Supplemental Material

Functional screening of candidate causal genes for insulin resistance in human preadipocytes and adipocytes

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Online Supplemental Methods

SGBS cell culture, adipogenic differentiation and cell treatment

SGBS preadipocytes were obtained as a gift from Dr. Martin Wabitsch's lab, and grown in OF medium (DMEMF12 supplemented with 10% FBS, 33um biotin, 17um panthotenat and 1% Penicillin/Streptomycin)^{1, 2}. The preadipocytes were differentiated into adipocytes using Quick-Diff medium (OF medium supplemented with 0.01mg/ml transferrin, 20 nm insulin, 100nm cortisol, 0.2nm T3, 25nm dexamethasone, 250um IBMX and 2um rosiglitazone) for the first three days, followed by maintenance medium (OF medium with 0.01mg/ml transferrin, 20nm insulin, 100nm cortisol and 0.2nm T3) for 12-20 days. Maintenance medium was exchanged every three days ^{1, 2}.

Lentivirus generation and CRISPR/Cas9-based targeting of SGBS preadipocytes

To construct sgRNA lentiviral plasmids, sgRNAs were designed using the on-line tool at <u>http://crispr.mit.edu/</u> and two oligonucleotides, 5'-CACCG-sgRNA sequence-3' and 5'-CAAA-(reverse compliment of sgRNA)-C-3' were synthesized. Oligonucleotides were annealed and ligated into LentiGuidePuro (Addgene #52963) plasmid after BsmBI digestion (Online Table II). Three sgRNAs were designed for each gene and the oligonucleotides were synthesized at Eurofins Scientific. The Cas9 lentiviral plasmid (lentiCas9-Blast) was purchased at Addgene (#52962). Cas9- and sgRNA-encoding lentivirus were packaged with the second-generation lentivirus system. A Cas9-expressing SGBS-preadipocytes cell line (SGBS-Cas9) was generated by transducing the cells with the lentiCas9-Blast lentivirus followed by 5ug/ml of blasticidin selection three days after transduction. Individual IR-genes were targeted by transduction of SGBS-Cas9 preadipocytes with the corresponding three sgRNA lentiviral particles. Three-day post infection, 3ug/ml puromycin was applied for four days to select for sgRNA-expressing cells.

Polymerase chain reaction (PCR), reverse transcription PCR, quantitative real-time PCR and next generation sequencing

Total mRNA was isolated from SGBS pre- and adipocytes using the trizol protocol (Life Technologies) and 1µg was used for reverse transcription of cDNA using the MaximaTh H Minus cDNA Synthesis Master Mix (Thermo Scientific, #FERM1662). Gene expression was quantified by qRT-PCR using 1µl of the reverse transcription reaction and the Fast SYBR[™] Green Master Mix (Thermo Scientific, #4385614). Primer sequences are provided in Online Table III. Genomic DNA of each knockout SGBS line was isolated by DNeasy Blood & Tissue Kit (QIAGEN, #69506). The genomic region of the targeted sites was amplified by PCR of isolated genomic DNA. Amplicons were 200-280 base pairs in length including the target-specific PCR primers (Online Table IV). The sites of interest (i.e. CRISPR cut site) are located within the first 100 base pairs from either the 5'-end or the 3'-end of the amplicon. The CRISPR/Cas9 targeting efficiency was calculated, using the results from pooled next generation sequencing (NGS) of the target-specific amplicons. For the pooled NGS, amplicons from each knockout cell line were barcoded prior to pooling.

Immunofluorescence and high content imaging

For immunofluorescence analyses, SGBS adipocytes were fixed with ice-cold methanol at -20°C for 15 min, and immunolabeled using the primary antibody for cEBPα (1:200, Abcam, #ab40761). Donkey anti-Rabbit Alexa Fluor 488 (1:1000, Life Technologies, #A10040) was used as the secondary antibody. LipidTox Red (1:1000, Life Technologies, #H34476) was applied to stain the lipid droplets. Nuclear DNA was stained by DAPI (1:500, Life Technologies, #62248). The secondary antibody only control was employed to validate its specificity and eliminate the background signal. Images were captured using a high content imaging system (Thermo Fisher Arrayscan XTi). The ratio of cEBPα/DAPI was quantified using an ArrayScan high-content analysis software (ThermoFisher scientific).

Lipid extraction and triglycerides measurement

SGBS adipocytes were washed twice with PBS and detached by scraping. A chloroform:methanol (2:1; v/v) mixture was used to extract lipid from the adipocytes, and evaporated to dry overnight in a fume hood. The dried lipid was suspended in 100 μ L of 1%

TritonX100 in absolute ethanol for 1 hour with constant rotation. This was then dried in a speedvac for 30 minutes and suspended in 100 μ L PBS with 1% Triton. 3 μ L of the suspension was used to measure the lipid levels. Triglyceride was quantified using Infinity Triglycerides Solution (VWR, #46100-346).

Lipolysis

To assist the induction of lipolysis, SGBS adipocytes were starved in serum-free DMEM (with 0.2% BSA) overnight to clear residual insulin and lipid in the differentiation medium. Lipolysis was induced by KRPH buffer (Life Technologies) supplemented with 10 μ M forskolin for 4 hours. Glycerol accumulated in the KRPH buffer was measured using the Free Glycerol Reagent (Sigma, #F6428).

Western blot

Adipocytes were harvested in Cell Lysis Buffer (Cell Signaling, #9803) supplemented with Halt[™] Protease and Phosphatase Inhibitor Cocktail (Thermo, #78440). The cell lysates of SGBS adipocytes were subjected to gel electrophoresis under heat denaturing conditions, using NuPAGE® Novex® 4-12% Bis-Tris Protein Gels (Life Technologies, #NP0323BOX) Primary antibodies for FST (Abcam, #ab157471), PEPD (Thermo, #OTI1B7), PDGFC (Abcam, #ab93899), MAP3K1 (Abcam, #ab212601), PPARG (Cell Signaling, #2443), ARL15 (Abcam, #ab178425) and HSP 90 (Santa Cruz Biotechnology, # sc-13119) were used to detect the protein expression in SCR and KO-adipocytes. Primary antibodies for phospho-AKT2 (Ser474), total AKT2 and β-actin were purchased from Cell Signaling (#8599 and #5239) and Sigma-Aldrich (#A5316), respectively. Anti-rabbit or mouse IgG, HRP-linked Antibody (1: 2000, R&D system, #HAF008 and #HAF018) was used as secondary antibodies for the corresponding species. The ratio of phospho-AKT2 (Ser474) to total AKT was quantified by analyzing the western blots using the NIH ImageJ software and data was normalized to β-actin level. All experiments were performed at least three times and the representative results were presented.

Phospho-AKT2 (Ser474) ELISA

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Adipocyte lysate was harvested as above and used for measurement of p-AKT2 (Ser474) and total protein. Phosphorylation of AKT2 (Ser474) was measured by Pathscan® phospho-akt2 (ser474) sandwich ELISA kit (Cell Signaling, #7048) according to the manufacturer's protocol.

LC-MS/MS-based 2-DeoxyGlucose-6-Phosphate detection

To measure the insulin induction of glucose uptake in SGBS adipocytes, cells were starved for 24 hours in glucose- and insulin-free 3FC medium to clear residual insulin and glucose. After starvation, cells were treated with 200 µm 2-DG with or without insulin (10nm) for 30 minutes. To extract metabolites from the treated adipocytes for 2-DG-phospate (2-DG-6P) quantification, the cells were lysed by adding precooled 80% methanol in -80 °C for 15 minutes. Cell were then scraped off the plates and thoroughly lysed by vortexing and trituration. We excluded the cell debris from the lysate by centrifugation and the supernatant was dried by a speedVac. For the detection of 2-DG-6P, dried samples were suspended with 60 µl of acetonitrile / methanol (75:25; v:v) containing 25 μ M of deuterated phenylalanine-d8 (Phe-d8, Cambridge Isotope Laboratories) as the internal standard. The suspension was transferred into the 250 µl insert vial (Microsolv Technology) and 20 µl of the sample was loaded onto the HILIC column (Atalantis HILIC 100A, 3um, 2.1mm X 150mm, Waters) using the HTS PAL autosampler (LEAP Technologies). Phe-d8 and 2-DG-6P were detected by the HPLC-coupled 4000 Q-TRAP mass spectrometry in MRM-based assay in negative mode. The MRM transition of Phe-d8 was 172.2 to 154 with the DP=-50 V, CE=-20V, CXP=-15V, and EP=-10V. Two different MRM transitions of 2DG-6P were applied, firstly, 243 to 78.9 with the DP=-70V, CE=-60V, CXP=-5V and EP=-10V, and secondly 243 to 96.8 with the DP=-70V, CE=-30V, CXP=-5V and EP=-10V. The source parameters were as follows: curtain gas (20psi), collision gas (4psi), lonspray voltage (-4500V), temperature (450°C), lon source gas 1 and 2 (40psi and 50psi, respectively) and the interface heater on. The detected peaks of compounds were integrated using MultiQuant 3.0.3 software (ABSciex) for the quantification.

Sanger sequencing based-off-target analysis

Potential off-target sites were predicted for the sgRNAs targeting *FST*, *PEPD*, and *PDGFC* using the publically accessible web tool, CCTop (Online Table V) ³. The predicted off-target sites with less than four base-pair mismatches were amplified for off-target analysis. Forward and reverse primers were designed ~150 base pairs upstream and downstream to the predicted site. These loci were amplified from the genomic DNA of SCR and KO-adipocytes and genotyped by Sanger sequencing (Online Table VI). Genome editing events were evaluated by the comparison between the sequence of the predicted site in SCR and KO adipocytes (Online Figure VI).

MRNA transfection

We used the mRNA Synthesis Kit (System Biosciences, # MR-KIT-1) to construct the transcription template plasmids encoding *FST*, *PEPD* and *PDGFC*. We produced the corresponding transcripts using *in vitro* transcription following the manufacturer's manual. Briefly, open reading frames (ORF) of *FST*, *PEPD* and *PDGFC* were amplified from Dharmacon plasmids, # MHS6278-202829884, # OHS6085-213573836 and # MHS1010-202700476 respectively. Restriction enzyme sites (EcoRI at the 5' end and BamHI at the 3' end) were appended using PCR (Online Table VII). The three ORFs were cloned individually into the multiple cloning site (MCS) of pMRNAXP mRNA Synthesis Vector (System Biosciences, # MR000PA-1). The ORFs were cloned into the expression vector using T4 DNA Ligase (NEB, # M0202S). The expression vectors were used as templates for *in vitro* transcription of the mRNA by T7 RNA Polymerase Mix in the mRNA synthesis kit, following the manufacturer's protocols. The *FST*, *PEPD* and *PDGFC* transcripts were delivered into preadipocytes and adipocytes (0.5ug per well of a 24-well plate) by RNAfection (System Biosciences, # MR750A-1).

Reference

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Online Figure I



Online Figure I. Evaluation of the IR-gene expression patterns during SGBS preadipocyte differentiation. RT-qPCR was used to analyze mRNA levels at differentiation day 0, 4, 8, 12, 16 and 20. Results were normalized to *RPLP0* mRNA, expression fold change was compared to day 0 and data are presented as line chart, mean \pm SD, n=3 (*, p < 0.05; **, p < 0.01).



Online Figure II. Knockout efficiency quantified by next generation sequencing (NGS) of the target sites in KO SGBS lines. The square chart for corresponding KO SGBS line displays percentage and size distribution of non-homologous end joining (NHEJ) generated by the three sgRNA targeting system, the size distribution indicated on the x-axis (minus as deletion, plus as insertion and zero as unedited or substitution). Indels are shown in blue and unedited sites or substitutions are shown in red. The total percentage of the three types of NHEJ including insertions, deletions and substitutions is presented in main Figure 1B. Total sequence reads per sample =150,000 - 300,000.



Online Figure III. Evaluation of gene knockout efficiency at the mRNA level. RT-qPCR was used to analyze mRNA levels of each gene in corresponding KO-adipocytes. Results were normalized to *RPLP0* mRNA. Expression fold change was compared to the gene level in SCR adipocytes and data are presented as bar graph, mean \pm SD, n=3 (*, p < 0.05; **, p < 0.01).



Online Figure IV

Online Figure IV. Optimization of the condition for insulin treatment. For this purpose, we used the level of AKT2 (Ser474) phosphorylation (p-AKT2) as an indicator. To minimize the basal pAKT2 level, 0, 4, 24 and 48 hours of starvation time were tested. For each starvation time point, we evaluated the levels of phosphor-AKT2 (Ser474), total AKT2 and β -actin of SGBS preadipocyte after the treatment of 0, 10, 100 and 1000nm insulin (Ins). The line charts display the ratio of phospho-AKT2 (Ser474) to total AKT2 and the ratio was normalized to the β -actin level of the same sample.



SYN2 3_12390484_T_C_b37 Adipose - Subcutaneous



Online Figure V. The effect of the 10 IR lead SNP genotypes on the expression of putative effector genes by eQTL studies in human subcutaneous adipose tissue. The chromosome number, SNP ID, reference and variant alleles, and human genome reference builds GRCh37/b37 (b37) are indicated under the gene name. The sample size is specified under the corresponding genotype. Data was extracted by the online tool, GTEx V7 eQTL Calculator. The detailed data and statistics are described in Online Table I.

