Table SI. P-values for comparison of N^6-methyladenosine-related enzyme expression in sequencing data from the GSE115313 dataset between diabetes mellitus and non-diabetes mellitus groups.

Genes	P-values
HNRNPA2B1	0.28045
HNRNPC	0.76416
IGF2BP1	0.90054
IGF2BP2	0.00025
IGF2BP3	0.51114
METTL14	0.94023
RBM15	0.14401
RBM15B	0.48326
VIRMA	0.82199
WTAP	0.78331
YTHDC2	0.74515
ZC3H13	0.06851

HNRNPA2B1, heterogeneous nuclear ribonucleoproteins A2/B1; HNRNPC, heterogeneous nuclear ribonucleoproteins C1/C2; IGF2BP1, insulin-like growth factor 2 mRNA-binding protein 1; IGF2BP2, insulin-like growth factor 2 mRNA binding protein 2; IGF2BP3, insulin-like growth factor 2 mRNA-binding protein 3; METTL14, methyltransferase-like protein 14; RBM15, RNA-binding protein 15; RBM15B, putative RNA-binding protein 15B; VIRMA, protein virilizer homolog; WTAP, pre-mRNA-splicing regulator WTAP; YTHDC2, 3'-5' RNA helicase YTHDC2; ZC3H13, zinc finger CCCH domain-containing protein 13.

Table SII. Correlation and predicted interactions of the candidate genes with IGF2BP2.

Gene	R	P-value	Predicted interaction with IGF2BP2
ACOT8	0.570	0.000	Positive
AKR1B10	0.710	0.000	Negative
ANG	0.560	0.000	Negative
CALML4	0.830	0.000	Positive
CDH1	0.80	0.000	Positive
CES2	0.800	0.000	Positive
COA6	0.220	$2.3\text{x}10^{-5}$	Positive
COX6B1	0.490	0.000	Positive
DHRS11	0.830	0.000	Negative
DPEP1	0.067	0.210	Negative
ECM1	-0.330	$1.5\text{x}10^{-10}$	Positive
EFEMP1	-0.260	$7.6\text{x}10^{-7}$	Positive
EIF1AY	-0.220	$5.0\text{x}10^{-5}$	Negative
EPS15	-0.510	$4.6\text{x}10^{-24}$	Positive
EPS8L2	0.830	0.000	Positive
FDX1	0.620	0.000	Positive
FGB	-0.110	0.033	Negative
GGT5	-0.220	$3.1\text{x}10^{-5}$	Negative
GLS	-0.250	$2.3\text{x}10^{-6}$	Positive
HBB	-0.057	0.290	Negative
HGS	$6.4\text{x}10^{-5}$	1.000	Positive
HLA-DRB1	0.180	0.001	Negative
HSD17B8	0.630	0.000	Negative
HSPB7	-0.490	$3.2\text{x}10^{-22}$	Positive
IGFBP7	-0.590	$1.2\text{x}10^{-33}$	Positive
IGHV3-48	0.410	$2.7\text{x}10^{-15}$	Negative
MDK	0.410	$8.9\text{x}10^{-16}$	Positive
MMAB	0.290	$4.6\text{x}10^{-8}$	Positive
MRPL18	-0.240	$4.0\text{x}10^{-6}$	Positive
MRPL51	-0.350	$9.1\text{x}10^{-12}$	Positive
MRPL53	-0.390	$7.7\text{x}10^{-14}$	Negative
MT-CO2	0.410	$8.9\text{x}10^{-16}$	Negative
MUC13	0.750	0.000	Negative
MVB12A	0.340	$8.0\text{x}10^{-11}$	Positive
MYO1A	0.800	0.000	Negative
NDUFA8	-0.450	$8.3\text{x}10^{-19}$	Positive
NDUFAF8	/	/	Negative
PADI4	-0.120	0.026	Negative
PBLD	0.770	0.000	Positive
PDLIM2	-0.650	$1.6\text{x}10^{-42}$	Positive
PKIG	-0.560	$8.5\text{x}10^{-30}$	Positive
PUS1	0.100	0.063	Positive
RNASE3	0.180	0.001	Negative
SCIN	0.730	0.000	Negative
SCO1	0.610	0.000	Positive
SDCBP2	0.800	0.000	Negative
TESC	-0.150	0.005	Positive
TIMM8A	0.380	$3.5\text{x}10^{-13}$	Negative
TIMM8B	0.076	0.160	Positive
TRAPPC6B	-0.590	$8.3\text{x}10^{-34}8$	Positive
UBA52	-0.380	$2.6\text{x}10^{-13}$	Positive

