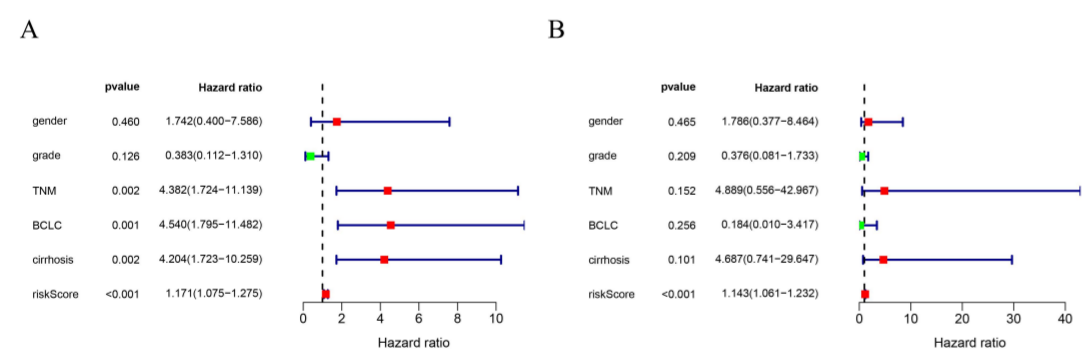
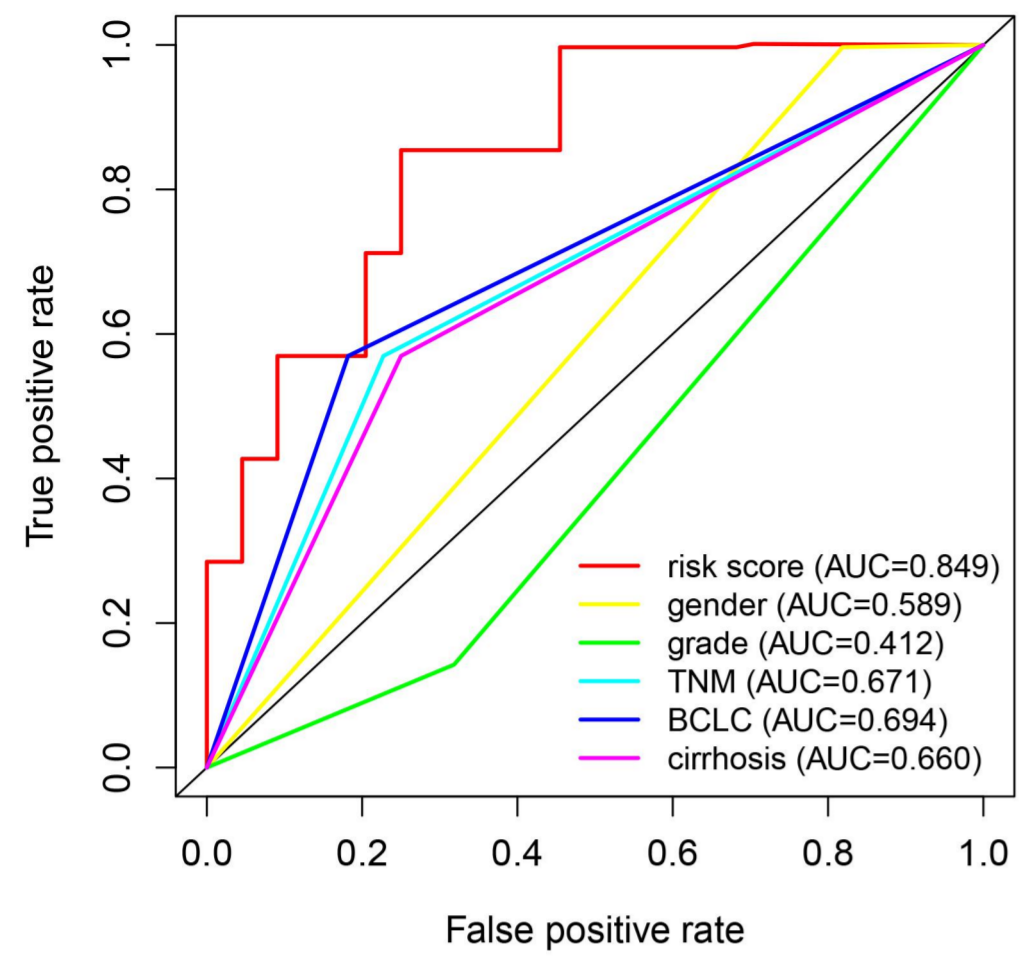


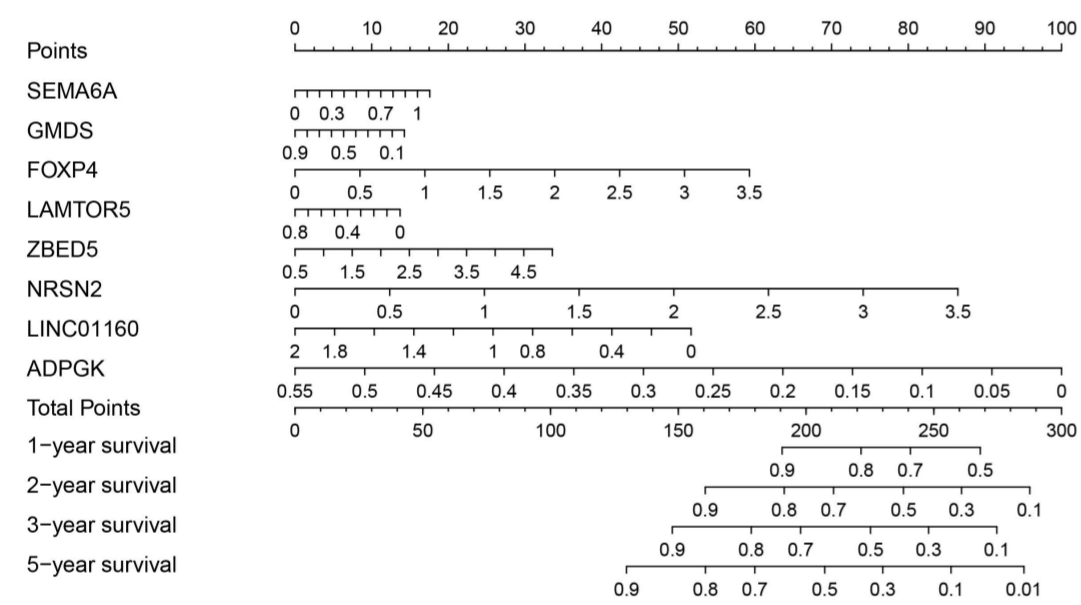
Supplement Figure 1. The prognostic differences in the high-risk and low-risk groups. A: Kaplan-Meier analysis based on the median cutoff value, P value less than 0.05 was considered significant. B:Kaplan-Meier analysis based on the best cutoff value. C:Risk score distribution plot in HCC patients. D: Risk score distribution plotsurvival status in HCC patients.



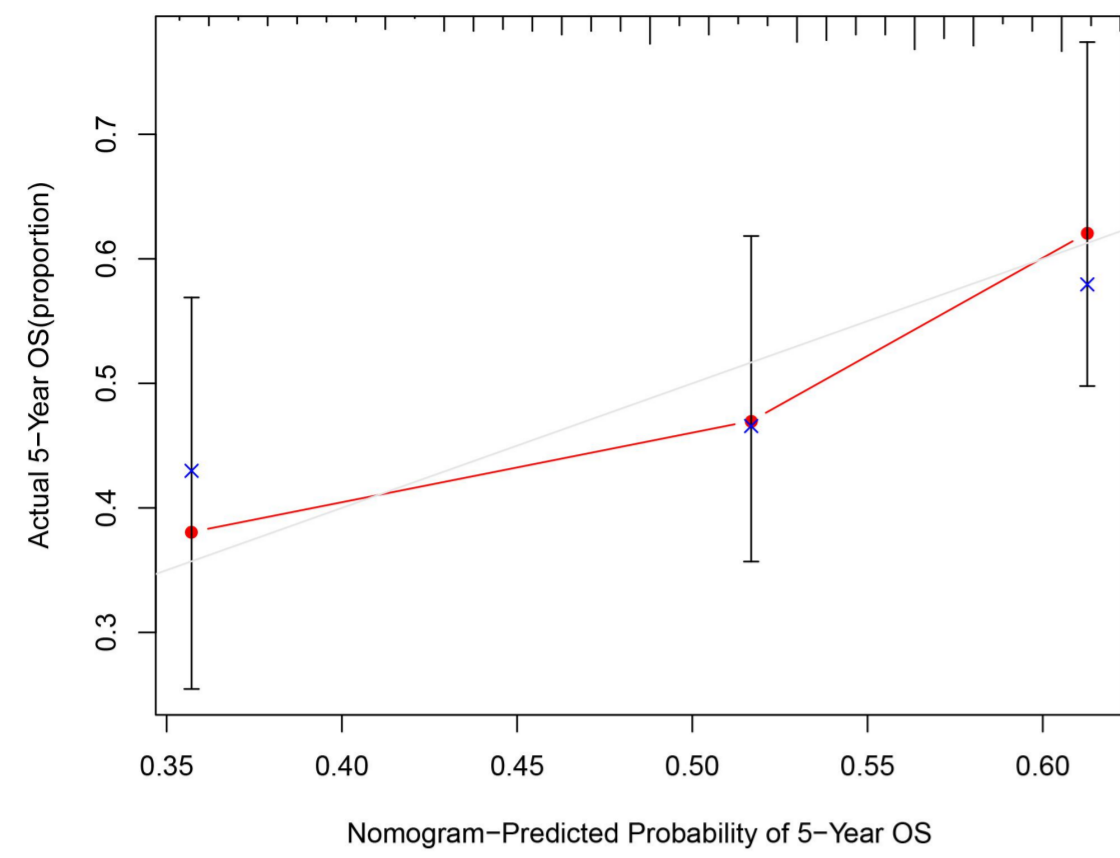
Supplement Figure 2. Regression analysis based on clinical dataset. A:Univariate Cox regression analysis. B: Multivariate Cox regression analysis.



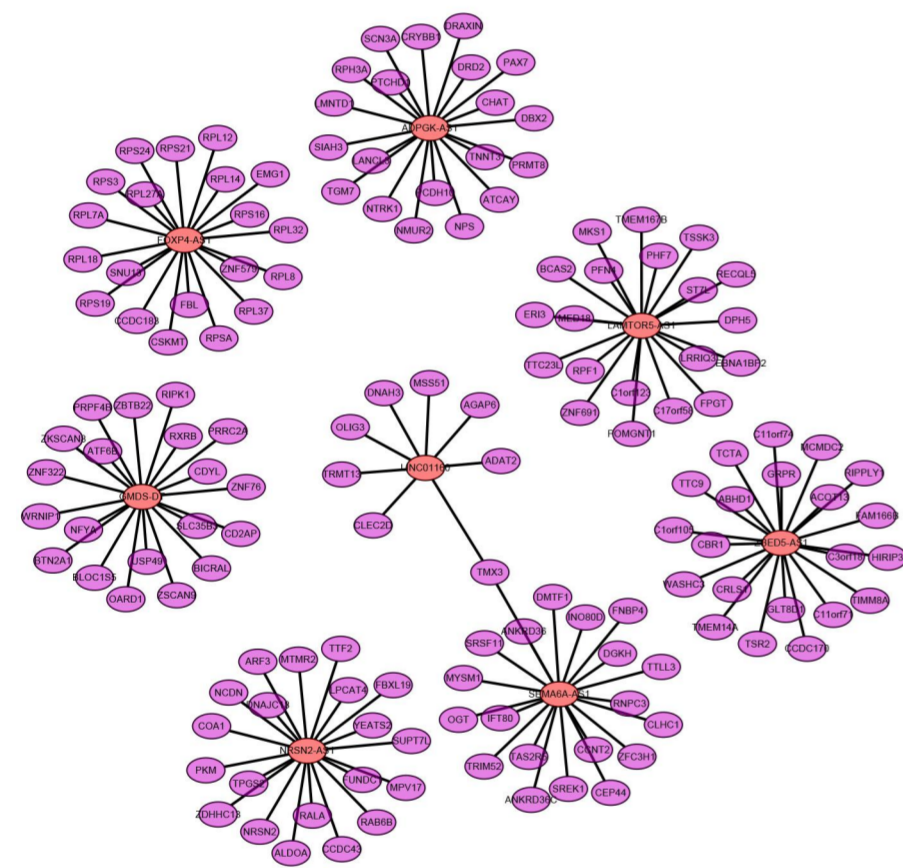
Supplement Figure 3. ROC curve of the risk score and clinical features based on clinical dataset.



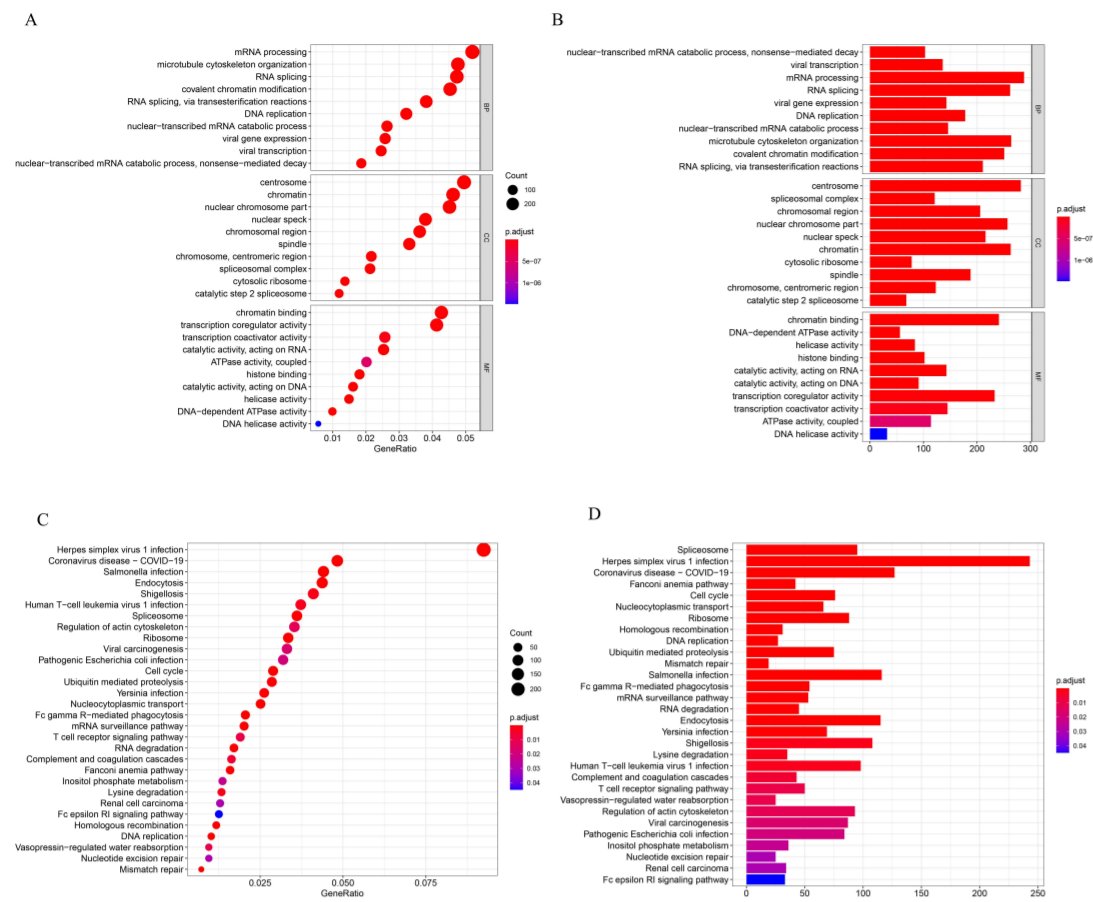
Supplement Figure 4. Nomogram that integrated both the risk signature and various clinicopathologic risk factors.



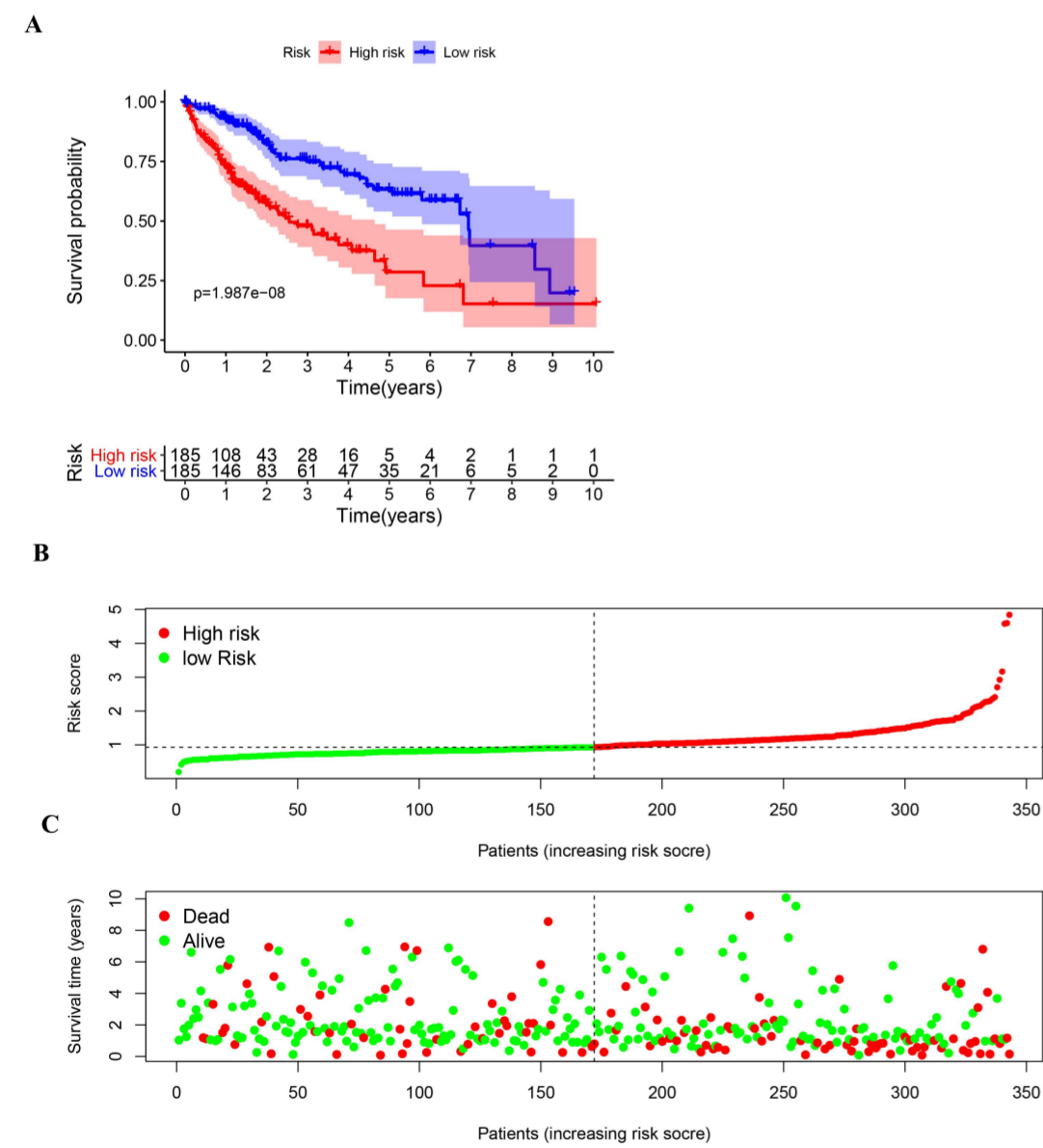
Supplement Figure 5. Calibration curve of Nomogram.



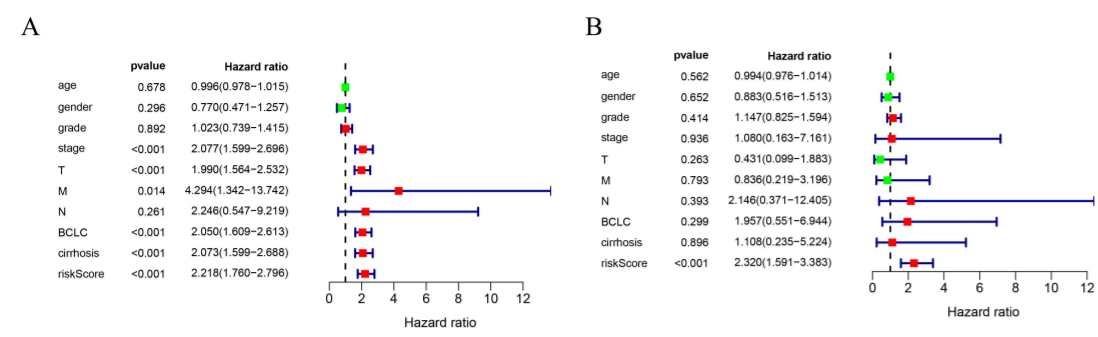
Supplement Figure 6. Visualization of the correlation between the expression level of the 8 lncRNAs and each protein coding genes (PCGs) using cytoscape.



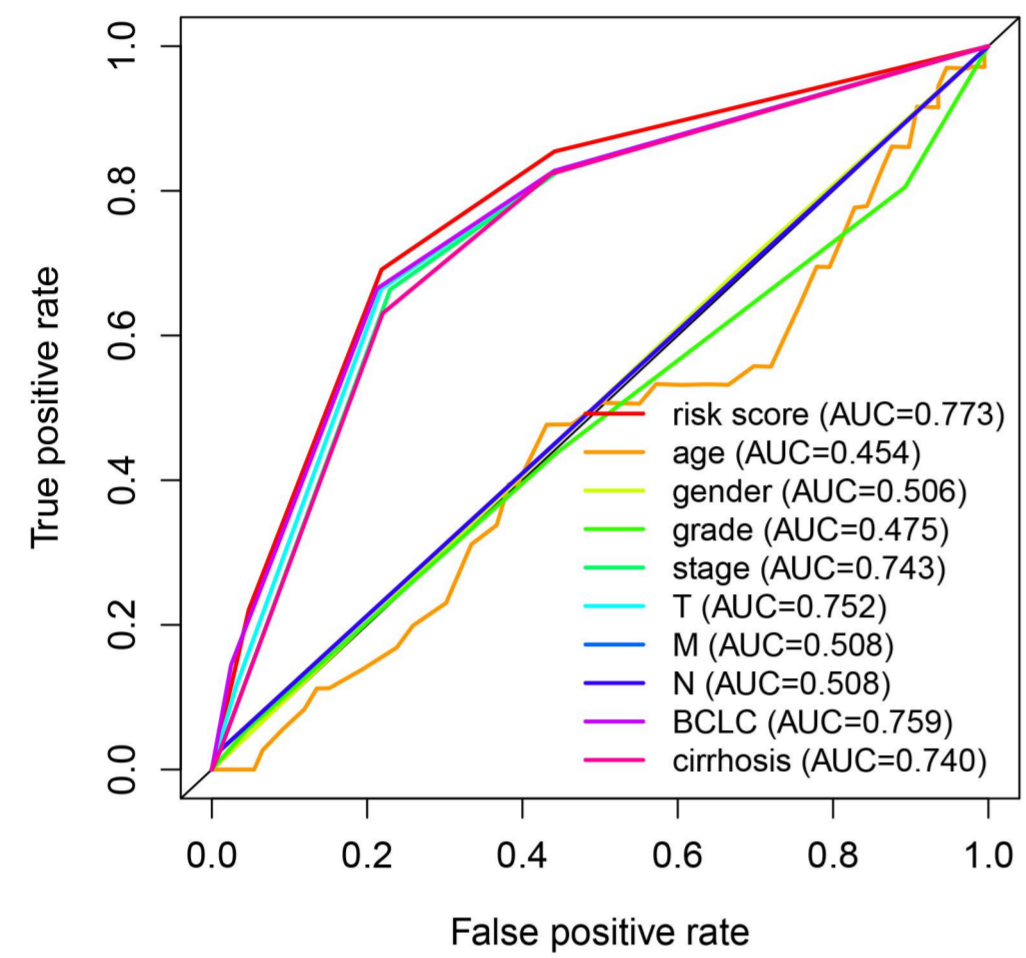
Supplement Figure 7. Gene Ontology (GO) pathway analysis and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis of the differentially expressed 8 lncRNAs. A: Barplot of GO pathway analysis; B: Dotplot of GO pathway analysis; C: Barplot of KEGG analysis; D: Dotplot of KEGG analysis



Supplement Figure 8. The prognostic differences in the high-risk and low-risk groups based on TCGA dataset. A: Kaplan-Meier analysis, P value less than 0.05 was considered significant. B: Risk score distribution plot in HCC patients. C: Risk score distribution plots survival status in HCC patients.



Supplement Figure 9. Regression analysis based on TCGA dataset. A: Univariate Cox regression analysis. B: Multivariate Cox regression analysis.



Supplement Figure 10. ROC curve of the risk score and clinical features based on TCGA dataset.

Supplement File: Supplement tables 1-4

Supplement table 1. The clinicopathological features of 251 HCC patients

Variable	N
Sex	
Female	35
Male	216
Age, years	
≤60	207
>60	44
Liver cirrhosis	
No	27
Yes	224
Lymph node metastasis	
No	212
Yes	39
Number of tumor	
< 3	205
≥ 3	46
Size of tumor, cm	
< 5	100
≥ 5	151
Metastasis	
No	212
Yes	39
BCLC stage	
0/A	135
B/C	116
TNM	
I/II	158
III/IV	90

Supplement table 2 Primers used for quantitative real-time PCR

Gene	Primer sequence
GMDS-DT	Forward 5'-TTGCTCCTCATTTCAGTGTC-3'
	Reverse 5'-TCAGGTGTCCAGGGTAAGA-3'
NRSN2-AS1	Forward 5'-CGGAGACGCAGGTCCAGAGGGAT-3'
	Reverse 5'-TATGCATCAACTGTTTATTGAAAGG-3'
FOXP4-AS1	Forward 5'-GTGAGCTTCTGGGTTTCGACA-3'
	Reverse 5'-ATTGAGGGTTAGGGCAGCAC-3'
LAMTOR5-AS1	Forward TGGCATTGTGAAGAGTGTC
	Reverse TTCCA AAAGACATCAAGACTC
SEMA6A-AS1	Forward 5'-GATTGATGAATGCTGGGGAG-3'
	Reverse 5'-TGAGGAAAAACCGCACTTAG-3'
ADPGK-AS1	Forward 5'-GCCGATGTCGACACAAGCG-3'
	Reverse 5'-AGCAAATGTGTTCCCATCCCT-3'
LINC01160	Forward: 5'-AGGAAGCAGTGCCGAATG-3'
	Reverse: 5'-AGGTGGAGCTAAATTGAGGG-3'
ZBED5-AS1	Forward 5'- TCGGGTGGGAAGTCGTTGC-3'
	Reverse 5'- CCTCCGCTTGCTCCCTTT-3'
β-actin	Forward 5'-GGGAAATCGTGCGTGACATTAAG-3'
	Reverse 5'- TGTGTTGGCGTACAGGTCTTTG-3'

Supplement table 3 Associations between the expression levels of the differentially expressed macrophage-associated lncRNAs and the clinicopathological characteristics of the patients with hepatocellular carcinoma based on clinical dataset

id	BCLC	cirrhosis	gender	grade	TNM
LINC01160	1.823(0.075)	-0.264(0.794)	<u>-2.255(0.029)</u>	1.591(0.119)	-0.196(0.847)
SEMA6A-AS1	-0.413(0.686)	-0.943(0.359)	<u>-2.402(0.020)</u>	1.48(0.145)	0.207(0.838)
FOXP4-AS1	0.297(0.769)	-0.607(0.550)	<u>-3.139(0.003)</u>	-0.652(0.522)	0.195(0.846)
GMDS-DT	-0.225(0.825)	-0.771(0.450)	0.882(0.404)	<u>3.98(2.324e-04)</u>	0.486(0.632)
LAMTOR5-AS1	-0.148(0.883)	-0.097(0.923)	0.131(0.898)	1.056(0.297)	1.291(0.204)
NRSN2-AS1	-0.613(0.552)	-0.811(0.430)	-1.848(0.071)	0.576(0.567)	-1.5(0.157)
ZBED5-AS1	0.868(0.390)	0.946(0.350)	-0.739(0.463)	1.242(0.223)	0.338(0.737)
ADPGK-A S1	1.503(0.140)	0.824(0.414)	1.018(0.342)	1.805(0.078)	1.411(0.166)
riskScore	0.922(0.361)	-0.85(0.408)	-1.876(0.067)	1.801(0.080)	-1.038(0.317)
risk	-0.568(0.577)	0.387(0.702)	1.575(0.145)	-1.468(0.154)	0.698(0.492)

A value greater than 0 indicates a positive correlation between lncRNA or riskscore and clinical characteristics, a value less than 0 indicates a negative correlation between the two, and a p<0.05 indicates statistical significance. Statistically significant data are underlined.

Supplement table 4 Associations between the expression levels of the differentially expressed macrophage-associated lncRNAs and the clinicopathological characteristics of the patients with hepatocellular carcinoma based on TCGA dataset

id	BCLC	cirrhosis	age	gender	grade	stage	T	M	N
LINC01160	0.558(0.906)	1.299(0.729)	53.332(0.347)	0.121(0.904)	2.028(0.567)	7.681(0.053)	4.48(0.214)	6.143(0.002)	-1.593(0.249)
NRSN2-AS1	4.032(0.258)	2.55(0.466)	60.985(0.137)	1.282(0.203)	<u>8.356(0.039)</u>	<u>17.762(4.924e-04)</u>	<u>17.024(6.988e-04)</u>	0.619(0.597)	-0.888(0.467)
GMDS-DT	0.714(0.870)	4.79(0.188)	47.305(0.582)	1.75(0.083)	0.804(0.848)	8.199(0.042)	3.892(0.273)	2.319(0.137)	-1.304(0.321)
LAMTOR5-AS1	0.493(0.920)	1.41(0.703)	49.807(0.481)	-2.2(0.029)	4.438(0.218)	4.388(0.222)	3.247(0.355)	<u>8.911(1.32e-04)</u>	-1.516(0.235)
SEMA6A-AS1	2.116(0.549)	5.379(0.146)	48.971(0.515)	<u>2.067(0.042)</u>	5.559(0.135)	7.843(0.049)	3.552(0.314)	<u>6.491(0.005)</u>	-0.937(0.448)
ADPGK-A S1	4.014(0.260)	2.271(0.518)	54.685(0.301)	0.074(0.941)	4.178(0.243)	7.145(0.067)	1.772(0.621)	<u>10.051(9.249e-20)</u>	1.129(0.342)
ZBED5-AS1	2.689(0.442)	2.723(0.436)	43.052(0.746)	<u>-3.745(2.426e-04)</u>	4.571(0.206)	2.588(0.460)	1.084(0.781)	1.531(0.260)	0.471(0.682)
FOXP4-AS1	<u>11.532(0.009)</u>	<u>12.024(0.007)</u>	42.138(0.778)	0.942(0.348)	6.853(0.077)	5.679(0.128)	6.358(0.095)	1.365(0.291)	-0.665(0.574)
riskScore	<u>11.683(0.009)</u>	<u>9.336(0.025)</u>	57.369(0.221)	0.604(0.547)	<u>8.995(0.029)</u>	<u>16.928(7.312e-04)</u>	<u>16.322(9.74e-04)</u>	0.109(0.923)	-1.162(0.363)
risk	<u>8.765(0.033)</u>	6.427(0.093)	65.022(0.075)	0.352(0.726)	7.76(0.051)	<u>12.543(0.006)</u>	<u>10.089(0.018)</u>	-0.58(0.620)	<u>14.2(8.438e-33)</u>

A value greater than 0 indicates a positive correlation between lncRNA or riskscore and clinical characteristics, a value less than 0 indicates a negative correlation between the two, and a p<0.05 indicates statistical significance. Statistically significant data are underlined.

