

SUPPLEMENTAL MATERIAL

For paper entitled “**FTO fuels diabetes-induced vascular endothelial dysfunction associated with inflammation by erasing m⁶A methylation of *TNIP1***”

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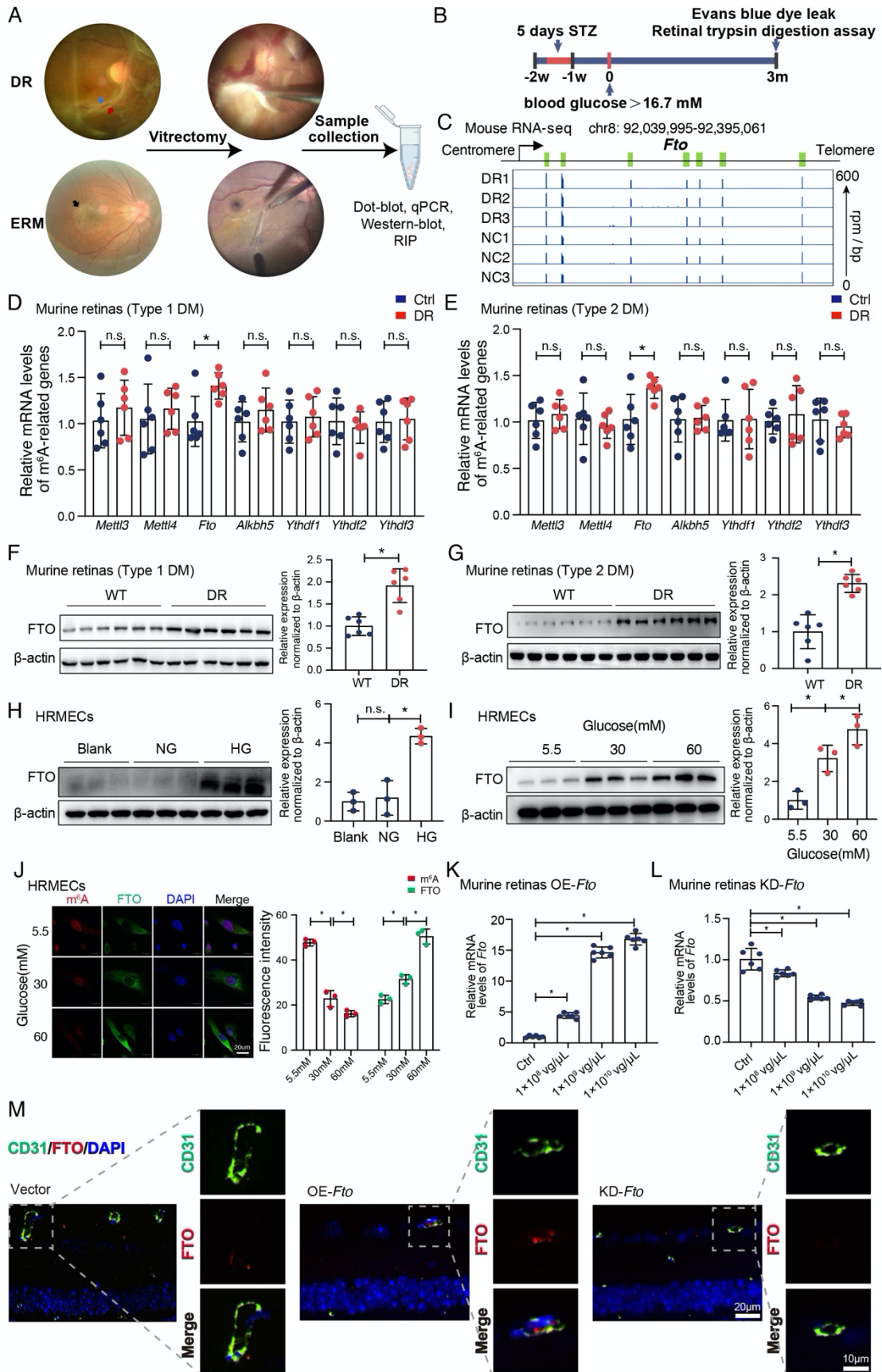
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#Chuandi Zhou, Xinping She and Chufeng Gu contributed equally to this paper.

*Zhi Zheng, Xun Xu and Haibing Chen are corresponding authors.

Supplemental material consisted of 11 supplemental figures and 6 supplemental tables.

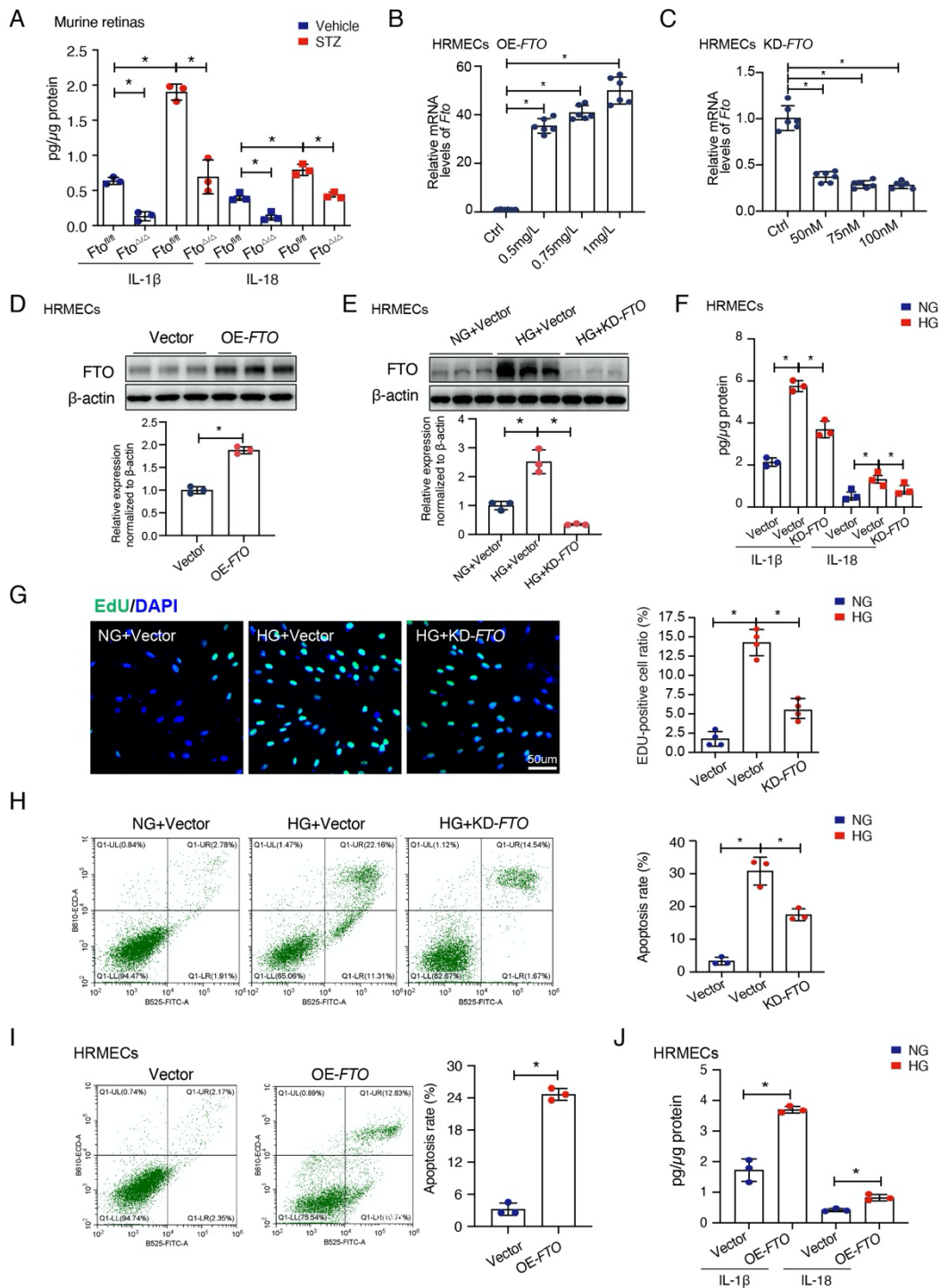
Supplemental Figure 1



Supplemental Figure 1. FTO is elevated upon high glucose both in vitro and in vivo.

(A) A diagram showing patient sample collection. Representative fundus photographs of recruited patients with diabetic retinopathy (DR) and idiopathic epiretinal membrane (ERM) (preoperative: the first column; intraoperative: the second column). Blue arrow: extensive fibrovascular membranes; Red arrow: neovascularization on fibrovascular membranes; Black arrow: epiretinal membrane formed on macular. (B) A schematic diagram of induction of diabetes and phenotype experiments in mice. (C) Gene tracks based on RNA-seq of *Fto* using Integrative Genomics Viewer (IGV) in normal and diabetic mouse retinas. DR, diabetic retinopathy; rpm/bp, reads per million mapped reads per base pair. (D and E) qRT-PCR reveals higher levels of *FTO* in murine retinas with type 1 (D, n=6) or type 2 (E, n=6) diabetes (Mann-Whitney U test). (F and G) Western blotting shows elevated expression of FTO in murine retinas with type 1 (F, n=6) or type 2 (G, n=6) diabetes (Student's t test). (H) Western-blotting shows upregulated FTO treated by high glucose in human retinal microvascular endothelial cells (HRMECs) (n=3). NG, normal glucose (5.5 mM) with D-mannitol as osmotic control; HG, high glucose (30 mM). (I) Western-blotting indicates FTO expression is elevated with increasing concentrations of glucose administered to HRMECs (n=3). (J) Immunofluorescence shows reduced level of m⁶A and upregulated FTO in HRMECs treated with increasing concentrations of glucose (n=3, scale bar: 20 μm). (K, L) qRT-PCR shows overexpression (K, n=6) and knockout (L, n=6) efficiency of *Fto* by intravitreal injection of adeno-associated virus (AAV). (M) Immunofluorescence shows successful transfection of AAV in retinal vascular endothelial cells to modulate the expression of FTO (scale bar: 10 μm; zoom figure: scale bar: 20 μm). For H-L, significant differences are determined by Kruskal-Wallis's test followed by Bonferroni's post hoc comparison test. Data are shown as the mean ± SD. *p<0.05. n.s., statistically not significant.

