328266162842801	0.1146921777111607	0.0756669372138185	EDN1	1	0.6666666666666667
GO:0045725	BP	GO:0045725	positive regulation of glycogen biosynthet	1/42	15/18903	0.0328266162842801	0.1146921777111607	0.0756669372138185	INSR	1	0.6666666666666667
GO:0048308	BP	GO:0048308	organelle inheritanc	1/42	15/18903	0.0328266162842801	0.1146921777111607	0.0756669372138185	MAPK1	1	0.6666666666666667
GO:0048313	BP	GO:0048313	Golgi inheritanc	1/42	15/18903	0.0328266162842801	0.1146921777111607	0.0756669372138185	MAPK1	1	0.6666666666666667

GO:0051299	BP	GO:0051299	centrosome separation	1/42	15/18903	0.0328266162842801	0.1146921777111607	0.0756669372138185	KIF11	1	0.6666666666666667
GO:0070262	BP	GO:0070262	peptidyl-serine dephosphorylation	1/42	15/18903	0.0328266162842801	0.1146921777111607	0.0756669372138185	DUSP1	1	0.6666666666666667
GO:0070831	BP	GO:0070831	basement membrane assembly	1/42	15/18903	0.0328266162842801	0.1146921777111607	0.0756669372138185	CLASP2	1	0.6666666666666667
GO:0097152	BP	GO:0097152	mesenchymal cell apoptotic process	1/42	15/18903	0.0328266162842801	0.1146921777111607	0.0756669372138185	MSX1	1	0.6666666666666667
GO:0120263	BP	GO:0120263	positive regulation of heterochromatin organization	1/42	15/18903	0.0328266162842801	0.1146921777111607	0.0756669372138185	CDK2	1	0.6666666666666667
GO:1904936	BP	GO:1904936	interneuron	1/42	15/18903	0.0328266162842801	0.1146921777111607	0.0756669372138185	PAFAH1B1	1	0.6666666666666667
GO:0045931	BP	GO:0045931	positive regulation of mitotic cell cycle	2/42	129/18903	0.0333105273971648	0.1159098002650297	0.0764702522403891	PAFAH1B1/RGCC	2	0.1550387596899224
GO:2000027	BP	GO:2000027	regulation of animal organ morphogenesis	2/42	129/18903	0.0333105273971648	0.1159098002650297	0.0764702522403891	MSX1/EDN1	2	0.1550387596899224
GO:0019058	BP	GO:0019058	viral life cycle	3/42	319/18903	0.0336804529640083	0.1169593001165076	0.0771626476574804	TOP2A/INSR/UVRAG	3	0.0940438871473354

GO:0071621	BP	GO:0071621	granulocyte positive	2/42	130/18903	0.0337841341816044	0.11708185773058	0.0772435030404038	MAPK1/EDN1	2	0.153846153846154
GO:0010595	BP	GO:0010595	regulation of endothelial cell migration	2/42	131/18903	0.0342603953905225	0.11810860393760 5	0.0779208878658693	PLK2/EDN1	2	0.152671755725191
GO:0034219	BP	GO:0034219	carbohydrate transmembrane transport	2/42	132/18903	0.0347392975076178	0.11810860393760 5	0.0779208878658693	INSR/EDN1	2	0.151515151515152
GO:0001767	BP	GO:0001767	establishment of lymphocyte polarity	1/42	16/18903	0.0349772559558 21	0.11810860393760 5	0.0779208878658693	CYP26B1	1	0.625
GO:0006266	BP	GO:0006266	DNA ligation	1/42	16/18903	0.0349772559558 21	0.11810860393760 5	0.0779208878658693	TOP2A	1	0.625
GO:0010715	BP	GO:0010715	regulation of extracellular matrix disassembl	1/42	16/18903	0.0349772559558 21	0.11810860393760 5	0.0779208878658693	CLASP2	1	0.625
GO:0034393	BP	GO:0034393	positive regulation of smooth muscle cell apoptotic	1/42	16/18903	0.0349772559558 21	0.11810860393760 5	0.0779208878658693	ATF4	1	0.625
GO:0042159	BP	GO:0042159	lipoprotein catabolic	1/42	16/18903	0.0349772559558 21	0.11810860393760 5	0.0779208878658693	ATM	1	0.625

GO:0042249	BP	GO:0042249	establishment of planar polarity of embryonic	1/42	16/18903	0.034977255955821	0.118108603937605	0.077920887658693	PAFAH1B1	1	0.625
GO:0045836	BP	GO:0045836	positive regulation of meiotic nuclear division	1/42	16/18903	0.034977255955821	0.118108603937605	0.077920887658693	MSX1	1	0.625
GO:0048385	BP	GO:0048385	regulation of retinoic acid receptor signaling	1/42	16/18903	0.034977255955821	0.118108603937605	0.077920887658693	CYP26B1	1	0.625
GO:0051447	BP	GO:0051447	negative regulation of meiotic cell cycle	1/42	16/18903	0.034977255955821	0.118108603937605	0.077920887658693	DUSP1	1	0.625
GO:0070875	BP	GO:0070875	positive regulation of glycogen metabolic	1/42	16/18903	0.034977255955821	0.118108603937605	0.077920887658693	INSR	1	0.625
GO:1902285	BP	GO:1902285	semaphorin-plexin signaling pathway involved in neuron projection guidance	1/42	16/18903	0.034977255955821	0.118108603937605	0.077920887658693	EDN1	1	0.625

GO:0031647	BP	GO:0031647	regulation of protein stability	3/42	325/18903	0.0353008949243138	0.118966795492963	0.078487070563176	MSX1/NDC80/MAPK1	3	0.0923076923076923
GO:0006661	BP	GO:0006661	phosphatidylinositol biosynthetic process	2/42	134/18903	0.0357049706230770	0.120092160523984	0.079229518102702 2	UVRAG/ATM	2	0.1492537313432840
GO:0071496	BP	GO:0071496	cellular response to external	3/42	328/18903	0.0361261531067577	0.120754518428109	0.079666501643729 1	GADD45A/ATF4/MAPK1	3	0.0914634146341463
GO:0003198	BP	GO:0003198	epithelial to mesenchymal transition involved in endocardia	1/42	17/18903	0.0371232270073301	0.120754518428109	0.079666501643729 1	MSX1	1	0.5882352941176470
GO:0007096	BP	GO:0007096	regulation of exit from mitosis	1/42	17/18903	0.0371232270073301	0.120754518428109	0.079666501643729 1	RGCC	1	0.5882352941176470
GO:0010470	BP	GO:0010470	regulation of gastrulation	1/42	17/18903	0.0371232270073301	0.120754518428109	0.079666501643729 1	CLASP2	1	0.5882352941176470
GO:0010831	BP	GO:0010831	positive regulation of myotube differentiation	1/42	17/18903	0.0371232270073301	0.120754518428109	0.079666501643729 1	CYP26B1	1	0.5882352941176470
GO:0033189	BP	GO:0033189	response to vitamin	1/42	17/18903	0.0371232270073301	0.120754518428109	0.079666501643729 1	CYP26B1	1	0.5882352941176470

GO:0051895	BP	GO:0051895	negative regulation of focal adhesion assembly	1/42	17/18903	0.03712322 70073301	0.12075451 8428109	0.07966650 16437291	CLASP2	1	0.58823529 4117647
GO:0071732	BP	GO:0071732	cellular response to nitric oxide	1/42	17/18903	0.03712322 70073301	0.12075451 8428109	0.07966650 16437291	CDK2	1	0.58823529 4117647
GO:0090399	BP	GO:0090399	replicativ e	1/42	17/18903	0.03712322 70073301	0.12075451 8428109	0.07966650 16437291	ATM	1	0.58823529 4117647
GO:0150118	BP	GO:0150118	negative regulation of cell-substrate junction organizati on	1/42	17/18903	0.03712322 70073301	0.12075451 8428109	0.07966650 16437291	CLASP2	1	0.58823529 4117647
GO:1900034	BP	GO:1900034	regulation of cellular response	1/42	17/18903	0.03712322 70073301	0.12075451 8428109	0.07966650 16437291	ATM	1	0.58823529 4117647
GO:1901096	BP	GO:1901096	regulation of autophagos ome maturation	1/42	17/18903	0.03712322 70073301	0.12075451 8428109	0.07966650 16437291	UVRAG	1	0.58823529 4117647
GO:1903358	BP	GO:1903358	regulation of Golgi organizati on	1/42	17/18903	0.03712322 70073301	0.12075451 8428109	0.07966650 16437291	MAPK1	1	0.58823529 4117647

GO:1904355	BP	GO:1904355	positive regulation of telomere	1/42	17/18903	0.0371232270073301	0.120754518428109	0.0796665016437291	MAPK1	1	0.588235294117647
GO:1905269	BP	GO:1905269	positive regulation of chromatin organization	1/42	17/18903	0.0371232270073301	0.120754518428109	0.0796665016437291	CDK2	1	0.588235294117647
GO:1905288	BP	GO:1905288	vascular associated smooth muscle cell apoptotic	1/42	17/18903	0.0371232270073301	0.120754518428109	0.0796665016437291	ATF4	1	0.588235294117647
GO:1905459	BP	GO:1905459	regulation of vascular associated smooth muscle cell	1/42	17/18903	0.0371232270073301	0.120754518428109	0.0796665016437291	ATF4	1	0.588235294117647
GO:0061041	BP	GO:0061041	regulation of wound healing	2/42	137/18903	0.0371729517472498	0.120754518428109	0.0796665016437291	CLASP2/EDN1	2	0.145985401459854
GO:0048638	BP	GO:0048638	regulation of developmental growth	3/42	332/18903	0.0372420477395103	0.120754518428109	0.0796665016437291	INSR/PAFAH1B1/EDN1	3	0.090361445783132
GO:0030879	BP	GO:0030879	mammary gland developmen	2/42	138/18903	0.0376674179496292	0.121902872457023	0.0804241115928668	MSX1/MAPK1	2	0.144927536231884

GO:0071214	BP	GO:0071214	cellular response to abiotic stimulus	3/42	335/18903	0.038090604423627	0.122665860086676	0.080927488545272	GADD45A/ATF4/ATM	3	0.089552238059702
GO:0104004	BP	GO:0104004	cellular response to environmen	3/42	335/18903	0.038090604423627	0.122665860086676	0.080927488545272	GADD45A/ATF4/ATM	3	0.089552238059702
GO:0006997	BP	GO:0006997	nucleus organizati on	2/42	139/18903	0.038164431682782	0.122665860086676	0.080927488545272	SUN2/PAFAH1B1	2	0.143884892086331
GO:0048813	BP	GO:0048813	dendrite morphogene sis	2/42	140/18903	0.038663979822874	0.122665860086676	0.080927488545272	CUL7/PAFAH1B1	2	0.142857142857143
GO:0046328	BP	GO:0046328	regulation of JNK cascade	2/42	141/18903	0.039166049127619	0.122665860086676	0.080927488545272	GADD45A/PAFAH1B1	2	0.141843971631206
GO:0001696	BP	GO:0001696	gastric acid secretion	1/42	18/18903	0.039264539268097	0.122665860086676	0.080927488545272	SNX10	1	0.555555555555556
GO:0008356	BP	GO:0008356	asymmetric cell division	1/42	18/18903	0.039264539268097	0.122665860086676	0.080927488545272	ASPM	1	0.555555555555556
GO:0032310	BP	GO:0032310	prostaglan din secretion	1/42	18/18903	0.039264539268097	0.122665860086676	0.080927488545272	EDN1	1	0.555555555555556
GO:0032354	BP	GO:0032354	response to follicle- stimulatin	1/42	18/18903	0.039264539268097	0.122665860086676	0.080927488545272	EDN1	1	0.555555555555556
GO:0033151	BP	GO:0033151	V(D)J recombinat ion	1/42	18/18903	0.039264539268097	0.122665860086676	0.080927488545272	ATM	1	0.555555555555556

GO:0035970	BP	GO:0035970	peptidyl-threonine dephosphorylation	1/42	18/18903	0.039264539268097	0.122665860086676	0.080927488545272	DUSP1	1	0.555555555555556
GO:0036035	BP	GO:0036035	osteoclast developmen	1/42	18/18903	0.039264539268097	0.122665860086676	0.080927488545272	PAFAH1B1	1	0.555555555555556
GO:0036499	BP	GO:0036499	PERK-mediated unfolded protein response	1/42	18/18903	0.039264539268097	0.122665860086676	0.080927488545272	ATF4	1	0.555555555555556
GO:0043217	BP	GO:0043217	myelin maintenanc	1/42	18/18903	0.039264539268097	0.122665860086676	0.080927488545272	NDRG1	1	0.555555555555556
GO:0051782	BP	GO:0051782	negative regulation of cell division	1/42	18/18903	0.039264539268097	0.122665860086676	0.080927488545272	ASPM	1	0.555555555555556
GO:0060263	BP	GO:0060263	regulation of respiratory burst	1/42	18/18903	0.039264539268097	0.122665860086676	0.080927488545272	INSR	1	0.555555555555556
GO:0061952	BP	GO:0061952	midbody abscission	1/42	18/18903	0.039264539268097	0.122665860086676	0.080927488545272	CEP55	1	0.555555555555556
GO:0086103	BP	GO:0086103	G protein-coupled receptor signaling pathway involved in heart process	1/42	18/18903	0.039264539268097	0.122665860086676	0.080927488545272	EDN1	1	0.555555555555556

GO:2000641	BP	GO:2000641	regulation of early endosome to late endosome transport	1/42	18/18903	0.0392645393268097	0.122665860086676	0.0809274888545272	MAPK1	1	0.555555555555556
GO:0000086	BP	GO:0000086	G2/M transition of mitotic cell cycle	2/42	142/18903	0.0396706266397399	0.123259732862495	0.0813192900648408	ATM/CDK2	2	0.140845070422535
GO:0035107	BP	GO:0035107	appendage morphogenesis	2/42	142/18903	0.0396706266397399	0.123259732862495	0.0813192900648408	MSX1/CYP26B1	2	0.140845070422535
GO:0035108	BP	GO:0035108	limb morphogenesis	2/42	142/18903	0.0396706266397399	0.123259732862495	0.0813192900648408	MSX1/CYP26B1	2	0.140845070422535
GO:0010212	BP	GO:0010212	response to ionizing	2/42	143/18903	0.040177699285553	0.124609096334904	0.0822095181796308	GADD45A/ATM	2	0.13986013986014
GO:0010508	BP	GO:0010508	positive regulation of autophagy	2/42	144/18903	0.0406872540732102	0.125227666364863	0.0826176131391401	PLK2/UVRAG	2	0.138888888888889
GO:0050921	BP	GO:0050921	positive regulation of chemotaxis	2/42	144/18903	0.0406872540732102	0.125227666364863	0.0826176131391401	MAPK1/EDN1	2	0.138888888888889
GO:0010506	BP	GO:0010506	regulation of autophagy	3/42	344/18903	0.0406958749381674	0.125227666364863	0.0826176131391401	PLK2/UVRAG/ATM	3	0.0872093023255814
GO:0007076	BP	GO:0007076	mitotic chromosome condensation	1/42	19/18903	0.0414012027818412	0.125227666364863	0.0826176131391401	SMC4	1	0.526315789473684

GO:0010759	BP	GO:0010759	positive regulation of macrophage chemotaxis	1/42	19/18903	0.0414012027818412	0.1252276663648631	0.0826176131391401	MAPK1	1	0.5263157894736841
GO:0030889	BP	GO:0030889	negative regulation of B cell proliferation	1/42	19/18903	0.0414012027818412	0.1252276663648631	0.0826176131391401	ATM	1	0.5263157894736841
GO:0035813	BP	GO:0035813	regulation of renal sodium excretion	1/42	19/18903	0.0414012027818412	0.1252276663648631	0.0826176131391401	EDN1	1	0.5263157894736841
GO:0036003	BP	GO:0036003	positive regulation of transcription from RNA polymerase II promoter	1/42	19/18903	0.0414012027818412	0.1252276663648631	0.0826176131391401	ATF4	1	0.5263157894736841
GO:0045091	BP	GO:0045091	regulation of single stranded viral RNA replication via double stranded DNA intermedia	1/42	19/18903	0.0414012027818412	0.1252276663648631	0.0826176131391401	TOP2A	1	0.5263157894736841

GO:0045947	BP	GO:0045947	negative regulation of translational initiation	1/42	19/18903	0.0414012027818412	0.126527666364863	0.0826176131391401	ATF4	1	0.526315789473684
GO:0060438	BP	GO:0060438	trachea developmen	1/42	19/18903	0.0414012027818412	0.126527666364863	0.0826176131391401	MAPK1	1	0.526315789473684
GO:0061003	BP	GO:0061003	positive regulation of dendritic spine morphogenesis	1/42	19/18903	0.0414012027818412	0.126527666364863	0.0826176131391401	PAFAH1B1	1	0.526315789473684
GO:1901978	BP	GO:1901978	positive regulation of cell cycle checkpoint	1/42	19/18903	0.0414012027818412	0.126527666364863	0.0826176131391401	NDC80	1	0.526315789473684
GO:1902170	BP	GO:1902170	cellular response to reactive nitrogen	1/42	19/18903	0.0414012027818412	0.126527666364863	0.0826176131391401	CDK2	1	0.526315789473684
GO:0045765	BP	GO:0045765	regulation of angiogenesis	3/42	349/18903	0.0421816989557029	0.126534609507645	0.0834798554895292	GADD45A/PLK2/RGCC	3	0.085959885386819
GO:0008584	BP	GO:0008584	male gonad developmen	2/42	147/18903	0.0422306802016987	0.126534609507645	0.0834798554895292	INSR/ASPM	2	0.136054421768707
GO:0035264	BP	GO:0035264	multicellular organism	2/42	147/18903	0.0422306802016987	0.126534609507645	0.0834798554895292	RMI1/ATM	2	0.136054421768707

GO:0002687	BP	GO:0002687	positive regulation of leukocyte migration	2/42	148/18903	0.0427500363154771	0.1265346095507645	0.0834798548952 92	MAPK1/EDN1	2	0.1351351351351 35
GO:0032147	BP	GO:0032147	activation of protein kinase activity	2/42	148/18903	0.0427500363154771	0.1265346095507645	0.0834798548952 92	INSR/RGCC	2	0.1351351351351 35
GO:0046546	BP	GO:0046546	development of primary male sexual	2/42	148/18903	0.0427500363154771	0.1265346095507645	0.0834798548952 92	INSR/ASPM	2	0.1351351351351 35
GO:0031346	BP	GO:0031346	positive regulation of cell projection organization	3/42	352/18903	0.0430863114761885	0.1265346095507645	0.0834798548952 92	CUL7/MARK4/PAFAH1B1	3	0.0852272727272727
GO:0061351	BP	GO:0061351	neural precursor cell proliferation	2/42	149/18903	0.0432718084 4084	0.1265346095507645	0.0834798548952 92	PAFAH1B1/ASPM	2	0.1342281879194 63
GO:0007265	BP	GO:0007265	Ras protein signal transduction	3/42	353/18903	0.0433900292595919	0.1265346095507645	0.0834798548952 92	PLK2/SSX2IP/CDK2	3	0.0849858356940 51
GO:0016050	BP	GO:0016050	vesicle organization	3/42	353/18903	0.0433900292595919	0.1265346095507645	0.0834798548952 92	UVRAG/SNX10/PAFAH1B1	3	0.0849858356940 51

GO:0006662	BP	GO:0006662	glycerol ether metabolic process	1/42	20/18903	0.0435332272196278	0.1265346095076454895292	0.0834798548952	PAFAH1B1	1	0.5
GO:0008334	BP	GO:0008334	histone mRNA metabolic process	1/42	20/18903	0.0435332272196278	0.1265346095076454895292	0.0834798548952	ATM	1	0.5
GO:0008340	BP	GO:0008340	determination of adult	1/42	20/18903	0.0435332272196278	0.1265346095076454895292	0.0834798548952	ATM	1	0.5
GO:0015732	BP	GO:0015732	prostaglandin transport	1/42	20/18903	0.0435332272196278	0.1265346095076454895292	0.0834798548952	EDN1	1	0.5
GO:0039692	BP	GO:0039692	single stranded viral RNA replication via double stranded DNA	1/42	20/18903	0.0435332272196278	0.1265346095076454895292	0.0834798548952	TOP2A	1	0.5
GO:0043586	BP	GO:0043586	intermedia tongue developmen	1/42	20/18903	0.0435332272196278	0.1265346095076454895292	0.0834798548952	CYP26B1	1	0.5
GO:0046485	BP	GO:0046485	ether lipid metabolic	1/42	20/18903	0.0435332272196278	0.1265346095076454895292	0.0834798548952	PAFAH1B1	1	0.5
GO:0060716	BP	GO:0060716	labyrinthine layer blood vessel developmen	1/42	20/18903	0.0435332272196278	0.1265346095076454895292	0.0834798548952	MAPK1	1	0.5

GO:0071243	BP	GO:0071243	cellular response to arsenic-containing	1/42	20/18903	0.0435332272196278	0.126534609507645	0.083479854895292	ATF4	1	0.5
GO:0071371	BP	GO:0071371	cellular response to gonadotrop	1/42	20/18903	0.0435332272196278	0.126534609507645	0.083479854895292	EDN1	1	0.5
GO:1903978	BP	GO:1903978	regulation of microglial cell activation	1/42	20/18903	0.0435332272196278	0.126534609507645	0.083479854895292	ATM	1	0.5
GO:2000678	BP	GO:2000678	negative regulation of transcription regulatory region DNA binding	1/42	20/18903	0.0435332272196278	0.126534609507645	0.083479854895292	MSX1	1	0.5
GO:2001014	BP	GO:2001014	regulation of skeletal muscle cell	1/42	20/18903	0.0435332272196278	0.126534609507645	0.083479854895292	CYP26B1	1	0.5
GO:0001890	BP	GO:0001890	placenta developmen	2/42	150/18903	0.0437959856576473	0.126867559130105	0.083699514846569	CUL7/MAPK1	2	0.1333333333333333
GO:0034614	BP	GO:0034614	cellular response to reactive oxygen	2/42	150/18903	0.0437959856576473	0.126867559130105	0.083699514846569	MAPK1/EDN1	2	0.1333333333333333

GO:1901342	BP	GO:1901342	regulation of vasculature	3/42	355/18903	0.0440007289776906	0.127245351367916	0.0839487592337519	GADD45A/PLK2/RGCC	3	0.0845070422535211
GO:0072507	BP	GO:0072507	divalent inorganic cation homeostasi	3/42	356/18903	0.0443077087851622	0.127744469068839	0.0842780467971373	ATF4/SNX10/EDN1	3	0.0842696629213483
GO:0046718	BP	GO:0046718	viral entry into host cell	2/42	151/18903	0.0443225552727163	0.127744469068839	0.0842780467971373	INSR/UVRAG	2	0.132450331125828
GO:0002089	BP	GO:0002089	lens morphogenesis in camera-type eye	1/42	21/18903	0.0456606224670341	0.128359582370381	0.0846838612170557	ATF4	1	0.476190476190476
GO:0008090	BP	GO:0008090	retrograde axonal transport	1/42	21/18903	0.0456606224670341	0.128359582370381	0.0846838612170557	PAFAH1B1	1	0.476190476190476
GO:0032305	BP	GO:0032305	positive regulation of icosanoid secretion	1/42	21/18903	0.0456606224670341	0.128359582370381	0.0846838612170557	EDN1	1	0.476190476190476
GO:0035812	BP	GO:0035812	renal sodium excretion	1/42	21/18903	0.0456606224670341	0.128359582370381	0.0846838612170557	EDN1	1	0.476190476190476
GO:0038083	BP	GO:0038083	peptidyl-tyrosine autophosphorylation	1/42	21/18903	0.0456606224670341	0.128359582370381	0.0846838612170557	INSR	1	0.476190476190476

GO:0045821	BP	GO:0045821	positive regulation of glycolytic process	1/42	21/18903	0.045660624670341	0.128359582370381	0.084683861217055 7	INSR	1	0.476190476190476
GO:0051315	BP	GO:0051315	attachment of mitotic spindle microtubules to kinetochor	1/42	21/18903	0.045660624670341	0.128359582370381	0.084683861217055 7	NDC80	1	0.476190476190476
GO:0060973	BP	GO:0060973	cell migration involved in heart developmen	1/42	21/18903	0.045660624670341	0.128359582370381	0.084683861217055 7	EDN1	1	0.476190476190476
GO:0061050	BP	GO:0061050	regulation of cell growth involved in cardiac muscle cell	1/42	21/18903	0.045660624670341	0.128359582370381	0.084683861217055 7	EDN1	1	0.476190476190476
GO:0071731	BP	GO:0071731	response to nitric oxide	1/42	21/18903	0.045660624670341	0.128359582370381	0.084683861217055 7	CDK2	1	0.476190476190476
GO:0097062	BP	GO:0097062	dendritic spine maintenanc	1/42	21/18903	0.045660624670341	0.128359582370381	0.084683861217055 7	INSR	1	0.476190476190476
GO:0099515	BP	GO:0099515	actin filament-based transport	1/42	21/18903	0.045660624670341	0.128359582370381	0.084683861217055 7	SUN2	1	0.476190476190476

GO:1901522	BP	GO:1901522	positive regulation of transcription from RNA polymerase II promoter involved in cellular	1/42	21/18903	0.0456606224670341	0.128359582370381	0.0846838612170557	ATF4	1	0.476190476190476
GO:1903204	BP	GO:1903204	negative regulation of oxidative stress-induced neuron death	1/42	21/18903	0.0456606224670341	0.128359582370381	0.0846838612170557	ATF4	1	0.476190476190476
GO:2000047	BP	GO:2000047	regulation of cell-cell adhesion mediated by	1/42	21/18903	0.0456606224670341	0.128359582370381	0.0846838612170557	RGCC	1	0.476190476190476
GO:0008544	BP	GO:0008544	epidermis developmen	3/42	362/18903	0.0461723381584051	0.129585316274081	0.0854925260465377	INSR/PAFAH1B1/CYP26B	3	0.082872928176795

GO:0070507	BP	GO:0070507	regulation of microtubule cytoskeleton organizati	2/42	155/18903	0.0464525053240046	0.130158247323561	0.0858705111769437	CLASP2/PAFAH1B1	2	0.129032258064516
GO:0008643	BP	GO:0008643	carbohydrate regulation of actin	2/42	156/18903	0.0469908480030516	0.130679197990473	0.0862142028060607	INSR/EDN1	2	0.128205128205128
GO:0032956	BP	GO:0032956	cytoskeleton organizati on	3/42	365/18903	0.0471192276099399	0.130679197990473	0.0862142028060607	CLASP2/RGCC/EDN1	3	0.0821917808219178
GO:0006268	BP	GO:0006268	DNA unwinding involved in DNA replicatio	1/42	22/18903	0.0477833983306284	0.130679197990473	0.0862142028060607	RPA1	1	0.454545454545455
GO:0007530	BP	GO:0007530	sex determinat ion	1/42	22/18903	0.0477833983306284	0.130679197990473	0.0862142028060607	INSR	1	0.454545454545455
GO:0010042	BP	GO:0010042	response to manganese	1/42	22/18903	0.0477833983306284	0.130679197990473	0.0862142028060607	ATF4	1	0.454545454545455
GO:0023019	BP	GO:0023019	signal transducti on involved in regulation of gene	1/42	22/18903	0.0477833983306284	0.130679197990473	0.0862142028060607	MSX1	1	0.454545454545455

GO:0032303	BP	GO:0032303	regulation of icosanoid secretion	1/42	22/18903	0.0477833983306284	0.1306791979990473	0.0862142028060607	EDN1	1	0.4545454545454545
GO:0035020	BP	GO:0035020	regulation of Rac protein signal transduction	1/42	22/18903	0.0477833983306284	0.1306791979990473	0.0862142028060607	SSX2IP	1	0.4545454545454545
GO:0035313	BP	GO:0035313	wound healing, spreading of epidermal cells	1/42	22/18903	0.0477833983306284	0.1306791979990473	0.0862142028060607	CLASP2	1	0.4545454545454545
GO:0035809	BP	GO:0035809	regulation of urine volume	1/42	22/18903	0.0477833983306284	0.1306791979990473	0.0862142028060607	EDN1	1	0.4545454545454545
GO:0044062	BP	GO:0044062	regulation of excretion	1/42	22/18903	0.0477833983306284	0.1306791979990473	0.0862142028060607	EDN1	1	0.4545454545454545
GO:0044321	BP	GO:0044321	response to leptin	1/42	22/18903	0.0477833983306284	0.1306791979990473	0.0862142028060607	EDN1	1	0.4545454545454545
GO:0051767	BP	GO:0051767	nitric-oxide synthase biosynthetic process	1/42	22/18903	0.0477833983306284	0.1306791979990473	0.0862142028060607	EDN1	1	0.4545454545454545

GO:0051769	BP	GO:0051769	regulation of nitric-oxide synthase biosynthetic process	1/42	22/18903	0.0477833983306284	0.130679197990473	0.0862142028060607	EDN1	1	0.454545454545455
GO:0060117	BP	GO:0060117	auditory receptor cell development	1/42	22/18903	0.0477833983306284	0.130679197990473	0.0862142028060607	PAFAH1B1	1	0.454545454545455
GO:0044409	BP	GO:0044409	entry into host	2/42	158/18903	0.0480744723197382	0.131056523266547	0.0864631391201459	INSR/UVRAG	2	0.126582278481013
GO:0097530	BP	GO:0097530	granulocyte	2/42	158/18903	0.0480744723197382	0.131056523266547	0.0864631391201459	MAPK1/EDN1	2	0.126582278481013
GO:0035051	BP	GO:0035051	cardiocyte differentiation	2/42	159/18903	0.0486197291972241	0.132332235590723	0.0873047768866564	MAPK1/EDN1	2	0.125786163522013
GO:0051017	BP	GO:0051017	actin filament bundle assembly	2/42	160/18903	0.0491672661161109	0.133610094588543	0.0881478380480513	CLASP2/RGCC	2	0.125
GO:0001675	BP	GO:0001675	acrosome assembly	1/42	23/18903	0.0499015645967221	0.133695584647243	0.0882042316321272	PAFAH1B1	1	0.434782608695652
GO:0002689	BP	GO:0002689	negative regulation of leukocyte chemotaxis	1/42	23/18903	0.0499015645967221	0.133695584647243	0.0882042316321272	DUSP1	1	0.434782608695652
GO:0014821	BP	GO:0014821	phasic smooth muscle contractio	1/42	23/18903	0.0499015645967221	0.133695584647243	0.0882042316321272	EDN1	1	0.434782608695652

GO:0033139	BP	GO:0033139	regulation of peptidyl-serine phosphorylation of STAT protein	1/42	23/18903	0.0499015645967221	0.133695584647243	0.0882042316321272	GADD45A	1	0.434782608695652
GO:0035493	BP	GO:0035493	SNARE complex assembly	1/42	23/18903	0.0499015645967221	0.133695584647243	0.0882042316321272	UVRAG	1	0.434782608695652
GO:0040019	BP	GO:0040019	positive regulation of embryonic developmen	1/42	23/18903	0.0499015645967221	0.133695584647243	0.0882042316321272	PAFAH1B1	1	0.434782608695652
GO:0046599	BP	GO:0046599	regulation of centriole replicatio	1/42	23/18903	0.0499015645967221	0.133695584647243	0.0882042316321272	PLK2	1	0.434782608695652
GO:0051457	BP	GO:0051457	maintenanc e of protein location	1/42	23/18903	0.0499015645967221	0.133695584647243	0.0882042316321272	SUN2	1	0.434782608695652
GO:0097150	BP	GO:0097150	neuronal stem cell population maintenanc	1/42	23/18903	0.0499015645967221	0.133695584647243	0.0882042316321272	ASPM	1	0.434782608695652
GO:0098687	CC	GO:0098687	chromosoma l region	10/42	388/19869	6.05776792788562e-09	9.38954028822271e-07	5.86646999332081e-07	SMC4/TOP2A /UVRAG/CLA SP2/NDC80/ SPDL1/PAFA H1B1/ATM/R PA1/CDK2	10	0.257731958762887

GO:0005819	CC	GO:0005819	spindle	10/42	426/19869	1.4727880311365e-08	1.1414107241307 9e-06	7.1313946770819 9e-07	PLK2/SHCBP1L/KIF11/CLASP2/MAPK1/SPDL1/PAFAH1B1/ASPM/ATM/MTUS	10	0.234741784037559
GO:0000793	CC	GO:0000793	condensed chromosome	8/42	273/19869	9.0299110479859 3e-08	4.6654540414594e-06	2.9149186540866 9e-06	SMC4/TOP2A/CLASP2/NDC80/SPDL1/PAFAH1B1/C	8	0.293040293040293
GO:0000775	CC	GO:0000775	chromosome, centromeric region	7/42	250/19869	8.5072503110732 8e-07	3.2965594955408 9e-05	2.0596500753124 8e-05	CNB1IP1/CDSMC4/TOP2A/UVRAG/CLASP2/NDC80/SPDL1/PAFA	7	0.28
GO:0005814	CC	GO:0005814	centriole	5/42	157/19869	1.9415050997271e-05	0.0006018665809154	0.0003760388824734 59	TOP2A/CCDC102B/CEP55/PLK2/CETN	5	0.318471337579618
GO:0005874	CC	GO:0005874	microtubule	7/42	466/19869	4.9471148528206 9e-05	0.0012780046703120 1	0.0007984816955429 88	KIF11/CEP57/CLASP2/PAFAH1B1/NDRG1/ASPM/M	7	0.150214592274678
GO:0000940	CC	GO:0000940	outer kinetochor	2/42	12/19869	0.0002840645732923 34	0.0060793589613126 4	0.0037983091642836 2	NDC80/SPDL1	2	1.66666666666667
GO:0072687	CC	GO:0072687	meiotic spindle	2/42	14/19869	0.0003906155048106 65	0.0060793589613126 4	0.0037983091642836 2	SHCBP1L/ASPM	2	1.42857142857143
GO:0000776	CC	GO:0000776	kinetochore	4/42	164/19869	0.0003922167071814 61	0.0060793589613126 4	0.0037983091642836 2	CLASP2/NDC80/SPDL1/PAFAH1B1	4	0.243902439024390
GO:0036064	CC	GO:0036064	ciliary basal body	4/42	164/19869	0.0003922167071814 61	0.0060793589613126 4	0.0037983091642836 2	RPGR/MARK4/SSX2IP/CETN2	4	0.243902439024390
GO:0000922	CC	GO:0000922	spindle pole	4/42	172/19869	0.0004695850850497 5	0.0063357749808176 1	0.0039585147588130 4	PLK2/KIF11/SPDL1/ASP	4	0.232558139534884

GO:0000779	CC	GO:0000779	condensed chromosome, centromeri	4/42	174/19869	0.00049051 1611418138	0.00633577 498081761	0.00395851 475881304	CLASP2/NDC 80/SPDL1/P AFAH1B1	4	0.22988505 7471264
GO:0072686	CC	GO:0072686	mitotic spindle	4/42	183/19869	0.00059298 345140763	0.00707018 730524482	0.00441736 660157911	KIF11/CLAS P2/MAPK1/A SPM	4	0.21857923 4972678
GO:0005876	CC	GO:0005876	spindle microtubul	3/42	87/19869	0.00082280 3450307804	0.00902907 006908036	0.00564125 26068278	KIF11/CLAS P2/PAFAH1B	3	0.34482758 6206897
GO:0030496	CC	GO:0030496	midbody	4/42	203/19869	0.00087378 0974427132	0.00902907 006908036	0.00564125 26068278	CEP55/MARK 4/UVRAG/AS	4	0.19704433 4975369
GO:0000228	CC	GO:0000228	nuclear chromosome	4/42	249/19869	0.00185434 026090698	0.01696805 58198318	0.01060143 38568728	SMC4/TOP2A /CCNB1IP1/ RPA1	4	0.16064257 0281124
GO:0031252	CC	GO:0031252	cell leading edge	5/42	421/19869	0.00186101 2573788	0.01696805 58198318	0.01060143 38568728	ATF4/INSR/ CLASP2/SSX 2IP/PAFAH1	5	0.11876484 5605701
GO:1902911	CC	GO:1902911	protein kinase complex	3/42	136/19869	0.00296269 603839023	0.02551210 4775027	0.01593965 1200696	CCNL1/INSR /CDK2	3	0.22058823 5294118
GO:0032590	CC	GO:0032590	dendrite membrane	2/42	41/19869	0.00339487 514589622	0.02650008 48149935	0.01655692 90524917	ATF4/INSR	2	0.48780487 804878
GO:0061695	CC	GO:0061695	transferase complex, transferring phosphorus-	4/42	295/19869	0.00341936 57825798	0.02650008 48149935	0.01655692 90524917	CCNL1/INSR /UVRAG/CDK 2	4	0.13559322 0338983
GO:0005871	CC	GO:0005871	containing kinesin complex	2/42	49/19869	0.00481700 183614977	0.03456802 19924866	0.02159767 75776487	KIF11/PAFA H1B1	2	0.40816326 5306122

GO:0000307	CC	GO:0000307	cyclin-dependent protein kinase holoenzyme complex	2/42	50/19869	0.0050110169445554	0.0345680219924866	0.0215976775776487	CCNL1/CDK2	2	0.4
GO:0001673	CC	GO:0001673	male germ cell nucleus	2/42	51/19869	0.0052085919797028 1	0.0345680219924866	0.0215976775776487	TOP2A/CDK2	2	0.392156862745098
GO:0000781	CC	GO:0000781	chromosome, telomeric	3/42	168/19869	0.0053524679214172 8	0.0345680219924866	0.0215976775776487	ATM/RPA1/CDK2	3	0.178571428571429
GO:0031256	CC	GO:0031256	leading edge membrane	3/42	177/19869	0.0061836599876829 8	0.0383386919236345	0.0239535460575509	ATF4/INSR/CLASP2	3	0.169491525423729
GO:0032589	CC	GO:0032589	neuron projection membrane	2/42	60/19869	0.0071444742014319 6	0.0425920577393059	0.0266109970255765	ATF4/INSR	2	0.333333333333333
GO:0043073	CC	GO:0043073	germ cell nucleus	2/42	66/19869	0.0085891937518146 5	0.0493083345011582	0.0308072446458849	TOP2A/CDK2	2	0.303030303030303
GO:0016607	CC	GO:0016607	nuclear speck	4/42	419/19869	0.0116005308541801	0.0642172243713 54	0.0401221367888935	GADD45A/CCNL1/ATF4/SMC4	4	0.095465393794 7494
GO:0000794	CC	GO:0000794	condensed nuclear chromosome	2/42	79/19869	0.0121256234296861	0.0648093666069432	0.0404921000192786	SMC4/CCNB1IP1	2	0.253164556962025
GO:0005901	CC	GO:0005901	caveola	2/42	82/19869	0.0130181552655853	0.0672604688721907	0.0420235187520648	INSR/MAPK1	2	0.243902439024 39
GO:0031514	CC	GO:0031514	motile cilium	3/42	244/19869	0.0147645560137682	0.0738227800688 41	0.0461235705693268	RPGR/PAFAH1B1/CETN2	3	0.122950819672131
GO:0005635	CC	GO:0005635	nuclear envelope	4/42	488/19869	0.0192707101405718	0.0792698468022184	0.0495268312788054	INSR/SUN2/PAFAH1B1/CETN2	4	0.081967213114754 1

GO:0005881	CC	GO:0005881	cytoplasmic	2/42	102/19869	0.0196627859546049	0.0792698468022184	0.0495268312788054	CLASP2/PAFAH1B1	2	0.196078431372549
GO:0000805	CC	GO:0000805	X chromosome	1/42	10/19869	0.0209432093800328	0.0792698468022184	0.0495268312788054	CDK2	1	1
GO:0031313	CC	GO:0031313	extrinsic component of endosome	1/42	10/19869	0.0209432093800328	0.0792698468022184	0.0495268312788054	SNX10	1	1
GO:0031617	CC	GO:0031617	NMS complex	1/42	10/19869	0.0209432093800328	0.0792698468022184	0.0495268312788054	NDC80	1	1
GO:0034451	CC	GO:0034451	centriolar satellite	2/42	108/19869	0.0218816042696854	0.0792698468022184	0.0495268312788054	CEP72/SSX2IP	2	0.185185185185185
GO:0005770	CC	GO:0005770	late endosome	3/42	288/19869	0.0228229057910357	0.0792698468022184	0.0495268312788054	INSR/UVRAG/MAPK1	3	0.104166666666667
GO:0000109	CC	GO:0000109	nucleotide-excision repair complex	1/42	11/19869	0.0230138264909666	0.0792698468022184	0.0495268312788054	CETN2	1	0.909090909090909
GO:0000235	CC	GO:0000235	astral microtubul	1/42	11/19869	0.0230138264909666	0.0792698468022184	0.0495268312788054	PAFAH1B1	1	0.909090909090909
GO:0005818	CC	GO:0005818	aster	1/42	11/19869	0.0230138264909666	0.0792698468022184	0.0495268312788054	PAFAH1B1	1	0.909090909090909
GO:0034992	CC	GO:0034992	microtubule organizing center attachment	1/42	11/19869	0.0230138264909666	0.0792698468022184	0.0495268312788054	SUN2	1	0.909090909090909
GO:0034993	CC	GO:0034993	meiotic nuclear membrane microtubule tethering	1/42	11/19869	0.0230138264909666	0.0792698468022184	0.0495268312788054	SUN2	1	0.909090909090909

GO:0106083	CC	GO:0106083	nuclear membrane protein complex	1/42	11/19869	0.0230138264909666	0.0792698468022184	0.0495268312788054	SUN2	1	0.909090909090909
GO:0106094	CC	GO:0106094	nuclear membrane microtubule tethering	1/42	11/19869	0.0230138264909666	0.0792698468022184	0.0495268312788054	SUN2	1	0.909090909090909
GO:0044853	CC	GO:0044853	plasma membrane raft	2/42	113/19869	0.0238064006549541	0.0802172195982151	0.0501187382209561	INSR/MAPK1	2	0.176991150442478
GO:0044615	CC	GO:0044615	nuclear pore nuclear basket	1/42	12/19869	0.0250801684834829	0.0827111939348905	0.0516769428998976	CETN2	1	0.833333333333333
GO:0043601	CC	GO:0043601	nuclear replisome	1/42	13/19869	0.0271422439693911	0.0850619658255387	0.0531456764410836	RPA1	1	0.769230769230769
GO:0097733	CC	GO:0097733	photoreceptor cell cilium	2/42	122/19869	0.0274393438146899	0.0850619658255387	0.0531456764410836	RPGR/CETN2	2	0.163934426229508
GO:1902554	CC	GO:1902554	serine/threonine protein kinase complex	2/42	122/19869	0.0274393438146899	0.0850619658255387	0.0531456764410836	CCNL1/CDK2	2	0.163934426229508
GO:0030894	CC	GO:0030894	replisome	1/42	15/19869	0.0312536297840920	0.0949865218928285	0.0593464177530745	RPA1	1	0.666666666666667
GO:0097731	CC	GO:0097731	9+0 non-motile cilium	2/42	134/19869	0.0326064492115046	0.0971923005342924	0.0607245612845834	RPGR/CETN2	2	0.149253731343284
GO:0000930	CC	GO:0000930	gamma-tubulin complex	1/42	16/19869	0.0333029572520617	0.0973954410201804	0.0608514809769548	MARK4	1	0.625

GO:0031253	CC	GO:0031253	cell projection membrane	3/42	344/19869	0.0359345603420255	0.1016716355229	0.0635231950295877	ATF4/INSR/CLASP2	3	0.0872093023255814
GO:0005639	CC	GO:0005639	integral component of nuclear inner membrane	1/42	18/19869	0.0373889240310019	0.1016716355229	0.0635231950295877	SUN2	1	0.5555555555555556
GO:0031143	CC	GO:0031143	pseudopodium	1/42	18/19869	0.0373889240310019	0.1016716355229	0.0635231950295877	MAPK1	1	0.5555555555555556
GO:0031229	CC	GO:0031229	intrinsic component of nuclear inner membrane	1/42	18/19869	0.0373889240310019	0.1016716355229	0.0635231950295877	SUN2	1	0.5555555555555556
GO:0005828	CC	GO:0005828	kinetochore	1/42	20/19869	0.0414580300339422	0.1107930111297604	0.0692221191129344	CLASP2	1	0.5
GO:0005680	CC	GO:0005680	anaphase-promoting complex	1/42	21/19869	0.0434862814692074	0.1142436210808935	0.0713780177549881	CUL7	1	0.4761904761904476
GO:1990391	CC	GO:1990391	DNA repair complex	1/42	22/19869	0.0455103431468723	0.1175683806462753	0.0734552906931974	ATM	1	0.4545454545454455
GO:0097729	CC	GO:0097729	9+2 motile cilium	2/42	165/19869	0.0475283018296412	0.1201119306527821	0.0750444696812194	RPGR/CETN2	2	0.1212121212121121
GO:0005875	CC	GO:0005875	microtubule associated	2/42	166/19869	0.0480447746111285	0.1201119306527821	0.0750444696812194	KIF11/PAFAH1B1	2	0.1204819277710843
GO:0097730	CC	GO:0097730	non-motile cilium	2/42	168/19869	0.0490839353677109	0.1207620603206273	0.0754506608826968	RPGR/CETN2	2	0.1190476190479047

GO:0008017	MF	GO:0008017	microtubule binding	9/42	271/18432	8.20308361117646e-09	1.27147795973235e-06	9.41195909071825e-07	MARK4/SUN2/KIF11/CEP57/CLASP2/PAFAH1B1/NDRG1/CETN2/MTUS1	9	0.33210332103321
GO:0015631	MF	GO:0015631	tubulin binding	9/42	375/18432	1.33725764402759e-07	1.03637467412138e-05	7.67163595784249e-06	MARK4/SUN2/KIF11/CEP57/CLASP2/PAFAH1B1/NDRG1/CETN2/MTUS1	9	0.24
GO:0043015	MF	GO:0043015	gamma-tubulin binding	3/42	34/18432	6.26719221220885e-05	0.00323804930964124	0.00239692614431847	MARK4/CEP57/NDRG1	3	0.882352941176471
GO:0035173	MF	GO:0035173	histone kinase activity	2/42	20/18432	0.000938339036022657	0.0321040577408181	0.0237646335738484	ATM/CDK2	2	1
GO:0051010	MF	GO:0051010	microtubule plus-end binding	2/42	21/18432	0.00103561476583284	0.0321040577408181	0.0237646335738484	CLASP2/PAFAH1B1	2	0.952380952380952
GO:0106310	MF	GO:0106310	protein serine kinase activity	5/42	363/18432	0.0013473467103423	0.0348064566838428	0.0257650511275984	MARK4/PLK2/MAPK1/ATM/CDK2	5	0.137741046831956
GO:0030332	MF	GO:0030332	cyclin binding	2/42	34/18432	0.00271516222307768	0.0546763913931471	0.0404735257174081	NDC80/CDK2	2	0.588235294117647
GO:0004674	MF	GO:0004674	protein serine/threonine kinase activity	5/42	430/18432	0.00282200729772753	0.0546763913931471	0.0404735257174081	MARK4/PLK2/MAPK1/ATM/CDK2	5	0.116279069767442

GO:0046982	MF	GO:0046982	protein heterodimerization activity	4/42	341/18432	0.007406957492096987	0.127564267919448	0.094427879139014 2	GADD45A/ATF4/TOP2A/PAFAH1B1	4	0.117302052785924	
GO:1990841	MF	GO:1990841	promoter-specific chromatin binding	2/42	63/18432	0.009066053524617 05	0.140523829631564	0.104021035177185	GADD45A/ATF4	2	0.317460317460317	
GO:0051219	MF	GO:0051219	phosphoprotein	2/42	92/18432	0.018641264770755 2	0.156590963166545	0.115914533006135	MAPK1/PAFAH1B1	2	0.217391304347826	
GO:0043130	MF	GO:0043130	ubiquitin binding	2/42	96/18432	0.020191047397037 4	0.156590963166545	0.115914533006135	TOP2A/MARK4	2	0.208333333333333	
GO:0008330	MF	GO:0008330	protein tyrosine/threonine phosphatase activity	1/42	10/18432	0.022559674137185 8	0.156590963166545	0.115914533006135	DUSP1	1	1	
GO:0008401	MF	GO:0008401	retinoic acid 4-hydroxylase activity	1/42	10/18432	0.022559674137185 8	0.156590963166545	0.115914533006135	CYP26B1	1	1	
GO:0016303	MF	GO:0016303	1-phosphatidylinositol-3-kinase activity	1/42	10/18432	0.022559674137185 8	0.156590963166545	0.115914533006135	ATM	1	1	
GO:0098505	MF	GO:0098505	G-rich strand telomeric DNA	1/42	10/18432	0.022559674137185 8	0.156590963166545	0.115914533006135	RPA1	1	1	
GO:0047485	MF	GO:0047485	protein N-terminus binding	2/42	106/18432	0.024291836447428 1	0.156590963166545	0.115914533006135	GADD45A/ATM	2	0.188679245283019	

GO:0002162	MF	GO:0002162	dystroglycan binding	1/42	11/18432	0.0247881234741874	0.156590963166545	0.115914533006135	CLASP2	1	0.909090909090909
GO:0043522	MF	GO:0043522	leucine zipper domain binding	1/42	11/18432	0.0247881234741874	0.156590963166545	0.115914533006135	ATF4	1	0.909090909090909
GO:0034452	MF	GO:0034452	dynactin binding	1/42	12/18432	0.027011612905493	0.156590963166545	0.115914533006135	PAFAH1B1	1	0.833333333333333
GO:0035004	MF	GO:0035004	phosphatidylinositol 3-kinase activity	1/42	12/18432	0.027011612905493	0.156590963166545	0.115914533006135	ATM	1	0.833333333333333
GO:0043047	MF	GO:0043047	single-stranded telomeric DNA	1/42	12/18432	0.027011612905493	0.156590963166545	0.115914533006135	RPA1	1	0.833333333333333
GO:0032182	MF	GO:0032182	ubiquitin-like protein binding	2/42	116/18432	0.0287032827446192	0.156590963166545	0.115914533006135	TOP2A/MARK4	2	0.172413793103448
GO:0008353	MF	GO:0008353	RNA polymerase II CTD heptapeptide repeat kinase activity	1/42	13/18432	0.0292301532017996	0.156590963166545	0.115914533006135	MAPK1	1	0.769230769230769
GO:0017017	MF	GO:0017017	MAP kinase tyrosine/serine/threonine phosphatase activity	1/42	13/18432	0.0292301532017996	0.156590963166545	0.115914533006135	DUSP1	1	0.769230769230769

GO:0031994	MF	GO:0031994	insulin-like growth factor I	1/42	13/18432	0.02923015 32017996	0.15659096 3166545	0.11591453 3006135	INSR	1	0.76923076 9230769
GO:0043560	MF	GO:0043560	insulin receptor substrate binding	1/42	13/18432	0.02923015 32017996	0.15659096 3166545	0.11591453 3006135	INSR	1	0.76923076 9230769
GO:0097157	MF	GO:0097157	pre-mRNA intronic binding	1/42	13/18432	0.02923015 32017996	0.15659096 3166545	0.11591453 3006135	RBM7	1	0.76923076 9230769
GO:0098847	MF	GO:0098847	sequence-specific single stranded DNA	1/42	14/18432	0.03144375 51109983	0.15659096 3166545	0.11591453 3006135	RPA1	1	0.71428571 4285714
GO:0003697	MF	GO:0003697	single-stranded DNA	2/42	124/18432	0.03244574 64427051	0.15659096 3166545	0.11591453 3006135	SMC4/RPA1	2	0.16129032 2580645
GO:0005545	MF	GO:0005545	1-phosphatidylinositol binding	1/42	15/18432	0.03365242 93582201	0.15659096 3166545	0.11591453 3006135	SNX10	1	0.66666666 6666667
GO:0004707	MF	GO:0004707	MAP kinase activity	1/42	16/18432	0.03585618 6645887	0.15659096 3166545	0.11591453 3006135	MAPK1	1	0.625
GO:0005159	MF	GO:0005159	insulin-like growth factor receptor	1/42	16/18432	0.03585618 6645887	0.15659096 3166545	0.11591453 3006135	INSR	1	0.625
GO:0005521	MF	GO:0005521	lamin binding	1/42	16/18432	0.03585618 6645887	0.15659096 3166545	0.11591453 3006135	SUN2	1	0.625
GO:0030275	MF	GO:0030275	LRR domain binding	1/42	16/18432	0.03585618 6645887	0.15659096 3166545	0.11591453 3006135	ATF4	1	0.625

GO:0019838	MF	GO:0019838	growth factor binding	2/42	132/18432	0.0363695140257783	0.156590963166545	0.115914533006135	INSR/CEP57	2	0.151515151515152
GO:0008574	MF	GO:0008574	plus-end-directed microtubule motor activity	1/42	17/18432	0.0380550376537536	0.156616662680724	0.115933556755171	KIF11	1	0.588235294117647
GO:0004708	MF	GO:0004708	MAP kinase kinase activity	1/42	18/18432	0.0402489930389579	0.156616662680724	0.115933556755171	MAPK1	1	0.555555555555556
GO:0033549	MF	GO:0033549	MAP kinase phosphatase activity	1/42	18/18432	0.0402489930389579	0.156616662680724	0.115933556755171	DUSP1	1	0.555555555555556
GO:0005520	MF	GO:0005520	insulin-like growth factor	1/42	19/18432	0.0424380634360067	0.156616662680724	0.115933556755171	INSR	1	0.526315789473684
GO:0008301	MF	GO:0008301	DNA binding, bending	1/42	19/18432	0.0424380634360067	0.156616662680724	0.115933556755171	TOP2A	1	0.526315789473684
GO:0052742	MF	GO:0052742	phosphatidylinositol kinase activity	1/42	19/18432	0.0424380634360067	0.156616662680724	0.115933556755171	ATM	1	0.526315789473684
GO:0001972	MF	GO:0001972	retinoic acid binding	1/42	20/18432	0.0446222594571217	0.157192050360315	0.116359480402542	CYP26B1	1	0.5
GO:0016500	MF	GO:0016500	protein-hormone receptor activity	1/42	20/18432	0.0446222594571217	0.157192050360315	0.116359480402542	INSR	1	0.5

GO:0031683	MF	GO:0031683	G-protein beta/gamma-subunit complex binding	1/42	22/18432	0.0489760707068921	0.1650280643384441	0.1221599932963367	CETN2	1	0.4545454545454455
GO:0050321	MF	GO:0050321	tau-protein kinase	1/42	22/18432	0.0489760707068921	0.1650280643384441	0.1221599932963367	MARK4	1	0.4545454545454455

Table S6	ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count	richFactor
GO:0030198	BP	GO:0030198	extracellular matrix organization	84/1414	318/18903	2.77935033598078e-25	8.114318891976 55e-22	5.19980625396496e-22	COL1A1/MMP2/COL1A2/TGFBI/COL14A1/COL12A1/COL5A1/COL5A2/COL3A1/SERPINH	84	0.264150943396226
GO:0043062	BP	GO:0043062	extracellular structure organization	84/1414	319/18903	3.50687594746 73e-25	8.114318891976 55e-22	5.19980625396496e-22	COL1A1/MMP2/COL1A2/TGFBI/COL14A1/COL12A1/COL5A1/COL5A2/COL3A1/SERPINH	84	0.263322884012539
GO:0045785	BP	GO:0045785	positive regulation of cell adhesion	107/1414	484/18903	5.52940551677772e-25	8.114318891976 55e-22	5.19980625396496e-22	THY1/SOX4/DAB2/LGALS1/ACTB/TPM1/RIN2/FLNA/RUNX1/ZFHX3/ABI3BP/GLI3/ANK	107	0.221074380165289
GO:0045229	BP	GO:0045229	external encapsulating structure	84/1414	321/18903	5.56442235006106e-25	8.114318891976 55e-22	5.19980625396496e-22	COL1A1/MMP2/COL1A2/TGFBI/COL14A1/COL12A1/COL5A1/COL5A2/COL3A1/SERPINH	84	0.261682242990654
GO:0042060	BP	GO:0042060	wound healing	96/1414	442/18903	6.36854985381362e-22	7.429550259458 97e-19	4.76099379 59773e-19	COL1A1/COL5A1/COL3A1/PDGFRA/AQP1/PDGFRB/MYL9/ACTG1/ACTB/TPM1/FLNA/FAP	96	0.217194570135747
GO:0022407	BP	GO:0022407	regulation of cell-cell adhesion	101/1414	490/18903	3.14429352074782e-21	3.056777351087e-18	1.95883970038167e-18	THY1/SOX4/GPNMB/LGALS1/ACTB/RUNX1/GLI3/ANK3/LAG3/PIEZO1/HES1/SPINT2/T	101	0.206122448979592
GO:0061448	BP	GO:0061448	connective tissue	70/1414	274/18903	2.25100031010346e-20	1.875726401261 93e-	1.20200031596653e-17	COL1A1/TGFBI/COL5A1/COL3A1/SERPINH1/EGR1/PDGFR	70	0.255474452554745
GO:0001667	BP	GO:0001667	ameboidal-type cell migration	99/1414	492/18903	4.82839187597348e-20	3.520501226569 16e-17	2.25600257257656e-17	GJA1/JUN/FOXP1/AQP1/TWIST1/FSTL1/SEMA3C/ZEB2/RIN2/FAP/PIK3R3/SMOC2/PL	99	0.201219512195122
GO:0007015	BP	GO:0007015	actin filament organization	94/1414	454/18903	5.74332290979281e-20	3.722311392535 72e-17	2.38532627516658e-17	CALD1/MARCKS/TPM4/CAPZB/ENAH/ITGB5/LIMA1/WIPF1/ACTG1/TPM1/FLNA/DPYSL3	94	0.20704845814978
GO:0001503	BP	GO:0001503	ossification	90/1414	429/18903	1.47233248856264e-19	8.588115405785 89e-17	5.50342385987994e-17	COL1A1/MMP2/COL1A2/TNC/CDH11/COL5A2/COL6A1/MRC2/TPM4/VCAN/ITGA11/TWIS	90	0.20979020979021
GO:0002504	BP	GO:0002504	antigen	24/1414	36/18903	4.081073809	2.1640821	1.38678402	CTSF/CTSL/HLA-DRB1/HLA-	24	0.666666666666667
GO:0071559	BP	GO:0071559	response to transforming	68/1414	277/18903	8.05419590310296e-19	3.915010391899 96e-	2.50881137297532e-16	COL1A1/COL1A2/COL3A1/LTBP2/JUN/MXRA5/ZFP36L1/L	68	0.245487364620939
GO:0051216	BP	GO:0051216	cartilage development	56/1414	201/18903	2.02261649147203e-18	9.075324611351 06e-	5.81563656 77872e-16	COL1A1/TGFBI/COL3A1/SERPINH1/ECM1/RSPO2/PRRX1/	56	0.278606965174129

GO:1901342	BP	GO:1901342	regulation of vasculature	78/1414	355/18903	2.49643359101009e-18	1.04012122402585e-	6.66528998622319e-16	THBS2/AQP1/TWIST1/ECM1/GPNMB/RUNX1/SMOC2/CCN6/	78 0.219718309859155
GO:0060326	BP	GO:0060326	cell chemotaxis	73/1414	319/18903	2.87847391104487e-18	1.11934255487498e-	7.17295498815463e-16	MMP2/NBL1/PDGFRA/PDGFRB/SMOC2/PTN/NR4A1/TRPV4/	73 0.22884012539185
GO:0002181	BP	GO:0002181	cytoplasmic translation	49/1414	161/18903	5.02484814645391e-18	1.83187120239l6e-	1.17389709 00038e-15	RPS26/RPL22L1/RPS21/RPS15A/RPL39/RPS3/RPL36/RP	49 0.304347826086957
GO:0032103	BP	GO:0032103	positive regulation of response to	91/1414	464/18903	9.42330350901514e-18	3.23330172753443e-15	2.07195979941255e-15	CADM1/PDGFRB/LGALS1/FLNA/HEXIM1/SMOC2/NEAT1/LAG3/PLCG2/PTN/PLA2G2A/NF	91 0.196120689655172
GO:0045765	BP	GO:0045765	regulation of angiogenesis	76/1414	349/18903	1.17362846377559e-17	3.80320823844613e-	2.43716647653048e-15	THBS2/AQP1/TWIST1/ECM1/GPNMB/RUNX1/SMOC2/CCN6/	76 0.217765042979943
GO:0022409	BP	GO:0022409	positive regulation of	72/1414	322/18903	1.89047462762894e-17	5.80375710682084e-	3.71915534776197e-15	THY1/SOX4/LGALS1/ACTB/RUNX1/GLI3/ANK3/PIEZO1/H	72 0.22360248447205
GO:0050900	BP	GO:0050900	leukocyte migration	82/1414	398/18903	1.99413581719957e-17	5.81589711086255e-	3.72693488782931e-15	MMP2/NBL1/THY1/ECM1/CD99/PTN/APOD/TRPV4/SAA1/V	82 0.206030150753769
GO:0002495	BP	GO:0002495	antigen	22/1414	34/18903	3.298846210	9.1629380	5.87178089	CTSF/CTSL/HLA-DRB1/HLA-	22 0.647058823529412
GO:0003158	BP	GO:0003158	endothelium	44/1414	139/18903	4.826294179	1.2796260	8.20008164	FOXP1/FSTL1/RBPJ/SLC40A	44 0.316546762589928
GO:0010631	BP	GO:0010631	epithelial cell	77/1414	366/18903	5.66436825619543e-17	1.43653330451473e-	9.20557056189931e-15	JUN/FOXP1/FSTL1/ZEB2/RIN2/FAP/PIK3R3/SMOC2/PLC	77 0.210382513661202
GO:0071560	BP	GO:0071560	cellular response to	64/1414	271/18903	6.88503388411562e-17	1.63165899060173e-	1.04559738612915e-14	COL1A1/COL1A2/COL3A1/LTBP2/JUN/ZFP36L1/LTBP1/F	64 0.236162361623616
GO:0007159	BP	GO:0007159	leukocyte cell-cell	83/1414	414/18903	6.99322385822279e-17	1.63165899060173e-	1.04559738612915e-14	THY1/SOX4/GPNMB/LGALS1/ACTB/RUNX1/GLI3/NT5E/LA	83 0.20048309178744
GO:1902903	BP	GO:1902903	regulation of supramolecula	79/1414	384/18903	8.54872979483092e-17	1.91787464974034e-	1.22900969641476e-14	AEBP1/CAPZB/LIMA1/ACTG1/TPM1/FLNA/TNXB/HSPA1A/	79 0.205729166666667
GO:0090132	BP	GO:0090132	epithelium migration	77/1414	369/18903	9.18979852583942e-17	1.98533684448968e-	1.27224072379165e-14	JUN/FOXP1/FSTL1/ZEB2/RIN2/FAP/PIK3R3/SMOC2/PLC	77 0.208672086720867
GO:0052547	BP	GO:0052547	regulation of peptidase activity	88/1414	459/18903	1.43667099436603e-16	2.99289353933467e-14	1.91790176 72909e-14	COL6A3/SERPINH1/PCOLCE/AQP1/ANTXR1/ECM1/TIMP2/ANOS1/TIMP4/PCSK1N/NR4A	88 0.191721132897603
GO:0090130	BP	GO:0090130	tissue migration	77/1414	374/18903	2.02946362889725e-16	4.08202115426127e-	2.61583497140259e-14	JUN/FOXP1/FSTL1/ZEB2/RIN2/FAP/PIK3R3/SMOC2/PLC	77 0.205882352941176
GO:0019886	BP	GO:0019886	antigen	20/1414	30/18903	3.850018685	7.4857196	4.79698819	CTSF/CTSL/HLA-DRB1/HLA-	20 0.666666666666667
GO:0032956	BP	GO:0032956	regulation of actin	75/1414	365/18903	5.62816907705693e-16	1.05900355569268e-	6.78629147457696e-14	PDGFRA/PDGFRB/CAPZB/LIMA1/ACTG1/TPM1/FLNA/NOTC	75 0.205479452054795

GO:0007178	BP	GO:0007178	transmembrane receptor	78/1414	390/18903	7.085363417 3776e-16	1.2771929 2030789e-	8.18448944 754134e-14	COL1A2/NBL1/COL3A1/LTBP 2/JUN/EGR1/LTBP1/FOS/DK	78 0.2
GO:0032970	BP	GO:0032970	regulation of actin	80/1414	406/18903	7.225675702 06762e-16	1.2771929 2030789e-	8.18448944 754134e-14	PDGFRA/PDGFRB/CAPZB/FRM D6/LIMA1/ACTG1/TPM1/FLN	80 0.197044334975369
GO:0001819	BP	GO:0001819	positive regulation of cytokine	89/1414	486/18903	1.773764945 37256e-15	3.0430502 7245828e- 13	1.95004313 344209e-13	CADM1/EGR1/FOXP1/TWIST1 /RUNX1/LUM/CHI3L1/H19/S ULF2/S100A13/PLCG2/HSPA	89 0.183127572016461
GO:0070482	BP	GO:0070482	response to oxygen levels	70/1414	337/18903	3.024526326 47545e-15	5.0405891 6066609e-	3.23010315 3478e-13	COL1A1/MMP2/EGR1/ZFP36L 1/AQP1/FOS/PDGFRB/TWIST	70 0.207715133531157
GO:0002478	BP	GO:0002478	antigen	22/1414	40/18903	4.401136042	7.1310629	4.56971756	CTSF/CTSL/HLA-DRB1/HLA-	22 0.55
GO:0019882	BP	GO:0019882	antigen	36/1414	108/18903	5.506130132	8.6803397	5.56252293	CTSF/ICAM1/CTSL/HLA-	36 0.333333333333333
GO:0002274	BP	GO:0002274	myeloid leukocyte	56/1414	237/18903	5.927140575 22071e-15	9.0981607 829638e-	5.83027041 069495e-13	JUN/FOXP1/RBPJ/NOTCH2/M T1G/S100A13/PLCG2/PLA2G	56 0.236286919831224
GO:0043542	BP	GO:0043542	endothelial cell	62/1414	281/18903	6.423841689 4e-15	9.6077611 7288979e-	6.15683180 541414e-13	FOXP1/FSTL1/RIN2/FAP/PI K3R3/SMOC2/PTN/NR4A1/SP	62 0.220640569395018
GO:0045446	BP	GO:0045446	endothelial	38/1414	121/18903	8.788557995	1.2815914	8.21267616	FSTL1/RBPJ/ZEB1/COL15A1	38 0.31404958677686
GO:0070371	BP	GO:0070371	ERK1 and ERK2 cascade	69/1414	340/18903	1.617758575 69982e-14	2.3015575 0537977e-	1.47488079 648526e-12	JUN/PDGFRA/ZFP36L1/PDGF RB/DAB2/GPNMB/NOTCH2/CH	69 0.202941176470588
GO:0008360	BP	GO:0008360	regulation of	43/1414	154/18903	1.690065354	2.3471788	1.50411580	TPM1/PALMD/PDPN/FN1/RHO	43 0.279220779220779
GO:0050920	BP	GO:0050920	regulation of chemotaxis	54/1414	230/18903	2.410250099 67383e-14	3.2695322 863715e-	2.09517701 442883e-12	NBL1/PDGFRA/PDGFRB/SEMA 3C/SMOC2/PTN/TRPV4/TUBB	54 0.234782608695652
GO:1903037	BP	GO:1903037	regulation of leukocyte	73/1414	377/18903	3.508510174 99305e-14	4.5653261 9105405e-	2.92554581 544803e-12	THY1/SOX4/GPNMB/LGALS1/ ACTB/RUNX1/GLI3/LAG3/HE	73 0.193633952254642
GO:0031589	BP	GO:0031589	cell-substrate	72/1414	369/18903	3.522024320 20285e-14	4.5653261 9105405e-	2.92554581 544803e-12	COL1A1/COL3A1/THY1/ANTX R1/ITGA11/ITGB5/DAB2/AC	72 0.195121951219512
GO:0030595	BP	GO:0030595	leukocyte chemotaxis	55/1414	240/18903	4.112543149 44794e-14	5.1636961 9895903e-	3.30899243 009438e-12	MMP2/NBL1/PTN/TRPV4/SAA 1/PDE4B/ANXA1/CCL20/VEG	55 0.229166666666667
GO:0070372	BP	GO:0070372	regulation of ERK1 and ERK2	65/1414	315/18903	4.160701548 96407e-14	5.1636961 9895903e-	3.30899243 009438e-12	JUN/PDGFRA/PDGFRB/DAB2/ GPNMB/NOTCH2/CHI3L1/PLA	65 0.206349206349206
GO:0052548	BP	GO:0052548	regulation of endopeptidase	79/1414	428/18903	4.593179136 13649e-14	5.5816695 6272587e-	3.57683752 465366e-12	COL6A3/SERPINH1/AQP1/TI MP2/ANOS1/TIMP4/PCSK1N/	79 0.184579439252336
GO:0043410	BP	GO:0043410	positive regulation of MAPK cascade	87/1414	496/18903	4.963645698 21256e-14	5.8356311 3800083e- 12	3.73958081 89414e-12	JUN/IGFBP4/PDGFRA/PDGFR B/GPNMB/NOTCH2/CDON/CHI 3L1/MAP2K6/GADD45B/PLCG	87 0.175403225806452
GO:0110053	BP	GO:0110053	regulation of actin	60/1414	278/18903	5.002255390 023e-14	5.8356311 3800083e-	3.73958081 89414e-12	CAPZB/LIMA1/ACTG1/TPM1/ FLNA/SCIN/GSN/PIK3R1/RH	60 0.215827338129496

GO:0036293	BP	GO:0036293	response to decreased	64/1414	309/18903	5.45801944414498e-14	6.21750525867698e-	3.98429284805362e-12	MMP2/EGR1/ZFP36L1/AQP1/FOS/TWIST1/LMNA/RBPJ/CR	64 0.207119741100324
GO:0071674	BP	GO:0071674	mononuclear cell	50/1414	206/18903	5.54277856079552e-14	6.21750525867698e-	3.98429284805362e-12	NBL1/ECM1/CD99/APOD/TRPV4/SAA1/SELENOK/ICAM1/A	50 0.242718446601942
GO:0050678	BP	GO:0050678	regulation of epithelial	77/1414	414/18903	6.40389238286983e-14	7.04790646590183e-	4.51642936476082e-12	JUN/ZFP36L1/TWIST1/DAB2/ECM1/SIX1/RBPJ/ZEB1/NO	77 0.185990338164251
GO:0045766	BP	GO:0045766	positive regulation of	47/1414	187/18903	7.88769556769932e-14	8.36525968116184e-	5.36061377242111e-12	AQP1/TWIST1/ECM1/RUNX1/SMOC2/CHI3L1/S100A1/ANG	47 0.251336898395722
GO:1904018	BP	GO:1904018	positive regulation of	47/1414	187/18903	7.88769556769932e-14	8.36525968116184e-	5.36061377242111e-12	AQP1/TWIST1/ECM1/RUNX1/SMOC2/CHI3L1/S100A1/ANG	47 0.251336898395722
GO:0050870	BP	GO:0050870	positive regulation of	56/1414	251/18903	8.06732092380245e-14	8.40297909795351e-	5.38478507526739e-12	THY1/SOX4/LGALS1/ACTB/RUNX1/GLI3/HES1/ZBTB16/V	56 0.223107569721116
GO:0019884	BP	GO:0019884	antigen	23/1414	49/18903	9.288658372	9.5053937	6.09123284	CTSF/CTSL/HLA-DRB1/HLA-	23 0.469387755102041
GO:0070374	BP	GO:0070374	positive regulation of	52/1414	223/18903	9.76185716461432e-14	9.81739876572334e-	6.29117146852005e-12	JUN/PDGFRA/PDGFRB/GPNMB/NOTCH2/CHI3L1/PLA2G2A/	52 0.233183856502242
GO:1903039	BP	GO:1903039	positive regulation of	59/1414	275/18903	1.07121989732712e-13	1.05905519679815e-	6.78662240037216e-12	THY1/SOX4/LGALS1/ACTB/RUNX1/GLI3/HES1/ZBTB16/V	59 0.214545454545455
GO:0048002	BP	GO:0048002	antigen	26/1414	64/18903	1.576439711	1.5325621	9.82094283	CTSF/CTSL/HLA-DRB1/HLA-	26 0.40625
GO:0060348	BP	GO:0060348	bone development	53/1414	233/18903	1.64598143619588e-13	1.57326589323427e-	1.00817800479575e-11	COL1A1/GJA1/COL3A1/SERPINH1/FOXP1/TWIST1/ECM1/	53 0.227467811158798
GO:0050921	BP	GO:0050921	positive	40/1414	144/18903	1.672252449	1.5732658	1.00817800	PDGFRB/SMOC2/PTN/TRPV4/	40 0.277777777777778
GO:0050673	BP	GO:0050673	epithelial cell	84/1414	481/18903	1.76380051677073e-13	1.6330553038609e-	1.04649216959947e-11	JUN/IGFBP4/ZFP36L1/TWIST1/DAB2/ECM1/SIX1/RBPJ/	84 0.174636174636175
GO:0061572	BP	GO:0061572	actin	43/1414	164/18903	1.873816662	1.7078082	1.09439522	CALD1/MARCKS/ITGB5/LIMA	43 0.26219512195122
GO:0002062	BP	GO:0002062	chondrocyte	35/1414	114/18903	2.132081274	1.9132969	1.22607621	TGFBI/COL3A1/SERPINH1/E	35 0.307017543859649
GO:0030099	BP	GO:0030099	myeloid cell differentiati	75/1414	407/18903	2.231387192 7086e-13	1.96928386673734e-	1.26195367749453e-11	MAFB/JUN/FOXP1/ZFP36L1/FOS/RBPJ/FLNA/KLF10/FBN	75 0.184275184275184
GO:0002683	BP	GO:0002683	negative regulation of immune system	80/1414	449/18903	2.26199244079208e-13	1.96928386673734e-11	1.26195367749453e-11	MAFB/NBL1/COL3A1/THY1/TWIST1/GPNMB/FBN1/RUNX1/GLI3/PSMB4/LAG3/APOD/NR	80 0.178173719376392
GO:0050867	BP	GO:0050867	positive regulation of cell	82/1414	467/18903	2.55152976491656e-13	2.18868722334681e-11	1.40255142340847e-11	THY1/PDGFRB/SOX4/LGALS1/ACTB/FLNA/RUNX1/GLI3/HES1/ZBTB16/VCAM1/CDKN1A	82 0.17558886509636
GO:0001666	BP	GO:0001666	response to hypoxia	61/1414	296/18903	2.70375365042947e-13	2.28565145550074e-	1.46468790429825e-11	MMP2/EGR1/ZFP36L1/AQP1/FOS/TWIST1/LMNA/RBPJ/CR	61 0.206081081081081

GO:0002685	BP	GO:0002685	regulation of leukocyte	52/1414	231/18903	4.316129778 82307e-13	3.5965692 8569643e-	2.30474839 768432e-11	NBL1/THY1/ECM1/CD99/PTN /APOD/TRPV4/PIK3R1/SELE	52 0.225108225108225
GO:0010632	BP	GO:0010632	regulation of epithelial	60/1414	292/18903	4.850655648 70143e-13	3.9850527 3223598e-	2.55369580 556542e-11	JUN/FOXP1/RIN2/SMOC2/PL CG2/PTN/SPARC/FGFR1/NRP	60 0.205479452054795
GO:0007596	BP	GO:0007596	blood coagulation	51/1414	225/18903	5.464510457 21069e-13	4.4270124 3012638e-	2.83691178 853145e-11	COL3A1/PDGFRA/MYL9/ACTG 1/ACTB/FLNA/FAP/PROCR/C	51 0.226666666666667
GO:0050863	BP	GO:0050863	regulation of T cell	70/1414	376/18903	8.608230275 06689e-13	6.8783297 5266647e-	4.40776145 735581e-11	THY1/SOX4/GPNMB/LGALS1/ ACTB/RUNX1/ZEB1/GLI3/LA	70 0.186170212765957
GO:0022604	BP	GO:0022604	regulation of cell	62/1414	312/18903	9.368123377 846e-13	7.3843599 5445618e-	4.73203500 920784e-11	CAPZB/DAB2/PTPRD/TPM1/F LNA/PALMD/SPARC/MELTF/P	62 0.198717948717949
GO:0003007	BP	GO:0003007	heart morphogenesis	55/1414	258/18903	9.672368720 30977e-13	7.5225235 6607559e-	4.82057281 765895e-11	COL5A1/JUN/TWIST1/SOX4/ SEMA3C/SIX1/RBPJ/TPM1/F	55 0.213178294573643
GO:0050817	BP	GO:0050817	coagulation	51/1414	230/18903	1.340486852 56861e-12	1.0288236 5934641e-	6.59289309 345034e-11	COL3A1/PDGFRA/MYL9/ACTG 1/ACTB/FLNA/FAP/PROCR/C	51 0.221739130434783
GO:1903706	BP	GO:1903706	regulation of hemopoiesis	74/1414	413/18903	1.375397378 42178e-12	1.0419081 6991354e-	6.67674106 736262e-11	MAFB/FOXP1/ZFP36L1/FOS/ SOX4/ACTB/KLF10/FBN1/RU	74 0.179176755447942
GO:0007179	BP	GO:0007179	transforming growth factor	49/1414	216/18903	1.509515009 47078e-12	1.1288462 884927e-	7.23385667 83141e-11	COL1A2/COL3A1/LTBP2/JUN /LTBP1/FOS/DKK3/ITGB5/D	49 0.226851851851852
GO:0051017	BP	GO:0051017	actin	41/1414	160/18903	1.543009477	1.1392878	7.30076836	CALD1/MARCKS/ITGB5/LIMA	41 0.25625
GO:0007599	BP	GO:0007599	hemostasis	51/1414	231/18903	1.598001117 06309e-12	1.1651425 6447862e-	7.46644995 61724e-11	COL3A1/PDGFRA/MYL9/ACTG 1/ACTB/FLNA/FAP/PROCR/C	51 0.220779220779221
GO:0001649	BP	GO:0001649	osteoblast differentiati	53/1414	246/18903	1.619415692 39501e-12	1.1661792 2638766e-	7.47309307 82257e-11	COL1A1/TNC/COL6A1/MRC2/ TPM4/VCAN/ITGA11/TWIST1	53 0.215447154471545
GO:0034612	BP	GO:0034612	response to tumor	54/1414	254/18903	1.745483314 35908e-12	1.2416346 5520202e-	7.95662548 047382e-11	COL1A1/FOXP1/ZFP36L1/FO S/CTSK/CHI3L1/HSPA1A/HE	54 0.21259842519685
GO:0050878	BP	GO:0050878	regulation of body fluid	71/1414	390/18903	1.803190432 24194e-12	1.2672300 953334e-	8.12064581 470021e-11	COL3A1/PDGFRA/AQP1/MYL9 /ACTG1/ACTB/FLNA/FAP/CD	71 0.182051282051282
GO:0002696	BP	GO:0002696	positive regulation of	78/1414	450/18903	1.957217700 26167e-12	1.3591012 9114599e-	8.70937350 078845e-11	THY1/SOX4/LGALS1/ACTB/R UNX1/GLI3/HES1/ZBTB16/V	78 0.173333333333333
GO:0010634	BP	GO:0010634	positive	43/1414	176/18903	2.535233546	1.7397667	1.11487483	JUN/FOXP1/RIN2/SMOC2/PL	43 0.244318181818182
GO:0097529	BP	GO:0097529	myeloid leukocyte	52/1414	242/18903	2.927078170 23066e-12	1.9853077 8685528e-	1.27222210 311984e-10	MMP2/NBL1/CD99/TRPV4/SA A1/PIK3R1/SELENOK/PDE4B	52 0.214876033057851
GO:0007162	BP	GO:0007162	negative regulation of	60/1414	308/18903	5.267992884 83588e-12	3.5319772 9853422e-	2.26335665 26379e-10	COL1A1/MMP2/TGFBI/GPNMB /RUNX1/GLI3/LAG3/MELTF/	60 0.194805194805195
GO:2001233	BP	GO:2001233	regulation of apoptotic	68/1414	374/18903	5.677054124 42362e-12	3.7629837 1679124e-	2.41138985 596032e-10	LMNA/HSPA1A/COL2A1/UBB/ HSPA1B/SNAI1/DDIT3/DNAJ	68 0.181818181818182

