

Table S3

Ontology ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue		
GO:0022613	BP	GO:0022613	ribonucleoprotein complex biogenesis	73/1133	412/29008	1.12E-27	5.96E-24	3.99E-24
GO:0008380	BP	GO:0008380	RNA splicing	68/1133	398/29008	6.62E-25	1.76E-21	1.18E-21
GO:0043484	BP	GO:0043484	regulation of RNA splicing	41/1133	157/29008	1.2E-22	2.12E-19	1.42E-19
GO:1903311	BP	GO:1903311	regulation of mRNA metabolic process	54/1133	293/29008	1.33E-21	1.76E-18	1.18E-18
GO:0043161	BP	GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	63/1133	423/29008	5.95E-20	6.33E-17	4.24E-17
GO:0006397	BP	GO:0006397	mRNA processing	66/1133	469/29008	1.64E-19	1.46E-16	9.76E-17
GO:0042254	BP	GO:0042254	ribosome biogenesis	50/1133	296/29008	2.01E-18	1.53E-15	1.02E-15
GO:0016570	BP	GO:0016570	histone modification	63/1133	461/29008	4.94E-18	3.29E-15	2.2E-15
GO:006325	BP	GO:006325	chromatin organization	64/1133	477/29008	6.83E-18	4.03E-15	2.7E-15
GO:0042274	BP	GO:0042274	ribosomal small subunit biogenesis	24/1133	72/29008	1.66E-16	8.82E-14	5.9E-14
GO:1903320	BP	GO:1903320	regulation of protein modification by small protein conjugation or removal	43/1133	248/29008	1.85E-16	8.93E-14	5.98E-14
GO:0034976	BP	GO:0034976	response to endoplasmic reticulum stress	43/1133	254/29008	4.54E-16	2.01E-13	1.35E-13
GO:0022618	BP	GO:0022618	ribonucleoprotein complex assembly	35/1133	171/29008	6.13E-16	2.05E-13	1.37E-13
GO:0000375	BP	GO:0000375	RNA splicing, via transesterification reactions	45/1133	279/29008	6.18E-16	2.05E-13	1.37E-13
GO:0000377	BP	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	45/1133	279/29008	6.18E-16	2.05E-13	1.37E-13
GO:0000398	BP	GO:0000398	mRNA splicing, via spliceosome	45/1133	279/29008	6.18E-16	2.05E-13	1.37E-13
GO:0006986	BP	GO:0006986	response to unfolded protein	29/1133	116/29008	7.11E-16	2.23E-13	1.49E-13
GO:0035966	BP	GO:0035966	response to topologically incorrect protein	31/1133	138/29008	1.83E-15	5.41E-13	3.62E-13
GO:0071826	BP	GO:0071826	ribonucleoprotein complex subunit organization	35/1133	178/29008	2.25E-15	6.29E-13	4.21E-13
GO:0031331	BP	GO:0031331	positive regulation of cellular catabolic process	55/1133	425/29008	7.09E-15	1.89E-12	1.26E-12
GO:0009896	BP	GO:0009896	positive regulation of catabolic process	60/1133	494/29008	7.69E-15	1.95E-12	1.3E-12
GO:0006913	BP	GO:0006913	nucleocytoplasmic transport	47/1133	327/29008	1.29E-14	2.98E-12	2E-12
GO:0051169	BP	GO:0051169	nuclear transport	47/1133	327/29008	1.29E-14	2.98E-12	2E-12
GO:0034248	BP	GO:0034248	regulation of cellular amide metabolic process	56/1133	448/29008	1.8E-14	4E-12	2.68E-12
GO:0002181	BP	GO:0002181	cytoplasmic translation	25/1133	96/29008	2.53E-14	5.26E-12	3.52E-12
GO:0006364	BP	GO:0006364	rRNA processing	37/1133	214/29008	2.57E-14	5.26E-12	3.52E-12
GO:0030099	BP	GO:0030099	myeloid cell differentiation	54/1133	426/29008	2.98E-14	5.87E-12	3.93E-12
GO:0006457	BP	GO:0006457	protein folding	32/1133	163/29008	3.71E-14	7.04E-12	4.72E-12
GO:2001233	BP	GO:2001233	regulation of apoptotic signaling pathway	52/1133	402/29008	3.96E-14	7.27E-12	4.87E-12
GO:0050684	BP	GO:0050684	regulation of mRNA processing	30/1133	148/29008	9.57E-14	1.7E-11	1.14E-11
GO:0016072	BP	GO:0016072	rRNA metabolic process	37/1133	224/29008	1.12E-13	1.92E-11	1.29E-11
GO:0006417	BP	GO:0006417	regulation of translation	50/1133	390/29008	1.74E-13	2.89E-11	1.94E-11
GO:0016032	BP	GO:0016032	viral process	46/1133	346/29008	4.4E-13	7.08E-11	4.75E-11
GO:0140694	BP	GO:0140694	non-membrane-bounded organelle assembly	48/1133	373/29008	4.63E-13	7.24E-11	4.85E-11
GO:0042176	BP	GO:0042176	regulation of protein catabolic process	49/1133	389/29008	5.93E-13	9.01E-11	6.04E-11
GO:0030098	BP	GO:0030098	lymphocyte differentiation	52/1133	441/29008	1.55E-12	2.3E-10	1.54E-10
GO:0043281	BP	GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	34/1133	210/29008	1.99E-12	2.86E-10	1.91E-10
GO:0034620	BP	GO:0034620	cellular response to unfolded protein	22/1133	88/29008	2.21E-12	3.09E-10	2.07E-10
GO:1903131	BP	GO:1903131	mononuclear cell differentiation	55/1133	489/29008	2.37E-12	3.23E-10	2.16E-10
GO:0035967	BP	GO:0035967	cellular response to topologically incorrect protein	24/1133	108/29008	3.5E-12	4.6E-10	3.08E-10
GO:0046631	BP	GO:0046631	alpha-beta T cell activation	31/1133	180/29008	3.55E-12	4.6E-10	3.08E-10
GO:2000116	BP	GO:2000116	regulation of cysteine-type endopeptidase activity	36/1133	239/29008	4.01E-12	5.08E-10	3.4E-10
GO:007264	BP	GO:007264	small GTPase mediated signal transduction	50/1133	425/29008	4.55E-12	5.63E-10	3.77E-10
GO:0006338	BP	GO:0006338	chromatin remodeling	33/1133	208/29008	7.42E-12	8.97E-10	6.01E-10
GO:0018205	BP	GO:0018205	peptidyl-lysine modification	46/1133	375/29008	7.72E-12	9.03E-10	6.05E-10
GO:0002683	BP	GO:0002683	negative regulation of immune system process	52/1133	460/29008	7.81E-12	9.03E-10	6.05E-10
GO:0031396	BP	GO:0031396	regulation of protein ubiquitination	33/1133	214/29008	1.64E-11	1.86E-09	1.24E-09
GO:0030522	BP	GO:0030522	intracellular receptor signaling pathway	33/1133	217/29008	2.41E-11	2.67E-09	1.78E-09
GO:0006402	BP	GO:0006402	mRNA catabolic process	34/1133	231/29008	3.03E-11	3.29E-09	2.2E-09
GO:0048024	BP	GO:0048024	regulation of mRNA splicing, via spliceosome	23/1133	110/29008	3.71E-11	3.95E-09	2.65E-09
GO:0043434	BP	GO:0043434	response to peptide hormone	43/1133	351/29008	3.88E-11	4.04E-09	2.71E-09
GO:0006401	BP	GO:0006401	rRNA catabolic process	37/1133	272/29008	4.36E-11	4.46E-09	2.99E-09
GO:0009615	BP	GO:0009615	response to virus	40/1133	312/29008	4.6E-11	4.53E-09	3.04E-09
GO:0010563	BP	GO:0010563	negative regulation of phosphorus metabolic process	50/1133	433/29008	4.69E-11	4.53E-09	3.04E-09
GO:0045936	BP	GO:0045936	negative regulation of phosphate metabolic process	50/1133	433/29008	4.69E-11	4.53E-09	3.04E-09
GO:1901652	BP	GO:1901652	response to peptide	47/1133	412/29008	5.82E-11	5.52E-09	3.7E-09
GO:1903322	BP	GO:1903322	positive regulation of protein modification by small protein conjugation or removal	26/1133	145/29008	7.65E-11	7.14E-09	4.78E-09
GO:0007249	BP	GO:0007249	I-kappaB kinase/NF-kappaB signaling	33/1133	228/29008	9.29E-11	8.45E-09	5.66E-09
GO:0036503	BP	GO:0036503	ERAD pathway	22/1133	105/29008	9.45E-11	8.45E-09	5.66E-09
GO:0072594	BP	GO:0072594	establishment of protein localization to organelle	47/1133	418/29008	9.54E-11	8.45E-09	5.66E-09
GO:0071824	BP	GO:0071824	protein-DNA complex subunit organization	30/1133	192/29008	9.74E-11	8.49E-09	5.69E-09
GO:0043543	BP	GO:0043543	protein acylation	34/1133	243/29008	1.23E-10	1.06E-08	7.09E-09
GO:0006333	BP	GO:0006333	chromatin assembly or disassembly	24/1133	127/29008	1.31E-10	1.11E-08	7.4E-09
GO:0006914	BP	GO:0006914	autophagy	48/1133	437/29008	1.35E-10	1.11E-08	7.4E-09
GO:0061919	BP	GO:0061919	process utilizing autophagic mechanism	48/1133	437/29008	1.35E-10	1.11E-08	7.4E-09
GO:0018209	BP	GO:0018209	peptidyl-serine modification	43/1133	365/29008	1.37E-10	1.11E-08	7.4E-09
GO:0061013	BP	GO:0061013	regulation of mRNA catabolic process	27/1133	161/29008	1.63E-10	1.29E-08	8.64E-09
GO:0001819	BP	GO:0001819	positive regulation of cytokine production	52/1133	500/29008	1.7E-10	1.33E-08	8.92E-09
GO:0043087	BP	GO:0043087	regulation of GTPase activity	40/1133	326/29008	1.77E-10	1.37E-08	9.14E-09
GO:1903037	BP	GO:1903037	regulation of leukocyte cell-cell adhesion	40/1133	333/29008	3.37E-10	2.56E-08	1.71E-08
GO:0097193	BP	GO:0097193	intrinsic apoptotic signaling pathway	38/1133	307/29008	3.91E-10	2.93E-08	1.96E-08
GO:0030433	BP	GO:0030433	ubiquitin-dependent ERAD pathway	19/1133	84/29008	4.47E-10	3.3E-08	2.21E-08
GO:0045862	BP	GO:0045862	positive regulation of proteolysis	41/1133	351/29008	4.76E-10	3.47E-08	2.32E-08
GO:0051090	BP	GO:0051090	regulation of DNA-binding transcription factor activity	46/1133	425/29008	5.32E-10	3.82E-08	2.56E-08
GO:0042326	BP	GO:0042326	negative regulation of phosphorylation	44/1133	396/29008	5.52E-10	3.92E-08	2.62E-08
GO:0018105	BP	GO:0018105	peptidyl-serine phosphorylation	40/1133	340/29008	6.27E-10	4.38E-08	2.94E-08
GO:0006354	BP	GO:0006354	DNA-templated transcription, elongation	19/1133	86/29008	6.87E-10	4.74E-08	3.18E-08
GO:1903362	BP	GO:1903362	regulation of cellular protein catabolic process	33/1133	246/29008	7E-10	4.77E-08	3.2E-08
GO:0006413	BP	GO:0006413	translational initiation	22/1133	117/29008	8.48E-10	5.71E-08	3.82E-08
GO:0007159	BP	GO:0007159	leukocyte cell-cell adhesion	42/1133	373/29008	9.07E-10	6.03E-08	4.04E-08
GO:0031056	BP	GO:0031056	regulation of histone modification	27/1133	174/29008	9.77E-10	6.38E-08	4.27E-08
GO:0034504	BP	GO:0034504	protein localization to nucleus	38/1133	317/29008	9.83E-10	6.38E-08	4.27E-08
GO:0071375	BP	GO:0071375	cellular response to peptide hormone stimulus	34/1133	264/29008	1.15E-09	7.37E-08	4.94E-08
GO:0043488	BP	GO:0043488	regulation of mRNA stability	25/1133	152/29008	1.17E-09	7.4E-08	4.96E-08
GO:0048872	BP	GO:0048872	homeostasis of number of cells	41/1133	363/29008	1.31E-09	8.19E-08	5.48E-08
GO:0006473	BP	GO:0006473	protein acetylation	29/1133	201/29008	1.36E-09	8.42E-08	5.64E-08
GO:0031647	BP	GO:0031647	regulation of protein stability	37/1133	307/29008	1.4E-09	8.58E-08	5.74E-08
GO:1901653	BP	GO:1901653	cellular response to peptide	37/1133	308/29008	1.54E-09	9.28E-08	6.22E-08
GO:0043487	BP	GO:0043487	regulation of RNA stability	26/1133	166/29008	1.62E-09	9.68E-08	6.48E-08
GO:0051168	BP	GO:0051168	nuclear export	25/1133	155/29008	1.78E-09	1.05E-07	7.04E-08
GO:0022407	BP	GO:0022407	regulation of cell-cell adhesion	47/1133	457/29008	1.85E-09	1.08E-07	7.25E-08
GO:0032868	BP	GO:0032868	response to insulin	32/1133	244/29008	2.24E-09	1.29E-07	8.66E-08
GO:0030183	BP	GO:0030183	B cell differentiation	26/1133	170/29008	2.73E-09	1.56E-07	1.04E-07
GO:0032869	BP	GO:0032869	cellular response to insulin stimulus	29/1133	206/29008	3.05E-09	1.73E-07	1.16E-07
GO:0034728	BP	GO:0034728	nucleosome organization	22/1133	125/29008	3.12E-09	1.74E-07	1.17E-07
GO:0030490	BP	GO:0030490	maturation of ssU-rRNA	14/1133	49/29008	3.34E-09	1.82E-07	1.22E-07
GO:0006605	BP	GO:0006605	protein targeting	34/1133	275/29008	3.35E-09	1.82E-07	1.22E-07
GO:0002029	BP	GO:0002029	protein polyubiquitination	32/1133	248/29008	3.36E-09	1.82E-07	1.22E-07
GO:0034470	BP	GO:0034470	ncRNA processing	40/1133	362/29008	3.92E-09	2.11E-07	1.41E-07
GO:0008286	BP	GO:0008286	insulin receptor signaling pathway	22/1133	127/29008	4.24E-09	2.25E-07	1.51E-07
GO:0043401	BP	GO:0043401	steroid hormone mediated signaling pathway	21/1133	117/29008	4.91E-09	2.58E-07	1.73E-07
GO:0033119	BP	GO:0033119	negative regulation of RNA splicing	11/1133	28/29008	5.57E-09	2.9E-07	1.94E-07
GO:2001242	BP	GO:2001242	regulation of intrinsic apoptotic signaling pathway	26/1133	176/29008	5.78E-09	2.98E-07	2E-07
GO:0050863	BP	GO:0050863	regulation of T cell activation	38/1133	339/29008	6.45E-09	3.3E-07	2.21E-07
GO:0043122	BP	GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	27/1133	190/29008	6.98E-09	3.53E-07	2.37E-07
GO:0042026	BP	GO:0042026	protein refolding	9/1133	18/29008	7.25E-09	3.64E-07	2.44E-07
GO:0030217	BP	GO:0030217	T cell differentiation	35/1133	299/29008	8.33E-09		

GO:0030518	BP	GO:0030518	Intracellular steroid hormone receptor signaling pathway	19/1133	110/29008	5E-08	1.94E-06	1.3E-06
GO:0001818	BP	GO:0001818	negative regulation of cytokine production	33/1133	292/29008	5.18E-08	1.99E-06	1.34E-06
GO:0019080	BP	GO:0019080	viral gene expression	15/1133	69/29008	5.37E-08	2.05E-06	1.38E-06
GO:0034249	BP	GO:0034249	negative regulation of cellular amide metabolic process	27/1133	209/29008	5.42E-08	2.06E-06	1.38E-06
GO:1903706	BP	GO:1903706	regulation of hemopoiesis	40/1133	398/29008	5.55E-08	2.09E-06	1.4E-06
GO:0006475	BP	GO:0006475	internal protein amino acid acetylation	23/1133	158/29008	5.69E-08	2.11E-06	1.41E-06
GO:0018393	BP	GO:0018393	internal peptidyl-lysine acetylation	23/1133	158/29008	5.69E-08	2.11E-06	1.41E-06
GO:0044270	BP	GO:0044270	cellular nitrogen compound catabolic process	41/1133	414/29008	5.71E-08	2.11E-06	1.41E-06
GO:0006446	BP	GO:0006446	regulation of translational initiation	14/1133	60/29008	5.74E-08	2.11E-06	1.41E-06
GO:0000956	BP	GO:0000956	nuclear-transcribed mRNA catabolic process	19/1133	111/29008	5.82E-08	2.12E-06	1.42E-06
GO:0042594	BP	GO:0042594	response to starvation	25/1133	184/29008	6.17E-08	2.23E-06	1.49E-06
GO:0048545	BP	GO:0048545	response to steroid hormone	28/1133	226/29008	7.62E-08	2.74E-06	1.83E-06
GO:0070661	BP	GO:0070661	leukocyte proliferation	37/1133	358/29008	8.54E-08	3.05E-06	2.04E-06
GO:1903050	BP	GO:1903050	regulation of proteolysis involved in cellular protein catabolic process	27/1133	214/29008	8.88E-08	3.15E-06	2.11E-06
GO:0019439	BP	GO:0019439	aromatic compound catabolic process	42/1133	437/29008	9.13E-08	3.22E-06	2.15E-06
GO:2001234	BP	GO:2001234	negative regulation of apoptotic signaling pathway	29/1133	242/29008	9.33E-08	3.26E-06	2.19E-06
GO:0042273	BP	GO:0042273	ribosomal large subunit biogenesis	15/1133	72/29008	9.8E-08	3.41E-06	2.28E-06
GO:0046651	BP	GO:0046651	lymphocyte proliferation	35/1133	330/29008	1.01E-07	3.48E-06	2.33E-06
GO:0009267	BP	GO:0009267	cellular response to starvation	23/1133	164/29008	1.15E-07	3.93E-06	2.63E-06
GO:2000117	BP	GO:2000117	negative regulation of cysteine-type endopeptidase activity	17/1133	94/29008	1.25E-07	4.28E-06	2.86E-06
GO:0051028	BP	GO:0051028	mRNA transport	19/1133	117/29008	1.38E-07	4.66E-06	3.12E-06
GO:0043154	BP	GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic pro	16/1133	84/29008	1.39E-07	4.66E-06	3.12E-06
GO:1903313	BP	GO:1903313	positive regulation of mRNA metabolic process	20/1133	129/29008	1.44E-07	4.78E-06	3.2E-06
GO:0043620	BP	GO:0043620	regulation of DNA-templated transcription in response to stress	13/1133	55/29008	1.45E-07	4.78E-06	3.2E-06
GO:0051170	BP	GO:0051170	import into nucleus	24/1133	179/29008	1.45E-07	4.78E-06	3.2E-06
GO:0051056	BP	GO:0051056	regulation of small GTPase mediated signal transduction	28/1133	233/29008	1.46E-07	4.78E-06	3.2E-06
GO:0016571	BP	GO:0016571	histone methylation	22/1133	154/29008	1.54E-07	5.04E-06	3.37E-06
GO:0043433	BP	GO:0043433	negative regulation of DNA-binding transcription factor activity	23/1133	167/29008	1.6E-07	5.2E-06	3.48E-06
GO:1901361	BP	GO:1901361	organic cyclic compound catabolic process	43/1133	463/29008	1.68E-07	5.42E-06	3.63E-06
GO:0034101	BP	GO:0034101	erythrocyte homeostasis	22/1133	155/29008	1.73E-07	5.55E-06	3.72E-06
GO:1903364	BP	GO:1903364	positive regulation of cellular protein catabolic process	21/1133	143/29008	1.83E-07	5.82E-06	3.9E-06
GO:0001558	BP	GO:0001558	regulation of cell growth	42/1133	450/29008	2.04E-07	6.46E-06	4.33E-06
GO:0042113	BP	GO:0042113	B cell activation	41/1133	434/29008	2.06E-07	6.48E-06	4.34E-06
GO:0002699	BP	GO:0002699	positive regulation of immune effector process	32/1133	296/29008	2.28E-07	7.14E-06	4.78E-06
GO:0005004	BP	GO:0005004	protein-DNA complex assembly	21/1133	145/29008	2.32E-07	7.19E-06	4.81E-06
GO:0005086	BP	GO:0005086	negative regulation of mRNA processing	10/1133	32/29008	2.34E-07	7.19E-06	4.81E-06
GO:0051085	BP	GO:0051085	chaperone cofactor-dependent protein refolding	10/1133	32/29008	2.34E-07	7.19E-06	4.81E-06
GO:0045785	BP	GO:0045785	positive regulation of cell adhesion	43/1133	471/29008	2.69E-07	8.23E-06	5.52E-06
GO:0016601	BP	GO:0016601	Rac protein signal transduction	12/1133	49/29008	2.88E-07	8.75E-06	5.86E-06
GO:0005057	BP	GO:0005057	nucleic acid transport	21/1133	147/29008	2.94E-07	8.83E-06	5.91E-06
GO:0005058	BP	GO:0005058	RNA transport	21/1133	147/29008	2.94E-07	8.83E-06	5.91E-06
GO:0017148	BP	GO:0017148	negative regulation of translation	24/1133	186/29008	2.99E-07	8.92E-06	5.98E-06
GO:0046634	BP	GO:0046634	regulation of alpha-beta T cell activation	18/1133	111/29008	3E-07	8.92E-06	5.98E-06
GO:0031398	BP	GO:0031398	positive regulation of protein ubiquitination	19/1133	123/29008	3.11E-07	9.18E-06	6.15E-06
GO:0052547	BP	GO:0052547	regulation of peptidase activity	41/1133	441/29008	3.15E-07	9.25E-06	6.2E-06
GO:0001666	BP	GO:0001666	response to hypoxia	26/1133	214/29008	3.24E-07	9.47E-06	6.34E-06
GO:0009755	BP	GO:0009755	hormone-mediated signaling pathway	22/1133	161/29008	3.4E-07	9.89E-06	6.62E-06
GO:0007519	BP	GO:0007519	skeletal muscle tissue development	25/1133	201/29008	3.47E-07	1E-05	6.72E-06
GO:0046626	BP	GO:0046626	regulation of insulin receptor signaling pathway	15/1133	79/29008	3.54E-07	1.02E-05	6.81E-06
GO:0017038	BP	GO:0017038	protein import	27/1133	229/29008	3.56E-07	1.02E-05	6.81E-06
GO:0019083	BP	GO:0019083	viral transcription	12/1133	50/29008	3.66E-07	1.03E-05	6.89E-06
GO:0043618	BP	GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress	12/1133	50/29008	3.66E-07	1.03E-05	6.89E-06
GO:0006064	BP	GO:0006064	regulation of gene silencing by miRNA	12/1133	50/29008	3.66E-07	1.03E-05	6.89E-06
GO:0032481	BP	GO:0032481	positive regulation of type I interferon production	14/1133	69/29008	3.69E-07	1.03E-05	6.91E-06
GO:2000058	BP	GO:2000058	regulation of ubiquitin-dependent protein catabolic process	22/1133	162/29008	3.79E-07	1.06E-05	7.08E-06
GO:0001933	BP	GO:0001933	negative regulation of protein phosphorylation	35/1133	349/29008	3.9E-07	1.08E-05	7.24E-06
GO:0051348	BP	GO:0051348	negative regulation of transferase activity	29/1133	259/29008	3.99E-07	1.1E-05	7.37E-06
GO:0043409	BP	GO:0043409	negative regulation of MAPK cascade	24/1133	189/29008	4.04E-07	1.11E-05	7.41E-06
GO:0051236	BP	GO:0051236	establishment of RNA localization	21/1133	150/29008	4.15E-07	1.13E-05	7.58E-06
GO:0031668	BP	GO:0031668	cellular response to extracellular stimulus	27/1133	231/29008	4.23E-07	1.15E-05	7.7E-06
GO:0005082	BP	GO:0005082	protein stabilization	24/1133	190/29008	4.45E-07	1.2E-05	8.05E-06
GO:0002831	BP	GO:0002831	regulation of response to biotic stimulus	34/1133	337/29008	4.95E-07	1.33E-05	8.91E-06
GO:0032922	BP	GO:0032922	circadian regulation of gene expression	14/1133	71/29008	5.34E-07	1.43E-05	9.56E-06
GO:0050777	BP	GO:0050777	negative regulation of immune response	25/1133	206/29008	5.54E-07	1.47E-05	9.87E-06
GO:0022411	BP	GO:0022411	cellular component disassembly	38/1133	402/29008	5.6E-07	1.47E-05	9.88E-06
GO:0006984	BP	GO:0006984	ER-nucleus signaling pathway	11/1133	43/29008	5.6E-07	1.47E-05	9.88E-06
GO:0031497	BP	GO:0031497	chromatin assembly	17/1133	104/29008	5.67E-07	1.48E-05	9.95E-06
GO:0033674	BP	GO:0033674	positive regulation of kinase activity	40/1133	435/29008	5.8E-07	1.51E-05	1.01E-05
GO:0042098	BP	GO:0042098	T cell proliferation	26/1133	221/29008	6.07E-07	1.58E-05	1.06E-05
GO:0005057	BP	GO:0005057	muscle tissue development	43/1133	486/29008	6.29E-07	1.62E-05	1.09E-05
GO:0002287	BP	GO:0002287	alpha-beta T cell activation involved in immune response	14/1133	72/29008	6.39E-07	1.63E-05	1.09E-05
GO:0098586	BP	GO:0098586	cellular response to virus	14/1133	72/29008	6.39E-07	1.63E-05	1.09E-05
GO:0071456	BP	GO:0071456	cellular response to hypoxia	17/1133	105/29008	6.52E-07	1.66E-05	1.11E-05
GO:0043558	BP	GO:0043558	regulation of translational initiation in response to stress	7/1133	15/29008	6.65E-07	1.68E-05	1.13E-05
GO:0009895	BP	GO:0009895	negative regulation of catabolic process	32/1133	311/29008	6.91E-07	1.74E-05	1.17E-05
GO:0001047	BP	GO:0001047	regulation of posttranscriptional gene silencing	12/1133	53/29008	7.21E-07	1.81E-05	1.21E-05
GO:0005086	BP	GO:0005086	negative regulation of cell activation	26/1133	223/29008	7.23E-07	1.81E-05	1.21E-05
GO:0042255	BP	GO:0042255	ribosome assembly	13/1133	63/29008	7.83E-07	1.94E-05	1.3E-05
GO:0002262	BP	GO:0002262	myeloid cell homeostasis	24/1133	196/29008	7.88E-07	1.94E-05	1.3E-05
GO:0034612	BP	GO:0034612	response to tumor necrosis factor	24/1133	196/29008	7.88E-07	1.94E-05	1.3E-05
GO:0030218	BP	GO:0030218	erythrocyte differentiation	20/1133	143/29008	7.9E-07	1.94E-05	1.3E-05
GO:0007517	BP	GO:0007517	muscle organ development	35/1133	360/29008	8.1E-07	1.97E-05	1.32E-05
GO:0006612	BP	GO:0006612	protein targeting to membrane	18/1133	119/29008	8.68E-07	2.1E-05	1.41E-05
GO:0018107	BP	GO:0018107	peptidyl-threonine phosphorylation	18/1133	119/29008	8.68E-07	2.1E-05	1.41E-05
GO:2001235	BP	GO:2001235	positive regulation of apoptotic signaling pathway	21/1133	157/29008	8.94E-07	2.14E-05	1.43E-05
GO:0009066	BP	GO:0009066	regulation of gene silencing by RNA	12/1133	54/29008	8.94E-07	2.14E-05	1.43E-05
GO:0016051	BP	GO:0016051	carbohydrate biosynthetic process	24/1133	198/29008	9.49E-07	2.25E-05	1.51E-05
GO:0031060	BP	GO:0031060	regulation of histone methylation	15/1133	85/29008	9.49E-07	2.25E-05	1.51E-05
GO:0006038	BP	GO:0006038	skeletal muscle organ development	25/1133	212/29008	9.51E-07	2.25E-05	1.51E-05
GO:0014706	BP	GO:0014706	striated muscle tissue development	41/1133	461/29008	9.99E-07	2.35E-05	1.57E-05
GO:0072659	BP	GO:0072659	protein localization to plasma membrane	31/1133	301/29008	1.01E-06	2.36E-05	1.58E-05
GO:0031669	BP	GO:0031669	cellular response to nutrient levels	24/1133	199/29008	1.04E-06	2.42E-05	1.62E-05
GO:0006458	BP	GO:0006458	'de novo' protein folding	10/1133	37/29008	1.06E-06	2.44E-05	1.64E-05
GO:0051084	BP	GO:0051084	'de novo' posttranslational protein folding	10/1133	37/29008	1.06E-06	2.44E-05	1.64E-05
GO:0062197	BP	GO:0062197	cellular response to chemical stress	33/1133	333/29008	1.08E-06	2.49E-05	1.67E-05
GO:0019058	BP	GO:0019058	viral life cycle	28/1133	257/29008	1.09E-06	2.49E-05	1.67E-05
GO:0034250	BP	GO:0034250	positive regulation of cellular amide metabolic process	21/1133	159/29008	1.1E-06	2.49E-05	1.67E-05
GO:0051098	BP	GO:0051098	regulation of binding	37/1133	397/29008	1.1E-06	2.49E-05	1.67E-05
GO:0071900	BP	GO:0071900	regulation of protein serine/threonine kinase activity	34/1133	349/29008	1.11E-06	2.49E-05	1.67E-05
GO:0050779	BP	GO:0050779	RNA destabilization	15/1133	86/29008	1.11E-06	2.49E-05	1.67E-05
GO:0061014	BP	GO:0061014	positive regulation of mRNA catabolic process	15/1133	86/29008	1.11E-06	2.49E-05	1.67E-05
GO:0002695	BP	GO:0002695	negative regulation of leukocyte activation	24/1133	200/29008	1.14E-06	2.53E-05	1.7E-05
GO:0046578	BP	GO:0046578	regulation of Ras protein signal transduction	24/1133	200/29008	1.14E-06	2.53E-05	1.7E-05
GO:0000245	BP	GO:0000245	spliceosomal complex assembly	11/1133	46/29008	1.17E-06	2.59E-05	1.73E-05
GO:0022409	BP	GO:0022409	positive regulation of cell-cell adhesion	30/1133	288/29008	1.18E-06	2.61E-05	1.75E-05
GO:0050852	BP	GO:0050852	T cell receptor signaling pathway	19/1133	134/29008	1.2E-06	2.62E-05	1.76E-05
GO:0006403	BP	GO:0006403	RNA localization	22/1133	174/29008	1.31E-06	2.63E-05	1.9E-05
GO:0050792	BP	GO:0050792	regulation of viral process	22/1133	174/29008	1.31E-06	2.63E-05	1.9E-05
GO:0071356	BP	GO:0071356	cellular response to tumor necrosis factor	22/1133	174/29008	1		