Supplemental Figure 2

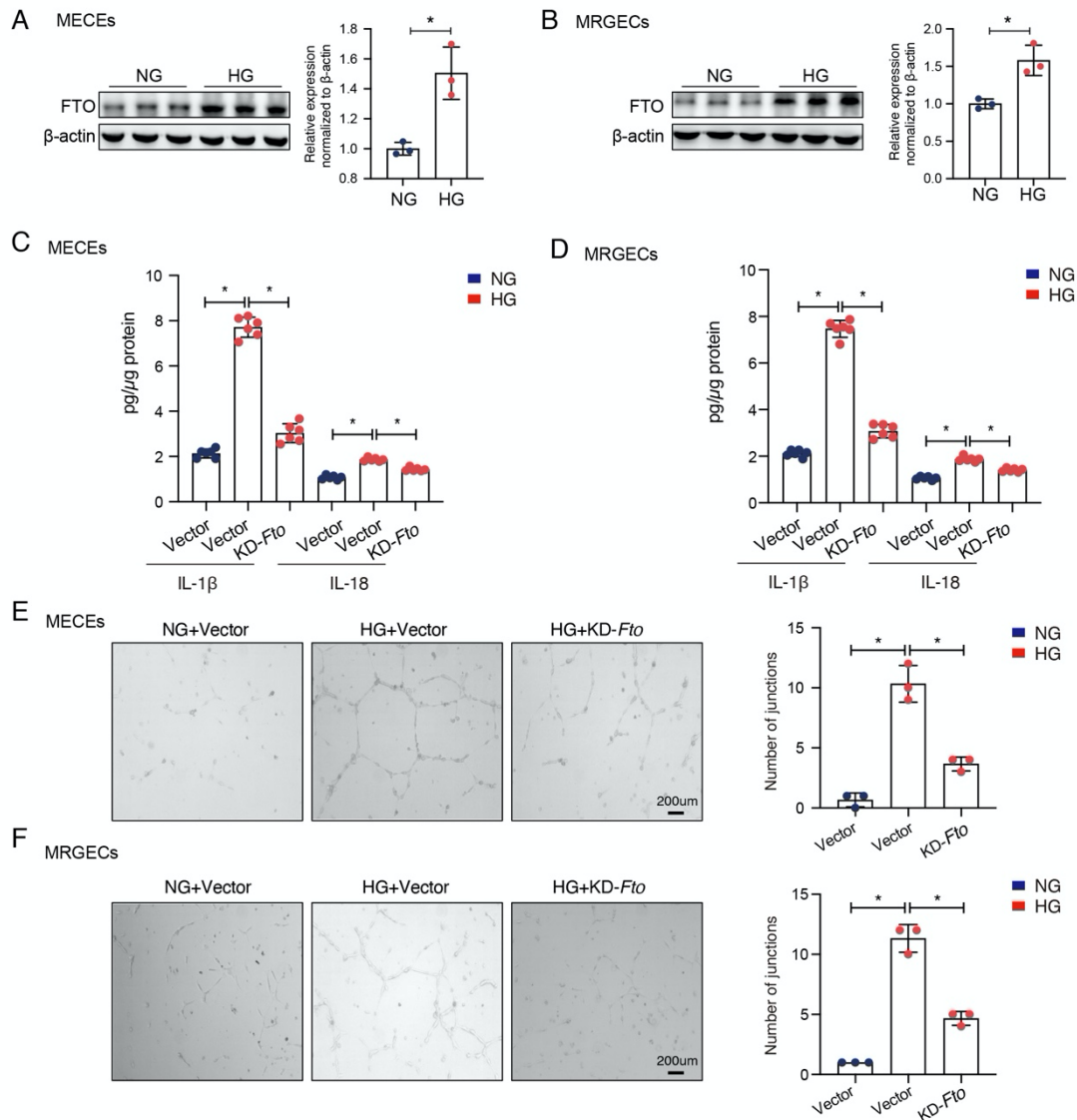


Supplemental Figure 2. FTO promotes inflammation, proliferation and apoptosis upon high glucose both *in vivo* and *in vitro*.

(A) ELISA assays demonstrate EC-specific *Fto*-deficient (*EC Fto* ^{Δ/Δ}) mice have lower levels of interleukin (IL)-1 β and IL-18 in retina after introduction of diabetes (n=3). (B, C) qRT-PCR shows overexpression (B, n=6) and knockout efficiency (C, n=6) of *FTO* by overexpression plasmid and small interfering RNA (siRNA), respectively. (D) Western-blotting shows upregulated FTO in human retinal microvascular endothelial cells (HRMECs) after transfecting with overexpressed

plasmid (n=3, Student's t test). (E) Western-blotting displays upregulated FTO upon high glucose in HRMECs, and FTO is successfully knockout by siRNA (n=3). (F) ELISA assays display an elevation of IL-1 β and IL-18 in HRMECs treated by high glucose, and this trend can be reversed by silencing *FTO* (n=3). (G) EdU assays indicates silencing *FTO* suppressed the proliferation of HRMECs induced by high glucose. The nuclei were stained with Hoechst (blue) (n=4, Scale bar: 50 μ m). (H) Flow cytometric analysis demonstrates *FTO* knockdown alleviates apoptosis of HRMECs treated by high glucose (n=3). (I) Flow cytometric analysis indicates *FTO* overexpression aggravates apoptosis of HRMECs (n=3, Student's t test). (J) ELISA assays display overexpressed *FTO* lead to an elevation of IL-1 β and IL-18 (n=3, Student's t test). NG, normal glucose (5.5 mM) with D-mannitol as osmotic control; HG, high glucose (30 mM). For A-C, E-H, significant differences are assessed by 1-way ANOVA or Kruskal-Wallis's test followed by Bonferroni's post hoc comparison test. Data are shown as the mean \pm SD. *p<0.05.

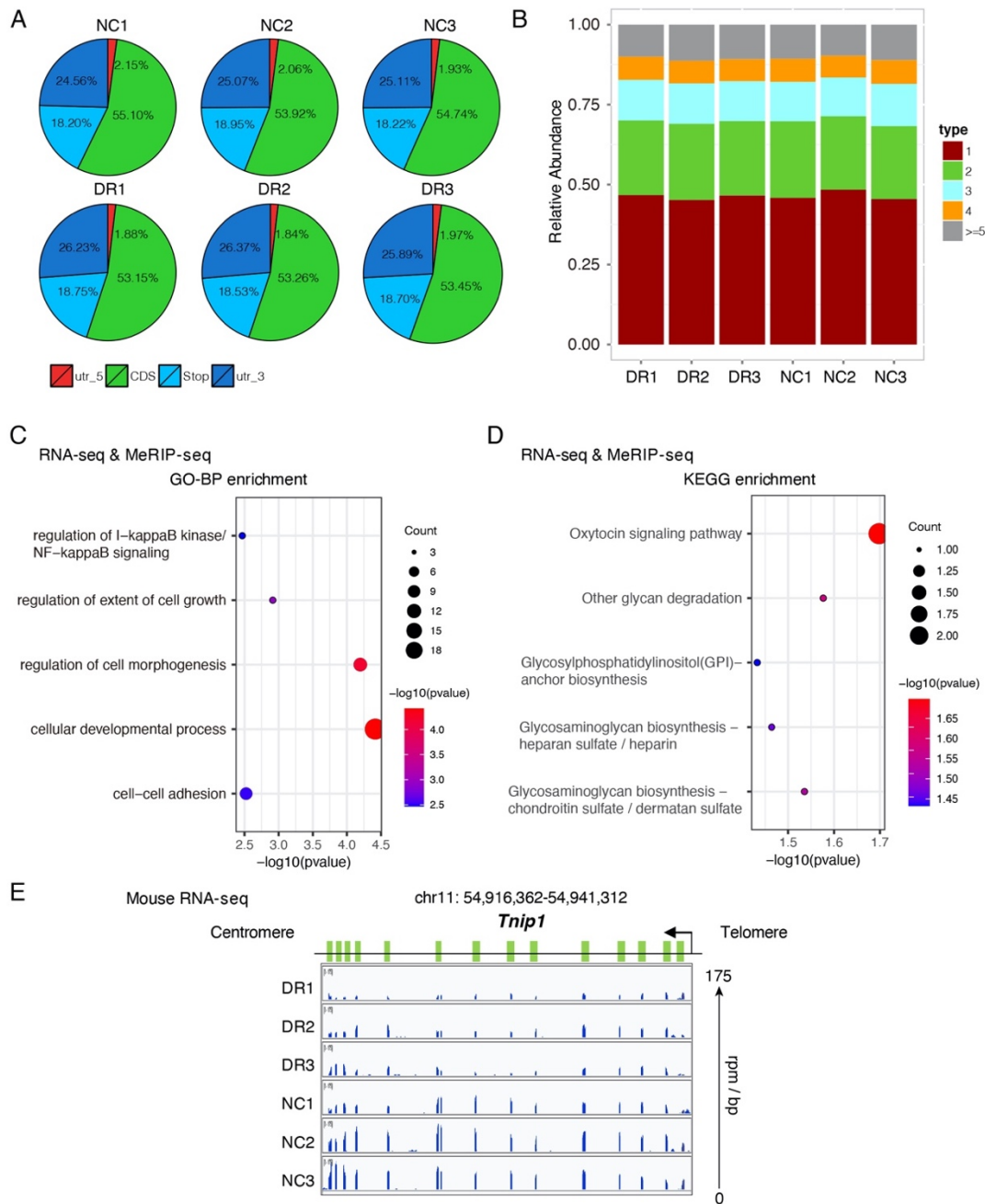
Supplemental Figure 3



Supplemental Figure 3. Silencing *Fto* inhibits inflammation and tube formation induced by high glucose in both mice cardiac endothelial cells (MECEs) and mice renal glomerular endothelial cells (MRGECs).

(A, B) Western-blotting displays upregulated FTO upon high glucose in both MECEs (A, n=3, Student's t test) and MRGECs (B, n=3, Student's t test). (C, D) ELISA assays show silencing *Fto* suppresses elevated interleukin-1 β (IL-1 β) and IL-18 stressed by high glucose in both MECEs (C, n=6) and MRGECs (D, n=6). (E, F) Silencing *Fto* inhibits tube formation induced by high glucose in both MECEs (E, n=3, scale bar: 200 μ m) and MRGECs (F, n=3, scale bar: 200 μ m). The average number of tube formation for each field was assessed. NG, normal glucose (5.5 mM) with D-mannitol as osmotic control; HG, high glucose (30 mM). For C-F, significant differences are determined by 1-way ANOVA or Kruskal-Wallis's test followed by Bonferroni's post hoc comparison test. Data are shown as the mean \pm SD. *p<0.05. n.s., statistically not significant.

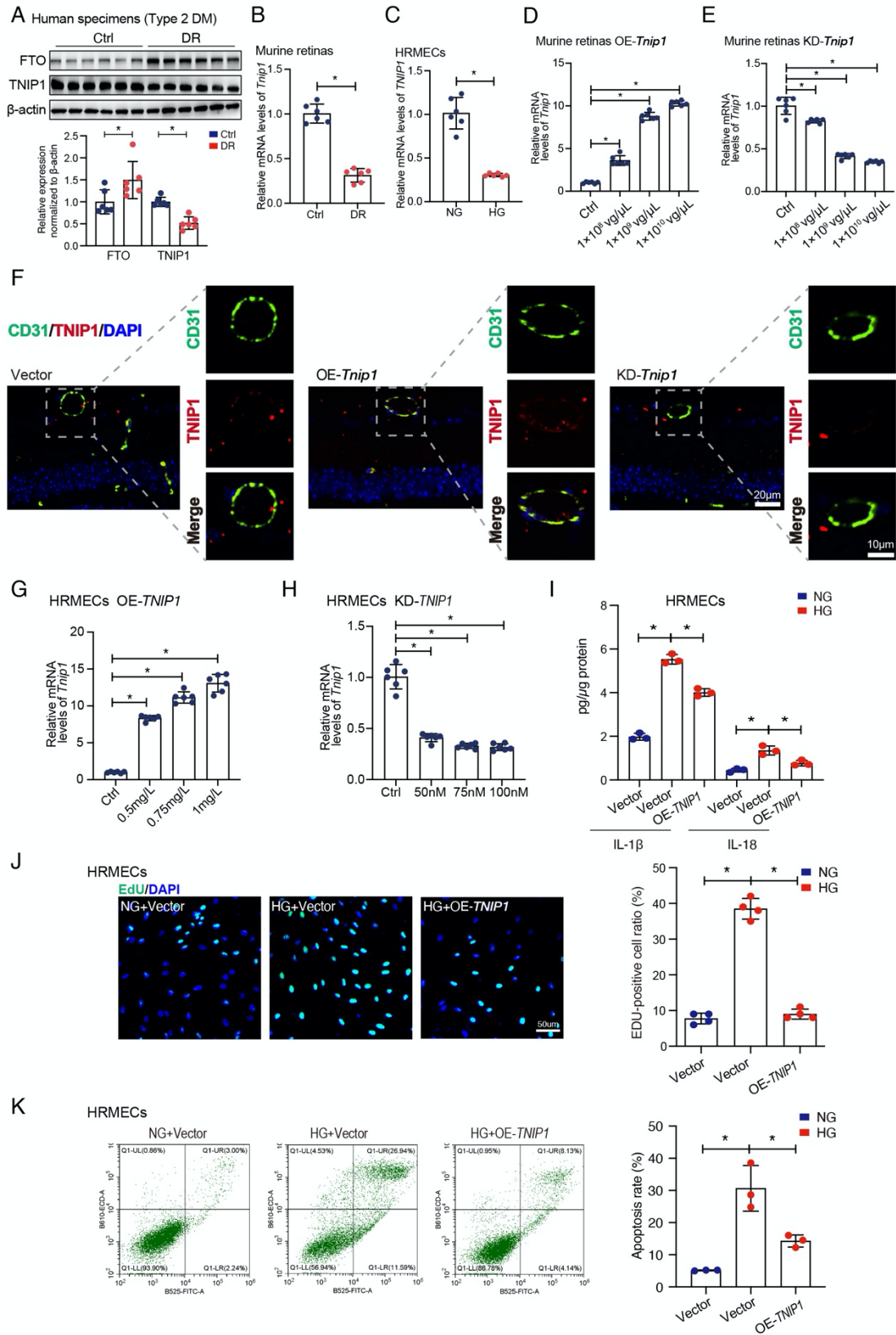
Supplemental Figure 4



Supplemental Figure 4. Enrichment analyses of differentially expressed genes in diabetes.

