

	PValue	Fold Enrichment	Genes
cell cycle	5.31303E-45	4.33698277	PRC1, DBP4, NTIC1, AURKA, AURKB, BRINP1, CDC48, OIP5, CDKN2C, INCENP, CCSPAP, CDC42, H2AFX, CCNA1, CCNA2, CDC45, ASCA, CDC45, LGT, SGC2, ESCO2, WEE1, NCAPO2, UHRF1, MAD2L1, SPAG5, MAPK4, CNTROB, DSDC1, TICRR, NEK2, ANLN, CHEK1, CHEK2, MYBL2, ROCI1, SPCL2, SPCL3, NPM2, FBD5, SNAI3, SKA1, SKA2, HELLS, ERCC1, CHAF1B, DDC1, MDC1, MDC2, MDC3, MDC4, MDC5, MDC6, MDC7, MDC8, MDC9, MDC10, MDC11, MDC12, MDC13, MDC14, MDC15, MDC16, MDC17, MDC18, MDC19, MDC20, MDC21, MDC22, MDC23, MDC24, MDC25, MDC26, MDC27, MDC28, MDC29, MDC30, MDC31, MDC32, MDC33, MDC34, MDC35, MDC36, MDC37, MDC38, MDC39, MDC40, MDC41, MDC42, MDC43, MDC44, MDC45, MDC46, MDC47, MDC48, MDC49, MDC50, MDC51, MDC52, MDC53, MDC54, MDC55, MDC56, MDC57, MDC58, MDC59, MDC60, MDC61, MDC62, MDC63, MDC64, MDC65, MDC66, MDC67, MDC68, MDC69, MDC70, MDC71, MDC72, MDC73, MDC74, MDC75, MDC76, MDC77, MDC78, MDC79, MDC80, MDC81, MDC82, MDC83, MDC84, MDC85, MDC86, MDC87, MDC88, MDC89, MDC90, MDC91, MDC92, MDC93, 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bone mineralization	0.005079142	4.295011876	ASPN, BMP2, ALOX15, PTN, GPNMB, PHEX, MMP13
lung development	0.005103086	2.42460479	LIF, WNT5A, ARG1, ALDH1A2, CDC40, FOXA1, MMP, IGFB1, PTN, ZFPM2, SPARC, MMP14, ADAMTS2, GLI1
response to wounding	0.005197655	3.333336851	IL6, CCL2, CYP1A1, GRNDC, AJRKA, NGFR, NDK, FABP5, GLI1
axon regeneration	0.005398911	6.710956057	NREP, DRHR, APOE, FOUR1, CHL1
platelet development	0.00592488	2.77912532	FRS1, WNT5A, INHBA, DHRS3, GSK1, GABRB3, LEF1, GAST, SNAI1, EPHB2, TWIST1
ERK1 and ERK2 cascade	0.00621168	4.95579234	CCL11, CCR3, DGAP3, OXTR, IGFB1, SOX9
spindle checkpoint	0.006281738	21.47505938	SPDL1, BIRC5, AURKB
development of primary male sexual characteristics	0.006281738	21.47505938	WNT5A, SFRP1, SFRP2
cellular response to interleukin-6	0.006804887	6.316195928	SELP, C16orf10328, ENTPO2, PPARGC1A
bone trabecula formation	0.006820388	9.544470837	SFRP1, COL1A1, FBX2, MMP2
attachment of spindle microtubules to kinetochore	0.006820388	9.544470837	SCOL1, NUP2, NDC80, CENPE
kinetochore assembly	0.006820388	9.544470837	APTD1, CENPA, CENPW, CENPH
protein K6 linked ubiquitination	0.006820388	9.544470837	UBE2B, BRCA1, UBE1T, BARD1
regulation of mitotic metaphase/anaphase transition	0.006820388	9.544470837	CDCA8, PLK1, CENPE, UBE2C
cellular response to transforming growth factor beta stimulus	0.007030209	3.168451384	WNT5A, ARG1, WNT4, SFRP1, EDN1, COL1A1, SOX9, PPARGC1A, DMB1
negative regulation of smooth muscle cell proliferation	0.007076612	3.955031991	NR4A1, HMOX1, ESRR2, NR3C1, IGFBP3, PPARGC1A, ADIPOQ
chromosome organization	0.007678612	3.955031991	CDC48, ILM, BNC1, BRCA2, CENPW, RAD54L, SMC2
negative regulation of neuron apoptotic process	0.007754363	2.147926938	KIF14, CCL2, GABRB3, LGMN, BIRC5, PPARGC1A, MOK, CCL12, BOK, APOE, NTRK1, HMOX1, NGFR, ADAM8, FAM2, CHL1
response to glucocorticoid	0.007845338	2.893312121	TYMS, IL6, PPARA, CYP19A, SPARC, MOK, ADIPOQ, SCGB1A1, IL10, ALDH3A1
positive regulation of GTPase activity	0.008181886	2.206341717	WNT5A, CCL2, EZR2, CCL9, CCL8, RGS16, ECT2, CCL7, CCL24, CCL11, CCL12, WNT4, COR7, NTRK1, ELMOD1
