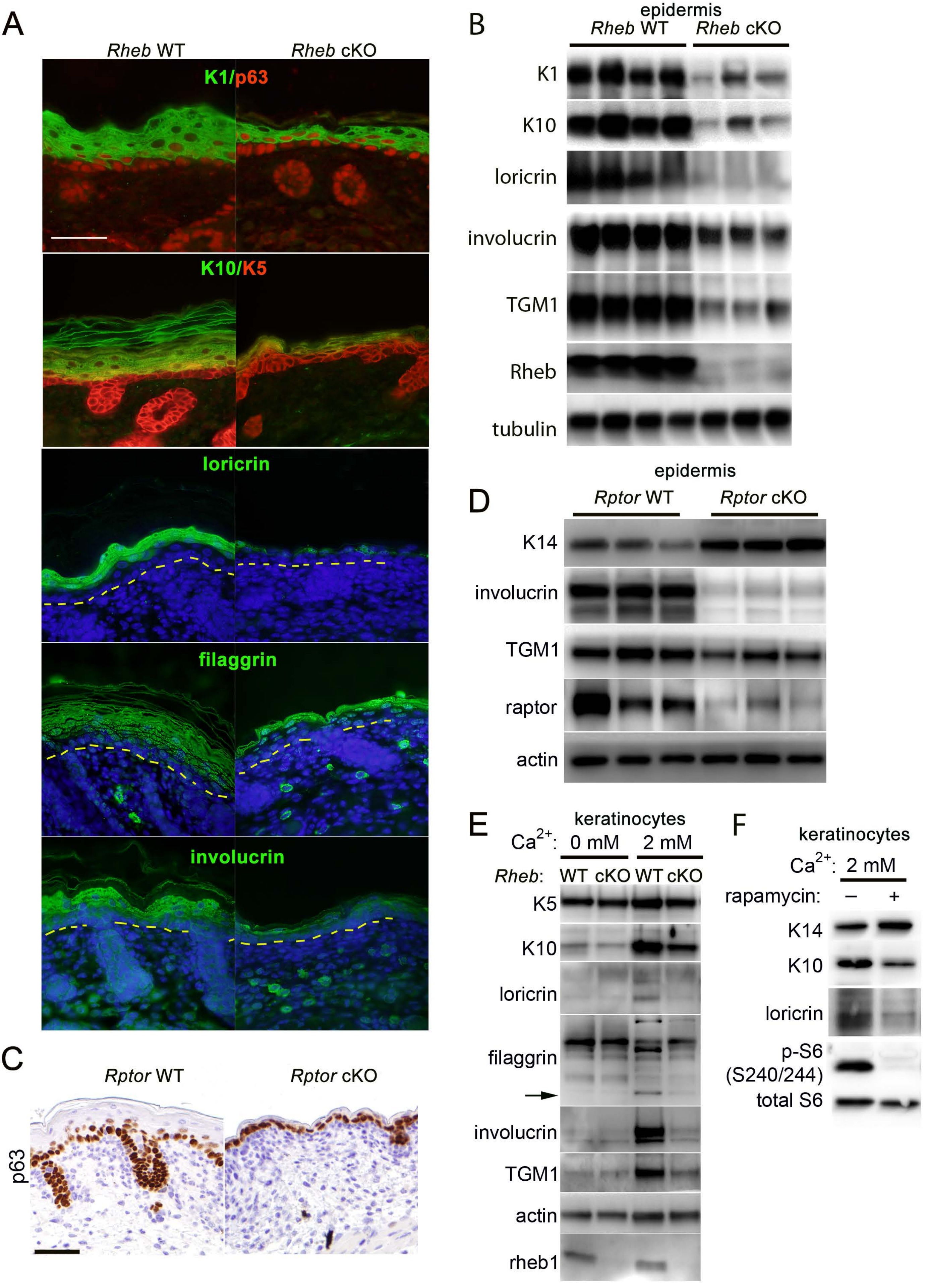
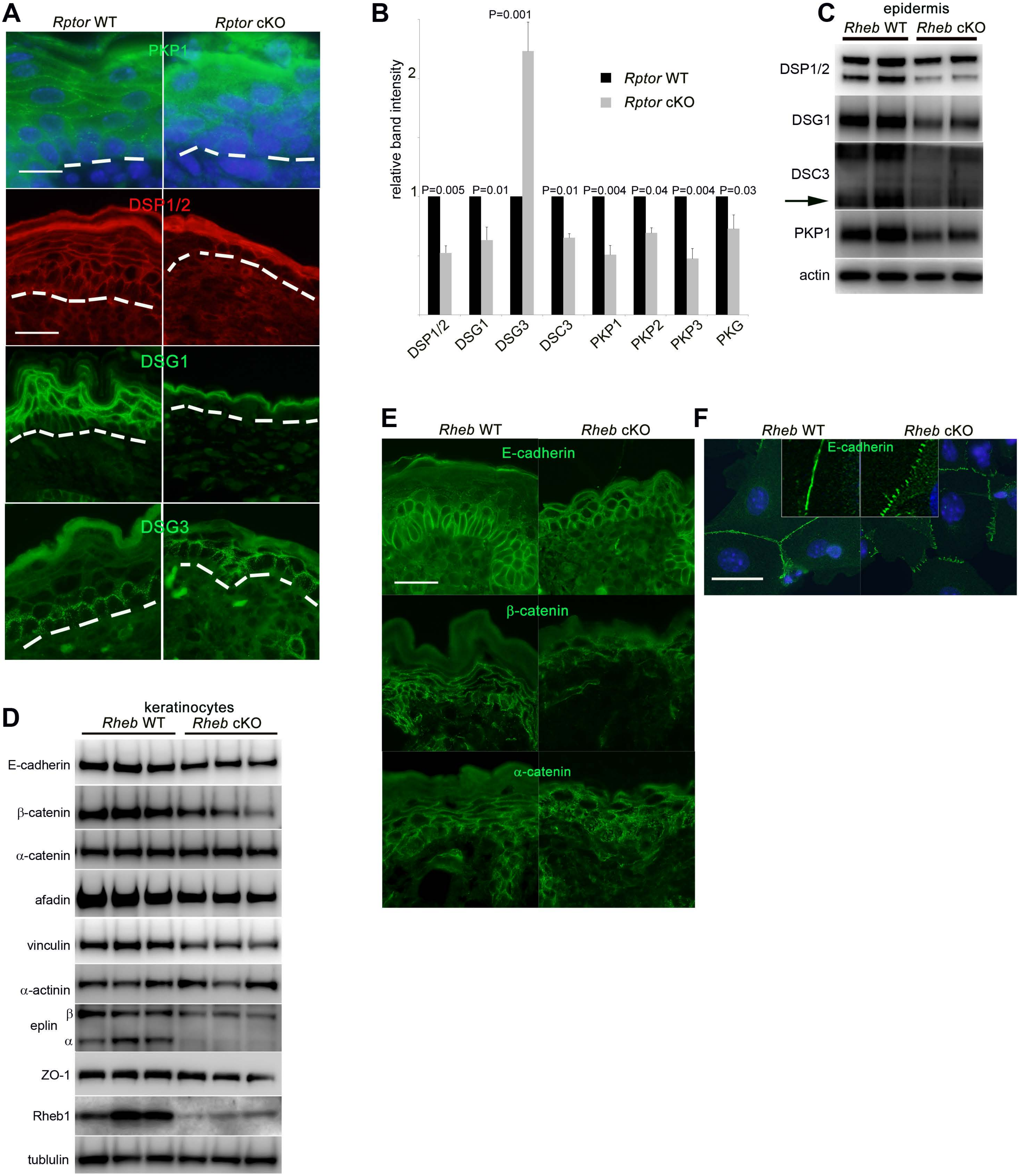
Supplementary Figure S1



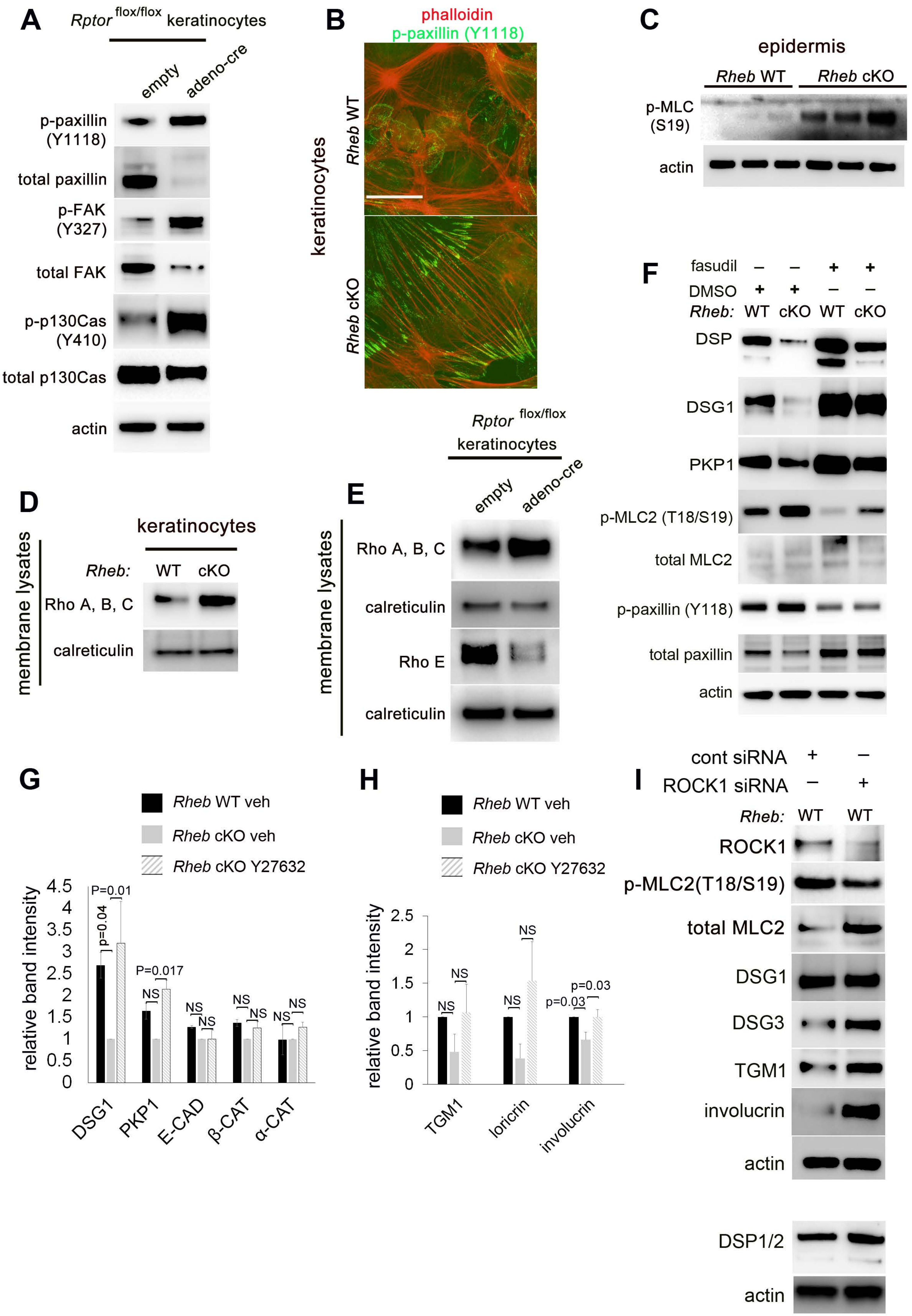
Supplementary Figure S1: Epidermal-specific mTORC1 loss-of-function models show impaired epidermal differentiation. (A) *Rheb* cKO P0 epidermis fails to express spinous (Keratin 1, 10) and granular layer (loricrin, filaggrin, involucrin) differentiation markers by immunofluorescence, while the basal layer is maintained or even slightly thicker than WT (p63 and Keratin 5). Scale bar= 30 µm. **(B)** *Rheb* cKO P0 epidermal protein lysates subjected to immunoblotting confirm downregulation of K1, K10, loricrin, involucrin and transglutaminase (TGM1) 1 expression compared to WT. **(C)** *Rptor* cKO P0 epidermis shows a similar but more severe phenotype compared to *Rheb* cKO, with near complete loss of suprabasal keratinocyte layers in the epidermis as demonstrated by basal marker p63 immunostaining. Scale bar= 30 µm. **(D)** Immunoblotting of *Rptor* cKO vs WT P0 epidermal protein lysates confirms relative downregulation of granular markers involucrin and TGM1 with slight up-regulation of basal marker keratin 14 (K14). **(E)** Calcium-induced differentiation is impaired in *Rheb* cKO cells subjected to calcium switch assay (transfer from 0.05 mM to 2 mM calcium concentration media). While WT cells up-regulate differentiation markers (K10, loricrin, filaggrin, involucrin and TGM1) in response to exposure to 2 mM calcium for 24 hours, cKO keratinocytes show an impaired response. Basal markers (K5) are unchanged in response to calcium. **(F)** mTORC1 inhibition by rapamycin (200 nM) in WT keratinocytes impairs expression of spinous (K10) and granular (loricrin) differentiation markers in 2 mM calcium. Phosphorylated S6 protein (p-S6) is markedly diminished by rapamycin, confirming mTORC1 inhibition.

Supplementary Figure S2



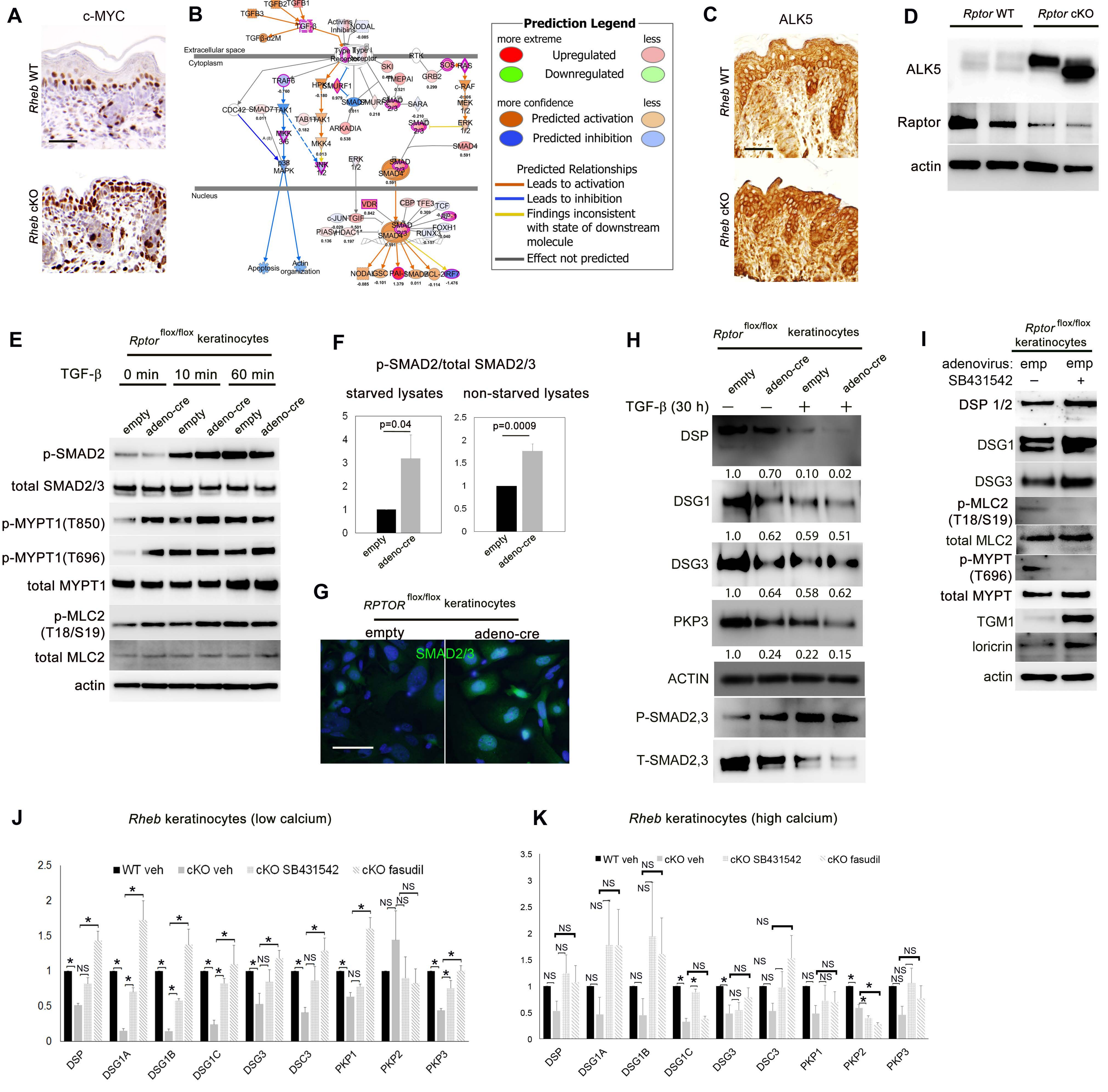
Supplementary Figure S2: mTORC1 loss-of-function is associated with decreased desmosomal, but not adherens, junctions. (A) Decreased expression of PKP1 (punctate dots), DSP1/2, DSG1 and DSG3 in *Rptor* cKO compared to WT P0 epidermis by immunofluorescence. Scale bar= 60 µm. **(B)** Densitometry quantification of immunoblot analysis shown in main Figure 3G (n=3; error bars represent SEM; p values indicated are by Student's T-test). **(C)** *Rheb* cKO P0 epidermal protein lysates subjected to immunoblotting confirm lower total levels of desmosomal proteins (DSP1/2, DSG1, DSC3 and PKP1). **(D)** *Rheb* cKO P0 cultured keratinocytes show normal protein expression of adherens junction components (E-cadherin, β-catenin, α-catenin), as well as adherens junctions components (afadin) and tight junction components (ZO-1) by immunoblotting. Some actin-binding proteins such as vinculin, afadin and EPLIN show decreased levels in cKO epidermis as well. **(E)** *Rheb* cKO P0 epidermis shows normal expression of adherens junction proteins by immunofluorescence. Scale bar = 30 µm. **(E)** *Rheb* cKO keratinocytes have normal membranous levels of E-cadherin, however the distribution of staining demonstrates immature adhesion zippers rather than mature adhesion bands by immunofluorescence. Scale bar = 50 µm.

Supplementary Figure S3



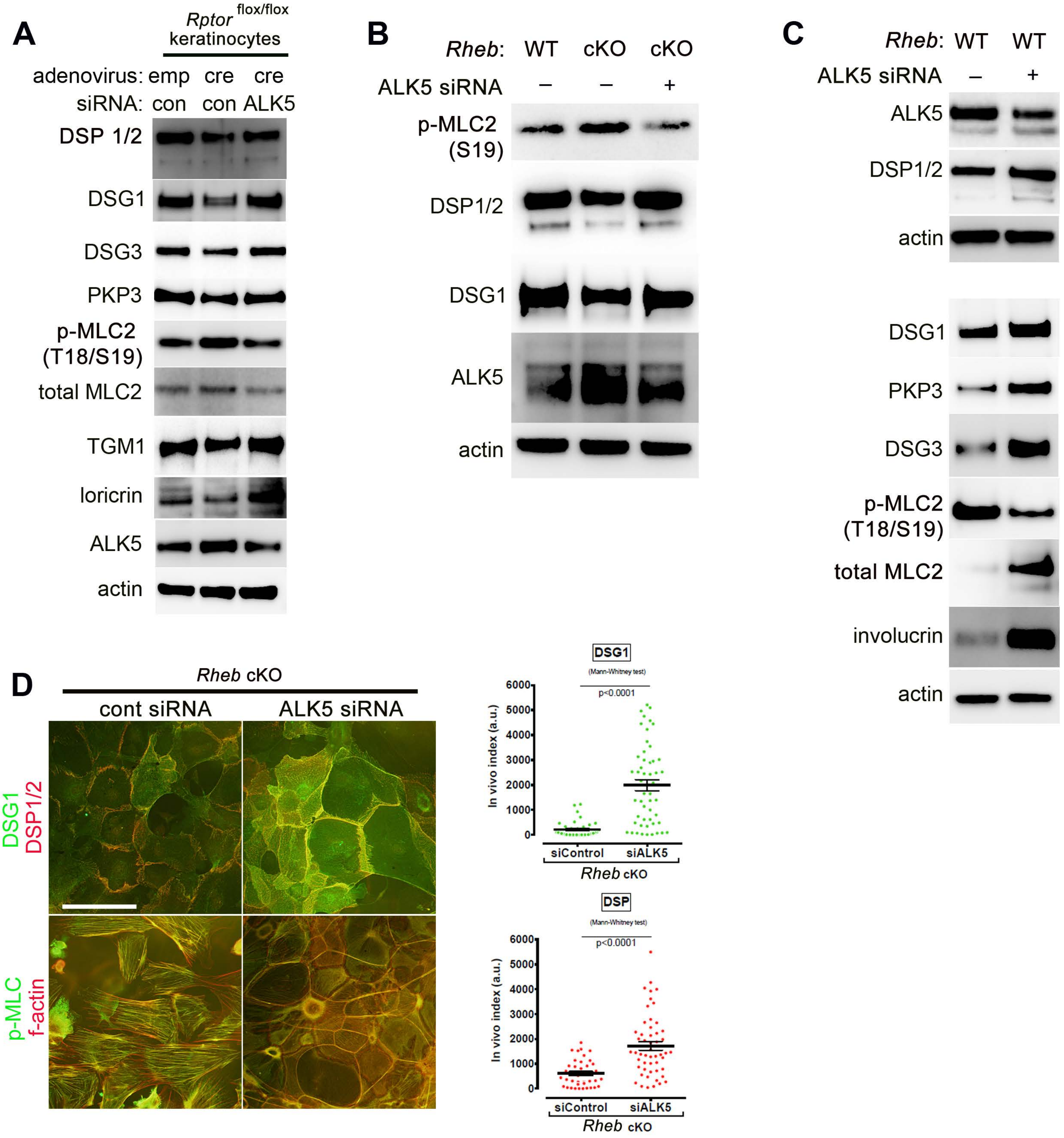
Supplementary Figure S3: mTORC1 loss-of-function is associated with increased Rho kinase activity and focal adhesion formation. (A) Increased biochemical evidence of focal adhesion formation in inducible *Rptor* KO keratinocytes, including increased phosphorylated paxillin (p-paxillin), focal adhesion kinase (p-FAK) and p130Cas (p-p130Cas), following calcium switch. **(B)** Immunofluorescence for p-paxillin and phallodin staining for f-actin demonstrates relatively rare focal adhesions in WT cells compared to *Rheb* cKO cells where focal adhesion and actin stress fiber formation is abundant. Scale bar = 30 µm. **(C)** Increased phosphorylated myosin light chain (p-MLC2) in *Rheb* cKO P0 epidermal lysates by immunoblotting compared to WT control. **(D), (E)** Lysates enriched for membrane proteins from *Rheb* cKO and *Rptor* inducible KO cultured keratinocytes demonstrate increased Rho A/B/C protein at the membrane in cells with mTORC1 loss-of-function compared to WT cells, consistent with increased Rho activity. Levels of ROCK inhibitor Rho E, by contrast, are decreased in membrane lysates from *Rptor* KO keratinocytes. Rho A/B/C and calreticulin in **(D)** were immunoblotted in parallel, contemporaneously. **(F)** Immunoblotting for desmosomal components (DSP1/2, DSG1, PKP1) in WT and *Rheb* cKO cells demonstrates rescue of total levels of desmosomal proteins with ROCK inhibition using fasudil (50 µM). ROCK activity suppression is documented by decreased p-MLC2 levels. Focal adhesion marker protein p-paxillin is also upregulated in *Rheb* cKO keratinocytes and is sensitive to ROCK inhibition. DSP, PKP1 and total MLC2 were immunoblotted in parallel, contemporaneously with the other markers. **(G)** Densitometry quantification of immunoblot experiments from **Figure 6C** (r=3; p-values by one-way ANOVA). **(H)** Densitometry quantification of immunoblot experiments from **Figure 6E** (r=3; p-values by one-way ANOVA). **(I)** . Immunoblotting of *Rheb* WT cells treated with ROCK1 siRNA (50nm) for ROCK1 and markers of ROCK activity, desmosomal and biochemical differentiation markers. DSP (lower panel**)** was immunoblotted separately from the upper panel using the same biological replicate. Error bars represent SEM throughout.

Supplementary Figure S4



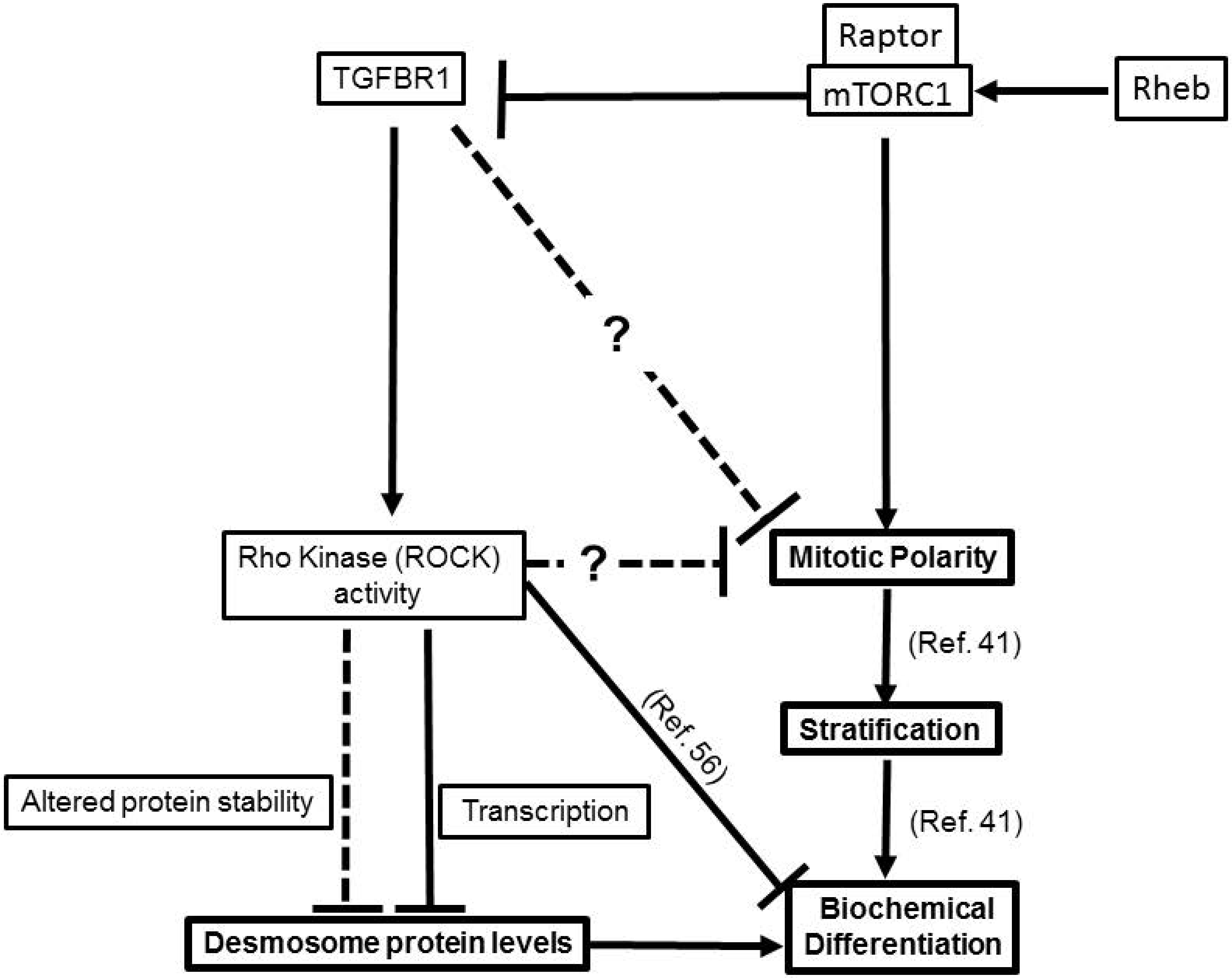
Supplementary Figure S4: ALK5 levels and TGF-β signaling are increased following mTORC1 loss-of-function and TGF-β signaling is necessary and sufficient to decrease desmosome levels in keratinocytes. (A) Immunohistochemistry for c-MYC shows more diffuse expression in Rheb cKO epidermis compared to WT where it is expressed predominantly in basal cells (scale bar=30 µm). **(B)** Ingenuity Pathway Analysis of the TGF- β signaling pathway from differential gene expression analysis of *Rheb* WT vs. cKO E18.5 epidermis. Genes within our data set whose expression showed greater than 2SD differential fold change are outlined in magenta and depicted in red (signifying up-regulation) or blue (signifying down-regulation). **(C)** Membranous ALK5 (TGF-β receptor I) levels are increased in *Rheb* cKO P0 epidermis compared to WT controls by immunohistochemistry (scale bar=30 µm). **(D)** ALK5 levels are increased by immunoblotting in *Rptor* cKO P0 epidermis compared to WT control. **(E)** Short-term treatment of *Rptor*$^{flox/flox}$ keratinocyte cultures treated with empty adenovirus or adenoviral-cre demonstrates increased TGF-β signaling (increased p-SMAD2 levels) and increased ROCK activation by immunoblotting (increased levels of p-MYPT1 and p-MLC2) in cells with mTORC1 inactivation with TGF-β treatment. ROCK activation is also increased in WT cells in response to TGF-β. **(F)** Densitometry analysis of phospho/total SMAD2, 3 expression in western blots from starved and non-starved *Rptor*$^{flox/flox}$ and inducible *Rptor* cKO keratinocytes demonstrates significant up-regulation in *Rptor* cKO keratinocytes (r=4; error bars represent SEM; p values indicated are by Student's T-test). **(G)** Immunofluorescence for SMAD2, 3 demonstrates increased nuclear localization in *Rptor*$^{flox/flox}$ keratinocyte cultures treated with adenoviral-cre (scale bar=50 µm). **(H)** Long term (30 h) TGF-β treatment of *Rptor*$^{flox/flox}$ keratinocyte cultures treated with empty adenovirus or adenoviral-cre increases p-SMAD2, 3 levels and suppresses DSP1/2, DSG1, DSG3 and PKP3 levels by immunoblotting. **(I)** By immunoblotting, basal p-MLC2 and p-MYPT1 levels are decreased, and desmosome proteins (DSP1/2, DSG1, DSG3) and differentiation markers (TGM1, loricrin) are increased in *Rptor*$^{flox/flox}$ keratinocyte cultures with empty vector, treated with ALK5 inhibitor SB431542. *Rheb* cKO keratinocytes show uniform down-regulation of desmosomal mRNA levels under low calcium **(J)** conditions as well as high calcium **(K)** conditions. ROCK inhibition with fasudil or ALK5 inhibition with SB431542 is sufficient to rescue desmosomal mRNA levels to WT levels for most of the desmosomal transcripts (r=3; error bars represent SEM; * indicates $p < 0.05$ by one-way ANOVA).

Supplementary Figure S5



Supplementary Figure S5: siRNA mediated depletion of ALK5 is sufficient to inhibit ROCK signaling and rescue desmosome levels in keratinocytes with mTORC1 loss-of-function. (A) Treatment of Inducible *Rptor* cKO keratinocytes with ALK5 siRNA partially suppresses p-MLC2 and ALK5 levels and rescues expression of desmosomal proteins (DSP, DSG1, DSG3, PKP3) and markers of biochemical differentiation (TGM1, loricrin) by immunoblotting. **(B)** Treatment of *Rheb* cKO keratinocytes with ALK5 siRNA partially suppresses p-MLC2 and ALK5 levels and rescues desmosomal protein expression by immunoblotting. **(C)** Treatment of *Rheb* WT keratinocytes with ALK5 siRNA partially suppresses p-MLC2 and ALK5 levels and rescues expression of desmosomal proteins (DSP, DSG1, DSG3, PKP3) and markers of biochemical differentiation (involucrin) by immunoblotting. DSP and ALK5 were immunoblotted separately using the same biological replicate. **(D)** Treatment of *Rheb* cKO keratinocytes with ALK5 siRNA increases membranous desmosomal protein levels (DSP1/2 and DSG1) and cortical f-actin (by phalloidin staining) and p-MLC2 levels by immunofluorescence (left panels) (scale bar=100 µm). Quantification of DSP and DSG1 border fluorescence (right panels) from representative images ($n>28$ cells, $r=3$; $p<0.001$ by Mann-Whitney test).

Supplementary Figure S6



Supplementary Figure S6: Tentative model outlining the downstream sequalae of mTORC1 loss-of-function in the epidermis. Solid lines represent pathways substantiated in this manuscript, or by previous studies (references 41,56). Dashed lines represent potential uncharacterized consequences of mTORC1 inhibition that are the subject of future study.

Methods:

Mice genotyping:

-Wild-type and floxed *Rptor*: 5’-CTC AGT AGT GGT ATG TGC TCA G-3’ (forward)
5’-GGG TAC AGT ATG TCA GCA CAG-3’ (reverse)
-Wild-type and floxed *Rheb:* 5’-GCC CAG AAC ATC TGT TCC AT-3’ (forward)
5’-GGT ACC CAC AAC CTG ACA CC-3’ (reverse)
-Recombined *Rheb:* 5’-ATA GCT GGA GCC ACC AAC AC-3’ (forward)
5’-GCC TCA GCT TCT CAA GCA AC-3’ (reverse)
-KRT14-cre: 5’- TTC CTC AGG AGT GTC TTC GC-3’ (transgene)
5’-GTC CAT GTC CTT CCT GA GC-3’ (transgene)
5’-CAA ATG TTG CTT GTC TGG TG-3’ (internal positive control forward)
5’-GTC AGT CGA GTG CAC AGT TT-3’ (internal positive control reverse)

Barrier function assay:

Embryos were euthanized, washed in ice-cold PBS, passaged through a gradient of ice-cold methanol and stained in 0.1% toluidine blue solution in water for 1-2 min on ice. After de-staining in PBS, embryos were photographed using a Motic SMZ 168 stereomicroscope (Motic Optics; Richmond, British Columbia) equipped with a Moticam 2300, 3.0 Megapixel digital color camera.

Primary mouse keratinocyte cultures: Newborn pups were decapitated, immersed in 7.5% povidone-iodine for 5 minutes and rinsed in 70% ethanol for 2 minutes. The trunk skin was removed and placed dermis-side down in a Petri dish containing 0.25% trypsin-EDTA (Invitrogen), overnight at 4 °C for 18h. The dermis was separated from the epidermis and keratinocytes isolated by scraping the basal surface of the epidermis. Keratinocyte cell suspensions were passed through a 100 micron cell strainer, centrifugated twice and plated on Petri dishes coated with fibronectin (F1141; Sigma), in calcium-free EMEM (BW06-174G; Lonza) supplemented with 10% chelated FBS (100-106; Gemini), 0.2 mM calcium (Lonza), 10 ng/ml epidermal growth factor (EGF)(Peprotech) and antibiotics. Chelation of Fetal Bovine Serum was carried out using

Chelex (100 resin, sodium, 200–400 dry mesh, 75–150 mm wet bead) (Bio-Rad) according to described protocols. The following day, media was replaced by EMEM containing 10% chelated FBS, EGF, 0.05 mM calcium and antibiotics.

Reagents and antibodies: Primary antibodies used were: Rheb (09-247, Millipore), 1:1000; Phospho-S6 Ribosomal Protein (Ser240/244) (5364, Cell Signaling), 1:800-1:1000; S6 Ribosomal Protein (2317, Cell Signaling), 1:1000; β-Actin (3700, Cell Signaling), 1:1000; Raptor (2280, Cell Signaling), 1:1000; Phospho-mTOR (S2448) (5536, Cell Signaling), 1:50; Phospho-4E-BP1 (Thr37/46) (2855, Cell Signaling), 1:1000; Phospho-Akt (S473) (4060, Cell Signaling), 1:1000; Phospho-Akt (T308) (5106, Cell Signaling), 1:500; Akt (pan) (4691, Cell Signaling), 1:1000; Phospho-FoxO1 (Thr24)/FoxO3a (Thr32)/FoxO4 (Thr28) (2599, Cell Signaling), 1:1000; FoxO1 (2880, Cell Signaling), 1:1000; Phospho-GSK-3β (Ser9) (9323, Cell Signaling), 1:1000; GSK-3β (sc-53931, Santa Cruz), 1:500; p63 (sc-8431, Santa Cruz), 1:50; Ki-67 (12202, Cell Signaling), 1:400; Phospho-Histone H3 (Ser10) (06-570, Millipore), 1:500-1:1000; Cleaved Caspase-3 (Asp175) (9664, Cell Signaling), 1:100; γ-tubulin (T-6557, Sigma-Aldrich), 1;5000; Acetyl-α-Tubulin (Lys40) (5335, Cell Signaling), 1:800; Survivin (2808, Cell Signaling), 1:400; Keratin1 (ab24643, Abcam), 1:1000; Keratin10 (PRB-159P, Covance), 1:1000; Keratin5 (PRB-160P, Covance), 1:1000; Keratin14 (CBL197, Millipore), 1:1000; Involucrin (PRB-140C, Covance), 1:1000; Loricrin (PRB-145P, Covance), 1:1000; Filaggrin (PRB-417P, Covance), 1:1000; TGM1 (ab103814, Abcam), 1:1000; β-Tubulin (2128, Cell signaling), 1:1000; DSP (10R-D108A, Fitzgerald), 1:500; DSG1 (sc-20114, Santa Cruz), 1:500; DSG3 (D218-3, MBL), 1:1000; DSC3 (sc-48750, Santa Cruz), 1:500; PKP1 (ab183512, Abcam), 1:1000; PKP2 (ab151402, Abcam), 1:1000; PKP3 (MA5-18080, ThermoFisher Scientific), 1:1000; E-Cadherin (3195, Cell Signaling); 1:1000; Pan-Cadherin (4068, Cell Signaling), 1:1000; β-Catenin (8480, Cell Signaling), 1:1000; α-E-Catenin Antibody (3236, Cell Signaling), 1:1000; γ-Catenin Antibody (2309, Cell Signaling) 1:1000; Vinculin (4650, Cell Signaling), 1:1000; Vinculin (V9264, Sigma-Aldrich), 1:50; α-Actinin (6487, Cell Signaling), 1:1000; EPLIN (sc-136399, Santa Cruz), 1:500; Afadin (13531, Cell Signaling), 1:1000; ZO-1 (13663, Cell

Signaling), 1:1000; Phospho-Myosin Light Chain 2 (Thr18/Ser19) (3674, Cell Signaling), 1:1000; Phospho-Myosin Light Chain 2 (Ser19) (3675, Cell Signaling), 1:1000; Myosin Light Chain 2 (8505, Cell Signaling), 1:500; Phospho-MYPT1 (Thr696) (5163, Cell Signaling), 1:1000; Phospho-MYPT1 (Thr853) (4563, Cell Signaling), 1:1000; MYPT1 (2634, Cell Signaling), 1:1000; Phospho-Paxillin (Tyr118) (2541, Cell Signaling), 1:50-1:1000; Paxillin (2542, Cell Signaling), 1:1000; Phospho-FAK (Tyr397) (3283, Cell Signaling), 1:1000; Fak (3285, Cell Signaling), 1:1000; Phospho-p130 Cas (Tyr410) (4011, Cell Signaling), 1:1000; p130 Cas (13846, Cell Signaling), 1:1000; ROCK1 (4035, Cell Signaling), 1;1000; ROCK2 (8236, Cell Signaling), 1;1000; RhoA (2117, Cell Signaling), 1:1000; RhoB (2098, Cell Signaling), 1:1000; Rho (A,B,C) (05-778, Millipore), 1:1000; RhoE/Rnd3 (05-723, Millipore), 1:1000; Calreticulin (12238, Cell Signaling), 1:1000; Na,K-ATPase (3010, Cell Signaling), 1:1000; ALK5 (ab31013, Abcam), 1:50-1:500; Smad2 (51-1300, ThermoFisher Scientific), 1:100; Smad3 (51-1500, ThermoFisher Scientific), 1:100; Phospho-Smad2 (Ser465/467) (3108, Cell Signaling), 1:1000; Phospho-Smad2 (Ser465/467)/Smad3 (Ser423/425), 1:1000; Smad2/3 (8685, Cell Signaling), 1:1000; Vimentin (5741, Cell Signaling), 1:1000.

Histology and immunostaining: Sections were deparaffinized in xylene (Sigma-Aldrich), hydrated in graded ethanol and rinsed in distilled water. Antigen retrieval was performed using citrate (10 mM, pH 6.0) or EDTA + 0.01% TWEEN 20 (1 mM, pH 8.0) buffers and HIER (heat-induced epitope retrieval) method, in accordance with the protocol specified for each antibody. All washing steps were done using 1X TBS-T buffer. Endogenous peroxidase activity was quenched by incubation with Dual Enzyme Block (Dako, Agilent Technologies) for 10 minutes at room temperature. Sections were incubated with each antibody overnight at 4°C diluted in antibody dilution buffer (Roche/ Ventana Medical Systems). For immunohistochemistry, a horseradish peroxidase–labeled polymer, Poly-HRP PowerVision Detection System (Novocastra/Leica Biosystems) was applied for 30 minutes at room temperature. Signal detection was performed using 3,3'-diaminobenzidine tetrahydrochloride (DAB) (Sigma-Aldrich) for 20 minutes at room temperature. Slides were counterstained for 30 seconds with Mayer's hematoxylin (Dako, Agilent Technologies), dehydrated, and mounted. For immunofluorescence, after primary antibody overnight reaction at 4°C, sections were incubated with secondary antibodies (Alexafluor-488 or Alexafluor-594 conjugated, anti-Rabbit or anti-Mouse IgG, Thermo Fisher Scientific) at a dilution of 1:200 for 1h 30min at room temperature. Subsequently they were washed 2x/5min in PBS, rinsed in distilled water, dehydrated in graded ethanol and mounted with ProLong Gold Antifade with DAPI (Thermo Fisher Scientific).

Protein lysate preparation and immunoblotting: Once dissociated, the epidermal sheet was homogenized using gentleMACS M tubes in the gentleMACS dissociator (Miltenyi Biotec). Tissues or cells were homogenized and lysed in ice-cold Urea lysis buffer (8M Urea, 60mM Tris pH 6.8, 1 % SDS [w/v],) supplemented with $NaVO_4$ (1 mM), NaF (1 mM) and 10 µl Halt Protease and Phosphatase Inhibitor Cocktail (78440, Thermo Fisher Scientific) in 1 ml buffer for 15 min on ice. Lysates were sheared by passing through 20,22,25 and 26 gauge needles progressively, centrifuged at 21,000 rpm for 10 minutes at 4°C and supernatants collected. Protein concentrations were quantified using the BCA Protein Assay Kit (23225, Pierce), and 5-10 ug of protein was resolved on a 1.5-mm, 3-8% Tris-Acetate or 4-12% Bis-Tris SDS-PAGE gel (Thermo Fisher Scientific). Protein was transferred to nitrocellulose membranes (Amersham Bioscience). Membranes were allowed to block for 1h at room temperature in 5% nonfat milk in 1X TBS-T and then incubated overnight with a primary antibody diluted in 5% BSA in 1X TBS-T. The secondary antibodies used were anti-rabbit or anti-mouse immunoglobulin as appropriate (Cell Signaling) and diluted at 1:1000 in 5% nonfat milk in 1X TBS-T . Blots were developed using a chemiluminescent development solution (Super Signal West Femto, Pierce) and bands were imaged on a chemiluminescent imaging system (ChemiDoc Touch imaging System, Bio-Rad) or MicroChemi Chemiluminescent imager (FroggaBio Inc.). Digital images were quantified using background correction on the Alpha Innotech system (Protein Simple) and all bands were normalized to their respective β-actin, tubulin or GAPDH expression levels as loading controls.

RNA isolation and RT-PCR: The following primers and probes were utilized: DSP(Mm01351876_m1), DSG1a(Mm00809994_s1),DSG1b(Mm00839130_mH), DSG1c(Mm00725121_g1) DSG3(Mm00659652_m1), DSC3(Mm00492270_m1), PKP1(Mm00451023_m1), PKP2(Mm00503159_m1), PKP3(Mm00451123_m1), actin (Mm02619580_g1) (TaqMan Gene Expression Assay, Applied Biosystems).

Immunocytochemistry: Cells were permeabilized and blocked in buffer containing 1X PBS, 5% normal donkey serum and 0.3% Triton X-100. Coverslips were incubated with indicated primary antibodies overnight at 4°C in antibody dilution buffer (ADB) containing 1X PBS, 1% BSA and 0.3% Triton X-100. After 3 PBS washes, coverslips were incubated with secondary antibodies (Alexafluor-488 or Alexafluor-594 conjugated, anti-Rabbit or anti-Mouse IgG, Thermo Scientific) in ADB (1:200) for 1 hour at room temperature. Nuclei were counterstained with DAPI.

Quantification of membrane localized of Dsp, Dsg and E-cadherin in cultured cells: Border index for each protein was calculated based on the method published by (Godsel et al, J Cell Biol, 2005). Briefly, all immunofluorescence procedures, epifluorescence acquisition settings, and image analysis parameters were maintained across all technical and biological replicates for the analysis of a protein stain. For each sampled cell, a region of interest was manually drawn around its borders using ImageJ, and the same threshold was applied to remove background noise. For each thresholded region of interest, the border index was calculated by multiplying the mean fluorescence intensity by the area of the region of interest and divided by the border perimeter. **Quantification of cell perimeter:** The perimeter of each cell was manually outlined as a region of interest and the perimeter was measured in pixels. **Quantification of nuclear Smad2/3 intensity:** Cells were stained with DAPI to mark nuclei (blue channel) and anti-total Smad2/3 (green channel). Images were analyzed using ImageJ. The blue channel was used to segment nuclei as follows: the Smooth function was used 3 times, then images were thresholded to remove background, converted to binary images on which a Watershed function was applied to separate overlapping nuclei. Then the analyze Particles function was used forautomatic detection of nuclear outlines. These nuclear outlines were applied to the green channel and mean fluorescence intensity of Smad2/3 within the regions was measured.

Transmission Electron Microscopy: Mouse skin samples were fixed in 2.5% glutaraldehyde, 3mM $MgCl_2$ and 1% sucrose, in 0.1 M sodium cacodylate buffer, pH 7.2 at 4^{o}C overnight, followed by 3 buffer rinses, 15 minutes each, in 3mM $MgCl_2$, 3% sucrose and 0.1 M sodium cacodylate. The samples were post-fixed in 1% osmium tetroxide in 0.1 M sodium cacodylate for 1 hour on ice in the dark, rinsed twice with distilled water for 5 minutes, stained with 2% aqueous uranyl acetate (0.22 µm filtered) for 1 hour in the dark, followed by dehydration in an ascending grade of ethanol (50%, 70%, 90% and 100%; thrice each) and embedded in an epoxy resin. The resin was allowed to polymerize at 37^{o}C overnight for 2-3 days followed by 60^{o}C overnight.

Microarray analysis: Mouse epidermis was separated from the dermis following incubation of E18.5 embryonic 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 was 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 RHEB WT and RHEB 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: *RHEB* cKO and *RHEB* WT. The list of 1,198 highly differentially expressed genes, with fold changes greater than 2 S.D. between RHEB WT versus RHEB cKO, is in **Supplementary Table S1**. These differentially expressed genes then underwent Canonical Pathway analysis using the Ingenuity Pathway Analysis platform (IPA, QIAGEN Redwood City, CA USA www.ingenuity.com).

