

Supplementary Table 2

GO ID	GO Term	GO Type	P value
GO:0034645	cellular macromolecule biosynthetic process	BP	1.05E-04
GO:0034644	cellular response to UV	BP	2.98E-02
GO:0010557	positive regulation of macromolecule biosynthetic process	BP	9.45E-03
GO:0010556	regulation of macromolecule biosynthetic process	BP	2.36E-03
GO:0019372	lipoxygenase pathway	BP	4.48E-02
GO:0031497	chromatin assembly	BP	9.64E-03
GO:0034641	cellular nitrogen compound metabolic process	BP	4.12E-03
GO:0043368	positive T cell selection	BP	4.11E-02
GO:0071702	organic substance transport	BP	3.91E-02
GO:0046637	regulation of alpha-beta T cell differentiation	BP	4.80E-02
GO:0071824	protein-DNA complex subunit organization	BP	4.40E-04
GO:0006290	pyrimidine dimer repair	BP	1.48E-02
GO:0071705	nitrogen compound transport	BP	3.46E-03
GO:0071826	ribonucleoprotein complex subunit organization	BP	7.08E-05
GO:0006294	nucleotide-excision repair, preincision complex assembly	BP	2.35E-02
GO:0006295	nucleotide-excision repair, DNA incision, 3'-to lesion	BP	9.68E-03
GO:0006293	nucleotide-excision repair, preincision complex stabilization	BP	9.68E-03
GO:0043482	cellular pigment accumulation	BP	2.61E-02
GO:0075071	modulation by symbiont of host autophagy	BP	8.90E-03
GO:0042274	ribosomal small subunit biogenesis	BP	5.41E-03
GO:0043485	endosome to pigment granule transport	BP	1.83E-02
GO:0043484	regulation of RNA splicing	BP	1.94E-02
GO:0006296	nucleotide-excision repair, DNA incision, 5'-to lesion	BP	7.80E-03
GO:0031124	mRNA 3'-end processing	BP	3.27E-04
GO:0034638	phosphatidylcholine catabolic process	BP	3.97E-02
GO:0035966	response to topologically incorrect protein	BP	4.92E-03
GO:0035967	cellular response to topologically incorrect protein	BP	9.54E-04
GO:0070972	protein localization to endoplasmic reticulum	BP	1.68E-03
GO:0031123	RNA 3'-end processing	BP	5.85E-03

GO:0070727	cellular macromolecule localization	BP	1.73E-03
GO:0022411	cellular component disassembly	BP	2.23E-02
GO:0043254	regulation of protein-containing complex assembly	BP	4.22E-03
GO:0007005	mitochondrion organization	BP	4.85E-03
GO:0034622	cellular protein-containing complex assembly	BP	4.62E-06
GO:1902902	negative regulation of autophagosome assembly	BP	3.04E-02
GO:0034620	cellular response to unfolded protein	BP	4.32E-03
GO:0034982	mitochondrial protein processing	BP	3.04E-02
GO:0044237	cellular metabolic process	BP	1.82E-02
GO:0000730	DNA recombinase assembly	BP	6.45E-03
GO:0006397	mRNA processing	BP	1.78E-06
GO:0008213	protein alkylation	BP	4.49E-02
GO:0007000	nucleolus organization	BP	8.90E-03
GO:0006396	RNA processing	BP	2.28E-03
GO:0031346	positive regulation of cell projection organization	BP	2.39E-02
GO:0034613	cellular protein localization	BP	2.42E-03
GO:0034976	response to endoplasmic reticulum stress	BP	1.87E-03
GO:0008104	protein localization	BP	9.35E-04
GO:0009314	response to radiation	BP	1.72E-02
GO:0061912	selective autophagy	BP	4.14E-02
GO:0016070	RNA metabolic process	BP	1.42E-03
GO:0042181	ketone biosynthetic process	BP	1.43E-02
GO:0016071	mRNA metabolic process	BP	2.59E-06
GO:0016192	vesicle-mediated transport	BP	4.69E-02
GO:0030490	maturation of SSU-rRNA	BP	2.34E-02
GO:0016072	rRNA metabolic process	BP	1.41E-02
GO:0018130	heterocycle biosynthetic process	BP	2.35E-02
GO:0016197	endosomal transport	BP	8.72E-04
GO:0061919	process utilizing autophagic mechanism	BP	6.08E-04
GO:0071840	cellular component organization or biogenesis	BP	1.22E-02
GO:0044249	cellular biosynthetic process	BP	9.58E-04
GO:0071712	ER-associated misfolded protein catabolic process	BP	2.61E-02

GO:0043153	entrainment of circadian clock by photoperiod	BP	2.35E-02
GO:0046660	female sex differentiation	BP	4.28E-02
GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	BP	3.56E-02
GO:0046545	development of primary female sexual characteristics	BP	2.54E-02
GO:0008585	female gonad development	BP	2.05E-02
GO:0001881	receptor recycling	BP	3.55E-02
GO:0036503	ERAD pathway	BP	2.05E-02
GO:0090304	nucleic acid metabolic process	BP	1.08E-03
GO:0045622	regulation of T-helper cell differentiation	BP	4.11E-02
GO:0046836	glycolipid transport	BP	8.90E-03
GO:0007062	sister chromatid cohesion	BP	1.12E-02
GO:0032259	methylation	BP	3.02E-02
GO:0052040	modulation by symbiont of host programmed cell death	BP	1.48E-02
GO:0035646	endosome to melanosome transport	BP	1.83E-02
GO:0015931	nucleobase-containing compound transport	BP	2.58E-02
GO:0032494	response to peptidoglycan	BP	2.61E-02
GO:0031167	rRNA methylation	BP	2.14E-02
GO:0070925	organelle assembly	BP	5.35E-03
GO:0043331	response to dsRNA	BP	2.65E-02
GO:0043330	response to exogenous dsRNA	BP	1.66E-02
GO:0033572	transferrin transport	BP	4.11E-02
GO:1990126	retrograde transport, endosome to plasma membrane	BP	3.64E-03
GO:0042254	ribosome biogenesis	BP	1.70E-02
GO:2000766	negative regulation of cytoplasmic translation	BP	1.17E-02
GO:0075044	positive regulation by symbiont of host autophagy	BP	8.90E-03
GO:0007059	chromosome segregation	BP	2.89E-02
GO:0010467	gene expression	BP	2.54E-02
GO:0051092	positive regulation of NF-kappaB transcription factor activity	BP	2.15E-02
GO:2000765	regulation of cytoplasmic translation	BP	2.57E-02
GO:0018298	protein-chromophore linkage	BP	3.97E-02
GO:0034654	nucleobase-containing compound biosynthetic process	BP	2.67E-02
GO:0033683	nucleotide-excision repair, DNA incision	BP	9.40E-03

GO:0042147	retrograde transport, endosome to Golgi	BP	4.74E-02
GO:0065003	protein-containing complex assembly	BP	9.99E-05
GO:0008380	RNA splicing	BP	6.77E-05
GO:0000422	autophagy of mitochondrion	BP	6.95E-03
GO:0051090	regulation of DNA-binding transcription factor activity	BP	2.00E-02
GO:0051091	positive regulation of DNA-binding transcription factor activity	BP	5.85E-03
GO:0009597	detection of virus	BP	6.45E-03
GO:0043476	pigment accumulation	BP	2.61E-02
GO:0045893	positive regulation of transcription, DNA-templated	BP	4.27E-02
GO:0065004	protein-DNA complex assembly	BP	2.71E-04
GO:0034248	regulation of cellular amide metabolic process	BP	2.75E-02
GO:0046470	phosphatidylcholine metabolic process	BP	4.04E-02
GO:0033036	macromolecule localization	BP	3.59E-03
GO:0035694	mitochondrial protein catabolic process	BP	4.36E-03
GO:0071427	mRNA-containing ribonucleoprotein complex export from nucleus	BP	3.02E-03
GO:0071426	ribonucleoprotein complex export from nucleus	BP	7.01E-03
GO:0046596	regulation of viral entry into host cell	BP	4.71E-02
GO:0090070	positive regulation of ribosome biogenesis	BP	1.83E-02
GO:0019080	viral gene expression	BP	3.39E-03
GO:0006900	vesicle budding from membrane	BP	9.50E-03
GO:0019083	viral transcription	BP	5.22E-03
GO:0033143	regulation of intracellular steroid hormone receptor signaling pathway	BP	5.41E-03
GO:0033144	negative regulation of intracellular steroid hormone receptor signaling pathway	BP	3.83E-02
GO:0000245	spliceosomal complex assembly	BP	9.83E-03
GO:0046483	heterocycle metabolic process	BP	7.20E-03
GO:0009059	macromolecule biosynthetic process	BP	1.13E-04
GO:0009058	biosynthetic process	BP	1.10E-03
GO:0048545	response to steroid hormone	BP	3.68E-02
GO:0001541	ovarian follicle development	BP	3.35E-02
GO:2000318	positive regulation of T-helper 17 type immune response	BP	2.20E-02
GO:2000316	regulation of T-helper 17 type immune response	BP	1.10E-02
GO:0072539	T-helper 17 cell differentiation	BP	1.94E-02

GO:0072538	T-helper 17 type immune response	BP	2.80E-02
GO:0072657	protein localization to membrane	BP	2.77E-02
GO:0045047	protein targeting to ER	BP	1.14E-03
GO:2000323	negative regulation of glucocorticoid receptor signaling pathway	BP	6.45E-03
GO:2000322	regulation of glucocorticoid receptor signaling pathway	BP	1.17E-02
GO:0045292	mRNA cis splicing, via spliceosome	BP	7.37E-03
GO:0015833	peptide transport	BP	6.60E-04
GO:2000321	positive regulation of T-helper 17 cell differentiation	BP	1.48E-02
GO:0033365	protein localization to organelle	BP	2.22E-02
GO:0070475	rRNA base methylation	BP	2.20E-02
GO:0090069	regulation of ribosome biogenesis	BP	4.48E-02
GO:0051607	defense response to virus	BP	1.02E-02
GO:0044085	cellular component biogenesis	BP	2.87E-04
GO:1901661	quinone metabolic process	BP	7.08E-03
GO:0044087	regulation of cellular component biogenesis	BP	2.77E-03
GO:2000319	regulation of T-helper 17 cell differentiation	BP	7.28E-03
GO:0000462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	BP	4.71E-02
GO:0048569	post-embryonic animal organ development	BP	3.97E-02
GO:1901663	quinone biosynthetic process	BP	4.99E-04
GO:0044089	positive regulation of cellular component biogenesis	BP	3.00E-02
GO:0060976	coronary vasculature development	BP	2.34E-02
GO:0036465	synaptic vesicle recycling	BP	2.11E-02
GO:0090150	establishment of protein localization to membrane	BP	3.40E-02
GO:0000398	mRNA splicing, via spliceosome	BP	1.57E-05
GO:0043043	peptide biosynthetic process	BP	6.69E-05
GO:0045582	positive regulation of T cell differentiation	BP	4.74E-02
GO:0044260	cellular macromolecule metabolic process	BP	2.18E-02
GO:0070646	protein modification by small protein removal	BP	1.33E-02
GO:0032091	negative regulation of protein binding	BP	2.64E-02
GO:0090161	Golgi ribbon formation	BP	3.49E-02
GO:0140238	presynaptic endocytosis	BP	4.35E-02
GO:0002551	mast cell chemotaxis	BP	2.61E-02

GO:1901976	regulation of cell cycle checkpoint	BP	3.04E-02
GO:2000234	positive regulation of rRNA processing	BP	1.83E-02
GO:0061724	lipophagy	BP	8.90E-03
GO:0044271	cellular nitrogen compound biosynthetic process	BP	7.40E-04
GO:0042093	T-helper cell differentiation	BP	3.93E-02
GO:0061726	mitochondrion disassembly	BP	6.95E-03
GO:2000117	negative regulation of cysteine-type endopeptidase activity	BP	4.93E-02
GO:0006914	autophagy	BP	6.08E-04
GO:2000112	regulation of cellular macromolecule biosynthetic process	BP	2.00E-03
GO:2000232	regulation of rRNA processing	BP	3.49E-02
GO:0048757	pigment granule maturation	BP	1.83E-02
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	BP	1.57E-05
GO:0000375	RNA splicing, via transesterification reactions	BP	1.77E-05
GO:0045003	double-strand break repair via synthesis-dependent strand annealing	BP	1.48E-02
GO:0060627	regulation of vesicle-mediated transport	BP	3.19E-02
GO:0000380	alternative mRNA splicing, via spliceosome	BP	3.88E-02
GO:0034499	late endosome to Golgi transport	BP	6.45E-03
GO:0006807	nitrogen compound metabolic process	BP	4.66E-02
GO:0070669	response to interleukin-2	BP	3.49E-02
GO:0000028	ribosomal small subunit assembly	BP	9.68E-03
GO:0060753	regulation of mast cell chemotaxis	BP	8.90E-03
GO:0006611	protein export from nucleus	BP	1.80E-02
GO:0006851	mitochondrial calcium ion transmembrane transport	BP	1.83E-03
GO:0050690	regulation of defense response to virus by virus	BP	2.35E-02
GO:0006614	SRP-dependent cotranslational protein targeting to membrane	BP	1.91E-03
GO:0006612	protein targeting to membrane	BP	1.55E-02
GO:0006613	cotranslational protein targeting to membrane	BP	2.42E-03
GO:0098876	vesicle-mediated transport to the plasma membrane	BP	1.56E-02
GO:0097428	protein maturation by iron-sulfur cluster transfer	BP	3.97E-02
GO:0060260	regulation of transcription initiation from RNA polymerase II promoter	BP	4.40E-02
GO:0060261	positive regulation of transcription initiation from RNA polymerase II promoter	BP	2.80E-02
GO:1902680	positive regulation of RNA biosynthetic process	BP	2.92E-02