Supplement File 2 The Top 10 Gene Ontology (GO) pathway.

ONTO LOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
BP	GO:000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	103/5534	118/17913	2.43E-37	1.51E-33	1.28E-33	RPS24/RPL18/RPS3/RPL14/RPS21/RPL7A/RPS19/RPL37/RPL27A/RPL8/RPL32/RPSA/RPL12/RPS16/RPL28/RPL35/RPS2/RPL37A/RPL6/RPS5/RPS7/RPL23A/RPL29/RPL24/RPS17/RPS8/RPL13A/RPL18A/RPS11/RPL7/RPL3/RPS9/RPL35A/RPL9/RPL31/RPL13/RPL2/RPL38/RPL36A/RPS18/RPL4/RPS6/RPLP0/RPL5/RPS10/RPL15/RPL27/RPS27A/RPL30/RPS20/RPL23/RPL11/RPS12/RPS3A/RPL36/RPL19/RPLP1/RPS13/RPS15/RPS15A/RPL10A/RPS28/RPS23/RPS14/RPS25/RPL17/PABPC1/EIF3E/DHX34/UBA52/RPL34/RPL41/RPS29/RPS27/RPL26/RPL21/RPL39/SMG9/RPS4X/PPP2R1A/RPL22/SMG1/RNPS1/NCBP2/EXOSC10/UPF3B/PNRC2/ETF1/PPP2CA/CASC3/PARN/EIF4A3/NCBP1/GSPT1/UPF3A/UPF2/SMG7/SMG8/SECISBP2/DCP1A/NBAS/UPF1/DCP2	103
BP	GO:0019083	viral transcription	136/5534	177/17913	1.53E-36	4.73E-33	4.03E-33	RPS24/RPL18/RPS3/RPL14/RPS21/RPL7A/RPS19/RPL37/RPL27A/RPL8/RPL32/RPSA/RPL12/RPS16/RPL28/RPL35/RPS2/RPL37A/RPL6/RPS5/RPS7/RPL23A/RPL29/RPL24/RPS17/RPS8/RPL13A/RPL18A/POLR2H/RPS11/RPL7/RPL3/RPS9/RPL35A/RPL9/RPL31/RPL13/RPL2/RPL38/RPL36A/RPS18/RPL4/RPS6/RPLP0/RPL5/RPS10/RPL15/RPL27/RPS27A/RPL30/RPS20/RPL23/RPL11/RPS12/RPS3A/RPL36/RPL19/RPLP1/RPS13/RPS15/RPS15A/RPL10A/RPS28/RPS23/RPS14/RPS25/RPL17/POLR2J/TARBP2/UBA52/RPL34/RPL41/RPS29/POLR2I/RPS27/HMGA2/RPL26/RPL21/RPL39/RPS4X/TFAP4/SUPT5H/RAE1/SMARCB1/RPL22/TRIM62/NUP93/HPN/CCNT2/SP1/CCNT1/RSF1/CHD1/SUPT4H1/NDC1/NUP107/NUP155/NUP205/TRIM32/NUP188/SMARCA4/NUP37/NUP85/NUP43/NUP62/TARDBP/HDAC1/DHX9/POLR2B/NELFA/AAAS/GTF2F2/GTF2F1/ZNF639/POLR2G/POLR2D/NUP35/CTDP1/NUP214/SNW1/TAF11/NUP153/TRIM27/POM121C/TPR/NUP160/NELFE/POM121/NUP54/EP300/REST/NUP133/NUP58/NUCKS1/NUP98/TRIM13	136
BP	GO:0006397	mRNA processing	288/5534	499/17913	3.34E-36	4.80E-33	4.09E-33	SNU13/POLR2H/SNRPD2/GEMIN7/SNRPF/SNRPA/SNRPD1/HSF1/CLASRP/SNRPB/LSM8/PRPF31/THOC5/POLR2J/CPSF1/SRRT/PABPC1/SRSF12/LSM4/LSM7/SNRPA1/TXNL4A/LSM2/SNRPG/ISY1/CPSF4/TSEN34/SNRPD3/POLR2I/PRPF6/ERCC2/RALY/AKAP8L/TBRG4/ARL6IP4/PP1H/SNRNP70/SUPT5H/SNRPE/SNRPC/PDCD11/ALYREF/SF3A2/RBM42/SYMPK/CELF2/SREK1/RNPC3/SRSF11/TIA1/PRPF38B/TRA2A/ZRANB2/PAN3/PNN/DDX17/HNRNPH1/DDX47/RBM25/DDX39B/KHDC4/RBM39/SRRM2/RBM5/SF3B1/ACIN1/PRPF40B/SRSF10/CCNT1/RBBP6/MBNL1/PABPC1L/PTBP3/TENT2/PCF11/CPSF6/CPSF7/RBM26/ZNF326/SRSF6/PRPF40A/U2SURP/USP49/PPWD1/SRSF2/U2AF1/DDX5/ERCC3/SFPQ/YTHDC1/SFSWAP/CDK13/HNRNPH3/SUGP2/PRPF4B/ZCCHC8/TTF2/ZC3H11A/SCAF11/PTBP2/CELF1/CDK12/SART3/SRSF1/RBM4/CCAR1/DDX42/THOC2/AKAP17A/BCAS2/PRPF38A/RBM17/RNPS1/NCBP2/HNRNPL/USP39/KHDRBS1/CWC27/RBM28/BARD1/EFTUD2/RBMX/HNRNPLL/CPSF3/SNRNP27/U2AF2/SF3A3/SNRNP200/CD2BP2/DDX23/FIP1L1/CSTF2/SRPK2/HNRNPU/CCAR2/DHX15/DDX1/YBX1/BUD31/UPF3B/FUS/RSRC1/KDM1A/HNRNPA2B1/WDR77/1WS1/NSRP1/DDX39A/MTPAP/CCNB1/DHX8/DDX20/TSEN54/HNRNPD/GTF2H1/HNRNPR/NUDT21/PNPT1/TARDBP/HNRNPU/SF3B3/SLBP/SMNDC1/STRAP/HNRNPA3/HNRNPC/DHX9/CHTOP/ZRSR2/MFAP1/GRSF1/PPP1R8/CWC22/SNRPB2/ZPR1/POLR2B/SRSF3/BUD13/PRPF4/SRSF9/PP1E/DNAJC8/TRA2B/HNRNPA0/ELAVL1/SNRNP40/DHX35/RBM15B/JMJD6/HTATSF1/HNRNPK/DHX38/CASC3/SF3B2/LSM1/GTF2F2/DDX46/HNRNPM/PDCD7/SCAF1/SF3B6/RBM10/XRN2/RNMT/CIR1/EIF4A3/NBDY/NCBP1/SF3B4/CDK11B/GTF2F1/ECD/WTAP/GEMIN2/HNRNPA1/GEMIN8/PTBP1/NONO/ZNF473/POLR2G/CPSF2/MTREX/SYNCRIP/SF1/POLR2D/SRSF7/AQR/SARNP/THRAP3/GEMIN5/RBM22/HNRNPA1L2/DDX41/WDR33/PRPF3/CRNKL1/SUGP1/SNW1/NOVA1/CDK11A/TSEN2/IK/ESS2/AHCYL1/DHX16/CMTR1/GTF2H4/SNRNP48/CDC5L/SRPK1/ZNF830/METTL3/SUPT6H/FAM172A/RBFOX2/WBP11/RBM27/GPATCH1/CWC25/NELFE/CDC73/KHSRP/POLDIP3/SF3A1/DHX36/PAN2/PP1L3/PP1L1/SLU7/SON/REST/CACTIN/SRSF4/CSTF2T/DYRK1A/PHRF1/RNF20/CSTF3/LSM11/GTF2H3/HNRNPF/TGS1/RAMAC/NUP98/ZCRB1/RNF40/PAPOLA/SRRM1	288
BP	GO:0008380	RNA splicing	262/5534	440/17913	3.52E-36	4.80E-33	4.09E-33	SNU13/POLR2H/SNRPD2/GEMIN7/SNRPF/SNRPA/SNRPD1/RPS13/CLASRP/SNRPB/LSM8/PRPF31/THOC5/POLR2J/CPSF1/SRRT/PABPC1/SRSF12/LSM4/LSM7/SNRPA1/TXNL4A/LSM2/SNRPG/ISY1/CPSF4/TSEN34/SNRPD3/POLR2I/PRPF6/RALY/PPP2R1A/AKAP8L/ARL6IP4/PP1H/SNRNP70/SNRPE/SNRPC/ALYREF/SF3A2/RBM42/SYMPK/CELF2/SREK1/RNPC3/SRSF11/TIA1/PRPF38B/TRA2A/ZRANB2/PNN/DDX17/LUC7L3/HNRNPH1/DDX47/RBM25/DDX39B/CLK4/KHDC4/RBM39/SRRM2/RBM5/ZNF638/SF3B1/CLK1/ACIN1/PRPF40B/C2orf49/SRSF10/CLK3/MBNL1/PTBP3/PCF11/CPSF7/ZNF326/SRSF6/PRPF40A/U2SURP/USP49/PPWD1/SRSF2/U2AF1/DDX5/SFPQ/YTHDC1/SFSWAP/CDK13/HNRNPH3/SUGP2/PRPF4B/ZCCHC8/TTF2/SCAF11/CLK2/PTBP2/CELF1/CDK12/SART3/SRSF1/RBM4/CCAR1/DDX42/THOC2/AKAP17A/BCAS2/PRPF38A/RBM17/RNPS1/NCBP2/HNRNPL/RRAGC/USP39/FAM98B/KHDRBS1/CWC27/RBM28/EFTUD2/RBMX/HNRNPLL/CPSF3/SNRNP27/U2AF2/DBR1/SF3A3/SNRNP200/CD2BP2/DDX23/FIP1L1/CSTF2/SRPK2/HNRNPU/CCAR2/DHX15/DDX1/YBX1/BUD31/UPF3B/FUS/RSRC1/KDM1A/HNRNPA2B1/WDR77/1WS1/NSRP1/DDX39A/USB1/DHX8/DDX20/TSEN54/HNRNPD/HNRNPR/NUDT21/TARDBP/HNRNPU/SF3B3/SMNDC1/STRAP/PPP1R9B/HNRNPA3/HNRNPC/DHX9/ZRSR2/MFAP1/RBM38/PPP1R8/CWC22/SNRPB2/ZPR1/POLR2B/SRSF3/BUD13/PRPF4/SRSF9/PP1E/DNAJC8/TRA2B/HNRNPA0/ELAVL1/SNRNP40/DHX35/RBM15B/JMJD6/PPP2CA/HTATSF1/HNRNPK/DHX38/CASC3/SF3B2/LSM1/GTF2F2/DDX46/HNRNPM/PDCD7/SCAF1/SF3B6/RBM10/CIR1/EIF4A3/NCBP1/SF3B4/GTF2F1/ECD/WTAP/GEMIN2/HNRNPA1/GEMIN8/PTBP1/NONO/POLR2G/CPSF2/MTREX/SYNCRIP/SF1/POLR2D/SRSF7/AQR/THRAP3/GEMIN5/RBM22/HNRNPA1L2/DDX41/WDR33/PRPF3/IVNS1ABP/CRNKL1/SUGP1/SNW1/NOVA1/TSEN2/IK/ESS2/DHX16/SNRNP48/CDC5L/SRPK1/ZNF830/METTL3/SUPT6H/FAM172A/RBFOX2/WBP11/GPATCH1/PP1G/CWC25/KHSRP/SF3A1/PP1L3/PP1L1/SLU7/SON/REST/CACTIN/SRSF4/CSTF2T/DYRK1A/CSTF3/HNRNPF/TGS1/NUP98/ZCRB1/PAPOLA/SRRM1	262
BP	GO:0019080	viral gene expression	143/5534	191/17913	4.00E-36	4.80E-33	4.09E-33	RPS24/RPL18/RPS3/RPL14/RPS21/RPL7A/RPS19/RPL37/RPL27A/RPL8/RPL32/RPSA/RPL12/RPS16/RPL28/RPL35/RPS2/RPL37A/RPL6/RPS5/RPS7/RPL23A/RPL29/RPL24/RPS17/RPS8/RPL13A/RPL18A/RPS11/RPL7/RPL3/RPS9/RPL35A/RPL9/RPL31/RPL13/RPL2/RPL38/RPL36A/RPS18/RPL4/RPS6/RPLP0/RPL5/RPS10/RPL15/RPL27/RPS27A/RPL30/RPS20/RPL23/RPL11/RPS12/RPS3A/RPL36/RPL19/RPLP1/RPS13/RPS15/RPS15A/RPL10A/RPS28/RPS23/RPS14/RPS25/RPL17/POLR2J/EIF3D/TARBP2/UBA52/RPL34/RPL41/RPS29/POLR2I/RPS27/HMGA2/RPL26/RPL21/RPL39/RPS4X/TFAP4/SUPT5H/RAE1/EIF3F/SMARCB1/RPL22/TRIM62/NUP93/HPN/CCNT2/SP1/CCNT1/RSF1/CHD1/SUPT4H1/NDC1/NUP107/NUP155/NUP205/TRIM32/SSB/NUP188/SMARCA4/NUP37/NUP85/NUP43/NUP62/DENR/TARDBP/HDAC1/DHX9/POLR2B/NELFA/AAAS/GTF2F2/GTF2F1/ZNF639/PTBP1/POLR2G/POLR2D/NUP35/CTDP1/NUP214/SNW1/TAF11/NUP153/TRIM27/POM121C/TPR/NUP160/NELFE/POM121/NUP54/EP300/REST/NUP133/NUP58/NUCKS1/NUP98/TRIM13/EIF2D	143
BP	GO:0006260	DNA replication	178/5534	260/17913	5.00E-36	4.80E-33	4.09E-33	RECQL4/HCRT/TONSL/TWINK/DSCC1/PPP2R1A/HMGA1/POLL/ALYREF/ING5/NAP1L1/CDT1/NUGGC/NF1C/MCMDC2/CENPX/ZNF365/GLI1/FGF10/ETAA1/POLI/ORC2/FAM111A/ATM/RBBP6/REV1/ATR/DDX11/ESCO1/MRE11/FBXW7/DNA2/ORC4/INO80/HELBG/GEN1/RFD3/TBRG1/ATRX/BOD1L1/KCTD13/RECQL5/CENPS/RPA3/FAF1/POLG2/GTPBP4/FBH1/RBBP8/TTF1/POLA1/CLSPN/RAD51/MCM10/BARD1/GINS3/DBF4B/TOPBP1/CHEK1/ORC1/MCIDAS/ORC6/CDC7/RBBP4/CDK2/MCM8/RHNO1/DBF4/RAD1/RFC2/MCM6/PNKP/TIPIN/MCM3/GINS1/RBBP7/CHAF1B/CDC6/S100A11/RAC1/MGME1/RFC4/PRIM2/TICRR/POLD3/MCM4/EXO1/SMARCAL1/GINS4/SET/CDC45/ATG7/SSRP1/BRCA1/MMS22L/MCM2/NASP/RBM14/POLD1/ATAD5/SUPT16H/CDK1/CDK2AP1/PCLAF/NCOA6/SLBP/BLM/DHX9/FBXO5/RRM2/BRCA2/RTF2/ZPR1/RRM1/KAT7/ESCO2/EHMT2/RFC3/PPP2CA/MCM7/PCNA/CHTF18/RFC5/FEN1/RPA1/POLA2/RPA2/RMI2/DTL/ORC5/HUS1/CHAF1A/CCNA2/DTD1/SIN3A/GMNN/WRN/WIZ/RNASEH2A/CACYBP/POLE3/E2F8/SETMAR/CCDC88A/WRNIP1/POLH/LIG3/RAD17/ZNF830/SMC3/PRIMPOL/RAD50/WAPL/CDAN1/RFC1/POLK/RAD9A/FANCM/KAT5/SMC1A/ATF1/USP37/PDS5A/REPINI/TIMELESS/ZRANB3/NUCKS1/RMI1/SLX4/STAG2/POLG/UPF1/NUP98/PURA/BRIP1/E4F1/ZMPSTE24/MCM9	178
BP	GO:0000956	nuclear-transcribed mRNA catabolic process	146/5534	197/17913	5.42E-36	4.80E-33	4.09E-33	RPS24/RPL18/RPS3/RPL14/RPS21/RPL7A/RPS19/RPL37/RPL27A/RPL8/RPL32/RPSA/RPL12/RPS16/RPL28/RPL35/RPS2/RPL37A/RPL6/RPS5/RPS7/RPL23A/RPL29/RPL24/RPS17/RPS8/RPL13A/RPL18A/RPS11/RPL7/RPL3/RPS9/RPL35A/RPL9/RPL31/RPL13/RPL2/RPL38/RPL36A/RPS18/RPL4/RPS6/RPLP0/RPL5/RPS10/RPL15/RPL27/RPS27A/RPL30/RPS20/RPL23/RPL11/RPS12/RPS3A/RPL36/RPL19/RPLP1/RPS13/RPS15/RPS15A/RPL10A/EXOSC4/RPS28/RPS23/RPS14/RPS25/EXOSC5/EXOSC7/RPL17/CNOT11/PABPC1/LSM4/LSM7/EIF3E/DHX34/UBA52/RPL34/RPL41/LSM2/EXOSC1/RPS29/RPS27/RPL26/RPL21/RPL39/SMG9/RPS4X/PPP2R1A/EXOSC2/RPL22/PAN3/CNOT6/CNOT2/ATM/SMG1/TENT2/DDX5/TUT4/TNRC6B/CSDE1/RNPS1/NCBP2/CNOT3/SSB/EXOSC10/UPF3B/MTPAP/CNOT9/EDC3/PNRC2/CNOT10/ETF1/PPP2CA/EXOSC3/CASC3/LSM1/CNOT8/PARN/EIF4A3/NBDY/NCBP1/AGO1/GSPT1/MLH1/THRAP3/SKIV2L/UPF3A/DDX6/DIS3L2/UPF2/SMG7/SMG8/SECISBP2/CNOT4/DHX36/PAN2/DCP1A/NBAS/EDC4/UPF1/DXO/EXOSC8/TTC37/CNOT1/DCP2/RC3H1/RPS3/SAPCD2/SPIRE2/AURKB/RANGRF/FKBP4/LZTS2/BCCIP/ARL2/DRG1/MYBL2/PPP2R1A/KAT2A/RAE1/ARHGFE2/GADD45A/KAT2B/HAUS4/CETN2/PLA2G3/MAP1A/FGF10/TRIM36/SLC39A12/IQCG/NEFL/TTL3/CFAP44/WDR73/PPP1R12A/SPICE1/CEP135/GCC2/TBK2/EFHC1/TAOK1/KIF3A/ZNF207/CCDC39/USP33/MARK2/C2CD3/PKD1/RNF19A/IFT172/CEP192/MTCL1/CFAP73/CEP295/CHMP3/ARHGFE10/CCDC78/DNAL1/MAP9/SS18/GAS2L3/SUN1/INO80/HAUS3/GEN1/HDGFL3/PKHD1/CLASP1/DNAAF4/ATRX/HOOK3/TUBG2/XPO1/TUBGCP6/ATXN7/MECP2/KIF2A/BICD1/KIAA0753/CCDC66/PHLDB1/CAMSA2/CEP97/CROCC/SSX21P/BBS4/MAPRE1/CEP19/GPSM2/RAB11A/KPNB1/NDE1/MAP4/KIF23/STIL/CHMP4B/CC2D2A/TTC26/KIF2C/DYNC1H1/CHEK1/SPDL1/MCIDAS/PLK1/KIF11/CDK2/INPP5J/TACC3/RAN/KIF20A/DCTN1/RNF4/PRC1/MAP1S/KIF18B/RACGAP1/JHY/STMN1/CSNK1D/KATN	146
BP	GO:0000226	microtubule cytoskeleton organization	264/5534	460/17913	1.08E-32	8.39E-30	7.15E-30	RPS24/RPL18/RPS3/RPL14/RPS21/RPL7A/RPS19/RPL37/RPL27A/RPL8/RPL32/RPSA/RPL12/RPS16/RPL28/RPL35/RPS2/RPL37A/RPL6/RPS5/RPS7/RPL23A/RPL29/RPL24/RPS17/RPS8/RPL13A/RPL18A/RPS11/RPL7/RPL3/RPS9/RPL35A/RPL9/RPL31/RPL13/RPL2/RPL38/RPL36A/RPS18/RPL4/RPS6/RPLP0/RPL5/RPS10/RPL15/RPL27/RPS27A/RPL30/RPS20/RPL23/RPL11/RPS12/RPS3A/RPL36/RPL19/RPLP1/RPS13/RPS15/RPS15A/RPL10A/RPS28/RPS23/RPS14/RPS25/RPL17/POLR2J/EIF3D/TARBP2/UBA52/RPL34/RPL41/RPS29/POLR2I/RPS27/HMGA2/RPL26/RPL21/RPL39/RPS4X/TFAP4/SUPT5H/RAE1/EIF3F/SMARCB1/RPL22/TRIM62/NUP93/HPN/CCNT2/SP1/CCNT1/RSF1/CHD1/SUPT4H1/NDC1/NUP107/NUP155/NUP205/TRIM32/SSB/NUP188/SMARCA4/NUP37/NUP85/NUP43/NUP62/DENR/TARDBP/HDAC1/DHX9/POLR2B/NELFA/AAAS/GTF2F2/GTF2F1/ZNF639/PTBP1/POLR2G/POLR2D/NUP35/CTDP1/NUP214/SNW1/TAF11/NUP153/TRIM27/POM121C/TPR/NUP160/NELFE/POM121/NUP54/EP300/REST/NUP133/NUP58/NUCKS1/NUP98/TRIM13/EIF2D	264