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

Probeset ID	RHEB_cKO vs. WT (p-val)	RHEB_cKO vs. WT Lin(FC)	RHEB_cKO vs. WT (Description)	RHEB_cKO vs. WT Log2(FC)	SD RHEB_cKO vs. WT Log2(FC)	Gene CytoLoc	Gene EntrezID	Gene EntrezID	Gene Symbol	Gene Title
TC0300000	0.000797	38.4788	RHEB_cKO up vs WT	5.26599	> +6σ	3 F1-F2|3	20201	20201	S100a8	S100 calcium binding protein A8 (calgranulin A)
TC0300002	0.000305	34.0958	RHEB_cKO up vs WT	5.09152	> +6σ	3 F1-F2|3	20202	20202	S100a9	S100 calcium binding protein A9 (calgranulin B)
TC0300000	0.00115	21.4185	RHEB_cKO up vs WT	4.42078	> +6σ	3 F1|3 40.	20760	20760	Sprr2f	small proline-rich protein 2F
TC0300000	0.002045	20.4921	RHEB_cKO up vs WT	4.357	> +6σ	3 F1|3	69520	69520	Lce3f	late cornified envelope 3F
TC0800000	0.001408	17.7214	RHEB_cKO up vs WT	4.14742	> +6σ	8|8	27358	27358	Defb3	defensin beta 3
TC0300000	0.003389	16.8731	RHEB_cKO up vs WT	4.07665	> +6σ	3 F1|3 40.	20761	20761	Sprr2g	small proline-rich protein 2G
TC0300002	7.08E-05	14.2322	RHEB_cKO up vs WT	3.83108	> +6σ	3 F1|3 40.	20754	20754	Sprr1b	small proline-rich protein 1B
TC0300000	0.002107	13.2807	RHEB_cKO up vs WT	3.73126	> +6σ	3 F1|3	630994	630994	Lce3d	late cornified envelope 3D
TC0300000	0.00107	11.9369	RHEB_cKO up vs WT	3.57736	> +6σ	3 F1|3 40.	20764	20764	Sprr2j-ps	small proline-rich protein 2J, pseudogene
TC0300000	0.000186	10.7404	RHEB_cKO up vs WT	3.42497	> +6σ	3 F1|3	381493	381493	S100a7a	S100 calcium binding protein A7A
TC0300002	0.003119	10.6727	RHEB_cKO up vs WT	3.41586	> +6σ	3 F1|3	545548	545548	Lce3a	late cornified envelope 3A
TC0300002	0.00028	9.93365	RHEB_cKO up vs WT	3.31232	> +6σ	3 F1|3 40.	20753	20753	Sprr1a	small proline-rich protein 1A
TC0100001	0.004786	9.7266	RHEB_cKO up vs WT	3.28194	> +6σ	1 H1|1 63.	19225	19225	Ptgs2	prostaglandin-endoperoxide synthase 2
TC1500002	0.000169	9.55391	RHEB_cKO up vs WT	3.25609	> +6σ	15 F2|15	406223	406223	Gm5414	predicted gene 5414
TC1600000	0.000109	9.02367	RHEB_cKO up vs WT	3.17371	> +6σ	16 B3|16	408196	408196	Gm5416	predicted gene 5416
TC0300000	0.000628	8.84585	RHEB_cKO up vs WT	3.145	> +6σ	3 F1|3 40.	20759	20759	Sprr2e	small proline-rich protein 2E
TC1500002	0.000366	8.33038	RHEB_cKO up vs WT	3.05838	> +6σ	15 F2|15	16687	16687	Krt6a	keratin 6A
TC1500001	2.76E-05	7.84124	RHEB_cKO up vs WT	2.97108	> +6σ	15 D3|15	11838	11838	Arc	activity regulated cytoskeletal-associated protein
TC0200001	0.00362	7.71179	RHEB_cKO up vs WT	2.94707	> +6σ	2 C2|2	241452	241452	Dhrs9	dehydrogenase/reductase (SDR family) member 9
TC0500000	0.000512	7.62878	RHEB_cKO up vs WT	2.93145	> +6σ	---	71920	71920	Epgn	epithelial mitogen
TC0800001	0.000581	7.52137	RHEB_cKO up vs WT	2.911	> +6σ	8 A3|8	211323	211323	Nrg1	neuregulin 1
TC0300000	0.003576	7.06496	RHEB_cKO up vs WT	2.82068	> +6σ	3 F1|3 40.	20758	20758	Sprr2d	small proline-rich protein 2D
TC0100003	0.003563	7.00865	RHEB_cKO up vs WT	2.80914	> +6σ	1 H3|1	666028	666028	Gm7897	predicted gene 7897
TC0300000	0.000604	6.88644	RHEB_cKO up vs WT	2.78376	> +6σ	3 F1|3 40.	20763	20763	Sprr2i	small proline-rich protein 2I
TC0600000	9.28E-05	6.77061	RHEB_cKO up vs WT	2.75928	> +6σ	6 B1|6 14.	14187	14187	Akr1b8	aldo-keto reductase family 1, member B8
TC0800000	0.002984	6.73769	RHEB_cKO up vs WT	2.75225	> +6σ	8 A1.3|8	56519	56519	Defb4	defensin beta 4
TC0700000	0.001038	6.67023	RHEB_cKO up vs WT	2.73774	> +6σ	7 B4|7 28.	69540	69540	Klk10	kallikrein related-peptidase 10
TC1100003	3.65E-05	6.26662	RHEB_cKO up vs WT	2.64769	> +6σ	11 D|11	16666	16666	Krt16	keratin 16
TC0900000	2.84E-05	6.21186	RHEB_cKO up vs WT	2.63503	> +6σ	9 A1|9 2.4	17392	17392	Mmp3	matrix metallopeptidase 3
TC1000001	0.001279	6.17593	RHEB_cKO up vs WT	2.62666	> +6σ	10|10 C3	67603	67603	Dusp6	dual specificity phosphatase 6
TC0100003	1.94E-05	5.86237	RHEB_cKO up vs WT	2.55148	> +6σ	1 E4|1	93672	93672	Il24	interleukin 24
TC1100003	4.53E-05	5.83589	RHEB_cKO up vs WT	2.54495	> +6σ	---	---	---	Gm11597	predicted gene 11597
TC0900000	0.00182	5.79621	RHEB_cKO up vs WT	2.53511	> +6σ	9|9 B	76509	76509	Plet1	placenta expressed transcript 1
TC1300000	0.000795	5.12175	RHEB_cKO up vs WT	2.35664	> +6σ	13 A3.2|1	218121	218121	Mboat1	membrane bound O-acyltransferase domain containing 1
TC1800000	0.001223	5.00993	RHEB_cKO up vs WT	2.32479	> +6σ	18 A2|18	13512	13512	Dsg3	desmoglein 3
TC0300000	0.002529	4.95249	RHEB_cKO up vs WT	2.30815	> +6σ	3 F1|3 40.	20762	20762	Sprr2h	small proline-rich protein 2H
TC0200004	0.006298	4.69922	RHEB_cKO up vs WT	2.23242	> +6σ	2 E5|2	329502	329502	Pla2g4e	phospholipase A2, group IVE
TC1500002	0.001025	4.61868	RHEB_cKO up vs WT	2.20748	> +6σ	15 F2|15	432985	432985	Gm5476	type II keratin Kb17P pseudogene
TC0100003	0.000206	4.59703	RHEB_cKO up vs WT	2.2007	> +6σ	1 H5|1	12334	12334	Capn2	calpain 2
TC0300000	0.01792	4.58465	RHEB_cKO up vs WT	2.19681	> +6σ	3 F1|3	242100	242100	Pglyrp3	peptidoglycan recognition protein 3
TC0300000	0.040014	4.49185	RHEB_cKO up vs WT	2.16731	> +6σ	3 F1|3	69514	69514	Lce3e	late cornified envelope 3E
TC0800000	0.001135	4.44329	RHEB_cKO up vs WT	2.15163	> +6σ	8|8	387216	387216	Mir23a	microRNA 23a
TC1100003	0.001712	4.39998	RHEB_cKO up vs WT	2.1375	> +6σ	11 D|11	217169	217169	Tns4	tensin 4
TC0300000	0.009364	4.34193	RHEB_cKO up vs WT	2.11834	> +6σ	3 F1|3	66344	66344	Lce3b	late cornified envelope 3B
TC0400001	0.000797	4.32072	RHEB_cKO up vs WT	2.11127	> +6σ	4 E2|4 78.	18158	18158	Nppb	natriuretic peptide type B
TC0X00002	0.001138	4.31771	RHEB_cKO up vs WT	2.11027	> +6σ	X C-D|X 39	14933	14933	Gk	glycerol kinase
TC0200000	0.001717	4.30934	RHEB_cKO up vs WT	2.10747	> +6σ	2 C1.1|2	71409	71409	Fmnl2	formin-like 2
TC1300001	0.001439	4.27612	RHEB_cKO up vs WT	2.0963	> +6σ	13 A3.3|1	97848	97848	Serpinb6c	serine (or cysteine) peptidase inhibitor, clade B, member 6c
TC1000003	0.000989	4.21317	RHEB_cKO up vs WT	2.0749	> +6σ	10 D2|10	15364	15364	Hmga2	high mobility group AT-hook 2
TC1800000	0.000177	4.14075	RHEB_cKO up vs WT	2.04989	> +6σ	18|18 E1	67951	67951	Tubb6	tubulin, beta 6 class V
TC0300002	0.008852	4.06674	RHEB_cKO up vs WT	2.02387	+6σ	3 F1|3 40.	229562	229562	Sprr4	small proline-rich protein 4
TC0300000	0.020518	3.97958	RHEB_cKO up vs WT	1.99262	+6σ	3|3 F1-F2	20129	20129	Rptn	repetin
TC1900000	0.000728	3.95121	RHEB_cKO up vs WT	1.9823	+6σ	19|19 C2	77125	77125	Il33	interleukin 33
TC0100003	0.001538	3.92505	RHEB_cKO up vs WT	1.97271	+6σ	1 F|1 62.5	19735	19735	Rgs2	regulator of G-protein signaling 2
TC0600001	0.007243	3.89992	RHEB_cKO up vs WT	1.96344	+6σ	6 G1|6	232431	232431	Gprc5a	G protein-coupled receptor, family C, group 5, member A
TC1800001	0.000307	3.88841	RHEB_cKO up vs WT	1.95918	+6σ	18 B2|18	15200	15200	Hbegf	heparin-binding EGF-like growth factor
TC0300000	0.0017	3.84409	RHEB_cKO up vs WT	1.94264	+6σ	3 F1-F2|3	20200	20200	S100a6	S100 calcium binding protein A6 (calcyclin)
TC0100003	0.002108	3.81185	RHEB_cKO up vs WT	1.93049	+6σ	1 H2.3|1	80914	80914	Uck2	uridine-cytidine kinase 2
TC0300003	0.00318	3.77507	RHEB_cKO up vs WT	1.9165	+6σ	3 H2|3 70.	16007	16007	Cyr61	cysteine rich protein 61
TC0700000	0.015803	3.6726	RHEB_cKO up vs WT	1.8768	+6σ	7 B4-B5|7	19144	19144	Klk6	kallikrein related-peptidase 6
TC1100003	0.007812	3.60834	RHEB_cKO up vs WT	1.85134	+6σ	11 D|11 5	16400	16400	Itga3	integrin alpha 3
TC1800000	0.002326	3.58938	RHEB_cKO up vs WT	1.84374	+6σ	18 A1|18	72504	72504	Taf4b	TATA-box binding protein associated factor 4b
TC0100001	0.008692	3.55466	RHEB_cKO up vs WT	1.82971	+6σ	1 E2.1|1	66957	66957	Serpinb11	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 11
TC0800000	1.24E-05	3.53624	RHEB_cKO up vs WT	1.82222	+6σ	8|8	387220	387220	Mir27a	microRNA 27a
TC0600001	0.000735	3.51779	RHEB_cKO up vs WT	1.81467	+6σ	6 D1|6 40.	21366	21366	Slc6a6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6
TC0900001	0.001951	3.48228	RHEB_cKO up vs WT	1.80003	+6σ	9 F1|9	235584	235584	Dusp7	dual specificity phosphatase 7
TC0200001	0.011685	3.47741	RHEB_cKO up vs WT	1.79801	+6σ	2 C2-C3|2	16403	16403	Itga6	integrin alpha 6
TC0500002	0.008744	3.43367	RHEB_cKO up vs WT	1.77975	+6σ	5 E3|5	71914	71914	Antxr2	anthrax toxin receptor 2
TC1300001	0.001238	3.37857	RHEB_cKO up vs WT	1.75641	+6σ	13 A4|13	66895	66895	Pxdc1	PX domain containing 1
TC0800003	0.001799	3.32285	RHEB_cKO up vs WT	1.73242	+6σ	---	---	---	Gm17709	predicted gene, 17709
TC0400002	0.008479	3.32193	RHEB_cKO up vs WT	1.73202	+6σ	4 B1|4	11828	11828	Aqp3	aquaporin 3
TC0700004	0.000135	3.29473	RHEB_cKO up vs WT	1.72016	+6σ	7|7 F3-F5	11501	11501	Adam8	a disintegrin and metallopeptidase domain 8
TC1200000	0.002762	3.28073	RHEB_cKO up vs WT	1.71401	+6σ	12 A1.1|1	18263	18263	Odc1	ornithine decarboxylase, structural 1
TC1400000	0.007538	3.27257	RHEB_cKO up vs WT	1.71043	+6σ	14 C3|14	16995	16995	Ltb4r1	leukotriene B4 receptor 1
TC1800001	0.00024	3.25484	RHEB_cKO up vs WT	1.70259	+6σ	18|18 E2	16891	16891	Lipg	lipase, endothelial
TC1500002	0.038914	3.25249	RHEB_cKO up vs WT	1.70155	+6σ	15 F2|15	109052	109052	Krt75	keratin 75
TC0300000	0.000684	3.24704	RHEB_cKO up vs WT	1.69912	+6σ	3 E1|3	99929	99929	Tiparp	TCDD-inducible poly(ADP-ribose) polymerase
TC1200001	0.010019	3.24517	RHEB_cKO up vs WT	1.69829	+6σ	12|12 D2	27260	27260	Plek2	pleckstrin 2
TC0100001	0.004146	3.24427	RHEB_cKO up vs WT	1.69789	+6σ	1 H2.1|1	67647	67647	4930523C	RIKEN cDNA 4930523C07 gene
TC1300001	0.003845	3.22514	RHEB_cKO up vs WT	1.68936	+6σ	13 A5|13	20238	20238	Atxn1	ataxin 1
TC0200003	0.00721	3.22368	RHEB_cKO up vs WT	1.68871	+6σ	2 B-C1|2	13830	13830	Stom	stomatin
TC0300001	0.002132	3.1643	RHEB_cKO up vs WT	1.66189	+6σ	3 F3|3	229731	229731	Slc25a24	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 24
TC0100003	0.002836	3.15927	RHEB_cKO up vs WT	1.65959	+6σ	1 H3|1	26388	26388	Ifi202b	interferon activated gene 202B
TC0400003	0.00084	3.15005	RHEB_cKO up vs WT	1.65537	+6σ	4|4 D3	67149	67149	Nkain1	Na+/K+ transporting ATPase interacting 1

TC17000015	0.000382	3.14671	RHEB_cKO up vs WT	1.65384	+6σ	17 A3.3|17	27279	27279	Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a
TC02000018	0.000228	3.13125	RHEB_cKO up vs WT	1.64674	+6σ	2 E5|2	99439	99439	Duox1	dual oxidase 1
TC05000006	0.015846	3.10094	RHEB_cKO up vs WT	1.63271	+6σ	5 C3.2|5	231293	231293	Cwh43	cell wall biogenesis 43 C-terminal homolog
TC04000036	0.002311	3.06675	RHEB_cKO up vs WT	1.61671	+6σ	4|4 D3	94242	94242	Tinagl1	tubulointerstitial nephritis antigen-like 1
TC04000012	0.037862	3.03854	RHEB_cKO up vs WT	1.60338	+6σ	---	---	---	Gm12840	predicted gene 12840
TC15000022	0.000134	3.03736	RHEB_cKO up vs WT	1.60282	+6σ	15 F2|15	432987	432987	Gm5478	predicted pseudogene 5478
TC03000003	0.030245	3.03565	RHEB_cKO up vs WT	1.60201	+6σ	3 B|3	18415	18415	Hspa4l	heat shock protein 4 like
TC11000020	0.003938	3.0342	RHEB_cKO up vs WT	1.60132	+6σ	11 E2|11 8	111241	111241	Hmga1-rs1	high mobility group AT-hook I, related sequence 1
TC0X000006	0.002403	3.01754	RHEB_cKO up vs WT	1.59337	+6σ	X|X B	75590	75590	Dusp9	dual specificity phosphatase 9
TC04000024	0.450121	3.0145	RHEB_cKO up vs WT	1.59192	+6σ	---	---	---	Gm13303	predicted gene 13303
TC01000038	0.000483	3.01073	RHEB_cKO up vs WT	1.59011	+6σ	1 E2.1|1 5	18788	18788	Serpinb2	serine (or cysteine) peptidase inhibitor, clade B, member 2
TC15000010	0.006292	3.00474	RHEB_cKO up vs WT	1.58724	+6σ	15|15 F	15370	15370	Nr4a1	nuclear receptor subfamily 4, group A, member 1
TC15000021	0.016427	2.97788	RHEB_cKO up vs WT	1.57429	+6σ	15 F1|15	67760	67760	Slc38a2	solute carrier family 38, member 2
TC11000009	0.0173	2.93686	RHEB_cKO up vs WT	1.55427	+6σ	11 B3|11 4	20670	20670	Sox15	SRY (sex determining region Y)-box 15
TC03000008	0.00939	2.92758	RHEB_cKO up vs WT	1.54971	+6σ	3 F1|3 40.	20765	20765	Sprr2k	small proline-rich protein 2K
TC18000013	0.006423	2.9234	RHEB_cKO up vs WT	1.54765	+6σ	18 D3|18	106878	106878	Smim3	small integral membrane protein 3
TC08000025	0.001733	2.91911	RHEB_cKO up vs WT	1.54553	+6σ	8 C2|8 40.	26364	26364	Adgre5	adhesion G protein-coupled receptor E5
TC0X000011	0.002878	2.90195	RHEB_cKO up vs WT	1.53702	+6σ	---	---	---	Gm14928	predicted gene 14928
TC12000001	0.01698	2.89631	RHEB_cKO up vs WT	1.53421	+6σ	---	---	---	Gm22303	predicted gene, 22303
TC04000034	0.004154	2.89503	RHEB_cKO up vs WT	1.53358	+6σ	4|4 D1	76574	76574	Mfsd2a	major facilitator superfamily domain containing 2A
TC0X000027	0.002694	2.89286	RHEB_cKO up vs WT	1.5325	+6σ	---	---	---	Gm9115	predicted gene 9115
TC08000030	0.002655	2.89014	RHEB_cKO up vs WT	1.53114	+6σ	8 E1|8 70.	20539	20539	Slc7a5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
TC08000006	0.00167	2.88347	RHEB_cKO up vs WT	1.52781	+6σ	8 B3.3|8	234344	234344	Naf1	nuclear assembly factor 1 ribonucleoprotein
TC0X000019	0.032636	2.86324	RHEB_cKO up vs WT	1.51765	+6σ	---	---	---	Gm26652	predicted gene, 26652
TC14000022	0.004807	2.84225	RHEB_cKO up vs WT	1.50703	+6σ	14 D1|14 3	19229	19229	Ptk2b	PTK2 protein tyrosine kinase 2 beta
TC04000028	0.01973	2.84022	RHEB_cKO up vs WT	1.506	+6σ	4 C1|4 34.	21923	21923	Tnc	tenascin C
TC04000004	0.351385	2.82231	RHEB_cKO up vs WT	1.49688	+6σ	---	---	---	Gm10600	predicted gene 10600
TC08000001	0.004036	2.81174	RHEB_cKO up vs WT	1.49147	+6σ	8 A1.3|8	244332	244332	Defb14	defensin beta 14
TC11000037	0.010257	2.80846	RHEB_cKO up vs WT	1.48978	+6σ	11 D|11 63	16664	16664	Krt14	keratin 14
TC17000021	0.005917	2.79185	RHEB_cKO up vs WT	1.48122	+6σ	17|17 C	71583	71583	9130008F2	RIKEN cDNA 9130008F23 gene
TC08000010	0.003112	2.78162	RHEB_cKO up vs WT	1.47592	+6σ	8 C5|8 46.	17750	17750	Mt2	metallothionein 2
TC05000008	0.004343	2.77443	RHEB_cKO up vs WT	1.47219	+6σ	5 E1|5 44.	11839	11839	Areg	amphiregulin
TC05000036	0.006398	2.76923	RHEB_cKO up vs WT	1.46949	+6σ	5 G3|5 88.	11987	11987	Slc7a1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
TC10000022	0.00206	2.76193	RHEB_cKO up vs WT	1.46567	+6σ	10 B4-B5.1	56200	56200	Ddx21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21
TC09000033	0.010264	2.75115	RHEB_cKO up vs WT	1.46003	+6σ	9 F|9 74.2	102680	102680	Slc6a20a	solute carrier family 6 (neurotransmitter transporter), member 20A
TC11000038	0.001401	2.7354	RHEB_cKO up vs WT	1.45175	+6σ	11 D|11 65	18612	18612	Etv4	ets variant 4
TC09000020	0.006021	2.72785	RHEB_cKO up vs WT	1.44776	+6σ	---	---	---	RP24-570C	NOP56 ribonucleoprotein (Nop56) pseudogene
TC01000014	0.006913	2.71295	RHEB_cKO up vs WT	1.43986	+6σ	1 G3-H1|1	11352	11352	Abl2	v-abl Abelson murine leukemia viral oncogene 2 (arg, Abelson-related gene)
TC01000038	0.07734	2.70829	RHEB_cKO up vs WT	1.43738	+6σ	1 E2.1|1	241197	241197	Serpinb10	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 10
TC03000008	0.064026	2.68853	RHEB_cKO up vs WT	1.42682	+6σ	3 F1|3	94060	94060	Lce3c	late cornified envelope 3C
TC04000004	0.34438	2.66305	RHEB_cKO up vs WT	1.41308	+6σ	---	1.01E+08	1.01E+08	Gm13301	predicted gene 13301
TC03000029	0.001488	2.65905	RHEB_cKO up vs WT	1.41091	+6σ	3 G3|3	74442	74442	Sgms2	sphingomyelin synthase 2
TC08000015	0.004259	2.65721	RHEB_cKO up vs WT	1.40991	+6σ	8 E2|8	16412	16412	Itgb1	integrin beta 1 (fibronectin receptor beta)
TC08000012	0.002616	2.65082	RHEB_cKO up vs WT	1.40644	+6σ	8 D3|8	21771	21771	Cirh1a	cirrhosis, autosomal recessive 1A (human)
TC17000005	0.009401	2.63512	RHEB_cKO up vs WT	1.39787	+6σ	17|17	11307	11307	Abcg1	ATP-binding cassette, sub-family G (WHITE), member 1
TC04000003	0.473544	2.63225	RHEB_cKO up vs WT	1.3963	+6σ	---	---	---	Gm10601	predicted pseudogene 10601
TC13000012	0.001813	2.62656	RHEB_cKO up vs WT	1.39317	+6σ	13|13 D2.	20620	20620	Plk2	polo-like kinase 2
TC13000002	0.023155	2.62243	RHEB_cKO up vs WT	1.39091	+6σ	13 A2-A3|	319181	319181	Hist1h2bg	histone cluster 1, H2bg
TC07000008	0.007607	2.62087	RHEB_cKO up vs WT	1.39004	+6σ	7 B4|7	243983	243983	Zdhhc13	zinc finger, DHHC domain containing 13
TC15000021	0.002635	2.61618	RHEB_cKO up vs WT	1.38746	+6σ	15 F1|15 5	19011	19011	Endou	endonuclease, polyU-specific
TC06000032	0.005444	2.61445	RHEB_cKO up vs WT	1.38651	+6σ	---	1.02E+08	1.02E+08	Mir7649	microRNA 7649
TC19000000	0.00129	2.60231	RHEB_cKO up vs WT	1.3798	+6σ	19 A|19 4.	14283	14283	Fosl1	fos-like antigen 1
TC11000034	0.124897	2.60171	RHEB_cKO up vs WT	1.37946	+6σ	11 C|11	76113	76113	Lpo	lactoperoxidase
TC04000037	0.000181	2.60055	RHEB_cKO up vs WT	1.37882	+6σ	4 D3|4 66.	55948	55948	Sfn	stratifin
TC05000034	0.006834	2.60023	RHEB_cKO up vs WT	1.37864	+6σ	5 G2|5	18787	18787	Serpine1	serine (or cysteine) peptidase inhibitor, clade E, member 1
TC06000024	0.026496	2.59717	RHEB_cKO up vs WT	1.37694	+6σ	6|6 D-E	54486	54486	Hpgds	hematopoietic prostaglandin D synthase
TC16000019	0.008612	2.59685	RHEB_cKO up vs WT	1.37676	+6σ	16 C3-C5|	11504	11504	Adamts1	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondir
TC14000016	0.006194	2.5938	RHEB_cKO up vs WT	1.37507	+6σ	14 B|14 19	30877	30877	Gnl3	guanine nucleotide binding protein-like 3 (nucleolar)
TC19000000	0.002755	2.59169	RHEB_cKO up vs WT	1.37389	+6σ	19 A|19	13340	13340	Slc29a2	solute carrier family 29 (nucleoside transporters), member 2
TC13000017	0.006704	2.58474	RHEB_cKO up vs WT	1.37002	+6σ	13|13 A4	73710	73710	Tubb2b	tubulin, beta 2B class IIB
TC13000016	0.013611	2.58412	RHEB_cKO up vs WT	1.36967	+6σ	---	---	---	Gm22358	predicted gene, 22358
TC10000026	0.009577	2.58177	RHEB_cKO up vs WT	1.36836	+6σ	10 C1|10	70683	70683	Utp20	UTP20 small subunit processome component
TC19000006	0.002707	2.58157	RHEB_cKO up vs WT	1.36825	+6σ	19 C3|19	70769	70769	Nolc1	nucleolar and coiled-body phosphoprotein 1
TC02000008	0.00444	2.56297	RHEB_cKO up vs WT	1.35781	+6σ	2 C1.1|2 3	14571	14571	Gpd2	glycerol phosphate dehydrogenase 2, mitochondrial
TC04000013	0.000539	2.56111	RHEB_cKO up vs WT	1.35677	+6σ	4 D2.2|4	230718	230718	Nt5c1a	5'-nucleotidase, cytosolic IA
TC13000000	0.003351	2.55859	RHEB_cKO up vs WT	1.35535	+6σ	13 A1|13 4	217995	217995	Heatr1	HEAT repeat containing 1
TC18000010	0.057416	2.54214	RHEB_cKO up vs WT	1.34604	+6σ	18 A2|18 1	13506	13506	Dsc2	desmocollin 2
TC02000042	0.01366	2.5343	RHEB_cKO up vs WT	1.34159	+6σ	2 E2|2 54.	12505	12505	Cd44	CD44 antigen
TC12000001	0.019766	2.53355	RHEB_cKO up vs WT	1.34116	+6σ	12|12 A3	19878	19878	Rock2	Rho-associated coiled-coil containing protein kinase 2
TC0X000018	0.009116	2.52905	RHEB_cKO up vs WT	1.3386	+6σ	---	---	---	Gm9432	predicted gene 9432
TC17000003	0.082411	2.52493	RHEB_cKO up vs WT	1.33625	+6σ	17 A3.3|17	213171	213171	Prss27	protease, serine 27
TC06000014	0.001486	2.52321	RHEB_cKO up vs WT	1.33526	+6σ	6 F2-F3|6	110109	110109	Nop2	NOP2 nucleolar protein
TC13000027	0.023185	2.50571	RHEB_cKO up vs WT	1.32522	+6σ	13 D2.2|13	16398	16398	Itga2	integrin alpha 2
TC06000018	0.002564	2.50452	RHEB_cKO up vs WT	1.32454	+6σ	6 A1|6	50799	50799	Slc25a13	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocato
TC06000032	0.016632	2.50259	RHEB_cKO up vs WT	1.32342	+6σ	6|6 63.11	1.01E+08	1.01E+08	Gm15987	predicted gene 15987
TC07000020	0.000371	2.50251	RHEB_cKO up vs WT	1.32338	+6σ	7 F5|7	76974	76974	Urah	urate (5-hydroxyiso-) hydrolase
TC11000037	0.006625	2.48972	RHEB_cKO up vs WT	1.31599	+6σ	11 D|11 63	16667	16667	Krt17	keratin 17
TC02000042	0.03051	2.4863	RHEB_cKO up vs WT	1.314	+6σ	2 E2|2	13661	13661	Ehf	ets homologous factor
TC07000007	0.022123	2.48243	RHEB_cKO up vs WT	1.31175	+6σ	7 B4|7 28.	69511	69511	Klk12	kallikrein related-peptidase 12
TC14000022	0.008936	2.47887	RHEB_cKO up vs WT	1.30968	+6σ	14 D1|14	68813	68813	Dock5	dedicator of cytokinesis 5
TC10000005	0.025972	2.47837	RHEB_cKO up vs WT	1.30939	+6σ	10 B4|10	432466	432466	Gm5424	argininosuccinate synthase pseudogene
TC09000033	0.008704	2.47695	RHEB_cKO up vs WT	1.30856	+6σ	9 F4|9	109332	109332	Cdcp1	CUB domain containing protein 1
TC15000003	0.006999	2.47589	RHEB_cKO up vs WT	1.30794	+6σ	15 D1|15 2	97998	97998	Deptor	DEP domain containing MTOR-interacting protein
TC04000004	0.360445	2.4742	RHEB_cKO up vs WT	1.30696	+6σ	4 A5|4	1E+08	1E+08	Gm10600	predicted gene 10600
TC02000044	0.071603	2.46668	RHEB_cKO up vs WT	1.30257	+6σ	2 E5|2	78390	78390	Pla2g4d	phospholipase A2, group IVD
TC13000001	0.010905	2.45669	RHEB_cKO up vs WT	1.29671	+6σ	13 A3.1|13	665622	665622	Hist1h2br	histone cluster 1 H2br
TC03000014	0.037614	2.45515	RHEB_cKO up vs WT	1.29581	+6σ	3 H2|3 72.	22262	22262	Uox	urate oxidase
TC10000012	0.005967	2.45345	RHEB_cKO up vs WT	1.29481	+6σ	---	---	---	Gm15664	predicted gene 15664
TC14000007	0.010926	2.44895	RHEB_cKO up vs WT	1.29216	+6σ	14|14 C1	57260	57260	Ltb4r2	leukotriene B4 receptor 2

TC07000020	0.108219	2.44806	RHEB_cKO up vs WT	1.29164	+6σ	---	---	---	Gm26143	predicted gene, 26143
TC01000034	0.086204	2.44491	RHEB_cKO up vs WT	1.28978	+6σ	1 H2.2|1 7	11931	11931	Atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide
TC15000015	0.039124	2.43971	RHEB_cKO up vs WT	1.28671	+6σ	15|15 20.	1.01E+08	1.01E+08	Gm19551	predicted gene, 19551
TC02000041	0.046132	2.43665	RHEB_cKO up vs WT	1.2849	+6σ	---	---	---	Gm13805	predicted gene 13805
TC07000007	0.273927	2.4361	RHEB_cKO up vs WT	1.28457	+6σ	7 B4|7 28.	13646	13646	Klk1b22	kallikrein 1-related peptidase b22
TC18000014	0.001773	2.42948	RHEB_cKO up vs WT	1.28065	+6σ	18 E1|18	54670	54670	Atp8b1	ATPase, class I, type 8B, member 1
TC14000003	0.034239	2.42672	RHEB_cKO up vs WT	1.27901	+6σ	14 B|14 2	11752	11752	Anxa8	annexin A8
TC11000004	0.008333	2.42292	RHEB_cKO up vs WT	1.27675	+6σ	---	---	---	Gm12141	predicted gene 12141
TC01000032	0.041196	2.41742	RHEB_cKO up vs WT	1.27347	+6σ	1 H1|1 65.	16782	16782	Lamc2	laminin, gamma 2
TC07000025	6.03E-05	2.41237	RHEB_cKO up vs WT	1.27045	+6σ	7 A3|7 9.9	12051	12051	Bcl3	B cell leukemia/lymphoma 3
TC10000000	0.006142	2.39678	RHEB_cKO up vs WT	1.2611	+6σ	X E3|X 56.	30058	30058	Timm8a1	translocase of inner mitochondrial membrane 8A1
TC15000010	0.005366	2.39656	RHEB_cKO up vs WT	1.26096	+6σ	15 F1|15	239667	239667	Dip2b	disco interacting protein 2 homolog B
TC05000017	0.008142	2.39453	RHEB_cKO up vs WT	1.25974	+6σ	5 G2|5 81.	14086	14086	Fscn1	fascin actin-bundling protein 1
TC09000004	0.009998	2.38879	RHEB_cKO up vs WT	1.25628	+6σ	9|9 B	58235	58235	Pvrl1	poliovirus receptor-related 1
TC08000019	0.003855	2.38599	RHEB_cKO up vs WT	1.25459	+6σ	8 A3|8	67920	67920	Mak16	MAK16 homolog
TC0X000015	0.006736	2.38293	RHEB_cKO up vs WT	1.25274	+6σ	X F3|X	56360	56360	Acot9	acyl-CoA thioesterase 9
TC0X000032	0.000221	2.38043	RHEB_cKO up vs WT	1.25122	+6σ	---	---	---	Gm15242	predicted gene 15242
TC09000002	0.000883	2.37946	RHEB_cKO up vs WT	1.25064	+6σ	9 A3|9 7.8	16835	16835	Ldlr	low density lipoprotein receptor
TC0X000034	0.011013	2.3746	RHEB_cKO up vs WT	1.24768	+6σ	X D|X 43.9	16186	16186	Il2rg	interleukin 2 receptor, gamma chain
TC05000006	0.006214	2.37218	RHEB_cKO up vs WT	1.24621	+6σ	5 C3.2|5	231287	231287	Atp10d	ATPase, class V, type 10D
TC03000008	0.006331	2.36885	RHEB_cKO up vs WT	1.24419	+6σ	3 F1-F2|3	20194	20194	S100a10	S100 calcium binding protein A10 (calpactin)
TC14000001	0.004403	2.36291	RHEB_cKO up vs WT	1.24056	+6σ	14 A2|14	218756	218756	Slc4a7	solute carrier family 4, sodium bicarbonate cotransporter, member 7
TC06000024	0.008184	2.35803	RHEB_cKO up vs WT	1.23758	+6σ	6 C1|6	232087	232087	Mat2a	methionine adenosyltransferase II, alpha
TC02000051	0.012744	2.357	RHEB_cKO up vs WT	1.23695	+6σ	2 H|2	20568	20568	Slpi	secretory leukocyte peptidase inhibitor
TC0X000003	0.009719	2.35554	RHEB_cKO up vs WT	1.23606	+6σ	X A3.3|X 2	16164	16164	Il13ra1	interleukin 13 receptor, alpha 1
TC11000019	0.020165	2.35227	RHEB_cKO up vs WT	1.23406	+6σ	11 E2|11	192897	192897	Itgb4	integrin beta 4
TC08000002	0.002577	2.35209	RHEB_cKO up vs WT	1.23394	+6σ	8 A1.3|8	654455	654455	Gm21944	defensin beta 48 pseudogene
TC14000000	0.002156	2.35045	RHEB_cKO up vs WT	1.23294	+6σ	14 A1|14	286940	286940	Flnb	filamin, beta
TC12000008	0.08041	2.33112	RHEB_cKO up vs WT	1.22103	+6σ	12 D2|12	14281	14281	Fos	FBJ osteosarcoma oncogene
TC09000007	0.006	2.32941	RHEB_cKO up vs WT	1.21996	+6σ	9 B|9 32.0	18746	18746	Pkm	pyruvate kinase, muscle
TC09000008	0.016451	2.32839	RHEB_cKO up vs WT	1.21934	+6σ	---	---	---	Gm22571	predicted gene, 22571
TC12000012	0.012503	2.3278	RHEB_cKO up vs WT	1.21897	+6σ	12 F1|12	68337	68337	Crip2	cysteine rich protein 2
TC15000011	0.020176	2.32714	RHEB_cKO up vs WT	1.21856	+6σ	15 A1|15	18414	18414	Osmr	oncostatin M receptor
TC04000038	0.010512	2.32374	RHEB_cKO up vs WT	1.21645	+6σ	4 E1|4 74.	27984	27984	Efhd2	EF hand domain containing 2
TC03000018	0.009815	2.32354	RHEB_cKO up vs WT	1.21632	+6σ	3 B|3 17.4	11747	11747	Anxa5	annexin A5
TC16000017	0.001758	2.31904	RHEB_cKO up vs WT	1.21353	+6σ	16|16 C1.	80859	80859	Nfkbiz	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, ze
TC07000036	0.038471	2.31636	RHEB_cKO up vs WT	1.21186	+6σ	7 D3|7	12173	12173	Bnc1	basonuclin 1
TC06000001	0.002841	2.31191	RHEB_cKO up vs WT	1.20908	+6σ	6 A3.1|6	19283	19283	Ptprz1	protein tyrosine phosphatase, receptor type Z, polypeptide 1
TC12000013	0.009546	2.31085	RHEB_cKO up vs WT	1.20843	+6σ	12 F2|12	52635	52635	Esyt2	extended synaptotagmin-like protein 2
TC09000022	0.002557	2.31073	RHEB_cKO up vs WT	1.20835	+6σ	9 A5.3|9	244871	244871	Zc3h12c	zinc finger CCCH type containing 12C
TC19000016	0.024585	2.31065	RHEB_cKO up vs WT	1.2083	+6σ	19 D1|19	12821	12821	Col17a1	collagen, type XVII, alpha 1
TC04000034	0.000176	2.30911	RHEB_cKO up vs WT	1.20734	+6σ	4 D2.2|4	442834	442834	D830031N	RIKEN cDNA D830031N03 gene
TC02000046	0.00019	2.30822	RHEB_cKO up vs WT	1.20678	+6σ	2 F1|2	269356	269356	Slc4a11	solute carrier family 4, sodium bicarbonate transporter-like, member 11
TC17000002	0.01256	2.30802	RHEB_cKO up vs WT	1.20666	+6σ	17 A3.2|1	75202	75202	Spaca6	sperm acrosome associated 6
TC13000015	0.008763	2.29914	RHEB_cKO up vs WT	1.2011	+6σ	13 A3.1|1	665596	665596	Hist1h2bq	histone cluster 1, H2bq
TC03000030	0.000417	2.29094	RHEB_cKO up vs WT	1.19594	+6σ	3 G3|3	75624	75624	Metap1	methionyl aminopeptidase 1
TC01000034	0.010828	2.28852	RHEB_cKO up vs WT	1.19442	+6σ	1 H2.3|1	80914	80914	Uck2	uridine-cytidine kinase 2
TC06000006	0.003826	2.28682	RHEB_cKO up vs WT	1.19334	+6σ	6 B3|6 25.	1.03E+08	1.03E+08	Halr1	Hoxa adjacent long noncoding RNA 1
TC17000014	0.166592	2.28502	RHEB_cKO up vs WT	1.19221	+6σ	17 A3-B|1	21826	21826	Thbs2	thrombospondin 2
TC15000004	0.004028	2.28498	RHEB_cKO up vs WT	1.19218	+6σ	15 D2-D3|	17869	17869	Myc	myelocytomatosis oncogene
TC19000010	0.00038	2.28278	RHEB_cKO up vs WT	1.19079	+6σ	19 A|19	56613	56613	Rps6ka4	ribosomal protein S6 kinase, polypeptide 4
TC06000001	0.018203	2.28167	RHEB_cKO up vs WT	1.19009	+6σ	6|6 A2	12390	12390	Cav2	caveolin 2
TC04000025	0.002033	2.27048	RHEB_cKO up vs WT	1.183	+6σ	4 B1|4	22004	22004	Tpm2	tropomyosin 2, beta
TC01000027	0.013046	2.26745	RHEB_cKO up vs WT	1.18107	+6σ	1 D|1 43.9	17975	17975	Ncl	nucleolin
TC19000004	0.152721	2.26732	RHEB_cKO up vs WT	1.18099	+6σ	19 C1|19	23972	23972	Papss2	3'-phosphoadenosine 5'-phosphosulfate synthase 2
TC07000041	0.008662	2.26426	RHEB_cKO up vs WT	1.17904	+6σ	7 F2|7	66922	66922	Rras2	related RAS viral (r-ras) oncogene 2
TC05000016	0.004909	2.25272	RHEB_cKO up vs WT	1.17167	+6σ	5 G2|5 76.	26433	26433	Plod3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3
TC06000019	0.032433	2.24876	RHEB_cKO up vs WT	1.16913	+6σ	6|6 8.16 c	1.01E+08	1.01E+08	Gm20186	predicted gene, 20186
TC08000011	0.004625	2.24718	RHEB_cKO up vs WT	1.16812	+6σ	8 D1|8 47.	14766	14766	Adgrg1	adhesion G protein-coupled receptor G1
TC0X000032	0.000395	2.24578	RHEB_cKO up vs WT	1.16722	+6σ	X F3-F4|X	20229	20229	Sat1	spermidine/spermine N1-acetyl transferase 1
TC07000017	0.119358	2.23776	RHEB_cKO up vs WT	1.16205	+6σ	7 F2|7 65.	20278	20278	Scnn1g	sodium channel, nonvoltage-gated 1 gamma
TC02000032	0.001076	2.23522	RHEB_cKO up vs WT	1.16042	+6σ	2 B|2 21.7	64292	64292	Ptges	prostaglandin E synthase
TC09000021	0.008606	2.22946	RHEB_cKO up vs WT	1.1567	+6σ	9 A5.1|9 2	102644	102644	Oaf	out at first homolog
TC04000019	0.000614	2.22912	RHEB_cKO up vs WT	1.15648	+6σ	4 E2|4	20810	20810	Srm	spermidine synthase
TC19000015	0.001374	2.22664	RHEB_cKO up vs WT	1.15487	+6σ	19 C3|19	107094	107094	Rrp12	ribosomal RNA processing 12 homolog (S. cerevisiae)
TC0X000008	0.010931	2.22379	RHEB_cKO up vs WT	1.15302	+6σ	---	---	---	Gm14788	predicted gene 14788
TC09000006	0.012828	2.22365	RHEB_cKO up vs WT	1.15293	+6σ	9 A5.3|9	67834	67834	Idh3a	isocitrate dehydrogenase 3 (NAD+) alpha
TC03000001	0.013558	2.22192	RHEB_cKO up vs WT	1.15181	+6σ	---	---	---	Gm5844	predicted gene 5844
TC15000010	0.000643	2.22023	RHEB_cKO up vs WT	1.15071	+6σ	15 F2|15	432986	432986	Gm5477	type II keratin Kb16P
TC02000011	0.034249	2.21384	RHEB_cKO up vs WT	1.14655	+6σ	---	---	---	Gm13669	predicted gene 13669
TC13000005	0.009522	2.20953	RHEB_cKO up vs WT	1.14374	+6σ	13 B1|13	70930	70930	Nol8	nucleolar protein 8
TC07000000	0.017956	2.20551	RHEB_cKO up vs WT	1.14111	+6σ	7 A1|7 1.9	50918	50918	Myadm	myeloid-associated differentiation marker
TC02000008	0.018738	2.20338	RHEB_cKO up vs WT	1.13972	+6σ	2|2 C3	227937	227937	Pkp4	plakophilin 4
TC09000014	0.005045	2.20335	RHEB_cKO up vs WT	1.1397	+6σ	9 F2|9	23918	23918	Impdh2	inosine 5'-phosphate dehydrogenase 2
TC17000026	0.011561	2.20033	RHEB_cKO up vs WT	1.13772	+6σ	17 E4|17	12193	12193	Zfp36l2	zinc finger protein 36, C3H type-like 2
TC09000008	0.048908	2.20029	RHEB_cKO up vs WT	1.13769	+6σ	9 C|9	76459	76459	Car12	carbonic anhydrase 12
TC09000027	0.005036	2.19655	RHEB_cKO up vs WT	1.13524	+6σ	9 E1|9 44.	15551	15551	Htr1b	5-hydroxytryptamine (serotonin) receptor 1B
TC18000014	0.186351	2.19445	RHEB_cKO up vs WT	1.13386	+6σ	18E1|18	408198	408198	Spink7	serine peptidase inhibitor, Kazal type 7 (putative)
TC02000020	0.00059	2.19416	RHEB_cKO up vs WT	1.13367	+6σ	2 F1|2	228608	228608	Smox	spermine oxidase
TC05000021	0.003034	2.19378	RHEB_cKO up vs WT	1.13342	+6σ	5 B1|5 17.	14208	14208	Ppm1g	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isofor
TC07000027	0.006303	2.19359	RHEB_cKO up vs WT	1.13329	+6σ	7 B1|7 17.	12336	12336	Capns1	calpain, small subunit 1
TC0X000007	0.022173	2.18835	RHEB_cKO up vs WT	1.12985	+6σ	X A7.3|X	245474	245474	Dkc1	dyskeratosis congenita 1, dyskerin
TC0Y000002	0.36544	2.18605	RHEB_cKO up vs WT	1.12832	+6σ	---	---	---	Gm21742	predicted gene, 21742
TC17000027	0.000382	2.1846	RHEB_cKO up vs WT	1.12737	+6σ	11 E1|11	16647	16647	Kpna2	karyopherin (importin) alpha 2
TC18000011	0.021829	2.18235	RHEB_cKO up vs WT	1.12588	+6σ	18 B3|18	72512	72512	Tmem173	transmembrane protein 173
TC07000010	0.015451	2.18181	RHEB_cKO up vs WT	1.12553	+6σ	---	---	---	Kansl2-ps	KAT8 regulatory NSL complex subunit 2, pseudogene
TC0X000009	0.010352	2.18179	RHEB_cKO up vs WT	1.12551	+6σ	X C3|X	17698	17698	Msn	moesin
TC01000004	0.010265	2.18136	RHEB_cKO up vs WT	1.12523	+6σ	1 C1.3|1	55989	55989	Nop58	NOP58 ribonucleoprotein
TC03000022	0.003023	2.18113	RHEB_cKO up vs WT	1.12508	+6σ	---	---	---	Gm3788	predicted gene 3788

