



GOTERM\_BP\_DIRECT GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway 8 0.030904736150815112 4.589448415178532E-6  
 ERBB3, FYN, MET, ZAP70, JAK1, JAK2, SYK, BTK 137 63 12723  
 11.792839763642682 0.004715987360594531 6.750781343167755E-4  
 0.007278264013244051

GOTERM\_BP\_DIRECT GO:0008284~positive regulation of cell proliferation 13  
 0.05022019624507456 1.22114800165754E-5 PTK2, AR, HDAC2, CRKL, HDAC1,  
 PTK2B, RELA, HCLS1, HIPK2, NPM1, RARA, RUNX2 137 245 12723  
 4.9277223298078345 0.012499130019830385 0.0015710023337063284  
 0.01936471110683957

GOTERM\_BP\_DIRECT GO:0034644~cellular response to UV 6  
 0.023178552113111334 1.7615765910380352E-5 EP300, YY1, TP53, ATR, TP73,  
 PIK3R1 137 31 12723 17.974570284906992  
 0.017980780180847034 0.0020140134478972005 0.027933593734874584

GOTERM\_BP\_DIRECT GO:0060396~growth hormone receptor signaling pathway  
 4 0.015452368075407556 2.3339342878108154E-5 PTK2, JAK2, PXN, PIK3R1  
 137 6 12723 61.912408759124084 0.023753149254344907  
 0.0024010931234985655 0.037007984969228414

GOTERM\_BP\_DIRECT GO:0030154~cell differentiation 9 0.034767828169667  
 6.755512575472914E-5 PTK2, PTK2B, FYN, ZAP70, SPI1, JAK1, SPIB, SYK, BTK 137  
 128 12723 6.529824361313868 0.06721834477769117  
 0.006305864054203969 0.10708347712982125

GOTERM\_BP\_DIRECT GO:0006351~transcription, DNA-templated 14  
 0.05408328826392645 1.0335304686352426E-4 MEF2A, AR, ESRRA, THRB, SMAD2,  
 ESR2, NR3C1, NCOA1, HDAC2, HDAC1, NCOA3, JUN, POU2F1, RARA 137 353  
 12723 3.68317445875809 0.10098821879020214 0.008155724735537495  
 0.16378418089590951

GOTERM\_BP\_DIRECT GO:0045087~innate immune response 10  
 0.03863092018851889 1.1729293597904384E-4 PTK2, PTK2B, FYN, RELA, ZAP70,  
 JAK1, JAK2, SRC, SYK, BTK 137 177 12723 5.246814301620685  
 0.11380548518587064 0.008592784157650413 0.185855592753608

GOTERM\_BP\_DIRECT GO:0042771~intrinsic apoptotic signaling pathway in response  
 to DNA damage by p53 class mediator 5 0.019315460094259444  
 1.555613303539516E-4 EP300, HIPK2, TP53, BRCA2, TP73 137 26 12723  
 17.85934868051656 0.14806124131237908 0.010625851456285695  
 0.24642337396514336

GOTERM\_BP\_DIRECT GO:0006978~DNA damage response, signal transduction by  
 p53 class mediator resulting in transcription of p21 class mediator 4  
 0.015452368075407556 1.8513428201494064E-4 HIPK2, TP53, BRCA2, TP73  
 137 11 12723 33.77040477770405 0.17362446351520733  
 0.01184837139127326 0.2932052249721928

GOTERM\_BP\_DIRECT GO:0007179~transforming growth factor beta receptor signaling pathway 6 0.023178552113111334 2.052111788914635E-4  
 PTK2, JUN, HIPK2, SMAD2, SRC, PXN 137 51 12723  
 10.925719192786605 0.19054103967845082 0.012357668176388614  
 0.32495342318400455

GOTERM\_BP\_DIRECT GO:0030833~regulation of actin filament polymerization 4  
 0.015452368075407556 2.449171971362344E-4 PAK3, HCLS1, RASA1, PIK3R2  
 137 12 12723 30.956204379562042 0.22298498935253774  
 0.013918650069296379 0.3877138514407741

GOTERM\_BP\_DIRECT GO:0030335~positive regulation of cell migration 8  
 0.030904736150815112 2.550421228568545E-4 EGFR, RACK1, PTK2, IRS2, PAK1,  
 TRIP6, GRB7, PIK3R1 137 117 12723 6.349990641961444  
 0.23104812382330975 0.01373256717953475 0.40371166297318295

GOTERM\_BP\_DIRECT GO:0048469~cell maturation 5  
 0.019315460094259444 3.141315788270849E-4 CEBPA, AXL, RUNX2, BTK, CTNNB1  
 137 31 12723 14.978808570755826 0.27646499870544594  
 0.016050119636528026 0.4970274976037192

GOTERM\_BP\_DIRECT GO:0009887~organ morphogenesis 5  
 0.019315460094259444 4.5165246242476187E-4 EP300, CRKL, THRB, RELA 137  
 34 12723 13.657148990983254 0.3720577797781941  
 0.02191380808319665 0.7138875019604751

GOTERM\_BP\_DIRECT GO:0048729~tissue morphogenesis 3  
 0.012929676056529656 4.634161675404009E-4  
 AR,CEACAM1,CTNNB1,EGFR,FRS2,MET,PAK1,RARA,RET,SMAD2,SOS1,SRC,TRAF6,WT1  
 137 4 12723 69.65145985401459 0.49913677815799895  
 0.028927629296560565 1.5566774834161675

GOTERM\_BP\_DIRECT GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB signaling 8  
 0.030904736150815112 4.843675873459568E-4  
 TRAF3IP2, TNFRSF1A, FYN, RELA, PRKCE, TRAF6, PRKCB, CTNNB1 137 130  
 12723 5.7149915777653 0.3928743326717269 0.022427385157659296  
 0.765411529086768

GOTERM\_BP\_DIRECT GO:0007229~integrin-mediated signaling pathway 6  
 0.023178552113111334 6.403261716582E-4 LAT, PTK2, PTK2B, ITGB2, SRC, SYK  
 137 65 12723 8.572487366647952 0.48301799210644925  
 0.028277161862875322 1.0106911646121541

GOTERM\_BP\_DIRECT GO:0010225~response to UV-C 3  
 0.011589276056555667 6.710584535404009E-4 YY1, BRCA2, WRN 137 4  
 12723 69.65145985401459 0.49913677815799895 0.028398229296570432  
 1.0589574834161675

GOTERM\_BP\_DIRECT GO:0090003~regulation of establishment of protein localization to plasma membrane 3  
 0.011589276056555667  
 6.710584535404009E-4 AR, PIK3R1, PIK3R2 137 4 12723  
 69.65145985401459 0.49913677815799895 0.028398229296570432

1.0589574834161675  
GOTERM\_BP\_DIRECT GO:0030522~intracellular receptor signaling pathway 3  
0.011589276056555667 6.710584535404009E-4 AR, NCOA1, NCOA3 137  
4 12723 69.65145985401459 0.49913677815799895  
0.028398229296570432 1.0589574834161675  
GOTERM\_BP\_DIRECT GO:0045453~bone resorption 4  
0.015452368075407556 7.279447575528191E-4 PTK2B, TRAF6, SRC, CTNNB1  
137 17 12723 21.851438385573207 0.5276599619269069  
0.02955664541477443 1.1482415967813853  
GOTERM\_BP\_DIRECT GO:0018105~peptidyl-serine phosphorylation 7  
0.027041644131963225 8.17459335903707E-4 PRKCA, HIPK2, MAP4K1, ATR,  
PRKCE, SYK, PRKCB 137 103 12723 6.311459145347601  
0.5692930916036385 0.031878041547504954 1.2885835541408208  
  
GOTERM\_BP\_DIRECT GO:0051091~positive regulation of sequence-specific DNA  
binding transcription factor activity 6 0.023178552113111334  
0.0010219059356810392 EP300, HIPK2, ESR2, PPARGC1A, ATF2, CTNNB1 137  
72 12723 7.739051094890511 0.6511458284535492  
0.038252898860837714 1.6084174342240631  
GOTERM\_BP\_DIRECT GO:0045669~positive regulation of osteoblast differentiation  
5 0.019315460094259444 0.001560468789322249 CEBPA, CEBPD, IL6ST,  
RUNX2, CTNNB1 137 47 12723 9.879639695604906  
0.7998199798448491 0.055828818977100236 2.446297426265398  
  
GOTERM\_BP\_DIRECT GO:0008285~negative regulation of cell proliferation 9  
0.034767828169667 0.0016037165672220211 CEBPA, KAT2B, HNF4A, TSG101,  
PTK2B, JUN, NPM1, ZBTB16, CTNNB1 137 205 12723 4.077158625600855  
0.8085548652604172 0.055410947198889726 2.5132902295239457  
  
GOTERM\_BP\_DIRECT GO:0009952~anterior/posterior pattern specification 6  
0.023178552113111334 0.0016403988573511462 CRKL, YY1, HIPK2, SMAD2, ZBTB16  
137 80 12723 6.965145985401461 0.8156645638116815  
0.05480744021391226 2.5700790009062113  
GOTERM\_BP\_DIRECT GO:0090330~regulation of platelet aggregation 3  
0.011589276056555667 0.0016542146407096477 PRKCA, ZAP70, SYK 137  
6 12723 46.434306569343065 0.8182733956928632  
0.0535225428310655 2.5914595244572736  
GOTERM\_BP\_DIRECT GO:0043524~negative regulation of neuron apoptotic process  
6 0.023178552113111334 0.0017335375867979055 BRAF, JUN, HIPK2, AXL,  
PPARGC1A, TP73 137 81 12723 6.879156528791565  
0.8325537975839501 0.05431586517158271 2.7141301702301113  
  
GOTERM\_BP\_DIRECT GO:0010332~response to gamma radiation 4  
0.015452368075407556 0.0018090633691630945 TP53, BRCA2, CHEK2, TP73

137	23	12723	16.15106315455411	0.8451073141976289
0.05494848614178005		2.8307940829769396		
GOTERM_BP_DIRECT		GO:0035556~intracellular signal transduction		10
0.03863092018851889		0.0022162989143147283	PRKCA, BRAF, ARHGEF7, ZAP70,	
JAK1, SMAD2, JAK2, PRKCE, SRC, PRKCB		137	266	12723
3.4913012458152677		0.8982586322188633		0.06500615465059711
3.4575911160603545				
GOTERM_BP_DIRECT		GO:0043066~negative regulation of apoptotic process		9
0.034767828169667		0.0022903777943246786	EGFR, PTK2, SIN3A, PTK2B, NPM1,	
TP53, RARA, PIK3R1, BARD1		137	217	12723
0.9057490961762152		0.065253447450078		3.571201679395275
GOTERM_BP_DIRECT		GO:0045892~negative regulation of transcription, DNA-		
templated	9	0.034767828169667	0.0028637723053117205	XRCC5,
COPS2, SUMO1, ID2, CEBPD, TSG101, POU2F1, SMAD2, RUNX2		137	225	12723
3.714744525547445		0.9478649165068092		0.07877710206062838
4.4463563716404035				
GOTERM_BP_DIRECT		GO:0002281~macrophage activation involved in immune		
response	3	0.011589276056555667	0.0030448109002816403	ZAP70,
PRKCE, SYK		137	8	12723
0.9567578446358621		0.08138690808338322		4.721120681680102
GOTERM_BP_DIRECT		GO:0061029~eyelid development in camera-type eye		
3		0.011589276056555667	0.0038874021940563516	EGFR, JUN, SOS1
9	12723	30.956204379562045		137
0.1001924733031635		5.990218610070375		0.9818997063064484
GOTERM_BP_DIRECT		GO:0031571~mitotic G1 DNA damage checkpoint		3
0.011589276056555667		0.0038874021940563516	CCND1, TP53, TP73	137
9	12723	30.956204379562045		0.9818997063064484
0.1001924733031635		5.990218610070375		
GOTERM_BP_DIRECT		GO:0050853~B cell receptor signaling pathway		4
0.015452368075407556		0.003927266296436534	CD19, ZAP70, SYK, PRKCB	137
30	12723	12.382481751824816		0.9826306514667185
0.09870648890544098		6.049867119585317		
GOTERM_BP_DIRECT		GO:0051897~positive regulation of protein kinase B signaling		
5		0.019315460094259444	0.004569855142309874	EGFR, PTK2, HCLS1, AXL,
SRC	137	63	12723	7.370524852276676
0.11125370613187935		7.006491154168659		0.9910646388986338
GOTERM_BP_DIRECT		GO:0050730~regulation of peptidyl-tyrosine phosphorylation		
3		0.011589276056555667	0.0048253267880044555	EGFR, ITGB2, PRKCE
137	10	12723	27.860583941605842	0.9931404706804025
0.11442226177759629		7.384270983209696		
GOTERM_BP_DIRECT		GO:0016477~cell migration		6
0.023178552113111334		0.005331852147520749	PLCG1, FYN, JAK1, JAK2, VAV2, SRC	

