Analysis Type: PANTHER Overrepresentation Test (Released 20200728)

Annotation Version and Release Date: PANTHER version 16.0 Released 2020-12-01

Reference List: Homo sapiens (all genes in database)
Test Type: FISHER
Correction: BONFERRONI

Cluster 1						
Genes List:	ABCA1,AURKA,AURKB,CDCA8,CENPU,DMD,INCENP,KIF11,NCAPH,PLK1,PLK2,PTEN,SPAG5,TPX2,SMC2,PRC1,USP13					
Biological Process						
Bonferroni count:	1810					
PANTHER GO-Slim Biological Process	Homo sapiens - REFLIST (20595)	BC_1.txt (17)	BC_1.txt (expected)	BC_1.txt (over/under)	BC_1.txt (fold Enrichment)	BC_1.txt (P-value)
regulation of cytokinesis (GO:0032465)	18	4	0.01	+	> 100	4.15E-06
regulation of cell division (GO:0051302)	21	4	0.02	+	> 100	7.17E-06
cytokinesis (GO:0000910)	50	5	0.04	+	> 100	1.23E-06
membrane fission (GO:0090148)	58	5	0.05	+	> 100	2.47E-06
cell division (GO:0051301)	61	5	0.05	+	99.3	3.14E-06
mitotic spindle organization (GO:0007052)	39	3	0.03	+	93.19	0.00949
microtubule cytoskeleton organization involved in mitosis (GO:1902850)	47	3	0.04	+	77.33	0.0161
mitotic sister chromatid segregation (GO:0000070)	61	3	0.05	+	59.58	0.0341
regulation of cell cycle process (GO:0010564)	110	4	0.09	+	44.05	0.00362
mitotic cell cycle (GO:0000278)	267	7	0.22	+	31.76	2.13E-06
mitotic cell cycle process (GO:1903047)	267	7	0.22	+	31.76	2.13E-06
mitotic nuclear division (GO:0140014)	267	7	0.22	+	31.76	2.13E-06
nuclear division (GO:0000280)	319	7	0.26	+	26.58	7.13E-06
organelle fission (GO:0048285)	340	7	0.28	+	24.94	1.1E-05
regulation of cell cycle (GO:0051726)	207	4	0.17	+	23.41	0.0414
cell cycle process	434	7	0.36	+	19.54	5.72E-05

(GO:0022402)						
cell cycle (GO:0007049)	473	7	0.39	+	17.93	0.000102
Unclassified (UNCLASSIFIED)	9793	7	8.08	-	0.87	0
Molecular Function						
Bonferroni count:	510					
PANTHER GO-Slim Molecular Function	Homo sapiens - REFLIST (20595)	BC_1.txt (17)	BC_1.txt (expected)	BC_1.txt (over/under)	BC_1.txt (fold Enrichment)	BC_1.txt (P-value)
Unclassified (UNCLASSIFIED)	10792	8	8.91	-	0.9	0
Cellular Component						
Bonferroni count:	438					
PANTHER GO-Slim Cellular Component	Homo sapiens - REFLIST (20595)	BC_1.txt (17)	BC_1.txt (expected)	BC_1.txt (over/under)	BC_1.txt (fold Enrichment)	BC_1.txt (P-value)
spindle midzone (GO:0051233)	15	4	0.01	+	> 100	5.33E-07
spindle pole (GO:0000922)	28	4	0.02	+	> 100	4.92E-06
spindle (GO:0005819)	77	6	0.06	+	94.4	1.86E-08
condensed nuclear chromosome (GO:0000794)	48	3	0.04	+	75.72	0.00415
chromosome, centromeric region (GO:0000775)	55	3	0.05	+	66.08	0.00612
condensed chromosome (GO:0000793)	69	3	0.06	+	52.67	0.0118
chromosomal region (GO:0098687)	83	3	0.07	+	43.79	0.02
centrosome (GO:0005813)	134	4	0.11	+	36.16	0.00187
centriole (GO:0005814)	149	4	0.12	+	32.52	0.00282
microtubule organizing center (GO:0005815)	194	4	0.16	+	24.98	0.00781
microtubule cytoskeleton (GO:0015630)	432	6	0.36	+	16.83	0.000395
cytoskeleton (GO:0005856)	667	6	0.55	+	10.9	0.00472
Unclassified (UNCLASSIFIED)	9302	6	7.68	-	0.78	0
Pathway						
Bonferroni count:	156					
PANTHER Pathways	Homo sapiens - REFLIST (20595)	BC_1.txt (17)	BC_1.txt (expected)	BC_1.txt (over/under)	BC_1.txt (fold Enrichment)	BC_1.txt (P-value)
Unclassified (UNCLASSIFIED)	17977	16	14.84	+	1.08	0
Cluster 2						
Genes List:	ABL1,ABL2,CAV1, CAV2,HBA1,HBB, HSPA1A,MYRIP,N OS3,PRKAR2A,PR KAR2B,RAB27B,R					

	IN1,PTGS2,SH2D3C,TRPC1,VAV2,ERN1,AKAP13,MAP2,PRKACA					
Biological Process						
Bonferroni count:	1810					
PANTHER GO-Slim Biological Process	Homo sapiens - REFLIST (20595)	BC_2.txt (24)	BC_2.txt (expected)	BC_2.txt (over/under)	BC_2.txt (fold Enrichment)	BC_2.txt (P-value)
intracellular signal transduction (GO:0035556)	786	8	0.92	+	8.73	0.00359
Unclassified (UNCLASSIFIED)	9793	5	11.41	-	0.44	0
Molecular Function						
Bonferroni count:	510					
PANTHER GO-Slim Molecular Function	Homo sapiens - REFLIST (20595)	BC_2.txt (24)	BC_2.txt (expected)	BC_2.txt (over/under)	BC_2.txt (fold Enrichment)	BC_2.txt (P-value)
kinase binding (GO:0019900)	196	5	0.23	+	21.89	0.00156
protein kinase binding (GO:0019901)	176	4	0.21	+	19.5	0.0266
small molecule binding (GO:0036094)	397	8	0.46	+	17.29	5.89E-06
nucleoside phosphate binding (GO:1901265)	254	5	0.3	+	16.89	0.00536
nucleotide binding (GO:0000166)	254	5	0.3	+	16.89	0.00536
carbohydrate derivative binding (GO:0097367)	272	5	0.32	+	15.77	0.00742
protein serine/threonine kinase activity (GO:0004674)	349	5	0.41	+	12.29	0.024
anion binding (GO:0043168)	500	6	0.58	+	10.3	0.00999
enzyme binding (GO:0019899)	703	7	0.82	+	8.54	0.00589
protein binding (GO:0005515)	2640	12	3.08	+	3.9	0.00615
Unclassified (UNCLASSIFIED)	10792	8	12.58	-	0.64	0
Cellular Component						
Bonferroni count:	438					
PANTHER GO-Slim Cellular Component	Homo sapiens - REFLIST (20595)	BC_2.txt (24)	BC_2.txt (expected)	BC_2.txt (over/under)	BC_2.txt (fold Enrichment)	BC_2.txt (P-value)
perinuclear region of cytoplasm (GO:0048471)	45	3	0.05	+	57.21	0.0101
Unclassified (UNCLASSIFIED)	9302	8	10.84	-	0.74	0
Pathway						
Bonferroni count:	156					
PANTHER Pathways	Homo sapiens - REFLIST (20595)	BC_2.txt (24)	BC_2.txt (expected)	BC_2.txt (over/under)	BC_2.txt (fold Enrichment)	BC_2.txt (P-value)
Histamine H2	25	3	0.03	+	> 100	0.000695

receptor mediated signaling pathway (P04386)						
Enkephalin release (P05913)	35	3	0.04	+	73.55	0.00178
GABA-B receptor II signaling (P05731)	36	3	0.04	+	71.51	0.00192
Endothelin signaling pathway (P00019)	85	6	0.1	+	60.57	1.23E-07
Beta2 adrenergic receptor signaling pathway (P04378)	47	3	0.05	+	54.77	0.00409
Beta1 adrenergic receptor signaling pathway (P04377)	47	3	0.05	+	54.77	0.00409
5HT1 type receptor mediated signaling pathway (P04373)	48	3	0.06	+	53.63	0.00434
Metabotropic glutamate receptor group II pathway (P00040)	49	3	0.06	+	52.54	0.0046
Dopamine receptor mediated signaling pathway (P05912)	59	3	0.07	+	43.63	0.00781
Muscarinic acetylcholine receptor 2 and 4 signaling pathway (P00043)	61	3	0.07	+	42.2	0.0086
Metabotropic glutamate receptor group III pathway (P00039)	70	3	0.08	+	36.78	0.0127
Unclassified (UNCLASSIFIED)	17977	12	20.95	-	0.57	0
Cluster 3						
Genes List:	ACTA1,BAIAP2,GSN,HIP1R,MTSS1,SPIRE1,GC,VCL					
Biological Process						
Bonferroni count:	1810					
PANTHER GO-Slim Biological Process	Homo sapiens - REFLIST (20595)	BC_3.txt (9)	BC_3.txt (expected)	BC_3.txt (over/under)	BC_3.txt (fold Enrichment)	BC_3.txt (P-value)
positive regulation of cellular component organization (GO:0051130)	139	3	0.06	+	49.39	0.0473
Unclassified (UNCLASSIFIED)	9793	4	4.28	-	0.93	0
Molecular Function						
Bonferroni count:	510					
PANTHER GO-Slim Molecular Function	Homo sapiens - REFLIST (20595)	BC_3.txt (9)	BC_3.txt (expected)	BC_3.txt (over/under)	BC_3.txt (fold Enrichment)	BC_3.txt (P-value)
Unclassified (UNCLASSIFIED)	10792	6	4.72	+	1.27	0
Cellular Component						
Bonferroni count:	438					

PANTHER GO-Slim Cellular Component	Homo sapiens - REFLIST (20595)	BC_3.txt (9)	BC_3.txt (expected)	BC_3.txt (over/under)	BC_3.txt (fold Enrichment)	BC_3.txt (P-value)
Unclassified (UNCLASSIFIED)	9302	4	4.06	-	0.98	0
Pathway						
Bonferroni count:	156					
PANTHER Pathways	Homo sapiens - REFLIST (20595)	BC_3.txt (9)	BC_3.txt (expected)	BC_3.txt (over/under)	BC_3.txt (fold Enrichment)	BC_3.txt (P-value)
Unclassified (UNCLASSIFIED)	17977	4	7.86	-	0.51	0
Cluster 4						
Genes List:	AGER,BTC,EGF,EGFR,ERBB3,ERRFI1,HGFAC,LINGO1,MET,NKD2,NRG1,SPINT1,TGFA,AREG,GPNMB,HGF					
Biological Process						
Bonferroni count:	1810					
PANTHER GO-Slim Biological Process	Homo sapiens - REFLIST (20595)	BC_4.txt (16)	BC_4.txt (expected)	BC_4.txt (over/under)	BC_4.txt (fold Enrichment)	BC_4.txt (P-value)
positive regulation of mitotic nuclear division (GO:0045840)	12	3	0.01	+	> 100	0.000314
regulation of epidermal growth factor receptor signaling pathway (GO:0042058)	17	4	0.01	+	> 100	2.6E-06
epidermal growth factor receptor signaling pathway (GO:0007173)	21	4	0.02	+	> 100	5.49E-06
ERBB signaling pathway (GO:0038127)	23	4	0.02	+	> 100	7.61E-06
positive regulation of mitotic cell cycle (GO:0045931)	21	3	0.02	+	> 100	0.00139
positive regulation of peptidyl-tyrosine phosphorylation (GO:0050731)	25	3	0.02	+	> 100	0.00225
regulation of peptidyl-tyrosine phosphorylation (GO:0050730)	30	3	0.02	+	> 100	0.00374
regulation of signaling receptor activity (GO:0010469)	32	3	0.02	+	> 100	0.00448
positive regulation of cell cycle process (GO:0090068)	34	3	0.03	+	> 100	0.00531
regulation of mitotic nuclear division (GO:0007088)	35	3	0.03	+	> 100	0.00576
positive regulation of cell cycle (GO:0045787)	37	3	0.03	+	> 100	0.00674

regulation of nuclear division (GO:0051783)	40	3	0.03	+	96.54	0.00841
peptidyl-tyrosine phosphorylation (GO:0018108)	51	3	0.04	+	75.72	0.0168
peptidyl-tyrosine modification (GO:0018212)	53	3	0.04	+	72.86	0.0188
positive regulation of cell population proliferation (GO:0008284)	90	5	0.07	+	71.51	1.42E-05
positive regulation of protein kinase activity (GO:0045860)	72	4	0.06	+	71.51	0.000544
positive regulation of kinase activity (GO:0033674)	128	7	0.1	+	70.39	8.71E-09
positive regulation of transferase activity (GO:0051347)	136	7	0.11	+	66.25	1.31E-08
transmembrane receptor protein tyrosine kinase signaling pathway (GO:0007169)	212	8	0.16	+	48.57	3.21E-09
regulation of kinase activity (GO:0043549)	206	7	0.16	+	43.74	2.18E-07
regulation of transferase activity (GO:0051338)	215	7	0.17	+	41.91	2.92E-07
regulation of cell population proliferation (GO:0042127)	167	5	0.13	+	38.54	0.00028
regulation of protein kinase activity (GO:0045859)	144	4	0.11	+	35.76	0.00786
cell population proliferation (GO:0008283)	190	5	0.15	+	33.87	0.000523
enzyme linked receptor protein signaling pathway (GO:0007167)	317	8	0.25	+	32.48	7.32E-08
positive regulation of phosphorylation (GO:0042327)	293	7	0.23	+	30.75	2.39E-06
positive regulation of phosphorus metabolic process (GO:0010562)	300	7	0.23	+	30.03	2.8E-06
positive regulation of phosphate metabolic process (GO:0045937)	300	7	0.23	+	30.03	2.8E-06
positive regulation of catalytic activity (GO:0043085)	323	7	0.25	+	27.9	4.63E-06
regulation of phosphorylation (GO:0042325)	393	7	0.31	+	22.93	1.75E-05
regulation of phosphorus metabolic process	419	7	0.33	+	21.5	2.7E-05

