

Supplementary Table S5. GO annotation enrichment.

Cellular Component			
Rank	GO Term	No. Targets	p-value
1	nucleus	361	3.10E-22
2	blood microparticle	66	1.92E-11
3	cytosol	425	4.47E-09
4	cytoplasm	396	4.47E-09
5	nucleoplasm	213	1.19E-08
6	extrinsic component of cytoplasmic side of plasma membrane	35	2.20E-08
7	cytoskeleton	41	3.89E-06
8	synapse	48	4.55E-06
9	voltage-gated calcium channel complex	19	1.75E-05
10	voltage-gated sodium channel complex	14	2.80E-05
11	postsynaptic membrane	56	2.80E-05
12	GABA-A receptor complex	16	0.000188
13	intracellular ribonucleoprotein complex	12	0.000188
14	cytosolic small ribosomal subunit	12	0.000189
15	cell junction	68	0.000262
16	neuron projection	62	0.000427
17	chloride channel complex	21	0.00084
18	neuronal postsynaptic density	14	0.003513
19	mast cell granule	8	0.008186
20	histone deacetylase complex	11	0.012368
21	focal adhesion	61	0.013928
22	extracellular matrix	30	0.015559
23	perinuclear region of cytoplasm	72	0.015651
24	spindle microtubule	9	0.015662
25	dendrite	57	0.016244
26	cornified envelope	7	0.016244
27	spherical high-density lipoprotein particle	7	0.01684
28	neuronal cell body	56	0.017332
29	centrosome	30	0.018536
30	microtubule cytoskeleton	18	0.019103
31	sarcolemma	18	0.019103
32	membrane	182	0.024995
33	receptor complex	34	0.025926
34	intermediate filament	12	0.027262
35	chylomicron	8	0.027375
36	nuclear speck	16	0.031762
37	inclusion body	6	0.032528
38	microtubule	25	0.032528
39	very-low-density lipoprotein particle	9	0.035254
40	centriole	9	0.035254
41	protein complex	43	0.044079
42	Z disc	17	0.048968

Molecular Function

Rank	GO Term	No. Targets	p-value
1	protein serine/threonine kinase activity	183	1.36E-58
2	ATP binding	367	1.98E-54
3	protein tyrosine kinase activity	65	1.83E-22
4	protein kinase activity	89	5.85E-20
5	non-membrane spanning protein tyrosine kinase activity	41	7.54E-17
6	transmembrane receptor protein tyrosine kinase activity	25	1.18E-09
7	RNA binding	54	2.13E-07
8	identical protein binding	96	4.20E-06
9	MAP kinase kinase kinase activity	15	2.54E-05
10	kinase activity	24	3.02E-05
11	protein serine/threonine/tyrosine kinase activity	18	7.81E-05
12	drug binding	42	0.000172
13	NAD-dependent histone deacetylase activity (H3-K14 specific)	11	0.000953
14	protein kinase C activity	11	0.000953
15	inhibitory extracellular ligand-gated ion channel activity	11	0.001021
16	voltage-gated sodium channel activity	13	0.001061
17	chloride channel activity	19	0.001173
18	GABA-A receptor activity	16	0.001296
19	cadherin binding	17	0.001669
20	serine-type endopeptidase inhibitor activity	22	0.001669
21	voltage-gated calcium channel activity	17	0.001696
22	cyclin-dependent protein serine/threonine kinase activity	12	0.001709
23	chromatin binding	36	0.001709
24	steroid hormone receptor activity	24	0.001719
25	magnesium ion binding	46	0.001743
26	high voltage-gated calcium channel activity	10	0.001743
27	enzyme binding	59	0.002362
28	calmodulin-dependent protein kinase activity	16	0.00278
29	protein kinase binding	51	0.003117
30	Rac GTPase binding	11	0.00385
31	chaperone binding	14	0.004229
32	protein phosphatase binding	17	0.007954
33	fibroblast growth factor binding	8	0.008516
34	tau-protein kinase activity	8	0.008516
35	protein homodimerization activity	91	0.008662
36	MAP kinase kinase kinase kinase activity	8	0.008752
37	receptor signaling protein tyrosine kinase activity	8	0.009002
38	histone deacetylase activity	10	0.009036
39	calmodulin binding	24	0.026661
40	transcription factor binding	31	0.026661
41	RNA polymerase II transcription factor activity, ligand-activated sequence-specific DNA binding	17	0.029695
42	DNA binding	45	0.031031
43	mRNA binding	11	0.03713
44	MAP kinase activity	8	0.044006