(A) Pie charts exhibit the distribution of m⁶A peak in different RNA regions (CDS, 5' UTR, 3' UTR and stop codon) in normal and diabetic murine retinas. (B) The distribution of the genes with 1, 2, 3, 4 and 5 or more m⁶A peaks in normal and diabetic murine retinas. (C) Gene ontology (GO) analysis for differentially expressed genes in diabetic retinas based on combined RNA-seq and MeRIP-seq. (D) Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis for differentially expressed genes in diabetic retinas based on combined RNA-seq and MeRIP-seq. DR, diabetic retinopathy. (E) Gene tracks based on RNA-seq of *Tnip1* using Integrative Genomics Viewer (IGV) in normal and diabetic mouse retinas. DR, diabetic retinopathy; rpm/bp, reads per million mapped reads per base pair.

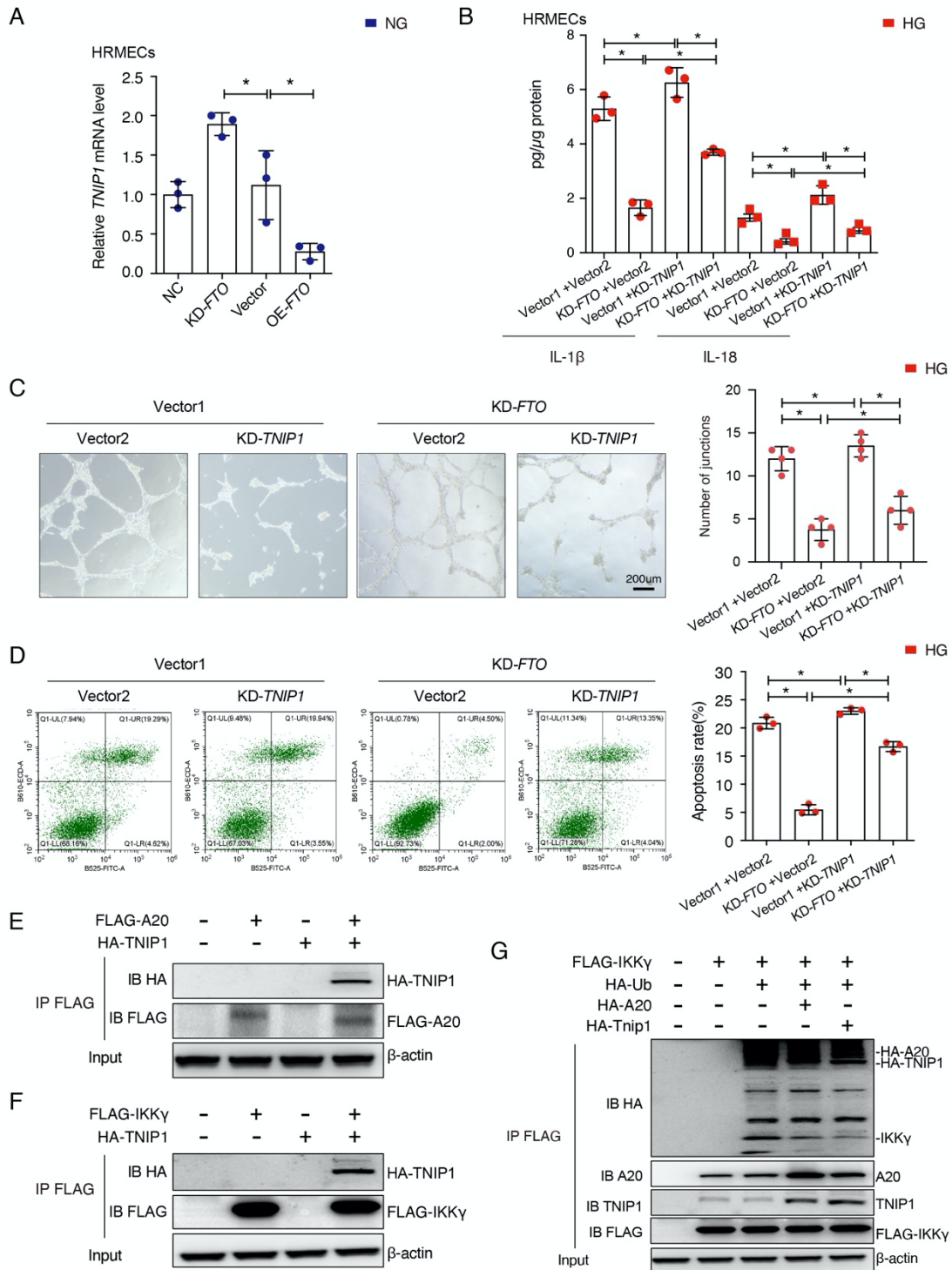
Supplemental Figure 5



Supplemental Figure 5. *TNIP1* attenuates inflammation, proliferation and apoptosis stressed by high glucose.

(A) Western blotting displays reduced expression of TNIP1, accompanied by upregulated FTO, in retinal fibrovascular membranes of patients with retinopathy due to type 2 diabetes (n=6, Student's t test). (B, C) qRT-PCR shows suppressed expression of *Tnip1* in both diabetic murine retinas (B, n=6, Student's t test) and human retinal microvascular endothelial cells (HRMECs) cultivated in high glucose (C, n=6, Student's t test). NG, normal glucose (5.5 mM) with D-mannitol as osmotic control; HG, high glucose (30 mM). (D, E) qRT-PCR shows overexpression (D, n=6) and knockout (E, n=6) efficiency of *Tnip1* by intravitreal injection of adeno-associated virus (AAV). (F) Immunofluorescence shows successful transfection of AAV in retinal vascular endothelial cells to modulate the expression *Tnip1* (scale bar: 10 μ m; zoom figure: scale bar: 20 μ m). (G, H) qRT-PCR shows overexpression (G, n=6) and knockout efficiency (H, n=6) of *Tnip1* by overexpression plasmid and small interfering RNA (siRNA), respectively. (I) ELISA assays demonstrate overexpressed *TNIP1* suppresses the enrichment of interleukin-1 β (IL-1 β) and IL-18 in human retinal microvascular endothelial cells (HRMECs) treated by high glucose (n=3). (J) EdU assays displays *TNIP1* impedes the proliferation of HRMECs cultivated in high glucose. The nuclei were stained with Hoechst (blue). (n=4, scale bar: 50 μ m). (K) Flow cytometric analysis demonstrates *TNIP1* alleviates apoptosis of HRMECs treated by high glucose (n=3). NG, normal glucose (5.5 mM) with D-mannitol as osmotic control; HG, high glucose (30 mM). For D-E, G-K significant differences are assessed by Kruskal-Wallis's test followed by Bonferroni's post hoc comparison test. Data are shown as the mean \pm SD. *p<0.05.

Supplemental Figure 6



Supplemental Figure 6. FTO regulates inflammation and apoptosis in diabetes-induced retinal vascular endothelium dysfunction via mediating *TNIP1*.

(A) FTO reduces mRNA level of *TNIP1* in human retinal microvascular endothelial cells (HRMECs) (n=3). (B) *TNIP1* knockout partially reverses the trend of decreased interleukin-1β (IL-1β) and IL-18 caused by silencing *FTO* in HRMECs (n=3). (C) Silencing *TNIP1* limits the suppression effect of tube formation induced by *FTO* knockdown. The average number of tube formation for each field

was assessed (n=4, scale bar: 200 μ m). (D) Silencing *TNIP1* partially reverses the trend of reduced apoptosis induced by *FTO* knockout in HRMECs (n=3). (E) Co-immunoprecipitation (Co-IP) assays reveal direct interaction between TNIP1 and A20. (F) Co-IP assays identify direct interaction between TNIP1 and IKK γ . (G) Co-IP assays indicate TNIP1 promotes A20-mediated deubiquitination of IKK γ . NG, normal glucose (5.5 mM) with D-mannitol as osmotic control; HG, high glucose (30 mM). All significant differences are assessed by 1-way ANOVA or Kruskal-Wallis's test followed by Bonferroni's post hoc comparison test. Data are shown as the mean \pm SD. *p<0.05.

Supplemental Figure 7

Range 1: 9 to 746 [Graphics](#)

Score	Expect	Identities	Gaps	Strand
248 bits(274)	2e-69	532/775(69%)	59/775(7%)	Plus/Plus
Human Query 9		TGTGTCATTTGGCTCCACCTTCATCTTGCAGAGCCAGCTGATCTCAGATTGCCAAGAAAC		68
Mouse Sbjct 9		TGGGTCATTTGGTTCCACCTTCATCTTTTCAGAGCCAGCTGACCTCAGATTGCCAA--AGT		67
Human Query 69		TAGAAG-CCACTTGCACG---GTGTGGCCAGAGCCTCAGCTGGATGAGAGGCTGAGATG		123
Mouse Sbjct 68		TTGAAGGCCATGTGCATGTTCTGTGTGACCCAAGCCTTGGCAG-AGGAGAGGCTGGGATG		126
Human Query 124		GGTGGCCAGCTTGTA-CACCAGTCCCTGAACTGAGCTGTTTACAGGACTGGGGAGGCTCC		182
Mouse Sbjct 127		GGTAGCTGGCTCACATCCCCAG--CCAAGCCTCGAACTGTTGACAAGACCAGGGAGAATCC		185
Human Query 183		ACCCAGAAGGCTTTCATTTGTACTCTGCTGGGAGTGACTGGGAAAAACTCCCTT-CCCTGC		241
Mouse Sbjct 186		ACCCATG-GGGGCCACCAGGT-TCTTATGGATGCAAGCAGGAGAAGCTCAACACCCTGC		243
Human Query 242		---TGCTGAGTGGAGAGAGGCCATCCGGCTTTGACCACCATCCGTTGCAGAAGCCT		297
Mouse Sbjct 244		CTCTTGCCAAGACAAG-GAAGCCTCACCTGGCTTTGACCTGCCATCCGTTGCTGAGGCCA		302
Human Query 298		CCAGGAGCAGCAATCCTAAGAGTGGGAGGCAGCCAAGACCCCTTCCCTTCAAAACCTCCC		357
Mouse Sbjct 303		CTGG---CTTCCATCCTAAGAATGAGGTGCAAC-AAGACCCCATTCACAGAAGCTCAA		358
Human Query 358		GGAAGTGGTTTCAGGCCCTCTAGTTGCCATGACCAATTTGTGTGTGTTAATTTTGC		417
Mouse Sbjct 359		AGACTTGGTTCAGGCTCTCCAGAGACCATACCCAACCTCATGTGCATGTGCCGTTTTTGC		418
Human Query 418		TTCAAGCTCTGTAGCAGGACTGCCCCAGCACAC---CCCTACCCCTCTGTGAGGAGC		473
Mouse Sbjct 419		TTCAAGCTCAGTAGCAGGACTGCCCCGAGCCCTGCTCCTTGCCCTCTGTGAGGAGT		478
Human Query 474		TGTGGGAAGTGTGGGTTTGTCTCCAGAACAGAAGAGAATGAT-GGATATTCTGGCTCTGG		532
Mouse Sbjct 479		TACGGAGAG---GGCTTTGTCTCTAGAGCAGAAGAGAATGATGGGACGGCCTGATGCTGT		535
Human Query 533		GGCCCTCTCCAC--CACCCTCACAGTAGCCTTGTCTGA-AGCCATCACAGA--TGGGA-G		586
Mouse Sbjct 536		CATGCTCTCCACTGCACCTGTGGCAG---CCTCCTGAGAGCCACCA-AGATCTGGGATG		590
Human Query 587		AAGGCCATGCCAGCCACGTCCGCCGAGGGCGCCAGCCTGAAGCTGCCAGGCCCTGAGGT		646
Mouse Sbjct 591		AAGGCCACACCAGCCATGTCTGCTGAAGGGCCCAAGCTGA-----GA---		633
Human Query 647		TCAGACCCTGGACCCATAGCTGGAGGCTGTGGTGCAGAAAGCCAGATTAGGGTGGCT		706
Mouse Sbjct 634		--TGACTCCGGCTCCACAGTTAGATGTTTATGGTGCAGAGGTCTATATTAAGGTAGCT		691
Human Query 707		GTCCATCCCTGGATAGCTATTTGCACGAATCATGGACATAAAATCCAAGTTGAAGA		761
Mouse Sbjct 692		GTCTGTGCTAGGCAGCCGTTTGCACAAATCTTGGACATAAAATCCAACCTGAAGA		746

Supplemental Figure 7. *TNPI* gene homology comparison between human and mouse.