(GO:0051174)						
regulation of phosphate metabolic process (GO:0019220)	419	7	0.33	+	21.5	2.7E-05
positive regulation of molecular function (GO:0044093)	421	7	0.33	+	21.4	2.79E-05
regulation of catalytic activity (GO:0050790)	646	7	0.5	+	13.95	0.000501
phosphorylation (GO:0016310)	704	7	0.55	+	12.8	0.000891
positive regulation of cellular metabolic process (GO:0031325)	768	7	0.6	+	11.73	0.00159
cell surface receptor signaling pathway (GO:0007166)	1003	9	0.78	+	11.55	2.43E-05
regulation of molecular function (GO:0065009)	806	7	0.63	+	11.18	0.00219
positive regulation of metabolic process (GO:0009893)	841	7	0.65	+	10.71	0.00291
phosphate-containing compound metabolic process (GO:0006796)	1090	7	0.85	+	8.27	0.0161
phosphorus metabolic process (GO:0006793)	1103	7	0.86	+	8.17	0.0174
positive regulation of cellular process (GO:0048522)	1295	7	1.01	+	6.96	0.0493
signal transduction (GO:0007165)	2062	9	1.6	+	5.62	0.011
signaling (GO:0023052)	2218	9	1.72	+	5.22	0.0201
cell communication (GO:0007154)	2230	9	1.73	+	5.19	0.021
response to stimulus (GO:0050896)	3027	10	2.35	+	4.25	0.0293
Unclassified (UNCLASSIFIED)	9793	5	7.61	-	0.66	0
Molecular Function						
Bonferroni count:	510					
PANTHER GO-Slim Molecular Function	Homo sapiens - REFLIST (20595)	BC_4.txt (16)	BC_4.txt (expected)	BC_4.txt (over/under)	BC_4.txt (fold Enrichment)	BC_4.txt (P-value)
transmembrane receptor protein tyrosine kinase activity (GO:0004714)	54	3	0.04	+	71.51	0.00558
protein tyrosine kinase activity (GO:0004713)	83	4	0.06	+	62.03	0.000264
transmembrane receptor protein kinase activity (GO:0019199)	64	3	0.05	+	60.34	0.0091
Unclassified	10792	9	8.38	+	1.07	0

(UNCLASSIFIED)						
Cellular Component						
Bonferroni count:	438					
PANTHER GO-Slim Cellular Component	Homo sapiens - REFLIST (20595)	BC_4.txt (16)	BC_4.txt (expected)	BC_4.txt (over/under)	BC_4.txt (fold Enrichment)	BC_4.txt (P-value)
Unclassified (UNCLASSIFIED)	9302	6	7.23	-	0.83	0
Pathway						
Bonferroni count:	156					
PANTHER Pathways	Homo sapiens - REFLIST (20595)	BC_4.txt (16)	BC_4.txt (expected)	BC_4.txt (over/under)	BC_4.txt (fold Enrichment)	BC_4.txt (P-value)
EGF receptor signaling pathway (P00018)	141	7	0.11	+	63.9	1.44E-09
Unclassified (UNCLASSIFIED)	17977	8	13.97	-	0.57	0
Cluster 5						
Genes List:	AHR,BAIAP2L1,DDB1,EPS8,SHANK1,SHANK2,SHANK3,WDTC1,DCAF4,FBXW5					
Biological Process						
Bonferroni count:	1810					
PANTHER GO-Slim Biological Process	Homo sapiens - REFLIST (20595)	BC_5.txt (10)	BC_5.txt (expected)	BC_5.txt (over/under)	BC_5.txt (fold Enrichment)	BC_5.txt (P-value)
dendritic spine organization (GO:0097061)	11	3	0.01	+	> 100	5.41E-05
regulation of dendritic spine development (GO:0060998)	13	3	0.01	+	> 100	8.32E-05
regulation of AMPA receptor activity (GO:2000311)	15	3	0.01	+	> 100	0.000121
neuromuscular junction development (GO:0007528)	15	3	0.01	+	> 100	0.000121
chemical synaptic transmission, postsynaptic (GO:0099565)	15	3	0.01	+	> 100	0.000121
ionotropic glutamate receptor signaling pathway (GO:0035235)	17	3	0.01	+	> 100	0.000169
regulation of neurotransmitter receptor activity (GO:0099601)	20	3	0.01	+	> 100	0.000263
regulation of synaptic transmission, glutamatergic (GO:0051966)	20	3	0.01	+	> 100	0.000263
dendrite morphogenesis (GO:0048813)	21	3	0.01	+	> 100	0.0003

synapse assembly (GO:0007416)	22	3	0.01	+	> 100	0.000341
regulation of dendrite development (GO:0050773)	22	3	0.01	+	> 100	0.000341
positive regulation of synaptic transmission (GO:0050806)	26	3	0.01	+	> 100	0.000541
regulation of synaptic plasticity (GO:0048167)	26	3	0.01	+	> 100	0.000541
positive regulation of cell projection organization (GO:0031346)	38	4	0.02	+	> 100	5.62E-06
glutamate receptor signaling pathway (GO:0007215)	29	3	0.01	+	> 100	0.000734
positive regulation of neuron projection development (GO:0010976)	30	3	0.01	+	> 100	0.000807
regulation of signaling receptor activity (GO:0010469)	32	3	0.02	+	> 100	0.000967
positive regulation of neuron differentiation (GO:0045666)	33	3	0.02	+	> 100	0.00105
dendrite development (GO:0016358)	35	3	0.02	+	> 100	0.00125
synaptic transmission, glutamatergic (GO:0035249)	36	3	0.02	+	> 100	0.00135
positive regulation of neurogenesis (GO:0050769)	39	3	0.02	+	> 100	0.00169
regulation of cation channel activity (GO:2001257)	40	3	0.02	+	> 100	0.00182
positive regulation of nervous system development (GO:0051962)	43	3	0.02	+	> 100	0.00224
developmental growth (GO:0048589)	44	3	0.02	+	> 100	0.00239
positive regulation of cell development (GO:0010720)	46	3	0.02	+	> 100	0.00271
head development (GO:0060322)	48	3	0.02	+	> 100	0.00306
brain development (GO:0007420)	48	3	0.02	+	> 100	0.00306
regulation of system process (GO:0044057)	48	3	0.02	+	> 100	0.00306
growth (GO:0040007)	54	3	0.03	+	> 100	0.0043
regulation of transmembrane transporter activity (GO:0022898)	57	3	0.03	+	> 100	0.00502
regulation of ion	57	3	0.03	+	> 100	0.00502

transmembrane transporter activity (GO:0032412)						
regulation of transporter activity (GO:0032409)	57	3	0.03	+	> 100	0.00502
regulation of cation transmembrane transport (GO:1904062)	62	3	0.03	+	99.65	0.00641
synapse organization (GO:0050808)	63	3	0.03	+	98.07	0.00671
regulation of plasma membrane bounded cell projection organization (GO:0120035)	89	4	0.04	+	92.56	0.000145
positive regulation of cell differentiation (GO:0045597)	67	3	0.03	+	92.22	0.00802
regulation of cell projection organization (GO:0031344)	91	4	0.04	+	90.53	0.000158
regulation of neuron projection development (GO:0010975)	74	3	0.04	+	83.49	0.0107
central nervous system development (GO:0007417)	79	3	0.04	+	78.21	0.0129
cell junction assembly (GO:0034329)	81	3	0.04	+	76.28	0.0139
regulation of ion transmembrane transport (GO:0034765)	82	3	0.04	+	75.35	0.0144
regulation of trans-synaptic signaling (GO:0099177)	83	3	0.04	+	74.44	0.0149
modulation of chemical synaptic transmission (GO:0050804)	83	3	0.04	+	74.44	0.0149
positive regulation of cellular component organization (GO:0051130)	139	5	0.07	+	74.08	6.89E-06
regulation of neuron differentiation (GO:0045664)	85	3	0.04	+	72.69	0.016
regulation of transmembrane transport (GO:0034762)	87	3	0.04	+	71.02	0.0171
positive regulation of developmental process (GO:0051094)	92	3	0.04	+	67.16	0.0201
regulation of neurogenesis (GO:0050767)	108	3	0.05	+	57.21	0.0321
regulation of ion transport (GO:0043269)	110	3	0.05	+	56.17	0.0339

regulation of nervous system development (GO:0051960)	118	3	0.06	+	52.36	0.0416
positive regulation of multicellular organismal process (GO:0051240)	118	3	0.06	+	52.36	0.0416
regulation of cell development (GO:0060284)	121	3	0.06	+	51.06	0.0448
animal organ morphogenesis (GO:0009887)	121	3	0.06	+	51.06	0.0448
regulation of cellular component organization (GO:0051128)	410	5	0.2	+	25.12	0.00136
plasma membrane bounded cell projection organization (GO:0120036)	395	4	0.19	+	20.86	0.048
Molecular Function						
Bonferroni count:	510					
PANTHER GO-Slim Molecular Function	Homo sapiens - REFLIST (20595)	BC_5.txt (10)	BC_5.txt (expected)	BC_5.txt (over/under)	BC_5.txt (fold Enrichment)	BC_5.txt (P-value)
signaling adaptor activity (GO:0035591)	11	3	0.01	+	> 100	1.52E-05
protein-macromolecule adaptor activity (GO:0030674)	84	3	0.04	+	73.55	0.00436
molecular adaptor activity (GO:0060090)	119	3	0.06	+	51.92	0.012
Unclassified (UNCLASSIFIED)	10792	4	5.24	-	0.76	0
Cellular Component						
Bonferroni count:	438					
PANTHER GO-Slim Cellular Component	Homo sapiens - REFLIST (20595)	BC_5.txt (10)	BC_5.txt (expected)	BC_5.txt (over/under)	BC_5.txt (fold Enrichment)	BC_5.txt (P-value)
dendritic spine (GO:0043197)	30	3	0.01	+	> 100	0.000195
neuron spine (GO:0044309)	30	3	0.01	+	> 100	0.000195
ionotropic glutamate receptor complex (GO:0008328)	35	3	0.02	+	> 100	0.000301
postsynaptic membrane (GO:0045211)	58	3	0.03	+	> 100	0.00128
neuron to neuron synapse (GO:0098984)	66	3	0.03	+	93.61	0.00186
asymmetric synapse (GO:0032279)	66	3	0.03	+	93.61	0.00186
postsynaptic density (GO:0014069)	66	3	0.03	+	93.61	0.00186
postsynaptic specialization (GO:0099572)	70	3	0.03	+	88.26	0.0022

synaptic membrane (GO:0097060)	78	3	0.04	+	79.21	0.00302
dendritic tree (GO:0097447)	108	3	0.05	+	57.21	0.00778
dendrite (GO:0030425)	108	3	0.05	+	57.21	0.00778
postsynapse (GO:0098794)	126	3	0.06	+	49.04	0.0122
ion channel complex (GO:0034702)	131	3	0.06	+	47.16	0.0137
somatodendritic compartment (GO:0036477)	134	3	0.07	+	46.11	0.0146
transmembrane transporter complex (GO:1902495)	136	3	0.07	+	45.43	0.0153
transporter complex (GO:1990351)	141	3	0.07	+	43.82	0.0169
receptor complex (GO:0043235)	213	4	0.1	+	38.68	0.00105
Pathway						
Bonferroni count:	156					
PANTHER Pathways	Homo sapiens - REFLIST (20595)	BC_5.txt (10)	BC_5.txt (expected)	BC_5.txt (over/under)	BC_5.txt (fold Enrichment)	BC_5.txt (P-value)
Ionotropic glutamate receptor pathway (P00037)	50	3	0.02	+	> 100	0.000297
Unclassified (UNCLASSIFIED)	17977	7	8.73	-	0.8	0
Cluster 6						
Genes List:	AMOT,FOS,FOSL1,JUN,MBD3,MECOM,PTPN14,RUNX2,SOX2,SOX9,TEAD1,TEAD3,TLE1,YAP1,ATF3,KLF4,POU5F1,FOSB,JUNB,AMOTL2,TEAD4					
Biological Process						
Bonferroni count:	1810					
PANTHER GO-Slim Biological Process	Homo sapiens - REFLIST (20595)	BC_6.txt (21)	BC_6.txt (expected)	BC_6.txt (over/under)	BC_6.txt (fold Enrichment)	BC_6.txt (P-value)
hippo signaling (GO:0035329)	17	6	0.02	+	> 100	9.21E-11
embryonic organ development (GO:0048568)	39	3	0.04	+	75.44	0.0184
vasculature development (GO:0001944)	55	3	0.06	+	53.49	0.0491
circulatory system development (GO:0072359)	110	4	0.11	+	35.66	0.00893
system development (GO:0048731)	804	8	0.82	+	9.76	0.00131
regulation of transcription by RNA polymerase II (GO:0006357)	1591	15	1.62	+	9.25	1.39E-09
transcription by	1635	15	1.67	+	9	2.06E-09

