Category	Term
UP_KEYWORDS	Phosphoprotein
GOTERM_CC_DIREC	GO:0005634~nucleus
UP_KEYWORDS	Nucleus
UP_KEYWORDS	Cytoplasm
GOTERM_CC_DIREC	GO:0005737~cytoplasm
UP_KEYWORDS	Acetylation
UP_KEYWORDS	Alternative splicing
UP_KEYWORDS	Meiosis
UP_KEYWORDS	Spermatogenesis
GOTERM_BP_DIREC	GO:0051321~meiotic cell cycle
UP_KEYWORDS	Zinc
GOTERM_MF_DIREC	GO:0005515~protein binding
GOTERM_BP_DIREC	GO:1904871~positive regulation of protein localization to Cajal body
GOTERM_BP_DIREC	GO:0007283~spermatogenesis
GOTERM_MF_DIREC	GO:0008270~zinc ion binding
GOTERM_CC_DIREC	GO:0005832~chaperonin-containing T-complex
GOTERM_CC_DIREC	GO:0005654~nucleoplasm
GOTERM_CC_DIREC	GO:0000795~synaptonemal complex
INTERPRO	IPR027410:TCP-1-like chaperonin intermediate domain
INTERPRO	IPR002194:Chaperonin TCP-1, conserved site
GOTERM_BP_DIREC	GO:0007286~spermatid development
UP_SEQ_FEATURE	splice variant
UP_KEYWORDS	Transcription regulation
INTERPRO	IPR017998:Chaperone tailless complex polypeptide 1 (TCP-1)
UP_KEYWORDS	Transcription
GOTERM_CC_DIREC	GO:0005829~cytosol
UP_KEYWORDS	Zinc-finger
GOTERM_CC_DIREC	GO:0002199~zona pellucida receptor complex
UP_KEYWORDS	Ligase
INTERPRO	IPR027409:GroEL-like apical domain
INTERPRO	IPR027413:GroEL-like equatorial domain
GOTERM_BP_DIREC	GO:1904851~positive regulation of establishment of protein localization to telom
INTERPRO	IPR002423:Chaperonin Cpn60/TCP-1
UP_KEYWORDS	Metal-binding
GOTERM_BP_DIREC	GO:0006457~protein folding
UP_KEYWORDS	Chromatin regulator
GOTERM_BP_DIREC	GO:1904874~positive regulation of telomerase RNA localization to Cajal body
UP_KEYWORDS	Cell cycle
UP_KEYWORDS	Coiled coil
GOTERM_BP_DIREC	GO:0006351~transcription, DNA-templated
UP_KEYWORDS	Ubl conjugation pathway
GOTERM_MF_DIREC	GO:0016874~ligase activity

UP_KEYWORDS	Differentiation
GOTERM_BP_DIREC	GO:0032212~positive regulation of telomere maintenance via telomerase
GOTERM_CC_DIREC	GO:0005874~microtubule
GOTERM_BP_DIREC	GO:0016569~covalent chromatin modification
GOTERM_BP_DIREC	GO:0007049~cell cycle
GOTERM_MF_DIREC	GO:0046872~metal ion binding
GOTERM_MF_DIREC	GO:0061630~ubiquitin protein ligase activity
UP_KEYWORDS	Oxidoreductase
GOTERM_BP_DIREC	GO:1901998~toxin transport
GOTERM_BP_DIREC	GO:0000209~protein polyubiquitination
GOTERM_MF_DIREC	GO:0016491~oxidoreductase activity
KEGG_PATHWAY	mmu01130:Biosynthesis of antibiotics
GOTERM_MF_DIREC	GO:0003824~catalytic activity
GOTERM_BP_DIREC	GO:0006355~regulation of transcription, DNA-templated
GOTERM_MF_DIREC	GO:0004842~ubiquitin-protein transferase activity
GOTERM_BP_DIREC	GO:0007130~synaptonemal complex assembly
GOTERM_BP_DIREC	GO:0007129~synapsis
GOTERM_CC_DIREC	GO:0044297~cell body
GOTERM_BP_DIREC	GO:0006974~cellular response to DNA damage stimulus
GOTERM_MF_DIREC	GO:0051082~unfolded protein binding
GOTERM_BP_DIREC	GO:0050821~protein stabilization
GOTERM_BP_DIREC	GO:0030154~cell differentiation
GOTERM_BP_DIREC	GO:0008152~metabolic process
UP_KEYWORDS	Chaperone
GOTERM_CC_DIREC	GO:0000794~condensed nuclear chromosome
GOTERM_BP_DIREC	GO:0055114~oxidation-reduction process
UP_KEYWORDS	DNA damage
GOTERM_CC_DIREC	GO:0005730~nucleolus
GOTERM_BP_DIREC	GO:0007126~meiotic nuclear division
UP_KEYWORDS	DNA-binding
UP_KEYWORDS	LIM domain
GOTERM_MF_DIREC	GO:0000166~nucleotide binding
INTERPRO	IPR013083:Zinc finger, RING/FYVE/PHD-type
UP_KEYWORDS	Aminoacyl-tRNA synthetase
INTERPRO	IPR006888:Cor1/Xlr/Xmr family
INTERPRO	IPR001781:Zinc finger, LIM-type
GOTERM_CC_DIREC	GO:0043209~myelin sheath
GOTERM_BP_DIREC	GO:0007339~binding of sperm to zona pellucida
INTERPRO	IPR001841:Zinc finger, RING-type
SMART	SM00132:LIM
UP_KEYWORDS	DNA repair
UP_KEYWORDS	Ubl conjugation
GOTERM_BP_DIREC	GO:0007140~male meiosis

GOTERM_CC_DIREC	GO:0005813~centrosome
GOTERM_MF_DIREC	GO:0004812~aminoacyl-tRNA ligase activity
UP_KEYWORDS	Flavoprotein
GOTERM_MF_DIREC	GO:0003730~mRNA 3'-UTR binding
INTERPRO	IPR013785:Aldolase-type TIM barrel
GOTERM_BP_DIREC	GO:0016567~protein ubiquitination
UP_KEYWORDS	Nucleotide-binding
UP_KEYWORDS	RNA-binding
GOTERM_BP_DIREC	GO:0045736~negative regulation of cyclin-dependent protein serine/threonine ki
GOTERM_CC_DIREC	GO:0005739~mitochondrion
UP_KEYWORDS	ATP-binding
GOTERM_BP_DIREC	GO:0006635~fatty acid beta-oxidation
GOTERM_MF_DIREC	GO:0003682~chromatin binding
GOTERM_MF_DIREC	GO:0016208~AMP binding
GOTERM_CC_DIREC	GO:0000801~central element
UP_SEQ_FEATURE	zinc finger region:RING-type
UP_KEYWORDS	NADP
GOTERM_BP_DIREC	GO:0048477~oogenesis
UP_KEYWORDS	Repressor
GOTERM_MF_DIREC	GO:0003723~RNA binding
GOTERM_CC_DIREC	GO:0005913~cell-cell adherens junction
UP_KEYWORDS	Cell division
UP_KEYWORDS	Lyase
GOTERM_BP_DIREC	GO:0006418~tRNA aminoacylation for protein translation
UP_KEYWORDS	Oogenesis
GOTERM_BP_DIREC	GO:0009566~fertilization
GOTERM_BP_DIREC	GO:0051026~chiasma assembly
UP_KEYWORDS	mRNA splicing
KEGG_PATHWAY	mmu00640:Propanoate metabolism
GOTERM_MF_DIREC	GO:0016829~lyase activity
KEGG_PATHWAY	mmu00310:Lysine degradation
GOTERM_MF_DIREC	GO:0098641~cadherin binding involved in cell-cell adhesion
KEGG_PATHWAY	mmu00970:Aminoacyl-tRNA biosynthesis
GOTERM_CC_DIREC	GO:0000800~lateral element
GOTERM_CC_DIREC	GO:0005694~chromosome
INTERPRO	IPR016040:NAD(P)-binding domain
GOTERM_BP_DIREC	GO:0000122~negative regulation of transcription from RNA polymerase II prom
UP_KEYWORDS	Microtubule
UP_KEYWORDS	FAD
GOTERM_CC_DIREC	GO:0005765~lysosomal membrane
GOTERM_BP_DIREC	GO:0006281~DNA repair
GOTERM_BP_DIREC	GO:0051865~protein autoubiquitination
GOTERM_MF_DIREC	GO:0031625~ubiquitin protein ligase binding

UP_SEQ_FEATURE	domain:LIM zinc-binding 1
UP_SEQ_FEATURE	domain:LIM zinc-binding 2
GOTERM_BP_DIREC	GO:0007131~reciprocal meiotic recombination
UP_SEQ_FEATURE	short sequence motif:"HIGH" region
SMART	SM00184:RING
GOTERM_BP_DIREC	GO:0007141~male meiosis I
GOTERM_CC_DIREC	GO:0005759~mitochondrial matrix
GOTERM_BP_DIREC	GO:0043161~proteasome-mediated ubiquitin-dependent protein catabolic proces
UP_KEYWORDS	Endosome
UP_KEYWORDS	Cytoskeleton
UP_KEYWORDS	Iron-sulfur
GOTERM_MF_DIRE	GO:0003677~DNA binding
UP_KEYWORDS	Protein transport
GOTERM_BP_DIREC	GO:0008380~RNA splicing
UP_KEYWORDS	Mitochondrion
GOTERM_CC_DIREC	GO:0001741~XY body
GOTERM_BP_DIREC	GO:0051301~cell division
UP_KEYWORDS	DNA replication
GOTERM_BP_DIREC	GO:0045893~positive regulation of transcription, DNA-templated
GOTERM_BP_DIREC	GO:0015937~coenzyme A biosynthetic process
INTERPRO	IPR017907:Zinc finger, RING-type, conserved site
GOTERM_MF_DIRE	GO:0003985~acetyl-CoA C-acetyltransferase activity
UP_KEYWORDS	mRNA processing
GOTERM_BP_DIREC	GO:0000711~meiotic DNA repair synthesis
GOTERM_BP_DIREC	GO:0090666~scaRNA localization to Cajal body
INTERPRO	IPR023753:Pyridine nucleotide-disulphide oxidoreductase, FAD/NAD(P)-bindin
UP_KEYWORDS	Isopeptide bond
GOTERM_MF_DIRE	GO:0003676~nucleic acid binding
GOTERM_MF_DIRE	GO:0030332~cyclin binding
UP_SEQ_FEATURE	domain:KH 2
UP_SEQ_FEATURE	domain:KH 1
INTERPRO	IPR012677:Nucleotide-binding, alpha-beta plait
UP_KEYWORDS	RNA-mediated gene silencing
GOTERM_MF_DIRE	GO:0004861~cyclin-dependent protein serine/threonine kinase inhibitor activity
KEGG_PATHWAY	mmu00071:Fatty acid degradation
GOTERM_CC_DIREC	GO:0005768~endosome
GOTERM_MF_DIRE	GO:0044822~poly(A) RNA binding
INTERPRO	IPR008927:6-phosphogluconate dehydrogenase, C-terminal-like
INTERPRO	IPR009080:Aminoacyl-tRNA synthetase, class 1a, anticodon-binding
GOTERM_BP_DIREC	GO:0048812~neuron projection morphogenesis
GOTERM_BP_DIREC	GO:0006302~double-strand break repair
UP_KEYWORDS	Transit peptide
GOTERM_CC_DIREC	GO:0030665~clathrin-coated vesicle membrane

