

Supplemental Table 1. GO enrichment analysis

Category	Term	Count	%	PValue	Genes	Fold Enrichment	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0038128~ERBB2 signaling pathway	6	4.87804878	5.78E-06	2549, 1956, 3845, 7316, 5295, 207	22.85662432	0.003283236	0.009288842
GOTERM_BP_DIRECT	GO:0070848~response to growth factor	5	4.06504065	3.57E-06	6657, 997, 10013, 1848, 4609	45.23706897	0.004045611	0.005725157
GOTERM_BP_DIRECT	GO:0071364~cellular response to epidermal growth factor stimulus	5	4.06504065	7.33E-05	5335, 1956, 1915, 207, 4609	21.93312435	0.027389688	0.117599411
GOTERM_BP_DIRECT	GO:0070141~response to UV-A	3	2.43902439	1.39E-04	595, 1956, 207	144.7586207	0.031086593	0.222758419
GOTERM_BP_DIRECT	GO:0032202~telomere assembly	3	2.43902439	1.39E-04	25913, 26277, 65057	144.7586207	0.031086593	0.222758419
GOTERM_BP_DIRECT	GO:0007049~cell cycle	9	7.317073171	1.24E-04	595, 23741, 1033, 672, 29117, 6737, 5596, 56288,	6.003813761	0.034545564	0.198412261
GOTERM_BP_DIRECT	GO:1901796~regulation of signal transduction by p53 class mediator	7	5.691056911	2.10E-04	10524, 147746, 672, 29117, 3066, 7316, 207	8.17185762	0.038946288	0.336062345
GOTERM_BP_DIRECT	GO:0045892~negative regulation of transcription, DNA-templated	12	9.756097561	6.29E-04	10524, 23741, 63976, 672, 2122, 51341, 253461, 29117, 10013, 3066, 3312,	3.481169235	0.076390112	1.004998176
GOTERM_BP_DIRECT	GO:0016233~telomere capping	4	3.25203252	5.01E-04	7013, 25913, 26277, 65057	25.17541229	0.07823914	0.802196509
GOTERM_BP_DIRECT	GO:0007173~epidermal growth factor receptor signaling pathway	5	4.06504065	5.83E-04	2549, 5335, 1956, 3845, 5295	12.92487685	0.07949838	0.931572646
GOTERM_BP_DIRECT	GO:0008283~cell proliferation	10	8.130081301	9.30E-04	10413, 2549, 1956, 200081, 3611, 6497, 5777, 207, 4609, 975	3.955153571	0.084365062	1.482648584
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	17	13.82113821	0.001047043	6657, 10413, 10524, 27161, 672, 1956, 5093, 7316, 22938, 207, 10987, 975, 253461, 3066, 27161, 2549,	2.508559176	0.087551769	1.668169315
GOTERM_BP_DIRECT	GO:0048015~phosphatidylinositol-mediated signaling	6	4.87804878	8.07E-04	1956, 5295, 4914, 207	8.19388419	0.087718017	1.288234541
GOTERM_BP_DIRECT	GO:0006513~protein monoubiquitination	4	3.25203252	9.05E-04	55658, 8452, 7706, 6737	20.67980296	0.089316907	1.443004121

GOTERM_BP_DIRECT	GO:0006468~protein phosphorylation	11	8.943089431	0.00115986	83732, 1859, 595, 10000, 5596, 9943, 3611, 5295, 4914, 207, 65125	3.491984271	0.089946494	1.846346811
GOTERM_BP_DIRECT	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	14	11.38211382	0.001294946	595, 6657, 10524, 63976, 51547, 7316, 2100, 22938, 23741, 51341, 8452, 3066, 6497, 4609	2.814750958	0.093551006	2.059295204
GOTERM_BP_DIRECT	GO:0018105~peptidyl-serine phosphorylation	6	4.87804878	0.00168561	1859, 10000, 147746, 3611, 207, 208	6.948413793	0.101082662	2.672699493
GOTERM_BP_DIRECT	GO:0050900~leukocyte migration	6	4.87804878	0.001514134	3676, 5335, 2335, 3845, 5777, 5295	7.119276427	0.102084838	2.403900075
GOTERM_BP_DIRECT	GO:0001934~positive regulation of protein phosphorylation	6	4.87804878	0.001807584	595, 1956, 3845, 4914, 207, 208	6.838989954	0.102612501	2.863479012