GO:1902105	BP	GO:1902105	regulation of leukocyte	61/1414	317/18903	6.038160875 2092e-12	3.9573699 3090958e-	2.53595615 232027e-10	MAFB/FOXP1/ZFP36L1/FOS/ SOX4/ACTB/KLF10/FBN1/RU	61 0.192429022082019
GO:0002573	BP	GO:0002573	myeloid leukocyte	48/1414	218/18903	8.008425128 72427e-12	5.1903493 0842763e-	3.32607223 76725e-10	MAFB/JUN/FOXP1/ZFP36L1/ FOS/RBPJ/KLF10/FBN1/RUN	48 0.220183486238532
GO:0030199	BP	GO:0030199	collagen	24/1414	64/18903	1.054064444	6.7564372	4.32965048	COL1A1/COL1A2/COL14A1/C	24 0.375
GO:0048545	BP	GO:0048545	response to steroid	63/1414	339/18903	1.307289366 01162e-11	8.2884987 7385408e-	5.31142395 733095e-10	COL1A1/FOSB/FOXP1/ZFP36 L1/AQP1/FOS/DAB2/LBH/CD	63 0.185840707964602
GO:0010594	BP	GO:0010594	regulation of endothelial	49/1414	230/18903	1.721482644 90341e-11	1.0797213 1910985e-	6.91905475 048332e-10	FOXP1/RIN2/SMOC2/PTN/SP ARC/FGFR1/NRP2/ETS1/FGF	49 0.21304347826087
GO:0048659	BP	GO:0048659	smooth muscle	42/1414	179/18903	1.867920639	1.1591043	7.42775609	MMP2/GJA1/JUN/FOXP1/PDG	42 0.23463687150838
GO:0032535	BP	GO:0032535	regulation of cellular	66/1414	367/18903	1.928950334 06059e-11	1.1843755 051132e-	7.58969821 191042e-10	AQP1/CAPZB/SEMA3C/LIMA1 /NTN1/SCIN/GSN/TRPV4/SP	66 0.17983651226158
GO:0043254	BP	GO:0043254	regulation of protein-	71/1414	410/18903	2.048871325 67151e-11	1.2449027 5444187e-	7.97756806 738983e-10	CAPZB/PIEZO1/PLCG2/HSPA 1A/HES1/HSPA1B/HSPA8/CR	71 0.173170731707317
GO:0033002	BP	GO:0033002	muscle cell proliferation	51/1414	247/18903	2.269219964 01814e-11	1.3645732 0104307e-	8.74443851 57118e-10	MMP2/GJA1/JUN/FOXP1/FOS /PDGFRB/SIX1/RBPJ/TPM1/	51 0.206477732793522
GO:0045861	BP	GO:0045861	negative regulation of	64/1414	352/18903	2.400895919 23495e-11	1.4290230 5070382e-	9.15744512 266735e-10	COL6A3/SERPINH1/AQP1/EC M1/TIMP2/GAS1/ANOS1/TIM	64 0.181818181818182
GO:0010466	BP	GO:0010466	negative regulation of	53/1414	263/18903	2.431852125 80021e-11	1.4328276 2119117e-	9.18182551 697666e-10	COL6A3/SERPINH1/AQP1/EC M1/TIMP2/ANOS1/TIMP4/PC	53 0.201520912547529
GO:1903131	BP	GO:1903131	mononuclear cell	78/1414	473/18903	2.534502620 2835e-11	1.4783753 7841136e-	9.47370400 48702e-10	MAFB/JUN/EGR1/FOXP1/ZFP 36L1/FOS/SOX4/KLF6/LGAL	78 0.164904862579281
GO:0150115	BP	GO:0150115	cell-	30/1414	101/18903	2.801394136	1.6178744	1.03676399	THY1/ACTG1/ACTN1/APOD/F	30 0.297029702970297
GO:0050727	BP	GO:0050727	regulation of inflammatory	71/1414	414/18903	3.248196209 62122e-11	1.8575224 0105104e-	1.19033485 452683e-09	TNC/SOCS3/FOXP1/LGALS1/ PSMB4/NT5E/NEAT1/PLCG2/	71 0.171497584541063
GO:0048660	BP	GO:0048660	regulation of	41/1414	175/18903	3.409144797	1.9306351	1.23718683	MMP2/GJA1/JUN/FOXP1/PDG	41 0.234285714285714
GO:0002687	BP	GO:0002687	positive	37/1414	148/18903	4.120406708	2.3109934	1.48092755	THY1/CD99/PTN/TRPV4/PIK	37 0.25
GO:0051251	BP	GO:0051251	positive regulation of	69/1414	400/18903	4.720627845 45414e-11	2.6224211 6405086e-	1.68049618 839175e-09	THY1/SOX4/LGALS1/ACTB/R UNX1/GLI3/HES1/ZBTB16/V	69 0.1725
GO:0010951	BP	GO:0010951	negative regulation of	51/1414	252/18903	4.911449960 48069e-11	2.7026875 1127206e-	1.73193235 448529e-09	COL6A3/SERPINH1/AQP1/TI MP2/ANOS1/TIMP4/PCSK1N/	51 0.202380952380952
GO:0001655	BP	GO:0001655	urogenital system	64/1414	360/18903	6.482183848 20992e-11	3.5336989 1463631e-	2.26445989 621185e-09	MMP2/TNC/EGR1/PDGFRA/AQ P1/PDGFRB/SOX4/SIX1/FBN	64 0.177777777777778
GO:0034329	BP	GO:0034329	cell junction assembly	72/1414	430/18903	7.338188646 84227e-11	3.9633013 3120657e-	2.53975710 379502e-09	THBS2/CDH11/GJA1/THY1/P TPRD/SIX1/ACTG1/ACTB/AC	72 0.167441860465116
GO:0001570	BP	GO:0001570	vasculogenesi	26/1414	81/18903	8.548365096	4.5745517	2.93145769	ZFP36L1/PDGFRB/RIN2/JUN	26 0.320987654320988

GO:0045926	BP	GO:0045926	negative regulation of	50/1414	249/18903	1.01787622646283e-10	5.39752002632518e-	3.45883108150193e-09	GJA1/FOXP1/SEMA3C/DAB2/FHL1/NTN1/MT1G/HSPA1A/M	50	0.200803212851406
GO:0051346	BP	GO:0051346	negative regulation of	65/1414	373/18903	1.10932115995282e-10	5.80334447296778e-	3.71889092432504e-09	COL6A3/SERPINH1/AQP1/ECM1/TIMP2/ANOS1/TIMP4/PC	65	0.17426273458445
GO:0071356	BP	GO:0071356	cellular response to	48/1414	234/18903	1.11430581342772e-10	5.80334447296778e-	3.71889092432504e-09	COL1A1/FOXP1/ZFP36L1/FOS/CTSK/CHI3L1/HSPA1A/HE	48	0.205128205128205
GO:0007229	BP	GO:0007229	integrin-	31/1414	113/18903	1.24763094	6.4402046	4.12700277	COL3A1/THY1/ITGA11/ITGB	31	0.274336283185841
GO:0045444	BP	GO:0045444	fat cell differentiati	49/1414	244/18903	1.55978340373655e-10	7.91977983799907e-	5.07514201498456e-09	MAFB/PDGFRA/ZFP36L1/SIX1/TBL1XR1/ID4/DIO2/RETR	49	0.200819672131148
GO:0034109	BP	GO:0034109	homotypic	28/1414	95/18903	1.56141724	7.91977985	5.07514201	PDGFRA/MYL9/ACTG1/CD99/	28	0.294736842105263
GO:0010038	BP	GO:0010038	response to metal ion	63/1414	360/18903	1.79676182252334e-10	9.03492388860023e-	5.78974703428348e-09	JUN/FOSB/AQP1/FOS/ACTG1/SLC40A1/FIBIN/CRIP1/AN	63	0.175
GO:0072001	BP	GO:0072001	renal system development	58/1414	318/18903	1.82989041801148e-10	9.12286393868458e-	5.84610065169479e-09	EGR1/PDGFRA/AQP1/PDGFRB/SOX4/SIX1/FBN1/NOTCH2/	58	0.182389937106918
GO:0007160	BP	GO:0007160	cell-matrix adhesion	48/1414	238/18903	2.05603580841399e-10	1.01634380258295e-	6.51291985341487e-09	COL3A1/THY1/ITGA11/ITGB5/ACTG1/RIN2/ACTN1/TNXB	48	0.201680672268908
GO:0042116	BP	GO:0042116	macrophage	30/1414	109/18903	2.26847164	1.1119323	7.12546909	JUN/FOXP1/PLCG2/NR1D1/J	30	0.275229357798165
GO:0090287	BP	GO:0090287	regulation of cellular	60/1414	338/18903	2.72948112423429e-10	1.32675528313822e-	8.50209427382101e-09	NBL1/LTBP1/DKK3/FSTL1/DAB2/ZEB2/RBPJ/FBN1/ZEB1	60	0.177514792899408
GO:0030282	BP	GO:0030282	bone	32/1414	123/18903	2.81479312	1.3569163	8.69537225	COL1A2/TWIST1/ECM1/RSPO	32	0.260162601626016
GO:0090092	BP	GO:0090092	regulation of transmembrane	54/1414	290/18903	3.53376002196157e-10	1.68954280394277e-	1.08269040879944e-08	NBL1/LTBP1/DKK3/FSTL1/DAB2/ZEB2/RBPJ/FBN1/ZEB1	54	0.186206896551724
GO:0072593	BP	GO:0072593	reactive oxygen	47/1414	235/18903	4.25153336323777e-10	2.01619464290776e-	1.29201497414267e-08	PDGFRB/CCN6/H19/FOXO1/PRDX4/PLCG2/CRYAB/GPX3/M	47	0.2
GO:0150116	BP	GO:0150116	regulation of	23/1414	69/18903	4.45103878	2.0937830	1.34173503	THY1/ACTG1/APOD/PIK3R1/	23	0.333333333333333
GO:0043434	BP	GO:0043434	response to peptide	69/1414	421/18903	4.76711642609127e-10	2.21977665903923e-	1.42247411 12271e-08	COL1A1/COL3A1/EGR1/SOCS3/ZFP36L1/FOS/FBN1/CTSK	69	0.163895486935867
GO:0045185	BP	GO:0045185	maintenance	27/1414	93/18903	4.82421073	2.2197766	1.42247411	NBL1/LTBP1/FLNA/FBN1/AN	27	0.290322580645161
GO:0001822	BP	GO:0001822	kidney development	56/1414	309/18903	4.83304707179808e-10	2.21977665903923e-	1.42247411 12271e-08	EGR1/PDGFRA/AQP1/PDGFRB/SOX4/SIX1/FBN1/NOTCH2/	56	0.181229773462783
GO:0071453	BP	GO:0071453	cellular	39/1414	175/18903	4.96371588	2.2479142	1.44050519	EGR1/ZFP36L1/AQP1/FOS/T	39	0.222857142857143
GO:1901654	BP	GO:1901654	response to	43/1414	205/18903	4.97138585	2.2479142	1.44050519	FOSB/FOXP1/POSTN/AQP1/F	43	0.209756097560976
GO:0045936	BP	GO:0045936	negative regulation of	71/1414	440/18903	5.38187145576493e-10	2.41480432319053e-	1.54745146068188e-08	JUN/THY1/SOCS3/HEXIM1/SH3BP5/H19/GADD45B/DNAJA	71	0.161363636363636
GO:0030168	BP	GO:0030168	platelet	33/1414	133/18903	5.70204888	2.5389352	1.62699683	COL3A1/PDGFRA/MYL9/ACTG	33	0.24812030075188

GO:0010563	BP	GO:0010563	negative regulation of	71/1414	441/18903	5.95872704018491e-10	2.6331253655605e-	1.68735563952924e-08	JUN/THY1/SOCS3/HEXIM1/SH3BP5/H19/GADD45B/DNAJA	71	0.160997732426304
GO:0071496	BP	GO:0071496	cellular response to	58/1414	328/18903	6.314192587230 6e-10	2.7640738 9272815e-	1.77126988785723e-08	COL1A1/POSTN/AQP1/FOS/KLF10/CTSK/LAMP2/FOXO1/P	58	0.176829268292683
GO:0010810	BP	GO:0010810	regulation of	45/1414	222/18903	6.349835447	2.7640738	1.77126988	COL1A1/THY1/DAB2/ACTG1/	45	0.202702702702703
GO:0002688	BP	GO:0002688	regulation of	32/1414	127/18903	6.812613718	2.9435537	1.88628392	NBL1/PTN/TRPV4/VEGFA/TN	32	0.251968503937008
GO:0008154	BP	GO:0008154	actin	42/1414	200/18903	7.601469462	3.2602478	2.08922740	CAPZB/ENAH/LIMA1/WIPF1/	42	0.21
GO:1901653	BP	GO:1901653	cellular response to	63/1414	373/18903	7.972204081275 76e-10	3.3942968 1796215e-	2.17512844353517e-08	GJA1/SOCS3/ZFP36L1/FOS/FBN1/PIK3R3/FOXO1/NR4A1	63	0.168900804289544
GO:2000379	BP	GO:2000379	positive	23/1414	71/18903	8.475962628	3.5826297	2.29581565	PDGFRB/H19/PLCG2/SOD2/C	23	0.323943661971831
GO:2000377	BP	GO:2000377	regulation of	35/1414	149/18903	8.559224158	3.5917952	2.30168913	PDGFRB/CCN6/H19/FOXO1/P	35	0.23489932885906
GO:0055076	BP	GO:0055076	transition	34/1414	143/18903	1.057843322	4.4074286	2.82436213	SLC40A1/MT1G/MT1M/MT1A/	34	0.237762237762238
GO:0002399	BP	GO:0002399	MHC class II	11/1414	16/18903	1.215539435	4.9709958	3.18550647	HLA-DRB1/HLA-DRA/HLA-	11	0.6875
GO:0002503	BP	GO:0002503	peptide	11/1414	16/18903	1.215539435	4.9709958	3.18550647	HLA-DRB1/HLA-DRA/HLA-	11	0.6875
GO:1901214	BP	GO:1901214	regulation of neuron death	57/1414	325/18903	1.218673766935 98e-09	4.9709958 619144e-	3.18550647507521e-08	JUN/EGR1/FOS/GPNMB/SIX1/RETREG1/UBB/DDIT3/SOD2	57	0.175384615384615
GO:0009612	BP	GO:0009612	response to	43/1414	211/18903	1.277752638	5.1757855	3.31673948	COL1A1/MMP2/JUN/FOSB/AQ	43	0.203791469194313
GO:0002237	BP	GO:0002237	response to molecule of	61/1414	360/18903	1.301913435413 19e-09	5.2372834 9570011e-	3.35614853658966e-08	FOXP1/FOS/DIO2/TIMP4/PLCG2/ZFP36/NR4A1/NFKBIA/	61	0.169444444444444
GO:0110148	BP	GO:0110148	biomineraliza	39/1414	181/18903	1.401243601	5.5982561	3.58746649	COL1A1/COL1A2/TWIST1/EC	39	0.215469613259669
GO:0008064	BP	GO:0008064	regulation of	36/1414	159/18903	1.448372886	5.7471830	3.68290162	CAPZB/LIMA1/SCIN/GSN/AR	36	0.226415094339623
GO:0001906	BP	GO:0001906	cell killing	40/1414	189/18903	1.509571697	5.9495484	3.81258114	CADM1/TUBB/LAG3/TUBB4B/	40	0.211640211640212
GO:0031214	BP	GO:0031214	biomineral	38/1414	174/18903	1.519883116	5.9499853	3.81286114	COL1A1/COL1A2/TWIST1/EC	38	0.218390804597701
GO:0010595	BP	GO:0010595	positive	32/1414	131/18903	1.581025722	6.1480820	3.93980515	FOXP1/RIN2/SMOC2/SPARC/	32	0.244274809160305
GO:0031532	BP	GO:0031532	actin	29/1414	111/18903	1.717840894	6.6358714	4.25238969	PDGFRA/ANTXR1/FLNA/NOTC	29	0.261261261261261
GO:0002064	BP	GO:0002064	epithelial	43/1414	213/18903	1.733229728	6.6512690	4.26225676	FRMD6/NOTCH2/COL15A1/FR	43	0.2018779342723
GO:0048661	BP	GO:0048661	positive	27/1414	98/18903	1.745497446	6.6545664	4.26436975	MMP2/GJA1/JUN/FOXP1/PDG	27	0.275510204081633
GO:1902905	BP	GO:1902905	positive	38/1414	176/18903	2.137335982	8.0955070	5.18775124	TPM1/TNXB/HSPA1A/HSPA1B	38	0.215909090909091
GO:0032496	BP	GO:0032496	response to lipopolysacch	58/1414	339/18903	2.287206606058 76e-09	8.6072749 2460692e-	5.51570163539195e-08	FOXP1/FOS/DIO2/TIMP4/PLCG2/ZFP36/NR4A1/NFKBIA/	58	0.171091445427729
GO:0034341	BP	GO:0034341	response to	33/1414	140/18903	2.348973355	8.7830522	5.62834304	ACTG1/IFITM1/GSN/IFITM2	33	0.235714285714286
GO:0030832	BP	GO:0030832	regulation of	36/1414	162/18903	2.482405702	9.2228487	5.91017274	CAPZB/LIMA1/SCIN/GSN/AR	36	0.222222222222222
GO:2001236	BP	GO:2001236	regulation of	35/1414	155/18903	2.633104914	9.7208233	6.22928417	LMNA/HSPA1A/COL2A1/HSPA	35	0.225806451612903
GO:0045216	BP	GO:0045216	cell-cell	42/1414	208/18903	2.654075370	9.7366173	6.23940525	CDH11/GJA1/ACTG1/ACTB/F	42	0.201923076923077
GO:0001909	BP	GO:0001909	leukocyte	32/1414	134/18903	2.897046806	1.0561546	6.76803500	CADM1/TUBB/LAG3/TUBB4B/	32	0.238805970149254
GO:0032271	BP	GO:0032271	regulation of	41/1414	201/18903	2.994822782	1.0850187	6.95300143	CAPZB/HSPA1A/HSPA1B/SCI	41	0.203980099502488

GO:0006898	BP	GO:0006898	receptor-mediated	48/1414	257/18903	3.02626846374967e-09	1.08964345364517e-	6.98263763 14328e-08	DAB2/PLCG2/TF/MAGI2/SDC BP/ANXA2/CTSL/CAV1/RABG	48 0.186770428015564
GO:0051235	BP	GO:0051235	maintenance of location	58/1414	342/18903	3.207175105 3029e-09	1.14769646559705e-	7.35465211 425936e-08	NBL1/THY1/LTBP1/FLNA/FB N1/ANK3/PLCG2/DDIT3/NFK	58 0.169590643274854
GO:0048771	BP	GO:0048771	tissue	38/1414	179/18903	3.523175095	1.2530902	8.03003515	MMP2/GJA1/SEMA3C/GPNMB/	38 0.212290502793296
GO:0060562	BP	GO:0060562	epithelial tube	57/1414	335/18903	3.870955283 78246e-09	1.36844134365473e-	8.76922629 200096e-08	FOXP1/TWIST1/SOX4/SIX1/ RSPO2/RBPJ/NOTCH2/GLI3/	57 0.170149253731343
GO:0007044	BP	GO:0007044	cell-	26/1414	95/18903	4.061883062	1.4272869	9.14632007	THY1/ACTG1/ACTN1/APOD/F	26 0.273684210526316
GO:0007265	BP	GO:0007265	Ras protein signal	59/1414	353/18903	4.122349366 6972e-09	1.43986011113442e-	9.22689101 868375e-08	COL1A2/COL3A1/JUN/PDGFR B/NOTCH2/NTN1/PDPN/FGF2	59 0.1671388101983
GO:0031960	BP	GO:0031960	response to	36/1414	165/18903	4.188247378	1.4541694	9.31858799	COL1A1/FOSB/ZFP36L1/AQP	36 0.218181818181818
GO:0006979	BP	GO:0006979	response to oxidative	68/1414	434/18903	4.362782831 27172e-09	1.50580545886437e-	9.64948105 502702e-08	COL1A1/MMP2/JUN/PDGFRA/ FOXP1/AQP1/FOS/PDGFRB/T	68 0.15668202764977
GO:0051098	BP	GO:0051098	regulation of binding	61/1414	372/18903	4.776058912 64183e-09	1.63875009631999e-	1.05014149 837716e-07	JUN/TWIST1/DAB2/ACTB/CC PG1/CDON/HES1/CTHRC1/DD	61 0.163978494623656
GO:0002443	BP	GO:0002443	leukocyte mediated	71/1414	463/18903	5.032580084 28304e-09	1.71666898430544e-	1.10007336 899286e-07	CADM1/C1R/TUBB/LAG3/S10 0A13/PLCG2/TUBB4B/C1S/C	71 0.153347732181425
GO:1904019	BP	GO:1904019	epithelial	32/1414	137/18903	5.198949771	1.7631089	1.12983296	ZFP36L1/H19/ZFP36/GSN/A	32 0.233576642335766
GO:0071675	BP	GO:0071675	regulation of	30/1414	123/18903	5.288999086	1.7832792	1.14275848	NBL1/ECM1/APOD/TRPV4/SE	30 0.24390243902439
GO:0036294	BP	GO:0036294	cellular	35/1414	159/18903	5.363658090	1.7980584	1.15222927	EGR1/ZFP36L1/AQP1/FOS/T	35 0.220125786163522
GO:0050866	BP	GO:0050866	negative regulation of	43/1414	221/18903	5.603062232 12124e-09	1.86758068571218e-	1.19678039 015113e-07	PDGFRA/GPNMB/RUNX1/GLI3 /LAG3/NR1D1/SERPINE2/IN	43 0.194570135746606
GO:0070665	BP	GO:0070665	positive	36/1414	167/18903	5.885931179	1.9507179	1.25005631	HES1/VCAM1/CDKN1A/PNP/S	36 0.215568862275449
GO:1904035	BP	GO:1904035	regulation of	28/1414	110/18903	6.143262467	2.0244999	1.29733720	ZFP36L1/H19/ZFP36/GSN/A	28 0.254545454545455
GO:0045637	BP	GO:0045637	regulation of	42/1414	214/18903	6.441251841	2.1107765	1.35262479	MAFB/FOXP1/ZFP36L1/FOS/	42 0.196261682242991
GO:0072676	BP	GO:0072676	lymphocyte	30/1414	124/18903	6.484134533	2.1129584	1.35402303	ECM1/CD99/APOD/SAA1/SEL	30 0.241935483870968
GO:0070997	BP	GO:0070997	neuron death	60/1414	368/18903	7.950315519 76474e-09	2.57071692451411e-	1.64736315 138903e-07	JUN/EGR1/FOS/GPNMB/SIX1 /RETREG1/UBB/DDIT3/SOD2	60 0.16304347826087
GO:0033674	BP	GO:0033674	positive regulation of kinase	74/1414	496/18903	7.977023201 38958e-09	2.57071692451411e- 07	1.64736315 138903e-07	EGR1/PDGFRA/PDGFRB/CHI3 L1/MAP2K6/FGFR1/GPRC5C/ BMP2/FGF2/CDKN1A/GPRC5A	74 0.149193548387097
GO:0071900	BP	GO:0071900	regulation of protein	63/1414	395/18903	8.076225234 20977e-09	2.58838581270031e-	1.65868570 310462e-07	THY1/PDGFRB/DAB2/ACTB/C CNL1/HEXIM1/TNXB/MAP2K6	63 0.159493670886076
GO:0043534	BP	GO:0043534	blood vessel	37/1414	177/18903	8.762235308	2.7929026	1.78974389	PIK3R3/NR4A1/FGFR1/ETS1	37 0.209039548022599
GO:0072678	BP	GO:0072678	T cell	22/1414	73/18903	8.993751018	2.8357053	1.81717268	ECM1/CD99/APOD/SELENOK/	22 0.301369863013699
GO:0150076	BP	GO:0150076	neuroinflamma	22/1414	73/18903	8.993751018	2.8357053	1.81717268	JUN/PLCG2/MMP3/NR1D1/NU	22 0.301369863013699

GO:0007266	BP	GO:0007266	Rho protein	32/1414	140/18903	9.146825701	2.8531248	1.82833538	COL1A2/COL3A1/PDGFRB/NT	32	0.228571428571429
GO:0030833	BP	GO:0030833	regulation of	32/1414	140/18903	9.146825701	2.8531248	1.82833538	CAPZB/SCIN/GSN/ARHGAP18	32	0.228571428571429
GO:0003206	BP	GO:0003206	cardiac	30/1414	126/18903	9.671966571	3.0008819	1.92302090	SOX4/SEMA3C/RBPJ/TPM1/N	30	0.238095238095238
GO:0002697	BP	GO:0002697	regulation of immune	61/1414	379/18903	9.840345593 98532e-09	3.0369701 5077864e-	1.94614687 854313e-07	CADM1/TWIST1/LAG3/PLCG2 /JUNB/RBP4/CFH/A2M/XBP1	61	0.160949868073879
GO:0061564	BP	GO:0061564	axon development	73/1414	490/18903	1.071503472 94335e-08	3.2805216 8702995e-	2.10221922 64779e-07	MMP2/TNC/CDH11/JUN/THY1 /ENAH/SEMA3C/ACTB/FLNA/	73	0.148979591836735
GO:0009266	BP	GO:0009266	response to	38/1414	186/18903	1.074197912	3.2805216	2.10221922	FOS/DIO2/IGFBP7/PCSK1N/	38	0.204301075268817
GO:0022408	BP	GO:0022408	negative	40/1414	202/18903	1.129086185	3.4289308	2.19732255	GPNMB/RUNX1/GLI3/LAG3/S	40	0.198019801980198
GO:0003151	BP	GO:0003151	outflow tract	23/1414	80/18903	1.134551087	3.4289308	2.19732255	JUN/TWIST1/SEMA3C/SIX1/	23	0.2875
GO:0045862	BP	GO:0045862	positive regulation of	60/1414	372/18903	1.199973046 3612e-08	3.6022425 5296372e-	2.30838393 271931e-07	PCOLCE/ANTXR1/DAB2/HSPA 1A/HSPA1B/MELTF/PCOLCE2	60	0.161290322580645
GO:0042326	BP	GO:0042326	negative regulation of	61/1414	381/18903	1.204247038 96438e-08	3.6022425 5296372e-	2.30838393 271931e-07	JUN/THY1/SOCS3/HEXIM1/S H3BP5/GADD45B/DNAJA1/BM	61	0.16010498687664
GO:2000116	BP	GO:2000116	regulation of	44/1414	235/18903	1.263884412	3.7613458	2.41034025	AQP1/NR4A1/CRYAB/GSN/CF	44	0.187234042553191
GO:0048762	BP	GO:0048762	mesenchymal cell	46/1414	252/18903	1.350523659 01005e-08	3.9987840 1167798e-	2.56249506 446417e-07	COL1A1/S100A4/TWIST1/SE MA3C/DAB2/SIX1/RBPJ/FLN	46	0.182539682539683
GO:0016049	BP	GO:0016049	cell growth	73/1414	493/18903	1.390487157 37088e-08	4.0963189 8431531e-	2.62499728 645613e-07	TNC/GJA1/IGFBP4/FOXP1/S EMA3C/DAB2/IGFBP7/FHL1/	73	0.148073022312373
GO:0030098	BP	GO:0030098	lymphocyte differentiati	65/1414	419/18903	1.424161648 51723e-08	4.1744396 4613116e-	2.67505845 748991e-07	MAFB/EGR1/FOXP1/ZFP36L1 /SOX4/KLF6/LGALS1/ACTB/	65	0.155131264916468
GO:1903053	BP	GO:1903053	regulation of	19/1414	57/18903	1.453885168	4.2402560	2.71723485	AEBP1/ANTXR1/RUNX1/FAP/	19	0.333333333333333
GO:0032623	BP	GO:0032623	interleukin-2	20/1414	63/18903	1.573133492	4.5426176	2.91099376	RUNX1/LAG3/PLCG2/ZFP36/	20	0.317460317460317
GO:0032663	BP	GO:0032663	regulation of	20/1414	63/18903	1.573133492	4.5426176	2.91099376	RUNX1/LAG3/PLCG2/ZFP36/	20	0.317460317460317
GO:0042026	BP	GO:0042026	protein	13/1414	27/18903	1.614953217	4.6404049	2.97365770	HSPA1A/HSPA1B/HSPA8/CRY	13	0.481481481481481
GO:0031668	BP	GO:0031668	cellular response to	47/1414	262/18903	1.660931928 65977e-08	4.7491254 6072178e-	3.04332780 117174e-07	COL1A1/POSTN/FOS/KLF10/ CTSK/LAMP2/FOXO1/TNRC6A	47	0.179389312977099
GO:0016032	BP	GO:0016032	viral process	65/1414	421/18903	1.719281289 99177e-08	4.8717603 5487352e-	3.12191451 905328e-07	JUN/ITGB5/LGALS1/GALNT1 /HEXIM1/IFITM1/HSPA1A/H	65	0.154394299287411
GO:0033627	BP	GO:0033627	cell adhesion	24/1414	88/18903	1.720525686	4.8717603	3.12191451	ITGA11/ITGB5/FBN1/ITGA1	24	0.272727272727273
GO:0032231	BP	GO:0032231	regulation of	27/1414	108/18903	1.732426090	4.8817591	3.12832191	ACTG1/TPM1/FLNA/PIK3R1/	27	0.25
GO:0071456	BP	GO:0071456	cellular	33/1414	151/18903	1.758311694	4.9308808	3.15980001	EGR1/ZFP36L1/AQP1/FOS/T	33	0.218543046357616
GO:0002263	BP	GO:0002263	cell activation	51/1414	297/18903	1.863288136 01514e-08	5.2002677 9778772e-	3.33242818 987146e-07	FOXP1/LGALS1/NOTCH2/S10 0A13/PLCG2/ITM2A/JUNB/X	51	0.171717171717172
GO:0001558	BP	GO:0001558	regulation of cell growth	65/1414	422/18903	1.887810107 84344e-08	5.2436173 138337e-	3.36020736 488824e-07	TNC/GJA1/IGFBP4/FOXP1/S EMA3C/DAB2/IGFBP7/FHL1/	65	0.154028436018957

GO:0001774	BP	GO:0001774	microglial	17/1414	47/18903	2.065467957	5.7098931	3.65900559	JUN/NR1D1/IFNGR2/TYROBP	17	0.361702127659574
GO:0051893	BP	GO:0051893	regulation of	20/1414	64/18903	2.128340581	5.8284556	3.73498265	THY1/ACTG1/APOD/SDC4/VE	20	0.3125
GO:0090109	BP	GO:0090109	regulation of	20/1414	64/18903	2.128340581	5.8284556	3.73498265	THY1/ACTG1/APOD/SDC4/VE	20	0.3125
GO:0070167	BP	GO:0070167	regulation of	26/1414	103/18903	2.559310353	6.9714891	4.46745971	TWIST1/ECM1/ASPN/LTBP3/	26	0.252427184466019
GO:0050679	BP	GO:0050679	positive	42/1414	224/18903	2.581590348	6.9714891	4.46745971	JUN/TWIST1/ECM1/RBPJ/NO	42	0.1875
GO:0097191	BP	GO:0097191	extrinsic	42/1414	224/18903	2.581590348	6.9714891	4.46745971	LMNA/HSPA1A/COL2A1/HSPA	42	0.1875
GO:0070527	BP	GO:0070527	platelet	21/1414	71/18903	2.817487225	7.5734575	4.85321229	PDGFRA/MYL9/ACTG1/ACTB/	21	0.295774647887324
GO:0001885	BP	GO:0001885	endothelial	20/1414	65/18903	2.859539584	7.6465884	4.90007591	COL15A1/ICAM1/VEGFA/AFD	20	0.307692307692308
GO:0001894	BP	GO:0001894	tissue homeostasis	48/1414	275/18903	2.870911841 54961e-08	7.6465884 8025519e-	4.90007591 893423e-07	GJA1/COL3A1/ACTG1/ACTB/ CTSK/LTBP3/COMP/COL2A1/	48	0.174545454545455
GO:0002690	BP	GO:0002690	positive	25/1414	97/18903	3.019462283	8.0056924	5.13019644	PTN/TRPV4/VEGFA/CD74/AI	25	0.257731958762887
GO:0002366	BP	GO:0002366	leukocyte activation	50/1414	293/18903	3.155276943 27525e-08	8.3279323 1227354e-	5.33669370 115285e-07	FOXP1/LGALS1/NOTCH2/S10 0A13/PLCG2/ITM2A/JUNB/X	50	0.170648464163823
GO:0007163	BP	GO:0007163	establishment	43/1414	234/18903	3.259235163	8.5635669	5.48769277	GJA1/AQP1/LMNA/ACTB/HES	43	0.183760683760684
GO:0051651	BP	GO:0051651	maintenance	42/1414	226/18903	3.365071971	8.8020021	5.64048646	THY1/FLNA/ANK3/PLCG2/DD	42	0.185840707964602
GO:0002396	BP	GO:0002396	MHC protein	11/1414	20/18903	3.528647026	9.1332125	5.85273221	HLA-DRB1/HLA-DRA/HLA-	11	0.55
GO:0002501	BP	GO:0002501	peptide	11/1414	20/18903	3.528647026	9.1332125	5.85273221	HLA-DRB1/HLA-DRA/HLA-	11	0.55
GO:0010952	BP	GO:0010952	positive	38/1414	194/18903	3.538669686	9.1332125	5.85273221	PCOLCE/ANTXR1/PCOLCE2/G	38	0.195876288659794
GO:0070663	BP	GO:0070663	regulation of leukocyte	47/1414	269/18903	3.868235078 42595e-08	9.9398304 9006985e-	6.36962799 14169e-07	GPNMB/HES1/VCAM1/CDKN1A /PNP/SELENOK/CD55/NMB/S	47	0.174721189591078
GO:0110149	BP	GO:0110149	regulation of	26/1414	105/18903	3.919630367	1.0027721	6.42594987	TWIST1/ECM1/ASPN/LTBP3/	26	0.247619047619048
GO:0060541	BP	GO:0060541	respiratory	40/1414	211/18903	4.024298873	1.0250539	6.56873606	COL3A1/PDGFRA/PDGFRB/SI	40	0.18957345971564
GO:0045667	BP	GO:0045667	regulation of	31/1414	141/18903	4.077532629	1.0340977	6.62669032	TWIST1/SMOC1/GLI3/IFITM	31	0.219858156028369
GO:0071216	BP	GO:0071216	cellular response to	46/1414	261/18903	4.107460463 368e-08	1.0371782 2003574e-	6.64643067 004773e-07	NOTCH2/PLCG2/ZFP36/DDIT 3/NFKBIA/NR1D1/XBP1/CD5	46	0.176245210727969
GO:0060537	BP	GO:0060537	muscle tissue development	64/1414	422/18903	4.408839424 08065e-08	1.1084810 5002855e-	7.10335244 778149e-07	GJA1/COL3A1/EGR1/PDGFRA /FOXP1/FOS/PDGFRB/TWIST	64	0.151658767772512
GO:0044089	BP	GO:0044089	positive regulation of	72/1414	498/18903	4.706926744 28483e-08	1.1783477 9825809e-	7.55107154 685134e-07	THBS2/THY1/PTPRD/TPM1/D PYSL3/PIEZO1/PLCG2/HSPA	72	0.144578313253012
GO:0046635	BP	GO:0046635	positive	21/1414	73/18903	4.830178321	1.1984356	7.67979847	RUNX1/GLI3/ZBTB16/PNP/C	21	0.287671232876712
GO:0051384	BP	GO:0051384	response to	31/1414	142/18903	4.847914537	1.1984356	7.67979847	FOSB/ZFP36L1/AQP1/FOS/C	31	0.21830985915493
GO:0030336	BP	GO:0030336	negative regulation of	58/1414	368/18903	4.848805459 18414e-08	1.1984356 8828055e-	7.67979847 705748e-07	GJA1/NBL1/COL3A1/THY1/T PM1/DPYSL3/IFITM1/APOD/	58	0.157608695652174
GO:1903844	BP	GO:1903844	regulation of	32/1414	150/18903	5.273786585	1.2979745	8.31766207	LTBP1/DKK3/DAB2/ZEB2/FB	32	0.213333333333333
GO:0060249	BP	GO:0060249	anatomical structure	54/1414	333/18903	5.334805930 07304e-08	1.3074757 5588723e-	8.37854748 239246e-07	GJA1/COL3A1/ACTG1/ACTB/ CTSK/LAMP2/LTBP3/COMP/C	54	0.162162162162162

GO:0034405	BP	GO:0034405	response to	14/1414	34/18903	5.391806297	1.3159165	8.43263781	MMP2/PDGFRB/PTGS2/KLF2/	14	0.411764705882353
GO:0031349	BP	GO:0031349	positive regulation of	51/1414	307/18903	5.651419391 96389e-08	1.3735303 8805522e-	8.80183783 371218e-07	CADM1/LGALS1/HEXIM1/NEA T1/LAG3/PLCG2/PLA2G2A/N	51	0.166123778501629
GO:0051258	BP	GO:0051258	protein polymerizatio	48/1414	281/18903	5.741216359 262e-08	1.3895649 3873756e-	8.90459021 259636e-07	CAPZB/MAP7D3/HSPA1A/UBE 2S/HSPA1B/SCIN/GSN/TRPV	48	0.170818505338078
GO:0032963	BP	GO:0032963	collagen	26/1414	107/18903	5.929196080	1.4291322	9.15814496	COL1A1/MMP2/COL1A2/COL5	26	0.242990654205607
GO:0002269	BP	GO:0002269	leukocyte	17/1414	50/18903	5.979749922	1.4295033	9.16052285	JUN/NR1D1/IFNGR2/TYROBP	17	0.34
GO:2001238	BP	GO:2001238	positive	17/1414	50/18903	5.979749922	1.4295033	9.16052285	ITM2C/TNFRSF12A/INHBA/P	17	0.34
GO:0071248	BP	GO:0071248	cellular	38/1414	198/18903	6.230636002	1.4833999	9.50590266	JUN/FOSB/AQP1/FOS/SLC40	38	0.191919191919192
GO:0031667	BP	GO:0031667	response to nutrient	69/1414	474/18903	6.854185029 06646e-08	1.6249350 347483e-	1.04128855 033362e-06	COL1A1/POSTN/FOS/KLF10/ TBL1XR1/CTSK/ZEB1/LAMP2	69	0.145569620253165
GO:0003205	BP	GO:0003205	cardiac	34/1414	167/18903	6.880832394	1.6249350	1.04128855	SOX4/SEMA3C/RBPJ/TPM1/N	34	0.203592814371257
GO:0002761	BP	GO:0002761	regulation of	28/1414	122/18903	6.944765588	1.6334200	1.04672591	MAFB/FOXP1/ZFP36L1/FOS/	28	0.229508196721311
GO:0062197	BP	GO:0062197	cellular response to	55/1414	345/18903	7.260867952 90293e-08	1.7009093 4816397e-	1.08997430 144825e-06	MMP2/JUN/PDGFRA/FOXP1/Z FP36L1/AQP1/FOS/TPM1/GP	55	0.159420289855072
GO:0034101	BP	GO:0034101	erythrocyte	30/1414	137/18903	7.386128655	1.7233315	1.10434285	MAFB/ZFP36L1/HSPA1A/HSP	30	0.218978102189781
GO:0055072	BP	GO:0055072	iron ion	23/1414	88/18903	8.075022331	1.8765579	1.20253320	SLC40A1/MELTF/TF/SLC39A	23	0.261363636363636
GO:1902107	BP	GO:1902107	positive	36/1414	184/18903	8.293962802	1.9050160	1.22076963	ZFP36L1/FOS/SOX4/ACTB/K	36	0.195652173913043
GO:1903708	BP	GO:1903708	positive	36/1414	184/18903	8.293962802	1.9050160	1.22076963	ZFP36L1/FOS/SOX4/ACTB/K	36	0.195652173913043
GO:0034332	BP	GO:0034332	adherens	17/1414	51/18903	8.347398901	1.9050160	1.22076963	CDH11/ACTB/BMP6/VEGFA/M	17	0.333333333333333
GO:0022612	BP	GO:0022612	gland	28/1414	123/18903	8.358121231	1.9050160	1.22076963	MMP2/TNC/SEMA3C/ID4/NOT	28	0.227642276422764
GO:0035633	BP	GO:0035633	maintenance	14/1414	35/18903	8.368563800	1.9050160	1.22076963	GJA1/ACTG1/ACTB/PTGS2/V	14	0.4
GO:0009636	BP	GO:0009636	response to	44/1414	250/18903	8.393435841	1.9050160	1.22076963	FOS/PDGFRB/GPX8/H19/MT1	44	0.176
GO:0045860	BP	GO:0045860	positive regulation of	63/1414	420/18903	8.474249110 95345e-08	1.9128320 1913871e-	1.22577828 5068e-06	EGR1/PDGFRB/CHI3L1/MAP2 K6/FGFR1/GPRC5C/BMP2/FG	63	0.15
GO:2000146	BP	GO:2000146	negative regulation of	59/1414	383/18903	8.493459505 51903e-08	1.9128320 1913871e-	1.22577828 5068e-06	GJA1/NBL1/COL3A1/THY1/T PM1/DPYSL3/IFITM1/APOD/	59	0.154046997389034
GO:0032835	BP	GO:0032835	glomerulus	20/1414	69/18903	8.734869701	1.9596344	1.25577013	EGR1/PDGFRA/AQP1/PDGFRB	20	0.289855072463768
GO:0001933	BP	GO:0001933	negative regulation of	54/1414	338/18903	8.861375072 13345e-08	1.9803984 9792163e-	1.26907613 959048e-06	JUN/THY1/SOCS3/HEXIM1/S H3BP5/GADD45B/DNAJA1/BM	54	0.159763313609467
GO:0038066	BP	GO:0038066	p38MAPK	18/1414	57/18903	8.980366396	1.9993311	1.28120856	ZFP36L1/MAP2K6/GADD45B/	18	0.315789473684211
GO:0048568	BP	GO:0048568	embryonic organ	66/1414	449/18903	9.123426810 91359e-08	2.0234581 2121897e-	1.29666954 594974e-06	MAFB/PDGFRA/SOCS3/ZFP36 L1/TWIST1/SIX1/RBPJ/PRR	66	0.146993318485523
GO:0050671	BP	GO:0050671	positive	31/1414	146/18903	9.503206424	2.0997046	1.34552974	HES1/VCAM1/CDKN1A/PNP/S	31	0.212328767123288
GO:0007517	BP	GO:0007517	muscle organ development	55/1414	348/18903	9.767369441 9488e-08	2.1418445 847702e-	1.37253379 059597e-06	COL6A3/COL3A1/EGR1/FOS/ ITGA11/TWIST1/SIX1/RBPJ	55	0.158045977011494

GO:0070661	BP	GO:0070661	leukocyte proliferation	55/1414	348/18903	9.767369441 9488e-08	2.1418445 847702e-	1.37253379 059597e-06	GPNMB/HES1/JUNB/VCAM1/C DKN1A/PNP/SELENOK/CD55/	55 0.158045977011494
GO:0050729	BP	GO:0050729	positive	32/1414	154/18903	1.009261217	2.2048766	1.41292591	LGALS1/NEAT1/PLCG2/PLA2	32 0.207792207792208
GO:0048732	BP	GO:0048732	gland development	65/1414	441/18903	1.030652557 13265e-07	2.2432075 9916223e-	1.43748909 284291e-06	MMP2/TNC/MAFB/JUN/CADM1 /PDGFRA/DKK3/SEMA3C/LBH	65 0.147392290249433
GO:0030041	BP	GO:0030041	actin	34/1414	170/18903	1.083311511	2.3490542	1.50531761	CAPZB/SCIN/GSN/AIF1/ARH	34 0.2
GO:0017015	BP	GO:0017015	regulation of	31/1414	147/18903	1.119270286	2.4180383	1.54952389	LTBP1/DKK3/DAB2/ZEB2/FB	31 0.210884353741497
GO:0001945	BP	GO:0001945	lymph vessel	13/1414	31/18903	1.250311319	2.6520239	1.69946621	PDPN/FGF2/VEGFA/PKD1/NR	13 0.419354838709677
GO:0035767	BP	GO:0035767	endothelial	13/1414	31/18903	1.250311319	2.6520239	1.69946621	SMOC2/NR4A1/FGFR1/FGF2/	13 0.419354838709677
GO:0061437	BP	GO:0061437	renal system	13/1414	31/18903	1.250311319	2.6520239	1.69946621	EGR1/PDGFRA/AQP1/PDGFRB	13 0.419354838709677
GO:0061440	BP	GO:0061440	kidney	13/1414	31/18903	1.250311319	2.6520239	1.69946621	EGR1/PDGFRA/AQP1/PDGFRB	13 0.419354838709677
GO:0150117	BP	GO:0150117	positive	13/1414	31/18903	1.250311319	2.6520239	1.69946621	THY1/PIK3R1/SDC4/VEGFA/	13 0.419354838709677
GO:0051495	BP	GO:0051495	positive	37/1414	195/18903	1.255111884	2.6525607	1.69981018	TPM1/HSPA1A/HSPA1B/SCIN	37 0.18974358974359
GO:0071346	BP	GO:0071346	cellular	27/1414	118/18903	1.265742038	2.6653694	1.70801823	ACTG1/GSN/GBP2/IFNGR2/C	27 0.228813559322034
GO:0071375	BP	GO:0071375	cellular response to	50/1414	306/18903	1.295923381 70752e-07	2.7191083 0413668e-	1.74245510 353783e-06	SOCS3/ZFP36L1/FOS/FBN1/ PIK3R3/FOXO1/NR4A1/SLC3	50 0.163398692810458
GO:0010755	BP	GO:0010755	regulation of	10/1414	18/18903	1.333223487	2.7873450	1.78618245	RUNX1/MELTF/SERPINE2/AN	10 0.555555555555556
GO:1901888	BP	GO:1901888	regulation of	38/1414	204/18903	1.405045392	2.9270106	1.87568277	THBS2/THY1/PTPRD/SIX1/A	38 0.186274509803922
GO:0071241	BP	GO:0071241	cellular	41/1414	229/18903	1.420690204	2.9426224	1.88568713	JUN/FOSB/AQP1/FOS/SLC40	41 0.179039301310044
GO:0002831	BP	GO:0002831	regulation of response to	56/1414	361/18903	1.422629069 35812e-07	2.9426224 686404e-	1.88568713 150082e-06	CADM1/FOXP1/HEXIM1/HTRA 1/LAG3/PLCG2/CFH/A2M/SE	56 0.155124653739612
GO:0022411	BP	GO:0022411	cellular component	69/1414	483/18903	1.430950336 60356e-07	2.9493757 2911963e-	1.89001474 624483e-06	MMP2/CAPZB/LIMA1/CTSK/F AP/LAMP2/VMP1/RETREG1/H	69 0.142857142857143
GO:0044403	BP	GO:0044403	biological process	50/1414	307/18903	1.438098759 62796e-07	2.9536725 5806687e-	1.89276823 403962e-06	JUN/ITGB5/LGALS1/EEA1/I FITM1/HSPA1A/HSPA1B/HSP	50 0.162866449511401
GO:0032946	BP	GO:0032946	positive	31/1414	149/18903	1.544309205	3.1606861	2.02542640	HES1/VCAM1/CDKN1A/PNP/S	31 0.208053691275168
GO:0032507	BP	GO:0032507	maintenance	19/1414	65/18903	1.577955363	3.2182565	2.06231854	ANK3/SCIN/GSN/TXN/INSIG	19 0.292307692307692
GO:0043281	BP	GO:0043281	regulation of	38/1414	205/18903	1.602610598	3.2571524	2.08724380	AQP1/NR4A1/CRYAB/GSN/CF	38 0.185365853658537
GO:0072331	BP	GO:0072331	signal	34/1414	173/18903	1.683350694	3.4093696	2.18478739	TWIST1/SOX4/HEXIM1/MAP2	34 0.196531791907514
GO:0050670	BP	GO:0050670	regulation of lymphocyte	42/1414	239/18903	1.714803470 69618e-07	3.4610548 9431517e-	2.21790825 876603e-06	GPNMB/HES1/VCAM1/CDKN1A /PNP/SELENOK/CD55/SDC4/	42 0.175732217573222
GO:0040013	BP	GO:0040013	negative regulation of	62/1414	419/18903	1.759492446 82048e-07	3.5312847 4914912e-	2.26291285 412914e-06	GJA1/NBL1/COL3A1/THY1/S EMA3C/TPM1/DPYSL3/IFITM	62 0.147971360381862
GO:0071280	BP	GO:0071280	cellular	12/1414	27/18903	1.767761266	3.5312847	2.26291285	AQP1/MT1G/MT1M/MT1A/MT1	12 0.444444444444444
GO:1903055	BP	GO:1903055	positive	12/1414	27/18903	1.767761266	3.5312847	2.26291285	RUNX1/TNXB/MELTF/PDPN/C	12 0.444444444444444
GO:0001890	BP	GO:0001890	placenta	31/1414	150/18903	1.809223886	3.6017757	2.30808479	SOCS3/ZFP36L1/RBPJ/NOTC	31 0.206666666666667

GO:0071774	BP	GO:0071774	response to	27/1414	120/18903	1.825672271	3.6221586	2.32114652	COL1A1/ZFP36L1/SMOC2/SU	27	0.225
GO:0048041	BP	GO:0048041	focal	22/1414	85/18903	1.855358858	3.6685790	2.35089359	THY1/ACTG1/ACTN1/APOD/S	22	0.258823529411765
GO:2001235	BP	GO:2001235	positive	29/1414	135/18903	1.878040820	3.6914918	2.36557652	UBB/DDIT3/ITM2C/TNFRSF1	29	0.214814814814815
GO:0002695	BP	GO:0002695	negative	37/1414	198/18903	1.879604101	3.6914918	2.36557652	GPNMB/RUNX1/GLI3/LAG3/N	37	0.186868686868687
GO:0006875	BP	GO:0006875	cellular metal ion	62/1414	420/18903	1.917448277 02985e-07	3.7531797 9862923e-	2.40510732 311303e-06	THY1/SLC40A1/FLNA/MT1G/ PLCG2/MT1M/MT1A/MT1E/MT	62	0.147619047619048
GO:0061028	BP	GO:0061028	establishment	16/1414	48/18903	2.003431941	3.9083673	2.50455441	ICAM1/VEGFA/AFDN/EZR/MS	16	0.333333333333333
GO:0030218	BP	GO:0030218	erythrocyte	28/1414	128/18903	2.038537061	3.9635955	2.53994565	MAFB/ZFP36L1/HSPA1A/HSP	28	0.21875
GO:0061900	BP	GO:0061900	glial cell	17/1414	54/18903	2.147985754	4.1625252	2.66742347	JUN/NR1D1/IFNGR2/TYROBP	17	0.314814814814815
GO:0051348	BP	GO:0051348	negative regulation of	46/1414	276/18903	2.270009014 24845e-07	4.3844246 9540106e-	2.80962077 713358e-06	THY1/HEXIM1/SH3BP5/GADD 45B/ZFP36/DNAJA1/BMP2/C	46	0.166666666666667
GO:0044344	BP	GO:0044344	cellular	26/1414	114/18903	2.306850897	4.4408783	2.84579730	COL1A1/ZFP36L1/SMOC2/SU	26	0.228070175438596
GO:1990845	BP	GO:1990845	adaptive	32/1414	160/18903	2.541394541	4.8763007	3.12482410	GJA1/RBPJ/ACOT13/DIO2/M	32	0.2
GO:0071219	BP	GO:0071219	cellular	41/1414	234/18903	2.601031871	4.9557016	3.17570567	PLCG2/ZFP36/NFKBIA/NR1D	41	0.175213675213675
GO:0002698	BP	GO:0002698	negative	27/1414	122/18903	2.608264037	4.9557016	3.17570567	TWIST1/A2M/CD55/TGFB1/A	27	0.221311475409836
GO:0030278	BP	GO:0030278	regulation of	27/1414	122/18903	2.608264037	4.9557016	3.17570567	TWIST1/ECM1/RBPJ/LTBP3/	27	0.221311475409836
GO:0097501	BP	GO:0097501	stress	10/1414	19/18903	2.625315565	4.9719044	3.18608871	MT1G/MT1M/MT1A/MT1E/MT1	10	0.526315789473684
GO:0031638	BP	GO:0031638	zymogen	19/1414	67/18903	2.677309226	5.0539626	3.23867316	C1R/RUNX1/MELTF/SERPINE	19	0.283582089552239
GO:0032944	BP	GO:0032944	regulation of mononuclear	42/1414	243/18903	2.743917008 47066e-07	5.1629896 4851915e-	3.30853965 944969e-06	GPNMB/HES1/VCAM1/CDKN1A /PNP/SELENOK/CD55/SDC4/	42	0.172839506172839
GO:0030865	BP	GO:0030865	cortical	18/1414	61/18903	2.846981902	5.3396930	3.42177449	EPB41L2/TRPV4/RHOC/RHOD	18	0.295081967213115
GO:0010761	BP	GO:0010761	fibroblast	17/1414	55/18903	2.893478159	5.3915356	3.45499620	AQP1/FGF2/TGFB1/SDC4/AR	17	0.309090909090909
GO:0014812	BP	GO:0014812	muscle cell	25/1414	108/18903	2.895899367	5.3915356	3.45499620	PDGFRB/SIX1/TPM1/DDIT3/	25	0.231481481481481
GO:0030217	BP	GO:0030217	T cell differentiati	48/1414	296/18903	2.902352487 39147e-07	5.3915356 8756511e-	3.45499620 60768e-06	MAFB/EGR1/FOXP1/ZFP36L1 /SOX4/ACTB/RUNX1/ZEB1/P	48	0.162162162162162
GO:0001837	BP	GO:0001837	epithelial to	33/1414	169/18903	2.977151643	5.4609199	3.49945894	COL1A1/S100A4/TWIST1/DA	33	0.195266272189349
GO:0002262	BP	GO:0002262	myeloid cell	33/1414	169/18903	2.977151643	5.4609199	3.49945894	MAFB/ZFP36L1/HSPA1A/HSP	33	0.195266272189349
GO:0007568	BP	GO:0007568	aging	33/1414	169/18903	2.977151643	5.4609199	3.49945894	MMP2/FOS/PDGFRB/COMP/CR	33	0.195266272189349
GO:1902904	BP	GO:1902904	negative	33/1414	169/18903	2.977151643	5.4609199	3.49945894	CAPZB/LIMA1/CHADL/HSPA8	33	0.195266272189349
GO:0002253	BP	GO:0002253	activation of immune	59/1414	397/18903	2.997688321 65827e-07	5.4813529 7185978e-	3.51255279 003746e-06	THY1/C1R/FOXP1/HEXIM1/P LCG2/CFH/CFB/C1S/A2M/CD	59	0.148614609571788
GO:0048705	BP	GO:0048705	skeletal	40/1414	227/18903	3.108631406	5.6664521	3.63116780	COL1A1/MMP2/COL3A1/SERP	40	0.176211453744493
GO:0046916	BP	GO:0046916	cellular	26/1414	116/18903	3.320848493	6.0344265	3.86697261	SLC40A1/MT1G/MT1M/MT1A/	26	0.224137931034483
GO:0001659	BP	GO:0001659	temperature	34/1414	178/18903	3.413147709	6.1447193	3.93765026	GJA1/EGR1/RBPJ/ACOT13/D	34	0.191011235955056
GO:0071772	BP	GO:0071772	response to	34/1414	178/18903	3.413147709	6.1447193	3.93765026	NBL1/EGR1/FSTL1/RBPJ/FB	34	0.191011235955056
GO:0071773	BP	GO:0071773	cellular	34/1414	178/18903	3.413147709	6.1447193	3.93765026	NBL1/EGR1/FSTL1/RBPJ/FB	34	0.191011235955056

GO:0018108	BP	GO:0018108	peptidyl-tyrosine	57/1414	380/18903	3.47801990246854e-07	6.2422431 0495353e-	4.00014531 940592e-06	THY1/PDGFRA/SOCS3/PDGFRB/SH3BP5/EFEMP1/MAP2K6/	57	0.15
GO:0031341	BP	GO:0031341	regulation of	24/1414	102/18903	3.607893621	6.4554734	4.13678729	CADM1/LAG3/CFH/CD55/ICA	24	0.235294117647059
GO:0030324	BP	GO:0030324	lung	35/1414	187/18903	3.840092902	6.8499271	4.38956056	COL3A1/PDGFRA/PDGFRB/RS	35	0.18716577540107
GO:0007409	BP	GO:0007409	axonogenesis	63/1414	438/18903	3.90621650070687e-07	6.9466344 0506804e-	4.45153234 724329e-06	CDH11/THY1/ENAH/SEMA3C/ACTB/NOTCH2/GLI3/ANOS1/	63	0.143835616438356
GO:0000302	BP	GO:0000302	response to	37/1414	204/18903	4.087886202	7.2135520	4.62257814	COL1A1/MMP2/JUN/PDGFRA/	37	0.181372549019608
GO:0031032	BP	GO:0031032	actomyosin	37/1414	204/18903	4.087886202	7.2135520	4.62257814	EPB41L2/PDGFRA/PDGFRB/I	37	0.181372549019608
GO:0043618	BP	GO:0043618	regulation of	14/1414	39/18903	4.093409451	7.2135520	4.62257814	JUN/EGR1/RBPJ/DDIT3/VEG	14	0.358974358974359
GO:0018212	BP	GO:0018212	peptidyl-tyrosine	57/1414	382/18903	4.14819475657794e-07	7.2880783 1780697e-	4.67033594 819539e-06	THY1/PDGFRA/SOCS3/PDGFRB/SH3BP5/EFEMP1/MAP2K6/	57	0.149214659685864
GO:0001952	BP	GO:0001952	regulation of	27/1414	125/18903	4.378245915	7.6691616	4.91454125	THY1/ACTG1/RIN2/APOD/PI	27	0.216
GO:0071229	BP	GO:0071229	cellular	22/1414	89/18903	4.422208054	7.7229759	4.94902641	COL1A1/MMP2/COL1A2/COL5	22	0.247191011235955
GO:1903034	BP	GO:1903034	regulation of	33/1414	172/18903	4.547023676	7.8959865	5.05989485	PDGFRA/ACTG1/FLNA/FAP/S	33	0.191860465116279
GO:0060317	BP	GO:0060317	cardiac	13/1414	34/18903	4.548348176	7.8959865	5.05989485	TWIST1/RBPJ/SNAI1/BMP2/	13	0.382352941176471
GO:0072012	BP	GO:0072012	glomerulus	12/1414	29/18903	4.583381089	7.9331934	5.08373770	EGR1/PDGFRA/AQP1/PDGFRB	12	0.413793103448276
GO:0071222	BP	GO:0071222	cellular	39/1414	222/18903	4.717251882	8.1407485	5.21674289	PLCG2/ZFP36/NFKBIA/NR1D	39	0.175675675675676
GO:0030003	BP	GO:0030003	cellular cation	69/1414	499/18903	4.94655655075351e-07	8.5112874 2198974e-	5.45419106 09302e-06	THY1/SLC40A1/FLNA/MT1G/PLCG2/MT1M/MT1A/MT1E/MT	69	0.138276553106212
GO:0006986	BP	GO:0006986	response to	29/1414	141/18903	4.962072205	8.5128726	5.45520693	SERPINH1/COMP/DNAJB1/HS	29	0.205673758865248
GO:0030500	BP	GO:0030500	regulation of	21/1414	83/18903	5.295892378	9.0324386	5.78815445	TWIST1/ECM1/LTBP3/COMP/	21	0.253012048192771
GO:0061515	BP	GO:0061515	myeloid cell	21/1414	83/18903	5.295892378	9.0324386	5.78815445	FOXP1/FLNA/FBN1/NOTCH2/	21	0.253012048192771
GO:0010959	BP	GO:0010959	regulation of metal ion	61/1414	423/18903	5.45088571861667e-07	9.2696840 8066794e-	5.94018572 558164e-06	THY1/PDGFRB/FLNA/VMP1/FHL1/ANK3/PLCG2/HES1/GEM	61	0.144208037825059
GO:0050777	BP	GO:0050777	negative	35/1414	190/18903	5.697039988	9.6601262	6.19038831	COL3A1/PSMB4/A2M/CD55/A	35	0.184210526315789
GO:0044409	BP	GO:0044409	entry into	31/1414	158/18903	6.048030821	1.0196001	6.53378687	ITGB5/LGALS1/IFITM1/HSP	31	0.19620253164557
GO:0097530	BP	GO:0097530	granulocyte	31/1414	158/18903	6.048030821	1.0196001	6.53378687	CD99/TRPV4/SAA1/SELENOK	31	0.19620253164557
GO:2001234	BP	GO:2001234	negative	40/1414	233/18903	6.277853762	1.0552945	6.76252349	LMNA/HSPA1A/COL2A1/HSPA	40	0.171673819742489
GO:1901655	BP	GO:1901655	cellular	24/1414	105/18903	6.374131874	1.0683997	6.84650401	POSTN/AQP1/FOS/SPP1/CFL	24	0.228571428571429
GO:0060485	BP	GO:0060485	mesenchyme development	49/1414	313/18903	6.43883563486612e-07	1.0761526 7215398e-	6.89618619 798208e-06	COL1A1/S100A4/ZFP36L1/PDGFRB/TWIST1/SEMA3C/DAB	49	0.156549520766773
GO:0030323	BP	GO:0030323	respiratory	35/1414	191/18903	6.482194568	1.0803040	6.92278884	COL3A1/PDGFRA/PDGFRB/RS	35	0.183246073298429
GO:1901216	BP	GO:1901216	positive	22/1414	91/18903	6.677513185	1.1034828	7.07132335	EGR1/FOS/DDIT3/NUPR1/DD	22	0.241758241758242
GO:2000117	BP	GO:2000117	negative	22/1414	91/18903	6.677513185	1.1034828	7.07132335	AQP1/NR4A1/CRYAB/PTGS2/	22	0.241758241758242
GO:0001936	BP	GO:0001936	regulation of	34/1414	183/18903	6.696947463	1.1034828	7.07132335	JUN/ECM1/CNMD/NR4A1/SPA	34	0.185792349726776
GO:0044000	BP	GO:0044000	movement in	34/1414	183/18903	6.696947463	1.1034828	7.07132335	ITGB5/LGALS1/IFITM1/HSP	34	0.185792349726776

GO:0001706	BP	GO:0001706	endoderm	17/1414	58/18903	6.752778639	1.1064313	7.09021790	MMP2/COL12A1/COL5A1/COL	17	0.293103448275862
GO:0048008	BP	GO:0048008	platelet-	17/1414	58/18903	6.752778639	1.1064313	7.09021790	PDGFRA/PDGFRB/PDGFRL/AP	17	0.293103448275862
GO:0046718	BP	GO:0046718	viral entry	30/1414	151/18903	6.919640793	1.1305956	7.24506691	ITGB5/LGALS1/IFITM1/HSP	30	0.198675496688742
GO:0030509	BP	GO:0030509	BMP signaling	32/1414	167/18903	6.959206366	1.1338840	7.26613990	NBL1/EGR1/FSTL1/RBPJ/FB	32	0.191616766467066
GO:0035051	BP	GO:0035051	cardiocyte	31/1414	159/18903	6.982985797	1.1345893	7.27065901	PDGFRA/FOXP1/PDGFRB/TWI	31	0.19496855345912
GO:0046651	BP	GO:0046651	lymphocyte proliferation	48/1414	305/18903	7.145805384 44233e-07	1.1577966 7590944e-	7.41937613 786249e-06	GPNMB/HES1/VCAM1/CDKN1A /PNP/SELENOK/CD55/SDC4/	48	0.157377049180328
GO:0048872	BP	GO:0048872	homeostasis of number of	47/1414	296/18903	7.172854007 49622e-07	1.1577966 7590944e-	7.41937613 786249e-06	MAFB/ZFP36L1/FSTL1/SOX4 /SLC40A1/CRISPLD1/HSPA1	47	0.158783783783784
GO:0032102	BP	GO:0032102	negative regulation of	62/1414	436/18903	7.185365963 98454e-07	1.1577966 7590944e-	7.41937613 786249e-06	NBL1/PDGFRA/SOCS3/SEMA3 C/FAP/HTRA1/PSMB4/NT5E/	62	0.142201834862385
GO:0031334	BP	GO:0031334	positive	35/1414	192/18903	7.366989063	1.1837919	7.58595858	PIEZO1/PLCG2/HSPA1A/HSP	35	0.182291666666667
GO:0071383	BP	GO:0071383	cellular	37/1414	209/18903	7.582186664	1.2135421	7.77660355	FOXP1/ZFP36L1/AQP1/DAB2	37	0.177033492822967
GO:0016055	BP	GO:0016055	Wnt signaling pathway	64/1414	456/18903	7.593740592 12687e-07	1.2135421 6092811e-	7.77660355 9522e-06	COL1A1/IGFBP4/EGR1/DKK3 /SOX4/DAB2/ZEB2/RSPO2/R	64	0.140350877192982
GO:0097581	BP	GO:0097581	lamellipodium	22/1414	92/18903	8.162775681	1.3009144	8.33650170	CAPZB/PDPN/PIK3R1/CD44/	22	0.239130434782609
GO:0042692	BP	GO:0042692	muscle cell differentiati	59/1414	409/18903	8.250141514 59239e-07	1.3112554 6197868e-	8.40276854 103473e-06	PDGFRA/FOXP1/PDGFRB/LMN A/MYL9/SIX1/ACTG1/RBPJ/	59	0.144254278728606
GO:0010720	BP	GO:0010720	positive regulation of	48/1414	307/18903	8.670681530 05874e-07	1.3743501 4578349e-	8.80709099 348929e-06	DAB2/PTPRD/FLNA/ID4/GLI 3/NTN1/HES1/PTN/TGM2/FN	48	0.156351791530945
GO:0097193	BP	GO:0097193	intrinsic apoptotic	47/1414	298/18903	8.732254028 48167e-07	1.3803587 4656189e-	8.84559522 326013e-06	CRIP1/HSPA1A/UBB/SNAI1/ DDIT3/DNAJA1/IVNS1ABP/S	47	0.157718120805369
GO:0198738	BP	GO:0198738	cell-cell signaling by	64/1414	458/18903	8.857056769 37246e-07	1.3963030 3069593e-	8.94776915 733759e-06	COL1A1/IGFBP4/EGR1/DKK3 /SOX4/DAB2/ZEB2/RSPO2/R	64	0.139737991266376
GO:0061041	BP	GO:0061041	regulation of	28/1414	137/18903	8.881033079	1.3963090	8.94780776	PDGFRA/ACTG1/FAP/SMOC2/	28	0.204379562043796
GO:0051099	BP	GO:0051099	positive	33/1414	177/18903	8.964178317	1.4055927	9.00729971	TWIST1/HES1/CTHRC1/BMP2	33	0.186440677966102
GO:0036230	BP	GO:0036230	granulocyte	15/1414	47/18903	9.098616900	1.4196594	9.09744146	PLA2G2A/ANXA1/TYROBP/FC	15	0.319148936170213
GO:0060411	BP	GO:0060411	cardiac	19/1414	72/18903	9.102565344	1.4196594	9.09744146	SOX4/SEMA3C/RBPJ/NOTCH2	19	0.263888888888889
GO:0003279	BP	GO:0003279	cardiac	24/1414	107/18903	9.185780557	1.4250174	9.13177680	SOX4/SEMA3C/RBPJ/NOTCH2	24	0.224299065420561
GO:0060840	BP	GO:0060840	artery	24/1414	107/18903	9.185780557	1.4250174	9.13177680	COL3A1/PDGFRB/SOX4/SIX1	24	0.224299065420561
GO:0030316	BP	GO:0030316	osteoclast	23/1414	100/18903	9.656919296	1.4941328	9.57468111	MAFB/FOXP1/FOS/KLF10/FB	23	0.23
GO:0010922	BP	GO:0010922	positive	13/1414	36/18903	9.831099439	1.5170582	9.72159123	PDGFRB/MAGI2/BMP2/CALM2	13	0.361111111111111
GO:0071621	BP	GO:0071621	granulocyte	27/1414	130/18903	9.943425924	1.5270384	9.78554604	TRPV4/SAA1/PDE4B/ANXA1/	27	0.207692307692308
GO:0030111	BP	GO:0030111	regulation of Wnt signaling	51/1414	336/18903	9.948133261 13925e-07	1.5270384 5558488e-	9.78554604 163587e-06	COL1A1/IGFBP4/EGR1/DKK3 /SOX4/DAB2/ZEB2/RSPO2/R	51	0.151785714285714
GO:0033631	BP	GO:0033631	cell-cell	9/1414	17/18903	1.001690992	1.5335599	9.82733724	PIEZO1/ITGA5/FERMT3/ADA	9	0.529411764705882

GO:0031098	BP	GO:0031098	stress-	41/1414	246/18903	1.014989923	1.5498524	9.93174213	ZFP36L1/MAP2K6/FOXO1/GA	41	0.166666666666667
GO:0010517	BP	GO:0010517	regulation of	18/1414	66/18903	1.037000085	1.5793267	1.01206192	PDGFRA/PDGFRB/FGFR1/FGF	18	0.272727272727273
GO:0051894	BP	GO:0051894	positive	11/1414	26/18903	1.065914991	1.6191359	1.03757240	THY1/SDC4/VEGFA/NRP1/RA	11	0.423076923076923
GO:1990778	BP	GO:1990778	protein localization	51/1414	337/18903	1.088983554 30112e-06	1.6498807 9798401e-	1.05727425 873501e-05	EPB41L2/DAB2/ACTB/FLNA/ ANK3/GPC6/PIK3R1/SQSTM1	51	0.1513353115727
GO:0001892	BP	GO:0001892	embryonic	21/1414	87/18903	1.224671106	1.8414983	1.18006635	SOCS3/ZFP36L1/RBPJ/HES1	21	0.241379310344828
GO:0045598	BP	GO:0045598	regulation of	29/1414	147/18903	1.228086512	1.8414983	1.18006635	ZFP36L1/SIX1/ID4/FOXO1/	29	0.197278911564626
GO:0106106	BP	GO:0106106	cold-induced	29/1414	147/18903	1.228086512	1.8414983	1.18006635	GJA1/RBPJ/ACOT13/DIO2/M	29	0.197278911564626
GO:0120161	BP	GO:0120161	regulation of	29/1414	147/18903	1.228086512	1.8414983	1.18006635	GJA1/RBPJ/ACOT13/DIO2/M	29	0.197278911564626
GO:0030308	BP	GO:0030308	negative	34/1414	188/18903	1.274087461	1.9055774	1.22112944	GJA1/FOXP1/SEMA3C/DAB2/	34	0.180851063829787
GO:0002449	BP	GO:0002449	lymphocyte mediated	54/1414	367/18903	1.293351104 77867e-06	1.9278949 7122304e-	1.23543090 452922e-05	CADM1/C1R/TUBB/LAG3/TUB B4B/C1S/CD55/ULBP2/TGFB	54	0.147138964577657
GO:0050730	BP	GO:0050730	regulation of	43/1414	266/18903	1.295619456	1.9278949	1.23543090	THY1/SOCS3/SH3BP5/PLCG2	43	0.161654135338346
GO:0030038	BP	GO:0030038	contractile	24/1414	109/18903	1.309740522	1.9341054	1.23941068	ITGB5/ACTG1/TPM1/PIK3R1	24	0.220183486238532
GO:0043149	BP	GO:0043149	stress fiber	24/1414	109/18903	1.309740522	1.9341054	1.23941068	ITGB5/ACTG1/TPM1/PIK3R1	24	0.220183486238532
GO:1903557	BP	GO:1903557	positive	24/1414	109/18903	1.309740522	1.9341054	1.23941068	TWIST1/PLCG2/PIK3R1/SEL	24	0.220183486238532
GO:0031669	BP	GO:0031669	cellular	39/1414	231/18903	1.329328357	1.9580738	1.25477006	COL1A1/POSTN/FOS/KLF10/	39	0.168831168831169
GO:0032943	BP	GO:0032943	mononuclear cell	48/1414	312/18903	1.391673999 35654e-06	2.0447441 9099413e-	1.31031005 480977e-05	GPNMB/HES1/VCAM1/CDKN1A /PNP/SELENOK/CD55/SDC4/	48	0.153846153846154
GO:0071276	BP	GO:0071276	cellular	13/1414	37/18903	1.412136033	2.0695953	1.32623513	JUN/FOS/MT1G/MT1M/MT1A/	13	0.351351351351351
GO:0072659	BP	GO:0072659	protein localization	45/1414	285/18903	1.437322717 00629e-06	2.1002627 4883704e-	1.34588737 782676e-05	DAB2/ACTB/FLNA/ANK3/PIK 3R1/SQSTM1/TGFB1/ATP1B3	45	0.157894736842105
GO:0071706	BP	GO:0071706	tumor	34/1414	189/18903	1.443863127	2.1002627	1.34588737	FOXP1/TWIST1/GPNMB/PLCG	34	0.17989417989418
GO:1903555	BP	GO:1903555	regulation of	34/1414	189/18903	1.443863127	2.1002627	1.34588737	FOXP1/TWIST1/GPNMB/PLCG	34	0.17989417989418
GO:0010811	BP	GO:0010811	positive	26/1414	125/18903	1.523154724	2.2100899	1.41626667	THY1/DAB2/RIN2/FLNA/ABI	26	0.208
GO:0070302	BP	GO:0070302	regulation of	35/1414	198/18903	1.550306589	2.2439052	1.43793618	FOXO1/GADD45B/GADD45G/D	35	0.176767676767677
GO:0010975	BP	GO:0010975	regulation of neuron	62/1414	446/18903	1.561077307 5353e-06	2.2539019 6407263e-	1.44434224 050491e-05	THY1/SEMA3C/DAB2/PTPRD/ PRRX1/FLNA/DPYSL3/NTN1/	62	0.139013452914798
GO:0003179	BP	GO:0003179	heart valve	16/1414	55/18903	1.601712251	2.3011792	1.47463837	TWIST1/SOX4/NOTCH2/SNAI	16	0.290909090909091
GO:0071385	BP	GO:0071385	cellular	16/1414	55/18903	1.601712251	2.3011792	1.47463837	ZFP36L1/AQP1/ZFP36/CFLA	16	0.290909090909091
GO:0035987	BP	GO:0035987	endodermal	15/1414	49/18903	1.653893369	2.3703095	1.51893840	MMP2/COL12A1/COL5A1/COL	15	0.306122448979592
GO:0045639	BP	GO:0045639	positive	23/1414	103/18903	1.672237455	2.3907257	1.53202146	ZFP36L1/FOS/KLF10/RUNX1	23	0.223300970873786
GO:0031639	BP	GO:0031639	plasminogen	11/1414	27/18903	1.677197961	2.3919549	1.53280915	RUNX1/MELTF/SERPINE2/AN	11	0.407407407407407
GO:0001935	BP	GO:0001935	endothelial	35/1414	199/18903	1.748277427	2.4872444	1.59387243	JUN/ECM1/CNMD/NR4A1/SPA	35	0.175879396984925
GO:0045669	BP	GO:0045669	positive	19/1414	75/18903	1.786416518	2.5353205	1.62468051	GLI3/IFITM1/CTHRC1/GDF1	19	0.253333333333333
GO:0061687	BP	GO:0061687	detoxificatio	9/1414	18/18903	1.870059636	2.6475868	1.69662283	MT1G/MT1M/MT1A/MT1E/MT1	9	0.5