Online Figure VI



Ref Seq	AAGGCCACTTGACTCCTGGGCCCTGACTCTGGCAGGCCACGTCTTCCCCATGAGCT
SCR	MMMAMMAMMAMMAMAMAMAMAMAMAMAMAMAMAMAMAM
PDGFC-KO	
CTA-223 Ref Seg	
	$\begin{tabular}{ c c c c c c c c c c c c c c c c c c c$
SCR	
PDGFC-KO	
<i>PRR5</i> (I) Ref Seq	AGAAATGCCAGCCCCTCCCGCGCGCACCTGCAGGGCTCCAGGTCTCCCAGCCCTTAGGCCT
SCR	Ang han and han
PEPD-KO	Ann harresser and a series for the series and the series of the series o
<i>CTD-203</i> Ref Seq	3D24.2 (E) TTCAAGGCAAAGAGCG <mark>CCA</mark> GTGGCACCTTCAGGGTTTCCTTCCCCAGCCAAAACGAGGGTC
SCR	Man Jaraan Amman Man Man Man Marka Marka
PEPD-KO	
<i>TTYH2</i> (I Ref Seq) TGTGCCCAGCAGCTGTGCAGGCAGCATTTCTGCACCGACAC <mark>TGG</mark> GCATCTCCAGTCTCTGT
SCP	$\mathbf{Sq42-off-1} \mathbf{PAM}$
JUN	
PEPD-KO	
<i>CTD-20</i> : Ref Seq	33D24.2 (E) CTGGCGGAAGAGGACCCCCGCTGTAGGTGCAGTAGCGCTGAGTCTCCTCTTAGCCCTGCAG
SCR	Mar All States
<i>РЕРД</i> -КО	where and marked and a second and a second as
OFD1P3 Ref Seq	BY(-) TTCAGGAAGCCATACCTGGGAGGAGGCCCACCGGGCCAACTCTATCTA
SCR	Mar And Mar And
<i>РЕРД</i> -КО	Mr. Anne Marken Anne Anne Marken Anne M

PTPRF(I)

Online Figure VI. Sequencing chromatograms of predicted off-targets sites in SCR and SGBS-KO adipocytes. The reference sequence (Ref Seq, 5'-3') was extracted from hg38. Predicted offtarget site positon is indicated with gene name (E = exonic; I = intronic; - = intergenic). Predicted offtarget site for corresponding sgRNA shown in the grey box under the Ref Seq.



Online Figure VII. GFP transcript expression in preadipocytes and adipocytes. Representative bright field (BF) and fluorescence images of GFP-expressing preadipocytes and adipocytes.

	Tissue	Adipose - Subcutaneous	oGRAMplusC4D GWAS ⁵¹	P_vari	6.48E-04	4.20E-02	3.53E-01	2.63E-01	2.00E-02	4.33E-03	1.80E-01	3.98E-01	9.43E-03	3.16E-01											
	gene expression	ion	n	ion	tion	n	tion	n	on	n	ion	CVD_CARDIC	OR_var	1.040	1.020	0.991	1.010	0.977	0.973	1.010	0.992	1.030	1.000	scular disease;	
_risk_alleles (RA)	Action of IR risk allele on g	Downregulati	Upregulatic	Downregulati	Downregulat	Upregulatic	Downregulat	Upregulatic	Downregulati	Upregulatic	Downregulat	E (European) T2D GWAS ³³	P_var	1.60E-39	2.30E-07	7.10E-08	6.70E-14	5.70E-26	7.42E-13	7.50E-03	1.40E-10	1.10E-20	9.80E-23	ype 2 diabetes; CVD,cardiovas	
eQTL analysis of IR	SNP_IR_RA	rs2943645_T	rs3822072_A	rs6822892_A	rs4865796_A	rs10195252_T	rs731839_G	rs2745353 T	rs4846565 G	rs459193 G	rs17036328 T	T2Dadj BMI_DIAMANTE	OR_var	1.110	1.040	0.958	1.060	0.923	0.957	0.980	0.950	1.080	0.896	iele; FI, fasting insulin; T2D, t	
	NES_var	-0.280	0.200	0.160	-0.120	-0.140	0.110	0.055	-0.007	0.017	0.064	CEMIC_European GWAS ⁴	P_IR_RA	2.26E-19	1.80E-08	2.60E-10	2.20E-12	1.30E-16	5.10E-12	4.10E-07	1.80E-09	1.12E-10	3.60E-12	insulin resistance; RA, risk all	
	P_var	1.70E-10	1.30E-07	3.10E-05	1.00E-02	1.20E-02	1.60E-02	2.40E-01	8.40E-01	6.90E-01	2.00E-01	Fladj BMI_MAGIC_GLY	Effect size _IR _RA	0.019	0.012	0.014	0.015	0.017	0.015	0.014	0.013	0.015	0.021	normalized effect size; IR, i	
IR loci	Lead SNP_ref_var	rs2943645_C_T	rs3822072_G_A	rs6822892 A G	rs4865796 G_A	rs10195252 T_C	rs731839 G A	rs2745353 C T	rs4846565 G A	rs459193 A G	rs17036328 T C	IR loci	Lead SNP_ref_var	rs2943645_C_T	rs3822072 G A	rs6822892 A G	rs4865796_G_A	rs10195252_T_C	rs731839_G_A	rs2745353 C T	rs4846565 G A	rs459193_A_G	rs17036328_T_C	; var, variant allele; NES BMI: OR, odds ratio.	
10	Transcript	IRS1	FAM13A	PDGFC	FST	GRB14	PEPD	RSP03	LYPLAL1	MAP3K1	SYN2	10	Locus	IRS1	FAM13A	PDGFC	FST	GRB14	PEPD	RSP03	LYPLAL1	MAP3K1	SYN2	Ref, reference allele adi BMI, adjusted to	

Online Table I: eQTL genes and GWAS of the 10 IR-SNPs.

