

Supplementary Table 6: Biological function analysis for protein coding genes with negative expressional correlation to lncRNAs of the signature (Only GO biological process terms with Benjamini corrected p value < E-2 are shown).

Annotation Cluster 1 Enrichment Score: 4.555732289721201					
Category	Term	Count	PValue	Genes	Benjamini
GOTERM_BP_FAT	GO:0007049~cell cycle	107	5.46E-08	SEPT4, RAD51C, SEPT3, RBM7, FOXO4, WTAP, CTNNB1, CUL2, MEI1, NUP37, TUBG1, CUL1, ZC3HC1, CGRRF1, CHTF8, HMG20B, PPP1CC, DCTN3, ESCO2, DCTN2, RAD1, HHEX, DCLRE1A, PPP1CA, MAD2L1, PSMA5, MAD2L2, SEPT7, UBA52, EID1, ANAPC13, TIPIN, CHEK1, ANAPC11, CHEK2, CDC34, CCNG1, ITGB1, PIN1, SPC24, PSMB5, TUBB, GADD45GIP1, PSMB3, PSMB2, FBXO5, CKAP2, SSSCA1, YEATS4, CCPG1, CDC20, PMF1, TET2, CDC27, SUV39H2, RNF8, PSMC3, UTP14C, SPIN1, KIAA0174, E2F6, MLH1, KIF2B, MCM7, EVI5, PSMD1, PSMD2, ZW10, PSMD9, ARL2, BANP, PBK, CDK5, EML4, PPM1G, PPM1D, RIF1, NSL1, UBC, HAUS7, PSME3, HAUS8, IL12B, GADD45A, ACVR1, DHH, PPP6C, HAUS6, HAUS2, BCCIP, CENPA, HINFP, BUB3, APC, MSH6, TXNL4B, GMNN, DLGAP5, CENPJ, SIRT2, PSMD13, GSPT1, PSMD11, PTP4A1, VPS24, TEX11, TP53INP1	1.80E-04
GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	62	7.42E-08	E2F6, FOXO4, KIF2B, CUL2, PSMD1, PSMD2, NUP37, CUL1, ZW10, PSMD9, ZC3HC1, PBK, DCTN3, EML4, DCTN2, PPM1D, DCLRE1A, MAD2L1, PSMA5, NSL1, UBC, HAUS7, PSME3, HAUS8, MAD2L2, SEPT7, GADD45A, UBA52, ACVR1, PPP6C, HAUS6, ANAPC13, HAUS2, TIPIN, CHEK1, CDC34, ANAPC11, CCNG1, ITGB1, PSMB5, SPC24, TUBB, CENPA, PSMB3, PSMB2, HINFP, FBXO5, BUB3, APC, SSSCA1, YEATS4, TXNL4B, DLGAP5, CDC20, PMF1, CDC27, SIRT2, RNF8, PSMD13, GSPT1, PSMC3, PSMD11	8.15E-05
GOTERM_BP_FAT	GO:0022402~cell cycle process	79	2.28E-06	RAD51C, E2F6, MLH1, RBM7, FOXO4, CTNNB1, KIF2B, CUL2, MEI1, PSMD1, PSMD2, NUP37, TUBG1, CUL1, ZW10, PSMD9, CGRRF1, ZC3HC1, PBK, DCTN3, EML4, DCTN2, RAD1, PPM1G, PPM1D, DCLRE1A, MAD2L1, PSMA5, NSL1, UBC, PSME3, HAUS7, IL12B, HAUS8, MAD2L2, SEPT7, GADD45A, UBA52, ACVR1, PPP6C, DHH, HAUS6, ANAPC13, HAUS2, TIPIN, CHEK1, CDC34, ANAPC11, CCNG1, ITGB1, PSMB5, SPC24, TUBB, CENPA, PSMB3, PSMB2, HINFP, FBXO5, BUB3, APC, SSSCA1, MSH6, YEATS4, TXNL4B, DLGAP5, CDC20, PMF1, CDC27, CENPJ, SIRT2, SUV39H2, RNF8, PSMD13, GSPT1, PSMC3, PSMD11, UTP14C, TP53INP1, TEX11	0.001072
GOTERM_BP_FAT	GO:0022403~cell cycle phase	59	2.95E-05	RAD51C, E2F6, MLH1, RBM7, FOXO4, KIF2B, MEI1, CUL2, NUP37, TUBG1, CUL1, ZW10, ZC3HC1, PBK, DCTN3, EML4, DCTN2, RAD1, DCLRE1A, PPM1D, MAD2L1, NSL1, HAUS7, HAUS8, MAD2L2, SEPT7, GADD45A, ACVR1, PPP6C, HAUS6, ANAPC13, HAUS2, TIPIN, CHEK1, CDC34, ANAPC11, CCNG1, ITGB1, SPC24, TUBB, HINFP, FBXO5, BUB3, APC, SSSCA1, MSH6, YEATS4, TXNL4B, DLGAP5, CDC20, PMF1, CDC27, SIRT2, SUV39H2, RNF8, PSMD13, GSPT1, UTP14C, TEX11	0.004621
GOTERM_BP_FAT	GO:0048285~organelle fission	38	4.25E-05	HAUS6, COX10, ANAPC13, HAUS2, TIPIN, ANAPC11, CCNG1, PEX11G, SPC24, KIF2B, FIS1, TUBB, FBXO5, NUP37, BUB3, ZW10, APC, SSSCA1, TXNL4B, YEATS4, ZC3HC1, DLGAP5, CDC20, PBK, PMF1,	0.005808

