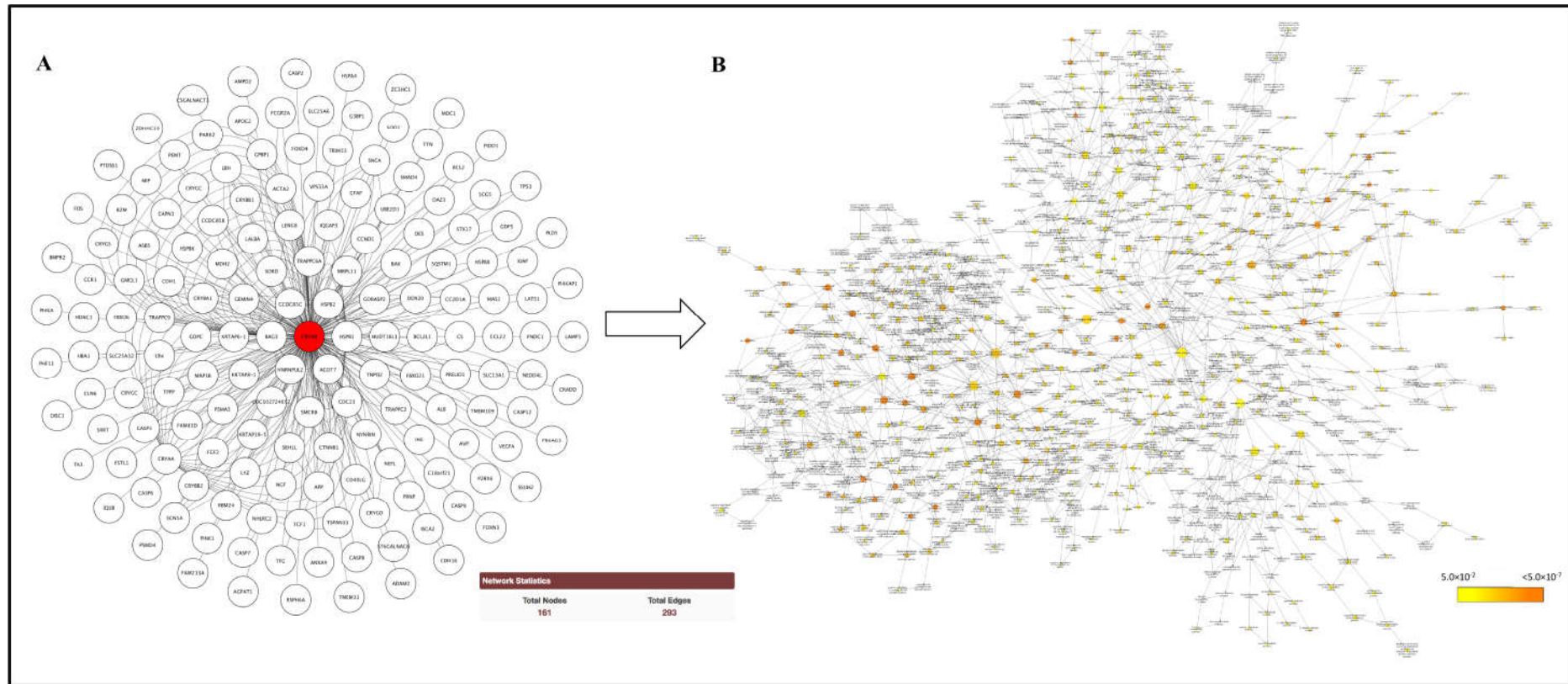


## Supplementary Materials



**Figure S1.** Schematic representation of (A) HSPB5 physical interaction with numerous targets and (B) the predominant biological functions resulting from the gene set network. All details are given in Supplementary Table S1. General Repository for Interaction Datasets (BioGRID), followed by BiNGO, a plug-in of Cytoscape 3.8.2 software were used for the Gene Ontology analysis ( $p < 0.05$ , all biological processes are visualized).