GO:0097191	BP	GO:0097191	extrinsic apoptotic signaling pathway	26/1133	238/29008	2.48E-06	4.79E-05	3.21E-05
GO:0006260	BP	GO:0006260	DNA replication	27/1133	253/29008	2.51E-06	4.82E-05	3.23E-05
GO:0061136	BP	GO:0061136	regulation of proteasomal protein catabolic process	22/1133	181/29008	2.54E-06	4.83E-05	3.23E-05
GO:0015931	BP	GO:0015931	nucleobase-containing compound transport	23/1133	195/29008	2.54E-06	4.83E-05	3.23E-05
GO:0030511	BP	GO:0030511	positive regulation of transforming growth factor beta receptor signaling pathway	9/1133	32/29008	2.55E-06	4.83E-05	3.23E-05
GO:1903846	BP	GO:1903846	positive regulation of cellular response to transforming growth factor beta stimulus	9/1133	32/29008	2.55E-06	4.83E-05	3.23E-05
GO:0010998	BP	GO:0010998	regulation of translational initiation by eIF2 alpha phosphorylation	6/1133	12/29008	2.64E-06	4.99E-05	3.34E-05
GO:0022294	BP	GO:0022294	CD4-positive, alpha-beta T cell differentiation involved in immune response	13/1133	70/29008	2.75E-06	5.18E-05	3.47E-05
GO:0027111	BP	GO:0027111	positive regulation of T cell mediated immunity	14/1133	81/29008	2.81E-06	5.27E-05	3.53E-05
GO:0006323	BP	GO:0006323	DNA packaging	20/1133	155/29008	2.85E-06	5.31E-05	3.56E-05
GO:0046632	BP	GO:0046632	alpha-beta T cell differentiation	18/1133	129/29008	2.87E-06	5.34E-05	3.57E-05
GO:1903039	BP	GO:1903039	positive regulation of leukocyte cell-cell adhesion	26/1133	240/29008	2.9E-06	5.38E-05	3.6E-05
GO:0006474	BP	GO:0006474	N-terminal protein amino acid acetylation	7/1133	18/29008	2.97E-06	5.48E-05	3.67E-05
GO:0033673	BP	GO:0033673	negative regulation of kinase activity	25/1133	228/29008	3.07E-06	5.66E-05	3.79E-05
GO:0034599	BP	GO:0034599	cellular response to oxidative stress	28/1133	271/29008	3.11E-06	5.7E-05	3.82E-05
GO:0036293	BP	GO:0036293	response to decreased oxygen levels	26/1133	241/29008	3.13E-06	5.73E-05	3.84E-05
GO:0032200	BP	GO:0032200	telomere organization	18/1133	130/29008	3.21E-06	5.85E-05	3.92E-05
GO:0022293	BP	GO:0022293	alpha-beta T cell differentiation involved in immune response	13/1133	71/29008	3.25E-06	5.9E-05	3.95E-05
GO:0006334	BP	GO:0006334	nucleosome assembly	14/1133	82/29008	3.27E-06	5.9E-05	3.95E-05
GO:0061157	BP	GO:0061157	mRNA destabilization	14/1133	82/29008	3.27E-06	5.9E-05	3.95E-05
GO:0051235	BP	GO:0051235	maintenance of location	32/1133	335/29008	3.44E-06	6.18E-05	4.14E-05
GO:0022604	BP	GO:0022604	regulation of cell morphogenesis	32/1133	337/29008	3.9E-06	6.98E-05	4.68E-05
GO:1903038	BP	GO:1903038	negative regulation of leukocyte cell-cell adhesion	19/1133	145/29008	3.98E-06	7.1E-05	4.75E-05
GO:0071559	BP	GO:0071559	response to transforming growth factor beta	25/1133	230/29008	4.21E-06	7.49E-05	5.02E-05
GO:0032944	BP	GO:0032944	regulation of mononuclear cell proliferation	26/1133	245/29008	4.24E-06	7.52E-05	5.04E-05
GO:0043255	BP	GO:0043255	regulation of carbohydrate biosynthetic process	16/1133	108/29008	4.59E-06	8.11E-05	5.43E-05
GO:0002253	BP	GO:0002253	activation of immune response	38/1133	439/29008	4.65E-06	8.19E-05	5.49E-05
GO:1901990	BP	GO:1901990	regulation of mitotic cell cycle phase transition	29/1133	293/29008	4.89E-06	8.58E-05	5.75E-05
GO:0071103	BP	GO:0071103	DNA conformation change	23/1133	203/29008	5.04E-06	8.82E-05	5.91E-05
GO:0045861	BP	GO:0045861	negative regulation of proteolysis	33/1133	358/29008	5.23E-06	9.12E-05	6.11E-05
GO:0031098	BP	GO:0031098	stress-activated protein kinase signaling cascade	26/1133	248/29008	5.3E-06	9.21E-05	6.17E-05
GO:2001056	BP	GO:2001056	positive regulation of cysteine-type endopeptidase activity	19/1133	148/29008	5.4E-06	9.35E-05	6.26E-05
GO:0071496	BP	GO:0071496	cellular response to external stimulus	29/1133	295/29008	5.58E-06	9.64E-05	6.46E-05
GO:0000462	BP	GO:0000462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU	9/1133	35/29008	5.78E-06	9.95E-05	6.66E-05
GO:0043491	BP	GO:0043491	protein kinase B signaling	23/1133	205/29008	5.95E-06	0.0001011	6.83E-05
GO:0034063	BP	GO:0034063	stress granule assembly	8/1133	27/29008	6.04E-06	0.0001030	6.92E-05
GO:0042692	BP	GO:0042692	muscle cell differentiation	37/1133	428/29008	6.37E-06	0.000106	7.27E-05
GO:0022408	BP	GO:0022408	negative regulation of cell-cell adhesion	23/1133	206/29008	6.45E-06	0.000109	7.34E-05
GO:0045638	BP	GO:0045638	negative regulation of myeloid cell differentiation	14/1133	87/29008	6.71E-06	0.000113	7.61E-05
GO:0034968	BP	GO:0034968	histone lysine methylation	17/1133	124/29008	6.85E-06	0.000115	7.74E-05
GO:0007623	BP	GO:0007623	circadian rhythm	24/1133	222/29008	7.14E-06	0.000119	8.03E-05
GO:0016236	BP	GO:0016236	macroautophagy	24/1133	222/29008	7.14E-06	0.000119	8.03E-05
GO:0043547	BP	GO:0043547	positive regulation of GTPase activity	25/1133	237/29008	7.17E-06	0.000119	8.03E-05
GO:0071346	BP	GO:0071346	cellular response to interferon-gamma	16/1133	112/29008	7.42E-06	0.000123	8.28E-05
GO:0051403	BP	GO:0051403	stress-activated MAPK cascade	25/1133	238/29008	7.72E-06	0.000128	8.59E-05
GO:0006470	BP	GO:0006470	protein dephosphorylation	25/1133	239/29008	8.3E-06	0.000137	9.21E-05
GO:0043254	BP	GO:0043254	regulation of protein-containing complex assembly	38/1133	451/29008	8.66E-06	0.000143	9.58E-05
GO:2001243	BP	GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	15/1133	101/29008	8.77E-06	0.000144	9.67E-05
GO:0008631	BP	GO:0008631	intrinsic apoptotic signaling pathway in response to oxidative stress	10/1133	46/29008	8.98E-06	0.000146	9.84E-05
GO:0051898	BP	GO:0051898	negative regulation of protein kinase B signaling	10/1133	46/29008	8.98E-06	0.000146	9.84E-05
GO:0002292	BP	GO:0002292	T cell differentiation involved in immune response	13/1133	78/29008	9.59E-06	0.000156	0.000104
GO:0050670	BP	GO:0050670	regulation of lymphocyte proliferation	25/1133	241/29008	9.6E-06	0.000156	0.000104
GO:0007163	BP	GO:0007163	establishment or maintenance of cell polarity	24/1133	226/29008	9.68E-06	0.000156	0.000104
GO:0071560	BP	GO:0071560	cellular response to transforming growth factor beta stimulus	24/1133	226/29008	9.68E-06	0.000156	0.000104
GO:0039531	BP	GO:0039531	regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway	7/1133	21/29008	9.78E-06	0.000156	0.000104
GO:0043555	BP	GO:0043555	regulation of translation in response to stress	7/1133	21/29008	9.78E-06	0.000156	0.000104
GO:2001236	BP	GO:2001236	regulation of extrinsic apoptotic signaling pathway	20/1133	168/29008	9.79E-06	0.000156	0.000104
GO:0051817	BP	GO:0051817	modulation of process of other organism involved in symbiotic interaction	12/1133	67/29008	9.8E-06	0.000156	0.000104
GO:1902105	BP	GO:1902105	regulation of leukocyte differentiation	30/1133	320/29008	9.93E-06	0.000158	0.000105
GO:0031365	BP	GO:0031365	N-terminal protein amino acid modification	8/1133	29/29008	1.09E-05	0.000172	0.000115
GO:0090502	BP	GO:0090502	RNA phosphodiester bond hydrolysis, endonucleolytic	8/1133	29/29008	1.09E-05	0.000172	0.000115
GO:0006094	BP	GO:0006094	gluconeogenesis	13/1133	79/29008	1.11E-05	0.000174	0.000116
GO:0033143	BP	GO:0033143	regulation of intracellular steroid hormone receptor signaling pathway	13/1133	79/29008	1.11E-05	0.000174	0.000116
GO:0008361	BP	GO:0008361	regulation of cell size	23/1133	213/29008	1.12E-05	0.000175	0.000117
GO:0046034	BP	GO:0046034	ATP metabolic process	26/1133	259/29008	1.16E-05	0.000180	0.000121
GO:0044770	BP	GO:0044770	cell cycle phase transition	40/1133	492/29008	1.18E-05	0.000183	0.000123
GO:1905475	BP	GO:1905475	regulation of protein localization to membrane	22/1133	199/29008	1.19E-05	0.000184	0.000123
GO:0044772	BP	GO:0044772	mitotic cell cycle phase transition	35/1133	406/29008	1.19E-05	0.000184	0.000123
GO:0048511	BP	GO:0048511	rhythmic process	29/1133	307/29008	1.2E-05	0.000185	0.000124
GO:0006979	BP	GO:0006979	response to oxidative stress	35/1133	407/29008	1.26E-05	0.000193	0.000129
GO:0000478	BP	GO:0000478	endonucleolytic cleavage involved in rRNA processing	6/1133	15/29008	1.29E-05	0.000197	0.000132
GO:0000479	BP	GO:0000479	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU	6/1133	15/29008	1.29E-05	0.000197	0.000132
GO:0043923	BP	GO:0043923	positive regulation by host of viral transcription	6/1133	15/29008	1.29E-05	0.000197	0.000132
GO:1900153	BP	GO:1900153	positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-cl	6/1133	15/29008	1.29E-05	0.000197	0.000132
GO:0038294	BP	GO:0038294	cellular response to decreased oxygen levels	17/1133	130/29008	1.3E-05	0.000197	0.000132
GO:0043367	BP	GO:0043367	CD4-positive, alpha-beta T cell differentiation	14/1133	92/29008	1.3E-05	0.000197	0.000132
GO:0070663	BP	GO:0070663	regulation of leukocyte proliferation	26/1133	261/29008	1.32E-05	0.000200	0.000134
GO:0150116	BP	GO:0150116	regulation of cell-substrate junction organization	12/1133	69/29008	1.34E-05	0.000201	0.000135
GO:0050856	BP	GO:0050856	regulation of T cell receptor signaling pathway	10/1133	48/29008	1.34E-05	0.000201	0.000135
GO:0007179	BP	GO:0007179	transforming growth factor beta receptor signaling pathway	21/1133	186/29008	1.35E-05	0.000202	0.000135
GO:1903829	BP	GO:1903829	positive regulation of cellular protein localization	27/1133	277/29008	1.35E-05	0.000202	0.000135
GO:0050870	BP	GO:0050870	positive regulation of T cell activation	23/1133	216/29008	1.41E-05	0.000209	0.000140
GO:0050868	BP	GO:0050868	negative regulation of T cell activation	17/1133	131/29008	1.44E-05	0.000213	0.000143
GO:0007162	BP	GO:0007162	negative regulation of cell adhesion	29/1133	310/29008	1.45E-05	0.000214	0.000143
GO:0007346	BP	GO:0007346	regulation of mitotic cell cycle	38/1133	462/29008	1.49E-05	0.000220	0.000147
GO:0032946	BP	GO:0032946	positive regulation of mononuclear cell proliferation	18/1133	145/29008	1.51E-05	0.000221	0.000148
GO:0072331	BP	GO:0072331	signal transduction by p53 class mediator	18/1133	145/29008	1.51E-05	0.000221	0.000148
GO:0051896	BP	GO:0051896	regulation of protein kinase B signaling	20/1133	173/29008	1.52E-05	0.000222	0.000148
GO:0000381	BP	GO:0000381	regulation of alternative mRNA splicing, via spliceosome	11/1133	59/29008	1.54E-05	0.000224	0.000150
GO:1901987	BP	GO:1901987	regulation of cell cycle phase transition	33/1133	378/29008	1.62E-05	0.000235	0.000158
GO:0042149	BP	GO:0042149	cellular response to glucose starvation	10/1133	49/29008	1.63E-05	0.000236	0.000158
GO:1900138	BP	GO:1900138	neuron projection extension	22/1133	203/29008	1.63E-05	0.000236	0.000158
GO:0071453	BP	GO:0071453	cellular response to oxygen levels	18/1133	146/29008	1.66E-05	0.000240	0.000160
GO:0008625	BP	GO:0008625	extrinsic apoptotic signaling pathway via death domain receptors	13/1133	82/29008	1.68E-05	0.000241	0.000161
GO:0019319	BP	GO:0019319	hexose biosynthetic process	13/1133	82/29008	1.68E-05	0.000241	0.000161
GO:0009314	BP	GO:0009314	response to radiation	36/1133	430/29008	1.7E-05	0.000243	0.000163
GO:0010212	BP	GO:0010212	response to ionizing radiation	17/1133	133/29008	1.78E-05	0.000258	0.000167
GO:0032434	BP	GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic process	17/1133	133/29008	1.78E-05	0.000258	0.000167
GO:0019221	BP	GO:0019221	cytokine-mediated signaling pathway	34/1133	397/29008	1.81E-05	0.000257	0.000172
GO:0006406	BP	GO:0006406	mRNA export from nucleus	11/1133	60/29008	1.82E-05	0.000257	0.000172
GO:0071427	BP	GO:0071427	mRNA-containing ribonucleoprotein complex export from nucleus	11/1133	60/29008	1.82E-05	0.000257	0.000172
GO:2000637	BP	GO:2000637	positive regulation of gene silencing by miRNA	8/1133	31/29008	1.87E-05	0.000263	0.000176
GO:0051651	BP	GO:0051651	maintenance of location in cell	23/1133	220/29008	1.9E-05	0.000266	0.000178
GO:0033120	BP	GO:0033120	positive regulation of RNA splicing	10/1133	50/29008	1.96E-05	0.000275	0.000184
GO:0032970	BP	GO:0032970	regulation of actin filament-based process	35/1133	416/29008	1.99E-05	0.000278	0.000186
GO:0031348	BP	GO:0031348	negative regulation of defense response	24/1133	236/29008	2E-05	0.000278	0.000186
GO:0030307	BP	GO:0030307	positive regulation of cell growth	22/1133	206/29008	2.		

GO:0070534	BP	GO:0070534	protein K63-linked ubiquitination	11/133	64/29008	3.42E-05	0.000438	0.000293
GO:0032680	BP	GO:0032680	regulation of tumor necrosis factor production	20/133	183/29008	3.45E-05	0.000439	0.000294
GO:1901343	BP	GO:1901343	negative regulation of vasculature development	15/133	113/29008	3.45E-05	0.000439	0.000294
GO:0002460	BP	GO:0002460	adaptive immune response based on somatic recombination of immune receptors b	38/133	480/29008	3.45E-05	0.000439	0.000294
GO:0032872	BP	GO:0032872	regulation of stress-activated MAPK cascade	21/133	198/29008	3.48E-05	0.000441	0.000295
GO:0046633	BP	GO:0046633	alpha-beta T cell proliferation	9/133	43/29008	3.48E-05	0.000441	0.000295
GO:0010950	BP	GO:0010950	positive regulation of endopeptidase activity	19/133	169/29008	3.63E-05	0.000458	0.000307
GO:0051101	BP	GO:0051101	regulation of DNA binding	16/133	127/29008	3.69E-05	0.000464	0.000311
GO:0018022	BP	GO:0018022	peptidyl-lysine methylation	17/133	141/29008	3.77E-05	0.000474	0.000317
GO:0051702	BP	GO:0051702	biological process involved in interaction with symbiont	15/133	114/29008	3.83E-05	0.000480	0.000321
GO:0006111	BP	GO:0006111	regulation of gluconeogenesis	10/133	54/29008	3.97E-05	0.000495	0.000332
GO:0043331	BP	GO:0043331	response to dsRNA	11/133	65/29008	3.97E-05	0.000495	0.000332
GO:0046364	BP	GO:0046364	monosaccharide biosynthetic process	13/133	89/29008	4.11E-05	0.000512	0.000343
GO:0061458	BP	GO:0061458	reproductive system development	38/133	484/29008	4.13E-05	0.000513	0.000343
GO:0016579	BP	GO:0016579	protein deubiquitination	15/133	115/29008	4.25E-05	0.000526	0.000352
GO:0006352	BP	GO:0006352	DNA-templated transcription, initiation	14/133	102/29008	4.29E-05	0.000526	0.000352
GO:0048525	BP	GO:0048525	negative regulation of viral process	14/133	102/29008	4.29E-05	0.000526	0.000352
GO:0150115	BP	GO:0150115	cell-substrate junction organization	14/133	102/29008	4.29E-05	0.000526	0.000352
GO:2000060	BP	GO:2000060	positive regulation of ubiquitin-dependent protein catabolic process	14/133	102/29008	4.29E-05	0.000526	0.000352
GO:0030575	BP	GO:0030575	nuclear body organization	6/133	18/29008	4.34E-05	0.000527	0.000353
GO:0039535	BP	GO:0039535	regulation of RIG-I signaling pathway	6/133	18/29008	4.34E-05	0.000527	0.000353
GO:1900151	BP	GO:1900151	regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependen	6/133	18/29008	4.34E-05	0.000527	0.000353
GO:0070302	BP	GO:0070302	regulation of stress-activated protein kinase signaling cascade	21/133	201/29008	4.34E-05	0.000527	0.000353
GO:0032388	BP	GO:0032388	positive regulation of intracellular transport	20/133	186/29008	4.35E-05	0.000527	0.000353
GO:1903555	BP	GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	20/133	186/29008	4.35E-05	0.000527	0.000353
GO:0070482	BP	GO:0070482	response to oxygen levels	27/133	296/29008	4.37E-05	0.000528	0.000353
GO:0070665	BP	GO:0070665	positive regulation of leukocyte proliferation	18/133	157/29008	4.45E-05	0.000536	0.000359
GO:1901216	BP	GO:1901216	positive regulation of neuron death	16/133	129/29008	4.47E-05	0.000537	0.000360
GO:0050671	BP	GO:0050671	positive regulation of lymphocyte proliferation	17/133	143/29008	4.52E-05	0.000543	0.000363
GO:0071478	BP	GO:0071478	cellular response to radiation	19/133	172/29008	4.63E-05	0.000553	0.000370
GO:0033233	BP	GO:0033233	regulation of protein sumoylation	7/133	29/29008	4.66E-05	0.000553	0.000370
GO:0035020	BP	GO:0035020	regulation of Rac protein signal transduction	7/133	29/29008	4.66E-05	0.000553	0.000370
GO:0046685	BP	GO:0046685	response to arsenic-containing substance	7/133	29/29008	4.66E-05	0.000553	0.000370
GO:0050857	BP	GO:0050857	positive regulation of antigen receptor-mediated signaling pathway	7/133	29/29008	4.66E-05	0.000553	0.000370
GO:0030308	BP	GO:0030308	negative regulation of cell growth	21/133	202/29008	4.67E-05	0.000553	0.000370
GO:0900068	BP	GO:0900068	positive regulation of cell cycle process	24/133	249/29008	4.78E-05	0.000563	0.000377
GO:0006919	BP	GO:0006919	activation of cysteine-type endopeptidase activity involved in apoptotic process	12/133	78/29008	4.78E-05	0.000563	0.000377
GO:0002698	BP	GO:0002698	negative regulation of immune effector process	16/133	130/29008	4.92E-05	0.000578	0.000387
GO:0032640	BP	GO:0032640	tumor necrosis factor production	20/133	188/29008	5.07E-05	0.000594	0.000398
GO:0009637	BP	GO:0009637	apoptotic mitochondrial changes	15/133	117/29008	5.21E-05	0.000610	0.000408
GO:0045637	BP	GO:0045637	regulation of myeloid cell differentiation	22/133	219/29008	5.24E-05	0.000612	0.000410
GO:0002821	BP	GO:0002821	positive regulation of adaptive immune response	18/133	159/29008	5.26E-05	0.000613	0.000410
GO:0045727	BP	GO:0045727	positive regulation of translation	16/133	131/29008	5.4E-05	0.000627	0.000420
GO:0051091	BP	GO:0051091	positive regulation of DNA-binding transcription factor activity	25/133	267/29008	5.41E-05	0.000627	0.000420
GO:010594	BP	GO:010594	regulation of endothelial cell migration	19/133	174/29008	5.42E-05	0.000628	0.000421
GO:0006405	BP	GO:0006405	RNA export from nucleus	12/133	79/29008	5.44E-05	0.000629	0.000421
GO:0018023	BP	GO:0018023	peptidyl-lysine trimethylation	10/133	56/29008	5.51E-05	0.000635	0.000425
GO:0036490	BP	GO:0036490	regulation of translation in response to endoplasmic reticulum stress	5/133	12/29008	5.67E-05	0.000651	0.000436
GO:0097201	BP	GO:0097201	negative regulation of transcription from RNA polymerase II promoter in response to	5/133	12/29008	5.67E-05	0.000651	0.000436
GO:0043542	BP	GO:0043542	endothelial cell migration	22/133	221/29008	6.01E-05	0.000687	0.000460
GO:0048639	BP	GO:0048639	positive regulation of developmental growth	22/133	221/29008	6.01E-05	0.000687	0.000460
GO:0002289	BP	GO:0002289	nuclear-transcribed mRNA poly(A) tail shortening	7/133	27/29008	6.08E-05	0.000691	0.000462
GO:0000469	BP	GO:0000469	cleavage involved in rRNA processing	7/133	27/29008	6.08E-05	0.000691	0.000462
GO:0006376	BP	GO:0006376	mRNA splice site selection	7/133	27/29008	6.08E-05	0.000691	0.000462
GO:1900076	BP	GO:1900076	regulation of cellular response to insulin stimulus	12/133	80/29008	6.18E-05	0.000700	0.000469
GO:0071706	BP	GO:0071706	tumor necrosis factor superfamily cytokine production	20/133	191/29008	6.34E-05	0.000716	0.000480
GO:0032496	BP	GO:0032496	response to lipopolysaccharide	32/133	388/29008	6.5E-05	0.000732	0.000490
GO:1902903	BP	GO:1902903	regulation of supramolecular fiber organization	32/133	388/29008	6.5E-05	0.000732	0.000490
GO:0051146	BP	GO:0051146	striated muscle cell differentiation	28/133	320/29008	6.63E-05	0.000745	0.000499
GO:0006281	BP	GO:0006281	DNA repair	38/133	485/29008	6.65E-05	0.000746	0.000499
GO:0048638	BP	GO:0048638	regulation of developmental growth	33/133	406/29008	6.68E-05	0.000747	0.000500
GO:0007033	BP	GO:0007033	vacuole organization	19/133	177/29008	6.85E-05	0.000764	0.000512
GO:0900257	BP	GO:0900257	regulation of muscle system process	24/133	255/29008	6.97E-05	0.000776	0.000520
GO:0045927	BP	GO:0045927	positive regulation of growth	28/133	321/29008	7E-05	0.000778	0.000521
GO:0051099	BP	GO:0051099	positive regulation of binding	20/133	193/29008	7.33E-05	0.000814	0.000545
GO:0007369	BP	GO:0007369	gastrulation	19/133	178/29008	7.39E-05	0.000817	0.000547
GO:0109076	BP	GO:0109076	viral release from host cell	8/133	37/29008	7.43E-05	0.000817	0.000547
GO:0035990	BP	GO:0035990	exit from host	8/133	37/29008	7.43E-05	0.000817	0.000547
GO:0035991	BP	GO:0035991	exit from host cell	8/133	37/29008	7.43E-05	0.000817	0.000547
GO:0046606	BP	GO:0046606	reproductive structure development	37/133	480/29008	7.59E-05	0.000833	0.000558
GO:0009411	BP	GO:0009411	response to UV	17/133	149/29008	7.62E-05	0.000834	0.000559
GO:0002237	BP	GO:0002237	response to molecule of bacterial origin	33/133	409/29008	7.69E-05	0.000840	0.000562
GO:010631	BP	GO:010631	epithelial cell migration	27/133	306/29008	7.71E-05	0.000840	0.000562
GO:1901342	BP	GO:1901342	regulation of vasculature development	27/133	306/29008	7.71E-05	0.000840	0.000562
GO:0032469	BP	GO:0032469	endoplasmic reticulum calcium ion homeostasis	7/133	28/29008	7.84E-05	0.000852	0.000570
GO:0006006	BP	GO:0006006	glucose metabolic process	22/133	225/29008	7.85E-05	0.000852	0.000570
GO:0000082	BP	GO:0000082	G1/S transition of mitotic cell cycle	20/133	194/29008	7.88E-05	0.000853	0.000571
GO:0010632	BP	GO:0010632	regulation of epithelial cell migration	23/133	241/29008	7.92E-05	0.000855	0.000573
GO:2001244	BP	GO:2001244	positive regulation of intrinsic apoptotic signaling pathway	11/133	70/29008	8.04E-05	0.000867	0.000580
GO:0031667	BP	GO:0031667	response to nutrient levels	30/133	358/29008	8.16E-05	0.000878	0.000588
GO:0070997	BP	GO:0070997	neuron death	34/133	428/29008	8.18E-05	0.000878	0.000588
GO:0900132	BP	GO:0900132	epithelium migration	27/133	308/29008	8.6E-05	0.000922	0.000617
GO:0010656	BP	GO:0010656	negative regulation of muscle cell apoptotic process	10/133	59/29008	8.74E-05	0.000935	0.000626
GO:0006983	BP	GO:0006983	ER overload response	5/133	13/29008	8.92E-05	0.000950	0.000636
GO:000213	BP	GO:000213	positive regulation of nuclear-transcribed mRNA poly(A) tail shortening	5/133	13/29008	8.92E-05	0.000950	0.000636
GO:1902106	BP	GO:1902106	negative regulation of leukocyte differentiation	14/133	109/29008	8.98E-05	0.000955	0.000639
GO:0030010	BP	GO:0030010	establishment of cell polarity	17/133	151/29008	9E-05	0.000955	0.000640
GO:0051402	BP	GO:0051402	neuron apoptotic process	27/133	309/29008	9.08E-05	0.000960	0.000643
GO:0045622	BP	GO:0045622	regulation of T-helper cell differentiation	8/133	38/29008	9.09E-05	0.000960	0.000643
GO:0009408	BP	GO:0009408	response to heat	13/133	96/29008	9.18E-05	0.000965	0.000646
GO:1901222	BP	GO:1901222	regulation of NIK/NF-kappaB signaling	13/133	96/29008	9.18E-05	0.000965	0.000646
GO:0030888	BP	GO:0030888	regulation of B cell proliferation	11/133	71/29008	9.18E-05	0.000965	0.000646
GO:0070646	BP	GO:0070646	protein modification by small protein removal	16/133	137/29008	9.28E-05	0.000972	0.000651
GO:1903052	BP	GO:1903052	positive regulation of proteolysis involved in cellular protein catabolic process	15/133	123/29008	9.31E-05	0.000972	0.000651
GO:0010720	BP	GO:0010720	positive regulation of cell development	31/133	378/29008	9.31E-05	0.000972	0.000651
GO:0900130	BP	GO:0900130	tissue migration	27/133	310/29008	9.59E-05	0.000999	0.000699
GO:0006109	BP	GO:0006109	regulation of carbohydrate metabolic process	20/133	197/29008	9.75E-05	0.001013	0.000678
GO:0002824	BP	GO:0002824	positive regulation of adaptive immune response based on somatic recombination of	17/133	152/29008	9.78E-05	0.001013	0.000678
GO:0051092	BP	GO:0051092	positive regulation of NF-kappaB transcription factor activity	17/133	152/29008	9.78E-05	0.001013	0.000678
GO:0006275	BP	GO:0006275	regulation of DNA replication	14/133	110/29008	9.93E-05	0.001026	0.000687
GO:0032647	BP	GO:0032647	regulation of interferon-alpha production	7/133	29/29008	9.98E-05	0.001026	0.000689
GO:0009266	BP	GO:0009266	response to temperature stimulus	18/133	167/29008	9.99E-05	0.001029	0.000689
GO:0002274	BP	GO:0002274	myeloid leukocyte activation	24/133	261/29008	0.000100	0.001030	0.000690
GO:0051656	BP	GO:0051656	establishment of organelle localization	33/133	415/29008	0.000101	0.001041	0.000697
GO:0002286	BP	GO:0002286	T cell activation involved in immune response	15/133	124/29008	0.000102	0.001045	0.000700
GO:0042158	BP	GO:0042158	lipoprotein biosynthetic process	13/133	97/29008	0.000102	0.001045	0.000700
GO:0050767	BP	GO:0050767	regulation of neurogenesis	35/133	451/29008	0.000102	0.001045	0.000702
GO:0043124	BP	GO:0043124	negative regulation of I-kappaB kinase/NF-kappaB signaling	9/133	49/29008	0.000102	0.001048	0.000702
GO:1901989								

GO:0036473	BP	GO:0036473	cell death in response to oxidative stress	13/1133	101/29008	0.000155	0.001478	0.000990
GO:0042116	BP	GO:0042116	macrophage activation	13/1133	101/29008	0.000155	0.001478	0.000990
GO:0043502	BP	GO:0043502	regulation of muscle adaptation	13/1133	101/29008	0.000155	0.001478	0.000990
GO:0045185	BP	GO:0045185	maintenance of protein location	13/1133	101/29008	0.000155	0.001478	0.000990
GO:0050772	BP	GO:0050772	positive regulation of axonogenesis	13/1133	101/29008	0.000155	0.001478	0.000990
GO:0032607	BP	GO:0032607	interferon-alpha production	7/1133	31/29008	0.000157	0.001488	0.000997
GO:0032801	BP	GO:0032801	receptor catabolic process	7/1133	31/29008	0.000157	0.001488	0.000997
GO:0072539	BP	GO:0072539	T-helper 17 cell differentiation	7/1133	31/29008	0.000157	0.001488	0.000997
GO:0032436	BP	GO:0032436	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	12/1133	88/29008	0.000158	0.001496	0.001002
GO:0010613	BP	GO:0010613	positive regulation of cardiac muscle hypertrophy	8/1133	41/29008	0.000160	0.001510	0.001011
GO:0071216	BP	GO:0071216	cellular response to biotic stimulus	28/1133	337/29008	0.000160	0.001510	0.001011
GO:0001667	BP	GO:0001667	ameboid-type cell migration	34/1133	444/29008	0.000164	0.001552	0.001039
GO:0032715	BP	GO:0032715	negative regulation of interleukin-6 production	9/1133	52/29008	0.000165	0.001559	0.001044
GO:1904950	BP	GO:1904950	negative regulation of establishment of protein localization	16/1133	144/29008	0.000167	0.001569	0.001051
GO:0050900	BP	GO:0050900	leukocyte migration	30/1133	373/29008	0.000168	0.001578	0.001057
GO:0032103	BP	GO:0032103	positive regulation of response to external stimulus	33/1133	427/29008	0.000172	0.001613	0.001080
GO:0030316	BP	GO:0030316	osteoclast differentiation	14/1133	116/29008	0.000176	0.001640	0.001099
GO:0043534	BP	GO:0043534	blood vessel endothelial cell migration	14/1133	116/29008	0.000176	0.001640	0.001099
GO:0051346	BP	GO:0051346	negative regulation of hydrolase activity	30/1133	374/29008	0.000176	0.001642	0.001100
GO:0002456	BP	GO:0002456	T cell mediated immunity	16/1133	145/29008	0.000181	0.001683	0.001127
GO:0010906	BP	GO:0010906	regulation of glucose metabolic process	15/1133	131/29008	0.000189	0.001571	0.001177
GO:0014742	BP	GO:0014742	positive regulation of muscle hypertrophy	8/1133	42/29008	0.000191	0.001763	0.001181
GO:1900744	BP	GO:1900744	regulation of p38MAPK cascade	8/1133	42/29008	0.000191	0.001763	0.001181
GO:0006888	BP	GO:0006888	endoplasmic reticulum to Golgi vesicle-mediated transport	14/1133	117/29008	0.000193	0.001776	0.001189
GO:0014812	BP	GO:0014812	muscle cell migration	14/1133	117/29008	0.000193	0.001776	0.001189
GO:0014743	BP	GO:0014743	regulation of muscle hypertrophy	11/1133	77/29008	0.000193	0.001776	0.001189
GO:1901532	BP	GO:1901532	regulation of hematopoietic progenitor cell differentiation	7/1133	32/29008	0.000194	0.001776	0.001189
GO:1905898	BP	GO:1905898	positive regulation of response to endoplasmic reticulum stress	7/1133	32/29008	0.000194	0.001776	0.001189
GO:0033235	BP	GO:0033235	positive regulation of protein sumoylation	5/1133	15/29008	0.000194	0.001776	0.001189
GO:0060211	BP	GO:0060211	regulation of nuclear-transcribed mRNA poly(A) tail shortening	5/1133	15/29008	0.000194	0.001776	0.001189
GO:0019318	BP	GO:0019318	hexose metabolic process	23/1133	256/29008	0.000195	0.001776	0.001189
GO:1901992	BP	GO:1901992	positive regulation of mitotic cell cycle phase transition	12/1133	90/29008	0.000196	0.001785	0.001196
GO:0002366	BP	GO:0002366	leukocyte activation involved in immune response	27/1133	324/29008	0.000196	0.001798	0.001204
GO:0000413	BP	GO:0000413	protein peptidyl-prolyl isomerization	6/1133	23/29008	0.000199	0.001805	0.001209
GO:1900101	BP	GO:1900101	regulation of endoplasmic reticulum unfolded protein response	6/1133	23/29008	0.000199	0.001805	0.001209
GO:0032615	BP	GO:0032615	interleukin-12 production	10/1133	65/29008	0.000201	0.001819	0.001218
GO:0050727	BP	GO:0050727	regulation of inflammatory response	28/1133	342/29008	0.000204	0.001843	0.001234
GO:0007030	BP	GO:0007030	Golgi organization	15/1133	132/29008	0.000206	0.001857	0.001244
GO:0002700	BP	GO:0002700	regulation of production of molecular mediator of immune response	18/1133	177/29008	0.000208	0.001872	0.001254
GO:0003300	BP	GO:0003300	cardiac muscle hypertrophy	13/1133	104/29008	0.000208	0.001872	0.001254
GO:0044262	BP	GO:0044262	cellular carbohydrate metabolic process	25/1133	291/29008	0.000211	0.001892	0.001267
GO:0035303	BP	GO:0035303	regulation of dephosphorylation	15/1133	133/29008	0.000224	0.002005	0.001343
GO:0016925	BP	GO:0016925	protein sumoylation	8/1133	43/29008	0.000226	0.002019	0.001352
GO:0046636	BP	GO:0046636	negative regulation of alpha-beta T cell activation	8/1133	43/29008	0.000226	0.002019	0.001352
GO:0060761	BP	GO:0060761	negative regulation of response to cytokine stimulus	10/1133	66/29008	0.000229	0.002039	0.001366
GO:0006816	BP	GO:0006816	calcium ion transport	33/1133	434/29008	0.000232	0.002063	0.001382
GO:0032102	BP	GO:0032102	negative regulation of response to external stimulus	31/1133	398/29008	0.000233	0.002071	0.001387
GO:0043523	BP	GO:0043523	regulation of neuron apoptotic process	24/1133	276/29008	0.000234	0.002072	0.001388
GO:0048641	BP	GO:0048641	regulation of skeletal muscle tissue development	7/1133	33/29008	0.000238	0.002106	0.001410
GO:0016458	BP	GO:0016458	gene silencing	22/1133	243/29008	0.000238	0.002106	0.001410
GO:0002263	BP	GO:0002263	cell activation involved in immune response	27/1133	328/29008	0.000241	0.002125	0.001423
GO:0006497	BP	GO:0006497	protein lipidation	12/1133	92/29008	0.000242	0.002130	0.001426
GO:0000466	BP	GO:0000466	maturational of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LS	6/1133	24/29008	0.000257	0.002251	0.001507
GO:0016578	BP	GO:0016578	histone deubiquitination	6/1133	24/29008	0.000257	0.002251	0.001507
GO:0032727	BP	GO:0032727	positive regulation of interferon-alpha production	6/1133	24/29008	0.000257	0.002251	0.001507
GO:0045580	BP	GO:0045580	regulation of T cell differentiation	17/1133	165/29008	0.000265	0.002315	0.001551
GO:0032651	BP	GO:0032651	regulation of interleukin-1 beta production	12/1133	93/29008	0.000268	0.002361	0.001565
GO:0043535	BP	GO:0043535	regulation of blood vessel endothelial cell migration	12/1133	93/29008	0.000268	0.002361	0.001565
GO:0001771	BP	GO:0001771	immunological synapse formation	5/1133	16/29008	0.000274	0.002381	0.001595
GO:0042921	BP	GO:0042921	glucocorticoid receptor signaling pathway	5/1133	16/29008	0.000274	0.002381	0.001595
GO:0017015	BP	GO:0017015	regulation of transforming growth factor beta receptor signaling pathway	14/1133	121/29008	0.000275	0.002383	0.001596
GO:1901800	BP	GO:1901800	positive regulation of proteasomal protein catabolic process	13/1133	107/29008	0.000277	0.002401	0.001608
GO:0032675	BP	GO:0032675	regulation of interleukin-6 production	17/1133	166/29008	0.000284	0.002459	0.001647
GO:0010922	BP	GO:0010922	positive regulation of phosphatase activity	7/1133	34/29008	0.000290	0.002501	0.001675
GO:1901224	BP	GO:1901224	positive regulation of NIK/NF-kappaB signaling	10/1133	68/29008	0.000294	0.002534	0.001697
GO:1903321	BP	GO:1903321	negative regulation of protein modification by small protein conjugation or removal	12/1133	94/29008	0.000296	0.002551	0.001709
GO:0043405	BP	GO:0043405	regulation of MAP kinase activity	19/1133	198/29008	0.000298	0.002559	0.001714
GO:0051271	BP	GO:0051271	negative regulation of cellular component movement	26/1133	315/29008	0.000299	0.002559	0.001714
GO:0042177	BP	GO:0042177	negative regulation of protein catabolic process	14/1133	122/29008	0.000299	0.002559	0.001714
GO:0042542	BP	GO:0042542	response to hydrogen peroxide	14/1133	122/29008	0.000299	0.002559	0.001714
GO:0014897	BP	GO:0014897	striated muscle hypertrophy	13/1133	108/29008	0.000304	0.002594	0.001737
GO:0045913	BP	GO:0045913	positive regulation of carbohydrate metabolic process	11/1133	81/29008	0.000304	0.002594	0.001737
GO:0042129	BP	GO:0042129	regulation of T cell proliferation	18/1133	183/29008	0.000315	0.002677	0.001793
GO:0060212	BP	GO:0060212	regulation of small molecule metabolic process	29/1133	369/29008	0.000315	0.002677	0.001793
GO:0050860	BP	GO:0050860	negative regulation of T cell receptor signaling pathway	6/1133	25/29008	0.000327	0.002773	0.001857
GO:0010660	BP	GO:0010660	regulation of muscle cell apoptotic process	12/1133	95/29008	0.000328	0.002773	0.001857
GO:1903900	BP	GO:1903900	regulation of viral life cycle	16/1133	153/29008	0.000335	0.002835	0.001899
GO:0002064	BP	GO:0002064	epithelial cell development	23/1133	266/29008	0.000339	0.002857	0.001914
GO:0031648	BP	GO:0031648	protein destabilization	9/1133	57/29008	0.000340	0.002863	0.001917
GO:0043666	BP	GO:0043666	regulation of phosphoprotein phosphatase activity	9/1133	57/29008	0.000340	0.002863	0.001917
GO:1901991	BP	GO:1901991	negative regulation of mitotic cell cycle phase transition	17/1133	169/29008	0.000351	0.002951	0.001977
GO:1903844	BP	GO:1903844	regulation of cellular response to transforming growth factor beta stimulus	14/1133	124/29008	0.000351	0.002973	0.001991
GO:0033044	BP	GO:0033044	regulation of chromosome organization	18/1133	185/29008	0.000359	0.003003	0.002011
GO:0050770	BP	GO:0050770	regulation of axonogenesis	18/1133	185/29008	0.000359	0.003003	0.002011
GO:0034502	BP	GO:0034502	protein localization to chromosome	12/1133	96/29008	0.000361	0.003015	0.002019
GO:0031341	BP	GO:0031341	regulation of cell killing	15/1133	139/29008	0.000363	0.003024	0.002025
GO:0014896	BP	GO:0014896	muscle hypertrophy	13/1133	110/29008	0.000365	0.003028	0.002028
GO:0032780	BP	GO:0032780	positive regulation of tumor necrosis factor production	13/1133	110/29008	0.000365	0.003028	0.002028
GO:0010907	BP	GO:0010907	positive regulation of glucose metabolic process	8/1133	46/29008	0.000367	0.003037	0.002034
GO:0030890	BP	GO:0030890	positive regulation of B cell proliferation	8/1133	46/29008	0.000367	0.003037	0.002034
GO:0045005	BP	GO:0045005	DNA-dependent DNA replication maintenance of fidelity	8/1133	46/29008	0.000367	0.003037	0.002034
GO:2000514	BP	GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	10/1133	70/29008	0.000374	0.003070	0.002056
GO:0031958	BP	GO:0031958	corticosteroid receptor signaling pathway	5/1133	17/29008	0.000376	0.003070	0.002056
GO:0032986	BP	GO:0032986	protein-DNA complex disassembly	5/1133	17/29008	0.000376	0.003070	0.002056
GO:0070262	BP	GO:0070262	peptidyl-serine dephosphorylation	5/1133	17/29008	0.000376	0.003070	0.002056
GO:0071243	BP	GO:0071243	cellular response to arsenic-containing substance	5/1133	17/29008	0.000376	0.003070	0.002056
GO:0071498	BP	GO:0071498	cellular response to fluid shear stress	5/1133	17/29008	0.000376	0.003070	0.002056
GO:1902916	BP	GO:1902916	positive regulation of protein polyubiquitination	5/1133	17/29008	0.000376	0.003070	0.002056
GO:0002244	BP	GO:0002244	hematopoietic progenitor cell differentiation	17/1133	170/29008	0.000377	0.003070	0.002056
GO:0007254	BP	GO:0007254	JNK cascade	17/1133	170/29008	0.000377	0.003070	0.002056
GO:0008154	BP	GO:0008154	actin polymerization or depolymerization	20/1133	218/29008	0.000378	0.003070	0.002060
GO:0007059	BP	GO:0007059	chromosome segregation	27/1133	338/29008	0.000388	0.003151	0.002112
GO:0006754	BP	GO:0006754	ATP biosynthetic process	9/1133	58/29008	0.000398	0.003153	0.002112
GO:0045058	BP	GO:0045058	T cell selection	9/1133	58/29008	0.000398	0.003153	0.002112
GO:0034614	BP	GO:0034614	cellular response to reactive oxygen species	15/1133	140/29008	0.000392	0.003167	0.002121
GO:0071987	BP	GO:0071987	leukocyte apoptotic process	15/1133	140/29008	0.000392	0.003167	0.002121
GO:0002718	BP	GO:0002718	regulation of cytokine production involved in immune response	12/1133	97/29008	0.000396	0.003210	0.002150
GO:1900246	BP	GO:1900246	positive regulation of RIG-I signaling pathway	4/1133	10/29008	0.000402	0.003231	0.00216