GO:0032233	BP	GO:0032233	positive	17/1414	62/18903	1.897807853	2.6803663	1.71762856	TPM1/RHOC/SDC4/LPAR1/RG	17	0.274193548387097
GO:0009267	BP	GO:0009267	cellular	32/1414	175/18903	2.023466248	2.8509368	1.82693329	FOS/KLF10/CTSK/LAMP2/FO	32	0.182857142857143
GO:0043523	BP	GO:0043523	regulation of	37/1414	218/18903	2.163816943	3.0413359	1.94894456	JUN/SIX1/RETREG1/DDIT3/	37	0.169724770642202
GO:0032640	BP	GO:0032640	tumor	33/1414	184/18903	2.198027741	3.0746033	1.97026290	FOXP1/TWIST1/GPNMB/PLCG	33	0.179347826086957
GO:0032680	BP	GO:0032680	regulation of	33/1414	184/18903	2.198027741	3.0746033	1.97026290	FOXP1/TWIST1/GPNMB/PLCG	33	0.179347826086957
GO:0051591	BP	GO:0051591	response to	21/1414	90/18903	2.210672411	3.0775303	1.97213860	COL1A1/FOSB/ZFP36L1/AQP	21	0.233333333333333
GO:0060191	BP	GO:0060191	regulation of	21/1414	90/18903	2.210672411	3.0775303	1.97213860	PDGFRA/PDGFRB/FGFR1/ANG	21	0.233333333333333
GO:0045619	BP	GO:0045619	regulation of	36/1414	210/18903	2.327252889	3.2321109	2.07119674	ZFP36L1/SOX4/ACTB/RUNX1	36	0.171428571428571
GO:0032760	BP	GO:0032760	positive	23/1414	105/18903	2.378248620	3.2950888	2.11155415	TWIST1/PLCG2/PIK3R1/SEL	23	0.219047619047619
GO:0031663	BP	GO:0031663	lipopolysacch	17/1414	63/18903	2.419436043	3.3442110	2.14303252	PLCG2/NFKBIA/CD55/TGFB1	17	0.26984126984127
GO:0007043	BP	GO:0007043	cell-cell	29/1414	152/18903	2.496692937	3.4428392	2.20623531	CDH11/GJA1/ACTG1/ACTB/S	29	0.190789473684211
GO:0060349	BP	GO:0060349	bone	22/1414	98/18903	2.545322779	3.5016197	2.24390297	COL1A1/COL3A1/SERPINH1/	22	0.224489795918367
GO:0019058	BP	GO:0019058	viral life cycle	48/1414	319/18903	2.634618864 59267e-06	3.6159369 028633e-	2.31715952 648138e-05	ITGB5/LGALS1/IFITM1/HSP A1A/HSPA1B/HSPA8/WWP2/G	48	0.150470219435737
GO:0051701	BP	GO:0051701	biological	35/1414	203/18903	2.797858644	3.8309646	2.45495331	ITGB5/LGALS1/IFITM1/HSP	35	0.172413793103448
GO:0043405	BP	GO:0043405	regulation of	33/1414	186/18903	2.809576203	3.8379995	2.45946138	PDGFRB/TNXB/MAP2K6/DNAJ	33	0.17741935483871
GO:0030835	BP	GO:0030835	negative	14/1414	45/18903	2.957057175	4.0112824	2.57050429	CAPZB/LIMA1/SCIN/GSN/TW	14	0.311111111111111
GO:0043620	BP	GO:0043620	regulation of	14/1414	45/18903	2.957057175	4.0112824	2.57050429	JUN/EGR1/RBPJ/DDIT3/VEG	14	0.311111111111111
GO:1900744	BP	GO:1900744	regulation of	14/1414	45/18903	2.957057175	4.0112824	2.57050429	GADD45B/GADD45G/BMP2/VE	14	0.311111111111111
GO:0009408	BP	GO:0009408	response to	24/1414	114/18903	3.043346068	4.1187558	2.63937523	IGFBP7/DNAJB1/HSPA1A/HS	24	0.210526315789474
GO:0035306	BP	GO:0035306	positive	17/1414	64/18903	3.066793310	4.1313176	2.64742507	PDGFRB/MAGI2/BMP2/CAMTA	17	0.265625
GO:0071384	BP	GO:0071384	cellular	17/1414	64/18903	3.066793310	4.1313176	2.64742507	ZFP36L1/AQP1/ZFP36/CFLA	17	0.265625
GO:0002548	BP	GO:0002548	monocyte	18/1414	71/18903	3.285032144	4.4151134	2.82928671	NBL1/ANXA1/CCL20/AIF1/C	18	0.253521126760563
GO:1990266	BP	GO:1990266	neutrophil	26/1414	130/18903	3.295359571	4.4188120	2.83165682	CD99/SAA1/SELENOK/PDE4B	26	0.2
GO:0036003	BP	GO:0036003	positive	9/1414	19/18903	3.316834908	4.4374078	2.84357333	RBPJ/DDIT3/VEGFA/CEBPB/	9	0.473684210526316
GO:0032743	BP	GO:0032743	positive	12/1414	34/18903	3.406520082	4.5469637	2.91377883	RUNX1/PLCG2/PNP/PDE4B/A	12	0.352941176470588
GO:0031529	BP	GO:0031529	ruffle	16/1414	58/18903	3.474498470	4.6271117	2.96513916	LIMA1/TPM1/CSPG4/ICAM1/	16	0.275862068965517
GO:0045088	BP	GO:0045088	regulation of	39/1414	240/18903	3.490760797	4.6381794	2.97223152	CADM1/HEXIM1/LAG3/PLCG2	39	0.1625
GO:0046634	BP	GO:0046634	regulation of	24/1414	115/18903	3.576842530	4.7417551	3.03860474	RUNX1/GLI3/JUNB/ZBTB16/	24	0.208695652173913
GO:0035966	BP	GO:0035966	response to	30/1414	163/18903	3.642473620	4.8178114	3.08734307	SERPINH1/COMP/DNAJB1/HS	30	0.184049079754601
GO:0010543	BP	GO:0010543	regulation of	15/1414	52/18903	3.799195868	5.0137351	3.21289462	PDGFRA/FLNA/PDPN/SERPIN	15	0.288461538461538
GO:0010273	BP	GO:0010273	detoxificatio	8/1414	15/18903	3.840963641	5.0334756	3.22554470	MT1G/MT1M/MT1A/MT1E/MT1	8	0.533333333333333
GO:1990169	BP	GO:1990169	stress	8/1414	15/18903	3.840963641	5.0334756	3.22554470	MT1G/MT1M/MT1A/MT1E/MT1	8	0.533333333333333
GO:2001028	BP	GO:2001028	positive	8/1414	15/18903	3.840963641	5.0334756	3.22554470	SMOC2/FGFR1/FGF2/VEGFA/	8	0.533333333333333
GO:0048246	BP	GO:0048246	macrophage	13/1414	40/18903	3.858693334	5.0334756	3.22554470	MMP2/TRPV4/SAA1/CSF1R/C	13	0.325
GO:0003170	BP	GO:0003170	heart valve	17/1414	65/18903	3.865930238	5.0334756	3.22554470	TWIST1/SOX4/RBPJ/NOTCH2	17	0.261538461538462

GO:0048247	BP	GO:0048247	lymphocyte	17/1414	65/18903	3.865930238	5.0334756	3.22554470	SAA1/CCL20/CCL3/GPR183/	17	0.261538461538462
GO:2001026	BP	GO:2001026	regulation of	10/1414	24/18903	3.937996136	5.1158867	3.27835524	SMOC2/FGFR1/FGF2/FGF1/V	10	0.416666666666667
GO:0048844	BP	GO:0048844	artery	19/1414	79/18903	4.127352806	5.3499664	3.42835785	COL3A1/PDGFRB/SOX4/SIX1	19	0.240506329113924
GO:0030042	BP	GO:0030042	actin	16/1414	59/18903	4.438800926	5.7409148	3.67888483	CAPZB/LIMA1/SCIN/GSN/PL	16	0.271186440677966
GO:0034599	BP	GO:0034599	cellular	44/1414	288/18903	4.547502621	5.8684917	3.76063852	MMP2/JUN/PDGFRA/FOXP1/A	44	0.152777777777778
GO:0035304	BP	GO:0035304	regulation of	21/1414	94/18903	4.639524566	5.9608693	3.81983578	PDGFRB/RCAN1/MAGI2/CAMT	21	0.223404255319149
GO:0051492	BP	GO:0051492	regulation of	21/1414	94/18903	4.639524566	5.9608693	3.81983578	ACTG1/TPM1/PIK3R1/RHOC/	21	0.223404255319149
GO:0072577	BP	GO:0072577	endothelial	17/1414	66/18903	4.847395802	6.2142548	3.98220994	ANGPTL4/ICAM1/RGCC/NDNF	17	0.257575757575758
GO:0001910	BP	GO:0001910	regulation of	20/1414	87/18903	4.891532836	6.2570857	4.00965676	CADM1/LAG3/ICAM1/HLA-	20	0.229885057471264
GO:0046638	BP	GO:0046638	positive	15/1414	53/18903	4.934885389	6.2987278	4.03634182	RUNX1/GLI3/ZBTB16/PNP/A	15	0.283018867924528
GO:0046637	BP	GO:0046637	regulation of	18/1414	73/18903	5.036068167	6.3874490	4.09319597	RUNX1/GLI3/JUNB/ZBTB16/	18	0.246575342465753
GO:0061035	BP	GO:0061035	regulation of	18/1414	73/18903	5.036068167	6.3874490	4.09319597	CTSK/GLI3/EFEMP1/LTBP3/	18	0.246575342465753
GO:0071230	BP	GO:0071230	cellular	19/1414	80/18903	5.037247647	6.3874490	4.09319597	COL1A1/MMP2/COL1A2/COL5	19	0.2375
GO:0046631	BP	GO:0046631	alpha-beta T	31/1414	174/18903	5.090906784	6.4414879	4.12782509	FOXP1/RUNX1/GLI3/JUNB/Z	31	0.17816091954023
GO:0061383	BP	GO:0061383	trabecula	14/1414	47/18903	5.253589208	6.6045522	4.23231974	COL1A1/MMP2/RBPJ/SLC40A	14	0.297872340425532
GO:0006458	BP	GO:0006458	'de novo'	13/1414	41/18903	5.265072513	6.6045522	4.23231974	DNAJB1/HSPA1A/HSPA1B/HS	13	0.317073170731707
GO:0042119	BP	GO:0042119	neutrophil	13/1414	41/18903	5.265072513	6.6045522	4.23231974	PLA2G2A/ANXA1/TYROBP/FC	13	0.317073170731707
GO:0046688	BP	GO:0046688	response to	13/1414	41/18903	5.265072513	6.6045522	4.23231974	AQP1/MT1G/MT1M/MT1A/MT1	13	0.317073170731707
GO:0043393	BP	GO:0043393	regulation of	34/1414	200/18903	5.314469349	6.6522102	4.26285987	DAB2/ACTB/CDON/CTHRC1/S	34	0.17
GO:0014909	BP	GO:0014909	smooth muscle	21/1414	95/18903	5.541306407	6.9065043	4.42581625	PDGFRB/TPM1/DDIT3/S100A	21	0.221052631578947
GO:1990874	BP	GO:1990874	vascular	21/1414	95/18903	5.541306407	6.9065043	4.42581625	MMP2/GJA1/JUN/TPM1/DDIT	21	0.221052631578947
GO:1901798	BP	GO:1901798	positive	11/1414	30/18903	5.698289723	7.0870200	4.54149406	HEXIM1/UBB/RPS20/PMAIP1	11	0.366666666666667
GO:0043535	BP	GO:0043535	regulation of	28/1414	150/18903	5.737914394	7.1211180	4.56334468	FGFR1/ETS1/FGF2/TGFB1/P	28	0.186666666666667
GO:0031579	BP	GO:0031579	membrane raft	10/1414	25/18903	6.123635183	7.5836866	4.85976724	GSN/ANXA2/CAV1/PTPRC/DO	10	0.4
GO:0042063	BP	GO:0042063	gliogenesis	46/1414	310/18903	6.169764582	7.6246264	4.88600223	COL3A1/MXRA8/SOX4/ID4/G	46	0.148387096774194
GO:0035924	BP	GO:0035924	cellular	18/1414	74/18903	6.194048692	7.6384537	4.89486300	PDGFRA/PDGFRB/GAS1/SMOC	18	0.243243243243243
GO:0030834	BP	GO:0030834	regulation of	15/1414	54/18903	6.363713036	7.8146396	5.00776620	CAPZB/LIMA1/SCIN/GSN/PL	15	0.277777777777778
GO:0050819	BP	GO:0050819	negative	15/1414	54/18903	6.363713036	7.8146396	5.00776620	PDGFRA/FAP/PROCR/SERPIN	15	0.277777777777778
GO:0051402	BP	GO:0051402	neuron	40/1414	255/18903	6.377726064	7.8153941	5.00824972	JUN/SIX1/RETREG1/DDIT3/	40	0.156862745098039
GO:0034446	BP	GO:0034446	substrate	23/1414	111/18903	6.433961504	7.8513174	5.03127005	ANTXR1/DAB2/FLNA/MELTF/	23	0.207207207207207
GO:1901222	BP	GO:1901222	regulation of	23/1414	111/18903	6.433961504	7.8513174	5.03127005	NFKBIA/PRDX1/RPS3/BIRC2	23	0.207207207207207
GO:0032635	BP	GO:0032635	interleukin-6	31/1414	176/18903	6.489380828	7.8859496	5.05346300	TWIST1/PLCG2/TRPV4/SELE	31	0.176136363636364
GO:0032675	BP	GO:0032675	regulation of	31/1414	176/18903	6.489380828	7.8859496	5.05346300	TWIST1/PLCG2/TRPV4/SELE	31	0.176136363636364
GO:0042594	BP	GO:0042594	response to	35/1414	211/18903	6.829672880	8.2822207	5.30740089	FOS/KLF10/CTSK/LAMP2/FO	35	0.165876777251185
GO:0002040	BP	GO:0002040	sprouting	32/1414	185/18903	6.862262076	8.3044760	5.32166251	PIK3R3/S100A1/NR4A1/FGF	32	0.172972972972973
GO:0071902	BP	GO:0071902	positive	37/1414	229/18903	7.043329503	8.5059505	5.45077107	PDGFRB/MAP2K6/FGFR1/BMP	37	0.161572052401747

GO:0048678	BP	GO:0048678	response to	20/1414	89/18903	7.069324292	8.5197042	5.45958472	MMP2/TNC/JUN/THY1/FLNA/	20 0.224719101123595
GO:2000249	BP	GO:2000249	regulation of	13/1414	42/18903	7.105715917	8.5283211	5.46510661	PDGFRA/NOTCH2/CSF1R/GMF	13 0.30952380952381
GO:2000403	BP	GO:2000403	positive	13/1414	42/18903	7.105715917	8.5283211	5.46510661	SELENOK/CCL20/AIF1/CCL3	13 0.30952380952381
GO:0097084	BP	GO:0097084	vascular	7/1414	12/18903	7.314873375	8.7613257	5.61442026	SGCB/COMP/HES1/VEGFA/AD	7 0.583333333333333
GO:0002704	BP	GO:0002704	negative	17/1414	68/18903	7.505735881	8.9531610	5.73735187	CD55/RABGEF1/PTPRC/BST2	17 0.25
GO:0060193	BP	GO:0060193	positive	17/1414	68/18903	7.505735881	8.9531610	5.73735187	PDGFRA/PDGFRB/FGFR1/FGF	17 0.25
GO:0043536	BP	GO:0043536	positive	18/1414	75/18903	7.585932536	9.0119642	5.77503407	FGFR1/ETS1/FGF2/TGFB1/P	18 0.24
GO:0050818	BP	GO:0050818	regulation of	18/1414	75/18903	7.585932536	9.0119642	5.77503407	PDGFRA/FAP/PROCR/SERPIN	18 0.24
GO:0051403	BP	GO:0051403	stress-	38/1414	239/18903	7.821639214	9.2730938	5.94237074	ZFP36L1/MAP2K6/FOXO1/GA	38 0.158995815899582
GO:0032872	BP	GO:0032872	regulation of	33/1414	195/18903	8.024220380	9.4939710	6.08391300	FOXO1/GADD45B/GADD45G/D	33 0.169230769230769
GO:0051051	BP	GO:0051051	negative regulation of	63/1414	479/18903	8.121525288587e-06	9.5896471 6767773e-	6.14522401 444118e-05	GJA1/TWIST1/ANK3/FOXO1/ HES1/GEM/CRYAB/WWP2/APO	63 0.131524008350731
GO:0010518	BP	GO:0010518	positive	15/1414	55/18903	8.149463331	9.6031958	6.15390628	PDGFRA/PDGFRB/FGFR1/FGF	15 0.272727272727273
GO:1901796	BP	GO:1901796	regulation of	22/1414	105/18903	8.410676737	9.8910236	6.33835167	TWIST1/SOX4/HEXIM1/MAP2	22 0.20952380952381
GO:0033673	BP	GO:0033673	negative	38/1414	240/18903	8.636358916	0.0001013	6.49533210	THY1/HEXIM1/SH3BP5/GADD	38 0.158333333333333
GO:0043030	BP	GO:0043030	regulation of	16/1414	62/18903	8.927848429	0.0001045	6.70107583	NR1D1/JUND/HSPD1/CD74/P	16 0.258064516129032
GO:0071498	BP	GO:0071498	cellular	9/1414	21/18903	9.198122726	0.0001073	6.87632290	MMP2/PTGS2/KLF2/KLF4/MT	9 0.428571428571429
GO:1901522	BP	GO:1901522	positive	9/1414	21/18903	9.198122726	0.0001073	6.87632290	JUN/RBPJ/DLX5/BMP2/XBP1	9 0.428571428571429
GO:0045580	BP	GO:0045580	regulation of	31/1414	179/18903	9.256059529	0.0001076	6.89534356	SOX4/ACTB/RUNX1/ZEB1/GL	31 0.173184357541899
GO:2000401	BP	GO:2000401	regulation of	17/1414	69/18903	9.272009086	0.0001076	6.89534356	ECM1/APOD/SELENOK/CCL20	17 0.246376811594203
GO:0032642	BP	GO:0032642	regulation of	21/1414	98/18903	9.278907128	0.0001076	6.89534356	EGR1/FOXP1/TWIST1/APOD/	21 0.214285714285714
GO:0031952	BP	GO:0031952	regulation of	13/1414	43/18903	9.491203821	0.0001098	7.03911127	JUN/GPNMB/CALM2/CAV1/VE	13 0.302325581395349
GO:0002703	BP	GO:0002703	regulation of	38/1414	241/18903	9.528557642	0.0001100	7.05282088	CADM1/LAG3/PLCG2/CD55/T	38 0.157676348547718
GO:0098754	BP	GO:0098754	detoxificatio	28/1414	154/18903	9.653911580	0.0001112	7.13148325	GPX8/H19/MT1G/PRDX4/MT1	28 0.181818181818182
GO:0061138	BP	GO:0061138	morphogenesis	32/1414	188/18903	9.679371259	0.0001113	7.13618755	SOCS3/SEMA3C/SIX1/RSPO2	32 0.170212765957447
GO:0030593	BP	GO:0030593	neutrophil	22/1414	106/18903	9.873604507	0.0001129	7.23838793	SAA1/PDE4B/CCL20/TNFAIP	22 0.207547169811321
GO:0042102	BP	GO:0042102	positive	22/1414	106/18903	9.873604507	0.0001129	7.23838793	HES1/VCAM1/PNP/SELENOK/	22 0.207547169811321
GO:0031647	BP	GO:0031647	regulation of protein	47/1414	325/18903	9.876088298 99131e-06	0.0001129 553393098	7.23838793 595834e-05	LMNA/SOX4/FLNA/LAMP2/HS PA1A/HSPA1B/DPM3/HSPA8/	47 0.144615384615385
GO:1903707	BP	GO:1903707	negative	23/1414	114/18903	1.024957541	0.0001169	7.49742348	MAFB/FBN1/RUNX1/GLI3/LA	23 0.201754385964912
GO:0042542	BP	GO:0042542	response to	25/1414	130/18903	1.042678460	0.0001187	7.61215299	COL1A1/MMP2/FOXP1/AQP1/	25 0.192307692307692
GO:0031397	BP	GO:0031397	negative	19/1414	84/18903	1.076836127	0.0001224	7.84619901	SOX4/HSPA1A/HSPA1B/DNAJ	19 0.226190476190476
GO:0030512	BP	GO:0030512	negative	21/1414	99/18903	1.095750364	0.0001241	7.95300877	LTBP1/FBN1/ASPN/HTRA1/H	21 0.212121212121212
GO:0032602	BP	GO:0032602	chemokine	21/1414	99/18903	1.095750364	0.0001241	7.95300877	EGR1/FOXP1/TWIST1/APOD/	21 0.212121212121212
GO:0003018	BP	GO:0003018	vascular	41/1414	270/18903	1.103602643	0.0001247	7.99447774	MMP2/COMP/TRPV4/SLC29A1	41 0.151851851851852
GO:2001242	BP	GO:2001242	regulation of	30/1414	172/18903	1.110161953	0.0001252	8.02520297	HSPA1A/UBB/SNAI1/DDIT3/	30 0.174418604651163

GO:0051604	BP	GO:0051604	protein maturation	48/1414	336/18903	1.11213809749518e-05	0.000125233620129	8.02520297542244e-05	MAFB/SERPINH1/C1R/SOX4/FLNA/RUNX1/GAS1/GLI3/PC	48	0.142857142857143	
GO:0002699	BP	GO:0002699	positive	40/1414	261/18903	1.126211619	0.0001265	8.11109919	CADM1/LAG3/PLCG2/RBP4/X	40	0.153256704980843	
GO:0002285	BP	GO:0002285	lymphocyte	34/1414	207/18903	1.141477693	0.0001280	8.20514493	FOXP1/LGALS1/NOTCH2/PLC	34	0.164251207729469	
GO:0043270	BP	GO:0043270	positive	43/1414	289/18903	1.143659950	0.0001280	8.20514493	THY1/PDGFRB/ACTB/FLNA/V	43	0.14878892733564	
GO:0006469	BP	GO:0006469	negative	35/1414	216/18903	1.157030295	0.0001292	8.28516753	THY1/HEXIM1/SH3BP5/GADD	35	0.162037037037037	
GO:0009743	BP	GO:0009743	response to	37/1414	234/18903	1.164168491	0.0001298	8.32034278	EGR1/ZFP36L1/SOX4/COL6A	37	0.158119658119658	
GO:0043552	BP	GO:0043552	positive	11/1414	32/18903	1.170579127	0.0001303	8.35019381	PDGFRA/PDGFRB/FGF2/TGFB	11	0.34375	
GO:0030856	BP	GO:0030856	regulation of	29/1414	164/18903	1.178196023	0.0001309	8.38851945	ZFP36L1/ZEB1/HES1/ZFP36	29	0.176829268292683	
GO:0072507	BP	GO:0072507	divalent inorganic	50/1414	356/18903	1.18072216688246e-05	0.000130934456262	8.39052314308511e-05	THY1/FLNA/NT5E/ANK3/MT1G/PLCG2/MT1M/MT1A/MT1E/	50	0.140449438202247	
GO:0014911	BP	GO:0014911	positive	13/1414	44/18903	1.255430722	0.0001386	8.88762857	PDGFRB/S100A11/LPAR1/AI	13	0.295454545454545	
GO:0021762	BP	GO:0021762	substantia	13/1414	44/18903	1.255430722	0.0001386	8.88762857	ACTB/S100A1/NDRG2/FGF2/	13	0.295454545454545	
GO:0046777	BP	GO:0046777	protein	36/1414	226/18903	1.287225406	0.0001419	9.09548784	JUN/THY1/PDGFRA/PDGFRB/	36	0.15929203539823	
GO:0031348	BP	GO:0031348	negative	41/1414	272/18903	1.322191332	0.0001455	9.32492834	SOCS3/HTRA1/PSMB4/NT5E/	41	0.150735294117647	
GO:1902106	BP	GO:1902106	negative	22/1414	108/18903	1.350895595	0.0001483	9.50942661	MAFB/FBN1/RUNX1/GLI3/LA	22	0.203703703703704	
GO:0043154	BP	GO:0043154	negative	18/1414	78/18903	1.360107057	0.0001491	9.55627257	AQP1/NR4A1/CRYAB/PTGS2/	18	0.230769230769231	
GO:0032922	BP	GO:0032922	circadian	17/1414	71/18903	1.395593987	0.0001527	9.78721091	EGR1/ID4/ZFHX3/ID3/NAMP	17	0.23943661971831	
GO:0010950	BP	GO:0010950	positive	30/1414	174/18903	1.402712681	0.0001532	9.81871226	GSN/CFLAR/CYCS/AKIRIN2/	30	0.172413793103448	
GO:1904705	BP	GO:1904705	regulation of	20/1414	93/18903	1.421826234	0.0001550	9.93390055	MMP2/GJA1/JUN/TPM1/NDRG	20	0.21505376344086	
GO:0032516	BP	GO:0032516	positive	9/1414	22/18903	1.453330068	0.0001578	0.00010116	PDGFRB/MAGI2/CALM2/PPP1	9	0.409090909090909	
GO:0061042	BP	GO:0061042	vascular	9/1414	22/18903	1.453330068	0.0001578	0.00010116	SMOC2/XBP1/VEGFA/NDNF/C	9	0.409090909090909	
GO:0007009	BP	GO:0007009	plasma	29/1414	166/18903	1.497248058	0.0001617	0.00010365	MAFB/COL5A1/VMP1/ANK3/S	29	0.174698795180723	
GO:0030225	BP	GO:0030225	macrophage	14/1414	51/18903	1.497416235	0.0001617	0.00010365	TSPAN2/INHBA/TGFB1/VEGF	14	0.274509803921569	
GO:1900047	BP	GO:1900047	negative	14/1414	51/18903	1.497416235	0.0001617	0.00010365	PDGFRA/FAP/COMP/SERPINE	14	0.274509803921569	
GO:0001101	BP	GO:0001101	response to	25/1414	133/18903	1.574846305	0.0001694	0.00010860	COL1A1/MMP2/COL1A2/COL5	25	0.18796992481203	
GO:0035303	BP	GO:0035303	regulation of	25/1414	133/18903	1.574846305	0.0001694	0.00010860	PDGFRB/RCAN1/MAGI2/BMP2	25	0.18796992481203	
GO:0090101	BP	GO:0090101	negative	28/1414	158/18903	1.587681048	0.0001705	0.00010929	NBL1/LTBP1/FBN1/ASPN/CI	28	0.177215189873418	
GO:0045582	BP	GO:0045582	positive	23/1414	117/18903	1.601044458	0.0001716	0.00011000	SOX4/ACTB/RUNX1/GLI3/ZB	23	0.196581196581197	
GO:0002063	BP	GO:0002063	chondrocyte	11/1414	33/18903	1.637631250	0.0001752	0.00011231	SERPINH1/ECM1/COMP/SULF	11	0.333333333333333	
GO:0006826	BP	GO:0006826	iron ion	15/1414	58/18903	1.646397651	0.0001758	0.00011271	SLC40A1/MELTF/TF/SLC39A	15	0.258620689655172	
GO:1900046	BP	GO:1900046	regulation of	17/1414	72/18903	1.700954659	0.0001810	0.00011602	PDGFRA/FAP/COMP/SERPINE	17	0.236111111111111	
GO:1903317	BP	GO:1903317	regulation of	17/1414	72/18903	1.700954659	0.0001810	0.00011602	SOX4/RUNX1/GAS1/MELTF/G	17	0.236111111111111	
GO:0038061	BP	GO:0038061	NIK/NF-kappaB	26/1414	142/18903	1.743361086	0.0001852	0.00011869	CHI3L1/NFKBIA/PRDX1/RPS	26	0.183098591549296	
GO:0060538	BP	GO:0060538	skeletal	30/1414	176/18903	1.764005923	0.0001870	0.00011988	EGR1/FOS/TWIST1/SIX1/CD	30	0.170454545454545	
GO:0001763	BP	GO:0001763	morphogenesis	33/1414	203/18903	1.900704273	0.0002012	0.00012894	SOCS3/SEMA3C/SIX1/RSPO2	33	0.16256157635468	

GO:0010043	BP	GO:0010043	response to	14/1414	52/18903	1.909125526	0.0002017	0.00012927	CRIP1/MT1G/MT1M/MT1A/MT	14	0.269230769230769
GO:0014068	BP	GO:0014068	positive	18/1414	80/18903	1.969446855	0.0002074	0.00013296	PDGFRA/PDGFRB/FGFR1/FN1	18	0.225
GO:0050808	BP	GO:0050808	synapse organization	57/1414	432/18903	1.970661899 43541e-05	0.0002074 886436716	0.00013296 2576570305	TNC/THBS2/TUBB/TUBA1A/P TPRD/SIX1/ACTG1/ACTB/FL	57	0.131944444444444
GO:0002763	BP	GO:0002763	positive	15/1414	59/18903	2.056346819	0.0002157	0.00013824	ZFP36L1/FOS/KLF10/RUNX1	15	0.254237288135593
GO:0043666	BP	GO:0043666	regulation of	15/1414	59/18903	2.056346819	0.0002157	0.00013824	PDGFRB/RCAN1/MAGI2/CALM	15	0.254237288135593
GO:0048144	BP	GO:0048144	fibroblast	21/1414	103/18903	2.075974183	0.0002173	0.00013931	COL3A1/JUN/PDGFRA/AQP1/	21	0.203883495145631
GO:0001701	BP	GO:0001701	in utero embryonic	53/1414	393/18903	2.084763078 22798e-05	0.0002179 287282312	0.00013965 2776660773	COL3A1/PDGFRA/SOCS3/ZFP 36L1/TWIST1/RBPJ/TBL1XR	53	0.134860050890585
GO:0034605	BP	GO:0034605	cellular	16/1414	66/18903	2.100914289	0.0002192	0.00014048	DNAJB1/HSPA1A/HSPA1B/TR	16	0.242424242424242
GO:0085029	BP	GO:0085029	extracellular	13/1414	46/18903	2.137486285	0.0002224	0.00014256	COL1A2/COL3A1/ANTXR1/TN	13	0.282608695652174
GO:0072006	BP	GO:0072006	nephron	27/1414	152/18903	2.139645396	0.0002224	0.00014256	EGR1/PDGFRA/AQP1/PDGFRB	27	0.177631578947368
GO:0061008	BP	GO:0061008	hepaticobilia	26/1414	144/18903	2.248959103	0.0002334	0.00014957	JUN/CADM1/NOTCH2/GLI3/H	26	0.180555555555556
GO:0140467	BP	GO:0140467	integrated	12/1414	40/18903	2.278061234	0.0002360	0.00015124	MAFB/JUN/FOS/JUNB/DDIT3	12	0.3
GO:0032868	BP	GO:0032868	response to	40/1414	269/18903	2.313715331	0.0002392	0.00015334	COL1A1/EGR1/SOCS3/ZFP36	40	0.148698884758364
GO:0072332	BP	GO:0072332	intrinsic	18/1414	81/18903	2.357166118	0.0002433	0.00015594	UBB/CDKN1A/NUPR1/CD44/D	18	0.222222222222222
GO:0060828	BP	GO:0060828	regulation of	39/1414	260/18903	2.382564829	0.0002453	0.00015721	COL1A1/IGFBP4/EGR1/DKK3	39	0.15
GO:0003012	BP	GO:0003012	muscle system process	59/1414	455/18903	2.384763218 84702e-05	0.0002453 319903974	0.00015721 3296020157	GJA1/CALD1/TPM4/FOXP1/L MNA/MYL9/SSPN/TPM1/FLNA	59	0.12967032967033
GO:0046683	BP	GO:0046683	response to	24/1414	128/18903	2.413234439	0.0002478	0.00015881	COL1A1/FOSB/ZFP36L1/AQP	24	0.1875
GO:0110020	BP	GO:0110020	regulation of	21/1414	104/18903	2.420399546	0.0002481	0.00015900	ACTG1/TPM1/PIK3R1/RHOC/	21	0.201923076923077
GO:0042267	BP	GO:0042267	natural	17/1414	74/18903	2.495409229	0.0002549	0.00016335	CADM1/TUBB/LAG3/TUBB4B/	17	0.22972972972973
GO:0048662	BP	GO:0048662	negative	17/1414	74/18903	2.495409229	0.0002549	0.00016335	TPM1/OGN/APOD/NDRG2/SOD	17	0.22972972972973
GO:0046686	BP	GO:0046686	response to	15/1414	60/18903	2.553931940	0.0002599	0.00016660	JUN/FOS/MT1G/MT1M/MT1A/	15	0.25
GO:2000351	BP	GO:2000351	regulation of	15/1414	60/18903	2.553931940	0.0002599	0.00016660	ANGPTL4/ICAM1/RGCC/NDNF	15	0.25
GO:0070613	BP	GO:0070613	regulation of	16/1414	67/18903	2.570319551	0.0002611	0.00016737	RUNX1/GAS1/MELTF/GSN/SE	16	0.238805970149254
GO:0006470	BP	GO:0006470	protein dephosphoryla	39/1414	261/18903	2.603275528 46874e-05	0.0002640 853244792	0.00016923 0780807185	PDGFRB/PTPRD/RCAN1/MAGI 2/CAMTA1/TGFB1/CALM2/PP	39	0.149425287356322
GO:0016311	BP	GO:0016311	dephosphoryla tion	49/1414	357/18903	2.660697404 87465e-05	0.0002694 418049068	0.00017266 3312951569	PDGFRB/PTPRD/RCAN1/TNS3 /MAGI2/BMP2/CAMTA1/TGFB	49	0.137254901960784
GO:0007584	BP	GO:0007584	response to	27/1414	154/18903	2.724523442	0.0002746	0.00017602	COL1A1/POSTN/STC2/SPP1/	27	0.175324675324675
GO:0043524	BP	GO:0043524	negative	27/1414	154/18903	2.724523442	0.0002746	0.00017602	JUN/SIX1/RETREG1/SOD2/C	27	0.175324675324675
GO:0050767	BP	GO:0050767	regulation of neurogenesis	51/1414	377/18903	2.726569648 68923e-05	0.0002746 818784249	0.00017602 1249386337	THY1/SEMA3C/PTPRD/ID4/G LI3/NTN1/HES1/PTN/SPP1/	51	0.135278514588859
GO:0045601	BP	GO:0045601	regulation of	13/1414	47/18903	2.753887925	0.0002764	0.00017717	ZEB1/BMP6/VEGFA/ROCK1/J	13	0.276595744680851
GO:0045646	BP	GO:0045646	regulation of	13/1414	47/18903	2.753887925	0.0002764	0.00017717	MAFB/ZFP36L1/HSPA1A/HSP	13	0.276595744680851

GO:0051101	BP	GO:0051101	regulation of	23/1414	121/18903	2.819894256	0.0002821	0.00018079	JUN/TWIST1/HES1/DDIT3/N	23	0.190082644628099
GO:0090100	BP	GO:0090100	positive	23/1414	121/18903	2.819894256	0.0002821	0.00018079	DAB2/ZEB2/RBPJ/NOTCH2/H	23	0.190082644628099
GO:0010592	BP	GO:0010592	positive	10/1414	29/18903	2.844820803	0.0002841	0.00018208	PIK3R1/HSP90AA1/ARPC2/T	10	0.344827586206897
GO:0031333	BP	GO:0031333	negative	26/1414	146/18903	2.883756927	0.0002875	0.00018425	CAPZB/CRYAB/SCIN/GSN/BI	26	0.178082191780822
GO:0097305	BP	GO:0097305	response to	38/1414	253/18903	2.925679779	0.0002912	0.00018661	FOSB/FOS/CTSK/CDO1/IGFB	38	0.150197628458498
GO:0061458	BP	GO:0061458	reproductive system	44/1414	310/18903	2.985885430 37238e-05	0.0002967 064687455	0.00019013 5015928491	MMP2/TNC/PDGFRA/PDGFRB/ ID4/CRIP1/GLI3/COL9A3/P	44	0.141935483870968
GO:0051693	BP	GO:0051693	actin	12/1414	41/18903	3.002842193	0.0002968	0.00019024	CAPZB/SCIN/GSN/TWF2/CAP	12	0.292682926829268
GO:0150077	BP	GO:0150077	regulation of	12/1414	41/18903	3.002842193	0.0002968	0.00019024	PLCG2/MMP3/NR1D1/NUPR1/	12	0.292682926829268
GO:1905314	BP	GO:1905314	semi-lunar	12/1414	41/18903	3.002842193	0.0002968	0.00019024	TWIST1/RBPJ/NOTCH2/SNAI	12	0.292682926829268
GO:0045621	BP	GO:0045621	positive	24/1414	130/18903	3.146192320	0.0003105	0.00019898	SOX4/ACTB/RUNX1/GLI3/ZB	24	0.184615384615385
GO:0007519	BP	GO:0007519	skeletal	28/1414	164/18903	3.217399675	0.0003170	0.00020314	EGR1/FOS/TWIST1/SIX1/CD	28	0.170731707317073
GO:0007492	BP	GO:0007492	endoderm	18/1414	83/18903	3.342099912	0.0003287	0.00021066	MMP2/COL12A1/COL5A1/COL	18	0.216867469879518
GO:0048017	BP	GO:0048017	inositol	30/1414	182/18903	3.414241426	0.0003352	0.00021484	PDGFRA/ZFP36L1/PDGFRB/T	30	0.164835164835165
GO:0032930	BP	GO:0032930	positive	8/1414	19/18903	3.438340121	0.0003370	0.00021600	TGFB1/TYROBP/ITGB2/CLEC	8	0.421052631578947
GO:1901215	BP	GO:1901215	negative	34/1414	218/18903	3.462762852	0.0003388	0.00021717	JUN/GPNMB/SIX1/RETREG1/	34	0.155963302752294
GO:0002224	BP	GO:0002224	toll-like	23/1414	123/18903	3.699254395	0.0003614	0.00023161	PLCG2/NFKBIA/NR1D1/PELI	23	0.186991869918699
GO:0031346	BP	GO:0031346	positive regulation of	48/1414	352/18903	3.787088363 94157e-05	0.0003693 994385764	0.00023671 8021129317	PTPRD/FLNA/DPYSL3/NTN1/ PTN/TUBB2B/FN1/PIK3R1/C	48	0.136363636363636
GO:0031099	BP	GO:0031099	regeneration	31/1414	192/18903	3.842479076	0.0003741	0.00023977	MMP2/TNC/JUN/THY1/PRRX1	31	0.161458333333333
GO:0072503	BP	GO:0072503	cellular	45/1414	323/18903	3.873796509	0.0003762	0.00024110	THY1/FLNA/MT1G/PLCG2/MT	45	0.139318885448916
GO:1904036	BP	GO:1904036	negative	15/1414	62/18903	3.876679059	0.0003762	0.00024110	ANGPTL4/CFLAR/NUPR1/ICA	15	0.241935483870968
GO:0010921	BP	GO:0010921	regulation of	18/1414	84/18903	3.959899127	0.0003836	0.00024587	PDGFRB/RCAN1/MAGI2/BMP2	18	0.214285714285714
GO:0030522	BP	GO:0030522	intracellular	39/1414	266/18903	4.014370870	0.0003883	0.00024884	FOXP1/TWIST1/DAB2/LBH/M	39	0.146616541353383
GO:0051250	BP	GO:0051250	negative	28/1414	166/18903	4.030669482	0.0003892	0.00024944	GPNMB/RUNX1/GLI3/LAG3/I	28	0.168674698795181
GO:0001569	BP	GO:0001569	branching	11/1414	36/18903	4.125434554	0.0003964	0.00025404	VEGFA/NRP1/PLXND1/GNA13	11	0.305555555555556
GO:0030224	BP	GO:0030224	monocyte	11/1414	36/18903	4.125434554	0.0003964	0.00025404	JUN/FOXP1/ZFP36L1/MT1G/	11	0.305555555555556
GO:0090218	BP	GO:0090218	positive	11/1414	36/18903	4.125434554	0.0003964	0.00025404	PDGFRA/PDGFRB/FGF2/TGFB	11	0.305555555555556
GO:0016525	BP	GO:0016525	negative	26/1414	149/18903	4.141811165	0.0003973	0.00025463	THBS2/CCN6/CNMD/SPARC/S	26	0.174496644295302
GO:0014706	BP	GO:0014706	striated	38/1414	257/18903	4.157324223	0.0003981	0.00025516	GJA1/PDGFRA/FOXP1/PDGFR	38	0.147859922178988
GO:0050731	BP	GO:0050731	positive	31/1414	193/18903	4.256122291	0.0004069	0.00026080	PLCG2/HES1/CSPG4/TGFB1/	31	0.160621761658031
GO:0002228	BP	GO:0002228	natural	17/1414	77/18903	4.306135420	0.0004110	0.00026343	CADM1/TUBB/LAG3/TUBB4B/	17	0.220779220779221
GO:0001889	BP	GO:0001889	liver	25/1414	141/18903	4.394728466	0.0004181	0.00026797	JUN/CADM1/NOTCH2/GLI3/H	25	0.177304964539007
GO:0070555	BP	GO:0070555	response to	25/1414	141/18903	4.394728466	0.0004181	0.00026797	MMP2/EGR1/CHI3L1/HES1/G	25	0.177304964539007
GO:0035307	BP	GO:0035307	positive	13/1414	49/18903	4.465864738	0.0004235	0.00027142	PDGFRB/MAGI2/CAMTA1/TGF	13	0.26530612244898
GO:0043114	BP	GO:0043114	regulation of	13/1414	49/18903	4.465864738	0.0004235	0.00027142	TRPV4/TGFB1/BMP6/VEGFA/	13	0.26530612244898

GO:0030193	BP	GO:0030193	regulation of	16/1414	70/18903	4.582041121	0.0004331	0.00027758	PDGFRA/FAP/SERPINE2/ANX	16	0.228571428571429
GO:0032722	BP	GO:0032722	positive	16/1414	70/18903	4.582041121	0.0004331	0.00027758	EGR1/TWIST1/TRPV4/SELEN	16	0.228571428571429
GO:0050680	BP	GO:0050680	negative	29/1414	176/18903	4.613578099	0.0004354	0.00027904	DAB2/ZEB1/CNMD/SPARC/TG	29	0.164772727272727
GO:0048608	BP	GO:0048608	reproductive structure	43/1414	306/18903	4.649809943 93529e-05	0.0004381 638352661	0.00028078 3523695505	MMP2/TNC/PDGFRA/PDGFRB/ ID4/CRIP1/GLI3/COL9A3/P	43	0.140522875816993
GO:0034614	BP	GO:0034614	cellular	26/1414	150/18903	4.659896384	0.0004383	0.00028088	MMP2/JUN/PDGFRA/FOXP1/A	26	0.173333333333333
GO:0042098	BP	GO:0042098	T cell	33/1414	212/18903	4.666439832	0.0004383	0.00028088	GPNMB/HES1/VCAM1/PNP/SE	33	0.155660377358491
GO:0043551	BP	GO:0043551	regulation of	14/1414	56/18903	4.721918422	0.0004428	0.00028376	PDGFRA/SOCS3/PDGFRB/PIK	14	0.25
GO:0002460	BP	GO:0002460	adaptive immune	50/1414	375/18903	4.762509256 08835e-05	0.0004459 023513766	0.00028574 2508547263	C1R/JUNB/C1S/CD55/TGFB1 /ICAM1/ANXA1/HSPD1/NFKB	50	0.133333333333333
GO:0051960	BP	GO:0051960	regulation of nervous	58/1414	456/18903	4.854035565 53388e-05	0.0004537 434207333	0.00029076 7211423934	THBS2/THY1/SEMA3C/PTPRD /ID4/GLI3/NTN1/HES1/PTN	58	0.12719298245614
GO:0002468	BP	GO:0002468	dendritic	7/1414	15/18903	4.862373583	0.0004537	0.00029080	HLA-DRB1/HLA-	7	0.466666666666667
GO:0050769	BP	GO:0050769	positive	35/1414	231/18903	4.948205913	0.0004610	0.00029546	PTPRD/ID4/GLI3/NTN1/HES	35	0.151515151515152
GO:0042554	BP	GO:0042554	superoxide	12/1414	43/18903	5.069671744	0.0004708	0.00030174	SOD2/TGFB1/TYROBP/CYBB/	12	0.27906976744186
GO:1904037	BP	GO:1904037	positive	12/1414	43/18903	5.069671744	0.0004708	0.00030174	H19/GSN/RGCC/ARRB2/CCL2	12	0.27906976744186
GO:0016485	BP	GO:0016485	protein	37/1414	250/18903	5.110013558	0.0004738	0.00030366	MAFB/C1R/RUNX1/GAS1/GLI	37	0.148
GO:0001764	BP	GO:0001764	neuron	29/1414	177/18903	5.130645211	0.0004743	0.00030399	COL3A1/TWIST1/NTN1/TUBB	29	0.163841807909605
GO:0007249	BP	GO:0007249	I-kappaB	41/1414	288/18903	5.131842473	0.0004743	0.00030399	GJA1/S100A4/ECM1/LGALS1	41	0.142361111111111
GO:2000181	BP	GO:2000181	negative	26/1414	151/18903	5.235583464	0.0004832	0.00030965	THBS2/CCN6/CNMD/SPARC/S	26	0.172185430463576
GO:0048738	BP	GO:0048738	cardiac	36/1414	241/18903	5.271559084	0.0004857	0.00031128	GJA1/PDGFRA/FOXP1/PDGFR	36	0.149377593360996
GO:0002577	BP	GO:0002577	regulation of	8/1414	20/18903	5.355241364	0.0004926	0.00031573	CD74/CD68/PYCARD/FGL2/F	8	0.4
GO:0003176	BP	GO:0003176	aortic valve	11/1414	37/18903	5.476420731	0.0005016	0.00032143	TWIST1/RBPJ/SNAI1/BMP2/	11	0.297297297297297
GO:0051084	BP	GO:0051084	'de novo'	11/1414	37/18903	5.476420731	0.0005016	0.00032143	DNAJB1/HSPA1A/HSPA1B/HS	11	0.297297297297297
GO:0002313	BP	GO:0002313	mature B cell	10/1414	31/18903	5.486424337	0.0005016	0.00032143	LGALS1/NOTCH2/PLCG2/ITM	10	0.32258064516129
GO:0060055	BP	GO:0060055	angiogenesis	10/1414	31/18903	5.486424337	0.0005016	0.00032143	SMOC2/XBP1/VEGFA/NDNF/C	10	0.32258064516129
GO:0003208	BP	GO:0003208	cardiac	16/1414	71/18903	5.509007560	0.0005028	0.00032225	SOX4/SEMA3C/RBPJ/TPM1/C	16	0.225352112676056
GO:0030195	BP	GO:0030195	negative	13/1414	50/18903	5.625261267	0.0005110	0.00032751	PDGFRA/FAP/SERPINE2/ANX	13	0.26
GO:0032964	BP	GO:0032964	collagen	13/1414	50/18903	5.625261267	0.0005110	0.00032751	COL1A1/COL5A1/SERPINH1/	13	0.26
GO:1902041	BP	GO:1902041	regulation of	13/1414	50/18903	5.625261267	0.0005110	0.00032751	CFLAR/ICAM1/PEA15/ATF3/	13	0.26
GO:0043200	BP	GO:0043200	response to	22/1414	118/18903	5.672889546	0.0005138	0.00032926	COL1A1/MMP2/COL1A2/COL5	22	0.186440677966102
GO:0051261	BP	GO:0051261	protein	22/1414	118/18903	5.672889546	0.0005138	0.00032926	CAPZB/LIMA1/HSPA8/SCIN/	22	0.186440677966102
GO:0048015	BP	GO:0048015	phosphatidyli	29/1414	178/18903	5.699449722	0.0005154	0.00033029	PDGFRA/ZFP36L1/PDGFRB/T	29	0.162921348314607
GO:0002042	BP	GO:0002042	cell	19/1414	94/18903	5.731339610	0.0005175	0.00033162	PIK3R3/NR4A1/FGF2/PTGS2	19	0.202127659574468
GO:0033632	BP	GO:0033632	regulation of	6/1414	11/18903	5.767543245	0.0005199	0.00033320	PIEZO1/FERMT3/SWAP70/PO	6	0.545454545454545
GO:1901343	BP	GO:1901343	negative	26/1414	152/18903	5.874427827	0.0005287	0.00033885	THBS2/CCN6/CNMD/SPARC/S	26	0.171052631578947

GO:0042476	BP	GO:0042476	odontogenesis	24/1414	135/18903	5.928539851	0.0005328	0.00034145	COL1A1/COL1A2/PDGFRA/AQ	24	0.177777777777778
GO:0001704	BP	GO:0001704	formation of	23/1414	127/18903	6.228885638	0.0005589	0.00035819	MMP2/COL12A1/COL5A1/GJA	23	0.181102362204724
GO:0030177	BP	GO:0030177	positive	25/1414	144/18903	6.294976780	0.0005640	0.00036144	COL1A1/SOX4/DAB2/ZEB2/R	25	0.173611111111111
GO:0060070	BP	GO:0060070	canonical Wnt	43/1414	310/18903	6.321634210	0.0005655	0.00036241	COL1A1/IGFBP4/EGR1/DKK3	43	0.138709677419355
GO:0002833	BP	GO:0002833	positive	30/1414	188/18903	6.358839990	0.0005680	0.00036399	CADM1/HEXIM1/LAG3/PLCG2	30	0.159574468085106
GO:0014910	BP	GO:0014910	regulation of	18/1414	87/18903	6.464473421	0.0005756	0.00036890	PDGFRB/TPM1/S100A11/LPA	18	0.206896551724138
GO:0048145	BP	GO:0048145	regulation of	18/1414	87/18903	6.464473421	0.0005756	0.00036890	JUN/PDGFRA/AQP1/PDGFRB/	18	0.206896551724138
GO:0042698	BP	GO:0042698	ovulation	16/1414	72/18903	6.597022675	0.0005848	0.00037475	MMP2/EGR1/PDGFRA/TIMP4/	16	0.222222222222222
GO:0045600	BP	GO:0045600	positive	16/1414	72/18903	6.597022675	0.0005848	0.00037475	ZFP36L1/SIX1/ZFP36/FRZB	16	0.222222222222222
GO:1901880	BP	GO:1901880	negative	16/1414	72/18903	6.597022675	0.0005848	0.00037475	CAPZB/LIMA1/SCIN/GSN/TW	16	0.222222222222222
GO:0014066	BP	GO:0014066	regulation of	21/1414	111/18903	6.647812541	0.0005884	0.00037706	PDGFRA/PDGFRB/TWIST1/FG	21	0.189189189189189
GO:0042113	BP	GO:0042113	B cell activation	47/1414	350/18903	6.659342880 73841e-05	0.0005885 446518688	0.00037715 0344011198	ZFP36L1/KLF6/LGALS1/RBP J/PIK3R3/NOTCH2/PLCG2/I	47	0.134285714285714
GO:0006929	BP	GO:0006929	substrate-	9/1414	26/18903	6.940906051	0.0006088	0.00039014	ITGA11/NTN1/CSPG4/FN1/S	9	0.346153846153846
GO:0051016	BP	GO:0051016	barbed-end	9/1414	26/18903	6.940906051	0.0006088	0.00039014	CAPZB/SCIN/GSN/TWF2/CAP	9	0.346153846153846
GO:0060343	BP	GO:0060343	trabecula	9/1414	26/18903	6.940906051	0.0006088	0.00039014	COL1A1/MMP2/SLC40A1/RBP	9	0.346153846153846
GO:1903306	BP	GO:1903306	negative	9/1414	26/18903	6.940906051	0.0006088	0.00039014	RABGEF1/SPI1/CD84/FCGR2	9	0.346153846153846
GO:1905523	BP	GO:1905523	positive	9/1414	26/18903	6.940906051	0.0006088	0.00039014	TRPV4/CSF1R/CCL3/C3AR1/	9	0.346153846153846
GO:0001913	BP	GO:0001913	T cell	13/1414	51/18903	7.037418778	0.0006163	0.00039497	HLA-DRB1/HLA-	13	0.254901960784314
GO:0014065	BP	GO:0014065	phosphatidyli	25/1414	145/18903	7.075483549	0.0006187	0.00039651	PDGFRA/ZFP36L1/PDGFRB/T	25	0.172413793103448
GO:0048010	BP	GO:0048010	vascular	14/1414	58/18903	7.164606271	0.0006246	0.00040030	MAPKAPK2/VEGFA/ITGA5/HS	14	0.241379310344828
GO:0060350	BP	GO:0060350	endochondral	14/1414	58/18903	7.164606271	0.0006246	0.00040030	COL1A1/COL3A1/SERPINH1/	14	0.241379310344828
GO:0045773	BP	GO:0045773	positive	11/1414	38/18903	7.190093475	0.0006259	0.00040113	NTN1/FN1/VEGFA/SHTN1/NR	11	0.289473684210526
GO:0051085	BP	GO:0051085	chaperone	10/1414	32/18903	7.448172159	0.0006465	0.00041429	DNAJB1/HSPA1A/HSPA1B/HS	10	0.3125
GO:0061036	BP	GO:0061036	positive	10/1414	32/18903	7.448172159	0.0006465	0.00041429	GLI3/SOX5/ZBTB16/BMP2/B	10	0.3125
GO:1901879	BP	GO:1901879	regulation of	18/1414	88/18903	7.566334651	0.0006557	0.00042024	CAPZB/LIMA1/SCIN/GSN/TR	18	0.204545454545455
GO:0045445	BP	GO:0045445	myoblast	21/1414	112/18903	7.614225834	0.0006589	0.00042227	ZFP36L1/SOX4/LGALS1/ACT	21	0.1875
GO:0150063	BP	GO:0150063	visual system development	51/1414	392/18903	7.630749884 88164e-05	0.0006594 098382002	0.00042256 207159789	COL5A1/COL5A2/JUN/THY1/ PDGFRA/AQP1/PDGFRB/TWIS	51	0.130102040816327
GO:0007411	BP	GO:0007411	axon guidance	35/1414	236/18903	7.721711705	0.0006658	0.00042670	ENAH/SEMA3C/NOTCH2/GLI3	35	0.148305084745763
GO:0002275	BP	GO:0002275	myeloid cell	19/1414	96/18903	7.739816568	0.0006658	0.00042670	S100A13/PLCG2/RABGEF1/T	19	0.197916666666667
GO:1903321	BP	GO:1903321	negative	19/1414	96/18903	7.739816568	0.0006658	0.00042670	SOX4/HSPA1A/HSPA1B/DNAJ	19	0.197916666666667
GO:0043409	BP	GO:0043409	negative	29/1414	181/18903	7.763100195	0.0006668	0.00042735	DAB2/FOXO1/DNAJA1/NDRG2	29	0.160220994475138
GO:0043122	BP	GO:0043122	regulation of	37/1414	255/18903	7.816677534	0.0006705	0.00042967	GJA1/S100A4/ECM1/LGALS1	37	0.145098039215686
GO:0030032	BP	GO:0030032	lamellipodium	16/1414	73/18903	7.869327916	0.0006730	0.00043130	CAPZB/PIK3R1/RHOD/HSP90	16	0.219178082191781
GO:0071677	BP	GO:0071677	positive	16/1414	73/18903	7.869327916	0.0006730	0.00043130	SELENOK/CCL20/AIF1/CCL3	16	0.219178082191781

GO:0072073	BP	GO:0072073	kidney	25/1414	146/18903	7.941542768	0.0006782	0.00043462	AQP1/SIX1/NOTCH2/GLI3/H	25	0.171232876712329
GO:0150105	BP	GO:0150105	protein	8/1414	21/18903	8.084736190	0.0006865	0.00043995	ACTG1/ACTB/PAK2/TJP1/VC	8	0.380952380952381
GO:0010715	BP	GO:0010715	regulation of	7/1414	16/18903	8.086015568	0.0006865	0.00043995	FAP/MELTF/PDPN/TGFB1/CS	7	0.4375
GO:0034112	BP	GO:0034112	positive	7/1414	16/18903	8.086015568	0.0006865	0.00043995	ANK3/PDPN/PLAUR/EMILIN2	7	0.4375
GO:0051014	BP	GO:0051014	actin	7/1414	16/18903	8.086015568	0.0006865	0.00043995	SCIN/GSN/GMFG/CAPG/CFL1	7	0.4375
GO:0035148	BP	GO:0035148	tube	26/1414	155/18903	8.232317790	0.0006979	0.00044726	TWIST1/SOX4/SIX1/CTHRC1	26	0.167741935483871
GO:0031623	BP	GO:0031623	receptor	22/1414	121/18903	8.391275047	0.0007098	0.00045491	PLCG2/MAGI2/SDCBP/ANXA2	22	0.181818181818182
GO:0006879	BP	GO:0006879	cellular iron	15/1414	66/18903	8.421276624	0.0007098	0.00045491	SLC40A1/TF/SLC39A14/CP/	15	0.227272727272727
GO:0030837	BP	GO:0030837	negative	15/1414	66/18903	8.421276624	0.0007098	0.00045491	CAPZB/SCIN/GSN/TMSB4X/T	15	0.227272727272727
GO:0097485	BP	GO:0097485	neuron	35/1414	237/18903	8.421866136	0.0007098	0.00045491	ENAH/SEMA3C/NOTCH2/GLI3	35	0.147679324894515
GO:0032272	BP	GO:0032272	negative	17/1414	81/18903	8.478185102	0.0007136	0.00045729	CAPZB/SCIN/GSN/TMSB4X/T	17	0.209876543209877
GO:0006909	BP	GO:0006909	phagocytosis	43/1414	314/18903	8.524388522	0.0007164	0.00045912	PLCG2/GSN/TGM2/ANXA1/TY	43	0.136942675159236
GO:0042129	BP	GO:0042129	regulation of	29/1414	182/18903	8.587393688	0.0007207	0.00046185	GPNMB/HES1/VCAM1/PNP/SE	29	0.159340659340659
GO:0046849	BP	GO:0046849	bone	18/1414	89/18903	8.830693122	0.0007400	0.00047425	GJA1/CTSK/NOTCH2/LTBP3/	18	0.202247191011236
GO:0031396	BP	GO:0031396	regulation of	32/1414	210/18903	9.151370758	0.0007658	0.00049077	SOX4/HSPA1A/UBB/UBE2S/H	32	0.152380952380952
GO:0045730	BP	GO:0045730	respiratory	11/1414	39/18903	9.342828758	0.0007770	0.00049794	SELENOK/CD55/CYBB/CLEC7	11	0.282051282051282
GO:0097242	BP	GO:0097242	amyloid-beta	11/1414	39/18903	9.342828758	0.0007770	0.00049794	MSR1/ITGB2/ITGAM/C5AR1/	11	0.282051282051282
GO:0002381	BP	GO:0002381	immunoglobuli	16/1414	74/18903	9.351788243	0.0007770	0.00049794	TGFB1/HSPD1/HLA-	16	0.216216216216216
GO:0006801	BP	GO:0006801	superoxide	16/1414	74/18903	9.351788243	0.0007770	0.00049794	H19/SOD2/TGFB1/PRDX1/SO	16	0.216216216216216
GO:0051145	BP	GO:0051145	smooth muscle	16/1414	74/18903	9.351788243	0.0007770	0.00049794	SIX1/SGCB/ZEB1/COMP/HES	16	0.216216216216216
GO:0051494	BP	GO:0051494	negative	27/1414	165/18903	9.376379924	0.0007779	0.00049854	CAPZB/LIMA1/SCIN/GSN/PI	27	0.163636363636364
GO:0008361	BP	GO:0008361	regulation of	29/1414	183/18903	9.489488932	0.0007862	0.00050384	AQP1/SEMA3C/NTN1/TRPV4/	29	0.158469945355191
GO:0031954	BP	GO:0031954	positive	9/1414	27/18903	9.723373199	0.0008033	0.00051480	GPNMB/CALM2/VEGFA/PDGFC	9	0.333333333333333
GO:0032967	BP	GO:0032967	positive	9/1414	27/18903	9.723373199	0.0008033	0.00051480	PDGFRB/RUNX1/INHBA/LARP	9	0.333333333333333
GO:0002526	BP	GO:0002526	acute	21/1414	114/18903	9.928935146	0.0008191	0.00052494	OSMR/SAA1/VCAM1/FN1/A2M	21	0.184210526315789
GO:0060395	BP	GO:0060395	SMAD protein	17/1414	82/18903	9.960246887	0.0008205	0.00052585	JUN/FOS/DAB2/CILP/GDF10	17	0.207317073170732
GO:0030888	BP	GO:0030888	regulation of	15/1414	67/18903	0.000101090	0.0008316	0.00053295	CDKN1A/PELI1/CD74/TYROB	15	0.223880597014925
GO:0051924	BP	GO:0051924	regulation of	38/1414	268/18903	0.000103522	0.0008504	0.00054500	THY1/PDGFRB/VMP1/PLCG2/	38	0.141791044776119
GO:0097178	BP	GO:0097178	ruffle	12/1414	46/18903	0.000104281	0.0008555	0.00054823	CSPG4/ICAM1/CAV1/EPS8L2	12	0.260869565217391
GO:0050728	BP	GO:0050728	negative	29/1414	184/18903	0.000104757	0.0008582	0.00054996	SOCS3/PSMB4/NT5E/ZFP36/	29	0.157608695652174
GO:1905517	BP	GO:1905517	macrophage	14/1414	60/18903	0.000106407	0.0008705	0.00055784	MMP2/TRPV4/SAA1/CSF1R/C	14	0.233333333333333
GO:0019216	BP	GO:0019216	regulation of lipid	46/1414	347/18903	0.000107984046872874	0.0008789324358332	0.000563236229374414	EGR1/PDGFRA/DKK3/PDGFRB/TWIST1/DAB2/NPC2/TBL1X	46	0.132564841498559
GO:0072015	BP	GO:0072015	podocyte	6/1414	12/18903	0.000108035	0.0008789	0.00056323	NOTCH2/MAGI2/IQGAP1/JAG	6	0.5
GO:2001214	BP	GO:2001214	positive	6/1414	12/18903	0.000108035	0.0008789	0.00056323	RIN2/ADM/RAP1A/RAMP2/CD	6	0.5
GO:0071622	BP	GO:0071622	regulation of	13/1414	53/18903	0.000108039	0.0008789	0.00056323	TRPV4/TNFAIP6/CD74/CSF1	13	0.245283018867925

GO:0048880	BP	GO:0048880	sensory system	51/1414	398/18903	0.000112424 35030589	0.0009133 304113290	0.00058527 9090948856	COL5A1/COL5A2/JUN/THY1/ PDGFRA/AQP1/PDGFRB/TWIS	51	0.128140703517588
GO:0001938	BP	GO:0001938	positive	21/1414	115/18903	0.000113049	0.0009171	0.00058771	JUN/ECM1/NR4A1/FGFR1/NR	21	0.182608695652174
GO:0070304	BP	GO:0070304	positive	23/1414	132/18903	0.000114987	0.0009315	0.00059695	GADD45B/GADD45G/TRPV4/I	23	0.174242424242424
GO:0030728	BP	GO:0030728	ovulation	8/1414	22/18903	0.000118741	0.0009553	0.00061219	MMP2/INHBA/PTGS2/TNFAIP	8	0.363636363636364
GO:0032928	BP	GO:0032928	regulation of	8/1414	22/18903	0.000118741	0.0009553	0.00061219	TGFB1/TYROBP/ITGB2/CLEC	8	0.363636363636364
GO:0060713	BP	GO:0060713	labyrinthine	8/1414	22/18903	0.000118741	0.0009553	0.00061219	SOCS3/ZFP36L1/SPINT2/AD	8	0.363636363636364
GO:0072574	BP	GO:0072574	hepatocyte	8/1414	22/18903	0.000118741	0.0009553	0.00061219	NOTCH2/PTN/CFLAR/XBP1/F	8	0.363636363636364
GO:0072575	BP	GO:0072575	epithelial	8/1414	22/18903	0.000118741	0.0009553	0.00061219	NOTCH2/PTN/CFLAR/XBP1/F	8	0.363636363636364
GO:0006882	BP	GO:0006882	cellular zinc	11/1414	40/18903	0.000120225	0.0009619	0.00061644	MT1G/MT1M/MT1A/MT1E/MT1	11	0.275
GO:0010762	BP	GO:0010762	regulation of	11/1414	40/18903	0.000120225	0.0009619	0.00061644	AQP1/FGF2/TGFB1/SDC4/SL	11	0.275
GO:0030866	BP	GO:0030866	cortical	11/1414	40/18903	0.000120225	0.0009619	0.00061644	EPB41L2/RAB13/LCP1/PLEK	11	0.275
GO:0035886	BP	GO:0035886	vascular	11/1414	40/18903	0.000120225	0.0009619	0.00061644	SGCB/COMP/HES1/SOD2/VEG	11	0.275
GO:0043550	BP	GO:0043550	regulation of	15/1414	68/18903	0.000120841	0.0009655	0.00061875	PDGFRA/SOCS3/PDGFRB/PIK	15	0.220588235294118
GO:1903729	BP	GO:1903729	regulation of	7/1414	17/18903	0.000128596	0.0010256	0.00065722	GSN/ANXA2/S100A10/MYH9/	7	0.411764705882353
GO:0034113	BP	GO:0034113	heterotypic	14/1414	61/18903	0.000128706	0.0010256	0.00065722	THY1/GLDN/VCAM1/CD44/IT	14	0.229508196721311
GO:0050821	BP	GO:0050821	protein	32/1414	214/18903	0.000131382	0.0010455	0.00066997	SOX4/FLNA/LAMP2/HSPA1A/	32	0.149532710280374
GO:0003382	BP	GO:0003382	epithelial	10/1414	34/18903	0.000131897	0.0010467	0.00067077	FRMD6/COL15A1/SPINT2/RO	10	0.294117647058824
GO:0090322	BP	GO:0090322	regulation of	10/1414	34/18903	0.000131897	0.0010467	0.00067077	H19/TGFB1/TYROBP/ITGB2/	10	0.294117647058824
GO:0032330	BP	GO:0032330	regulation of	13/1414	54/18903	0.000132654	0.0010498	0.00067279	GLI3/EFEMP1/LTBP3/SOX5/	13	0.240740740740741
GO:1902743	BP	GO:1902743	regulation of	13/1414	54/18903	0.000132654	0.0010498	0.00067279	CAPZB/PDPN/PIK3R1/CD44/	13	0.240740740740741
GO:1903320	BP	GO:1903320	regulation of	36/1414	252/18903	0.000133575	0.0010537	0.00067529	EGR1/SOX4/HSPA1A/UBB/UB	36	0.142857142857143
GO:0010714	BP	GO:0010714	positive	9/1414	28/18903	0.000133830	0.0010537	0.00067529	PDGFRB/RUNX1/INHBA/LARP	9	0.321428571428571
GO:0032703	BP	GO:0032703	negative	9/1414	28/18903	0.000133830	0.0010537	0.00067529	LAG3/ZFP36/LAPTM5/PTPRC	9	0.321428571428571
GO:0060560	BP	GO:0060560	developmental	34/1414	233/18903	0.000133869	0.0010537	0.00067529	SEMA3C/SIX1/NTN1/SPP1/N	34	0.145922746781116
GO:0034620	BP	GO:0034620	cellular	19/1414	100/18903	0.000137007	0.0010755	0.00068926	HSPA1A/HSPA1B/HSPA8/DDI	19	0.19
GO:0098869	BP	GO:0098869	cellular	19/1414	100/18903	0.000137007	0.0010755	0.00068926	GPX8/H19/PRDX4/GPX3/SOD	19	0.19
GO:0045664	BP	GO:0045664	regulation of	30/1414	196/18903	0.000137876	0.0010809	0.00069269	NBL1/TCF4/SIX1/ID4/ZFHX	30	0.153061224489796
GO:0002221	BP	GO:0002221	pattern	29/1414	187/18903	0.000140096	0.0010956	0.00070214	MAP2K6/PLCG2/HSPA1A/HSP	29	0.155080213903743
GO:0001818	BP	GO:0001818	negative regulation of	48/1414	371/18903	0.000140131 690136657	0.0010956 945691248	0.00070214 1430330564	TWIST1/GPNMB/LAG3/ZFP36 /DDIT3/APOD/NDRG2/FN1/I	48	0.129380053908356
GO:0046632	BP	GO:0046632	alpha-beta T	21/1414	117/18903	0.000145723	0.0011378	0.00072918	FOXP1/RUNX1/GLI3/JUNB/Z	21	0.179487179487179
GO:0048511	BP	GO:0048511	rhythmic	41/1414	302/18903	0.000149086	0.0011625	0.00074501	MMP2/EGR1/PDGFRA/TWIST1	41	0.135761589403974
GO:0019221	BP	GO:0019221	cytokine-mediated	60/1414	496/18903	0.000150341 261533139	0.0011708 151916192	0.00075028 012044716	EGR1/ECM1/IFITM1/HSPA1A /HSPA1B/NFKBIA/OSMR/IFI	60	0.120967741935484
GO:0046545	BP	GO:0046545	development	20/1414	109/18903	0.000152308	0.0011845	0.00075908	MMP2/PDGFRA/COL9A3/UBB/	20	0.18348623853211

GO:0001914	BP	GO:0001914	regulation of	11/1414	41/18903	0.000153298	0.0011906	0.00076299	HLA-DRB1/HLA-	11	0.268292682926829
GO:1903036	BP	GO:1903036	positive	16/1414	77/18903	0.000153623	0.0011916	0.00076360	ACTG1/FLNA/SMOC2/PTN/XB	16	0.207792207792208
GO:0030183	BP	GO:0030183	B cell	25/1414	152/18903	0.000154322	0.0011954	0.00076605	ZFP36L1/KLF6/LGALS1/RBP	25	0.164473684210526
GO:0022617	BP	GO:0022617	extracellular	14/1414	62/18903	0.000154938	0.0011970	0.00076707	MMP2/CTSK/FAP/MELTF/PDP	14	0.225806451612903
GO:0045428	BP	GO:0045428	regulation of	14/1414	62/18903	0.000154938	0.0011970	0.00076707	SOD2/PTGS2/CAV1/HSP90AA	14	0.225806451612903
GO:0003231	BP	GO:0003231	cardiac	22/1414	126/18903	0.000155497	0.0011997	0.00076882	SOX4/SEMA3C/RBPJ/TPM1/H	22	0.174603174603175
GO:0030900	BP	GO:0030900	forebrain development	49/1414	383/18903	0.000157810774076982	0.0012159976818904	0.00077923389939145	COL3A1/FAT4/FOXP1/AQP1/RBPJ/ID4/ZEB1/GLI3/CDON	49	0.127937336814621
GO:0071320	BP	GO:0071320	cellular	13/1414	55/18903	0.000161950	0.0012446	0.00079757	ZFP36L1/AQP1/HSPA5/AHR/	13	0.236363636363636
GO:1904645	BP	GO:1904645	response to	13/1414	55/18903	0.000161950	0.0012446	0.00079757	MMP2/GJA1/MMP3/VCAM1/IC	13	0.236363636363636
GO:0002819	BP	GO:0002819	regulation of	30/1414	198/18903	0.000165764	0.0012722	0.00081527	JUNB/CD55/TGFB1/ANXA1/A	30	0.151515151515152
GO:0050650	BP	GO:0050650	chondroitin	8/1414	23/18903	0.000170179	0.0013009	0.00083370	DSE/CYTL1/XYLT1/CHST3/C	8	0.347826086956522
GO:0072576	BP	GO:0072576	liver	8/1414	23/18903	0.000170179	0.0013009	0.00083370	NOTCH2/PTN/CFLAR/XBP1/F	8	0.347826086956522
GO:0150146	BP	GO:0150146	cell junction	8/1414	23/18903	0.000170179	0.0013009	0.00083370	PIK3R1/C1QC/C1QA/C1QB/I	8	0.347826086956522
GO:0043627	BP	GO:0043627	response to	15/1414	70/18903	0.000170606	0.0013025	0.00083469	MMP2/PDGFRB/GLI3/TNFRSF	15	0.214285714285714
GO:0050654	BP	GO:0050654	chondroitin	10/1414	35/18903	0.000172370	0.0013091	0.00083893	DSEL/DSE/CYTL1/XYLT1/CH	10	0.285714285714286
GO:0090050	BP	GO:0090050	positive	10/1414	35/18903	0.000172370	0.0013091	0.00083893	FGF2/PTGS2/ANXA1/VEGFA/	10	0.285714285714286
GO:2000352	BP	GO:2000352	negative	10/1414	35/18903	0.000172370	0.0013091	0.00083893	ANGPTL4/ICAM1/NDNF/NFE2	10	0.285714285714286
GO:2000406	BP	GO:2000406	positive	10/1414	35/18903	0.000172370	0.0013091	0.00083893	SELENOK/CCL20/AIF1/PYCA	10	0.285714285714286
GO:0032869	BP	GO:0032869	cellular	31/1414	208/18903	0.000176497	0.0013387	0.00085790	SOCS3/ZFP36L1/PIK3R3/FO	31	0.149038461538462
GO:0008630	BP	GO:0008630	intrinsic	19/1414	102/18903	0.000179750	0.0013616	0.00087258	CRIP1/SNAI1/SOD2/PIK3R1	19	0.186274509803922
GO:0097066	BP	GO:0097066	response to	9/1414	29/18903	0.000181253	0.0013712	0.00087873	HES1/CTSL/CTSS/CTSH/CTS	9	0.310344827586207
GO:0032092	BP	GO:0032092	positive	17/1414	86/18903	0.000184053	0.0013906	0.00089115	CTHRC1/BMP2/RAN/ANXA2/C	17	0.197674418604651
GO:0034333	BP	GO:0034333	adherens	6/1414	13/18903	0.000187933	0.0014126	0.00090525	ACTB/PAK2/HIPK1/SMAD7/V	6	0.461538461538462
GO:0034616	BP	GO:0034616	response to	6/1414	13/18903	0.000187933	0.0014126	0.00090525	KLF2/KLF4/ABCA1/NFE2L2/	6	0.461538461538462
GO:0070424	BP	GO:0070424	regulation of	6/1414	13/18903	0.000187933	0.0014126	0.00090525	HSPA1A/HSPA1B/BIRC2/TLR	6	0.461538461538462
GO:0072310	BP	GO:0072310	glomerular	6/1414	13/18903	0.000187933	0.0014126	0.00090525	NOTCH2/MAGI2/IQGAP1/JAG	6	0.461538461538462
GO:1905475	BP	GO:1905475	regulation of	27/1414	172/18903	0.000191017	0.0014339	0.00091892	DAB2/ACTB/ANK3/GPC6/GSN	27	0.156976744186047
GO:0010591	BP	GO:0010591	regulation of	11/1414	42/18903	0.000193785	0.0014491	0.00092865	CAPZB/PIK3R1/HSP90AA1/A	11	0.261904761904762
GO:0034142	BP	GO:0034142	toll-like	11/1414	42/18903	0.000193785	0.0014491	0.00092865	NFKBIA/NR1D1/PELI1/CD14	11	0.261904761904762
GO:0055069	BP	GO:0055069	zinc ion	11/1414	42/18903	0.000193785	0.0014491	0.00092865	MT1G/MT1M/MT1A/MT1E/MT1	11	0.261904761904762
GO:0001954	BP	GO:0001954	positive	13/1414	56/18903	0.000196637	0.0014573	0.00093387	THY1/RIN2/SDC4/VEGFA/NR	13	0.232142857142857
GO:0010718	BP	GO:0010718	positive	13/1414	56/18903	0.000196637	0.0014573	0.00093387	COL1A1/TWIST1/DAB2/SNAI	13	0.232142857142857
GO:0043370	BP	GO:0043370	regulation of	13/1414	56/18903	0.000196637	0.0014573	0.00093387	RUNX1/JUNB/ANXA1/NFKBIZ	13	0.232142857142857
GO:0030510	BP	GO:0030510	regulation of	20/1414	111/18903	0.000196756	0.0014573	0.00093387	NBL1/FSTL1/RBPJ/FBN1/NO	20	0.18018018018018
GO:0071347	BP	GO:0071347	cellular	20/1414	111/18903	0.000196756	0.0014573	0.00093387	MMP2/EGR1/HES1/GBP2/NR1	20	0.18018018018018