**Table S1.** Enriched biological functions related to HSPB5 network.

GO ID	GO Description	Corrected <i>p</i> -Value
10941	regulation of cell death	1.3106E-13
43067	regulation of programmed cell death	3.3024E-13
42981	regulation of apoptosis	1.0456E-12
60548	negative regulation of cell death	1.3226E-12
43066	negative regulation of apoptosis	3.1712E-10
10035	response to inorganic substance	3.1712E-10
43069	negative regulation of programmed cell death	3.1712E-10
9628	response to abiotic stimulus	9.3241E-10
6916	anti-apoptosis	1.2442E-9
9266	response to temperature stimulus	1.5475E-9
48522	positive regulation of cellular process	1.0653E-8
9408	response to heat	7.2713E-8
48518	positive regulation of biological process	8.0915E-8
2088	lens development in camera-type eye	1.2106E-7
31399	regulation of protein modification process	2.1695E-7
48523	negative regulation of cellular process	2.4370E-7
32270	positive regulation of cellular protein metabolic process	2.4370E-7
10038	response to metal ion	2.4774E-7
32268	regulation of cellular protein metabolic process	2.5105E-7
42221	response to chemical stimulus	3.9729E-7
51247	positive regulation of protein metabolic process	4.5582E-7
31401	positive regulation of protein modification process	4.5582E-7
51246	regulation of protein metabolic process	4.7231E-7
8219	cell death	6.0996E-7
90066	regulation of anatomical structure size	6.3460E-7
16265	death	6.4982E-7
48519	negative regulation of biological process	7.7189E-7
43010	camera-type eye development	1.2266E-6
6950	response to stress	1.4899E-6
1836	release of cytochrome c from mitochondria	2.3185E-6
32535	regulation of cellular component size	4.9176E-6
42493	response to drug	9.1544E-6
1654	eye development	9.3503E-6
8361	regulation of cell size	9.6696E-6
65008	regulation of biological quality	9.9022E-6
43523	regulation of neuron apoptosis	1.1505E-5
8637	apoptotic mitochondrial changes	1.5474E-5
46668	regulation of retinal cell programmed cell death	1.5792E-5
51049	regulation of transport	1.7983E-5
9892	negative regulation of metabolic process	2.3064E-5
7005	mitochondrion organization	2.3841E-5
10033	response to organic substance	2.4464E-5
51239	regulation of multicellular organismal process	2.7010E-5
7423	sensory organ development	2.8008E-5
10604	positive regulation of macromolecule metabolic process	2.8008E-5

9893	positive regulation of metabolic process	3.5530E-5
1558	regulation of cell growth	3.6071E-5
50896	response to stimulus	3.9011E-5
43065	positive regulation of apoptosis	3.9011E-5
9314	response to radiation	4.0362E-5
31325	positive regulation of cellular metabolic process	4.0362E-5
43068	positive regulation of programmed cell death	4.0362E-5
9607	response to biotic stimulus	4.0846E-5
60341	regulation of cellular localization	4.3170E-5
10942	positive regulation of cell death	4.3170E-5
40008	regulation of growth	5.6766E-5
6915	apoptosis	5.6766E-5
302	response to reactive oxygen species	5.6766E-5
10605	negative regulation of macromolecule metabolic process	5.7230E-5
51789	response to protein stimulus	5.9250E-5
51259	protein oligomerization	6.6096E-5
12501	programmed cell death	6.8345E-5
1934	positive regulation of protein amino acid phosphorylation	6.9774E-5
51881	regulation of mitochondrial membrane potential	8.4773E-5
43281	regulation of caspase activity	8.4773E-5
52548	regulation of endopeptidase activity	1.3401E-4
32879	regulation of localization	1.3401E-4
42327	positive regulation of phosphorylation	1.3401E-4
6508	proteolysis	1.4239E-4
45937	positive regulation of phosphate metabolic process	1.5387E-4
10562	positive regulation of phosphorus metabolic process	1.5387E-4
51094	positive regulation of developmental process	1.5387E-4
33554	cellular response to stress	1.6177E-4
52547	regulation of peptidase activity	1.7449E-4
1932	regulation of protein amino acid phosphorylation	1.9430E-4
7006	mitochondrial membrane organization	2.0786E-4
30307	positive regulation of cell growth	2.0909E-4
10039	response to iron ion	2.0909E-4
34097	response to cytokine stimulus	2.1716E-4
10646	regulation of cell communication	2.2072E-4
51130	positive regulation of cellular component organization	2.2347E-4
6917	induction of apoptosis	2.3339E-4
22402	cell cycle process	2.3339E-4
9416	response to light stimulus	2.3547E-4
12502	induction of programmed cell death	2.3576E-4
6979	response to oxidative stress	2.4764E-4
43524	negative regulation of neuron apoptosis	2.6452E-4
51128	regulation of cellular component organization	3.0405E-4
45793	positive regulation of cell size	3.2010E-4
51704	multi-organism process	3.2010E-4
43933	macromolecular complex subunit organization	3.3609E-4
278	mitotic cell cycle	3.3609E-4
50789	regulation of biological process	3.3609E-4