137	105	12723	5.306777893639208	0.9959397093362428
0.12287622314298241		8.129049611354755		
GOTERM_BP_DIRECT		GO:0042993~positive regulation of transcription factor import into nucleus	3	0.011589276056555667
0.005856480678072418		HCLS1, PIK3R1, PIK3R2	137	11
0.9976419211210563		0.13124622386610385	12723	25.327803583278037
			8.894528071979336	
GOTERM_BP_DIRECT		GO:0071480~cellular response to gamma radiation	3	0.011589276056555667
0.005856480678072418		XRCC5, ATR, WRN	137	11
12723		25.327803583278037	0.9976419211210563	0.13124622386610385
8.894528071979336				
GOTERM_BP_DIRECT		GO:0048514~blood vessel morphogenesis	3	0.011589276056555667
0.006978793374280826		SOS1, RASA1, SYK	137	12
12723		23.217153284671532	0.9992633199006299	
0.15120699068461252		10.512058526725932		
GOTERM_BP_DIRECT		GO:0043923~positive regulation by host of viral transcription	3	0.011589276056555667
0.006978793374280826		EP300, SP1, JUN	137	12
12723		23.217153284671532	0.9992633199006299	
0.15120699068461252		10.512058526725932		
GOTERM_BP_DIRECT		GO:0050852~T cell receptor signaling pathway	4	0.015452368075407556
0.00711864368542506		PLCG1, FYN, ZAP70, TRAF6	137	37
12723		10.039850069047148	0.9993627988560473	
0.15085095939249682		10.711721342901726		
GOTERM_BP_DIRECT		GO:0010165~response to X-ray	3	0.011589276056555667
0.008190227431753206		TP53, BRCA2, TP73	137	13
12723		21.431218416619874	0.9997904755581981	
0.16818482097840237		12.227816053598872		
GOTERM_BP_DIRECT		GO:0006302~double-strand break repair	4	0.015452368075407556
0.00824424433245782		BRCA2, WRN, CHEK2, PARP1	137	39
12723		9.524985962942168	0.9998019059300758	
0.16591553704313844		12.303597795003984		
GOTERM_BP_DIRECT		GO:0048538~thymus development	4	0.015452368075407556
0.00824424433245782		CRKL, BRAF, CTNNB1	137	39
12723		9.524985962942168	0.9998019059300758	
0.16591553704313844		12.303597795003984		
GOTERM_BP_DIRECT		GO:0045893~positive regulation of transcription, DNA-templated	8	0.030904736150815112
0.010271021325308185		AR, TRIP4, NPM1, BRCA2, ZBTB16, ESR2, CHEK2, PPARGC1A	137	224
12723		3.3167361835245046	0.999975913431926	0.19871506504391845
15.103116109553739				
GOTERM_BP_DIRECT		GO:0045766~positive regulation of angiogenesis	5	0.019315460094259444
0.010561254583453826		PRKCA, PLCG1, PTK2B, HIPK2, PRKCB	137	80
12723		5.804288321167883	0.9999821934296923	0.20003116732698956
15.497082175677079				

GOTERM_BP_DIRECT	GO:0007569~cell aging	3	0.011589276056555667		
0.010872472319078877	NPM1, BRCA2, WRN	137	15	12723	
18.573722627737226	0.9999871217391284			0.20164298745566633	
15.91762926739838					
GOTERM_BP_DIRECT	GO:0006303~double-strand break repair via nonhomologous end joining	3	0.011589276056555667	0.012339369364973186	XRCC5, XRCC6
137	16	12723	17.412864963503647	0.9999972076176735	
0.2217886749105228	17.87356990933673				
GOTERM_BP_DIRECT	GO:0043525~positive regulation of neuron apoptotic process	3	0.011589276056555667	0.012339369364973186	TP53, FOXO3, CTNNB1
137	16	12723	17.412864963503647	0.9999972076176735	
0.2217886749105228	17.87356990933673				
GOTERM_BP_DIRECT	GO:0030225~macrophage differentiation	3	0.011589276056555667	0.012339369364973186	CEBPA, SPI1, SPIB
16	12723	17.412864963503647	0.9999972076176735		
0.2217886749105228	17.87356990933673				
GOTERM_BP_DIRECT	GO:0046677~response to antibiotic	3	0.011589276056555667	0.012339369364973186	TP53, JAK1, JAK2
16	12723	17.412864963503647	0.9999972076176735		
0.2217886749105228	17.87356990933673				
GOTERM_BP_DIRECT	GO:0070374~positive regulation of ERK1 and ERK2 cascade	6	0.023178552113111334	0.013608602688121654	EGFR, BRAF, PTK2B, JUN, RAP1A, SRC
137	132	12723	4.221300597213006	0.999999257401208	
0.23769303258233188	19.531465180530617				
GOTERM_BP_DIRECT	GO:0033209~tumor necrosis factor-mediated signaling pathway	3	0.011589276056555667	0.013887559312464789	PTK2B, JAK2, FOXO3
0.999999445079226	0.23797955725445175	137	17	12723	16.388578789179906
					19.891615115209373
GOTERM_BP_DIRECT	GO:0000723~telomere maintenance	3	0.011589276056555667	0.013887559312464789	XRCC5, XRCC6
12723	16.388578789179906	0.999999445079226	0.23797955725445175		
19.891615115209373					
GOTERM_BP_DIRECT	GO:0051092~positive regulation of NF-kappaB transcription factor activity	5	0.019315460094259444	0.014041479466406723	AR, RELA, NPM1, TRAF6, PRKCB
0.9999995274978309	0.2364115867553479	137	87	12723	5.33727661716587
					20.089688252092884
GOTERM_BP_DIRECT	GO:0042981~regulation of apoptotic process	6	0.023178552113111334	0.015760776591550424	TNFRSF1A, FYN, JAK2, WRN, TRAF6, FRS2
137	137	12723	4.067238531621291	0.9999999217132293	
0.25733264524141	22.271210144154253				
GOTERM_BP_DIRECT	GO:0045444~fat cell differentiation	4			

0.015452368075407556	0.018034640613624874	CCND1, EP300, CEBPD, ATF2	
137	52	12723	7.143739472206625
0.28447314460059026	25.07076541206754		0.9999999927714273
GOTERM_BP_DIRECT	GO:0007050~cell cycle arrest		4
0.015452368075407556	0.018034640613624874	CCND1, TSG101, TP53, TP73	
137	52	12723	7.143739472206625
0.28447314460059026	25.07076541206754		0.9999999927714273
GOTERM_BP_DIRECT	GO:0007283~spermatogenesis		6
0.023178552113111334	0.020722342195596342	DNMT3A, YY1, AXL, BRCA2, RARA, H2AFX	
137	147	12723	3.79055563831372
0.3150371060281867	28.25796103397291		0.999999995704423
GOTERM_BP_DIRECT	GO:0060395~SMAD protein signal transduction		4
0.015452368075407556	0.02092143855575059	HNF4A, JUN, HIPK2, SMAD2	
137	55	12723	6.754080955540809
0.31303882159577345	28.48893201811109		0.999999996516087
GOTERM_BP_DIRECT	GO:0090241~negative regulation of histone H4 acetylation		
2	0.007726184037703778	0.021265175720108217	CTBP1, SPI1
2	12723	92.86861313868611	0.999999997573432
0.3128781327922687	28.88606126965452		
GOTERM_BP_DIRECT	GO:0007172~signal complex assembly		2
0.007726184037703778	0.021265175720108217	PTK2, PTK2B	137
12723	92.86861313868611	0.999999997573432	0.3128781327922687
28.88606126965452			
GOTERM_BP_DIRECT	GO:0043366~beta selection		2
0.007726184037703778	0.021265175720108217	ZAP70, SYK	137
12723	92.86861313868611	0.999999997573432	0.3128781327922687
28.88606126965452			
GOTERM_BP_DIRECT	GO:0006954~inflammatory response		7
0.027041644131963225	0.021797320061524916	LAT, TNFRSF1A, RELA, AXL, ZAP70, JAK2, SYK	
137	203	12723	3.2023659702995215
0.999999998614157	0.3149926534592714	29.496789196982753	
GOTERM_BP_DIRECT	GO:0010634~positive regulation of epithelial cell migration		
3	0.011589276056555667	0.022783190799986808	JUN, PRKCE, SRC
22	12723	12.663901791639018	0.9999999950948
0.3223672770293362	30.615281963698838		
GOTERM_BP_DIRECT	GO:0032870~cellular response to hormone stimulus		
3	0.011589276056555667	0.022783190799986808	NCOA1, NCOA3, JUN
137	22	12723	12.663901791639018
0.3223672770293362	30.615281963698838		0.9999999950948
GOTERM_BP_DIRECT	GO:0007507~heart development		5
0.019315460094259444	0.022995012951041564	EP300, CRKL, CASP7, GAB1	
137	101	12723	4.597456095974561
0.32055204948008	30.853419097572377		0.9999999960764



GOTERM_BP_DIRECT		GO:0046777~protein autophosphorylation	5
0.019315460094259444	0.02374104648534236	EGFR, MAP4K1, ATR, PAK1, CHEK2	
137	102	12723	4.552382996994418
0.3248558311952673	31.686049502544343		0.999999999982136
GOTERM_BP_DIRECT		GO:0009749~response to glucose	3
0.011589276056555667	0.02684702540011092	IRS2, HNF4A, SMAD2	137
24	12723	11.608576642335766	0.999999999993293
0.35465817772906727	35.05263048626313		
GOTERM_BP_DIRECT		GO:0042177~negative regulation of protein catabolic process	3
0.011589276056555667	0.028980411534981397	EGFR, FYN, RELA	137
25	12723	11.144233576642335	0.99999999999301
0.37250137085781765	37.274264593299776		
GOTERM_BP_DIRECT		GO:0071222~cellular response to lipopolysaccharide	4
0.015452368075407556	0.029786587826840582	RELA, AXL, RARA, TRAF6	137
63	12723	5.896419881821341	0.99999999999702
0.3761935197329185	38.09509427425929		
GOTERM_BP_DIRECT		GO:0007249~I-kappaB kinase/NF-kappaB signaling	3
0.011589276056555667	0.031179237416534035	RELA, TRAF6, BTK	137
26	12723	10.715609208309937	0.99999999999932
0.3855047688541887	39.48939437049442		
GOTERM_BP_DIRECT		GO:0070141~response to UV-A	2
0.007726184037703778	0.031728813492429994	EGFR, CCND1	137
12723	61.912408759124084	0.99999999999962	0.3863851471841593
40.03148086606344			
GOTERM_BP_DIRECT		GO:0043551~regulation of phosphatidylinositol 3-kinase activity 2	3
0.007726184037703778	0.031728813492429994	PIK3R1, PIK3R2	137
137	3	12723	61.912408759124084
0.3863851471841593	40.03148086606344		0.99999999999962
GOTERM_BP_DIRECT		GO:0018076~N-terminal peptidyl-lysine acetylation	2
0.007726184037703778	0.031728813492429994	EP300, KAT2B	137
12723	61.912408759124084	0.99999999999962	0.3863851471841593
40.03148086606344			
GOTERM_BP_DIRECT		GO:0007265~Ras protein signal transduction	3
0.011589276056555667	0.03344188241390676	LAT, JUN, TP53	137
12723	10.31873479318735	0.99999999999994	0.39814756015133035
41.69215280267581			
GOTERM_BP_DIRECT		GO:0030155~regulation of cell adhesion	3
0.011589276056555667	0.035766752615894806	PTK2, PTK2B, JAK2	137
28	12723	9.950208550573516	1.0
43.8770738151194		0.41487193133861	
GOTERM_BP_DIRECT		GO:0042493~response to drug	4
0.015452368075407556	0.03618427130269515	CCND1, PTPRM, JUN, CTNNB1	
137	68	12723	5.462859596393302
44.26124044371497		1.0	0.41413113677060476

GOTERM_BP_DIRECT	GO:0071277~cellular response to calcium ion	3
0.011589276056555667	0.03815228045383198	MEF2A, BRAF, JUN 137
29	12723	9.607097910898565 1.0 0.426773159716629
46.03909516886008		
GOTERM_BP_DIRECT	GO:2001237~negative regulation of extrinsic apoptotic signaling pathway	3
0.011589276056555667	0.04059692432160905	AR, 137
RELA, SRC 137	30 12723	9.286861313868613 1.0
0.44275907024816163	48.173558379719914	
GOTERM_BP_DIRECT	GO:0001942~hair follicle development	3
0.011589276056555667	0.04059692432160905	EGFR, SOS1, RELA 137
30 12723	9.286861313868613	1.0 0.44275907024816163
48.173558379719914		
GOTERM_BP_DIRECT	GO:2000301~negative regulation of synaptic vesicle exocytosis	2
0.007726184037703778	0.04208139850599557	BRAF, 137
RAP1A 137	4 12723	46.43430656934306 1.0
0.4503143603110744	49.43080220492719	
GOTERM_BP_DIRECT	GO:0044027~hypermethylation of CpG island	2
0.007726184037703778	0.04208139850599557	DNMT3A, SPI1 137 4
12723 46.43430656934306		1.0 0.4503143603110744
49.43080220492719		
GOTERM_BP_DIRECT	GO:0031052~chromosome breakage	2
0.007726184037703778	0.04208139850599557	CD19, BRCA2 137 4
12723 46.43430656934306		1.0 0.4503143603110744
49.43080220492719		
GOTERM_BP_DIRECT	GO:0002283~neutrophil activation involved in immune response	2
0.007726184037703778	0.04208139850599557	ZAP70, SYK 137 4
137 4 12723	46.43430656934306	1.0 0.4503143603110744
49.43080220492719		
GOTERM_BP_DIRECT	GO:1990182~exosomal secretion	2
0.007726184037703778	0.04208139850599557	COPS5, TSG101 137 4
12723 46.43430656934306		1.0 0.4503143603110744
49.43080220492719		
GOTERM_BP_DIRECT	GO:0010387~COP9 signalosome assembly	2
0.007726184037703778	0.04208139850599557	GPS1, COPS8 137 4
12723 46.43430656934306		1.0 0.4503143603110744
49.43080220492719		
GOTERM_BP_DIRECT	GO:0048660~regulation of smooth muscle cell proliferation	2
0.007726184037703778	0.04208139850599557	XRCC5, CTNNB1 137 4
4 12723	46.43430656934306	1.0 0.4503143603110744
49.43080220492719		
GOTERM_BP_DIRECT	GO:0030218~erythrocyte differentiation	3
0.011589276056555667	0.0430991682148068	HCLS1, SPI1, JAK2 137
31 12723	8.987285142453496	1.0 0.45394146357351217
50.27620592994455		