GO:0030206	BP	GO:0030206	chondroitin	7/1414	18/18903	0.000196873	0.0014573	0.00093387	DSE/XYLT1/CHST3/CSGALNA	7	0.388888888888889
GO:0036035	BP	GO:0036035	osteoclast	7/1414	18/18903	0.000196873	0.0014573	0.00093387	FOXP1/FBN1/NOTCH2/FAM20	7	0.388888888888889
GO:0097067	BP	GO:0097067	cellular	7/1414	18/18903	0.000196873	0.0014573	0.00093387	CTSL/CTSS/CTSH/CTSB/KLF	7	0.388888888888889
GO:0033628	BP	GO:0033628	regulation of	12/1414	49/18903	0.000200573	0.0014809	0.00094901	PIEZO1/LYN/FERMT3/NCKAP	12	0.244897959183673
GO:2000404	BP	GO:2000404	regulation of	12/1414	49/18903	0.000200573	0.0014809	0.00094901	ECM1/APOD/SELENOK/CCL20	12	0.244897959183673
GO:1903510	BP	GO:1903510	mucopolysacch	18/1414	95/18903	0.000210972	0.0015557	0.00099695	DSEL/DSE/XYLT1/CHST3/CS	18	0.189473684210526
GO:0021915	BP	GO:0021915	neural tube	26/1414	164/18903	0.000211855	0.0015602	0.00099986	MARCKS/ZFP36L1/TWIST1/S	26	0.158536585365854
GO:0001654	BP	GO:0001654	eye development	49/1414	388/18903	0.000215562511277762	0.0015855941088060	0.0010160781543072	COL5A1/COL5A2/JUN/THY1/PDGFRA/AQP1/PDGFRB/TWIS	49	0.126288659793814
GO:2000027	BP	GO:2000027	regulation of	22/1414	129/18903	0.000220684	0.0016212	0.00103891	DAB2/SIX1/RSPO2/CTHRC1/	22	0.170542635658915
GO:0050869	BP	GO:0050869	negative	10/1414	36/18903	0.000222800	0.0016326	0.00104623	INHBA/ID2/TYROBP/LAPTM5	10	0.277777777777778
GO:0060323	BP	GO:0060323	head	10/1414	36/18903	0.000222800	0.0016326	0.00104623	COL1A1/MMP2/PDGFRA/CRIS	10	0.277777777777778
GO:1903038	BP	GO:1903038	negative	24/1414	147/18903	0.000232313	0.0017002	0.00108953	GPNMB/RUNX1/GLI3/LAG3/S	24	0.163265306122449
GO:0035914	BP	GO:0035914	skeletal	15/1414	72/18903	0.000237226	0.0017316	0.00110969	EGR1/FOS/SIX1/CDON/NR4A	15	0.208333333333333
GO:0008347	BP	GO:0008347	glial cell	13/1414	57/18903	0.000237501	0.0017316	0.00110969	COL3A1/GLI3/NTN1/CSPG4/	13	0.228070175438596
GO:0043388	BP	GO:0043388	positive	13/1414	57/18903	0.000237501	0.0017316	0.00110969	TWIST1/HES1/TXN/TGFB1/C	13	0.228070175438596
GO:0036303	BP	GO:0036303	lymph vessel	8/1414	24/18903	0.000238616	0.0017354	0.00111212	PDPN/FGF2/VEGFA/PKD1/CL	8	0.333333333333333
GO:0071294	BP	GO:0071294	cellular	8/1414	24/18903	0.000238616	0.0017354	0.00111212	MT1G/MT1M/MT1A/MT1E/MT1	8	0.333333333333333
GO:0010464	BP	GO:0010464	regulation of	9/1414	30/18903	0.000241866	0.0017503	0.00112167	LMNA/SIX1/PRRX1/ZEB1/FG	9	0.3
GO:0030204	BP	GO:0030204	chondroitin	9/1414	30/18903	0.000241866	0.0017503	0.00112167	DSEL/DSE/XYLT1/CHST3/CS	9	0.3
GO:0060325	BP	GO:0060325	face	9/1414	30/18903	0.000241866	0.0017503	0.00112167	COL1A1/MMP2/PDGFRA/CRIS	9	0.3
GO:0070168	BP	GO:0070168	negative	9/1414	30/18903	0.000241866	0.0017503	0.00112167	ECM1/ASPN/LTBP3/TGFB1/R	9	0.3
GO:0002347	BP	GO:0002347	response to	11/1414	43/18903	0.000242971	0.0017562	0.00112540	NOTCH2/TXNIP/HSPD1/KLF4	11	0.255813953488372
GO:0035023	BP	GO:0035023	regulation of	17/1414	88/18903	0.000245948	0.0017755	0.00113778	COL3A1/PDGFRB/LPAR1/EPS	17	0.193181818181818
GO:0002456	BP	GO:0002456	T cell	20/1414	113/18903	0.000252212	0.0018184	0.00116531	CD55/ICAM1/HSPD1/HLA-	20	0.176991150442478
GO:0048754	BP	GO:0048754	branching	25/1414	157/18903	0.000259178	0.0018644	0.00119475	SIX1/RSPO2/GLI3/BMP2/FG	25	0.159235668789809
GO:0043010	BP	GO:0043010	camera-type eye	44/1414	340/18903	0.000259221611239856	0.0018644138820740	0.0011947510435625	JUN/THY1/PDGFRA/AQP1/PDGFRB/TWIST1/FBN1/ZEB1/N	44	0.129411764705882
GO:0048857	BP	GO:0048857	neural	14/1414	65/18903	0.000263132	0.0018878	0.00120979	ACTB/S100A1/NDRG2/FGF2/	14	0.215384615384615
GO:0080164	BP	GO:0080164	regulation of	14/1414	65/18903	0.000263132	0.0018878	0.00120979	SOD2/PTGS2/CAV1/HSP90AA	14	0.215384615384615
GO:0008585	BP	GO:0008585	female gonad	19/1414	105/18903	0.000265734	0.0019042	0.00122025	MMP2/PDGFRA/COL9A3/UBB/	19	0.180952380952381
GO:0071901	BP	GO:0071901	negative	21/1414	122/18903	0.000266383	0.0019065	0.00122173	HEXIM1/DNAJA1/BMP2/CDKN	21	0.172131147540984
GO:0031345	BP	GO:0031345	negative	29/1414	194/18903	0.000267031	0.0019088	0.00122320	THY1/CAPZB/SEMA3C/DAB2/	29	0.149484536082474
GO:0042176	BP	GO:0042176	regulation of protein	46/1414	361/18903	0.000270873547108329	0.0019339111386571	0.00123928617635982	DAB2/TIMP2/FLNA/TIMP4/FOXO1/HSPA1A/UBB/HSPA1B/	46	0.127423822714681
GO:0032984	BP	GO:0032984	protein-	34/1414	242/18903	0.000278301	0.0019845	0.00127171	CAPZB/LIMA1/LAMP2/VMP1/	34	0.140495867768595

GO:0002335	BP	GO:0002335	mature B cell	10/1414	37/18903	0.000285035	0.0020251	0.00129772	LGALS1/NOTCH2/PLCG2/ITM	10	0.27027027027027
GO:0034110	BP	GO:0034110	regulation of	10/1414	37/18903	0.000285035	0.0020251	0.00129772	ANK3/PDPN/SERPINE2/PLAU	10	0.27027027027027
GO:1902745	BP	GO:1902745	positive	10/1414	37/18903	0.000285035	0.0020251	0.00129772	PIK3R1/HSP90AA1/ARPC2/T	10	0.27027027027027
GO:0002483	BP	GO:0002483	antigen	7/1414	19/18903	0.000291659	0.0020596	0.00131984	HLA-DRB1/HLA-	7	0.368421052631579
GO:0010759	BP	GO:0010759	positive	7/1414	19/18903	0.000291659	0.0020596	0.00131984	TRPV4/CSF1R/C3AR1/C5AR1	7	0.368421052631579
GO:0010801	BP	GO:0010801	negative	7/1414	19/18903	0.000291659	0.0020596	0.00131984	CALM2/SPRY2/DDIT4/SPRED	7	0.368421052631579
GO:0032026	BP	GO:0032026	response to	7/1414	19/18903	0.000291659	0.0020596	0.00131984	ANK3/TNFRSF11B/BMP6/CCN	7	0.368421052631579
GO:0043031	BP	GO:0043031	negative	7/1414	19/18903	0.000291659	0.0020596	0.00131984	NR1D1/PTPRC/VSIG4/FCGR2	7	0.368421052631579
GO:0001709	BP	GO:0001709	cell fate	11/1414	44/18903	0.000302295	0.0021295	0.00136467	PRRX1/NOTCH2/TNXB/HES1/	11	0.25
GO:0071526	BP	GO:0071526	semaphorin-	11/1414	44/18903	0.000302295	0.0021295	0.00136467	SEMA3C/FLNA/NRP2/NRP1/P	11	0.25
GO:0042117	BP	GO:0042117	monocyte	6/1414	14/18903	0.000308090	0.0021599	0.00138414	FOXP1/MT1G/FN1/ADAM9/AD	6	0.428571428571429
GO:0043301	BP	GO:0043301	negative	6/1414	14/18903	0.000308090	0.0021599	0.00138414	RABGEF1/SPI1/CD84/FCGR2	6	0.428571428571429
GO:0071801	BP	GO:0071801	regulation of	6/1414	14/18903	0.000308090	0.0021599	0.00138414	GSN/LCP1/RHOA/MSN/ASAP1	6	0.428571428571429
GO:1902043	BP	GO:1902043	positive	6/1414	14/18903	0.000308090	0.0021599	0.00138414	PEA15/ATF3/PMAIP1/STK4/	6	0.428571428571429
GO:0010812	BP	GO:0010812	negative	14/1414	66/18903	0.000311303	0.0021746	0.00139355	COL1A1/MELTF/APOD/SPOCK	14	0.212121212121212
GO:0031343	BP	GO:0031343	positive	14/1414	66/18903	0.000311303	0.0021746	0.00139355	CADM1/LAG3/HLA-	14	0.212121212121212
GO:0060389	BP	GO:0060389	pathway-	14/1414	66/18903	0.000311303	0.0021746	0.00139355	DAB2/GDF10/BMP2/SDCBP/I	14	0.212121212121212
GO:0120162	BP	GO:0120162	positive	18/1414	98/18903	0.000315400	0.0021953	0.00140684	GJA1/DIO2/GADD45G/LCN2/	18	0.183673469387755
GO:1990868	BP	GO:1990868	response to	18/1414	98/18903	0.000315400	0.0021953	0.00140684	CCL20/CCL3/CCL3L1/CXCL8	18	0.183673469387755
GO:1990869	BP	GO:1990869	cellular	18/1414	98/18903	0.000315400	0.0021953	0.00140684	CCL20/CCL3/CCL3L1/CXCL8	18	0.183673469387755
GO:0030010	BP	GO:0030010	establishment	24/1414	150/18903	0.000316968	0.0022036	0.00141215	GJA1/HES1/GSN/SPRY2/HSP	24	0.16
GO:0110150	BP	GO:0110150	negative	9/1414	31/18903	0.000318366	0.0022061	0.00141375	ECM1/ASPN/LTBP3/TGFB1/R	9	0.290322580645161
GO:1900745	BP	GO:1900745	positive	9/1414	31/18903	0.000318366	0.0022061	0.00141375	GADD45B/GADD45G/BMP2/VE	9	0.290322580645161
GO:0007369	BP	GO:0007369	gastrulation	29/1414	196/18903	0.000318462	0.0022061	0.00141375	MMP2/COL12A1/COL5A1/GJA	29	0.147959183673469
GO:0051146	BP	GO:0051146	striated	39/1414	293/18903	0.000321028	0.0022213	0.00142345	PDGFRA/FOXP1/PDGFRB/LMN	39	0.133105802047782
GO:0055006	BP	GO:0055006	cardiac cell	17/1414	90/18903	0.000325179	0.0022447	0.00143847	PDGFRA/FOXP1/PDGFRB/LMN	17	0.188888888888889
GO:0030330	BP	GO:0030330	DNA damage	15/1414	74/18903	0.000325186	0.0022447	0.00143847	TWIST1/SOX4/SNAI1/NDRG1	15	0.202702702702703
GO:0001911	BP	GO:0001911	negative	8/1414	25/18903	0.000328037	0.0022590	0.00144766	PTPRC/ARRB2/FCGR2B/NCKA	8	0.32
GO:0070423	BP	GO:0070423	nucleotide-	8/1414	25/18903	0.000328037	0.0022590	0.00144766	MAP2K6/HSPA1A/HSPA1B/NF	8	0.32
GO:0043242	BP	GO:0043242	negative	16/1414	82/18903	0.000329099	0.0022610	0.00144892	CAPZB/LIMA1/SCIN/GSN/TW	16	0.195121951219512
GO:0048708	BP	GO:0048708	astrocyte	16/1414	82/18903	0.000329099	0.0022610	0.00144892	ID4/TSPAN2/HES1/NR1D1/S	16	0.195121951219512
GO:0046660	BP	GO:0046660	female sex	21/1414	124/18903	0.000335063	0.0022993	0.00147344	MMP2/PDGFRA/COL9A3/UBB/	21	0.169354838709677
GO:0010717	BP	GO:0010717	regulation of	19/1414	107/18903	0.000341294	0.0023314	0.00149401	COL1A1/TWIST1/DAB2/SNAI	19	0.177570093457944
GO:0062207	BP	GO:0062207	regulation of	19/1414	107/18903	0.000341294	0.0023314	0.00149401	HSPA1A/HSPA1B/NR1D1/PEL	19	0.177570093457944
GO:0001912	BP	GO:0001912	positive	13/1414	59/18903	0.000341337	0.0023314	0.00149401	CADM1/LAG3/HLA-	13	0.220338983050847
GO:0045010	BP	GO:0045010	actin	13/1414	59/18903	0.000341337	0.0023314	0.00149401	SCIN/GSN/GMFG/IQGAP2/AR	13	0.220338983050847

GO:0010977	BP	GO:0010977	negative	23/1414	142/18903	0.000349416	0.0023810	0.00152579	THY1/SEMA3C/DAB2/FLNA/D	23	0.161971830985915
GO:0014074	BP	GO:0014074	response to	23/1414	142/18903	0.000349416	0.0023810	0.00152579	COL1A1/FOSB/ZFP36L1/AQP	23	0.161971830985915
GO:2001237	BP	GO:2001237	negative	18/1414	99/18903	0.000358998	0.0024434	0.00156581	LMNA/HSPA1A/COL2A1/HSPA	18	0.181818181818182
GO:0043516	BP	GO:0043516	regulation of	10/1414	38/18903	0.000361155	0.0024524	0.00157155	TWIST1/SOX4/SNAI1/CD44/	10	0.263157894736842
GO:0045920	BP	GO:0045920	negative	10/1414	38/18903	0.000361155	0.0024524	0.00157155	ANXA1/RABGEF1/SPI1/CD84	10	0.263157894736842
GO:0021872	BP	GO:0021872	forebrain	12/1414	52/18903	0.000364062	0.0024664	0.00158051	GLI3/HES1/UBB/NRP2/INHB	12	0.230769230769231
GO:0051496	BP	GO:0051496	positive	12/1414	52/18903	0.000364062	0.0024664	0.00158051	TPM1/RHOC/SDC4/LPAR1/RG	12	0.230769230769231
GO:1901224	BP	GO:1901224	positive	14/1414	67/18903	0.000366830	0.0024822	0.00159069	RPS3/LAPTM5/CD14/CD86/T	14	0.208955223880597
GO:0060021	BP	GO:0060021	roof of mouth	17/1414	91/18903	0.000372478	0.0025118	0.00160965	PDGFRA/TWIST1/PRRX1/GLI	17	0.186813186813187
GO:0010712	BP	GO:0010712	regulation of	11/1414	45/18903	0.000373356	0.0025118	0.00160965	PDGFRB/RUNX1/FAP/INHBA/	11	0.244444444444444
GO:0010799	BP	GO:0010799	regulation of	11/1414	45/18903	0.000373356	0.0025118	0.00160965	CHI3L1/TGFB1/CALM2/SPRY	11	0.244444444444444
GO:0030574	BP	GO:0030574	collagen	11/1414	45/18903	0.000373356	0.0025118	0.00160965	MMP2/MRC2/CTSK/FAP/RETR	11	0.244444444444444
GO:0062208	BP	GO:0062208	positive	11/1414	45/18903	0.000373356	0.0025118	0.00160965	HSPA1A/HSPA1B/PELI1/CAV	11	0.244444444444444
GO:1904375	BP	GO:1904375	regulation of	21/1414	125/18903	0.000374870	0.0025191	0.00161431	EPB41L2/DAB2/ACTB/GPC6/	21	0.168
GO:0090257	BP	GO:0090257	regulation of	35/1414	256/18903	0.000384912	0.0025836	0.00165565	FOXP1/LMNA/MYL9/TPM1/FO	35	0.13671875
GO:2001056	BP	GO:2001056	positive	23/1414	143/18903	0.000387498	0.0025980	0.00166485	GSN/CFLAR/CYCS/RPS3/HSP	23	0.160839160839161
GO:0043123	BP	GO:0043123	positive	28/1414	189/18903	0.000392078	0.0026257	0.00168260	GJA1/S100A4/ECM1/LGALS1	28	0.148148148148148
GO:0009615	BP	GO:0009615	response to virus	50/1414	409/18903	0.000404771 6657361	0.0027076 067961452	0.00173508 472359837	NPC2/HTRA1/H19/IFITM1/R PS15A/IVNS1ABP/IFITM2/S	50	0.122249388753056
GO:0043406	BP	GO:0043406	positive	20/1414	117/18903	0.000405368	0.0027084	0.00173565	PDGFRB/MAP2K6/FGFR1/FGF	20	0.170940170940171
GO:0009144	BP	GO:0009144	purine	34/1414	247/18903	0.000408213	0.0027243	0.00174583	NT5E/H19/NDUFB1/ATP5ME/	34	0.137651821862348
GO:0046685	BP	GO:0046685	response to	9/1414	32/18903	0.000413800	0.0027522	0.00176367	TNFRSF11B/GSTO1/ATF4/AT	9	0.28125
GO:0061384	BP	GO:0061384	heart	9/1414	32/18903	0.000413800	0.0027522	0.00176367	RBPJ/RBP4/TGFBR3/FKBP1A	9	0.28125
GO:1990776	BP	GO:1990776	response to	9/1414	32/18903	0.000413800	0.0027522	0.00176367	COL3A1/INHBA/PTGS2/CAV1	9	0.28125
GO:0032332	BP	GO:0032332	positive	7/1414	20/18903	0.000419871	0.0027830	0.00178344	GLI3/SOX5/ZBTB16/BMP6/G	7	0.35
GO:0055093	BP	GO:0055093	response to	7/1414	20/18903	0.000419871	0.0027830	0.00178344	COL1A1/MMP2/PDGFRB/FOXO	7	0.35
GO:1903978	BP	GO:1903978	regulation of	7/1414	20/18903	0.000419871	0.0027830	0.00178344	NR1D1/PTPRC/CCL3/TREM2/	7	0.35
GO:0072091	BP	GO:0072091	regulation of	17/1414	92/18903	0.000425605	0.0028172	0.00180532	GJA1/ZFP36L1/RBPJ/PRRX1	17	0.184782608695652
GO:2000347	BP	GO:2000347	positive	5/1414	10/18903	0.000425987	0.0028172	0.00180532	PTN/CFLAR/XBP1/FGF1/TNF	5	0.5
GO:0030100	BP	GO:0030100	regulation of	30/1414	209/18903	0.000429417	0.0028366	0.00181779	DAB2/PLCG2/TF/MAGI2/SDC	30	0.143540669856459
GO:0045670	BP	GO:0045670	regulation of	14/1414	68/18903	0.000430605	0.0028413	0.00182076	MAFB/FOS/KLF10/FBN1/NOT	14	0.205882352941176
GO:0009409	BP	GO:0009409	response to	12/1414	53/18903	0.000438995	0.0028893	0.00185156	FOS/DIO2/PCSK1N/FOXO1/N	12	0.226415094339623
GO:0048146	BP	GO:0048146	positive	12/1414	53/18903	0.000438995	0.0028893	0.00185156	JUN/PDGFRA/AQP1/PDGFRB/	12	0.226415094339623
GO:0006809	BP	GO:0006809	nitric oxide	15/1414	76/18903	0.000439821	0.0028893	0.00185156	SOD2/PTGS2/CAV1/HSP90AA	15	0.197368421052632
GO:0048863	BP	GO:0048863	stem cell	34/1414	248/18903	0.000439871	0.0028893	0.00185156	PDGFRA/TWIST1/SEMA3C/LB	34	0.137096774193548
GO:0019883	BP	GO:0019883	antigen	8/1414	26/18903	0.000442983	0.0028967	0.00185630	HLA-DRB1/HLA-	8	0.307692307692308

GO:0035872	BP	GO:0035872	nucleotide-	8/1414	26/18903	0.000442983	0.0028967	0.00185630	MAP2K6/HSPA1A/HSPA1B/NF	8	0.307692307692308
GO:0060669	BP	GO:0060669	embryonic	8/1414	26/18903	0.000442983	0.0028967	0.00185630	SOCS3/ZFP36L1/SPINT2/AD	8	0.307692307692308
GO:0072010	BP	GO:0072010	glomerular	8/1414	26/18903	0.000442983	0.0028967	0.00185630	NOTCH2/MAGI2/IQGAP1/JAG	8	0.307692307692308
GO:0002286	BP	GO:0002286	T cell	20/1414	118/18903	0.000454425	0.0029682	0.00190212	FOXP1/JUNB/ICAM1/ANXA1/	20	0.169491525423729
GO:2001243	BP	GO:2001243	negative	18/1414	101/18903	0.000462080	0.0030148	0.00193199	HSPA1A/SNAI1/DNAJA1/IVN	18	0.178217821782178
GO:0055001	BP	GO:0055001	muscle cell	28/1414	191/18903	0.000466234	0.0030385	0.00194718	PDGFRA/FOXP1/PDGFRB/LMN	28	0.146596858638743
GO:0045834	BP	GO:0045834	positive	24/1414	154/18903	0.000471423	0.0030689	0.00196666	PDGFRA/PDGFRB/TWIST1/DA	24	0.155844155844156
GO:0010649	BP	GO:0010649	regulation of	6/1414	15/18903	0.000481067	0.0031103	0.00199315	ANK3/CALM2/CAV1/SLC8A1/	6	0.4
GO:0032488	BP	GO:0032488	Cdc42 protein	6/1414	15/18903	0.000481067	0.0031103	0.00199315	NTN1/APOE/SHTN1/NRP1/AB	6	0.4
GO:0061307	BP	GO:0061307	cardiac	6/1414	15/18903	0.000481067	0.0031103	0.00199315	TWIST1/SEMA3C/HES1/CITE	6	0.4
GO:0061308	BP	GO:0061308	cardiac	6/1414	15/18903	0.000481067	0.0031103	0.00199315	TWIST1/SEMA3C/HES1/CITE	6	0.4
GO:1902563	BP	GO:1902563	regulation of	6/1414	15/18903	0.000481067	0.0031103	0.00199315	PLA2G2A/ITGB2/SPI1/ITGA	6	0.4
GO:2000345	BP	GO:2000345	regulation of	6/1414	15/18903	0.000481067	0.0031103	0.00199315	PTN/CFLAR/XBP1/FGF1/LIM	6	0.4
GO:1900024	BP	GO:1900024	regulation of	13/1414	61/18903	0.000481505	0.0031103	0.00199315	DAB2/FLNA/MELTF/PDPN/NR	13	0.213114754098361
GO:0051962	BP	GO:0051962	positive	37/1414	279/18903	0.000484276	0.0031247	0.00200240	THBS2/PTPRD/ID4/GLI3/NT	37	0.132616487455197
GO:2000106	BP	GO:2000106	regulation of	17/1414	93/18903	0.000485141	0.0031268	0.00200376	FOXP1/ANXA1/PRELID1/TCP	17	0.182795698924731
GO:0008625	BP	GO:0008625	extrinsic	16/1414	85/18903	0.000501763	0.0032268	0.00206784	PIK3R1/CFLAR/ICAM1/PEA1	16	0.188235294117647
GO:0034103	BP	GO:0034103	regulation of	16/1414	85/18903	0.000501763	0.0032268	0.00206784	GPNMB/RUNX1/LTBP3/TF/SP	16	0.188235294117647
GO:0048645	BP	GO:0048645	animal organ	14/1414	69/18903	0.000503593	0.0032350	0.00207310	SIX1/RBPJ/GLI3/HES1/BMP	14	0.202898550724638
GO:0043297	BP	GO:0043297	apical	15/1414	77/18903	0.000509062	0.0032666	0.00209331	SNAI1/RHOC/RAB13/AFDN/R	15	0.194805194805195
GO:0006936	BP	GO:0006936	muscle contraction	44/1414	351/18903	0.000517427450900212	0.0033166531001109	0.00212537290705223	GJA1/CALD1/TPM4/MYL9/SSPN/TPM1/FLNA/COMP/SULF2	44	0.125356125356125
GO:0043583	BP	GO:0043583	ear	31/1414	221/18903	0.000520104	0.0033301	0.00213402	MAFB/PDGFRB/TWIST1/SIX1	31	0.14027149321267
GO:0030857	BP	GO:0030857	negative	12/1414	54/18903	0.000526521	0.0033675	0.00215798	ZEB1/HES1/FRZB/SPRY2/CA	12	0.222222222222222
GO:0048839	BP	GO:0048839	inner ear	28/1414	193/18903	0.000552466	0.0035296	0.00226184	MAFB/PDGFRB/SIX1/RBPJ/P	28	0.145077720207254
GO:0034314	BP	GO:0034314	Arp2/3	11/1414	47/18903	0.000557940	0.0035451	0.00227181	GMFG/IQGAP2/ARPC1B/ARPC	11	0.234042553191489
GO:0060711	BP	GO:0060711	labyrinthine	11/1414	47/18903	0.000557940	0.0035451	0.00227181	SOCS3/ZFP36L1/RBPJ/HES1	11	0.234042553191489
GO:0097028	BP	GO:0097028	dendritic	11/1414	47/18903	0.000557940	0.0035451	0.00227181	RBPJ/NOTCH2/CEBPB/SPI1/	11	0.234042553191489
GO:0120163	BP	GO:0120163	negative	11/1414	47/18903	0.000557940	0.0035451	0.00227181	RBPJ/ACOT13/MAP2K6/DDIT	11	0.234042553191489
GO:1902622	BP	GO:1902622	regulation of	11/1414	47/18903	0.000557940	0.0035451	0.00227181	CD99/SELENOK/TNFAIP6/CD	11	0.234042553191489
GO:1990000	BP	GO:1990000	amyloid	10/1414	40/18903	0.000564558	0.0035832	0.00229622	FUS/CRYAB/GSN/APOE/TREM	10	0.25
GO:0031102	BP	GO:0031102	neuron	13/1414	62/18903	0.000568145	0.0035832	0.00229622	MMP2/TNC/JUN/THY1/PRRX1	13	0.209677419354839
GO:0060393	BP	GO:0060393	regulation of	13/1414	62/18903	0.000568145	0.0035832	0.00229622	DAB2/GDF10/BMP2/SDCBP/I	13	0.209677419354839
GO:0090303	BP	GO:0090303	positive	13/1414	62/18903	0.000568145	0.0035832	0.00229622	ACTG1/SMOC2/XBP1/ANXA1/	13	0.209677419354839
GO:0035967	BP	GO:0035967	cellular	20/1414	120/18903	0.000568195	0.0035832	0.00229622	HSPA1A/HSPA1B/HSPA8/DDI	20	0.166666666666667
GO:0051897	BP	GO:0051897	positive	20/1414	120/18903	0.000568195	0.0035832	0.00229622	CHI3L1/H19/FGFR1/FGF2/T	20	0.166666666666667

GO:0048638	BP	GO:0048638	regulation of	42/1414	332/18903	0.000568236	0.0035832	0.00229622	FOXP1/SEMA3C/SIX1/RBPJ/	42 0.126506024096386
GO:0050770	BP	GO:0050770	regulation of	24/1414	156/18903	0.000570848	0.0035958	0.00230428	THY1/SEMA3C/NTN1/SPP1/F	24 0.153846153846154
GO:0051592	BP	GO:0051592	response to	23/1414	147/18903	0.000578580	0.0036406	0.00233298	JUN/FOSB/FOS/ACTG1/PLCG	23 0.156462585034014
GO:0050772	BP	GO:0050772	positive	15/1414	78/18903	0.000587401	0.0036715	0.00235279	NTN1/FN1/TIAM2/VEGFA/DI	15 0.192307692307692
GO:0061045	BP	GO:0061045	negative	15/1414	78/18903	0.000587401	0.0036715	0.00235279	PDGFRA/FAP/SERPINE2/FGF	15 0.192307692307692
GO:0090049	BP	GO:0090049	regulation of	15/1414	78/18903	0.000587401	0.0036715	0.00235279	FGF2/PTGS2/ANXA1/VEGFA/	15 0.192307692307692
GO:0034143	BP	GO:0034143	regulation of	8/1414	27/18903	0.000588563	0.0036715	0.00235279	NR1D1/PELI1/CD14/LYN/TR	8 0.296296296296296
GO:0036296	BP	GO:0036296	response to	8/1414	27/18903	0.000588563	0.0036715	0.00235279	COL1A1/MMP2/PDGFRB/FOXO	8 0.296296296296296
GO:0071549	BP	GO:0071549	cellular	8/1414	27/18903	0.000588563	0.0036715	0.00235279	AQP1/CFLAR/EIF4E/DDIT4/	8 0.296296296296296
GO:2000737	BP	GO:2000737	negative	8/1414	27/18903	0.000588563	0.0036715	0.00235279	LBH/HES1/ZFP36/HSPA9/ZF	8 0.296296296296296
GO:0007042	BP	GO:0007042	lysosomal	7/1414	21/18903	0.000589383	0.0036715	0.00235279	ATP6V0C/ATP6V0B/GRN/PPT	7 0.333333333333333
GO:1902307	BP	GO:1902307	positive	7/1414	21/18903	0.000589383	0.0036715	0.00235279	ANK3/FXYD1/GLRX/ATP1B3/	7 0.333333333333333
GO:0032677	BP	GO:0032677	regulation of	18/1414	103/18903	0.000589787	0.0036715	0.00235279	CHI3L1/HSPA1A/HSPA1B/DD	18 0.174757281553398
GO:0090596	BP	GO:0090596	sensory organ	36/1414	272/18903	0.000594844	0.0036990	0.00237043	MAFB/COL5A1/COL5A2/THY1	36 0.132352941176471
GO:0006457	BP	GO:0006457	protein	31/1414	223/18903	0.000607306	0.0037725	0.00241751	WIPF1/LTBP4/PPIC/PRDX4/	31 0.139013452914798
GO:0010976	BP	GO:0010976	positive	24/1414	157/18903	0.000627089	0.0038912	0.00249361	FLNA/DPYSL3/PTN/TUBB2B/	24 0.152866242038217
GO:0070169	BP	GO:0070169	positive	12/1414	55/18903	0.000628262	0.0038944	0.00249562	PTN/FAM20C/BMP2/TGFB1/B	12 0.218181818181818
GO:0032874	BP	GO:0032874	positive	21/1414	130/18903	0.000642090	0.0039759	0.00254784	GADD45B/GADD45G/TRPV4/I	21 0.161538461538462
GO:0072175	BP	GO:0072175	epithelial	22/1414	139/18903	0.000642942	0.0039769	0.00254851	TWIST1/SOX4/SIX1/CTHRC1	22 0.158273381294964
GO:0140694	BP	GO:0140694	non-membrane-bounded	47/1414	386/18903	0.000649066426900174	0.0040105979535049	0.00257006565780834	PDGFRA/PDGFRB/MYL9/TUBB/ACTG1/TPM1/FLNA/TNNT3/	47 0.121761658031088
GO:0032637	BP	GO:0032637	interleukin-8	18/1414	104/18903	0.000664304	0.0040960	0.00262484	CHI3L1/HSPA1A/HSPA1B/DD	18 0.173076923076923
GO:0042100	BP	GO:0042100	B cell	18/1414	104/18903	0.000664304	0.0040960	0.00262484	CDKN1A/PELI1/HSPD1/CD74	18 0.173076923076923
GO:0043087	BP	GO:0043087	regulation of GTPase	46/1414	376/18903	0.000665556170554704	0.0040994605521072	0.00262701046144584	THY1/CCPG1/ASAP2/RGS16/TGM2/TIAM2/SPRY2/CCL20/	46 0.122340425531915
GO:0032757	BP	GO:0032757	positive	13/1414	63/18903	0.000667590	0.0041033	0.00262948	CHI3L1/HSPA1A/HSPA1B/DD	13 0.206349206349206
GO:0045453	BP	GO:0045453	bone	13/1414	63/18903	0.000667590	0.0041033	0.00262948	CTSK/LTBP3/TF/SPP1/TNFR	13 0.206349206349206
GO:0060563	BP	GO:0060563	neuroepitheli	9/1414	34/18903	0.000675453	0.0041232	0.00264226	SOX4/TUBB/HES1/FAM20C/B	9 0.264705882352941
GO:0001974	BP	GO:0001974	blood vessel	11/1414	48/18903	0.000675536	0.0041232	0.00264226	SEMA3C/RBPJ/FLNA/TGFB1/	11 0.229166666666667
GO:0006953	BP	GO:0006953	acute-phase	11/1414	48/18903	0.000675536	0.0041232	0.00264226	SAA1/FN1/A2M/SERPINA1/S	11 0.229166666666667
GO:0010171	BP	GO:0010171	body	11/1414	48/18903	0.000675536	0.0041232	0.00264226	COL1A1/MMP2/PDGFRA/CDON	11 0.229166666666667
GO:1904738	BP	GO:1904738	vascular	11/1414	48/18903	0.000675536	0.0041232	0.00264226	TPM1/DDIT3/DOCK4/MEF2C/	11 0.229166666666667
GO:0043299	BP	GO:0043299	leukocyte	15/1414	79/18903	0.000675782	0.0041232	0.00264226	S100A13/RABGEF1/VAMP8/I	15 0.189873417721519
GO:2000514	BP	GO:2000514	regulation of	15/1414	79/18903	0.000675782	0.0041232	0.00264226	RUNX1/JUNB/CD55/ANXA1/N	15 0.189873417721519
GO:0061077	BP	GO:0061077	chaperone-	14/1414	71/18903	0.000681474	0.0041536	0.00266173	DNAJB1/HSPA1A/HSPA1B/HS	14 0.197183098591549
GO:1905954	BP	GO:1905954	positive	19/1414	113/18903	0.000690467	0.0042040	0.00269404	DAB2/ABCA5/MAP2K6/NFKBI	19 0.168141592920354

GO:0016064	BP	GO:0016064	immunoglobuli	30/1414	215/18903	0.000692846	0.0042097	0.00269769	C1R/C1S/CD55/TGFB1/HSPD	30	0.13953488372093
GO:0050803	BP	GO:0050803	regulation of	30/1414	215/18903	0.000692846	0.0042097	0.00269769	THBS2/TUBB/TUBA1A/PTPRD	30	0.13953488372093
GO:0030513	BP	GO:0030513	positive	10/1414	41/18903	0.000697223	0.0042319	0.00271191	RBPJ/NOTCH2/HES1/CCN1/N	10	0.24390243902439
GO:0048675	BP	GO:0048675	axon	20/1414	122/18903	0.000705834	0.0042797	0.00274255	SEMA3C/NTN1/NRP2/FN1/VE	20	0.163934426229508
GO:0061097	BP	GO:0061097	regulation of	17/1414	96/18903	0.000708641	0.0042923	0.00275059	THY1/SH3BP5/GPRC5A/CAV1	17	0.177083333333333
GO:0030214	BP	GO:0030214	hyaluronan	6/1414	16/18903	0.000721192	0.0043412	0.00278198	FGF2/TGFB1/CD44/HEXB/HY	6	0.375
GO:0046184	BP	GO:0046184	aldehyde	6/1414	16/18903	0.000721192	0.0043412	0.00278198	DKK3/DAB2/BMP2/BMP6/TKT	6	0.375
GO:0048268	BP	GO:0048268	clathrin coat	6/1414	16/18903	0.000721192	0.0043412	0.00278198	DAB2/FCHO2/PICALM/EPS15	6	0.375
GO:0060841	BP	GO:0060841	venous blood	6/1414	16/18903	0.000721192	0.0043412	0.00278198	SEMA3C/VEGFA/EFNB2/HEG1	6	0.375
GO:0070431	BP	GO:0070431	nucleotide-	6/1414	16/18903	0.000721192	0.0043412	0.00278198	HSPA1A/HSPA1B/NFKBIA/TL	6	0.375
GO:2001212	BP	GO:2001212	regulation of	6/1414	16/18903	0.000721192	0.0043412	0.00278198	RIN2/ADM/RAP1A/RAMP2/CD	6	0.375
GO:0002604	BP	GO:0002604	regulation of	5/1414	11/18903	0.000732914	0.0043757	0.00280404	CD74/CD68/FGL2/FCGR2B/T	5	0.454545454545455
GO:0032060	BP	GO:0032060	bleb assembly	5/1414	11/18903	0.000732914	0.0043757	0.00280404	PMP22/LPAR1/EMP3/EMP1/R	5	0.454545454545455
GO:0033212	BP	GO:0033212	iron import	5/1414	11/18903	0.000732914	0.0043757	0.00280404	SLC39A14/STEAP4/STEAP2/	5	0.454545454545455
GO:0042989	BP	GO:0042989	sequestering	5/1414	11/18903	0.000732914	0.0043757	0.00280404	SCIN/GSN/TMSB4X/TMSB10/	5	0.454545454545455
GO:0061418	BP	GO:0061418	regulation of	5/1414	11/18903	0.000732914	0.0043757	0.00280404	EGR1/RBPJ/VEGFA/CITED2/	5	0.454545454545455
GO:0071803	BP	GO:0071803	positive	5/1414	11/18903	0.000732914	0.0043757	0.00280404	LCP1/RHOA/MSN/ASAP1/FSC	5	0.454545454545455
GO:0098883	BP	GO:0098883	synapse	5/1414	11/18903	0.000732914	0.0043757	0.00280404	C1QC/C1QA/C1QB/ITGAM/TR	5	0.454545454545455
GO:1990440	BP	GO:1990440	positive	5/1414	11/18903	0.000732914	0.0043757	0.00280404	DDIT3/CEBPB/ATF4/HSPA5/	5	0.454545454545455
GO:0002707	BP	GO:0002707	negative	12/1414	56/18903	0.000745978	0.0044364	0.00284296	CD55/PTPRC/ARRB2/AHR/FC	12	0.214285714285714
GO:0110151	BP	GO:0110151	positive	12/1414	56/18903	0.000745978	0.0044364	0.00284296	PTN/FAM20C/BMP2/TGFB1/B	12	0.214285714285714
GO:2000630	BP	GO:2000630	positive	12/1414	56/18903	0.000745978	0.0044364	0.00284296	JUN/EGR1/FOS/KCNQ1OT1/E	12	0.214285714285714
GO:0032370	BP	GO:0032370	positive	16/1414	88/18903	0.000746888	0.0044364	0.00284296	DAB2/ABCA5/MAP2K6/NFKBI	16	0.181818181818182
GO:0043367	BP	GO:0043367	CD4-positive,	16/1414	88/18903	0.000746888	0.0044364	0.00284296	FOXP1/RUNX1/JUNB/ANXA1/	16	0.181818181818182
GO:0010758	BP	GO:0010758	regulation of	8/1414	28/18903	0.000770455	0.0045532	0.00291781	TRPV4/CSF1R/C3AR1/C5AR1	8	0.285714285714286
GO:0010818	BP	GO:0010818	T cell	8/1414	28/18903	0.000770455	0.0045532	0.00291781	CCL3/GPR183/CXCL16/ADAM	8	0.285714285714286
GO:0031342	BP	GO:0031342	negative	8/1414	28/18903	0.000770455	0.0045532	0.00291781	PTPRC/ARRB2/FCGR2B/NCKA	8	0.285714285714286
GO:0044331	BP	GO:0044331	cell-cell	8/1414	28/18903	0.000770455	0.0045532	0.00291781	BMP6/RGCC/VEGFA/AFDN/TJ	8	0.285714285714286
GO:1903672	BP	GO:1903672	positive	8/1414	28/18903	0.000770455	0.0045532	0.00291781	S100A1/FGF2/FGF1/VEGFA/	8	0.285714285714286
GO:0048644	BP	GO:0048644	muscle organ	15/1414	80/18903	0.000775216	0.0045721	0.00292990	COL3A1/RBPJ/TPM1/COL11A	15	0.1875
GO:1903201	BP	GO:1903201	regulation of	15/1414	80/18903	0.000775216	0.0045721	0.00292990	FOXP1/STK26/MMP3/SOD2/T	15	0.1875
GO:0050918	BP	GO:0050918	positive	13/1414	64/18903	0.000781298	0.0046033	0.00294991	GPNMB/FGF2/VEGFA/CCL3/C	13	0.203125
GO:0046328	BP	GO:0046328	regulation of	22/1414	141/18903	0.000783154	0.0046096	0.00295393	GADD45B/GADD45G/DNAJA1/	22	0.156028368794326
GO:0034284	BP	GO:0034284	response to	29/1414	207/18903	0.000790133	0.0046460	0.00297725	EGR1/SOX4/COL6A2/SLC29A	29	0.140096618357488
GO:0009410	BP	GO:0009410	response to xenobiotic	51/1414	432/18903	0.000798302488926089	0.0046893236836917	0.00300500571174701	COL1A1/MMP2/JUN/FOSB/FOS/SEMA3C/TIMP4/MAP2K6/S	51	0.118055555555556

GO:0002902	BP	GO:0002902	regulation of	7/1414	22/18903	0.000809016	0.0047331	0.00303311	FOXP1/ORMDL3/CD74/LYN/B	7	0.318181818181818
GO:0006907	BP	GO:0006907	pinocytosis	7/1414	22/18903	0.000809016	0.0047331	0.00303311	CAV1/MAPKAPK2/PYCARD/DO	7	0.318181818181818
GO:0010042	BP	GO:0010042	response to	7/1414	22/18903	0.000809016	0.0047331	0.00303311	FIBIN/SOD2/PTGS2/ATF4/H	7	0.318181818181818
GO:0030449	BP	GO:0030449	regulation of	7/1414	22/18903	0.000809016	0.0047331	0.00303311	CFH/A2M/CD55/CD59/VSIG4	7	0.318181818181818
GO:0010862	BP	GO:0010862	positive	11/1414	49/18903	0.000813026	0.0047518	0.00304509	DAB2/GDF10/BMP2/SDCBP/I	11	0.224489795918367
GO:0002709	BP	GO:0002709	regulation of	16/1414	89/18903	0.000848525	0.0049544	0.00317487	CD55/HSPD1/HLA-	16	0.179775280898876
GO:0001893	BP	GO:0001893	maternal	9/1414	35/18903	0.000849596	0.0049556	0.00317570	PTN/JUNB/STC2/SPP1/PTGS	9	0.257142857142857
GO:0010463	BP	GO:0010463	mesenchymal	10/1414	42/18903	0.000854547	0.0049746	0.00318783	LMNA/SIX1/PRRX1/ZEB1/BM	10	0.238095238095238
GO:0045429	BP	GO:0045429	positive	10/1414	42/18903	0.000854547	0.0049746	0.00318783	SOD2/PTGS2/HSP90AA1/KLF	10	0.238095238095238
GO:0035710	BP	GO:0035710	CD4-positive,	19/1414	115/18903	0.000860814	0.0050011	0.00320481	FOXP1/RUNX1/JUNB/CD55/A	19	0.165217391304348
GO:1990748	BP	GO:1990748	cellular	19/1414	115/18903	0.000860814	0.0050011	0.00320481	GPX8/H19/PRDX4/GPX3/SOD	19	0.165217391304348
GO:0019724	BP	GO:0019724	B cell	30/1414	218/18903	0.000871256	0.0050517	0.00323724	C1R/C1S/CD55/TGFB1/HSPD	30	0.137614678899083
GO:0044706	BP	GO:0044706	multi-	30/1414	218/18903	0.000871256	0.0050517	0.00323724	MMP2/GJA1/FOSB/FOS/VMP1	30	0.137614678899083
GO:0007565	BP	GO:0007565	female	27/1414	189/18903	0.000873268	0.0050583	0.00324149	MMP2/GJA1/FOSB/FOS/VMP1	27	0.142857142857143
GO:0045137	BP	GO:0045137	development	32/1414	238/18903	0.000892184	0.0051628	0.00330842	MMP2/PDGFRA/PDGFRB/COL9	32	0.134453781512605
GO:1902414	BP	GO:1902414	protein	17/1414	98/18903	0.000902282	0.0052160	0.00334255	ACTG1/ACTB/GPC6/HSPB1/L	17	0.173469387755102
GO:0071260	BP	GO:0071260	cellular	14/1414	73/18903	0.000909837	0.0052545	0.00336720	COL1A1/AQP1/PIEZO1/FGF2	14	0.191780821917808
GO:0055074	BP	GO:0055074	calcium ion	39/1414	309/18903	0.000916935	0.0052902	0.00339011	THY1/FLNA/NT5E/PLCG2/DD	39	0.12621359223301
GO:0044703	BP	GO:0044703	multi-	29/1414	209/18903	0.000922495	0.0053118	0.00340394	MMP2/GJA1/FOSB/FOS/VMP1	29	0.138755980861244
GO:0050807	BP	GO:0050807	regulation of	29/1414	209/18903	0.000922495	0.0053118	0.00340394	THBS2/TUBB/TUBA1A/PTPRD	29	0.138755980861244
GO:0071322	BP	GO:0071322	cellular	23/1414	152/18903	0.000928921	0.0053435	0.00342426	ZFP36L1/SOX4/MAP2K6/SLC	23	0.151315789473684
GO:0006959	BP	GO:0006959	humoral	40/1414	320/18903	0.000958270	0.0055041	0.00352715	C1R/RBPJ/NOTCH2/RPL39/T	40	0.125
GO:0072009	BP	GO:0072009	nephron	19/1414	116/18903	0.000958719	0.0055041	0.00352715	AQP1/SIX1/NOTCH2/GLI3/H	19	0.163793103448276
GO:0006029	BP	GO:0006029	proteoglycan	16/1414	90/18903	0.000961681	0.0055066	0.00352878	DSEL/SULF2/DSE/COL2A1/C	16	0.177777777777778
GO:0010586	BP	GO:0010586	miRNA	16/1414	90/18903	0.000961681	0.0055066	0.00352878	JUN/EGR1/FOS/KCNQ1OT1/E	16	0.177777777777778
GO:0006022	BP	GO:0006022	aminoglycan	21/1414	134/18903	0.000961994	0.0055066	0.00352878	PDGFRB/DSEL/CHI3L1/DSE/	21	0.156716417910448
GO:0043280	BP	GO:0043280	positive	20/1414	125/18903	0.000965888	0.0055235	0.00353959	GSN/CFLAR/CYCS/RPS3/HSP	20	0.16
GO:0038084	BP	GO:0038084	vascular	11/1414	50/18903	0.000972914	0.0055474	0.00355489	PDGFRA/PDGFRB/SMOC2/NRP	11	0.22
GO:0061082	BP	GO:0061082	myeloid	11/1414	50/18903	0.000972914	0.0055474	0.00355489	TWIST1/PLCG2/TGFB1/RABG	11	0.22
GO:1904707	BP	GO:1904707	positive	11/1414	50/18903	0.000972914	0.0055474	0.00355489	MMP2/GJA1/JUN/FGF2/GNAI	11	0.22
GO:0010575	BP	GO:0010575	positive	8/1414	29/18903	0.000994914	0.0056507	0.00362111	SULF2/TGFB1/PTGS2/ATF4/	8	0.275862068965517
GO:0010955	BP	GO:0010955	negative	8/1414	29/18903	0.000994914	0.0056507	0.00362111	GAS1/SERPINE2/NOL3/CTSZ	8	0.275862068965517
GO:0034123	BP	GO:0034123	positive	8/1414	29/18903	0.000994914	0.0056507	0.00362111	PELI1/CAV1/CD14/CYBA/RT	8	0.275862068965517
GO:1903318	BP	GO:1903318	negative	8/1414	29/18903	0.000994914	0.0056507	0.00362111	GAS1/SERPINE2/NOL3/CTSZ	8	0.275862068965517
GO:1904062	BP	GO:1904062	regulation of cation	47/1414	394/18903	0.001008229 78439131	0.0057208 213349751	0.00366600 85647896	THY1/TWIST1/FLNA/VMP1/F HL1/ANK3/NDUFA4/PLCG2/G	47	0.119289340101523

GO:0046209	BP	GO:0046209	nitric oxide	15/1414	82/18903	0.001011638	0.0057345	0.00367482	SOD2/PTGS2/CAV1/HSP90AA	15	0.182926829268293
GO:0032755	BP	GO:0032755	positive	17/1414	99/18903	0.001014914	0.0057475	0.00368314	TWIST1/PLCG2/TRPV4/SELE	17	0.171717171717172
GO:0061005	BP	GO:0061005	cell	12/1414	58/18903	0.001037090	0.0058465	0.00374660	NOTCH2/GLI3/HES1/MAGI2/	12	0.206896551724138
GO:0021879	BP	GO:0021879	forebrain	10/1414	43/18903	0.001039873	0.0058465	0.00374660	HES1/UBB/NRP2/INHBA/FGF	10	0.232558139534884
GO:0033574	BP	GO:0033574	response to	10/1414	43/18903	0.001039873	0.0058465	0.00374660	FOXP1/SPP1/CFLAR/CA9/NC	10	0.232558139534884
GO:0060412	BP	GO:0060412	ventricular	10/1414	43/18903	0.001039873	0.0058465	0.00374660	SOX4/RBPJ/HES1/FGFRL1/F	10	0.232558139534884
GO:0071364	BP	GO:0071364	cellular	10/1414	43/18903	0.001039873	0.0058465	0.00374660	COL1A1/ZFP36L1/FOS/DAB2	10	0.232558139534884
GO:0071548	BP	GO:0071548	response to	10/1414	43/18903	0.001039873	0.0058465	0.00374660	AQP1/FIBIN/CFLAR/EIF4E/	10	0.232558139534884
GO:0002921	BP	GO:0002921	negative	6/1414	17/18903	0.001044427	0.0058465	0.00374660	A2M/CD55/CD59/VSIG4/FCG	6	0.352941176470588
GO:0010566	BP	GO:0010566	regulation of	6/1414	17/18903	0.001044427	0.0058465	0.00374660	EGR1/DKK3/DAB2/BMP2/BMP	6	0.352941176470588
GO:0010763	BP	GO:0010763	positive	6/1414	17/18903	0.001044427	0.0058465	0.00374660	AQP1/TGFB1/SLC8A1/THBS1	6	0.352941176470588
GO:0072224	BP	GO:0072224	metanephric	6/1414	17/18903	0.001044427	0.0058465	0.00374660	EGR1/PDGFRA/AQP1/PDGFRB	6	0.352941176470588
GO:1901550	BP	GO:1901550	regulation of	6/1414	17/18903	0.001044427	0.0058465	0.00374660	VEGFA/ROCK1/VCL/CDH5/CL	6	0.352941176470588
GO:1903140	BP	GO:1903140	regulation of	6/1414	17/18903	0.001044427	0.0058465	0.00374660	VEGFA/ROCK1/VCL/CDH5/CL	6	0.352941176470588
GO:0050766	BP	GO:0050766	positive	14/1414	74/18903	0.001046255	0.0058512	0.00374956	PLCG2/FCER1G/PTPRC/CLEC	14	0.189189189189189
GO:0090263	BP	GO:0090263	positive	18/1414	108/18903	0.001048810	0.0058598	0.00375511	COL1A1/SOX4/ZEB2/RSPO2/	18	0.166666666666667
GO:0050854	BP	GO:0050854	regulation of	13/1414	66/18903	0.001057896	0.0058916	0.00377544	THY1/FOXP1/RPS3/LAPTM5/	13	0.196969696969697
GO:0006026	BP	GO:0006026	aminoglycan	9/1414	36/18903	0.001058529	0.0058916	0.00377544	CHI3L1/CHI3L2/FGF2/TGFB	9	0.25
GO:0035909	BP	GO:0035909	aorta	9/1414	36/18903	0.001058529	0.0058916	0.00377544	COL3A1/PDGFRB/SOX4/SIX1	9	0.25
GO:0071711	BP	GO:0071711	basement	9/1414	36/18903	0.001058529	0.0058916	0.00377544	COL3A1/SPINT2/CAV1/CTSS	9	0.25
GO:0071887	BP	GO:0071887	leukocyte	19/1414	117/18903	0.001066001	0.0059275	0.00379847	FOXP1/GLI3/ANXA1/CTSL/P	19	0.162393162393162
GO:0002822	BP	GO:0002822	regulation of	26/1414	182/18903	0.001077443	0.0059854	0.00383559	JUNB/CD55/TGFB1/ANXA1/H	26	0.142857142857143
GO:0030901	BP	GO:0030901	midbrain	16/1414	91/18903	0.001087378	0.0060348	0.00386727	ACTB/S100A1/HES1/NDRG2/	16	0.175824175824176
GO:0048143	BP	GO:0048143	astrocyte	7/1414	23/18903	0.001088506	0.0060354	0.00386760	NR1D1/C1QA/C5AR1/TREM2/	7	0.304347826086957
GO:0002429	BP	GO:0002429	immune	39/1414	312/18903	0.001101439	0.0060955	0.00390613	THY1/FOXP1/PLCG2/PDE4B/	39	0.125
GO:0002757	BP	GO:0002757	immune	39/1414	312/18903	0.001101439	0.0060955	0.00390613	THY1/FOXP1/PLCG2/PDE4B/	39	0.125
GO:0050848	BP	GO:0050848	regulation of	15/1414	83/18903	0.001151006	0.0063577	0.00407418	RCAN1/PLCG2/SELENOK/CAM	15	0.180722891566265
GO:2001057	BP	GO:2001057	reactive	15/1414	83/18903	0.001151006	0.0063577	0.00407418	SOD2/PTGS2/CAV1/HSP90AA	15	0.180722891566265
GO:0045165	BP	GO:0045165	cell fate	36/1414	282/18903	0.001153226	0.0063640	0.00407818	SIX1/RBPJ/PRRX1/NOTCH2/	36	0.127659574468085
GO:0002887	BP	GO:0002887	negative	5/1414	12/18903	0.001179256	0.0064648	0.00414279	RABGEF1/SPI1/CD84/FCGR2	5	0.416666666666667
GO:0003157	BP	GO:0003157	endocardium	5/1414	12/18903	0.001179256	0.0064648	0.00414279	RBPJ/STK4/SOX18/KDR/SOX	5	0.416666666666667
GO:0021979	BP	GO:0021979	hypothalamus	5/1414	12/18903	0.001179256	0.0064648	0.00414279	UBB/NRP2/NDNF/NRP1/SEMA	5	0.416666666666667
GO:0045602	BP	GO:0045602	negative	5/1414	12/18903	0.001179256	0.0064648	0.00414279	ZEB1/VEGFA/JAG1/NOTCH4/	5	0.416666666666667
GO:0061309	BP	GO:0061309	cardiac	5/1414	12/18903	0.001179256	0.0064648	0.00414279	TWIST1/SEMA3C/HES1/CDC4	5	0.416666666666667
GO:0061795	BP	GO:0061795	Golgi lumen	5/1414	12/18903	0.001179256	0.0064648	0.00414279	ATP6V0C/ATP6V0B/ATP6V1F	5	0.416666666666667
GO:1904667	BP	GO:1904667	negative	5/1414	12/18903	0.001179256	0.0064648	0.00414279	RPS20/RPS15/RPS7/RPL11/	5	0.416666666666667

GO:0009205	BP	GO:0009205	purine	32/1414	242/18903	0.001181803	0.0064727	0.00414784	NT5E/H19/NDUFB1/ATP5ME/	32	0.132231404958678
GO:0002718	BP	GO:0002718	regulation of	19/1414	118/18903	0.001183375	0.0064752	0.00414946	TWIST1/PLCG2/CD55/TGFB1	19	0.161016949152542
GO:0006816	BP	GO:0006816	calcium ion transport	51/1414	440/18903	0.001200222 48505659	0.0065612 912421134	0.00420459 729140823	THY1/PDGFRB/FLNA/VMP1/P LCG2/HES1/GEM/DDIT3/STC	51	0.115909090909091
GO:0046578	BP	GO:0046578	regulation of	27/1414	193/18903	0.001201929	0.0065644	0.00420663	COL3A1/PDGFRB/NOTCH2/SQ	27	0.139896373056995
GO:0001656	BP	GO:0001656	metanephros	16/1414	92/18903	0.001226699	0.0066809	0.00428130	EGR1/PDGFRA/AQP1/PDGFRB	16	0.173913043478261
GO:0009791	BP	GO:0009791	post-	16/1414	92/18903	0.001226699	0.0066809	0.00428130	SEMA3C/FBN1/EFEMP1/SCUB	16	0.173913043478261
GO:0032273	BP	GO:0032273	positive	16/1414	92/18903	0.001226699	0.0066809	0.00428130	HSPA1A/HSPA1B/RPS3/HSP9	16	0.173913043478261
GO:0042771	BP	GO:0042771	intrinsic	10/1414	44/18903	0.001256808	0.0068258	0.00437413	CDKN1A/NUPR1/CD44/DDIT4	10	0.227272727272727
GO:1904407	BP	GO:1904407	positive	10/1414	44/18903	0.001256808	0.0068258	0.00437413	SOD2/PTGS2/HSP90AA1/KLF	10	0.227272727272727
GO:1905521	BP	GO:1905521	regulation of	10/1414	44/18903	0.001256808	0.0068258	0.00437413	TRPV4/CSF1R/CCL3/C3AR1/	10	0.227272727272727
GO:0008406	BP	GO:0008406	gonad	31/1414	233/18903	0.001264771	0.0068575	0.00439442	MMP2/PDGFRA/PDGFRB/COL9	31	0.133047210300429
GO:0021700	BP	GO:0021700	developmental	38/1414	304/18903	0.001266165	0.0068575	0.00439442	MMP2/RBPJ/HES1/DDIT3/ZB	38	0.125
GO:0051047	BP	GO:0051047	positive	38/1414	304/18903	0.001266165	0.0068575	0.00439442	AQP1/SOX4/DAB2/MAP2K6/R	38	0.125
GO:0048562	BP	GO:0048562	embryonic	37/1414	294/18903	0.001288452	0.0069717	0.00446762	MAFB/PDGFRA/TWIST1/SIX1	37	0.125850340136054
GO:0050868	BP	GO:0050868	negative	20/1414	128/18903	0.001304178	0.0070502	0.00451796	GPNMB/RUNX1/GLI3/LAG3/S	20	0.15625
GO:0010092	BP	GO:0010092	specification	9/1414	37/18903	0.001307152	0.0070598	0.00452407	SIX1/RBPJ/GLI3/BMP2/FGF	9	0.243243243243243
GO:0032386	BP	GO:0032386	regulation of	41/1414	336/18903	0.001333043	0.0071930	0.00460941	DAB2/FLNA/GAS1/GLI3/ANK	41	0.12202380952381
GO:0030516	BP	GO:0030516	regulation of	16/1414	93/18903	0.001380789	0.0074437	0.00477009	SEMA3C/NTN1/FN1/VEGFA/A	16	0.172043010752688
GO:0030879	BP	GO:0030879	mammary gland	21/1414	138/18903	0.001410389	0.0075959	0.00486762	LBH/CDO1/GLI3/NTN1/SLC2	21	0.152173913043478
GO:0002886	BP	GO:0002886	regulation of	12/1414	60/18903	0.001416832	0.0075959	0.00486762	RABGEF1/TYROBP/VAMP8/IT	12	0.2
GO:0043407	BP	GO:0043407	negative	12/1414	60/18903	0.001416832	0.0075959	0.00486762	DNAJA1/BMP2/SPRY2/CAV1/	12	0.2
GO:0045599	BP	GO:0045599	negative	12/1414	60/18903	0.001416832	0.0075959	0.00486762	ID4/FOXO1/DDIT3/TRPV4/S	12	0.2
GO:0055008	BP	GO:0055008	cardiac	12/1414	60/18903	0.001416832	0.0075959	0.00486762	RBPJ/TPM1/COL11A1/BMP2/	12	0.2
GO:1903670	BP	GO:1903670	regulation of	12/1414	60/18903	0.001416832	0.0075959	0.00486762	S100A1/FGF2/FGF1/VEGFA/	12	0.2
GO:0034504	BP	GO:0034504	protein	38/1414	306/18903	0.001427715	0.0076472	0.00490050	COL1A1/LMNA/SIX1/FLNA/G	38	0.124183006535948
GO:0051928	BP	GO:0051928	positive	20/1414	129/18903	0.001437366	0.0076836	0.00492382	THY1/PDGFRB/VMP1/PLCG2/	20	0.155038759689922
GO:0003181	BP	GO:0003181	atrioventricu	7/1414	24/18903	0.001438461	0.0076836	0.00492382	TWIST1/SOX4/BMP2/CCN1/E	7	0.291666666666667
GO:0050855	BP	GO:0050855	regulation of	7/1414	24/18903	0.001438461	0.0076836	0.00492382	FOXP1/FCGR2B/LYN/CMTM3/	7	0.291666666666667
GO:0022900	BP	GO:0022900	electron	25/1414	176/18903	0.001442612	0.0076987	0.00493351	P4HA2/NDUFA4/NDUFB1/UQC	25	0.142045454545455
GO:0042177	BP	GO:0042177	negative	18/1414	111/18903	0.001449263	0.0077246	0.00495010	TIMP2/FLNA/TIMP4/SERPIN	18	0.162162162162162
GO:0002367	BP	GO:0002367	cytokine	19/1414	120/18903	0.001451436	0.0077246	0.00495010	TWIST1/PLCG2/CD55/TGFB1	19	0.158333333333333
GO:0002821	BP	GO:0002821	positive	19/1414	120/18903	0.001451436	0.0077246	0.00495010	CD55/TGFB1/AKIRIN2/HSPD	19	0.158333333333333
GO:0003159	BP	GO:0003159	morphogenesis	6/1414	18/18903	0.001468203	0.0077502	0.00496650	FOXP1/RBPJ/FGF1/CXCR4/R	6	0.333333333333333
GO:0034138	BP	GO:0034138	toll-like	6/1414	18/18903	0.001468203	0.0077502	0.00496650	PELI1/CAV1/UNC93B1/COLE	6	0.333333333333333
GO:0043117	BP	GO:0043117	positive	6/1414	18/18903	0.001468203	0.0077502	0.00496650	TRPV4/TGFB1/BMP6/VEGFA/	6	0.333333333333333

GO:0048569	BP	GO:0048569	post-	6/1414	18/18903	0.001468203	0.0077502	0.00496650	FBN1/EFEMP1/VEGFA/KLF4/	6	0.333333333333333
GO:0061154	BP	GO:0061154	endothelial	6/1414	18/18903	0.001468203	0.0077502	0.00496650	FOXP1/RBPJ/FGF1/CXCR4/R	6	0.333333333333333
GO:0086103	BP	GO:0086103	G protein-	6/1414	18/18903	0.001468203	0.0077502	0.00496650	PDE4B/CAV1/CDC42/GNAI2/	6	0.333333333333333
GO:0150078	BP	GO:0150078	positive	6/1414	18/18903	0.001468203	0.0077502	0.00496650	PLCG2/NUPR1/CCL3/TREM2/	6	0.333333333333333
GO:2000641	BP	GO:2000641	regulation of	6/1414	18/18903	0.001468203	0.0077502	0.00496650	DAB2/EZR/MSN/RDX/SNX3/C	6	0.333333333333333
GO:2000811	BP	GO:2000811	negative	6/1414	18/18903	0.001468203	0.0077502	0.00496650	PIK3R3/CAV1/ITGA5/MCL1/	6	0.333333333333333
GO:0034767	BP	GO:0034767	positive	26/1414	186/18903	0.001483270	0.0078227	0.00501293	THY1/FLNA/VMP1/ANK3/NDU	26	0.139784946236559
GO:0030501	BP	GO:0030501	positive	10/1414	45/18903	0.001509222	0.0079308	0.00508226	PTN/FAM20C/BMP2/TGFB1/B	10	0.222222222222222
GO:0030890	BP	GO:0030890	positive	10/1414	45/18903	0.001509222	0.0079308	0.00508226	CDKN1A/PELI1/CD74/PTPRC	10	0.222222222222222
GO:1904646	BP	GO:1904646	cellular	10/1414	45/18903	0.001509222	0.0079308	0.00508226	GJA1/VCAM1/ICAM1/FCGR2B	10	0.222222222222222
GO:2000516	BP	GO:2000516	positive	10/1414	45/18903	0.001509222	0.0079308	0.00508226	CD55/ANXA1/NFKBIZ/HLA-	10	0.222222222222222
GO:1903035	BP	GO:1903035	negative	16/1414	94/18903	0.001550857	0.0081423	0.00521776	PDGFRA/FAP/SPP1/SERPINE	16	0.170212765957447
GO:0034121	BP	GO:0034121	regulation of	14/1414	77/18903	0.001562503	0.0081961	0.00525222	NR1D1/PELI1/BIRC2/CAV1/	14	0.181818181818182
GO:0032612	BP	GO:0032612	interleukin-1	20/1414	130/18903	0.001581961	0.0082832	0.00530808	EGR1/FOXP1/S100A13/SAA1	20	0.153846153846154
GO:0032652	BP	GO:0032652	regulation of	20/1414	130/18903	0.001581961	0.0082832	0.00530808	EGR1/FOXP1/S100A13/SAA1	20	0.153846153846154
GO:0001916	BP	GO:0001916	positive	8/1414	31/18903	0.001599317	0.0083441	0.00534708	HLA-DRB1/HLA-	8	0.258064516129032
GO:0010039	BP	GO:0010039	response to	8/1414	31/18903	0.001599317	0.0083441	0.00534708	SLC40A1/TF/BMP6/MAP1LC3	8	0.258064516129032
GO:0060390	BP	GO:0060390	regulation of	8/1414	31/18903	0.001599317	0.0083441	0.00534708	DAB2/CILP/BMP2/TGFB1/BM	8	0.258064516129032
GO:0010742	BP	GO:0010742	macrophage	9/1414	38/18903	0.001600737	0.0083441	0.00534708	ABCA5/PLA2G2A/NFKBIA/SE	9	0.236842105263158
GO:0048009	BP	GO:0048009	insulin-like	9/1414	38/18903	0.001600737	0.0083441	0.00534708	IGFBP4/CILP/IGFBP6/PIK3	9	0.236842105263158
GO:0002700	BP	GO:0002700	regulation of	26/1414	187/18903	0.001603213	0.0083495	0.00535057	TWIST1/PLCG2/RBP4/XBP1/	26	0.13903743315508
GO:0014015	BP	GO:0014015	positive	13/1414	69/18903	0.001622703	0.0084411	0.00540921	NTN1/HES1/PTN/SERPINE2/	13	0.188405797101449
GO:0009141	BP	GO:0009141	nucleoside	34/1414	267/18903	0.001623678	0.0084411	0.00540921	NT5E/H19/NDUFB1/ATP5ME/	34	0.127340823970037
GO:0010001	BP	GO:0010001	glial cell	30/1414	227/18903	0.001668137	0.0086643	0.00555228	MXRA8/SOX4/ID4/GLI3/TSP	30	0.13215859030837
GO:0033273	BP	GO:0033273	response to	15/1414	86/18903	0.001669593	0.0086643	0.00555228	COL1A1/POSTN/STC2/SPP1/	15	0.174418604651163
GO:0002705	BP	GO:0002705	positive	21/1414	140/18903	0.001694659	0.0087866	0.00563062	CADM1/LAG3/PLCG2/CD55/T	21	0.15
GO:0048592	BP	GO:0048592	eye	23/1414	159/18903	0.001718444	0.0089020	0.00570458	COL5A1/COL5A2/THY1/AQP1	23	0.144654088050314
GO:1900407	BP	GO:1900407	regulation of	16/1414	95/18903	0.001738175	0.0089962	0.00576496	FOXP1/H19/STK26/MMP3/SO	16	0.168421052631579
GO:0000041	BP	GO:0000041	transition	17/1414	104/18903	0.001773980	0.0091653	0.00587329	SLC40A1/MELTF/TF/SLC39A	17	0.163461538461538
GO:1902882	BP	GO:1902882	regulation of	17/1414	104/18903	0.001773980	0.0091653	0.00587329	FOXP1/H19/STK26/MMP3/SO	17	0.163461538461538
GO:0043491	BP	GO:0043491	protein	29/1414	218/18903	0.001785898	0.0092187	0.00590752	ZFP36L1/PIK3R3/CHI3L1/H	29	0.13302752293578
GO:0098876	BP	GO:0098876	vesicle-	22/1414	150/18903	0.001789853	0.0092309	0.00591537	ANK3/STEAP2/RAB13/ARL4C	22	0.146666666666667
GO:0045916	BP	GO:0045916	negative	5/1414	13/18903	0.001798832	0.0092407	0.00592162	A2M/CD55/CD59/VSIG4/SER	5	0.384615384615385
GO:0060213	BP	GO:0060213	positive	5/1414	13/18903	0.001798832	0.0092407	0.00592162	TNRC6A/ZFP36/BTG2/TOB1/	5	0.384615384615385
GO:0060670	BP	GO:0060670	branching	5/1414	13/18903	0.001798832	0.0092407	0.00592162	SOCS3/SPINT2/ADM/FGFR2/	5	0.384615384615385
GO:1903054	BP	GO:1903054	negative	5/1414	13/18903	0.001798832	0.0092407	0.00592162	ANTXR1/FAP/CHADL/TGFB1/	5	0.384615384615385

GO:0055010	BP	GO:0055010	ventricular	10/1414	46/18903	0.001801250	0.0092407	0.00592162	RBPJ/TPM1/COL11A1/TGFB1	10	0.217391304347826
GO:1904752	BP	GO:1904752	regulation of	10/1414	46/18903	0.001801250	0.0092407	0.00592162	TPM1/DOCK4/MEF2C/GNA13/	10	0.217391304347826
GO:0090090	BP	GO:0090090	negative	21/1414	141/18903	0.001854172	0.0095038	0.00609024	IGFBP4/EGR1/DKK3/DAB2/G	21	0.148936170212766
GO:0003148	BP	GO:0003148	outflow tract	7/1414	25/18903	0.001870292	0.0095278	0.00610564	SEMA3C/NRP2/FGFR2/NRP1/	7	0.28
GO:0046641	BP	GO:0046641	positive	7/1414	25/18903	0.001870292	0.0095278	0.00610564	CD55/PTPRC/IL18/HLA-	7	0.28
GO:0046697	BP	GO:0046697	decidualizati	7/1414	25/18903	0.001870292	0.0095278	0.00610564	PTN/JUNB/STC2/SPP1/PTGS	7	0.28
GO:0046885	BP	GO:0046885	regulation of	7/1414	25/18903	0.001870292	0.0095278	0.00610564	EGR1/DKK3/DAB2/STC2/BMP	7	0.28
GO:0086064	BP	GO:0086064	cell	7/1414	25/18903	0.001870292	0.0095278	0.00610564	GJA1/CALM2/CAV1/ATP1B1/	7	0.28
GO:0098581	BP	GO:0098581	detection of	7/1414	25/18903	0.001870292	0.0095278	0.00610564	HLA-	7	0.28
GO:2000209	BP	GO:2000209	regulation of	7/1414	25/18903	0.001870292	0.0095278	0.00610564	PIK3R3/CAV1/ITGA5/MCL1/	7	0.28
GO:0008543	BP	GO:0008543	fibroblast	15/1414	87/18903	0.001880798	0.0095730	0.00613457	SMOC2/SULF2/FGFRL1/FGFR	15	0.172413793103448
GO:0009199	BP	GO:0009199	ribonucleosid	32/1414	249/18903	0.001888092	0.0096017	0.00615299	NT5E/H19/NDUFB1/ATP5ME/	32	0.1285140562249
GO:0042149	BP	GO:0042149	cellular	11/1414	54/18903	0.001893385	0.0096058	0.00615563	XBP1/UPP1/ATF4/HSPA5/PM	11	0.203703703703704
GO:0045778	BP	GO:0045778	positive	11/1414	54/18903	0.001893385	0.0096058	0.00615563	PTN/ZBTB16/FAM20C/BMP2/	11	0.203703703703704
GO:0120032	BP	GO:0120032	regulation of	27/1414	199/18903	0.001893841	0.0096058	0.00615563	CAPZB/DPYSL3/PIK3R1/ICA	27	0.135678391959799
GO:0061614	BP	GO:0061614	miRNA	12/1414	62/18903	0.001904552	0.0096434	0.00617970	JUN/EGR1/FOS/ETS1/BMP2/	12	0.193548387096774
GO:0061951	BP	GO:0061951	establishment	12/1414	62/18903	0.001904552	0.0096434	0.00617970	ANK3/AFDN/RAB31/RAB10/A	12	0.193548387096774
GO:0048588	BP	GO:0048588	developmental	30/1414	229/18903	0.001913032	0.0096779	0.00620183	FOXP1/SEMA3C/NTN1/SPP1/	30	0.131004366812227
GO:0034250	BP	GO:0034250	positive	24/1414	170/18903	0.001931068	0.0097607	0.00625487	SOX4/LARP6/RPS4X/PPP1R1	24	0.141176470588235
GO:0045807	BP	GO:0045807	positive	16/1414	96/18903	0.001944082	0.0098052	0.00628339	DAB2/PLCG2/TF/MAGI2/ANX	16	0.166666666666667
GO:0032570	BP	GO:0032570	response to	9/1414	39/18903	0.001944915	0.0098052	0.00628339	FOSB/FOS/TGFB1/CAV1/TXN	9	0.230769230769231
GO:0090077	BP	GO:0090077	foam cell	9/1414	39/18903	0.001944915	0.0098052	0.00628339	ABCA5/PLA2G2A/NFKBIA/SE	9	0.230769230769231
GO:0030203	BP	GO:0030203	glycosaminogl	19/1414	123/18903	0.001949245	0.0098101	0.00628651	PDGFRB/DSEL/DSE/XYLT1/C	19	0.154471544715447
GO:0097237	BP	GO:0097237	cellular	19/1414	123/18903	0.001949245	0.0098101	0.00628651	GPX8/H19/PRDX4/GPX3/SOD	19	0.154471544715447
GO:0035265	BP	GO:0035265	organ growth	25/1414	180/18903	0.001979319	0.0099529	0.00637800	FOXP1/PDGFRB/ECM1/RSPO2	25	0.138888888888889
GO:0003180	BP	GO:0003180	aortic valve	8/1414	32/18903	0.001994490	0.0099861	0.00639930	TWIST1/SNAI1/TGFB1/RB1/	8	0.25
GO:0007435	BP	GO:0007435	salivary	8/1414	32/18903	0.001994490	0.0099861	0.00639930	SEMA3C/TGM2/TGFB1/FGFR2	8	0.25
GO:0010644	BP	GO:0010644	cell	8/1414	32/18903	0.001994490	0.0099861	0.00639930	GJA1/ANK3/CALM2/CAV1/AT	8	0.25
GO:0048710	BP	GO:0048710	regulation of	8/1414	32/18903	0.001994490	0.0099861	0.00639930	ID4/HES1/NR1D1/SERPINE2	8	0.25
GO:0060674	BP	GO:0060674	placenta	8/1414	32/18903	0.001994490	0.0099861	0.00639930	SOCS3/RBPJ/NOTCH2/HES1/	8	0.25
GO:0000028	BP	GO:0000028	ribosomal	6/1414	19/18903	0.002011224	0.0099996	0.00640793	RPL38/RPS27L/RPS27/RPS1	6	0.315789473684211
GO:0002283	BP	GO:0002283	neutrophil	6/1414	19/18903	0.002011224	0.0099996	0.00640793	TYROBP/FCER1G/ITGB2/SPI	6	0.315789473684211
GO:0060977	BP	GO:0060977	coronary	6/1414	19/18903	0.002011224	0.0099996	0.00640793	PDGFRB/FGF2/VEGFA/TGFBR	6	0.315789473684211
GO:0061298	BP	GO:0061298	retina	6/1414	19/18903	0.002011224	0.0099996	0.00640793	PDGFRA/PDGFRB/NRP1/CYP1	6	0.315789473684211
GO:0071800	BP	GO:0071800	podosome	6/1414	19/18903	0.002011224	0.0099996	0.00640793	GSN/LCP1/RHOA/MSN/ASAP1	6	0.315789473684211
GO:0097284	BP	GO:0097284	hepatocyte	6/1414	19/18903	0.002011224	0.0099996	0.00640793	H19/GSN/CFLAR/RB1/STK4/	6	0.315789473684211

GO:2001185	BP	GO:2001185	regulation of	6/1414	19/18903	0.002011224	0.0099996	0.00640793	RUNX1/NCKAP1L/HLA-	6	0.315789473684211
GO:0002437	BP	GO:0002437	inflammatory	14/1414	79/18903	0.002012735	0.0099996	0.00640793	RBPJ/NOTCH2/PSMB4/A2M/H	14	0.177215189873418
GO:0071695	BP	GO:0071695	anatomical	32/1414	250/18903	0.002014056	0.0099996	0.00640793	MMP2/RBPJ/HES1/DDIT3/ZB	32	0.128
GO:0043433	BP	GO:0043433	negative	26/1414	190/18903	0.002014322	0.0099996	0.00640793	TWIST1/FLNA/ID3/HES1/DD	26	0.136842105263158
GO:1904064	BP	GO:1904064	positive	24/1414	171/18903	0.002090985	0.0103678	0.00664388	THY1/FLNA/VMP1/ANK3/PLC	24	0.140350877192982
GO:0002244	BP	GO:0002244	hematopoietic	20/1414	133/18903	0.002092048	0.0103678	0.00664388	PDGFRA/SOX4/HES1/ZFP36/	20	0.150375939849624
GO:0002312	BP	GO:0002312	B cell	15/1414	88/18903	0.002113793	0.0104666	0.00670724	LGALS1/NOTCH2/PLCG2/ITM	15	0.170454545454545
GO:0070849	BP	GO:0070849	response to	10/1414	47/18903	0.002137280	0.0105650	0.00677027	COL1A1/ZFP36L1/FOS/DAB2	10	0.212765957446809
GO:1902895	BP	GO:1902895	positive	10/1414	47/18903	0.002137280	0.0105650	0.00677027	JUN/EGR1/FOS/ETS1/BMP2/	10	0.212765957446809
GO:0072089	BP	GO:0072089	stem cell	19/1414	124/18903	0.002144297	0.0105907	0.00678675	GJA1/ZFP36L1/RBPJ/PRRX1	19	0.153225806451613
GO:0032414	BP	GO:0032414	positive	18/1414	115/18903	0.002178462	0.0107503	0.00688905	VMP1/ANK3/NDUFA4/PLCG2/	18	0.156521739130435
GO:0001841	BP	GO:0001841	neural tube	17/1414	106/18903	0.002189134	0.0107893	0.00691404	TWIST1/SOX4/CTHRC1/SPIN	17	0.160377358490566
GO:0060491	BP	GO:0060491	regulation of	27/1414	201/18903	0.002190063	0.0107893	0.00691404	CAPZB/DPYSL3/PIK3R1/ICA	27	0.134328358208955
GO:0070542	BP	GO:0070542	response to	12/1414	63/18903	0.002195601	0.0108075	0.00692567	FOXO1/ID3/HES1/PTGS2/PI	12	0.19047619047619
GO:0002931	BP	GO:0002931	response to	11/1414	55/18903	0.002209666	0.0108401	0.00694659	EGR1/RCAN1/MAP2K6/SQSTM	11	0.2
GO:0003229	BP	GO:0003229	ventricular	11/1414	55/18903	0.002209666	0.0108401	0.00694659	RBPJ/TPM1/COL11A1/TGFB1	11	0.2
GO:0043525	BP	GO:0043525	positive	11/1414	55/18903	0.002209666	0.0108401	0.00694659	DDIT3/NUPR1/ATF4/TYROBP	11	0.2
GO:2000107	BP	GO:2000107	negative	11/1414	55/18903	0.002209666	0.0108401	0.00694659	FOXP1/ORMDL3/CD74/HCLS1	11	0.2
GO:0010324	BP	GO:0010324	membrane	21/1414	143/18903	0.002211668	0.0108408	0.00694704	PLCG2/GSN/AIF1/MSR1/ITG	21	0.146853146853147
GO:1990138	BP	GO:1990138	neuron	24/1414	172/18903	0.002262044	0.0110785	0.00709931	SEMA3C/NTN1/NRP2/FN1/VE	24	0.13953488372093
GO:0019932	BP	GO:0019932	second-	38/1414	314/18903	0.002267307	0.0110949	0.00710986	AQP1/RCAN1/PLCG2/RASD1/	38	0.121019108280255
GO:0001953	BP	GO:0001953	negative	9/1414	40/18903	0.002345664	0.0114304	0.00732485	APOD/PIK3R1/THBS1/SEMA3	9	0.225
GO:0010863	BP	GO:0010863	positive	9/1414	40/18903	0.002345664	0.0114304	0.00732485	PDGFRA/PDGFRB/FGFR1/FGF	9	0.225
GO:0032965	BP	GO:0032965	regulation of	9/1414	40/18903	0.002345664	0.0114304	0.00732485	PDGFRB/RUNX1/INHBA/LARP	9	0.225
GO:0042307	BP	GO:0042307	positive	9/1414	40/18903	0.002345664	0.0114304	0.00732485	FLNA/GLI3/PIK3R1/RAN/TG	9	0.225
GO:0098751	BP	GO:0098751	bone cell	9/1414	40/18903	0.002345664	0.0114304	0.00732485	FOXP1/FLNA/FBN1/NOTCH2/	9	0.225
GO:0033622	BP	GO:0033622	integrin	7/1414	26/18903	0.002396143	0.0116278	0.00745135	PIEZO1/FN1/PLEK/FERMT3/	7	0.269230769230769
GO:0035751	BP	GO:0035751	regulation of	7/1414	26/18903	0.002396143	0.0116278	0.00745135	ATP6V0C/ATP6V0B/GRN/PPT	7	0.269230769230769
GO:0035994	BP	GO:0035994	response to	7/1414	26/18903	0.002396143	0.0116278	0.00745135	JUN/FOS/NFKBIA/GSN/SLC8	7	0.269230769230769
GO:0036119	BP	GO:0036119	response to	7/1414	26/18903	0.002396143	0.0116278	0.00745135	PDGFRB/DDIT3/TLR4/IQGAP	7	0.269230769230769
GO:1900151	BP	GO:1900151	regulation of	7/1414	26/18903	0.002396143	0.0116278	0.00745135	ZFP36L1/ZFP36/ZFP36L2/T	7	0.269230769230769
GO:0035567	BP	GO:0035567	non-canonical	13/1414	72/18903	0.002416838	0.0116918	0.00749232	DAB2/CTHRC1/FRZB/GPC6/M	13	0.180555555555556
GO:0070265	BP	GO:0070265	necrotic cell	13/1414	72/18903	0.002416838	0.0116918	0.00749232	CFLAR/NUPR1/PELI1/BIRC2	13	0.180555555555556
GO:0007040	BP	GO:0007040	lysosome	16/1414	98/18903	0.002417335	0.0116918	0.00749232	ATP6V0C/CHMP4B/ATP6V0B/	16	0.163265306122449
GO:0080171	BP	GO:0080171	lytic vacuole	16/1414	98/18903	0.002417335	0.0116918	0.00749232	ATP6V0C/CHMP4B/ATP6V0B/	16	0.163265306122449
GO:0014013	BP	GO:0014013	regulation of	17/1414	107/18903	0.002425406	0.0117211	0.00751111	ID4/NTN1/HES1/PTN/NR1D1	17	0.158878504672897

