SUPPLEMENTARY METHODS

Biochemical assays. Serum alanine aminotransferase (ALT), alkaline phosphatase (ALP), and total bilirubin (TBIL) levels were determined using a Catalyst Dx Chemistry Analyzer (IDEXX Laboratories, Westbrook, ME). Tissue bile acid concentration was evaluated using the Total Bile Acid Assays and following manufacturer's instructions (Cell Biolabs Inc., CA).

Immunohistochemistry. Paraformaldehyde fixed (4%) and paraffin embedded 4 µm thick liver sections were used. Section were deparaffinized, and antigen retrieval was performed using heat-mediated epitope retrieval solution (ThermoFisher Scientific). Sections were blocked for one hour in PBS containing 3% normal goat serum. Slides were incubated overnight with primary antibodies listed in Supplementary Table 1. Conventional and and multiplex immunostaining showing more than three markers was performed as previously described, and images were analyzed using the trainable classification software Ilastik (v 1.3.3) (Berg et al., Nat Methods. 2019 Dec;16(12):1226-1232. doi: 10.1038/s41592-019-0582-9. Epub 2019 Sep 30) and CellProfiler v3.1.9 (Lamprecht et al., Biotechniques. 2007 Jan;42(1):71-5. doi: 10.2144/000112257) (Guillot et al., Cancers (Basel). 2020 Aug 28;12(9):E2449. doi: 10.3390/cancers12092449).

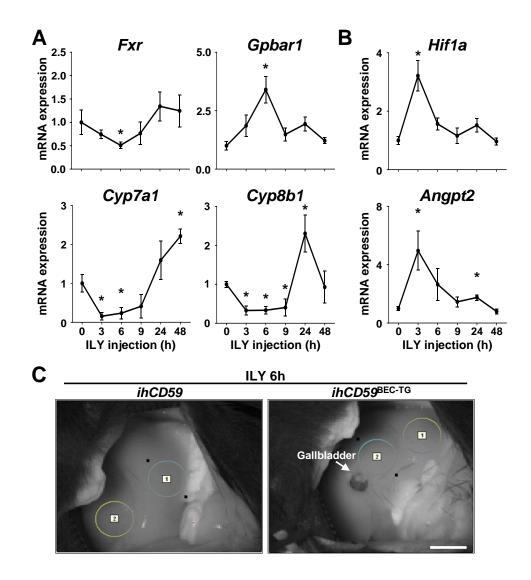
TUNEL staining. Liver injury was assessed by Terminal deoxynucleotidyl transferase dUTP nick end labeling (TUNEL) staining on formaldehyde fixed paraffin embedded tissue sections as per manufacturer's instructions and revealed either after HRP based coloration (ApopTag Peroxidase In Situ Apoptosis Detection Kit, Millipore Sigma, St. Louis, MO) or by fluorescence (DeadEnd Fluorometric TUNEL System, Promega, Madison, WI).

Liver microcirculation (additional information). Briefly, liver was exposed and scanned by using moorFLPI-2 blood flow imager (Moor Instruments, Wilmington, DE, USA) to determine the red blood cell velocity in 1.5% isoflurane anesthetized mice with core temperatures maintained at 37.2 ± 0.1 °C. Hepatic microcirculation was assessed in a 5 mm diametric region of both left and medial lobes placed onto the free part of the liver lobes, and quantified by using the Moor Instruments analysis software. Data are expressed in arbitrary units.

Non-parenchymal cell isolation and FACS analysis. For non-parenchymal collagen-

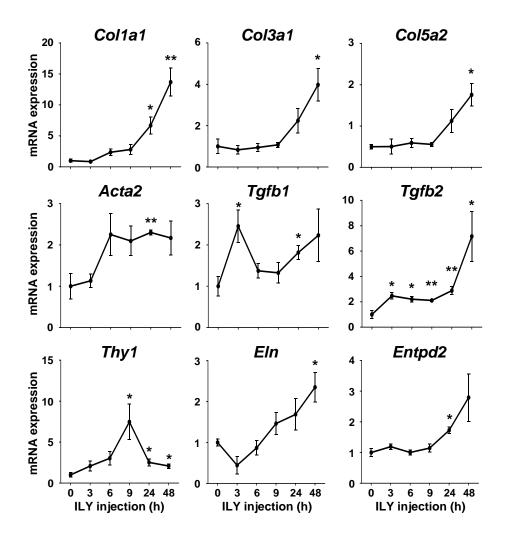
expressing cell isolation, livers from tamoxifen and ILY injected *ihCD59*^{BEC-TG} Coll1^{GFP} mice were perfused with GBSS containing 0.5 g/L collagenase IV (Millipore Sigma, St. Louis, MO), collected and minced with scissors, and further digested for 20 minutes at 37°C under agitation in GBSS containing 0.5 g/L collagenase IV and 0.5 g/L pronase (Millipore Sigma, St. Louis, MO). Cells were then passed through a 70 µm cell strainer, and HCs were removed after three consecutive low speed centrifugations (60 g 5 minutes). Red blood cells were lysed using ACK Lysing Buffer (ThermoFisher Scientific, Carlsbad, CA). For non-parenchymal immune cell isolation, livers from *ihCD59* or *ihCD59*^{BEC-TG} mice were excised and cut into small pieces using scissors, before being forced through a 100 µm and a 70 µm cell strainer to obtain single cell suspensions. Hepatocytes were pelleted by low speed centrifugation (60 g 5 minutes) and discarded. Supernatant was centrifuged for 10 minutes at 400 g and pellet was resuspended in 37.5% Percoll solution containing 100 U/mL heparin and centrifuged at 850 g for 30 minutes with the off-brake setting. Red blood cells were lysed using ACK Lysing Buffer (ThermoFisher Scientific, Carlsbad, CA). Pellet was then resuspended, and cells were stained for flow cytometry using fluorochrome-conjugated antibodies listed in Supplementary Table 1 and diluted in PBS+2% FBS.

Quantitative RT-PCR. Total RNA was extracted from snap-frozen liver tissue or cell lysates using the RNeasy Mini Kit (Qiagen, Germantown, MD), following manufacturer's instructions. High-Capacity cDNA Reverse Transcription Kit (ThermoFisher Scientific, Carlsbad, CA) was used for reverse transcription. Real-time PCR was performed on a QuantStudio 6 Flex Real-Time PCR System (ThermoFisher Scientific, Carlsbad, CA), using BrightGreen 2X qPCR MasterMix-ROX (Applied Biological Materials Inc., Richmond, BC). Oligonucleotides used for PCR amplification are listed in Supplementary Table 3.

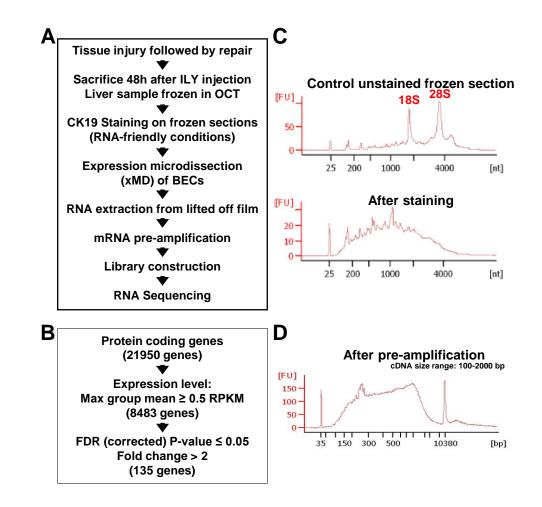


Supplementary Figure 1: Acute BEC death induces cholestasis and liver ischemia

ihCD59 and *ihCD59*^{BEC-TG} mice were intraperitoneally injected with Tamoxifen (50 mg/kg) to induce hCD59 expression in Sox9⁺ cells, every two days for a total of three injections. Following one-week tamoxifen wash-out period, ILY was injected intravenously (140 µg/kg). Liver samples were collected at the indicated time points post ILY injection for qRT-PCR. (A) Alternative representation of quantitative RT-PCR data depicted in Figure 1D (n=3-7). (B) Hypoxia-inducible factor 1-alpha (*Hif1a*) and Angiopoietin 2 (*Angpt2*) gene expression were assessed. Data are represented as mean \pm SEM. **p*<0.05 as compared to ILY injected *ihCD59* mice (n=3-6 per group). (C) Representative grayscale images corresponding to the flux images displayed in Figure 1E, showing the areas of interest (circled and labelled 1 and 2) used for liver blood microcirculation measurements. Scale bar: 5 mm.

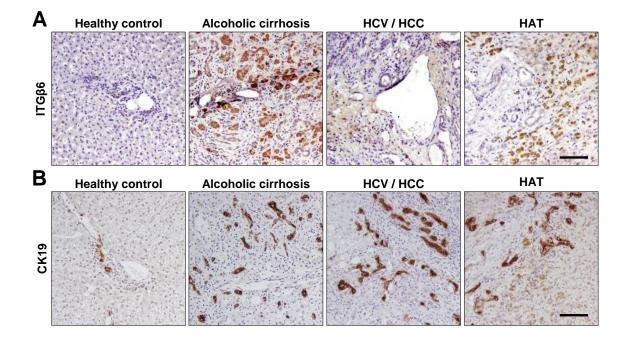


Supplementary Figure 2: Fibrogenesis accompanies bile duct repair after acute injury *ihCD59* and *ihCD59*^{BEC-TG} mice were treated as described in Supplementary Figure 1. Relative mRNA expression of fibrogenesis-associated genes depicted in Figure 2D. Data are represented as mean \pm SEM. **p*<0.05; ***p*<0.01 as compared to *ihCD59* mice (n=3-7 per group).

