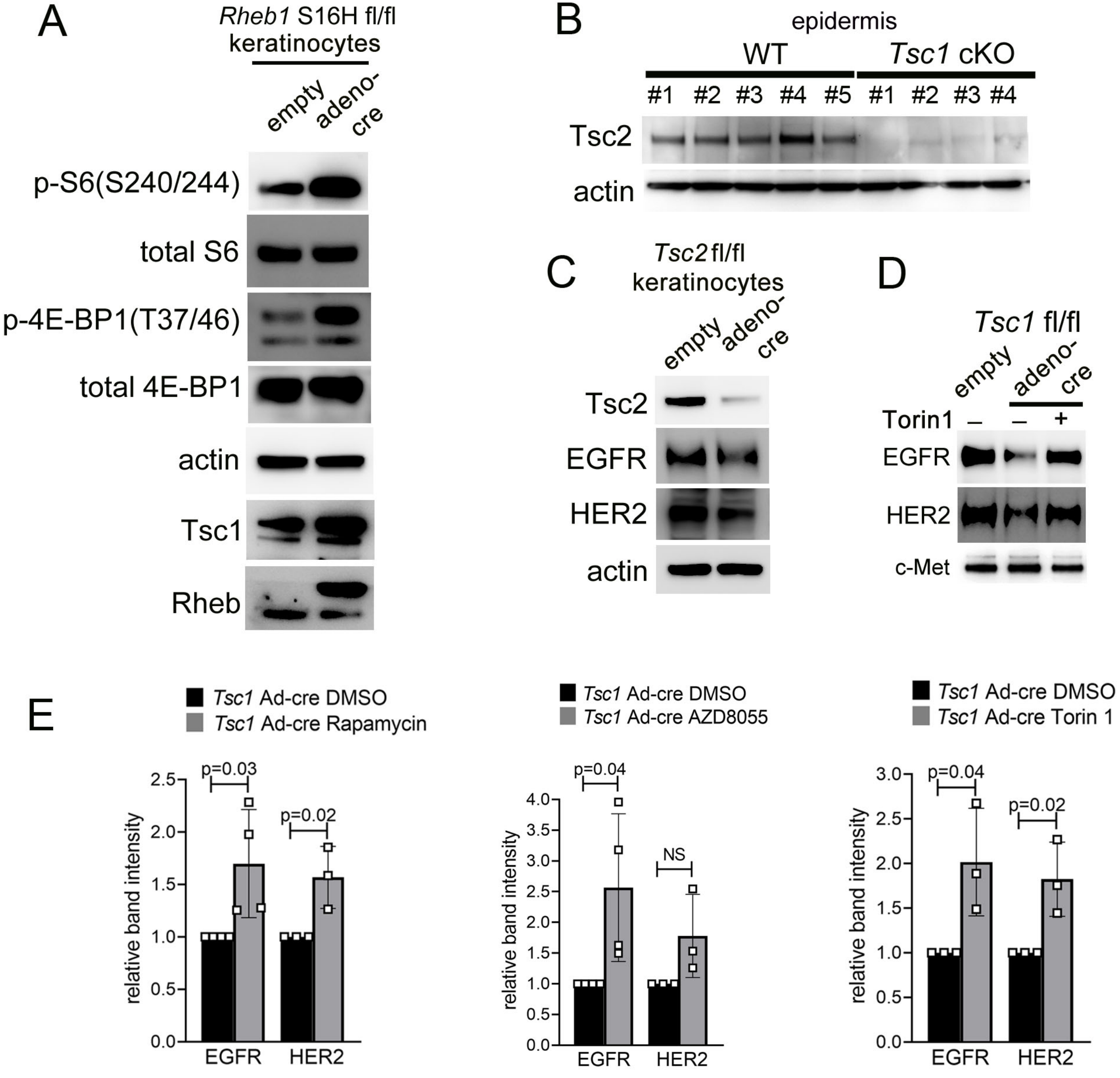
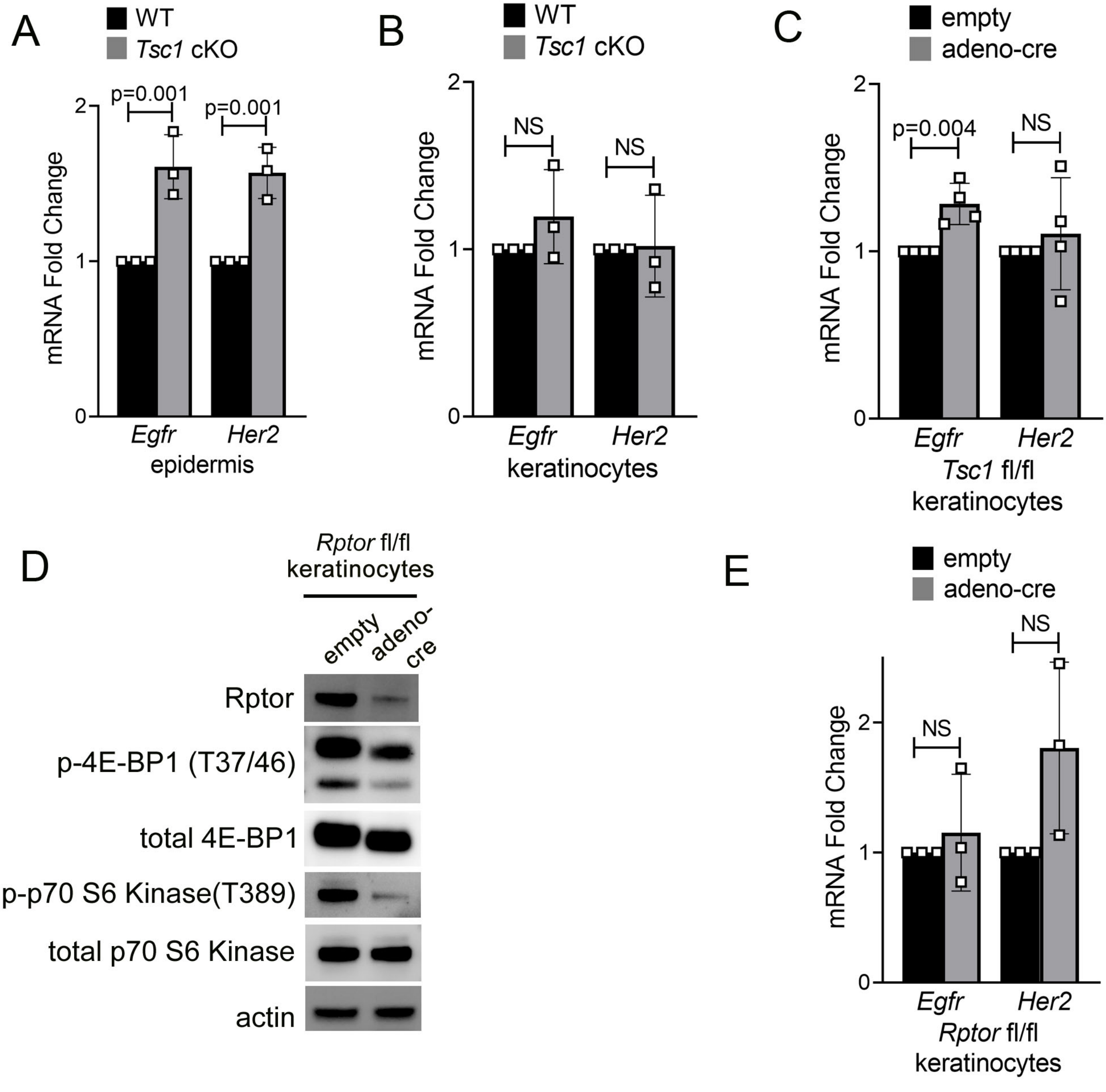
S1


A
Rheb1 S16H fl/fl keratinocytes
empty
adeno-cre
p-S6(S240/244)
total S6
p-4E-BP1(T37/46)
total 4E-BP1
actin
Tsc1
Rheb
B
epidermis
WT
Tsc1 cKO
#1
#2
#3
#4
#5
#1
#2
#3
#4
Tsc2
actin
C
Tsc2 fl/fl keratinocytes
empty
adeno-cre
Tsc2
EGFR
HER2
actin
D
Tsc1 fl/fl
empty
adeno-cre
Torin1 – – +
EGFR
HER2
c-Met
E
Tsc1 Ad-cre DMSO
Tsc1 Ad-cre Rapamycin
p=0.03
p=0.02
relative band intensity
0.0
0.5
1.0
1.5
2.0
2.5
EGFR
HER2
Tsc1 Ad-cre DMSO
Tsc1 Ad-cre AZD8055
p=0.04
NS
relative band intensity
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0
EGFR
HER2
Tsc1 Ad-cre DMSO
Tsc1 Ad-cre Torin 1
p=0.04
p=0.02
relative band intensity
0.0
0.5
1.0
1.5
2.0
2.5
3.0
EGFR
HER2

Supplemental Figure Legends

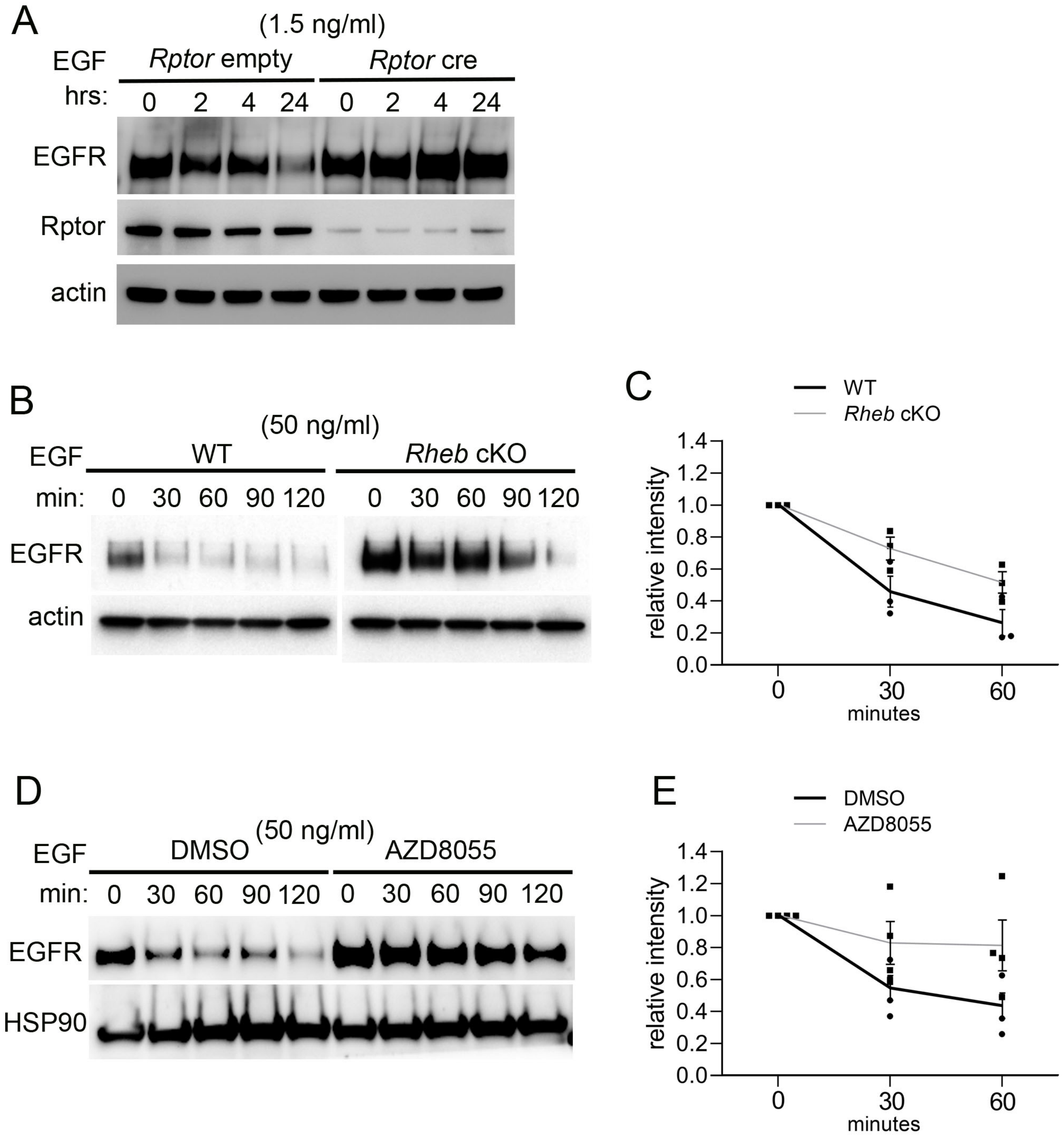
Supplemental Figure S1: Epidermal-specific mTORC1 gain-of-function models show increased mTORC1 activation and down-regulate EGFR and HER2 protein expression in a mTORC1-sensitive manner. (**A**) Immunoblotting of *Rheb1* S16H $^{flox/flox}$ keratinocyte cultures infected with empty or adenoviral cre recombinase for markers of mTORC1 (p-S6, p-4E-BP1) activity. **(B)** *Tsc1* cKO epidermal lysates also show decreased expression of TSC2 by immunoblotting of the same experiment as in Figure 2A. **(C)** Immunoblotting of *Tsc2* $^{flox/flox}$ keratinocyte cultures infected with empty or adenoviral cre recombinase showing decreased EGFR and HER2 protein expression. **(D)** Expression of EGFR and HER2 was decreased in *Tsc1* cre keratinocytes compared to empty controls, and up-regulated in response to Torin1 (1µM, 24 hrs), by immunoblot analyses. Immunoblots are contemporaneous and parallel from the same biological replicate and represent the same experiment as depicted in Figure 7B. **(E)** Densitometry quantification of representative immunoblot experiments shown in Figures 2E and S1D ($r \geq 3$; error bars represent STDEV; p-values by Student's T-test).

S2


A
WT
Tsc1 cKO
mRNA Fold Change
0
1
2
p=0.001
p=0.001
Egfr
Her2
epidermis
B
WT
Tsc1 cKO
mRNA Fold Change
0
1
2
NS
NS
Egfr
Her2
keratinocytes
C
empty
adeno-cre
mRNA Fold Change
0
1
2
p=0.004
NS
Egfr
Her2
Tsc1 fl/fl
keratinocytes
D
Rptor fl/fl
keratinocytes
empty
adeno-cre
Rptor
p-4E-BP1 (T37/46)
total 4E-BP1
p-p70 S6 Kinase(T389)
total p70 S6 Kinase
actin
E
empty
adeno-cre
mRNA Fold Change
0
1
2
NS
NS
Egfr
Her2
Rptor fl/fl
keratinocytes

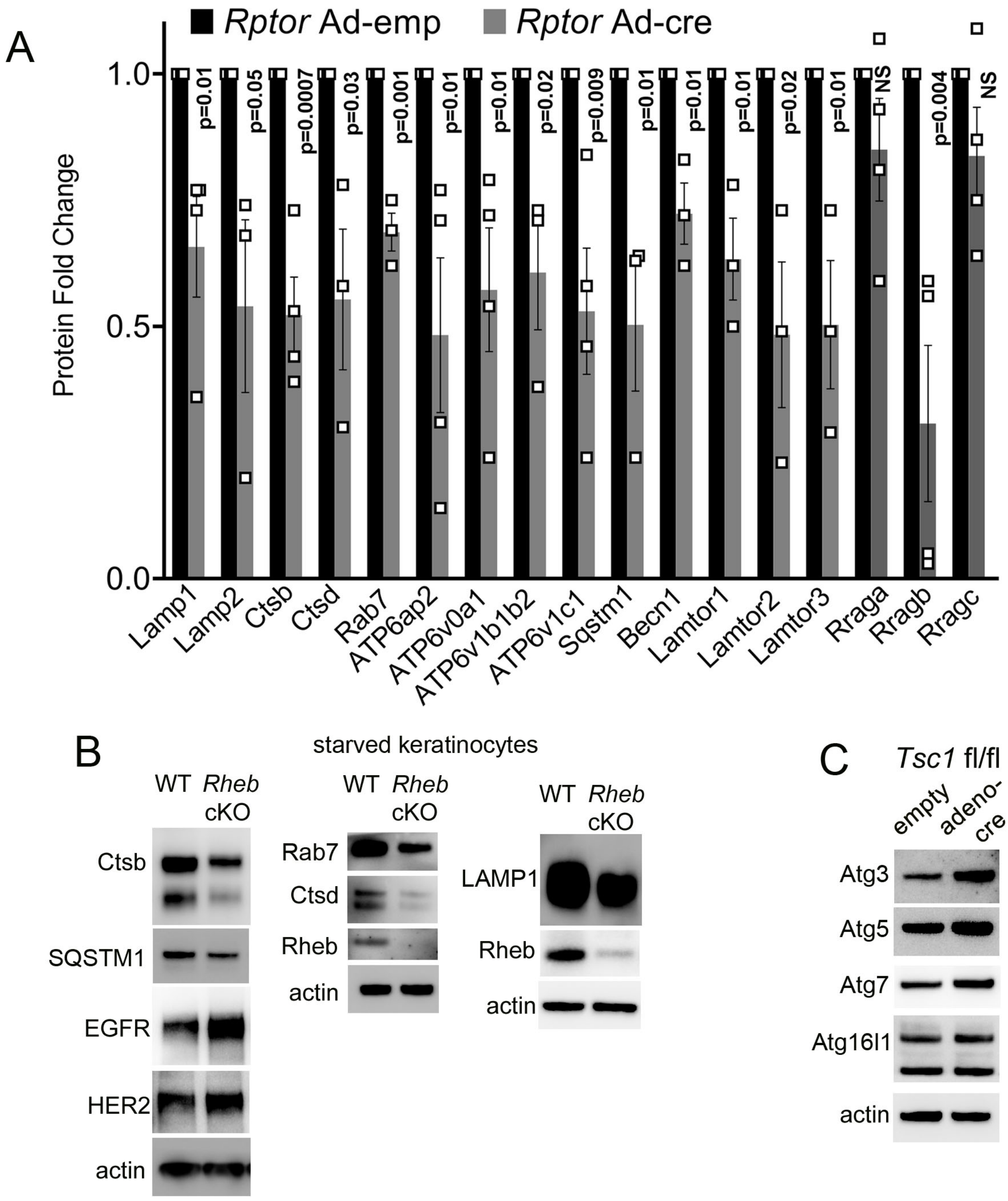
Supplemental Figure S2: EGFR and HER2 transcription are unchanged with epidermal/ keratinocyte *Tsc1* or *Rptor* loss. *Egfr* and *Her2* mRNA levels in (**A**) *Tsc1* cKO epidermal lysates, (**B**) *Tsc1* cKO keratinocyte lysates and(**C**) *Tsc1* cre keratinocyte lysates are minimally altered compared to their respective controls. (r≥3; error bars represent STDEV; p-values by Student's T-test). (**D**) Immunoblotting of *Rptor* $^{\text{flox/flox}}$ keratinocyte cultures infected with empty or adenoviral cre recombinase for markers of mTORC1 (p-4E-BP1, p-p70 S6K) activity. This represents the same experiment depicted in Figure 3A (right panel). (**E**) EGFR and HER2 mRNA levels in *Rptor* cre keratinocyte lysates are minimally altered compared to their respective controls. (r=3; error bars represent STDEV; p-values by Student's T-test).

S3


A
(1.5 ng/ml)
EGF
Rptor empty
Rptor cre
hrs: 0 2 4 24 0 2 4 24
EGFR
Rptor
actin
B
(50 ng/ml)
EGF
WT
Rheb cKO
min: 0 30 60 90 120 0 30 60 90 120
EGFR
actin
C
WT
Rheb cKO
relative intensity
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
0
30
60
minutes
D
(50 ng/ml)
EGF
DMSO
AZD8055
min: 0 30 60 90 120 0 30 60 90 120
EGFR
HSP90
E
DMSO
AZD8055
relative intensity
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
0
30
60
minutes

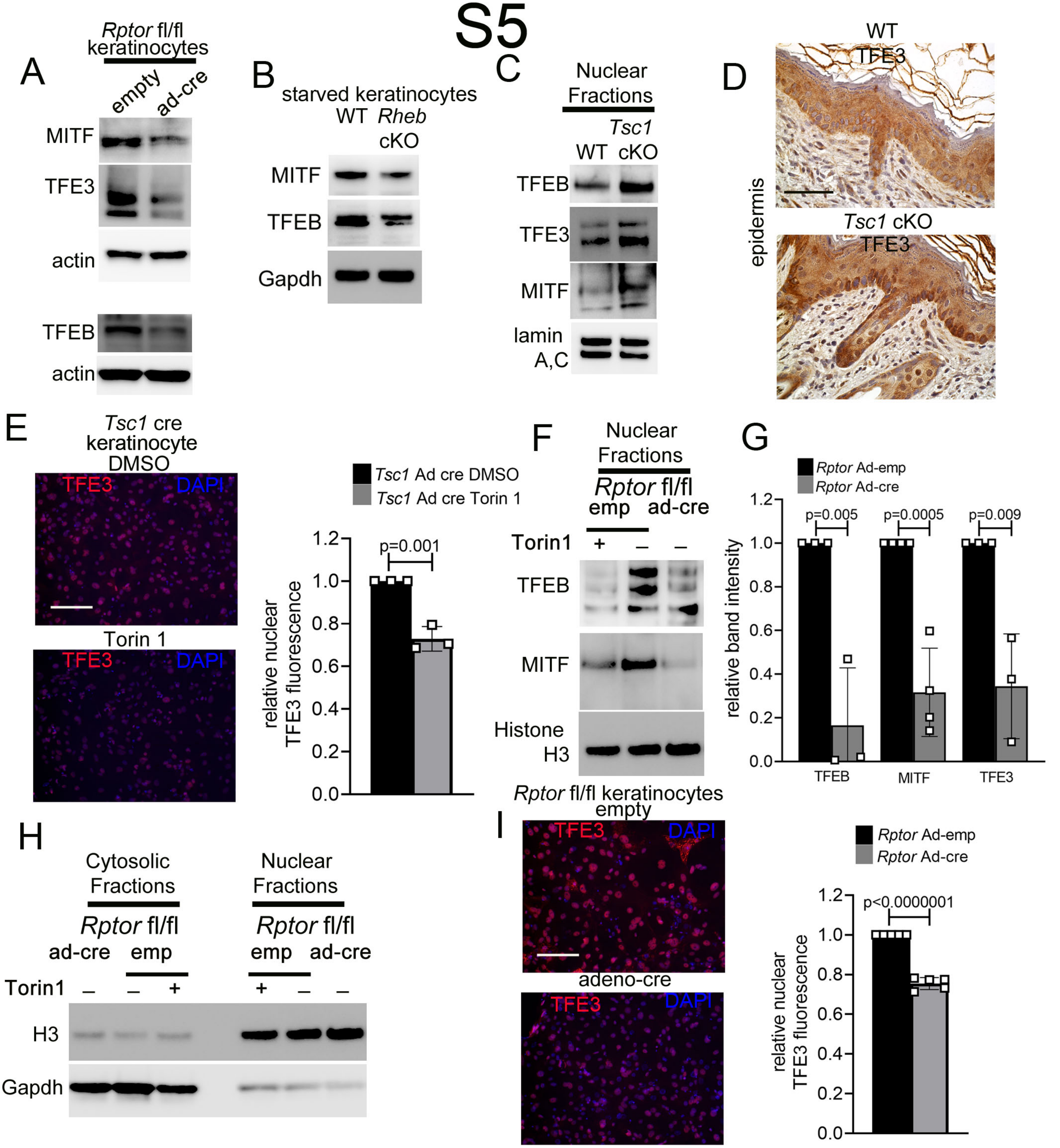
Supplemental Figure S3: mTORC1 inhibition attenuates EGF-induced EGFR degradation. **(A)** Starved empty and *Rptor* cre keratinocytes were stimulated with EGF (1.5 ng/ml) for the indicated times and immunoblotted for EGFR. **(B)** Starved WT and *Rheb* cKO keratinocytes were stimulated with EGF for the indicated times and immunoblotted for EGFR. EGFR degradation curves are presented in **(C)**. Error bars represent STDEV. Immunoblots are representative of three independent experiments. **(D)** Starved DMSO and AZD8055-treated (500 nM) keratinocytes were stimulated with EGF for the indicated times and immunoblotted for EGFR. EGFR degradation curves are presented in **(E)**. Error bars represent STDEV. Immunoblots are representative of three independent experiments.

S4


A
■ Rptor Ad-emp
■ Rptor Ad-cre
Protein Fold Change
1.0
0.5
0.0
p=0.01
p=0.05
p=0.0007
p=0.03
p=0.001
p=0.01
p=0.01
p=0.02
p=0.009
p=0.01
p=0.01
p=0.01
p=0.02
p=0.01
NS
p=0.004
NS
Lamp1
Lamp2
Ctsb
Ctsd
Rab7
ATP6ap2
ATP6v0a1
ATP6v1b1b2
ATP6v1c1
Sqstm1
Becn1
Lamtor1
Lamtor2
Lamtor3
Rraga
Rragb
Rragc
B
starved keratinocytes
WT
Rheb cKO
Ctsb
SQSTM1
EGFR
HER2
actin
WT
Rheb cKO
Rab7
Ctsd
Rheb
actin
WT
Rheb cKO
LAMP1
Rheb
actin
C
Tsc1 fl/fl
empty
adeno-cre
Atg3
Atg5
Atg7
Atg16l1
actin

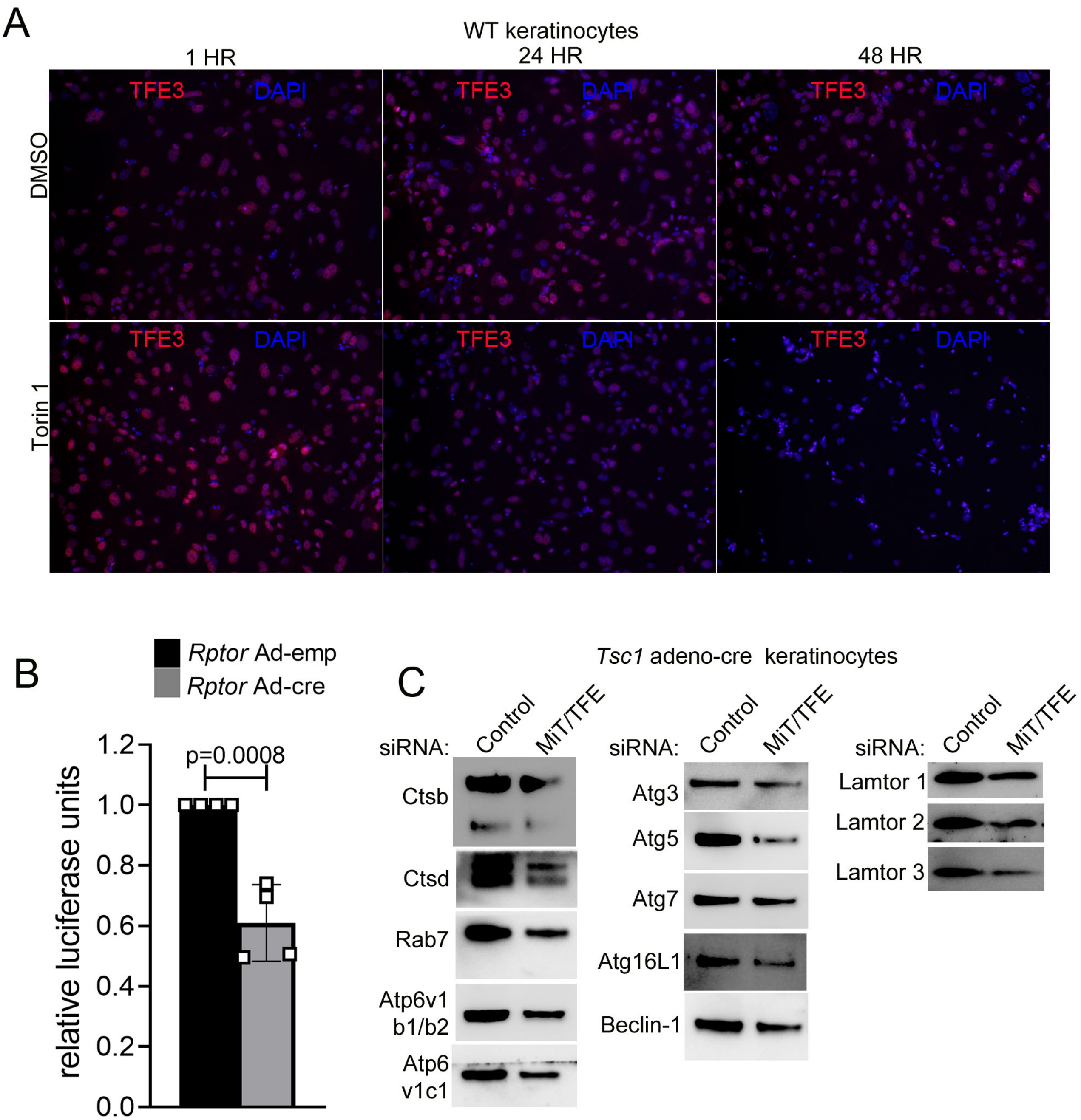
Supplemental Figure S4: mTORC1 promotes MiT/TFE-dependent lysosomal biogenesis. (A) Densitometry quantification of representative immunoblot experiments shown in Figure. 4F, (r≥3; error bars represent SEM; p-values by Student's T-test). **(B)** Expression of lysosomal proteins is decreased in *Rheb* cKO keratinocytes compared to WT controls, by immunoblot analyses. Ctsb, SQSTM1, EGFR, HER2 and actin are contemporaneous parallel immunoblots on the same biological replicate. Ctsd, Rab7, Rheb and paired actin are non-contemporaneous immunoblots from the same biological replicate. LAMP1, Rheb and paired actin were immunoblotted separately using a different biological replicate. **(C)** Expression of multiple MiT/TFE-inducible **a**u**t**opha**g**y related genes (ATG) is increased in *Tsc1* cre keratinocytes compared to empty controls, by immunoblot analyses.

S5


A
Rptor fl/fl keratinocytes
empty
ad-cre
MITF
TFE3
actin
TFEB
actin
B
starved keratinocytes
WT
Rheb cKO
MITF
TFEB
Gapdh
C
Nuclear Fractions
Tsc1
WT
cKO
TFEB
TFE3
MITF
lamin A,C
D
WT TFE3
Tsc1 cKO TFE3
epidermis
E
Tsc1 cre keratinocyte DMSO
TFE3
DAPI
Torin 1
TFE3
DAPI
Tsc1 Ad cre DMSO
Tsc1 Ad cre Torin 1
relative nuclear TFE3 fluorescence
p=0.001
0.0
0.2
0.4
0.6
0.8
1.0
1.2
F
Nuclear Fractions
Rptor fl/fl
emp
ad-cre
Torin1
+
–
–
TFEB
MITF
Histone H3
G
Rptor Ad-emp
Rptor Ad-cre
relative band intensity
p=0.005
p=0.0005
p=0.009
0.0
0.2
0.4
0.6
0.8
1.0
1.2
TFEB
MITF
TFE3
H
Cytosolic Fractions
Rptor fl/fl
ad-cre
emp
Torin1
–
–
+
Nuclear Fractions
Rptor fl/fl
emp
ad-cre
+
–
–
H3
Gapdh
I
Rptor fl/fl keratinocytes empty
TFE3
DAPI
adeno-cre
TFE3
DAPI
Rptor Ad-emp
Rptor Ad-cre
relative nuclear TFE3 fluorescence
p<0.0000001
0.0
0.2
0.4
0.6
0.8
1.0
1.2

Supplemental Figure S5: mTORC1 drives MiT/TFE expression and nuclear localization. (A) Immunoblotting showing decreased expression of MiT/TFE proteins in *Rptor* cre keratinocyte lysates compared to empty controls. TFEB and its paired actin were immunoblotted separately on a different biological replicate. **(B)** Immunoblotting showing decreased expression of MiT/TFE proteins in *Rheb* cKO keratinocyte lysates compared to WT controls. **(C)** Subcellular fractionation and immunoblotting of nuclear lysates demonstrates nuclear enrichment of MiT/TFE proteins in *Tsc1* cKO keratinocytes compared to WT controls. Lamin A/C is used to normalize for nuclear protein. **(D)** Immunohistochemistry showing increased expression of TFE3 in basal epidermal nuclei of P7 *Tsc1* cKO epidermal sections, compared to WT controls. Scale bar=150 µm. **(E)** Immunofluorescence showing decreased nuclear localization of TFE3 in *Tsc1* cre, Torin1-treated keratinocyte cultures (1µM, 24 hrs), compared to DMSO controls. (left panel; Scale bar=150 µm). Quantification of nuclear TFE3 fluorescence (right panel; r=3, n> 1268 cells, p=0.001 by Student's T-test. **(F)** MiT/TFE proteins are decreased in nuclear-fraction immunoblots of *Rptor* cre keratinocytes compared to controls. Lamin A/C and Histone H3 are used to normalize for nuclear protein. Immunoblots are contemporaneous and parallel from the same biological replicate. **(G)** Densitometry quantification of representative immunoblot experiments shown in **(F)** (r≥3; error bars represent STDEV; p-values by Student's T-test). **(H)** Enrichment of nuclear proteins in nuclear extracts of subcellular fractionation experiments is shown using Histone H3 as a control for nuclear protein in the same experiment as Supplementary Figure 5F. **(I)** Immunofluorescence showing decreased nuclear localization of TFE3 in *Rptor* cre keratinocyte cultures, compared to empty controls. (left panel; Scale bar=150 µm). Quantification of nuclear TFE3 fluorescence (right panel; r=5, n> 320 cells, p<0.0000001 by Student's T-test.

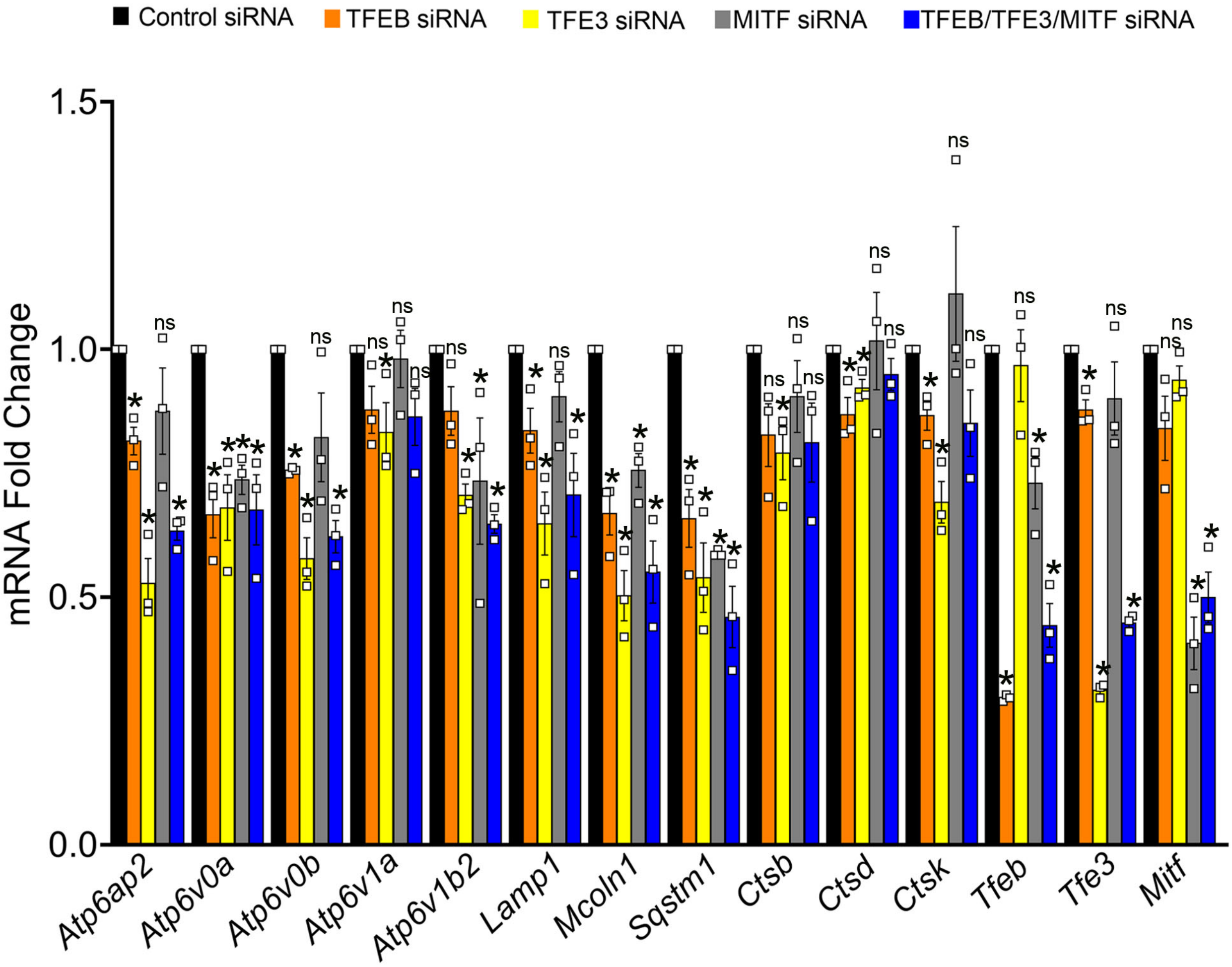
S6


A
WT keratinocytes
1 HR
24 HR
48 HR
DMSO
Torin 1
TFE3
DAPI
B
Rptor Ad-emp
Rptor Ad-cre
relative luciferase units
p=0.0008
0.0
0.2
0.4
0.6
0.8
1.0
1.2
C
Tsc1 adeno-cre keratinocytes
siRNA:
Control
MiT/TFE
Ctsb
Ctsd
Rab7
Atp6v1 b1/b2
Atp6 v1c1
Atg3
Atg5
Atg7
Atg16L1
Beclin-1
Lamtor 1
Lamtor 2
Lamtor 3

Supplemental Figure S6: mTORC1 drives MiT/TFE expression and nuclear localization.