Online Table I

PPAR6 sg1CCATTCTGGCCCACCAACTTCACCGCCATTCTGGCCCACCAACTTAMACAATTGGTGGGCCAGCAAGGCPPAR6 sg2CTCCGTGGATCTTCCTCCGTAACACCGCCGCGGATCTTCCGTAATAMACCTACGGAGAGTCTCCACGGAGGCIRS1 sg4ACGCTTCTTCGTACTGCGCGCACCGACGCCCCCCGGAGAGGCGAAMACCGC GCA TGCAAAGAAGC GTCIRS1 sg5GCGAGCCCTCCGGAGAGGGACACCGACGCCCCCCGCGAGAGGCGAAMACCGC GCA TGCAAAGAAGC GTCIRS1 sg6TCGTAGTACTCGAGGCGCGCCACCGACGCCGCCCTCCGGAGAGGCGCCAMACCGC GCA GCA GGA CCC GC GC CT CRS1 sg8AGCGCCGGCGCCCGCCGAGCCACCGACGCCGCGCCCCCCCGCGAAAMACCGC CGC GC CT CG CG CC CT CCGRB14 sg7AGCGCCGGGCGCCCACGACCCACCGCAGGCGCCCCCCCGCAAAMACCGT CG CG GG CGT CG CC CT CCGLUT4 sg10CCCCCCAGGCAGCGCACGACCCACCGGCAGCCCCACGACCAMACGGT CG CG GG CGT CG CC CT CCGLUT4 sg11GAACTCTCAGTGGTCTACCCACCGGCAGCTCCAATGGAGGCGCCAMACGGT CG CG GG CGT CG CC CT CCCOBLL1 sg13GAACTCCCAGGGGTGCCACCCCACCGGAAGTCCAATGAGAGGTGCAMACGGT AGG ACC ACT GG AGG TC CCOBLL1 sg14GAACTCCCAGGGCTTACTTGCACCGGCAGAATCCACTGGGCTTTCAMACGGT AGA AC AAT TAT ACT GACCOBLL1 sg15GGAGCCAATTTAGCAGGCACCGGCGCAAATTTAGCATCAMACGGT AGA AC CAC TG AGC AAT TAT ACT GCANKRD55 sg18GGGAGCCACATTGAGAGGGGCACCGGCGCACACGCGTTTAMACGA CG GT GC CAC CCANCCBS Sg28TGTGTGTGCGCACAGCGGGCACCGGCAGAGTTTTACACTGCAMACGA CG CG GG CT CAC CC GAC CCANCCBS CG GGTTTCCAACGGGGGGACACCCCTGGGGAAGACGGCGACACGCTAACCGA CG CG CG CAC CCCACCGGCAGAGGGACACCCCGGGGGANKRD55 sg18GGGACCCAATTTACACTGCCACCGGCAGAGGGCACCCCCGCGGGGGAAGACGCCGCGGGGAAGAGGACCCC
PPARG sg2CTCCGTGGATCTCTCCGTAACACCGATCGTGGATCTCTCCGTAAAAACTTACGGAGAGATCCCTCCGGAGGCPRARG sg3AAGGATGCTTCGTGATATGAAACGACGATGCCTCCGGAGAGCGAAAACGACGATTCCAACGAGACATTCCATCPRS1 sg4ACGCTTCTTGGTACTGGCGCCACCGACGCGCCCCCGGAGAGCGAAAACCGC CGC CT CC GGA GC CACGACGCGCGCPRS1 sg4GCGAGCCCCCCGGAGAGCGACACCGATGCGTAGTGCTCGGGGAGCCAAAACCGC CG CT CT CC GGA GC ACGACGCGCGCGCPRBR sg4AGGCGAGGCCCCCCGCGGAGCCACCGAGCGCGGGGGCCCCCCCGGGAGCCAAAACCGC CG CT CT CC GA TC CAC GACPRBR sg4AGGGGCGACGCCCCCACACCCACCGAGCGCGGGGGCCCCCCCCGCAAAACGC CG GC GC TC CC CAC CACPRBR sg4AGGGCAGAGCCCCCCACACCCACCGAGCGCGCGCGCGCGCGCGCAGCAAACGC CG GC CT CC CAC CACPRBR sg4AGGGCACACCCCCACACCACACCGGGGGCCCCCCCCCCCACACCAAACGC CG GC CT CC CC CT CCPRBR sg4AGGGCACACCCCCACACCACACCGGAGCCCCCCCCACACCAAACGC CG GC CT CC CC CC CT CCPRBR sg4AGGGCACACCCCCCCCCACACCCACCGGAGCCCCCCCCCACACCAAAACGC CAC GG CC CC CC CC CCPRBR sg4CGCCTCCAGGGAGCGCCCCACACACCACCGGAGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
PPAR6 sg3AATGGAATGTCTTCGTAATGCACCGAAGAATGGAATGTCTTCGTAATGAAACCATTACGAAGACATTCACTCIRS1 sg4ACGCTTCTTCGTACTGCGGGCACCGAACCCTTCGGAGAGCGGAAACCGC GCA GAAGACACTCCCTCIRS1 sg4CGCGAGCCTCCGGAGAGCGCCACCGACCGCTCCGGAGAGCGGAAACCGC GCA GAAGAAGC GTCIRS1 sg4TCGTAGTACTCGAGGCGCGCCACCGACCGCCCCCGGAGAAACCGC CC CGAG GGC CC GCG CCGRB14 sg8ATGGCAGAGCGCCCCCACGACCCACCGACCGCCGCGGGCCCCCCCGCGAAAACGC CGG GC CC GC GC CCGRB14 sg9GAGGGCGACGCCCACGACCCACCGACGCCCCCCACGACCAAACGC CGG GC CC GC CC CC CC CCGLUT4 sg10CCCCTCAGCAGCGAGGCACCCCCACCGGACCTCCAGCAGCCAAACGT CAC CG GC CC CACCGACGCCGLUT4 sg11CTGCAGTTTGGTCACACATCACCGGAGCTCACAACGTAAACGCT CAC GC GC CC CAC CAC CCCOBLL1 sg13GAACTCCACTGCTTCATCACACCGGAGCTACAATGGCCAGGCCACGACCAAACGCT CAC GG AC CC CAC AAA TT AC GACCOBLL1 sg14TCAGTATTTTGGTCTCAGCCACCGGGCCATGCATTGGTTCCATCAAAACGCT GAG ACC CAA TT AC GACCOBLL1 sg15GGGGAGCCAACGACGCTTCAAGACACCGGGGGCCACGACGCTTTGAGAGCGCGCAAACGCT GA GA CC AAA TT AC GACCARKRD55 sg18GGGGAGCCAACGACGTTCACCGGGGCGCACGACGCTTTTGGTGCGACACGAGGAAACGT CT GT GG CAC CAC CACARAL5 sg20TGTGGTGCAACACGAGAGCACCGGAGGCGGCGCGCGCGCGCGGCGCGCGCGCGCGCG
IRST sg4ACGCTTCTTCGTACTGCGCGCACCGGAGCTTCTTGGTACTGCGGAAACCGC GCA GTA CAAAAGAGC GTCIRST sg5GCGAGCCCTCCGGAGAGCGACACCGGCGGAGCCCCCGAGAGCGAAAACCGC GCC CTC GA GGA CTC CACGRB14 sg7AGCGCGCGGGCCCACGCCGCACCGAGCGCGGGGCCCCGCGGAGCAAACCGC GC GC GG GC CTC GA GG CT CAC GGGRB14 sg8ATGGGCAGAGCCCACGCAGAGCACCGAGGGCGAGGGCCACGCCGCAGACAAACCGC CGC GG GG CTC GA CC CAC CG GG GC T CG CC CTCGRB14 sg9GAGGGCGACGCCACGCAGAGCCACCGAGGGGCGACGCCCACGACCAAACCGT CGC GG GG CG CG CC CC CC CGLU74 sg10CCCCTCAGCAGCGAGTGCTCACCGGCGGCAGCGCCACGACCAAACGC CA CG GC CT CA CC GA GG GGGLU74 sg11CGGCATCAATGAGACGTGCCACCGGCGCAGCGCAACACATAAACGGT CA CT CG CTG CT CAT CT GA GG GGCOBLL1 sg12GAACTCCACATGAGACGTGCCACCGGCAGCACAATTGGCTCTACCAAACGGT AGA CC AAAT TA ACT GA CCOBLL1 sg14TGGTATATTTGGTCTACCCACCGGTGCCAGCCATAATTGGTCTACCAAACCGA CAC AAA TT AC TG ACCOBLL1 sg15AGAATCCACTGCTTTCATCACACCGTGGCGCAGCATAATTTGGTCTACCAAACCGA CAA TT AC TG CCANKRD55 sg16GGGAGCCAATATTAACATGCCACCGGGGGCCACGGTTATAAACCGA CAC GAT TT AT TAT GC TC CCANKRD55 sg18GGGAGCCAATATTAACATGCCACCGGTGGCGACGCGGGGAGCCAGCGTTATAAACCGA CG TG CAC CAC CACARL15 sg19GCGCGCGTGCAACGAGGGCACCGGTGGCGACGCGGGGGAGCGGGGGGAGGGTGCAGCGGGGAAACCGA CG GT GC CC CAC CACARL15 sg19GGGGACCAACGAGGCACCGGTGGGAGGGGAAGGGGCGAGGGGAGGGGAGGGGA
IRST sg5GCGAGCCTCCGGAGAGCCACACCGGCGAGCCCTCCGAGAGCGCAAAACTC GC AG GG CT CC GC AGIRST sg5TCGTAGTACTCGAGGCGCGCCACCGTCGTAGTACTCGAGGCGCGCAAAACTC GG AC GG CT CT G CG AC GGRB14 sg7AGCCGCGGGCCACGACCCACCGAGGCGCCCGCGGGCAAACCGC GG CG CC CG GG CT CT CC CC ATCGRB14 sg9GAGGGCGACGCCACGACCCACCGAGGGCGACGCCCACGACCAAACCGT CG CT G CT CT C CC ATCGRB14 sg1CCCCTCAGCAGCGCACGACCCACCGGAGGCGCCCCCAGGACCAAACCGT CG CT G CT G CC C CT CCGLUT4 sg10CCCCTCAGCAGCTGCCCACCGGCGCCACGACCAAACCGC TG CT C CT G AG GG CT CT CCGLUT4 sg11GAACTCCCAGTGTCTACCCACCGGCGCCACGACCCCAAACCGC AG CT CT G CT G AG GT TC CCOBLL1 sg13GAACTCCCAGTGTCTACCCACCGGCAGCATAAATGACCGTGGCAAACCGC AGC GAA AT AT CT GACCOBLL1 sg14TCAGTATTTGGTCTCACCCACCGGGCCATAAATCCATGCAAACCGA AGC ATT AAG GAA CG ACT GG CACANKRD55 sg16TGGCCAGGCATATAACTTGGCACCGGGGCCATTTATACATGCAAACCGA CACT GA GC TT CCANKRD55 sg16GGCAGCCAATTAACTTGCCACCGGGGCCATTATTACATGCAAACCGA CACT GA CC ACAARL15 sg20TGTGTGCAACAGAGCCACCGGGCGCATTATTCAACATGCAAACCAC CAC GA TT CA CAC CACARL15 sg21AGGTCATATTCTGGTGCAACGGGGCACCGGAGCTGAATTACATGCAAACCAC CAC GA AT TA CAC TC CAC CACFST sg25AAGTGGTGAAGTGAACGTGGCACCGGAGCGCATTATTCGTGCGAAAAACCAC CAC GA AGA CC CC CAC TCFST sg27AGGGGCGACTTATACGTGGCACCGGAGCGCCGCTCTCGGGAACGCCGAAAAAACCAC CAG GG TC CAC CAC CACFST sg27AGGGGGCACTCAAGGGGCACCGGAGCGCCCTCTGGGGACCCCGAAACCAGGGAAACCCC CG GA AGA CAC GG GG CC CT CC </td
IRS1 996TCGTAGTACTCGAGGCGCGCCACCGTCGTAGTACTCGAGGCGCGAAACGCG CGC CTC GAG TAC TAC GACGRB14 937AGCGGCGGGGCCCCGCGAGCCACCGATGGCAGAGCGCCCCGCGAGCAAACGC CGG GC CT CG CCG CCG CCGRB14 939GAGGGGCGACGCCCAGGCGCACCGATGGCAGAGCGCCCCGAGCCAAACGT CG CG GG CG CT CG CC CTCGLUT4 9310CCCCTCAGCAGGGAGGGCCCACCGGCGCCTCAGCAGCGAGGGCCAAACGT CAC TCG CG GG CG CT CG CC CTCGLUT4 9311CTGCAGTTTGGGTACAACATCACCGCGCCCTCAGCAGGGGCGACCCCACGAAACGT CAC TCG CG GC GC CC ACGGLUT4 9312GAGCTACAATGAGACGTGGCCACCGGAGCTACAATGAGACGTGGCAAACGT CAC TCG AGG GAC CAA CAGCOBLL1 9313GAACTCTCAGTGGTCCTACCCACCGGAGCACCACTGCAGTGGTCCTACCAAACGGT AGA ACC ACT GA GG TCCCOBLL1 9314TCAGTATATTGGTCTCAGCCACCGGAGAATCCACTGCTTTCATCACAACGGA GA CC AAA TAT ACT GA CCANKRD55 9317CGCCGGGCAGACACTGGGTTTCCACCGGGGAGCCAATATTAACATGCAAACGCA CG CA GA CC AAAANKRD55 9318GGGAGCCAATATTAACATGCCACCGGGGAGCCAATATTAACATGCAAACGT CG TG CGA CC CACARL15 9319GCAGGTAAATTGGTCGGGCCACCGGCGGGCAAACTTGGGGTGAACGGGAAACGT CG TG CGA CC CACARL15 9319GGGGCGAATGGAGGGACACCGGTGGAACGGGAAACGGGGAAAACCTC TG GA CC AACARL15 9321AGGTCAATTCTGGGGAACACCGGTGGAACGGGAAACGGGGAACGGGGAACGCGGAGAGCGCACGGGAAACCTC CG AAC AAA TA GA CTCFAM13A 9223GAACTGCAGAGGTGAACGGACACCGGAAGCACCTGGTGAACGGGAAACCTC CG TA CAC TTC CACFAM13A 9224TAGGGGAATGGTACGGAACACCGGAGCACCTCGTGGAACGGGGACCCGCGGGAAACCTC CG CACAC GA GA CAC CT TCFAM13A 9224TAGGGGAATGGTACGTGACACCGGAGCACCTCGTGGAACGG
GRB14 sg7AGCCGCGGGTCCCGTCCGGACACCGACGGCGCCCGGGACAAACTCC GGA CGA GAC CC CGG CTCGRB14 sg8ATGGCAGAGGCGCACGAGCCACCGATGGGCAGAGCGCCCACGACCAAACGT CG GGC GT CG CGC CTCGLUT4 sg10CCCCTCAGCAGCGAGGTGACTCACCGCTCAGCAGCGCCACGACCAAACGT CTG GGC CGT CG CCC TCCGLUT4 sg11GAGCTCACATGAGACGTGGCCACCGGCGCTCAGGAGCGCCCACGACCAAACGT CTG CGC CGT CG CCC TCCCOBL1 sg13GAACTCTCAGTGGTCCTACCCACCGGAGCTCACATGAGACGTGGCAAACGT CG CG CT CA CAC AGA GG CTCOBL1 sg13GAACTCTCAGTGGTCTACCCACCGGAACTCTCAGTGGTCCTACCAAACGGT AGA AC CAC TGA GG ATT CTCOBL1 sg14TCAGTATATTGGTCTCAGCCACCGGAACTCTCAGTGGTCTTACCAAACGA CAC GG CA AAT TA CT GCCOBL1 sg15GGCAAGCCAAATGTGTGCACCGGGCAATAACTTGTCAAACGAC CAC AGA TT AT CG CT GC CCCANKRD55 sg16TGCCAGGCAATAATTAACATGCCACCGGCGCAGCAATATTAACATGCAAACGAC CAC GA TGA TTA TG CT GC CCCANKRD55 sg19GCAAGGTTTGGACAACAGACCACCGGCAGGCAATATTAACATGCAAACGAC CG TG CT CA ACA CT CCCANKRD55 sg19GCAAGGTTTGGACACAGACTCACCGGCAGGTATTACACTGCAAACGAC CG TG CA CAC ACA CAANKRD55 sg19GCAAGGTTTCGACACAGACTTCACCGGCAGGTTGGACACGAGGTTTAAACGAC CG CT G CA CA CA CAANKRD55 sg19GCAGGCTATATTCTGGTGCCACCGGCAGGTTGGACACGAGGTTATAAACGAC CG GC CT CC CA CACARL15 sg20TGTGGTCGACACGACGTGCACCGGCGAGTTGGACACGAGCTAAACCT CA CT CA CA CA CA CAFST sg25AGGTGGATAGTACGTGACACCGGGGGTGCAACGCTGAAACCT CA CAT CA CAT CA CT CA CTFST sg26GAGCACCTCGTGGGACAGGGCGCAGGCCACCGGAGGTGGACTGCGGGGGATAAAACCT CA CG GA CA CT
GRB14 sg8ATGGGCAGAGCGCGCGGAGCCACCGATGGCAGAGGGCCAGCGCGCGCAAAGCGT CGC GGC GCT CG CCC ATCGRB14 sg9GAGGGCGACGCCCACGACCCACCGAGGGGGCGACGCCACGACCAAAGCGT CGC GG CGT CG CC CTCGLUT4 sg10CTGCAGTTTGGGTACAACATCACCGCCCCTCAGCAGGAGTGGCCAACGGT CCC TCG CG CG CT CAT TG AGC CCCGLUT4 sg11GAGCTACAATGAGCGTGCCACCGGAGCTACAATGAGACGTGCAAAGCGT CAC TGG CG CT CAT TG TAC CCCCOBLL1 sg13GAACTCCACTGCTTTCAGCCACCGGAGCTACAATGAGACGTGCAAAGCCT CAC TGG AGT TCCCOBLL1 sg14TCAGTATATTGGTCTAGCCACCGGACGACTCTCAGGGCATAACTTGTGAAAGCGT AGA ACC TG GA GAT TCCANKRD55 sg16TGGCCAGGCATAACTTGCCACCGGGGAGCCATAATTTGGCTCTACCAAACGA TGG ATG ATT TCANKRD55 sg17CCCTTGATGCATGCGGTTTCCACCGGGGAGCCATAATTTGGCACACGGGAAACGCA CG AG GAC TC AAG GGCANKRD55 sg18GGGAGCCAATATTAACTGCCACCGGGGGAGCCATATATTCGGCACACGAGCAAACGA CG GA GC CAC ACAANKRD55 sg18GGGAGCCAATATTACATGCCACCGGGGGGGCACGAGTTTGAAACGA CG CG AG CT CAAC TG CCANKRD55 sg18GGGAGCCAATATTACATGCCACCGGGGGGGACTGAACTGCAAACGA CC GC AG CA CA CAARL15 sg21TGTGGTCGACACGAGGCACCGGAGGTTGGACGAGGGAACCT CT GA CCA CCARL15 sg23AGGCCATGAAGGAGCACCGGAGGTGATGGAGCGGAGGAACCCA CCA CCA CAC CAAC CT CFST sg25AAGGGGAGTGGAACGGGACACCGGAGGTGCTCCGGGGGATTGTCCGGGATATAAACCT CAG CG ACC AC CA CG AGG CG CT CCFST sg26GACACCTCGTGGACCGAGGCACCGGAGGGGGCGTCTTCCGGGGATATAAACCT CAG GG AAAAT AAG AG CCCACGGAGGGGACACCAGAGGCACCGGAGGGGGGCGCCTGCAAACCC CAG GG AAA AT AAG AG CCL0C64