GO:200045	BP	GO:200045	regulation of G1/S transition of mitotic cell cycle	14/133	128/29008	0.000491	0.003772	0.002526
GO:001890	BP	GO:001890	placenta development	17/133	174/29008	0.000493	0.003778	0.002531
GO:002635	BP	GO:002635	interleukin-6 production	17/133	174/29008	0.000493	0.003778	0.002531
GO:005085	BP	GO:005085	regulation of B cell receptor signaling pathway	5/133	18/29008	0.000504	0.003837	0.002570
GO:190037	BP	GO:190037	regulation of cellular response to hypoxia	5/133	18/29008	0.000504	0.003837	0.002570
GO:1902176	BP	GO:1902176	negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	5/133	18/29008	0.000504	0.003837	0.002570
GO:2000319	BP	GO:2000319	regulation of T-helper 17 cell differentiation	5/133	18/29008	0.000504	0.003837	0.002570
GO:002685	BP	GO:002685	regulation of leukocyte migration	20/133	223/29008	0.000506	0.003847	0.002577
GO:007064	BP	GO:007064	mitotic sister chromatid cohesion	6/133	27/29008	0.000512	0.003868	0.002591
GO:0032781	BP	GO:0032781	positive regulation of ATPase activity	6/133	27/29008	0.000512	0.003868	0.002591
GO:040033	BP	GO:040033	negative regulation of translation, ncRNA-mediated	6/133	27/29008	0.000512	0.003868	0.002591
GO:044974	BP	GO:044974	regulation of translation, ncRNA-mediated	6/133	27/29008	0.000512	0.003868	0.002591
GO:010657	BP	GO:010657	muscle cell apoptotic process	12/133	100/29008	0.000527	0.003977	0.002604
GO:0033209	BP	GO:0033209	tumor necrosis factor-mediated signaling pathway	10/133	73/29008	0.000528	0.003977	0.002604
GO:0030336	BP	GO:0030336	negative regulation of cell migration	24/133	293/29008	0.000559	0.004199	0.002812
GO:0051258	BP	GO:0051258	protein polymerization	24/133	293/29008	0.000559	0.004199	0.002812
GO:002832	BP	GO:002832	negative regulation of response to biotic stimulus	13/133	115/29008	0.000562	0.004213	0.002822
GO:0050764	BP	GO:0050764	regulation of phagocytosis	13/133	115/29008	0.000562	0.004213	0.002822
GO:0060324	BP	GO:0060324	face development	9/133	61/29008	0.000571	0.004270	0.002860
GO:010332	BP	GO:010332	response to gamma radiation	8/133	49/29008	0.000573	0.004270	0.002860
GO:0032873	BP	GO:0032873	negative regulation of stress-activated MAPK cascade	8/133	49/29008	0.000573	0.004270	0.002860
GO:0070303	BP	GO:0070303	negative regulation of stress-activated protein kinase signaling cascade	8/133	49/29008	0.000573	0.004270	0.002860
GO:010506	BP	GO:010506	regulation of autophagy	22/133	259/29008	0.000574	0.004273	0.002862
GO:016441	BP	GO:016441	posttranscriptional gene silencing	16/133	161/29008	0.000592	0.004401	0.002948
GO:2001144	BP	GO:2001144	positive regulation of DNA-templated transcription, initiation	7/133	38/29008	0.000594	0.004407	0.002952
GO:045444	BP	GO:045444	fat cell differentiation	22/133	260/29008	0.000605	0.004481	0.003001
GO:0071888	BP	GO:0071888	macrophage apoptotic process	4/133	11/29008	0.000612	0.004532	0.003036
GO:1903828	BP	GO:1903828	negative regulation of cellular protein localization	14/133	131/29008	0.000621	0.004588	0.003073
GO:016577	BP	GO:016577	histone demethylation	6/133	28/29008	0.000630	0.004636	0.003105
GO:0070076	BP	GO:0070076	histone lysine demethylation	6/133	28/29008	0.000630	0.004636	0.003105
GO:1902175	BP	GO:1902175	regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	6/133	28/29008	0.000630	0.004636	0.003105
GO:0011704	BP	GO:0011704	formation of primary germ layer	12/133	102/29008	0.000632	0.004636	0.003105
GO:006476	BP	GO:006476	protein deacetylation	12/133	102/29008	0.000632	0.004636	0.003105
GO:043112	BP	GO:043112	receptor metabolic process	18/133	194/29008	0.000635	0.004653	0.003118
GO:0001960	BP	GO:0001960	negative regulation of cytokine-mediated signaling pathway	9/133	62/29008	0.000645	0.004723	0.003163
GO:007492	BP	GO:007492	endoderm development	10/133	75/29008	0.000656	0.004791	0.003209
GO:1901796	BP	GO:1901796	regulation of signal transduction by p53 class mediator	10/133	75/29008	0.000656	0.004791	0.003209
GO:002753	BP	GO:002753	cytoplasmic pattern recognition receptor signaling pathway	8/133	50/29008	0.000659	0.004801	0.003216
GO:0007039	BP	GO:0007039	protein catabolic process in the vacuole	5/133	19/29008	0.000662	0.004801	0.003216
GO:0051571	BP	GO:0051571	positive regulation of histone H3-K4 methylation	5/133	19/29008	0.000662	0.004801	0.003216
GO:0071786	BP	GO:0071786	endoplasmic reticulum tubular network organization	5/133	19/29008	0.000662	0.004801	0.003216
GO:140467	BP	GO:140467	integrated stress response signaling	5/133	19/29008	0.000662	0.004801	0.003216
GO:042100	BP	GO:042100	B cell proliferation	13/133	117/29008	0.000663	0.004801	0.003216
GO:0007178	BP	GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	29/133	387/29008	0.000681	0.004921	0.003296
GO:0034644	BP	GO:0034644	cellular response to UV	11/133	89/29008	0.000692	0.004990	0.003342
GO:010959	BP	GO:010959	regulation of metal ion transport	32/133	443/29008	0.000692	0.004990	0.003342
GO:0001706	BP	GO:0001706	endoderm formation	7/133	39/29008	0.000700	0.005017	0.003360
GO:0001782	BP	GO:0001782	B cell homeostasis	7/133	39/29008	0.000700	0.005017	0.003360
GO:018208	BP	GO:018208	peptidyl-proline modification	7/133	39/29008	0.000700	0.005017	0.003360
GO:0031297	BP	GO:0031297	replication fork processing	7/133	39/29008	0.000700	0.005017	0.003360
GO:0030312	BP	GO:0030312	muscle system process	31/133	425/29008	0.000710	0.005083	0.003404
GO:0003158	BP	GO:0003158	endothelium development	14/133	133/29008	0.000723	0.005167	0.003461
GO:0010675	BP	GO:0010675	regulation of cellular carbohydrate metabolic process	16/133	164/29008	0.000724	0.005174	0.003466
GO:0030865	BP	GO:0030865	cortical cytoskeleton organization	9/133	63/29008	0.000727	0.005180	0.003469
GO:043966	BP	GO:043966	histone H3 acetylation	9/133	63/29008	0.000727	0.005180	0.003469
GO:0002704	BP	GO:0002704	negative regulation of leukocyte mediated immunity	10/133	76/29008	0.000730	0.005185	0.003473
GO:2000573	BP	GO:2000573	positive regulation of DNA biosynthetic process	10/133	76/29008	0.000730	0.005185	0.003473
GO:044930	BP	GO:044930	negative regulation of mitotic cell cycle	20/133	231/29008	0.000789	0.005598	0.003750
GO:0442593	BP	GO:0442593	glucose homeostasis	23/133	283/29008	0.000802	0.005679	0.003804
GO:0051147	BP	GO:0051147	regulation of muscle cell differentiation	15/133	150/29008	0.000813	0.005742	0.003846
GO:1902806	BP	GO:1902806	regulation of cell cycle G1/S phase transition	15/133	150/29008	0.000813	0.005742	0.003846
GO:0051893	BP	GO:0051893	regulation of focal adhesion assembly	9/133	64/29008	0.000817	0.005758	0.003857
GO:0090109	BP	GO:0090109	regulation of cell-substrate junction assembly	9/133	64/29008	0.000817	0.005758	0.003857
GO:0033144	BP	GO:0033144	negative regulation of intracellular steroid hormone receptor signaling pathway	7/133	40/29008	0.000820	0.005758	0.003857
GO:0090224	BP	GO:0090224	regulation of spindle organization	7/133	40/29008	0.000820	0.005758	0.003857
GO:1902749	BP	GO:1902749	regulation of cell cycle G2/M phase transition	12/133	105/29008	0.000820	0.005758	0.003857
GO:0033135	BP	GO:0033135	regulation of peptidyl-serine phosphorylation	16/133	166/29008	0.000828	0.005790	0.003878
GO:1903578	BP	GO:1903578	regulation of ATP metabolic process	11/133	91/29008	0.000835	0.005848	0.003917
GO:0032609	BP	GO:0032609	interferon-gamma production	14/133	135/29008	0.000838	0.005856	0.003924
GO:0033500	BP	GO:0033500	carbohydrate homeostasis	23/133	284/29008	0.000841	0.005871	0.003932
GO:0001776	BP	GO:0001776	leukocyte homeostasis	13/133	120/29008	0.000843	0.005880	0.003938
GO:0002643	BP	GO:0002643	regulation of tolerance induction	5/133	20/29008	0.000855	0.005907	0.003956
GO:0003159	BP	GO:0003159	morphogenesis of an endothelium	5/133	20/29008	0.000855	0.005907	0.003956
GO:0032695	BP	GO:0032695	negative regulation of interleukin-12 production	5/133	20/29008	0.000855	0.005907	0.003956
GO:0033962	BP	GO:0033962	P-body assembly	5/133	20/29008	0.000855	0.005907	0.003956
GO:0445623	BP	GO:0445623	negative regulation of T-helper cell differentiation	5/133	20/29008	0.000855	0.005907	0.003956
GO:0445722	BP	GO:0445722	positive regulation of gluconeogenesis	5/133	20/29008	0.000855	0.005907	0.003956
GO:0061154	BP	GO:0061154	endothelial tube morphogenesis	5/133	20/29008	0.000855	0.005907	0.003956
GO:0060203	BP	GO:0060203	aminoglycan biosynthetic process	8/133	52/29008	0.000862	0.005936	0.003976
GO:0445581	BP	GO:0445581	negative regulation of T cell differentiation	8/133	52/29008	0.000862	0.005936	0.003976
GO:2000059	BP	GO:2000059	negative regulation of ubiquitin-dependent protein catabolic process	8/133	52/29008	0.000862	0.005936	0.003976
GO:016055	BP	GO:016055	Wnt signaling pathway	32/133	449/29008	0.000866	0.005951	0.003986
GO:0007051	BP	GO:0007051	spindle organization	17/133	183/29008	0.000875	0.006004	0.004022
GO:0061418	BP	GO:0061418	regulation of transcription from RNA polymerase II promoter in response to hypoxia	4/133	12/29008	0.000890	0.006106	0.004089
GO:016575	BP	GO:016575	histone deacetylation	10/133	78/29008	0.000897	0.006135	0.004109
GO:0071277	BP	GO:0071277	cellular response to calcium ion	10/133	78/29008	0.000897	0.006135	0.004109
GO:010821	BP	GO:010821	regulation of mitochondrial organization	14/133	136/29008	0.000901	0.006156	0.004123
GO:006611	BP	GO:006611	protein export from nucleus	9/133	65/29008	0.000916	0.006250	0.004186
GO:0051924	BP	GO:0051924	regulation of calcium ion transport	23/133	286/29008	0.000924	0.006291	0.004214
GO:0032271	BP	GO:0032271	regulation of protein polymerization	20/133	234/29008	0.000926	0.006291	0.004214
GO:0000470	BP	GO:0000470	maturation of LSU-rRNA	6/133	30/29008	0.000929	0.006291	0.004214
GO:1902751	BP	GO:1902751	positive regulation of cell cycle G2/M phase transition	6/133	30/29008	0.000929	0.006291	0.004214
GO:1902914	BP	GO:1902914	regulation of protein polyubiquitination	6/133	30/29008	0.000929	0.006291	0.004214
GO:0448659	BP	GO:0448659	smooth muscle cell proliferation	17/133	184/29008	0.000929	0.006291	0.004214
GO:198738	BP	GO:198738	cell-cell signaling by wnt	32/133	451/29008	0.000931	0.006297	0.004216
GO:043368	BP	GO:043368	positive T cell selection	7/133	41/29008	0.000936	0.006445	0.004317
GO:044627	BP	GO:044627	negative regulation of insulin receptor signaling pathway	7/133	41/29008	0.000936	0.006445	0.004317
GO:006874	BP	GO:006874	cellular calcium ion homeostasis	34/133	490/29008	0.000964	0.006494	0.004350
GO:0033555	BP	GO:0033555	multicellular organismal response to stress	12/133	107/29008	0.000971	0.006528	0.004373
GO:0440013	BP	GO:0440013	negative regulation of locomotion	26/133	341/29008	0.000979	0.006577	0.004405
GO:0443370	BP	GO:0443370	regulation of CD4-positive, alpha-beta T cell differentiation	8/133	53/29008	0.000982	0.006585	0.004411
GO:2000146	BP	GO:2000146	negative regulation of cell motility	24/133	306/29008	0.001025	0.006858	0.004594
GO:1903051	BP	GO:1903051	negative regulation of proteolysis involved in cellular protein catabolic process	9/133	66/29008	0.001025	0.006858	0.004594
GO:0002285	BP	GO:0002285	lymphocyte activation involved in immune response	19/133	219/29008	0.001029	0.006876	0.004605
GO:0009749	BP	GO:0009749	response to glucose	17/133	186/29008	0.001048	0.006944	0.004685
GO:0007006	BP	GO:0007006	mitochondrial membrane organization	12/133	108/29008	0.001054	0.007071	0.004700
GO:0071901	BP	GO:0071901	negative regulation of protein serine/threonine kinase activity	12/133	108/29008	0.001054	0.007071	0.004700
GO:0051251	BP	GO:0051251	positive regulation of lymphocyte activation	31/133	436/29008	0.001074	0.007140	0.004782
GO:0446777	BP	GO:0446777	protein autophosphorylation	20/133	237/29008	0.001083	0.007198	0.004809

GO:0032608	BP	GO:0032608	interferon-beta production	9/1133	68/29008	0.0012731	0.008131	0.0054468
GO:0032648	BP	GO:0032648	regulation of interferon-beta production	9/1133	68/29008	0.0012731	0.008131	0.0054468
GO:0001824	BP	GO:0001824	blastocyst development	15/1133	157/29008	0.0012951	0.008241	0.005520
GO:0008360	BP	GO:0008360	regulation of cell shape	15/1133	157/29008	0.0012951	0.008241	0.005520
GO:0071322	BP	GO:0071322	cellular response to carbohydrate stimulus	15/1133	157/29008	0.0012951	0.008241	0.005520
GO:0070444	BP	GO:0070444	cell-substrate junction assembly	11/1133	96/29008	0.0013051	0.008297	0.0055571
GO:0034284	BP	GO:0034284	response to monosaccharide	17/1133	190/29008	0.0013231	0.008366	0.005604
GO:0002260	BP	GO:0002260	lymphocyte homeostasis	10/1133	82/29008	0.0013261	0.008366	0.005604
GO:0072332	BP	GO:0072332	intrinsic apoptotic signaling pathway by p53 class mediator	10/1133	82/29008	0.0013261	0.008366	0.005604
GO:0006482	BP	GO:0006482	protein demethylation	6/1133	32/29008	0.0013271	0.008366	0.005604
GO:0008214	BP	GO:0008214	protein dealkylation	6/1133	32/29008	0.0013271	0.008366	0.005604
GO:0022037	BP	GO:0022037	metencephalon development	13/1133	126/29008	0.0013271	0.008366	0.005604
GO:0043123	BP	GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	13/1133	126/29008	0.0013271	0.008366	0.005604
GO:0003236	BP	GO:0003236	cell chemotaxis	24/1133	312/29008	0.0013341	0.008401	0.005627
GO:0002367	BP	GO:0002367	cytokine production involved in immune response	12/1133	111/29008	0.001340	0.008417	0.005638
GO:0071482	BP	GO:0071482	cellular response to light stimulus	12/1133	111/29008	0.001340	0.008417	0.005638
GO:0007035	BP	GO:0007035	vacuolar acidification	5/1133	22/29008	0.001361	0.008538	0.005719
GO:0006261	BP	GO:0006261	DNA-dependent DNA replication	14/1133	142/29008	0.001372	0.008585	0.005750
GO:0048675	BP	GO:0048675	axon extension	14/1133	142/29008	0.001372	0.008585	0.005750
GO:0016482	BP	GO:0016482	cytosolic transport	15/1133	158/29008	0.001381	0.008630	0.005780
GO:0030041	BP	GO:0030041	actin filament polymerization	17/1133	191/29008	0.001401	0.008748	0.005859
GO:0002706	BP	GO:0002706	regulation of lymphocyte mediated immunity	19/1133	225/29008	0.001413	0.008800	0.005894
GO:0009206	BP	GO:0009206	purine ribonucleoside triphosphate biosynthetic process	9/1133	69/29008	0.001414	0.008800	0.005894
GO:0032507	BP	GO:0032507	maintenance of protein location in cell	9/1133	69/29008	0.001414	0.008800	0.005894
GO:0002209	BP	GO:0002209	behavioral defense response	8/1133	56/29008	0.001420	0.008801	0.005895
GO:0034340	BP	GO:0034340	response to type I interferon	8/1133	56/29008	0.001420	0.008801	0.005895
GO:1901861	BP	GO:1901861	regulation of muscle tissue development	8/1133	56/29008	0.001420	0.008801	0.005895
GO:0010389	BP	GO:0010389	regulation of G2/M transition of mitotic cell cycle	11/1133	97/29008	0.001421	0.008803	0.005896
GO:0001906	BP	GO:0001906	cell killing	21/1133	260/29008	0.001430	0.008843	0.005923
GO:140014	BP	GO:140014	mitotic nuclear division	22/1133	278/29008	0.001450	0.008960	0.006011
GO:0031397	BP	GO:0031397	negative regulation of protein ubiquitination	10/1133	83/29008	0.001456	0.008986	0.006019
GO:0003048	BP	GO:0003048	bone development	20/1133	243/29008	0.001465	0.009030	0.006048
GO:0046328	BP	GO:0046328	regulation of JNK cascade	14/1133	143/29008	0.001467	0.009033	0.006051
GO:0030219	BP	GO:0030219	megakaryocyte differentiation	7/1133	44/29008	0.001472	0.009042	0.006056
GO:0072599	BP	GO:0072599	establishment of protein localization to endoplasmic reticulum	7/1133	44/29008	0.001472	0.009042	0.006056
GO:0010810	BP	GO:0010810	regulation of cell-substrate adhesion	19/1133	226/29008	0.001488	0.009119	0.006108
GO:0030595	BP	GO:0030595	leukocyte chemotaxis	19/1133	226/29008	0.001488	0.009119	0.006108
GO:0110053	BP	GO:0110053	regulation of actin filament organization	22/1133	279/29008	0.001518	0.009292	0.006224
GO:0001952	BP	GO:0001952	regulation of cell-matrix adhesion	13/1133	128/29008	0.001533	0.009372	0.006277
GO:0030516	BP	GO:0030516	regulation of axon extension	12/1133	113/29008	0.001565	0.009531	0.006384
GO:0009145	BP	GO:0009145	purine nucleoside triphosphate biosynthetic process	9/1133	70/29008	0.001568	0.009531	0.006384
GO:0090316	BP	GO:0090316	positive regulation of intracellular protein transport	14/1133	144/29008	0.001568	0.009531	0.006384
GO:0032786	BP	GO:0032786	positive regulation of DNA-templated transcription, elongation	6/1133	33/29008	0.001568	0.009531	0.006384
GO:0150117	BP	GO:0150117	positive regulation of cell-substrate junction organization	6/1133	33/29008	0.001568	0.009531	0.006384
GO:0007568	BP	GO:0007568	aging	21/1133	262/29008	0.001571	0.009531	0.006384
GO:0032886	BP	GO:0032886	regulation of microtubule-based process	21/1133	262/29008	0.001571	0.009531	0.006384
GO:0050769	BP	GO:0050769	positive regulation of neurogenesis	23/1133	298/29008	0.001591	0.009642	0.006458
GO:0031529	BP	GO:0031529	ruffle organization	8/1133	57/29008	0.001596	0.009648	0.006482
GO:0006809	BP	GO:0006809	nitric oxide biosynthetic process	10/1133	84/29008	0.001596	0.009648	0.006482
GO:0042157	BP	GO:0042157	lipoprotein metabolic process	13/1133	129/29008	0.001645	0.009923	0.006653
GO:0030111	BP	GO:0030111	regulation of Wnt signaling pathway	24/1133	317/29008	0.001651	0.009945	0.006682
GO:0051222	BP	GO:0051222	positive regulation of protein transport	24/1133	317/29008	0.001651	0.009945	0.006682
GO:0022626	CC	GO:0022626	cytosolic ribosome	46/1136	114/28886	1.34E-34	8.24E-32	5.16E-32
GO:0005840	CC	GO:0005840	ribosome	57/1136	239/28886	1.36E-28	6.82E-26	2.27E-26
GO:0044391	CC	GO:0044391	ribosomal subunit	52/1136	197/28886	1.77E-28	6.82E-26	2.27E-26
GO:0022627	CC	GO:0022627	cytosolic small ribosomal subunit	23/1136	47/28886	2.51E-20	3.86E-18	2.42E-18
GO:0015935	CC	GO:0015935	small ribosomal subunit	28/1136	80/28886	1.33E-19	1.63E-17	1.02E-17
GO:0022625	CC	GO:0022625	cytosolic large ribosomal subunit	24/1136	63/28886	5.34E-18	5.47E-16	3.43E-16
GO:0005844	CC	GO:0005844	polysome	24/1136	77/28886	1.1E-15	9.68E-14	6.06E-14
GO:0016607	CC	GO:0016607	nuclear speck	50/1136	343/28886	1.34E-15	1.02E-13	6.47E-14
GO:0035770	CC	GO:0035770	ribonucleoprotein granule	40/1136	250/28886	4.2E-14	2.87E-12	1.8E-12
GO:0042788	CC	GO:0042788	polysomal ribosome	16/1136	35/28886	9.92E-14	3.64E-12	2.28E-12
GO:0036464	CC	GO:0036464	cytoplasmic ribonucleoprotein granule	38/1136	232/28886	8.48E-14	4.74E-12	2.97E-12
GO:0015934	CC	GO:0015934	large ribosomal subunit	27/1136	122/28886	2.06E-13	1.06E-11	6.61E-12
GO:0005635	CC	GO:0005635	nuclear envelope	49/1136	423/28886	1.66E-11	7.86E-10	4.92E-10
GO:0031248	CC	GO:0031248	protein acetyltransferase complex	20/1136	90/28886	2.47E-10	1.01E-08	6.35E-09
GO:1902493	CC	GO:1902493	acetyltransferase complex	20/1136	90/28886	2.47E-10	1.01E-08	6.35E-09
GO:0043209	CC	GO:0043209	myelin sheath	30/1136	215/28886	1.88E-09	7.23E-08	4.53E-08
GO:0005667	CC	GO:0005667	transcription regulator complex	48/1136	475/28886	2.76E-09	9.99E-08	6.26E-08
GO:0010494	CC	GO:0010494	cytoplasmic stress granule	17/1136	74/28886	3.16E-09	1.08E-07	6.76E-08
GO:0005774	CC	GO:0005774	vacuolar membrane	30/1136	228/28886	7.61E-09	2.46E-07	1.54E-07
GO:0034399	CC	GO:0034399	nuclear periphery	20/1136	115/28886	2.22E-08	6.83E-07	4.28E-07
GO:0031965	CC	GO:0031965	nuclear membrane	30/1136	241/28886	2.76E-08	8.07E-07	5.06E-07
GO:0016605	CC	GO:0016605	PML body	16/1136	76/28886	3.46E-08	9.68E-07	6.06E-07
GO:0030139	CC	GO:0030139	endocytic vesicle	27/1136	205/28886	4.14E-08	1.11E-06	6.93E-07
GO:0031300	CC	GO:0031300	intrinsic component of organelle membrane	37/1136	366/28886	1.77E-07	4.54E-06	2.84E-06
GO:0061695	CC	GO:0061695	transferase complex, transferring phosphorus-containing groups	28/1136	242/28886	3.68E-07	8.81E-06	5.52E-06
GO:0031301	CC	GO:0031301	integral component of organelle membrane	35/1136	346/28886	3.72E-07	8.81E-06	5.52E-06
GO:0005776	CC	GO:0005776	autophagosome	14/1136	75/28886	1.17E-06	2.86E-05	1.66E-05
GO:0031414	CC	GO:0031414	N-terminal protein acetyltransferase complex	6/1136	11/28886	1.42E-06	3.13E-05	1.96E-05
GO:0016363	CC	GO:0016363	nuclear matrix	15/1136	89/28886	1.89E-06	4.02E-05	2.52E-05
GO:0045335	CC	GO:0045335	phagocytic vesicle	17/1136	113/28886	2.06E-06	4.22E-05	2.64E-05
GO:0005681	CC	GO:0005681	spliceosomal complex	24/1136	206/28886	2.18E-06	4.3E-05	2.69E-05
GO:0000123	CC	GO:0000123	histone acetyltransferase complex	14/1136	79/28886	2.23E-06	4.3E-05	2.69E-05
GO:0098562	CC	GO:0098562	cytoplasmic side of membrane	23/1136	194/28886	2.61E-06	4.86E-05	3.05E-05
GO:0001650	CC	GO:0001650	fibrillar center	19/1136	142/28886	3.21E-06	5.8E-05	3.63E-05
GO:0000932	CC	GO:0000932	P-body	14/1136	83/28886	4.1E-06	7.21E-05	4.52E-05
GO:0005684	CC	GO:0005684	U2-type spliceosomal complex	15/1136	95/28886	4.4E-06	7.51E-05	4.7E-05
GO:0008023	CC	GO:0008023	transcription elongation factor complex	11/1136	53/28886	5.54E-06	9.21E-05	5.77E-05
GO:0070603	CC	GO:0070603	SWI/SNF superfamily-type complex	13/1136	75/28886	6.6E-06	0.0001061	6.69E-05
GO:1904949	CC	GO:1904949	ATPase complex	13/1136	76/28886	7.68E-06	0.000121	7.59E-05
GO:0019866	CC	GO:0019866	organelle inner membrane	41/1136	500/28886	8.81E-06	0.000135	8.49E-05
GO:0034708	CC	GO:0034708	methyltransferase complex	15/1136	101/28886	9.51E-06	0.000141	8.88E-05
GO:0001726	CC	GO:0001726	ruffle	19/1136	153/28886	9.68E-06	0.000141	8.88E-05
GO:0032279	CC	GO:0032279	asymmetric synapse	31/1136	337/28886	1.19E-05	0.000164	0.000102
GO:0016234	CC	GO:0016234	inclusion body	13/1136	79/28886	1.19E-05	0.000164	0.000102
GO:0005769	CC	GO:0005769	early endosome	30/1136	321/28886	1.2E-05	0.000164	0.000102
GO:0030684	CC	GO:0030684	prebosome	13/1136	80/28886	1.37E-05	0.000183	0.000114
GO:0140534	CC	GO:0140534	endoplasmic reticulum protein-containing complex	17/1136	130/28886	1.42E-05	0.000185	0.000116
GO:0090575	CC	GO:0090575	RNA polymerase II transcription regulator complex	20/1136	172/28886	1.54E-05	0.000196	0.000123
GO:0014069	CC	GO:0014069	postsynaptic density	30/1136	328/28886	1.82E-05	0.000228	0.000143
GO:0071013	CC	GO:0071013	catalytic step 2 spliceosome	14/1136	95/28886	2.05E-05	0.000251	0.000157
GO:0000139	CC	GO:0000139	Golgi membrane	26/1136	267/28886	2.21E-05	0.000267	0.000167
GO:0009898	CC	GO:0009898	cytoplasmic side of plasma membrane	20/1136	177/28886	2.34E-05	0.000273	0.000171
GO:1902554	CC	GO:1902554	serine/threonine protein kinase complex	13/1136	84/28886	2.35E-05	0.000273	0.000171
GO:0098572	CC	GO:0098572	postsynaptic specialization	31/1136	351/28886	2.63E-05	0.000299	0.000187
GO:0016514	CC	GO:0016514	SWI/SNF complex	6/1136	17/28886	3.11E-05	0.000347	0.000217
GO:0005770	CC	GO:0005770	late endosome	24/1136	242/28886	3.36E-05	0.000369	0.000231
GO:0030496	CC							

GO:0000791	CC	GO:0000791	euchromatin	8/1136	46/28886	0.0003851	0.0026841	0.0016811
GO:0005767	CC	GO:0005767	secondary lysosome	5/1136	17/28886	0.0003889	0.0026841	0.0016811
GO:0005801	CC	GO:0005801	cis-Golgi network	10/1136	73/28886	0.0005561	0.0030651	0.0023841
GO:0008287	CC	GO:0008287	protein serine/threonine phosphatase complex	8/1136	49/28886	0.0005999	0.0040096	0.0025111
GO:1902293	CC	GO:1902293	phosphatase complex	8/1136	49/28886	0.0005999	0.0040096	0.0025111
GO:0042611	CC	GO:0042611	MHC protein complex	7/1136	38/28886	0.0006181	0.0040921	0.0025631
GO:0072686	CC	GO:0072686	mitotic spindle	16/1136	161/28886	0.0006371	0.0041711	0.0026131
GO:1905368	CC	GO:1905368	peptidase complex	12/1136	102/28886	0.0006711	0.0043341	0.0027151
GO:0032045	CC	GO:0032045	guanyl-nucleotide exchange factor complex	5/1136	19/28886	0.0006831	0.0043341	0.0027151
GO:1902773	CC	GO:1902773	GTPase activator complex	5/1136	19/28886	0.0006831	0.0043341	0.0027151
GO:0032993	CC	GO:0032993	protein-DNA complex	16/1136	163/28886	0.0007291	0.0045771	0.0028671
GO:0005759	CC	GO:0005759	mitochondrial matrix	23/1136	280/28886	0.0007601	0.0047231	0.0029591
GO:0033106	CC	GO:0033106	cis-Golgi network membrane	6/1136	29/28886	0.0007791	0.0049001	0.0030691
GO:0009803	CC	GO:0009803	sex chromosome	7/1136	40/28886	0.0008531	0.0051751	0.0032421
GO:0005052	CC	GO:0005052	proteasome complex	9/1136	64/28886	0.0008561	0.0051751	0.0032421
GO:0071564	CC	GO:0071564	npBAF complex	4/1136	12/28886	0.0009114	0.0054581	0.0034191
GO:0032806	CC	GO:0032806	carboxy-terminal domain protein kinase complex	5/1136	21/28886	0.0011201	0.0062621	0.0041511
GO:0031228	CC	GO:0031228	intrinsic component of Golgi membrane	8/1136	54/28886	0.0011631	0.0068171	0.0042701
GO:0005657	CC	GO:0005657	replication fork	9/1136	67/28886	0.0011991	0.0069621	0.0043611
GO:0019908	CC	GO:0019908	nuclear cyclin-dependent protein kinase holoenzyme complex	4/1136	13/28886	0.0012791	0.0073061	0.0045781
GO:0019898	CC	GO:0019898	extrinsic component of membrane	24/1136	309/28886	0.0012831	0.0073061	0.0045781
GO:0030134	CC	GO:0030134	COPII-coated ER to Golgi transport vesicle	8/1136	55/28886	0.0013151	0.0074231	0.0046501
GO:0001741	CC	GO:0001741	XY body	5/1136	22/28886	0.0014031	0.0077771	0.0048711
GO:0035145	CC	GO:0035145	exon-exon junction complex	5/1136	22/28886	0.0014031	0.0077771	0.0048711
GO:0031256	CC	GO:0031256	leading edge membrane	15/1136	158/28886	0.0014761	0.0081081	0.0050791
GO:1905369	CC	GO:1905369	endopeptidase complex	9/1136	70/28886	0.0016431	0.0089461	0.0056041
GO:0030662	CC	GO:0030662	coated vesicle membrane	10/1136	84/28886	0.0016781	0.0090591	0.0056751
GO:0190034	CC	GO:0190034	distal axon	27/1136	371/28886	0.0017241	0.0092021	0.0057641
GO:0005652	CC	GO:0005652	nuclear lamina	4/1136	14/28886	0.0017351	0.0092021	0.0057641
GO:0003735	MF	GO:0003735	structural constituent of ribosome	52/1102	166/28438	7.76E-33	6.66E-30	4.79E-30
GO:0044389	MF	GO:0044389	ubiquitin-like protein ligase binding	65/1102	330/28438	1.13E-27	4.84E-25	3.48E-25
GO:0031625	MF	GO:0031625	ubiquitin protein ligase binding	62/1102	313/28438	1.37E-26	3.82E-24	2.82E-24
GO:0140297	MF	GO:0140297	DNA-binding transcription factor binding	67/1102	431/28438	2.19E-22	4.7E-20	3.39E-20
GO:003729	MF	GO:003729	mRNA binding	59/1102	366/28438	1.2E-20	2.06E-18	1.48E-18
GO:0061629	MF	GO:0061629	RNA polymerase II-specific DNA-binding transcription factor binding	55/1102	329/28438	4.39E-20	6.28E-18	4.52E-18
GO:0003712	MF	GO:0003712	transcription coregulator activity	61/1102	480/28438	3.77E-16	4.62E-14	3.32E-14
GO:0030695	MF	GO:0030695	GTPase regulator activity	52/1102	421/28438	1.84E-13	1.75E-11	1.26E-11
GO:0060589	MF	GO:0060589	nucleoside-triphosphatase regulator activity	52/1102	421/28438	1.84E-13	1.75E-11	1.26E-11
GO:0051082	MF	GO:0051082	unfolded protein binding	23/1102	88/28438	2.13E-13	1.75E-11	1.26E-11
GO:0019787	MF	GO:0019787	ubiquitin-like protein transferase activity	53/1102	437/28438	2.24E-13	1.75E-11	1.26E-11
GO:0004942	MF	GO:0004942	ubiquitin-protein transferase activity	51/1102	415/28438	3.83E-13	2.74E-11	1.97E-11
GO:0005096	MF	GO:0005096	GTPase activator activity	50/1102	405/28438	5.48E-13	3.62E-11	2.6E-11
GO:0042393	MF	GO:0042393	histone binding	40/1102	287/28438	2.55E-12	1.56E-10	1.12E-10
GO:0016922	MF	GO:0016922	nuclear receptor binding	28/1102	156/28438	9.91E-12	5.67E-10	4.07E-10
GO:0005085	MF	GO:0005085	guanyl-nucleotide exchange factor activity	31/1102	197/28438	3.23E-11	1.73E-09	1.25E-09
GO:0031072	MF	GO:0031072	heat shock protein binding	26/1102	147/28438	8.82E-11	4.45E-09	3.2E-09
GO:0051020	MF	GO:0051020	GTPase binding	39/1102	313/28438	1.5E-10	7.13E-09	5.13E-09
GO:0003713	MF	GO:0003713	transcription coactivator activity	34/1102	253/28438	2.99E-10	1.35E-08	9.72E-09
GO:0003730	MF	GO:0003730	mRNA 3'-UTR binding	21/1102	106/28438	6.5E-10	2.79E-08	2E-08
GO:0061659	MF	GO:0061659	ubiquitin-like protein ligase activity	38/1102	321/28438	1.12E-09	4.9E-08	3.3E-08
GO:0061630	MF	GO:0061630	ubiquitin protein ligase activity	37/1102	310/28438	1.48E-09	5.76E-08	4.14E-08
GO:0031267	MF	GO:0031267	small GTPase binding	34/1102	277/28438	3.3E-09	1.23E-07	8.85E-08
GO:0008022	MF	GO:0008022	protein C-terminus binding	30/1102	230/28438	8.18E-09	2.92E-07	2.1E-07
GO:0140658	MF	GO:0140658	ATP-dependent chromatin remodeler activity	11/1102	31/28438	1.17E-08	4.01E-07	2.88E-07
GO:0043021	MF	GO:0043021	ribonucleoprotein complex binding	24/1102	168/28438	3.67E-08	1.21E-06	8.71E-07
GO:0047485	MF	GO:0047485	protein N-terminus binding	21/1102	133/28438	4.46E-08	1.42E-06	1.02E-06
GO:0140097	MF	GO:0140097	catalytic activity, acting on DNA	28/1102	223/28438	4.84E-08	1.48E-06	1.07E-06
GO:0001221	MF	GO:0001221	transcription coregulator binding	17/1102	90/28438	5.75E-08	1.7E-06	1.22E-06
GO:0002039	MF	GO:0002039	p53 binding	15/1102	78/28438	1.88E-07	5.38E-06	3.87E-06
GO:0051787	MF	GO:0051787	misfolded protein binding	9/1102	25/28438	2.22E-07	6.15E-06	4.42E-06
GO:0050681	MF	GO:0050681	androgen receptor binding	10/1102	33/28438	3.01E-07	8.06E-06	5.8E-06
GO:0005543	MF	GO:0005543	phospholipid binding	41/1102	457/28438	6.5E-07	1.89E-05	1.21E-05
GO:0004674	MF	GO:0004674	protein serine/threonine kinase activity	40/1102	441/28438	6.72E-07	1.7E-05	1.22E-05
GO:0046332	MF	GO:0046332	SMAD binding	15/1102	86/28438	1E-06	2.46E-05	1.77E-05
GO:0003714	MF	GO:0003714	transcription corepressor activity	23/1102	187/28438	1.07E-06	2.56E-05	1.84E-05
GO:0008094	MF	GO:0008094	ATP-dependent activity, acting on DNA	17/1102	110/28438	1.15E-06	2.66E-05	1.91E-05
GO:0044183	MF	GO:0044183	protein folding chaperone	10/1102	38/28438	1.29E-06	2.91E-05	2.09E-05
GO:0019207	MF	GO:0019207	kinase regulator activity	25/1102	229/28438	3.39E-06	7.45E-05	5.36E-05
GO:0108310	MF	GO:0108310	protein serine kinase activity	26/1102	246/28438	3.98E-06	8.38E-05	6.03E-05
GO:0003725	MF	GO:0003725	double-stranded RNA binding	14/1102	84/28438	4.01E-06	8.38E-05	6.03E-05
GO:0090079	MF	GO:0090079	translation regulator activity, nucleic acid binding	16/1102	108/28438	4.15E-06	8.47E-05	6.09E-05
GO:0051087	MF	GO:0051087	chaperone binding	16/1102	109/28438	4.69E-06	9.36E-05	6.73E-05
GO:0016410	MF	GO:0016410	N-acetyltransferase activity	15/1102	99/28438	6.21E-06	0.0001211	8.7E-05
GO:0004388	MF	GO:0004388	helicase activity	19/1102	151/28438	6.48E-06	0.0001231	8.88E-05
GO:0051721	MF	GO:0051721	protein phosphatase 2A binding	9/1102	37/28438	8.9E-06	0.0001661	0.0001191
GO:0046982	MF	GO:0046982	protein heterodimerization activity	29/1102	307/28438	1.03E-05	0.0001881	0.0001351
GO:0019902	MF	GO:0019902	phosphatase binding	24/1102	230/28438	1.14E-05	0.0002041	0.0001461
GO:0048156	MF	GO:0048156	tau protein binding	7/1102	22/28438	1.32E-05	0.0002281	0.0001641
GO:0140030	MF	GO:0140030	modification-dependent protein binding	22/1102	202/28438	1.33E-05	0.0002281	0.0001641
GO:0032182	MF	GO:0032182	ubiquitin-like protein binding	15/1102	106/28438	1.45E-05	0.0002441	0.0001751
GO:0001046	MF	GO:0001046	core promoter sequence-specific DNA binding	10/1102	49/28438	1.52E-05	0.0002501	0.0001801
GO:0030331	MF	GO:0030331	estrogen receptor binding	10/1102	50/28438	1.83E-05	0.0002911	0.0002091
GO:0034212	MF	GO:0034212	peptide N-acetyltransferase activity	10/1102	50/28438	1.83E-05	0.0002911	0.0002091
GO:0003743	MF	GO:0003743	translation initiation factor activity	11/1102	61/28438	1.99E-05	0.0003041	0.0002191
GO:0070063	MF	GO:0070063	RNA polymerase binding	11/1102	61/28438	1.99E-05	0.0003041	0.0002191
GO:0019903	MF	GO:0019903	protein phosphatase binding	20/1102	182/28438	2.85E-05	0.0004141	0.0002981
GO:0032183	MF	GO:0032183	SUMO binding	6/1102	17/28438	2.86E-05	0.0004141	0.0002981
GO:0043422	MF	GO:0043422	protein kinase B binding	6/1102	17/28438	2.86E-05	0.0004141	0.0002981
GO:0051019	MF	GO:0051019	mitogen-activated protein kinase binding	8/1102	33/28438	2.9E-05	0.0004141	0.0002981
GO:0008080	MF	GO:0008080	N-acetyltransferase activity	12/1102	75/28438	2.96E-05	0.0004161	0.0002991
GO:1900782	MF	GO:1900782	protein tyrosine kinase binding	15/1102	113/28438	3.15E-05	0.0004351	0.0003131
GO:0045182	MF	GO:0045182	translation regulator activity	17/1102	141/28438	3.42E-05	0.0004651	0.0003341
GO:0008135	MF	GO:0008135	translation factor activity, RNA binding	13/1102	90/28438	4.27E-05	0.0005721	0.0004111
GO:0042826	MF	GO:0042826	histone deacetylase binding	16/1102	132/28438	5.39E-05	0.0007111	0.0005111
GO:0016887	MF	GO:0016887	ATP hydrolysis activity	22/1102	223/28438	6.12E-05	0.0007951	0.0005711
GO:0097718	MF	GO:0097718	disordered domain specific binding	8/1102	37/28438	7.03E-05	0.0008991	0.0006461
GO:0046966	MF	GO:0046966	thyroid hormone receptor binding	7/1102	28/28438	7.46E-05	0.0009401	0.0006761
GO:0001227	MF	GO:0001227	DNA-binding transcription repressor activity, RNA polymerase II-specific	28/1102	328/28438	8.86E-05	0.0011011	0.0007921
GO:00314								