GO:0006874	BP	GO:0006874	cellular	35/1414	284/18903	0.002444753	0.0118048	0.00756476	THY1/FLNA/PLCG2/DDIT3/S	35	0.123239436619718
GO:0051056	BP	GO:0051056	regulation of	37/1414	305/18903	0.002464395	0.0118898	0.00761923	COL3A1/PDGFRB/NOTCH2/CD	37	0.121311475409836
GO:0035850	BP	GO:0035850	epithelial	10/1414	48/18903	0.002521949	0.0121475	0.00778438	NOTCH2/MAGI2/MTSS1/MEF2	10	0.208333333333333
GO:0002218	BP	GO:0002218	activation of	12/1414	64/18903	0.002521979	0.0121475	0.00778438	HEXIM1/PLCG2/HSP90AA1/T	12	0.1875
GO:0120193	BP	GO:0120193	tight	14/1414	81/18903	0.002565365	0.0123462	0.00791169	ACTG1/SNAI1/RAB13/AFDN/	14	0.172839506172839
GO:0001836	BP	GO:0001836	release of	11/1414	56/18903	0.002567456	0.0123462	0.00791169	LMNA/SOD2/PLAUR/PRELID1	11	0.196428571428571
GO:0032411	BP	GO:0032411	positive	19/1414	126/18903	0.002583947	0.0123961	0.00794368	VMP1/ANK3/NDUFA4/PLCG2/	19	0.150793650793651
GO:0043244	BP	GO:0043244	regulation of	19/1414	126/18903	0.002583947	0.0123961	0.00794368	CAPZB/LIMA1/SCIN/GSN/TR	19	0.150793650793651
GO:0051100	BP	GO:0051100	negative	23/1414	164/18903	0.002584214	0.0123961	0.00794368	JUN/DAB2/ACTB/DDIT3/NFK	23	0.140243902439024
GO:0006596	BP	GO:0006596	polyamine	5/1414	14/18903	0.002627022	0.0125396	0.00803562	SRM/SAT1/OAZ1/ODC1/SMS	5	0.357142857142857
GO:0032486	BP	GO:0032486	Rap protein	5/1414	14/18903	0.002627022	0.0125396	0.00803562	RAP2B/RAP1A/RAP1B/PLK2/	5	0.357142857142857
GO:0048388	BP	GO:0048388	endosomal	5/1414	14/18903	0.002627022	0.0125396	0.00803562	ATP6V0C/ATP6V0B/ATP6V1F	5	0.357142857142857
GO:0048711	BP	GO:0048711	positive	5/1414	14/18903	0.002627022	0.0125396	0.00803562	HES1/SERPINE2/BMP2/ID2/	5	0.357142857142857
GO:0051764	BP	GO:0051764	actin	5/1414	14/18903	0.002627022	0.0125396	0.00803562	MARCKS/FLNA/DPYSL3/AIF1	5	0.357142857142857
GO:0061043	BP	GO:0061043	regulation of	5/1414	14/18903	0.002627022	0.0125396	0.00803562	SMOC2/XBP1/CXCR4/SLC12A	5	0.357142857142857
GO:0006937	BP	GO:0006937	regulation of	24/1414	174/18903	0.002640049	0.0125812	0.00806227	MYL9/TPM1/TNNT3/NR4A1/T	24	0.137931034482759
GO:0030178	BP	GO:0030178	negative	24/1414	174/18903	0.002640049	0.0125812	0.00806227	IGFBP4/EGR1/DKK3/DAB2/G	24	0.137931034482759
GO:0070098	BP	GO:0070098	chemokine-	15/1414	90/18903	0.002651984	0.0126174	0.00808551	CCL20/CCL3/CCL3L1/CXCL8	15	0.166666666666667
GO:2000177	BP	GO:2000177	regulation of	15/1414	90/18903	0.002651984	0.0126174	0.00808551	ID4/GLI3/CDON/FOXO1/PTN	15	0.166666666666667
GO:0008637	BP	GO:0008637	apoptotic	17/1414	108/18903	0.002682572	0.0127422	0.00816545	LMNA/HSPA1A/SOD2/SLC25A	17	0.157407407407407
GO:0061387	BP	GO:0061387	regulation of	17/1414	108/18903	0.002682572	0.0127422	0.00816545	SEMA3C/NTN1/SPP1/FN1/VE	17	0.157407407407407
GO:0006700	BP	GO:0006700	C21-steroid	6/1414	20/18903	0.002693232	0.0127616	0.00817792	EGR1/DKK3/DAB2/BMP2/BMP	6	0.3
GO:0044794	BP	GO:0044794	positive	6/1414	20/18903	0.002693232	0.0127616	0.00817792	HSPA8/CSF1R/APOE/CFL1/S	6	0.3
GO:0071243	BP	GO:0071243	cellular	6/1414	20/18903	0.002693232	0.0127616	0.00817792	GSTO1/ATF4/ATF3/HMOX1/D	6	0.3
GO:0060415	BP	GO:0060415	muscle tissue	13/1414	73/18903	0.002743355	0.0129886	0.00832335	COL3A1/RBPJ/TPM1/COL11A	13	0.178082191780822
GO:0045124	BP	GO:0045124	regulation of	9/1414	41/18903	0.002809288	0.0132792	0.00850958	LTBP3/TF/SPP1/TNFRSF11B	9	0.219512195121951
GO:0050850	BP	GO:0050850	positive	9/1414	41/18903	0.002809288	0.0132792	0.00850958	PLCG2/CAMTA1/LMCD1/CCL3	9	0.219512195121951
GO:2000045	BP	GO:2000045	regulation of	25/1414	185/18903	0.002882276	0.0135903	0.00870898	GPNMB/ACTB/FHL1/CDKN1A/	25	0.135135135135135
GO:1902117	BP	GO:1902117	positive	14/1414	82/18903	0.002885250	0.0135903	0.00870898	SDCBP/SDC4/LCP1/RHOA/MS	14	0.170731707317073
GO:1905897	BP	GO:1905897	regulation of	14/1414	82/18903	0.002885250	0.0135903	0.00870898	HSPA1A/DDIT3/PIK3R1/XBP	14	0.170731707317073
GO:2000736	BP	GO:2000736	regulation of	14/1414	82/18903	0.002885250	0.0135903	0.00870898	PDGFRA/LBH/LTBP3/SOX5/H	14	0.170731707317073
GO:0031100	BP	GO:0031100	animal organ	12/1414	65/18903	0.002886765	0.0135903	0.00870898	GLI3/CEBPB/ADM/TGFBR3/C	12	0.184615384615385
GO:0043300	BP	GO:0043300	regulation of	10/1414	49/18903	0.002960134	0.0139222	0.00892162	RABGEF1/VAMP8/ITGB2/SPI	10	0.204081632653061
GO:0046822	BP	GO:0046822	regulation of	17/1414	109/18903	0.002962024	0.0139222	0.00892162	FLNA/GLI3/APOD/PIK3R1/R	17	0.155963302752294
GO:0002532	BP	GO:0002532	production of	16/1414	100/18903	0.002982616	0.0139964	0.00896919	H19/APOD/ALOX5AP/VAMP8/	16	0.16
GO:0036473	BP	GO:0036473	cell death in	16/1414	100/18903	0.002982616	0.0139964	0.00896919	FOXP1/STK26/MMP3/SOD2/T	16	0.16

GO:0007431	BP	GO:0007431	salivary	8/1414	34/18903	0.003012523	0.0140688	0.00901560	SEMA3C/TGM2/TGFB1/FGFR2	8	0.235294117647059
GO:0010765	BP	GO:0010765	positive	8/1414	34/18903	0.003012523	0.0140688	0.00901560	ANK3/FXYD1/GLRX/ATP1B3/	8	0.235294117647059
GO:0055094	BP	GO:0055094	response to	8/1414	34/18903	0.003012523	0.0140688	0.00901560	GAS5/FCER1G/ITGB2/CD68/	8	0.235294117647059
GO:0090022	BP	GO:0090022	regulation of	8/1414	34/18903	0.003012523	0.0140688	0.00901560	TNFAIP6/CD74/C3AR1/CXCL	8	0.235294117647059
GO:0090162	BP	GO:0090162	establishment	8/1414	34/18903	0.003012523	0.0140688	0.00901560	HES1/FRMD4B/CDC42/RHOA/	8	0.235294117647059
GO:1902624	BP	GO:1902624	positive	8/1414	34/18903	0.003012523	0.0140688	0.00901560	CD99/SELENOK/CD74/C3AR1	8	0.235294117647059
GO:0001783	BP	GO:0001783	B cell	7/1414	27/18903	0.003028796	0.0141110	0.00904259	FOXP1/ORMDL3/CD74/LYN/B	7	0.259259259259259
GO:0003171	BP	GO:0003171	atrioventricu	7/1414	27/18903	0.003028796	0.0141110	0.00904259	TWIST1/SOX4/BMP2/CCN1/E	7	0.259259259259259
GO:0042730	BP	GO:0042730	fibrinolysis	7/1414	27/18903	0.003028796	0.0141110	0.00904259	FAP/ANXA2/PLAUR/THBS1/S	7	0.259259259259259
GO:0007548	BP	GO:0007548	sex	35/1414	288/18903	0.003080657	0.0143411	0.00919008	MMP2/PDGFRA/PDGFRB/COL9	35	0.121527777777778
GO:0045471	BP	GO:0045471	response to	19/1414	128/18903	0.003096726	0.0144044	0.00923065	FOS/CTSK/CDO1/SOD2/VCAM	19	0.1484375
GO:0003281	BP	GO:0003281	ventricular	13/1414	74/18903	0.003105032	0.0144171	0.00923874	SOX4/RBPJ/HES1/FGFRL1/F	13	0.175675675675676
GO:2000628	BP	GO:2000628	regulation of	13/1414	74/18903	0.003105032	0.0144171	0.00923874	JUN/EGR1/FOS/KCNQ1OT1/E	13	0.175675675675676
GO:0002768	BP	GO:0002768	immune	40/1414	341/18903	0.003106857	0.0144171	0.00923874	THY1/FOXP1/PLCG2/PDE4B/	40	0.117302052785924
GO:0032609	BP	GO:0032609	interferon-	18/1414	119/18903	0.003193306	0.0147947	0.00948073	DDIT3/INHBA/PDE4B/HSPD1	18	0.151260504201681
GO:0032649	BP	GO:0032649	regulation of	18/1414	119/18903	0.003193306	0.0147947	0.00948073	DDIT3/INHBA/PDE4B/HSPD1	18	0.151260504201681
GO:1905477	BP	GO:1905477	positive	16/1414	101/18903	0.003303799	0.0152861	0.00979563	ANK3/PIK3R1/SQSTM1/NMT1	16	0.158415841584158
GO:0046034	BP	GO:0046034	ATP metabolic	28/1414	217/18903	0.003304611	0.0152861	0.00979563	NT5E/H19/NDUFB1/ATP5ME/	28	0.129032258064516
GO:0016050	BP	GO:0016050	vesicle organization	41/1414	353/18903	0.003321440 56815916	0.0153517 930539401	0.00983771 411922025	AQP1/ZEB2/EEA1/SERPINE2 /SDCBP/ATP6V0C/SQSTM1/R	41	0.11614730878187
GO:1902115	BP	GO:1902115	regulation of	27/1414	207/18903	0.003327241	0.0153664	0.00984709	PTPRD/HSPA1A/HSPA1B/GSN	27	0.130434782608696
GO:0000910	BP	GO:0000910	cytokinesis	25/1414	187/18903	0.003330423	0.0153689	0.00984871	SEPTIN11/ANK3/RHOC/CHMP	25	0.133689839572193
GO:0014002	BP	GO:0014002	astrocyte	9/1414	42/18903	0.003342399	0.0153755	0.00985294	TSPAN2/NR1D1/C1QA/C5AR1	9	0.214285714285714
GO:0031670	BP	GO:0031670	cellular	9/1414	42/18903	0.003342399	0.0153755	0.00985294	COL1A1/POSTN/XBP1/FOLR2	9	0.214285714285714
GO:0071604	BP	GO:0071604	transforming	9/1414	42/18903	0.003342399	0.0153755	0.00985294	COL3A1/LTBP1/LUM/FN1/PT	9	0.214285714285714
GO:1900274	BP	GO:1900274	regulation of	9/1414	42/18903	0.003342399	0.0153755	0.00985294	PDGFRA/PDGFRB/FGFR1/FGF	9	0.214285714285714
GO:0045931	BP	GO:0045931	positive	19/1414	129/18903	0.003383343	0.0155516	0.00996578	SMOC2/HES1/ANXA1/RGCC/D	19	0.147286821705426
GO:0045620	BP	GO:0045620	negative	11/1414	58/18903	0.003423126	0.0157221	0.01007502	RUNX1/GLI3/LAG3/INHBA/A	11	0.189655172413793
GO:0045661	BP	GO:0045661	regulation of	13/1414	75/18903	0.003504591	0.0160583	0.01029049	ZFP36L1/SOX4/ACTB/CDON/	13	0.173333333333333
GO:0050810	BP	GO:0050810	regulation of	13/1414	75/18903	0.003504591	0.0160583	0.01029049	EGR1/DKK3/DAB2/IGFBP7/S	13	0.173333333333333
GO:0120192	BP	GO:0120192	tight	13/1414	75/18903	0.003504591	0.0160583	0.01029049	ACTG1/SNAI1/RAB13/AFDN/	13	0.173333333333333
GO:0048639	BP	GO:0048639	positive	23/1414	168/18903	0.003519573	0.0161143	0.01032636	RBPJ/NTN1/FN1/FGF2/VEGF	23	0.136904761904762
GO:0060445	BP	GO:0060445	branching	6/1414	21/18903	0.003534772	0.0161215	0.01033098	SEMA3C/TGM2/FGFR2/NRP1/	6	0.285714285714286
GO:0071605	BP	GO:0071605	monocyte	6/1414	21/18903	0.003534772	0.0161215	0.01033098	TWIST1/APOD/TRPV4/SELEN	6	0.285714285714286
GO:0071637	BP	GO:0071637	regulation of	6/1414	21/18903	0.003534772	0.0161215	0.01033098	TWIST1/APOD/TRPV4/SELEN	6	0.285714285714286
GO:2000047	BP	GO:2000047	regulation of	6/1414	21/18903	0.003534772	0.0161215	0.01033098	BMP6/RGCC/VEGFA/AFDN/TJ	6	0.285714285714286

GO:0008277	BP	GO:0008277	regulation of	20/1414	139/18903	0.003534964	0.0161215	0.01033098	RGS16/SLC39A14/PDE4B/AD	20	0.143884892086331
GO:0019722	BP	GO:0019722	calcium-	27/1414	208/18903	0.003558504	0.0162162	0.01039165	RCAN1/PLCG2/VCAM1/SELEN	27	0.129807692307692
GO:0002440	BP	GO:0002440	production of molecular	39/1414	333/18903	0.003567621 49838105	0.0162450 711944236	0.01041014 33425787	TWIST1/PLCG2/RBP4/XBP1/ CD55/DNAJB9/TGFB1/RABGE	39	0.117117117117117
GO:0120034	BP	GO:0120034	positive	17/1414	111/18903	0.003593623	0.0163507	0.01047783	DPYSL3/PIK3R1/HSP90AA1/	17	0.153153153153153
GO:0051851	BP	GO:0051851	modulation by	14/1414	84/18903	0.003623312	0.0164729	0.01055616	JUN/EEA1/HSPA8/SAP30/CS	14	0.166666666666667
GO:0090150	BP	GO:0090150	establishment	33/1414	270/18903	0.003637388	0.0165240	0.01058892	ANK3/SDCBP/CHMP4B/RABGE	33	0.122222222222222
GO:0022898	BP	GO:0022898	regulation of	35/1414	291/18903	0.003646016	0.0165323	0.01059424	TWIST1/ACTB/VMP1/FHL1/A	35	0.120274914089347
GO:0061351	BP	GO:0061351	neural	21/1414	149/18903	0.003651503	0.0165323	0.01059424	ID4/GLI3/CDON/SOX5/FOXO	21	0.140939597315436
GO:0030212	BP	GO:0030212	hyaluronan	8/1414	35/18903	0.003653390	0.0165323	0.01059424	FGF2/TGFB1/CD44/TNFAIP6	8	0.228571428571429
GO:0043372	BP	GO:0043372	positive	8/1414	35/18903	0.003653390	0.0165323	0.01059424	ANXA1/NFKBIZ/HLA-	8	0.228571428571429
GO:1905898	BP	GO:1905898	positive	8/1414	35/18903	0.003653390	0.0165323	0.01059424	DDIT3/PIK3R1/XBP1/CAV1/	8	0.228571428571429
GO:0022406	BP	GO:0022406	membrane	15/1414	93/18903	0.003667406	0.0165572	0.01061020	VMP1/VCAM1/ICAM1/RAB13/	15	0.161290322580645
GO:0051781	BP	GO:0051781	positive	15/1414	93/18903	0.003667406	0.0165572	0.01061020	LBH/PTN/FGF2/TGFB1/FGF1	15	0.161290322580645
GO:0070301	BP	GO:0070301	cellular	15/1414	93/18903	0.003667406	0.0165572	0.01061020	FOXP1/AQP1/STK26/TXN/AN	15	0.161290322580645
GO:0002679	BP	GO:0002679	respiratory	5/1414	15/18903	0.003700000	0.0165633	0.01061412	SELENOK/NCF1/TREM2/GRN/	5	0.333333333333333
GO:0002903	BP	GO:0002903	negative	5/1414	15/18903	0.003700000	0.0165633	0.01061412	FOXP1/ORMDL3/CD74/SLC39	5	0.333333333333333
GO:0032905	BP	GO:0032905	transforming	5/1414	15/18903	0.003700000	0.0165633	0.01061412	COL3A1/LUM/TYROBP/ATP6A	5	0.333333333333333
GO:0035358	BP	GO:0035358	regulation of	5/1414	15/18903	0.003700000	0.0165633	0.01061412	TWIST1/BMP2/FABP5/CITED	5	0.333333333333333
GO:0043129	BP	GO:0043129	surfactant	5/1414	15/18903	0.003700000	0.0165633	0.01061412	VEGFA/CTSH/EPAS1/ADGRF5	5	0.333333333333333
GO:0043518	BP	GO:0043518	negative	5/1414	15/18903	0.003700000	0.0165633	0.01061412	TWIST1/SNAI1/CD44/PTTG1	5	0.333333333333333
GO:0060211	BP	GO:0060211	regulation of	5/1414	15/18903	0.003700000	0.0165633	0.01061412	TNRC6A/ZFP36/BTG2/TOB1/	5	0.333333333333333
GO:0060347	BP	GO:0060347	heart	5/1414	15/18903	0.003700000	0.0165633	0.01061412	RBP4/TGFBR3/FKBP1A/ADAM	5	0.333333333333333
GO:0071639	BP	GO:0071639	positive	5/1414	15/18903	0.003700000	0.0165633	0.01061412	TWIST1/TRPV4/SELENOK/CL	5	0.333333333333333
GO:0090280	BP	GO:0090280	positive	5/1414	15/18903	0.003700000	0.0165633	0.01061412	PDGFRB/CCL3/CCL2/PDGFB/	5	0.333333333333333
GO:1900153	BP	GO:1900153	positive	5/1414	15/18903	0.003700000	0.0165633	0.01061412	ZFP36L1/ZFP36/ZFP36L2/T	5	0.333333333333333
GO:0000303	BP	GO:0000303	response to	7/1414	28/18903	0.003781577	0.0168896	0.01082322	H19/SOD2/PRDX1/SOD3/GLR	7	0.25
GO:0003416	BP	GO:0003416	endochondral	7/1414	28/18903	0.003781577	0.0168896	0.01082322	ECM1/COMP/COL27A1/FGFR3	7	0.25
GO:1903319	BP	GO:1903319	positive	7/1414	28/18903	0.003781577	0.0168896	0.01082322	SOX4/MELTF/GSN/ANXA2/EN	7	0.25
GO:0051090	BP	GO:0051090	regulation of DNA-binding	50/1414	454/18903	0.003826397 54244541	0.0170563 079108074	0.01092999 8897611	TWIST1/FLNA/GLI3/ID3/PL CG2/HSPA1A/HES1/HSPA1B/	50	0.110132158590308
GO:0009746	BP	GO:0009746	response to	26/1414	199/18903	0.003827654	0.0170563	0.01092999	EGR1/SOX4/COL6A2/SLC29A	26	0.130653266331658
GO:0032388	BP	GO:0032388	positive	26/1414	199/18903	0.003827654	0.0170563	0.01092999	DAB2/FLNA/GLI3/ANK3/PIK	26	0.130653266331658
GO:0042306	BP	GO:0042306	regulation of	11/1414	59/18903	0.003929217	0.0174821	0.01120289	FLNA/GLI3/APOD/PIK3R1/R	11	0.186440677966102
GO:0071709	BP	GO:0071709	membrane	11/1414	59/18903	0.003929217	0.0174821	0.01120289	MAFB/PTPRD/ANK3/ANXA2/C	11	0.186440677966102
GO:0001937	BP	GO:0001937	negative	13/1414	76/18903	0.003944862	0.0175295	0.01123327	CNMD/SPARC/RGCC/CAV1/CC	13	0.171052631578947

GO:0048259	BP	GO:0048259	regulation of	17/1414	112/18903	0.003948824	0.0175295	0.01123327	DAB2/PLCG2/TF/MAGI2/SDC	17	0.151785714285714
GO:0045622	BP	GO:0045622	regulation of	9/1414	43/18903	0.003951892	0.0175295	0.01123327	JUNB/ANXA1/NFKBIZ/HLA-	9	0.209302325581395
GO:0045687	BP	GO:0045687	positive	9/1414	43/18903	0.003951892	0.0175295	0.01123327	HES1/PTN/SERPINE2/BMP2/	9	0.209302325581395
GO:0022602	BP	GO:0022602	ovulation	10/1414	51/18903	0.004017680	0.0177538	0.01137701	MMP2/PDGFRA/MAP2K6/A2M/	10	0.196078431372549
GO:0032873	BP	GO:0032873	negative	10/1414	51/18903	0.004017680	0.0177538	0.01137701	FOXO1/DNAJA1/TREM2/TAOK	10	0.196078431372549
GO:0043277	BP	GO:0043277	apoptotic	10/1414	51/18903	0.004017680	0.0177538	0.01137701	TGM2/ANXA1/TYROBP/CCL2/	10	0.196078431372549
GO:0050873	BP	GO:0050873	brown fat	10/1414	51/18903	0.004017680	0.0177538	0.01137701	SIX1/DIO2/TRPV4/METRNL/	10	0.196078431372549
GO:0070303	BP	GO:0070303	negative	10/1414	51/18903	0.004017680	0.0177538	0.01137701	FOXO1/DNAJA1/TREM2/TAOK	10	0.196078431372549
GO:0050764	BP	GO:0050764	regulation of	16/1414	103/18903	0.004031874	0.0177896	0.01139994	PLCG2/TGM2/FCER1G/PTPRC	16	0.155339805825243
GO:1903076	BP	GO:1903076	regulation of	16/1414	103/18903	0.004031874	0.0177896	0.01139994	DAB2/ACTB/PIK3R1/SQSTM1	16	0.155339805825243
GO:0051302	BP	GO:0051302	regulation of	25/1414	190/18903	0.004111950	0.0181292	0.01161756	LBH/PTN/FGF2/TGFB1/CALM	25	0.131578947368421
GO:1903531	BP	GO:1903531	negative	21/1414	151/18903	0.004278271	0.0188483	0.01207834	GJA1/FOXO1/PIM3/INHBA/N	21	0.139072847682119
GO:0030968	BP	GO:0030968	endoplasmic	13/1414	77/18903	0.004428779	0.0194966	0.01249382	DDIT3/STC2/PIK3R1/XBP1/	13	0.168831168831169
GO:0002011	BP	GO:0002011	morphogenesis	11/1414	60/18903	0.004493222	0.0196456	0.01258930	COL5A1/FLNA/NOTCH2/PDPN	11	0.183333333333333
GO:0002711	BP	GO:0002711	positive	11/1414	60/18903	0.004493222	0.0196456	0.01258930	CD55/HSPD1/HLA-	11	0.183333333333333
GO:0045638	BP	GO:0045638	negative	15/1414	95/18903	0.004506365	0.0196456	0.01258930	MAFB/ZFP36L1/FBN1/ZFP36	15	0.157894736842105
GO:0002088	BP	GO:0002088	lens	14/1414	86/18903	0.004508341	0.0196456	0.01258930	CDON/CRYAB/FGF2/SPRY2/A	14	0.162790697674419
GO:0001765	BP	GO:0001765	membrane raft	4/1414	10/18903	0.004538588	0.0196456	0.01258930	ANXA2/CAV1/S100A10/CAV2	4	0.4
GO:0001915	BP	GO:0001915	negative	4/1414	10/18903	0.004538588	0.0196456	0.01258930	PTPRC/FCGR2B/NCKAP1L/IL	4	0.4
GO:0002291	BP	GO:0002291	T cell	4/1414	10/18903	0.004538588	0.0196456	0.01258930	ICAM1/HLA-	4	0.4
GO:0003183	BP	GO:0003183	mitral valve	4/1414	10/18903	0.004538588	0.0196456	0.01258930	TWIST1/SOX4/EFNA1/BMPR2	4	0.4
GO:0014012	BP	GO:0014012	peripheral	4/1414	10/18903	0.004538588	0.0196456	0.01258930	MMP2/TNC/APOD/MAP1B	4	0.4
GO:0018401	BP	GO:0018401	peptidyl-	4/1414	10/18903	0.004538588	0.0196456	0.01258930	P4HA2/PRDX4/P4HA1/EGLN3	4	0.4
GO:0031666	BP	GO:0031666	positive	4/1414	10/18903	0.004538588	0.0196456	0.01258930	BMP6/CD14/LY96/SASH1	4	0.4
GO:0035747	BP	GO:0035747	natural	4/1414	10/18903	0.004538588	0.0196456	0.01258930	CCL3/CCL2/CCL4/CCL5	4	0.4
GO:0045657	BP	GO:0045657	positive	4/1414	10/18903	0.004538588	0.0196456	0.01258930	ZFP36L1/HLA-	4	0.4
GO:0046886	BP	GO:0046886	positive	4/1414	10/18903	0.004538588	0.0196456	0.01258930	EGR1/DAB2/BMP6/ADM	4	0.4
GO:0050861	BP	GO:0050861	positive	4/1414	10/18903	0.004538588	0.0196456	0.01258930	FOXP1/CMTM3/SLC39A10/PR	4	0.4
GO:0051342	BP	GO:0051342	regulation of	4/1414	10/18903	0.004538588	0.0196456	0.01258930	SLC39A14/CALM2/CALM3/CA	4	0.4
GO:0062042	BP	GO:0062042	regulation of	4/1414	10/18903	0.004538588	0.0196456	0.01258930	TWIST1/JAG1/ENG/TGFBR2	4	0.4
GO:1902946	BP	GO:1902946	protein	4/1414	10/18903	0.004538588	0.0196456	0.01258930	NRP1/EZR/MSN/RDX	4	0.4
GO:1990034	BP	GO:1990034	calcium ion	4/1414	10/18903	0.004538588	0.0196456	0.01258930	CALM2/ATP2B1/CALM3/CALM	4	0.4
GO:2000048	BP	GO:2000048	negative	4/1414	10/18903	0.004538588	0.0196456	0.01258930	BMP6/RGCC/VEGFA/NOTCH4	4	0.4
GO:2000271	BP	GO:2000271	positive	4/1414	10/18903	0.004538588	0.0196456	0.01258930	NUPR1/STK17A/STK17B/BTG	4	0.4
GO:0002223	BP	GO:0002223	stimulatory	6/1414	22/18903	0.004556931	0.0196456	0.01258930	PLCG2/TYROBP/CLEC7A/LYN	6	0.272727272727273
GO:0051220	BP	GO:0051220	cytoplasmic	6/1414	22/18903	0.004556931	0.0196456	0.01258930	FLNA/NFKBIA/MDFI/TMSB4X	6	0.272727272727273

GO:0051444	BP	GO:0051444	negative	6/1414	22/18903	0.004556931	0.0196456	0.01258930	RPS20/SMAD7/RPS15/RPS7/	6	0.272727272727273
GO:0061318	BP	GO:0061318	renal	6/1414	22/18903	0.004556931	0.0196456	0.01258930	NOTCH2/MAGI2/IQGAP1/JAG	6	0.272727272727273
GO:0072112	BP	GO:0072112	podocyte	6/1414	22/18903	0.004556931	0.0196456	0.01258930	NOTCH2/MAGI2/IQGAP1/JAG	6	0.272727272727273
GO:1990840	BP	GO:1990840	response to	6/1414	22/18903	0.004556931	0.0196456	0.01258930	PLCG2/TYROBP/CLEC7A/LYN	6	0.272727272727273
GO:1990858	BP	GO:1990858	cellular	6/1414	22/18903	0.004556931	0.0196456	0.01258930	PLCG2/TYROBP/CLEC7A/LYN	6	0.272727272727273
GO:1900026	BP	GO:1900026	positive	9/1414	44/18903	0.004644913	0.0199194	0.01276474	DAB2/FLNA/NRP1/ARPC2/RA	9	0.204545454545455
GO:1904706	BP	GO:1904706	negative	9/1414	44/18903	0.004644913	0.0199194	0.01276474	TPM1/NDRG2/SOD2/CDKN1A/	9	0.204545454545455
GO:0002762	BP	GO:0002762	negative	10/1414	52/18903	0.004647869	0.0199194	0.01276474	MAFB/FBN1/PIK3R1/INHBA/	10	0.192307692307692
GO:0010939	BP	GO:0010939	regulation of	10/1414	52/18903	0.004647869	0.0199194	0.01276474	CFLAR/NUPR1/PELI1/BIRC2	10	0.192307692307692
GO:0099172	BP	GO:0099172	presynapse	10/1414	52/18903	0.004647869	0.0199194	0.01276474	PTPRD/FARP1/GPC6/SDCBP/	10	0.192307692307692
GO:0000305	BP	GO:0000305	response to	7/1414	29/18903	0.004668242	0.0199194	0.01276474	H19/SOD2/PRDX1/SOD3/GLR	7	0.241379310344828
GO:0001773	BP	GO:0001773	myeloid	7/1414	29/18903	0.004668242	0.0199194	0.01276474	RBPJ/NOTCH2/SPI1/PYCARD	7	0.241379310344828
GO:0001958	BP	GO:0001958	endochondral	7/1414	29/18903	0.004668242	0.0199194	0.01276474	COL1A1/COL2A1/DLX5/BMP6	7	0.241379310344828
GO:0003094	BP	GO:0003094	glomerular	7/1414	29/18903	0.004668242	0.0199194	0.01276474	AQP1/SULF2/CYBA/GAS6/AD	7	0.241379310344828
GO:0003209	BP	GO:0003209	cardiac	7/1414	29/18903	0.004668242	0.0199194	0.01276474	SOX4/NOTCH2/BMP2/CCN1/H	7	0.241379310344828
GO:0010800	BP	GO:0010800	positive	7/1414	29/18903	0.004668242	0.0199194	0.01276474	CHI3L1/TGFB1/CALM2/CAB3	7	0.241379310344828
GO:0036075	BP	GO:0036075	replacement	7/1414	29/18903	0.004668242	0.0199194	0.01276474	COL1A1/COL2A1/DLX5/BMP6	7	0.241379310344828
GO:0070977	BP	GO:0070977	bone	7/1414	29/18903	0.004668242	0.0199194	0.01276474	ZBTB16/XYLT1/BMP2/RFLNB	7	0.241379310344828
GO:0090025	BP	GO:0090025	regulation of	7/1414	29/18903	0.004668242	0.0199194	0.01276474	NBL1/AIF1/LYN/LGMN/DUSP	7	0.241379310344828
GO:0050792	BP	GO:0050792	regulation of	22/1414	162/18903	0.004689504	0.0199955	0.01281350	LGALS1/HEXIM1/IFITM1/ZF	22	0.135802469135802
GO:0002702	BP	GO:0002702	positive	19/1414	133/18903	0.004759609	0.0202796	0.01299555	PLCG2/RBP4/XBP1/CD55/DN	19	0.142857142857143
GO:0070830	BP	GO:0070830	bicellular	12/1414	69/18903	0.004796397	0.0204214	0.01308644	SNAI1/RAB13/AFDN/PAK2/R	12	0.173913043478261
GO:0010212	BP	GO:0010212	response to	20/1414	143/18903	0.004897271	0.0208357	0.01335192	EGR1/CRYAB/SOD2/VCAM1/C	20	0.13986013986014
GO:1902806	BP	GO:1902806	regulation of	27/1414	213/18903	0.004928534	0.0209534	0.01342736	GPNMB/ACTB/FHL1/PLCG2/C	27	0.126760563380282
GO:0070373	BP	GO:0070373	negative	13/1414	78/18903	0.004959373	0.0210692	0.01350154	DAB2/NDRG2/SPRY2/ATF3/P	13	0.166666666666667
GO:0001738	BP	GO:0001738	morphogenesis	15/1414	96/18903	0.004980862	0.0210990	0.01352065	DAB2/ACTG1/ACTB/CTHRC1/	15	0.15625
GO:0014033	BP	GO:0014033	neural crest	15/1414	96/18903	0.004980862	0.0210990	0.01352065	TWIST1/SEMA3C/SIX1/HES1	15	0.15625
GO:0032091	BP	GO:0032091	negative	15/1414	96/18903	0.004980862	0.0210990	0.01352065	DAB2/ACTB/SLPI/CDKN1A/C	15	0.15625
GO:0046330	BP	GO:0046330	positive	15/1414	96/18903	0.004980862	0.0210990	0.01352065	GADD45B/GADD45G/TRPV4/S	15	0.15625
GO:0055007	BP	GO:0055007	cardiac	18/1414	124/18903	0.004985685	0.0211041	0.01352392	PDGFRA/FOXP1/PDGFRB/LMN	18	0.145161290322581
GO:0034349	BP	GO:0034349	glial cell	5/1414	16/18903	0.005054003	0.0213314	0.01366956	CCL2/TREM2/RB1/GAS6/PRK	5	0.3125
GO:0045986	BP	GO:0045986	negative	5/1414	16/18903	0.005054003	0.0213314	0.01366956	KCNMA1/PTGS2/DOCK4/RGS2	5	0.3125
GO:1902285	BP	GO:1902285	semaphorin-	5/1414	16/18903	0.005054003	0.0213314	0.01366956	NRP2/NRP1/PLXND1/PLXNB2	5	0.3125
GO:1905906	BP	GO:1905906	regulation of	5/1414	16/18903	0.005054003	0.0213314	0.01366956	CRYAB/APOE/TREM2/APP/PF	5	0.3125
GO:0042255	BP	GO:0042255	ribosome	11/1414	61/18903	0.005119634	0.0215616	0.01381708	RPL23A/RPL38/NOP53/RPS2	11	0.180327868852459
GO:0046456	BP	GO:0046456	icosanoid	11/1414	61/18903	0.005119634	0.0215616	0.01381708	PTGS2/ANXA1/FABP5/PTGES	11	0.180327868852459

GO:1902893	BP	GO:1902893	regulation of	11/1414	61/18903	0.005119634	0.0215616	0.01381708	JUN/EGR1/FOS/ETS1/BMP2/	11	0.180327868852459
GO:0003230	BP	GO:0003230	cardiac	8/1414	37/18903	0.005246538	0.0219691	0.01407825	SOX4/NOTCH2/BMP2/CCN1/N	8	0.216216216216216
GO:0010934	BP	GO:0010934	macrophage	8/1414	37/18903	0.005246538	0.0219691	0.01407825	TWIST1/PLCG2/TGFB1/MAPK	8	0.216216216216216
GO:0010935	BP	GO:0010935	regulation of	8/1414	37/18903	0.005246538	0.0219691	0.01407825	TWIST1/PLCG2/TGFB1/MAPK	8	0.216216216216216
GO:0044319	BP	GO:0044319	wound	8/1414	37/18903	0.005246538	0.0219691	0.01407825	COL5A1/FLNA/PDPN/RHOC/C	8	0.216216216216216
GO:0051385	BP	GO:0051385	response to	8/1414	37/18903	0.005246538	0.0219691	0.01407825	FOSB/FOS/CCND1/CYBB/SGK	8	0.216216216216216
GO:0070229	BP	GO:0070229	negative	8/1414	37/18903	0.005246538	0.0219691	0.01407825	FOXP1/ORMDL3/CD74/SLC39	8	0.216216216216216
GO:0071402	BP	GO:0071402	cellular	8/1414	37/18903	0.005246538	0.0219691	0.01407825	GAS5/FCER1G/ITGB2/CD68/	8	0.216216216216216
GO:0090505	BP	GO:0090505	epiboly	8/1414	37/18903	0.005246538	0.0219691	0.01407825	COL5A1/FLNA/PDPN/RHOC/C	8	0.216216216216216
GO:0050864	BP	GO:0050864	regulation of	26/1414	204/18903	0.005327476	0.0222920	0.01428518	ZFP36L1/CDKN1A/INHBA/XB	26	0.127450980392157
GO:0048260	BP	GO:0048260	positive	10/1414	53/18903	0.005353200	0.0223516	0.01432333	DAB2/PLCG2/TF/MAGI2/ANX	10	0.188679245283019
GO:0052372	BP	GO:0052372	modulation by	10/1414	53/18903	0.005353200	0.0223516	0.01432333	LGALS1/IFITM1/GSN/IFITM	10	0.188679245283019
GO:0060071	BP	GO:0060071	Wnt signaling	10/1414	53/18903	0.005353200	0.0223516	0.01432333	DAB2/CTHRC1/GPC6/MAGI2/	10	0.188679245283019
GO:0006754	BP	GO:0006754	ATP	16/1414	106/18903	0.005365964	0.0223728	0.01433696	H19/NDUFB1/ATP5ME/ATP6V	16	0.150943396226415
GO:1901890	BP	GO:1901890	positive	16/1414	106/18903	0.005365964	0.0223728	0.01433696	THBS2/THY1/PTPRD/SDC4/C	16	0.150943396226415
GO:0009749	BP	GO:0009749	response to	25/1414	194/18903	0.005388071	0.0224490	0.01438574	EGR1/SOX4/COL6A2/SLC29A	25	0.128865979381443
GO:0014823	BP	GO:0014823	response to	12/1414	70/18903	0.005404144	0.0224999	0.01441836	MMP2/FOS/ZEB1/SOD2/METR	12	0.171428571428571
GO:0010596	BP	GO:0010596	negative	15/1414	97/18903	0.005495048	0.0228620	0.01465043	FGF2/TGFB1/RGCC/KLF4/AP	15	0.154639175257732
GO:0002292	BP	GO:0002292	T cell	13/1414	79/18903	0.005539772	0.0230317	0.01475914	FOXP1/JUNB/ANXA1/NFKBIZ	13	0.164556962025316
GO:0002065	BP	GO:0002065	columnar/cubo	17/1414	116/18903	0.005670372	0.0235578	0.01509633	SOX4/TUBB/HES1/FAM20C/C	17	0.146551724137931
GO:1903532	BP	GO:1903532	positive	33/1414	278/18903	0.005685827	0.0236052	0.01512670	SOX4/DAB2/MAP2K6/RBP4/S	33	0.118705035971223
GO:0001778	BP	GO:0001778	plasma	7/1414	30/18903	0.005702871	0.0236088	0.01512897	ANXA2/CHMP4B/S100A10/MY	7	0.233333333333333
GO:0002474	BP	GO:0002474	antigen	7/1414	30/18903	0.005702871	0.0236088	0.01512897	FCER1G/IFI30/B2M/HLA-	7	0.233333333333333
GO:0006027	BP	GO:0006027	glycosaminogl	7/1414	30/18903	0.005702871	0.0236088	0.01512897	FGF2/TGFB1/CD44/HEXB/GN	7	0.233333333333333
GO:0043032	BP	GO:0043032	positive	7/1414	30/18903	0.005702871	0.0236088	0.01512897	JUND/HSPD1/CCL3/TREM2/T	7	0.233333333333333
GO:0045089	BP	GO:0045089	positive	20/1414	145/18903	0.005725842	0.0236871	0.01517914	CADM1/HEXIM1/LAG3/PLCG2	20	0.137931034482759
GO:0051457	BP	GO:0051457	maintenance	6/1414	23/18903	0.005781081	0.0238817	0.01530387	TXN/SP100/CHCHD10/SUN2/	6	0.260869565217391
GO:0072311	BP	GO:0072311	glomerular	6/1414	23/18903	0.005781081	0.0238817	0.01530387	NOTCH2/MAGI2/IQGAP1/JAG	6	0.260869565217391
GO:0035904	BP	GO:0035904	aorta	11/1414	62/18903	0.005813084	0.0239630	0.01535596	COL3A1/PDGFRB/SOX4/SIX1	11	0.17741935483871
GO:0070228	BP	GO:0070228	regulation of	11/1414	62/18903	0.005813084	0.0239630	0.01535596	FOXP1/PRELID1/ORMDL3/CD	11	0.17741935483871
GO:1903409	BP	GO:1903409	reactive	11/1414	62/18903	0.005813084	0.0239630	0.01535596	CCN6/H19/PLCG2/SOD2/CFL	11	0.17741935483871
GO:0051048	BP	GO:0051048	negative	23/1414	175/18903	0.005836519	0.0240426	0.01540698	GJA1/FOXO1/PIM3/INHBA/N	23	0.131428571428571
GO:0031330	BP	GO:0031330	negative	30/1414	247/18903	0.005881839	0.0241998	0.01550774	FUS/TIMP2/TIMP4/ZFP36/Q	30	0.121457489878543
GO:0002444	BP	GO:0002444	myeloid	16/1414	107/18903	0.005882985	0.0241998	0.01550774	S100A13/RABGEF1/TYROBP/	16	0.149532710280374
GO:0016358	BP	GO:0016358	dendrite	29/1414	237/18903	0.006036968	0.0247983	0.01589123	PTPRD/NTN1/FARP1/PTN/LP	29	0.122362869198312
GO:0034764	BP	GO:0034764	positive	29/1414	237/18903	0.006036968	0.0247983	0.01589123	THY1/FLNA/VMP1/ANK3/NDU	29	0.122362869198312

GO:0014020	BP	GO:0014020	primary	15/1414	98/18903	0.006051261	0.0248395	0.01591764	TWIST1/CTHRC1/SPINT2/TG	15	0.153061224489796
GO:0099024	BP	GO:0099024	plasma	19/1414	136/18903	0.006069784	0.0248980	0.01595514	PLCG2/GSN/AIF1/MSR1/ITG	19	0.139705882352941
GO:0045744	BP	GO:0045744	negative	10/1414	54/18903	0.006139521	0.0251664	0.01612711	PDE4B/ADM/PLEK/ARRB2/CX	10	0.185185185185185
GO:0040036	BP	GO:0040036	regulation of	8/1414	38/18903	0.006218751	0.0254375	0.01630086	SMOC2/SULF2/FAM20C/FGF2	8	0.210526315789474
GO:0048821	BP	GO:0048821	erythrocyte	8/1414	38/18903	0.006218751	0.0254375	0.01630086	KLF2/CITED2/NCKAP1L/PTB	8	0.210526315789474
GO:0090504	BP	GO:0090504	epiboly	8/1414	38/18903	0.006218751	0.0254375	0.01630086	COL5A1/FLNA/PDPN/RHOC/C	8	0.210526315789474
GO:0099173	BP	GO:0099173	postsynapse	22/1414	166/18903	0.006266080	0.0256132	0.01641342	PTPRD/ACTG1/ACTB/ACTN1/	22	0.132530120481928
GO:0002920	BP	GO:0002920	regulation of	9/1414	46/18903	0.006311222	0.0257436	0.01649698	CFH/A2M/CD55/CD59/PTPRC	9	0.195652173913043
GO:0044788	BP	GO:0044788	modulation by	9/1414	46/18903	0.006311222	0.0257436	0.01649698	EEA1/HSPA8/CSF1R/APOE/C	9	0.195652173913043
GO:0048701	BP	GO:0048701	embryonic	9/1414	46/18903	0.006311222	0.0257436	0.01649698	PDGFRA/TWIST1/SIX1/PRRX	9	0.195652173913043
GO:0001838	BP	GO:0001838	embryonic	18/1414	127/18903	0.006409401	0.0261075	0.01673021	TWIST1/SOX4/SIX1/CTHRC1	18	0.141732283464567
GO:0006911	BP	GO:0006911	phagocytosis,	18/1414	127/18903	0.006409401	0.0261075	0.01673021	PLCG2/GSN/AIF1/MSR1/ITG	18	0.141732283464567
GO:0032526	BP	GO:0032526	response to	16/1414	108/18903	0.006439578	0.0261939	0.01678554	COL1A1/MMP2/AQP1/PDGFRB	16	0.148148148148148
GO:0090398	BP	GO:0090398	cellular	16/1414	108/18903	0.006439578	0.0261939	0.01678554	TWIST1/LMNA/PRELP/MAP2K	16	0.148148148148148
GO:0044091	BP	GO:0044091	membrane	11/1414	63/18903	0.006578320	0.0266344	0.01706786	MAFB/PTPRD/ANK3/ANXA2/C	11	0.174603174603175
GO:2001244	BP	GO:2001244	positive	11/1414	63/18903	0.006578320	0.0266344	0.01706786	UBB/DDIT3/NUPR1/RPS3/CA	11	0.174603174603175
GO:0035296	BP	GO:0035296	regulation of	20/1414	147/18903	0.006666086	0.0266344	0.01706786	MMP2/COMP/SOD2/KCNMA1/P	20	0.136054421768707
GO:0097746	BP	GO:0097746	blood vessel	20/1414	147/18903	0.006666086	0.0266344	0.01706786	MMP2/COMP/SOD2/KCNMA1/P	20	0.136054421768707
GO:0032412	BP	GO:0032412	regulation of	33/1414	281/18903	0.006670308	0.0266344	0.01706786	VMP1/FHL1/ANK3/NDUFA4/P	33	0.117437722419929
GO:0003174	BP	GO:0003174	mitral valve	4/1414	11/18903	0.006713260	0.0266344	0.01706786	TWIST1/SOX4/EFNA1/BMPR2	4	0.363636363636364
GO:0019065	BP	GO:0019065	receptor-	4/1414	11/18903	0.006713260	0.0266344	0.01706786	CTSL/CAV1/EPS15/CAV2	4	0.363636363636364
GO:0032342	BP	GO:0032342	aldosterone	4/1414	11/18903	0.006713260	0.0266344	0.01706786	DKK3/DAB2/BMP2/BMP6	4	0.363636363636364
GO:0034350	BP	GO:0034350	regulation of	4/1414	11/18903	0.006713260	0.0266344	0.01706786	CCL2/TREM2/GAS6/PRKCH	4	0.363636363636364
GO:0042167	BP	GO:0042167	heme	4/1414	11/18903	0.006713260	0.0266344	0.01706786	SLCO2B1/HMOX1/BLVRB/BLV	4	0.363636363636364
GO:0042451	BP	GO:0042451	purine	4/1414	11/18903	0.006713260	0.0266344	0.01706786	NT5E/PNP/ADK/APRT	4	0.363636363636364
GO:0042455	BP	GO:0042455	ribonucleosid	4/1414	11/18903	0.006713260	0.0266344	0.01706786	NT5E/PNP/ADK/APRT	4	0.363636363636364
GO:0042487	BP	GO:0042487	regulation of	4/1414	11/18903	0.006713260	0.0266344	0.01706786	RSPO2/BMP2/TNFRSF11B/RU	4	0.363636363636364
GO:0045060	BP	GO:0045060	negative	4/1414	11/18903	0.006713260	0.0266344	0.01706786	GLI3/CD74/PTPRC/DOCK2	4	0.363636363636364
GO:0045628	BP	GO:0045628	regulation of	4/1414	11/18903	0.006713260	0.0266344	0.01706786	ANXA1/CD86/IL18/BCL6	4	0.363636363636364
GO:0046129	BP	GO:0046129	purine	4/1414	11/18903	0.006713260	0.0266344	0.01706786	NT5E/PNP/ADK/APRT	4	0.363636363636364
GO:0046149	BP	GO:0046149	pigment	4/1414	11/18903	0.006713260	0.0266344	0.01706786	SLCO2B1/HMOX1/BLVRB/BLV	4	0.363636363636364
GO:0048505	BP	GO:0048505	regulation of	4/1414	11/18903	0.006713260	0.0266344	0.01706786	RBPJ/HES1/SERPINE2/JAG1	4	0.363636363636364
GO:0048563	BP	GO:0048563	post-	4/1414	11/18903	0.006713260	0.0266344	0.01706786	FBN1/EFEMP1/BAX/KDR	4	0.363636363636364
GO:0060174	BP	GO:0060174	limb bud	4/1414	11/18903	0.006713260	0.0266344	0.01706786	SOX4/SEMA3C/COL2A1/FGFR	4	0.363636363636364
GO:0060315	BP	GO:0060315	negative	4/1414	11/18903	0.006713260	0.0266344	0.01706786	CALM2/GSTO1/CALM3/CALM1	4	0.363636363636364
GO:0061314	BP	GO:0061314	Notch	4/1414	11/18903	0.006713260	0.0266344	0.01706786	RBPJ/NOTCH2/SNAI1/JAG1	4	0.363636363636364

GO:0071394	BP	GO:0071394	cellular	4/1414	11/18903	0.006713260	0.0266344	0.01706786	SPP1/NCF1/NCOA4/MSN	4	0.363636363636364
GO:0071679	BP	GO:0071679	commissural	4/1414	11/18903	0.006713260	0.0266344	0.01706786	VEGFA/NRP1/NFIB/NCAM1	4	0.363636363636364
GO:0090084	BP	GO:0090084	negative	4/1414	11/18903	0.006713260	0.0266344	0.01706786	DNAJB1/HSPA1A/HSPA1B/DN	4	0.363636363636364
GO:1901844	BP	GO:1901844	regulation of	4/1414	11/18903	0.006713260	0.0266344	0.01706786	CALM2/CAV1/CALM3/CALM1	4	0.363636363636364
GO:2000727	BP	GO:2000727	positive	4/1414	11/18903	0.006713260	0.0266344	0.01706786	TGFB1/ARRB2/MEF2C/EFNB2	4	0.363636363636364
GO:0030307	BP	GO:0030307	positive	22/1414	167/18903	0.006721786	0.0266344	0.01706786	NTN1/FN1/SDCBP/VEGFA/CX	22	0.131736526946108
GO:0019885	BP	GO:0019885	antigen	5/1414	17/18903	0.006724660	0.0266344	0.01706786	B2M/HLA-B/HLA-E/HLA-	5	0.294117647058824
GO:0036005	BP	GO:0036005	response to	5/1414	17/18903	0.006724660	0.0266344	0.01706786	SPP1/CSF1R/TREM2/TLR4/B	5	0.294117647058824
GO:0038065	BP	GO:0038065	collagen-	5/1414	17/18903	0.006724660	0.0266344	0.01706786	COL1A1/ITGA11/DDR2/COL4	5	0.294117647058824
GO:0042481	BP	GO:0042481	regulation of	5/1414	17/18903	0.006724660	0.0266344	0.01706786	RSPO2/BMP2/TNFRSF11B/RU	5	0.294117647058824
GO:0048875	BP	GO:0048875	chemical	5/1414	17/18903	0.006724660	0.0266344	0.01706786	VEGFA/CTSH/EPAS1/ADGRF5	5	0.294117647058824
GO:0051412	BP	GO:0051412	response to	5/1414	17/18903	0.006724660	0.0266344	0.01706786	FOSB/FOS/CCND1/ATP2B1/C	5	0.294117647058824
GO:0055119	BP	GO:0055119	relaxation of	5/1414	17/18903	0.006724660	0.0266344	0.01706786	GSN/PDE4B/ATP1B1/SLC8A1	5	0.294117647058824
GO:0072109	BP	GO:0072109	glomerular	5/1414	17/18903	0.006724660	0.0266344	0.01706786	EGR1/PDGFRB/CFLAR/CD34/	5	0.294117647058824
GO:1900034	BP	GO:1900034	regulation of	5/1414	17/18903	0.006724660	0.0266344	0.01706786	DNAJB1/IER5/MAPKAPK2/DN	5	0.294117647058824
GO:2000651	BP	GO:2000651	positive	5/1414	17/18903	0.006724660	0.0266344	0.01706786	ANK3/GLRX/ATP1B1/ACTN4/	5	0.294117647058824
GO:0071214	BP	GO:0071214	cellular	38/1414	335/18903	0.006730536	0.0266344	0.01706786	COL1A1/MMP2/EGR1/ZFP36L	38	0.113432835820896
GO:0104004	BP	GO:0104004	cellular	38/1414	335/18903	0.006730536	0.0266344	0.01706786	COL1A1/MMP2/EGR1/ZFP36L	38	0.113432835820896
GO:0009145	BP	GO:0009145	purine	17/1414	118/18903	0.006735994	0.0266380	0.01707012	H19/NDUFB1/ATP5ME/ATP6V	17	0.144067796610169
GO:0071692	BP	GO:0071692	protein	41/1414	368/18903	0.006812648	0.0269228	0.01725268	NBL1/LTBP2/LTBP1/SOX4/C	41	0.111413043478261
GO:0014855	BP	GO:0014855	striated	13/1414	81/18903	0.006862920	0.0271031	0.01736822	FOS/SIX1/RBPJ/RUNX1/RBP	13	0.160493827160494
GO:0061311	BP	GO:0061311	cell surface	7/1414	31/18903	0.006899740	0.0271383	0.01739076	RBPJ/NOTCH2/SNAI1/BMP2/	7	0.225806451612903
GO:0071295	BP	GO:0071295	cellular	7/1414	31/18903	0.006899740	0.0271383	0.01739076	COL1A1/POSTN/FOLR2/ATP2	7	0.225806451612903
GO:0097205	BP	GO:0097205	renal	7/1414	31/18903	0.006899740	0.0271383	0.01739076	AQP1/SULF2/CYBA/GAS6/AD	7	0.225806451612903
GO:0098868	BP	GO:0098868	bone growth	7/1414	31/18903	0.006899740	0.0271383	0.01739076	ECM1/COMP/COL27A1/FGFR3	7	0.225806451612903
GO:1900027	BP	GO:1900027	regulation of	7/1414	31/18903	0.006899740	0.0271383	0.01739076	ICAM1/CAV1/EPS8L2/RHOG/	7	0.225806451612903
GO:1902042	BP	GO:1902042	negative	7/1414	31/18903	0.006899740	0.0271383	0.01739076	CFLAR/ICAM1/PEA15/HMOX1	7	0.225806451612903
GO:0048706	BP	GO:0048706	embryonic	18/1414	128/18903	0.006951475	0.0273234	0.01750935	COL1A1/PDGFRA/TWIST1/SI	18	0.140625
GO:0031103	BP	GO:0031103	axon	10/1414	55/18903	0.007012822	0.0275459	0.01765198	MMP2/TNC/JUN/FLNA/PTN/A	10	0.181818181818182
GO:0045927	BP	GO:0045927	positive	31/1414	261/18903	0.007134124	0.0280035	0.01794522	RBPJ/NTN1/FN1/FGF2/SDCB	31	0.118773946360153
GO:0035150	BP	GO:0035150	regulation of	20/1414	148/18903	0.007181401	0.0281097	0.01801321	MMP2/COMP/SOD2/KCNMA1/P	20	0.135135135135135
GO:0046546	BP	GO:0046546	development	20/1414	148/18903	0.007181401	0.0281097	0.01801321	PDGFRA/PDGFRB/COL9A3/PR	20	0.135135135135135
GO:0007097	BP	GO:0007097	nuclear	6/1414	24/18903	0.007228621	0.0281097	0.01801321	LMNA/NTN1/CDC42/SUN2/SY	6	0.25
GO:0021884	BP	GO:0021884	forebrain	6/1414	24/18903	0.007228621	0.0281097	0.01801321	UBB/NRP2/FGFR2/NDNF/NRP	6	0.25
GO:0032528	BP	GO:0032528	microvillus	6/1414	24/18903	0.007228621	0.0281097	0.01801321	STK26/GLDN/TWF2/EZR/POD	6	0.25
GO:0035357	BP	GO:0035357	peroxisome	6/1414	24/18903	0.007228621	0.0281097	0.01801321	TWIST1/BMP2/FABP5/CITED	6	0.25

GO:0036010	BP	GO:0036010	protein	6/1414	24/18903	0.007228621	0.0281097	0.01801321	NRP1/EZR/MSN/ARF6/VPS35	6	0.25
GO:0036120	BP	GO:0036120	cellular	6/1414	24/18903	0.007228621	0.0281097	0.01801321	PDGFRB/TLR4/IQGAP1/PDGF	6	0.25
GO:0051043	BP	GO:0051043	regulation of	6/1414	24/18903	0.007228621	0.0281097	0.01801321	TIMP2/TIMP4/APOE/ADAM9/	6	0.25
GO:0060706	BP	GO:0060706	cell	6/1414	24/18903	0.007228621	0.0281097	0.01801321	SNAI1/SPINT2/MDFI/STK4/	6	0.25
GO:0060907	BP	GO:0060907	positive	6/1414	24/18903	0.007228621	0.0281097	0.01801321	PLCG2/MAPKAPK2/CD74/LAP	6	0.25
GO:0061162	BP	GO:0061162	establishment	6/1414	24/18903	0.007228621	0.0281097	0.01801321	CDC42/RHOA/MSN/MAP1B/FA	6	0.25
GO:0120255	BP	GO:0120255	olefinic	6/1414	24/18903	0.007228621	0.0281097	0.01801321	EGR1/DKK3/DAB2/BMP2/BMP	6	0.25
GO:1904666	BP	GO:1904666	regulation of	6/1414	24/18903	0.007228621	0.0281097	0.01801321	UBE2S/RPS20/RPS15/RPS7/	6	0.25
GO:0045732	BP	GO:0045732	positive	26/1414	209/18903	0.007287742	0.0282642	0.01811228	DAB2/FOXO1/HSPA1A/HSPA1	26	0.124401913875598
GO:0010769	BP	GO:0010769	regulation of	15/1414	100/18903	0.007299421	0.0282642	0.01811228	DAB2/PTPRD/FLNA/MELTF/P	15	0.15
GO:1990830	BP	GO:1990830	cellular	15/1414	100/18903	0.007299421	0.0282642	0.01811228	SOCS3/PCOLCE2/NRP2/SRM/	15	0.15
GO:0030521	BP	GO:0030521	androgen	9/1414	47/18903	0.007299787	0.0282642	0.01811228	FOXP1/DAB2/DNAJA1/PMEPA	9	0.191489361702128
GO:0090199	BP	GO:0090199	regulation of	9/1414	47/18903	0.007299787	0.0282642	0.01811228	LMNA/PLAUR/PRELID1/NOL3	9	0.191489361702128
GO:0009595	BP	GO:0009595	detection of	8/1414	39/18903	0.007321677	0.0282642	0.01811228	FAP/HLA-	8	0.205128205128205
GO:0030279	BP	GO:0030279	negative	8/1414	39/18903	0.007321677	0.0282642	0.01811228	ECM1/RBPJ/LTBP3/RFLNB/C	8	0.205128205128205
GO:0032373	BP	GO:0032373	positive	8/1414	39/18903	0.007321677	0.0282642	0.01811228	ABCA5/NFKBIA/ANXA2/CAV1	8	0.205128205128205
GO:0032376	BP	GO:0032376	positive	8/1414	39/18903	0.007321677	0.0282642	0.01811228	ABCA5/NFKBIA/ANXA2/CAV1	8	0.205128205128205
GO:0042401	BP	GO:0042401	cellular	8/1414	39/18903	0.007321677	0.0282642	0.01811228	SRM/SAT1/OAZ1/ODC1/SMS/	8	0.205128205128205
GO:0071634	BP	GO:0071634	regulation of	8/1414	39/18903	0.007321677	0.0282642	0.01811228	LTBP1/LUM/FN1/PTGS2/TYR	8	0.205128205128205
GO:0032409	BP	GO:0032409	regulation of	37/1414	326/18903	0.007356153	0.0283786	0.01818553	TWIST1/ACTB/VMP1/FHL1/A	37	0.113496932515337
GO:0048593	BP	GO:0048593	camera-type	18/1414	129/18903	0.007530091	0.0290304	0.01860323	THY1/AQP1/TWIST1/ZEB1/N	18	0.13953488372093
GO:0051896	BP	GO:0051896	regulation of	24/1414	189/18903	0.007551871	0.0290951	0.01864471	CHI3L1/H19/DDIT3/FGFR1/	24	0.126984126984127
GO:0002706	BP	GO:0002706	regulation of	23/1414	179/18903	0.007648646	0.0294485	0.01887117	CADM1/LAG3/CD55/TGFB1/H	23	0.128491620111732
GO:0050852	BP	GO:0050852	T cell	19/1414	139/18903	0.007660589	0.0294750	0.01888817	THY1/PLCG2/PDE4B/RPS3/N	19	0.136690647482014
GO:0050851	BP	GO:0050851	antigen	30/1414	252/18903	0.007779386	0.0299124	0.01916844	THY1/FOXP1/PLCG2/PDE4B/	30	0.119047619047619
GO:0072594	BP	GO:0072594	establishment of protein	48/1414	449/18903	0.007862419 53957058	0.0302117 873348585	0.01936027 44504647	LMNA/FLNA/LAMP2/GLI3/HS PA8/DDIT3/DNAJA1/NFKBIA	48	0.106904231625835
GO:1990823	BP	GO:1990823	response to	15/1414	101/18903	0.007996332	0.0307061	0.01967705	SOCS3/PCOLCE2/NRP2/SRM/	15	0.148514851485149
GO:0001843	BP	GO:0001843	neural tube	14/1414	92/18903	0.008254077	0.0316236	0.02026500	TWIST1/CTHRC1/SPINT2/TG	14	0.152173913043478
GO:0002028	BP	GO:0002028	regulation of	14/1414	92/18903	0.008254077	0.0316236	0.02026500	ANK3/FXYD1/GLRX/SERPINE	14	0.152173913043478
GO:0002862	BP	GO:0002862	negative	7/1414	32/18903	0.008273211	0.0316236	0.02026500	PSMB4/HLA-	7	0.21875
GO:0010743	BP	GO:0010743	regulation of	7/1414	32/18903	0.008273211	0.0316236	0.02026500	ABCA5/PLA2G2A/NFKBIA/MS	7	0.21875
GO:0045671	BP	GO:0045671	negative	7/1414	32/18903	0.008273211	0.0316236	0.02026500	MAFB/FBN1/PIK3R1/TNFRSF	7	0.21875
GO:0061037	BP	GO:0061037	negative	7/1414	32/18903	0.008273211	0.0316236	0.02026500	CTSK/GLI3/EFEMP1/LTBP3/	7	0.21875
GO:0061099	BP	GO:0061099	negative	7/1414	32/18903	0.008273211	0.0316236	0.02026500	THY1/SH3BP5/GPRC5A/CAV1	7	0.21875
GO:0051147	BP	GO:0051147	regulation of	21/1414	160/18903	0.008304375	0.0317219	0.02032801	FOXP1/ZEB1/PIEZO1/SOD2/	21	0.13125

GO:0032613	BP	GO:0032613	interleukin-	11/1414	65/18903	0.008343680	0.0318304	0.02039751	PLCG2/HSPD1/HLA-	11	0.169230769230769
GO:0032653	BP	GO:0032653	regulation of	11/1414	65/18903	0.008343680	0.0318304	0.02039751	PLCG2/HSPD1/HLA-	11	0.169230769230769
GO:0032611	BP	GO:0032611	interleukin-1	16/1414	111/18903	0.008368258	0.0318824	0.02043087	EGR1/FOXP1/HSPB1/SERPIN	16	0.144144144144144
GO:0032651	BP	GO:0032651	regulation of	16/1414	111/18903	0.008368258	0.0318824	0.02043087	EGR1/FOXP1/HSPB1/SERPIN	16	0.144144144144144
GO:0003197	BP	GO:0003197	endocardial	9/1414	48/18903	0.008402365	0.0319498	0.02047402	TWIST1/RBPJ/SNAI1/BMP2/	9	0.1875
GO:0045581	BP	GO:0045581	negative	9/1414	48/18903	0.008402365	0.0319498	0.02047402	RUNX1/GLI3/LAG3/ANXA1/C	9	0.1875
GO:0046850	BP	GO:0046850	regulation of	9/1414	48/18903	0.008402365	0.0319498	0.02047402	LTBP3/TF/SPP1/TNFRSF11B	9	0.1875
GO:0042310	BP	GO:0042310	vasoconstrict	13/1414	83/18903	0.008424875	0.0320145	0.02051550	MMP2/COMP/PTGS2/CAV1/AD	13	0.156626506024096
GO:0032732	BP	GO:0032732	positive	12/1414	74/18903	0.008471153	0.0321484	0.02060135	EGR1/S100A13/SAA1/HSPB1	12	0.162162162162162
GO:0045123	BP	GO:0045123	cellular	12/1414	74/18903	0.008471153	0.0321484	0.02060135	THY1/CD99/VCAM1/ICAM1/C	12	0.162162162162162
GO:1903829	BP	GO:1903829	positive regulation of	48/1414	451/18903	0.008514165 11816219	0.0322907 185528219	0.02069249 21871151	EPB41L2/SOX4/FLNA/GLI3/ ANK3/RBP4/PIK3R1/RAN/SQ	48	0.106430155210643
GO:0009309	BP	GO:0009309	amine	8/1414	40/18903	0.008565680	0.0324649	0.02080416	SRM/SAT1/OAZ1/ODC1/SMS/	8	0.2
GO:0008217	BP	GO:0008217	regulation of	24/1414	191/18903	0.008573012	0.0324716	0.02080845	COL1A2/TPM1/SOD2/PTGS2/	24	0.12565445026178
GO:0032355	BP	GO:0032355	response to	17/1414	121/18903	0.008632265	0.0326748	0.02093867	COL1A1/MMP2/PDGFRB/CRYA	17	0.140495867768595
GO:0001946	BP	GO:0001946	lymphangiogen	5/1414	18/18903	0.008746374	0.0327666	0.02099744	PDPN/CLEC14A/SOX18/TIE1	5	0.277777777777778
GO:0002076	BP	GO:0002076	osteoblast	5/1414	18/18903	0.008746374	0.0327666	0.02099744	JUND/BGLAP/SATB2/RUNX2/	5	0.277777777777778
GO:0006595	BP	GO:0006595	polyamine	5/1414	18/18903	0.008746374	0.0327666	0.02099744	SRM/SAT1/OAZ1/ODC1/SMS	5	0.277777777777778
GO:0008356	BP	GO:0008356	asymmetric	5/1414	18/18903	0.008746374	0.0327666	0.02099744	SOX5/ZBTB16/ACTR2/ACTR3	5	0.277777777777778
GO:0036499	BP	GO:0036499	PERK-mediated	5/1414	18/18903	0.008746374	0.0327666	0.02099744	DDIT3/PPP1R15A/ATF4/HSP	5	0.277777777777778
GO:0051770	BP	GO:0051770	positive	5/1414	18/18903	0.008746374	0.0327666	0.02099744	MAP2K6/NAMPT/CCL2/TLR4/	5	0.277777777777778
GO:0051917	BP	GO:0051917	regulation of	5/1414	18/18903	0.008746374	0.0327666	0.02099744	FAP/PLAUR/THBS1/PLAT/TH	5	0.277777777777778
GO:0060263	BP	GO:0060263	regulation of	5/1414	18/18903	0.008746374	0.0327666	0.02099744	CLEC7A/NCF1/GRN/RAC1/RP	5	0.277777777777778
GO:0060391	BP	GO:0060391	positive	5/1414	18/18903	0.008746374	0.0327666	0.02099744	DAB2/BMP2/TGFB1/BMP6/BM	5	0.277777777777778
GO:0060602	BP	GO:0060602	branch	5/1414	18/18903	0.008746374	0.0327666	0.02099744	SIX1/SPRY2/FGF1/FGFR2/S	5	0.277777777777778
GO:0060644	BP	GO:0060644	mammary gland	5/1414	18/18903	0.008746374	0.0327666	0.02099744	LBH/FGF2/CEBPB/ID2/MGMT	5	0.277777777777778
GO:0072567	BP	GO:0072567	chemokine (C-	5/1414	18/18903	0.008746374	0.0327666	0.02099744	FOXP1/KLF4/CD74/MBP/TLR	5	0.277777777777778
GO:0072673	BP	GO:0072673	lamellipodium	5/1414	18/18903	0.008746374	0.0327666	0.02099744	PDPN/CD44/PLEKHO1/SNX2/	5	0.277777777777778
GO:0150079	BP	GO:0150079	negative	5/1414	18/18903	0.008746374	0.0327666	0.02099744	NR1D1/PTPRC/TREM2/GRN/C	5	0.277777777777778
GO:1902683	BP	GO:1902683	regulation of	5/1414	18/18903	0.008746374	0.0327666	0.02099744	GPC6/TYROBP/ADAM10/STX7	5	0.277777777777778
GO:2000341	BP	GO:2000341	regulation of	5/1414	18/18903	0.008746374	0.0327666	0.02099744	FOXP1/KLF4/CD74/MBP/TLR	5	0.277777777777778
GO:0021854	BP	GO:0021854	hypothalamus	6/1414	25/18903	0.008920725	0.0332277	0.02129293	UBB/NRP2/NDNF/NRP1/BAX/	6	0.24
GO:0043567	BP	GO:0043567	regulation of	6/1414	25/18903	0.008920725	0.0332277	0.02129293	IGFBP4/CILP/IGFBP6/BMP2	6	0.24
GO:0045649	BP	GO:0045649	regulation of	6/1414	25/18903	0.008920725	0.0332277	0.02129293	INHBA/TGFB1/ID2/C1QC/HC	6	0.24
GO:0050927	BP	GO:0050927	positive	6/1414	25/18903	0.008920725	0.0332277	0.02129293	VEGFA/CXCL8/PGF/S1PR1/K	6	0.24
GO:0061339	BP	GO:0061339	establishment	6/1414	25/18903	0.008920725	0.0332277	0.02129293	CDC42/RHOA/MSN/MAP1B/FA	6	0.24

GO:0071450	BP	GO:0071450	cellular	6/1414	25/18903	0.008920725	0.0332277	0.02129293	H19/SOD2/PRDX1/SOD3/GLR	6	0.24
GO:0071451	BP	GO:0071451	cellular	6/1414	25/18903	0.008920725	0.0332277	0.02129293	H19/SOD2/PRDX1/SOD3/GLR	6	0.24
GO:0090023	BP	GO:0090023	positive	6/1414	25/18903	0.008920725	0.0332277	0.02129293	CD74/C3AR1/CXCL8/C5AR1/	6	0.24
GO:2000679	BP	GO:2000679	positive	6/1414	25/18903	0.008920725	0.0332277	0.02129293	TWIST1/TGFB1/GTF2B/KLF4	6	0.24
GO:0090175	BP	GO:0090175	regulation of	10/1414	57/18903	0.009044867	0.0336686	0.02157547	DAB2/CTHRC1/GPC6/MAGI2/	10	0.175438596491228
GO:0045666	BP	GO:0045666	positive	14/1414	93/18903	0.009066904	0.0337076	0.02160046	NBL1/TCF4/ZEB1/CDON/FGF	14	0.150537634408602
GO:0060606	BP	GO:0060606	tube closure	14/1414	93/18903	0.009066904	0.0337076	0.02160046	TWIST1/CTHRC1/SPINT2/TG	14	0.150537634408602
GO:0043500	BP	GO:0043500	muscle	17/1414	122/18903	0.009351614	0.0346698	0.02221706	FOXP1/LMNA/FOXO1/GSN/CF	17	0.139344262295082
GO:0071479	BP	GO:0071479	cellular	12/1414	75/18903	0.009417165	0.0346698	0.02221706	EGR1/CRYAB/CDKN1A/HSPA5	12	0.16
GO:0007254	BP	GO:0007254	JNK cascade	22/1414	172/18903	0.009425726	0.0346698	0.02221706	GADD45B/GADD45G/DNAJA1/	22	0.127906976744186
GO:0001553	BP	GO:0001553	luteinization	4/1414	12/18903	0.009480262	0.0346698	0.02221706	MMP2/PDGFRA/A2M/INHBA	4	0.333333333333333
GO:0001886	BP	GO:0001886	endothelial	4/1414	12/18903	0.009480262	0.0346698	0.02221706	COL15A1/COL18A1/NOTCH4/	4	0.333333333333333
GO:0002424	BP	GO:0002424	T cell	4/1414	12/18903	0.009480262	0.0346698	0.02221706	HSPD1/HLA-DRB1/AHR/HLA-	4	0.333333333333333
GO:0006705	BP	GO:0006705	mineralocorti	4/1414	12/18903	0.009480262	0.0346698	0.02221706	DKK3/DAB2/BMP2/BMP6	4	0.333333333333333
GO:0014745	BP	GO:0014745	negative	4/1414	12/18903	0.009480262	0.0346698	0.02221706	LMNA/FOXO1/NOL3/IGFBP5	4	0.333333333333333
GO:0014889	BP	GO:0014889	muscle	4/1414	12/18903	0.009480262	0.0346698	0.02221706	GSN/CFLAR/NOL3/GATM	4	0.333333333333333
GO:0031953	BP	GO:0031953	negative	4/1414	12/18903	0.009480262	0.0346698	0.02221706	JUN/CAV1/PTPRC/ENG	4	0.333333333333333
GO:0032817	BP	GO:0032817	regulation of	4/1414	12/18903	0.009480262	0.0346698	0.02221706	FCGR3A/IL18/HLA-	4	0.333333333333333
GO:0032908	BP	GO:0032908	regulation of	4/1414	12/18903	0.009480262	0.0346698	0.02221706	LUM/TYROBP/ATP6AP2/THBS	4	0.333333333333333
GO:0034135	BP	GO:0034135	regulation of	4/1414	12/18903	0.009480262	0.0346698	0.02221706	LYN/TREM2/CYBA/TNFAIP3	4	0.333333333333333
GO:0034145	BP	GO:0034145	positive	4/1414	12/18903	0.009480262	0.0346698	0.02221706	PELI1/CD14/NINJ1/PTPN22	4	0.333333333333333
GO:0038063	BP	GO:0038063	collagen-	4/1414	12/18903	0.009480262	0.0346698	0.02221706	COL1A1/DDR2/COL4A1/COL4	4	0.333333333333333
GO:0040034	BP	GO:0040034	regulation of	4/1414	12/18903	0.009480262	0.0346698	0.02221706	RBPJ/HES1/SERPINE2/JAG1	4	0.333333333333333
GO:0042447	BP	GO:0042447	hormone	4/1414	12/18903	0.009480262	0.0346698	0.02221706	DIO2/SPP1/HSD17B11/ECE1	4	0.333333333333333
GO:0043380	BP	GO:0043380	regulation of	4/1414	12/18903	0.009480262	0.0346698	0.02221706	HLA-DRB1/HLA-	4	0.333333333333333
GO:0043383	BP	GO:0043383	negative T	4/1414	12/18903	0.009480262	0.0346698	0.02221706	GLI3/CD74/PTPRC/DOCK2	4	0.333333333333333
GO:0071472	BP	GO:0071472	cellular	4/1414	12/18903	0.009480262	0.0346698	0.02221706	ZFP36L1/AQP1/TRPV4/FBP1	4	0.333333333333333
GO:0072110	BP	GO:0072110	glomerular	4/1414	12/18903	0.009480262	0.0346698	0.02221706	EGR1/PDGFRB/CFLAR/PDGFB	4	0.333333333333333
GO:0099010	BP	GO:0099010	modification	4/1414	12/18903	0.009480262	0.0346698	0.02221706	CTTNBP2/PFN1/CYFIP1/RHO	4	0.333333333333333
GO:1900152	BP	GO:1900152	negative	4/1414	12/18903	0.009480262	0.0346698	0.02221706	TOB1/PABPC1/YBX1/HNRNPU	4	0.333333333333333
GO:1900272	BP	GO:1900272	negative	4/1414	12/18903	0.009480262	0.0346698	0.02221706	PTN/TYROBP/APOE/APP	4	0.333333333333333
GO:1902950	BP	GO:1902950	regulation of	4/1414	12/18903	0.009480262	0.0346698	0.02221706	FCGR2B/APOE/VPS35/FYN	4	0.333333333333333
GO:1905245	BP	GO:1905245	regulation of	4/1414	12/18903	0.009480262	0.0346698	0.02221706	LYN/GRN/PICALM/EFNA1	4	0.333333333333333
GO:0042552	BP	GO:0042552	myelination	19/1414	142/18903	0.009573129	0.0349875	0.02242064	ID4/TSPAN2/PTN/NDRG1/TY	19	0.133802816901408
GO:0070509	BP	GO:0070509	calcium ion	9/1414	49/18903	0.009626867	0.0351178	0.02250420	PDGFRB/HES1/TRPV4/CCL3/	9	0.183673469387755
GO:0099054	BP	GO:0099054	presynapse	9/1414	49/18903	0.009626867	0.0351178	0.02250420	PTPRD/FARP1/GPC6/SDCBP/	9	0.183673469387755