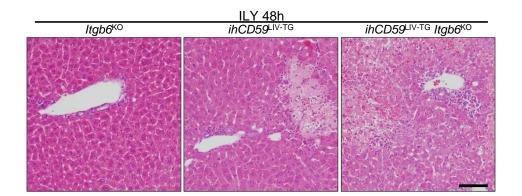


Supplementary Figure 3: Purification and next generation transcriptome (RNAseq) analysis of regenerating BECs

(A) Detailed experimental design. Liver tissue from two *ihCD59* (control group) and two *ihCD59*^{BEC-TG} (injury group) mice was collected after 48 hours of ILY injection and frozen. Messenger RNA from purified BECs was pre-amplified and sequenced. (B) Number of genes throughout RNAseq analysis and filtering pipeline. (C) Quality assessment was performed by Bioanalyzer on RNA extracted from unstained or RNA-friendly stained liver tissue sections. Representative plots are shown, revealing acceptable RNA quality after staining (average mRNA length of 1,000 nucleotides shows limited degradation). (D) Size profile of pre-amplified mRNA (cDNA) using Ovation RNA-seq System V2. Representative plot.

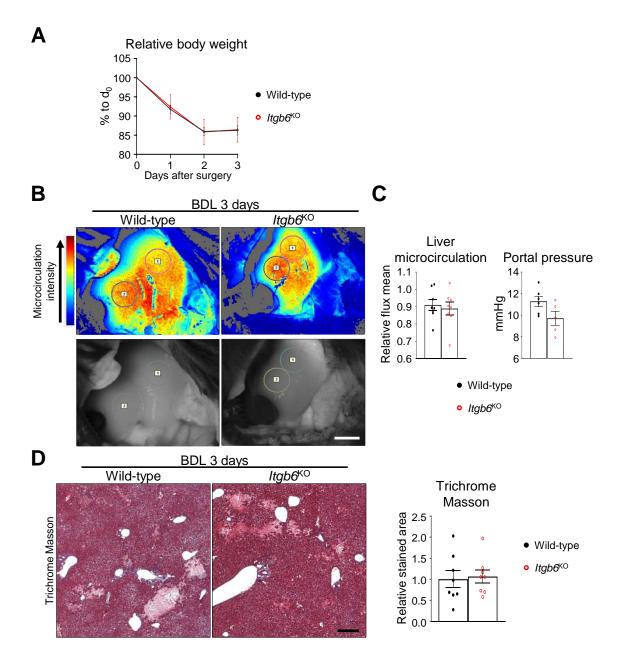


Supplementary Figure 4: Integrin $\alpha\nu\beta6$ expression is increased in human ductular reaction Representative images of (A) integrin $\alpha\nu\beta6$ (ITG $\beta6$) and (B) cytokeratin-19 (CK19) staining performed on human liver sections of patients suffering from various chronic liver diseases. HCV / HCC: hepatitis C virus infection and hepatocellular carcinoma; HAT: hepatic artery thrombosis. Scale bars: 100 µm.



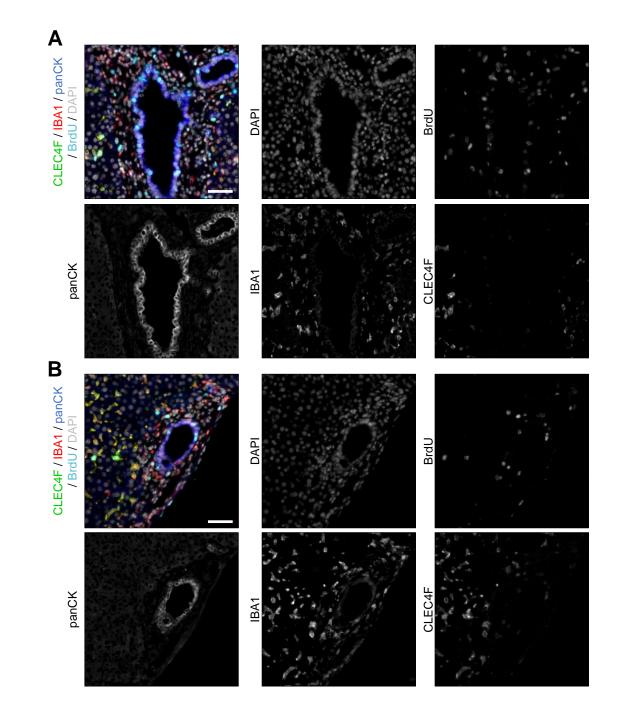
Supplementary Figure 5: Combined acute hepatocyte and BEC death leads to mononuclear cell infiltrates and tissue necrosis.

ihCD59^{LIV-TG} and *ihCD59*^{LIV-TG} *Itgb6*^{KO} mice were injected intravenously with ILY, and samples were collected at the indicated time points after ILY injection. Hematoxylin-eosin staining showing tissue injury and inflammation in ILY injected mice. Scale bar: 100 µm.



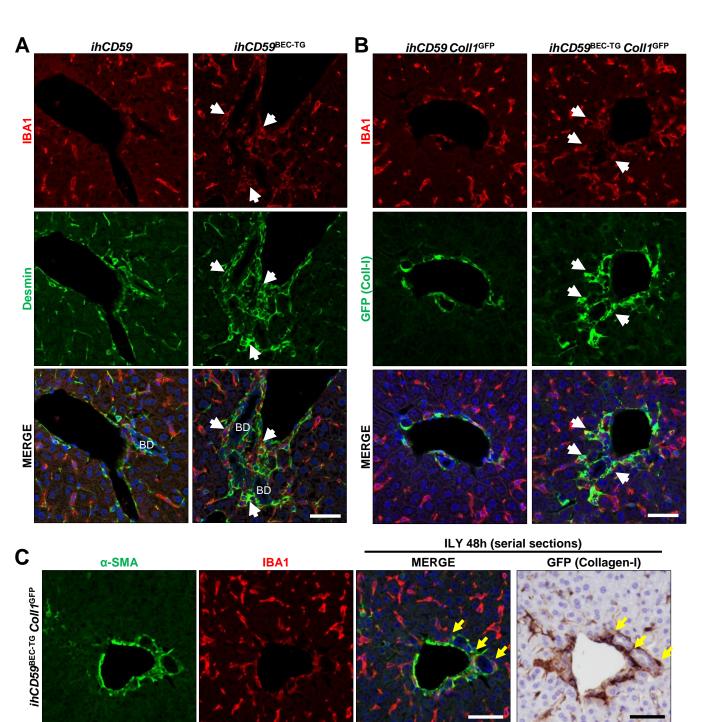
Supplementary Figure 6: Integrin $\alpha\nu\beta6$ deficiency does not alter early fibrogenesis or liver microcirculation following bile duct ligation

(A) Relative body weight following bile duct ligation surgery performed on wild-type and *ltgb6*^{KO} mice (n=8 per group). **(B)** Liver microcirculation and portal pressure were measured as described in Figure 1E. Representative flux images of wild-type and *ltgb6*^{KO} mice, three days after BDL surgery. Scale bar: 5 mm. **(C)** Relative blood flux mean and portal pressure values. Portal pressure measurement (n=6 wild-type and n=5 *ltgb6*^{KO}). **(D)** Trichrome Masson staining was performed on liver sections, and the stained area was quantified (n=8 per group). Scale bar: 200 μm.



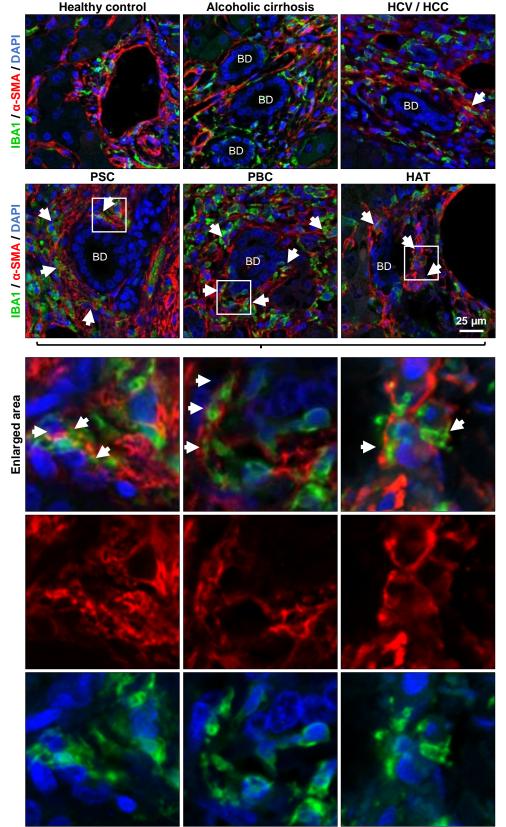
Supplementary Figure 7: Integrin $\alpha\nu\beta6$ deficiency reduces BEC proliferation following bile duct ligation

Single channel pictures from multiplex fluorescence immunostaining (Figure 5E) are depicted in grayscale, obtained from **(A)** wild-type, or **(B)** *Itgb6*^{KO} FFPE liver, 3 days after bile duct ligation. Scale bars: 50 μ m.