				DCTN3, CDC27, SIRT2, DCTN2, EML4, RNF8, DCLRE1A, MAD2L1, NSL1, HAUS7, HAUS8, MAD2L2, SEPT7	
Annotation Cluster 2 Enrichment Score: 4.4572626214809095					
Category	Term	Count	PValue	Genes	Benjamini
GOTERM_BP_FAT	GO:0051340~regulation of ligase activity	24	6.77E-08	SMAD7, CDC20, ANAPC11, FEM1A, CDC27, PIN1, PSMB5, PSMD13, MAD2L1, PSMA5, PSMC3, PSMD11, PSMB3, PSMB2, PSMD1, UBC, PSMD2, FBXO5, PSME3, NHEJ1, UBA52, CUL1, BUB3, PSMD9	1.12E-04
GOTERM_BP_FAT	GO:0051438~regulation of ubiquitin-protein ligase activity	23	1.49E-07	SMAD7, CDC20, ANAPC11, FEM1A, CDC27, PIN1, PSMB5, PSMD13, MAD2L1, PSMA5, PSMC3, PSMD11, PSMB3, PSMB2, PSMD1, UBC, PSMD2, FBXO5, PSME3, UBA52, BUB3, CUL1, PSMD9	1.22E-04
GOTERM_BP_FAT	GO:0051444~negative regulation of ubiquitin-protein ligase activity	20	9.50E-07	SMAD7, CDC20, ANAPC11, CDC27, PSMB5, PSMD13, MAD2L1, PSMA5, PSMC3, PSMD11, PSMB3, PSMB2, PSMD1, UBC, PSMD2, FBXO5, PSME3, UBA52, BUB3, PSMD9	6.26E-04
GOTERM_BP_FAT	GO:0051352~negative regulation of ligase activity	20	9.50E-07	SMAD7, CDC20, ANAPC11, CDC27, PSMB5, PSMD13, MAD2L1, PSMA5, PSMC3, PSMD11, PSMB3, PSMB2, PSMD1, UBC, PSMD2, FBXO5, PSME3, UBA52, BUB3, PSMD9	6.26E-04
GOTERM_BP_FAT	GO:0031397~negative regulation of protein ubiquitination	21	1.15E-06	SMAD7, CDC20, ANAPC11, CDC27, CDK5, PSMB5, PSMD13, MAD2L1, PSMA5, PSMC3, PSMD11, PSMB3, PSMB2, PSMD1, UBC, PSMD2, FBXO5, PSME3, UBA52, BUB3, PSMD9	6.30E-04
GOTERM_BP_FAT	GO:0051439~regulation of ubiquitin-protein ligase activity during mitotic cell cycle	20	2.49E-06	CDC20, ANAPC11, CDC27, PSMB5, PSMD13, MAD2L1, PSMA5, PSMC3, PSMD11, PSMB3, PSMB2, PSMD1, UBC, PSMD2, FBXO5, PSME3, UBA52, BUB3, CUL1, PSMD9	0.001026
GOTERM_BP_FAT	GO:0051436~negative regulation of ubiquitin-protein ligase activity during mitotic cell cycle	19	2.67E-06	CDC20, ANAPC11, CDC27, PSMB5, PSMD13, MAD2L1, PSMC3, PSMD11, PSMA5, PSMB3, PSMB2, PSMD1, UBC, PSMD2, FBXO5, PSME3, UBA52, BUB3, PSMD9	9.77E-04
GOTERM_BP_FAT	GO:0051351~positive regulation of ligase activity	20	3.91E-06	CDC20, ANAPC11, CDC27, PIN1, PSMB5, PSMD13, PSMC3, PSMD11, PSMA5, PSMB3, PSMB2, PSMD1, UBC, PSMD2, FBXO5, PSME3, NHEJ1, UBA52, CUL1, PSMD9	0.001288
GOTERM_BP_FAT	GO:0031396~regulation of protein ubiquitination	24	3.94E-06	SMAD7, CDC20, ANAPC11, FEM1A, CDC27, CDK5, PIN1, PSMB5, PSMD13, MAD2L1, PSMA5, PSMC3, PSMD11, PSMB3, PSMB2, PSMD1, UBC, PSMD2, FBXO5, PSME3, UBA52, BUB3, CUL1, PSMD9	0.001178
GOTERM_BP_FAT	GO:0051443~positive regulation of ubiquitin-protein ligase activity	19	8.41E-06	CDC20, ANAPC11, CDC27, PIN1, PSMB5, PSMD13, PSMC3, PSMD11, PSMA5, PSMB3, PSMB2, PSMD1, UBC, PSMD2, FBXO5, PSME3, UBA52, CUL1, PSMD9	0.001977
GOTERM_BP_FAT	GO:0031145~anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	18	1.17E-05	CDC20, ANAPC11, CDC27, PSMB5, MAD2L1, PSMD13, PSMC3, PSMD11, PSMA5, PSMB3, PSMB2, PSMD1, UBC, PSMD2, PSME3, UBA52, BUB3, PSMD9	0.002401
GOTERM_BP_FAT	GO:0010498~proteasomal protein catabolic process	23	1.89E-05	TBL1XR1, CDC20, EDEM3, ANAPC11, EDEM1, CDC27, SELS, PSMB5, PSMD13, MAD2L1, PSMA5, PSMC3, PSMD11, PSMB3, PSMB2, PPP2CB, PSMD1, UBC, PSMD2, PSME3, UBA52, BUB3, PSMD9	0.003273