GOTERM_CC_DIREC	GO:0030897~HOPS complex
GOTERM_CC_DIREC	GO:0070062~extracellular exosome
KEGG_PATHWAY	mmu01212:Fatty acid metabolism
GOTERM_MF_DIREC	GO:0051536~iron-sulfur cluster binding
UP_KEYWORDS	WD repeat
GOTERM_MF_DIREC	GO:0070403~NAD+ binding
GOTERM_BP_DIREC	GO:0045786~negative regulation of cell cycle
INTERPRO	IPR004087:K Homology domain
GOTERM_CC_DIREC	GO:0016023~cytoplasmic, membrane-bounded vesicle
GOTERM_CC_DIREC	GO:0031965~nuclear membrane
GOTERM_CC_DIREC	GO:0055037~recycling endosome
UP_KEYWORDS	Developmental protein
GOTERM_BP_DIREC	GO:0042138~meiotic DNA double-strand break formation
GOTERM_CC_DIREC	GO:0000790~nuclear chromatin
GOTERM_BP_DIREC	GO:0007050~cell cycle arrest
GOTERM_BP_DIREC	GO:0000902~cell morphogenesis
GOTERM_CC_DIREC	GO:0031410~cytoplasmic vesicle
KEGG_PATHWAY	mmu00620:Pyruvate metabolism
SMART	SM00322:KH
UP_SEQ_FEATURE	chain:X-linked lymphocyte-regulated protein 3C
UP_SEQ_FEATURE	chain:X-linked lymphocyte-regulated protein 3B
UP_SEQ_FEATURE	chain:X-linked lymphocyte-regulated protein 3A
GOTERM_BP_DIREC	GO:0031146~SCF-dependent proteasomal ubiquitin-dependent protein catabolic
GOTERM_MF_DIREC	GO:0003697~single-stranded DNA binding
GOTERM_BP_DIREC	GO:0046685~response to arsenic-containing substance
GOTERM_BP_DIREC	GO:0016973~poly(A)+ mRNA export from nucleus
GOTERM_MF_DIREC	GO:0008134~transcription factor binding
UP_KEYWORDS	Methylation
GOTERM_MF_DIREC	GO:0008013~beta-catenin binding
GOTERM_BP_DIREC	GO:0031047~gene silencing by RNA
SMART	SM00360:RRM
UP_KEYWORDS	Hydrolase
GOTERM_MF_DIREC	GO:0005524~ATP binding
KEGG_PATHWAY	mmu05215:Prostate cancer
INTERPRO	IPR019775:WD40 repeat, conserved site
GOTERM_CC_DIREC	GO:0010008~endosome membrane
GOTERM_BP_DIREC	GO:0015031~protein transport
KEGG_PATHWAY	mmu05219:Bladder cancer
KEGG_PATHWAY	mmu04144:Endocytosis
GOTERM_BP_DIREC	GO:0097352~autophagosome maturation
GOTERM_MF_DIREC	GO:0016787~hydrolase activity
INTERPRO	IPR000504:RNA recognition motif domain
GOTERM_BP_DIREC	GO:0030097~hemopoiesis

UP_KEYWORDS	Activator
INTERPRO	IPR020472:G-protein beta WD-40 repeat
INTERPRO	IPR001680:WD40 repeat
GOTERM_MF_DIREC	GO:0019901~protein kinase binding
GOTERM_BP_DIREC	GO:0006417~regulation of translation
UP_SEQ_FEATURE	short sequence motif:"KMSKS" region
KEGG_PATHWAY	mmu01100:Metabolic pathways
GOTERM_MF_DIREC	GO:0050660~flavin adenine dinucleotide binding
PIR_SUPERFAMILY	PIRSF000429:acetyl-CoA acetyltransferase
GOTERM_BP_DIREC	GO:0051973~positive regulation of telomerase activity
UP_SEQ_FEATURE	zinc finger region:C2H2-type 6
GOTERM_MF_DIREC	GO:0003712~transcription cofactor activity
UP_SEQ_FEATURE	repeat:WD 3
GOTERM_BP_DIREC	GO:0045944~positive regulation of transcription from RNA polymerase II promo
INTERPRO	IPR014729:Rossmann-like alpha/beta/alpha sandwich fold
GOTERM_BP_DIREC	GO:0006260~DNA replication
GOTERM_MF_DIREC	GO:0042393~histone binding
KEGG_PATHWAY	mmu04931:Insulin resistance
GOTERM_BP_DIREC	GO:0010212~response to ionizing radiation
KEGG_PATHWAY	mmu00030:Pentose phosphate pathway
INTERPRO	IPR002155:Thiolase
INTERPRO	IPR020610:Thiolase, active site
INTERPRO	IPR003000:Sirtuin family
INTERPRO	IPR026590:Sirtuin family, catalytic core domain
GOTERM_BP_DIREC	GO:0034587~piRNA metabolic process
GOTERM_BP_DIREC	GO:0043407~negative regulation of MAP kinase activity
GOTERM_CC_DIREC	GO:0005667~transcription factor complex
UP_SEQ_FEATURE	repeat:WD 2
UP_SEQ_FEATURE	repeat:WD 1
INTERPRO	IPR019956:Ubiquitin subgroup
GOTERM_MF_DIREC	GO:0097371~MDM2/MDM4 family protein binding
SMART	SM00320:WD40
UP_SEQ_FEATURE	repeat:WD 4
GOTERM_CC_DIREC	GO:0080008~Cul4-RING E3 ubiquitin ligase complex
GOTERM_BP_DIREC	GO:0045732~positive regulation of protein catabolic process
GOTERM_CC_DIREC	GO:0005856~cytoskeleton
UP_KEYWORDS	Translation regulation
INTERPRO	IPR004088:K Homology domain, type 1
UP_SEQ_FEATURE	domain:Deacetylase sirtuin-type
GOTERM_BP_DIREC	GO:0006397~mRNA processing
UP_KEYWORDS	Lipid metabolism
UP_SEQ_FEATURE	zinc finger region:C2H2-type 10
GOTERM_BP_DIREC	GO:0043046~DNA methylation involved in gamete generation

KEGG_PATHWAY	mmu00380:Tryptophan metabolism
KEGG_PATHWAY	mmu01200:Carbon metabolism
INTERPRO	IPR020613:Thiolase, conserved site
INTERPRO	IPR020617:Thiolase, C-terminal
INTERPRO	IPR020616:Thiolase, N-terminal
INTERPRO	IPR003530:Long hematopoietin receptor, soluble alpha chain, conserved site
UP_SEQ_FEATURE	nucleotide phosphate-binding region:FAD
UP_KEYWORDS	Cytoplasmic vesicle
GOTERM_CC_DIREC	GO:0000242~pericentriolar material
UP_SEQ_FEATURE	zinc finger region:C2H2-type 11
UP_KEYWORDS	NAD
GOTERM_CC_DIREC	GO:0035861~site of double-strand break
KEGG_PATHWAY	mmu05212:Pancreatic cancer
KEGG_PATHWAY	mmu05214:Glioma
GOTERM_BP_DIREC	GO:0035855~megakaryocyte development
GOTERM_BP_DIREC	GO:0046512~sphingosine biosynthetic process
GOTERM_BP_DIREC	GO:0090244~Wnt signaling pathway involved in somitogenesis
GOTERM_BP_DIREC	GO:0050687~negative regulation of defense response to virus
GOTERM_BP_DIREC	GO:0048642~negative regulation of skeletal muscle tissue development
GOTERM_BP_DIREC	GO:0002318~myeloid progenitor cell differentiation
GOTERM_BP_DIREC	GO:0021978~telencephalon regionalization
GOTERM_BP_DIREC	GO:0031062~positive regulation of histone methylation
GOTERM_CC_DIREC	GO:0005929~cilium
GOTERM_CC_DIREC	GO:0031201~SNARE complex
UP_KEYWORDS	Golgi apparatus
UP_KEYWORDS	Lysosome
GOTERM_CC_DIREC	GO:0042470~melanosome
GOTERM_BP_DIREC	GO:0042787~protein ubiquitination involved in ubiquitin-dependent protein catal
GOTERM_BP_DIREC	GO:0070936~protein K48-linked ubiquitination
UP_SEQ_FEATURE	zinc finger region:C2H2-type 7
GOTERM_CC_DIREC	GO:0043234~protein complex
GOTERM_BP_DIREC	GO:0007005~mitochondrion organization
GOTERM_BP_DIREC	GO:0007275~multicellular organism development
SMART	SM00055:FCH
KEGG_PATHWAY	mmu04115:p53 signaling pathway
GOTERM_MF_DIREC	GO:0050750~low-density lipoprotein particle receptor binding
GOTERM_BP_DIREC	GO:0006511~ubiquitin-dependent protein catabolic process
UP_KEYWORDS	Protein biosynthesis
INTERPRO	IPR003008:Tubulin/FtsZ, GTPase domain
INTERPRO	IPR001060:FCH domain
GOTERM_BP_DIREC	GO:0009953~dorsal/ventral pattern formation
GOTERM_BP_DIREC	GO:0016192~vesicle-mediated transport
GOTERM_CC_DIREC	GO:0001673~male germ cell nucleus

UP_KEYWORDS	Chromosome
INTERPRO	IPR008984:SMAD/FHA domain
UP_SEQ_FEATURE	zinc finger region:C2H2-type 1
GOTERM_CC_DIREC	GO:0005793~endoplasmic reticulum-Golgi intermediate compartment
GOTERM_BP_DIREC	GO:0032088~negative regulation of NF-kappaB transcription factor activity
GOTERM_MF_DIREC	GO:0035612~AP-2 adaptor complex binding
GOTERM_MF_DIREC	GO:0019887~protein kinase regulator activity
GOTERM_BP_DIREC	GO:0001890~placenta development
GOTERM_BP_DIREC	GO:0090181~regulation of cholesterol metabolic process
GOTERM_BP_DIREC	GO:0051123~RNA polymerase II transcriptional preinitiation complex assembly
KEGG_PATHWAY	mmu05213:Endometrial cancer
GOTERM_BP_DIREC	GO:0043153~entrainment of circadian clock by photoperiod
GOTERM_BP_DIREC	GO:0043393~regulation of protein binding
INTERPRO	IPR000253:Forkhead-associated (FHA) domain
GOTERM_CC_DIREC	GO:0005669~transcription factor TFIID complex