							AL2/CEP126/KIF4A/EML2/CENPA/XRCC2/DNAF5/MAD2L1/PLK4/CENPE/RAC1/CEP152/WDR62/HNRNPU/NCKAP5L/HAUS6/BICD2/HAUS2/SPC25/KIF18A/ATAT1/CDC20/SKA1/MDM1/NDC80/BRCA1/HAUS1/CENPJ/AUNIP/NUP62/INTS13/RBM14/EZR/WRAP73/E2F4/TTK/ABL1/RCC1/NUSAP1/CCNB1/KIFC1/CDK1/CFAP157/SASS6/PCLAF/TUBG1/TTL1/TRIM37/S			
							G01/TTL/CCNF/RHOA/GSK3B/CCDC40/KIF24/FBX05/HAUS8/TPX2/FLNA/GAPDH/BRCA2/SDCCAG8/EFNA5/CKAP5/CDK5R1/CHD3/CEP131/ZPR1/CLTC/CHORDC1/NEK2/CEP250/CAMS			
							AP1/CEP68/KNSTRN/TMEM67/ODF2/AAAS/PCNT/SPEF1/SKA3/MARK1/CLIP3/FIGNL1/KATNA1/PAK1/PSRC1/SP1RE1/HAUS5/GBA2/MCPH1/DNAH7/CEP63/SPAG1/BORA/CKAP2/MLH1			
							/BRSK1/DYNLT1/AURKA/CHMP1A/NIN/DOCK7/CNTROB/SRGAP2/CRMP1/FER/TRAF3IP1/LRRC6/NPM1/CUL7/CUL9/RANBP9/NUMA1/GOLGA2/PIBF1/SMC3/DLG1/TPR/SETD2/CETN3/			
							CLASP2/STAG1/CEP350/SMC1A/SPAST/CCP110/PRUNE1/PDCD61P/SLK/TUBGCP4/SON/TOGARAM1/TUBGCP5/DYRK1A/STAG2/TUBB/ZW10/CEP70/ABRAXAS2/VAMP4/NEK7/GNAI1/CN			
							P/CEP85/FOPNL/CDK5RAP2/TUBGCP3/GAS8/UVRAG			
							FBL/TRIM28/PRMT1/BEND3/PIH1D1/HDAC10/RUVBL2/AURKB/SUPT3H/HMGA2/DNMT3A/AKAP8L/KAT2A/HDAC11/SMARCB1/ING5/KMT5C/SETD7/KAT2B/PINK1/SIRT3/PRMT8/PAX7/			
							HDAC9/JAK2/TWIST1/SPI1/DPF1/EYA1/GATA3/MYSM1/OGT/BAZ2A/KANSL1L/PCGF3/MLLT6/NA40/TET3/PAXBP1/KMT2A/ATM/MTF2/KMT2D/EP400/KANSL1/TET2/SRCAP/HDAC7/			
							SETD5/BRD8/RIF1/SUPT7L/EZH1/PRDM4/PRDM2/YEATS2/USP3/KMT2E/USP49/NIPBL/SFPQ/KDM5C/PPHLN1/SUDS3/NSD1/DR1/MAP3K12/SETD1B/KDM3A/MSL2/KANSL3/MUC1/ASX			
							L1/EPC1/AKAP8/MIER1/TADA2A/ATRX/UIMC1/SART3/SMARCA1/EPC2/MSL1/NSD2/TAF1/RSF1/CTCF/ZNF335/ATXN7/SDR16C5/ARID4B/CHD1/MECP2/NSD3/KDM2A/DMP1/H2AFY			
							/PRMT2/RUVBL1/PPP5C/NEK11/PHF19/CHEK1/CDK2/EED/KANSL2/PHC1/PHF20/MCRS1/HCF1/BRPF1/ACTL6A/HDAC2/EZH2/MORF4L1/MAPK3/UBE2N/SET/KDM1A/WAC/DNMT1/NA			
							50/BRCA1/HAT1/DPF2/IWS1/MSL3/RBM14/JADE2/HUWE1/RPS6KA4/UBE2E1/MBD2/CCNB1/CDK1/TRRAP/KMT5A/TRIM37/PWP1/PCGF2/HDAC1/HASPIN/TRIP12/CHTOP/CUL4B/UHRF			
							1/PRKCD/BRCA2/BAZ1B/MECOM/SUV39H2/SETD1A/ATXN7L3/LDB1/MAP3K7/KAT7/EHMT2/GTF3C4/PKN1/JMJD6/UBE2A/CXCC1/ATF7IP/USP22/WDR82/RNF2/USP21/VRK1/KDM4A/C			
							TBP1/HELLS/USP36/SIRT6/OTUB1/SUZ12/CCNA2/PRKD2/SIN3A/RLF/UBR5/DBB1/AURKA/PYGO2/APBB1/EYA3/ATF2/PHB/RTF1/SNW1/SAP30/POLE3/SETMAR/BRCC3/ZNF451/KDM			
							1B/C6orf89/JARID2/PHF1/BRPF3/PAXIP1/SETDB1/VEGFA/UBR2/ING3/MORC2/ASH1L/DCAF1/RING1/SETD2/BCOR/SUPT6H/KAT8/PHF2/PRKCA/SETD6/CREBBP/NELFE/CDC73/BR			
							D1/MCM3AP/KAT5/ZNF304/ZNF274/KAT14/EP300/YEATS4/CBX8/REST/BMI1/RCOR1/SMAD4/ELK4/EHMT1/KMT5B/RNF8/KMT2C/RNF20/MPHOSPH8/CRTC2/SIRT7/KDM5A/RBBP5/TA			
							F5/CARM1/NCOA3/RNF40/USP7/KDM5B/CLOCK/DOT1L/ZMPSTE24			
							SNU13/POLR2H/SNRPD2/GEMIN7/SNRPF/SNRPA/SNRPD1/SNRPB/LSM8/PRPF31/POLR2J/CPSF1/SRR1/PABPC1/SRSF12/LSM4/LSM7/SNRPA1/TXNL4A/LSM2/SNRPG/ISY1/CPSF4/SN			
							RPD3/POLR2I/PRPF6/RALY/PIH/SNRNP70/SNRPE/SNRPC/ALYREF/SF3A2/RBM42/SYMPK/CELP2/SREK1/RNPC3/SRSF11/TIA1/TRA2A/PNN/DDX17/HNRNPH1/RBM25/DDX39B/KHDC			
							4/SRRM2/RBM5/SF3B1/PRPF40B/SRSF10/PCF11/CPSF7/SRSF6/PRPF40A/U2SURP/USP49/PPWD1/SRSF2/U2AF1/DDX5/SFPQ/YTHDC1/SFSWAP/CDK13/HNRNPH3/PRPF4B/ZCCHC8/S			
							CAF11/PTBP2/CELF1/SART3/SRSF1/RBM4/CCAR1/DDX42/BCAS2/PRPF38A/RBM17/RNPS1/NCBP2/HNRNPL/USP39/KHDRBS1/CWC27/EFTUD2/RBMX/CPSF3/SNRNP27/U2AF2/DBR1/S			
							F3A3/SNRNP200/CD2BP2/DDX23/FIP1L1/CSTF2/SRPK2/HNRNPU/DHX15/DDX1/YBX1/BUD31/UPF3B/FUS/RSRC1/KDM1A/HNRNPA2B1/WDR77/NSRP1/DDX39A/DHX8/DDX20/HNRNPD/			
							HNRNPR/NUDT21/HNRNPU1/SF3B3/SMNDC1/STRAP/HNRNPA3/HNRNPC/DHX9/ZRSR2/MFAP1/CWC22/SNRPB2/POLR2B/SRSF3/BUD13/PRPF4/SRSF9/PIIE/DNAJC8/TRA2B/HNRNPA0/			
							ELAVL1/SNRNP40/DHX35/RBM15B/JMJD6/HTATSF1/HNRNPK/DHX38/CASC3/SF3B2/LSM1/GTF2F2/DDX46/HNRNPM/PDCD7/SF3B6/RBM10/EIF4A3/NCBP1/SF3B4/GTF2F1/WTAP/GEM			
							IN2/HNRNPA1/GEMIN8/PTBP1/POLR2G/CPSF2/MTREX/SYNCRIP/SF1/POLR2D/SRSF7/AQR/THRAP3/GEMIN5/RBM22/DDX41/WDR33/PRPF3/CRNKL1/SUGP1/SNW1/NOVA1/IK/ESS2/D			
							HX16/SNRNP48/CDC5L/SRPK1/METTL3/FAM172A/RBFOX2/WBP11/GPATC1/CWC25/KHSRP/SF3A1/PPIL3/PPIL1/SLU7/SON/REST/CACTIN/SRSF4/CSTF2/DYRK1A/CSTF3/HNRNPF			
							/TGS1/NUP98/ZCRB1/PAPOLA/SRRM1			
							RPS7/HSF1/MZT2A/SF11/NME1/MZT2B/RUVBL2/H2AFX/LZTS2/SSNA1/ATF4/BCCIP/RABL6/DYLNLR1/ARL2/DCAF13/KAT2A/KAT2B/HAUS4/LRRC45/CETN2/ODF2L/LCK/AKNA/NLRC			
							5/CEP44/CCDC14/RIC8B/PPP1R12A/OFD1/CEP95/CEP290/ORC2/CEP170/BBS1/SPICE1/CEP135/EFHC1/IFT140/ZNF12/CNTRL/KIF3A/RBBP6/CEP164/WDR60/USP33/C2CD3/AHI			
							1/NEDD1/POC5/RNF19A/MAK/ITSN2/TRAF5/DDX11/CEP192/DYNC1L12/CEP295/ARHGEF10/RAD51D/SCLT1/PATJ/HOOK2/PKN2/CAPRIN2/HAUS3/GEN1/PKHD1/CLASP1/SPPL2B/RA			
							BL2B/IQCB1/HOOK3/RPGRIP1L/FBXW11/TUBG2/TUBGCP6/MECP2/KIF2A/CEP162/BICD1/KIAA0753/CCDC66/CAMSAP2/CEP97/CROCC/MKS1/BCAS2/SSX2IP/BBS4/DCTN2/MAPRE1/			
							DCTN5/CEP19/MASTL/CEP89/IFT52/CEP55/GPSM2/RAB11A/NDE1/RABEP2/KIF23/STIL/GNAI3/CALM2/BBS7/TTC26/CHD4/CCT5/DYNC1L11/DCLRE1B/CEP112/RILPL1/IFT22/DY			
							NC1H1/CHEK1/DYNC1I2/CDC25B/CEP41/PLK1/DYNC2L11/CDK2/OLA1/DCTN1/TTL5/CSNK1D/CEP126/XRCC2/PRICKLE3/RAD18/IST1/MCM3/PLK4/CEP152/WDR62/HNRNPU/NCKAP			
							5L/ADGRB2/HAUS6/DLGA5/BICD2/CKAP2L/HAUS2/CCT8/CDC45/CDC20/MDM1/CENPF/NDC80/SLF1/DPF2/MARCKS/HAUS1/CENPJ/AUNIP/NUP62/TXNDC9/MKKS/WRAP73/TBC1D31/			
							CCNB2/TRIP4/CCNB1/CDK1/SASS6/PCLAF/WDR35/NUDT21/TUBG1/CDC42/SGO1/CCT4/KIF15/CCNF/GSK3B/HASPIN/DHX9/ACTR8/HAUS8/KIF20B/BRCA2/SDCCAG8/CKAP5/HMMR/C			
							HD3/CEP131/FBF1/TCTEX1D2/NEK2/CEP250/CEP68/TMEM67/RAP1GAP2/ODF2/PCNA/AAAS/C7orf31/UNC119/PCNT/DNM2/ALMS1/EEF1AKMT3/NPH4/RAB23/ACTR1A/DTL/KATNA1			
							/FLOT1/B9D2/CDC27/HAUS5/ANKRD26/ATP6V1D/BOD1/CIR1/CCDC77/CEP63/C4orf47/CTSC/FAM161A/CKAP2/BRSK1/NME7/MZT1/CTDP1/WRN/AURKA/POC1B/NIN/TCP1/EYA3/CN			
							TROB/E2F1/CRMP1/RABGAP1/CCDC81/DYNLL1/TSEN2/NPM1/BICDL1/ALDOB/ZNF322/CUL7/KIF13A/PHF1/NUMA1/EXOC7/PIBF1/NEK9/PLEKHA7/CETN3/MI1B/CEP350/CSPP1/PPP			
							4R3B/SPAST/DCAF12/CCP110/TUBGCP4/ZFYVE26/TUBGCP5/DCTN4/SMAD4/APEX1/CEP70/ACTR1B/ABRAXAS2/TBCD1/ERCC6L2/CDKL5/GNAI1/TNKS2/CCDC15/CEP85/KIAA0586/			
							TCHP/FOPNL/CDK5RAP2/TUBGCP3/UVRAG/BBS9			
							SNU13/SNRPD2/SNRPF/SNRPA/SNRPD1/SNRPB/LSM8/PRPF31/PABPC1/LSM4/LSM7/SNRPA1/TXNL4A/LSM2/SNRPG/ISY1/SNRPD3/PRPF6/RALY/PIH/SNRNP70/SNRPE/SNRPC/ALYR			
							EF/SF3A2/SREK1/RNPC3/PNN/HNRNPH1/DDX39B/KHDC4/SRRM2/RBM5/SF3B1/PPWD1/SRSF2/U2AF1/DDX5/HNRNPH3/PRPF4B/ZCCHC8/TF2/PTBP2/SRSF1/AKAP17A/BCAS2/PRPF3			
							8A/RBM17/USP39/CWC27/RBM28/EFTUD2/RBMX/U2AF2/SF3A3/SNRNP200/DDX23/HNRNPU/DHX15/YBX1/BUD31/HNRNPA2B1/WAC/DHX8/HNRNPR/SF3B3/SMNDC1/HNRNPA3/HNRNPF/			
							ZRSR2/MFAP1/PPP1R8/CWC22/SNRPB2/BUD13/PRPF4/PIIE/TRA2B/SNRNP40/DHX35/HNRNPK/DHX38/CASC3/SF3B2/HNRNPM/RHEB/PDCD7/SF3B6/EIF4A3/SF3B4/GEMIN2/HNRNPA			
							1/MTREX/SYNCRIP/SF1/AQR/RBM22/HNRNPA1L2/DDX41/PRPF3/IVNS1ABP/CRNKL1/SUGP1/SNW1/IK/ESS2/DHX16/SNRNP48/CDC5L/ZNF830/GPATC1/CWC25/SF3A1/PPIL3/PPIL			
							1/SLU7/CACTIN/UPF1/HNRNPF/ZCRB1/SRRM1			
							RECQL4/HSF1/WRAP53/THOC5/H2AFX/AURKB/DSCC1/PPP2R1A/CENPM/DNMT3A/RANGAP1/ALYREF/KMT5C/H2AFY2/CDT1/KAT2B/CENPX/IKZF1/RASSF2/PML/TEP1/PPP1R12A/ORC2			
							/ZNF276/ATM/HIST4H4/SCMH1/KANSL1/MBD6/ZNF207/RIF1/MBD5/EZH1/ATR/DYNC1L12/SMCHD1/TP53BP1/RAD51D/MRE11/DNA2/ORC4/PKHD1/CLASP1/ATRX/CTCF/XPO1/THOC2			
							/CENPS/ITGB3BP/DCTN2/DCTN5/H2AFY/CBX3/RCC2/NDE1/PPP1CB/BUB1B/BUB1/RAD51/DYNC1L11/DCLRE1B/KIF2C/SGO2/CBX1/CHEK1/ORC1/ERCC6L/SPDL1/ZWILCH/PLK1/CDK			
							2/CENPI/NUP107/DCTN1/CDC48/CBX5/CENPH/CENPL/CENPA/CENPK/MSH2/MCM6/NCAPG/MCM3/MAD2L1/CENPE/SSB/EZH2/HNRNPU/MCM4/SPC25/KIF18A/KDM1A/HNRNPA2B1/XRCC			
							1/DNMT1/SKA1/INCENP/CENPF/NDC80/HAT1/MCM2/NUP37/NUP85/NUP43/KNTC1/HJURP/POLD1/TTK/NABP2/CCNB1/CDK1/NUF2/PHF6/BLM/MTBP/SGO1/CENPB/ZWINT/CDCA5/PPP			
							1CC/NCAPD3/BRCA2/BAZ1B/DSN1/XRCC5/CKAP5/SUV39H2/OIP5/CENPW/POLR2B/CENPN/CENPQ/ESCO2/NEK2/NAT10/KNSTRN/PIF1/BIRC5/PPP2CA/MCM7/PCNA/ACD/FEN1/RPA1/			
							PRKDC/RPA2/SKA3/WDR82/NABP1/BUB3/ORC5/BOD1/CENPT/RAD21/HELLS/HIST1H4H/SIRT6/SIN3A/DBB1/WRN/CENPU/DYNLL1/GAR1/WRNIP1/DAXX/RAD17/SMC3/TPR/TOX4/SMC			
							6/RAD50/KAT8/POT1/WAPL/PDS5B/PHF2/NUP160/CLASP2/STAG1/CDC73/SMC1A/TINF2/CENPC/LRIF1/DHX36/H3F3B/PDS5A/NUP133/DCTN4/SLX4/KMT5B/APEX1/STAG2/RNF8/U			
							PF1/PPP1R10/ZW10/NGDN/AHCTF1/TNKS2/MIS12/NUP98/PURA/AURKB/UVRAG/DOT1L			
							IPO4/TRIM28/TONSL/BEND3/RUVBL2/THOC5/P3H4/CHRAC1/CHRAC2/CPSP9/KAT2A/ALYREF/TPPT/SMARCB1/KMT5C/H2AFY2/AR/RUNX2/RUNX3/SPI1/EOMES/IKZF1/DPF1/			
							PML/GATA3/ZEB2/ACTB/ZNF385A/ETAA1/ORC2/SP1/ATM/HIST4H4/PURB/ZMIZ2/PHF12/EP400/CREB1/BRD8/RIF1/CPSF6/ATR/PAWR/DDX11/SINHCAF/POG2/BPTF/USP3/TCF12/			
							SMCHD1/TP53BP1/SS18/RAD51D/MRE11/SUDS3/DNA2/ORC4/INO80/HELB/MUC1/HMGXB4/ATRX/DFFB/SMARCA1/TAF1/RSF1/TAF4/THOC2/BCAS2/RPA3/SMARCD1/H2AFY/UBE2I/S			
							MAD2/CBX3/MTA3/PPP1CB/MTA2/POLA1/BUB1/CHD4/RUVBL1/RAD51/CSNK2A1/DCLRE1B/SMARCD3/RBMX/CBX1/ORC1/H2AFZ/PLK1/RBBP4/DVL3/EED/CBX5/MCRS1/CENPA/ACTL6A			
							/MSH2/MCM6/HDAC2/TIPIN/MCM3/RBBP7/CHAF1B/SSB/EZH2/CCAR2/POLR3D/ASF1B/TCF3/MORF4L1/POLD3/MCM4/BUD31/SFR1/SMARCAL1/EME1/KDM1A/SMARCA4/XRCC1/INCENP			
							/NDC80/BRCA1/HAT1/MMS22L/MCM2/DPF2/RAD51AP1/NASP/POLD1/RARG/E2F4/GATAD2A/MBD2/RCC1/NABP2/CCNB1/CDK1/BRD9/TRRAP/TARDBP/BLM/SGO1/CENPB/PCGF2/DFFA/			
							HDAC1/CDCA5/HNRNPC/DHX9/PPP1CC/ACTR8/NCAPD3/NCOR2/UHRF1/BRCA2/BAZ1B/XRCC5/CHD3/SETD1A/MSH6/POLR2B/LDB1/ESCO2/NAT10/EHMT2/PIF1/HMG2/MCM7/PCNA/AC			
							D/HNRNPK/FEN1/SMARCA5/RPA1/PRKDC/SMARCE1/RPA2/CREB3L1/WDR82/RNF2/NABP1/ORC5/CHAF1A/HIST1H4H/SIRT6/SUZ12/MLH1/SIN3A/TBP/DBB1/TCP1/RFX3/SMARCC2/E2			
							F1/FER/HIF1A/POLE3/GAR1/SMARCC1/WRNIP1/BICRAL/CDC5L/MLH3/NFRKB/ING3/SMC3/TTC21B/GATAD2B/RING1/SMAD3/TOX4/RAD50/ARID1A/UHRF2/POT1/WAPL/YY1/INO80E			
							/ANP32E/CREBBP/CDC73/KAT5/TINF2/CALCOCO1/CENPC/HIST1H3E/LRIF1/H3F3B/REPIN1/TIMELESS/YEATS4/ZRANB3/CBX8/MTA1/TBX6/SMAD4/YY1AP1/NUCKS1/SLX4/KMT5B/			
							APEX1/UPF1/PPP1R10/PLCB1/MPHOSPH8/PPARD/ETV3/TNKS2/SIRT7/TAF5/NCOA3/GABPA/PURA/SRF			
BP	G0:00 16569	covalent chromatin modification	251/5534	433/179 13	4.51 E-32	3.10 E-29	2.64 E-29			25 1
BP	G0:00 00375	RNA splicing, via transesterification reactions	211/5534	348/179 13	7.23 E-31	4.48 E-28	3.82 E-28			21 1
CC	G0:00 05813	centrosome	282/5692	473/186 78	3.41 E-40	2.43 E-37	1.67 E-37			28 2
CC	G0:00 05681	spliceosomal complex	121/5692	160/186 78	4.30 E-32	1.53 E-29	1.05 E-29			12 1
CC	G0:00 98687	chromosomal region	206/5692	337/186 78	9.91 E-32	2.35 E-29	1.62 E-29			20 6
CC	G0:00 44454	nuclear chromosome part	257/5692	469/186 78	1.50 E-28	2.67 E-26	1.84 E-26			25 7

CC	G0:00 16607	nuclear speck	216/5692	386/186 78	8.89 E-26	1.27 E-23	8.72 E-24	REXO4/SURF2/PRPF31/H2AFX/TIMM50/NXT1/SNRPA1/PRPF6/AKAP8L/ARL6IP4/PIIH/SNRNP70/ALYREF/SF3A2/GADD45A/NUGGC/NR3C1/NAMPT/AR/GLI3/FEV/LPXN/IL16/IL15/LIMK1/PYHIN1/SREK1/SRSF11/FNBP4/PNISR/PNN/DDX17/LUC7L3/BAZ2A/POLI/RBM25/DDX39B/MAML1/CCNL1/ZNF621/RBM39/SRRM2/S100BPB/CCNL2/ZNF638/SF3B1/ACIN1/PRPF40B/EP400/FAM76B/SRSF10/CLK3/NFKBIZ/RBBP6/CPSF6/GPATCH2/SMURF2/SNURF/TCF12/KMT2E/SRSF6/PRPF40A/SRSF2/U2AF1/SFPQ/YTHDC1/NXF1/CDK13/SMC4/PRPF4B/SETD1B/DENND1B/RNF34/CLK2/ATXN2L/CDK12/SART3/RNF169/SRSF1/RBM4/DDX42/THOC2/AKAP17A/PHF7/BCAS2/SPOP/HEXIM2/RNPS1/CARMIL1/AAGAB/GLIS2/PIAS2/BARD1/EFTUD2/UNC45A/U2AF2/CDYL/PIAS3/SF3A3/CD2BP2/DGKZ/DUSP11/HNRNPU/HAUS6/POLR3D/DHX15/TCF3/MORF4L1/RSRC1/WAC/SAP130/STK17A/NCAPG2/NSRP1/DDX39A/RBM14/GATAD2A/TARDBP/NFATC4/AP5Z1/ARHGAP18/SMNDC1/BNIP3L/PPP1CC/EIF4ENIF1/TRIP12/CHTOP/PPP1R8/MECOM/CWC22/SNRPB2/SETD1A/OIP5/RUFY1/SRSF3/PRPF4/PIIE/PSPC1/EHMT2/LUC7L2/SNRNP40/MBD1/RBM15B/TOE1/ZMIZ1/CXXC1/RMI2/CASC3/SF3B2/USP22/HP1BP3/DDX46/MAML2/RBM10/CIR1/EIF4A3/CBX4/WTAP/NONO/USP36/ZC3H18/POLR2D/SARNP/THRAP3/CBL1/WRN/APBB1/PRPF3/MSX2/STK19/TRIM69/CRNKL1/SNW1/RFXAP/HIF1A/IK/RCHY1/BRD2/GTF2H4/MAPK14/CDC5L/ZNF830/PIAS1/GATAD2B/METTL3/RING1/SMC6/PUM1/RREB1/TAB1/RBM27/ERBIN/PP1G/CWC25/BRD1/POLDIP3/PPP4R3B/PIP5K1A/SF3A1/DHX36/YLPM1/SLU7/SON/CACTIN/SRSF4/APEX1/DYRK1A/PLCB1/BCLAF1/TEPSIN/SPRTN/TRIP11/GLYR1/MAML3/FOXO4/SRRM1 IPO4/TRIM28/HSF1/BEND3/EXOSC4/RUVBL2/EXOSC5/CHAC1/H2AFX/DSCC1/EIF3E/PELP1/CSNK2B/NOP53/HMGA2/DNMT3A/AKAP8L/HMGA1/COPS9/KAT2A/TFPT/SMARCB1/KMT5C/H2AFY2/AR/PINK1/RUNX2/RUNX3/CCND2/FANK1/SPI1/EOMES/IKZF1/DPF1/PML/GATA3/ZEB2/ACTB/ZNF385A/BAZ2A/ORC2/SP1/FAM111A/HIST4H4/MAU2/PHF12/EP400/CREB1/L3MBTL1/BRD8/RIF1/CPSF6/PAWR/DDX11/SINHCAF/POGZ/BPTF/USP3/TCF12/KMT2E/ESCO1/ICE2/SFPQ/SS18/SUDS3/MED1/INO80/MUC1/HMGXB4/ATRX/DFFB/SMARCD1/TAF1/RSF1/TAF4/ICE1/SDR16C5/MECP2/SMARCD1/H2AFY/FBH1/SMAD2/CBX3/MTA3/MTA2/POLA1/CHD4/RUVBL1/RAD51/CSNK2A1/SMARCD3/RBMX/CBX1/CHEK1/H2AFZ/PLK1/RBBP4/RAN/DVL3/EED/CBX5/MCRS1/CENPA/UBA1/ACTL6A/IST1/HDAC2/TIPIN/RBBP7/CHAF1B/EZH2/CCAR2/POLR3D/ASF1B/TCF3/MORF4L1/CSNK2A2/BUD31/EXOSC10/SFR1/EME1/KDM1A/SMARCA4/XRCC1/DNMT1/INCENP/CENPF/HMGNA4/HAT1/SLF1/MCM2/DPF2/RAD51AP1/NASP/RARG/E2F4/GATAD2A/MBD2/RCC1/BRD9/TRRAP/TARDBP/MTBP/CENPB/PCGF2/DFFA/HDAC1/CDA5/HNRNPC/DHX9/ACTR8/NCAPD3/LOXL2/NCOR2/UHRF1/PARBP/BAZ1B/SUV39H2/CBX2/CHD3/SETD1A/MSH6/OIP5/LDB1/ESCO2/EHMT2/HMGB2/CDK4/MCM7/PCNA/UBE2A/HNRNPK/SMARCA5/EXOSC3/SMARCE1/RPA2/CREB3L1/WDR82/HP1BP3/RNF2/RAD21/HMGN1/HELLS/HTRA2/WDR76/CHAF1A/HIST1H4H/STRT6/SUZ12/SIN3A/TBP/TCP1/RFX3/PHC2/SMARCC2/E2F1/ZC3H8/FER/HIF1A/SMARCC1/BICRAL/LEMD2/KDM1B/NFRKB/UBR2/ING3/MORC2/SMC3/TTC21B/GATAD2B/RING1/SLF2/DDX6/SMAD3/TOX4/ARID1A/UHRF2/H2AFV/WAPL/YY1/INO80E/ANP32E/PDS5B/STAG1/CREBBP/KAT5/CALCOCO1/CENPC/HIST1H3E/H3F3B/PDS5A/TIMELESS/YEATS4/CBX8/MTA1/TBX6/SMAD4/YY1AP1/SOS1/NUCKS1/SLX4/TOP2B/SOS2/STAG2/CREB3L2/UPF1/RNF20/PPP1R10/PLCB1/MPHOSPH8/PPARD/ETV3/AHCTF1/TTC37/SIRT7/HIST1H2BN/TAF5/GLYR1/NCOA3/GABPA/RNF40/SMC8/SRF RPS24/RPL18/RPS3/RPL14/RPS21/RPL7A/RPS19/RPL37/RPL27A/RPL8/RPL32/RPSA/RPL12/RPS16/RPL28/RPL35/RPS2/RPL37A/RPL6/RPS5/RPS7/RPL23A/RPL29/RPL24/RPS17/RPS8/RPL13A/RPL18A/RPS11/RPL7/RPL3/RPS9/RPL35A/RPL9/RPL31/RPL13/RPL2/RPL38/RPL36A/RPS18/RPL4/RPS6/RPLP0/RPL5/RPS10/RPL15/RPL27/RPS27A/RPL30/RPS20/RPL23/RPL11/RPS12/RPS3A/RPL36/RPL19/RPLP1/RPS13/RPS15/RPS15A/RPL10A/RPS28/RPS23/RPS14/RPS25/RPL17/UBA52/RPL34/RPL41/RPS29/RPS27/RPL26/RPL21/RPL39/RPS4X/RPL22/GEMIN5/EIF2D RPS3/HSF1/MZT2A/MZT2B/AURKB/BCCIP/ERCC2/KAT2A/RANGAP1/RAE1/ARHGEF2/NR3C1/ACOT13/HAUS4/MAP7D1/LRMP/CEP44/WDR73/CEP95/CEP170/SPICE1/EFHC1/MAPKB1/ATM/KLHL42/KATNBL1/KIF3A/ZNF207/WDR60/RIF1/MAK/YEATS2/DDX11/MTCL1/CEP295/MAP9/DID01/INO80/HAUS3/PKHD1/CLASP1/IQCB1/TUBG2/LATS1/SPIN1/TUBGCP6/ECT2/KIF2A/CEP162/TTC23L/MAPRE1/CEP19/CEP89/CBX3/GPSM2/RAB11A/RCC2/NDE1/MAP4/KIF23/CALM2/MAEA/BUB1B/SHCBP1/TMEM201/DYNC1L11/TOPBP1/SPDL1/SPDL1/CDC25B/PLK1/CDC7/KIF11/TACC3/KIF20A/DCTN1/PRC1/MAP1S/KIF18B/RACGAP1/CSNK1D/KATNAL2/KIF4A/EML2/CIAO1/CDC6/MAD2L1/CENPE/WDR62/HNRNPU/HAUS6/DLGA5/CKAP2L/HAUS2/FAM110A/KIF18A/ATA1/CDC20/SAK1/ARL8B/INCENP/CENPF/NUP85/HAUS1/KNTC1/AUNIP/NUP62/PKP4/TTK/ANXA11/CCNB1/CDK1/TUBG1/CDC42/AGBL5/SGO1/KIF15/HASPIN/FBX05/HAUS8/TPX2/KIF20B/CKAP5/CLTC/FBF1/TCTEX1D2/MMS19/NEK2/KNSTRN/TBL1XR1/ODF2/PPP2CA/CTTN/AAAS/UNC119/ALMS1/SKA3/SPAG8/KATNA1/KIF14/CD27/PSRC1/HAUS5/BOD1/VRK1/RAD21/CEP63/FAM161A/CKAP2/DYNLT1/MZT1/CTDP1/AURKA/POC1B/NIN/CRMP1/DYNLL1/IK/NPM1/BRCC3/MAPK14/NUMA1/GOLGA2/SMC3/TPR/MAPK1/CLASP2/STAG1/CEP350/CSPP1/CUL3/SMC1A/SPAST/TUBGCP4/MAD2L1BP/TUBGCP5/DCTN4/STAG2/ZW10/BIRC6/ABRAXAS2/TBCCD1/NEK7/CEP85/CDK5RAP2/TUBGCP3/PARP4/E4F1 HSF1/AURKB/DSCC1/PPP2R1A/CENPM/DNMT3A/RANGAP1/KMT5C/CDT1/KAT2B/CENPX/IKZF1/RASSF2/PPP1R12A/ORC2/ZNF276/KANSL1/ZNF207/DYNC1L12/TP53BP1/PKHD1/CLASP1/ATRX/CTCF/XPO1/CENPS/ITGB3BP/DCTN2/DCTN5/H2AFY/CBX3/RCC2/NDE1/BUB1B/BUB1/DYNC1L11/KIF2C/SGO2/CBX1/ERCC6L/SPDL1/ZWILCH/PLK1/CENPI/NUP107/DCTN1/CDCA8/CBX5/CENPH/CENPL/CENPA/CENPK/NCAPG/MAD2L1/CENPE/HNRNPU/SPC25/KIF18A/DNMT1/SAK1/INCENP/CENPF/NDC80/NUP37/NUP85/NUP43/KNTC1/HJURP/TTK/CCNB1/NUP2/PHF6/MTBP/SGO1/CENPB/ZWINT/CDCA5/PPP1CC/NCAPD3/BAZ1B/DSN1/CKAP5/SUV39H2/CENPW/CENPN/CENPQ/ESCO2/NEK2/KNSTRN/BIRC5/PPP2CA/SKA3/BUB3/BOD1/CE NPT/RAD21/HELLS/SIN3A/CENPU/DYNLL1/DAXX/SMC3/TPR/KAT8/WAPL/PDS5B/PHF2/NUP160/CLASP2/STAG1/SMC1A/CENPC/PDS5A/NUP133/DCTN4/KMT5B/STAG2/ZW10/NGDN/AHCTF1/MIS12/NUP98/UVRAG SNRPD2/SNRPF/SNRPD1/SNRPB/PABPC1/SNRPA1/LSM2/SNRPG/ISY1/SNRPD3/PRPF6/RALY/SNRPE/ALYREF/SF3A2/PNN/HNRNPH1/SRRM2/SF3B1/PPWD1/U2AF1/DDX5/PRPF4B/ZCC8/SRSF1/BCAS2/CWC27/EFTUD2/RBMX/SF3A3/SNRNP200/DDX23/HNRNPU/BUD31/HNRNPA2B1/DHX8/HNRNPR/SF3B3/HNRNPA3/HNRNPC/CWC22/SNRPB2/PIIE/SNRNP40/DHX35/HNRNPK/DHX38/SF3B2/HNRNPM/EIF4A3/HNRNPA1/MTREX/SYNCRIP/AQR/RBM22/DDX41/CRNKL1/SNW1/ESS2/CDC5L/GPATCH1/SF3A1/PPIL3/PPIL1/SLU7/CACTIN/HNRNPF/SRRM1 TRIM28/HSF1/RUVBL2/ARID3A/PELP1/CSNK2B/HMGA2/DNMT3A/HMGA1/KAT2A/SUPT5H/SMARCB1/H2AFY2/CDT1/SETD7/KAT2B/AR/BEND6/NKX6-1/DMRT1/GLI3/TFAP2B/RUNX2/M EIS3/GLI1/TSHZ3/PRDM1/EOMES/MEOX1/CGAS/HOXC13/HOXD10/ACTB/CCNT2/PHF21A/MLLT6/ZNF354B/PWWP2A/MRNIP/EP400/MBD6/CCNT1/L3MBTL1/MLLT3/HDAC7/MITF/ZNF431/MBD5/EZH1/DDX11/USP3/DDX5/SFPQ/NSD1/MED1/ERCC6/MNT/ATRX/RNF169/NSD2/CTCF/BAHCC1/CENPS/HESX1/SMARCD1/H2AFY/SMAD2/MTA3/MTA2/POLA1/THRA/FAAP24/C HD4/RAD51/RBL1/SMARCD3/RBMX/CBX1/NAP1L4/ORC1/H2AFZ/RBBP4/MCM8/CDYL/RAN/RNF4/CBX5/SIN3B/CENPA/HCF1/ACTL6A/MSH2/HDAC2/MEIS1/CHAF1B/EZH2/POLQ/HNRN PU/CTBP2/POLR3D/DDX11/YBX1/TICRR/TOP2A/FUS/EXO1/KDM1A/SMARCA4/WAC/DNMT1/SSRP1/CENPF/RBPJ/HMGNA4/NUP62/POLD1/E2F4/MBD2/RCC1/PRDM11/HINFP/CDK1/HNRNP D/GTF2H1/PCLAF/MED12/NUDT21/NCOA6/TRIM37/CENPB/HDAC1/CDCA5/HNRNPC/DHX9/CHD8/CKS2/UHRF1/RERE/UBE2T/CBX2/MSH6/POLR2B/LDB1/POLR1A/UBTF/ADNP/NCOA5/T TC5/EHMT2/PKN1/PCNA/SMARCA5/SMARCE1/CREB3L1/HP1BP3/RNF2/VRK1/CBX4/GTF2F1/HMGN1/NONO/CHAF1A/STRT6/ACTN4/SP3/SUZ12/MLH1/SIN3A/GMNN/DNTTIP1/WRN/PYG O2/APBB1/CIC/ATF2/SMARCC2/SSBP1/TOP1/SMARCC1/FABP1/BRD2/PBX2/JARID2/ZKSCAN3/MLH3/SETDB1/MORC2/TNRC18/ASH1L/SMC3/GATAD2B/PRIMPOL/MLLT10/TPR/RING1 /SMAD3/ARID1A/SAFB/BRD3/PATZ1/CREBBP/NELFE/STAT5B/FANCM/MCM3AP/YAP1/SMC1A/CALCOCO1/SATB2/ZNF304/H3F3B/ZNF274/EP300/MTA1/REST/BMI1/SMAD4/ELK4/NUC KS1/TOP2B/APEX1/RNF8/POLG/UPF1/RNF20/MPHOSPH8/CRTC2/POLR3A/SIRT7/KDM5A/URI1/NUP98/PBRM1/GABPA/FOXO4/DHX30/SRF/CLOCK/BRIP1/ZIC2/MCM9 RECQL4/RUVBL2/DSCC1/ERCC2/CHD2/CHD6/DDX11/BPTF/ERCC3/RAD51D/MRE11/DNA2/TF2/INO80/HELB/ERCC6/ATRX/CHD1/RAD51C/FBH1/CHD4/RUVBL1/RAD51/ERCC6L/RBBP 4/XRCC2/RFC2/MCM6/POLQ/RFC4/MCM4/TOP2A/SMARCAL1/SMARCA4/GTF2H1/BLM/DHX9/CHD8/XRCC5/CHD3/PIF1/RFC3/MCM7/CHTF18/RFC5/WRN/RECQL/RAD54B/GTF2H4/RAD50 /RFC1/FANCM/DHX36/TOP2B/GTF2H3/BRIP1 RECQL4/RUVBL2/TWINK/ERCC2/DDX56/DDX17/DDX47/DDX39B/EP400/CHD2/SRCAP/YTHDC2/HELZ/CHD6/DDX11/DDX5/ERCC3/MRE11/DNA2/TF2/HELB/EIF4A1/ATRX/SMARCD1/C HD1/DDX42/BTAF1/RECQL5/FBH1/DDX27/RAD54L/CHD4/RUVBL1/ERCC6L/DDX52/MCM8/SNRNP200/DDX23/MCM6/MCM3/DHX15/DDX1/MCM4/SMARCAL1/SMARCA4/MCM2/DDX39A/DHX 8/DDX20/BLM/DHX9/CHD8/XRCC5/CHD3/PIF1/DDX55/MCM7/SMARCA5/GTF2F2/DDX46/DDX31/EIF4A3/HELLS/DDX18/AQR/WRN/DDX41/RECQL/DDX49/DDX50/RAD54B/DHX16/EIF4 A2/HLTF/DDX6/RAD50/FANCM/DHX36/UPF1/ERCC6L2/HELQ/DHX30/BRIP1/MCM9 TONSL/WRAP53/PIH1D1/H2AFX/ING5/PYGO1/JAK2/MYSM1/BAZ2A/MLLT6/PHIP/KMT2A/MTF2/PWWP2A/CHD2/L3MBTL1/MLLT3/ZMYND8/EZH1/SPIN3/YEATS2/BPTF/USP3/KMT2E/U SP49/TP53BP1/ATAD2B/ATRX/UMC1/SART3/TAF1/RSF1/SPIN1/CHD1/NCAPD2/PHF19/RBBP4/CDYL/CBX5/CHAF1B/ASF1B/PTMA/SET/SMARCA4/MCM2/DPF2/NCAPG2/NASP/HJURP /MSL3/RCC1/HINFP/PHF6/BRD9/PWP1/CHD8/NCAPD3/UHRF1/BAZ1B/CBX2/MSH6/TBL1XR1/PKN1/SMARCA5/SPIN4/VRK1/KDM4A/CBX4/SUZ12/PYGO2/APBB1/FAM156A/NPM1/DEK/ BRD2/MBTD1/KDM1B/PHF1/DAXX/ING3/MLLT10/UHRF2/SUPT6H/KAT8/ANP32E/BRD3/PHF2/SPY2D1/BRD1/MCM3AP/IP07/ZMYND11/CBX8/RNF8/RNF20/MPHOSPH8/KDM5A/RBBP5/ GLYR1/CARM1/IP09/KDM5B EMG1/PUS1/WDR4/EXOSC4/EXOSC5/TRMT1/EXOSC7/SARS2/POLR1C/POP7/CD3EAP/METTL1/TRMT2A/QARS/FARSB/DDX56/EXOSC2/RPP30/WARS/TRDMT1/RNASE6/PAN3/DDX17/CNO T6/SLFN13/DDX39B/AGO3/CNOT2/TRMT10B/YTHDC2/TENT2/TYW5/TRMT13/DGCR8/DDX5/TUT4/EIF4A1/POLR2M/TRIT1/METTL2A/NARS/DROSHA/WARS2/RNASEH1/NSUN4/NT5C3A/	21 6 26 3 78 18 8 12 3 68 24 1 56 84 10 2 14 3
CC	G0:00 00785	chromatin	263/5692	500/186 78	1.45 E-25	1.72 E-23	1.18 E-23		
CC	G0:00 22626	cytosolic ribosome	78/5692	95/1867 8	2.42 E-25	2.46 E-23	1.70 E-23		
CC	G0:00 05819	spindle	188/5692	326/186 78	1.09 E-24	9.69 E-23	6.68 E-23		
CC	G0:00 00775	chromosome, centromeric region	123/5692	185/186 78	4.28 E-24	3.39 E-22	2.33 E-22		
CC	G0:00 71013	catalytic step 2 spliceosome	68/5692	82/1867 8	9.53 E-23	6.79 E-21	4.68 E-21		
MF	G0:00 03682	chromatin binding	241/5644	437/169 69	1.48 E-21	1.50 E-18	1.26 E-18		
MF	G0:00 08094	DNA-dependent ATPase activity	56/5644	72/1696 9	1.09 E-14	5.54 E-12	4.64 E-12		
MF	G0:00 04386	helicase activity	84/5644	128/169 69	6.10 E-14	2.06 E-11	1.73 E-11		
MF	G0:00 42393	histone binding	102/5644	174/169 69	5.02 E-12	1.27 E-09	1.07 E-09		
MF	G0:01 40098	catalytic activity, acting on RNA	143/5644	268/169 69	7.21 E-12	1.46 E-09	1.22 E-09		

