

**Table S1. Direct human LIN28A binding partners are enriched for glucose and diabetes related genes.**

Table showing metabolic pathway gene sets are represented.

<b>Gene set name</b>	<b>Size</b>	<b>Description</b>	<b>p value</b>
DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP	1398	Genes up-regulated in CD34+ [Gene ID=947] cells isolated from bone marrow of CML (chronic myelogenous leukemia) patients, compared to those from normal donors.	< 1.0E-13
DANG_BOUND_BY_MYC	1053	Genes whose promoters are bound by MYC [Gene ID=4609], according to MYC Target Gene Database.	< 1.0E-13
GRADE_COLON_CANCER_UP	737	Up-regulated genes in colon carcinoma tumors compared to the matched normal mucosa samples.	< 1.0E-13
REACTOME_DIABETES_PATHWAYS	383	Genes involved in Diabetes pathways	< 1.0E-13
REACTOME_METABOLISM_OF_PROTEINS	215	Genes involved in Metabolism of proteins	< 1.0E-13
REACTOME_GLUCOSE_REGULATION_OF_INSULIN_SECRETION	161	Genes involved in Glucose Regulation of Insulin Secretion	< 1.0E-13
REACTOME_INSULIN_SYNTHESIS_AND_SECRETION	129	Genes involved in Insulin Synthesis and Secretion	< 1.0E-13
REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT	114	Genes involved in Regulation of beta-cell development	< 1.0E-13
REACTOME_TRANSLATION	120	Genes involved in Translation	< 1.0E-13
REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA_CELLS	101	Genes involved in Regulation of gene expression in beta cells	< 1.0E-13
KEGG_RIBOSOME	88	Ribosome	< 1.0E-13
LI_AMPLIFIED_IN_LUNG_CANCER	165	Genes with increased copy number that correlates with increased expression across six different lung adenocarcinoma cell lines.	7.51E-13
REACTOME_INTEGRATION_OF_ENERGY_METABOLISM	229	Genes involved in Integration of energy metabolism	1.50E-12

## Table S2. Primers used for wild-type and mutant UTR cloning.

The targets of the *let-7* family were predicted by [TargetScan](#) 5.1. 3'UTRs from mouse and human genomic or cDNA clones were cloned by PCR using the primers listed below and cloned into the XbaI site of the pTK-RL vector (Promega).

### primers used for UTR cloning

hIGF1-utr-547F	attaaatctagaCGTCGTCAAGAAGCACACCAA
hIGF1-utr-2577R	attaaatctagaGTCTGGAAAACAGGCAGAGG
mPIK3IP1-utr-F1	attaaatctagaCGCAGGTGCCCATGTAAACAC
mPIK3IP1-utr-R1	attaaatctagaTGCAAGGTAAAACCATGTCTTG
hEIF4EBP2-utr-F1	attaaatctagaCATGCAGTTGGGGATGAT
hEIF4EBP2-utr-R1	attaaatctagaTTAATTAAAAACAGAACAGGGATACA
mLin28a-utr-F	attaaatctagaCGGCCAGGAGTCAGGGTATTCT
mLin28a-utr-R	attaaatctagaCAGTACCAACTCTGGAGTACCA
hINSR-utr-2351F	attaaatctagaCAGGTGAATGGGGGATAGTG
hINSR-utr-2747R	attaaatctagaGCCATCTCTCACCAAAGGAA
hRPS6KA3-utr-5231R	attaaatctagaTGATGCGATTTAACACCAA
hRPS6KA3-utr-4014F	attaaatctagaCTTCAACCCAGGTTGCTTAC
hRPS6KA3-utr-3139F	attaaatctagaCGCAACAGACCCCAACTTAA
hIRS2-utr-1303R	attaaatctagaACATTCTGCCGGTCAAGTTC
hIRS2-utr-379F	attaaatctagaCGGAGAGTGCACCCGTACCTA
hRICTOR-utr-1667F	attaaatctagaCGGCTGTAAGCTGCTGCTTATGTTG
hRICTOR-utr2339R	attaaatctagaGACCTGTCTAGTAAATCATGGAG
hIGF1R-utr-63F	attaaatctagaCGAGAGAGTTTTAACAATCC
hIGF1R-utr-2720R	attaaatctagaCTGTGGCGTGGATGAGGT
hEIF4G2-utr-7F	attaaatctagaCGCCAAAGCCTTAAATTTGTGC
hEIF4G2-utr-717R	attaaatctagaAGGGCATGAACATGACTTGA
hAKT2-utr-1566F	attaaatctagaCAACCACTCTGGGCTTTG
hAKT2-utr-3800R	attaaatctagaGCAGAGAGGTAATCAGCACCA
hTSC1-utr-1F	attaaatctagaCGAATGATGGTCAATCAGTGTAA
hTSC1-utr-1098R	attaaatctagaGAAAAGCTGCCCTCTTCT
mHmgal-utr-F1	attaaatctagaTGCTCCATAGCCACTGAGG
mHmgal-utr-R1	attaaatctagaCCTACACCCTTTTCCCATCA

### Site Directed mutagenesis sequences

human IGF1 wild-type	ggggcaatatgtcatctac <b>CTACCTC</b> aaaggggtggtataaggtt
human IGF1 let-7 site mutated	ggggcaatatgtcatctac <b>cgaacgc</b> aaaggggtggtataaggtt
human INSR wild-type	atagtgatthttcttttttcagcacagt <b>CTACCTC</b> agtgtattggttaagatgtgattcaatc
human INSR let-7 site 1 mutated	atagtgatthttcttttttcagcacagt <b>cgaacgc</b> agtgtattggttaagatgtgattcaatc
human INSR wild-type	atggacatctttgagatttcagaatt <b>CTACCTC</b> ggaaccggtctgaatcag
human INSR let-7 site 2 mutated	atggacatctttgagatttcagaatt <b>cgaacgc</b> ggaaccggtctgaatcag
human IGF1R wild-type	atccattcacaagcctcct <b>TACCTCA</b> agtggatcttcagaactgc
human IGF1R let-7 site 1 mutated	atccattcacaagcctcct <b>cgaacgc</b> agtggatcttcagaactgc
human IRS2 wild-type	ctcaaacgaccacagtc <b>CTACCTC</b> agttcaaggtaaagccgg
human IRS2 let-7 site mutated	ctcaaacgaccacagtc <b>cgaacgc</b> agttcaaggtaaagccgg