GO:0006743	ubiquinone metabolic process	BP	7.63E-04
GO:2000027	regulation of animal organ morphogenesis	BP	4.78E-02
GO:0071383	cellular response to steroid hormone stimulus	BP	5.10E-03
GO:0006744	ubiquinone biosynthetic process	BP	4.99E-04
GO:0006986	response to unfolded protein	BP	1.75E-02
GO:0072594	establishment of protein localization to organelle	BP	2.87E-02
GO:0070059	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	BP	4.57E-02
GO:2000144	positive regulation of DNA-templated transcription, initiation	BP	4.71E-02
GO:0072599	establishment of protein localization to endoplasmic reticulum	BP	1.44E-03
GO:0036498	IRE1-mediated unfolded protein response	BP	1.43E-02
GO:0060491	regulation of cell projection assembly	BP	4.61E-02
GO:0035162	embryonic hemopoiesis	BP	1.33E-03
GO:0043933	protein-containing complex subunit organization	BP	9.04E-06
GO:1901360	organic cyclic compound metabolic process	BP	1.01E-02
GO:1901362	organic cyclic compound biosynthetic process	BP	3.58E-02
GO:0048024	regulation of mRNA splicing, via spliceosome	BP	3.46E-02
GO:1902107	positive regulation of leukocyte differentiation	BP	2.15E-02
GO:0080090	regulation of primary metabolic process	BP	4.27E-02
GO:1903311	regulation of mRNA metabolic process	BP	7.86E-03
GO:1903432	regulation of TORC1 signaling	BP	4.71E-02
GO:0006725	cellular aromatic compound metabolic process	BP	9.11E-03
GO:0071166	ribonucleoprotein complex localization	BP	2.10E-03
GO:0097531	mast cell migration	BP	3.04E-02
GO:0006605	protein targeting	BP	1.62E-02
GO:0035264	multicellular organism growth	BP	4.28E-02
GO:0097659	nucleic acid-templated transcription	BP	6.60E-03
GO:1902115	regulation of organelle assembly	BP	2.44E-02
GO:1902236	negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	BP	8.43E-03
GO:1902116	negative regulation of organelle assembly	BP	9.40E-03
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	BP	4.36E-03
GO:1902235	regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	BP	4.62E-03
GO:0006412	translation	BP	3.51E-05

GO:0006413	translational initiation	BP	2.80E-04
GO:0030522	intracellular receptor signaling pathway	BP	1.24E-02
GO:0006417	regulation of translation	BP	9.09E-03
GO:0045184	establishment of protein localization	BP	8.03E-04
GO:0006415	translational termination	BP	2.54E-02
GO:0071352	cellular response to interleukin-2	BP	3.04E-02
GO:0071478	cellular response to radiation	BP	2.04E-02
GO:2001141	regulation of RNA biosynthetic process	BP	1.18E-02
GO:0016584	nucleosome positioning	BP	3.97E-02
GO:0039694	viral RNA genome replication	BP	3.83E-02
GO:0030518	intracellular steroid hormone receptor signaling pathway	BP	1.25E-02
GO:0002293	alpha-beta T cell differentiation involved in immune response	BP	4.57E-02
GO:0002294	CD4-positive, alpha-beta T cell differentiation involved in immune response	BP	4.35E-02
GO:1903506	regulation of nucleic acid-templated transcription	BP	1.14E-02
GO:1902415	regulation of mRNA binding	BP	1.83E-02
GO:1903508	positive regulation of nucleic acid-templated transcription	BP	2.90E-02
GO:0016571	histone methylation	BP	3.44E-02
GO:0071103	DNA conformation change	BP	2.19E-02
GO:0038110	interleukin-2-mediated signaling pathway	BP	2.61E-02
GO:0016579	protein deubiquitination	BP	8.51E-03
GO:0042921	glucocorticoid receptor signaling pathway	BP	3.04E-02
GO:0050657	nucleic acid transport	BP	2.89E-02
GO:0050658	RNA transport	BP	2.89E-02
GO:0048102	autophagic cell death	BP	2.20E-02
GO:0002181	cytoplasmic translation	BP	6.72E-03
GO:0031958	corticosteroid receptor signaling pathway	BP	3.49E-02
GO:0060215	primitive hemopoiesis	BP	1.17E-02
GO:0002183	cytoplasmic translational initiation	BP	3.83E-02
GO:1901566	organonitrogen compound biosynthetic process	BP	2.54E-02
GO:0006996	organelle organization	BP	3.08E-03
GO:0006515	protein quality control for misfolded or incompletely synthesized proteins	BP	2.35E-02
GO:0032802	low-density lipoprotein particle receptor catabolic process	BP	3.49E-02

GO:0071493	cellular response to UV-B	BP	1.17E-02
GO:0006997	nucleus organization	BP	2.45E-02
GO:0006518	peptide metabolic process	BP	4.01E-04
GO:0051641	cellular localization	BP	8.92E-04
GO:0051640	organelle localization	BP	7.58E-03
GO:1903513	endoplasmic reticulum to cytosol transport	BP	2.35E-02
GO:1901576	organic substance biosynthetic process	BP	8.16E-04
GO:1903753	negative regulation of p38MAPK cascade	BP	1.48E-02
GO:0006644	phospholipid metabolic process	BP	3.76E-02
GO:0006886	intracellular protein transport	BP	6.91E-04
GO:0030970	retrograde protein transport, ER to cytosol	BP	2.35E-02
GO:0002287	alpha-beta T cell activation involved in immune response	BP	4.57E-02
GO:0006405	RNA export from nucleus	BP	1.25E-02
GO:0071360	cellular response to exogenous dsRNA	BP	5.28E-03
GO:0006406	mRNA export from nucleus	BP	3.02E-03
GO:0071482	cellular response to light stimulus	BP	2.12E-02
GO:0006403	RNA localization	BP	3.15E-02
GO:0006888	endoplasmic reticulum to Golgi vesicle-mediated transport	BP	1.38E-02
GO:0051656	establishment of organelle localization	BP	4.70E-02
GO:0050684	regulation of mRNA processing	BP	1.68E-03
GO:0051653	spindle localization	BP	2.19E-02
GO:0051650	establishment of vesicle localization	BP	3.95E-02
GO:0071359	cellular response to dsRNA	BP	1.10E-02
GO:0051649	establishment of localization in cell	BP	3.10E-03
GO:0051648	vesicle localization	BP	2.64E-02
GO:0030968	endoplasmic reticulum unfolded protein response	BP	1.52E-03
GO:0048488	synaptic vesicle endocytosis	BP	4.35E-02
GO:0006335	DNA replication-dependent nucleosome assembly	BP	3.04E-02
GO:0006333	chromatin assembly or disassembly	BP	2.07E-02
GO:0006334	nucleosome assembly	BP	1.30E-02
GO:0031532	actin cytoskeleton reorganization	BP	2.54E-02
GO:0032984	protein-containing complex disassembly	BP	2.66E-02

GO:0030325	adrenal gland development	BP	1.41E-02
GO:0046907	intracellular transport	BP	1.36E-04
GO:0051028	mRNA transport	BP	5.61E-03
GO:0043401	steroid hormone mediated signaling pathway	BP	3.13E-03
GO:0002097	tRNA wobble base modification	BP	1.10E-02
GO:0030433	ubiquitin-dependent ERAD pathway	BP	2.59E-02
GO:0006107	oxaloacetate metabolic process	BP	1.17E-02
GO:0009615	response to virus	BP	6.21E-04
GO:0051276	chromosome organization	BP	3.28E-02
GO:1903146	regulation of autophagy of mitochondrion	BP	1.32E-02
GO:0051168	nuclear export	BP	3.22E-02
GO:0016241	regulation of macroautophagy	BP	1.39E-02
GO:0016242	negative regulation of macroautophagy	BP	3.55E-02
GO:0045724	positive regulation of cilium assembly	BP	1.41E-02
GO:0070911	global genome nucleotide-excision repair	BP	1.75E-02
GO:0120032	regulation of plasma membrane bounded cell projection assembly	BP	4.38E-02
GO:0045727	positive regulation of translation	BP	2.73E-02
GO:0070914	UV-damage excision repair	BP	3.04E-02
GO:0120035	regulation of plasma membrane bounded cell projection organization	BP	4.68E-02
GO:1901096	regulation of autophagosome maturation	BP	3.04E-02
GO:1905214	regulation of RNA binding	BP	2.61E-02
GO:1901097	negative regulation of autophagosome maturation	BP	4.36E-03
GO:0051294	establishment of spindle orientation	BP	4.11E-02
GO:0006323	DNA packaging	BP	1.49E-02
GO:0051293	establishment of spindle localization	BP	1.54E-02
GO:0031503	protein-containing complex localization	BP	2.38E-02
GO:0090735	DNA repair complex assembly	BP	6.45E-03
GO:0015031	protein transport	BP	3.92E-04
GO:0016236	macroautophagy	BP	7.49E-03
GO:0044403	symbiotic process	BP	8.40E-03
GO:0009889	regulation of biosynthetic process	BP	4.32E-03
GO:0034723	DNA replication-dependent nucleosome organization	BP	3.04E-02

GO:0032543	mitochondrial translation	BP	2.63E-02
GO:0006378	mRNA polyadenylation	BP	1.78E-02
GO:0034728	nucleosome organization	BP	1.75E-02
GO:0006139	nucleobase-containing compound metabolic process	BP	5.59E-03
GO:0009649	entrainment of circadian clock	BP	3.55E-02
GO:0009648	photoperiodism	BP	3.29E-02
GO:0022618	ribonucleoprotein complex assembly	BP	4.99E-05
GO:0000956	nuclear-transcribed mRNA catabolic process	BP	1.55E-02
GO:0042754	negative regulation of circadian rhythm	BP	3.97E-02
GO:0019219	regulation of nucleobase-containing compound metabolic process	BP	8.82E-03
GO:0043603	cellular amide metabolic process	BP	8.27E-04
GO:0043604	amide biosynthetic process	BP	1.89E-04
GO:0010508	positive regulation of autophagy	BP	2.10E-03
GO:0006376	mRNA splice site selection	BP	2.81E-02
GO:0010507	negative regulation of autophagy	BP	2.32E-03
GO:0009416	response to light stimulus	BP	2.09E-02
GO:0031325	positive regulation of cellular metabolic process	BP	4.68E-02
GO:0032774	RNA biosynthetic process	BP	7.23E-03
GO:0031323	regulation of cellular metabolic process	BP	2.39E-02
GO:0031328	positive regulation of cellular biosynthetic process	BP	1.31E-02
GO:0031329	regulation of cellular catabolic process	BP	2.42E-02
GO:0031326	regulation of cellular biosynthetic process	BP	3.13E-03
GO:0051238	sequestering of metal ion	BP	4.48E-02
GO:0016050	vesicle organization	BP	3.27E-02
GO:0051236	establishment of RNA localization	BP	3.13E-02
GO:0022607	cellular component assembly	BP	5.67E-04
GO:0042886	amide transport	BP	1.01E-03
GO:0022613	ribonucleoprotein complex biogenesis	BP	1.48E-04
GO:0009891	positive regulation of biosynthetic process	BP	1.80E-02
GO:0009895	negative regulation of catabolic process	BP	4.67E-02
GO:1902017	regulation of cilium assembly	BP	6.85E-03
GO:0061024	membrane organization	BP	2.23E-02