RNA polymerase II (GO:0006366)						
multicellular organism development (GO:0007275)	906	8	0.92	+	8.66	0.00318
regulation of transcription, DNA-templated (GO:0006355)	1984	16	2.02	+	7.91	1.34E-09
regulation of nucleic acid-templated transcription (GO:1903506)	1984	16	2.02	+	7.91	1.34E-09
regulation of RNA biosynthetic process (GO:2001141)	1984	16	2.02	+	7.91	1.34E-09
anatomical structure development (GO:0048856)	1126	9	1.15	+	7.84	0.00131
nucleic acid-templated transcription (GO:0097659)	2047	16	2.09	+	7.67	2.16E-09
transcription, DNA-templated (GO:0006351)	2047	16	2.09	+	7.67	2.16E-09
RNA biosynthetic process (GO:0032774)	2054	16	2.09	+	7.64	2.28E-09
regulation of cellular macromolecule biosynthetic process (GO:2000112)	2112	16	2.15	+	7.43	3.5E-09
regulation of RNA metabolic process (GO:0051252)	2113	16	2.15	+	7.43	3.53E-09
regulation of macromolecule biosynthetic process (GO:0010556)	2120	16	2.16	+	7.4	3.71E-09
regulation of cellular biosynthetic process (GO:0031326)	2134	16	2.18	+	7.35	4.11E-09
regulation of biosynthetic process (GO:0009889)	2141	16	2.18	+	7.33	4.32E-09
regulation of nucleobase-containing compound metabolic process (GO:0019219)	2161	16	2.2	+	7.26	4.98E-09
developmental process (GO:0032502)	1271	9	1.3	+	6.94	0.00359
nucleobase-containing compound biosynthetic process (GO:0034654)	2297	16	2.34	+	6.83	1.27E-08
heterocycle biosynthetic process (GO:0018130)	2322	16	2.37	+	6.76	1.5E-08
aromatic compound biosynthetic process (GO:0019438)	2323	16	2.37	+	6.75	1.51E-08

organic cyclic compound biosynthetic process (GO:1901362)	2350	16	2.4	+	6.68	1.81E-08
regulation of gene expression (GO:0010468)	2410	16	2.46	+	6.51	2.66E-08
cellular macromolecule biosynthetic process (GO:0034645)	2580	16	2.63	+	6.08	7.55E-08
macromolecule biosynthetic process (GO:0009059)	2590	16	2.64	+	6.06	8.01E-08
cellular nitrogen compound biosynthetic process (GO:0044271)	2597	16	2.65	+	6.04	8.35E-08
RNA metabolic process (GO:0016070)	2659	16	2.71	+	5.9	1.2E-07
regulation of nitrogen compound metabolic process (GO:0051171)	2715	16	2.77	+	5.78	1.65E-07
regulation of primary metabolic process (GO:0080090)	2743	16	2.8	+	5.72	1.92E-07
regulation of cellular metabolic process (GO:0031323)	2835	16	2.89	+	5.53	3.18E-07
nucleic acid metabolic process (GO:0090304)	2918	16	2.98	+	5.38	4.93E-07
regulation of macromolecule metabolic process (GO:0060255)	2931	16	2.99	+	5.35	5.27E-07
cellular biosynthetic process (GO:0044249)	2966	16	3.02	+	5.29	6.31E-07
organic substance biosynthetic process (GO:1901576)	3004	16	3.06	+	5.22	7.66E-07
biosynthetic process (GO:0009058)	3011	16	3.07	+	5.21	7.93E-07
gene expression (GO:0010467)	3048	16	3.11	+	5.15	9.55E-07
regulation of metabolic process (GO:0019222)	3093	16	3.15	+	5.07	1.19E-06
nucleobase-containing compound metabolic process (GO:0006139)	3150	16	3.21	+	4.98	1.57E-06
heterocycle metabolic process (GO:0046483)	3198	16	3.26	+	4.91	1.97E-06
cellular aromatic compound metabolic process (GO:0006725)	3214	16	3.28	+	4.88	2.13E-06
organic cyclic compound metabolic process (GO:1901360)	3262	16	3.33	+	4.81	2.66E-06

cellular nitrogen compound metabolic process (GO:0034641)	3483	16	3.55	+	4.51	7.14E-06
cellular macromolecule metabolic process (GO:0044260)	4233	16	4.32	+	3.71	0.000131
regulation of cellular process (GO:0050794)	5092	19	5.19	+	3.66	6.73E-07
regulation of biological process (GO:0050789)	5324	19	5.43	+	3.5	1.52E-06
biological regulation (GO:0065007)	5797	19	5.91	+	3.21	7.22E-06
macromolecule metabolic process (GO:0043170)	5051	16	5.15	+	3.11	0.00173
nitrogen compound metabolic process (GO:0006807)	5350	16	5.46	+	2.93	0.00397
primary metabolic process (GO:0044238)	5603	16	5.71	+	2.8	0.0077
cellular metabolic process (GO:0044237)	5684	16	5.8	+	2.76	0.00945
organic substance metabolic process (GO:0071704)	5910	16	6.03	+	2.66	0.0164
metabolic process (GO:0008152)	6178	16	6.3	+	2.54	0.0307
Molecular Function						
Bonferroni count:	510					
PANTHER GO-Slim Molecular Function	Homo sapiens - REFLIST (20595)	BC_6.txt (21)	BC_6.txt (expected)	BC_6.txt (over/under)	BC_6.txt (fold Enrichment)	BC_6.txt (P-value)
RNA polymerase II cis-regulatory region sequence-specific DNA binding (GO:0000978)	1054	15	1.07	+	13.96	9.89E-13
cis-regulatory region sequence-specific DNA binding (GO:0000987)	1057	15	1.08	+	13.92	1.03E-12
DNA-binding transcription factor activity, RNA polymerase II-specific (GO:0000981)	1226	15	1.25	+	12	8.94E-12
DNA-binding transcription factor activity (GO:0003700)	1313	15	1.34	+	11.2	2.42E-11
RNA polymerase II transcription regulatory region sequence-specific DNA binding (GO:0000977)	1337	15	1.36	+	11	3.15E-11
transcription regulator activity (GO:0140110)	1559	17	1.59	+	10.69	2.18E-13

transcription regulatory region sequence-specific DNA binding (GO:0000976)	1377	15	1.4	+	10.68	4.84E-11
regulatory region nucleic acid binding (GO:0001067)	1377	15	1.4	+	10.68	4.84E-11
sequence-specific double-stranded DNA binding (GO:1990837)	1403	15	1.43	+	10.49	6.34E-11
sequence-specific DNA binding (GO:0043565)	1436	15	1.46	+	10.24	8.89E-11
double-stranded DNA binding (GO:0003690)	1451	15	1.48	+	10.14	1.03E-10
DNA binding (GO:0003677)	1648	15	1.68	+	8.93	6.52E-10
molecular function regulator (GO:0098772)	2358	17	2.4	+	7.07	2.04E-10
nucleic acid binding (GO:0003676)	2248	15	2.29	+	6.54	5.63E-08
heterocyclic compound binding (GO:1901363)	2595	15	2.65	+	5.67	4.33E-07
organic cyclic compound binding (GO:0097159)	2632	15	2.68	+	5.59	5.29E-07
binding (GO:0005488)	5963	16	6.08	+	2.63	0.00525
molecular_function (GO:0003674)	9803	19	10	+	1.9	0.0371
Cellular Component						
Bonferroni count:	438					
PANTHER GO-Slim Cellular Component	Homo sapiens - REFLIST (20595)	BC_6.txt (21)	BC_6.txt (expected)	BC_6.txt (over/under)	BC_6.txt (fold Enrichment)	BC_6.txt (P-value)
transcription regulator complex (GO:0005667)	200	6	0.2	+	29.42	1.94E-05
nuclear chromatin (GO:0000790)	704	9	0.72	+	12.54	5.97E-06
chromatin (GO:0000785)	738	9	0.75	+	11.96	8.93E-06
nuclear chromosome (GO:0000228)	787	9	0.8	+	11.22	1.55E-05
chromosome (GO:0005694)	898	9	0.92	+	9.83	4.74E-05
nuclear lumen (GO:0031981)	1398	9	1.43	+	6.31	0.0019
membrane-enclosed lumen (GO:0031974)	1494	9	1.52	+	5.91	0.00327
intracellular organelle lumen (GO:0070013)	1494	9	1.52	+	5.91	0.00327
organelle lumen (GO:0043233)	1494	9	1.52	+	5.91	0.00327
intracellular non-membrane-bounded organelle (GO:0043232)	1959	9	2	+	4.51	0.0287

non-membrane-bounded organelle (GO:0043228)	1959	9	2	+	4.51	0.0287
nucleus (GO:0005634)	3956	17	4.03	+	4.21	7.99E-07
membrane-bounded organelle (GO:0043227)	5999	19	6.12	+	3.11	3.26E-06
intracellular membrane-bounded organelle (GO:0043231)	5903	17	6.02	+	2.82	0.000449
intracellular organelle (GO:0043229)	6633	19	6.76	+	2.81	2.02E-05
organelle (GO:0043226)	6781	19	6.91	+	2.75	3.01E-05
intracellular (GO:0005622)	8253	19	8.42	+	2.26	0.00102
Pathway						
Bonferroni count:	156					
PANTHER Pathways	Homo sapiens - REFLIST (20595)	BC_6.txt (21)	BC_6.txt (expected)	BC_6.txt (over/under)	BC_6.txt (fold Enrichment)	BC_6.txt (P-value)
Apoptosis signaling pathway (P00006)	118	4	0.12	+	33.24	0.00101
TGF-beta signaling pathway (P00052)	102	3	0.1	+	28.84	0.0249
Gonadotropin-releasing hormone receptor pathway (P06664)	231	5	0.24	+	21.23	0.000515
Unclassified (UNCLASSIFIED)	17977	13	18.33	-	0.71	0
Cluster 7						
Genes List:	AP4B1,BUB1B,CDC20,CDC27,PTTG1,BUB1					
Biological Process						
Bonferroni count:	1810					
PANTHER GO-Slim Biological Process	Homo sapiens - REFLIST (20595)	BC_7.txt (6)	BC_7.txt (expected)	BC_7.txt (over/under)	BC_7.txt (fold Enrichment)	BC_7.txt (P-value)
negative regulation of mitotic sister chromatid segregation (GO:0033048)	14	3	0	+	> 100	1.69E-05
negative regulation of sister chromatid segregation (GO:0033046)	14	3	0	+	> 100	1.69E-05
negative regulation of mitotic sister chromatid separation (GO:2000816)	14	3	0	+	> 100	1.69E-05
negative regulation of mitotic nuclear division (GO:0045839)	14	3	0	+	> 100	1.69E-05
negative regulation of chromosome separation	15	3	0	+	> 100	2.02E-05

(GO:1905819)						
negative regulation of chromosome segregation (GO:0051985)	15	3	0	+	> 100	2.02E-05
negative regulation of nuclear division (GO:0051784)	18	3	0.01	+	> 100	3.3E-05
regulation of mitotic sister chromatid separation (GO:0010965)	19	3	0.01	+	> 100	3.82E-05
mitotic sister chromatid separation (GO:0051306)	20	3	0.01	+	> 100	4.39E-05
regulation of chromosome separation (GO:1905818)	21	3	0.01	+	> 100	5.02E-05
regulation of mitotic sister chromatid segregation (GO:0033047)	21	3	0.01	+	> 100	5.02E-05
regulation of mitotic metaphase/anaphase transition (GO:0030071)	15	2	0	+	> 100	0.0174
regulation of sister chromatid segregation (GO:0033045)	24	3	0.01	+	> 100	7.25E-05
regulation of chromosome segregation (GO:0051983)	26	3	0.01	+	> 100	9.05E-05
regulation of mitotic nuclear division (GO:0007088)	35	3	0.01	+	> 100	0.000209
negative regulation of chromosome organization (GO:2001251)	37	3	0.01	+	> 100	0.000244
negative regulation of cell cycle process (GO:0010948)	39	3	0.01	+	> 100	0.000284
regulation of nuclear division (GO:0051783)	40	3	0.01	+	> 100	0.000305
chromosome separation (GO:0051304)	41	3	0.01	+	> 100	0.000328
meiotic chromosome segregation (GO:0045132)	43	3	0.01	+	> 100	0.000375
negative regulation of mitotic cell cycle (GO:0045930)	58	3	0.02	+	> 100	0.000889
mitotic sister chromatid segregation (GO:0000070)	61	3	0.02	+	> 100	0.00103
regulation of chromosome organization (GO:0033044)	68	3	0.02	+	> 100	0.00141
sister chromatid segregation	79	3	0.02	+	> 100	0.00218

(GO:0000819)						
negative regulation of organelle organization (GO:0010639)	85	3	0.02	+	> 100	0.0027
meiotic cell cycle process (GO:1903046)	91	3	0.03	+	> 100	0.0033
meiotic nuclear division (GO:0140013)	91	3	0.03	+	> 100	0.0033
meiotic cell cycle (GO:0051321)	91	3	0.03	+	> 100	0.0033
negative regulation of cell cycle (GO:0045786)	93	3	0.03	+	> 100	0.00351
regulation of mitotic cell cycle (GO:0007346)	103	3	0.03	+	99.98	0.00474
nuclear chromosome segregation (GO:0098813)	109	3	0.03	+	94.47	0.0056
regulation of cell cycle process (GO:0010564)	110	3	0.03	+	93.61	0.00575
negative regulation of cellular component organization (GO:0051129)	114	3	0.03	+	90.33	0.00638
chromosome segregation (GO:0007059)	125	3	0.04	+	82.38	0.00837
reproductive process (GO:0022414)	179	3	0.05	+	57.53	0.0241
reproduction (GO:0000003)	179	3	0.05	+	57.53	0.0241
regulation of cell cycle (GO:0051726)	207	3	0.06	+	49.75	0.037
Molecular Function						
Bonferroni count:	510					
PANTHER GO-Slim Molecular Function	Homo sapiens - REFLIST (20595)	BC_7.txt (6)	BC_7.txt (expected)	BC_7.txt (over/under)	BC_7.txt (fold Enrichment)	BC_7.txt (P-value)
Unclassified (UNCLASSIFIED)	10792	3	3.14	-	0.95	0
Cellular Component						
Bonferroni count:	438					
PANTHER GO-Slim Cellular Component	Homo sapiens - REFLIST (20595)	BC_7.txt (6)	BC_7.txt (expected)	BC_7.txt (over/under)	BC_7.txt (fold Enrichment)	BC_7.txt (P-value)
Pathway						
Bonferroni count:	156					
PANTHER Pathways	Homo sapiens - REFLIST (20595)	BC_7.txt (6)	BC_7.txt (expected)	BC_7.txt (over/under)	BC_7.txt (fold Enrichment)	BC_7.txt (P-value)
Unclassified (UNCLASSIFIED)	17977	6	5.24	+	1.15	0
Cluster 8						
Genes List:	AR,BAG1,CDK7,POLR2A,PRKCB,PR					