-LOG10(pval)	PValue
24.98	1.04E-25
19.54	2.91E-20
17.10	7.97E-18
16.99	1.02E-17
15.11	7.84E-16
14.88	1.33E-15
13.58	2.60E-14
12.08	8.29E-13
11.04	9.02E-12
10.88	1.31E-11
9.35	4.45E-10
9.09	8.13E-10
8.95	1.12E-09
8.84	1.46E-09
8.70	1.99E-09
8.41	3.92E-09
8.29	5.07E-09
8.00	1.00E-08
7.95	1.11E-08
7.95	1.11E-08
7.74	1.84E-08
7.72	1.91E-08
7.66	2.20E-08
7.53	2.96E-08
7.43	3.70E-08
7.28	5.22E-08
7.09	8.19E-08
6.79	1.63E-07
6.78	1.66E-07
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6.56	2.78E-07
6.55	2.82E-07
6.30	5.05E-07
6.23	5.85E-07
6.18	6.55E-07
6.17	6.83E-07
6.15	7.09E-07
5.99	1.03E-06
5.92	1.20E-06
5.91	1.23E-06
5.90	1.26E-06
5.62	2.41E-06

5.61	2.45E-06
5.56	2.75E-06
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3.84	1.43E-04
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2.02	0.009539144
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1.87	0.013413737
1.87	0.013527783
1.85	0.01414431
1.84	0.014380483
1.84	0.014455737
1.84	0.014506014
1.84	0.014506014
1.81	0.015313462
1.81	0.015425361
1.81	0.015523244
1.81	0.015597806
1.81	0.015597806
1.81	0.015597806
1.80	0.015750068
1.80	0.015981008
1.79	0.016111785
1.79	0.016111785
1.79	0.016128779
1.79	0.016269378
1.77	0.017077814
1.75	0.017622787
1.75	0.01795926
1.74	0.018379035
1.73	0.01845088
1.73	0.018499358
1.73	0.018501768
1.73	0.018686304
1.73	0.018689368
1.72	0.018882267
1.72	0.01914578
1.71	0.019559106
1.70	0.019956233
1.70	0.020073658
1.69	0.020194375

1.69	0.020405066
1.68	0.020986368
1.68	0.021106784
1.67	0.021545825
1.67	0.021570033
1.66	0.021871185
1.65	0.022421625
1.65	0.02249181
1.64	0.022879628
1.63	0.023234479
1.63	0.023432192
1.63	0.023683998
1.62	0.023761645
1.62	0.02383603
1.62	0.02385583
1.62	0.023867898
1.62	0.024011429
1.62	0.024039571
1.61	0.024430741
1.59	0.025880899
1.58	0.026062671
1.58	0.026062671
1.58	0.026062671
1.58	0.026062671
1.58	0.026134027
1.58	0.026410762
1.56	0.02779221
1.55	0.027899397
1.55	0.027899397
1.55	0.028223953
1.55	0.028272646
1.55	0.028407052
1.54	0.028951306
1.53	0.02961998
1.51	0.030556989
1.51	0.030572189
1.51	0.030761549
1.51	0.030767995
1.51	0.031006899
1.51	0.031042787
1.51	0.031185625
1.49	0.032022892
1.49	0.03214278

1.49	0.032176864
1.49	0.032464258
1.47	0.033896686
1.47	0.033896686
1.47	0.033896686
1.47	0.033896686
1.47	0.033958106
1.47	0.03403281
1.47	0.034198976
1.46	0.034581509
1.45	0.035526026
1.44	0.036064651
1.44	0.036558592
1.44	0.036558592
1.43	0.037078838
1.43	0.037216944
1.43	0.037216944
1.43	0.037216944
1.43	0.037216944
1.43	0.037216944
1.43	0.037216944
1.43	0.037216944
1.42	0.038374315
1.41	0.038546577
1.41	0.038970979
1.41	0.039164026
1.40	0.039727178
1.40	0.03972881
1.40	0.040073911
1.39	0.040603553
1.39	0.040704964
1.39	0.040755953
1.39	0.041198057
1.38	0.041375364
1.38	0.041506618
1.38	0.041626051
1.38	0.041952029
1.37	0.042263467
1.37	0.042355144
1.37	0.042355144
1.36	0.043236221
1.36	0.043539017
1.35	0.044382482

1.35	0.044578962
1.35	0.044836054
1.34	0.045234425
1.34	0.045366499
1.34	0.045622845
1.34	0.046019034
1.34	0.046019034
1.33	0.046544241
1.33	0.046619541
1.33	0.046619541
1.33	0.046840264
1.32	0.048035125
1.32	0.048035125
1.31	0.048868518
1.30	0.049975469

Genes
ALS2, LDHA, RUSC1, XRCC6, PGD, VPS52, VPS53, WTAP, CIAPIN1, CUL3, HMHA1, PGAM
ALS2, MEF2B, TEX19.2, LDHA, RUSC1, XRCC6, PGD, CHMP7, ASCC1, WTAP, CIAPIN1, SO
MEF2B, RUSC1, XRCC6, CHMP7, ASCC1, WTAP, CIAPIN1, SOHLH2, TAF7L, NONO, DCPS,
RBPMS2, TEX19.2, LDHA, DZIP3, RUSC1, CHMP7, PGD, RAB1B, CCT2, CCT3, CIAPIN1, TA
ALS2, RBPMS2, TEX19.2, LDHA, DZIP3, RUSC1, XRCC6, PGD, NELL2, CHMP7, RAB1B, CC
PDP1, RBPMS2, ALS2, LDHA, PGD, XRCC6, VPS52, VPS53, RAB1B, CCT2, CCT3, VPS33B, W
ALS2, MEF2B, DZIP3, RUSC1, CHMP7, VPS52, VPS53, WTAP, TAF7L, BC026585, NONO, HM
CCNB1IP1, TEX19.2, NBN, FKBP6, MAEL, SYCE1, MOV10L1, SYCP2, SYCP1, SIRT2, CDK2,
TEX19.2, RNF17, NKD1, FKBP6, NANOS2, ADAD1, SPINK2, MAEL, MOV10L1, SOHLH2, TA
CCNB1IP1, TEX19.2, NBN, FKBP6, MAEL, SYCE1, MOV10L1, SYCP2, SYCP1, SIRT2, CDK2,
LMO1, DZIP3, THRB, LMO4, RBM4, RBM5, ZFP583, TRIM47, HMHA1, ZFP90, GATA3, GIT2,
TEX101, ALS2, TEX19.2, XRCC6, CCT3, WTAP, TAF7L, NONO, CUL3, MEI4, INSIG2, DNAJB
CCT7, CCT5, TCP1, CCT4, CCT8, CCT2, CCT6A, CCT3
TEX19.2, NKD1, RNF17, FKBP6, NEK1, NANOS2, ARID4B, ADAD1, SPINK2, MAEL, MLH1,
ZMAT1, PPARA, ZBTB32, ZFP385A, AEBP1, LMO1, DZIP3, THRB, AGTPBP1, LMO4, RBM4,
CCT7, CCT5, TCP1, CCT4, CCT8, CCT2, CCT6A, CCT3
XRCC6, RBM4, MAEL, RBM5, CNP, MAF1, WTAP, ACSS2, CBX8, CIAPIN1, CTNNBL1, NON
CCNB1IP1, TEX12, REC8, SYCP3, FKBP6, MLH1, SYCE1, HORMAD1, HORMAD2, SYCP2, S
CCT7, CCT5, TCP1, CCT4, CCT8, CCT2, CCT6A, CCT3
CCT7, CCT5, TCP1, CCT4, CCT8, CCT2, CCT6A, CCT3
1700013H16RIK, RNF17, XLR3C, XLR3B, ADAD1, XLR3A, SPINK2, GM1140, TAF7L, DDX25
ALS2, MEF2B, DZIP3, RUSC1, CHMP7, VPS52, VPS53, WTAP, TAF7L, BC026585, NONO, HM
AKNA, RALY, MEF2B, THRB, LMO4, XRCC6, ASCC1, ZFP583, CBX8, MAF1, SOHLH2, TAF
CCT7, CCT5, TCP1, CCT4, CCT8, CCT2, CCT6A, CCT3
AKNA, RALY, MEF2B, THRB, LMO4, XRCC6, ASCC1, ZFP583, CBX8, MAF1, SOHLH2, TAF
ALS2, LDHA, BTRC, MAEL, VPS53, MAF1, GBF1, ATXN10, HTRA1, PDE4A, SH3BGR, VPS4
THRB, DZIP3, RBM4, RBM5, ZFP583, TRIM47, HMHA1, GATA3, ZFP90, GIT2, RBCK1, RNF3
CCT7, CCT5, TCP1, CCT4, CCT8, CCT2, CCT6A, CCT3
NARS, DZIP3, FARS2, PPIL2, NHLRC1, ACSS2, TTLL1, TTC3, TTLL11, RBX1, QRSL1, WARS
CCT7, CCT5, TCP1, CCT4, CCT8, CCT2, CCT6A, CCT3
CCT7, CCT5, TCP1, CCT4, CCT8, CCT2, CCT6A, CCT3
CCT7, CCT5, TCP1, CCT4, CCT8, CCT2, CCT6A
CCT7, CCT5, TCP1, CCT4, CCT8, CCT2, CCT6A, CCT3
PDP1, LMO1, DZIP3, THRB, LMO4, RBM4, RBM5, NT5DC2, ZFP583, CIAPIN1, HMHA1, TRI
HSP90AB1, FKBP9, P4HB, TCP1, FKBP6, TMX4, CWC27, PPIL2, CCT2, CCT6A, CCT3, CCT7,
USP3, PHF20, NR3C1, CBX8, MEN1, TSPYL2, SMARCD3, ASF1B, CHD5, EHMT1, IKZF1, BA
CCT7, CCT5, TCP1, CCT4, CCT8, CCT2, CCT6A, CCT3
MAD1L1, NBN, ZFP385A, MAEA, MLH1, WTAP, CDC45, ZFYVE19, CDKN2D, VPS4A, ACTR
RALY, CEP72, 1700013H16RIK, DZIP3, TRMT2A, CHMP7, VPS52, RBM5, VPS53, WTAP, TA
AKNA, RALY, MEF2B, THRB, LMO4, XRCC6, ASCC1, ZFP583, CBX8, MAF1, SOHLH2, TAF
DZIP3, BTRC, SENP8, FAM63A, CUL3, DCAF11, RBCK1, E4F1, FBXL15, RNF34, DCAF17, RN
NARS, DZIP3, FARS2, PPIL2, NHLRC1, ACSS2, TTLL1, TTC3, TTLL11, RBX1, QRSL1, WARS

