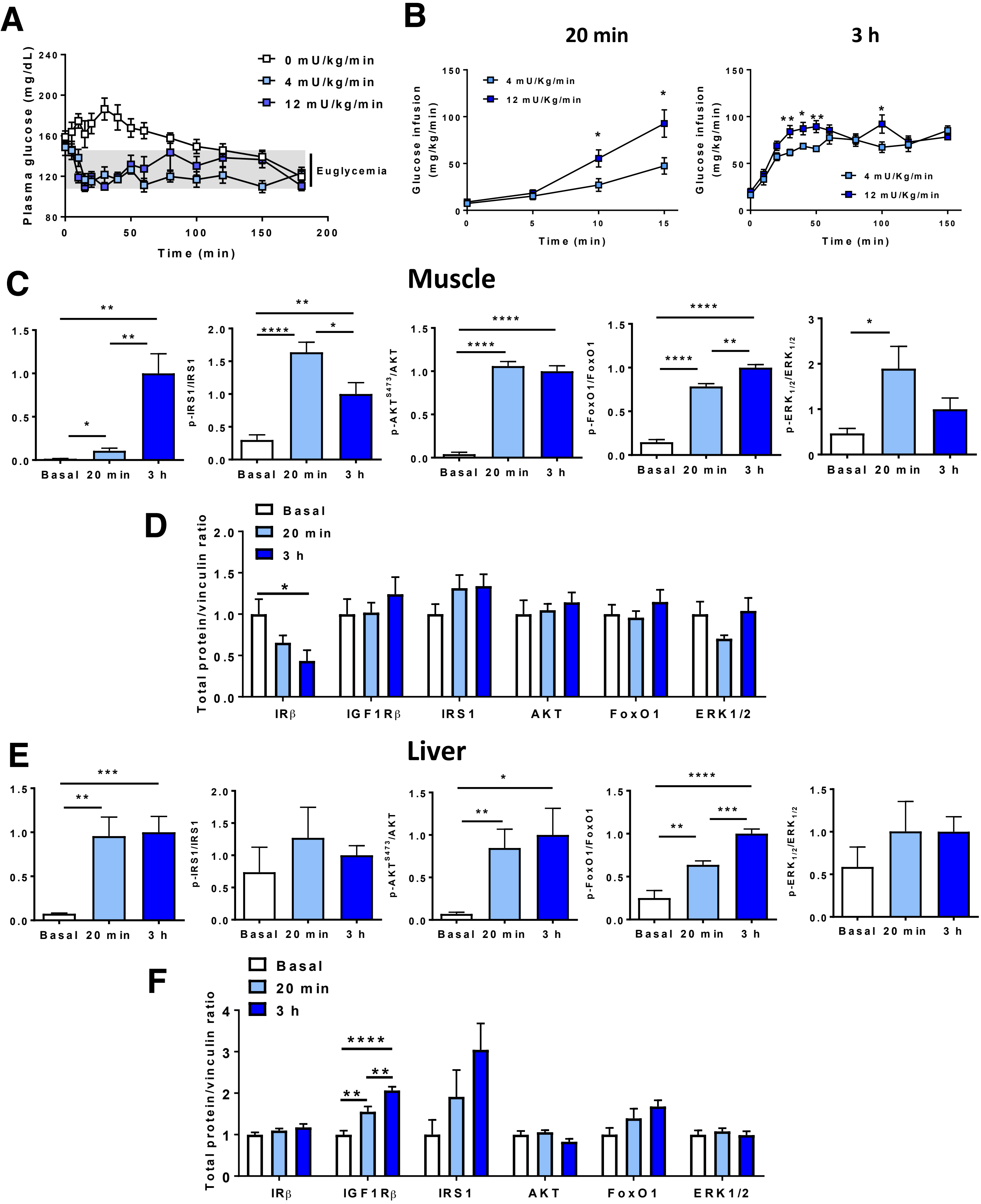
**Cell Reports, Volume *26***

# Supplemental Information

# Multi-dimensional Transcriptional Remodeling by Physiological Insulin *In Vivo*

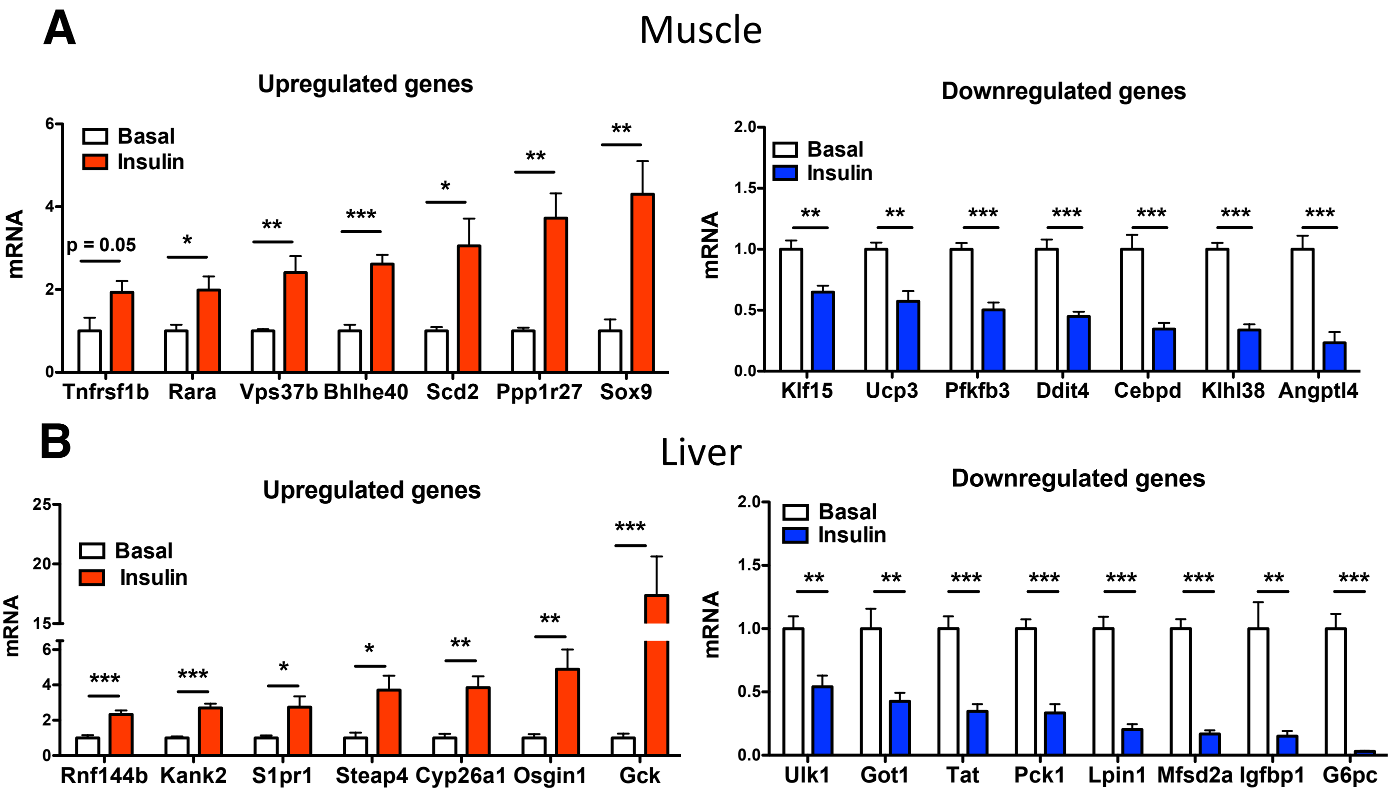
**Thiago M. Batista, Ruben Garcia-Martin, Weikang Cai, Masahiro Konishi, Brian T. O'Neill, Masaji Sakaguchi, Jong Hun Kim, Dae Young Jung, Jason K. Kim, and C. Ronald Kahn**