GO:1903426	BP	GO:1903426	regulation of	9/1414	49/18903	0.009626867	0.0351178	0.02250420	CCN6/H19/PLCG2/SOD2/CFL	9	0.183673469387755
GO:0009895	BP	GO:0009895	negative	37/1414	332/18903	0.009739775	0.0355075	0.02275391	FUS/TIMP2/FLNA/TIMP4/ZF	37	0.11144578313253
GO:0001782	BP	GO:0001782	B cell	7/1414	33/18903	0.009837599	0.0356193	0.02282552	CD74/LYN/NCKAP1L/MEF2C/	7	0.212121212121212
GO:0002431	BP	GO:0002431	Fc receptor	7/1414	33/18903	0.009837599	0.0356193	0.02282552	RABGEF1/FCER1G/PTPRC/FC	7	0.212121212121212
GO:0007035	BP	GO:0007035	vacuolar	7/1414	33/18903	0.009837599	0.0356193	0.02282552	ATP6V0C/ATP6V0B/GRN/PPT	7	0.212121212121212
GO:0038094	BP	GO:0038094	Fc-gamma	7/1414	33/18903	0.009837599	0.0356193	0.02282552	FCER1G/PTPRC/FCGR3A/FCG	7	0.212121212121212
GO:0045577	BP	GO:0045577	regulation of	7/1414	33/18903	0.009837599	0.0356193	0.02282552	ZFP36L1/INHBA/XBP1/ZFP3	7	0.212121212121212
GO:0048799	BP	GO:0048799	animal organ	7/1414	33/18903	0.009837599	0.0356193	0.02282552	ZBTB16/XYLT1/BMP2/RFLNB	7	0.212121212121212
GO:0051497	BP	GO:0051497	negative	7/1414	33/18903	0.009837599	0.0356193	0.02282552	PIK3R1/PFN1/PAK2/TJP1/S	7	0.212121212121212
GO:0060351	BP	GO:0060351	cartilage	7/1414	33/18903	0.009837599	0.0356193	0.02282552	COL1A1/SERPINH1/COMP/CO	7	0.212121212121212
GO:0090169	BP	GO:0090169	regulation of	7/1414	33/18903	0.009837599	0.0356193	0.02282552	HSPA1A/HSPA1B/CHMP4B/NU	7	0.212121212121212
GO:0090279	BP	GO:0090279	regulation of	7/1414	33/18903	0.009837599	0.0356193	0.02282552	PDGFRB/HES1/CCL3/CCL2/S	7	0.212121212121212
GO:1902253	BP	GO:1902253	regulation of	7/1414	33/18903	0.009837599	0.0356193	0.02282552	UBB/CD44/PTTG1IP/CD74/R	7	0.212121212121212
GO:0007219	BP	GO:0007219	Notch	23/1414	183/18903	0.009896824	0.0358115	0.02294869	POSTN/SIX1/RBPJ/NOTCH2/	23	0.12568306010929
GO:0048704	BP	GO:0048704	embryonic	14/1414	94/18903	0.009941488	0.0359328	0.02302646	PDGFRA/TWIST1/SIX1/PRRX	14	0.148936170212766
GO:0006040	BP	GO:0006040	amino sugar	8/1414	41/18903	0.009961169	0.0359328	0.02302646	CHI3L1/CHST3/CSGALNACT1	8	0.195121951219512
GO:0032733	BP	GO:0032733	positive	8/1414	41/18903	0.009961169	0.0359328	0.02302646	PLCG2/HSPD1/CLEC7A/CD83	8	0.195121951219512
GO:0072210	BP	GO:0072210	metanephric	8/1414	41/18903	0.009961169	0.0359328	0.02302646	EGR1/PDGFRA/AQP1/PDGFRB	8	0.195121951219512
GO:0072595	BP	GO:0072595	maintenance	8/1414	41/18903	0.009961169	0.0359328	0.02302646	TXN/INSIG1/HSPA5/SP100/	8	0.195121951219512
GO:0006413	BP	GO:0006413	translational	17/1414	123/18903	0.010117959	0.0364759	0.02337445	RPS3/EIF1/PPP1R15A/EIF1	17	0.138211382113821
GO:0015980	BP	GO:0015980	energy	37/1414	333/18903	0.010193128	0.0367242	0.02353356	NDUFA4/NDUFB1/ATP5ME/UQ	37	0.111111111111111
GO:0033619	BP	GO:0033619	membrane	10/1414	58/18903	0.010216063	0.0367841	0.02357195	TIMP2/TIMP4/TGFB1/CTSH/	10	0.172413793103448
GO:0045727	BP	GO:0045727	positive	19/1414	143/18903	0.010289591	0.0370260	0.02372696	SOX4/LARP6/RPS4X/PPP1R1	19	0.132867132867133
GO:0045685	BP	GO:0045685	regulation of	12/1414	76/18903	0.010443221	0.0375325	0.02405154	ID4/HES1/PTN/NR1D1/SERP	12	0.157894736842105
GO:0060420	BP	GO:0060420	regulation of	12/1414	76/18903	0.010443221	0.0375325	0.02405154	FOXP1/RBPJ/RUNX1/RBP4/F	12	0.157894736842105
GO:1904377	BP	GO:1904377	positive	11/1414	67/18903	0.010455587	0.0375538	0.02406520	EPB41L2/PIK3R1/SQSTM1/T	11	0.164179104477612
GO:0016197	BP	GO:0016197	endosomal	29/1414	247/18903	0.010527615	0.0377892	0.02421607	EEA1/SQSTM1/CHMP4B/GOLT	29	0.117408906882591
GO:0002824	BP	GO:0002824	positive	16/1414	114/18903	0.010732192	0.0384999	0.02467146	CD55/TGFB1/HSPD1/NFKBIZ	16	0.140350877192982
GO:0010259	BP	GO:0010259	multicellular	6/1414	26/18903	0.010878100	0.0388560	0.02489969	COMP/CRYAB/INHBA/GNA13/	6	0.230769230769231
GO:0010882	BP	GO:0010882	regulation of	6/1414	26/18903	0.010878100	0.0388560	0.02489969	CALM2/GSTO1/ATP1B1/SLC8	6	0.230769230769231
GO:0010954	BP	GO:0010954	positive	6/1414	26/18903	0.010878100	0.0388560	0.02489969	MELTF/GSN/ANXA2/ENO1/S1	6	0.230769230769231
GO:0043931	BP	GO:0043931	ossification	6/1414	26/18903	0.010878100	0.0388560	0.02489969	ZBTB16/XYLT1/BMP2/RFLNB	6	0.230769230769231
GO:0046639	BP	GO:0046639	negative	6/1414	26/18903	0.010878100	0.0388560	0.02489969	RUNX1/GLI3/ANXA1/BCL6/S	6	0.230769230769231
GO:0050857	BP	GO:0050857	positive	6/1414	26/18903	0.010878100	0.0388560	0.02489969	FOXP1/RPS3/PTPRC/CMTM3/	6	0.230769230769231
GO:0050926	BP	GO:0050926	regulation of	6/1414	26/18903	0.010878100	0.0388560	0.02489969	VEGFA/CXCL8/PGF/S1PR1/K	6	0.230769230769231
GO:0051209	BP	GO:0051209	release of	17/1414	124/18903	0.010933367	0.0390295	0.02501087	THY1/FLNA/PLCG2/DDIT3/F	17	0.137096774193548

GO:0060043	BP	GO:0060043	regulation of	9/1414	50/18903	0.010981242	0.0391765	0.02510503	RBPJ/RUNX1/RBP4/FGF2/FG	9	0.18
GO:0030048	BP	GO:0030048	actin	18/1414	134/18903	0.011032904	0.0393367	0.02520772	GJA1/FRMD6/WIPF1/TPM1/F	18	0.134328358208955
GO:0007272	BP	GO:0007272	ensheathment	19/1414	144/18903	0.011048276	0.0393434	0.02521202	ID4/TSPAN2/PTN/NDRG1/TY	19	0.131944444444444
GO:0008366	BP	GO:0008366	axon	19/1414	144/18903	0.011048276	0.0393434	0.02521202	ID4/TSPAN2/PTN/NDRG1/TY	19	0.131944444444444
GO:0007213	BP	GO:0007213	G protein-	5/1414	19/18903	0.011151784	0.0396153	0.02538623	RGS10/GNAQ/GNAI2/PLCB1/	5	0.263157894736842
GO:0010544	BP	GO:0010544	negative	5/1414	19/18903	0.011151784	0.0396153	0.02538623	PDGFRA/SERPINE2/APOE/PD	5	0.263157894736842
GO:0099563	BP	GO:0099563	modification	5/1414	19/18903	0.011151784	0.0396153	0.02538623	CTTNBP2/PFN1/CYFIP1/CDC	5	0.263157894736842
GO:2000136	BP	GO:2000136	regulation of	5/1414	19/18903	0.011151784	0.0396153	0.02538623	SIX1/RBPJ/HES1/GNG5/BMP	5	0.263157894736842
GO:1903050	BP	GO:1903050	regulation of	27/1414	227/18903	0.011267978	0.0400037	0.02563513	DAB2/HSPA1A/UBB/HSPA1B/	27	0.118942731277533
GO:0032456	BP	GO:0032456	endocytic	13/1414	86/18903	0.011276448	0.0400094	0.02563879	RAB13/ARL4C/CMTM6/RAB8B	13	0.151162790697674
GO:0007566	BP	GO:0007566	embryo	10/1414	59/18903	0.011499093	0.0407498	0.02611324	MMP2/GJA1/VMP1/IGFBP7/S	10	0.169491525423729
GO:0043903	BP	GO:0043903	regulation of	10/1414	59/18903	0.011499093	0.0407498	0.02611324	LGALS1/IFITM1/GSN/IFITM	10	0.169491525423729
GO:0045022	BP	GO:0045022	early	8/1414	42/18903	0.011518526	0.0407939	0.02614149	DAB2/FLNA/EEA1/EZR/MSN/	8	0.19047619047619
GO:0032729	BP	GO:0032729	positive	12/1414	77/18903	0.011553580	0.0408684	0.02618924	PDE4B/HSPD1/HLA-	12	0.155844155844156
GO:0045824	BP	GO:0045824	negative	12/1414	77/18903	0.011553580	0.0408684	0.02618924	A2M/ARRB2/VSIG4/SAMHD1/	12	0.155844155844156
GO:0000289	BP	GO:0000289	nuclear-	7/1414	34/18903	0.011607064	0.0409830	0.02626270	TNRC6A/ZFP36/BTG2/TOB1/	7	0.205882352941176
GO:0035308	BP	GO:0035308	negative	7/1414	34/18903	0.011607064	0.0409830	0.02626270	PPP1R15A/NCKAP1L/YWHAB/	7	0.205882352941176
GO:0070570	BP	GO:0070570	regulation of	7/1414	34/18903	0.011607064	0.0409830	0.02626270	THY1/PRRX1/FLNA/PTN/SPP	7	0.205882352941176
GO:0048640	BP	GO:0048640	negative	16/1414	115/18903	0.011627664	0.0410309	0.02629339	FOXP1/SEMA3C/NTN1/RBP4/	16	0.139130434782609
GO:0000288	BP	GO:0000288	nuclear-	11/1414	68/18903	0.011654228	0.0410501	0.02630572	ZFP36L1/TNRC6A/ZFP36/BT	11	0.161764705882353
GO:0030239	BP	GO:0030239	myofibril	11/1414	68/18903	0.011654228	0.0410501	0.02630572	PDGFRA/PDGFRB/MYL9/ACTG	11	0.161764705882353
GO:0042093	BP	GO:0042093	T-helper cell	11/1414	68/18903	0.011654228	0.0410501	0.02630572	FOXP1/JUNB/ANXA1/NFKBIZ	11	0.161764705882353
GO:0051283	BP	GO:0051283	negative	17/1414	125/18903	0.011799930	0.0415383	0.02661852	THY1/FLNA/PLCG2/DDIT3/F	17	0.136
GO:0003073	BP	GO:0003073	regulation of	14/1414	96/18903	0.011888214	0.0417986	0.02678534	TPM1/SOD2/ADM/CTSZ/CYBA	14	0.145833333333333
GO:0070664	BP	GO:0070664	negative	14/1414	96/18903	0.011888214	0.0417986	0.02678534	GPNMB/SDC4/PELI1/CEBPB/	14	0.145833333333333
GO:1901136	BP	GO:1901136	carbohydrate	22/1414	176/18903	0.012171194	0.0427678	0.02740641	NT5E/CHI3L1/FBXO2/CHI3L	22	0.125
GO:0030850	BP	GO:0030850	prostate	9/1414	51/18903	0.012473434	0.0437244	0.02801946	MMP2/TNC/ID4/CRIP1/GLI3	9	0.176470588235294
GO:0050982	BP	GO:0050982	detection of	9/1414	51/18903	0.012473434	0.0437244	0.02801946	PIEZO1/COL11A1/SERPINE2	9	0.176470588235294
GO:0060324	BP	GO:0060324	face	9/1414	51/18903	0.012473434	0.0437244	0.02801946	COL1A1/MMP2/PDGFRA/CRIS	9	0.176470588235294
GO:0060425	BP	GO:0060425	lung	9/1414	51/18903	0.012473434	0.0437244	0.02801946	RSPO2/SPRY2/FGFR2/CTSZ/	9	0.176470588235294
GO:0002832	BP	GO:0002832	negative	16/1414	116/18903	0.012580830	0.0440480	0.02822678	HTRA1/A2M/ARRB2/VSIG4/S	16	0.137931034482759
GO:0051702	BP	GO:0051702	biological	16/1414	116/18903	0.012580830	0.0440480	0.02822678	JUN/EEA1/HSPA8/FN1/HSPD	16	0.137931034482759
GO:0043547	BP	GO:0043547	positive	32/1414	283/18903	0.012664195	0.0443132	0.02839677	THY1/ASAP2/RGS16/TGM2/T	32	0.113074204946996
GO:0003084	BP	GO:0003084	positive	4/1414	13/18903	0.012894230	0.0446306	0.02860014	CYBA/RHOA/NR2F2/WNK1	4	0.307692307692308
GO:0006787	BP	GO:0006787	porphyrin-	4/1414	13/18903	0.012894230	0.0446306	0.02860014	SLCO2B1/HMOX1/BLVRB/BLV	4	0.307692307692308
GO:0031392	BP	GO:0031392	regulation of	4/1414	13/18903	0.012894230	0.0446306	0.02860014	PTGS2/ANXA1/FABP5/CD74	4	0.307692307692308

GO:0032341	BP	GO:0032341	aldosterone	4/1414	13/18903	0.012894230	0.0446306	0.02860014	DKK3/DAB2/BMP2/BMP6	4	0.307692307692308
GO:0032530	BP	GO:0032530	regulation of	4/1414	13/18903	0.012894230	0.0446306	0.02860014	TWF2/EZR/PODXL/FSCN1	4	0.307692307692308
GO:0033015	BP	GO:0033015	tetrapyrrole	4/1414	13/18903	0.012894230	0.0446306	0.02860014	SLCO2B1/HMOX1/BLVRB/BLV	4	0.307692307692308
GO:0034144	BP	GO:0034144	negative	4/1414	13/18903	0.012894230	0.0446306	0.02860014	NR1D1/LYN/TREM2/TNFAIP3	4	0.307692307692308
GO:0043379	BP	GO:0043379	memory T cell	4/1414	13/18903	0.012894230	0.0446306	0.02860014	HLA-DRB1/HLA-	4	0.307692307692308
GO:0051280	BP	GO:0051280	negative	4/1414	13/18903	0.012894230	0.0446306	0.02860014	CALM2/GSTO1/CALM3/CALM1	4	0.307692307692308
GO:0051451	BP	GO:0051451	myoblast	4/1414	13/18903	0.012894230	0.0446306	0.02860014	SIX1/ANXA1/PLEKHO1/ROCK	4	0.307692307692308
GO:0060100	BP	GO:0060100	positive	4/1414	13/18903	0.012894230	0.0446306	0.02860014	PLCG2/NCKAP1L/TREM2/RAB	4	0.307692307692308
GO:0075509	BP	GO:0075509	endocytosis	4/1414	13/18903	0.012894230	0.0446306	0.02860014	CTSL/CAV1/EPS15/CAV2	4	0.307692307692308
GO:1901857	BP	GO:1901857	positive	4/1414	13/18903	0.012894230	0.0446306	0.02860014	NUPR1/PRELID1/IFNAR1/IS	4	0.307692307692308
GO:1903651	BP	GO:1903651	positive	4/1414	13/18903	0.012894230	0.0446306	0.02860014	DAB2/EZR/MSN/RDX	4	0.307692307692308
GO:1905155	BP	GO:1905155	positive	4/1414	13/18903	0.012894230	0.0446306	0.02860014	PLCG2/NCKAP1L/TREM2/RAB	4	0.307692307692308
GO:1905907	BP	GO:1905907	negative	4/1414	13/18903	0.012894230	0.0446306	0.02860014	CRYAB/APOE/TREM2/PFDN2	4	0.307692307692308
GO:2001046	BP	GO:2001046	positive	4/1414	13/18903	0.012894230	0.0446306	0.02860014	FLNA/LIMS1/LIMS2/LAMB1	4	0.307692307692308
GO:2001198	BP	GO:2001198	regulation of	4/1414	13/18903	0.012894230	0.0446306	0.02860014	CEBPB/FCGR2B/HLA-	4	0.307692307692308
GO:0002753	BP	GO:0002753	cytoplasmic	10/1414	60/18903	0.012900267	0.0446306	0.02860014	MAP2K6/HSPA1A/HSPA1B/NF	10	0.166666666666667
GO:0055002	BP	GO:0055002	striated	11/1414	69/18903	0.012954851	0.0447398	0.02867014	PDGFRA/PDGFRB/MYL9/ACTG	11	0.159420289855072
GO:0055021	BP	GO:0055021	regulation of	11/1414	69/18903	0.012954851	0.0447398	0.02867014	FOXP1/RBPJ/RUNX1/RBP4/F	11	0.159420289855072
GO:0061180	BP	GO:0061180	mammary gland	11/1414	69/18903	0.012954851	0.0447398	0.02867014	LBH/NTN1/FGF2/CEBPB/FGF	11	0.159420289855072
GO:0006942	BP	GO:0006942	regulation of	14/1414	97/18903	0.012966579	0.0447538	0.02867911	TNNT3/NR4A1/TRPV4/PDE4B	14	0.144329896907216
GO:0002418	BP	GO:0002418	immune	6/1414	27/18903	0.013120758	0.0450726	0.02888340	HSPD1/HLA-	6	0.222222222222222
GO:0002710	BP	GO:0002710	negative	6/1414	27/18903	0.013120758	0.0450726	0.02888340	PTPRC/AHR/FCGR2B/NCKAP1	6	0.222222222222222
GO:0003401	BP	GO:0003401	axis	6/1414	27/18903	0.013120758	0.0450726	0.02888340	SIX1/MAGI2/SPRY2/FGF1/F	6	0.222222222222222
GO:0010875	BP	GO:0010875	positive	6/1414	27/18903	0.013120758	0.0450726	0.02888340	NFKBIA/CAV1/APOE/TREM2/	6	0.222222222222222
GO:0014829	BP	GO:0014829	vascular	6/1414	27/18903	0.013120758	0.0450726	0.02888340	COMP/SLC8A1/DOCK4/ATP2B	6	0.222222222222222
GO:0036037	BP	GO:0036037	CD8-positive,	6/1414	27/18903	0.013120758	0.0450726	0.02888340	RUNX1/NCKAP1L/HLA-	6	0.222222222222222
GO:0044342	BP	GO:0044342	type B	6/1414	27/18903	0.013120758	0.0450726	0.02888340	IGFBP4/NR4A1/NR1D1/NUPR	6	0.222222222222222
GO:1901623	BP	GO:1901623	regulation of	6/1414	27/18903	0.013120758	0.0450726	0.02888340	CCL3/CCL2/CCL4/ADAM10/W	6	0.222222222222222
GO:0060236	BP	GO:0060236	regulation of	8/1414	43/18903	0.013248042	0.0454831	0.02914643	HSPA1A/HSPA1B/CHMP4B/PK	8	0.186046511627907
GO:0010721	BP	GO:0010721	negative	23/1414	188/18903	0.013428622	0.0460759	0.02952633	THY1/SEMA3C/FBN1/ID4/NT	23	0.122340425531915
GO:0009206	BP	GO:0009206	purine	16/1414	117/18903	0.013594095	0.0463215	0.02968369	H19/NDUFB1/ATP5ME/ATP6V	16	0.136752136752137
GO:0021782	BP	GO:0021782	glial cell	16/1414	117/18903	0.013594095	0.0463215	0.02968369	MXRA8/SOX4/ID4/TSPAN2/N	16	0.136752136752137
GO:0006119	BP	GO:0006119	oxidative	19/1414	147/18903	0.013594580	0.0463215	0.02968369	NDUFA4/NDUFB1/ATP5ME/UQ	19	0.129251700680272
GO:0008584	BP	GO:0008584	male gonad	19/1414	147/18903	0.013594580	0.0463215	0.02968369	PDGFRA/PDGFRB/COL9A3/PR	19	0.129251700680272
GO:0002719	BP	GO:0002719	negative	7/1414	35/18903	0.013595482	0.0463215	0.02968369	TWIST1/TGFB1/RABGEF1/BS	7	0.2
GO:0014808	BP	GO:0014808	release of	7/1414	35/18903	0.013595482	0.0463215	0.02968369	CALM2/GSTO1/NOL3/CCL3/S	7	0.2

GO:0032633	BP	GO:0032633	interleukin-4	7/1414	35/18903	0.013595482	0.0463215	0.02968369	DDIT3/CEBPB/HLA-	7	0.2
GO:0032673	BP	GO:0032673	regulation of	7/1414	35/18903	0.013595482	0.0463215	0.02968369	DDIT3/CEBPB/HLA-	7	0.2
GO:0043276	BP	GO:0043276	anoikis	7/1414	35/18903	0.013595482	0.0463215	0.02968369	PIK3R3/CAV1/ITGA5/MCL1/	7	0.2
GO:0048048	BP	GO:0048048	embryonic eye	7/1414	35/18903	0.013595482	0.0463215	0.02968369	TWIST1/FBN1/ZEB1/EFEMP1	7	0.2
GO:0060914	BP	GO:0060914	heart	7/1414	35/18903	0.013595482	0.0463215	0.02968369	SIX1/RBPJ/HES1/BMP2/GNG	7	0.2
GO:0062098	BP	GO:0062098	regulation of	7/1414	35/18903	0.013595482	0.0463215	0.02968369	CFLAR/NUPR1/PELI1/BIRC2	7	0.2
GO:0098657	BP	GO:0098657	import into	29/1414	252/18903	0.013631096	0.0464157	0.02974407	ACTB/TRPV4/SLC29A1/SLC3	29	0.115079365079365
GO:0051282	BP	GO:0051282	regulation of	17/1414	127/18903	0.013695001	0.0466061	0.02986608	THY1/FLNA/PLCG2/DDIT3/F	17	0.133858267716535
GO:0002888	BP	GO:0002888	positive	5/1414	20/18903	0.013971301	0.0472432	0.03027435	TYROBP/ITGB2/SPI1/ITGAM	5	0.25
GO:0014856	BP	GO:0014856	skeletal	5/1414	20/18903	0.013971301	0.0472432	0.03027435	FOS/SIX1/CFLAR/FGF2/CAV	5	0.25
GO:0035455	BP	GO:0035455	response to	5/1414	20/18903	0.013971301	0.0472432	0.03027435	IFITM1/IFITM2/BST2/IFNA	5	0.25
GO:0042053	BP	GO:0042053	regulation of	5/1414	20/18903	0.013971301	0.0472432	0.03027435	ITGB2/ITGAM/ALDH2/NR4A2	5	0.25
GO:0042069	BP	GO:0042069	regulation of	5/1414	20/18903	0.013971301	0.0472432	0.03027435	ITGB2/ITGAM/ALDH2/NR4A2	5	0.25
GO:0045655	BP	GO:0045655	regulation of	5/1414	20/18903	0.013971301	0.0472432	0.03027435	FOXP1/ZFP36L1/HLA-	5	0.25
GO:0061323	BP	GO:0061323	cell	5/1414	20/18903	0.013971301	0.0472432	0.03027435	SIX1/RBPJ/HES1/GNG5/BMP	5	0.25
GO:0072376	BP	GO:0072376	protein	5/1414	20/18903	0.013971301	0.0472432	0.03027435	FLNA/FN1/F13A1/PRCP/THB	5	0.25
GO:0098543	BP	GO:0098543	detection of	5/1414	20/18903	0.013971301	0.0472432	0.03027435	HLA-	5	0.25
GO:1903579	BP	GO:1903579	negative	5/1414	20/18903	0.013971301	0.0472432	0.03027435	H19/NUPR1/DDIT4/PID1/FB	5	0.25
GO:2000269	BP	GO:2000269	regulation of	5/1414	20/18903	0.013971301	0.0472432	0.03027435	NUPR1/STK17A/STK17B/GAS	5	0.25
GO:0002720	BP	GO:0002720	positive	12/1414	79/18903	0.014044363	0.0474627	0.03041503	PLCG2/CD55/MAPKAPK2/CD7	12	0.151898734177215
GO:0043392	BP	GO:0043392	negative	9/1414	52/18903	0.014111342	0.0476615	0.03054239	JUN/DDIT3/NFKBIA/MDFI/T	9	0.173076923076923
GO:0045055	BP	GO:0045055	regulated	28/1414	242/18903	0.014172795	0.0478413	0.03065764	S100A13/SCIN/STEAP2/RAB	28	0.115702479338843
GO:0002294	BP	GO:0002294	CD4-positive,	11/1414	70/18903	0.014362610	0.0483980	0.03101439	FOXP1/JUNB/ANXA1/NFKBIZ	11	0.157142857142857
GO:0006081	BP	GO:0006081	cellular	11/1414	70/18903	0.014362610	0.0483980	0.03101439	DKK3/DAB2/BMP2/BMP6/TKT	11	0.157142857142857
GO:0051881	BP	GO:0051881	regulation of	11/1414	70/18903	0.014362610	0.0483980	0.03101439	CCN6/UBB/SOD2/PRELID1/P	11	0.157142857142857
GO:0060135	BP	GO:0060135	maternal	10/1414	61/18903	0.014425881	0.0485832	0.03113304	PTN/JUNB/STC2/SPP1/PTGS	10	0.163934426229508
GO:0032147	BP	GO:0032147	activation of	19/1414	148/18903	0.014539156	0.0489364	0.03135939	CHI3L1/GPRC5C/GPRC5A/TX	19	0.128378378378378
GO:0048864	BP	GO:0048864	stem cell	13/1414	89/18903	0.014824585	0.0498683	0.03195659	TWIST1/SEMA3C/HES1/NRP2	13	0.146067415730337
GO:0006509	BP	GO:0006509	membrane	8/1414	44/18903	0.015159849	0.0509374	0.03264165	TIMP2/TIMP4/APOE/ADAM9/	8	0.181818181818182
GO:0045663	BP	GO:0045663	positive	8/1414	44/18903	0.015159849	0.0509374	0.03264165	SOX4/ACTB/CDON/BOC/MEF2	8	0.181818181818182
GO:0061326	BP	GO:0061326	renal tubule	14/1414	99/18903	0.015349030	0.0515434	0.03302997	AQP1/SIX1/NOTCH2/GLI3/H	14	0.141414141414141
GO:0070227	BP	GO:0070227	lymphocyte	12/1414	80/18903	0.015433394	0.0517968	0.03319240	FOXP1/GLI3/PRELID1/ORMD	12	0.15
GO:0014072	BP	GO:0014072	response to	6/1414	28/18903	0.015667807	0.0522529	0.03348462	FOSB/PEA15/MAP1LC3A/AIF	6	0.214285714285714
GO:0031664	BP	GO:0031664	regulation of	6/1414	28/18903	0.015667807	0.0522529	0.03348462	CD55/BMP6/CD14/LY96/SAS	6	0.214285714285714
GO:0032801	BP	GO:0032801	receptor	6/1414	28/18903	0.015667807	0.0522529	0.03348462	TGFB1/ANXA2/LAPTM5/APOE	6	0.214285714285714
GO:0032878	BP	GO:0032878	regulation of	6/1414	28/18903	0.015667807	0.0522529	0.03348462	GSN/SHTN1/RAP1B/ROCK1/C	6	0.214285714285714

GO:0043278	BP	GO:0043278	response to	6/1414	28/18903	0.015667807	0.0522529	0.03348462	FOSB/PEA15/MAP1LC3A/AIF	6	0.214285714285714
GO:0051647	BP	GO:0051647	nucleus	6/1414	28/18903	0.015667807	0.0522529	0.03348462	LMNA/NTN1/CDC42/SUN2/SY	6	0.214285714285714
GO:0060547	BP	GO:0060547	negative	6/1414	28/18903	0.015667807	0.0522529	0.03348462	NUPR1/PELI1/BIRC2/CAV1/	6	0.214285714285714
GO:0071624	BP	GO:0071624	positive	6/1414	28/18903	0.015667807	0.0522529	0.03348462	CD74/C3AR1/CXCL8/C5AR1/	6	0.214285714285714
GO:1902883	BP	GO:1902883	negative	6/1414	28/18903	0.015667807	0.0522529	0.03348462	H19/TXN/MCTP1/NFE2L2/DD	6	0.214285714285714
GO:1903649	BP	GO:1903649	regulation of	6/1414	28/18903	0.015667807	0.0522529	0.03348462	DAB2/EZR/MSN/RDX/SNX3/C	6	0.214285714285714
GO:1904385	BP	GO:1904385	cellular	6/1414	28/18903	0.015667807	0.0522529	0.03348462	INHBA/CAV1/CYBA/NFE2L2/	6	0.214285714285714
GO:0000423	BP	GO:0000423	mitophagy	7/1414	36/18903	0.015816342	0.0525269	0.03366024	RETREG1/MAP1LC3B/SQSTM1	7	0.194444444444444
GO:0016486	BP	GO:0016486	peptide	7/1414	36/18903	0.015816342	0.0525269	0.03366024	PCSK1N/CPE/CTSL/CTSZ/AT	7	0.194444444444444
GO:0018149	BP	GO:0018149	peptide	7/1414	36/18903	0.015816342	0.0525269	0.03366024	COL3A1/TGM2/FN1/ANXA1/N	7	0.194444444444444
GO:0031112	BP	GO:0031112	positive	7/1414	36/18903	0.015816342	0.0525269	0.03366024	HSPA1A/HSPA1B/TRPV4/RPS	7	0.194444444444444
GO:0032232	BP	GO:0032232	negative	7/1414	36/18903	0.015816342	0.0525269	0.03366024	PIK3R1/PFN1/PAK2/TJP1/S	7	0.194444444444444
GO:0070306	BP	GO:0070306	lens fiber	7/1414	36/18903	0.015816342	0.0525269	0.03366024	FGF2/SPRY2/ATF4/MAF/SPR	7	0.194444444444444
GO:1903514	BP	GO:1903514	release of	7/1414	36/18903	0.015816342	0.0525269	0.03366024	CALM2/GSTO1/NOL3/CCL3/S	7	0.194444444444444
GO:0021537	BP	GO:0021537	telencephalon	29/1414	255/18903	0.015822023	0.0525269	0.03366024	COL3A1/FAT4/FOXP1/AQP1/	29	0.113725490196078
GO:0002287	BP	GO:0002287	alpha-beta T	11/1414	71/18903	0.015882643	0.0526383	0.03373161	FOXP1/JUNB/ANXA1/NFKBIZ	11	0.154929577464789
GO:0002293	BP	GO:0002293	alpha-beta T	11/1414	71/18903	0.015882643	0.0526383	0.03373161	FOXP1/JUNB/ANXA1/NFKBIZ	11	0.154929577464789
GO:0032715	BP	GO:0032715	negative	11/1414	71/18903	0.015882643	0.0526383	0.03373161	NMB/RABGEF1/KLF2/ARRB2/	11	0.154929577464789
GO:0030838	BP	GO:0030838	positive	9/1414	53/18903	0.015902781	0.0526452	0.03373605	PYCARD/NCKAP1L/GRB2/PFN	9	0.169811320754717
GO:2000677	BP	GO:2000677	regulation of	9/1414	53/18903	0.015902781	0.0526452	0.03373605	TWIST1/DDIT3/TGFB1/GTF2	9	0.169811320754717
GO:0030166	BP	GO:0030166	proteoglycan	10/1414	62/18903	0.016082189	0.0531788	0.03407796	DSEL/DSE/CYTL1/XYLT1/CH	10	0.161290322580645
GO:0046824	BP	GO:0046824	positive	10/1414	62/18903	0.016082189	0.0531788	0.03407796	FLNA/GLI3/PIK3R1/RAN/TG	10	0.161290322580645
GO:0010639	BP	GO:0010639	negative	39/1414	366/18903	0.016161748	0.0534116	0.03422714	CAPZB/LMNA/LIMA1/HSPA1A	39	0.10655737704918
GO:0010821	BP	GO:0010821	regulation of	19/1414	150/18903	0.016582469	0.0547709	0.03509825	LMNA/HSPA1A/SQSTM1/SLC2	19	0.126666666666667
GO:0019080	BP	GO:0019080	viral gene	14/1414	100/18903	0.016659431	0.0549940	0.03524120	JUN/GALNT1/HEXIM1/ZFP36	14	0.14
GO:0007033	BP	GO:0007033	vacuole	25/1414	213/18903	0.016704209	0.0551106	0.03531593	VMP1/MAP1LC3B/ATP6V0C/R	25	0.117370892018779
GO:0060048	BP	GO:0060048	cardiac	18/1414	140/18903	0.016821558	0.0554664	0.03554393	GJA1/TPM1/FLNA/MAP2K6/G	18	0.128571428571429
GO:0046661	BP	GO:0046661	male sex	21/1414	171/18903	0.016911700	0.0554938	0.03556148	PDGFRA/PDGFRB/COL9A3/PR	21	0.12280701754386
GO:0008212	BP	GO:0008212	mineralocorti	4/1414	14/18903	0.017001114	0.0554938	0.03556148	DKK3/DAB2/BMP2/BMP6	4	0.285714285714286
GO:0030007	BP	GO:0030007	cellular	4/1414	14/18903	0.017001114	0.0554938	0.03556148	KCNMA1/ATP1B3/ATP1B1/SL	4	0.285714285714286
GO:0034309	BP	GO:0034309	primary	4/1414	14/18903	0.017001114	0.0554938	0.03556148	DKK3/DAB2/BMP2/BMP6	4	0.285714285714286
GO:0035791	BP	GO:0035791	platelet-	4/1414	14/18903	0.017001114	0.0554938	0.03556148	PDGFRB/PDGFRL/PTPN12/PD	4	0.285714285714286
GO:0043584	BP	GO:0043584	nose	4/1414	14/18903	0.017001114	0.0554938	0.03556148	SIX1/GLI3/DLX5/SMCHD1	4	0.285714285714286
GO:0043922	BP	GO:0043922	negative	4/1414	14/18903	0.017001114	0.0554938	0.03556148	JUN/CCL3/CCL4/CCL5	4	0.285714285714286
GO:0045059	BP	GO:0045059	positive	4/1414	14/18903	0.017001114	0.0554938	0.03556148	CD74/PTPRC/DOCK2/CD3D	4	0.285714285714286
GO:0046598	BP	GO:0046598	positive	4/1414	14/18903	0.017001114	0.0554938	0.03556148	LGALS1/HLA-	4	0.285714285714286

GO:0050930	BP	GO:0050930	induction of	4/1414	14/18903	0.017001114	0.0554938	0.03556148	VEGFA/CXCL8/PGF/CXCL12	4	0.285714285714286
GO:0071236	BP	GO:0071236	cellular	4/1414	14/18903	0.017001114	0.0554938	0.03556148	CRIP1/HSPA5/MEF2C/ACTR2	4	0.285714285714286
GO:0075294	BP	GO:0075294	positive	4/1414	14/18903	0.017001114	0.0554938	0.03556148	LGALS1/HLA-	4	0.285714285714286
GO:0090715	BP	GO:0090715	immunological	4/1414	14/18903	0.017001114	0.0554938	0.03556148	HLA-DRB1/HLA-	4	0.285714285714286
GO:1901533	BP	GO:1901533	negative	4/1414	14/18903	0.017001114	0.0554938	0.03556148	HES1/ZFP36/HSPA9/NFE2L2	4	0.285714285714286
GO:1901841	BP	GO:1901841	regulation of	4/1414	14/18903	0.017001114	0.0554938	0.03556148	GEM/PDE4B/CALM3/CALM1	4	0.285714285714286
GO:1902287	BP	GO:1902287	semaphorin-	4/1414	14/18903	0.017001114	0.0554938	0.03556148	NRP1/PLXND1/PLXNB2/ECE1	4	0.285714285714286
GO:1902947	BP	GO:1902947	regulation of	4/1414	14/18903	0.017001114	0.0554938	0.03556148	EGR1/HSP90AA1/C5AR1/RB1	4	0.285714285714286
GO:2001171	BP	GO:2001171	positive	4/1414	14/18903	0.017001114	0.0554938	0.03556148	ENO1/PID1/TMSB4X/TREM2	4	0.285714285714286
GO:0018210	BP	GO:0018210	peptidyl-	16/1414	120/18903	0.017018714	0.0555202	0.03557839	GALNT1/CHI3L1/TGFB1/CAL	16	0.133333333333333
GO:0030502	BP	GO:0030502	negative	5/1414	21/18903	0.017232717	0.0559056	0.03582540	ECM1/LTBP3/RFLNB/CCL3/S	5	0.238095238095238
GO:0034755	BP	GO:0034755	iron ion	5/1414	21/18903	0.017232717	0.0559056	0.03582540	SLC40A1/SLC39A14/SLC25A	5	0.238095238095238
GO:0060973	BP	GO:0060973	cell	5/1414	21/18903	0.017232717	0.0559056	0.03582540	PDGFRB/TWIST1/SEMA3C/CD	5	0.238095238095238
GO:0071636	BP	GO:0071636	positive	5/1414	21/18903	0.017232717	0.0559056	0.03582540	LUM/PTGS2/ATP6AP2/THBS1	5	0.238095238095238
GO:0071731	BP	GO:0071731	response to	5/1414	21/18903	0.017232717	0.0559056	0.03582540	AQP1/FOXO1/MMP3/CFLAR/T	5	0.238095238095238
GO:0097062	BP	GO:0097062	dendritic	5/1414	21/18903	0.017232717	0.0559056	0.03582540	FCGR2B/APOE/TREM2/VPS35	5	0.238095238095238
GO:0099515	BP	GO:0099515	actin	5/1414	21/18903	0.017232717	0.0559056	0.03582540	MYO5A/SUN2/MYO1B/ACTN4/	5	0.238095238095238
GO:0140131	BP	GO:0140131	positive	5/1414	21/18903	0.017232717	0.0559056	0.03582540	CCL3/CCL4/ADAM10/WNK1/C	5	0.238095238095238
GO:1904754	BP	GO:1904754	positive	5/1414	21/18903	0.017232717	0.0559056	0.03582540	DOCK4/DDR2/ADAMTS1/IGFB	5	0.238095238095238
GO:2000725	BP	GO:2000725	regulation of	5/1414	21/18903	0.017232717	0.0559056	0.03582540	BMP2/TGFB1/ARRB2/MEF2C/	5	0.238095238095238
GO:0032781	BP	GO:0032781	positive	8/1414	45/18903	0.017263852	0.0559444	0.03585025	TPM1/VMP1/DNAJB1/TNNT3/	8	0.177777777777778
GO:0098927	BP	GO:0098927	vesicle-	8/1414	45/18903	0.017263852	0.0559444	0.03585025	DAB2/FLNA/EEA1/EZR/MSN/	8	0.177777777777778
GO:0046890	BP	GO:0046890	regulation of	22/1414	182/18903	0.017449914	0.0565160	0.03621651	EGR1/DKK3/DAB2/IGFBP7/S	22	0.120879120879121
GO:0014009	BP	GO:0014009	glial cell	9/1414	54/18903	0.017855433	0.0576698	0.03695589	SOX4/NTN1/HES1/CSF1R/LY	9	0.166666666666667
GO:0033157	BP	GO:0033157	regulation of	26/1414	225/18903	0.017864358	0.0576698	0.03695589	FLNA/GLI3/ANK3/APOD/PIK	26	0.115555555555556
GO:0032481	BP	GO:0032481	positive	10/1414	63/18903	0.017875371	0.0576698	0.03695589	PLCG2/NMB/HSP90AA1/HSPD	10	0.158730158730159
GO:0032615	BP	GO:0032615	interleukin-	10/1414	63/18903	0.017875371	0.0576698	0.03695589	FOXP1/PLCG2/HSPD1/LAPTM	10	0.158730158730159
GO:0032655	BP	GO:0032655	regulation of	10/1414	63/18903	0.017875371	0.0576698	0.03695589	FOXP1/PLCG2/HSPD1/LAPTM	10	0.158730158730159
GO:0032731	BP	GO:0032731	positive	10/1414	63/18903	0.017875371	0.0576698	0.03695589	EGR1/HSPB1/TYROBP/CCL3/	10	0.158730158730159
GO:0099072	BP	GO:0099072	regulation of	10/1414	63/18903	0.017875371	0.0576698	0.03695589	GPC6/AP2A2/ADAM10/RAP1A	10	0.158730158730159
GO:0007259	BP	GO:0007259	receptor	21/1414	172/18903	0.017952796	0.0578875	0.03709544	SOCS3/PTPRD/HES1/CAV1/F	21	0.122093023255814
GO:0051208	BP	GO:0051208	sequestering	17/1414	131/18903	0.018193149	0.0586301	0.03757131	THY1/FLNA/PLCG2/DDIT3/F	17	0.129770992366412
GO:0006887	BP	GO:0006887	exocytosis	39/1414	369/18903	0.018211572	0.0586571	0.03758859	S100A13/SCIN/STEAP2/SDC	39	0.105691056910569
GO:0018107	BP	GO:0018107	peptidyl-	15/1414	111/18903	0.018262231	0.0586915	0.03761064	CHI3L1/TGFB1/CALM2/SPRY	15	0.135135135135135
GO:0043588	BP	GO:0043588	skin	33/1414	302/18903	0.018278590	0.0586915	0.03761064	COL1A1/COL1A2/MAFB/COL5	33	0.109271523178808
GO:0033144	BP	GO:0033144	negative	7/1414	37/18903	0.018282630	0.0586915	0.03761064	FOXP1/DAB2/LBH/RHOA/PER	7	0.189189189189189

GO:0048846	BP	GO:0048846	axon	7/1414	37/18903	0.018282630	0.0586915	0.03761064	SEMA3C/NRP2/VEGFA/NRP1/	7	0.189189189189189
GO:0060416	BP	GO:0060416	response to	7/1414	37/18903	0.018282630	0.0586915	0.03761064	PIK3R1/LYN/ASS1/IGFBP5/	7	0.189189189189189
GO:1902284	BP	GO:1902284	neuron	7/1414	37/18903	0.018282630	0.0586915	0.03761064	SEMA3C/NRP2/VEGFA/NRP1/	7	0.189189189189189
GO:0044843	BP	GO:0044843	cell cycle	31/1414	280/18903	0.018349468	0.0588737	0.03772738	GPNMB/ACTB/ID4/FHL1/PLC	31	0.110714285714286
GO:0097696	BP	GO:0097696	receptor	22/1414	183/18903	0.018482013	0.0592664	0.03797901	SOCS3/PTPRD/HES1/TGFB1/	22	0.120218579234973
GO:0006446	BP	GO:0006446	regulation of	12/1414	82/18903	0.018520181	0.0592806	0.03798811	EIF1/PPP1R15A/EIF1B/EIF	12	0.146341463414634
GO:0003156	BP	GO:0003156	regulation of	6/1414	29/18903	0.018537259	0.0592806	0.03798811	SIX1/BMP2/FGF2/FGF1/CIT	6	0.206896551724138
GO:0007263	BP	GO:0007263	nitric oxide	6/1414	29/18903	0.018537259	0.0592806	0.03798811	RASD1/VEGFA/NDNF/APOE/D	6	0.206896551724138
GO:0060441	BP	GO:0060441	epithelial	6/1414	29/18903	0.018537259	0.0592806	0.03798811	RSPO2/SPRY2/FGFR2/CTSZ/	6	0.206896551724138
GO:1902175	BP	GO:1902175	regulation of	6/1414	29/18903	0.018537259	0.0592806	0.03798811	SOD2/HSPB1/NOL3/TREM2/M	6	0.206896551724138
GO:0009306	BP	GO:0009306	protein	38/1414	359/18903	0.019147816	0.0611995	0.03921782	LTBP2/SOX4/CAVIN1/COMP/	38	0.105849582172702
GO:1903578	BP	GO:1903578	regulation of	11/1414	73/18903	0.019279890	0.0615879	0.03946670	H19/NUPR1/DDIT4/ENO1/PI	11	0.150684931506849
GO:0042742	BP	GO:0042742	defense	40/1414	382/18903	0.019450966	0.0621004	0.03979510	FOXP1/AQP1/RBPJ/NOTCH2/	40	0.104712041884817
GO:0048565	BP	GO:0048565	digestive	17/1414	132/18903	0.019477833	0.0621521	0.03982827	COL3A1/PDGFRA/GLI3/HES1	17	0.128787878787879
GO:0060419	BP	GO:0060419	heart growth	14/1414	102/18903	0.019534359	0.0622409	0.03988514	FOXP1/RBPJ/RUNX1/RBP4/F	14	0.137254901960784
GO:0035272	BP	GO:0035272	exocrine	8/1414	46/18903	0.019569668	0.0622409	0.03988514	SEMA3C/TGM2/TGFB1/FGFR2	8	0.173913043478261
GO:0046596	BP	GO:0046596	regulation of	8/1414	46/18903	0.019569668	0.0622409	0.03988514	LGALS1/IFITM1/GSN/IFITM	8	0.173913043478261
GO:0060443	BP	GO:0060443	mammary gland	8/1414	46/18903	0.019569668	0.0622409	0.03988514	GLI3/NTN1/CAV1/FGFR2/CS	8	0.173913043478261
GO:1990090	BP	GO:1990090	cellular	8/1414	46/18903	0.019569668	0.0622409	0.03988514	HES1/MAGI2/HSPA5/ARF6/R	8	0.173913043478261
GO:2001239	BP	GO:2001239	regulation of	8/1414	46/18903	0.019569668	0.0622409	0.03988514	HSPA1A/COL2A1/HSPA1B/FG	8	0.173913043478261
GO:0000768	BP	GO:0000768	syncytium	10/1414	64/18903	0.019811514	0.0629072	0.04031211	CDON/CFLAR/TYROBP/CD53/	10	0.15625
GO:0019229	BP	GO:0019229	regulation of	10/1414	64/18903	0.019811514	0.0629072	0.04031211	MMP2/PTGS2/CAV1/ADM/TBX	10	0.15625
GO:0140253	BP	GO:0140253	cell-cell	10/1414	64/18903	0.019811514	0.0629072	0.04031211	CDON/CFLAR/TYROBP/CD53/	10	0.15625
GO:0035592	BP	GO:0035592	establishment	38/1414	360/18903	0.019918031	0.0631912	0.04049415	LTBP2/SOX4/CAVIN1/COMP/	38	0.105555555555556
GO:0002686	BP	GO:0002686	negative	9/1414	55/18903	0.019976813	0.0631912	0.04049415	NBL1/APOD/RABGEF1/TNFAI	9	0.163636363636364
GO:0042743	BP	GO:0042743	hydrogen	9/1414	55/18903	0.019976813	0.0631912	0.04049415	PRDX4/GPX3/MMP3/SOD2/PR	9	0.163636363636364
GO:1900087	BP	GO:1900087	positive	9/1414	55/18903	0.019976813	0.0631912	0.04049415	ANXA1/RGCC/CCND1/AIF1/D	9	0.163636363636364
GO:1902991	BP	GO:1902991	regulation of	9/1414	55/18903	0.019976813	0.0631912	0.04049415	LYN/APOE/RTN3/IFNGR1/RT	9	0.163636363636364
GO:1903202	BP	GO:1903202	negative	9/1414	55/18903	0.019976813	0.0631912	0.04049415	SOD2/TXN/ATF4/HSPB1/NOL	9	0.163636363636364
GO:2000648	BP	GO:2000648	positive	9/1414	55/18903	0.019976813	0.0631912	0.04049415	GJA1/PRRX1/ID4/LTBP3/FG	9	0.163636363636364
GO:0016331	BP	GO:0016331	morphogenesis	19/1414	153/18903	0.020059227	0.0634175	0.04063917	TWIST1/SOX4/SIX1/CTHRC1	19	0.124183006535948
GO:0098742	BP	GO:0098742	cell-cell	31/1414	282/18903	0.020079728	0.0634480	0.04065867	CDH11/CADM1/FAT4/PTPRD/	31	0.109929078014184
GO:0055013	BP	GO:0055013	cardiac	12/1414	83/18903	0.020226430	0.0638769	0.04093355	PDGFRA/FOXP1/PDGFRB/LMN	12	0.144578313253012
GO:0033135	BP	GO:0033135	regulation of	18/1414	143/18903	0.020485095	0.0646588	0.04143459	TXN/TGFB1/PTGS2/SPRY2/C	18	0.125874125874126
GO:0050886	BP	GO:0050886	endocrine	13/1414	93/18903	0.020809175	0.0656107	0.04204459	GJA1/AQP1/DAB2/SPP1/INH	13	0.139784946236559
GO:0055017	BP	GO:0055017	cardiac	13/1414	93/18903	0.020809175	0.0656107	0.04204459	FOXP1/RBPJ/RUNX1/RBP4/F	13	0.139784946236559

GO:0051222	BP	GO:0051222	positive	32/1414	294/18903	0.020912854	0.0656279	0.04205560	SOX4/FLNA/GLI3/ANK3/RBP	32	0.108843537414966
GO:0010881	BP	GO:0010881	regulation of	5/1414	22/18903	0.020960889	0.0656279	0.04205560	CALM2/GSTO1/SLC8A1/CALM	5	0.227272727272727
GO:0033630	BP	GO:0033630	positive	5/1414	22/18903	0.020960889	0.0656279	0.04205560	PIEZO1/NCKAP1L/ADAM9/PO	5	0.227272727272727
GO:0035089	BP	GO:0035089	establishment	5/1414	22/18903	0.020960889	0.0656279	0.04205560	CDC42/RHOA/MSN/FAT1/FSC	5	0.227272727272727
GO:0043371	BP	GO:0043371	negative	5/1414	22/18903	0.020960889	0.0656279	0.04205560	RUNX1/ANXA1/BCL6/SMAD7/	5	0.227272727272727
GO:0045061	BP	GO:0045061	thymic T cell	5/1414	22/18903	0.020960889	0.0656279	0.04205560	GLI3/CD74/PTPRC/DOCK2/C	5	0.227272727272727
GO:0051767	BP	GO:0051767	nitric-oxide	5/1414	22/18903	0.020960889	0.0656279	0.04205560	MAP2K6/NAMPT/CCL2/TLR4/	5	0.227272727272727
GO:0051769	BP	GO:0051769	regulation of	5/1414	22/18903	0.020960889	0.0656279	0.04205560	MAP2K6/NAMPT/CCL2/TLR4/	5	0.227272727272727
GO:0072111	BP	GO:0072111	cell	5/1414	22/18903	0.020960889	0.0656279	0.04205560	EGR1/PDGFRB/CFLAR/BMP2/	5	0.227272727272727
GO:1900424	BP	GO:1900424	regulation of	5/1414	22/18903	0.020960889	0.0656279	0.04205560	FOXP1/EMILIN2/GRN/CYBA/	5	0.227272727272727
GO:1903428	BP	GO:1903428	positive	5/1414	22/18903	0.020960889	0.0656279	0.04205560	H19/PLCG2/SOD2/TLR4/CYB	5	0.227272727272727
GO:2000810	BP	GO:2000810	regulation of	5/1414	22/18903	0.020960889	0.0656279	0.04205560	SNAI1/ROCK1/TJP1/CLDN5/	5	0.227272727272727
GO:2001044	BP	GO:2001044	regulation of	5/1414	22/18903	0.020960889	0.0656279	0.04205560	FLNA/LIMS1/LIMS2/LAMB1/	5	0.227272727272727
GO:0140448	BP	GO:0140448	signaling	7/1414	38/18903	0.021006731	0.0657084	0.04210718	PCSK1N/CPE/CTSL/CTSZ/AT	7	0.184210526315789
GO:0000082	BP	GO:0000082	G1/S	28/1414	250/18903	0.021009123	0.0657084	0.04210718	GPNMB/ACTB/ID4/FHL1/CDK	28	0.112
GO:0003015	BP	GO:0003015	heart process	29/1414	261/18903	0.021044573	0.0657840	0.04215562	GJA1/TPM1/FLNA/MAP2K6/S	29	0.111111111111111
GO:0009201	BP	GO:0009201	ribonucleosid	16/1414	123/18903	0.021071723	0.0658336	0.04218740	H19/NDUFB1/ATP5ME/ATP6V	16	0.130081300813008
GO:0046620	BP	GO:0046620	regulation of	14/1414	103/18903	0.021105153	0.0659027	0.04223171	FOXP1/RBPJ/RUNX1/RBP4/F	14	0.135922330097087
GO:0010633	BP	GO:0010633	negative	15/1414	113/18903	0.021176226	0.0660539	0.04232861	FGF2/TGFB1/RGCC/KLF4/AP	15	0.132743362831858
GO:0061640	BP	GO:0061640	cytoskeleton-	15/1414	113/18903	0.021176226	0.0660539	0.04232861	SEPTIN11/ANK3/RHOC/CHMP	15	0.132743362831858
GO:0009651	BP	GO:0009651	response to	6/1414	30/18903	0.021745856	0.0671483	0.04302989	ZFP36L1/AQP1/TRPV4/HSP9	6	0.2
GO:0021602	BP	GO:0021602	cranial nerve	6/1414	30/18903	0.021745856	0.0671483	0.04302989	MAFB/SIX1/GLI3/NRP2/CIT	6	0.2
GO:0045940	BP	GO:0045940	positive	6/1414	30/18903	0.021745856	0.0671483	0.04302989	DAB2/NR1D1/BMP6/FGF1/AD	6	0.2
GO:0060142	BP	GO:0060142	regulation of	6/1414	30/18903	0.021745856	0.0671483	0.04302989	CFLAR/TYROBP/CD53/PLEKH	6	0.2
GO:0070293	BP	GO:0070293	renal	6/1414	30/18903	0.021745856	0.0671483	0.04302989	AQP1/GSN/SGK1/GAS6/MLLT	6	0.2
GO:0071480	BP	GO:0071480	cellular	6/1414	30/18903	0.021745856	0.0671483	0.04302989	EGR1/CRYAB/CDKN1A/HSPA5	6	0.2
GO:1900101	BP	GO:1900101	regulation of	6/1414	30/18903	0.021745856	0.0671483	0.04302989	PIK3R1/XBP1/DNAJB9/PPP1	6	0.2
GO:2000108	BP	GO:2000108	positive	6/1414	30/18903	0.021745856	0.0671483	0.04302989	ANXA1/PRELID1/LYN/MEF2C	6	0.2
GO:0001787	BP	GO:0001787	natural	4/1414	15/18903	0.021837883	0.0671483	0.04302989	FCGR3A/IL18/HLA-	4	0.266666666666667
GO:0009163	BP	GO:0009163	nucleoside	4/1414	15/18903	0.021837883	0.0671483	0.04302989	NT5E/PNP/ADK/APRT	4	0.266666666666667
GO:0009886	BP	GO:0009886	post-	4/1414	15/18903	0.021837883	0.0671483	0.04302989	FBN1/EFEMP1/BAX/KDR	4	0.266666666666667
GO:0014857	BP	GO:0014857	regulation of	4/1414	15/18903	0.021837883	0.0671483	0.04302989	SIX1/CFLAR/FGF2/CAV2	4	0.266666666666667
GO:0019511	BP	GO:0019511	peptidyl-	4/1414	15/18903	0.021837883	0.0671483	0.04302989	P4HA2/PRDX4/P4HA1/EGLN3	4	0.266666666666667
GO:0032352	BP	GO:0032352	positive	4/1414	15/18903	0.021837883	0.0671483	0.04302989	EGR1/DAB2/BMP6/ADM	4	0.266666666666667
GO:0034404	BP	GO:0034404	nucleobase-	4/1414	15/18903	0.021837883	0.0671483	0.04302989	NT5E/PNP/ADK/APRT	4	0.266666666666667
GO:0042994	BP	GO:0042994	cytoplasmic	4/1414	15/18903	0.021837883	0.0671483	0.04302989	NFKBIA/MDFI/TMSB4X/PKD1	4	0.266666666666667

GO:0045064	BP	GO:0045064	T-helper 2	4/1414	15/18903	0.021837883	0.0671483	0.04302989	ANXA1/CD86/IL18/BCL6	4	0.266666666666667
GO:0045989	BP	GO:0045989	positive	4/1414	15/18903	0.021837883	0.0671483	0.04302989	TRPV4/GSTO1/HSP90AA1/RG	4	0.266666666666667
GO:0051284	BP	GO:0051284	positive	4/1414	15/18903	0.021837883	0.0671483	0.04302989	CALM2/GSTO1/CALM3/CALM1	4	0.266666666666667
GO:0060099	BP	GO:0060099	regulation of	4/1414	15/18903	0.021837883	0.0671483	0.04302989	PLCG2/NCKAP1L/TREM2/RAB	4	0.266666666666667
GO:0060413	BP	GO:0060413	atrial septum	4/1414	15/18903	0.021837883	0.0671483	0.04302989	SOX4/NOTCH2/CCN1/BMPR2	4	0.266666666666667
GO:0070262	BP	GO:0070262	peptidyl-	4/1414	15/18903	0.021837883	0.0671483	0.04302989	PPP1R15A/DUSP1/PPP1CA/S	4	0.266666666666667
GO:0072148	BP	GO:0072148	epithelial	4/1414	15/18903	0.021837883	0.0671483	0.04302989	RBPJ/PDPN/NRP1/NR2F2	4	0.266666666666667
GO:0097531	BP	GO:0097531	mast cell	4/1414	15/18903	0.021837883	0.0671483	0.04302989	RABGEF1/VEGFA/SWAP70/PG	4	0.266666666666667
GO:1900426	BP	GO:1900426	positive	4/1414	15/18903	0.021837883	0.0671483	0.04302989	EMILIN2/GRN/CYBA/MMRN2	4	0.266666666666667
GO:1905153	BP	GO:1905153	regulation of	4/1414	15/18903	0.021837883	0.0671483	0.04302989	PLCG2/NCKAP1L/TREM2/RAB	4	0.266666666666667
GO:2001279	BP	GO:2001279	regulation of	4/1414	15/18903	0.021837883	0.0671483	0.04302989	PTGS2/ANXA1/FABP5/CD74	4	0.266666666666667
GO:0045333	BP	GO:0045333	cellular	27/1414	240/18903	0.021958301	0.0674830	0.04324437	NDUFA4/NDUFB1/ATP5ME/UQ	27	0.1125
GO:0006606	BP	GO:0006606	protein	20/1414	165/18903	0.022043544	0.0675568	0.04329169	LMNA/FLNA/GLI3/NFKBIA/A	20	0.121212121212121
GO:0021675	BP	GO:0021675	nerve	12/1414	84/18903	0.022046830	0.0675568	0.04329169	MAFB/SIX1/GLI3/SULF2/HE	12	0.142857142857143
GO:0002701	BP	GO:0002701	negative	8/1414	47/18903	0.022086567	0.0675568	0.04329169	TWIST1/TGFB1/RABGEF1/BS	8	0.170212765957447
GO:0002861	BP	GO:0002861	regulation of	8/1414	47/18903	0.022086567	0.0675568	0.04329169	PSMB4/HLA-	8	0.170212765957447
GO:0046633	BP	GO:0046633	alpha-beta T	8/1414	47/18903	0.022086567	0.0675568	0.04329169	CD55/PTPRC/DOCK2/IL18/H	8	0.170212765957447
GO:0071470	BP	GO:0071470	cellular	8/1414	47/18903	0.022086567	0.0675568	0.04329169	ZFP36L1/AQP1/TRPV4/PTGS	8	0.170212765957447
GO:0072583	BP	GO:0072583	clathrin-	8/1414	47/18903	0.022086567	0.0675568	0.04329169	DAB2/MAGI2/BMP2K/AP2A2/	8	0.170212765957447
GO:0090224	BP	GO:0090224	regulation of	8/1414	47/18903	0.022086567	0.0675568	0.04329169	HSPA1A/HSPA1B/CHMP4B/PK	8	0.170212765957447
GO:0140353	BP	GO:0140353	lipid export	8/1414	47/18903	0.022086567	0.0675568	0.04329169	DAB2/MAP2K6/SPP1/INHBA/	8	0.170212765957447
GO:0009142	BP	GO:0009142	nucleoside	17/1414	134/18903	0.022254560	0.0679993	0.04357527	H19/NDUFB1/ATP5ME/ATP6V	17	0.126865671641791
GO:0043467	BP	GO:0043467	regulation of	17/1414	134/18903	0.022254560	0.0679993	0.04357527	NDUFA4/COX7A1/TRPV4/PHL	17	0.126865671641791
GO:0030705	BP	GO:0030705	cytoskeleton-	24/1414	208/18903	0.022558289	0.0688913	0.04414686	TUBB/TUBA1A/UBB/HSPA8/R	24	0.115384615384615
GO:0006892	BP	GO:0006892	post-Golgi	14/1414	104/18903	0.022768970	0.0694983	0.04453585	ANK3/STEAP2/LAPTM5/MYO5	14	0.134615384615385
GO:0042445	BP	GO:0042445	hormone	27/1414	241/18903	0.023030311	0.0702593	0.04502347	EGR1/PDGFRA/DKK3/DAB2/C	27	0.112033195020747
GO:1903522	BP	GO:1903522	regulation of	29/1414	263/18903	0.023058541	0.0703086	0.04505509	MMP2/GJA1/TPM1/FLNA/S10	29	0.110266159695817
GO:0032350	BP	GO:0032350	regulation of	7/1414	39/18903	0.024000337	0.0731420	0.04687081	EGR1/DKK3/DAB2/STC2/BMP	7	0.179487179487179
GO:0048488	BP	GO:0048488	synaptic	10/1414	66/18903	0.024136359	0.0734798	0.04708724	ACTG1/ACTB/FCHO2/ITSN2/	10	0.151515151515152
GO:0140238	BP	GO:0140238	presynaptic	10/1414	66/18903	0.024136359	0.0734798	0.04708724	ACTG1/ACTB/FCHO2/ITSN2/	10	0.151515151515152
GO:0003014	BP	GO:0003014	renal system	16/1414	125/18903	0.024155173	0.0734987	0.04709937	AQP1/SULF2/GSN/KCNMA1/A	16	0.128
GO:0042982	BP	GO:0042982	amyloid	13/1414	95/18903	0.024403886	0.0742168	0.04755952	ITM2B/ITM2A/ITM2C/LYN/A	13	0.136842105263158
GO:0010332	BP	GO:0010332	response to	9/1414	57/18903	0.024754732	0.0751790	0.04817616	EGR1/CRYAB/SOD2/CDKN1A/	9	0.157894736842105
GO:0002673	BP	GO:0002673	regulation of	8/1414	48/18903	0.024823408	0.0751790	0.04817616	OSMR/PTGS2/PTGES/ALOX5A	8	0.166666666666667
GO:0008038	BP	GO:0008038	neuron	8/1414	48/18903	0.024823408	0.0751790	0.04817616	CRTAC1/EMB/CXCR4/NRP1/Y	8	0.166666666666667
GO:0032924	BP	GO:0032924	activin	8/1414	48/18903	0.024823408	0.0751790	0.04817616	MAGI2/INHBA/GDF6/CITED2	8	0.166666666666667

GO:0035305	BP	GO:0035305	negative	8/1414	48/18903	0.024823408	0.0751790	0.04817616	PPP1R15A/NCKAP1L/YWHAB/	8	0.166666666666667
GO:0048483	BP	GO:0048483	autonomic	8/1414	48/18903	0.024823408	0.0751790	0.04817616	SOX4/SIX1/HES1/NRP2/VCA	8	0.166666666666667
GO:0060976	BP	GO:0060976	coronary	8/1414	48/18903	0.024823408	0.0751790	0.04817616	PDGFRB/ADAMTS6/FGF2/VEG	8	0.166666666666667
GO:1990089	BP	GO:1990089	response to	8/1414	48/18903	0.024823408	0.0751790	0.04817616	HES1/MAGI2/HSPA5/ARF6/R	8	0.166666666666667
GO:0007623	BP	GO:0007623	circadian	24/1414	210/18903	0.024976193	0.0756025	0.04844752	EGR1/KLF10/ID4/ZFHX3/ID	24	0.114285714285714
GO:0018209	BP	GO:0018209	peptidyl-	35/1414	332/18903	0.025082793	0.0757793	0.04856081	GALNT1/STK38L/TXN/TGFB1	35	0.105421686746988
GO:0002053	BP	GO:0002053	positive	5/1414	23/18903	0.025177502	0.0757793	0.04856081	SIX1/PRRX1/FGFR2/KDR/TG	5	0.217391304347826
GO:0003283	BP	GO:0003283	atrial septum	5/1414	23/18903	0.025177502	0.0757793	0.04856081	SOX4/NOTCH2/CCN1/NPHP3/	5	0.217391304347826
GO:0010893	BP	GO:0010893	positive	5/1414	23/18903	0.025177502	0.0757793	0.04856081	DAB2/NR1D1/BMP6/FGF1/AD	5	0.217391304347826
GO:0019430	BP	GO:0019430	removal of	5/1414	23/18903	0.025177502	0.0757793	0.04856081	H19/SOD2/PRDX1/SOD3/NFE	5	0.217391304347826
GO:0046794	BP	GO:0046794	transport of	5/1414	23/18903	0.025177502	0.0757793	0.04856081	CTSL/CAV1/BST2/EPS15/CA	5	0.217391304347826
GO:0090335	BP	GO:0090335	regulation of	5/1414	23/18903	0.025177502	0.0757793	0.04856081	SIX1/TRPV4/METRNL/PTGS2	5	0.217391304347826
GO:1900120	BP	GO:1900120	regulation of	5/1414	23/18903	0.025177502	0.0757793	0.04856081	PHLDA2/ANXA2/B2M/NRP1/A	5	0.217391304347826
GO:1900543	BP	GO:1900543	negative	5/1414	23/18903	0.025177502	0.0757793	0.04856081	H19/NUPR1/DDIT4/PID1/FB	5	0.217391304347826
GO:1901673	BP	GO:1901673	regulation of	5/1414	23/18903	0.025177502	0.0757793	0.04856081	HSPA1A/HSPA1B/CHMP4B/HN	5	0.217391304347826
GO:2001169	BP	GO:2001169	regulation of	5/1414	23/18903	0.025177502	0.0757793	0.04856081	H19/ENO1/PID1/TMSB4X/TR	5	0.217391304347826
GO:0002220	BP	GO:0002220	innate immune	6/1414	31/18903	0.025308924	0.0760963	0.04876396	PLCG2/TYROBP/CLEC7A/LYN	6	0.193548387096774
GO:0032148	BP	GO:0032148	activation of	6/1414	31/18903	0.025308924	0.0760963	0.04876396	TXN/FGF1/IL18/CCDC88A/G	6	0.193548387096774
GO:0010822	BP	GO:0010822	positive	11/1414	76/18903	0.025343236	0.0761210	0.04877978	SLC25A5/PLAUR/NMT1/PYCA	11	0.144736842105263
GO:0021536	BP	GO:0021536	diencephalon	11/1414	76/18903	0.025343236	0.0761210	0.04877978	RBPJ/HES1/UBB/NRP2/BMP2	11	0.144736842105263
GO:0023061	BP	GO:0023061	signal release	47/1414	470/18903	0.025529207 9514915	0.0766258 182793552	0.04910324 75317369	GJA1/AQP1/SOX4/DAB2/MAP 2K6/FOXO1/LTBP4/RBP4/NR	47	0.1
GO:0090316	BP	GO:0090316	positive	19/1414	157/18903	0.025537560	0.0766258	0.04910324	FLNA/GLI3/ANK3/PIK3R1/R	19	0.121019108280255
GO:1904951	BP	GO:1904951	positive	33/1414	310/18903	0.025617836	0.0768271	0.04923227	SOX4/FLNA/GLI3/ANK3/RBP	33	0.106451612903226
GO:0071478	BP	GO:0071478	cellular	22/1414	189/18903	0.025710833	0.0770664	0.04938560	MMP2/EGR1/AQP1/CRIP1/CR	22	0.116402116402116
GO:0038127	BP	GO:0038127	ERBB	16/1414	126/18903	0.025818505	0.0773494	0.04956695	RBPJ/EFEMP1/GPRC5A/TGFB	16	0.126984126984127
GO:0006970	BP	GO:0006970	response to	12/1414	86/18903	0.026046406	0.0779521	0.04995316	ZFP36L1/AQP1/TRPV4/KCNM	12	0.13953488372093
GO:0007260	BP	GO:0007260	tyrosine	12/1414	86/18903	0.026046406	0.0779521	0.04995316	SOCS3/HES1/CAV1/FGFR3/C	12	0.13953488372093
GO:0030518	BP	GO:0030518	intracellular	15/1414	116/18903	0.026187830	0.0783351	0.05019864	FOXP1/DAB2/LBH/DNAJA1/W	15	0.129310344827586
GO:0007032	BP	GO:0007032	endosome	13/1414	96/18903	0.026364172	0.0787818	0.05048488	EEA1/ATP6V0C/SQSTM1/CHM	13	0.135416666666667
GO:0072080	BP	GO:0072080	nephron	13/1414	96/18903	0.026364172	0.0787818	0.05048488	AQP1/SIX1/NOTCH2/GLI3/H	13	0.135416666666667
GO:0043954	BP	GO:0043954	cellular	10/1414	67/18903	0.026536494	0.0792562	0.05078884	CSF1R/FCGR2B/MTSS1/APOE	10	0.149253731343284
GO:0060759	BP	GO:0060759	regulation of	21/1414	179/18903	0.026705059	0.0797188	0.05108531	ECM1/HSPA1A/HSPA1B/CAV1	21	0.11731843575419
GO:0043001	BP	GO:0043001	Golgi to	7/1414	40/18903	0.027274355	0.0810607	0.05194520	ANK3/RAB31/RAB10/VAMP2/	7	0.175
GO:0050732	BP	GO:0050732	negative	9/1414	58/18903	0.027425100	0.0810607	0.05194520	THY1/SOCS3/SH3BP5/GPRC5	9	0.155172413793103
GO:0002730	BP	GO:0002730	regulation of	4/1414	16/18903	0.027432509	0.0810607	0.05194520	PLCG2/CLEC7A/BST2/TLR4	4	0.25

GO:0006825	BP	GO:0006825	copper ion	4/1414	16/18903	0.027432509	0.0810607	0.05194520	CP/STEAP4/STEAP2/STEAP3	4	0.25
GO:0021783	BP	GO:0021783	preganglionic	4/1414	16/18903	0.027432509	0.0810607	0.05194520	SIX1/HES1/NRP2/NRP1	4	0.25
GO:0023035	BP	GO:0023035	CD40	4/1414	16/18903	0.027432509	0.0810607	0.05194520	ITGA5/CD86/TREM2/TNFAIP	4	0.25
GO:0030033	BP	GO:0030033	microvillus	4/1414	16/18903	0.027432509	0.0810607	0.05194520	STK26/EZR/PODXL/FSCN1	4	0.25
GO:0030852	BP	GO:0030852	regulation of	4/1414	16/18903	0.027432509	0.0810607	0.05194520	RUNX1/C1QC/EVI2B/HCLS1	4	0.25
GO:0036376	BP	GO:0036376	sodium ion	4/1414	16/18903	0.027432509	0.0810607	0.05194520	FXYD1/ATP1B3/ATP1B1/SLC	4	0.25
GO:0043517	BP	GO:0043517	positive	4/1414	16/18903	0.027432509	0.0810607	0.05194520	PMAIP1/SPRED1/DDX5/RPL2	4	0.25
GO:0045651	BP	GO:0045651	positive	4/1414	16/18903	0.027432509	0.0810607	0.05194520	TGFB1/ID2/HCLS1/RB1	4	0.25
GO:0050872	BP	GO:0050872	white fat	4/1414	16/18903	0.027432509	0.0810607	0.05194520	PDGFRA/TBL1XR1/RETREG1/	4	0.25
GO:0061101	BP	GO:0061101	neuroendocrin	4/1414	16/18903	0.027432509	0.0810607	0.05194520	HES1/BMP2/FGF2/JAG1	4	0.25
GO:0061684	BP	GO:0061684	chaperone-	4/1414	16/18903	0.027432509	0.0810607	0.05194520	LAMP2/HSPA8/HSP90AA1/CT	4	0.25
GO:0090030	BP	GO:0090030	regulation of	4/1414	16/18903	0.027432509	0.0810607	0.05194520	DKK3/DAB2/BMP2/BMP6	4	0.25
GO:0090336	BP	GO:0090336	positive	4/1414	16/18903	0.027432509	0.0810607	0.05194520	SIX1/METRNL/PTGS2/HNRNP	4	0.25
GO:0099170	BP	GO:0099170	postsynaptic	4/1414	16/18903	0.027432509	0.0810607	0.05194520	EIF4E/CYFIP1/PLCB1/RNF1	4	0.25
GO:1900044	BP	GO:1900044	regulation of	4/1414	16/18903	0.027432509	0.0810607	0.05194520	BIRC2/DDX3X/SASH1/PTPN2	4	0.25
GO:1901201	BP	GO:1901201	regulation of	4/1414	16/18903	0.027432509	0.0810607	0.05194520	ANTXR1/TGFB1/RGCC/TIE1	4	0.25
GO:1902931	BP	GO:1902931	negative	4/1414	16/18903	0.027432509	0.0810607	0.05194520	DKK3/BMP2/PLEK/APOE	4	0.25
GO:0006024	BP	GO:0006024	glycosaminogl	11/1414	77/18903	0.027641512	0.0815956	0.05228798	PDGFRB/DSEL/DSE/XYLT1/C	11	0.142857142857143
GO:0006919	BP	GO:0006919	activation of	11/1414	77/18903	0.027641512	0.0815956	0.05228798	CFLAR/CYCS/HSPD1/RPS27L	11	0.142857142857143
GO:0051170	BP	GO:0051170	import into	20/1414	169/18903	0.027695073	0.0817123	0.05236280	LMNA/FLNA/GLI3/NFKBIA/A	20	0.118343195266272
GO:0043457	BP	GO:0043457	regulation of	8/1414	49/18903	0.027788586	0.0819468	0.05251304	COX7A1/TRPV4/NUPR1/NOP5	8	0.163265306122449
GO:0019915	BP	GO:0019915	lipid storage	12/1414	87/18903	0.028233525	0.0830071	0.05319251	NFKBIA/HILPDA/CAV1/MSR1	12	0.137931034482759
GO:0050672	BP	GO:0050672	negative	12/1414	87/18903	0.028233525	0.0830071	0.05319251	GPNMB/SDC4/PELI1/CEBPB/	12	0.137931034482759
GO:0071277	BP	GO:0071277	cellular	12/1414	87/18903	0.028233525	0.0830071	0.05319251	JUN/FOSB/FOS/PLCG2/JUNB	12	0.137931034482759
GO:0099175	BP	GO:0099175	regulation of	12/1414	87/18903	0.028233525	0.0830071	0.05319251	PTPRD/HSPA8/NRP2/ARF4/S	12	0.137931034482759
GO:1900182	BP	GO:1900182	positive	12/1414	87/18903	0.028233525	0.0830071	0.05319251	FLNA/GLI3/PIK3R1/RAN/TG	12	0.137931034482759
GO:2000134	BP	GO:2000134	negative	12/1414	87/18903	0.028233525	0.0830071	0.05319251	GPNMB/FHL1/CDKN1A/INHBA	12	0.137931034482759
GO:0006576	BP	GO:0006576	cellular	13/1414	97/18903	0.028437609	0.0835650	0.05355002	SRM/SAT1/OAZ1/ODC1/ITGB	13	0.134020618556701
GO:0098739	BP	GO:0098739	import across	23/1414	202/18903	0.028805970	0.0846048	0.05421635	TRPV4/SLC39A14/SLC7A2/S	23	0.113861386138614
GO:0018105	BP	GO:0018105	peptidyl-	33/1414	313/18903	0.028898595	0.0848341	0.05436331	STK38L/TXN/TGFB1/PTGS2/	33	0.105431309904153
GO:0006949	BP	GO:0006949	syncytium	10/1414	68/18903	0.029102402	0.0853036	0.05466417	CDON/CFLAR/TYROBP/CD53/	10	0.147058823529412
GO:0042987	BP	GO:0042987	amyloid	10/1414	68/18903	0.029102402	0.0853036	0.05466417	LYN/APOE/RTN3/IFNGR1/RT	10	0.147058823529412
GO:1902808	BP	GO:1902808	positive	10/1414	68/18903	0.029102402	0.0853036	0.05466417	PLCG2/ANXA1/RGCC/CCND1/	10	0.147058823529412
GO:0001516	BP	GO:0001516	prostaglandin	6/1414	32/18903	0.029240242	0.0854500	0.05475799	PTGS2/ANXA1/FABP5/PTGES	6	0.1875
GO:0002758	BP	GO:0002758	innate immune	6/1414	32/18903	0.029240242	0.0854500	0.05475799	PLCG2/TYROBP/CLEC7A/LYN	6	0.1875
GO:0031116	BP	GO:0031116	positive	6/1414	32/18903	0.029240242	0.0854500	0.05475799	HSPA1A/HSPA1B/RPS3/RAC1	6	0.1875