GO:0006264	mitochondrial DNA replication	BP	2.36E-03
GO:0006357	regulation of transcription by RNA polymerase II	BP	1.58E-02
GO:0006479	protein methylation	BP	4.49E-02
GO:0048193	Golgi vesicle transport	BP	1.35E-03
GO:0006355	regulation of transcription, DNA-templated	BP	1.29E-02
GO:0032527	protein exit from endoplasmic reticulum	BP	6.00E-04
GO:0051128	regulation of cellular component organization	BP	1.20E-02
GO:0016043	cellular component organization	BP	1.68E-02
GO:0030100	regulation of endocytosis	BP	3.76E-02
GO:0038066	p38MAPK cascade	BP	2.49E-02
GO:0019438	aromatic compound biosynthetic process	BP	3.14E-02
GO:0006351	transcription, DNA-templated	BP	8.07E-03
GO:0051252	regulation of RNA metabolic process	BP	4.32E-03
GO:0006369	termination of RNA polymerase II transcription	BP	3.83E-02
GO:0006366	transcription by RNA polymerase II	BP	7.06E-03
GO:0009755	hormone-mediated signaling pathway	BP	2.89E-02
GO:0010506	regulation of autophagy	BP	2.13E-04
GO:1903008	organelle disassembly	BP	2.71E-03
GO:0030218	erythrocyte differentiation	BP	4.58E-02
GO:0098787	mRNA cleavage involved in mRNA processing	BP	3.49E-02
GO:0000819	sister chromatid segregation	BP	2.58E-02
GO:0016032	viral process	BP	3.47E-03
GO:0051254	positive regulation of RNA metabolic process	BP	1.53E-02
GO:0098789	pre-mRNA cleavage required for polyadenylation	BP	3.04E-02
GO:0043631	RNA polyadenylation	BP	1.91E-02
GO:0045935	positive regulation of nucleobase-containing compound metabolic process	BP	2.41E-02
GO:0006364	rRNA processing	BP	1.02E-02
GO:0040001	establishment of mitotic spindle localization	BP	3.83E-02
GO:0030135	coated vesicle	CC	2.00E-02
GO:0030136	clathrin-coated vesicle	CC	3.42E-02
GO:0031227	intrinsic component of endoplasmic reticulum membrane	CC	1.41E-02
GO:0030132	clathrin coat of coated pit	CC	5.25E-03

GO:0008278	cohesin complex	CC	3.91E-02
GO:0033588	Elongator holoenzyme complex	CC	1.00E-02
GO:0015935	small ribosomal subunit	CC	6.80E-03
GO:0015934	large ribosomal subunit	CC	4.94E-02
GO:0000323	lytic vacuole	CC	1.24E-02
GO:0034663	endoplasmic reticulum chaperone complex	CC	2.05E-02
GO:0030176	integral component of endoplasmic reticulum membrane	CC	1.05E-02
GO:0043231	intracellular membrane-bounded organelle	CC	2.39E-03
GO:0043233	organelle lumen	CC	2.73E-03
GO:0005840	ribosome	CC	9.52E-03
GO:0000153	cytoplasmic ubiquitin ligase complex	CC	4.45E-02
GO:0000151	ubiquitin ligase complex	CC	3.26E-02
GO:0055038	recycling endosome membrane	CC	4.45E-02
GO:0005851	eukaryotic translation initiation factor 2B complex	CC	7.27E-03
GO:0005739	mitochondrion	CC	6.40E-03
GO:0034399	nuclear periphery	CC	3.05E-02
GO:0070531	BRCA1-A complex	CC	1.32E-02
GO:0044391	ribosomal subunit	CC	3.91E-03
GO:0005829	cytosol	CC	2.61E-02
GO:0016604	nuclear body	CC	2.06E-02
GO:0016607	nuclear speck	CC	5.36E-03
GO:0005764	lysosome	CC	1.24E-02
GO:0005766	primary lysosome	CC	2.59E-02
GO:0097422	tubular endosome	CC	4.92E-03
GO:0036020	endolysosome membrane	CC	3.53E-03
GO:0005773	vacuole	CC	3.42E-03
GO:0005654	nucleoplasm	CC	5.05E-04
GO:0005774	vacuolar membrane	CC	3.70E-02
GO:0036019	endolysosome	CC	9.99E-03
GO:0005776	autophagosome	CC	2.35E-02
GO:0005740	mitochondrial envelope	CC	3.17E-02
GO:0005743	mitochondrial inner membrane	CC	3.29E-02

GO:0097525	spliceosomal snRNP complex	CC	2.24E-02
GO:0005634	nucleus	CC	5.87E-03
GO:0005759	mitochondrial matrix	CC	2.49E-02
GO:0031974	membrane-enclosed lumen	CC	2.73E-03
GO:0005687	U4 snRNP	CC	3.40E-02
GO:0031975	envelope	CC	1.49E-02
GO:0072686	mitotic spindle	CC	1.13E-02
GO:0005681	spliceosomal complex	CC	4.99E-04
GO:0031966	mitochondrial membrane	CC	2.88E-02
GO:0031967	organelle envelope	CC	1.49E-02
GO:0031965	nuclear membrane	CC	4.42E-02
GO:0070013	intracellular organelle lumen	CC	2.73E-03
GO:1990904	ribonucleoprotein complex	CC	6.01E-05
GO:0071013	catalytic step 2 spliceosome	CC	3.73E-03
GO:0120114	Sm-like protein family complex	CC	4.61E-02
GO:0005790	smooth endoplasmic reticulum	CC	4.15E-02
GO:0016363	nuclear matrix	CC	3.84E-02
GO:0030532	small nuclear ribonucleoprotein complex	CC	2.91E-02
GO:0031981	nuclear lumen	CC	1.39E-02
GO:0019866	organelle inner membrane	CC	1.57E-02
GO:0031616	spindle pole centrosome	CC	4.45E-02
GO:0042582	azurophil granule	CC	2.59E-02
GO:0030128	clathrin coat of endocytic vesicle	CC	2.92E-02
GO:0030122	AP-2 adaptor complex	CC	2.47E-02
GO:0000836	Hrd1p ubiquitin ligase complex	CC	1.67E-02
GO:0022626	cytosolic ribosome	CC	3.72E-03
GO:0000835	ER ubiquitin ligase complex	CC	2.05E-02
GO:0022627	cytosolic small ribosomal subunit	CC	6.61E-04
GO:0000839	Hrd1p ubiquitin ligase ERAD-L complex	CC	1.32E-02
GO:0031314	extrinsic component of mitochondrial inner membrane	CC	3.91E-02
GO:0031300	intrinsic component of organelle membrane	CC	2.13E-02
GO:0031301	integral component of organelle membrane	CC	2.22E-02

GO:0031304	intrinsic component of mitochondrial inner membrane	CC	2.67E-02
GO:0031305	integral component of mitochondrial inner membrane	CC	2.67E-02
GO:0035615	clathrin adaptor activity	MF	4.62E-02
GO:0017069	snRNA binding	MF	6.29E-03
GO:0042043	neurexin family protein binding	MF	3.60E-02
GO:0005068	transmembrane receptor protein tyrosine kinase adaptor activity	MF	3.13E-02
GO:1990446	U1 snRNP binding	MF	4.51E-03
GO:0000978	RNA polymerase II cis-regulatory region sequence-specific DNA binding	MF	2.08E-02
GO:0000977	RNA polymerase II transcription regulatory region sequence-specific DNA binding	MF	1.43E-02
GO:0000976	transcription regulatory region sequence-specific DNA binding	MF	7.39E-03
GO:0043021	ribonucleoprotein complex binding	MF	2.60E-03
GO:0032554	purine deoxyribonucleotide binding	MF	4.51E-03
GO:0070990	snRNP binding	MF	3.35E-04
GO:0032552	deoxyribonucleotide binding	MF	6.66E-03
GO:0030374	nuclear receptor transcription coactivator activity	MF	2.97E-02
GO:0000987	cis-regulatory region sequence-specific DNA binding	MF	2.78E-02
GO:0000981	DNA-binding transcription factor activity, RNA polymerase II-specific	MF	4.89E-02
GO:0015929	hexosaminidase activity	MF	4.10E-02
GO:0043565	sequence-specific DNA binding	MF	1.02E-02
GO:0008168	methyltransferase activity	MF	4.99E-02
GO:0051082	unfolded protein binding	MF	4.42E-02
GO:0008135	translation factor activity, RNA binding	MF	3.63E-02
GO:0046625	sphingolipid binding	MF	1.64E-02
GO:0046983	protein dimerization activity	MF	4.29E-02
GO:0003743	translation initiation factor activity	MF	2.47E-02
GO:0003723	RNA binding	MF	4.75E-05
GO:1990837	sequence-specific double-stranded DNA binding	MF	1.45E-02
GO:0034452	dynactin binding	MF	2.69E-02
GO:0003735	structural constituent of ribosome	MF	4.98E-03
GO:0003676	nucleic acid binding	MF	1.41E-05
GO:0003677	DNA binding	MF	5.39E-03
GO:0140110	transcription regulator activity	MF	1.25E-02

GO:0001046	core promoter sequence-specific DNA binding	MF	1.75E-02
GO:1901363	heterocyclic compound binding	MF	6.83E-04
GO:0036002	pre-mRNA binding	MF	1.35E-02
GO:0016645	oxidoreductase activity, acting on the CH-NH group of donors	MF	2.23E-02
GO:0016646	oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor	MF	6.53E-03
GO:0003697	single-stranded DNA binding	MF	3.84E-02
GO:0019901	protein kinase binding	MF	3.71E-02
GO:0019900	kinase binding	MF	4.25E-02
GO:0019902	phosphatase binding	MF	2.67E-02
GO:0003690	double-stranded DNA binding	MF	1.65E-02
GO:0045182	translation regulator activity	MF	1.13E-02
GO:0051861	glycolipid binding	MF	1.64E-02
GO:0042803	protein homodimerization activity	MF	1.85E-02
GO:0001067	regulatory region nucleic acid binding	MF	7.48E-03
GO:0031702	type 1 angiotensin receptor binding	MF	9.19E-03
GO:0031701	angiotensin receptor binding	MF	1.21E-02
GO:0070273	phosphatidylinositol-4-phosphate binding	MF	2.68E-02
GO:0008757	S-adenosylmethionine-dependent methyltransferase activity	MF	2.42E-02
GO:0019899	enzyme binding	MF	2.42E-02
GO:0030674	protein-macromolecule adaptor activity	MF	7.61E-03
GO:0097159	organic cyclic compound binding	MF	9.30E-04
GO:0060090	molecular adaptor activity	MF	1.00E-02
GO:0031748	D1 dopamine receptor binding	MF	1.53E-02
GO:0005161	platelet-derived growth factor receptor binding	MF	4.10E-02
GO:0051117	ATPase binding	MF	4.29E-02

Supplementary Table 3

ID	Term
GO:0032802	low-density lipoprotein particle receptor catabolic process
GO:0035264	multicellular organism growth
GO:0006107	oxaloacetate metabolic process
GO:0019372	lipoxygenase pathway
GO:0046836	glycolipid transport
GO:0006264	mitochondrial DNA replication
GO:0051238	sequestering of metal ion
GO:0006294	nucleotide-excision repair, preincision complex assembly
GO:0030325	adrenal gland development
GO:0060976	coronary vasculature development
GO:0070911	global genome nucleotide-excision repair
GO:0071103	DNA conformation change
GO:0097428	protein maturation by iron-sulfur cluster transfer
GO:2000027	regulation of animal organ morphogenesis
GO:0031503	protein-containing complex localization
GO:0002097	tRNA wobble base modification
GO:0031532	actin cytoskeleton reorganization
GO:0032091	negative regulation of protein binding
GO:0006851	mitochondrial calcium ion transmembrane transport
GO:0034982	mitochondrial protein processing
GO:0042886	amide transport
GO:0015833	peptide transport
GO:0070646	protein modification by small protein removal
GO:0016579	protein deubiquitination
GO:0090161	Golgi ribbon formation
GO:0034499	late endosome to Golgi transport
GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process
GO:2000117	negative regulation of cysteine-type endopeptidase activity
GO:0006644	phospholipid metabolic process
GO:0046470	phosphatidylcholine metabolic process

GO:0034638	phosphatidylcholine catabolic process
GO:0048569	post-embryonic animal organ development
GO:0036498	IRE1-mediated unfolded protein response
GO:0006290	pyrimidine dimer repair
GO:0070669	response to interleukin-2
GO:0038110	interleukin-2-mediated signaling pathway
GO:0071352	cellular response to interleukin-2
GO:0090735	DNA repair complex assembly
GO:0045003	double-strand break repair via synthesis-dependent strand annealing
GO:0000730	DNA recombinase assembly
GO:0071478	cellular response to radiation
GO:0000819	sister chromatid segregation
GO:1901976	regulation of cell cycle checkpoint
GO:0048102	autophagic cell death
GO:0038066	p38MAPK cascade
GO:1903753	negative regulation of p38MAPK cascade
GO:0032984	protein-containing complex disassembly
GO:0006415	translational termination
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0000819	sister chromatid segregation
GO:0006997	nucleus organization
GO:0007000	nucleolus organization
GO:0043331	response to dsRNA
GO:0032494	response to peptidoglycan
GO:0043330	response to exogenous dsRNA
GO:2000318	positive regulation of T-helper 17 type immune response
GO:0046660	female sex differentiation
GO:0046545	development of primary female sexual characteristics
GO:0001541	ovarian follicle development
GO:0008585	female gonad development
GO:0016197	endosomal transport
GO:0098876	vesicle-mediated transport to the plasma membrane