GOTERM_BP_FAT	GO:0043161~proteasomal ubiquitin-dependent protein catabolic process	23	1.89E-05	TBL1XR1, CDC20, EDEM3, ANAPC11, EDEM1, CDC27, SELS, PSMB5, PSMD13, MAD2L1, PSMA5, PSMC3, PSMD11, PSMB3, PSMB2, PPP2CB, PSMD1, UBC, PSMD2, PSME3, UBA52, BUB3, PSMD9	0.003273
GOTERM_BP_FAT	GO:0051437~positive regulation of ubiquitin-protein ligase activity during mitotic cell cycle	18	2.23E-05	CDC20, ANAPC11, CDC27, PSMB5, PSMD13, PSMC3, PSMD11, PSMA5, PSMB3, PSMB2, PSMD1, UBC, PSMD2, FBXO5, PSME3, UBA52, CUL1, PSMD9	0.003657
GOTERM_BP_FAT	GO:0031398~positive regulation of protein ubiquitination	20	3.44E-05	SMAD7, CDC20, ANAPC11, CDC27, PIN1, PSMB5, PSMD13, PSMC3, PSMD11, PSMA5, PSMB3, PSMB2, PSMD1, UBC, PSMD2, FBXO5, PSME3, UBA52, CUL1, PSMD9	0.005129