TEX19.2, RNF17, NKD1, FKBP6, FHL1, CAMK2G, NANOS2, RBM4, ADAD1, SPINK2, MAEL,
CCT7, PRKCQ, CCT5, TCP1, CCT4, OBFC1, CCT8, CCT2, CCT6A, CCT3
RUSC1, TUBA3B, TUBA3A, KLC4, CCT2, KIF9, CCT3, KLC2, TTLL1, TTLL11, CYLD, DYNC
USP3, PHF20, NR3C1, CBX8, MEN1, TSPYL2, SMARCD3, ASF1B, CHD5, EHMT1, IKZF1, BA
MAD1L1, ZFP385A, NBN, MAEA, NEK3, USP3, USP2, NEK1, MLH1, SYCP2, WTAP, SYCP1,
PDP1, LMO1, DZIP3, THRB, LMO4, RBM4, RBM5, NT5DC2, ZFP583, CIAPIN1, HMHA1, TRI
CCNB1IP1, PELI1, DZIP3, BTRC, PPIL2, NHLRC1, RBX1, CUL3, RNF8, MED7, RNF6, UHRF1,
CYB5R3, LDHA, CYP2S1, PGD, EGLN2, SESN1, HADHA, BC026585, SESN3, MTHFD2, FMO
CCT7, CCT5, TCP1, CCT4, RAB28, CCT8, CCT2, CCT6A, CCT3
PELI1, DZIP3, RUSC1, BTRC, PPIL2, NHLRC1, CUL3, TMEM129, RNF114, DDB2, RBCK1, RN
CYB5R3, LDHA, CYP2S1, PGD, EGLN2, SESN1, HADHA, BC026585, SESN3, MTHFD2, FMO
LDHA, ACY1, ALDOC, BCKDHB, PGD, TKTL1, ACSS2, ACAT2, ACAT1, HADHA, PYCR1, P
PDP1, LDHA, ABHD8, ALDOC, XRCC6, ECHDC1, NFS1, PPM1B, TKTL1, ACSS2, PPCDC, AC
AKNA, RALY, MEF2B, THRB, LMO4, XRCC6, ASCC1, ZFP583, MAF1, CBX8, SOHLH2, TAF
MAEA, DZIP3, BTRC, PPIL2, NHLRC1, TTC3, RBX1, CUL3, FBXO6, RBCK1, RNF167, RNF34
TEX12, REC8, SYCP3, SYCE1, HORMAD1, SYCP1, TEX11
REC8, MEI4, STRA8, SYCP3, MAEL, MLH1, HORMAD1, SYCP1
TCP1, CCT2, CCT3, CCT6A, CCT7, ACOT7, CCT5, CCT4, PACRG, CCT8, CACYBP, GNB4, GS
ZFP385A, NBN, USP3, APLF, NEK1, XRCC6, MAEL, MLH1, MUM1, CHCHD6, RBX1, MEN1,
HSP90AB1, CCT7, CCT5, TCP1, CCT4, DNAJB11, CCT8, CCT2, CCT6A, DNAJB1, CCT3, HSP
TCP1, USP2, FLOT2, CCT2, CCT6A, CCT3, CCT7, LAMP1, CCT5, MSX1, CCT4, COG7, RASS
TEX19.2, RBM4, SPINK2, MAEL, MOV10L1, CSPG5, TNFSF12, DLK1, SOHLH2, TAF7L, STR
CRTC1, XRCC6, ECHDC1, TKTL1, ACSS2, ACAT2, GPAT2, CIAPIN1, ACAT1, HADHA, ACA
HSP90AB1, P4HB, TCP1, LYRM7, ANP32B, CCT2, CCT6A, CCT3, CCT7, PSMG1, CCT5, CCT
CCNB1IP1, REC8, SYCP3, MLH1, HORMAD1, TUBG1, ADD3, SYCP1, TEX11
CYB5R3, LDHA, TMX4, CYP2S1, PGD, EGLN2, SESN1, HADHA, BC026585, SESN3, MTHFD
ZFP385A, NBN, USP3, APLF, XRCC6, MLH1, MUM1, RBX1, NONO, AEN, FBXO6, POLN, FA
NBN, 1700013H16RIK, ZFP385A, CPT2, LMO1, RBM4, XRCC6, MAF1, CIAPIN1, NONO, RBM
REC8, SYCP3, FKBP6, MLH1, HORMAD1, HORMAD2, BOLL
ZMAT1, AKNA, PPARA, MEF2B, AEBP1, THRB, XRCC6, ARID4B, MAEL, PHF20, ZFP583, S
ABLIM1, LMO1, LHX2, LMO4, FHL1, LHX3, LIMD2, LHX6, FHL4, SCEL, PXN
RBPMS2, RALY, TRMT2A, RBM4, XRCC6, RBM5, RAB1B, CCT2, CCT3, ACSS2, NONO, RA
DZIP3, USP3, PPIL2, PHF20, NHLRC1, TTC3, RBX1, CXXC1, TRIM47, ZFYVE19, RSPRY1, R
WARS, CARS, NARS, RARS2, FARS2, CARS2, LARS2, SARS2
XLR4A, 1700013H16RIK, XLR4C, XLR3C, XLR4B, XLR3B, XLR3A, GM1140, SYCP3, XLR5C,
ABLIM1, LMO1, LHX2, LMO4, FHL1, LHX3, LIMD2, LHX6, FHL4, SCEL, PXN
ACTB, EEF1A1, TCP1, ATP5B, STIP1, CNP, CCT2, CCT3, SIRT2, SLC25A12, CCT5, ACTR1A,
CCT7, CCT5, TCP1, CCT4, CCT8, CCT2, CCT6A, CCT3
CCNB1IP1, RNF17, CGRRF1, DZIP3, DTX3, NHLRC1, TTC3, RBX1, RNF8, TRIM47, RNF6, U
ABLIM1, LMO1, LHX2, LMO4, FHL1, LHX3, LIMD2, LHX6, FHL4, SCEL, PXN
NBN, APLF, NEIL3, XRCC6, CINP, MLH1, MUM1, RAD54L, CDK2, UIMC1, RBX1, NONO, RN
RALY, HSP90AB1, MAD1L1, ZFP385A, LDHA, RUSC1, XRCC6, ARID4B, H2-D1, CCT3, MAF
TDRKH, MAEL, BRDT, MLH1, MOV10L1, SYCP2, TEX11

IQCB1, ALS2, CEP72, NEK3, USP2, NEK1, BCL2L1, MAF1, CYLD, CDC45, ZFYVE19, TSPYL
WARS, CARS, NARS, RARS2, FARS2, CARS2, LARS2, SARS2
CYB5R3, RNLS, PPCDC, ACADVL, FMO5, TXNRD3, ETFDH, TXNRD2, SMOX, ACAD9, MT
ZFP385A, SERBP1, RBM4, DAZL, IGF2BP3, ANGEL2, RNF20, BOLL, FXR1
HYAL2, UMPS, ALDOC, TYW1, NPL, DERA, GMPR, DUS3L
DZIP3, BTRC, PPIL2, NHLRC1, RBX1, OS9, CUL3, TMEM129, DCAF11, E4F1, RNF34, FBXL1
HSP90AB1, NARS, APLF, ATP5B, PRKAG1, PRKAG2, XRCC6, RAB1B, MOV10L1, CCT2, CC
RBPMS2, ADAD2, RALY, FIP1L1, ZFP385A, DZIP3, TRMT2A, NANOS2, ADAD1, RBM4, RB
MEN1, HHEX, HEXIM2, INCA1, CDK5RAP1, FBXO7
PDP1, HSP90AB1, CYB5R3, LDHA, CPT2, NARS, COX10, AGTPBP1, ATP5B, RAB1B, MPV17
HSP90AB1, NARS, PRKAG1, ATP5B, PRKAG2, XRCC6, MOV10L1, CCT2, CCT3, ACSS2, TTL
ACADVL, ACAT2, HADH, ACAT1, HADHA, ACAT3, SLC25A17, PEX7
USP3, MLH1, NR3C1, HDGFRP2, CALCOCO1, MEN1, NONO, CDC45, SMARCD3, LHX2, GA
CYB5R3, PRKAG1, PRKAG2, ACSS2, PRPS1
TEX12, SYCE1, SYCP1, TEX11
RNF17, CGRRF1, DTX3, NHLRC1, RBX1, RNF8, TRIM47, UHRF1, RNF114, RNF208, RSPRY1
RNLS, PTGR1, SDR39U1, GMDS, PGD, QDPR, GMPR, TECR, PYCR1, FMO5, TXNRD3, TXNR
MEI4, STRA8, ZSCAN21, MLH1, DAZL, HORMAD1, SOHLH2
ZBTB32, AEBP1, CNBP, MAF1, CBX8, MEN1, NONO, HEXIM2, ZFP90, E4F1, FIZ1, THAP11,
RALY, ADAD2, ZMAT1, RBPMS2, ZFP385A, FIP1L1, DZIP3, TRMT2A, NANOS2, ADAD1, RB
EGFR, HSP90AB1, DBNL, LDHA, BAIAP2L1, FLOT2, FLOT1, SNX1, MPP7, KLC2, GCN1L1, S
PARD6A, MAD1L1, MAEA, ZC3HC1, NEK3, DSN1, NEK1, CINP, SYCE1, SYCP2, SYCP1, CD
FECH, GMDS, APLF, NEIL3, ALDOC, XRCC6, NPL, ECHDC1, PPCDC, HADHA, UMPS, TYW
WARS, CARS, NARS, RARS2, CARS2, LARS2, SARS2
STRA8, ZSCAN21, DAZL, HORMAD1, SOHLH2
REC8, STRA8, TDRKH, SPINK2, MAEL, BCL2L1, SYCP2, TEX11
CCNB1IP1, SYCP3, SYCP1, TEX11
RALY, ZFP326, RBM4, RBM5, SAP18, PRPF3, WTAP, DCPS, NONO, RBM4B, HNRNPM, SUG
LDHA, ECHDC1, ACAT2, ACSS2, ACAT1, HADHA
FECH, GMDS, APLF, NEIL3, ALDOC, XRCC6, NPL, ECHDC1, PPCDC, HADHA, UMPS, TYW
EHMT1, PLOD1, PLOD2, ACAT2, HADH, ACAT1, ALDH9A1, HADHA
EGFR, HSP90AB1, DBNL, LDHA, BAIAP2L1, SNX1, MPP7, KLC2, GCN1L1, SLC9A3R2, SCY
QRSL1, WARS, CARS, NARS, RARS2, FARS2, CARS2, LARS2, SARS2
REC8, MEI4, SYCP3, SYCP2, SYCP1
CCNB1IP1, MAD1L1, NBN, EHMT1, FKBP6, DSN1, XRCC6, MLH1, SYCE1, SYCP2, SYCP1, D
LDHA, PTGR1, SDR39U1, GMDS, PGD, QDPR, VAT1, HADHA, NAE1, BC026585, PYCR1, MT
PPARA, AEBP1, LMO1, THRB, USP3, USP2, MAEL, TRIB3, CBX8, SUFU, MEN1, NR1H2, CU
NIN, TUBA3B, RUSC1, TUBA3A, KLC4, KLC2, KIF9, GAS8, TTLL1, EML5, SIRT2, TTLL11, F
ACADVL, CYB5R3, RNLS, FMO5, TXNRD3, ETFDH, TXNRD2, SMOX, ACAD9, MTO1, PRO
HSP90AB1, SPHK2, FLOT1, SNAPIN, ATP11C, VPS33B, DAGLB, TMEM175, DIRC2, DRAM2,
NBN, USP3, APLF, NEIL3, XRCC6, CINP, MLH1, MUM1, RAD54L, CDK2, UIMC1, RBX1, NO
RNF8, UHRF1, RNF208, DDB2, RAD18, ASB4, RNF146, RNF41
EGFR, TCP1, USP2, RELA, TRIB3, CCT2, TANK, NAE1, CUL3, RNF8, AKTIP, ARRB1, PACR