GOTERM_BP_DIRECT	GO:0000209~protein polyubiquitination	7	5.691056911	0.001673224	997, 26270, 55658, 8452, 6737, 10013, 7316	5.507121439	0.105958339	2.653307453
GOTERM_BP_DIRECT	GO:0018107~peptidyl-threonine phosphorylation	4	3.25203252	0.002216797	1859, 9943, 207, 65125	15.23774955	0.113218778	3.500970319
GOTERM_BP_DIRECT	GO:0000165~MAPK cascade	8	6.504065041	0.002177262	369, 8452, 1956, 5596, 3845, 7316, 1848, 4609	4.420110555	0.116542695	3.439552558
GOTERM_BP_DIRECT	GO:0032211~negative regulation of telomere maintenance via telomerase	3	2.43902439	0.00293416	7013, 26277, 65057	36.18965517	0.135204966	4.609052656
GOTERM_BP_DIRECT	GO:0045893~positive regulation of transcription, DNA-templated	11	8.943089431	0.002832105	6657, 10524, 63976, 672, 2122, 29117, 3066, 2100, 3611, 4609,	3.091931704	0.136339899	4.452144031
GOTERM_BP_DIRECT	GO:0006974~cellular response to DNA damage stimulus	7	5.691056911	0.003089552	10413, 595, 672, 253461, 254394, 207, 4609	4.87168435	0.136355537	4.847504016
GOTERM_BP_DIRECT	GO:0016567~protein ubiquitination	9	7.317073171	0.003284553	997, 63891, 9820, 672, 8452, 55236, 6737, 26260, 207	3.629046201	0.13897122	5.145944901
GOTERM_BP_DIRECT	GO:0022011~myelination in peripheral nervous system	3	2.43902439	0.00400956	3611, 6497, 56288	31.01970443	0.161125015	6.247854001
GOTERM_BP_DIRECT	GO:0000398~mRNA splicing, via spliceosome	7	5.691056911	0.00424897	988, 9343, 5093, 56339, 3312, 2521, 22938	4.564461013	0.164153312	6.609080693

GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell proliferation	10	8.130081301	0.004743523	10413, 8452, 1956, 2335, 3845, 3066, 3611, 5777, 4609, 975	3.106408169	0.170076132	7.351141159
GOTERM_BP_DIRECT	GO:0051974~negative regulation of telomerase activity	3	2.43902439	0.004605787	7013, 25913, 26277	28.95172414	0.17093763	7.145030623
GOTERM_BP_DIRECT	GO:0000082~G1/S transition of mitotic cell cycle	5	4.06504065	0.005299858	595, 997, 1033, 8452, 4171	7.096010818	0.182413661	8.17929409
GOTERM_BP_DIRECT	GO:0006464~cellular protein modification process	5	4.06504065	0.005869297	997, 369, 55236, 207, 208	6.893267652	0.194188068	9.019762279
GOTERM_BP_DIRECT	GO:0050680~negative regulation of epithelial cell proliferation	4	3.25203252	0.00666317	6657, 55764, 4163, 26277	10.33990148	0.200341011	10.17945062
GOTERM_BP_DIRECT	GO:0007004~telomere maintenance via telomerase	3	2.43902439	0.006622013	7013, 25913, 65057	24.12643678	0.204605648	10.11967184
GOTERM_BP_DIRECT	GO:0046777~protein autophosphorylation	6	4.87804878	0.006602811	1859, 147746, 1956, 4914, 207, 65125	5.049719326	0.209732746	10.09176835
GOTERM_BP_DIRECT	GO:0070932~histone H3 deacetylation	3	2.43902439	0.008968324	51547, 10013, 3066	20.67980296	0.2537217	13.46875065
GOTERM_BP_DIRECT	GO:0035019~somatic stem cell population maintenance	4	3.25203252	0.010043882	10413, 6657, 63976, 6497	8.908222812	0.272995834	14.96453948
GOTERM_BP_DIRECT	GO:0098609~cell-cell adhesion	7	5.691056911	0.010889259	7112, 27236, 392, 7706, 5093, 5315, 3312	3.739152564	0.285704987	16.12315839