51716	cellular response to stimulus	3.4538E-4
45595	regulation of cell differentiation	4.0199E-4
77	DNA damage checkpoint	4.4934E-4
3008	system process	4.5090E-4
51726	regulation of cell cycle	4.5180E-4
51412	response to corticosterone stimulus	4.8546E-4
51051	negative regulation of transport	4.8546E-4
70271	protein complex biogenesis	4.9255E-4
6461	protein complex assembly	4.9255E-4
60284	regulation of cell development	5.3505E-4
9411	response to UV	5.5304E-4
43086	negative regulation of catalytic activity	5.6912E-4
31570	DNA integrity checkpoint	5.9515E-4
45597	positive regulation of cell differentiation	6.1827E-4
51248	negative regulation of protein metabolic process	6.7369E-4
9636	response to toxin	6.8659E-4
42542	response to hydrogen peroxide	6.8659E-4
10647	positive regulation of cell communication	7.0631E-4
50790	regulation of catalytic activity	7.2451E-4
22607	cellular component assembly	8.0667E-4
65007	biological regulation	8.9663E-4
8635	activation of caspase activity by cytochrome c	8.9663E-4
31400	negative regulation of protein modification process	8.9663E-4
50793	regulation of developmental process	9.3990E-4
51385	response to mineralocorticoid stimulus	9.5287E-4
44092	negative regulation of molecular function	9.8814E-4
48545	response to steroid hormone stimulus	9.9975E-4
30308	negative regulation of cell growth	9.9975E-4
7626	locomotory behavior	1.0103E-3
35466	regulation of signaling pathway	1.0379E-3
51260	protein homooligomerization	1.0379E-3
50794	regulation of cellular process	1.0414E-3
51240	positive regulation of multicellular organismal process	1.0773E-3
9605	response to external stimulus	1.0773E-3
35468	positive regulation of signaling pathway	1.0809E-3
9719	response to endogenous stimulus	1.0869E-3
65003	macromolecular complex assembly	1.0889E-3
46902	regulation of mitochondrial membrane permeability	1.1765E-3
226	microtubule cytoskeleton organization	1.1792E-3
44265	cellular macromolecule catabolic process	1.1920E-3
6996	organelle organization	1.1920E-3
8624	induction of apoptosis by extracellular signals	1.2131E-3
45471	response to ethanol	1.3433E-3
45792	negative regulation of cell size	1.3433E-3
7010	cytoskeleton organization	1.3676E-3
30163	protein catabolic process	1.4035E-3
10243	response to organic nitrogen	1.4126E-3
44085	cellular component biogenesis	1.4282E-3

30264	nuclear fragmentation involved in apoptotic nuclear change	1.4282E-3
46670	positive regulation of retinal cell programmed cell death	1.4282E-3
71763	nuclear membrane organization	1.4282E-3
60732	positive regulation of inositol phosphate biosynthetic process	1.4282E-3
43627	response to estrogen stimulus	1.5801E-3
42325	regulation of phosphorylation	1.6492E-3
8284	positive regulation of cell proliferation	1.6492E-3
32269	negative regulation of cellular protein metabolic process	1.7003E-3
48678	response to axon injury	1.7342E-3
7017	microtubule-based process	1.7374E-3
35239	tube morphogenesis	1.7986E-3
7610	behavior	1.8708E-3
22603	regulation of anatomical structure morphogenesis	1.9134E-3
65009	regulation of molecular function	1.9385E-3
51707	response to other organism	1.9846E-3
10720	positive regulation of cell development	2.0471E-3
45927	positive regulation of growth	2.1720E-3
7049	cell cycle	2.2484E-3
9611	response to wounding	2.4096E-3
51603	proteolysis involved in cellular protein catabolic process	2.4327E-3
31103	axon regeneration	2.4327E-3
32387	negative regulation of intracellular transport	2.4327E-3
51174	regulation of phosphorus metabolic process	2.4327E-3
19220	regulation of phosphate metabolic process	2.4327E-3
44057	regulation of system process	2.4993E-3
44257	cellular protein catabolic process	2.5543E-3
45926	negative regulation of growth	2.5677E-3
9991	response to extracellular stimulus	2.6650E-3
6997	nucleus organization	2.6650E-3
43085	positive regulation of catalytic activity	2.9188E-3
32880	regulation of protein localization	2.9642E-3
19217	regulation of fatty acid metabolic process	3.0738E-3
16043	cellular component organization	3.1605E-3
42770	DNA damage response, signal transduction	3.2152E-3
9725	response to hormone stimulus	3.4533E-3
90199	regulation of release of cytochrome c from mitochondria	3.4688E-3
10919	regulation of inositol phosphate biosynthetic process	3.4688E-3
9057	macromolecule catabolic process	3.5246E-3
31102	neuron projection regeneration	3.5851E-3
51436	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	3.7131E-3
32386	regulation of intracellular transport	3.8874E-3
31145	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	3.9594E-3
23056	positive regulation of signaling process	4.0498E-3
51437	positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	4.2169E-3
44248	cellular catabolic process	4.2492E-3