GO:0035456	BP	GO:0035456	response to	6/1414	32/18903	0.029240242	0.0854500	0.05475799	IFITM1/IFITM2/BST2/MNDA	6	0.1875
GO:0046457	BP	GO:0046457	prostanoid	6/1414	32/18903	0.029240242	0.0854500	0.05475799	PTGS2/ANXA1/FABP5/PTGES	6	0.1875
GO:1903715	BP	GO:1903715	regulation of	6/1414	32/18903	0.029240242	0.0854500	0.05475799	COX7A1/TRPV4/NUPR1/NOP5	6	0.1875
GO:0006417	BP	GO:0006417	regulation of translation	48/1414	486/18903	0.029361089 0024708	0.0857602 564603968	0.05495676 51729035	ZFP36L1/SOX4/DIO2/TNRC6 A/ZFP36/LARP6/RPS3/EIF1	48	0.0987654320987654
GO:0046879	BP	GO:0046879	hormone	31/1414	291/18903	0.029517322	0.0861734	0.05522154	GJA1/AQP1/SOX4/DAB2/FOX	31	0.106529209621993
GO:0006941	BP	GO:0006941	striated	21/1414	181/18903	0.029720177	0.0866788	0.05554544	GJA1/TPM1/FLNA/MAP2K6/T	21	0.116022099447514
GO:0042770	BP	GO:0042770	signal	21/1414	181/18903	0.029720177	0.0866788	0.05554544	TWIST1/SOX4/SNAI1/NDRG1	21	0.116022099447514
GO:0001759	BP	GO:0001759	organ	5/1414	24/18903	0.029900891	0.0867720	0.05560516	SIX1/BMP2/FGF2/FGF1/SPR	5	0.208333333333333
GO:0006123	BP	GO:0006123	mitochondrial	5/1414	24/18903	0.029900891	0.0867720	0.05560516	NDUFA4/COX7A1/CYCS/COX5	5	0.208333333333333
GO:0030859	BP	GO:0030859	polarized	5/1414	24/18903	0.029900891	0.0867720	0.05560516	CDC42/RHOA/MSN/RAB10/FA	5	0.208333333333333
GO:0035162	BP	GO:0035162	embryonic	5/1414	24/18903	0.029900891	0.0867720	0.05560516	VEGFA/ATF4/STK4/KDR/TGF	5	0.208333333333333
GO:0035988	BP	GO:0035988	chondrocyte	5/1414	24/18903	0.029900891	0.0867720	0.05560516	COMP/FGFR3/DDR2/SMAD7/B	5	0.208333333333333
GO:0040037	BP	GO:0040037	negative	5/1414	24/18903	0.029900891	0.0867720	0.05560516	SULF2/FGF2/SPRY2/THBS1/	5	0.208333333333333
GO:0061484	BP	GO:0061484	hematopoietic	5/1414	24/18903	0.029900891	0.0867720	0.05560516	FSTL1/SOX4/CRISPLD1/EMC	5	0.208333333333333
GO:0071676	BP	GO:0071676	negative	5/1414	24/18903	0.029900891	0.0867720	0.05560516	NBL1/APOD/CCL2/DUSP1/PL	5	0.208333333333333
GO:2000353	BP	GO:2000353	positive	5/1414	24/18903	0.029900891	0.0867720	0.05560516	RGCC/CCL2/THBS1/PDCD4/E	5	0.208333333333333
GO:2000738	BP	GO:2000738	positive	5/1414	24/18903	0.029900891	0.0867720	0.05560516	LTBP3/SOX5/PTN/FGF2/SOX	5	0.208333333333333
GO:0050830	BP	GO:0050830	defense	15/1414	118/18903	0.029986934	0.0869785	0.05573744	PLA2G2A/RPL39/GBP2/LYZ/	15	0.127118644067797
GO:0043537	BP	GO:0043537	negative	11/1414	78/18903	0.030085973	0.0871357	0.05583823	FGF2/TGFB1/RGCC/KLF4/AP	11	0.141025641025641
GO:0055117	BP	GO:0055117	regulation of	11/1414	78/18903	0.030085973	0.0871357	0.05583823	PDE4B/CALM2/GSTO1/CAV1/	11	0.141025641025641
GO:0140115	BP	GO:0140115	export across	11/1414	78/18903	0.030085973	0.0871357	0.05583823	GJA1/SLC40A1/FXYD1/CALM	11	0.141025641025641
GO:0010574	BP	GO:0010574	regulation of	9/1414	59/18903	0.030291781	0.0875145	0.05608097	SULF2/NDRG2/TGFB1/PTGS2	9	0.152542372881356
GO:0045604	BP	GO:0045604	regulation of	9/1414	59/18903	0.030291781	0.0875145	0.05608097	ZFP36L1/HES1/ZFP36/FGF2	9	0.152542372881356
GO:0051653	BP	GO:0051653	spindle	9/1414	59/18903	0.030291781	0.0875145	0.05608097	GJA1/SPRY2/ACTR2/ACTR3/	9	0.152542372881356
GO:0097352	BP	GO:0097352	autophagosome	9/1414	59/18903	0.030291781	0.0875145	0.05608097	LAMP2/VMP1/MAP1LC3B/CHM	9	0.152542372881356
GO:1903078	BP	GO:1903078	positive	9/1414	59/18903	0.030291781	0.0875145	0.05608097	PIK3R1/SQSTM1/TREM2/RHO	9	0.152542372881356
GO:1902600	BP	GO:1902600	proton	19/1414	160/18903	0.030339234	0.0876082	0.05614102	TWIST1/NDUFA4/ATP5ME/CO	19	0.11875
GO:0033138	BP	GO:0033138	positive	14/1414	108/18903	0.030414857	0.0877832	0.05625311	TXN/TGFB1/PTGS2/SPRY2/C	14	0.12962962962963
GO:0032945	BP	GO:0032945	negative	12/1414	88/18903	0.030550649	0.0881315	0.05647631	GPNMB/SDC4/PELI1/CEBPB/	12	0.136363636363636
GO:0014912	BP	GO:0014912	negative	7/1414	41/18903	0.030838835	0.0888310	0.05692460	TPM1/AIF1/MEF2C/GNA13/R	7	0.170731707317073
GO:0045454	BP	GO:0045454	cell redox	7/1414	41/18903	0.030838835	0.0888310	0.05692460	PRDX4/DDIT3/TXN/PRDX1/G	7	0.170731707317073
GO:0120178	BP	GO:0120178	steroid	7/1414	41/18903	0.030838835	0.0888310	0.05692460	EGR1/DKK3/DAB2/BMP2/BMP	7	0.170731707317073
GO:0097553	BP	GO:0097553	calcium ion	21/1414	182/18903	0.031320646	0.0901743	0.05778542	THY1/FLNA/PLCG2/DDIT3/T	21	0.115384615384615
GO:0051148	BP	GO:0051148	negative	10/1414	69/18903	0.031839275	0.0915771	0.05868434	FOXP1/BMP2/XBP1/BHLHE41	10	0.144927536231884
GO:1902305	BP	GO:1902305	regulation of	10/1414	69/18903	0.031839275	0.0915771	0.05868434	ANK3/FXYD1/GLRX/ATP1B3/	10	0.144927536231884

GO:0002708	BP	GO:0002708 positive	15/1414	119/18903	0.032031597	0.0920849	0.05900972	CADM1/LAG3/CD55/TGFB1/H	15	0.126050420168067
GO:0071326	BP	GO:0071326 cellular	17/1414	140/18903	0.032396835	0.0930890	0.05965318	SOX4/SLC29A1/PIM3/SLC39	17	0.121428571428571
GO:0033209	BP	GO:0033209 tumor	14/1414	109/18903	0.032588594	0.0935939	0.05997672	HSPA1A/HSPA1B/NFKBIA/BI	14	0.128440366972477
GO:0036465	BP	GO:0036465 synaptic	11/1414	79/18903	0.032680939	0.0937668	0.06008751	ACTG1/ACTB/CYFIP1/FCHO2	11	0.139240506329114
GO:0061333	BP	GO:0061333 renal tubule	11/1414	79/18903	0.032680939	0.0937668	0.06008751	SIX1/GLI3/HES1/BMP2/FGF	11	0.139240506329114
GO:0062012	BP	GO:0062012 regulation of	35/1414	339/18903	0.032784811	0.0940185	0.06024885	IGFBP4/EGR1/DKK3/TWIST1	35	0.103244837758112
GO:0045787	BP	GO:0045787 positive	37/1414	362/18903	0.032915023	0.0942541	0.06039979	PDGFRB/CCPG1/SMOC2/PLCG	37	0.102209944751381
GO:0009060	BP	GO:0009060 aerobic	22/1414	194/18903	0.033238901	0.0942541	0.06039979	NDUFA4/NDUFB1/ATP5ME/UQ	22	0.11340206185567
GO:0061136	BP	GO:0061136 regulation of	22/1414	194/18903	0.033238901	0.0942541	0.06039979	DAB2/HSPA1A/UBB/HSPA1B/	22	0.11340206185567
GO:0019079	BP	GO:0019079 viral genome	16/1414	130/18903	0.033336650	0.0942541	0.06039979	IFITM1/HSPA8/SLPI/IFITM	16	0.123076923076923
GO:0022029	BP	GO:0022029 telencephalon	9/1414	60/18903	0.033360872	0.0942541	0.06039979	COL3A1/GLI3/DIXDC1/CXCR	9	0.15
GO:2000649	BP	GO:2000649 regulation of	9/1414	60/18903	0.033360872	0.0942541	0.06039979	ANK3/FXYD1/GLRX/ATP1B1/	9	0.15
GO:0002828	BP	GO:0002828 regulation of	6/1414	33/18903	0.033551941	0.0942541	0.06039979	ECM1/ANXA1/CD74/CD86/IL	6	0.181818181818182
GO:0030511	BP	GO:0030511 positive	6/1414	33/18903	0.033551941	0.0942541	0.06039979	DAB2/ZEB2/SDCBP/TGFBR3/	6	0.181818181818182
GO:0048147	BP	GO:0048147 negative	6/1414	33/18903	0.033551941	0.0942541	0.06039979	SOD2/NUPR1/CAV1/FTH1/IF	6	0.181818181818182
GO:0048841	BP	GO:0048841 regulation of	6/1414	33/18903	0.033551941	0.0942541	0.06039979	SEMA3C/VEGFA/NRP1/SEMA3	6	0.181818181818182
GO:0050858	BP	GO:0050858 negative	6/1414	33/18903	0.033551941	0.0942541	0.06039979	THY1/LAPTM5/FCGR2B/EZR/	6	0.181818181818182
GO:0050974	BP	GO:0050974 detection of	6/1414	33/18903	0.033551941	0.0942541	0.06039979	COL11A1/SERPINE2/CXCR4/	6	0.181818181818182
GO:1903846	BP	GO:1903846 positive	6/1414	33/18903	0.033551941	0.0942541	0.06039979	DAB2/ZEB2/SDCBP/TGFBR3/	6	0.181818181818182
GO:0001542	BP	GO:0001542 ovulation	3/1414	10/18903	0.033656989	0.0942541	0.06039979	MMP2/NRIP1/ADAMTS1	3	0.3
GO:0003056	BP	GO:0003056 regulation of	3/1414	10/18903	0.033656989	0.0942541	0.06039979	DOCK4/ATP2B1/RHOA	3	0.3
GO:0003093	BP	GO:0003093 regulation of	3/1414	10/18903	0.033656989	0.0942541	0.06039979	CYBA/GAS6/PDGFB	3	0.3
GO:0003253	BP	GO:0003253 cardiac	3/1414	10/18903	0.033656989	0.0942541	0.06039979	TWIST1/SEMA3C/CDC42	3	0.3
GO:0003266	BP	GO:0003266 regulation of	3/1414	10/18903	0.033656989	0.0942541	0.06039979	SIX1/HES1/GNG5	3	0.3
GO:0007343	BP	GO:0007343 egg	3/1414	10/18903	0.033656989	0.0942541	0.06039979	MYH9/PLAT/PLCB1	3	0.3
GO:0010572	BP	GO:0010572 positive	3/1414	10/18903	0.033656989	0.0942541	0.06039979	FLNA/PLEK/TLR4	3	0.3
GO:0010764	BP	GO:0010764 negative	3/1414	10/18903	0.033656989	0.0942541	0.06039979	FGF2/RAC1/HYAL2	3	0.3
GO:0021561	BP	GO:0021561 facial nerve	3/1414	10/18903	0.033656989	0.0942541	0.06039979	SIX1/NRP2/NRP1	3	0.3
GO:0021610	BP	GO:0021610 facial nerve	3/1414	10/18903	0.033656989	0.0942541	0.06039979	SIX1/NRP2/NRP1	3	0.3
GO:0030953	BP	GO:0030953 astral	3/1414	10/18903	0.033656989	0.0942541	0.06039979	EZR/RAB11A/NUMA1	3	0.3
GO:0032819	BP	GO:0032819 positive	3/1414	10/18903	0.033656989	0.0942541	0.06039979	FCGR3A/IL18/HLA-E	3	0.3
GO:0033007	BP	GO:0033007 negative	3/1414	10/18903	0.033656989	0.0942541	0.06039979	RABGEF1/CD84/HMOX1	3	0.3
GO:0035768	BP	GO:0035768 endothelial	3/1414	10/18903	0.033656989	0.0942541	0.06039979	FGFR1/FGF2/FGF1	3	0.3
GO:0044341	BP	GO:0044341 sodium-	3/1414	10/18903	0.033656989	0.0942541	0.06039979	CEBPB/ATF4/SFRP4	3	0.3
GO:0044351	BP	GO:0044351 macropinocyto	3/1414	10/18903	0.033656989	0.0942541	0.06039979	MAPKAPK2/PYCARD/DOCK2	3	0.3
GO:0051409	BP	GO:0051409 response to	3/1414	10/18903	0.033656989	0.0942541	0.06039979	DDIT3/DNAJA1/DUSP6	3	0.3

GO:0060346	BP	GO:0060346	bone	3/1414	10/18903	0.033656989	0.0942541	0.06039979	COL1A1/MMP2/CHAD	3	0.3
GO:0060368	BP	GO:0060368	regulation of	3/1414	10/18903	0.033656989	0.0942541	0.06039979	RABGEF1/PTPRC/LYN	3	0.3
GO:0060502	BP	GO:0060502	epithelial	3/1414	10/18903	0.033656989	0.0942541	0.06039979	FGFR2/CDC42/NFIB	3	0.3
GO:0061626	BP	GO:0061626	pharyngeal	3/1414	10/18903	0.033656989	0.0942541	0.06039979	HES1/ADGRF5/BMPR2	3	0.3
GO:0070391	BP	GO:0070391	response to	3/1414	10/18903	0.033656989	0.0942541	0.06039979	CD14/TREM2/TLR4	3	0.3
GO:0071223	BP	GO:0071223	cellular	3/1414	10/18903	0.033656989	0.0942541	0.06039979	CD14/TREM2/TLR4	3	0.3
GO:0071476	BP	GO:0071476	cellular	3/1414	10/18903	0.033656989	0.0942541	0.06039979	TRPV4/FBP1/CAB39	3	0.3
GO:0098974	BP	GO:0098974	postsynaptic	3/1414	10/18903	0.033656989	0.0942541	0.06039979	ACTG1/ACTB/FARP1	3	0.3
GO:1902959	BP	GO:1902959	regulation of	3/1414	10/18903	0.033656989	0.0942541	0.06039979	LYN/PICALM/EFNA1	3	0.3
GO:1903980	BP	GO:1903980	positive	3/1414	10/18903	0.033656989	0.0942541	0.06039979	CCL3/TREM2/CTSC	3	0.3
GO:1905461	BP	GO:1905461	positive	3/1414	10/18903	0.033656989	0.0942541	0.06039979	SOD2/ATF4/PDCD4	3	0.3
GO:2000425	BP	GO:2000425	regulation of	3/1414	10/18903	0.033656989	0.0942541	0.06039979	TGM2/CCL2/TREM2	3	0.3
GO:2000544	BP	GO:2000544	regulation of	3/1414	10/18903	0.033656989	0.0942541	0.06039979	FGFR1/FGF2/FGF1	3	0.3
GO:0002371	BP	GO:0002371	dendritic	4/1414	17/18903	0.033804155	0.0942541	0.06039979	PLCG2/CLEC7A/BST2/TLR4	4	0.235294117647059
GO:0003198	BP	GO:0003198	epithelial to	4/1414	17/18903	0.033804155	0.0942541	0.06039979	RBPJ/SNAI1/ENG/TGFBR2	4	0.235294117647059
GO:0009084	BP	GO:0009084	glutamine	4/1414	17/18903	0.033804155	0.0942541	0.06039979	OAT/GLUL/GLUD1/ASS1	4	0.235294117647059
GO:0032328	BP	GO:0032328	alanine	4/1414	17/18903	0.033804155	0.0942541	0.06039979	SLC3A2/SLC6A6/SLC38A2/S	4	0.235294117647059
GO:0034134	BP	GO:0034134	toll-like	4/1414	17/18903	0.033804155	0.0942541	0.06039979	LYN/TREM2/CYBA/TNFAIP3	4	0.235294117647059
GO:0045198	BP	GO:0045198	establishment	4/1414	17/18903	0.033804155	0.0942541	0.06039979	CDC42/RHOA/MSN/FAT1	4	0.235294117647059
GO:0048557	BP	GO:0048557	embryonic	4/1414	17/18903	0.033804155	0.0942541	0.06039979	PDGFRA/GLI3/FGFR2/ID2	4	0.235294117647059
GO:0061548	BP	GO:0061548	ganglion	4/1414	17/18903	0.033804155	0.0942541	0.06039979	SIX1/NRP2/NRP1/CYP1B1	4	0.235294117647059
GO:0070206	BP	GO:0070206	protein	4/1414	17/18903	0.033804155	0.0942541	0.06039979	COL1A2/STEAP4/CD74/ALOX	4	0.235294117647059
GO:0071732	BP	GO:0071732	cellular	4/1414	17/18903	0.033804155	0.0942541	0.06039979	AQP1/FOXO1/MMP3/CFLAR	4	0.235294117647059
GO:0072378	BP	GO:0072378	blood	4/1414	17/18903	0.033804155	0.0942541	0.06039979	FLNA/FN1/F13A1/THBD	4	0.235294117647059
GO:0080154	BP	GO:0080154	regulation of	4/1414	17/18903	0.033804155	0.0942541	0.06039979	LHFPL2/MYH9/PLAT/PLCB1	4	0.235294117647059
GO:0090083	BP	GO:0090083	regulation of	4/1414	17/18903	0.033804155	0.0942541	0.06039979	DNAJB1/HSPA1A/HSPA1B/DN	4	0.235294117647059
GO:0090594	BP	GO:0090594	inflammatory	4/1414	17/18903	0.033804155	0.0942541	0.06039979	TGFB1/TLR4/HMOX1/GRN	4	0.235294117647059
GO:0090713	BP	GO:0090713	immunological	4/1414	17/18903	0.033804155	0.0942541	0.06039979	HLA-DRB1/HLA-	4	0.235294117647059
GO:0090288	BP	GO:0090288	negative	15/1414	120/18903	0.034176295	0.0952462	0.06103554	NBL1/FBN1/HTRA1/SULF2/C	15	0.125
GO:0019083	BP	GO:0019083	viral	8/1414	51/18903	0.034434925	0.0957839	0.06138012	JUN/HEXIM1/ZFP36/GTF2B/	8	0.156862745098039
GO:0045058	BP	GO:0045058	T cell	8/1414	51/18903	0.034434925	0.0957839	0.06138012	GLI3/CTSL/CD74/PTPRC/CD	8	0.156862745098039
GO:0046580	BP	GO:0046580	negative	8/1414	51/18903	0.034434925	0.0957839	0.06138012	SPRY2/RABGEF1/FBP1/BCL6	8	0.156862745098039
GO:0051489	BP	GO:0051489	regulation of	8/1414	51/18903	0.034434925	0.0957839	0.06138012	CAPZB/DPYSL3/PIK3R1/NRP	8	0.156862745098039
GO:0070296	BP	GO:0070296	sarcoplasmic	7/1414	42/18903	0.034702896	0.0964833	0.06182830	CALM2/GSTO1/NOL3/CCL3/S	7	0.166666666666667
GO:0019835	BP	GO:0019835	cytolysis	5/1414	25/18903	0.035145933	0.0971133	0.06223202	PLA2G2A/TGFB1/LYZ/NINJ1	5	0.2
GO:0021801	BP	GO:0021801	cerebral	5/1414	25/18903	0.035145933	0.0971133	0.06223202	COL3A1/GLI3/RTN4/SYNE2/	5	0.2

GO:0022030	BP	GO:0022030	telencephalon	5/1414	25/18903	0.035145933	0.0971133	0.06223202	COL3A1/GLI3/RTN4/SYNE2/	5	0.2
GO:0032331	BP	GO:0032331	negative	5/1414	25/18903	0.035145933	0.0971133	0.06223202	GLI3/EFEMP1/LTBP3/CHADL	5	0.2
GO:0032816	BP	GO:0032816	positive	5/1414	25/18903	0.035145933	0.0971133	0.06223202	TYROBP/FCGR3A/IL18/HLA-	5	0.2
GO:0034114	BP	GO:0034114	regulation of	5/1414	25/18903	0.035145933	0.0971133	0.06223202	THY1/CD44/KLF4/MBP/WNK1	5	0.2
GO:0045932	BP	GO:0045932	negative	5/1414	25/18903	0.035145933	0.0971133	0.06223202	KCNMA1/PTGS2/DOCK4/RGS2	5	0.2
GO:0045980	BP	GO:0045980	negative	5/1414	25/18903	0.035145933	0.0971133	0.06223202	H19/NUPR1/DDIT4/PID1/FB	5	0.2
GO:0050860	BP	GO:0050860	negative	5/1414	25/18903	0.035145933	0.0971133	0.06223202	THY1/LAPTM5/EZR/ELF1/PT	5	0.2
GO:0060396	BP	GO:0060396	growth	5/1414	25/18903	0.035145933	0.0971133	0.06223202	PIK3R1/LYN/JAK1/PTK2/LE	5	0.2
GO:0071378	BP	GO:0071378	cellular	5/1414	25/18903	0.035145933	0.0971133	0.06223202	PIK3R1/LYN/JAK1/PTK2/LE	5	0.2
GO:1901071	BP	GO:1901071	glucosamine-	5/1414	25/18903	0.035145933	0.0971133	0.06223202	CHI3L1/CHST3/CHI3L2/PGM	5	0.2
GO:2000114	BP	GO:2000114	regulation of	5/1414	25/18903	0.035145933	0.0971133	0.06223202	GSN/SHTN1/RAP1B/ROCK1/C	5	0.2
GO:0062013	BP	GO:0062013	positive	18/1414	152/18903	0.035178671	0.0971577	0.06226049	TWIST1/DAB2/FOXO1/NR1D1	18	0.118421052631579
GO:0097306	BP	GO:0097306	cellular	13/1414	100/18903	0.035369314	0.0975918	0.06253868	FOS/SOD2/INHBA/KLF2/CYB	13	0.13
GO:1901992	BP	GO:1901992	positive	13/1414	100/18903	0.035369314	0.0975918	0.06253868	ANXA1/RGCC/CCND1/AIF1/R	13	0.13
GO:2001259	BP	GO:2001259	positive	11/1414	80/18903	0.035430548	0.0977146	0.06261733	ANK3/PLCG2/CALM2/GSTO1/	11	0.1375
GO:1902850	BP	GO:1902850	microtubule	19/1414	163/18903	0.035785496	0.0986468	0.06321475	GJA1/FLNA/HSPA1A/HSPA1B	19	0.116564417177914
GO:1903900	BP	GO:1903900	regulation of	17/1414	142/18903	0.036436484	0.1003939	0.06433431	LGALS1/IFITM1/GSN/SLPI/	17	0.119718309859155
GO:1905952	BP	GO:1905952	regulation of	21/1414	185/18903	0.036510296	0.1005498	0.06443420	DAB2/ABCA5/MAP2K6/NFKBI	21	0.113513513513514
GO:0006956	BP	GO:0006956	complement	16/1414	132/18903	0.037645743	0.1036279	0.06640671	C1R/CFH/CFB/C1S/A2M/CD5	16	0.121212121212121
GO:0051057	BP	GO:0051057	positive	10/1414	71/18903	0.037845399	0.1041284	0.06672741	COL3A1/PDGFRB/NOTCH2/CD	10	0.140845070422535
GO:0042773	BP	GO:0042773	ATP synthesis	13/1414	101/18903	0.037927333	0.1042554	0.06680885	NDUFA4/NDUFB1/UQCR11/CO	13	0.128712871287129
GO:0042775	BP	GO:0042775	mitochondrial	13/1414	101/18903	0.037927333	0.1042554	0.06680885	NDUFA4/NDUFB1/UQCR11/CO	13	0.128712871287129
GO:0048013	BP	GO:0048013	ephrin	8/1414	52/18903	0.038130122	0.1045632	0.06700608	MMP2/RBPJ/SIPA1L1/LYN/E	8	0.153846153846154
GO:1902930	BP	GO:1902930	regulation of	8/1414	52/18903	0.038130122	0.1045632	0.06700608	DKK3/DAB2/BMP2/BMP6/FGF	8	0.153846153846154
GO:0021799	BP	GO:0021799	cerebral	6/1414	34/18903	0.038254414	0.1045632	0.06700608	COL3A1/GLI3/DIXDC1/RTN4	6	0.176470588235294
GO:0035025	BP	GO:0035025	positive	6/1414	34/18903	0.038254414	0.1045632	0.06700608	COL3A1/PDGFRB/LPAR1/LPA	6	0.176470588235294
GO:0036336	BP	GO:0036336	dendritic	6/1414	34/18903	0.038254414	0.1045632	0.06700608	GPR183/SPI1/CXCR4/CDC42	6	0.176470588235294
GO:0045648	BP	GO:0045648	positive	6/1414	34/18903	0.038254414	0.1045632	0.06700608	HSPA1A/HSPA1B/ETS1/INHB	6	0.176470588235294
GO:0061081	BP	GO:0061081	positive	6/1414	34/18903	0.038254414	0.1045632	0.06700608	PLCG2/MAPKAPK2/CD74/LAP	6	0.176470588235294
GO:0099174	BP	GO:0099174	regulation of	6/1414	34/18903	0.038254414	0.1045632	0.06700608	PTPRD/FARP1/GPC6/ARF6/V	6	0.176470588235294
GO:0110110	BP	GO:0110110	positive	6/1414	34/18903	0.038254414	0.1045632	0.06700608	SIX1/BMP2/FGF2/FGF1/CD3	6	0.176470588235294
GO:1901797	BP	GO:1901797	negative	6/1414	34/18903	0.038254414	0.1045632	0.06700608	TWIST1/SNAI1/CD44/NOP53	6	0.176470588235294
GO:1905207	BP	GO:1905207	regulation of	6/1414	34/18903	0.038254414	0.1045632	0.06700608	BMP2/TGFB1/ARRB2/MEF2C/	6	0.176470588235294
GO:1905606	BP	GO:1905606	regulation of	6/1414	34/18903	0.038254414	0.1045632	0.06700608	PTPRD/FARP1/GPC6/ARF6/V	6	0.176470588235294
GO:0048525	BP	GO:0048525	negative	12/1414	91/18903	0.038318211	0.1045976	0.06702813	HEXIM1/IFITM1/ZFP36/GSN	12	0.131868131868132
GO:0106027	BP	GO:0106027	neuron	12/1414	91/18903	0.038318211	0.1045976	0.06702813	SIPA1L1/FCGR2B/APOE/TRE	12	0.131868131868132

GO:0006023	BP	GO:0006023	aminoglycan	11/1414	81/18903	0.038338733	0.1045976	0.06702813	PDGFRB/DSEL/DSE/XYLT1/C	11	0.135802469135802
GO:0097061	BP	GO:0097061	dendritic	11/1414	81/18903	0.038338733	0.1045976	0.06702813	SIPA1L1/FCGR2B/APOE/TRE	11	0.135802469135802
GO:0055123	BP	GO:0055123	digestive	17/1414	143/18903	0.038588655	0.1052303	0.06743353	COL3A1/PDGFRA/GLI3/HES1	17	0.118881118881119
GO:0022904	BP	GO:0022904	respiratory	15/1414	122/18903	0.038775270	0.1056404	0.06769634	NDUFA4/NDUFB1/UQCR11/CO	15	0.122950819672131
GO:1901989	BP	GO:1901989	positive	15/1414	122/18903	0.038775270	0.1056404	0.06769634	PLCG2/ANXA1/RGCC/PPP1R1	15	0.122950819672131
GO:0007595	BP	GO:0007595	lactation	7/1414	43/18903	0.038874674	0.1058124	0.06780655	CDO1/SLC29A1/XBP1/CAV1/	7	0.162790697674419
GO:0051602	BP	GO:0051602	response to	7/1414	43/18903	0.038874674	0.1058124	0.06780655	MMP2/NR4A1/SOD2/BTG2/AI	7	0.162790697674419
GO:0034763	BP	GO:0034763	negative	18/1414	154/18903	0.039293659	0.1069029	0.06850539	TWIST1/ANK3/GEM/OAZ1/CA	18	0.116883116883117
GO:0007052	BP	GO:0007052	mitotic	16/1414	133/18903	0.039945207	0.1086248	0.06960884	FLNA/HSPA1A/HSPA1B/RAN/	16	0.120300751879699
GO:0002820	BP	GO:0002820	negative	9/1414	62/18903	0.040128705	0.1089714	0.06983094	CD55/PTPRC/AHR/FCGR2B/N	9	0.145161290322581
GO:0032387	BP	GO:0032387	negative	9/1414	62/18903	0.040128705	0.1089714	0.06983094	CRYAB/APOD/TXN/INSIG1/S	9	0.145161290322581
GO:0060038	BP	GO:0060038	cardiac	9/1414	62/18903	0.040128705	0.1089714	0.06983094	RBPJ/RUNX1/RBP4/FGF2/FG	9	0.145161290322581
GO:0001823	BP	GO:0001823	mesonephros	13/1414	102/18903	0.040613947	0.1098070	0.07036642	SIX1/GLI3/HES1/ZBTB16/B	13	0.127450980392157
GO:0019218	BP	GO:0019218	regulation of	13/1414	102/18903	0.040613947	0.1098070	0.07036642	EGR1/DKK3/DAB2/IGFBP7/S	13	0.127450980392157
GO:0000027	BP	GO:0000027	ribosomal	5/1414	26/18903	0.040923989	0.1098070	0.07036642	RPL23A/RPL38/NOP53/RPL1	5	0.192307692307692
GO:0002433	BP	GO:0002433	immune	5/1414	26/18903	0.040923989	0.1098070	0.07036642	PTPRC/FCGR2B/LYN/PTK2/F	5	0.192307692307692
GO:0032515	BP	GO:0032515	negative	5/1414	26/18903	0.040923989	0.1098070	0.07036642	PPP1R15A/NCKAP1L/GNAI2/	5	0.192307692307692
GO:0033598	BP	GO:0033598	mammary gland	5/1414	26/18903	0.040923989	0.1098070	0.07036642	CEBPB/ID2/CCND1/BAX/RTN	5	0.192307692307692
GO:0038096	BP	GO:0038096	Fc-gamma	5/1414	26/18903	0.040923989	0.1098070	0.07036642	PTPRC/FCGR2B/LYN/PTK2/F	5	0.192307692307692
GO:0044346	BP	GO:0044346	fibroblast	5/1414	26/18903	0.040923989	0.1098070	0.07036642	NUPR1/STK17A/STK17B/GAS	5	0.192307692307692
GO:0045672	BP	GO:0045672	positive	5/1414	26/18903	0.040923989	0.1098070	0.07036642	FOS/KLF10/NOTCH2/TYROBP	5	0.192307692307692
GO:0048596	BP	GO:0048596	embryonic	5/1414	26/18903	0.040923989	0.1098070	0.07036642	TWIST1/ZEB1/CITED2/HIPK	5	0.192307692307692
GO:0060314	BP	GO:0060314	regulation of	5/1414	26/18903	0.040923989	0.1098070	0.07036642	CALM2/GSTO1/CALM3/FKBP1	5	0.192307692307692
GO:0060333	BP	GO:0060333	interferon-	5/1414	26/18903	0.040923989	0.1098070	0.07036642	IFNGR2/IFNGR1/SP100/JAK	5	0.192307692307692
GO:0060384	BP	GO:0060384	innervation	5/1414	26/18903	0.040923989	0.1098070	0.07036642	SULF2/VCAM1/SERPINE2/NR	5	0.192307692307692
GO:1903901	BP	GO:1903901	negative	5/1414	26/18903	0.040923989	0.1098070	0.07036642	IFITM1/GSN/IFITM2/BST2/	5	0.192307692307692
GO:1904753	BP	GO:1904753	negative	5/1414	26/18903	0.040923989	0.1098070	0.07036642	TPM1/MEF2C/GNA13/RHOA/N	5	0.192307692307692
GO:1905048	BP	GO:1905048	regulation of	5/1414	26/18903	0.040923989	0.1098070	0.07036642	ANTXR1/TIMP2/MBP/PICALM	5	0.192307692307692
GO:2000050	BP	GO:2000050	regulation of	5/1414	26/18903	0.040923989	0.1098070	0.07036642	DAB2/PLEKHA4/RNF213/NPH	5	0.192307692307692
GO:0002693	BP	GO:0002693	positive	4/1414	18/18903	0.040963521	0.1098070	0.07036642	THY1/CD99/ICAM1/PLVAP	4	0.222222222222222
GO:0006957	BP	GO:0006957	complement	4/1414	18/18903	0.040963521	0.1098070	0.07036642	CFH/CFB/CFD/VSIG4	4	0.222222222222222
GO:0006978	BP	GO:0006978	DNA damage	4/1414	18/18903	0.040963521	0.1098070	0.07036642	CDKN1A/RPS27L/SP100/RPL	4	0.222222222222222
GO:0009125	BP	GO:0009125	nucleoside	4/1414	18/18903	0.040963521	0.1098070	0.07036642	NT5E/TYMP/PNP/UPP1	4	0.222222222222222
GO:0032354	BP	GO:0032354	response to	4/1414	18/18903	0.040963521	0.1098070	0.07036642	INHBA/TGFBR3/CYP1B1/PLA	4	0.222222222222222
GO:0043116	BP	GO:0043116	negative	4/1414	18/18903	0.040963521	0.1098070	0.07036642	VEGFA/ADM/RAMP2/CLDN5	4	0.222222222222222
GO:0043217	BP	GO:0043217	myelin	4/1414	18/18903	0.040963521	0.1098070	0.07036642	NDRG1/CXCR4/EPB41L3/PLE	4	0.222222222222222

GO:0048486	BP	GO:0048486	parasympathet	4/1414	18/18903	0.040963521	0.1098070	0.07036642	SIX1/HES1/NRP2/NRP1	4	0.222222222222222
GO:0050665	BP	GO:0050665	hydrogen	4/1414	18/18903	0.040963521	0.1098070	0.07036642	SOD2/CYBB/CYBA/FYN	4	0.222222222222222
GO:0071786	BP	GO:0071786	endoplasmic	4/1414	18/18903	0.040963521	0.1098070	0.07036642	RTN3/RAB10/RTN4/ARL6IP1	4	0.222222222222222
GO:0090520	BP	GO:0090520	sphingolipid	4/1414	18/18903	0.040963521	0.1098070	0.07036642	RAC1/EZR/S1PR1/PLPP3	4	0.222222222222222
GO:0060996	BP	GO:0060996	dendritic	12/1414	92/18903	0.041190775	0.1103655	0.07072429	LPAR1/ARF4/SIPA1L1/APOE	12	0.130434782608696
GO:0010770	BP	GO:0010770	positive	11/1414	82/18903	0.041409213	0.1108489	0.07103409	DAB2/PTPRD/FLNA/NRP1/AR	11	0.134146341463415
GO:0042509	BP	GO:0042509	regulation of	11/1414	82/18903	0.041409213	0.1108489	0.07103409	SOCS3/HES1/CAV1/FGFR3/C	11	0.134146341463415
GO:0070507	BP	GO:0070507	regulation of	18/1414	155/18903	0.041477505	0.1109808	0.07111860	HSPA1A/HSPA1B/TRPV4/CHM	18	0.116129032258065
GO:0009914	BP	GO:0009914	hormone	31/1414	300/18903	0.042051140	0.1124641	0.07206911	GJA1/AQP1/SOX4/DAB2/FOX	31	0.103333333333333
GO:0097300	BP	GO:0097300	programmed	8/1414	53/18903	0.042081649	0.1124941	0.07208834	CFLAR/NUPR1/PELI1/BIRC2	8	0.150943396226415
GO:0006939	BP	GO:0006939	smooth muscle	14/1414	113/18903	0.042414690	0.1133325	0.07262558	COMP/SULF2/KCNMA1/PTGS2	14	0.123893805309735
GO:0031128	BP	GO:0031128	developmental	6/1414	35/18903	0.043356262	0.1148718	0.07361200	SIX1/BMP2/FGF2/FGF1/HIP	6	0.171428571428571
GO:0071398	BP	GO:0071398	cellular	6/1414	35/18903	0.043356262	0.1148718	0.07361200	ID3/HES1/PID1/ASS1/PLCB	6	0.171428571428571
GO:0090075	BP	GO:0090075	relaxation of	6/1414	35/18903	0.043356262	0.1148718	0.07361200	GSN/KCNMA1/PDE4B/ATP1B1	6	0.171428571428571
GO:1903539	BP	GO:1903539	protein	6/1414	35/18903	0.043356262	0.1148718	0.07361200	GPC6/ADAM10/RAP1A/VPS35	6	0.171428571428571
GO:0042181	BP	GO:0042181	ketone	7/1414	44/18903	0.043361262	0.1148718	0.07361200	EGR1/DKK3/DAB2/BMP2/BMP	7	0.159090909090909
GO:0046640	BP	GO:0046640	regulation of	7/1414	44/18903	0.043361262	0.1148718	0.07361200	CD55/PTPRC/IL18/HLA-	7	0.159090909090909
GO:0042472	BP	GO:0042472	inner ear	13/1414	103/18903	0.043431884	0.1148718	0.07361200	MAFB/SIX1/PRRX1/ZEB1/NT	13	0.12621359223301
GO:0002158	BP	GO:0002158	osteoclast	3/1414	11/18903	0.043760887	0.1148718	0.07361200	JUNB/NMB/TNFAIP3	3	0.272727272727273
GO:0010917	BP	GO:0010917	negative	3/1414	11/18903	0.043760887	0.1148718	0.07361200	PRELID1/PMAIP1/BAX	3	0.272727272727273
GO:0021903	BP	GO:0021903	rostrocaudal	3/1414	11/18903	0.043760887	0.1148718	0.07361200	HES1/ATP6AP2/SOX17	3	0.272727272727273
GO:0030320	BP	GO:0030320	cellular	3/1414	11/18903	0.043760887	0.1148718	0.07361200	TBXAS1/SLC12A2/WNK1	3	0.272727272727273
GO:0030644	BP	GO:0030644	cellular	3/1414	11/18903	0.043760887	0.1148718	0.07361200	TBXAS1/SLC12A2/WNK1	3	0.272727272727273
GO:0033625	BP	GO:0033625	positive	3/1414	11/18903	0.043760887	0.1148718	0.07361200	PIEZO1/PLEK/RAP1B	3	0.272727272727273
GO:0033860	BP	GO:0033860	regulation of	3/1414	11/18903	0.043760887	0.1148718	0.07361200	CYBA/GNAI2/GNAI3	3	0.272727272727273
GO:0034115	BP	GO:0034115	negative	3/1414	11/18903	0.043760887	0.1148718	0.07361200	KLF4/MBP/WNK1	3	0.272727272727273
GO:0035581	BP	GO:0035581	sequestering	3/1414	11/18903	0.043760887	0.1148718	0.07361200	NBL1/LTBP1/FBN1	3	0.272727272727273
GO:0035766	BP	GO:0035766	cell	3/1414	11/18903	0.043760887	0.1148718	0.07361200	FGFR1/FGF2/FGF1	3	0.272727272727273
GO:0044557	BP	GO:0044557	relaxation of	3/1414	11/18903	0.043760887	0.1148718	0.07361200	KCNMA1/SLC8A1/RGS2	3	0.272727272727273
GO:0044857	BP	GO:0044857	plasma	3/1414	11/18903	0.043760887	0.1148718	0.07361200	CAV1/COLEC12/CAV2	3	0.272727272727273
GO:0045837	BP	GO:0045837	negative	3/1414	11/18903	0.043760887	0.1148718	0.07361200	PRELID1/PMAIP1/BAX	3	0.272727272727273
GO:0046643	BP	GO:0046643	regulation of	3/1414	11/18903	0.043760887	0.1148718	0.07361200	SOX4/PTPRC/NCKAP1L	3	0.272727272727273
GO:0048251	BP	GO:0048251	elastic fiber	3/1414	11/18903	0.043760887	0.1148718	0.07361200	COL3A1/TNXB/LTBP3	3	0.272727272727273
GO:0051386	BP	GO:0051386	regulation of	3/1414	11/18903	0.043760887	0.1148718	0.07361200	SPRY2/CYFIP1/SPRY1	3	0.272727272727273
GO:0061299	BP	GO:0061299	retina	3/1414	11/18903	0.043760887	0.1148718	0.07361200	NRP1/CYP1B1/COL4A1	3	0.272727272727273
GO:0070587	BP	GO:0070587	regulation of	3/1414	11/18903	0.043760887	0.1148718	0.07361200	KLF4/MBP/WNK1	3	0.272727272727273

GO:0070934	BP	GO:0070934	CRD-mediated	3/1414	11/18903	0.043760887	0.1148718	0.07361200	PABPC1/YBX1/HNRNPU	3 0.272727272727273
GO:0071609	BP	GO:0071609	chemokine (C-	3/1414	11/18903	0.043760887	0.1148718	0.07361200	TRPV4/SIRPA/DDX3X	3 0.272727272727273
GO:0071649	BP	GO:0071649	regulation of	3/1414	11/18903	0.043760887	0.1148718	0.07361200	TRPV4/SIRPA/DDX3X	3 0.272727272727273
GO:0072124	BP	GO:0072124	regulation of	3/1414	11/18903	0.043760887	0.1148718	0.07361200	EGR1/CFLAR/PDGFB	3 0.272727272727273
GO:0072697	BP	GO:0072697	protein	3/1414	11/18903	0.043760887	0.1148718	0.07361200	EPB41L2/EZR/NUMA1	3 0.272727272727273
GO:0097250	BP	GO:0097250	mitochondrial	3/1414	11/18903	0.043760887	0.1148718	0.07361200	COX7A1/HIGD1A/HIGD2A	3 0.272727272727273
GO:0097278	BP	GO:0097278	complement-	3/1414	11/18903	0.043760887	0.1148718	0.07361200	CFH/CD55/CD59	3 0.272727272727273
GO:1901731	BP	GO:1901731	positive	3/1414	11/18903	0.043760887	0.1148718	0.07361200	PDPN/EMILIN2/IL6ST	3 0.272727272727273
GO:1904238	BP	GO:1904238	pericyte cell	3/1414	11/18903	0.043760887	0.1148718	0.07361200	SPI1/CD34/PDGFB	3 0.272727272727273
GO:1904847	BP	GO:1904847	regulation of	3/1414	11/18903	0.043760887	0.1148718	0.07361200	FGFR1/FGF2/FGF1	3 0.272727272727273
GO:1905668	BP	GO:1905668	positive	3/1414	11/18903	0.043760887	0.1148718	0.07361200	EZR/MSN/RDX	3 0.272727272727273
GO:2000644	BP	GO:2000644	regulation of	3/1414	11/18903	0.043760887	0.1148718	0.07361200	ANXA2/LAPTM5/APOE	3 0.272727272727273
GO:2000833	BP	GO:2000833	positive	3/1414	11/18903	0.043760887	0.1148718	0.07361200	DAB2/SPP1/BMP6	3 0.272727272727273
GO:2001204	BP	GO:2001204	regulation of	3/1414	11/18903	0.043760887	0.1148718	0.07361200	FBN1/NOTCH2/TYROBP	3 0.272727272727273
GO:0042471	BP	GO:0042471	ear	15/1414	124/18903	0.043802040	0.1148718	0.07361200	MAFB/TWIST1/SIX1/PRRX1/	15 0.120967741935484
GO:0010573	BP	GO:0010573	vascular	9/1414	63/18903	0.043837594	0.1148718	0.07361200	SULF2/NDRG2/TGFB1/PTGS2	9 0.142857142857143
GO:0021885	BP	GO:0021885	forebrain	9/1414	63/18903	0.043837594	0.1148718	0.07361200	COL3A1/GLI3/DIXDC1/CXCR	9 0.142857142857143
GO:0070059	BP	GO:0070059	intrinsic	9/1414	63/18903	0.043837594	0.1148718	0.07361200	HSPA1A/DDIT3/SELENOK/XB	9 0.142857142857143
GO:0019646	BP	GO:0019646	aerobic	12/1414	93/18903	0.044210272	0.1157963	0.07420446	NDUFA4/NDUFB1/UQCR11/CO	12 0.129032258064516
GO:0031331	BP	GO:0031331	positive regulation of	42/1414	429/18903	0.044346144 0424372	0.1161001 15888481	0.07439911 0599402	ZFP36L1/TWIST1/DAB2/KCN Q1OT1/FOXO1/TNRC6A/HSPA	42 0.0979020979020979
GO:0042246	BP	GO:0042246	tissue	10/1414	73/18903	0.044590949	0.1165840	0.07470922	RUNX1/PTN/APOD/CFLAR/CD	10 0.136986301369863
GO:0045665	BP	GO:0045665	negative	10/1414	73/18903	0.044590949	0.1165840	0.07470922	ID4/GLI3/HES1/EIF4E/DIX	10 0.136986301369863
GO:1904888	BP	GO:1904888	cranial	10/1414	73/18903	0.044590949	0.1165840	0.07470922	PDGFRA/TWIST1/SIX1/PRRX	10 0.136986301369863
GO:0014032	BP	GO:0014032	neural crest	11/1414	83/18903	0.044645472	0.1166220	0.07473357	TWIST1/SEMA3C/HES1/NRP2	11 0.132530120481928
GO:0061912	BP	GO:0061912	selective	11/1414	83/18903	0.044645472	0.1166220	0.07473357	RETREG1/MAP1LC3B/SQSTM1	11 0.132530120481928
GO:1900180	BP	GO:1900180	regulation of	16/1414	135/18903	0.044843842	0.1170877	0.07503203	LMNA/FLNA/GLI3/APOD/PIK	16 0.118518518518519
GO:0050768	BP	GO:0050768	negative	17/1414	146/18903	0.045596278	0.1189991	0.07625686	THY1/SEMA3C/ID4/NTN1/HE	17 0.116438356164384
GO:0031113	BP	GO:0031113	regulation of	8/1414	54/18903	0.046294904	0.1207684	0.07739064	HSPA1A/HSPA1B/RPS3/RAC1	8 0.148148148148148
GO:0002092	BP	GO:0002092	positive	5/1414	27/18903	0.047242905	0.1230213	0.07883437	PLCG2/MAGI2/VEGFA/ARRB2	5 0.185185185185185
GO:0002407	BP	GO:0002407	dendritic	5/1414	27/18903	0.047242905	0.1230213	0.07883437	GPR183/SPI1/CXCR4/GAS6/	5 0.185185185185185
GO:0030325	BP	GO:0030325	adrenal gland	5/1414	27/18903	0.047242905	0.1230213	0.07883437	PDGFRA/DKK3/ARID5B/CITE	5 0.185185185185185
GO:0090200	BP	GO:0090200	positive	5/1414	27/18903	0.047242905	0.1230213	0.07883437	PLAUR/PYCARD/PMAIP1/BAX	5 0.185185185185185
GO:1900542	BP	GO:1900542	regulation of	12/1414	94/18903	0.047379574	0.1233222	0.07902715	H19/NUPR1/DDIT4/ENO1/PI	12 0.127659574468085
GO:0043401	BP	GO:0043401	steroid	16/1414	136/18903	0.047446742	0.1233319	0.07903339	FOXP1/DAB2/LBH/DNAJA1/N	16 0.117647058823529
GO:0071333	BP	GO:0071333	cellular	16/1414	136/18903	0.047446742	0.1233319	0.07903339	SOX4/SLC29A1/PIM3/SLC39	16 0.117647058823529

GO:1903052	BP	GO:1903052	positive	16/1414	136/18903	0.047446742	0.1233319	0.07903339	DAB2/HSPA1A/HSPA1B/NUPR	16	0.117647058823529
GO:0048524	BP	GO:0048524	positive	9/1414	64/18903	0.047769134	0.1241146	0.07953496	LGALS1/HLA-	9	0.140625
GO:0035050	BP	GO:0035050	embryonic	11/1414	84/18903	0.048050747	0.1247907	0.07996822	NOTCH2/HES1/CITED2/MEF2	11	0.130952380952381
GO:0008631	BP	GO:0008631	intrinsic	7/1414	45/18903	0.048168680	0.1249212	0.08005186	SOD2/HSPB1/NOL3/TREM2/M	7	0.155555555555556
GO:0031295	BP	GO:0031295	T cell	7/1414	45/18903	0.048168680	0.1249212	0.08005186	LGALS1/CAV1/LYN/CD86/MA	7	0.155555555555556
GO:1901021	BP	GO:1901021	positive	7/1414	45/18903	0.048168680	0.1249212	0.08005186	VMP1/PLCG2/CALM2/GSTO1/	7	0.155555555555556
GO:0017157	BP	GO:0017157	regulation of	23/1414	213/18903	0.048242097	0.1249212	0.08005186	SDCBP/SDC4/ANXA2/ANXA1/	23	0.107981220657277
GO:0001736	BP	GO:0001736	establishment	10/1414	74/18903	0.048250920	0.1249212	0.08005186	DAB2/CTHRC1/GPC6/MAGI2/	10	0.135135135135135
GO:0007164	BP	GO:0007164	establishment	10/1414	74/18903	0.048250920	0.1249212	0.08005186	DAB2/CTHRC1/GPC6/MAGI2/	10	0.135135135135135
GO:2000573	BP	GO:2000573	positive	10/1414	74/18903	0.048250920	0.1249212	0.08005186	PDGFRB/SMOC2/FGF2/RGCC/	10	0.135135135135135
GO:0001678	BP	GO:0001678	cellular	18/1414	158/18903	0.048553448	0.1251365	0.08018984	SOX4/FOXO1/SLC29A1/PIM3	18	0.113924050632911
GO:0051607	BP	GO:0051607	defense	31/1414	304/18903	0.048749491	0.1251365	0.08018984	HTRA1/IFITM1/IFITM2/SEL	31	0.101973684210526
GO:0033280	BP	GO:0033280	response to	6/1414	36/18903	0.048864247	0.1251365	0.08018984	STC2/SPP1/PTGS2/ATP2B1/	6	0.166666666666667
GO:0033687	BP	GO:0033687	osteoblast	6/1414	36/18903	0.048864247	0.1251365	0.08018984	JUNB/CTHRC1/BMP2/FGFR2/	6	0.166666666666667
GO:0045777	BP	GO:0045777	positive	6/1414	36/18903	0.048864247	0.1251365	0.08018984	TPM1/ID2/CYBA/RHOA/NR2F	6	0.166666666666667
GO:0048261	BP	GO:0048261	negative	6/1414	36/18903	0.048864247	0.1251365	0.08018984	SDCBP/ANXA2/RABGEF1/RAC	6	0.166666666666667
GO:0062237	BP	GO:0062237	protein	6/1414	36/18903	0.048864247	0.1251365	0.08018984	GPC6/ADAM10/RAP1A/VPS35	6	0.166666666666667
GO:0001502	BP	GO:0001502	cartilage	4/1414	19/18903	0.048913318	0.1251365	0.08018984	SOX5/COL2A1/COL11A1/PKD	4	0.210526315789474
GO:0002281	BP	GO:0002281	macrophage	4/1414	19/18903	0.048913318	0.1251365	0.08018984	PLCG2/TYROBP/TREM2/GRN	4	0.210526315789474
GO:0002544	BP	GO:0002544	chronic	4/1414	19/18903	0.048913318	0.1251365	0.08018984	VCAM1/THBS1/CCL5/TNFAIP	4	0.210526315789474
GO:0002923	BP	GO:0002923	regulation of	4/1414	19/18903	0.048913318	0.1251365	0.08018984	CD55/PTPRC/FCGR2B/TREM2	4	0.210526315789474
GO:0009226	BP	GO:0009226	nucleotide-	4/1414	19/18903	0.048913318	0.1251365	0.08018984	UGDH/PGM3/NANS/UAP1	4	0.210526315789474
GO:0010744	BP	GO:0010744	positive	4/1414	19/18903	0.048913318	0.1251365	0.08018984	PLA2G2A/MSR1/IL18/PRKCH	4	0.210526315789474
GO:0014067	BP	GO:0014067	negative	4/1414	19/18903	0.048913318	0.1251365	0.08018984	TWIST1/SERPINE2/NOP53/T	4	0.210526315789474
GO:0030889	BP	GO:0030889	negative	4/1414	19/18903	0.048913318	0.1251365	0.08018984	TYROBP/MNDA/FCGR2B/LYN	4	0.210526315789474
GO:0042772	BP	GO:0042772	DNA damage	4/1414	19/18903	0.048913318	0.1251365	0.08018984	CDKN1A/RPS27L/SP100/RPL	4	0.210526315789474
GO:0043652	BP	GO:0043652	engulfment of	4/1414	19/18903	0.048913318	0.1251365	0.08018984	TREM2/RHOG/RAC1/THBS1	4	0.210526315789474
GO:0045953	BP	GO:0045953	negative	4/1414	19/18903	0.048913318	0.1251365	0.08018984	ARRB2/HLA-B/HLA-E/HLA-A	4	0.210526315789474
GO:0048245	BP	GO:0048245	eosinophil	4/1414	19/18903	0.048913318	0.1251365	0.08018984	CCL3/CCL2/CCL4/CCL5	4	0.210526315789474
GO:0055003	BP	GO:0055003	cardiac	4/1414	19/18903	0.048913318	0.1251365	0.08018984	PDGFRA/PDGFRB/NEBL/MEF2	4	0.210526315789474
GO:0060216	BP	GO:0060216	definitive	4/1414	19/18903	0.048913318	0.1251365	0.08018984	ZFP36L2/TGFBR3/HIPK1/TE	4	0.210526315789474
GO:0097202	BP	GO:0097202	activation of	4/1414	19/18903	0.048913318	0.1251365	0.08018984	CYCS/PYCARD/LGMN/IFI16	4	0.210526315789474
GO:0097494	BP	GO:0097494	regulation of	4/1414	19/18903	0.048913318	0.1251365	0.08018984	BLOC1S1/PICALM/RAB11A/C	4	0.210526315789474
GO:1901659	BP	GO:1901659	glycosyl	4/1414	19/18903	0.048913318	0.1251365	0.08018984	NT5E/PNP/ADK/APRT	4	0.210526315789474
GO:1902170	BP	GO:1902170	cellular	4/1414	19/18903	0.048913318	0.1251365	0.08018984	AQP1/FOXO1/MMP3/CFLAR	4	0.210526315789474
GO:1902176	BP	GO:1902176	negative	4/1414	19/18903	0.048913318	0.1251365	0.08018984	SOD2/HSPB1/NOL3/NFE2L2	4	0.210526315789474

GO:2000251	BP	GO:2000251	positive	4/1414	19/18903	0.048913318	0.1251365	0.08018984	HCLS1/NRP1/CDC42/TEK	4 0.210526315789474
GO:0032479	BP	GO:0032479	regulation of	13/1414	105/18903	0.049471916	0.1264547	0.08103453	PLCG2/NMB/HSP90AA1/HSPD	13 0.123809523809524
GO:0032606	BP	GO:0032606	type I	13/1414	105/18903	0.049471916	0.1264547	0.08103453	PLCG2/NMB/HSP90AA1/HSPD	13 0.123809523809524
GO:0005925	CC	GO:0005925	focal adhesion	135/1454	422/19869	9.545946062 66903e-52	6.2621406 1711088e-49	4.40118355 310425e-49	TNC/GJA1/MARCKS/THY1/MR C2/EPB41L2/TPM4/ITGA11/ PDGFRB/ENAH/ITGB5/DAB2/ LIMA1/ACTG1/CD99/ACTB/F	135 0.319905213270142
GO:0030055	CC	GO:0030055	cell-substrate junction	136/1454	432/19869	3.358256090 10307e-51	1.1015079 9755381e-48	7.74166403 929023e-49	TNC/GJA1/MARCKS/THY1/MR C2/EPB41L2/TPM4/ITGA11/ PDGFRB/ENAH/ITGB5/DAB2/ LIMA1/ACTG1/CD99/ACTB/F	136 0.314814814814815
GO:0062023	CC	GO:0062023	collagen-containing extracellular matrix	128/1454	433/19869	8.010452158 49353e-45	1.7516188 7199059e-42	1.23108001 59369e-42	COL1A1/MMP2/COL1A2/TNC/ TGFBI/THBS2/COL14A1/COL 12A1/COL5A1/COL6A3/COL5 A2/COL3A1/LTBP2/S100A4/	128 0.295612009237875
GO:0005788	CC	GO:0005788	endoplasmic reticulum	80/1454	312/19869	8.285980667 02927e-24	1.3589008 293928e-	9.55068297 936532e-22	COL1A1/COL1A2/TNC/COL14 A1/COL12A1/COL5A1/COL6A	80 0.256410256410256
GO:0034774	CC	GO:0034774	secretory granule lumen	81/1454	322/19869	1.658815737 66208e-23	2.1763662 4781264e-	1.52960272 230735e-21	ECM1/TUBB/NPC2/TIMP2/AC TN1/CHI3L1/ISLR/PRDX4/T	81 0.251552795031056
GO:0060205	CC	GO:0060205	cytoplasmic vesicle lumen	81/1454	325/19869	3.171559701 00904e-23	3.4675719 3976989e-	2.43709324 393327e-21	ECM1/TUBB/NPC2/TIMP2/AC TN1/CHI3L1/ISLR/PRDX4/T	81 0.249230769230769
GO:0031983	CC	GO:0031983	vesicle lumen	81/1454	327/19869	4.860736703 23184e-23	4.5552046 8188584e-	3.20150778 348202e-21	ECM1/TUBB/NPC2/TIMP2/AC TN1/CHI3L1/ISLR/PRDX4/T	81 0.247706422018349
GO:0022626	CC	GO:0022626	cytosolic ribosome	44/1454	105/19869	5.783215872 6134e-23	4.7422370 1554299e-	3.33295862 132193e-21	RPS26/RPS21/RPS15A/RPL3 9/APOD/RPS4Y1/RPL36AL/R	44 0.419047619047619
GO:0031252	CC	GO:0031252	cell leading edge	91/1454	421/19869	2.673962010 64202e-21	1.9490211 9886796e-19	1.36981913 527626e-19	THY1/ANTXR1/CAPZB/ENAH/ LIMA1/WIPF1/ACTB/TPM1/D PYSL3/ACTN1/FAP/PIEZO1/	91 0.216152019002375
GO:0005775	CC	GO:0005775	vacuolar lumen	51/1454	176/19869	4.429220837 53896e-18	2.7845103 40676e-16	1.95702106 741991e-16	VCAN/PDGFRB/TUBB/NPC2/C TSK/LAMP2/OGN/LUM/PRELP	51 0.289772727272727
GO:0030139	CC	GO:0030139	endocytic vesicle	75/1454	343/19869	4.669148437 10915e-18	2.7845103 40676e-16	1.95702106 741991e-16	ITGB5/ACTG1/RIN2/LAMP2/ UBB/SPARC/TF/GSN/SAA1/A TP6V0C/LPAR1/ATP6V0B/CT	75 0.21865889212828
GO:0101002	CC	GO:0101002	ficolin-1-rich granule	50/1454	185/19869	2.255674504 06245e-16	1.2331020 6222081e-	8.66653888 402943e-15	TIMP2/LAMP2/PRDX4/HSPA1 A/HSPA1B/HSPA8/GSN/PNP/	50 0.27027027027027

GO:0030027	CC	GO:0030027	lamellipodium	52/1454	203/19869	6.64248589490481e-16	3.35190057465966e-14	2.35579661697838e-14	ANTXR1/CAPZB/ENAH/ACTB/DPYSL3/FAP/PIEZO1/GSN/T	52	0.25615763546798
GO:0032432	CC	GO:0032432	actin	31/1454	79/19869	1.284549840	6.0190335	4.23032203	MARCKS/TPM4/MYL9/LIMA1/	31	0.392405063291139
GO:0005581	CC	GO:0005581	collagen	32/1454	86/19869	2.719070882	1.1891403	8.35756523	COL1A1/COL1A2/COL14A1/C	32	0.372093023255814
GO:0030667	CC	GO:0030667	secretory granule	66/1454	313/19869	3.19118951355413e-15	1.30838770055719e-14	9.19566451932046e-14	LAMP2/SPARC/SERPINA5/SLC44A2/CPE/ATP6V0C/CD55/	66	0.210862619808307
GO:0043202	CC	GO:0043202	lysosomal	34/1454	98/19869	4.276252340	1.6501303	1.15975140	VCAN/PDGFRB/NPC2/CTSK/L	34	0.346938775510204
GO:0070820	CC	GO:0070820	tertiary	44/1454	164/19869	1.893395405	6.9003743	4.84974963	TIMP2/LAMP2/QSOX1/ATP6V	44	0.268292682926829
GO:0005774	CC	GO:0005774	vacuolar membrane	82/1454	461/19869	3.92281456707265e-14	1.35440334526298e-12	9.51907357550038e-13	COL6A1/DAB2/LAMP2/VMP1/ABCA5/IFITM1/HSPA8/ITM2C/SLC44A2/SLC39A14/CP/I	82	0.177874186550976
GO:0044391	CC	GO:0044391	ribosomal subunit	47/1454	188/19869	4.44992471693047e-14	1.45957530715319e-12	1.02582475 05345e-12	RPS26/RPS21/RPS15A/RPL39/RPS4Y1/MRPS24/MRPS6/R	47	0.25
GO:0022627	CC	GO:0022627	cytosolic	22/1454	45/19869	7.133291266	2.2283043	1.56610605	RPS26/RPS21/RPS15A/RPS4	22	0.488888888888889
GO:0001726	CC	GO:0001726	ruffle	45/1454	178/19869	1.00020996605611e-13	2.98244426242187e-12	2.09613380 44621e-12	LIMA1/WIPF1/TPM1/ACTN1/FAP/PLCG2/S100B/TRPV4/C	45	0.252808988764045
GO:0001725	CC	GO:0001725	stress fiber	27/1454	70/19869	1.446585234	3.9539996	2.77896637	TPM4/MYL9/LIMA1/SEPTIN1	27	0.385714285714286
GO:0097517	CC	GO:0097517	contractile	27/1454	70/19869	1.446585234	3.9539996	2.77896637	TPM4/MYL9/LIMA1/SEPTIN1	27	0.385714285714286
GO:0098857	CC	GO:0098857	membrane microdomain	64/1454	327/19869	3.17551316752886e-13	8.33254655159574e-13	5.85631481001113e-12	GJA1/SERPINH1/THY1/TUBB/CAVIN1/LAMP2/PDPN/FXYD	64	0.195718654434251
GO:0042611	CC	GO:0042611	MHC protein	16/1454	25/19869	6.782581528	1.7112974	1.20274117	HLA-DRB1/HLA-	16	0.64
GO:0005840	CC	GO:0005840	ribosome	51/1454	232/19869	8.48850904952456e-13	1.97003814708204e-13	1.38459035369373e-11	RPS26/RPL22L1/RPS21/RPS15A/RPL39/APOD/RPS4Y1/M	51	0.219827586206897
GO:0045121	CC	GO:0045121	membrane raft	63/1454	326/19869	8.79453710122359e-13	1.97003814708204e-13	1.38459035369373e-11	GJA1/SERPINH1/THY1/TUBB/CAVIN1/PDPN/FXYD1/CFLA	63	0.193251533742331
GO:0005765	CC	GO:0005765	lysosomal membrane	74/1454	418/19869	9.00932079458252e-13	1.97003814708204e-13	1.38459035369373e-11	COL6A1/DAB2/LAMP2/ABCA5/IFITM1/HSPA8/ITM2C/SLC	74	0.177033492822967
GO:0098852	CC	GO:0098852	lytic vacuole membrane	74/1454	418/19869	9.00932079458252e-13	1.97003814708204e-13	1.38459035369373e-11	COL6A1/DAB2/LAMP2/ABCA5/IFITM1/HSPA8/ITM2C/SLC	74	0.177033492822967
GO:0042641	CC	GO:0042641	actomyosin	27/1454	78/19869	3.002277528	6.3532066	4.46518695	TPM4/MYL9/LIMA1/SEPTIN1	27	0.346153846153846
GO:0005938	CC	GO:0005938	cell cortex	60/1454	312/19869	3.82377340726688e-12	7.83873548490104e-13	5.50925247 49465e-11	CALD1/MARCKS/EPB41L2/TPM4/CAPZB/MYL9/SEPTIN11/	60	0.192307692307692
GO:0031091	CC	GO:0031091	platelet	29/1454	91/19869	5.077850005	9.6665122	6.79385809	THBS2/ACTN1/ISLR/SPARC/	29	0.318681318681319
GO:0005766	CC	GO:0005766	primary	39/1454	155/19869	5.157437937	9.6665122	6.79385809	TUBB/NPC2/LAMP2/TUBB4B/	39	0.251612903225806
GO:0042582	CC	GO:0042582	azurophil	39/1454	155/19869	5.157437937	9.6665122	6.79385809	TUBB/NPC2/LAMP2/TUBB4B/	39	0.251612903225806
GO:1904813	CC	GO:1904813	ficolin-1-	34/1454	124/19869	8.987324436	1.6376902	1.15100821	TIMP2/PRDX4/HSPA1A/HSPA	34	0.274193548387097

GO:0030666	CC	GO:0030666	endocytic vesicle	44/1454	194/19869	1.03069177676933e-11	1.82738866367751e-	1.28433285412508e-10	LAMP2/UBB/TF/ATP6V0C/ATP6V0B/CAV1/HLA-	44	0.22680412371134
GO:0030175	CC	GO:0030175	filopodium	31/1454	108/19869	2.024012789	3.4940852	2.45572742	ANTXR1/ENAH/FARP1/TRPV4	31	0.287037037037037
GO:0030016	CC	GO:0030016	myofibril	48/1454	233/19869	4.56406982169664e-11	7.6769994949564e-	5.39558051795716e-10	MMP2/CALD1/TPM4/CAPZB/MYL9/ACTG1/TPM1/FLNA/ACT	48	0.206008583690987
GO:0022625	CC	GO:0022625	cytosolic	22/1454	59/19869	5.726073332	9.3907602	6.60005294	RPL39/RPL36AL/RPL36/RPL	22	0.372881355932203
GO:0042613	CC	GO:0042613	MHC class II	12/1454	17/19869	9.893262473	1.5829219	1.11251578	HLA-DRB1/HLA-	12	0.705882352941177
GO:0098858	CC	GO:0098858	actin-based cell	46/1454	223/19869	1.10221885470249e-10	1.72156087782103e-	1.20995453022298e-09	PDGFRA/ANTXR1/ENAH/FARP1/TRPV4/PDPN/SLC26A2/VC	46	0.20627802690583
GO:0009897	CC	GO:0009897	external side of plasma membrane	74/1454	462/19869	1.24618430969457e-10	1.90115559804566e-09	1.33617803585366e-09	THY1/PDGFRA/ANTXR1/ITGA11/CTSK/NT5E/ITGA10/LAG3/SERPINA5/TF/SCUBE1/OS	74	0.16017316017316
GO:0005912	CC	GO:0005912	adherens	40/1454	179/19869	1.441638901	2.1493525	1.51061683	CDH11/ACTB/TRPV4/NDRG1/	40	0.223463687150838
GO:0043292	CC	GO:0043292	contractile fiber	48/1454	242/19869	1.81157119216483e-10	2.64086822680029e-	1.85606592320046e-09	MMP2/CALD1/TPM4/CAPZB/MYL9/ACTG1/TPM1/FLNA/ACT	48	0.198347107438017
GO:0005583	CC	GO:0005583	fibrillar	10/1454	12/19869	2.463522452	3.4384483	2.41662448	COL1A1/COL1A2/COL5A1/CO	10	0.833333333333333
GO:0098643	CC	GO:0098643	banded	10/1454	12/19869	2.463522452	3.4384483	2.41662448	COL1A1/COL1A2/COL5A1/CO	10	0.833333333333333
GO:0015935	CC	GO:0015935	small	24/1454	77/19869	5.760103441	7.8721413	5.53273093	RPS26/RPS21/RPS15A/RPS4	24	0.311688311688312
GO:0031093	CC	GO:0031093	platelet	22/1454	67/19869	9.803963718	1.3125306	9.22478218	ACTN1/ISLR/SPARC/QSOX1/	22	0.328358208955224
GO:0005604	CC	GO:0005604	basement	27/1454	99/19869	1.393917984	1.8288203	1.28533910	TNC/TGFBI/THBS2/COL5A1/	27	0.272727272727273
GO:0042581	CC	GO:0042581	specific	35/1454	160/19869	3.658217558	4.7054719	3.30711927	TIMP2/CHI3L1/SLC44A2/QS	35	0.21875
GO:0002102	CC	GO:0002102	podosome	14/1454	30/19869	5.660445668	7.1408699	5.01877571	TPM4/SCIN/GSN/VCAM1/PTP	14	0.466666666666667
GO:0098644	CC	GO:0098644	complex of	12/1454	22/19869	7.315039115	9.0540861	6.36343025	COL1A1/COL1A2/COL5A1/CO	12	0.545454545454545
GO:0030017	CC	GO:0030017	sarcomere	41/1454	214/19869	1.089826783	1.3099149	9.20639807	MMP2/TPM4/CAPZB/MYL9/TP	41	0.191588785046729
GO:0030863	CC	GO:0030863	cortical	27/1454	108/19869	1.098251824	1.3099149	9.20639807	CALD1/EPB41L2/TPM4/CAPZ	27	0.25
GO:0045177	CC	GO:0045177	apical part of cell	65/1454	435/19869	2.75096019081098e-08	3.22255336637858e-	2.26488827739701e-07	GJA1/THY1/AQP1/PDGFRB/ACTG1/CTSK/FAP/TF/STK26/	65	0.149425287356322
GO:0030135	CC	GO:0030135	coated vesicle	51/1454	310/19869	3.93749979551887e-08	4.53157871203575e-	3.18490288169393e-07	DAB2/COPZ2/HSPA8/TF/STEAP2/ATP6V0C/SERPINA1/AT	51	0.164516129032258
GO:0072562	CC	GO:0072562	blood	31/1454	145/19869	4.942200584	5.5897992	3.92864583	C1R/ACTG1/ACTB/HSPA1A/H	31	0.213793103448276
GO:0031256	CC	GO:0031256	leading edge	35/1454	177/19869	5.600938078	6.2274836	4.37682583	THY1/ANTXR1/TPM1/FAP/PI	35	0.19774011299435
GO:0098576	CC	GO:0098576	lumenal side	14/1454	35/19869	6.373134201	6.9531120	4.88681493	HSPA8/HLA-DRB1/HLA-	14	0.4
GO:0045335	CC	GO:0045335	phagocytic	30/1454	139/19869	6.465546241	6.9531120	4.88681493	ITGB5/ACTG1/LAMP2/GSN/A	30	0.215827338129496
GO:0031253	CC	GO:0031253	cell projection	54/1454	344/19869	7.97909596821805e-08	8.40589723753162e-	5.90786744229597e-07	THY1/MXRA8/AQP1/ANTXR1/LIMA1/TPM1/FAP/PIEZO1/P	54	0.156976744186047
GO:0098562	CC	GO:0098562	cytoplasmic	38/1454	204/19869	8.072736676	8.4058972	5.90786744	RPS26/FARP1/GEM/DNAJA1/	38	0.186274509803922

GO:0042788 CC	GO:0042788	polysomal	13/1454	31/19869	9.683681468	9.9257735	6.97607316	RPS26/RPS21/RPL39/RPL36	13	0.419354838709677
GO:0035578 CC	GO:0035578	azurophil	23/1454	91/19869	1.064639804	1.0744672	7.55161513	TUBB/NPC2/TUBB4B/SDCBP/	23	0.252747252747253
GO:0005884 CC	GO:0005884	actin	26/1454	114/19869	1.510830535	1.5016739	1.05541271	TPM4/WIPF1/ACTG1/ACTB/T	26	0.228070175438596
GO:0005770 CC	GO:0005770	late endosome	47/1454	288/19869	1.703143163 90264e-07	1.6516904 3984068e-	1.16084790 219868e-06	LAMP2/ABCA5/HSPA8/DDIT3 /TF/SLC39A14/IFITM2/STE	47	0.163194444444444
GO:0070821 CC	GO:0070821	tertiary	20/1454	73/19869	1.712118138	1.6516904	1.16084790	ATP6V0C/CD59/CYSTM1/FCE	20	0.273972602739726
GO:0030136 CC	GO:0030136	clathrin-	38/1454	211/19869	2.004516291	1.9057430	1.33940219	DAB2/HSPA8/TF/STEAP2/AT	38	0.180094786729858
GO:0042470 CC	GO:0042470	melanosome	25/1454	110/19869	2.799496756	2.5865772	1.81790893	GPNMB/HSPA8/RAN/SDCBP/S	25	0.227272727272727
GO:0048770 CC	GO:0048770	pigment	25/1454	110/19869	2.799496756	2.5865772	1.81790893	GPNMB/HSPA8/RAN/SDCBP/S	25	0.227272727272727
GO:0071556 CC	GO:0071556	integral	12/1454	29/19869	3.621589464	3.2544694	2.28731966	HLA-DRB1/HLA-	12	0.413793103448276
GO:0098553 CC	GO:0098553	lumenal side	12/1454	29/19869	3.621589464	3.2544694	2.28731966	HLA-DRB1/HLA-	12	0.413793103448276
GO:0005844 CC	GO:0005844	polysome	18/1454	66/19869	7.562281963	6.7038607	4.71163513	RPS26/RPS21/RPL39/RPS4Y	18	0.272727272727273
GO:0030665 CC	GO:0030665	clathrin-	27/1454	132/19869	8.965583044	7.8418966	5.51147420	DAB2/HSPA8/TF/ATP6V0C/A	27	0.204545454545455
GO:0009898 CC	GO:0009898	cytoplasmic	32/1454	173/19869	9.796401713	8.4558414	5.94296946	FARP1/GEM/GNG5/CHMP4B/S	32	0.184971098265896
GO:0031258 CC	GO:0031258	lamellipodium	10/1454	22/19869	1.221235760	1.0404294	7.31238910	ANTXR1/FAP/PIEZO1/CSPG4	10	0.454545454545455
GO:0005769 CC	GO:0005769	early endosome	58/1454	414/19869	1.341422454 61942e-06	1.1281706 7978248e-	7.92905580 463298e-06	GPNMB/EEA1/MELTF/TF/SLC 39A14/STEAP4/VCAM1/STEA	58	0.140096618357488
GO:0044309 CC	GO:0044309	neuron spine	32/1454	176/19869	1.448729766	1.2029958	8.45494520	SEPTIN11/ACTN1/EEA1/PAL	32	0.181818181818182
GO:0005767 CC	GO:0005767	secondary	9/1454	18/19869	1.557226958	1.2769261	8.97454484	LAMP2/SQSTM1/FTL/MAP1LC	9	0.5
GO:0015934 CC	GO:0015934	large	24/1454	115/19869	2.456386324	1.9893696	1.39817701	RPL39/RPL36AL/MRPL44/RP	24	0.208695652173913
GO:0019897 CC	GO:0019897	extrinsic	31/1454	172/19869	2.546241027	2.0369928	1.43164771	CDH11/EEA1/FARP1/TF/SCU	31	0.180232558139535
GO:0030662 CC	GO:0030662	coated	34/1454	198/19869	2.640047744	2.0865919	1.46650718	DAB2/COPZ2/HSPA8/TF/ATP	34	0.171717171717172
GO:0030669 CC	GO:0030669	clathrin-	18/1454	72/19869	3.001109750	2.3437238	1.64722565	TF/HLA-DRB1/HLA-	18	0.25
GO:0016324 CC	GO:0016324	apical plasma membrane	52/1454	368/19869	3.624672902 94352e-06	2.7917135 7680293e-	1.96208367 560925e-05	GJA1/THY1/AQP1/PDGFRB/C TSK/TF/STK26/TRPV4/ECRG	52	0.141304347826087
GO:0030864 CC	GO:0030864	cortical	19/1454	80/19869	3.670170829	2.7917135	1.96208367	CALD1/EPB41L2/ACTN1/GSN	19	0.2375
GO:0043197 CC	GO:0043197	dendritic	31/1454	175/19869	3.702425018	2.7917135	1.96208367	SEPTIN11/ACTN1/PALMD/FA	31	0.177142857142857
GO:0101003 CC	GO:0101003	ficolin-1-	16/1454	61/19869	5.388929688	4.0172021	2.82338660	LAMP2/ATP6V0C/CD55/FCER	16	0.262295081967213
GO:0032587 CC	GO:0032587	ruffle	21/1454	97/19869	5.601912912	4.1290504	2.90199628	TPM1/FAP/PLCG2/TRPV4/PD	21	0.216494845360825
GO:1904724 CC	GO:1904724	tertiary	15/1454	55/19869	6.257972026	4.5578711	3.20338183	TIMP2/QSOX1/ILF2/FTH1/T	15	0.272727272727273
GO:0044754 CC	GO:0044754	autolysosome	7/1454	12/19869	6.322656618	4.5578711	3.20338183	LAMP2/SQSTM1/FTL/MAP1LC	7	0.583333333333333
GO:0035579 CC	GO:0035579	specific	20/1454	91/19869	7.308425519	5.2112251	3.66257480	SLC44A2/CD59/PLAUR/ORMD	20	0.21978021978022
GO:0005902 CC	GO:0005902	microvillus	20/1454	93/19869	1.033434596	7.2896031	5.12330903	PDGFRA/PDPN/SLC26A2/VCA	20	0.21505376344086
GO:0035577 CC	GO:0035577	azurophil	15/1454	58/19869	1.270191454	8.8376658	6.21132481	LAMP2/ATP6V0C/VAMP8/CD6	15	0.258620689655172
GO:0005903 CC	GO:0005903	brush border	21/1454	102/19869	1.279844896	8.8376658	6.21132481	AQP1/CAPZB/LIMA1/FLNA/A	21	0.205882352941176
GO:0098636 CC	GO:0098636	protein	14/1454	52/19869	1.493047760	0.0001020	7.17055832	TNC/ITGA11/ITGB5/LGALS1	14	0.269230769230769