GOTERM_BP_DIRECT	GO:0045742~positive regulation of epidermal growth factor receptor signaling pathway	3	2.43902439	0.011630644	10551, 7316, 207	18.09482759	0.29534057	17.12705237
GOTERM_BP_DIRECT	GO:0071300~cellular response to retinoic acid	4	3.25203252	0.012281262	10413, 3066, 22938, 4609	8.271921182	0.302507006	17.99874737
GOTERM_BP_DIRECT	GO:0031647~regulation of protein stability	4	3.25203252	0.012281262	10013, 3845, 3312, 975	8.271921182	0.302507006	17.99874737
GOTERM_BP_DIRECT	GO:0061621~canonical glycolysis	3	2.43902439	0.013574329	5315, 5213, 5211	16.70291777	0.321922075	19.70572899
GOTERM_BP_DIRECT	GO:0005978~glycogen biosynthetic process	3	2.43902439	0.013574329	7316, 207, 208	16.70291777	0.321922075	19.70572899
GOTERM_BP_DIRECT	GO:0030154~cell differentiation	9	7.317073171	0.014127827	23741, 988, 10551, 2122, 51341, 5777, 1848, 4745, 207	2.81997313	0.326038753	20.42617054

GOTERM_BP_DIRECT	GO:0007623~circadian rhythm	4	3.25203252	0.014782209	1859, 1956, 56339, 4914	7.72045977	0.331796654	21.27010455
GOTERM_BP_DIRECT	GO:0016236~macroautophagy	4	3.25203252	0.015314382	55054, 10013, 7316, 26100	7.618874773	0.335069994	21.95023321
GOTERM_BP_DIRECT	GO:0097421~liver regeneration	3	2.43902439	0.016733213	595, 1956, 4609	14.97502973	0.335171676	23.73670262
GOTERM_BP_DIRECT	GO:0051973~positive regulation of telomerase activity	3	2.43902439	0.016733213	25913, 65057, 4609	14.97502973	0.335171676	23.73670262
GOTERM_BP_DIRECT	GO:0014066~regulation of phosphatidylinositol 3-kinase signaling	4	3.25203252	0.016410913	2549, 1956, 5295, 207	7.42351901	0.335685933	23.33428839
GOTERM_BP_DIRECT	GO:0008286~insulin receptor signaling pathway	4	3.25203252	0.016410913	2549, 5295, 207, 208	7.42351901	0.335685933	23.33428839
GOTERM_BP_DIRECT	GO:0007050~cell cycle arrest	5	4.06504065	0.016074095	6657, 1033, 8452, 3611, 4609	5.133284422	0.335976906	22.91162009
GOTERM_BP_DIRECT	GO:0032869~cellular response to insulin stimulus	4	3.25203252	0.015857277	5295, 207, 208, 4609	7.519928348	0.338370859	22.63838363
GOTERM_BP_DIRECT	GO:0090004~positive regulation of establishment of protein localization to plasma membrane	3	2.43902439	0.017849146	10551, 5295, 207	14.47586207	0.347288776	25.11477212
GOTERM_BP_DIRECT	GO:0046326~positive regulation of glucose import	3	2.43902439	0.017849146	5295, 207, 208	14.47586207	0.347288776	25.11477212
GOTERM_BP_DIRECT	GO:0042493~response to drug	7	5.691056911	0.018241285	595, 7013, 3066, 4914, 1848, 4609, 999	3.333257713	0.347654126	25.59345631
GOTERM_BP_DIRECT	GO:1990090~cellular response to nerve growth factor stimulus	3	2.43902439	0.018995776	988, 4914, 207	14.00889878	0.35345948	26.50640362
GOTERM_BP_DIRECT	GO:0042787~protein ubiquitination involved in ubiquitin-dependent protein catabolic process	5	4.06504065	0.021019236	55658, 8452, 55236, 7706, 7316	4.730673879	0.366014112	28.90323569
GOTERM_BP_DIRECT	GO:1990646~cellular response to prolactin	2	1.62601626	0.02040632	988, 4609	96.50574713	0.368493389	28.18507644
GOTERM_BP_DIRECT	GO:0044346~fibroblast apoptotic process	2	1.62601626	0.02040632	8452, 4609	96.50574713	0.368493389	28.18507644