GRB14 sg9GAGGGCGACCCCACGACCCACCGGAGGGCGACGCCACGACCAAACGT CG GG CGT CGC CCC TCCGLUT4 sg10CTCGAGTTGGGTACAACATCACCGCCCCAGCAGCGAGTACATAAACGT CG CTG CTG AGG GGCGLUT4 sg11GAGCTACAATGAGACGTGGCCACCGGCGAGTCACAACTGGGTACAACATAAACGT CC CAC CG CC AGC CAAAC TG CAG AGG CTGDL11 sg13GAACTCTCAGTGGTCCTACCCACCGGAGCTACAATGAGACGTGGCAAACGT CG CTG CT CAT TG AGC TCCCOBLL1 sg14TCAGTATATTGGTCTCAGCCACCGGAGATCCACTGCTTTCATCAAAACGT GA AG ACC ACT GA G AGT TCCCOBL1 sg15AGAATCCACTGCTTTCATCACACCGGAGACCACTGCTTTCATCAAAACGT GA AACGT GA AAC CAC TG AG AGC ACT GA GANKRD55 sg16TGGCCAGGCATAAACTTGTGCACCGGGGAGCCAATATTACATGCAAACGG TGA ATAT AT G G CT CCCANKRD55 sg17CCCTTGATGCATGCGGTTTCCACCGGGGAGCCACATATTAACATGCAAACGG TGT TGA TAT TG CC T GGC CACANKRD55 sg18GGGAGCCAATATTAACAGGCACCGGGGAGCCACAGAGCTTAAAACGAT CAA GG AG CA TC AG GGCANKRD55 sg19GCAGAGTTTGGACAACAGACCACCGGGGAGCCACAGAGCTTAAAACGAT CG TGT GG AC CA CACARL15 sg20TTGGGTCGAACGAGAGTCACCGGGGGAGCTGAACGGTGAAAACTA ACG T GG AGC CA CACARL15 sg21AGGTGAATGGTAAACTGACACCGGAGGCTGCAACGGCGAAACCAG CG CG AG AT TG AGC CTFAM13A sg23GAATCGATGGAAGGTGACACCGAGGGGGAGCTGCAACGGGGAAACCAG CG CG AG CT CAC TCFST sg26AGCGACCTCGTGGACCGAGGCACCGAAGGGGGACCCTGGTGGAGGGGAGCGCGGAGGAAACCCA CG GG AA CG GC GC TCFST sg26AGCGACCCCGGAGGCTCGAGGCACCGACGGGGGCGCGGGGGGGGGGGGGGGGGGGGGGG
GLUT4 sg10CCCCTCAGCAGCGAGTGACTCACCGGCCCTCAGCAGCGAGTGACTAAACAGT CAC TG CTG CTG AGG GGGGLUT4 sg11CTGCAGTTTGGGTACAACATCACCGGAGCTTACAATGAGACGTGACAAACCTG TTG TAC CCAAAC TGC AGCCOBLL1 sg13GAACTCTCAGTGGTCCTACCCACCGGAGCTTACAATGAGACGTGACAAACGGT AGG ACC ACT GA GAG TTCCOBLL1 sg14TCAGTATATTTGGTCTCAGCCACCGGCACATGATTTTTGGTCTCAGCAAACGGT AGG ACC CAT GT AGC TCCCOBLL1 sg15AGAATCCACTGCTTTCATCACACCGTGAGATCACTGCTTTCATCAAAACGAT GAAAG CAG TGG ATT CTCANKRD55 sg16TGGCCAGCACTAACTTGTGCACCGGGCAGCACTAAACTTGTGAAACCGA CAG TTT ATG CCT GGC CACANKRD55 sg17CCCTTGATGCATGCGGTTTCCACCGGCGCAGAGCCATAATACATGGAAACCGA CAG TG TAC TAG GGCANKRD55 sg18GGAGCCAATATTAACATGCCACCGGCGAGCCATAATACATGGAAACCGA CGA TGC ATC CAG GGCANKRD55 sg18GGAGCCAATATTACAGTGCCACCGGCGAGGCCATAATACATGGAAACCGA CGA TGC ATC CAG GGCARL15 sg20TGTGTGCGACACAGAGCCACCGGCGAGCCATATTACAGGCAAACCTA ACG TG TG CGA ACC TCARL15 sg21AGGTCATATTCTGGTCGTGCCACCGGAGCTGAATTTCTGGTCGTGCAAACCAC AGA TT GA CC TCAM13A sg22CTTCGACTGAAGTGTAACGTGCACCGGAGCTGATAGTGAACGCTGAAACCAC CG TG CAC CT CAC TCFXH sg25AAGTGGAGAGTTTCAGCGGCACCGGAGCGTGTCTTCCGCTGAAAACCAC AGC TTA CAT TC CC TCCFST sg27AGGCGCCCTCGTGGGACTGAGGCACCGGAGCGCGTTCTTCCGCTGAAAACCAC AGG CAC CAT GTG AGCL0C646736 sg28CTCACATGGTCCAGAGGCACCGGCAAGAGAGATCCTCCAAACCGA CGG GGA CC ACT GG GG CCG CT CCL0C646736 sg28CTCACATGGTCACAAGAACACCGGCAAAGAGGATCCCCGGGGATAAACCGC AGG GG AC
GLUT4 sg11CTGCAGTTTGGGTACAACATCACCGCTGCAGTTTGGGTACAACATAAACATG TTG TAC CCAAC TG CAGCGLUT4 sg13GACCTACAATGAGACGTGGCCACCGGAGCTACAATGAGAGCTGGCAAACGCC ACG TGC ACT TGT AGC TCCCOBLL1 sg13GAACTCCACTGGTCCTACCCACCGGAACTCTAGTGGTCCTACCAAACGGT AGG ACC ACT GAG AGT TCCCOBLL1 sg14TCAGTATATTTGGTCTCAGCCACCGGAACTCTACTGGTGCTACCAAACGAT GA AAG CAA TGT ACT TCANKRD55 sg16AGAATCCACTGCTTTCATCACACCGGGGCAGCAATACTTGTGAAACGAA AGC CAC TGG ATG CAC CAGANKRD55 sg17CCCTTGATGCATGCGGTTTCCACCGGGGGCAGCAATATTAACATGCAAACGAA ACC GAC TGT TAA TAT TGG CTC CCCANL15 sg19GGCAGCCAATATTAACATGCCACCGGGGGCGCAACATTTGACACAGCAAAACGAC CGC TGT TGT CCAAAC TCT CCCARL15 sg10TGTGGTCGACACGACGTTATCACCGGTGGTCGACACGACGTATAAACGAC CG CG GC CA CACARL15 sg21AGGTCATATTCTGGTCGTCCCACCGGTGGCGCACACGACGTATAAACGAC CG CG ACC CAC CACARL13 sg22CTTCGACTGAAGTTCGAAGGCACCGGTGGATGATACGTGAAAACCAC CAG TTA CAT CAC CC TACFAM13A sg23GAATCGAGGCTGCAACGCTGCACCGGAACTGAGGTGCAACGCTGAAACCAC CG TTAC CAT TCC CAC TCCFST sg25AAGTGGATGATTTCACGGCACCGGAACTCATGGGAACGCTGAAAACCCC CGG TCC AGA GT G TCCFST sg26GAGCACCTCGTGGACCGAGGCACCGGACGCTCGTGGAAGCTGCTGAAAACCCC CAG CGA CG CT CAC TCFST sg27AGCGGCGTTCAGGAGAACCACCGGACACCTCGTGGGAACCCTGGGGGATATAAACCCA AGG CGA CGA TGT G AGCL0C646736 sg29ATCTTATTTTTACGGGGGCACCGGACACCACGGCGATAAACATCATAAACCCA AGG CGA CGA TGT GA GCL0C646736 sg29ATCTTATTTTTTCGCGGGGGCACCGGCAAACCACACACATCATTGAACCATAC
GLUT4 sg12GAGCTACAATGAGACGTGGCCACCGGAGCTACAATGAGACGTGGCAAACGCT ACT TC AT TGT AGC TCCCOBLL1 sg13GAACTCTCAGTGGTCCTACCCACCGGAGCTACAATGAGACGTGGCAAACGGT AGA ACC ACT GAG AGT TCCCOBLL1 sg14TCAGTATATTTGGTCTCAGCCACCGGCAGAATCTCAGTGCTCAGCAAACGGT AGA ACC AAT AT ACT GACCOBLL1 sg15AGAATCCACTGCTTTCATCACACCGGCAGAAACCTGCTTCATCAAAACGAT GAG ACC AAA TA ACT GACANKRD55 sg16TGGCCAGGCATAAACTTGTGCACCGGGGCAGGCATAAACTTGTGAAACGAA ACC GCA TGC ATC AGG GG CTCANKRD55 sg17CCCTTGATGCATGCGGTTTCCACCGGCGCAGGCATAAACTTGTGAAACGAA ACC GCA TGC ATC AAG GGCANKRD55 sg18GGCAGCCAATATTAACATGCCACCGGCGCAGGCCAATATTAACATGCAAACGAC GC TG TGC TGC CCCARL15 sg21GCGAGCTGCAACGACGACGTTATCACCGGCGCGGCGCGCAGCGCTTATAAACGAC CG CG TGT CGA CCA CACARL15 sg21AGGTCATATTCTGGTGCGCCACCGGCGGCGCGCGCGCGCGCAAACCAC AGC TG TGT CGA CCA CACARL15 sg21AGGTCATATTCTGGTGGTGCCACCGGAGCGCGCGCGCGAAACCAC CG CG GAC CGA CCA CACARL13 sg23GAATCGAGGCTGCAACGCTGCACCGGAGCGCGACGAGGTAAAAACCCA CG CG AGA TT CAC CC TACFAM13A sg24TAGGGTGAATGGTAACGTGACACCGGAGCACTCGTGGGACGAGGAAACCCA CGG CC GT TC CC CACFST sg25AAGTGGACTCGTGGGGCGATCACCGGAGCACCTGGTGGACCGAGGAAACCCA CG CG CG TC CC CACFST sg27AGCGCCCGTTCTCGCTGGCACCGGAGCACCTCGTGGGACCGAGGAAACCCC CAC CG GA AAAC CG C CG CC CCL0C646736 sg28CTCACATGGTCAAGAGAACCACCGCCAAGGCGCCGTTCTTCGCTGGAAACCTC CG AAA AAT AAG ATCL0C646736 sg30CCAAAGAAGAACACCCCCCACCGCCAAGCGCGCCCCAAACCGC CAC C
COBLL1 sg13GAACTCTCAGTGGTCCTACCCACCGGAACTCTCAGTGGTCCTACCAAACGGT AGG ACC ACT GAG AGT TCCCOBLL1 sg14TCAGTATATTTGGTCTCAGCCACCGTCAGTATATTTGGTCTCAGCAAACGGT GAG ACC AAA TA TA CT GACCOBLL1 sg15AGAATCCACTGCTTTCATCACACCGTCAGTATATTTGGTCTCAGCAAACGGT GAG ACC AAA TA TA CT GACANKRD55 sg16TGGCCAGGCATAAACTTGTGCACCGTGGCCAGGCATAAACTTGTGAAACCGA CGA TGC ATC AAG GGCANKRD55 sg17CCCTTGATGCATGCGGTTTCCACCGGCGCAGGCATAAACTTGTGAAACGGA ACC GCA TGC ATC AAG GGCANKRD55 sg18GGGAGCCAATATTAACATGCCACCGGCGCAGGCATATACATACATGCAAACGGA ACC GCA TG TAA TAT TGG CTC CCCARL15 sg19GCAGAGTTTGGACACGACGCCACCGGCGCGGCGCATATTTAACATGCAAACGCA CGA CTG AAAC TTC GGC CACARL15 sg21AGGTCATATTCTGGTCGTGCCACCGGCGGCGCACGTATAAACGAC CGA CCA GAA TAT GAC CTARL15 sg21AGGTCATATTCTGGTCGAGCCACCGGCGCGCGCGCGCGCGCGCGCAGGGAAACCCC CG AG CCA GAA TAT GAC CTARL13 sg22CTTCGACTGAAGGTAGAGTGCAACGTGCACCGGAGTGCAACGCGGAAACCCA CGT TGC ACC CT CA CAFAM13A sg23GAATCGAGGTGCAACGTGCACCGAGGTGCAACGGTGAAACCCA CGT TAC CAT TCC CAC CACFST sg26GAGCACCTCGTGGACCGAGGCACCGAGGTGCAACGTGGATGCGGGGTAAACCCA CG TTC CAC CAC CC CAC CTCFST sg27AGCGGCCGTTCTCGGGGATATCACCGGCACTCGTGGGCGCTTCTTCCCCCAAACCCA CG GA AAA CG AG TG CAC CAT TCL0C646736 sg28CTCACATGGTCCGGCGCTCCCACCGACGTGCACCACACCATCCTAAACCGA GG GA AC GG CG CC TCL0C646736 sg30CCAAAGAAGAAGATACCTCCCACCGGCACTCGAGGAAACCGACCCCCGAGGAAACCGA GCG GG CG TAC CAT TCLVPLAL1 sg31AAAGTGGCATCAAGAGAAC
COBLL1 sg14TCAGTATATTTGGTCTCAGCCACCGTCAGTATATTTGGTCTCAGCAAACGCT GAG ACC AAA TAT ACT GACCOBLL1 sg15AGAATCCACTGCTTTCTCATCACACCGAGGAATCCACTGCTTCATCAAAACGAC GAG TG GAAT GCT TCANKRD55 sg16TGGCCAGGCATAAACTTGTGCACCGGCGCAGGCATAAACTTGTGAAACGAC AGA TTT ATG CCT GGC CACANKRD55 sg17CCCTTGATGCATGCGGTTTCCACCGGCGCAGGCATAATTAACATGCAAACGAC AGA TTT ATG CCT GGC CACANKRD55 sg18GGGAGCCAATATTAACATGCCACCGGCGCAGGCGATATATTAACATGCAAACGAC GAC TGT TAA TAT TGG CT CCCARL15 sg19GCAGAGTTTGGACAACGACCACCGGCGCCGAGAGCTGGACACAGACAAACGAC TGT TAT TT GG CT CCC CAARL15 sg21AGGTCATATTCTGGTCGTGCCACCGGCGCGAGAGTTGGACACAGAGAAACGAC CGA CCG AGA TAT GAC CTCFAM13A sg22CTTCGACTGAAGGTTCGAGAGCACCGGCTGCAACGCGGAAACCCC CGA GCT GC ACC CACFAM13A sg23GAATCGAGGTGAAACGTGACACCGGAGGTGCAACGCTGAAACCCA CGT TG AAC TT CAGT CGA AGCFST sg25AAGTGGATGGTAACGTGACACCGAGGTGCAACGCGGAAACCCA CGT TG AAAT CAT CAC CT TCFST sg26GAGCACCTCGTGGACCGAGGCACCGAGGGGCGTTCTTCGCTGAAAACCCA CGG TG AAAT CAT CAC CT TCFST sg27AGCGGCGGTTCTTCGCTGGACACCGACGGCGCGTTCTTCGCTGGAAAACCCA GGA AAAT AAG AAT CAG CG CG CTCL0C646736 sg28ATCTTATTTTTACGTGGGGCACCGAAGGGCGCCTCAAGGAGAACAAACCGA GGT AAA AAT AAG AAT CAG CG AAACT TC CC CGACAGACGCACCTCGL0C646736 sg30CCAAAGAAGAAGAACCCACCGAAGTGGCATCAAGAAGAACAAACGG ACG GGA CAT TC TT TTT TG CCL0C646736 sg30CCAAAGAAGAAGAACCCACCGACGCACCTCGTCGTAAACGG ACG CG GG CG CT CT CCLVPLAL1 sg31AAAGTGGCATCAAGAGAAC
COBLL1 sg15AGAATCCACTGCTTTCATCACACCGAGAATCCACTGCTTTCATCAAAACTGA TGA AAG CAG TGG ATT CTCANKRD55 sg16TGGCCAGGCATAAACTTGTGCACCGGTGCCCAGGCATAACTTGTGAAACCAC AAG TTT ATG CCT GGC CACANKRD55 sg17CCCTTGATGCATGCGGTTTCCACCGGCGGGCATGACGTGCGAAACCAC AAG TTT ATG CCT GGC CACANKRD55 sg18GGGAGCCAATATTAACATGCCACCGGGGAGCCAATATTAACATGCAAACGA AACG CA CTG TAT AT TG CCT CCCARL15 sg20TGTGGTCGACACGACGTTATCACCGGCGAGAGTTTGGACAACAGACAAACGCA CGA CCG AC CA CACARL15 sg21AGGTCATATTCTGGTCGTGCCACCGGAGGTCATATTCTGGTGGTGCAAACGA CGA CCG AC CA CACAAA1TC AGGCTGCAACGTGCAACGCGTGCACCGGAGTCAATTTCTGGTCGTGCAAACGCA CGA CCA GA TAT GAC CTCFAM13A sg22CTTCGACTGAAGGTCGAAACGTGACACCGGAATCGAGGCTGCAACGCGTAAACCAC GG TG C CAC CG CA CCFAM13A sg23GAATCGAGGCTGCAACGCTGCACCGGAATGGAATGGTAACGTGAAAACCTC CG TG C ACC CTC GACFST sg25AAGTGGATGATTTTCAACGGCACCGGAGCGCGTTCTTCGCTGAAAACCCA CGT TG C AGC CTC CAC GA GT TCCFST sg26GAGCACCTCGTGGACCGAGGCACCGGAGCACCTCGTGGACCGAGGAAACCCA CGG TC ACG AG GT CC CCFST sg27AGCGGCCGTTTTCCGCTGACACCGACGACGCTCGTGGACCGAGGAAACCCA CGG TC ACG AG CG CC CTLOC646736 sg28CTCACATGGTTCCGGGGGCACCGACAGGGCGCTCTTGCCTTGAAAACCACA AGC GAA CAC GG CG CC CTLOC646736 sg30CCAAAGAAGAAGAACCCACCGCAAAGGAAGAAGAAGAACCTCCAAACGGA GG ATT CTT CTT GT GA GC CTTLYPLAL1 sg31AAAGTGGCATCAACATACTCACCGGCAAGCGCCCCCGGAACTCAACATACATAAACGGA GG GG GG ATT CAT CCCLYPLAL1 sg34GGGGAATCGCGCCCTGCTGCCACCGGCAAGCGACCCCCCG
ANKRD55 sg16TGGCCAGGCATAAACTTGTGCACCGTGGCCAGGCATAAACTTGTGAAACCAC AAG TTT ATG CCT GGC CACANKRD55 sg17CCCTTGATGCATGCGGGTTTCCACCGGCCCTTGATGCATGCGGTTTCAAACGAA ACC GCA TG CAC AG GGCANKRD55 sg18GGGAGCCAATATTAACATGCCACCGGCGCAGGCCATAACAGCAAACGCA TGT TAT TG CCT CGC CACARL15 sg19GCAGAGTTTGGACAACAGACCACCGGCGCAGGCTTGGACAACAGACAAACGTC TGT TGT CCA AAC TC GCARL15 sg20TGTGGTCGACACGACGATTATCACCGGTGGTCGACACGACGTTATAAACGTC GC TG TGT CGA CCA CCAARL15 sg21AGGTCATATTCTGGTCGTGCCACCGGCGCTGAACGAGGTTCGAAGGGGAAACCCA CGA CCA GAA TAT GAC CTCAM13A sg22CTTCGACTGAAGTGGTAACGTGACACCGGAATCGAGGCTGCAACGCGGAAACCAC AGG TGC AGC CTC GAT CCFAM13A sg24TAGGGTGAATGGTAACGTGACACCGGAATCGAGGCTGCAACGCTGAAACCAC CGT TAC CAT TC CC CAT CCFST sg25AAGTGGATGATTTCAACGGCACCGAAGGGTGCAACGGTGAAAACCCC TGG ACC CAG AGG TGC TCCFST sg26GAGCACCTCGTGGACCGAGGCACCGGAGGCGTTCTTGGTTGAAAACCCC AGG GAA CGG CCG CTCL0C646736 sg28CTCACATGGTTCCGGGGATATCACCGGCGTTCTTGCTTGAAAACCCA CAG GAA CAG CGC CCTL0C646736 sg30CCAAAGAAGAAGATACCTCCACCGCAAAGAAGAAGATACCTCCAAACCGA GGT ATA GT TG AG GC CAT TTLVPLAL1 sg31AAATGGCACTAAAGAAGACCACCGGCAGTCAAGCATCAACATAAACCGA AGG GGG CG CAT TC CCCMAP3K1 sg36GGGGAATCGCCCCGCCGCCGCACCGGCAGGCCGCCGCCGAAACCGA GGG GGG CGG CT GC CCC TGCMAP3K1 sg36CAAGGGGAGAGCCCGAAGCACCGCCGCAGGCCGGCCGAAACCGA CGG GGG GGA CTG GCC TT GCMAP3K1 sg36CAAGGGGAGAGCCCGAAGCACCGCCGCAGGCCGGCCGAAACCGA CGG