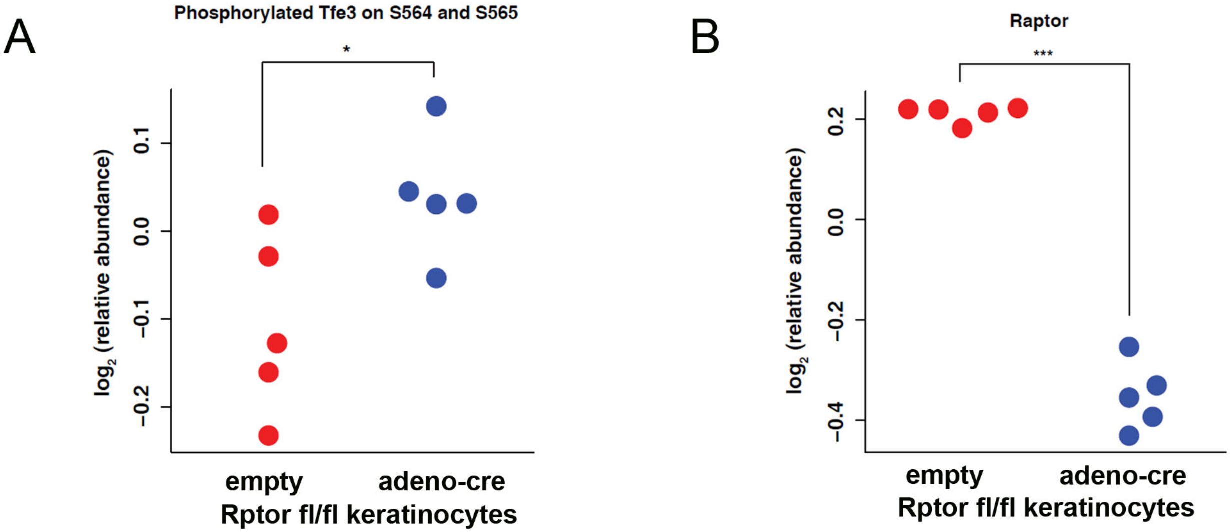
(A) Immunofluorescence showing increased nuclear localization of TFE3 in WT keratinocytes treated with Torin1 for 1hr (left panel), and decreased nuclear localization of TFE3 in response to Torin1 treatment in excess of 24hrs (middle, right panels). (Scale bar=150 µm). **(B)** 4X-CLEAR luciferase reporter activity is decreased in *Rptor* cre keratinocytes, compared to controls. Renilla is used to normalize for luciferase activity. (r=4; error bars represent STDEV; p-values by Student's T-test). **(C)** *Tsc1* cre keratinocytes transfected with triple (TFEB, TFE3 and MITF siRNA) show decreased expression of multiple lysosomal proteins, compared to negative control siRNA, by immunoblot analyses.

S7


Control siRNA
TFEB siRNA
TFE3 siRNA
MITF siRNA
TFEB/TFE3/MITF siRNA
mRNA Fold Change
1.5
1.0
0.5
0.0
Atp6ap2
Atp6v0a
Atp6v0b
Atp6v1a
Atp6v1b2
Lamp1
Mcoln1
Sqstm1
Ctsb
Ctsd
Ctsk
Tfeb
Tfe3
Mitf
ns
*

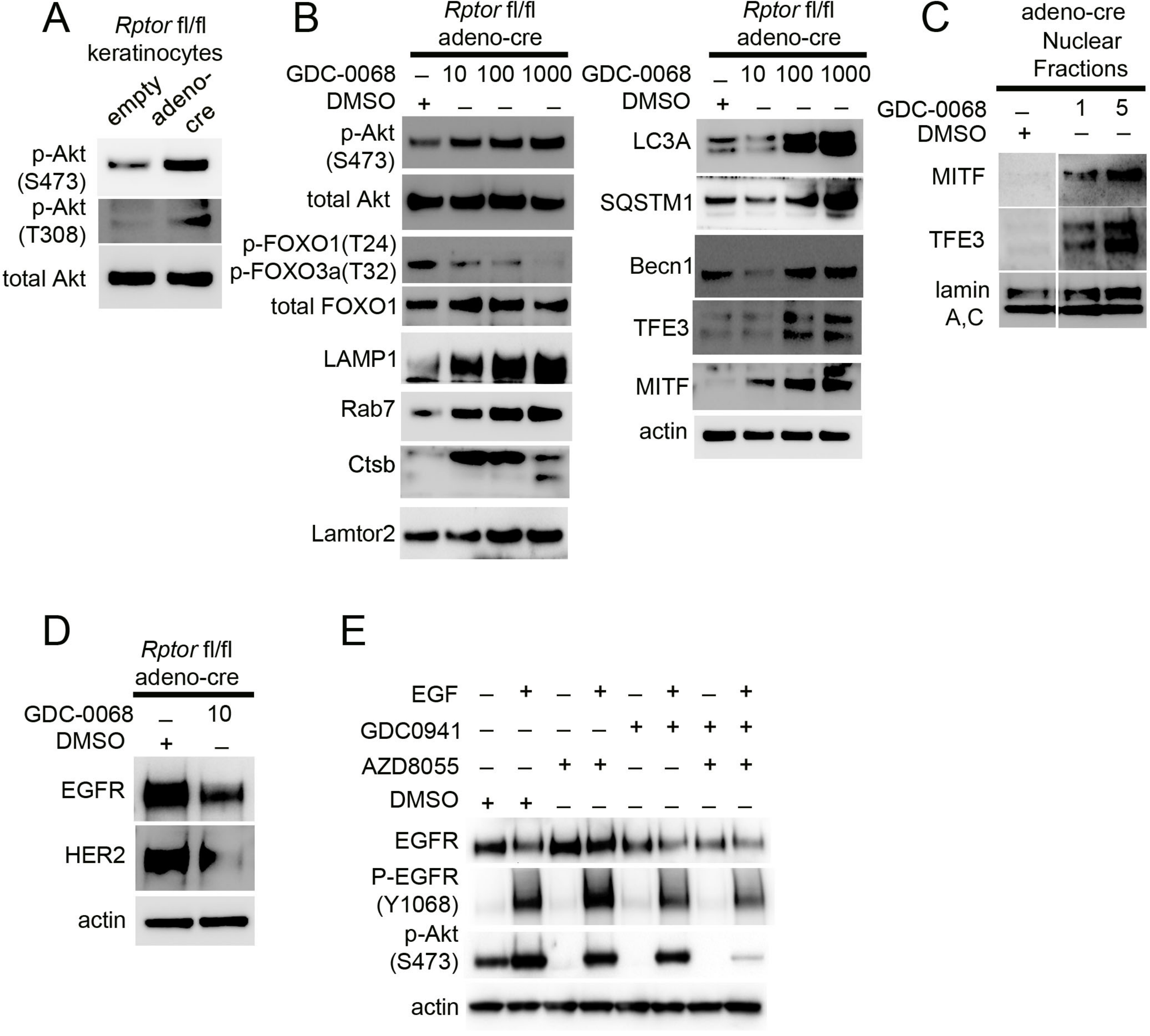
Supplemental Figure S7: MiT/TFE transcription factors drive lysosomal gene expression in *Tsc1* KO keratinocytes. (A) Quantitative real time PCR (qRT-PCR) showing down-regulation of lysosomal CLEAR gene transcripts in *Tsc1* cre keratinocytes, following transient transfection with TFEB, TFE3, MITF or combined triple (TFEB, TFE3 and MITF) siRNA, compared to control siRNA (r=3, error bars represent SEM; * indicate p values < 0.05 by Student's t-test).

S8


A
Phosphorylated Tfe3 on S564 and S565
*
$\log_2$ (relative abundance)
0.1
0.0
−0.1
−0.2
empty
adeno-cre
Rptor fl/fl keratinocytes
B
Raptor
***
$\log_2$ (relative abundance)
0.2
0.0
−0.2
−0.4
empty
adeno-cre
Rptor fl/fl keratinocytes

Supplemental Figure S8: (A) Phosphorylated TFE3: The relative abundance of phosphorylated TFE3 (S564/565) levels was measured by conducting a TMT-based phosphoprotoeme analysis of control or *Rptor* KO mouse primary keratinocytes. **(B)** Total RPTOR: The relative abundance of RPTOR was measured by conducting a TMT-based total proteome analysis of control or *Rptor* KO mouse primary keratinocytes.

S9


A
Rptor fl/fl keratinocytes
empty
adeno-cre
p-Akt (S473)
p-Akt (T308)
total Akt
B
Rptor fl/fl adeno-cre
GDC-0068 – 10 100 1000
DMSO + – – –
p-Akt (S473)
total Akt
p-FOXO1(T24)
p-FOXO3a(T32)
total FOXO1
LAMP1
Rab7
Ctsb
Lamtor2
Rptor fl/fl adeno-cre
GDC-0068 – 10 100 1000
DMSO + – – –
LC3A
SQSTM1
Becn1
TFE3
MITF
actin
C
Rptor fl/fl adeno-cre Nuclear Fractions
GDC-0068 – 1 5
DMSO + – –
MITF
TFE3
lamin A,C
D
Rptor fl/fl adeno-cre
GDC-0068 – 10
DMSO + –
EGFR
HER2
actin
E
EGF – + – + – + – +
GDC0941 – – – – + + + +
AZD8055 – – + + – – + +
DMSO + + – – – – – –
EGFR
P-EGFR (Y1068)
p-Akt (S473)
actin

Supplemental Figure S9: Inhibition of hyperactive AKT in mTORC1-inhibited cells rescues autophagy/ lysosomal biogenesis and downregulates EGFR expression. (A) Immunoblotting showing increased activation of AKT signaling in *Rptor* cre keratinocytes, compared to empty controls. **(B)** Immunoblotting showing a dose-dependent increase in expression of lysosomal, autophagy and MiT/TFE proteins in GDC0068-treated *Rptor* cre keratinocytes (10nM-1000nM for 8hrs). Immunoblots are contemporaneous and parallel from the same biological replicate. **(C)** Immunoblotting of nuclear lysates from GDC0068-treated *Rptor* cre keratinocytes showing a dose-dependent increase in nuclear localization of MiT/TFE proteins (1, 5μM; 8 hrs). All samples were run on the same gel; intermediate lanes between DMSO and GDC were irrelevant and cropped out of the figure. **(D)** Immunoblotting showing decreased expression of EGFR and HER2 in GDC0068-treated *Rptor* cre keratinocytes (10nM 24hrs). **(E)** EGF-stimulated, EGFR auto-phosphorylation is enhanced and EGFR degradation is attenuated in AZD8055-treated keratinocytes (500nM, 24hrs). Pretreatment of AZD8055-treated keratinocytes with the PI3K α/δ inhibitor GDC-0941 (1 μM), prior to EGF stimulation, decreased EGF-induced EGFR auto-phosphorylation and increased EGF-stimulated EGFR degradation.

Supplemental Methods

Microarray analysis: Mouse epidermis was separated from the dermis following incubation of E19.5 pup skin with 3.8% Ammonium thiocynate (A7149, Sigma-Aldrich) for 10 minutes at room temperature. The epidermal sheet was homogenized in TRIzol and total RNA prepared using the TRIzol RNA extraction protocol (Thermo Fisher Scientific) at the Johns Hopkins Deep Sequencing & Microarray Core Facility. Integrity and concentration of RNA were evaluated using the Bioanalyzer 2100 (Agilent Technologies, Santa Clara, CA USA). Labeled cDNA probes were synthesized from reverse-transcribed mRNA templates and hybridized to the Affymetrix GeneChip® Mouse Transcriptome Array MTA 1.0 (Affymetrix Inc., Santa Clara, CA USA). Samples from six biological replicates each of *Rptor* WT and *Rptor* cKO mice were analyzed. Raw data generated as CEL files by the Affymetrix Expression Console were imported into the Partek Genomics Suite v6.6 for analysis. Data were normalized and log2 transformed with the RMA (Robust Multi-Array Average) algorithm, underwent quality control, and were compared using a two tailed one-way ANOVA between their two biological classes: *Rptor* cKO and *Rptor* WT. The list of 1,176 highly differentially expressed genes, with fold changes greater than 2 S.D. between *Rptor* WT versus *Rptor* cKO, is in Supplementary table S1 online. **Gene Set Enrichment Analysis, GSEA:** (http://www.broad.mit.edu/gsea/) was used to evaluate whether lysosomal gene expression was differentially regulated in this comparison. A set of 360 lysosomal genes was downloaded from the Mouse Lysosome Gene Database, mLGDB, (http://lysosome.unipg.it/mouse.php) and mapped to our dataset and uploaded to GSEA. This subset of 360 genes was compared to the universe of all the array, collapsed to genes, and the results indicated a Normalized Enrichment Score (NES) of -5.5024543 with Nominal p-value, FDR q-value, and FWER p-values of 0.0, all of which indicate the great likelihood that these lysosomal genes are more highly expressed in *Rptor* WT than in *Rptor* cKO cells.

Phosphoproteome analysis

Protein extraction, digestion, and labeling: The mouse primary keratinocytes were sonicated in 8 M urea and 50 mM triethylammonium bicarbonate (TEAB) with 35% amplitude for 1 min. Protein lysates were centrifuged at 16,000 x g at 4°C to exclude cell debris pelleting at the bottom of a tube, and protein concentration was estimated using a bicinchoninic acid (BCA) assay. A total of 1 mg of each sample was reduced with 10 mM dithiothreitol at room temperature (RT) for one hour and alkylated with 30 mM iodoacetamide for 20 minutes in the dark. The protein samples were digested with Lys-C (1:100) at 37°C for 3 h followed by sequencing-grade trypsin (1:50) overnight at 37°C. The resulting peptides were desalted with Sep-Pak C18 Plus Light cartridges (Waters Corporation, Milford, MA) and labeled with 10-plex TMT reagent according to the manufacturer's instructions (Thermo Fisher Scientific). The labeling reaction was performed for one hour at RT, followed by quenching with 100 mM Tris-HCl (pH 8.0). The peptides were pooled and pre-fractionated by basic pH reversed-phase liquid chromatography (bRPLC) into 96 fractions, followed by concatenation into 24 fractions by combining every 24th fractions. Briefly, Agilent 1260 offline LC system was used for bRPLC fractionation, which includes a binary pump, VWD detector, an autosampler, and an automatic fraction collector. In brief, lyophilized samples were reconstituted in solvent A (10 mM TEAB, pH 8.5) and loaded onto XBridge C_{18}, 5 µm 250 × 4.6 mm column (Waters, Milford, MA). Peptides were resolved using a gradient of 3 to 50% solvent B (10 mM TEAB in acetonitrile, pH 8.5) at a flow rate of 1 ml per min over 50 min collecting 96 fractions. Subsequently, 10% of the fractions were concatenated into 24 fractions for total proteome analysis and the remaining samples were concatenated into 12 fractions for phosphopeptide enrichment. The concatenated samples were vacuum dried using a SpeedVac.

Phosphopeptide enrichment

The enrichment of phosphopeptides was conducted as described by Mertins et al. (PMID: 23749302). Briefly, nickel ions were stripped out from Ni-NTA superflow agarose beads (QIAGEN) by washing with water thrice, incubating with 100 mM EDTA, pH 8.0 at RT for 30 min with rotation and washing with water thrice. Subsequently, the beads were chelated with iron ions by incubating in 10 mM $FeCl_3$ (Sigma, 451469) at RT for 30 min with rotation and washing with water thrice. The dried peptide fractions (0.75 mg of peptide per fraction) were reconstituted in 750 µl of 60% acetonitrile/0.1% trifluoroacetic acid followed by diluting with a 1 volume of 100% acetonitrile/0.1% trifluoroacetic acid to obtain a final 80% acetonitrile/0.1% trifluoroacetic acid peptide solution at a concentration of 0.5 µg/µl. The prepared 10 µl of beads (20 ul of slurry) was added to each fraction and incubated at RT for 30 min. To elute phosphopeptides from the beads, Empore C_{18} StageTips (3M, 2315) were prepared by equilibrating with 100 µl of methanol twice, 50 µl of 50% acetonitrile/0.1% formic acid twice and 100 µl of 1% formic acid twice. The peptide-bead mixture was loaded onto the prepared StageTips and washed with 50 µl of 80% acetonitrile/0.1% trifluoroacetic acid twice followed by 100 µl of 1% formic acid once. The phosphopeptides were eluted from the beads to the C_{18} disk with 70 µl of 500 mM dibasic sodium phosphate, pH 7.0 (Sigma, S9763) thrice. To elute the phosphopeptides from the C_{18} disk, the StageTips were washed with 100 µl of 1% FA thrice followed by elution with 60 µl of 50% acetonitrile/0.1% formic acid. The eluted solution was completely dried in a SpeedVac.

Mass spectrometry

The peptides were analyzed on an Orbitrap Fusion Lumos Tribrid Mass Spectrometer coupled with the RSLCnano nano-flow liquid chromatography system (Thermo Fisher Scientific). The peptides from each fraction were reconstituted in 15 µl 0.5% formic acid and all the 15 µl were loaded on an Acclaim PepMap100 Nano-Trap Column (100 µm × 2 cm, Thermo Fisher Scientific) packed with 5 µm C_{18} particles at a flow rate of 5 µl per minute. Peptides were resolved at 250-nl/min flow rate using a linear gradient of 10% to 35% solvent B (0.1% formic acid in 95% acetonitrile) over 95 minutes on an EASY-Spray column (50 cm x 75 µm ID, Thermo Fisher Scientific) packed with 2 µm C18 particles, which was fitted with an EASY-Spray ion source that was operated at a voltage of 2.0 kV. Mass spectrometry analysis was carried out in a data-dependent manner with a full scan in the mass-to-charge ratio (*m/z*) range of 300 to 1,500 in the "Top Speed" setting, three seconds per cycle. MS1 and MS2 were acquired for the precursor ions and the peptide fragmentation ions, respectively. MS1 scans were measured at a resolution of 120,000 at an *m/z* of 200. MS2 scans were acquired by fragmenting precursor ions using the higher-energy collisional dissociation method and detected at a mass resolution of 50,000, at an *m/z* of 200. Automatic gain control for MS1 was set to one million ions for MS1 and was set to 0.05 million ions for MS2. Maximum ion injection time was set to 50 ms for MS1 and 100 ms for MS2. Higher-energy collisional dissociation was set to 35 with a stepped collision energy of 5% for MS2. Precursor isolation window was set to 1.6 *m/z* with 0.4 *m/z* of offset. Dynamic exclusion was set to 35 seconds, and singly-charged ions were rejected. Internal calibration was carried out using the lock mass option (*m/z* 445.1200025) from ambient air.

Data analysis

Proteome Discoverer (v 2.1; Thermo Scientific) suite was used for quantitation and identification. During MS/MS preprocessing, the top 10 peaks in each window of 100 *m/z* were selected for database search. The tandem mass spectrometry data were then searched using SEQUEST algorithms against a mouse RefSeq database (version 85) with common contaminant proteins. The search parameters used were as follows: a) trypsin as a proteolytic enzyme (with up to two missed cleavages); b) peptide mass error tolerance of 10 ppm; c) fragment mass error tolerance of 0.02 Da; and d) carbamidomethylation of cysteine (+57.02146 Da) and TMT tags (+229.162932 Da) on lysine and peptide N-termini as a fixed modification; d) oxidation (+15.99492 Da) of methionine and phosphorylation (+79.966331 Da) of serine, threonine and tyrosine as a variable modification. For the total proteome analysis, the phosphorylation of serine, threonine and tyrosine as a variable modification was not considered. The minimum peptide length was set to 6 amino acids. Peptides and proteins were filtered at a 1 % false-discovery rate (FDR) at the PSM level using percolator node and at the protein level using protein FDR validator node, respectively. The protein quantification was performed with the following parameters and methods. The most confident centroid option was used for the integration mode while the reporter ion tolerance was set to 20 ppm. The MS order was set to MS2 and the activation type was set to HCD. Unique and razor peptides both were used for peptide quantification while protein groups were considered for peptide uniqueness. Reporter ion abundance was computed based on signal-to-noise ratios and the missing intensity values were replaced with the minimum value. The quantification value corrections for isobaric tags, average reporter signal-to-noise threshold, and data normalization were disabled. Protein grouping was performed with strict parsimony principle to generate the final protein groups. All proteins sharing the same set or subset of identified peptides were grouped while protein groups with no unique peptides were filtered out. Proteome Discoverer iterated through all spectra and selected PSM with the highest number of unambiguous and unique peptides. Subsequent to protein identification and quantification, the protein table was exported to Perseus 1.5.2.6 software for the generation of a volcano plot (77). Before generating a volcano plot, the signal-to-noise values of the reporter ions were divided by the median value followed by dividing each column by the median value of the corresponding column to remove any systemic deviation. Finally, each value was log2-transformed.

Supplemental Table S1: Differentially expressed genes (>2SD) in *Rptor* cKO vs WT epidermis at E18.5

Transcript ID	*cKO_Rptor vs. WT (p-value)*	*cKO_Rptor vs. WT Lin(FC)*	*cKO_Rptor vs. WT Log2(FC)*	*cKO_Rptor vs. WT (Description)*	*SD cKO_Rptor vs. WT*	*Entrez Gene Symbol*	*Gene Title*	*CytoLoc*	*Entrez Gene ID*
TC1500002268.mm.1	0.0015847	7.16066	2.84009	Null_Rptor up vs WT	> +6σ	Krt6a	keratin 6A	15 F2|15 56.97 cM	16687
TC0800001984.mm.1	1.25E-05	5.60296	2.48619	Null_Rptor up vs WT	+6σ	Nrg1	neuregulin 1	8|8 A3	211323
TC0400002812.mm.1	0.0013004	5.50825	2.46159	Null_Rptor up vs WT	+6σ	Tnc	tenascin C	4 C1|4 34.06 cM	21923
TC1000001207.mm.1	0.001357	5.40408	2.43405	Null_Rptor up vs WT	+6σ	Dusp6	dual specificity phosphatase 6	10|10 D1	67603
TC1100003762.mm.1	0.0052178	4.7451	2.24644	Null_Rptor up vs WT	+6σ	Krt16	keratin 16	11|11 D	16666
TC0100000718.mm.1	0.0014564	4.71737	2.23798	Null_Rptor up vs WT	+6σ	Ccl20	chemokine (C-C motif) ligand 20	1 C5|1 42.69 cM	20297
TC1000001490.mm.1	0.0002876	4.16394	2.05795	Null_Rptor up vs WT	+6σ	Wif1	Wnt inhibitory factor 1	10|10 D2	24117
TC0900000598.mm.1	0.002125	4.0978	2.03485	Null_Rptor up vs WT	+6σ	Plet1	placenta expressed transcript 1	9|9 A5.3	76509
TC0300003087.mm.1	0.0007718	4.04175	2.01498	Null_Rptor up vs WT	+6σ	Cyr61	cysteine rich protein 61	3 H2|3 70.18 cM	16007
TC1500000658.mm.1	0.0001324	4.02012	2.00724	Null_Rptor up vs WT	+6σ	Lgals1	lectin, galactose binding, soluble 1	15 E1|15 37.7 cM	16852
TC1500002265.mm.1	0.004063	3.88215	1.95686	Null_Rptor up vs WT	+6σ	Gm5476	type II keratin Kb17P pseudogene	15 F2|15	432985
TC0700000961.mm.1	0.0004185	3.54195	1.82454	Null_Rptor up vs WT	+6σ	Ndn	necdin	7 34.36 cM|7 C	17984
TC0400003917.mm.1	1.90E-05	3.44293	1.78364	Null_Rptor up vs WT	+6σ	Pdpn	podoplanin	4|4 E1	14726
TC1600001616.mm.1	0.0296254	3.37469	1.75476	Null_Rptor up vs WT	+6σ	Upk1b	uroplakin 1B	16|16 B4	22268
TC0500000928.mm.1	0.0025462	3.291	1.71853	Null_Rptor up vs WT	+6σ	Anxa3	annexin A3	5 E3|5 47.29 cM	11745
TC1700001598.mm.1	0.0019203	3.29065	1.71837	Null_Rptor up vs WT	+6σ	Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	17|17 A3.3	27279
TC0600003074.mm.1	9.80E-05	3.2824	1.71475	Null_Rptor up vs WT	+6σ	Slc2a3	solute carrier family 2 (facilitated glucose transporter), member 3	6 F1|6 57.82 cM	20527
TC1900001415.mm.1	0.0435191	3.19623	1.67637	Null_Rptor up vs WT	+6σ	Acta2	actin, alpha 2, smooth muscle, aorta	19|19 C1	11475
TC0300001704.mm.1	0.0889976	3.17032	1.66463	Null_Rptor up vs WT	+6σ	Cpa3	carboxypeptidase A3, mast cell	3 A2|3 6.25 cM	12873
TC0600000277.mm.1	0.0006221	3.16241	1.66102	Null_Rptor up vs WT	+6σ	Mest	mesoderm specific transcript	6 A3.3|6 12.53 cM	17294
TC0500000855.mm.1	0.0021985	3.11358	1.63857	Null_Rptor up vs WT	+6σ	Epgn	epithelial mitogen	5|5 E1	71920
TC1100003814.mm.1	0.0008212	3.10228	1.63333	Null_Rptor up vs WT	+6σ	Etv4	ets variant 4	11 D|11 65.48 cM	18612
TC0600000334.mm.1	0.0051704	3.07901	1.62247	Null_Rptor up vs WT	+6σ	Gm19966	predicted gene, 19966	6|6 15.12 cM	1E+08
TC0700000005.mm.1	0.0002161	3.05785	1.61252	Null_Rptor up vs WT	+6σ	Myadm	myeloid-associated differentiation marker	7 A1|7 1.92 cM	50918

TC0100001028.mm.1	0.0042242	3.0244	1.59665	Null_Rptor up vs WT	+6σ	Serpinb11	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 11	1|1 E2.1	66957
TC1200000951.mm.1	0.0008295	3.0221	1.59555	Null_Rptor up vs WT	+6σ	Flrt2	fibronectin leucine rich transmembrane protein 2	12|12 E	399558
TC0100003715.mm.1	0.0004945	2.94696	1.55923	Null_Rptor up vs WT	+6σ	Capn2	calpain 2	1|1 H5	12334
TC1700001484.mm.1	0.0079487	2.78524	1.4778	Null_Rptor up vs WT	+6σ	Thbs2	thrombospondin 2	17 A2|17 8.95 cM	21826
TC0300001031.mm.1	6.68E-06	2.76468	1.46711	Null_Rptor up vs WT	+6σ	Ngf	nerve growth factor	3 F2.2|3 45.25 cM	18049
TC1400002844.mm.1	6.25E-05	2.70965	1.43811	Null_Rptor up vs WT	+6σ	Gm3591	predicted gene 3591	14 A1|14	1E+08
TC1000001190.mm.1	0.0200542	2.70309	1.43461	Null_Rptor up vs WT	+6σ	Lum	lumican	10 C3|10 50.32 cM	17022
TC1100003584.mm.1	0.0021416	2.64827	1.40505	Null_Rptor up vs WT	+6σ	Itga3	integrin alpha 3	11 D|11 59.01 cM	16400
TC1700000752.mm.1	0.0036175	2.61492	1.38677	Null_Rptor up vs WT	+6σ	Zfp57	zinc finger protein 57	17 B1|17	22715
TC1400002794.mm.1	0.0001593	2.60363	1.38052	Null_Rptor up vs WT	+6σ	Gm3173	predicted gene 3173	14 A1|14	1E+08
TC1400002108.mm.1	0.0621104	2.58323	1.36918	Null_Rptor up vs WT	+6σ	Cma1	chymase 1, mast cell	14 C3|14 28.19 cM	17228
TC0200003512.mm.1	0.0035883	2.56212	1.35734	Null_Rptor up vs WT	+6σ	Rnd3	Rho family GTPase 3	2|2 C1.1	74194
TC1500002266.mm.1	0.001589	2.53906	1.3443	Null_Rptor up vs WT	+6σ	Gm5414	predicted gene 5414	15|15 F2	406223
TC1600001379.mm.1	0.0008179	2.52361	1.33549	Null_Rptor up vs WT	+6σ	Etv5	ets variant 5	16|16 B1	104156
TC0100001510.mm.1	0.0475777	2.52044	1.33368	Null_Rptor up vs WT	+6σ	Dpt	dermatopontin	1|1 H2.2	56429
TC0700000773.mm.1	0.0002201	2.51885	1.33277	Null_Rptor up vs WT	+6σ	Klk10	kallikrein related-peptidase 10	7 B3|7 28.26 cM	69540
TC1300002711.mm.1	0.0016092	2.50926	1.32726	Null_Rptor up vs WT	+6σ	Fst	follistatin	13|13 D2.2	14313
TC1100001692.mm.1	0.000168	2.50743	1.32621	Null_Rptor up vs WT	+6σ	Mdk-ps1	midkine pseudogene 1	11 E1|11 66.39 cM	17243
TC1400002666.mm.1	0.0273826	2.50467	1.32462	Null_Rptor up vs WT	+6σ	Spry2	sprouty homolog 2 (Drosophila)	14 E2.3|14 56.16 cM	24064
TC1400002786.mm.1	0.0009382	2.48685	1.31432	Null_Rptor up vs WT	+6σ	Gm3020	predicted gene 3020	14 A1|14	1E+08
TC0300002415.mm.1	0.118454	2.47889	1.3097	Null_Rptor up vs WT	+6σ	Lce3a	late cornified envelope 3A	3 F1|3	545548
TC0900000047.mm.1	0.16701	2.45389	1.29507	Null_Rptor up vs WT	+6σ	Mmp3	matrix metallopeptidase 3	9 A1|9 2.46 cM	17392
TC1400002787.mm.1	0.0001053	2.44511	1.2899	Null_Rptor up vs WT	+6σ	Gm3002	alpha-takusan pseudogene	14 A1|14	1E+08
TC0700004515.mm.1	0.0033879	2.44164	1.28785	Null_Rptor up vs WT	+6σ	Ifitm3	interferon induced transmembrane protein 3	7|7 F5	66141
TC1400002845.mm.1	0.0001935	2.42721	1.2793	Null_Rptor up vs WT	+6σ	Gm2897	predicted gene 2897	14 A1|14	1E+08
TC1400002841.mm.1	0.0006801	2.42052	1.27532	Null_Rptor up vs WT	+6σ	Gm3468	predicted gene 3468	-	1E+08
TC1400002848.mm.1	0.0002042	2.41252	1.27054	Null_Rptor up vs WT	+6σ	Gm10406	predicted gene 10406	14|14 A1	1E+08
TC1400002784.mm.1	0.0007441	2.40875	1.26829	Null_Rptor up vs WT	+6σ	Gm3020	predicted gene 3020	14 A1|14	1E+08

TC1400002856.mm.1	0.0008273	2.39786	1.26175	Null_Rptor up vs WT	+6σ	Gm3383	predicted gene 3383	14 A1|14	1E+08
TC1400001517.mm.1	0.0006627	2.38646	1.25487	Null_Rptor up vs WT	+6σ	Gm2237	predicted gene 2237	14 A3|14	1E+08
TC1400002838.mm.1	0.0008377	2.38454	1.25371	Null_Rptor up vs WT	+6σ	Gm3383	predicted gene 3383	14 A1|14	1E+08
TC0900002254.mm.1	0.0045312	2.3827	1.2526	Null_Rptor up vs WT	+6σ	Ncam1	neural cell adhesion molecule 1	9 A5.3|9 26.83 cM	17967
TC1400002853.mm.1	0.0005709	2.38253	1.2525	Null_Rptor up vs WT	+6σ	Gm2897	predicted gene 2897	14 A1|14	1E+08
TC1700001954.mm.1	0.020055	2.38142	1.25182	Null_Rptor up vs WT	+6σ	Tnf	tumor necrosis factor	17 B1|17 18.59 cM	21926
TC1500002267.mm.1	0.002943	2.37727	1.24931	Null_Rptor up vs WT	+6σ	Gm5478	predicted pseudogene 5478	15 F2|15	432987
TC1400002843.mm.1	0.0012134	2.37157	1.24584	Null_Rptor up vs WT	+6σ	Gm3411	predicted gene 3411	14 A1|14	1E+08
TC1600000536.mm.1	0.001803	2.36866	1.24407	Null_Rptor up vs WT	+3σ	Fstl1	follistatin-like 1	16 B3|16 26.48 cM	14314
TC1400002783.mm.1	0.001157	2.36328	1.24079	Null_Rptor up vs WT	+3σ	Gm2956	predicted gene 2956	14 A1|14	1E+08
TC0700000265.mm.1	0.0128846	2.35891	1.23812	Null_Rptor up vs WT	+3σ	Mill1	MHC I like leukocyte 1	7 A3|7 9.15 cM	266815
TC0100001451.mm.1	0.0116121	2.35869	1.23798	Null_Rptor up vs WT	+3σ	4930523C07Rik	RIKEN cDNA 4930523C07 gene	1|1 H1	67647
TC0900002751.mm.1	0.0021466	2.3563	1.23652	Null_Rptor up vs WT	+3σ	Htr1b	5-hydroxytryptamine (serotonin) receptor 1B	9 E1|9 44.61 cM	15551
TC0500003637.mm.1	0.0005256	2.34701	1.23082	Null_Rptor up vs WT	+3σ	Slc7a1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	5 G3|5 88.48 cM	11987
TC0400001921.mm.1	0.019409	2.33745	1.22494	Null_Rptor up vs WT	+3σ	Nppb	natriuretic peptide type B	4 E2|4 78.57 cM	18158
TC1000003023.mm.1	8.10E-05	2.33679	1.22453	Null_Rptor up vs WT	+3σ	Hmga2	high mobility group AT-hook 2	10 D2|10 67.94 cM	15364
TC1400002847.mm.1	8.96E-05	2.32907	1.21976	Null_Rptor up vs WT	+3σ	Gm3667	predicted gene 3667	14 A1|14	1E+08
TC1400002792.mm.1	0.0002406	2.32783	1.21899	Null_Rptor up vs WT	+3σ	Gm2897	predicted gene 2897	14 A1|14	1E+08
TC1100000648.mm.1	0.0169604	2.32387	1.21653	Null_Rptor up vs WT	+3σ	Gm12238	predicted gene 12238	11|11 B1.3	1E+08
TC0600000331.mm.1	0.000987	2.32264	1.21576	Null_Rptor up vs WT	+3σ	Cald1	caldesmon 1	6 B1|6 15.07 cM	109624
TC1400000040.mm.1	8.26E-06	2.32209	1.21543	Null_Rptor up vs WT	+3σ	Gm3317	predicted gene 3317	14 A1|14	666329
TC1400002785.mm.1	0.0008205	2.31802	1.21289	Null_Rptor up vs WT	+3σ	Gm2897	predicted gene 2897	14 A1|14	1E+08
TC1400002854.mm.1	0.0003458	2.31375	1.21023	Null_Rptor up vs WT	+3σ	Gm3558	predicted gene 3558	14 A1|14	1E+08
TC1400002788.mm.1	7.33E-05	2.31215	1.20923	Null_Rptor up vs WT	+3σ	Gm5796	predicted gene 5796	14 A1|14	545007
TC1600001277.mm.1	9.06E-05	2.3018	1.20276	Null_Rptor up vs WT	+3σ	2610318N02Rik	RIKEN cDNA 2610318N02 gene	16|16 A3	70458
TC1500001712.mm.1	0.0215487	2.29688	1.19968	Null_Rptor up vs WT	+3σ	Arc	activity regulated cytoskeletal-associated protein	15 D3|15 34.25 cM	11838

