

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benfactors	Benamins	FDR
GOTERM BP	DIRECT GO004594--negative regulation of transcription from RNA polymerase II promoter	70	15.11879	8.36E-15	CNCT2, ZNF292, THRB, FOXA2, ZBK1, M	427	981	16792	2.806192839	2.33E-11	2.33E-11	1.49E-11
GOTERM BP	DIRECT GO003106--negative regulation of apoptotic process	70	8.423248	1.17E-10	MDTH, MCL1, XIAP, TRAF, FOXO1, PTEN,	427	981	16792	2.707594181	2.7E-07	1.64E-07	2.09E-07
GOTERM BP	DIRECT GO000122--positive regulation of transcription from RNA polymerase II promoter	50	10.799136	3.07E-10	BMI1, THRB, FGF9, MITF, DICER1, EBH1, M	427	720	16792	2.703993397	8.58E-07	2.80E-07	5.48E-07
GOTERM BP	DIRECT GO004893--positive regulation of transcription, DNA-templated	41	8.852919	3.32E-10	FOXA2, FOXA2, CRLF3, MITF, FOXO1, FOX	427	515	16792	3.137701905	9.28E-07	1.23E-07	5.93E-07
GOTERM BP	DIRECT GO000828--positive regulation of cell proliferation	35	5.1599252	3.53E-08	EFZF3, FGF9, BTG, PTEN, IL13RA, TGFBR	427	466	16792	2.953633979	9.87E-05	1.97E-05	6.31E-05
GOTERM BP	DIRECT GO000285--negative regulation of cell proliferation	29	6.263489	1.10E-06	DLCL1, CYP11B, BAP1, ZEB1, SRF, PTEN, A	427	396	16792	2.871899	0.00368831	4.43E-04	0.001963875
GOTERM BP	DIRECT GO007265--RAS protein signal transduction	12	2.5917927	1.39E-06	PLD1, CYP11A, KRAS, CRKL, RRG, F3, MA	427	70	16792	6.78518903	0.003869596	4.80E-04	0.002737527
GOTERM BP	DIRECT GO0010628--positive regulation of gene expression	12	4.75101628	1.39E-06	BCR4L3, RFX4, POU5F1, MITF, TCF7L2, R	427	60	16792	2.320144583	0.00222402	0.00022402	0.000463992
GOTERM BP	DIRECT GO000636--transcription from RNA polymerase II promoter	12	6.9114471	7.75E-06	CNCT2, ZNF292, MITF, DREK, NR3C1, FO	427	513	16792	2.453043312	0.021426216	0.002165655	0.018863437
GOTERM BP	DIRECT GO001666--response to hypoxia	17	3.6717063	8.16E-06	LDHA, CYP11A, ACTN2, CREB1, SMAD4, P	427	172	16792	3.886825336	0.022550738	0.002071388	0.014573055
GOTERM BP	DIRECT GO0016032--viral process	23	4.9676026	8.41E-06	VAC14, RCR1, KRAS, RBLM3, TP53, AC	427	299	16792	3.025400533	0.023237681	0.001957409	0.015022026
GOTERM BP	DIRECT GO0049537--transcription from RNA polymerase II promoter	29	6.263489	1.05E-05	MDM1, RFX4, POU5F1, MITF, ZEB1, FOX	427	441	16792	2.584012383	0.023966363	0.002186457	0.015013136
GOTERM BP	DIRECT GO0007173--epidermal growth factor receptor signaling pathway	10	2.1967022	1.05E-05	EGFR, PDK1, KRAS, PDK3, GRB2, PI3	427	56	16792	7.022415524	0.029024198	0.002101626	0.018818474
GOTERM BP	DIRECT GO0007050--cell cycle arrest	15	3.2397408	1.43E-05	TP53, SMAD3, CDK6, TCF7L2, TGFBR2, N	427	141	16792	4.183566605	0.039902111	0.002678486	0.025475378
GOTERM BP	DIRECT GO0007136--cellular response to epidermal growth factor stimulus	8	1.7278618	1.55E-05	ZFP641, EGFR, BAG1, PDK1, FGF9, GRB2, PI3	427	33	16792	9.534461074	0.165317588	0.002711812	0.02757912
GOTERM BP	DIRECT GO0007001--phosphatidylinositol-mediated signaling	12	2.8077554	1.56E-05	EGFR, RAS, PDK1, FGF9, GRB2, PI3K	427	106	16792	4.82941982	0.04256915	0.022559927	0.02789488
GOTERM BP	DIRECT GO0001837--epithelial to mesenchymal transition	8	1.2727618	1.91E-05	NOTCH1, GSK3B, FOXM1, HGF, SNAI2, CI	427	34	16792	9.25306516	0.052119849	0.002969317	0.034196239
GOTERM BP	DIRECT GO0001701--in utero embryonic development	17	3.6717063	2.33E-05	GNAL3, SMAD4, GJA1, SMAD2, KEAP1, S	427	187	16792	3.575047903	0.063152608	0.003427532	0.0416721
GOTERM BP	DIRECT GO0000974--cellular response to DNA damage stimulus	18	3.887689	2.36E-05	XIAP, CENPL, TP53BP1, ZMAT3, TP53, FG	427	208	16792	3.4031706	0.063931543	0.00297883	0.020524772
GOTERM BP	DIRECT GO0030770--DNA damage response, signal transduction by p53 class mediator	19	4.295898	2.50E-05	SIHX2, TP53, DRB1, FOXO3, MDM2, S	427	15	16792	1.73021077	0.067467206	0.00322071	0.044422458
GOTERM BP	DIRECT GO0007145--cellular response to hypoxia	12	2.5917927	3.13E-05	ZFP641, DNMT3A, ERO1A, GATA6, BC	427	96	16792	4.915908607	0.083812469	0.003970923	0.020551572
GOTERM BP	DIRECT GO0001571--positive regulation of histone H3-K4 methylation	6	1.2958963	4.94E-05	SMAD4, DNMT1, OGT, MYB, DNMT3B, T	427	17	16792	13.87959774	0.12891784	0.005982858	0.058150639
GOTERM BP	DIRECT GO0008283--cell proliferation	24	5.1835853	6.46E-05	EGFR, MORF4L1, CDV3, PLAGL1, FSCN1,	427	366	16792	2.57823708	0.165314435	0.007509002	0.12394827
GOTERM BP	DIRECT GO0001407--angiogenesis	8	1.2397408	8.28E-05	EGFR, MORF4L1, CDV3, PLAGL1, FSCN1,	427	172	16792	4.29251767	0.30028248	0.01827585	0.22484524
GOTERM BP	DIRECT GO0008286--insulin receptor signaling pathway	10	2.1967022	1.55E-04	IGF1R, EIF4E2P2, GRB2, PI3K2A, ATP2	427	78	16792	5.041734222	0.35186477	0.01654574	0.2768012
GOTERM BP	DIRECT GO0010718--positive regulation of epithelial to mesenchymal transition	7	1.511879	1.59E-04	NOTCH1, EGFR, SMAD3, SMAD4, SMAD2,	427	33	16792	8.41377844	0.359609749	0.016370576	0.2048381
GOTERM BP	DIRECT GO0004997--DNA damage response, signal transduction by p53 class mediator res	9	1.943845	1.64E-04	TNKS1BP1, CDKN1A, CDKN2C, EP300, N	427	62	16792	5.908544252	0.367281782	0.016216099	0.20246871
GOTERM BP	DIRECT GO0004997--DNA damage response, signal transduction by p53 class mediator res	12	4.5917927	1.64E-04	PHLPP1, MCL1, PDK1, PLG1, GJA1, GAT	427	115	16792	4.055332361	0.365834097	0.01708234	0.1931477
GOTERM BP	DIRECT GO0007192--extrinsic apoptotic signaling pathway in absence of ligand	7	1.511879	1.89E-04	MCL1, BCL2, GSK3B, MKNK2, EP300, C	427	34	16792	8.964632015	0.41128317	0.01750365	0.37888256
GOTERM BP	DIRECT GO0035924--cellular response to vascular endothelial growth factor stimulus	6	1.2958963	2.37E-04	VCAM1, NOTCH1, FLT1, MAPK14, VEGFR	427	23	16792	10.28838311	0.484161208	0.021127206	0.402277563
GOTERM BP	DIRECT GO0035924--cellular response to vascular endothelial growth factor stimulus	12	4.5917927	2.50E-04	SIHX2, TP53, DRB1, FOXO3, MDM2, S	427	115	16792	4.055332361	0.365834097	0.01708234	0.1931477
GOTERM BP	DIRECT GO0030335--positive regulation of cell migration	15	3.2397408	2.59E-04	EGFR, FLT1, ACTN2, PDXL, SMAD3, H	427	184	16792	2.88385848	0.51578531	0.021236847	0.462235958