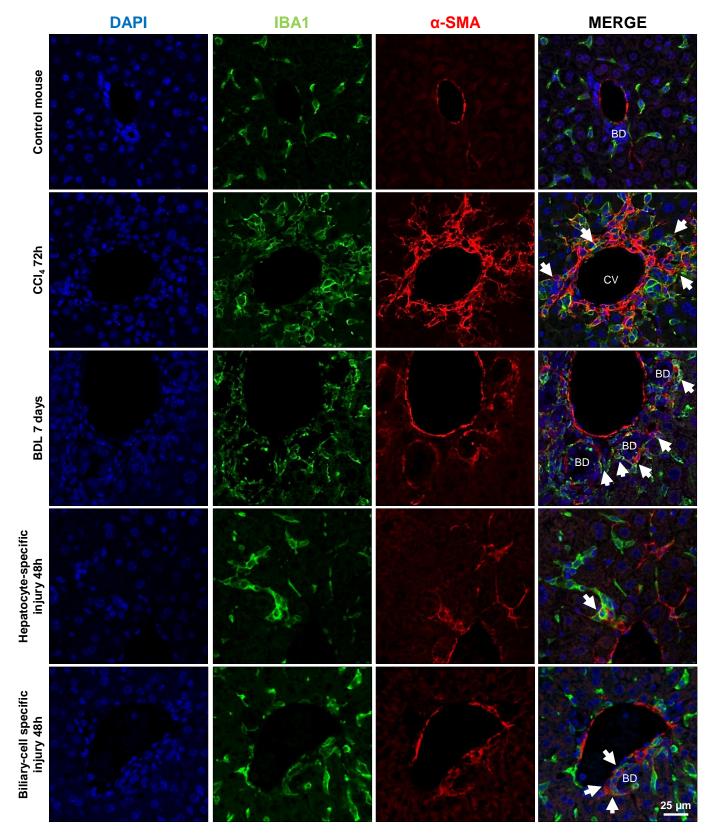
Supplementary Figure 8: Monocytes and fibrogenic cells are in close interaction during bile duct repair.

Single channel pictures from data presented in Figure 6A-C. (A) IBA1 (red) and Desmin (green), and (B) IBA1 (red) GFP (Collagen-I, green) immunostaining was performed, 48 hours after ILY administration. (C) IBA1 (red) and α -SMA (green) co-staining, and GFP (collagen-I) staining were performed on serial liver sections from *ihCD59*^{BEC-TG} *Coll1*^{GFP} mice, 48h after ILY injection. Yellow arrows indicate cell clusters of IBA1⁺, α -SMA⁺ and GFP⁺ cells. Scale bars: 50 µm.



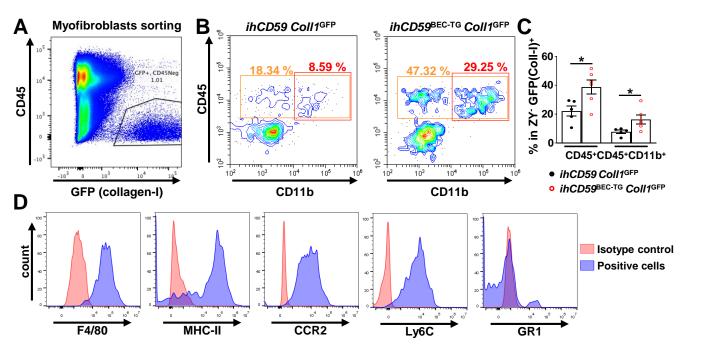
Supplementary Figure 9: IBA1⁺ macrophages and α-SMA⁺ fibroblasts accumulate around injured bile ducts in patients suffering liver disease of various etiologies

Representative images of IBA1 (green) and α -SMA (red) staining performed on various chronic liver diseases from patients. An enlarged area with single channel pictures is depicted in the lower panel. White arrows indicate positive cell clusters. Quantification is depicted in Figure 6D. BD: bile duct-like structures; HCV/HCC: Hepatitis C virus infection and hepatocellular carcinoma; PSC: primary sclerosing cholangitis; PBC: primary biliary cholangitis; HAT: hepatic artery thrombosis.



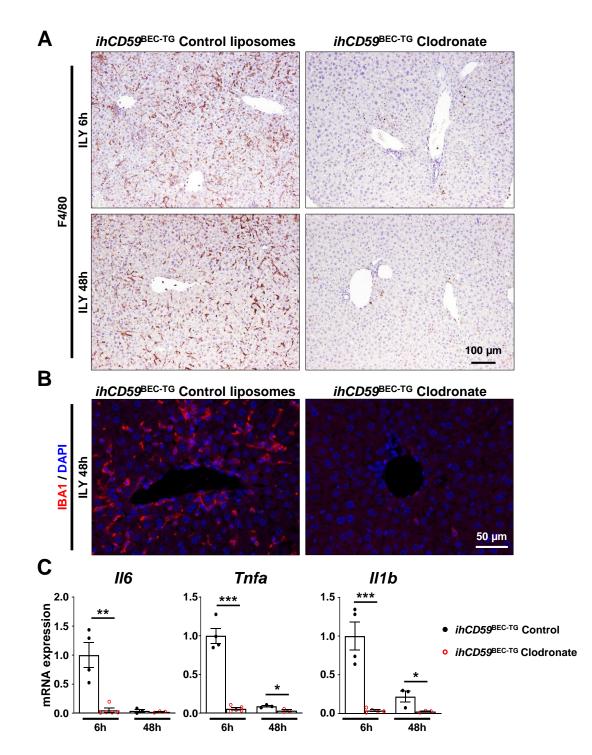
Supplementary Figure 10: IBA1⁺ macrophages and α -SMA⁺ fibroblasts accumulate around injured bile ducts in different murine models of liver injury

Representative images of the IBA1 (green) and α -SMA (red) staining performed on mouse samples from different liver injury models. Quantification is depicted in Figure 6D. White arrows indicate double positive cells. CV: central vein, BD: bile duct-like structures, BDL: Bile duct ligation and section.



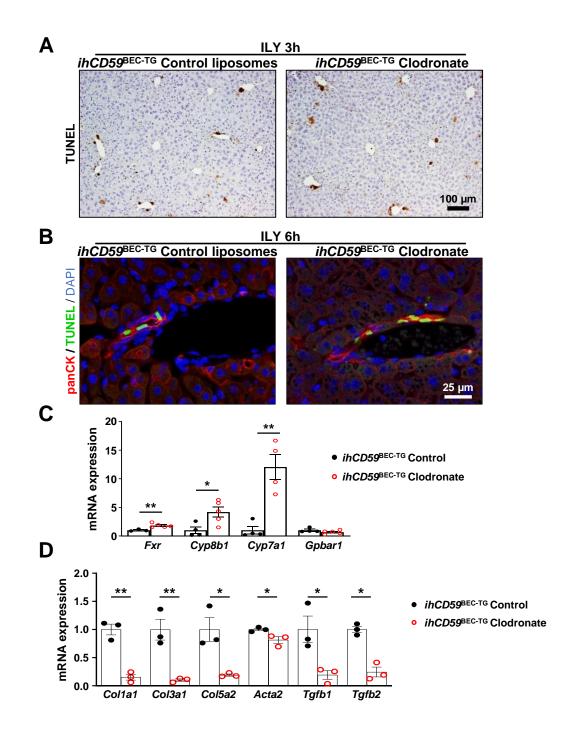
Supplementary Figure 11: Monocytes, an alternative source of fibrogenic cells?

(A) Collagen-I producing (GFP⁺) CD45^{NEG} fibroblasts were sorted from carbon tetrachloride (CCI₄) injected *Coll1*^{GFP} mouse livers. (B) *ihCD59*^{BEC-TG}*Coll1*^{GFP} mice were injected with ILY, and euthanized 48 hours after ILY injection. Representative flow cytometry data obtained from liver non-parenchymal cell fraction analysis are shown. After doublets exclusion and SSC/FSC gating, live (Zombie Yellow negative) and GFP (collagen-I) -positive cells were assessed for CD45 and CD11b expression. (C) Flow cytometry results from 5-6 mice per group show percentages of ZY⁻GFP⁺CD45⁺ and ZY⁻GFP⁺CD45⁺CD11b⁺ among ZY⁻GFP⁺ cells. (D) Representative F4/80, MHC-II, CCR2, Ly6C and GR1 expression in ZY⁻GFP⁺CD45⁺CD11b⁺ cells from *ihCD59*^{BEC-TG}*Coll1*^{GFP} mice as assessed by FACS, 48 hours after ILY injection. **p*<0.05 as compared to control *ihCD59CollI*^{GFP} mice, unpaired Student's t test (n=5-6 per group).