MF	GO:01 40097	catalytic activity, acting on DNA	91/5644	152/169 69	1.38 E-11	2.34 E-09	1.96 E-09	CPSF3/DBR1/SNRNP200/METTL6/DDX23/YARS2/DHX15/QTRT2/DDX1/EXOSC10/EXO1/FTSJ1/POPI/GARS/POLR3F/TRMT9B/USB1/TRNT1/DHX8/DDX20/MARS/PNPT1/IARS/ERI1/RP P25/DIMT1/EDC3/LARS/DHX9/EPRS/MRM2/PPP1R8/DALRD3/POLR1A/PIF1/JMJD6/TOE1/ZCCHC4/TARS/FEN1/EXOSC3/HARS2/RPP38/TRMT2B/KARS/DARS2/PCIF1/CNOT8/PARN/X RN2/RNMT/EIF4A3/NSUN3/BUD23/DDX18/POLR3C/POLR2D/MED20/MED21/RNASEH2A/RAD54B/QRSL1/RIDA/RNASE4/AZGP1/ANG/AARS2/DHX16/CMTR1/CDKAL1/EIF4A2/PRIMPOL/ METTL3/DDX6/DIS3L2/TYW1/VARS2/RPAP1/DHX36/PAN2/SLU7/AARSD1/VARS/ALKBH8/APEX1/FARS2/MRM1/UPF1/RPP21/TDP2/POLR3A/TGS1/CNOT1/DCP2/ISG20L2/RAMAC/DHX 30 RPS3/RECQL4/NME1/RUVBL2/TWNK/CHRAC1/HMGA2/ERCC2/DNMT3A/SMUG1/POLL/TEP1/POLI/CHD2/TDG/DDX11/ERCC3/MRE11/DNA2/HELB/GEN1/POLM/ATRX/DFFB/CHD1/RECQL5 /MUTYH/RAD51C/FBH1/RBBP8/POLA1/RAD54L/CHD4/RUVBL1/DCLRE1C/ERCC6L/RAD1/MCM6/POLQ/MGME1/DDX1/POLD3/MCM4/TOP2A/EXO1/SMARCAL1/XRCC1/DNMT1/POLD1/BLM/ DHX9/CHD8/APEX2/XRCC5/CHD3/DKC1/EXD2/PIF1/MUS81/MCM7/PCNA/FEN1/POLA2/LIG1/NEIL3/WRN/RECQL/RAD54B/TOP1/POLE3/SETMAR/POLH/LIG3/PRIMPOL/RAD50/RAD9A /FANCM/DHX36/ZRANB3/EXO5/SLX4/TOP2B/APEX1/FAN1/POLG/THAP9/TDP2/TOP3B/DCLRE1A/BRIP1/MCM9 REX04/TRIM28/TONSL/RUVBL2/SOX12/PFDN5/SUPT3H/PRPF6/HMGA2/UBE2L3/RALY/DNMT3A/HMGA1/KAT2A/RFXANK/HSBP1/SMARCB1/LPIN2/KAT2B/IL31RA/BEND6/TFAP2B/TFE C/HDAC9/PRRX1/BATF3/FEV/CIIITA/LPXN/TRERF1/GATA3/MYSM1/DDX17/NR2C2/TCERG1/MAML1/N4BP2L2/CNOT2/ZMIZ2/PHF12/SUPT20H/SP4/CREB1/SRCAP/HDAC7/TDG/KLF7/ ZNF136/ZMYND8/SUPT7L/EZH1/MAK/PAWR/GON4L/MED23/MRTFB/SRSF2/TP53BP1/MED14/SS18/NSD1/GPS2/MED1/MEIS2/MUC1/ASXL1/MNT/CBFA2T2/MED15/NFE2L3/ATN1/TAF1 /CTCF/TAF4/CCAR1/SDR16C5/MECP2/NSD3/BCL10/SPEN/PSMC3IP/SMARCD1/PRMT2/RBBP8/TRIP13/KCTD1/E2F6/RUVBL1/PIAS2/SMARCD3/MCIDAS/CDYL/RNF4/TRIM32/MED22/ HCFC1/PPP1R13L/ACTL6A/EZH2/HNRNPU/CTBP2/TCF3/DDX1/BUD31/MRTFA/FUS/SFR1/KDM1A/SMARCA4/BRC1A/DPF2/WDR77/RBM14/MED17/ABL1/MYCBP/TRIP4/HINFP/GMEB1/T RRAP/MED12/SOX4/NFATC4/NCOA6/KMT5A/MED7/HDAC1/YBX3/DHX9/NFYC/NCOR2/RERE/MED24/AEBP2/ATXN7L3/GTF2A2/LDB1/PTPN14/GRIP1/MMS19/HMGB2/TBL1XR1/PKN1/JM JD6/HSF2/BCL9L/MAP3K10/SMARCE1/ZNF85/BHLHE41/ATF7IP/SUB1/MTF1/USP22/USP21/MAML2/TFDP1/CIR1/CBX4/GTF2F1/ECD/CTBP1/SIRT6/ACTN4/TSG101/NME2/PSMD9/S F1/GMNN/THRAP3/MED21/MSX2/SMARCC2/SNW1/RFXAP/SAP30/E2F8/MED19/SMARCC1/NPM1/NR1I3/RXR/RNF451/TAF11/ABT1/DAXX/PIAS1/SCAI/TCF20/SMAD3/UBE3A/BOR/A RID1A/RBFOX2/YY1/NPAT/PHF2/BCL9/CREBBP/KAT5/YAP1/CALCOCO1/GMEB2/ZNF274/HMGB1/EP300/ZMYND11/GTF2A1/MTA1/MED13/SMAD4/ELK4/ZFX/APEX1/SERTAD2/RNF20/ BIRC2/CASP8AP2/TDP2/KDM5A/URI1/SUFU/NUP98/TRIP11/CARM1/MAML3/NCOA3/GABPA/PIAS4/KDM5B/E4F1/TFDP2/OLIG3 REX04/TRIM28/SOX12/SUPT3H/PRPF6/UBE2L3/HMGA1/KAT2A/SMARCB1/LPIN2/KAT2B/IL31RA/TFAP2B/TFEC/PRRX1/CIIITA/TRERF1/GATA3/MYSM1/DDX17/NR2C2/TCERG1/MAML 1/ZMIZ2/SP4/SRCAP/KLF7/SUPT7L/MAK/MED23/MRTFB/MED14/SS18/GPS2/MED1/ASXL1/MNT/NFE2L3/TAF1/TAF4/CCAR1/NSD3/BCL10/PSMC3IP/SMARCD1/PRMT2/RUVBL1/PIAS 2/SMARCD3/MCIDAS/RNF4/TRIM32/HCFC1/ACTL6A/CTBP2/TCF3/BUD31/MRTFA/FUS/SFR1/KDM1A/SMARCA4/BRC1A/WDR77/RBM14/MED17/ABL1/MYCBP/TRIP4/HINFP/GMEB1/MED 12/SOX4/NFATC4/NCOA6/MED7/DHX9/NFYC/RERE/MED24/ATXN7L3/GTF2A2/GRIP1/MMS19/HMGB2/PKN1/JMJD6/HSF2/BCL9L/SMARCE1/SUB1/MTF1/USP22/USP21/MAML2/TFDP1/ GTF2F1/ECD/ACTN4/TSG101/NME2/PSMD9/THRAP3/MED21/SMARCC2/SNW1/RFXAP/SMARCC1/NPM1/NR1I3/RXR/RNF451/TAF11/ABT1/DAXX/PIAS1/TCF20/UBE3A/ARID1A/YY1/NPAT/PHF 2/BCL9/CREBBP/KAT5/YAP1/CALCOCO1/GMEB2/HMGB1/EP300/GTF2A1/MTA1/MED13/ZFX/APEX1/SERTAD2/RNF20/BIRC2/KDM5A/NUP98/TRIP11/CARM1/MAML3/NCOA3/GABPA/E4 F1 RECQL4/RUVBL2/CD320/DSCC1/ERCC2/DDX56/ATP5F1E/LONP2/MYO1B/TNNT3/ATP13A2/ABCD2/DDX17/DDX39B/KIF3A/CHD2/YTHDC2/CHD6/DDX11/BPTF/DDX5/ERCC3/RAD51D/A BCC1/MRE11/DNA2/TTF2/INO80/HELB/ERCC6/EIF4A1/ATRX/ATP1A3/CHD1/RAD51C/FBH1/ATP1B3/CHD4/RUVBL1/RAD51/ATP2C1/DYNC1H1/ERCC6L/DYNC2LI1/RBBP4/SNRNP200 /XRCC2/RFC2/DDX23/MCM6/POLQ/RFC4/DDX1/MCM4/CCT8/TOP2A/SMARCAL1/KIF18A/SMARCA4/ATP6V1E1/ATP6V1F/ATP1A1/ATP13A1/NSF/ATP5F1B/ATAD5/DHX8/DDX20/ATP7A /GTF2H1/BLM/ATP6V1E2/ABCC4/DHX9/CHD8/KIF20B/XRCC5/CHD3/ABCB9/PIF1/RFC3/MCM7/CHTF18/RFC5/DYNC2H1/YME1L1/ATP10D/KATNA1/KIF14/MYO3A/EIF4A3/ATP5F1A/ DDX18/WRN/RECQL/RAD54B/TAP1/ABCB4/GTF2H4/EIF4A2/RAD50/ATP6AP1L/RFC1/HSP90AB1/FANCM/SPAST/DHX36/ATP8B1/TOP2B/RALBP1/UPF1/GTF2H3/DHX30/BRIP1	91
MF	GO:00 03712	transcription coregulator activity	233/5644	494/169 69	5.72 E-11	8.29 E-09	6.95 E-09	RRAP/MED12/SOX4/NFATC4/NCOA6/KMT5A/MED7/HDAC1/YBX3/DHX9/NFYC/NCOR2/RERE/MED24/AEBP2/ATXN7L3/GTF2A2/LDB1/PTPN14/GRIP1/MMS19/HMGB2/TBL1XR1/PKN1/JM JD6/HSF2/BCL9L/MAP3K10/SMARCE1/ZNF85/BHLHE41/ATF7IP/SUB1/MTF1/USP22/USP21/MAML2/TFDP1/CIR1/CBX4/GTF2F1/ECD/CTBP1/SIRT6/ACTN4/TSG101/NME2/PSMD9/S F1/GMNN/THRAP3/MED21/MSX2/SMARCC2/SNW1/RFXAP/SAP30/E2F8/MED19/SMARCC1/NPM1/NR1I3/RXR/RNF451/TAF11/ABT1/DAXX/PIAS1/SCAI/TCF20/SMAD3/UBE3A/BOR/A RID1A/RBFOX2/YY1/NPAT/PHF2/BCL9/CREBBP/KAT5/YAP1/CALCOCO1/GMEB2/ZNF274/HMGB1/EP300/ZMYND11/GTF2A1/MTA1/MED13/SMAD4/ELK4/ZFX/APEX1/SERTAD2/RNF20/ BIRC2/CASP8AP2/TDP2/KDM5A/URI1/SUFU/NUP98/TRIP11/CARM1/MAML3/NCOA3/GABPA/PIAS4/KDM5B/E4F1/TFDP2/OLIG3 REX04/TRIM28/SOX12/SUPT3H/PRPF6/UBE2L3/HMGA1/KAT2A/SMARCB1/LPIN2/KAT2B/IL31RA/TFAP2B/TFEC/PRRX1/CIIITA/TRERF1/GATA3/MYSM1/DDX17/NR2C2/TCERG1/MAML 1/ZMIZ2/SP4/SRCAP/KLF7/SUPT7L/MAK/MED23/MRTFB/MED14/SS18/GPS2/MED1/ASXL1/MNT/NFE2L3/TAF1/TAF4/CCAR1/NSD3/BCL10/PSMC3IP/SMARCD1/PRMT2/RUVBL1/PIAS 2/SMARCD3/MCIDAS/RNF4/TRIM32/HCFC1/ACTL6A/CTBP2/TCF3/BUD31/MRTFA/FUS/SFR1/KDM1A/SMARCA4/BRC1A/WDR77/RBM14/MED17/ABL1/MYCBP/TRIP4/HINFP/GMEB1/MED 12/SOX4/NFATC4/NCOA6/MED7/DHX9/NFYC/RERE/MED24/ATXN7L3/GTF2A2/GRIP1/MMS19/HMGB2/PKN1/JMJD6/HSF2/BCL9L/SMARCE1/SUB1/MTF1/USP22/USP21/MAML2/TFDP1/ GTF2F1/ECD/ACTN4/TSG101/NME2/PSMD9/THRAP3/MED21/SMARCC2/SNW1/RFXAP/SMARCC1/NPM1/NR1I3/RXR/RNF451/TAF11/ABT1/DAXX/PIAS1/TCF20/UBE3A/ARID1A/YY1/NPAT/PHF 2/BCL9/CREBBP/KAT5/YAP1/CALCOCO1/GMEB2/HMGB1/EP300/GTF2A1/MTA1/MED13/ZFX/APEX1/SERTAD2/RNF20/BIRC2/KDM5A/NUP98/TRIP11/CARM1/MAML3/NCOA3/GABPA/E4 F1 RECQL4/RUVBL2/CD320/DSCC1/ERCC2/DDX56/ATP5F1E/LONP2/MYO1B/TNNT3/ATP13A2/ABCD2/DDX17/DDX39B/KIF3A/CHD2/YTHDC2/CHD6/DDX11/BPTF/DDX5/ERCC3/RAD51D/A BCC1/MRE11/DNA2/TTF2/INO80/HELB/ERCC6/EIF4A1/ATRX/ATP1A3/CHD1/RAD51C/FBH1/ATP1B3/CHD4/RUVBL1/RAD51/ATP2C1/DYNC1H1/ERCC6L/DYNC2LI1/RBBP4/SNRNP200 /XRCC2/RFC2/DDX23/MCM6/POLQ/RFC4/DDX1/MCM4/CCT8/TOP2A/SMARCAL1/KIF18A/SMARCA4/ATP6V1E1/ATP6V1F/ATP1A1/ATP13A1/NSF/ATP5F1B/ATAD5/DHX8/DDX20/ATP7A /GTF2H1/BLM/ATP6V1E2/ABCC4/DHX9/CHD8/KIF20B/XRCC5/CHD3/ABCB9/PIF1/RFC3/MCM7/CHTF18/RFC5/DYNC2H1/YME1L1/ATP10D/KATNA1/KIF14/MYO3A/EIF4A3/ATP5F1A/ DDX18/WRN/RECQL/RAD54B/TAP1/ABCB4/GTF2H4/EIF4A2/RAD50/ATP6AP1L/RFC1/HSP90AB1/FANCM/SPAST/DHX36/ATP8B1/TOP2B/RALBP1/UPF1/GTF2H3/DHX30/BRIP1	23 3
MF	GO:00 03713	transcription coactivator activity	145/5644	285/169 69	4.69 E-10	5.94 E-08	4.98 E-08	REX04/TRIM28/SOX12/SUPT3H/PRPF6/UBE2L3/HMGA1/KAT2A/SMARCB1/LPIN2/KAT2B/IL31RA/TFAP2B/TFEC/PRRX1/CIIITA/TRERF1/GATA3/MYSM1/DDX17/NR2C2/TCERG1/MAML 1/ZMIZ2/SP4/SRCAP/KLF7/SUPT7L/MAK/MED23/MRTFB/MED14/SS18/GPS2/MED1/ASXL1/MNT/NFE2L3/TAF1/TAF4/CCAR1/NSD3/BCL10/PSMC3IP/SMARCD1/PRMT2/RUVBL1/PIAS 2/SMARCD3/MCIDAS/RNF4/TRIM32/HCFC1/ACTL6A/CTBP2/TCF3/BUD31/MRTFA/FUS/SFR1/KDM1A/SMARCA4/BRC1A/WDR77/RBM14/MED17/ABL1/MYCBP/TRIP4/HINFP/GMEB1/MED 12/SOX4/NFATC4/NCOA6/MED7/DHX9/NFYC/RERE/MED24/ATXN7L3/GTF2A2/GRIP1/MMS19/HMGB2/PKN1/JMJD6/HSF2/BCL9L/SMARCE1/SUB1/MTF1/USP22/USP21/MAML2/TFDP1/ GTF2F1/ECD/ACTN4/TSG101/NME2/PSMD9/THRAP3/MED21/SMARCC2/SNW1/RFXAP/SMARCC1/NPM1/NR1I3/RXR/RNF451/TAF11/ABT1/DAXX/PIAS1/TCF20/UBE3A/ARID1A/YY1/NPAT/PHF 2/BCL9/CREBBP/KAT5/YAP1/CALCOCO1/GMEB2/HMGB1/EP300/GTF2A1/MTA1/MED13/ZFX/APEX1/SERTAD2/RNF20/BIRC2/KDM5A/NUP98/TRIP11/CARM1/MAML3/NCOA3/GABPA/E4 F1 RECQL4/RUVBL2/CD320/DSCC1/ERCC2/DDX56/ATP5F1E/LONP2/MYO1B/TNNT3/ATP13A2/ABCD2/DDX17/DDX39B/KIF3A/CHD2/YTHDC2/CHD6/DDX11/BPTF/DDX5/ERCC3/RAD51D/A BCC1/MRE11/DNA2/TTF2/INO80/HELB/ERCC6/EIF4A1/ATRX/ATP1A3/CHD1/RAD51C/FBH1/ATP1B3/CHD4/RUVBL1/RAD51/ATP2C1/DYNC1H1/ERCC6L/DYNC2LI1/RBBP4/SNRNP200 /XRCC2/RFC2/DDX23/MCM6/POLQ/RFC4/DDX1/MCM4/CCT8/TOP2A/SMARCAL1/KIF18A/SMARCA4/ATP6V1E1/ATP6V1F/ATP1A1/ATP13A1/NSF/ATP5F1B/ATAD5/DHX8/DDX20/ATP7A /GTF2H1/BLM/ATP6V1E2/ABCC4/DHX9/CHD8/KIF20B/XRCC5/CHD3/ABCB9/PIF1/RFC3/MCM7/CHTF18/RFC5/DYNC2H1/YME1L1/ATP10D/KATNA1/KIF14/MYO3A/EIF4A3/ATP5F1A/ DDX18/WRN/RECQL/RAD54B/TAP1/ABCB4/GTF2H4/EIF4A2/RAD50/ATP6AP1L/RFC1/HSP90AB1/FANCM/SPAST/DHX36/ATP8B1/TOP2B/RALBP1/UPF1/GTF2H3/DHX30/BRIP1	14 5
MF	GO:00 42623	ATPase activity, coupled	114/5644	218/169 69	4.44 E-09	5.01 E-07	4.19 E-07	RECQL4/RUVBL2/TWNK/ERCC2/CHD2/DDX11/ERCC3/MRE11/DNA2/HELB/CHD1/RECQL5/FBH1/CHD4/RUVBL1/MCM6/MCM4/BLM/DHX9/CHD8/XRCC5/CHD3/PIF1/MCM7/WRN/RECQL/RA D54B/RAD50/FANCM/DHX36/BRIP1/MCM9	11 4
MF	GO:00 03678	DNA helicase activity	32/5644	42/1696 9	1.46 E-08	1.48 E-06	1.24 E-06	RECQL4/RUVBL2/TWNK/ERCC2/CHD2/DDX11/ERCC3/MRE11/DNA2/HELB/CHD1/RECQL5/FBH1/CHD4/RUVBL1/MCM6/MCM4/BLM/DHX9/CHD8/XRCC5/CHD3/PIF1/MCM7/WRN/RECQL/RA D54B/RAD50/FANCM/DHX36/BRIP1/MCM9	32

MF:Molecular Function, CC: Cellular ComponentBP: Biological Process, a p<0.05 indicates statistical significance.Statistically significant

Supplement File 3 The Top 10 Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway

ID	Description	GeneRatio	BgRatio	pvalue	padjust	qvalue	geneID	Count
hsa03040	Spliceosome	95/2629	147/8105	7.27E-16	2.42E-13	2.12E-13	SNU13/SNRPD2/SNRPF/SNRPA/SNRPD1/SNRPB/LSM8/PRPF31/CCDC12/LSM4/LSM7/SNRPA1/TXNL4A/LSM2/SNRPG/ISY1/SNRPD3/PRPF6/PIIH/SNRNP70/SNRPE/SNRPC/ALYREF/SF3A2/PRPF38B/TRA2A/TCERG1/RBM25/DDX39B/SF3B1/ACIN1/PRPF40B/SRSF10/SRSF6/PRPF40A/U2SURP/SRSF2/U2AF1/DDX5/SRSF1/DDX42/THOC2/BCAS2/PRPF38A/RBM17/NCBP2/USP39/EFTUD2/RBMX/SNRNP27/U2AF2/SF3A3/SNRNP200/DDX23/HNRNPU/DHX15/BUD31/FUS/DHX8/SF3B3/SMNDC1/HNRNPA3/HNRNPC/SNRPB2/SRSF3/PRPF4/SRSF9/PP1E/TRA2B/SNRNP40/HNRNPK/DHX38/SF3B2/DDX46/HNRNPM/SF3B6/EIF4A3/NCBP1/SF3B4/HNRNPA1/SRSF7/AQR/RBM22/HNRNPA1L2/PRPF3/CRNKL1/SNW1/DHX16/CDC5L/HSPA1L/WBP11/SF3A1/PPIL1/SLU7/SRSF4/PIK3R2/ZNF589/ZNF7/ALYREF/PIK3CD/IFNA1/FASLG/JAK2/PILRA/POU2F2/HLA-DQA1/HLA-DOA/SYK/CARD9/HLA-DMB/ZNF267/CGAS/PML/IFNG/LTA/HLA-DPB1/ZNF169/ZNF23/ZNF337/ZNF514/ZNF700/ZNF107/ZNF587/ZNF621/ZNF888/ZNF354B/ZNF182/ZNF12/ZNF195/ZNF841/ZNF432/ZNF224/ZNF605/ZNF26/ZNF84/ZNF791/ZNF708/RBAK/ZNF19/IRAK4/CASP8/ZNF248/ZNF736/ZNF641/ZNF737/ZNF431/ZNF136/ZNF333/ZNF91/ZFP90/ZNF8/TRAF5/ZNF713/ZNF33B/SRSF6/ZNF721/SRSF2/ZNF785/PILRB/NXF1/ZNF562/ZNF780B/ZNF43/ZNF273/POU2F1/TSC1/ZNF33A/SRSF1/ZNF44/ZNF124/ZNF519/ZNF550/ZNF439/ZNF611/ZNF558/TNF/ZNF101/IRF9/ZNF302/ZNF100/EIF2B3/BAK1/CYCS/ZNF714/PPP1CB/ZNF768/ZNF93/ZNF765/HCF1/ZNF430/EIF2B5/ZNF845/ZNF766/IKKBK/ZNF480/ZNF320/ZNF354A/ZNF486/ZNF675/ZNF816/PPP1CC/ZNF133/ZNF783/SRSF3/MAP3K7/ZNF160/SRSF9/ZNF436/AKT3/ZNF468/ZNF630/ZFP69B/TRAF2/ZNF283/ZNF81/ZNF211/ZNF229/ZNF718/ZFP69/ZNF85/ZNF761/ZNF544/RHEB/IKBEK/ZNF286A/ZNF2/ZNF506/ZNF607/ZNF37A/ZNF808/SRC/ZNF461/ZNF860/ZNF473/NECTIN1/ZNF529/ZNF316/ZNF551/ZNF14/MAVS/SRSF7/ZNF205/PIK3CB/ZNF382/ZNF669/ZNF426/ZNF778/ZNF132/ZNF530/TAP1/TRAF3/EIF2B2/C3/ZNF184/ZNF627/DAXX/ZFP14/ZNF546/ZNF189/SRPK1/ZNF606/ZNF343/ZNF212/ZNF383/ZNF543/ZNF567/ZNF764/ZNF234/ZNF74/ZNF3/ZNF616/ZNF443/ZNF317/TAB1/ZNF585A/ZNF527/ZNF235/ZNF548/ZNF561/ZNF571/ZNF891/ZNF45/ZNF689/ZNF528/ZNF510/ZNF41/ZNF225/ZNF417/ZNF112/ZSCAN32/ZNF799/ZNF304/ZNF180/ZNF253/ZNF619/ZNF441/ZNF324B/ZNF200/ZNF282/ZNF599/ZNF701/ZNF17/ZNF780A/ZNF440/ZNF227/ZNF623/ZNF786/ZNF585B/ZNF554/ZNF566/ZNF782/ZNF792/ZNF398/APAF1/ZNF772/ZNF300/ZNF140/SRSF4/ZNF573/BIRC2/ZNF823/TYK2/ZNF420/ZNF600/ZNF30/ZNF77/ZNF595/ZNF674/PIK3CA/ZNF658/ZNF613/ZNF620/TRAF6/ZNF559-ZNF177/ZNF836/ZNF181/ZNF155/ZNF793/RPS24/RPL18/RPS3/RPL14/RPS21/RPL7A/RPS19/RPL37/RPL27A/RPL8/RPL32/RPSA/RPL12/RPS16/RPL28/RPL35/RPS2/RPL37A/RPL6/RPS5/RPS7/RPL23A/RPL29/RPL24/RPS17/RPS8/RPL13A/RPL18A/RPS11/RPL7/RPL3/RPS9/RPL35A/RPL9/RPL31/RPL13/RPLP2/PIK3R2/RPL38/RPL36A/RPS18/RPL4/RPS6/RPLP0/RPL5/RPS10/RPL15/RPL27/RPS27A/RPL30/RPS20/RPL23/RPL11/RPS12/RPS3A/RPL36/RPL19/RPLP1/RPS13/RPS15/RPS15A/RPL10A/RPS28/RPS23/RPS14/RPS25/RPL17/UBA52/RPL34/RPL41/RPS29/RPS27/RPL26/RPL21/RPL39/RPS4X/FAU/RPL22/IL6ST/C6/C1R/C1S/TLR7/PIK3CD/IFNA1/C3AR1/FCGR2A/TLR8/MAPK10/CYBB/SYK/NLRP3/CASP1/CGAS/F2/IRAK4/ADAM17/TNF/IRF9/MAPK3/IKKBK/MAP3K7/IKBEK/MAPK13/PLCG1/MAVS/MAPK9/PIK3CB/TRAF3/C2/CFB/FGFB/C3/FGG/MBL2/FGA/F13B/C8A/MASP2/C8B/MAPK14/MAPK1/PRKCA/TYK2/PIK3CA/TRAF6/RSL24D1	95
hsa05168	Herpes simplex virus 1 infection	243/2629	495/8105	1.58E-15	2.63E-13	2.31E-13	8/ZFP69/ZNF85/ZNF761/ZNF544/RHEB/IKBEK/ZNF286A/ZNF2/ZNF506/ZNF607/ZNF37A/ZNF808/SRC/ZNF461/ZNF860/ZNF473/NECTIN1/ZNF529/ZNF316/ZNF551/ZNF14/MAVS/SRSF7/ZNF205/PIK3CB/ZNF382/ZNF669/ZNF426/ZNF778/ZNF132/ZNF530/TAP1/TRAF3/EIF2B2/C3/ZNF184/ZNF627/DAXX/ZFP14/ZNF546/ZNF189/SRPK1/ZNF606/ZNF343/ZNF212/ZNF383/ZNF543/ZNF567/ZNF764/ZNF234/ZNF74/ZNF3/ZNF616/ZNF443/ZNF317/TAB1/ZNF585A/ZNF527/ZNF235/ZNF548/ZNF561/ZNF571/ZNF891/ZNF45/ZNF689/ZNF528/ZNF510/ZNF41/ZNF225/ZNF417/ZNF112/ZSCAN32/ZNF799/ZNF304/ZNF180/ZNF253/ZNF619/ZNF441/ZNF324B/ZNF200/ZNF282/ZNF599/ZNF701/ZNF17/ZNF780A/ZNF440/ZNF227/ZNF623/ZNF786/ZNF585B/ZNF554/ZNF566/ZNF782/ZNF792/ZNF398/APAF1/ZNF772/ZNF300/ZNF140/SRSF4/ZNF573/BIRC2/ZNF823/TYK2/ZNF420/ZNF600/ZNF30/ZNF77/ZNF595/ZNF674/PIK3CA/ZNF658/ZNF613/ZNF620/TRAF6/ZNF559-ZNF177/ZNF836/ZNF181/ZNF155/ZNF793/RPS24/RPL18/RPS3/RPL14/RPS21/RPL7A/RPS19/RPL37/RPL27A/RPL8/RPL32/RPSA/RPL12/RPS16/RPL28/RPL35/RPS2/RPL37A/RPL6/RPS5/RPS7/RPL23A/RPL29/RPL24/RPS17/RPS8/RPL13A/RPL18A/RPS11/RPL7/RPL3/RPS9/RPL35A/RPL9/RPL31/RPL13/RPLP2/PIK3R2/RPL38/RPL36A/RPS18/RPL4/RPS6/RPLP0/RPL5/RPS10/RPL15/RPL27/RPS27A/RPL30/RPS20/RPL23/RPL11/RPS12/RPS3A/RPL36/RPL19/RPLP1/RPS13/RPS15/RPS15A/RPL10A/RPS28/RPS23/RPS14/RPS25/RPL17/UBA52/RPL34/RPL41/RPS29/RPS27/RPL26/RPL21/RPL39/RPS4X/FAU/RPL22/IL6ST/C6/C1R/C1S/TLR7/PIK3CD/IFNA1/C3AR1/FCGR2A/TLR8/MAPK10/CYBB/SYK/NLRP3/CASP1/CGAS/F2/IRAK4/ADAM17/TNF/IRF9/MAPK3/IKKBK/MAP3K7/IKBEK/MAPK13/PLCG1/MAVS/MAPK9/PIK3CB/TRAF3/C2/CFB/FGFB/C3/FGG/MBL2/FGA/F13B/C8A/MASP2/C8B/MAPK14/MAPK1/PRKCA/TYK2/PIK3CA/TRAF6/RSL24D1	243
hsa05171	Coronavirus disease - COVID-19	127/2629	232/8105	1.01E-12	1.12E-10	9.81E-11	RPS24/RPL18/RPS3/RPL14/RPS21/RPL7A/RPS19/RPL37/RPL27A/RPL8/RPL32/RPSA/RPL12/RPS16/RPL28/RPL35/RPS2/RPL37A/RPL6/RPS5/RPS7/RPL23A/RPL29/RPL24/RPS17/RPS8/RPL13A/RPL18A/RPS11/RPL7/RPL3/RPS9/RPL35A/RPL9/RPL31/RPL13/RPLP2/PIK3R2/RPL38/RPL36A/RPS18/RPL4/RPS6/RPLP0/RPL5/RPS10/RPL15/RPL27/RPS27A/RPL30/RPS20/RPL23/RPL11/RPS12/RPS3A/RPL36/RPL19/RPLP1/RPS13/RPS15/RPS15A/RPL10A/RPS28/RPS23/RPS14/RPS25/RPL17/UBA52/RPL34/RPL41/RPS29/RPS27/RPL26/RPL21/RPL39/RPS4X/FAU/RPL22/IL6ST/C6/C1R/C1S/TLR7/PIK3CD/IFNA1/C3AR1/FCGR2A/TLR8/MAPK10/CYBB/SYK/NLRP3/CASP1/CGAS/F2/IRAK4/ADAM17/TNF/IRF9/MAPK3/IKKBK/MAP3K7/IKBEK/MAPK13/PLCG1/MAVS/MAPK9/PIK3CB/TRAF3/C2/CFB/FGFB/C3/FGG/MBL2/FGA/F13B/C8A/MASP2/C8B/MAPK14/MAPK1/PRKCA/TYK2/PIK3CA/TRAF6/RSL24D1	127
hsa03460	Fanconi anemia pathway	42/2629	54/8105	8.80E-12	7.31E-10	6.42E-10	CENPX/POLI/EME2/REV1/ATR/FANCL/FANCF/CENPS/RPA3/RAD51C/FANCI/FAAP24/RAD51/FANCD2/FANCB/EME1/BRCA1/USP1/PALB2/BLM/FANCG/BRCA2/PMS2/UBE2T/FANCE/MUS81/RPA1/RPA2/RMI2/MLH1/TELO2/FANCA/POLH/WDR48/POLK/FANCM/RMI1/SLX4/FANI/FAAP100/TOP3B/BRIP1	42
hsa04110	Cell cycle	76/2629	126/8105	8.87E-11	5.89E-09	5.17E-09	CDC25A/RBX1/E2F5/ANAPC7/GADD45A/CCND2/ORC2/ATM/ATR/ORC4/SMAD2/YWHAQ/YWHAB/BUB1B/BUB1/E2F3/RBL1/ANAPC4/CHEK1/ORC1/ORC6/CDC25B/PLK1/PKMYT1/CDC7/CDK2/YWHAH/DBF4/MCM6/HDAC2/MCM3/CDC6/MAD2L1/E2F2/MCM4/CDC45/CDC20/ANAPC1/YWHAQ/YWHAZ/MCM2/ZBTB17/E2F4/TTK/ABL1/CCNB2/CCNB1/CDK1/HDAC1/GSK3B/TGFB2/CDK4/MCM7/PCNA/PRKDC/TFDP1/BUB3/CD27/PTTG1/ORC5/ANAPC13/RAD21/CCND3/CCNA2/ANAPC5/E2F1/SMC3/SMAD3/STAG1/CREBBP/SMC1A/EP300/CDC23/SMAD4/STAG2/TFDP2	76
hsa03013	Nucleocytoplasmic transport	66/2629	108/8105	7.07E-10	3.91E-08	3.44E-08	IPO4/THOC5/NXT1/RANGAP1/RAE1/ALYREF/NUP93/PNN/DDX39B/ACIN1/NXF1/TNPO2/XPO1/THOC2/UBE2I/RNPS1/NCBP2/KPNB1/NDC1/XPO6/NUP107/RAN/NUP155/NUP205/XPO7/KPNA2/UPF3B/NUP188/KPNA4/NUP37/NUP85/NUP43/NUP62/CSE1L/IPO13/AAAS/XPOT/CASC3/SUMO2/EIF4A3/NCBP1/TNPO1/TNPO3/KPNA6/XPO4/XPO5/NUP35/NUP214/NUP153/POM121C/UPF3A/TPR/UPF2/NUP160/IPO7/POM121/NUP54/IPO11/NUP133/NUP58/UPF1/AHCTF1/IPO5/NUP98/IPO9/SRRM1	66
hsa03010	Ribosome	88/2629	158/8105	1.01E-09	4.81E-08	4.22E-08	RPS24/RPL18/RPS3/RPL14/RPS21/RPL7A/RPS19/RPL37/RPL27A/RPL8/RPL32/RPSA/RPL12/RPS16/RPL28/RPL35/RPS2/RPL37A/RPL6/RPS5/RPS7/RPL23A/RPL29/RPL24/RPS17/RPS8/RPL13A/RPL18A/RPS11/RPL7/RPL3/RPS9/RPL35A/RPL9/RPL31/RPL13/RPLP2/RPL38/RPL36A/RPS18/RPL4/RPS6/RPLP0/RPL5/RPS10/RPL15/RPL27/RPS27A/RPL30/RPS20/RPL23/RPL11/RPS12/RPS3A/RPL36/RPL19/RPLP1/RPS13/RPS15/RPS15A/RPL10A/RPS28/RPS23/RPS14/RPS25/RPL17/UBA52/RPL34/RPL41/RPS29/RPS27/RPL26/RPL21/RPL39/RPS4X/MRPL11/MRPL14/FAU/RPL22/MRPL13/MRPL35/MRPL3/MRPL10/MRPL9/MRPL17/MRPS10/MRPL30/RSL24D1	88
hsa03440	Homologous recombination	31/2629	41/8105	1.66E-08	6.89E-07	6.06E-07	RAD52/ATM/RAD51D/MRE11/UIMC1/RPA3/RAD51C/RBBP8/RAD54L/RAD51/BARD1/BABAM2/TOPBP1/XRCC2/POLD3/EME1/BRCA1/PALB2/POLD1/BLM/BRCA2/MUS81/RPA1/RPA2/RAD54B/SSBP1/BRCC3/RAD50/ABRAXAS1/TOP3B/BRIP1	31
hsa03030	DNA replication	27/2629	36/8105	1.92E-07	7.06E-06	6.20E-06	DNA2/RPA3/POLA1/RNASEH1/RFC2/MCM6/MCM3/RFC4/PRIM2/POLD3/MCM4/MCM2/POLD1/RFC3/MCM7/PCNA/RFC5/FEN1/RPA1/POLA2/RPA2/LIG1/RNASEH2A/SSBP1/RNASEH2B/POLE3/RFC1	27
hsa04120	Ubiquitin mediated proteolysis	75/2629	142/8105	3.32E-07	1.10E-05	9.68E-06	RPS27A/UBA52/RBX1/UBE2L3/UBE2S/UBE2C/ELOC/UBE2M/ANAPC7/PML/MAP3K1/CBL/FANCL/SMURF2/FBXW7/UBA6/FBXW11/KLHL9/UBE3B/CBLB/UBE2I/UBE2Z/PIAS2/ANAPC4/PIAS3/TRIM32/UBA1/UBE2Q2/UBA2/SAE1/RNF7/UBE2N/CDC20/ANAPC1/BRCA1/HUWE1/UBE2E1/TRIM37/RHOBTB2/UBE2D2/TRIP12/UBA3/CUL4B/ERCC8/UBE2J2/UBE2A/CUL2/UBE2D1/UBE2E3/SMURF1/CDC27/ANAPC13/ANAPC5/UBR5/DBB1/RCHY1/CUL7/UBE20/PIAS1/PPIL2/UBE3A/CUL5/HERC2/CUL3/NHLRC1/VHL/CDC23/BTRC/FBXW8/BIRC2/BIRC6/CUL4A/PIAS4/TRAF6/HERC4	75