GOTERM_BP_DIRECT	GO:0060830~ciliary receptor clustering involved in smoothened signaling pathway	2	1.62601626	0.02040632	55764, 57728	96.50574713	0.368493389	28.18507644
GOTERM_BP_DIRECT	GO:0035556~intracellular signal transduction	8	6.504065041	0.020893894	10000, 5335, 369, 9943, 5777, 207, 208, 65125	2.873620262	0.369784396	28.75692174
GOTERM_BP_DIRECT	GO:0045787~positive regulation of cell cycle	3	2.43902439	0.022615229	595, 6737, 4609	12.77281947	0.382232564	30.74180594

GOTERM_BP_DIRECT	GO:0042059~negative regulation of epidermal growth factor receptor signaling pathway	3	2.43902439	0.025173289	55658, 1956, 7316	12.06321839	0.409663565	33.59594535
GOTERM_BP_DIRECT	GO:0000723~telomere maintenance	3	2.43902439	0.025173289	7013, 25913, 65057	12.06321839	0.409663565	33.59594535
GOTERM_BP_DIRECT	GO:0000320~re-entry into mitotic cell cycle	2	1.62601626	0.027116266	595, 4609	72.37931034	0.427738547	35.68969918
GOTERM_BP_DIRECT	GO:0010748~negative regulation of plasma membrane long-chain fatty acid transport	2	1.62601626	0.027116266	207, 208	72.37931034	0.427738547	35.68969918
GOTERM_BP_DIRECT	GO:0034446~substrate adhesion-dependent cell spreading	3	2.43902439	0.02784327	3676, 2335, 3611	11.42831216	0.430660653	36.45708018
GOTERM_BP_DIRECT	GO:0030326~embryonic limb morphogenesis	3	2.43902439	0.030621696	65057, 6497, 57728	10.85689655	0.456471889	39.31141831
GOTERM_BP_DIRECT	GO:0071681~cellular response to indole-3-methanol	2	1.62601626	0.033780647	672, 999	57.90344828	0.478583075	42.41047262
GOTERM_BP_DIRECT	GO:0006986~response to unfolded protein	3	2.43902439	0.033505165	23197, 26270, 3312	10.33990148	0.481465657	42.14623861
GOTERM_BP_DIRECT	GO:0051091~positive regulation of sequence-specific DNA binding transcription factor activity	4	3.25203252	0.035446544	7706, 6737, 2100, 207	5.514614122	0.489668308	43.98439533
GOTERM_BP_DIRECT	GO:0043066~negative regulation of apoptotic process	8	6.504065041	0.036942579	369, 1956, 396, 3066, 7316, 5295, 207, 4609	2.545206518	0.498579469	45.36337063
GOTERM_BP_DIRECT	GO:0080009~mRNA methylation	2	1.62601626	0.04039977	25962, 56339	48.25287356	0.513907663	48.42922924
GOTERM_BP_DIRECT	GO:0070200~establishment of protein localization to telomere	2	1.62601626	0.04039977	25913, 65057	48.25287356	0.513907663	48.42922924
GOTERM_BP_DIRECT	GO:0006979~response to oxidative stress	4	3.25203252	0.039830743	2549, 1956, 9943, 207	5.263949843	0.514267044	47.935962
GOTERM_BP_DIRECT	GO:0000186~activation of MAPKK activity	3	2.43902439	0.039573973	5335, 1956, 4914	9.44077961	0.517479773	47.71193208
GOTERM_BP_DIRECT	GO:0060831~smoothened signaling pathway involved in dorsal/ventral neural tube patterning	2	1.62601626	0.046973941	55764, 57728	41.35960591	0.563451723	53.81926248
GOTERM_BP_DIRECT	GO:2000617~positive regulation of histone H3-K9 acetylation	2	1.62601626	0.046973941	672, 55011	41.35960591	0.563451723	53.81926248
GOTERM_BP_DIRECT	GO:0010870~positive regulation of receptor biosynthetic process	2	1.62601626	0.046973941	10013, 3066	41.35960591	0.563451723	53.81926248

GOTERM_BP_DIRECT	GO:0032287~peripheral nervous system myelin maintenance	2	1.62601626	0.046973941	207, 208	41.35960591	0.563451723	53.81926248