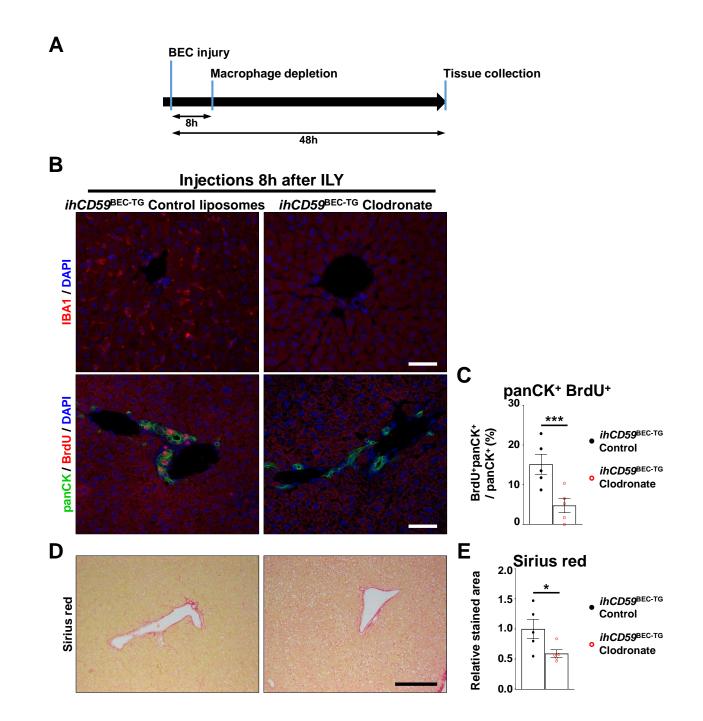
Supplementary Figure 12: Liver inflammation is impaired after macrophage depletion using clodronate-loaded liposomes

Following tamoxifen injections and wash out period, macrophages were depleted using clodronateloaded liposomes 24 hours prior to ILY injection. Macrophage depletion was verified by **(A)** F4/80 immunostaining, and **(B)** IBA1 immunostaining. **(C)** Inflammation-related relative gene expression was assessed on liver homogenates by qRT-PCR. Data are represented as mean \pm SEM. *p<0.05; **p<0.01; ***p<0.005 as compared to control liposome injected mice, unpaired Student's t test (n=3-5 per group).



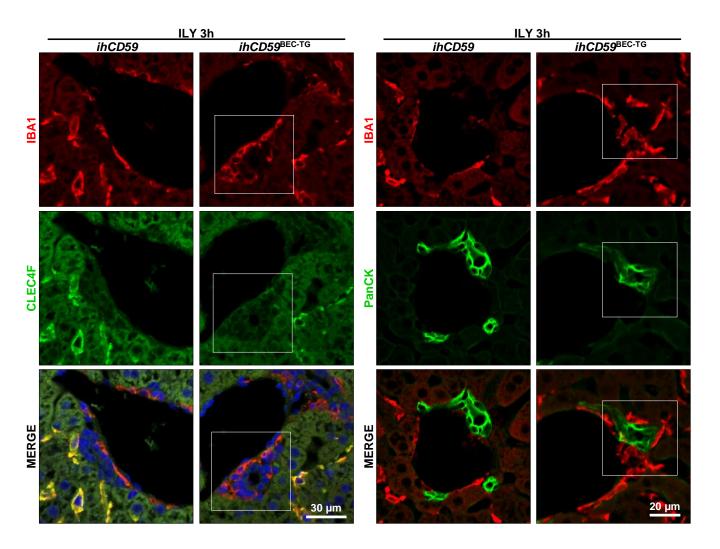
Supplementary Figure 13: Macrophage depletion reduces cholestasis and bile duct repair after BEC injury (representative fields)

(A) TUNEL, and (B) panCK (red) TUNEL (green) representative images used for the quantifications presented in Figure 7A. (C) Quantitative RT-PCR data depicted in Figure 7C. (D) Quantitative RT-PCR data depicted in Figure 7E. Data are represented as mean \pm SEM. *p<0.05; **p<0.01 as compared to control liposome injected *ihCD59*^{BEC-TG} mice, unpaired Student's t test (n=3-5 per group).



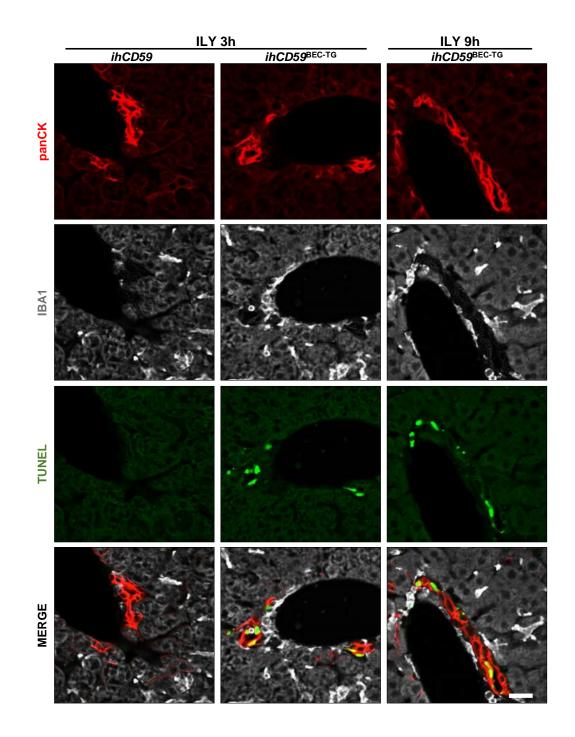
Supplementary Figure 14: Macrophage depletion 8 hours after ILY injection reduces BEC proliferation

(A) Experimental design: Mice were injected with clodronate-loaded or control liposomes 8 hours after ILY injection. Tissues were collected 48 hours after the initial BEC injury. (B) IBA1 (red, upper panel), panCK and BrdU (green and red, respectively, lower panel) were performed on liver sections obtained from control- or clodronate-loaded liposome injected mice. Scale bars: 50 μ m. (C) Quantification of proliferating BECs. (D) Sirius red staining was performed (scale bar: 200 μ m), and (E) relative stained area was quantified in both groups. **p<0.01; ***p<0.005 as compared to control liposome injected *ihCD59*^{BEC-TG} mice, unpaired Student's t test (n=5 per group).



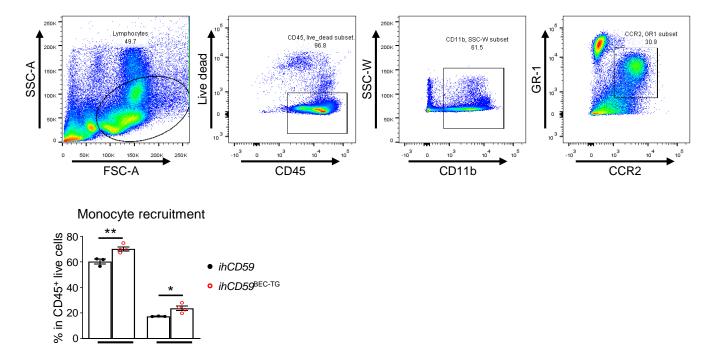
Supplementary Figure 15: Monocytes are recruited around damaged bile ducts following acute BEC injury

IBA1 (red) and CLEC4F (green, left panel) or pan-cytokeratin (PanCK, right panel in green) immunostaining was performed on liver sections, 3 hours after ILY injection. Single channel images of the representative fields presented in Figure 8A.



Supplementary Figure 16: Recruited monocytes accumulate around injured BECs

ihCD59^{BEC-TG} mice were treated as described in Supplementary Figure 1. Liver tissue sections (Formalin-Fixed Paraffin-Embedded) were subjected to immunostaining. Representative immunostaining showing monocyte (IBA1, grey) accumulation in contact with damaged BECs (panCK, red and TUNEL, green). Scale bar: 20 µm.

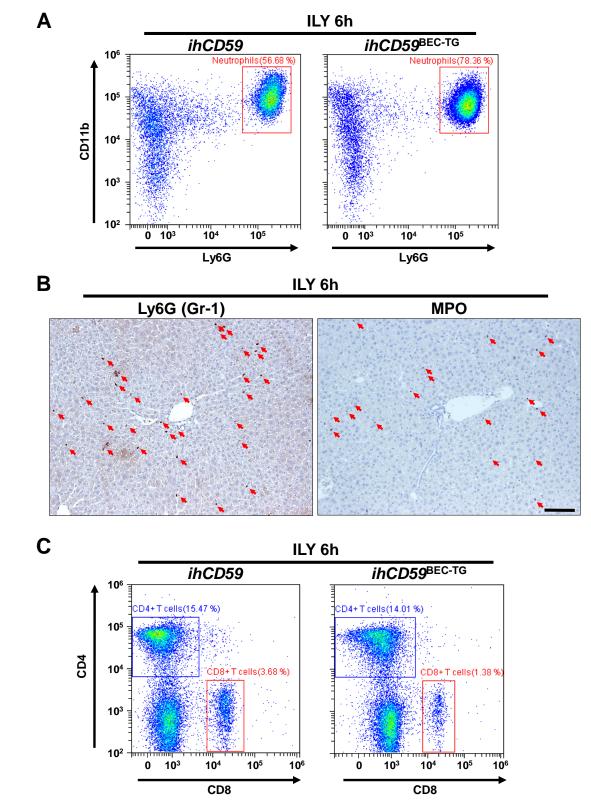


CD11b+

CD11b⁺ CCR2⁺

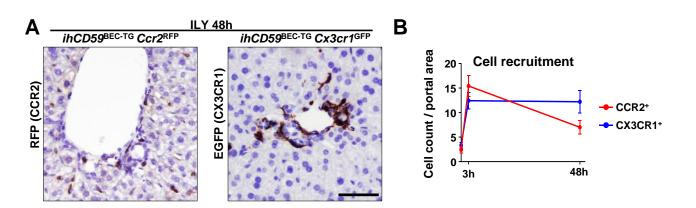
Supplementary Figure 17: Circulating monocytes are recruited in the liver after acute biliary epithelial cell injury

Non-parenchymal cells were isolated and hepatocytes, CD3⁺ and CD19⁺ cells were removed. CCR2⁺ CD11b⁺ cells in the CD45⁺ cell population was evaluated by flow cytometry. *p<0.05; **p<0.01 as indicated, unpaired Student's t test (n=3-4 per group).