GOTERM BP	DIRECT GO0006915--apoptotic process	30	6.4794816	2.87E-04	DLCL1, PHLPP1, XIAP, CARD11, STK17B, F	427	567	16792	2.08071511	0.522500207	0.02352673	0.51203577
GOTERM BP	DIRECT GO0038128--ERBB2 signaling pathway	7	1.511879	3.15E-04	EGFR, CUL5, KRAS, GRB2, EBI3, ERBIN, S	427	38	16792	7.244176014	0.614570578	0.028117089	0.605758287
GOTERM BP	DIRECT GO0179154--cytoskeletal protein phosphorylation	12	2.5917927	3.92E-04	PHLPP1, MCL1, PDK1, PLG1, GJA1, GAT	427	115	16792	4.055332361	0.365834097	0.01708234	0.1931477
GOTERM BP	DIRECT GO0004134--positive regulation of fibroblast proliferation	8	1.2727618	4.07E-04	BMI1, EGFR, WNT1, CDKN1A, JUN, BIC	427	54	16792	8.26039039	0.679955129	0.030242945	0.75237343
GOTERM BP	DIRECT GO0030306--actin cytoskeleton organization	12	2.5917927	4.78E-04	DLCL1, PEN1, RND3, SMAD1, F3LN, PDI	427	130	16792	3.63040864	0.67558706	0.0439368	0.81189932
GOTERM BP	DIRECT GO0032355--response to estradiol	12	2.1967022	4.99E-04	DNMT3A, CDKN1B, ETS1, EZH2, MBD4, J	427	91	16792	4.321484676	0.75237343	0.053157648	0.88792746
GOTERM BP	DIRECT GO0001570--vasculogenesis	8	1.2727618	6.23E-04	ZFP641, VEGFA, GJA1, ZEB1, YAP1, EP	427	104	16792	3.61791244	0.87646615	0.01827585	0.22484524
GOTERM BP	DIRECT GO0001889--liver development	9	1.943845	5.60E-04	NOTCH1, KRAS, CADM1, GATA6, BC	427	74	16792	4.78283457	0.9127602	0.037491047	0.999607271
GOTERM BP	DIRECT GO004570--positive regulation of DNA replication	7	1.511879	6.23E-04	EGFR, IGF1R, JUN, NPAT, SHL1, AREG, A	427	42	16792	6.52442849	0.82744727	0.040620281	1.166992039
GOTERM BP	DIRECT GO0008584--male zoonid development	10	2.1967022	6.34E-04	FGF9, GATRA4, BCL2, GATA4, HOXA9, M	427	94	16792	4.183566605	0.83060958	0.004379848	1.102992079
GOTERM BP	DIRECT GO003106--negative regulation of apoptotic process	4	1.0316717	8.91E-04	PHLPP1, MCL1, PDK1, PLG1, GJA1, GAT	427	79	16792	2.496619312	0.852763629	0.01708234	0.21403222
GOTERM BP	DIRECT GO0030336--negative regulation of cell migration	10	2.1967022	6.85E-04	RECK, DLCL1, CYP11B, RAP2B, BCL2, P	427	95	16792	4.139259151	0.852466059	0.041661027	1.2611299
GOTERM BP	DIRECT GO0050821--protein stabilization	12	2.5917927	7.00E-04	PNP1, CDKN1A, FBXW7, EP300, PBE2, C	427	136	16792	8.99899435	0.888896263	0.041679748	1.2149139
GOTERM BP	DIRECT GO0008111--negative regulation of anionics	5	1.0799136	7.48E-04	NOTCH1, MCL1, BCL2, FDKS, SNAI2	427	17	16792	11.56633147	0.87646615	0.04351917	1.32746055
GOTERM BP	DIRECT GO0001701--in utero embryonic development	17	3.6717063	8.41E-04	PHLPP1, MCL1, PDK1, PLG1, GJA1, GAT	427	115	16792	4.055332361	0.365834097	0.01708234	0.1931477
GOTERM BP	DIRECT GO0045892--negative regulation of transcription, DNA-templated	26	6.155508	0.001002	TP53BP1, MAPK14, BRIP1, CKE2, RAD1	427	499	16792	2.490525361	0.933785816	0.033495811	0.51578531
GOTERM BP	DIRECT GO0000771--intrinsic apoptotic signaling pathway in response to DNA damage	6	1.2958963	0.001017	CDKN1A, EP300, TP53, CHEK2, PMAIP1, I	427	31	16792	7.11392309	0.940995228	0.01791194	1.792109664
GOTERM BP	DIRECT GO0007147--cellular response to ionizing radiation	6	1.2958963	0.001017	CDKN1A, GRB2, MAPK14, TP53, SNAI2, C	427	31	16792	7.11392309	0.940995228	0.02597114	1.912109664
GOTERM BP	DIRECT GO003106--negative regulation of apoptotic process	15	3.2397408	0.001294	NOTCH1, MCL1, PDK1, PLG1, GJA1, GAT	427	115	16792	4.055332361	0.365834097	0.01708234	0.1931477
GOTERM BP	DIRECT GO0007129--cellular response to amino acid stimulus	7	1.511879	0.001458	EGFR, DNMT3A, DPC1, DNMT1, ZEB1, S	427	47	16792	5.85993733	0.959462322	0.057634	0.202381873
GOTERM BP	DIRECT GO0006915--apoptotic process	9	1.943845	0.001202	TNFRSF10A, ILPS, DNMT1, TNFRSF10	427	83	16792	4.264213764	0.967663662	0.059656468	1.2128715
GOTERM BP	DIRECT GO0006915--apoptotic process	30	6.4794816	0.001202	TNFRSF10A, ILPS, DNMT1, TNFRSF10	427	567	16792	2.08071511	0.522500207	0.02352673	0.51203577
GOTERM BP	DIRECT GO0038128--ERBB2 signaling pathway	7	1.511879	3.15E-04	EGFR, CUL5, KRAS, GRB2, EBI3, ERBIN, S	427	38	16792	7.244176014	0.614570578	0.028117089	0.605758287
GOTERM BP	DIRECT GO0179154--cytoskeletal protein phosphorylation	12	2.5917927	3.92E-04	PHLPP1, MCL1, PDK1, PLG1, GJA1, GAT	427	115	16792	4.055332361	0.365834097	0.01708234	0.1931477
GOTERM BP	DIRECT GO0004134--positive regulation of fibroblast proliferation	8	1.2727618	4.07E-04	BMI1, EGFR, WNT1, CDKN1A, JUN, BIC	427	54	16792	8.26039039	0.679955129	0.030242945	0.75237343
GOTERM BP	DIRECT GO0030306--actin cytoskeleton organization	12	2.5917927	4.78E-04	DLCL1, PEN1, RND3, SMAD1, F3LN, PDI	427	130	16792	3.63040864	0.67558706	0.0439368	0.81189932
GOTERM BP	DIRECT GO0032355--response to estradiol	12	2.1967022	4.99E-04	DNMT3A, CDKN1B, ETS1, EZH2, MBD4, J	427	91	16792	4.321484676	0.75237343	0.053157648	0.88792746
GOTERM BP	DIRECT GO0001570--vasculogenesis	8	1.2727618	6.23E-04	ZFP641, VEGFA, GJA1, ZEB1, YAP1, EP	427	104	16792	3.61791244	0.87646615	0.01827585	0.22484524
GOTERM BP	DIRECT GO0001889--liver development	9	1.943845	5.60E-04	NOTCH1, KRAS, CADM1, GATA6, BC	427	74	16792	4.78283457	0.9127602	0.037491047	0.999607271
GOTERM BP	DIRECT GO004570--positive regulation of DNA replication	7	1.511879	6.23E-04	EGFR, IGF1R, JUN, NPAT, SHL1, AREG, A	427	42	16792	6.52442849	0.82744727	0.040620281	1.166992039
GOTERM BP	DIRECT GO0008584--male zoonid development	10	2.1967022	6.34E-04	FGF9, GATRA4, BCL2							

GOTERM	BP	DIRECT	GO:0001658--branching involved in ureteric bud morphogenesis	5	1.0799136	0.021394	WNT1, LHX1, BCL2, SMAD4, CTNWB1	427	42	16792	4.681610349	1.026303109	32.0476115
GOTERM	BP	DIRECT	GO:0045123--positive regulation of I-kappaB kinase-NF-kappaB signaling	10	2.1598272	0.0217992	MTDH, TNFRSF10B, MAP3K3, TRIM8, TBK1	427	161	16792	2.442579913	1.036400591	32.5485456
GOTERM	BP	DIRECT	GO:0071070--cytoskeleton organization	7	1.1598272	0.0217992	YEATS4, PNM3, BRWD1, WASF3, TUBB	427	161	16792	2.442579913	1.036400591	32.5485456
GOTERM	BP	DIRECT	GO:0006338--chromatin remodeling	7	1.511879	0.0220654	MORF4L1, ATXN1, SRSB, SMARCD3, TRIM7	427	86	16792	3.200914983	1.036786841	32.5485456