32502	developmental process	4.2492E-3
9653	anatomical structure morphogenesis	4.7128E-3
51352	negative regulation of ligase activity	4.7165E-3
51444	negative regulation of ubiquitin-protein ligase activity	4.7165E-3
6986	response to unfolded protein	4.7165E-3
819	sister chromatid segregation	4.7421E-3
31324	negative regulation of cellular metabolic process	4.7762E-3
51329	interphase of mitotic cell cycle	4.7837E-3
46686	response to cadmium ion	4.9962E-3
51402	neuron apoptosis	4.9962E-3
9056	catabolic process	5.1147E-3
51223	regulation of protein transport	5.1147E-3
43170	macromolecule metabolic process	5.1147E-3
51046	regulation of secretion	5.1147E-3
51439	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	5.1501E-3
48878	chemical homeostasis	5.1909E-3
33043	regulation of organelle organization	5.3521E-3
31667	response to nutrient levels	5.4875E-3
51325	interphase	5.5629E-3
35295	tube development	5.5967E-3
46688	response to copper ion	5.6787E-3
51443	positive regulation of ubiquitin-protein ligase activity	5.6787E-3
48856	anatomical structure development	5.6787E-3
75	cell cycle checkpoint	5.6836E-3
14070	response to organic cyclic substance	5.6836E-3
70141	response to UV-A	5.7084E-3
14012	axon regeneration in the peripheral nervous system	5.7084E-3
43497	regulation of protein heterodimerization activity	5.7084E-3
60561	apoptosis involved in morphogenesis	5.7084E-3
7178	transmembrane receptor protein serine/threonine kinase signaling pathway	5.8328E-3
43623	cellular protein complex assembly	5.9856E-3
7154	cell communication	6.1286E-3
70201	regulation of establishment of protein localization	6.3399E-3
737	DNA catabolic process, endonucleolytic	6.3399E-3
70997	neuron death	6.3399E-3
6309	DNA fragmentation involved in apoptotic nuclear change	6.3399E-3
51351	positive regulation of ligase activity	6.4437E-3
10629	negative regulation of gene expression	7.0016E-3
9267	cellular response to starvation	7.2401E-3
6873	cellular ion homeostasis	7.5724E-3
30534	adult behavior	7.6136E-3
51641	cellular localization	7.8168E-3
9987	cellular process	8.0794E-3
22403	cell cycle phase	8.2496E-3
30509	BMP signaling pathway	8.3094E-3
46928	regulation of neurotransmitter secretion	8.3094E-3
43525	positive regulation of neuron apoptosis	8.3094E-3
31397	negative regulation of protein ubiquitination	8.3094E-3

