

Supplementary Table S5

Event 1 (LINC00665)

N.A.

Event 2 (NSUN4)

(Event #2)	Term	Ont	N	DE	P.DE	FDR
GO:0098798	mitochondrial protein complex	CC	262	82	9.50E-32	2.18E-27
GO:0005743	mitochondrial inner membrane	CC	473	108	3.62E-28	4.14E-24
GO:0019866	organelle inner membrane	CC	532	115	1.05E-27	8.03E-24
GO:0005737	cytoplasm	CC	11625	1021	2.04E-27	1.17E-23
GO:0044429	mitochondrial part	CC	1036	172	1.62E-26	7.44E-23
GO:0005740	mitochondrial envelope	CC	739	137	7.77E-26	2.97E-22
GO:0005515	protein binding	MF	11807	1025	2.97E-25	9.71E-22
GO:0031966	mitochondrial membrane	CC	698	130	9.78E-25	2.80E-21
GO:0044424	intracellular part	CC	15063	1227	7.88E-24	2.01E-20
GO:0005622	intracellular	CC	15073	1227	1.20E-23	2.74E-20
GO:0005739	mitochondrion	CC	1573	220	1.79E-23	3.72E-20
GO:0044444	cytoplasmic part	CC	9735	869	5.35E-22	1.02E-18
GO:0044446	intracellular organelle part	CC	9811	868	1.47E-20	2.60E-17
GO:0043229	intracellular organelle	CC	13294	1103	2.85E-20	4.66E-17
GO:0043231	intracellular membrane-bounded organelle	CC	11488	982	4.79E-20	7.31E-17
GO:0044422	organelle part	CC	10112	882	5.46E-19	7.82E-16
GO:0043226	organelle	CC	14144	1151	1.14E-18	1.53E-15
GO:0098800	inner mitochondrial membrane protein complex	CC	135	44	2.19E-18	2.79E-15
GO:0043227	membrane-bounded organelle	CC	13019	1075	6.22E-18	7.50E-15
GO:0005488	binding	MF	15267	1217	1.34E-17	1.54E-14
GO:0031967	organelle envelope	CC	1182	164	3.48E-17	3.62E-14
GO:0031975	envelope	CC	1182	164	3.48E-17	3.62E-14
GO:0006415	translational termination	BP	104	37	4.19E-17	4.17E-14
GO:0098803	respiratory chain complex	CC	85	33	1.00E-16	9.58E-14
GO:0000313	organellar ribosome	CC	87	33	2.28E-16	2.01E-13
GO:0005761	mitochondrial ribosome	CC	87	33	2.28E-16	2.01E-13
GO:0070125	mitochondrial translational elongation	BP	88	33	3.40E-16	2.89E-13
GO:0070126	mitochondrial translational termination	BP	89	33	5.04E-16	4.13E-13
GO:0070469	respiratory chain	CC	100	35	5.32E-16	4.21E-13
GO:0042775	mitochondrial ATP synthesis coupled electron transport	BP	97	34	1.32E-15	1.01E-12
GO:0042773	ATP synthesis coupled electron transport	BP	98	34	1.89E-15	1.39E-12
GO:0044455	mitochondrial membrane part	CC	229	54	2.61E-15	1.87E-12
GO:0003674	molecular function	MF	17697	1350	8.83E-15	6.13E-12
GO:0006996	organelle organization	BP	3885	391	1.62E-14	1.09E-11
GO:0022904	respiratory electron transport chain	BP	117	36	2.03E-14	1.29E-11
GO:0005746	mitochondrial respiratory chain	CC	88	31	2.02E-14	1.29E-11
GO:0006119	oxidative phosphorylation	BP	145	40	4.35E-14	2.69E-11
GO:0022900	electron transport chain	BP	186	46	4.68E-14	2.82E-11
GO:0071840	cellular component organization or biogenesis	BP	6697	606	1.09E-13	6.38E-11
GO:1902494	catalytic complex	CC	1370	171	1.42E-13	8.12E-11
GO:0003824	catalytic activity	MF	5710	530	1.59E-13	8.88E-11
GO:1901564	organonitrogen compound metabolic process	BP	7040	630	2.22E-13	1.21E-10
GO:0031974	membrane-enclosed lumen	CC	5740	530	4.24E-13	2.16E-10
GO:0043233	organelle lumen	CC	5740	530	4.24E-13	2.16E-10
GO:0070013	intracellular organelle lumen	CC	5740	530	4.24E-13	2.16E-10