ABLIM1, LMO1, LHX2, LMO4, FHL1, LHX3, LHX6, PXN
ABLIM1, LMO1, LHX2, LMO4, FHL1, LHX3, LHX6, PXN
CCNB1IP1, CNTD1, STRA8, MLH1, SYCP1, TEX11
WARS, CARS, RARS2, CARS2, LARS2
CGRRF1, DZIP3, DTX3, NHLRC1, TTC3, RNF8, TRIM47, RNF6, UHRF1, RNF114, RSPRY1, RA
REC8, DMRTC2, BRDT, MOV10L1, UBB
PDP1, LYRM7, RARS2, FARS2, NFS1, LARS2, BCL2L1, ACAT1, SARS2, ISCA1, HAGH, ALAS
CUL3, RNF6, MAEA, DZIP3, ARRB1, SIAH1B, BTRC, PCBP2, RBCK1, NHLRC1, RNF34, SIRT
SNX17, RUSC1, SNX16, VPS52, SNX1, VPS53, VPS33B, DTNBP1, TMEM175, TMEM9B, RAB
CEP72, MAD1L1, MAEA, RUSC1, TTLL1, TTLL11, ZFYVE19, RAB28, ACTR1A, DYNC2H1, C
ISCA1, FECH, TYW1, PRIM2, NFS1, ETFDH, CDK5RAP1, CIAPIN1
ZMAT1, AKNA, PPARA, ZBTB32, AEBP1, THRB, XRCC6, ARID4B, MAEL, PHF20, ZFP583, S
RAB3A, ARFGAP3, AP1M2, SNX17, SNX16, CHMP7, SNX7, BET1, VPS52, NUP93, SNX1, VPS
RALY, ZFP326, RBM4, RBM5, SAP18, PRPF3, WTAP, DCPS, NONO, RBM4B, HNRNPM, SUG
CYB5R3, PDP1, CPT2, COX10, AGTPBP1, ATP5B, MPV17, GPAT2, CIAPIN1, MTHFD2, ALAS
1700013H16RIK, DMRTC2, SCML2, MAEL, RAD18
PARD6A, MAD1L1, MAEA, ZC3HC1, NEK3, DSN1, NEK1, CINP, SYCE1, SYCP2, SYCP1, CD
CDC45, CCDC88A, STRA8, GINS3, POLD2, PRIM2, CINP, POLN, CHAF1B, NFIA
DEAF1, PPARA, CNBP, BTRC, XRCC6, CALCOCO1, CXXC1, MEN1, NR1H2, TASP1, PRMT2,
ACOT7, PPCDC, ACAT1, DCAKD
RNF17, DTX3, NHLRC1, RNF8, TRIM47, UHRF1, RNF114, RNF208, RBCK1, RAD18, PEX10,
ACAT2, ACAT1, ACAT3
RALY, FIP1L1, ZFP326, RBM4, RBM5, DDX1, SAP18, PRPF3, WTAP, DCPS, NONO, RBM4B,
TEX12, SYCP3, SYCP1
TCP1, CCT4, CCT2
RNLS, FMO5, TXNRD3, ETFDH, TXNRD2, SMOX, MTO1, RETSAT
RALY, MAD1L1, ATG12, FHL1, XRCC6, ARID4B, STIP1, IGF2BP3, PPM1B, CCT3, NR3C1, M
RALY, ZMAT1, RBPMS2, ZBTB32, ZFP385A, NARS, RBM4, RBM5, ASCC1, ZFP583, NONO,
CUL3, USP2, INCA1, CDK5RAP3, CDK2
PCBP3, PCBP2, TDRKH, IGF2BP3, FXR1
PCBP3, PCBP2, TDRKH, IGF2BP3, FXR1
RALY, RBPMS2, RBM46, TRMT2A, RBM45, RBM4, NXF2, G3BP2, RBM5, NXF3, IGF2BP3, N
FKBP6, TDRKH, CNOT10, RBM4, MAEL, PIWIL1, MOV10L1
CDKN1C, HEXIM2, CDKN2D, INCA1
ACADVL, CPT2, ACAT2, HADH, ACAT1, ALDH9A1, HADHA
RAB3A, SNX17, RUSC1, SNX16, SNX7, VPS52, SNX1, VPS53, VPS33B, DTNBP1, TMEM175,
RALY, HSP90AB1, ZFP385A, DZIP3, TRMT2A, RBM4, XRCC6, RBM5, H2-D1, CCT3, NAP1L4
PYCR1, PGD, HADH, HADHA
CARS, RARS2, CARS2, LARS2
EGFR, ALS2, DBNL, NTF5, NEK3, ILK, UBB, DTNBP1
RNF8, NBN, APLF, TDP1, XRCC6, DDX1, RAD54L, UIMC1
PDP1, CPT2, CCDC90B, COX10, ATP5B, FARS2, NFS1, ACAT1, HADHA, MTHFD2, ALAS1, E
DBNL, AP1M2, VAMP3, AP3B1

AKTIP, STX17, VPS16, VPS33B
LDHA, THRB, PGD, RAB1B, TSPAN8, CNP, CCT2, CCT3, DNASE1L1, MMRN2, CUL3, PLOD
ACADVL, CPT2, ACAT2, HADH, ACAT1, TECR, HADHA
ISCA1, FECH, TYW1, PRIM2, NFS1, ETFDH, CDK5RAP1, CIAPIN1
TBL3, BTRC, WDR70, WDR91, TSSC1, WIPI1, EML5, PEX7, BRWD1, DCAF11, WDR61, WDS
SIRT6, SIRT7, HADH, SIRT2
MEN1, BMP4, TAF6, GATA3, MOV10L1, RNF167
PCBP3, PCBP2, TDRKH, ASCC1, IGF2BP3, FXR1
HYAL2, NTF5, CCDC88A, ARRB1, SNX17, RUSC1, RAB11B, PDGFRB, RGS19, COMMD7, SL
EGFR, ZC3HC1, NUP93, TRIB3, FAM188A, PHF20, BCL2L1, WTAP, SLC16A3, APEH, RNF6,
RAB11B, SDCCAG3, VPS52, VPS53, VAMP3, FCHSD1, ATP11C, VPS16, TUBG1, VPS33B, LD
RBPMS2, MAEL, MOV10L1, CSPG5, TNFSF12, WTAP, SOHLH2, TAF7L, DDX25, DYNC2H1,
MEI4, STRA8, HORMAD1
ACTB, ZFP385A, USP3, THRB, RELA, SCML2, CBX8, STAT3, CALCOCO1, KLHDC3, MEN1,
MEN1, CDKN1C, CGRRF1, SGSM3, CDKN2D, RASSF1, ILK, VASH1, MLF1
EGFR, CUL3, MSX1, GATA3, MAEL, STRADB, CAP1, THOC5, MED1
AP1M2, SNX17, RUSC1, SNX7, BCL2L1, VPS33B, DTNBP1, SYNGR2, SYNPR, STX17, RAB11
HAGH, LDHA, ACAT2, ACSS2, ACAT1, ALDH9A1
PCBP3, PCBP2, TDRKH, ASCC1, IGF2BP3, FXR1
XLR3C, XLR3B, XLR3A
XLR3C, XLR3B, XLR3A
XLR3C, XLR3B, XLR3A
BTRC, FBXO6, FBXL15, FBXO9, RBX1
CNBP, CDC45, SSBP2, NEIL3, TDP1, OBFC1, PRIM2, MLH1, NCL
FECH, SERPINF1, RBM4, NR3C1
HHEX, NXF2, NUP93, NXF3
PPARA, NBN, RELA, LMO4, BCL2L1, HDAC11, NR3C1, SUFU, SIRT2, STAT3, TAF7L, HHEX
RAB3A, CNBP, RAB1B, CNP, NR3C1, HADHA, NONO, TRIM47, FMO5, HNRNPM, PRMT2, A
CTNNBIP1, PRMT2, BTRC, RGS19, SLC9A3R2, SUFU, CALCOCO1, PXN, HDAC6
FKBP6, TDRKH, CNOT10, RBM4, MAEL, PIWIL1, MOV10L1
RALY, RBPMS2, RBM46, RBM45, RBM4, G3BP2, RBM5, IGF2BP3, NCL, BOLL, NONO, RBM
PDP1, NPEPL1, AGTPBP1, ATP5B, XRCC6, SENP8, MOV10L1, CNP, FAM63A, AFMID, DNAS
HSP90AB1, NARS, PRKAG1, ATP5B, PRKAG2, XRCC6, MLH1, MOV10L1, CCT2, CCT3, ACS
HSP90AB1, EGFR, CCND1, RELA, ARAF, PDGFRA, PDGFRB, PIK3R3, CDK2
BRWD1, TBL3, WDR61, WDSUB1, BTRC, DDB2, FBXW2, GNB4, WDR70, CHAF1B, TSSC1,
EGFR, TMEM175, LAMP1, SNX17, VPS52, SNX1, VPS53, ABCB6, WIPI1, DTNBP1, GRB14
RAB3A, ARFGAP3, AP1M2, SNX17, SNX16, CHMP7, SNX7, VPS52, BET1, NUP93, SNX1, VPS
EGFR, CCND1, RASSF1, ARAF, DAPK2, DAPK3
PARD6A, H2-K1, EGFR, ARFGAP3, CHMP7, H2-D1, SNX1, CYTH2, LDLRAP1, GBF1, SH3GL
STX17, SNAPIN, MCOLN1, VPS16
PDP1, NPEPL1, AGTPBP1, ATP5B, XRCC6, SENP8, MOV10L1, CNP, TMEM62, FAM63A, AFM
RALY, RBPMS2, RBM46, RBM45, RBM4, G3BP2, RBM5, IGF2BP3, NCL, BOLL, NONO, RBM
MEN1, HHEX, ZBTB32, IKZF1, PDGFRB, ROGDI, TXNRD2, CIAPIN1, MELK