# Figure S1, Blood glucose levels, glucose infusion during clamp experiment and western blot quantification, Related to Figure 1



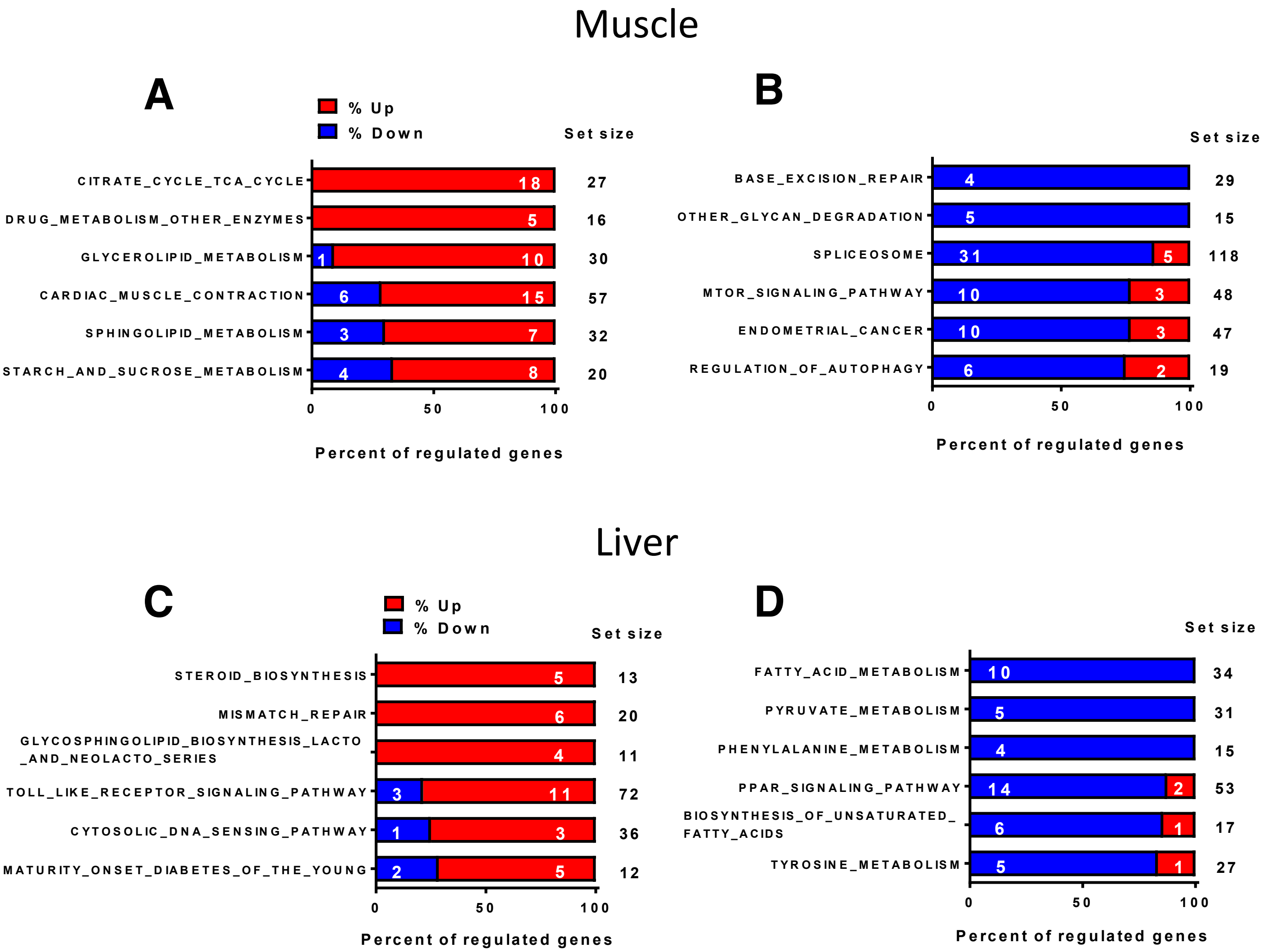
(A) Blood glucose and (B) glucose infusion rates during euglycemic clamp experiments. For blood glucose, mice from 20 and 180 min time-points are shown together (n = 6-12). Western blot quantification in muscle showing (C) phospho/total ratios and (D) total/vinculin ratios. Western blot quantification in liver showing (E) phospho/total ratios and (F) total/vinculin ratios. Data are means ± SEM, n = 5-6. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$, One-way ANOVA.