55082	cellular chemical homeostasis	8.3094E-3
32847	regulation of cellular pH reduction	8.4005E-3
71681	cellular response to indole-3-methanol	8.4005E-3
71680	response to indole-3-methanol	8.4005E-3
2326	B cell lineage commitment	8.4005E-3
2360	T cell lineage commitment	8.4005E-3
10821	regulation of mitochondrion organization	8.4005E-3
7021	tubulin complex assembly	8.4005E-3
48608	reproductive structure development	8.4101E-3
1541	ovarian follicle development	8.6387E-3
42592	homeostatic process	8.7978E-3
44093	positive regulation of molecular function	8.9894E-3
42127	regulation of cell proliferation	8.9894E-3
45913	positive regulation of carbohydrate metabolic process	8.9894E-3
43154	negative regulation of caspase activity	8.9894E-3
10676	positive regulation of cellular carbohydrate metabolic process	8.9894E-3
31396	regulation of protein ubiquitination	9.1271E-3
51438	regulation of ubiquitin-protein ligase activity	9.1271E-3
10565	regulation of cellular ketone metabolic process	9.1271E-3
50953	sensory perception of light stimulus	9.3559E-3
7601	visual perception	9.3559E-3
3012	muscle system process	9.5278E-3
23034	intracellular signaling pathway	9.9988E-3
51224	negative regulation of protein transport	1.0380E-2
48729	tissue morphogenesis	1.0422E-2
51340	regulation of ligase activity	1.0465E-2
10740	positive regulation of intracellular protein kinase cascade	1.0567E-2
9967	positive regulation of signal transduction	1.0567E-2
6511	ubiquitin-dependent protein catabolic process	1.0795E-2
8344	adult locomotory behavior	1.0947E-2
43122	regulation of I-kappaB kinase/NF-kappaB cascade	1.1056E-2
46889	positive regulation of lipid biosynthetic process	1.1056E-2
48538	thymus development	1.1056E-2
8634	negative regulation of survival gene product expression	1.1225E-2
48739	cardiac muscle fiber development	1.1225E-2
32469	endoplasmic reticulum calcium ion homeostasis	1.1225E-2
8406	gonad development	1.1317E-2
70887	cellular response to chemical stimulus	1.1601E-2
45786	negative regulation of cell cycle	1.1690E-2
43632	modification-dependent macromolecule catabolic process	1.1690E-2
19941	modification-dependent protein catabolic process	1.1690E-2
19538	protein metabolic process	1.1995E-2
30262	apoptotic nuclear change	1.2096E-2
19725	cellular homeostasis	1.2322E-2
50801	ion homeostasis	1.2989E-2
48754	branching morphogenesis of a tube	1.3229E-2
19216	regulation of lipid metabolic process	1.3268E-2
33077	T cell differentiation in the thymus	1.3268E-2

43255	regulation of carbohydrate biosynthetic process	1.3268E-2
10595	positive regulation of endothelial cell migration	1.3268E-2
51588	regulation of neurotransmitter transport	1.3268E-2
34599	cellular response to oxidative stress	1.3482E-2
7612	learning	1.4385E-2
45165	cell fate commitment	1.4521E-2
85	G2 phase of mitotic cell cycle	1.4541E-2
51319	G2 phase	1.4541E-2
10332	response to gamma radiation	1.4590E-2
46890	regulation of lipid biosynthetic process	1.5117E-2
34621	cellular macromolecular complex subunit organization	1.5532E-2
48285	organelle fission	1.5728E-2
43161	proteasomal ubiquitin-dependent protein catabolic process	1.5728E-2
10498	proteasomal protein catabolic process	1.5728E-2
51969	regulation of transmission of nerve impulse	1.5728E-2
31398	positive regulation of protein ubiquitination	1.5763E-2
42594	response to starvation	1.5763E-2
6921	cellular component disassembly involved in apoptosis	1.5813E-2
31668	cellular response to extracellular stimulus	1.6369E-2
51346	negative regulation of hydrolase activity	1.6642E-2
71496	cellular response to external stimulus	1.6962E-2
51384	response to glucocorticoid stimulus	1.6962E-2
48869	cellular developmental process	1.6993E-2
9409	response to cold	1.7077E-2
1658	branching involved in ureteric bud morphogenesis	1.7077E-2
10466	negative regulation of peptidase activity	1.7077E-2
60688	regulation of morphogenesis of a branching structure	1.7077E-2
50808	synapse organization	1.7156E-2
6919	activation of caspase activity	1.7156E-2
40014	regulation of multicellular organism growth	1.7156E-2
10623	developmental programmed cell death	1.7646E-2
31109	microtubule polymerization or depolymerization	1.7646E-2
43496	regulation of protein homodimerization activity	1.7646E-2
60052	neurofilament cytoskeleton organization	1.7646E-2
44238	primary metabolic process	1.7646E-2
48468	cell development	1.8062E-2
7568	aging	1.8113E-2
48731	system development	1.8226E-2
61138	morphogenesis of a branching epithelium	1.8352E-2
30003	cellular cation homeostasis	1.8505E-2
45137	development of primary sexual characteristics	1.8505E-2
23051	regulation of signaling process	1.8505E-2
7275	multicellular organismal development	1.8558E-2
8584	male gonad development	1.8558E-2
60675	ureteric bud morphogenesis	1.9728E-2
1666	response to hypoxia	2.0108E-2
31644	regulation of neurological system process	2.0108E-2
48646	anatomical structure formation involved in morphogenesis	2.0108E-2