GO:1990226	MF	GO:1990226	histone methyltransferase binding	4/1102	13/28438	0.0012111	0.0092771	0.0066691
GO:1990405	MF	GO:1990405	protein antigen binding	4/1102	13/28438	0.0012111	0.0092771	0.0066691
GO:0042288	MF	GO:0042288	MHC class I protein binding	7/1102	43/28438	0.0012231	0.0092891	0.0066781
GO:0070182	MF	GO:0070182	DNA polymerase binding	5/1102	22/28438	0.0013141	0.0098921	0.0071121



Dnaja1/Foxp1/Pges3/Rnf18/Nrc21/Fkbp4/Parp1/Sirt1/Daxx/Ep300/Drgk1/Lbh/Cnot1/Arf1/Per1/Ncoa2/Cnot2/Safb/Cair	19
Kf2/Hsp90ab1/Kf4/Zp36/Smad7/Mul1/At2b1/Lapm5/Rel/Inpp5d/Rnf125/Crebbp/Nmi/Parp1/Sirt1/Crb2/Ant2/Bank1/Nrk11/Spa/Cd2ap/Sars/C1qbp/Rabgef1/Ccr7/Cd200/Bst2/Irak3/Relb/Pmi/Zc3h12a/Ptrpr/Bcl6	33
Jun/Zfp36/Ef3/Ef3a/Chd1/Sp100/Rel1/Ep300/Cnt2/Inpp5k/Snr1/Cde1/Sp1/Ttim11/Nucks1	15
Gapdh/Zfp36/Rp13a/Rc3h2/Rps3/Dhx36/Ddx4/Zfp362/Ce1f1/Bank1/Rock1/Ef2ak3/Tnrc6a/Bmi1/Cnot1/Pan3/Cnot2/Rn3/Yhdh3/Ef4e2/Larp1/Tnrc6c/Pmi/Zc3h12a/Apoe/Cair/Tnrc6b	27
Jun/Hsp90aa1/Fos/Nkbia/Mef2c/Foxp1/Zfp36/Gpr171/Smad7/Syk/Rc3h2/Pcid2/Clec2d/Inpp5d/Hspb1/Sar1/Kf10/Malt1/Myc/Ets1/Zfp362/Nkbid/Ldb1/Sh2b3/Pipr2/Hax1/Stat1/Pk3r1/Ciptm1/It4ra/Hspa9b/Ctnnb1/Ccr7/F	40
Phf14/Artd5a/Atf2/Morf42/Naas50/Pxip1/Crebbp/H4/Sirt1/Ldb1/Phf20/Ep300/Ogt/Mecp2/lws1/Per1/Brd8/Epc1/Ep400/Fcn/Kmt2a/Phf20/1/Kat5a	23
Zfp36/Rc3h2/Pcid2/Dhx36/Lmd2/Pabpc4/Kyru/Ahcy/Zfp362/Ce1f1/Hnmpa0/Ef3a/Smg5/Smg1/Npm1/Zc3hav1/N5c/Cde1/Taf15/Rock1/Casc3/Magoh/Tnrc6a/Cnot1/Pan3/Myd88/Sid2/Cnot2/Yhdh3/Fus/Rnaset2a/Larp1/	23
Ppp1r15a/Elf1/Rp13a/Elf3k/Ppp1r15b/Tmed2/Elf4g2/Npm1/Bank1/Elf2ak3/Larp1/Rps6kb1/Pmi/Dnajc3	41
Zfp36/Rc3h2/Pcid2/Dhx36/Zfp362/Elf3e/Smg5/Smg1/Cde1/Casc3/Magoh/Tnrc6a/Cnot1/Pan3/Cnot2/Tnrc6c/Secisbp2/Zc3h12a/Tnrc6b	19
Jun/Zfp36/Atf2/Pmaip1/Kf10/Hnmp1/Bcl2/Sirt1/Foxo1/Pik3c3/Nfe2l2/Gabarap/Sik2/Pkag1/Pk3r4/Elf2ak3/Tnrc6a/Fnip1/Hgd1a/Larp1/Wpi2/Map1c3a/Fcn/Zc3h12a	25
Dnaja1/Foxp1/Zfp36/Akap13/Pges3/Rnf18/Nrc21/Fkbp4/Parp1/Sirt1/Zfp362/Tb11v/Daxx/Ep300/Drgk1/Lbh/Cnot1/Arf1/Per1/Ncoa2/Pk3r1/Cnot2/Rps6kb1/Crebr1/Safb/Cair	38
Hsp41/Mef2c/Syk/Satb1/Rs2/Rc3h2/H2-Ab1/Rps3/Lapm5/Inpp5d/Toig1/Malt1/Dhps/Rasa3/SH2b3/Bcl2/Ich/Siglecq/Cblb/Tnfrsf13c/Fkbp1a/Btla/Cd55/Cd86/Cnd3/Dock8/Myd88/Hst/Cd19/Ctnnb1/Ccr7/Dock2/Cd81/F	27
Hspa1a/Hspa1b/Ubb/Hsp90ab1/Rps7/Smad7/Gpx1/Lapm5/Arh1/Tmem259/Cenk1d/Xpo1/Cank2a1/Gabarap/Drgk1/Smarrc1/Ogt/Usf7/Herpud1/Zfand2a/Dnajb2/Chfr/Pten/Arh2/Pmi/Apoe/Usp19	27
Zfp36/Rc3h2/Pcid2/Dhx36/Lmd2/Pabpc4/Kyru/Ahcy/Zfp362/Ce1f1/Hnmpa0/Ef3a/Exrn1/Smg5/Smg1/Npm1/Zc3hav1/N5c/Cde1/Taf15/Rock1/Casc3/Magoh/Tnrc6a/Cnot1/Pan3/Myd88/Sid2/Cnot2/Yhdh3/Fus/Rnaset2a	42
Dnaja1/Hsp41/Gpx1/Pfaur/Tp11/Hsp41/Sgk3/Map2k1/Bcl2/Sirt1/Arnt2/Rb1cc1/Nfe2l2/Siah2/Eno1/Ghnm/Herpud1/Vns1abp/Ptg1p/Zmynd11/Birc6/Higd1a/Rnf34/Cdk11b/Ctnnb1/Fcrr/Rps6kb1/Phip/Ptpr1	29
Rp38/Rps2/Rp24/Rp14/Rp35a/Rp7a/Wdr74/Nrk/Npm1/Rrs1/Dhx30/Nhp2/Zfp622/Pea1/Ebna1b2	15
Hsp41/Mef2c/Syk/Satb1/Rs2/Rc3h2/H2-Ab1/Rps3/Lapm5/Inpp5d/Malt1/Dhps/Rasa3/Bcl2/Ich/Siglecq/Cblb/Tnfrsf13c/Fkbp1a/Btla/Cd55/Cd86/Cnd3/Dock8/Myd88/Hst/Cd19/Ctnnb1/Ccr7/Dock2/Cd81/Msn/Ptpr	35
Jun/Atf3/Atf2/Pmaip1/Kf10/Hnmp1/Bcl2/Sirt1/Foxo1/Pik3c3/Nfe2l2/Gabarap/Sik2/Pkag1/Pk3r4/Elf2ak3/Tnrc6a/Fnip1/Hgd1a/Wpi2/Map1c3a/Fcn/Zc3h12a	23
Hspa1b/Nk4a1/Kf4/Gpx1/Pfaur/Pcid2/Ar6p1/Arnt2/Siah2/Cank2a1/Akt2/Mical1/Herpud1/Fnip1/Rnf34/Srf/Fcrr	17
Zfp36/Myc1c/Pcid2/Snf7/Ret2/Rae1/Xpo1/Nup88/Nup210/lws1/Casc3/Magoh/Poldip3/Sid2/Eny2/Ranbp2/Akap8/Pabpn1/Chtop/Nxf1	38
Hspa1b/Nk4a1/Kf4/Gpx1/Pfaur/Ar6p1/Arnt2/Siah2/Cenk2a1/Akt2/Mical1/Herpud1/Fnip1/Rnf34/Srf/Fcrr	19
Hspa2/Zfp36/Rc3h2/Daxp1/Dhx36/Zfp362/Ce1f1/Srrmp70/Zc3hav1/Snr1/Rock1/Tnrc6a/Cnot1/Pan3/Cnot2/Yhdh3/Tnrc6c/Paf1/Zc3h12a/Tnrc6b	20
Dnajb1/Kf2/Jun/Ppp1r15a/Atf3/Cited2/Egr1/Arnt/Hif1an/Nfe2l2/Elf2ak3/Bclaf1/Atf8	13
Hspa90ab1/Nkbia/Syk/Bach2/Atf2/Mtbp31/Nup50/Ipo7/Nup88/Pkag1/Kpnb1/Ppp3ca/Pttg1p/Ing1/Pk3r1/Rbnm2/Ppp2ca/Ranbp2/Trpo1/Phip/Pmi/Zc3h12a/Cse11	24
Cytl1/P2ry10/Donmd4a/Ralgap1/Akap13/Cdc42se2/Dgkz/Rasa3/Map2k1/Dynt1c/Kras/Gabarap/Camk2d/Ogt/Arfge1/Rasa2/Cd2ap/Arhgap25/Rabgef1/Dock2/Ralgs2/Dnm2/Gpr65/Fcn/Apoe/Bcl6/Arhgap26/Iqsec1	28
Kmt2a/Arnd4/Satb1/Crebbp/Setd3/Sirt1/Mt2/Kmt2c/Ogt/Snr1/Mecp2/Ermt1/lws1/Atrx/Pax5/Rf1/Ctnnb1/Paf1/Kmt2a/Ned1/Chtop/Pmtt1	22
Nkbia/Kf4/Sirt1/Itch/Nkbid/Arnt2/Med13/Sr/Usp7/Tax1bp1/Cebpg/Bhhd40/Faf1/Cd200/Irak3/Pel1/Chuk/Zc3h12a/Kat5a	43
Zfp36/Rc3h2/Pcid2/Dhx36/Lmd2/Pabpc4/Kyru/Ahcy/Zfp362/Ce1f1/Hnmpa0/Nfe2l2/Elf3e/Smg5/Smg1/Npm1/Zc3hav1/N5c/Cde1/Taf15/Rock1/Casc3/Magoh/Tnrc6a/Cnot1/Pan3/Myd88/Sid2/Cnot2/Yhdh3/Fus/Rnaset2a	23
Kf2/Rps24/Zfp36/Rps19/Kmt2a/Rps17/Inpp5d/Tmod3/Tcaa1/Cited2/Ets1/Ldb1/Sh2b3/Pipr2/Cebpg/Stat1/Ptbp3/Hspa9b/Sp1/Bcl6/Dnase2a/Pmtt1	21
Hspa1a/Hspa1b/Hsp90aa1/Smad7/Lapm5/Arh1/Tmem259/Cenk1d/Gabarap/Drgk1/Herpud1/Zfand2a/Dnajb2/Ptg1p/Chfr/Pten/Faf1/Atrp1/Man/Apoe	22
Serfat1/Macf1/Foxp1/Smad7/Mul1/Atf1/Rnf18/Adam10/Bcl11a/Nrc31/Lamtora2/Bcl2/Sirt1/Elf4g2/Trf1/Ptpr1/Atf5g1/Zfyw27/Dip2b/Golga4/Npm1/Cank2a1/Elf2b2/Eno1/Mecp2/Dnajb2/Der2/Mdnl/Sfr/Sk11/Bst2/Dnm1	42
Hsp41/Mef2c/Foxp1/Syk/Ms4a1/Rs2/H2-Ab1/Pcid2/Lapm5/Inpp5d/Toig1/Srk3gp1/Malt1/Bcl11a/Bc2/Zfp362/Siglecq/Ptpr/Nfat1/Ep300/Pkcb/Cdnf1c/Bank1/Tnfrsf13c/Dnajb2/Pipr2/Btla/Cebpg/Cd86/Fnip1/Pk3r1/Bir	21
Hspa90/Hsp41/Foxp1/Syk/Rps19/Artd5a/Lapm5/Malt1/Myc18a/Dhx36/Sirt1/Cd84/Nkbid/H2-Q7/Ptpr/Fbox38/Dnm15/Rap1a/H2-M3/DG58/Cd55/Stat1/Ankrd17/Cd86/H2-Q6/H4a/Rabgef1/Ccr7/H2-Q4/Cd81/Ptpr/H2-	32
Cempa/Nap111/Senp6/Rnf4/Smarc5/Sart3/Ref1/Daxx/Trf4/Npm1/Gt2a2/Cabin1/Anp32b/Atrv/Gtfn25/Ub1/Npm1/Smarc2/Nap114/Nasp/Kat5a	21
Snf7/Sap18/Actin1/Hnmp1/Npm1/Cdk9/Cnt1/C1qbp/Ptbp3/Srf10	8
Dnajb1/Hspa90/Hspa1/Hspa1a/Hspa1b/Hsph1/Pges3/Srt13/Hspa9b/Hspa14	10
Hsp90aa1/Hsp41/Hsp41/Smad7/Syk/Hga4/H2-Ab1/Rps3/Pfaur/Lims1/Sart1/Malt1/Cited2/Dhps/Rasa3/Ets1/Ntkbid/Ldb1/Ptpr/H2-Eb2/Plekha2/Tnfrsf13c/Jak1/Igapp1/Cd55/Ppp3ca/Rnk1/Nat5/Cd86/C1qbp/Dock8/Hst61	43
Dynt1c/Kras/Gabarap/Camk2d/Ogt/Elmo1/Rhob/Nisch/Dock2/Dnm2/Rhoh/Dnl1	12
Zfp36/Myc1c/Pcid2/Snf7/Ret2/Rae1/Xpo1/Npm1/Nup88/Nup210/lws1/Casc3/Magoh/Poldip3/Sid2/Eny2/Ranbp2/Akap8/Pabpn1/Chtop/Nxf1	21
Zfp36/Myc1c/Pcid2/Snf7/Ret2/Rae1/Xpo1/Npm1/Nup88/Nup210/lws1/Casc3/Magoh/Poldip3/Sid2/Eny2/Ranbp2/Akap8/Pabpn1/Chtop/Nxf1	21
Gapdh/Zfp36/Rp13a/Rc3h2/Rps3/Dhx36/Ddx4/Zfp362/Ce1f1/Bank1/Elf2ak3/Tnrc6a/Cnot1/Pan3/Cnot2/Rn3/Ef4e2/Larp1/Tnrc6c/Pmi/Zc3h12a/Apoe/Cair/Tnrc6b	27
Hsp41/Smad7/Syk/Rc3h2/H2-Ab1/Malt1/Rasa3/Itch/Nkbid/Cblb/Btla/Cd55/H4a/Ccr7/Cd81/Zc3h12a/Ptrpr/Bcl6	18
Ubb/Birc3/Rps2/Smad7/Lapm5/Nmi/Ube2d1/Cblb/Npm1/Birc2/Gabarap/Cdk9/Dnajb2/Pttg1p/Chfr/Fbox33/Pten/Mycbp2/Pel1	41
Hspa1b/Nk4a1/Gapdh/Hsp41/Kf4/Syk/Gpx1/Mul1/Rps3/Pfaur/Pcid2/Lapm5/Pmaip1/Casp2/Pcd2/Malt1/Myc/Sirt1/Ar6p1/Arnt2/Fis1/Siah2/Cank2a1/Drgk1/Akt2/Mical1/Herpud1/Anp32b/Elf2ak3/Bmi1/Fnip1/Stat1/Birc6/	19
Chhd2/Atf2/Natc3/Lmd1/Cited2/Egr1/Map2k1/Myc/Bcl2/Armi/Cr1/Sirt1/Hif1an/Nfe2l2/Ep300/Pkcb/Birc2/Eno1/Cank2d/Ogt/Mecp2/Pgk1/Hga1/Pten/Pmi/Usp19	22
Dnaja1/Foxp1/Akap13/Pges3/Rnf18/Nrc21/Fkbp4/Parp1/Sirt1/Daxx/Ep300/Drgk1/Lbh/Cnot1/Arf1/Per1/Ncoa2/Cnot2/Prcc/Prcb1/Safb/Cair	26
Nk4a1/Fos/Mef2c/Cf2/Mbml1/Foxp1/Naca/Mef2d/Gpx1/Atf3/Tsc22d3/Natc3/Cited2/Egr1/Gpccp1/Myc/Bcl2/Ep300/Cnt2/Snr1/Ppp3ca/Pax5/Ctnnb1/Rps6kb1/Usp19	25
Sirt1/Ptpr/Pkcb/Lmbd1/Sik2/Inpp5k/Ogt/Ptpr2/Pk3r1/Cnd3/Rps6kb1/Nucks1/Soccs3/Osbp8/Ptpr1	15
Hspa90ab1/Hsp90aa1/Nkbia/Hsp41/Syk/Atf2/Mtbp31/Nup50/Ipo7/Nup88/Kpnb1/Ppp3ca/Pex7/Pttg1p/Ing1/Pk3r1/Rbnm2/Ppp2ca/Ranbp2/Trpo1/Phip/Pmi/Zc3h12a/Apoe/Hspa4/Cse11	27
Jun/Zfp36/Chd1/Sp100/Rel1/Ep300/Cnt2/Inpp5k/Snr1/Sp1/Ttim11/Nucks1	12
Dnajb1/Kf2/Jun/Ppp1r15a/Atf3/Cited2/Egr1/Arnt/Hif1an/Nfe2l2/Elf2ak3/Atf8	12
Zfp36/Lmd1/Map2k1/Ddx8/Mecp2/Nkbl1/Ppp3ca/Elf4e2/Tnrc6c/Zc3h12a/Pum2/Tnrc6b	14
Hsp90aa1/Gapdh/Hsp41/Syk/G3bp1/Dhx36/Setd2/Ztb20/Zc3hav1/Hnar1/Stat1/Myd88/Riok3/Chuk	12
Hspa1a/Hspa1b/Hsp90ab1/Rps7/Smad7/Lapm5/Arh1/Cenk1d/Xpo1/Cank2a1/Gabarap/Drgk1/Smarrc1/Ogt/Usf7/Herpud1/Zfand2a/Dnajb2/Chfr/Pten/Arh2/Pmi	35
Jun/Dnajb1/Ppp1r15a/Smad7/Dusp1/Hspb1/Ppb1/Sbg4d45b/Hpk3/Sirt1/Tmed2/Arnt2/Ptpr/Cbbl/SH2b3/Npm1/Mical1/Inpp5k/Ogt/Ptpr2/Ube2b/Gadd45g/Sik38/Rabgef1/Pten/Ppp2ca/Irak3/Zc3h12a/Soccs3/Ptpr/Dnaj	22
Dnaja1/Wnk1/Rp37/Zfp36/Smad7/Dusp1/Rs2/Hspb1/Pxd3/Gadd45b/Hpk3/Sirt1/Ptpr/Cbbl/SH2b3/Npm1/Pk3ip1/Inpp5k/Ptpr2/Gadd45g/Sik38/Pten/Ppp2ca/Irak3/Pmi/Ptpr/Dnajc3/Apoe/Ptpr1	29
Dnaja1/Hsp41/Kf4/Atf3/Dusp1/Dusp5/Elf3a/Hpk3/Itch/Foxo1/Ptpr1/Sh2b3/Inpp5k/Ptpr2/Sik38/Per1/Zmynd11/Dusp16/Pten/Fcn/Plcn/Ptpr/Apoe/Ptpr1	24
Zfp36/Myc1c/Pcid2/Snf7/Ret2/Rae1/Xpo1/Npm1/Nup88/Nup210/lws1/Casc3/Magoh/Poldip3/Sid2/Eny2/Ranbp2/Akap8/Pabpn1/Chtop/Nxf1	21
Jun/Fos/Atf3/Hga1/Phf1/Kf10/Hnmp1/Bcl2/Sirt1/Foxo1/Pik3c3/Nfe2l2/Gabarap/Sik2/Pkag1/Snr1/Pk3r4/Elf2ak3/Tnrc6a/Fnip1/Hgd1a/Wpi2/Map1c3a/Fcn/Zc3h12a/Ptrpr	27
Hsp90ab1/Hsp90aa1/Gapdh/Hsp41/Hsp41/Rps7/Smad7/Mul1/Pges3/Tb1x/Usp36/Ep300/Npm1/Ube2b/Usf7/Naat5/Pk3r1/Pten/Golga7/Pmi/Rab3gap1/Usp19/Cair/Hytk	24
Hsp90aa1/Hsp41/Foxp1/Syk/Mul1/Rps19/Clec2d/Rnf125/Matrx3/Nmi/Itch/Cd84/Arnt2/Fbox38/Tspan32/H2-M3/Zc3hav1/Ptpr2/Cd55/Ptpr1/Ankrd17/C1qbp/Stat1/Mdnl/Yhdh3/Usp15/Ttim12a/Irak3/Pmi/Riok3/Zc3h12a/Pl	14
Kdm5a/K3/Crem/Egr1/Sirt1/Cank1d/Ogt/Per1/Ncoa2/Bhhd40/Mycbp2/Relb/Pmi/Kmt2a	34
Smad7/Gpx1/Mul1/Rps19/Rc3h2/Clec2d/Inpp5d/Rnf125/Nmi/Cr1/Itch/Cd84/Arnt2/Ptpr2/Cd55/C1qbp/Yhdh3/It4ra/Usp15/Rabgef1/Irak3/Riok3/Zc3h12a/Ptrpr/Bcl6	25
Hspa2/Cf2/Nat1/Mat1/Capp/Sptbn1/Tmod3/Ptbp1/Alg12/Actin1/Myc/Dedd2/Ets1/Rb1cc1/Smarrc1/Snnp/Fis1/Gabarap/Drgk1/Smarrc1/Mical1/Cebpg/Ptpr/Plek/Arf1a/Pk3r1/Uvrag/Filii/Wpi2/Map1c3a/Rnk3/Vk1/Scaf	38
Cdc47/Ppp1r15b/Elm1/Tmed2/Nfe2l2/Ptpr2/Elf2ak3/Tmco1/Atf6/Bcl2/11/Ptpr1	11
Nap111/Ubt1/Smarc5/Sart3/Ref1/Sirt1/Daxx/Npm1/Cabin1/Anp32b/Atrv/Ub1/Smarc2/Paf1/Nap114/Nasp/Kat5a	17
Hsp90ab1/Hsp90aa1/Hsp41/Syk/Akap13/Trf4/Rps3/Zfp91/Zeb2/Dgkz/Malt1/Egr1/Map2k1/Cab39/Sirt1/Arnt2/Daxx/Kras/Cdc25b/Npm1/Rap1a/Igapp1/Pk3r4/Stat1/Map4k2/Zfp622/Cd86/Hgd1a/Cnd3/Cd19/Ccr7/Sk11	40
Syk/Satb1/Rc3h2/H2-Ab1/Rps3/Lapm5/Arh1/Dhps/Rasa3/Itch/Cbbl/Tnfrsf13c/Fkbp1a/Btla/Cd55/Cd86/Cnd3/Dock8/Myd88/Hst/Ctnnb1/Ccr7/Dock2/Cd81/Msn/Ptpr	26
Nk4a1/Fos/Mef2c/Cf2/Cacopy/Mbml1/Foxp1/Naca/Mef2d/Gpx1/Akap13/Atf3/Tsc22d3/Natc3/S1/pr1/Hrd1/Kdm6b/Cited2/Egr1/Nrc31/Gpccp1/Myc/Bcl2/Carp1/Sirt1/Arnt2/Ep300/Cnt2/Fkbp1a/Camk2d/Snr1/Ube4	43
Foxp1/Smad7/Rc3h2/Malt1/H4a/Nkbid/H2-M3/Gadd45g/Ly9/H4a/Ccr7/Relb/Zc3h12a/Bcl6	14
Hsp90aa1/Atf2/Rnf125/Crebbp/Wdy4/Zc3hav1/Nrk1/Ankrd17/C1qbp/Usp15/Riok3/Chuk/Zc3h12a/Pum2	14
Chhd2/Atf2/Cited2/Egr1/Map2k1/Myc/Bcl2/Armi/Hif1an/Nfe2l2/Eno1/Ogt/Pgk1/Hgd1a/Pten/Usp19	7
Ppp1r15a/Ppp1r15b/Tmed2/Npm1/Elf2ak3/Pmi/Dnajc3	17
Hsp90ab1/Rps7/Zfp36/Azn1/H10ra/Herc1/Dhx36/Srx12/Bcl2/Elf4g2/Hnmpa0/Usp36/Pdx3/Smg1/Cank2a1/Ddrgk1/Ctsa/Smarrc1/Ogt/Usf7/Taf15/Spce/Myd88/Fus/Dbl/Larp1/Secisbp2/Irak3/Mycbp2/Pmi/Usp19/Larp4b	32
Zfp36/Lmd1/Map2k1/Ddx8/Mecp2/Nkbl1/Ppp3ca/Elf4e2/Tnrc6c/Zc3h12a/Pum2/Tnrc6b	12
Smad7/Rc3h2/H2-Ab1/Pag1/Lapm5/Tnfap82/Inpp5d/Hspb1/Itch/Cd84/Nkbid/Cblb/SH2b3/Bank1/Tspan32/Ptpr2/Btla/Cd86/H4a/Rabgef1/Cnr2/Cd200/Pel1/Zc3h12a/Apoe/Bcl6	16
Rps5/Rps3/Rps27/Rps2/Rps19/Rp24/Rps28/Atf1/Rs1/Dhx30/Mps7/C1qbp	23
Kf2/Pkcb/Hps24/Zfp36/Rps19/Kmt2a/Rps17/Inpp5d/Tmod3/Tcaa1/Cited2/Ets1/Ldb1/Sh2b3/Pipr2/Cebpg/Stat1/Ptbp3/Hspa9b/Sp1/Bcl2/11/Bcl6/Dnase2a/Pmtt1	24
Nkbia/Birc3/Zfp36/Syk/Rps3/Lapm5/Lims1/Adam10/Sirt1/Zfp362/Trf1/Nfe2l2/Ikbb/Birc2/Tnfrsf13c/Inpp5k/Ptpr2/Nkbl1/Stat1/Rps6kb1/Zfand6/Chuk/Zc3h12a/Ptpr8	20
Kf2/Zfp36/Rps19/Kmt2a/Inpp5d/Tmod3/Tcaa1/Cited2/Ets1/Ldb1/Sh2b3/Pipr2/Cebpg/Stat1/Ptbp3/Hspa9b/Sp1/Bcl6/Dnase2a/Pmtt1	24
Nk4a1/Fos/Mef2c/Cf2/Mbml1/Foxp1/Naca/Smad7/Mef2d/Gpx1/Kf4/Atf3/Tsc22d3/Natc3/S1/pr1/Cited2/Egr1/Gpccp1/Myc/Bcl2/Sirt1/Ep300/Cnt2/Fkbp1a/Chkb/Snr1/Ube4b/Ppp3ca/Pax5/Mts1/Ctnnb1/Rps6kb1/Chd2/Cf	35
Macf1/Vps37b/Naca/Myc1c/Zdhxc3/Exoc4/Zdhxc18/Ar6p1/Fis1/Akt2/Inpp5k/Ogt/Srpr/Rabgef1/Tram1/Golga7/Sec63/Gd1	18
Ppp1r15a/Wnk1/Smad7/Atf2/Cik1/Map2k1/Cab39/Bcl2/Hpk3/Pkcb/Cank2a1/Camk2d/Inpp5k/Ogt/Rock1/Sbk1/Wk1/Phip	21
Ubb/Rps7/Atf3/Rps3/Pmaip1/Casp2/Myc/Dedd2/Sirt1/Daxx/Fis1/Ptpr2/Elf2ak3/Trp53np1/Pten/Faf1/Bclaf1/Fcn/Pmi/Bcl2/11/Ptrpr	18
Zfp36/Lmd1/Map2k1/Ddx8/Mecp2/Nkbl1/Ppp3ca/Elf4e2/Tnrc6c/Zc3h12a/Pum2/Tnrc6b	12
Gapdh/Atf3/Rs2/Pges3/B3gn7/Nrc31/Sirt1/Chst12/Foxo1/Ep300/Gr1/Akt2/Inpp5k/Ogt/Ptpr2/Usf7/Nrk1/Plek/B3gn2/Sup20/Pgk1/Cf2/Sk111/Ranbp2	24
Kmt2c/Sirt1/Mt2/Ogt/Snr1/Mecp2/Hes1/Atrx/Pax5/Rf1/Ctnnb1/Paf1/Kmt2a/Ned1/Chtop	15
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Macf1/Nat/Sptbn1/Zdhxc3/Tmed2/Zfyw27/Ikbb/Vamp3/Golga4/Bsg/Cank2a1/Tspan32/Rap1a/Camk2d/Akt2/Inpp5k/Pgmc1/Rock1/Wamp/Rer1/Rhog/Atp2c1/Pk3r1/Cf2c/Ppp2r6a/Golga7/Vts1/Cd81/Sys1/Myadm/Rapp	31
Jun/Atf3/Atf2/Pmaip1/Kf10/Hnmp1/Bcl2/Sirt1/Foxo1/Pik3c3/Nfe2l2/Gabarap/Sik2/Pkag1/Snr1/Pk3r4/Elf2ak3/Tnrc6a/Fnip1/Hgd1a/Wpi2/Map1c3a/Fcn/Zc3h12a	24
Dnajb1/Hspa90/Hspa1/Hspa1a/Hspa1b/Hsph1/Pges3/Srt13/Hspa9b/Hspa14	10
Dnajb1/Hspa90/Hspa1/Hspa1a/Hspa1b/Hsph1/Pges3/Srt13/Hspa9b/Hspa14	10
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Hsp90ab1/Hsp90aa1/Vps37b/Tm2b/Rab43/Pcbp1/Tmim59/Vapa/Bcl2/Ddx4/Arb1/bst1/Bsg/Zc3hav1/Inpp5k/Alg162/Fam111a/Uvrag/Larp1/Bcl2/Tim12a/Pmi/Tim11/Zc3h12a/Nucks1/Apoe/Srk2	28
Itfgr1/Dhx36/Hnmp1/Nfe2l2/Ef3a/Npm1/Elf2ak3/C1qbp/Poldip3/Yhdh3/Larp1/Rps6kb1/Usf16/Secisbp2/Sp1/Dnajc3/Apoe/Larp4/Larp4b/Vim/Ef2a3	21
Jun/Hsp90ab1/Kf4/Hga4/Pfaur/Pxip1/Sp100/H4/Myc/Hnmp1/Hpk3/Ref1/Parp1/Sirt1/Arnt2/Ef3a/Kr1/Ep300/Snarp/Cblb/Dnrf1/Eno1/Srv/Cdk9/Mecp2/Ppp3ca/Rock1/Ep4b1/Elf2ak3/Dnajb2/Ctnnb1/Ppp2ca/Btlf1/Nsd1	34
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Zfp36/Rc3h2/Dhx36/Zfp362/Ce1f1/Rock1/Tnrc6a/Cnot1/Pan3/Cnot2/Yhdh3/Tnrc6c/Zc3h12a/Zc3h12a/Tnrc6b	15
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Smad7/Rc3h2/H2-Ab1/Pag1/Lapm5/Tnfap82/Inpp5d/Hspb1/Itch/Cd84/Nkbid/Cblb/Bank1/Tspan32/Ptpr2/Btla/Cd86/H4a/Rabgef1/Cnr2/Cd200/Pel1/Zc3h12a/Bcl6	24
Cytl1/P2ry10/Donmd4a/Akap13/Cdc42se2/Dgkz/Rasa3/Map2k1/Dynt1c/Kras/Gabarap/Camk2d/Ogt/Arfge1/Rasa2/Rabgef1/Dock2/Ralgs2/Dnm2/Gpr65/Fcn/Apoe/Bcl6/Iqsec1	28
Mbml1/Sf3b1/Isv1/Rbm5/Scaf11/Ce1f1/Ce1f2/Luc72/Srf10/Setx/Srpk2	11
Hsp90aa1/Hsp41/Hsp41/Smad7/Syk/Hga4/H2-Ab1/Rps3/Pfaur/Sar1/Malt1/Cited2/Dhps/Rasa3/Ets1/Nkbid/H2-Eb2/Tnfrsf13c/Jak1/Cd55/Nat5/Cd86/Dock8/Hst61/H4a/Ccr7/Rhoh/Cd81/Ptpr/Bcl6	30
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Zfp36/Myc1c/Pcid2/Snf7/Dhx36/Setd2/Rae1/Xpo1/Npm1/Nup88/Nup210/lws1/Casc3/Magoh/Poldip3/Sid2/Eny2/Ranbp2/Akap8/Pabpn1/Chtop/Nxf1	22