# Figure S2, Validation of significantly regulated genes by high insulin at 3h, Related to Figure 2 and Figure 3



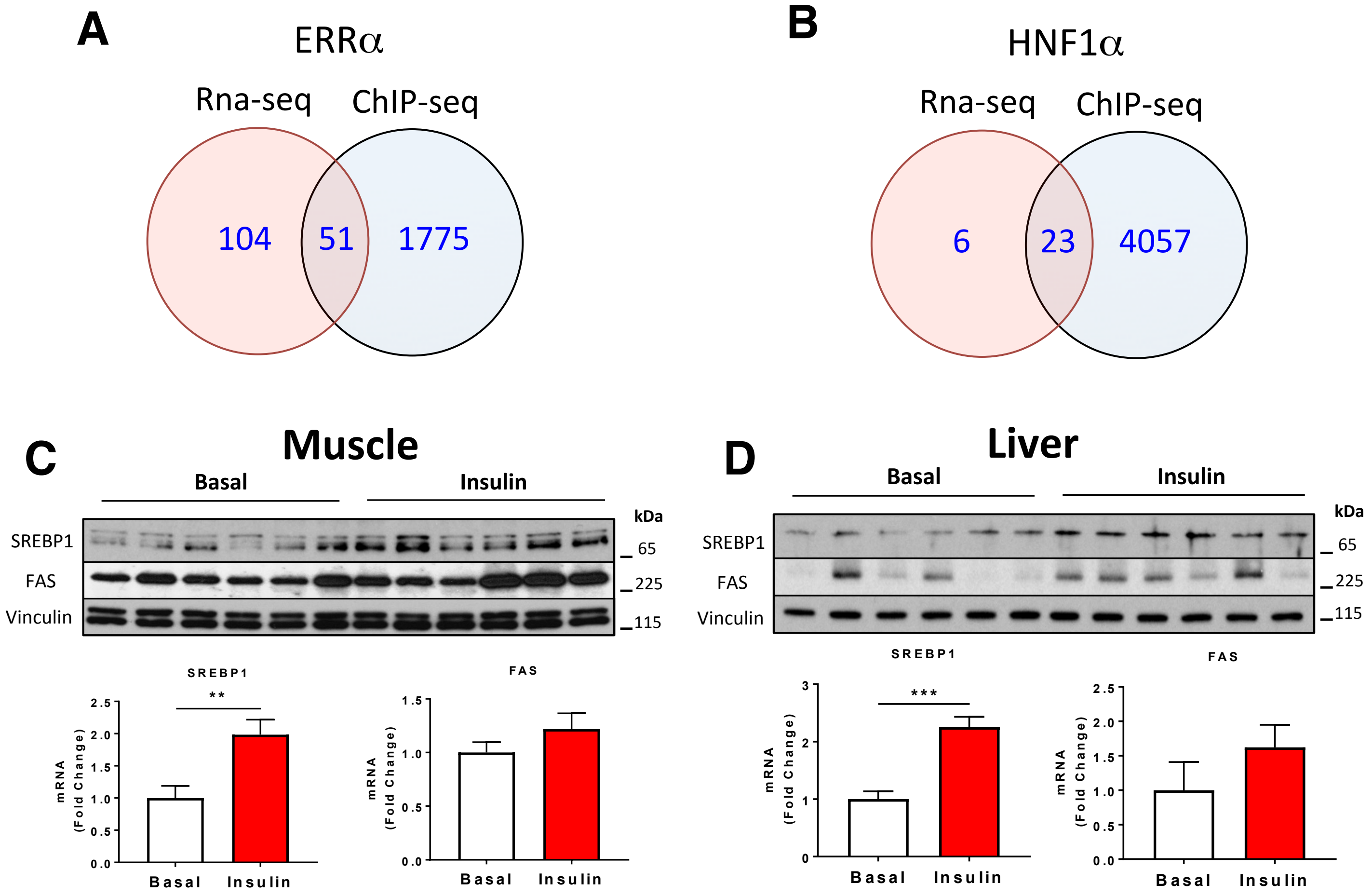
Semi-quantitative qPCR analysis in (A) muscle and (B) liver normalized to TBP. Data are means ± SEM, n=6, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, Student's *t* test

# Figure S3, KEGG pathways regulated by insulin in muscle and liver, Related to Figure 2 and Figure 3



Significant (FDR < 0.05) insulin-regulated pathways in (A, B) skeletal muscle and (C, D) liver at 3 h assessed by mroast analysis. Plots are percentage of up and down-regulated genes over total regulated genes (FDR < 0.1) within each pathway. Numbers of regulated genes are indicated inside bars. Set size represents the total number of genes annotated in each pathway from KEGG database. Pathway analysis was performed using a set in which data from low and high insulin samples was combined (n = 12).