	KCD,RIPK4,RPRD1B,TGFB1I1,FOXA1,TMF1,CCNK,SMN1,PIK3CG					
Biological Process						
Bonferroni count:	1810					
PANTHER GO-Slim Biological Process	Homo sapiens - REFLIST (20595)	BC_8.txt (15)	BC_8.txt (expected)	BC_8.txt (over/under)	BC_8.txt (fold Enrichment)	BC_8.txt (P-value)
Unclassified (UNCLASSIFIED)	9793	5	7.13	-	0.7	0
Molecular Function						
Bonferroni count:	510					
PANTHER GO-Slim Molecular Function	Homo sapiens - REFLIST (20595)	BC_8.txt (15)	BC_8.txt (expected)	BC_8.txt (over/under)	BC_8.txt (fold Enrichment)	BC_8.txt (P-value)
phosphotransferase activity, alcohol group as acceptor (GO:0016773)	555	5	0.4	+	12.37	0.0178
transferase activity, transferring phosphorus-containing groups (GO:0016772)	714	6	0.52	+	11.54	0.00347
kinase activity (GO:0016301)	613	5	0.45	+	11.2	0.0285
Unclassified (UNCLASSIFIED)	10792	3	7.86	-	0.38	0
Cellular Component						
Bonferroni count:	438					
PANTHER GO-Slim Cellular Component	Homo sapiens - REFLIST (20595)	BC_8.txt (15)	BC_8.txt (expected)	BC_8.txt (over/under)	BC_8.txt (fold Enrichment)	BC_8.txt (P-value)
RNA polymerase II, holoenzyme (GO:0016591)	63	3	0.05	+	65.38	0.00608
nuclear DNA-directed RNA polymerase complex (GO:0055029)	82	3	0.06	+	50.23	0.013
DNA-directed RNA polymerase complex (GO:0000428)	83	3	0.06	+	49.63	0.0135
RNA polymerase complex (GO:0030880)	84	3	0.06	+	49.04	0.014
transferase complex, transferring phosphorus-containing groups (GO:0061695)	188	5	0.14	+	36.52	8.33E-05
transferase complex (GO:1990234)	482	5	0.35	+	14.24	0.0078
nucleoplasm (GO:0005654)	504	5	0.37	+	13.62	0.00965
nuclear lumen (GO:0031981)	1398	7	1.02	+	6.87	0.0117
membrane-enclosed lumen (GO:0031974)	1494	7	1.09	+	6.43	0.0179
intracellular organelle lumen (GO:0070013)	1494	7	1.09	+	6.43	0.0179

organelle lumen (GO:0043233)	1494	7	1.09	+	6.43	0.0179
Unclassified (UNCLASSIFIED)	9302	3	6.77	-	0.44	0
Pathway						
Bonferroni count:	156					
PANTHER Pathways	Homo sapiens - REFLIST (20595)	BC_8.txt (15)	BC_8.txt (expected)	BC_8.txt (over/under)	BC_8.txt (fold Enrichment)	BC_8.txt (P-value)
VEGF signaling pathway (P00056)	68	4	0.05	+	80.76	2.83E-05
B cell activation (P00010)	70	3	0.05	+	58.84	0.00293
Endothelin signaling pathway (P00019)	85	3	0.06	+	48.46	0.00514
Apoptosis signaling pathway (P00006)	118	4	0.09	+	46.54	0.000237
FGF signaling pathway (P00021)	123	3	0.09	+	33.49	0.015
Angiogenesis (P00005)	175	4	0.13	+	31.38	0.00109
EGF receptor signaling pathway (P00018)	141	3	0.1	+	29.21	0.0223
Unclassified (UNCLASSIFIED)	17977	8	13.09	-	0.61	0
Cluster 9						
Genes List:	ARRB2,CNR1,GRM2,HTR2A,INSR,IRS1,MAP1A,NDUFB10,NTF3,NTRK3,PTPN1,PTPN3,SORT1,ADRB1,EDNRA,ANKS1B,GLUL,PON2,GRB14,BDNF					
Biological Process						
Bonferroni count:	1810					
PANTHER GO-Slim Biological Process	Homo sapiens - REFLIST (20595)	BC_9.txt (20)	BC_9.txt (expected)	BC_9.txt (over/under)	BC_9.txt (fold Enrichment)	BC_9.txt (P-value)
transmembrane receptor protein tyrosine kinase signaling pathway (GO:0007169)	212	6	0.21	+	29.14	8.09E-05
cellular response to endogenous stimulus (GO:0071495)	244	5	0.24	+	21.1	0.00598
response to endogenous stimulus (GO:0009719)	259	5	0.25	+	19.88	0.00795
enzyme linked receptor protein signaling pathway (GO:0007167)	317	6	0.31	+	19.49	0.000823
positive regulation of phosphorylation (GO:0042327)	293	5	0.28	+	17.57	0.0143
positive regulation of phosphorus metabolic process	300	5	0.29	+	17.16	0.016

(GO:0010562)						
positive regulation of phosphate metabolic process (GO:0045937)	300	5	0.29	+	17.16	0.016
regulation of cell communication (GO:0010646)	813	7	0.79	+	8.87	0.0137
regulation of signaling (GO:0023051)	813	7	0.79	+	8.87	0.0137
signal transduction (GO:0007165)	2062	11	2	+	5.49	0.00133
signaling (GO:0023052)	2218	11	2.15	+	5.11	0.00277
cell communication (GO:0007154)	2230	11	2.17	+	5.08	0.00292
cellular response to stimulus (GO:0051716)	2522	11	2.45	+	4.49	0.00989
Unclassified (UNCLASSIFIED)	9793	6	9.51	-	0.63	0
Molecular Function						
Bonferroni count:	510					
PANTHER GO-Slim Molecular Function	Homo sapiens - REFLIST (20595)	BC_9.txt (20)	BC_9.txt (expected)	BC_9.txt (over/under)	BC_9.txt (fold Enrichment)	BC_9.txt (P-value)
transmembrane signaling receptor activity (GO:0004888)	669	6	0.65	+	9.24	0.0161
molecular transducer activity (GO:0060089)	783	6	0.76	+	7.89	0.0385
signaling receptor activity (GO:0038023)	783	6	0.76	+	7.89	0.0385
Unclassified (UNCLASSIFIED)	10792	7	10.48	-	0.67	0
Cellular Component						
Bonferroni count:	438					
PANTHER GO-Slim Cellular Component	Homo sapiens - REFLIST (20595)	BC_9.txt (20)	BC_9.txt (expected)	BC_9.txt (over/under)	BC_9.txt (fold Enrichment)	BC_9.txt (P-value)
Unclassified (UNCLASSIFIED)	9302	5	9.03	-	0.55	0
Pathway						
Bonferroni count:	156					
PANTHER Pathways	Homo sapiens - REFLIST (20595)	BC_9.txt (20)	BC_9.txt (expected)	BC_9.txt (over/under)	BC_9.txt (fold Enrichment)	BC_9.txt (P-value)
Heterotrimeric G-protein signaling pathway-Gi alpha and Gs alpha mediated pathway (P00026)	166	4	0.16	+	24.81	0.00304
Unclassified (UNCLASSIFIED)	17977	8	17.46	-	0.46	0
Cluster 10						
Genes List:	ATAD2,CSF2RB,ESR1,PBXIP1,PGR,					

	PIK3CA,PIK3R1,THRB,ZBTB17,NR2F1,GFI1					
Biological Process						
Bonferroni count:	1810					
PANTHER GO-Slim Biological Process	Homo sapiens - REFLIST (20595)	BC_10.txt (12)	BC_10.txt (expected)	BC_10.txt (over/under)	BC_10.txt (fold Enrichment)	BC_10.txt (P-value)
regulation of transcription by RNA polymerase II (GO:0006357)	1591	7	0.93	+	7.55	0.0168
transcription by RNA polymerase II (GO:0006366)	1635	7	0.95	+	7.35	0.0202
Molecular Function						
Bonferroni count:	510					
PANTHER GO-Slim Molecular Function	Homo sapiens - REFLIST (20595)	BC_10.txt (12)	BC_10.txt (expected)	BC_10.txt (over/under)	BC_10.txt (fold Enrichment)	BC_10.txt (P-value)
RNA polymerase II cis-regulatory region sequence-specific DNA binding (GO:0000978)	1054	6	0.61	+	9.77	0.00659
cis-regulatory region sequence-specific DNA binding (GO:0000987)	1057	6	0.62	+	9.74	0.00669
DNA-binding transcription factor activity (GO:0003700)	1313	6	0.77	+	7.84	0.0229
RNA polymerase II transcription regulatory region sequence-specific DNA binding (GO:0000977)	1337	6	0.78	+	7.7	0.0254
transcription regulatory region sequence-specific DNA binding (GO:0000976)	1377	6	0.8	+	7.48	0.03
regulatory region nucleic acid binding (GO:0001067)	1377	6	0.8	+	7.48	0.03
sequence-specific double-stranded DNA binding (GO:1990837)	1403	6	0.82	+	7.34	0.0333
sequence-specific DNA binding (GO:0043565)	1436	6	0.84	+	7.17	0.0379
double-stranded DNA binding (GO:0003690)	1451	6	0.85	+	7.1	0.0402
Cellular Component						
Bonferroni count:	438					
PANTHER GO-Slim Cellular Component	Homo sapiens - REFLIST (20595)	BC_10.txt (12)	BC_10.txt (expected)	BC_10.txt (over/under)	BC_10.txt (fold Enrichment)	BC_10.txt (P-value)
Unclassified	9302	3	5.42	-	0.55	0

(UNCLASSIFIED)						
Pathway						
Bonferroni count:	156					
PANTHER Pathways	Homo sapiens - REFLIST (20595)	BC_10.txt (12)	BC_10.txt (expected)	BC_10.txt (over/under)	BC_10.txt (fold Enrichment)	BC_10.txt (P-value)
Unclassified (UNCLASSIFIED)	17977	7	10.47	-	0.67	0
Cluster 11						
Genes List:	BTK,CDCP1,GP6, HCK,IL6,IL6R,IL6 ST,LIFR,LYN,OSM ,PLAUR,SYK,TYK 2,YES1,FAS,LIF,F GR,PLAU,RPS6KA 2					
Biological Process						
Bonferroni count:	1810					
PANTHER GO-Slim Biological Process	Homo sapiens - REFLIST (20595)	BC_11.txt (21)	BC_11.txt (expected)	BC_11.txt (over/under)	BC_11.txt (fold Enrichment)	BC_11.txt (P-value)
protein autophosphorylation (GO:0046777)	40	4	0.04	+	98.07	0.00019
peptidyl-tyrosine phosphorylation (GO:0018108)	51	5	0.05	+	96.15	4.39E-06
peptidyl-tyrosine modification (GO:0018212)	53	5	0.05	+	92.52	5.26E-06
regulation of cell population proliferation (GO:0042127)	167	6	0.17	+	35.24	2.83E-05
cell population proliferation (GO:0008283)	190	6	0.19	+	30.97	5.97E-05
protein phosphorylation (GO:0006468)	541	7	0.55	+	12.69	0.00137
phosphorylation (GO:0016310)	704	7	0.72	+	9.75	0.00777
cell surface receptor signaling pathway (GO:0007166)	1003	9	1.02	+	8.8	0.000498
signal transduction (GO:0007165)	2062	10	2.1	+	4.76	0.0232
signaling (GO:0023052)	2218	10	2.26	+	4.42	0.0441
cell communication (GO:0007154)	2230	10	2.27	+	4.4	0.0463
Unclassified (UNCLASSIFIED)	9793	9	9.99	-	0.9	0
Molecular Function						
Bonferroni count:	510					
PANTHER GO-Slim Molecular Function	Homo sapiens - REFLIST (20595)	BC_11.txt (21)	BC_11.txt (expected)	BC_11.txt (over/under)	BC_11.txt (fold Enrichment)	BC_11.txt (P-value)
cytokine binding (GO:0019955)	65	4	0.07	+	60.35	0.000336
cytokine receptor activity	50	3	0.05	+	58.84	0.0105

(GO:0004896)						
protein tyrosine kinase activity (GO:0004713)	83	4	0.08	+	47.26	0.000855
protein kinase activity (GO:0004672)	467	5	0.48	+	10.5	0.0472
Unclassified (UNCLASSIFIED)	10792	10	11	-	0.91	0
Cellular Component						
Bonferroni count:	438					
PANTHER GO-Slim Cellular Component	Homo sapiens - REFLIST (20595)	BC_11.txt (21)	BC_11.txt (expected)	BC_11.txt (over/under)	BC_11.txt (fold Enrichment)	BC_11.txt (P-value)
extrinsic component of cytoplasmic side of plasma membrane (GO:0031234)	56	4	0.06	+	70.05	0.000164
cytoplasmic side of plasma membrane (GO:0009898)	69	4	0.07	+	56.85	0.000362
cytoplasmic side of membrane (GO:0098562)	75	4	0.08	+	52.3	0.000498
extrinsic component of plasma membrane (GO:0019897)	87	4	0.09	+	45.09	0.000879
extrinsic component of membrane (GO:0019898)	134	4	0.14	+	29.28	0.00461
side of membrane (GO:0098552)	292	8	0.3	+	26.87	1.39E-07
leaflet of membrane bilayer (GO:0097478)	292	8	0.3	+	26.87	1.39E-07
external side of plasma membrane (GO:0009897)	217	4	0.22	+	18.08	0.0292
Unclassified (UNCLASSIFIED)	9302	9	9.48	-	0.95	0
Pathway						
Bonferroni count:	156					
PANTHER Pathways	Homo sapiens - REFLIST (20595)	BC_11.txt (21)	BC_11.txt (expected)	BC_11.txt (over/under)	BC_11.txt (fold Enrichment)	BC_11.txt (P-value)
Interleukin signaling pathway (P00036)	86	4	0.09	+	45.61	0.0003
B cell activation (P00010)	70	3	0.07	+	42.03	0.00844
Parkinson disease (P00049)	97	4	0.1	+	40.44	0.000475
Unclassified (UNCLASSIFIED)	17977	7	18.33	-	0.38	0
Cluster 12						
Genes List:	CCNA2,CCNB1,CCND1,CCNE1,CCP110,CDK1,CDK6,CDKN1A,CDKN1B,CDKN3,DDB2,GADD45G,MXD1,RPS6KA1,SCML2,AK					

	T3,FBXO31,CCNF,GADD45A,CDKN2D					
Biological Process						
Bonferroni count:	1810					
PANTHER GO-Slim Biological Process	Homo sapiens - REFLIST (20595)	BC_12.txt (21)	BC_12.txt (expected)	BC_12.txt (over/under)	BC_12.txt (fold Enrichment)	BC_12.txt (P-value)
regulation of cyclin-dependent protein kinase activity (GO:1904029)	28	5	0.03	+	> 100	2.77E-07
regulation of cyclin-dependent protein serine/threonine kinase activity (GO:0000079)	28	5	0.03	+	> 100	2.77E-07
G1/S transition of mitotic cell cycle (GO:0000082)	31	4	0.03	+	> 100	7.39E-05
cell cycle G1/S phase transition (GO:0044843)	33	4	0.03	+	> 100	9.3E-05
mitotic cell cycle phase transition (GO:0044772)	84	8	0.09	+	93.4	4.05E-11
cell cycle phase transition (GO:0044770)	90	8	0.09	+	87.17	6.82E-11
regulation of protein serine/threonine kinase activity (GO:0071900)	89	7	0.09	+	77.13	7.58E-09
regulation of mitotic cell cycle phase transition (GO:1901990)	53	3	0.05	+	55.51	0.0441
regulation of cell cycle (GO:0051726)	207	11	0.21	+	52.12	8.35E-14
regulation of protein kinase activity (GO:0045859)	144	7	0.15	+	47.67	1.9E-07
regulation of kinase activity (GO:0043549)	206	7	0.21	+	33.33	2.12E-06
regulation of transferase activity (GO:0051338)	215	7	0.22	+	31.93	2.83E-06
mitotic cell cycle (GO:0000278)	267	8	0.27	+	29.38	2.87E-07
mitotic cell cycle process (GO:1903047)	267	8	0.27	+	29.38	2.87E-07
mitotic nuclear division (GO:0140014)	267	8	0.27	+	29.38	2.87E-07
nuclear division (GO:0000280)	319	8	0.33	+	24.59	1.13E-06
organelle fission (GO:0048285)	340	8	0.35	+	23.08	1.85E-06
cell cycle (GO:0007049)	473	11	0.48	+	22.81	5.51E-10
protein phosphorylation (GO:0006468)	541	12	0.55	+	21.75	5.27E-11
regulation of protein phosphorylation	327	7	0.33	+	20.99	4.76E-05