GOTERM	BP	DIRECT	GO:0045648--positive regulation of erythrocyte differentiation	4	0.8639309	0.0221001	ACVR1B, ETS1, MAPK14, FOXO3	427	24	16792	6.524544489	1.036447858	32.91821221
GOTERM	BP	DIRECT	GO:0048570--cell motility	4	0.8639309	0.0221001	PLD1, ETS1, FSCN1, EPHA2	427	24	16792	6.524544489	1.036447858	32.91821221
GOTERM	BP	DIRECT	GO:0096090--negative regulation of canonical Wnt signaling pathway	10	1.5982709	0.0233918	CYLD, NOTCH1, PSMAD1, MAPK14, GSK3	427	161	16792	2.412609091	1.026303109	36.6767853
GOTERM	BP	DIRECT	GO:0010629--negative regulation of gene expression	9	1.9438445	0.0236627	ACVR1B, CDKN1A, TBK1, CREB1, GJA1,	427	137	16792	2.583428777	1.037944374	34.74145165
GOTERM	BP	DIRECT	GO:2000134--regulatory regulation of G1/S transition of mitotic cell cycle	4	0.8639309	0.0246521	CDKN1A, BCL2, E2F1, PTEN	427	25	16792	6.290820439	1.039041216	35.97774174
GOTERM	BP	DIRECT	GO:0019010--signal transduction by protein phosphorylation	1	1.0799136	0.0249488	ACVR1B, PRKCB1, CAB39, KDR, TGFBR2	427	44	16792	4.458809073	1.026303109	36.32491197
GOTERM	BP	DIRECT	GO:0051272--positive regulation of cellular component movement	3	0.6479482	0.0252512	ACTN4, ETS1, VEGFA	427	10	16792	11.797568008	1.039350713	36.6767853
GOTERM	BP	DIRECT	GO:0006983--ER overload response	3	0.6479482	0.0252512	GSK3B, TP53, PPP1R15B	427	10	16792	11.797568008	1.039350713	36.6767853
GOTERM	BP	DIRECT	GO:0053265--organ growth	3	0.6479482	0.0252512	BCL2, NLGN4, SMAD2	427	10	16792	11.797568008	1.039350713	36.6767853
GOTERM	BP	DIRECT	GO:0045616--regulation of hematopoiesis differentiation	3	0.6479482	0.0252512	CYLD, NOTCH1, PSMAD1, MAPK14, GSK3	427	10	16792	11.797568008	1.039350713	36.6767853
GOTERM	BP	DIRECT	GO:0090009--primitive streak formation	3	0.6479482	0.0252512	FOXO2, LHX1, SRF	427	10	16792	11.797568008	1.039350713	36.6767853
GOTERM	BP	DIRECT	GO:0003184--planary valve morphogenesis	3	0.6479482	0.0252512	NOTCH2, NOTCH1, TGFBR2	427	10	16792	11.797568008	1.039350713	36.6767853
GOTERM	BP	DIRECT	GO:0051146--striated muscle cell differentiation	3	0.6479482	0.0252512	SPAG9, KRAS, MAPK14	427	10	16792	11.797568008	1.039350713	36.6767853
GOTERM	BP	DIRECT	GO:0047982--cellular response to hypoxia	3	0.6479482	0.0252512	WASF3, PRKCB1, HIF1A	427	11	16792	11.797568008	1.039350713	36.6767853
GOTERM	BP	DIRECT	GO:0071363--cellular response to growth factor stimulus	5	1.0799136	0.0268516	PFN1, SHC1, MAPK7, THBS1, CTNWB1	427	45	16792	4.369502992	1.041059971	38.50881676
GOTERM	BP	DIRECT	GO:0002314--activation of protein kinase activity	5	1.0799136	0.0268516	SLC11A1, HMGB1, VEGFA, CAB39, TGFBR2	427	45	16792	4.369502992	1.041059971	38.50881676
GOTERM	BP	DIRECT	GO:0007160--cell-matrix adhesion	7	1.511879	0.0268879	VCAM1, TIAM1, FERMT2, PKD1, SRF, BCL2	427	90	16792	3.085620529	1.040871896	38.549740662
GOTERM	BP	DIRECT	GO:0002053--positive regulation of mesenchymal cell proliferation	4	0.8639309	0.027358	CYLD, NOTCH1, PSMAD1, MAPK14, GSK3	427	48	16792	6.058081066	1.041200248	39.09570495
GOTERM	BP	DIRECT	GO:0000186--activation of MAPK3 cascade	5	1.0799136	0.0283891	EGFR, CRKL, PLCG1, MAPK3, FRS2	427	46	16792	4.274513797	1.026843033	40.71149142
GOTERM	BP	DIRECT	GO:0045165--cell fate commitment	5	1.0799136	0.0283891	WNT1, WNT16, GATA6, GATA4, SMAD2	427	46	16792	4.274513797	1.026843033	40.71149142
GOTERM	BP	DIRECT	GO:0010595--positive regulation of endothelial cell migration	1	1.0799136	0.0283891	ROCK2, ETS1, VEGFA, THBS1, KDR	427	46	16792	4.274513797	1.026843033	40.71149142
GOTERM	BP	DIRECT	GO:0000255--regulation of transcription, DNA-templated	5	1.1015119	0.0290287	WASF3, PRKCB1, HIF1A, CTNWB1	427	1504	16792	1.333511834	1.026378845	40.85289652
GOTERM	BP	DIRECT	GO:0032728--positive regulation of interferon-beta production	4	0.8639309	0.0302114	POLR3F, HMGB1, TBK1, FLOT1	427	27	16792	5.826003399	1.043766624	42.19310906
GOTERM	BP	DIRECT	GO:0003109--hair follicle morphogenesis	4	0.8639309	0.0302114	NOTCH1, BCL2, CTNWB1, TGFBR2	427	27	16792	5.826003399	1.043766624	42.19310906
GOTERM	BP	DIRECT	GO:0003249--response to miramydip dipeptide	3	0.6479482	0.0303518	NOTCH1, MAPK3, ERBB1	427	11	16792	10.725512174	1.043702535	42.34361782
GOTERM	BP	DIRECT	GO:0004927--positive regulation of protein chemotaxis	3	0.6479482	0.0303518	VEGFA, SMAD3, KDR	427	11	16792	10.725512174	1.043702535	42.34361782
GOTERM	BP	DIRECT	GO:0046854--phosphatidylinositol phosphorylation	4	0.9676026	0.0313884	DLC1, EGFR, FGF, GRB2, E2H2, BPC, PTEN	427	565	16792	1.600862158	1.045560226	43.43817325
GOTERM	BP	DIRECT	GO:0004854--phosphatidylinositol phosphorylation	4	1.511879	0.0323619	EGFR, GRB2, PIK3CA, FGF, BPC, IRS1, FRS2	427	16792	2.928496686	1.045399899	44.44066776	
GOTERM	BP	DIRECT	GO:0001317--positive regulation of cell cycle	4	0.8639309	0.0323619	EIF4E, ARPC2, ARPC1, ARPC3, ARPC4, ARPC5, ARPC6, ARPC7, ARPC8, ARPC9, ARPC10, ARPC11, ARPC12, ARPC13, ARPC14, ARPC15, ARPC16, ARPC17, ARPC18, ARPC19, ARPC20, ARPC21, ARPC22, ARPC23, ARPC24, ARPC25, ARPC26, ARPC27, ARPC28, ARPC29, ARPC30, ARPC31, ARPC32, ARPC33, ARPC34, ARPC35, ARPC36, ARPC37, ARPC38, ARPC39, ARPC40, ARPC41, ARPC42, ARPC43, ARPC44, ARPC45, ARPC46, ARPC47, ARPC48, ARPC49, ARPC50, ARPC51, ARPC52, ARPC53, ARPC54, ARPC55, ARPC56, ARPC57, ARPC58, ARPC59, ARPC60, ARPC61, ARPC62, ARPC63, ARPC64, ARPC65, ARPC66, ARPC67, ARPC68, ARPC69, ARPC70, ARPC71, ARPC72, ARPC73, ARPC74, ARPC75, ARPC76, ARPC77, ARPC78, ARPC79, ARPC80, ARPC81, ARPC82, ARPC83, ARPC84, ARPC85, ARPC86, ARPC87, ARPC88, ARPC89, ARPC90, ARPC91, ARPC92, ARPC93, ARPC94, ARPC95, ARPC96, ARPC97, ARPC98, ARPC99, ARPC100	427	16792	2.928496686	1.045399899	44.44066776	
GOTERM	BP	DIRECT	GO:0090020--positive regulation of release of cytochrome c from mitochondria	4	0.8639309	0.0323725	MFF, TP53, PMAIP1, BCL2L1	427	28	16792	5.617391219	1.045845683	45.13311915
GOTERM	BP	DIRECT	GO:0001569--patterning of blood vessels	4	0.8639309	0.0332173	VEGFA, SRF, CTNWB1	427	28	16792	5.617391219	1.045845683	45.13311915
GOTERM	BP	DIRECT	GO:0007126--cellular response to mechanical stimulus	6	1.2958963	0.0341294	TNFRSF10A, EGFR, TNFRSF10B, GJA1, C	427	71	16792	3.732323696	1.046548828	46.22634813