GOTERM_BP_DIRECT		GO:0030900~forebrain development		3
0.011589276056555667	0.0430991682148068	FYN, FRS2, SRC	137	31
12723	8.987285142453496	1.0	0.45394146357351217	
50.27620592994455				
GOTERM_BP_DIRECT		GO:0030097~hemopoiesis		3
0.011589276056555667	0.04565752135807581	BRCA2, ZBTB16, RUNX2	137	
32	12723	8.706432481751824	1.0	0.469189815828735
52.34317599645439				
GOTERM_BP_DIRECT		GO:0008283~cell proliferation		5
0.019315460094259444	0.04610621059536462	XRCC5, EGFR, COPS2, IRS2,		
MAP4K1	137	126	12723	3.685262426138338
0.4681618288378825	52.697281141909095			1.0
GOTERM_BP_DIRECT		GO:0001764~neuron migration		4
0.015452368075407556	0.046226605933652354	PTK2, FYN, AXL, CTNNB1	137	
75	12723	4.952992700729927	1.0	0.46473200570163653
52.79187668437342				
GOTERM_BP_DIRECT		GO:0034599~cellular response to oxidative stress		3
0.011589276056555667	0.050936716314078895	FOXO3, PARP1, PPARGC1A	137	
34	12723	8.194289394589953	1.0	0.4942044196474731
56.35656802504669				
GOTERM_BP_DIRECT		GO:0008630~intrinsic apoptotic signaling pathway in response to DNA damage	3	
0.011589276056555667	0.050936716314078895			
TNFRSF1A, CHEK2, PIK3R1	137	34	12723	8.194289394589953
0.4942044196474731	56.35656802504669			1.0
GOTERM_BP_DIRECT		GO:0001302~replicative cell aging		2
0.007726184037703778	0.05232410074655598	WRN, CHEK2	137	5
12723	37.14744525547445	1.0	0.4993947625384151	
57.35747118093204				
GOTERM_BP_DIRECT		GO:0042475~odontogenesis of dentin-containing tooth		3
0.011589276056555667	0.05924047012722322	TRAF6, RUNX2, CTNNB1		
137	37	12723	7.529887551785362	1.0
62.03429982209816				0.5400052196350187
GOTERM_BP_DIRECT		GO:0008286~insulin receptor signaling pathway		3
0.011589276056555667	0.062105540833818716	IRS2, PIK3R1, PIK3R2	137	
38	12723	7.331732616212064	1.0	0.5530831814899266
63.827095263542446				
GOTERM_BP_DIRECT		GO:0001889~liver development		3
0.011589276056555667	0.062105540833818716	CEBPA, JUN, RELA	137	
38	12723	7.331732616212064	1.0	0.5530831814899266
63.827095263542446				
GOTERM_BP_DIRECT		GO:0010870~positive regulation of receptor biosynthetic process	2	
0.007726184037703778	0.062458077967384305	HDAC2, HDAC1		
137	6	12723	30.956204379562042	1.0
64.04212770334514				0.5508259435482167

GOTERM\_BP\_DIRECT GO:2000144~positive regulation of DNA-templated transcription, initiation 2 0.007726184037703778 0.062458077967384305  
 JUN, CTNNB1 137 6 12723 30.956204379562042 1.0  
 0.5508259435482167 64.04212770334514

GOTERM\_BP\_DIRECT GO:0042129~regulation of T cell proliferation 2  
 0.007726184037703778 0.062458077967384305 SOS1, CTNNB1 137 6  
 12723 30.956204379562042 1.0 0.5508259435482167  
 64.04212770334514

GOTERM\_BP\_DIRECT GO:0071498~cellular response to fluid shear stress 2  
 0.007726184037703778 0.062458077967384305 PTK2B, SRC 137 6  
 12723 30.956204379562042 1.0 0.5508259435482167  
 64.04212770334514

GOTERM\_BP\_DIRECT GO:0031065~positive regulation of histone deacetylation 2  
 0.007726184037703778 0.062458077967384305 CTBP1, TP53 137 6  
 12723 30.956204379562042 1.0 0.5508259435482167  
 64.04212770334514

GOTERM\_BP\_DIRECT GO:0030851~granulocyte differentiation 2  
 0.007726184037703778 0.062458077967384305 CEBPA, SPI1 137 6  
 12723 30.956204379562042 1.0 0.5508259435482167  
 64.04212770334514

GOTERM\_BP\_DIRECT GO:0051974~negative regulation of telomerase activity 2  
 0.007726184037703778 0.062458077967384305 TP53, SRC 137 6  
 12723 30.956204379562042 1.0 0.5508259435482167  
 64.04212770334514

GOTERM\_BP\_DIRECT GO:0010976~positive regulation of neuron projection development 3  
 0.011589276056555667 0.06797343295386908 PTK2B, FYN, RAP1A 137 40 12723 6.965145985401461 1.0  
 0.5781746970078119 67.25415331960696

GOTERM\_BP\_DIRECT GO:0010763~positive regulation of fibroblast migration 2  
 0.007726184037703778 0.07248447581163689 ARHGEF7, PRKCE 137 7  
 12723 26.533889468196037 1.0 0.5982002321895259  
 69.67930404353879

GOTERM\_BP\_DIRECT GO:0060017~parathyroid gland development 2  
 0.007726184037703778 0.07248447581163689 CRKL 137 7 12723  
 26.533889468196037 1.0 0.5982002321895259 69.67930404353879

GOTERM\_BP\_DIRECT GO:2000394~positive regulation of lamellipodium morphogenesis 2  
 0.007726184037703778 0.07248447581163689  
 ARHGEF7, SRC 137 7 12723 26.533889468196037 1.0  
 0.5982002321895259 69.67930404353879

GOTERM\_BP\_DIRECT GO:0045084~positive regulation of interleukin-12 biosynthetic process 2  
 0.007726184037703778 0.07248447581163689  
 RELA, TRAF6 137 7 12723 26.533889468196037 1.0  
 0.5982002321895259 69.67930404353879

GOTERM\_BP\_DIRECT GO:0046641~positive regulation of alpha-beta T cell  
 proliferation 2 0.007726184037703778 0.07248447581163689  
 ZAP70, SYK 137 7 12723 26.533889468196037 1.0  
 0.5982002321895259 69.67930404353879  
 GOTERM\_BP\_DIRECT GO:0048617~embryonic foregut morphogenesis 2  
 0.007726184037703778 0.07248447581163689 SMAD2, CTNNB1 137 7  
 12723 26.533889468196037 1.0 0.5982002321895259  
 69.67930404353879  
 GOTERM\_BP\_DIRECT GO:0046638~positive regulation of alpha-beta T cell  
 differentiation 2 0.007726184037703778 0.07248447581163689  
 ZAP70, SYK 137 7 12723 26.533889468196037 1.0  
 0.5982002321895259 69.67930404353879  
 GOTERM\_BP\_DIRECT GO:0050821~protein stabilization 4  
 0.015452368075407556 0.08148377841325066 SUMO1, EP300, CHEK2, PIK3R1  
 137 95 12723 3.9102573953131 1.0 0.638673001575449  
 74.02320748610825  
 GOTERM\_BP\_DIRECT GO:0006281~DNA repair 4 0.015452368075407556  
 0.08148377841325066 RFC1, MDC1, NPM1, ATR 137 95 12723  
 3.9102573953131 1.0 0.638673001575449 74.02320748610825  
  
 GOTERM\_BP\_DIRECT GO:0036120~cellular response to platelet-derived growth  
 factor stimulus 2 0.007726184037703778 0.08240442794403974 FYN, SRC  
 137 8 12723 23.21715328467153 1.0 0.6387350367602949  
 74.43307543064552  
 GOTERM\_BP\_DIRECT GO:0090399~replicative senescence 2  
 0.007726184037703778 0.08240442794403974 TP53, ATR 137 8  
 12723 23.21715328467153 1.0 0.6387350367602949  
 74.43307543064552  
 GOTERM\_BP\_DIRECT GO:0031666~positive regulation of lipopolysaccharide-  
 mediated signaling pathway 2 0.007726184037703778 0.08240442794403974  
 PRKCA, TRAF6 137 8 12723 23.21715328467153 1.0  
 0.6387350367602949 74.43307543064552  
 GOTERM\_BP\_DIRECT GO:0001701~in utero embryonic development 5  
 0.019315460094259444 0.0830681032465312 SIN3A, PLCG1, COPS3, SMAD2,  
 CTNNB1 137 154 12723 3.015214712295004 1.0  
 0.6376129687968766 74.72477294843733  
 GOTERM\_BP\_DIRECT GO:0007417~central nervous system development 3  
 0.011589276056555667 0.08338750725628336 FYN, ZBTB16, SRC 137  
 45 12723 6.191240875912409 1.0 0.6349312444517322  
 74.86404271778935  
 GOTERM\_BP\_DIRECT GO:0030520~intracellular estrogen receptor signaling  
 pathway 2 0.007726184037703778 0.09221905616380124 TRIP4, SRC  
 137 9 12723 20.637469586374696 1.0 0.6695417520687516  
 78.44182670550158

GOTERM\_BP\_DIRECT GO:0033630~positive regulation of cell adhesion mediated by integrin 2 0.007726184037703778 0.09221905616380124 ZAP70, SYK 137 9 12723 20.637469586374696 1.0 0.6695417520687516 78.44182670550158

GOTERM\_BP\_DIRECT GO:0042511~positive regulation of tyrosine phosphorylation of Stat1 protein 2 0.007726184037703778 0.09221905616380124 TNFRSF1A, IL6ST 137 9 12723 20.637469586374696 1.0 0.6695417520687516 78.44182670550158

GOTERM\_BP\_DIRECT GO:0051492~regulation of stress fiber assembly 2 0.007726184037703778 0.09221905616380124 PIK3R1, PIK3R2 137 9 12723 20.637469586374696 1.0 0.6695417520687516 78.44182670550158

GOTERM\_BP\_DIRECT GO:0001525~angiogenesis 4 0.015452368075407556 0.09379527811599347 PTK2, PTK2B, JUN, NCL 137 101 12723 3.677964876779649 1.0 0.672011696702598 79.02787937025242

GOTERM\_BP\_DIRECT GO:0030324~lung development 3 0.011589276056555667 0.09640486357924165 CEBPA, EP300, SMAD2 137 49 12723 5.685833457470579 1.0 0.6785607350737112 79.96544624095317

GOTERM\_BP\_DIRECT GO:0006357~regulation of transcription from RNA polymerase II promoter 6 0.023178552113111334 0.09767604373061749 SP1, SPI1, SPIB, RUNX2, ATF2, PRKCB 137 228 12723 2.4439108720706875 1.0 0.679647916124801 80.40779167997474

GOTERM\_BP\_DIRECT GO:0032092~positive regulation of protein binding 3 0.011589276056555667 0.09974496655627385 EP300, ARHGEF7, HIPK2 137 50 12723 5.572116788321168 1.0 0.6837991508686363 81.10822112939256

GOTERM\_CC\_DIRECT GO:0008180~COP9 signalosome 10 0.03863092018851889 6.148414777864875E-12 GPS1, LAT, COPS2, PLCG1, COPS5, COPS6, COPS3, COPS4, COPS7A, COPS8 139 30 14445 34.64028776978417 1.0267853234324775E-9 1.0267853234324775E-9 7.478406782723823E-9

GOTERM\_CC\_DIRECT GO:0005654~nucleoplasm 39 0.15066058873522367 1.2504730995822602E-10 XRCC5, TAF1C, MEF2A, COPS5, COPS6, COPS3, COPS4, COPS7A, NR3C1, FOXO3, PXN, ATF1, ATF2, MDC1, PTK2B, NPM1, GIT2, POU2F1, H2AFX, RUNX2, DNMT3B, KPNB1, DHX9, DNMT3A, CTBP1, TRIP4, BRCA2, CDC20, WRN, NCL, TP73, CCND1, CBLB, NCOA3, RFC1, SP1, JUN, KPNA2, BARD1 139 1277 14445 3.1737773446082596 2.0882899853802428E-8 1.0441450037923516E-8 1.520969683532769E-7