Vps37b/Tm25/Zfp36/Top2b/Crebbp/Sp100/Tmem58/Vapa/Bcl2/Ref1/Dynt1c/Bsg/Zc3hav1/Inpp5k/Fam111a/Stat1/Larp1/Bst1/Trm12a/Pmi/Tim111/Srk2	22
Nkbia/Birc3/Zfp36/Syk/Rps3/Lapm5/Lims1/Sirt1/Zfp362/Trf1/Nfe2l2/Ikbb/Birc2/Tnfrsf13c/Inpp5k/Ptpr2/Nkbl1/Stat1/Zfand6/Chuk/Zc3h12a/Ptpr8	22
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Serfat1/Pcid2/Nrc31/Setd2/Map2k1/Ldb1/Wd43/Zmynd11/Rtfl1/Ctnnb1/Paf1/Sufl16/Zmiz2	13
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Hspa1a/Hsp90ab1/Hsp90aa1/Pges3/Dhx36/Sp100/Myc/Parp1/Doire1c/Smg5/Smg1/Pona/Nhp2/Atrv/Tnks2/Ctnnb1/Pmi/Gn3	11
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Atad1/Smad7/Dynt1c/Pcid2/Zdhxc3/Adam10/Fkbp4/Setd2/Map2k1/Rae1/Xpo1/Snarp1/Npm1/Lar1a/Nup88/Rs1/lws1/Pcm1/Rcc2/Vamp2/Poldip3/Eny2/Akap8/Akap8/Pabpn1/Chtop/Nxf1/Iqsec1	28
Hspa90/Jun/Hsp90ab1/Gapdh/Hsp41/Hsp41/Rps37b/Tm25/Gpx1/Chd1/Tmim59/Vapa/Ar6b/Dynt1c/Itf1/Ep300/Bsg/Inpp5k/Snr1/Myd88/Uvrag/Tm12a/Sp1/Pmi/Tim11/Zc3h12a/Nucks1/Bcl2/11/Apoe	28
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Hspd1/Foxp1/Zfp36/Syk/Artd5a/Ifng1/Hspb1/Cd2/Sirt1/Cd84/Arb2/Pprj/Zbtb20/Tspo/Pik3r1/Myd88/Ccr7/Irak3/Zc3h12a/Ptprc	20
Klf2/Klf4/Atf2/Tcf4/Pde3b/Krt1/Sh2b3/Mecp2/Rock1/Sars/Pgk1/Stat1/Cttnb1/Ficn/Pml	15
Hspa8/Hspd1/MeF2c/Smad7/Artd5a/Bach2/Rc3h2/H2-Ab1/Hnp5d/Tcig1/Malt1/Hf4/Or11/Nkbid/H2-Q7/Fbxo38/H2-Eb2/Tnfrsf13c/Dennd1b/H2-M3/Gadd45g/Cd55/C1qbp/H2-O6/Ly9/Myd88/Cd19/Il4ra/Ccr7/H2-Q4/Cd81b/	38
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Syk/Rasa3/Itch/Ccib/Blla/Cd55/Dock2/Cd81/Ptprc	9
Hspd1/Syk/Mul1/Rps3/Laptn5/Pmaip1/Casp2/Pdcd2/Malt1/Myc/Sirt1/Fis1/Anp32b/Elf2ak3/Stat1/Ppp2ca/Pml/Cyfp2/Bcl2l11	19
Jun/Kf4/Plaur/Sp100/Irf4/Myc/Hpk3/Rsf1/Parp1/Sirt1/Ep300/Odrgr1/Sn/Cttnb1/Nsd1/Hspa4	16
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Hspa8/Jun/Gapdh/Hspd1/Gpx1/Chd1/Napa/Ep300/Inpp5k/Snw1/Myd88/Sp1/Zc3h12a/Nucks1/Apoe	15
N3c1/Sirt1/Foxo1/Ep300/Ogt/Ptpr2/Usf7/Supt20/Skt11/Ranbp2	10
Nkbia/Mul1/Pmaip1/Dhx36/Npm1/Zc3hav1/Nkbl1/Stat1/Irak3/Pell1/Rlk3	11
Gapdh/ATF3/N3c1/Sirt1/Foxo1/Ep300/Ogt/Ptpr2/Usf7/Supt20/Pgk1/Sk11/Ranbp2	13
Ubb/Hsp90ab1/Junb/Artd4b/Hgs4/Plaur/Dazap1/Xist/Pdx3/Cited2/Fkbp4/Setd2/Map2k1/Bcl2/Arnt/Sirt1/Tmed2/Jmyd1c/Arnt2/Birc2/Elf2b2/Nduf6/Fndc3a/Bptf/Atrx/Arid1a/Birc6/Cttnb1/Pten/Akap9/Ppap/Sk11/Sp1/Socs3	38
Erf1/Stambp1/Sart3/Rch/Usp36/Znan1/Usf7/Usf4/Dnaj2/Usf15/Eny2/Usf16/Usf24/Zc3h12a/Usf19	15
Jun/Dhx36/Myc/Sub1/Ubtf/Smarca5/Rsf1/Med13/Gt2a2/Gt2h5/Tiam/Bdp1/Bclaf1/Setx	14
Trim25/Zfp36/Crebbp/Sp100/Trim59/Zc3hav1/Inpp5k/Fam111a/Stat1/Bat2/Trim12a/Pml/Trim11/Srpk2	14
Macf1/Actg1/Lims1/Lamtor2/Bcl2/Ldb1/Ptprj/Iqgapp1/Rock1/Rcc2/Pik3r1/Pten/Tin1/Iqsec1	14
Hspa1a/Hspa1b/Smad7/Laptn5/Arh1/Cank1d/Gabarap/Ddrgk1/Herpud1/Zhand2a/Dnaj2/Chfr/Pten/Arh2	14
Neat1/Ets1/Daxx/Serbp1/Pml/Srpk2	6
Rrf125/Zc3hav1/Ankrd17/C1qbp/Usf15/Pum2	6
Zfp36/Dhx36/Zfp362/Cnot1/Tnrc6c/Tnrc6b	6
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MeF2c/Syk/Irs2/Rps3/Dhps/Rasa3/Stgga1/Bcl2/Tnfrsf13c/Cd55/Cd86/Myd88/Il6st/Ccr7/Cd81/Pell1/Ptprc/Bcl6	18
Jun/Fos/Atf2/Pmaip1/Casp2/Egr1/N3c1/Parp1/Daxx/Atp5g1/Itk/Ikbb/Fis1/Cttnb1/Bcl2l11/Apoe/Srpk2	16
MeF2c/Syk/Irs2/Rps3/Dhps/Rasa3/Bcl2/Tnfrsf13c/Cd55/Cd86/Myd88/Il6st/Ccr7/Cd81/Pell1/Ptprc/Bcl6	17
Rhob/Crebbp/Dhx36/Egr1/Rf4/Parp1/Sirt1/Ep300/Npm1/Ak2/Pcna/Trp53inp1/Pik3r1/Sde2/GH2h5/Sk11/Nucks1/Nipbl/Cnd2	19
Mul1/Egr1/Arnt/Usa2/Cttnb1/Sae1/Gn3	7
Dynl1c/Kras/Gabarap/Camk2d/Ogt/Deck2/Dnm2	7
Dhx36/Nr3c1/Rf4/Daxx/Zhand2a/Zc3h12a/Sic3ba2	7
Foxp1/Rps3/Pkcb/Stap1/Ccr7/Cd81/Ptprc	7
Sertad1/Foxp1/Mul1/Hnf1b/Rnf6/Bcl11a/Bcl2/Sirt1/Ptprj/Dip2b/Eno1/Mecp2/Dnaj2/Mndal/Sk11/Bst2/Smarca2/Ficn/Pml/Rad/Bcl6	21
Kmt2e/Azin1/Pcd2/Tmod3/Crebbp/Cdc25b/Npm1/Camk2d/Ube2b/Nsf1c/Mecp2/Anp32b/Rcc2/Arnt/Ankrd17/Cnd3/Cxcr5/Paf1/Phip/Rad21/Usp18/Lmnb1/Numa1/Cnd2	24
Hspd1/Mul1/Laptn5/Pmaip1/Casp2/Pdcd2/Myc/Anp32b/Elf2ak3/Stat1/Pml/Bcl2l11	12
Smad7/Rps19/Rc3h2/Clec2d/Cr1/Cd84/Arb2/Siglec/Cd55/Il4ra/Rabge1/Bst2/Irak3/Zc3h12a/Ptprc/Bcl6	16
Hspd1/Foxp1/Zfp36/Syk/Artd5a/Ifng1/Hspb1/Cd2/Sirt1/Cd84/Arb2/Pprj/Zbtb20/Tspo/Pik3r1/Myd88/Ccr7/Irak3/Zc3h12a/Ptprc	20
Jun/Hspd1/Gpx1/Mul1/Atf2/Plaur/Pmaip1/Bcl2/Arb2/Chchd10/Fis1/Ghlim/Hgd1a/Sfn/Bcl2l11	15
Jun/Fos/Nkbia/MeF2c/Foxp1/Zfp36/Gpr171/Clec2d/Inpp5k/Klf10/Myc/Ets1/Ldb1/Ptpr2/Hax1/Stat1/Pik3r1/Hspa9/Cttnb1/Paf1/Tb2/Pmt1	22
Hspa8/Hspd1/Artd5a/H2-Ab1/Malt1/Nkbid/H2-Q7/Fbxo38/Tnfrsf13c/Dennd1b/H2-M3/Cd55/H2-Q6/H2-Q4/Cd81/Ptprc/H2-T23	18
Dhx36/Hnmp1/Erf6/Npm1/C1qbp/Poldip3/Ythdf3/Larp1/Rps6kb1/Usp16/Secisbp2/Dnaj3/Larp4/Larp4/Vim/Elf2a3x	16
Trim25/Trappc9/Atf2/Rps3/Hnf1d/Malt1/Pdx3/Crebbp/Sp100/Cd84/Traf1/Ep300/Pkcb/Ikbb/Kras/Npm1/Ddrgk1/Ppp3ca/Myd88/Cttnb1/Pten/Cd200/Trim12a/Irak3/Chuk	25
Klf4/MeF2c/Rhob/Foxp1/Hspb1/Sp100/Sirt1/Ets1/Nfe2l2/Krt1/Bsg/Mecp2/Sp1/Zc3h12a/Prcp/Apoe/P2rx4/Calr/Atp5a1	19
Pcd2/Setd2/Rae1/Npm1/Nup88/Iws1/Poldip3/Eno2/Akap8/Pabpn1/Chtop/Nxf1	12
Kmt2e/Artd4b/Setd2/Sirt1/Ogt/Mecp2/Iws1/Atrx/Rtf1/Kmt2a	10
Ppp1r1/Sa/Ppp1r1/Sa/Cited2/Elf2ak3/Dnaj3	5
Dnaj1b/Jun/Ppp1r1/Sa/Cited2/Hif1an	5
Nr4a1/Klf4/MeF2c/Rhob/Foxp1/Gpx1/Hspbl/Sp100/Sirt1/Ets1/Nfe2l2/Krt1/Bsg/Mecp2/Pten/Sp1/Zc3h12a/Prcp/Apoe/P2rx4/Calr/Atp5a1	22
Macf1/MeF2c/Naca/Smad7/Mul1/Bcl11a/N3c1/Bcl2/Sirt1/Ce1f1/Atf1/Atp5g1/Zfyve27/Golga4/Elf2b2/Mecp2/Rps6kb1/Dbnl/Apoe/Chd7/Nipbl/Gd1	22
Zfp36/Tnrc6a/Cnot1/Par3/Cnot2/Tnrc6c/Tnrc6b	7
Rps21/Fct1/Bms1/Npm1/Abt1/Rs1/Nhp2	7
Mtnl1/Sy1/Ce1f1/Ce1f2/Luc72/Srfl0/Setx	7
Atp2b1/Myo1c/Sirt1/Ptprj/Pkcb/Lmnb1/Inpp5k/Ptpr2/Rps6kb1/Nucks1/Socs3/Osbp8	12
Hspd1/Foxp1/Zfp36/Syk/Artd5a/Ifng1/Hspb1/Cd2/Sirt1/Cd84/Arb2/Pprj/Zbtb20/Tspo/Pik3r1/Myd88/Ccr7/Irak3/Zc3h12a/Ptprc	20
Pde4b/Nkbia/MeF2c/Foxp1/Zfp36/Rpl13a/Artd5a/Malt1/Pdx3/Sbno2/Cd84/Hnmpa/Ogt/Cd55/Stap1/Nkfb1/Hnar1/Cd86/Stat1/Myd88/Ccr7/Cnr2/Trim12a/Paf1/Irak3/Pabpn1/Pel1/Chuk/Zc3h12a/Ptpr8/Ly86/Vim	32
Hspa8/MeF2c/Cf2/Actg1/Srh2/Capg/Akap13/Myo1c/Rps3/Sptbn1/S1pr1/Tmod3/Fkbp4/Arpc5/Fchd2/Inpp5k/Mecp2/Argef1/Plek/Hax1/Bln1/Pik1/Mtss1/Fil/Akap9/Gpr65/Emi4/Dbnl/Cyfp2/Myadm/Apoe/Numa1	32
MeF2c/Cf2/Capg/Actg1/Foxp1/Naca/Gpx1/Akap13/Nfat3/Plekho1/Tmod3/Kdm6b/Nr3c1/Bcl2/Carp1/Sirt1/Arb2/Daxx/Kras/Camk2d/Ppp3ca/Artd1a/Epc1/Il4ra/Fil/Spag9/Cd81/Chuk	28
Hspa1a/Rps3/Pds5a/Merf2/Bcl11/Snchd1/Neil1/Pcd4/Setd2/Emys/Parp1/Sirt1/Tdp2/Dlce1/Smg1/Topbp1/Npm1/Pcna/Ube2b/Usf7/Cdk3/Cebpg/Atrx/Namc4a/Rfc1/Fam111a/Uvrag/GH2h5/Tonf/Fus/Setx/Trip12/Pm	38
Macf1/MeF2c/Foxp1/Naca/Smad7/Mul1/Hnf1b/Rnf6/Bcl2/Bcl11a/N3c1/Bcl2/Sirt1/Daxx/Ce1f1/Atf1/Atp5g1/Zfyve27/Dip2b/Golga4/Elf2b2/Mecp2/Trks2/Pten/Rps6kb1/Dnm2/Plac8/Dbnl/Bcl2l11/Apoe/Chd7/Nipbl/Gd1	33
Hspa8/Atf2/Rab43/Laptn5/Tppl1/Tcig1/Atg12/Mtbp1/Ar8b/Rb1/cc1/Pik3c3/Snapi/Gabarap/Nsf11c/Trp53inp1/Wip2/Map1lc3a/Hexa/Rab3gapp1	19
Nr4a1/Pde4b/Klf4/MeF2c/Foxp1/Smad7/Atp2b1/Nr3c1/Map2k1/Parp1/Foxo1/Nfatc1/Eno1/Camk2d/Sn/Cdk9/Ppp3ca/Cdk9/Ppp3ca/Roc1/Bln1/Akap9/Zc3h12a/P2rx4	24
Macf1/MeF2c/Naca/Smad7/Mul1/Adam10/Bcl11a/N3c1/Bcl2/Sirt1/Elf1qg2/Ce1f1/Atf1/Atp5g1/Zfyve27/Golga4/Cank2a1/Elf2b2/Mecp2/Deaf2/Sfn/Rps6kb1/Cd81/Dbnl/Apoe/Chd7/Nipbl/Gd1	28
Hsp90ab1/Klf4/Plaur/Hf4/Myc/Hnmp1/Hpk3/Parp1/Elf3a/Krt11/Ep300/Odrgr1/Eno1/Cdk9/Epb41/Elf2ak3/Cttnb1/Ppp2ca/Apoe/Hspa4	20
Wrk1/Klf4/Macf1/Dusp1/Dusp5/Kdm6b/Exoc4/Setd2/Ldb1/Lmnb1/Supt20/Artd4a/Rtf1/Cttnb1/Tnrc6c/Paf1/Kdm6a/Nsd1/Myadm	19
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Vps37b/Trim25/Vapa/Arf8b/Itf1/Trim12a/Pml/Trim11	8
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Gpx1/Pmaip1/Crebbp/Dhx36/Bcl2/Parp1/Sirt1/Ep300/Npm1/Pcna/Ube2b/Ube4b/Trp53inp1/Pik3r1/Sde2/Sk11/Pml	17
Pde4b/Nkbia/MeF2c/Foxp1/Zfp36/Rpl13a/Artd5a/Malt1/Pdx3/Sbno2/Cd84/Hnmpa/Ogt/Cd55/Stap1/Nkfb1/Hnar1/Cd86/Stat1/Myd88/Ccr7/Cnr2/Trim12a/Paf1/Irak3/Pabpn1/Pel1/Chuk/Zc3h12a/Ptpr8/Ly86/Vim	33
Jun/Nr4a1/Klf4/Macf1/MeF2c/Rhob/Foxp1/Gpx1/Zeb2/Hspb1/Sp100/Sirt1/Ets1/Nfe2l2/Krt1/Bsg/Mecp2/Rock1/Pten/Sp1/Zc3h12a/Prcp/Apoe/P2rx4/Iqsec1/Calr/Atp5a1	27
Klf2/Ppp1r1/Sa/Klf4/Rhob/Atf2/Hspb1/Adam10/Sp100/Sirt1/Ets1/Nfe2l2/Tcf4/Pde3b/Krt1/Pkcb/Sh2b3/Jak1/Mecp2/Rock1/Sars/Pgk1/Stat1/Cttnb1/Sp1/Ficn/Pml/Zc3h12a	27
Cdc47/Bcl2/Fis1/Camk2d/Herpud1/Tmco1/Pml	7
Gapdh/ATF3/Ins2/Pmaip1/Nr3c1/Myc/Sirt1/Foxo1/Ep300/Eno1/Ak2/Inpp5k/Ogt/Ptpr2/Usf7/Supt20/Pgk1/Ncoo2/Nisch/Pik3r1/Sk11/Ranbp2	22
Klf4/Kmt2e/Casp2/Dgkz/Crebbp/Bcl2/Nfatc1/Zfp655/Camk2d/Anp32b/Ppp3ca/Ankrd17/Cnd3/Sde2/Pten/Rps6kb1/Pml/Nasp/Gpr132/Cnd2	20
Jun/Kf4/Macf1/MeF2c/Rhob/Foxp1/Hspb1/Sp100/Sirt1/Ets1/Nfe2l2/Krt1/Bsg/Mecp2/Pten/Sp1/Zc3h12a/Prcp/Apoe/P2rx4/Iqsec1/Calr/Atp5a1	23
Ubb/Rps7/Rps3/Pmaip1/Sirt1/Fis1/Ptpr2/Elf2ak3/Bclaf1/Ficn/Bcl2l11	11
Jun/Zfp36/Atf3/Atf2/Pmaip1/Klf10/Kym/Hnmp1/Bcl2/Alcy/Sirt1/Foxo1/Pik3c3/Nfe2l2/Gabarap/Skag2/Pkag1/Snw1/Pik4/Elf2ak3/Tnrc6a/Frip1/Hgd1a/Larp1/Wip2/Map1lc3a/Rps6kb1/Ficn/Zc3h12a/Apoe	30
Ubb/Jun/Hsp90ab1/Fos/Gapdh/Hspbl/Hspd1/MeF2c/Gpx1/Atf2/Pmaip1/Casp2/Pdx3/Egr1/Nr3c1/Tmem259/Bcl2/Parp1/Sirt1/Arnt2/Daxx/Atp5g1/Ikbb/Fis1/Kras/Npm1/Ak2/Mecp2/Rock1/Cttnb1/Cd200/Bcl2l11/Apoe/Si	34
Jun/Nr4a1/Klf4/Macf1/MeF2c/Rhob/Foxp1/Gpx1/Zeb2/Hspb1/Sp100/Sirt1/Ets1/Nfe2l2/Krt1/Bsg/Mecp2/Rock1/Pten/Sp1/Zc3h12a/Prcp/Apoe/P2rx4/Iqsec1/Calr/Atp5a1	27
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Cdc47/Ppp1r1/Sa/Elf2ak3/Tmco1/Bcl2l11	5
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Hsp90ab1/Hsp90aa1/Cytl1/Cenpa/Tcig1/Myo18a/Exoc4/Krt1/Map4/Nsf1c/Argef1/Dock8/Ccr7/Dock2/Sk11/Msn/Numa1	17
Jun/Hsp90ab1/Gapdh/Hspbl/Hspd1/MeF2c/Gpx1/Atf2/Pmaip1/Casp2/Pdx3/Egr1/Nr3c1/Bcl2/Parp1/Sirt1/Arnt2/Fis1/Kras/Npm1/Ak2/Mecp2/Rock1/Cttnb1/Bcl2l11/Apoe/Srpk2	27
Smad7/Rc3h2/Malt1/Nkbid/Il4ra/Ccr7/Zc3h12a/Bcl6	8
Hspa1a/Hspa1b/Hsp90ab1/Hsp90aa1/Dnaj1/Pde4b/Ier5/Dhx36/Daxx/Elf2b2/Xytl1/Trp53inp1/Hspa4	13
Birc3/Rc3h2/Rps3/Laptn5/Lims1/Crebbp/Nmi/Ep300/Bcl2/Nfat5/Cd86/Zc3h12a/Calr	11
MeF2c/Irs2/Inpp5b/Bcl2/Siglec/Tnfrsf13c/Blla/Cd81/Pell1/Ptprc/Bcl6	13
Erf1/Stambp1/Serp6/Sart3/Rch/Usp36/Znan1/Usf7/Usf4/Dnaj2/Usf15/Eny2/Usf16/Usf24/Zc3h12a/Usf19	16
Hspa1a/Hspa1b/Smad7/Laptn5/Arh1/Tmem259/Cank1d/Gabarap/Ddrgk1/Herpud1/Zhand2a/Dnaj2/Chfr/Pten/Arh2	15
Macf1/Smad7/Nap111/Zeb2/Lims1/Dhx36/Bcl11a/Map2k1/Myc/Bcl2/Itf1/Cux1/Atp5g1/Zfyve27/Golga4/Elf2b2/Snw1/Tspo/Bln1/C1qbp/Il6st/Cttnb1/Sk11/Dnm2/Dbnl/Myadm/Apoe/Ned9/Vim/Calr/Gd1	31
Jun/Nr4a1/Klf4/Macf1/MeF2c/Rhob/Foxp1/Gpx1/Zeb2/Hspb1/Sp100/Sirt1/Ets1/Nfe2l2/Krt1/Bsg/Mecp2/Rock1/Pten/Sp1/Zc3h12a/Prcp/Apoe/P2rx4/Iqsec1/Calr/Atp5a1	27
Ins2/Pmaip1/Nr3c1/Myc/Sirt1/Foxo1/Ep300/Zbts20/Akt2/Inpp5k/Ogt/Ptpr2/Usf7/Nfkb1/Plek/Supt20/Ncoo2/Ctkc/Sk11/Ranbp2	20
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Trim25/Trappc9/Rps3/Malt1/Pdx3/Cd84/Traf1/Ep300/Pkcb/Ikbb/Kras/Npm1/Ddrgk1/Myd88/Trim12a/Irak3/Chuk	17
Jun/Cacyp3/Pds5a/Orc3/Bcar3/Npm1/Pcna/Atrx/Ankrd17/Faf1/Nucks1/Donson/Esco1	14
Hspd1/Dhx36/Nmi/Setd2/Zc3hav1/Stat1/Chuk	7
Hspa1a/Hspa1b/Hsp90ab1/Hsp90aa1/Dnaj1/Pde4b/Ier5/Dhx36/Arb2/Daxx/Elf2b2/Xytl1/Elf2ak3/Trp53inp1/Rnf64/Plac8/Dnaj3/Hspa4	18
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Foxp1/Smad7/Rc3h2/Malt1/Hf4/Nkbid/H2-M3/Gadd45g/Ly9/Il4ra/Ccr7/Cd81/Relb/Zc3h12a/Bcl6	15
Ppap1/Znfhc3/Atg12/Znfhc18/Pik3c3/Uvgg/Nm2/Dbs/Wip2/Golga7/Dpm1/Apoe/Rab3gapp1	13
Macf1/Nap111/Zeb2/Hnf1b/H2/Dhx36/Bcl11a/Hes8/Map2k1/Myc/Stat1/Cux1/Atp5g1/Zfyve27/Dip2b/Golga4/Dnajb11/Elf2b2/Snw1/Mecp2/Ppp3ca/Pcm1/Tspo/Bln1/Il6st/Bhh4d0/Cttnb1/Pten/Sk11/Trim11/Dbnl/Apoe/Chd7/	35
Trim59/Sirt1/Nkbid/Per1/Zmynd11/Stat1/Rhoh/Rlk3/Zc3h12a	9
Kmt2e/Tmod3/Crebbp/Cdc25b/Npm1/Camk2d/Mecp2/Anp32b/Rcc2/Ankrd17/Cnd3/Paf1/Lmnb1/Cnd2	14
Sat2/Cpx1/Mul1/Capp/Pcd2/Sptbn1/S1pr1/Tmod3/Fkbp4/Nas10/Parp1/Arb2/Npm1/Map4/Inpp5k/Ghlim/Argef1/Tspo/Atrx/Hgd1a/Pik3r1/Trks2/Filfil/Dnm2/Ficn/Emi4/Pml/Rad21/Myadm	30
Syk/Rasa3/Itch/Ccib/Blla/Cd55/Cd81/Ptprc	8
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Hspa8/Hspd1/Smad7/Syk/Artd5a/Clec2d/Malt1/Dhx36/Cr1/Cd84/Arb2/H2-Q7/Fbxo38/Dennd1b/H2-M3/Cd55/Stap1/H2-Q6/Il4ra/Rabge1/Bst2/H2-Q4/Cd81/Ptprc/H2-T23/Bcl6	25
Kmt2e/Artd4b/Sat1/Crebbp/Srpp3/Setd2/Myc/Cntf1/Parp1/Sirt1/Mt2/Kmt2c/Ogt/Snw1/Mecp2/Ehmt1/Iws1/Atrx/Pax5/Rhf1/Zc3h13/Cttnb1/Paf1/Kmt2a/Nsd1/Chtop/Pmt1	27
Hspbl/Syk/H2-Ab1/Malt1/Rasa3/Nkbid/Cd55/Il4ra/Ccr7/Cd81/Ptprc	11
Klf4/Kmt2e/Casp2/Dgkz/Crebbp/Bcl2/Nfatc1/Zfp655/Camk2d/Anp32b/Ppp3ca/Ankrd17/Cnd3/Sde2/Pten/Rps6kb1/Paf1/Pml/Nasp/Gpr132/Cnd2	21
Ubb/Jun/Hsp90ab1/Fos/Hspbl/Hspd1/MeF2c/Atf2/Pmaip1/Casp2/Pdx3/Egr1/Nr3c1/Tmem259/Bcl2/Parp1/Sirt1/Arnt2/Daxx/Atp5g1/Ikbb/Fis1/Kras/Npm1/Mecp2/Rock1/Cttnb1/Cd200/Bcl2l11/Apoe/Srpk2	31
Rrf125/Zc3hav1/Ankrd17/C1qbp/Usf15/Rmk3/Pum2	7
Neat1/Rps19/Ubtf/Smarca5/Sirt1/Ets1/Daxx/Usf36/Nsf1c/Reep3/Pe1/Bln1/Serbp1/Akap8/Pml/Srpk2	16
Sptbn1/Adam10/Map2k1/Cank2a1/Rap1a/Camk2d/Pgrmc1/Epb41/Rer1/Rhog/Atp2c1/Pik3r1/Ctco/Ppp2r5a/Vi1b/Numa1	16
Shias5/Rps3/Tp1/Pmaip1/Casp2/Myc/Bcl2/Sirt1/Ep300/Snw1/Pik3r1/Sfn/Pml/Bcl2l11	14
Dnaj1a/Foxp1/Rnf6/Fkbp4/Sirt1/Daxx/Ep300/Artd1a	8
Klf4/MeF2c/Foxp1/Nfat3/Nr3c1/Parp1/Sirt1/Foxo1/Nfatc1/Camk2d/Cdk9/Ppp3ca/Rock1/Tbce/P2rx4	15
Sertad1/Foxp1/Mul1/Hnf1b/Rnf6/Cited2/Bcl11a/Bcl2/Sirt1/Ptprj/Dip2b/Eno1/Mecp2/Dnaj2/Mndal/Pten/Sk11/Bst2/Smarca2/Plac8/Ficn/Pml/Rad/Bcl6	24
Tmed2/Nfe2l2/Ptpr2/Elf2ak3/Ptpn1	5
Laptn5/Itch/Mylp/Apoe/Ptpr1	5
Dnaj1a/Dusp1/Hpk3/Ptprj/Sh2b3/Inpp5k/Sk38/Irak3/Apoe/Ptpr1	10
MeF2c/Foxp1/Nr3c1/Parp1/Sirt1/Foxo1/Camk2d/Cdk9/Ppp3ca/Rock1/P2rx4	11
Hsp90aa1/Mul1/Rrf125/Itch/Tspan32/Zc3hav1/C1qbp/Stat1/Pml/Rlk3/Zc3h12a	11
Hspa8/Cf2/Nsf1/Capp/Sptbn1/Exoc4/Vamp3/Golga4/Vamp2/Atp2c1/Dnm2/Golga7/Vh1b/Sy1	21
Macf1/Nsf1/Laptn5/Sptbn1/Exoc4/Vamp3/Golga4/Vamp2/Atp2c1/Dnm2/Golga7/Vh1b/Sy1	23
Klf2/Foxp1/Tmod3/Cited2/Pahpc4/Ep300/Sh2b3/Nros/Rabgap1/Ptbp3/Ff1/Bcl6	12
Hspa1b/H4a1/Gapdh/Klf4/Cpx1/Plaur/Pcd2/Arfp1/Arb2/Sat2/Cank2a1/Atf2/Mical1/Herpud1/Bln1/Frip1/RhG4/Sfn/Fcrr	19
Macf1/Dynl1/Zeb2/Hspb1/Dhx36/Bcl11a/Map2k1/Sirt1/Dynl1c/Itf1/Nfe2l2/Cux1/Ep300/Atp5g1/Zfyve27/Rala/Ikbb/Fbxo38/Golga4/Elf2b2/Rap1a/Iqgapp1/Kidins220/Plekhhm1/Tmem30a/Pik3r1/Ccr7/Sk11/Dnm2/Setx/Dnk	34
Dnaj1a/Dusp1/Hspb1/Gadd45b/Hpk3/Sirt1/Ptprj/Ccib/Sh2b3/Npm1/Inpp5k/Ptpr2/Gadd45g/Sk38/Pten/Irak3/Ptprc/Dnaj3/Apoe/Ptpr1	6
Pcd2/Iws1/Poldip3/Eny2/Pabpn1/Nxf1	20
Klf2/Ppp1r1/Sa/Klf4/Rhob/Atf2/Hspb1/Sp100/Sirt1/Ets1/Nfe2l2/Tcf4/Pde3b/Krt1/Pkcb/Sh2b3/Jak1/Mecp2/Rock1/Sars/Pgk1/Stat1/Cttnb1/Sp1/Ficn/Pml/Zc3h12a	26
Hspd1/Foxp1/Syk/Laptn5/Rel/Arb2/Nkbl1/C1qbp/Ccr7/Irak3	10