a p<0.05 indicates statistical significance. Statistically significant

Supplement File 4. The data of LncRNA microarray.

P-value and FDR		Fold change and Regulation		Annotations			Group--Raw Intensity		Group--Normalized Intensity		Raw Intensity						Normalized Intensity						
P-value	FDR	Fold Change	Regulation	type	seqname	relations	Associate d_gene_name	group-M1 (raw)	group-M2 (raw)	group-M1 (normalized)	group-M2 (normalized)	[U937-M1-1, M1](raw)	[U937-M1-2, M1](raw)	[U937-M1-3, M1](raw)	[U937-M1-2, M2](raw)	[U937-M1-3, M2](raw)	[U937-M1-1, M1](normalized)	[U937-M1-2, M1](normalized)	[U937-M1-3, M1](normalized)	[U937-M2-1, M2](normalized)	[U937-M2-2, M2](normalized)	[U937-M2-3, M2](normalized)	
2.5662	0.0007	2.4642		noncod				1081.7	4269.9	10.40301	11.70413	1029.916		1280.466									
9E-05	98285	014	down	ing	uc003hrl.1	intergenic		48533	12	1	1	9	934.8625	2	3668.314	4438.904	4702.518	10.373772	10.338708	10.4965515	11.634016	11.743604	11.734772
4.2028	0.0003	2.5933		noncod	ENST0000			2373.2	10108.	11.55855	12.93335	2356.152	2103.607	2659.875		10009.49	10939.56						
7E-07	32251	214	down	ing	0560415	intergenic		11567	78433	7	8	3	2	9377.293	5	5	5	11.578867	11.520314	11.57649	12.952816	12.912685	12.934573
6.5944	0.0011	2.5882		noncod				9.7465	35.146					31.47279			37.22803						
1E-05	84473	38	down	ing	NR_038863	intergenic		66	936	3.521968	4.893938	10.42352	9.203723	9.612455	2	36.73998	5	3.6444488	3.5067835	3.4146712	4.8946333	4.968136	4.819045
0.0001	0.0017	2.4712		noncod	ENST0000	bidirectio		32.057	110.69			28.08492	30.43747		108.2028	106.6654	117.2018						
39873	16782	345	down	ing	0434547	nal	STK24	345	004	5.233518	6.53875	9	5	37.64963	8	05	36	5.0890093	5.270131	5.341414	6.642829	6.481902	6.491519
0.0449	0.0892	2.9028		noncod	HMLincRN			13.637	47.181				11.23162		43.16044		46.66665						
45449	30443	249	down	ing	A921+	intergenic intron		088	555	3.776246	5.313703	6.042284	9	23.63735	2	51.71757	3	2.8500438	3.8060446	4.6726484	5.333574	5.4542084	5.153327
0.0001	0.0016	8.1501		noncod	ENST0000	sense-ove		6.0345	64.977				4.999999	7.155351	54.44042		70.51572						
33579	758	111	down	ing	0445310	rlapping intron	KCNQ5	81	555	2.736288	5.763108	5.948393	5	6	2	69.97652	4	2.8287086	2.3528795	3.0272765	5.6624274	5.8770294	5.749867
0.0001	0.0016	8.1501		noncod	ENST0000	sense-ove		6.0345	64.977				4.999999	7.155351	54.44042		70.51572						
33579	758	111	down	ing	0445310	rlapping intron	KCNQ5	81	555	2.736288	5.763108	5.948393	5	6	2	69.97652	4	2.8287086	2.3528795	3.0272765	5.6624274	5.8770294	5.749867
0.0001	0.0016	8.1501		noncod	ENST0000	sense-ove		6.0345	64.977				4.999999	7.155351	54.44042		70.51572						
33579	758	111	down	ing	0445310	rlapping intron	KCNQ5	81	555	2.736288	5.763108	5.948393	5	6	2	69.97652	4	2.8287086	2.3528795	3.0272765	5.6624274	5.8770294	5.749867
0.0001	0.0016	8.1501		noncod	ENST0000	sense-ove		6.0345	64.977				4.999999	7.155351	54.44042		70.51572						
33579	758	111	down	ing	0445310	rlapping intron	KCNQ5	81	555	2.736288	5.763108	5.948393	5	6	2	69.97652	4	2.8287086	2.3528795	3.0272765	5.6624274	5.8770294	5.749867
0.0001	0.0016	8.1501		noncod	ENST0000	sense-ove		6.0345	64.977				4.999999	7.155351	54.44042		70.51572						
33579	758	111	down	ing	0445310	rlapping intron	KCNQ5	81	555	2.736288	5.763108	5.948393	5	6	2	69.97652	4	2.8287086	2.3528795	3.0272765	5.6624274	5.8770294	5.749867
0.0008	0.0049	2.2078		noncod		natural		54.004	171.04					138.5932	168.4875	206.0533							
22081	82574	253	down	ing	NR_036497	antisense	LPP	237	4723	5.990044	7.13267	47.13774	48.79725	66.07772	9	5	3	5.844401	5.9656796	6.1600523	6.989405	7.1209073	7.2876987
8.9243	0.0013	2.9768		noncod	ENST0000			25.812	108.24			26.87691		28.26438	94.94488		129.9589						
8E-05	79735	369	down	ing	0413311	intergenic		163	4845	4.918667	6.492447	7	22.29519	3	5	99.83067	8	5.021068	4.8108964	4.924037	6.4495635	6.385105	6.6426735
2.3115	0.0007	2.4521		noncod	ENST0000			873.38	3431.4	10.09784	11.39189	813.8710		1034.831	3023.494		3774.761						
2E-05	58104	541	down	ing	0523028			1677	49967	5	5	3	771.4428	2	4	3496.094	5	10.038029	10.051138	10.204368	11.349338	11.40947	11.416876
0.0177	0.0440	2.0032		noncod		sense-ove	APITD1-	86.840	241.46				54.74469	111.5544	226.9637	222.6812	274.7588						
56464	72255	177	down	ing	NR_036462	rlapping exon	CORT	155	7957	6.631547	7.633867	94.22128	4	9	8	4	5	6.842588	6.1327	6.9193544	7.687953	7.510281	7.703366
0.0177	0.0440	2.0032		noncod		sense-ove	APITD1-	86.840	241.46				54.74469	111.5544	226.9637	222.6812	274.7588						
56464	72255	177	down	ing	NR_036462	rlapping exon	CORT	155	7957	6.631547	7.633867	94.22128	4	9	8	4	5	6.842588	6.1327	6.9193544	7.687953	7.510281	7.703366
0.0177	0.0440	2.0032		noncod		sense-ove	APITD1-	86.840	241.46				54.74469	111.5544	226.9637	222.6812	274.7588						
56464	72255	177	down	ing	NR_036462	rlapping exon	CORT	155	7957	6.631547	7.633867	94.22128	4	9	8	4	5	6.842588	6.1327	6.9193544	7.687953	7.510281	7.703366
0.0177	0.0440	2.0032		noncod		sense-ove	APITD1-	86.840	241.46				54.74469	111.5544	226.9637	222.6812	274.7588						
56464	72255	177	down	ing	NR_036462	rlapping exon	APITD1	155	7957	6.631547	7.633867	94.22128	4	9	8	4	5	6.842588	6.1327	6.9193544	7.687953	7.510281	7.703366
2.5590	0.0003	2.3660		noncod		sense-ove		23.002	76.574			22.65916	21.82514			79.35078							
6E-06	67353	326	down	ing	NR_046236	rlapping exon	CMPK2	863	708	4.759054	6.001524	4	6	24.52428	68.11146	4	82.26188	4.7718234	4.7772913	4.728046	5.977593	6.0567675	5.97021
2.5590	0.0003	2.3660		noncod		sense-ove		23.002	76.574			22.65916	21.82514			79.35078							
6E-06	67353	326	down	ing	NR_046236	rlapping exon	CMPK2	863	708	4.759054	6.001524	4	6	24.52428	68.11146	4	82.26188	4.7718234	4.7772913	4.728046	5.977593	6.0567675	5.97021
2.5590	0.0003	2.3660		noncod		sense-ove		23.002	76.574			22.65916	21.82514			79.35078							
6E-06	67353	326	down	ing	NR_046236	rlapping exon	CMPK2	863	708	4.759054	6.001524	4	6	24.52428	68.11146	4	82.26188	4.7718234	4.7772913	4.728046	5.977593	6.0567675	5.97021
0.0392	0.0805	2.3796		noncod				6.9777	21.730			4.999999		6.705812	25.20876		17.93993						
89809	00531	085	down	ing	CR744969	intergenic		45	648	2.934401	4.185126	5	9.227424	5	1	22.04325	2	2.3494408	3.5104606	2.9433026	4.5792	4.2373905	3.7387862
0.0358	0.0751	2.2404	down	noncod	ENST0000	natural	MRPS2	9.8432	28.744	3.432464	4.596229	10.39105	5.576054	13.56254	31.02889	23.66726	31.53608	3.6396437	2.7670274	3.8907197	4.8733153	4.337325	4.5780473

3.9188	0.0009	3.9697		noncod		intronic		52.738	303.36			53.52718	51.40325			336.5515								
E-05	3994	664	down	ing	NR_033897	antisense	EPHA1	494	7457	5.970563	7.959617	53.28504	7	5	285.2255	288.3253	7	6.021994	6.0989413	5.7907543	8.009592	7.8799334	7.9893265	
9.8940	0.0003	3.6476		noncod	ENST0000	intronic		7.2307	36.916			6.698681				41.86835								
7E-07	32251	246	down	ing	0583250	antisense	EFCAB5	91	128	3.095217	4.962174	7.102574	4	7.891119	32.10752	36.77251	5	3.0906076	3.044423	3.150621	4.9216094	4.968952	4.995962	
9.8940	0.0003	3.6476		noncod	ENST0000	natural		7.2307	36.916			6.698681				41.86835								
7E-07	32251	246	down	ing	0583250	antisense	EFCAB5	91	128	3.095217	4.962174	7.102574	4	7.891119	32.10752	36.77251	5	3.0906076	3.044423	3.150621	4.9216094	4.968952	4.995962	
0.0006	0.0043	2.3166		noncod				8.2531	26.698			7.390439			21.96019									
56517	30983	509	down	ing	uc004adp.4	intergenic		89	092	3.275525	4.487566	8.019195	5	9.349932	6	30.7821	27.35198	3.2599874	3.186904	3.3796837	4.3840394	4.7132564	4.3654013	
8.5435	0.0003	3.4332		noncod	ENST0000			107.82	549.97			102.1837	116.9670	498.1540	533.3426	618.4280								
6E-07	32251	17	down	ing	0451149	intergenic		4443	4923	7.011928	8.791489	104.3226	2	1	8	5	4	6.993974	7.0495014	6.99231	8.7924595	8.740712	8.841297	
						exon																		
0.0001	0.0017	2.0039		noncod	ENST0000	sense-ove		40.487	115.05			41.49882			98.33926	112.0404	134.7761							
38102	08048	234	down	ing	0433131	rlapping	HEATR1	538	1935	5.579054	6.581882	5	36.02731	43.93648	4	3	1	5.6554174	5.522148	5.559597	6.500326	6.551972	6.6933465	
0.0001	0.0017	2.0039		noncod	ENST0000	natural		40.487	115.05			41.49882			98.33926	112.0404	134.7761							
38102	08048	234	down	ing	0433131	antisense	LGALS8	538	1935	5.579054	6.581882	5	36.02731	43.93648	4	3	1	5.6554174	5.522148	5.559597	6.500326	6.551972	6.6933465	
0.0001	0.0017	2.0039		noncod	ENST0000	natural		40.487	115.05			41.49882			98.33926	112.0404	134.7761							
38102	08048	234	down	ing	0433131	antisense	LGALS8	538	1935	5.579054	6.581882	5	36.02731	43.93648	4	3	1	5.6554174	5.522148	5.559597	6.500326	6.551972	6.6933465	
0.0001	0.0017	2.0039		noncod	ENST0000	natural		40.487	115.05			41.49882			98.33926	112.0404	134.7761							
38102	08048	234	down	ing	0433131	antisense	LGALS8	538	1935	5.579054	6.581882	5	36.02731	43.93648	4	3	1	5.6554174	5.522148	5.559597	6.500326	6.551972	6.6933465	
0.0001	0.0017	2.0039		noncod	ENST0000	natural		40.487	115.05			41.49882			98.33926	112.0404	134.7761							
38102	08048	234	down	ing	0433131	antisense	LGALS8	538	1935	5.579054	6.581882	5	36.02731	43.93648	4	3	1	5.6554174	5.522148	5.559597	6.500326	6.551972	6.6933465	
0.0004	0.0034	2.0796		noncod	TCONS_00			74.842	224.48			63.57900			181.8180	250.9039								
50973	59524	948	down	ing	019201	intergenic		151	5013	6.464659	7.521031	72.75472	2	88.19273	2	240.7331	2	6.465887	6.3548903	6.5731997	7.3688235	7.621515	7.572754	
7.0169	0.0001	3.5103		noncod		natural	TNFRSF	84.072	429.23							463.0993								
4E-08	15486	579	down	ing	NR_037844	antisense	14	007	0477	6.64075	8.452368	83.73657	76.61976	91.85969	395.0498	429.5423	3	6.6701026	6.620752	6.631396	8.475148	8.439768	8.442189	
0.0047	0.0165	4.2404		noncod	ENST0000			6.2703	32.903			4.999999			4.999999	28.77158	35.62569							
44934	10145	646	down	ing	0447389	intergenic		64	204	2.71369	4.797913	5	8.811092	5	7	34.31233	4	2.3494408	3.4437895	2.3478405	4.7627616	4.8735237	4.7574525	
3.1317	0.0008	2.2227		noncod	TCONS_00			243.30	827.33			228.3984	229.8042	271.7077										
4E-05	59046	135	down	ing	001989	intergenic		348	6467	8.214331	9.366653	7	4	3	797.5721	794.2895	890.1478	8.152609	8.259376	8.231007	9.448804	9.293162	9.357992	
9.9276	0.0003	3.1470		noncod		natural	RNASEH	44.141	200.42						47.56395	174.6853	208.2583							
2E-07	32251	486	down	ing	uc021vdo.1	antisense	1	622	7517	5.710132	7.364131	43.69465	41.16626	7	2	3	218.3389	5.733557	5.718646	5.6781926	7.311791	7.4119263	7.3686767	
						intron																		
0.0357	0.0749	3.6668		noncod	ENST0000	sense-ove		9.2250	38.741			5.692446	4.999999		24.54413	47.73418								
23567	90684	762	down	ing	0416076	rlapping	VCL	22	413	3.108345	4.982896	7	5	16.98262	2	43.94592	8	2.7693734	2.3528795	4.2027817	4.543318	5.2198253	5.185546	
						intron																		
0.0357	0.0749	3.6668		noncod	ENST0000	sense-ove		9.2250	38.741			5.692446	4.999999		24.54413	47.73418								
23567	90684	762	down	ing	0416076	rlapping	VCL	22	413	3.108345	4.982896	7	5	16.98262	2	43.94592	8	2.7693734	2.3528795	4.2027817	4.543318	5.2198253	5.185546	
						exon																		
0.0014	0.0070	2.5188		noncod		sense-ove		44.661	158.47			53.24257			46.47352	139.2242	178.0018							
25562	8064	676	down	ing	NR_034039	rlapping	SORD	394	0273	5.704206	7.036981	7	34.26808	6	6	158.1847	6	6.0206165	5.448952	5.643049	6.9951267	7.0305033	7.0853133	
1.3019	0.0006	3.2584		noncod				7.1447	32.729			7.339312												
4E-05	13906	682	down	ing	NR_038378	intergenic		98	503	3.08386	4.788054	6	6.695949	7.399131	28.59355	35.17081	34.42415	3.1377585	3.0435169	3.0703037	4.7528553	4.9036856	4.70762	
0.0011	0.0060	2.6189		noncod		bidirectio		40.857	150.33			32.17753			46.49368	141.6233	138.4482	170.9301						
32761	76647	475	down	ing	uc002iil.3	nal	FMNL1	285	391	5.577673	6.96666	2	43.90064	3	7	1	5	5.2797375	5.8093057	5.643976	7.018398	6.851829	7.0297537	
0.0019	0.0089	2.1265		noncod	ENST0000			41.559	124.01			39.95480	32.39145	52.33172	100.0423	142.7879								
94421	32953	628	down	ing	0545923	intergenic		329	3455	5.594414	6.682938	7	7	2	05	129.2101	6	5.601924	5.3657794	5.81554	6.526972	6.7498198	6.772022	
0.0001	0.0018	4.0883		noncod	ENST0000	intronic		23.899	135.33						30.29327	130.7359	128.8787	146.4045						
55466	2573	023	down	ing	0411949	antisense	NAB1	911	9757	4.786819	6.818321	19.5316	21.87486	4	3	8	6	4.5481987	4.7817445	5.0305147	6.899744	6.74662	6.8085995	
						intron																		
0.0001	0.0016	2.1448		noncod		sense-ove		103.50	321.53			103.5166			121.2528	291.2723	349.2617							
34471	81257	997	down	ing	uc001zhh.2	rlapping	SCG5	1673	154	6.939887	8.040797	8	85.73552	2	4	324.0605	8	6.981347	6.791881	7.0464334	8.041466	8.040053	8.040873	
						intron																		
0.0001	0.0016	2.1448		noncod		sense-ove		103.50	321.53			103.5166			121.2528	291.2723	349.2617							
34471	81257	997	down	ing	uc001zhh.2	rlapping	SCG5	1673	154	6.939887	8.040797	8	85.73552	2	4	324.0605	8	6.981347	6.791881	7.0464334	8.041466	8.040053	8.040873	
0.0033	0.0128	2.4901		noncod	ENST0000			19.449	66.612			24.41247			19.37664	59.53627	70.95759	69.34389						
33086	06241	118	down	ing	0573220	intergenic		224	59	4.485813	5.802024	6	14.55855	6	8	6	5	4.8770204	4.1868896	4.39353	5.785018	5.8953586	5.725695	
0.0054	0.0181	3.9334		noncod		natural		11.164	56.620			10.70619			16.52639	50.59296	58.92474							
03441	1889	981	down	ing	NR_040093	antisense	NREP	94	759	3.595554	5.571367	9	6.262227	4	4	60.34457	4	3.6861372	2.937103	4.1634226	5.557795	5.667175	5.4891315	
0.0054	0.0181	3.9334		noncod		natural		11.164	56.620			10.70619			16.52639	50.59296	58.92474							
03441	1889	981	down	ing	NR_040093	antisense	NREP	94	759	3.595554	5.571367	9	6.262227	4	4	60.34457	4	3.6861372	2.937103	4.1634226	5.557795	5.667175	5.4891315	
0.0054	0.0181	3.9334		noncod		natural		11.164	56.620			10.70619			16.52639	50.59296	58.92474							
03441	1889	981	down	ing	NR_040093	antisense	NREP	94	759	3.595554	5.571367													

03441	1889	981		ing		antisense		94	759			9		4	4			4					
0.0054	0.0181	3.9334		noncod		natural		11.164	56.620			10.70619		16.52639	50.59296			58.92474					
03441	1889	981	down	ing	NR_040093	antisense	NREP	94	759	3.595554	5.571367	9	6.262227	4	4	60.34457	4	3.6861372	2.937103	4.1634226	5.557795	5.667175	5.4891315
0.0054	0.0181	3.9334		noncod		natural		11.164	56.620			10.70619		16.52639	50.59296			58.92474					
03441	1889	981	down	ing	NR_040093	antisense	NREP	94	759	3.595554	5.571367	9	6.262227	4	4	60.34457	4	3.6861372	2.937103	4.1634226	5.557795	5.667175	5.4891315
0.0054	0.0181	3.9334		noncod		natural		11.164	56.620			10.70619		16.52639	50.59296			58.92474					
03441	1889	981	down	ing	NR_040093	antisense	NREP	94	759	3.595554	5.571367	9	6.262227	4	4	60.34457	4	3.6861372	2.937103	4.1634226	5.557795	5.667175	5.4891315
0.0054	0.0181	3.9334		noncod		natural		11.164	56.620			10.70619		16.52639	50.59296			58.92474					
03441	1889	981	down	ing	NR_040093	antisense	NREP	94	759	3.595554	5.571367	9	6.262227	4	4	60.34457	4	3.6861372	2.937103	4.1634226	5.557795	5.667175	5.4891315
0.0054	0.0181	3.9334		noncod		natural		11.164	56.620			10.70619		16.52639	50.59296			58.92474					
03441	1889	981	down	ing	NR_040093	antisense	NREP	94	759	3.595554	5.571367	9	6.262227	4	4	60.34457	4	3.6861372	2.937103	4.1634226	5.557795	5.667175	5.4891315
0.0054	0.0181	3.9334		noncod		natural		11.164	56.620			10.70619		16.52639	50.59296			58.92474					
03441	1889	981	down	ing	NR_040093	antisense	STARD4	94	759	3.595554	5.571367	9	6.262227	4	4	60.34457	4	3.6861372	2.937103	4.1634226	5.557795	5.667175	5.4891315
0.0017	0.0081	2.2812		noncod	ENST0000	natural		21.570	67.142			18.98577		28.36309	62.06432								
50483	40443	897	down	ing	0422153	antisense	RFX5	278	191	4.626523	5.816373	1	17.36197	4	3	70.21018	69.15207	4.5055556	4.444511	4.9295034	5.844524	5.883112	5.721483
0.0017	0.0081	2.2812		noncod	ENST0000	natural		21.570	67.142			18.98577		28.36309	62.06432								
50483	40443	897	down	ing	0422153	antisense	RFX5	278	191	4.626523	5.816373	1	17.36197	4	3	70.21018	69.15207	4.5055556	4.444511	4.9295034	5.844524	5.883112	5.721483
4.2790	0.0009	3.7695		noncod	ENST0000	intronic		22.933				4.999999	4.999999	4.999999	19.67062	20.21757	28.91372						
8E-05	67147	285	down	ing	0556874	antisense	GPHN	5	975	2.350054	4.264438	5	5	5	4	7	3	2.3494408	2.3528795	2.3478405	4.231636	4.111099	4.450578
4.2790	0.0009	3.7695		noncod	ENST0000	intronic		22.933				4.999999	4.999999	4.999999	19.67062	20.21757	28.91372						
8E-05	67147	285	down	ing	0556874	antisense	GPHN	5	975	2.350054	4.264438	5	5	5	4	7	3	2.3494408	2.3528795	2.3478405	4.231636	4.111099	4.450578
0.0016	0.0078	2.1546		noncod	ENST0000			18.304	54.653			15.35758	17.94630	21.60894	56.90236	49.61345							
52941	11303	996	down	ing	0563377			279	075	4.416253	5.52374	9	6	2	3	3	57.44341	4.2069507	4.4933023	4.5485067	5.7241783	5.393774	5.4532676
0.0006	0.0044	3.3616		noncod	ENST0000	intronic		11.551	53.101			13.12810		13.10443	48.31978	54.51217	56.47266						
75983	05718	468	down	ing	0454380	antisense	C5orf56	341	541	3.733981	5.483149	9	8.421474	9	2	3	8	3.9783065	3.3801665	3.84347	5.4907575	5.529472	5.429218
0.0006	0.0044	3.3616		noncod	ENST0000	intronic		11.551	53.101			13.12810		13.10443	48.31978	54.51217	56.47266						
75983	05718	468	down	ing	0454380	antisense	C5orf56	341	541	3.733981	5.483149	9	8.421474	9	2	3	8	3.9783065	3.3801665	3.84347	5.4907575	5.529472	5.429218
0.0006	0.0044	3.3616		noncod	ENST0000	intronic		11.551	53.101			13.12810		13.10443	48.31978	54.51217	56.47266						
75983	05718	468	down	ing	0454380	antisense	C5orf56	341	541	3.733981	5.483149	9	8.421474	9	2	3	8	3.9783065	3.3801665	3.84347	5.4907575	5.529472	5.429218
0.0006	0.0044	3.3616		noncod	ENST0000	intronic		11.551	53.101			13.12810		13.10443	48.31978	54.51217	56.47266						
75983	05718	468	down	ing	0454380	antisense	C5orf56	341	541	3.733981	5.483149	9	8.421474	9	2	3	8	3.9783065	3.3801665	3.84347	5.4907575	5.529472	5.429218
5.4008	0.0004	3.6296		noncod	TCONS_00			89.885	477.22				77.55453	100.3999	417.5123								
7E-06	45438	224	down	ing	008952	intergenic		55	7853	6.735097	8.594917	91.70219	5	25	6	499.1222	515.049	6.804621	6.639413	6.7612576	8.545616	8.646338	8.592796
0.0044	0.0158	2.8318		noncod	ENST0000	natural	SLC25A1	8.0829	31.382						25.53610	30.63584	37.97614						
90951	67327	261	down	ing	0443935	antisense	8	46	698	3.21516	4.716893	5.563613	9.596536	9.088689	6	1	7	2.7320914	3.5703702	3.3430183	4.5982323	4.705322	4.8471236
0.0127	0.0343	2.0319		noncod		sense-ove		8.7341	24.908						26.87909	26.81891							
14035	39084	406	down	ing	NR_036633	rlapping	VAPB	47	847	3.363273	4.386131	9.901275	8.156075	8.145091	3	8	21.02853	3.5661576	3.3295407	3.1941197	4.6699457	4.5170274	3.9714196
0.0127	0.0343	2.0319		noncod		sense-ove		8.7341	24.908						26.87909	26.81891							
14035	39084	406	down	ing	NR_036633	rlapping	VAPB	47	847	3.363273	4.386131	9.901275	8.156075	8.145091	3	8	21.02853	3.5661576	3.3295407	3.1941197	4.6699457	4.5170274	3.9714196
0.0007	0.0046	4.8293		noncod	ENST0000			5.5678	34.433			4.999999		4.999999		33.66362	41.51729						
29558	18154	167	down	ing	0452402	intergenic		49	773	2.580887	4.852706	5	6.703549	5	28.1204	8	2	2.3494408	3.0453799	2.3478405	4.7329044	4.8444076	4.9808064
0.0004	0.0032	2.0014		noncod	ENST0000	bidirectio	ERCC6L	98.954	287.03			104.3028		110.3303	244.8017	307.0070	309.2998						
00768	16094	85	down	ing	0427259	nal	2	507	6217	6.875658	7.876729	1	82.23035	6	6	2	7	6.993661	6.7299	6.903414	7.797011	7.966799	7.8663774
0.0003	0.0031	5.8996		noncod	ENST0000			9.8193	78.360				6.926466			83.69318							
79063	01019	848	down	ing	0436551	intergenic		76	835	3.471934	6.032572	9.126652	5	13.40501	69.03587	4	82.35345	3.444596	3.0944822	3.8767238	5.99771	6.128417	5.9715886
4.1091	0.0004	3.1108		noncod	ENST0000			195.89	933.03			196.8106	171.0016	219.8828		1014.416							
6E-06	1588	938	down	ing	0442067	intergenic		8397	1433	7.887532	9.524862	7	3	9	810.8729	973.8045	9	7.9261885	7.8115125	7.924896	9.473179	9.5690365	9.532369
3.0824	0.0008	2.7553		noncod	TCONS_00	sense-ove	RP11-73	36.800	143.08			32.60212	35.95380	41.84490	129.5316		154.4713						
6E-05	55922	511	down	ing	011946	rlapping	O6.4	279	0017	5.435716	6.897952	3	8	6	6	145.237	9	5.298253	5.5186825	5.490212	6.8879113	6.917085	6.8888597
0.0030	0.0118	2.1038		noncod	ENST0000	natural		11.618	33.853						29.98384	39.15006	32.42531						
06837	62229	401	down	ing	0547042	antisense	FKBP4	512	076	3.757699	4.830724	9.732487	11.27843	13.84462	9	3	6	3.5431156	3.8121052	3.9178748	4.8225117	5.049631	4.620028
2.5297	0.0007	2.4478		noncod	ENST0000	bidirectio		107.04	382.74					125.4458	349.6921	373.5778	424.9532						
8E-05	92371	965	down	ing	0528692	nal	LRRRC8C	6942	109	6.992967	8.28451	98.49023	97.20478	16	7	8	2	6.908799	6.9762917	7.0938106	8.289558	8.242472	8.321499
2.7305	0.0008	3.1108		noncod	ENST0000			95.797	437.05				84.37775	110.9000	372.9489	479.3133	458.8955						
E-05	27901	285	down	ing	0434661	intergenic		148	26	6.83038	8.467679	92.11361	4	8	4	2	4	6.8109407	6.769559	6.9106407	8.384217	8.591843	8.426977
0.0255	0.0581	2.2857		noncod	ENST0000			28.149	86.427			16.70526		33.91219									
04945	0262	95	down	ing	0579301	intergenic		061	5	4.983742	6.176438	1	33.82973	3	82.49816	77.92195	98.86239	4.325797	5.429393	5.196035	6.25048	6.032934	6.245899
0.0057	0.0189	2.8697		noncod		natural		10.159	38.815			11.87475		12.25204	37.22733	37.38753	41.83215						
54004	79307	649	down	ing	uc010beg.1	antisense	SLC30A4	914	674	3.514855	5.035788	1	6.352941	9	3	5	3	3					