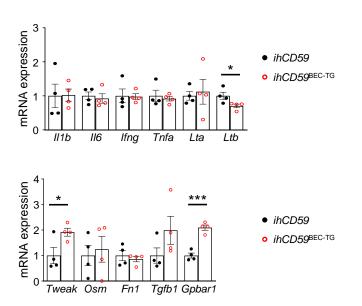
Supplementary Figure 18: Neutrophils accumulate in the liver after BEC injury, but not in the vicinity of bile ducts while T lymphocytes do not seem to be involved

(A) Non-parenchymal liver cells were isolated and analyzed by FACS staining, 6 hours after ILY injection. Neutrophils were identified as Zombie Yellow⁻ CD45⁺ CD3⁻ CD19⁻ CD11b⁺ Ly6G⁺ cells. (B) Paraffin embedded liver sections from *ihCD59*^{BEC-TG} mice were stained for Ly6G (left panel) or myeloperoxidase (MPO, right panel) to reveal neutrophil localization. Scale bar: 100 μ m. (C) Leukocytes were gated as Zombie Yellow⁻ CD45⁺ CD3⁺, and CD4⁺ or CD8a⁺ T-lymphocyte recruitment was evaluated.



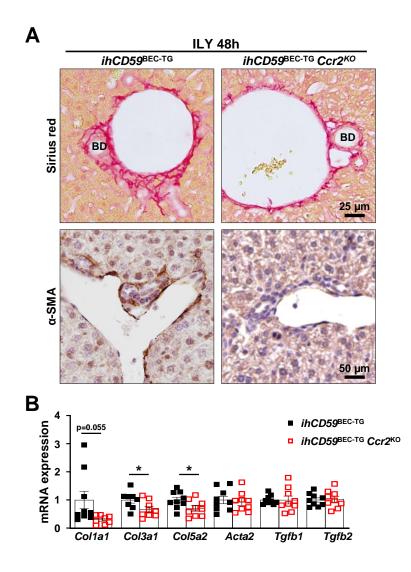
Supplementary Figure 19: Freshly recruited monocytes accumulate around injured BECs 48 hours post-injury

ihCD59 Cx3cr1^{GFP}, *ihCD59*^{BEC-TG} Cx3cr1^{GFP}, *ihCD59* Ccr2^{RFP} and *ihCD59*^{BEC-TG}Ccr2^{RFP} mice were treated as described in Supplementary Figure 1. Liver tissues were subjected to immunostaining. **(A)** GFP or RFP immunostaining, as appropriate. **(D)** GFP⁺ or RFP⁺ cell count, showing CCR2⁺ or CX3CR1⁺ cell accumulation in portal areas (n=5-7 per group). Scale bar: 50 µm.



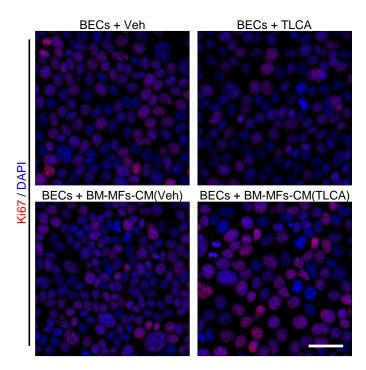
Supplementary Figure 20: Macrophage characterization during bile duct repair

Liver macrophages were isolated from *ihCD59* and *ihCD59*^{BEC-TG} mice, 48 hours after ILY injection. Gene expression analysis was performed by qRT-PCR. Statistical analysis of qRT-PCR data shown in Figure 6J. *p<0.05; ***p<0.005 as indicated, unpaired Student's t test (n=4 per group).



Supplementary Figure 21: Macrophage depletion or Ccr2-deficiency reduces portal fibrosis in a model of acute and targeted biliary epithelial cell death *ihCD59*^{BEC-TG} and *ihCD59*^{BEC-TG} *Ccr2*^{KO} mice were also injected with ILY and liver tissue was

ihCD59^{BEC-TG} and *ihCD59*^{BEC-TG} *Ccr2*^{KO} mice were also injected with ILY and liver tissue was collected after 48 hours. (A) Representative pictures obtained after Sirius red, α -SMA or PanCK (green) and BrdU (red) staining used for quantification in Figure 8F. (B) Statistical analysis of qRT-PCR data shown in Figure 8G, **p*<0.05; ***p*<0.01 as indicated, unpaired Student's t test (n=8-9 per group).

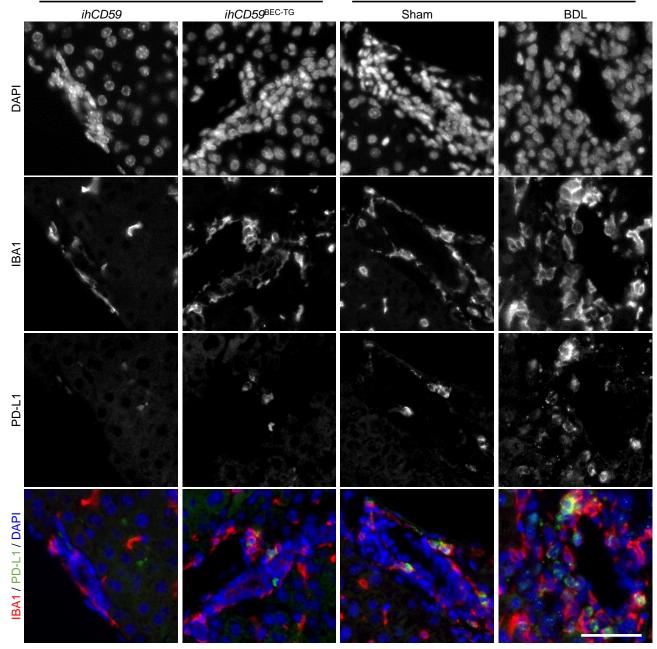


Supplementary Figure 22: Cultured BECs proliferation is increased in the presence of bile acid-activated macrophages.

Conditionned-media from TLCA-treated bone-marrow derived macrophages (BM-MFs-CM) was added to BECs for 24 hours, and Ki67 staining was performed. Scale bar: 40 µm.

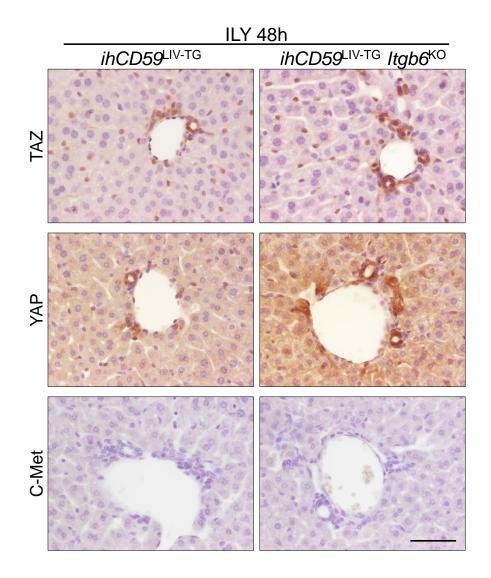






Supplementary Figure 23: PD-L1+ macrophages accumulate around bile ducts

Liver FFPE section from mice that were injected with ILY and killed 48 hours later, or 3 days after sham or BDL-surgery, were subjected to IBA1 (red) and PD-L1 (green) immunostaining. Corresponding single channel pictures from Figure 4D are shown. Scale bar: 50 µm.



Supplementary Figure 24: YAP/TAZ and cMet signaling are not altered in *ihCD59*LIV-TG *ltgb6*^{KO} animals

Liver FFPE section from *ihCD59*^{LIV-TG}, or *ihCD59*^{LIV-TG} *Itgb6*^{KO} mice sacrificed 48 hours after ILY injection, were stained for TAZ, YAP, and cMet. Scale bar: 100 µm.