TC17000025	0.00502	2.17687	RHEB_cKO up vs WT	1.12226	+6σ	17 E3|17	260409	260409	Cdc42ep3	CDC42 effector protein (Rho GTPase binding) 3
TC09000026	7.27E-06	2.17452	RHEB_cKO up vs WT	1.1207	+6σ	9 D|9 42.3	50772	50772	Mapk6	mitogen-activated protein kinase 6
TC08000006	0.019563	2.17224	RHEB_cKO up vs WT	1.11919	+6σ	8 B3.2|8	15446	15446	Hpgd	hydroxyprostaglandin dehydrogenase 15 (NAD)
TC11000011	0.014234	2.17019	RHEB_cKO up vs WT	1.11782	+6σ	---	---	---	Gm12346	predicted gene 12346
TC04000023	0.008556	2.16965	RHEB_cKO up vs WT	1.11746	+6σ	---	---	---	Gm11902	predicted gene 11902
TC19000009	0.009041	2.16955	RHEB_cKO up vs WT	1.1174	+6σ	---	---	---	Gm8034	predicted gene 8034
TC08000001	0.210172	2.16738	RHEB_cKO up vs WT	1.11595	+6σ	8 A1.3|8	116746	116746	Defb6	defensin beta 6
TC06000022	0.004977	2.16498	RHEB_cKO up vs WT	1.11435	+6σ	6|6 B3	71720	71720	Osbpl3	oxysterol binding protein-like 3
TC03000027	0.002386	2.16494	RHEB_cKO up vs WT	1.11433	+6σ	3 F2.3|3 4	99738	99738	Kcnc4	potassium voltage gated channel, Shaw-related subfamily, member 4
TC0X000017	0.004594	2.15963	RHEB_cKO up vs WT	1.11078	+6σ	---	---	---	Gm14373	predicted gene 14373
TC06000028	0.002428	2.15571	RHEB_cKO up vs WT	1.10816	+6σ	---	---	---	Gm16433	predicted gene 16433
TC08000009	0.001099	2.15474	RHEB_cKO up vs WT	1.10752	+6σ	8|8	723960	723960	Mir24-2	microRNA 24-2
TC02000035	0.023976	2.15374	RHEB_cKO up vs WT	1.10685	+6σ	---	---	---	Gm13487	predicted gene 13487
TC08000010	0.014473	2.15308	RHEB_cKO up vs WT	1.1064	+6σ	8 C5|8 46.	17748	17748	Mt1	metallothionein 1
TC01000024	0.007174	2.15305	RHEB_cKO up vs WT	1.10638	+6σ	1|1 C1-C3	93691	93691	Klf7	Kruppel-like factor 7 (ubiquitous)
TC07000025	0.002915	2.15068	RHEB_cKO up vs WT	1.10479	+6σ	7 A3|7 9.9	52118	52118	Pvr	poliovirus receptor
TC05000000	0.00137	2.14988	RHEB_cKO up vs WT	1.10425	+6σ	---	---	---	Gm26825	predicted gene, 26825
TC10000012	0.011318	2.14347	RHEB_cKO up vs WT	1.09995	+6σ	10 D1|10	237542	237542	Osbpl8	oxysterol binding protein-like 8
TC16000004	0.005072	2.14145	RHEB_cKO up vs WT	1.09859	+6σ	16 B3|16	22042	22042	Tfrc	transferrin receptor
TC09000016	0.031583	2.1399	RHEB_cKO up vs WT	1.09755	+6σ	9 F4|9	319626	319626	9530059O	RIKEN cDNA 9530059O14 gene
TC01000002	0.000911	2.13783	RHEB_cKO up vs WT	1.09614	+6σ	1 B|1	226971	226971	Plekhb2	pleckstrin homology domain containing, family B (evectins) member 2
TC10000017	0.007113	2.1368	RHEB_cKO up vs WT	1.09545	+6σ	---	---	---	Gm8355	predicted pseudogene 8355
TC14000012	0.003423	2.13597	RHEB_cKO up vs WT	1.09489	+6σ	---	---	---	Tpm3-rs7	tropomyosin 3, related sequence 7
TC03000006	0.042616	2.13398	RHEB_cKO up vs WT	1.09355	+6σ	---	---	---	Gm25188	predicted gene, 25188
TC03000010	0.002299	2.13389	RHEB_cKO up vs WT	1.09349	+6σ	3 F2.2|3 4	18049	18049	Ngf	nerve growth factor
TC15000010	0.011517	2.13315	RHEB_cKO up vs WT	1.09299	+6σ	15 F1|15	207214	207214	Larp4	La ribonucleoprotein domain family, member 4
TC08000004	0.003808	2.12944	RHEB_cKO up vs WT	1.09048	+6σ	---	---	---	Gm6180	predicted pseudogene 6180
TC04000026	0.001297	2.12861	RHEB_cKO up vs WT	1.08991	+6σ	4 B1|4	381605	381605	Tbc1d2	TBC1 domain family, member 2
TC04000036	0.001526	2.12789	RHEB_cKO up vs WT	1.08943	+6σ	4 D2.2|4	230779	230779	Serinc2	serine incorporator 2
TC02000019	0.007555	2.12606	RHEB_cKO up vs WT	1.08818	+6σ	2 F3|2	20017	20017	Polr1b	polymerase (RNA) I polypeptide B
TC0X000004	0.006711	2.12255	RHEB_cKO up vs WT	1.0858	+6σ	---	---	---	Gm14584	predicted gene 14584
TC03000017	0.000314	2.1215	RHEB_cKO up vs WT	1.08509	+6σ	11 E1|11	16647	16647	Kpna2	karyopherin (importin) alpha 2
TC15000023	0.012999	2.12106	RHEB_cKO up vs WT	1.08479	+6σ	15 D3|15	18810	18810	Plec	plectin
TC06000016	0.022411	2.12069	RHEB_cKO up vs WT	1.08454	+6σ	6 G1|6 66.	13730	13730	Emp1	epithelial membrane protein 1
TC10000004	0.00077	2.12044	RHEB_cKO up vs WT	1.08436	+6σ	10 B2-B3|	19072	19072	Prep	prolyl endopeptidase
TC06000030	0.000378	2.11745	RHEB_cKO up vs WT	1.08233	+6σ	6 F1|6	111173	111173	Erc1	ELKS/RAB6-interacting/CAST family member 1
TC09000028	0.02476	2.11655	RHEB_cKO up vs WT	1.08171	+6σ	9 E3.3|9 5	11933	11933	Atp1b3	ATPase, Na+/K+ transporting, beta 3 polypeptide
TC13000000	0.002088	2.11484	RHEB_cKO up vs WT	1.08055	+6σ	13 A1|13	23849	23849	Klf6	Kruppel-like factor 6
TC17000024	0.017475	2.11197	RHEB_cKO up vs WT	1.07859	+6σ	17 E1.1|17	106572	106572	Rab31	RAB31, member RAS oncogene family
TC08000025	0.002022	2.11168	RHEB_cKO up vs WT	1.07839	+6σ	8 C|8	24015	24015	Abce1	ATP-binding cassette, sub-family E (OABP), member 1
TC14000021	0.005201	2.10994	RHEB_cKO up vs WT	1.0772	+6σ	14|14 C1	56532	56532	Ripk3	receptor-interacting serine-threonine kinase 3
TC07000026	0.081052	2.10818	RHEB_cKO up vs WT	1.076	+6σ	7 A3|7	72383	72383	Cnfn	cornifelin
TC07000003	0.003999	2.10728	RHEB_cKO up vs WT	1.07538	+6σ	7 A3|7	18793	18793	Plaur	plasminogen activator, urokinase receptor
TC02000007	0.006273	2.10114	RHEB_cKO up vs WT	1.07117	+6σ	---	---	---	Gm13588	predicted gene 13588
TC02000041	0.072358	2.1	RHEB_cKO up vs WT	1.07039	+6σ	---	---	---	Gm13797	predicted gene 13797
TC02000041	0.006381	2.09929	RHEB_cKO up vs WT	1.0699	+6σ	---	---	---	Gm10800	predicted gene 10800
TC19000000	0.000312	2.09896	RHEB_cKO up vs WT	1.06968	+6σ	19 B1-3|1	19697	19697	Rela	v-rel reticuloendotheliosis viral oncogene homolog A (avian)
TC02000029	0.023779	2.09853	RHEB_cKO up vs WT	1.06938	+6σ	2 A1|2	170768	170768	Pfkfb3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3
TC15000017	0.000651	2.0954	RHEB_cKO up vs WT	1.06723	+6σ	15 D3|15	12181	12181	Bop1	block of proliferation 1
TC05000000	0.012228	2.09439	RHEB_cKO up vs WT	1.06653	+6σ	5 A2-A3|5	12571	12571	Cdk6	cyclin-dependent kinase 6
TC0X000024	0.038167	2.09346	RHEB_cKO up vs WT	1.06589	+6σ	X A7.3|X 3	192176	192176	Flna	filamin, alpha
TC04000032	0.006253	2.09288	RHEB_cKO up vs WT	1.06549	+6σ	---	---	---	Gm20731	predicted gene, 20731
TC05000021	0.014558	2.09075	RHEB_cKO up vs WT	1.06402	+6σ	5 B1|5	68567	68567	Cgref1	cell growth regulator with EF hand domain 1
TC05000004	0.007984	2.09062	RHEB_cKO up vs WT	1.06393	+6σ	---	---	---	Gm7816	predicted pseudogene 7816
TC11000036	0.004928	2.08952	RHEB_cKO up vs WT	1.06317	+6σ	11 D|11 5	140486	140486	Igf2bp1	insulin-like growth factor 2 mRNA binding protein 1
TC05000019	0.010485	2.08839	RHEB_cKO up vs WT	1.06239	+6σ	---	---	---	Gm15459	predicted gene 15459
TC19000014	0.008358	2.08829	RHEB_cKO up vs WT	1.06232	+6σ	19 C3|19	57753	57753	Noc3l	NOC3 like DNA replication regulator
TC14000014	0.058044	2.08734	RHEB_cKO up vs WT	1.06167	+6σ	14 A1|14	13421	13421	Dnase1l3	deoxyribonuclease 1-like 3
TC01000036	0.022822	2.08623	RHEB_cKO up vs WT	1.0609	+6σ	1 H4|1	11566	11566	Adss	adenylosuccinate synthetase, non muscle
TC16000007	6.24E-05	2.08416	RHEB_cKO up vs WT	1.05947	+6σ	16 C1.2|16	224250	224250	Cldnd1	claudin domain containing 1
TC12000017	0.000526	2.0807	RHEB_cKO up vs WT	1.05707	+6σ	12|12 C	217578	217578	Baz1a	bromodomain adjacent to zinc finger domain 1A
TC02000036	0.003607	2.07733	RHEB_cKO up vs WT	1.05473	+6σ	2 C3|2 34.	16420	16420	Itgb6	integrin beta 6
TC19000013	0.008574	2.07549	RHEB_cKO up vs WT	1.05345	+6σ	19 C1|19	52874	52874	Pum3	pumilio RNA-binding family member 3
TC11000034	0.011285	2.07498	RHEB_cKO up vs WT	1.0531	+6σ	11|11 B5	56321	56321	Aatf	apoptosis antagonizing transcription factor
TC04000033	0.002314	2.07382	RHEB_cKO up vs WT	1.05229	+6σ	4 D2.1|4	107995	107995	Cdc20	cell division cycle 20
TC06000013	0.022103	2.0738	RHEB_cKO up vs WT	1.05228	+6σ	6 F1|6 56.	330409	330409	Cecr2	cat eye syndrome chromosome region, candidate 2
TC02000031	0.02012	2.07187	RHEB_cKO up vs WT	1.05093	+6σ	2 A3|2 18.	18128	18128	Notch1	notch 1
TC04000029	0.000776	2.07171	RHEB_cKO up vs WT	1.05082	+6σ	4 C3|4 39.	68268	68268	Zdhhc21	zinc finger, DHHC domain containing 21
TC05000019	0.003854	2.06626	RHEB_cKO up vs WT	1.04702	+6σ	---	---	---	Gm10108	predicted pseudogene 10108
TC08000029	0.012221	2.06593	RHEB_cKO up vs WT	1.04679	+6σ	8 E1|8 57.	101943	101943	Sf3b3	splicing factor 3b, subunit 3
TC17000013	0.015053	2.06585	RHEB_cKO up vs WT	1.04674	+6σ	---	---	---	Gm5812	predicted gene 5812
TC02000005	0.010166	2.06537	RHEB_cKO up vs WT	1.0464	+6σ	2 B|2	14299	14299	Ncs1	neuronal calcium sensor 1
TC04000037	0.034485	2.06123	RHEB_cKO up vs WT	1.0435	+6σ	4 D3|4 67.	230824	230824	Grhl3	grainyhead-like 3 (Drosophila)
TC10000026	0.006193	2.05928	RHEB_cKO up vs WT	1.04214	+6σ	10 C|10 41	12952	12952	Cry1	cryptochrome 1 (photolyase-like)
TC01000004	0.004273	2.05901	RHEB_cKO up vs WT	1.04195	+6σ	1|1 C2	66882	66882	Bzw1	basic leucine zipper and W2 domains 1
TC01000019	0.020418	2.05848	RHEB_cKO up vs WT	1.04158	+6σ	---	---	---	Gm15452	predicted gene 15452
TC03000009	0.039454	2.05819	RHEB_cKO up vs WT	1.04137	+6σ	---	---	---	Gm12428	predicted gene 12428
TC05000022	0.008231	2.05685	RHEB_cKO up vs WT	1.04043	+6σ	5 B2|5	75416	75416	Nop14	NOP14 nucleolar protein
TC19000004	0.006765	2.05557	RHEB_cKO up vs WT	1.03954	+6σ	19 C1|19	16452	16452	Jak2	Janus kinase 2
TC09000025	0.022362	2.05467	RHEB_cKO up vs WT	1.03891	+6σ	9 D|9	76886	76886	Fam81a	family with sequence similarity 81, member A
TC18000003	0.002458	2.05333	RHEB_cKO up vs WT	1.03796	+6σ	18 C/D|18	13653	13653	Egr1	early growth response 1
TC05000003	0.045454	2.05284	RHEB_cKO up vs WT	1.03762	+6σ	5 B1|5	20537	20537	Slc5a1	solute carrier family 5 (sodium/glucose cotransporter), member 1
TC12000013	0.001982	2.05214	RHEB_cKO up vs WT	1.03713	+6σ	12 A1.1|12	11852	11852	Rhob	ras homolog family member B
TC12000002	0.000822	2.0517	RHEB_cKO up vs WT	1.03682	+6σ	12 A2|12	104943	104943	Fam110c	family with sequence similarity 110, member C
TC02000041	0.006701	2.05171	RHEB_cKO up vs WT	1.03682	+6σ	---	---	---	Gm13772	predicted gene 13772
TC18000010	0.076462	2.04962	RHEB_cKO up vs WT	1.03536	+6σ	18 A2|18 1	13507	13507	Dsc3	desmocollin 3
TC16000001	0.039752	2.04925	RHEB_cKO up vs WT	1.0351	+6σ	16 A1|16 1	20583	20583	Snai2	snail family zinc finger 2
TC19000007	0.002735	2.04903	RHEB_cKO up vs WT	1.03494	+6σ	19 D2|19	67788	67788	Sfr1	SWI5 dependent recombination repair 1
TC01000016	0.003645	2.04877	RHEB_cKO up vs WT	1.03476	+6σ	1 H3|1	236312	236312	Pyhin1	pyrin and HIN domain family, member 1

TC01000013	0.04023	2.04818	RHEB_cKO up vs WT	1.03434	+6σ		1 F|1	1E+08	1E+08	Gm15583	predicted gene 15583
TC15000015	0.015386	2.04787	RHEB_cKO up vs WT	1.03412	+6σ		15 C|15 20	14042	14042	Ext1	exostoses (multiple) 1
TC01000006	0.027594	2.04611	RHEB_cKO up vs WT	1.03289	+6σ		1 C3|1	67534	67534	Ttll4	tubulin tyrosine ligase-like family, member 4
TC13000024	0.040958	2.04529	RHEB_cKO up vs WT	1.03231	+6σ		X A2-A3.1|	18824	18824	Plp2	proteolipid protein 2
TC11000009	0.003366	2.04496	RHEB_cKO up vs WT	1.03207	+6σ		11 B4|11 4	18432	18432	Mybbp1a	MYB binding protein (P160) 1a
TC06000018	0.003665	2.04302	RHEB_cKO up vs WT	1.0307	+6σ		6 A1|6	27053	27053	Asns	asparagine synthetase
TC08000015	0.000955	2.04256	RHEB_cKO up vs WT	1.03038	+6σ		8 E1|8	22152	22152	Tubb3	tubulin, beta 3 class III
TC05000029	0.002114	2.04216	RHEB_cKO up vs WT	1.03009	+6σ		5 F|5	100608	100608	Noc4l	NOC4 like
TC19000003	0.001038	2.04134	RHEB_cKO up vs WT	1.02952	+6σ		6 B2.3|6 2	13063	13063	Cycs	cytochrome c, somatic
TC06000008	0.007807	2.0403	RHEB_cKO up vs WT	1.02878	+6σ		6 C1|6 32.	20019	20019	Polr1a	polymerase (RNA) I polypeptide A
TC04000026	0.005491	2.03986	RHEB_cKO up vs WT	1.02847	+6σ		---	---	---	Amd-ps4	S-adenosylmethionine decarboxylase, pseudogene 4
TC03000002	0.002035	2.03958	RHEB_cKO up vs WT	1.02827	+6σ		3|3 B	76295	76295	Atp11b	ATPase, class VI, type 11B
TC02000018	0.000502	2.0387	RHEB_cKO up vs WT	1.02765	+6σ		2 F1|2	214968	214968	Sema6d	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semap
TC10000000	0.093213	2.03868	RHEB_cKO up vs WT	1.02764	+6σ		10 A1|10	76142	76142	Ppp1r14c	protein phosphatase 1, regulatory (inhibitor) subunit 14c
TC02000019	0.013934	2.03794	RHEB_cKO up vs WT	1.02711	+6σ		2|2 F3	67134	67134	Nop56	NOP56 ribonucleoprotein
TC10000030	0.025235	2.03461	RHEB_cKO up vs WT	1.02475	+6σ		10 D2|10	73914	73914	Irak3	interleukin-1 receptor-associated kinase 3
TC05000027	0.010304	2.02945	RHEB_cKO up vs WT	1.02109	+3σ		5 E2|5	231452	231452	Sdad1	SDA1 domain containing 1
TC01000016	0.012304	2.02855	RHEB_cKO up vs WT	1.02045	+3σ		1 H3|1 79.	21346	21346	Tagln2	transgelin 2
TC17000011	0.010006	2.02673	RHEB_cKO up vs WT	1.01915	+3σ		17 E1.3|17	72515	72515	Wdr43	WD repeat domain 43
TC17000004	0.004533	2.02507	RHEB_cKO up vs WT	1.01797	+3σ		17 A3.3|17	15361	15361	Hmga1	high mobility group AT-hook 1
TC10000020	0.007253	2.02019	RHEB_cKO up vs WT	1.01449	+3σ		10 B1|10	1E+08	1E+08	Amd2	S-adenosylmethionine decarboxylase 2
TC14000026	0.005114	2.02005	RHEB_cKO up vs WT	1.01439	+3σ		14 E2.2|14	72662	72662	Dis3	DIS3 homolog, exosome endoribonuclease and 3'-5' exoribonuclease
TC0X000030	0.021409	2.01973	RHEB_cKO up vs WT	1.01416	+3σ		---	---	---	Gm5762	predicted gene 5762
TC09000024	0.006252	2.01958	RHEB_cKO up vs WT	1.01405	+3σ		9 D|9	17127	17127	Smad3	SMAD family member 3
TC08000029	0.014696	2.01785	RHEB_cKO up vs WT	1.01282	+3σ		8 E1|8 62.0	17132	17132	Maf	avian musculoaponeurotic fibrosarcoma oncogene homolog
TC07000020	0.00911	2.01654	RHEB_cKO up vs WT	1.01188	+3σ		---	---	---	Gm15542	predicted gene 15542
TC13000009	0.00117	2.01202	RHEB_cKO up vs WT	1.00865	+3σ		13 C3|13	80289	80289	Lysmd3	LysM, putative peptidoglycan-binding, domain containing 3
TC13000003	0.001698	2.01104	RHEB_cKO up vs WT	1.00794	+3σ		---	---	---	Gm11366	predicted gene 11366
TC0Y000002	0.373038	2.00844	RHEB_cKO up vs WT	1.00608	+3σ		---	---	---	Gm21857	predicted gene, 21857
TC10000007	0.003707	2.00564	RHEB_cKO up vs WT	1.00406	+3σ		10 B5.3-C1	110279	110279	Bcr	breakpoint cluster region
TC12000006	0.00091	2.00429	RHEB_cKO up vs WT	1.00309	+3σ		12 C3|12 3	15251	15251	Hif1a	hypoxia inducible factor 1, alpha subunit
TC02000000	0.115277	2.00404	RHEB_cKO up vs WT	1.00291	+3σ		2 A1|2	74186	74186	Ccdc3	coiled-coil domain containing 3
TC05000017	0.028417	2.00355	RHEB_cKO up vs WT	1.00256	+3σ		5 G2|5 81.	17425	17425	Foxk1	forkhead box K1
TC02000024	0.00078	2.00231	RHEB_cKO up vs WT	1.00167	+3σ		2 H2-3|2 8	21969	21969	Top1	topoisomerase (DNA) I
TC07000002	0.000168	1.99666	RHEB_cKO up vs WT	0.997588	+3σ		7 A3|7 9.6	13870	13870	Ercc1	excision repair cross-complementing rodent repair deficiency, complementati
TC17000013	6.03E-05	1.99623	RHEB_cKO up vs WT	0.997281	+3σ		17 E5|17	14236	14236	Foxn2	forkhead box N2
TC04000024	0.002517	1.99601	RHEB_cKO up vs WT	0.997118	+3σ		4 A5|4	230082	230082	Nol6	nucleolar protein family 6 (RNA-associated)
TC14000021	0.029665	1.99558	RHEB_cKO up vs WT	0.996806	+3σ		14 D1-E1|1	14619	14619	Gjb2	gap junction protein, beta 2
TC04000002	0.000735	1.99367	RHEB_cKO up vs WT	0.995425	+3σ		4 A3|4	68493	68493	Ndufaf4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4
TC16000016	0.017179	1.9936	RHEB_cKO up vs WT	0.995375	+3σ		2 H1|2 76.	269378	269378	Ahcy	S-adenosylhomocysteine hydrolase
TC05000022	0.002576	1.99304	RHEB_cKO up vs WT	0.994971	+3σ		5 B3|5 20.	22388	22388	Wdr1	WD repeat domain 1
TC0M00000	0.00726	1.99284	RHEB_cKO up vs WT	0.994827	+3σ		---	---	---	mt-Ts2	mitochondrially encoded tRNA serine 2
TC15000017	0.000748	1.99085	RHEB_cKO up vs WT	0.993382	+3σ		---	---	---	Gm7935	predicted pseudogene 7935
TC0X000019	0.095379	1.99066	RHEB_cKO up vs WT	0.993249	+3σ		---	---	---	Gm26652	predicted gene, 26652
TC10000031	0.037007	1.99066	RHEB_cKO up vs WT	0.993245	+3σ		10 D3|10	108037	108037	Shmt2	serine hydroxymethyltransferase 2 (mitochondrial)
TC10000011	0.019743	1.98946	RHEB_cKO up vs WT	0.992377	+3σ		10|10 C3	67972	67972	Atp2b1	ATPase, Ca++ transporting, plasma membrane 1
TC16000014	0.015678	1.98943	RHEB_cKO up vs WT	0.992352	+3σ		16 B1|16	210530	210530	P3h2	prolyl 3-hydroxylase 2
TC06000009	0.031064	1.98779	RHEB_cKO up vs WT	0.991168	+3σ		6 D1|6 37.	21802	21802	Tgfa	transforming growth factor alpha
TC01000038	0.014654	1.98666	RHEB_cKO up vs WT	0.990347	+3σ		1 H4|1 83.	226747	226747	Ahctf1	AT hook containing transcription factor 1
TC07000030	0.004794	1.98093	RHEB_cKO up vs WT	0.986181	+3σ		7 B4|7	108961	108961	E2f8	E2F transcription factor 8
TC05000003	0.007578	1.97844	RHEB_cKO up vs WT	0.984361	+3σ		5 B2|5 17.	71729	71729	Rgs12	regulator of G-protein signaling 12
TC11000022	0.011492	1.97769	RHEB_cKO up vs WT	0.983815	+3σ		11 A2|11	66249	66249	Pno1	partner of NOB1 homolog
TC13000017	0.013558	1.97702	RHEB_cKO up vs WT	0.983325	+3σ		---	---	---	Gm11394	predicted gene 11394
TC03000029	0.017202	1.97657	RHEB_cKO up vs WT	0.982998	+3σ		3 G3|3	214133	214133	Tet2	tet methylcytosine dioxygenase 2
TC09000022	0.012221	1.97651	RHEB_cKO up vs WT	0.982954	+3σ		9 A5.3|9 2	235320	235320	Zbtb16	zinc finger and BTB domain containing 16
TC11000036	0.010398	1.97468	RHEB_cKO up vs WT	0.981621	+3σ		11|11 D	16211	16211	Kpnb1	karyopherin (importin) beta 1
TC09000010	0.012676	1.97445	RHEB_cKO up vs WT	0.981452	+3σ		---	---	---	Gm9531	predicted gene 9531
TC09000000	0.002286	1.97319	RHEB_cKO up vs WT	0.98053	+3σ		---	---	---	Gm10718	predicted gene 10718
TC07000007	0.003636	1.97305	RHEB_cKO up vs WT	0.980427	+3σ		---	---	---	Gm15470	predicted gene 15470
TC15000023	0.010937	1.97144	RHEB_cKO up vs WT	0.979249	+3σ		15 F3|15 5	16402	16402	Itga5	integrin alpha 5 (fibronectin receptor alpha)
TC0Y000002	0.425048	1.97142	RHEB_cKO up vs WT	0.979234	+3σ		X and Y|X	17318	17318	Mid1	midline 1
TC05000035	0.000504	1.97133	RHEB_cKO up vs WT	0.979168	+3σ		5 G2|5	75788	75788	Smurf1	SMAD specific E3 ubiquitin protein ligase 1
TC03000022	0.095164	1.96718	RHEB_cKO up vs WT	0.976127	+3σ		---	19870	19870	Snord73a	small nucleolar RNA, C/D box U73A
TC07000045	0.04845	1.96688	RHEB_cKO up vs WT	0.975907	+3σ		7 F5|7	66141	66141	Ifitm3	interferon induced transmembrane protein 3
TC09000005	0.002074	1.96481	RHEB_cKO up vs WT	0.974387	+3σ		9 A5.2|9 2	14012	14012	Mpzl2	myelin protein zero-like 2
TC18000005	0.00974	1.96267	RHEB_cKO up vs WT	0.972819	+3σ		18 D1-D2|	70425	70425	Csnk1g3	casein kinase 1, gamma 3
TC16000009	0.018017	1.96252	RHEB_cKO up vs WT	0.972706	+3σ		---	---	---	Gm23406	predicted gene, 23406
TC02000026	0.010278	1.96108	RHEB_cKO up vs WT	0.97165	+3σ		2|2 H3-H4	21420	21420	Tfap2c	transcription factor AP-2, gamma
TC10000018	0.01265	1.96057	RHEB_cKO up vs WT	0.971274	+3σ		10 A3|10 8	21929	21929	Tnfaip3	tumor necrosis factor, alpha-induced protein 3
TC07000034	0.037153	1.96042	RHEB_cKO up vs WT	0.971161	+3σ		7 C|7	50794	50794	Klf13	Kruppel-like factor 13
TC10000013	0.002756	1.96006	RHEB_cKO up vs WT	0.970898	+3σ		10 D1|10	21664	21664	Phlda1	pleckstrin homology like domain, family A, member 1
TC01000032	0.026861	1.95997	RHEB_cKO up vs WT	0.970835	+3σ		---	---	---	Gm7278	predicted gene 7278
TC10000030	0.009574	1.9596	RHEB_cKO up vs WT	0.970562	+3σ		10|10	791076	791076	Mir763	microRNA 763
TSUnmappe	0.009574	1.9596	RHEB_cKO up vs WT	0.970562	+3σ		10|10	791076	791076	Mir763	microRNA 763
TC07000045	0.011468	1.95937	RHEB_cKO up vs WT	0.970392	+3σ		7 F5|7 88.1	79202	79202	Tnfrsf22	tumor necrosis factor receptor superfamily, member 22
TC11000014	0.001682	1.95895	RHEB_cKO up vs WT	0.970082	+3σ		11 D|11	98238	98238	Lrrc59	leucine rich repeat containing 59
TC06000020	0.042003	1.95819	RHEB_cKO up vs WT	0.96952	+3σ		6 B1|6 17.	78781	78781	Zc3hav1	zinc finger CCCH type, antiviral 1
TC13000015	0.015841	1.95759	RHEB_cKO up vs WT	0.969076	+3σ		13 A3.1|13	319161	319161	Hist1h4n	histone cluster 1, H4n
TC04000013	0.011233	1.95608	RHEB_cKO up vs WT	0.967962	+3σ		4 D2.1|4 5	20525	20525	Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1
TC01000029	0.002341	1.95554	RHEB_cKO up vs WT	0.967568	+3σ		1|1 E2	66942	66942	Ddx18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18
TC17000010	0.002687	1.95386	RHEB_cKO up vs WT	0.966326	+3σ		17 E1.2|17	70351	70351	Ppp4r1	protein phosphatase 4, regulatory subunit 1
TC04000017	0.000206	1.95373	RHEB_cKO up vs WT	0.966235	+3σ		4 D-E|4 73	13836	13836	Epha2	Eph receptor A2
TC09000013	0.009811	1.95312	RHEB_cKO up vs WT	0.965779	+3σ		9 F1|9 58.1	15983	15983	Ifrd2	interferon-related developmental regulator 2
TC18000006	0.006122	1.95285	RHEB_cKO up vs WT	0.965579	+3σ		18 E1|18	58801	58801	Pmaip1	phorbol-12-myristate-13-acetate-induced protein 1
TC07000029	0.049961	1.95252	RHEB_cKO up vs WT	0.965334	+3σ		---	---	---	Cd9-ps	Cd9 antigen, pseudogene
TC0X000016	0.012652	1.95169	RHEB_cKO up vs WT	0.964724	+3σ		X F3-F4|X	18700	18700	Piga	phosphatidylinositol glycan anchor biosynthesis, class A
TC12000015	0.240535	1.94996	RHEB_cKO up vs WT	0.963447	+3σ		12 A3|12	20666	20666	Sox11	SRY (sex determining region Y)-box 11
TC0M00000	0.06087	1.94924	RHEB_cKO up vs WT	0.962911	+3σ		---	---	---	mt-Tk	mitochondrially encoded tRNA lysine
TC07000003	0.003228	1.94807	RHEB_cKO up vs WT	0.962044	+3σ		7 A3|7	16534	16534	Kcnn4	potassium intermediate/small conductance calcium-activated channel, subfan

TC13000018	0.009147	1.94761	RHEB_cKO up vs WT	0.961702	+3σ	13|13 A5	66143	66143	Eef1e1	eukaryotic translation elongation factor 1 epsilon 1
TC02000034	0.010255	1.94694	RHEB_cKO up vs WT	0.961211	+3σ	---	---	---	Gm13461	predicted gene 13461
TC02000017	0.044633	1.94492	RHEB_cKO up vs WT	0.959709	+3σ	2|2	732489	732489	Mir674	microRNA 674
TC10000015	0.00549	1.9439	RHEB_cKO up vs WT	0.958957	+3σ	10 D3|10 7	14421	14421	B4galnt1	beta-1,4-N-acetyl-galactosaminyl transferase 1
TC05000029	0.056567	1.94238	RHEB_cKO up vs WT	0.957826	+3σ	---	1.02E+08	1.02E+08	Mir7026	microRNA 7026
TC03000026	0.026104	1.94103	RHEB_cKO up vs WT	0.956822	+3σ	3 F3|3 44.	11928	11928	Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide
TC09000019	0.054458	1.94084	RHEB_cKO up vs WT	0.956682	+3σ	9|9 A4	68743	68743	Anln	anillin, actin binding protein
TC18000004	0.003466	1.93949	RHEB_cKO up vs WT	0.955676	+3σ	18 C|18	13664	13664	Eif1a	eukaryotic translation initiation factor 1A
TC08000009	0.000963	1.93755	RHEB_cKO up vs WT	0.954231	+3σ	8 C2|8	68278	68278	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
TC12000017	0.000345	1.93707	RHEB_cKO up vs WT	0.953879	+3σ	12|12 C1-	18035	18035	Nfkbia	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, al
TC16000013	0.01839	1.93584	RHEB_cKO up vs WT	0.95296	+3σ	---	---	---	Gm6493	predicted gene 6493
TC10000010	0.008136	1.93555	RHEB_cKO up vs WT	0.952743	+3σ	10 C1|10	103136	103136	Pwp1	PWP1 homolog, endonuclein
TC15000015	0.017743	1.93493	RHEB_cKO up vs WT	0.952282	+3σ	15 D1|15 2	15117	15117	Has2	hyaluronan synthase 2
TC16000018	0.062407	1.93448	RHEB_cKO up vs WT	0.951949	+3σ	16 C1.3|1	72020	72020	Zfp654	zinc finger protein 654
TC05000035	0.015368	1.93447	RHEB_cKO up vs WT	0.95194	+3σ	5 G2|5	66898	66898	Baiap2l1	BAI1-associated protein 2-like 1
TC04000003	0.42491	1.9317	RHEB_cKO up vs WT	0.949868	+3σ	4 A5|4	1E+08	1E+08	Gm3893	predicted gene 3893
TC05000023	0.002053	1.9315	RHEB_cKO up vs WT	0.94972	+3σ	5 B3|5	14181	14181	Fgfbp1	fibroblast growth factor binding protein 1
TC11000039	0.007748	1.93092	RHEB_cKO up vs WT	0.94929	+3σ	11 E1|11	71795	71795	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1
TC0X000019	0.01471	1.93	RHEB_cKO up vs WT	0.948599	+3σ	---	1.01E+08	1.01E+08	LOC10050	uncharacterized LOC100503338
TC13000017	0.097632	1.92811	RHEB_cKO up vs WT	0.947189	+3σ	13 A4|13 1	66222	66222	Serpinb1a	serine (or cysteine) peptidase inhibitor, clade B, member 1a
TC10000012	0.012804	1.9281	RHEB_cKO up vs WT	0.947177	+3σ	10 D1|10 5	52679	52679	E2f7	E2F transcription factor 7
TC04000009	0.021108	1.92778	RHEB_cKO up vs WT	0.94694	+3σ	4 C4|4	66902	66902	Mtap	methylthioadenosine phosphorylase
TC18000003	0.015782	1.92775	RHEB_cKO up vs WT	0.946918	+3σ	18B2|18	436583	436583	Snora74a	small nucleolar RNA, H/ACA box 74A
TC02000045	0.010282	1.92649	RHEB_cKO up vs WT	0.945978	+3σ	2 E5|2	213696	213696	Duoxa1	dual oxidase maturation factor 1
TC10000026	0.02398	1.92592	RHEB_cKO up vs WT	0.94555	+3σ	10 C-D1|1	13713	13713	Elk3	ELK3, member of ETS oncogene family
TC0X000020	0.025648	1.92582	RHEB_cKO up vs WT	0.945469	+3σ	X A3.3|X	104369	104369	Snora69	small nucleolar RNA, H/ACA box 69
TC15000020	0.037716	1.92573	RHEB_cKO up vs WT	0.945409	+3σ	15|15 F1	66871	66871	Cpne8	copine VIII
TC03000006	0.015779	1.92421	RHEB_cKO up vs WT	0.944267	+3σ	3|3 F1	67738	67738	Ppid	peptidylprolyl isomerase D (cyclophilin D)
TC19000014	0.033242	1.92384	RHEB_cKO up vs WT	0.943986	+3σ	19 C2|19	226101	226101	Myof	myoferlin
TC07000020	0.005169	1.92203	RHEB_cKO up vs WT	0.942634	+3σ	7 F5|7 86.	12476	12476	Cd151	CD151 antigen
TC17000022	0.001719	1.92126	RHEB_cKO up vs WT	0.942054	+3σ	17 C|17 23	53414	53414	Bysl	bystin-like
TC13000025	0.012511	1.92125	RHEB_cKO up vs WT	0.942047	+3σ	13 D1|13 5	238799	238799	Tnpo1	transportin 1
TSUnmappe	0.071798	1.92072	RHEB_cKO up vs WT	0.941646	+3σ	9|9	1E+08	1E+08	Snord14e	small nucleolar RNA, C/D box 14E
TC0X000002	0.026255	1.91813	RHEB_cKO up vs WT	0.939704	+3σ	---	---	---	Gm1848	predicted gene 1848
TC18000014	0.011004	1.91616	RHEB_cKO up vs WT	0.938222	+3σ	---	---	---	Amd-ps3	S-adenosylmethionine decarboxylase, pseudogene 3
TC05000013	0.009097	1.91403	RHEB_cKO up vs WT	0.93661	+3σ	5 F|5	76199	76199	Med13l	mediator complex subunit 13-like
TC13000025	0.004536	1.91393	RHEB_cKO up vs WT	0.936541	+3σ	13 D1|13 5	544971	544971	Bdp1	B double prime 1, subunit of RNA polymerase III transcription initiation factor
TC02000036	2.71E-05	1.91389	RHEB_cKO up vs WT	0.936508	+3σ	2|2 C3	319876	319876	Cobll1	Cobl-like 1
TC0X000023	0.014328	1.91389	RHEB_cKO up vs WT	0.936505	+3σ	X A6|X	434782	434782	Gm5637	predicted pseudogene 5637
TC08000012	0.000668	1.91368	RHEB_cKO up vs WT	0.936347	+3σ	8 D3|8	104394	104394	E2f4	E2F transcription factor 4
TC19000011	0.005224	1.91348	RHEB_cKO up vs WT	0.936196	+3σ	19 A|19	20908	20908	Stx3	syntaxin 3
TC04000025	0.044079	1.91332	RHEB_cKO up vs WT	0.93608	+3σ	4 B1|4	50798	50798	Gne	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase
TC07000003	0.007896	1.9119	RHEB_cKO up vs WT	0.935006	+3σ	6 C1|6	19240	19240	Tmsb10	thymosin, beta 10
TC05000034	0.010686	1.91131	RHEB_cKO up vs WT	0.934565	+3σ	---	---	---	Got2-ps1	glutamate oxaloacetate transaminase 2, mitochondrial, pseudogene 1
TC14000015	0.012773	1.91087	RHEB_cKO up vs WT	0.93423	+3σ	14 A3|14 1	11750	11750	Anxa7	annexin A7
TC19000000	0.001105	1.90774	RHEB_cKO up vs WT	0.931863	+3σ	19 A|19	56708	56708	Clcf1	cardiotrophin-like cytokine factor 1
TC09000017	0.021033	1.90739	RHEB_cKO up vs WT	0.931602	+3σ	9 A1|9	83996	83996	Mmp1b	matrix metallopeptidase 1b (interstitial collagenase)
TC0X000006	0.037146	1.90699	RHEB_cKO up vs WT	0.931294	+3σ	X|X A5	14266	14266	Aff2	AF4/FMR2 family, member 2
TC09000009	0.03144	1.9068	RHEB_cKO up vs WT	0.931155	+3σ	9 C|9 38.5	12306	12306	Anxa2	annexin A2
TC19000012	0.030736	1.90644	RHEB_cKO up vs WT	0.930878	+3σ	19 B|19 13	16952	16952	Anxa1	annexin A1
TC14000025	0.009354	1.9043	RHEB_cKO up vs WT	0.929258	+3σ	9 A5.1|9 2	15481	15481	Hspa8	heat shock protein 8
TC01000003	0.010418	1.90225	RHEB_cKO up vs WT	0.927704	+3σ	9 A5.1|9 2	15481	15481	Hspa8	heat shock protein 8
TC13000003	0.017518	1.90192	RHEB_cKO up vs WT	0.927457	+3σ	---	---	---	Gm11395	predicted gene 11395
TC11000021	0.007049	1.9014	RHEB_cKO up vs WT	0.927061	+3σ	11 A1|11	67815	67815	Sec14l2	SEC14-like lipid binding 2
TC01000037	0.015369	1.899	RHEB_cKO up vs WT	0.925239	+3σ	1 H5|1 84.	13800	13800	Enah	enabled homolog (Drosophila)
TC12000005	0.017856	1.89868	RHEB_cKO up vs WT	0.924999	+3σ	12 C1|12	328110	328110	Prpf39	pre-mRNA processing factor 39
TC13000001	0.02079	1.8985	RHEB_cKO up vs WT	0.924862	+3σ	13 A2-A3|1	319183	319183	Hist1h2bj	histone cluster 1, H2bj
TC14000013	0.002876	1.8985	RHEB_cKO up vs WT	0.924861	+3σ	14 E5|14	70572	70572	Ipo5	importin 5
TC18000003	0.015466	1.89691	RHEB_cKO up vs WT	0.92365	+3σ	18 B2|18	67936	67936	Wdr55	WD repeat domain 55
TC16000012	0.003431	1.89509	RHEB_cKO up vs WT	0.922264	+3σ	16|16 B1	66409	66409	Rsl1d1	ribosomal L1 domain containing 1
TC11000017	0.002911	1.89379	RHEB_cKO up vs WT	0.921273	+3σ	---	---	---	Gm11653	predicted gene 11653
TC18000005	0.035158	1.89314	RHEB_cKO up vs WT	0.920785	+3σ	18 D3|18 3	20496	20496	Slc12a2	solute carrier family 12, member 2
TC14000026	0.027413	1.89299	RHEB_cKO up vs WT	0.920668	+3σ	14 E2.3|14	24064	24064	Spry2	sprouty homolog 2 (Drosophila)
TC07000024	0.001221	1.89297	RHEB_cKO up vs WT	0.920654	+3σ	7 A3|7	67369	67369	Qpctl	glutaminyl-peptide cyclotransferase-like
TC06000025	0.009087	1.89216	RHEB_cKO up vs WT	0.920034	+3σ	9 A5.1|9 2	15481	15481	Hspa8	heat shock protein 8
TC09000026	0.05602	1.89093	RHEB_cKO up vs WT	0.919099	+3σ	9 D|9	208994	208994	Fam83b	family with sequence similarity 83, member B
TC11000027	0.058156	1.89048	RHEB_cKO up vs WT	0.918752	+3σ	11 B1.3|11	245827	245827	Fat2	FAT atypical cadherin 2
TC06000000	0.019867	1.8884	RHEB_cKO up vs WT	0.917161	+3σ	6 A1|6	94192	94192	C1galt1	core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransfe
TC01000003	0.008069	1.88762	RHEB_cKO up vs WT	0.916569	+3σ	9 A5.1|9 2	15481	15481	Hspa8	heat shock protein 8
TC16000013	0.00542	1.88734	RHEB_cKO up vs WT	0.916357	+3σ	16 B1|16	104156	104156	Etv5	ets variant 5
TC09000000	0.00992	1.8871	RHEB_cKO up vs WT	0.916172	+3σ	9 A1|9	76863	76863	Dcun1d5	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)
TC10000001	0.022624	1.88694	RHEB_cKO up vs WT	0.916045	+3σ	10 A3|10	26408	26408	Map3k5	mitogen-activated protein kinase kinase kinase 5
TC09000000	0.001535	1.88641	RHEB_cKO up vs WT	0.915644	+3σ	---	---	---	Gm11168	predicted gene 11168
TC04000002	0.008672	1.8863	RHEB_cKO up vs WT	0.915561	+3σ	4 A5|4 14.	100019	100019	Mdn1	midasin AAA ATPase 1
TC13000002	0.002376	1.88587	RHEB_cKO up vs WT	0.915233	+3σ	13 A3.1|13	68024	68024	Hist1h2bc	histone cluster 1, H2bc
TC01000010	0.001989	1.88529	RHEB_cKO up vs WT	0.914789	+3σ	1 E2.3|1	67949	67949	Nifk	nucleolar protein interacting with the FHA domain of MKI67
TC14000005	0.003894	1.88454	RHEB_cKO up vs WT	0.914211	+3σ	---	---	---	Gm3534	predicted pseudogene 3534
TC05000025	0.007831	1.88409	RHEB_cKO up vs WT	0.913871	+3σ	5|5 D	433904	433904	Ociad2	OCIA domain containing 2
TC10000013	0.04043	1.88355	RHEB_cKO up vs WT	0.913455	+3σ	10 D2|10	216345	216345	Zfc3h1	zinc finger, C3H1-type containing
TC12000004	0.015567	1.88313	RHEB_cKO up vs WT	0.91313	+3σ	12 C1|12	1E+08	1E+08	1700047I1	RIKEN cDNA 1700047I17 gene 2
TC01000003	0.009943	1.87972	RHEB_cKO up vs WT	0.91052	+3σ	1|1 C1	73674	73674	Wdr75	WD repeat domain 75
TC02000042	0.006874	1.87964	RHEB_cKO up vs WT	0.910458	+3σ	2 E2|2	98956	98956	Nat10	N-acetyltransferase 10
TC04000029	0.040791	1.87863	RHEB_cKO up vs WT	0.909681	+3σ	4 C4|4 40.	230376	230376	Haus6	HAUS augmin-like complex, subunit 6
TC0X000020	0.00473	1.87788	RHEB_cKO up vs WT	0.909103	+3σ	---	---	---	Gm15432	predicted gene 15432
TC0X000012	0.005672	1.87775	RHEB_cKO up vs WT	0.909007	+3σ	X E3|X	54004	54004	Diaph2	diaphanous related formin 2
TC04000026	0.00712	1.87727	RHEB_cKO up vs WT	0.908638	+3σ	4 B1|4 26.	28028	28028	Mrpl50	mitochondrial ribosomal protein L50
TC14000012	0.021514	1.87665	RHEB_cKO up vs WT	0.908158	+3σ	14|14	75957	75957	Mir17hg	Mir17 host gene (non-protein coding)
TC02000013	0.011627	1.87518	RHEB_cKO up vs WT	0.90703	+3σ	2 E1|2	59015	59015	Nup160	nucleoporin 160
TC04000024	0.004434	1.87295	RHEB_cKO up vs WT	0.905315	+3σ	4 A5|4 21.	12804	12804	Cntfr	ciliary neurotrophic factor receptor

TC1000001	0.002878	1.87185	RHEB_cKO up vs WT	0.904463	+3σ	10 C2|10	75089	75089	Uhrf1bp1l	UHRF1 (ICBP90) binding protein 1-like
TC1300001	0.046612	1.87165	RHEB_cKO up vs WT	0.904314	+3σ	13 A3.3|1	22151	22151	Tubb2a	tubulin, beta 2A class IIA
TC1600000	0.007802	1.87035	RHEB_cKO up vs WT	0.90331	+3σ	16 C1.1|1	28185	28185	Tomm70a	translocase of outer mitochondrial membrane 70 homolog A (yeast)
TC1600001	0.04604	1.86977	RHEB_cKO up vs WT	0.902859	+3σ	16 B1|16	17217	17217	Mcm4	minichromosome maintenance complex component 4
TC07000001	0.026181	1.86921	RHEB_cKO up vs WT	0.902426	+3σ	---	---	---	Gm4879	predicted pseudogene 4879
TC0300002	0.011748	1.8676	RHEB_cKO up vs WT	0.901185	+3σ	---	---	---	Gm9774	predicted pseudogene 9774
TC0200000	0.006226	1.86707	RHEB_cKO up vs WT	0.900776	+3σ	---	---	---	Gm13422	predicted gene 13422
TC0X00002	0.008206	1.86626	RHEB_cKO up vs WT	0.900148	+3σ	---	---	---	Gm14933	predicted gene 14933
TC0700003	0.00812	1.86601	RHEB_cKO up vs WT	0.899953	+3σ	7 D1|7	83962	83962	Btbd1	BTB (POZ) domain containing 1
TC0800002	0.011043	1.86415	RHEB_cKO up vs WT	0.898522	+3σ	8|8 B3.2	108150	108150	Galnt7	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltran
TC0400001	0.01251	1.86396	RHEB_cKO up vs WT	0.898373	+3σ	---	---	---	Gm12891	predicted gene 12891
TC1000002	0.023022	1.86349	RHEB_cKO up vs WT	0.898009	+3σ	---	---	---	Gm24119	predicted gene, 24119
TC0400002	0.054363	1.86334	RHEB_cKO up vs WT	0.897888	+3σ	---	---	---	Gm22888	predicted gene, 22888
TC09000021	0.052045	1.86297	RHEB_cKO up vs WT	0.897607	+3σ	9 A5.2|9 2	12402	12402	Cbl	Casitas B-lineage lymphoma
TC0300003	0.117515	1.8628	RHEB_cKO up vs WT	0.897469	+3σ	3 H2|3	229933	229933	Clca2	chloride channel accessory 2
TC0200000	0.04023	1.86275	RHEB_cKO up vs WT	0.897433	+3σ	2 B|2 21.8	11898	11898	Ass1	argininosuccinate synthetase 1
TC1000002	0.003722	1.86211	RHEB_cKO up vs WT	0.896935	+3σ	10 C1|10	17319	17319	Mif	macrophage migration inhibitory factor
TC0500000	0.339829	1.8621	RHEB_cKO up vs WT	0.896933	+3σ	5 E1|5	13874	13874	Ereg	epiregulin
TC1000002	0.016737	1.86102	RHEB_cKO up vs WT	0.896093	+3σ	10 B1|10	1E+08	1E+08	Amd2	S-adenosylmethionine decarboxylase 2
TC1900000	0.074916	1.86074	RHEB_cKO up vs WT	0.895874	+3σ	19 C2|19	16551	16551	Kif11	kinesin family member 11
TC0300000	0.026223	1.8604	RHEB_cKO up vs WT	0.89561	+3σ	3|3 E-F	20195	20195	S100a11	S100 calcium binding protein A11
TC1100001	0.01293	1.85871	RHEB_cKO up vs WT	0.894302	+3σ	---	---	---	Gm11625	predicted gene 11625
TC1800000	0.026411	1.85837	RHEB_cKO up vs WT	0.89404	+3σ	18 B3|18	56070	56070	Tcerg1	transcription elongation regulator 1 (CA150)
TC0500003	0.018425	1.85707	RHEB_cKO up vs WT	0.893032	+3σ	5 G2|5	107939	107939	Pom121	nuclear pore membrane protein 121
TC1200001	0.013851	1.8565	RHEB_cKO up vs WT	0.892582	+3σ	12|12 C3	66244	66244	Nemf	nuclear export mediator factor
TC1500000	0.367121	1.85627	RHEB_cKO up vs WT	0.892406	+3σ	15 D3|15	72373	72373	Psca	prostate stem cell antigen
TC1100002	0.031087	1.85437	RHEB_cKO up vs WT	0.890927	+3σ	11 B2|11	20425	20425	Shmt1	serine hydroxymethyltransferase 1 (soluble)
TC1200000	0.067519	1.8541	RHEB_cKO up vs WT	0.89072	+3σ	12 C3|12	319565	319565	Syne2	spectrin repeat containing, nuclear envelope 2
TC1700000	0.023516	1.85235	RHEB_cKO up vs WT	0.889354	+3σ	---	---	---	Gm25447	predicted gene, 25447
TC0900000	0.004409	1.84978	RHEB_cKO up vs WT	0.887351	+3σ	---	---	---	Gm10721	predicted gene 10721
TC0200003	0.010198	1.84975	RHEB_cKO up vs WT	0.887332	+3σ	---	---	---	Gm13552	predicted gene 13552
TC1600002	0.168799	1.84825	RHEB_cKO up vs WT	0.886158	+3σ	16 C3.3|1	16699	16699	Krtap13	keratin associated protein 13
TC1000003	0.007051	1.84793	RHEB_cKO up vs WT	0.885908	+3σ	10|10 D3	73192	73192	Xpot	exportin, tRNA (nuclear export receptor for tRNAs)
TC1300002	0.015429	1.84788	RHEB_cKO up vs WT	0.88587	+3σ	13 C1|13	69716	69716	Trip13	thyroid hormone receptor interactor 13
TC0900000	0.065716	1.84691	RHEB_cKO up vs WT	0.885116	+3σ	---	---	---	Gm22455	predicted gene, 22455
TC1100001	0.054184	1.84482	RHEB_cKO up vs WT	0.883483	+3σ	11 E1|11	77097	77097	Tanc2	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2
TC1700001	0.013513	1.8447	RHEB_cKO up vs WT	0.883389	+3σ	17 A3.3|1	52009	52009	Hn1l	hematological and neurological expressed 1-like
TC09000001	0.038221	1.84468	RHEB_cKO up vs WT	0.883374	+3σ	9 A3|9 7.6	15894	15894	Icam1	intercellular adhesion molecule 1
TC1300000	0.052016	1.84382	RHEB_cKO up vs WT	0.882695	+3σ	13 B1|13	328258	328258	Slc25a48	solute carrier family 25, member 48
TC1400001	0.004637	1.84377	RHEB_cKO up vs WT	0.882662	+3σ	---	---	---	Gm21738	predicted gene, 21738
TC0400002	0.06363	1.84366	RHEB_cKO up vs WT	0.882574	+3σ	4 A3|4	70568	70568	Cpne3	copine III
TC1300002	0.065194	1.84261	RHEB_cKO up vs WT	0.881748	+3σ	13 D2.3|1	52552	52552	Parp8	poly (ADP-ribose) polymerase family, member 8
TC1300002	4.49E-05	1.84255	RHEB_cKO up vs WT	0.881701	+3σ	13 D1|13	328329	328329	Mast4	microtubule associated serine/threonine kinase family member 4
TC1100003	0.044536	1.84248	RHEB_cKO up vs WT	0.881651	+3σ	11|11	1E+08	1E+08	Snord4a	small nucleolar RNA, C/D box 4A
TC09000001	0.030508	1.84223	RHEB_cKO up vs WT	0.881455	+3σ	9|9 A3	75316	75316	Taf1d	TATA-box binding protein associated factor, RNA polymerase I, D
TC1100002	0.002231	1.8408	RHEB_cKO up vs WT	0.880334	+3σ	11|11 A2-	29856	29856	Smtn	smoothelin
TC0500002	0.013598	1.84015	RHEB_cKO up vs WT	0.879825	+3σ	5 C3.3|5	231327	231327	Ppat	phosphoribosyl pyrophosphate amidotransferase
TC0900001	0.004584	1.83896	RHEB_cKO up vs WT	0.878889	+3σ	---	---	---	Gm16379	predicted pseudogene 16379
TC1700001	0.00459	1.83875	RHEB_cKO up vs WT	0.878722	+3σ	17|17 B3	66973	66973	Mrps18b	mitochondrial ribosomal protein S18B
TC02000031	0.00936	1.83864	RHEB_cKO up vs WT	0.878637	+3σ	2 A3|2	67512	67512	Agpat2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltrar
TC1100003	0.022031	1.83731	RHEB_cKO up vs WT	0.877599	+3σ	11 B5|11	15218	15218	Foxn1	forkhead box N1
TC0800000	0.016195	1.83673	RHEB_cKO up vs WT	0.877143	+3σ	8 B3.3|8 3	17925	17925	Myo9b	myosin IXb
TC1300000	0.005905	1.8364	RHEB_cKO up vs WT	0.876881	+3σ	13|13 B2	212880	212880	Ddx46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46
TC0500003	0.003101	1.83617	RHEB_cKO up vs WT	0.876699	+3σ	5 G2|5 82.	19353	19353	Rac1	RAS-related C3 botulinum substrate 1
TC0100002	0.010051	1.83513	RHEB_cKO up vs WT	0.875884	+3σ	1 C1.2|1	15510	15510	Hspd1	heat shock protein 1 (chaperonin)
TC0500000	0.127741	1.83491	RHEB_cKO up vs WT	0.875707	+3σ	5 A1|5	20349	20349	Sema3e	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (ser
TC11000031	0.00575	1.83435	RHEB_cKO up vs WT	0.875266	+3σ	11 B4|11	276829	276829	Smtnl2	smoothelin-like 2
TC0200001	0.055183	1.83367	RHEB_cKO up vs WT	0.874736	+3σ	---	---	---	Gm18953	predicted gene, 18953
TC0800001	0.010133	1.83234	RHEB_cKO up vs WT	0.873687	+3σ	8 C5|8 44.	54352	54352	Irx5	Iroquois related homeobox 5 (Drosophila)
TC1800000	0.006708	1.83102	RHEB_cKO up vs WT	0.872648	+3σ	18 B1|18	12385	12385	Ctnna1	catenin (cadherin associated protein), alpha 1
TC0100001	0.006621	1.83052	RHEB_cKO up vs WT	0.872253	+3σ	---	---	---	Gm4204	predicted gene 4204
TC0700000	0.008135	1.83031	RHEB_cKO up vs WT	0.872091	+3σ	7 A1|7	14113	14113	Fbl	fibrillarin
TC0800000	0.002405	1.8303	RHEB_cKO up vs WT	0.872077	+3σ	8 A4-B1|8	13685	13685	Eif4ebp1	eukaryotic translation initiation factor 4E binding protein 1
TC0400001	0.039873	1.83001	RHEB_cKO up vs WT	0.871853	+3σ	---	---	---	Anp32b-ps	Bacidic (leucine-rich) nuclear phosphoprotein 32 family, member B, pseudoge
TC09000001	0.007109	1.82898	RHEB_cKO up vs WT	0.871037	+3σ	9|9 A4	60507	60507	Qtrt1	queuine tRNA-ribosyltransferase 1
TC1100003	0.016391	1.82833	RHEB_cKO up vs WT	0.87053	+3σ	11 C|11	237887	237887	Slfn10-ps	schlafen 10, pseudogene
TC0700001	0.010187	1.82743	RHEB_cKO up vs WT	0.869814	+3σ	7 F1|7	233726	233726	Ipo7	importin 7
TC1800000	0.010069	1.82732	RHEB_cKO up vs WT	0.869729	+3σ	18 B1|18	225348	225348	Wdr36	WD repeat domain 36
TC1000001	0.006137	1.82709	RHEB_cKO up vs WT	0.869548	+3σ	---	---	---	Gm8394	predicted gene 8394
TC0500000	0.004009	1.82651	RHEB_cKO up vs WT	0.869088	+3σ	---	---	---	Gm5560	predicted pseudogene 5560
TC0500002	0.019569	1.82582	RHEB_cKO up vs WT	0.868548	+3σ	---	---	---	Gm15484	predicted gene 15484
TC11000031	0.00603	1.82566	RHEB_cKO up vs WT	0.868414	+3σ	11 B4|11	12261	12261	C1qbp	complement component 1, q subcomponent binding protein
TC0500002	0.175226	1.82478	RHEB_cKO up vs WT	0.867723	+3σ	5 E1|5	13874	13874	Ereg	epiregulin
TC0100000	0.022416	1.82448	RHEB_cKO up vs WT	0.867484	+3σ	1 D|1	227333	227333	Dgkd	diacylglycerol kinase, delta
TC14000021	0.062202	1.82413	RHEB_cKO up vs WT	0.867208	+3σ	14 C3|14	14623	14623	Gjb6	gap junction protein, beta 6
TC1200000	0.005153	1.82363	RHEB_cKO up vs WT	0.866812	+3σ	12 A1.1|1	20969	20969	Sdc1	syndecan 1
TC0200000	0.035733	1.82309	RHEB_cKO up vs WT	0.866388	+3σ	---	---	---	Gm25966	predicted gene, 25966
TC0700004	0.004528	1.82298	RHEB_cKO up vs WT	0.866299	+3σ	7 F4|7 69.	56347	56347	Eif3c	eukaryotic translation initiation factor 3, subunit C
TC0900000	0.004148	1.82254	RHEB_cKO up vs WT	0.865951	+3σ	---	---	---	Gm10717	predicted gene 10717
TC1200000	0.006163	1.82215	RHEB_cKO up vs WT	0.865639	+3σ	---	---	---	Gm17138	predicted gene 17138
TC0900001	0.108098	1.82197	RHEB_cKO up vs WT	0.865502	+3σ	9 E1|9	235505	235505	Cd109	CD109 antigen
TC0300000	0.022221	1.82162	RHEB_cKO up vs WT	0.865226	+3σ	2 A7.2|2	229279	229279	Hnrnpa3	heterogeneous nuclear ribonucleoprotein A3
TC1700000	0.008511	1.82133	RHEB_cKO up vs WT	0.864992	+3σ	17|17 C	27226	27226	Pla2g7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma
TC09000001	0.024711	1.82122	RHEB_cKO up vs WT	0.864907	+3σ	---	---	---	Gm5611	predicted gene 5611
TC1500000	0.086023	1.82053	RHEB_cKO up vs WT	0.864362	+3σ	---	---	---	Gm22519	predicted gene, 22519
TC0600000	0.002241	1.81969	RHEB_cKO up vs WT	0.863689	+3σ	6 B2.3|6 2	56524	56524	Mpp6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)
TC10000031	0.062951	1.81956	RHEB_cKO up vs WT	0.863588	+3σ	10 D3|10	13139	13139	Dgka	diacylglycerol kinase, alpha
TC0500003	0.019079	1.81802	RHEB_cKO up vs WT	0.862365	+3σ	5 G3|5 89.	15505	15505	Hsph1	heat shock 105kDa/110kDa protein 1
TC1300000	0.014043	1.81795	RHEB_cKO up vs WT	0.862309	+3σ	13 A5|13	75678	75678	Ippk	inositol 1,3,4,5,6-pentakisphosphate 2-kinase