(GO:0001932)						
regulation of protein modification process (GO:0031399)	378	7	0.39	+	18.16	0.000126
cell cycle process (GO:0022402)	434	8	0.44	+	18.08	1.21E-05
regulation of phosphorylation (GO:0042325)	393	7	0.4	+	17.47	0.000164
phosphorylation (GO:0016310)	704	12	0.72	+	16.72	1.12E-09
regulation of phosphorus metabolic process (GO:0051174)	419	7	0.43	+	16.38	0.000251
regulation of phosphate metabolic process (GO:0019220)	419	7	0.43	+	16.38	0.000251
regulation of cellular protein metabolic process (GO:0032268)	571	7	0.58	+	12.02	0.00196
regulation of protein metabolic process (GO:0051246)	608	7	0.62	+	11.29	0.00297
phosphate-containing compound metabolic process (GO:0006796)	1090	12	1.11	+	10.8	1.74E-07
phosphorus metabolic process (GO:0006793)	1103	12	1.12	+	10.67	2E-07
regulation of catalytic activity (GO:0050790)	646	7	0.66	+	10.63	0.00443
regulation of molecular function (GO:0065009)	806	7	0.82	+	8.52	0.0187
cellular protein modification process (GO:0006464)	1383	12	1.41	+	8.51	2.64E-06
protein modification process (GO:0036211)	1383	12	1.41	+	8.51	2.64E-06
macromolecule modification (GO:0043412)	1481	12	1.51	+	7.95	5.73E-06
cellular protein metabolic process (GO:0044267)	1906	13	1.94	+	6.69	6.82E-06
protein metabolic process (GO:0019538)	2236	13	2.28	+	5.7	4.74E-05
organonitrogen compound metabolic process (GO:1901564)	2699	13	2.75	+	4.72	0.000451
cellular macromolecule metabolic process (GO:0044260)	4233	16	4.32	+	3.71	0.000131
macromolecule metabolic process (GO:0043170)	5051	16	5.15	+	3.11	0.00173
nitrogen compound	5350	16	5.46	+	2.93	0.00397

metabolic process (GO:0006807)						
regulation of cellular process (GO:0050794)	5092	15	5.19	+	2.89	0.0162
primary metabolic process (GO:0044238)	5603	16	5.71	+	2.8	0.0077
regulation of biological process (GO:0050789)	5324	15	5.43	+	2.76	0.0291
cellular metabolic process (GO:0044237)	5684	16	5.8	+	2.76	0.00945
organic substance metabolic process (GO:0071704)	5910	16	6.03	+	2.66	0.0164
metabolic process (GO:0008152)	6178	16	6.3	+	2.54	0.0307
Unclassified (UNCLASSIFIED)	9793	4	9.99	-	0.4	0
Molecular Function						
Bonferroni count:	510					
PANTHER GO-Slim Molecular Function	Homo sapiens - REFLIST (20595)	BC_12.txt (21)	BC_12.txt (expected)	BC_12.txt (over/under)	BC_12.txt (fold Enrichment)	BC_12.txt (P-value)
cyclin-dependent protein serine/threonine kinase regulator activity (GO:0016538)	36	6	0.04	+	> 100	1.33E-09
cyclin-dependent protein kinase activity (GO:0097472)	63	9	0.06	+	> 100	6.67E-15
cyclin-dependent protein serine/threonine kinase activity (GO:0004693)	63	9	0.06	+	> 100	6.67E-15
cyclin binding (GO:0030332)	65	9	0.07	+	> 100	8.65E-15
protein kinase regulator activity (GO:0019887)	71	6	0.07	+	82.88	5.89E-08
kinase regulator activity (GO:0019207)	89	6	0.09	+	66.12	2.14E-07
protein kinase binding (GO:0019901)	176	6	0.18	+	33.43	1.08E-05
protein serine/threonine kinase activity (GO:0004674)	349	11	0.36	+	30.91	6.09E-12
kinase binding (GO:0019900)	196	6	0.2	+	30.02	2.01E-05
protein kinase activity (GO:0004672)	467	11	0.48	+	23.1	1.36E-10
phosphotransferase activity, alcohol group as acceptor (GO:0016773)	555	11	0.57	+	19.44	8.51E-10
kinase activity (GO:0016301)	613	11	0.63	+	17.6	2.45E-09

transferase activity, transferring phosphorus-containing groups (GO:0016772)	714	11	0.73	+	15.11	1.23E-08
enzyme regulator activity (GO:0030234)	402	6	0.41	+	14.64	0.00125
enzyme binding (GO:0019899)	703	6	0.72	+	8.37	0.0288
catalytic activity, acting on a protein (GO:0140096)	1551	11	1.58	+	6.96	4.03E-05
transferase activity (GO:0016740)	1572	11	1.6	+	6.86	4.62E-05
Unclassified (UNCLASSIFIED)	10792	7	11	-	0.64	0
Cellular Component						
Bonferroni count:	438					
PANTHER GO-Slim Cellular Component	Homo sapiens - REFLIST (20595)	BC_12.txt (21)	BC_12.txt (expected)	BC_12.txt (over/under)	BC_12.txt (fold Enrichment)	BC_12.txt (P-value)
cyclin-dependent protein kinase holoenzyme complex (GO:0000307)	29	6	0.03	+	> 100	3.56E-10
serine/threonine protein kinase complex (GO:1902554)	52	6	0.05	+	> 100	8.74E-09
protein kinase complex (GO:1902911)	59	6	0.06	+	99.73	1.78E-08
centrosome (GO:0005813)	134	5	0.14	+	36.59	0.000106
centriole (GO:0005814)	149	5	0.15	+	32.91	0.000176
transferase complex, transferring phosphorus-containing groups (GO:0061695)	188	6	0.19	+	31.3	1.36E-05
microtubule organizing center (GO:0005815)	194	5	0.2	+	25.28	0.000626
transferase complex (GO:1990234)	482	7	0.49	+	14.24	0.000155
microtubule cytoskeleton (GO:0015630)	432	5	0.44	+	11.35	0.0282
catalytic complex (GO:1902494)	858	7	0.87	+	8	0.00679
nucleus (GO:0005634)	3956	15	4.03	+	3.72	0.000132
intracellular membrane-bounded organelle (GO:0043231)	5903	15	6.02	+	2.49	0.0268
membrane-bounded organelle (GO:0043227)	5999	15	6.12	+	2.45	0.033
Unclassified (UNCLASSIFIED)	9302	5	9.48	-	0.53	0
Pathway						

Bonferroni count:	156					
PANTHER Pathways	Homo sapiens - REFLIST (20595)	BC_12.txt (21)	BC_12.txt (expected)	BC_12.txt (over/under)	BC_12.txt (fold Enrichment)	BC_12.txt (P-value)
Cell cycle (P00013)	22	3	0.02	+	> 100	0.000322
p53 pathway (P00059)	89	9	0.09	+	99.17	3.72E-14
p53 pathway feedback loops 2 (P04398)	51	4	0.05	+	76.92	4.09E-05
PI3 kinase pathway (P00048)	57	3	0.06	+	51.62	0.00468
Interleukin signaling pathway (P00036)	86	4	0.09	+	45.61	0.0003
Unclassified (UNCLASSIFIED)	17977	8	18.33	-	0.44	0
Cluster 13						
Genes List:	CDH1,CDK5RAP2,CEP135,CEP152,CTNNA1,ECT2,KCNQ1,LIMA1,PLK4,RACGAP1,WDR62,PTPRM,AKAP9,CEP170,TUBG1,KIF23					
Biological Process						
Bonferroni count:	1810					
PANTHER GO-Slim Biological Process	Homo sapiens - REFLIST (20595)	BC_13.txt (17)	BC_13.txt (expected)	BC_13.txt (over/under)	BC_13.txt (fold Enrichment)	BC_13.txt (P-value)
microtubule cytoskeleton organization involved in mitosis (GO:1902850)	47	3	0.04	+	77.33	0.0161
cell cycle process (GO:0022402)	434	5	0.36	+	13.96	0.0388
Unclassified (UNCLASSIFIED)	9793	6	8.08	-	0.74	0
Molecular Function						
Bonferroni count:	510					
PANTHER GO-Slim Molecular Function	Homo sapiens - REFLIST (20595)	BC_13.txt (17)	BC_13.txt (expected)	BC_13.txt (over/under)	BC_13.txt (fold Enrichment)	BC_13.txt (P-value)
Unclassified (UNCLASSIFIED)	10792	7	8.91	-	0.79	0
Cellular Component						
Bonferroni count:	438					
PANTHER GO-Slim Cellular Component	Homo sapiens - REFLIST (20595)	BC_13.txt (17)	BC_13.txt (expected)	BC_13.txt (over/under)	BC_13.txt (fold Enrichment)	BC_13.txt (P-value)
spindle (GO:0005819)	77	3	0.06	+	47.2	0.0161
microtubule cytoskeleton (GO:0015630)	432	5	0.36	+	14.02	0.00919
cytoskeleton (GO:0005856)	667	6	0.55	+	10.9	0.00472
Unclassified (UNCLASSIFIED)	9302	7	7.68	-	0.91	0

Pathway						
Bonferroni count:	156					
PANTHER Pathways	Homo sapiens - REFLIST (20595)	BC_13.txt (17)	BC_13.txt (expected)	BC_13.txt (over/under)	BC_13.txt (fold Enrichment)	BC_13.txt (P-value)
Unclassified (UNCLASSIFIED)	17977	15	14.84	+	1.01	0
Cluster 14						
Genes List:	CDH2,CTNNA2,CTNNB1,EFNB3,EPHA2,EPHA3,EPHA4,ID2,JUP,PDLIM5,PPARGC1A,PRKAA2,TCF4,TCF7L2,IQGAP1,FHIT,NR5A2,SATB1,EFNA1,EFNA5,ID1					
Biological Process						
Bonferroni count:	1810					
PANTHER GO-Slim Biological Process	Homo sapiens - REFLIST (20595)	BC_14.txt (21)	BC_14.txt (expected)	BC_14.txt (over/under)	BC_14.txt (fold Enrichment)	BC_14.txt (P-value)
axon guidance (GO:0007411)	104	6	0.11	+	56.58	1.85E-06
neuron projection guidance (GO:0097485)	104	6	0.11	+	56.58	1.85E-06
axonogenesis (GO:0007409)	140	7	0.14	+	49.04	1.57E-07
axon development (GO:0061564)	143	7	0.15	+	48.01	1.81E-07
cell morphogenesis involved in neuron differentiation (GO:0048667)	158	7	0.16	+	43.45	3.55E-07
neuron projection morphogenesis (GO:0048812)	177	7	0.18	+	38.79	7.62E-07
cell projection morphogenesis (GO:0048858)	178	7	0.18	+	38.57	7.91E-07
plasma membrane bounded cell projection morphogenesis (GO:0120039)	178	7	0.18	+	38.57	7.91E-07
cell morphogenesis involved in differentiation (GO:0000904)	178	7	0.18	+	38.57	7.91E-07
cell part morphogenesis (GO:0032990)	180	7	0.18	+	38.14	8.53E-07
cellular component morphogenesis (GO:0032989)	204	7	0.21	+	33.65	1.98E-06
taxis (GO:0042330)	176	6	0.18	+	33.43	3.83E-05
chemotaxis (GO:0006935)	176	6	0.18	+	33.43	3.83E-05
neuron projection development (GO:0031175)	216	7	0.22	+	31.78	2.92E-06
neuron development (GO:0048666)	235	7	0.24	+	29.21	5.15E-06
cell morphogenesis	241	7	0.25	+	28.49	6.11E-06

(GO:0000902)						
transmembrane receptor protein tyrosine kinase signaling pathway (GO:0007169)	212	6	0.22	+	27.76	0.000112
neuron differentiation (GO:0030182)	320	7	0.33	+	21.45	4.12E-05
generation of neurons (GO:0048699)	348	7	0.35	+	19.73	7.24E-05
neurogenesis (GO:0022008)	366	7	0.37	+	18.76	0.000102
enzyme linked receptor protein signaling pathway (GO:0007167)	317	6	0.32	+	18.56	0.00114
cell development (GO:0048468)	382	7	0.39	+	17.97	0.000135
plasma membrane bounded cell projection organization (GO:0120036)	395	7	0.4	+	17.38	0.000169
cell projection organization (GO:0030030)	401	7	0.41	+	17.12	0.000187
locomotion (GO:0040011)	384	6	0.39	+	15.32	0.00341
nervous system development (GO:0007399)	479	7	0.49	+	14.33	0.000613
anatomical structure morphogenesis (GO:0009653)	492	7	0.5	+	13.95	0.000732
response to external stimulus (GO:0009605)	611	7	0.62	+	11.24	0.00307
cell differentiation (GO:0030154)	802	9	0.82	+	11.01	7.5E-05
cellular developmental process (GO:0048869)	806	9	0.82	+	10.95	7.83E-05
movement of cell or subcellular component (GO:0006928)	595	6	0.61	+	9.89	0.0405
system development (GO:0048731)	804	8	0.82	+	9.76	0.00131
multicellular organism development (GO:0007275)	906	8	0.92	+	8.66	0.00318
developmental process (GO:0032502)	1271	11	1.3	+	8.49	1.84E-05
response to chemical (GO:0042221)	822	7	0.84	+	8.35	0.0213
anatomical structure development (GO:0048856)	1126	9	1.15	+	7.84	0.00131
multicellular organismal process (GO:0032501)	1385	10	1.41	+	7.08	0.000624
regulation of transcription by	1591	9	1.62	+	5.55	0.0225