# Figure S4, Motif enrichment and ChIP-Seq comparisons, SREBP1 protein expression and target genes, Related to Figure 4

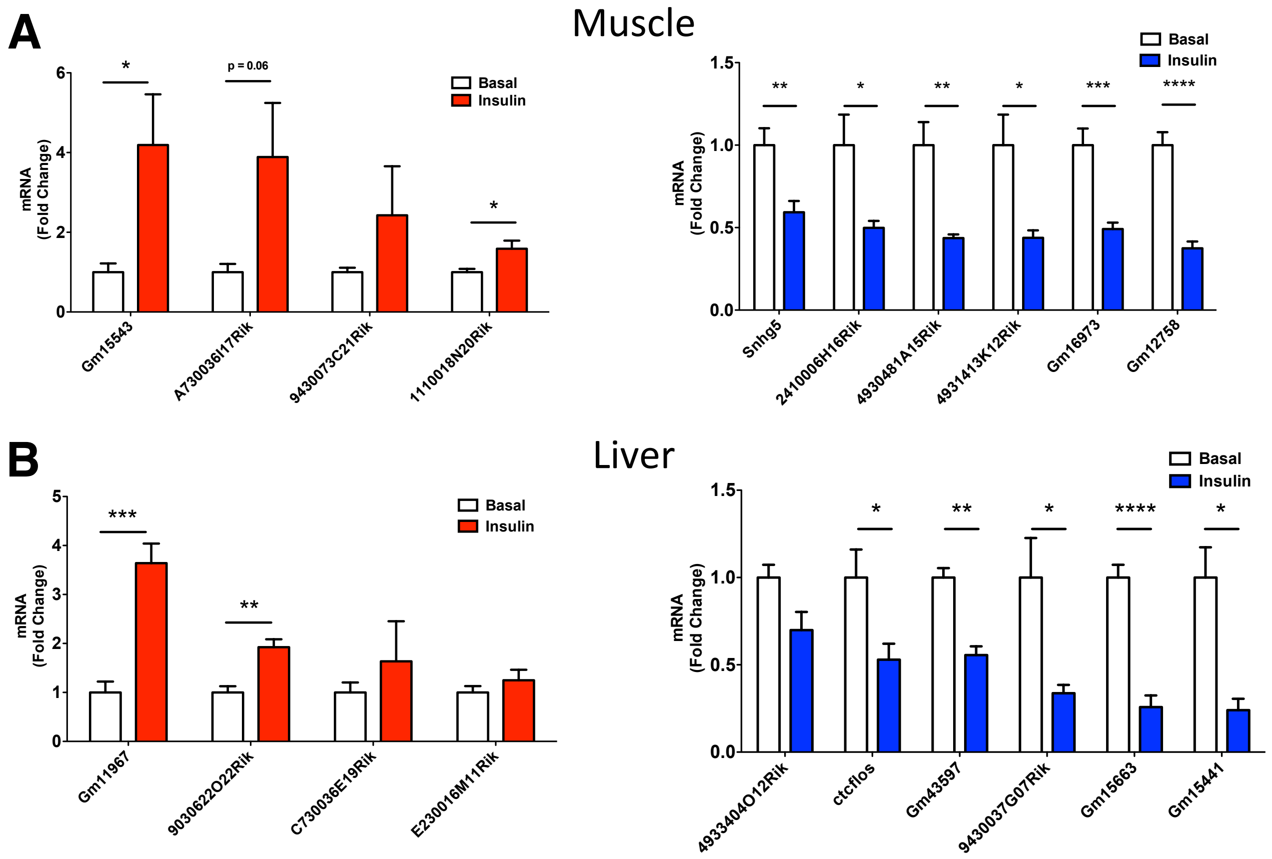


**E**

| Tissue | TRANSFAC Motif | Significantly regulated genes (FDR < 0.1) | |
|---|---|---|---|
| | | Up | Down |
| Muscle | M00220 – SREBP1 | Vps26a, Hk2, Stx6, Bdnf, Tug1, Abr, Rnf115 | Chd2, Cnppd1, Eif4b, Dvl2, Setd2, Atf7ip, Eif4g1, Sppl3, Zfyve26, Pias4, Sdf2, Ube4b, Aspscr1, Rnf146, Polr3c, Epc1, Alg1, Fam179b, Slc36a1, Mfsd5, Grn, Rab22a, Hoxa7 |
| Liver | M00221 – SREBP1 | Ift80, Rara, Notch2, Inpp4a | Foxp2, Ube2b, Zfyve1, Pdp2, Tex2, Sik3, Cebpb, Jund, Elovl5, Hyal1, Tom1l1, Inca1 |

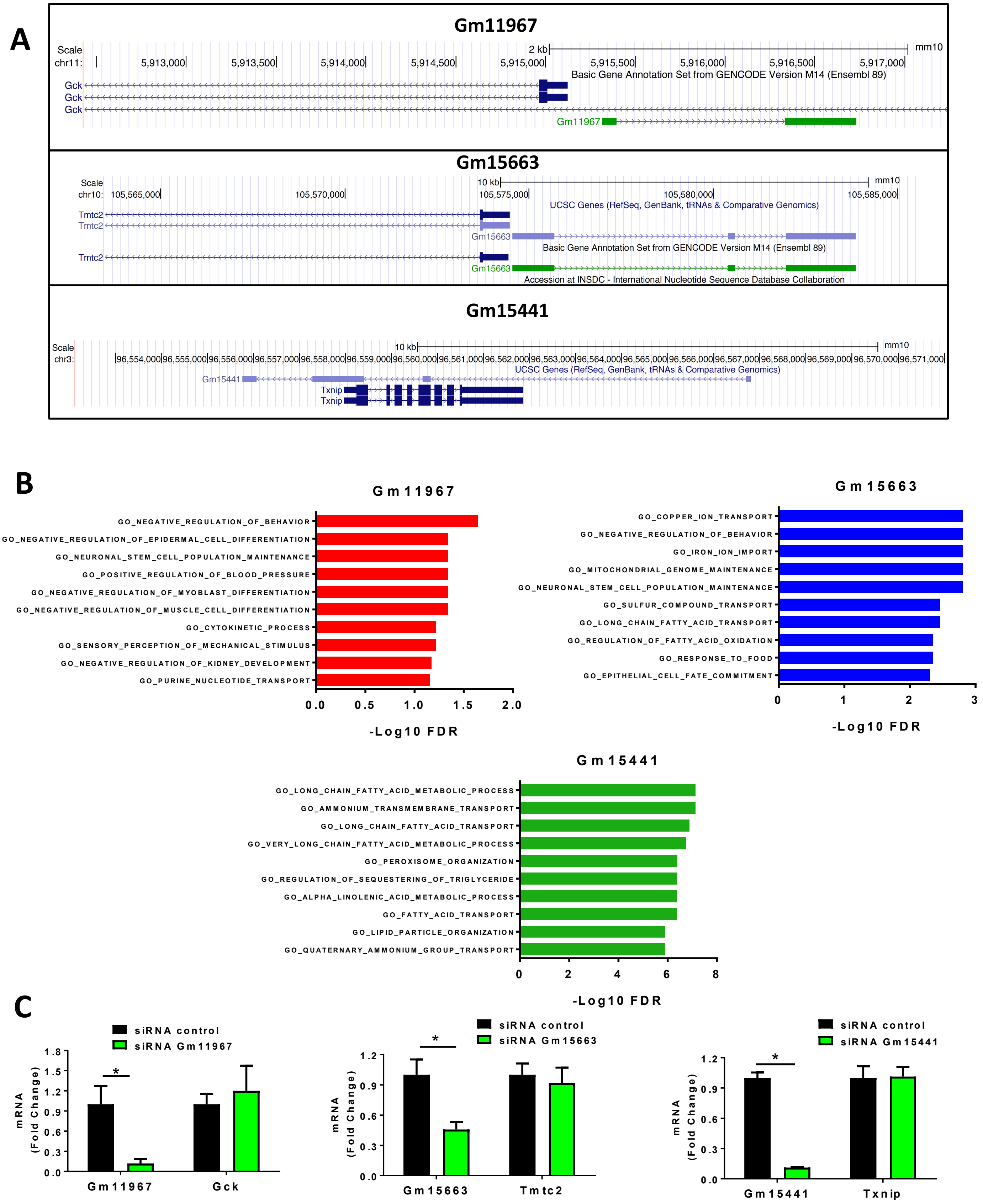
Overlap between transcription factor motif enrichment analysis (RNA-Seq) and ChIP-Seq analysis of (A) ERRα and (B) HNF1α. Protein expression of mature SREBP1 isoform and FAS in (C) muscle and (D) liver in response to high insulin at 3h. Data are means ± SEM, n=6, ** $p < 0.01$, *** $p < 0.001$, Student's *t* test. (E) Significantly regulated genes showing enrichment of SREBP1 motifs within promoter regions.