TC10000011	0.005069	1.81719	RHEB_cKO up vs WT	0.861708	+3σ		10 C3|10	216238	216238	Eea1	early endosome antigen 1
TC03000025	0.025526	1.81623	RHEB_cKO up vs WT	0.860946	+3σ		3|3 F3	19221	19221	Ptgfrn	prostaglandin F2 receptor negative regulator
TC11000006	0.015138	1.81582	RHEB_cKO up vs WT	0.860623	+3σ		11|11 B2	73158	73158	Larp1	La ribonucleoprotein domain family, member 1
TC18000001	0.014244	1.81569	RHEB_cKO up vs WT	0.860515	+3σ		---	---	---	Gm6457	predicted pseudogene 6457
TC09000006	0.000518	1.81455	RHEB_cKO up vs WT	0.859609	+3σ		9 A5.3|9	73699	73699	Ppp2r1b	protein phosphatase 2, regulatory subunit A, beta
TC02000048	0.002452	1.81327	RHEB_cKO up vs WT	0.858597	+3σ		---	---	---	Gm14121	predicted gene 14121
TC05000020	0.003813	1.81212	RHEB_cKO up vs WT	0.857681	+3σ		5|5 A3-B	19248	19248	Ptpn12	protein tyrosine phosphatase, non-receptor type 12
TC18000014	0.007809	1.81165	RHEB_cKO up vs WT	0.857308	+3σ		18 E1|18	70223	70223	Nars	asparaginyl-tRNA synthetase
TC09000016	0.004994	1.81142	RHEB_cKO up vs WT	0.857123	+3σ		9|9 A1	67618	67618	Aasdhppt	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase
TC11000037	0.022131	1.81015	RHEB_cKO up vs WT	0.856105	+3σ		---	---	---	Gm10039	predicted pseudogene 10039
TC0X000023	0.065608	1.80898	RHEB_cKO up vs WT	0.855175	+3σ		---	---	---	Gm14681	predicted gene 14681
TC05000013	0.001952	1.80778	RHEB_cKO up vs WT	0.854218	+3σ		5 F|5	231713	231713	Naa25	N(alpha)-acetyltransferase 25, NatB auxiliary subunit
TC10000006	0.006449	1.80744	RHEB_cKO up vs WT	0.85395	+3σ		10 B5.3|1	52696	52696	Zwint	ZW10 interactor
TC15000018	0.025851	1.80629	RHEB_cKO up vs WT	0.85303	+3σ		15 E1|15	1E+08	1E+08	Snord43	small nucleolar RNA, C/D box 43
TC01000024	0.051294	1.80544	RHEB_cKO up vs WT	0.852348	+3σ		1 C2|1	77300	77300	Raph1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1
TC07000029	0.017794	1.805	RHEB_cKO up vs WT	0.851998	+3σ		7 B3|7	434175	434175	Gm5593	predicted gene 5593
TC14000020	0.00446	1.80458	RHEB_cKO up vs WT	0.851665	+3σ		14 C1|14	27374	27374	Prmt5	protein arginine N-methyltransferase 5
TC08000002	0.064997	1.80279	RHEB_cKO up vs WT	0.850231	+3σ		8 A2|8 11.	20377	20377	Sfrp1	secreted frizzled-related protein 1
TC16000015	0.029124	1.80141	RHEB_cKO up vs WT	0.84913	+3σ		16 B3|16	1E+08	1E+08	BC117090	cDNA sequence BC1179090
TC16000020	0.011111	1.8003	RHEB_cKO up vs WT	0.848236	+3σ		16 C3.3|1	207932	207932	Urb1	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)
TC13000007	0.064739	1.80017	RHEB_cKO up vs WT	0.848137	+3σ		---	---	---	Gm24539	predicted gene, 24539
TC17000006	0.002169	1.80004	RHEB_cKO up vs WT	0.848033	+3σ		17 B1|17 1	114584	114584	Clic1	chloride intracellular channel 1
TC15000014	0.007738	1.79911	RHEB_cKO up vs WT	0.84728	+3σ		15 B3.2|1	67429	67429	Nudcd1	NudC domain containing 1
TC06000014	0.000388	1.79903	RHEB_cKO up vs WT	0.847222	+3σ		6 F3|6 59.	21937	21937	Tnfrsf1a	tumor necrosis factor receptor superfamily, member 1a
TC07000030	0.001923	1.79875	RHEB_cKO up vs WT	0.846996	+3σ		7 B4|7	101612	101612	Grwd1	glutamate-rich WD repeat containing 1
TC15000017	0.077859	1.79866	RHEB_cKO up vs WT	0.846924	+3σ		15 D3|15 3	110454	110454	Ly6a	lymphocyte antigen 6 complex, locus A
TC11000010	0.021378	1.79837	RHEB_cKO up vs WT	0.846691	+3σ		11 B5|11	104662	104662	Tsr1	TSR1 20S rRNA accumulation
TC19000009	0.000741	1.79765	RHEB_cKO up vs WT	0.846111	+3σ		19 A|19	66961	66961	Neat1	nuclear paraspeckle assembly transcript 1 (non-protein coding)
TC16000011	0.007822	1.7974	RHEB_cKO up vs WT	0.845913	+3σ		16 A1|16 4	52502	52502	Carhsp1	calcium regulated heat stable protein 1
TC17000006	0.004193	1.79732	RHEB_cKO up vs WT	0.845847	+3σ		---	---	---	Gm8741	predicted gene 8741
TC13000026	0.019198	1.79672	RHEB_cKO up vs WT	0.845369	+3σ		13 D2.2|1	72198	72198	Skiv2l2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)
TC10000024	0.006534	1.79591	RHEB_cKO up vs WT	0.844717	+3σ		10 C1|10	216161	216161	Sbno2	strawberry notch homolog 2 (Drosophila)
TC08000007	0.015955	1.79491	RHEB_cKO up vs WT	0.84391	+3σ		8 B3.3|8	71780	71780	Isyna1	myo-inositol 1-phosphate synthase A1
TC05000009	0.021242	1.79469	RHEB_cKO up vs WT	0.843732	+3σ		5 E3|5 47.	11745	11745	Anxa3	annexin A3
TC10000029	0.034615	1.79459	RHEB_cKO up vs WT	0.843657	+3σ		10 D2|10	72068	72068	Cnot2	CCR4-NOT transcription complex, subunit 2
TC02000030	0.007396	1.79453	RHEB_cKO up vs WT	0.843605	+3σ		---	---	---	Gm13316	predicted gene 13316
TC09000031	0.037464	1.79386	RHEB_cKO up vs WT	0.843065	+3σ		9 F3|9 68.	21813	21813	Tgfbr2	transforming growth factor, beta receptor II
TC12000024	0.071881	1.79372	RHEB_cKO up vs WT	0.842954	+3σ		12 F1|12 6	16450	16450	Jag2	jagged 2
TC03000014	0.002318	1.79368	RHEB_cKO up vs WT	0.84292	+3σ		---	---	---	Gm2574	predicted pseudogene 2574
TC02000042	0.001672	1.79296	RHEB_cKO up vs WT	0.842344	+3σ		2 E2|2	228413	228413	Prrg4	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)
TC15000021	0.005584	1.7926	RHEB_cKO up vs WT	0.842053	+3σ		15 F1|15	22337	22337	Vdr	vitamin D receptor
TC16000007	0.050368	1.79239	RHEB_cKO up vs WT	0.841881	+3σ		---	---	---	Gm9027	predicted gene 9027
TC18000009	0.100379	1.79175	RHEB_cKO up vs WT	0.84137	+3σ		18|18 A2	19877	19877	Rock1	Rho-associated coiled-coil containing protein kinase 1
TC07000042	0.018475	1.79174	RHEB_cKO up vs WT	0.84136	+3σ		7 F2|7	76179	76179	Usp31	ubiquitin specific peptidase 31
TC0M00000	0.162623	1.79144	RHEB_cKO up vs WT	0.841119	+3σ		---	---	---	mt-Th	mitochondrially encoded tRNA histidine
TC03000008	0.028051	1.79051	RHEB_cKO up vs WT	0.840374	+3σ		---	---	---	Gm6097	predicted pseudogene 6097
TC09000033	0.017477	1.79015	RHEB_cKO up vs WT	0.840078	+3σ		9 D|9	225215	225215	Rsl24d1	ribosomal L24 domain containing 1
TC16000014	0.033307	1.78861	RHEB_cKO up vs WT	0.838838	+3σ		16 B2|16 2	224105	224105	Pak2	p21 protein (Cdc42/Rac)-activated kinase 2
TC11000028	0.019695	1.78853	RHEB_cKO up vs WT	0.838776	+3σ		11 B1.3|1	216766	216766	Gemin5	gem (nuclear organelle) associated protein 5
TC03000014	0.011862	1.78825	RHEB_cKO up vs WT	0.838552	+3σ		3|3 H3	69219	69219	Ddah1	dimethylarginine dimethylaminohydrolase 1
TC01000026	0.00051	1.7867	RHEB_cKO up vs WT	0.837296	+3σ		1 C4|1	23874	23874	Farsb	phenylalanyl-tRNA synthetase, beta subunit
TC14000003	0.00247	1.78662	RHEB_cKO up vs WT	0.837234	+3σ		14 B|14	74427	74427	Eaf1	ELL associated factor 1
TC06000031	0.052928	1.78575	RHEB_cKO up vs WT	0.836528	+3σ		6 F3|6 59.	12527	12527	Cd9	CD9 antigen
TC08000012	0.049123	1.78568	RHEB_cKO up vs WT	0.836475	+3σ		8 D3|8 53.	12560	12560	Cdh3	cadherin 3
TC04000041	0.005014	1.78539	RHEB_cKO up vs WT	0.836237	+3σ		4 D3|4	212632	212632	Iffo2	intermediate filament family orphan 2
TC16000010	0.023592	1.78538	RHEB_cKO up vs WT	0.836227	+3σ		---	---	---	Gm9242	predicted pseudogene 9242
TC06000007	0.01348	1.78476	RHEB_cKO up vs WT	0.835732	+3σ		6 B3|6	68140	68140	Tigd2	tigger transposable element derived 2
TC10000010	0.235661	1.78472	RHEB_cKO up vs WT	0.835701	+3σ		10 C1|10	216225	216225	Slc5a8	solute carrier family 5 (iodide transporter), member 8
TC01000022	0.016493	1.78452	RHEB_cKO up vs WT	0.835535	+3σ		1 B|1	72097	72097	2010300C	RIKEN cDNA 2010300C02 gene
TC11000031	0.001648	1.78434	RHEB_cKO up vs WT	0.835389	+3σ		11 B4|11 4	18643	18643	Pfn1	profilin 1
TC15000018	0.026674	1.78385	RHEB_cKO up vs WT	0.834997	+3σ		15 E1|15 3	17886	17886	Myh9	myosin, heavy polypeptide 9, non-muscle
TC08000001	0.009879	1.78327	RHEB_cKO up vs WT	0.834528	+3σ		8|8 A1-A3	21781	21781	Tfdp1	transcription factor Dp 1
TC06000001	0.043802	1.78239	RHEB_cKO up vs WT	0.833809	+3σ		6 A2|6 7.8	17295	17295	Met	met proto-oncogene
TC0X000016	0.002641	1.7823	RHEB_cKO up vs WT	0.83374	+3σ		---	---	---	Gm16459	predicted gene 16459
TC08000016	0.014214	1.78199	RHEB_cKO up vs WT	0.833489	+3σ		8|8 A1.2	20419	20419	Shcbp1	Shc SH2-domain binding protein 1
TC10000024	0.003976	1.7797	RHEB_cKO up vs WT	0.831638	+3σ		10 B5-C1|	12822	12822	Col18a1	collagen, type XVIII, alpha 1
TC02000044	0.000152	1.77843	RHEB_cKO up vs WT	0.830601	+3σ		2 E5|2	98878	98878	Ehd4	EH-domain containing 4
TC0M00000	0.033093	1.77806	RHEB_cKO up vs WT	0.830308	+3σ		---	---	---	mt-Tr	mitochondrially encoded tRNA arginine
TC08000026	0.001265	1.77772	RHEB_cKO up vs WT	0.830026	+3σ		---	---	---	Gm3272	predicted pseudogene 3272
TC05000023	0.004781	1.77712	RHEB_cKO up vs WT	0.829542	+3σ		5 B3|5	231225	231225	Tapt1	transmembrane anterior posterior transformation 1
TC04000012	0.091382	1.77636	RHEB_cKO up vs WT	0.828924	+3σ		---	---	---	Gm25099	predicted gene, 25099
TC16000006	0.019257	1.77604	RHEB_cKO up vs WT	0.828664	+3σ		16 B4|16	212547	212547	Nepro	nucleolus and neural progenitor protein
TC09000012	0.058871	1.77596	RHEB_cKO up vs WT	0.828598	+3σ		9 E3.3|9 5	19659	19659	Rbp1	retinol binding protein 1, cellular
TC04000020	0.013113	1.7758	RHEB_cKO up vs WT	0.82847	+3σ		4 E2|4	74035	74035	Nol9	nucleolar protein 9
TC10000016	0.012603	1.77497	RHEB_cKO up vs WT	0.827794	+3σ		10 D3|10	237615	237615	Ankrd52	ankyrin repeat domain 52
TC03000023	0.005318	1.77426	RHEB_cKO up vs WT	0.82722	+3σ		3 F1|3 38.	16905	16905	Lmna	lamin A
TC04000008	0.004824	1.77351	RHEB_cKO up vs WT	0.82661	+3σ		---	---	---	Gm11185	predicted gene 11185
TC02000035	0.018404	1.77313	RHEB_cKO up vs WT	0.826295	+3σ		2 C1.1|2	74194	74194	Rnd3	Rho family GTPase 3
TC05000034	0.022254	1.77279	RHEB_cKO up vs WT	0.82602	+3σ		5 G2|5	83701	83701	Srrt	serrate RNA effector molecule homolog (Arabidopsis)
TC12000013	0.046508	1.77263	RHEB_cKO up vs WT	0.825888	+3σ		12 F2|12	76044	76044	Ncapg2	non-SMC condensin II complex, subunit G2
TC17000006	6.45E-05	1.77257	RHEB_cKO up vs WT	0.825844	+3σ		17 B1|17	57315	57315	Wdr46	WD repeat domain 46
TC09000000	0.001688	1.77251	RHEB_cKO up vs WT	0.825795	+3σ		---	---	---	Gm10719	predicted gene 10719
TC05000002	0.018104	1.77244	RHEB_cKO up vs WT	0.825737	+3σ		5|5	1E+08	1E+08	Snord93	small nucleolar RNA, C/D box 93
TC0X000026	0.005439	1.77215	RHEB_cKO up vs WT	0.825504	+3σ		X C3|X	76130	76130	Las1l	LAS1-like (S. cerevisiae)
TC02000004	0.046869	1.7715	RHEB_cKO up vs WT	0.824975	+3σ		---	---	---	Gm23969	predicted gene, 23969
TC07000027	0.000855	1.77144	RHEB_cKO up vs WT	0.824923	+3σ		---	---	---	Gm10169	predicted pseudogene 10169
TC0X000007	0.016256	1.77133	RHEB_cKO up vs WT	0.824834	+3σ		---	---	---	Gm5940	predicted gene 5940
TC07000004	0.008812	1.7712	RHEB_cKO up vs WT	0.824727	+3σ		7 A3|7	16801	16801	Arhgef1	Rho guanine nucleotide exchange factor (GEF) 1
TC15000016	0.029842	1.77085	RHEB_cKO up vs WT	0.824438	+3σ		15 D2|15	20442	20442	St3gal1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1

TC16000006	0.028165	1.77051	RHEB_cKO up vs WT	0.824167	+3σ	16 B4|16	72117	72117	Naa50	N(alpha)-acetyltransferase 50, NatE catalytic subunit
TC05000008	0.010057	1.77051	RHEB_cKO up vs WT	0.824166	+3σ	5 E2|5 47.	52398	52398	Sept11	septin 11
TC01000018	0.030587	1.77039	RHEB_cKO up vs WT	0.824066	+3σ	1 H6|1	77065	77065	Ints7	integrator complex subunit 7
TC07000046	0.033852	1.77013	RHEB_cKO up vs WT	0.823859	+3σ	7 F5|7	101772	101772	Ano1	anoctamin 1, calcium activated chloride channel
TC13000001	0.044612	1.76963	RHEB_cKO up vs WT	0.823448	+3σ	13 A3.1|13	1E+08	1E+08	Hist1h4m	histone cluster 1, H4m
TC08000030	0.011459	1.76941	RHEB_cKO up vs WT	0.823272	+3σ	---	---	---	Gm15899	predicted gene 15899
TC02000017	0.019618	1.76857	RHEB_cKO up vs WT	0.822586	+3σ	2 E5|2	114715	114715	Spred1	sprouty protein with EVH-1 domain 1, related sequence
TC01000008	0.015251	1.76826	RHEB_cKO up vs WT	0.822329	+3σ	---	---	---	Gm5832	predicted gene 5832
TC08000024	0.02519	1.76811	RHEB_cKO up vs WT	0.822209	+3σ	8 B3.3|8	104370	104370	Snora68	small nucleolar RNA, H/ACA box 68
TC06000031	0.00396	1.76808	RHEB_cKO up vs WT	0.822187	+3σ	---	---	---	Gm4691	predicted gene 4691
TC17000011	0.071089	1.76753	RHEB_cKO up vs WT	0.821736	+3σ	17|17 E3	268977	268977	Ltbp1	latent transforming growth factor beta binding protein 1
TC16000020	0.014665	1.76682	RHEB_cKO up vs WT	0.821158	+3σ	16 C3-C4|1	14450	14450	Gart	phosphoribosylglycinamide formyltransferase
TC15000000	0.149515	1.76663	RHEB_cKO up vs WT	0.821001	+3σ	15 A1|15 3	16880	16880	Lifr	leukemia inhibitory factor receptor
TC17000011	0.008853	1.76661	RHEB_cKO up vs WT	0.820985	+3σ	17 E2|17	74196	74196	Ttc27	tetratricopeptide repeat domain 27
TC03000025	0.015699	1.76594	RHEB_cKO up vs WT	0.820439	+3σ	3 F2.2|3	269470	269470	Wdr3	WD repeat domain 3
TC04000021	0.008288	1.76548	RHEB_cKO up vs WT	0.820061	+3σ	4|4 E	21936	21936	Tnfrsf18	tumor necrosis factor receptor superfamily, member 18
TC11000003	0.015103	1.76542	RHEB_cKO up vs WT	0.820011	+3σ	11 A4|11	211347	211347	Pank3	pantothenate kinase 3
TC18000011	0.025555	1.76499	RHEB_cKO up vs WT	0.819656	+3σ	18 C|18 18	15526	15526	Hspa9	heat shock protein 9
TC12000018	0.03292	1.76434	RHEB_cKO up vs WT	0.819128	+3σ	12 C3-D|12	20663	20663	Sos2	son of sevenless homolog 2 (Drosophila)
TC09000000	0.001799	1.76389	RHEB_cKO up vs WT	0.818757	+3σ	---	---	---	Gm10715	predicted gene 10715
TC14000001	0.099169	1.76388	RHEB_cKO up vs WT	0.818756	+3σ	14 A3|14 1	18792	18792	Plau	plasminogen activator, urokinase
TC11000023	0.001695	1.76328	RHEB_cKO up vs WT	0.818259	+3σ	---	---	---	Gm12033	predicted gene 12033
TC08000011	0.005062	1.76276	RHEB_cKO up vs WT	0.817838	+3σ	8 D1|8	1E+08	1E+08	Gm15210	inosine 5-phosphate dehydrogenase 2
TC07000030	0.090161	1.76235	RHEB_cKO up vs WT	0.8175	+3σ	7 B4|7 30.	20208	20208	Saa1	serum amyloid A 1
TC11000024	0.030465	1.76213	RHEB_cKO up vs WT	0.817322	+3σ	11 A4|11	18148	18148	Npm1	nucleophosmin 1
TC02000015	0.004541	1.76213	RHEB_cKO up vs WT	0.817317	+3σ	---	---	---	Gm13882	predicted gene 13882
TC12000008	0.002352	1.76197	RHEB_cKO up vs WT	0.817188	+3σ	12|12 D3	78920	78920	Dlst	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate cor
TC01000032	0.023247	1.76182	RHEB_cKO up vs WT	0.817065	+3σ	1 G3|1 65.	13211	13211	Dhx9	DEAH (Asp-Glu-Ala-His) box polypeptide 9
TC15000012	0.001879	1.76048	RHEB_cKO up vs WT	0.815966	+3σ	15 A1|15 5	110960	110960	Tars	threonyl-tRNA synthetase
TC12000020	0.00857	1.76001	RHEB_cKO up vs WT	0.81558	+3σ	---	---	---	Gm3695	predicted gene 3695
TC19000017	0.012286	1.75984	RHEB_cKO up vs WT	0.81544	+3σ	19 D3|19	107368	107368	Pdzd8	PDZ domain containing 8
TC03000007	0.019964	1.7596	RHEB_cKO up vs WT	0.815247	+3σ	3 F1|3	229504	229504	Isg20l2	interferon stimulated exonuclease gene 20-like 2
TC14000021	0.007121	1.75944	RHEB_cKO up vs WT	0.815113	+3σ	14 D1|14	71844	71844	Nupl1	nucleoporin like 1
TC16000007	0.044727	1.75859	RHEB_cKO up vs WT	0.814422	+3σ	16 B5|16	224171	224171	C330027C0	RIKEN cDNA C330027C09 gene
TC14000009	0.034457	1.75681	RHEB_cKO up vs WT	0.812962	+3σ	14 D1|14	14714	14714	Gnrh1	gonadotropin releasing hormone 1
TC10000029	0.014673	1.75639	RHEB_cKO up vs WT	0.812611	+3σ	10 D2|10	12461	12461	Cct2	chaperonin containing Tcp1, subunit 2 (beta)
TC04000016	0.029479	1.75385	RHEB_cKO up vs WT	0.810524	+3σ	4 D3-E|4 6	20544	20544	Slc9a1	solute carrier family 9 (sodium/hydrogen exchanger), member 1
TC13000021	0.098284	1.75313	RHEB_cKO up vs WT	0.809932	+3σ	---	---	---	Gm24095	predicted gene, 24095
TC04000037	0.018657	1.75255	RHEB_cKO up vs WT	0.809452	+3σ	4 D3|4	100017	100017	Ldlrap1	low density lipoprotein receptor adaptor protein 1
TC11000017	0.010809	1.75109	RHEB_cKO up vs WT	0.80825	+3σ	---	---	---	Gm11652	predicted gene 11652
TC01000000	0.023269	1.75084	RHEB_cKO up vs WT	0.808051	+3σ	---	---	---	Gm6161	predicted gene 6161
TC07000035	0.020823	1.7508	RHEB_cKO up vs WT	0.808016	+3σ	7 D3|7 45.	29875	29875	Iqgap1	IQ motif containing GTPase activating protein 1
TC10000005	0.031643	1.75059	RHEB_cKO up vs WT	0.807838	+3σ	---	---	---	Gm7399	predicted gene 7399
TC0X000021	0.031111	1.75031	RHEB_cKO up vs WT	0.807612	+3σ	X A5|X	72065	72065	Rap2c	RAP2C, member of RAS oncogene family
TC01000038	0.005442	1.75031	RHEB_cKO up vs WT	0.807611	+3σ	1 H6|1 97.	54139	54139	Irf6	interferon regulatory factor 6
TC17000011	0.052532	1.75011	RHEB_cKO up vs WT	0.807446	+3σ	17|17	1E+08	1E+08	Snord53	small nucleolar RNA, C/D box 53
TC02000046	0.481809	1.7499	RHEB_cKO up vs WT	0.807276	+3σ	6|6 59.32	1.01E+08	1.01E+08	Mir3098	microRNA 3098
TC12000006	0.060475	1.74948	RHEB_cKO up vs WT	0.806928	+3σ	12 D2|12	108156	108156	Mthfd1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltet
TC0Y000001	0.000742	1.74915	RHEB_cKO up vs WT	0.806658	+3σ	Y|Y	1E+08	1E+08	Gapdh-ps1	glyceraldehyde-3-phosphate dehydrogenase, pseudogene 15
TC16000005	0.000449	1.74907	RHEB_cKO up vs WT	0.806585	+3σ	16 B3|16	433016	433016	Gm5483	predicted gene 5483
TC03000026	0.004244	1.74836	RHEB_cKO up vs WT	0.806	+3σ	3|3 F3	53975	53975	Ddx20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20
TC09000013	0.004578	1.74833	RHEB_cKO up vs WT	0.805974	+3σ	9 F1-F2|9 5	15586	15586	Hyal1	hyaluronoglucosaminidase 1
TC11000042	0.007643	1.74675	RHEB_cKO up vs WT	0.804675	+3σ	11 E2|11	20973	20973	Syngr2	synaptogyrin 2
TC08000021	0.008541	1.7466	RHEB_cKO up vs WT	0.804549	+3σ	---	---	---	Gm10313	predicted pseudogene 10313
TC05000024	0.006279	1.74658	RHEB_cKO up vs WT	0.804531	+3σ	5 C1|5	666377	666377	Gm8069	predicted pseudogene 8069
TC05000000	9.38E-05	1.74652	RHEB_cKO up vs WT	0.804487	+3σ	---	---	---	Tubb4b-ps	tubulin, beta 4B class IVB, pseudogene 1
TC09000032	0.006398	1.74643	RHEB_cKO up vs WT	0.804407	+3σ	9 F3|9	108737	108737	Oxsr1	oxidative-stress responsive 1
TC01000006	0.021279	1.74617	RHEB_cKO up vs WT	0.804195	+3σ	1 C4|1 40.	195434	195434	Utp14b	UTP14B small subunit processome component
TC05000019	0.019266	1.74565	RHEB_cKO up vs WT	0.803767	+3σ	---	---	---	Gm8991	predicted pseudogene 8991
TC12000023	0.011631	1.74552	RHEB_cKO up vs WT	0.80366	+3σ	12 F1|12 6	15519	15519	Hsp90aa1	heat shock protein 90, alpha (cytosolic), class A member 1
TC19000004	0.031111	1.74522	RHEB_cKO up vs WT	0.803405	+3σ	19 C1|19	59028	59028	Rcl1	RNA terminal phosphate cyclase-like 1
TC0X000020	0.005547	1.74504	RHEB_cKO up vs WT	0.803257	+3σ	X A3.3|X	77286	77286	Nkrf	NF-kappaB repressing factor
TC12000023	0.192822	1.74473	RHEB_cKO up vs WT	0.803004	+3σ	12|12 59.1	1.01E+08	1.01E+08	Gm19576	predicted gene, 19576
TC07000024	0.064932	1.74432	RHEB_cKO up vs WT	0.802662	+3σ	7 A2|7 8.6	259300	259300	Ehd2	EH-domain containing 2
TC14000013	0.018939	1.74379	RHEB_cKO up vs WT	0.802227	+3σ	---	---	---	Gm6254	predicted gene 6254
TC19000006	0.00933	1.74373	RHEB_cKO up vs WT	0.802178	+3σ	19|19 D1	93685	93685	Entpd7	ectonucleoside triphosphate diphosphohydrolase 7
TC05000004	0.002707	1.74359	RHEB_cKO up vs WT	0.802058	+3σ	5 B3|5 20.	17089	17089	Lyar	Ly1 antibody reactive clone
TC08000003	0.031593	1.74317	RHEB_cKO up vs WT	0.801711	+3σ	8 A4|8 20.	14782	14782	Gsr	glutathione reductase
TC13000005	0.006286	1.74277	RHEB_cKO up vs WT	0.801383	+3σ	13 A5|13 2	16468	16468	Jarid2	jumonji, AT rich interactive domain 2
TC02000032	0.001746	1.74227	RHEB_cKO up vs WT	0.800969	+3σ	---	---	---	Gm13394	predicted gene 13394
TC11000036	0.008961	1.74151	RHEB_cKO up vs WT	0.800336	+3σ	11 D|11 60	19155	19155	Npepps	aminopeptidase puromycin sensitive
TC13000014	0.011777	1.74143	RHEB_cKO up vs WT	0.800276	+3σ	13 A1|13	69237	69237	Gtpbp4	GTP binding protein 4
TC13000006	0.001286	1.74116	RHEB_cKO up vs WT	0.800045	+3σ	13 B1|13 2	14057	14057	Sfxn1	sideroflexin 1
TC10000013	0.013175	1.73999	RHEB_cKO up vs WT	0.799078	+3σ	10 D2|10 5	52705	52705	Krr1	KRR1, small subunit (SSU) processome component, homolog (yeast)
TC19000007	0.001299	1.73962	RHEB_cKO up vs WT	0.798775	+3σ	19|19 D2	20874	20874	Slk	STE20-like kinase
TC03000020	0.002508	1.73694	RHEB_cKO up vs WT	0.796548	+3σ	---	---	---	Gm8349	predicted gene 8349
TC19000001	0.05434	1.73631	RHEB_cKO up vs WT	0.796022	+3σ	---	---	---	Pcna-ps2	proliferating cell nuclear antigen pseudogene 2
TC07000003	0.002363	1.73609	RHEB_cKO up vs WT	0.795845	+3σ	7 A3|7	72434	72434	Lypd3	Ly6/Plaur domain containing 3
TC16000014	0.067744	1.73609	RHEB_cKO up vs WT	0.795841	+3σ	16 B2|16	224088	224088	Atp13a3	ATPase type 13A3
TC13000023	0.007007	1.73505	RHEB_cKO up vs WT	0.79498	+3σ	13 C1|13	18570	18570	Pdcd6	programmed cell death 6
TC12000004	0.013803	1.73496	RHEB_cKO up vs WT	0.794901	+3σ	12 C1|12	1E+08	1E+08	1700047I1	RIKEN cDNA 1700047I17 gene 2
TC10000008	0.011553	1.73489	RHEB_cKO up vs WT	0.794841	+3σ	10 C1|10 3	19205	19205	Ptbp1	polypyrimidine tract binding protein 1
TC03000005	0.01123	1.73474	RHEB_cKO up vs WT	0.794719	+3σ	3 E1|3 30.9	28030	28030	Gfm1	G elongation factor, mitochondrial 1
TC12000023	0.262738	1.73331	RHEB_cKO up vs WT	0.793526	+3σ	12 F1|12	70059	70059	Degs2	delta(4)-desaturase, sphingolipid 2
TC17000001	0.011695	1.73296	RHEB_cKO up vs WT	0.79324	+3σ	17 A2|17 8	12648	12648	Chd1	chromodomain helicase DNA binding protein 1
TC05000014	0.004764	1.73289	RHEB_cKO up vs WT	0.79318	+3σ	5 G1.2|5	319804	319804	Glt1d1	glycosyltransferase 1 domain containing 1
TC17000027	0.003054	1.73232	RHEB_cKO up vs WT	0.792709	+3σ	17 E4|17 5	225055	225055	Fbxo11	F-box protein 11
TSUnmappe	0.019275	1.73205	RHEB_cKO up vs WT	0.792482	+3σ	13|13 A3.3	13557	13557	E2f3	E2F transcription factor 3
TC05000016	0.005315	1.73183	RHEB_cKO up vs WT	0.792297	+3σ	5 G2|5 78.	27979	27979	Eif3b	eukaryotic translation initiation factor 3, subunit B

TC0900002З	0.029087	1.7315	RHEB_cKO up vs WT	0.792021	+3σ	9 A5.3|9	77591	77591	Ddx10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10
TC0300001	0.007727	1.73126	RHEB_cKO up vs WT	0.791826	+3σ	3 G1-G2|3	108058	108058	Camk2d	calcium/calmodulin-dependent protein kinase II, delta
TC0500002	0.00407	1.73122	RHEB_cKO up vs WT	0.79179	+3σ	5 A3|5 10.	20817	20817	Srpk2	serine/arginine-rich protein specific kinase 2
TC1500000	0.004817	1.73118	RHEB_cKO up vs WT	0.791752	+3σ	15|15 B3.	67724	67724	Pop1	processing of precursor 1, ribonuclease P/MRP family, (S. cerevisiae)
TC0700002	0.00011	1.73051	RHEB_cKO up vs WT	0.791194	+3σ	7 F5|7	56460	56460	Pkp3	plakophilin 3
TC1500001	0.060001	1.73015	RHEB_cKO up vs WT	0.7909	+3σ	15 D2|15	17988	17988	Ndrg1	N-myc downstream regulated gene 1
TC1700000	0.012425	1.72957	RHEB_cKO up vs WT	0.790415	+3σ	---	---	---	Gm16580	predicted gene 16580
TC1300001	0.022238	1.72952	RHEB_cKO up vs WT	0.790372	+3σ	13 D1|13	68018	68018	Col4a3bp	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein
TC1800001	0.040502	1.72864	RHEB_cKO up vs WT	0.789633	+3σ	---	---	---	Gm7665	predicted pseudogene 7665
TC17000001	0.016058	1.72677	RHEB_cKO up vs WT	0.788077	+3σ	17|17	1E+08	1E+08	Snora20	small nucleolar RNA, H/ACA box 20
TC1000000	0.004372	1.72656	RHEB_cKO up vs WT	0.7879	+3σ	10 A1|10	270685	270685	Mthfd1l	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like
TC11000001	0.01274	1.72515	RHEB_cKO up vs WT	0.786721	+3σ	11 A1-A4|	13649	13649	Egfr	epidermal growth factor receptor
TC0100002	0.007971	1.72503	RHEB_cKO up vs WT	0.786624	+3σ	1 B|1	14200	14200	Fhl2	four and a half LIM domains 2
TC0700003	0.007173	1.72495	RHEB_cKO up vs WT	0.786551	+3σ	---	---	---	Gm3200	predicted pseudogene 3200
TC1300000	0.007919	1.72436	RHEB_cKO up vs WT	0.78606	+3σ	13 A1|13	69617	69617	Pitrm1	pitrilysin metallepetidase 1
TC1500002	0.034275	1.72372	RHEB_cKO up vs WT	0.785527	+3σ	---	1.02E+08	1.02E+08	Mir6963	microRNA 6963
TC0800001	0.00341	1.72365	RHEB_cKO up vs WT	0.785463	+3σ	8 C3|8	257632	257632	Nod2	nucleotide-binding oligomerization domain containing 2
TC1500001	0.002622	1.72352	RHEB_cKO up vs WT	0.785362	+3σ	15 B3.1|1	70790	70790	Ubr5	ubiquitin protein ligase E3 component n-recognin 5
TC1100003	0.002687	1.72346	RHEB_cKO up vs WT	0.785304	+3σ	11 E1|11	16647	16647	Kpna2	karyopherin (importin) alpha 2
TC1900000	0.039796	1.72204	RHEB_cKO up vs WT	0.784115	+3σ	19 A|19	225929	225929	Patl1	protein associated with topoisomerase II homolog 1 (yeast)
TC0300001	0.016905	1.72109	RHEB_cKO up vs WT	0.78332	+3σ	---	---	---	Gm10254	predicted gene 10254
TC0100000	0.008977	1.72088	RHEB_cKO up vs WT	0.783147	+3σ	---	---	---	Gm15659	predicted gene 15659
TC0900000	0.003702	1.72082	RHEB_cKO up vs WT	0.783096	+3σ	---	1.01E+08	1.01E+08	LOC10086	NHP2-like protein 1
TC04000011	0.002367	1.72027	RHEB_cKO up vs WT	0.782639	+3σ	4 C7|4	16975	16975	Lrp8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor
TC0300002	0.019507	1.72015	RHEB_cKO up vs WT	0.782532	+3σ	3 G3|3	99683	99683	Sec24b	Sec24 related gene family, member B (S. cerevisiae)
TC0900001	0.008785	1.7201	RHEB_cKO up vs WT	0.782491	+3σ	9 F1|9 59.	19882	19882	Mst1r	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
TC1500001	0.005076	1.71997	RHEB_cKO up vs WT	0.782385	+3σ	15|15 C	18458	18458	Pabpc1	poly(A) binding protein, cytoplasmic 1
TC1100002	0.005028	1.71958	RHEB_cKO up vs WT	0.782056	+3σ	---	---	---	Gm12286	predicted gene 12286
TC1900000	0.024303	1.71958	RHEB_cKO up vs WT	0.782053	+3σ	19 B|19	83921	83921	Tmem2	transmembrane protein 2
TC0400001	0.011962	1.71909	RHEB_cKO up vs WT	0.781641	+3σ	4 D2.2-D2.	80912	80912	Pum1	pumilio RNA-binding family member 1
TC1700000	0.015349	1.71889	RHEB_cKO up vs WT	0.781474	+3σ	17 A3.2|1	22710	22710	Zfp52	zinc finger protein 52
TC07000011	0.079156	1.71847	RHEB_cKO up vs WT	0.781127	+3σ	7 D3|7	18584	18584	Pde8a	phosphodiesterase 8A
TC0500001	0.00571	1.71795	RHEB_cKO up vs WT	0.780684	+3σ	5 G1.3|5	12466	12466	Cct6a	chaperonin containing Tcp1, subunit 6a (zeta)
TC1700001	0.045184	1.71764	RHEB_cKO up vs WT	0.780426	+3σ	17 A3.3|1	1E+08	1E+08	Snora78	small nucleolar RNA, H/ACA box 7
TC0200003	0.001342	1.71562	RHEB_cKO up vs WT	0.778727	+3σ	---	---	---	Gm13642	predicted gene 13642
TC09000001	0.038058	1.71534	RHEB_cKO up vs WT	0.778495	+3σ	---	---	---	Gm23455	predicted gene, 23455
TC1300002	0.00429	1.71504	RHEB_cKO up vs WT	0.778242	+3σ	---	---	---	Gm2445	predicted gene 2445
TC1600001	0.008062	1.71493	RHEB_cKO up vs WT	0.778149	+3σ	16 A1|16	17470	17470	Cd200	CD200 antigen
TC0100003	0.004096	1.7136	RHEB_cKO up vs WT	0.777032	+3σ	1|1 H1	12301	12301	Cacybp	calcyclin binding protein
TC1600000	0.153897	1.71352	RHEB_cKO up vs WT	0.776962	+3σ	16 C3.3|1	117172	117172	2310034C	RIKEN cDNA 2310034C09 gene
TC1100000	0.0349	1.71302	RHEB_cKO up vs WT	0.776545	+3σ	11 A1|11	74522	74522	Morc2a	microrchidia 2A
TC0100003	0.01575	1.71292	RHEB_cKO up vs WT	0.776459	+3σ	1 E4|1	226419	226419	Dyrk3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3
TC0600002	0.002264	1.71268	RHEB_cKO up vs WT	0.776254	+3σ	---	---	---	Gm5138	predicted gene 5138
TC0400000	0.003543	1.71186	RHEB_cKO up vs WT	0.775566	+3σ	---	---	---	Gm12416	predicted gene 12416
TC0200001	0.023389	1.71151	RHEB_cKO up vs WT	0.775274	+3σ	2 E5|2	1E+08	1E+08	Inafm2	InaF motif containing 2
TC1000001	0.010287	1.71149	RHEB_cKO up vs WT	0.775255	+3σ	---	---	---	Gm8330	predicted gene 8330
TC1000002	0.000194	1.71123	RHEB_cKO up vs WT	0.775032	+3σ	10 C1|10	70294	70294	Rnf126	ring finger protein 126
TC0700001	0.00997	1.71046	RHEB_cKO up vs WT	0.774387	+3σ	7 F3|7 74.	12237	12237	Bub3	BUB3 mitotic checkpoint protein
TC0800001	0.012864	1.70999	RHEB_cKO up vs WT	0.773992	+3σ	8 A1.3|8	244334	244334	Defb8	defensin beta 8
TC0500001	0.064282	1.70961	RHEB_cKO up vs WT	0.773671	+3σ	5 A3|5 8.1	14677	14677	Gnai1	guanine nucleotide binding protein (G protein), alpha inhibiting 1
TC1700002	0.001674	1.70782	RHEB_cKO up vs WT	0.772157	+3σ	17 E3|17	668830	668830	Gm9386	predicted pseudogene 9386
TC1800000	0.012226	1.7076	RHEB_cKO up vs WT	0.771967	+3σ	---	---	---	Gm5507	predicted gene 5507
TC0X00001	0.04753	1.70732	RHEB_cKO up vs WT	0.771734	+3σ	X A1.1|X 8	12361	12361	Cask	calcium/calmodulin-dependent serine protein kinase (MAGUK family)
TC0400000	0.003407	1.70711	RHEB_cKO up vs WT	0.771557	+3σ	---	---	---	Gm11912	predicted gene 11912
TC1400000	0.030595	1.70683	RHEB_cKO up vs WT	0.771318	+3σ	14 C1|14	218975	218975	Mapk1ip1l	mitogen-activated protein kinase 1 interacting protein 1-like
TC0300003	0.009849	1.70539	RHEB_cKO up vs WT	0.770099	+3σ	3 F2.2|3	70465	70465	Wdr77	WD repeat domain 77
TC0700000	0.005705	1.70535	RHEB_cKO up vs WT	0.770071	+3σ	7 B4|7 29.	211548	211548	Nomo1	nodal modulator 1
TC1200002	0.016663	1.70496	RHEB_cKO up vs WT	0.769742	+3σ	12 A1.2|1	211914	211914	Asap2	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2
TC1500001	0.008213	1.70485	RHEB_cKO up vs WT	0.769643	+3σ	15 D3|15	17068	17068	Ly6d	lymphocyte antigen 6 complex, locus D
TC0500001	0.031196	1.70447	RHEB_cKO up vs WT	0.769327	+3σ	---	---	---	Gm7332	predicted gene 7332
TC1700002	0.021238	1.70429	RHEB_cKO up vs WT	0.769167	+3σ	17 E4|17	72416	72416	Lrpprc	leucine-rich PPR-motif containing
TC1800001	0.003732	1.7042	RHEB_cKO up vs WT	0.769097	+3σ	18|18 D3	17714	17714	Grpel2	GrpE-like 2, mitochondrial
TC1000002	0.112755	1.70326	RHEB_cKO up vs WT	0.768295	+3σ	10|10	1E+08	1E+08	Snord98	small nucleolar RNA, C/D box 98
TC1000002	0.058766	1.7023	RHEB_cKO up vs WT	0.767487	+3σ	10|10	71207	71207	Nudt4	nudix (nucleoside diphosphate linked moiety X)-type motif 4
TC0600001	0.034799	1.7023	RHEB_cKO up vs WT	0.767482	+3σ	---	---	---	Gm20400	predicted gene 20400
TC0100001	0.02896	1.70227	RHEB_cKO up vs WT	0.767464	+3σ	---	---	---	Gm6397	predicted gene 6397
TC0200005	0.013897	1.70166	RHEB_cKO up vs WT	0.76694	+3σ	2 B|2	227699	227699	Nup188	nucleoporin 188
TC0300000	0.002944	1.70072	RHEB_cKO up vs WT	0.766148	+3σ	---	---	---	Gm10293	predicted pseudogene 10293
TC0800001	0.020283	1.70071	RHEB_cKO up vs WT	0.766141	+3σ	8 C5|8	270086	270086	Ogfod1	2-oxoglutarate and iron-dependent oxygenase domain containing 1
TC0200001	0.052011	1.70022	RHEB_cKO up vs WT	0.765726	+3σ	2 E5|2	271842	271842	Rpusd2	RNA pseudouridylate synthase domain containing 2
TC1000002	0.003142	1.70021	RHEB_cKO up vs WT	0.765715	+3σ	10 C1|10	208228	208228	Mob3a	MOB kinase activator 3A
TC1900000	0.01405	1.69984	RHEB_cKO up vs WT	0.765397	+3σ	19 C3|19	226182	226182	Taf5	TATA-box binding protein associated factor 5
TC0800003	0.007823	1.6994	RHEB_cKO up vs WT	0.765021	+3σ	8 E1|8	142682	142682	Zcchc14	zinc finger, CCHC domain containing 14
TC0300002	0.045978	1.69839	RHEB_cKO up vs WT	0.764164	+3σ	3 G3|3 62.	18033	18033	Nfkb1	nuclear factor of kappa light polypeptide gene enhancer in B cells 1, p105
TC1900000	0.001283	1.69735	RHEB_cKO up vs WT	0.763288	+3σ	19 A|19	12631	12631	Cfl1	cofilin 1, non-muscle
TC1200001	0.003915	1.69715	RHEB_cKO up vs WT	0.763112	+3σ	12 A1.1|1	627110	627110	Tubb2a-ps	tubulin, beta 2a, pseudogene 2
TC1600001	0.008523	1.69684	RHEB_cKO up vs WT	0.762848	+3σ	16 B1|16	12053	12053	Bcl6	B cell leukemia/lymphoma 6
TC1700001	0.002924	1.69659	RHEB_cKO up vs WT	0.762642	+3σ	---	---	---	Gm27023	predicted gene, 27023
TC1700000	0.005941	1.69646	RHEB_cKO up vs WT	0.762527	+3σ	17 B1|17	72462	72462	Rrp1b	ribosomal RNA processing 1 homolog B (S. cerevisiae)
TC1300001	0.015289	1.6963	RHEB_cKO up vs WT	0.76239	+3σ	13 D2.1|1	75616	75616	Smim15	small integral membrane protein 15
TC1100000	0.013913	1.69616	RHEB_cKO up vs WT	0.762269	+3σ	11|11	1E+08	1E+08	Gm12238	predicted gene 12238
TC0900001	0.044204	1.69613	RHEB_cKO up vs WT	0.762247	+3σ	9 E1|9	14860	14860	Gsta4	glutathione S-transferase, alpha 4
TC0700002	0.003004	1.69594	RHEB_cKO up vs WT	0.762083	+3σ	---	---	---	Gm2308	predicted gene 2308
TC0500000	0.002875	1.69524	RHEB_cKO up vs WT	0.761491	+3σ	---	---	---	Gm5559	predicted gene 5559
TC0900001	0.001368	1.69486	RHEB_cKO up vs WT	0.761168	+3σ	9 F2|9 59.	235623	235623	Scap	SREBF chaperone
TC0500002	0.001473	1.69464	RHEB_cKO up vs WT	0.760981	+3σ	5 B3|5 21.	15476	15476	Hs3st1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1
TC0600001	0.001895	1.69416	RHEB_cKO up vs WT	0.760569	+3σ	---	---	---	Gm4575	predicted gene 4575
TC1000000	0.00721	1.69396	RHEB_cKO up vs WT	0.7604	+3σ	---	---	---	Gm8055	predicted pseudogene 8055
TC0700002	0.029156	1.69291	RHEB_cKO up vs WT	0.759503	+3σ	7 F5|7	11772	11772	Ap2a2	adaptor-related protein complex 2, alpha 2 subunit