Annotation Cluster 3 Enrichment Score: 4.339863612496553

Category	Term	Count	PValue	Genes	Benjamini
GOTERM_BP_FAT	GO:0045184~establishment of protein localization	95	3.60E-05	COPA, SEC24A, MSR1, RAB9B, LMAN2L, UNC50, CHMP7, USE1, EIF5A, FGF10, PEX3, CLTC, CANX, VPS33A, AIP, FAM125A, HOMER3, DNAJC14, NECAP1, NUP37, STAM, NUP35, RAMP1, ZW10, RAMP3, SCAMP2, SNUPN, RAB4B, FUT10, AP4M1, NLRP3, TIMM23, TIMM44, YIF1A, CDK5, PRKCB, TRAM1L1, MYRIP, ATG4C, VAMP7, TOMM20, RAB14, SNX11, LCP2, BID, RAB3C, NUP160, SNX14, MTX1, PPT1, SEC62, SFT2D1, SLC11A1, RAB43, TOMM6, TMED3, STX18, HINFP, SEC22C, SCG5, SNAP23, APPBP2, STX11, STX10, TRAM1, EXOC2, SNX20, EIF4ENIF1, SYS1, RAB2B, RILP, GDI2, RAB8B, CUBN, VTA1, SNAPIN, RAB33A, SELS, ABCG1, LIN7A, PREB, RAB32, SCFD1, RAB30, COG6, YWHAH, TOM1L1, RAB34, VPS24, TRPC4AP, SEC13, YIPF5, NUTF2, SSR4, F2R	0.005141
GOTERM_BP_FAT	GO:0015031~protein transport	94	4.26E-05	COPA, SEC24A, MSR1, RAB9B, LMAN2L, UNC50, CHMP7, USE1, EIF5A, FGF10, PEX3, CLTC, CANX, VPS33A, AIP, FAM125A, HOMER3, DNAJC14, NECAP1, NUP37, STAM, NUP35, RAMP1, ZW10, RAMP3, SCAMP2, SNUPN, RAB4B, FUT10, AP4M1, NLRP3, TIMM23, TIMM44, YIF1A, CDK5, PRKCB, TRAM1L1, MYRIP, ATG4C, VAMP7, TOMM20, RAB14, SNX11, LCP2, BID, RAB3C, NUP160, SNX14, MTX1, PPT1, SEC62, SFT2D1, SLC11A1, RAB43, TOMM6, TMED3, STX18, SEC22C, SCG5, SNAP23, APPBP2, STX11, STX10, TRAM1, EXOC2, SNX20, EIF4ENIF1, SYS1, RAB2B, RILP, GDI2, RAB8B, CUBN, VTA1, SNAPIN, RAB33A, SELS, ABCG1, LIN7A, PREB, RAB32, SCFD1, RAB30, COG6, YWHAH, TOM1L1, RAB34, VPS24, TRPC4AP, SEC13, YIPF5, NUTF2, SSR4, F2R	0.005592
GOTERM_BP_FAT	GO:0008104~protein localization	105	6.24E-05	RAB9B, LMAN2L, UNC50, CHMP7, USE1, FGF10, EIF5A, VPS33A, IL10, AIP, CTNBN1, FAM125A, HOMER3, GRIN2C, NUP37, STAM, NUP35, CUTA, SCAMP2, FUT10, AP4M1, YIF1A, TRAM1L1, VAMP7, RAB14, PALM, MTX1, PPT1, SLC11A1, TOMM6, STX18, SUPT7L, STX11, TRAM1, STX10, SYS1, RILP, CUBN, RAB8B, SNAPIN, RAB33A, ABCG1, LIN7A, SEC13, YIPF5, NUTF2, COPA, SEC24A, MSR1, ALG2, PEX3, CLTC, CANX, DNAJC14, TMSB15B, NECAP1, RAMP1, ZW10, RAMP3, SNUPN, RAB4B, NLRP3, TIMM23, TIMM44, CDK5, PRKCB, MYRIP, ATG4C, TOMM20, LCP2, SNX11, BID, RAB3C, NUP160, SNX14, SEC62, SFT2D1, RAB43, TMED3, SH3GLB1, HINFP, SCG5, SEC22C, SNAP23,	0.007869

				APPBP2, ERCC3, EXOC2, SNX20, EIF4ENIF1, RAB2B, GDI2, VTA1, SELS, PREB, RAB32, SCFD1, RAB30, YWHAH, COG6, TOM1L1, RAB34, VPS24, TRPC4AP, SSR4, F2R	
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Annotation Cluster 4 Enrichment Score: 3.984160160453971