canonical Wnt signaling pathway	0.008254842	2.654220523	WNT5A, DKK1, WNT4, SFRP1, GATA4, SFRP4, LEF1, PTKRR, CDH3, WNT2B, GLI1
cellular response to hypoxia	0.008389594	2.501948996	CCNB1, EP2, SFRP1, FNDC1, HMOX1, EDN1, PTN, ADAM8, PPARGC1A, CCNA3, PCK1, TWIST1
cell-cell signaling	0.008389594	2.501948996	WNT5A, WNT4, WSP1, CCR3, CXCL13, GATA4, EDN1, FAX1, ADORA2A, ADRA1A, F2RBP1, WNT2B
drug metabolic process	0.008431956	5.965244273	CYP1A1, FMO1, FMO3, CYP2B6, CYP2C19
mitotic spindle assembly checkpoint	0.008431956	5.965244273	MAJL2L, PLK1, BUB1, BUB3B, CENPE
positive regulation of microphage activation	0.008431956	5.965244273	WNT5A, IGFBP1, IL10, RAB18B, IFI202
response to mechanical stimulus	0.008526966	3.067865626	CCNB1, CCL2, TNC, COL3A1, GATA4, BOKRB1, DCN, MMP14, MMP2
double-strand break repair	0.008526966	3.067865626	UG1, BRCA2, CHEK2, POLQ, RAD54L, CDC45, BRCA1, ESCO2, TRIP13
positive regulation of epithelial cell proliferation	0.008542585	2.255857891	WNT5A, IL6, SFRP1, CCR1, BNC1, IGFB1, GAST, SOX9, TBX18, TBX1
positive regulation of neutrophil chemotaxis	0.00866485	4.601798439	CXCL1, CSAR1, COR7, CXCL3, EDN1, THBS4
reciprocal meiotic recombination	0.00866485	4.601798439	RAD51C, RAD51B, CHTF18, TEX11, RAD51, TRIP13
glucose homeostasis	0.009091051	2.200512958	CAVI, IL6, PACH, FFA2, EDN1, FOXA1, MLXIP, ADIPOQ, PCK1, GPR39, ADRA1B, ADRA2A, NGFR, NR1H4
positive regulation of keratinocyte proliferation	0.00940958	8.590023753	TGFB1, HAS2, REG3G, CDH3
complement activation, alternative pathway	0.00940958	8.590023753	C3FB, C3, CFB, C3D
cellular response to vitamin D	0.00940958	8.590023753	SFRP1, TNC, PTH, FGF33
hair regeneration	0.010076618	4.443115724	TYMS, HMOX1, EZR2, ALDH3A1, IL10, GLI1
response to vitamin A	0.010293992	5.651331416	ARG1, TYMS, ALDH1A2, CYP1A1, GATA4
estrous cycle	0.010293992	5.651331416	HAS1, OXTR, PTH, HAS2, ESRR2
embryo development	0.010917761	2.183189177	WNT5A, CKB1B, BMP2, LRAT, MEG3, BUB1, OXK2, BIRC5, DLK1, RACGAP1
positive regulation of smoothened signaling pathway	0.011642942	4.295011876	SFRP1, FOXA1, CDC2A, PRKDC, GAST, GLI1
positive regulation of protein kinase C activity	0.01217634	16.10629454	WNT5A, CENP, ROR2
regulation of mitotic centrosome separation	0.01217634	16.10629454	KIF11, NDC, CHEK1
positive regulation of cell-substrate adhesion	0.012477343	3.579176584	ALOX5, PLAG2, CDC38, PTN, WIT, DBN1, SPP1
positive regulation of interleukin-8 secretion	0.012495993	7.809112503	WNT5A, FNA4, FPR2, PYCARD
one-carbon metabolic process	0.013363241	4.156485106	MTHFD2, DHFR, CARI3, ALDH1L2, CARS, CARI3
cellification	0.013722621	2.400203885	BMP2, ALOX15, PTN, MGP, SPARC, MMP14, SOX9, COL11A1, COL5A2, SPT1, TWIST1
regulation of cell cycle	0.015618352	2.30089922	CONE2, EP2, CCNE1, FIGL1, DTL, PRR11, CNCF, FOXA1, SKP2, MASTL, CCN3, 2810417H13R1K
bone morphogenesis	0.015948923	4.002578534	DHRS3, SFRP2, CYP26B1, HAS2, PAPP2A, MMP13
positive regulation of leukocyte migration	0.017400538	4.880955114	CCL12, SELP, CCL3, BDNFB1, AOC3
skin development	0.017549596	2.962077156	FRS1, COL3A1, J3B3, COL1A1, NGFR, ADAMTS2, COL5A2, COL3A1
cellular response to lipopolysaccharide	0.018227114	1.849526445	WNT5A, HMOX2, IL6, CCL2, CXCL3, PPARGC1A, IL10, RAB18B, RAB17A, CXCL10, ARG1, MIR47, PYCARD, GBT10, SPON2, NR1H4, CD14, TNF93