TC01000005	0.06866	1.69228	RHEB_cKO up vs WT	0.758965	+3σ	---	---	---	Gm26457	predicted gene, 26457
TC0X000003	0.003435	1.69189	RHEB_cKO up vs WT	0.758633	+3σ	X A4|X 21.	11740	11740	Slc25a5	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocato
TC13000027	0.119202	1.69182	RHEB_cKO up vs WT	0.758576	+3σ	13 D2.2|13	14313	14313	Fst	follistatin
TC08000008	0.007143	1.69178	RHEB_cKO up vs WT	0.758545	+3σ	---	---	---	Gm7984	predicted gene 7984
TC18000010	0.00393	1.6916	RHEB_cKO up vs WT	0.758387	+3σ	18 A2|18	106957	106957	Slc39a6	solute carrier family 39 (metal ion transporter), member 6
TC03000026	0.002701	1.6904	RHEB_cKO up vs WT	0.757365	+3σ	3|3 F3	15257	15257	Hipk1	homeodomain interacting protein kinase 1
TC15000004	0.015014	1.69017	RHEB_cKO up vs WT	0.757172	+3σ	15 D1|15	76740	76740	Efr3a	EFR3 homolog A
TC03000004	0.027065	1.68986	RHEB_cKO up vs WT	0.756901	+3σ	3 E1|3	74012	74012	Rap2b	RAP2B, member of RAS oncogene family
TC14000004	0.018571	1.68952	RHEB_cKO up vs WT	0.756613	+3σ	---	---	---	Gm7324	predicted gene 7324
TC09000008	0.10063	1.68918	RHEB_cKO up vs WT	0.756325	+3σ	---	---	---	Gm23136	predicted gene, 23136
TC01000031	0.101195	1.68872	RHEB_cKO up vs WT	0.755932	+3σ	1 E4|1	329252	329252	Lgr6	leucine-rich repeat-containing G protein-coupled receptor 6
TC02000021	0.064496	1.68864	RHEB_cKO up vs WT	0.755865	+3σ	2|2 H1	24128	24128	Xrn2	5'-3' exoribonuclease 2
TC15000020	0.036646	1.68798	RHEB_cKO up vs WT	0.755294	+3σ	15 E3|15	105847	105847	Lmf2	lipase maturation factor 2
TC02000047	0.014327	1.68796	RHEB_cKO up vs WT	0.75528	+3σ	2|2 G3	66580	66580	Esf1	ESF1 nucleolar pre-rRNA processing protein homolog
TC17000016	0.033865	1.68773	RHEB_cKO up vs WT	0.755082	+3σ	6|6 B1	68011	68011	Snrpg	small nuclear ribonucleoprotein polypeptide G
TC02000036	0.006966	1.68691	RHEB_cKO up vs WT	0.754387	+3σ	2|2 C3	56878	56878	Rbms1	RNA binding motif, single stranded interacting protein 1
TC04000030	0.001092	1.6866	RHEB_cKO up vs WT	0.754118	+3σ	---	---	---	Gm12671	predicted gene 12671
TC03000012	0.015913	1.68657	RHEB_cKO up vs WT	0.75409	+3σ	3 G1|3	99480	99480	Dnttip2	deoxynucleotidyltransferase, terminal, interacting protein 2
TC02000048	0.000457	1.68649	RHEB_cKO up vs WT	0.754021	+3σ	2 G3|2 73.	21824	21824	Thbd	thrombomodulin
TC02000047	0.002105	1.68635	RHEB_cKO up vs WT	0.753908	+3σ	---	---	---	Gm14111	predicted gene 14111
TC07000004	0.012584	1.68623	RHEB_cKO up vs WT	0.753801	+3σ	7 A3|7 13.	21803	21803	Tgfb1	transforming growth factor, beta 1
TC11000010	0.032688	1.68599	RHEB_cKO up vs WT	0.753595	+3σ	11 B4|11 4	246788	246788	Trpv3	transient receptor potential cation channel, subfamily V, member 3
TC16000012	0.006211	1.68573	RHEB_cKO up vs WT	0.753372	+3σ	16 A1|16	106205	106205	Zc3h7a	zinc finger CCCH type containing 7 A
TC08000002	0.019315	1.68511	RHEB_cKO up vs WT	0.752845	+3σ	8 A2|8 11.	20516	20516	Slc20a2	solute carrier family 20, member 2
TC13000001	0.028986	1.68421	RHEB_cKO up vs WT	0.75207	+3σ	13 A2-A3|	319191	319191	Hist1h2ai	histone cluster 1, H2ai
TC16000019	0.004132	1.68405	RHEB_cKO up vs WT	0.751938	+3σ	16 C3.3|16	12469	12469	Cct8	chaperonin containing Tcp1, subunit 8 (theta)
TC01000026	0.003468	1.68309	RHEB_cKO up vs WT	0.751109	+3σ	---	---	---	Gm5529	predicted pseudogene 5529
TC01000002	0.031118	1.68306	RHEB_cKO up vs WT	0.751091	+3σ	1 B|1	50785	50785	Hs6st1	heparan sulfate 6-O-sulfotransferase 1
TC04000017	0.03569	1.68267	RHEB_cKO up vs WT	0.750753	+3σ	4 D3|4 69.	15530	15530	Hspg2	perlecan (heparan sulfate proteoglycan 2)
TC09000000	0.004625	1.68247	RHEB_cKO up vs WT	0.750578	+3σ	9|9 A1-A2	17386	17386	Mmp13	matrix metallopeptidase 13
TC03000020	0.000331	1.68213	RHEB_cKO up vs WT	0.750286	+3σ	3 D|3 28.6	20439	20439	Siah2	seven in absentia 2
TC05000034	0.01899	1.68201	RHEB_cKO up vs WT	0.750183	+3σ	---	---	---	Gm15502	predicted gene 15502
TC01000037	0.011478	1.68194	RHEB_cKO up vs WT	0.750127	+3σ	1 H6|1	226844	226844	Mfsd7b	major facilitator superfamily domain containing 7B
TC01000035	0.004426	1.68176	RHEB_cKO up vs WT	0.74997	+3σ	1|1 80.65	1.01E+08	1.01E+08	Gm16340	interferon-activable protein 203-like
TC13000027	0.001413	1.68174	RHEB_cKO up vs WT	0.749958	+3σ	13|13	72465	72465	Zfp131	zinc finger protein 131
TC03000007	0.005667	1.68133	RHEB_cKO up vs WT	0.749599	+3σ	3 F1|3	66614	66614	Gpatch4	G patch domain containing 4
TC05000010	0.04368	1.68117	RHEB_cKO up vs WT	0.749465	+3σ	5 E5|5	433926	433926	Lrrc8b	leucine rich repeat containing 8 family, member B
TC08000030	0.004253	1.68104	RHEB_cKO up vs WT	0.749357	+3σ	8 E1|8 71.9	11821	11821	Aprt	adenine phosphoribosyl transferase
TC03000024	0.010116	1.681	RHEB_cKO up vs WT	0.74932	+3σ	3 F1-F2|3	319176	319176	Hist2h2ac	histone cluster 2, H2ac
TC12000016	0.322836	1.68037	RHEB_cKO up vs WT	0.748776	+3σ	12 B1|12	380755	380755	Lsmem1	leucine-rich single-pass membrane protein 1
TC0X000017	0.260775	1.68011	RHEB_cKO up vs WT	0.748552	+3σ	---	---	---	Gm21887	predicted gene, 21887
TC01000023	0.023889	1.68005	RHEB_cKO up vs WT	0.748503	+3σ	1 C1.1|1 2	14660	14660	Gls	glutaminase
TC19000015	0.002016	1.67985	RHEB_cKO up vs WT	0.748334	+3σ	19|19 D1	66583	66583	Exosc1	exosome component 1
TC17000021	0.004187	1.6797	RHEB_cKO up vs WT	0.748201	+3σ	17 C|17	20807	20807	Srf	serum response factor
TC02000052	0.096307	1.67958	RHEB_cKO up vs WT	0.748097	+3σ	2 H3|2 95.	12162	12162	Bmp7	bone morphogenetic protein 7
TC19000016	0.010328	1.67922	RHEB_cKO up vs WT	0.747788	+3σ	19 D2|19 4	1E+08	1E+08	Nutf2-ps1	nuclear transport factor 2, pseudogene 1
TC13000015	0.04714	1.67905	RHEB_cKO up vs WT	0.747646	+3σ	13 A2-A3|	319185	319185	Hist1h2bl	histone cluster 1, H2bl
TC04000024	0.029822	1.6789	RHEB_cKO up vs WT	0.747512	+3σ	4 A5|4 20.	14595	14595	B4galt1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1
TC04000004	0.499126	1.67736	RHEB_cKO up vs WT	0.746188	+3σ	4 A5|4	1E+08	1E+08	Gm2163	predicted gene 2163
TC02000025	0.016259	1.67713	RHEB_cKO up vs WT	0.745998	+3σ	2 H3|2 87.	110750	110750	Cse1l	chromosome segregation 1-like (S. cerevisiae)
TC05000024	0.00031	1.67676	RHEB_cKO up vs WT	0.74568	+3σ	5 C3.1|5	212285	212285	Arap2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2
TC14000000	0.028517	1.67671	RHEB_cKO up vs WT	0.745629	+3σ	14 A1|14	66082	66082	Abhd6	abhydrolase domain containing 6
TC15000004	0.019933	1.6763	RHEB_cKO up vs WT	0.74528	+3σ	15 D1|15	239463	239463	Fam83a	family with sequence similarity 83, member A
TC01000019	0.0094	1.6761	RHEB_cKO up vs WT	0.745109	+3σ	1 A3|1	433273	433273	Gm5523	glyceraldehyde-3-phosphate dehydrogenase pseudogene
TC19000005	0.01252	1.67589	RHEB_cKO up vs WT	0.744927	+3σ	19 C2|19	74493	74493	Tnks2	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2
TC16000009	0.0216	1.67587	RHEB_cKO up vs WT	0.744912	+3σ	16 C3.3|16	12013	12013	Bach1	BTB and CNC homology 1, basic leucine zipper transcription factor 1
TC08000015	0.008975	1.67578	RHEB_cKO up vs WT	0.744831	+3σ	8 E2|8	382038	382038	Urb2	URB2 ribosome biogenesis 2 homolog (S. cerevisiae)
TC07000000	0.011486	1.67542	RHEB_cKO up vs WT	0.744527	+3σ	7 A1|7 2.7	19943	19943	Rpl28	ribosomal protein L28
TC09000013	0.066716	1.675	RHEB_cKO up vs WT	0.744162	+3σ	9 F1|9	235559	235559	Topbp1	topoisomerase (DNA) II binding protein 1
TC02000050	0.002015	1.67423	RHEB_cKO up vs WT	0.743496	+3σ	---	---	---	Gm11451	predicted gene 11451
TC16000004	0.019532	1.67413	RHEB_cKO up vs WT	0.743409	+3σ	16 B3|16	66667	66667	Hspbap1	Hspb associated protein 1
TC11000012	0.011142	1.67401	RHEB_cKO up vs WT	0.743305	+3σ	11|11 B5	78394	78394	Ddx52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52
TC15000016	0.005458	1.67393	RHEB_cKO up vs WT	0.74324	+3σ	15 D3|15	239528	239528	Ago2	argonaute RISC catalytic subunit 2
TC17000013	0.00086	1.67311	RHEB_cKO up vs WT	0.742532	+3σ	17 A1|17	22350	22350	Ezr	ezrin
TC14000005	0.053223	1.67247	RHEB_cKO up vs WT	0.741982	+3σ	14 C1|14 2	93834	93834	Peli2	pellino 2
TC0X000032	0.038598	1.67232	RHEB_cKO up vs WT	0.741855	+3σ	X F4|X 72.4	20603	20603	Sms	spermine synthase
TC07000023	0.066051	1.6717	RHEB_cKO up vs WT	0.741318	+3σ	---	---	---	Gm10179	predicted gene 10179
TC10000000	0.004368	1.67163	RHEB_cKO up vs WT	0.741252	+3σ	10 A1|10	69912	69912	Nup43	nucleoporin 43
TC08000023	0.015308	1.67123	RHEB_cKO up vs WT	0.740908	+3σ	8 B3.1|8	77113	77113	Klhl2	kelch-like 2, Mayven
TC02000050	0.001988	1.67122	RHEB_cKO up vs WT	0.740905	+3σ	---	---	---	Gm14287	predicted gene 14287
TC10000020	0.013607	1.67035	RHEB_cKO up vs WT	0.74015	+3σ	10 B1|10	67239	67239	Rpf2	ribosome production factor 2 homolog
TC16000015	0.016564	1.6703	RHEB_cKO up vs WT	0.740103	+3σ	16 B3|16	1E+08	1E+08	BC100530	cDNA sequence BC100530
TC19000011	0.023421	1.67022	RHEB_cKO up vs WT	0.740041	+3σ	19 A|19 9.	21888	21888	Tle4	transducin-like enhancer of split 4
TC03000007	0.005839	1.67001	RHEB_cKO up vs WT	0.739857	+3σ	3 F|3 38.79	12462	12462	Cct3	chaperonin containing Tcp1, subunit 3 (gamma)
TC07000029	0.030343	1.66933	RHEB_cKO up vs WT	0.739267	+3σ	7 B4|7	27212	27212	Snord35b	small nucleolar RNA, C/D box 35B
TC13000025	0.017952	1.66923	RHEB_cKO up vs WT	0.73918	+3σ	13 D1|13	68927	68927	Ptcd2	pentatricopeptide repeat domain 2
TC15000022	0.052347	1.66889	RHEB_cKO up vs WT	0.738885	+3σ	15 F2|15 5	110308	110308	Krt5	keratin 5
TC14000010	0.094521	1.6688	RHEB_cKO up vs WT	0.738815	+3σ	14|14	1E+08	1E+08	Snora31	small nucleolar RNA, H/ACA box 31
TC07000009	0.001206	1.6684	RHEB_cKO up vs WT	0.738461	+3σ	---	---	---	Gm7336	predicted gene 7336
TC02000028	0.02633	1.66836	RHEB_cKO up vs WT	0.73843	+3σ	---	---	---	Gm14398	predicted gene 14398
TC01000038	0.018502	1.66816	RHEB_cKO up vs WT	0.738256	+3σ	1 H6|1	215193	215193	Diexf	digestive organ expansion factor homolog (zebrafish)
TC17000025	0.014105	1.6678	RHEB_cKO up vs WT	0.73795	+3σ	17 E3|17	12607	12607	Cebpz	CCAAT/enhancer binding protein zeta
TC11000034	0.004434	1.6676	RHEB_cKO up vs WT	0.737775	+3σ	11 C|11	70422	70422	Ints2	integrator complex subunit 2
TC02000022	0.006517	1.66697	RHEB_cKO up vs WT	0.737228	+3σ	2 G3|2	14225	14225	Fkbp1a	FK506 binding protein 1a
TC03000002	0.018944	1.66653	RHEB_cKO up vs WT	0.736849	+3σ	3 A3|3	56456	56456	Actl6a	actin-like 6A
TC09000004	0.012993	1.66651	RHEB_cKO up vs WT	0.736826	+3σ	9 A5.1|9 2	15481	15481	Hspa8	heat shock protein 8
TC11000015	0.005086	1.66649	RHEB_cKO up vs WT	0.736814	+3σ	---	---	---	Gm11557	predicted gene 11557
TC03000013	0.016468	1.66578	RHEB_cKO up vs WT	0.736202	+3σ	3 G3|3 63.	67547	67547	Slc39a8	solute carrier family 39 (metal ion transporter), member 8
TC02000047	0.075024	1.66562	RHEB_cKO up vs WT	0.736059	+3σ	2 F3|2 67.7	16449	16449	Jag1	jagged 1

TC13000024	0.02399	1.66538	RHEB_cKO up vs WT	0.735847	+3σ	13 D1|13	105372	105372	Utp15	UTP15 small subunit processome component
TC16000012	0.013088	1.6643	RHEB_cKO up vs WT	0.734912	+3σ	16 A3|16 1	94112	94112	Med15	mediator complex subunit 15
TC04000021	0.009556	1.66399	RHEB_cKO up vs WT	0.734645	+3σ	4 E2|4	57741	57741	Noc2l	NOC2 like nucleolar associated transcriptional repressor
TC02000040	0.040721	1.66295	RHEB_cKO up vs WT	0.733746	+3σ	---	---	---	Gm13767	predicted gene 13767
TC08000020	0.032691	1.66208	RHEB_cKO up vs WT	0.732992	+3σ	---	---	---	Gm10131	predicted pseudogene 10131
TC09000022	0.005452	1.66175	RHEB_cKO up vs WT	0.7327	+3σ	---	---	---	Gm7286	predicted gene 7286
TC15000016	0.009551	1.66159	RHEB_cKO up vs WT	0.732564	+3σ	15 D1|15	223601	223601	Fam49b	family with sequence similarity 49, member B
TC15000001	0.001239	1.66102	RHEB_cKO up vs WT	0.732067	+3σ	---	---	---	Gm2606	predicted pseudogene 2606
TC08000001	0.007246	1.66079	RHEB_cKO up vs WT	0.731866	+3σ	8 A1.3|8	654452	654452	Defa-ps12	defensin, alpha, pseudogene 12
TC08000030	0.003359	1.65997	RHEB_cKO up vs WT	0.731157	+3σ	8 E1|8	68533	68533	Mphosph6	M phase phosphoprotein 6
TC01000027	0.030174	1.65986	RHEB_cKO up vs WT	0.73106	+3σ	1|1	1E+08	1E+08	Snora75	small nucleolar RNA, H/ACA box 75
TC02000048	0.008596	1.65969	RHEB_cKO up vs WT	0.730911	+3σ	---	---	---	Gm14108	predicted gene 14108
TC0X000028	0.006438	1.6596	RHEB_cKO up vs WT	0.730832	+3σ	---	---	---	Gm5944	predicted gene 5944
TC0X000024	0.035284	1.65956	RHEB_cKO up vs WT	0.730804	+3σ	X C1|X 37.	15161	15161	Hcfc1	host cell factor C1
TC08000004	0.015034	1.6591	RHEB_cKO up vs WT	0.730402	+3σ	8 A4|8 21.	52065	52065	Mfhas1	malignant fibrous histiocytoma amplified sequence 1
TC15000021	0.018522	1.65894	RHEB_cKO up vs WT	0.730258	+3σ	15 F1|15 5	19082	19082	Prkag1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit
TC13000027	0.014116	1.65877	RHEB_cKO up vs WT	0.73011	+3σ	13 C1|13 3	28114	28114	Nsun2	NOL1/NOP2/Sun domain family member 2
TC01000000	0.002587	1.65876	RHEB_cKO up vs WT	0.730105	+3σ	---	---	---	Gm2383	predicted gene 2383
TC01000014	0.051093	1.65867	RHEB_cKO up vs WT	0.730027	+3σ	1 H2.1|1	14455	14455	Gas5	growth arrest specific 5
TC02000022	0.00557	1.65814	RHEB_cKO up vs WT	0.729568	+3σ	---	---	---	Gm14130	predicted gene 14130
TC03000017	0.08134	1.65739	RHEB_cKO up vs WT	0.728913	+3σ	3|3 B	13605	13605	Ect2	ect2 oncogene
TC0X000007	0.068517	1.65734	RHEB_cKO up vs WT	0.728871	+3σ	---	---	---	Gm8503	predicted gene 8503
TC17000023	0.002964	1.65726	RHEB_cKO up vs WT	0.728797	+3σ	---	---	---	Gm4518	predicted gene 4518
TC16000021	0.019184	1.65671	RHEB_cKO up vs WT	0.728319	+3σ	16 C4|16	72388	72388	Ripk4	receptor-interacting serine-threonine kinase 4
TC13000011	0.005206	1.65664	RHEB_cKO up vs WT	0.728261	+3σ	13 D1|13	218506	218506	Mrps27	mitochondrial ribosomal protein S27
TC07000024	0.004131	1.65663	RHEB_cKO up vs WT	0.728249	+3σ	7 A3|7	22323	22323	Vasp	vasodilator-stimulated phosphoprotein
TC09000014	0.055588	1.65641	RHEB_cKO up vs WT	0.728061	+3σ	9 F2|9 59.8	12530	12530	Cdc25a	cell division cycle 25A
TC13000026	0.034417	1.65628	RHEB_cKO up vs WT	0.727943	+3σ	13 D2.1|13	67263	67263	Zswim6	zinc finger SWIM-type containing 6
TC09000023	0.005159	1.65553	RHEB_cKO up vs WT	0.727293	+3σ	9|9 C	56434	56434	Tspan3	tetraspanin 3
TC11000005	0.066022	1.65498	RHEB_cKO up vs WT	0.726814	+3σ	11 B1.2|11	14584	14584	Gfpt2	glutamine fructose-6-phosphate transaminase 2
TC10000019	0.001715	1.65435	RHEB_cKO up vs WT	0.726261	+3σ	---	---	---	Gm10327	predicted pseudogene 10327
TC11000010	0.007219	1.65434	RHEB_cKO up vs WT	0.726254	+3σ	11 B4|11	74148	74148	Cluh	clustered mitochondria (cluA/CLU1) homolog
TC02000045	0.026384	1.65384	RHEB_cKO up vs WT	0.72582	+3σ	2 F1|2	215387	215387	Ncaph	non-SMC condensin I complex, subunit H
TC09000031	0.002165	1.6538	RHEB_cKO up vs WT	0.725788	+3σ	9 F2|9	104831	104831	Ptpn23	protein tyrosine phosphatase, non-receptor type 23
TC15000009	0.008293	1.65272	RHEB_cKO up vs WT	0.724842	+3σ	---	---	---	Gm4335	predicted gene 4335
TC12000010	0.021708	1.6522	RHEB_cKO up vs WT	0.724386	+3σ	12|12 F1	18789	18789	Papola	poly (A) polymerase alpha
TC07000046	0.002807	1.65132	RHEB_cKO up vs WT	0.723618	+3σ	7 A3|7	233033	233033	Samd4b	sterile alpha motif domain containing 4B
TC09000002	0.058601	1.65128	RHEB_cKO up vs WT	0.723588	+3σ	9 A4|9	78658	78658	Ncapd3	non-SMC condensin II complex, subunit D3
TC02000029	0.026465	1.65087	RHEB_cKO up vs WT	0.72323	+3σ	---	---	---	Gm13294	predicted gene 13294
TC07000009	0.041889	1.65004	RHEB_cKO up vs WT	0.722498	+3σ	---	---	---	Gm7551	predicted gene 7551
TC03000008	0.000177	1.64999	RHEB_cKO up vs WT	0.722456	+3σ	---	---	---	Gm4202	predicted gene 4202
TC07000046	0.028814	1.64984	RHEB_cKO up vs WT	0.72233	+3σ	7 F3|7 65.5	18817	18817	Plk1	polo-like kinase 1
TC11000022	0.005784	1.6496	RHEB_cKO up vs WT	0.722113	+3σ	---	---	---	Gm12017	predicted gene 12017
TC17000006	0.016755	1.64933	RHEB_cKO up vs WT	0.72188	+3σ	17 B1|17	57390	57390	Psors1c2	psoriasis susceptibility 1 candidate 2 (human)
TC01000017	0.031875	1.64871	RHEB_cKO up vs WT	0.721339	+3σ	1|1	108909	108909	Aida	axin interactor, dorsalization associated
TC09000026	0.003598	1.64817	RHEB_cKO up vs WT	0.720866	+3σ	---	---	---	Gm3671	predicted gene 3671
TC01000016	0.005502	1.64817	RHEB_cKO up vs WT	0.720865	+3σ	1|1 H3	78825	78825	Desi2	desumoylating isopeptidase 2
TC12000020	0.003572	1.64765	RHEB_cKO up vs WT	0.720412	+3σ	12 D1|12	67963	67963	Npc2	Niemann-Pick type C2
TC14000011	0.028049	1.64747	RHEB_cKO up vs WT	0.720251	+3σ	14 D3|14	13709	13709	Elf1	E74-like factor 1
TC0X000017	0.035403	1.64737	RHEB_cKO up vs WT	0.720164	+3σ	X A2-A3.1|	18824	18824	Plp2	proteolipid protein 2
TC02000003	0.081827	1.64678	RHEB_cKO up vs WT	0.719649	+3σ	---	---	---	Gm13378	predicted gene 13378
TC0X000015	0.020281	1.64678	RHEB_cKO up vs WT	0.719644	+3σ	---	---	---	Amd-ps1	S-adenosylmethionine decarboxylase, pseudogene 1
TC04000008	0.033073	1.64653	RHEB_cKO up vs WT	0.719425	+3σ	---	---	---	Gm12418	predicted gene 12418
TC03000006	0.006415	1.64633	RHEB_cKO up vs WT	0.719253	+3σ	---	---	---	Gm10291	predicted pseudogene 10291
TC06000017	0.013957	1.64611	RHEB_cKO up vs WT	0.719056	+3σ	6 G3|6	71323	71323	Rassf8	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8
TC19000013	0.010915	1.64584	RHEB_cKO up vs WT	0.718823	+3σ	19|19 C3	67979	67979	Atad1	ATPase family, AAA domain containing 1
TC03000007	0.015006	1.64552	RHEB_cKO up vs WT	0.718544	+3σ	3 F1|3	94232	94232	Ubqln4	ubiquilin 4
TC02000036	0.002356	1.64519	RHEB_cKO up vs WT	0.718254	+3σ	2|2 C3	14425	14425	Galnt3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltrans
TC01000038	0.003261	1.64393	RHEB_cKO up vs WT	0.717149	+3σ	1 H6|1	226849	226849	Ppp2r5a	protein phosphatase 2, regulatory subunit B', alpha
TC17000013	0.002979	1.64367	RHEB_cKO up vs WT	0.716924	+3σ	17 E4|17	56468	56468	Socs5	suppressor of cytokine signaling 5
TC03000031	0.016152	1.64319	RHEB_cKO up vs WT	0.7165	+3σ	3 H3|3 78.	19352	19352	Rabggtb	Rab geranylgeranyl transferase, b subunit
TC10000032	0.003443	1.64295	RHEB_cKO up vs WT	0.716291	+3σ	10 C1|10	103466	103466	Nt5dc3	5'-nucleotidase domain containing 3
TC13000015	0.012354	1.64287	RHEB_cKO up vs WT	0.716221	+3σ	13 A2-A3|1	319158	319158	Hist1h4i	histone cluster 1, H4i
TC0X000018	0.061436	1.6425	RHEB_cKO up vs WT	0.715892	+3σ	X A1.1|X	26896	26896	Med14	mediator complex subunit 14
TC02000052	0.023826	1.64249	RHEB_cKO up vs WT	0.715888	+3σ	2 H3|2 89.	228913	228913	Zfp217	zinc finger protein 217
TC11000010	0.065739	1.64249	RHEB_cKO up vs WT	0.715886	+3σ	11 B5|11 4	192159	192159	Prpf8	pre-mRNA processing factor 8
TC01000019	0.00297	1.64246	RHEB_cKO up vs WT	0.715856	+3σ	---	---	---	Gm10566	predicted gene 10566
TC08000000	0.048888	1.64161	RHEB_cKO up vs WT	0.715112	+3σ	---	---	---	Gm16589	predicted gene 16589
TC16000012	0.001085	1.64103	RHEB_cKO up vs WT	0.714598	+3σ	16 A1|16 6	14852	14852	Gspt1	G1 to S phase transition 1
TC11000035	0.018528	1.6408	RHEB_cKO up vs WT	0.714396	+3σ	11 D|11	217109	217109	Utp18	UTP18 small subunit processome component
TC09000031	0.043411	1.64043	RHEB_cKO up vs WT	0.714072	+3σ	9 F3|9	68292	68292	Stt3b	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevis
TC06000013	0.013362	1.6401	RHEB_cKO up vs WT	0.713788	+3σ	6 F1|6 57.5	17113	17113	M6pr	mannose-6-phosphate receptor, cation dependent
TC08000024	0.002299	1.6399	RHEB_cKO up vs WT	0.713609	+3σ	---	---	---	Gm10358	predicted gene 10358
TC06000034	0.014579	1.63986	RHEB_cKO up vs WT	0.713576	+3σ	6 G3|6	71177	71177	Asun	asunder, spermatogenesis regulator
TC04000018	0.010416	1.63986	RHEB_cKO up vs WT	0.713574	+3σ	---	---	---	Gm13169	predicted gene 13169
TC17000009	0.041795	1.63922	RHEB_cKO up vs WT	0.713013	+3σ	---	---	---	Trp53-ps	transformation related protein 53, pseudogene
TC02000055	0.012834	1.63875	RHEB_cKO up vs WT	0.712595	+3σ	2|2 H2	75710	75710	Rbm12	RNA binding motif protein 12
TC19000003	0.009866	1.63856	RHEB_cKO up vs WT	0.712428	+3σ	10|10 C1	66118	66118	Sarnp	SAP domain containing ribonucleoprotein
TC01000024	0.018891	1.63847	RHEB_cKO up vs WT	0.712348	+3σ	1|1 C1-C2	57750	57750	Wdr12	WD repeat domain 12
TC07000036	0.088167	1.63834	RHEB_cKO up vs WT	0.712234	+3σ	7 D3|7 48.	80982	80982	Cemip	cell migration inducing protein, hyaluronan binding
TC11000008	0.125545	1.63822	RHEB_cKO up vs WT	0.712129	+3σ	11|11	1E+08	1E+08	Snord118	small nucleolar RNA, C/D box 118
TC09000000	0.010975	1.63811	RHEB_cKO up vs WT	0.712035	+3σ	---	---	---	Gm10720	predicted gene 10720
TC0M00000	0.015957	1.63766	RHEB_cKO up vs WT	0.711636	+3σ	---	---	---	mt-Tq	mitochondrially encoded tRNA glutamine
TC03000010	0.000808	1.63762	RHEB_cKO up vs WT	0.711602	+3σ	3 F2.2|3	229672	229672	Bcl2l15	BCLl2-like 15
TC18000007	0.012042	1.63719	RHEB_cKO up vs WT	0.711222	+3σ	18 E2|18 4	17191	17191	Mbd2	methyl-CpG binding domain protein 2
TC13000005	0.019717	1.63713	RHEB_cKO up vs WT	0.71117	+3σ	13 A5|13	105148	105148	Iars	isoleucine-tRNA synthetase
TC11000028	0.002466	1.63686	RHEB_cKO up vs WT	0.710933	+3σ	11 B|11 37	14248	14248	Flii	flightless I actin binding protein
TC12000013	0.021107	1.63675	RHEB_cKO up vs WT	0.710833	+3σ	12 A1.1|12	1E+08	1E+08	Gm3625	predicted gene 3625
TC08000024	0.007199	1.63601	RHEB_cKO up vs WT	0.710177	+3σ	8 C1|8 35.	16795	16795	Large	like-glycosyltransferase

TC06000034	0.008008	1.63594	RHEB_cKO up vs WT	0.710124	+3σ	6 G2|6 77.	16653	16653	Kras	Kirsten rat sarcoma viral oncogene homolog
TC02000046	0.062938	1.63558	RHEB_cKO up vs WT	0.709801	+3σ	2 F|2 62.9	16176	16176	Il1b	interleukin 1 beta
TC07000012	0.072712	1.6353	RHEB_cKO up vs WT	0.709552	+3σ	7|7 D3-E1.	13032	13032	Ctsc	cathepsin C
TC08000032	0.005921	1.6349	RHEB_cKO up vs WT	0.709201	+3σ	8 E1|8	22224	22224	Usp10	ubiquitin specific peptidase 10
TC19000011	0.015116	1.63482	RHEB_cKO up vs WT	0.709134	+3σ	19 B|19 7.	108673	108673	Ccdc86	coiled-coil domain containing 86
TC02000026	0.009434	1.6348	RHEB_cKO up vs WT	0.709111	+3σ	2 H4|2 97.	19334	19334	Rab22a	RAB22A, member RAS oncogene family
TC11000004	0.02247	1.63478	RHEB_cKO up vs WT	0.709092	+3σ	11 B1.2|11	14694	14694	Rack1	receptor for activated C kinase 1
TC12000014	0.003797	1.63451	RHEB_cKO up vs WT	0.708862	+3σ	12 A1.3|12	434693	434693	Mrto4-ps2	mRNA turnover 4, pseudogene 2
TC03000000	0.008462	1.63436	RHEB_cKO up vs WT	0.708722	+3σ	3 A1-A3|3	16592	16592	Fabp5	fatty acid binding protein 5, epidermal
TC09000021	0.045406	1.63413	RHEB_cKO up vs WT	0.70852	+3σ	9 A5.2|9 2	12402	12402	Cbl	Casitas B-lineage lymphoma
TC16000003	0.08468	1.63397	RHEB_cKO up vs WT	0.708384	+3σ	16 B1|16 1	22061	22061	Trp63	transformation related protein 63
TC08000027	0.00306	1.63378	RHEB_cKO up vs WT	0.708213	+3σ	8 D1|8 47.	14719	14719	Got2	glutamatic-oxaloacetic transaminase 2, mitochondrial
TC02000045	0.018019	1.63369	RHEB_cKO up vs WT	0.708133	+3σ	2 F1|2 61.	73338	73338	Itpripl1	inositol 1,4,5-triphosphate receptor interacting protein-like 1
TC12000008	0.023045	1.63309	RHEB_cKO up vs WT	0.707608	+3σ	---	---	---	Gm2075	predicted gene 2075
TC03000015	0.079325	1.63265	RHEB_cKO up vs WT	0.707211	+3σ	3 H3|3 77.	51886	51886	Fubp1	far upstream element (FUSE) binding protein 1
TC02000022	0.003978	1.63247	RHEB_cKO up vs WT	0.707056	+3σ	---	---	---	Gm14148	predicted gene 14148
TC13000019	0.016656	1.6323	RHEB_cKO up vs WT	0.706905	+3σ	13 A5|13	218210	218210	Nup153	nucleoporin 153
TC15000021	0.019561	1.63209	RHEB_cKO up vs WT	0.706719	+3σ	15|15 F2	69612	69612	Kansl2	KAT8 regulatory NSL complex subunit 2
TC05000019	0.00173	1.63169	RHEB_cKO up vs WT	0.706366	+3σ	---	---	---	Gm10481	predicted gene 10481
TC12000014	0.002651	1.63147	RHEB_cKO up vs WT	0.706177	+3σ	---	---	---	Gm4929	predicted gene 4929
TC13000015	0.009334	1.63126	RHEB_cKO up vs WT	0.705989	+3σ	13 A2-A3|	319167	319167	Hist1h2ag	histone cluster 1, H2ag
TC0X000023	0.058643	1.6308	RHEB_cKO up vs WT	0.705583	+3σ	X A6|X	671878	671878	Gm14680	predicted gene 14680
TC06000029	0.003147	1.63058	RHEB_cKO up vs WT	0.705386	+3σ	6|6 F	58186	58186	Rad18	RAD18 E3 ubiquitin protein ligase
TC12000010	0.061734	1.63052	RHEB_cKO up vs WT	0.705336	+3σ	---	---	---	Gm17052	predicted gene 17052
TC12000000	0.002248	1.63046	RHEB_cKO up vs WT	0.70528	+3σ	12 A1.1|12	626534	626534	Gm6682	tubulin, alpha 1C pseudogene
TC17000011	0.026136	1.6304	RHEB_cKO up vs WT	0.705225	+3σ	17 E3|17	12211	12211	Birc6	baculoviral IAP repeat-containing 6
TC0X000025	0.008164	1.63014	RHEB_cKO up vs WT	0.704995	+3σ	---	---	---	Gm8822	predicted gene 8822
TC04000016	0.076149	1.63006	RHEB_cKO up vs WT	0.704923	+3σ	4 D2.3|4	100342	100342	Fam46b	family with sequence similarity 46, member B
TC10000007	0.001937	1.62998	RHEB_cKO up vs WT	0.704855	+3σ	10 C1|10 3	20509	20509	Slc19a1	solute carrier family 19 (folate transporter), member 1
TC01000018	0.001037	1.62904	RHEB_cKO up vs WT	0.704021	+3σ	1 H6|1	226856	226856	Lpgat1	lysophosphatidylglycerol acyltransferase 1
TC0X000008	0.002142	1.62852	RHEB_cKO up vs WT	0.703564	+3σ	---	---	---	Gm14777	predicted gene 14777
TC02000041	0.003349	1.62837	RHEB_cKO up vs WT	0.703429	+3σ	---	---	---	Gm13810	predicted gene 13810
TC17000002	0.010883	1.62835	RHEB_cKO up vs WT	0.703409	+3σ	17|17	387248	387248	Mirlet7e	microRNA let7e
TC13000019	0.010193	1.62827	RHEB_cKO up vs WT	0.703338	+3σ	---	---	---	Gm7251	predicted pseudogene 7251
TC03000027	0.136671	1.62825	RHEB_cKO up vs WT	0.703324	+3σ	3 F2.3|3	229700	229700	Rbm15	RNA binding motif protein 15
TC08000031	0.000903	1.62806	RHEB_cKO up vs WT	0.703156	+3σ	8 E2|8	244668	244668	Sipa1l2	signal-induced proliferation-associated 1 like 2
TC11000041	0.063128	1.62789	RHEB_cKO up vs WT	0.703007	+3σ	11 E2|11 8	20382	20382	Srsf2	serine/arginine-rich splicing factor 2
TC03000005	0.005966	1.62783	RHEB_cKO up vs WT	0.702953	+3σ	---	---	---	Gm5139	predicted gene 5139
TC0X000021	0.04868	1.62781	RHEB_cKO up vs WT	0.702931	+3σ	---	---	---	Gm7803	predicted gene 7803
TC0X000018	0.00223	1.62772	RHEB_cKO up vs WT	0.702856	+3σ	---	---	---	Gm7129	predicted gene 7129
TC15000014	0.000109	1.62746	RHEB_cKO up vs WT	0.702623	+3σ	15 B3.1|15	21847	21847	Klf10	Kruppel-like factor 10
TC07000039	0.016198	1.62735	RHEB_cKO up vs WT	0.702526	+3σ	---	---	---	Gm16464	predicted gene 16464
TC17000001	0.003946	1.62624	RHEB_cKO up vs WT	0.70154	+3σ	---	---	---	Gm3222	predicted pseudogene 3222
TC01000011	0.049415	1.62545	RHEB_cKO up vs WT	0.700843	+3σ	1 E4|1	226412	226412	R3hdm1	R3H domain containing 1
TC19000012	0.00416	1.62498	RHEB_cKO up vs WT	0.700418	+3σ	---	---	---	Gm8825	predicted gene 8825
TC14000020	0.030022	1.62468	RHEB_cKO up vs WT	0.700158	+3σ	14 C2|14 2	114741	114741	Supt16	suppressor of Ty 16
TC08000009	0.065868	1.62449	RHEB_cKO up vs WT	0.699985	+3σ	8 C3|8	330814	330814	Adgrl1	adhesion G protein-coupled receptor L1
TC03000005	0.020137	1.6243	RHEB_cKO up vs WT	0.699816	+3σ	---	---	---	Gm20657	predicted gene 20657
TC04000025	0.013464	1.62315	RHEB_cKO up vs WT	0.6988	+3σ	---	---	---	Gm12444	predicted gene 12444
TC08000012	0.03292	1.62297	RHEB_cKO up vs WT	0.698638	+3σ	8|8 D2	66164	66164	Nip7	NIP7, nucleolar pre-rRNA processing protein
TC02000049	0.00019	1.62286	RHEB_cKO up vs WT	0.698538	+3σ	2 H1|2	16418	16418	Eif6	eukaryotic translation initiation factor 6
TC04000034	0.002235	1.62217	RHEB_cKO up vs WT	0.697928	+3σ	4|4 D1	12331	12331	Cap1	CAP, adenylate cyclase-associated protein 1 (yeast)
TC12000001	0.024147	1.62212	RHEB_cKO up vs WT	0.69788	+3σ	---	---	---	Gm22748	predicted gene, 22748
TC01000002	0.008007	1.62194	RHEB_cKO up vs WT	0.697718	+3σ	1 B|1	26921	26921	Map4k4	mitogen-activated protein kinase kinase kinase kinase 4
TC11000005	0.003295	1.62113	RHEB_cKO up vs WT	0.696999	+3σ	11 B1.3|11	19052	19052	Ppp2ca	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
TC18000014	0.002324	1.62059	RHEB_cKO up vs WT	0.696516	+3σ	18 E1|18 3	11555	11555	Adrb2	adrenergic receptor, beta 2
TC04000029	0.035545	1.62047	RHEB_cKO up vs WT	0.696417	+3σ	4 C3|4	101739	101739	Psip1	PC4 and SFRS1 interacting protein 1
TC05000016	0.00458	1.62045	RHEB_cKO up vs WT	0.696396	+3σ	5 G2|5	433956	433956	Dnaaf5	dynein, axonemal assembly factor 5
TC01000029	0.005842	1.62042	RHEB_cKO up vs WT	0.696365	+3σ	1|1 E2	64143	64143	Ralb	v-ral simian leukemia viral oncogene B
TC12000012	0.163429	1.61902	RHEB_cKO up vs WT	0.695117	+3σ	12|12	387199	387199	Mir203	microRNA 203
TC03000020	0.005778	1.61898	RHEB_cKO up vs WT	0.695085	+3σ	---	---	---	Gm8177	predicted gene 8177
TC01000022	0.046562	1.61887	RHEB_cKO up vs WT	0.694989	+3σ	1 C1.1|1	227059	227059	Slc39a10	solute carrier family 39 (zinc transporter), member 10
TC14000009	0.071357	1.61843	RHEB_cKO up vs WT	0.694599	+3σ	14 D1|14 3	210925	210925	Ints9	integrator complex subunit 9
TC10000016	0.015494	1.6183	RHEB_cKO up vs WT	0.694476	+3σ	10|10 C1	66118	66118	Sarnp	SAP domain containing ribonucleoprotein
TC01000038	0.004502	1.61822	RHEB_cKO up vs WT	0.694403	+3σ	1 C1|1	75623	75623	Tex30	testis expressed 30
TC04000027	0.001555	1.61817	RHEB_cKO up vs WT	0.694363	+3σ	---	---	---	Gm12537	predicted gene 12537
TC07000003	0.015054	1.61808	RHEB_cKO up vs WT	0.694281	+3σ	7|7 9.95 cM	1.01E+08	1.01E+08	Gm19345	predicted gene, 19345
TC17000016	0.019198	1.61785	RHEB_cKO up vs WT	0.69408	+3σ	---	---	---	Gm5430	predicted gene 5430
TC10000004	0.01779	1.61692	RHEB_cKO up vs WT	0.693246	+3σ	10 B3|10 2	52014	52014	Nus1	NUS1 dehydrodolichyl diphosphate synthase subunit
TC09000005	0.073393	1.61685	RHEB_cKO up vs WT	0.693189	+3σ	9 A5.2|9 2	15270	15270	H2afx	H2A histone family, member X
TC0X000015	0.01576	1.61677	RHEB_cKO up vs WT	0.693113	+3σ	---	---	---	Gm15191	predicted gene 15191
TC19000006	0.009972	1.61658	RHEB_cKO up vs WT	0.692942	+3σ	19 C3|19	226169	226169	Pprc1	peroxisome proliferative activated receptor, gamma, coactivator-related 1
TC08000006	0.001724	1.61623	RHEB_cKO up vs WT	0.692629	+3σ	---	---	---	Gm10284	predicted pseudogene 10284
TC10000012	0.029776	1.61552	RHEB_cKO up vs WT	0.691996	+3σ	10 D1|10 5	53605	53605	Nap1l1	nucleosome assembly protein 1-like 1
TC07000001	0.025871	1.6147	RHEB_cKO up vs WT	0.691267	+3σ	7|7 A2	21849	21849	Trim28	tripartite motif-containing 28
TC0X000004	0.00204	1.61432	RHEB_cKO up vs WT	0.690923	+3σ	X A6|X 29.	15452	15452	Hprt	hypoxanthine guanine phosphoribosyl transferase
TC02000012	0.027501	1.61417	RHEB_cKO up vs WT	0.690793	+3σ	---	---	---	Gm13691	predicted gene 13691
TC02000032	0.019894	1.61405	RHEB_cKO up vs WT	0.690687	+3σ	2 B|2	72500	72500	Ier5l	immediate early response 5-like
TC06000008	0.00589	1.61393	RHEB_cKO up vs WT	0.690575	+3σ	6|6 C3	12332	12332	Capg	capping protein (actin filament), gelsolin-like
TC11000039	0.003278	1.61379	RHEB_cKO up vs WT	0.690451	+3σ	11 E1|11 6	56095	56095	Ftsj3	FtsJ RNA methyltransferase homolog 3 (E. coli)
TC03000005	0.005687	1.61374	RHEB_cKO up vs WT	0.69041	+3σ	3 E1|3	97112	97112	Nmd3	NMD3 ribosome export adaptor
TC13000001	0.036374	1.61373	RHEB_cKO up vs WT	0.690395	+3σ	13 A2-A3|	319187	319187	Hist1h2bn	histone cluster 1, H2bn
TC14000022	0.006494	1.61351	RHEB_cKO up vs WT	0.690204	+3σ	14|14 C3	18130	18130	Ints6	integrator complex subunit 6
TC02000044	0.025167	1.61292	RHEB_cKO up vs WT	0.689679	+3σ	2 F1|2 60.	20402	20402	Zfp106	zinc finger protein 106
TC0X000025	0.001583	1.61241	RHEB_cKO up vs WT	0.689214	+3σ	---	---	---	Gm14760	predicted gene 14760
TC04000003	0.417074	1.61234	RHEB_cKO up vs WT	0.689155	+3σ	---	---	---	Gm13302	predicted gene 13302
TC09000001	0.018448	1.61234	RHEB_cKO up vs WT	0.689153	+3σ	---	---	---	Gm24357	predicted gene, 24357
TC05000003	0.018092	1.61186	RHEB_cKO up vs WT	0.688728	+3σ	5 B1|5	69719	69719	Cad	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydro
TC15000010	0.000814	1.61119	RHEB_cKO up vs WT	0.688124	+3σ	15 F1|15	22146	22146	Tuba1c	tubulin, alpha 1C