GOTERM\_CC\_DIRECT GO:0005634~nucleus 54 0.20860696901800202 1.1698209396836041E-8 MEF2A, SPI1, FOXO3, BTK, CTNNB1, SPIB, H2AFX, CCNA1, TOP2A, CASP2, SYK, EGFR, CTBP1, AR, RELA, ESR2, PRKCE, PPARGC1A, PRKCB, CCND1, NCOA1, NCOA3, RFC1, HNF4A, NEDD9, CTNND1, NR3C1, SRC, WT1, ATF2, RACK1, PTK2,

SUMO1, MDC1, POU2F1, RUNX2, PIK3R1, PIK3R2, DHX9, ESRRA, TRIP4, KAT2B, CEBPD, HCLS1, BRCA2, SMAD2, ATR, HDAC2, SP1, HDAC1, ID2, JAK1, JAK2, PARP1 139 2601 14445 2.1575265738965923 1.9535990731789354E-6 6.512001151648406E-7 1.422871174217022E-5

GOTERM\_CC\_DIRECT GO:0000790~nuclear chromatin 13  
0.05022019624507456 2.6898437905241945E-8 MEF2A, AR, THRB, TP53, SPI1, SMAD2, NCOA1, NCOA3, SP1, JUN, RARA, H2AFX, RUNX2 139 154 14445 8.772540409231055 4.4920291041306015E-6 1.1230091677694176E-6 3.2716980347125E-5

GOTERM\_CC\_DIRECT GO:0031234~extrinsic component of cytoplasmic side of plasma membrane 9 0.034767828169667 3.491830785856014E-8 PTK2, PTK2B, FYN, ZAP70, JAK1, JAK2, SRC, SYK, BTK 139 53 14445 17.646939052531557 5.831340520789929E-6 1.1662708244708497E-6 4.247166864868035E-5

GOTERM\_CC\_DIRECT GO:0005667~transcription factor complex 13  
0.05022019624507456 4.122304832023394E-8 CTBP1, MEF2A, HCLS1, RELA, YY1, TP53, SMAD2, TP73, EP300, SIN3A, JUN, PARP1, RUNX2 139 160 14445 8.443570143884891 6.884225512981956E-6 1.1473742099754602E-6 5.0140218466054876E-5

GOTERM\_CC\_DIRECT GO:0005737~cytoplasm 48 0.18542841690489067 2.5869857725779827E-6 XRCC5, COPS2, MEF2A, COPS3, COPS7A, MAP4K1, NR3C1, PXN, CTNNB1, TUBB, SIN3A, PAK3, CASP7, GAB1, NPM1, RARA, PAK1, RUNX2, KPNB1, FRS2, CASP2, MAP2K6, RASA1, DHX9, DNMT3A, AR, TRIP4, HCLS1, RELA, CDC20, SMAD2, WRN, VAV2, PRKCB, CCND1, CBLB, HDAC2, EP300, NCOA3, HNF4A, ID2, HIPK2, TUBA4A, JAK1, JAK2, PARP1, TRIP6, BARD1 139 2555 14445 1.9523293302735503 4.3193387254336635E-4 6.171626445139466E-5 0.0031465452945855787

GOTERM\_CC\_DIRECT GO:0005829~cytosol 24 0.09271420845244534 9.436401489693372E-6 PRKCA, IRS2, ARHGEF7, RELA, COPS4, TP53, CTNND1, FOXO3, PRKCE, SRC, TP73, CTNNB1, BTK, RACK1, PTK2, PLCG1, HDAC1, PPP2CA, ZAP70, TRAF6, KPNA2, GRB7, CABLES1, PIK3R1 139 880 14445 2.8342053629823414 0.0015746454270336718 1.9696641008559723E-4 0.011477036288976006

GOTERM\_CC\_DIRECT GO:0005925~focal adhesion 13  
0.05022019624507456 2.957209996583211E-5 EGFR, PTK2, MDC1, ARHGEF7, PTK2B, NPM1, GIT2, JAK1, TRIP6, GRB7, PXN, CTNNB1, PIK3R2 139 299 14445 4.518298404754458 0.004926438815137546 5.485843300332416E-4 0.035963065267374805

GOTERM\_CC\_DIRECT GO:0005911~cell-cell junction 8  
0.030904736150815112 3.9159517065102034E-5 LAT, PLCG1, ZAP70, CTNND1, PAK1, FRS2, CEACAM1, PIK3R1 139 97 14445 8.570792850255879 0.006518429658924241 6.537629435982018E-4 0.04761991582471481

GOTERM\_CC\_DIRECT GO:0016605~PML body 6

0.023178552113111334	2.0794545258598335E-4	SUMO1, HIPK2, TP53, ATR, ZBTB16,			
CHEK2 139 57	14445 10.93903824308974		0.034134319686368486		
0.0031523392512891046	0.2526339071720285				
GOTERM_CC_DIRECT	GO:0030027~lamellipodium				7
0.027041644131963225	2.3355429860840563E-4	PTK2, PTPRM, PLCG1, ARHGEF7,			
PTK2B, PXN, CTNNB1 139	91 14445 7.993912562257886				
0.03825710341372268	0.003245399211855071	0.28370567004712965			
GOTERM_CC_DIRECT	GO:0043564~Ku70:Ku80 complex				3
0.011589276056555667	2.7013507855005195E-4	XRCC5, XRCC6 139			3
14445 103.92086330935253	0.04411594288840481	0.0034646497755213			
0.3280745086744363					
GOTERM_CC_DIRECT	GO:0017053~transcriptional repressor complex				5
0.019315460094259444	8.049167623539272E-4	CCND1, CTBP1, SIN3A, JUN,			
ZBTB16 139	44 14445 11.809189012426422				
0.1258254656921105	0.009559389126518658	0.9746461499908432			
GOTERM_CC_DIRECT	GO:0045121~membrane raft				6
0.023178552113111334	0.002360915890638573	EGFR, TNFRSF1A, CBLB, FYN,			
ZAP70, BTK 139	97 14445 6.428094637691909				
0.3261441815895936	0.025972693860492613	2.8340783317965523			
GOTERM_CC_DIRECT	GO:0016580~Sin3 complex 3		0.011589276056555667		
0.0024432825648811464	SIN3A, HDAC2, HDAC1 139	8 14445			
38.9703237410072	0.3353717823254204	0.025209757098052843			
2.931608314063716					
GOTERM_CC_DIRECT	GO:0042101~T cell receptor complex				3
0.011589276056555667	0.004709950857543438	ZAP70, CEACAM1, SYK 139			
11 14445	28.34205362982342	0.545437546696834			
0.045318636470075724	5.580559444730482				
GOTERM_CC_DIRECT	GO:0005730~nucleolus 13		0.05022019624507456		
0.008354933697538147	DHX9, ESRRA, TSG101, TP53, ZBTB16, WRN, NCL, GTF2B,				
SUMO1, UBTF, NPM1, TRAF6, PARP1 139	569 14445 2.37429037437888				
0.7536828408330458	0.07488835409176409	9.701492303188664			
GOTERM_CC_DIRECT	GO:0048471~perinuclear region of cytoplasm				9
0.034767828169667	0.009665694885338923	EGFR, RACK1, PTPRM, PTK2B,			
RAP1A, PRKCE, TRAF6, SRC, CTNNB1 139	309 14445 3.026821261437452				
0.8025011907637198	0.08182715065993995	11.142587010928008			
GOTERM_CC_DIRECT	GO:000044255~cellular lipid metabolic process				14
0.019368546094259444		0.00550346170175947			
CD19,EGFR,ERBB3,FRS2,FYN,GAB1,IRS2,MET,PDGFRB,PIK3R1,PIK3R2,PLCG1,PPARGC1A,PPP2					
CA,SRC,TNFRSF1A,VAV1 134	119 14445 3.0151472988786514				



0.9226052174548297	0.32482971939986514	49.48210029335738		
GOTERM_CC_DIRECT	GO:0036464~cytoplasmic ribonucleoprotein granule			
3	0.011589276056555667	0.01689663114503008	DHX9, TUBB, NCL	139
21	14445	14.84583761562179		0.9419150282620943
0.1326324123526652	18.720179371164548			
GOTERM_CC_DIRECT	GO:0000120~RNA polymerase I transcription factor complex			
2	0.007726184037703778	0.019016343565696273	TAF1C, TAF1A	139
2	14445	103.92086330935253		0.9594943214574391
0.1415969858985584	20.826317564922313			
GOTERM_CC_DIRECT	GO:0000784~nuclear chromosome, telomeric region			4
0.015452368075407556	0.046446821168226494		XRCC5, BRCA2, WRN, PARP1	
139	84	14445	4.948612538540597	0.9996446949720422
0.30303791585926965	43.92502964570173			
GOTERM_CC_DIRECT	GO:0005856~cytoskeleton			4
0.052061818790944715	PTK2B, JAK1, JAK2, PRKCE	139	88	14445
4.72367560497057	0.9998674857124242			0.32172981605307927
47.81186793372429				
GOTERM_CC_DIRECT	GO:0043234~protein complex			5
0.019315460094259444	0.05459346170176767		CD19, ARHGEF7, BRCA2, PAK1,	
KPNB1	139	149	14445	3.4872772922601514
0.9999152174548297	0.32337801939988786	49.48210029335738		
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome			29
0.11202966854670479	0.07853047994008439		TAF1B, THRB, TSG101, IL6ST,	
			COPS6, MRAS, COPS4, CTNND1, ITGB2, SRC, CTNNB1, RACK1, TUBB, PPP2CA, H2AFX, KPNB1,	
			CEACAM1, PRKCA, AXL, NCL, PRKCB, CRKL, CD19, NCOA3, RFC1, RAP1A, TUBA4A, CRK	
139	2241	14445	1.3448036751321835	0.9999988296312287
0.42092754251903075	63.01917387565095			
GOTERM_CC_DIRECT	GO:0043005~neuron projection			4
0.015452368075407556	0.08107749210818542		BRAF, ARHGEF7, RAP1A, MARK4	
139	106	14445	3.92154201167368	0.9999992628183912
0.4190517063310002	64.24346221296717			
GOTERM_CC_DIRECT	GO:0001726~ruffle			3
0.08533627231318329	PLCG1, PAK1, RASA1	139	51	14445
6.1129919593736775	0.9999996606379349			0.42403653360263827
66.20774919939672				
GOTERM_MF_DIRECT	GO:0004715~non-membrane spanning protein tyrosine kinase activity			9
PTK2, PTK2B, FYN, ZAP70, JAK1, JAK2, SRC, SYK, BTK	0.034767828169667			4.221323048806749E-9
22.561414392059557	8.020510631201461E-7	124	39	12123
5.246527934321676E-6				
GOTERM_MF_DIRECT	GO:0005524~ATP binding			34
3.613896857945997E-8	XRCC5, ERBB3, MAP4K1, CHEK2, SRC, BTK, AKT1, PTK2, PAK3,			0.13134512864096423

PTK2B, ZAP70, PAK1, RUNX2, TOP2A, MAP2K6, SYK, PRKCA, EGFR, DHX9, BRAF, MET, TP53, AXL, ATR, WRN, PRKCE, MARK4, PRKCB, RFC1, FYN, HIPK2, PDGFRB, JAK1, JAK2 124  
 1171 12123 2.838640808793146 6.866380583558929E-  
 3.433196185120835E-6 4.491579311816096E-5  
 GOTERM\_MF\_DIRECT GO:0051222~positive regulation of protein transport 16  
 0.01313451286409642 5.273288269545826E-7  
 DHX9,EGFR,FYN,GNB2L1,HCLS1,IRS2,ITGB2,JAK2,PAK1,PIK3R1,PIK3R2,PRKCE,SRC,SYK,TP53,T  
 SG101 114 1171 12123 2.248975855893929 6.879388355558939E-5  
 3.961754186096835E-5 4.835579311816096E-5  
 GOTERM\_MF\_DIRECT GO:0003682~chromatin binding 14  
 0.05408328826392645 7.779324399294104E-6 EGFR, DNMT3A, MEF2A, KAT2B,  
 RELA, TP53, SMAD2, TP73, PRKCB, ATF2, NCOA1, SIN3A, JUN, RUNX2 124 291  
 12123 4.703525108081144 0.001476985566719935 4.925711087001572E-4  
 0.009668207996804679  
 GOTERM\_MF\_DIRECT GO:0003684~damaged DNA binding 7  
 0.027041644131963225 8.359360334489398E-6 XRCC5, EP300, XRCC6, TP53,  
 H2AFX, TP73 124 48 12123 14.257560483870968  
 0.0015870244448208393 3.9699245315605314E-4 0.010389046967307358  
  