enter exit morphogenesis	0.018338977	2.884382423	WNT5A, MARRS, ALDH1A3, ROR2, PRKDC, F2R2, COL11A1, PTPRG, EPHB2
positive regulation of tumor necrosis factor production	0.019139213	2.911874589	CCR7, CCL3, CCR5, PYCARD, PFA, SPON2, CD14, TWIST1
protein phosphorylation	0.019173439	1.454040479	WNT5A, STK33, NFK2, PASK, FANCD2, TTK, AJRKA, CHEK1, AURKB, CHEK2, EPHB1, EPHB2, CCNE1, SPEG, BUB1, MASTL, DCLK1, MATK, CDCK7, CDK1, BMP2, CAMK1G, BIRC5, PBK, GSK2, NFK1, WEE1, CCNE1, LAMM1, PLK4, PLK1, MAPK4, NTRK1, MAP3K19, ROR2, BUB1B, CIT, GTFB3, MELK
stem cell differentiation	0.019528037	3.789716362	LIF, AZM, PPH19, EDN1, ETV4, SHC4
response to gamma radiation	0.019528037	3.789716362	CCL2, FANCD2, BRCA2, CHEK2, CCL7, CXCL10
brown fat cell differentiation	0.019528037	3.789716362	MRAP, LGI1, EPB2, FABP4, UCP1, ADIPOQ
bone morphogenesis	0.019671052	12.88503563	GAST, COL5A2, COL1A1
muscle cell chemotaxis	0.019671052	12.88503563	CCL11, CHGA, CCR3
double-strand break repair via break-induced resection	0.019671052	12.88503563	CCD1, GINS2, CDC45
regulation of vascular endothelial growth factor production	0.019671052	12.88503563	IL6, CCL2, APOA
metaphase/anaphase transition of mitotic cell cycle	0.019671052	12.88503563	BUB1B, CIT, TACC3
protein localization to chromosome, centromeric region	0.019671052	12.88503563	CENPA, BUB1B, GSG2
osteoclast fusion	0.019671052	12.88503563	CD18B, ADAM8, DCSTAMP
regulation of cell-cell adhesion	0.020209974	6.607710579	WNT1, LEF1, EFNA5, ADAM8
leukocyte migration involved in inflammatory response	0.020209974	6.607710579	CCL2, ADAM8, ITGAM, AOC3
positive regulation of gene expression	0.02032758	1.560843915	E2F1, HMOX2, TNC, DGAP3, PFA, CDH3, SOX9, LIF, ALDH1A2, SLC11A1, OSR1, ITGB8, GATA4, CYP26B1, NFY3, ETV4, TWIST1, CD28, FN1, CDK1, IL6, TSCB, BMP2, PTGER3, LEFT1, BRCA1, INHBA, CCR5, SFRP4
acute immune response	0.020923949	1.559910188	HMOX2, HMOX1, C3, FOXA1, CCR7, MARCH3, CYP, MERV, CLEC4E, PTPRG2, CLEC4A2, CLEC4D, C1P, PFK3, SPOR2, C1D, NR1H4, MATK, CBL, BPIA1, CBL, PADI4, C1QA, C1QB, THMS8B, SUP, TREM2, C1S1, CD14
acute-phase response	0.021951886	3.691439751	IL6, SAA3, REG3G, UGT1A1, FN1, CD163
negative regulation of apoptotic process	0.022976337	1.4417788439	WNT5A, STL, FIGL1, IL6, UNQ, ARNT2, PHL2, AURKA, SOX9, INS16, IL10, TBMPI, OSR1, NAPI1, HNP, NR1H4, NELL3, SPT1, FN1, TWIST1, KIF14, CCL1, IL6, CENPF, LEF1, IGFB1, BIRC5, GAST, AMIGO2, PROK2, MAO2L1, SFRP1, PLK1, SERPINB2, NGFR, PCD1, BARD1, TEX11
positive regulation of vascular endothelial growth factor production	0.02348617	4.473970105	CSAR1, CYP1B1, C3, GATA4, BRCA1
positive regulation of urine volume	0.024849449	6.135731252	PTGER3, EDN1, HAS2, NR3C1
cellular response to follicle-stimulating hormone stimulus	0.024849449	6.135731252	INHBA, GATA4, EFNA5, PPARGC1A
positive regulation of protein import into nucleus, translocation	0.024849449	6.135731252	CDK1, IL6, IGFB1, BRCA1
microtubule depolymerization	0.024849449	6.135731252	KIF14, KIF20C, KIF18A, KIF18B
positive regulation of fat cell differentiation	0.025337432	3.067865626	BMP2, ZBTB7C, SFRP1, SFRP2, IGFB1, FRZB, THY1
negative regulation of cell migration	0.025733638	2.226543888	WNT4, SLURP1, PDGF, CYP19A1, SFRP1, CCR5, SFRP2, PTPN, PTPRR1, CHRD, ADIPOQ