TC05000002	0.037592	1.61116	RHEB_cKO up vs WT	0.688101	+3σ	5 B1|5 15.	433864	433864	Nom1	nucleolar protein with MIF4G domain 1
TC0X000027	0.07448	1.61099	RHEB_cKO up vs WT	0.687951	+3σ	---	---	---	Gm9103	predicted gene 9103
TC15000014	0.009041	1.61044	RHEB_cKO up vs WT	0.687453	+3σ	15|15 C	54375	54375	Azin1	antizyme inhibitor 1
TC04000027	0.063884	1.61031	RHEB_cKO up vs WT	0.687336	+3σ	4|4 C1	54366	54366	Ctnnal1	catenin (cadherin associated protein), alpha-like 1
TC05000029	0.014148	1.61015	RHEB_cKO up vs WT	0.687193	+3σ	---	---	---	Rps19-ps8	ribosomal protein S19, pseudogene 8
TC02000040	0.065388	1.60988	RHEB_cKO up vs WT	0.686954	+3σ	2 E1-2|2 5	19271	19271	Ptprj	protein tyrosine phosphatase, receptor type, J
TC03000012	0.041557	1.60973	RHEB_cKO up vs WT	0.686822	+3σ	3|3 G3	29815	29815	Bcar3	breast cancer anti-estrogen resistance 3
TC04000026	0.017961	1.60963	RHEB_cKO up vs WT	0.686725	+3σ	4 B1|4	269536	269536	Tex10	testis expressed gene 10
TC13000018	0.001334	1.60946	RHEB_cKO up vs WT	0.686577	+3σ	13 A3.3|13	105245	105245	Txndc5	thioredoxin domain containing 5
TC07000026	0.001187	1.60938	RHEB_cKO up vs WT	0.686504	+3σ	7 A3|7	233011	233011	Itpkc	inositol 1,4,5-trisphosphate 3-kinase C
TC16000001	0.012364	1.60905	RHEB_cKO up vs WT	0.686206	+3σ	16 A1|16	67203	67203	Nde1	nudE neurodevelopment protein 1
TC14000011	0.123518	1.60888	RHEB_cKO up vs WT	0.686058	+3σ	14 E2.2|14	12224	12224	Klf5	Kruppel-like factor 5
TC17000016	0.002306	1.60869	RHEB_cKO up vs WT	0.685884	+3σ	17 A3.3|17	213773	213773	Tbl3	transducin (beta)-like 3
TC16000010	0.002224	1.60838	RHEB_cKO up vs WT	0.685609	+3σ	16 C4|16	338467	338467	Morc3	microrchidia 3
TC02000049	0.010902	1.60794	RHEB_cKO up vs WT	0.685209	+3σ	2 H1|2 76.	269378	269378	Ahcy	S-adenosylhomocysteine hydrolase
TC05000029	0.000981	1.60757	RHEB_cKO up vs WT	0.684877	+3σ	---	---	---	Gm10359	predicted gene 10359
TC08000020	0.003533	1.60745	RHEB_cKO up vs WT	0.684772	+3σ	---	---	---	Gm5787	predicted gene 5787
TC13000017	0.007995	1.60737	RHEB_cKO up vs WT	0.684704	+3σ	13|13 A3.3	13557	13557	E2f3	E2F transcription factor 3
TC13000025	0.00022	1.60732	RHEB_cKO up vs WT	0.68466	+3σ	13 D1|13	621312	621312	Gm6211	predicted gene 6211
TC01000018	0.013234	1.60716	RHEB_cKO up vs WT	0.684513	+3σ	---	---	---	Gm3809	predicted gene 3809
TC07000013	0.063114	1.60692	RHEB_cKO up vs WT	0.684296	+3σ	---	---	---	Gm24412	predicted gene, 24412
TC05000022	0.012244	1.60677	RHEB_cKO up vs WT	0.684166	+3σ	5 B2|5	24116	24116	Nelfa	negative elongation factor complex member A, Whsc2
TC11000013	0.075717	1.60668	RHEB_cKO up vs WT	0.684078	+3σ	11 C|11 52	110809	110809	Srsf1	serine/arginine-rich splicing factor 1
TC11000016	0.094468	1.60634	RHEB_cKO up vs WT	0.683779	+3σ	---	---	---	Gm11585	predicted gene 11585
TC08000021	0.000757	1.60622	RHEB_cKO up vs WT	0.683666	+3σ	---	---	---	Gm2193	predicted gene 2193
TC0M000000	0.230049	1.60593	RHEB_cKO up vs WT	0.683407	+3σ	---	---	---	mt-Tn	mitochondrially encoded tRNA asparagine
TC07000016	0.012979	1.60573	RHEB_cKO up vs WT	0.683233	+3σ	7 F1|7	53322	53322	Nucb2	nucleobindin 2
TC16000003	0.003244	1.60562	RHEB_cKO up vs WT	0.68313	+3σ	---	---	---	Gm5809	predicted pseudogene 5809
TC06000024	0.04466	1.60537	RHEB_cKO up vs WT	0.682906	+3σ	6 C1|6	69956	69956	Ptcd3	pentatricopeptide repeat domain 3
TC11000026	0.00952	1.60525	RHEB_cKO up vs WT	0.682799	+3σ	---	---	---	Gm12182	predicted gene 12182
TC19000012	0.034409	1.60488	RHEB_cKO up vs WT	0.682461	+3σ	19 A|19 10	107272	107272	Psat1	phosphoserine aminotransferase 1
TC03000010	0.004344	1.60465	RHEB_cKO up vs WT	0.682258	+3σ	3 F2.2|3	329727	329727	Dennd2c	DENN/MADD domain containing 2C
TC15000017	0.01167	1.60425	RHEB_cKO up vs WT	0.681903	+3σ	15 D3|15	105732	105732	Fam83h	family with sequence similarity 83, member H
TC09000008	0.094725	1.60419	RHEB_cKO up vs WT	0.681846	+3σ	---	---	---	Gm23344	predicted gene, 23344
TC16000001	0.009689	1.60408	RHEB_cKO up vs WT	0.681746	+3σ	16 A2|16	70120	70120	Yars2	tyrosyl-tRNA synthetase 2 (mitochondrial)
TC02000023	0.004327	1.60404	RHEB_cKO up vs WT	0.681707	+3σ	---	---	---	Gm14240	predicted gene 14240
TC04000032	0.009872	1.60399	RHEB_cKO up vs WT	0.681667	+3σ	---	---	---	Gm12749	predicted gene 12749
TC10000024	0.011823	1.60328	RHEB_cKO up vs WT	0.68103	+3σ	10 C1|10 3	110816	110816	Pwp2	PWP2 periodic tryptophan protein homolog (yeast)
TSUnmappe	0.239832	1.60327	RHEB_cKO up vs WT	0.681022	+3σ	10 B1|10	19850	19850	Rnu3a	U3A small nuclear RNA
TC12000024	0.000414	1.60312	RHEB_cKO up vs WT	0.680887	+3σ	12 F1|12 6	217866	217866	Cdc42bpb	CDC42 binding protein kinase beta
TC01000020	0.050759	1.60286	RHEB_cKO up vs WT	0.680651	+3σ	1|1 A3-A5	17215	17215	Mcm3	minichromosome maintenance complex component 3
TC11000037	0.013818	1.60268	RHEB_cKO up vs WT	0.68049	+3σ	11 D|11 63	20848	20848	Stat3	signal transducer and activator of transcription 3
TC16000016	0.021047	1.60248	RHEB_cKO up vs WT	0.680306	+3σ	16 B4|16	106248	106248	Qtrtd1	queuine tRNA-ribosyltransferase domain containing 1
TC03000011	0.00312	1.60219	RHEB_cKO up vs WT	0.680048	+3σ	3 F3|3	26442	26442	Psma5	proteasome (prosome, macropain) subunit, alpha type 5
TC03000027	0.117268	1.60202	RHEB_cKO up vs WT	0.679891	+3σ	3 F3|3	76123	76123	Gpsm2	G-protein signalling modulator 2 (AGS3-like, C. elegans)
TC19000007	0.04836	1.60138	RHEB_cKO up vs WT	0.679316	+3σ	19 D2|19	13006	13006	Smc3	structural maintenance of chromosomes 3
TC14000024	0.073549	-1.61384	RHEB_cKO down vs WT	-0.6905	-3σ	14 D3|14	380916	380916	Lrch1	leucine-rich repeats and calponin homology (CH) domain containing 1
TC08000030	0.029497	-1.61399	RHEB_cKO down vs WT	-0.69063	-3σ	8 E1|8	192156	192156	Mvd	mevalonate (diphospho) decarboxylase
TC11000028	0.035105	-1.6152	RHEB_cKO down vs WT	-0.69171	-3σ	11 B1.3|11	14923	14923	Guk1	guanylate kinase 1
TC12000011	0.370411	-1.61524	RHEB_cKO down vs WT	-0.69175	-3σ	12 E-F1|12	13386	13386	Dlk1	delta-like 1 homolog (Drosophila)
TC01000013	0.055432	-1.61557	RHEB_cKO down vs WT	-0.69204	-3σ	1 G3|1	226518	226518	Nmnat2	nicotinamide nucleotide adenylyltransferase 2
TC10000003	0.002015	-1.61588	RHEB_cKO down vs WT	-0.69232	-3σ	10 B2|10 2	140742	140742	Sesn1	sestrin 1
TC07000045	0.051006	-1.61631	RHEB_cKO down vs WT	-0.69271	-3σ	---	---	---	Gm10153	predicted gene 10153
TC01000038	0.063514	-1.61775	RHEB_cKO down vs WT	-0.69399	-3σ	1 H3|1 80.	15951	15951	Ifi204	interferon activated gene 204
TC14000019	0.00507	-1.6184	RHEB_cKO down vs WT	-0.69457	-3σ	---	---	---	Gm6055	predicted gene 6055
TC14000020	0.225342	-1.61851	RHEB_cKO down vs WT	-0.69467	-3σ	14 C1|14	11731	11731	Ang2	angiogenin, ribonuclease A family, member 2
TC13000017	0.142573	-1.61859	RHEB_cKO down vs WT	-0.69473	-3σ	13 A3.3|13	73102	73102	Slc22a23	solute carrier family 22, member 23
TC10000022	0.011594	-1.61869	RHEB_cKO down vs WT	-0.69483	-3σ	10 B4|10	70423	70423	Tspan15	tetraspanin 15
TC16000017	0.064455	-1.62017	RHEB_cKO down vs WT	-0.69614	-3σ	16 C1.1|16	56277	56277	Tmem45a	transmembrane protein 45a
TC11000029	0.007431	-1.62046	RHEB_cKO down vs WT	-0.69641	-3σ	11 B2|11 3	11671	11671	Aldh3a2	aldehyde dehydrogenase family 3, subfamily A2
TC06000033	0.002597	-1.62071	RHEB_cKO down vs WT	-0.69663	-3σ	6 G2|6 74.	16832	16832	Ldhb	lactate dehydrogenase B
TC11000031	0.281554	-1.621	RHEB_cKO down vs WT	-0.69689	-3σ	11 B4|11	216892	216892	Spns2	spinster homolog 2
TC10000000	0.028249	-1.62111	RHEB_cKO down vs WT	-0.69698	-3σ	10 A2|10 4	22634	22634	Plagl1	pleiomorphic adenoma gene-like 1
TC17000028	0.006803	-1.62113	RHEB_cKO down vs WT	-0.697	-3σ	17 B1|17 1	15024	15024	H2-T10	histocompatibility 2, T region locus 10
TC11000012	0.000996	-1.62141	RHEB_cKO down vs WT	-0.69725	-3σ	11 B5|11 5	16882	16882	Lig3	ligase III, DNA, ATP-dependent
TC19000004	0.242978	-1.62149	RHEB_cKO down vs WT	-0.69732	-3σ	19 C1|19	78753	78753	Lipm	lipase, family member M
TC05000033	0.012018	-1.6218	RHEB_cKO down vs WT	-0.6976	-3σ	5 G2|5 74.	17969	17969	Ncf1	neutrophil cytosolic factor 1
TC12000008	0.004433	-1.6219	RHEB_cKO down vs WT	-0.69769	-3σ	12|12 E	14874	14874	Gstz1	glutathione transferase zeta 1 (maleylacetoacetate isomerase)
TC12000013	0.022711	-1.62212	RHEB_cKO down vs WT	-0.69788	-3σ	---	---	---	Gm3625	predicted gene 3625
TC04000011	0.084667	-1.62212	RHEB_cKO down vs WT	-0.69788	-3σ	4 C7|4	74754	74754	Dhcr24	24-dehydrocholesterol reductase
TC01000002	0.369945	-1.62236	RHEB_cKO down vs WT	-0.69809	-3σ	1 B|1 18.6	16178	16178	Il1r2	interleukin 1 receptor, type II
TC04000004	0.29067	-1.62244	RHEB_cKO down vs WT	-0.69817	-3σ	4 B1|4	53614	53614	Reck	reversion-inducing-cysteine-rich protein with kazal motifs
TC01000000	0.013535	-1.62317	RHEB_cKO down vs WT	-0.69881	-3σ	1|1 A2	12421	12421	Rb1cc1	RB1-inducible coiled-coil 1
TC13000004	0.053265	-1.62335	RHEB_cKO down vs WT	-0.69898	-3σ	13 A5|13 2	14538	14538	Gcnt2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme
TC03000012	0.260082	-1.62369	RHEB_cKO down vs WT	-0.69928	-3σ	3 G1|3	71994	71994	Cnn3	calponin 3, acidic
TC13000027	0.376178	-1.62505	RHEB_cKO down vs WT	-0.70048	-3σ	13 D2.3|13	16392	16392	Isl1	ISL1 transcription factor, LIM/homeodomain
TC07000019	0.142044	-1.62535	RHEB_cKO down vs WT	-0.70075	-3σ	7 F3|7 76.3	360216	360216	Zranb1	zinc finger, RAN-binding domain containing 1
TC18000006	0.1924	-1.62595	RHEB_cKO down vs WT	-0.70128	-3σ	18 E1|18 3	16149	16149	Cd74	CD74 antigen (invariant polypeptide of major histocompatibility complex, clas
TC11000035	0.000483	-1.62638	RHEB_cKO down vs WT	-0.70167	-3σ	11 D|11	76408	76408	Abcc3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3
TC16000002	0.005108	-1.62734	RHEB_cKO down vs WT	-0.70252	-3σ	16 A3|16 1	11877	11877	Arvcf	armadillo repeat gene deleted in velo-cardio-facial syndrome
TC10000024	0.265462	-1.62755	RHEB_cKO down vs WT	-0.7027	-3σ	10 B5-C1|1	12833	12833	Col6a1	collagen, type VI, alpha 1
TC03000009	0.207005	-1.62776	RHEB_cKO down vs WT	-0.70289	-3σ	3 F2.1|3 40	13040	13040	Ctss	cathepsin S
TC14000022	0.038429	-1.62885	RHEB_cKO down vs WT	-0.70385	-3σ	14 D1|14	219151	219151	Scara3	scavenger receptor class A, member 3
TC03000012	0.050812	-1.62957	RHEB_cKO down vs WT	-0.70449	-3σ	3 G1|3 52.	14066	14066	F3	coagulation factor III
TC08000015	0.025964	-1.63168	RHEB_cKO down vs WT	-0.70636	-3σ	8 E2|8	73647	73647	Capn9	calpain 9
TC04000016	0.023481	-1.63325	RHEB_cKO down vs WT	-0.70774	-3σ	4 D3|4	100163	100163	Pafah2	platelet-activating factor acetylhydrolase 2
TC15000019	0.081785	-1.63356	RHEB_cKO down vs WT	-0.70802	-3σ	15 E1|15	23970	23970	Pacsin2	protein kinase C and casein kinase substrate in neurons 2
TC19000014	0.153015	-1.63426	RHEB_cKO down vs WT	-0.70864	-3σ	19 C3|19 3	20411	20411	Sorbs1	sorbin and SH3 domain containing 1
TC06000004	0.068618	-1.63459	RHEB_cKO down vs WT	-0.70893	-3σ	6 B2.1|6	109218	109218	Tmem139	transmembrane protein 139

TC16000004	0.00122	-1.63462	RHEB_cKO down vs WT	-0.70896	-3σ		16 B3|16 2	13026	13026	Pcyt1a	phosphate cytidylyltransferase 1, choline, alpha isoform
TC02000002	0.004004	-1.63496	RHEB_cKO down vs WT	-0.70926	-3σ		2|2 11.87	1.01E+08	1.01E+08	Gm20038	predicted gene, 20038
TC10000008	0.089908	-1.63595	RHEB_cKO down vs WT	-0.71013	-3σ		10 C1|10 3	50492	50492	Thop1	thimet oligopeptidase 1
TC17000027	0.057688	-1.63657	RHEB_cKO down vs WT	-0.71068	-3σ		17 B1|17 1	14961	14961	H2-Ab1	histocompatibility 2, class II antigen A, beta 1
TC12000007	0.058247	-1.63674	RHEB_cKO down vs WT	-0.71082	-3σ		12 C3|12	69522	69522	2310002D0	RIKEN cDNA 2310002D06 gene
TC01000035	0.156048	-1.63675	RHEB_cKO down vs WT	-0.71084	-3σ		1 H3|1 79.	14127	14127	Fcer1g	Fc receptor, IgE, high affinity I, gamma polypeptide
TC11000040	0.028163	-1.637	RHEB_cKO down vs WT	-0.71106	-3σ		11 E2|11	328035	328035	Fads6	fatty acid desaturase domain family, member 6
TC08000002	0.102759	-1.63711	RHEB_cKO down vs WT	-0.71115	-3σ		8|8 A3	56229	56229	Thsd1	thrombospondin, type I, domain 1
TC04000016	0.01538	-1.63789	RHEB_cKO down vs WT	-0.71184	-3σ		4 D3|4 68.	15356	15356	Hmgcl	3-hydroxy-3-methylglutaryl-Coenzyme A lyase
TC07000004	0.016614	-1.63877	RHEB_cKO down vs WT	-0.71261	-3σ		7 A3|7 14.	13094	13094	Cyp2b9	cytochrome P450, family 2, subfamily b, polypeptide 9
TC19000009	0.03167	-1.63935	RHEB_cKO down vs WT	-0.71312	-3σ		19 A|19	75221	75221	Dpp3	dipeptidylpeptidase 3
TC18000004	0.301399	-1.63986	RHEB_cKO down vs WT	-0.71357	-3σ		18 B3|18	433178	433178	Spink14	serine peptidase inhibitor, Kazal type 14
TC15000018	0.007718	-1.64056	RHEB_cKO down vs WT	-0.71419	-3σ		15 E1|15 3	52609	52609	Cbx7	chromobox 7
TC13000012	0.014417	-1.64246	RHEB_cKO down vs WT	-0.71586	-3σ		13 D2.2|13	77318	77318	Ankrd55	ankyrin repeat domain 55
TC06000013	0.33486	-1.64265	RHEB_cKO down vs WT	-0.71603	-3σ		6 F1|6	50530	50530	Mfap5	microfibrillar associated protein 5
TC12000024	0.032987	-1.64299	RHEB_cKO down vs WT	-0.71633	-3σ		12|12 F2	21981	21981	Ppp1r13b	protein phosphatase 1, regulatory (inhibitor) subunit 13B
TC07000003	0.043396	-1.64373	RHEB_cKO down vs WT	-0.71697	-3σ		7 A3|7	1E+08	1E+08	Gm4598	predicted gene 4598
TC05000022	0.013485	-1.64522	RHEB_cKO down vs WT	-0.71828	-3σ		5|5 B2	17160	17160	Man2b2	mannosidase 2, alpha B2
TC13000014	0.000327	-1.64581	RHEB_cKO down vs WT	-0.7188	-3σ		13 A1|13 5	83924	83924	Gpr137b	G protein-coupled receptor 137B
TC09000017	0.103869	-1.64617	RHEB_cKO down vs WT	-0.71911	-3σ		9|9 A3	71946	71946	Endod1	endonuclease domain containing 1
TC14000007	0.041287	-1.64725	RHEB_cKO down vs WT	-0.72006	-3σ		---	---	---	Traj14	T cell receptor alpha joining 14
TC01000012	0.139041	-1.64782	RHEB_cKO down vs WT	-0.72056	-3σ		1 F|1	329260	329260	Dennd1b	DENN/MADD domain containing 1B
TC02000006	0.000215	-1.64932	RHEB_cKO down vs WT	-0.72187	-3σ		2 B|2 23.5	227753	227753	Gsn	gelsolin
TC19000003	0.114229	-1.64976	RHEB_cKO down vs WT	-0.72226	-3σ		19 A-B|19	14675	14675	Gna14	guanine nucleotide binding protein, alpha 14
TC19000016	0.12169	-1.65014	RHEB_cKO down vs WT	-0.72259	-3σ		---	---	---	Gm10197	predicted gene 10197
TC11000011	0.0252	-1.65315	RHEB_cKO down vs WT	-0.72521	-3σ		11 B5|11	216961	216961	Coro6	coronin 6
TC13000012	0.081033	-1.65374	RHEB_cKO down vs WT	-0.72573	-3σ		13 D2.1|13	74559	74559	Elovl7	ELOVL family member 7, elongation of long chain fatty acids (yeast)
TC06000015	0.002179	-1.65377	RHEB_cKO down vs WT	-0.72576	-3σ		6 F3|6	408064	408064	BC064078	cDNA sequence BC064078
TC09000023	0.349165	-1.65417	RHEB_cKO down vs WT	-0.7261	-3σ		9 B|9 31.6	16949	16949	Loxl1	lysyl oxidase-like 1
TC02000019	0.005845	-1.65438	RHEB_cKO down vs WT	-0.72629	-3σ		2 F1|2 61.	99138	99138	Stard7	START domain containing 7
TC19000013	0.009121	-1.65541	RHEB_cKO down vs WT	-0.72719	-3σ		19 C1|19	240614	240614	Ranbp6	RAN binding protein 6
TC19000012	0.008888	-1.65567	RHEB_cKO down vs WT	-0.72742	-3σ		19 B|19	1E+08	1E+08	Gm3775	predicted gene 3775
TC02000034	0.035602	-1.65585	RHEB_cKO down vs WT	-0.72757	-3σ		2 B|2	76899	76899	Golga1	golgi autoantigen, golgin subfamily a, 1
TC08000025	0.405637	-1.65664	RHEB_cKO down vs WT	-0.72826	-3σ		8 C2|8	13617	13617	Ednra	endothelin receptor type A
TC12000012	0.012413	-1.65677	RHEB_cKO down vs WT	-0.72837	-3σ		12 F1|12	104759	104759	Pld4	phospholipase D family, member 4
TC09000025	0.078253	-1.6572	RHEB_cKO down vs WT	-0.72875	-3σ		9 C|9	235442	235442	Rab8b	RAB8B, member RAS oncogene family
TC08000024	0.082465	-1.6573	RHEB_cKO down vs WT	-0.72884	-3σ		---	---	---	Gm11034	predicted gene 11034
TC02000051	0.323349	-1.65841	RHEB_cKO down vs WT	-0.7298	-3σ		2 H3|2	209232	209232	Wfdc5	WAP four-disulfide core domain 5
TC14000001	0.02892	-1.65876	RHEB_cKO down vs WT	-0.7301	-3σ		---	---	---	Gm15935	predicted gene 15935
TC03000002	0.027976	-1.65895	RHEB_cKO down vs WT	-0.73027	-3σ		3 A3|3	67576	67576	4930429B2	RIKEN cDNA 4930429B21 gene
TC0X000000	0.025669	-1.65971	RHEB_cKO down vs WT	-0.73093	-3σ		X A1.1|X 3	54636	54636	Wdr45	WD repeat domain 45
TC03000003	0.014902	-1.66047	RHEB_cKO down vs WT	-0.7316	-3σ		3 C|3	211666	211666	Mgst2	microsomal glutathione S-transferase 2
TC07000005	0.002005	-1.66272	RHEB_cKO down vs WT	-0.73354	-3σ		7 A3|7	51798	51798	Ech1	enoyl coenzyme A hydratase 1, peroxisomal
TC01000008	0.04647	-1.66322	RHEB_cKO down vs WT	-0.73398	-3σ		---	---	---	Gm15369	predicted gene 15369
TC08000015	0.117521	-1.66389	RHEB_cKO down vs WT	-0.73456	-3σ		8 E2|8	69581	69581	Rhou	ras homolog family member U
TC10000009	0.00322	-1.66444	RHEB_cKO down vs WT	-0.73503	-3σ		10 C1|10 3	70615	70615	Ankrd24	ankyrin repeat domain 24
TC02000015	0.008899	-1.66459	RHEB_cKO down vs WT	-0.73516	-3σ		---	---	---	Gm14013	predicted gene 14013
TC11000034	0.197345	-1.66519	RHEB_cKO down vs WT	-0.73569	-3σ		11 C|11	66569	66569	Gdpd1	glycerophosphodiester phosphodiesterase domain containing 1
TC01000003	0.080613	-1.66758	RHEB_cKO down vs WT	-0.73776	-3σ		1 C1.1|1	227102	227102	Ormdl1	ORM1-like 1 (S. cerevisiae)
TC19000015	0.354945	-1.66826	RHEB_cKO down vs WT	-0.73834	-3σ		19 C3|19	545291	545291	Hpse2	heparanase 2
TC03000004	0.10744	-1.66864	RHEB_cKO down vs WT	-0.73868	-3σ		3 D|3	229333	229333	C130079G	RIKEN cDNA C130079G13 gene
TC12000006	0.000137	-1.67021	RHEB_cKO down vs WT	-0.74003	-3σ		12 C3|12	210762	210762	Ppp1r36	protein phosphatase 1, regulatory subunit 36
TC12000010	0.153298	-1.67056	RHEB_cKO down vs WT	-0.74033	-3σ		12 E|12	68149	68149	Otub2	OTU domain, ubiquitin aldehyde binding 2
TC04000032	0.127185	-1.67061	RHEB_cKO down vs WT	-0.74037	-3σ		4 C7|4	29864	29864	Rnf11	ring finger protein 11
TC02000023	0.169985	-1.6712	RHEB_cKO down vs WT	-0.74088	-3σ		2 H1|2	98932	98932	Myl9	myosin, light polypeptide 9, regulatory
TC12000008	0.306501	-1.67165	RHEB_cKO down vs WT	-0.74128	-3σ		12 D2|12	217721	217721	Mfsd7c	major facilitator superfamily domain containing 7C
TC19000014	0.178186	-1.67337	RHEB_cKO down vs WT	-0.74276	-3σ		19 C2|19 3	15925	15925	Ide	insulin degrading enzyme
TC09000020	0.331172	-1.67482	RHEB_cKO down vs WT	-0.74401	-3σ		9 A5.1|9	244810	244810	AW551984	expressed sequence AW551984
TC09000011	0.032674	-1.67571	RHEB_cKO down vs WT	-0.74477	-3σ		9 E3.3|9	22038	22038	Plscr1	phospholipid scramblase 1
TC14000021	0.500465	-1.67652	RHEB_cKO down vs WT	-0.74547	-3σ		14 C3|14 2	17228	17228	Cma1	chymase 1, mast cell
TC01000014	0.37071	-1.67746	RHEB_cKO down vs WT	-0.74628	-3σ		1 H2.1|1	474332	474332	Dnm3os	dynamin 3, opposite strand
TC04000040	0.010476	-1.67868	RHEB_cKO down vs WT	-0.74733	-3σ		4 E2|4 80.	100198	100198	H6pd	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)
TC15000000	0.104153	-1.67869	RHEB_cKO down vs WT	-0.74734	-3σ		15 A|15 2.	13132	13132	Dab2	disabled 2, mitogen-responsive phosphoprotein
TC05000007	0.376096	-1.67897	RHEB_cKO down vs WT	-0.74757	-3σ		5 C3.3|5 3	18595	18595	Pdgfra	platelet derived growth factor receptor, alpha polypeptide
TC03000005	0.016911	-1.68022	RHEB_cKO down vs WT	-0.74865	-3σ		3 E1|3	242083	242083	Ppm1l	protein phosphatase 1 (formerly 2C)-like
TC07000014	0.084007	-1.68064	RHEB_cKO down vs WT	-0.74901	-3σ		7 E3|7	207728	207728	Pde2a	phosphodiesterase 2A, cGMP-stimulated
TC15000023	0.111285	-1.68107	RHEB_cKO down vs WT	-0.74938	-3σ		15 D1|15	83492	83492	Gsdmc	gasdermin C
TC07000011	0.000102	-1.68145	RHEB_cKO down vs WT	-0.7497	-3σ		7 D3|7	233424	233424	Tmc3	transmembrane channel-like gene family 3
TC05000029	0.014675	-1.68251	RHEB_cKO down vs WT	-0.75061	-3σ		5 E5|5	67266	67266	Fam69a	family with sequence similarity 69, member A
TC08000017	0.081707	-1.68314	RHEB_cKO down vs WT	-0.75115	-3σ		8 A1.1|8 6	14456	14456	Gas6	growth arrest specific 6
TC11000006	0.013731	-1.68451	RHEB_cKO down vs WT	-0.75233	-3σ		11 B1.3|11	20362	20362	Sept8	septin 8
TC15000001	0.01874	-1.68464	RHEB_cKO down vs WT	-0.75244	-3σ		---	1.02E+08	1.02E+08	Mir7212	microRNA 7212
TC02000055	0.021542	-1.68643	RHEB_cKO down vs WT	-0.75397	-3σ		2 H3|2	407243	407243	Tmem189	transmembrane protein 189
TC08000011	0.028416	-1.68694	RHEB_cKO down vs WT	-0.75441	-3σ		8 C5|8	434341	434341	Nlrc5	NLR family, CARD domain containing 5
TC01000002	0.002025	-1.68757	RHEB_cKO down vs WT	-0.75495	-3σ		1 B|1 17.9	18143	18143	Npas2	neuronal PAS domain protein 2
TC04000033	0.030785	-1.68778	RHEB_cKO down vs WT	-0.75513	-3σ		4 D1|4 53.	14073	14073	Faah	fatty acid amide hydrolase
TC03000022	0.019241	-1.68794	RHEB_cKO down vs WT	-0.75526	-3σ		3 F1|3	80890	80890	Trim2	tripartite motif-containing 2
TC09000001	0.005622	-1.68884	RHEB_cKO down vs WT	-0.75603	-3σ		9|9 A3	75747	75747	Sesn3	sestrin 3
TC12000005	0.097828	-1.68895	RHEB_cKO down vs WT	-0.75613	-3σ		12 C2|12	1.01E+08	1.01E+08	Abhd12b	abhydrolase domain containing 12B
TC05000026	0.093035	-1.69033	RHEB_cKO down vs WT	-0.75731	-3σ		5 C3.3|5	56183	56183	Nmu	neuromedin U
TC07000004	0.019323	-1.69109	RHEB_cKO down vs WT	-0.75795	-3σ		7 A3|7 14.	13089	13089	Cyp2b13	cytochrome P450, family 2, subfamily b, polypeptide 13
TC08000010	0.054472	-1.69303	RHEB_cKO down vs WT	-0.75961	-3σ		8 C5|8	69543	69543	Capns2	calpain, small subunit 2
TC02000015	0.056209	-1.69361	RHEB_cKO down vs WT	-0.76011	-3σ		2 E2|2	22034	22034	Traf6	TNF receptor-associated factor 6
TC07000003	0.144987	-1.69367	RHEB_cKO down vs WT	-0.76015	-3σ		7 A3|7	69547	69547	Nkpd1	NTPase, KAP family P-loop domain containing 1
TC01000033	0.004498	-1.69381	RHEB_cKO down vs WT	-0.76027	-3σ		1|1 H1	15064	15064	Mr1	major histocompatibility complex, class I-related
TC15000003	0.34821	-1.69538	RHEB_cKO down vs WT	-0.76161	-3σ		15 D1|15 2	18133	18133	Nov	nephroblastoma overexpressed gene
TC04000004	0.035461	-1.69625	RHEB_cKO down vs WT	-0.76235	-3σ		4|4 B1	56323	56323	Dnajb5	DnaJ heat shock protein family (Hsp40) member B5
TC07000022	0.050341	-1.69633	RHEB_cKO down vs WT	-0.76242	-3σ		7 A2-B1|7	18616	18616	Peg3	paternally expressed 3
TC06000002	0.252139	-1.69716	RHEB_cKO down vs WT	-0.76312	-3σ		6|6 A3	77042	77042	Hyal4	hyaluronoglucosaminidase 4

TC10000008	0.00135	-1.6975	RHEB_cKO down vs WT	-0.76341	-3σ	10 C1|10 3	18483	18483	Palm	paralemmin
TC07000005	0.037386	-1.69892	RHEB_cKO down vs WT	-0.76462	-3σ	7 A3|7	60594	60594	Capn12	calpain 12
TC11000027	0.087079	-1.70088	RHEB_cKO down vs WT	-0.76628	-3σ	11 B1.3|11	52570	52570	Ccdc69	coiled-coil domain containing 69
TC09000006	0.027026	-1.70096	RHEB_cKO down vs WT	-0.76635	-3σ	9 A5.3|9	58233	58233	Dnaja4	DnaJ heat shock protein family (Hsp40) member A4
TC15000019	0.115068	-1.70188	RHEB_cKO down vs WT	-0.76713	-3σ	15 E1|15	319953	319953	Ttll1	tubulin tyrosine ligase-like 1
TC02000024	0.130357	-1.70253	RHEB_cKO down vs WT	-0.76768	-3σ	2 H3|2	76080	76080	Ttpal	tocopherol (alpha) transfer protein-like
TC08000029	0.005892	-1.7041	RHEB_cKO down vs WT	-0.76901	-3σ	8 E1|8	76527	76527	Il34	interleukin 34
TC08000001	0.149244	-1.70505	RHEB_cKO down vs WT	-0.76982	-3σ	8 A1.1|8 7	26889	26889	Cln8	ceroid-lipofuscinosis, neuronal 8
TC04000032	2.43E-05	-1.7052	RHEB_cKO down vs WT	-0.76994	-3σ	4 C7|4 51.	12580	12580	Cdkn2c	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)
TC06000012	0.024207	-1.70592	RHEB_cKO down vs WT	-0.77055	-3σ	6 F1|6 53.	28006	28006	Fam21	family with sequence similarity 21
TC06000019	0.053794	-1.7063	RHEB_cKO down vs WT	-0.77087	-3σ	6 A3.1|6	319832	319832	Tmem229a	transmembrane protein 229A
TC05000006	0.205716	-1.70834	RHEB_cKO down vs WT	-0.77259	-3σ	5 C3.2|5	70701	70701	Nipal1	NIPA-like domain containing 1
TC12000000	0.340038	-1.70881	RHEB_cKO down vs WT	-0.77299	-3σ	12 A1.1|12	23967	23967	Osr1	odd-skipped related 1 (Drosophila)
TC02000015	0.206029	-1.71225	RHEB_cKO down vs WT	-0.7759	-3σ	2|2 E3	13711	13711	Elf5	E74-like factor 5
TC04000039	0.009824	-1.71233	RHEB_cKO down vs WT	-0.77596	-3σ	---	---	---	Gm13080	predicted gene 13080
TC09000017	0.392497	-1.71476	RHEB_cKO down vs WT	-0.77801	-3σ	9 A2|9	244698	244698	Hephl1	hephaestin-like 1
TC09000014	0.031488	-1.715	RHEB_cKO down vs WT	-0.77821	-3σ	9 F2|9	16578	16578	Kif9	kinesin family member 9
TC01000017	0.071607	-1.71522	RHEB_cKO down vs WT	-0.7784	-3σ	1 H5|1 84.	320404	320404	Itpkb	inositol 1,4,5-trisphosphate 3-kinase B
TC13000022	0.002468	-1.71698	RHEB_cKO down vs WT	-0.77987	-3σ	13 B3|13	66129	66129	Aaed1	AhpC/TSA antioxidant enzyme domain containing 1
TC08000024	0.011971	-1.71781	RHEB_cKO down vs WT	-0.78057	-3σ	8|8 C1	70807	70807	Arrdc2	arrestin domain containing 2
TC08000024	0.007066	-1.7194	RHEB_cKO down vs WT	-0.7819	-3σ	8 B3.3|8	546071	546071	Mast3	microtubule associated serine/threonine kinase 3
TC14000003	0.371977	-1.71998	RHEB_cKO down vs WT	-0.78239	-3σ	14 B|14 20	14560	14560	Gdf10	growth differentiation factor 10
TC01000030	0.043818	-1.72056	RHEB_cKO down vs WT	-0.78288	-3σ	1 E4|1 56.	54354	54354	Rassf5	Ras association (RalGDS/AF-6) domain family member 5
TC05000011	0.005811	-1.72127	RHEB_cKO down vs WT	-0.78347	-3σ	5 F|5	72392	72392	Tmem175	transmembrane protein 175
TC07000015	0.021792	-1.72365	RHEB_cKO down vs WT	-0.78547	-3σ	7|7 F2	19024	19024	Ppfibp2	PTPRF interacting protein, binding protein 2 (liprin beta 2)
TC07000013	0.014174	-1.72392	RHEB_cKO down vs WT	-0.78569	-3σ	7|7 E2	72461	72461	Prcp	prolylcarboxypeptidase (angiotensinase C)
TC08000017	0.001452	-1.72504	RHEB_cKO down vs WT	-0.78663	-3σ	8 A1.3|8 1	11601	11601	Angpt2	angiopoietin 2
TC11000018	0.001174	-1.72505	RHEB_cKO down vs WT	-0.78664	-3σ	11|11 E1	26399	26399	Map2k6	mitogen-activated protein kinase kinase 6
TC10000020	0.033698	-1.7254	RHEB_cKO down vs WT	-0.78693	-3σ	---	---	---	Gm15199	predicted gene 15199
TC19000006	0.032729	-1.72728	RHEB_cKO down vs WT	-0.7885	-3σ	19 C3|19 3	20250	20250	Scd2	stearoyl-Coenzyme A desaturase 2
TC19000006	0.058753	-1.72768	RHEB_cKO down vs WT	-0.78884	-3σ	19 C3|19	226122	226122	Ubtd1	ubiquitin domain containing 1
TC03000014	0.039617	-1.72863	RHEB_cKO down vs WT	-0.78963	-3σ	3 G3|3	69117	69117	Adh6a	alcohol dehydrogenase 6A (class V)
TC04000041	0.179753	-1.72867	RHEB_cKO down vs WT	-0.78967	-3σ	4 E2|4 87.	79554	79554	Cptp	ceramide-1-phosphate transfer protein
TC07000012	0.003096	-1.73101	RHEB_cKO down vs WT	-0.79162	-3σ	7 E1|7 51.	23859	23859	Dlg2	discs, large homolog 2 (Drosophila)
TC05000029	0.011846	-1.73128	RHEB_cKO down vs WT	-0.79184	-3σ	5 F|5 52.2	14020	14020	Evi5	ecotropic viral integration site 5
TC08000024	0.016142	-1.73509	RHEB_cKO down vs WT	-0.79501	-3σ	8|8 C2	78514	78514	Arhgap10	Rho GTPase activating protein 10
TC17000006	0.02478	-1.73557	RHEB_cKO down vs WT	-0.79541	-3σ	17 B2|17	70274	70274	Ly6g6e	lymphocyte antigen 6 complex, locus G6E
TC09000004	0.187011	-1.73599	RHEB_cKO down vs WT	-0.79576	-3σ	9|9 B	53376	53376	Usp2	ubiquitin specific peptidase 2
TC09000011	0.002808	-1.73618	RHEB_cKO down vs WT	-0.79592	-3σ	9 E2|9	12040	12040	Bckdhb	branched chain ketoacid dehydrogenase E1, beta polypeptide
TC18000014	0.120752	-1.737	RHEB_cKO down vs WT	-0.7966	-3σ	18 E1|18	328967	328967	Arhgef37	Rho guanine nucleotide exchange factor (GEF) 37
TC02000005	0.059278	-1.73855	RHEB_cKO down vs WT	-0.79788	-3σ	---	---	---	Gm13608	predicted gene 13608
TC17000016	0.011704	-1.74061	RHEB_cKO down vs WT	-0.7996	-3σ	17 A3.3|17	106581	106581	Fam234a	family with sequence similarity 234, member A
TC05000027	0.031106	-1.74178	RHEB_cKO down vs WT	-0.80056	-3σ	5 E3|5	231474	231474	Paqr3	progestin and adipoQ receptor family member III
TC11000003	0.005499	-1.74385	RHEB_cKO down vs WT	-0.80228	-3σ	11 A4|11	78372	78372	Snrnp25	small nuclear ribonucleoprotein 25 (U11/U12)
TC03000007	0.011693	-1.74415	RHEB_cKO down vs WT	-0.80253	-3σ	3 E3-F1|3	21827	21827	Thbs3	thrombospondin 3
TC05000025	0.0254	-1.74468	RHEB_cKO down vs WT	-0.80296	-3σ	5 C3.2|5 3	21682	21682	Tec	tec protein tyrosine kinase
TC11000032	0.022524	-1.74635	RHEB_cKO down vs WT	-0.80434	-3σ	11 B5|11	216965	216965	Taok1	TAO kinase 1
TC11000008	0.132777	-1.74711	RHEB_cKO down vs WT	-0.80497	-3σ	11 B3|11	14457	14457	Gas7	growth arrest specific 7
TC07000001	0.226603	-1.74794	RHEB_cKO down vs WT	-0.80566	-3σ	7 A1|7	381845	381845	Rnf225	ring finger protein 225
TC04000019	0.01259	-1.74844	RHEB_cKO down vs WT	-0.80607	-3σ	4 E2|4	269604	269604	Gpr157	G protein-coupled receptor 157
TC10000015	0.188829	-1.74875	RHEB_cKO down vs WT	-0.80632	-3σ	10 D3|10	70061	70061	Sdr9c7	4short chain dehydrogenase/reductase family 9C, member 7
TC02000038	0.094536	-1.74885	RHEB_cKO down vs WT	-0.8064	-3σ	2 C3|2 45.	14231	14231	Fkbp7	FK506 binding protein 7
TC12000010	0.033478	-1.75092	RHEB_cKO down vs WT	-0.80811	-3σ	12|12 F1	74521	74521	Ppp4r4	protein phosphatase 4, regulatory subunit 4
TC07000022	0.100258	-1.75125	RHEB_cKO down vs WT	-0.80839	-3σ	7 A1|7 3.8	22776	22776	Zim1	zinc finger, imprinted 1
TC10000001	0.258562	-1.75235	RHEB_cKO down vs WT	-0.80929	-3σ	10 A2|10	17684	17684	Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal doma
TC07000026	0.058222	-1.75279	RHEB_cKO down vs WT	-0.80966	-3σ	7 A3|7	243881	243881	Cyp2b23	cytochrome P450, family 2, subfamily b, polypeptide 23
TC14000001	0.008295	-1.75358	RHEB_cKO down vs WT	-0.81031	-3σ	14|14 A3	21834	21834	Thrb	thyroid hormone receptor beta
TC17000016	0.030134	-1.75368	RHEB_cKO down vs WT	-0.81038	-3σ	17|17 A3	50817	50817	Capn15	calpain 15
TC06000015	0.083777	-1.75428	RHEB_cKO down vs WT	-0.81088	-3σ	8 C1|8	21968	21968	Tom1	target of myb1 trafficking protein
TC04000015	0.126627	-1.75441	RHEB_cKO down vs WT	-0.81098	-3σ	4 D2.2|4	66260	66260	Tmem54	transmembrane protein 54
TC11000006	0.080404	-1.75521	RHEB_cKO down vs WT	-0.81164	-3σ	---	---	---	Gm12226	predicted pseudogene 12226
TC12000016	0.037037	-1.75563	RHEB_cKO down vs WT	-0.81199	-3σ	12 B1|12 1	11861	11861	Arl4a	ADP-ribosylation factor-like 4A
TC03000019	0.017246	-1.75718	RHEB_cKO down vs WT	-0.81327	-3σ	3|3 C	70804	70804	Pgrmc2	progesterone receptor membrane component 2
TC18000002	0.035053	-1.75727	RHEB_cKO down vs WT	-0.81334	-3σ	18 A2|18	68591	68591	Mocos	molybdenum cofactor sulfurase
TC11000018	0.040876	-1.7586	RHEB_cKO down vs WT	-0.81443	-3σ	11 E2|11	26941	26941	Slc9a3r1	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1
TC07000043	0.02151	-1.76331	RHEB_cKO down vs WT	-0.81829	-3σ	7 F3|7	114660	114660	Etos1	ectopic ossification 1
TC16000018	0.002338	-1.76432	RHEB_cKO down vs WT	-0.81912	-3σ	16 C1.3|16	224273	224273	Crybg3	beta-gamma crystallin domain containing 3
TC07000009	0.004609	-1.76643	RHEB_cKO down vs WT	-0.82083	-3σ	7|7 C	73724	73724	Mcee	methylmalonyl CoA epimerase
TC04000038	0.00048	-1.76665	RHEB_cKO down vs WT	-0.82102	-3σ	4 D3|4 70.	17965	17965	Nbl1	neuroblastoma, suppression of tumorigenicity 1
TC04000007	0.360863	-1.76825	RHEB_cKO down vs WT	-0.82232	-3σ	4 B3|4 33.	18405	18405	Orm1	orosomucoid 1
TC06000001	0.007611	-1.77097	RHEB_cKO down vs WT	-0.82454	-3σ	6 A1|6	16543	16543	Mdfic	MyoD family inhibitor domain containing
TC10000000	0.368211	-1.77132	RHEB_cKO down vs WT	-0.82483	-3σ	10 A1|10	83397	83397	Akap12	A kinase (PRKA) anchor protein (gravin) 12
TC19000000	0.076782	-1.77135	RHEB_cKO down vs WT	-0.82485	-3σ	19 A|19	621603	621603	Aldh3b2	aldehyde dehydrogenase 3 family, member B2
TC10000005	0.108588	-1.77217	RHEB_cKO down vs WT	-0.82552	-3σ	10 B4|10	57319	57319	Smpdl3a	sphingomyelin phosphodiesterase, acid-like 3A
TC10000000	0.007744	-1.77347	RHEB_cKO down vs WT	-0.82657	-3σ	10 A2|10	66848	66848	Fuca2	fucosidase, alpha-L- 2, plasma
TC04000032	0.021872	-1.77501	RHEB_cKO down vs WT	-0.82783	-3σ	4 C7|4	140475	140475	Bsnd	Bartter syndrome, infantile, with sensorineural deafness (Barttin)
TC03000024	0.306309	-1.77608	RHEB_cKO down vs WT	-0.82869	-3σ	3 F1|3	74175	74175	Crct1	cysteine-rich C-terminal 1
TC18000010	0.018774	-1.7808	RHEB_cKO down vs WT	-0.83253	-3σ	18|18 A2	64291	64291	Osbpl1a	oxysterol binding protein-like 1A
TC02000010	0.187681	-1.784	RHEB_cKO down vs WT	-0.83512	-3σ	2 C3|2	56508	56508	Rapgef4	Rap guanine nucleotide exchange factor (GEF) 4
TC16000005	0.364763	-1.7866	RHEB_cKO down vs WT	-0.83721	-3σ	16 B3|16 2	14314	14314	Fstl1	follistatin-like 1
TC16000020	0.097165	-1.7866	RHEB_cKO down vs WT	-0.83722	-3σ	16 C3.3|16	16703	16703	Krtap8-1	keratin associated protein 8-1
TC04000035	0.088219	-1.78735	RHEB_cKO down vs WT	-0.83783	-3σ	4 D1-D3|4	14621	14621	Gjb4	gap junction protein, beta 4
TC03000002	0.023552	-1.78743	RHEB_cKO down vs WT	-0.83789	-3σ	3 A3|3	69276	69276	Sec62	SEC62 homolog (S. cerevisiae)
TC18000000	0.317196	-1.788	RHEB_cKO down vs WT	-0.83834	-3σ	18 A1|18	140792	140792	Colec12	collectin sub-family member 12
TC15000015	0.08431	-1.78837	RHEB_cKO down vs WT	-0.83864	-3σ	15 D1|15 2	1.01E+08	1.01E+08	Gm19510	predicted gene, 19510
TC0X000029	0.004472	-1.78876	RHEB_cKO down vs WT	-0.83896	-3σ	X E3|X	215201	215201	Trmt2b	TRM2 tRNA methyltransferase 2B
TC18000013	0.363345	-1.78886	RHEB_cKO down vs WT	-0.83904	-3σ	18 C|18 24	12583	12583	Cdo1	cysteine dioxygenase 1, cytosolic
TC02000004	0.055949	-1.78965	RHEB_cKO down vs WT	-0.83968	-3σ	2 A3|2	67839	67839	Gpsm1	G-protein signalling modulator 1 (AGS3-like, C. elegans)
TC01000004	0.057391	-1.78999	RHEB_cKO down vs WT	-0.83995	-3σ	---	---	---	Gm11581	predicted gene 11581