GO:0032543	mitochondrial translation	BP	135	37	4.83E-13	2.41E-10
GO:0005759	mitochondrial matrix	CC	469	79	5.34E-13	2.60E-10
GO:0005747	mitochondrial respiratory chain complex I	CC	50	22	6.16E-13	2.82E-10
GO:0030964	NADH dehydrogenase complex	CC	50	22	6.16E-13	2.82E-10
GO:0045271	respiratory chain complex I	CC	50	22	6.16E-13	2.82E-10
GO:0031090	organelle membrane	CC	2903	300	2.64E-12	1.19E-09
GO:0045333	cellular respiration	BP	193	44	3.41E-12	1.50E-09
GO:0016043	cellular component organization	BP	6512	583	4.31E-12	1.86E-09
GO:0005654	nucleoplasm	CC	3512	349	4.43E-12	1.88E-09
GO:0044237	cellular metabolic process	BP	11301	928	5.69E-12	2.37E-09
GO:0006120	mitochondrial electron transport, NADH to ubiquinone	BP	55	22	6.39E-12	2.61E-09
GO:0000315	organellar large ribosomal subunit	CC	57	22	1.49E-11	5.90E-09
GO:0005762	mitochondrial large ribosomal subunit	CC	57	22	1.49E-11	5.90E-09
GO:0043624	cellular protein complex disassembly	BP	217	46	1.64E-11	6.37E-09
GO:0010257	NADH dehydrogenase complex assembly	BP	64	23	2.90E-11	1.09E-08
GO:0032981	mitochondrial respiratory chain complex I assembly	BP	64	23	2.90E-11	1.09E-08
GO:0140053	mitochondrial gene expression	BP	162	38	4.10E-11	1.51E-08
GO:0007005	mitochondrion organization	BP	530	81	4.61E-11	1.68E-08
GO:0005829	cytosol	CC	5085	468	4.70E-11	1.68E-08
GO:0016655	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor	MF	60	22	4.92E-11	1.73E-08
GO:0009144	purine nucleoside triphosphate metabolic process	BP	342	60	6.40E-11	2.22E-08
GO:0003954	NADH dehydrogenase activity	MF	46	19	9.01E-11	2.99E-08
GO:0008137	NADH dehydrogenase (ubiquinone) activity	MF	46	19	9.01E-11	2.99E-08
GO:0050136	NADH dehydrogenase (quinone) activity	MF	46	19	9.01E-11	2.99E-08
GO:0009123	nucleoside monophosphate metabolic process	BP	375	63	1.39E-10	4.48E-08
GO:0046034	ATP metabolic process	BP	305	55	1.38E-10	4.48E-08
GO:0009167	purine ribonucleoside monophosphate metabolic process	BP	340	59	1.45E-10	4.54E-08
GO:1990204	oxidoreductase complex	CC	112	30	1.43E-10	4.54E-08
GO:0006414	translational elongation	BP	133	33	1.60E-10	4.96E-08
GO:0009126	purine nucleoside monophosphate metabolic process	BP	341	59	1.63E-10	4.98E-08
GO:0009161	ribonucleoside monophosphate metabolic process	BP	354	60	2.66E-10	8.03E-08
GO:0006091	generation of precursor metabolites and energy	BP	526	78	4.54E-10	1.35E-07
GO:0006807	nitrogen compound metabolic process	BP	10812	881	6.29E-10	1.85E-07
GO:0009205	purine ribonucleoside triphosphate metabolic process	BP	335	57	6.41E-10	1.86E-07
GO:0009141	nucleoside triphosphate metabolic process	BP	362	60	6.58E-10	1.89E-07
GO:0015980	energy derivation by oxidation of organic compounds	BP	285	51	8.49E-10	2.40E-07
GO:0032984	protein-containing complex disassembly	BP	329	56	8.92E-10	2.49E-07
GO:0009199	ribonucleoside triphosphate metabolic process	BP	341	57	1.27E-09	3.51E-07
GO:0043412	macromolecule modification	BP	4373	403	1.98E-09	5.39E-07
GO:0044267	cellular protein metabolic process	BP	5276	471	3.77E-09	1.02E-06
GO:0033108	mitochondrial respiratory chain complex assembly	BP	96	25	9.02E-09	2.40E-06
GO:0034641	cellular nitrogen compound metabolic process	BP	7161	609	1.26E-08	3.33E-06
GO:0044238	primary metabolic process	BP	11287	905	1.31E-08	3.41E-06
GO:0055114	oxidation-reduction process	BP	999	119	1.53E-08	3.95E-06
GO:0044281	small molecule metabolic process	BP	2115	216	1.65E-08	4.19E-06