Hsp1/Foxp1/Gpx1/Hsp1/Alk2/Bcl2/Parp1/Sirt1/Nfe2l3/Zfp822/Cnmb1/Paap/Pml	13
Juv/Hsp1/Jund/Foxp1/SyK/Ingr1/Myo18a/Sbno2/Nmi/Cd84/Stap1/Itra/Cd200	13
Klf4/Mef2c/Foxp1/Nr3c1/Parp1/Sirt1/Foxo1/Nfatc1/Cank2/Cdk9/Ppp3ca/Rock1/P2rx4	13
Nkbia/Sp100/Os9/Ankd1/3c/Chcd10/Nros/Si/Tspo/Rer1/Vps13a/Tnrc6a/Faf1/Pml	13
Macf1/Zeb2/Bcl11a/Map2k1/ist1/Atg5g1/Zfyve27/Golga4/Eif2b2/Sk11/Dnml/Apoe/Gdl1	13
Hsp1/Dhx36/Nmi/Setd2/Zc3hav1/Staf1/Chuk	7
Laptm5/Irch/Pk3/4/Myip/Uvrag/Apoe/Ptpn1	7
Smad7/Rc3h2/Malt1/IrH4/Nkbid/Ly9/Zc3h12a	7
Hspa1a/Hspa1b/Smad7/Arh1/Csnk1d/Gabarap/Ddrgk1/Herpud1/Zfand2a/Dnajb2/Chfr/Arh2	12
Mef2c/Nr3c1/Parp1/Sirt1/Cank2d/Cdk9/Ppp3ca/Rock1	8
Pde4b/Nkbia/Mef2c/Zfp36/SyK/And5a/Malt1/Cdcd47/Ppp115b/Sbno2/Cd84/Ogt/Cd55/Stap1/Nkbl1/Eif2ak3/Cd98/Stat1/Myd88/Tim12a/Paf1/Pabp1/Tmco1/Zc3h12a/Bcl2l11/Ppf8/Ly86/Vm	28
Juv/Nr4a1/Klf4/Macfl1/Mef2c/Rhob/Foxp1/Gpx1/Irta4/Zeb2/Hsp1/Sp100/Lamor2/Sirt1/Ets1/Nfe2l3/Krl1/Bsig/Iqgap1/Mecp2/Rock1/Rcc2/C1qbp/Yhd3/Pten/Sp1/Fml/Zc3h12a/Prpc/Apoe/P2rx4/Iqsec1/Catr/Atp5a1	34
Klf2/Inpp5d/Cd84/Arb2/Bank1/Rabgef1/Cd200/Irak3/Zc3h12a	9
Dnaj1/Hsp1/Klf7/Sp100/Os9/Srx12/Pde3b/Inpp5k/Ogt/Ppp3ca/Der10/Eny2/Cd200/Ppp3ca/Apoe/Gdl1	16
Pde4b/Wnk1/SyK/Rpl13a/Rps19/Irta4/Dusp1/S1pr1/Gpm3/Ano6/Adam10/Pprj/Bsg/Stap1/Rock1/Rhog/C1qbp/Dock8/Myd88/Cxcr5/Rabgef1/Ccr7/Chr2/Cd200/Rhob/Cd81/ManV/P2rx4/Catr/Ill17ra	30
Hsp90aa1/Wnk1/Nkbia/Hsp1/SyK/Rps19/S1pr1/Gpm3/Ano6/Hsp1/Adam10/Mat3/Nmi/Ets1/Pprj/H2-M3/Ak2/Zc3hav1/Stap1/Papc1/Ankrd17/C1qbp/Mnda/Usp15/Ccr7/Tim12a/Cd81/Rlok3/Pum2/Ly86/P2rx4/Catr/Ill1	33
Foxo/Foxp1/Jumb/Clec2d/Inpp5d/Klf10/Tcrg1/Sbno2/Nfatc1/Pk3r1/Cnmb1/Cd81/Chuk/Tob2	14
Nr4a1/Klf4/Mef2c/Gpx1/Hsp1/Sirt1/Ets1/Nfe2l3/Mecp2/Sp1/Prpc/Apoe/P2rx4/Atp5a1	14
Hspa1b/Ppp115a/Nr4a1/Gapdh/Wnk1/Klf4/Gpx1/Kdm5a/Plaur/Pcid2/Bod1/Neil1/Tmed2/Ar6ip1/Arb2/lkbbk/Siah2/Cank2a1/Ak2/Mical1/Herpud1/Arfgef1/Rock1/Rcc2/Bin1/Fnip1/Broc6/Rnf54/SrnV/Fcmr	30
Hspa8/Hsp1/Smad7/Artd5a/Malt1/Cr11/H2-Q7/Fbox38/Denn1b/H2-M3/Cd55/H2-Q6/H2-Q4/Cd81/Ptprc/H2-T23	16
Irs2/Pmaip1/Nr3c1/Sirt1/Foxo1/Ep300/Ak2/Inpp5k/Ogt/Ptpn2/Usp7/Supt20/Ncoa2/Sk11/Ranbp2	15
Mef2c/Nr3c1/Parp1/Sirt1/Cank2d/Cdk9/Ppp3ca/Rock1	8
Hsp1/Dusp1/Rell1/Gadd45b/Gadd45g/Per1/Zc3h12a/Pmt1	8
Pgap1/Tmed5/Vapa/Tmed2/Sec24b/Axon1/Ergic3/Copb2/Tmed9/Preb/Ergic2/Trappc6b/Copa/Sec24c	14
Mef2c/Naca/Plekho1/Egr1/Myc/Bcl2/Arpc5/Nfe2l2/Igapp1/Cank2/Rock1/Ill6st/Rps6kb1/Gna13	14
Mef2c/Foxp1/Nr3c1/Parp1/Sirt1/Foxo1/Cank2d/Cdk9/Ppp3ca/Rock1/P2rx4	11
Pdcd2/Dhx36/Nbp2/Bcl2/Fnip1/Hspa9/Fcn	7
Tmen259/Sirt1/Ptprc/Herpud1/Eif2ak3/Pk3r1/Arf6	7
Mul1/Arnt/Uba2/Sae1/Gn3	5
Zfp36/Tnrc6a/Cnot1/Tnrc6c/Tnrc6b	5
Gapdh/Atf3/Irs2/Pmaip1/Nr3c1/Myc/Sirt1/Foxo1/Ep300/Man2b1/Eno1/Ak2/Inpp5k/Ogt/Ptpn2/Usp7/Supt20/Pgk1/Ncoa2/Nisch/Pk3r1/Sk11/Ranbp2	23
Kmt2b/Tmod3/Crebip/Cdc25b/Cank2d/Mecp2/Anp3z/Rcc2/Ankrd17/Cord3/Lmb1/Cend2	12
Hsp1/Foxp1/Smad7/SyK/Rc3h2/Malt1/Sbno2/Nmi/Ir4-Cd84/Nkbid/H2-M3/Gadd45g/Vamp2/Ly9/Myd88/Cd19l/Itra/Rabgef1/Ccr7/Dock2/Cd81/Rellb/Zc3h12a/Ptprc/Bcl6/Dock11	27
Fkbp4/Fkbp1a/Nkr/Pp1g/Pp1w1/Ranbp2	6
Ddrgk1/Ptprc2/Pk3r1/Atf6/Crebfr/Ptpn1	6
Hsp1/Foxp1/SyK/Laptm5/Rell/Arnt2/Nkbl1/C1qbp/Ccr7/Irak3	10
Nkbia/Pk3ap1/Hsp1/Foxp1/Zfp36/Gpx1/Rps19/Tnfrs2/Gpm3/Sbno2/Nmi/Alk2/Ets1/Celf1/Siglecg/Ptprc2/Stap1/Nkbl1/Myd88/Rabgef1/Ccr7/Cnr2/Cd200/Cd81/Socs3/Apoe/Bcl6/Ill17ra	28
Tmed5/Rab43/Lysmd3/Myo18a/Map2k1/Csnk1d/Tmed2/Nfil1c/Arfgef1/Tmed9/Ctic/Akap9/Dnm2/Wk1/Vti1b	15
Foxp1/Smad7/Artd5a/Laptm5/Malt1/Dhx36/Sirt1/Siglecg/Denn1b/Dnajb9/Cd55/Cd86/Itra/Bat2/Irak3/Cd81/Ptprc/Bcl6	18
Mef2c/Foxp1/Akap13/Nfatc3/Nr3c1/Parp1/Sirt1/Foxo1/Cank2d/Cdk9/Ppp3ca/Rock1/P2rx4	13
Irs2/Pges3/Pmaip1/B3gn1/Nr3c1/Sirt1/Foxo1/Rb1/cc1/Ep300/Got1/Ak2/Inpp5k/Ogt/Ccg2/Ptprc2/Usp7/Mecp2/Plek/B3gn1/Supt20/Ncoa2/Ill6st/Pten/Sk11/Ranbp2	25
Hsp90ab1/Ppp115a/Mef2c/Bod1/Ppp115b/lkbbk/Smg5/Iqgap1/Inpp5k/Rock1/Plek/Ppp25a/Ppp2ca/Ptprc/Hsp90b1	15
Mul1/Bcl11a/Egr1/Arnt/Uba2/Cnmb1/Sae1/Gn3	8
Smad7/Rc3h2/Irch/Cblb/Bta/Itra/Zc3h12a/Bcl6	8
Klf4/Mul1/Sk2b3/Ptprc2/Stap1/Ill6st/Yhd3/Rabgef1/Irak3/Ptprc	10
Pde4b/Atf2b1/Msa41/Nfatc3/Ano6/Ahnac/Diaph1/Mcur1/Bcl2/Cd84/Arb2/Nfatc1/Pkcb/Fkbp1a/Cank2d/Inpp5k/Siv/Ppp3ca/Spoo/Ep41/Bin1/Atp2c1/Cd19/Dbl/Cnmb1/Ppp2ca/Tmco1/Pml/Ptprc/Radi/Cld7/P2rx4/Cherp	33
Zfp36/Gpx1/Mul1/Rps19/Dusp1/Tnfrs2/Bcl2/Rnf125/Chd8/Nmi/Sig6a1/Ets1/Irch/Arb2/Siglecg/Sh2b3/Ptprc2/Stap1/Nkbl1/Yhl1/C1qbp/Yhd3/Usf15/Rab22b/Irak3/Rok3/Socs3/Apoe	30
Juv/Hsp90ab1/Hsp1/Hsp1/Mef2c/Artd5a/Pmaip1/Casp2/Pdxc3/Egr1/Nr3c1/Bcl2/Parp1/Sirt1/Arnt/Fia1/Kras/Npm1/Mecp2/Rock1/Cnmb1/Bcl2l11/Apoe/Spk2	24
Mef2c/Naca/Tsc2d3/Bcl2/Cnmb1/Rps6kb1/Usp19	7
Zfp36/Fam172a/Snchd1/Lind1/Map2k1/Ubatf1/Smarc5/Ddx6/Sirt1/Celf1/Celf2/Mecp2/Nkbl1/Ppp3ca/Tnrc6a/Cnot1/Cnot2/Eif4e2/Tnrc6c/Zc3h12a/Pum2/Tnrc6b	22
Hsp1/Foxp1/Smad7/SyK/Rc3h2/Malt1/Sbno2/Nmi/Ir4-Cd84/Nkbid/H2-M3/Gadd45g/Vamp2/Ly9/Myd88/Cd19l/Itra/Rabgef1/Ccr7/Dock2/Cd81/Rellb/Zc3h12a/Ptprc/Bcl6/Dock11	27
Pgap1/Zfhc3/Atg12/Zfhc18/Pk3c3/Ugcg/Nnt2/Dbl/Wip2/Golga7/Dpm1/Rab3gap1	12
Rps21/Fch1/Npm1/Abt1/Rrs1/Res1	6
Sart3/Usp36/Usf7/Usf15/Eny2/Usf16	6
Hsp1/Dhx36/Setd2/Zc3hav1/Staf1/Chuk	6
Hsp90aa1/Smad7/SyK/Rc3h2/Hsp1/Sirt1/Malt1/Nkbid/Sh2b3/Ptprc2/Ciptm1/Itra/Ccr7/Rhoh/Zc3h12a/Ptprc/Bcl6	17
Foxp1/Hsp1/Malt1/Egr1/Ir8100582/4Rk/Arb2/Itra1/Myd88/Mnda/Ccr7/Pml/Zc3h12a	12
Klf4/Mef2c/Hsp1/Sirt1/Ets1/Nfe2l3/Mecp2/Sp1/Prpc/Apoe/P2rx4/Atp5a1	12
Dock8/Ccr7/Dock2/Cd81/Mn	5
Ptges3/Nr3c1/Artd1a/Per1/Ncoa2	5
Hsp90ab1/Smad7/Zeb2/Cited2/Crebip/Sirt1/Ep300/Got1/Nros/Snw1/Sk11/Dnm2/Flcn/Glg1	14
Hspa1a/Hspa1b/Smad7/Arh1/Tmen259/Csnk1d/Gabarap/Ddrgk1/Herpud1/Zfand2a/Dnajb2/Chfr/Arh2	13
Klf2/Hsp1/SyK/And5a/Laptm5/Inpp5d/Cd84/Arb2/Bsg/Bank1/Zbtb20/Myd88/Rabgef1/Cd200/Irak3/Zc3h12a/Ill17ra	17
Hsp90ab1/Ppp115a/Mef2c/Ppp115b/Plek/Ppp2ca/Ptprc	7
Rc3h2/Rps3/Laptm5/Lims1/Crebip/Nmi/Ep300/Nfat5/Cd86/Calr	10
Dnaj1/Rps7/Smad7/Rps3/Arb2/Ogt/Irns1/abp/Usf4/Dnajb2/Cnmb1/Trip12	12
Dnaj1/SyK/Akap13/Dusp1/Rps3/Zeb2/Hpk3/Ptprj/Kras/Sh2b3/Iqgap1/Inpp5k/Sh2b3/Map4k2/Ccr7/Irak3/Ptprc/Apoe/Ptpn1	19
Klf4/Mef2c/Rhob/Dusp1/Tmod3/Cited2/Sp100/Bc9/Cic4/Ptprj/Nfe2l3/Krl1/Mecp2/Stap1/Bin1/Trip53/Nip1/Nisch/Rabgef1/Pten/Cd200/Bat2/Flcn/Gna13/Apoe/Osbpl9/Calr	26
Hsp90ab1/Rps7/Arnt1/Srx12/Cank2a1/Ddrgk1/Ctss/Smarcc1/Ogt/Usf7/Irak3/Myc2b/Pml/Usf19	14
Hsp1/Rhob/Foxp1/Gpx1/Rps3/Pdxc3/Kdm6b/Ppp115b/Bcl2/Sirt1/Nfe2l2/Oser1/Psapp/Setx	14
Mef2c/Foxp1/Akap13/Nfatc3/Nr3c1/Parp1/Sirt1/Foxo1/Cank2d/Cdk9/Ppp3ca/Rock1/P2rx4	13
Irs2/Pmaip1/Myc/Sirt1/Foxo1/Zbtb20/Ak2/Ptprc2/Nkbl1/Supt20/Sk11	11
SyK/H2-Ab1/Rps3/Laptm5/Dhps/Rasa3/Irch/Cblb/Tnfrs13c/Bta/Cd55/Cd86/Ill6st/Cnmb1/Ccr7/Cd81/Pel1/Ptprc	29
Irs2/Pmaip1/Egr1/Nr3c1/Map2k1/Myc/Erlin1/Parp1/Sirt1/Foxo1/Ep300/Zbtb20/Eno1/Ak2/Inpp5k/Ogt/Ptprc2/Usf7/Nkbl1/Plek/Eif2ak3/Supt20/Ncoa2/Dbl/Sk11/Lpgat1/Ranbp2/Flcn/Apoe	18
Laptm5/Dgkz/Eif1/Ptprj/Cblb/Ptprc2	6
Hspa8/Gapdh/Naca/Bcl2/Sirt1/Arb2/Nfe2l2/Npm1/Cank2d/Pk3r1/Pten/Zc3h12a	12
Vps2b/Tim25/Top2b/Tim59/Vapa/Bcl2/Bsg/Zc3hav1/Inpp5k/Fam111a/Larp1/Bst2/Tim12a/Pml/Tim11/Spk2	16
Gpx1/Artd4b/Cic4/Jmd1c/Sec24a/lkbbk/Rap1a/Com2/WnnFndc3a/Rock1/Atrx/Myd88/Sid2/Ill6st/Siv/Akap9/Spao/Sic4a7/MnV/Myadm/Cdc88c/Vm	23
Mul1/Crebip/Sirt1/Foxd3/Ep300/Npm1/Myip/Chfr/Cdc88c	9
Hsp90ab1/Ppp115a/Bod1/Ppp115b/lkbbk/Rock1/Ppp2ca/Ptprc/Hsp90b1	9
Klf4/Pcid2/Casp2/Dgkz/Bcl2/Zfp36/Zfp655/Topbp1/Chfr/Sde2/Pten/Irk/Pml/Rad21/Donson/Gpr132/Foxn3	17
Hsp90ab1/Smad7/Zeb2/Cited2/Crebip/Sirt1/Ep300/Got1/Nros/Snw1/Sk11/Dnm2/Flcn/Glg1	14
Pcid2/Dhx36/Senp6/Naa10/Rnf4/Myc/Parp1/Smg5/Smg1/Atrx/Chfr/Tnks2/Cnmb1/Irk/Pml/Rad21/Gn3/Numa1	18
Macf1/Zeb2/Irfd1/Rnf6/Bcl11a/Map2k1/ist1/Atg5g1/Zfyve27/Dip2b/Golga4/Eif2b2/Pten/Sk11/I/Dbn1/Apoe/Vim/Gdl1	12
Cempa7/Pp1/Setd2/Daxx/Rcc2/Atrx/Tnks2/Irk/Pml/Rad21/Gn3/Nepbl	18
Hspa8/Hsp90ab1/SyK/Clec2d/Cr11/Arb2/H2-Q7/H2-M3/Cd55/Stap1/H2-Q6/H2-Q4/Bcl2l11/Ptprc/H2-T23	15
Mef2c/Foxp1/Akap13/Nfatc3/Nr3c1/Parp1/Sirt1/Foxo1/Cank2d/Cdk9/Ppp3ca/Rock1/P2rx4	13
Hsp1/SyK/And5a/Ingr1/Hsp1/Cd84/Ptprj/Zbtb20/Pk3r1/Myd88/Ccr7/Ptprc	13
Irs2/Pmaip1/Sirt1/Foxo1/Ak2/Ptprc2/Supt20/Sk11	8
Mef2c/Irs2/Bcl2/Tnfrs13c/Cd81/Pel1/I/Dbn1/Ptprc/Bcl6	8
Bod1/Pcna/Cdk9/Atrx/Fam111a/Tnfrs1/Nucks1/Donson	8
Smad7/Rc3h2/Malt1/Nkbid/Cd55/Itra/Ccr7/Cd81/Zc3h12a/Bcl6	10
Ptges3/Nr3c1/Artd1a/Per1/Ncoa2	5
Myc/Smarccl1/Smarcc1/Cebpg/Ard1a	5
Ppp115a/Dusp1/Ppp115b/Ppp3ca/Ppp2r2a	5
Dhx36/Daxx/Zfand2a/Zc3h12a/Sic38a2	5
Klf2/Klf4/Mef2c/Nfe2l3/Nfat1	5
Birc3/Nmi/UBE2d1/Birc2/Gabarap	17
Atf2/Pdcd2/Cned2/Dhx36/Nbp2/Bcl2/Siglecg/Nfe2l2/Pm2c/Rrs1/Fnip1/Hspa9/Chd2/Flcn/Samd9/Ptprc/Pid4	15
Dnaj1/Itra4/Atf2/Gadd45b/Hpk3/Irch/Rbl1cc1/Traf1/Gadd45b/Nkbl1/Map4k2/Zfp622/Per1/Zmynd11/Myd88/Spag9/Lmb1	20
Ct2/Sah2/Capp/Myo1c/Sp1bn1/Tmod3/Diaph1/Ptsp1/Arpc5/Fchs2/Mical1/Arfgef1/Plek/Hax1/Bmi1/Mts1/Filii/Dnml/Cyfp2/Myadm	17
Top2b/Rps3/Pcid2/Pds5a/Naa50/Naa10/Arhb/Nudo/Cank2a1/Rrs1/Ube2b/Krpb1/Rcc2/Atx/Tk1/Chfr/Top2b/Uvrag/Cnmb1/Irk/Akap8/Emi4/Rad21/Pum2/Esco1/Npbl/Numa1	27
Atp5a/Map2k1/Atpsc1/Myc/Parp1/Atpsg1/Eno1/Flcn/Atpsa1	9
SyK/Irf4/Bcl2/Ptprc2/Ly9/Ccr7/Dock2/Sk11/Ptprc	9
Juv/Fos/Hsp1/Rhob/Foxp1/Rps3/Pdxc3/Kdm6b/Parp1/Sirt1/Nfe2l2/Oser1/Psapp/Setx/Chuk	15
Mef2c/Foxp1/Tac2d3/Irs2/Plekho2/Sig6a1/Myc/Sirt1/Nkbid/Fnip1/Dock8/Pten/Fcmr/Ccr7/Bcl2l11	15
Smad7/Artd5a/Laptm5/Malt1/Dhx36/Sirt1/Denn1b/Cd55/Bat2/Irak3/Cd81/Bcl6	12
Zc3hav1/Ankrd17/Usf15/Pum2	4
Laptm5/Irch/Apoe/Ptpn1	17
Nkbia/Pk3ap1/Hsp1/Rnf125/Nmi/Ir4/Arb2/Zc3hav1/Ankrd17/Cd86/C1qbp/Myd88/Usf15/Irak3/Pel1/Rlok3/Pum2	4
H13/Aup1/Os9/Herpud1/Der2/Set11	6
Zfp36/Dx6/Tnrc6a/Eif4e2/Tnrc6c/Tnrc6b	6
Rnf125/Zc3hav1/Ankrd17/C1qbp/Usf15/Pum2	6
H13/Aup1/Os9/Herpud1/Der2/Set11	6
Smad7/Artd5a/Rc3h2/Malt1/Nkbid/Zc3h12a	6
Hspa8/Top2b/Pcbp1/Vapa/Bcl2/Zc3hav1/Inpp5k/Atg162/Fam111a/Larp1/Bst2/Zc3h12a/Nuck1/Spk2	14
Iff30/H2-Ab1/Arhb/H2-Q7/Wty/H2-Eb2/H2-M3/H2-Q6/Paap/Ccr7/H2-Q4/Rellb/H2-T23/Calr	14
Rhob/Lrcc6/Crebip/Dhx36/Egr1/Rnf4/Parp1/Sirt1/Sic12a6/Ep300/Got1/Npm1/Ak2/Pcna/Rcsd1/Trip53/Nip1/Pk3r1/Sde2/GH2H5/Cnmb1/Pten/Sk11/Rellb/Nucks1/Nipbl/Cend2	26
Rhob/Lrcc6/Crebip/Dhx36/Egr1/Rnf4/Parp1/Sirt1/Sic12a6/Ep300/Got1/Npm1/Ak2/Pcna/Rcsd1/Trip53/Nip1/Pk3r1/Sde2/GH2H5/Cnmb1/Pten/Sk11/Rellb/Nucks1/Nipbl/Cend2	26
Hspa8/Ano6/Myo18a/Ptprj/Rap1a/Stap1/Ccr7/Dock2/Dnm2/Ptprc/Calr	11
Rc3h2/Pcid2/Cited2/Bcl2/Nk2/Kmt2a/Samd9/Bcl2l11	8
Gpx1/Klf7/Irs2/Cdcd186/Egr1/Sirt1/Nadk/Pde3b/Pkcb/Eif2b2/Zbtb20/Siv/Ogt/Nkbl1/Ppp3ca/Vamp2/Side2/Eny2/Ppp2ca	19
Hsp1/SyK/And5a/Ingr1/Hsp1/Cd2/Cd84/Ptprj/Zbtb20/Pk3r1/Myd88/Ccr7/Ptprc	13
Mef2c/Foxp1/Tac2d3/Irs2/Sig6a1/Myc/Sirt1/Nkbid/Fnip1/Dock8/Pten/Fcmr/Ccr7	13
Top2b/Pcid2/Pds5a/Naa50/Naa10/Nudo/Rrs1/Krpb1/Atrx/Chfr/Cnmb1/Irk/Akap8/Emi4/Rad21/Esco1/Npbl/Numa1	13
Hsp90ab1/Hsp90aa1/Macfl1/Mef2c/Foxp1/Klf7/Irta4/Top2b/Rp24/Zeb2/Irfd1/Rnf6/Bcl11a/Map2k1/Bcl2/Ist1/Atpsg1/Zfyve27/Dip2b/Golga4/Bsg/Eif2b2/Groc10/B3gn2/Rhog/Tbce/Pten/Sk11/Dnm2/Rhob/Myc2b/Dbln1/Arp	35
Klf4/Plaur/Irf4/Myc/Hpk3/Parp1/Ep300/Ddrgk1/Cnmb1	17
Gpx1/Cept1/Pgap1/Inpp5d/Dgkz/Gpcpd1/Sirt1/Prpla7/Pk3c3/Scd1/Mboat7/Smg1/Chkb/Inpp5k/Mecp2/Plek/Hadha/Pk3r1/Ill6st/Sel1/Ill6st/16a/Dbl/Pten/Erlin1/Lpgat1/Dpm1/Socs3/Apoe/Dgka	29
Hsp90aa1/Hsp1/SyK/Rps19/Mat3/Nmi/Fbox38/H2-M3/Zc3hav1/Papc1/Ankrd17/Mnda/Usf15/Tim12a/Rlok3/Pum2/Ly86	17
Juv/Fos/Hsp1/Rhob/Foxp1/Gpx1/Rps3/Pdxc3/Kdm6b/Ppp115b/Bcl2/Parp1/Sirt1/Nfe2l2/Oser1/Psapp/Setx/Chuk	18
Hsp90ab1/Ppp115a/Mef2c/Bod1/Ppp115b/lkbbk/Rock1/Plek/Ppp2ca/Ptprc/Hsp90b1	11
Ubb/Mul1/Pmaip1/Pdxc3/Myc/Bcl2/Parp1/Atpsg1/Got1/Ak2/Tspo	11
Rps21/Fch1/Erns1/Pop7/Npm1/Faf1/Fip11/Rrs1/Hnp2/Zc3h12a	10
Foxp1/Hsp1/Malt1/Egr1/Ir8100582/4Rk/Arb2/Itra1/Myd88/Mnda/Ccr7/Pml/Zc3h12a	12
Pk3ap1/Rnf125/Irf4/Arb2/Zc3hav1/Ankrd17/C1qbp/Usf15/Irak3/Pel1/Rlok3/Pum2	12
Gapdh/Atf3/Irs2/Pmaip1/Nr3c1/Myc/Sirt1/Foxo1/Ep300/Man2b1/Eno1/Ak2/Inpp5k/Ogt/Ptprc2/Usf7/Supt20/Pgk1/Ncoa2/Nisch/Pk3r1/Sk11/Ranbp2	23
Cept1/Pgap1/Inpp5d/Dgkz/Gpcpd1/Prpla7/Pk3c3/Mboat7/Smg1/Chkb/Inpp5k/Mecp2/Plek/Hadha/Pk3r1/Abhd16a/Dbl/Pten/Erlin1/Lpgat1/Dpm1/Socs3/Dgka	23
Hsp90ab1/SyK/Akap13/Rps3/Zeb2/Map2k1/Cab39/Sirt1/Kras/Iqgap1/Map4k2/Higd1a/Ccn3/Ccr7/Sk11/Ppp2ca/Ptprc/Ptpn1/Cend2	19
Macf1/Irfd1/Rnf6/Bcl11a/ist1/Atpsg1/Zfyve27/Dip2b/Golga4/Eif2b2/Dnm2/Dnml/Apoe/Gdl1	14

Kf4/Km2e/Casp2/Dgkz/Crebbp/Bcl2/Zfp655/Anp32b/Ankrd17/Ccnd3/Sde2/Pten/Pml/Cnd2	14
Hsp90ab1/Junb/Igfa4/Dazap1/Xist/Pdx3/Clec2/Setd2/Map2k1/Arnt/Tmed2/Birc2/Bptf/Arid1a/Birc6/Sp1/Socs3	17
Klf2/Hspd1/Syk/Arid5a/Laptm5/Inpp5d/Cd84/Arnt2/Bsg/Bank1/Zbtb20/Myd88/Rabgef1/Cd200/Irak3/Zc3h12a/Il17ra	17
Foxp1/Pkcb/Stap1/Cd19/Cd81	5
Chch2/Map2k1/Eno1/Ogt/Usp19	5
Hsp17/Gpx1/Hspb1/Sirt1/Nfe22	5
Smad7/Rc3h2/Mat1/Nkbid/Zc3h12a	5
Wnk1/Igfa4/Dusp1/Gpsm3/Ano6/Adam10/Ptpry/Stap1/Rhog/C1qbp/Dock8/Myd88/Rabgef1/Ccr7/Cd200/Rhoc/Cd81/Men/P2rx4/Calr	20
Pds5a/Naa50/Naa10/Atrv/Rad21/Nipbl	6
Dnajb1/Ahsa1/Dnajb11/Zc3hav1/Dnajb2/Chtop	6
Zfp36/Ddx6/Tnrc6a/Eif4e2/Tnrc6c/Tnrc6b	6
Zfp36/Ddx6/Tnrc6a/Eif4e2/Tnrc6c/Tnrc6b	6
Hspa8/Gapdh/Naca/Bcl2/Sirt1/Arnt2/Nfe22/Npm1/Camk2d/Pik3r1/Pten/Zc3h12a	12
Nkbia/Syk/Laptm5/Lims1/Tnfr1/Ikbbk/Tnfr13c/Ptpr2/Sirt1/Chuk	10
Klf4/Mef2c/Rhoc/Dusp1/Cited2/Sp100/Bcl2/Cic4/Ptpry/Nfe22/Krt11/Mecp2/Stap1/Trip53inp1/Nisch/Rabgef1/Pten/Cd200/Bst2/Fcn/Gna13/ApoE/Osbp8/Calr	24
Hsp90aa1/Sah2/Capp/Myc1c/Rps3/Sptbn1/Tmod3/Fkbp4/Clec2/Setd2/Map2k1/Arnt/Tmed2/Birc2/Bptf/Arid1a/Birc6/Sp1/Socs3	24
Mu1/Rps19/Clec2d/Rnf125/Nm/Ich/Arnt2/Ptpr2/C1qbp/Yhd3/Usp15/Irak3/Rlok3	13
Hspa8/Syk/Ano6/Myo18a/Ptpry/Rap1a/Stap1/Pten/Ccr7/Dock2/Dnm2/Ptprc/Calr	13
Igfa4/Crebbp/Map2k1/Ankrd11/Ep300/Rab3gap1/Chd7/Kat5a/Nipbl	9
Gpx1/Egr1/Rnf4/Myc/Bcl2/Gt2h5/Pml/Ptprc	8
Dnajb1/Hsp17/Dusp1/Hipk3/Ich/Foxo1/Per1/Zmynd11	8
Dnajb1/Hsp17/Dusp1/Hipk3/Ich/Foxo1/Per1/Zmynd11	8
Iti1/Oa1/Ap6/Oa1/Hec1/Map2k1/Bcl2/Sirt1/Eif4g2/Foxo1/Usp36/Smg1/Csa/Rock1/Tspo/Trip53inp1/Larp1/Sik11/Trim12a/Fln/Atf/Zc3h12a/Bcl211/Rab3gap1	22
Zfp36/Lmd1/Map2k1/Ddx6/Ceif1/Ceif2/Mecp2/Nkbf1/Ppp3ca/Tnrc6a/Cnot1/Eif4e2/Tnrc6c/Zc3h12a/Pum2/Tnrc6b	16
Juv/Dhx36/Myc/Sub1/Med13/Bclaf1/Setx	7
Nr4a1/Klf4/Zfp36/Lnrc8/Gpx1/Atf2/Sirt1/Zfp36/2Tb1/x/Foxo1/Scf1/Ep300/Zad2/Eif2ak3/Lamb3/Opk3/Arh4/Plac8/Fcn/Zc3h12a/Osbp8/Nipbl	22
Mef2c/Plekho2/Stgal1/Sirt1	4
Dnajb1/Hsp17/Sp100/Oa9/Sirt1/Inpp5k/Ogt/Nsf1c/Der2/Cic4/Ppp2r5a/Ppp2ca/Fcn/Gd1	14
Kdm5a/Kdm6b/Umj1c/Ube2b/Kdm6a/Kdm7a	6
Kdm5a/Kdm6b/Umj1c/Ube2b/Kdm6a/Kdm7a	6
Hsp17/Gpx1/Hspb1/Parp1/Sirt1/Nfe22	6
Macf1/Dusp1/Dusp5/Kdm6b/Exoc4/Setd2/Arid1a/Rf1/Cnmb1/Tnrc6c/Paf1/Kdm6a	12
Kdm5a/Mor4d2/Sirt1/Tb1/x/Ep300/Fry/Per1/Akap8/Pml/Ek4/Bcl6/Nipbl	12
Atad1/Nsf/Syk/Laptm5/Plekhh1/Ich/Arnt2/Vamp3/Lmbd1/Pik3r4/Myip/Ctcf/Uvrag/Dnm2/Cd81/ApoE/Ptpn1/Iqsec1	18
Mu1/Sh2b3/Ptpr2/Stap1/Nest1/Yhd3/Rabgef1/Irak3/Ptprc	9
Dusp1/Dusp5/Setd2/Lb1/Bptf/Ankrd17/Rf1/Cnmb1/Tnrc6c/Paf1	10
Ubb/Rpe7/Rp137/Rps20/Pmaip1/Sirt1/Npm1/Rs1/Ptfg1p/Rnf34	10
Nkbia/Rnf125/Zc3hav1/Ankrd17/C1qbp/Usp15/Rlok3/Pum2	8
Tpp1/Tcrg1/Nps13a/Paap/Cd81	5
Kmt2e/Snw1/Rf1/Cnmb1/Kmt2a	5
Arfip1/Zfyve27/Reep3/Rh3/Rab3gap1	5
Tmed2/Nfe22/Ptpr2/Eif2ak3/Ptpr1	5
Hspd1/Mef2c/Irs2/Inpp5d/Bcl2/Siglecg/Tnfr13c/Bta/Cd18/Cd81/Pell1/Ptprc/Bcl6	13
Juv/Hsp90ab1/Fos/Smad7/Atf2/Zeb2/Sptbn1/Cited2/Crebbp/Egr1/Sub1/Parp1/Sirt1/Arnt2/Ep300/Got1/Nros/Snw1/Myd88/Usp15/Sk11/Dnm2/Fcn/Pml/Zyx/Glg1/Hexa/Vim/Numa1	29
Crebbp/Dhx36/Parp1/Sirt1/Ep300/Npm1/Pcna/Trip53inp1/Pik3r1/Sde2/Sk11	11
Pde4b/Wnk1/Atp2b1/Fyd5/Ntacc3/Ahnak/Diaph1/Bcl2/Cd84/Arnt2/Ikbbk/Fkbp1a/Camk2d/Akt2/Inpp5k/Sri/Tspo/Ep41/Vamp2/Bin1/Per1/Cd19/Dbl/Cnmb1/Pten/Akap9/Dnm2/Ppp2ca/Pml/Rrad/Chd7/P2rx4	32
Dusp1/Dusp5/Setd2/Rf1/Cnmb1/Tnrc6c/Paf1	7
Mef2c/Rc3h2/Bcl2/Ikbbk/Tnfr13c/Bcl211/Dock11	7
Fkbp4/P4ha1/Fkbp1a/Nktr/Pp1g/Pow1/Ranbp2	7
Bod1/Pcna/Cdk9/Atrv/Fam111a/Tonf1/Nucks1	7
Nr4a1/Pde4b/Klf4/Mef2c/Foxp1/Smad7/Atf2b1/Akap13/Ntacc3/Tmed3/Nr3c1/Map2k1/Parp1/Sirt1/Foxo1/Ntacc1/Fkbp1a/Eno1/Camk2d/Nufs6/Sri/Cdk9/Ppp3ca/Grc10/Rock1/Rcad1/Bin1/Tbce/Akap9/Zc3h12a/P2rx4	31
Rhoc/Foxp1/Gpx1/Kdm6b/Cic4/Ikbbk/Bsg/Rap1a/Cnm2/Rock1/Myd88/Cnmb1/Msn/Myadm	14
Irs2/Pmaip1/Nr3c1/Sirt1/Foxo1/Ep300/Akt2/Inpp5k/Ogt/Ptpr2/Usp7/Plek/Supt20/Ncca2/Sk11/Ranbp2	16
Rhoc/Ikbbk/Rock1/Ep41/Plek/Rhog/Rhoc/Tnfr1/Calr	9
Phf14/Pbxip1/Rf4/Sirt1/Ldb1/Ep300/Par1/Kmt2a/Kat5a	9
Smad7/Clec2a/Cr1/Cd84/Arnt2/Cd55/Rabgef1/Bst2/Ptprc/Bcl6	10
Hsp90ab1/Hsp90aa1/Klf4/Pges2/Myc/Arnt2/Npm1/Camk2c/Pcna/Cnmb1	10
Kf4/Rp24/Atf2/Pcid2/Casp2/Dgkz/Bcl2/Zfp362/Zfp655/Toppb1/Chfr/Sde2/Cnmb1/Pten/Vk/Pml/Rad21/Donson/Gpr132/Foxn3	20
Gpx1/Klf7/Ccdc188/Dhps/Map2k1/Sirt1/Nadk/Foxo1/Ptpry/Pde3b/Zbtb20/Inpp5k/Sri/Ogt/Ptpr2/Ppp3ca/Pik3r1/Sid2/Eny2/Sk11/Ppp2ca/Nucks1/Ptprc	23
Mef2c/Foxp1/Naca/Ntacc3/Nr3c1/Bcl2/Sirt1/Arnt2/Daxx/Ntacc1/Cnrd2/Cdk9/Mecp2/Ankrd17/Ep21	15
Klf4/Km2e/Casp2/Dgkz/Crebbp/Bcl2/Zfp655/Anp32b/Ankrd17/Ccnd3/Sde2/Pten/Pml/Cnd2	15
Macf1/Actg1/Lims1/Ldb1/Ptpry/Iqgap1/Rock1/Rcc2/Pten	9
Macf1/Actg1/Lims1/Ldb1/Ptpry/Iqgap1/Rock1/Rcc2/Pten	9
Foxp1/Sirt1/Lbn/Cnot1/Per1/Cnot2/Calr	7
Hspa1a/Hspa1b/Serp8/Rnf4/Rae1/Ctcf/Numa1	7
Cdc25b/Iqgap1/Npm1/Camk2d/Mecp2/Rcc2/Chfr/Rad21/Donson/Lmb1/Gpr132/Foxn3	12
Hsp90ab1/Hsp90aa1/Ppp1r15a/Smad7/Bcl2/Bcar3/Arnt2/Akt2/Inpp5k/Ogt/Hax1/Fnip1/Pten/Akap9/Php/Nsd1	16
Map2k1/Myc/Parp1/Ep300/Fis1/Zbtb20/Eno1/Ogt/Tspo/Cox7a2/Fcn	11
Pde4b/Hsp17/Arid5a/Laptm5/Tcrg1/Cd2/Tnfr13c/H2-M3/Gadd45g/Ceblpg/Iifar1/C1qbp/Ccr7/Zc3h12a	14
Gpx1/Klf7/Ccdc188/Dhps/Map2k1/Sirt1/Nadk/Foxo1/Ptpry/Pde3b/Zbtb20/Inpp5k/Sri/Ogt/Ptpr2/Ppp3ca/Pik3r1/Sid2/Eny2/Sk11/Ppp2ca/Nucks1/Ptprc	23
Pde4b/Mef2c/Tacc22d/Rc3h2/Pmaip1/Mir142hg/Tcrg1/Bcl2/Ikbbk/Sh2b3/Tnfr13c/Bcl211/Dock11	13
Ich/Ctcf/Cd86/Ccr7/Irak3	5
Rhoc/Foxp1/Bsg/Cnm2/Cnmb1	5
Arnt2/Nkx1/C1qbp/Ccr7/Irak3	5
Lmd1/Ddx6/Cnot1/Pan3/Cnot2	5
Smad7/Rc3h2/Ira4/Zc3h12a/Bcl6	5
Sirt1/Foxo1/Ptpr2/Supt20/Sk11	5
Rhoc/Foxp1/Bsg/Cnm2/Cnmb1	5
B3gnt7/Chst12/Nkx1/Yy11/B3gnt2/Ccnd3/Ctcf/Hexa	8
Smad7/Rc3h2/Hsp17/Nkbid/Ptpr2/Ira4/Zc3h12a/Bcl6	8
Hsp90ab1/Rps7/Cenk2a1/Odrpk1/Smarcc1/Ogt/Usp7/Pml	8
Wnk1/Klf4/Map1/Rps12/Rnf13/Zeb2/G3bp1/Cmah/Pbxip1/Lmd1/Chd8/Egr1/Myc/Csrk1d/Ldb1/Foxo1/Zran1/Cenk1g3/Siah2/Cenk2a1/Ube2b/Nkbf1/Rf1/Tks2/Cnmb1/Pten/Sk11/Cenk1a1/Paf1/Kdm6a/ApoE/Ccdc88c	32
Hspa1a/Hspa1b/Ubb5/Rps3/Serp8/Rnf4/Csrk1d/Ndc80/Rae1/Map4/Kpn1/Mecp2/Atrv/Tbce/Ctcf/Uvrag/Numa1	17
Cited2/Egr1/Hf1/an/Nfe22	4
Kdm5a/Mor4d2/Sirt1/Tb1/x/Per1/Akap8/Pml/Ek4/Bcl6/Nipbl	10
Juv/Fos/Wnk1/Mef2c/Junb/Junb/Ntacc3/Cic4/Iqgap1/Fus	10
Gpx1/Mu1/Ptsr/Pmaip1/Arnt2/Chchd10/Ep300/Rala/Fis1/Gshim/Tspo/Hgd1a/Fcn/Bcl211	14
Sp100/Xpo1/Anp32b/Xpo8/Srh/Hspa8/Rbm22/Calr/Ceif1	9
Pde4b/Atp2b1/Ntacc3/Ahnak/Diaph1/Bcl2/Cd84/Arnt2/Fkbp1a/Camk2d/Inpp5k/Sri/Tspo/Ep41/Bin1/Cd19/Dbl/Cnmb1/Ppp2ca/Pml/Rrad/Chd7/P2rx4	23
Hsp90aa1/Sah2/Capp/Myc1c/Rps3/Sptbn1/Tmod3/Fkbp4/Arpc6/Fchs2d/Mecp2/Arfgef1/Hax1/Bin1/Fil/Akap9/Dnbl/Cyp2/Myadm/Numa1	20
Rp35/Rp7a/Nkx1/Npm1/Nip2/Pes1	6
Cdc25b/Npm1/Camk2d/Mecp2/Rcc2/Lmb1	6
Birc3/Nmi/Ube2d1/Birc2/Gabarap/Trip12	6
Juv/Klf4/Mef2c/Foxp1/Mef2d/S1pr1/Naa35/Egr1/Myc/Camk2d/Pik3r1/Myd88/Cnmb1/Pten/Psp6kb1/Gna13/ApoE	17
Wnk1/Klf4/Map1/Rps12/Rnf13/Zeb2/G3bp1/Cmah/Pbxip1/Lmd1/Chd8/Egr1/Myc/Csrk1d/Ldb1/Foxo1/Zran1/Cenk1g3/Siah2/Cenk2a1/Ube2b/Nkbf1/Rf1/Tks2/Cnmb1/Pten/Sk11/Cenk1a1/Paf1/Kdm6a/ApoE/Ccdc88c	32
Irs4/Bcl2/Ptpr2/Ly9/Dock2/Sk11/Ptprc	7
Ptpry/Pkcb/Lmbd1/Inpp5k/Ptpr2/Rps8kb1/Seca3	7
P2ry10/Atp2b1/Msa4a1/S1pr1/Tcrg1/Anxa7/Ccdc47/Diaph1/Mcur1/Bcl2/Pkcb/Fis1/Got1/Fkbp1a/Camk2d/Siv/Cd55/Herpud1/Atp2c1/Nfss/Cd19/Cxcr5/Dbl/Ccr7/Cu15/Gpr65/Tmco1/Pml/Gna13/Ptpr/ApoE/Chd7/P2rx4/Chc	34
Mef2c/Fbx20/Bcl2/Mecp2/Ppp3ca/Tspo/Git2/Dbl/Pten/Psp6kb1/ApoE/P2rx4	12
Klf4/Mef2c/Rhoc/Dusp1/Cited2/Sp100/Stgal1/Bcl2/Cic4/Ptpry/Nfe22/Krt11/Mecp2/Stap1/Trip53inp1/Nisch/Rabgef1/Pten/Cd200/Bst2/Fcn/Gna13/ApoE/Osbp8/Calr	26
Smad7/Rc3h2/Mat1/Nkbid/Ira4/Ccr7/Zc3h12a/Bcl6	8
Klf4/Mef2c/Rhoc/Dusp1/Cited2/Sp100/Bcl2/Cic4/Ptpry/Nfe22/Krt11/Mecp2/Stap1/Trip53inp1/Nisch/Rabgef1/Pten/Cd200/Bst2/Fcn/Gna13/ApoE/Osbp8/Calr	24
Hsp90ab1/Rps7/Cenk2a1/Odrpk1/Smarcc1/Ogt/Usp7/Pml/Usp19	8
Hspd1/Foxp1/Smad7/Rc3h2/Mat1/Ira4/Nkbid/H2-M3/Gadd45g/Ly9/Cd19/Ira4/Ccr7/Cd81/Relb/Zc3h12a/Ptprc/Bcl6/Dock11	19
Gpx1/Klf7/Irs2/Ccdc188/Egr1/Sirt1/Nadk/Pkcb/Eif2b2/Zbtb20/Sri/Ogt/Ppp3ca/Vamp2/Sid2/Eny2/Ppp2ca	17
Hsp90aa1/Mu1/Atf2/Pmaip1/Myc/Chchd3/Bcl3/Dynl1c/Chchd10/Gshim/Bcl211/Hspa4	12
Dnajb1/Dusp1/Hipk3/Sirt1/Ptpry/Sh2b3/Inpp5k/Sk38/Pten/Irak3/ApoE/Ptpn1	12
Hsp90aa1/Hsp17/Hsp17/Mef2c/Syk/Irs2/H2-Ab1/Rps3/Pcid2/Inpp5d/Sart1/SH3bp1/Mat1/Dhps/Rasa3/Bcl2/Nkbid/H2-Eb2/Tnfr13c/Cd55/Cd86/Dock8/Myd88/Irs1/Kra4/Rhoc/Cd81/Pell1/Ptprc/Bcl6	31
Hspa8/Jun/Sk17b/Wnk1/Syk/Ck1c/Csrk1g3/Smg1/Cank2a1/Iqgap1/Sk2/Camk2d/Eif2ak3/Hspa9/Sk11/Ppp2ca/Irak3/Wk1/Ptprc/Ck4	20
Klf2/Rc3h2/Bcl2/Tmed2/Cic4/Daxx/Ceif1/Ankrd11/Ep300/Ndus8/Ccm2/Kmt2c/Atx/Lncprnt/Tnks2/Plac8/Kdm6a/Chd7/Nipbl	19
Hsp90ab1/Ppp1r15a/Ppp1r15b/Ppp2ca/Ptprc	5
Cabin1/Atrv/Ubn1/Nasp/Supt16	5
Juv/Fos/Nkbia/Nkx1/Chuk	5
Dhx36/Myc/Parp1/Smg5/Smg1/Atrv/Tnks2/Cnmb1/Pml/Gn3	10
Btb9/Ch8/Crebbp/Egr1/Mecp2/ApoE/Ccnd2	7
Sp100/Oa9/Ankrd13c/Chchd10/Tspo/Rer1/Pml	7
Smad7/Rc3h2/Cr11/Cd55/Ira4/Zc3h12a/Ptprc/Bcl6	8
Macf1/Atp5g1/Zfyve27/Golga4/Eif2b2/Dnbl/ApoE/Gd1	8
Kdm5a/Sirt1/Ep300/Fry/Akap8/Pml/Bcl6/Nipbl	8
Laptm5/Dgkz/Eif1/Ptpry/Ctcf/Ptpr2	6
Vps37b/Tm25/Vapa/Trim12a/Pml/Tfm11	6
Klf7/Sp100/Oa9/Snx12/Pde4b/Inpp5k/Ogt/Ppp3ca/Der2/Eny2/Cd200/Ppp2ca/ApoE/Gd1	14
Kmt2e/Arnd4/Satb1/Crebbp/Snrp3/Setd2/Myc/Cntrl/Parp1/Sirt1/Mt2/Kmt2c/Ogt/Snw1/Mecp2/Ehmt1/Avs1/Atrv/Pax5/Rf1/Zc3h13/Cnmb1/Paf1/Kmt2a/Ned1/Chtop/Pmt1	27
Rhoc/Foxp1/Hsp17/Sirt1/Ets1/Nfe22/Bsg/Sp1/Zc3h12a/P2rx4/Calr/Atf5a1	12
Igfa4/Lims1/Sf6g1/Vamp3/Rcc2/C1qbp/Lamb3/Dnm2/Myadm/Nedd9/Calr/Parvg	12
Macf1/Nsf/Sptbn1/Vamp3/Golga4/Vamp2/Atp2c1/Golga7/Sy11	9
Rab43/Tcrg1/Atg12/Rb1ccc1/Pk3c3/Gabarap/Nsf1c/Trip53inp1/Wp2/Map1lc3a/Rab3gap1	11
Rps3/Tp11/Pmaip1/Smchd1/Setd2/Myc/Parp1/Sirt1/Smg1/Npm1/Pcna/Cdk9/Ceblpg/Nmcc4a/Ptfg1p/Fus/Bclaf1/Trip12/Pml	19
Juv/Fos/Wnk1/Mef2c/Junb/Junb/Ntacc3/Sic3oa5/Tcrg1/Anxa7/Bcl2/Cic4/Daxx/Nfe22/Iqgap1/Mecp2/Ppp3ca/Fus/Ppp2ca/Chuk/Glut1/P2rx4/Gd1	23
Foxp1/Arid5a/Laptm5/Mat1/Dhx36/Sirt1/Denn1b/Dnajb9/Cd55/Cd86/Ira4/Cd81/Ptprc	13
Kmt2e/Tmod3/Crebbp/Cdc25b/Camk2d/Mecp2/Anp32b/Rcc2/Ankrd17/Ccnd3/Rps6kb1/Lmb1/Cnd2	13
Rps2/Rpl13a/Eif2e2/Eif2sx	4
Klf2/Snw1/Cnot1/Calr	4
Ptpry/Rap1a/Rabgef1/Ptprc	4
Sart3/Ichv/Dnajb2/Zc3h12a	4
Erlin1/Nkx1/Plek/ApoE	4
Hnmp1/Eif3e/Cdk9/Nucks1	4
Gpx1/Klf7/Irs2/Ccdc188/Egr1/Sirt1/Nadk/Pkcb/Eif2b2/Zbtb20/Sri/Ogt/Ppp3ca/Vamp2/Sid2/Eny2/Ppp2ca	17
Pds5a/Naa50/Naa10/Atrv/Cnmb1/Rad21/Escoc1/Nipbl	8