1894	tissue homeostasis	2.0467E-2
32355	response to estradiol stimulus	2.0467E-2
6954	inflammatory response	2.0467E-2
34622	cellular macromolecular complex assembly	2.0782E-2
51649	establishment of localization in cell	2.0782E-2
31960	response to corticosteroid stimulus	2.0790E-2
60	protein import into nucleus, translocation	2.0879E-2
50772	positive regulation of axonogenesis	2.0879E-2
1782	B cell homeostasis	2.0879E-2
1963	synaptic transmission, dopaminergic	2.0879E-2
6878	cellular copper ion homeostasis	2.0879E-2
6998	nuclear envelope organization	2.0879E-2
30154	cell differentiation	2.0888E-2
48534	hemopoietic or lymphoid organ development	2.1056E-2
60255	regulation of macromolecule metabolic process	2.1667E-2
16044	cellular membrane organization	2.1888E-2
61024	membrane organization	2.2235E-2
2009	morphogenesis of an epithelium	2.2270E-2
1776	leukocyte homeostasis	2.2270E-2
6936	muscle contraction	2.2270E-2
10627	regulation of intracellular protein kinase cascade	2.2834E-2
10212	response to ionizing radiation	2.2834E-2
51651	maintenance of location in cell	2.2834E-2
40007	growth	2.3153E-2
9891	positive regulation of biosynthetic process	2.3530E-2
8306	associative learning	2.3840E-2
34637	cellular carbohydrate biosynthetic process	2.3840E-2
70482	response to oxygen levels	2.4506E-2
32501	multicellular organismal process	2.4506E-2
70306	lens fiber cell differentiation	2.4506E-2
55070	copper ion homeostasis	2.4506E-2
32026	response to magnesium ion	2.4506E-2
43280	positive regulation of caspase activity	2.4665E-2
10952	positive regulation of peptidase activity	2.4665E-2
7416	synapse assembly	2.5349E-2
48513	organ development	2.7020E-2
46474	glycerophospholipid biosynthetic process	2.7020E-2
50769	positive regulation of neurogenesis	2.7020E-2
7611	learning or memory	2.7020E-2
9790	embryonic development	2.7020E-2
7569	cell aging	2.7020E-2
48747	muscle fiber development	2.7020E-2
2520	immune system development	2.7888E-2
60429	epithelium development	2.8392E-2
43123	positive regulation of I-kappaB kinase/NF-kappaB cascade	2.8403E-2
45723	positive regulation of fatty acid biosynthetic process	2.8403E-2
6107	oxaloacetate metabolic process	2.8403E-2
7080	mitotic metaphase plate congression	2.8403E-2

48070	regulation of developmental pigmentation	2.8403E-2
19222	regulation of metabolic process	2.8403E-2
70	mitotic sister chromatid segregation	2.8585E-2
8585	female gonad development	2.8850E-2
22602	ovulation cycle process	3.0225E-2
46651	lymphocyte proliferation	3.0654E-2
8152	metabolic process	3.1887E-2
42110	T cell activation	3.2161E-2
7167	enzyme linked receptor protein signaling pathway	3.2517E-2
34614	cellular response to reactive oxygen species	3.2635E-2
6839	mitochondrial transport	3.2635E-2
45736	negative regulation of cyclin-dependent protein kinase activity	3.2635E-2
42100	B cell proliferation	3.2635E-2
7617	mating behavior	3.2635E-2
32225	regulation of synaptic transmission, dopaminergic	3.2635E-2
55080	cation homeostasis	3.2635E-2
51960	regulation of nervous system development	3.3361E-2
1763	morphogenesis of a branching structure	3.3472E-2
60627	regulation of vesicle-mediated transport	3.3472E-2
46546	development of primary male sexual characteristics	3.3472E-2
31669	cellular response to nutrient levels	3.3472E-2
32943	mononuclear cell proliferation	3.4146E-2
9966	regulation of signal transduction	3.4756E-2
23033	signaling pathway	3.4767E-2
32989	cellular component morphogenesis	3.4821E-2
51241	negative regulation of multicellular organismal process	3.4821E-2
7346	regulation of mitotic cell cycle	3.4821E-2
9617	response to bacterium	3.5610E-2
7548	sex differentiation	3.5610E-2
46545	development of primary female sexual characteristics	3.5683E-2
90305	nucleic acid phosphodiester bond hydrolysis	3.5683E-2
45833	negative regulation of lipid metabolic process	3.5683E-2
70661	leukocyte proliferation	3.5683E-2
280	nuclear division	3.5719E-2
7067	mitosis	3.5719E-2
14059	regulation of dopamine secretion	3.5719E-2
51310	metaphase plate congression	3.5719E-2
10559	regulation of glycoprotein biosynthetic process	3.5719E-2
43536	positive regulation of blood vessel endothelial cell migration	3.5719E-2
6833	water transport	3.5719E-2
31571	G1/S DNA damage checkpoint	3.5719E-2
60749	mammary gland alveolus development	3.5719E-2
8088	axon cargo transport	3.5719E-2
32729	positive regulation of interferon-gamma production	3.5719E-2
45321	leukocyte activation	3.5719E-2
30097	hemopoiesis	3.5719E-2
33157	regulation of intracellular protein transport	3.5934E-2
31099	regeneration	3.5934E-2