GO:0009055	electron transfer activity	MF	114	27	2.12E-08	5.34E-06
GO:0072521	purine-containing compound metabolic process	BP	613	82	2.15E-08	5.36E-06
GO:0009150	purine ribonucleotide metabolic process	BP	542	74	4.56E-08	1.12E-05
GO:0006163	purine nucleotide metabolic process	BP	575	77	5.56E-08	1.36E-05
GO:0022411	cellular component disassembly	BP	546	74	6.18E-08	1.49E-05
GO:0019693	ribose phosphate metabolic process	BP	577	77	6.44E-08	1.52E-05
GO:0006626	protein targeting to mitochondrion	BP	98	24	6.44E-08	1.52E-05
GO:0044260	cellular macromolecule metabolic process	BP	8352	690	8.49E-08	1.97E-05
GO:0006753	nucleoside phosphate metabolic process	BP	716	90	8.49E-08	1.97E-05
GO:0016491	oxidoreductase activity	MF	748	93	8.62E-08	1.98E-05
GO:0072655	establishment of protein localization to mitochondrion	BP	137	29	9.20E-08	2.09E-05
GO:0016651	oxidoreductase activity, acting on NAD(P)H	MF	107	25	9.32E-08	2.09E-05
GO:0009117	nucleotide metabolic process	BP	709	89	1.07E-07	2.37E-05
GO:0006796	phosphate-containing compound metabolic process	BP	3320	309	1.26E-07	2.78E-05
GO:0009259	ribonucleotide metabolic process	BP	557	74	1.39E-07	3.04E-05
GO:0016071	mRNA metabolic process	BP	877	104	1.61E-07	3.48E-05
GO:0006464	cellular protein modification process	BP	4160	374	1.71E-07	3.60E-05
GO:0036211	protein modification process	BP	4160	374	1.71E-07	3.60E-05
GO:0046700	heterocycle catabolic process	BP	695	87	1.68E-07	3.60E-05
GO:0070585	protein localization to mitochondrion	BP	141	29	1.77E-07	3.69E-05
GO:0019538	protein metabolic process	BP	5986	513	1.80E-07	3.69E-05
GO:0044270	cellular nitrogen compound catabolic process	BP	696	87	1.79E-07	3.69E-05
GO:0044464	cell part	CC	17521	1310	2.31E-07	4.67E-05
GO:0034655	nucleobase-containing compound catabolic process	BP	648	82	2.42E-07	4.87E-05
GO:0006793	phosphorus metabolic process	BP	3347	309	2.74E-07	5.47E-05
GO:0055086	nucleobase-containing small molecule metabolic process	BP	801	96	3.01E-07	5.94E-05
GO:0006839	mitochondrial transport	BP	256	42	3.16E-07	6.18E-05
GO:0008152	metabolic process	BP	12552	982	3.32E-07	6.44E-05
GO:2001234	negative regulation of apoptotic signaling pathway	BP	230	39	3.46E-07	6.67E-05
GO:0046907	intracellular transport	BP	1847	186	5.03E-07	9.53E-05
GO:1901361	organic cyclic compound catabolic process	BP	745	90	5.03E-07	9.53E-05
GO:0044391	ribosomal subunit	CC	190	34	5.36E-07	1.01E-04
GO:0005623	cell	CC	17590	1312	6.18E-07	1.15E-04
GO:0032991	protein-containing complex	CC	6151	521	6.57E-07	1.21E-04
GO:0019637	organophosphate metabolic process	BP	1177	128	7.78E-07	1.43E-04
GO:0019439	aromatic compound catabolic process	BP	712	86	9.10E-07	1.65E-04
GO:0043933	protein-containing complex subunit organization	BP	2290	221	9.38E-07	1.69E-04
GO:0065002	intracellular protein transmembrane transport	BP	56	16	1.09E-06	1.95E-04
GO:1901135	carbohydrate derivative metabolic process	BP	1266	135	1.13E-06	2.00E-04
GO:1901575	organic substance catabolic process	BP	2175	211	1.20E-06	2.11E-04
GO:0003723	RNA binding	MF	1950	192	1.49E-06	2.60E-04
GO:0009056	catabolic process	BP	2615	246	1.52E-06	2.64E-04
GO:1990542	mitochondrial transmembrane transport	BP	101	22	1.93E-06	3.29E-04
GO:0043487	regulation of RNA stability	BP	183	32	1.92E-06	3.29E-04
GO:0071806	protein transmembrane transport	BP	65	17	1.97E-06	3.35E-04