GOTERM_BP_DIRECT	GO:0043161~proteasome-mediated ubiquitin-dependent protein catabolic process	5	4.06504065	0.050924179	10524, 997, 55658, 8452, 7316	3.565483268	0.588098813	56.7989742
GOTERM_BP_DIRECT	GO:0044829~positive regulation by host of viral genome replication	2	1.62601626	0.053503461	5479, 3312	36.18965517	0.595905303	58.64621739
GOTERM_BP_DIRECT	GO:0031659~positive regulation of cyclin-dependent protein serine/threonine kinase activity involved in G1/S transition of mitotic cell cycle	2	1.62601626	0.053503461	1956, 207	36.18965517	0.595905303	58.64621739
GOTERM_BP_DIRECT	GO:0006002~fructose 6-phosphate metabolic process	2	1.62601626	0.053503461	5213, 5211	36.18965517	0.595905303	58.64621739
GOTERM_BP_DIRECT	GO:0048146~positive regulation of fibroblast proliferation	3	2.43902439	0.052830116	1956, 2335, 4609	8.042145594	0.596484423	58.17125657
GOTERM_BP_DIRECT	GO:0016032~viral process	6	4.87804878	0.054771574	10524, 9820, 5335, 3312, 5295, 22938	2.904855265	0.59945869	59.52701217
GOTERM_BP_DIRECT	GO:0070198~protein localization to chromosome, telomeric region	2	1.62601626	0.059988631	26277, 65057	32.16858238	0.628677479	62.96888831
GOTERM_BP_DIRECT	GO:0010907~positive regulation of glucose metabolic process	2	1.62601626	0.059988631	207, 208	32.16858238	0.628677479	62.96888831
GOTERM_BP_DIRECT	GO:0070933~histone H4 deacetylation	2	1.62601626	0.059988631	51547, 3066	32.16858238	0.628677479	62.96888831
GOTERM_BP_DIRECT	GO:0043406~positive regulation of MAP kinase activity	3	2.43902439	0.061803027	1956, 3845, 3611	7.360607832	0.634845617	64.10014607
GOTERM_BP_DIRECT	GO:0048661~positive regulation of smooth muscle cell proliferation	3	2.43902439	0.063656067	1956, 207, 4609	7.237931034	0.635993788	65.22199178
GOTERM_BP_DIRECT	GO:0051289~protein homotetramerization	3	2.43902439	0.063656067	978, 1429, 5211	7.237931034	0.635993788	65.22199178
GOTERM_BP_DIRECT	GO:0051092~positive regulation of NF-kappaB transcription factor activity	4	3.25203252	0.063304284	7706, 3845, 7316, 4914	4.353642728	0.638891722	65.01158018
GOTERM_BP_DIRECT	GO:0051146~striated muscle cell differentiation	2	1.62601626	0.066429751	3845, 207	28.95172414	0.647281232	66.83993351
GOTERM_BP_DIRECT	GO:0035721~intracellular retrograde transport	2	1.62601626	0.066429751	55764, 57728	28.95172414	0.647281232	66.83993351
GOTERM_BP_DIRECT	GO:0043586~tongue development	2	1.62601626	0.066429751	63976, 1956	28.95172414	0.647281232	66.83993351

GOTERM_BP_DIRECT	GO:0000086~G2/M transition of mitotic cell cycle	4	3.25203252	0.067917322	10383, 7013, 7846, 7316	4.226529071	0.650841753	67.67831104
GOTERM_BP_DIRECT	GO:0009611~response to wounding	3	2.43902439	0.069325925	6657, 2335, 4609	6.893267652	0.653854806	68.45382559
GOTERM_BP_DIRECT	GO:0030512~negative regulation of transforming growth factor beta receptor signaling pathway	3	2.43902439	0.071251678	63976, 7316, 6497	6.785560345	0.659550868	69.48585636
GOTERM_BP_DIRECT	GO:0043627~response to estrogen	3	2.43902439	0.073194782	595, 672, 7706	6.681167109	0.660512623	70.49503401
GOTERM_BP_DIRECT	GO:0030857~negative regulation of epithelial cell differentiation	2	1.62601626	0.072827116	10413, 595	26.31974922	0.663206417	70.30651524