GOTERM	BP	DIRECT	GO:0049853--T cell receptor signaling pathway	1	1.9438445	0.0341294	PP2R1A, CD3E, CD3D, CD3EAP, CD3G, CD3GAP, CD3GAP2, CD3GAP3, CD3GAP4, CD3GAP5, CD3GAP6, CD3GAP7, CD3GAP8, CD3GAP9, CD3GAP10, CD3GAP11, CD3GAP12, CD3GAP13, CD3GAP14, CD3GAP15, CD3GAP16, CD3GAP17, CD3GAP18, CD3GAP19, CD3GAP20, CD3GAP21, CD3GAP22, CD3GAP23, CD3GAP24, CD3GAP25, CD3GAP26, CD3GAP27, CD3GAP28, CD3GAP29, CD3GAP30, CD3GAP31, CD3GAP32, CD3GAP33, CD3GAP34, CD3GAP35, CD3GAP36, CD3GAP37, CD3GAP38, CD3GAP39, CD3GAP40, CD3GAP41, CD3GAP42, CD3GAP43, CD3GAP44, CD3GAP45, CD3GAP46, CD3GAP47, CD3GAP48, CD3GAP49, CD3GAP50, CD3GAP51, CD3GAP52, CD3GAP53, CD3GAP54, CD3GAP55, CD3GAP56, CD3GAP57, CD3GAP58, CD3GAP59, CD3GAP60, CD3GAP61, CD3GAP62, CD3GAP63, CD3GAP64, CD3GAP65, CD3GAP66, CD3GAP67, CD3GAP68, CD3GAP69, CD3GAP70, CD3GAP71, CD3GAP72, CD3GAP73, CD3GAP74, CD3GAP75, CD3GAP76, CD3GAP77, CD3GAP78, CD3GAP79, CD3GAP80, CD3GAP81, CD3GAP82, CD3GAP83, CD3GAP84, CD3GAP85, CD3GAP86, CD3GAP87, CD3GAP88, CD3GAP89, CD3GAP90, CD3GAP91, CD3GAP92, CD3GAP93, CD3GAP94, CD3GAP95, CD3GAP96, CD3GAP97, CD3GAP98, CD3GAP99, CD3GAP100	427	16792	3.732323696	1.046548828	46.22634813	
GOTERM	BP	DIRECT	GO:0036092--ubiquitin-protein ligase complex assembly	5	1.0799136	0.0353134	GRB2, PIK3CA, FGF, IRS1, FRS2	427	49	16792	4.012808871	1.047284065	47.19315221
GOTERM	BP	DIRECT	GO:0061158--3-TUR-mediated RNAi destabilization	3	0.6479482	0.0358207	ZFP541, QKI, TRIM71	427	12	16792	9.831833773	1.047611196	47.8839659
GOTERM	BP	DIRECT	GO:0048596--embryonic carcinoma-type eye morphogenesis	3	0.6479482	0.0358207	FOXO2, ZEB1, CITED2	427	12	16792	9.831833773	1.047611196	47.8839659
GOTERM	BP	DIRECT	GO:0049327--ubiquitin-mediated inhibition of translation	3	0.6479482	0.0358207	TRIM71, TRIM72, TRIM73, TRIM74, TRIM75, TRIM76, TRIM77, TRIM78, TRIM79, TRIM80, TRIM81, TRIM82, TRIM83, TRIM84, TRIM85, TRIM86, TRIM87, TRIM88, TRIM89, TRIM90, TRIM91, TRIM92, TRIM93, TRIM94, TRIM95, TRIM96, TRIM97, TRIM98, TRIM99, TRIM100	427	12	16792	9.831833773	1.047611196	47.8839659
GOTERM	BP	DIRECT	GO:0042149--cellular response to glucose starvation	4	0.8639309	0.0363728	BCL2, TP53, PMAIP1	427	29	16792	5.424210611	1.0478755	48.41459323
GOTERM	BP	DIRECT	GO:0007409--axogenesis	5	1.511879	0.0383136	PARD6B, NOTCH1, CREB1, BCL2, GSK3B	427	98	16792	2.808692049	1.056579277	50.41241714
GOTERM	BP	DIRECT	GO:0001654--eye development	4	0.8639309	0.0396766	HMGB1, RAB18, FGF, TGFBR2	427	30	16792	5.244033591	1.050494352	51.48451714
GOTERM	BP	DIRECT	GO:0009791--positive regulation of gene expression	4	0.8639309	0.0396766	CDKN1A, C/EBP, CTNWB1	427	30	16792	5.244033591	1.050494352	51.48451714
GOTERM	BP	DIRECT	GO:1900740--positive regulation of protein insertion into mitochondrial membrane	4	0.8639309	0.0396766	BCL2, TP53, PMAIP1, BCL2L1	427	30	16792	5.244033591	1.050494352	51.48451714
GOTERM	BP	DIRECT	GO:0042542--response to hydrogen peroxide	5	1.0799136	0.0400596	LDHA, JNK1, ABL2, AREG, PPP1R15B	427	51	16792	3.855443817	1.050261823	51.82004749
GOTERM	BP	DIRECT	GO:0006367--transcription initiation from RNA polymerase II promoter	1	1.9438445	0.0401438	NOTCH1, NOTCH1, E2F3, NRBP1, RARG,	427	152	16792	2.338487441	1.050483027	51.90834271
GOTERM	BP	DIRECT	GO:0046852--ubiquitin-mediated inhibition of translation	3	0.6479482	0.041636	WNT1, WNT16, GATA6, GATA4, SMAD2	427	152	16792	2.338487441	1.050483027	51.90834271
GOTERM	BP	DIRECT	GO:0061029--cytidyl development in carcinoma-type eye	3	0.6479482	0.041636	EGFR, JNK1, PTFN	427	13	16792	9.0751216	1.051566833	53.22294391
GOTERM	BP	DIRECT	GO:0007267--protein localization to membrane	3	0.6479482	0.041636	CPIA1, TIAM1, FERMT2	427	13	16792	9.0751216	1.051566833	53.22294391
GOTERM	BP	DIRECT	GO:0007267--protein localization to membrane	3	0.6479482	0.041636	NCOA2, HFE, GDF2	427	13	16792	9.0751216	1.051566833	53.22294391
GOTERM	BP	DIRECT	GO:0007267--protein localization to membrane	3	0.6479482	0.041636	NOTCH1, NOTCH1, E2F3, NRBP1, RARG,	427	13	16792	9.0751216	1.051566833	53.22294391
GOTERM	BP	DIRECT	GO:0006413--airial septum morphogenesis	3	0.6479482	0.041636	NOTCH2, GATGA, TGFBR2	427	13	16792	9.0751216	1.051566833	53.22294391
GOTERM	BP	DIRECT	GO:0003198--epithelial to mesenchymal transition involved in endocardial cushion	3	0.6479482	0.041636	NOTCH1, SMAD2, SNAI2	427	13	16792	9.0751216	1.051566833	53.22294391
GOTERM	BP	DIRECT	GO:2000273--positive regulation of receptor activity	3	0.6479482	0.041636	NCOA2, HFE, GDF2	427	13	16792	9.0751216	1.051566833	53.22294391
GOTERM	BP	DIRECT	GO:0049627--positive regulation of protein phosphorylation	3	0.6479482	0.041636	NOTCH1, NOTCH1, E2F3, NRBP1, RARG,	427	13	16792	9.0751216	1.051566833	53.22294391
GOTERM	BP	DIRECT	GO:0007623--circadian rhythm	6	1.2958963	0.0417531	EGFR, EP300, JNK1, CREB1, GSK3B, C/EBP	427	75	16792	3.146042155	1.051441529	53.30924148
GOTERM	BP	DIRECT	GO:0010468--regulation of gene expression	7	1.511879	0.0418503	ZFP541, BMI1, DNMT3A, LHX1, CLC2	427	100	16792	2.752786885	1.051328414	53.40947486
GOTERM	BP	DIRECT	GO:0004097--response to cytokine	5	1.0799136	0.0425621	MCL1, JNK1, CD274, SRF	427	52	16792	3.781300667	1.051722539	54.02091895
GOTERM	BP	DIRECT	GO:0003760--positive regulation of angiogenesis	4	0.8639309	0.0425621	MTS1, MAPK7, EPHA2, PMAIP1	427	52	16792	3.781300667	1.051722539	54.02091895
GOTERM	BP	DIRECT	GO:0004008--regulation of growth	4	0.8639309	0.0447891	GNA13, DCL1, FGF9, GARRB1, GJA1, DEJ	427	1161	16792	1.348489469	1.053145606	55.89796354
GOTERM	BP	DIRECT	GO:0001843--neural tube closure	5	1.0799136	0.0451508	MORF4L1, YEATS4, ZMAT3, SHC1	427	53	16792	3.709953571	1.053279866	56.1949842
GOTERM	BP	DIRECT	GO:0009349--positive regulation of protein catabolic process	6	1.2958963	0.0458918	HDAC1, PEN1, RARG, TRIM71, MTS1, FERMT2	427	77	16792	3.064532674	1.052612257	56.79821962
GOTERM	BP												

GOTERM BP DIRECT GO:0008361--regulation of cell size	3	0.6479482	0.0903805	RARG, CREB1, MSN	427	20	16792	5.89882904	1	0.703279228	81.59190734
GOTERM BP DIRECT GO:0001892--embryonic placenta development	3	0.6479482	0.0903805	EGFR, PKD1, CITED2	427	20	16792	5.89882904	1	0.703279228	81.59190734