GO:0016310	phosphorylation	BP	2417	229	2.26E-06	3.81E-04
GO:0031981	nuclear lumen	CC	4594	399	2.47E-06	4.13E-04
GO:0034470	ncRNA processing	BP	384	53	2.65E-06	4.39E-04
GO:0009894	regulation of catabolic process	BP	979	108	3.07E-06	5.07E-04
GO:1901360	organic cyclic compound metabolic process	BP	6839	566	3.50E-06	5.73E-04
GO:0015934	large ribosomal subunit	CC	121	24	3.89E-06	6.31E-04
GO:0017144	drug metabolic process	BP	851	96	4.35E-06	7.02E-04
GO:0009057	macromolecule catabolic process	BP	1396	143	4.89E-06	7.84E-04
GO:0097190	apoptotic signaling pathway	BP	602	73	5.27E-06	8.39E-04
GO:0006139	nucleobase-containing compound metabolic process	BP	6411	532	6.53E-06	1.03E-03
GO:0007007	inner mitochondrial membrane organization	BP	44	13	7.33E-06	1.15E-03
GO:0043488	regulation of mRNA stability	BP	177	30	7.61E-06	1.18E-03
GO:0005634	nucleus	CC	7932	643	7.62E-06	1.18E-03
GO:0044451	nucleoplasm part	CC	1126	119	7.67E-06	1.18E-03
GO:0046483	heterocycle metabolic process	BP	6570	543	7.96E-06	1.22E-03
GO:0044248	cellular catabolic process	BP	2324	218	8.22E-06	1.25E-03
GO:0006886	intracellular protein transport	BP	1119	118	9.29E-06	1.40E-03
GO:0071704	organic substance metabolic process	BP	12093	938	9.40E-06	1.41E-03
GO:0005840	ribosome	CC	272	40	9.65E-06	1.44E-03
GO:0061013	regulation of mRNA catabolic process	BP	199	32	1.18E-05	1.75E-03
GO:1903311	regulation of mRNA metabolic process	BP	324	45	1.25E-05	1.84E-03
GO:0000314	organellar small ribosomal subunit	CC	28	10	1.29E-05	1.87E-03
GO:0005763	mitochondrial small ribosomal subunit	CC	28	10	1.29E-05	1.87E-03
GO:0070069	cytochrome complex	CC	34	11	1.41E-05	2.04E-03
GO:0006725	cellular aromatic compound metabolic process	BP	6615	544	1.44E-05	2.06E-03
GO:0070647	protein modification by small protein conjugation or removal	BP	1108	116	1.54E-05	2.18E-03
GO:0044085	cellular component biogenesis	BP	3355	297	1.79E-05	2.53E-03
GO:0044743	protein transmembrane import into intracellular organelle	BP	41	12	1.83E-05	2.57E-03
GO:0051649	establishment of localization in cell	BP	2242	209	1.94E-05	2.71E-03
GO:0044428	nuclear part	CC	5023	424	2.04E-05	2.83E-03
GO:0008121	ubiquinol-cytochrome-c reductase activity	MF	10	6	2.10E-05	2.89E-03
GO:0016681	oxidoreductase activity, acting on diphenols and related substances as donors, cytoch	MF	10	6	2.10E-05	2.89E-03
GO:0006364	rRNA processing	BP	214	33	2.12E-05	2.90E-03
GO:0051641	cellular localization	BP	2927	263	2.15E-05	2.91E-03
GO:0043604	amide biosynthetic process	BP	876	95	2.40E-05	3.23E-03
GO:0006402	mRNA catabolic process	BP	364	48	2.60E-05	3.49E-03
GO:2001233	regulation of apoptotic signaling pathway	BP	406	52	2.73E-05	3.64E-03
GO:0034613	cellular protein localization	BP	1872	178	2.93E-05	3.88E-03
GO:0006401	RNA catabolic process	BP	397	51	3.00E-05	3.95E-03
GO:0044265	cellular macromolecule catabolic process	BP	1162	119	3.21E-05	4.20E-03
GO:0009451	RNA modification	BP	163	27	3.25E-05	4.23E-03
GO:0009060	aerobic respiration	BP	87	18	3.38E-05	4.38E-03
GO:0042254	ribosome biogenesis	BP	297	41	3.45E-05	4.44E-03
GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	BP	15	7	3.52E-05	4.51E-03
GO:0006914	autophagy	BP	496	60	3.83E-05	4.84E-03