Hsp90aa1/Rel/Crebbp/Nmi/Zbt20/Zc3hav1/fnar1/Relb/Riok3	9
Hsp90aa1/Rel/Crebbp/Nmi/Zbt20/Zc3hav1/fnar1/Relb/Riok3	9
Klf4/Junb/Rpl13/Sk3b1/Matr3/Ctcd2/N4bp2/Wdr74/Med21/Cnot1/Cnot2/Cdk11b/Rfl1/Sp1/Nasp	15
Rhob/Cdc42e2/Plekho1/Anx7/Sk3bp1/Lmd1/1Diaph1/Epb41/Arhgap15/Rhog/Rhoq/Phip/Brd1/Gna13/Msn	15
Gpx1/Klf7/Ccdc186/Sirt1/Nadk/Pde3b/Prkcb/Zbt20/Sri/Ogt/Ppp3ca/Vamp2/Sit2/Eny2/Ppp2ca	15
Mac1/Actg1/Lims1/Bcl2/Ldb1/Pprj/Iqgarp1/Rock1/Rcc2/Pten/Tin1	11
Gpx1/Klf7/Ar2/Ccdc186/Egr1/Sirt1/Nadk/Pde3b/Prkcb/Zbt20/Sri/Ogt/Ppp3ca/Vamp2/Sit2/Eny2/Ppp2ca	17
Me2c/Tsc2d3/Rc3h2/Pmaip1/Tcirg1/Bcl2/lkbbk/Tnfrs13c/Bcl2l11/Dock11	10
Ubb/Shias5/Rps7/Pmaip1/Sirt1/Ep300/Snr1/Ptlig1p/Sk11/Pmi	10
Kdm5a/Kdm6b/Umj1c/Ube2b/Kdm6a/Kdm7a	6
Kdm5a/Kdm6b/Umj1c/Ube2b/Kdm6a/Kdm7a	6
Ah2/Rere/Herc1/Map2k1/Bcl2/Ldb1/Sec24b/Wnn/Arcn1/Mecc2/Ogdh/Ptap/Slc4a7	13
Gapdh/Tim25/Akap13/Dhx3b/Prkcb/lkbbk/Zc3hav1/Ankr17/Myd88/Ctmb1/Tim12a/Pel1/Chuk	13
Nk4a1/Pde4b/Wnk1/Syk/Rpl13a/Rps19/Dusp1/S1pr1/Gsm3/Ano6/Hsp11/Adam10/Arnt2/Ppry/Bsg/Stap1/Rhog/C1qbp/Cxcr5/Ccr7/Cnr2/P2rx4/Ca1r/Il17ra	24
Smad7/Arid5a/Laptm5/Malt1/Dhx36/Sirt1/Dennd1b/Cd55/Baz2/Itih3/Cd81/Bcl6	12
Crebbp/Dhx36/Parp1/Sirt1/Ep300/Npm1/Akt2/Pcna/Trip5inp1/Pik3r1/Soe2/Sk11	12
Atp6v0a1/Tcirg1/Clic4/Snarp1/Dmx1	5
Orc3/Bod1/Poik4/Polg/Topbp1/Npm1/Pcna/Cdk9/AtrX/Fam111a/Tons1/Nucks1/Donson/Spk2	14
Hsp90ab1/Hsp90aa1/Mact1/Irf1/Rnf48/Atpsg1/Zlyve27/Dig2b/Golga4/Eif2b/Dnm2/Dbl/Apoe/Gdi1	14
Laptm5/Plekhl1/Map2k1/Srx12/Arf8b/Pik3c3/Vamp3/Usip7/Mecc2/Ctcs/Snf10/Vti1b/Spag9/Sys1/Msn	15
Sit2/Capp/Myo1c/Sptbn1/Tmod3/Diaph1/Ptstbp1/Arpc5/Fchs2d/Argef1/Hax1/Bin1/Mts1/Flil1/Dbln1/Cyfp2/Myadm	14
Hspa8/Hspd1/Smad7/Arid5a/Ctcd2/Malt1/Cr11/Arnt2/H2-Q7/Fbx38/Dennd1b/H2-M3/Cd55/H2-Q6/H2-Q4/Cd81/Ptprc/H2-T23/Bcl6	17
Atp5a/Map2k1/Atp5c1/Myo/Parp1/Atpsg1/Eno1/Ficn/Atp5a1	9
Sp100/Onk3/Anrd13c/Chchd10/Tspo/Perr1/Vps13a/Tnrc6a/Pmi	9
Me2c/Fbx20/Bcl2/Ep300/Mecc2/Ddb/Rps6bk1/Apoe	8
Mu1/Sp100/Sec22d3/Ptbn2/fnar1/Stat1/Myd88/Ythd3	8
Me2c/Naca/Tsc22d3/Bcl2/Ctmb1/Rps6bk1/Ficn/Usip9	8
Cdc25b/Topbp1/Camk2d/Mecc2/Rcc2/Chfr/Rad21/Donson/Lmnb1/Gpr132/Foxn3	11
Hspa8/Hsp90ab1/Gapdh/Rpl30/Syk/Rps19/Ctcd2/Cr11/Arf8b/Arnt2/H2-Q7/H2-M3/Cd55/Stap1/Ceppg/H2-Q6/Myd88/H2-Q4/Bcl2l11/Ptprc/H2-T23	21
Hspa1a/Hspa1b/Rpl24/Pcid2/Pds5a/Naa50/Naa10/Nudo/Frs1/Nsf11c/Kpnb1/Reep3/Atrv/Ctcs/Cdk11b/Nk/Akap6/Phip/Emi4/Rad21/Nipbl/Numa1	22
Dnaj1/Rps7/Smad7/Rps3/Arnt2/Ctfl/Nms1/abp/Tspo/Usip4/Trip12	10
Me2c/Foxp1/Me2f/Rpl13/Akap13/Ah2/Ppsa2/Ano6/Ctcd2/Ankr11/Ep300/Sh2b3/Yf11/Rabgap11/Pev7/Fil1/Opa3/Glg1/Ptprc/Foxn3	20
Dnaj1/Traf4/Gadd45b/Hpk3/Irb1/Bcl11/Traf1/Gadd45g/Map4k2/Zfp822/Per1/Zmynd11/Myd88/Lmnb1	14
Me2c/Ep300/Sh2b3/Rabgap11/Fil1/S1pr1/Pmt1	7
Mact1/Herpud1/Zland2a/Sprp1/Tfam1/Sec63/Rab3gap1	7
Mact1/Actg1/Lims1/Sit2/Ldb1/Bcl2/Ldb1/Pprj/Plekha2/Iqgarp1/Rock1/Rcc2/C1qbp/Pik3r1/Pten/Dnm2/Myadm/Bcl6/Nedd9/Calr	19
Pde4b/Wnk1/Syk/Rpl13a/Rps19/Dusp1/S1pr1/Gsm3/Ano6/Adam10/Ppry/Bsg/Stap1/C1qbp/Cxcr5/Ccr7/Cnr2/Ca1r/Il17ra	24
Ctcd2/Actg1/Sit2/Capp/Myo1c/Sptbn1/S1pr1/Tmod3/Arpc5/Fchs2d/Inpp5k/Argef1/Plek/Hax1/Bin1/Pik3r1/Mts1/Fil1/Gpr56/Dbln1/Cyfp2/Myadm	22
Mact1/Actg1/Lims1/Bcl2/Ldb1/Pprj/Plekha2/Iqgarp1/Rock1/Rcc2/Pik3r1/Pten/Bcl6	12
Mact1/Irf1/Rnf48/Atpsg1/Zlyve27/Dig2b/Golga4/Eif2b/Dnm2/Dbln1/Apoe/Gdi1	13
Atp5a/Map2k1/Atp5c1/Myo/Parp1/Atpsg1/Eno1/Ficn/Atp5a1	9
Hsp90ab1/Myo1c/Pmaip1/Fis1/Akt2/Anp32b/Pcm1/Vamp2/Tmen30a/Pik3r1/Shv/Rbm22/Cd81/Zc3h12a	14
Map2k1/Ccnt2/Cntn1/Cnmb1/Scab9/Supt16	16
Lims1/Pprj/Iqgarp1/Rock1/Pik3r1/Iqsec1	6
Pdm2/Inpp5d/Map2k1/Bcl2/Polg/Sirt1/Umj1c/c/Kras/Npm1/Ndufs6/Pax5/Lncrpnt/Baz2b/Pten/Pmi/Gna13/Sec63/Apoe/Bcl6/Kat5a/Calr	21
Hspa1a/Hspa1b/hsp1/Mact1/Azin1/Rps3/Serp6/Fkbp4/Rnf4/Diaph1/Sirt1/Rae1/Xpo1/Npm1/Mecc2/Rock1/Ctcs/Akap9/Sk11/Emi4/Numa1	21
Mact1/Nap111/Zeb2/Dhx36/Bcl11a/Map2k1/Myo1st1/Cux1/Atpsg1/Zlyve27/Golga4/Eif2b/Snr1/Tspo/Bin1/I6st4/Ctmb1/Sk11/Dbln1/Apoe/Vim/Gdi1	23
Tcirg1/Inpp5k/Stap1/Rcc2/Plek/Rhog/Plekhl1/Dbln1	8
Klf2/Hsp90aa1/Klf4/Dynll1/H2-M3/Akt2/Tspo/Dnm2/Zc3h12a/P2rx4	10
Pgap1/Zfh3c3/Alg12/Zfh3c3/Pik3c3/Ugc9/Nm12/Dbl/Wip1/Golga7/Dpm1/Apoe/Rab3gap1	13
Wnk1/Mact1/Rps12/Rnf212/Zh3c2/G3bp1/Cmah/Pmp1/Lmd1/Chd8/Egr1/Cank1d/Foxo1/Zrnb1/Cank1g3/Siah2/Cskn2a1/Ube2b/Nfk1b1/Tnfr2/Sk11/Cank1a1/Apoe/Ccdc8b	24
Hsp90ab1/Ar2/Myo1c/Pmaip1/Myo18a/Sirt1/Nadk/Fis1/Bsg/Akt2/Sra/Ang32b/Pcm1/Vamp2/Cd2ap/At2c1/Tmem30a/Pik3r1/Shv/Rbm22/Cd81/Zc3h12a/Gliud1/Crebrf	24
Rps8/Uba2/Rps5/Rpl18/Rplp2/Rpsa/Rpl19/Rpl9-ps6/Rps24/Rps26/Rps4x/Fau/Rpl8/Rp38/Rps21/Rps7/Rp37/Rps27/Rps20/Rpl30/Rps16/Rps2/Rpl13a/Rpl18a/Rpl13/Rps19/Rps13/Rps35/Rpl21/Rps12/Rps27a/Rp28/Rplc	46
Rps8/Uba2/Rps5/Rpl18/Rplp2/Rpsa/Rpl19/Rpl9-ps6/Rps24/Rps26/Rps4x/Fau/Rpl8/Rp38/Rps21/Rps7/Rp37/Rps27/Rps20/Rpl30/Rps16/Rps2/Rpl13a/Rpl18a/Rpl13/Rps19/Rps13/Rps35/Rpl21/Rps12/Rps27a/Rp28/Rplc	47
Rps8/Uba2/Rps5/Rpl18/Rplp2/Rpsa/Rpl19/Rpl9-ps6/Rps24/Rps26/Rps4x/Fau/Rpl8/Rp38/Rps21/Rps7/Rp37/Rps27/Rps20/Rpl30/Rps16/Rps2/Rpl13a/Rpl18a/Rpl13/Rps19/Rps13/Rps35/Rpl21/Rps12/Rps27a/Rp28/Rplc	46
Rps8/Uba2/Rps5/Rpsa/Rps24/Rps26/Rps4x/Fau/Rpl21/Rps7/Rps27/Rps20/Rps16/Rps2/Rps19/Rps13/Rps12/Rps27a/Rps3/Rps10/Rps17/Rps28/Larp4	23
Rps8/Uba2/Rps5/Rpsa/Rps24/Rps26/Rps4x/Fau/Rpl21/Rps7/Rps27/Rps20/Rps16/Rps2/Rps19/Rps13/Rps12/Rps27a/Rps3/Rps10/Rps17/Rps28/Larp4	23
Uba2/Spt18/Rplp2/Rpl19/Rpl9-ps6/Rpl8/Rp38/Rpl37/Rp30/Rpl13a/Rpl18a/Rpl13/Rp35/Rpl21/Rps12/Rp28/Rpl24/Rpl14/Rp31/Rpl35a/Rpl15/Rpl36a/Rpl7a/Rpl39	28
Rpl18/Rpl19/Rps26/Rps4x/Rpl8/Rp38/Rps21/Rp30/Rpl18a/Rpl13/Rps13/Rps35/Rp39/Rps19/Rps13/Rps12/Rps27a/Rps3/Rpl39/Naa38/Fus/Larp1/Larp4/Larp4b/Vim/Calr	24
Hspa1a/Hspa1b/Me2c/Malt1/Rbm39/Pmaip1/Snr1/Alps4a1/Pmi/STb1/Rsf7/Sap18/Pebp1/Sarf1/Dgkz/Dhx36/Srm2/Ndc1/Actn1/Ujsg36/Npm1/Snmp70/Dennd1b/Tcf12/Snrw1/Gcc10/Luc72/Pokip3/Smm1/Soe2/Zc3h13f1	50
Rps4x/Tuba1a/Mbn1/Tim25/Tubb5/Zfp36/Rp28/Rc3h2/Pcbp1/G3bp1/Lmd1/Dhx36/Lam2/Pabpc4/Hmnp/Ddx6/Celf1/Iqgarp1/Dhx30/Cdk9/Kpnb1/Rock1/Tnrc6a/Cnot1/Poik3/Par3/Cnot2/Blnk/Ythd3/Eif4e2/Larp1/Tnrc6	40
Rpl18/R19/Rps26/Rpl8/Rp38/Rps21/Rp30/Rpl18a/Rpl13/Rps13/Rp35a/Rpl7a/Rp39/Larp1/Larp4b	36
Rps4x/Tuba1a/Mbn1/Tim25/Tubb5/Zfp36/Rp28/Rc3h2/Pcbp1/G3bp1/Lmd1/Dhx36/Lam2/Pabpc4/Ddx6/Celf1/Iqgarp1/Cdk9/Kpnb1/Rock1/Tnrc6a/Cnot1/Poik3/Par3/Cnot2/Blnk/Ythd3/Eif4e2/Larp1/Tnrc6c/Tim12a/Aba	38
Uba2/Spt18/Rplp2/Rpl19/Rpl9-ps6/Rpl8/Rp38/Rpl37/Rp30/Rpl13a/Rpl18a/Rpl13/Rp35/Rpl21/Rps12/Rp28/Rp24/Rpl14/Rp31/Rpl35a/Rpl15/Rpl36a/Rpl7a/Rp39/Mrps12/Npm1/Mrps15	27
N4a1/Gapdh/Caopy/Shias5/Tubb5/Myo1c/Pcid2/Rnf8/Anxa7/Vapa/Bcl2/Nup50/Parp1/Sirt1/Brnp/Ph20/Rb1cc1/Rae1/Xpo1/Pto1/Unc50/Nup88/Nup210/Nmm/Kpnb1/Mrps23/Pcm1/Casc3/Dnajb2/Bin1/Ankr117/Epc1/Eny2	49
Ph1/4/Atf2/Naa35/Morf4i2/Gm16286/Naa50/Crebbp/Naa10/Ph20/Ep300/Naa38/Ogt/Naa15/Supt20/Brd9/Epc1/Eny2/Ep400/Ph20l1/Kat6a	20
Ph1/4/Atf2/Naa35/Morf4i2/Gm16286/Naa50/Crebbp/Naa10/Ph20/Ep300/Naa38/Ogt/Naa15/Supt20/Brd9/Epc1/Eny2/Ep400/Ph20l1/Kat6a	20
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Mbn1/Tim25/Zfp36/Rc3h2/G3bp1/Dhx36/Pabpc4/Ddx6/Celf1/Kpnb1/Rock1/Ythd3/Larp1/Abr22/Pum2/Larp4/Larp4b	17
Hspa8/Hsp90ab1/Laptm5/Atpsv0a1/Tcirg1/Lamor2/Arf8b/H2-Q7/Rb1cc1/Mar2b1/H2-B6/Gabarap/H2-M3/Lmbrd1/Cyb561a3/Atg162/Vps13a/Frip1/H2-Q6/Sit2/Uvrag/Lamor3/Map11c3a/Vti1b/H2-Q4/Spag9/Ficn/Atpsv0	30
Sarb1/Sf5b1/Matr3/Clic4/Npm1/Snr1/Zfp326/Srm1/Ppig/Scat8/Akap8/Lbr/Lmri/Rad21/Ebna1/bp2/Lmnb1/Numa1	16
N4a1/Gapdh/Rnf6/Vapa/Bcl2/Nup50/Sirt1/Brnp/Ph20/Rb1cc1/Xpo1/Unc50/Nmm/Kpnb1/Mrps23/Pcm1/Casc3/Dnajb2/Ankr117/Epc1/Tnrc18/Ctmb1/Ranbp2/Lbr/Pmi/Pum2/4/Ostp8/Lmnb1/Cnd2	30
Sarb1/Rnf6/Crebbp/Sp100/Rnf4/Hpk3/Sirt1/Daxx/Tdp2/Ei2a/Topbp1/Cdk9/Atrv/Chfr/Pmi/Kat6a	16
Fth1/Ftfl1/Actg1/Syk/Capp/Myo1c/Rab43/Tcirg1/Sk3bp1/Rpl13a/Rpl18a/Rpl18a/Rpl13/Rp35/Rpl21/Rps12/Rp28/Rp24/Rpl14/Rp31/Rpl35a/Rpl15/Rpl36a/Rpl7a/Rp39/Mrps12/Npm1/Mrps15	47
Mu1/Atfp21/H13/Atp6v0a1/Ccdc47/Aup1/Mcur1/Chchd3/Anfip1/Chchd10/H2-Q7/Scd1/Cux1/Zlyve27/Fis1/Unc50/Ktn1/Coq2/Ghntm/Vp23b/Srx3/Rer1/Ergic3/Dnajb2/Der2/Preb/Atpm2/Tfam1/Golga7/Tmco1/Sys1/Atf6	37
Pripap2/Tcoa1/Poik4/Rplc/Rb1cc1/Pik3c3/lkbbk/Ccnt2/Poia2/GT2a2/Pkag1/Pcna/Snr1/Cnppd1/Pik34/Cdk9/Poia1/Ccnt1/Pik31/Ccnt3/Uvrag/Ppns1/GH2b/Rf1/Paf1/Chuk/Socs3/Ccnt2	28
Mu1/Atfp21/H13/Atp6v0a1/Ccdc47/Aup1/Mcur1/Chchd3/Anfip1/Chchd10/H2-Q7/Scd1/Cux1/Zlyve27/Fis1/Unc50/Ktn1/Coq2/Ghntm/Vp23b/Srx3/Rer1/Ergic3/Der2/Preb/Atpm2/Tfam1/Tmco1/Sys1/Atf6/Sic25a3/H2-T22	35
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Sarb1/Sf5b1/Matr3/Clic4/Npm1/Snr1/Zfp326/Srm1/Ppig/Scat8/Akap8/Pmi/Rad21/Lmnb1/Numa1	15
Actg1/Syk/Capp/Myo1c/Rab43/Tcirg1/Myo18a/H2-Q7/Pik3c3/Vamp3/Rap1a/Uvrag/Zyx/H2-T23/Pid4/Vim/Calr	17
Hspa8/Pten/Sf5b1/Sarb1/Srm2/Snrp3/lay1/Lsm2/Rbm17/Rbm5/Snmp70/Snr1/Prl/Slb5/Casc3/Magoh/Luc72/Srm1/Lsm8/lk/Rbm22/Pwtd1/Hnmp11/Mtap1a/PspB	24
Ph1/4/Atf2/Morf4i2/Crebbp/Ph20/Ep300/Ogr/Supt20/Brd8/Epc1/Eny2/Ep400/Ph20l1/Kat6a	20
Cytl1/Sla/Syk/Atp2b1/H13/Rasa3/Gng5/Cd2/Traf1/lkbbk/Kras/Birc2/Iqgarp1/Ppp3ca/Gng2/Mts1/Pten/Cnr2/Gna13/Chuk/Msn/Ptprc/Ptgn1	23
Klf6/Smad7/Sp140/Traf4/Arf4/Malt1/Znrfd2/Ubt/Smarc5/Sirt1/Rae1/Herc4/Wdr43/Pipco1/Cd2ap/Fam111a/Mn1/Pax5/Nop56	19
Zfp36/Lmd1/Lsm2/Ddx4/Tnrc6a/Cnot1/Par3/Cnot2/Ythd3/Eif4e2/Tnrc6c/Tim12a/Zc3h12a/Tnrc6b	14
Sf3b1/Sarb1/Srm2/Snrp3/lay1/Lsm2/Snmp70/Snr1/Casc3/Luc72/Lsm8/lk/Rbm22/Map1a/PrpB	15
Afh4/Ccnt2/Snr1/Cdk9/Afh1/Ccnt1/Tons1/Rf1/Paf1/Ccnt1/Supt16	11
Arid1b/Smarc5/Rf1/Smarc1/Brd9/Csnk2a1/Smarcc1/Bptf/Arid1a/Brd8/Ep400/Smarc2/Chd4	13
Arid1b/Smarc5/Rf1/Smarc1/Brd9/Csnk2a1/Smarcc1/Bptf/Arid1a/Brd8/Ep400/Smarc2/Chd4	13
Hspd1/Rps3/Timm8b/Atps5e/Pmpcb/Ndufs3/Ndufc1/Atp5c1/Mcur1/Chchd3/Bcl2/Nduf1/Polg/Cox7b/Sirt1/Ak2/Chchd10/Atpsg1/Tufm/Unc50/Ndufs8/Coq2/Nmm/Ghntm/Cade1/Sfkn3/Sic25a51/Ndufs8/Cox7a2/Hadha/Higd1	41
Tex10/Pelp1/Kdm6b/Chd8/Snrp3/Sirt1/Ph20/Mit2/Kmt2c/Rioc1/Zc3h13/Kdm6a/Kmt2a/Nsd1/Pmt1	15
Hsp90aa1/Mact1/Myo1c/Rps3/Plekho1/Tmod3/Diaph1/Pprj/Iqgarp1/Akt2/Inpp5k/Rfog1/Plek/Cd2ap/Dnm2/Dbln1/Atpsv1b2/Tin1/Myadm	19
Hspa8/Pde4b/Mact1/Rpl8/Nsf/Rp38/Rps27/Rp30/Rpl18a/Rps19/Rps13/Rpl14/Rps3/Sptbn1/fhngp1/Hsp1/Adam10/Eif3a/Bcl11a/Nr3c1/Exoc4/Eif4g2/Arnt2/Map4/Ncoa2/Myd88/Ctmb1/Ppp2ca/Dbln1/P2rx4/Iqsec1	31
Hspa1a/Hspa1b/Hsp90ab1/Gpx1/Arh1/Tdp2/Cabin1/Herpud1/Dnajb2/Peap/Ranbp2/Pabpn1/Nxf1	13
Hspd1/Rhob/H2-Ab1/Plekhl1/Phd3/Map2k1/Srx12/Uhrf1p11/Ich1/Tmem127/H2-Q7/Hmnp3/Siah2/Mon2/Rap1a/H2-M3/Rcc2/Rabgarp1/Der12/H2-Q6/Uvrag/Rabgef1/Vti1b/H2-Q4/Sam99/H2-T23/Apoe/Pk4/Phn1/Tmem11	30
Rps7/Ftfl1/Bms1/Wdr74/Rpl1/Rs1/Zfp622/Rioc1/Pes1/Phospho10/Rioc3/Nop56/Ebna1/bp2	17
Ganab/St3b/H13/Rnf125/P4ha1/Aup1/Sec11c/Arfip1/Dnajb11/Krtcap2/Sprp/Der2/Sel1/Faf1/Sec63/Hsp90b1/Calr	13
Jun/Fos/Jund/Smad7/Junb/Hmnpab/Cnem/Atf2/Tcoa1/Crebbp/Amt/Ldb1/Mxd4/Tcf4/GH2a2/Tcf12/Cebpa/GH2b/Ctmb1/Chd4	20
Pde4b/Mact1/Rpl8/Nsf/Rp38/Rps27/Rp30/Rpl18a/Rps19/Rps13/Rpl14/Rps3/Sptbn1/fhngp1/Hsp1/Adam10/Eif3a/Bcl11a/Nr3c1/Exoc4/Eif4g2/Arnt2/Map4/Ncoa2/Myd88/Ctmb1/Ppp2ca/Dbln1/P2rx4/Iqsec1	30
Pmn/Sf5b1/Sarb1/Srm2/Snrp3/lay1/Lsm2/Snr1/Magoh/Srm1/Rbm22/Pwtd1/Hnmp11/PprfB	14
Rnf125/B3gn7/Stegal1/Mbtps1/H2-Q7/B3gn75/Cux1/Ujgoc/H2-M3/Unc50/Tvp23b/Yf11/Argef1/Rer1/B3gn12/Ergic3/Copt2/H2-Q6/Atpm21/Dnm2/Golga7/H2-Q4/Sys1/Glg1/H2-T23/Numa1	26
Cytl1/Sla/Syk/Atp2b1/Gng5/Cd2/Traf1/lkbbk/Kras/Birc2/Iqgarp1/Ppp3ca/Gng2/Mts1/Pten/Cnr2/Gna13/Chuk/Msn/Ptprc	23
Rb1cc1/lkbbk/Ccnt2/Pcna/Snr1/Cnppd1/Cdk9/Ccnt1/Ccnt3/Uvrag/GH2b/Chuk/Ccnt2	10
Hspa8/Pde4b/Mact1/Rpl8/Nsf/Rp38/Rps27/Rp30/Rpl18a/Rps19/Rps13/Rpl14/Rps3/Sptbn1/fhngp1/Hsp1/Adam10/Eif3a/Bcl11a/Nr3c1/Exoc4/Eif4g2/Arnt2/Map4/Ncoa2/Myd88/Ctmb1/Ppp2ca/Dbln1/P2rx4/Iqsec1	31
Arid1b/Smarcc1/Brd9/Smarcc1/Arid1a/Smarc2	6
Hspa8/Gapdh/Rhob/H2-Ab1/Tp11/Tcirg1/Map2k1/Lamor2/Pik3c3/H2-Eb2/Rap1a/Kidins220/Zc3hav1/Pik34/Cyb561a3/Der12/Ccz1/Uvrag/Lamor3/Psap/Map11c3a/Bst2/Vti1b/Apoe	24
Vps37b/Capp/Hepacam2/Arf8b/Clic4/Ist1/Nudo/Pik3c3/Cel2/Iqgarp1/Mical1/Rcc2/Birc6/Uvrag/Ficn/Emi4/Hsp90b1/Gln3/Safb/Gdi1	20
Hspa8/Pde4b/Mact1/Rpl8/Nsf/Rp38/Rps27/Rp30/Rpl18a/Rps19/Rps13/Rpl14/Rps3/Sptbn1/fhngp1/Hsp1/Adam10/Eif3a/Bcl11a/Nr3c1/Exoc4/Eif4g2/Arnt2/Map4/Ncoa2/Myd88/Ctmb1/Ppp2ca/Dbln1/P2rx4/Iqsec1	31
Rb1cc1/lkbbk/Ccnt2/Pkag1/Pcna/Snr1/Cnppd1/Cdk9/Ccnt1/Ccnt3/Uvrag/GH2b/Chuk/Ccnt2	10
Sf3b1/Sarb1/Srm2/Snrp3/Lsm2/Ppp58b/Lsm8/lk/Map1a/PrpB	14
Hspa8/Hsp90ab1/Laptm5/Arf8b/H2-Q7/H2-Eb2/H2-M3/Lmbrd1/Cyb561a3/Vps13a/Frip1/H2-Q6/Sit2/Vti1b/H2-Q4/Spag9/Ficn/H2-T23/Uba1	19
Hspa8/Hsp90ab1/Laptm5/Arf8b/H2-Q7/H2-Eb2/H2-M3/Lmbrd1/Cyb561a3/Vps13a/Frip1/H2-Q6/Sit2/Vti1b/H2-Q4/Spag9/Ficn/H2-T23/Uba1	19
Sf3b1/Sarb1/Snrp3/Lsm2/Sarb1/Snmp70/Argef1/Luc72/Lsm8/U2surp/PrpB	11
Myo1c/Pcid2/Nup50/Rae1/Nup88/Nup210/Kpnb1/Eny2/Ranbp2/Lbr/Nxf1	10
Sf3b1/Sarb1/Snrp3/Lsm2/Sarb1/Snmp70/Luc72/Lsm8/U2surp/PrpB	11
Hspa8/Hsp1/Mact1/Tuba1a/Tubb5/Dynll1/Tp11/Bod1/Eif3a/Ptbp1/Klf21b/Fkbp4/Tuba1b/Rnf4/Map2k1/Cank1d/Dynll1c/Daxx/Nudo/Gabarap/Iqgarp1/Map4/Reep3/Rcc2/Tbca/Rass3/Ncoa2/Ctcs/Map11c3a/Dnm2/Emi4/Bcl	4
Fth1/Pk3c3/Plekhl1/Map11c3a	5
Hsp90aa1/Mact1/Myo1c/Rps3/Plekho1/Diaph1/Pprj/Akt2/Inpp5k/Plek/Dnm2	11
Tex10/Pelp1/Kdm6b/Chd8/Sirt1/Ph20/Mit2/Kmt2c/Kdm6a/Kmt2a/Nsd1	11
Hspd1/Rps3/Timm8b/Atps5e/Pmpcb/Ndufs3/Ndufc1/Atp5c1/Mcur1/Chchd3/Bcl2/Nduf1/Polg/Cox7b/Ak2/Chchd10/Atpsg1/Tufm/Ndufs8/Coq2/Ghntm/Cade1/Sfkn3/Sic25a51/Ndufs8/Cox7a2/Hadha/Higd1a/Ndufs5/Mtx1/H	35
Sarb1/Tgp2b/Cenpa/Ddx6/Sirt1/Daxx/Ube2b/Mecc2/Cbx1/AtrX/Uhr2/Pmi/Uba1	13
Sf3b1/Sarb1/Srm2/Snrp3/Lsm2/Lsm8/lk/Map1a/PrpB	9
Cyfp/Mact1/Rhob/Akap13/Sptbn1/Hpp5d/Fry/Exoc4/Map2k1/Ptstbp1/Ich1/Daxx/Pkcb/Iqgarp1/Eno1/Akt2/Epb41/Cd2ap/Rhog/Fry/Ctmb1/Rhoq/Dbln1/Myadm/Osbpl8/Numa1	27
H13/Ccdc47/Aup1/Arfip1/H2-Q7/Scd1/Zlyve27/Kfn1/Ergic3/Dnajb2/Der2/Preb/Tram1/Tmco1/Atf6/H2-T23/Calr	18
Arid1b/Smarcc1/Smarcc1/Arid1a/Smarc2	6
Hspa8/Hspa1a/Hspa1b/Hspdl/Brc3/Tuba1a/Tubb5/Atp2b1/Ms4a1/Myo1c/Pag1/Tpp1/Ahnak/Tuba1b/Lamor2/Cd2/Cr11/Cbb/Kras/Bsg/Birc2/Iqgarp1/Cd55/Pgk1/I6st4/Lamor3/Ctmb1/Ppp2ca/Ptprc/Myadm/Atps5a1	31
Hspa8/Hspa1a/Hspa1b/Hspdl/Brc3/Tuba1a/Tubb5/Atp2b1/Ms4a1/Myo1c/Pag1/Tpp1/Ahnak/Tuba1b/Lamor2/Cd2/Cr11/Cbb/Kras/Bsg/Birc2/Iqgarp1/Cd55/Pgk1/I6st4/Lamor3/Ctmb1/Ppp2ca/Ptprc/Myadm/Atps5a1	31
Hsp90aa1/Mact1/Atfp21/Adrgfs/Myo1c/Rps3/Sptbn1/Plekho1/Tmod3/Dgkz/Exoc4/Diaph1/Arpc5/Dynt1c/Ldb1/Pprj/Iqgarp1/Akt2/Inpp5k/Rock1/Plek/Cd2ap/Hax1/Dock4/Ctmb1/Dnm2/Dbln1/Atpsv1b2/Tin1/Myadm/Vim/A	32
Hspd1/Nsf/Trapp8/Plekhl1/Ccdc186/Arf5c/Myo18a/Adam10/Atph/Stegal1/Mbtps1/Inpp5k/Yf11/Argef1/Vamp2/Atp11b/Birc6/Atp2c1/Akap9/Dnm2/Golga7/Wk11/Trappc8b/Sys1/Glg1/Pid4	26
Sf3b1/Sarb1/Snrp3/Lsm2/Sarb1/Snmp70/Argef1/Luc72/Lsm8/U2surp/PrpB	11
Cnt2/Pcna/Snr1/Cnppd1/Cdk9/Ccnt1/Ccnt3/Ccnt2	8
Ah2/Morf42/Ph20/Brd8/Epc1/Ep400/Ph20l1	7
Mrps6/Tomm6/Mrps12/Atps5e/Mrps52/Pmpcb/Ndufs3/Ndufc1/Atp5c1/Chchd3/Nduf1/Polg/Chchd10/Atpsg1/Ndufs6/Mrps7/Mrps23/Ndufs8/Hadha/Ndufs5/Mtx1/Mrpl15/Atps5a1	23
Dynll1/Capp/Rps3/Tp1/Hepacam2/Bod1/Diaph1/Myo/Arf8b/Csnk1d/Tb11x/Nudo/Rae1/Cdc25b/Npm1/Map4/Nsf11c/Cbx1/Rcc2/Epb41/Birc6/Ctcs/Ik/Ficn/Emi4/Nedd9/Numa1	27
H13/Ccdc47/Aup1/Arfip1/H2-Q7/Scd1/Zlyve27/Kfn1/Ergic3/Der2/Preb/Tram1/Tmco1/Atf6/H2-T23/Calr	18
Wdr74/Rpl1/Rs1/Zfp622/Pes1/Ebna1/bp2	6
Hspd1/Tmed5/Atph/Tmed2/Sec24b/Vamp3/Lmbrd1/Arcn1/Vamp2/Ergic3/Copt2/Hax1/Tmed9/Ctcs/Ergic2/Dnm2/Vti1b/Copa/Sec24c	19