GO:0001881	receptor recycling
GO:0033572	transferrin transport
GO:0048102	autophagic cell death
GO:0052040	modulation by symbiont of host programmed cell death
GO:0075071	modulation by symbiont of host autophagy
GO:0035694	mitochondrial protein catabolic process
GO:1903753	negative regulation of p38MAPK cascade
GO:0043476	pigment accumulation
GO:0043482	cellular pigment accumulation
GO:0048757	pigment granule maturation
GO:0043485	endosome to pigment granule transport
GO:0035646	endosome to melanosome transport
GO:0042181	ketone biosynthetic process
GO:1901661	quinone metabolic process
GO:0006743	ubiquinone metabolic process
GO:1901663	quinone biosynthetic process
GO:0006744	ubiquinone biosynthetic process
GO:0032259	methylation
GO:0006479	protein methylation
GO:0008213	protein alkylation
GO:0031497	chromatin assembly
GO:0016571	histone methylation
GO:0031167	rRNA methylation
GO:0097531	mast cell migration
GO:0002551	mast cell chemotaxis
GO:0030218	erythrocyte differentiation
GO:0035162	embryonic hemopoiesis
GO:0060753	regulation of mast cell chemotaxis
GO:0060215	primitive hemopoiesis
GO:0007059	chromosome segregation
GO:0051656	establishment of organelle localization
GO:0000819	sister chromatid segregation

GO:0006997	nucleus organization
GO:0007062	sister chromatid cohesion
GO:0032984	protein-containing complex disassembly
GO:1901976	regulation of cell cycle checkpoint
GO:0016236	macroautophagy
GO:0000819	sister chromatid segregation
GO:0032984	protein-containing complex disassembly
GO:0043254	regulation of protein-containing complex assembly
GO:0016241	regulation of macroautophagy
GO:0006415	translational termination
GO:1901096	regulation of autophagosome maturation
GO:0051648	vesicle localization
GO:0051650	establishment of vesicle localization
GO:0030100	regulation of endocytosis
GO:0140238	presynaptic endocytosis
GO:0036465	synaptic vesicle recycling
GO:0006900	vesicle budding from membrane
GO:0048488	synaptic vesicle endocytosis
GO:0009895	negative regulation of catabolic process
GO:0016236	macroautophagy
GO:0010506	regulation of autophagy
GO:0010507	negative regulation of autophagy
GO:0016241	regulation of macroautophagy
GO:0016242	negative regulation of macroautophagy
GO:1903311	regulation of mRNA metabolic process
GO:0045727	positive regulation of translation
GO:0043631	RNA polyadenylation
GO:1903311	regulation of mRNA metabolic process
GO:0031123	RNA 3'-end processing
GO:0000956	nuclear-transcribed mRNA catabolic process
GO:0050684	regulation of mRNA processing
GO:0031124	mRNA 3'-end processing

GO:0098787	mRNA cleavage involved in mRNA processing
GO:0006378	mRNA polyadenylation
GO:0006369	termination of RNA polymerase II transcription
GO:0098789	pre-mRNA cleavage required for polyadenylation
GO:0060261	positive regulation of transcription initiation from RNA polymerase II promoter
GO:0032259	methylation
GO:0071824	protein-DNA complex subunit organization
GO:0006479	protein methylation
GO:0008213	protein alkylation
GO:0031497	chromatin assembly
GO:0034723	DNA replication-dependent chromatin organization
GO:0065004	protein-DNA complex assembly
GO:0016571	histone methylation
GO:0006335	DNA replication-dependent chromatin assembly
GO:0034728	nucleosome organization
GO:0006334	nucleosome assembly
GO:0060260	regulation of transcription initiation from RNA polymerase II promoter
GO:2000144	positive regulation of DNA-templated transcription, initiation
GO:0002293	alpha-beta T cell differentiation involved in immune response
GO:0046637	regulation of alpha-beta T cell differentiation
GO:0045622	regulation of T-helper cell differentiation
GO:0002294	CD4-positive, alpha-beta T cell differentiation involved in immune response
GO:2000319	regulation of T-helper 17 cell differentiation
GO:2000321	positive regulation of T-helper 17 cell differentiation
GO:0042093	T-helper cell differentiation
GO:0072539	T-helper 17 cell differentiation
GO:0072538	T-helper 17 type immune response
GO:0032494	response to peptidoglycan
GO:0002287	alpha-beta T cell activation involved in immune response
GO:2000316	regulation of T-helper 17 type immune response
GO:1902107	positive regulation of leukocyte differentiation
GO:2000318	positive regulation of T-helper 17 type immune response

GO:0043368	positive T cell selection
GO:0045582	positive regulation of T cell differentiation
GO:0009314	response to radiation
GO:0009649	entrainment of circadian clock
GO:0009416	response to light stimulus
GO:0048569	post-embryonic animal organ development
GO:0071478	cellular response to radiation
GO:0009648	photoperiodism
GO:0043153	entrainment of circadian clock by photoperiod
GO:0071482	cellular response to light stimulus
GO:0034644	cellular response to UV
GO:0006290	pyrimidine dimer repair
GO:0070914	UV-damage excision repair
GO:1901976	regulation of cell cycle checkpoint
GO:0033683	nucleotide-excision repair, DNA incision
GO:0071493	cellular response to UV-B
GO:2000322	regulation of glucocorticoid receptor signaling pathway
GO:0006295	nucleotide-excision repair, DNA incision, 3'-to lesion
GO:0006296	nucleotide-excision repair, DNA incision, 5'-to lesion
GO:2000323	negative regulation of glucocorticoid receptor signaling pathway
GO:0016032	viral process
GO:0051092	positive regulation of NF-kappaB transcription factor activity
GO:0019080	viral gene expression
GO:0044403	biological process involved in symbiotic interaction
GO:0019083	viral transcription
GO:0039694	viral RNA genome replication
GO:0009615	response to virus
GO:0030522	intracellular receptor signaling pathway
GO:0043331	response to dsRNA
GO:0009597	detection of virus
GO:0032494	response to peptidoglycan
GO:0046596	regulation of viral entry into host cell

GO:0010508	positive regulation of autophagy
GO:0043330	response to exogenous dsRNA
GO:0051607	defense response to virus
GO:0071359	cellular response to dsRNA
GO:0071360	cellular response to exogenous dsRNA
GO:0002183	cytoplasmic translational initiation
GO:0051090	regulation of DNA-binding transcription factor activity
GO:0051091	positive regulation of DNA-binding transcription factor activity
GO:0009314	response to radiation
GO:0042754	negative regulation of circadian rhythm
GO:0009649	entrainment of circadian clock
GO:0009416	response to light stimulus
GO:0030522	intracellular receptor signaling pathway
GO:0009755	hormone-mediated signaling pathway
GO:0048545	response to steroid hormone
GO:0009648	photoperiodism
GO:0043153	entrainment of circadian clock by photoperiod
GO:0043401	steroid hormone mediated signaling pathway
GO:0051607	defense response to virus
GO:0071383	cellular response to steroid hormone stimulus
GO:0030518	intracellular steroid hormone receptor signaling pathway
GO:0033143	regulation of intracellular steroid hormone receptor signaling pathway
GO:0006290	pyrimidine dimer repair
GO:0031958	corticosteroid receptor signaling pathway
GO:0033144	negative regulation of intracellular steroid hormone receptor signaling pathway
GO:0042921	glucocorticoid receptor signaling pathway
GO:2000322	regulation of glucocorticoid receptor signaling pathway
GO:2000323	negative regulation of glucocorticoid receptor signaling pathway
GO:0051090	regulation of DNA-binding transcription factor activity
GO:0051091	positive regulation of DNA-binding transcription factor activity
GO:0007059	chromosome segregation
GO:0051648	vesicle localization

GO:0051656	establishment of organelle localization
GO:0051653	spindle localization
GO:0051650	establishment of vesicle localization
GO:0016197	endosomal transport
GO:0016236	macroautophagy
GO:0098876	vesicle-mediated transport to the plasma membrane
GO:0000819	sister chromatid segregation
GO:0006888	endoplasmic reticulum to Golgi vesicle-mediated transport
GO:0016050	vesicle organization
GO:0048193	Golgi vesicle transport
GO:0090150	establishment of protein localization to membrane
GO:0140238	presynaptic endocytosis
GO:1902115	regulation of organelle assembly
GO:0036465	synaptic vesicle recycling
GO:0051293	establishment of spindle localization
GO:0001881	receptor recycling
GO:0006900	vesicle budding from membrane
GO:0042147	retrograde transport, endosome to Golgi
GO:0051294	establishment of spindle orientation
GO:0070972	protein localization to endoplasmic reticulum
GO:0040001	establishment of mitotic spindle localization
GO:0032527	protein exit from endoplasmic reticulum
GO:0048488	synaptic vesicle endocytosis
GO:0051092	positive regulation of NF-kappaB transcription factor activity
GO:0051656	establishment of organelle localization
GO:0009895	negative regulation of catabolic process
GO:0016197	endosomal transport
GO:0016236	macroautophagy
GO:0010506	regulation of autophagy
GO:0016050	vesicle organization
GO:0031346	positive regulation of cell projection organization
GO:0032984	protein-containing complex disassembly

GO:0043254	regulation of protein-containing complex assembly
GO:0060491	regulation of cell projection assembly
GO:1902115	regulation of organelle assembly
GO:1903008	organelle disassembly
GO:0000422	autophagy of mitochondrion
GO:0046596	regulation of viral entry into host cell
GO:0010507	negative regulation of autophagy
GO:0010508	positive regulation of autophagy
GO:0061912	selective autophagy
GO:0016241	regulation of macroautophagy
GO:0061726	mitochondrion disassembly
GO:0120032	regulation of plasma membrane bounded cell projection assembly
GO:1902116	negative regulation of organelle assembly
GO:0006605	protein targeting
GO:0016242	negative regulation of macroautophagy
GO:0061724	lipophagy
GO:1901096	regulation of autophagosome maturation
GO:1902017	regulation of cilium assembly
GO:1903146	regulation of autophagy of mitochondrion
GO:0045724	positive regulation of cilium assembly
GO:1901097	negative regulation of autophagosome maturation
GO:1903432	regulation of TORC1 signaling
GO:1902902	negative regulation of autophagosome assembly
GO:0051091	positive regulation of DNA-binding transcription factor activity
GO:0006403	RNA localization
GO:0035966	response to topologically incorrect protein
GO:0034976	response to endoplasmic reticulum stress
GO:0048569	post-embryonic animal organ development
GO:0006986	response to unfolded protein
GO:0016197	endosomal transport
GO:0035967	cellular response to topologically incorrect protein
GO:0098876	vesicle-mediated transport to the plasma membrane

GO:1903513	endoplasmic reticulum to cytosol transport
GO:0006888	endoplasmic reticulum to Golgi vesicle-mediated transport
GO:0030968	endoplasmic reticulum unfolded protein response
GO:0048193	Golgi vesicle transport
GO:0072594	establishment of protein localization to organelle
GO:0090150	establishment of protein localization to membrane
GO:1903008	organelle disassembly
GO:0000422	autophagy of mitochondrion
GO:0006900	vesicle budding from membrane
GO:0034620	cellular response to unfolded protein
GO:0036498	IRE1-mediated unfolded protein response
GO:0061726	mitochondrion disassembly
GO:0070059	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress
GO:0070972	protein localization to endoplasmic reticulum
GO:0072599	establishment of protein localization to endoplasmic reticulum
GO:0006515	protein quality control for misfolded or incompletely synthesized proteins
GO:0006605	protein targeting
GO:0032527	protein exit from endoplasmic reticulum
GO:0036503	ERAD pathway
GO:0006612	protein targeting to membrane
GO:0030970	retrograde protein transport, ER to cytosol
GO:1902235	regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway
GO:1902236	negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway
GO:0045047	protein targeting to ER
GO:0071712	ER-associated misfolded protein catabolic process
GO:0006613	cotranslational protein targeting to membrane
GO:0030433	ubiquitin-dependent ERAD pathway
GO:0006614	SRP-dependent cotranslational protein targeting to membrane
GO:0016032	viral process
GO:0000380	alternative mRNA splicing, via spliceosome
GO:0045292	mRNA cis splicing, via spliceosome
GO:0019080	viral gene expression

GO:0032259	methylation
GO:0006403	RNA localization
GO:0071166	ribonucleoprotein complex localization
GO:0039694	viral RNA genome replication
GO:0051236	establishment of RNA localization
GO:0009895	negative regulation of catabolic process
GO:0022613	ribonucleoprotein complex biogenesis
GO:1905214	regulation of RNA binding
GO:0015931	nucleobase-containing compound transport
GO:0042254	ribosome biogenesis
GO:0071826	ribonucleoprotein complex subunit organization
GO:0072594	establishment of protein localization to organelle
GO:0090069	regulation of ribosome biogenesis
GO:1902415	regulation of mRNA binding
GO:0050658	RNA transport
GO:0022618	ribonucleoprotein complex assembly
GO:0042274	ribosomal small subunit biogenesis
GO:0006413	translational initiation
GO:0050657	nucleic acid transport
GO:0051028	mRNA transport
GO:0002181	cytoplasmic translation
GO:0006405	RNA export from nucleus
GO:0006415	translational termination
GO:0006417	regulation of translation
GO:0006611	protein export from nucleus
GO:0032543	mitochondrial translation
GO:0043631	RNA polyadenylation
GO:0051168	nuclear export
GO:1903311	regulation of mRNA metabolic process
GO:0002183	cytoplasmic translational initiation
GO:0000028	ribosomal small subunit assembly
GO:0006406	mRNA export from nucleus