# Figure S5, Validation of significantly regulated ncRNA genes by high insulin at 3 h, Related to Figure 6



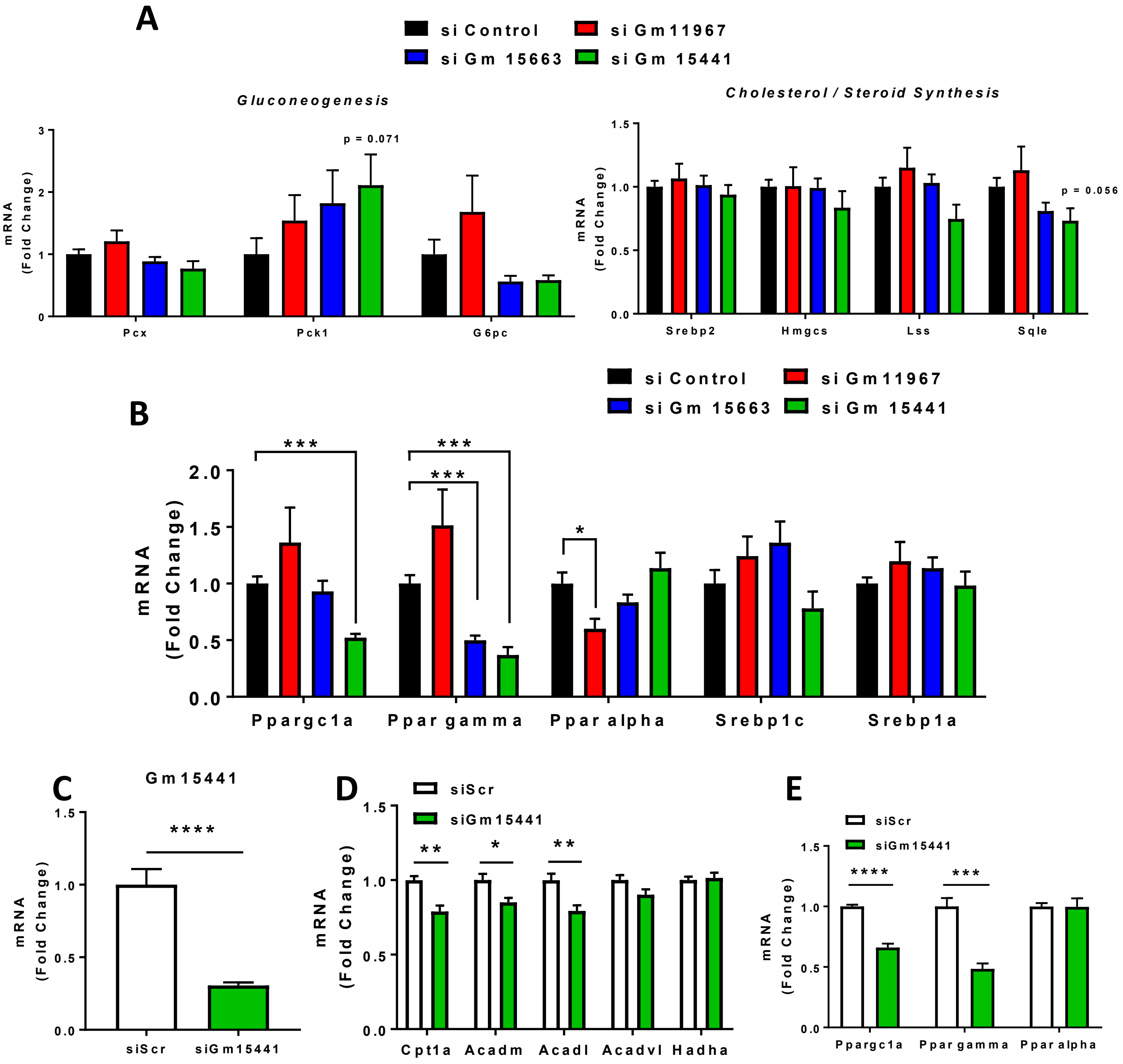
Semi-quantitative qPCR analysis in (A) muscle and (B) liver normalized to TBP. Data are means ± SEM, n=6, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$, Student’s *t* test.

# Figure S6, lncRNA loci, GO analysis and knockdown efficiency in primary hepatocytes, Related to Figure 7



(A) Genome browser screen shots from UCSC (GRCm38/mm10) indicating the position of the indicated LncRNAs and neighboring genes. (B) Top 10 significantly (FDR < 0.1) enriched GO Biological Process terms from mRNA-lncRNA correlation analysis (C) Semi-quantitative qPCR analysis, normalized to TBP, showing knockdown efficiency of lncRNAs in primary hepatocytes and no effects on neighboring genes. Data are means ± SEM, n= 4-5, * $p < 0.05$, Student's *t* test.

# Figure S7, Effects of lncRNA knockdown in primary and AML-12 hepatocytes, Related to Figure 7



Semi-quantitative qPCR analysis of (A) genes involved in gluconeogenesis and cholesterol/steroid synthesis and (B) gene expression of major transcriptional regulators of lipid metabolism in primary hepatocytes transfected with siRNAs against *Gm11967*, *Gm15663*, *Gm15441* or scramble controls, normalized to 18S. Data are means ± SEM. For each condition, hepatocyte cultures from 4-5 mice were used, * $p < 0.05$, *** $p < 0.001$, Student's t test. (C) Knockdown efficiency and expression of (D) fatty oxidation genes and (E) transcriptional regulators of lipid metabolism in AML-12 hepatocytes after transfection with siRNAs against Gm15441 or scramble controls, normalized to TBP. Data are means ± SEM. n = 5-6 biological replicates, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$, Student's t test.