embryonic limb morphogenesis	0.026204694	2.728921688	FRS1, WNT5A, ALDH1A1, CYP26B1, LEF1, PRKDC, FBX2, TWIST1
metabolic process	0.027030449	1.484237386	SCAT1, ALPLP2, IL6, ENPP5, ARS1, RAS1, ALDH1A2, ALDH3A1, MTHFD2, ALDH1A2, UGT1A9, UGT1A7C, UGT1A7, UGT1A6B, CH13, ALDH1A3, ACAA1B, DCTD, CAMK1G, ACADL, NELL3, FBP1, NPL, UGT1A1, UGT1A10, HMGCS2, DNPH1, RRM1, CENP, ZRANB3, GLB1L3, THY1
positive regulation of mesenchymal cell proliferation	0.027311027	3.480442062	WNT5A, PRRK2, GAST, SOX9, TBX18, CHRD
positive regulation of bone mineralization	0.027311027	3.480442062	BMP2, WNT4, OSR1, FANCD2, CD276, FBX2
chromosome organization involved in meiotic cell cycle	0.028046531	10.73752969	CONE2, CCNE1, RAD51
intramembranous ossification	0.028046531	10.73752969	CTSK, COL1A1, MMP2
negative regulation of centrosome duplication	0.028046531	10.73752969	KIF20B, KIF1C, CNCF
regulation of branching involved in mammary gland duct morphogenesis	0.028046531	10.73752969	CAVI, WNT5A, ETV4
negative regulation of gastric acid secretion	0.028046531	10.73752969	PTGER3, GPR39, OXTR
cellular glucuronidation	0.028046531	10.73752969	UGT1A2, UGT1A5, UGT1A1
complement activation	0.030011125	5.72662502	C4B, C3, CFB, C1B1
positive regulation of T cell chemotaxis	0.030011125	5.72662502	WNT5A, CCR7, CXCL13, TNFSF14
regulation of double-strand break repair via homologous recombination	0.030011125	5.72662502	RAD51AP1, FIGL1, CHEK1, RAD51
hematopoietic stem cell proliferation	0.030011125	5.72662502	WNT5A, PRK4, SFRP, WNT2B
positive regulation of leukocyte chemotaxis	0.030011125	5.72662502	CDK3, CXCL13, PFA, CXCL10
mitotic cell cycle	0.030285636	3.90779885	RRM1, CENP, KIF18B, CENPW, CENPE, AURKA
response to steroid hormone	0.030734383	4.126819112	HMOX2, ARH1, ADRA1B, OXTR, SFRP1
positive regulation of JAK-STAT cascade	0.030734383	4.126819112	IL6, CYP1B1, IL6, CCL5, IL10
positive regulation of fibroblast proliferation	0.03082618	2.643084232	CCNB1, EP2, WNT5A, CCDC1, IGFB1, NGFR, CCNA2, FN1
negative regulation of cell growth	0.031351362	2.661626701	INHBA, SFRP1, CDKN2C, SFRP2, TRD, PRCR1, FBP1, BOKRB1, GAST, FRZB, WY1, DCSTAMP
positive regulation of smooth muscle cell proliferation	0.032245816	2.415941581	CSAR1, IL6, WSP1, HMOX1, EDN1, SKP2, IGFB1, CCR1, PPARGC1A
positive regulation of cyclin-dependent protein serine/threonine kinase activity	0.03479316	3.978928249	STL1, CDC8, CKB1B, PRCR1, CKB2
cellular response to interleukin-4	0.03479316	3.978928249	ARG1, LEF1, MCM2, NFY3, DCSTAMP
microtubule bundle formation	0.03479316	3.978928249	CAPN1, PRK1, PLK1, PRCR1, NF2B2A
cell proliferation in forebrain	0.035690959	5.368744846	KIF14, DDXD2, RRM1, FABP1
negative regulation of smooth muscle cell migration	0.035690959	5.368744846	NR4A3, IGFBP3, PPARGC1A, ADIPOQ
DNA-dependent DNA replication	0.035690959	5.368744846	RFC3, RFC4, POLQ, POLQ
inner cell mass cell proliferation	0.035690959	5.368744846	GINS1, NCAQD2, BRCA2, CHEK1
positive regulation of osteoblast differentiation	0.038155426	2.526477574	BMP2, WNT4, SFRP2, FAM20C, CD276, FBG1, FBG2, IFI204
central cortex development	0.038155426	2.526477574	KIF14, LHX2, COL3A1, H2AFX, CDH2, CDH3, MOK, ASPM
hematopoietic progenitor cell differentiation	0.038533994	2.191313259	STON2, INHBA, SFRP1, K2P, ANLN, CACCA1, TOP2A, BMPN3, ESCO2, PPRF2