GO:0008380	RNA splicing
GO:0031123	RNA 3'-end processing
GO:0043484	regulation of RNA splicing
GO:0045727	positive regulation of translation
GO:0000956	nuclear-transcribed mRNA catabolic process
GO:0006364	rRNA processing
GO:0016072	rRNA metabolic process
GO:0050684	regulation of mRNA processing
GO:2000232	regulation of rRNA processing
GO:2000765	regulation of cytoplasmic translation
GO:0000375	RNA splicing, via transesterification reactions
GO:0030490	maturation of SSU-rRNA
GO:0031124	mRNA 3'-end processing
GO:0031167	rRNA methylation
GO:2000234	positive regulation of rRNA processing
GO:2000766	negative regulation of cytoplasmic translation
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006378	mRNA polyadenylation
GO:0000245	spliceosomal complex assembly
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
GO:0000398	mRNA splicing, via spliceosome
GO:0000462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
GO:0048024	regulation of mRNA splicing, via spliceosome
GO:0070475	rRNA base methylation
GO:0006376	mRNA splice site selection
GO:0006807	nitrogen compound metabolic process
GO:0009058	biosynthetic process
GO:0033036	macromolecule localization
GO:0044237	cellular metabolic process
GO:0051640	organelle localization
GO:0051641	cellular localization
GO:0061919	process utilizing autophagic mechanism

GO:0071840	cellular component organization or biogenesis
GO:0006725	cellular aromatic compound metabolic process
GO:0016043	cellular component organization
GO:0034641	cellular nitrogen compound metabolic process
GO:0044085	cellular component biogenesis
GO:0044249	cellular biosynthetic process
GO:0046483	heterocycle metabolic process
GO:0051649	establishment of localization in cell
GO:0070727	cellular macromolecule localization
GO:1901360	organic cyclic compound metabolic process
GO:1901576	organic substance biosynthetic process
GO:0006139	nucleobase-containing compound metabolic process
GO:0006914	autophagy
GO:0009889	regulation of biosynthetic process
GO:0031323	regulation of cellular metabolic process
GO:0044087	regulation of cellular component biogenesis
GO:0044260	cellular macromolecule metabolic process
GO:0046907	intracellular transport
GO:0051128	regulation of cellular component organization
GO:0080090	regulation of primary metabolic process
GO:0006996	organelle organization
GO:0008104	protein localization
GO:0009059	macromolecule biosynthetic process
GO:0009891	positive regulation of biosynthetic process
GO:0010467	gene expression
GO:0016192	vesicle-mediated transport
GO:0018130	heterocycle biosynthetic process
GO:0019438	aromatic compound biosynthetic process
GO:0022411	cellular component disassembly
GO:0022607	cellular component assembly
GO:0031325	positive regulation of cellular metabolic process
GO:0043603	cellular amide metabolic process

GO:0043933	protein-containing complex organization
GO:0044089	positive regulation of cellular component biogenesis
GO:0044271	cellular nitrogen compound biosynthetic process
GO:0045184	establishment of protein localization
GO:0060627	regulation of vesicle-mediated transport
GO:0061024	membrane organization
GO:0071702	organic substance transport
GO:0071705	nitrogen compound transport
GO:1901362	organic cyclic compound biosynthetic process
GO:1901566	organonitrogen compound biosynthetic process
GO:0006518	peptide metabolic process
GO:0010556	regulation of macromolecule biosynthetic process
GO:0019219	regulation of nucleobase-containing compound metabolic process
GO:0031326	regulation of cellular biosynthetic process
GO:0031329	regulation of cellular catabolic process
GO:0034248	regulation of cellular amide metabolic process
GO:0034645	cellular macromolecule biosynthetic process
GO:0034654	nucleobase-containing compound biosynthetic process
GO:0072657	protein localization to membrane
GO:0090304	nucleic acid metabolic process
GO:0007005	mitochondrion organization
GO:0010557	positive regulation of macromolecule biosynthetic process
GO:0015031	protein transport
GO:0031328	positive regulation of cellular biosynthetic process
GO:0033365	protein localization to organelle
GO:0043604	amide biosynthetic process
GO:0045935	positive regulation of nucleobase-containing compound metabolic process
GO:0051276	chromosome organization
GO:0065003	protein-containing complex assembly
GO:0070925	organelle assembly
GO:0006412	translation
GO:0006886	intracellular protein transport

GO:0016070	RNA metabolic process
GO:0043043	peptide biosynthetic process
GO:0051252	regulation of RNA metabolic process
GO:0120035	regulation of plasma membrane bounded cell projection organization
GO:2000112	regulation of cellular macromolecule biosynthetic process
GO:0006396	RNA processing
GO:0032774	RNA biosynthetic process
GO:0051254	positive regulation of RNA metabolic process
GO:0016071	mRNA metabolic process
GO:0097659	nucleic acid-templated transcription
GO:2001141	regulation of RNA biosynthetic process
GO:0006397	mRNA processing
GO:1902680	positive regulation of RNA biosynthetic process
GO:0006351	transcription, DNA-templated
GO:0006355	regulation of transcription, DNA-templated
GO:1903506	regulation of nucleic acid-templated transcription
GO:1903508	positive regulation of nucleic acid-templated transcription
GO:0006357	regulation of transcription by RNA polymerase II
GO:0006366	transcription by RNA polymerase II
GO:0045893	positive regulation of transcription, DNA-templated

Ontology Source	Term	PValue	GOGroups
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Supplementary Table 4

multiMir input list

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 hsa-miR-1307-3p
 hsa-miR-23a-5p
 hsa-miR-23a-3p
 hsa-miR-27a-5p
 hsa-miR-27a-3p
 hsa-miR-24-2-5p
 hsa-miR-3188
 hsa-miR-4258
 hsa-miR-4530
 hsa-miR-4754
 hsa-miR-4999-5p
 hsa-miR-4999-3p
 hsa-miR-636

Database Mature_mirna_acc Mature_mirna_Target_symbol

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tarbase	MIMAT0000084	hsa-miR-27a-3p	FKBP14
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tarbase	MIMAT0000084	hsa-miR-27a-3p	PLEKHA8
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tarbase	MIMAT0000084	hsa-miR-27a-3p	ENPP2
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mirtarbase	MIMAT0000078	hsa-miR-23a-3p	UBALD1
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tarbase	MIMAT0000084	hsa-miR-27a-3p	CTCF
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tarbase	MIMAT0000084	hsa-miR-27a-3p	PLA2G15
tarbase	MIMAT0004501	hsa-miR-27a-5p	CYB5D2
tarbase	MIMAT0000078	hsa-miR-23a-3p	ZZEF1
tarbase	MIMAT0000084	hsa-miR-27a-3p	ZZEF1
tarbase	MIMAT0004501	hsa-miR-27a-5p	ZZEF1
tarbase	MIMAT0000078	hsa-miR-23a-3p	ZNF594
tarbase	MIMAT0000084	hsa-miR-27a-3p	ZNF594
tarbase	MIMAT0004501	hsa-miR-27a-5p	DVL2
tarbase	MIMAT0000084	hsa-miR-27a-3p	PHF23

tarbase	MIMAT0000084	hsa-miR-27a-3p	TMEM102
tarbase	MIMAT0000084	hsa-miR-27a-3p	PEMT
tarbase	MIMAT0000084	hsa-miR-27a-3p	CPD
tarbase	MIMAT0000084	hsa-miR-27a-3p	ACLY
tarbase	MIMAT0005951	hsa-miR-1307-3p	ACLY
mirtarbase	MIMAT0004496	hsa-miR-23a-5p	RAB5C
tarbase	MIMAT0000084	hsa-miR-27a-3p	ATXN7L3
tarbase	MIMAT0000084	hsa-miR-27a-3p	STRADA
tarbase	MIMAT0000084	hsa-miR-27a-3p	FDXR
tarbase	MIMAT0004501	hsa-miR-27a-5p	FDXR
tarbase	MIMAT0004501	hsa-miR-27a-5p	TMEM94
mirtarbase	MIMAT0000084	hsa-miR-27a-3p	H3-3B
mirtarbase	MIMAT0000084	hsa-miR-27a-3p	H3-3B
tarbase	MIMAT0000078	hsa-miR-23a-3p	H3-3B
tarbase	MIMAT0000084	hsa-miR-27a-3p	H3-3B
mirtarbase	MIMAT0003306	hsa-miR-636	UNK
tarbase	MIMAT0000078	hsa-miR-23a-3p	DNAJC16
mirtarbase	MIMAT0019069	hsa-miR-4530	STK11
tarbase	MIMAT0000084	hsa-miR-27a-3p	CIRBP
tarbase	MIMAT0000084	hsa-miR-27a-3p	MOB3A
mirtarbase	MIMAT0000084	hsa-miR-27a-3p	AP3D1
tarbase	MIMAT0000084	hsa-miR-27a-3p	AP3D1
tarbase	MIMAT0005951	hsa-miR-1307-3p	AP3D1
tarbase	MIMAT0000084	hsa-miR-27a-3p	MPND
tarbase	MIMAT0000084	hsa-miR-27a-3p	SH3GL1
tarbase	MIMAT0004501	hsa-miR-27a-5p	SH3GL1
mirtarbase	MIMAT0005951	hsa-miR-1307-3p	TNFAIP8L1
tarbase	MIMAT0000078	hsa-miR-23a-3p	SAFB
tarbase	MIMAT0000084	hsa-miR-27a-3p	SAFB
tarbase	MIMAT0000084	hsa-miR-27a-3p	MICOS13
mirtarbase	MIMAT0004496	hsa-miR-23a-5p	HSD11B1L
tarbase	MIMAT0000084	hsa-miR-27a-3p	SLC25A23

tarbase	MIMAT0000084	hsa-miR-27a-3p	XAB2
mirTarbase	MIMAT0005951	hsa-miR-1307-3p	RPS28
tarbase	MIMAT0000084	hsa-miR-27a-3p	RAB11B
tarbase	MIMAT0000084	hsa-miR-27a-3p	RAB11B
tarbase	MIMAT0000084	hsa-miR-27a-3p	ZNF414
tarbase	MIMAT0000084	hsa-miR-27a-3p	MRPL4
tarbase	MIMAT0000084	hsa-miR-27a-3p	MRPL4
tarbase	MIMAT0000084	hsa-miR-27a-3p	ILF3
tarbase	MIMAT0005951	hsa-miR-1307-3p	ILF3
mirTarbase	MIMAT0000084	hsa-miR-27a-3p	CARM1
tarbase	MIMAT0000084	hsa-miR-27a-3p	CARM1
tarbase	MIMAT0000084	hsa-miR-27a-3p	ZSWIM4
tarbase	MIMAT0004496	hsa-miR-23a-5p	ZSWIM4
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tarbase	MIMAT0000084	hsa-miR-27a-3p	USHBP1
mirTarbase	MIMAT0000084	hsa-miR-27a-3p	DPY19L3
tarbase	MIMAT0004501	hsa-miR-27a-5p	ANKRD27
mirTarbase	MIMAT0000084	hsa-miR-27a-3p	ZFP36
mirTarbase	MIMAT0000084	hsa-miR-27a-3p	ZFP36
mirTarbase	MIMAT0000084	hsa-miR-27a-3p	ZFP36
tarbase	MIMAT0000084	hsa-miR-27a-3p	ZFP36
mirTarbase	MIMAT0000084	hsa-miR-27a-3p	ZFP36
mirTarbase	MIMAT0000084	hsa-miR-27a-3p	ZFP36
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tarbase	MIMAT0000084	hsa-miR-27a-3p	PLEKHG2
mirTarbase	MIMAT0004501	hsa-miR-27a-5p	RPS16
tarbase	MIMAT0004501	hsa-miR-27a-5p	RPS16
tarbase	MIMAT0000084	hsa-miR-27a-3p	SUPT5H
mirTarbase	MIMAT0000084	hsa-miR-27a-3p	SZRD1
mirTarbase	MIMAT0016879	hsa-miR-4258	SZRD1

tarbase	MIMAT0000084	hsa-miR-27a-3p	SZRD1
tarbase	MIMAT0000084	hsa-miR-27a-3p	SERTAD1
mirTarbase	MIMAT0000084	hsa-miR-27a-3p	SERTAD3
tarbase	MIMAT0000084	hsa-miR-27a-3p	SERTAD3
tarbase	MIMAT0000084	hsa-miR-27a-3p	SERTAD3
tarbase	MIMAT0000084	hsa-miR-27a-3p	BLVRB
mirTarbase	MIMAT0000078	hsa-miR-23a-3p	ITPKC
tarbase	MIMAT0000084	hsa-miR-27a-3p	ITPKC
tarbase	MIMAT0000084	hsa-miR-27a-3p	C19orf54
mirTarbase	MIMAT0005951	hsa-miR-1307-3p	SNRPA
tarbase	MIMAT0000084	hsa-miR-27a-3p	SNRPA
tarbase	MIMAT0000084	hsa-miR-27a-3p	ERCC1
tarbase	MIMAT0000084	hsa-miR-27a-3p	ZC3H4
tarbase	MIMAT0005951	hsa-miR-1307-3p	FTL
mirTarbase	MIMAT0003306	hsa-miR-636	ZNF813
tarbase	MIMAT0000084	hsa-miR-27a-3p	TFPT
mirTarbase	MIMAT0000078	hsa-miR-23a-3p	RPS5
tarbase	MIMAT0000084	hsa-miR-27a-3p	ZNF132
tarbase	MIMAT0000084	hsa-miR-27a-3p	EIF2B4
tarbase	MIMAT0000084	hsa-miR-27a-3p	TTC31
mirTarbase	MIMAT0005951	hsa-miR-1307-3p	CCDC142
tarbase	MIMAT0000084	hsa-miR-27a-3p	CCDC142
tarbase	MIMAT0000084	hsa-miR-27a-3p	TMEM127
mirTarbase	MIMAT0005951	hsa-miR-1307-3p	CIAO1
tarbase	MIMAT0000084	hsa-miR-27a-3p	EIF5B
tarbase	MIMAT0000084	hsa-miR-27a-3p	CREB3L4
tarbase	MIMAT0000084	hsa-miR-27a-3p	CREB3L4
tarbase	MIMAT0000084	hsa-miR-27a-3p	HAX1
mirTarbase	MIMAT0015070	hsa-miR-3188	CKS1B
tarbase	MIMAT0000084	hsa-miR-27a-3p	SHC1
tarbase	MIMAT0004501	hsa-miR-27a-5p	SHC1
tarbase	MIMAT0000084	hsa-miR-27a-3p	TAGLN2