Antigen	Application(s)	Manufacturer	Catalog #	Host species	Dilution
BrdU	IHC-P	BD Biosciences, San Jose, CA	550803	Biotin-conjugated	1/20
BrdU	IHC-P	Abcam, Cambridge, UK	6326	Rat	1/200
c-MET	IHC-P	R&D Systems, Minneapolis, MN	AF2480	Rabbit	1/200
CCR2	FC	BioLegend, San Diego, CA	150604	Rat	1/200
CD11b	FC	BD Biosciences, San Jose, CA	550993	Rat	1/200
CD11b	FC	ThermoFisher Scientific, Carlsbad, CA	45-0112-82	Rat	1/200
CD3	FC	BioLegend, San Diego, CA	100216	Rat	1/200
CD4	FC	ThermoFisher Scientific, Carlsbad, CA	47-0042-80	Rat	1/200
CD8a	FC	BD Biosciences, San Jose, CA	553031	Rat	1/200
CD45	FC	ThermoFisher Scientific, Carlsbad, CA	25-0451-82	Rat	1/200
CD45	FC	ThermoFisher Scientific, Carlsbad, CA	69-0451-82	Rat	1/200
СК19	IHC-P, xMD	Developmental Studies Hybridoma Bank, Iowa City, IA *	TROMA-III	Rat	1/4
CLEC4F	IHC-P	R&D Systems, Minneapolis, MN	MAB2784	Rat	1/200
Desmin	IHC-P	Abcam, Cambridge, UK	ab15200	Rabbit	1/100
F4/80	FC	ThermoFisher Scientific, Carlsbad, CA	12-4801-82	Rat	1/200
F4/80	IHC-P	Bio-Rad , Hercules, CA	MCA497R	Rat	1/500
GFP	IHC-P	Cell Signaling, Danvers, MA	2955	Mouse	1/100
GFP	IHC-P	Cell Signaling , Danvers, MA	2956	Rabbit	1/400
IBA1	IHC-P	VWR, Arlington Heights, IL	100369-764	Rabbit	1/1,000
IBA1	IHC-P	Millipore Sigma, St. Louis, MO	MABN92-25UG	Mouse	1/500
ITGB6	IHC-P	ProteinTech, Chicago, IL	19695	Rabbit	1/100
Ki67	ICC	Dako by Agilent, Santa Clara, CA	M7249	Rat	1/100
Ly6C	FC	BioLegend, San Diego, CA	128024	Rat	1/200
Ly6G / Gr1	IHC-P	BioXCell, West Lebanon, NH	BE0075	Rat	1/100
Ly6G / Gr1	FC	ThermoFisher Scientific, Carlsbad, CA	17-9668-80	Rat	1/200
Ly6G / Gr1	FC	ThermoFisher Scientific, Carlsbad, CA	48-9668-82	Rat	1/200
МНС-ІІ	FC	ThermoFisher Scientific, Carlsbad, CA	47-5321-82	Rat	1/200
МРО	IHC-P	Biocare Medical , Concord, CA	PP023AA	Rabbit	RTU
panCK	IHC-P	Cell Signaling , Danvers, MA	4545	Mouse	1/500
panCK	IHC-P	Agilent Dako, Santa Clara, CA	Z0622	Rabbit	1/200
PD-L1	IHC-P	P Cell Signaling , Danvers, MA		Rabbit	1/200
RFP	IHC-P	Rockland, PA	600-401-379	Rabbit	1/250
TAZ	IHC-P	Cell Signaling, Danvers, MA	72804	Rabbit	1/200
ΥΑΡ	IHC-P	Cell Signaling, Danvers, MA	14074	Rabbit	1/400
α-SMA	A IHC-P Agilent Dako, Santa Clara, CA		M085129-2	Mouse	1/200

Supplementary Table 1: Primary antibodies used in this study

FC: Flow cytometry; IHC-P: immunohistochemistry paraffin sections; xMD: expression microdissection. The monoclonal anti-mouse cytokeratin-19 (CK19/TROMA-III) antibody developed by R. Kemler, was obtained from the Developmental Studies Hybridoma Bank developed under the auspices of the NICHD and maintained by The University of Iowa, Department of Biology (Iowa City, IA 52242).