GOTERM_BP_DIRECT	GO:0030183~B cell differentiation	3	2.43902439	0.075154916	3676, 5295, 4914	6.579937304	0.666028668	71.4812829
GOTERM_BP_DIRECT	GO:0006006~glucose metabolic process	3	2.43902439	0.07713176	207, 208, 4609	6.481729285	0.671426762	72.44456607
GOTERM_BP_DIRECT	GO:0035690~cellular response to drug	3	2.43902439	0.081134314	9343, 1956, 4609	6.293853073	0.686240321	74.3022696
GOTERM_BP_DIRECT	GO:0032479~regulation of type I interferon production	2	1.62601626	0.085491759	6737, 7316	22.27055703	0.697428939	76.19083764
GOTERM_BP_DIRECT	GO:0061029~eyelid development in camera-type eye	2	1.62601626	0.085491759	1956, 3066	22.27055703	0.697428939	76.19083764
GOTERM_BP_DIRECT	GO:0048546~digestive tract morphogenesis	2	1.62601626	0.085491759	10551, 1956	22.27055703	0.697428939	76.19083764
GOTERM_BP_DIRECT	GO:2001275~positive regulation of glucose import in response to insulin stimulus	2	1.62601626	0.085491759	5295, 208	22.27055703	0.697428939	76.19083764
GOTERM_BP_DIRECT	GO:0060644~mammary gland epithelial cell differentiation	2	1.62601626	0.085491759	207, 208	22.27055703	0.697428939	76.19083764
GOTERM_BP_DIRECT	GO:0071260~cellular response to mechanical stimulus	3	2.43902439	0.08519996	1956, 396, 207	6.116561438	0.70041356	76.06855085
GOTERM_BP_DIRECT	GO:0018108~peptidyl-tyrosine phosphorylation	4	3.25203252	0.087826565	1859, 1956, 5777, 4914	3.784539103	0.70338961	77.14841744
GOTERM_BP_DIRECT	GO:0010243~response to organonitrogen compound	2	1.62601626	0.09175962	595, 4259	20.67980296	0.707582365	78.68029021
GOTERM_BP_DIRECT	GO:0048009~insulin-like growth factor receptor signaling pathway	2	1.62601626	0.09175962	5295, 207	20.67980296	0.707582365	78.68029021
GOTERM_BP_DIRECT	GO:0034968~histone lysine methylation	2	1.62601626	0.09175962	63976, 2122	20.67980296	0.707582365	78.68029021
GOTERM_BP_DIRECT	GO:0030334~regulation of cell migration	3	2.43902439	0.091411418	2549, 207, 208	5.868592731	0.710208083	78.54865796

GOTERM_BP_DIRECT	GO:0006260~DNA replication	4	3.25203252	0.090471647	10524, 672, 254394, 4171	3.73570634	0.710418453	78.18957858
GOTERM_BP_DIRECT	GO:0000729~DNA double-strand break processing	2	1.62601626	0.097984894	10524, 672	19.30114943	0.720423208	80.90957521
GOTERM_BP_DIRECT	GO:0045725~positive regulation of glycogen biosynthetic process	2	1.62601626	0.097984894	207, 208	19.30114943	0.720423208	80.90957521
GOTERM_BP_DIRECT	GO:0042993~positive regulation of transcription factor import into nucleus	2	1.62601626	0.097984894	5295, 999	19.30114943	0.720423208	80.90957521
GOTERM_BP_DIRECT	GO:0048026~positive regulation of mRNA splicing, via spliceosome	2	1.62601626	0.097984894	3312, 22938	19.30114943	0.720423208	80.90957521
GOTERM_BP_DIRECT	GO:0006412~translation	5	4.06504065	0.095982425	27161, 9343, 1956, 207, 10987	2.860842306	0.720508994	80.21752504
GOTERM_BP_DIRECT	GO:0001843~neural tube closure	3	2.43902439	0.097751386	55764, 4522, 6497	5.639946261	0.723418419	80.8300607
GOTERM_BP_DIRECT	GO:0031295~T cell costimulation	3	2.43902439	0.099891925	5777, 5295, 207	5.567639257	0.723805304	81.54748031