negative regulation of cytokinesis	0.038827341	9.203596878	E2F1, E2F3, AURKB
glomerular visceral epithelial cell differentiation	0.038827341	9.203596878	KLF15, BASP1, WT1
strand invasion	0.038827341	9.203596878	RAD51C, RAD51B, RAD51
protein localization to chromatin	0.038827341	9.203596878	PLK1, EZH2, ESCO2
positive regulation of male gonad development	0.038827341	9.203596878	ZFPM2, SOX9, WT1
positive regulation of ubiquitin protein ligase activity	0.038827341	9.203596878	PLK1, CDCR4, UBE6
cooper on import	0.038827341	9.203596878	STEAP4, STEAP1, ATP7B
positive regulation of mitotic cell cycle spindle assembly checkpoint	0.038827341	9.203596878	MAO2L1, NDC80
spermatogenesis	0.041492221	1.477396653	E2F1, TSNAPK1, RAD51C, HMOX2, INS16, SOX9, WT1, GLI1, GATA4, RPL38L, CYP26B1, H2AFX, CCNA1, ASPM, TRIP13, BRCA2, BPR1, C300027G0R1K, CDC25C, RACGAP1, CCNB1, PROK2, CLGN, SPATAB1, MYCBAP1, CHTF18, CIT, ADAMTS2
04161675197	0.04161675197	0.04161675197	C1QA, C1QB, C1B, C1, C1, C1S1, C1QC
neural crest cell development	0.041880472	5.052951149	ALDH1A2, EDN1, CYP26A1, SOX9

negative regulation of peptidyl-tyrosine phosphorylation	0.041880472	5.052955149	SFRP1, SFRP2, IGF1, ERRF1
non-canonical Wnt signaling pathway	0.041880472	5.052955149	WNT5A, WNT4, SFRP4, FRZB
positive regulation of calcium ion-dependent exocytosis	0.041880472	5.052955149	CACNA1, CACNA1G, DCC2B, SCAMP5
positive regulation of cytosolic calcium ion concentration	0.043483714	1.886322784	CXCL1, CAV3, MCHR1, CSAR1, PTGER3, CCR5, CXCL13, PMCH, CXCL2, EDN1, ADRA1B, CACNA1G, OXTR
sprouting angiogenesis	0.043738484	3.102596445	EPF1, E2F8, LEF1, ESM1, LOXL2
stochastic cell cycle checkpoint	0.043738484	3.102596445	MDC1, RNF13, TTK, CHEK1, ZWILCH
somitogenesis	0.044817824	2.884382425	WNT5A, SFRP1, CRB2, SFRP2, ROR2, LEF1, TBX18
positive regulation of peptidyl-tyrosine phosphorylation	0.045489758	2.126243503	LIF, IL6, IL5, CSPG4, IGF1, CD4, EFNA6, TREM2, ADIPOQ, THBS4
positive regulation of peptide activity	0.0460849	2.119257627	WNTC1, ASX, SCOR54B, CSF1R, CD139, SERPINE2, SFR, COL3A1, BIRC5, NAPI1, TMPT1
response to toxic substance	0.046483937	2.247339935	CDK1, TMS, CYP1B1, CYP2P2, CYP1A1, ARNT2, PONT1, INMT, RAD51
cellular response to glucose stimulus	0.046542922	2.419725001	SERPINF1, LGALS1, GATA4, MLXIP, AQPI, IGF1, CMA1, PPARGC1A
negative regulation of JAK-STAT cascade	0.046714792	2.996519914	ASPN, FLRT3, PDGN, DCN, LRRC15, NYX
positive regulation of protein phosphorylation	0.048941025	1.176841189	WNT5A, BMP2, PTGER3, CS, VEGFA, CHEK2, SOX9, ADIPOQ, NTRK1, FND0C1, GATA4, CLIP3, GPNMB, CD6, RND0C1
DNA damage checkpoint	0.048745495	3.579176564	E2F1, CLIPB1, CHEK1, H2AFX, CHEK2
cell fate commitment	0.049480485	2.388117709	WNT5A, BMP2, WNT4, SOX12, ROR2, GAST1, SOX9, WNT2B
cerebellar cortex development	0.050200236	8.053147288	RIF1, DDXC1, E2F8
tube morphogenesis	0.050200236	8.053147288	WNT4, GATA4, FOXA1
negative regulation of retinoic acid receptor signaling pathway	0.050200236	8.053147288	DIRX53, CYP28B1, E2H2
positive regulation of acute inflammatory response	0.050200236	8.053147288	IL6, ADAM8, AOC3
pyrimidine nucleotide metabolic process	0.050200236	8.053147288	DCTD, NME4, DCK