ANKRD55 sg17CCCTTGATGCATGCGGTTTCCACCGCCCTTGATGCATGCGGTTTCAAACGAAACC GCATGCATC AAG GGCANKRD55 sg18GGGAGCCAATATTAACATGCCACCGGGGAGCCAATATTAACATGCAAACGCC TGT TAA TAT TGC CTC CCCARL15 sg19GCAGAGTTTGGACAACAGACCACCGGCAGAGTTGGACACCGACGTTATAAACGT CGT TGT TG TCCAAAC TCT GCCARL15 sg20TGTGGTCGACACGACGTTATCACCGGCGGCGCACGCTTGTAAACGCA CGA CCA GAC TGT CGA CCA CACARL15 sg21AGGTCATATTCTGGTCGTGCCACCGGAGGTCATATTCTGGTCGTGCAAACGCA CGA CCA GAC CA GAC CA CACFAM13A sg22CTTCGACTGAAGTTCGAGAGCACCGGAGGTCGAACGCTGAAACCCA CGT TGC AGC CTC GAT CCFAM13A sg24TAGGGTGAATGGTAACGTGACACCGGAAGTGGAATGGTAACGTGAAAACCCA CGT TGC AGC CTC GAT CCFST sg25AAGTGGATGATTTTCAGCGCACCGGAGGCACCTCGTGGACCGAGGAAACCCC CGT TGC AGA CGT CCFST sg27AGCGGCCGTTCTTCGCTTGACACCGGAGGCGCCGTTCTCGCGTGAAAACCCA CGA CCA CGA GG GC CTCLOC646736 sg28CTCACATGGTTCCGGGGATCACCGGACGCACCTCGTGGACCGGGGAAACCTC CGG GAA CAG CAC TGT GA GCLOC646736 sg20CCTAAAGGGCATCAAGAAACCACCGCAAAGTGGCATCAAGAAGAAAAACGT CT CT CT CT TC TC TT CTLYPLAL1 sg31AAAGTGGCATCAAGAAACACACCGCAAAGTGGCATCAAGAAGAAAAACGT CAC TG GT TG ACA GAT TCLYPLAL1 sg34GGGGAATCGCGCCCGTCGCACCGGAGGAATGCGCCCCGCCGAAACCGA CGA GGA GG GC CAT TC CCCMAP3K1 sg36GCGGCACATCAACTGCCCCCCCGCACCGGCGCCCGCCGCCGCCGCCGAAACCGA GG GG CG CG CT CC CCCMAP3K1 sg36CAAGGGCAGAGCCCCGAAGCACCGCCGGAGGCCCCGCGCGGAGGACCCGCCCGAAACCGA GG GG CG CG CT CC CCCMAP3K1 sg36CAAGGGCCGAGGCCCCGGCCACCGCCGCG
ANKRD55 sg18GGGAGCCAATATTAACATGCCACCGGGGAGCCAATATTAACATGCAAACGCA TGT TAA TAT TGG CTC CCCARL15 sg19GCAGAGTTTGGACAACAGACCACCGGCAGAGTTTGGACAACAGACAAACGT TGT TGT CCA AAC TCT GCCARL15 sg20TGTGGTCGACACGACGACGTTATCACCGGTGTGGTCGACACGACGACGTTATAAACGT CG TGT CGA CCA CACARL15 sg21AGGTCATATTCTGGTCGTGCCACCGAGGTCATATTCTGGTCGTGCAAACGCA CGA CCA GAC TAT GAC CTCFAM13A sg22CTTCGACTGAAGTTCGAGAGCACCGAGGTCGAACGCTGAAACCGC CGA CCA GAC TAT CAC CT CAG AGCFAM13A sg23GAATCGAGGCTGCAACGCTGCACCGAGGTGCAACGGCTGAAACCAG CGT TGC AGC CTC GA TCCFAM13A sg24TAGGGTGAATGGTAACGTGACACCGTAGGGTGAATGGTAACGTGAAAACCCC CGT TC CAT CAC TC CAC TCCFST sg25AAGTGGATGGTAACGTGACACCGGAGGCGGCCGTTCTTCACCTGAAACCCC CGG TCC ACG AGG TGC TCCFST sg26GAGCACCTCGTGGACCGAGGCACCGGAGCGGCCGTTCTTCGCTTGAAAACTCA AGC GAA GAA CGG CCG CTCLOC646736 sg28CTCACATGGTTCCGGGGATATCACCGCACAGTGATGGTACCTGGGAAACCCC CAG GGT AAC AAT AGA ATCLOC646736 sg29ATCTTATTTTTACGCTGGGGCACCGCAAAGAAGAAGAACACCCAAACCTAAACGT CT TC TT TG CCLVPLAL1 sg31AAAGTGGCATCAAGAAGAACCACCGAAAGTGGCCTCAAGAAGAACAAACTGA CAT TG ATT GAT TG CAT GTAAACAGG AGG AGG AGG CGC GAT TCLVPLAL1 sg33ACATGACATCAATGATTCACACCGGACATGCCCCCGCCGAAACCGA CGA GG GG GG GG GC GC TG TCC CCCAAACCGA CGA GG GG GG GG GG GC GC TG CC CCCMAP3K1 sg36GGGGAATCGCGCCCCGCCGCACCGGCAGGCAGCGCCCCGCCGAAACCGG GG GG GG GG GG CG GC TG CC CCCCAAACCGG GG GG GG GG GG CG CG CT TG CCCCCMAP3K1 sg36CAAGGCAGGAGGCCCG
ARL15 sg19GCAGAGTTTGGACAACAGACCACCGGCAGAGTTTGGACAACAGACAAACGTC TGT TGT CCA AAC TCT GCCARL15 sg20TGTGGTCGACACGACGTTATCACCGGTGTGGTCGACACGACGTTATAAACGTC TGT TGT CCA AAC TCT GCCARL15 sg21AGGTCATATTCTGGTCGTGCCACCGAGGTCGATATTCTGGTCGTGCAAACGTC ACC GA CCA CCA CACARL13 sg22CTTCGACTGAAGTTCGAGAGCACCGCAGGTCGAACGTGGAACGCTGAAACCAC CCA CCA CAC CAC CAC CACCGATGAGTTCGAGAGFAM13A sg23GAATCGAGGCTGCAACGTGCACCGAAGGGTGCAACGCTGAAACCAC CGT TCC AAC TC AGT CCA CCT CACFST sg25AAGTGGATGATTTCAACGGCACCGAAGTGGATGGTAACGTGAAAACCCC GTTG AAAATC ATC CAC TTCFST sg26GAGCACCTCGTGGACCGAGGCACCGGAGCGCCGTTCTTCGCTTGAAAACTCA AGC GAA CAG GG TGC TCCLOC646736 sg28CTCACATGGTTCCGGGATATCACCGAAGGGAGCACCTCGTGGGACAAACCCC CAG GGT AAAAT AAG ATCLOC646736 sg29ATCTTATTTTACGCTGGGGCACCGAAAGTGGCATCAAGAGAAACAAACCG CAG GGT ATC TTC TTT GGCLYPLAL1 sg31AAAGGGAACATCAACATCACCGAAAGTGGCATCAAGAAGAAACAAACTGA CAT TGA CAT TTCLYPLAL1 sg34GGGGAATCGCGCCCTGTCGTCACCGGCAGATCCAACAATACATAAACTGA CAT TGA CAT TTCMAP3K1 sg34GGGGAATCGCGCCCGCTGTCACCGGCAGGCAGCCCGCCGTCGTAAACCGA AGG AGG CGC GAT TCC CCCMAP3K1 sg36CAAGGCGAGCAGCCCCGCCGCACCGCAAGGCGGCCCGCTGTCGTAAACCGA GCG GGC GG CTG TCC CCCMAP3K1 sg38CAAGGCGAGCAGCCCCGCCGCACCGCAGGCGCGCCGCCGCCGAAACCCG GG GG GG GG CTG CT CG CCT TGCMAP3K1 sg36CAAGGCGAGGAGCCCGGAGGCACCGTCGCGCGCGGGCGAGGCGCCGCGCAAACCCG GG GG GG CG CT CT CC CCCMAP3K1 sg38CAAGGGCAGGAGCCCGGAGGCACCGTCGCGCGG
ARL15 sg20TGTGGTCGACACGACGTTAT AGGTCATATTCTGGTCGTGCCACCGTGTGGTCGACACGACGTTAT CACCGAGGTCATATTCTGGTCGTGCAAACATAACG TCG TGT CGA CCA CAC AAACCCA CGA CCA GAA TAT GAC CTC AAACCCA CGA CCA GAC CTC GAT GC AAACCCA CGT TGC AGC CTC GAT CC AAACCCA CGT TGC AGC CTC GAT TCC AACCCA CGT TAC CAT TCA CCC TAC AAACCCA CGT TAC CAT TCA CCC TAC AAACCCA CGT TAC CAT CAC CTC CAC AACCCA CGT TGC AGC CTC CAC TCC AGCGGCCGTTCTTCGCTTGA LOC646736 sg20AAACTCA GGTCCACGGGG CACCGAGGGGGGTCATACCTCC CACCGAGGAGAAGAACAACCAT CAC CAC GAG GGA CCAC CAT GTG AGC CACCGACCGCCGATCTTTTTTTACGCTGGGG CACCGACCACCACGAGGAGACCCCCCAAAGAAGAAGAACAAC
ARL15 sg21AGGTCATATTCTGGTCGTGCCACCGAGGTCATATTCTGGTCGTGCAAACGCA CGA CCA GAA TAT GAC CTCFAM13A sg22CTTCGACTGAAGTTCGAGAGCACCGCGCTTGGACGAGGTTCGAGAGAAACCTC TCG AAC TTC AGT CGA AGCFAM13A sg23GAATCGAGGCTGCAACGCTGCACCGGAATCGAGGCTGCAACGCTGAAACCAG CGT TGC AGC CTC GAT TCCFAM13A sg24TAGGGTGAATGGTAACGTGACACCGAGGTGAATGGTAACGTGAAAACTCA CGT TAC CAT TCA CCC TACFST sg25AAGTGGATGATTTTCAACGGCACCGAGGCGCCTCGTGGACCGAGGAAACCCG TTG AAAATC ATC CAC TTCFST sg27AGCGCCGTTCTTCGCTTGACACCGAGGCGCCGTTCTTCGCTGAAAACCCC CGG TCC ACG AGG TGC TCCLOC646736 sg28CTCACATGGTTCCGGGGATATCACCGACGCCCAGGGCGTTCTTCGGTGGAAAACCAC AGC GAA CAT GG AGCLOC646736 sg30CCAAAGAAGAAGATACCTCCCACCGCAAAGAAGAAGAAGATCCTCCAAACGGT GTT GAC AGT TTC AACGGA GGT ATT CT TTT TTG GCLYPLAL1 sg31AAAGTGGCATCAAGAAGAACCACCGACATGGCACCATACATCACCGACATGAACCATACATAAACGT TCT CTT GAT GCC ACT TTCLYPLAL1 sg33ACATGACATCAATTGATTCACACCGGCAAAGTGGCATCAAGAAGAACAAACTG ATT GGT TTG ACA GAT TTCCACCGGACATGCGCCCCGCTGTCGTMAP3K1 sg36GGGGAATCGCGCCCGCTGTCGTCACCGCAAGGCGGCAGCAGCGCGCCCGAAACCGG CG GGC GGA CTG GCG GCCAAACCGG CG GC GGC TGC TCG CCT TGCMAP3K1 sg36CAAGGCGAGCAGCGCGCCGCACCGCCAGGCGGGCAGCAGCGCCCCGAAACCGG GCG GGC GGA CTG GCC CTT GCAAACCGG GCG GC TGC CCT GCCPDGFC sg37CTGGAATTTACTACTCCAGGAGCACCGCTGAGGGGGCCCGAGGCCCGGAGGAAACCCT CGG GCT TGC CCT GCCAAACCCT CGG GCT TCC CCT GC CACCGCAGGCGAGGCCCGAAGAAACCT CGG GCT TCC CCT GC CACCGCAGGGAGGCCCGAAGGCCCCGAAGMAP3K1 sg36CAAGCCCCGA
FAM13A sg22CTTCGACTGAAGTTCGAGAGCACCGCTTCGACTGAAGTTCGAGAGAAACCTC TCG AAC TTC AGT CGA AGCFAM13A sg23GAATCGAGGCTGCAACGCTGCACCGGAATCGAGGCTGCAACGCTGAAACCAG CGT TGC AGC CTC GAT TCCFAM13A sg24TAGGGTGAATGGTAACGTGACACCGGAGGTGAATGGTAACGTGAAAACCCG CGT TGC AGC CTC GAT TCCFST sg25AAGTGGATGATTTTCAACGGCACCGAAGTGGATGATTTTCAACGGAAACCCG TTG AAA ATC ATC CAC TTCFST sg26GAGCACCTCGTGGACCGAGGCACCGAGGGGCCGTTCTTCGCTTGAAAACCCC CGG TCC ACG AGG TGC TCCLOC646736 sg28CTCACATGGTTCCGGGGATATCACCGACGCGCCGTTCTTCGCTGGAAACCCC CAG CG AAA CAG CGC CCG CTCLOC646736 sg30CCAAAGAAGAAGATACCTCCCACCGAAAGTGGCATCAAGAAGAACAAACCCC CAG CGT AAA AAT AAG ATCLYPLAL1 sg31AAAGTGGCATCAAGAAGAACCACCGAAAGTGGCATCAAAGAAGAACAAACGGA GGT ATC TTT CTT GAT GCC ACT TTCLYPLAL1 sg33ACATGACATCAATCAATCAATCAACATCACCGGAAATCGGCCCCGTCGTAAACCGA CGG AGG CGC GAT TCC CCCMAP3K1 sg34GGGGAATCGCGCCCGCTGGCACCGGAAGGCAGCCGCCGCTAAACCGA CGG GGC GGA CTG GCG GCCMAP3K1 sg36CCAAGGCGAGCAGCGCCCGCACCGGCAGGCGCGCCGAAACCGA CGG GGC GGA CTG GCG GCCMAP3K1 sg36CAAGGCGAGCAGCGCCCGCACCGCCAGGCGGCGCCGAAACCGA GCG GGC GGA CTG GCG GCCMAP3K1 sg36CAAGGCGAGCAGCGCCCGCACCGCCGCAGCCGCGCGAAACCG AGG GGC GGA CTG CCG CCT TCPDGFC sg38TCAGCAGGAGACGCCCGAGGCACCGCCGCAGGCAGGCGCCGCAAACCG GG GGA GT GA GTAAT TCC AGCPDGFC sg38TCAGCAGGAGAGCCCCGAAGCACCGCTCGCCGCGAGAAACCG CTG CTG CCT GCC GCCGPDGFC sg38TCAGCAGGAGAGCCCCGAAGCACCGCTCGCCGCAGAAACCGG
FAM13A sg23GAATCGAGGCTGCAACGCTGCACCGGAATCGAGGCTGCAACGCTGAAACCAG CGT TGC AGC CTC GAT TCCFAM13A sg24TAGGGTGAATGGTAACGTGACACCGGAGGGTGAATGGTAACGTGAAAACCAG CGT TGC AGC CTC GAT TCCFST sg25AAGTGGATGATTTTCAACGGCACCGGAGGCACCTCGTGGACCGAGGAAACCCG TTG AAAATC ATC CAC TTCFST sg26GAGCACCTCGTGGACCGAGGCACCGGAGCGCCGTTCTTCGCTTGAAAACCCG TG CACG AGG TGC CCCLOC646736 sg28CTCACATGGTTCCGGGATATCACCGGCGCTCACATGGTTCCGGGATATAAACCCC CAG CG AAA CAC CG CCG CTCLOC646736 sg29ATCTTATTTTTACGCTGGGGCACCGGCCAAAGAAGAAGATACCTCCAAACCGG AGC ACC CAG CG AAA AAT AAG ATCLOC646736 sg30CCAAAGAAGAAGAACCACCAACATCACCGAAAGGAGGAAGATACCTCCAAACGGA GGT ATC TTC TTC TTT GGCLYPLAL1 sg31AAAGTGGCATCAAGAAGAACCACCGAAATCGTCAAAACCATACATAAACCGT CAT GGT TTG ACA GAT TTCLYPLAL1 sg33ACATGACATCAATCAATCAATCAACCAATCAATCGAACCAATCAAT
FAM13A sg24TAGGGTGAATGGTAACGTGACACCGTAGGGTGAATGGTAACGTGAAAACTCA CGT TAC CAT TCA CCC TACFST sg25AAGTGGATGATTTTCAACGGCACCGAAGTGGATGATTTTCAACGGAAACCCG TTG AAA ATC ATC CAC TTCFST sg26GAGCACCTCGTGGACCGAGGCACCGGAGCACCTCGTGGACCGAGGAAACCCT CGG TCC ACG AGG TGC TCCFST sg27AGCGGCCGTTCTTCGCTTGACACCGAGCGGCCGTTCTTCGCTTGAAAACTA ACC AGC GAA GAA CGG CCG CTCLOC646736 sg28CTCACATGGTTCCGGGATATCACCGCTCACATGGTTCCGGGATATAAACTA TCC CGG AAC CAT GTG AGCLOC646736 sg30CCAAAGAAGAAGATACCTCCCACCGCCCAAAGAAGAAGATACCTCCAAACGGG GGT ATC TTC TTT GTT GGCLYPLAL1 sg31AAAGTGGCATCAAGAAGAACCACCGAAAGTGGCATCAAGAAGAACAAACGTT CTT CTT GAT GCC ACT TTCLYPLAL1 sg33ACATGACATCAATGATTCACACCGGACATGACATCAATTGATTCAAAACTG ATT GGT TTG ACA GAT TTCLYPLAL1 sg34GGGGAATCGCGCCTCGTCGTCACCGGCGGCATCAAGAAGAACAAACTG ATC AAT TGA TGT CAT GTCMAP3K1 sg36CCAAGGCGAGCAGCGCCCCGCACCGGCGGAATCGCGCCTCGTCGTAAACCGA GCG GGC GGA CTG GCG GCCMAP3K1 sg36CAAGGCGAGCAGCGCCCCGCACCGGCAGGCAGCAGCGCCCCGAAACCGG GCG GGC GGA CTG GCG GCCMAP3K1 sg36CAAGGCGAGCAGCGCCCCGCACCGGCGGAGCAGCGCCCCGAAACCGG GCG GCG CGC TGC TCG CCT TGCPDGFC sg37CTGGAATTACTACTCAGGTCACCGCTGGGAGAGGAGCCCGAAGAAACCCT CGG GCT TCT CCT GCT GACPDGFC sg38TCAGCAGGAGAAGCCCCGAAGCACCGTCAGGCAGGCGCCCGAGGAAACCCT CGG GCT TCT CCT GCT GAC