TNPI homology analysis with Basic Local Alignment Search Tool (BLAST) between human and mouse genomes.

Supplemental Figure 8

Range 1: 12 to 744 [Graphics](#)

	Score	Expect	Identities	Gaps	Strand
	233 bits(258)	4e-65	530/774(68%)	65/774(8%)	Plus/Plus
Human Query	12				71
Rat Sbjct	12				71
Human Query	72				125
Rat Sbjct	72				130
Human Query	126				183
Rat Sbjct	131				184
Human Query	184				241
Rat Sbjct	185				243
Human Query	242				298
Rat Sbjct	244				302
Human Query	299				357
Rat Sbjct	303				357
Human Query	358				417
Rat Sbjct	358				417
Human Query	418				473
Rat Sbjct	418				476
Human Query	474				532
Rat Sbjct	477				535
Human Query	533				587
Rat Sbjct	536				591
Human Query	588				647
Rat Sbjct	592				635
Human Query	648				707
Rat Sbjct	636				691
Human Query	708				761
Rat Sbjct	692				744

Supplemental Figure 8. *TNIP1* gene homology comparison between human and rat.

TNIP1 homology analysis with Basic Local Alignment Search Tool (BLAST) between human and rat genomes.

Supplemental Figure 9

		Range 1: 24 to 1560					
		Score	Expect	Identities	Gaps	Strand	Frame
		1764 bits(1955)	0.0()	1321/1547(85%)	11/1547(0%)	Plus/Plus	
Human	Query	2	CGGTGGCGAAGGCGGCTTTAGTGGCAGCATGAAGCGCACCCGACTGCCGAGGAACGAGA	61			
Mouse	Sbjct	24	CGGTGGCGAAGGCGGCTTTAGTAGCAGCATGAAGCGCGTCCAGACCAGGAGGAACGAGA	83			
Human	Query	62	GCGCGAAGCTAAGAACTGAGGCTTCTTGAAGAGCTTGAAGACACTTGGCTCCCTTATCT	121			
Mouse	Sbjct	84	GCGGGAAGCTAAGAACTGAGGCTCCTTGAAGAGCTTGAAGACACTTGGCTTCTTACCT	143			
Human	Query	122	GACCCCAAAGATGATGAATTCATCAGCAGTGGCAGCTGAAATATCCTAAACTAATTC	181			
Mouse	Sbjct	144	GACCCCAAAGATGATGAGTTCTATCAGCAGTGGCAGCTGAAATATCCTAAACTGTTT	203			
Human	Query	182	CCGAGAAGCCAGCAGTGTATCTGAGGAGCTCCATAAAGAGGTTCAAGAAGCCTTTCTCAC	241			
Mouse	Sbjct	204	CCGAGAAGCCAGCAGCATACCAGAGGAGTGCATAAAGAGGTTCCCGAGGCTTTCTCAC	263			
Human	Query	242	ACTGCACAAGCATGGCTGCTTATTCGGGACCTGGTTAGGATCCAAGGCAAAGATCTGCT	301			
Mouse	Sbjct	264	ACTGCATAAGCATGGCTGCTTGTTCGGGACCTGGTTAGGATCCAAGGCAAAGATGTGCT	323			
Human	Query	302	CACCTCCGTTATCTCGCATCCTCATTGGTAATCCAGGCTGCACCTACAAGTACCTGAAC	361			
Mouse	Sbjct	324	CACCCCACTGCTCGCATCCTCATCGGGGACCCAGGCTGCACCTACAAGTACTTGAAC	383			
Human	Query	362	CAGGCTCTTTACGGTCCCTGGCCAGTGAAGGGTCTAATATAAAACACACCCAGGCTGA	421			
Mouse	Sbjct	384	CAGACTCTTTACGGTCCCTGGCCCGTGAAGGGTGCACGGTCAAGTACACAGAGGCTGA	443			
Human	Query	422	AATAGCCCGTCTGTGTGAGACCTTCCTCAAGCTCAATGACTACCTGCAGATAGAAACC	481			
Mouse	Sbjct	444	GATCGCCGCTGCATGTGAGACCTTCCTAAAGCTCAATGACTACCTCCAGGTGAGAGCC	503			
Human	Query	482	CCAGGCTTTGGAAGAAGTGTGTCGCAAGAGAGGCTAATGAGGATGCTGTCATTTGTG	541			
Mouse	Sbjct	504	CCAGGCTTTGGAAGAAGTGGTGTGTCAGAGAGAAGGCCAATGAAGACGCTGTGCCACTGTG	563			
Human	Query	542	TATGTCGAGATTTCCCGAGGTTGGGATGGGTTTCATCCTACACGGACAAGATGAAGT	601			
Mouse	Sbjct	564	CATG---GCAGGTTCCCGAGGCTGGGCTGGGCGCTCCTGCGATG-----ATGAAGT	614			
Human	Query	602	GGACATTAAGAGCAGAGCAGCATACAACCTAACTTTGCTGAATTTTCATGGATCCTCAGAA	661			
Mouse	Sbjct	615	GGACCTTAAGAGCAGAGCAGCCTACAACCTGACTTTGCTAAACTTCATGGATCCTCAGAA	674			
Human	Query	662	AATGCCATACCTGAAAGAGAACCTTATTTGGCATGGGGAAATGGCAGTGAAGTGGCA	721			
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Human	Query	722	TCATGATGAAATCTGTTGGACAGGTCAGCCGTTGGCAGTGTACAGTTATAGCTGTGAAG	781			
Mouse	Sbjct	735	TCACGATGAGAACCTGTTGGACAGGTCAGCCGTTGGCAGTGTACAGCTATAGCTGCGAAG	794			
Human	Query	782	CCCTGAAGAGGAAAGTGAAGGATGACTCTCATC-TCGAAGGACAGGATCCTGATATTGGC	840			
Mouse	Sbjct	795	CTCTGAGGATGAAAGTGAAGGACGAGTC-CAGCTTCGAAGGACAGATCCTGACTTTGGC	853			
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Human	Query	1501	ACATCGTTTCAAGACTCAGAGGTCAGCTTCTGGAAGCAAAACCCCTAG	1547			
Mouse	Sbjct	1514	ACGTGTTTCCGAGCTCAGAGGCCAGCTGCTGGAAGCAAGATCCTAG	1560			

Supplemental Figure 9. *FTO* gene homology comparison between human and mouse.

FTO homology analysis with Basic Local Alignment Search Tool (BLAST) between human and mouse genomes.

Supplemental Figure 10

Range 1: 1 to 1509

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	1677 bits(1859)	0.00	1285/1519(85%)	11/1519(0%)	Plus/Plus	
Human	Query	30	ATGAAGCGCACCCGACTGCCGAGGAACGAGAGCGCGAAGCTAAGAACTGAGGCTTCTT			89
Rat	Sbjct	1	ATGAAGCGCGTCCAGACC CGGAGGAACGGGAGCGGGAAGCTAAGAACTGAGGCTTCCTC			60
Human	Query	90	GAAGAGCTTGAAGACACTTGGCTCCCTTATCTGACCCCAAGATGATGAATTCATCAG			149
Rat	Sbjct	61	GAGGAGCTTGAAGACACTTGGCTTCCTTACCTGACCCCAAGATGACGAGTTCATCAG			120
Human	Query	150	CAGTGGCAGCTGAAATATCCTAAACTAATTCCTCCGAGAAGCCAGCAGTGTATCTGAGGAG			209
Rat	Sbjct	121	CAGTGGCAGCTGAAATATCCTAAACTGGTTCCTCCGAGAGGCTGGCAGCATACCCGAGGAG			180
Human	Query	210	CTCCATAAAGAGGTTCAAGAAGCCTTCTCAGACTGCACAAGCATGGCTGCTTATTCGG			269
Rat	Sbjct	181	CTGCACAAAGAGGTCCTCCGAGGCTTCTCAGACTGCACAAGCATGGCTGCTTGTTCGG			240
Human	Query	270	GACCTGGTTAGGATCCAAGGCAAGATCTGCTCACTCCGGTATCTCGCATCCTCATTGGT			329
Rat	Sbjct	241	GACCTGGTGGAGATCCAAGGCAAGAGCTGCTCACCCGGTGTCTCGCATCCTCATTGGG			300
Human	Query	330	AATCCAGGCTGCACCTACAAGTACCTGAACACCAGGCTTTTACGGTCCCCTGGCCAGTG			389
Rat	Sbjct	301	GACCCGGCTGCACCTACAAGTACTTGAACACCAGGCTTTTACCGTCCCTGGCCAGTG			360
Human	Query	390	AAAGGCTAATATAAAACACACCGAGGCTGAAATAGCCGCTGCTGTGAGACCTTCCTC			449
Rat	Sbjct	361	AAGGGCTGCACCATCAATTACACAGAGGCGGAGATTGCCGCGCATGTCAGACCTTCCTC			420
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Rat	Sbjct	421	AAGCTCAATGACTACCTGCAGGTCGAGACCATCCAGGCTTTGAAGAACTGGCTATCAAA			480
Human	Query	510	GAGAAGGCTAATGAGGATGCTGTGCCATTGTGTATGCTGCAGATTTCCTCCAGGGTTGGG			569
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Human	Query	570	ATGGGTTTACCTTACAACGGACAAGATGAAGTGGACATTAAGAGCAGAGCAGCATACAAC			629
Rat	Sbjct	538	GTGGGACCGTCTCGCATG-----ATGAAGTGGACCTTAAGAGCAGAGCAGCTTACAAC			591
Human	Query	630	GTAACTTTGCTGAATTCATGGATCCTCAGAAAATGCCATACCTGAAGAGGAACTTAT			689
Rat	Sbjct	592	GTGACTTTGCTAAACTTCATGGATCCTCAGAAAATGCCGACTTGAAGAGGAGCCCTAT			651
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Rat	Sbjct	652	TTCCGCATGGGAAAGATGGCGGTGAGCTGGCACCATGACGAGAACTTGGTGGACAGGTCA			711
Human	Query	750	GCGGTGGCAGTGTACAGTTATAGCTGTGAAGGCCCTGAAGAGGAAAGTGAAGTACTCT			809
Rat	Sbjct	712	GCCGTGCGGTGTACAGCTATAGCTGTGAAGGCTCCGAGGATGAAAGCATGACGAGTCT-			770
Human	Query	810	CATC--TCGAAGGCAGGGATCCTGATATTTGGCATGTTGGTTTTAAGATCTCATGGACAT			868
Rat	Sbjct	771	CAGCTTCGAAGGCAGAGATCCCGATACGTGGCATGTTGGTTTTAAGATCTCATGGACAT			830
Human	Query	869	AGAGACACCTGGTTTGGGATACCCCTTACCAGGAGACTGCTATTTATGCTTGATGA			928
Rat	Sbjct	831	CGAGACGCCAGGCTTGACAATTCCTTCCACCAGGAGACTGCTATTTATGCTTGATGA			890
Human	Query	929	TCTCAATGCCACCCACCAACTGTGTTTTGGCCGGTTCACAACCTCGGTTTATGTTCCAC			988
Rat	Sbjct	891	CCTCAATGCCACCCACCAACTGTGTTTTGGCTGGCTCACAGCCTCGGTTTATGCTCCAC			950
Human	Query	989	CCACCAGTGGCAGAGTGTCAACAGGAACCTTGGATTATATTTTACAACGCTGTGAGTT			1048
Rat	Sbjct	951	CCACCAGTGGCAGAGTGTCAACAGGACCTTGGATTATATCTTACAACGCTGCCAGTT			1010
Human	Query	1049	GGCTCTGCAGAATGTCTGTGACGATGTGGACAATGATGATGCTCTTTGAAATCCTTTGA			1108
Rat	Sbjct	1011	GGCACTGCAGAATGTTCTCAATGACTCGGACAATGGCGACGCTCTCGCTGAAGTCCATCGA			1070
Human	Query	1109	GCCTGCAGTTTGAACAAGGAGAAGARATTCATAATGAGGTCGAGTTTGAGTGGCTGAG			1168
Rat	Sbjct	1071	GCCTGCAGTCTGAACAAGGAGAAGAGATCCACAACGAGGTCGAGTTTGAGTGGCTGAG			1130
Human	Query	1169	GCAGTTTGGTTTCAAGGCAATCGATACAGAAAAGTGCAGTACTGGTGGTGTCAACCCAT			1228
Rat	Sbjct	1131	GCAGTTCTGGTTTCAAGGAAATCGATACAAAATTTGCACTGATTTGGTGGTGTGAGCCAT			1190
Human	Query	1229	GGCTCAACTGGAAGCACTGTGGAAGAAGATGGAGGGTGTGACAAAATGCTGTGCTTCATGA			1288
Rat	Sbjct	1191	GACTCAGTGGAGGGCTGTGGAAGAAGATGGAGAGTGTGACAAAATGCCGTGCTTCGTGA			1250
Human	Query	1289	AGTTAAAAGAGAGGGGCTCCCGTGGAAACAAGGAATGAAATCTTGACTGCCATCCTTGC			1348
Rat	Sbjct	1251	AGTTAAGAGAGAGGGGCTCTCCGTGGAAACAAGGAGTGAATTTCTGTCTGCCCTCTGAT			1310
Human	Query	1349	CTCGTCACTGCACGCCAGAACCTGAGGAGAGAATGGCATGCCAGGTGCCAGTACGAAAT			1408
Rat	Sbjct	1311	CCCACTCACCATGCGCCAGAACTGAGGAAAGAAATGGCACGCCAGGTGCCAGGCCGAGT			1370
Human	Query	1409	TGCCCCAACATTACCTGCTGATCAGAAGCCAGAATGTCCGCCACTTGGGAAAAGGATGA			1468
Rat	Sbjct	1371	TGTCCGAACCTTACCAGCACAGCAGAAACCAGACTGCCGCCATATTGGGAGAAGGATGA			1430
Human	Query	1469	TGCTTCGATGCCTTGCCTTTGACCTCACAGACATCGTTTCAAGAACTCAGAGGTCAGCT			1528
Rat	Sbjct	1431	CCCTTCTATGCTCTGCCCTTGGACTCACAGATGTGGTCTCTGAGATCAGAAGCCAGCT			1490
Human	Query	1529	TCTGGAAGCAAAACCCCTAG	1547		
Rat	Sbjct	1491	TCTGGAAGCAAGATCCTAG	1509		