tarbase	MIMAT0000084	hsa-miR-27a-3p	TAGLN2
tarbase	MIMAT0004501	hsa-miR-27a-5p	ATG16L1
tarbase	MIMAT0000078	hsa-miR-23a-3p	FARP2
tarbase	MIMAT0000084	hsa-miR-27a-3p	FARP2
tarbase	MIMAT0000084	hsa-miR-27a-3p	NAPB
tarbase	MIMAT0000084	hsa-miR-27a-3p	APMAP
tarbase	MIMAT0004501	hsa-miR-27a-5p	APMAP
tarbase	MIMAT0000084	hsa-miR-27a-3p	RALY
tarbase	MIMAT0021017	hsa-miR-4999-5p	CEP250
tarbase	MIMAT0000084	hsa-miR-27a-3p	RBM39
tarbase	MIMAT0000078	hsa-miR-23a-3p	SRSF6
tarbase	MIMAT0000084	hsa-miR-27a-3p	SRSF6
mirTarbase	MIMAT0000078	hsa-miR-23a-3p	SERINC3
mirTarbase	MIMAT0000078	hsa-miR-23a-3p	SERINC3
mirTarbase	MIMAT0000078	hsa-miR-23a-3p	SERINC3
mirTarbase	MIMAT0000078	hsa-miR-23a-3p	SERINC3
mirTarbase	MIMAT0000078	hsa-miR-23a-3p	SERINC3
mirTarbase	MIMAT0000078	hsa-miR-23a-3p	SERINC3
tarbase	MIMAT0000078	hsa-miR-23a-3p	SERINC3
tarbase	MIMAT0004501	hsa-miR-27a-5p	SERINC3

Target_entrez	Target_ensembl	Experiment	Support_type	Pubmed_id	Methylation status
64332	ENSG00000144802	Degradome sequencing	positive		gained-close
55033	ENSG00000106080	Degradome sequencing	negative		gained-close
55033	ENSG00000106080	Degradome sequencing	positive		gained-close
84725	ENSG00000106086	Degradome sequencing//De	positive		gained-close
10863	ENSG00000042980	PAR-CLIP	Functional MTI (Weak)	22012620	gained-close
157777	ENSG00000178460	Degradome sequencing	negative		gained-close
157777	ENSG00000178460	Degradome sequencing	positive		gained-close
5168	ENSG00000136960	Degradome sequencing	negative		gained-close
84159	ENSG00000150347	Degradome sequencing	negative		gained-close
84159	ENSG00000150347	Degradome sequencing//De	positive		gained-close
3434	ENSG00000185745	Degradome sequencing	positive		gained-close
10346	ENSG00000132274	Degradome sequencing	negative		gained-close
10346	ENSG00000132274	Degradome sequencing	positive		gained-close
11010	ENSG00000139278	Degradome sequencing	positive		gained-close
10561	ENSG00000137965	Degradome sequencing	positive		gained-close
160897	ENSG00000152749	Degradome sequencing	positive		gained-close
64135	ENSG00000115267	Degradome sequencing	positive		gained-close
5087	ENSG00000185630	Degradome sequencing	negative		gained-close
5087	ENSG00000185630	Degradome sequencing	positive		gained-close
3454	ENSG00000142166	Degradome sequencing	positive		gained-open
5316	ENSG00000160199	PAR-CLIP	Functional MTI (Weak)	20371350	gained-open
23786	ENSG00000099968	PAR-CLIP	Functional MTI (Weak)	23446348	gained-open
529	ENSG00000131100	Degradome sequencing	positive		gained-open
23753	ENSG00000128228	Degradome sequencing	positive		gained-open
23753	ENSG00000128228	Degradome sequencing	positive		gained-open
27156	ENSG00000100218	Degradome sequencing	negative		gained-open
27156	ENSG00000100218	Degradome sequencing	positive		gained-open
9609	ENSG00000100228	Degradome sequencing	positive		gained-open
22880	ENSG00000133422	Degradome sequencing	positive		gained-open
6767	ENSG00000100380	Degradome sequencing	positive		gained-open

150368	ENSG00000177096	Degradome sequencing	negative		gained-open
4668	ENSG00000198951	Degradome sequencing	negative		gained-open
4668	ENSG00000198951	Degradome sequencing//De	positive		gained-open
84271	ENSG00000100227	Degradome sequencing//De	positive		gained-open
78987	ENSG00000163703	Degradome sequencing//De	positive		gained-open
10236	ENSG00000125944	Degradome sequencing//De	positive		gained-open
54859	ENSG00000163832	Degradome sequencing	positive		gained-open
4134	ENSG00000047849	Degradome sequencing//De	positive		gained-open
4134	ENSG00000047849	Degradome sequencing	positive		gained-open
4134	ENSG00000047849	Degradome sequencing	positive		gained-open
11180	ENSG00000178252	Degradome sequencing//De	positive		gained-open
11180	ENSG00000178252	Degradome sequencing	positive		gained-open
11070	ENSG00000126062	Degradome sequencing	negative		gained-open
23200	ENSG00000058063	Degradome sequencing//De	positive		gained-open
152687	ENSG00000272602	Degradome sequencing	positive		gained-open
152687	ENSG00000272602	Degradome sequencing	positive		gained-open
152687	ENSG00000272602	Degradome sequencing	positive		gained-open
3064	ENSG00000197386	Degradome sequencing//De	positive		gained-open
3064	ENSG00000197386	Degradome sequencing//De	positive		gained-open
5156	ENSG00000134853	Degradome sequencing	negative		gained-open
81608	ENSG00000145216	Degradome sequencing	positive		gained-open
1843	ENSG00000120129	Degradome sequencing	positive		gained-open
153222	ENSG00000164463	Degradome sequencing//De	positive		gained-open
285598	ENSG00000175414	HITS-CLIP	Functional MTI (Weak)	23824327	gained-open
57179	ENSG00000122203	PAR-CLIP	Functional MTI (Weak)	23592263	gained-open
57179	ENSG00000122203	PAR-CLIP	Functional MTI (Weak)	20371350	gained-open
57179	ENSG00000122203	Degradome sequencing	positive		gained-open
10960	ENSG00000169223	PAR-CLIP	Functional MTI (Weak)	20371350	gained-open
10960	ENSG00000169223	Degradome sequencing	negative		gained-open
821	ENSG00000127022	Degradome sequencing//De	positive		gained-open
821	ENSG00000127022	Degradome sequencing//De	positive		gained-open
821	ENSG00000127022	Degradome sequencing//De	positive		gained-open

821	ENSG00000127022	Degradome sequencing	positive			gained-open
3008	ENSG00000168298	PAR-CLIP	Functional MTI (Weak)	23446348		gained-open
3008	ENSG00000168298	Degradome sequencing	negative			gained-open
3008	ENSG00000168298	Degradome sequencing	positive			gained-open
3017	ENSG00000158373	Degradome sequencing	negative			gained-open
3017	ENSG00000158373	Degradome sequencing	positive			gained-open
8348	ENSG00000274641	Degradome sequencing	negative			gained-open
8348	ENSG00000274641	Degradome sequencing	positive			gained-open
80232	ENSG00000162923	Degradome sequencing//De	positive			gained-open
221927	ENSG00000106009	CLASH	Functional MTI (Weak)	23622248		gained-open
23288	ENSG00000106012	Degradome sequencing	negative			gained-open
10652	ENSG00000106636	Degradome sequencing	positive			gained-open
4191	ENSG00000146701	Degradome sequencing	positive			gained-open
23038	ENSG00000142784	PAR-CLIP	Functional MTI (Weak)	26701625		gained-open
23038	ENSG00000142784	PAR-CLIP	Functional MTI (Weak)	26701625		gained-open
23038	ENSG00000142784	Degradome sequencing	positive			gained-open
84958	ENSG00000142765	Degradome sequencing	positive			gained-open
4289	ENSG00000128585	Sequencing	Functional MTI (Weak)	20371350		gained-open
4289	ENSG00000128585	Degradome sequencing	positive			gained-open
4289	ENSG00000128585	Degradome sequencing//De	positive			gained-open
665	ENSG00000104765	Degradome sequencing//De	positive			gained-open
665	ENSG00000104765	Degradome sequencing//De	positive			gained-open
137994	ENSG00000165046	Degradome sequencing	positive			gained-open
54904	ENSG00000147548	Degradome sequencing//De	positive			gained-open
137964	ENSG00000158669	Degradome sequencing	negative			gained-open
137964	ENSG00000158669	Degradome sequencing	positive			gained-open
7071	ENSG00000155090	PAR-CLIP	Functional MTI (Weak)	23592263		gained-open
7071	ENSG00000155090	Degradome sequencing//De	positive			gained-open
7071	ENSG00000155090	Degradome sequencing	positive			gained-open
7071	ENSG00000155090	Degradome sequencing	positive			gained-open
6118	ENSG00000117748	Degradome sequencing	positive			gained-open
6118	ENSG00000117748	Degradome sequencing	positive			gained-open

65263	ENSG00000104524	Degradome sequencing	positive		gained-open
92400	ENSG00000119446	Degradome sequencing//De	positive		gained-open
92400	ENSG00000119446	Degradome sequencing//De	positive		gained-open
26995	ENSG00000167112	PAR-CLIP	Functional MTI (Weak)	23592263	gained-open
26995	ENSG00000167112	PAR-CLIP	Functional MTI (Weak)	22012620	gained-open
26995	ENSG00000167112	HITS-CLIP	Functional MTI (Weak)	21572407	gained-open
26995	ENSG00000167112	HITS-CLIP	Functional MTI (Weak)	19536157	gained-open
26995	ENSG00000167112	PAR-CLIP	Functional MTI (Weak)	23446348	gained-open
51117	ENSG00000167113	Degradome sequencing	negative		gained-open
51490	ENSG00000198917	Degradome sequencing	positive		gained-open
84895	ENSG00000148343	PAR-CLIP	Functional MTI (Weak)	23592263	gained-open
84895	ENSG00000148343	Degradome sequencing	positive		gained-open
9919	ENSG00000148396	CLASH	Functional MTI (Weak)	23622248	gained-open
9919	ENSG00000148396	Degradome sequencing//De	positive		gained-open
10383	ENSG00000188229	Degradome sequencing//De	positive		gained-open
10383	ENSG00000188229	Degradome sequencing//De	positive		gained-open
10383	ENSG00000188229	Degradome sequencing	positive		gained-open
9282	ENSG00000180182	HITS-CLIP	Functional MTI (Weak)	22473208	gained-open
9282	ENSG00000180182	Degradome sequencing//De	positive		gained-open
10084	ENSG00000102103	Degradome sequencing	negative		gained-open
10730	ENSG00000136758	Degradome sequencing	negative		gained-open
3185	ENSG00000169813	HITS-CLIP	Functional MTI (Weak)	22473208	gained-open
3185	ENSG00000169813	PAR-CLIP	Functional MTI (Weak)	20371350	gained-open
3185	ENSG00000169813	Degradome sequencing//De	positive		gained-open
4791	ENSG00000077150	Degradome sequencing	positive		gained-open
10121	ENSG00000138107	Degradome sequencing	positive		gained-open
84833	ENSG00000173915	Degradome sequencing//De	positive		gained-open
84833	ENSG00000173915	Degradome sequencing//De	positive		gained-open
10487	ENSG00000131236	Degradome sequencing//De	positive		gained-open
10078	ENSG00000184281	Degradome sequencing	negative		gained-open
10078	ENSG00000184281	Degradome sequencing	positive		gained-open
391	ENSG00000177105	Degradome sequencing	negative		gained-open