RNA polymerase II (GO:0006357)						
transcription by RNA polymerase II (GO:0006366)	1635	9	1.67	+	5.4	0.0281
signaling (GO:0023052)	2218	11	2.26	+	4.86	0.00524
cell communication (GO:0007154)	2230	11	2.27	+	4.84	0.00552
signal transduction (GO:0007165)	2062	10	2.1	+	4.76	0.0232
regulation of cellular metabolic process (GO:0031323)	2835	13	2.89	+	4.5	0.000807
regulation of metabolic process (GO:0019222)	3093	13	3.15	+	4.12	0.00224
regulation of cellular process (GO:0050794)	5092	19	5.19	+	3.66	6.73E-07
regulation of biological process (GO:0050789)	5324	19	5.43	+	3.5	1.52E-06
biological regulation (GO:0065007)	5797	19	5.91	+	3.21	7.22E-06
cellular process (GO:0009987)	9951	20	10.15	+	1.97	0.0116
Molecular Function						
Bonferroni count:	510					
PANTHER GO-Slim Molecular Function	Homo sapiens - REFLIST (20595)	BC_14.txt (21)	BC_14.txt (expected)	BC_14.txt (over/under)	BC_14.txt (fold Enrichment)	BC_14.txt (P-value)
cadherin binding (GO:0045296)	50	3	0.05	+	58.84	0.0105
transmembrane receptor protein tyrosine kinase activity (GO:0004714)	54	3	0.06	+	54.48	0.0131
transmembrane receptor protein kinase activity (GO:0019199)	64	3	0.07	+	45.97	0.0213
transcription coactivator activity (GO:0003713)	78	3	0.08	+	37.72	0.0377
protein tyrosine kinase activity (GO:0004713)	83	3	0.08	+	35.45	0.045
molecular_function (GO:0003674)	9803	20	10	+	2	0.00274
Cellular Component						
Bonferroni count:	438					
PANTHER GO-Slim Cellular Component	Homo sapiens - REFLIST (20595)	BC_14.txt (21)	BC_14.txt (expected)	BC_14.txt (over/under)	BC_14.txt (fold Enrichment)	BC_14.txt (P-value)
adherens junction (GO:0005912)	68	4	0.07	+	57.69	0.000343
extrinsic component of plasma membrane (GO:0019897)	87	3	0.09	+	33.82	0.0443
cell-cell junction (GO:0005911)	129	4	0.13	+	30.41	0.00399

anchoring junction (GO:0070161)	168	4	0.17	+	23.35	0.011
intrinsic component of plasma membrane (GO:0031226)	798	6	0.81	+	7.37	0.0496
cellular anatomical entity (GO:0110165)	11122	20	11.34	+	1.76	0.0312
cellular_component (GO:0005575)	11293	20	11.52	+	1.74	0.0348
Pathway						
Bonferroni count:	156					
PANTHER Pathways	Homo sapiens - REFLIST (20595)	BC_14.txt (21)	BC_14.txt (expected)	BC_14.txt (over/under)	BC_14.txt (fold Enrichment)	BC_14.txt (P-value)
Alzheimer disease-presenilin pathway (P00004)	127	4	0.13	+	30.89	0.00134
Cadherin signaling pathway (P00012)	164	4	0.17	+	23.92	0.00356
Wnt signaling pathway (P00057)	317	4	0.32	+	12.37	0.0437
Unclassified (UNCLASSIFIED)	17977	12	18.33	-	0.65	0
Cluster 15						
Genes List:	COL1A1,FN1,IL1R1,IRAK1,KDR,KRT19,PDGFA,PDGFB,PDGFRA,PDGFRB,PELI1,PELI2,RASA1,TGM2,MBP,PELI3,PDGFC					
Biological Process						
Bonferroni count:	1810					
PANTHER GO-Slim Biological Process	Homo sapiens - REFLIST (20595)	BC_15.txt (18)	BC_15.txt (expected)	BC_15.txt (over/under)	BC_15.txt (fold Enrichment)	BC_15.txt (P-value)
regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)	9	3	0.01	+	> 100	0.000222
phosphatidylinositol 3-kinase signaling (GO:0014065)	16	3	0.01	+	> 100	0.000972
positive regulation of MAP kinase activity (GO:0043406)	34	3	0.03	+	> 100	0.00772
inositol lipid-mediated signaling (GO:0048017)	35	3	0.03	+	98.07	0.00838
phosphatidylinositol-mediated signaling (GO:0048015)	35	3	0.03	+	98.07	0.00838
positive regulation of protein serine/threonine kinase activity (GO:0071902)	39	3	0.03	+	88.01	0.0114
protein autophosphorylation (GO:0046777)	40	3	0.03	+	85.81	0.0122
positive regulation	56	4	0.05	+	81.73	0.000348

of cell migration (GO:0030335)						
positive regulation of ERK1 and ERK2 cascade (GO:0070374)	45	3	0.04	+	76.28	0.0171
positive regulation of cell motility (GO:2000147)	60	4	0.05	+	76.28	0.000453
positive regulation of cellular component movement (GO:0051272)	61	4	0.05	+	75.03	0.000482
positive regulation of locomotion (GO:0040017)	61	4	0.05	+	75.03	0.000482
regulation of ERK1 and ERK2 cascade (GO:0070372)	48	3	0.04	+	71.51	0.0205
ERK1 and ERK2 cascade (GO:0070371)	48	3	0.04	+	71.51	0.0205
regulation of MAP kinase activity (GO:0043405)	56	3	0.05	+	61.29	0.0319
positive regulation of kinase activity (GO:0033674)	128	6	0.11	+	53.63	2.12E-06
positive regulation of transferase activity (GO:0051347)	136	6	0.12	+	50.48	3.02E-06
regulation of cell migration (GO:0030334)	111	4	0.1	+	41.23	0.00479
regulation of cell motility (GO:2000145)	118	4	0.1	+	38.79	0.00607
regulation of locomotion (GO:0040012)	123	4	0.11	+	37.21	0.00712
regulation of cellular component movement (GO:0051270)	125	4	0.11	+	36.61	0.00758
regulation of kinase activity (GO:0043549)	206	6	0.18	+	33.33	3.34E-05
transmembrane receptor protein tyrosine kinase signaling pathway (GO:0007169)	212	6	0.19	+	32.38	3.95E-05
regulation of transferase activity (GO:0051338)	215	6	0.19	+	31.93	4.28E-05
positive regulation of phosphorylation (GO:0042327)	293	6	0.26	+	23.43	0.000257
positive regulation of phosphorus metabolic process (GO:0010562)	300	6	0.26	+	22.88	0.000295
positive regulation of phosphate metabolic process (GO:0045937)	300	6	0.26	+	22.88	0.000295
cell migration	263	5	0.23	+	21.75	0.00483

(GO:0016477)						
enzyme linked receptor protein signaling pathway (GO:0007167)	317	6	0.28	+	21.66	0.000405
positive regulation of catalytic activity (GO:0043085)	323	6	0.28	+	21.25	0.000452
positive regulation of molecular function (GO:0044093)	421	7	0.37	+	19.02	7.49E-05
localization of cell (GO:0051674)	304	5	0.27	+	18.82	0.00968
cell motility (GO:0048870)	304	5	0.27	+	18.82	0.00968
regulation of phosphorylation (GO:0042325)	393	6	0.34	+	17.47	0.0014
regulation of phosphorus metabolic process (GO:0051174)	419	6	0.37	+	16.38	0.00202
regulation of phosphate metabolic process (GO:0019220)	419	6	0.37	+	16.38	0.00202
locomotion (GO:0040011)	384	5	0.34	+	14.9	0.0295
cell surface receptor signaling pathway (GO:0007166)	1003	10	0.88	+	11.41	4.34E-06
regulation of catalytic activity (GO:0050790)	646	6	0.56	+	10.63	0.0238
regulation of molecular function (GO:0065009)	806	7	0.7	+	9.94	0.00569
phosphorylation (GO:0016310)	704	6	0.62	+	9.75	0.0385
signal transduction (GO:0007165)	2062	10	1.8	+	5.55	0.00382
signaling (GO:0023052)	2218	10	1.94	+	5.16	0.00745
cell communication (GO:0007154)	2230	10	1.95	+	5.13	0.00782
cellular response to stimulus (GO:0051716)	2522	10	2.2	+	4.54	0.0238
response to stimulus (GO:0050896)	3027	11	2.65	+	4.16	0.0147
Unclassified (UNCLASSIFIED)	9793	4	8.56	-	0.47	0
Molecular Function						
Bonferroni count:	510					
PANTHER GO-Slim Molecular Function	Homo sapiens - REFLIST (20595)	BC_15.txt (18)	BC_15.txt (expected)	BC_15.txt (over/under)	BC_15.txt (fold Enrichment)	BC_15.txt (P-value)
growth factor receptor binding (GO:0070851)	39	3	0.03	+	88.01	0.0032
transmembrane receptor protein tyrosine kinase activity (GO:0004714)	54	3	0.05	+	63.56	0.0081

transmembrane receptor protein kinase activity (GO:0019199)	64	3	0.06	+	53.63	0.0132
protein tyrosine kinase activity (GO:0004713)	83	3	0.07	+	41.36	0.0279
catalytic activity, acting on a protein (GO:0140096)	1551	8	1.36	+	5.9	0.0118
transferase activity (GO:0016740)	1572	8	1.37	+	5.82	0.013
Unclassified (UNCLASSIFIED)	10792	5	9.43	-	0.53	0
Cellular Component						
Bonferroni count:	438					
PANTHER GO-Slim Cellular Component	Homo sapiens - REFLIST (20595)	BC_15.txt (18)	BC_15.txt (expected)	BC_15.txt (over/under)	BC_15.txt (fold Enrichment)	BC_15.txt (P-value)
Unclassified (UNCLASSIFIED)	9302	9	8.13	+	1.11	0
Pathway						
Bonferroni count:	156					
PANTHER Pathways	Homo sapiens - REFLIST (20595)	BC_15.txt (18)	BC_15.txt (expected)	BC_15.txt (over/under)	BC_15.txt (fold Enrichment)	BC_15.txt (P-value)
Angiogenesis (P00005)	175	7	0.15	+	45.77	1.7E-08
PDGF signaling pathway (P00047)	147	5	0.13	+	38.92	2.52E-05
Unclassified (UNCLASSIFIED)	17977	7	15.71	-	0.45	0
Cluster 16						
Genes List:	EGLN1,EIF4A1,EIF4G1,EPAS1,FOXO3,HIF1A,MUC1,PABPC1,PDCD4,FBP1,ESRRA					
Biological Process						
Bonferroni count:	1810					
PANTHER GO-Slim Biological Process	Homo sapiens - REFLIST (20595)	BC_16.txt (11)	BC_16.txt (expected)	BC_16.txt (over/under)	BC_16.txt (fold Enrichment)	BC_16.txt (P-value)
cellular response to hypoxia (GO:0071456)	8	3	0	+	> 100	3.37E-05
response to hypoxia (GO:0001666)	22	3	0.01	+	> 100	0.000468
response to oxygen levels (GO:0070482)	22	3	0.01	+	> 100	0.000468
response to decreased oxygen levels (GO:0036293)	22	3	0.01	+	> 100	0.000468
response to abiotic stimulus (GO:0009628)	97	3	0.05	+	57.91	0.0322
Unclassified (UNCLASSIFIED)	9793	4	5.23	-	0.76	0

Molecular Function						
Bonferroni count:	510					
PANTHER GO-Slim Molecular Function	Homo sapiens - REFLIST (20595)	BC_16.txt (11)	BC_16.txt (expected)	BC_16.txt (over/under)	BC_16.txt (fold Enrichment)	BC_16.txt (P-value)
nucleic acid binding (GO:0003676)	2248	7	1.2	+	5.83	0.021
Cellular Component						
Bonferroni count:	438					
PANTHER GO-Slim Cellular Component	Homo sapiens - REFLIST (20595)	BC_16.txt (11)	BC_16.txt (expected)	BC_16.txt (over/under)	BC_16.txt (fold Enrichment)	BC_16.txt (P-value)
Pathway						
Bonferroni count:	156					
PANTHER Pathways	Homo sapiens - REFLIST (20595)	BC_16.txt (11)	BC_16.txt (expected)	BC_16.txt (over/under)	BC_16.txt (fold Enrichment)	BC_16.txt (P-value)
Unclassified (UNCLASSIFIED)	17977	7	9.6	-	0.73	0
Cluster 17						
Genes List:	GRK5,MCM4,MCM5,MCM7,NFKBIA,REL,MAP3K8					
Biological Process						
Bonferroni count:	1810					
PANTHER GO-Slim Biological Process	Homo sapiens - REFLIST (20595)	BC_17.txt (7)	BC_17.txt (expected)	BC_17.txt (over/under)	BC_17.txt (fold Enrichment)	BC_17.txt (P-value)
pre-replicative complex assembly involved in nuclear cell cycle DNA replication (GO:0006267)	7	3	0	+	> 100	5.21E-06
double-strand break repair via break-induced replication (GO:0000727)	11	3	0	+	> 100	1.58E-05
cell cycle DNA replication (GO:0044786)	15	3	0.01	+	> 100	3.54E-05
nuclear DNA replication (GO:0033260)	15	3	0.01	+	> 100	3.54E-05
DNA replication initiation (GO:0006270)	17	3	0.01	+	> 100	4.94E-05
DNA-dependent DNA replication (GO:0006261)	60	3	0.02	+	> 100	0.00171
double-strand break repair via homologous recombination (GO:0000724)	64	3	0.02	+	> 100	0.00206
recombinational repair (GO:0000725)	66	3	0.02	+	> 100	0.00226
DNA replication (GO:0006260)	77	3	0.03	+	> 100	0.00353
protein-DNA complex assembly	91	3	0.03	+	96.99	0.00575