astrocyte cell migration	0.050200236	8.053147288	CCL12, CCL2, MMP14
positive regulation of glucose transport	0.050200236	8.053147288	CS, CLIP3, AOC3
attachment of mitotic spindle microtubules to kinetochore	0.050200236	8.053147288	KIF5C, NCDB, CENPE
maintenance of epithelial cell apical/basal polarity	0.050200236	8.053147288	CRB2, LHX2, LINC7A
lipopolysaccharide-mediated signaling pathway	0.053887305	3.463719255	CCL12, CCL2, TREM2, CDK, CD14
cellular response to ionizing radiation	0.053887305	3.463719255	RAD51AP1, BLM, FUS1, ECT2, RAD51
angiogenesis	0.054686328	1.817388489	COL18A1, CYP1B1, CCL2, MMP19, CSPG4, CDC4B, ESM1, MMP14, MMP2, EPHB1, EPHB2, NRCAM, PROCR, CCL12, HMOX1, TGFBI, ADAM8, FN1
retinoid metabolic process	0.055749559	4.521065133	ALDH1A2, DHRS3, APO1, APOE
oocyte maturation	0.055749559	4.521065133	CNNB1, FBXO5, BRCA2, TRIP13
negative regulation of cAMP biosynthetic process	0.055749559	4.521065133	PTGER3, EDN1, ADRA2A, APLP1
seminiferous tubule development	0.055749559	4.521065133	GATA4, KIF18A, BRP1, WT1
response to nicotine	0.056712251	2.863341251	LYR31, DHFR, NTRK1, HMOX1, EDN1, ABAT
positive regulation of mitotic cell cycle	0.056921645	3.355478029	CNNB1, CDT1, FOXA1, BRCA2, BIRC5
response to axon injury	0.056921645	3.355478029	ARG1, CDK1, POLR1, LGALS1, NTRK1
negative regulation of G1/S transition of mitotic cell cycle	0.056921645	3.355478029	E2F1, SLFN1F, E2H2, GPNMB, GSG2
heart development	0.062413013	1.963311493	BMP2, COL1A1, FBN1, EDN1, OXTR, CENPE, SPARC, SOX9, MMP13, BMP2, DNAH5, WT1, ALDH1A2, OSR1, GATA4, CDC135, PTN, VCAN, ZFP62
amine metabolic process	0.062594478	7.158353127	CYP1A1, INMT, AOC3
positive regulation of exit from mitosis	0.062594478	7.158353127	BIRC5, UBE2C, CCOA5
nitric metabolic process	0.062594478	7.158353127	CYP1B1, CYP1A1, FMO1
lung vasculature development	0.062594478	7.158353127	LIF, IGF1, ERRF1
positive regulation of cAMP metabolic process	0.062594478	7.158353127	CHGA, FF4, CXCL10
regulation of chromosome segregation	0.062594478	7.158353127	KIF5C, INNO3, BUB1
negative regulation of histone acetylation	0.062594478	7.158353127	MSK3, BRCA1, TWIST1
negative regulation of collagen biosynthetic process	0.062594478	7.158353127	IL6, CYBB, ERRF1
mitotic recombination	0.062594478	7.158353127	RAD51B, APTD1, TOP2A
positive regulation of cell-cell adhesion	0.063359546	4.256011876	WNT5A, CCL2, CCR5, TBX18
DNA metabolic process	0.063359546	4.256011876	MK067, TOP2A, TK1, RAD51
retinal ganglion cell axon guidance	0.063359546	4.256011876	NRCAM, EFNA5, EPHB1, EPHB2
response to hypoxia	0.064398587	1.877734574	BMP2, CCL2, CYP1A1, ARNT, EDN1, EGR1, MMP14, TACC3, ADIPOQ, MMP2, ALDH3A1, HMOX1, ABAT, CYBB, LOXL2
positive regulation of release of sequestered calcium ion into cytosol	0.065345321	3.253736876	P2RX3, CTRP9, CEMIP, BDKRB1, CXCL10
regulation of neuron apoptotic process	0.065345321	3.253736876	RIF1, G4MB3, TGLN3, ESR2, FAM2
positive regulation of apoptotic process	0.069411985	1.147447062	BMP2, IL6, CYP1B1, ESR2, FRZB, ECT2, MMP2, WT1, ALDH1A2, SFRP1, BOK, SFRP2, ALDH1A3, HMOX1, SFRP4, PTCARD, PTN, NGFR, CLIP3, IGFBP3, TOP2A, MELK, BARD1
regulation of blood pressure	0.0701544	2.426034719	CALCA, CSAR1, HMOX1, EDN1, COL1A2, NRP3, AOC3