209	protein polyubiquitination	3.6744E-2
3006	reproductive developmental process	3.6744E-2
60562	epithelial tube morphogenesis	3.6744E-2
42698	ovulation cycle	3.7120E-2
7369	gastrulation	3.7120E-2
22008	neurogenesis	3.7418E-2
2237	response to molecule of bacterial origin	3.7531E-2
2521	leukocyte differentiation	3.7531E-2
10594	regulation of endothelial cell migration	3.8592E-2
30335	positive regulation of cell migration	3.8592E-2
3013	circulatory system process	3.8829E-2
8015	blood circulation	3.8829E-2
87	M phase of mitotic cell cycle	3.9248E-2
71310	cellular response to organic substance	3.9248E-2
50804	regulation of synaptic transmission	3.9248E-2
33138	positive regulation of peptidyl-serine phosphorylation	3.9248E-2
8625	induction of apoptosis via death domain receptors	3.9248E-2
45773	positive regulation of axon extension	3.9248E-2
42044	fluid transport	3.9248E-2
32330	regulation of chondrocyte differentiation	3.9248E-2
10675	regulation of cellular carbohydrate metabolic process	4.0076E-2
6066	alcohol metabolic process	4.0076E-2
31328	positive regulation of cellular biosynthetic process	4.0076E-2
904	cell morphogenesis involved in differentiation	4.0076E-2
46660	female sex differentiation	4.0076E-2
46661	male sex differentiation	4.0076E-2
7059	chromosome segregation	4.0076E-2
45017	glycerolipid biosynthetic process	4.0076E-2
42391	regulation of membrane potential	4.1530E-2
30183	B cell differentiation	4.1530E-2
50679	positive regulation of epithelial cell proliferation	4.1530E-2
6109	regulation of carbohydrate metabolic process	4.1530E-2
46649	lymphocyte activation	4.1530E-2
51222	positive regulation of protein transport	4.1530E-2
48871	multicellular organismal homeostasis	4.1530E-2
43434	response to peptide hormone stimulus	4.1530E-2
9651	response to salt stress	4.1530E-2
14048	regulation of glutamate secretion	4.1530E-2
10165	response to X-ray	4.1530E-2
51354	negative regulation of oxidoreductase activity	4.1530E-2
22414	reproductive process	4.1530E-2
48609	reproductive process in a multicellular organism	4.1530E-2
32504	multicellular organism reproduction	4.1530E-2
51235	maintenance of location	4.1530E-2
50877	neurological system process	4.1530E-2
16567	protein ubiquitination	4.1530E-2
51336	regulation of hydrolase activity	4.1530E-2
3	reproduction	4.1530E-2