GO:0061919	process utilizing autophagic mechanism	BP	496	60	3.83E-05	4.84E-03
GO:1903214	regulation of protein targeting to mitochondrion	BP	44	12	4.00E-05	5.04E-03
GO:0034660	ncRNA metabolic process	BP	562	66	4.05E-05	5.06E-03
GO:0070727	cellular macromolecule localization	BP	1883	178	4.07E-05	5.06E-03
GO:0010033	response to organic substance	BP	3302	290	4.23E-05	5.24E-03
GO:0016679	oxidoreductase activity, acting on diphenols and related substances as donors	MF	11	6	4.35E-05	5.36E-03
GO:1905368	peptidase complex	CC	89	18	4.65E-05	5.70E-03
GO:0045184	establishment of protein localization	BP	2113	196	4.89E-05	5.93E-03
GO:1903955	positive regulation of protein targeting to mitochondrion	BP	32	10	4.88E-05	5.93E-03
GO:0006986	response to unfolded protein	BP	176	28	4.94E-05	5.96E-03
GO:0031329	regulation of cellular catabolic process	BP	871	93	5.25E-05	6.30E-03
GO:0016072	rRNA metabolic process	BP	253	36	5.36E-05	6.40E-03
GO:1901565	organonitrogen compound catabolic process	BP	1296	129	5.54E-05	6.58E-03
GO:0006412	translation	BP	714	79	5.93E-05	7.00E-03
GO:0043603	cellular amide metabolic process	BP	1157	117	6.42E-05	7.54E-03
GO:0042407	cristae formation	BP	33	10	6.56E-05	7.67E-03
GO:0043043	peptide biosynthetic process	BP	739	81	6.62E-05	7.70E-03
GO:1901566	organonitrogen compound biosynthetic process	BP	1957	182	8.16E-05	9.44E-03
GO:0070646	protein modification by small protein removal	BP	299	40	8.64E-05	9.95E-03
GO:0016462	pyrophosphatase activity	MF	914	95	1.19E-04	1.36E-02
GO:0006473	protein acetylation	BP	204	30	1.20E-04	1.36E-02
GO:0030687	preribosome, large subunit precursor	CC	23	8	1.20E-04	1.36E-02
GO:0016817	hydrolase activity, acting on acid anhydrides	MF	917	95	1.33E-04	1.50E-02
GO:0016818	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	MF	917	95	1.33E-04	1.50E-02
GO:0006518	peptide metabolic process	BP	894	93	1.35E-04	1.51E-02
GO:0016236	macroautophagy	BP	295	39	1.36E-04	1.51E-02
GO:1903747	regulation of establishment of protein localization to mitochondrion	BP	72	15	1.38E-04	1.52E-02
GO:0033605	positive regulation of catecholamine secretion	BP	13	6	1.43E-04	1.57E-02
GO:2000757	negative regulation of peptidyl-lysine acetylation	BP	18	7	1.44E-04	1.58E-02
GO:0008104	protein localization	BP	2765	244	1.47E-04	1.59E-02
GO:0010506	regulation of autophagy	BP	327	42	1.46E-04	1.59E-02
GO:1903533	regulation of protein targeting	BP	81	16	1.62E-04	1.75E-02
GO:0000278	mitotic cell cycle	BP	1017	103	1.66E-04	1.79E-02
GO:0031252	cell leading edge	CC	403	49	1.68E-04	1.80E-02
GO:1903749	positive regulation of establishment of protein localization to mitochondrion	BP	58	13	1.75E-04	1.87E-02
GO:0009058	biosynthetic process	BP	6339	513	1.76E-04	1.87E-02
GO:0042180	cellular ketone metabolic process	BP	248	34	1.77E-04	1.87E-02
GO:0022613	ribonucleoprotein complex biogenesis	BP	502	58	1.80E-04	1.88E-02
GO:1901576	organic substance biosynthetic process	BP	6259	507	1.80E-04	1.88E-02
GO:0035966	response to topologically incorrect protein	BP	199	29	1.81E-04	1.88E-02
GO:0016787	hydrolase activity	MF	2533	225	1.90E-04	1.97E-02
GO:0033036	macromolecule localization	BP	3116	270	2.07E-04	2.14E-02
GO:0030150	protein import into mitochondrial matrix	BP	19	7	2.14E-04	2.20E-02
GO:0009394	2'-deoxyribonucleotide metabolic process	BP	31	9	2.19E-04	2.23E-02
GO:0140098	catalytic activity, acting on RNA	MF	386	47	2.19E-04	2.23E-02