GOTERM BP DIRECT GO:0050900--leukocyte migration	7	1.5118179	0.0904229	KRAS, PLCG1, GRB2, PODXL, SHC1, MSN	427	122	16792	2.236582693	1	0.701808594	81.60722802
GOTERM BP DIRECT GO:0018108--peptidyl-tyrosine phosphorylation	8	1.7278618	0.095068	EGFR, EPHA7, FLT1, FGF9, BTC, ABI2, EF	427	153	16792	2.056236702	1	0.719050631	83.21497142
GOTERM BP DIRECT GO:1904837--beta-catenin-TCT complex assembly	4	0.8639309	0.0951529	EP300, TCF7L2, TCF7L1, CTNNB1	427	43	16792	3.658188552	1	0.717767028	83.24306628
GOTERM BP DIRECT GO:0030135--regulation of cell adhesion	4	0.8639309	0.0951529	ROCK2, PPP1R12A, PKD1, SRF	427	43	16792	3.658188552	1	0.717767028	83.24306628
GOTERM BP DIRECT GO:0051726--regulation of cell cycle	7	1.5118179	0.0959169	CCNE2, EP300, JUN, BAP1, USP16, PTEN,	427	124	16792	2.219989424	1	0.719158105	83.49406179
GOTERM BP DIRECT GO:0007169--transmembrane receptor protein tyrosine kinase signaling pathway	6	1.2958963	0.0971905	EGFR, IGF1R, MTS1, FLT1, KDR, IL13RA	427	96	16792	2.457845433	1	0.722502511	83.90457031
GOTERM BP DIRECT GO:0007621--negative regulation of female receptivity	2	0.4319654	0.0976886	THRB, AVPR1A	427	4	16792	19.66276347	1	0.72282582	84.06248713
GOTERM BP DIRECT GO:0003219--cardiac right ventricle formation	2	0.4319654	0.0976886	NOTCH1, SMARCD3	427	4	16792	19.66276347	1	0.72282582	84.06248713
GOTERM BP DIRECT GO:1901031--regulation of response to reactive oxygen species	2	0.4319654	0.0976886	SESN2, SESN1	427	4	16792	19.66276347	1	0.72282582	84.06248713
GOTERM BP DIRECT GO:0046498--S-adenosylhomocysteine metabolic process	2	0.4319654	0.0976886	DNMT3A, DNMT3B	427	4	16792	19.66276347	1	0.72282582	84.06248713
GOTERM BP DIRECT GO:0060534--trachea cartilage development	2	0.4319654	0.0976886	RARG, SRF	427	4	16792	19.66276347	1	0.72282582	84.06248713
GOTERM BP DIRECT GO:0060429--epithelium development	2	0.4319654	0.0976886	LHX1, SNAI2	427	4	16792	19.66276347	1	0.72282582	84.06248713
GOTERM BP DIRECT GO:0072177--mesonephric duct development	2	0.4319654	0.0976886	LHX1, PKD1	427	4	16792	19.66276347	1	0.72282582	84.06248713
GOTERM BP DIRECT GO:0055522--monoubiquitinated histone H2A deubiquitination	2	0.4319654	0.0976886	BAP1, USP16	427	4	16792	19.66276347	1	0.72282582	84.06248713
GOTERM BP DIRECT GO:0090403--oxidative stress-induced premature senescence	2	0.4319654	0.0976886	WNT16, TP53	427	4	16792	19.66276347	1	0.72282582	84.06248713
GOTERM BP DIRECT GO:1904954--canonical Wnt signaling pathway involved in midbrain dopaminergic	2	0.4319654	0.0976886	WNT1, CTNNB1	427	4	16792	19.66276347	1	0.72282582	84.06248713
GOTERM BP DIRECT GO:0061419--positive regulation of transcription from RNA polymerase II promoter	2	0.4319654	0.0976886	NOTCH1, VEGFA	427	4	16792	19.66276347	1	0.72282582	84.06248713
GOTERM BP DIRECT GO:1903347--negative regulation of bicellular tight junction assembly	2	0.4319654	0.0976886	ROCK2, IKKKB	427	4	16792	19.66276347	1	0.72282582	84.06248713
GOTERM BP DIRECT GO:0007161--calcium-independent cell-matrix adhesion	2	0.4319654	0.0976886	PKD1, FNI	427	4	16792	19.66276347	1	0.72282582	84.06248713
GOTERM BP DIRECT GO:0002520--immune system development	2	0.4319654	0.0976886	TROVE2, SMAD3	427	4	16792	19.66276347	1	0.72282582	84.06248713
GOTERM BP DIRECT GO:0090400--stress-induced premature senescence	2	0.4319654	0.0976886	CDKN1A, MAPK14	427	4	16792	19.66276347	1	0.72282582	84.06248713
GOTERM BP DIRECT GO:0003273--cell migration involved in endocardial cushion formation	2	0.4319654	0.0976886	NOTCH1, SNAI2	427	4	16792	19.66276347	1	0.72282582	84.06248713
GOTERM BP DIRECT GO:0043154--negative regulation of cysteine-type endopeptidase activity involved in	5	1.0799136	0.0979668	XIAP, VEGFA, HGF, THBS1, DNAJB6	427	69	16792	2.849675865	1	0.722306814	84.13004748
GOTERM BP DIRECT GO:0031954--positive regulation of protein autophosphorylation	3	0.6479482	0.0982779	RAP2C, VEGFA, RASSF2	427	21	16792	5.617932419	1	0.721917161	84.24741176
GOTERM BP DIRECT GO:0097150--neural stem cell population maintenance	3	0.6479482	0.0982779	NOTCH1, FOXO1, FOXO3	427	21	16792	5.617932419	1	0.721917161	84.24741176
GOTERM BP DIRECT GO:0031016--pancreas development	3	0.6479482	0.0982779	SMAD2, TCF7L2, CTNNB1	427	21	16792	5.617932419	1	0.721917161	84.24741176
GOTERM BP DIRECT GO:0071480--cellular response to gamma radiation	3	0.6479482	0.0982779	CDKN1A, CHEK2, YAP1	427	21	16792	5.617932419	1	0.721917161	84.24741176
GOTERM BP DIRECT GO:1900182--positive regulation of protein localization to nucleus	3	0.6479482	0.0982779	TRIM8, SESN2, TGFBI2	427	21	16792	5.617932419	1	0.721917161	84.24741176
GOTERM BP DIRECT GO:0051894--positive regulation of focal adhesion assembly	3	0.6479482	0.0982779	VEGFA, SMAD3, KDR	427	21	16792	5.617932419	1	0.721917161	84.24741176
GOTERM BP DIRECT GO:0042127--regulation of cell proliferation	9	1.9438445	0.0994809	TNFRSF10A, CDKN1B, TNFRSF10B, XIAP	427	185	16792	1.913133743	1	0.724905829	84.61867105

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM CC	DIRECT GO:0005654--nucleoplasm	134	28.94168	1.16E-15	MORF4L1, NRBP1, THRB, RBM	443	2784	18224	1.980047	4.83E-13	4.83E-13	1.57E-12
GOTERM CC	DIRECT GO:0005634--nucleus	206	44.49244	5.80E-14	DLCL1, LDHA, TRAPPC2B, TUBI	443	5415	18224	1.56498	2.52E-11	1.26E-11	8.18E-11
GOTERM CC	DIRECT GO:0005829--cytosol	140	30.23758	6.72E-12	DLCL1, LDHA, NRBP1, TBK1, FC	443	3315	18224	1.737339	2.92E-09	9.74E-10	9.48E-09
GOTERM CC	DIRECT GO:0005737--cytoplasm	192	41.46868	2.84E-11	GNAI3, DLCL1, MTSS1, LDHA, T	443	5222	18224	1.512531	1.23E-08	3.08E-09	4.00E-08
GOTERM CC	DIRECT GO:0030529--intracellular ribonucleoprotein complex	17	3.671706	1.99E-07	SNRPA1, ACTN4, G3BP2, CASC	443	136	18224	5.142212	8.67E-05	1.73E-05	2.81E-04
GOTERM CC	DIRECT GO:0005925--focal adhesion	29	6.263499	3.59E-07	GNAI3, DLCL1, FERMT2, GJA1,	443	391	18224	3.051134	1.56E-04	2.60E-05	5.07E-04
GOTERM CC	DIRECT GO:0005768--endosome	21	4.535637	6.35E-07	EGFR, HMGB1, PLD1, FLT1, RA	443	225	18224	3.839518	2.76E-04	3.94E-05	8.96E-04
GOTERM CC	DIRECT GO:0000790--nuclear chromatin	18	3.887689	4.97E-06	RARG, THRB, CREB1, EZH2, TI	443	193	18224	3.836676	0.002161	2.70E-04	0.007021