AKNA, PPARA, MEF2B, CRTC1, RBM4, XRCC6, GCN1L1, CALCOCO1, CXXC1, NR1H2, NO
TBL3, DCAF11, WDR61, WDSUB1, BTRC, FBXW2, GNB4, WDR70, PEX7
TBL3, BTRC, WDR70, WDR91, TSSC1, WIPI1, EML5, PEX7, BRWD1, DCAF11, WDR61, WDS
HSP90AB1, PRKAG1, PRKAG2, TRIB3, BCL2L1, GCN1L1, PXN, SUFU, CYLD, CDKN2D, ST
RBM4B, ZFP385A, NANOS2, DDX25, CNOT10, ADAD1, PIWIL1, DAZL, IGF2BP3, GCN1L1,
WARS, CARS, CARS2, LARS2
LDHA, SEC1, COX10, ALG1, ATP5B, CYP2S1, PGD, ACSS2, GPAT2, AFMID, PIGK, MTHFD2
ACADVL, CYB5R3, FMO5, TXNRD3, TXNRD2, ACAD9, MTO1, DUS3L
ACAT2, ACAT1, ACAT3
PRKCQ, TCP1, CCT4, OBFC1, CCT2
PRDM9, ZFP120, IKZF1, ZSCAN21, ZFP647, ZFP90, BNC1, ZFP672, ZFP629, E4F1, ZFP583, FI
RALY, ZFP212, MED16, DDX1, PHF21A, CALCOCO1, MED1
TBL3, MPV17, WDR70, WDR91, TSSC1, WIPI1, EML5, PEX7, BRWD1, DCAF11, WDR61, WD
AKNA, MEF2B, PPARA, LMO1, THRB, LMO4, ARID4B, XRCC6, SOHLH2, MEN1, STRA8, G
WARS, CARS, RARS2, CARS2, LARS2, PAPSS1
CDC45, CCDC88A, STRA8, GINS3, POLD2, PRIM2, CINP, POLN, E4F1, CHAF1B, NFIA
RNF8, UHRF1, USP3, ANP32B, PHF21A, BRDT, ASF1B, CHAF1B, RNF20, NCL, UIMC1
NR1H2, PRKCQ, PPARA, RELA, PRKAG1, PRKAG2, TRIB3, SLC27A3, PIK3R3, STAT3
RNF8, AEN, NEK1, XRCC6, CYP2R1, RAD54L, UIMC1
ALDOC, PGD, DERA, TKTL1, PRPS1
ACAT2, ACAT1, ACAT3
ACAT2, ACAT1, ACAT3
SIRT6, SIRT7, SIRT2
SIRT6, SIRT7, SIRT2
FKBP6, TDRKH, MAEL, PIWIL1, MOV10L1
BMP4, PTPN6, HYAL2, SMPD1, CDK5RAP3, GBA
DEAF1, MEF2B, IKZF1, RELA, LMO4, XRCC6, ASCC1, SAP18, DAZAP2, ECSIT, CDK2, MED
TBL3, MPV17, WDR70, WDR91, TSSC1, WIPI1, EML5, PEX7, BRWD1, DCAF11, WDR61, WD
TBL3, MPV17, WDR70, WDR91, TSSC1, WIPI1, EML5, PEX7, BRWD1, DCAF11, WDR61, WD
UHRF1, UBC, UBB, GM1821
PPARA, CDK5RAP3, BCL2L1
TBL3, BTRC, WDR70, WDR91, TSSC1, WIPI1, EML5, PEX7, BRWD1, DCAF11, WDR61, WDS
TBL3, MPV17, WDR70, WDR91, TSSC1, EML5, PEX7, BRWD1, DCAF11, WDR61, WDSUB1,
DCAF11, DDB2, DCAF17, RBX1
NKD1, SGSM3, SNX1, EGLN2, TRIB3, TNFSF12, NSF
CEP72, MAD1L1, MAEA, RUSC1, TTLL1, TTLL11, ZFYVE19, RAB28, ACTR1A, DYNC2H1, C
ZFP385A, NANOS2, DDX25, CNOT10, PIWIL1, DAZL, IGF2BP3, GCN1L1, BOLL
PCBP3, PCBP2, TDRKH, ASCC1, IGF2BP3, FXR1
SIRT6, SIRT7, SIRT2
RALY, FIP1L1, ZFP326, RBM4, RBM5, DDX1, SAP18, PRPF3, WTAP, DCPS, NONO, RBM4B,
PLD3, CYB5R3, CPT2, CHKB, PRKAG1, PRKAG2, PLBD1, PNPLA2, GPAT2, TECR, LDLRAP
PRDM9, ZFP120, ZFP647, ZFP90, ZFP672, ZFP629, ZFP583, FIZ1, ZFP526
FKBP6, TDRKH, MAEL, MOV10L1

ACAT2, HADH, ACAT1, ALDH9A1, HADHA, AFMID
ALDOC, PGD, IDH1, ENO3, TKTL1, ACAT2, ACSS2, ACAT1, HADHA, PRPS1
ACAT2, ACAT1, ACAT3
ACAT2, ACAT1, ACAT3
ACAT2, ACAT1, ACAT3
GM13305, IL11RA2, IL11RA1
ACADVL, CYB5R3, FMO5, TXNRD3, ETFDH, TXNRD2, MTO1
AP1M2, SNX17, RUSC1, SNX7, BCL2L1, VPS33B, SYNGR2, DTNBP1, SYNPR, STX17, RAB11
TCP1, NIN, NEK1, TUBG1
PRDM9, ZFP647, ZFP90, ZFP672, ZFP629, ZFP583, FIZ1, ZFP526
CYB5R3, RNLS, LDHA, SIRT6, SIRT7, HADHA, SIRT2, MTHFD2, HADH, HSD17B7, ALDH9A
RNF8, NBN, APLF, RAD18, KDM4D
EGFR, CCND1, RELA, ARAF, BCL2L1, PIK3R3, STAT3
EGFR, CCND1, CAMK2G, ARAF, PDGFRA, PDGFRB, PIK3R3
PTPN6, ZFP385A, VPS33B, MED1
ACER3, SPHK2, GBA
DKK1, SFRP2, RGS19
HTRA1, PCBP2, PPM1B
TSC22D3, DKK1, USP2
SLC37A4, JAM3, MLF1
BMP4, LHX2, OTX2
MEN1, RNF20, TET1
TUBA3B, TUBA3A, ANKMY2, GAS8, SUFU, TTLL11, SLC25A31, CCT4, SPAG4, PACRG, CC
STX17, SYN2, BET1, SNAP47, VAMP3, YKT6
GAL3ST3, ARFGAP3, SEC1, AP1M2, SLC39A13, RUSC1, VPS52, BET1, SNX1, VPS53, CSPG5,
SPHK2, SNX16, PLBD1, SNAPIN, VPS33B, TMEM175, LAMP1, DIRC2, DRAM2, TMEM9B, S
HSP90AB1, P4HB, LAMP1, CCT4, SERPINF1, FLOT1, CNP, GCHFR, HSPA8
CUL3, UHRF1, MAEA, DZIP3, SIAH1B, RNF34, RNF146, FBXO7, SPOP, RBX1, OS9
RNF8, RNF6, PELI1, RNF34, TTC3, RNF146
PRDM9, ZFP120, ZSCAN21, ZFP647, ZFP90, ZFP672, ZFP629, E4F1, ZFP583, FIZ1, ZFP526
ALS2, RAB3A, ATG12, PRKAG1, SNX17, XRCC6, SNX1, STIP1, NR3C1, KLC2, PEX3, MEN1,
RAB3A, NRF1, MSTO1, AGTPBP1, COX10, PRKAG1, PRKAG2, FANCG
RBPMS2, MAEL, MOV10L1, CSPG5, TNFSF12, WTAP, SOHLH2, TAF7L, DDX25, DYNC2H1,
HMHA1, PACSIN3, FCHSD1, FCHO1
CCND1, SIAH1B, SHISA5, DDB2, SESN1, CDK2, SESN3
DKK1, SNX17, LDLRAP1, SLC9A3R2
RNF8, CUL3, CYLD, RNF6, USP3, USP2, SIAH1B, BTRC, RNF20, TTC3, RBX1, HDAC6
QRSL1, WARS, EEF1A1, CARS, NARS, RARS2, FARS2, CARS2, LARS2, EEFSEC, SARS2
MSTO1, TUBA3B, TUBA3A, TUBG1
HMHA1, PACSIN3, FCHSD1, FCHO1
LHX2, LHX3, OTX2, DYNC2H1, TGIF1, FBXL15
ARFGAP3, AP1M2, BET1, VPS33B, CUL3, GBF1, SCYL1, ARF2, STX17, VPS4A, VAMP3, YK
REC8, SYCP3, MLH1, SYCP1

CCNB1IP1, MAD1L1, NBN, EHMT1, FKBP6, DSN1, XRCC6, SYCE1, SYCP2, SYCP1, DAPK3,
RNF8, NBN, APLF, PPP1R8, RASIP1, SLC4A1AP
ZBTB32, IKZF1, ZFP414, ZHX1, ZFP672, ZFP629, ZFP583, PRDM9, ZFP120, ZSCAN21, ZFP647
NUCB1, SLC35C2, P4HB, GBF1, SCYL1, STX17, RAB1B
CYLD, PELI1, PRMT2, ARRB1, RBCK1, CDK5RAP3, COMMD7
ARRB1, LDLRAP1, FCHO1
HSP90AB1, GCN1L1, CDK5RAP1
HSP90AB1, CDKN1C, HTRA1, LHX3, IL11RA1, ETNK2
ACADVL, DGAT2, THRB
4933416C03RIK, TAF12, TAF7L
EGFR, CCND1, ILK, ARAF, MLH1, PIK3R3
RBM4B, USP2, CRTC1, RBM4
CYLD, SMARCD3, SNAPIN, LDLRAP1
RNF8, NBN, APLF, PPP1R8, SLC4A1AP
4933416C03RIK, TAF12, TAF6, TAF7L

Count	%	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
420	50.48076923	825	7617	22680	1.515843747	3.49E-23	3.49E-23
348	41.82692308	753	6019	19662	1.509689436	1.56E-17	1.56E-17
267	32.09134615	825	4534	22680	1.618895617	2.66E-15	1.33E-15
261	31.37019231	825	4404	22680	1.629229626	3.42E-15	1.14E-15
359	43.14903846	753	6631	19662	1.413670307	4.17E-13	2.08E-13
198	23.79807692	825	3125	22680	1.741824	4.45E-13	1.11E-13
266	31.97115385	825	4779	22680	1.530148947	8.71E-12	1.74E-12
23	2.764423077	825	90	22680	7.025454545	2.77E-10	4.61E-11
31	3.725961538	825	188	22680	4.533075435	3.01E-09	4.31E-10
23	2.764423077	715	95	18082	6.122723592	3.40E-08	3.40E-08
132	15.86538462	825	2099	22680	1.728823249	1.49E-07	1.86E-08
230	27.64423077	685	4092	17446	1.431520289	7.00E-07	7.00E-07
8	0.961538462	715	8	18082	25.28951049	2.93E-06	1.47E-06
45	5.408653846	715	407	18082	2.796137523	3.79E-06	1.26E-06
84	10.09615385	685	1075	17446	1.990105585	1.71E-06	8.56E-07
8	0.961538462	753	9	19662	23.21027003	2.10E-06	7.01E-07
125	15.02403846	753	1935	19662	1.68679288	2.72E-06	6.80E-07
12	1.442307692	753	31	19662	10.10769824	5.37E-06	1.07E-06
8	0.961538462	774	10	20594	21.28578811	1.46E-05	1.46E-05
8	0.961538462	774	10	20594	21.28578811	1.46E-05	1.46E-05
25	3.004807692	715	160	18082	3.951486014	4.79E-05	1.20E-05
261	31.37019231	743	4691	18012	1.348801993	3.36E-05	3.36E-05
112	13.46153846	825	1799	22680	1.711496286	7.35E-06	8.17E-07
8	0.961538462	774	11	20594	19.35071647	3.88E-05	1.94E-05
114	13.70192308	825	1859	22680	1.685833048	1.24E-05	1.24E-06
114	13.70192308	753	1784	19662	1.668563415	2.80E-05	4.66E-06
99	11.89903846	825	1565	22680	1.739041534	2.74E-05	2.49E-06
8	0.961538462	753	13	19662	16.06864848	8.76E-05	1.25E-05
34	4.086538462	825	330	22680	2.832396694	5.55E-05	4.62E-06
8	0.961538462	774	14	20594	15.20413437	3.66E-04	1.22E-04
8	0.961538462	774	14	20594	15.20413437	3.66E-04	1.22E-04
7	0.841346154	715	9	18082	19.66961927	7.34E-04	1.47E-04
8	0.961538462	774	15	20594	14.19052541	6.64E-04	1.66E-04
176	21.15384615	825	3395	22680	1.425154639	1.95E-04	1.50E-05
20	2.403846154	715	128	18082	3.951486014	0.00170516	2.84E-04
29	3.485576923	825	270	22680	2.952727273	2.28E-04	1.63E-05
8	0.961538462	715	15	18082	13.48773893	0.001846602	2.64E-04
49	5.889423077	825	626	22680	2.151844322	3.44E-04	2.30E-05
161	19.35096154	825	3076	22680	1.438893486	4.00E-04	2.50E-05
116	13.94230769	715	1885	18082	1.556277569	0.003197399	4.00E-04
49	5.889423077	825	631	22680	2.134793257	4.20E-04	2.47E-05
35	4.206730769	685	362	17446	2.462434972	0.002067729	6.90E-04