TC11000011	0.011208	-1.79003	RHEB_cKO down vs WT	-0.83999	-3σ	11 B5|11	68385	68385	Tlcd1	TLC domain containing 1
TC07000044	0.094629	-1.79144	RHEB_cKO down vs WT	-0.84112	-3σ	7|7 F4	55987	55987	Cpxm2	carboxypeptidase X 2 (M14 family)
TC16000021	0.051976	-1.79405	RHEB_cKO down vs WT	-0.84322	-3σ	16 C3.3|16	16155	16155	Il10rb	interleukin 10 receptor, beta
TC0X000009	0.265509	-1.79584	RHEB_cKO down vs WT	-0.84466	-3σ	X C3|X 42.	11835	11835	Ar	androgen receptor
TC08000009	0.002425	-1.79826	RHEB_cKO down vs WT	-0.8466	-3σ	8 C3|8 41.	102093	102093	Phkb	phosphorylase kinase beta
TC12000002	0.082889	-1.79881	RHEB_cKO down vs WT	-0.84705	-3σ	12 B-C1|12	22160	22160	Twist1	twist basic helix-loop-helix transcription factor 1
TC11000007	0.28535	-1.80157	RHEB_cKO down vs WT	-0.84926	-3σ	11 B2|11 3	76293	76293	Mfap4	microfibrillar-associated protein 4
TC19000006	4.26E-05	-1.80185	RHEB_cKO down vs WT	-0.84948	-3σ	19 C3|19	26456	26456	Sema4g	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and
TC07000024	0.013902	-1.80336	RHEB_cKO down vs WT	-0.85069	-3σ	7 A3|7 9.9	11812	11812	Apoc1	apolipoprotein C-I
TC01000000	0.003295	-1.80414	RHEB_cKO down vs WT	-0.85132	-3σ	1 A1|1	319263	319263	Pcmtd1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1
TC03000005	0.054714	-1.80635	RHEB_cKO down vs WT	-0.85308	-3σ	3 E1|3 29.	17380	17380	Mme	membrane metallo endopeptidase
TC03000027	0.000984	-1.80681	RHEB_cKO down vs WT	-0.85345	-3σ	3 F2.3|3	329735	329735	4933431E2	RIKEN cDNA 4933431E20 gene
TC05000018	0.011118	-1.80882	RHEB_cKO down vs WT	-0.85505	-3σ	---	---	---	Gm6054	predicted gene 6054
TC08000024	0.078425	-1.80922	RHEB_cKO down vs WT	-0.85537	-3σ	8 B3.3|8	65972	65972	Ifi30	interferon gamma inducible protein 30
TC02000025	0.084758	-1.80966	RHEB_cKO down vs WT	-0.85572	-3σ	2 H3|2 85.	19025	19025	Ctsa	cathepsin A
TC02000028	0.00056	-1.81048	RHEB_cKO down vs WT	-0.85637	-3σ	2 H4|2	245867	245867	Pcmtd2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2
TC10000018	0.120935	-1.81137	RHEB_cKO down vs WT	-0.85708	-3σ	10 A4|10	11846	11846	Arg1	arginase, liver
TC09000029	0.004798	-1.81264	RHEB_cKO down vs WT	-0.8581	-3σ	9 E3.3|9	213208	213208	Il20rb	interleukin 20 receptor beta
TC12000009	0.02492	-1.81415	RHEB_cKO down vs WT	-0.8593	-3σ	12 D3|12	71349	71349	5430427M	RIKEN cDNA 5430427M07 gene
TC14000017	0.075585	-1.81473	RHEB_cKO down vs WT	-0.85976	-3σ	14 B|14	432839	432839	Gprin2	G protein regulated inducer of neurite outgrowth 2
TC01000025	0.033823	-1.81679	RHEB_cKO down vs WT	-0.86139	-3σ	1 C3|1	381269	381269	Mreg	melanoregulin
TC12000003	0.012815	-1.81758	RHEB_cKO down vs WT	-0.86202	-3σ	12 A3|12	217463	217463	Snx13	sorting nexin 13
TC12000003	0.004683	-1.81772	RHEB_cKO down vs WT	-0.86213	-3σ	12 B1|12 1	238130	238130	Dock4	dedicator of cytokinesis 4
TC15000017	0.001497	-1.81893	RHEB_cKO down vs WT	-0.86309	-3σ	15 D3|15	78725	78725	D730001G	RIKEN cDNA D730001G18 gene
TC19000010	0.00803	-1.81926	RHEB_cKO down vs WT	-0.86335	-3σ	19 A|19	56072	56072	Lgals12	lectin, galactose binding, soluble 12
TC14000017	0.03209	-1.82108	RHEB_cKO down vs WT	-0.86479	-3σ	14 B|14	26419	26419	Mapk8	mitogen-activated protein kinase 8
TC01000001	0.125533	-1.82364	RHEB_cKO down vs WT	-0.86682	-3σ	1|1 A5	74229	74229	Paqr8	progestin and adipoQ receptor family member VIII
TC02000016	0.050212	-1.82407	RHEB_cKO down vs WT	-0.86717	-3σ	---	---	---	Gm13929	predicted gene 13929
TC08000011	0.0664	-1.82655	RHEB_cKO down vs WT	-0.86912	-3σ	8 D3|8	72361	72361	Ces2g	carboxylesterase 2G
TC06000019	0.024528	-1.82718	RHEB_cKO down vs WT	-0.86962	-3σ	6 A3.3|6 1	22214	22214	Ube2h	ubiquitin-conjugating enzyme E2H
TC10000005	0.001011	-1.82789	RHEB_cKO down vs WT	-0.87018	-3σ	10 B4|10	216001	216001	Micu1	mitochondrial calcium uptake 1
TC18000013	0.155183	-1.82978	RHEB_cKO down vs WT	-0.87167	-3σ	18 D2|18	320253	320253	March3	membrane-associated ring finger (C3HC4) 3
TC14000019	0.125357	-1.83018	RHEB_cKO down vs WT	-0.87199	-3σ	14 C1|14	114874	114874	Ddhd1	DDHD domain containing 1
TC09000026	0.00414	-1.83087	RHEB_cKO down vs WT	-0.87253	-3σ	9 D|9	546143	546143	Ccpg1os	cell cycle progression 1, opposite strand
TC07000016	0.180234	-1.83134	RHEB_cKO down vs WT	-0.8729	-3σ	7 F1|7 57.	11535	11535	Adm	adrenomedullin
TC03000026	0.001522	-1.83169	RHEB_cKO down vs WT	-0.87317	-3σ	3 F2.2|3	242125	242125	Mab21l3	mab-21-like 3 (C. elegans)
TC04000011	0.006167	-1.83276	RHEB_cKO down vs WT	-0.87402	-3σ	---	---	---	Gm12727	predicted gene 12727
TC18000001	0.04451	-1.83286	RHEB_cKO down vs WT	-0.8741	-3σ	18 A2|18	67664	67664	Rnf125	ring finger protein 125
TC0X000015	0.007521	-1.83553	RHEB_cKO down vs WT	-0.8762	-3σ	X F3|X	54609	54609	Ubqln2	ubiquilin 2
TC01000008	0.004679	-1.83653	RHEB_cKO down vs WT	-0.87698	-3σ	1 D|1	22236	22236	Ugt1a2	UDP glucuronosyltransferase 1 family, polypeptide A2
TC09000012	0.0202	-1.8374	RHEB_cKO down vs WT	-0.87766	-3σ	9|9	319707	319707	C430002N	RIKEN cDNA C430002N11 gene
TC02000017	0.013852	-1.83842	RHEB_cKO down vs WT	-0.87846	-3σ	2 E4-E5|2	56357	56357	Ivd	isovaleryl coenzyme A dehydrogenase
TC0X000025	0.048956	-1.83906	RHEB_cKO down vs WT	-0.87897	-3σ	---	---	---	Gm8876	predicted gene 8876
TC01000033	0.028419	-1.83977	RHEB_cKO down vs WT	-0.87953	-3σ	1 G3|1 67.	20652	20652	Soat1	sterol O-acyltransferase 1
TC13000022	0.058674	-1.84013	RHEB_cKO down vs WT	-0.87981	-3σ	13 B3|13	66631	66631	Mfsd14b	major facilitator superfamily domain containing 14B
TC04000038	0.081645	-1.84055	RHEB_cKO down vs WT	-0.88014	-3σ	4 D3|4	26971	26971	Pla2g2f	phospholipase A2, group IIF
TC11000037	0.032317	-1.84119	RHEB_cKO down vs WT	-0.88064	-3σ	---	---	---	Gm14180	predicted gene 14180
TC13000006	0.014701	-1.84121	RHEB_cKO down vs WT	-0.88065	-3σ	---	1E+08	1E+08	Gm10782	predicted gene 10782
TC10000017	0.00299	-1.84193	RHEB_cKO down vs WT	-0.88122	-3σ	10|10 A	56535	56535	Pex3	peroxisomal biogenesis factor 3
TC18000011	0.049579	-1.84216	RHEB_cKO down vs WT	-0.8814	-3σ	18 B1|18 1	170459	170459	Stard4	StAR-related lipid transfer (START) domain containing 4
TC04000033	0.01986	-1.84221	RHEB_cKO down vs WT	-0.88143	-3σ	4 D2.1|4	68625	68625	Cfap57	cilia and flagella associated protein 57
TC07000042	0.045822	-1.8426	RHEB_cKO down vs WT	-0.88174	-3σ	7 F2|7 65.	12585	12585	Cdr2	cerebellar degeneration-related 2
TC15000017	0.049797	-1.84478	RHEB_cKO down vs WT	-0.88345	-3σ	15 D3|15	223645	223645	Mroh6	maestro heat-like repeat family member 6
TC02000017	0.046522	-1.84489	RHEB_cKO down vs WT	-0.88354	-3σ	2 E5|2	69065	69065	Chac1	ChaC, cation transport regulator 1
TC12000007	0.003375	-1.84514	RHEB_cKO down vs WT	-0.88373	-3σ	12 D1|12 3	26897	26897	Acot1	acyl-CoA thioesterase 1
TC03000024	0.129188	-1.84627	RHEB_cKO down vs WT	-0.88462	-3σ	3 F1|3	631101	631101	Lce1k	late cornified envelope 1K
TC01000003	0.381647	-1.84677	RHEB_cKO down vs WT	-0.885	-3σ	1 C1.1|1 2	12825	12825	Col3a1	collagen, type III, alpha 1
TC15000019	0.003338	-1.84936	RHEB_cKO down vs WT	-0.88703	-3σ	15 E2|15	223739	223739	5031439G	RIKEN cDNA 5031439G07 gene
TC12000019	0.042773	-1.85135	RHEB_cKO down vs WT	-0.88858	-3σ	12 C3|12	81535	81535	Sgpp1	sphingosine-1-phosphate phosphatase 1
TC05000005	0.112635	-1.85153	RHEB_cKO down vs WT	-0.88872	-3σ	5 C1|5 27.	20657	20657	Sod3	superoxide dismutase 3, extracellular
TC08000013	0.04642	-1.85252	RHEB_cKO down vs WT	-0.88949	-3σ	8 E1|8	93739	93739	Gabarapl2	gamma-aminobutyric acid (GABA) A receptor-associated protein-like 2
TC03000009	0.006614	-1.85252	RHEB_cKO down vs WT	-0.88949	-3σ	3 F2.1|3	213121	213121	Ankrd35	ankyrin repeat domain 35
TSUnmappe	0.013063	-1.85311	RHEB_cKO down vs WT	-0.88995	-3σ	5 G2|5 76.	11423	11423	Ache	acetylcholinesterase
TC03000024	0.191658	-1.85436	RHEB_cKO down vs WT	-0.89092	-3σ	3 F1|3	67828	67828	Lce1f	late cornified envelope 1F
TC0X000028	0.250034	-1.85598	RHEB_cKO down vs WT	-0.89218	-3σ	X|X A2-A3	16431	16431	Itm2a	integral membrane protein 2A
TC03000013	0.050635	-1.85686	RHEB_cKO down vs WT	-0.89287	-3σ	3 G3|3	170439	170439	Elovl6	ELOVL family member 6, elongation of long chain fatty acids (yeast)
TC08000025	0.088113	-1.85696	RHEB_cKO down vs WT	-0.89294	-3σ	8 C3|8 38.	74841	74841	Usp38	ubiquitin specific peptidase 38
TC06000012	0.05326	-1.85878	RHEB_cKO down vs WT	-0.89435	-3σ	---	---	---	Gm17482	predicted gene, 17482
TC04000000	0.040076	-1.86072	RHEB_cKO down vs WT	-0.89586	-3σ	4|4 A1-A2	60599	60599	Trp53inp1	transformation related protein 53 inducible nuclear protein 1
TC14000021	0.000206	-1.86088	RHEB_cKO down vs WT	-0.89598	-3σ	14 C2|14	68514	68514	Micu2	mitochondrial calcium uptake 2
TC08000019	0.024812	-1.86171	RHEB_cKO down vs WT	-0.89663	-3σ	8 A2|8	83436	83436	Plekha2	pleckstrin homology domain-containing, family A (phosphoinositide binding s
TC08000027	0.378863	-1.86278	RHEB_cKO down vs WT	-0.89746	-3σ	8 D2|8 50.	12552	12552	Cdh11	cadherin 11
TC11000019	0.005985	-1.86325	RHEB_cKO down vs WT	-0.89783	-3σ	11 E2|11	20698	20698	Sphk1	sphingosine kinase 1
TC02000037	0.006474	-1.86336	RHEB_cKO down vs WT	-0.8979	-3σ	---	---	---	Gm13652	predicted gene 13652
TC07000014	0.000767	-1.86338	RHEB_cKO down vs WT	-0.89792	-3σ	7|7 F1	69710	69710	Arap1	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1
TC15000022	0.188083	-1.8642	RHEB_cKO down vs WT	-0.89855	-3σ	15 F3|15	332131	332131	Krt78	keratin 78
TC11000021	0.002088	-1.86491	RHEB_cKO down vs WT	-0.89911	-3σ	11 A1|11 2	21452	21452	Tcn2	transcobalamin 2
TC07000005	0.001474	-1.8662	RHEB_cKO down vs WT	-0.9001	-3σ	7 B1|7	68458	68458	Ppp1r14a	protein phosphatase 1, regulatory (inhibitor) subunit 14A
TC01000018	0.234517	-1.8664	RHEB_cKO down vs WT	-0.90026	-3σ	1 H6|1 98.	12490	12490	Cd34	CD34 antigen
TC14000007	0.005849	-1.86755	RHEB_cKO down vs WT	-0.90115	-3σ	14 C3|14	277154	277154	Nynrin	NYN domain and retroviral integrase containing
TC11000004	0.00282	-1.87038	RHEB_cKO down vs WT	-0.90333	-3σ	11 A5-B1.1	11492	11492	Adam19	a disintegrin and metallopeptidase domain 19 (meltrin beta)
TC04000013	0.090559	-1.87406	RHEB_cKO down vs WT	-0.90617	-3σ	---	---	---	Gm12892	predicted gene 12892
TC07000018	0.13851	-1.87549	RHEB_cKO down vs WT	-0.90727	-3σ	7|7 F4	68616	68616	Gdpd3	glycerophosphodiester phosphodiesterase domain containing 3
TC07000028	0.061757	-1.87596	RHEB_cKO down vs WT	-0.90763	-3σ	7 B2|7	243923	243923	Rgs9bp	regulator of G-protein signalling 9 binding protein
TC10000008	0.06995	-1.8769	RHEB_cKO down vs WT	-0.90835	-3σ	10 C1|10	67112	67112	Fgf22	fibroblast growth factor 22
TC12000007	0.012321	-1.87748	RHEB_cKO down vs WT	-0.9088	-3σ	12 C3|12	11847	11847	Arg2	arginase type II
TC07000030	0.013832	-1.87847	RHEB_cKO down vs WT	-0.90956	-3σ	7 B4|7 29.	14344	14344	Fut2	fucosyltransferase 2
TC01000004	0.025196	-1.87988	RHEB_cKO down vs WT	-0.91064	-3σ	1 C|1 30.5	12477	12477	Ctla4	cytotoxic T-lymphocyte-associated protein 4
TC08000025	0.041851	-1.88097	RHEB_cKO down vs WT	-0.91147	-3σ	8 C2|8 39.	16168	16168	Il15	interleukin 15

TC14000009	0.002216	-1.88363	RHEB_cKO down vs WT	-0.91352	-3σ	14 D2|14	105653	105653	Phyhip	phytanoyl-CoA hydroxylase interacting protein
TC14000015	0.077797	-1.88434	RHEB_cKO down vs WT	-0.91406	-3σ	14 A3|14	78787	78787	Usp54	ubiquitin specific peptidase 54
TC03000022	0.046811	-1.88445	RHEB_cKO down vs WT	-0.91415	-3σ	3 E3|3	24088	24088	Tlr2	toll-like receptor 2
TC05000015	0.068192	-1.88701	RHEB_cKO down vs WT	-0.9161	-3σ	5 G2|5 75.	15507	15507	Hspb1	heat shock protein 1
TC09000001	0.018986	-1.88715	RHEB_cKO down vs WT	-0.91621	-3σ	9|9 A3	69137	69137	Vstm5	V-set and transmembrane domain containing 5
TC07000016	0.077815	-1.88756	RHEB_cKO down vs WT	-0.91652	-3σ	7 E2-E3|7	11717	11717	Ampd3	adenosine monophosphate deaminase 3
TC19000007	0.000381	-1.88787	RHEB_cKO down vs WT	-0.91676	-3σ	19 D2|19 4	27360	27360	Add3	adducin 3 (gamma)
TC18000004	0.003685	-1.88976	RHEB_cKO down vs WT	-0.9182	-3σ	18 B3|18	269016	269016	Sh3rf2	SH3 domain containing ring finger 2
TC11000011	0.025197	-1.89409	RHEB_cKO down vs WT	-0.92151	-3σ	11 B5|11 4	11676	11676	Aldoc	aldolase C, fructose-bisphosphate
TC07000043	0.226137	-1.89556	RHEB_cKO down vs WT	-0.92262	-3σ	7 F3|7 69.8	76560	76560	Prss8	protease, serine 8 (prostasin)
TC11000031	0.038917	-1.89572	RHEB_cKO down vs WT	-0.92275	-3σ	11 B4|11	83429	83429	Ctns	cystinosis, nephropathic
TC04000037	0.036173	-1.89806	RHEB_cKO down vs WT	-0.92453	-3σ	4 D3|4 69.	12260	12260	C1qb	complement component 1, q subcomponent, beta polypeptide
TC17000028	0.003578	-1.89909	RHEB_cKO down vs WT	-0.92531	-3σ	17 B1|17 1	15039	15039	H2-T22	histocompatibility 2, T region locus 22
TC16000011	0.058934	-1.90059	RHEB_cKO down vs WT	-0.92645	-3σ	16 A1|16	239691	239691	AU021092	expressed sequence AU021092
TC03000021	0.092271	-1.90093	RHEB_cKO down vs WT	-0.92671	-3σ	---	---	---	Gm20689	predicted gene 20689
TC10000022	0.005395	-1.9034	RHEB_cKO down vs WT	-0.92858	-3σ	10 B4|10	237360	237360	Adamts14	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin
TC04000010	0.030741	-1.90423	RHEB_cKO down vs WT	-0.92921	-3σ	4 C6|4 45.	26563	26563	Ror1	receptor tyrosine kinase-like orphan receptor 1
TC0X000016	0.061967	-1.90442	RHEB_cKO down vs WT	-0.92935	-3σ	X F5|X 76.	70008	70008	Ace2	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2
TC03000011	0.018725	-1.90485	RHEB_cKO down vs WT	-0.92967	-3σ	3 F3|3	20661	20661	Sort1	sortilin 1
TC19000000	0.111528	-1.90669	RHEB_cKO down vs WT	-0.93107	-3σ	19 A|19	73458	73458	Aldh3b3	aldehyde dehydrogenase 3 family, member B3
TC12000020	0.004464	-1.90704	RHEB_cKO down vs WT	-0.93134	-3σ	12 D1|12 3	104776	104776	Aldh6a1	aldehyde dehydrogenase family 6, subfamily A1
TC19000006	0.036429	-1.9072	RHEB_cKO down vs WT	-0.93146	-3σ	19 C3|19 3	20249	20249	Scd1	stearoyl-Coenzyme A desaturase 1
TC13000001	0.109686	-1.90984	RHEB_cKO down vs WT	-0.93345	-3σ	---	---	---	Tcrg-C3	T cell receptor gamma, constant 3
TC03000023	0.000532	-1.91063	RHEB_cKO down vs WT	-0.93405	-3σ	3 F1|3	20615	20615	Snapin	SNAP-associated protein
TC11000037	0.34516	-1.91338	RHEB_cKO down vs WT	-0.93612	-3σ	11 D|11	107656	107656	Krt9	keratin 9
TC03000022	0.108717	-1.9139	RHEB_cKO down vs WT	-0.93652	-3σ	3 F1|3	229474	229474	Fhdc1	FH2 domain containing 1
TC04000035	0.010925	-1.91583	RHEB_cKO down vs WT	-0.93797	-3σ	4 D2.2|4	76850	76850	Ago4	argonaute RISC catalytic subunit 4
TC16000003	0.094261	-1.91657	RHEB_cKO down vs WT	-0.93853	-3σ	16 B1|16	71338	71338	Tprg	transformation related protein 63 regulated
TC07000015	0.156152	-1.91674	RHEB_cKO down vs WT	-0.93865	-3σ	7 E3|7 55.9	20597	20597	Smpd1	sphingomyelin phosphodiesterase 1, acid lysosomal
TC16000021	0.079922	-1.91683	RHEB_cKO down vs WT	-0.93872	-3σ	16 A1|16 5	58239	58239	Dexi	dexamethasone-induced transcript
TC01000022	0.047599	-1.91691	RHEB_cKO down vs WT	-0.93878	-3σ	1 B|1	1E+08	1E+08	Gm16894	predicted gene, 16894
TC03000002	0.255087	-1.91949	RHEB_cKO down vs WT	-0.94073	-3σ	3 B|3	329628	329628	Fat4	FAT atypical cadherin 4
TC14000009	0.009349	-1.92018	RHEB_cKO down vs WT	-0.94124	-3σ	14|14 C3	20680	20680	Sox7	SRY (sex determining region Y)-box 7
TC04000038	0.010976	-1.92263	RHEB_cKO down vs WT	-0.94308	-3σ	4 D3|4 70.	18784	18784	Pla2g5	phospholipase A2, group V
TC15000011	0.01957	-1.9235	RHEB_cKO down vs WT	-0.94373	-3σ	15 A2|15 3	20512	20512	Slc1a3	solute carrier family 1 (glial high affinity glutamate transporter), member 3
TC04000021	0.002642	-1.92533	RHEB_cKO down vs WT	-0.9451	-3σ	4 A1|4 2.3	18619	18619	Penk	preproenkephalin
TC19000000	0.242554	-1.92838	RHEB_cKO down vs WT	-0.94739	-3σ	19 A|19	70445	70445	Cd248	CD248 antigen, endosialin
TC09000027	0.057963	-1.92908	RHEB_cKO down vs WT	-0.94791	-3σ	9 E3.1|9 40	17436	17436	Me1	malic enzyme 1, NADP(+)-dependent, cytosolic
TC05000020	0.159663	-1.93075	RHEB_cKO down vs WT	-0.94916	-3σ	5 A3|5 11.	213948	213948	Atg9b	autophagy related 9B
TC11000016	0.065157	-1.93129	RHEB_cKO down vs WT	-0.94957	-3σ	11 D|11 63	14459	14459	Gast	gastrin
TC11000011	0.044913	-1.93204	RHEB_cKO down vs WT	-0.95013	-3σ	11 B5|11 4	52466	52466	Slc46a1	solute carrier family 46, member 1
TC17000016	0.009608	-1.93271	RHEB_cKO down vs WT	-0.95063	-3σ	17 B1|17 1	26378	26378	Decr2	2-4-dienoyl-Coenzyme A reductase 2, peroxisomal
TC04000015	0.124284	-1.93324	RHEB_cKO down vs WT	-0.95102	-3σ	---	---	---	Gm12968	predicted gene 12968
TC07000035	0.003023	-1.93362	RHEB_cKO down vs WT	-0.9513	-3σ	7 D3|7	16790	16790	Anpep	alanyl (membrane) aminopeptidase
TC02000003	0.044125	-1.93461	RHEB_cKO down vs WT	-0.95205	-3σ	2 A3|2 16.	215274	215274	Il1f10	interleukin 1 family, member 10
TC17000017	0.081796	-1.93536	RHEB_cKO down vs WT	-0.9526	-3σ	17 A3.3|17	20815	20815	Srpk1	serine/arginine-rich protein specific kinase 1
TC18000013	0.368043	-1.93696	RHEB_cKO down vs WT	-0.95379	-3σ	18 D1|18 2	16948	16948	Lox	lysyl oxidase
TC01000012	0.208739	-1.93969	RHEB_cKO down vs WT	-0.95583	-3σ	1 E4|1	71884	71884	Chit1	chitinase 1 (chitotriosidase)
TC09000024	0.040241	-1.93996	RHEB_cKO down vs WT	-0.95603	-3σ	9|9 C	74090	74090	Paqr5	progestin and adipoQ receptor family member V
TC01000005	0.116856	-1.94424	RHEB_cKO down vs WT	-0.9592	-3σ	1 C3|1 33.	17756	17756	Map2	microtubule-associated protein 2
TC09000023	0.031197	-1.94496	RHEB_cKO down vs WT	-0.95974	-3σ	9 B|9	244895	244895	Peak1	pseudopodium-enriched atypical kinase 1
TC08000011	0.017444	-1.94622	RHEB_cKO down vs WT	-0.96067	-3σ	8 D1|8	244608	244608	Ccdc113	coiled-coil domain containing 113
TC01000023	0.070676	-1.94704	RHEB_cKO down vs WT	-0.96128	-3σ	1 C1.1|1 2	17912	17912	Myo1b	myosin IB
TC16000013	0.133393	-1.94828	RHEB_cKO down vs WT	-0.9622	-3σ	16 B1|16 1	239759	239759	Liph	lipase, member H
TC09000011	0.0354	-1.94929	RHEB_cKO down vs WT	-0.96295	-3σ	---	---	---	Gm11114	predicted gene 11114
TC15000015	0.388398	-1.95058	RHEB_cKO down vs WT	-0.9639	-3σ	15|15 D2	18606	18606	Enpp2	ectonucleotide pyrophosphatase/phosphodiesterase 2
TC10000026	0.173615	-1.95256	RHEB_cKO down vs WT	-0.96537	-3σ	10 C1|10	270757	270757	Bpifc	BPI fold containing family C
TC03000004	0.008842	-1.95362	RHEB_cKO down vs WT	-0.96615	-3σ	3 D|3	676914	676914	Gm9696	arylacetamide deacetylase-like 2 pseudogene
TC16000007	0.015546	-1.95839	RHEB_cKO down vs WT	-0.96967	-3σ	16 C1.1|16	320712	320712	Abi3bp	ABI gene family, member 3 (NESH) binding protein
TC03000019	0.062599	-1.95875	RHEB_cKO down vs WT	-0.96993	-3σ	3 C|3 26.6	26422	26422	Nbea	neurobeachin
TC09000023	0.027281	-1.96205	RHEB_cKO down vs WT	-0.97236	-3σ	9 A5.3|9	94180	94180	Acsbg1	acyl-CoA synthetase bubblegum family member 1
TC0X000028	0.074399	-1.96621	RHEB_cKO down vs WT	-0.97542	-3σ	X E1|X	67071	67071	Rps6ka6	ribosomal protein S6 kinase polypeptide 6
TC19000014	0.155037	-1.96839	RHEB_cKO down vs WT	-0.97702	-3σ	19 C3|19 3	17060	17060	Blnk	B cell linker
TC01000006	0.005426	-1.96857	RHEB_cKO down vs WT	-0.97715	-3σ	1|1 C3	56695	56695	Pnkd	paroxysmal nonkinesiogenic dyskinesia
TC06000019	0.000496	-1.9723	RHEB_cKO down vs WT	-0.97988	-3σ	6 A2|6	30785	30785	Cttnbp2	cortactin binding protein 2
TC04000026	0.126771	-1.9733	RHEB_cKO down vs WT	-0.98061	-3σ	---	---	---	2310081O	RIKEN cDNA 2310081O03 gene
TC15000009	0.033935	-1.97412	RHEB_cKO down vs WT	-0.98121	-3σ	---	---	---	Gm26760	predicted gene, 26760
TC13000018	0.004548	-1.97544	RHEB_cKO down vs WT	-0.98217	-3σ	13 A4|13	109254	109254	Adtrp	androgen dependent TFPI regulating protein
TC03000012	0.071713	-1.97661	RHEB_cKO down vs WT	-0.98303	-3σ	3 G1|3	214137	214137	Arhgap29	Rho GTPase activating protein 29
TC14000009	0.008584	-1.97754	RHEB_cKO down vs WT	-0.98371	-3σ	14 D1|14 3	12759	12759	Clu	clusterin
TC0X000026	0.011101	-1.97838	RHEB_cKO down vs WT	-0.98432	-3σ	X|X C2	94190	94190	Ophn1	oligophrenin 1
TSUnmappe	0.119818	-1.97839	RHEB_cKO down vs WT	-0.98433	-3σ	9 C|9 37.4	19883	19883	Rora	RAR-related orphan receptor alpha
TC01000015	0.070154	-1.97892	RHEB_cKO down vs WT	-0.98471	-3σ	1|1 H1	74895	74895	Ccdc181	coiled-coil domain containing 181
TC03000019	0.086551	-1.97898	RHEB_cKO down vs WT	-0.98476	-3σ	---	---	---	Gm21954	predicted gene, 21954
TC17000016	0.013766	-1.97961	RHEB_cKO down vs WT	-0.98522	-3σ	17 A3.3|17	224617	224617	Tbc1d24	TBC1 domain family, member 24
TC11000036	0.007547	-1.97964	RHEB_cKO down vs WT	-0.98524	-3σ	11 D|11	56013	56013	Srcin1	SRC kinase signaling inhibitor 1
TC04000018	0.01095	-1.9797	RHEB_cKO down vs WT	-0.98528	-3σ	4 E1|4	20148	20148	Dhrs3	dehydrogenase/reductase (SDR family) member 3
TC03000000	0.064547	-1.9837	RHEB_cKO down vs WT	-0.9882	-3σ	3 A1|3	66371	66371	Chmp4c	charged multivesicular body protein 4C
TC0X000006	0.20142	-1.98458	RHEB_cKO down vs WT	-0.98883	-3σ	X B|X 37.3	12111	12111	Bgn	biglycan
TC13000021	0.001797	-1.98542	RHEB_cKO down vs WT	-0.98944	-3σ	13 B3|13	218294	218294	Cdc14b	CDC14 cell division cycle 14B
TC14000017	0.044778	-1.98753	RHEB_cKO down vs WT	-0.99098	-3σ	14 B|14	69134	69134	Fam25c	family with sequence similarity 25, member C
TC04000001	0.030975	-1.98921	RHEB_cKO down vs WT	-0.9922	-3σ	4 A3|4 7.7	50500	50500	Ttpa	tocopherol (alpha) transfer protein
TC06000000	0.324454	-1.99445	RHEB_cKO down vs WT	-0.99599	-3σ	6 A1|6 1.8	12843	12843	Col1a2	collagen, type I, alpha 2
TC08000005	0.312152	-1.99567	RHEB_cKO down vs WT	-0.99687	-3σ	8 B1.1|8	53318	53318	Pdlim3	PDZ and LIM domain 3
TC04000034	0.017497	-1.99602	RHEB_cKO down vs WT	-0.99713	-3σ	---	1.02E+08	1.02E+08	Mir7015	microRNA 7015
TC08000029	0.004355	-1.9963	RHEB_cKO down vs WT	-0.99733	-3σ	8 E1|8	234740	234740	Tmem231	transmembrane protein 231
TC15000021	0.003125	-1.99753	RHEB_cKO down vs WT	-0.99822	-3σ	15 F1|15 5	74775	74775	Lmbr1l	limb region 1 like
TC01000015	0.122419	-1.99805	RHEB_cKO down vs WT	-0.99859	-3σ	1 H2.2|1 7	116914	116914	Slc19a2	solute carrier family 19 (thiamine transporter), member 2
TC08000027	0.105779	-1.99861	RHEB_cKO down vs WT	-0.999	-3σ	8 D1|8 47.	13000	13000	Csnk2a2	casein kinase 2, alpha prime polypeptide

TC02000003	0.164754	-1.99934	RHEB_cKO down vs WT	-0.99952	-3σ	2 A3|2 16.	54450	54450	Il1f5	interleukin 1 family, member 5 (delta)
TC13000003	0.027977	-2.00352	RHEB_cKO down vs WT	-1.00254	-3σ	13 A3.3|13	20706	20706	Serpinb9b	serine (or cysteine) peptidase inhibitor, clade B, member 9b
TC12000021	0.000848	-2.00369	RHEB_cKO down vs WT	-1.00266	-3σ	12|12 F1	24000	24000	Ptpn21	protein tyrosine phosphatase, non-receptor type 21
TC06000004	0.01843	-2.0068	RHEB_cKO down vs WT	-1.0049	-3σ	6 B2.1|6	54324	54324	Arhgef5	Rho guanine nucleotide exchange factor (GEF) 5
TC02000043	0.010018	-2.00693	RHEB_cKO down vs WT	-1.00499	-3σ	2 E5|2 59.	19419	19419	Rasgrp1	RAS guanyl releasing protein 1
TC07000038	0.00906	-2.01047	RHEB_cKO down vs WT	-1.00753	-3σ	7 F1|7	50877	50877	Neu3	neuraminidase 3
TC08000005	0.00479	-2.01568	RHEB_cKO down vs WT	-1.01127	-3σ	8|8 B2	14081	14081	Acsl1	acyl-CoA synthetase long-chain family member 1
TC05000036	0.004421	-2.01782	RHEB_cKO down vs WT	-1.0128	-3σ	5 G3|5	71706	71706	Slc46a3	solute carrier family 46, member 3
TC01000009	0.01915	-2.02008	RHEB_cKO down vs WT	-1.01441	-3σ	1 D|1	208777	208777	Sned1	sushi, nidogen and EGF-like domains 1
TC07000017	0.009609	-2.02097	RHEB_cKO down vs WT	-1.01505	-3σ	7 F3|7	30949	30949	Lcmt1	leucine carboxyl methyltransferase 1
TC01000010	0.132848	-2.02317	RHEB_cKO down vs WT	-1.01662	-3σ	1|1 D	20725	20725	Serpinb8	serine (or cysteine) peptidase inhibitor, clade B, member 8
TC04000036	0.00472	-2.02366	RHEB_cKO down vs WT	-1.01696	-3σ	4 D2.3|4	269589	269589	Sytl1	synaptotagmin-like 1
TC08000024	0.106495	-2.025	RHEB_cKO down vs WT	-1.01792	-3σ	8 B3.3|8	74015	74015	Fcho1	FCH domain only 1
TC01000012	0.033778	-2.02988	RHEB_cKO down vs WT	-1.0214	-3σ	1 E4|1 59.	21956	21956	Tnnt2	troponin T2, cardiac
TC01000008	0.117409	-2.0311	RHEB_cKO down vs WT	-1.02226	-3σ	---	---	---	Gm15374	predicted gene 15374
TC15000003	0.171427	-2.0313	RHEB_cKO down vs WT	-1.0224	-3σ	15|15 D	12818	12818	Col14a1	collagen, type XIV, alpha 1
TC11000039	0.011934	-2.03228	RHEB_cKO down vs WT	-1.0231	-3σ	11 D|11 69	21763	21763	Tex2	testis expressed gene 2
TC0X000003	0.006494	-2.03533	RHEB_cKO down vs WT	-1.02526	-3σ	X A3.2|X	75974	75974	Dock11	dedicator of cytokinesis 11
TC07000007	0.028353	-2.03597	RHEB_cKO down vs WT	-1.02572	-3σ	---	---	---	Gm2058	predicted gene 2058
TC04000000	0.066135	-2.03637	RHEB_cKO down vs WT	-1.026	-3σ	---	---	---	A830012C1	RIKEN cDNA A830012C17 gene
TC01000016	0.028538	-2.0374	RHEB_cKO down vs WT	-1.02673	-3σ	1 H4|1	226744	226744	Cnst	consortin, connexin sorting protein
TC06000021	0.052957	-2.04135	RHEB_cKO down vs WT	-1.02952	-3σ	6 B1|6	434008	434008	Tmem178b	transmembrane protein 178B
TC03000024	0.046954	-2.04178	RHEB_cKO down vs WT	-1.02983	-3σ	3|3 F2	22156	22156	Tuft1	tuftelin 1
TC11000041	0.047099	-2.04296	RHEB_cKO down vs WT	-1.03066	-3σ	11 E2|11 8	21858	21858	Timp2	tissue inhibitor of metalloproteinase 2
TC04000022	0.365014	-2.04309	RHEB_cKO down vs WT	-1.03075	-3σ	4 A1|4	208890	208890	Slc26a7	solute carrier family 26, member 7
TC11000009	0.08305	-2.0438	RHEB_cKO down vs WT	-1.03125	-6σ	11 B3|11	80515	80515	Chd3os	chromodomain helicase DNA binding protein 3, opposite strand
TC16000008	0.01229	-2.04391	RHEB_cKO down vs WT	-1.03133	-6σ	16|16	387229	387229	Mir99a	microRNA 99a
TC10000031	0.010635	-2.04488	RHEB_cKO down vs WT	-1.03202	-6σ	---	---	---	Gm15900	predicted gene 15900
TC09000033	0.010197	-2.04896	RHEB_cKO down vs WT	-1.03489	-6σ	9 F|9 74.5	17281	17281	Fyco1	FYVE and coiled-coil domain containing 1
TC15000020	0.010743	-2.05031	RHEB_cKO down vs WT	-1.03584	-6σ	15|15 E	11883	11883	Arsa	arylsulfatase A
TC18000013	0.000356	-2.05137	RHEB_cKO down vs WT	-1.03659	-6σ	18 C|18	20358	20358	Sema6a	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semap
TC01000025	0.235587	-2.05253	RHEB_cKO down vs WT	-1.0374	-6σ	1 C3|1 36.	16011	16011	Igfbp5	insulin-like growth factor binding protein 5
TC03000011	0.046746	-2.05631	RHEB_cKO down vs WT	-1.04005	-6σ	---	---	---	Gm10961	predicted gene 10961
TC14000023	0.041196	-2.05747	RHEB_cKO down vs WT	-1.04087	-6σ	14 D2|14	213019	213019	Pdlim2	PDZ and LIM domain 2
TC19000013	0.002651	-2.05801	RHEB_cKO down vs WT	-1.04125	-6σ	19 C1|19 2	226090	226090	Ermp1	endoplasmic reticulum metallopeptidase 1
TC01000002	0.020142	-2.05872	RHEB_cKO down vs WT	-1.04174	-6σ	1 B|1 15.2	94220	94220	Cnnm4	cyclin M4
TC07000007	0.129367	-2.05928	RHEB_cKO down vs WT	-1.04214	-6σ	7 B4|7 28.	68668	68668	Klk5	kallikrein related-peptidase 5
TC18000008	0.000924	-2.05951	RHEB_cKO down vs WT	-1.0423	-6σ	18 E3|18	207259	207259	Zbtb7c	zinc finger and BTB domain containing 7C
TC14000010	0.006712	-2.06079	RHEB_cKO down vs WT	-1.0432	-6σ	14 D3|14 3	16432	16432	Itm2b	integral membrane protein 2B
TC17000003	0.039704	-2.06187	RHEB_cKO down vs WT	-1.04395	-6σ	17 A3.3|17	212733	212733	Ccdc64b	coiled-coil domain containing 64B
TC19000007	0.004285	-2.06248	RHEB_cKO down vs WT	-1.04438	-6σ	19 D2|19 4	18569	18569	Pdcd4	programmed cell death 4
TC03000008	0.067968	-2.06473	RHEB_cKO down vs WT	-1.04596	-6σ	3 F2.1|3	229574	229574	Flg2	filaggrin family member 2
TC05000023	0.000279	-2.06935	RHEB_cKO down vs WT	-1.04918	-6σ	5 B3|5	70693	70693	Adgra3	adhesion G protein-coupled receptor A3
TC01000035	0.068238	-2.0704	RHEB_cKO down vs WT	-1.04991	-6σ	1 H3|1	15490	15490	Hsd17b7	hydroxysteroid (17-beta) dehydrogenase 7
TC08000008	0.122033	-2.0706	RHEB_cKO down vs WT	-1.05005	-6σ	8 C1|8 35.	15368	15368	Hmox1	heme oxygenase 1
TC17000024	0.05036	-2.07362	RHEB_cKO down vs WT	-1.05215	-6σ	17 E1.1|17	19274	19274	Ptprm	protein tyrosine phosphatase, receptor type, M
TC19000016	0.053144	-2.07699	RHEB_cKO down vs WT	-1.05449	-6σ	19 C3|19 3	13074	13074	Cyp17a1	cytochrome P450, family 17, subfamily a, polypeptide 1
TC05000008	0.000315	-2.08701	RHEB_cKO down vs WT	-1.06144	-6σ	5 E2|5	231440	231440	Parm1	prostate androgen-regulated mucin-like protein 1
TC13000000	0.093413	-2.09356	RHEB_cKO down vs WT	-1.06596	-6σ	13 A1|13 5	14706	14706	Gng4	guanine nucleotide binding protein (G protein), gamma 4
TC09000031	0.066736	-2.0984	RHEB_cKO down vs WT	-1.06929	-6σ	9 F3|9	70031	70031	Cmtm8	CKLF-like MARVEL transmembrane domain containing 8
TC11000027	0.034198	-2.09948	RHEB_cKO down vs WT	-1.07003	-6σ	11 B1.3|11	246049	246049	Slc36a2	solute carrier family 36 (proton/amino acid symporter), member 2
TC13000005	0.371694	-2.10091	RHEB_cKO down vs WT	-1.07101	-6σ	13|13 B1	66695	66695	Aspn	asporin
TC13000013	0.15148	-2.10191	RHEB_cKO down vs WT	-1.0717	-6σ	13 A1|13	70405	70405	Calml3	calmodulin-like 3
TC11000006	0.006155	-2.10281	RHEB_cKO down vs WT	-1.07232	-6σ	11 B1.3|11	215335	215335	Slc36a1	solute carrier family 36 (proton/amino acid symporter), member 1
TC07000027	0.004073	-2.10291	RHEB_cKO down vs WT	-1.07239	-6σ	7 B1|7	76718	76718	Catsperg2	catsper channel auxiliary subunit gamma 2
TC03000008	0.050686	-2.10303	RHEB_cKO down vs WT	-1.07247	-6σ	3 F2.1|3	99681	99681	Tchh	trichohyalin
TC0X000002	0.037458	-2.10326	RHEB_cKO down vs WT	-1.07263	-6σ	X A1.3|X	19733	19733	Rgn	regucalcin
TC11000037	0.031723	-2.10772	RHEB_cKO down vs WT	-1.07568	-6σ	11 D|11 62	268482	268482	Krt12	keratin 12
TC16000020	0.140028	-2.10846	RHEB_cKO down vs WT	-1.07619	-6σ	16 C3.3|16	71363	71363	Krtap7-1	keratin associated protein 7-1
TC03000024	0.139238	-2.10971	RHEB_cKO down vs WT	-1.07705	-6σ	3 F1|3	66195	66195	Lce1g	late cornified envelope 1G
TC05000028	0.331805	-2.11566	RHEB_cKO down vs WT	-1.08111	-6σ	5 E4|5 50.	13602	13602	Sparcl1	SPARC-like 1
TC05000010	0.001051	-2.11664	RHEB_cKO down vs WT	-1.08178	-6σ	5 F|5	433931	433931	Pigg	phosphatidylinositol glycan anchor biosynthesis, class G
TC14000023	0.000564	-2.1179	RHEB_cKO down vs WT	-1.08263	-6σ	14 D3|14 3	1.01E+08	1.01E+08	Gm20290	predicted gene, 20290
TC10000011	0.332483	-2.11833	RHEB_cKO down vs WT	-1.08293	-6σ	10 C3|10 5	17022	17022	Lum	lumican
TC15000022	0.228862	-2.1186	RHEB_cKO down vs WT	-1.08311	-6σ	15 F3|15	406220	406220	Krt77	keratin 77
TC04000016	0.001621	-2.12145	RHEB_cKO down vs WT	-1.08505	-6σ	4 D3|4	230837	230837	Asap3	ArfGAP with SH3 domain, ankyrin repeat and PH domain 3
TC07000006	0.005923	-2.12274	RHEB_cKO down vs WT	-1.08593	-6σ	7 B1|7 20.	18624	18624	Pepd	peptidase D
TC01000018	0.068687	-2.12415	RHEB_cKO down vs WT	-1.08689	-6σ	1 H6|1 97.	22782	22782	Slc30a1	solute carrier family 30 (zinc transporter), member 1
TC15000023	0.003845	-2.12854	RHEB_cKO down vs WT	-1.08986	-6σ	15 F3|15	67488	67488	Calcoco1	calcium binding and coiled coil domain 1
TC10000015	0.053478	-2.1305	RHEB_cKO down vs WT	-1.09119	-6σ	10 D3|10 7	107605	107605	Rdh1	retinol dehydrogenase 1 (all trans)
TC03000008	0.100278	-2.13113	RHEB_cKO down vs WT	-1.09162	-6σ	3 F1|3	73719	73719	Lce1c	late cornified envelope 1C
TC09000029	0.190572	-2.13211	RHEB_cKO down vs WT	-1.09228	-6σ	9 F1|9	56318	56318	Acpp	acid phosphatase, prostate
TC04000016	0.022262	-2.13303	RHEB_cKO down vs WT	-1.0929	-6σ	4 D3|4	71904	71904	Paqr7	progestin and adipoQ receptor family member VII
TC11000037	0.051619	-2.13362	RHEB_cKO down vs WT	-1.0933	-6σ	11 D|11 63	16665	16665	Krt15	keratin 15
TC19000015	0.039597	-2.13803	RHEB_cKO down vs WT	-1.09628	-6σ	19 C3|19 3	20249	20249	Scd1	stearoyl-Coenzyme A desaturase 1
TC15000000	0.007315	-2.13946	RHEB_cKO down vs WT	-1.09725	-6σ	15 A1|15 1	20363	20363	Sepp1	selenoprotein P, plasma, 1
TC07000037	0.094002	-2.14052	RHEB_cKO down vs WT	-1.09796	-6σ	7|7 F1	67800	67800	Dgat2	diacylglycerol O-acyltransferase 2
TC04000041	0.01574	-2.14242	RHEB_cKO down vs WT	-1.09924	-6σ	4 E2|4	66469	66469	Fam213b	family with sequence similarity 213, member B
TC03000024	0.191886	-2.1436	RHEB_cKO down vs WT	-1.10003	-6σ	3 F1|3	66533	66533	2310050C0	RIKEN cDNA 2310050C09 gene
TC06000015	0.010268	-2.14849	RHEB_cKO down vs WT	-1.10332	-6σ	6 F3|6	57436	57436	Gabarapl1	gamma-aminobutyric acid (GABA) A receptor-associated protein-like 1
TC03000024	0.16839	-2.14967	RHEB_cKO down vs WT	-1.10412	-6σ	3 F1|3	73730	73730	Lce1l	late cornified envelope 1L
TC09000001	0.013923	-2.15058	RHEB_cKO down vs WT	-1.10473	-6σ	9|9 A3	75747	75747	Sesn3	sestrin 3
TC01000024	0.003731	-2.15461	RHEB_cKO down vs WT	-1.10743	-6σ	1 C2|1	241075	241075	Plekhm3	pleckstrin homology domain containing, family M, member 3
TC13000009	0.017488	-2.1635	RHEB_cKO down vs WT	-1.11337	-6σ	13 C3|13	105171	105171	Arrdc3	arrestin domain containing 3
TC17000010	0.008377	-2.16514	RHEB_cKO down vs WT	-1.11446	-6σ	17 E1.1|17	14158	14158	Fer	fer (fms/fps related) protein kinase
TC15000012	0.009577	-2.16564	RHEB_cKO down vs WT	-1.11479	-6σ	15|15 A2	68070	68070	Pdzd2	PDZ domain containing 2
TC15000020	0.010718	-2.16781	RHEB_cKO down vs WT	-1.11624	-6σ	15 E3|15 4	16564	16564	Kif21a	kinesin family member 21A
TC13000005	0.135976	-2.17174	RHEB_cKO down vs WT	-1.11885	-6σ	13 B|13 24	15904	15904	Id4	inhibitor of DNA binding 4
TC16000021	0.095697	-2.17449	RHEB_cKO down vs WT	-1.12068	-6σ	16 C4|16	207781	207781	C2cd2	C2 calcium-dependent domain containing 2

TC03000008	0.001301	-2.1772	RHEB_cKO down vs WT	-1.12247	-6σ	3|3 F2	19885	19885	Rorc	RAR-related orphan receptor gamma
TC01000011	0.102276	-2.17891	RHEB_cKO down vs WT	-1.12361	-6σ	1 E4|1	226418	226418	Yod1	YOD1 OTU deubiquitinating enzyme 1 homologue (S. cerevisiae)
TC07000008	0.004106	-2.18033	RHEB_cKO down vs WT	-1.12455	-6σ	7 B4|7	66065	66065	Hsd17b14	hydroxysteroid (17-beta) dehydrogenase 14
TC15000015	0.000293	-2.18398	RHEB_cKO down vs WT	-1.12696	-6σ	15 D1|15 2	20649	20649	Sntb1	syntrophin, basic 1
TC01000008	0.306842	-2.18502	RHEB_cKO down vs WT	-1.12765	-6σ	1 D|1	13345	13345	Twist2	twist basic helix-loop-helix transcription factor 2
TC10000016	0.016005	-2.18728	RHEB_cKO down vs WT	-1.12914	-6σ	10 A1|10	670558	670558	H60c	histocompatibility 60c
TC13000021	0.076425	-2.18751	RHEB_cKO down vs WT	-1.12929	-6σ	13 B1|13	114304	114304	Slc28a3	solute carrier family 28 (sodium-coupled nucleoside transporter), member 3
TC10000022	0.02305	-2.18813	RHEB_cKO down vs WT	-1.1297	-6σ	10 B4|10 3	20397	20397	Sgpl1	sphingosine phosphate lyase 1
TC03000024	0.117148	-2.18837	RHEB_cKO down vs WT	-1.12986	-6σ	3 F1|3	68720	68720	Lce1b	late cornified envelope 1B
TC02000002	0.025301	-2.18984	RHEB_cKO down vs WT	-1.13083	-6σ	2 A2-A3|2	67448	67448	Plxdc2	plexin domain containing 2
TC06000012	0.020492	-2.1912	RHEB_cKO down vs WT	-1.13172	-6σ	6|6	71779	71779	March8	membrane-associated ring finger (C3HC4) 8
TC12000019	0.002122	-2.19863	RHEB_cKO down vs WT	-1.13661	-6σ	12 C3|12	66375	66375	Dhrs7	dehydrogenase/reductase (SDR family) member 7
TC08000010	0.000563	-2.20453	RHEB_cKO down vs WT	-1.14047	-6σ	8 C3|8	66887	66887	Lonp2	lon peptidase 2, peroxisomal
TC19000001	0.001804	-2.20736	RHEB_cKO down vs WT	-1.14232	-6σ	19 A|19	225898	225898	Eml3	echinoderm microtubule associated protein like 3
TC15000001	0.000709	-2.20815	RHEB_cKO down vs WT	-1.14284	-6σ	15 B1|15	223431	223431	Tiaf2	TGF-beta1-induced anti-apoptotic factor 2
TC03000028	0.001316	-2.2092	RHEB_cKO down vs WT	-1.14353	-6σ	3 G-H1|3 5	19299	19299	Abcd3	ATP-binding cassette, sub-family D (ALD), member 3
TC05000029	0.011368	-2.21074	RHEB_cKO down vs WT	-1.14453	-6σ	5 F|5	243197	243197	Mfsd7a	major facilitator superfamily domain containing 7A
TC01000009	0.066969	-2.21583	RHEB_cKO down vs WT	-1.14785	-6σ	1 D|1	404545	404545	Ano7	anoctamin 7
TC19000004	0.225603	-2.22127	RHEB_cKO down vs WT	-1.15138	-6σ	19 C1|19	70166	70166	Lipn	lipase, family member N
TC08000023	0.054128	-2.22272	RHEB_cKO down vs WT	-1.15233	-6σ	8 B3.1|8 3	12876	12876	Cpe	carboxypeptidase E
TC01000028	0.029058	-2.22333	RHEB_cKO down vs WT	-1.15272	-6σ	1 D|1	71874	71874	2310007B0	RIKEN cDNA 2310007B03 gene
TC15000000	0.025011	-2.22808	RHEB_cKO down vs WT	-1.1558	-6σ	15 A1|15	223337	223337	Ugt3a2	UDP glycosyltransferases 3 family, polypeptide A2
TC13000006	0.038675	-2.23245	RHEB_cKO down vs WT	-1.15863	-6σ	13 B-C1|13	21810	21810	Tgfbi	transforming growth factor, beta induced
TC0X000033	0.011686	-2.23865	RHEB_cKO down vs WT	-1.16263	-6σ	X F5|X	76763	76763	Mospd2	motile sperm domain containing 2
TC11000030	0.000967	-2.24113	RHEB_cKO down vs WT	-1.16423	-6σ	11 B3|11 4	11684	11684	Alox12	arachidonate 12-lipoxygenase
TC05000026	0.258736	-2.24675	RHEB_cKO down vs WT	-1.16784	-6σ	5 E1|5	243083	243083	Tmprss11f	transmembrane protease, serine 11f
TC03000024	0.117025	-2.2468	RHEB_cKO down vs WT	-1.16787	-6σ	3 F1|3	73722	73722	Lce1a2	late cornified envelope 1A2
TC04000038	0.000459	-2.25018	RHEB_cKO down vs WT	-1.17004	-6σ	4 D3|4	68943	68943	Pink1	PTEN induced putative kinase 1
TC01000031	0.006054	-2.25543	RHEB_cKO down vs WT	-1.1734	-6σ	1 E4|1 58.	12227	12227	Btg2	B cell translocation gene 2, anti-proliferative
TC04000032	0.012275	-2.2603	RHEB_cKO down vs WT	-1.17652	-6σ	---	---	---	Gm12818	predicted gene 12818
TC19000012	0.00886	-2.26083	RHEB_cKO down vs WT	-1.17685	-6σ	19 B|19 13	26358	26358	Aldh1a7	aldehyde dehydrogenase family 1, subfamily A7
TC09000007	0.223887	-2.26252	RHEB_cKO down vs WT	-1.17793	-6σ	9 B|9 31.6	13070	13070	Cyp11a1	cytochrome P450, family 11, subfamily a, polypeptide 1
TC14000013	0.007693	-2.26509	RHEB_cKO down vs WT	-1.17957	-6σ	14 E5|14	69634	69634	Clybl	citrate lyase beta like
TC03000008	0.190048	-2.26678	RHEB_cKO down vs WT	-1.18064	-6σ	3 F2.1|3	381457	381457	Crnn	cornulin
TC09000026	0.014428	-2.26811	RHEB_cKO down vs WT	-1.18149	-6σ	9 D|9	64008	64008	Aqp9	aquaporin 9
TC04000019	0.014481	-2.26888	RHEB_cKO down vs WT	-1.18198	-6σ	4 E2|4	67087	67087	Ctnnbip1	catenin beta interacting protein 1
TC08000004	0.0011	-2.26926	RHEB_cKO down vs WT	-1.18222	-6σ	8 A4|8	244416	244416	Ppp1r3b	protein phosphatase 1, regulatory (inhibitor) subunit 3B
TC19000010	0.070469	-2.27195	RHEB_cKO down vs WT	-1.18393	-6σ	19 A|19	22287	22287	Scgb1a1	secretoglobin, family 1A, member 1 (uteroglobin)
TC14000020	0.017752	-2.27209	RHEB_cKO down vs WT	-1.18402	-6σ	14 C2|14	29811	29811	Ndrg2	N-myc downstream regulated gene 2
TC03000011	0.019457	-2.273	RHEB_cKO down vs WT	-1.1846	-6σ	3 F2.3|3	72121	72121	Dennd2d	DENN/MADD domain containing 2D
TC03000024	0.024508	-2.27622	RHEB_cKO down vs WT	-1.18664	-6σ	3 F2.1|3	545551	545551	BC021767	cingulin pseudogene
TC03000024	0.15926	-2.27815	RHEB_cKO down vs WT	-1.18787	-6σ	3 F1|3	76585	76585	Lce1i	late cornified envelope 1I
TC03000021	0.201969	-2.28325	RHEB_cKO down vs WT	-1.19109	-6σ	3 E1|3	109222	109222	Rarres1	retinoic acid receptor responder (tazarotene induced) 1
TC16000016	0.054399	-2.2896	RHEB_cKO down vs WT	-1.1951	-6σ	16 B5|16	433022	433022	Plcxd2	phosphatidylinositol-specific phospholipase C, X domain containing 2
TC03000024	0.041812	-2.29304	RHEB_cKO down vs WT	-1.19726	-6σ	---	---	---	Gm15264	predicted gene 15264
TC03000015	0.009426	-2.29666	RHEB_cKO down vs WT	-1.19954	-6σ	3 H4|3	433667	433667	Ankrd13c	ankyrin repeat domain 13c
TC03000004	0.019484	-2.29747	RHEB_cKO down vs WT	-1.20005	-6σ	3 D|3	67758	67758	Aadac	arylacetamide deacetylase (esterase)
TC04000014	0.000287	-2.29762	RHEB_cKO down vs WT	-1.20014	-6σ	4 D2.2|4	230726	230726	Rhbdl2	rhomboid, veinlet-like 2 (Drosophila)
TC11000027	0.038189	-2.29779	RHEB_cKO down vs WT	-1.20025	-6σ	---	---	---	Gm12220	predicted gene 12220
TC03000023	0.111396	-2.30765	RHEB_cKO down vs WT	-1.20643	-6σ	3|3	78382	78382	Lce6a	late cornified envelope 6A
TC03000023	0.124619	-2.30782	RHEB_cKO down vs WT	-1.20653	-6σ	3 F1|3 40.	16447	16447	Ivl	involucrin
TC07000004	0.019862	-2.31655	RHEB_cKO down vs WT	-1.21198	-6σ	7 A3|7 14.	13088	13088	Cyp2b10	cytochrome P450, family 2, subfamily b, polypeptide 10
TC09000011	0.074425	-2.31664	RHEB_cKO down vs WT	-1.21204	-6σ	9|9 E3.2	23959	23959	Nt5e	5' nucleotidase, ecto
TC16000020	0.012356	-2.3182	RHEB_cKO down vs WT	-1.21301	-6σ	16 C3.3|16	69699	69699	2310079G	RIKEN cDNA 2310079G19 gene
TC11000012	0.006744	-2.32196	RHEB_cKO down vs WT	-1.21534	-6σ	11|11 B5	217026	217026	Heatr6	HEAT repeat containing 6
TC01000029	0.005462	-2.3316	RHEB_cKO down vs WT	-1.22132	-6σ	1|1 E2	72999	72999	Insig2	insulin induced gene 2
TC03000008	0.007072	-2.33574	RHEB_cKO down vs WT	-1.22388	-6σ	3 F2.1|3 40	20342	20342	Selenbp2	selenium binding protein 2
TC13000019	0.076949	-2.33606	RHEB_cKO down vs WT	-1.22408	-6σ	---	---	---	Hsp25-ps1	heat shock protein 25, pseudogene 1
TC01000022	8.72E-05	-2.3406	RHEB_cKO down vs WT	-1.22688	-6σ	1|1 B	53945	53945	Slc40a1	solute carrier family 40 (iron-regulated transporter), member 1
TC03000004	0.002509	-2.34142	RHEB_cKO down vs WT	-1.22738	-6σ	3 E1|3	622434	622434	Arhgef26	Rho guanine nucleotide exchange factor (GEF) 26
TC05000009	0.010058	-2.34319	RHEB_cKO down vs WT	-1.22848	-6σ	5 E4|5	74596	74596	Cds1	CDP-diacylglycerol synthase 1
TC02000011	0.042796	-2.34338	RHEB_cKO down vs WT	-1.22859	-6σ	2|2 D	70599	70599	Ssfa2	sperm specific antigen 2
TC06000032	0.002066	-2.34361	RHEB_cKO down vs WT	-1.22873	-6σ	6 F3|6	677440	677440	Clec2j	C-type lectin domain family 2, member J
TC19000001	0.010439	-2.34841	RHEB_cKO down vs WT	-1.23169	-6σ	19 A|19	225845	225845	Pla2g16	phospholipase A2, group XVI
TC01000027	0.007468	-2.35304	RHEB_cKO down vs WT	-1.23452	-6σ	1 C5|1	71781	71781	Slc16a14	solute carrier family 16 (monocarboxylic acid transporters), member 14
TC0X000026	0.028648	-2.35438	RHEB_cKO down vs WT	-1.23535	-6σ	X C3|X	236900	236900	Pdk3	pyruvate dehydrogenase kinase, isoenzyme 3
TC10000007	0.005943	-2.35702	RHEB_cKO down vs WT	-1.23697	-6σ	10 C1|10 3	216136	216136	Ilvbl	ilvB (bacterial acetolactate synthase)-like
TC06000004	0.00253	-2.35801	RHEB_cKO down vs WT	-1.23757	-6σ	6 B2.1|6	76263	76263	Gstk1	glutathione S-transferase kappa 1
TC04000011	0.000481	-2.36699	RHEB_cKO down vs WT	-1.24305	-6σ	4 D1|4	639774	639774	Skint8	selection and upkeep of intraepithelial T cells 8
TC06000018	0.009913	-2.36726	RHEB_cKO down vs WT	-1.24322	-6σ	6 A1|6 1.9	269823	269823	Pon3	paraoxonase 3
TC08000020	0.093352	-2.37017	RHEB_cKO down vs WT	-1.24499	-6σ	8|8 B1.1	71908	71908	Cldn23	claudin 23
TC09000019	0.057442	-2.37257	RHEB_cKO down vs WT	-1.24645	-6σ	9 A4|9	244757	244757	Glb1l2	galactosidase, beta 1-like 2
TC02000004	0.056944	-2.37495	RHEB_cKO down vs WT	-1.2479	-6σ	2 A3|2	69454	69454	Clic3	chloride intracellular channel 3
TC15000012	0.007333	-2.37716	RHEB_cKO down vs WT	-1.24924	-6σ	15|15 A2	75646	75646	Rai14	retinoic acid induced 14
TC04000041	0.022645	-2.38227	RHEB_cKO down vs WT	-1.25234	-6σ	4 E2|4 87.	83771	83771	Tas1r3	taste receptor, type 1, member 3
TC09000012	0.020447	-2.385	RHEB_cKO down vs WT	-1.25399	-6σ	9 E3.3|9 5	19660	19660	Rbp2	retinol binding protein 2, cellular
TC11000034	0.01665	-2.38562	RHEB_cKO down vs WT	-1.25437	-6σ	11 C|11	77864	77864	Ypel2	yippee-like 2 (Drosophila)
TC19000004	0.016502	-2.3865	RHEB_cKO down vs WT	-1.25489	-6σ	19 C1|19 2	17330	17330	Minpp1	multiple inositol polyphosphate histidine phosphatase 1
TC06000012	0.006847	-2.38663	RHEB_cKO down vs WT	-1.25498	-6σ	6 E3|6 52.	108960	108960	Irak2	interleukin-1 receptor-associated kinase 2
TC13000003	0.013251	-2.38826	RHEB_cKO down vs WT	-1.25596	-6σ	---	---	---	Gm11379	predicted gene 11379
TC04000010	0.078529	-2.38975	RHEB_cKO down vs WT	-1.25686	-6σ	4 C6|4 49.	67916	67916	Plpp3	phospholipid phosphatase 3
TC09000018	0.017397	-2.40396	RHEB_cKO down vs WT	-1.26541	-6σ	9|9 A4	94226	94226	S1pr5	sphingosine-1-phosphate receptor 5
TC03000011	0.007855	-2.40592	RHEB_cKO down vs WT	-1.26659	-6σ	3 F2.3|3	14866	14866	Gstm5	glutathione S-transferase, mu 5
TC17000016	0.041283	-2.40605	RHEB_cKO down vs WT	-1.26667	-6σ	17 A3.3|17	69259	69259	Kctd5	potassium channel tetramerisation domain containing 5
TC08000024	0.018991	-2.4081	RHEB_cKO down vs WT	-1.2679	-6σ	8 B3.3|8	382014	382014	Ano8	anoctamin 8
TC19000016	0.006414	-2.41128	RHEB_cKO down vs WT	-1.2698	-6σ	19 D2|19 5	14732	14732	Gpam	glycerol-3-phosphate acyltransferase, mitochondrial
TC04000016	0.028882	-2.41338	RHEB_cKO down vs WT	-1.27106	-6σ	4 D3|4 67.	230828	230828	Il22ra1	interleukin 22 receptor, alpha 1
TC04000011	0.003855	-2.41943	RHEB_cKO down vs WT	-1.27467	-6σ	4 C7|4	69908	69908	Rab3b	RAB3B, member RAS oncogene family
TC03000024	0.139369	-2.42574	RHEB_cKO down vs WT	-1.27842	-6σ	3 F1|3	545547	545547	Lce1j	late cornified envelope 1J