TC0500000200.mm.1	0.0327513	2.29687	1.19967	Null_Rptor up vs WT	+3σ	Snord93	small nucleolar RNA, C/D box 93	5 A3|5	1E+08
TC1400002781.mm.1	0.0004139	2.29523	1.19864	Null_Rptor up vs WT	+3σ	Gm10340	predicted gene 10340	14 A1|14	1E+08
TC1500002278.mm.1	0.200364	2.2927	1.19705	Null_Rptor up vs WT	+3σ	Krt4	keratin 4	15 F2|15 57.13 cM	16682
TC1400002791.mm.1	0.0002223	2.27112	1.1834	Null_Rptor up vs WT	+3σ	Gm3264	predicted gene 3264	14 A1|14	1E+08
TC1000003135.mm.1	0.0064043	2.26784	1.18132	Null_Rptor up vs WT	+3σ	Il23a	interleukin 23, alpha subunit p19	10|10 D3	83430
TC1800001338.mm.1	0.0008828	2.26338	1.17848	Null_Rptor up vs WT	+3σ	Ppic	peptidylprolyl isomerase C	18|18 D1	19038
TC1800001193.mm.1	0.0166379	2.26091	1.17691	Null_Rptor up vs WT	+3σ	Hbegf	heparin-binding EGF-like growth factor	18 B2|18 19.46 cM	15200
TC1400002793.mm.1	0.0001836	2.25191	1.17115	Null_Rptor up vs WT	+3σ	Gm3264	predicted gene 3264	14 A1|14	1E+08
TC1400002849.mm.1	9.44E-05	2.24611	1.16743	Null_Rptor up vs WT	+3σ	Gm3696	predicted gene 3696	14|14 A1	1E+08
TC1400002846.mm.1	0.0001497	2.24346	1.16572	Null_Rptor up vs WT	+3σ	Gm3636	predicted gene 3636	14 A1|14	1E+08
TC1800001430.mm.1	0.0060224	2.2395	1.16318	Null_Rptor up vs WT	+3σ	Afap1l1	actin filament associated protein 1-like 1	18|18 E1	106877
TC0100003422.mm.1	0.0138132	2.23615	1.16102	Null_Rptor up vs WT	+3σ	Atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide	1 H2.2|1 71.75 cM	11931
TC1400000046.mm.1	2.94E-05	2.23232	1.15855	Null_Rptor up vs WT	+3σ	Gm3317	predicted gene 3317	14 A1|14	666329
TC0100001338.mm.1	0.0127984	2.22635	1.15468	Null_Rptor up vs WT	+3σ	Ptgs2	prostaglandin-endoperoxide synthase 2	1 G1|1 63.84 cM	19225
TC0200005130.mm.1	0.0771127	2.21337	1.14624	Null_Rptor up vs WT	+3σ	Tnnc2	troponin C2, fast	2|2 H3	21925
TC1400002780.mm.1	0.0013277	2.21154	1.14505	Null_Rptor up vs WT	+3σ	Gm2897	predicted gene 2897	14 A1|14	1E+08
TC1200001151.mm.1	0.0038026	2.21044	1.14433	Null_Rptor up vs WT	+3σ	DQ267102	snoRNA DQ267102	12 F1|12	1E+08
TC1700001641.mm.1	0.0048805	2.20552	1.14112	Null_Rptor up vs WT	+3σ	Snora78	small nucleolar RNA, H/ACA box 7	17|17 A3.3	1E+08
TC1400002851.mm.1	0.0001973	2.20254	1.13917	Null_Rptor up vs WT	+3σ	Gm3739	predicted gene 3739	14 A1|14	1E+08
TC0M00000027.mm.1	0.0177378	2.18266	1.12609	Null_Rptor up vs WT	+3σ	ND6	NADH dehydrogenase subunit 6	-	17722
TC0100003867.mm.1	0.0057263	2.17998	1.12431	Null_Rptor up vs WT	+3σ	Serpinb10	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 10	1|1 E2.1	241197
TC1500000777.mm.1	0.0009787	2.16774	1.11619	Null_Rptor up vs WT	+3σ	Mpped1	metallophosphoesterase domain containing 1	15 E1|15 39.44 cM	223726
TC1000002458.mm.1	0.0050905	2.16047	1.11135	Null_Rptor up vs WT	+3σ	Syde1	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	10|10 C1	71709
TC0500000848.mm.1	0.0274343	2.15827	1.10987	Null_Rptor up vs WT	+3σ	Cxcl1	chemokine (C-X-C motif) ligand 1	5 E1|5 44.78 cM	14825
TC1700002107.mm.1	0.0405782	2.15803	1.10972	Null_Rptor up vs WT	+3σ	9130008F23Rik	RIKEN cDNA 9130008F23 gene	17|17 B2	71583
TC1100003460.mm.1	0.066245	2.14876	1.10351	Null_Rptor up vs WT	+3σ	A130040M12Rik	RIKEN cDNA A130040M12 gene	11 C|11	319269
TC1900000923.mm.1	0.0033906	2.14733	1.10255	Null_Rptor up vs WT	+3σ	Syt12	synaptotagmin XII	19|19 A	171180
TC1500000392.mm.1	0.0162573	2.14289	1.09956	Null_Rptor up vs WT	+3σ	Deptor	DEP domain containing MTOR-interacting protein	15 D1|15 21.96	97998

								cM	
TC0800002558.mm.1	4.33E-05	2.13478	1.09409	Null_Rptor up vs WT	+3σ	Adgre5	adhesion G protein-coupled receptor E5	8 C2|8 40.22 cM	26364
TC1400001393.mm.1	0.0001881	2.13356	1.09326	Null_Rptor up vs WT	+3σ	Gm3500	predicted gene 3500	14 A1|14	1E+08
TC0700002644.mm.1	0.0021876	2.13336	1.09313	Null_Rptor up vs WT	+3σ	Axl	AXL receptor tyrosine kinase	7 A3|7 14.02 cM	26362
TC0600003169.mm.1	0.0005312	2.13196	1.09218	Null_Rptor up vs WT	+3σ	Ccnd2	cyclin D2	6 F3|6 61.92 cM	12444
TC1300000330.mm.1	0.0044328	2.1262	1.08828	Null_Rptor up vs WT	+3σ	Mboat1	membrane bound O-acyltransferase domain containing 1	13|13 A3.2	218121
TC1000002205.mm.1	0.0024682	2.11972	1.08388	Null_Rptor up vs WT	+3σ	Edar	ectodysplasin-A receptor	10 B4|10 29.37 cM	13608
TC0400001390.mm.1	0.0003918	2.1184	1.08297	Null_Rptor up vs WT	+3σ	Oxct2b	3-oxoacid CoA transferase 2B	4|4 D2.2	353371
TC0400002529.mm.1	0.0053855	2.11332	1.07951	Null_Rptor up vs WT	+3σ	Tpm2	tropomyosin 2, beta	4|4 A5	22004
TC0900001598.mm.1	0.0483432	2.10914	1.07666	Null_Rptor up vs WT	+3σ	Snora62	small nucleolar RNA, H/ACA box 62	9|9 F4	104433
TC0400002808.mm.1	0.0008966	2.10904	1.07659	Null_Rptor up vs WT	+3σ	Tnfsf15	tumor necrosis factor (ligand) superfamily, member 15	4|4 C1	326623
TC0300001480.mm.1	0.0017901	2.09227	1.06507	Null_Rptor up vs WT	+3σ	Gm17501	predicted gene, 17501	3|3	1E+08
TC0300000838.mm.1	0.054772	2.09152	1.06455	Null_Rptor up vs WT	+3σ	Lce3f	late cornified envelope 3F	3|3 F1	69520
TC0X00003437.mm.1	0.0003666	2.08181	1.05784	Null_Rptor up vs WT	+3σ	Il2rg	interleukin 2 receptor, gamma chain	X D|X 43.9 cM	16186
TC1800001429.mm.1	0.0003928	2.08163	1.05772	Null_Rptor up vs WT	+3σ	Grpel2	GrpE-like 2, mitochondrial	18|18 E1	17714
TC0300002376.mm.1	0.0633806	2.07956	1.05628	Null_Rptor up vs WT	+3σ	S100a9	S100 calcium binding protein A9 (calgranulin B)	3 F1|3 39.91 cM	20202
TC0700004156.mm.1	0.005776	2.07731	1.05472	Null_Rptor up vs WT	+3σ	Snord14a	small nucleolar RNA, C/D box 14A	7|7 F1	1E+08
TC0100000523.mm.1	0.0002365	2.07157	1.05073	Null_Rptor up vs WT	+3σ	Zdbf2	zinc finger, DBF-type containing 2	1|1 C2	73884
TC0X00002447.mm.1	0.0062982	2.06627	1.04703	Null_Rptor up vs WT	+3σ	Flna	filamin, alpha	X A7.3|X 37.89 cM	192176
TC1000002497.mm.1	0.0002295	2.06207	1.04409	Null_Rptor up vs WT	+3σ	Adamtsl5	ADAMTS-like 5	10|10 C1	66548
TC0800003059.mm.1	0.0188833	2.06079	1.0432	Null_Rptor up vs WT	+3σ	Slc7a5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	8 E1|8 70.8 cM	20539
TC0100003599.mm.1	0.0005662	2.06068	1.04312	Null_Rptor up vs WT	+3σ	Ifi202b	interferon activated gene 202B	1|1 H3	26388
TC0100001222.mm.1	0.0320666	2.05768	1.04102	Null_Rptor up vs WT	+3σ	Chil1	chitinase-like 1	1 E4|1 58.15 cM	12654
TC1800000301.mm.1	0.0141798	2.05746	1.04087	Null_Rptor up vs WT	+3σ	Egr1	early growth response 1	18 B1|18 18.76 cM	13653
TC1500001980.mm.1	0.001265	2.05618	1.03997	Null_Rptor up vs WT	+3σ	Scube1	signal peptide, CUB domain, EGF-like 1	15|15 E1	64706
TC0100000372.mm.1	0.0026763	2.05513	1.03923	Null_Rptor up vs WT	+3σ	Cavin2	caveolae associated 2	1|1 C1.1	20324
TC0800000282.mm.1	0.0054095	2.03398	1.02431	Null_Rptor up vs WT	+3σ	Dkk4	dickkopf WNT signaling pathway inhibitor 4	8|8 A2	234130

TC1400002839.mm.1	8.06E-05	2.02907	1.02082	Null_Rptor up vs WT	+3σ	Gm3500	predicted gene 3500	14 A1|14	1E+08
TC1500001728.mm.1	0.0054181	2.0215	1.01543	Null_Rptor up vs WT	+3σ	Ly6a	lymphocyte antigen 6 complex, locus A	15 D3|15 34.29 cM	110454
TC1300001242.mm.1	0.0041053	2.01916	1.01375	Null_Rptor up vs WT	+3σ	Plk2	polo like kinase 2	13|13 D2.1	20620
TC0900002541.mm.1	5.02E-05	2.01641	1.01179	Null_Rptor up vs WT	+3σ	Tpm1	tropomyosin 1, alpha	9 C|9 36.27 cM	22003
TC0400001912.mm.1	0.0005477	2.01186	1.00853	Null_Rptor up vs WT	+3σ	Vmn2r-ps20	vomeronasal 2, receptor, pseudogene 20	4|4 E1	1E+08
TC0700004610.mm.1	0.0105119	2.01175	1.00845	Null_Rptor up vs WT	+3σ	Ccnd1	cyclin D1	7 F5|7 88.92 cM	12443
TC1500000542.mm.1	0.245061	2.01155	1.00831	Null_Rptor up vs WT	+3σ	Psca	prostate stem cell antigen	15|15 D3	72373
TC1600001884.mm.1	0.003699	2.01068	1.00768	Null_Rptor up vs WT	+3σ	Robo2	roundabout guidance receptor 2	16|16 C3.1	268902
TC1400002857.mm.1	0.0050013	2.00812	1.00584	Null_Rptor up vs WT	+3σ	Gm10021	predicted gene 10021	14 A1|14	622931
TC1400002790.mm.1	0.0022259	2.00669	1.00482	Null_Rptor up vs WT	+3σ	2610042L04Rik	RIKEN cDNA 2610042L04 gene	14|14 A1	554327
TC0900000500.mm.1	0.0027291	2.00532	1.00383	Null_Rptor up vs WT	+3σ	Mcam	melanoma cell adhesion molecule	9|9 A5.1	84004
TC0X00000689.mm.1	8.09E-05	1.9929	0.994867	Null_Rptor up vs WT	+3σ	Dusp9	dual specificity phosphatase 9	X|X A7.3	75590
TC1300001642.mm.1	0.022185	1.99128	0.993693	Null_Rptor up vs WT	+3σ	Hist1h3c	histone cluster 1, H3c	13|13 A3.1	319148
TC1100001916.mm.1	0.0011219	1.9721	0.97973	Null_Rptor up vs WT	+3σ	Itgb4	integrin beta 4	11 E2|11 80.91 cM	192897
TC1500002142.mm.1	0.0031096	1.97009	0.97826	Null_Rptor up vs WT	+3σ	Slc38a2	solute carrier family 38, member 2	15|15 F1	67760
TC0M00000011.mm.1	0.0914543	1.96971	0.97798	Null_Rptor up vs WT	+3σ	ND3	NADH dehydrogenase subunit 3	-	17718
TC1500000395.mm.1	0.0301031	1.96799	0.976727	Null_Rptor up vs WT	+3σ	Col14a1	collagen, type XIV, alpha 1	15|15 D1	12818
TC0600002233.mm.1	0.0061816	1.96668	0.975763	Null_Rptor up vs WT	+3σ	Tmem176b	transmembrane protein 176B	6 B2.3|6 23.75 cM	65963
TC1400002112.mm.1	0.100575	1.95657	0.968323	Null_Rptor up vs WT	+3σ	Mcpt4	mast cell protease 4	14 C3|14 28.19 cM	17227
TC1700002481.mm.1	0.0280911	1.95275	0.965506	Null_Rptor up vs WT	+3σ	Tgif1	TGFB-induced factor homeobox 1	17|17 E1.3	21815
TC0600000128.mm.1	0.0013193	1.95265	0.965433	Null_Rptor up vs WT	+3σ	Cav1	caveolin 1, caveolae protein	6|6 A2	12389
TC0200001847.mm.1	0.0116711	1.95121	0.964366	Null_Rptor up vs WT	+3σ	Duox1	dual oxidase 1	2|2 E5	99439
TC0500000338.mm.1	0.002397	1.94195	0.957503	Null_Rptor up vs WT	+3σ	Gm5864	PDZ and LIM domain protein 1 pseudogene	5|5 B1	545743
TC0200000833.mm.1	0.0061646	1.94066	0.95655	Null_Rptor up vs WT	+3σ	Fmnl2	formin-like 2	2|2 C1.1	71409
TC0300002280.mm.1	0.0132172	1.93864	0.955047	Null_Rptor up vs WT	+3σ	Gm19382	predicted gene, 19382	3 F1|3 38.19 cM	1E+08
TC0600000232.mm.1	0.001112	1.93695	0.953783	Null_Rptor up vs WT	+3σ	Flnc	filamin C, gamma	6 A3.3|6 12.36 cM	68794
TC0100000610.mm.1	0.077257	1.92999	0.94859	Null_Rptor up vs WT	+3σ	Igfbp2	insulin-like growth factor binding protein 2	1 C3|1 36.94 cM	16008
TC0700001646.mm.1	0.0014751	1.92925	0.948037	Null_Rptor up vs WT	+3σ	Parva	parvin, alpha	7|7 F1	57342

TC0200004217.mm.1	0.0085749	1.92852	0.947497	Null_Rptor up vs WT	+3σ	Fjx1	four jointed box 1 (Drosophila)	2|2 E2	14221
TC1300002392.mm.1	0.000812	1.92531	0.945093	Null_Rptor up vs WT	+3σ	Vcan	versican	13 C3|13 45.5 cM	13003
TC1200001686.mm.1	0.0030021	1.92442	0.944427	Null_Rptor up vs WT	+3σ	Stxbp6	syntaxin binding protein 6 (amisyn)	12|12 B2-B3	217517
TC1300001032.mm.1	0.0015304	1.92346	0.943703	Null_Rptor up vs WT	+3σ	Gm20379	predicted gene, 20379	13|13 47.63 cM	1E+08
TC1500002141.mm.1	0.0029956	1.92295	0.94332	Null_Rptor up vs WT	+3σ	Slc38a1	solute carrier family 38, member 1	15|15 F1	105727
TC0300002760.mm.1	0.0004388	1.92211	0.942693	Null_Rptor up vs WT	+3σ	Fam102b	family with sequence similarity 102, member B	3|3 F3	329739
TC0300001081.mm.1	0.0059758	1.91935	0.940616	Null_Rptor up vs WT	+3σ	Rhoc	ras homolog family member C	3|3 F2.2	11853
TSUnmapped00000184.mm.1	0.0072828	1.9172	0.939003	Null_Rptor up vs WT	+3σ	Rnu2-10	U2 small nuclear RNA 10	11 D|11 65.48 cM	19848
TC0100001617.mm.1	0.0137316	1.91394	0.936543	Null_Rptor up vs WT	+3σ	Tagln2	transgelin 2	1 H3|1 79.89 cM	21346
TC0400002103.mm.1	0.0246206	1.91261	0.93554	Null_Rptor up vs WT	+3σ	Tnfrsf4	tumor necrosis factor receptor superfamily, member 4	4 E2|4 87.68 cM	22163
TC1200000263.mm.1	0.0078786	1.91257	0.93551	Null_Rptor up vs WT	+3σ	Lamb1	laminin B1	12 A2|12 13.39 cM	16777
TC1000001189.mm.1	0.0007203	1.91196	0.93505	Null_Rptor up vs WT	+3σ	Dcn	decorin	10 C3|10 50.27 cM	13179
TC1900000054.mm.1	0.0003049	1.90963	0.93329	Null_Rptor up vs WT	+3σ	Rin1	Ras and Rab interactor 1	19|19 A	225870
TC1700000835.mm.1	0.041122	1.90863	0.93254	Null_Rptor up vs WT	+3σ	Pla2g7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	17|17 B3	27226
TC1800001234.mm.1	0.0005431	1.90733	0.931553	Null_Rptor up vs WT	+3σ	Spry4	sprouty homolog 4 (Drosophila)	18 B3|18 20.5 cM	24066
TC1700001139.mm.1	0.0093367	1.90654	0.930953	Null_Rptor up vs WT	+3σ	Snord92	small nucleolar RNA, C/D box 92	17 E1.3|17	1E+08
TC1300000087.mm.1	0.0002915	1.89316	0.920793	Null_Rptor up vs WT	+3σ	Nid1	nidogen 1	13 A1|13 5.26 cM	18073
TC0300000809.mm.1	0.0283344	1.88708	0.916153	Null_Rptor up vs WT	+3σ	S100a6	S100 calcium binding protein A6 (calcyclin)	3 F1|3 39.35 cM	20200
TC1200001461.mm.1	0.006709	1.88271	0.91281	Null_Rptor up vs WT	+3σ	Greb1	gene regulated by estrogen in breast cancer protein	12|12 A1.1	268527
TC0700003028.mm.1	0.002108	1.87931	0.910203	Null_Rptor up vs WT	+3σ	Emp3	epithelial membrane protein 3	7 B3|7 29.6 cM	13732
TC1500001078.mm.1	0.0097816	1.8792	0.910117	Null_Rptor up vs WT	+3σ	Gm5477	type II keratin Kb16P	15 F2|15	432986
TC0400001823.mm.1	0.0283144	1.87813	0.909297	Null_Rptor up vs WT	+3σ	Anp32b-ps1	Bacidic (leucine-rich) nuclear phosphoprotein 32 family, member B, pseudogene 1	4|4 E1	621961
TC0200005402.mm.1	0.0117801	1.87486	0.90678	Null_Rptor up vs WT	+3σ	Lama5	laminin, alpha 5	2 H4|2 102.7 cM	16776
TC0600001095.mm.1	0.007636	1.87397	0.906097	Null_Rptor up vs WT	+3σ	Fgd5	FYVE, RhoGEF and PH domain containing 5	6|6 D1	232237
TC0600003155.mm.1	0.0084025	1.87163	0.904297	Null_Rptor up vs WT	+3σ	Ntf3	neurotrophin 3	6 F3|6 60.45 cM	18205
TC0700002	7.25E-05	1.87113	0.90391	Null_Rptor up	+3σ	B4galn	beta-1,4-N-acetyl-	7|7 F5	330671

037.mm.1				vs WT		t4	galactosaminyl transferase 4		
TC0800000509.mm.1	0.0077766	1.87084	0.903687	Null_Rptor up vs WT	+3σ	Fat1	FAT atypical cadherin 1	8 B1.1|8 24.81 cM	14107
TC1100001448.mm.1	0.0471968	1.86129	0.896307	Null_Rptor up vs WT	+3σ	Col1a1	collagen, type I, alpha 1	11 59.01 cM|11 D	12842
TC0300000816.mm.1	0.163943	1.85942	0.894853	Null_Rptor up vs WT	+3σ	Pglyrp3	peptidoglycan recognition protein 3	3|3 F1	242100
TC0700002216.mm.1	0.0005911	1.85326	0.890063	Null_Rptor up vs WT	+3σ	Zim1	zinc finger, imprinted 1	7 A1|7 3.87 cM	22776
TC1200002020.mm.1	0.125721	1.84857	0.886407	Null_Rptor up vs WT	+3σ	Adam4	a disintegrin and metallopeptidase domain 4	12|12 D1	11498
TC1100001395.mm.1	0.0038154	1.84728	0.8854	Null_Rptor up vs WT	+3σ	Tmem100	transmembrane protein 100	11|11 C	67888
TC1100003604.mm.1	0.0008372	1.84687	0.88508	Null_Rptor up vs WT	+3σ	Igf2bp1	insulin-like growth factor 2 mRNA binding protein 1	11 D|11 59.08 cM	140486
TC1500000654.mm.1	0.0430648	1.84639	0.88471	Null_Rptor up vs WT	+3σ	Cdc42ep1	CDC42 effector protein (Rho GTPase binding) 1	15|15 E1	104445
TC1100002783.mm.1	8.23E-05	1.8455	0.88401	Null_Rptor up vs WT	+3σ	Sparc	secreted acidic cysteine rich glycoprotein	11 B1.3|11 33.04 cM	20692
TC0X00003023.mm.1	0.0005486	1.84321	0.882223	Null_Rptor up vs WT	+3σ	Bex1	brain expressed X-linked 1	X F1|X 57.4 cM	19716
TC0400001209.mm.1	0.0001029	1.84239	0.88158	Null_Rptor up vs WT	+3σ	Trabd2b	TraB domain containing 2B	4 D1|4	666048
TC0100003272.mm.1	0.0099829	1.84074	0.880287	Null_Rptor up vs WT	+3σ	Lamc2	laminin, gamma 2	1 G3|1 65.26 cM	16782
TC0900001297.mm.1	0.0031625	1.84036	0.87999	Null_Rptor up vs WT	+3σ	Slco2a1	solute carrier organic anion transporter family, member 2a1	9 F1|9 54.72 cM	24059
TC0900000573.mm.1	0.0141427	1.8368	0.877193	Null_Rptor up vs WT	+3σ	Cadm1	cell adhesion molecule 1	9|9 A5.3	54725
TC0200004507.mm.1	0.0182105	1.83246	0.87378	Null_Rptor up vs WT	+3σ	Duoxa1	dual oxidase maturation factor 1	2|2 E5	213696
TC0400003848.mm.1	0.0113836	1.83036	0.87213	Null_Rptor up vs WT	+3σ	Ccnd3-ps	cyclin D3, pseudogene	4|4 D3	626000
TC0800001599.mm.1	0.0141651	1.82735	0.86975	Null_Rptor up vs WT	+3σ	Itgb1	integrin beta 1 (fibronectin receptor beta)	8|8 E2	16412
TC0100000116.mm.1	0.0011712	1.82456	0.867547	Null_Rptor up vs WT	+3σ	Tfap2b	transcription factor AP-2 beta	1|1 A3	21419
TC0400002475.mm.1	0.0046172	1.82449	0.867497	Null_Rptor up vs WT	+3σ	Cntfr	ciliary neurotrophic factor receptor	4 A5|4 21.81 cM	12804
TC1700001234.mm.1	0.0033456	1.8225	0.865917	Null_Rptor up vs WT	+3σ	Gm6594	high mobility group nucleosomal binding domain 2 pseudogene	17|17 E3	625514
TC0400003627.mm.1	0.0226059	1.81926	0.86335	Null_Rptor up vs WT	+3σ	Tinagl1	tubulointerstitial nephritis antigen-like 1	4|4 D2.2	94242
TC0700002445.mm.1	0.0051521	1.81694	0.861513	Null_Rptor up vs WT	+3σ	Hif3a	hypoxia inducible factor 3, alpha subunit	7|7 A2	53417
TC1100003318.mm.1	0.0502412	1.81657	0.86122	Null_Rptor up vs WT	+3σ	Wsb1	WD repeat and SOCS box-containing 1	11|11 B5	78889
TC0100002461.mm.1	0.0046348	1.81204	0.857613	Null_Rptor up vs WT	+3σ	Klf7	Kruppel-like factor 7 (ubiquitous)	1|1 C2	93691
TC1100003233.mm.1	0.0057181	1.81017	0.856127	Null_Rptor up vs WT	+3σ	Doc2b	double C2, beta	11|11 B5	13447
TC0500000496.mm.1	0.0075986	1.80819	0.85455	Null_Rptor up vs WT	+3σ	Gm7931	non-histone chromosomal protein HMG-17-like	5|5 B3	1E+08
TC0100001696.mm.1	0.0587697	1.80678	0.853423	Null_Rptor up vs WT	+3σ	A730054J21Rik	RIKEN cDNA A730054J21 gene	1|1	320862
TC0800002843.mm.1	0.0480532	1.80498	0.851983	Null_Rptor up vs WT	+3σ	Lcat	lecithin cholesterol acyltransferase	8 D3|8 53.06 cM	16816

TC0900001908.mm.1	0.0084368	1.80488	0.8519	Null_Rptor up vs WT	+3σ	Anln	anillin, actin binding protein	9|9 A3	68743
TC0900003300.mm.1	0.006392	1.8008	0.848637	Null_Rptor up vs WT	+3σ	Cdcp1	CUB domain containing protein 1	9|9 F4	109332
TC0900001113.mm.1	0.0008031	1.7996	0.847677	Null_Rptor up vs WT	+3σ	Tpbg	trophoblast glycoprotein	9|9 E3.1	21983
TC0100002544.mm.1	0.0013187	1.79496	0.843953	Null_Rptor up vs WT	+3σ	Fn1	fibronectin 1	1 C3|1 36.05 cM	14268
TC0700004179.mm.1	0.0252104	1.79313	0.842483	Null_Rptor up vs WT	+3σ	Gprc5b	G protein-coupled receptor, family C, group 5, member B	7|7 F2	64297
TC0700000292.mm.1	0.111394	1.79155	0.84121	Null_Rptor up vs WT	+3σ	Gpr4	G protein-coupled receptor 4	7|7 A3	319197
TC0200004563.mm.1	0.1849	1.78608	0.8368	Null_Rptor up vs WT	+3σ	Mal	myelin and lymphocyte protein, T cell differentiation protein	2|2 F1	17153
TC1700001846.mm.1	0.0091643	1.78567	0.836466	Null_Rptor up vs WT	+3σ	Pglyrp2	peptidoglycan recognition protein 2	17|17 B1	57757
TC0300001486.mm.1	0.009541	1.7853	0.83617	Null_Rptor up vs WT	+3σ	Syde2	synapse defective 1, Rho GTPase, homolog 2 (C. elegans)	3|3 H2	214804
TC1800000704.mm.1	0.0155601	1.78467	0.835653	Null_Rptor up vs WT	+3σ	Tubb6	tubulin, beta 6 class V	18|18 E1	67951
TC0200004129.mm.1	0.0103755	1.7834	0.834627	Null_Rptor up vs WT	+3σ	Mdk	midkine	2 E1|2 50.63 cM	17242
TC0600000871.mm.1	0.0010192	1.78241	0.833827	Null_Rptor up vs WT	+3σ	Lrrtm1	leucine rich repeat transmembrane neuronal 1	6|6 C3	74342
TC0500000499.mm.1	0.0015325	1.78019	0.832033	Null_Rptor up vs WT	+3σ	Slit2	slit homolog 2 (Drosophila)	5|5 B3	20563
TC0800001182.mm.1	0.0004075	1.77986	0.831767	Null_Rptor up vs WT	+3σ	Cmtm3	CKLF-like MARVEL transmembrane domain containing 3	8|8 D3	68119
TC0X00002211.mm.1	0.0153385	1.77896	0.831037	Null_Rptor up vs WT	+3σ	Gpc3	glypican 3	X|X A5	14734
TC1900000350.mm.1	0.002759	1.77851	0.830667	Null_Rptor up vs WT	+3σ	Tmem2	transmembrane protein 2	19|19 B	83921
TC1100001667.mm.1	0.0136412	1.7758	0.82847	Null_Rptor up vs WT	+3σ	Rnu2-10	U2 small nuclear RNA 10	11 D|11 65.48 cM	19848
TC1700000211.mm.1	0.0001285	1.77294	0.82614	Null_Rptor up vs WT	+3σ	Spaca6	sperm acrosome associated 6	17|17 A3.2	75202
TC0700001008.mm.1	0.0031623	1.77269	0.825943	Null_Rptor up vs WT	+3σ	Igf1r	insulin-like growth factor I receptor	7 C|7 37.27 cM	16001
TC1100003097.mm.1	0.003356	1.76813	0.822223	Null_Rptor up vs WT	+3σ	Cxcl16	chemokine (C-X-C motif) ligand 16	11|11 B3	66102
TC0X00000682.mm.1	0.0250017	1.76725	0.82151	Null_Rptor up vs WT	+3σ	Zfp275	zinc finger protein 275	X A7.3|X 37.29 cM	27081
TC0200004126.mm.1	0.0025499	-1.82942	-0.871383	Null_Rptor down vs WT	-3σ	Atg13	autophagy related 13	2|2 E1	51897
TC0500000297.mm.1	0.0054418	-1.83072	-0.872413	Null_Rptor down vs WT	-3σ	Slc35f6	solute carrier family 35, member F6	5|5 B1	74919
TC0800001092.mm.1	0.0222055	-1.83132	-0.872883	Null_Rptor down vs WT	-3σ	Mt4	metallothionein 4	8 C5|8 46.26 cM	17752
TC0X00001799.mm.1	0.0027878	-1.83264	-0.873927	Null_Rptor down vs WT	-3σ	Ebp	phenylalkylamine Ca2+ antagonist (emopamil) binding protein	X A1.1|X 3.7 cM	13595
TC0300001497.mm.1	0.0012559	-1.83287	-0.874103	Null_Rptor down vs WT	-3σ	Ttll7	tubulin tyrosine ligase-like family, member 7	3|3 H2	70892
TC0500002598.mm.1	0.0249814	-1.833	-0.87420	Null_Rptor down vs WT	-3σ	Usp46	ubiquitin specific peptidase 46	5|5 C3.3	69727

			7						
TC1100003269.mm.1	0.103277	-1.83345	-0.874563	Null_Rptor down vs WT	-3σ	Taok1	TAO kinase 1	11|11 B5	216965
TC1100002673.mm.1	0.0133538	-1.83364	-0.874713	Null_Rptor down vs WT	-3σ	Rufy1	RUN and FYVE domain containing 1	11|11 B1.3	216724
TC0100003320.mm.1	0.0010086	-1.83417	-0.875127	Null_Rptor down vs WT	-3σ	Tor3a	torsin family 3, member A	1|1 G3	30935
TC0900002347.mm.1	0.0377119	-1.83479	-0.875614	Null_Rptor down vs WT	-3σ	Peak1	pseudopodium-enriched atypical kinase 1	9|9 B	244895
TC1500000344.mm.1	0.0144528	-1.83485	-0.875663	Null_Rptor down vs WT	-3σ	Emc2	ER membrane protein complex subunit 2	15|15 B3.2	66736
TC1100000205.mm.1	0.0085496	-1.83525	-0.875973	Null_Rptor down vs WT	-3σ	Peli1	pellino 1	11 A3.1|11 13.81 cM	67245
TC0300000903.mm.1	0.0182793	-1.83555	-0.876213	Null_Rptor down vs WT	-3σ	Ctss	cathepsin S	3 F2.1|3 40.74 cM	13040
TC0500003632.mm.1	0.0001297	-1.8376	-0.877827	Null_Rptor down vs WT	-3σ	Slc46a3	solute carrier family 46, member 3	5|5 G3	71706
TC0500000987.mm.1	0.0734605	-1.83813	-0.87824	Null_Rptor down vs WT	-3σ	Gpat3	glycerol-3-phosphate acyltransferase 3	5|5 E4	231510
TC1700001688.mm.1	0.0034519	-1.83967	-0.879447	Null_Rptor down vs WT	-3σ	Decr2	2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	17 A3.3|17 13.06 cM	26378
TC0600000661.mm.1	0.0226027	-1.84019	-0.879854	Null_Rptor down vs WT	-3σ	Gars	glycyl-tRNA synthetase	6 B3|6 27.29 cM	353172
TC1800001535.mm.1	0.0293912	-1.84106	-0.88054	Null_Rptor down vs WT	-3σ	Rab27b	RAB27B, member RAS oncogene family	18 E2|18 43.89 cM	80718
TC1100003422.mm.1	0.0052101	-1.84122	-0.88066	Null_Rptor down vs WT	-3σ	Usp32	ubiquitin specific peptidase 32	11|11 C	237898
TC0200005094.mm.1	0.0635951	-1.8413	-0.880726	Null_Rptor down vs WT	-3σ	Serinc3	serine incorporator 3	2|2 H3	26943
TC1300002536.mm.1	0.0174309	-1.84137	-0.880777	Null_Rptor down vs WT	-3σ	Ocln	occludin	13 D1|13 53.23 cM	18260
TC1500002313.mm.1	0.0446641	-1.84318	-0.882193	Null_Rptor down vs WT	-3σ	Nfe2	nuclear factor, erythroid derived 2	15 F3|15 58.62 cM	18022
TC0700002669.mm.1	0.0129915	-1.84379	-0.882674	Null_Rptor down vs WT	-3σ	Pld3	phospholipase D family, member 3	7|7 A3	18807
TC1100002597.mm.1	0.0868449	-1.84415	-0.882953	Null_Rptor down vs WT	-3σ	Nipal4	NIPA-like domain containing 4	11|11 B1.1	214112
TC0400003792.mm.1	0.0352107	-1.84416	-0.882963	Null_Rptor down vs WT	-3σ	C1qb	complement component 1, q subcomponent, beta polypeptide	4 D3|4 69.05 cM	12260
TC0600002114.mm.1	0.0191596	-1.84434	-0.883107	Null_Rptor down vs WT	-3σ	Parp12	poly (ADP-ribose) polymerase family, member 12	6|6 B1	243771
TC1400002141.mm.1	0.0083443	-1.84473	-0.883413	Null_Rptor down vs WT	-3σ	Gjb6	gap junction protein, beta 6	14 C3|14 30.1 cM	14623
TC1600000464.mm.1	0.0137939	-1.84534	-0.883887	Null_Rptor down vs WT	-3σ	Osbpl11	oxysterol binding protein-like 11	16|16 B3	106326