(GO:0065004)						
double-strand break repair (GO:0006302)	99	3	0.03	+	89.16	0.00736
DNA biosynthetic process (GO:0071897)	101	3	0.03	+	87.39	0.0078
DNA recombination (GO:0006310)	109	3	0.04	+	80.98	0.00975
protein-DNA complex subunit organization (GO:0071824)	119	3	0.04	+	74.17	0.0126
cellular response to stress (GO:0033554)	500	4	0.17	+	23.54	0.0211
Unclassified (UNCLASSIFIED)	9793	3	3.33	-	0.9	0
Molecular Function						
Bonferroni count:	510					
PANTHER GO-Slim Molecular Function	Homo sapiens - REFLIST (20595)	BC_17.txt (7)	BC_17.txt (expected)	BC_17.txt (over/under)	BC_17.txt (fold Enrichment)	BC_17.txt (P-value)
DNA replication origin binding (GO:0003688)	18	3	0.01	+	> 100	1.62E-05
single-stranded DNA binding (GO:0003697)	39	3	0.01	+	> 100	0.00014
Unclassified (UNCLASSIFIED)	10792	3	3.67	-	0.82	0
Cellular Component						
Bonferroni count:	438					
PANTHER GO-Slim Cellular Component	Homo sapiens - REFLIST (20595)	BC_17.txt (7)	BC_17.txt (expected)	BC_17.txt (over/under)	BC_17.txt (fold Enrichment)	BC_17.txt (P-value)
MCM core complex (GO:0097373)	30	3	0.01	+	> 100	5.71E-05
MCM complex (GO:0042555)	30	3	0.01	+	> 100	5.71E-05
Unclassified (UNCLASSIFIED)	9302	3	3.16	-	0.95	0
Pathway						
Bonferroni count:	156					
PANTHER Pathways	Homo sapiens - REFLIST (20595)	BC_17.txt (7)	BC_17.txt (expected)	BC_17.txt (over/under)	BC_17.txt (fold Enrichment)	BC_17.txt (P-value)
Toll receptor signaling pathway (P00054)	58	3	0.02	+	> 100	0.000134
Apoptosis signaling pathway (P00006)	118	3	0.04	+	74.8	0.00106
Cluster 18						
Genes List:	MDM2,RBBP6,RNF144B,RRM1,RRM2B,TP63,TP73,RRM2,PPP1R13L,SIAH1					
Biological Process						
Bonferroni count:	1810					

PANTHER GO-Slim Biological Process	Homo sapiens - REFLIST (20595)	BC_18.txt (10)	BC_18.txt (expected)	BC_18.txt (over/under)	BC_18.txt (fold Enrichment)	BC_18.txt (P-value)
nucleotide biosynthetic process (GO:0009165)	117	3	0.06	+	52.81	0.0406
nucleoside phosphate biosynthetic process (GO:1901293)	119	3	0.06	+	51.92	0.0427
nucleobase-containing compound biosynthetic process (GO:0034654)	2297	7	1.12	+	6.28	0.0346
heterocycle biosynthetic process (GO:0018130)	2322	7	1.13	+	6.21	0.0372
aromatic compound biosynthetic process (GO:0019438)	2323	7	1.13	+	6.21	0.0373
organic cyclic compound biosynthetic process (GO:1901362)	2350	7	1.14	+	6.13	0.0403
Molecular Function						
Bonferroni count:	510					
PANTHER GO-Slim Molecular Function	Homo sapiens - REFLIST (20595)	BC_18.txt (10)	BC_18.txt (expected)	BC_18.txt (over/under)	BC_18.txt (fold Enrichment)	BC_18.txt (P-value)
ubiquitin protein ligase activity (GO:0061630)	191	3	0.09	+	32.35	0.0479
Cellular Component						
Bonferroni count:	438					
PANTHER GO-Slim Cellular Component	Homo sapiens - REFLIST (20595)	BC_18.txt (10)	BC_18.txt (expected)	BC_18.txt (over/under)	BC_18.txt (fold Enrichment)	BC_18.txt (P-value)
Pathway						
Bonferroni count:	156					
PANTHER Pathways	Homo sapiens - REFLIST (20595)	BC_18.txt (10)	BC_18.txt (expected)	BC_18.txt (over/under)	BC_18.txt (fold Enrichment)	BC_18.txt (P-value)
P53 pathway feedback loops 1 (P04392)	7	3	0	+	> 100	1.54E-06
De novo pyrimidine deoxyribonucleotide biosynthesis (P02739)	15	3	0.01	+	> 100	1.04E-05
De novo purine biosynthesis (P02738)	30	3	0.01	+	> 100	6.95E-05
p53 pathway feedback loops 2 (P04398)	51	4	0.02	+	> 100	1.47E-06
p53 pathway (P00059)	89	5	0.04	+	> 100	6.85E-08
Unclassified (UNCLASSIFIED)	17977	3	8.73	-	0.34	0
Other than Core						
Genes List:	ABCC8,ABCG5,A					

	BCG8,ACE2,ACKR1,ACSS1,ACTN2,ACVR2A,ACVRL1,ADAMTS13,ADCYAP1,ADCYAP1R1,ADRA2A,AGR2,AGT,ALK,ALOX5,ANGPT2,ANGPTL2,ANK2,ANK3,APOE,ARHGDIB,ARPIN,ASF1B,ATP6V1B2,BAX,BCL2L1,BMP1,BMP2,BMP4,BMP7,BMPR1A,BMPR1B,BMPR2,BRCA2,C3,C8A,C9,CABP1,CACNA1C,CACNA1D,CALCRL,CAMK2A,CAMK2B,CAMK2D,CAMK2G,CASK,CASKIN1,CASP6,CASP7,CBFA2T3,CBFB,CCL11,CCL14,CCL16,CCL2,CCL4,CCL5,CCL8,CCNC,CCR1,CCR5,CD28,CD4,CD44,CD86,CD9,CDH23,CDK8,CDT1,CEACAM1,CEACAM5,CEBPA,CFB,CFH,CFTR,CHD3,CHD4,CHRD,CHRM3,CLDN18,CLDN19,CLEC1B,CLEC7A,CNTN1,CNTNAP4,COL3A1,COPS5,COTL1,CRYAB,CTSS,CXCL1,CXCL5,CXCL8,CXCR1,CXCR4,CYFIP1,DAB2,DCC,DCUN1D2,DDR1,DISC1,DLAT,DLC1,DNMT1,DOCK2,DPP4,DSP,E2F2,ELN,ENG,ETFA,ETFB,EXO1,EZH2,EZR,F13A1,F2,F3,F7,F8,F9,FANCD2,FANCI,FBLN5,FCGR2B,FGF10,FGF12,FGF13,FGF2,FGF5,FGF7,FGFR2,FGFR3,FGFR4,FHL2,FKBP1A,FLT1,FOXM1,FOXO1,FSCN1,FYCO1,GATA1,GATA2,GATA3,GDNF,GFRA1,GINS3,GPC3,GRIA2,GRIA3,GRIN2A,GTF2H1,GTF2H5,HAVCR2,HBEGF,HDAC5,HJURP,HLA-C,HLA-DMA,HLA-DMB,HLA-DOA,HLA-G,HMGA1,HMGB1,HSPB1,HTRA1,ICAM1,IFIT3,IFNGR1,IGF2,IGFBP1,IGFBP3,IL16,IL1B,IL1RAP,IL2RA,IL2RB,IL2RG,IL32,IM					

	MT,INHBA,ITGA2, ITGA3,ITGA4,ITG A5,ITGA7,ITGAL,I TGAV,ITGAX,ITG B2,ITGB6,ITK,JAK 3,JARID2,KANK1, KCNJ11,KCNMA1, KCNN2,KIF15,KIF 21A,KIF5B,KLF1, KRT14,KRT18,KR T5,KRT6A,KRT8,L CN2,LCP2,LDB1,L DB2,LGALS3,LHX 4,LILRB2,LMNB1, LMO3,LRG1,LRP1 ,LRRK2,LYL1,MA P1LC3A,MAPK14, MAPT,MASP1,MB L2,MCAM,MCL1, MCM2,MCM6,ME D25,MFN2,MKI67, MLPH,MMP14,M MP9,MRPL12,MR PS27,MST1,MST1 R,MTA3,MUC2,M YB,MYO10,MYO6, NCF1,NCF2,NCF4, NCKAP1,NDUFA9 ,NEDD4L,NFIB,NF IC,NOD2,NOS1,N OTUM,NR2F2,NR 4A1,NRP1,NTN1, NTN4,NUF2,OBSC N,OBSL1,OCLN,O GDH,OGDHL,OLF M4,ORAI2,ORC1,P ARD3,PDE5A,PDK 3,PDPN,PGF,PINK 1,PLXNA2,PLXNB 1,PODXL,PPARA,P PBP,PRDM14,PRK CH,PRKG1,PRL,P RLR,PRTN3,PTGE S3,PTN,PTPN13,P TPRC,PTPRR,PTP RZ1,RAB27A,RAC 2,RAMP1,RAPH1, RASIP1,RASSF5,R BBP8,RBL1,RCOR 1,REN,RET,RGMA ,RGS4,RILP,RND1, RNF165,ROBO1,R UNX1,RUVBL2,R XRA,RYR2,S,S100 A8,S100A9,SCN1A ,SCN5A,SDC1,SD C2,SDC4,SELE,SE MA3A,SERPINA5, SERPINC1,SETD7, SH3GL3,SH3RF3,S IAH2,SIRT3,SLC1 1A2,SLC12A2,SLC 15A3,SLC25A4,SL C38A9,SLC8A1,SL C9A3R1,SLIT2,SM AD6,SNCA,SNCAI P,SNTA1,SPARC,S PC24,SPI1,SPTA1, SPTB,SPTLC3,SPT SSB,SQSTM1,SRE BF1,STAT1,STIP1, STK11,STK26,STK 4,STUB1,TAL1,TB XA2R,TCAP,TEK, TF,TFDP1,TFDP2,					

	TFRC,TGFB2,TGFB3,TGFBR1,TGFBR2,TGFBR3,TIAM1,TLR2,TNFRSF10D,TNFRSF13B,TNFSF10,TNFSF13B,TNIK,TNKS2,TNS1,TOM1L2,TOP2A,TRIB1,TRPC3,TTK,TTN,UBB,UBE2B,UBE2M,UBR1,UNC5B,UNC5C,USH1C,USH1G,USP11,USP2,USP33,VDR,VLDLR,VWF,WAS,WASF1,WIPF1,WNT7A,ZFPM1,ZNF827					
Biological Process						
Bonferroni count:	1810					
PANTHER GO-Slim Biological Process	Homo sapiens - REFLIST (20595)	3_Otherthan_Core_Genes.txt (418)	3_Otherthan_Core_Genes.txt (expected)	3_Otherthan_Core_Genes.txt (over/under)	3_Otherthan_Core_Genes.txt (fold Enrichment)	3_Otherthan_Core_Genes.txt (P-value)
positive chemotaxis (GO:0050918)	9	5	0.18	+	27.37	0.0095
neutrophil migration (GO:1990266)	49	13	0.99	+	13.07	3.94E-07
granulocyte chemotaxis (GO:0071621)	49	13	0.99	+	13.07	3.94E-07
leukocyte chemotaxis (GO:0030595)	58	15	1.18	+	12.74	2.17E-08
positive regulation of ERK1 and ERK2 cascade (GO:0070374)	45	11	0.91	+	12.04	2.04E-05
granulocyte migration (GO:0097530)	55	13	1.12	+	11.65	1.34E-06
cell chemotaxis (GO:0060326)	64	15	1.3	+	11.55	7.2E-08
myeloid leukocyte migration (GO:0097529)	61	14	1.24	+	11.31	4.12E-07
regulation of ERK1 and ERK2 cascade (GO:0070372)	48	11	0.97	+	11.29	3.64E-05
ERK1 and ERK2 cascade (GO:0070371)	48	11	0.97	+	11.29	3.64E-05
leukocyte migration (GO:0050900)	71	15	1.44	+	10.41	2.56E-07
response to interleukin-1 (GO:0070555)	35	7	0.71	+	9.85	0.0314
lymphocyte migration (GO:0072676)	36	7	0.73	+	9.58	0.0368
inflammatory response (GO:0006954)	128	20	2.6	+	7.7	2.87E-08
transmembrane receptor protein serine/threonine kinase signaling pathway (GO:0007178)	97	15	1.97	+	7.62	1.15E-05

BMP signaling pathway (GO:0030509)	52	8	1.06	+	7.58	0.043
cellular response to BMP stimulus (GO:0071773)	53	8	1.08	+	7.44	0.0486
response to BMP (GO:0071772)	53	8	1.08	+	7.44	0.0486
cell migration (GO:0016477)	263	39	5.34	+	7.31	2.42E-17
response to growth factor (GO:0070848)	131	19	2.66	+	7.15	2.91E-07
cellular response to growth factor stimulus (GO:0071363)	131	19	2.66	+	7.15	2.91E-07
taxis (GO:0042330)	176	25	3.57	+	7	5.44E-10
chemotaxis (GO:0006935)	176	25	3.57	+	7	5.44E-10
positive regulation of MAPK cascade (GO:0043410)	103	14	2.09	+	6.7	0.000158
localization of cell (GO:0051674)	304	39	6.17	+	6.32	2.29E-15
cell motility (GO:0048870)	304	39	6.17	+	6.32	2.29E-15
cytokine-mediated signaling pathway (GO:0019221)	139	17	2.82	+	6.03	2.73E-05
positive regulation of cell population proliferation (GO:0008284)	90	11	1.83	+	6.02	0.00978
positive regulation of protein phosphorylation (GO:0001934)	241	29	4.89	+	5.93	3.05E-10
positive regulation of phosphorus metabolic process (GO:0010562)	300	36	6.09	+	5.91	3.49E-13
positive regulation of phosphate metabolic process (GO:0045937)	300	36	6.09	+	5.91	3.49E-13
positive regulation of phosphorylation (GO:0042327)	293	35	5.95	+	5.89	1.05E-12
MAPK cascade (GO:0000165)	146	17	2.96	+	5.74	5.29E-05
positive regulation of protein modification process (GO:0031401)	261	30	5.3	+	5.66	3.4E-10
cellular response to cytokine stimulus (GO:0071345)	148	17	3	+	5.66	6.34E-05
locomotion (GO:0040011)	384	44	7.79	+	5.65	6.46E-16
enzyme linked receptor protein signaling pathway (GO:0007167)	317	36	6.43	+	5.6	1.67E-12
regulation of MAPK cascade (GO:0043408)	133	15	2.7	+	5.56	0.000504