cell-matrix adhesion	0.070408776	2.202570183	ITGB8, COL1A1, MSLN, NID2, ADAMTSL2, ADAM8, COL3A1, FN1
response to hormone	0.071098772	2.684326423	MMP19, MSH1, ADRA1B, FLH2, MMP16, TMPT1
positive regulation of phagocytosis	0.071098772	2.684326423	SLC11A1, GCF1, FCGR2B, CS, PTCARD, FTY3
T cell activation	0.071454293	3.158089698	IL6, CD8A, CD278, CD4, CD28
negative regulation of ossification	0.071500559	4.090487501	CALCA, SFRP1, THP1, SOX9
termination of axon lifespan	0.071500559	4.090487501	MEG3, ROR4B, RAD51, ANKLE1
Wnt signaling pathway	0.072629655	1.813150001	WNT5A, DIXD1, TRAB20B, LEF1, CELA1, FRZB, WNT2B, CPZ, DKK2, CCNE1, WNT4, WSP1, SFRP1, SFRP2, SFRP4, ROR2
negative regulation of protein kinase activity	0.074658516	2.03447931	ASPN, CAV3, FLRT2, IL6, PDGN, FABP4, DCN, LRRC15, NYX
nucleotide biosynthetic process	0.075980703	6.442517815	DCTD, TMS, DHFR
anabolism-promoting complex-dependent catabolic process	0.075980703	6.442517815	CDK20, UBE2C, UBE2E
artery smooth muscle contraction	0.075980703	6.442517815	EDN1, CACNA1G, SMPD3
regulation of microtubule polymerization or depolymerization	0.075980703	6.442517815	SKA3, SKA1, SKA1
dorsoventral pattern formation	0.076256687	2.625916289	LHX2, EDN1, GAST, HHP, CHR2, GLI1
positive regulation of T cell proliferation	0.076425589	2.34883462	CCR7, IL6, CD278, CD4, CD6, PDCD1LG2, CD28
regulation of transcription from RNA polymerase II promoter	0.07690457	1.406427063	HMOB2, E2H2, FLH2, MYBL2, SOX9, WT1, MSX3, GATA4, NR1H4, BATF3, MAFB, SOX12, FOXA1, MLXIP, BRP1, LEF1, UCP1, SNAI1, HMO4, BNC1, CKS2, SP6, NFEDL3, ZFP367, IFI204
positive regulation of blood pressure	0.077843728	3.078586219	CALCA, NRP3, ABAT, BDNF, ADIPOQ
extracellular matrix disassembly	0.080042563	3.904556251	LAMA1, MMP19, MMP13, MMP12
positive regulation of interleukin-1 beta secretion	0.080042563	3.904556251	WNT5A, CCR7, CCR5, PTCARD
response to cytokine	0.0806781	2.120965519	THBS, ALDH1A2, COL3A1, SERPINA3, OXTR, SPARC, SCGB1A1, TMPT1
growth	0.084580852	2.862847138	GDF3, HMO4, BMP2, CNNB2, GDF6
inner ear development	0.085853034	2.277657813	C1QB, BMP2, IGF1, SPARC, LGR5, IFI204, LINTA
protein complex assembly	0.085853034	2.277657813	CNNB1, CDT1, CLGN, GANN, MGP, PF4, SOX9
phosphorylation	0.088002827	1.286320754	STK3, NEK2, PASK, FAMDC, DCK, TTK, AURKA, CHEK1, AURKB, CHEK2, ITPKA, EPHB1, EPHB2, TK1, SPEG, BUB1, MASTL, DCLK1, MATK, CDCK7, CCK1, CAMK1G, AKS, PRK, GSG2, NEK11, WEE1, NME4, PLK4, PLK1, MAPK4, NTRK1, MAPK19, ROR2, BUB1B, CIT, MELK
cochlea morphogenesis	0.088002827	3.734732936	WNT5A, FRZB, SOX9, TBX18
positive regulation of cardiac muscle cell proliferation	0.088002827	3.734732936	CNNB1, CDK1, GATA4, ZFPM2
ventricular cardiac muscle cell development	0.089978417	5.856834377	CNNB1, CDK1, FLH2
negative regulation of immune response	0.089978417	5.856834377	FCGR2B, COL3A1, FCRLB
regulation of cellular protein localization	0.089978417	5.856834377	CNNB2, WNT5A, CCNE1
cell-like receptor 4 signaling pathway	0.089978417	5.856834377	NR1H4, CD14, THP93
negative regulation of tumor necrosis factor-mediated signaling pathway	0.089978417	5.856834377	TRAP, ADIPOQ, NR1H4
positive regulation of insulin-like growth factor receptor signaling pathway	0.089978417	5.856834377	IGF1, CDH3, IGFBP3