# Table S3 – Regulation of Mitochondrial DNA-encoded genes in muscle by high insulin at 3 h, Related to Figure 2

| Ensembl accession n° | Gene symbol | Fold change (Ins/Basal) | FDR |
|---|---|---|---|
| | **16 rRNA** | | |
| ENSMUSG00000064339 | mt-Rnr2 | 1.87 | 0.0933 |
| | **Electron transport chain** | | |
| ENSMUSG00000064351 | mt-Co1 | 1.59 | 0.0542 |
| ENSMUSG00000064341 | mt-Nd1 | 1.74 | 0.063 |
| ENSMUSG00000064345 | mt-Nd2 | 1.68 | 0.0771 |
| ENSMUSG00000064360 | mt-Nd3 | 2.14 | 0.0765 |
| ENSMUSG00000064363 | mt-Nd4 | 1.68 | 0.0755 |
| ENSMUSG00000064367 | mt-Nd5 | 1.62 | 0.0392 |
| ENSMUSG00000064368 | mt-Nd6 | 1.52 | 0.0545 |
| | **tRNA** | | |
| ENSMUSG00000064347 | mt-Ta | 2.53 | 0.042 |
| ENSMUSG00000064361 | mt-Tr | 3.5 | 0.0465 |
| ENSMUSG00000064348 | mt-Tn | 2.7 | 0.0578 |
| ENSMUSG00000064349 | mt-Tc | 2.32 | 0.0493 |
| ENSMUSG00000064343 | mt-Tq | 2.92 | 0.0311 |
| ENSMUSG00000064359 | mt-Tg | 3.01 | 0.025 |
| ENSMUSG00000064364 | mt-Th | 2.75 | 0.0175 |
| ENSMUSG00000064342 | mt-Ti | 4.43 | 0.02 |
| ENSMUSG00000064340 | mt-Tl1 | 2.72 | 0.00348 |
| ENSMUSG00000064372 | mt-Tp | 6.49 | 0.0345 |
| ENSMUSG00000064346 | mt-Tw | 3.42 | 0.00306 |

# Table S4, Genes inversely regulated by insulin and diabetic models (STZ and HFD), Related to Figure 5

| | | Log2 Fold Change | | | FDR | | |
|---|---|---|---|---|---|---|---|
| **Ensembl accession n°** | **Gene Symbol** | **Ins 3h High vs Basal** | **HFD vs Chow** | **STZ vs Vehicle** | **Ins 3h High vs Basal** | **HFD vs Chow** | **STZ vs Vehicle** |
| ***Muscle*** | | | | | | | |
| ENSMUSG00000018893 | Mb | 1.85 | -3.25 | -1.28 | 0.0216 | 5.09E-06 | 0.0204 |
| ENSMUSG00000021622 | Ckmt2 | 1.28 | -2.12 | -1.68 | 0.00514 | 0.000934 | 0.00613 |
| ENSMUSG00000002416 | Ndufb2 | 0.91 | -2.86 | -0.805 | 0.0289 | 1.23E-05 | 0.0602 |
| ENSMUSG00000022551 | Cyc1 | 0.869 | -1.53 | -0.659 | 0.00441 | 0.0106 | 0.0568 |
| ENSMUSG00000046668 | Cxxc5 | 0.82 | -1.59 | -0.618 | 0.0976 | 1.30E-05 | 0.082 |
| ENSMUSG00000038375 | Trp53inp2 | 0.733 | -2.52 | -0.761 | 0.0183 | 0.000196 | 0.0357 |
| ENSMUSG00000026664 | Phyh | 0.699 | -0.589 | -1.16 | 0.0169 | 0.0461 | 0.00882 |
| ENSMUSG00000022186 | Oxct1 | 0.637 | -1.96 | -1.23 | 0.0319 | 0.000287 | 0.0204 |
| ENSMUSG00000025968 | Ndufs1 | 0.578 | -1.56 | -0.856 | 0.0214 | 0.0145 | 0.041 |
| ENSMUSG00000032279 | Idh3a | 0.542 | -1.08 | -0.88 | 0.0281 | 0.00455 | 0.0486 |
| ENSMUSG00000027332 | Ivd | 0.536 | -0.551 | -1.1 | 0.0477 | 0.00245 | 0.0555 |
| ENSMUSG00000024181 | Mrpl28 | 0.502 | -0.657 | -0.65 | 0.0833 | 0.000478 | 0.0556 |
| ENSMUSG00000026895 | Ndufa8 | 0.491 | -1.5 | -0.671 | 0.0931 | 0.000937 | 0.0414 |
| ENSMUSG00000019179 | Mdh2 | 0.441 | -1.26 | -0.673 | 0.0827 | 0.00589 | 0.0435 |
| ENSMUSG00000032216 | Nedd4 | -0.354 | 0.792 | 0.657 | 0.0822 | 0.000489 | 0.0878 |
| ENSMUSG00000027651 | Rprd1b | -0.376 | 0.434 | 0.699 | 0.0416 | 0.00463 | 0.0602 |
| ENSMUSG00000026473 | Glul | -0.515 | 0.564 | 1.31 | 0.0436 | 0.00683 | 0.0142 |
| ENSMUSG00000028329 | Xpa | -0.67 | 0.359 | 0.982 | 0.0757 | 0.0632 | 0.0238 |
| ENSMUSG00000074340 | Ovgp1 | -0.864 | 0.57 | 0.816 | 0.0248 | 0.00544 | 0.0841 |
| ENSMUSG00000054640 | Slc8a1 | -0.874 | 0.41 | 0.808 | 0.0464 | 0.044 | 0.0718 |
| ENSMUSG00000048249 | Crebrf | -0.897 | 0.874 | 1.07 | 0.0156 | 2.00E-04 | 0.075 |
| ENSMUSG00000031939 | Taf1d | -0.99 | 0.939 | 1.4 | 0.00744 | 0.00435 | 0.028 |
| ***Liver*** | | | | | | | |
| ENSMUSG00000052562 | Slc22a30 | 0.903 | -0.606 | -1.02 | 0.0104 | 0.0139 | 0.0106 |
| ENSMUSG00000022010 | Tsc22d1 | 0.814 | -0.58 | -0.707 | 0.00849 | 0.00818 | 0.0768 |
| ENSMUSG00000022508 | Bcl6 | 0.765 | -1.21 | -1.34 | 0.0857 | 0.000451 | 0.0364 |
| ENSMUSG00000067071 | Hes6 | 0.741 | -0.752 | -1.3 | 0.0859 | 0.000302 | 2.32E-06 |
| ENSMUSG00000020484 | Xbp1 | 0.737 | -0.408 | -0.245 | 0.0254 | 0.0681 | 0.0368 |
| ENSMUSG00000073155 | 1810058I24Rik | 0.681 | -0.379 | -0.419 | 0.00455 | 0.00194 | 0.0256 |
| ENSMUSG00000038267 | Slc22a23 | 0.41 | -0.51 | -0.249 | 0.0175 | 0.00676 | 0.0144 |
| ENSMUSG00000037242 | Clic4 | -0.412 | 0.277 | 0.157 | 0.0303 | 0.0152 | 0.0835 |
| ENSMUSG00000029178 | Klf3 | -0.469 | 1.4 | 0.284 | 0.0598 | 2.55E-06 | 0.0925 |
| ENSMUSG00000030934 | Oat | -0.528 | 0.202 | 0.53 | 0.0535 | 0.0959 | 0.000591 |
| ENSMUSG00000071076 | Jund | -0.601 | 0.541 | 0.241 | 0.0346 | 0.00027 | 0.0972 |
| ENSMUSG00000037573 | Tob1 | -0.752 | 0.405 | 0.31 | 0.00422 | 0.0944 | 0.0186 |
| ENSMUSG00000031596 | Slc7a2 | -0.967 | 0.263 | 0.484 | 6.08E-05 | 0.0541 | 0.00555 |
| ENSMUSG00000022091 | Sorbs3 | -1.14 | 0.374 | 0.926 | 7.02E-06 | 0.0013 | 7.71E-05 |
| ENSMUSG00000034634 | Ly6d | -1.22 | 0.885 | 2.8 | 0.0537 | 2.16E-07 | 0.000418 |
| ENSMUSG00000020423 | Btg2 | -1.26 | 0.612 | 1.17 | 0.0138 | 6.75E-05 | 0.000229 |
| ENSMUSG00000032715 | Trib3 | -1.35 | 0.23 | 0.426 | 0.0296 | 0.063 | 0.00764 |
| ENSMUSG00000041773 | Enc1 | -1.67 | 0.198 | 0.483 | 0.000285 | 0.079 | 0.00575 |
| ENSMUSG00000037887 | Dusp8 | -1.82 | 0.272 | 0.238 | 0.0176 | 0.0436 | 0.0717 |
| ENSMUSG00000028654 | Mycl | -2.11 | 0.261 | 0.206 | 1.07E-06 | 0.0394 | 0.0343 |