1408	ENSG00000121671	PAR-CLIP	Functional MTI (Weak)	23592263	gained-open
1408	ENSG00000121671	PAR-CLIP	Functional MTI (Weak)	26701625	gained-open
1408	ENSG00000121671	Degradome sequencing//De	positive		gained-open
1643	ENSG00000134574	Degradome sequencing	negative		gained-open
221092	ENSG00000214753	Degradome sequencing	positive		gained-open
221092	ENSG00000214753	Degradome sequencing	positive		gained-open
283237	ENSG00000162222	Degradome sequencing	negative		gained-open
25824	ENSG00000126432	Degradome sequencing	positive		gained-open
2197	ENSG00000149806	CLASH	Functional MTI (Weak)	23622248	gained-open
741	ENSG00000174276	Degradome sequencing	positive		gained-open
10534	ENSG00000173465	Degradome sequencing	negative		gained-open
23625	ENSG00000176973	Degradome sequencing	negative		gained-open
4926	ENSG00000137497	Degradome sequencing	positive		gained-open
4926	ENSG00000137497	Degradome sequencing	positive		gained-open
4926	ENSG00000137497	Degradome sequencing//De	positive		gained-open
25973	ENSG00000162396	PAR-CLIP	Functional MTI (Weak)	23592263	gained-open
25973	ENSG00000162396	Degradome sequencing	positive		gained-open
894	ENSG00000118971	Degradome sequencing	negative		gained-open
171017	ENSG00000126746	PAR-CLIP	Functional MTI (Weak)	23592263	gained-open
8078	ENSG00000111667	HITS-CLIP	Functional MTI (Weak)	23313552	gained-open
8078	ENSG00000111667	Degradome sequencing	positive		gained-open
83461	ENSG00000111665	Degradome sequencing	negative		gained-open
3887	ENSG00000205426	Degradome sequencing	positive		gained-open
11213	ENSG00000090376	Degradome sequencing	negative		gained-open
11213	ENSG00000090376	Degradome sequencing	positive		gained-open
255394	ENSG00000166046	Degradome sequencing	positive		gained-open
1407	ENSG00000008405	Degradome sequencing	positive		gained-open
160760	ENSG00000196850	PAR-CLIP	Functional MTI (Weak)	22012620	gained-open
160760	ENSG00000196850	PAR-CLIP	Functional MTI (Weak)	21572407	gained-open
160760	ENSG00000196850	PAR-CLIP	Functional MTI (Weak)	20371350	gained-open
160760	ENSG00000196850	Degradome sequencing	positive		gained-open
10019	ENSG00000111252	Degradome sequencing//De	positive		gained-open

10019	ENSG00000111252	Degradome sequencing	positive		gained-open
10019	ENSG00000111252	Degradome sequencing	positive		gained-open
9761	ENSG00000110917	Degradome sequencing	positive		gained-open
79676	ENSG00000111325	Degradome sequencing	positive		gained-open
55206	ENSG00000139697	Degradome sequencing//De	positive		gained-open
55206	ENSG00000139697	Degradome sequencing	positive		gained-open
387893	ENSG00000183955	PAR-CLIP	Functional MTI (Weak)	23592263	gained-open
2353	ENSG00000170345	PAR-CLIP	Functional MTI (Weak)	23592263	gained-open
53981	ENSG00000165934	Degradome sequencing	positive		gained-open
4140	ENSG00000075413	Degradome sequencing	positive		gained-open
56204	ENSG00000047346	Degradome sequencing	negative		gained-open
84231	ENSG00000131653	PAR-CLIP	Functional MTI (Weak)	26701625	gained-open
84231	ENSG00000131653	Degradome sequencing	positive		gained-open
54985	ENSG00000103145	Degradome sequencing	negative		gained-open
124402	ENSG00000153443	CLASH	Functional MTI (Weak)	23622248	gained-open
124402	ENSG00000153443	Degradome sequencing	negative		gained-open
124454	ENSG00000103356	Degradome sequencing	positive		gained-open
56061	ENSG00000103353	Degradome sequencing//De	positive		gained-open
3835	ENSG00000079616	CLASH	Functional MTI (Weak)	23622248	gained-open
78994	ENSG00000156858	Degradome sequencing	negative		gained-open
1540	ENSG00000083799	Degradome sequencing	positive		gained-open
10664	ENSG00000102974	Degradome sequencing//De	positive		gained-open
23659	ENSG00000103066	Degradome sequencing	negative		gained-open
23659	ENSG00000103066	Degradome sequencing//De	positive		gained-open
124936	ENSG00000167740	Degradome sequencing	negative		gained-open
23140	ENSG00000074755	Degradome sequencing//De	positive		gained-open
23140	ENSG00000074755	Degradome sequencing	positive		gained-open
23140	ENSG00000074755	Degradome sequencing	positive		gained-open
84622	ENSG00000180626	Degradome sequencing	positive		gained-open
84622	ENSG00000180626	Degradome sequencing	negative		gained-open
1856	ENSG00000004975	Degradome sequencing	negative		gained-open
79142	ENSG00000040633	Degradome sequencing	negative		gained-open

284114	ENSG00000181284	Degradome sequencing	negative		gained-open
10400	ENSG00000133027	Degradome sequencing	positive		gained-open
1362	ENSG00000108582	Degradome sequencing	positive		gained-open
47	ENSG00000131473	Degradome sequencing//De	positive		gained-open
47	ENSG00000131473	Degradome sequencing	positive		gained-open
5878	ENSG00000108774	PAR-CLIP	Functional MTI (Weak)	27292025	gained-open
56970	ENSG00000087152	Degradome sequencing	negative		gained-open
92335	ENSG00000266173	Degradome sequencing	positive		gained-open
2232	ENSG00000161513	Degradome sequencing	negative		gained-open
2232	ENSG00000161513	Degradome sequencing	negative		gained-open
9772	ENSG00000177728	Degradome sequencing	positive		gained-open
3021	ENSG00000132475	PAR-CLIP	Functional MTI (Weak)	24398324	gained-open
3021	ENSG00000132475	PAR-CLIP	Functional MTI (Weak)	20371350	gained-open
3021	ENSG00000132475	Degradome sequencing	positive		gained-open
3021	ENSG00000132475	Degradome sequencing	positive		gained-open
85451	ENSG00000132478	PAR-CLIP	Functional MTI (Weak)	22012620	gained-open
23341	ENSG00000116138	Degradome sequencing//De	positive		gained-open
6794	ENSG00000118046	PAR-CLIP	Functional MTI (Weak)	26701625	gained-open
1153	ENSG00000099622	Degradome sequencing	positive		gained-open
126308	ENSG00000172081	Degradome sequencing	negative		gained-open
8943	ENSG00000065000	PAR-CLIP	Functional MTI (Weak)	23592263	gained-open
8943	ENSG00000065000	Degradome sequencing//De	positive		gained-open
8943	ENSG00000065000	Degradome sequencing	positive		gained-open
84954	ENSG00000008382	Degradome sequencing	negative		gained-open
6455	ENSG00000141985	Degradome sequencing	negative		gained-open
6455	ENSG00000141985	Degradome sequencing	positive		gained-open
126282	ENSG00000185361	HITS-CLIP	Functional MTI (Weak)	23824327	gained-open
6294	ENSG00000160633	Degradome sequencing	positive		gained-open
6294	ENSG00000160633	Degradome sequencing	positive		gained-open
125988	ENSG00000174917	Degradome sequencing	negative		gained-open
374875	ENSG00000167733	HITS-CLIP	Functional MTI (Weak)	19536157	gained-open
79085	ENSG00000125648	Degradome sequencing//De	positive		gained-open

56949	ENSG00000076924	Degradome sequencing	negative		gained-open
6234	ENSG00000233927	CLASH	Functional MTI (Weak)	23622248	gained-open
9230	ENSG00000185236	Degradome sequencing	negative		gained-open
9230	ENSG00000185236	Degradome sequencing	positive		gained-open
84330	ENSG00000133250	Degradome sequencing	positive		gained-open
51073	ENSG00000105364	Degradome sequencing	negative		gained-open
51073	ENSG00000105364	Degradome sequencing	positive		gained-open
3609	ENSG00000129351	Degradome sequencing	positive		gained-open
3609	ENSG00000129351	Degradome sequencing	positive		gained-open
10498	ENSG00000142453	HITS-CLIP	Functional MTI (Weak)	22473208	gained-open
10498	ENSG00000142453	Degradome sequencing	positive		gained-open
65249	ENSG00000132003	Degradome sequencing	positive		gained-open
65249	ENSG00000132003	Degradome sequencing	positive		gained-open
65249	ENSG00000132003	Degradome sequencing	positive		gained-open
65249	ENSG00000132003	Degradome sequencing	positive		gained-open
83878	ENSG00000130307	Degradome sequencing	positive		gained-open
147991	ENSG00000178904	Sequencing	Functional MTI (Weak)	20371350	gained-open
84079	ENSG00000105186	Degradome sequencing	positive		gained-open
7538	ENSG00000128016	PAR-CLIP	Functional MTI (Weak)	23446348	gained-open
7538	ENSG00000128016	HITS-CLIP	Functional MTI (Weak)	23313552	gained-open
7538	ENSG00000128016	PAR-CLIP	Functional MTI (Weak)	26701625	gained-open
7538	ENSG00000128016	Degradome sequencing//De	positive		gained-open
7538	ENSG00000128016	PAR-CLIP	Functional MTI (Weak)	23446348	gained-open
7538	ENSG00000128016	HITS-CLIP	Functional MTI (Weak)	23313552	gained-open
7538	ENSG00000128016	PAR-CLIP	Functional MTI (Weak)	26701625	gained-open
7538	ENSG00000128016	Degradome sequencing//De	positive		gained-open
64857	ENSG00000090924	Degradome sequencing	negative		gained-open
6217	ENSG00000105193	PAR-CLIP	Functional MTI (Weak)	20371350	gained-open
6217	ENSG00000105193	Degradome sequencing//De	positive		gained-open
6829	ENSG00000196235	Degradome sequencing	positive		gained-open
26099	ENSG00000055070	HITS-CLIP	Functional MTI (Weak)	22473208	gained-open
26099	ENSG00000055070	HITS-CLIP	Functional MTI (Weak)	23824327	gained-open

26099	ENSG00000055070	Degradome sequencing//De	positive		gained-open
29950	ENSG00000197019	Degradome sequencing	negative		gained-open
29946	ENSG00000167565	HITS-CLIP	Functional MTI (Weak)	22473208	gained-open
29946	ENSG00000167565	Degradome sequencing	negative		gained-open
29946	ENSG00000167565	Degradome sequencing	positive		gained-open
645	ENSG00000090013	Degradome sequencing	positive		gained-open
80271	ENSG00000086544	CLASH	Functional MTI (Weak)	23622248	gained-open
80271	ENSG00000086544	Degradome sequencing	negative		gained-open
284325	ENSG00000188493	Degradome sequencing	negative		gained-open
6626	ENSG00000077312	CLASH	Functional MTI (Weak)	23622248	gained-open
6626	ENSG00000077312	Degradome sequencing	positive		gained-open
2067	ENSG00000012061	Degradome sequencing	negative		gained-open
23211	ENSG00000130749	Degradome sequencing//De	positive		gained-open
2512	ENSG00000087086	Degradome sequencing	positive		gained-open
126017	ENSG00000198346	PAR-CLIP	Functional MTI (Weak)	20371350	gained-open
29844	ENSG00000105619	Degradome sequencing	negative		gained-open
6193	ENSG00000083845	CLASH	Functional MTI (Weak)	23622248	gained-open
7691	ENSG00000131849	Degradome sequencing	negative		gained-open
8890	ENSG00000115211	Degradome sequencing//De	positive		gained-open
64427	ENSG00000115282	Degradome sequencing	negative		gained-open
84865	ENSG00000135637	HITS-CLIP	Functional MTI (Weak)	23824327	gained-open
84865	ENSG00000135637	Degradome sequencing	negative		gained-open
55654	ENSG00000135956	Degradome sequencing	positive		gained-open
9391	ENSG00000144021	HITS-CLIP	Functional MTI (Weak)	23824327	gained-open
9669	ENSG00000158417	Degradome sequencing	positive		gained-open
148327	ENSG00000143578	Degradome sequencing	negative		gained-open
148327	ENSG00000143578	Degradome sequencing	positive		gained-open
10456	ENSG00000143575	Degradome sequencing	positive		gained-open
1163	ENSG00000173207	PAR-CLIP	Functional MTI (Weak)	22100165	gained-open
6464	ENSG00000160691	Degradome sequencing	positive		gained-open
6464	ENSG00000160691	Degradome sequencing	positive		gained-open
8407	ENSG00000158710	Degradome sequencing	negative		gained-open