45	steroid binding	13	0.047011
46	microtubule binding	14	0.049088
Biological Process			
Rank	GO Term	No. Targets	p-value
1	protein phosphorylation	182	9.45E-51
2	protein autophosphorylation	117	4.21E-42
3	intracellular signal transduction	99	3.10E-19
4	peptidyl-tyrosine phosphorylation	49	3.92E-16
5	peptidyl-serine phosphorylation	63	3.91E-13
6	peptidyl-tyrosine autophosphorylation	37	3.91E-13
7	transmembrane receptor protein tyrosine kinase signaling pathway	44	1.61E-12
8	peptidyl-threonine phosphorylation	42	1.61E-12
9	regulation of mitotic cell cycle	38	9.69E-12
10	innate immune response	165	1.96E-08
11	signal transduction	159	7.03E-08
12	signal transduction by protein phosphorylation	20	3.80E-07
13	cell differentiation	42	5.62E-07
14	membrane depolarization during action potential	22	6.16E-07
15	activation of protein kinase activity	24	3.96E-06
16	stress-activated protein kinase signaling cascade	20	3.98E-06
17	regulation of apoptotic process	56	4.45E-06
18	cell migration	41	5.10E-06
19	cell cycle	30	1.23E-05
20	axon guidance	93	4.43E-05
21	transcription, DNA-templated	57	0.000104
22	visual learning	20	0.000108
23	regulation of cell proliferation	44	0.000158
24	neurological system process	30	0.000182
25	rRNA processing	19	0.000235
26	activation of MAPK activity	36	0.000258
27	vascular endothelial growth factor receptor signaling pathway	70	0.000286
28	positive regulation of phosphatidylinositol 3-kinase signaling	23	0.000288
29	positive regulation of protein phosphorylation	36	0.000459
30	negative regulation of apoptotic process	87	0.000615
31	regulation of membrane potential	41	0.000744
32	platelet degranulation	38	0.000778
33	apoptotic process	77	0.0011
34	activation of MAPKK activity	53	0.001447
35	microtubule cytoskeleton organization	15	0.001453
36	positive regulation of transcription by RNA polymerase II	11	0.00148
37	neurotrophin TRK receptor signaling pathway	76	0.001517
38	transcription initiation from RNA polymerase II promoter	50	0.001631
39	rhythmic process	19	0.001848
40	phosphorylation	16	0.002104
41	positive regulation of cell proliferation	75	0.002104
42	regulation of transcription, DNA-templated	45	0.002112
43	positive regulation of neuron projection development	21	0.002541

44	insulin receptor signaling pathway	61	0.002743
45	Fc-epsilon receptor signaling pathway	77	0.002953
46	regulation of cell motility	10	0.0032
47	regulation of ERK1 and ERK2 cascade	10	0.0032
48	negative regulation of neuron apoptotic process	35	0.00322
49	B cell activation	12	0.003371
50	epidermal growth factor receptor signaling pathway	67	0.003838
51	neutrophil degranulation	15	0.004007
52	wound healing	20	0.004423
53	Ras protein signal transduction	54	0.004423
54	MAPK cascade	56	0.005159
55	positive regulation of protein binding	13	0.005757
56	G2/M transition of mitotic cell cycle	25	0.005802
57	platelet activation	58	0.005802
58	negative regulation of transcription, DNA-templated	37	0.006723
59	fibroblast growth factor receptor signaling pathway	63	0.006723
60	behavioral response to cocaine	11	0.006966
61	establishment of cell polarity	11	0.006966
62	positive regulation of telomere capping	9	0.007068
63	negative regulation of transcription from RNA polymerase II promoter	50	0.007721
64	synaptic transmission, cholinergic	19	0.007762
65	positive regulation of ERK1 and ERK2 cascade	43	0.009358
66	membrane depolarization	15	0.009573
67	activation of JUN kinase activity	15	0.009573
68	chloride transmembrane transport	23	0.009585
69	phosphatidylinositol-mediated signaling	31	0.013218
70	cell proliferation	51	0.013218
71	positive regulation of transcription from RNA polymerase II promoter	82	0.013821
72	mitotic cell cycle	42	0.013821
73	cornification	10	0.01536
74	positive regulation of phospholipase C activity	8	0.01615
75	adaptive immune response	24	0.016209
76	intracellular receptor signaling pathway	15	0.022408
77	positive regulation of phosphatidylinositol 3-kinase activity	15	0.022408
78	nervous system development	29	0.022675
79	toll-like receptor signaling pathway	28	0.023106
80	keratinization	11	0.023735
81	gamma-aminobutyric acid signaling pathway	16	0.024365
82	cardiac muscle contraction	17	0.026132
83	positive regulation of peptidyl-serine phosphorylation	21	0.028016
84	protein stabilization	19	0.028016
85	positive regulation of cell differentiation	9	0.033968
86	Rho protein signal transduction	13	0.037855
87	regulation of protein binding	7	0.038245
88	cellular response to histamine	7	0.038245
89	regulation of cell shape	22	0.046859
90	positive regulation of apoptotic process	42	0.047884
91	cellular response to retinoic acid	16	0.047884
92	response to amphetamine	17	0.048786

93	SRP-dependent cotranslational protein targeting to membrane	18	0.048798
94	response to drug	85	0.049567