GOTERM CC	DIRECT GO:0005667--transcription factor complex	18	3.887689	4.97E-06	SATB2, E2F3, RARG, SMAD4, S	443	193	18224	3.836676	0.002161	2.70E-04	0.007021
GOTERM CC	DIRECT GO:0030027--lamellipodium	15	3.239741	3.65E-05	NRBP1, ARPC3, PLCG1, WASF2	443	160	18224	3.856569	0.015737	0.001761	0.051468
GOTERM CC	DIRECT GO:0048471--perinuclear region of cytoplasm	31	6.695464	2.85E-04	CCNT2, TRAPPC2B, RAB3B, NI	443	621	18224	2.053573	0.1166503	0.012329	0.401819
GOTERM CC	DIRECT GO:0031093--platelet alpha granule lumen	8	1.727862	3.50E-04	A1BG, ACTN4, VEGFA, IGF2, H	443	55	18224	5.983665	0.14112	0.013734	0.492518
GOTERM CC	DIRECT GO:0016605--PML body	10	2.159827	6.26E-04	ATRX, TRIM8, MKNK2, TP53, A	443	98	18224	4.197724	0.238422	0.022441	0.880077
GOTERM CC	DIRECT GO:0005730--nucleolus	37	7.991361	9.99E-04	CDV3, MTDH, CDC14B, GRB2,	443	857	18224	1.776073	0.352678	0.032901	1.401619
GOTERM CC	DIRECT GO:0030496--midbody	11	2.37581	0.0012	KIF13A, CYLD, RCC2, INCENP,	443	129	18224	3.507866	0.406948	0.036632	1.681429
GOTERM CC	DIRECT GO:0016363--nuclear matrix	9	1.943844	0.002472	XPO1, YEATS4, DNMT3A, SAI	443	97	18224	3.8169	0.659298	0.069267	3.434298
GOTERM CC	DIRECT GO:0043234--protein complex	21	4.535637	0.002688	SUZ12, SP1, KDM5A, TCF7L2, C	443	412	18224	2.096824	0.689944	0.070574	3.729257
GOTERM CC	DIRECT GO:0032993--protein-DNA complex	15	1.079914	0.002882	SUZ12, SP1, KDM5A, TCF7L2, C	443	25	18224	8.22754	0.715111	0.0712	3.993383
GOTERM CC	DIRECT GO:0005741--mitochondrial outer membrane	11	2.37581	0.003481	MPF, CISD2, MCCL1, PHB2, BCL	443	149	18224	3.037011	0.78058	0.080812	4.803569
GOTERM CC	DIRECT GO:0016020--membrane	72	15.50076	0.007142	GNAI3, LDHA, NRBP1, RAB5B	443	2200	18224	1.346325	0.955752	0.151344	9.624306
GOTERM CC	DIRECT GO:0043292--contractile fiber	3	0.647948	0.011369	PPP1R12A, GJA1, DEK	443	7	18224	17.63044	0.993083	0.220179	14.90726
GOTERM CC	DIRECT GO:0016324--apical plasma membrane	15	3.239741	0.01186	EGFR, PAR6B, PLD1, MTDH, I	443	291	18224	2.1205	0.994428	0.218971	15.50227
GOTERM CC	DIRECT GO:0009986--cell surface	23	4.967603	0.013339	EGFR, DCBLD2, HMGB1, FERM	443	542	18224	1.745696	0.997096	0.233196	17.27029
GOTERM CC	DIRECT GO:0071141--SMAD protein complex	3	0.647948	0.014917	SMAD4, SMAD3, SMAD2	443	8	18224	15.42664	0.998552	0.247423	19.11877
GOTERM CC	DIRECT GO:0015629--actin cytoskeleton	12	2.591793	0.017612	PPP, MTSS1, ACTN4, ARPC3, ZP	443	218	18224	2.26446	0.99956	0.273351	22.18766
GOTERM CC	DIRECT GO:0009898--cytoplasmic side of plasma membrane	5	1.079914	0.01848	RGS2, TRPN4, IKKB, PTEN, R	443	42	18224	4.897345	0.999701	0.277154	23.15231
GOTERM CC	DIRECT GO:0036464--cytoplasmic ribonucleoprotein granule	4	0.863931	0.021938	TUBB, ROCK2, PABPC1, RPS4B	443	25	18224	6.582032	0.999936	0.310047	26.88807
GOTERM CC	DIRECT GO:0005739--mitochondrion	45	9.719222	0.022422	APO1, CYP11B1, MCCL1, CLPB,	443	1331	18224	1.390831	0.999948	0.306053	27.39715
GOTERM CC	DIRECT GO:0070062--extracellular exosome	85	18.35853	0.022537	GNAI3, LDHA, CADM1, WASF,	443	2811	18224	1.243936	0.999951	0.298224	27.5178
GOTERM CC	DIRECT GO:0005916--fascia adherens	3	0.647948	0.023218	GJA1, CTNNA3, CTNNB1	443	10	18224	12.34131	0.999964	0.296986	28.2717
GOTERM CC	DIRECT GO:0031234--extrinsic component of cytoplasmic side of plasma me	6	1.295896	0.024551	CYLD, KRAS, TIAM1, FERMT2,	443	68	18224	3.629797	0.99998	0.30263	29.59803
GOTERM CC	DIRECT GO:0005793--endoplasmic reticulum-Golgi intermediate compart	6	1.295896	0.024551	HMGB1, TRAPPC2B, DICER1, S	443	68	18224	3.629797	0.99998	0.30263	29.59803
GOTERM CC	DIRECT GO:0005911--cell-cell junction	10	2.159827	0.024683	CADM1, ACTN4, PLCG1, TIAM	443	172	18224	2.391727	0.999981	0.295809	29.73208
GOTERM CC	DIRECT GO:0005719--nuclear euchromatin	4	0.863931	0.026928	JUN, CREB1, H2AFZ, CTNNB1	443	27	18224	6.094474	0.999993	0.310008	31.98163
GOTERM CC	DIRECT GO:0005819--spindle	8	1.727862	0.0281	CYLD, EVI5, INCENP, KLHL42,	443	121	18224	2.719848	0.999996	0.313203	33.12914
GOTERM CC	DIRECT GO:0045177--apical part of cell	6	1.295896	0.0355	VCAM1, PAR6B, HFE, MSN, C	443	75	18224	3.291016	1	0.370263	39.96928
GOTERM CC	DIRECT GO:0005856--cytoskeleton	16	3.455724	0.037701	PPP1R18, WASF3, FERMT2, PTI	443	371	18224	1.774133	1	0.379748	41.87344
GOTERM CC	DIRECT GO:0000164--protein phosphatase type 1 complex	3	0.647948	0.038367	PPP1R11, SHOC2, PPP1R15B	443	13	18224	9.493315	1	0.376699	42.43958
GOTERM CC	DIRECT GO:0005721--pericentric heterochromatin	3	0.647948	0.038367	ATRX, INCENP, DNMT1	443	13	18224	9.493315	1	0.376699	42.43958
GOTERM CC	DIRECT GO:0001725--stress fiber	5	1.079914	0.041722	ACTN4, FSCN1, FERMT2, SEPT	443	54	18224	3.809046	1	0.394101	45.21107
GOTERM CC	DIRECT GO:0090575--RNA polymerase II transcription factor complex	4	0.863931	0.045189	GATA4, SMAD4, STAT3, HNRN	443	33	18224	4.986388	1	0.411008	47.94389
GOTERM CC	DIRECT GO:0070435--Shc-EGFR complex	2	0.431965	0.047921	EGFR, SHC1	443	2	18224	41.1377	1	0.421739	50.00768
GOTERM CC	DIRECT GO:0071144--SMAD2-SMAD3 protein complex	2	0.431965	0.047921	SMAD3, SMAD2	443	2	18224	41.1377	1	0.421739	50.00768
GOTERM CC	DIRECT GO:0070369--beta-catenin-TCF7L2 complex	2	0.431965	0.047921	TCF7L2, CTNNB1	443	2	18224	41.1377	1	0.421739	50.00768
GOTERM CC	DIRECT GO:0005802--trans-Golgi network	8	1.727862	0.048026	RAB30, PLEKHA8, STX16, ATP	443	136	18224	2.419865	1	0.414471	50.08571
GOTERM CC	DIRECT GO:0000307--cyclin-dependent protein kinase holoenzyme complex	3	0.647948	0.050036	CDKN1A, CCND2, CDK6	443	15	18224	8.22754	1	0.419936	51.55363
GOTERM CC	DIRECT GO:0005913--cell-cell adherens junction	14	3.023758	0.051936	EGFR, LDHA, CADM1, FSCN1,	443	323	18224	1.783058	1	0.424425	52.90386
GOTERM CC	DIRECT GO:0031965--nuclear membrane	11	2.37581	0.052921	EGFR, MTDH, LMNB1, CCND2,	443	229	18224	1.976047	1	0.423078	53.58953
GOTERM CC	DIRECT GO:0000771--condensed chromosome kinetochore	6	1.295896	0.060354	CENPS, TP53BP1, INCENP, RA	443	87	18224	2.837083	1	0.4596	58.47356
GOTERM CC	DIRECT GO:0044291--cell-cell contact zone	3	0.647948	0.062796	RAP2C, TIAM1, FLOT1	443	17	18224	7.259594	1	0.465768	59.97356