8407	ENSG00000158710	Degradome sequencing	positive		gained-open
55054	ENSG00000085978	Degradome sequencing	positive		gained-open
9855	ENSG00000006607	Degradome sequencing	positive		gained-open
9855	ENSG00000006607	Degradome sequencing	positive		gained-open
63908	ENSG00000125814	Degradome sequencing	positive		gained-open
57136	ENSG00000101474	Degradome sequencing	positive		gained-open
57136	ENSG00000101474	Degradome sequencing	positive		gained-open
22913	ENSG00000125970	Degradome sequencing	negative		gained-open
11190	ENSG00000126001	Degradome sequencing	positive		gained-open
9584	ENSG00000131051	Degradome sequencing	positive		gained-open
6431	ENSG00000124193	Degradome sequencing	positive		gained-open
6431	ENSG00000124193	Degradome sequencing	positive		gained-open
10955	ENSG00000132824	PAR-CLIP	Functional MTI (Weak)	23592263	gained-open
10955	ENSG00000132824	PAR-CLIP	Functional MTI (Weak)	24398324	gained-open
10955	ENSG00000132824	PAR-CLIP	Functional MTI (Weak)	23446348	gained-open
10955	ENSG00000132824	PAR-CLIP	Functional MTI (Weak)	21572407	gained-open
10955	ENSG00000132824	PAR-CLIP	Functional MTI (Weak)	20371350	gained-open
10955	ENSG00000132824	HITS-CLIP	Functional MTI (Weak)	23313552	gained-open
10955	ENSG00000132824	Degradome sequencing	positive		gained-open
10955	ENSG00000132824	Degradome sequencing	negative		gained-open

Supplementary Table 5

Category	Term	Count	PValue
CHROMOSOME	19	38	8.290670249285834E-14

Category	Term	Count	PValue
GOTERM_BP_DIRECT	GO:0009615~response to virus	6	0.0029224520696824272
GOTERM_BP_DIRECT	GO:0070314~G1 to G0 transition	3	0.0033204727581969545
GOTERM_BP_DIRECT	GO:0051607~defense response to virus	8	0.005254639133481927
GOTERM_BP_DIRECT	GO:0014823~response to activity	4	0.009748562135664815
GOTERM_BP_DIRECT	GO:0071360~cellular response to exogenous dsRNA	3	0.010779355225003989
GOTERM_BP_DIRECT	GO:0009416~response to light stimulus	3	0.011978288248549072
GOTERM_BP_DIRECT	GO:2000850~negative regulation of glucocorticoid secretion	2	0.017557238017843844
GOTERM_BP_DIRECT	GO:0009785~blue light signaling pathway	2	0.017557238017843844
GOTERM_BP_DIRECT	GO:0030325~adrenal gland development	3	0.018785433673132335
GOTERM_BP_DIRECT	GO:0000380~alternative mRNA splicing, via spliceosome	3	0.02030212587656299
GOTERM_BP_DIRECT	GO:0045893~positive regulation of DNA-templated transcription	13	0.024396995618732313
GOTERM_BP_DIRECT	GO:0032868~response to insulin	4	0.029637311260757054
GOTERM_BP_DIRECT	GO:0000398~mRNA splicing, via spliceosome	6	0.03329803734388822
GOTERM_BP_DIRECT	GO:0032785~negative regulation of DNA-templated transcription, elongation	2	0.03480796005449397
GOTERM_BP_DIRECT	GO:0048536~spleen development	3	0.04208563798548127

Category	Term	Count	PValue
REACTOME_PATHWAY	R-HSA-2262752~Cellular responses to stress	22	1.9070830564443992E-4
REACTOME_PATHWAY	R-HSA-8953897~Cellular responses to stimuli	22	2.416907413863659E-4
REACTOME_PATHWAY	R-HSA-199991~Membrane Trafficking	17	0.001679802725067504
REACTOME_PATHWAY	R-HSA-5653656~Vesicle-mediated transport	17	0.0030650860861799302
REACTOME_PATHWAY	R-HSA-72203~Processing of Capped Intron-Containing Pre-mRNA	10	0.0044026314743659326
REACTOME_PATHWAY	R-HSA-199977~ER to Golgi Anterograde Transport	7	0.0072935275325331315
REACTOME_PATHWAY	R-HSA-9735869~SARS-CoV-1 modulates host translation machinery	4	0.007857835188963972

REACTOME_PATHWAY	R-HSA-72737~Cap-dependent Translation Initiation	6	0.010703134762210412
REACTOME_PATHWAY	R-HSA-72613~Eukaryotic Translation Initiation	6	0.010703134762210412
REACTOME_PATHWAY	R-HSA-5617472~Activation of anterior HOX genes in hindbrain development during	6	0.011067862097530882
REACTOME_PATHWAY	R-HSA-5619507~Activation of HOX genes during differentiation	6	0.011067862097530882
REACTOME_PATHWAY	R-HSA-8953854~Metabolism of RNA	16	0.01427947788929096
REACTOME_PATHWAY	R-HSA-72766~Translation	9	0.015913239892024672
REACTOME_PATHWAY	R-HSA-948021~Transport to the Golgi and subsequent modification	7	0.016930605377080105
REACTOME_PATHWAY	R-HSA-392499~Metabolism of proteins	34	0.017717232720305377
REACTOME_PATHWAY	R-HSA-9754678~SARS-CoV-2 modulates host translation machinery	4	0.01883283453158449
REACTOME_PATHWAY	R-HSA-446203~Asparagine N-linked glycosylation	9	0.019773561206452538
REACTOME_PATHWAY	R-HSA-72695~Formation of the ternary complex, and subsequently, the 43S complex	4	0.019827546687847444
REACTOME_PATHWAY	R-HSA-9678108~SARS-CoV-1 Infection	6	0.020795594813650307
REACTOME_PATHWAY	R-HSA-9692914~SARS-CoV-1-host interactions	5	0.021893044044196237
REACTOME_PATHWAY	R-HSA-6807878~COPI-mediated anterograde transport	5	0.02580659499482982
REACTOME_PATHWAY	R-HSA-72649~Translation initiation complex formation	4	0.02759024364848599
REACTOME_PATHWAY	R-HSA-72187~mRNA 3'-end processing	4	0.02759024364848599
REACTOME_PATHWAY	R-HSA-72702~Ribosomal scanning and start codon recognition	4	0.02759024364848599
REACTOME_PATHWAY	R-HSA-72163~mRNA Splicing - Major Pathway	7	0.027604144336805945
REACTOME_PATHWAY	R-HSA-72662~Activation of the mRNA upon binding of the cap-binding complex	4	0.02881331051035884
REACTOME_PATHWAY	R-HSA-4839726~Chromatin organization	8	0.030569306289699495
REACTOME_PATHWAY	R-HSA-3247509~Chromatin modifying enzymes	8	0.030569306289699495
REACTOME_PATHWAY	R-HSA-72172~mRNA Splicing	7	0.03239033045846365
REACTOME_PATHWAY	R-HSA-5696398~Nucleotide Excision Repair	5	0.03289395281338822
REACTOME_PATHWAY	R-HSA-72706~GTP hydrolysis and joining of the 60S ribosomal subunit	5	0.03682443168678437
REACTOME_PATHWAY	R-HSA-73856~RNA Polymerase II Transcription Termination	4	0.03961401305532686
REACTOME_PATHWAY	R-HSA-204005~COPII-mediated vesicle transport	4	0.03961401305532686
REACTOME_PATHWAY	R-HSA-2299718~Condensation of Prophase Chromosomes	4	0.047265884781812255
REACTOME_PATHWAY	R-HSA-3700989~Transcriptional Regulation by TP53	9	0.04806463804291128

Supplementary Table 6

Cluster #	STIM/UNSTIM	Gene list modulated by BUT	Clusters genes
Cluster 2	STIM	gained-open_RNU12	RNU12
Cluster 2	STIM	gained-open_DUSP1	DUSP1
Cluster 2	STIM	gained-open_SYTL1	SYTL1
Cluster 2	STIM	gained-open_FOS	FOS
Cluster 2	STIM	gained-open_TMC8	TMC8
Cluster 2	STIM	gained-open_CIRBP	CIRBP
Cluster 2	STIM	gained-open_ZFP36	ZFP36
Cluster 2	STIM	gained-open_RASGRP2	RASGRP2
Cluster 2	UNSTIM	gained-open_RNU12	RNU12
Cluster 2	UNSTIM	gained-open_DUSP1	DUSP1
Cluster 2	UNSTIM	gained-open_SYTL1	SYTL1
Cluster 2	UNSTIM	gained-open_FOS	FOS
Cluster 2	UNSTIM	gained-open_CIRBP	CIRBP
Cluster 2	UNSTIM	gained-open_RASGRP2	RASGRP2
Cluster 4	STIM	gained-open_LINC00996	LINC00996
Cluster 4	STIM	gained-open_DDB2	DDB2
Cluster 4	STIM	gained-open_STARD10	STARD10
Cluster 4	STIM	gained-open_TAGLN2	TAGLN2
Cluster 4	UNSTIM	gained-open_LINC00996	LINC00996
Cluster 4	UNSTIM	gained-open_DDB2	DDB2
Cluster 4	UNSTIM	gained-open_STARD10	STARD10
Cluster 4	UNSTIM	gained-open_TAGLN2	TAGLN2
Average expression (stim_avg_log_FC)		n marker genes	n corrispondenze nostri geni e geni marker
Cluster 2	0,852237722		199 14
Cluster 4	0,715947628		92 8

Cluster #	STIM/UNSTIM	Gene list modulated by BUT	Clusters genes
Cluster 3	STIM	gained-close_IFI44	IFI44
Cluster 3	STIM	gained-close_IFIH1	IFIH1
Cluster 3	STIM	gained-close_IFIT1	IFIT1
Cluster 3	UNSTIM	gained-close_IFI44	IFI44
Cluster 3	UNSTIM	gained-close_IFIH1	IFIH1
Cluster 3	UNSTIM	gained-close_IFIT1	IFIT1
Cluster 6	STIM	gained-close_ARID5B	ARID5B
Cluster 6	STIM	gained-close_TRIM22	TRIM22
Cluster 6	UNSTIM	gained-close_ARID5B	ARID5B

	Average expression (stim_avg_log_FC)	n marker genes	n corrispondenze nostri geni e geni marker
cluster 3	0,810618317	63	6
cluster 6	0,869220663	93	3

stim_avg_logFC	stim_pct.1	stim_pct.2	stim_p_val_adj	diff(pct.1,pct.2)	Expression level or Notes
1,17038179	0,291	0,038	5,21084E-86	0,253	high expressed gene
1,52325049	0,736	0,185	8,5452E-164	0,551	high expressed gene
0,52399874	0,211	0,053	7,61785E-30	0,158	high expressed gene
1,4415796	0,576	0,141	4,0808E-115	0,435	high expressed gene
0,47800877	0,165	0,062	1,00886E-11	0,103	high expressed gene
0,44878241	0,75	0,589	4,36833E-18	0,161	high expressed gene
0,70075309	0,532	0,356	1,59604E-16	0,176	high expressed gene
0,416438734	0,17	0,054	1,14072E-15	0,116	high expressed gene
1,010199448	0,257	0,035	3,50226E-95	0,222	high expressed gene
1,361159557	0,657	0,219	3,5302E-143	0,438	high expressed gene
0,515590217	0,208	0,055	5,09136E-38	0,153	high expressed gene
1,500981135	0,524	0,144	1,3565E-125	0,38	high expressed gene
0,378320272	0,751	0,612	2,64732E-18	0,139	high expressed gene
0,461883858	0,195	0,062	2,23789E-26	0,133	high expressed gene
1,11811584	0,644	0,16	1,16837E-69	0,484	high expressed gene
0,44868364	0,256	0,075	2,58783E-15	0,181	high expressed gene
0,543370731	0,352	0,106	5,10591E-22	0,246	high expressed gene
0,366531366	0,653	0,422	7,24424E-06	0,231	high expressed gene
1,339512035	0,804	0,217	1,852E-108	0,587	high expressed gene
0,712084685	0,304	0,063	2,65721E-40	0,241	high expressed gene
0,816237318	0,428	0,101	1,35761E-49	0,327	high expressed gene
0,383045408	0,688	0,417	9,42645E-10	0,271	high expressed gene

100*(n nostri geni/n marker genes) Average pct diff
7,035175879 0,244142857
8,695652174 0,321

stim_avg_logFC	stim_pct.1	stim_pct.2	stim_p_val_adj	diff(pct.1,pct.2)	Expression level or Notes
0,674819968	0,199	0,036	6,63E-28	0,163	high expressed gene
0,762824646	0,254	0,061	2,25E-25	0,193	high expressed gene
1,033166569	0,305	0,026	1,71E-88	0,279	high expressed gene
0,546591161	0,17	0,024	5,83821E-35	0,146	high expressed gene
0,78407663	0,235	0,043	1,57769E-38	0,192	high expressed gene
1,062230929	0,269	0,019	1,7317E-107	0,25	high expressed gene
0,914559738	0,53	0,177	1,64737E-31	0,353	high expressed gene
0,657406974	0,35	0,167	7,50678E-08	0,183	high expressed gene
1,035695276	0,52	0,126	6,00151E-29	0,394	high expressed gene

100*(n nostri geni/n marker genes) Average pct diff

9,523809524	0,203833333
3,225806452	0,31

Supplementary Table 7

Fluorochrome	Specificity	Clone
BV605	CD3	SK7 Leu-4
BV650	CD8	RPA-T8
PerCp5.5	CD16	3G8
PeCy7	CD19	H1B19
PeCy5	CD33	Wm53
BV786	CD56	NCAm16.2
FITC	CD57	NK1
APC	CD69	FN50
BV711	CD158a	HP3E4, DX27, DX9
BV421	NKG2C/CD159c	134591
BV480	NKG2A/CD159a	131411
PE-CF594	CD279 (PD-1)	MIH4
PE	KLRG1	2F1