Jun/KH4/Myo/Srt1/Pok2a/Ogt/Cnbn1/Sp1	8
Fh1/Ft1/Pk3c3/Pkhm1/Map1/c3a	5
Tmed5/H2-Q7/H2-M3/H2-Q6/Atp2c1/Pk3r1/Akap9/H2-Q4/Trapp6b/H2-T23	10
Ppp1r1Sa/le5/Ppp1r15b/Ppp3ca/Ppp2a/Ppp25a/Ppp2ca/Tox4	8
Ppp1r1Sa/le5/Ppp1r15b/Ppp3ca/Ppp2a/Ppp25a/Ppp2ca/Tox4	8
H2-Ab1/H2-Q7/H2-Eb2/H2-M3/H2-Q6/H2-Q4/H2-T23	7
Dyn1l1/Capp/Rps3/Hepacam2/Dlaph1/Tb1x/Nudo/Rae1/Map4/Rcc2/Epb41/Ctcr/Ic/Flcn/Em4/Numa1	16
Hsp1/Pmb3/Sec11c/Pmd3/Ubr1/Pamb6/Pmd2/Zland2a/Supt20/Dnajb2/Eny2/Pamd11	12
Lamtor2/Pde3b/Rap1a/Elmo1/Lamtor3	5
Lamtor2/Pde3b/Rap1a/Elmo1/Lamtor3	5
Fos/Jund/Kdm5a/Cenpa/Orc3/Pol44/I44/Parp1/Nfe2l2/Npm1/Tonsi/Cnrb1/Sp1/Chd4/Denson/Kat6a	16
Hsp1/Hspa1b/Hsp1/Mrps6/Rps3/Mps12/Mpl52/Pmpcb/Acs1/Adh2/Polg/Tufm/Dhx30/Mps7/Mrps23/Cipp/C1qbp/Hadha/Tfam/Hspa9/Glut1/Ppnr1/Mrpl15	23
H2-Q7/H2-M3/H2-Q6/Atp2c1/H2-Q4/H2-T23	6
Xst/Smchd1/Daxx/Birc2/Smarca1/Ube2b/Usp7	7
Hsp1/Pmb3/Pmd3/Ubr1/Pamb6/Pmd2/Zland2a/Dnajb2/Pamd11	9
Smarca1/Smarca1/Arid1a/Smarca2	4
Ccnt2/Snw1/Cdk9/Ccnt1/GItH5	5
Cux1/Unc50/Tvp23b/Rer1/Ergic3/Atp2c1/Golga7/Sys1	8
Pol44/Smarca5/Pcna/Ube2b/Rfc1/Tonsi/Denson/Zmiz2/Bcl6	9
Ccnt2/Snw1/Cdk9/Ccnt1	4
Cytl1/Sla/Syk/Gng5/Rb1cc1/Pk3c3/Kras/Nmt2/Iqgap1/Eno1/Pk3r4/Vps13a/Gng2/Pk3r1/Cnrb1/Wip2/Cnr2/Pmi/Gna13/Zc3h12a/Socs3/Bcl211/Apoe/Numa1	24
Tmed5/Tmed2/Sec24b/Ergic3/Tmed9/Ergic2/Wt1b/Sec24c	8
Daxx/Birc2/Smarca1/Ube2b/Usp7	5
Pnr1/Sap18/Acin1/Cas3/Magoh	15
Hsp90aa1/Macr1/Atp2b1/Adgre5/Myo1c/Rps3/Sptbn1/Plekho1/Dlaph1/Ppr/Akt2/Inpp5b/Plek/Dock8/Dnm2	5
Hsp1/Pmb3/Pmd3/Ubr1/Pamb6/Pmd2/Zland2a/Dnajb2/Pamd11	9
Atp4b/Sec24b/Vamp3/Arcn1/Vamp2/Copb2/Ctic/Vt1b/Copa/Sec24c	10
Hspa9/Hsp90ab1/Hsp90aa1/Ac1g/Hga4/Fkbp4/Exoc4/Arpc5/Polg/Srt1/Dynl1c/Atp5y1/Zlyve27/Pkcb/Got1/Iqgap1/Fkbp1a/Mical1/Ssi/Bin1/Git2/Dnm2/Ppp2ca/Srf10/Setx/Copa/P2rx4	27
Pcna/Nm/Lbr/Lmb1	4
Rps8/Uba25/Rps5/Rpl18/Rplp2/Rpsa/Rpl19/Rpl19-ps6/Rps24/Rps26/Rps4x/Fau/Rpl8/Rpl38/Rps21/Rps7/Rpl37/Rps27/Rps20/Rpl30/Rps16/Rps2/Rpl13a/Rpl18a/Rpl13/Mps6/Rps19/Rps13/Rpl35/Rpl21/Rps12/Rps27a/Rpl1	52
Hspa8/Hspa1a/Hspa1b/Ubb/Jun/Hsp90ab1/Dnaj1/Uba25/Nkbia/Hsp1/Cacypb/Actg1/Tubb5/Smad7/Syk/Mu1/Rps27a/H13/Htt/Hat4/H2-Ab1/Laptn5/Arh1/SH3kbp1/Tuba1b/Myc/Aap1/Ubc/Bcl2/Erln1/Ithc/A	65
Hspa8/Hspa1a/Hspa1b/Ubb/Jun/Hsp90ab1/Hsp90aa1/Dnaj1/Uba25/Nkbia/Hsp1/Cacypb/Actg1/Tubb5/Smad7/Syk/Mu1/Rps27a/H13/Htt/Hat4/H2-Ab1/Laptn5/Arh1/SH3kbp1/Tuba1b/Myc/Aap1/Ubc/Bcl2/Erln1/Arb2	62
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Jun/Dnaj1/Nr4a1/Fos/Nkbia/Klf4/Jund/Foxp1/Arid5a/Atf2/Irf1/RH6/Hsp1/Cited2/Crebbp/Fkbp4/RH4/Hes6/Arnt/Parp1/Srt1/Nkbid/Ldb1/Htt/an/Daxx/Nfe2l2/Smarca1/Ntfc1/Ep300/Pkcb/Npm1/Med13/Gt2a2/Ddrgk1	55
Dnaj1/Hspa1a/Trm25/Naca/Kdm5a/Arid5a/Rbm3/Med15/Sap18/Rere/Pbox1/Lmd1/Cited2/Crebbp/Bcl11a/Nr3c1/Nmi1/H4/N4bp2/Sub1/Hpk3/Rf1/Srt1/Ets1/Tb1x/Ldb1/Jmj1c/Daxx/Tcf4/Ep300/Pkcb/Npm1/Med13	61
Jun/Cytl1/Demnd4/Eef1b2/Ralgapa1/Akap13/Srt1/Gpsm3/Rasa3/Lamtor2/Bcar3/Gd2/Krt11/Phy/EI2b2/Demnd1b/Rap1a/Rabgarp1/Iqgap1/Tagap/Elmo1/Argef1/Rasa2/Rcc2/Ahgap15/Rabgarp1/Git2/Ccz1/Fnip1/Preb/Do	52
Jun/Cytl1/Demnd4/Eef1b2/Ralgapa1/Akap13/Srt1/Gpsm3/Rasa3/Lamtor2/Bcar3/Gd2/Krt11/Phy/EI2b2/Demnd1b/Rap1a/Rabgarp1/Iqgap1/Tagap/Elmo1/Argef1/Rasa2/Rcc2/Ahgap15/Rabgarp1/Git2/Ccz1/Fnip1/Preb/Do	52
Dnaj1/Hspa8/Hspa1a/Hspa1b/Hsp90ab1/Hsp90aa1/Dnaj1/Naca/Pges3/Nudc3/Nudo/S13/Npm1/Dnajb1/Ube4b/Dnajb2/Bce/Hspa9/Hspa14/Srf10/Hsp90b1/Calr	23
Birc3/Trm25/Mu1/Htt/Rc3h2/Zfp1/RH213/RH6/RH125/Arh1/Mat1/Ube3b/RH4/Trm59/Neur3/Znr2/Ubr1/Ithc/Brap/Fbx3/Ube2l1/Ube2d1/Herc4/Ctbl/Siah2/Birc2/Ube2b/Cul1/Ube2h/Myip/Ube4b/Med21/Ube2	53
Birc3/Trm25/Mu1/Htt/Rc3h2/Zfp1/RH213/RH6/RH125/Arh1/Mat1/Ube3b/RH4/Trm59/Neur3/Znr2/Ubr1/Ithc/Brap/Fbx3/Ube2l1/Ube2d1/Herc4/Ctbl/Siah2/Birc2/Ube2b/Cul1/Ube2h/Myip/Ube4b/Med21/Chf1	51
Jun/Cytl1/Demnd4/Eef1b2/Ralgapa1/Akap13/Srt1/Rasa3/Lamtor2/Bcar3/Gd2/Phy/EI2b2/Demnd1b/Rap1a/Rabgarp1/Iqgap1/Tagap/Elmo1/Argef1/Rasa2/Rcc2/Ahgap15/Rabgarp1/Git2/Ccz1/Fnip1/Preb/Dock8/Ragge1/	50
PH4/Kdm5a/Kmt2e/Nap111/Chd1/Chd8/Sbn2/Smarca5/Sart3/Rf1/Srt1/Tb1x/Daxx/Mt2/Brd9/Pkcb/Npm1/Ipo7/Smarca1/Kmt2e/Arg32b/Bpt/Atrv/Zmynd11/Sta1/Sbn1/Ing1/Usp15/Tonsi/Uhr2/Usp16/Smarca2/Nap1	40
Nr4a1/Jund/Foxp1/Arid5a/Rnf6/Fkbp4/Rnf4/Rnf4/Srt1/Daxx/Smarca1/Ep300/Pkcb/Med13/Pcna/Snw1/Cnot1/Arid1a/Bdb/Stat1/Ncoa2/Pk3r1/Fus/Cnrb1/Frp12/Nsd1/Tob2/Calr	28
Cytl1/Demnd4/Eef1b2/Akap13/Srt1/Lamtor2/Bcar3/EI2b2/Demnd1b/Rap1a/Rabgarp1/Iqgap1/Ccz1/Fnip1/Preb/Dock8/Ragge1b/Bap7/Gapv1/Lamtor3/Rabgarp1/Dock2/Ralgs2/Myctb2/Fcn/Ragge1/Rab3garp1/Cdc	31
Dnaj1/Hspa8/Hspa1a/Hspa1b/Hsp90ab1/Dnaj1/Nkbia/Zp36/Pges3/Rps3/Ahsa1/Nr3c1/Fkbp4/S13/Fkbp1a/Dnajb9/Kpnb1/Nkib1/EI2a3/Dnajb2/Ctic/Tfam/Hspa9/Fat1/Hspa14/Usp19	26
Hsp90aa1/Nst/Akap13/Myo1c/Cdc42se2/Sptbn1/Ccdc186/Exoc4/Lsm2/Map2k1/Dlaph1/Tmem127/Gd2/Xpo1/Golga4/Ipo7/Demnd1b/Rap1a/Rabgarp1/Iqgap1/Eno1/Mical1/Kpnb1/Xpo6/Rock1/Rcc2/Rabgarp1/Bin1/Preb/Ri	39
Trm25/Naca/Kdm5a/Rbm39/Rere/Cited2/Crebbp/Nr3c1/Irf4/Sub1/Srt1/Ets1/Daxx/Ep300/Pkcb/Npm1/Med13/Birc2/Kmt2c/Snw1/Med21/Cebp2/Brd9/Ncoa2/Eny2/Fus/Cnrb1/Usp16/Smarca2/Tm12a/Pml/Nucks1/Zmiz2/	34
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Birc3/Trm25/Mu1/Htt/Rc3h2/Rnf6/RH125/Arh1/Ube3b/RH4/Trm59/Neur3/Znr2/Ubr1/Ithc/Brap/Ube2d1/Herc4/Ctbl/Siah2/Birc2/Cul1/Myip/Ube4b/Med21/Chf1/Rnf4/Rabgarp1/Uhr2/Tm12a/Ranp2/Arh2/Myctb2/Pel1	38
Birc3/Trm25/Mu1/Htt/Rc3h2/Rnf6/RH125/Arh1/Ube3b/RH4/Trm59/Neur3/Znr2/Ubr1/Ithc/Brap/Ube2d1/Herc4/Ctbl/Siah2/Birc2/Cul1/Myip/Ube4b/Med21/Chf1/Rnf4/Rabgarp1/Uhr2/Tm12a/Arh2/Myctb2/Pel1/Frp12/	37
Nst/Akap13/Myo1c/Cdc42se2/Ccdc186/Exoc4/Lsm2/Map2k1/Dlaph1/Tmem127/Gd2/Xpo1/Golga4/Ipo7/Demnd1b/Rap1a/Rabgarp1/Iqgap1/Mical1/Kpnb1/Xpo6/Rock1/Rcc2/Rabgarp1/Rabgarp1/Ranp2/Tpno1/Myctb2/Cyfl	34
Nst/Dynl1/Top2b/Myo1c/Dgkz/Pdx3/Nei1/Map2k1/Srt1/Dynl1c/Tb1x/Tcf4/Ep300/For2a/Prrc2/Pcna/Usf7/Epb41/Vamp2/Cd2ap/Pk3r1/Ctfc/Cnrb1/Sae1/Ppp2ca/Sp1/Dbn1/Nipbl/Numa1/Foxn3	30
Htt/Chd1/Chd8/Smarca5/Atrv/And1a/Ep400/Smarca2/Chd2/Chd4/Chd7	11
Rpsa/Ef1l/Rps35/Xist/EI3k/Ccdc47/Srnp3/Naas10/Ithc/Npm1/Srnp70/Cank2a1/Naas15/Spr1/C1qbp/Der1/Yhd3/Larp1/Serbp1/Secisbp2/Nemf/Tmco1/Zc3h12a/Prrt1	24
Hspa1a/Hsp1a/Rps21/Pe1p1/Srnt2/Exoc4/Map2k1/Parp1/Daxx/Smarca1/EI3a/Npm1/Birc2/Csrn2a1/Smarca1/Mecp2/Epb41/Hax1/Tnks2/Nipbl/Hypk	21
Top2b/Htt/Pges3/Rps3/G3bp1/Nei1/Polid1/Chd1/Chd8/Dhx36/Smarca5/Polg/Tdp2/Dclre1c/Pcna/Bptf/Atrv/Rfc1/Arid1a/Top3b/Ep400/Smarca2/Chd2/Batf1/Chd4/Chd7/Pid4/Dnaase2a	28
KH4/Crebbp/Foxo1/Met2/Ep300/Cnt2/Cdk9/Ehmt1/Nkib1/Per1/Sta1/Cnot2/Tmn/Cnrb1/Sp1/Chd4	17
Hsp21/Mu1/Pges3/Rnf125/Chd8/Crebbp/Srt1/Daxx/Ep300/Npm1/Usp7/Ehmt1/Plt1p/RH34/Sk11	15
Hspa8/Hspa1a/Hspa1b/Dnajb11/Dnajb9/Der2/Hspa9/Hspa14/Dnajc3	9
Foxp1/Arid5a/Rnf6/RH4/Daxx/Ep300/Pkcb/Snw1/Nsd1/Calr	10
Hspa8/Phd1a1/Capp/Myo1c/Sptbn1/Tp1/Plekhb2/Anxa7/Sgk3/Snx12/Krt11/Fchs2/Pxd1/Npm1/Gitp/Demnd1b/Iqgap1/Ogt/Nsf1c/Rasa2/Epb41/Vamp2/Snx30/Bin1/Nc4/Nisch/Rnf34/Mts1/Flii/Pasp/Wip2/Map1/c3a/Ar	41
Skt17b/Wnk1/Syk/Akap13/Cik1/Sgk3/Map2k1/Hpk3/Csnk1/Pkcb/Ikbb/Csnk1g3/Smg1/Cank2a1/Sik2/Cank2/Act2/Pk3r1/Pk3r4/Sk38/Cdk9/Map4k2/Rock1/EI2a3/Riok1/Tk1/Mast4/Cnd3/Map3k2/Cdk1b/Sbk1/S	40
Jun/Fos/Smad7/Zeb2/Cited2/Crebbp/Parp1/Purb/Pp7/Fkbp1a/Tcf12/Snw1/Usp15/Cnrb1/Pml	15
Dnaj1/Hspa1a/Arid5a/Sap18/Rere/Pbox1/Lmd1/Cited2/Crebbp/Bcl11a/N4bp2/Dnajc3/Srt1/Tb1x/Daxx/Tcf4/Snw1/Mecp2/C1qbp/Zmynd11/Irf2bp2/Nsd1/Tob2	23
Top2b/Htt/G3bp1/Chd1/Chd8/Dhx36/Smarca5/Bptf/Atrv/Rfc1/Arid1a/Ep400/Smarca2/Chd2/Batf1/Chd4/Chd7	17
Dnaj1/Hspa8/Hspa1a/Hspa1b/Hsp90ab1/Hsp90aa1/Hsp1/Ccdc47/Hspa9/Hspa14	10
Hsp90ab1/Wnk1/Klf4/Hpk3/Mat1/Map2k1/Cab39/Daxx/Cnt2/Npm1/Iqgap1/Klfn5220/Pkag1/Cnppd1/Cnt1/Pk3r1/Cnd3/Lamtor3/Sk111/Rhhv/Cnt1/Socs3/Dnajc3/Cnt2/Cnt2	25
Skt17b/Wnk1/Sgk3/Hpk3/Csnk1/Ikbb/Csnk1g3/Smg1/Cank2a1/Sik2/Akt2/Pk3r4/Sk38/Map4k2/Rock1/EI2a3/Riok1/Tk1/Mast4/Sk111/Rps6k1/Csnk1a1/Vnk1/Riok3/Srp2	26
Hspa1a/Hsp90ab1/Hsp1/Mor1l/Rc3h2/Dhx36/Tuba1b/Srtpb/Dhx30/Ctic/Sid2/H2/Msr/Vim	14
Ei1/EI3/Eef1b2/Pcbp1/EI3a/EI3a/EI4g2/EI3e/Tufm/Purb/EI2b2/EI1ax/EI4e2/Larp1/Fnip1/Hspa9/Lbr/Dnajc3	16
Dnajb1/Hspa8/Hspa1a/Hspa1b/Hsp90ab1/Dnaj1/Hsp1/Pges3/Ahsa1/S13/Birc2/Dnajb9/Dnajb2/Bin1/Fat2/Hpa2/Nipbl/Hypk	16
Atf2/Gm16286/Naa50/Crebbp/Naa10/Srt1/Smarca1/Ep300/Nmt2/Ogt/Naa15/Epc1/Cers4/Kat6a/Esco1	15
Htt/G3bp1/Chd1/Chd8/Dhx36/Smarca5/Ddx6/Ddx50/Dhx30/Atrv/Ddx47/Ep400/Smarca2/Chd2/Setx/Chd4/Ddx24/Chd7/Ddx52	19
Bod1/Bcl2/Foxo1/Smg5/Ppp2a2a/Rps6k1/Ppp2ca/Ptpn1/Vim	9
Nr4a1/Mef2c/Mef2d/Ralgapa1/Atf3/Top2b/Cenpa/Atf2/Bcl11a/Hes6/Vapa/Bcl2/Arnt/Tcf4/Ikbb/Gtf2a2/Sr/Tcf12/Zfp318/Uba2/Pk3r1/Bhhe40/Sae1/Ppp2ca/raK3/Pml/Atf6/Chuk/Hexa	29
Ppp1r1Sa/Wnk1/Syk/fns2/Bod1/Pstpip1/Chcd3/Bcl2/Foxo1/Siglec9/Ikbb/Smg5/Jak1/Iqgap1/Cabin1/EI2a3/Pk3r1/Ppp2a2/Cnrb1/Rps6k1/Ppp2ca/Hsp90b1/Ptpn1/Vim	24
Hsp90ab1/Hsp90aa1/Fkbp4/Bin1/Ppp2a2/Ppp2ca/Apoe	7
Hsp21/Kdm5a/Kmt2e/Laptn5/Chd1/Chd8/Daxx/Mt2/Zranb1/Brd9/Bptf/Atrv/Dnajb2/Zmynd11/Ing1/Usp15/Zland6/Phip/Pmi/Kmt2a/Pprf/Kdm7a	22
Pe1p1/Hsp1/Rnf4/Aup1/Rae1/Birc2/Nsf1c/Tax1/Top1/Uba2/Dnajb2/Fat1/Usp16/Serbp1/Pmi/Herc2	15
Fos/Foxp1/Klf10/Egr1/Nr3c1/Myc/Ubtff/Pol2a/Npm1/Sta1	10
Arid5a/Rnf4/Parp1/Pcna/Cnot1/Ncoa2/Pk3r1/Fus/Cnrb1/Nsd1	10
Atf2/Gm16286/Naa50/Crebbp/Naa10/Ep300/Naa15/Epc1/Kat6a/Esco1	10
Ei1/EI3/EI3k/EI3a/EI4g2/EI3e/Tufm/Purb/EI2b2/EI1ax/EI4e2/EI2e2/EI2e3x	17
Zfp36/Cnt2/Wdr43/Arp32b/Zfp326/Cnt1/Bin1/RH11/Fat1/Scal8/Pabpn1	11
Ppp1r1Sa/fns2/Bod1/Pstpip1/Bcl2/Foxo1/Nkbb/Smg5/Jak1/Iqgap1/Cabin1/EI2a3/Pk3r1/Ppp2a2/Cnrb1/Rps6k1/Ppp2ca/Hsp90b1/Ptpn1/Vim	20
Pe1p1/Rnf4/Uba2/Setp1/Pmi/Herc2	6
Srt1/Arb2/Pde3b/Npm1/Ppp2ca/Seq5	6
Dusp1/Srt1/Arb2/Ppp1/Ntate1/Iqgap1/Spag9/Prrt1	8
Atf2/Gm16286/Naa50/Crebbp/Naa10/Smarca1/Ep300/Ogt/Naa15/Epc1/Kat6a/Esco1	12
Hsp90aa1/EI3a/Nr3c1/Cd2/Ctbl/Sh2b3/Bank1/Ptpn2/Pcna/Stat1/Pk3r1/Bink/Pten/Need9/Ptpn1	10
Ei1/EI3/Eef1b2/Pcbp1/EI3k/EI3a/EI4g2/EI3e/Tufm/Purb/EI2b2/EI1ax/EI2a3/EI4e2/Larp1/EI2e2/EI2e3x	15
Ei1/EI3/Eef1b2/EI3k/EI3a/EI4g2/EI3e/Tufm/EI2b2/EI1ax/EI4e2/EI2e2/EI2e3x	13
Hspa1a/Hspa1b/Hsp90ab1/Hsp90aa1/Klf4/Mef2c/Mef2d/Top2b/Dhx36/Parp1/Smg5/Mecp2/Sp1/Akap8/Chd4/Nipbl	16
Hspa8/Hspa1a/Hspa1b/Hsp90ab1/Hsp90aa1/Hsp1/Atad1/Nst/Rnf213/Atf5e/Klf21b/Atf5c/Smarca5/Rfc1/Hspa9/Hspa14/Smarca2/Hsp90b1/Hspa4/Atf5a1	22
Hspa1a/Hsp90ab1/Hsp90aa1/Gapdh/Crebbp/Ctic/Cnrb1/Numa1	8
Arid5a/Med13/Brd9/Ncoa2/Fus/Trip12/Nsd1	7
Jun/Foxp1/Atf3/Satb1/Crem/Bach2/Ntact3/Pdm2/Zeb2/Mynn/Bcl11a/Nr3c1/Hes6/Myc/Foxp4/Foxo1/Mxd4/Ntact1/Purb/Zbtb20/Zbtb21/Eno1/Nkbf1/Zfp148/EV3/Bhhe40/Ccd21b/Bcl6	28
Kdm5a/Kdm6b/Crebbp/Sbn2/Jmj1c/Foxo1/Ep300/Mecp2/Per1/Sbn1/Kdm6a/Tox4/Bcl6	13
Jun/Foxp1/Atf3/Satb1/Crem/Bach2/Ntact3/Pdm2/Zeb2/Mynn/Bcl11a/Nr3c1/Hes6/Myc/Foxp4/Foxo1/Mxd4/Ntact1/Purb/Zbtb20/Zbtb21/Eno1/Nkbf1/Zfp148/EV3/Bhhe40/Ccd21b/Bcl6	28
Phd1a1/Capp/Pkxb2/Sgk3/Snx12/Krt11/Fchs2/Pxd1/Npm1/Demnd1b/Iqgap1/Ogt/Epb41/Snx30/Nc4/Nisch/Rnf34/Flii/Wip2/Arp22/Tin1/Osbp8/Svx29/Numa1	24
Rps5/Rpl18/Rps4/Rpl8/Rpl37/Mrps6/Rps13/Rps3/Npm1/Rs1/Mps7	11
Srnp3/Sart3/Cnt2/Srnp70/Cdk9/Cnt1/Rbm22/Prrt8	8
Rps3/Rnf125/Arh1/Rnf4/Aup1/Siah2/Uba2/Arh2	8
Tsc22d3/Crebbp/Sht1/Tcf4/Tcf12/Bhhe40/Sp1	7
Laptn5/Daxx/Dnajb2/Usp15/Pmi	5
Ube2l1/Ube2f1/Ube2d1/Ube2h/Ube2i/Ube2j/Birc6/Ube2g1	8
H2-Q7/H2-Eb2/H2-M3/H2-Q6/Dock2/H2-Q4/H2-T23	7
Zfp36/fns2/Arb2-Q7/H2-M3/H2-Q6/H2-Q4/H2-T23/Srpk2	9
Hsp90ab1/Wnk1/Hsp1/Map2k1/Cab39/Daxx/Cnt2/Npm1/Iqgap1/Klfn5220/Pkag1/Cnppd1/Cnt1/Cnd3/Sk111/Cnrb1/Dnajc3/Cnt2/Cnt2	19
KH4/Smad7/Kdm6/Chd8/Tb1x/Foxo1/Pprj/Tcf4/Ep300/Csnk2a1/Cd2ap/Cnrb1	12
Rpsa/EI3k/Cdc47/Naas10/Naas15/C1qbp/Yhd3/Serbp1/Tmco1/Zc3h12a	10
Hspa8/Hsp90ab1/Nkbia/H2-Ab1/Tp1/Fkbp4/Brp/H2-Q7/H2-Eb2/Gtp/H2-M3/Fkbp1a/Ogt/Kpnb1/Ppp3ca/Ntrf/Fex7/H2-Q6/Hadha/Pk3r1/Ctic/Dbi/Peap/Rps6k1/Ppp2ca/Hsp90b1/Ptpn1/Vim	33
Crebbp/Foxo1/Ep300/Cnt2/Cdk9/Nkib1/Tfam	7
Syk/Fkbp4/Bcar3/Pde3b/Ctbl/Stap1/Epb41/Pk3r1/Sfr/RH1/Cank1a1/Scal8/Socs3	13
Arid5a/Rc3h2/Dazap1/Csd1/Zc3h12a	5
Fkbp4/Fkbp3/Fkbp1a/Nktr/Ppfg/Ppwd1/Ranb2	7
KH4/Atf2/Egr1/Srt1/Foxo1/Polr2a/Mecp2/Stat1/Chd7/Nipbl	10
Cited2/Egr1/Ets1/Pcna/Stat1/Sp1	6
Atf2/Gm16286/Naa50/Crebbp/Naa10/Smarca1/Ep300/Ogt/Naa15/Epc1/Kat6a/Esco1	12
Foxp1/Mat1/Cd2/Ahcy/Ldb1/Tcf4/Zlyve27/Myd88/Pabpn1/Ccdc88c	10
Atf2/Zdhc3/Gm16286/Naa50/Crebbp/Naa10/Zdhc18/Srt1/Smarca1/Ep300/Ctbl/Mboat7/Nmt2/Kmt2c/Ogt/Naa15/Epc1/Hadha/Lggt1/Cers4/Kat6a/Esco1	22
Rps24/EI3l/Rps19/Celf1/EI2a3/Larp1/EI2a2	7
Atf2/Zdhc3/Gm16286/Naa50/Crebbp/Naa10/Zdhc18/Srt1/Smarca1/Ep300/Mboat7/Nmt2/Ogt/Naa15/Epc1/Hadha/Lggt1/Cers4/Kat6a/Esco1	20
Dnajb1/Dnaj1a/Rps3/Nr3c1/S13/Fkbp1a/Dnajb9/Dnajb2	8
Arid1b/Rnf4/Smarca5/Cabin1/Arid1a/Nap1/Map114/Wk1/Supt16	8
Ube2l1/Ube2e1/Ube2d1/Ube2b/Ube2h/Birc6/Ube2g1	7
Rps7/Rps13/Dhx36/Celf1/Larp1/Gn3	6
Fkbp4/Fkbp3/Fkbp1a/Nktr/Ppfg/Ppwd1/Ranb2	7
Hsp90ab1/Rhob/Tuba1a/Ubb5/Rab43/Arf5c/Bms1/Fkbp4/Tuba1b/Rasd1/Ar18b/Rala/Tufm/Xras/Gimap6/EI2b2/Rap1a/Srpr/Rhog/Drm2/A44a/Rhoh/Gna13/Glut1/Rrad/Gn3/EI2e3x	27
Gm16286/Naa50/Naas10/Naas15	4
Ubb/Uba52/Rps27a/Ubc	4
Atf2/Naas50/Crebbp/Ep300/Epc1/Kat6a/Esco1	7
Sh2/Dusp1/Dusp5/Ssu72/Ppp1/Cdc25b/Ppr2/Ppp3ca/Dusp16/Pp4a2/Pten/Ppp2a5/Ppm1g/Ppp2ca/Ppcc/Ptpn1	16
Ei3a/Nr3c1/Cd2/Ctbl/Sh2b3/Ppnr2/Pcna/Stat1/Pk3r1/Ptpn1	10
Wnk1/Rps7/Rpl37/Rps20/Smad7/Dynl1/Icd3/Dgkz/Bcl2/Daxx/Cank2d/Cd55/Fry/Frip1	14
Nkbia/Nkbid/Htt/Av/Ep300/Npm1/Fat1	6
Akap13/Map2k1/Iqgap1/Spag9	4
Ppp3ca/Ntrf/Ppp1/Ppwd1	4

Hsp90ab1/Cbx1/Cttnb1/Nop56	4
Hga4/H2-Ab1/Ep400/Ppp2ca	4
Tubb5/H2-G7/H2-M3/H2-Q6/H2-Q4/H2-T23/Atp5a1	7
Hsp90ab1/Hsp90aa1/Ptges3/Pcna/Ncoa2	5