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	GOTERM_CC_DIRECT	GO:0034364~high-density lipoprotein particle					
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Total Map Direct 60:0006657-tity and total-axidation 5 7 15:1 2276.0 0006 COD1, EG2, EH4ADH, ACA1B, SLC27A2 Total Map Direct 60:000567-tity and total degradation 5 5 22:6 65:5:6 0015 COD1, Mup2, Direct COD20647 COD1 COD1 <td>KEGG_PATHWAY GOTERM_BP_DIRECT KEGG_PATHWAY</td> <td>GO:0042593~glucose homeostasis mmu00830:Retinol metabolism</td> <td>7 9.3 7 9.3</td> <td>10.7</td> <td>4.09E-05 4.45E-05</td> <td>1.23E-03 1.38E-03</td> <td>GGPC, MUP1, MUP2, MUP2, MUP18, MUP3, MUP3 CIPAALU, UGTIALO, CYP28U, UGT281, CYP3ALA, CYP2C40, RETSAT MUP7, MUP1, MUP, MUP3, SEPNILE, MUP10, SEPNIA6, POGFRI, MUP18, MUP17, MUP15, MUP14, MUP9, MUP11, ANGPTL4</td>	KEGG_PATHWAY GOTERM_BP_DIRECT KEGG_PATHWAY	GO:0042593~glucose homeostasis mmu00830:Retinol metabolism	7 9.3 7 9.3	10.7	4.09E-05 4.45E-05	1.23E-03 1.38E-03	GGPC, MUP1, MUP2, MUP2, MUP18, MUP3, MUP3 CIPAALU, UGTIALO, CYP28U, UGT281, CYP3ALA, CYP2C40, RETSAT MUP7, MUP1, MUP, MUP3, SEPNILE, MUP10, SEPNIA6, POGFRI, MUP18, MUP17, MUP15, MUP14, MUP9, MUP11, ANGPTL4
Total Map Direct 60:0006657-tity and total-axidation 5 7 15:1 2276.0 0006 COD1, EG2, EH4ADH, ACA1B, SLC27A2 Total Map Direct 60:000567-tity and total degradation 5 5 22:6 65:5:6 0015 COD1, Mup2, Direct COD20647 COD1 COD1 <td>KEGG_PATHWAY GOTERM_BP_DIRECT KEGG_PATHWAY GOTERM_CC_DIRECT</td> <td>GC:0042593°giucose homeostasis mmu0883:Retinol metabolism GC:0005576°extracellular region</td> <td>7 9.3 7 9.3 15 20.0</td> <td>10.7 10.0 3.6</td> <td>4.09E-05 4.45E-05 4.47E-05</td> <td>1.23E-03 1.38E-03 2.86E-03</td> <td>GGPC, MUP1, MUP3, MUP2, MUP18, MUP9, MUP11 CYPAAI0, UGTIA10, CYP289, UGT281, CYP3AIA, CYP2C40, RETSAT MUP7, MUP1, MUP3, MUP2, SEPINIA1E, MUP10, SEPINIA6, PDGFRL, MUP18, MUP17, MUP15, MUP14, MUP3, MUP11, ANGPTL4 ETMPL, ACXX, CH276, SIGE, EHAAD, CYP289, UGT281, CYP2C40, UPP2, AKA, LPIN2, LPIN1, CYPA410, UGTLA10, TOO2, GBPC, HYKK,</td>	KEGG_PATHWAY GOTERM_BP_DIRECT KEGG_PATHWAY GOTERM_CC_DIRECT	GC:0042593°giucose homeostasis mmu0883:Retinol metabolism GC:0005576°extracellular region	7 9.3 7 9.3 15 20.0	10.7 10.0 3.6	4.09E-05 4.45E-05 4.47E-05	1.23E-03 1.38E-03 2.86E-03	GGPC, MUP1, MUP3, MUP2, MUP18, MUP9, MUP11 CYPAAI0, UGTIA10, CYP289, UGT281, CYP3AIA, CYP2C40, RETSAT MUP7, MUP1, MUP3, MUP2, SEPINIA1E, MUP10, SEPINIA6, PDGFRL, MUP18, MUP17, MUP15, MUP14, MUP3, MUP11, ANGPTL4 ETMPL, ACXX, CH276, SIGE, EHAAD, CYP289, UGT281, CYP2C40, UPP2, AKA, LPIN2, LPIN1, CYPA410, UGTLA10, TOO2, GBPC, HYKK,
OFEM. BP. DIRECT 00:0005584*response to sitilenoid 4 53 22::53:E04 00:15 SCIDAL, MUPJ, MUP3, CYP289 VESG. FATHWAM mmu00271:E1xty aid argination 6 6 11::6 7::55 00:15 SCIDAL, MUPJ, MUP3, CYP289 VESG. FATHWAM mmu0027:E1xty aid argination 2 2 11::6 7::55 00:15 SCIDAL, MUPJ, MUP3, CYP289 OTEMM, P. DIRECT 00:000582**rtysaol 2 <td>KEGG_PATHWAY GOTERM_BP_DIRECT KEGG_PATHWAY GOTERM_CC_DIRECT KEGG_PATHWAY</td> <td>GO:004293*plucose homeotatais mmu00830.Petinol metabolism GO:0005576*extracellular region mmu01100.Metabolic pathways</td> <td>7 9.3 7 9.3 15 20.0 21 28.0</td> <td>10.7 10.0 3.6 2.4</td> <td>4.09E-05 4.45E-05 4.47E-05 4.74E-05</td> <td>1.23E-03 1.38E-03 2.86E-03 9.79E-04</td> <td>GGEC, MUPI, MUPIS, MUPIS, MUPIS, MUPIS, MUPIS CYPAAIQ, UGTLAIQ, CYP289, UGT281, CYP3AIA3, CYP2C4Q, RETSAT MUPI, MUPIS, MUPIS, MUPIS, SEIPINAIE, MUPIQ, SEPINAIG, POGFRL, MUPIR, MUPIS, MUPIS, MUPIA, MUPIS, MUPII, ANGPTL4 MUPIS, MURI, CYP29, GNE, EHHADH, CYP289, UGT281, CYP2C40, UPP2, AKA, LPINZ, LPINI, CYPAHQ, UGTLAIQ, TDOZ, GGPC, HYKK, HMGCS2, HOC, CYP34IA, ACAAIB</td>	KEGG_PATHWAY GOTERM_BP_DIRECT KEGG_PATHWAY GOTERM_CC_DIRECT KEGG_PATHWAY	GO:004293*plucose homeotatais mmu00830.Petinol metabolism GO:0005576*extracellular region mmu01100.Metabolic pathways	7 9.3 7 9.3 15 20.0 21 28.0	10.7 10.0 3.6 2.4	4.09E-05 4.45E-05 4.47E-05 4.74E-05	1.23E-03 1.38E-03 2.86E-03 9.79E-04	GGEC, MUPI, MUPIS, MUPIS, MUPIS, MUPIS, MUPIS CYPAAIQ, UGTLAIQ, CYP289, UGT281, CYP3AIA3, CYP2C4Q, RETSAT MUPI, MUPIS, MUPIS, MUPIS, SEIPINAIE, MUPIQ, SEPINAIG, POGFRL, MUPIR, MUPIS, MUPIS, MUPIA, MUPIS, MUPII, ANGPTL4 MUPIS, MURI, CYP29, GNE, EHHADH, CYP289, UGT281, CYP2C40, UPP2, AKA, LPINZ, LPINI, CYPAHQ, UGTLAIQ, TDOZ, GGPC, HYKK, HMGCS2, HOC, CYP34IA, ACAAIB
For Edge (PM-WW) mmu000171stry add degradation 5 6.7 11.6 7.15 Feb 0.011 (CPMA10, ACX1, E02, EHMAH), ACX14 FORM CD, DIRECT 6.0005829*-cytosid 21 28.0 2.1 9.16 Feb 0.0005(AR3, MP11.4) SOTEM, DC, DIRECT 6.0005629*-frig add catabilic process 3 4 2.2 2.8.0 0.011 (CPMA10, ACX1, E02, EHMAH), MIP2, EVRA, GPCPD, INMT, STARDA, LIK1, HDC, CPNE1, CESIF, MUP18, GS2, FABP1, YOD, MD SOTEM, BP, DIRECT 6.000551*-frig add catabilic process 5 6.7 8.5 2.29E-08 0.008 (CPMA10, ACX1, E02, 2HMAH), MIP2, ACA18, SLC2PA2 SOTEM, BP, DIRECT 6.000551*-frig add metabolic process 9 2.0 3.2 2.8E-08 0.008 (CPMA10, ACX1, EVRADS, GPCP), ACA18, SLC2PA2 SOTEM, BP, DIRECT 6.000552*Find metabolic process 9 2.0 3.2 2.6E-08 0.005 (CPMA10, ACX1, BSC2PA SOTEM, BP, DIRECT 6.000562*Find metabolic process 9 2.0 3.2 2.6E-08 0.005 (CPMA10, ACX1, BSC2PA SOTEM, BP, DIRECT 6.0005679*reprotisment 1.1 1.12 2.9 3.8 4.001 0.005 (CPMA10, ACX1, BSC2PA	KEGG_PATHWAY GOTERM_BP_DIRECT KEGG_PATHWAY GOTERM_CC_DIRECT KEGG_PATHWAY GOTERM_BP_DIRECT	G0 2002393*glucose homeotasis mmu00883.0Fcm lon etabalism G0 2005576*extracellular region mmu01103.Metabolic pathways G0 2007139************************************	7 9.3 7 9.3 15 20.0 21 28.0 4 5.3	10.7 10.0 3.6 2.4 41.0	4.09E-05 4.45E-05 4.47E-05 4.74E-05 9.99E-05	1.23E-03 1.38E-03 2.86E-03 9.79E-04 2.76E-03	GGPC, MUP1, MUP3, MUP2, MUP18, MUP9, MUP11 CMP4A10, UGTLA10, CMP289, UG7281, CMP3A1A, CMP2C40, RETSAT MUP7, MUP1, MUP, MUP, MUP, MUP3, SEPINAL MUP10, SEPINALA, POGFRL, MUP13, MUP15, MUP14, MUP9, MUP11, ANGPTL4 ETNPPL, ACXXL, CMP28, GNE, EHHADH, CMP289, UGT281, CMP2C40, UPP2, AK4, LPIN2, LPIN1, CMP4410, UGTLA10, TD02, GGPC, HYKK, HMGCS2, HDC, CYP3A41A, ACA1B MUP1, UGT281, MUP18, MUP11
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Bit Net Public Time Control UP Public Time Contro Public Public Publi	KEGG_PATHWAY GOTERM_BP_DIRECT KEGG_PATHWAY GOTERM_CC_DIRECT KEGG_PATHWAY GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	GO.002593-glucose homeostasis mmu00880.Retinol metabolism GO.0005576-restracellular region mmu0100.Metabolic pathways GO.001394-recllular regionse to testosterone stimulus GO.0005637-fatty avid beta-oxidation GO.0036547-response to stillbenid	7 9.3 7 9.3 15 20.0 21 28.0 4 5.3 5 6.7 4 5.3	10.7 10.0 3.6 2.4 41.0 16.1 22.5	4.09E-05 4.45E-05 4.47E-05 9.99E-05 2.27E-04 6.53E-04	1.23E-03 1.38E-03 2.86E-03 9.79E-04 2.76E-03 0.006 0.015	GGPC, MUP1, MUP3, MUP2, MUP3, MUP3, MUP3, MUP3, MUP3, C(PP4A10, UGTLA10, CP289, UG7881, CP33A14, CY32400, RETSAT MUP7, MUP1, MUP, MUP, MUP3, MUP3, SEPINAG, MUP13, MUP13, MUP17, MUP15, MUP14, MUP9, MUP11, ANGPTL4 ETNPPL, ACXXL, CP239, ONE, EHHADH, CYP289, UGT281, CY92C40, UP92, AK4, LPIN2, LPIN1, CYP4A10, UGTLA10, TD02, GGPC, HYKK, HMGS2, HOC, CY924, ACA341, ACA341 MUP1, UGT281, MUP18, MUP11 ACCXL, EG2, EHHADH, ACA41, SLC27A2 SICO14, MUP1, MUP3, CYP289