GO:0031400	negative regulation of protein modification process	BP	618	68	2.23E-04	2.26E-02
GO:0071310	cellular response to organic substance	BP	2707	238	2.25E-04	2.27E-02
GO:0015833	peptide transport	BP	2034	185	2.32E-04	2.33E-02
GO:0005750	mitochondrial respiratory chain complex III	CC	14	6	2.35E-04	2.34E-02
GO:0045275	respiratory chain complex III	CC	14	6	2.35E-04	2.34E-02
GO:0015031	protein transport	BP	1998	182	2.42E-04	2.41E-02
GO:0016579	protein deubiquitination	BP	283	37	2.49E-04	2.46E-02
GO:1901363	heterocyclic compound binding	MF	6241	503	3.21E-04	3.16E-02
GO:0051128	regulation of cellular component organization	BP	2507	221	3.37E-04	3.28E-02
GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress	BP	121	20	3.37E-04	3.28E-02
GO:0016853	isomerase activity	MF	158	24	3.38E-04	3.29E-02
GO:0030163	protein catabolic process	BP	931	94	3.53E-04	3.41E-02
GO:0007050	cell cycle arrest	BP	237	32	3.57E-04	3.42E-02
GO:0072594	establishment of protein localization to organelle	BP	549	61	3.56E-04	3.42E-02
GO:0005010	insulin-like growth factor-activated receptor activity	MF	3	3	3.60E-04	3.43E-02
GO:0044249	cellular biosynthetic process	BP	6168	497	3.66E-04	3.45E-02
GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	BP	104	18	3.69E-04	3.45E-02
GO:0034620	cellular response to unfolded protein	BP	140	22	3.63E-04	3.45E-02
GO:0019692	deoxyribose phosphate metabolic process	BP	33	9	3.68E-04	3.45E-02
GO:0035067	negative regulation of histone acetylation	BP	15	6	3.67E-04	3.45E-02
GO:0034708	methyltransferase complex	CC	113	19	3.75E-04	3.50E-02
GO:0051130	positive regulation of cellular component organization	BP	1258	121	3.80E-04	3.52E-02
GO:0051173	positive regulation of nitrogen compound metabolic process	BP	3200	274	3.98E-04	3.68E-02
GO:0034612	response to tumor necrosis factor	BP	312	39	4.31E-04	3.96E-02
GO:2000737	negative regulation of stem cell differentiation	BP	21	7	4.36E-04	3.98E-02
GO:0031970	organelle envelope lumen	CC	88	16	4.35E-04	3.98E-02
GO:0016241	regulation of macroautophagy	BP	171	25	4.65E-04	4.23E-02
GO:1905369	endopeptidase complex	CC	64	13	4.89E-04	4.43E-02
GO:0016567	protein ubiquitination	BP	822	84	4.95E-04	4.46E-02
GO:0042886	amide transport	BP	2065	185	4.97E-04	4.46E-02
GO:0051247	positive regulation of protein metabolic process	BP	1713	157	5.06E-04	4.53E-02
GO:0007006	mitochondrial membrane organization	BP	134	21	5.08E-04	4.53E-02
GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	BP	98	17	5.16E-04	4.59E-02
GO:0044271	cellular nitrogen compound biosynthetic process	BP	5029	411	5.20E-04	4.60E-02
GO:1902600	proton transmembrane transport	BP	163	24	5.39E-04	4.75E-02
GO:0071495	cellular response to endogenous stimulus	BP	1393	131	5.50E-04	4.82E-02