 GOTERM\_MF\_DIRECT GO:0004674~protein serine/threonine kinase activity 12  
 0.04635710422622267 1.305117429054945E-5 PRKCA, AKT1, BRAF, PAK3, HIPK2,  
 ATR, PAK1, CHEK2, PRKCE, MARK4, SYK, PRKCB 124 218 12123  
 5.381621781592187 0.0024766672832859937 4.958248975862611E-4  
 0.016219617546853193  
 GOTERM\_MF\_DIRECT GO:0000978~RNA polymerase II core promoter proximal  
 region sequence-specific DNA binding 14 0.05408328826392645  
 1.4793826822208473E-5 CEBPA, ESRRA, MEF2A, CEBPD, RELA, SPI1, SMAD2, NR3C1,  
 TP73, HDAC2, HDAC1, SP1, JUN, RUNX2 124 309 12123  
 4.42953335421234 0.002806901153705743 4.683649308649951E-4  
 0.018385152047029063  
 GOTERM\_MF\_DIRECT GO:0000980~RNA polymerase II distal enhancer sequence-  
 specific DNA binding 7 0.027041644131963225 1.674175439486251E-5  
 HDAC2, HDAC1, JUN, RELA, SPI1, ZBTB16, ATF2 124 54 12123  
 12.673387096774194 0.003175906069535994 4.543196173615316E-4  
 0.020805723747152616  
 GOTERM\_MF\_DIRECT GO:0003713~transcription coactivator activity 9  
 0.034767828169667 2.4204206564254807E-5 CEBPA, EP300, KAT2B, TRIP4, JUN,  
 NPM1, RARA, PPARGC1A, CTNNB1 124 117 12123 7.5204714640198524  
 0.004588296361970334 5.746916643560862E-4 0.03007836276256448  
  
 GOTERM\_MF\_DIRECT GO:0001077~transcriptional activator activity, RNA  
 polymerase II core promoter proximal region sequence-specific binding 11  
 0.04249401220737078 3.118619610481633E-5 CEBPA, ESRRA, MEF2A, CEBPD,  
 RELA, SPI1, SMAD2, NR3C1, RUNX2, TP73, ATF2 124 197 12123

5.459022433273293	0.005907948685251574	6.581688292387478E-4		
0.0387532759775433				
GOTERM_MF_DIRECT	GO:0031490~chromatin DNA binding			6
0.023178552113111334	1.4572422466865148E-4	EP300, THRB, RELA, RARA, FOXO3,		
PPARGC1A	124	50	12123	11.731935483870968
0.02730977670789836	0.002765131986569247	0.18096456845032582		
GOTERM_MF_DIRECT	GO:0004402~histone acetyltransferase activity			5
0.019315460094259444	1.47821850638598E-4	NCOA1, EP300, KAT2B, NCOA3,		
ATF2	124	27	12123	18.10483870967742
0.027697421002769618	0.002550217900589624	0.1835672612723882		
GOTERM_MF_DIRECT	GO:0005102~receptor binding			6
0.023178552113111334	1.9264325654005E-4	PTK2, PTK2B, FYN, ZAP70, JAK1,		
SYK	124	53	12123	11.067863664029215
0.0030458307488757663	0.23916586499024284	0.035943855399535596		
GOTERM_MF_DIRECT	GO:0005496~steroid binding			4
0.015452368075407556	5.182570561426679E-4	ESRRA, AR, NR3C1, ESR2	124	
16	12123	24.441532258064516		0.0937992014771376
0.0075478604103171865	0.642218613825063			
GOTERM_MF_DIRECT	GO:0003714~transcription corepressor activity			7
0.027041644131963225	5.876475682104388E-4	COPS2, CCND1, CTBP1, TSG101,		
HIPK2, RARA, DNMT3B	124	102	12123	6.709440227703984
0.10567484075683675	0.007945824931281487	0.7279181029497539		
GOTERM_MF_DIRECT	GO:0042162~telomeric DNA binding			4
0.015452368075407556	7.440667312562704E-4	XRCC5, XRCC6, NCL	124	
18	12123	21.725806451612904		0.13187997861568235
0.00938404579469021	0.9208514986247973			
GOTERM_MF_DIRECT	GO:0043565~sequence-specific DNA binding			12
0.04635710422622267	9.586671867318054E-4	ESRRA, AR, THRB, JUN, TP53,		
POU2F1, SPIB, FOXO3, NR3C1, PPARGC1A, TP73, ATF2	124	355	12123	
3.3047705588368923	0.16659380813939328	0.011325016828697021		
1.1849869406224567				
GOTERM_MF_DIRECT	GO:0004871~signal transducer activity			7
0.027041644131963225	0.001261063013497183	PTK2, CBLB, IRS2, PLCG1, PTK2B,		
GAB1, CTNNB1	124	118	12123	5.799685620557681
0.21317795656209548	0.014004144777855498	1.556084112117928		
GOTERM_MF_DIRECT	GO:0004716~receptor signaling protein tyrosine kinase activity			3
0.011589276056555667	0.002074066895983236	EGFR, ERBB3,		
SYK	124	7	12123	41.89976958525346
0.021677260099485562	2.5474495411428433	0.3259708655159578		
GOTERM_MF_DIRECT	GO:0001164~RNA polymerase I CORE element sequence-			

specific DNA binding 3 0.011589276056555667 0.0027470899565724314  
TAF1B, TAF1C, UBTB 124 8 12123 36.662298387096776  
0.40706193279338665 0.02713378271107958 3.361170016244208

GOTERM\_MF\_DIRECT GO:0000981~RNA polymerase II transcription factor activity,  
sequence-specific DNA binding 7 0.027041644131963225  
0.004076215668952959 SP1, JUN, RELA, SPI1, SPIB, FOXO3, RUNX2 124  
149 12123 4.593039618965143 0.5397860346028603  
0.03805998792758125 4.949830087640416

GOTERM\_MF\_DIRECT GO:0030374~ligand-dependent nuclear receptor  
transcription coactivator activity 4 0.015452368075407556  
0.0052646181483895415 NCOA1, NCOA3, PPARGC1A, PRKCB 124 35  
12123 11.173271889400922 0.6331931139766194 0.04663560678658363  
6.349915778613435

GOTERM\_MF\_DIRECT GO:0001228~transcriptional activator activity, RNA  
polymerase II transcription regulatory region sequence-specific binding 5  
0.019315460094259444 0.007380014336076073 EP300, HNF4A, TP53, FOXO3, ATF1  
124 76 12123 6.431982173174873 0.7552217206696359  
0.06196952307634074 8.795288953599867

GOTERM\_MF\_DIRECT GO:0008270~zinc ion binding 19  
0.07339874835818588 0.008543885448565602 PRKCA, ESRRA, AR, TRIP4, THRB,  
NR3C1, ESR2, GTF2B, PXN, PRKCB, CBLB, EP300, HNF4A, PIAS3, RARA, TRIP6, PARP1, TRAF6,  
BARD1 124 966 12123 1.9229362853135645  
0.8041317027037322 0.06842927429349288 10.115534831696271

GOTERM\_MF\_DIRECT GO:0003705~transcription factor activity, RNA polymerase II  
distal enhancer sequence-specific binding 4 0.015452368075407556  
0.008771990650391963 CEBPA, MEF2A, HNF4A, JUN 124 42 12123  
9.311059907834101 0.8125102869464433 0.06737426875254748  
10.372218865954741

GOTERM\_MF\_DIRECT GO:0003700~transcription factor activity, sequence-specific  
DNA binding 13 0.05022019624507456 0.009419704681336792 ESRRA,  
CTBP1, AR, RELA, TP53, SMAD2, NR3C1, TP73, CTNNB1, ATF2, SIN3A, JUN, POU2F1  
124 546 12123 2.327764976958526 0.8344077157606387  
0.06940309485718443 11.097413855848925

GOTERM\_MF\_DIRECT GO:0000979~RNA polymerase II core promoter sequence-  
specific DNA binding 4 0.015452368075407556 0.00997280788430303  
EP300, HNF4A, SPI1, RUNX2 124 44 12123 8.887829912023461  
0.8510798756495882 0.07062600762076776 11.712405315045826

GOTERM\_MF\_DIRECT GO:0004714~transmembrane receptor protein tyrosine  
kinase activity 3 0.011589276056555667 0.012570690777186136  
ERBB3, MET, AXL 124 17 12123 17.252846299810248  
0.9096053658065251 0.08517375215161838 14.548978897153242

GOTERM\_MF\_DIRECT GO:0001106~RNA polymerase II transcription corepressor activity 3 0.011589276056555667 0.014049018782848883 CTBP1, SIN3A, HDAC1 124 18 12123 16.294354838709676 0.9319995990155843 0.09154382514218073 16.1254769500757

GOTERM\_MF\_DIRECT GO:0003707~steroid hormone receptor activity 4 0.015452368075407556 0.014899745481741831 ESRRA, HNF4A, THRB, RARA 124 51 12123 7.667931688804553 0.9422858979852045 0.09367160977886713 17.020528456192764

GOTERM\_MF\_DIRECT GO:0004003~ATP-dependent DNA helicase activity 3 0.011589276056555667 0.015598660840384512 XRCC5, XRCC6 124 19 12123 15.436757215619695 0.9495667205908078 0.09477353939192756 17.749277957010644

GOTERM\_MF\_DIRECT GO:0004702~receptor signaling protein serine/threonine kinase activity 4 0.015452368075407556 0.01569713003411466 PAK3, MAP4K1, PAK1, MAP2K6 124 52 12123 7.520471464019852 0.9505162316623135 0.09241795470288128 17.851476119307684

GOTERM\_MF\_DIRECT GO:0035403~histone kinase activity (H3-T6 specific) 2 0.007726184037703778 0.020189894041385683 PRKCA, PRKCB 124 2 12123 97.76612903225806 0.9792525960175757 0.11405835339809178 22.392070787499343

GOTERM\_MF\_DIRECT GO:0003886~DNA (cytosine-5-)-methyltransferase activity 2 0.007726184037703778 0.020189894041385683 DNMT3A, DNMT3B 124 2 12123 97.76612903225806 0.9792525960175757 0.11405835339809178 22.392070787499343

GOTERM\_MF\_DIRECT GO:0035257~nuclear hormone receptor binding 2 0.007726184037703778 0.03013269109017194 NCOA1, NCOA3 124 3 12123 65.1774193548387 0.9970122725724909 0.161515225332986 31.63209118563489

GOTERM\_MF\_DIRECT GO:0003677~DNA binding 12 0.04635710422622267 0.03645645284566028 DNMT3A, NCOA1, MEF2A, RFC1, SOS1, RELA, HIPK2, SMAD2, H2AFX, WRN, PARP1, PPARGC1A 124 588 12123 1.9952271231073073 0.9991379032968113 0.1874140785159999 36.97064338636652

GOTERM\_MF\_DIRECT GO:0008134~transcription factor binding 3 0.011589276056555667 0.036917937669383345 SUMO1, JUN, PPARGC1A 124 30 12123 9.776612903225807 0.9992129073165417 0.184704538004538 37.344809208215516

GOTERM\_MF\_DIRECT GO:0004468~lysine N-acetyltransferase activity, acting on acetyl phosphate as donor 2 0.007726184037703778 0.03997540387918093 EP300, KAT2B 124 4 12123 48.88306451612903 0.9995698218096547 0.19371193172907486 39.77262549344744

GOTERM\_MF\_DIRECT GO:0046935~1-phosphatidylinositol-3-kinase regulator activity 2 0.007726184037703778 0.03997540387918093 PIK3R1, PIK3R2 124 4 12123 48.88306451612903 0.9995698218096547 0.19371193172907486 39.77262549344744

GOTERM\_MF\_DIRECT GO:0046790~virion binding 2 0.007726184037703778 0.04971903167961923 TSG101, HIPK2 124 5 12123 39.10645161290323 0.9999380721510837 0.2303962254437989 46.944428117898596

GOTERM\_MF\_DIRECT GO:0016922~ligand-dependent nuclear receptor binding 2 0.007726184037703778 0.04971903167961923 NCOA1, NCOA3 124 5 12123 39.10645161290323 0.9999380721510837 0.2303962254437989 46.944428117898596

GOTERM\_MF\_DIRECT GO:0044822~poly(A) RNA binding 15 0.057946380282778334 0.06380528897057869 XRCC5, DHX9, NCL, RACK1, SUMO1, CRKL, HDAC2, UBTG, JUN, NPM1, TRIP6, PARP1, KPNA2, KPNB1 124 884 12123 1.6589275288279084 0.9999963727722677 0.2808310700980592 55.932261468193936

GOTERM\_MF\_DIRECT GO:0001078~transcriptional repressor activity, RNA polymerase II core promoter proximal region sequence-specific binding 4 0.015452368075407556 0.06857567468523915 ESRRB, RELB, YY1, SPI1 124 93 12123 4.204994797086369 0.9999986258333032 0.29255396241649945 58.643240335508295

GOTERM\_MF\_DIRECT GO:0004708~MAP kinase kinase activity 2 0.007726184037703778 0.06891298003399249 PAK3, MAP2K6 124 7 12123 27.933179723502306 0.9999987172213046 0.287632998930188 58.82899813032547