7267	cell-cell signaling	4.1530E-2
6259	DNA metabolic process	4.1530E-2
51272	positive regulation of cellular component movement	4.1530E-2
40017	positive regulation of locomotion	4.1530E-2
32848	negative regulation of cellular pH reduction	4.1530E-2
90200	positive regulation of release of cytochrome c from mitochondria	4.1530E-2
32976	release of matrix enzymes from mitochondria	4.1530E-2
70495	negative regulation of thrombin receptor signaling pathway	4.1530E-2
70494	regulation of thrombin receptor signaling pathway	4.1530E-2
33693	neurofilament bundle assembly	4.1530E-2
21747	cochlear nucleus development	4.1530E-2
46370	fructose biosynthetic process	4.1530E-2
50747	positive regulation of lipoprotein metabolic process	4.1530E-2
46674	induction of retinal programmed cell death	4.1530E-2
50812	regulation of acyl-CoA biosynthetic process	4.1530E-2
1711	endodermal cell fate commitment	4.1530E-2
14041	regulation of neuron maturation	4.1530E-2
14042	positive regulation of neuron maturation	4.1530E-2
6060	sorbitol metabolic process	4.1530E-2
6062	sorbitol catabolic process	4.1530E-2
51124	synaptic growth at neuromuscular junction	4.1530E-2
51160	L-xylitol catabolic process	4.1530E-2
51164	L-xylitol metabolic process	4.1530E-2
42999	regulation of Golgi to plasma membrane CFTR protein transport	4.1530E-2
43002	negative regulation of Golgi to plasma membrane CFTR protein transport	4.1530E-2
43004	cytoplasmic sequestering of CFTR protein	4.1530E-2
51315	attachment of spindle microtubules to kinetochore involved in mitotic sister chromatid segregation	4.1530E-2
43217	myelin maintenance	4.1530E-2
43369	CD4-positive or CD8-positive, alpha-beta T cell lineage commitment	4.1530E-2
43375	CD8-positive, alpha-beta T cell lineage commitment	4.1530E-2
51581	negative regulation of neurotransmitter uptake	4.1530E-2
51585	negative regulation of dopamine uptake	4.1530E-2
51611	regulation of serotonin uptake	4.1530E-2
51612	negative regulation of serotonin uptake	4.1530E-2
51621	regulation of norepinephrine uptake	4.1530E-2
51622	negative regulation of norepinephrine uptake	4.1530E-2
2477	antigen processing and presentation of exogenous peptide antigen via MHC class Ib	4.1530E-2
2481	antigen processing and presentation of exogenous protein antigen via MHC class Ib, TAP-dependent	4.1530E-2
2525	acute inflammatory response to non-antigenic stimulus	4.1530E-2
2575	basophil chemotaxis	4.1530E-2
14916	regulation of lung blood pressure	4.1530E-2
10822	positive regulation of mitochondrion organization	4.1530E-2
6808	regulation of nitrogen utilization	4.1530E-2
51913	regulation of synaptic plasticity by chemical substance	4.1530E-2
51914	positive regulation of synaptic plasticity by chemical substance	4.1530E-2

51915	induction of synaptic plasticity by chemical substance	4.1530E-2
51945	negative regulation of catecholamine uptake involved in synaptic transmission	4.1530E-2
60215	primitive hemopoiesis	4.1530E-2
60266	negative regulation of respiratory burst involved in inflammatory response	4.1530E-2
60268	negative regulation of respiratory burst	4.1530E-2
60319	primitive erythrocyte differentiation	4.1530E-2
19407	hexitol catabolic process	4.1530E-2
19519	pentitol metabolic process	4.1530E-2
19527	pentitol catabolic process	4.1530E-2
31987	locomotion involved in locomotory behavior	4.1530E-2
60697	positive regulation of phospholipid catabolic process	4.1530E-2
48668	collateral sprouting	4.1530E-2
48669	collateral sprouting in the absence of injury	4.1530E-2
32287	myelin maintenance in the peripheral nervous system	4.1530E-2
48743	positive regulation of skeletal muscle fiber development	4.1530E-2
32621	interleukin-18 production	4.1530E-2
16238	chaperone-mediated autophagy	4.1530E-2
46907	intracellular transport	4.1908E-2
44262	cellular carbohydrate metabolic process	4.2121E-2
16486	peptide hormone processing	4.2148E-2
19098	reproductive behavior	4.2148E-2
60395	SMAD protein signal transduction	4.2148E-2
48732	gland development	4.2359E-2
55002	striated muscle cell development	4.4786E-2
9615	response to virus	4.5859E-2
10638	positive regulation of organelle organization	4.5859E-2
50000	chromosome localization	4.6700E-2
30104	water homeostasis	4.6700E-2
51303	establishment of chromosome localization	4.6700E-2
10862	positive regulation of pathway-restricted SMAD protein phosphorylation	4.6700E-2
61035	regulation of cartilage development	4.6700E-2
45944	positive regulation of transcription from RNA polymerase II promoter	4.6710E-2
10769	regulation of cell morphogenesis involved in differentiation	4.6914E-2
90092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	4.6914E-2
48593	camera-type eye morphogenesis	4.8988E-2
48638	regulation of developmental growth	4.8988E-2
1817	regulation of cytokine production	4.9769E-2
48666	neuron development	4.9918E-2

All biological processes. Significance level  $p < 0.05$ .