IGF2BP2, insulin-like growth factor 2 mRNA binding protein 2; ACOT8, acyl-CoA thioesterase 8; AKR1B10, aldo-keto reductase family 1 member B10; ANG, angiogenin; CALML4, calmodulin like 4; CDH1, cadherin 1; CES2, carboxylesterase 2; COA6, cytochrome c oxidase assembly factor 6; COX6B1, cytochrome c oxidase subunit 6B1; DHRS11, dehydrogenase/reductase 11; DPEP1, dipeptidase 1; ECM1, extracellular matrix protein 1; EFEMP1, EGF containing fibulin extracellular matrix protein 1; EIF1AY, eukaryotic translation initiation factor 1A Y-linked; EPS15, epidermal growth factor receptor pathway substrate 15; EPS8L2, EPS8 like 2; FDX1, ferredoxin 1; FGB, fibrinogen beta chain; GGT5, gamma-glutamyltransferase 5; GLS, glutaminase; HBB, hemoglobin subunit beta; HGS, hepatocyte growth factor-regulated tyrosine kinase substrate; HLA-DRB1, major histocompatibility complex, class II, DR beta 1; HSD17B8, hydroxysteroid 17-beta dehydrogenase 8 ; HSPB7, heat shock protein family B (small) member 7; IGFBP7, insulin like growth factor binding protein 7; IGHV3-48, immunoglobulin heavy variable 3-48; MDK, midkine; MMAB, metabolism of cobalamin associated B; MRPL18, mitochondrial ribosomal protein L18; MRPL51, mitochondrial ribosomal protein L51; MRPL53, mitochondrial ribosomal protein L53; MT-CO2, mitochondrially encoded cytochrome c oxidase II; MUC13, mucin 13; MVB12A, multivesicular body subunit 12A; MYO1A, myosin IA; NDUFA8, NADH:ubiquinone oxidoreductase subunit A8; NDUFAF8, NADH:ubiquinone oxidoreductase complex assembly factor 8; PADI4, peptidyl arginine deiminase 4; PBLD, phenazine biosynthesis like protein domain containing protein; PDLIM2, PDZ and LIM domain 2; PKIG, cAMP-dependent protein kinase inhibitor gamma; PUS1, pseudouridine synthase 1; RNASE3, ribonuclease A family member 3; SCIN, scinderin; SCO1, synthesis of cytochrome c oxidase 1; SDCBP2, syndecan binding protein 2; TESC, tescalcin; TIMM8A, translocase of inner mitochondrial membrane 8A; TIMM8B, translocase of inner mitochondrial membrane 8B; TRAPPC6B, trafficking protein particle complex subunit 6B; UBA52, ubiquitin A-52 residue ribosomal protein fusion product 1.

Table SIII. Details of the Venn diagram.

Section	Genes
Genes positively correlated with IGF2BP2	ACOT8, AKR1B10, ANG, CALML4, CDH1, CES2, COA6, COX6B1, DHRS11, EPS8L2, FDX1, HLA-DRB1, HSD17B8, IGHV3-48, MDK, MMAB, MT-CO2, MUC13, MVB12A, MYO1A, PBLD, RNASE3, SCIN, SCO1, SDCBP2, TIMM8A, TIMM8B
Genes predicted to interact with IGF2BP2	ACOT8, CALML4, CDH1, CES2, COA6, COX6B1, ECM1, EFEMP1, EPS15, EPS8L2, FDX1, GLS, HGS, HSPB7, IGFBP7, MDK, MMAB, MRPL18, MRPL51, MVB12A, NDUFA8, PBLD, PDLIM2, PKIG, PUS1, SCO1, TESC, TIMM8B, TRAPPC6B, UBA52
Overlapping genes	ACOT8, CALML4, CDH1, CES2, COA6, COX6B1, EPS8L2, FDX1, MDK, MMAB, MVB12A, PBLD, SCO1, TIMM8B

IGF2BP2, insulin-like growth factor 2 mRNA binding protein 2; ACOT8, acyl-CoA thioesterase 8; AKR1B10, aldo-keto reductase family 1 member B10; ANG, angiogenin; CALML4, calmodulin like 4; CDH1, cadherin 1; CES2, carboxylesterase 2; COA6, cytochrome c oxidase assembly factor 6; COX6B1, cytochrome c oxidase subunit 6B1; DHRS11, dehydrogenase/reductase 11; EPS8L2, epidermal growth factor receptor pathway substrate 8; FDX1, ferredoxin 1; HLA-DRB1, major histocompatibility complex, class II, DR Beta 1; HSD17B8, hydroxysteroid 17-beta dehydrogenase 8; IGHV3-48, immunoglobulin heavy variable 3-48; MDK, midkine; MMAB, metabolism of cobalamin associated B; MT-CO2, mitochondrially encoded cytochrome c oxidase II; MUC13, mucin 13; MVB12A, multivesicular body subunit 12A; MYO1A, myosin IA; PBLD, phenazine biosynthesis like protein domain containing protein; RNASE3, ribonuclease A family member 3; SCIN, scinderin; SCO1, synthesis of cytochrome c oxidase 1; SDCBP2, syndecan binding protein 2; TIMM8A, translocase of inner mitochondrial membrane 8A; TIMM8B, translocase of inner mitochondrial membrane 8B; ECM1, extracellular matrix protein 1; EFEMP1, EGF containing fibulin extracellular matrix protein 1; EPS15, epidermal growth factor receptor pathway substrate 15; GLS, glutaminase; HGS, hepatocyte growth factor-regulated tyrosine kinase substrate; HSPB7, heat shock protein family B (small) member 7; IGFBP7, insulin like growth factor binding protein 7; MRPL18, mitochondrial ribosomal protein L18; MRPL51, mitochondrial ribosomal protein L51; NDUFA8, NADH:ubiquinone oxidoreductase subunit A8; PDLIM2, PDZ and LIM domain 2; PKIG, cAMP-dependent protein kinase inhibitor gamma; PUS1, pseudouridine synthase 1; TESC, tescalcin; TRAPPC6B, trafficking protein particle complex subunit 6B; UBA52, ubiquitin a-52 residue ribosomal protein fusion product 1.