Supplemental Figure 10. *FTO* gene homology comparison between human and rat.

FTO homology analysis with Basic Local Alignment Search Tool (BLAST) between human and rat genomes.

Supplemental Figure 11

Range 1: 52 to 1560

	Score	Expect	Identities	Gaps	Strand	Frame
	2228 bits(1206)	0.0)	1408/1509(93%)	0/1509(0%)	Plus/Plus	
Rat Query	1		ATGAAGCGCGTCCAGACCGCGGAGGAACGGGAGCGGGAAGCTAAGAAACTGAGGCTCCTC			60
Mouse Sbjct	52		ATGAAGCGCGTCCAGACCGCGGAGGAACGAGAGCGGGAAGCTAAGAAACTGAGGCTCCTT			111
Rat Query	61		GAGGAGCTTGAAGACACTTGGCTTCCTTACCTGACCCCCAAGATGACGAGTCTATCAG			120
Mouse Sbjct	112		GAGGAGCTTGAAGACACTTGGCTTCCTTACCTGACCCCCAAGATGATGAGTCTATCAG			171
Rat Query	121		CAGTGGCAGCTGAAATATCCTAAACTGGTTTTCCGAGAGGCTGGCAGCATACCCGAGGAG			180
Mouse Sbjct	172		CAGTGGCAGCTGAAATACCTAAACTGGTTTTCCGAGAGGCGGCAGCATACCAAGAGGAG			231
Rat Query	181		CTGCACAAAGAGTCCCCGAGGCTTCTCAGACTGCACAAGCATGGCTGCTTGTTCGG			240
Mouse Sbjct	232		CTGCATAAGGAGTCCCCGAGGCTTCTCAGACTGCATAAGCATGGCTGCTTGTTCGG			291
Rat Query	241		GACCTGGTGGAGTCCAAGGCAAGACGTGCTACCCCGTGTCTCGCATCCTCATGGG			300
Mouse Sbjct	292		GACCTGGTGGAGTCCAAGGCAAGATGTGCTACCCCAAGTGTCTCGCATCCTCATCGGG			351
Rat Query	301		GACCCCGGCTGCACCTACAAGTACTTGAACACCAAGGCTTTCACCTGCCCTGGCCAGTG			360
Mouse Sbjct	352		GACCCAGGCTGCACCTACAGTACTTGAACACCAAGACTCTTCACGCTGCCCTGGCCCGTG			411
Rat Query	361		AAGGGCTGCACCATCAATTACACAGAGGCCGAGATTGCCCGCCATGTGAGACTTCTCTC			420
Mouse Sbjct	412		AAGGGCTGCACGCTCAAGTACACAGAGGCTGAGATGCCCGTGCATGTGAGACTTCTCTA			471
Rat Query	421		AAGCTCAATGACTACCTACAGGTCGAGACCATCCAGGCTTGAAGAAGTGGCTATCAAA			480
Mouse Sbjct	472		AAGCTCAATGACTACCTCCAGGTCGAGACCATCCAGGCTTGAAGAAGTGGCTATCAGA			531
Rat Query	481		GAGAAGGCCAATGAAGACGCTGTGCCCTGTGTCATGGCAGAGTTCGCCAGGGCTGGCGTG			540
Mouse Sbjct	532		GAGAAGGCCAATGAAGACGCTGTGCCACTGTGTCATGGCAGAGTTCGCCAGGGCGCGGTG			591
Rat Query	541		GGACCGTCTGCGATGATGAAGTGGACCTTAAGAGCAGAGCAGCTACAACTGACTTTG			600
Mouse Sbjct	592		GGCCCGTCTGCGATGATGAAGTGGACCTTAAGAGCAGAGCAGCTACAACTGACTTTG			651
Rat Query	601		CTAAACTTCATGGATCCTCAGAAAATGCCGACTTGAAGAGGAGGCCATTTTCGGCATG			660
Mouse Sbjct	652		CTAAACTTCATGGATCCTCAGAAATGCCGACTTGAAGAGGAGGCCATTTTCGGCATG			711
Rat Query	661		GGGAAGATGGCGTGAGCTGGCACCATGACGAGAAGTGGTGGACAGGTCAGCCGTGGCG			720
Mouse Sbjct	712		GGGAAGATGGCGTGAGCTGGCACCATGACGAGAAGTGGTGGACAGGTCAGCCGTGGCA			771
Rat Query	721		GTGTACAGCTATAGCTGTGAAGGCTCCGAGGATGAAAGCGATGACGAGTCCAGCTTCGAA			780
Mouse Sbjct	772		GTGTACAGCTATAGCTGCGAAGGCTCTGAGGATGAAAGTGAAGACGAGTCCAGCTTCGAA			831
Rat Query	781		GGCAGAGATCCCGATACGTGGCATGTTGGTTTTAAGATCTCATGGGACATCGAGACGCCA			840
Mouse Sbjct	832		GGCAGAGATCCCGATACGTGGCATGTTGGTTTTAAGATCTCTTGGGACATCGAGACCCCA			891
Rat Query	841		GGCTTGACAAATTCCTCTTCCAGGGGAGACTGCTATTTCATGTGGATGACCTCAATGCC			900
Mouse Sbjct	892		GGATTAACAATCCCTCTTCCAGGGGAGACTGCTATTTCATGTGGATGACCTCAATGCC			951
Rat Query	901		ACCCACCAGCACTGTGTTTTGGCTGGCTCACAGCCTCGGTTTAGCTCCACCACCAGCGTG			960
Mouse Sbjct	952		ACCCACCAGCACTGTGTTTTGGCTGGCTCACAGCCTCGGTTTAGTTCACCTACCCGTGTG			1011
Rat Query	961		GCAGAGTGTCAACAGGCACCTGGATTATATCTTACAACGCTGCCAGTGGCAGTGCAG			1020
Mouse Sbjct	1012		GCAGAGTGTCAACAGGCACCTGGATTATATCTTAGAACGCTGTCAGTTGGCGTGCAG			1071
Rat Query	1021		AATGTTCTCAATGACTCGGCAATGGCGACGCTCGCTGAAGTCCCTCGAGCTGCAGTT			1080
Mouse Sbjct	1072		AATGTTCTCAATGACTCAGACGATGGCGACGCTCGGTTGAAATCCCTTGGATCTGCAGTT			1131
Rat Query	1081		CTGAAACAAGGAGAAGAGATCCACAACGAGTTCGAGTTTGAAGTGGCTGAGGAGTTCTGG			1140
Mouse Sbjct	1132		TTGAAACAAGGAGAAGAAATCCATAATGAGTGGAGTTTGAAGTGGCTGAGGAGTTCTGG			1191
Rat Query	1141		TTTCAAGGAAATCGATACAAAATTTGCACTGATGGTGGTGTGAGCCATGACTCAGTG			1200
Mouse Sbjct	1192		TTTCAAGGCAATCGATACAAAATTTGCACCGATTGGTGGTGTGAGCCATGACTCAGTG			1251
Rat Query	1201		GAGGGCTGTGGAAGAAGATGGAGAGTGTGACAAAATGCCGCTTCCGTGAAGTTAAGAGA			1260
Mouse Sbjct	1252		GAGGGCTGTGGAAGAAGATGGAGAGCATGACAAAATGCCGCTTCCGTGAAGTTAAGAGA			1311
Rat Query	1261		GAGGGCTCTCCGTGGAACAAGGAGTGAATTTCTGTCTGCCCTCCTGATCCCACTCAC			1320
Mouse Sbjct	1312		GAGGGCTCTCCGTGGAACAAGGAGTGAATTTCTGTCTGCCATCCTGGTCCCCTCAC			1371
Rat Query	1321		ATGCGCCAGAATCTGAGGAAAGAAATGGCACGCGAGTCCAGGCCGAGTTGTCGGAAT			1380
Mouse Sbjct	1372		GTGCGCCAGAATCTGAGGAAAGAAATGGCACGCGAGTCCAGGCCGAGTTGTCGGAAT			1431
Rat Query	1381		CTACCAGCACAGCAGAAAACAGACTGCCGCCATATTGGGAGAAGGATGACCTTCTATG			1440
Mouse Sbjct	1432		TTACCAGTACAGCAGAAAACAGACTGCCGCCATATTGGGAGAAGGATGACCTTCCATG			1491
Rat Query	1441		CCTCTGCCCTTTGACCTCACAGATGTGGTCTCTGAGATCAGAAGCCAGCTTCTGGAAGCA			1500
Mouse Sbjct	1492		CCTCTGCCCTTTGACCTCACAGAGTGGTTCAGAGCTCAGAGGCCAGCTGCTGGAAGCA			1551
Rat Query	1501		AGATCCTAG 1509			
Mouse Sbjct	1552		AGATCCTAG 1560			

Supplemental Figure 11. *Fto* gene homology comparison between rat and mouse.

Fto homology analysis with Basic Local Alignment Search Tool (BLAST) between rat and mouse genomes.