0.0024	0.0101	2.5343		noncod	ENST0000			46.741	166.04			35.56189			170.0614	167.9241	160.1399								
02371	52317	5	down	ing	0567401	intergenic	HEATR5	894	187	5.768282	7.109898	3	48.63437	56.02942	8	5	8	5.427608	5.96122	5.9160194	7.2740216	7.117118	6.9385552		
0.0004	0.0032	2.5766		noncod	ENST0000	natural		26.369	94.373			26.22827		31.60089	94.86555										
13182	80729	11	down	ing	0551799	antisense	A	695	702	4.940243	6.305718	1	21.27992	5	5	90.56949	97.68606	4.9866333	4.741627	5.09247	6.448612	6.240159	6.2283835		
0.0001	0.0020	2.4992		noncod	ENST0000	natural		46.889	167.37			50.83503		49.04449	154.8252	189.3204									
88908	30877	17	down	ing	0452431	antisense	PCBP1	461	0313	5.794417	7.115893	7	40.78885	5	157.9653	1	3	5.957259	5.7046013	5.7213893	7.170998	7.0004797	7.1762004		
0.0001	0.0016	4.1452		noncod	ENST0000			38.405	228.82						205.7202	213.5446									
3612	97185	372	down	ing	0567068	intergenic		043	3613	5.500356	7.55181	32.97234	41.91557	40.32722	1	3	267.206	5.315956	5.746097	5.4390135	7.543829	7.4463515	7.66525		
4.4829	0.0009	2.8335		noncod		sense-ove		42.242	171.71			42.64312			156.4322	162.3099	196.4042								
8E-05	92889	67	down	ing	NR_033746	rlapping	DMKN	316	5497	5.647934	7.150553	7	41.44164	42.64218	8	4	7	5.694929	5.7290273	5.519846	7.1568694	7.069551	7.2252398		
4.4829	0.0009	2.8335		noncod		sense-ove		42.242	171.71			42.64312			156.4322	162.3099	196.4042								
8E-05	92889	67	down	ing	NR_033746	rlapping	DMKN	316	5497	5.647934	7.150553	7	41.44164	42.64218	8	4	7	5.694929	5.7290273	5.519846	7.1568694	7.069551	7.2252398		
4.4829	0.0009	2.8335		noncod		sense-ove		42.242	171.71			42.64312			156.4322	162.3099	196.4042								
8E-05	92889	67	down	ing	NR_033746	rlapping	DMKN	316	5497	5.647934	7.150553	7	41.44164	42.64218	8	4	7	5.694929	5.7290273	5.519846	7.1568694	7.069551	7.2252398		
4.4829	0.0009	2.8335		noncod		sense-ove		42.242	171.71			42.64312			156.4322	162.3099	196.4042								
8E-05	92889	67	down	ing	NR_033746	rlapping	DMKN	316	5497	5.647934	7.150553	7	41.44164	42.64218	8	4	7	5.694929	5.7290273	5.519846	7.1568694	7.069551	7.2252398		
4.4829	0.0009	2.8335		noncod		sense-ove		42.242	171.71			42.64312			156.4322	162.3099	196.4042								
8E-05	92889	67	down	ing	NR_033746	rlapping	DMKN	316	5497	5.647934	7.150553	7	41.44164	42.64218	8	4	7	5.694929	5.7290273	5.519846	7.1568694	7.069551	7.2252398		
4.4829	0.0009	2.8335		noncod		sense-ove		42.242	171.71			42.64312			156.4322	162.3099	196.4042								
8E-05	92889	67	down	ing	NR_033746	rlapping	DMKN	316	5497	5.647934	7.150553	7	41.44164	42.64218	8	4	7	5.694929	5.7290273	5.519846	7.1568694	7.069551	7.2252398		
4.4829	0.0009	2.8335		noncod		sense-ove		42.242	171.71			42.64312			156.4322	162.3099	196.4042								
8E-05	92889	67	down	ing	NR_033746	rlapping	DMKN	316	5497	5.647934	7.150553	7	41.44164	42.64218	8	4	7	5.694929	5.7290273	5.519846	7.1568694	7.069551	7.2252398		
0.0395	0.0809	2.0523		noncod	TCONS_00			13.778	37.086					19.79115	36.41490	31.74657	43.09710								
69237	17368	716	down	ing	018558	intergenic		808	197	3.926641	4.963933	8.269676	13.27559	9	6	8	7	3.3053422	4.0502133	4.424368	5.0908093	4.759735	5.041255		
0.0049	0.0171	3.4588		noncod	ENST0000	natural		56.540	261.87				38.99296		235.9108	288.5317	261.1685								
96121	20911	119	down	ing	0425290	antisense	ADO	722	0393	5.962016	7.752293	41.68103	6	88.94817	9	7	2	5.6612396	5.639869	6.58494	7.7453327	7.8805456	7.631		
0.0025	0.0106	3.5447		noncod	ENST0000	intronic		5.8861	25.750			4.999999	4.999999		19.88254	28.13669	29.23161								
75632	75194	276	down	ing	0422204	antisense	C5orf56	73	286	2.604979	4.430654	5	5	7.658519	2	8	7	2.3494408	2.3528795	3.112616	4.244882	4.5809593	4.4661193		
0.0025	0.0106	3.5447		noncod	ENST0000	intronic		5.8861	25.750			4.999999	4.999999		19.88254	28.13669	29.23161								
75632	75194	276	down	ing	0422204	antisense	C5orf56	73	286	2.604979	4.430654	5	5	7.658519	2	8	7	2.3494408	2.3528795	3.112616	4.244882	4.5809593	4.4661193		
0.0025	0.0106	3.5447		noncod	ENST0000	intronic		5.8861	25.750			4.999999	4.999999		19.88254	28.13669	29.23161								
75632	75194	276	down	ing	0422204	antisense	C5orf56	73	286	2.604979	4.430654	5	5	7.658519	2	8	7	2.3494408	2.3528795	3.112616	4.244882	4.5809593	4.4661193		
0.0179	0.0443	2.6875		noncod		natural		12.199	42.769			6.801275		16.73576		39.13875	46.97263								
61698	99041	18	down	ing	NR_027334	antisense	MZF1	014	185	3.745077	5.171351	3	13.06	7	42.19617	2	3	3.028495	4.0259337	4.1808014	5.3011208	5.049034	5.1638985		
0.0179	0.0443	2.6875		noncod		natural		12.199	42.769			6.801275		16.73576		39.13875	46.97263								
61698	99041	18	down	ing	NR_027334	antisense	MZF1	014	185	3.745077	5.171351	3	13.06	7	42.19617	2	3	3.028495	4.0259337	4.1808014	5.3011208	5.049034	5.1638985		
0.0179	0.0443	2.6875		noncod		natural		12.199	42.769			6.801275		16.73576		39.13875	46.97263								
61698	99041	18	down	ing	NR_027334	antisense	MZF1	014	185	3.745077	5.171351	3	13.06	7	42.19617	2	3	3.028495	4.0259337	4.1808014	5.3011208	5.049034	5.1638985		
0.0005	0.0037	2.6727		noncod				193.96	774.53				151.8393	246.7876											
26024	91057	502	down	ing	NR_026885	intergenic		191	9267	7.850196	9.268521	183.2587	9	4	660.3851	811.3903	851.8424	7.824573	7.634449	8.091566	9.184458	9.327621	9.293484		
0.0004	0.0035	7.2133		noncod	ENST0000	intronic		13.634	130.93			11.61304			126.9216	127.2108									
63716	08194	504	down	ing	0518880	antisense	FABP5	445	8027	3.923579	6.774249	1	9.349904	19.94039	9	9	138.6815	3.804884	3.530779	4.4350753	6.8619614	6.7289724	6.731813		
0.0176	0.0438	2.0650		noncod		natural		20.780	57.135					30.38160		62.34634	54.42390								
69755	81104	972	down	ing	NR_038953	antisense	LRP8	548	386	4.540574	5.586784	16.16828	15.79176	3	54.63591	4	4	4.280131	4.306189	5.0354033	5.6675634	5.714142	5.378647		
0.0176	0.0438	2.0650		noncod		natural		20.780	57.135					30.38160		62.34634	54.42390								
69755	81104	972	down	ing	NR_038953	antisense	MAGOH	548	386	4.540574	5.586784	16.16828	15.79176	3	54.63591	4	4	4.280131	4.306189	5.0354033	5.6675634	5.714142	5.378647		
0.0176	0.0438	2.0650		noncod		natural		20.780	57.135					30.38160		62.34634	54.42390								
69755	81104	972	down	ing	NR_038953	antisense	LRP8	548	386	4.540574	5.586784	16.16828	15.79176	3	54.63591	4	4	4.280131	4.306189	5.0354033	5.6675634	5.714142	5.378647		
0.0176	0.0438	2.0650		noncod		natural		20.780	57.135					30.38160		62.34634	54.42390								
69755	81104	972	down	ing	NR_038953	antisense	LRP8	548	386	4.540574	5.586784	16.16828	15.79176	3	54.63591	4	4	4.280131	4.306189	5.0354033	5.6675634	5.714142	5.378647		
0.0176	0.0438	2.0650		noncod		natural		20.780	57.135					30.38160		62.34634	54.42390								
69755	81104	972	down	ing	NR_038953	antisense	LRP8	548	386	4.540574	5.586784	16.16828	15.79176	3	54.63591	4	4	4.280131	4.306189	5.0354033	5.6675634	5.714142	5.378647		
0.0176	0.0438	2.0650		noncod		natural		20.780	57.135					30.38160		62.34634	54.42390								
69755	81104	972	down	ing	NR_038953	antisense	LRP8	548	386	4.540574	5.586784	16.16828	15.79176	3	54.63591	4	4	4.280131	4.306189	5.0354033	5.6675634	5.714142	5.378647		

42779	51886	226		ing		antisense		589	0297			8			7	8	4						
0.0003	0.0029	2.0202		noncod				13.765	39.178				13.16755	14.71770	31.01331	38.96557							
4843	37506	802	down	ing	NR_026788	intergenic		872	46	4.017445	5.032	13.41235	9	8	5	6	47.55649	4.009138	4.036271	4.0069256	4.8721027	5.043382	5.180516
0.0193	0.0469	2.7666		noncod	TCONS_00			10.893	38.614				5.709855		36.81799	40.37468							
3884	69461	33	down	ing	010939	intergenic		379	088	3.557505	5.025636	11.77848	6	15.1918	7	38.64958	7	3.8247697	2.7988997	4.0488453	5.1060705	5.031788	4.93905
9.2125	0.0014	2.2954		noncod		natural	TRNAU1	615.78	2254.3				10.79591	553.5503		693.1950	2064.121	2145.686	2553.288				
4E-05	02723	908	down	ing	uc001bqn.3	antisense	AP	184	657	9.597116	9	5	600.6001	7	8	5	8	9.474893	9.68783	9.628625	10.816121	10.717035	10.8546
0.0004	0.0036	3.4357		noncod	ENST0000	natural		46.856	228.53				36.33818		58.95102	203.3199	214.2563	268.0323					
88573	33673	421	down	ing	0541940	antisense	SSPN	512	622	5.767752	7.548373	4	45.28033	3	9	5	2	5.4588933	5.854325	5.9900365	7.524916	7.4508944	7.6693096
0.0004	0.0036	3.4357		noncod	ENST0000	natural		46.856	228.53				36.33818		58.95102	203.3199	214.2563	268.0323					
88573	33673	421	down	ing	0541940	antisense	SSPN	512	622	5.767752	7.548373	4	45.28033	3	9	5	2	5.4588933	5.854325	5.9900365	7.524916	7.4508944	7.6693096
0.0001	0.0018	2.9695		noncod	ENST0000	intronic		34.885	145.77				35.36892		142.0892	141.5231	153.7216						
58973	43399	616	down	ing	0514270	antisense	OCLN	169	7997	5.35795	6.9282	29.40133	7	39.88525	3	3	3	5.1554294	5.496031	5.42239	7.0221663	6.880668	6.881766
0.0001	0.0018	2.9695		noncod	ENST0000	intronic		34.885	145.77				35.36892		142.0892	141.5231	153.7216						
58973	43399	616	down	ing	0514270	antisense	OCLN	169	7997	5.35795	6.9282	29.40133	7	39.88525	3	3	3	5.1554294	5.496031	5.42239	7.0221663	6.880668	6.881766
9.6932	0.0005	2.1574		noncod		sense-ove		208.50	682.79				199.2392	187.8215	238.4525		738.0328						
2E-06	49154	959	down	ing	NR_046106	rlapping	NOL8	447	4913	7.979391	9.088749	6	6	9	600.9877	709.3642	4	7.9454165	7.949214	8.043543	9.048321	9.128879	9.089047
9.6932	0.0005	2.1574		noncod		sense-ove		208.50	682.79				199.2392	187.8215	238.4525		738.0328						
2E-06	49154	959	down	ing	NR_046106	rlapping	NOL8	447	4913	7.979391	9.088749	6	6	9	600.9877	709.3642	4	7.9454165	7.949214	8.043543	9.048321	9.128879	9.089047
9.6932	0.0005	2.1574		noncod		natural		208.50	682.79				199.2392	187.8215	238.4525		738.0328						
2E-06	49154	959	down	ing	NR_046106	antisense	CENPP	447	4913	7.979391	9.088749	6	6	9	600.9877	709.3642	4	7.9454165	7.949214	8.043543	9.048321	9.128879	9.089047
0.0003	0.0029	2.1590		noncod	ENST0000	bidirectio		43.677	133.50				38.72342	45.63911		127.3476	129.6579	143.5150					
56616	87585	953	down	ing	0444410	nal	PCBP1	209	6918	5.689894	6.800321	3	4	46.66909	94	7	9	5.5530186	5.8668146	5.6498494	6.8666854	6.755043	6.779235
6.1286	0.0004	2.2450		noncod		natural	FAM211	1190.0	4286.6	10.54483			1187.039	1071.650	1311.533	3746.615	4546.697	4566.622					
4E-06	7214	979	down	ing	NR_027170	antisense	A	745	45133	2	11.71161	3	3	9	5	3	6	10.571324	10.530873	10.532299	11.662023	11.778482	11.694326
6.1286	0.0004	2.2450		noncod		natural	FAM211	1190.0	4286.6	10.54483			1187.039	1071.650	1311.533	3746.615	4546.697	4566.622					
4E-06	7214	979	down	ing	NR_027170	antisense	A	745	45133	2	11.71161	3	3	9	5	3	6	10.571324	10.530873	10.532299	11.662023	11.778482	11.694326
0.0001	0.0015	2.1762		noncod		intronic	FAM211	930.65	3247.2	10.18700			951.1203		1062.526		3464.060	3478.498					
1868	73059	475	down	ing	NR_045025	antisense	A	5487	21533	7	11.30885	6	778.3199	2	2799.106	3	3	10.253954	10.065527	10.24154	11.240263	11.39223	11.294056
0.0001	0.0015	2.1762		noncod		intronic	FAM211	930.65	3247.2	10.18700			951.1203		1062.526		3464.060	3478.498					
1868	73059	475	down	ing	NR_045025	antisense	A	5487	21533	7	11.30885	6	778.3199	2	2799.106	3	3	10.253954	10.065527	10.24154	11.240263	11.39223	11.294056
0.0010	0.0059	3.6705		noncod	TCONS_00			5.8584	28.645				4.999999	5.755028		24.95868	36.18377						
96786	7	541	down	ing	013515	intergenic		25	539	2.707761	4.583759	6.820246	5	7	24.79416	3	3	3.0323143	2.3528795	2.7380893	4.558418	4.4150963	4.7777624
0.0219	0.0517	2.2938		noncod	ENST0000	natural		9.5120	28.264				5.673619	13.79826	24.27641		30.72284						
48071	78458	282	down	ing	0534988	antisense	NUDT22	57	145	3.378894	4.576651	9.064284	3	8	3	29.79318	3	3.4339576	2.788996	3.9137275	4.5273366	4.6670685	4.535548
0.0219	0.0517	2.2938		noncod	ENST0000	natural		9.5120	28.264				5.673619	13.79826	24.27641		30.72284						
48071	78458	282	down	ing	0534988	antisense	NUDT22	57	145	3.378894	4.576651	9.064284	3	8	3	29.79318	3	3.4339576	2.788996	3.9137275	4.5273366	4.6670685	4.535548
0.0219	0.0517	2.2938		noncod	ENST0000	natural		9.5120	28.264				5.673619	13.79826	24.27641		30.72284						
48071	78458	282	down	ing	0534988	antisense	DNAJC4	57	145	3.378894	4.576651	9.064284	3	8	3	29.79318	3	3.4339576	2.788996	3.9137275	4.5273366	4.6670685	4.535548
0.0219	0.0517	2.2938		noncod	ENST0000	natural		9.5120	28.264				5.673619	13.79826	24.27641		30.72284						
48071	78458	282	down	ing	0534988	antisense	NUDT22	57	145	3.378894	4.576651	9.064284	3	8	3	29.79318	3	3.4339576	2.788996	3.9137275	4.5273366	4.6670685	4.535548
0.0175	0.0436	2.1555		noncod	ENST0000			44.447	132.08				32.34224		142.9837	142.0911	111.1828						
51099	58298	414	down	ing	0439157	intergenic		829	5883	5.669386	6.777437	7	40.33211	60.66913	2	1	2	5.286143	5.689642	6.0323744	7.0291524	6.8865294	6.4166284
7.5168	0.0012	2.0631		noncod				948.97	3169.4	10.22479	11.26966	858.7229		1094.419	2751.925	3271.164	3485.163						
E-05	57709	761	down	ing	uc010lcl.3	intergenic		002	179	8	5	6	893.7675	6	5	6	6	10.11333	10.27216	10.288905	11.213822	11.299354	11.29582
0.0003	0.0030	3.1425		noncod	ENST0000	natural	TRNAU1	24.892	110.30				23.66432	23.08717	105.6754								
6798	43618	779	down	ing	0464612	antisense	AP	008	3105	4.875806	6.527754	27.92452	6	7	15	99.4246	125.8093	5.0812244	4.90541	4.640783	6.6110206	6.379003	6.5932393
0.0006	0.0042	3.4121		noncod		natural		23.128	110.83				28.10436	19.64899	21.63070		107.0169						
43579	78864	913	down	ing	NR_001459	antisense	GLRX5	019	3923	4.755832	6.52653	2	3	1	93.54646	1	131.9384	5.090216	4.627254	4.5500245	6.4270477	6.486173	6.6663694
0.0005	0.0040	2.4475		noncod	ENST0000	sense-ove		18.990	64.427				15.28125		53.16488	68.49682							
90505	58656	852	down	ing	0569353	rlapping	VPS35	85	851	4.458813	5.750172	18.34972	1	23.34158	6	6	71.62184	4.460173	4.25995	4.6563168	5.6312833	5.8476267	5.771607
0.0210	0.0501	2.7170		noncod	ENST0000	natural		6.3698	21.273				4.999999		20.06227	22.45427	21.30424						
69732	22791	491	down	ing	0433905	antisense	ZBTB46	39	601	2.729332	4.171373	5	9.109519	5	9	5	9	2.3494408	3.490716	2.3478405	4.257619	4.264249	3.9922512
0.0306	0.0669	2.5972		noncod	ENST0000	intronic		7.4416	25.649				8.644073		4.999999	29.77104	25.71864	21.46012					
7649	35902	337	down	ing	0585088	antisense	ANK1	47	94	3.04613	4.423106	5	8.680868	5	2	9	9	3.3682942	3.422255	2.3478405	4.8107142	4.456415	4.002188
0.0306	0.0669	2.5972		noncod	ENST0000	intronic		7.4416	25.649				8.644073		4.999999	29.77104	25.71864	21.46012					
7649	35902	337	down	ing	0585088	antisense	ANK1	47	94	3.04613	4.423106	5	8.680868	5	2	9	9	3.3682942	3.422255	2.3478405	4.8107142	4.456415	4.002188
0.0306	0.0669	2.5972		noncod	ENST0000	intronic		7.4416	25.649				8.644073		4.999999	29.77104	25.71864	21.46012					
7649	35902	337	down	ing	0585088	antisense	ANK1	47	94	3.04613	4.4231												

7.4379	0.0012	2.4458		noncod		natural	KIAA091	118.15	423.56			104.7522	109.2950	140.4292	380.8243	430.2962							
7E-05	50298	366	down	ing	NR_038357	antisense	3	8857	4567	7.13901	8.429338	8	1	8	4	6	459.5731	7.0009336	7.1505475	7.2655478	8.416065	8.443575	8.428373
7.4379	0.0012	2.4458		noncod		natural	KIAA091	118.15	423.56			104.7522	109.2950	140.4292	380.8243	430.2962							
7E-05	50298	366	down	ing	NR_038357	antisense	3	8857	4567	7.13901	8.429338	8	1	8	4	6	459.5731	7.0009336	7.1505475	7.2655478	8.416065	8.443575	8.428373
9.3414	0.0014	2.0188		noncod		sense-ove		95.011	279.02						103.1822	242.7755		291.1341					
3E-05	08434	969	down	ing	NR_030774	lapping	UPRT	78	637	6.825607	7.839174	90.21283	91.64028	3	9	303.1694	2	6.781271	6.891142	6.8044086	7.784679	7.9485216	7.7843227
0.0061	0.0198	2.0624		noncod	ENST0000	sense-ove	TIMM23	57.833	166.54					40.74430		152.7428	160.4594	186.4338					
13664	49673	307	down	ing	0429104	lapping	B	885	5367	6.066485	7.11083	68.06136	5	64.69599	4	1	5	6.369539	5.7028594	6.127056	7.126536	7.050896	7.1550593
0.0067	0.0214	2.0537		noncod	ENST0000			28.570	80.486			34.04797	20.26795	31.39611	75.30949		86.02109						
88202	62385	069	down	ing	0502249			682	443	5.039305	6.077535	4	8	4	4	80.12874	5	5.3617816	4.672024	5.084108	6.124164	6.0712924	6.037148
3.5512	0.0004	2.9035		noncod	ENST0000	bidirectio		182.27	805.56			181.7082	172.1732	192.9581			900.5329						
6E-06	05245	315	down	ing	0436656	nal	ZBTB37	9883	612	7.788129	9.325938	7	5	3	701.9317	814.2337	6	7.813784	7.821701	7.728903	9.270519	9.330796	9.376499
3.5512	0.0004	2.9035		noncod	ENST0000	bidirectio		182.27	805.56			181.7082	172.1732	192.9581			900.5329						
6E-06	05245	315	down	ing	0436656	nal	ZBTB37	9883	612	7.788129	9.325938	7	5	3	701.9317	814.2337	6	7.813784	7.821701	7.728903	9.270519	9.330796	9.376499
4.7262	0.0010	2.3624		noncod	ENST0000	bidirectio		251.19	913.63			232.7831	248.0871	272.7072			1008.523						
8E-05	22563	192	down	ing	0437416	nal	CNIH3	2547	0333	8.26146	9.501725	9	7	8	856.555	875.8123	7	8.18317	8.366496	8.234714	9.551873	9.429223	9.524079
0.0045	0.0160	2.9796		noncod	ENST0000			15.733	64.942				20.28331	15.31292			62.17827						
5806	5755	291	down	ing	0457457	intergenic		539	005	4.178522	5.753655	11.60437	8	9	52.74861	6	79.89913	3.803632	4.673446	4.058488	5.6187353	5.710944	5.931285
0.0014	0.0072	2.0213		noncod	ENST0000	intronic		119.87	354.29			112.3130	98.81299	148.4953			370.4393						
91881	94997	445	down	ing	0549565	antisense	CNPY2	3802	431	7.149327	8.164642	2	6	9	283.4199	3	409.0237	7.106003	6.9995627	7.342414	7.9998794	8.229554	8.264492
0.0014	0.0072	2.0213		noncod	ENST0000	natural		119.87	354.29			112.3130	98.81299	148.4953			370.4393						
91881	94997	445	down	ing	0549565	antisense	CNPY2	3802	431	7.149327	8.164642	2	6	9	283.4199	3	409.0237	7.106003	6.9995627	7.342414	7.9998794	8.229554	8.264492
0.0014	0.0072	2.0213		noncod	ENST0000	natural		119.87	354.29			112.3130	98.81299	148.4953			370.4393						
91881	94997	445	down	ing	0549565	antisense	CS	3802	431	7.149327	8.164642	2	6	9	283.4199	3	409.0237	7.106003	6.9995627	7.342414	7.9998794	8.229554	8.264492
0.0027	0.0110	8.8551		noncod	ENST0000			9.0017	95.161			7.375683	4.999999	14.62946			108.8028						
24145	67758	503	down	ing	0426124	intergenic		17	457	3.165525	6.312042	3	5	9	85.06734	91.61414	9	3.1460724	2.3528795	3.9976237	6.29196	6.2580605	6.3861055
0.0028	0.0115	3.3244		noncod	ENST0000			5.7775	23.988				4.999999	4.999999			22.63135	26.44951					
96404	37184	017	down	ing	0559960	intergenic		9	741	2.612487	4.345582	7.332772	5	5	22.88536	1	2	3.1367412	2.3528795	2.3478405	4.4415627	4.2756476	4.319535
0.0003	0.0029	2.0782		noncod	ENST0000	natural		58.963	176.01				59.38683			167.7211	169.2811	191.0425					
41056	01541	201	down	ing	0369391	antisense	TCF7L2	939	498	6.134266	7.189614	59.29918	7	58.2058	9	9	6	6.169638	6.2605667	5.972593	7.2548294	7.1257167	7.188297
0.0003	0.0029	2.0782		noncod	ENST0000	natural		58.963	176.01				59.38683			167.7211	169.2811	191.0425					
41056	01541	201	down	ing	0369391	antisense	TCF7L2	939	498	6.134266	7.189614	59.29918	7	58.2058	9	9	6	6.169638	6.2605667	5.972593	7.2548294	7.1257167	7.188297
0.0003	0.0029	2.0782		noncod	ENST0000	natural		58.963	176.01				59.38683			167.7211	169.2811	191.0425					
41056	01541	201	down	ing	0369391	antisense	TCF7L2	939	498	6.134266	7.189614	59.29918	7	58.2058	9	9	6	6.169638	6.2605667	5.972593	7.2548294	7.1257167	7.188297
0.0003	0.0029	2.0782		noncod	ENST0000	natural		58.963	176.01				59.38683			167.7211	169.2811	191.0425					
41056	01541	201	down	ing	0369391	antisense	TCF7L2	939	498	6.134266	7.189614	59.29918	7	58.2058	9	9	6	6.169638	6.2605667	5.972593	7.2548294	7.1257167	7.188297
0.0003	0.0029	2.0782		noncod	ENST0000	natural		58.963	176.01				59.38683			167.7211	169.2811	191.0425					
41056	01541	201	down	ing	0369391	antisense	TCF7L2	939	498	6.134266	7.189614	59.29918	7	58.2058	9	9	6	6.169638	6.2605667	5.972593	7.2548294	7.1257167	7.188297
0.0003	0.0029	2.0782		noncod	ENST0000	natural		58.963	176.01				59.38683			167.7211	169.2811	191.0425					
41056	01541	201	down	ing	0369391	antisense	TCF7L2	939	498	6.134266	7.189614	59.29918	7	58.2058	9	9	6	6.169638	6.2605667	5.972593	7.2548294	7.1257167	7.188297
0.0003	0.0029	2.0782		noncod	ENST0000	natural		58.963	176.01				59.38683			167.7211	169.2811	191.0425					
41056	01541	201	down	ing	0369391	antisense	TCF7L2	939	498	6.134266	7.189614	59.29918	7	58.2058	9	9	6	6.169638	6.2605667	5.972593	7.2548294	7.1257167	7.188297
0.0003	0.0029	2.0782		noncod	ENST0000	natural		58.963	176.01				59.38683			167.7211	169.2811	191.0425					
41056	01541	201	down	ing	0369391	antisense	TCF7L2	939	498	6.134266	7.189614	59.29918	7	58.2058	9	9	6	6.169638	6.2605667	5.972593	7.2548294	7.1257167	7.188297
0.0003	0.0029	2.0782		noncod	ENST0000	natural		58.963	176.01				59.38683			167.7211	169.2811	191.0425					
41056	01541	201	down	ing	0369391	antisense	TCF7L2	939	498	6.134266	7.189614	59.29918	7	58.2058	9	9	6	6.169638	6.2605667	5.972593	7.2548294	7.1257167	7.188297
0.0003	0.0029	2.0782		noncod	ENST0000	natural		58.963	176.01				59.38683			167.7211	169.2811	191.0425					
41056	01541	201	down	ing	0369391	antisense	TCF7L2	939	498	6.134266	7.189614	59.29918	7	58.2058	9	9	6	6.169638	6.2605667	5.972593	7.2548294	7.1257167	7.188297
0.0003	0.0029	2.0782		noncod	ENST0000	natural		58.963	176.01				59.38683			167.7211	169.2811	191.0425					
41056	01541	201	down	ing	0369391	antisense	TCF7L2	939	498	6.134266	7.189614	59.29918	7	58.2058	9	9	6	6.169638	6.2605667	5.972593	7.2548294	7.1257167	7.188297
0.0094	0.0274	2.0167		noncod	TCONS_00			26.329	73.126			20.31811	24.96099			80.85857							
30336	65701	098	down	ing	006466	intergenic		32	078	4.926553	5.938556	33.70885	5	5	69.30875	69.21091	4	5.348635	4.677127	4.753896	6.0040307	5.8630714	5.9485664
2.2817	0.0007	2.0343		noncod		intronic		211.82	653.56			212.1106				238.2046							
9E-05	58104	305	down	ing	uc003vcp.1	antisense	MLL5	0203	39	8.002467	9.027021	9	185.1453	2	577.0285	652.8151	730.8481	8.039097	7.9263277	8.041976	8.99118	9.01548	9.074403
2.2817	0.0007	2.0343		noncod		intronic		211.82	653.56			212.1106				238.2046							
9E-05	58104	305	down	ing	uc003vcp.1	antisense	MLL5	0203	39	8.002467	9.027021	9	185.1453	2	577.0285	652.8151	730.8481	8.039097	7.9263277	8.041976	8.99118	9.01548	9.074403
0.0071	0.0222	2.2340		noncod	ENST0000			65.777	204.40			56.65174	91.93352	186.6661	225.2315	201.3263							
0452	10365	41	down	ing	0450360			86	8033	6.236898	7.396554	48.74831	5	5	8	5	7	5.894421	6.1835556	6.6327186	7.406239	7.5264482	7.25