GOTERM\_MF\_DIRECT GO:0003690~double-stranded DNA binding 3 0.011589276056555667 0.07330977948448444 TP53, TP73, CTNNA1 124 44 12123 6.665872434017595 0.999999478120573 0.29729991784261134 61.181210723816406

GOTERM\_MF\_DIRECT GO:0001948~glycoprotein binding 3 0.011589276056555667 0.07330977948448444 FYN, ITGB2, RASA1 124 44 12123 6.665872434017595 0.999999478120573 0.29729991784261134 61.181210723816406

GOTERM\_MF\_DIRECT GO:0044212~transcription regulatory region DNA binding 4 0.015452368075407556 0.075725943084578 XRCC5, AR, TP53, CTNNA1 124 97 12123 4.031592949783838 0.9999996822065061 0.29969187237181305 62.42056963092677

GOTERM\_MF\_DIRECT GO:0001047~core promoter binding 3 0.011589276056555667 0.07622617486659616 HDAC1, FOXO3, GTF2B 124 45 12123 6.517741935483871 0.9999997132694484 0.2955531493724409 62.67257015052572

GOTERM\_MF\_DIRECT GO:0032041~NAD-dependent histone deacetylase activity (H3-K14 specific) 2 0.007726184037703778 0.08772233417582018 HDAC2,

HDAC1	124	9	12123	21.725806451612904	0.999999973445501
	0.327300165670223		68.05274148868136		
GOTERM_MF_DIRECT			GO:0004697~protein kinase C activity		2
	0.007726184037703778		0.08772233417582018	PRKCA, PRKCB	124 9
	12123	21.725806451612904		0.999999973445501	0.327300165670223
	68.05274148868136				
GOTERM_MF_DIRECT			GO:0000977~RNA polymerase II regulatory region sequence-specific DNA binding		5
		5	0.019315460094259444		0.09455946587502334
	MEF2A, KAT2B, RELA, RARA, ATF1	124	170	12123	2.875474383301708
	0.9999999936410233		0.34256465402143965		70.90436219639557
GOTERM_MF_DIRECT			GO:0004861~cyclin-dependent protein serine/threonine kinase inhibitor activity		2
		2	0.007726184037703778		0.09698518318541795
	CCND1, KAT2B	124	10	12123	19.553225806451614
	0.9999999961803242		0.34385386313367383		71.85846248895616

### Pathways of the most significant top 3 modules

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits
Pop Total	Fold Enrichment	Bonferroni		Benjamini		FDR	
KEGG_PATHWAY	ptr05200:Pathways in cancer	33		0.12748203662211233			
4.06222408442244347E-17	SPI1, ZBTB16, CTNNB1, AKT1, PTK2, SOS1, RARA, TRAF6, PIK3R1, PIK3R2, PRKCA, CEBPA, EGFR, RET, AR, CTBP1, BRAF, RELA, MET, TP53, BRCA2, SMAD2, PRKCB, CCND1, CBLB, HDAC2, EP300, CRKL, PLCG1, JUN, PDGFRB, JAK1, CRK	112	392	6946	5.2208910349854225	6.490363801958665E-13	
3.2451819009793326E-13	4.951594689828198E-12						
KEGG_PATHWAY	ptr04012:ErbB signaling pathway	19		0.07339874835818588			
6.66455335549225E-16	EGFR, PRKCA, BRAF, ERBB3, SRC, PRKCB, AKT1, CBLB, PTK2, CRKL, PLCG1, PAK3, SOS1, JUN, GAB1, PAK1, CRK, PIK3R1, PIK3R2	112	86	6946	13.701619601328904	1.0524914273446484E-13	1.0524914273446484E-13
7.993605777301127E-13	1.0524914273446484E-13						
KEGG_PATHWAY	ptr04510:Focal adhesion	24		0.09271420845244534			
1.0917196785286268E-13	PRKCA, EGFR, BRAF, MET, VAV2, VAV1, SRC, PXN, CTNNB1, PRKCB, AKT1, PTK2, CCND1, CRKL, PAK3, FYN, SOS1, JUN, RAP1A, PDGFRB, PAK1, CRK, PIK3R1, PIK3R2	112	209	6946	1.7243317884663156E-11	5.747735620786898E-12	1.3149481503660354E-10
1.7243317884663156E-11	5.747735620786898E-12						
KEGG_PATHWAY	ptr05205:Proteoglycans in cancer						23
0.08885111643359345	5.006186535166335E-13	PRKCA, EGFR, BRAF, ERBB3, HCLS1, MRAS, MET, TP53, SRC, PXN, CTNNB1, PRKCB, AKT1, CBLB, PTK2, CCND1, PLCG1, SOS1, GAB1, PAK1, FRS2, PIK3R1, PIK3R2	112	202	6946	7.061439179632249	7.909473076495033E-11
7.909473076495033E-11	1.9773738202388813E-11	6.031730670486013E-10					
KEGG_PATHWAY	ptr05211:Renal cell carcinoma	14		0.05408328826392645			
2.1889651294939067E-11	BRAF, MET, AKT1, EP300, CRKL, PAK3, SOS1, JUN, GAB1, RAP1A, PAK1, CRK, PIK3R1, PIK3R2	112	66	6946	3.458556996349671E-9	6.917113548610132E-10	2.6374624706448913E-8
3.458556996349671E-9	6.917113548610132E-10	2.6374624706448913E-8					
KEGG_PATHWAY	ptr04650:Natural killer cell mediated cytotoxicity						17
0.06567256432048212	2.4357118430481532E-11	PRKCA, BRAF, ITGB2, VAV2, VAV1, PRKCB, LAT, PLCG1, PTK2B, FYN, SOS1, ZAP70, PAK1, PIK3R1, SYK, PIK3R2, SH3BP2	112	115	6946	9.167857142857141	3.848417362561918E-9
115	6946	9.167857142857141					
6.414029307677538E-10	2.9347668739632127E-8						
KEGG_PATHWAY	ptr04919:Thyroid hormone signaling pathway						17
0.06567256432048212	2.4357118430481532E-11	PRKCA, KAT2B, THRB, TP53, SRC, CTNNB1, PRKCB, AKT1, NCOA1, CCND1, EP300, SIN3A, HDAC2, NCOA3, PLCG1, PIK3R1, PIK3R2	112	115	6946	9.167857142857141	3.848417362561918E-9
112	115	6946					
6.414029307677538E-10	2.9347668739632127E-8						
KEGG_PATHWAY	ptr04722:Neurotrophin signaling pathway						17
0.06567256432048212	6.929992858517413E-11	BRAF, RELA, TP53, FOXO3, TP73, AKT1, CRKL, PLCG1, SOS1, JUN, GAB1, RAP1A, TRAF6, CRK, FRS2, PIK3R1, PIK3R2	112	123	6946	8.5715737514518	1.0949383955072278E-8
123	6946	8.5715737514518					
8.349897440140808E-8	1.0949383955072278E-8	1.564197771308784E-9					



KEGG\_PATHWAY ptr05166:HTLV-I infection 23 0.08885111643359345  
7.542771310943016E-11 KAT2B, MRAS, RELA, TP53, SPI1, ITGB2, SMAD2, CDC20, ATR,  
CHEK2, ATF1, ATF2, CTNNB1, AKT1, TNFRSF1A, CCND1, EP300, JUN, PDGFRB, JAK1, ANAPC7,  
PIK3R1, PIK3R2 112 259 6946 5.5073772752344174  
1.191757081908662E-8 1.4896963662636153E-9 9.088226837761226E-8

KEGG\_PATHWAY ptr04666:Fc gamma R-mediated phagocytosis 14  
0.05408328826392645 7.145917199401994E-10 PRKCA, VAV2, PRKCE, VAV1, PRKCB,  
AKT1, LAT, CRKL, PLCG1, PAK1, CRK, PIK3R1, PIK3R2, SYK 112 86 6946  
10.095930232558139 1.1290548529441224E-7 1.2545054550727741E-8  
8.61006632657535E-7

KEGG\_PATHWAY ptr04015:Rap1 signaling pathway 20 0.07726184037703777  
8.285203926600969E-10 EGFR, PRKCA, BRAF, MRAS, MET, CTNND1, ITGB2, SRC, CTNNB1,  
PRKCB, AKT1, LAT, CRKL, PLCG1, RAP1A, PDGFRB, CRK, MAP2K6, PIK3R1, PIK3R2 112  
214 6946 5.796061415220294 1.3090620887279414E-7  
1.3090621697742222E-8 9.982784598960848E-7

KEGG\_PATHWAY ptr05223:Non-small cell lung cancer 12  
0.04635710422622267 8.575155047585538E-10 EGFR, PRKCA, AKT1, CCND1, BRAF,  
PLCG1, SOS1, TP53, FOXO3, PIK3R1, PRKCB, PIK3R2 112 56 6946  
13.28954081632653 1.3548744037805704E-7 1.2317040831710813E-8  
1.0332145139457793E-6

KEGG\_PATHWAY ptr05220:Chronic myeloid leukemia 13  
0.05022019624507456 1.7100975949436502E-9 AKT1, CBLB, CCND1, CTBP1, CRKL,  
HDAC2, BRAF, SOS1, RELA, TP53, CRK, PIK3R1, PIK3R2 112 75 6946  
10.749761904761904 2.7019538750838734E-7 2.2516285058671315E-8  
2.0604848049998736E-6

KEGG\_PATHWAY ptr04062:Chemokine signaling pathway 18  
0.069535656339334 1.9401334418732787E-9 BRAF, RELA, FOXO3, VAV2, VAV1,  
PXN, SRC, AKT1, PTK2, CRKL, PTK2B, SOS1, RAP1A, JAK2, PAK1, CRK, PIK3R1, PIK3R2 112  
176 6946 6.34273538961039 3.065410284497361E-7  
2.3580082442187233E-8 2.3376533042629433E-6

KEGG\_PATHWAY ptr04010:MAPK signaling pathway 21 0.08112493239588967  
2.903210504352453E-9 PRKCA, EGFR, BRAF, MRAS, RELA, TP53, MAP4K1, ATF2, PRKCB,  
AKT1, TNFRSF1A, CRKL, SOS1, JUN, RAP1A, PDGFRB, PAK1, TRAF6, CRK, RASA1, MAP2K6  
112 257 6946 5.067607003891051 4.5870714648899025E-7  
3.276480320391073E-8 3.498058187556552E-6

KEGG\_PATHWAY ptr05214:Glioma 12 0.04635710422622267  
4.571938909208427E-9 EGFR, PRKCA, AKT1, CCND1, BRAF, PLCG1, SOS1, TP53, PDGFRB,  
PIK3R1, PRKCB, PIK3R2 112 65 6946 11.44945054945055  
7.223660930533171E-7 4.81577557831514E-8 5.508697542566665E-6

KEGG\_PATHWAY ptr04660:T cell receptor signaling pathway 14  
0.05408328826392645 7.908437025596503E-9 RELA, VAV2, VAV1, AKT1, LAT,  
PLCG1, FYN, PAK3, JUN, SOS1, ZAP70, PAK1, PIK3R1, PIK3R2 112 104 6946  
8.348557692307692 1.2495322728733882E-6 7.809581281659206E-8  
9.528820787974013E-6