FST sg25AAGTGGATGATTTTCAACGGCACCGAAGTGGATGATTTTCAACGGAAACCCG TTG AAAATC ATC CAC TTCFST sg26GAGCACCTCGTGGACCGAGGCACCGGAGCACCTCGTGGACCGAGGAAACCCT CGG TCC ACG AGG TGC TCCFST sg27AGCGGCCGTTCTTCGCTTGACACCGAGCGGCCGTTCTTCGCTTGAAAACTCA AGC GAA GAA CGG CCG CTCLOC646736 sg28CTCACATGGTTCCGGGATATCACCGCTCACATGGTTCCGGGATATAAACCCC CAG CGT AAAAT AAG ATCLOC646736 sg30CCAAAGAAGAAGATACCTCCCACCGCCAAAGAAGAAGATACCTCCAAACGGA GGT ATC TTC TTC TTC TTC GTLOC646736 sg30CCAAAGAAGAAGATACCTCCCACCGCCAAAGAAGAAGATACCTCCAAACGGA GGT ATC TTC TTC TTC TTC GGCLYPLAL1 sg31AAAGTGGCATCAAGAAGAACCACCGAAAGTGGCATCAAGAAGAACAAACGTT CTT CTT GAT GCC ACT TTCLYPLAL1 sg33ACATGACATCAATTGATTCACACCGACAGACCATCAATTGATTCAAAACTGA ATC AAT TGA TGT CAT GTCLYPLAL1 sg34GGGGAATCGCGCCTCGTCGTCACCGGCGGCAAGCCGCCCGAAACACG ACG AGG CGC GAT TCC CCCMAP3K1 sg36CAAGGCGAGCAGCGCCCGCACCGGCAGGCGGCCCGAAACCGG ACG AGG CGC GGC TGC TCG CCT TGCMAP3K1 sg36CAAGGCGAGCAGCGCCCGGCACCGCTGGAATTTACTACTCAGGTAAACCGG GCG CGC TGC TCG CCT TGCPDGFC sg37CTGGAATTTACTACTACAGGTCACCGCTGGAAGGCGCCCCGAAACACC TGA GTA GTA AAT TCC AGCPDGFC sg38TCAGCAGGAGAGCCCGAAGCACCGTCAGCAGGAGGAGCCCGAAGAAACCTT CGG GCT TCT CCT GCT GAC
FST sg26GAGCACCTCGTGGACCGAGGCACCGGAGCACCTCGTGGACCGAGGAAACCCT CGG TCC ACG AGG TGC TCCFST sg27AGCGGCCGTTCTTCGCTTGACACCGAGCGGCCGTTCTTCGCTTGAAAACTCA AGC GAA GAA CGG CCG CTCLOC646736 sg28CTCACATGGTTCCGGGATATCACCGACGCTCACATGGTTCCGGGATATAAACTCA AGC GAA GAA CGG CCG CTCLOC646736 sg29ATCTTATTTTTACGCTGGGGCACCGATCTTATTTTTACGCTGGGGAAACCCC CAG CGT AAA AAT AAG ATCLOC646736 sg30CCAAAGAAGAAGATACCTCCCACCGCCAAAGAAGAAGATACCTCCAAACGGA GGT ATC TTC TTC TTT GGCLYPLAL1 sg31AAAGTGGCATCAAGAAGAACCACCGAAAGTGGCATCAAGAAGAACAAACGTT CTT CTT GAT GCC ACT TTCLYPLAL1 sg32AAATCTGTCAAACCATACATCACCGACATGACATCAATGAACAACATAAACTGA ATC GT TG ACA GAT TTCLYPLAL1 sg33ACATGACATCAATTGATTCACACCGGCGCAGCCCGCCAGTCCGTCGTAAACACG ACG AGG CGC GAT TCC CCCMAP3K1 sg34GGGGAATCGCGCCTCGTCGTCACCGGCGGCAGCAGCGCGCCCGAAACCGA GCG GGC GGA CTG GCG GCCMAP3K1 sg36CAAGGCGAGCAGCGCGCCCGCACCGCCGAAGCCGCGCCCGAAACCGG GCG GGC GGA CTG GCG GCCPDGFC sg37CTGGAATTTACTACTCAGGTCACCGTCAGCAGGAGAAGCCCGAAGAAACCCT TGA GTA GTA AAT TCC AGCPDGFC sg38TCAGCAGGAGAAGCCCCGAAGCACCGTCAGCGGGGAGAGCCCGAAGAAACCCT TGA GTA GTA AAT TCC AGC
FST sg27AGCGGCCGTTCTTCGCTTGACACCGAGCGGCCGTTCTTCGCTTGAAAACTCA AGC GAA GAA CGG CCG CTCLOC646736 sg28CTCACATGGTTCCGGGATATCACCGCTCACATGGTTCCGGGATATAAACTA TCC CGG AAC CAT GTG AGCLOC646736 sg29ATCTTATTTTTACGCTGGGGCACCGATCTTATTTTTACGCTGGGGAAACCCC CAG CGT AAA AAT AAG ATCLOC646736 sg30CCAAAGAAGAAGATACCTCCCACCGCCAAAGAAGAAGAAGAACCTCCAAACGGA GGT ATC TTC TTC TTT GGCLVPLAL1 sg31AAAGTGGCATCAAGAAGAACCACCGACAAGAAGAAGAAGAACAAACGTT CTT CTT GAT GCC ACT TTCLYPLAL1 sg32AAATCTGTCAAACCATACATCACCGACATGACATCAATGAACAACATAAACATG TAT GGT TTG ACA GAT TTCLYPLAL1 sg33ACATGACATCAATTGATTCACACCGGCGCAGCCCGCCCGTCGTAAACCGA AGC AGG CGC GAT TCC CCCMAP3K1 sg34GGGGAATCGCGCCTCGTCGTCACCGGCGGCGCCGCCAGTCCGCCGCCGAAACCGA GCG GGC GGA CTG GCG GCCMAP3K1 sg36CAAGGCGAGCAGCGCCCCGCACCGCCGAGGCGGCGCCCGAAACCGG GCG GGC GGC TGC TCC CCT TGCPDGFC sg37CTGGAATTTACTACTCAGGTCACCGCTCGGCGGCGGAGAGCGCCCGAAGAAACCCT GA GTA GTA AAT TCC AGCPDGFC sq38TCAGCAGGAGAAGCCCCGAAGCACCGTCAGCGGGGAGAGCCCGAAGAAACCTT CGG GCT TCT CCT GCT GAC
LOC646736 sg28CTCACATGGTTCCGGGATATCACCGCTCACATGGTTCCGGGATATAAACATA TCC CGG AAC CAT GTG AGCLOC646736 sg29ATCTTATTTTTACGCTGGGGCACCGATCTTATTTTTACGCTGGGGAAACCC CAG CGT AAA AAT AAG ATCLOC646736 sg30CCAAAGAAGAAGAAGATACCTCCCACCGCCAAAGAAGAAGAAGATACCTCCAAACGGA GGT ATC TTC TTC TTT GGCLYPLAL1 sg31AAAGTGGCATCAAGAAGAACCACCGACAAGAAGAAGAAGAACAAACCGT CTT CTT GAT GCC ACT TTCLYPLAL1 sg32AAATCTGTCAAACCATACATCACCGACATGACATCAATGAACCATACATAAACATG TAT GGT TTG ACA GAT TTCLYPLAL1 sg33ACATGACATCAATTGATTCACACCGACATGACATCAATTGATTCAAAACTGA ATC AAT TGA TGT CAT GTCLYPLAL1 sg34GGGGAATCGCGCCTCGTCGTCACCGGGGGGAATCGCGCCTCGTCGTAAACAGG ACG AGG CGC GAT TCC CCCMAP3K1 sg35GCCGCCAGTCCGCCCGCTCGCACCGGCGCGCCGCCGCCGCCGAAACCGA GCG GGC GGA CTG GCG GCCMAP3K1 sg36CAAGGCGAGCAGCGCGCCCGCACCGCCGAAGCCGGCGCCCGAAACCGG GCG CGC TGC TCG CCT TGCPDGFC sg37CTGGAATTTACTACTCAGGTCACCGTCAGCAGGAGAAGCCCGAAGAAACCCT GA GTA GTA AAT TCC AGCPDGFC sq38TCAGCAGGAGAAGCCCCGAAGCACCGTCAGCGGGAGAAGCCCGAAGAAACCTT CGG GCT TCT CCT GCT GAC
LOC646736 sg29ATCTTATTTTTACGCTGGGGCACCGATCTTATTTTTACGCTGGGGAAACCCC CAG CGT AAA AAT AAG ATCLOC646736 sg30CCAAAGAAGAAGAAGATACCTCCCACCGCCAAAGAAGAAGAAGATACCTCCAAACGGA GGT ATC TTC TTC TTT GGCLYPLAL1 sg31AAAGTGGCATCAAGAAGAACCACCGCAAAGTGGCATCAAGAAGAACAAACGTT CTT CTT GAT GCC ACT TTCLYPLAL1 sg32AAATCTGTCAAACCATACATCACCGAAATCGCACCATACATAAACCGGA GGT ATC ATT GAT GCC ACT TTCLYPLAL1 sg33ACATGACATCAATTGATTCACACCGACATGACATCAATTGATTCAAAACTGA ATC AAT TGA TGT CAT GTCLYPLAL1 sg34GGGGAATCGCGCCTCGTCGTCACCGGGGGGAATCGCGCCTCGTCGTAAACACG ACG AGG CGC GAT TCC CCCMAP3K1 sg35GCCGCCAGTCCGCCCGCTCGCACCGGCGCGCAGTCCGCCCGCCGAAACCGA GCG GGC GGA CTG GCG GCCMAP3K1 sg36CAAGGCGAGCAGCGCGCCCGCACCGCCGAGGCGGCGCCCGAAACCGG GCG CGC TGC TCG CCT TGCPDGFC sg37CTGGAATTTACTACTCAGGTCACCGTCAGCAGGAGAAGCCCGAAGAAACCCT GA GTA GTA AAT TCC AGCPDGFC sg38TCAGCAGGAGAAGCCCCGAAGCACCGTCAGCAGGAGAAGCCCGAAGAAACCCT CG GCT TCT CCT GCT GAC
LOC646736 sg30CCAAAGAAGAAGAAGATACCTCCCACCGCCAAAGAAGAAGAAGATACCTCCAAACGGA GGT ATC TTC TTC TTT GGCLYPLAL1 sg31AAAGTGGCATCAAGAAGAACCACCGAAAGTGGCATCAAGAAGAACAAACGTT CTT CTT GAT GCC ACT TTCLYPLAL1 sg32AAATCTGTCAAACCATACATCACCGAAAGTGGCATCAAGAAGAACAAACGTT CTT CTT GAT GCC ACT TTCLYPLAL1 sg33ACATGACATCAATTGATTCACACCGACATGACATCAATTGATTCAAAACTGA ATC AAT TGA TGT CAT GTCMAP3K1 sg34GGGGAATCGCGCCTCGTCGTCACCGGGGGGAATCGCGCCTCGTCGTAAACACG ACG AGG CGC GAT TCC CCCMAP3K1 sg35GCCGCCAGTCCGCCCGCTCGCACCGGCGCGCGCGCGCGCCGCAAACCGA GCG GGC GGA CTG GCG GCCMAP3K1 sg36CAAGGCGAGCAGCGCGCCCGCACCGCCGAGGCGGCGCCGAAACCGG GCG CGC TGC TCG CCT TGCPDGFC sg37CTGGAATTTACTACTCAGGTCACCGTCAGCAGGAGAAGCCCGAAGAAACCCT GA GTA GTA AAT TCC AGCPDGFC sg38TCAGCAGGAGAAGCCCCGAAGCACCGTCAGCAGGAGAAGCCCGAAGAAACCT CGG GCT TCT CCT GCT GAC
LYPLAL1 sg31AAAGTGGCATCAAGAAGAACCACCGAAAGTGGCATCAAGAAGAACAAACGTT CTT CTT GAT GCC ACT TTCLYPLAL1 sg32AAATCTGTCAAACCATACATCACCGAAATCTGTCAAACCATACATAAACATG TAT GGT TTG ACA GAT TTCLYPLAL1 sg33ACATGACATCAATTGATTCACACCGACATGACATCAATTGATTCAAAACTGA ATC AAT TGA TGT CAT GTCLYPLAL1 sg33ACATGACATCAATTGATTCACACCGGCGGCAATCGCGCCTCGTCGTAAACACG ACG AGG CGC GAT TCC CCCMAP3K1 sg34GGGGAATCGCGCCCGCTCGCACCGGGCGCCAGTCCGCCCGCTCGAAACCGA GCG GGC GGA CTG GCG GCCMAP3K1 sg35GCCGCCAGTCCGCCCGCCCGCACCGGCGAGCAGCGCGCCCGAAACCGG GCG GGC GGA CTG GCG GCCMAP3K1 sg36CAAGGCGAGCAGCGCGCCCGCACCGCCGAAGGCGAGCAGCGCGCCCGAAACCGG GCG CGC TGC TCG CCT TGCPDGFC sg37CTGGAATTTACTACTCAGGTCACCGTCAGCAGGAGAAGCCCGAAGAAACCCT TGG GT GAAAT TCC AGCPDGFC sq38TCAGCAGGAGAAGCCCCGAAGCACCGTCAGCAGGAGAAGCCCGAAGAAACCTT CGG GCT TCT CCT GCT GAC
LYPLAL1 sg32AAATCTGTCAAACCATACATCACCGAAATCTGTCAAACCATACATAAACATG TAT GGT TTG ACA GAT TTCLYPLAL1 sg33ACATGACATCAATTGATTCACACCGACATGACATCAATTGATTCAAAACTGA ATC AAT TGA TGT CAT GTCMAP3K1 sg34GGGGAATCGCGCCTCGTCGTCACCGGGGGGAATCGCGCCCGCTCGAAACACG ACG AGG CGC GAT TCC CCCMAP3K1 sg35GCCGCCAGTCCGCCCGCTCGCACCGGCGCCAGTCCGCCCGCCCGAAACCGA GCG GGC GGA CTG GCG GCCMAP3K1 sg36CAAGGCGAGCAGCGCGCCCGCACCGCCAAGGCGAGCAGCGCGCCCGAAACCGG GCG GGC GGA CTG CCG CCT TGCPDGFC sg37CTGGAATTTACTACTCAGGTCACCGCTCAGCAGGAGAAGCCCCGAAGAAACCCT CG GCT TCT CCT GCT GACPDGFC sq38TCAGCAGGAGAAGCCCCGAAGCACCGTCAGCAGGAGAAGCCCCGAAGAAACCTT CGG GCT TCT CCT GCT GAC
LYPLAL1 sg33ACATGACATCAATTGATTCACACCGACATGACATCAATTGATTCAAAACTGA ATC AAT TGA TGT CAT GTCMAP3K1 sg34GGGGAATCGCGCCTCGTCGTCACCGGGGGGAATCGCGCCCGCTCGAAACACG ACG AGG CGC GAT TCC CCCMAP3K1 sg35GCCGCCAGTCCGCCCGCTCGCACCGGCGCCGCCAGTCCGCCCGCCCGAAACCGA GCG GGC GGA CTG GCG GCCMAP3K1 sg36CAAGGCGAGCAGCGCGCCCGCACCGCCAAGGCGAGCAGCGCGCCCGAAACCGG GCG CGC TGC TCG CCT TGCPDGFC sg37CTGGAATTTACTACTCAGGTCACCGCTCGCAGGAGAAGCCCCGAAGAAACACC TGA GTA GTA AAT TCC AGCPDGFC sn38TCAGCAGGAGAAGCCCCGAAGCACCGTCAGCAGGAGAAGCCCCGAAGAAACCTT CGG GCT TCT CCT GCT GAC
MAP3K1 sg34GGGGAATCGCGCCTCGTCGTCACCGGGGGGAATCGCGCCTCGTCGTAAACACG ACG AGG CGC GAT TCC CCCMAP3K1 sg35GCCGCCAGTCCGCCCGCTCGCACCGGCGCCCGCCAGTCCGCCCGCCCGAAACCGA GCG GGC GGA CTG GCG GCCMAP3K1 sg36CAAGGCGAGCAGCGCGCCCGCACCGCCAAGGCGAGCAGCGCGCCCGAAACCGG GCG CGC TGC TCG CCT TGCPDGFC sg37CTGGAATTTACTACTCAGGTCACCGCTCGCAGGAGAAGCCCCGAAGAAACACC TGA GTA GTA AAT TCC AGCPDGFC sg38TCAGCAGGAGAAGCCCCGAAGCACCGTCAGCAGGAGAAGCCCCGAAGAAACCTT CGG GCT TCT CCT GCT GAC
MAP3K1 sg35 GCCGCCAGTCCGCCCGCTCG CACCGGCCGCCAGTCCGCCCGCTCG AAACCGA GCG GGC GGA CTG GCG GCC MAP3K1 sg36 CAAGGCGAGCAGCGCGCCCG CACCGCAAGGCGAGCAGCGCGCCCG AAACCGG GCG GGC GGA CTG GCG GCC PDGFC sg37 CTGGAATTTACTACTCAGGT CACCGCTGGAATTTACTACTCAGGT AAACACC TGA GTA GTA AAT TCC AGC PDGFC sg38 TCAGCAGGAGAAGCCCCGAAG CACCGTCAGCAGGAGAAGCCCCGAAG AAACCTT CGG GCT TCT CCT GCT GAC
MAP3K1 sg36 CAAGGCGAGCAGCGCGCCCG CACCGCAAGGCGAGCAGCGCGCCCG AAACCGG GCG CGC TGC TCG CCT TGC PDGFC sg37 CTGGAATTTACTACTCAGGT CACCGCTGGAATTTACTACTCAGGT AAACACC TGA GTA GTA AAT TCC AGC PDGFC sg38 TCAGCAGGAGAAGCCCCGAAG CACCGTCAGCAGGAGAAGCCCCGAAG AAACCTT CGG GCT TCT CCT GCT GAC
PDGFC sg37 CTGGAATTTACTACTCAGGT CACCGCTGGAATTTACTACTCAGGT AAACACC TGA GTA GTA AAT TCC AGC PDGFC sg38 TCAGCAGGAGAAGCCCCGAAG CACCGTCAGCAGGAGAAGCCCCGAAG AAACACC TGG GT TCT CCT GCT GAC
PDGFC sg39 CCCCTGTCTCTGGCCGGCCA CACCGCCCCTGTCTCTGGCCGGCCA AAACTGG CCG GCC AGA GAC AGG GGC
PEPD sg40 TGTGCAGGCCGGCTCCATCG CACCGTGTGCAGGCCGGCTCCATCG AAACCGA TGG AGC CGG CCT GCA CAC
PEPD sg41 TGAAACCCTGAAGGTGCCGC CACCGTGAAACCCTGAAGGTGCCGC AAACGCG GCA CCT TCA GGG TTT CAC
PEPD sg42 CAGCGCTACTGCACCGACAC CACCGCAGCGCTACTGCACCGACAC AAACGTG TCG GTG CAG TAG CGC TGC
RSP03 sg43 TGGCAGCCTTGACTAACGTT CACCGTGGCAGCCTTGACTAACGTT AAACAAC GTT AGT CAA GGC TGC CAC
RSP03 sg44 CGAGTTCCATAATATCCACT CACCGCGAGTTCCATAATATCCACT AAACAGT GGA TAT TAT GGA ACT CGC
RSP03 sg45 GCCCAGACTATTTTTGCTC CACCGGCCCAGACTATTTTTTGCTC AAACGAG CAA AAA ATA GTC TGG GCC
SLC30A10 sq46 TGAGCGCCGGCTACATCGCC CACCGTGAGCGCCGGCTACATCGCC AAACGGC GAT GTA GCC GGC GCT CAC
SLC30A10 sg47 CTCGGCGCGGGGCGTAGCCGT CACCGCTCGGCGCGGGGCGTAGCCGT AAACACG GCT ACG CCC GCG CCG AGC
SLC30A10 sg48 GCTACTCTGGCAAGACGTGC CACCGGCTACTCTGGCAAGACGTGC AAACGCA CGT CTT GCC AGA GTA GCC
SYN2 sg49 CGGTCATGTAGCCGTTGGGC CACCGCGGTCATGTAGCCGTTGGGC AAACGCC CAA CGG CTA CAT GAC CGC
SYN2 sg50 TGATGAACTTCCTGCGGCGC CACCGTGATGAACTTCCTGCGGCGC AAACGCG CCG CAG GAA GTT CAT CAC
SYN2 sg51 GCAGCCCGCGCCGACGCCGT CACCGGCAGCCCGCGCCGACGCCGT AAACACG GCG TCG GCG CGG GCT GCC