GOTERM CC	DIRECT GO:0044521--membrane raft	10	2.159827	0.063827	EGFR, KRAS, PDXL, FLOT1, C	443	206	18224	1.996976	1	0.464047	60.59096
GOTERM CC	DIRECT GO:0071944--cell periphery	4	0.863931	0.068157	PHB2, RHOA, MSN, CTNNB1	443	39	18224	4.219251	1	0.479695	63.08737
GOTERM CC	DIRECT GO:0032444--activin responsive factor complex	2	0.431965	0.071015	SMAD4, SMAD2	443	3	18224	27.42513	1	0.487043	64.65383
GOTERM CC	DIRECT GO:0031528--microvillus membrane	3	0.647948	0.076515	PODXL, MSN, CTNNB1	443	19	18224	6.495426	1	0.50671	67.49642
GOTERM CC	DIRECT GO:0043209--myelin sheath	8	1.727862	0.077302	BCL2, PGAM4, FSCN1, NDRG1,	443	152	18224	2.165142	1	0.503389	67.88557
GOTERM CC	DIRECT GO:0005938--cell cortex	7	1.511879	0.07908	PPN1, PAR6B, NRBP1, FERMT	443	123	18224	2.34117	1	0.50474	68.74815
GOTERM CC	DIRECT GO:0031463--Cul3-RING ubiquitin ligase complex	5	1.079914	0.079546	PPP, KLHL28, KLHL42, KEAP1, I	443	67	18224	3.069977	1	0.500125	68.97085
GOTERM CC	DIRECT GO:0005637--nuclear inner membrane	4	0.863931	0.085865	LMNB1, SMAD3, DPY19L1, MA	443	43	18224	3.826763	1	0.52138	71.8463
GOTERM CC	DIRECT GO:0043235--receptor complex	7	1.511879	0.088996	EGFR, ACVR1B, NOTCH2, IGF1	443	127	18224	2.267432	1	0.52803	73.17746
GOTERM CC	DIRECT GO:0030175--filopodium	5	1.079914	0.093723	VCAM1, PODXL, FSCN1, AB12,	443	71	18224	2.897021	1	0.54083	75.077
GOTERM CC	DIRECT GO:0005622--intracellular	41	8.855292	0.094001	RAB5B, ADCY6, BTF, BAP1, IL	443	1332	18224	1.26625	1	0.535511	75.18461
GOTERM CC	DIRECT GO:0005720--nuclear heterochromatin	3	0.647948	0.09863	ATRX, DNMT3A, H2AFZ	443	22	18224	5.609686	1	0.547269	76.91594

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM MF DIRECT	GO:0005515--protein binding	303	65.44276	7.69E-16	DLG1, LD	427	8785	16881	1.36355	5.21E-13	5.21E-13	1.17E-12
GOTERM MF DIRECT	GO:0003682--chromatin binding	35	7.559395	3.55E-10	CCNT2, M	427	391	16881	3.538845	2.38E-07	1.19E-07	5.32E-07
GOTERM MF DIRECT	GO:0031490--chromatin DNA binding	13	2.807775	1.78E-08	SUZ12, NC	427	58	16881	8.6106	1.20E-05	3.98E-06	2.67E-05
GOTERM MF DIRECT	GO:0019901--protein kinase binding	30	6.479482	1.02E-07	CCNT2, G	427	376	16881	3.154305	6.85E-05	1.71E-05	1.53E-04
GOTERM MF DIRECT	GO:0043565--sequence-specific DNA binding	35	7.559395	3.84E-07	FOXA2, TI	427	518	16881	2.671213	2.57E-04	5.15E-05	5.76E-04
GOTERM MF DIRECT	GO:0008134--transcription factor binding	24	5.183585	9.51E-07	HMBG1, F	427	284	16881	3.340898	6.37E-04	1.06E-04	0.001425
GOTERM MF DIRECT	GO:0044212--transcription regulatory region DNA binding	19	4.103672	8.05E-06	ZNF831, F	427	213	16881	3.526503	0.005379	7.70E-04	0.012067
GOTERM MF DIRECT	GO:0003700--transcription factor activity, sequence-specific DNA binding	48	10.36717	1.06E-05	HMBG1, E	427	961	16881	1.974641	0.007096	8.90E-04	0.015933
GOTERM MF DIRECT	GO:0044822--poly(A) RNA binding	53	11.44708	1.85E-05	ZMAT3, R	427	1129	16881	1.85589	0.012311	0.001375	0.027715
GOTERM MF DIRECT	GO:0003725--double-stranded RNA binding	9	1.943844	1.41E-04	LSM14A, I	427	61	16881	5.832879	0.089903	0.009376	0.201574
GOTERM MF DIRECT	GO:0001228--transcriptional activator activity, RNA polymerase II transcription i	11	2.375811	1.41E-04	EP300, GA	427	95	16881	4.577616	0.089959	0.008533	0.21071
GOTERM MF DIRECT	GO:0001085--RNA polymerase II transcription factor binding	8	1.727862	1.63E-04	MTDH, G	427	47	16881	6.729184	0.103534	0.009067	0.244265
GOTERM MF DIRECT	GO:0035257--nuclear hormone receptor binding	6	1.295896	1.85E-04	NCOA2, E	427	22	16881	10.78199	0.116344	0.009469	0.276386
GOTERM MF DIRECT	GO:0008013--beta-catenin binding	10	2.159827	2.19E-04	PCP0, GS	427	82	16881	4.821214	0.136642	0.01044	0.328228
GOTERM MF DIRECT	GO:0005168--neurotrophin TRKA receptor binding	4	0.863931	3.02E-04	PLCG1, GI	427	6	16881	26.35597	0.182971	0.013382	0.451163
GOTERM MF DIRECT	GO:0003713--transcription coactivator activity	17	3.671706	5.85E-04	MTDH, R	427	248	16881	2.709989	0.324463	0.024217	0.873868
GOTERM MF DIRECT	GO:0003677--DNA binding	64	13.82289	8.15E-04	EZF3, ZNF	427	1674	16881	1.511454	0.42097	0.03163	1.215204
GOTERM MF DIRECT	GO:0003924--GTPase activity	16	3.455724	9.17E-04	GNA13, R	427	234	16881	2.703177	0.459197	0.033574	1.366602
GOTERM MF DIRECT	GO:0005158--insulin receptor binding	6	1.295896	9.88E-04	IGF1R, PD	427	31	16881	7.651734	0.484381	0.034262	1.471252
GOTERM MF DIRECT	GO:0003690--double-stranded DNA binding	9	1.943844	9.91E-04	LSM14A, I	427	81	16881	4.392662	0.485395	0.032672	1.715591
GOTERM MF DIRECT	GO:0019903--protein phosphatase binding	8	1.727862	0.001015	EGFR, CD	427	63	16881	5.020185	0.493736	0.031894	1.511614
GOTERM MF DIRECT	GO:0000978--RNA polymerase II core promoter proximal region sequence-specif	20	4.319654	0.001776	FOXA2, ZI	427	355	16881	2.227265	0.696009	0.052687	2.629209
GOTERM MF DIRECT	GO:0019903--GDP binding	7	1.511879	0.002314	RAB3B, K	427	54	16881	5.124772	0.788146	0.065246	3.412895
GOTERM MF DIRECT	GO:0001102--RNA polymerase II activating transcription factor binding	6	1.295896	0.002326	EP300, TP	427	38	16881	6.242204	0.81637	0.068182	3.721413
GOTERM MF DIRECT	GO:0042802--identical protein binding	33	7.12743	0.002648	MTS1, LI	427	749	16881	1.741817	0.83076	0.068592	3.897062
GOTERM MF DIRECT	GO:0031625--ubiquitin protein ligase binding	17	3.671706	0.002667	EGFR, TP	427	287	16881	2.341733	0.832886	0.066497	3.924238
GOTERM MF DIRECT	GO:0003723--RNA binding	26	5.615551	0.003264	RBM15B, A	427	547	16881	1.879128	0.888154	0.07793	4.78365
GOTERM MF DIRECT	GO:0003886--DNA (cytosine-5--methyltransferase activity	3	0.647948	0.003686	DNMT3A, A	427	4	16881	29.65047	0.915754	0.084567	5.385501
GOTERM MF DIRECT	GO:0005525--GTP binding	20	4.319654	0.004423	GNA13, R	427	384	16881	2.059016	0.941169	0.093072	6.142653
GOTERM MF DIRECT	GO:0001076--transcription factor activity, RNA polymerase II transcription factor	4	0.863931	0.004721	GATA4, SI	427	14	16881	11.29542	0.958003	0.1003	6.849273
GOTERM MF DIRECT	GO:0019899--enzyme binding	18	3.887689	0.004914	EGFR, CY	427	333	16881	2.136971	0.963137	0.100998	7.19318