KEGG\_PATHWAY ptr04664:Fc epsilon RI signaling pathway 12  
0.04635710422622267 1.2073635138230801E-8 AKT1, LAT, PLCG1, FYN, SOS1,  
VAV2, VAV1, MAP2K6, PIK3R1, SYK, BTK, PIK3R2 112 71 6946  
10.481891348088531 1.907632536490844E-6 1.1221377937964405E-7  
1.454743865370034E-5  
KEGG\_PATHWAY ptr05215:Prostate cancer 13 0.05022019624507456  
1.2896892012046021E-8 EGFR, AKT1, AR, CCND1, EP300, BRAF, SOS1, RELA, TP53,  
PDGFRB, PIK3R1, CTNNB1, PIK3R2 112 89 6946 9.05878812199037  
2.0377068727928105E-6 1.132060463149287E-7 1.5539375086692786E-5  
KEGG\_PATHWAY ptr05203:Viral carcinogenesis 18 0.069535656339334  
1.59613847025422E-8 KAT2B, IL6ST, RELA, TP53, CDC20, GTF2B, PXN, SRC, ATF2,  
CCND1, EP300, HDAC2, JUN, JAK1, CCNA1, PIK3R1, SYK, PIK3R2 112 202  
6946 5.526343705799152 2.5218956162254003E-6 1.3273150678561052E-7  
1.923176056184417E-5  
KEGG\_PATHWAY ptr05221:Acute myeloid leukemia 11 0.04249401220737078  
1.6617996959072337E-8 CEBPA, AKT1, CCND1, BRAF, SOS1, RELA, SPI1, RARA, ZBTB16,  
PIK3R1, PIK3R2 112 57 6946 11.968358395989975  
2.6256400974533634E-6 1.3128216858060426E-7 2.0022908076011703E-5  
KEGG\_PATHWAY ptr04014:Ras signaling pathway 19 0.07339874835818588  
1.9427863130115166E-8 EGFR, PRKCA, MRAS, RELA, MET, PRKCB, AKT1, LAT, PLCG1,  
PAK3, SOS1, GAB1, ZAP70, RAP1A, PDGFRB, PAK1, RASA1, PIK3R1, PIK3R2 112  
231 6946 5.101035868893012 3.0695976878103437E-6  
1.4617153210050304E-7 2.3408495697374576E-5  
KEGG\_PATHWAY ptr04670:Leukocyte transendothelial migration 14  
0.05408328826392645 3.0328363017694345E-8 PRKCA, PTK2, PLCG1, PTK2B,  
RAP1A, CTNND1, ITGB2, VAV2, VAV1, PXN, PIK3R1, CTNNB1, PRKCB, PIK3R2 112 116  
6946 7.484913793103448 4.791869952391892E-6 2.1781276871024602E-7  
3.654242927142448E-5  
KEGG\_PATHWAY ptr04810:Regulation of actin cytoskeleton 18  
0.069535656339334 4.3455101312590525E-8 EGFR, BRAF, ARHGEF7, MRAS,  
ITGB2, VAV2, VAV1, SRC, PXN, PTK2, CRKL, PAK3, SOS1, PDGFRB, PAK1, CRK, PIK3R1, PIK3R2  
112 216 6946 5.168154761904763 6.865882583473315E-6  
2.985176142944468E-7 5.2358739177638114E-5  
KEGG\_PATHWAY ptr05100:Bacterial invasion of epithelial cells 12  
0.04635710422622267 4.381793497005127E-8 PTK2, CBLB, CRKL, HCLS1, MET,  
GAB1, CRK, SRC, PXN, PIK3R1, CTNNB1, PIK3R2 112 80 6946  
9.30267857142857 6.923209907805372E-6 2.8846803645787844E-7  
5.279591472895362E-5  
KEGG\_PATHWAY ptr05212:Pancreatic cancer 11 0.04249401220737078  
8.352035619369864E-8 EGFR, AKT1, CCND1, BRAF, RELA, TP53, BRCA2, JAK1, SMAD2,  
PIK3R1, PIK3R2 112 67 6946 10.182036247334755  
1.3196129758918929E-5 5.278485338822136E-7 1.0063305452279181E-4  
KEGG\_PATHWAY ptr05161:Hepatitis B 15 0.057946380282778334  
9.065400017044947E-8 PRKCA, RELA, TP53, SRC, ATF2, PRKCB, AKT1, CCND1, EP300,

PTK2B, JUN, JAK1, CCNA1, PIK3R1, PIK3R2 112 150 6946  
 6.201785714285713 1.4323230101642714E-5 5.508972590329009E-7  
 1.092283246961756E-4  
 KEGG\_PATHWAY ptr05213:Endometrial cancer 10 0.03863092018851889  
 1.0161619691855087E-7 EGFR, AKT1, CCND1, BRAF, SOS1, TP53, FOXO3, PIK3R1,  
 CTNNB1, PIK3R2 112 52 6946 11.926510989010989  
 1.6055231039535656E-5 5.946427834579993E-7 1.2243658585875394E-4  
 KEGG\_PATHWAY ptr04662:B cell receptor signaling pathway 11  
 0.04249401220737078 1.1150306785879505E-7 AKT1, CD19, JUN, SOS1, RELA,  
 VAV2, VAV1, PIK3R1, SYK, BTK, PIK3R2 112 69 6946  
 9.886904761904761 1.7617330521857433E-5 6.29195720192044E-7  
 1.3434919446941862E-4  
 KEGG\_PATHWAY ptr05206:MicroRNAs in cancer 19 0.07339874835818588  
 1.3566158206478892E-7 EGFR, PRKCA, DNMT3A, IRS2, ERBB3, EZH2, MET, TP53, PRKCE,  
 PRKCB, CCND1, EP300, CRKL, PLCG1, SOS1, PDGFRB, DNMT1, CRK, DNMT3B 112  
 262 6946 4.497478189749182 2.1434301704537084E-5  
 7.391215000041029E-7 1.634575818032502E-4  
 KEGG\_PATHWAY ptr05169:Epstein-Barr virus infection 13  
 0.05022019624507456 2.1506894205243143E-7 RELA, TP53, AKT1, CD19, HDAC2,  
 JUN, JAK1, TRAF6, CCNA1, PIK3R1, MAP2K6, SYK, PIK3R2 112 114 6946  
 7.0722117794486214 3.398031916179711E-5 1.132695908734327E-6  
 2.591347766700558E-4  
 KEGG\_PATHWAY ptr05202:Transcriptional misregulation in cancer 15  
 0.057946380282778334 3.737614971436662E-7 CEBPA, RELA, MET, TP53, SPI1,  
 ZBTB16, ATF1, WT1, PTK2, SIN3A, HDAC2, SP1, ID2, RARA, RUNX2 112 168  
 6946 5.537308673469387 5.905258392069346E-5 1.9049764949929937E-6  
 4.503417194712256E-4  
 KEGG\_PATHWAY ptr04380:Osteoclast differentiation 13  
 0.05022019624507456 1.3609438072116097E-6 RELA, SPI1, BTK, AKT1, TNFRSF1A,  
 FYN, JUN, JAK1, TRAF6, PIK3R1, MAP2K6, SYK, PIK3R2 112 135 6946  
 5.972089947089947 2.1500615072378437E-4 6.71964204368436E-6  
 0.0016397794753264527  
 KEGG\_PATHWAY ptr04917:Prolactin signaling pathway 10  
 0.03863092018851889 1.4134963944135898E-6 AKT1, CCND1, SOS1, RELA, JAK2,  
 FOXO3, ESR2, SRC, PIK3R1, PIK3R2 112 70 6946 8.85969387755102  
 2.2330765128530938E-4 6.767631285931053E-6 0.0017030987545130216  
 KEGG\_PATHWAY ptr05231:Choline metabolism in cancer 11  
 0.04249401220737078 5.8530699658683605E-6 EGFR, PRKCA, AKT1, PLCG1, SP1,  
 JUN, SOS1, PDGFRB, PIK3R1, PRKCB, PIK3R2 112 105 6946  
 6.497108843537415 9.243602766282333E-4 2.7199270123845487E-5  
 0.007052095588044871  
 KEGG\_PATHWAY ptr04068:FoxO signaling pathway 12 0.04635710422622267  
 6.237144176094152E-6 EGFR, AKT1, IRS2, CCND1, PRMT1, EP300, BRAF, SOS1, SMAD2,  
 FOXO3, PIK3R1, PIK3R2 112 130 6946 5.724725274725275

9.849864351793025E-4	2.8155942273899726E-5	0.007514833045896285		
KEGG_PATHWAY	ptr05160:Hepatitis C	12	0.04635710422622267	
7.779746712167533E-6	EGFR, AKT1, TNFRSF1A, BRAF, PPP2CA, SOS1, RELA, TP53, JAK1, TRAF6, PIK3R1, PIK3R2	112	133	6946
0.001228449599255943	3.4143993802304706E-5	0.009373360276354603		
KEGG_PATHWAY	ptr04370:VEGF signaling pathway	9	0.034767828169667	
7.816269687023508E-6	PRKCA, AKT1, PTK2, PLCG1, SRC, PXN, PIK3R1, PRKCB, PIK3R2	112	65	6946
112	65	6946	8.587087912087913	0.0012342131686713387
3.337715748408243E-5	0.009417362765373749			
KEGG_PATHWAY	ptr05210:Colorectal cancer	9	0.034767828169667	
8.77734265496146E-6	AKT1, CCND1, BRAF, JUN, TP53, SMAD2, PIK3R1, CTNNB1, PIK3R2	112	66	6946
0.0013858650267104533	3.649476104505833E-5	0.010575246804334082		
KEGG_PATHWAY	ptr05162:Measles	12	0.04635710422622267	
8.984276122616465E-6	RACK1, AKT1, CCND1, FYN, RELA, TP53, JAK1, JAK2, TRAF6, TP73, PIK3R1, PIK3R2	112	135	6946
0.0014185149592752522	3.639733770521847E-5	0.010824555047606044		
KEGG_PATHWAY	ptr05218:Melanoma	9	0.034767828169667	
1.3682429584728333E-5	EGFR, AKT1, CCND1, BRAF, MET, TP53, PDGFRB, PIK3R1, PIK3R2	112	70	6946
112	70	6946	7.973724489795919	0.0021595035738247725
5.404450614376888E-5	0.016484618932022244			
KEGG_PATHWAY	ptr04915:Estrogen signaling pathway	10		
0.03863092018851889	1.8312224548568613E-5	EGFR, AKT1, SP1, JUN, SOS1, ESR2, SRC, PIK3R1, ATF2, PIK3R2	112	95
0.0028891762445494296	7.056721661857779E-5	0.022062041019987877		
KEGG_PATHWAY	ptr04520:Adherens junction	9	0.034767828169667	
1.8723744780873655E-5	EGFR, EP300, PTPRM, FYN, MET, CTNND1, SMAD2, SRC, CTNNB1	112	73	6946
0.002954007679281556	7.043512341187164E-5	0.02255777746772436		
KEGG_PATHWAY	ptr04071:Sphingolipid signaling pathway	11		
0.04249401220737078	1.9280074483294574E-5	PRKCA, AKT1, TNFRSF1A, FYN, PPP2CA, RELA, TP53, PRKCE, PIK3R1, PRKCB, PIK3R2	112	120
5.6849702380952385	0.003041645928246295	7.084123795986219E-5		
0.023227954567683895				
KEGG_PATHWAY	ptr04151:PI3K-Akt signaling pathway	18		
0.069535656339334	2.497265503514049E-5	EGFR, RELA, MET, TP53, FOXO3, ATF2, AKT1, PTK2, CCND1, CD19, SOS1, PPP2CA, PDGFRB, JAK1, JAK2, PIK3R1, SYK, PIK3R2	112	341
112	341	6946	3.2736698785085885	0.003937954603943639
8.967163297268765E-5	0.03008522896222887			
KEGG_PATHWAY	ptr05230:Central carbon metabolism in cancer	8		
0.030904736150815112	6.45562548033304E-5	EGFR, AKT1, RET, MET, TP53, PDGFRB, PIK3R1, PIK3R2	112	64
0.010148371716974358	2.266458120983028E-4	0.07775565145673458		
KEGG_PATHWAY	ptr04066:HIF-1 signaling pathway	9		

0.034767828169667	1.0083704284430331E-4	EGFR, PRKCA, AKT1, EP300, PLCG1, RELA, PIK3R1, PRKCB, PIK3R2	112	92	6946	6.0669642857142865
0.015806796422547897	3.463108054350128E-4					0.12143019719020876
KEGG_PATHWAY	ptr05164:Influenza A		12			0.04635710422622267
1.0615728400147388E-4	AKT1, TNFRSF1A, EP300, JUN, RELA, JAK1, JAK2, KPNA2, MAP2K6, PIK3R1, ATF2, PIK3R2		112	176	6946	4.228490259740259
0.016633845302948203	3.5682443397910824E-4					0.12783319245252
KEGG_PATHWAY	ptr04152:AMPK signaling pathway		10			0.03863092018851889
1.1689054365524689E-4	AKT1, IRS2, CCND1, HNF4A, PPP2CA, FOXO3, CCNA1, PPARGC1A, PIK3R1, PIK3R2		112	120	6946	5.168154761904763
0.01830026418184494	3.8471317453048215E-4					0.14074969629309653
KEGG_PATHWAY	ptr04110:Cell cycle		10			0.03863092018851889
1.699719823571371E-4	CCND1, EP300, HDAC2, TP53, SMAD2, CDC20, ATR, ANAPC7, CHEK2, CCNA1		112	126	6946	4.922052154195011
0.026500391004939283	5.479693164470723E-4					0.2046058720574062
KEGG_PATHWAY	ptr05142:Chagas disease (American trypanosomiasis)					9
0.034767828169667	2.715370449080709E-4	AKT1, TNFRSF1A, PPP2CA, JUN, RELA, SMAD2, TRAF6, PIK3R1, PIK3R2	112	106	6946	5.265667115902965
0.04200112851934834	8.578054545081981E-4					0.32668276675966723
KEGG_PATHWAY	ptr04668:TNF signaling pathway		9			0.034767828169667
2.8962985762010787E-4	AKT1, TNFRSF1A, JUN, RELA, CASP7, MAP2K6, PIK3R1, ATF2, PIK3R2		112	107	6946	5.216455273698265
8.970120661765391E-4	0.34841518428684326					0.04473658158505356
KEGG_PATHWAY	ptr04910:Insulin signaling pathway					10
0.03863092018851889	3.3731941852345866E-4	AKT1, CBLB, IRS2, CRKL, BRAF, SOS1, CRK, PPARGC1A, PIK3R1, PIK3R2			112	138
4.494047619047619	0.05190963459752107					6946
0.4056773019866844						0.0010245797423676928
KEGG_PATHWAY	ptr04630:Jak-STAT signaling pathway					10
0.03863092018851889	4.620974799948094E-4	AKT1, CCND1, EP300, PIAS3, IL6ST, SOS1, JAK1, JAK2, PIK3R1, PIK3R2	112	144	6946	4.306795634920635
0.07042545520963706	0.0013769431470130877					0.555358897169933
KEGG_PATHWAY	ptr04540:Gap junction		8			0.030904736150815112
4.816751596326377E-4	EGFR, PRKCA, TUBB, SOS1, PDGFRB, TUBA4A, SRC, PRKCB		112	88	6946	5.637987012987013
0.0014086922302233296	0.5788252102135294					0.07329779406780024
KEGG_PATHWAY	ptr05222:Small cell lung cancer		8			0.030904736150815112
5.52244086839362E-4	AKT1, PTK2, CCND1, RELA, TP53, TRAF6, PIK3R1, PIK3R2		112	90	6946	5.512698412698412
0.0015856264276652432	0.663368817860488					0.08357831689527018
KEGG_PATHWAY	ptr04064:NF-kappa B signaling pathway					8
0.030904736150815112	5.52244086839362E-4	LAT, TNFRSF1A, PLCG1, RELA, ZAP70, TRAF6, SYK, BTK	112	90	6946	5.512698412698412
0.08357831689527018	0.0015856264276652432					0.663368817860488