Event 3 (SRRM2)

(Event #3)	Term	Ont	N	DE	P.DE	FDR
GO:0005737	cytoplasm	CC	11625	201	4.35E-07	9.96E-03
GO:0044444	cytoplasmic part	CC	9735	173	2.49E-06	2.85E-02

Event 4 (ELOVL7)

(Event #4)	Term	Ont	N	DE	P.DE	FDR
GO:0009615	response to virus	BP	326	26	2.46E-12	5.64E-08
GO:0051607	defense response to virus	BP	238	20	3.59E-10	4.11E-06
GO:0060337	type I interferon signaling pathway	BP	95	13	1.26E-09	7.20E-06
GO:0071357	cellular response to type I interferon	BP	95	13	1.26E-09	7.20E-06
GO:0034340	response to type I interferon	BP	99	13	2.12E-09	9.69E-06
GO:0005737	cytoplasm	CC	11625	214	7.04E-08	2.69E-04
GO:0044444	cytoplasmic part	CC	9735	183	1.16E-06	3.79E-03
GO:0001730	2'-5'-oligoadenylate synthetase activity	MF	3	3	3.08E-06	8.81E-03
GO:0044424	intracellular part	CC	15063	252	5.53E-06	1.38E-02
GO:0005622	intracellular	CC	15073	252	6.02E-06	1.38E-02
GO:0098586	cellular response to virus	BP	56	7	1.65E-05	3.44E-02
GO:0045071	negative regulation of viral genome replication	BP	59	7	2.34E-05	4.47E-02

Event 5 (DRC1)

N.A.