# Table S7, Primer sequences used in the study, Related to STAR Methods

| Primer | Sequence | | Primer | Sequence | | Primer | Sequence | |
|---|---|---|---|---|---|---|---|---|
| Coding Genes | | | Coding Genes | | | Non-Coding Genes | | |
| Tbp | F | ACCCTTCACCAATGACTCCTATG | Mfsd2a | F | AGAAGCAGCAACTGTCCATTT | Gm15543 | F | GAGAGGCACAGGAAGGACTG |
| | R | TGACTGCAGCAAATCGCTTGG | | R | CTCGGCCCACAAAAAGGATAAT | | R | CAGCCAGACAGCAGAGACTG |
| Tnfrsf1b | F | GACTGTGAGGCAAGCATGTAT | Igfbp1 | F | CTGCCAAACTGCAACAAGAATG | A730036I17Rik | F | CAGGGGTGGAGGAAGTACAA |
| | R | GGTTCTGCTGTTTAGTGCAGG | | R | GGTCCCCTCTAGTCTCCAGA | | R | CTCTCTCCGCACACACTGAA |
| Rara | F | TTCTTTCCCCCTATGCTGGGT | G6pc | F | CTGTTTGGACAACGCCCGTAT | 9430073C21Rik | F | TAGCTGCTTTGCTCCCTGAG |
| | R | GGGAGGGCTGGGTACTATCTC | | R | AGGTGACAGGGAACTGCTTTA | | R | AGTCCCAGGTCAACAAGCTG |
| Vps37b | F | ACAACGCTTCCTTGGAGACTC | Gck var1 | F | CTGGGCTACTTCTGCTTTGG | 1110018N20Rik | F | CTGAGAGCGTAACCCAGGAG |
| | R | CGCTTGCTCTGGTAGACATCA | | R | CGTAGGTGGGCAACATCTTT | | R | AATGGCTGCTGCTTCTGTTT |
| Bhlhe40 | F | ACGGAGACCTGTCAGGGATG | Gck var2 | F | TCGGGAGTCAGGAACATCTC | Snhg5 | F | GCACGTTCACAAGGACAATG |
| | R | GGCAGTTTGTAAGTTTCCTTGC | | R | CGTAGGTGGGCAACATCTTT | | R | ACTGGCATCTCTCGCAAGTT |
| Scd2 | F | GCATTTGGGAGCCTTGTACG | Txnip | F | TATGTACGCCCCTGAGTTCC | 2410006H16Rik | F | ATCATGGGATCGTGCTCTTC |
| | R | AGCCGTGCCTTGTATGTTCTG | | R | GTTCCCCGCTGTAGAGACTG | | R | TCATGGTGGGATGATACTGC |
| Ppp1r27 | F | TGCTAGTCAAATACGGGGCTG | Tmtc2 | F | GCAAGGACGCTATGAGGAAG | 4930481A15Rik | F | CTCCATCTGTCCCTCCTCAG |
| | R | CCGGGTCAATAAGGTCGGAG | | R | GGTGAGATGAGCAGGGATGT | | R | CAGCCAGTGATTGAGCAAAA |
| Sox9 | F | CGGAACAGACTCACATCTCTCC | Cd36 | F | TCAATGGAAAGGATAACATAAGCA | 4931413K12Rik | F | CTGCCCTCTCTCACCACTTC |
| | R | GCTTGCACGTCGGTTTTGG | | R | TTCAACAAAAGGTGGAAAGGA | | R | CTGTTCTAAGGGACGGCTTG |
| Klf15 | F | GAGACCTTCTCGTCACCGAAA | Fatp1 | F | TTCTCGTGGGCCAGATCAAC | Gm16973 | F | AAGTCTGGGCTCACACTGCT |
| | R | GCTGGAGACATCGCTGTCAT | | R | AGCACGTCACCTGAGAGGTA | | R | GACAGGTGGGAAGGACAGAA |
| Ucp3 | F | CTGCACCGCCAGATGAGTTT | Cpt1a | F | AGTGGCCTCACAGACTCCAG | Gm12758 | F | TACCATTATGCCTGGCTTCC |
| | R | ATCATGGCTTGAAATCGGACC | | R | GCCCATGTTGTACAGCTTCC | | R | GAACTGTGCAGGAGCTGGAT |
| Pfkfb3 | F | CGATGCTGGTGTGTGTGAG | Hadha | F | CTGGTCAGCAGAGCAGAAGA | 2810425M01Rik | F | CCTCTGACGAAGGGAACTTG |
| | R | TCTCTTGGCGCTCTAATTCC | | R | ATTGGCAGTCTCAGTCGCTT | | R | CCACTCTGGTTAGGGTCCTG |
| Ddit4 | F | GTGCTGCGTCTGGACTCTC | Acadm | F | GCGAGCAGAAATGAAACTCC | 2310015A10Rik | F | GCATGAGCGGTTTCTCTTTC |
| | R | CCGGTACTTAGCGTCAGGG | | R | AGCTCTAGACGAAGCCACGA | | R | AGCAGGTGACCATACCCAAG |
| Cebpd | F | CGACTTCAGCGCCTACATTGA | Acadl | F | TCTTGCGATCAGCTCTTTCA | Gm26908 | F | CCTCCTCGTCCAGTCTTCTG |
| | R | CTAGCGACAGACCCCACAC | | R | GGTACATGTGGGAGTACCCG | | R | GCGGCACCCTCTACATTAAA |
| Klhl38 | F | TGAGGAGTTACCAGATGGGGT | Acadvl | F | CTGATGAGCTCCCAGGGTAA | Gm9828 | F | TTGTCCAGTAGGCTGCAGTG |