Supplemental Table 1. Differentially expressed genes based on combined methylated RNA immunoprecipitation sequencing (MeRIP-seq) and RNA-seq in diabetes

Gene_ID	Gene_Name	m ⁶ A log ₂ fold change	RNA log ₂ fold change
ENSRNOG00000010370	<i>Tnip1</i>	-2.403344934	-1.877649774
ENSRNOG00000006565	<i>Fstl4</i>	-2.116491664	0.933593991
ENSRNOG00000001335	<i>Zkscan1</i>	-1.501391236	0.676768574
ENSRNOG00000008869	<i>Ppp1r9a</i>	-1.035297836	0.703270304
ENSRNOG00000024711	<i>Sdk2</i>	-0.926931718	0.755600279
ENSRNOG00000009403	<i>Dcaf17</i>	-0.890179084	0.831494151
ENSRNOG00000043102	<i>Bahcc1</i>	-0.786528769	0.628833773
ENSRNOG00000013570	<i>Rad54l2</i>	-0.77675958	0.623855184
ENSRNOG00000006050	<i>Med19</i>	-0.74638501	-0.593321028
ENSRNOG00000014452	<i>Zfhx3</i>	-0.733215313	0.700445655
ENSRNOG00000007528	<i>Kcnh7</i>	-0.728463539	1.240004352
ENSRNOG00000013257	<i>Hecw2</i>	-0.727604057	0.872840955
ENSRNOG00000048174	<i>Uqcrq</i>	-0.720206759	-0.684999835
ENSRNOG00000016046	<i>Hecw1</i>	-0.670929796	0.663801235
ENSRNOG00000004269	<i>Myt1l</i>	-0.657111855	0.629508064
ENSRNOG00000015269	<i>Atf7</i>	-0.630214394	0.604309124
ENSRNOG00000014866	<i>Pign</i>	-0.628593726	0.724600424
ENSRNOG00000007319	<i>Trib3</i>	-0.60789811	0.898044
ENSRNOG00000030352	<i>Pcdhga9</i>	-0.599882549	0.745519586
ENSRNOG00000007030	<i>Epha7</i>	0.607385619	0.704355376
ENSRNOG00000003742	<i>Cdkl5</i>	0.614003318	0.882585524
ENSRNOG000000052894	<i>Epg5</i>	0.624900984	0.677217193
ENSRNOG00000011585	<i>Fat3</i>	0.635607055	0.86493989
ENSRNOG00000045696	/	0.670009641	-0.720027611
ENSRNOG00000000924	<i>Slc7a1</i>	0.688531053	1.916719941
ENSRNOG00000001622	<i>Impg2</i>	0.708175115	0.649446802
ENSRNOG00000001141	<i>Srrm4</i>	0.708357455	0.669713596
ENSRNOG00000029131	<i>Aabr07024637.1</i>	0.723300489	0.657155156
ENSRNOG00000002291	<i>Brwd3</i>	0.763101043	0.68355021
ENSRNOG00000011151	<i>Tenm4</i>	0.773635986	0.688185311
ENSRNOG00000002341	<i>Trim25</i>	0.77387041	0.777095165
ENSRNOG00000024832	<i>Gpr158</i>	0.843450113	0.773135615
ENSRNOG00000056658	<i>Xylt1</i>	0.868167806	0.65151631
ENSRNOG00000056656	/	0.881474402	1.058279742
ENSRNOG00000059479	<i>Adcyl1</i>	0.93522769	0.587940421
ENSRNOG00000018830	<i>Aff3</i>	0.976309003	0.792163902
ENSRNOG00000008425	<i>Nav1</i>	1.038821314	0.719154598
ENSRNOG00000006943	<i>Aabr07072108.1</i>	1.090522518	-1.181784135
ENSRNOG00000010964	<i>Akap13</i>	1.099207994	0.846206833
ENSRNOG00000000478	/	1.199220997	-0.823773518
ENSRNOG00000001216	<i>Trpm2</i>	1.45803698	-0.640956169
ENSRNOG00000053240	<i>Soga1</i>	1.475450762	0.834672276
ENSRNOG00000052247	<i>Manba</i>	1.820481272	0.587818667

Supplemental Table 2. Genes regulated by *Fto* based on combined analyses of methylated RNA immunoprecipitation sequencing (MeRIP-seq) and RNA-seq in diabetic retinas

Gene_ID	Gene_name	m ⁶ A log ₂ fold change	RNA log ₂ fold change
ENSRNOG00000061371	<i>Aabr07035541.3</i>	-1.501391236	-2.986475067
ENSRNOG00000022673	<i>Slc22a20</i>	-1.709196683	1.413439099
ENSRNOG00000017410	<i>Loxhd1</i>	-1.394557866	1.324649995
ENSRNOG00000010370	<i>Tnip1</i>	-2.403344934	-1.877649774
ENSRNOG00000051494	<i>Aabr07002870.2</i>	-1.599254974	4.299916654
ENSRNOG00000010906	<i>Ccl5</i>	-1.139213224	-1.258196724
ENSRNOG00000029749	<i>Pabpc4l</i>	-5.766610799	2.305523471
ENSRNOG00000015441	<i>Il4r</i>	-2.223895882	1.25294364
ENSRNOG00000028632	<i>Bcl2l14</i>	-1.029716879	1.413439099
ENSRNOG00000028744	<i>Mtnr1a</i>	-3.037795763	2.039296856
ENSRNOG00000042623	<i>Sh2d4b</i>	-1.326540478	-1.24398034
ENSRNOG00000032869	<i>Crygf</i>	-4.863984696	-2.35602882

Supplemental Table 3. Clinical characteristics of patients with diabetic retinopathy and idiopathic epiretinal membrane

Variables	DR (n=30)	ERM (n=30)	p
Age (y)	51.5(41.0-57.0)	59.0(56.5-66.0)	<0.001*
Gender			0.121
Male	18(60.0)	12(40.0)	
Female	12(40.0)	18(60.0)	
Diabetes duration (y)	12.5(10.0-17.5)	NA	NA
Type of diabetes			NA
Type 1 diabetes	10(33.3)	NA	
Type 2 diabetes	20(66.7)	NA	
Glycated hemoglobin (%)	7.1(6.4-8.6)	5.4(4.9-5.9)	<0.001*
Fasting blood glucose (mmol/L)	6.2(5.9-8.5)	5.6(4.8-6.3)	0.002*
Systolic blood pressure (mmHg)	129.5(121.5-140.3)	134.5(123.8-142.5)	0.317
Diastolic blood pressure (mmHg)	78.5(70.0-86.0)	80.0(72.8-90.0)	0.552
Low density lipoprotein (mmol/L)	2.8(1.7-3.0)	2.7(2.3-2.9)	0.915
BMI (kg/m ²)	24.0(21.8-26.4)	24.8(22.7-26.4)	0.313
Insulin use	26(86.7%)	0	<0.001*
LogMAR BCVA	0.8(0.3-1.2)	0.7(0.5-1.0)	0.305

Data are presented as median (interquartile range)/n (%).

DR: diabetic retinopathy; ERM: epiretinal membrane; BMI: body mass index; LogMAR, logarithm of the minimum angle of resolution; BCVA: best-corrected visual acuity; NA: not available.

*Statistically significant.

Supplemental Table 4. Oligonucleotides sequences for small interfering RNA (siRNA), overexpression plasmid, virus, and probes

Oligonucleotides name	Species	Sequence (5'-3')
<i>FTO</i> -siRNA	human	CGGTGGCAGTGTACAGTTA
<i>TNIP1</i> -siRNA	human	CAGGAGAGCGUUACCAUGUGGTT
NC-siRNA	human	TTCTCCGAACGTGTCACGT
LV- <i>FTO</i> -OE	human	NM_001363894.1
LV- <i>TNIP1</i> -OE	human	NM_001252385.2
AAV- <i>Fto</i> -shRNA	mouse	Top strand: AATTCGTTGAAAGAGGAGCCCTATTTCTCGAGGA AATAGGGCTCCTCTTTCAATTTTTTG Bottom strand: GATCCAAAAAATTGAAAGAGGAGCCCTATTTCTC GAGGAAATAGGGCTCCTCTTTCAACG
AAV- <i>Fto</i> -OE	mouse	NM_011936.2
AAV- <i>Tnip1</i> -shRNA	mouse	Top strand: AATTCGCGAGTTCAACAGGTTGGCCTCCAAATTCA AGAGATTTGGAGGCCAACCTGTTGAACTCGTTTTT TG Bottom strand: GATCCAAAAACGAGTTCAACAGGTTGGCCTCCA AATCTCTTGAATTTGGAGGCCAACCTGTTGAACTC GCG
AAV- <i>Tnip1</i> -OE	mouse	NM_021327.4
WT probe	/	TAAGAGTGGGAGGCAGCCAAGACCCCCTTCCTTCA AAACCTCCCGGA
MT probe	/	TAAGAGTGGGAGGCAGCCAAGTCCCCTTCCTTCA AAACCTCCCGGA

LV: lentivirus; AAV: adeno-associated virus; OE, overexpression; WT: wildtype; MT: mutant type.

Supplemental Table 5. Primers used in this study

Gene name	Application	Species	Sequence (5'-3')
<i>TNIP1</i>	qPCR	human	F: GTTCAACCGACTGGCATCCAA R: AGACGCACCCTCTTTGTTGC
<i>METTL3</i>	qPCR	human	F: TCCATCTGTCTTGCCATCT R: TCGCTTTACCTCAATCAACTC
<i>METTL14</i>	qPCR	human	F: AATGGCCGTTCTGTGCTCAT R: AAGGACCCATCACAGGCAAG
<i>FTO</i>	qPCR	human	F: GCTGACCTGGATGTAGATGTT R: GGAGAGATGTGTTAATGGCAT
<i>ALKBH5</i>	qPCR	human	F: CCTTGGTTTTGTTGCCTGTT R: ATCAGCCTCTGTCCCCTATTG
<i>YTHDF1</i>	qPCR	human	F: GGAACAACATCTATCAGCACA R: GACCTTGAGACCCACTTGTC
<i>YTHDF2</i>	qPCR	human	F: GCTACAAGCACACCACTTCCAT R: GCCTTTTATTTCCCACGACC
<i>YTHDF3</i>	qPCR	human	F: CCTGTCAGTGCTTCACCTTCT R: CGTCCATTCTTCAGATTCCAA
<i>β-actin</i>	qPCR	human	F: GCACCGCAAATGCTTCTA R: GGTCTTTACGGATGTCAACG
<i>TNIP1</i>	m ⁶ A RIP	human	F: AGAGTGGGAGGCAGCCA R: TGAAACCACTTCCGGGAG
<i>Tnip1</i>	m ⁶ A RIP	mouse	F: ATCCTAAGAATGAGGTGCAAC R: AACCAAGTCTTTGAGGTTCT
<i>Cre</i> expressioin	Genotyping PCR	mouse	F: CCAGGCTGACCAAGCTGAG R: CCTGGCGATCCCTGAACA
<i>Fto</i> flox	Genotyping PCR	mouse	F: AAAGTTTGAAGGAGGGGAGAAGTG R: ACCAAAGAGGGGAGACAGTTACG
<i>Fto</i> ^{Δ/Δ}	Genotyping PCR	mouse	F: CTGAATAGCCCCCTCCCAATGACC R: ATAAAAATGACAGGAAGCCAAGAA

PCR: polymerase chain reaction.

Supplemental Table 6. Antibodies and reagents used in this study

Chemicals and Reagents	Catalog Number	Company
Human IL-18 ELISA Kit	ab215539	Abcam
Mouse IL-18BP ELISA Kit	ab254509	Abcam
Human IL-1 beta ELISA Kit	ab214025	Abcam
Mouse IL-1 beta ELISA Kit	ab197742	Abcam
Rabbit monoclonal to FTO	ab280081	Abcam
Anti-YTHDF1 antibody [EPR22349-41]	ab220162	Abcam
Rabbit recombinant multiclonal [RM1006] to CD31	ab281583	Abcam
Mouse monoclonal to beta Actin	ab8226	Abcam
Rabbit Anti-Mouse IgG H&L(HRP)	ab6728	Abcam
Goat Anti-Rabbit IgG H&L(HRP)	ab6721	Abcam
Pierce Magnetic RNA-Protein Pull-Down Kit	20164	Thermo Fisher Scientific
Rhodamine phalloidin	R415	Thermo Fisher Scientific
Imprint® RNA Immunoprecipitation Kit	RIP-12RXN	Sigma-Aldrich
Dual-Glo Luciferase® Assay System	E2920	Promega
GloMax® 96 Microplate Luminometer	E6521	Promega
Rabbit polyclonal antibody to TNIP1	15104-1-AP	Proteintech
Ubiquitin antibody	10201-2-AP	Proteintech
Rabbit polyclonal antibody to HA	51064-2	Proteintech
NF-κB p105/p50 (D4P4D) Rabbit mAb	13586	CST
m ⁶ A Rabbit mAb	D9D9W	CST
DYKDDDDK Tag (D6W5B) Rabbit mAb	14793S	CST
Rabbit monoclonal to A20	5630S	CST
Anti-rabbit IgG, HRP-linked Antibody	7074	CST
Anti-mouse IgG, HRP-linked Antibody	7076	CST
Rabbit monoclonal to FLAG M2	14793	CST

Unedited blot and gel images.