Online Table II: SgRNA sequences and primers for sgRNA plasmid cloning.

Gene	Primer Forward (5'-3')	Primer reverse(5'-3')
PPARG	CGTGGATCTCTCCGTAATGG	GAGATGCAGGCTCCACTTTG
IRS1	GATGGCTTCTCGGACGTGCG	GTTTGGGGGCGCTCGACTTG
GRB14	CACTTCCCTGCAAGATGGGC	GATGGCATTTCCGGAACATC
GLUT4	CGGGCTTCCAACAGATAGGC	GCCACGTCTCATTGTAGCTC
COBLL1	CCGCAGGACGCCCCAGCCAG	ACCACTGAGAGTTCAACGTC
ANKRD55	CAGCACCCCTTCTGTGTTTG	AGGATAGAAGGGTCTTCCCG
ARL15	GAGGCGTTTCTGTACATGG	CGTTATCGGGGCTTTCACTG
FAM13A	CACCGAGAATGGCATTCCAG	AGCAGACATCACCGTCCTTC
FST	TTCATGGAGGACCGCAGTGC	GTGTGTTGTCATTCACGTCC
LOC646736	AATGAACAAGTCCACCCCAG	GGAGGTATCTTCTTCTTGG
LYPLAL1	ATTTATCCAACAGCTCCTCC	CAGTAAGCACTTGACACATG
MAP3K1	AAGTGCGGAGTGTGGAGCTG	CTGGAAGCCGGTCCCACTC
PDGFC	CTTCTCCTGCTGACATCTGC	CTTGGGCTGTGAATACTTCC
PEPD	TTGAACCGGCAGCGCCTGTG	GTGACACCGAACGCCCAGTG
RSPO3	TATGGAATACATCGGCAGCC	GAGCATGTTGCACAGCCTCC
SLC30A10	GACTCCTTCAACATGCTCTC	AGGAAGACCGCGTTGCTCAG
SYN2	ATGATGAACTTCCTGCGGCG	GGTCGGTCATGTAGCCGTTG