signal transduction by protein phosphorylation (GO:0023014)	152	17	3.09	+	5.51	9.05E-05
response to cytokine (GO:0034097)	155	17	3.15	+	5.4	0.000117
regulation of cell migration (GO:0030334)	111	12	2.25	+	5.33	0.0117
regulation of locomotion (GO:0040012)	123	13	2.5	+	5.21	0.00607
positive regulation of transferase activity (GO:0051347)	136	14	2.76	+	5.07	0.0034
regulation of cell motility (GO:2000145)	118	12	2.39	+	5.01	0.0207
positive regulation of multicellular organismal process (GO:0051240)	118	12	2.39	+	5.01	0.0207
positive regulation of kinase activity (GO:0033674)	128	13	2.6	+	5	0.00907
animal organ morphogenesis (GO:0009887)	121	12	2.46	+	4.89	0.0261
transmembrane receptor protein tyrosine kinase signaling pathway (GO:0007169)	212	21	4.3	+	4.88	1.73E-05
regulation of cellular component movement (GO:0051270)	125	12	2.54	+	4.73	0.0352
positive regulation of cellular protein metabolic process (GO:0032270)	340	32	6.9	+	4.64	7.38E-09
positive regulation of protein metabolic process (GO:0051247)	366	34	7.43	+	4.58	2.14E-09
regulation of protein phosphorylation (GO:0001932)	327	30	6.64	+	4.52	6.33E-08
regulation of phosphorylation (GO:0042325)	393	36	7.98	+	4.51	6.62E-10
regulation of cell population proliferation (GO:0042127)	167	15	3.39	+	4.43	0.00698
cellular response to organic substance (GO:0071310)	468	42	9.5	+	4.42	1.23E-11
response to endogenous stimulus (GO:0009719)	259	23	5.26	+	4.38	2.28E-05
regulation of phosphorus metabolic process (GO:0051174)	419	37	8.5	+	4.35	8.55E-10
regulation of phosphate metabolic	419	37	8.5	+	4.35	8.55E-10

process (GO:0019220)						
cellular response to endogenous stimulus (GO:0071495)	244	21	4.95	+	4.24	0.000162
movement of cell or subcellular component (GO:0006928)	595	51	12.08	+	4.22	7.2E-14
response to organic substance (GO:0010033)	551	47	11.18	+	4.2	1.62E-12
positive regulation of signal transduction (GO:0009967)	294	25	5.97	+	4.19	1.18E-05
protein phosphorylation (GO:0006468)	541	46	10.98	+	4.19	3.75E-12
cell population proliferation (GO:0008283)	190	16	3.86	+	4.15	0.00721
cell part morphogenesis (GO:0032990)	180	15	3.65	+	4.11	0.0162
regulation of protein modification process (GO:0031399)	378	31	7.67	+	4.04	3.97E-07
positive regulation of intracellular signal transduction (GO:1902533)	185	15	3.75	+	3.99	0.0219
positive regulation of cell communication (GO:0010647)	321	26	6.52	+	3.99	1.49E-05
positive regulation of signaling (GO:0023056)	321	26	6.52	+	3.99	1.49E-05
neuron projection development (GO:0031175)	216	17	4.38	+	3.88	0.00843
cellular component morphogenesis (GO:0032989)	204	16	4.14	+	3.86	0.0167
cellular response to chemical stimulus (GO:0070887)	590	46	11.97	+	3.84	7.2E-11
positive regulation of catalytic activity (GO:0043085)	323	25	6.56	+	3.81	6.67E-05
neuron development (GO:0048666)	235	18	4.77	+	3.77	0.00633
cell surface receptor signaling pathway (GO:0007166)	1003	75	20.36	+	3.68	1.96E-18
positive regulation of cellular metabolic process (GO:0031325)	768	57	15.59	+	3.66	3.64E-13
phosphorylation (GO:0016310)	704	52	14.29	+	3.64	1.04E-11
positive regulation of metabolic process (GO:0009893)	841	60	17.07	+	3.52	2.96E-13
positive regulation	707	50	14.35	+	3.48	1.74E-10

of nitrogen compound metabolic process (GO:0051173)						
response to chemical (GO:0042221)	822	58	16.68	+	3.48	1.59E-12
anatomical structure morphogenesis (GO:0009653)	492	34	9.99	+	3.4	3.43E-06
neuron differentiation (GO:0030182)	320	22	6.49	+	3.39	0.00285
positive regulation of macromolecule metabolic process (GO:0010604)	753	50	15.28	+	3.27	1.61E-09
multicellular organism development (GO:0007275)	906	60	18.39	+	3.26	7.09E-12
positive regulation of response to stimulus (GO:0048584)	504	33	10.23	+	3.23	2.07E-05
regulation of cellular protein metabolic process (GO:0032268)	571	37	11.59	+	3.19	3.35E-06
regulation of protein metabolic process (GO:0051246)	608	39	12.34	+	3.16	1.56E-06
positive regulation of molecular function (GO:0044093)	421	27	8.54	+	3.16	0.000676
response to external stimulus (GO:0009605)	611	39	12.4	+	3.14	1.78E-06
system development (GO:0048731)	804	51	16.32	+	3.13	4.68E-09
generation of neurons (GO:0048699)	348	22	7.06	+	3.11	0.0102
neurogenesis (GO:0022008)	366	23	7.43	+	3.1	0.00687
nervous system development (GO:0007399)	479	30	9.72	+	3.09	0.000244
animal organ development (GO:0048513)	385	24	7.81	+	3.07	0.00482
regulation of multicellular organismal process (GO:0051239)	329	20	6.68	+	3	0.0461
defense response (GO:0006952)	395	24	8.02	+	2.99	0.00729
anatomical structure development (GO:0048856)	1126	68	22.85	+	2.98	6.09E-12
positive regulation of biological process (GO:0048518)	1455	87	29.53	+	2.95	6.31E-16
positive regulation of cellular process (GO:0048522)	1295	76	26.28	+	2.89	4.65E-13
cell development	382	22	7.75	+	2.84	0.0402

(GO:0048468)						
developmental process (GO:0032502)	1271	73	25.8	+	2.83	5.83E-12
regulation of catalytic activity (GO:0050790)	646	37	13.11	+	2.82	7.19E-05
cellular developmental process (GO:0048869)	806	46	16.36	+	2.81	1.59E-06
cell differentiation (GO:0030154)	802	45	16.28	+	2.76	4.05E-06
regulation of signal transduction (GO:0009966)	728	40	14.78	+	2.71	5.77E-05
regulation of intracellular signal transduction (GO:1902531)	441	24	8.95	+	2.68	0.0411
multicellular organismal process (GO:0032501)	1385	74	28.11	+	2.63	1.24E-10
regulation of cell communication (GO:0010646)	813	41	16.5	+	2.48	0.000395
regulation of signaling (GO:0023051)	813	41	16.5	+	2.48	0.000395
regulation of response to stimulus (GO:0048583)	1004	50	20.38	+	2.45	2.15E-05
regulation of molecular function (GO:0065009)	806	40	16.36	+	2.45	0.00079
phosphate-containing compound metabolic process (GO:0006796)	1090	54	22.12	+	2.44	8.53E-06
phosphorus metabolic process (GO:0006793)	1103	54	22.39	+	2.41	1.08E-05
response to stress (GO:0006950)	967	47	19.63	+	2.39	0.000155
signal transduction (GO:0007165)	2062	99	41.85	+	2.37	2.46E-12
immune system process (GO:0002376)	676	32	13.72	+	2.33	0.0425
cell communication (GO:0007154)	2230	103	45.26	+	2.28	6.99E-12
signaling (GO:0023052)	2218	102	45.02	+	2.27	1.21E-11
cellular response to stimulus (GO:0051716)	2522	114	51.19	+	2.23	4.7E-13
cellular protein modification process (GO:0006464)	1383	62	28.07	+	2.21	2.14E-05
protein modification process (GO:0036211)	1383	62	28.07	+	2.21	2.14E-05
response to stimulus (GO:0050896)	3027	134	61.44	+	2.18	2.07E-15
negative regulation of cellular process	1045	45	21.21	+	2.12	0.00625

(GO:0048523)						
macromolecule modification (GO:0043412)	1481	62	30.06	+	2.06	0.000202
cellular protein metabolic process (GO:0044267)	1906	69	38.68	+	1.78	0.00688
regulation of cellular process (GO:0050794)	5092	174	103.35	+	1.68	1.62E-10
protein metabolic process (GO:0019538)	2236	75	45.38	+	1.65	0.0321
regulation of biological process (GO:0050789)	5324	177	108.06	+	1.64	9.13E-10
regulation of cellular metabolic process (GO:0031323)	2835	94	57.54	+	1.63	0.00372
biological regulation (GO:0065007)	5797	189	117.66	+	1.61	4.72E-10
regulation of nitrogen compound metabolic process (GO:0051171)	2715	87	55.1	+	1.58	0.0395
regulation of metabolic process (GO:0019222)	3093	99	62.78	+	1.58	0.00856
cellular process (GO:0009987)	9951	255	201.97	+	1.26	0.000567
biological_process (GO:0008150)	10802	269	219.24	+	1.23	0.0026
Unclassified (UNCLASSIFIED)	9793	149	198.76	-	0.75	0
Molecular Function						
Bonferroni count:	510					
PANTHER GO-Slim Molecular Function	Homo sapiens - REFLIST (20595)	3_Otherthan_Core_Genes.txt (418)	3_Otherthan_Core_Genes.txt (expected)	3_Otherthan_Core_Genes.txt (over/under)	3_Otherthan_Core_Genes.txt (fold Enrichment)	3_Otherthan_Core_Genes.txt (P-value)
transmembrane receptor protein serine/threonine kinase activity (GO:0004675)	10	6	0.2	+	29.56	0.000206
fibroblast growth factor receptor binding (GO:0005104)	24	6	0.49	+	12.32	0.0121
transmembrane receptor protein kinase activity (GO:0019199)	64	15	1.3	+	11.55	2.03E-08
growth factor activity (GO:0008083)	39	9	0.79	+	11.37	0.000193
chemokine receptor binding (GO:0042379)	51	11	1.04	+	10.63	1.76E-05
growth factor receptor binding (GO:0070851)	39	8	0.79	+	10.11	0.00186
growth factor binding (GO:0019838)	35	7	0.71	+	9.85	0.00884
transmembrane receptor protein	54	9	1.1	+	8.21	0.00209

tyrosine kinase activity (GO:0004714)						
cytokine receptor binding (GO:0005126)	100	16	2.03	+	7.88	6.52E-07
cytokine activity (GO:0005125)	129	19	2.62	+	7.26	6.47E-08
receptor ligand activity (GO:0048018)	245	31	4.97	+	6.23	3.54E-12
signaling receptor activator activity (GO:0030546)	247	31	5.01	+	6.18	4.33E-12
protein tyrosine kinase activity (GO:0004713)	83	10	1.68	+	5.94	0.00825
receptor regulator activity (GO:0030545)	276	31	5.6	+	5.53	6.57E-11
G protein-coupled receptor binding (GO:0001664)	139	12	2.82	+	4.25	0.026
protein kinase activity (GO:0004672)	467	32	9.48	+	3.38	3.56E-06
signaling receptor binding (GO:0005102)	680	43	13.8	+	3.12	8.63E-08
protein serine/threonine kinase activity (GO:0004674)	349	22	7.08	+	3.11	0.003
phosphotransferase activity, alcohol group as acceptor (GO:0016773)	555	32	11.26	+	2.84	0.000151
kinase activity (GO:0016301)	613	32	12.44	+	2.57	0.00116
transmembrane signaling receptor activity (GO:0004888)	669	32	13.58	+	2.36	0.00669
molecular transducer activity (GO:0060089)	783	37	15.89	+	2.33	0.00218
signaling receptor activity (GO:0038023)	783	37	15.89	+	2.33	0.00218
transferase activity, transferring phosphorus-containing groups (GO:0016772)	714	32	14.49	+	2.21	0.0235
protein binding (GO:0005515)	2640	112	53.58	+	2.09	2.09E-11
catalytic activity, acting on a protein (GO:0140096)	1551	57	31.48	+	1.81	0.0118
binding (GO:0005488)	5963	166	121.03	+	1.37	0.00177
molecular_function (GO:0003674)	9803	242	198.96	+	1.22	0.016
Unclassified (UNCLASSIFIED)	10792	176	219.04	-	0.8	0
Cellular Component						
Bonferroni count:	438					

PANTHER GO-Slim Cellular Component	Homo sapiens - REFLIST (20595)	3_Otherthan_Core_Genes.txt (418)	3_Otherthan_Core_Genes.txt (expected)	3_Otherthan_Core_Genes.txt (over/under)	3_Otherthan_Core_Genes.txt (fold Enrichment)	3_Otherthan_Core_Genes.txt (P-value)
receptor complex (GO:0043235)	213	28	4.32	+	6.48	2.73E-11
transcription regulator complex (GO:0005667)	200	16	4.06	+	3.94	0.0032
cell surface (GO:0009986)	325	19	6.6	+	2.88	0.029
extracellular space (GO:0005615)	1051	58	21.33	+	2.72	6.72E-09
neuron projection (GO:0043005)	384	21	7.79	+	2.69	0.0301
extracellular region (GO:0005576)	1203	63	24.42	+	2.58	8.34E-09
intrinsic component of plasma membrane (GO:0031226)	798	34	16.2	+	2.1	0.0461
cellular anatomical entity (GO:0110165)	11122	271	225.73	+	1.2	0.00422
cellular_component (GO:0005575)	11293	272	229.2	+	1.19	0.0126
Unclassified (UNCLASSIFIED)	9302	146	188.8	-	0.77	0
Pathway						
Bonferroni count:	156					
PANTHER Pathways	Homo sapiens - REFLIST (20595)	3_Otherthan_Core_Genes.txt (418)	3_Otherthan_Core_Genes.txt (expected)	3_Otherthan_Core_Genes.txt (over/under)	3_Otherthan_Core_Genes.txt (fold Enrichment)	3_Otherthan_Core_Genes.txt (P-value)
Axon guidance mediated by Slit/Robo (P00008)	25	7	0.51	+	13.8	0.0004
TGF-beta signaling pathway (P00052)	102	18	2.07	+	8.69	4.38E-09
Blood coagulation (P00011)	48	8	0.97	+	8.21	0.0022
Axon guidance mediated by netrin (P00009)	36	6	0.73	+	8.21	0.0267
Ionotropic glutamate receptor pathway (P00037)	50	7	1.01	+	6.9	0.0205
Gonadotropin-releasing hormone receptor pathway (P06664)	231	25	4.69	+	5.33	1.03E-08
Inflammation mediated by chemokine and cytokine signaling pathway (P00031)	255	25	5.18	+	4.83	6.94E-08
FGF signaling pathway (P00021)	123	12	2.5	+	4.81	0.00261
CCKR signaling map (P06959)	172	16	3.49	+	4.58	0.000188
Integrin signalling pathway (P00034)	193	15	3.92	+	3.83	0.00301
Unclassified (UNCLASSIFIED)	17977	255	364.86	-	0.7	0