Figure 1E

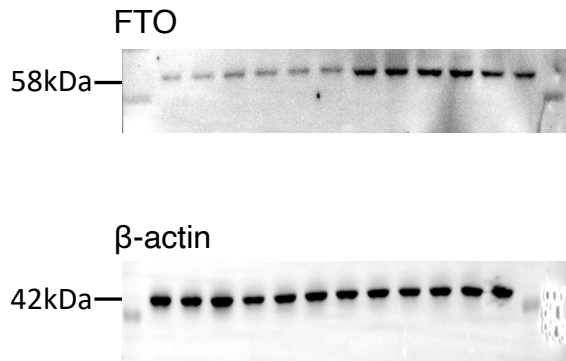


Figure 1F

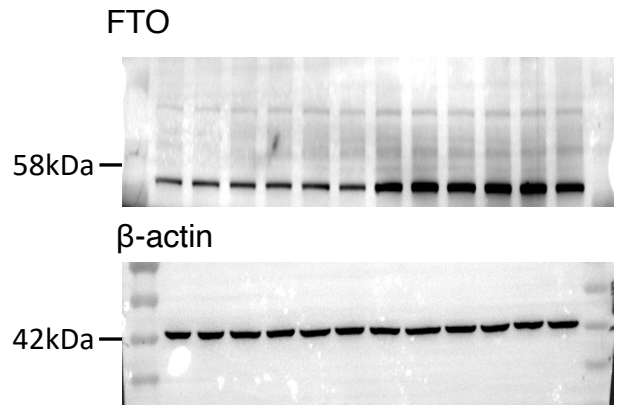


Figure 2D

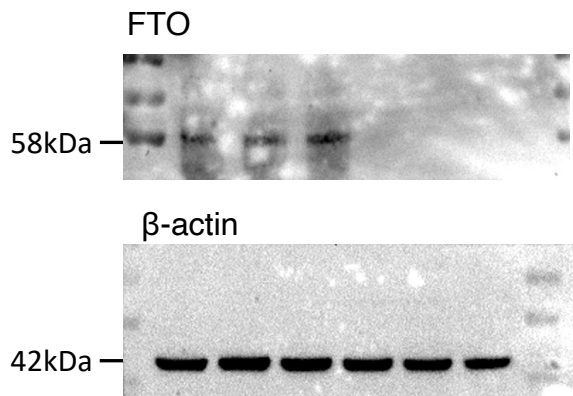


Figure 4A

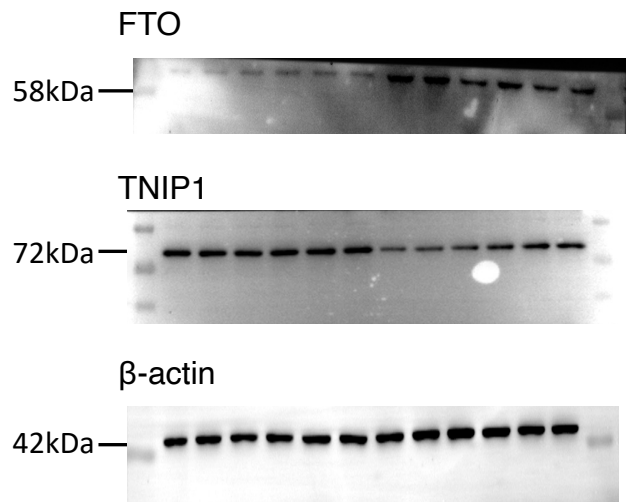


Figure 4B

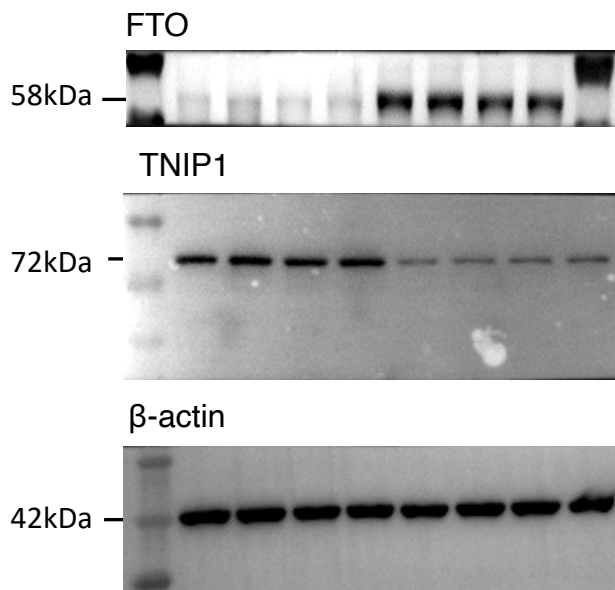


Figure 4C

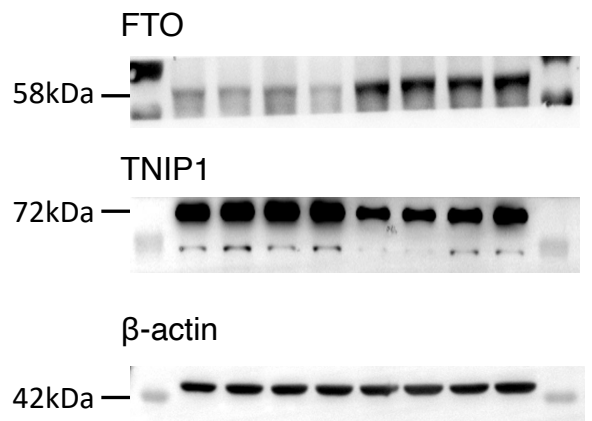


Figure 6A

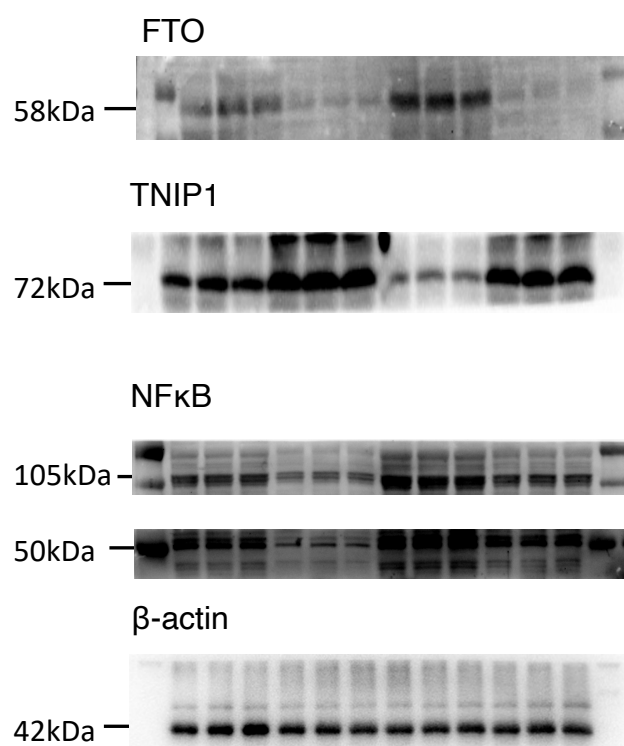


Figure 6B

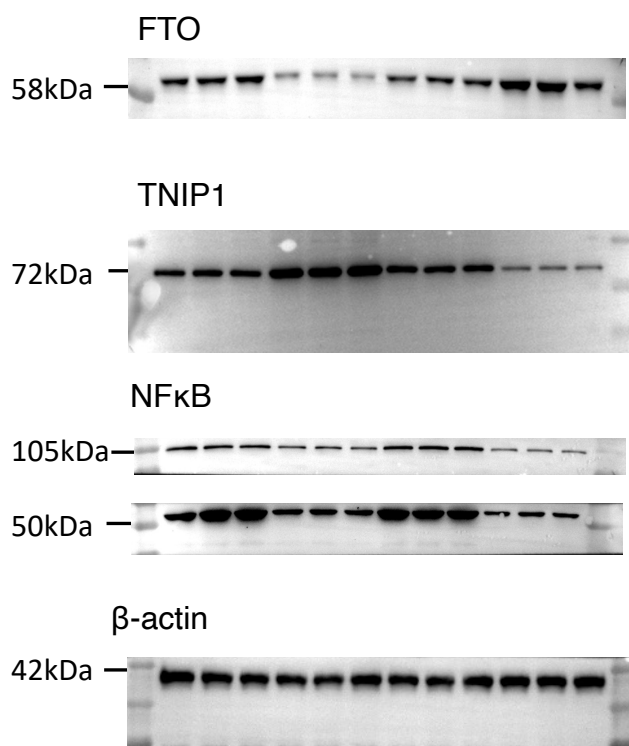


Figure 7F

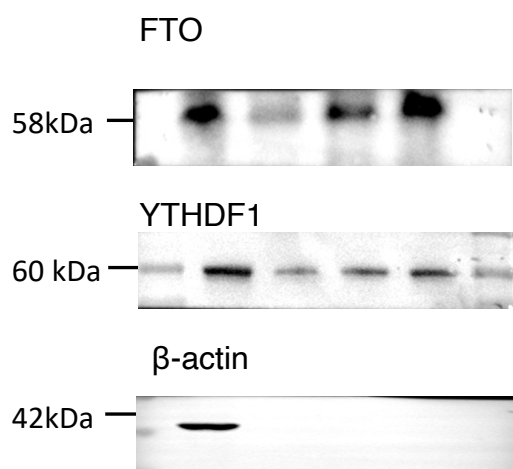


Figure S1F

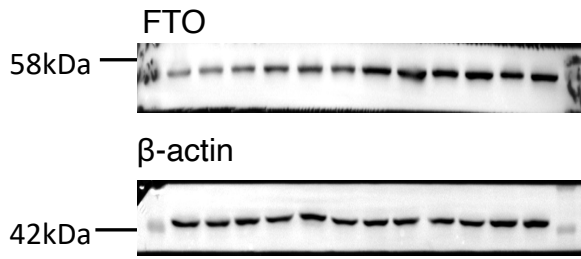


Figure S1G

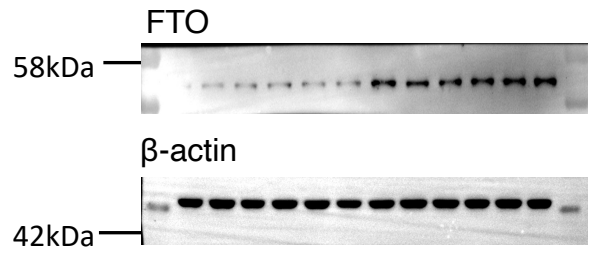


Figure S1H

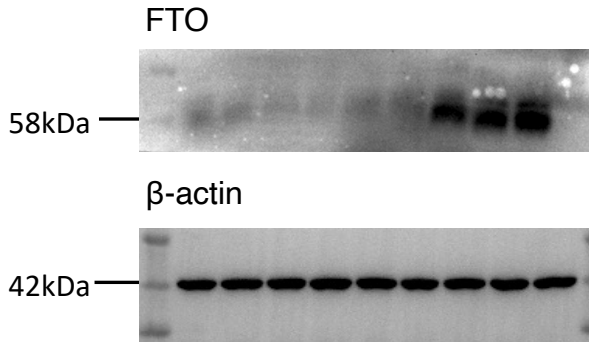


Figure S1I

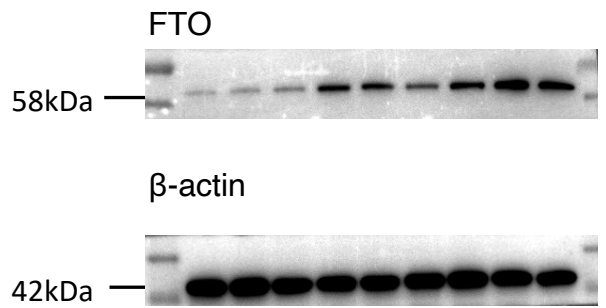


Figure S2D

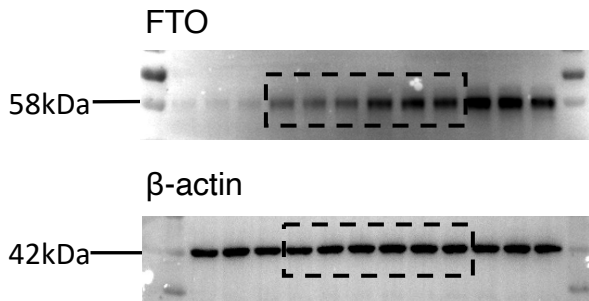