77457	49035	517		ing	0439104	nal		1	478		4	6		3	2								
0.0009	0.0055	2.6262		noncod	ENST0000	bidirectio		6.7506	24.785		5.470502	7.444878		19.96769	26.25658								
77457	49035	517	down	ing	0439104	nal	BUD13	1	478	2.988694	4.381699	4	6	7.336448	3	2	28.13216	2.7082143	3.196879	3.0609875	4.252485	4.484412	4.4081993
0.0006	0.0041	2.2961		noncod				39.518	127.94		33.01076	41.32577	44.22007	111.9353	126.8648	145.0458							
05853	2655	53	down	ing	uc001jby.3	intergenic		871	867	5.537487	6.736706	5	5	4	1	2	8	5.317957	5.7241783	5.570327	6.690606	6.7251797	6.794333
3.8982	0.0004	3.8850		noncod	ENST0000			742.76	4651.5		11.82731	670.6564	857.4007	3992.425									
2E-06	13042	971	down	ing	0422183	intergenic		623	20933	9.869361	1	700.2415	3	6	8	4850.534	5111.603	9.819267	9.847395	9.94142	11.744423	11.875824	11.861687
0.0001	0.0018	2.5010		noncod	ENST0000			274.23	1059.4				285.5073	891.0644	1129.452	1157.934							
64379	82305	406	down	ing	0519852	intergenic		1607	8375	8.383277	9.705806	298.7517	238.4358	2	5	5	3	8.543079	8.308352	8.2984	9.6053095	9.790697	9.72141
0.0030	0.0119	3.4615		noncod	ENST0000			13.532	66.259			16.35125	13.66214	10.58405									
32974	36196	136	down	ing	0537764	intergenic		484	987	3.977753	5.769156	2	1	8	48.85307	80.76074	69.16615	4.2946606	4.0914316	3.547166	5.5049725	6.0805707	5.721924
8.5639	0.0013	2.3549		noncod	ENST0000			589.80	2191.9		10.75717	534.3226	714.3346	2033.851	2189.277	2352.630							
E-05	46636	308	down	ing	0514265	intergenic		683	19833	9.521488	3	3	520.7632	6	8	3	4	9.41857	9.478252	9.667642	10.785771	10.744246	10.741501
7.0164	0.0012	2.5010		noncod	ENST0000	bidirectio		18.488	64.843		18.89124	16.98494		57.23015		66.08890							
2E-05	17883	739	down	ing	0508123	nal	MRPS30	48	177	4.439669	5.762216	7	3	19.58925	6	71.21047	5	4.498585	4.4098864	4.4105344	5.730973	5.8995566	5.6561193
						intron																	
0.0024	0.0103	3.9493		noncod	ENST0000	sense-ove		5.8437	29.138		7.531284	4.999999	4.999999	23.84376	26.84325	36.72892							
54982	03216	922	down	ing	0366153	rlapping	CLHC1	61	648	2.625427	4.607058	3	5	5	3	4	8	3.175561	2.3528795	2.3478405	4.5011945	4.518459	4.8015194
						intron																	
0.0024	0.0103	3.9493		noncod	ENST0000	sense-ove		5.8437	29.138		7.531284	4.999999	4.999999	23.84376	26.84325	36.72892							
54982	03216	922	down	ing	0366153	rlapping	CLHC1	61	648	2.625427	4.607058	3	5	5	3	4	8	3.175561	2.3528795	2.3478405	4.5011945	4.518459	4.8015194
1.4754	0.0003	2.0992		noncod	ENST0000			454.44	1506.8		10.21373	445.5879	406.6695	511.0626	1345.704	1556.466	1618.316						
2E-06	33887	039	down	ing	0538790	intergenic		0053	29433	9.143891	3	2	6	8	6	9	8	9.153605	9.107879	9.170188	10.196393	10.243347	10.201459
0.0002	0.0025	2.5454		noncod	ENST0000			185.09	714.32		192.5568	186.6912	176.0443			797.1640							
84788	97381	16	down	ing	0560029	intergenic		7487	3053	7.808849	9.15675	8	4	4	652.1595	693.6456	6	7.895686	7.9395347	7.591325	9.165402	9.103353	9.201495
3.3513	0.0008	3.2506		noncod	ENST0000	bidirectio		39.367	183.29			36.24891		151.6453	189.4587	208.7837							
3E-05	74299	052	down	ing	0534499	nal	RAB30	891	596	5.531923	7.232632	35.67958	3	46.17518	9	1	8	5.43203	5.531081	5.632659	7.1147184	7.278205	7.3049717
0.0005	0.0038	2.8433		noncod	ENST0000			6.5310	26.037		7.138479	5.361821		22.78143	23.01739	32.31336							
31406	17685	126	down	ing	0422178	intergenic		77	397	2.941611	4.449184	7	7	7.09293	3	1	6	3.0976863	2.7125454	3.014602	4.4342194	4.298573	4.6147594
0.0004	0.0035	2.3476		noncod	ENST0000			140.85	488.56		125.4461	125.4279	171.6926										
79514	94667	089	down	ing	0561706	intergenic		5583	0367	7.395367	8.626559	5	9	1	470.798	435.9482	558.9349	7.27157	7.360917	7.5536127	8.715439	8.458841	8.705396
0.0001	0.0019	2.0422		noncod	ENST0000			86.471	254.18			84.38386	98.83095	229.2935	252.1481	281.1192							
67029	02049	298	down	ing	0584023	intergenic		027	699	6.679648	7.709793	76.19826	5	6	6	8	3	6.533102	6.7698135	6.736027	7.7059474	7.685364	7.7380667
4.7348	0.0004	2.2599		noncod		intronic		3334.6	12134.	12.04691	13.22320	3284.659		10752.74	12470.32	13181.63							
E-06	28594	494	down	ing	uc010tki.2	antisense	GAS6	868	90267	5	6	4	2916.999	3802.402	2	7	9	12.075972	11.989416	12.075357	13.183156	13.247196	13.2392645
6.8605	0.0012	2.6477		noncod				234.27	955.19		227.8795	205.2713	269.6696		1061.967	1001.191							
3E-05	03844	694	down	ing	uc010rog.2	intergenic		3503	91	8.151095	9.555873	3	3	5	802.4389	3	1	8.15056	8.0839205	8.218805	9.456802	9.696715	9.514101
0.0003	0.0030	2.2096		noncod	ENST0000			64.989	208.04			62.01394		177.0665	227.8348	219.2323							
66044	34272	342	down	ing	0507736	intergenic		278	4573	6.273895	7.417703	68.58209	3	64.3718	9	1	2	6.3814526	6.320715	6.1195173	7.333308	7.545493	7.3745346
8.2846	0.0013	5.7932		noncod	TCONS_00			35.688		4.999999	4.999999	4.999999	25.41628		45.58146								
3E-05	2029	29	down	ing	012765	intergenic		5	441	2.350054	4.884421	5	5	5	36.06757	7	2.3494408	2.3528795	2.3478405	4.591678	4.9401402	5.1214457	
0.0064	0.0206	3.7478		noncod				16.111	82.787			19.13049	10.17025	65.34830	89.79027								
55759	93177	304	down	ing	AW340022	intergenic		335	614	4.196389	6.102444	19.03325	7	9	5	6	93.22426	4.5095835	4.5880957	3.4914863	5.917451	6.2281685	6.161713
0.0001	0.0015	2.5709		noncod	ENST0000			11.849	42.514			10.40100	12.58528	35.59255		46.08819							
22485	96353	807	down	ing	0553470	intergenic		144	968	3.796995	5.159314	12.56115	1	1	2	45.86416	2	3.9166594	3.6870985	3.7872286	5.061447	5.2797375	5.1367583
0.0079	0.0242	2.2752		noncod	ENST0000			9.1069	28.371				11.35736	23.35983	34.44036	27.31462							
88729	8681	258	down	ing	0554946	intergenic		15	608	3.385189	4.571199	9.322197	6.64118	9	3	5	5	3.4794168	3.0309849	3.645166	4.4710417	4.8793087	4.3632464
						intron																	
0.0001	0.0014	2.4027		noncod	ENST0000	sense-ove	RP11-102	210.69	762.64			178.5983	254.8252	690.0765									
00504	53298	624	down	ing	0566734	rlapping	IN1.1	0583	318	7.984951	9.249645	198.6482	1	4	4	783.7689	814.0841	7.94217	7.872197	8.140487	9.2462435	9.2744465	9.228246
0.0003	0.0027	2.8254		noncod		natural		77.549	313.05			59.29988	94.88885	280.8547	327.5613	330.7465							
17132	81667	766	down	ing	NR_039978	antisense	SEC24B	523	42	6.502882	8.001377	78.45983	5	5	4	4	2	6.571786	6.257758	6.679103	7.986562	8.054401	7.9631667
0.0003	0.0027	2.8254		noncod		natural		77.549	313.05			59.29988	94.88885	280.8547	327.5613	330.7465							
17132	81667	766	down	ing	NR_039978	antisense	SEC24B	523	42	6.502882	8.001377	78.45983	5	5	4	4	2	6.571786	6.257758	6.679103	7.986562	8.054401	7.9631667
0.0003	0.0029	2.1875		noncod	ENST0000	natural		49.819	156.57			52.14407		133.8749		180.4264							
40704	01272	435	down	ing	0434512	antisense	INTS6	589	754	5.887251	7.016563	46.12484	7	51.18985	8	155.4312	4	5.816167	6.0604606	5.785126	6.939786	7.0058646	7.1040382
						exon																	
0.0303	0.0663	2.7805		noncod		sense-ove		15.792	56.619					51.99548	54.68129								
42602	43294	898	down	ing	uc001iuv.1	rlapping	SVIL	608	987	4.098355	5.573746	8.355505	23.20838	15.81394	7	3	63.18318	3.3195055	4.8735237	4.102037	5.597259	5.5339007	5.5900793
						intron																	
0.0303	0.0663	2.7805		noncod		sense-ove		15.792	56.619					51.99548	54.68129								
42602	43294	898	down	ing	uc001iuv.1	rlapping	SVIL																

27937	76536	454		ing	0446201		908	082			1	3	2	5									
0.0008	0.0049	2.2081		noncod			24.246	74.536		19.97868	25.49521	27.26677	67.59640										
1037	2975	111	down	ing	AK125162	intergenic	89	522	4.82098	5.963793	5	3	5	74.42017	81.59299	4.5816507	5.0068765	4.874413	5.967075	5.965301	5.9590025		
8.2046	0.0005	2.7128		noncod			960.64	4185.2	10.23656	11.67636			1072.320	3754.390	4232.380	4569.122							
7E-06	13475	347	down	ing	uc002suy.1	intergenic	6633	978	2	4	985.4242	824.195	7	4	4	6	10.307639	10.144277	10.2577715	11.666502	11.666502	11.696087	
0.0024	0.0102	2.2788		noncod	ENST0000	natural	24.379	78.096			29.08063	20.24455	23.81336	62.41613									
42698	67657	86	down	ing	0501016	antisense	515	389	4.831282	6.019611	1	3	2	8	81.74383	90.1292	5.1383266	4.670215	4.6853056	5.853085	6.096178	6.1095705	
						intron																	
0.0001	0.0016	2.8700		noncod	ENST0000	sense-ove	41.164	168.64			38.73947	35.62955	49.12351	135.8050	181.9811	188.1393							
28618	37487	812	down	ing	0435858	rlapping	FAM46A	182	185	5.594621	7.115713	5	5	6	5	4	6	5.5536404	5.5062838	5.723939	6.957538	7.2226014	7.1669984
0.0001	0.0015	2.1196		noncod	ENST0000	natural	EXOSC1	249.79	808.55			231.2858	220.1430		694.6615								
15243	51192	075	down	ing	0435388	antisense	0	751	702	8.245602	9.3294	6	7	297.9636	6	848.2753	882.7342	8.170729	8.198006	8.3680725	9.257219	9.383644	9.347336
0.0001	0.0015	2.1196		noncod	ENST0000	natural	EXOSC1	249.79	808.55			231.2858	220.1430		694.6615								
15243	51192	075	down	ing	0435388	antisense	0	751	702	8.245602	9.3294	6	7	297.9636	6	848.2753	882.7342	8.170729	8.198006	8.3680725	9.257219	9.383644	9.347336
						intron																	
0.0025	0.0106	3.0750		noncod	ENST0000	sense-ove	8.7850	36.655			6.172610	11.47591	29.06989	41.45277	39.44496								
57177	18151	966	down	ing	0514241	rlapping	MAST4	09	88	3.31832	4.938952	8.706505	3	2	7	8	5	3.3777184	2.9157968	3.6614456	4.778758	5.136211	4.901887
						intron																	
0.0025	0.0106	3.0750		noncod	ENST0000	sense-ove	8.7850	36.655			6.172610	11.47591	29.06989	41.45277	39.44496								
57177	18151	966	down	ing	0514241	rlapping	MAST4	09	88	3.31832	4.938952	8.706505	3	2	7	8	5	3.3777184	2.9157968	3.6614456	4.778758	5.136211	4.901887
0.0036	0.0136	2.2423		noncod	ENST0000		16.699	52.080				18.91770		42.10514	52.58632	61.55036							
29415	16967	049	down	ing	0568246	intergenic	572	611	4.279135	5.444117	13.04431	7	18.1367	5	3	5	3.9687643	4.5731707	4.295469	5.2973413	5.480962	5.554048	
4.9945	0.0010	2.3289		noncod			58.607	197.21			54.76823		62.93561	185.6467	187.0991	218.8882							
3E-05	40957	653	down	ing	NR_036586	intergenic	408	1363	6.124745	7.344434	8	58.11837	6	3	2	4	6.061634	6.225508	6.0870924	7.3996277	7.2626195	7.3710546	
0.0154	0.0396	2.7744		noncod	ENST0000	natural	7.6518	26.911			4.999999			30.71814	29.25539								
11327	71075	543	down	ing	0554650	antisense	FBXO34	97	679	3.021916	4.49412	7.785701	5	10.16999	20.7615	2	4	3.2214277	2.3528795	3.491442	4.3049927	4.709773	4.4675956
0.0004	0.0034	2.0680		noncod	ENST0000		65.714	192.77			65.08098				198.1176								
55147	72952	048	down	ing	0426641		439	1193	6.268061	7.316301	6	53.44085	78.62148	182.0191	198.1768	8	6.3036847	6.0967865	6.403713	7.370158	7.3431215	7.2356234	
0.0005	0.0039	3.4410		noncod	ENST0000	intronic	6.4489	30.891			6.250605		29.39665	25.67761	37.59997								
68908	644	814	down	ing	0583950	antisense	CRLF3	7	416	2.910644	4.693506	5.338203	6	7.758102	6	6	2.6700172	2.933452	3.128464	4.7923813	4.455136	4.833002	
0.0006	0.0041	3.0754		noncod		bidirectio	44.099	192.87			52.31368		45.62793	165.3676	199.6948								
07323	28197	279	down	ing	NR_027447	nal	MAN1B1	613	0107	5.688129	7.308917	3	34.35722	7	3	9	213.5478	5.996727	5.4531035	5.614558	7.2356234	7.353431	7.3376956
0.0005	0.0038	5.5077		noncod		bidirectio	TNFRSF	14.335	106.06				19.57675		109.2441	112.9339							
38459	42439	906	down	ing	NR_033928	nal	10A	731	6823	4.011772	6.473246	13.81571	9.61473	2	96.02243	25	14	4.0528817	3.5728722	4.4095626	6.4671926	6.514807	6.437738
0.0152	0.0394	2.4319		noncod	ENST0000		7.1850	24.261			9.582787	5.727289	27.75619	20.30204	24.72541								
63366	41617	873	down	ing	0510261	intergenic	09	218	3.066257	4.348392	6.244949	5	7	3	4	8	2.8997483	3.5672464	2.7317748	4.7146053	4.1172633	4.213308	
0.0192	0.0467	2.3627		noncod	ENST0000		16.148	49.520			13.54275	24.70454	44.29227		54.82282								
33085	8793	594	down	ing	0393264	intergenic	86	35	4.142777	5.38325	10.19928	1	8	4	49.44595	6	3.6114755	4.0779595	4.738897	5.3721523	5.3886104	5.3889875	
0.0051	0.0174	2.0871		noncod	ENST0000	intronic	10.532	29.751					13.65896		29.49362	29.87421							
13904	02654	682	down	ing	0323689	antisense	PFN2	761	164	3.592768	4.654315	9.820537	8.118785	2	29.88565	8	4	3.5551653	3.3241272	3.899012	4.8161592	4.65032	4.496466
0.0051	0.0174	2.0871		noncod	ENST0000	intronic	10.532	29.751					13.65896		29.49362	29.87421							
13904	02654	682	down	ing	0323689	antisense	PFN2	761	164	3.592768	4.654315	9.820537	8.118785	2	29.88565	8	4	3.5551653	3.3241272	3.899012	4.8161592	4.65032	4.496466
5.7751	0.0011	3.5943		noncod	ENST0000		66.549	346.94			72.17277		297.1757		365.3950								
4E-05	11797	444	down	ing	0450998	intergenic	745	4277	6.297464	8.143193	5	56.02001	71.45645	8	378.262	5	6.4559426	6.167478	6.2689724	8.068668	8.260838	8.100073	
0.0080	0.0243	3.1261		noncod	ENST0000	natural	RASGRF	12.658	52.535			18.65243			51.41516								
26114	63644	275	down	ing	0316148	antisense	1	725	672	3.823042	5.467419	3	9.069472	10.25427	5	49.07451	57.11734	4.482973	3.4847856	3.5013676	5.5803533	5.3768444	5.4450583
0.0080	0.0243	3.1261		noncod	ENST0000	natural	RASGRF	12.658	52.535			18.65243			51.41516								
26114	63644	275	down	ing	0316148	antisense	1	725	672	3.823042	5.467419	3	9.069472	10.25427	5	49.07451	57.11734	4.482973	3.4847856	3.5013676	5.5803533	5.3768444	5.4450583
0.0080	0.0243	3.1261		noncod	ENST0000	natural	RASGRF	12.658	52.535			18.65243			51.41516								
26114	63644	275	down	ing	0316148	antisense	1	725	672	3.823042	5.467419	3	9.069472	10.25427	5	49.07451	57.11734	4.482973	3.4847856	3.5013676	5.5803533	5.3768444	5.4450583
2.8319	0.0008	2.1171		noncod		natural	FAM211	1046.0	3557.5	10.36046	11.44259	1033.748	897.1539	1207.152	3131.701								
E-05	32888	547	down	ing	NR_027165	antisense	A	18277	89133	4	1	2	3	7	4	3715.861	3825.205	10.378134	10.277965	10.425293	11.400935	11.490358	11.436479
2.8319	0.0008	2.1171		noncod		natural	FAM211	1046.0	3557.5	10.36046	11.44259	1033.748	897.1539	1207.152	3131.701								
E-05	32888	547	down	ing	NR_027165	antisense	A	18277	89133	4	1	2	3	7	4	3715.861	3825.205	10.378134	10.277965	10.425293	11.400935	11.490358	11.436479
8.1480	0.0005	2.2118		noncod	ENST0000	bidirectio	46.416	145.66			50.68660	140.0811	141.1513	155.7753									
6E-06	13475	624	down	ing	0434781	nal	PCBP1	302	929	5.78254	6.927802	45.34233	43.21997	7	8	8	1	5.7917233	5.7860947	5.769802	7.003644	6.8772445	6.9025164
0.0060	0.0196	2.1951		noncod		bidirectio	7.3053	21.913			5.578911	6.782410		20.16006		26.50460							
42407	74772	552	down	ing	uc004bav.1	nal	TEX10	26	218	3.069737	4.20406	3	6	9.554656	5	19.07498	8	2.7380893	3.0640666	3.407054	4.2636147	4.0249834	4.3235807
0.0060	0.0196	2.1951		noncod		bidirectio	7.3053	21.913			5.578911	6.782410		20.16006		26.50460							
42407	74772	552	down	ing	uc004bav.1	nal	TEX10	26	218	3.069737	4.20406	3	6	9.554656	5	19.07498	8	2.7380893	3.0640666	3.407054	4.2636147	4.0249834	4.3235807
						intron																	

0.0002	0.0023	2.3819		noncod		natural		37.307	124.29			34.84917		117.4484	129.9306	125.4969							
43376	52417	539	down	ing	uc002ued.3	antisense	CERS6	511	2017	5.449949	6.702094	32.50414	4	44.56922	6	8	1	5.2938075	5.47466	5.581379	6.7593594	6.757209	6.5897145
0.0002	0.0023	2.3819		noncod		natural		37.307	124.29			34.84917		117.4484	129.9306	125.4969							
43376	52417	539	down	ing	uc002ued.3	antisense	CERS6	511	2017	5.449949	6.702094	32.50414	4	44.56922	6	8	1	5.2938075	5.47466	5.581379	6.7593594	6.757209	6.5897145
0.0001	0.0020	3.8410		noncod	ENST0000	natural	MARVE	26.890	145.09			30.87118	22.65255	27.14745	145.1899	132.9057	157.1881						
83019	05675	333	down	ing	0562763	antisense	LD3	395	461	4.976805	6.9183	1	2	1	7	2	4	5.223666	4.836671	4.870079	7.0528364	6.787272	6.914791
0.0001	0.0020	3.8410		noncod	ENST0000	natural	MARVE	26.890	145.09			30.87118	22.65255	27.14745	145.1899	132.9057	157.1881						
83019	05675	333	down	ing	0562763	antisense	LD3	395	461	4.976805	6.9183	1	2	1	7	2	4	5.223666	4.836671	4.870079	7.0528364	6.787272	6.914791
0.0045	0.0161	6.3737		noncod	ENST0000			11.132	86.520			6.400569	7.245514	19.75281		92.56943							
87765	46363	722	down	ing	0422542	intergenic		967	608	3.505729	6.177876	4	4	7	78.88951	5	88.10288	2.9364173	3.1590824	4.421687	6.18596	6.2754235	6.0722456
0.0014	0.0070	2.3258		noncod	ENST0000	intronic		34.708	116.60							143.0436							
28836	92858	252	down	ing	0444873	antisense	BCL11A	187	54	5.356859	6.574602	33.21858	33.06719	37.83879	83.93799	122.8346	1	5.3267207	5.394818	5.349039	6.2718067	6.6771154	6.7748837
0.0014	0.0070	2.3258		noncod	ENST0000	intronic		34.708	116.60							143.0436							
28836	92858	252	down	ing	0444873	antisense	BCL11A	187	54	5.356859	6.574602	33.21858	33.06719	37.83879	83.93799	122.8346	1	5.3267207	5.394818	5.349039	6.2718067	6.6771154	6.7748837
0.0014	0.0070	2.3258		noncod	ENST0000	intronic		34.708	116.60							143.0436							
28836	92858	252	down	ing	0444873	antisense	BCL11A	187	54	5.356859	6.574602	33.21858	33.06719	37.83879	83.93799	122.8346	1	5.3267207	5.394818	5.349039	6.2718067	6.6771154	6.7748837
0.0013	0.0069	2.0216		noncod				128.22	380.34			140.3932	101.4777	142.8121	322.5729	385.5401	432.9262						
74723	07575	426	down	ing	uc021pvt.1	intergenic		7703	6467	7.257195	8.272723	2	1	8	7	6	7	7.442274	7.038856	7.290456	8.176735	8.290999	8.350436
0.0021	0.0093	3.0342		noncod	ENST0000			11.193	48.340			12.21941	11.86258			55.77200							
35416	62939	724	down	ing	0512319	intergenic		28	546	3.720127	5.321478	1	9	9.497839	34.44534	7	54.80429	3.8770602	3.884255	3.399066	5.015753	5.560338	5.388342
3.2743	0.0003	2.0957		noncod	ENST0000			783.70	2641.8			11.01951		733.7792	2476.601	2619.915	2828.978						
8E-06	96799	307	down	ing	0573141	intergenic		3313	319	9.95206	3	749.3286	4	868.0021	6	8	3	9.915541	9.984207	9.956432	11.061747	10.997589	10.999204
0.0043	0.0153	2.9961		noncod	ENST0000	natural		13.778	56.544			17.42568		14.52895		62.33919							
15404	98347	442	down	ing	0578500	antisense	GINS4	501	105	3.969958	5.553065	8	9.380858	8	43.0823	5	64.21082	4.386653	3.5347545	3.9884653	5.330579	5.714	5.614615
1.1533	0.0003	2.8488		noncod	ENST0000			443.26	1978.6			10.61451	421.9067	400.3393	1761.529	2193.961							
4E-06	32251	118	down	ing	0430893	intergenic		041	075	9.10415	1	7	6	507.5351	3	1980.332	2	9.068751	9.085131	9.158569	10.594982	10.603522	10.645028
1.0687	0.0005	2.5712		noncod	ENST0000	bidirectio	TMEM16	82.054	306.39					269.7698	318.1291	331.2972							
1E-05	61762	331	down	ing	0504769	nal	1B	03	8773	6.607828	7.970288	84.5767	75.55634	86.02905	7	8	7	6.686054	6.600971	6.536458	7.9297633	8.015123	7.965978
0.0005	0.0040	2.2489		noncod		natural		19.541	61.928					22.75097	50.09335	77.35950							
91721	62386	53	down	ing	NR_024052	antisense	TRIM39	601	069	4.512688	5.681941	18.65754	17.21629	3	3	58.33135	5	4.4835734	4.4321346	4.6223555	5.5404935	5.620627	5.8847036
0.0051	0.0174	2.6665		noncod	TCONS_00			6.1027	21.477			4.999999	7.481693			20.81115	22.85828						
10297	00192	938	down	ing	020994	intergenic		59	648	2.769705	4.184703	5	7	5.826585	20.76351	2	2	2.3494408	3.2030466	2.7566285	4.3050895	4.15405	4.0949707
0.0002	0.0023	2.4522		noncod	ENST0000			18.274	62.222						57.69577	60.25476							
38128	26737	556	down	ing	0440645	intergenic		64	206	4.412244	5.706354	15.6341	17.10225	22.08757	4	5	68.71608	4.2326536	4.420596	4.583483	5.7425237	5.6653476	5.7111893
0.0080	0.0244	2.1883		noncod		sense-ove		22.890	68.526			28.86055	16.38789	23.42299		71.40427							
87814	9296	95	down	ing	NR_028463	rlapping	ATXN3	482	151	4.715799	5.845672	2	6	7	64.59782	4	69.57636	5.1279774	4.358985	4.6604333	5.9026117	5.9034305	5.730973
0.0080	0.0244	2.1883		noncod		sense-ove		22.890	68.526			28.86055	16.38789	23.42299		71.40427							
87814	9296	95	down	ing	NR_028463	rlapping	ATXN3	482	151	4.715799	5.845672	2	6	7	64.59782	4	69.57636	5.1279774	4.358985	4.6604333	5.9026117	5.9034305	5.730973
0.0080	0.0244	2.1883		noncod		sense-ove		22.890	68.526			28.86055	16.38789	23.42299		71.40427							
87814	9296	95	down	ing	NR_028463	rlapping	ATXN3	482	151	4.715799	5.845672	2	6	7	64.59782	4	69.57636	5.1279774	4.358985	4.6604333	5.9026117	5.9034305	5.730973
0.0080	0.0244	2.1883		noncod		sense-ove		22.890	68.526			28.86055	16.38789	23.42299		71.40427							
87814	9296	95	down	ing	NR_028463	rlapping	ATXN3	482	151	4.715799	5.845672	2	6	7	64.59782	4	69.57636	5.1279774	4.358985	4.6604333	5.9026117	5.9034305	5.730973
0.0080	0.0244	2.1883		noncod		sense-ove		22.890	68.526			28.86055	16.38789	23.42299		71.40427							
87814	9296	95	down	ing	NR_028463	rlapping	ATXN3	482	151	4.715799	5.845672	2	6	7	64.59782	4	69.57636	5.1279774	4.358985	4.6604333	5.9026117	5.9034305	5.730973
0.0080	0.0244	2.1883		noncod		sense-ove		22.890	68.526			28.86055	16.38789	23.42299		71.40427							
87814	9296	95	down	ing	NR_028463	rlapping	ATXN3	482	151	4.715799	5.845672	2	6	7	64.59782	4	69.57636	5.1279774	4.358985	4.6604333	5.9026117	5.9034305	5.730973
0.0080	0.0244	2.1883		noncod		sense-ove		22.890	68.526			28.86055	16.38789	23.42299		71.40427							
87814	9296	95	down	ing	NR_028463	rlapping	ATXN3	482	151	4.715799	5.845672	2	6	7	64.59782	4	69.57636	5.1279774	4.358985	4.6604333	5.9026117	5.9034305	5.730973
0.0080	0.0244	2.1883		noncod		sense-ove		22.890	68.526			28.86055	16.38789	23.42299		71.40427							
87814	9296	95	down	ing	NR_028463	rlapping	ATXN3	482	151	4.715799	5.845672	2	6	7	64.59782	4	69.57636	5.1279774	4.358985	4.6604333	5.9026117	5.9034305	5.730973
0.0080	0.0244	2.1883		noncod		sense-ove		22.890	68.526			28.86055	16.38789	23.42299		71.40427							
87814	9296	95	down	ing	NR_028463	rlapping	ATXN3	482	151	4.715799	5.845672	2	6	7	64.59782	4	69.57636	5.1279774	4.358985	4.6604333	5.9026117	5.9034305	5.730973