| | R | CAGTCAGGATCTTGCTTTGTCTT | | R | TTGGGCCTCTCTAATACCCA | | R | CTGGAAAGCATTCCGAACAT |
| Angptl4 | F | CATCCTGGGACGAGATGAACT | Srebp1c | F | GAGCCATGGATTGCACATTT | 2410006H16Rik | F | ATCATGGGATCGTGCTCTTC |
| | R | TGACAAGCGTTACCACAGGC | | R | CTCAGGAGAGTTGGCACCTG | | R | TCATGGTGGGATGATACTGC |
| Rnf144b | F | CATGACTGCGGAAAACCCAC | Srebp1a | F | GAACTGGACACAGCGGTTTT | Gm15622 | F | CGTTGACTTTCTGCCCCTAA |
| | R | CTGGCACTCTTGGAGCATGG | | R | GGCCAGAGAAGCAGAAGAGA | | R | GCTTGTGTGCTCTCAGTTCG |
| Kank2 | F | GGAGGAAATTCGGATGGATCTG | Pparg | F | TCAGCTCTGTGGACCTCTCC | Gm16559 | F | ATGGGATTTCTGCCCTCTCT |
| | R | ACTTTCAGTTCTCGCTCTGTGA | | R | ACCCTTGCATCCTTCACAAG | | R | TGTAGCTTCGTGTCGGATGA |
| S1pr1 | F | ATGGTGTCCACTAGCATCCC | Ppara | F | AACATCGAGTGTCGAATATGTGG | Gm42940 | F | CCCGAGTTTGCATTCTCAAT |
| | R | CGATGTTCAACTTGCCTGTGTAG | | R | CCGAATAGTTCGCCGAAAGAA | | R | AGGTGTTTTCCCCAATCACA |
| Steap4 | F | GGGAAGTCACTGGGATTGAAAA | Pcx | F | GGGATGCCCACCAGTCACT | B430119L08Rik | F | ATCCTGTGCTGCCCTACAGT |
| | R | CCGAATAGCTCAGGACCTCTG | | R | CATAGGGCGCAATCTTTTTGA | | R | AATGCCACTGCTGTCTTCCT |
| Cyp26a1 | F | AAGCTCTGGGACCTGTACTGT | Srebp2 | F | GCGTTCTGGAGACCATGGA | Malat1 | F | CTTTGCGGGTGTTGTAGGTT |
| | R | CTCCGCTGAAGCACCATCT | | R | ACAAAGTTGCTCTGAAAACAAATCA | | R | CAAAACTGGGAGGTTGTGCT |
| Osgin1 | F | CCTCCGGTATCTGCCTGTC | Hmgcs | F | TGCTGGAAAGTATACCATCGGCCT | Gm11967 | F | TGATGATCGGATGCTTTGAA |
| | R | GGAAAGGTACTCTAGGTCCTGG | | R | GCCGCCCAATGCAATCATAGGAAA | | R | CAGAGTTGTCCTGGGTGCTT |
| Gck | F | TGAGCCGGATGCAGAAGGA | Lss | F | TGTTCGTTGGTCAGTGGATG | 9030622O22Rik | F | GCTGAAGCCCTTTGATCTTG |
| | R | GCAACATCTTTACACTGGCCT | | R | GATAGCAAATGAAGTGTCCCAG | | R | CATCAGTCCCATTGTGTTGC |
| Ulk1 | F | AAGTTCGAGTTCTCTCGCAAG | Sqle | F | TTGTTGCGGATGGACTCTTCTCCA | C730036E19Rik | F | GCCAGTAAATCCGAAGACCA |
| | R | CGATGTTTTCGTGCTTTAGTTCC | | R | GTTGACCAGAACAAGCTCCGCAAA | | R | GGCATGTCCATTCCTGACTT |
| Got1 | F | GCGCCTCCATCAGTCTTTG | Ppargc1a | F | TGATGTGAATGACTTGGATACAGACA | E230016M11Rik | F | AATCTCTCCAGCCCGACTCT |
| | R | ATTCATCTGTGCGGTACGCTC | | R | GCTCATTGTTGTACTGGTTGGATATG | | R | TGTGATGACTTCAGCCTTGG |
| Tat | F | TGCTGGATGTTCGCGTCAATA | 18S | F | GTTCCGACCATAAACGATGCC | 4933404O12Rik | F | TGTGATCTTGGAACCCTGAG |
| | R | CGGCTTCACCTTCATGTTGTC | | R | TGGTGGTGCCCTTCCGTCAAT | | R | AAGGGGAATGAACACACTGC |
| Pck1 | F | TGACAGACTCGCCCTATGTG | Lpin1 | F | CATGCTTCGGAAAGTCCTTCA | Ctcflos | F | CCCAGAACAAGAAGAGCTGG |
| | R | CCCAGTTGTTGACCAAAGGC | | R | GGTTATTCTTTGGCGTCAACCT | | R | GCTAGTTGCGGGAAGACTTG |
| | | | | | | Gm43597 | F | ACCAACAGCCTCGCTCTAAA |
| | | | | | | | R | TCTACAGCCCAGCAGGTTCT |
| | | | | | | 9430037G07Rik | F | CGTTCCTTAGTCCCAGTTTGG |
| | | | | | | | R | CTGGTCATGCAGTTCTGCTG |
| | | | | | | Gm15663 | F | ATTTTCTTGGCACTGGGTTG |
| | | | | | | | R | AGCAAGCAGAGCAGAACTCC |
| | | | | | | Gm15441 | F | TTCTGGTGAATGCTCTGGTG |
| | | | | | | | R | GAGATGGCTTGGTGGTTGAT |