Figure S2E

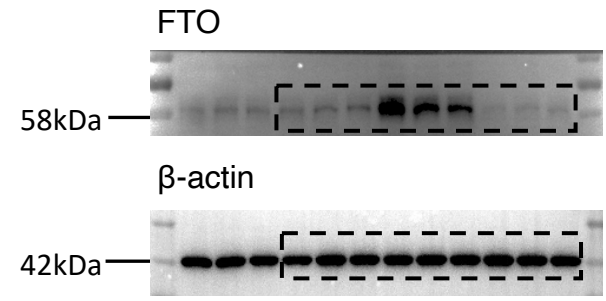


Figure S3A

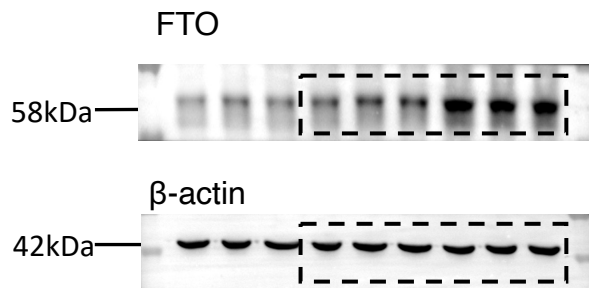


Figure S3B

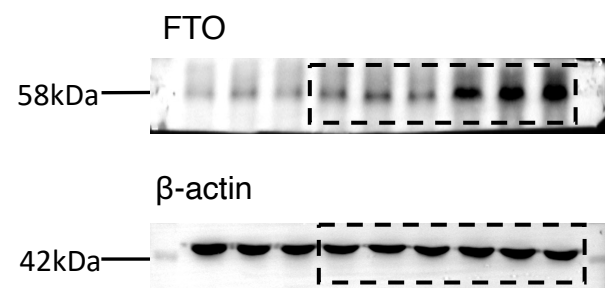


Figure S5A

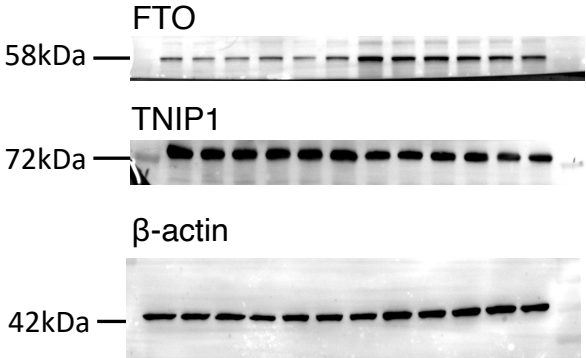


Figure S6G

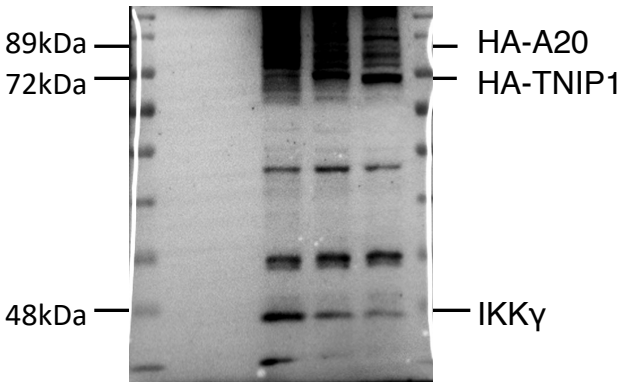


Figure S6E

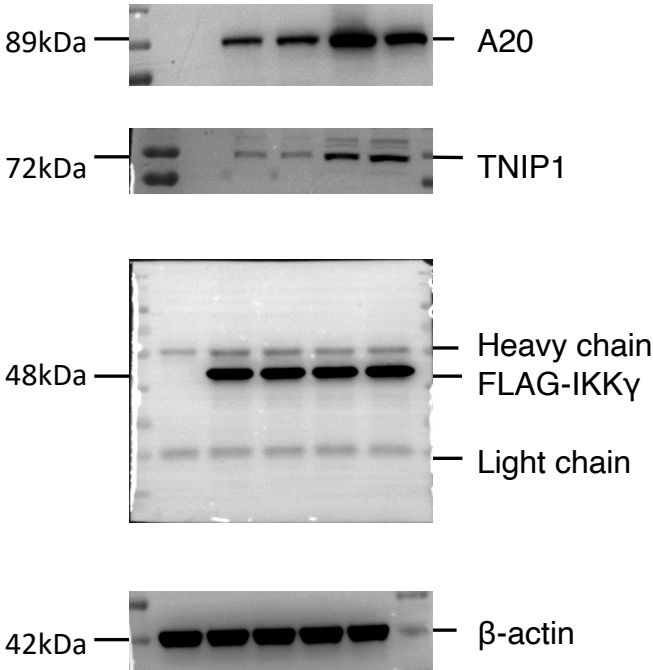
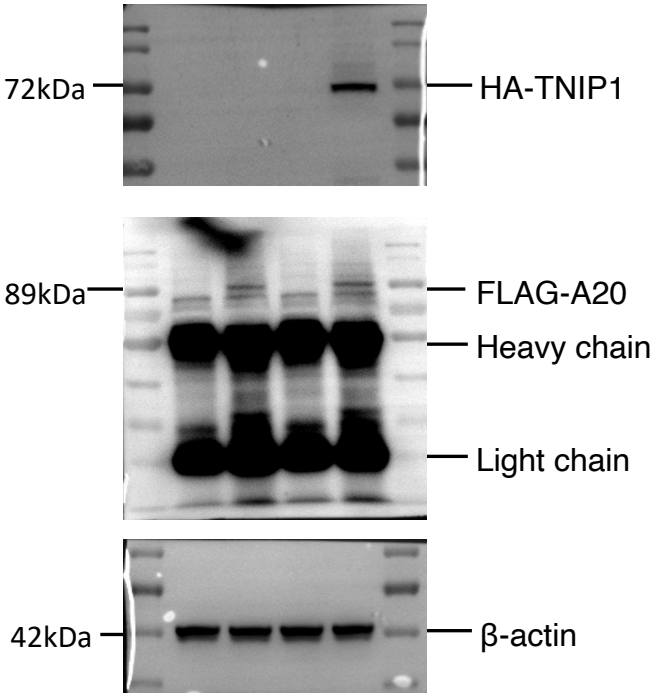


Figure S6F

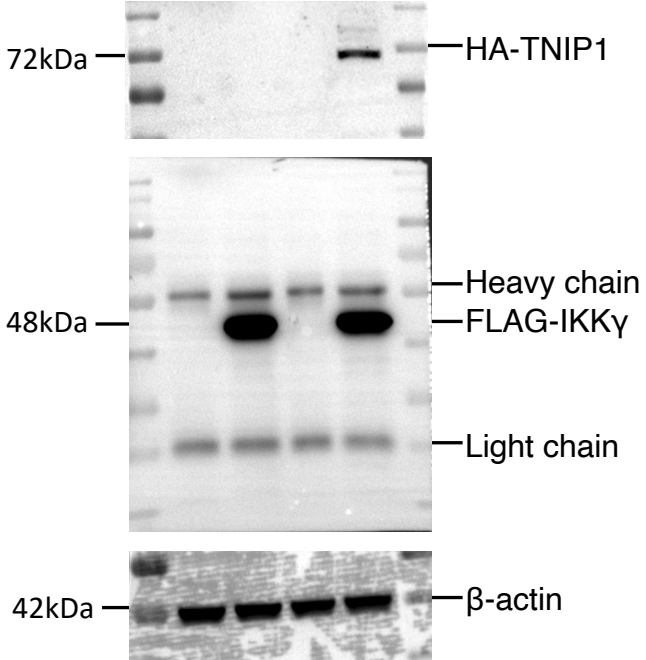


Figure 2C

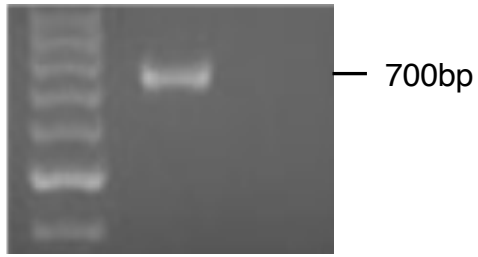


Figure 4D

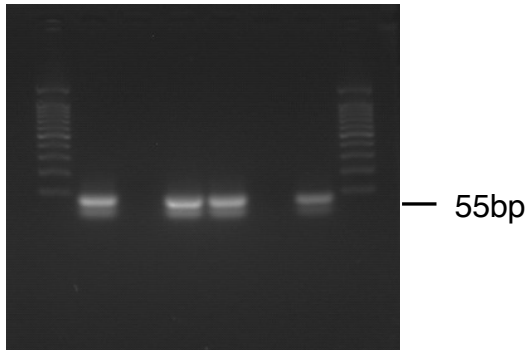


Figure 4E

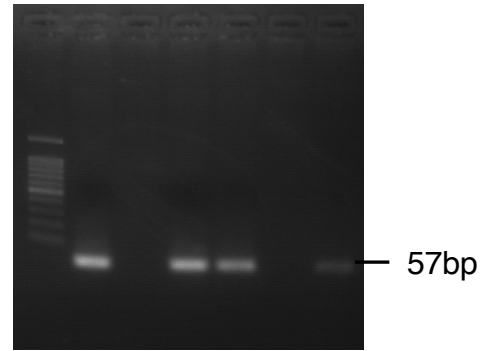


Figure 4F

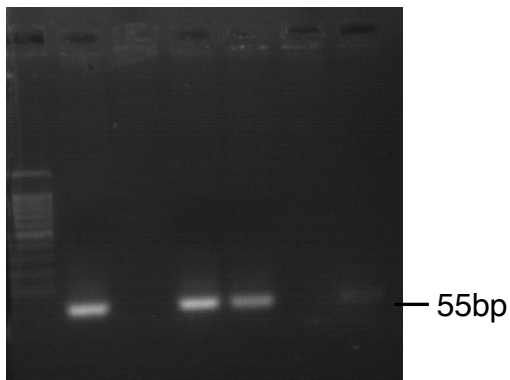


Figure 7A

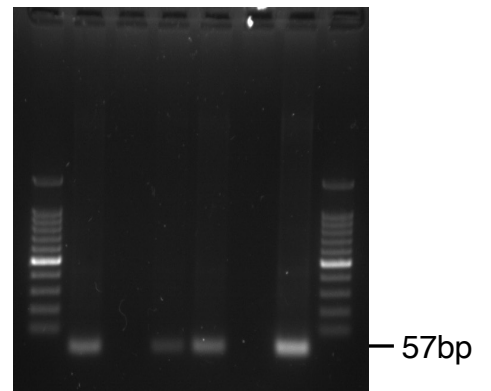


Figure 7B

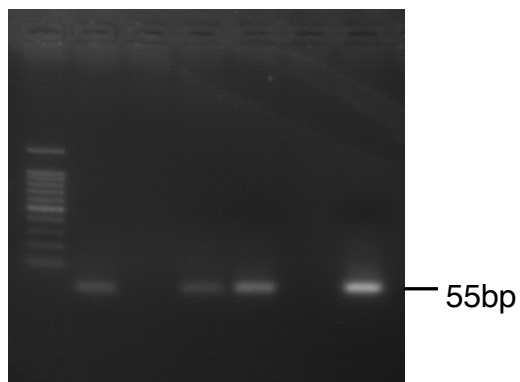


Figure 7F