Category	Term	Count	PValue	Genes	Benjamini
GOTERM_BP_FAT	GO:0044265~cellular macromolecule catabolic process	94	5.92E-06	RNASEH1, MLH1, SENP7, USP50, CUL2, MAP1LC3C, PSMD1, PSMD2, FBXL12, RNF34, FBXO22, CUL1, KLHL20, USP13, PSMD9, TBL1XR1, ZC3HC1, ADAM10, UBE2MP1, DTL, FBXL20, DFFB, RELA, RING1, UBE2J1, UBE2J2, RNASEH2A, PJA1, MAD2L1, ATG4C, PIAS4, PSMA5, MED8, FBXO18, UBE2M, UBC, RNF25, UCHL5, CAND2, UBE2W, PSME3, SPOPL, UBA52, ASB6, DNAH12, APH1A, ANAPC13, APH1B, RNH1, PPT1, CDC34, ANAPC11, EDEM3, FEM1A, EDEM1, SMUG1, PSMB5, FBXW9, UBE2D4, RPA2, SUMO1, PSMB3, PPP2CB, PSMB2, RNF11, FBXO5, RNF167, PPIL5, FBXO3, ERCC3, NTHL1, FBXO8, BUB3, ERCC1, UBL7, UPF2, RNASE2, CDC20, CDC27, SELS, RNF8, DNASE2, UBE2E3, TXNDC12, GMCL1, PSMD13, TOM1L1, GSPT1, PSMC3, PSMD11, DCP1A, ZRANB1, UBXN6, OGG1, RNF111	0.001624
GOTERM_BP_FAT	GO:0009057~macromolecule catabolic process	99	8.50E-06	USE1, RNASEH1, USP50, CUL2, RNF34, FBXO22, CUL1, ZC3HC1, UBE2MP1, DTL, RELA, DFFB, UBE2J1, UBE2J2, RNASEH2A, MAD2L1, PIAS4, PSMA5, FBXO18, RNF25, UBA52, ASB6, DNAH12, ANAPC13, PPT1, ANAPC11, CDC34, FBXW9, PSMB5, UBE2D4, PSMB3, PSMB2, RNF11, FBXO5, RNF167, FBXO3, PPIL5, NTHL1, FBXO8, CDC20, CDC27, ABCG1, RNF8, DNASE2, TXNDC12, UBE2E3, PSMC3, DCP1A, MLH1, SENP7, MAP1LC3C, PSMD1, PSMD2, FBXL12, KLHL20, PSMD9, USP13, TBL1XR1, CLN3, ADAM10, FBXL20, RING1, CDK5, PJA1, ATG4C, MED8, UBE2M, UBC, UCHL5, UBE2W, CAND2, PSME3, SPOPL, APH1A, APH1B, RNH1, EDEM3, EDEM1, FEM1A, SMUG1, NGLY1, RPA2, SUMO1, PPP2CB, ERCC3, BUB3, ERCC1, UBL7, UPF2, RNASE2, SELS, PSMD13, GMCL1, TOM1L1, GSPT1, PSMD11, ZRANB1, UBXN6, OGG1, RNF111	0.001864
GOTERM_BP_FAT	GO:0030163~protein catabolic process	79	7.43E-05	USE1, SENP7, USP50, CUL2, MAP1LC3C, PSMD1, PSMD2, FBXL12, RNF34, FBXO22, KLHL20, CUL1, USP13, PSMD9, TBL1XR1, CLN3, ZC3HC1, ADAM10, UBE2MP1, FBXL20, DTL, RELA, RING1, UBE2J1, UBE2J2, PJA1, MAD2L1, ATG4C, PIAS4, PSMA5, FBXO18, MED8, UBE2M, UBC, RNF25, UCHL5, CAND2, UBE2W, PSME3, SPOPL, UBA52, ASB6, DNAH12, APH1A, ANAPC13, APH1B, PPT1, CDC34, EDEM3, ANAPC11, FEM1A, EDEM1, PSMB5, FBXW9, UBE2D4, SUMO1, PSMB3, PPP2CB, PSMB2, RNF11, FBXO5, RNF167, PPIL5, FBXO3, FBXO8, BUB3, UBL7, CDC20, CDC27, SELS, RNF8, UBE2E3, GMCL1, PSMD13, TOM1L1, PSMC3, PSMD11, ZRANB1, UBXN6, RNF111	0.009016

Annotation Cluster 5 Enrichment Score: 3.4037107915296896

Category	Term	Count	PValue	Genes	Benjamini
GOTERM_BP_FAT	GO:0006354~RNA elongation	16	8.04E-06	POLR2F, POLR2L, TAF5, ELL, POLR2I, POLR2D, GTF2B, POLR2B, TAF11, ADRM1, TAF13, GTF2E2,	0.002035

				GTF2F1, TCEB3, TCEA2, ERCC3	
GOTERM_BP_FAT	GO:0006368~RNA elongation from RNA polymerase II promoter	15	1.79E-05	POLR2F, POLR2L, TAF5, ELL, POLR2I, POLR2D, GTF2B, POLR2B, TAF11, ADRM1, TAF13, GTF2E2, GTF2F1, TCEB3, ERCC3	0.003264