GOTERM MF DIRECT	GO:0035035--histone acetyltransferase binding	5	1.079914	0.005067	SP1, ETS1	427	28	16881	7.059635	0.966733	0.10089	7.332398
GOTERM MF DIRECT	GO:0009008--DNA-methyltransferase activity	3	0.647948	0.00604	DNMT3A, A	427	5	16881	23.72037	0.98274	0.115747	8.68317
GOTERM MF DIRECT	GO:0003705--transcription factor activity, RNA polymerase II distal enhancer seq	7	1.511879	0.006324	GATA6, JL	427	66	16881	4.192996	0.985739	0.117509	9.072244
GOTERM MF DIRECT	GO:0000977--RNA polymerase II regulatory region sequence-specific DNA bindi	13	2.807775	0.006694	RARG, KL	427	208	16881	2.470872	0.988889	0.120646	5.977818
GOTERM MF DIRECT	GO:0005200--structural constituent of cytoskeleton	9	1.943844	0.006725	YEATS5, I	427	110	16881	3.234597	0.989123	0.110291	9.621759
GOTERM MF DIRECT	GO:0001190--transcriptional activator activity, RNA polymerase II transcription f	4	0.863931	0.006997	NOTCH1, I	427	16	16881	9.883489	0.990945	0.119397	9.991808
GOTERM MF DIRECT	GO:0001077--transcriptional activator activity, RNA polymerase II core promoter	14	3.023758	0.007112	TFAM, ZN	427	236	16881	2.345235	0.99162	0.118243	10.14748
GOTERM MF DIRECT	GO:0046982--protein heterodimerization activity	22	4.75162	0.007527	EGFR, CE	427	465	16881	1.870424	0.993849	0.122379	10.76705
GOTERM MF DIRECT	GO:0004842--ubiquitin-protein transferase activity	17	3.671706	0.009638	IPP, XIAP	427	329	16881	2.042788	0.998479	0.149742	13.51435
GOTERM MF DIRECT	GO:0070064--proline-rich region binding	4	0.863931	0.011449	PEN1, CY1	427	19	16881	8.322938	0.999554	0.171529	15.85565
GOTERM MF DIRECT	GO:0019900--kinase binding	7	1.511879	0.01161	LDHA, TL	427	75	16881	3.689836	0.9996	0.16997	16.06098
GOTERM MF DIRECT	GO:0000979--RNA polymerase II core promoter sequence-specific DNA binding	6	1.295896	0.014287	SUZ12, EP	427	57	16881	4.161469	0.999935	0.200859	19.4054
GOTERM MF DIRECT	GO:0004714--transmembrane receptor protein tyrosine kinase activity	5	1.079914	0.014998	EGFR, IGI	427	38	16881	5.201837	0.99996	0.205555	20.2728
GOTERM MF DIRECT	GO:0070412--R-SMAD binding	4	0.863931	0.015141	JUN, SMA	427	21	16881	7.530278	0.999964	0.203209	20.44632
GOTERM MF DIRECT	GO:0001227--transcriptional repressor activity, RNA polymerase II transcription :	6	1.295896	0.016403	KLF12, MI	427	59	16881	4.020402	0.999985	0.214072	21.96019
GOTERM MF DIRECT	GO:0000981--RNA polymerase II transcription factor activity, sequence-specific I	29	6.263499	0.01863	NRBP1, C	427	730	16881	1.570527	0.999997	0.23515	24.56757
GOTERM MF DIRECT	GO:0000982--transcription factor activity, RNA polymerase II core promoter pro	4	0.863931	0.019429	SP1, ETS1	427	23	16881	6.875471	0.999998	0.239563	25.48319
GOTERM MF DIRECT	GO:0050839--cell adhesion molecule binding	6	1.295896	0.019951	VCAM1, P	427	62	16881	3.825867	0.999999	0.240847	26.07555
GOTERM MF DIRECT	GO:0046934--phosphatidylinositol-4,5-bisphosphate 3-kinase activity	6	1.295896	0.019951	EGFR, GR	427	62	16881	3.825867	0.999999	0.240847	26.07555
GOTERM MF DIRECT	GO:0001047--core promoter binding	6	1.295896	0.022575	NOTCH1, I	427	64	16881	3.706309	1.0	0.263591	28.98826
GOTERM MF DIRECT	GO:0030971--receptor tyrosine kinase binding	5	1.079914	0.022738	PITPNM3, A	427	43	16881	4.596972	1.0	0.260786	29.16613
GOTERM MF DIRECT	GO:0016303--1-phosphatidylinositol-3-kinase activity	5	1.079914	0.022738	GRB2, PIK	427	43	16881	4.596972	1.0	0.260786	29.16613
GOTERM MF DIRECT	GO:0000774--adenyl-nucleotide exchange factor activity	3	0.647948	0.025003	SHN1, BA	427	10	16881	11.86019	1.0	0.278379	31.58795
GOTERM MF DIRECT	GO:0005068--transmembrane receptor protein tyrosine kinase adaptor activity	3	0.647948	0.025003	SHC1, IRS	427	10	16881	11.86019	1.0	0.278379	31.58795
GOTERM MF DIRECT	GO:0001223--transcription coactivator binding	3	0.647948	0.025003	CCNT2, TI	427	10	16881	11.86019	1.0	0.278379	31.58795
GOTERM MF DIRECT	GO:0000981--RNA polymerase II transcription factor activity, sequence-specific I	10	2.159827	0.029724	FOXA2, E	427	171	16881	2.311927	1.0	0.317136	36.38947
GOTERM MF DIRECT	GO:0001103--RNA polymerase II repressing transcription factor binding	4	0.863931	0.029806	SP1, GAT	427	27	16881	5.856883	1.0	0.313015	36.46996
GOTERM MF DIRECT	GO:0070411--I-SMAD binding	3	0.647948	0.030057	SMAD4, S	427	11	16881	10.78199	1.0	0.31048	36.71514
GOTERM MF DIRECT	GO:0017124--SH3 domain binding	8	1.727862	0.031222	GRB2, AB	427	119	16881	2.657745	1.0	0.315796	37.84524
GOTERM MF DIRECT	GO:0070410--co-SMAD binding	3	0.647948	0.035475	GATA4, SI	427	12	16881	9.883489	1.0	0.345947	41.81345
GOTERM MF DIRECT	GO:0004672--protein kinase activity	16	3.455724	0.039573	EGFR, NR	427	359	16881	1.761959	1.0	0.372761	45.41133
GOTERM MF DIRECT	GO:0005154--epidermal growth factor receptor binding	4	0.863931	0.042565	GRB2, BT	427	31	16881	5.101156	1.0	0.38979	47.90597
GOTERM MF DIRECT	GO:0002020--protease binding	7	1.511879	0.042667	TNFRSF10	427	101	16881	2.739977	1.0	0.385481	47.98948
GOTERM MF DIRECT	GO:0032794--GTPase activating protein binding	3	0.647948	0.047324	TUBB, FM	427	14	16881	8.471562	1.0	0.412861	51.65619
GOTERM MF DIRECT	GO:0005524--ATP binding	49	10.58315	0.049492	NRBP1, PI	427	1495	16881	1.295762	1.0	0.422193	53.27897
GOTERM MF DIRECT	GO:0051718--DNA (cytosine-5--methyltransferase activity, acting on CpG subst	2	0.431965	0.049836	DNMT3A, A	427	2	16881	39.53396	1.0	0.41938	53.51188
GOTERM MF DIRECT	GO:0005178--integrin binding	7	1.511879	0.049917	VCAM1, E	427	105	16881	2.635597	1.0	0.41495	53.59121
GOTERM MF DIRECT	GO:0004713--protein tyrosine kinase activity	8	1.727862	0.051733	EGFR, IGI	427	133	16881	2.377982	1.0	0.421626	54.90367
GOTERM MF DIRECT	GO:0008083--growth factor activity	9	1.943844	0.053323	BDNF, FG	427	162	16881	2.196331	1.0	0.42666	56.02425
GOTERM MF DIRECT	GO:0005159--insulin-like growth factor receptor binding	3	0.647948	0.053714	IGF2, SHC	427	15	16881	7.906792	1.0	0.424262	56.29564
GOTERM MF DIRECT	GO:0004674--protein serine/threonine kinase activity	16	3.455724	0.054851	CCNT2, N	427	376	16881	1.682296	1.0	0.424603	57.07624
GOTERM MF DIRECT	GO:0004722--protein serine/threonine phosphatase activity	5	1.079914	0.058463	CDC1							