TC0500001408.mm.1	0.0292857	-1.84752	-0.885587	Null_Rptor down vs WT	-3σ	Tmem120b	transmembrane protein 120B	5|5 F	330189
TC0100003301.mm.1	0.0626181	-1.84812	-0.886057	Null_Rptor down vs WT	-3σ	Mr1	major histocompatibility complex, class I-related	1|1 G3	15064
TC1400001605.mm.1	0.0135129	-1.85093	-0.888247	Null_Rptor down vs WT	-3σ	Tmem254b	transmembrane protein 254b	14 A3|14	1E+08
TC0300003113.mm.1	0.0440865	-1.85147	-0.888674	Null_Rptor down vs WT	-3σ	Adgrl2	adhesion G protein-coupled receptor L2	3|3 H3	99633
TC0300002042.mm.1	0.0007462	-1.85207	-0.889137	Null_Rptor down vs WT	-3σ	Serp1	stress-associated endoplasmic reticulum protein 1	3 D|3 28.58 cM	28146
TC0600000444.mm.1	0.0260349	-1.8525	-0.889473	Null_Rptor down vs WT	-3σ	Ephb6	Eph receptor B6	6|6 B2.1	13848
TC1100000421.mm.1	0.0319217	-1.85306	-0.889907	Null_Rptor down vs WT	-3σ	Gm9972	predicted gene 9972	-	791397
TC0100003563.mm.1	0.0077019	-1.85307	-0.88992	Null_Rptor down vs WT	-3σ	Pea15a	phosphoprotein enriched in astrocytes 15A	1 H3|1 79.54 cM	18611
TC1400000368.mm.1	0.118178	-1.85415	-0.890756	Null_Rptor down vs WT	-3σ	Anxa8	annexin A8	14 B|14 20.8 cM	11752
TC1800000098.mm.1	0.002848	-1.85429	-0.89087	Null_Rptor down vs WT	-3σ	Riok3	RIO kinase 3	18 A1|18 6.15 cM	66878
TC0900003311.mm.1	0.004313	-1.85541	-0.891737	Null_Rptor down vs WT	-3σ	Fyco1	FYVE and coiled-coil domain containing 1	9 F4|9 74.52 cM	17281
TC1200000416.mm.1	0.0365332	-1.85586	-0.892087	Null_Rptor down vs WT	-3σ	Scfd1	Sec1 family domain containing 1	12|12 B3	76983
TC0200000380.mm.1	0.0511748	-1.8573	-0.893207	Null_Rptor down vs WT	-3σ	Il1f10	interleukin 1 family, member 10	2 A3|2 16.32 cM	215274
TC0500000291.mm.1	0.002202	-1.85812	-0.893847	Null_Rptor down vs WT	-3σ	Drc1	dynein regulatory complex subunit 1	5|5 B1	381738
TC0600002116.mm.1	0.0048296	-1.85833	-0.894003	Null_Rptor down vs WT	-3σ	Kdm7a	lysine (K)-specific demethylase 7A	6|6 B1	338523
TC0300002724.mm.1	0.0049767	-1.8601	-0.89538	Null_Rptor down vs WT	-3σ	Gstm2	glutathione S-transferase, mu 2	3|3 F2.3	14863
TC0700002716.mm.1	0.0233303	-1.8616	-0.89654	Null_Rptor down vs WT	-3σ	Psmd8	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	7|7 B1	57296
TC0400000654.mm.1	0.0592691	-1.86169	-0.89661	Null_Rptor down vs WT	-3σ	Ugcg	UDP-glucose ceramide glucosyltransferase	4 32.44 cM|4 B3	22234
TC0700001198.mm.1	0.007007	-1.86188	-0.89676	Null_Rptor down vs WT	-3σ	Stard5	StAR-related lipid transfer (START) domain containing 5	7 D3|7 47.43 cM	170460
TC0100002642.mm.1	0.0309326	-1.86343	-0.897963	Null_Rptor down vs WT	-3σ	Ap1s3	adaptor-related protein complex AP-1, sigma 3	1|1 C4	252903
TC0100001024.mm.1	0.007983	-1.86416	-0.898527	Null_Rptor down vs WT	-3σ	Serpinb5	serine (or cysteine) peptidase inhibitor, clade B, member 5	1|1 E2.1	20724
TC1200002263.mm.1	0.0622585	-1.86568	-0.899703	Null_Rptor down vs WT	-3σ	Asb2	ankyrin repeat and SOCS box-containing 2	12 E|12 52.9 cM	65256
TC0400001160.mm.1	0.024244	-1.86575	-0.899753	Null_Rptor down vs WT	-3σ	Rab3b	RAB3B, member RAS oncogene family	4|4 C7	69908
TC0700002024.mm.1	0.0301855	-1.86705	-0.90076	Null_Rptor down vs WT	-3σ	Urah	urate (5-hydroxyiso-) hydrolase	7|7 F4	76974

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TC0600001808.mm.1	0.0107562	-1.86936	-0.902543	Null_Rptor down vs WT	-3σ	Pon2	paraoxonase 2	6 A1|6 1.99 cM	330260
TC0100001724.mm.1	0.0058729	-1.8707	-0.903577	Null_Rptor down vs WT	-3σ	Tmem63a	transmembrane protein 63a	1|1 H4	208795
TC0900003115.mm.1	0.0132799	-1.87236	-0.904857	Null_Rptor down vs WT	-3σ	Nbeal2	neurobeachin-like 2	9|9 F2	235627
TC0600001647.mm.1	0.0039477	-1.8743	-0.90635	Null_Rptor down vs WT	-3σ	Pik3c2g	phosphatidylinositol-4-phosphate 3-kinase catalytic subunit type 2 gamma	6 G2|6 69.7 cM	18705
TC0700000647.mm.1	0.0124515	-1.8749	-0.90681	Null_Rptor down vs WT	-3σ	Pepd	peptidase D	7 B2|7 20.7 cM	18624
TC1300001882.mm.1	0.0157876	-1.87507	-0.906947	Null_Rptor down vs WT	-3σ	Ranbp9	RAN binding protein 9	13|13 A4	56705
TC0700000903.mm.1	0.0006558	-1.87586	-0.90755	Null_Rptor down vs WT	-3σ	Htatip2	HIV-1 Tat interactive protein 2	7|7 B4	53415
TC1900000465.mm.1	0.0313362	-1.87594	-0.90761	Null_Rptor down vs WT	-3σ	Minpp1	multiple inositol polyphosphate histidine phosphatase 1	19 C1|19 27.25 cM	17330
TC0500003638.mm.1	0.0550366	-1.87632	-0.907907	Null_Rptor down vs WT	-3σ	Ubl3	ubiquitin-like 3	5|5 G3	24109
TC0700003485.mm.1	0.0012472	-1.87641	-0.907973	Null_Rptor down vs WT	-3σ	Mctp2	multiple C2 domains, transmembrane 2	7|7 D1	244049
TC0600001992.mm.1	0.0053438	-1.87898	-0.909953	Null_Rptor down vs WT	-3σ	Ube2h	ubiquitin-conjugating enzyme E2H	6 A3.3|6 12.52 cM	22214
TC1700000352.mm.1	0.0608923	-1.88096	-0.911467	Null_Rptor down vs WT	-3σ	Hs3st6	heparan sulfate (glucosamine) 3-O-sulfotransferase 6	17|17 A3.3	328779
TC0700002359.mm.1	0.0245941	-1.88101	-0.911507	Null_Rptor down vs WT	-3σ	Chmp2a	charged multivesicular body protein 2A	7 A1|7	68953
TC0400003327.mm.1	0.0238383	-1.88168	-0.912023	Null_Rptor down vs WT	-3σ	Faah	fatty acid amide hydrolase	4 D1|4 53.08 cM	14073
TC1900001414.mm.1	0.0132025	-1.88683	-0.915967	Null_Rptor down vs WT	-3σ	Ankrd22	ankyrin repeat domain 22	19 C1|19 29.33 cM	52024
TC1800000509.mm.1	0.0047623	-1.88717	-0.916223	Null_Rptor down vs WT	-3σ	Hsd17b4	hydroxysteroid (17-beta) dehydrogenase 4	18|18 D1	15488
TC1700002332.mm.1	0.020506	-1.88747	-0.916453	Null_Rptor down vs WT	-3σ	2410015M20Rik	RIKEN cDNA 2410015M20 gene	17|17 D	224904
TC0700000763.mm.1	0.0338094	-1.88795	-0.91682	Null_Rptor down vs WT	-3σ	Vsig10l	V-set and immunoglobulin domain containing 10 like	7|7 B3	75690
TC0X00001558.mm.1	0.100105	-1.88797	-0.916837	Null_Rptor down vs WT	-3σ	Ubqln2	ubiquilin 2	X|X F3	54609
TC1300002201.mm.1	0.0452472	-1.88829	-0.91708	Null_Rptor down vs WT	-3σ	Aaed1	AhpC/TSA antioxidant enzyme domain containing 1	13|13 B3	66129
TC1100000093.mm.1	0.0019589	-1.88971	-0.918167	Null_Rptor down vs WT	-3σ	Ogdh	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	11|11 A1	18293
TC0700002043.mm.1	0.0256859	-1.8908	-0.918997	Null_Rptor down vs WT	-3σ	Rassf7	Ras association (RalGDS/AF-6) domain family (N-terminal) member 7	7|7 F5	66985
TC1900001485.mm.1	0.0420479	-1.89333	-0.92092	Null_Rptor down vs WT	-3σ	Sorbs1	sorbin and SH3 domain containing 1	19 C3|19	20411

			3					34.25 cM	
TC0800000754.mm.1	0.0040259	-1.89346	-0.921027	Null_Rptor down vs WT	-3σ	Ell	elongation factor RNA polymerase II	8|8 B3.3	13716
TC1100001777.mm.1	0.032951	-1.8936	-0.92113	Null_Rptor down vs WT	-3σ	Psmc5	protease (prosome, macropain) 26S subunit, ATPase 5	11|11 E1	19184
TC0700001906.mm.1	0.0092796	-1.89388	-0.921347	Null_Rptor down vs WT	-3σ	Tacc2	transforming, acidic coiled-coil containing protein 2	7|7 F3	57752
TC1400002090.mm.1	0.0080164	-1.89407	-0.921493	Null_Rptor down vs WT	-3σ	Emc9	ER membrane protein complex subunit 9	14|14 C3	85308
TC0600003045.mm.1	0.0106764	-1.89713	-0.923816	Null_Rptor down vs WT	-3σ	Atp6v1e1	ATPase, H+ transporting, lysosomal V1 subunit E1	6 F1|6 57.01 cM	11973
TC1900000401.mm.1	0.0090046	-1.89757	-0.924153	Null_Rptor down vs WT	-3σ	Gm3873	predicted gene 3873	19 B|19	1E+08
TC0800000146.mm.1	0.0702249	-1.90024	-0.92618	Null_Rptor down vs WT	-3σ	Cln8	ceroid-lipofuscinosis, neuronal 8	8 A1.1|8 7.59 cM	26889
TC1800001041.mm.1	0.0449007	-1.90268	-0.928036	Null_Rptor down vs WT	-3σ	Dsc3	desmocollin 3	18 A2|18 11.11 cM	13507
TC1300002095.mm.1	0.0277314	-1.90272	-0.928064	Null_Rptor down vs WT	-3σ	Ubqln1	ubiquilin 1	13 B1|13 30.95 cM	56085
TC0900003307.mm.1	0.0004998	-1.90287	-0.92818	Null_Rptor down vs WT	-3σ	Slc6a20a	solute carrier family 6 (neurotransmitter transporter), member 20A	9 F4|9 74.26 cM	102680
TC0100001589.mm.1	0.0206362	-1.90295	-0.92824	Null_Rptor down vs WT	-3σ	Nectin4	nectin cell adhesion molecule 4	1|1 H3	71740
TC1200000792.mm.1	0.0003901	-1.90301	-0.928283	Null_Rptor down vs WT	-3σ	Psen1	presenilin 1	12 D1|12 38.84 cM	19164
TC1100000314.mm.1	0.011459	-1.90375	-0.928843	Null_Rptor down vs WT	-3σ	Psme4	proteasome (prosome, macropain) activator subunit 4	11|11 A4	103554
TC1200000258.mm.1	0.0034508	-1.90594	-0.930503	Null_Rptor down vs WT	-3σ	Sh3yl1	Sh3 domain YSC-like 1	12|12 A2	24057
TC1200001722.mm.1	0.0459308	-1.90609	-0.93062	Null_Rptor down vs WT	-3σ	Hectd1	HECT domain E3 ubiquitin protein ligase 1	12 B3|12 22.11 cM	207304
TC0900000586.mm.1	0.0757369	-1.90844	-0.932393	Null_Rptor down vs WT	-3σ	Gm5617	predicted gene 5617	9|9 A5.3	434402
TC0900002889.mm.1	0.0763874	-1.909	-0.932817	Null_Rptor down vs WT	-3σ	Pxylp1	2-phosphoxylose phosphatase 1	9|9 E3.3	235534
TC0400001670.mm.1	0.0079701	-1.90987	-0.933477	Null_Rptor down vs WT	-3σ	Hmgcl	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	4 D3|4 68.14 cM	15356
TC0400001411.mm.1	0.0014253	-1.91153	-0.93473	Null_Rptor down vs WT	-3σ	Mycbp	MYC binding protein	4|4 D2.2	56309
TC1100004251.mm.1	0.000237	-1.91492	-0.937287	Null_Rptor down vs WT	-3σ	Rab40b	Rab40B, member RAS oncogene family	11|11 E2	217371
TC1000003153.mm.1	0.0111692	-1.91676	-0.938667	Null_Rptor down vs WT	-3σ	Erbb3	erb-b2 receptor tyrosine kinase 3	10 D3|10 77.1 cM	13867
TC0200003435.mm.1	0.0101733	-1.91803	-0.939627	Null_Rptor down vs WT	-3σ	Golga1	golgi autoantigen, golgin subfamily a, 1	2|2 B	76899

TC0700000433.mm.1	0.0152605	-1.91873	-0.94015	Null_Rptor down vs WT	-3σ	Cyp2b13	cytochrome P450, family 2, subfamily b, polypeptide 13	7 A3|7 14.11 cM	13089
TC0400003319.mm.1	0.0073621	-1.91939	-0.94065	Null_Rptor down vs WT	-3σ	Cyp4b1-ps1	cytochrome P450, family 4, subfamily b, polypeptide 1, pseudogene 1	4|4 D1	1E+08
TC1100001989.mm.1	0.0088501	-1.91997	-0.941083	Null_Rptor down vs WT	-3σ	Engase	endo-beta-N-acetylglucosaminidase	11|11 E2	217364
TC1600001473.mm.1	0.0084364	-1.92063	-0.941583	Null_Rptor down vs WT	-3σ	Acap2	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2	16|16 B2	78618
TC1900000160.mm.1	0.006123	-1.92463	-0.944583	Null_Rptor down vs WT	-3σ	Bscl2	Berardinelli-Seip congenital lipodystrophy 2 (seipin)	19 A|19 5.76 cM	14705
TC0X00003335.mm.1	0.0073092	-1.92724	-0.94654	Null_Rptor down vs WT	-3σ	Mospd2	motile sperm domain containing 2	X|X F5	76763
TC0700003019.mm.1	0.0231975	-1.9278	-0.946957	Null_Rptor down vs WT	-3σ	Sult2b1	sulfotransferase family, cytosolic, 2B, member 1	7|7 B3	54200
TC0600001252.mm.1	0.0064095	-1.9279	-0.947027	Null_Rptor down vs WT	-3σ	Il17rc	interleukin 17 receptor C	6|6 E3	171095
TC0700002047.mm.1	0.0275982	-1.92843	-0.947427	Null_Rptor down vs WT	-3σ	Eps8l2	EPS8-like 2	7|7 F5	98845
TC0100002604.mm.1	0.0236836	-1.93001	-0.948606	Null_Rptor down vs WT	-3σ	Tuba4a	tubulin, alpha 4A	1|1 C4	22145
TC0900000100.mm.1	0.0012373	-1.93012	-0.94869	Null_Rptor down vs WT	-3σ	Sesn3	sestrin 3	9|9 A1	75747
TC1200002526.mm.1	0.043091	-1.93101	-0.949354	Null_Rptor down vs WT	-3σ	Serpina3h	serine (or cysteine) peptidase inhibitor, clade A, member 3H	12|12 E	546546
TC0200005317.mm.1	0.0182666	-1.93173	-0.949897	Null_Rptor down vs WT	-3σ	Prelid3b	PRELI domain containing 3B	2|2 H4	66390
TC0200000593.mm.1	0.0381385	-1.93194	-0.950047	Null_Rptor down vs WT	-3σ	Ptrh1	peptidyl-tRNA hydrolase 1 homolog	2|2 B	329384
TC0700001942.mm.1	0.0182742	-1.93219	-0.95024	Null_Rptor down vs WT	-3σ	Zranb1	zinc finger, RAN-binding domain containing 1	7 F3|7 76.32 cM	360216
TC0700000652.mm.1	0.0077803	-1.93243	-0.950413	Null_Rptor down vs WT	-3σ	Cebpa	CCAAT/enhancer binding protein (C/EBP), alpha	7 B2|7 21.02 cM	12606
TC1600001047.mm.1	0.0038371	-1.93285	-0.950727	Null_Rptor down vs WT	-3σ	Dopey2	dopey family member 2	16|16 C4	70028
TC1600000168.mm.1	0.0453041	-1.93516	-0.95245	Null_Rptor down vs WT	-3σ	Mpv17l	Mpv17 transgene, kidney disease mutant-like	16|16 A1	93734
TC0100000332.mm.1	0.109258	-1.93618	-0.95321	Null_Rptor down vs WT	-3σ	Tpp2	tripeptidyl peptidase II	1 C1.1|1 23.5 cM	22019
TC0100000021.mm.1	0.0200694	-1.93648	-0.953437	Null_Rptor down vs WT	-3σ	Rb1cc1	RB1-inducible coiled-coil 1	1|1 A1	12421
TC1700000418.mm.1	0.0056857	-1.93748	-0.954183	Null_Rptor down vs WT	-3σ	Atp6v0e	ATPase, H+ transporting, lysosomal V0 subunit E	17|17 A3.3	11974
TC1000001799.mm.1	0.0660699	-1.94282	-0.95815	Null_Rptor down vs WT	-3σ	Heca	hdc homolog, cell cycle regulator	10|10 A3	380629
TC1100001454.mm.1	0.0676782	-1.94519	-0.959913	Null_Rptor down vs WT	-3σ	Dlx3	distal-less homeobox 3	11 D|11 59.01 cM	13393
TC0100000627.mm.1	0.0027628	-1.94745	-0.96159	Null_Rptor down vs WT	-3σ	Pnkd	paroxysmal nonkinesiogenic dyskinesia	1|1 C3	56695
TC0900001838.mm.1	0.0044702	-1.94882	-0.962603	Null_Rptor down vs WT	-3σ	Zfp266	zinc finger protein 266	9|9 A3	77519

TC1100003303.mm.1	0.0081671	-1.94915	-0.962847	Null_Rptor down vs WT	-3σ	Nlk	nemo like kinase	11|11 B5	18099
TC1600000138.mm.1	0.0185146	-1.95057	-0.963897	Null_Rptor down vs WT	-3σ	Snx29	sorting nexin 29	16|16 A1	74478
TC1100000907.mm.1	0.0206575	-1.95247	-0.9653	Null_Rptor down vs WT	-3σ	Trappc1	trafficking protein particle complex 1	11 B3|11 42.51 cM	245828
TC1900000646.mm.1	0.0001735	-1.95252	-0.965337	Null_Rptor down vs WT	-3σ	Scd2	stearoyl-Coenzyme A desaturase 2	19 C3|19 37.98 cM	20250
TC1400002152.mm.1	0.0045312	-1.95423	-0.966597	Null_Rptor down vs WT	-3σ	Micu2	mitochondrial calcium uptake 2	14|14 C3	68514
TC1500000066.mm.1	0.0414677	-1.95429	-0.966647	Null_Rptor down vs WT	-3σ	Lmbrd2	LMBR1 domain containing 2	15|15 A1	320506
TC0300000453.mm.1	0.0640804	-1.95545	-0.9675	Null_Rptor down vs WT	-3σ	Tsc22d2	TSC22 domain family, member 2	3|3 D	72033
TC0800001106.mm.1	0.0077481	-1.95575	-0.96772	Null_Rptor down vs WT	-3σ	Herpud1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	8|8 C5	64209
TC0600000454.mm.1	0.0030773	-1.95603	-0.96793	Null_Rptor down vs WT	-3σ	Gstk1	glutathione S-transferase kappa 1	6|6 B2.1	76263
TC0800001078.mm.1	0.0114782	-1.95701	-0.968653	Null_Rptor down vs WT	-3σ	Lpcat2	lysophosphatidylcholine acyltransferase 2	8|8 C5	270084
TC1600002080.mm.1	0.0095608	-1.95706	-0.968687	Null_Rptor down vs WT	-3σ	Tmem50b	transmembrane protein 50B	16|16 C3.3	77975
TC0900002495.mm.1	0.0100535	-1.95721	-0.9688	Null_Rptor down vs WT	-3σ	Rab11a	RAB11A, member RAS oncogene family	9|9 C	53869
TC1100002871.mm.1	0.0066942	-1.96109	-0.971653	Null_Rptor down vs WT	-3σ	Tom1l2	target of myb1-like 2 (chicken)	11|11 B2	216810
TC0600000606.mm.1	0.0122175	-1.96111	-0.971673	Null_Rptor down vs WT	-3σ	Nfe2l3	nuclear factor, erythroid derived 2, like 3	6 B3|6 24.84 cM	18025
TC0300000580.mm.1	0.0066474	-1.96535	-0.974783	Null_Rptor down vs WT	-3σ	Ppm1l	protein phosphatase 1 (formerly 2C)-like	3|3 E1	242083
TC0300001306.mm.1	0.0090368	-1.96755	-0.976403	Null_Rptor down vs WT	-3σ	Elovl6	ELOVL family member 6, elongation of long chain fatty acids (yeast)	3|3 G3	170439
TC0400000721.mm.1	0.027877	-1.96901	-0.977474	Null_Rptor down vs WT	-3σ	Orm2	orosomucoid 2	4 B3|4 33.96 cM	18406
TC1400002523.mm.1	0.0267435	-1.96986	-0.978093	Null_Rptor down vs WT	-3σ	Pcdh20	protocadherin 20	14|14 E1	219257
TC1300001776.mm.1	0.0550654	-1.97088	-0.978837	Null_Rptor down vs WT	-3σ	Serpinb6c	serine (or cysteine) peptidase inhibitor, clade B, member 6c	13 A3.3|13 13.99 cM	97848
TC1600000861.mm.1	0.0034171	-1.97104	-0.97896	Null_Rptor down vs WT	-3σ	Usp25	ubiquitin specific peptidase 25	16|16 C3.1	30940
TC1000000744.mm.1	0.0017317	-1.97347	-0.980733	Null_Rptor down vs WT	-3σ	Lss	lanosterol synthase	10 C1|10 39.1 cM	16987
TC1100000956.mm.1	0.072528	-1.97422	-0.981283	Null_Rptor down vs WT	-3σ	Pld2	phospholipase D2	11 B3|11 42.99 cM	18806
TC0700004080.mm.1	0.0028563	-1.97563	-0.98231	Null_Rptor down vs WT	-3σ	Tmem9b	TMEM9 domain family, member B	7|7 E3	56786

TC1000001772.mm.1	0.0058178	-1.97597	-0.982563	Null_Rptor down vs WT	-3σ	Pex3	peroxisomal biogenesis factor 3	10|10 A2	56535
TC0100002324.mm.1	0.00766	-1.9767	-0.983093	Null_Rptor down vs WT	-3σ	Mfsd6	major facilitator superfamily domain containing 6	1|1 C1.1	98682
TC0300001124.mm.1	0.0101953	-1.97948	-0.985123	Null_Rptor down vs WT	-3σ	Gstm5	glutathione S-transferase, mu 5	3|3 F2.3	14866
TC0700001672.mm.1	0.0039491	-1.97999	-0.985493	Null_Rptor down vs WT	-3σ	Calcb	calcitonin-related polypeptide, beta	7|7 F1	116903
TC0100002830.mm.1	0.017374	-1.98218	-0.987087	Null_Rptor down vs WT	-3σ	2310007B03Rik	RIKEN cDNA 2310007B03 gene	1|1 D	71874
TC1500001207.mm.1	0.0049932	-1.98406	-0.988453	Null_Rptor down vs WT	-3σ	Rai14	retinoic acid induced 14	15|15 A1	75646
TC1700000335.mm.1	0.0302843	-1.98527	-0.989333	Null_Rptor down vs WT	-3σ	Abca3	ATP-binding cassette, sub-family A (ABC1), member 3	17|17 A3.3	27410
TC1100001315.mm.1	0.0236166	-1.98556	-0.989543	Null_Rptor down vs WT	-3σ	Rnft1	ring finger protein, transmembrane 1	11|11 C	76892
TC0900003341.mm.1	0.0204844	-1.98596	-0.989837	Null_Rptor down vs WT	-3σ	Snx14	sorting nexin 14	9|9 E3.1	244962
TC0100000129.mm.1	0.04688	-1.98641	-0.990163	Null_Rptor down vs WT	-3σ	Paqr8	progestin and adipoQ receptor family member VIII	1|1 A4	74229
TC0600002797.mm.1	0.0451453	-1.98823	-0.991483	Null_Rptor down vs WT	-3σ	Tmf1	TATA element modulatory factor 1	6|6 D3	232286
TC0400004117.mm.1	0.0504573	-1.98856	-0.991723	Null_Rptor down vs WT	-3σ	Tprgl	transformation related protein 63 regulated like	4|4 E2	67808
TC1300000045.mm.1	0.0021569	-1.98873	-0.99185	Null_Rptor down vs WT	-3σ	Idi1	isopentenyl-diphosphate delta isomerase	13|13 A1	319554
TC0X00002453.mm.1	0.0050528	-1.98968	-0.99254	Null_Rptor down vs WT	-3σ	G6pdx	glucose-6-phosphate dehydrogenase X-linked	X A7.3|X 38.0 cM	14381
TC0200000651.mm.1	0.0061609	-1.99121	-0.993647	Null_Rptor down vs WT	-3σ	Ptgs1	prostaglandin-endoperoxide synthase 1	2 B|2 24.19 cM	19224
TC0200002457.mm.1	0.0338021	-1.99337	-0.99521	Null_Rptor down vs WT	-3σ	Lpin3	lipin 3	2|2 H2	64899
TC0700002221.mm.1	0.0027842	-1.99486	-0.996287	Null_Rptor down vs WT	-3σ	Zfp954	zinc finger protein 954	7|7 A1	232853
TC0800001928.mm.1	0.0224703	-1.99571	-0.996903	Null_Rptor down vs WT	-3σ	Hook3	hook microtubule tethering protein 3	8|8 A2	320191
TC0700001736.mm.1	0.0089795	-1.99827	-0.998753	Null_Rptor down vs WT	-3σ	Eef2k	eukaryotic elongation factor-2 kinase	7|7 F2	13631
TC0300000812.mm.1	0.0854922	-1.99897	-0.999256	Null_Rptor down vs WT	-3σ	Pglyrp4	peptidoglycan recognition protein 4	3|3 F1	384997
TC0X00000668.mm.1	0.0031318	-1.99949	-0.999633	Null_Rptor down vs WT	-3σ	Nsdhl	NAD(P) dependent steroid dehydrogenase-like	X A7.3|X 37.29 cM	18194
TC1400001035.mm.1	0.0116815	-2.00063	-1.00045	Null_Rptor down vs WT	-3σ	Med4	mediator complex subunit 4	14|14 D3	67381
TC0200001810.mm.1	0.0036797	-2.00329	-1.00237	Null_Rptor down vs WT	-3σ	Ckmt1	creatine kinase, mitochondrial 1, ubiquitous	2 E5|2 60.37 cM	12716
TC0900002780.mm.1	0.0070049	-2.00512	-1.00369	Null_Rptor down vs WT	-3σ	Me1	malic enzyme 1, NADP(+)-dependent, cytosolic	9 E3.1|9 46.58	17436

								cM	
TC1400000578.mm.1	0.0369523	-2.00703	-1.00506	Null_Rptor down vs WT	-3σ	Ang	angiogenin, ribonuclease, RNase A family, 5	14 C1|14 26.37 cM	11727
TC1100001161.mm.1	0.0176374	-2.00804	-1.00579	Null_Rptor down vs WT	-3σ	Slc46a1	solute carrier family 46, member 1	11 B5|11 46.74 cM	52466
TC0X00002865.mm.1	0.0356083	-2.0088	-1.00633	Null_Rptor down vs WT	-3σ	Rps6ka6	ribosomal protein S6 kinase polypeptide 6	X|X E1	67071
TC0300001103.mm.1	0.0068318	-2.00937	-1.00675	Null_Rptor down vs WT	-3σ	Dennd2d	DENN/MADD domain containing 2D	3|3 F2.3	72121
TC0300000849.mm.1	0.0280038	-2.0107	-1.0077	Null_Rptor down vs WT	-3σ	Tchh	trichohyalin	3|3 F2.1	99681
TC1200001658.mm.1	0.0020566	-2.0133	-1.00956	Null_Rptor down vs WT	-3σ	Arl4a	ADP-ribosylation factor-like 4A	12 B1|12 18.06 cM	11861
TC1300002052.mm.1	0.0062298	-2.01517	-1.0109	Null_Rptor down vs WT	-3σ	Rab24	RAB24, member RAS oncogene family	13 B1|13 29.8 cM	19336
TC1600001045.mm.1	0.0004112	-2.01537	-1.01104	Null_Rptor down vs WT	-3σ	Cbr3	carbonyl reductase 3	16 C4|16 54.58 cM	109857
TC0600001536.mm.1	0.0114885	-2.01728	-1.01241	Null_Rptor down vs WT	-3σ	Gabarapl1	gamma-aminobutyric acid (GABA) A receptor-associated protein-like 1	6|6 F3	57436
TC1100004173.mm.1	0.0037659	-2.0173	-1.01242	Null_Rptor down vs WT	-3σ	Cbx4	chromobox 4	11 E2|11 83.34 cM	12418
TC0900001423.mm.1	0.0512498	-2.01844	-1.01324	Null_Rptor down vs WT	-3σ	Nckipsd	NCK interacting protein with SH3 domain	9|9 F2	80987
TC0200002533.mm.1	0.001174	-2.02099	-1.01506	Null_Rptor down vs WT	-3σ	Snx21	sorting nexin family member 21	2|2 H3	101113
TC0900003282.mm.1	0.0029113	-2.02111	-1.01515	Null_Rptor down vs WT	-3σ	Ano10	anoctamin 10	9|9 F4	102566
TC1700000665.mm.1	0.0075543	-2.02143	-1.01537	Null_Rptor down vs WT	-3σ	Ly6g6e	lymphocyte antigen 6 complex, locus G6E	17|17 B1	70274
TC0400002744.mm.1	0.0164123	-2.02485	-1.01781	Null_Rptor down vs WT	-3σ	Ptgr1	prostaglandin reductase 1	4|4 B3	67103
TC0300000494.mm.1	0.0013327	-2.02492	-1.01787	Null_Rptor down vs WT	-3σ	Arhgef26	Rho guanine nucleotide exchange factor (GEF) 26	3|3 E1	622434
TC1100000014.mm.1	0.0158745	-2.02604	-1.01866	Null_Rptor down vs WT	-3σ	Pla2g3	phospholipase A2, group III	11|11 A1	237625
TC1400000322.mm.1	0.0005966	-2.02621	-1.01879	Null_Rptor down vs WT	-3σ	Nt5dc2	5'-nucleotidase domain containing 2	14|14 B	70021
TC0700001581.mm.1	0.0205814	-2.03097	-1.02217	Null_Rptor down vs WT	-3σ	Ppfibp2	PTPRF interacting protein, binding protein 2 (liprin beta 2)	7|7 E3	19024
TC1900001019.mm.1	0.0025354	-2.03108	-1.02225	Null_Rptor down vs WT	-3σ	Prdx5	peroxiredoxin 5	19 A|19 5.08 cM	54683
TC0800003204.mm.1	0.0001785	-2.03162	-1.02263	Null_Rptor down vs WT	-3σ	Gm9909	predicted gene 9909	8 E2|8	628856
TC1500002270.mm.1	0.089099	-2.03447	-1.02465	Null_Rptor down vs WT	-3σ	Krt71	keratin 71	15 F2|15 57.0 cM	56735
TC0300002346.mm.1	0.0244435	-2.03552	-1.0254	Null_Rptor down vs WT	-3σ	Efna3	ephrin A3	3 F1|3 39.06 cM	13638
TC0X00001625.mm.1	0.0133609	-2.03731	-1.02667	Null_Rptor down vs WT	-3σ	Sh3kbp1	SH3-domain kinase binding protein 1	X|X F4	58194
TC0400003230.mm.1	0.00789	-2.03815	-1.02726	Null_Rptor down vs WT	-3σ	Cpt2	carnitine palmitoyltransferase 2	4 C7|4 50.18 cM	12896
TC0200002087.mm.1	0.0209528	-2.03895	-1.02782	Null_Rptor down vs WT	-3σ	Sptlc3	serine palmitoyltransferase, long chain base subunit 3	2|2 F3	228677