GO:0030018	CC	GO:0030018	Z disc	24/1454	130/19869	2.212457305	0.0001496	0.00010516	MYL9/FLNA/ACTN1/ANK3/CR	24	0.184615384615385
GO:0045334	CC	GO:0045334	clathrin-	19/1454	90/19869	2.252233639	0.0001507	0.00010595	TF/HLA-DRB1/HLA-	19	0.211111111111111
GO:0019898	CC	GO:0019898	extrinsic component of	44/1454	316/19869	2.855030631 82367e-05	0.0001891 818277248	0.00013296 1554145536	CDH11/SOCS3/PIK3R3/EEA1 /FARP1/UBB/TF/SCUBE1/PI	44	0.139240506329114
GO:0035580	CC	GO:0035580	specific	15/1454	62/19869	3.009485315	0.0001974	0.00013875	TIMP2/CHI3L1/QSOX1/SLPI	15	0.241935483870968
GO:0098862	CC	GO:0098862	cluster of	27/1454	159/19869	3.347855037	0.0002174	0.00015282	AQP1/CAPZB/LIMA1/FLNA/A	27	0.169811320754717
GO:0030134	CC	GO:0030134	COPII-coated	19/1454	95/19869	4.974566231	0.0003199	0.00022485	SERPINA1/CD59/TMED5/HLA	19	0.2
GO:0030427	CC	GO:0030427	site of	28/1454	173/19869	5.872569206	0.0003740	0.00026287	THY1/FLNA/DPYSL3/PCDH9/	28	0.161849710982659
GO:0030133	CC	GO:0030133	transport vesicle	53/1454	423/19869	8.617251678 36386e-05	0.0005435 497212506	0.00038201 9861854592	SSPN/SLC40A1/DPYSL3/GAL NT15/COPZ2/FGFRL1/CPE/S	53	0.125295508274232
GO:0031234	CC	GO:0031234	extrinsic	19/1454	99/19869	8.947506699	0.0005590	0.00039288	FARP1/GNG5/S100A6/PLEKH	19	0.191919191919192
GO:0031674	CC	GO:0031674	I band	24/1454	143/19869	0.000108178	0.0006694	0.00047052	MYL9/FLNA/ACTN1/ANK3/CR	24	0.167832167832168
GO:0055037	CC	GO:0055037	recycling	30/1454	198/19869	0.000113209	0.0006940	0.00048781	TUBA1A/MELTF/TF/NDRG1/R	30	0.151515151515152
GO:0030670	CC	GO:0030670	phagocytic	16/1454	77/19869	0.000119306	0.0007246	0.00050932	LAMP2/ATP6V0C/ATP6V0B/C	16	0.207792207792208
GO:0016323	CC	GO:0016323	basolateral	33/1454	229/19869	0.000141819	0.0008535	0.00059987	CADM1/AQP1/SLC40A1/ANK3	33	0.14410480349345
GO:0012507	CC	GO:0012507	ER to Golgi	14/1454	63/19869	0.000147683	0.0008807	0.00061900	CD59/HLA-DRB1/HLA-	14	0.222222222222222
GO:0005905	CC	GO:0005905	clathrin-	15/1454	71/19869	0.000158651	0.0009376	0.00065897	DAB2/TF/HSPD1/LRP10/AP1	15	0.211267605633803
GO:0031527	CC	GO:0031527	filopodium	7/1454	18/19869	0.000171683	0.0010055	0.00070674	ANTXR1/PDPN/VASP/ARF6/U	7	0.388888888888889
GO:0044291	CC	GO:0044291	cell-cell	15/1454	72/19869	0.000187022	0.0010857	0.00076307	GJA1/ACTN1/PCDH9/ANK3/F	15	0.208333333333333
GO:0044853	CC	GO:0044853	plasma	20/1454	113/19869	0.000189130	0.0010883	0.00076490	CAVIN1/FXYD1/KCNMA1/PTG	20	0.176991150442478
GO:0045178	CC	GO:0045178	basal part of	37/1454	272/19869	0.000192936	0.0011005	0.00077351	CADM1/AQP1/SLC40A1/FAP/	37	0.136029411764706
GO:0055038	CC	GO:0055038	recycling	18/1454	97/19869	0.000211623	0.0011967	0.00084111	NDRG1/PDLIM4/RAB13/VAMP	18	0.185567010309278
GO:0009925	CC	GO:0009925	basal plasma	35/1454	254/19869	0.000220904	0.0012385	0.00087049	CADM1/AQP1/SLC40A1/ANK3	35	0.137795275590551
GO:0005901	CC	GO:0005901	caveola	16/1454	82/19869	0.000257558	0.0014318	0.00100633	CAVIN1/FXYD1/KCNMA1/PTG	16	0.195121951219512
GO:0008305	CC	GO:0008305	integrin	9/1454	31/19869	0.000270358	0.0014903	0.00104747	ITGA11/ITGB5/ITGA10/ITG	9	0.290322580645161
GO:0042383	CC	GO:0042383	sarcolemma	22/1454	136/19869	0.000351701	0.0019226	0.00135127	COL6A3/COL6A1/AQP1/COL6	22	0.161764705882353
GO:0031901	CC	GO:0031901	early	27/1454	183/19869	0.000376136	0.0020392	0.00143321	GPNMB/EEA1/SLC39A14/STE	27	0.147540983606557
GO:0032154	CC	GO:0032154	cleavage	12/1454	54/19869	0.000432310	0.0023245	0.00163375	LIMA1/RHOC/RHOA/ARF6/MY	12	0.222222222222222
GO:0043209	CC	GO:0043209	myelin sheath	11/1454	47/19869	0.000463700	0.0024730	0.00173813	TSPAN2/ANXA2/PMP22/CALM	11	0.234042553191489
GO:0030426	CC	GO:0030426	growth cone	25/1454	167/19869	0.000488230	0.0025828	0.00181532	THY1/FLNA/DPYSL3/PCDH9/	25	0.149700598802395
GO:0043034	CC	GO:0043034	costamere	6/1454	16/19869	0.000641638	0.0033673	0.00236663	ANK3/SDC4/AHNAK/PLEC/VC	6	0.375
GO:0031904	CC	GO:0031904	endosome	9/1454	35/19869	0.000725776	0.0037786	0.00265572	CTSK/CTSL/PDLIM4/CTSS/C	9	0.257142857142857
GO:0098978	CC	GO:0098978	glutamatergic	40/1454	324/19869	0.000807631	0.0041717	0.00293197	CDH11/PTPRD/ACTB/ACTN1/	40	0.123456790123457
GO:0030904	CC	GO:0030904	retromer	5/1454	12/19869	0.001067406	0.0054704	0.00384477	SNX2/SNX6/VPS29/VPS35/S	5	0.416666666666667
GO:0046658	CC	GO:0046658	anchored	12/1454	62/19869	0.001582639	0.0080481	0.00565643	THY1/GAS1/MELTF/GPC6/UL	12	0.193548387096774
GO:0044194	CC	GO:0044194	cytolytic	5/1454	13/19869	0.001630483	0.0082276	0.00578260	RNF19B/SERPINB1/SRGN/AR	5	0.384615384615385

GO:0030658	CC	GO:0030658	transport	29/1454	222/19869	0.001705463	0.0085403	0.00600235	CPE/ATP6V0C/RAB1A/CD59/	29	0.130630630630631
GO:0032153	CC	GO:0032153	cell division	13/1454	72/19869	0.001993292	0.0099060	0.00696221	LIMA1/SEPTIN11/RHOC/RHO	13	0.180555555555556
GO:0098984	CC	GO:0098984	neuron to	41/1454	351/19869	0.002032401	0.0100244	0.00704544	CADM1/CAPZB/PTPRD/DNAJB	41	0.116809116809117
GO:0014069	CC	GO:0014069	postsynaptic	38/1454	321/19869	0.002297253	0.0112462	0.00790413	CADM1/CAPZB/DNAJB1/CRYA	38	0.118380062305296
GO:0005834	CC	GO:0005834	heterotrimeri	8/1454	34/19869	0.002628474	0.0127724	0.00897677	GNG5/GNAQ/GNA13/GNAI2/G	8	0.235294117647059
GO:0005811	CC	GO:0005811	lipid droplet	16/1454	102/19869	0.002946900	0.0142144	0.00999026	HILPDA/DHRS3/ANXA2/GOS2	16	0.156862745098039
GO:0005802	CC	GO:0005802	trans-Golgi	32/1454	262/19869	0.003019882	0.0144601	0.01016295	TGFBI/POSTN/FLNA/PCSK1N	32	0.122137404580153
GO:0032279	CC	GO:0032279	asymmetric	38/1454	327/19869	0.003166855	0.0149474	0.01050539	CADM1/CAPZB/DNAJB1/CRYA	38	0.116207951070336
GO:0005865	CC	GO:0005865	striated	6/1454	21/19869	0.003167209	0.0149474	0.01050539	TPM4/TPM1/TNNT3/TPM3/TP	6	0.285714285714286
GO:0043296	CC	GO:0043296	apical	21/1454	151/19869	0.003324970	0.0155658	0.01094007	MXRA8/FRMD6/ACTG1/ACTB/	21	0.139072847682119
GO:0031528	CC	GO:0031528	microvillus	7/1454	28/19869	0.003345715	0.0155658	0.01094007	PDPN/SLC26A2/CA9/EZR/MS	7	0.25
GO:0070160	CC	GO:0070160	tight	19/1454	132/19869	0.003456741	0.0159691	0.01122351	GJA1/MXRA8/ACTB/ANK3/US	19	0.143939393939394
GO:0099572	CC	GO:0099572	postsynaptic	39/1454	342/19869	0.003907799	0.0179266	0.01259930	CADM1/CAPZB/DNAJB1/HSPA	39	0.114035087719298
GO:0000421	CC	GO:0000421	autophagosome	10/1454	52/19869	0.003980109	0.0181316	0.01274333	LAMP2/VMP1/MAP1LC3B/CHM	10	0.192307692307692
GO:0098791	CC	GO:0098791	Golgi apparatus	43/1454	387/19869	0.004086607 42401619	0.0184883 756562388	0.01299407 66005016	TGFBI/POSTN/GALNT1/FLNA /ASAP2/PCSK1N/SULF2/XYL	43	0.111111111111111
GO:0036019	CC	GO:0036019	endolysosome	7/1454	29/19869	0.004136054	0.0185839	0.01306122	CTSK/CTSL/CTSS/CTSB/LGM	7	0.241379310344828
GO:0005641	CC	GO:0005641	nuclear	4/1454	10/19869	0.004191511	0.0186604	0.01311499	TUBB/PTGES/APP/CACYBP	4	0.4
GO:0030176	CC	GO:0030176	integral	22/1454	164/19869	0.004209972	0.0186604	0.01311499	RETREG1/DPM3/INSIG1/HSP	22	0.134146341463415
GO:0005796	CC	GO:0005796	Golgi lumen	16/1454	106/19869	0.004354727	0.0191724	0.01347488	VCAN/OGN/LUM/PRELP/GPC6	16	0.150943396226415
GO:0036464	CC	GO:0036464	cytoplasmic	30/1454	248/19869	0.004594602	0.0200937	0.01412235	ZFP36L1/TUBB/TUBA1A/ACT	30	0.120967741935484
GO:0001772	CC	GO:0001772	immunological	9/1454	45/19869	0.004705834	0.0204438	0.01436846	ICAM1/HLA-DRB1/HLA-	9	0.2
GO:0016528	CC	GO:0016528	sarcoplasm	14/1454	89/19869	0.005092295	0.0219772	0.01544615	ANK3/S100A1/SERTAD1/CTH	14	0.157303370786517
GO:0033116	CC	GO:0033116	endoplasmic	13/1454	80/19869	0.005152017	0.0220896	0.01552517	GALNT1/VMP1/PIEZO1/COPZ	13	0.1625
GO:0071682	CC	GO:0071682	endocytic	6/1454	23/19869	0.005194437	0.0221269	0.01555135	SPARC/SAA1/CTSL/HSP90AA	6	0.260869565217391
GO:0031092	CC	GO:0031092	platelet	5/1454	17/19869	0.006128917	0.0257728	0.01811380	SPARC/LHFPL2/APLP2/PECA	5	0.294117647058824
GO:0043020	CC	GO:0043020	NADPH oxidase	5/1454	17/19869	0.006128917	0.0257728	0.01811380	CYBB/NCF1/NCF2/CYBA/RAC	5	0.294117647058824
GO:0002116	CC	GO:0002116	semaphorin	4/1454	11/19869	0.006208105	0.0257754	0.01811559	NRP2/NRP1/PLXND1/PLXNB2	4	0.363636363636364
GO:0005614	CC	GO:0005614	interstitial	4/1454	11/19869	0.006208105	0.0257754	0.01811559	TNC/COL14A1/VIT/VWA1	4	0.363636363636364
GO:0031233	CC	GO:0031233	intrinsic	6/1454	24/19869	0.006504117	0.0268345	0.01886000	THY1/CD59/CD14/FOLR2/AD	6	0.25
GO:0032588	CC	GO:0032588	trans-Golgi	15/1454	101/19869	0.006585438	0.0270002	0.01897646	HLA-DRB1/HLA-	15	0.148514851485149
GO:0008287	CC	GO:0008287	protein	10/1454	56/19869	0.006872532	0.0280023	0.01968074	PPP1R15A/PPP1R3C/PPP1R1	10	0.178571428571429
GO:0030496	CC	GO:0030496	midbody	25/1454	203/19869	0.007300934	0.0295642	0.02077848	GEM/RAN/ANXA2/CHMP4B/HS	25	0.123152709359606
GO:0031227	CC	GO:0031227	intrinsic	22/1454	172/19869	0.007395153	0.0297620	0.02091751	RETREG1/DPM3/INSIG1/HSP	22	0.127906976744186
GO:1905360	CC	GO:1905360	GTPase	8/1454	40/19869	0.007538096	0.0301523	0.02119182	GNG5/GNAQ/GNA13/GNAI2/G	8	0.2
GO:0036379	CC	GO:0036379	myofilament	6/1454	25/19869	0.008037740	0.0319561	0.02245952	TPM4/TPM1/TNNT3/TPM3/TP	6	0.24

GO:0005793	CC	GO:0005793	endoplasmic	18/1454	133/19869	0.008280837	0.0327242	0.02299940	SERPINH1/GALNT1/VMP1/PI	18	0.135338345864662
GO:1903293	CC	GO:1903293	phosphatase	10/1454	58/19869	0.008824482	0.0346638	0.02436257	PPP1R15A/PPP1R3C/PPP1R1	10	0.172413793103448
GO:0031902	CC	GO:0031902	late endosome	20/1454	155/19869	0.009402085	0.0367129	0.02580271	LAMP2/ABCA5/SLC39A14/IF	20	0.129032258064516
GO:0005776	CC	GO:0005776	autophagosome	16/1454	115/19869	0.009562664	0.0369951	0.02600110	LAMP2/VMP1/HSPA8/MAP1LC	16	0.139130434782609
GO:0014704	CC	GO:0014704	intercalated	9/1454	50/19869	0.009587164	0.0369951	0.02600110	GJA1/ACTN1/ANK3/FXYD1/A	9	0.18
GO:0035770	CC	GO:0035770	ribonucleopro	30/1454	265/19869	0.011485382	0.0440608	0.03096705	ZFP36L1/TUBB/TUBA1A/ACT	30	0.113207547169811
GO:0001931	CC	GO:0001931	uropod	4/1454	13/19869	0.011955330	0.0450729	0.03167837	EZR/MSN/MYH9/ICAM2	4	0.307692307692308
GO:0031254	CC	GO:0031254	cell trailing	4/1454	13/19869	0.011955330	0.0450729	0.03167837	EZR/MSN/MYH9/ICAM2	4	0.307692307692308
GO:0043218	CC	GO:0043218	compact	4/1454	13/19869	0.011955330	0.0450729	0.03167837	ANXA2/PMP22/MBP/CLDN5	4	0.307692307692308
GO:0005798	CC	GO:0005798	Golgi-	13/1454	89/19869	0.012535558	0.0469904	0.03302601	GJA1/ITM2B/COPZ2/STK26/	13	0.146067415730337
GO:0150034	CC	GO:0150034	distal axon	31/1454	278/19869	0.012643306	0.0471250	0.03312062	THY1/ACTG1/ACTB/FLNA/DP	31	0.111510791366906
GO:0031362	CC	GO:0031362	anchored	5/1454	20/19869	0.012785282	0.0473850	0.03330332	THY1/CD59/CD14/FOLR2/HY	5	0.25
GO:0001891	CC	GO:0001891	phagocytic	6/1454	28/19869	0.014175204	0.0522412	0.03671637	ANXA1/AIF1/LCP1/TLR4/RA	6	0.214285714285714
GO:0098685	CC	GO:0098685	Schaffer	11/1454	72/19869	0.015103906	0.0553528	0.03890332	CDH11/CAPZB/PTPRD/ACTG1	11	0.152777777777778
GO:0070469	CC	GO:0070469	respirasome	14/1454	101/19869	0.015197342	0.0553858	0.03892652	NDUFA4/NDUFB1/UQCR11/CO	14	0.138613861386139
GO:0090575	CC	GO:0090575	RNA	28/1454	249/19869	0.015466613	0.0556927	0.03914220	MAFB/JUN/TCF4/FOS/RUNX1	28	0.112449799196787
GO:0030132	CC	GO:0030132	clathrin coat	4/1454	14/19869	0.015783676	0.0556927	0.03914220	AP2A2/PICALM/EPS15/AP2S	4	0.285714285714286
GO:0031089	CC	GO:0031089	platelet	4/1454	14/19869	0.015783676	0.0556927	0.03914220	ECM1/CDC37L1/SELENOP/TI	4	0.285714285714286
GO:0098554	CC	GO:0098554	cytoplasmic	4/1454	14/19869	0.015783676	0.0556927	0.03914220	RPS26/DNAJA1/RPS29/RPS2	4	0.285714285714286
GO:0042827	CC	GO:0042827	platelet	5/1454	21/19869	0.015790930	0.0556927	0.03914220	ECM1/LAMP2/CDC37L1/SELE	5	0.238095238095238
GO:0097038	CC	GO:0097038	perinuclear	5/1454	21/19869	0.015790930	0.0556927	0.03914220	PIK3R1/CYBB/CYBA/ADAM10	5	0.238095238095238
GO:0016328	CC	GO:0016328	lateral	10/1454	64/19869	0.017259521	0.0605467	0.04255373	ANK3/ANXA1/RAB13/ATP1B1	10	0.15625
GO:0031970	CC	GO:0031970	organelle	13/1454	94/19869	0.019208258	0.0667548	0.04691694	TUBB/CYCS/TXNIP/PRELID1	13	0.138297872340426
GO:0090665	CC	GO:0090665	glycoprotein	5/1454	22/19869	0.019232732	0.0667548	0.04691694	SSPN/FLNA/SGCB/UTRN/SNT	5	0.227272727272727
GO:0005923	CC	GO:0005923	bicellular	16/1454	127/19869	0.023068279	0.0794490	0.05583868	MXRA8/ANK3/USP53/MAGI2/	16	0.125984251968504
GO:0044295	CC	GO:0044295	axonal growth	5/1454	23/19869	0.023132258	0.0794490	0.05583868	FLNA/HSP90AA1/BOC/SHTN1	5	0.217391304347826
GO:0005874	CC	GO:0005874	microtubule	46/1454	466/19869	0.023604069020227	0.0806472358191091	0.0566808236340978	TUBB/TUBA1A/TUBB4B/TUBB2A/TRPV4/TUBB2B/NDRG1/S	46	0.0987124463519313
GO:0017053	CC	GO:0017053	transcription	11/1454	77/19869	0.023998560	0.0811497	0.05703401	JUN/RBPJ/TBL1XR1/GLI3/Z	11	0.142857142857143
GO:0035861	CC	GO:0035861	site of	11/1454	77/19869	0.023998560	0.0811497	0.05703401	LMNA/SAMHD1/ARPC5/ARPC3	11	0.142857142857143
GO:0016469	CC	GO:0016469	proton-	8/1454	50/19869	0.027654864	0.0930338	0.06538640	ATP5ME/ATP6V0C/ATP6V0B/	8	0.16
GO:0016010	CC	GO:0016010	dystrophin-	4/1454	17/19869	0.031504428	0.1047999	0.07365596	SSPN/SGCB/UTRN/SNTB2	4	0.235294117647059
GO:0000220	CC	GO:0000220	vacuolar	3/1454	10/19869	0.031791461	0.1047999	0.07365596	ATP6V0C/ATP6V0B/ATP6AP2	3	0.3
GO:0071203	CC	GO:0071203	WASH complex	3/1454	10/19869	0.031791461	0.1047999	0.07365596	CAPZB/CAPZA1/WASHC4	3	0.3
GO:0097197	CC	GO:0097197	tetraspanin-	3/1454	10/19869	0.031791461	0.1047999	0.07365596	PDPN/SAMHD1/ADAM10	3	0.3
GO:0016460	CC	GO:0016460	myosin II	5/1454	26/19869	0.037747287	0.1225852	0.08615587	MYL9/MYL12A/MYH9/MYL6/M	5	0.192307692307692

GO:0033177	CC	GO:0033177	proton-	5/1454	26/19869	0.037747287	0.1225852	0.08615587	ATP5ME/ATP6V0C/ATP6V0B/	5	0.192307692307692
GO:0046930	CC	GO:0046930	pore complex	5/1454	26/19869	0.037747287	0.1225852	0.08615587	SLC25A5/AFDN/BAX/ADAM10	5	0.192307692307692
GO:0031968	CC	GO:0031968	organelle	25/1454	235/19869	0.038217380	0.1229196	0.08639091	UBB/PLA2G2A/PTGS2/PPP1R	25	0.106382978723404
GO:0000164	CC	GO:0000164	protein	4/1454	18/19869	0.038225020	0.1229196	0.08639091	PPP1R15A/PPP1R3C/PPP1CA	4	0.222222222222222
GO:0005771	CC	GO:0005771	multivesicula	9/1454	63/19869	0.038971425	0.1241031	0.08722271	STEAP3/CHMP4B/CTSL/CD74	9	0.142857142857143
GO:0044304	CC	GO:0044304	main axon	9/1454	63/19869	0.038971425	0.1241031	0.08722271	THY1/ANK3/SPOCK1/EPB41L	9	0.142857142857143
GO:1990204	CC	GO:1990204	oxidoreductas	15/1454	125/19869	0.039624560	0.1255734	0.08825607	NDUFA4/NDUFB1/UQCR11/ND	15	0.12
GO:0034992	CC	GO:0034992	microtubule	3/1454	11/19869	0.041385220	0.1274587	0.08958105	SUN2/SYNE1/SYNE2	3	0.272727272727273
GO:0034993	CC	GO:0034993	meiotic	3/1454	11/19869	0.041385220	0.1274587	0.08958105	SUN2/SYNE1/SYNE2	3	0.272727272727273
GO:0106083	CC	GO:0106083	nuclear	3/1454	11/19869	0.041385220	0.1274587	0.08958105	SUN2/SYNE1/SYNE2	3	0.272727272727273
GO:0106094	CC	GO:0106094	nuclear	3/1454	11/19869	0.041385220	0.1274587	0.08958105	SUN2/SYNE1/SYNE2	3	0.272727272727273
GO:1904090	CC	GO:1904090	peptidase	3/1454	11/19869	0.041385220	0.1274587	0.08958105	SERPINA5/CTSB/PLAT	3	0.272727272727273
GO:1905370	CC	GO:1905370	serine-type	3/1454	11/19869	0.041385220	0.1274587	0.08958105	CFH/PLAUR/THBD	3	0.272727272727273
GO:0019867	CC	GO:0019867	outer	25/1454	237/19869	0.041626432	0.1276025	0.08968213	UBB/PLA2G2A/PTGS2/PPP1R	25	0.105485232067511
GO:0033176	CC	GO:0033176	proton-	5/1454	27/19869	0.043631989	0.1331283	0.09356578	ATP6V0C/ATP6V0B/ATP6V1F	5	0.185185185185185
GO:0051233	CC	GO:0051233	spindle	6/1454	36/19869	0.044684477	0.1357084	0.09537914	GEM/CDC42/ARL8B/NUMA1/A	6	0.166666666666667
GO:0032433	CC	GO:0032433	filopodium	4/1454	19/19869	0.045700649	0.1381549	0.09709864	MYO5A/CYFIP1/ABI1/MYO10	4	0.210526315789474
GO:0016459	CC	GO:0016459	myosin	8/1454	56/19869	0.049952565	0.1502589	0.10560562	MYL9/MYO5A/MYL12A/MYH9/	8	0.142857142857143
GO:0005201	MF	GO:0005201	extracellular matrix	67/1421	173/18432	1.835246492 42479e-30	1.8205645 204854e-	1.44694697 139597e-27	COL1A1/COL1A2/TNC/TGFBI /THBS2/COL14A1/COL12A1/	67	0.38728323699422
GO:0045296	MF	GO:0045296	cadherin binding	90/1421	333/18432	7.165206674 05136e-27	3.5539425 1032947e- 24	2.82459989 413919e-24	CDH11/CALD1/CAPZB/LIMA1 /FLNA/TAGLN2/PPFIBP1/RP	90	0.27027027027027
GO:0003779	MF	GO:0003779	actin binding	94/1421	439/18432	3.846816217 63527e-20	1.2720138 9596473e- 17	1.01097029 719608e-17	S26/ANK3/DNAJB1/HSPA1A/ CALD1/S100A4/MARCKS/EPB 41L2/TPM4/ANTXR1/CAPZB/ ENAH/LIMA1/WIPF1/TPM1/F	94	0.214123006833713
GO:0005178	MF	GO:0005178	integrin binding	49/1421	156/18432	3.942829267 21468e-18	9.7782165 8269241e-	7.77152400 300999e-16	TGFBI/COL5A1/COL3A1/CCN 5/THY1/ITGA11/ITGB5/GPN	49	0.314102564102564
GO:0019838	MF	GO:0019838	growth factor binding	44/1421	132/18432	1.612034294 30937e-17	3.1982760 399098e-	2.54192355 03952e-15	COL1A1/COL1A2/COL5A1/CO L3A1/LTBP2/COL6A1/IGFBP	44	0.333333333333333
GO:0005518	MF	GO:0005518	collagen	31/1421	69/18432	5.149983187	8.5146388	6.76725860	TGFBI/COL14A1/SERPINH1/	31	0.449275362318841
GO:0005539	MF	GO:0005539	glycosaminogl ycan binding	60/1421	237/18432	7.816332817 58107e-17	1.1076860 2214863e-	8.80365906 822289e-15	THBS2/COL5A1/LTBP2/CCN5 /PCOLCE/VCAN/POSTN/FSTL	60	0.253164556962025
GO:0051015	MF	GO:0051015	actin filament	56/1421	219/18432	5.240871853 98813e-16	6.4986810 9894528e-	5.16501712 978567e-14	MARCKS/TPM4/ANTXR1/CAPZ B/LIMA1/TPM1/FLNA/ACTN1	56	0.255707762557078

GO:0003735	MF	GO:0003735	structural constituent	49/1421	176/18432	9.28312763834181e-16	1.02320695747056e-	8.13223696037195e-14	RPS26/RPL22L1/RPS21/RPS15A/RPL39/RPS4Y1/MRPS24	49	0.278409090909091
GO:0008201	MF	GO:0008201	heparin binding	45/1421	171/18432	1.29268300565 8e-13	1.28234154161274e-	1.01917849603983e-11	THBS2/COL5A1/LTBP2/CCN5/PCOLCE/POSTN/FSTL1/GPN	45	0.263157894736842
GO:0030020	MF	GO:0030020	extracellular	21/1421	41/18432	2.208553160	1.9917133	1.58297255	COL1A1/COL1A2/COL14A1/C	21	0.51219512195122
GO:0023026	MF	GO:0023026	MHC class II	16/1421	27/18432	8.279803748	6.8446377	5.43997632	HSPA8/HSP90AA1/ATP1B1/H	16	0.592592592592593
GO:0048407	MF	GO:0048407	platelet-derived	10/1421	11/18432	7.371247794	5.6248290	4.47049765	COL1A1/COL1A2/COL5A1/CO	10	0.909090909090909
GO:1901681	MF	GO:1901681	sulfur compound	52/1421	270/18432	6.14647084090078e-10	4.35521362441467e-	3.46143357882703e-08	THBS2/COL5A1/LTBP2/CCN5/PCOLCE/POSTN/FSTL1/GPN	52	0.192592592592593
GO:0004857	MF	GO:0004857	enzyme inhibitor	66/1421	395/18432	1.70219310018768e-09	1.12571703692412e-	8.94696583888122e-08	COL6A3/SERPINH1/SOCS3/TIMP2/HEXIM1/SH3BP5/PPP1	66	0.167088607594937
GO:0023023	MF	GO:0023023	MHC protein	16/1421	36/18432	2.379127406	1.4750589	1.17234633	HSPA8/HSP90AA1/ATP1B1/H	16	0.444444444444444
GO:0044548	MF	GO:0044548	S100 protein	10/1421	14/18432	5.403337406	3.1530062	2.50594409	S100A1/S100B/ANXA2/S100	10	0.714285714285714
GO:0061134	MF	GO:0061134	peptidase regulator	45/1421	232/18432	6.92367441338593e-09	3.81571389893269e-	3.03265037171115e-07	COL6A3/SERPINH1/PCOLCE/TIMP2/ANOS1/TIMP4/PCSK1	45	0.193965517241379
GO:0019199	MF	GO:0019199	transmembrane	23/1421	79/18432	1.529766443	7.9869911	6.34789510	PDGFRA/LTBP1/PDGFRB/PDG	23	0.291139240506329
GO:0043394	MF	GO:0043394	proteoglycan	15/1421	36/18432	2.217663691	1.0999611	8.74226371	TNC/COL5A1/GPNMB/CTSK/C	15	0.416666666666667
GO:0050840	MF	GO:0050840	extracellular	18/1421	56/18432	1.042400299	4.8587314	3.86161912	TGFBI/ECM1/LGALS1/SMOC1	18	0.321428571428571
GO:0005200	MF	GO:0005200	structural	26/1421	107/18432	1.077541251	4.8587314	3.86161912	LMNA/TUBB/TUBA1A/ACTG1/	26	0.242990654205607
GO:0140297	MF	GO:0140297	DNA-binding transcription	70/1421	476/18432	1.16815299554066e-07	5.03829465902754e-	4.00433223642999e-06	JUN/FOXP1/FOS/TWIST1/ACTB/RBPJ/PRRX1/FLNA/ID4/	70	0.147058823529412
GO:0061629	MF	GO:0061629	RNA polymerase	56/1421	350/18432	1.32696393271 55e-07	5.48478425522407e-	4.35919291931539e-06	JUN/FOXP1/FOS/ACTB/RBPJ/PRRX1/ID4/NOTCH2/HES1/	56	0.16
GO:0004866	MF	GO:0004866	endopeptidase	34/1421	180/18432	8.914334236	3.5372078	2.81129951	COL6A3/SERPINH1/TIMP2/A	34	0.188888888888889
GO:0046332	MF	GO:0046332	SMAD binding	20/1421	78/18432	1.249790349	4.7684308	3.78985008	COL1A2/COL5A2/COL3A1/JU	20	0.256410256410256
GO:0001540	MF	GO:0001540	amyloid-beta	21/1421	85/18432	1.320549961	4.8517983	3.85610885	ITM2B/ITM2A/CRYAB/ITM2C	21	0.247058823529412
GO:0019955	MF	GO:0019955	cytokine	29/1421	144/18432	1.446156679	5.1235265	4.07207275	NBL1/LTBP1/LTBP3/COMP/L	29	0.201388888888889
GO:0003924	MF	GO:0003924	GTPase activity	51/1421	331/18432	1.52032332747054e-06	5.20055427879578e-	4.13329282132644e-05	TUBB/SEPTIN11/TUBB4B/RGS16/GEM/RASD1/TUBB2A/TU	51	0.154078549848943
GO:0004714	MF	GO:0004714	transmembrane	17/1421	60/18432	1.737091663	5.7439830	4.56519879	PDGFRA/PDGFRB/PDGFRL/EF	17	0.283333333333333
GO:0061135	MF	GO:0061135	endopeptidase	35/1421	194/18432	1.883850623	6.0283219	4.79118545	COL6A3/SERPINH1/TIMP2/A	35	0.180412371134021
GO:0030021	MF	GO:0030021	extracellular	10/1421	22/18432	1.964747663	6.0907177	4.84077631	VCAN/ASPN/OGN/LUM/PRELP	10	0.454545454545455
GO:0030414	MF	GO:0030414	peptidase	34/1421	187/18432	2.195492138	6.5997824	5.24537037	COL6A3/SERPINH1/TIMP2/A	34	0.181818181818182
GO:0019211	MF	GO:0019211	phosphatase	10/1421	23/18432	3.235828663	9.4410059	7.50351600	MAP2K6/BMP2/CALM2/PPP1R	10	0.434782608695652
GO:0019887	MF	GO:0019887	protein	37/1421	218/18432	4.337003807	0.0001229	9.76967173	SOCS3/CCNL1/HEXIM1/SH3B	37	0.169724770642202
GO:0019209	MF	GO:0019209	kinase	25/1421	121/18432	4.661885823	0.0001284	0.00010209	MAP2K6/GPRC5C/BMP2/CDKN	25	0.206611570247934

GO:0031625	MF	GO:0031625	ubiquitin protein	46/1421	299/18432	5.090068736 61107e-06	0.0001364 688699113	0.00010846 2631115838	JUN/TUBB/ACTG1/DIO2/FOX O1/HSPA1A/UBB/HSPA1B/HS	46	0.153846153846154
GO:0019207	MF	GO:0019207	kinase	40/1421	246/18432	5.353495848	0.0001397	0.00011107	SOCS3/CCNL1/HEXIM1/PIK3	40	0.16260162601626
GO:0030295	MF	GO:0030295	protein	24/1421	115/18432	5.985181842	0.0001522	0.00012099	MAP2K6/GPRC5C/BMP2/CDKN	24	0.208695652173913
GO:0097718	MF	GO:0097718	disordered	12/1421	35/18432	6.594447822	0.0001635	0.00012998	HSPA1A/FN1/CALM2/HSP90A	12	0.342857142857143
GO:0044183	MF	GO:0044183	protein	17/1421	68/18432	1.116707968	0.0002701	0.00021474	WIPF1/DNAJB1/HSPA1A/HSP	17	0.25
GO:0044389	MF	GO:0044389	ubiquitin-like protein	47/1421	318/18432	1.201006481 57968e-05	0.0002836 662927921	0.00022545 2093910571	JUN/TUBB/ACTG1/DIO2/FOX O1/HSPA1A/UBB/HSPA1B/HS	47	0.147798742138365
GO:0004867	MF	GO:0004867	serine-type	21/1421	98/18432	1.466151023	0.0003382	0.00026882	COL6A3/SERPINH1/ANOS1/P	21	0.214285714285714
GO:0030246	MF	GO:0030246	carbohydrate binding	42/1421	275/18432	1.546201948 43777e-05	0.0003485 982574659	0.00027705 8674492796	MRC2/VCAN/LGALS1/GALNT1 /P4HA2/CHI3L1/GALNT15/P	42	0.152727272727273
GO:0098631	MF	GO:0098631	cell adhesion	16/1421	64/18432	2.011746731	0.0004434	0.00035246	ITGA11/ITGA10/GLDN/ANXA	16	0.25
GO:0017124	MF	GO:0017124	SH3 domain	24/1421	125/18432	2.616562628	0.0005642	0.00044846	ENAH/WIPF1/DPYSL3/SH3BP	24	0.192
GO:0140416	MF	GO:0140416	transcription	9/1421	23/18432	2.837414317	0.0005988	0.00047597	ID4/ID3/DNAJB1/HSPA1A/D	9	0.391304347826087
GO:0042277	MF	GO:0042277	peptide binding	47/1421	330/18432	3.161492730 11859e-05	0.0006533 751642245	0.00051928 9047118163	SLC40A1/CRIP1/ITM2B/PPI C/ITM2A/CRYAB/NFKBIA/IT	47	0.142424242424242
GO:0032395	MF	GO:0032395	MHC class II	6/1421	10/18432	3.327298782	0.0006694	0.00053207	HLA-DRB1/HLA-DRA/HLA-	6	0.6
GO:0005161	MF	GO:0005161	platelet-	7/1421	14/18432	3.374276245	0.0006694	0.00053207	PDGFRA/PDGFRB/VEGFA/ITG	7	0.5
GO:0003925	MF	GO:0003925	G protein	12/1421	41/18432	4.044303297	0.0007866	0.00062521	RAB1A/RAP2B/RAC1/RAB5C/	12	0.292682926829268
GO:0051087	MF	GO:0051087	chaperone	21/1421	105/18432	4.378743505	0.0008353	0.00066390	DNAJB1/HES1/HSPA8/DNAJA	21	0.2
GO:0060090	MF	GO:0060090	molecular adaptor	63/1421	492/18432	4.642839730 32948e-05	0.0008689 994363182	0.00069066 2752336997	COL1A2/COL14A1/DAB2/SEP TIN11/FUS/RETREG1/ANK3/	63	0.128048780487805
GO:0005080	MF	GO:0005080	protein	14/1421	55/18432	5.289798271	0.0009717	0.00077233	MARCKS/FLNA/TRPV4/SQSTM	14	0.254545454545455
GO:0002020	MF	GO:0002020	protease	25/1421	139/18432	5.616220505	0.0010129	0.00080508	COL1A1/COL1A2/COL3A1/EC	25	0.179856115107914
GO:0140375	MF	GO:0140375	immune	26/1421	148/18432	6.083778753	0.0010533	0.00083718	OSMR/CD44/IFNGR2/HLA-	26	0.175675675675676
GO:0008009	MF	GO:0008009	chemokine	13/1421	49/18432	6.101221505	0.0010533	0.00083718	CCL20/CCL3/CCL3L1/CXCL1	13	0.26530612244898
GO:0050431	MF	GO:0050431	transforming	9/1421	25/18432	6.158707257	0.0010533	0.00083718	LTBP1/LTBP3/LTBP4/TGFBR	9	0.36
GO:0005126	MF	GO:0005126	cytokine	40/1421	273/18432	6.348167580	0.0010673	0.00084830	ECM1/OSMR/PIK3R1/CFLAR/	40	0.146520146520147
GO:0034713	MF	GO:0034713	type I	6/1421	11/18432	6.841022962	0.0011310	0.00089893	TGFB1/SNX6/FKBP1A/SMAD7	6	0.545454545454545
GO:0001968	MF	GO:0001968	fibronectin	10/1421	31/18432	7.085896960	0.0011523	0.00091584	MMP2/CTSK/IGFBP6/SDC4/C	10	0.32258064516129
GO:0042605	MF	GO:0042605	peptide	11/1421	37/18432	7.207343020	0.0011531	0.00091651	HLA-DRB1/HLA-DRA/HLA-	11	0.297297297297297
GO:0072542	MF	GO:0072542	protein	7/1421	16/18432	9.799817708	0.0015430	0.00122640	CALM2/PPP1R15A/CALM3/PP	7	0.4375
GO:0016504	MF	GO:0016504	peptidase	12/1421	45/18432	0.000110351	0.0016969	0.00134872	PCOLCE/PCOLCE2/FN1/CAV1	12	0.266666666666667
GO:0044325	MF	GO:0044325	transmembrane	23/1421	128/18432	0.000111193	0.0016969	0.00134872	FLNA/ACTN1/FHL1/ANK3/FX	23	0.1796875
GO:0033218	MF	GO:0033218	amide binding	53/1421	408/18432	0.000125263 705931023	0.0018827 514588420	0.00149637 186191924	SLC40A1/CRIP1/ITM2B/PPI C/ITM2A/CRYAB/NFKBIA/IT	53	0.129901960784314

GO:0005525	MF	GO:0005525	GTP binding	50/1421	379/18432	0.000131437731004703	0.0019460631217412	0.00154669066021245	TUBB/SEPTIN11/TUBA1A/TUBB4B/GEM/RASD1/TUBB2A/T	50	0.131926121372032
GO:0009055	MF	GO:0009055	electron	22/1421	122/18432	0.000147225	0.0021477	0.00170699	P4HA2/NDUFA4/NDUFB1/UQC	22	0.180327868852459
GO:0043539	MF	GO:0043539	protein	13/1421	54/18432	0.000179259	0.0025771	0.00204829	MAP2K6/BMP2/CKS2/CALM2/	13	0.240740740740741
GO:0051082	MF	GO:0051082	unfolded	22/1421	124/18432	0.000187900	0.0026628	0.00211635	SERPINH1/TUBB4B/DNAJB1/	22	0.17741935483871
GO:0017134	MF	GO:0017134	fibroblast	8/1421	23/18432	0.000209807	0.0029313	0.00232981	S100A13/FGFRL1/FGFR1/FG	8	0.347826086956522
GO:0015026	MF	GO:0015026	coreceptor	12/1421	48/18432	0.000215399	0.0029677	0.00235868	GPC6/CSPG4/TGFBR3/CD4/C	12	0.25
GO:0005024	MF	GO:0005024	transforming	6/1421	13/18432	0.000221997	0.0029759	0.00236523	LTBP1/LTBP4/TGFBR3/ENG/	6	0.461538461538462
GO:0035259	MF	GO:0035259	nuclear	6/1421	13/18432	0.000221997	0.0029759	0.00236523	NR4A1/CEBPB/YWHAH/NR4A2	6	0.461538461538462
GO:0016209	MF	GO:0016209	antioxidant	17/1421	85/18432	0.000227148	0.0030044	0.00238784	GPX8/PRDX4/GPX3/SOD2/TX	17	0.2
GO:0140678	MF	GO:0140678	molecular	18/1421	93/18432	0.000231620	0.0030232	0.00240281	TIMP2/ID4/ID3/DNAJB1/HS	18	0.193548387096774
GO:0098641	MF	GO:0098641	cadherin	7/1421	18/18432	0.000237605	0.0030611	0.00243290	ANXA2/ANXA1/S100A11/RAB	7	0.388888888888889
GO:0042379	MF	GO:0042379	chemokine	15/1421	71/18432	0.000279543	0.0035552	0.00282561	CCL20/CCL3/CCL3L1/CXCL1	15	0.211267605633803
GO:0004713	MF	GO:0004713	protein	23/1421	138/18432	0.000350780	0.0044047	0.00350079	PDGFRA/PDGFRB/PDGFRL/EF	23	0.166666666666667
GO:0140313	MF	GO:0140313	molecular	6/1421	14/18432	0.000363188	0.0045035	0.00357931	C1R/PRDX4/CDKN1A/LAPTM5	6	0.428571428571429
GO:0019003	MF	GO:0019003	GDP binding	15/1421	73/18432	0.000384210	0.0047053	0.00373975	GEM/RAN/RHEB/RAP2B/RAB3	15	0.205479452054795
GO:0048306	MF	GO:0048306	calcium-	16/1421	81/18432	0.000398157	0.0048167	0.00382824	S100A4/S100A1/S100A13/T	16	0.197530864197531
GO:0140677	MF	GO:0140677	molecular	13/1421	59/18432	0.000456272	0.0054532	0.00433415	HTRA1/DNAJB1/DNAJA1/DNA	13	0.220338983050847
GO:0042608	MF	GO:0042608	T cell	5/1421	10/18432	0.000490404	0.0057766	0.00459118	HLA-DRB1/HLA-	5	0.5
GO:0031072	MF	GO:0031072	heat shock	21/1421	124/18432	0.000499529	0.0057766	0.00459118	DNAJB1/HSPA1A/HSPA1B/ZF	21	0.169354838709677
GO:0019001	MF	GO:0019001	guanyl nucleotide	50/1421	401/18432	0.000506624143581629	0.0057766798900342	0.0045911855238069	TUBB/SEPTIN11/TUBA1A/TUBB4B/GEM/RASD1/TUBB2A/T	50	0.124688279301746
GO:0032561	MF	GO:0032561	guanyl ribonucleotid	50/1421	401/18432	0.000506624143581629	0.0057766798900342	0.0045911855238069	TUBB/SEPTIN11/TUBA1A/TUBB4B/GEM/RASD1/TUBB2A/T	50	0.124688279301746
GO:0005543	MF	GO:0005543	phospholipid binding	57/1421	474/18432	0.000535013990421176	0.0060310668011114	0.00479336697159642	THY1/EEA1/PLA2G2A/HSPA8/SERPINA5/SCIN/GSN/SDCB	57	0.120253164556962
GO:0008083	MF	GO:0008083	growth factor	25/1421	162/18432	0.000656660	0.0073191	0.00581713	OGN/EFEMP1/CCN6/MIA/CLE	25	0.154320987654321
GO:0098632	MF	GO:0098632	cell-cell	12/1421	54/18432	0.000689408	0.0075931	0.00603486	GLDN/ANXA2/ANXA1/S100A1	12	0.222222222222222
GO:0005546	MF	GO:0005546	phosphatidyli	16/1421	85/18432	0.000696548	0.0075931	0.00603486	SCIN/GSN/SDCBP/ANXA2/PL	16	0.188235294117647
GO:0019864	MF	GO:0019864	IgG binding	5/1421	11/18432	0.000842066	0.0089355	0.00710176	FCER1G/FCGR2A/FCGR3A/FC	5	0.454545454545455
GO:0005523	MF	GO:0005523	tropomyosin	6/1421	16/18432	0.000846713	0.0089355	0.00710176	CALD1/TNNT3/NEBL/S100A6	6	0.375
GO:0016722	MF	GO:0016722	oxidoreductas	6/1421	16/18432	0.000846713	0.0089355	0.00710176	CP/STEAP4/STEAP2/STEAP3	6	0.375
GO:0140662	MF	GO:0140662	ATP-dependent	10/1421	41/18432	0.000881425	0.0092039	0.00731509	HSPA1A/HSPA1B/HSPA8/HSP	10	0.24390243902439
GO:0070851	MF	GO:0070851	growth factor	22/1421	140/18432	0.001054418	0.0108956	0.00865964	PDGFRA/PDGFRB/ECM1/EFEM	22	0.157142857142857
GO:0019208	MF	GO:0019208	phosphatase	19/1421	114/18432	0.001104469	0.0112951	0.00897718	ZEB2/PPP1R14B/RCAN1/MAP	19	0.166666666666667
GO:0047485	MF	GO:0047485	protein N-	18/1421	106/18432	0.001182865	0.0119734	0.00951628	RBPJ/TBL1XR1/HSPA1A/RPS	18	0.169811320754717

GO:0046875	MF	GO:0046875	ephrin	8/1421	29/18432	0.001211278	0.0121372	0.00964643	AQP1/SDCBP/SIPA1L1/LYN/	8	0.275862068965517
GO:0030169	MF	GO:0030169	low-density	6/1421	17/18432	0.001223724	0.0121393	0.00964809	MSR1/STAB1/TREM2/PLTP/C	6	0.352941176470588
GO:0030674	MF	GO:0030674	protein-macromolecule	43/1421	347/18432	0.001364658 44636576	0.0133235 48651343	0.01058928 04964515	COL1A2/COL14A1/DAB2/FUS /RETREG1/ANK3/COL11A2/H	43	0.123919308357349
GO:0038024	MF	GO:0038024	cargo	15/1421	82/18432	0.001369961	0.0133235	0.01058928	DAB2/PRG4/SCARA3/LRP10/	15	0.182926829268293
GO:1901981	MF	GO:1901981	phosphatidyli	26/1421	180/18432	0.001407252	0.0135533	0.01077191	SCIN/GSN/SDCBP/PHLDA1/P	26	0.144444444444444
GO:0071813	MF	GO:0071813	lipoprotein	8/1421	30/18432	0.001541464	0.0145631	0.01157450	HSPD1/MSR1/STAB1/APOE/T	8	0.266666666666667
GO:0071814	MF	GO:0071814	protein-lipid	8/1421	30/18432	0.001541464	0.0145631	0.01157450	HSPD1/MSR1/STAB1/APOE/T	8	0.266666666666667
GO:0016765	MF	GO:0016765	transferase	12/1421	59/18432	0.001573607	0.0147265	0.01170439	DTWD1/SRM/GSTO1/RABGGTB	12	0.203389830508475
GO:0001664	MF	GO:0001664	G protein-	37/1421	289/18432	0.001605673	0.0148862	0.01183128	FLNA/HSPA1A/HSPA1B/CTHR	37	0.1280276816609
GO:0001221	MF	GO:0001221	transcription	18/1421	109/18432	0.001641380	0.0149380	0.01187246	FOS/TWIST1/SIX1/HES1/ZB	18	0.165137614678899
GO:1902936	MF	GO:1902936	phosphatidyli	18/1421	109/18432	0.001641380	0.0149380	0.01187246	SCIN/GSN/SDCBP/ANXA2/PL	18	0.165137614678899
GO:0005160	MF	GO:0005160	transforming	7/1421	24/18432	0.001714705	0.0153186	0.01217494	TGFB1/TGFBR3/SNX6/FKBP1	7	0.291666666666667
GO:0005540	MF	GO:0005540	hyaluronic	7/1421	24/18432	0.001714705	0.0153186	0.01217494	VCAN/HAPLN1/ACAN/CD44/T	7	0.291666666666667
GO:0030546	MF	GO:0030546	signaling receptor	57/1421	498/18432	0.001729524 71339299	0.0153186 474614808	0.01217494 37061217	NBL1/SEMA3C/GPNMB/FBN1/ OGN/EFEMP1/CCN6/MIA/CLE	57	0.114457831325301
GO:1990782	MF	GO:1990782	protein	19/1421	119/18432	0.001857030	0.0163024	0.01295682	PLCG2/PIK3R1/SQSTM1/HSP	19	0.159663865546218
GO:0004675	MF	GO:0004675	transmembrane	6/1421	19/18432	0.002347019	0.0204231	0.01623192	LTBP1/LTBP4/TGFBR3/ENG/	6	0.315789473684211
GO:0004860	MF	GO:0004860	protein	13/1421	70/18432	0.002426907	0.0209347	0.01663847	SOCS3/HEXIM1/SH3BP5/CDK	13	0.185714285714286
GO:0035091	MF	GO:0035091	phosphatidyli	35/1421	277/18432	0.002634442	0.0225290	0.01790559	THY1/EEA1/SCIN/GSN/SDCB	35	0.126353790613718
GO:0001848	MF	GO:0001848	complement	7/1421	26/18432	0.002844683	0.0241190	0.01916930	CFH/CFB/CD59/ITGB2/VSIG	7	0.269230769230769
GO:0005172	MF	GO:0005172	vascular	5/1421	14/18432	0.003000457	0.0252241	0.02004766	VEGFA/ITGA5/CCDC88A/PGF	5	0.357142857142857
GO:0048018	MF	GO:0048018	receptor ligand	55/1421	491/18432	0.003285085 96840538	0.0273849 183248583	0.02176496 58587849	NBL1/SEMA3C/GPNMB/FBN1/ OGN/EFEMP1/CCN6/MIA/CLE	55	0.112016293279022
GO:0019210	MF	GO:0019210	kinase	13/1421	74/18432	0.004019478	0.0332276	0.02640867	SOCS3/HEXIM1/SH3BP5/CDK	13	0.175675675675676
GO:0048185	MF	GO:0048185	activin	5/1421	15/18432	0.004217714	0.0345782	0.02748210	TGFBR3/FKBP1A/SMAD7/ENG	5	0.333333333333333
GO:0019902	MF	GO:0019902	phosphatase	26/1421	195/18432	0.004322837	0.0351496	0.02793619	FOXO1/CARHSP1/PIK3R1/MA	26	0.133333333333333
GO:0043236	MF	GO:0043236	laminin	7/1421	28/18432	0.004471321	0.0357705	0.02842970	ECM1/LGALS1/CTSS/ADAM9/	7	0.25
GO:0043495	MF	GO:0043495	protein-	7/1421	28/18432	0.004471321	0.0357705	0.02842970	RETREG1/SLC9A3R2/EPB41L	7	0.25
GO:0005522	MF	GO:0005522	profilin	4/1421	10/18432	0.005062257	0.0389283	0.03093946	ENAH/WIPF1/ACTG1/VASP	4	0.4
GO:0016175	MF	GO:0016175	superoxide-	4/1421	10/18432	0.005062257	0.0389283	0.03093946	CYBB/NCF1/NCF2/CYBA	4	0.4
GO:0030957	MF	GO:0030957	Tat protein	4/1421	10/18432	0.005062257	0.0389283	0.03093946	ACTB/DNAJA1/GABARAPL1/M	4	0.4
GO:0050786	MF	GO:0050786	RAGE receptor	4/1421	10/18432	0.005062257	0.0389283	0.03093946	S100A4/S100A13/S100B/HM	4	0.4
GO:0070008	MF	GO:0070008	serine-type	4/1421	10/18432	0.005062257	0.0389283	0.03093946	CPVL/TPP1/CTSA/PRCP	4	0.4
GO:0042056	MF	GO:0042056	chemoattracta	8/1421	36/18432	0.005274056	0.0400286	0.03181395	GPNMB/FGF2/VEGFA/CCL3/P	8	0.222222222222222
GO:0004602	MF	GO:0004602	glutathione	6/1421	22/18432	0.005286044	0.0400286	0.03181395	GPX8/GPX3/PTGES/ALOX5AP	6	0.272727272727273

GO:0051787	MF	GO:0051787	misfolded	7/1421	29/18432	0.005508607	0.0410867	0.03265490	HSPA1A/HSPA1B/HSPA8/DNA	7	0.241379310344828
GO:0051861	MF	GO:0051861	glycolipid	7/1421	29/18432	0.005508607	0.0410867	0.03265490	THY1/MANF/LYN/TREM2/TPP	7	0.241379310344828
GO:0001222	MF	GO:0001222	transcription	9/1421	44/18432	0.005656264	0.0413332	0.03285080	HES1/ZBTB16/NR1D1/ETS1/	9	0.204545454545455
GO:0001618	MF	GO:0001618	virus	13/1421	77/18432	0.005696983	0.0413332	0.03285080	ITGB5/HSPA1A/HSPA1B/CD5	13	0.168831168831169
GO:0005521	MF	GO:0005521	lamin binding	5/1421	16/18432	0.005749987	0.0413332	0.03285080	SUN2/SYNE1/PPP1CC/IFI27	5	0.3125
GO:0008191	MF	GO:0008191	metalloendope	5/1421	16/18432	0.005749987	0.0413332	0.03285080	TIMP2/TIMP4/SPOCK1/BST2	5	0.3125
GO:0031435	MF	GO:0031435	mitogen-	5/1421	16/18432	0.005749987	0.0413332	0.03285080	DIXDC1/DAZAP2/MAP3K11/S	5	0.3125
GO:0005516	MF	GO:0005516	calmodulin	26/1421	200/18432	0.006038982	0.0430983	0.03425367	CALD1/MARCKS/AEBP1/EEA1	26	0.13
GO:0051020	MF	GO:0051020	GTPase	36/1421	303/18432	0.006321570	0.0447888	0.03559723	RIN2/FLNA/FARP1/NDRG1/R	36	0.118811881188119
GO:0140272	MF	GO:0140272	exogenous	13/1421	78/18432	0.006366153	0.0447888	0.03559723	ITGB5/HSPA1A/HSPA1B/CD5	13	0.166666666666667
GO:0035035	MF	GO:0035035	histone	6/1421	23/18432	0.006692811	0.0467554	0.03716023	EGR1/GLI3/CEBPB/CITED2/	6	0.260869565217391
GO:0001851	MF	GO:0001851	complement	4/1421	11/18432	0.007473795	0.0518461	0.04120627	CFH/ITGB2/VSIG4/ITGAM	4	0.363636363636364
GO:0005001	MF	GO:0005001	transmembrane	5/1421	17/18432	0.007635930	0.0521084	0.04141469	PTPRD/PTPRC/PTPRE/PTPRB	5	0.294117647058824
GO:0019198	MF	GO:0019198	transmembrane	5/1421	17/18432	0.007635930	0.0521084	0.04141469	PTPRD/PTPRC/PTPRE/PTPRB	5	0.294117647058824
GO:0015453	MF	GO:0015453	oxidoreductio	12/1421	71/18432	0.007669183	0.0521084	0.04141469	NDUFA4/NDUFB1/COX7A1/ND	12	0.169014084507042
GO:0019865	MF	GO:0019865	immunoglobuli	6/1421	24/18432	0.008352179	0.0559821	0.04449347	FCER1G/FCGR2A/FCGR3A/FC	6	0.25
GO:0042974	MF	GO:0042974	nuclear	6/1421	24/18432	0.008352179	0.0559821	0.04449347	HMGA1/NR4A2/NRIP1/ACTN4	6	0.25
GO:0004601	MF	GO:0004601	peroxidase	10/1421	55/18432	0.008610527	0.0573264	0.04556188	GPX8/PRDX4/GPX3/PRDX1/P	10	0.181818181818182
GO:0048020	MF	GO:0048020	CCR chemokine	9/1421	47/18432	0.008834911	0.0584282	0.04643753	CCL20/CCL3/CCL3L1/CCL2/	9	0.191489361702128
GO:0005125	MF	GO:0005125	cytokine	29/1421	237/18432	0.009009529	0.0591884	0.04704173	GDF10/SPP1/NAMPT/BMP2/F	29	0.122362869198312
GO:0050699	MF	GO:0050699	WW domain	7/1421	32/18432	0.009704163	0.0633324	0.05033530	ENAH/TCEAL6/TCEAL2/TCEA	7	0.21875
GO:0005547	MF	GO:0005547	phosphatidyli	8/1421	40/18432	0.010196659	0.0661116	0.05254419	FUNDC2/ADAP2/IQGAP2/IQG	8	0.2
GO:0008179	MF	GO:0008179	adenylate	4/1421	12/18432	0.010534593	0.0674213	0.05358513	CALM2/CAP1/CALM3/CALM1	4	0.333333333333333
GO:0017154	MF	GO:0017154	semaphorin	4/1421	12/18432	0.010534593	0.0674213	0.05358513	NRP2/NRP1/PLXND1/PLXNB2	4	0.333333333333333
GO:0017022	MF	GO:0017022	myosin	12/1421	74/18432	0.010633994	0.0676212	0.05374400	CALD1/MYL9/GSN/LARP6/PY	12	0.162162162162162
GO:0016684	MF	GO:0016684	oxidoreductas	10/1421	57/18432	0.011060233	0.0698837	0.05554217	GPX8/PRDX4/GPX3/PRDX1/P	10	0.175438596491228
GO:0070888	MF	GO:0070888	E-box binding	9/1421	49/18432	0.011604241	0.0728570	0.05790524	TCF4/TWIST1/ZEB1/HES1/S	9	0.183673469387755
GO:0001965	MF	GO:0001965	G-protein	6/1421	26/18432	0.012519829	0.0776229	0.06169310	LPAR1/RGS1/RGS10/CCDC88	6	0.230769230769231
GO:0070696	MF	GO:0070696	transmembrane	6/1421	26/18432	0.012519829	0.0776229	0.06169310	MAGI2/BMP2/INHBA/BMP6/P	6	0.230769230769231
GO:0005520	MF	GO:0005520	insulin-like	5/1421	19/18432	0.012614492	0.0777240	0.06177348	IGFBP4/IGFBP7/IGFBP6/IG	5	0.263157894736842
GO:0019843	MF	GO:0019843	rRNA binding	11/1421	67/18432	0.012915188	0.0790856	0.06285559	CAVIN1/RPS4Y1/MRPS6/RPS	11	0.164179104477612
GO:0042287	MF	GO:0042287	MHC protein	8/1421	42/18432	0.013656982	0.0831148	0.06605799	TUBB/LAG3/TUBB4B/COL2A1	8	0.19047619047619
GO:0031994	MF	GO:0031994	insulin-like	4/1421	13/18432	0.014301712	0.0859836	0.06833800	IGFBP4/IGFBP6/IGFBP5/IT	4	0.307692307692308
GO:0050998	MF	GO:0050998	nitric-oxide	4/1421	13/18432	0.014301712	0.0859836	0.06833800	ACTB/CAV1/CD74/CALM3	4	0.307692307692308
GO:0001671	MF	GO:0001671	ATPase	6/1421	27/18432	0.015071643	0.0889944	0.07073095	DNAJB1/DNAJA1/DNAJB4/AT	6	0.222222222222222
GO:0008198	MF	GO:0008198	ferrous iron	6/1421	27/18432	0.015071643	0.0889944	0.07073095	CDO1/TF/FTL/FTH1/EGLN3/	6	0.222222222222222

GO:0038187	MF	GO:0038187	pattern	6/1421	27/18432	0.015071643	0.0889944	0.07073095	CD14/CLEC7A/MARCO/TLR4/	6	0.222222222222222
GO:0008013	MF	GO:0008013	beta-catenin	13/1421	87/18432	0.015593845	0.0914761	0.07270333	GJA1/TCF4/TBL1XR1/GLI3/	13	0.149425287356322
GO:0048156	MF	GO:0048156	tau protein	8/1421	43/18432	0.015676352	0.0914761	0.07270333	ACTB/S100B/HSP90AA1/APO	8	0.186046511627907
GO:0016505	MF	GO:0016505	peptidase	5/1421	20/18432	0.015773786	0.0915064	0.07272739	RPS27L/EBAG9/PYCARD/CTS	5	0.25
GO:0001786	MF	GO:0001786	phosphatidyls	10/1421	61/18432	0.017497855	0.1009178	0.08020742	HSPA8/SCIN/ANXA2/TREM2/	10	0.163934426229508
GO:0015036	MF	GO:0015036	disulfide	8/1421	44/18432	0.017903038	0.1026578	0.08159036	QSOX1/GLRX/TXN/GLRX2/GS	8	0.181818181818182
GO:0032036	MF	GO:0032036	myosin heavy	4/1421	14/18432	0.018822214	0.1073082	0.08528637	MYL9/MYL12A/PDLIM2/MYL1	4	0.285714285714286
GO:0001846	MF	GO:0001846	opsonin	5/1421	21/18432	0.019419191	0.1094536	0.08699147	CFH/ITGB2/VSIG4/ITGAM/C	5	0.238095238095238
GO:0036122	MF	GO:0036122	BMP binding	5/1421	21/18432	0.019419191	0.1094536	0.08699147	NBL1/COMP/CHRDL2/ENG/BM	5	0.238095238095238
GO:0019903	MF	GO:0019903	protein	19/1421	149/18432	0.020633493	0.1152923	0.09163199	FOXO1/PIK3R1/PPP1R15A/P	19	0.12751677852349
GO:0016922	MF	GO:0016922	nuclear	18/1421	139/18432	0.020687542	0.1152923	0.09163199	FOXP1/NR4A1/HMGA1/JUND/	18	0.129496402877698
GO:0003785	MF	GO:0003785	actin monomer	6/1421	29/18432	0.021211519	0.1163810	0.09249724	LIMA1/TMSB4X/MTSS1/TMSB	6	0.206896551724138
GO:0001530	MF	GO:0001530	lipopolysacch	7/1421	37/18432	0.021234847	0.1163810	0.09249724	PSMB4/HSPD1/CD14/TREM2/	7	0.189189189189189
GO:0035198	MF	GO:0035198	miRNA binding	7/1421	37/18432	0.021234847	0.1163810	0.09249724	SOCS3/SOX4/KCNQ1OT1/NEA	7	0.189189189189189
GO:0055106	MF	GO:0055106	ubiquitin-	5/1421	22/18432	0.023575999	0.1266660	0.10067153	RPS20/RPS15/RPS7/RPL11/	5	0.227272727272727
GO:0005545	MF	GO:0005545	1-	4/1421	15/18432	0.024132941	0.1266660	0.10067153	EEA1/SCIN/SNX10/PICALM	4	0.266666666666667
GO:0015929	MF	GO:0015929	hexosaminidas	4/1421	15/18432	0.024132941	0.1266660	0.10067153	HEXB/OGA/HYAL2/CEMIP2	4	0.266666666666667
GO:0022858	MF	GO:0022858	alanine	4/1421	15/18432	0.024132941	0.1266660	0.10067153	SLC3A2/SLC6A6/SLC38A2/S	4	0.266666666666667
GO:0031005	MF	GO:0031005	filamin	4/1421	15/18432	0.024132941	0.1266660	0.10067153	DPYSL3/NEBL/RFLNB/PDLIM	4	0.266666666666667
GO:0046965	MF	GO:0046965	nuclear	4/1421	15/18432	0.024132941	0.1266660	0.10067153	HMGA1/NR4A2/NRIP1/TACC1	4	0.266666666666667
GO:0051371	MF	GO:0051371	muscle alpha-	4/1421	15/18432	0.024132941	0.1266660	0.10067153	PDLIM4/PDLIM2/PALLD/PDL	4	0.266666666666667
GO:0070700	MF	GO:0070700	BMP receptor	4/1421	15/18432	0.024132941	0.1266660	0.10067153	BMP2/BMP6/PYCARD/CDH5	4	0.266666666666667
GO:0008157	MF	GO:0008157	protein	6/1421	30/18432	0.024835399	0.1296669	0.10305658	PPP1R15A/PPP1R3C/PPP1R1	6	0.2
GO:0005044	MF	GO:0005044	scavenger	8/1421	47/18432	0.025929551	0.1346707	0.10703353	PRG4/SCARA3/MSR1/STAB1/	8	0.170212765957447
GO:0004869	MF	GO:0004869	cysteine-type	9/1421	56/18432	0.026476564	0.1367955	0.10872229	SPOCK1/PTTG1/BIRC2/NOL3	9	0.160714285714286
GO:0015035	MF	GO:0015035	protein-	7/1421	39/18432	0.027767912	0.1427241	0.11343423	QSOX1/GLRX/TXN/GLRX2/PG	7	0.179487179487179
GO:0072341	MF	GO:0072341	modified	13/1421	94/18432	0.028013099	0.1432422	0.11384596	HSPA8/SCIN/ANXA2/PTGES/	13	0.138297872340426
GO:0033612	MF	GO:0033612	receptor	6/1421	31/18432	0.028849670	0.1459552	0.11600218	MAGI2/BMP2/INHBA/BMP6/P	6	0.193548387096774
GO:0071889	MF	GO:0071889	14-3-3	6/1421	31/18432	0.028849670	0.1459552	0.11600218	ZFP36L1/ZFP36/DDIT4/ARR	6	0.193548387096774
GO:0097110	MF	GO:0097110	scaffold	10/1421	66/18432	0.028985059	0.1459552	0.11600218	PLCG2/HSP90AA1/CD163/LY	10	0.151515151515152
GO:0005092	MF	GO:0005092	GDP-	4/1421	16/18432	0.030260593	0.1500925	0.11929044	EIF5/ARHGDIB/CCDC88A/GD	4	0.25
GO:0010851	MF	GO:0010851	cyclase	4/1421	16/18432	0.030260593	0.1500925	0.11929044	CALM2/CALM3/RGS2/CALM1	4	0.25
GO:0050664	MF	GO:0050664	oxidoreductas	4/1421	16/18432	0.030260593	0.1500925	0.11929044	CYBB/NCF1/NCF2/CYBA	4	0.25
GO:0003725	MF	GO:0003725	double-	11/1421	76/18432	0.030741702	0.1517202	0.12058410	ACTN1/TUBB4B/SLC3A2/MRP	11	0.144736842105263
GO:0045309	MF	GO:0045309	protein	9/1421	58/18432	0.032471231	0.1593789	0.12667105	SOCS3/PIK3R3/PLCG2/PIK3	9	0.155172413793103
GO:0019888	MF	GO:0019888	protein	13/1421	96/18432	0.032614836	0.1593789	0.12667105	PPP1R14B/RCAN1/PTN/CALM	13	0.135416666666667

GO:0030971	MF	GO:0030971	receptor	11/1421	77/18432	0.033462946	0.1613502	0.12823780	PIK3R1/SQSTM1/TOB1/DOK2	11	0.142857142857143
GO:0050750	MF	GO:0050750	low-density	5/1421	24/18432	0.033506193	0.1613502	0.12823780	DAB2/DNAJA1/APOE/PICALM	5	0.208333333333333
GO:0070412	MF	GO:0070412	R-SMAD	5/1421	24/18432	0.033506193	0.1613502	0.12823780	JUN/FOS/RGCC/PMEPA1/DDX	5	0.208333333333333
GO:0016651	MF	GO:0016651	oxidoreductas	12/1421	87/18432	0.034519140	0.1654250	0.13147641	NDUFA4/NDUFB1/NDUFA6/DC	12	0.137931034482759
GO:0008137	MF	GO:0008137	NADH	7/1421	41/18432	0.035543008	0.1679102	0.13345160	NDUFA4/NDUFB1/NDUFA6/ND	7	0.170731707317073
GO:0016667	MF	GO:0016667	oxidoreductas	9/1421	59/18432	0.035795282	0.1679102	0.13345160	QSOX1/GLRX/TXN/GLRX2/GS	9	0.152542372881356
GO:0005114	MF	GO:0005114	type II	3/1421	10/18432	0.036391841	0.1679102	0.13345160	TGFB1/TGFBR3/ENG	3	0.3
GO:0005381	MF	GO:0005381	iron ion	3/1421	10/18432	0.036391841	0.1679102	0.13345160	SLC40A1/SLC39A14/SLC25A	3	0.3
GO:0008239	MF	GO:0008239	dipeptidyl-	3/1421	10/18432	0.036391841	0.1679102	0.13345160	FAP/CTSC/PRCP	3	0.3
GO:0008330	MF	GO:0008330	protein	3/1421	10/18432	0.036391841	0.1679102	0.13345160	DUSP6/DUSP1/DUSP2	3	0.3
GO:0016176	MF	GO:0016176	superoxide-	3/1421	10/18432	0.036391841	0.1679102	0.13345160	NCF1/NCF2/PDGFB	3	0.3
GO:0019869	MF	GO:0019869	chloride	3/1421	10/18432	0.036391841	0.1679102	0.13345160	VAMP8/STX7/WNK1	3	0.3
GO:0017081	MF	GO:0017081	chloride	4/1421	17/18432	0.037222027	0.1701578	0.13523792	VAMP8/SGK1/STX7/WNK1	4	0.235294117647059
GO:0046933	MF	GO:0046933	proton-	4/1421	17/18432	0.037222027	0.1701578	0.13523792	ATP5ME/ATP6V0C/ATP5F1E/	4	0.235294117647059
GO:0004725	MF	GO:0004725	protein	13/1421	98/18432	0.037737522	0.1717230	0.13648191	PTPRD/PTPN12/PTPRC/DUSP	13	0.13265306122449
GO:0005154	MF	GO:0005154	epidermal	6/1421	33/18432	0.038101553	0.1718033	0.13654575	EFEMP1/ARF4/ITGA5/SNX2/	6	0.181818181818182
GO:0030291	MF	GO:0030291	protein	6/1421	33/18432	0.038101553	0.1718033	0.13654575	HEXIM1/CDKN1A/SPRY2/HSP	6	0.181818181818182
GO:0008022	MF	GO:0008022	protein C-	21/1421	181/18432	0.039224547	0.1756598	0.13961077	TCF4/DAB2/ECM1/ZBTB16/F	21	0.116022099447514
GO:0030247	MF	GO:0030247	polysaccharid	5/1421	25/18432	0.039310965	0.1756598	0.13961077	PRG4/PPP1R3C/HLA-	5	0.2
GO:0008307	MF	GO:0008307	structural	7/1421	42/18432	0.039920213	0.1767895	0.14050864	TPM4/MYL9/TPM1/NEBL/PLE	7	0.166666666666667
GO:0050136	MF	GO:0050136	NADH	7/1421	42/18432	0.039920213	0.1767895	0.14050864	NDUFA4/NDUFB1/NDUFA6/ND	7	0.166666666666667
GO:0003743	MF	GO:0003743	translation	8/1421	51/18432	0.040113686	0.1768567	0.14056211	EIF1/EIF1B/EIF2S2/EIF4E	8	0.156862745098039
GO:0008376	MF	GO:0008376	acetylgalacto	6/1421	34/18432	0.043360277	0.1903247	0.15126617	GALNT1/GALNT15/CSGALNAC	6	0.176470588235294
GO:0035615	MF	GO:0035615	clathrin	4/1421	18/18432	0.045024742	0.1950416	0.15501508	DAB2/AP1S2/AP2A2/AP2S1	4	0.222222222222222
GO:0043395	MF	GO:0043395	heparan	4/1421	18/18432	0.045024742	0.1950416	0.15501508	COMP/CFH/PTPRC/APOE	4	0.222222222222222
GO:0045236	MF	GO:0045236	CXCR	4/1421	18/18432	0.045024742	0.1950416	0.15501508	CXCL8/CXCL2/CXCL3/CXCL1	4	0.222222222222222
GO:0004364	MF	GO:0004364	glutathione	5/1421	26/18432	0.045689807	0.1952425	0.15517476	GSTO1/PTGES/ALOX5AP/LTC	5	0.192307692307692
GO:0030507	MF	GO:0030507	spectrin	5/1421	26/18432	0.045689807	0.1952425	0.15517476	EPB41L2/ANK3/DYNC1I1/PT	5	0.192307692307692
GO:0048027	MF	GO:0048027	mRNA 5'-UTR	5/1421	26/18432	0.045689807	0.1952425	0.15517476	LARP6/RPL41/DDX3X/RPS7/	5	0.192307692307692
GO:0031267	MF	GO:0031267	small GTPase	29/1421	272/18432	0.047180449	0.1952425	0.15517476	RIN2/FLNA/FARP1/NDRG1/R	29	0.106617647058824
GO:0008199	MF	GO:0008199	ferric iron	3/1421	11/18432	0.047236108	0.1952425	0.15517476	TF/FTL/FTH1	3	0.272727272727273
GO:0019855	MF	GO:0019855	calcium	3/1421	11/18432	0.047236108	0.1952425	0.15517476	CALM2/SLC30A1/CALM1	3	0.272727272727273
GO:0031996	MF	GO:0031996	thioesterase	3/1421	11/18432	0.047236108	0.1952425	0.15517476	RAC1/CDC42/ARF6	3	0.272727272727273
GO:0035256	MF	GO:0035256	G protein-	3/1421	11/18432	0.047236108	0.1952425	0.15517476	SLC9A3R2/CALM3/FYN	3	0.272727272727273
GO:0047134	MF	GO:0047134	protein-	3/1421	11/18432	0.047236108	0.1952425	0.15517476	TXN/PGK1/SELENOT	3	0.272727272727273
GO:0097371	MF	GO:0097371	MDM2/MDM4	3/1421	11/18432	0.047236108	0.1952425	0.15517476	RPS20/RPS15/RPL37	3	0.272727272727273

GO:0097493	MF	GO:0097493 structural	3/1421	11/18432	0.047236108	0.1952425	0.15517476	FBN1/EMILIN2/AHNAK	3	0.272727272727273
GO:0140296	MF	GO:0140296 general	8/1421	53/18432	0.048833798	0.2010088	0.15975765	JUN/TCF4/GTF2B/ATF4/AHR	8	0.150943396226415
GO:0003954	MF	GO:0003954 NADH	7/1421	44/18432	0.049691562	0.2035650	0.16178926	NDUFA4/NDUFB1/NDUFA6/ND	7	0.159090909090909
GO:0051219	MF	GO:0051219 phosphoprotei	12/1421	92/18432	0.049865221	0.2035650	0.16178926	SOCS3/PIK3R3/PLCG2/PIK3	12	0.130434782608696