49	5.889423077	825	646	22680	2.085223755	8.16E-04	4.54E-05
10	1.201923077	715	32	18082	7.902972028	0.007141498	7.96E-04
32	3.846153846	753	327	19662	2.555259086	0.001830735	2.29E-04
28	3.365384615	715	266	18082	2.662053736	0.018746985	0.001890704
48	5.769230769	715	614	18082	1.977030136	0.029954331	0.002760921
175	21.03365385	685	3355	17446	1.328467153	0.024628077	0.006214714
22	2.644230769	685	199	17446	2.815625573	0.031773983	0.006437138
45	5.408653846	825	639	22680	1.935979513	0.013609638	7.21E-04
9	1.081730769	715	35	18082	6.503016983	0.126470412	0.01120453
15	1.802884615	715	103	18082	3.682938421	0.127826573	0.01046539
45	5.408653846	685	604	17446	1.897496012	0.050471593	0.008594493
22	2.644230769	295	214	7720	2.690321559	0.014953475	0.014953475
38	4.567307692	685	479	17446	2.020474529	0.058712267	0.008606523
126	15.14423077	715	2279	18082	1.398191453	0.167598058	0.013017378
29	3.485576923	685	326	17446	2.265612825	0.074999552	0.009697802
7	0.841346154	715	21	18082	8.42983683	0.270706243	0.020825339
8	0.961538462	715	30	18082	6.743869464	0.294139943	0.021535862
14	1.682692308	753	102	19662	3.583938755	0.070879785	0.0081353
34	4.086538462	715	420	18082	2.047246087	0.311315847	0.021700639
12	1.442307692	685	75	17446	4.074978102	0.124568047	0.014673267
16	1.923076923	715	128	18082	3.161188811	0.342043597	0.022988131
53	6.370192308	715	780	18082	1.718389815	0.344387142	0.021975202
36	4.326923077	715	463	18082	1.966355027	0.398637894	0.025107335
19	2.283653846	825	191	22680	2.734697763	0.070840901	0.003667025
9	1.081730769	753	44	19662	5.340999638	0.116194231	0.012275826
47	5.649038462	715	676	18082	1.758294368	0.463830205	0.029245001
27	3.245192308	825	336	22680	2.209090909	0.084809773	0.004211267
54	6.490384615	753	842	19662	1.674612713	0.133243817	0.012915646
7	0.841346154	715	24	18082	7.376107226	0.507201984	0.031654348
86	10.33653846	825	1604	22680	1.473951485	0.091497452	0.00435221
11	1.322115385	825	74	22680	4.086486486	0.105144832	0.004818501
106	12.74038462	685	1936	17446	1.39445919	0.249460368	0.028288454
33	3.966346154	774	445	20594	1.973120808	0.381561213	0.091637193
8	0.961538462	825	38	22680	5.787559809	0.120404585	0.005331289
13	1.5625	774	101	20594	3.424693632	0.409729766	0.08411317
11	1.322115385	774	74	20594	3.955129548	0.430694743	0.07732381
19	2.283653846	753	192	19662	2.583955843	0.205468998	0.018984422
8	0.961538462	715	36	18082	5.61989122	0.68736221	0.049296087
24	2.884615385	774	286	20594	2.232774977	0.499360225	0.08284937
11	1.322115385	409	74	10425	3.788905042	0.140255313	0.140255313
23	2.764423077	825	279	22680	2.26627566	0.178111252	0.00781531
80	9.615384615	825	1505	22680	1.461310782	0.191226401	0.008129707
7	0.841346154	715	28	18082	6.322377622	0.822996016	0.069608016

32	3.846153846	753	435	19662	1.920849934	0.311339057	0.028285058
8	0.961538462	685	39	17446	5.2243309	0.457272689	0.054043727
14	1.682692308	825	130	22680	2.960559441	0.263563741	0.011266885
9	1.081730769	685	53	17446	4.324858835	0.575926456	0.06899196
8	0.961538462	774	44	20594	4.837679117	0.783901446	0.156524584
28	3.365384615	715	362	18082	1.956094734	0.95882762	0.119794174
89	10.69711538	825	1754	22680	1.394920701	0.337753861	0.014610712
38	4.567307692	825	601	22680	1.738193919	0.3573264	0.015129835
6	0.721153846	715	22	18082	6.897139224	0.975638896	0.133138164
91	10.9375	753	1721	19662	1.380680648	0.534543669	0.053158974
72	8.653846154	825	1363	22680	1.452197692	0.382010009	0.015914767
8	0.961538462	715	44	18082	4.598092816	0.982807906	0.139716077
33	3.966346154	685	466	17446	1.803571317	0.749486642	0.101007182
5	0.600961538	685	14	17446	9.095933264	0.770838033	0.099889359
4	0.480769231	753	7	19662	14.92088788	0.606304126	0.060253484
18	2.163461538	743	186	18012	2.346025268	0.958193651	0.79553399
16	1.923076923	825	175	22680	2.513454545	0.464142335	0.019924214
7	0.841346154	715	34	18082	5.206663924	0.993644436	0.165279233
34	4.086538462	825	534	22680	1.750357508	0.52315889	0.022877131
48	5.769230769	685	780	17446	1.56729927	0.854243787	0.120487927
24	2.884615385	753	316	19662	1.983155984	0.736214909	0.079914598
26	3.125	825	372	22680	1.921407625	0.565904684	0.024970557
14	1.682692308	825	146	22680	2.63611457	0.583686618	0.025444714
7	0.841346154	715	36	18082	4.917404817	0.998945629	0.210513692
5	0.600961538	825	17	22680	8.085561497	0.610556238	0.026584132
8	0.961538462	715	49	18082	4.128899672	0.99954228	0.226096791
4	0.480769231	715	8	18082	12.64475524	0.999557766	0.220537476
19	2.283653846	825	240	22680	2.176363636	0.642720572	0.028185095
6	0.721153846	295	27	7720	5.815442561	0.540926805	0.322450596
14	1.682692308	685	139	17446	2.565184057	0.938624659	0.160057377
8	0.961538462	295	52	7720	4.026075619	0.561842131	0.240472438
22	2.644230769	685	279	17446	2.008277739	0.942937444	0.155024359
9	1.081730769	295	66	7720	3.568567026	0.568543803	0.189535162
5	0.600961538	753	17	19662	7.67986876	0.838164425	0.101589248
25	3.004807692	753	344	19662	1.89764199	0.847029515	0.09905055
17	2.043269231	774	199	20594	2.272979887	0.990326567	0.371134075
45	5.408653846	715	729	18082	1.561080894	0.999900051	0.250117677
20	2.403846154	825	264	22680	2.082644628	0.71741481	0.033579353
12	1.442307692	825	118	22680	2.79568567	0.722068375	0.033132887
19	2.283653846	753	234	19662	2.120168897	0.879078611	0.105231491
24	2.884615385	715	318	18082	1.908642301	0.999971102	0.271465034
8	0.961538462	715	52	18082	3.890693921	0.999980072	0.272640674
22	2.644230769	685	284	17446	1.972920736	0.971933199	0.180047876

8	0.961538462	743	50	18012	3.878761777	0.999358637	0.913761458
8	0.961538462	743	50	18012	3.878761777	0.999358637	0.913761458
6	0.721153846	715	28	18082	5.419180819	0.999989012	0.278374834
5	0.600961538	743	17	18012	7.130076795	0.999585643	0.857326346
19	2.283653846	409	234	10425	2.06961946	0.717789375	0.468765
5	0.600961538	715	19	18082	6.655134339	0.999999752	0.344585744
16	1.923076923	753	188	19662	2.222259897	0.957588421	0.146164471
14	1.682692308	715	149	18082	2.376195616	0.999999908	0.354641836
28	3.365384615	825	443	22680	1.737574389	0.879856569	0.052885327
56	6.730769231	825	1073	22680	1.434753876	0.885003293	0.052635438
8	0.961538462	825	61	22680	3.605365127	0.885360367	0.051457169
94	11.29807692	685	1847	17446	1.296182802	0.997157941	0.265518786
34	4.086538462	825	577	22680	1.61991492	0.905945395	0.054728273
19	2.283653846	715	241	18082	1.993778835	0.999999996	0.398792859
55	6.610576923	825	1058	22680	1.429111531	0.918757988	0.056708194
5	0.600961538	753	21	19662	6.217036615	0.982842528	0.17600164
26	3.125	715	374	18082	1.758094312	0.999999998	0.398503639
10	1.201923077	825	95	22680	2.893779904	0.923493587	0.056744174
36	4.326923077	715	576	18082	1.580594406	0.999999999	0.399872311
4	0.480769231	715	11	18082	9.196185633	0.999999999	0.399033691
14	1.682692308	774	163	20594	2.285284	0.999988367	0.644017871
3	0.360576923	685	4	17446	19.10145985	0.999472202	0.314317025
21	2.524038462	825	307	22680	1.880485638	0.947329828	0.063321984
3	0.360576923	715	4	18082	18.96713287	1	0.424411029
3	0.360576923	715	4	18082	18.96713287	1	0.424411029
8	0.961538462	774	63	20594	3.378696526	0.999994105	0.633388949
50	6.009615385	825	953	22680	1.442335209	0.958758115	0.066963436
66	7.932692308	685	1237	17446	1.358875074	0.999736917	0.324651098
5	0.600961538	685	22	17446	5.788321168	0.999781632	0.318290252
5	0.600961538	743	21	18012	5.771966929	0.999999967	0.968166995
5	0.600961538	743	21	18012	5.771966929	0.999999967	0.968166995
20	2.403846154	774	281	20594	1.893753391	0.999998285	0.639845129
7	0.841346154	825	51	22680	3.773262032	0.966523292	0.069724576
4	0.480769231	685	12	17446	8.489537713	0.999842026	0.316527424
7	0.841346154	295	49	7720	3.738498789	0.921752876	0.399250141
33	3.966346154	753	544	19662	1.583972932	0.996636472	0.228063466
60	7.211538462	685	1113	17446	1.372971059	0.999927146	0.327639326
4	0.480769231	774	13	20594	8.186841582	0.9999997	0.65797129
4	0.480769231	774	13	20594	8.186841582	0.9999997	0.65797129
8	0.961538462	715	63	18082	3.211366411	1	0.513706716
8	0.961538462	715	63	18082	3.211366411	1	0.513706716
30	3.605769231	825	510	22680	1.617112299	0.981363424	0.079622568
4	0.480769231	753	13	19662	8.034324241	0.998417157	0.244496588