TC1600000441.mm.1	0.0022308	-2.04007	-1.02862	Null_Rptor down vs WT	-3σ	Gm20056	calcium-binding protein p22-like	16 B3|16 22.67 cM	1E+08
TC1000000852.mm.1	0.0044017	-2.04133	-1.02951	Null_Rptor down vs WT	-3σ	Reep6	receptor accessory protein 6	10|10 C1	70335
TC0700000517.mm.1	0.0340144	-2.04419	-1.03153	Null_Rptor down vs WT	-3σ	Capn12	calpain 12	7|7 B1	60594
TC0900003233.mm.1	0.0097483	-2.0448	-1.03196	Null_Rptor down vs WT	-3σ	Plcd1	phospholipase C, delta 1	9|9 F3	18799
TC1800001000.mm.1	0.0038003	-2.04486	-1.032	Null_Rptor down vs WT	-3σ	Osbpl1a	oxysterol binding protein-like 1A	18|18 A1	64291
TC0300000823.mm.1	0.236178	-2.04697	-1.03349	Null_Rptor down vs WT	-3σ	Sprr2b	small proline-rich protein 2B	3 F1|3 40.14 cM	20756
TC1200001971.mm.1	0.0081375	-2.04819	-1.03435	Null_Rptor down vs WT	-3σ	Atp6v1d	ATPase, H+ transporting, lysosomal V1 subunit D	12 C3|12 35.51 cM	73834
TSUnmapped00000036.mm.1	0.0029652	-2.04856	-1.03461	Null_Rptor down vs WT	-3σ	Ache	acetylcholinesterase	5 G2|5 76.32 cM	11423
TC1500001942.mm.1	0.0331973	-2.0495	-1.03527	Null_Rptor down vs WT	-3σ	Naga	N-acetyl galactosaminidase, alpha	15 E1|15 38.56 cM	17939
TC1000002224.mm.1	0.0218075	-2.0506	-1.03605	Null_Rptor down vs WT	-3σ	Ddit4	DNA-damage-inducible transcript 4	10|10 B4	74747
TC0600002466.mm.1	0.0087331	-2.05188	-1.03695	Null_Rptor down vs WT	-3σ	Rmnd5a	required for meiotic nuclear division 5 homolog A	6|6 C1	68477
TC0400003034.mm.1	0.0006386	-2.05216	-1.03714	Null_Rptor down vs WT	-3σ	Cdkn2b	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	4 C4|4 42.15 cM	12579
TC0700003570.mm.1	0.0051276	-2.05228	-1.03723	Null_Rptor down vs WT	-3σ	Anpep	alanyl (membrane) aminopeptidase	7|7 D2	16790
TC0100002499.mm.1	0.0031816	-2.05598	-1.03982	Null_Rptor down vs WT	-3σ	Lancl1	LanC (bacterial lantibiotic synthetase component C)-like 1	1|1 C3	14768
TC0500001038.mm.1	0.0055999	-2.05622	-1.03999	Null_Rptor down vs WT	-3σ	Lrrc8b	leucine rich repeat containing 8 family, member B	5|5 E5	433926
TC1200002166.mm.1	0.0032428	-2.05677	-1.04038	Null_Rptor down vs WT	-3σ	Lysmd1	LysM, putative peptidoglycan-binding, domain containing 1	3|3 F2.1	217779
TC1600000967.mm.1	0.168128	-2.05736	-1.0408	Null_Rptor down vs WT	-3σ	Gm10229	predicted gene 10229	16|16 C3.3	1E+08
TC1000001167.mm.1	0.207601	-2.05745	-1.04086	Null_Rptor down vs WT	-3σ	4732465J04Rik	RIKEN cDNA 4732465J04 gene	10|10 C2	414105
TC1400000991.mm.1	0.0044339	-2.05767	-1.04101	Null_Rptor down vs WT	-3σ	Bin3	bridging integrator 3	14|14 D2	57784
TC1300000144.mm.1	0.0188899	-2.05795	-1.04121	Null_Rptor down vs WT	-3σ	Tcrg-C3	T cell receptor gamma, constant 3	13|13 A2	107575
TC1700000487.mm.1	0.0705229	-2.05928	-1.04214	Null_Rptor down vs WT	-3σ	Mapk13	mitogen-activated protein kinase 13	17|17 A3.3	26415
TC0200002537.mm.1	0.012709	-2.06026	-1.04282	Null_Rptor down vs WT	-3σ	Ctsa	cathepsin A	2 H3|2 85.27 cM	19025
TC1000000815.mm.1	0.0508346	-2.0615	-1.0437	Null_Rptor down vs WT	-3σ	Fgf22	fibroblast growth factor 22	10|10 C1	67112
TC0400003545.mm.1	0.0195876	-2.06162	-1.04378	Null_Rptor down vs WT	-3σ	Ago4	argonaute RISC catalytic subunit 4	4|4 D2.2	76850
TC1100001430.mm.1	0.0205726	-2.06175	-1.04387	Null_Rptor down vs WT	-3σ	Tob1	transducer of ErbB-2.1	11|11 D	22057
TC0700000886.mm.1	0.0094711	-2.06376	-1.04528	Null_Rptor down vs WT	-3σ	Tmem86a	transmembrane protein 86A	7|7 B3	67893
TC1000000011.mm.1	0.0329272	-2.0641	-1.04551	Null_Rptor down vs WT	-3σ	Plekhg1	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	10|10 A1	213783
TC1000000	0.017182	-2.06669	-1.04732	Null_Rptor	-3σ	Thop1	thimet oligopeptidase 1	10	50492

879.mm.1				down vs WT				C1|10 39.72 cM	
TC0500002940.mm.1	0.0042824	-2.0695	-1.04928	Null_Rptor down vs WT	-3σ	Tmed5	transmembrane p24 trafficking protein 5	5|5 F	73130
TC0900002529.mm.1	0.0112851	-2.07092	-1.05027	Null_Rptor down vs WT	-3σ	Aph1b	aph1 homolog B, gamma secretase subunit	9|9 C	208117
TC0700004288.mm.1	0.0018755	-2.07149	-1.05067	Null_Rptor down vs WT	-3σ	Nupr1	nuclear protein transcription regulator 1	7|7 F3	56312
TC1500001935.mm.1	0.0065307	-2.07154	-1.0507	Null_Rptor down vs WT	-3σ	Desi1	desumoylating isopeptidase 1	15 E1|15 38.34 cM	28075
TC0800000844.mm.1	0.0186893	-2.07373	-1.05223	Null_Rptor down vs WT	-3σ	Tom1	target of myb1 trafficking protein	8|8 C1	21968
TC1700000496.mm.1	0.024585	-2.07493	-1.05306	Null_Rptor down vs WT	-3σ	Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	17 A3.3|17 15.12 cM	12575
TC0100002471.mm.1	0.0044423	-2.07604	-1.05383	Null_Rptor down vs WT	-3σ	Plekhm3	pleckstrin homology domain containing, family M, member 3	1|1 C2	241075
TC0500000599.mm.1	0.0074023	-2.07649	-1.05415	Null_Rptor down vs WT	-3σ	Klf3	Kruppel-like factor 3 (basic)	5|5 C3.1	16599
TC0300002610.mm.1	0.0027988	-2.07654	-1.05418	Null_Rptor down vs WT	-3σ	Mab21l3	mab-21-like 3 (C. elegans)	3|3 F2.2	242125
TC1500001717.mm.1	0.0108164	-2.07948	-1.05622	Null_Rptor down vs WT	-3σ	Lynx1	Ly6/neurotoxin 1	15|15 D3	23936
TC0900000497.mm.1	0.0860605	-2.08021	-1.05673	Null_Rptor down vs WT	-3σ	Usp2	ubiquitin specific peptidase 2	9|9 A5.1	53376
TC0700000855.mm.1	0.0008335	-2.08149	-1.05761	Null_Rptor down vs WT	-3σ	Fut1	fucosyltransferase 1	7 B3|7 29.39 cM	14343
TC1400001157.mm.1	0.0104875	-2.08265	-1.05842	Null_Rptor down vs WT	-3σ	Klf5	Kruppel-like factor 5	14|14 E2.2	12224
TC0800002428.mm.1	0.0457796	-2.08385	-1.05925	Null_Rptor down vs WT	-3σ	Ano8	anoctamin 8	8|8 B3.3	382014
TC1100003406.mm.1	0.0348387	-2.08818	-1.06224	Null_Rptor down vs WT	-3σ	Dusp14	dual specificity phosphatase 14	11 C|11 51.29 cM	56405
TC0100003309.mm.1	0.0327425	-2.09148	-1.06453	Null_Rptor down vs WT	-3σ	Qsox1	quiescin Q6 sulfhydryl oxidase 1	1|1 G3	104009
TC0500001526.mm.1	0.0174847	-2.09218	-1.06501	Null_Rptor down vs WT	-3σ	Rabgef1	RAB guanine nucleotide exchange factor (GEF) 1	5|5 G1.3	56715
TC1400001188.mm.1	0.0284211	-2.09713	-1.06842	Null_Rptor down vs WT	-3σ	Scel	sciellin	14|14 E2.3	64929
TC1300002762.mm.1	0.0284794	-2.09865	-1.06946	Null_Rptor down vs WT	-3σ	Trgj1	T cell receptor gamma joining 1	13|13 A2	1E+08
TC0300003240.mm.1	0.0095269	-2.09939	-1.06997	Null_Rptor down vs WT	-3σ	Bnipl	BCL2/adenovirus E1B 19kD interacting protein like	3|3 F2.1	171388
TC0700003517.mm.1	0.0177126	-2.10134	-1.07131	Null_Rptor down vs WT	-3σ	Slco3a1	solute carrier organic anion transporter family, member 3a1	7|7 D1	108116
TC1300002037.mm.1	0.0097149	-2.10339	-1.07271	Null_Rptor down vs WT	-3σ	Cltb	clathrin, light polypeptide (Lcb)	13|13 B1	74325
TC0400002251.mm.1	0.0056182	-2.10703	-1.07521	Null_Rptor down vs WT	-3σ	Ripk2	receptor (TNFRSF)-interacting serine-threonine kinase 2	4 A2|4 6.7 cM	192656
TC1800000682.mm.1	0.006011	-2.10875	-1.07639	Null_Rptor down vs WT	-3σ	Sec11c	SEC11 homolog C, signal peptidase complex subunit	18|18 E1	66286
TC0800001436.mm.1	0.0029637	-2.10884	-1.07645	Null_Rptor down vs WT	-3σ	6430548M08Rik	RIKEN cDNA 6430548M08 gene	8|8 E1	234797
TC0X00003098.mm.1	0.0026578	-2.10911	-1.07664	Null_Rptor down vs WT	-3σ	Acsl4	acyl-CoA synthetase long-chain family member 4	X|X F2	50790
TC0700001287.mm.1	0.0005668	-2.11548	-1.08098	Null_Rptor down vs WT	-3σ	Dlg2	discs, large homolog 2 (Drosophila)	7 E1|7 51.07 cM	23859
TC1600002	0.136194	-2.11571	-1.08114	Null_Rptor	-3σ	231007	RIKEN cDNA 2310079G19	16|16	69699

008.mm.1				down vs WT		9G19Rik	gene	C3.3	
TC0700001590.mm.1	0.0425491	-2.11814	-1.0828	Null_Rptor down vs WT	-3σ	Olfr479	olfactory receptor 479	7|7 E3	257891
TC1000002099.mm.1	0.0419453	-2.12367	-1.08656	Null_Rptor down vs WT	-3σ	Prdm1	PR domain containing 1, with ZNF domain	10 B2|10 23.24 cM	12142
TC0400001969.mm.1	0.0076442	-2.12417	-1.0869	Null_Rptor down vs WT	-3σ	Gpr157	G protein-coupled receptor 157	4|4 E2	269604
TC0300001909.mm.1	0.0143317	-2.12779	-1.08935	Null_Rptor down vs WT	-3σ	Pgrmc2	progesterone receptor membrane component 2	3|3 B	70804
TC1300001266.mm.1	0.0029838	-2.13026	-1.09103	Null_Rptor down vs WT	-3σ	Slc38a9	solute carrier family 38, member 9	13|13 D2.2	268706
TC1100004003.mm.1	0.033533	-2.1314	-1.0918	Null_Rptor down vs WT	-3σ	Abca5	ATP-binding cassette, sub-family A (ABC1), member 5	11|11 E1	217265
TC1000000789.mm.1	0.0351327	-2.13211	-1.09228	Null_Rptor down vs WT	-3σ	Ilvbl	ilvB (bacterial acetolactate synthase)-like	10 C1|10 39.72 cM	216136
TC0700000435.mm.1	0.0151333	-2.13496	-1.09421	Null_Rptor down vs WT	-3σ	Cyp2b9	cytochrome P450, family 2, subfamily b, polypeptide 9	7 A3|7 14.11 cM	13094
TC1800000564.mm.1	0.0429841	-2.13595	-1.09488	Null_Rptor down vs WT	-3σ	Gramd3	GRAM domain containing 3	18|18 D3	107022
TC0400002694.mm.1	0.0089306	-2.13633	-1.09513	Null_Rptor down vs WT	-3σ	Klf4	Kruppel-like factor 4 (gut)	4 B3|4 29.76 cM	16600
TC0400002849.mm.1	0.008255	-2.13726	-1.09576	Null_Rptor down vs WT	-3σ	Megf9	multiple EGF-like-domains 9	4|4 C2	230316
TC0100003421.mm.1	0.0463966	-2.13743	-1.09588	Null_Rptor down vs WT	-3σ	Blzf1	basic leucine zipper nuclear factor 1	1|1 H2.2	66352
TC1000000122.mm.1	0.0122133	-2.13956	-1.09731	Null_Rptor down vs WT	-3σ	Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	10|10 A2	17684
TC0300000766.mm.1	0.0029151	-2.1401	-1.09768	Null_Rptor down vs WT	-3σ	Pmvk	phosphomevalonate kinase	3|3 F1	68603
TC0200004512.mm.1	0.0403687	-2.14339	-1.0999	Null_Rptor down vs WT	-3σ	Slc30a4	solute carrier family 30 (zinc transporter), member 4	2 E5|2 60.65 cM	22785
TC0800001797.mm.1	0.0130327	-2.14382	-1.10018	Null_Rptor down vs WT	-3σ	Angpt2	angiopoietin 2	8 A1.3|8 10.3 cM	11601
TC0800001927.mm.1	0.0154163	-2.14578	-1.1015	Null_Rptor down vs WT	-3σ	Fnta	farnesyltransferase, CAAX box, alpha	8 A2|8 14.27 cM	14272
TC1200000303.mm.1	0.0104938	-2.14763	-1.10274	Null_Rptor down vs WT	-3σ	Snx13	sorting nexin 13	12|12 A3	217463
TC0400000485.mm.1	0.061245	-2.14941	-1.10394	Null_Rptor down vs WT	-3σ	Frmpd1	FERM and PDZ domain containing 1	4|4 B1	666060
TC0300002334.mm.1	0.0037093	-2.15214	-1.10577	Null_Rptor down vs WT	-3σ	Fdps	farnesyl diphosphate synthetase	3 F1|3 39.01 cM	110196
TC1800000956.mm.1	0.0069706	-2.15618	-1.10848	Null_Rptor down vs WT	-3σ	Mpp7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	18|18 A1	75739
TC1500001968.mm.1	0.0078841	-2.15661	-1.10877	Null_Rptor down vs WT	-3σ	A4galt	alpha 1,4-galactosyltransferase	15|15 E1	239559
TC0200002442.mm.1	0.093175	-2.1567	-1.10883	Null_Rptor down vs WT	-3σ	Fam83d	family with sequence similarity 83, member D	2|2 H1	71878
TC1000002535.mm.1	0.001785	-2.15962	-1.11078	Null_Rptor down vs WT	-3σ	Tjp3	tight junction protein 3	10|10 C1	27375
TC0200004848.mm.1	0.0017994	-2.16536	-1.11461	Null_Rptor down vs WT	-3σ	Abhd12	abhydrolase domain containing 12	2|2 G3	76192
TC0400003567.mm.1	0.0105811	-2.16627	-1.11521	Null_Rptor down vs WT	-3σ	Gjb4	gap junction protein, beta 4	4 D2.2|4 61.51 cM	14621
TSUnmapp	0.0187471	-2.16699	-1.11569	Null_Rptor	-3σ	Sts	steroid sulfatase	X;Y|XY	20905

ed00000053.mm.1				down vs WT				75.0 cM	
TC1800000791.mm.1	0.019318	-2.1685	-1.1167	Null_Rptor down vs WT	-3σ	Myo5b	myosin VB	18 E2|18 50.7 cM	17919
TC0500001451.mm.1	0.0593172	-2.17066	-1.11813	Null_Rptor down vs WT	-3σ	Atp6v0a2	ATPase, H+ transporting, lysosomal V0 subunit A2	5|5 F	21871
TC1400001942.mm.1	0.0451909	-2.17093	-1.11831	Null_Rptor down vs WT	-3σ	Gm6055	microtubule-associated protein 1 light chain 3 pseudogene 2	14|14 C1	606520
TC1100003066.mm.1	0.0038502	-2.17166	-1.1188	Null_Rptor down vs WT	-3σ	Tmem102	transmembrane protein 102	11|11 B3	380705
TC0700002631.mm.1	0.126269	-2.17223	-1.11918	Null_Rptor down vs WT	-3σ	Cnfn	cornifelin	7|7 A3	72383
TC0800002403.mm.1	0.0253279	-2.17362	-1.1201	Null_Rptor down vs WT	-3σ	Ifi30	interferon gamma inducible protein 30	8|8 B3.3	65972
TC0900002533.mm.1	0.0067838	-2.17396	-1.12032	Null_Rptor down vs WT	-3σ	Rab8b	RAB8B, member RAS oncogene family	9|9 C	235442
TC0400004157.mm.1	0.0599197	-2.17525	-1.12118	Null_Rptor down vs WT	-3σ	Tas1r3	taste receptor, type 1, member 3	4 E2|4 87.65 cM	83771
TC1100003705.mm.1	0.262417	-2.17551	-1.12135	Null_Rptor down vs WT	-3σ	Krt28	keratin 28	11|11 D	70843
TC1600001660.mm.1	0.005887	-2.17595	-1.12164	Null_Rptor down vs WT	-3σ	BC016579	cDNA sequence, BC016579	16|16 B5	212998
TC1100003092.mm.1	0.011111	-2.17775	-1.12284	Null_Rptor down vs WT	-3σ	Alox12e	arachidonate lipoxygenase, epidermal	11 B3|11 42.99 cM	11685
TC0800003069.mm.1	0.0022255	-2.17873	-1.12349	Null_Rptor down vs WT	-3σ	Mvd	mevalonate (diphospho) decarboxylase	8|8 E1	192156
TC0400003832.mm.1	0.0029176	-2.1793	-1.12386	Null_Rptor down vs WT	-3σ	Pla2g5	phospholipase A2, group V	4 D3|4 70.57 cM	18784
TC0900000116.mm.1	0.0021906	-2.1809	-1.12492	Null_Rptor down vs WT	-3σ	Vstm5	V-set and transmembrane domain containing 5	9|9 A2	69137
TC0X00000519.mm.1	0.0228679	-2.18212	-1.12573	Null_Rptor down vs WT	-3σ	Ints6l	integrator complex subunit 6 like	X|X A6	236790
TC0100000836.mm.1	0.0033385	-2.18307	-1.12636	Null_Rptor down vs WT	-3σ	Ugt1a2	UDP glucuronosyltransferase 1 family, polypeptide A2	1|1 D	22236
TC1600001573.mm.1	0.0112486	-2.1851	-1.1277	Null_Rptor down vs WT	-3σ	BC100530	cDNA sequence BC100530	16|16 B3	1E+08
TC1400001174.mm.1	0.0104931	-2.18653	-1.12864	Null_Rptor down vs WT	-3σ	Uchl3	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	14 E2.3|14 50.9 cM	50933
TC0100001190.mm.1	0.0079704	-2.18967	-1.13072	Null_Rptor down vs WT	-3σ	Nuak2	NUAK family, SNF1-like kinase, 2	1|1 E4	74137
TC1900000609.mm.1	0.0014536	-2.19113	-1.13168	Null_Rptor down vs WT	-3σ	Pi4k2a	phosphatidylinositol 4-kinase type 2 alpha	19 C3|19 35.74 cM	84095
TC1500001714.mm.1	0.0840703	-2.19266	-1.13268	Null_Rptor down vs WT	-3σ	Slurp1	secreted Ly6/Plaur domain containing 1	15|15 D3	57277
TC0800002313.mm.1	0.0029625	-2.19296	-1.13288	Null_Rptor down vs WT	-3σ	Msmo1	methylsterol monoxygenase 1	8|8 B3.1	66234
TC0500003064.mm.1	0.0201133	-2.19392	-1.13351	Null_Rptor down vs WT	-3σ	Gltp	glycolipid transfer protein	5|5 F	56356
TC1700000356.mm.1	0.0245922	-2.19609	-1.13494	Null_Rptor down vs WT	-3σ	Spsb3	splA/ryanodine receptor domain and SOCS box containing 3	17|17 A3.3	79043
TC0400001250.mm.1	0.0006938	-2.19691	-1.13547	Null_Rptor down vs WT	-3σ	Pik3r3	phosphoinositide-3-kinase regulatory subunit 3	4|4 D1	18710
TC1000002239.mm.1	0.0181704	-2.19827	-1.13637	Null_Rptor down vs WT	-3σ	Sgpl1	sphingosine phosphate lyase 1	10 B4|10 32.14 cM	20397
TC1500001041.mm.1	0.0008176	-2.19864	-1.13661	Null_Rptor down vs WT	-3σ	Mettl7a3	methyltransferase like 7A3	15 F1|15	668178
TC0900001	0.0028327	-2.19868	-1.13664	Null_Rptor	-3σ	Sh3bgr	SH3 domain binding	9|9 E2	212531

099.mm.1				down vs WT		l2	glutamic acid-rich protein like 2		
TC1200001030.mm.1	0.0044407	-2.19928	-1.13703	Null_Rptor down vs WT	-3σ	Ifi27	interferon, alpha-inducible protein 27	12 E|12 52.93 cM	52668
TC0300003232.mm.1	0.0057725	-2.20018	-1.13762	Null_Rptor down vs WT	-3σ	Glt28d2	glycosyltransferase 28 domain containing 2	3|3 F1	320302
TC1100003564.mm.1	0.034859	-2.20183	-1.1387	Null_Rptor down vs WT	-3σ	Epn3	epsin 3	11|11 D	71889
TC0500002799.mm.1	0.0006492	-2.20248	-1.13913	Null_Rptor down vs WT	-3σ	Paqr3	progestin and adipoQ receptor family member III	5|5 E3	231474
TC1800000929.mm.1	0.0532879	-2.20605	-1.14146	Null_Rptor down vs WT	-3σ	Map3k8	mitogen-activated protein kinase kinase kinase 8	18 A1|18 2.73 cM	26410
TC0900001887.mm.1	0.0116779	-2.20653	-1.14178	Null_Rptor down vs WT	-3σ	Rab3d	RAB3D, member RAS oncogene family	9|9 A3	19340
TC1100002988.mm.1	0.0101714	-2.20793	-1.1427	Null_Rptor down vs WT	-3σ	Map2k4	mitogen-activated protein kinase kinase 4	11 B3|11 40.53 cM	26398
TC0X00000156.mm.1	0.0619318	-2.20872	-1.14321	Null_Rptor down vs WT	-3σ	AA414768	expressed sequence AA414768	X|X A1.1	245350
TC1200000200.mm.1	0.0090733	-2.20922	-1.14354	Null_Rptor down vs WT	-3σ	Grhl1	grainyhead-like 1 (Drosophila)	12|12 A1.3	195733
TC1400000581.mm.1	0.0119046	-2.211	-1.1447	Null_Rptor down vs WT	-3σ	Rnase2b	ribonuclease, RNase A family, 2B (liver, eosinophil-derived neurotoxin)	14|14 C1	54159
TC1000002586.mm.1	0.0222897	-2.21251	-1.14568	Null_Rptor down vs WT	-3σ	Appl2	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	10|10 C1	216190
TC0700004620.mm.1	0.0232139	-2.2178	-1.14913	Null_Rptor down vs WT	-3σ	Sbsn	suprabasin	7 B1|7	282619
TC0600001458.mm.1	0.0125049	-2.221	-1.15121	Null_Rptor down vs WT	-3σ	Scnn1a	sodium channel, nonvoltage-gated 1 alpha	6 F3|6 59.32 cM	20276
TC1300002453.mm.1	0.0245261	-2.22483	-1.1537	Null_Rptor down vs WT	-3σ	Pde8b	phosphodiesterase 8B	13|13 D1	218461
TC1300001318.mm.1	0.0037775	-2.2249	-1.15374	Null_Rptor down vs WT	-3σ	Mocs2	molybdenum cofactor synthesis 2	13|13 D2.2	17434
TC0800001872.mm.1	0.0010421	-2.22878	-1.15625	Null_Rptor down vs WT	-3σ	Polb	polymerase (DNA directed), beta	8 A2|8 11.42 cM	18970
TC1100001935.mm.1	0.0011068	-2.23024	-1.1572	Null_Rptor down vs WT	-3σ	Sphk1	sphingosine kinase 1	11|11 E2	20698
TC1600001419.mm.1	0.0070093	-2.23223	-1.15848	Null_Rptor down vs WT	-3σ	Cldn1	claudin 1	16|16 B2	12737
TC0500002234.mm.1	0.0010204	-2.23358	-1.15936	Null_Rptor down vs WT	-3σ	Gm5553	predicted gene 5553	5|5 B2	433874
TC1100001583.mm.1	0.0142068	-2.23433	-1.15984	Null_Rptor down vs WT	-3σ	Rapgefl1	Rap guanine nucleotide exchange factor (GEF)-like 1	11|11 D	268480
TC1100002102.mm.1	0.0671098	-2.23458	-1.16001	Null_Rptor down vs WT	-3σ	Slc35e4	solute carrier family 35, member E4	11|11 A1	103710
TC1100003399.mm.1	0.0197571	-2.24242	-1.16506	Null_Rptor down vs WT	-3σ	Ccl6	chemokine (C-C motif) ligand 6	11 C|11 50.85 cM	20305
TC0500003243.mm.1	0.0011781	-2.24272	-1.16525	Null_Rptor down vs WT	-3σ	Hcar2	hydroxycarboxylic acid receptor 2	5|5 F	80885
TC0300001410.mm.1	0.0200779	-2.25412	-1.17256	Null_Rptor down vs WT	-3σ	Adh6a	alcohol dehydrogenase 6A (class V)	3|3 G3	69117
TC0700002223.mm.1	0.0123279	-2.25673	-1.17423	Null_Rptor down vs WT	-3σ	Zfp772	zinc finger protein 772	7|7 A1	232855
TC1100003677.mm.1	0.0093744	-2.25802	-1.17506	Null_Rptor down vs WT	-3σ	Mien1	migration and invasion enhancer 1	11|11 D	103742
TC0100002890.mm.1	0.0010549	-2.25857	-1.17541	Null_Rptor down vs WT	-3σ	Gm7160	predicted gene 7160	1|1 E2.1	635504
TC0100003102.mm.1	0.0009222	-2.26051	-1.17665	Null_Rptor down vs WT	-3σ	Btg2	B cell translocation gene 2, anti-proliferative	1 E4|1 58.1 cM	12227

TC0900002115.mm.1	0.0045788	-2.26096	-1.17693	Null_Rptor down vs WT	-3σ	Sc5d	sterol-C5-desaturase	9|9 A5.1	235293
TC0400000425.mm.1	0.0296386	-2.26374	-1.17871	Null_Rptor down vs WT	-3σ	Phf24	PHD finger protein 24	4|4 A5	230085
TC1500000235.mm.1	0.0757091	-2.26412	-1.17895	Null_Rptor down vs WT	-3σ	Laptm4b	lysosomal-associated protein transmembrane 4B	15|15 B3.1	114128
TC0600000775.mm.1	0.003306	-2.2642	-1.179	Null_Rptor down vs WT	-3σ	Gng12	guanine nucleotide binding protein (G protein), gamma 12	6 C1|6 30.68 cM	14701
TC1300000460.mm.1	0.0096745	-2.26601	-1.18016	Null_Rptor down vs WT	-3σ	Gcnt2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	13 A3.3|13 20.12 cM	14538
TC0700001660.mm.1	0.0073729	-2.26666	-1.18057	Null_Rptor down vs WT	-3σ	Arntl	aryl hydrocarbon receptor nuclear translocator-like	7 F1|7 59.17 cM	11865
TC0700002102.mm.1	0.0135465	-2.26862	-1.18181	Null_Rptor down vs WT	-3σ	Dhcr7	7-dehydrocholesterol reductase	7|7 F5	13360
TC1000002776.mm.1	0.0013928	-2.27591	-1.18645	Null_Rptor down vs WT	-3σ	4930430F08Rik	RIKEN cDNA 4930430F08 gene	10|10 D1	68281
TC0700003806.mm.1	0.0002389	-2.27628	-1.18668	Null_Rptor down vs WT	-3σ	Neu3	neuraminidase 3	7|7 E1	50877
TC0500001590.mm.1	0.0108103	-2.28008	-1.18908	Null_Rptor down vs WT	-3σ	Hspb1	heat shock protein 1	5 G2|5 75.51 cM	15507
TC1900001691.mm.1	0.0011585	-2.28182	-1.19018	Null_Rptor down vs WT	-3σ	Gpam	glycerol-3-phosphate acyltransferase, mitochondrial	19 D2|19 50.81 cM	14732
TC0100003888.mm.1	0.0181467	-2.28324	-1.19108	Null_Rptor down vs WT	-3σ	Ifi204	interferon activated gene 204	1 H3|1 80.63 cM	15951
TC0900001155.mm.1	0.0222252	-2.28372	-1.19138	Null_Rptor down vs WT	-3σ	Ctsh	cathepsin H	9 E3.1|9 47.4 cM	13036
TC0600001807.mm.1	0.0006414	-2.28454	-1.1919	Null_Rptor down vs WT	-3σ	Pon3	paraoxonase 3	6 A1|6 1.99 cM	269823
TC1000002050.mm.1	0.0045914	-2.28698	-1.19345	Null_Rptor down vs WT	-3σ	Fig4	FIG4 phosphoinositide 5-phosphatase	10|10 B1	103199
TC0800001137.mm.1	0.0054746	-2.28889	-1.19465	Null_Rptor down vs WT	-3σ	Ccdc113	coiled-coil domain containing 113	8|8 C5	244608
TC1100001886.mm.1	0.0180646	-2.28929	-1.1949	Null_Rptor down vs WT	-3σ	Slc9a3r1	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	11|11 E2	26941
TC0700000707.mm.1	0.0135222	-2.29261	-1.19699	Null_Rptor down vs WT	-3σ	Gm2058	ubiquitin-conjugating enzyme E2H pseudogene	7|7 B3	1E+08
TC0500000260.mm.1	0.0346994	-2.29505	-1.19853	Null_Rptor down vs WT	-3σ	Insig1	insulin induced gene 1	5|5 B1	231070
TC0400003361.mm.1	0.0756508	-2.29521	-1.19862	Null_Rptor down vs WT	-3σ	Plk3	polo like kinase 3	4|4 D1	12795
TC1100002069.mm.1	0.0056793	-2.29932	-1.20121	Null_Rptor down vs WT	-3σ	Metrnl	meteorin, glial cell differentiation regulator-like	11|11 E2	210029
TC1100003072.mm.1	0.0188927	-2.29979	-1.2015	Null_Rptor down vs WT	-3σ	Kctd11	potassium channel tetramerisation domain containing 11	11|11 B3	216858
TC0200000382.mm.1	0.0269279	-2.3005	-1.20195	Null_Rptor down vs WT	-3σ	Il1rn	interleukin 1 receptor antagonist	2 A3|2 16.36 cM	16181
TC0X00002689.mm.1	0.0024416	-2.30202	-1.2029	Null_Rptor down vs WT	-3σ	Ophn1	oligophrenin 1	X|X C3	94190
TC0300000736.mm.1	0.0048192	-2.30241	-1.20315	Null_Rptor down vs WT	-3σ	Rit1	Ras-like without CAAX 1	3|3 F1	19769
TC0200002491.mm.1	0.0069438	-2.30414	-1.20423	Null_Rptor down vs WT	-3σ	Ttpal	tocopherol (alpha) transfer protein-like	2|2 H3	76080
TC0100002562.mm.1	0.0305734	-2.31258	-1.2095	Null_Rptor down vs WT	-3σ	Igfbp5	insulin-like growth factor binding protein 5	1 C3|1 36.94 cM	16011

TC0800002402.mm.1	0.0051753	-2.3129	-1.2097	Null_Rptor down vs WT	-3σ	Mpv17l2	MPV17 mitochondrial membrane protein-like 2	8|8 B3.3	234384
TC0X00001782.mm.1	0.0199227	-2.31409	-1.21045	Null_Rptor down vs WT	-3σ	Ccdc120	coiled-coil domain containing 120	X A1.1|X 3.48 cM	54648
TC1400002393.mm.1	0.026847	-2.31578	-1.2115	Null_Rptor down vs WT	-3σ	Gm20290	predicted gene, 20290	14 D3|14 38.89 cM	1E+08
TC0800002535.mm.1	0.0498591	-2.31869	-1.21331	Null_Rptor down vs WT	-3σ	Usp38	ubiquitin specific peptidase 38	8 C2|8 38.68 cM	74841
TC1500001389.mm.1	0.0149049	-2.31873	-1.21334	Null_Rptor down vs WT	-3σ	Zfp706	zinc finger protein 706	15|15 B3.1	68036
TC0600002323.mm.1	0.0021991	-2.31897	-1.21349	Null_Rptor down vs WT	-3σ	Nod1	nucleotide-binding oligomerization domain containing 1	6|6 B3	107607
TC0900002944.mm.1	0.003025	-2.32165	-1.21515	Null_Rptor down vs WT	-3σ	Ppp2r3a	protein phosphatase 2, regulatory subunit B'', alpha	9|9 E4	235542
TC0400003285.mm.1	0.0296202	-2.3257	-1.21767	Null_Rptor down vs WT	-3σ	Slc5a9	solute carrier family 5 (sodium/glucose cotransporter), member 9	4|4 D1	230612
TC0600001289.mm.1	0.0852318	-2.32987	-1.22025	Null_Rptor down vs WT	-3σ	Rho	rhodopsin	6 E3|6 53.72 cM	212541
TC0200004826.mm.1	0.003808	-2.33004	-1.22035	Null_Rptor down vs WT	-3σ	Zfp120	zinc finger protein 120	2|2 G3	104348
TC1400002689.mm.1	0.0017039	-2.33246	-1.22185	Null_Rptor down vs WT	-3σ	Slitrk6	SLIT and NTRK-like family, member 6	14|14 E3	239250
TC0700002652.mm.1	0.0093837	-2.3329	-1.22213	Null_Rptor down vs WT	-3σ	Cyp2b23	cytochrome P450, family 2, subfamily b, polypeptide 23	7|7 A3	243881
TC1600002168.mm.1	0.027639	-2.33622	-1.22418	Null_Rptor down vs WT	-3σ	Vasn	vasorin	16|16 A1	246154
TC1300001263.mm.1	3.88E-06	-2.3382	-1.2254	Null_Rptor down vs WT	-3σ	Ankrd55	ankyrin repeat domain 55	13|13 D2.2	77318
TC1100003702.mm.1	0.125501	-2.33828	-1.22545	Null_Rptor down vs WT	-3σ	Krt25	keratin 25	11|11 D	70810
TC1600000512.mm.1	0.0084043	-2.33876	-1.22574	Null_Rptor down vs WT	-3σ	Stfa1	stefin A1	16 B3|16 25.45 cM	20861
TC0400001192.mm.1	0.0385716	-2.34007	-1.22655	Null_Rptor down vs WT	-3σ	Skint8	selection and upkeep of intraepithelial T cells 8	4|4 D1	639774
TC1200000614.mm.1	0.0281172	-2.34101	-1.22713	Null_Rptor down vs WT	-3σ	Daam1	dishevelled associated activator of morphogenesis 1	12|12 C3	208846
TC0700000852.mm.1	0.0188645	-2.34406	-1.22901	Null_Rptor down vs WT	-3σ	Hsd17b14	hydroxysteroid (17-beta) dehydrogenase 14	7|7 B3	66065
TC0200000277.mm.1	0.0756742	-2.34687	-1.23074	Null_Rptor down vs WT	-3σ	Gm20038	predicted gene, 20038	2|2 11.87 cM	1E+08
TC0300000264.mm.1	0.0031784	-2.34809	-1.23149	Null_Rptor down vs WT	-3σ	Acad9	acyl-Coenzyme A dehydrogenase family, member 9	3|3 B	229211
TC0100001220.mm.1	0.0617323	-2.34826	-1.23159	Null_Rptor down vs WT	-3σ	Chit1	chitinase 1 (chitotriosidase)	1|1 E4	71884
TC1000001020.mm.1	0.0133887	-2.36532	-1.24203	Null_Rptor down vs WT	-3σ	Tcp11l2	t-complex 11 (mouse) like 2	10|10 C1	216198
TC1100000494.mm.1	0.0053791	-2.36563	-1.24223	Null_Rptor down vs WT	-3σ	Trim7	tripartite motif-containing 7	11|11 B1.2	94089
TC1900000604.mm.1	0.0105335	-2.36593	-1.24241	Null_Rptor down vs WT	-3σ	Ubtd1	ubiquitin domain containing 1	19|19 C3	226122
TC0800002992.mm.1	0.0179841	-2.36643	-1.24271	Null_Rptor down vs WT	-3σ	Maf	avian musculoaponeurotic fibrosarcoma oncogene homolog	8 E1|8 62.61 cM	17132
TC0100003401.mm.1	0.0005403	-2.36679	-1.24293	Null_Rptor down vs WT	-3σ	Fmo1	flavin containing monooxygenase 1	1 H2.1|1 70.34 cM	14261
TC1100001	0.0064991	-2.37051	-1.2452	Null_Rptor	-3σ	Ift20	intraflagellar transport 20	11|11	55978