Online Table III: Primers for qRT-PCR.

Online Table IV

Gene	Primer Forward (5'-3')	Primer reverse (5'-3')
PPARG	TTCTCTAGGACTTAACTTCACAGC	TGCAACCACTGGATCTGTTCT
IRS1	CACCCGGTTGTTTTTCGGAG	TTGTGCCGCCACTTCTTCTC
GRB14	ACAATGACCACTTCCCTGCAA	TCCAGGGTTGCCTACCTGT
GLUT4	ATGCTGTGTCTTTGTGTCTGC	ATGGAGCTGGGTCCCTCA
COBLL1	CAAAAGCCAAGGCACCACTT	ACCACTGAGAGTTCAACGTC
ANKRD55	AGGCCAATAAAGCCTGCTCA	TGTGACAGGCACAAGTCAGT
ARL15	CACTTTGCTGCAAGGGACCA	AGGGAGGGGATAAATTGCACA
FAM13A	CCAGGACTTACCCAAGAAGGT	GTGCCCAGCCTAGTAAAGTTGT
FST	CCCACCCTTGTCTCTTCACAG	ACCTTTACAGGGGATGCAGT
LOC646736	TGCAAAACTGGGAGAGCTTCA	CACTAAGGCTCCACTCACCAT
LYPLAL1	CATATTCCCTTTTCCTTTCT	TGAACAGTGATAAATTACCA
MAP3K1	TGTAGCCCGCGAGAGAAAAT	AGCTCCACACTCCGCACTTT
PDGFC	CCAGTCAGCCAAATGAGCCT	ACACACAGCGAGAAACAAGC
PEPD	CTCTGCAGACCCTCGTTTTG	ATCACACACCTGCTCACTTG
RSPO3	TTGTCTCCACAGTGCATCCT	TCGTGTGGGCACTTACTTGT
SLC30A10	ACAATCTGGGAGGCGGGTA	TCCACGAAGATGGTGAAGCA
SYN2	CCAGCCCTTTAAGCCAGA	AGCTGAAGAAGCTGCTGCCCA

Online Table	IV: Primers for	PCR of targeted	I genomic site.
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	Coordinates (hg38)	strand	ММ	target_seq	PAM	Position	gene name				
	chr5:53483023-53483045	+	0	AAGTGGATGATTTTCAACGG	GGG	E	FST (on-target				
	chrX:115338062-115338084	+	2	AA <mark>C</mark> TGGATGATTTTCAA <mark>G</mark> GG	TGG	-	LUZP4				
F 0 T	sg26: GAGCACCTCGTGGA) 	ternet een	D 447	Destri					
F31		strand			PAN	Position	gene name				
	<u>chr5:53482977-53482999</u>	+	0	GAGCACCICGIGGACCGAGG	AGG	E	FST (on-target				
	sg27: GCGGCCGTTCTTCG	CTTGA									
	Coordinates (hg38)	strand	MM	target_seq	PAM	Position	gene name				
	chr5:53482896-53482918	-	0	AGCGGCCGTTCTTCGCTTGA	CGG	E	FST (on-target				
	<u>chr6:1384949-1384971</u>	+	3	TGAGGCCGGTCTTCGCTTGA	GGG	E	RP4-668J24.2				
	sg37: CTGGAATTTACTACT	CAGGT									
	Coordinates (hg38)	strand	ММ	target_seg	PAM	Position	gene name				
	chr4:156970811-156970833	+	0	CTGGAATTTACTACTCAGGT	TGG	E	PDGFC (on-				
	chr21:45784281-45784303	-	3	CAGGAATTTTCTACACAGGT	AGG	I	PCBP3				
	chr18:41841371-41841393	-	3	CTG A AATTTA <mark>G</mark> TACACAGGT	AGG	-	AC011225.1				
	Sg38: TCAGCAGGAGAGAGCC	strand	ММ	target seg	PAM	Position	gene name				
	chr4:156970876-156970898	+	0		AGG	E	PDGFC (on-				
DGFC	chr17:9735253-9735275	-	3	GCAACAGGAGAAGCCCAAAG	TGG	-	USP43				
	chr2:165988057-165988079	-	3	TCATCAGGTGAAGCCAGAAG	AGG		SCN1A				
	chr2:47056412-47056434	+	3	TCACCTGGAGAAGCCCTAAG	AGG	I	Metazoa_SRI				
	sg39: CCCCTGTCTCTGGC	CGGCC		torgot cog	DAM	Position	aono nomo				
	cooldinates (11938)	Stranu			CCC	FOSILION					
	chr20:61E04202_61E0422E	T	2		000						
	<u>clii20.81304203-81304223</u>	-	3 2	CCCCAGIGIGIGGCCGGCC		1					
	<u>CHI1:43567087-43567109</u>	+	3	GCCCTGACTCTGGCAGGCCA		1	PIPKF				
	<u>CN122.41431649-41431871</u>	+	3	GUULIGIGIUIGGUAGGUUA	GGG	-	CTA-223H9.9				
	sg40: TGTGCAGGCCGGCT	ССАТСС	3								
	Coordinates (hg38)	strand	ММ	target_seq	PAM	Position	gene name				
	chr19:33512655-33512677	-	0	TGTGCAGGCCGGCTCCATCG	TGG	E	PEPD (on-tar				
	sg41: TGAAACCCTGAAGGT	GCCGC		<u> </u>							
	Coordinates (hg38)	strand	ММ	target_seq	PAM	Position	gene name				
	chr19:33512733-33512755	-	0	TGAAACCCTGAAGGTGCCGC	TGG	Е	PEPD (on-tar				
PFPD	chr22:44704534-44704556	-	3	TGGAGCCCTGCAGGTGCCG	GGG	I	PRR5				
	chr17:55561520-55561542	-	2	GGAAACCCTGAAGGTGCCAC	TGG	E	CTD-2033D24				
	sg42: CAGCGCTACTGCAC	GACAC									
	Coordinates (hg38)	strand	ММ	target_seq	PAM	Position	gene name				
		<u> </u>	0	CAGCGCTACTGCACCGACAC	CGG	E	PEPD (on-tar				
	chr19:33512609-33512631	-									
	chr19:33512609-33512631 chr17:74222922-74222944	+	3	CAGCATTTCTGCACCGACAC	TGG	I	TTYH2				
	chr19:33512609-33512631 chr17:74222922-74222944 chr17:55561396-55561418	+	3 1	CAGCATTTCTGCACCGACAC CAGCGCTACTGCACCTACAC	TGG CGG	I E	TTYH2 CTD-2033D24				

Online Table V. Predicted off-target sites of the nine sgRNAs by CCTop.

Position of the off-site	Name of the off-site	Primer Forward (5'-3')	Primer reverse (5'-3')			
LUZP4 (-)	sg25-0ff-1	GGCTTGTGTGGGTGTAGGTT	GGACAACCGTAAGTTGGGGA			
RP4-668J24.2 (E)	sg27-0ff-1	CAACTCGCCACCCCTAAACG	CCAGGTCTGAGGGTGCTTGA			
PCBP3 (I)	sg37-off-1	GTAGCTCTGAATGTGCTGATTC	GAG GTA GGA GGT AGG GGT AG			
AC011225.1 (-)	sg37-off-2	AGCTTCTCCCAGGGTATCAA	GCT GAA ATT GAG TAC TGT ATG ATG			
USP43 (-)	sg38-off-1	TTCTGGAGCACCAAGTCACG	GCACTTCATGTCTGTACTCAAGTT			
SCN1A (I)	sg38-off-2	AGGCAAAGTCAGTCCATTGT	CACAGTGAAGTCCAGTGCAGA			
Metazoa_SRP (I)	sg38-off-3	AGCCATGGTGAATTCTTTTGGG	GCCCACTTTCCATGGGCTA			
CDH4 (I)	sg39-off-1	CACGCCTGTCTTGGGAACAA	ACCACAATCCGAACATCTGAGT			
PTPRF (I)	sg39-off-2	TCCCAAAGACCTTCCTCGTGT	CCAACACCTGGGGACACTCG			
CTA-223H9.9 (-)	sg39-off-3	CCCAAGGTTGGGTGGTCAG	ACTTCTGGACAGGTTGCAGG			
PRR5 (I)	sg41-off-1	TCTTCTCAGAGTTCAGGGAGGC	CAGTTAAGGGCAGTGAACGGG			
CTD-2033D24.2 (E)	sg41-off-2	GTAGCGCTGAGTCTCCTCTT	CCCTTTCTGAGCTTTAATTTTCTCA			
TTYH2 (I)	sg42-off-1	GGAATCAGATGCCTGGGGTG	TGGAATTGATTTGTGCTGGAGTC			
CTD-2033D24.2 (E)	sg42-off-2	GATGAAGCCGTAGCAGCCT	AAGGAAACCCTGAAGGTGCC			
OFD1P3Y (-)	sg42-off-3	AGCACTCACAAACACACAATGC	GCCTGCCTAGTTTTGTAGGG			
Predicted off-target site positon is indicated with gene name (E = exonic; I = intronic; - = intergenic).						

Online Table VI. Primers for PCR of predicted off-target genomic sites.

Online Table VII

Gene name	Primer Forward (5'-3')	Primer reverse (5'-3')
FST	GAAGAAATATAAGAGAATTCGCCACCATGGTCCGCGCGAGGCACCAG	CCGCAGAAGGCAGCGGATCCCTACCACTCTAGAATAGAA
PEPD	GAAGAAATATAAGAGAATTCGCCACCATGGCGGCGGCCACCGGACCC	CCGCAGAAGGCAGCGGATCCCTACTTGGGGCCAGAGAAGGG
PDGFC	GAAGAAATATAAGAGAATTCGCCACCATGAGCCTCTTCGGGCTTCTC	CCGCAGAAGGCAGCGGATCCCTATCCTCCTGTGCTCCCTCT

Online Table VII. Primers for cloning of mRNA expression constructs.