TC07000021	0.012098	-2.42853	RHEB_cKO down vs WT	-1.28008	-6σ	7 F5|7	1.01E+08	1.01E+08	Bc1	brain cytoplasmic RNA 1
TC1000001	0.045753	-2.43004	RHEB_cKO down vs WT	-1.28098	-6σ	10|10 A2	56016	56016	Hebp2	heme binding protein 2
TC1400002	0.013856	-2.43305	RHEB_cKO down vs WT	-1.28276	-6σ	14 D2|14	268759	268759	9930012K	RIKEN cDNA 9930012K11 gene
TC0400001	0.005782	-2.43659	RHEB_cKO down vs WT	-1.28486	-6σ	4|4 E1	71890	71890	Mad2l2	MAD2 mitotic arrest deficient-like 2
TC04000011	0.005248	-2.44088	RHEB_cKO down vs WT	-1.2874	-6σ	4 D1|4	320640	320640	Skint4	selection and upkeep of intraepithelial T cells 4
TC1500000	0.384561	-2.4441	RHEB_cKO down vs WT	-1.2893	-6σ	15 B3.1|1	107587	107587	Osr2	odd-skipped related 2
TC0500001	0.014474	-2.44613	RHEB_cKO down vs WT	-1.2905	-6σ	5 F|5 57.8	57816	57816	Tesc	tescalcin
TC0400001	0.008696	-2.44879	RHEB_cKO down vs WT	-1.29207	-6σ	4 D3|4 68.	71665	71665	Fuca1	fucosidase, alpha-L- 1, tissue
TC0X00000	0.000749	-2.45248	RHEB_cKO down vs WT	-1.29424	-6σ	X|X C2	71584	71584	Gdpd2	glycerophosphodiester phosphodiesterase domain containing 2
TC1000002	0.002797	-2.46018	RHEB_cKO down vs WT	-1.29876	-6σ	10 B2|10	11630	11630	Aim1	absent in melanoma 1
TC0500000	0.001805	-2.46186	RHEB_cKO down vs WT	-1.29975	-6σ	5 B1|5	80911	80911	Acox3	acyl-Coenzyme A oxidase 3, pristanoyl
TC0300002	0.088657	-2.46822	RHEB_cKO down vs WT	-1.30347	-6σ	3 F1|3	67127	67127	Lce1a1	late cornified envelope 1A1
TC0X000021	0.033949	-2.46985	RHEB_cKO down vs WT	-1.30442	-6σ	X A4|X	208884	208884	Zdhhc9	zinc finger, DHHC domain containing 9
TC0600003	0.039421	-2.47301	RHEB_cKO down vs WT	-1.30627	-6σ	6 A1|6	170772	170772	Glcci1	glucocorticoid induced transcript 1
TC0700000	0.001934	-2.48552	RHEB_cKO down vs WT	-1.31355	-6σ	---	---	---	Gm14377	predicted gene 14377
TC1000002	0.003413	-2.48562	RHEB_cKO down vs WT	-1.31361	-6σ	10 C1|10	27375	27375	Tjp3	tight junction protein 3
TC0500002	0.105186	-2.4868	RHEB_cKO down vs WT	-1.31429	-6σ	5|5 D	16924	16924	Lnx1	ligand of numb-protein X 1
TC1100003	0.000877	-2.48804	RHEB_cKO down vs WT	-1.31501	-6σ	---	---	---	Gm11611	predicted gene 11611
TC0400003	0.005998	-2.48839	RHEB_cKO down vs WT	-1.31521	-6σ	4 D1|4	230612	230612	Slc5a9	solute carrier family 5 (sodium/glucose cotransporter), member 9
TC0900000	0.002441	-2.49209	RHEB_cKO down vs WT	-1.31735	-6σ	9 A5.2|9	59095	59095	Fxyd6	FXYD domain-containing ion transport regulator 6
TC0700000	0.00636	-2.50216	RHEB_cKO down vs WT	-1.32317	-6σ	7 B2|7	245886	245886	Ankrd27	ankyrin repeat domain 27 (VPS9 domain)
TC1100000	0.009222	-2.50944	RHEB_cKO down vs WT	-1.32736	-6σ	11|11 A4	216616	216616	Efemp1	epidermal growth factor-containing fibulin-like extracellular matrix protein 1
TC0300000	0.014518	-2.51599	RHEB_cKO down vs WT	-1.33113	-6σ	3|3	1E+08	1E+08	Sprr2a2	small proline-rich protein 2A2
TC0300002	0.025319	-2.53783	RHEB_cKO down vs WT	-1.34359	-6σ	3 F2.1|3 4	70737	70737	Cgn	cingulin
TC04000011	0.02117	-2.54007	RHEB_cKO down vs WT	-1.34487	-6σ	4 D1|4	639781	639781	Skint1	selection and upkeep of intraepithelial T cells 1
TC0300000	0.003747	-2.54401	RHEB_cKO down vs WT	-1.3471	-6σ	3 F2.1|3 4	20341	20341	Selenbp1	selenium binding protein 1
TC1400001	0.114568	-2.54471	RHEB_cKO down vs WT	-1.3475	-6σ	14|14 D2	67516	67516	Kctd4	potassium channel tetramerisation domain containing 4
TSUnmappe	0.012715	-2.55336	RHEB_cKO down vs WT	-1.3524	-6σ	X;Y|XY 75.	20905	20905	Sts	steroid sulfatase
TC0300002	0.141383	-2.56568	RHEB_cKO down vs WT	-1.35934	-6σ	3 F1|3	69611	69611	Lce1d	late cornified envelope 1D
TC0400000	0.041258	-2.56894	RHEB_cKO down vs WT	-1.36117	-6σ	4 B1|4	666060	666060	Frmpd1	FERM and PDZ domain containing 1
TC14000021	0.352033	-2.57326	RHEB_cKO down vs WT	-1.3636	-6σ	14 C3|14	17227	17227	Mcpt4	mast cell protease 4
TC1300002	0.018032	-2.57371	RHEB_cKO down vs WT	-1.36385	-6σ	13 D1|13	218461	218461	Pde8b	phosphodiesterase 8B
TC1700001	0.029278	-2.57386	RHEB_cKO down vs WT	-1.36393	-6σ	---	---	---	Gm5815	predicted pseudogene 5815
TC0900003	0.009067	-2.57685	RHEB_cKO down vs WT	-1.36561	-6σ	9 F4|9	102566	102566	Ano10	anoctamin 10
TC1100002	0.033412	-2.57857	RHEB_cKO down vs WT	-1.36657	-6σ	11 B1.3|1	30805	30805	Slc22a4	solute carrier family 22 (organic cation transporter), member 4
TC0700001	0.024026	-2.58324	RHEB_cKO down vs WT	-1.36918	-6σ	7 E3|7	207278	207278	Fchsd2	FCH and double SH3 domains 2
TC0100002	0.065807	-2.58443	RHEB_cKO down vs WT	-1.36984	-6σ	---	---	---	Gm8080	predicted gene 8080
TC0900001	0.003637	-2.58463	RHEB_cKO down vs WT	-1.36996	-6σ	9 E2|9	212531	212531	Sh3bgrl2	SH3 domain binding glutamic acid-rich protein like 2
TC0800000	0.000956	-2.58838	RHEB_cKO down vs WT	-1.37205	-6σ	8|8 C1	72281	72281	Sh2d4a	SH2 domain containing 4A
TC0100003	0.021788	-2.60262	RHEB_cKO down vs WT	-1.37997	-6σ	1 E4|1	14270	14270	Srgap2	SLIT-ROBO Rho GTPase activating protein 2
TC0700000	0.049674	-2.61392	RHEB_cKO down vs WT	-1.38622	-6σ	7 B4|7	67893	67893	Tmem86a	transmembrane protein 86A
TC1400002	0.143177	-2.62074	RHEB_cKO down vs WT	-1.38997	-6σ	14 E5|14	56643	56643	Slc15a1	solute carrier family 15 (oligopeptide transporter), member 1
TC16000001	0.01118	-2.62445	RHEB_cKO down vs WT	-1.39202	-6σ	---	74478	74478	Snx29	sorting nexin 29
TC1300002	0.043476	-2.6333	RHEB_cKO down vs WT	-1.39687	-6σ	13 A2|13	21638	21638	Tcrg-V4	T cell receptor gamma, variable 4
TC0900000	0.062307	-2.63534	RHEB_cKO down vs WT	-1.39799	-6σ	9 A5.3|9 2	16173	16173	Il18	interleukin 18
TC0200001	0.005407	-2.64328	RHEB_cKO down vs WT	-1.40233	-6σ	2 F1-F3|2	12010	12010	B2m	beta-2 microglobulin
TC0700002	0.004858	-2.6436	RHEB_cKO down vs WT	-1.4025	-6σ	7 B1|7	320225	320225	Catsperg1	catsper channel auxiliary subunit gamma 1
TC0600003	0.025776	-2.65362	RHEB_cKO down vs WT	-1.40796	-6σ	6 G1|6	67729	67729	Mansc1	MANSC domain containing 1
TC0700004	0.009791	-2.65902	RHEB_cKO down vs WT	-1.41089	-6σ	7 F5|7	71345	71345	Ano9	anoctamin 9
TC0400002	0.017257	-2.6626	RHEB_cKO down vs WT	-1.41284	-6σ	4|4 C1	67103	67103	Ptgr1	prostaglandin reductase 1
TC0100001	0.405785	-2.66285	RHEB_cKO down vs WT	-1.41297	-6σ	1|1 H2	56429	56429	Dpt	dermatopontin
TC0700003	0.002155	-2.6741	RHEB_cKO down vs WT	-1.41905	-6σ	7|7 D1	108116	108116	Slco3a1	solute carrier organic anion transporter family, member 3a1
TC1500000	0.054849	-2.67562	RHEB_cKO down vs WT	-1.41987	-6σ	15 B3.1|1	114128	114128	Laptm4b	lysosomal-associated protein transmembrane 4B
TC0800001	0.089825	-2.67792	RHEB_cKO down vs WT	-1.42111	-6σ	8 C5|8 44.	17390	17390	Mmp2	matrix metallopeptidase 2
TC0100002	0.011474	-2.67869	RHEB_cKO down vs WT	-1.42153	-6σ	1E2.1|1	394252	394252	Serpinb3d	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3D
TC0100002	0.08064	-2.68286	RHEB_cKO down vs WT	-1.42377	-6σ	1 C1.1|1	329154	329154	Ankrd44	ankyrin repeat domain 44
TC0300003	0.015277	-2.68289	RHEB_cKO down vs WT	-1.42379	-6σ	3 H2|3	26377	26377	Dapp1	dual adaptor for phosphotyrosine and 3-phosphoinositides 1
TC0300002	0.128197	-2.68502	RHEB_cKO down vs WT	-1.42493	-6σ	3 F1|3	68694	68694	Lce1e	late cornified envelope 1E
TC0400003	0.0098	-2.69633	RHEB_cKO down vs WT	-1.431	-6σ	---	---	---	Gm12736	predicted gene 12736
TC0200000	0.048306	-2.69736	RHEB_cKO down vs WT	-1.43155	-6σ	2 B|2	108897	108897	Aif1l	allograft inflammatory factor 1-like
TC0800000	0.024334	-2.69822	RHEB_cKO down vs WT	-1.43201	-6σ	8|8 B3.2	71306	71306	Mfap3l	microfibrillar-associated protein 3-like
TC0400003	0.0053	-2.70302	RHEB_cKO down vs WT	-1.43457	-6σ	4 E1|4 72.	18599	18599	Padi1	peptidyl arginine deiminase, type I
TC1800000	0.009608	-2.7037	RHEB_cKO down vs WT	-1.43493	-6σ	18 B2|18	240215	240215	Slc4a9	solute carrier family 4, sodium bicarbonate cotransporter, member 9
TC0700003	0.059775	-2.71214	RHEB_cKO down vs WT	-1.43943	-6σ	---	---	---	Gm23233	predicted gene, 23233
TC0500000	1.27E-05	-2.71625	RHEB_cKO down vs WT	-1.44162	-6σ	5|5 E4	231532	231532	Arhgap24	Rho GTPase activating protein 24
TC0200001	0.016777	-2.72224	RHEB_cKO down vs WT	-1.44479	-6σ	2 E5|2	96957	96957	Tmem62	transmembrane protein 62
TC1500001	0.011302	-2.72718	RHEB_cKO down vs WT	-1.44741	-6σ	15 E|15 3	17939	17939	Naga	N-acetyl galactosaminidase, alpha
TC1500001	0.010494	-2.73701	RHEB_cKO down vs WT	-1.4526	-6σ	15 E1|15	239559	239559	A4galt	alpha 1,4-galactosyltransferase
TC1100000	0.018628	-2.74095	RHEB_cKO down vs WT	-1.45468	-6σ	11 A1|11	237625	237625	Pla2g3	phospholipase A2, group III
TC0300002	0.012785	-2.74528	RHEB_cKO down vs WT	-1.45695	-6σ	3 F2.3|3	69206	69206	2010016I1	RIKEN cDNA 2010016I18 gene
TC1200002	0.052173	-2.75666	RHEB_cKO down vs WT	-1.46292	-6σ	12 E|12	71907	71907	Serpina9	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitr
TC0400003	0.015269	-2.77088	RHEB_cKO down vs WT	-1.47035	-6σ	4|4	77173	77173	8030443G	RIKEN cDNA 8030443G20 gene
TC0900001	0.02943	-2.77602	RHEB_cKO down vs WT	-1.47302	-6σ	---	---	---	Gm26870	predicted gene, 26870
TC1100001	0.003727	-2.77753	RHEB_cKO down vs WT	-1.4738	-6σ	---	---	---	Gm26888	predicted gene, 26888
TC0500002	0.001749	-2.78056	RHEB_cKO down vs WT	-1.47538	-6σ	5|5 E3	67111	67111	Naaa	N-acylethanolamine acid amidase
TC0700004	0.050403	-2.78179	RHEB_cKO down vs WT	-1.47601	-6σ	7 F5|7	54123	54123	Irf7	interferon regulatory factor 7
TC1200001	0.039326	-2.78365	RHEB_cKO down vs WT	-1.47698	-6σ	12 C1|12	112407	112407	Egln3	egl-9 family hypoxia-inducible factor 3
TC0200002	0.076473	-2.7852	RHEB_cKO down vs WT	-1.47778	-6σ	2 H1|2	545481	545481	Arhgap40	Rho GTPase activating protein 40
TC0X00002	0.018632	-2.79746	RHEB_cKO down vs WT	-1.48412	-6σ	X|X A4	70380	70380	Mospd1	motile sperm domain containing 1
TC0700000	0.009414	-2.80455	RHEB_cKO down vs WT	-1.48777	-6σ	7 A3|7	13107	13107	Cyp2f2	cytochrome P450, family 2, subfamily f, polypeptide 2
TC1000000	0.01534	-2.81232	RHEB_cKO down vs WT	-1.49176	-6σ	10 A4|10	52665	52665	Echdc1	enoyl Coenzyme A hydratase domain containing 1
TC0200004	0.001965	-2.82078	RHEB_cKO down vs WT	-1.49609	-6σ	2|2 H2	59038	59038	Pxmp4	peroxisomal membrane protein 4
TC1600001	0.077676	-2.82799	RHEB_cKO down vs WT	-1.49978	-6σ	16 B4|16	207798	207798	Gramd1c	GRAM domain containing 1C
TC0X00000	0.000785	-2.82839	RHEB_cKO down vs WT	-1.49998	-6σ	X C3|X 42.	15203	15203	Heph	hephaestin
TC0500000	0.004114	-2.82845	RHEB_cKO down vs WT	-1.50001	-6σ	5 A2|5	108151	108151	Sema3d	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (ser
TC1000001	0.002271	-2.84893	RHEB_cKO down vs WT	-1.51042	-6σ	10 A1|10	64009	64009	Syne1	spectrin repeat containing, nuclear envelope 1
TC0800001	0.097073	-2.85413	RHEB_cKO down vs WT	-1.51305	-6σ	8|8 A3	75767	75767	Rab11fip1	RAB11 family interacting protein 1 (class I)
TC1500001	0.006327	-2.85678	RHEB_cKO down vs WT	-1.51439	-6σ	15 D3|15	106068	106068	Slc45a4	solute carrier family 45, member 4
TC1100003	0.023873	-2.85732	RHEB_cKO down vs WT	-1.51466	-6σ	11 C|11 5	20305	20305	Ccl6	chemokine (C-C motif) ligand 6

TC0600001	0.019652	-2.88287	RHEB_cKO down vs WT	-1.52751	-6σ	6 E3|6 53.	212541	212541	Rho	rhodopsin
TC0400001	0.011496	-2.88946	RHEB_cKO down vs WT	-1.5308	-6σ	4 C6|4 47.	13131	13131	Dab1	disabled 1
TC0900001	0.028388	-2.89241	RHEB_cKO down vs WT	-1.53227	-6σ	9 E1|9 43.	17920	17920	Myo6	myosin VI
TC1600002	0.066462	-2.90791	RHEB_cKO down vs WT	-1.53998	-6σ	---	---	---	2310043M	RIKEN cDNA 2310043M15 gene
TC1700000	0.340647	-2.90864	RHEB_cKO down vs WT	-1.54034	-6σ	17 A3.3|1	17229	17229	Tpsb2	tryptase beta 2
TC0300002	0.094665	-2.91922	RHEB_cKO down vs WT	-1.54558	-6σ	3 F1|3	67718	67718	Lce1h	late cornified envelope 1H
TC1300000	0.022106	-2.93163	RHEB_cKO down vs WT	-1.5517	-6σ	13 A3.1|1	14756	14756	Gpld1	glycosylphosphatidylinositol specific phospholipase D1
TC0100000	0.047144	-2.93777	RHEB_cKO down vs WT	-1.55472	-6σ	1 c1|1 28.	71872	71872	Aox4	aldehyde oxidase 4
TC0100002	0.095078	-2.95484	RHEB_cKO down vs WT	-1.56308	-6σ	1 E2.1|1	20248	20248	Serpinb3a	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3A
TC1800001	0.051673	-2.97274	RHEB_cKO down vs WT	-1.5718	-6σ	18 E3|18	66255	66255	Hsbp1l1	heat shock factor binding protein 1-like 1
TC1700001	0.004772	-2.97279	RHEB_cKO down vs WT	-1.57182	-6σ	---	---	---	Gm8597	predicted gene 8597
TC1000001	0.02658	-2.97343	RHEB_cKO down vs WT	-1.57213	-6σ	10|10 6.6	1.01E+08	1.01E+08	Gm20125	predicted gene, 20125
TC0300002	0.005068	-2.97931	RHEB_cKO down vs WT	-1.57498	-6σ	3|3 G3	99887	99887	Tmem56	transmembrane protein 56
TC0X00003	0.099853	-2.98038	RHEB_cKO down vs WT	-1.57549	-6σ	X F5|X 77.	54156	54156	Egfl6	EGF-like-domain, multiple 6
TC1700002	0.004587	-2.98216	RHEB_cKO down vs WT	-1.57636	-6σ	17 D|17	171168	171168	Acer1	alkaline ceramidase 1
TC0500002	0.002897	-2.98539	RHEB_cKO down vs WT	-1.57792	-6σ	5 C3.1|5	11980	11980	Atp8a1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1
TC0300000	0.041905	-2.99139	RHEB_cKO down vs WT	-1.58081	-6σ	---	1.03E+08	1.03E+08	Gm35439	predicted gene, 35439
TC0400000	0.019779	-2.99479	RHEB_cKO down vs WT	-1.58246	-6σ	4 A5|4	230085	230085	Phf24	PHD finger protein 24
TC1100003	0.061768	-2.99611	RHEB_cKO down vs WT	-1.58309	-6σ	11 C|11	74617	74617	Scpep1	serine carboxypeptidase 1
TC0400001	0.010744	-2.99708	RHEB_cKO down vs WT	-1.58356	-6σ	4 C7|4	230598	230598	Nrd1	nardilysin, N-arginine dibasic convertase, NRD convertase 1
TC1500000	0.049913	-3.00334	RHEB_cKO down vs WT	-1.58657	-6σ	15 B1|15	66270	66270	Fam134b	family with sequence similarity 134, member B
TC1500000	0.025176	-3.00364	RHEB_cKO down vs WT	-1.58671	-6σ	15|15 E3	116939	116939	Pnpla3	patatin-like phospholipase domain containing 3
TC0600002	0.032531	-3.01202	RHEB_cKO down vs WT	-1.59073	-6σ	6|6 27.26	110175	110175	Ggct	gamma-glutamyl cyclotransferase
TC0400001	0.002943	-3.02033	RHEB_cKO down vs WT	-1.59471	-6σ	4 D1|4	328505	328505	Skint7	selection and upkeep of intraepithelial T cells 7
TC1100003	0.017783	-3.02462	RHEB_cKO down vs WT	-1.59676	-6σ	11 D|11	66708	66708	Krtap3-2	keratin associated protein 3-2
TC1400000	0.008485	-3.02669	RHEB_cKO down vs WT	-1.59774	-6σ	14 C1|14	54159	54159	Rnase2b	ribonuclease, RNase A family, 2B (liver, eosinophil-derived neurotoxin)
TC0900001	0.043741	-3.02804	RHEB_cKO down vs WT	-1.59838	-6σ	9 D|9	235493	235493	Fam214a	family with sequence similarity 214, member A
TC1900001	0.0025	-3.03161	RHEB_cKO down vs WT	-1.60008	-6σ	19 B|19	381217	381217	Fam189a2	family with sequence similarity 189, member A2
TC1600001	0.016099	-3.03311	RHEB_cKO down vs WT	-1.6008	-6σ	16 B5|16	212998	212998	BC016579	cDNA sequence, BC016579
TC1000002	0.017533	-3.03345	RHEB_cKO down vs WT	-1.60096	-6σ	10 C1|10	216190	216190	Appl2	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper c
TC1100000	0.028654	-3.03497	RHEB_cKO down vs WT	-1.60168	-6σ	11 A5|11	319767	319767	Atp10b	ATPase, class V, type 10B
TC0400003	0.021126	-3.03712	RHEB_cKO down vs WT	-1.6027	-6σ	4 D2.2|4	69780	69780	Smap2	small ArfGAP 2
TC0700004	0.005174	-3.04309	RHEB_cKO down vs WT	-1.60554	-6σ	7|7 F5	12176	12176	Bnip3	BCL2/adenovirus E1B interacting protein 3
TC0500000	0.055863	-3.04924	RHEB_cKO down vs WT	-1.60845	-6σ	5 B1|5	665270	665270	Plb1	phospholipase B1
TC0100001	0.077676	-3.0706	RHEB_cKO down vs WT	-1.61852	-6σ	1|1 D	116872	116872	Serpinb7	serine (or cysteine) peptidase inhibitor, clade B, member 7
TC1200001	0.045867	-3.07444	RHEB_cKO down vs WT	-1.62032	-6σ	12|12 A3	68775	68775	Atp6v1c2	ATPase, H+ transporting, lysosomal V1 subunit C2
TC1700002	0.039971	-3.08456	RHEB_cKO down vs WT	-1.62507	-6σ	17 B3|17	78249	78249	Adgrf4	adhesion G protein-coupled receptor F4
TC1300000	0.043518	-3.08579	RHEB_cKO down vs WT	-1.62564	-6σ	---	---	---	Gm11295	predicted gene 11295
TC0400002	0.003315	-3.09478	RHEB_cKO down vs WT	-1.62984	-6σ	4 A1|4	242285	242285	Sdr16c5	short chain dehydrogenase/reductase family 16C, member 5
TC0400003	0.002584	-3.09788	RHEB_cKO down vs WT	-1.63128	-6σ	4 D1|4	242627	242627	Skint5	selection and upkeep of intraepithelial T cells 5
TC0300002	0.086813	-3.0983	RHEB_cKO down vs WT	-1.63148	-6σ	3 F2|3	66203	66203	Lce1m	late cornified envelope 1M
TC1100001	0.003746	-3.1	RHEB_cKO down vs WT	-1.63227	-6σ	---	---	---	Gm11433	predicted gene 11433
TC0X00002	0.118286	-3.11986	RHEB_cKO down vs WT	-1.64148	-6σ	X E3|X	331524	331524	Xkrx	X-linked Kx blood group related, X-linked
TC0100003	0.003637	-3.12612	RHEB_cKO down vs WT	-1.64437	-6σ	1 B|1	78321	78321	Ankrd23	ankyrin repeat domain 23
TC1100000	0.061186	-3.14001	RHEB_cKO down vs WT	-1.65077	-6σ	11 A1|11	75219	75219	Dusp18	dual specificity phosphatase 18
TC1300000	0.009981	-3.17431	RHEB_cKO down vs WT	-1.66644	-6σ	13 A1|13	17101	17101	Lyst	lysosomal trafficking regulator
TC0200004	0.020565	-3.21598	RHEB_cKO down vs WT	-1.68526	-6σ	2 E3|2 54.	12359	12359	Cat	catalase
TC0900001	0.018413	-3.21774	RHEB_cKO down vs WT	-1.68605	-6σ	9 F3|9	73748	73748	Gadl1	glutamate decarboxylase-like 1
TC1300002	0.020443	-3.23537	RHEB_cKO down vs WT	-1.69393	-6σ	---	1.03E+08	1.03E+08	Gm32089	predicted gene, 32089
TC1100001	0.005254	-3.25924	RHEB_cKO down vs WT	-1.70454	-6σ	11 E2|11	69602	69602	Otop3	otopetrin 3
TC0X00002	0.110937	-3.26358	RHEB_cKO down vs WT	-1.70645	-6σ	X|X C2	57385	57385	P2ry4	pyrimidinergic receptor P2Y, G-protein coupled, 4
TC0500000	0.047562	-3.26421	RHEB_cKO down vs WT	-1.70674	-6σ	5 B3|5	76943	76943	Psapl1	prosaposin-like 1
TC0400000	0.045243	-3.26937	RHEB_cKO down vs WT	-1.70901	-6σ	4 A3|4	14590	14590	Ggh	gamma-glutamyl hydrolase
TC0300001	0.015824	-3.27731	RHEB_cKO down vs WT	-1.71251	-6σ	---	---	---	Adh6b	alcohol dehydrogenase 6B (class V)
TC1300002	0.007206	-3.29474	RHEB_cKO down vs WT	-1.72017	-6σ	13 D1|13	15212	15212	Hexb	hexosaminidase B
TC0700003	0.008972	-3.30219	RHEB_cKO down vs WT	-1.72342	-6σ	7 D3|7	65098	65098	Zfand6	zinc finger, AN1-type domain 6
TC1500001	0.122902	-3.30657	RHEB_cKO down vs WT	-1.72533	-6σ	15 D3|15	57277	57277	Slurp1	secreted Ly6/Plaur domain containing 1
TC1400002	0.008075	-3.30877	RHEB_cKO down vs WT	-1.72629	-6σ	14 C3|14	68631	68631	Cryl1	crystallin, lambda 1
TC0900003	0.004505	-3.31859	RHEB_cKO down vs WT	-1.73057	-6σ	---	---	---	Gm26797	predicted gene, 26797
TC0200004	0.003884	-3.33254	RHEB_cKO down vs WT	-1.73662	-6σ	2 F3|2	74182	74182	Gpcpd1	glycerophosphocholine phosphodiesterase 1
TC1100000	0.020193	-3.33523	RHEB_cKO down vs WT	-1.73779	-6σ	11 A1|11	626870	626870	Gm11992	predicted gene 11992
TC1100000	0.045612	-3.35112	RHEB_cKO down vs WT	-1.74464	-6σ	11 A4|11	20868	20868	Stk10	serine/threonine kinase 10
TC1200002	0.049123	-3.35679	RHEB_cKO down vs WT	-1.74708	-6σ	12|12 F1	94040	94040	Clmn	calmin
TC0600002	0.019643	-3.37954	RHEB_cKO down vs WT	-1.75683	-6σ	6 B3|6	107569	107569	Nt5c3	5'-nucleotidase, cytosolic III
TC1200000	0.016064	-3.41452	RHEB_cKO down vs WT	-1.77168	-6σ	12 A1.3|1	67216	67216	Mboat2	membrane bound O-acyltransferase domain containing 2
TSUnmappe	0.020697	-3.42105	RHEB_cKO down vs WT	-1.77444	-6σ	---	74478	74478	Snx29	sorting nexin 29
TC1600001	0.08777	-3.44002	RHEB_cKO down vs WT	-1.78242	-6σ	16 B1|16	625123	625123	Gm6557	predicted gene 6557
TC0600000	0.0026	-3.44459	RHEB_cKO down vs WT	-1.78433	-6σ	6 B1|6	208665	208665	Akr1d1	aldo-keto reductase family 1, member D1
TC0200002	0.003246	-3.44931	RHEB_cKO down vs WT	-1.78631	-6σ	2 H1|2	71878	71878	Fam83d	family with sequence similarity 83, member D
TC0200001	0.075035	-3.45878	RHEB_cKO down vs WT	-1.79026	-6σ	2 E5|2	623781	623781	Gm14137	predicted gene 14137
TC0400003	0.002778	-3.46712	RHEB_cKO down vs WT	-1.79374	-6σ	4 D2.2|4 6	14622	14622	Gjb5	gap junction protein, beta 5
TC1400002	0.026058	-3.48365	RHEB_cKO down vs WT	-1.8006	-6σ	14 C2|14	214922	214922	Slc39a2	solute carrier family 39 (zinc transporter), member 2
TC1300002	0.01683	-3.48685	RHEB_cKO down vs WT	-1.80192	-6σ	13 C1|13	74338	74338	Slc6a19	solute carrier family 6 (neurotransmitter transporter), member 19
TC1500000	0.00297	-3.48808	RHEB_cKO down vs WT	-1.80243	-6σ	15 B1|15	11732	11732	Ank	progressive ankylosis
TC0300002	0.017354	-3.50069	RHEB_cKO down vs WT	-1.80764	-6σ	3 F1|3	545541	545541	Gm5849	predicted gene 5849
TC0900000	0.01335	-3.50602	RHEB_cKO down vs WT	-1.80984	-6σ	9 A1|9 2.4	12362	12362	Casp1	caspase 1
TC0X00002	0.03236	-3.51034	RHEB_cKO down vs WT	-1.81161	-6σ	X|X	74305	74305	1700111N	RIKEN cDNA 1700111N16 gene
TC1700001	0.029869	-3.51148	RHEB_cKO down vs WT	-1.81208	-6σ	17 E4|17	13819	13819	Epas1	endothelial PAS domain protein 1
TC0300002	0.014121	-3.53484	RHEB_cKO down vs WT	-1.82165	-6σ	3 F2.1|3 4	13601	13601	Ecm1	extracellular matrix protein 1
TC0300001	0.442133	-3.57185	RHEB_cKO down vs WT	-1.83667	-6σ	3 A2|3 6.2	12873	12873	Cpa3	carboxypeptidase A3, mast cell
TC1200002	0.056683	-3.59153	RHEB_cKO down vs WT	-1.8446	-6σ	12|12 F1	68054	68054	Serpina12	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitr
TC0500003	0.005037	-3.62522	RHEB_cKO down vs WT	-1.85807	-6σ	5 G2|5	330217	330217	Gal3st4	galactose-3-O-sulfotransferase 4
TC1900000	0.111567	-3.71028	RHEB_cKO down vs WT	-1.89153	-6σ	19 C1|19	240633	240633	Lipk	lipase, family member K
TC0500002	0.053328	-3.75755	RHEB_cKO down vs WT	-1.90979	-6σ	5 E4|5	15442	15442	Hpse	heparanase
TC1000001	0.012811	-3.77144	RHEB_cKO down vs WT	-1.91512	-6σ	10 D3|10	407790	407790	Ndufa4l2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2
TC1300000	0.355309	-3.80585	RHEB_cKO down vs WT	-1.92822	-6σ	13 A5|13	18295	18295	Ogn	osteoglycin
TC1100002	0.029143	-3.80739	RHEB_cKO down vs WT	-1.9288	-6σ	11 A1|11	12808	12808	Cobl	cordon-bleu WH2 repeat
TC0900002	0.02788	-3.83179	RHEB_cKO down vs WT	-1.93802	-6σ	9|9 B	56857	56857	Slc37a2	solute carrier family 37 (glycerol-3-phosphate transporter), member 2
TC1100003	0.085427	-3.85339	RHEB_cKO down vs WT	-1.94613	-6σ	11 D|11	94179	94179	Krt23	keratin 23

TC03000024	0.054365	-3.87193	RHEB_cKO down vs WT	-1.95305	-6σ	3|3 F2	71790	71790	Anxa9	annexin A9
TC07000004	0.07897	-3.88793	RHEB_cKO down vs WT	-1.959	-6σ	7 A3|7 15.	13090	13090	Cyp2b19	cytochrome P450, family 2, subfamily b, polypeptide 19
TC11000024	0.000592	-3.96062	RHEB_cKO down vs WT	-1.98573	-6σ	11 A4|11	216643	216643	Gabrp	gamma-aminobutyric acid (GABA) A receptor, pi
TC17000003	0.006454	-3.96094	RHEB_cKO down vs WT	-1.98584	-6σ	17 A3.3|17	27410	27410	Abca3	ATP-binding cassette, sub-family A (ABC1), member 3
TC07000029	0.026853	-3.96217	RHEB_cKO down vs WT	-1.98629	-6σ	7 B4|7 29.	50722	50722	Dkkl1	dickkopf-like 1
TC12000010	0.030656	-4.00325	RHEB_cKO down vs WT	-2.00117	-6σ	12 E|12 51	12652	12652	Chga	chromogranin A
TC08000011	0.083968	-4.01199	RHEB_cKO down vs WT	-2.00432	-6σ	8 D3|8	71903	71903	Ces2f	carboxylesterase 2F
TC04000032	0.012381	-4.04952	RHEB_cKO down vs WT	-2.01775	-6σ	4 D1|4	230613	230613	Skint10	selection and upkeep of intraepithelial T cells 10
TC0X000009	0.011144	-4.15559	RHEB_cKO down vs WT	-2.05505	-6σ	X C3|X	245533	245533	Awat1	acyl-CoA wax alcohol acyltransferase 1
TC09000030	0.006445	-4.19241	RHEB_cKO down vs WT	-2.06778	≤ -6σ	9 F1|9 58.	76257	76257	Slc38a3	solute carrier family 38, member 3
TC08000009	0.019544	-4.29258	RHEB_cKO down vs WT	-2.10185	≤ -6σ	8|8 C3	71310	71310	Tbc1d9	TBC1 domain family, member 9
TC04000032	0.004665	-4.48222	RHEB_cKO down vs WT	-2.16421	≤ -6σ	4 D1|4	230622	230622	Skint6	selection and upkeep of intraepithelial T cells 6
TC02000045	0.076472	-4.50337	RHEB_cKO down vs WT	-2.17101	≤ -6σ	2 F|2 62.9	16175	16175	Il1a	interleukin 1 alpha
TC11000007	0.021182	-4.51402	RHEB_cKO down vs WT	-2.17441	≤ -6σ	11 B2|11 3	16515	16515	Kcnj12	potassium inwardly-rectifying channel, subfamily J, member 12
TC04000011	0.014375	-4.55217	RHEB_cKO down vs WT	-2.18655	≤ -6σ	4 D1|4	329919	329919	Skint2	selection and upkeep of intraepithelial T cells 2
TC10000024	0.021549	-4.60782	RHEB_cKO down vs WT	-2.20408	≤ -6σ	10 C1|10	12365	12365	Casp14	caspase 14
TC12000002	0.004303	-4.63035	RHEB_cKO down vs WT	-2.21112	≤ -6σ	---	407816	407816	BC023202	cDNA sequence BC023202
TC11000040	0.035428	-4.70469	RHEB_cKO down vs WT	-2.2341	≤ -6σ	11 E1|11	217265	217265	Abca5	ATP-binding cassette, sub-family A (ABC1), member 5
TC03000008	0.0202	-4.72121	RHEB_cKO down vs WT	-2.23916	≤ -6σ	3 F1|3	1E+08	1E+08	Sprr2a3	small proline-rich protein 2A3
TC08000001	0.021832	-4.73975	RHEB_cKO down vs WT	-2.24481	≤ -6σ	8 A3|8 10.	52123	52123	Agpat5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltrar
TC08000030	0.014767	-4.91304	RHEB_cKO down vs WT	-2.29662	≤ -6σ	8 E1|8	74032	74032	Sdr42e1	short chain dehydrogenase/reductase family 42E, member 1
TC05000005	0.045286	-5.04732	RHEB_cKO down vs WT	-2.33552	≤ -6σ	5 C1|5 28.	20531	20531	Slc34a2	solute carrier family 34 (sodium phosphate), member 2
TC10000023	0.085121	-5.05488	RHEB_cKO down vs WT	-2.33768	≤ -6σ	10|10 B5.3	71733	71733	Susd2	sushi domain containing 2
TC06000015	0.00067	-5.08151	RHEB_cKO down vs WT	-2.34526	≤ -6σ	6 F3|6	70809	70809	Clec2g	C-type lectin domain family 2, member g
TC04000005	0.013863	-5.11751	RHEB_cKO down vs WT	-2.35544	≤ -6σ	---	---	---	Gm12436	predicted gene 12436
TC04000039	0.021081	-5.21732	RHEB_cKO down vs WT	-2.38331	≤ -6σ	4 E1|4	329993	329993	Gm438	predicted gene 438
TC14000020	0.014236	-5.22352	RHEB_cKO down vs WT	-2.38502	≤ -6σ	14 B-C1|14	19752	19752	Rnase1	ribonuclease, RNase A family, 1 (pancreatic)
TC16000014	0.00925	-5.24403	RHEB_cKO down vs WT	-2.39068	≤ -6σ	16 B2|16	224079	224079	Atp13a4	ATPase type 13A4
TC07000004	0.005024	-5.25908	RHEB_cKO down vs WT	-2.39481	≤ -6σ	7 A3|7	13108	13108	Cyp2g1	cytochrome P450, family 2, subfamily g, polypeptide 1
TC04000011	0.009431	-5.27255	RHEB_cKO down vs WT	-2.3985	≤ -6σ	4 D1|4	195564	195564	Skint3	selection and upkeep of intraepithelial T cells 3
TC02000016	0.000625	-5.28608	RHEB_cKO down vs WT	-2.4022	≤ -6σ	2 E3|2	269328	269328	Muc15	mucin 15
TC17000014	0.005265	-5.29328	RHEB_cKO down vs WT	-2.40416	≤ -6σ	17 A1|17 8	381058	381058	Unc93a	unc-93 homolog A (C. elegans)
TC06000010	0.011056	-5.32506	RHEB_cKO down vs WT	-2.4128	≤ -6σ	6 D1|6	243535	243535	BC048671	cDNA sequence BC048671
TC18000012	0.048071	-5.54078	RHEB_cKO down vs WT	-2.47009	≤ -6σ	18 B3|18	225443	225443	Gm94	predicted gene 94
TC04000040	0.001256	-5.57402	RHEB_cKO down vs WT	-2.47872	≤ -6σ	4 E2|4	12353	12353	Car6	carbonic anhydrase 6
TC10000011	0.025598	-5.58734	RHEB_cKO down vs WT	-2.48216	≤ -6σ	10 C2-D1|	15109	15109	Hal	histidine ammonia lyase
TC13000004	0.007846	-5.62003	RHEB_cKO down vs WT	-2.49058	≤ -6σ	13|13 14.3	1.01E+08	1.01E+08	Gm19865	predicted gene, 19865
TC07000040	0.023221	-5.79831	RHEB_cKO down vs WT	-2.53563	≤ -6σ	7 E3|7	244202	244202	Nlrp10	NLR family, pyrin domain containing 10
TC07000034	0.028944	-5.83652	RHEB_cKO down vs WT	-2.54511	≤ -6σ	7 C|7	67867	67867	Lrrc28	leucine rich repeat containing 28
TC01000034	0.032147	-5.85961	RHEB_cKO down vs WT	-2.5508	≤ -6σ	1|1 H1	55990	55990	Fmo2	flavin containing monooxygenase 2
TC11000012	0.015846	-5.91921	RHEB_cKO down vs WT	-2.5654	≤ -6σ	11 C|11	66107	66107	Wfdc21	WAP four-disulfide core domain 21
TC03000008	0.03535	-5.96672	RHEB_cKO down vs WT	-2.57694	≤ -6σ	3|3 F2	66198	66198	Them5	thioesterase superfamily member 5
TC14000004	0.007535	-6.09067	RHEB_cKO down vs WT	-2.6066	≤ -6σ	---	---	---	Gm16439	predicted pseudogene 16439
TC06000017	0.031542	-6.16782	RHEB_cKO down vs WT	-2.62476	≤ -6σ	6 G3|6	330450	330450	Far2	fatty acyl CoA reductase 2
TC08000013	0.000847	-6.31305	RHEB_cKO down vs WT	-2.65834	≤ -6σ	8 E1|8	209239	209239	Gan	giant axonal neuropathy
TC02000006	0.011905	-6.52146	RHEB_cKO down vs WT	-2.7052	≤ -6σ	---	---	---	Gm13536	predicted gene 13536
TC02000043	0.000821	-6.53526	RHEB_cKO down vs WT	-2.70825	≤ -6σ	2 E3|2	170442	170442	Bbox1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase 1 (gamma-butyrobetaine
TC03000014	0.006757	-6.63564	RHEB_cKO down vs WT	-2.73024	≤ -6σ	3 G3|3 64.	11522	11522	Adh1	alcohol dehydrogenase 1 (class I)
TC05000013	0.000276	-7.14073	RHEB_cKO down vs WT	-2.83607	≤ -6σ	5 F|5 60.6	243262	243262	Oas1f	2'-5' oligoadenylate synthetase 1F
TC08000013	0.000949	-7.1534	RHEB_cKO down vs WT	-2.83863	≤ -6σ	---	---	---	Gm20204	predicted gene, 20204
TC01000038	0.01914	-7.26425	RHEB_cKO down vs WT	-2.86081	≤ -6σ	1|1 E1-E2	381286	381286	Serpinb3c	serine (or cysteine) peptidase inhibitor, clade B, member 3C
TC15000017	0.027046	-7.41249	RHEB_cKO down vs WT	-2.88996	≤ -6σ	15 D3|15	69462	69462	2300005B0	RIKEN cDNA 2300005B03 gene
TC11000006	0.016477	-8.08311	RHEB_cKO down vs WT	-3.01491	≤ -6σ	11 B1.3|11	73988	73988	4930438A0	RIKEN cDNA 4930438A08 gene
TC01000032	0.002413	-8.13554	RHEB_cKO down vs WT	-3.02424	≤ -6σ	1|1 G2	74091	74091	Npl	N-acetylneuraminate pyruvate lyase
TC02000008	0.006117	-8.15908	RHEB_cKO down vs WT	-3.02841	≤ -6σ	2|2 C3	76747	76747	Dapl1	death associated protein-like 1
TC08000014	0.006037	-8.53742	RHEB_cKO down vs WT	-3.0938	≤ -6σ	8 E1|8	15486	15486	Hsd17b2	hydroxysteroid (17-beta) dehydrogenase 2
TC17000014	0.004599	-9.00995	RHEB_cKO down vs WT	-3.17152	≤ -6σ	17 A1|17	667055	667055	Gm9992	predicted gene 9992
TC05000027	0.0064	-10.6801	RHEB_cKO down vs WT	-3.41685	≤ -6σ	5 E2|5 44.	12223	12223	Btc	betacellulin, epidermal growth factor family member
TC04000027	0.008304	-11.5792	RHEB_cKO down vs WT	-3.53347	≤ -6σ	4 B3|4 32.	30936	30936	Slc46a2	solute carrier family 46, member 2
TC04000032	0.003223	-15.398	RHEB_cKO down vs WT	-3.94468	≤ -6σ	4 D1|4	329918	329918	Skint9	selection and upkeep of intraepithelial T cells 9