165.mm.1				down vs WT				B5	
TC1300000013.mm.1	0.0238052	-2.37206	-1.24614	Null_Rptor down vs WT	-3σ	Calm4	calmodulin 4	13|13 A1	80796
TC1700000314.mm.1	0.0071902	-2.37244	-1.24637	Null_Rptor down vs WT	-3σ	Bicdl2	BICD family like cargo adaptor 2	17|17 A3.3	212733
TC0800000991.mm.1	0.0005107	-2.37671	-1.24897	Null_Rptor down vs WT	-3σ	Gpt2	glutamic pyruvate transaminase (alanine aminotransferase) 2	8|8 C3	108682
TC0500002075.mm.1	0.0865589	-2.37743	-1.2494	Null_Rptor down vs WT	-3σ	Atg9b	autophagy related 9B	5 A3|5 11.49 cM	213948
TC0600003017.mm.1	0.0070005	-2.38146	-1.25185	Null_Rptor down vs WT	-3σ	Adipor2	adiponectin receptor 2	6 F1|6 56.78 cM	68465
TC0700002632.mm.1	0.0378402	-2.38314	-1.25287	Null_Rptor down vs WT	-3σ	Lipe	lipase, hormone sensitive	7 A3|7 13.78 cM	16890
TC0700004520.mm.1	0.0133947	-2.38327	-1.25294	Null_Rptor down vs WT	-3σ	Ano9	anoctamin 9	7|7 F5	71345
TC1300000255.mm.1	0.0951364	-2.3857	-1.25441	Null_Rptor down vs WT	-3σ	Hist1h2bc	histone cluster 1, H2bc	13|13 A3.1	68024
TC1600002024.mm.1	0.145481	-2.38907	-1.25645	Null_Rptor down vs WT	-3σ	Krtap22-2	keratin associated protein 22-2	16|16 C3.3	68740
TC1700001805.mm.1	0.0025225	-2.39637	-1.26085	Null_Rptor down vs WT	-3σ	Glo1	glyoxalase 1	17 A3.3|17 15.69 cM	109801
TC1500000605.mm.1	0.0010854	-2.39887	-1.26236	Null_Rptor down vs WT	-3σ	Gpt	glutamic pyruvic transaminase, soluble	15 D3|15 36.28 cM	76282
TC0500003286.mm.1	0.0106868	-2.40037	-1.26326	Null_Rptor down vs WT	-3σ	Tmem132d	transmembrane protein 132D	5|5 G1.2-G1.3	243274
TC0200000638.mm.1	0.0017574	-2.40092	-1.26359	Null_Rptor down vs WT	-3σ	Gm13443	glyoxalase 1 pseudogene	2|2 B	654354
TC0100000485.mm.1	0.101346	-2.40112	-1.26371	Null_Rptor down vs WT	-3σ	Ctla4	cytotoxic T-lymphocyte-associated protein 4	1 C2|1 30.58 cM	12477
TC1900001080.mm.1	0.0287552	-2.40175	-1.26408	Null_Rptor down vs WT	-3σ	Scgb1a1	secretoglobin, family 1A, member 1 (uteroglobin)	19|19 A	22287
TC1400000513.mm.1	0.0147667	-2.40746	-1.26751	Null_Rptor down vs WT	-3σ	Lgals3	lectin, galactose binding, soluble 3	14|14 C1	16854
TC0500000397.mm.1	0.0012751	-2.40913	-1.26851	Null_Rptor down vs WT	-3σ	Acox3	acyl-Coenzyme A oxidase 3, pristanoyl	5|5 B3	80911
TC0300001581.mm.1	0.0019828	-2.41331	-1.27101	Null_Rptor down vs WT	-3σ	Ankrd13c	ankyrin repeat domain 13c	3|3 H4	433667
TC1300000090.mm.1	0.0025993	-2.41367	-1.27123	Null_Rptor down vs WT	-3σ	Gng4	guanine nucleotide binding protein (G protein), gamma 4	13 A1|13 5.29 cM	14706
TC1500000073.mm.1	0.0166898	-2.41479	-1.2719	Null_Rptor down vs WT	-3σ	Ugt3a2	UDP glycosyltransferases 3 family, polypeptide A2	15|15 A1	223337
TC1300001353.mm.1	0.0015903	-2.41606	-1.27266	Null_Rptor down vs WT	-3σ	Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	13 D2.3|13	208715
TC0X00001067.mm.1	0.0020711	-2.42006	-1.27504	Null_Rptor down vs WT	-3σ	Atp7a	ATPase, Cu++ transporting, alpha polypeptide	X D|X 47.36 cM	11977
TC0300001137.mm.1	0.0052089	-2.42321	-1.27692	Null_Rptor down vs WT	-3σ	Sort1	sortilin 1	3|3 F2.3-F3	20661
TC0900003040.mm.1	0.0201958	-2.435	-1.28392	Null_Rptor down vs WT	-3σ	Slc38a3	solute carrier family 38, member 3	9 F1|9 58.69 cM	76257
TC0500001225.mm.1	0.0093311	-2.4394	-1.28652	Null_Rptor down vs WT	-3σ	Mvk	mevalonate kinase	5 F|5 55.99 cM	17855
TC1000000142.mm.1	0.0086434	-2.44067	-1.28728	Null_Rptor down vs WT	-3σ	Ifngr1	interferon gamma receptor 1	10 A3|10 8.49 cM	15979

TC0300003013.mm.1	0.0092874	-2.44072	-1.28731	Null_Rptor down vs WT	-3σ	Dapp1	dual adaptor for phosphotyrosine and 3-phosphoinositides 1	3|3 G3	26377
TC1700001766.mm.1	0.0203119	-2.44136	-1.28768	Null_Rptor down vs WT	-3σ	Srpk1	serine/arginine-rich protein specific kinase 1	17|17 A3.3	20815
TC0400001512.mm.1	0.026541	-2.44144	-1.28773	Null_Rptor down vs WT	-3σ	Tmem54	transmembrane protein 54	4|4 D2.2	66260
TC1400002193.mm.1	0.0058013	-2.44568	-1.29024	Null_Rptor down vs WT	-3σ	Spryd7	SPRY domain containing 7	14|14 D1	66674
TC0700002646.mm.1	0.0031078	-2.45014	-1.29287	Null_Rptor down vs WT	-6σ	Cyp2s1	cytochrome P450, family 2, subfamily s, polypeptide 1	7|7 A3	74134
TC1400002333.mm.1	0.0110422	-2.45137	-1.29359	Null_Rptor down vs WT	-6σ	Pdlim2	PDZ and LIM domain 2	14|14 D2	213019
TC0300002838.mm.1	0.0229776	-2.45412	-1.29521	Null_Rptor down vs WT	-6σ	Tmem56	transmembrane protein 56	3|3 G1	99887
TC0100002552.mm.1	0.0105964	-2.46022	-1.29879	Null_Rptor down vs WT	-6σ	Mreg	melanoregulin	1|1 C3	381269
TC1600001154.mm.1	0.0196424	-2.46355	-1.30074	Null_Rptor down vs WT	-6σ	Ppl	periplakin	16 A1|16 2.5 cM	19041
TC1100004254.mm.1	0.0079132	-2.46756	-1.30309	Null_Rptor down vs WT	-6σ	Zfp750	zinc finger protein 750	11|11 E2	319530
TC1500000388.mm.1	0.0100186	-2.46864	-1.30372	Null_Rptor down vs WT	-6σ	Mal2	mal, T cell differentiation protein 2	15|15 D1	105853
TC1100001095.mm.1	0.0087567	-2.46986	-1.30443	Null_Rptor down vs WT	-6σ	Fam57a	family with sequence similarity 57, member A	11|11 B5	116972
TC0400001405.mm.1	0.0030723	-2.47437	-1.30706	Null_Rptor down vs WT	-6σ	Rhbdl2	rhomboid, veinlet-like 2 (Drosophila)	4|4 D2.2	230726
TC1300000958.mm.1	0.0236348	-2.47722	-1.30872	Null_Rptor down vs WT	-6σ	Arrdc3	arrestin domain containing 3	13|13 C2	105171
TC0900001782.mm.1	0.0766134	-2.47931	-1.30994	Null_Rptor down vs WT	-6σ	Hephl1	hephaestin-like 1	9|9 A2	244698
TC0700000033.mm.1	0.0504461	-2.48116	-1.31102	Null_Rptor down vs WT	-6σ	Eps8l1	EPS8-like 1	7|7 A1	67425
TC0800000424.mm.1	0.0012849	-2.48128	-1.31108	Null_Rptor down vs WT	-6σ	Ppp1r3b	protein phosphatase 1, regulatory (inhibitor) subunit 3B	8|8 A4	244416
TC0X00002637.mm.1	0.0043528	-2.48178	-1.31138	Null_Rptor down vs WT	-6σ	Pdk3	pyruvate dehydrogenase kinase, isoenzyme 3	X|X C3	236900
TC1900001353.mm.1	0.0234104	-2.48225	-1.31165	Null_Rptor down vs WT	-6σ	Ranbp6	RAN binding protein 6	19|19 C1	240614
TC0200000383.mm.1	0.0077077	-2.48278	-1.31196	Null_Rptor down vs WT	-6σ	Psd4	pleckstrin and Sec7 domain containing 4	2|2 A3	215632
TC1600001358.mm.1	0.0444505	-2.49164	-1.3171	Null_Rptor down vs WT	-6σ	Teddm3	transmembrane epididymal family member 3	16|16 B1	66561
TC0100001010.mm.1	0.0111489	-2.49283	-1.31778	Null_Rptor down vs WT	-6σ	Gm10193	predicted gene 10193	1 E2.1|1	1E+08
TC1700001053.mm.1	0.0228022	-2.49782	-1.32067	Null_Rptor down vs WT	-6σ	Fer	fer (fms/fps related) protein kinase	17|17 E1.1	14158
TC1600000787.mm.1	0.0029121	-2.49972	-1.32177	Null_Rptor down vs WT	-6σ	Stx19	syntaxin 19	16|16 C1.3	68159
TC1800000809.mm.1	0.0221002	-2.50583	-1.32529	Null_Rptor down vs WT	-6σ	Zbtb7c	zinc finger and BTB domain containing 7C	18|18 E3	207259
TC0900000637.mm.1	0.0004022	-2.5063	-1.32556	Null_Rptor down vs WT	-6σ	Exph5	exophilin 5	9|9 A5.3	320051
TC0500002528.mm.1	0.0036395	-2.50816	-1.32663	Null_Rptor down vs WT	-6σ	Atp8a1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	5|5 C3.1	11980
TC1100001109.mm.1	0.0293649	-2.50895	-1.32708	Null_Rptor down vs WT	-6σ	Blmh	bleomycin hydrolase	11|11 B5	104184
TC1100000859.mm.1	0.0612397	-2.51266	-1.32922	Null_Rptor down vs WT	-6σ	Gas7	growth arrest specific 7	11|11 B3	14457
TC1600001572.mm.1	0.015406	-2.51444	-1.33024	Null_Rptor down vs WT	-6σ	BC117090	cDNA sequence BC1179090	16|16 B3	1E+08
TC1400002332.mm.1	0.0388374	-2.51485	-1.33047	Null_Rptor down vs WT	-6σ	9930012K11Rik	RIKEN cDNA 9930012K11 gene	14|14 D2	268759
TC0700001	0.0201854	-2.51747	-1.33198	Null_Rptor	-6σ	Ampd3	adenosine monophosphate	7 E3|7	11717

631.mm.1				down vs WT			deaminase 3	57.85 cM	
TC1400000747.mm.1	0.0188392	-2.51787	-1.3322	Null_Rptor down vs WT	-6σ	Lrp10	low-density lipoprotein receptor-related protein 10	14|14 C2	65107
TC1300001784.mm.1	0.0278129	-2.51983	-1.33333	Null_Rptor down vs WT	-6σ	Slc22a23	solute carrier family 22, member 23	13|13 A3.3	73102
TSUnmapped00000002.mm.1	0.0310939	-2.51985	-1.33334	Null_Rptor down vs WT	-6σ	Vsig10l	V-set and immunoglobulin domain containing 10 like	7|7 B3	75690
TC1100001108.mm.1	0.0756542	-2.52094	-1.33396	Null_Rptor down vs WT	-6σ	Tmigd1	transmembrane and immunoglobulin domain containing 1	11|11 B5	66601
TC1400000835.mm.1	0.0051143	-2.52354	-1.33545	Null_Rptor down vs WT	-6σ	Cab39l	calcium binding protein 39-like	14|14 C3	69008
TC0300002257.mm.1	0.0092888	-2.52707	-1.33746	Null_Rptor down vs WT	-6σ	Fam160a1	family with sequence similarity 160, member A1	3|3 F1	229488
TC0800002577.mm.1	0.0204286	-2.5307	-1.33954	Null_Rptor down vs WT	-6σ	Zswim4	zinc finger SWIM-type containing 4	8|8 C2	212168
TC1900001346.mm.1	0.0013976	-2.53075	-1.33957	Null_Rptor down vs WT	-6σ	Ermp1	endoplasmic reticulum metallopeptidase 1	19 C1|19 24.17 cM	226090
TC1300002017.mm.1	0.0030713	-2.53305	-1.34087	Null_Rptor down vs WT	-6σ	Sptlc1	serine palmitoyltransferase, long chain base subunit 1	13|13 B1	268656
TC0500000527.mm.1	0.0652008	-2.53397	-1.3414	Null_Rptor down vs WT	-6σ	Sod3	superoxide dismutase 3, extracellular	5 C1|5 27.92 cM	20657
TC1100003753.mm.1	0.0364839	-2.53444	-1.34167	Null_Rptor down vs WT	-6σ	Krt35	keratin 35	11|11 D	53617
TC1000000265.mm.1	0.0029033	-2.53569	-1.34238	Null_Rptor down vs WT	-6σ	Echdc1	enoyl Coenzyme A hydratase domain containing 1	10 A4|10 16.59 cM	52665
TC0700002230.mm.1	0.0085756	-2.53635	-1.34275	Null_Rptor down vs WT	-6σ	Gm3912	predicted gene 3912	7 A1|7	1E+08
TC0700001816.mm.1	0.0035277	-2.53692	-1.34308	Null_Rptor down vs WT	-6σ	Ypel3	yippee-like 3 (Drosophila)	7|7 F3	66090
TC0700002606.mm.1	0.0065665	-2.53838	-1.34391	Null_Rptor down vs WT	-6σ	Pinlyp	phospholipase A2 inhibitor and LY6/PLAUR domain containing	7|7 A3	641361
TC1500001348.mm.1	0.0051217	-2.53867	-1.34407	Null_Rptor down vs WT	-6σ	Nipal2	NIPA-like domain containing 2	15|15 B3.1	223473
TC1300002210.mm.1	0.0127581	-2.53952	-1.34456	Null_Rptor down vs WT	-6σ	Mfsd14b	major facilitator superfamily domain containing 14B	13|13 B3	66631
TC0100002350.mm.1	0.0673861	-2.54021	-1.34495	Null_Rptor down vs WT	-6σ	Ankrd44	ankyrin repeat domain 44	1|1 C1.2	329154
TSUnmapped00000020.mm.1	0.0112683	-2.54323	-1.34666	Null_Rptor down vs WT	-6σ	Snx29	sorting nexin 29	16|16 A1	74478
TC0400002531.mm.1	0.0805385	-2.54578	-1.34811	Null_Rptor down vs WT	-6σ	Gba2	glucosidase beta 2	4|4 A5	230101
TC1200002029.mm.1	0.0255835	-2.54597	-1.34822	Null_Rptor down vs WT	-6σ	Map3k9	mitogen-activated protein kinase kinase kinase 9	12|12 D1	338372
TC1500000782.mm.1	0.0062463	-2.54808	-1.34941	Null_Rptor down vs WT	-6σ	Pnpla3	patatin-like phospholipase domain containing 3	15|15 E2	116939
TC1100003704.mm.1	0.0812629	-2.54824	-1.3495	Null_Rptor down vs WT	-6σ	Krt27	keratin 27	11 D|11 62.92 cM	16675
TC0300000710.mm.1	0.0129011	-2.55338	-1.35241	Null_Rptor down vs WT	-6σ	Crabp2	cellular retinoic acid binding protein II	3 F1|3	12904
TC0800000271.mm.1	0.0093738	-2.55352	-1.35249	Null_Rptor down vs WT	-6σ	Thsd1	thrombospondin, type I, domain 1	8|8 A2	56229
TC1400002142.mm.1	0.0029788	-2.56189	-1.35721	Null_Rptor down vs WT	-6σ	Cryl1	crystallin, lambda 1	14 C3|14 30.1 cM	68631
TC1700001465.mm.1	0.0050858	-2.56503	-1.35897	Null_Rptor down vs WT	-6σ	Unc93a	unc-93 homolog A (C. elegans)	17 A1|17 8.78 cM	381058

TC1100000343.mm.1	0.0508173	-2.57016	-1.36186	Null_Rptor down vs WT	-6σ	Stk10	serine/threonine kinase 10	11 18.97 cM|11 A4	20868
TC1600000215.mm.1	0.0122718	-2.57375	-1.36387	Null_Rptor down vs WT	-6σ	Snap29	synaptosomal-associated protein 29	16|16 A3	67474
TC1600001671.mm.1	0.0549164	-2.57469	-1.3644	Null_Rptor down vs WT	-6σ	Plcxd2	phosphatidylinositol-specific phospholipase C, X domain containing 2	16|16 B5	433022
TC0300002413.mm.1	0.026015	-2.57579	-1.36501	Null_Rptor down vs WT	-6σ	Lce1l	late cornified envelope 1L	3|3 F1	73730
TC1700001835.mm.1	0.0439704	-2.57859	-1.36658	Null_Rptor down vs WT	-6σ	Ephx3	epoxide hydrolase 3	17|17 B1	71932
TC0700002703.mm.1	0.02428	-2.58124	-1.36807	Null_Rptor down vs WT	-6σ	Acp7	acid phosphatase 7, tartrate resistant	7|7 B1	101744
TC0700002496.mm.1	0.0339315	-2.58175	-1.36835	Null_Rptor down vs WT	-6σ	Apoc1	apolipoprotein C-I	7 A3|7 9.94 cM	11812
TC0X00000229.mm.1	0.0739083	-2.58343	-1.36929	Null_Rptor down vs WT	-6σ	Slc6a14	solute carrier family 6 (neurotransmitter transporter), member 14	X|X A2	56774
TC0200002876.mm.1	0.0270242	-2.58392	-1.36956	Null_Rptor down vs WT	-6σ	Camk1d	calcium/calmodulin-dependent protein kinase ID	2|2 A1	227541
TC1900000941.mm.1	0.0062789	-2.58879	-1.37228	Null_Rptor down vs WT	-6σ	Dpp3	dipeptidylpeptidase 3	19|19 A	75221
TC1100000994.mm.1	0.006163	-2.5915	-1.37379	Null_Rptor down vs WT	-6σ	Ggt6	gamma-glutamyltransferase 6	11|11 B4	71522
TC1100003462.mm.1	0.0039048	-2.60008	-1.37856	Null_Rptor down vs WT	-6σ	Ypel2	yippee-like 2 (Drosophila)	11|11 C	77864
TC1700002117.mm.1	0.0167307	-2.60264	-1.37997	Null_Rptor down vs WT	-6σ	Adgrf2	adhesion G protein-coupled receptor F2	17|17 B3	435529
TC1600000295.mm.1	0.0667732	-2.60395	-1.3807	Null_Rptor down vs WT	-6σ	Gm6551	predicted gene 6551	16|16 B1	625060
TC0400001110.mm.1	0.0029164	-2.61316	-1.38579	Null_Rptor down vs WT	-6σ	Ttc22	tetratricopeptide repeat domain 22	4|4 C7	230576
TC1000002093.mm.1	0.0185644	-2.61394	-1.38623	Null_Rptor down vs WT	-6σ	Crybg1	crystallin beta-gamma domain containing 1	10 B2|10 23.14 cM	11630
TC0900002521.mm.1	0.0095538	-2.6161	-1.38742	Null_Rptor down vs WT	-6σ	Snx22	sorting nexin 22	9|9 C	382083
TC0700002727.mm.1	0.0087051	-2.61671	-1.38775	Null_Rptor down vs WT	-6σ	Catsperg2	cation channel sperm associated auxiliary subunit gamma 2	7|7 B1	76718
TC0900000103.mm.1	0.0067323	-2.61925	-1.38915	Null_Rptor down vs WT	-6σ	Sesn3	sestrin 3	9|9 A1	75747
TC0600003489.mm.1	0.0626857	-2.62111	-1.39018	Null_Rptor down vs WT	-6σ	Glcci1	glucocorticoid induced transcript 1	6|6 A1	170772
TC0100001111.mm.1	0.0018764	-2.6226	-1.391	Null_Rptor down vs WT	-6σ	Slc35f5	solute carrier family 35, member F5	1|1 E2.3	74150
TC1400001331.mm.1	0.005822	-2.62623	-1.39299	Null_Rptor down vs WT	-6σ	Clybl	citrate lyase beta like	14|14 E5	69634
TC0600001514.mm.1	0.0167243	-2.62823	-1.39409	Null_Rptor down vs WT	-6σ	Tom1	target of myb1 trafficking protein	8|8 C1	21968
TC0200004476.mm.1	0.0033236	-2.63004	-1.39509	Null_Rptor down vs WT	-6σ	Tgm5	transglutaminase 5	2|2 E5	74176
TC0100001570.mm.1	0.0214739	-2.63089	-1.39555	Null_Rptor down vs WT	-6σ	Olfml2b	olfactomedin-like 2B	1|1 H3	320078
TC0300000312.mm.1	0.0005897	-2.63443	-1.39749	Null_Rptor down vs WT	-6σ	Larp1b	La ribonucleoprotein domain family, member 1B	3|3 B	214048
TC1400001906.mm.1	0.0516717	-2.63548	-1.39807	Null_Rptor down vs WT	-6σ	Ddhd1	DDHD domain containing 1	14|14 C1	114874
TC0200004974.mm.1	0.0572949	-2.64086	-1.40101	Null_Rptor down vs WT	-6σ	Fam83c	family with sequence similarity 83, member C	2|2 H1	71405
TC0500000934.mm.1	0.0044042	-2.64232	-1.40181	Null_Rptor down vs WT	-6σ	Bmp2k	BMP2 inducible kinase	5|5 E3	140780
TC0400003694.mm.1	0.0055043	-2.64246	-1.40188	Null_Rptor down vs WT	-6σ	Sytl1	synaptotagmin-like 1	4|4 D2.3	269589
TC0900002312.mm.1	0.0665017	-2.64267	-1.40199	Null_Rptor down vs WT	-6σ	Elmod1	ELMO/CED-12 domain containing 1	9|9 A5.3	270162

TC1700002786.mm.1	0.027734	-2.64533	-1.40345	Null_Rptor down vs WT	-6σ	Ly6g6c	lymphocyte antigen 6 complex, locus G6C	17|17 B1	68468
TC0200004558.mm.1	0.0026506	-2.65533	-1.40889	Null_Rptor down vs WT	-6σ	Prom2	prominin 2	2|2 F1	192212
TC0800002441.mm.1	0.0116961	-2.65579	-1.40914	Null_Rptor down vs WT	-6σ	Fcho1	FCH domain only 1	8|8 B3.3	74015
TC0300000367.mm.1	0.0119603	-2.65597	-1.40924	Null_Rptor down vs WT	-6σ	Mgst2	microsomal glutathione S-transferase 2	3|3 C	211666
TC0400003267.mm.1	0.0235369	-2.65908	-1.41093	Null_Rptor down vs WT	-6σ	Rnf11	ring finger protein 11	4|4 C7	29864
TC0500000459.mm.1	0.0047599	-2.66756	-1.41552	Null_Rptor down vs WT	-6σ	Cpeb2	cytoplasmic polyadenylation element binding protein 2	5|5 B3	231207
TC1100000641.mm.1	0.0331009	-2.67006	-1.41687	Null_Rptor down vs WT	-6σ	Gm2a	GM2 ganglioside activator protein	11 B1.3|11 32.13 cM	14667
TC1800000331.mm.1	0.0095832	-2.67085	-1.4173	Null_Rptor down vs WT	-6σ	Slc4a9	solute carrier family 4, sodium bicarbonate cotransporter, member 9	18|18 B2	240215
TC1500000175.mm.1	0.0052015	-2.67133	-1.41756	Null_Rptor down vs WT	-6σ	Ank	progressive ankylosis	15 B1|15 10.23 cM	11732
TC0200000511.mm.1	0.0141159	-2.67233	-1.4181	Null_Rptor down vs WT	-6σ	Slc27a4	solute carrier family 27 (fatty acid transporter), member 4	2 B|2 20.64 cM	26569
TC0800000845.mm.1	0.0645014	-2.67281	-1.41836	Null_Rptor down vs WT	-6σ	Hmox1	heme oxygenase 1	8 35.59 cM|8 C1	15368
TC0400002945.mm.1	0.0071177	-2.67692	-1.42057	Null_Rptor down vs WT	-6σ	Ttc39b	tetratricopeptide repeat domain 39B	4|4 C3	69863
TC0100001031.mm.1	0.0145816	-2.67801	-1.42116	Null_Rptor down vs WT	-6σ	Serpinb8	serine (or cysteine) peptidase inhibitor, clade B, member 8	1|1 E2.1	20725
TC0100003058.mm.1	0.0030441	-2.67865	-1.42151	Null_Rptor down vs WT	-6σ	Srgap2	SLIT-ROBO Rho GTPase activating protein 2	1|1 E4	14270
TC0600000995.mm.1	0.0187538	-2.67913	-1.42177	Null_Rptor down vs WT	-6σ	Asprv1	aspartic peptidase, retroviral-like 1	6|6 D1	67855
TC1100001156.mm.1	0.0067869	-2.68268	-1.42368	Null_Rptor down vs WT	-6σ	Aldoc	aldolase C, fructose-bisphosphate	11 B5|11 46.74 cM	11676
TC1400000912.mm.1	0.0059781	-2.6862	-1.42557	Null_Rptor down vs WT	-6σ	Sox7	SRY (sex determining region Y)-box 7	14|14 D1	20680
TC1400001746.mm.1	0.000649	-2.68644	-1.4257	Null_Rptor down vs WT	-6σ	2610528A11Rik	RIKEN cDNA 2610528A11 gene	14|14 B	70045
TC0400001194.mm.1	0.0211084	-2.68658	-1.42577	Null_Rptor down vs WT	-6σ	Skint1	selection and upkeep of intraepithelial T cells 1	4|4 D1	639781
TC1500002071.mm.1	0.0037045	-2.69085	-1.42806	Null_Rptor down vs WT	-6σ	Kif21a	kinesin family member 21A	15 E3|15 45.86 cM	16564
TC0700000775.mm.1	0.0192326	-2.69312	-1.42928	Null_Rptor down vs WT	-6σ	Klk8	kallikrein related-peptidase 8	7 B3|7 28.26 cM	259277
TC0100000551.mm.1	0.0203252	-2.69893	-1.43239	Null_Rptor down vs WT	-6σ	Map2	microtubule-associated protein 2	1 C3|1 33.49 cM	17756
TC1900000141.mm.1	0.0058543	-2.7029	-1.43451	Null_Rptor down vs WT	-6σ	Pla2g16	phospholipase A2, group XVI	19|19 A	225845
TC0600003212.mm.1	0.0037169	-2.70392	-1.43505	Null_Rptor down vs WT	-6σ	Clec2j	C-type lectin domain family 2, member J	6|6 F3	677440
TC0900000532.mm.1	0.0130684	-2.70642	-1.43638	Null_Rptor down vs WT	-6σ	Mpzl3	myelin protein zero-like 3	9 A5.2|9 24.84 cM	319742
TC0100002702.mm.1	0.0021727	-2.70762	-1.43702	Null_Rptor down vs WT	-6σ	Slc16a14	solute carrier family 16 (monocarboxylic acid transporters), member 14	1|1 C5	71781
TC1000001573.mm.1	0.0064325	-2.71389	-1.44036	Null_Rptor down vs WT	-6σ	Rdh1	retinol dehydrogenase 1 (all trans)	10 D3|10	107605

								75.21 cM	
TC0300000806.mm.1	0.0515149	-2.71407	-1.44046	Null_Rptor down vs WT	-6σ	S100a3	S100 calcium binding protein A3	3 F1|3 39.26 cM	20197
TC0100003056.mm.1	0.0251257	-2.71845	-1.44279	Null_Rptor down vs WT	-6σ	Rassf5	Ras association (RalGDS/AF-6) domain family member 5	1 E4|1 56.91 cM	54354
TC0600003329.mm.1	0.0142261	-2.71973	-1.44346	Null_Rptor down vs WT	-6σ	Plbd1	phospholipase B domain containing 1	6|6 G1	66857
TC0300002399.mm.1	0.0541831	-2.72103	-1.44415	Null_Rptor down vs WT	-6σ	Lce6a	late cornified envelope 6A	3|3 F1	78382
TC0300000205.mm.1	0.0011601	-2.72499	-1.44625	Null_Rptor down vs WT	-6σ	Gpr160	G protein-coupled receptor 160	3|3 A3	71862
TC1900001227.mm.1	0.001469	-2.72526	-1.44639	Null_Rptor down vs WT	-6σ	Ostf1	osteoclast stimulating factor 1	19 B|19 13.17 cM	20409
TC1000000372.mm.1	0.0011733	-2.74658	-1.45764	Null_Rptor down vs WT	-6σ	Sesn1	sestrin 1	10 B2|10 22.77 cM	140742
TC1000000566.mm.1	0.0226006	-2.74898	-1.4589	Null_Rptor down vs WT	-6σ	Lrrc20	leucine rich repeat containing 20	10|10 B4	216011
TC0300002052.mm.1	0.0050824	-2.75468	-1.46188	Null_Rptor down vs WT	-6σ	Gpr87	G protein-coupled receptor 87	3|3 D	84111
TC0300002382.mm.1	0.0393227	-2.76167	-1.46554	Null_Rptor down vs WT	-6σ	Lor	loricrin	3 F1|3 40.14 cM	16939
TC0200001637.mm.1	0.0025568	-2.76314	-1.46631	Null_Rptor down vs WT	-6σ	Muc15	mucin 15	2|2 E3	269328
TC0900000892.mm.1	0.0041437	-2.77173	-1.47079	Null_Rptor down vs WT	-6σ	Rora	RAR-related orphan receptor alpha	9 C|9 37.45 cM	19883
TC0500002633.mm.1	0.0206167	-2.77347	-1.47169	Null_Rptor down vs WT	-6σ	Nmu	neuromedin U	5|5 C3.3	56183
TC0200003548.mm.1	0.0023827	-2.7741	-1.47202	Null_Rptor down vs WT	-6σ	Gm13502	predicted gene 13502	2|2 C1.1	207933
TC0300003085.mm.1	0.0219658	-2.77882	-1.47447	Null_Rptor down vs WT	-6σ	Clca2	chloride channel accessory 2	3|3 H2	229933
TC1600002177.mm.1	0.0177762	-2.78303	-1.47666	Null_Rptor down vs WT	-6σ	Dexi	dexamethasone-induced transcript	16 A1|16 5.67 cM	58239
TC1900001521.mm.1	0.0180055	-2.78463	-1.47748	Null_Rptor down vs WT	-6σ	Avpi1	arginine vasopressin-induced 1	19|19 C3	69534
TC0400000084.mm.1	0.0098847	-2.78867	-1.47958	Null_Rptor down vs WT	-6σ	Trp53inp1	transformation related protein 53 inducible nuclear protein 1	4|4 A1	60599
TC0400003321.mm.1	0.0012727	-2.78919	-1.47985	Null_Rptor down vs WT	-6σ	Cyp4b1	cytochrome P450, family 4, subfamily b, polypeptide 1	4 D1|4 53.06 cM	13120
TC0800002856.mm.1	0.0533726	-2.80835	-1.48972	Null_Rptor down vs WT	-6σ	Smpd3	sphingomyelin phosphodiesterase 3, neutral	8|8 D3	58994
TC0200002436.mm.1	0.0377525	-2.80933	-1.49023	Null_Rptor down vs WT	-6σ	Arhgap40	Rho GTPase activating protein 40	2|2 H1	545481
TC1300000284.mm.1	0.0261949	-2.8116	-1.49139	Null_Rptor down vs WT	-6σ	Gpld1	glycosylphosphatidylinositol specific phospholipase D1	13 A3.1|13 10.79 cM	14756
TC0900002985.mm.1	0.0523362	-2.81698	-1.49415	Null_Rptor down vs WT	-6σ	Acpp	acid phosphatase, prostate	9|9 F1	56318
TC0600001258.mm.1	0.0063092	-2.8224	-1.49692	Null_Rptor down vs WT	-6σ	Irak2	interleukin-1 receptor-associated kinase 2	6 E3|6 52.82 cM	108960
TC1400002017.mm.1	0.0151738	-2.8227	-1.49707	Null_Rptor down vs WT	-6σ	Ndrg2	N-myc downstream regulated gene 2	14|14 C1	29811
TC1900000763.mm.1	0.0004762	-2.83335	-1.50251	Null_Rptor down vs WT	-6σ	Pdcd4	programmed cell death 4	19 D2|19 48.73	18569

								cM	
TC1400002799.mm.1	0.0202597	-2.8334	-1.50253	Null_Rptor down vs WT	-6σ	Slc39a2	solute carrier family 39 (zinc transporter), member 2	14|14 C1	214922
TC0300002377.mm.1	0.0865851	-2.83565	-1.50368	Null_Rptor down vs WT	-6σ	Gm5849	predicted gene 5849	3|3 F1	545541
TC0200000376.mm.1	0.0939798	-2.83747	-1.50461	Null_Rptor down vs WT	-6σ	Il1f9	interleukin 1 family, member 9	2 A3|2 16.24 cM	215257
TC0700004201.mm.1	0.0026516	-2.83837	-1.50506	Null_Rptor down vs WT	-6σ	Cdr2	cerebellar degeneration-related 2	7 F2|7 65.04 cM	12585
TC0100003874.mm.1	0.0075148	-2.83955	-1.50566	Null_Rptor down vs WT	-6σ	Ankrd23	ankyrin repeat domain 23	1|1 B	78321
TC0400003320.mm.1	0.0032948	-2.84077	-1.50628	Null_Rptor down vs WT	-6σ	Cyp4b1-ps2	cytochrome P450, family 4, subfamily b, polypeptide 1, pseudogene 2	4|4 D1	631037
TC0200004676.mm.1	0.0003377	-2.8544	-1.51319	Null_Rptor down vs WT	-6σ	Gpcpd1	glycerophosphocholine phosphodiesterase 1	2 F2|2	74182
TC0500002945.mm.1	0.001043	-2.86077	-1.5164	Null_Rptor down vs WT	-6σ	Mfsd7a	major facilitator superfamily domain containing 7A	5|5 F	243197
TC1800000160.mm.1	0.0010831	-2.86762	-1.51985	Null_Rptor down vs WT	-6σ	Rnf125	ring finger protein 125	18|18 A2	67664
TC1100003146.mm.1	0.0491938	-2.86791	-1.52	Null_Rptor down vs WT	-6σ	Spns2	spinster homolog 2	11|11 B4	216892
TC0300002450.mm.1	0.0053258	-2.87265	-1.52238	Null_Rptor down vs WT	-6σ	Tuft1	tuftelin 1	3|3 F2.1	22156
TC1100003466.mm.1	0.0193838	-2.87373	-1.52293	Null_Rptor down vs WT	-6σ	Gdpd1	glycerophosphodiester phosphodiesterase domain containing 1	11|11 C	66569
TC1700000562.mm.1	0.0047256	-2.879	-1.52557	Null_Rptor down vs WT	-6σ	Cyp4f39	cytochrome P450, family 4, subfamily f, polypeptide 39	17|17 B1	320997
TC0100000292.mm.1	0.0254414	-2.88154	-1.52684	Null_Rptor down vs WT	-6σ	Il1r2	interleukin 1 receptor, type II	1 B|1 18.65 cM	16178
TC0900001056.mm.1	0.024117	-2.88211	-1.52713	Null_Rptor down vs WT	-6σ	Cd109	CD109 antigen	9|9 E1	235505
TC1500000432.mm.1	0.0017391	-2.88301	-1.52757	Null_Rptor down vs WT	-6σ	Sqle	squalene epoxidase	15|15 D1	20775
TC0800001341.mm.1	0.0221913	-2.88844	-1.53029	Null_Rptor down vs WT	-6σ	Gabarapl2	gamma-aminobutyric acid (GABA) A receptor-associated protein-like 2	8|8 E1	93739
TC0400001193.mm.1	0.0171301	-2.89831	-1.53521	Null_Rptor down vs WT	-6σ	Skint7	selection and upkeep of intraepithelial T cells 7	4|4 D1	328505
TC0700000999.mm.1	0.0370799	-2.89875	-1.53543	Null_Rptor down vs WT	-6σ	Cers3	ceramide synthase 3	7|7 C	545975
TC1100000773.mm.1	0.0393503	-2.90797	-1.54001	Null_Rptor down vs WT	-6σ	Kcnj12	potassium inwardly-rectifying channel, subfamily J, member 12	11 B2|11 37.96 cM	16515
TC1500001718.mm.1	0.0240207	-2.91186	-1.54194	Null_Rptor down vs WT	-6σ	Ly6d	lymphocyte antigen 6 complex, locus D	15 D3|15 34.27 cM	17068
TC0500002753.mm.1	0.0002316	-2.91335	-1.54268	Null_Rptor down vs WT	-6σ	Naaa	N-acylethanolamine acid amidase	5|5 E2	67111
TC0200001801.mm.1	0.0048506	-2.91483	-1.54341	Null_Rptor down vs WT	-6σ	Tmem62	transmembrane protein 62	2|2 E5	96957
TC1700002526.mm.1	0.00447	-2.92163	-1.54677	Null_Rptor down vs WT	-6σ	Xdh	xanthine dehydrogenase	17 E2|17 45.25 cM	22436
TC0300002245.mm.1	0.0062009	-2.92832	-1.55007	Null_Rptor down vs WT	-6σ	Fhdc1	FH2 domain containing 1	3|3 F1	229474
TC1200001028.mm.1	0.0106053	-2.92873	-1.55027	Null_Rptor down vs WT	-6σ	Otub2	OTU domain, ubiquitin aldehyde binding 2	12|12 E	68149
TC0400001668.mm.1	0.0044215	-2.93079	-1.55129	Null_Rptor down vs WT	-6σ	Fuca1	fucosidase, alpha-L- 1, tissue	4 D3|4 68.01 cM	71665