skin morphogenesis	0.089978417	5.856834377	COL1A2, COL1A1, ERRF1
hepatocyte differentiation	0.089978417	5.856834377	CYP1A1, E2F1, E2F8
negative regulation of interleukin-1 beta production	0.089978417	5.856834377	MEFV, AQPI, ERRF1
telomere maintenance via recombination	0.089978417	5.856834377	RAD51C, BRCA2, RAD51
apoptotic cell migration	0.089978417	5.856834377	CCL2, GSPB4, FN1
negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	0.09079592	2.243652921	IL6, SFRP2, RAG1, IGF1, LEF1, BIRC5, NAPI1
negative regulation of interleukin-13 production	0.090859924	21.47505938	LEF1, SCGB1A1
actomyosin contractile ring assembly	0.090859924	21.47505938	KIF23, RACAP1
positive regulation of antigen processing and presentation of peptide antigen via MHC class II	0.090859924	21.47505938	PTCARD, TREM2
positive regulation of DNA endoreplication	0.090859924	21.47505938	E2F1, E2F8
urter urothelium development	0.090859924	21.47505938	OSR1, SOX9
neutrophil neuroblast division	0.090859924	21.47505938	LEF1, ASPM
clUMP biosynthetic process	0.090859924	21.47505938	DCTD, DUT
positive regulation of eesinophil migration	0.090859924	21.47505938	CCL24, ADAM8
gonade assembly involved in female meiosis I	0.090859924	21.47505938	FBXO5, AURKA
minus-end-directed vesicle transport along microtubule	0.090859924	21.47505938	KIF5B, KIF1
sequestering of TGFbeta in extracellular matrix	0.090859924	21.47505938	FN1, FN2
negative regulation of endodermal cell differentiation	0.090859924	21.47505938	COL3A2, COL5A1
regulation of median disassembly; neuron differentiation	0.090859924	21.47505938	SFRP1, SFRP2
flavone metabolic process	0.090859924	21.47505938	PPARGC1A, UGT1A1
centrosome separation	0.090859924	21.47505938	NIK2, CENTRON
posterior mesencephalic tubule development	0.090859924	21.47505938	CRT1, WT1
lymphocyte chemotaxis across high endothelial venule	0.090859924	21.47505938	CCR7, CXCL13
mitotic recombination-dependent replication fork processing	0.090859924	21.47505938	BRCA2, RAD51
cellular response to developmental stimulus	0.091441025	2.902035052	ARG1, IL6, CCL2, SERPINF1, ERRF1
regulation of mitotic cell cycle	0.091441025	2.902035052	CKS1B, PLK1, CKS2, FBXO5, BIRC5
base-excision repair	0.091441025	2.902035052	NEIL3, LIG1, UNL, POLQ, FEN1
negative regulation of interferon-gamma production	0.093056247	2.477891467	WNT5A, SLC11A1, ULBP1, PTCARD, CD14, RAET1B
transmembrane receptor protein tyrosine kinase signaling pathway	0.093848649	1.932763344	DDK2, NTRK1, CSRP4, ROR2, SHC2, EPHB1, EPHB2, SHC4, MATK
response to ethanol	0.09502357	1.835475181	CDK1, TMS, CCL2, NTRK1, TNC, ABAT, SPARC, ADIPOQ, CD14, CAR3
sperm motility	0.095891229	2.10857878	LRKKR, CCL20A, CACNA1I, ENK4, INSL3, WT1, DNHA5
nitride ear morphogenesis	0.098361064	3.579176564	CSR1, EDN1, PTCARD, GAST
epithelial tube branching involved in lung morphogenesis	0.098361064	3.579176564	LAMA1, FOXA1, HHP, SOX9
xenobiotic metabolic process	0.098361064	3.579176564	CYP1B1, CYP28B1, CYP2B6A1, CYP2B10
cellular response to gamma radiation	0.098361064	3.579176564	H2AFX, CHEK2, DDX45, RAD51

positive regulation of synaptic transmission, glutamatergic	0.098361064	3.579176564	NTRK1, OXTR, ROR2, NGFR
protein kinase B signaling	0.098635776	2.825965708	CCL12, LINGO1, CCL2, IGF1, SOX9