KEGG\_PATHWAY ptr04210:Apoptosis 7 0.027041644131963225  
8.308753352381348E-4 AKT1, TNFRSF1A, RELA, CASP7, TP53, PIK3R1, PIK3R2  
112 70 6946 6.201785714285714 0.12307417750264926  
0.0023424819389964435 0.9965334598408093

KEGG\_PATHWAY ptr05216:Thyroid cancer 5 0.019315460094259444  
0.00122874421271398 CCND1, RET, BRAF, TP53, CTNNB1 112 30 6946  
10.336309523809526 0.17655700828535192 0.0034022860560535273  
1.4704967735307717

KEGG\_PATHWAY ptr04750:Inflammatory mediator regulation of TRP channels 8  
0.030904736150815112 0.0012356820128127937 PRKCA, PLCG1, PRKCE, MAP2K6,  
SRC, PIK3R1, PRKCB, PIK3R2 112 103 6946 4.816920943134535  
0.17746026162805117 0.0033625835238756396 1.4787429740675373

KEGG\_PATHWAY ptr04024:cAMP signaling pathway 11 0.04249401220737078  
0.001236838074220549 AKT1, EP300, BRAF, JUN, RELA, RAP1A, PAK1, VAV2, VAV1,  
PIK3R1, PIK3R2 112 199 6946 3.4281227566403443  
0.17761067706172795 0.0033087743618368526 1.4801169956998428

KEGG\_PATHWAY ptr04550:Signaling pathways regulating pluripotency of stem cells  
9 0.034767828169667 0.0015665791658920861 AKT1, ID2, IL6ST, JAK1,  
SMAD2, JAK2, PIK3R1, CTNNB1, PIK3R2 112 138 6946  
4.044642857142858 0.21941652212253526 0.004120049053059294  
1.8713099329473737

KEGG\_PATHWAY ptr04931:Insulin resistance 8 0.030904736150815112  
0.001811336025114746 AKT1, TNFRSF1A, IRS2, RELA, PRKCE, PPARGC1A, PIK3R1, PIK3R2  
112 110 6946 4.51038961038961 0.24907582635792525  
0.004684902913483557 2.1607590389464693

KEGG\_PATHWAY ptr04150:mTOR signaling pathway 6 0.023178552113111334  
0.0022243631821245347 PRKCA, AKT1, BRAF, PIK3R1, PRKCB, PIK3R2 112  
58 6946 6.41564039408867 0.2966079342851645  
0.005658780682132991 2.647429578166871

KEGG\_PATHWAY ptr05152:Tuberculosis 10 0.03863092018851889  
0.002250390299635508 AKT1, TNFRSF1A, EP300, RELA, JAK1, ITGB2, JAK2, TRAF6, SRC,  
SYK 112 180 6946 3.445436507936508 0.299501002859075  
0.005634263613758517 2.678022892879839

KEGG\_PATHWAY ptr04932:Non-alcoholic fatty liver disease (NAFLD) 9  
0.034767828169667 0.0036519289367965132 CEBPA, AKT1, TNFRSF1A, IRS2, JUN,  
RELA, CASP7, PIK3R1, PIK3R2 112 158 6946 3.532662748643762  
0.4390149004689773 0.008991534294087167 4.312487482540384

KEGG\_PATHWAY ptr05219:Bladder cancer 5 0.019315460094259444  
0.003968514286362476 EGFR, CCND1, BRAF, TP53, SRC 112 41 6946  
7.563153310104529 0.46648747854127737 0.009619171364325996  
4.678184403794406

KEGG\_PATHWAY ptr05140:Leishmaniasis 6 0.023178552113111334  
0.0047496460212710515 JUN, RELA, JAK1, ITGB2, JAK2, TRAF6 112 69  
6946 5.392857142857142 0.5286865495940164 0.01133274821709429

5.575016851159919

KEGG\_PATHWAY ptr04611:Platelet activation 8 0.030904736150815112  
0.005466548148081314 AKT1, FYN, RAP1A, SRC, PIK3R1, SYK, BTK, PIK3R2 112 134  
6946 3.7025586353944564 0.5794046263052266 0.012843437087857401  
6.391289907374286

KEGG\_PATHWAY ptr04920:Adipocytokine signaling pathway 6  
0.023178552113111334 0.005694308959329625 AKT1, TNFRSF1A, IRS2, RELA, JAK2,  
PPARGC1A 112 72 6946 5.168154761904762  
0.5943530864465087 0.013181067111055489 6.64926335059417

KEGG\_PATHWAY ptr04620:Toll-like receptor signaling pathway 7  
0.027041644131963225 0.005927293100068388 AKT1, JUN, RELA, TRAF6, MAP2K6,  
PIK3R1, PIK3R2 112 103 6946 4.214805825242718  
0.6090981672710836 0.013520788121981209 6.912478324238769

KEGG\_PATHWAY ptr04310:Wnt signaling pathway 8 0.030904736150815112  
0.006659118963503931 PRKCA, CCND1, CTBP1, EP300, JUN, TP53, PRKCB, CTNNB1  
112 139 6946 3.5693730729701953 0.6520371617969074  
0.014967704767785306 7.734842257655162

KEGG\_PATHWAY ptr05146:Amoebiasis 7 0.027041644131963225  
0.007117730602028389 PRKCA, PTK2, RELA, ITGB2, PIK3R1, PRKCB, PIK3R2 112 107  
6946 4.057242990654205 0.6765215665797064 0.01577042011195673  
8.246789975773527

KEGG\_PATHWAY ptr04725:Cholinergic synapse 7 0.027041644131963225  
0.008117922110945728 PRKCA, AKT1, FYN, JAK2, PIK3R1, PRKCB, PIK3R2 112  
110 6946 3.946590909090909 0.7241412152649235  
0.017728007102292942 9.354279731333682

KEGG\_PATHWAY ptr05145:Toxoplasmosis 7 0.027041644131963225  
0.009215716974812958 AKT1, TNFRSF1A, RELA, JAK1, JAK2, TRAF6, MAP2K6 112  
113 6946 3.841814159292036 0.7684210012126961  
0.01983938204990554 10.555722995181094

KEGG\_PATHWAY ptr04914:Progesterone-mediated oocyte maturation 6  
0.023178552113111334 0.011342168167917275 AKT1, BRAF, ANAPC7, CCNA1,  
PIK3R1, PIK3R2 112 85 6946 4.377731092436974  
0.8350813594462656 0.024061245561991518 12.841503707722469

KEGG\_PATHWAY ptr04912:GnRH signaling pathway 6 0.023178552113111334  
0.017683394721721722 EGFR, PTK2B, JUN, SOS1, MAP2K6, SRC 112 95  
6946 3.916917293233083 0.9403329301830765 0.03688873454025443  
19.343627933309214

KEGG\_PATHWAY ptr04720:Long-term potentiation 5 0.019315460094259444  
0.023000618531072943 PRKCA, EP300, BRAF, RAP1A, PRKCB 112 68  
6946 4.560136554621849 0.9746896806007453 0.04722411122033576  
24.449562676386684

KEGG\_PATHWAY ptr04960:Aldosterone-regulated sodium reabsorption 4  
0.015452368075407556 0.02392290099560635 PRKCA, PIK3R1, PRKCB, PIK3R2  
112 39 6946 6.36080586080586 0.9781982432500362

0.04847113481660903	25.30441588343324			
KEGG_PATHWAY	ptr04115:p53 signaling pathway	5	0.019315460094259444	
0.0264685579939309	CCND1, TP53, ATR, CHEK2, TP73	112	71	6946
4.367454728370221	0.9855689735111921		0.052888202247566296	
27.61813949371711				
KEGG_PATHWAY	ptr05133:Pertussis	5	0.019315460094259444	
0.03155683893486991	JUN, RELA, CASP7, ITGB2, TRAF6	112	75	6946
4.1345238095238095	0.9936945863264056		0.06211784378617857	
32.04706290538289				
KEGG_PATHWAY	ptr04390:Hippo signaling pathway	7		
0.027041644131963225	0.035393521698484684	CCND1, ID2, PPP2CA, ITGB2,		
SMAD2, TP73, CTNNB1	112	153	6946	2.837418300653595
0.9966323453975672	0.06869572979602057		35.22068816816451	
KEGG_PATHWAY	ptr05168:Herpes simplex infection	8		
0.030904736150815112	0.03614380886764709	TNFRSF1A, EP300, JUN, RELA, TP53,		
JAK1, JAK2, TRAF6	112	195	6946	2.544322344322344
0.9970219353092404	0.06929081142976834		35.82518895900547	
KEGG_PATHWAY	ptr04930:Type II diabetes mellitus	4		
0.015452368075407556	0.04303611666921663	IRS2, PRKCE, PIK3R1, PIK3R2		
112	49	6946	5.06268221574344	0.9990417110215235
0.08126770755336832	41.14115047686602			
KEGG_PATHWAY	ptr04350:TGF-beta signaling pathway	5		
0.019315460094259444	0.04497904051848684	EP300, ID2, SP1, PPP2CA, SMAD2		
112	84	6946	3.6915391156462585	0.9993049137916541
0.08388019251785728	42.564970696209116			
KEGG_PATHWAY	ptr04925:Aldosterone synthesis and secretion	5		
0.019315460094259444	0.04497904051848684	PRKCA, PRKCE, ATF1, ATF2, PRKCB		
112	84	6946	3.6915391156462585	0.9993049137916541
0.08388019251785728	42.564970696209116			
KEGG_PATHWAY	ptr04330:Notch signaling pathway	4		
0.015452368075407556	0.045266877941365066	CTBP1, EP300, KAT2B, HDAC2		
112	50	6946	4.961428571428571	0.9993372429542751
0.0834440514096948	42.77319754642952			
KEGG_PATHWAY	ptr04360:Axon guidance	6	0.023178552113111334	
0.05077026586742797	PTK2, PAK3, FYN, MET, PAK1, RASA1	112	126	
6946	2.953231292517007	0.9997341291390701	0.09231051835685788	
46.62366353771592				
KEGG_PATHWAY	ptr04923:Regulation of lipolysis in adipocytes	4		
0.015452368075407556	0.05725889416421014	AKT1, IRS2, PIK3R1, PIK3R2		
112	55	6946	4.51038961038961	0.9999100489740655
0.10266716520678387	50.85760458325106			
KEGG_PATHWAY	ptr04020:Calcium signaling pathway	7		
0.027041644131963225	0.0663925714012458	EGFR, PRKCA, PLCG1, PTK2B, ERBB3,		
PDGFRB, PRKCB	112	179	6946	2.4252793296089385



0.9999806821321326	0.1172949262758759	56.296955425218954	
KEGG_PATHWAY	ptr04070:Phosphatidylinositol signaling system		5
0.019315460094259444	0.06919654953375681	PRKCA, PLCG1, PIK3R1, PRKCB,	
PIK3R2 112 97	6946 3.1967967599410896		0.9999879894870219
0.12080354808083216	57.852482058393036		
KEGG_PATHWAY	ptr04922:Glucagon signaling pathway		5
0.019315460094259444	0.07129145720363492	AKT1, PRMT1, EP300, PPARGC1A,	
ATF2 112 98	6946 3.1641763848396502		0.9999915869863751
0.12304565505326848	58.98132815682503		
KEGG_PATHWAY	ptr04730:Long-term depression	4	0.015452368075407556
0.08826193717960942	PRKCA, BRAF, PPP2CA, PRKCB		112 66 6946
3.7586580086580086	0.9999995434655311		0.14974399791693627
67.15438230264894			
KEGG_PATHWAY	ptr04144:Endocytosis	8	0.030904736150815112
0.0904199774475127	EGFR, CBLB, TSG101, GIT2, SH3KBP1, SMAD2, TRAF6, SRC		
112 241	6946 2.0586840545346767		0.999999686047253
0.15172440945444132	68.07896216835734		
KEGG_PATHWAY	ptr05031:Amphetamine addiction	4	0.015452368075407556
0.09452779170558474	PRKCA, JUN, ATF2, PRKCB	112	68 6946
3.6481092436974785	0.9999998464429518		0.1567861822210297
69.7732567740473			