4	0.480769231	753	13	19662	8.034324241	0.998417157	0.244496588
125	15.02403846	753	2674	19662	1.220622372	0.998466721	0.236631524
7	0.841346154	295	51	7720	3.591890994	0.954227443	0.40190864
8	0.961538462	685	64	17446	3.183576642	0.99997762	0.348379825
18	2.163461538	825	256	22680	1.932954545	0.98603399	0.083474962
4	0.480769231	685	13	17446	7.83649635	0.999984376	0.346650558
6	0.721153846	715	36	18082	4.214918415	1	0.537888908
6	0.721153846	774	38	20594	4.201142391	0.999999975	0.688784043
13	1.5625	753	151	19662	2.248014564	0.99924243	0.249800274
17	2.043269231	753	226	19662	1.964143426	0.999281554	0.243006602
11	1.322115385	753	116	19662	2.476095618	0.99932472	0.236914002
50	6.009615385	825	976	22680	1.408345753	0.991416626	0.090771248
3	0.360576923	715	5	18082	15.17370629	1	0.567925654
17	2.043269231	753	228	19662	1.946914098	0.999592237	0.243266183
9	1.081730769	715	81	18082	2.80994561	1	0.563136133
9	1.081730769	715	81	18082	2.80994561	1	0.563136133
37	4.447115385	753	646	19662	1.49555339	0.999744301	0.248154569
6	0.721153846	295	39	7720	4.026075619	0.978832773	0.423486957
6	0.721153846	409	38	10425	4.024578561	0.983410539	0.744958554
3	0.360576923	743	5	18012	14.54535666	1	0.989957549
3	0.360576923	743	5	18012	14.54535666	1	0.989957549
3	0.360576923	743	5	18012	14.54535666	1	0.989957549
5	0.600961538	715	25	18082	5.057902098	1	0.585457191
9	1.081730769	685	83	17446	2.761656846	0.999999038	0.401384584
4	0.480769231	715	14	18082	7.225574426	1	0.586127544
4	0.480769231	715	14	18082	7.225574426	1	0.586127544
23	2.764423077	685	342	17446	1.712801468	0.999999155	0.393118899
49	5.889423077	825	960	22680	1.403181818	0.995825085	0.101855878
9	1.081730769	685	84	17446	2.728779979	0.999999631	0.399996556
7	0.841346154	715	53	18082	3.340124027	1	0.611694991
17	2.043269231	409	229	10425	1.892196325	0.991331773	0.694871645
77	9.254807692	825	1646	22680	1.286026731	0.997961843	0.112323812
76	9.134615385	685	1507	17446	1.284415792	0.999999889	0.413665977
9	1.081730769	295	88	7720	2.67642527	0.990253115	0.439457909
13	1.5625	774	161	20594	2.148410291	1	0.784261838
11	1.322115385	753	122	19662	2.354320423	0.999959354	0.286105938
35	4.206730769	715	592	18082	1.49515687	1	0.626069294
6	0.721153846	295	41	7720	3.829681687	0.991152123	0.408614038
19	2.283653846	295	278	7720	1.78856237	0.991722345	0.380857339
4	0.480769231	715	15	18082	6.743869464	1	0.635679973
77	9.254807692	685	1533	17446	1.279245409	0.99999997	0.428347085
17	2.043269231	774	241	20594	1.87685891	1	0.791404883
9	1.081730769	715	86	18082	2.646576679	1	0.640413219

34	4.086538462	825	624	22680	1.497902098	0.998977788	0.121834749
9	1.081730769	774	91	20594	2.631484794	1	0.787392809
18	2.163461538	774	263	20594	1.8210275	1	0.771295801
27	3.245192308	685	434	17446	1.584452891	0.999999993	0.443101961
11	1.322115385	715	121	18082	2.299046408	1	0.657886114
4	0.480769231	743	15	18012	6.464602961	1	0.996102543
63	7.572115385	295	1278	7720	1.290045357	0.996389284	0.400259987
8	0.961538462	685	72	17446	2.829845904	0.999999997	0.447246166
3	0.360576923	76	6	1807	11.88815789	0.823759756	0.823759756
5	0.600961538	715	28	18082	4.515984016	1	0.6785604
13	1.5625	743	152	18012	2.073351279	1	0.994508669
7	0.841346154	685	57	17446	3.127724421	0.999999999	0.454620827
18	2.163461538	743	243	18012	1.795723045	1	0.990832867
53	6.370192308	715	995	18082	1.347079453	1	0.681301894
6	0.721153846	774	44	20594	3.628259338	1	0.795323729
11	1.322115385	715	123	18082	2.26166354	1	0.675221219
11	1.322115385	685	124	17446	2.259312456	0.999999999	0.449646179
10	1.201923077	295	110	7720	2.379044684	0.997605649	0.395217817
7	0.841346154	715	57	18082	3.105729358	1	0.677373731
5	0.600961538	295	30	7720	4.361581921	0.998501038	0.393608465
3	0.360576923	774	7	20594	11.40310078	1	0.808411679
3	0.360576923	774	7	20594	11.40310078	1	0.808411679
3	0.360576923	774	7	20594	11.40310078	1	0.808411679
3	0.360576923	774	7	20594	11.40310078	1	0.808411679
5	0.600961538	715	29	18082	4.360260429	1	0.695870538
6	0.721153846	715	43	18082	3.528768906	1	0.693545213
18	2.163461538	753	267	19662	1.760329469	0.999999725	0.385741985
18	2.163461538	743	248	18012	1.759518951	1	0.993048333
18	2.163461538	743	248	18012	1.759518951	1	0.993048333
4	0.480769231	774	18	20594	5.91271892	1	0.819131704
3	0.360576923	685	7	17446	10.91511992	1	0.495977145
18	2.163461538	409	262	10425	1.751152504	0.999474103	0.779107916
17	2.043269231	743	230	18012	1.791819299	1	0.990812423
4	0.480769231	753	18	19662	5.802567508	0.9999999	0.395667541
7	0.841346154	715	60	18082	2.95044289	1	0.740347064
56	6.730769231	753	1113	19662	1.31378887	0.999999941	0.396081106
9	1.081730769	825	101	22680	2.449684968	0.999970635	0.175727208
6	0.721153846	774	47	20594	3.396668316	1	0.8322698
3	0.360576923	743	7	18012	10.38954047	1	0.990039979
21	2.524038462	715	322	18082	1.649315901	1	0.74016956
24	2.884615385	825	417	22680	1.582210595	0.999974628	0.175021255
9	1.081730769	743	90	18012	2.42422611	1	0.987677484
4	0.480769231	715	18	18082	5.61989122	1	0.746844248

6	0.721153846	295	47	7720	3.340786152	0.999699802	0.439744306
10	1.201923077	295	116	7720	2.255990649	0.999721118	0.420533916
3	0.360576923	774	8	20594	9.977713178	1	0.848629735
3	0.360576923	774	8	20594	9.977713178	1	0.848629735
3	0.360576923	774	8	20594	9.977713178	1	0.848629735
3	0.360576923	774	8	20594	9.977713178	1	0.848629735
7	0.841346154	743	59	18012	2.87620047	1	0.986876044
27	3.245192308	825	489	22680	1.517902956	0.999990506	0.186586623
4	0.480769231	753	19	19662	5.497169218	0.999999992	0.422225423
8	0.961538462	743	75	18012	2.585841184	1	0.983755448
13	1.5625	825	183	22680	1.95290611	0.999994337	0.191001126
5	0.600961538	753	33	19662	3.956296028	0.999999997	0.430222775
7	0.841346154	295	65	7720	2.818252934	0.999902574	0.438574317
7	0.841346154	295	65	7720	2.818252934	0.999902574	0.438574317
4	0.480769231	715	19	18082	5.324107471	1	0.790603784
3	0.360576923	715	8	18082	9.483566434	1	0.786675249
3	0.360576923	715	8	18082	9.483566434	1	0.786675249
3	0.360576923	715	8	18082	9.483566434	1	0.786675249
3	0.360576923	715	8	18082	9.483566434	1	0.786675249
3	0.360576923	715	8	18082	9.483566434	1	0.786675249
3	0.360576923	715	8	18082	9.483566434	1	0.786675249
3	0.360576923	715	8	18082	9.483566434	1	0.786675249
17	2.043269231	753	257	19662	1.727223402	0.999999999	0.441556763
6	0.721153846	753	49	19662	3.197333117	0.999999999	0.434164327
38	4.567307692	825	753	22680	1.387323434	0.999998286	0.204599118
16	1.923076923	825	249	22680	1.766484118	0.999998397	0.202414706
9	1.081730769	753	101	19662	2.326772119	1	0.435489882
11	1.322115385	715	134	18082	2.076004592	1	0.80327483
6	0.721153846	715	48	18082	3.161188811	1	0.801210747
11	1.322115385	743	129	18012	2.067169551	1	0.989424714
34	4.086538462	753	628	19662	1.413682848	1	0.435117137
8	0.961538462	715	81	18082	2.497729431	1	0.801914047
53	6.370192308	715	1029	18082	1.302569539	1	0.800694869
4	0.480769231	409	20	10425	5.097799511	0.999984443	0.842000788
7	0.841346154	295	67	7720	2.73412598	0.999972829	0.461212226
4	0.480769231	685	20	17446	5.093722628	1	0.627768165
12	1.442307692	715	154	18082	1.970611207	1	0.801955881
11	1.322115385	825	147	22680	2.057142857	0.999999455	0.213673278
4	0.480769231	774	21	20594	5.068044789	1	0.897172923
4	0.480769231	774	21	20594	5.068044789	1	0.897172923
6	0.721153846	715	49	18082	3.096674754	1	0.807197288
15	1.802884615	715	213	18082	1.780951443	1	0.804955184
4	0.480769231	753	21	19662	4.973629292	1	0.455739304

23	2.764423077	825	409	22680	1.545943543	0.999999757	0.220962409
6	0.721153846	774	52	20594	3.070065593	1	0.901560639
18	2.163461538	743	263	18012	1.659166159	1	0.991615972
7	0.841346154	753	68	19662	2.687954066	1	0.454993903
7	0.841346154	715	66	18082	2.682220809	1	0.815627445
3	0.360576923	685	9	17446	8.489537713	1	0.655688658
3	0.360576923	685	9	17446	8.489537713	1	0.655688658
6	0.721153846	715	50	18082	3.034741259	1	0.817705188
3	0.360576923	715	9	18082	8.42983683	1	0.813981789
3	0.360576923	715	9	18082	8.42983683	1	0.813981789
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4	0.480769231	715	21	18082	4.817049617	1	0.819339449
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