						exon																		
0.0080	0.0244	2.1883		noncod		sense-ove	22.890	68.526		28.86055	16.38789	23.42299		71.40427										
87814	9296	95	down	ing	NR_028463	rlapping	ATXN3	482	151	4.715799	5.845672	2	6	7	64.59782	4	69.57636	5.1279774	4.358985	4.6604333	5.9026117	5.9034305	5.730973	
5.2284	0.0003	2.1601		noncod		natural	FAM211	218.83	720.69			212.0680	205.4084		643.6482		778.9988							
8E-07	32251	513	down	ing	NR_027168	antisense	A	4927	1197	8.057036	9.168169	5	3	239.0283	5	739.4265	4	8.038513	8.085703	8.046893	9.146422	9.189331	9.168753	
5.2284	0.0003	2.1601		noncod		natural	FAM211	218.83	720.69			212.0680	205.4084		643.6482		778.9988							
8E-07	32251	513	down	ing	NR_027168	antisense	A	4927	1197	8.057036	9.168169	5	3	239.0283	5	739.4265	4	8.038513	8.085703	8.046893	9.146422	9.189331	9.168753	
0.0112	0.0313	2.2623		noncod	TCONS_00			8.7886	26.444			7.777993	6.302048		26.66202		25.45404							
5164	04701	324	down	ing	006034	intergenic		67	291	3.306279	4.484089	7	7	12.28596	4	27.2168	8	3.2201793	2.9457877	3.7528687	4.6565514	4.53751	4.258207	
0.0023	0.0099	2.3171		noncod	ENST0000	bidirectio		8.1484	26.072						24.45214	28.35301	25.41111							
25483	24399	631	down	ing	0433521	nal	ACADM	1	095	3.249527	4.461886	9.345493	6.493676	8.606061	8	8	8	3.4833403	2.9943097	3.2709303	4.53735	4.5928864	4.2554226	
0.0023	0.0099	2.3171		noncod	ENST0000	bidirectio		8.1484	26.072						24.45214	28.35301	25.41111							
25483	24399	631	down	ing	0433521	nal	ACADM	1	095	3.249527	4.461886	9.345493	6.493676	8.606061	8	8	8	3.4833403	2.9943097	3.2709303	4.53735	4.5928864	4.2554226	
0.0003	0.0028	5.2541		noncod		bidirectio		23.058	171.58			21.57130	27.67350	19.93175			200.1888							
31133	57402	4	down	ing	NR_036502	nal	PRKCQ	854	4753	4.753336	7.146791	8	4	1	151.8787	162.6867	6	4.6975617	5.1278934	4.434553	7.1163325	7.074276	7.2497635	
0.0003	0.0028	5.2541		noncod		bidirectio		23.058	171.58			21.57130	27.67350	19.93175			200.1888							
31133	57402	4	down	ing	NR_036502	nal	PRKCQ	854	4753	4.753336	7.146791	8	4	1	151.8787	162.6867	6	4.6975617	5.1278934	4.434553	7.1163325	7.074276	7.2497635	
2.2446	0.0007	2.1282		noncod	TCONS_00			58.363	177.64						53.81603	170.6211	170.1408	192.1698						
6E-05	52542	864	down	ing	028205	intergenic		565	3933	6.113489	7.203182	55.321	6	65.95366	7	1	2	6.0763764	6.107018	6.1570735	7.2787194	7.133854	7.1969714	
0.0011	0.0062	3.8767		noncod	ENST0000	natural		5.8440	30.558						4.999999		27.30387	40.74388						
75064	33438	331	down	ing	0425754	antisense	LRRC7	26	87	2.706359	4.661201	6.579924	5	5.952153	23.62885	5	5	2.9804106	2.3528795	2.785788	4.4878383	4.541643	4.954121	
0.0044	0.0157	3.0593		noncod	ENST0000			8.6139	37.685						7.299819	25.06395								
5182	53664	509	down	ing	0559505	intergenic		88	617	3.333201	4.946426	10.91351	7.628636	5	1	38.25628	49.73662	3.7115679	3.2333481	3.0546856	4.5714703	5.020121	5.247687	
7.1627	0.0004	2.2036		noncod	ENST0000			64.681	206.13						62.84702		181.6254	204.2542	232.5402					
6E-06	9593	802	down	ing	0459633	intergenic		388	9963	6.265872	7.405787	3	61.57173	69.62541	1	1	7	6.254113	6.3111615	6.2323427	7.3668504	7.386773	7.4637384	
8.0467	0.0012	2.0082		noncod	ENST0000	natural		59.822	173.15						59.12005		149.6550	175.0552	194.7667					
8E-05	95149	222	down	ing	0418945	antisense	PNISR	249	9007	6.154594	7.160513	55.52925	6	64.81744	1	4	7	6.0821896	6.2518425	6.129749	7.0957704	7.1716237	7.2141438	
8.0467	0.0012	2.0082		noncod	ENST0000	natural		59.822	173.15						59.12005		149.6550	175.0552	194.7667					
8E-05	95149	222	down	ing	0418945	antisense	PNISR	249	9007	6.154594	7.160513	55.52925	6	64.81744	1	4	7	6.0821896	6.2518425	6.129749	7.0957704	7.1716237	7.2141438	
0.0032	0.0127	2.2926		noncod	ENST0000			9.2438	29.197						11.91554		25.04650	36.63868						
90055	0274	716	down	ing	0499203	intergenic		92	019	3.414584	4.611614	7.60606	8.210066	9	25.90587	3	3	3.1879692	3.3403382	3.7154458	4.617491	4.420505	4.7968464	
2.6337	0.0003	4.7138		noncod	ENST0000	natural	HIST2H3	785.29	5988.0			12.18672			723.1087	914.3793	5618.145	6074.532	6271.610					
E-06	67353	734	down	ing	0435113	antisense	PS2	1763	962	9.949813	6	718.3872	6	3	5	7	4	9.857149	9.960411	10.03188	12.229614	12.194796	12.135769	
0.0035	0.0132	2.1137		noncod		natural	CXorf40	30.064	89.463						35.39581		29.23137	70.20312	98.81093					
12997	99727	897	down	ing	NR_027456	antisense	B	653	06	5.136035	6.215867	3	25.56677	5	5	6	99.37512	5.4212866	5.010571	4.9762464	6.02462	6.368649	6.2543306	
2.4179	0.0003	2.1297		noncod	ENST0000			65.323	200.11						65.20112		72.46773	184.1462	202.6723					
7E-06	67353	106	down	ing	0564464	intergenic		207	5563	6.275179	7.365837	6	58.30076	5	6	3	213.5281	6.3059773	6.229431	6.290129	7.385109	7.3751526	7.337248	
0.0093	0.0273	3.1887		noncod	ENST0000	intronic		7.6775	30.984						4.999999	10.02650		26.56889	37.78994					
70682	62391	728	down	ing	0429588	antisense	CLDN14	38	823	3.026343	4.699344	8.006106	5	9	28.59563	2	8	3.2575603	2.3528795	3.4685895	4.7529645	4.504842	4.8402267	
0.0093	0.0273	3.1887		noncod	ENST0000	intronic		7.6775	30.984						4.999999	10.02650		26.56889	37.78994					
70682	62391	728	down	ing	0429588	antisense	CLDN14	38	823	3.026343	4.699344	8.006106	5	9	28.59563	2	8	3.2575603	2.3528795	3.4685895	4.7529645	4.504842	4.8402267	
0.0093	0.0273	3.1887		noncod	ENST0000	intronic		7.6775	30.984						4.999999	10.02650		26.56889	37.78994					
70682	62391	728	down	ing	0429588	antisense	CLDN14	38	823	3.026343	4.699344	8.006106	5	9	28.59563	2	8	3.2575603	2.3528795	3.4685895	4.7529645	4.504842	4.8402267	
0.0093	0.0273	3.1887		noncod	ENST0000	intronic		7.6775	30.984						4.999999	10.02650		26.56889	37.78994					
70682	62391	728	down	ing	0429588	antisense	CLDN14	38	823	3.026343	4.699344	8.006106	5	9	28.59563	2	8	3.2575603	2.3528795	3.4685895	4.7529645	4.504842	4.8402267	
1.4131	0.0003	4.1591		noncod	ENST0000	intronic		25.155							4.999999	4.999999	4.999999	20.98671	29.44107					
3E-06	32251	83	down	ing	0583956	antisense	SLC46A1	5	75	2.350054	4.406354	5	5	5	7	25.03946	2	2.3494408	2.3528795	2.3478405	4.321988	4.419878	4.4771953	
1.4131	0.0003	4.1591		noncod	ENST0000	natural		25.155							4.999999	4.999999	4.999999	20.98671	29.44107					
3E-06	32251	83	down	ing	0583956	antisense	SLC46A1	5	75	2.350054	4.406354	5	5	5	7	25.03946	2	2.3494408	2.3528795	2.3478405	4.321988	4.419878	4.4771953	
0.0015	0.0076	5.8846		noncod	TCONS_00			6.0692	44.928						4.999999		4.999999	47.00655	50.28775					
79647	01788	63	down	ing	005211	intergenic		67	394	2.679043	5.236003	5	8.207802	5	37.49087	4	8	2.3494408	3.339847	2.3478405	5.1318183	5.3151674	5.261022	
8.682E-05	58431	576	down	ing	014652	intergenic		85.678	252.81						84.55830		227.3469	291.1449						
0.0033	0.0129	2.2360		noncod	ENST0000	bidirectio		10.756	33.585						12.40594	10.90885	29.35173	29.59732	41.80647					
75267	31147	233	down	ing	0519655	nal	RIPK2	675	178	3.652464	4.8134	8.955218	8	8	4	6	3	3.414297	3.952275	3.5908213	4.7901278	4.6563168	4.9937544	
0.0267	0.0602	2.2544		noncod	ENST0000	intronic		11.774	34.749						6.620833	14.33925		37.67486						
32794	77805	865	down	ing	0424434	antisense	GNAS	078	851	3.701328	4.874127	14.36215	4	1	30.31027	36.26442	2	4.1095295	3.0246658	3.9697883	4.8384266	4.9481087	4.835845	
0.0267	0.0602	2.2544		noncod	ENST0000	intronic		11.774	34.749						6.620833	14.33925		37.67486						
32794	77805	865	down	ing	0424434	antisense	GNAS	078	851	3.701328	4.874127	14.36215	4	1	30.31027	36.26442	2	4.1095295	3.0246658	3.9697883	4.8384266	4.9481087	4.835845	
0.																								

0.0009	0.0054	2.0458		noncod	ENST0000	natural	C10orf13	35.453	102.86						117.2964	101.3341							
58501	79222	403	down	ing	0528844	antisense	7	473	0137	5.391231	6.423925	33.6398	35.95426	36.76636	89.94975	7	9	5.345747	5.518859	5.309088	6.3755193	6.6151614	6.281094
0.0009	0.0054	2.0458		noncod	ENST0000	natural	C10orf13	35.453	102.86						117.2964	101.3341							
58501	79222	403	down	ing	0528844	antisense	7	473	0137	5.391231	6.423925	33.6398	35.95426	36.76636	89.94975	7	9	5.345747	5.518859	5.309088	6.3755193	6.6151614	6.281094
0.0149	0.0388	4.3995		noncod	ENST0000	natural	KANSL1	14.721	81.727									93.70344					
82972	83562	251	down	ing	0452057	antisense	L	66	068	3.9578	6.095148	4	4	14.48263	71.37206	80.1057	5	3.0417259	4.8470635	3.9846098	6.04601	6.071122	6.1683106
2.6456	0.0008	5.0853		noncod	ENST0000	natural	CABLES	52.910	391.51									380.1045	429.5011				
E-05	11796	971	down	ing	0585184	antisense	1	041	8283	5.973439	8.3198	3	56.61057	54.72691	364.9492	2	3	5.8553333	6.1826897	5.8822947	8.35217	8.270165	8.337064
2.6456	0.0008	5.0853		noncod	ENST0000	natural	CABLES	52.910	391.51									380.1045	429.5011				
E-05	11796	971	down	ing	0585184	antisense	1	041	8283	5.973439	8.3198	3	56.61057	54.72691	364.9492	2	3	5.8553333	6.1826897	5.8822947	8.35217	8.270165	8.337064
2.6456	0.0008	5.0853		noncod	ENST0000	natural	CABLES	52.910	391.51									380.1045	429.5011				
E-05	11796	971	down	ing	0585184	antisense	1	041	8283	5.973439	8.3198	3	56.61057	54.72691	364.9492	2	3	5.8553333	6.1826897	5.8822947	8.35217	8.270165	8.337064
0.0002	0.0024	3.9532		noncod		sense-ove		26.722	146.45				20.94476	25.19449	34.02844	136.1067	140.8719	162.3770					
55334	15391	779	down	ing	NR_036536	rlapping	MATR3	568	1887	4.948655	6.931704	5	2	6	2	3	1	4.653913	4.9912033	5.200848	6.9626994	6.873717	6.958696
0.0002	0.0024	3.9532		noncod		sense-ove		26.722	146.45				20.94476	25.19449	34.02844	136.1067	140.8719	162.3770					
55334	15391	779	down	ing	NR_036536	rlapping	MATR3	568	1887	4.948655	6.931704	5	2	6	2	3	1	4.653913	4.9912033	5.200848	6.9626994	6.873717	6.958696
4.2881	0.0004	2.7382		noncod	ENST0000			85.319	340.35						94.56196	307.2654	336.8444	376.9679					
9E-06	1588	055	down	ing	0536487	intergenic		915	9303	6.663439	8.11667	79.36188	82.0359	6	7	8	6	6.5895205	6.7262864	6.67451	8.116226	8.092336	8.141447
0.0001	0.0020	5.3470		noncod	ENST0000	bidirectio		26.539	202.12				24.51940	31.02590	24.07295	192.1294	192.5280						
87769	27053	058	down	ing	0414676	nal	SOX12	42	7163	4.961407	7.380138	2	6	2	3	6	221.724	4.883148	5.30101	4.700062	7.44548	7.3031387	7.391795
0.0001	0.0019	2.0935		noncod		natural		282.35	911.25				251.0817	282.8200	313.1521								
77772	74985	901	down	ing	uc001edd.3	antisense	SLC16A1	1333	3633	8.428255	9.494234	7	7	6	812.3746	916.6203	1004.766	8.289025	8.559913	8.435828	9.475567	9.487802	9.519334
0.0041	0.0150	2.0789		noncod	ENST0000	intronic		32.906	93.599				26.16383	27.95173	44.60445			93.43809	102.7101				
76553	41242	742	down	ing	0560280	antisense	RORA	676	175	5.235642	6.291514	7	3	8	84.64924	5	9	4.982148	5.1423497	5.582429	6.284144	6.289319	6.3010793
0.0041	0.0150	2.0789		noncod	ENST0000	intronic		32.906	93.599				26.16383	27.95173	44.60445			93.43809	102.7101				
76553	41242	742	down	ing	0560280	antisense	RORA	676	175	5.235642	6.291514	7	3	8	84.64924	5	9	4.982148	5.1423497	5.582429	6.284144	6.289319	6.3010793
0.0041	0.0150	2.0789		noncod	ENST0000	intronic		32.906	93.599				26.16383	27.95173	44.60445			93.43809	102.7101				
76553	41242	742	down	ing	0560280	antisense	RORA	676	175	5.235642	6.291514	7	3	8	84.64924	5	9	4.982148	5.1423497	5.582429	6.284144	6.289319	6.3010793
5.7150	0.0011	6.4684		noncod				20.916	192.69				23.54896	20.47711		185.1634	182.8885	210.0469					
4E-05	11797	165	down	ing	uc010zan.1	intergenic		556	967	4.62005	7.313462	7	2	18.72359	7	7	7	4.826275	4.6876507	4.346224	7.395023	7.229826	7.3155384
1.5410	0.0003	8.3607		noncod	TCONS_00			92.224	1165.3				91.29111	87.08095		1137.171	1084.489	1274.318					
9E-06	36928	461	down	ing	029753	intergenic		277	26367	6.781037	9.844669	5	6	98.30076	1	9	1	6.798129	6.8156223	6.7293606	9.947874	9.728054	9.858079
0.0015	0.0074	2.2980		noncod				23.951	75.793				24.89671		29.20426			83.80398					
43055	57412	027	down	ing	uc010ady.1	intergenic		045	732	4.786455	5.986835	7	17.75215	8	67.5096	76.06761	6	4.906971	4.4772906	4.975102	5.96458	5.9966183	5.9993067
0.0395	0.0808	2.2415		noncod				8.2145	24.158				12.83890	5.446217	6.358431	21.91213		28.36043					
31805	77296	81	down	ing	NR_024429	intergenic		19	509	3.185505	4.350021	9	5	3	4	22.20296	2	3.9479108	2.734554	2.874049	4.380165	4.248934	4.4209647
2.9603	0.0008	2.6059		noncod	ENST0000			42.230	156.96				40.38313		44.56879	148.9698	148.3158	173.6048					
E-05	46163	711	down	ing	0464115	intergenic		962	3517	5.646259	7.02808	3	41.74096	4	8	3	4	5.617246	5.740179	5.581352	7.089458	6.9421153	7.052667
1.0486	0.0005	2.2316		noncod		natural		350.72	1226.2				360.4580	310.1046	381.6085	1090.826	1268.566	1319.393					
7E-05	59979	07	down	ing	NR_003138	antisense	GLRX5	3753	62067	8.752571	9.910654	7	4	5	3	8	1	8.828341	8.698169	8.731203	9.886253	9.940674	9.905035
0.0001	0.0015	2.4448		noncod				425.18	1629.8		10.32583			406.6515	496.5237	1414.316	1678.319	1796.946					
11924	34055	862	down	ing	NR_024397	intergenic		2273	60833	9.036069	7	372.3715	5	7	2	8	5	8.875593	9.10768	9.124935	10.26837	10.352867	10.356273
0.0174	0.0434	3.0516		noncod	ENST0000			8.1516	31.449				4.999999	10.56810		29.71766							
3489	58591	266	down	ing	0455355			91	13	3.125707	4.735285	5	1	8.886973	9	32.89787	31.73185	2.3494408	3.7151432	3.3125367	4.8078938	4.81164	4.5863223
0.0410	0.0831	3.0967		noncod	ENST0000	bidirectio		10.894	39.781				11.93241	4.999999	15.75080			48.08685					
12027	72593	648	down	ing	0412856	nal	SEPT7	407	669	3.430763	5.061525	9	5	1	34.71117	36.54698	7	3.8428216	2.3528795	4.0965877	5.02723	4.9598103	5.197534
0.0410	0.0831	3.0967		noncod	ENST0000	bidirectio		10.894	39.781				11.93241	4.999999	15.75080			48.08685					
12027	72593	648	down	ing	0412856	nal	SEPT7	407	669	3.430763	5.061525	9	5	1	34.71117	36.54698	7	3.8428216	2.3528795	4.0965877	5.02723	4.9598103	5.197534
0.0410	0.0831	3.0967		noncod	ENST0000	bidirectio		10.894	39.781				11.93241	4.999999	15.75080			48.08685					
12027	72593	648	down	ing	0412856	nal	SEPT7	407	669	3.430763	5.061525	9	5	1	34.71117	36.54698	7	3.8428216	2.3528795	4.0965877	5.02723	4.9598103	5.197534
1.5416	0.0006	3.7686		noncod	ENST0000	sense-ove		109.47	618.16				108.5079	100.3751	119.5472			714.6799					
1E-05	62721	37	down	ing	0432513	rlapping	SASH3	6747	551	7.034336	8.948379	04	1	26	581.6685	558.1481	3	7.053011	7.022969	7.0270295	9.003476	8.797667	9.043995
0.0046	0.0162	2.4750		noncod	ENST0000	intronic		14.498	50.135				11.25606			44.17826							
41345	59917	797	down	ing	0576956	antisense	PDE7B	896	988	4.063619	5.371094	9	14.00233	18.23829	5	40.20433	66.02537	3.7587986	4.1286163	4.3034425	5.367836	5.0903034	5.655143
0.0001	0.0014	2.9010		noncod	ENST0000			97.104	413.45							349.3617	433.9482	457.0494					
0188	66171	296	down	ing	0458422	intergenic		663	3157	6.851774	8.388339	84.72392	97.27057	109.3195	6	7	4	6.688924	6.9778214	6.8885756	8.288466	8.453479	8.423071
0.0001	0.0016	2.0633		noncod				369.82	1190.7				334.4935	360.4230	414.5559			1168.488	1270.054				
25876	1124	578	down	ing	uc010vhg.2	intergenic		4187	893	8.83253	9.877524	6	3	7	1133.825	5	4	8.712159	8.923827	8.861605	9.944113	9.835437	9.853023
0.0001	0.0019	2.7921		noncod	ENST0000	intronic		25.132	97.894														

rlapping																							
0.0010	0.0057	2.6118		noncod	ENST0000		29.096	105.91			23.99125	28.32860	97.38994	101.4265	118.9244								
22011	07123	009	down	ing	0565095	intergenic	666	365	5.085165	6.47021	34.97013	9	8	6	75	3	5.403021	4.9244313	4.928043	6.486603	6.411656	6.512371	
2.9698	0.0008	2.6826		noncod		natural	58.677	227.43			59.09413	56.73642	60.20153	213.6976	216.0012	252.6004							
5E-05	46163	274	down	ing	NR_040677	antisense	SIAH1	364	31	6.123808	7.547454	5	3	4	3	2	5	6.1639423	6.186526	6.0209546	7.5977283	7.4617257	7.582909
2.9698	0.0008	2.6826		noncod		natural	58.677	227.43			59.09413	56.73642	60.20153	213.6976	216.0012	252.6004							
5E-05	46163	274	down	ing	NR_040677	antisense	SIAH1	364	31	6.123808	7.547454	5	3	4	3	2	5	6.1639423	6.186526	6.0209546	7.5977283	7.4617257	7.582909
7.5833	0.0012	2.4433		noncod	ENST0000	natural	69.018	242.97			62.52474				242.2428	263.7860							
7E-05	6185	074	down	ing	0551187	antisense	CA7	281	6117	6.357892	7.646727	2	70.41708	74.11302	222.8995	1	4	6.2466803	6.5051064	6.3218884	7.662899	7.6306305	7.6466517
7.5833	0.0012	2.4433		noncod	ENST0000	natural	69.018	242.97			62.52474				242.2428	263.7860							
7E-05	6185	074	down	ing	0551187	antisense	CA7	281	6117	6.357892	7.646727	2	70.41708	74.11302	222.8995	1	4	6.2466803	6.5051064	6.3218884	7.662899	7.6306305	7.6466517
3.8872	0.0004	2.3752		noncod		natural	135.24	476.77			132.2109	125.5995			470.6956								
6E-06	13042	813	down	ing	uc003fua.2	antisense	ATP13A3	9632	3417	7.352529	8.600627	7	25	147.9384	454.7317	5	504.8929	7.356474	7.363718	7.3373938	8.669765	8.567358	8.564758
0.0005	0.0039	2.0509		noncod	ENST0000		37.429	107.76			34.37656	41.95913	111.2250	107.8384									
66572	54211	796	down	ing	0437865	intergenic	566	5305	5.463955	6.500268	35.953	4	3	9	25	104.2324	5.442953	5.4542084	5.494703	6.6805964	6.495097	6.3251104	
2.8976	0.0008	2.8786		noncod	ENST0000		36.451	149.25			33.74408	34.18996	41.42111		150.4289	172.6849							
5E-05	4204	385	down	ing	0366140	intergenic	721	9003	5.423766	6.949152	7	4	2	124.6631	9	2	5.3493376	5.445181	5.476778	6.8377748	6.9630637	7.046618	
0.0040	0.0147	2.1112		noncod	ENST0000	natural	MCM3A	10.434	31.114			11.61677				36.81018	33.29142						
40608	00798	382	down	ing	0444998	antisense	P	339	121	3.619897	4.697987	1	9.904417	9.78183	23.24075	4	8	3.805516	3.6155956	3.4385803	4.463733	4.970549	4.659678
0.0001	0.0018	2.3164		noncod	ENST0000		139.96	477.10			118.6680	171.7708	424.8470	492.8560									
56038	28421	176	down	ing	0566217	intergenic	4382	081	7.384446	8.596341	129.4542	76	7	5	8	513.5993	7.321094	7.278205	7.554039	8.571651	8.627896	8.589477	
0.0005	0.0039	2.9058		noncod		intronic	7.1621	28.674			5.562821				24.14741								
75026	91668	348	down	ing	NR_046711	antisense	POU6F2	66	904	3.057317	4.59627	7.41217	4	8.511506	3	29.48929	32.38801	3.154076	2.7632878	3.2545874	4.5208163	4.6501746	4.6178184
0.0005	0.0039	2.9058		noncod		intronic	7.1621	28.674			5.562821				24.14741								
75026	91668	348	down	ing	NR_046711	antisense	POU6F2	66	904	3.057317	4.59627	7.41217	4	8.511506	3	29.48929	32.38801	3.154076	2.7632878	3.2545874	4.5208163	4.6501746	4.6178184
0.0007	0.0046	2.0108		noncod		intronic	349.33	1088.1			350.6152	280.8809	416.4957	917.2773	1162.197								
4454	88398	949	down	ing	uc001vfn.3	antisense	INTS6	0637	10147	8.733723	9.741561	3	2	6	4	1	1184.856	8.783673	8.550476	8.86702	9.646135	9.82799	9.750557
0.0007	0.0046	2.0108		noncod		natural	349.33	1088.1			350.6152	280.8809	416.4957	917.2773	1162.197								
4454	88398	949	down	ing	uc001vfn.3	antisense	INTS6	0637	10147	8.733723	9.741561	3	2	6	4	1	1184.856	8.783673	8.550476	8.86702	9.646135	9.82799	9.750557
0.0301	0.0660	2.1275		noncod	ENST0000	bidirectio	CAMSAP	8.5011	24.761			6.647501	12.06857	6.787408		28.36767							
70187	76601	433	down	ing	0423793	nal	1	61	383	3.288211	4.3774	5	2	4	19.61586	8	26.30061	2.9965703	3.9114215	2.9566426	4.227593	4.593584	4.3110228
0.0060	0.0197	2.1614		noncod		natural	16.618	50.483			20.00136	15.51500	14.34006		44.95203								
68982	29316	119	down	ing	uc003nog.1	antisense	HLA-A	813	601	4.27858	5.390554	8	9	1	42.36592	4	64.13285	4.583483	4.282256	3.9700003	5.3073497	5.2517586	5.612553
0.0060	0.0197	2.1614		noncod		natural	16.618	50.483			20.00136	15.51500	14.34006		44.95203								
68982	29316	119	down	ing	uc003nog.1	antisense	HLA-A	813	601	4.27858	5.390554	8	9	1	42.36592	4	64.13285	4.583483	4.282256	3.9700003	5.3073497	5.2517586	5.612553
0.0001	0.0018	2.5915		noncod	ENST0000	natural	33.403	122.52			31.26651	33.10196			126.2908								
55619	25875	631	down	ing	0563278	antisense	SIN3A	096	689	5.303409	6.677231	35.84081	6	3	108.2061	133.0837	7	5.438374	5.3119564	5.1598964	6.6429596	6.7892904	6.5994444
0.0001	0.0018	2.5915		noncod	ENST0000	natural	33.403	122.52			31.26651	33.10196			126.2908								
55619	25875	631	down	ing	0563278	antisense	SIN3A	096	689	5.303409	6.677231	35.84081	6	3	108.2061	133.0837	7	5.438374	5.3119564	5.1598964	6.6429596	6.7892904	6.5994444
0.0001	0.0018	2.5915		noncod	ENST0000	natural	33.403	122.52			31.26651	33.10196			126.2908								
55619	25875	631	down	ing	0563278	antisense	MAN2C1	096	689	5.303409	6.677231	35.84081	6	3	108.2061	133.0837	7	5.438374	5.3119564	5.1598964	6.6429596	6.7892904	6.5994444
0.0001	0.0018	2.5915		noncod	ENST0000	natural	33.403	122.52			31.26651	33.10196			126.2908								
55619	25875	631	down	ing	0563278	antisense	MAN2C1	096	689	5.303409	6.677231	35.84081	6	3	108.2061	133.0837	7	5.438374	5.3119564	5.1598964	6.6429596	6.7892904	6.5994444
0.0001	0.0018	2.5915		noncod	ENST0000	natural	33.403	122.52			31.26651	33.10196			126.2908								
55619	25875	631	down	ing	0563278	antisense	SIN3A	096	689	5.303409	6.677231	35.84081	6	3	108.2061	133.0837	7	5.438374	5.3119564	5.1598964	6.6429596	6.7892904	6.5994444
0.0001	0.0016	2.4618		noncod	ENST0000		58.916	209.15			51.54037				188.2673								
30108	50653	93	down	ing	0431981	intergenic	642	9693	6.122179	7.421947	58.49441	5	66.71514	193.5736	8	245.6381	6.1507516	6.0429688	6.1728163	7.4554224	7.269914	7.5405045	
2.4418	0.0003	3.4907		noncod			392.79	2158.2		10.72996				425.0518		2250.011	2376.482						
6E-06	67353	019	down	ing	uc001utv.3	intergenic	9373	86867	8.926446	3	393.8579	359.4884	2	1848.367	2	4	8.962129	8.919567	8.897642	10.648577	10.7846365	10.756676	
0.0003	0.0029	2.0661		noncod	ENST0000	natural	CTDSPL	181.57	561.99			194.2453	152.3626	198.1039	470.6766	588.4784							
53312	66772	96	down	ing	0560750	antisense	2	0657	3073	7.769433	8.81641	9	7	1	7	5	626.8241	7.9070597	7.637979	7.763261	8.714774	8.871556	8.862901
						intron																	
0.0004	0.0035	2.5127		noncod	ENST0000	sense-ove	C17orf10	13.998	48.425			14.50489	11.32797	16.16255	46.68882	50.15085	48.43673						
70082	43082	148	down	ing	0579188	rlapping	1	473	471	4.023986	5.353233	1	05	8	4	6	3	4.1223726	3.8173096	4.1322765	5.4433975	5.409064	5.207238
						intron																	
0.0004	0.0035	2.5127		noncod	ENST0000	sense-ove	C17orf10	13.998	48.425			14.50489	11.32797	16.16255	46.68882	50.15085	48.43673						
70082	43082	148	down	ing	0579188	rlapping	1	473	471	4.023986	5.353233	1	05	8	4	6	3	4.1223726	3.8173096	4.1322765	5.4433975	5.409064	5.207238
0.0001	0.0015	2.0444		noncod			375.50	1208.0			367.4104	331.8568	427.2465	1001.804		1328.096							
18749	73059	352	down	ing	NR_045026	intergenic	4607	10033	8.854905	9.886608	3	7	2	8	1294.129	3	8.854281	8.804669	8.905766	9.766023	9.977861	9.915939	
0.0076	0.0235	2.6607		noncod			7.3506	26.865			5.307070				7.239350	25.78813	22.44684						
81568	66702	815	down	ing	uc002nsx.1	intergenic	59	923	3.08551	4.497													



CERTIFICATE OF EDITING

This is to certify that the paper titled Prognostic value of macrophage-associated long non-coding RNA expression for hepatocellular carcinoma commissioned to us by Guanyu Chen has been edited for English language, grammar, punctuation, and spelling by Enago, the editing brand of Crimson Interactive Consulting Co., Ltd.

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