TC1200002354.mm.1	0.0208323	-2.93341	-1.55258	Null_Rptor down vs WT	-6σ	Degs2	delta(4)-desaturase, sphingolipid 2	12|12 F1	70059
TC0800002745.mm.1	0.0065555	-2.93887	-1.55526	Null_Rptor down vs WT	-6σ	Csnk2a2	casein kinase 2, alpha prime polypeptide	8 C5|8 47.12 cM	13000
TC1000001566.mm.1	0.0021983	-2.96617	-1.5686	Null_Rptor down vs WT	-6σ	Ndufa4l2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	10|10 D3	407790
TC1000002846.mm.1	0.0049302	-2.96765	-1.56932	Null_Rptor down vs WT	-6σ	Nav3	neuron navigator 3	10|10 D1	260315
TC0100001174.mm.1	0.012435	-2.97812	-1.5744	Null_Rptor down vs WT	-6σ	Slc26a9	solute carrier family 26, member 9	1|1 E4	320718
TC0800002542.mm.1	2.55E-06	-2.98376	-1.57713	Null_Rptor down vs WT	-6σ	Il15	interleukin 15	8 C2|8 39.33 cM	16168
TC1800001368.mm.1	0.0307142	-2.98419	-1.57734	Null_Rptor down vs WT	-6σ	March3	membrane-associated ring finger (C3HC4) 3	18 D3|18	320253
TC0500000675.mm.1	0.0376369	-2.98472	-1.57759	Null_Rptor down vs WT	-6σ	Nipal1	NIPA-like domain containing 1	5|5 C3.2	70701
TC0800002056.mm.1	0.0413704	-2.98567	-1.57805	Null_Rptor down vs WT	-6σ	Cldn23	claudin 23	8|8 A4	71908
TC0700004346.mm.1	0.0203673	-2.98795	-1.57916	Null_Rptor down vs WT	-6σ	Prss8	protease, serine 8 (prostasin)	7 F3|7 69.84 cM	76560
TC1900001270.mm.1	0.0067731	-2.99129	-1.58077	Null_Rptor down vs WT	-6σ	Fam189a2	family with sequence similarity 189, member A2	19|19 B	381217
TC0400000659.mm.1	0.0023841	-2.99457	-1.58235	Null_Rptor down vs WT	-6σ	Hsdl2	hydroxysteroid dehydrogenase like 2	4|4 B3	72479
TC1500002250.mm.1	0.0033362	-2.99549	-1.58279	Null_Rptor down vs WT	-6σ	Galnt6	polypeptide N-acetylgalactosaminyltransferase 6	15|15 F1	207839
TC0700003015.mm.1	0.0038122	-2.9974	-1.58371	Null_Rptor down vs WT	-6σ	Fut2	fucosyltransferase 2	7 B3|7 29.41 cM	14344
TC0500003466.mm.1	0.0006367	-3.00185	-1.58585	Null_Rptor down vs WT	-6σ	Cyp3a13	cytochrome P450, family 3, subfamily a, polypeptide 13	5 G2|5 76.89 cM	13113
TC0300000068.mm.1	0.049635	-3.00328	-1.58654	Null_Rptor down vs WT	-6σ	Chmp4c	charged multivesicular body protein 4C	3|3 A1	66371
TC0300000832.mm.1	0.0578722	-3.00372	-1.58675	Null_Rptor down vs WT	-6σ	Lce1c	late cornified envelope 1C	3|3 F1	73719
TC0500002608.mm.1	0.054049	-3.00467	-1.58721	Null_Rptor down vs WT	-6σ	Lnx1	ligand of numb-protein X 1	5|5 C3.3	16924
TC0400001307.mm.1	0.0120507	-3.0053	-1.58751	Null_Rptor down vs WT	-6σ	Elovl1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	4|4 D2.1	54325
TC0X00002158.mm.1	0.0145811	-3.00948	-1.58951	Null_Rptor down vs WT	-6σ	Zdhhc9	zinc finger, DHHC domain containing 9	X|X A5	208884
TC0700004351.mm.1	0.0121097	-3.01356	-1.59147	Null_Rptor down vs WT	-6σ	Pycard	PYD and CARD domain containing	7|7 F3	66824
TC0500002580.mm.1	0.0010471	-3.01659	-1.59292	Null_Rptor down vs WT	-6σ	Tec	tec protein tyrosine kinase	5 C3.2|5 38.44 cM	21682
TC0X00000961.mm.1	0.0024194	-3.02023	-1.59466	Null_Rptor down vs WT	-6σ	Gdpd2	glycerophosphodiester phosphodiesterase domain containing 2	X|X C3	71584
TC1100002156.mm.1	0.0009015	-3.02637	-1.59759	Null_Rptor down vs WT	-6σ	Myl7	myosin, light polypeptide 7, regulatory	11 A1|11 3.88 cM	17898
TC1900000684.mm.1	0.0065037	-3.04518	-1.60653	Null_Rptor down vs WT	-6σ	Elovl3	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3	19 C3|19 38.75 cM	12686
TC0600002641.mm.1	0.0127954	-3.04521	-1.60654	Null_Rptor down vs WT	-6σ	Mxd1	MAX dimerization protein 1	6 D1|6 37.75 cM	17119
TC0200003139.mm.1	0.020849	-3.04669	-1.60724	Null_Rptor down vs WT	-6σ	Cysrt1	cysteine rich tail 1	2|2 A3	67859

TC0500002936.mm.1	0.0020563	-3.0565	-1.61188	Null_Rptor down vs WT	-6σ	Fam69a	family with sequence similarity 69, member A	5 F|5	67266
TC1800000448.mm.1	0.0521934	-3.05836	-1.61276	Null_Rptor down vs WT	-6σ	Spink5	serine peptidase inhibitor, Kazal type 5	18 B3|18 23.74 cM	72432
TC0100001161.mm.1	0.0170964	-3.06253	-1.61472	Null_Rptor down vs WT	-6σ	AA986860	expressed sequence AA986860	1|1 E4	212439
TC0700000575.mm.1	0.0116756	-3.06321	-1.61504	Null_Rptor down vs WT	-6σ	Dmkn	dermokine	7|7 B1	73712
TC1500000165.mm.1	0.0099673	-3.0634	-1.61513	Null_Rptor down vs WT	-6σ	Retreg1	reticulophagy regulator 1	15|15 B1	66270
TC0700000379.mm.1	0.0779209	-3.06341	-1.61514	Null_Rptor down vs WT	-6σ	Lypd5	Ly6/Plaur domain containing 5	7|7 A3	76942
TC0400001953.mm.1	0.0155108	-3.07148	-1.61893	Null_Rptor down vs WT	-6σ	Ctnnbip1	catenin beta interacting protein 1	4|4 E2	67087
TC0300000880.mm.1	0.0004895	-3.07389	-1.62006	Null_Rptor down vs WT	-6σ	Selenbp1	selenium binding protein 1	3 F2.1|3 40.74 cM	20341
TC0500000997.mm.1	0.0005592	-3.07754	-1.62178	Null_Rptor down vs WT	-6σ	Arhgap24	Rho GTPase activating protein 24	5|5 E5	231532
TC0600002958.mm.1	0.0137146	-3.08125	-1.62352	Null_Rptor down vs WT	-6σ	Tmem40	transmembrane protein 40	6|6 E3	94346
TC1600001575.mm.1	0.003027	-3.0959	-1.63036	Null_Rptor down vs WT	-6σ	Stfa3	stefin A3	16 B3|16 25.55 cM	20863
TC1200000839.mm.1	0.0564927	-3.10174	-1.63308	Null_Rptor down vs WT	-6σ	Flvcr2	feline leukemia virus subgroup C cellular receptor 2	12|12 D2	217721
TC1800000152.mm.1	0.0112389	-3.10494	-1.63457	Null_Rptor down vs WT	-6σ	Dsg1c	desmoglein 1 gamma	18 A2|18 11.26 cM	211924
TC0900000722.mm.1	0.07233	-3.11133	-1.63753	Null_Rptor down vs WT	-6σ	Cyp11a1	cytochrome P450, family 11, subfamily a, polypeptide 1	9 B|9 31.63 cM	13070
TC0400003568.mm.1	2.43E-05	-3.11787	-1.64056	Null_Rptor down vs WT	-6σ	Gjb5	gap junction protein, beta 5	4 D2.2|4 61.51 cM	14622
TC0800002310.mm.1	0.0090371	-3.12301	-1.64294	Null_Rptor down vs WT	-6σ	Cpe	carboxypeptidase E	8 B3.1|8 32.3 cM	12876
TC0400001161.mm.1	0.0186702	-3.13368	-1.64786	Null_Rptor down vs WT	-6σ	Nrd1	nardilysin, N-arginine dibasic convertase, NRD convertase 1	4|4 C7	230598
TC0900001182.mm.1	0.0014856	-3.13445	-1.64821	Null_Rptor down vs WT	-6σ	Slc9a9	solute carrier family 9 (sodium/hydrogen exchanger), member 9	9|9 E3.3	331004
TC1500000663.mm.1	0.0013377	-3.13644	-1.64913	Null_Rptor down vs WT	-6σ	Gcat	glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	15 E1|15 37.7 cM	26912
TC0900001638.mm.1	0.0021088	-3.13793	-1.64981	Null_Rptor down vs WT	-6σ	Abhd5	abhydrolase domain containing 5	9|9 F4	67469
TC0800002925.mm.1	0.0011232	-3.1435	-1.65237	Null_Rptor down vs WT	-6σ	Il34	interleukin 34	8|8 E1	76527
TC1000001366.mm.1	0.0156568	-3.15571	-1.65796	Null_Rptor down vs WT	-6σ	Cpm	carboxypeptidase M	10|10 D2	70574
TC0200004943.mm.1	0.0015805	-3.16026	-1.66004	Null_Rptor down vs WT	-6σ	Pxmp4	peroxisomal membrane protein 4	2|2 H1	59038
TC0700002506.mm.1	0.0090133	-3.16698	-1.66311	Null_Rptor down vs WT	-6σ	Ceacam19	carcinoembryonic antigen-related cell adhesion molecule 19	7|7 A3	319930
TC0300000480.mm.1	0.0004565	-3.17081	-1.66485	Null_Rptor down vs WT	-6σ	Gm9696	arylacetamide deacetylase-like 2 pseudogene	3|3 D	676914
TC1100000324.mm.1	0.028478	-3.17232	-1.66554	Null_Rptor down vs WT	-6σ	Cpeb4	cytoplasmic polyadenylation element binding protein 4	11|11 A4	67579
TC0300000482.mm.1	0.0034888	-3.18523	-1.6714	Null_Rptor down vs WT	-6σ	Aadac	arylacetamide deacetylase	3|3 D	67758

TC1100000333.mm.1	0.0010101	-3.1894	-1.67328	Null_Rptor down vs WT	-6σ	Snrnp25	small nuclear ribonucleoprotein 25 (U11/U12)	11|11 A4	78372
TC0700002855.mm.1	0.0008763	-3.19242	-1.67465	Null_Rptor down vs WT	-6σ	Rgs9bp	regulator of G-protein signalling 9 binding protein	7|7 B2	243923
TC0200004227.mm.1	0.0015769	-3.19303	-1.67493	Null_Rptor down vs WT	-6σ	Cat	catalase	2 E2|2 54.43 cM	12359
TC1700001699.mm.1	0.0362685	-3.19557	-1.67607	Null_Rptor down vs WT	-6σ	Dusp1	dual specificity phosphatase 1	17 A3.3|17 13.28 cM	19252
TC1600001374.mm.1	0.0109287	-3.20195	-1.67895	Null_Rptor down vs WT	-6σ	Liph	lipase, member H	16 B1|16 12.95 cM	239759
TC0100001158.mm.1	0.0138393	-3.20764	-1.68151	Null_Rptor down vs WT	-6σ	Yod1	YOD1 deubiquitinase	1|1 E4	226418
TC0200000561.mm.1	0.0234683	-3.20801	-1.68168	Null_Rptor down vs WT	-6σ	Aif1l	allograft inflammatory factor 1-like	2|2 B	108897
TC1400002738.mm.1	0.0196833	-3.21027	-1.68269	Null_Rptor down vs WT	-6σ	Slc15a1	solute carrier family 15 (oligopeptide transporter), member 1	14|14 E5	56643
TC0400001107.mm.1	0.0104911	-3.21096	-1.68301	Null_Rptor down vs WT	-6σ	Dhcr24	24-dehydrocholesterol reductase	4|4 C7	74754
TC0100002305.mm.1	0.0177849	-3.21596	-1.68525	Null_Rptor down vs WT	-6σ	Nabp1	nucleic acid binding protein 1	1|1 C1.1	109019
TC1900001498.mm.1	0.0166673	-3.21731	-1.68585	Null_Rptor down vs WT	-6σ	Blnk	B cell linker	19 C3|19 34.26 cM	17060
TC1700001143.mm.1	0.0068405	-3.21881	-1.68653	Null_Rptor down vs WT	-6σ	Clip4	CAP-GLY domain containing linker protein family, member 4	17|17 E1.3	78785
TC0600003362.mm.1	0.0126191	-3.22007	-1.68709	Null_Rptor down vs WT	-6σ	Gm5724	predicted gene 5724	6|6 G2	435927
TC1700000694.mm.1	0.0399694	-3.22298	-1.68839	Null_Rptor down vs WT	-6σ	Cdsn	corneodesmosin	17|17 B1	386463
TC0900001070.mm.1	0.0123483	-3.22393	-1.68882	Null_Rptor down vs WT	-6σ	Myo6	myosin VI	9 E1|9 43.98 cM	17920
TC1700001936.mm.1	0.0171677	-3.23541	-1.69395	Null_Rptor down vs WT	-6σ	Hspa1a	heat shock protein 1A	17 B1|17 18.51 cM	193740
TC1200001018.mm.1	0.0160333	-3.23718	-1.69474	Null_Rptor down vs WT	-6σ	Chga	chromogranin A	12 E|12 51.66 cM	12652
TC0X00000359.mm.1	0.114454	-3.23936	-1.69571	Null_Rptor down vs WT	-6σ	Rhox10	reproductive homeobox 10	X|X A3.3	434769
TC1700001400.mm.1	0.0065002	-3.24785	-1.69949	Null_Rptor down vs WT	-6σ	Gm9992	predicted gene 9992	17|17 A1	667055
TC0100002969.mm.1	0.0104261	-3.25066	-1.70073	Null_Rptor down vs WT	-6σ	Insig2	insulin induced gene 2	1|1 E2.3	72999
TC0700000447.mm.1	0.0084976	-3.25108	-1.70092	Null_Rptor down vs WT	-6σ	Cyp2f2	cytochrome P450, family 2, subfamily f, polypeptide 2	7|7 A3	13107
TC1600002158.mm.1	0.0174303	-3.25443	-1.7024	Null_Rptor down vs WT	-6σ	C2cd2	C2 calcium-dependent domain containing 2	16|16 C4	207781
TC0X00002238.mm.1	0.0089402	-3.25499	-1.70265	Null_Rptor down vs WT	-6σ	Mospd1	motile sperm domain containing 1	X|X A5	70380
TC0700002717.mm.1	0.0066142	-3.2677	-1.70827	Null_Rptor down vs WT	-6σ	Catsperg1	cation channel sperm associated auxiliary subunit gamma 1	7|7 B1	320225
TC0600001751.mm.1	0.0148965	-3.28366	-1.71531	Null_Rptor down vs WT	-6σ	Far2	fatty acyl CoA reductase 2	6|6 G3	330450
TC0300002403.mm.1	0.0330832	-3.29228	-1.71909	Null_Rptor down vs WT	-6σ	Lce1a2	late cornified envelope 1A2	3|3 F1	73722
TC0Y0000	0.0492519	-3.2945	-1.72006	Null_Rptor	-6σ	Eif2s3y	eukaryotic translation	Y|Y A1	26908

0006.mm.1				down vs WT			initiation factor 2, subunit 3, structural gene Y-linked		
TC0800001531.mm.1	0.0054202	-3.30123	-1.723	Null_Rptor down vs WT	-6σ	Rhou	ras homolog family member U	8|8 E1	69581
TC0800000700.mm.1	0.0042125	-3.30492	-1.72462	Null_Rptor down vs WT	-6σ	Sh2d4a	SH2 domain containing 4A	8|8 B3.3	72281
TC0700000776.mm.1	0.0169921	-3.30502	-1.72466	Null_Rptor down vs WT	-6σ	Klk7	kallikrein related-peptidase 7 (chymotryptic, stratum corneum)	7 B3|7 28.27 cM	23993
TC0900002920.mm.1	0.0306964	-3.3059	-1.72504	Null_Rptor down vs WT	-6σ	Esyt3	extended synaptotagmin-like protein 3	9 E3.3|9 51.54 cM	272636
TC0300000060.mm.1	0.0029834	-3.31526	-1.72912	Null_Rptor down vs WT	-6σ	Fabp5	fatty acid binding protein 5, epidermal	3|3 A1	16592
TC0700000304.mm.1	0.0309657	-3.31612	-1.7295	Null_Rptor down vs WT	-6σ	Nkpd1	NTPase, KAP family P-loop domain containing 1	7|7 A3	69547
TC0200005052.mm.1	0.004366	-3.32063	-1.73146	Null_Rptor down vs WT	-6σ	Mafb	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)	2 H2|2 80.92 cM	16658
TC0700004474.mm.1	0.0004506	-3.32341	-1.73266	Null_Rptor down vs WT	-6σ	Bnip3	BCL2/adenovirus E1B interacting protein 3	7|7 F4	12176
TC1000001668.mm.1	0.0151327	-3.32536	-1.73351	Null_Rptor down vs WT	-6σ	H60c	histocompatibility 60c	10 A1|10	670558
TC0200000419.mm.1	0.0174689	-3.32535	-1.73351	Null_Rptor down vs WT	-6σ	Clic3	chloride intracellular channel 3	2|2 A3	69454
TC1300000912.mm.1	0.0052486	-3.33673	-1.73844	Null_Rptor down vs WT	-6σ	Ell2	elongation factor RNA polymerase II 2	13|13 C1	192657
TC1500002111.mm.1	0.0224352	-3.34096	-1.74026	Null_Rptor down vs WT	-6σ	Twf1	twinfilin actin binding protein 1	15|15 E3	19230
TC1100002754.mm.1	0.0015937	-3.34452	-1.7418	Null_Rptor down vs WT	-6σ	Slc22a4	solute carrier family 22 (organic cation transporter), member 4	11 B1.3|11 32.07 cM	30805
TC0500003740.mm.1	0.0039126	-3.35561	-1.74658	Null_Rptor down vs WT	-6σ	Gal3st4	galactose-3-O-sulfotransferase 4	5|5 G2	330217
TC0900002934.mm.1	0.004494	-3.36192	-1.74928	Null_Rptor down vs WT	-6σ	Il20rb	interleukin 20 receptor beta	9|9 E3.3	213208
TC1500000002.mm.1	0.0014554	-3.36613	-1.75109	Null_Rptor down vs WT	-6σ	Selenop	selenoprotein P	15 A1|15 1.84 cM	20363
TC0300001236.mm.1	0.008152	-3.36672	-1.75134	Null_Rptor down vs WT	-6σ	F3	coagulation factor III	3 G1|3 52.94 cM	14066
TC0900002452.mm.1	0.0035727	-3.36989	-1.7527	Null_Rptor down vs WT	-6σ	Paqr5	progestin and adipoQ receptor family member V	9|9 B	74090
TC0400003867.mm.1	0.0020508	-3.37031	-1.75288	Null_Rptor down vs WT	-6σ	Padi1	peptidyl arginine deiminase, type I	4 D3|4 72.62 cM	18599
TC0300000875.mm.1	5.17E-05	-3.37744	-1.75593	Null_Rptor down vs WT	-6σ	Selenbp2	selenium binding protein 2	3 F2.1|3 40.74 cM	20342
TC0700001197.mm.1	0.0005525	-3.37977	-1.75693	Null_Rptor down vs WT	-6σ	Tmc3	transmembrane channel-like gene family 3	7|7 D3	233424
TC0300000822.mm.1	0.191444	-3.38244	-1.75806	Null_Rptor down vs WT	-6σ	Sprr2a3	small proline-rich protein 2A3	3 F1|3	1E+08
TC1400000942.mm.1	0.0011216	-3.38708	-1.76004	Null_Rptor down vs WT	-6σ	Clu	clusterin	14 D1|14 34.36 cM	12759
TC0100001500.mm.1	0.0372689	-3.38958	-1.76111	Null_Rptor down vs WT	-6σ	Slc19a2	solute carrier family 19 (thiamine transporter), member 2	1 H2.2|1 71.56 cM	116914
TC1100000422.mm.1	0.006077	-3.39039	-1.76145	Null_Rptor down vs WT	-6σ	Atp10b	ATPase, class V, type 10B	11|11 A5	319767
TC0900002767.mm.1	0.0110287	-3.39063	-1.76155	Null_Rptor down vs WT	-6σ	Elovl4	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4	9|9 E2	83603
TC1100003	0.0229138	-3.39772	-1.76457	Null_Rptor	-6σ	Krt10	keratin 10	11 D|11	16661

706.mm.1				down vs WT				62.92 cM	
TC1300002481.mm.1	0.0038935	-3.41177	-1.77052	Null_Rptor down vs WT	-6σ	Hexb	hexosaminidase B	13 D1|13 50.66 cM	15212
TC0X00000670.mm.1	0.008104	-3.41183	-1.77055	Null_Rptor down vs WT	-6σ	Zfp185	zinc finger protein 185	X A7.3|X 37.29 cM	22673
TC0500002645.mm.1	0.0041283	-3.41455	-1.7717	Null_Rptor down vs WT	-6σ	Gm20558	predicted gene, 20558	5|5 C3.3	330108
TC1300000089.mm.1	0.0033418	-3.41714	-1.77279	Null_Rptor down vs WT	-6σ	Lyst	lysosomal trafficking regulator	13 A1|13 5.28 cM	17101
TC1900000309.mm.1	0.0004602	-3.41771	-1.77303	Null_Rptor down vs WT	-6σ	Gna14	guanine nucleotide binding protein, alpha 14	19 A|19 11.29 cM	14675
TC1100000025.mm.1	0.0379412	-3.42621	-1.77661	Null_Rptor down vs WT	-6σ	Dusp18	dual specificity phosphatase 18	11|11 A1	75219
TC1500001040.mm.1	0.0039127	-3.45467	-1.78855	Null_Rptor down vs WT	-6σ	Mettl7a1	methyltransferase like 7A1	15|15 F1	70152
TC1100003071.mm.1	0.0361445	-3.46066	-1.79105	Null_Rptor down vs WT	-6σ	Tmem95	transmembrane protein 95	11|11 B3	1E+08
TC0400004127.mm.1	0.0028564	-3.46538	-1.79301	Null_Rptor down vs WT	-6σ	Fam213b	family with sequence similarity 213, member B	4|4 E2	66469
TC1900001562.mm.1	0.0080077	-3.47019	-1.79502	Null_Rptor down vs WT	-6σ	Scd1	stearoyl-Coenzyme A desaturase 1	19 C3|19 37.98 cM	20249
TC1300001270.mm.1	0.0203417	-3.47234	-1.79591	Null_Rptor down vs WT	-6σ	Plpp1	phospholipid phosphatase 1	13|13 D2.2	19012
TC0400001013.mm.1	0.0033451	-3.48662	-1.80183	Null_Rptor down vs WT	-6σ	Ror1	receptor tyrosine kinase-like orphan receptor 1	4 C6|4 45.71 cM	26563
TC0100003505.mm.1	0.0020508	-3.48948	-1.80301	Null_Rptor down vs WT	-6σ	Hsd17b7	hydroxysteroid (17-beta) dehydrogenase 7	1|1 H3	15490
TC0300002409.mm.1	0.0386427	-3.49141	-1.80381	Null_Rptor down vs WT	-6σ	Lce1i	late cornified envelope 1I	3|3 F1	76585
TC0600001070.mm.1	0.0147077	-3.51043	-1.81165	Null_Rptor down vs WT	-6σ	BC048671	cDNA sequence BC048671	6|6 D1	243535
TC1500002155.mm.1	0.005351	-3.5147	-1.8134	Null_Rptor down vs WT	-6σ	Endou	endonuclease, polyU-specific	15 F1|15 53.7 cM	19011
TC0700000774.mm.1	0.0350079	-3.52245	-1.81658	Null_Rptor down vs WT	-6σ	Klk9	kallikrein related-peptidase 9	7 B3|7 28.26 cM	101533
TC1300001868.mm.1	0.0076405	-3.54318	-1.82504	Null_Rptor down vs WT	-6σ	Adtrp	androgen dependent TFPI regulating protein	13|13 A4	109254
TC0100002903.mm.1	0.0176955	-3.55085	-1.82816	Null_Rptor down vs WT	-6σ	Serpinb3a	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3A	1|1 E2.1	20248
TC0900000599.mm.1	0.025247	-3.55196	-1.82862	Null_Rptor down vs WT	-6σ	Il18	interleukin 18	9 A5.3|9 27.75 cM	16173
TC0900002322.mm.1	0.0109493	-3.57232	-1.83686	Null_Rptor down vs WT	-6σ	Acsbg1	acyl-CoA synthetase bubblegum family member 1	9|9 A5.3	94180
TC0300000092.mm.1	0.0047827	-3.58177	-1.84067	Null_Rptor down vs WT	-6σ	Car13	carbonic anhydrase 13	3|3 A1	71934
TC0Y00000235.mm.1	0.0488691	-3.582	-1.84077	Null_Rptor down vs WT	-6σ	Ddx3y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	Y|Y A1	26900
TC0300000656.mm.1	0.00323	-3.59273	-1.84508	Null_Rptor down vs WT	-6σ	Tmem154	transmembrane protein 154	3|3 F1	320782
TC1600002035.mm.1	0.0506351	-3.59505	-1.84601	Null_Rptor down vs WT	-6σ	Krtap8-1	keratin associated protein 8-1	16|16 C3.3	16703
TC0700000778.mm.1	0.0161774	-3.6114	-1.85256	Null_Rptor down vs WT	-6σ	Klk5	kallikrein related-peptidase 5	7 B3|7 28.3 cM	68668
TC0300000955.mm.1	0.0005781	-3.61411	-1.85364	Null_Rptor down vs WT	-6σ	Ankrd35	ankyrin repeat domain 35	3|3 F2.1	213121

TC0300000750.mm.1	0.0069698	-3.61432	-1.85372	Null_Rptor down vs WT	-6σ	Gba	glucosidase, beta, acid	3 F1|3 39.01 cM	14466
TC0400002265.mm.1	0.0129859	-3.62277	-1.85709	Null_Rptor down vs WT	-6σ	Gm11868	cytochrome b5 reductase 4 pseudogene	4|4 A3	667251
TC0200000379.mm.1	0.0276965	-3.636	-1.86235	Null_Rptor down vs WT	-6σ	Il1f5	interleukin 1 family, member 5 (delta)	2 A3|2 16.31 cM	54450
TC0Y00000005.mm.1	0.0642706	-3.63721	-1.86283	Null_Rptor down vs WT	-6σ	Kdm5d	lysine (K)-specific demethylase 5D	Y|Y A1	20592
TC0700000770.mm.1	0.0127823	-3.63757	-1.86297	Null_Rptor down vs WT	-6σ	Klk13	kallikrein related-peptidase 13	7|7 B3	626834
TC0300002482.mm.1	0.0308875	-3.64795	-1.86709	Null_Rptor down vs WT	-6σ	Ecm1	extracellular matrix protein 1	3 F2.1|3 40.91 cM	13601
TC1300000691.mm.1	0.0140889	-3.65236	-1.86883	Null_Rptor down vs WT	-6σ	Tgfbi	transforming growth factor, beta induced	13 B1|13 30.09 cM	21810
TC1800000200.mm.1	0.0017169	-3.65316	-1.86915	Null_Rptor down vs WT	-6σ	Mocos	molybdenum cofactor sulfurase	18|18 A2	68591
TC1600001639.mm.1	0.0428501	-3.65364	-1.86933	Null_Rptor down vs WT	-6σ	Gramd1c	GRAM domain containing 1C	16|16 B4	207798
TC1200001742.mm.1	0.0012297	-3.65379	-1.86939	Null_Rptor down vs WT	-6σ	Egln3	egl-9 family hypoxia-inducible factor 3	12|12 C1	112407
TC1900001612.mm.1	0.018902	-3.66435	-1.87356	Null_Rptor down vs WT	-6σ	Cyp17a1	cytochrome P450, family 17, subfamily a, polypeptide 1	19 C3|19 38.97 cM	13074
TC0300002419.mm.1	0.0296983	-3.67776	-1.87883	Null_Rptor down vs WT	-6σ	Lce1m	late cornified envelope 1M	3 F1|3	66203
TC0400003829.mm.1	0.0102877	-3.67997	-1.87969	Null_Rptor down vs WT	-6σ	Pla2g2f	phospholipase A2, group IIF	4|4 D3	26971
TC0800001952.mm.1	0.0334242	-3.68239	-1.88064	Null_Rptor down vs WT	-6σ	Rab11fip1	RAB11 family interacting protein 1 (class I)	8|8 A2	75767
TC0500000337.mm.1	0.0371457	-3.68622	-1.88214	Null_Rptor down vs WT	-6σ	Plb1	phospholipase B1	5|5 B1	665270
TC0700001554.mm.1	0.0154017	-3.68797	-1.88283	Null_Rptor down vs WT	-6σ	Smpd1	sphingomyelin phosphodiesterase 1, acid lysosomal	7 E3|7 55.9 cM	20597
TC1400002608.mm.1	0.0019476	-3.68957	-1.88345	Null_Rptor down vs WT	-6σ	Klf12	Kruppel-like factor 12	14 E2.2-E2.3|14 50.9 cM	16597
TC0300002405.mm.1	0.0910112	-3.69347	-1.88498	Null_Rptor down vs WT	-6σ	Lce1e	late cornified envelope 1E	3|3 F1	68694
TC1500002280.mm.1	0.0145727	-3.70847	-1.89082	Null_Rptor down vs WT	-6σ	Krt78	keratin 78	15|15 F2	332131
TC0X00002872.mm.1	0.0301578	-3.70913	-1.89108	Null_Rptor down vs WT	-6σ	Pof1b	premature ovarian failure 1B	X|X E1	69693
TC1900001454.mm.1	0.0114553	-3.72308	-1.8965	Null_Rptor down vs WT	-6σ	Ide	insulin degrading enzyme	19 C2|19 32.24 cM	15925
TC1300001779.mm.1	0.0254259	-3.73036	-1.89932	Null_Rptor down vs WT	-6σ	Tubb2a	tubulin, beta 2A class IIA	13 A3.3|13 14.03 cM	22151
TC0300002396.mm.1	0.0178195	-3.73444	-1.90089	Null_Rptor down vs WT	-6σ	Ivl	involucrin	3 F1|3 40.14 cM	16447
TC0200001514.mm.1	0.0112436	-3.75239	-1.90781	Null_Rptor down vs WT	-6σ	Traf6	TNF receptor-associated factor 6	2|2 E2	22034
TC1100003707.mm.1	0.0004354	-3.76277	-1.91179	Null_Rptor down vs WT	-6σ	Krt12	keratin 12	11 D|11 62.92 cM	268482
TC1700001614.mm.1	0.0145051	-3.76319	-1.91196	Null_Rptor down vs WT	-6σ	Kctd5	potassium channel tetramerisation domain containing 5	17|17 A3.3	69259

TC0200000274.mm.1	0.0088763	-3.77211	-1.91537	Null_Rptor down vs WT	-6σ	Plxdc2	plexin domain containing 2	2|2 A2-A3	67448
TC0900000539.mm.1	0.014665	-3.79074	-1.92248	Null_Rptor down vs WT	-6σ	Tmprss13	transmembrane protease, serine 13	9|9 A5.2	214531
TC0900001050.mm.1	0.0028222	-3.79454	-1.92393	Null_Rptor down vs WT	-6σ	Gm10639	predicted gene 10639	9|9 E1	1E+08
TC0900002044.mm.1	0.0027638	-3.8012	-1.92645	Null_Rptor down vs WT	-6σ	Slc37a2	solute carrier family 37 (glycerol-3-phosphate transporter), member 2	9|9 A4	56857
TC0400004173.mm.1	0.009226	-3.80401	-1.92752	Null_Rptor down vs WT	-6σ	Plekhn1	pleckstrin homology domain containing, family N member 1	4|4 E2	231002
TC0800000916.mm.1	0.0367338	-3.80498	-1.92789	Null_Rptor down vs WT	-6σ	Tbc1d9	TBC1 domain family, member 9	8|8 C2	71310
TC1800001274.mm.1	0.0304204	-3.81978	-1.93349	Null_Rptor down vs WT	-6σ	Spink1	serine peptidase inhibitor, Kazal type 1	18|18 B3	20730
TC0Y00000233.mm.1	0.0703433	-3.82113	-1.934	Null_Rptor down vs WT	-6σ	Uty	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome	Y|Y A1	22290
TC0800001398.mm.1	0.0024709	-3.82624	-1.93593	Null_Rptor down vs WT	-6σ	Gan	giant axonal neuropathy	8|8 E1	209239
TC1200001908.mm.1	0.0029331	-3.82711	-1.93626	Null_Rptor down vs WT	-6σ	Dhrs7	dehydrogenase/reductase (SDR family) member 7	12|12 C3	66375
TC0900001123.mm.1	0.005609	-3.83132	-1.93784	Null_Rptor down vs WT	-6σ	Cyb5r4	cytochrome b5 reductase 4	9|9 E3.1	266690
TC0300002414.mm.1	0.0953467	-3.84252	-1.94205	Null_Rptor down vs WT	-6σ	2310050C09Rik	RIKEN cDNA 2310050C09 gene	3|3 F1	66533
TC1000001577.mm.1	0.019643	-3.85402	-1.94636	Null_Rptor down vs WT	-6σ	Sdr9c7	4short chain dehydrogenase/reductase family 9C, member 7	10|10 D3	70061
TC1800000154.mm.1	0.0105463	-3.87029	-1.95244	Null_Rptor down vs WT	-6σ	Dsg1b	desmoglein 1 beta	18 A2|18 11.32 cM	225256
TC0200001164.mm.1	0.0014407	-3.88557	-1.95813	Null_Rptor down vs WT	-6σ	Ssfa2	sperm specific antigen 2	2|2 C3	70599
TC0300002401.mm.1	0.0296292	-3.88766	-1.9589	Null_Rptor down vs WT	-6σ	Lce1a1	late cornified envelope 1A1	3|3 F1	67127
TC1100001890.mm.1	0.0012152	-3.88831	-1.95914	Null_Rptor down vs WT	-6σ	Otop3	otopetrin 3	11|11 E2	69602
TC1400002000.mm.1	0.000828	-3.89585	-1.96194	Null_Rptor down vs WT	-6σ	Rnase1	ribonuclease, RNase A family, 1 (pancreatic)	14 C1|14 26.4 cM	19752
TC0500000992.mm.1	0.0037189	-3.89847	-1.96291	Null_Rptor down vs WT	-6σ	Cds1	CDP-diacylglycerol synthase 1	5|5 E4	74596
TC0700001534.mm.1	0.0257021	-3.90901	-1.9668	Null_Rptor down vs WT	-6σ	Gm4887	predicted gene 4887	7|7 E3	233637
TC0800001079.mm.1	0.0118368	-3.91122	-1.96762	Null_Rptor down vs WT	-6σ	Capns2	calpain, small subunit 2	8|8 C5	69543
TC0800000646.mm.1	0.0072207	-3.91878	-1.9704	Null_Rptor down vs WT	-6σ	Mfap3l	microfibrillar-associated protein 3-like	8|8 B3.1	71306
TC0300000481.mm.1	0.0181182	-3.92239	-1.97173	Null_Rptor down vs WT	-6σ	Aadacl2	arylacetamide deacetylase like 2	3|3 D	639634
TC0700000576.mm.1	0.0089202	-3.92467	-1.97257	Null_Rptor down vs WT	-6σ	Krtdap	keratinocyte differentiation associated protein	7|7 B1	64661
TC1100003506.mm.1	0.0122435	-3.95705	-1.98443	Null_Rptor down vs WT	-6σ	Scpep1	serine carboxypeptidase 1	11|11 C	74617
TC1200002296.mm.1	0.0207191	-3.95835	-1.9849	Null_Rptor down vs WT	-6σ	Clmn	calmin	12|12 E	94040
TC1800001421.mm.1	0.0042044	-3.98114	-1.99318	Null_Rptor down vs WT	-6σ	Arhgef37	Rho guanine nucleotide exchange factor (GEF) 37	18|18 E1	328967
TC0700003658.mm.1	0.010295	-3.98791	-1.99563	Null_Rptor down vs WT	-6σ	Zfand6	zinc finger, AN1-type domain 6	7|7 D3	65098
TC1200000718.mm.1	0.0013027	-3.99017	-1.99645	Null_Rptor down vs WT	-6σ	Rdh12	retinol dehydrogenase 12	12|12 C3	77974
TC0400003448.mm.1	0.009934	-4.00945	-2.0034	Null_Rptor down vs WT	-6σ	Smap2	small ArfGAP 2	4|4 D2.2	69780

TC1300000919.mm.1	0.0220507	-4.04681	-2.01679	Null_Rptor down vs WT	-6σ	Glrx	glutaredoxin	13 C1|13 40.95 cM	93692
TC0300002406.mm.1	0.0390905	-4.06201	-2.02219	Null_Rptor down vs WT	-6σ	Lce1f	late cornified envelope 1F	3|3 F1	67828
TC0500001304.mm.1	0.0007258	-4.07558	-2.02701	Null_Rptor down vs WT	-6σ	Tesc	tescalcin	5 F|5 57.84 cM	57816
TC0300002402.mm.1	0.0220563	-4.10572	-2.03764	Null_Rptor down vs WT	-6σ	Lce1b	late cornified envelope 1B	3|3 F1	68720
TC1000001807.mm.1	0.0057368	-4.11157	-2.03969	Null_Rptor down vs WT	-6σ	Hebp2	heme binding protein 2	10|10 A3	56016
TC0900003275.mm.1	0.0004178	-4.11694	-2.04157	Null_Rptor down vs WT	-6σ	Higd1a	HIG1 domain family, member 1A	9|9 F4	56295
TC0800001198.mm.1	0.0113989	-4.13232	-2.04695	Null_Rptor down vs WT	-6σ	Ces2g	carboxylesterase 2G	8|8 D3	72361
TC0400001662.mm.1	0.0088023	-4.14115	-2.05003	Null_Rptor down vs WT	-6σ	Il22ra1	interleukin 22 receptor, alpha 1	4 D3|4 67.99 cM	230828
TC1100000469.mm.1	0.0284165	-4.14918	-2.05283	Null_Rptor down vs WT	-6σ	Fndc9	fibronectin type III domain containing 9	11|11 B1.1	320116
TC0200004599.mm.1	0.0621886	-4.19047	-2.06711	Null_Rptor down vs WT	-6σ	Il1a	interleukin 1 alpha	2 F1|2 62.9 cM	16175
TC1500002275.mm.1	0.0192804	-4.20474	-2.07202	Null_Rptor down vs WT	-6σ	Krt1	keratin 1	15 F2|15 57.06 cM	16678
TC1100000903.mm.1	0.0217229	-4.20789	-2.0731	Null_Rptor down vs WT	-6σ	Alox12b	arachidonate 12-lipoxygenase, 12R type	11 B3|11 42.38 cM	11686
TC1800001045.mm.1	0.0131323	-4.22682	-2.07957	Null_Rptor down vs WT	-6σ	Dsc1	desmocollin 1	18|18 A2	13505
TC1800001138.mm.1	0.0008648	-4.22942	-2.08046	Null_Rptor down vs WT	-6σ	Stard4	StAR-related lipid transfer (START) domain containing 4	18 B1|18 18.18 cM	170459
TC0600002342.mm.1	0.0120759	-4.24296	-2.08507	Null_Rptor down vs WT	-6σ	Nt5c3	5'-nucleotidase, cytosolic III	6|6 B3	107569
TC1200000715.mm.1	0.0097716	-4.2497	-2.08736	Null_Rptor down vs WT	-6σ	Arg2	arginase type II	12|12 C3	11847
TC1900000020.mm.1	0.0191435	-4.25497	-2.08915	Null_Rptor down vs WT	-6σ	Aldh3b3	aldehyde dehydrogenase 3 family, member B3	19|19 A	73458
TC1500001725.mm.1	0.0162948	-4.26464	-2.09242	Null_Rptor down vs WT	-6σ	2010109I03Rik	RIKEN cDNA 2010109I03 gene	15|15 D3	67038
TC1300002102.mm.1	0.0073419	-4.27164	-2.09479	Null_Rptor down vs WT	-6σ	Slc28a3	solute carrier family 28 (sodium-coupled nucleoside transporter), member 3	13|13 B1	114304
TC0600000359.mm.1	1.70E-05	-4.27199	-2.09491	Null_Rptor down vs WT	-6σ	Akr1d1	aldo-keto reductase family 1, member D1	6|6 B1	208665
TC1900001388.mm.1	0.0090067	-4.28743	-2.10011	Null_Rptor down vs WT	-6σ	Asah2	N-acylsphingosine amidohydrolase 2	19|19 C1	54447
TC0100002543.mm.1	0.0167803	-4.30754	-2.10686	Null_Rptor down vs WT	-6σ	Abca12	ATP-binding cassette, sub-family A (ABC1), member 12	1|1 C3	74591
TC0400004158.mm.1	0.0053996	-4.31933	-2.11081	Null_Rptor down vs WT	-6σ	Cptp	ceramide-1-phosphate transfer protein	4 E2|4 87.66 cM	79554
TC0X00000954.mm.1	0.0004315	-4.34107	-2.11805	Null_Rptor down vs WT	-6σ	Awat1	acyl-CoA wax alcohol acyltransferase 1	X|X C3	245533
TC0400001196.mm.1	0.0036548	-4.36895	-2.12729	Null_Rptor down vs WT	-6σ	Skint3	selection and upkeep of intraepithelial T cells 3	4|4 D1	195564
TC1300002303.mm.1	0.0092832	-4.38824	-2.13364	Null_Rptor down vs WT	-6σ	Slc6a19	solute carrier family 6 (neurotransmitter transporter), member 19	13|13 C1	74338
TC1400001064.mm.1	0.0695162	-4.38894	-2.13387	Null_Rptor down vs WT	-6σ	Kctd4	potassium channel tetramerisation domain	14|14 D3	67516

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TC1200001468.mm.1	0.0134116	-4.38936	-2.13401	Null_Rptor down vs WT	-6σ	Atp6v1c2	ATPase, H+ transporting, lysosomal V1 subunit C2	12|12 A1.1	68775
TC0600001368.mm.1	0.0098333	-4.39823	-2.13692	Null_Rptor down vs WT	-6σ	Tuba8	tubulin, alpha 8	6|6 F1	53857
TC1200001939.mm.1	0.0116854	-4.43895	-2.15022	Null_Rptor down vs WT	-6σ	Sgpp1	sphingosine-1-phosphate phosphatase 1	12|12 C3	81535
TC1800000153.mm.1	0.0119545	-4.44769	-2.15306	Null_Rptor down vs WT	-6σ	Dsg1a	desmoglein 1 alpha	18 A2|18 11.29 cM	13510
TC0200005436.mm.1	0.0001895	-4.45623	-2.15582	Null_Rptor down vs WT	-6σ	Ptk6	PTK6 protein tyrosine kinase 6	2 H4|2 103.62 cM	20459
TC1700001626.mm.1	0.0212934	-4.47066	-2.16049	Null_Rptor down vs WT	-6σ	Dnase1l2	deoxyribonuclease 1-like 2	17|17 A3.3	66705
TC0900003177.mm.1	0.0105203	-4.47163	-2.1608	Null_Rptor down vs WT	-6σ	Cmtm8	CKLF-like MARVEL transmembrane domain containing 8	9|9 F3	70031
TC1400002222.mm.1	0.0003596	-4.4783	-2.16295	Null_Rptor down vs WT	-6σ	Tdh	L-threonine dehydrogenase	14|14 D1	58865
TC1800001655.mm.1	0.0182964	-4.49081	-2.16698	Null_Rptor down vs WT	-6σ	Hsbp1l1	heat shock factor binding protein 1-like 1	18|18 E3	66255
TC0300002418.mm.1	0.0152478	-4.52515	-2.17797	Null_Rptor down vs WT	-6σ	Crct1	cysteine-rich C-terminal 1	3|3 F1	74175
TC0700003793.mm.1	0.0117904	-4.54136	-2.18312	Null_Rptor down vs WT	-6σ	Dgat2	diacylglycerol O-acyltransferase 2	7|7 E1	67800
TC1600001561.mm.1	0.0141722	-4.54196	-2.18331	Null_Rptor down vs WT	-6σ	Csta1	cystatin A1	16|16 B3	209294
TC0100000933.mm.1	0.0037094	-4.60484	-2.20315	Null_Rptor down vs WT	-6σ	Ano7	anoctamin 7	1|1 D	404545
TC0400001195.mm.1	0.0040749	-4.60534	-2.20331	Null_Rptor down vs WT	-6σ	Skint4	selection and upkeep of intraepithelial T cells 4	4|4 D1	320640
TC1600001752.mm.1	0.0129016	-4.6062	-2.20358	Null_Rptor down vs WT	-6σ	Tmem45a	transmembrane protein 45a	16|16 C1.1	56277
TC0900002719.mm.1	0.0017306	-4.65838	-2.21983	Null_Rptor down vs WT	-6σ	Gsta2	glutathione S-transferase, alpha 2 (Yc2)	9 E1|9 43.65 cM	14858
TC1200000760.mm.1	0.0054071	-4.72017	-2.23884	Null_Rptor down vs WT	-6σ	Ttc9	tetratricopeptide repeat domain 9	12|12 D1	69480
TC1900001246.mm.1	0.0036743	-4.74858	-2.2475	Null_Rptor down vs WT	-6σ	Aldh1a7	aldehyde dehydrogenase family 1, subfamily A7	19 B|19 13.95 cM	26358
TC1200000206.mm.1	0.0042316	-4.77974	-2.25693	Null_Rptor down vs WT	-6σ	Mboat2	membrane bound O-acyltransferase domain containing 2	12|12 A1.3	67216
TC0200002264.mm.1	0.028486	-4.82538	-2.27064	Null_Rptor down vs WT	-6σ	Sdcbp2	syndecan binding protein (syntenin) 2	2|2 G3	228765
TC0700002997.mm.1	0.004828	-4.84106	-2.27532	Null_Rptor down vs WT	-6σ	Dkkl1	dickkopf-like 1	7 B3|7 29.19 cM	50722
TC1000002380.mm.1	0.0085682	-4.84325	-2.27598	Null_Rptor down vs WT	-6σ	Susd2	sushi domain containing 2	10|10 C1	71733
TC1900000493.mm.1	0.0140323	-4.84588	-2.27676	Null_Rptor down vs WT	-6σ	Lipm	lipase, family member M	19|19 C1	78753
TC0200004457.mm.1	0.0015201	-4.84985	-2.27794	Null_Rptor down vs WT	-6σ	Pla2g4f	phospholipase A2, group IVF	2|2 E5	271844
TC0500002875.mm.1	0.0072301	-4.85854	-2.28052	Null_Rptor down vs WT	-6σ	Slc10a6	solute carrier family 10 (sodium/bile acid cotransporter family), member 6	5|5 E5	75750
TC0300000751.mm.1	0.0190637	-4.88589	-2.28862	Null_Rptor down vs WT	-6σ	AI464196	expressed sequence AI464196	3|3	1E+08
TC0400000718.mm.1	0.0224025	-4.91384	-2.29685	Null_Rptor down vs WT	-6σ	Orm1	orosomucoid 1	4 B3|4 33.96 cM	18405
TC0700004065.mm.1	0.0092471	-4.93343	-2.30259	Null_Rptor down vs WT	-6σ	Nlrp10	NLR family, pyrin domain containing 10	7|7 E3	244202

TC1300001204.mm.1	0.0065962	-4.94444	-2.30581	Null_Rptor down vs WT	-6σ	Elovl7	ELOVL family member 7, elongation of long chain fatty acids (yeast)	13|13 D2.1	74559
TC1100003757.mm.1	0.0089717	-4.96148	-2.31077	Null_Rptor down vs WT	-6σ	Krt15	keratin 15	11 D|11 63.41 cM	16665
TC1900000021.mm.1	0.008566	-4.97316	-2.31416	Null_Rptor down vs WT	-6σ	Aldh3b2	aldehyde dehydrogenase 3 family, member B2	19|19 A	621603
TC0200004450.mm.1	0.0043551	-4.98362	-2.31719	Null_Rptor down vs WT	-6σ	6330405D24Rik	RIKEN cDNA 6330405D24 gene	2|2 E5	70715
TC0900001005.mm.1	0.0054654	-4.99476	-2.32042	Null_Rptor down vs WT	-6σ	Fam214a	family with sequence similarity 214, member A	9|9 D	235493
TC0400000169.mm.1	0.0027418	-5.00859	-2.3244	Null_Rptor down vs WT	-6σ	Ggh	gamma-glutamyl hydrolase	4|4 A3	14590
TC1100002233.mm.1	0.013834	-5.01207	-2.32541	Null_Rptor down vs WT	-6σ	Cobl	cordon-bleu WH2 repeat	11 A1|11 7.3 cM	12808
TC0900001542.mm.1	0.0006299	-5.03177	-2.33107	Null_Rptor down vs WT	-6σ	Gadl1	glutamate decarboxylase-like 1	9|9 F3	73748
TC1600001574.mm.1	0.0150423	-5.05282	-2.33709	Null_Rptor down vs WT	-6σ	Stfa2	stefin A2	16 B3|16 25.52 cM	20862
TC0800000172.mm.1	0.0062582	-5.06365	-2.34018	Null_Rptor down vs WT	-6σ	Agpat5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	8 A1.3|8 10.3 cM	52123
TC1100002492.mm.1	0.0007528	-5.10757	-2.35264	Null_Rptor down vs WT	-6σ	Gabrp	gamma-aminobutyric acid (GABA) A receptor, pi	11|11 A4	216643
TC1700000489.mm.1	0.0139312	-5.11347	-2.3543	Null_Rptor down vs WT	-6σ	Pnpla1	patatin-like phospholipase domain containing 1	17|17 A3.3	433091
TC0300002408.mm.1	0.0266026	-5.12104	-2.35644	Null_Rptor down vs WT	-6σ	Lce1h	late cornified envelope 1H	3|3 F1	67718
TC1500002343.mm.1	0.0155373	-5.12354	-2.35714	Null_Rptor down vs WT	-6σ	Gsdmc	gasdermin C	15|15 D1	83492
TC0600000270.mm.1	0.0374341	-5.15288	-2.36538	Null_Rptor down vs WT	-6σ	Cpa4	carboxypeptidase A4	6|6 A3.3	71791
TC1100000902.mm.1	0.0169016	-5.15888	-2.36706	Null_Rptor down vs WT	-6σ	Aloxe3	arachidonate lipoxygenase 3	11 B3|11 42.38 cM	23801
TC1100001577.mm.1	0.018789	-5.1674	-2.36944	Null_Rptor down vs WT	-6σ	Gsdma	gasdermin A	11|11 D	57911
TC0300000479.mm.1	0.001312	-5.18622	-2.37468	Null_Rptor down vs WT	-6σ	C130079G13Rik	RIKEN cDNA C130079G13 gene	3|3 D	229333
TC0300002473.mm.1	0.0146379	-5.19602	-2.37741	Null_Rptor down vs WT	-6σ	Anxa9	annexin A9	3|3 F2.1	71790
TC0400003296.mm.1	0.004021	-5.21766	-2.3834	Null_Rptor down vs WT	-6σ	Skint5	selection and upkeep of intraepithelial T cells 5	4|4 D1	242627
TC1900000491.mm.1	0.0141631	-5.24179	-2.39006	Null_Rptor down vs WT	-6σ	Lipn	lipase, family member N	19|19 C1	70166
TC1400001724.mm.1	0.0123718	-5.24733	-2.39158	Null_Rptor down vs WT	-6σ	Fam25c	family with sequence similarity 25, member C	14|14 B	69134
TC1600001357.mm.1	0.0200333	-5.31424	-2.40986	Null_Rptor down vs WT	-6σ	Gm6557	predicted gene 6557	16 B1|16	625123
TC0300002410.mm.1	0.0483214	-5.36941	-2.42476	Null_Rptor down vs WT	-6σ	Lce1j	late cornified envelope 1J	3|3 F1	545547
TC0600001522.mm.1	0.0109959	-5.37476	-2.4262	Null_Rptor down vs WT	-6σ	Clec2g	C-type lectin domain family 2, member g	6|6 F3	70809
TC0X00001663.mm.1	0.0028146	-5.42053	-2.43843	Null_Rptor down vs WT	-6σ	Ace2	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	X F5|X 76.12 cM	70008
TC1600000367.mm.1	0.0066596	-5.49626	-2.45845	Null_Rptor down vs WT	-6σ	Tprg	transformation related protein 63 regulated	16|16 B1	71338
TC0100003884.mm.1	0.0038664	-5.5014	-2.4598	Null_Rptor down vs WT	-6σ	Serpinb3b	serine (or cysteine) peptidase inhibitor, clade B	1|1 E2.1	383548

							(ovalbumin), member 3B		
TC0200005105.mm.1	0.0121898	-5.51079	-2.46226	Null_Rptor down vs WT	-6σ	Wfdc5	WAP four-disulfide core domain 5	2|2 H3	209232
TC0100001029.mm.1	0.0069735	-5.56699	-2.4769	Null_Rptor down vs WT	-6σ	Serpinb7	serine (or cysteine) peptidase inhibitor, clade B, member 7	1|1 E2.1	116872
TC0900000031.mm.1	0.0091517	-5.57206	-2.47821	Null_Rptor down vs WT	-6σ	Casp1	caspase 1	9 A1|9 2.46 cM	12362
TC0X00002427.mm.1	0.0133992	-5.64716	-2.49753	Null_Rptor down vs WT	-6σ	Trex2	three prime repair exonuclease 2	X|X A7.3	24102
TC0700001815.mm.1	0.0064119	-5.66881	-2.50305	Null_Rptor down vs WT	-6σ	Gdpd3	glycerophosphodiester phosphodiesterase domain containing 3	7|7 F3	68616
TC0300000846.mm.1	0.0119764	-5.70973	-2.51342	Null_Rptor down vs WT	-6σ	Hrnr	hornerin	3 F2.1|3	68723
TC1100003090.mm.1	0.0012846	-5.71748	-2.51538	Null_Rptor down vs WT	-6σ	Alox12	arachidonate 12-lipoxygenase	11 B3|11 42.99 cM	11684
TC1400001034.mm.1	0.0120244	-5.73485	-2.51976	Null_Rptor down vs WT	-6σ	Itm2b	integral membrane protein 2B	14 D3|14 38.88 cM	16432
TC0900003169.mm.1	0.00242	-5.75293	-2.5243	Null_Rptor down vs WT	-6σ	Ccr4	chemokine (C-C motif) receptor 4	9 F3|9 64.49 cM	12773
TC0700000152.mm.1	0.0258675	-5.77404	-2.52958	Null_Rptor down vs WT	-6σ	Rnf225	ring finger protein 225	7|7 A1	381845
TC0X00002704.mm.1	0.0147112	-5.79991	-2.53603	Null_Rptor down vs WT	-6σ	P2ry4	pyrimidinergic receptor P2Y, G-protein coupled, 4	X|X C3	57385
TC0300002407.mm.1	0.0427009	-5.80133	-2.53638	Null_Rptor down vs WT	-6σ	Lce1g	late cornified envelope 1G	3|3 F1	66195
TC1900000489.mm.1	0.0119018	-5.82944	-2.54336	Null_Rptor down vs WT	-6σ	Lipk	lipase, family member K	19|19 C1	240633
TC0400002137.mm.1	0.0177159	-5.83864	-2.54563	Null_Rptor down vs WT	-6σ	Sdr16c6	short chain dehydrogenase/reductase family 16C, member 6	4|4 A1	242286
TC0900001234.mm.1	0.003196	-5.8438	-2.54691	Null_Rptor down vs WT	-6σ	Rbp2	retinol binding protein 2, cellular	9 E3.3|9 51.37 cM	19660
TC1300000258.mm.1	0.005445	-5.89183	-2.55872	Null_Rptor down vs WT	-6σ	Hist1h1c	histone cluster 1, H1c	13|13 A3.1	50708
TC1300000014.mm.1	0.0045853	-5.90297	-2.56144	Null_Rptor down vs WT	≤ -6σ	Calm5	calmodulin 5	13|13 A1	494124
TC0300002114.mm.1	0.0026945	-5.92472	-2.56675	Null_Rptor down vs WT	≤ -6σ	Rarres1	retinoic acid receptor responder (tazarotene induced) 1	3|3 E1	109222
TC0300000844.mm.1	0.0424611	-5.94179	-2.5709	Null_Rptor down vs WT	≤ -6σ	Flg	filaggrin	3 F2.1|3 40.16 cM	14246
TC0400002136.mm.1	0.0078304	-5.96032	-2.57539	Null_Rptor down vs WT	≤ -6σ	Sdr16c5	short chain dehydrogenase/reductase family 16C, member 5	4|4 A1	242285
TC0800001410.mm.1	0.0080058	-5.96079	-2.5755	Null_Rptor down vs WT	≤ -6σ	Hsd17b2	hydroxysteroid (17-beta) dehydrogenase 2	8|8 E1	15486
TC1200002288.mm.1	0.0115999	-5.97376	-2.57864	Null_Rptor down vs WT	≤ -6σ	Serpina12	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 12	12|12 E	68054
TC1100003709.mm.1	0.0141158	-6.06352	-2.60016	Null_Rptor down vs WT	≤ -6σ	Krt23	keratin 23	11|11 D	94179
TC0700000430.mm.1	0.0001638	-6.06878	-2.60141	Null_Rptor down vs WT	≤ -6σ	Cyp2b10	cytochrome P450, family 2, subfamily b, polypeptide 10	7 A3|7 14.11 cM	13088
TC1100000118.mm.1	0.0028491	-6.08486	-2.60522	Null_Rptor down vs WT	≤ -6σ	Gm11992	predicted gene 11992	11|11 A1	626870
TC0800000538.mm.1	0.0016891	-6.08832	-2.60604	Null_Rptor down vs WT	≤ -6σ	Acsl1	acyl-CoA synthetase long-chain family member 1	8|8 B1.1	14081

TC0200004308.mm.1	0.0004135	-6.25152	-2.64421	Null_Rptor down vs WT	≤ -6σ	Bbox1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase 1 (gamma-butyrobetaine hydroxylase)	2|2 E3	170442
TC0900001049.mm.1	0.0030178	-6.2529	-2.64453	Null_Rptor down vs WT	≤ -6σ	Gm3776	predicted gene 3776	9 E1|9	1E+08
TC0500000536.mm.1	0.0066939	-6.27451	-2.6495	Null_Rptor down vs WT	≤ -6σ	Slc34a2	solute carrier family 34 (sodium phosphate), member 2	5 C1|5 28.92 cM	20531
TC0200001658.mm.1	0.0001356	-6.28448	-2.65179	Null_Rptor down vs WT	≤ -6σ	Gm13929	L-threonine dehydrogenase pseudogene	2|2 E3	433463
TC0700001630.mm.1	0.0193598	-6.38534	-2.67476	Null_Rptor down vs WT	≤ -6σ	Adm	adrenomedullin	7 E3|7 57.7 cM	11535
TC0700002700.mm.1	0.0108959	-6.40512	-2.67923	Null_Rptor down vs WT	≤ -6σ	Nccrp1	non-specific cytotoxic cell receptor protein 1 homolog (zebrafish)	7|7 B1	233038
TC0800003011.mm.1	0.0066293	-6.45469	-2.69035	Null_Rptor down vs WT	≤ -6σ	Sdr42e1	short chain dehydrogenase/reductase family 42E, member 1	8|8 E1	74032
TC0700003448.mm.1	0.0061106	-6.59514	-2.7214	Null_Rptor down vs WT	≤ -6σ	Lrrc28	leucine rich repeat containing 28	7|7 C	67867
TC0500000407.mm.1	0.0072423	-6.59976	-2.72241	Null_Rptor down vs WT	≤ -6σ	Psapl1	prosaposin-like 1	5|5 B3	76943
TC0X00002988.mm.1	0.0188784	-6.60292	-2.7231	Null_Rptor down vs WT	≤ -6σ	Xkrx	X-linked Kx blood group related, X-linked	X|X E3	331524
TC0100003402.mm.1	0.0334537	-6.71183	-2.74671	Null_Rptor down vs WT	≤ -6σ	Fmo2	flavin containing monooxygenase 2	1|1 H2.1	55990
TC0400003953.mm.1	0.0147494	-6.76914	-2.75897	Null_Rptor down vs WT	≤ -6σ	Gm438	predicted gene 438	4|4 E1	329993
TC0400001199.mm.1	0.0020406	-6.80018	-2.76557	Null_Rptor down vs WT	≤ -6σ	Skint2	selection and upkeep of intraepithelial T cells 2	4 D1|4	329919
TC0100003885.mm.1	0.0031494	-6.80735	-2.76709	Null_Rptor down vs WT	≤ -6σ	Serpinb3c	serine (or cysteine) peptidase inhibitor, clade B, member 3C	1|1 E2.1	381286
TC0500002843.mm.1	0.0033376	-6.84418	-2.77488	Null_Rptor down vs WT	≤ -6σ	Hpse	heparanase	5|5 E4	15442
TC0400004062.mm.1	0.0005019	-6.91123	-2.78894	Null_Rptor down vs WT	≤ -6σ	Car6	carbonic anhydrase 6	4|4 E2	12353
TC1600000507.mm.1	0.0209159	-6.96801	-2.80075	Null_Rptor down vs WT	≤ -6σ	Stfa2l1	stefin A2 like 1	16|16 B3	268885
TC0600002324.mm.1	0.0074882	-6.97534	-2.80226	Null_Rptor down vs WT	≤ -6σ	Ggct	gamma-glutamyl cyclotransferase	6 B3|6 27.26 cM	110175
TC0200000894.mm.1	0.0068266	-6.99336	-2.80599	Null_Rptor down vs WT	≤ -6σ	Dapl1	death associated protein-like 1	2|2 C1.1	76747
TC0700000443.mm.1	0.0215982	-7.0847	-2.82471	Null_Rptor down vs WT	≤ -6σ	Cyp2b19	cytochrome P450, family 2, subfamily b, polypeptide 19	7 A3|7 15.44 cM	13090
TC1200000210.mm.1	0.0016066	-7.31484	-2.87083	Null_Rptor down vs WT	≤ -6σ	BC023202	cDNA sequence BC023202	-	407816
TC0300002412.mm.1	0.032317	-7.42429	-2.89225	Null_Rptor down vs WT	≤ -6σ	Kprp	keratinocyte expressed, proline-rich	3|3 F1	433619
TC0500002738.mm.1	0.012385	-7.52146	-2.91101	Null_Rptor down vs WT	≤ -6σ	Btc	betacellulin, epidermal growth factor family member	5 E2|5 44.78 cM	12223
TC0400003292.mm.1	0.0019391	-7.53686	-2.91396	Null_Rptor down vs WT	≤ -6σ	Skint10	selection and upkeep of intraepithelial T cells 10	4|4 D1	230613
TC0200001965.mm.1	0.001203	-7.5387	-2.91432	Null_Rptor down vs WT	≤ -6σ	Tgm3	transglutaminase 3, E polypeptide	2|2 F1	21818
TC0300002404.mm.1	0.0156542	-7.8093	-2.96519	Null_Rptor down vs WT	≤ -6σ	Lce1d	late cornified envelope 1D	3|3 F1	69611
TC1000002613.mm.1	0.0161352	-7.88334	-2.97881	Null_Rptor down vs WT	≤ -6σ	Bpifc	BPI fold containing family C	10|10 C1	270757
TC1700001299.mm.1	0.0042587	-8.03238	-3.00583	Null_Rptor down vs WT	≤ -6σ	Epas1	endothelial PAS domain protein 1	17|17 E4	13819
TC1700002114.mm.1	0.0059394	-8.21238	-3.0378	Null_Rptor down vs WT	≤ -6σ	Adgrf4	adhesion G protein-coupled receptor F4	17|17 B3	78249
TC0300001	0.0008964	-8.24032	-3.0427	Null_Rptor	≤ -	Adh1	alcohol dehydrogenase 1	3 G3|3	11522

409.mm.1				down vs WT	6σ		(class I)	64.16 cM	
TC0900002196.mm.1	0.0040114	-8.47361	-3.08298	Null_Rptor down vs WT	≤ -6σ	Tmprss4	transmembrane protease, serine 4	9|9 A5.2	214523
TC0700000444.mm.1	0.0040213	-8.72233	-3.12471	Null_Rptor down vs WT	≤ -6σ	Cyp2g1	cytochrome P450, family 2, subfamily g, polypeptide 1	7|7 A3	13108
TC0300000843.mm.1	0.0246021	-8.83677	-3.14352	Null_Rptor down vs WT	≤ -6σ	Flg2	filaggrin family member 2	3|3 F2.1	229574
TC0100000430.mm.1	0.0053046	-8.91048	-3.1555	Null_Rptor down vs WT	≤ -6σ	Aox4	aldehyde oxidase 4	1 C1.3|1 28.97 cM	71872
TC1300001373.mm.1	0.0061717	-9.0399	-3.17631	Null_Rptor down vs WT	≤ -6σ	Calml3	calmodulin-like 3	13|13 A1	70405
TC1100000684.mm.1	0.00073	-9.04376	-3.17692	Null_Rptor down vs WT	≤ -6σ	4930438A08Rik	RIKEN cDNA 4930438A08 gene	11|11 B1.3	73988
TC1500001716.mm.1	0.0128739	-9.10238	-3.18624	Null_Rptor down vs WT	≤ -6σ	Slurp2	secreted Ly6/Plaur domain containing 2	15|15 D3	69462
TC0800001197.mm.1	0.0104501	-9.11741	-3.18862	Null_Rptor down vs WT	≤ -6σ	Ces2f	carboxylesterase 2F	8|8 D3	71903
TC1700002340.mm.1	0.0045111	-9.32504	-3.22111	Null_Rptor down vs WT	≤ -6σ	Acer1	alkaline ceramidase 1	17|17 D	171168
TSUnmapped00000043.mm.1	0.0061303	-9.5086	-3.24923	Null_Rptor down vs WT	≤ -6σ	Rora	RAR-related orphan receptor alpha	9 C|9 37.45 cM	19883
TC0500001350.mm.1	0.0007639	-9.53049	-3.25255	Null_Rptor down vs WT	≤ -6σ	Oas1f	2'-5' oligoadenylate synthetase 1F	5 F|5 60.64 cM	243262
TC0200003897.mm.1	0.0082736	-9.62044	-3.2661	Null_Rptor down vs WT	≤ -6σ	4833423E24Rik	RIKEN cDNA 4833423E24 gene	2|2 D	228151
TC0200001762.mm.1	0.0062075	-9.93624	-3.3127	Null_Rptor down vs WT	≤ -6σ	Gm14137	predicted gene 14137	2|2 E5	623781
TC0400002765.mm.1	0.0079213	-10.1945	-3.34972	Null_Rptor down vs WT	≤ -6σ	Slc46a2	solute carrier family 46, member 2	4 B3|4 32.81 cM	30936
TC0300000862.mm.1	0.010113	-11.2206	-3.48808	Null_Rptor down vs WT	≤ -6σ	Them5	thioesterase superfamily member 5	3|3 F2.1	66198
TC0100001025.mm.1	0.0037791	-11.8853	-3.57111	Null_Rptor down vs WT	≤ -6σ	Serpinb12	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 12	1|1 E2.1	71869
TC0200000373.mm.1	0.0171877	-11.9641	-3.58064	Null_Rptor down vs WT	≤ -6σ	Il1f8	interleukin 1 family, member 8	2 A3|2 16.21 cM	69677
TC0400003293.mm.1	0.0039654	-12.6722	-3.66359	Null_Rptor down vs WT	≤ -6σ	Skint6	selection and upkeep of intraepithelial T cells 6	4|4 D1	230622
TC1600001443.mm.1	0.0010717	-13.0658	-3.70772	Null_Rptor down vs WT	≤ -6σ	Atp13a4	ATPase type 13A4	16|16 B2	224079
TC0500002684.mm.1	0.0146473	-13.2077	-3.72331	Null_Rptor down vs WT	≤ -6σ	Tmprss11f	transmembrane protease, serine 11f	5|5 E1	243083
TC1800001275.mm.1	0.0067775	-14.2672	-3.83463	Null_Rptor down vs WT	≤ -6σ	Gm94	predicted gene 94	18|18 B3	225443
TC1000002460.mm.1	0.005806	-14.6018	-3.86808	Null_Rptor down vs WT	≤ -6σ	Casp14	caspase 14	10|10 C1	12365
TC0100003280.mm.1	0.0059591	-17.4968	-4.12902	Null_Rptor down vs WT	≤ -6σ	Npl	N-acetylneuraminate pyruvate lyase	1|1 G3	74091
TC1000001133.mm.1	0.0059089	-33.7395	-5.07637	Null_Rptor down vs WT	≤ -6σ	Hal	histidine ammonia lyase	10 C2|10 48.49 cM	15109
TC0400003290.mm.1	0.0019111	-37.7905	-5.23995	Null_Rptor down vs WT	≤ -6σ	Skint9	selection and upkeep of intraepithelial T cells 9	4|4 D1	329918
TC1100001267.mm.1	0.0099905	-41.1841	-5.36402	Null_Rptor down vs WT	≤ -6σ	Wfdc21	WAP four-disulfide core domain 21	11|11 C	66107