Bit Net Public Time Control UP Public Time Contro Public Public Publi	KEGG_PATHWAY GOTERM_BP_DIRECT KEGG_PATHWAY GOTERM_CC_DIRECT KEGG_PATHWAY GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	GO.002593-glucose homeostasis mmu00880.Retinol metabolism GO.0005576-restracellular region mmu0100.Metabolic pathways GO.001394-recllular regionse to testosterone stimulus GO.0005637-fatty avid beta-oxidation GO.0036547-response to stillbenid	7 9.3 7 9.3 15 20.0 21 28.0 4 5.3 5 6.7 4 5.3	10.7 10.0 3.6 2.4 41.0 16.1 22.5	4.09E-05 4.45E-05 4.47E-05 9.99E-05 2.27E-04 6.53E-04	1.23E-03 1.38E-03 2.86E-03 9.79E-04 2.76E-03 0.006 0.015	GGPC, MUP1, MUP3, MUP2, MUP3, MUP3, MUP3, MUP3, MUP3, MUP1 (CPP4A10, UGTLA10, CP289, UGT281, CP32A14, CY24C40, RETSAT MUP7, MUP1, MUP, MUP, MUP3, MUP3, SEPINAG, PDGFRL, MUP18, MUP17, MUP15, MUP14, MUP9, MUP11, ANGPTL4 ETNPPL, ACXXL, CP29, ONE, EHHADH, CP289, UGT281, CP2C40, UPP2, AK4, LPIN2, LPIN1, CYP4A10, UGTLA10, TD02, GGPC, HYKK, HMGS2, HOC, CP34A14, ACA3B MUP1, UGT281, MUP18, MUP11 ACCXL, EG2, EHHADH, ACA4B, SLC27A2 SICO14, MUP1, MUP3, CP289
Bit Science Sc	KEGG_PATHWAY GOTERM_BP_DIRECT KEGG_PATHWAY GOTERM_CC_DIRECT KEGG_PATHWAY GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	GO:004293*plucose homeotasis mm/00830*femention lerabolism GO:0005576*extracellular region mm/01100.Metabolic pathways GO:0001394*rellular regionse to testosterone stimulus GO:000656*dest ya did beta-oxidiation GO:000656*dest ya did beta-oxidiation GO:0005654*response to stilbenoid mm/002071:Fatty acid degradation	7 9.3 7 9.3 15 20.0 21 28.0 4 5.3 5 6.7 4 5.3 5 6.7	10.7 10.0 3.6 2.4 41.0 16.1 22.5 11.6	4.09E-05 4.45E-05 4.47E-05 9.99E-05 2.27E-04 6.53E-04 7.15E-04	1.23E-03 1.38E-03 2.86E-03 9.79E-04 2.76E-03 0.006 0.015 0.011	GBCC_MUP1, MUP2, MUP2, MUP3, MUP3, MUP3, MUP3, MUP3 CYP4A10, UGTLA10, CYP289, UGT281, CYP3A41A, CYP2C40, RETSAT MUP2, MUP3, MUP3, MUP2, SRIPINALE, MUP10, SEIPINAS, POGFRL, MLP18, MUP17, MLP15, MUP14, MUP3, MUP1, ANGPTL4 ETNPPL, ACXX, CYP29, GNE, EHHADH, CYP289, UGT281, CYP2C40, UPP2, AKA, LPIN2, LPIN1, CYPA410, UGTLA10, TD02, G6PC, HYKK, HMGS2, HOC, CYPA3H, ACAA18 MUP2, UGT281, MUP18, MUP11 ACXX, EG2, EHHADH, ACAA18, SLC27A2 SLCD1A1, MUP1, MUP3, CYP289 CYPA410, ACXXL, EG2, EHHADH, ACAA18 CYP4A10, ACXXL, EG2, EHHADH, ACAA18 CYPA410, ACXXL, EG2, EHHADH, ACMA18
OP SOTEMA BP_DIRECT COUNDEST2-metabolic process 9 12.0 3.7.2 233.E.8 0.0.07/ IGTIAID ACOXE, FC2, HMACKS2, GKE, EHMADH, MY2, ACAAB, SLC27A2 SOTEMA BP_DIRECT COUNDEST-thyt and metabolic process 6 6.0 2.23.E.8 0.0.08/ ICMAD, SQCAADAB, SLC27A2 GOTEMA BP_DIRECT COUNDEST-metabolic process 6 6.2 2.25.E.8 0.0.08/ ICMAD, SQCAADAB, SLC27A2 GOTEMA BP_DIRECT COUNDEST-metabolic process 9 2.0 3.6 2.0E.6.8 0.0.007/ ISCTABA, SPC, UPN2, GACABB, SLC27A2, UPN1 GOTEMA BP_DIRECT COUNDEST-metabolic process 9 2.0 3.6 2.0E.6.8 0.0.005 LANGE, SLC2AAL, UPN2, GACABB, SLC27A2, UPN1, RETSAT GOTEMA CP_DIRECT COUNDEST®-metabolic process 5 7.0 0.0.05 LANGE, SLC2AAL, UPN2, GACABB, SLC27A2, UPN1, RETSAT GOTEMA LP_DIRECT COUNDEST®-metabolic process 5 6.7 C.0.05 LANGE, GACABB, SLC27A2, UPN1, RETSAT GOTEMA LP_DIRECT COUNDEST®-metabolic process 5 C.7 LANGE, SLC27A2, UPN2, MY28, CY28, LANGE, SLC27A2, UPN2, GACABB, SLC27A2, UPN2, GACABB, SLC27A2, UPN2, GACABB, SLC27A2, UPN2, GACABB, SLC27A2, UPN1, RETSAT GOTEMA	KEGG_PATHWAY GOTERM_GP_DIRECT KEGG_PATHWAY GOTERM_CC_DIRECT KEGG_PATHWAY GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_GP_DIRECT	GO.2002593*plucose homestasis mmu00830.844*cml metabolism GO.2005576*extracellular region mmu10103Metabolic pathways GO.2007394*cml lular response to testosterone stimulus GO.20056554*response to stilloenoid mmu00203.044*cml lular response to testosterone stimulus GO.20056554*response to stilloenoid mmu00071.64*ad degradation GO.2005654*response to stilloenoid GO.2005654*response to stilloenoid GO.2005654*response to stilloenoid GO.2005654*response to stilloenoid	7 9.3 7 9.3 15 20.0 21 28.0 4 5.3 5 6.7 4 5.3 5 6.7 21 28.0	10.7 10.0 3.6 2.4 41.0 16.1 22.5 11.6 2.1	4.09E-05 4.45E-05 4.47E-05 9.99E-05 2.27E-04 6.53E-04 7.15E-04 9.16E-04	1.23E-03 1.38E-03 2.86E-03 9.79E-04 2.76E-03 0.006 0.015 0.011 0.029	GBPC, MUP2, MUP2, MUP2, MUP2, MUP3, MUP3, MUP11 (CPVAID (05TLA) (CPV28), UST28), CPVAID, CPVAID, CPVAOD, BETSAT MUP2, MUP2, MUP3, MUP2, SEPHIALE, MUP10, SEPPIAE, POSFIL, MUP18, MUP15, MUP15, MUP14, MUP3, MUP11, ANGPTL4 ETNPFL, ACCX1, CPV280, GNE, EHHADH, CPV289, UGT281, CPV2C40, UPP2, ACA, LPN2, LPN1, CPVALD, UGTLA1D, TDO2, GBPC, HYKK, HMGCS2, HDC, CPV3ALD, ACAALB MUP1, UGT281, MUP18, MUP11 ACCX1, ECD, EHHADH, ACAALB, SICZPA2 SICC01A1, MUP1, MUP3, CPV289 (CPVALD, ACCX2, ECD, EHHADH, ACAALB TXNIF, MUP1, GNE, MUP2, EHHADH, MUP2, LPN2, GPCPD1, INMT, STARD4, ULK1, HDC, CPNE1, CES1F, MUP18, GYS2, FABP1, YOD1, MUP9, MUP1, GNE, MUP2, GNE2, EHHADH, MUP2, LPN2, GPCPD1, INMT, STARD4, ULK1, HDC, CPNE1, CES1F, MUP18, GYS2, FABP1, YOD1, MUP9, MUP1, GNE, MUP2, BEHADH, MUP2, LPN2, GPCPD1, INMT, STARD4, ULK1, HDC, CPNE1, CES1F, MUP18, GYS2, FABP1, YOD1, MUP9, MUP1, GNE, MUP2, BHHADH, MUP2, LPN2, GPCPD1, INMT, STARD4, ULK1, HDC, CPNE1, CES1F, MUP18, GYS2, FABP1, YOD1, MUP9, MUP1, GNE, MUP2, GNE2, HHADH, ACAALB
SOTEM. #P. DIRECT 60.0006317-fatty add metabolic process 6 8.0 5.2 2.55 E63 0.008 [VPAA10, 40X2, EHKADN, [VPL2, ACALB, SLC27A2 SOTEM. #P. DIRECT 0.00065297-lipid metabolic process 9 12.0 3.6 3.04E.68 0.005 [AVL2, NMP2S, SLC2FA2, LPNA, SUC2FA2, LPNA GOTEM, M. P. DIRECT 0.00065297-lipid metabolic process 9 12.0 3.5 3.04E.68 0.005 [AVL2, NMP2S, MCL2, MMP3, MCL2,	KEGG PATHWAY GOTERM, BP DIRECT KEGG PATHWAY GOTERM, CC DIRECT KEGG PATHWAY GOTERM, BP DIRECT GOTERM, BP DIRECT GOTERM, BP DIRECT KEGG PATHWAY GOTERM, CC DIRECT	G0:0002593*plicose homeostasis mm/00830.Petrion Imetabolism G0:0005576*extracellular region mm/01100.Metabolic pathways G0:0001394*rcellular regionse to testosterone stimulus G0:00006574*rsty add beta-oxidation G0:0000554*response to stilbenoid mmu0001/1-fatty add deta-oxidation G0:000565*response to stilbenoid mmu0001/1-fatty add deta-oxidation G0:000562*response to stilbenoid G0:000562*response G0:000562*response G0:000562*response G0:000562*response G0:000562*response G0:000562*response G0:000562*response G0:000562*response	7 9.3 7 9.3 15 20.0 4 5.3 5 6.7 4 5.3 5 6.7 21 28.0 3 4.0	10.7 10.0 3.6 2.4 41.0 16.1 122.5 11.6 2.1 42.3	4.09E-05 4.45E-05 4.47E-05 9.99E-05 2.27E-04 6.53E-04 7.15E-04 9.16E-04 2.03E-03	1.23E-03 1.38E-03 2.86E-03 9.79E-04 2.76E-03 0.006 0.015 0.011 0.029 0.044	GePC_MUP1_MUP2_MUP2_MUP13_MUP3_MUP3_MUP1_ CYPAA10, UGTLA10, CYP289, UGT281, CYP3A43A, CYP3C40, RETSAT MUP2_MUP3_MUP3_MUP2_SEPINAALE_MUP10_SEPINA6, POGFRL_MUP18, MUP17, MUP15, MUP14, MUP3, MUP11, ANGPTL4 ETNPPL_ACX1, CYP219, GNE_EHHADH, CYP289, UGT281, CYP3C40, UPP2, AKA, LPIN2, LPIN1, CYPAA10, UGTLA10, TD02, G6PC, HYKK, HMGS2, H0C, CYP304A, ACAA18 MUP1_UGT281, MUP18, MUP11 ACX0, EQ2_EHHADH, ACAA18, SIC27A2 SICO1A1, MUP1, MUP3, GYP289 CYPAA10, ACX1, EG2_EHHADH, ACAA18 TXNIF, MUP1, GNE, MUP3, EHHADH, MUP2, LPIN2, GPCP1, INMT, STARD4, ULK1, HDC, CPNE1, CES1F, MUP18, GYS2, FABP1, YOD1, MUP9, CAR3, MUP11 CAR3, MUP11
SOTEM. JP. DIRECT 00.004232*sodum-independent organic anion transport 3 40 37.6 2.66E.68 0.0071kLC028_3 SLC01A1, SLC22A2 SLC2A2A5 SOTEM. JP. DIRECT 00.005827*negative regulation of transcription, DNA-templated 9 12.0 3.6 3.46E.68 0.0056 [MuP1, NND2, KLF10, MUP3, MUP2, MUP3, MUP3, MUP2, MUP3, MUP	KEGG PATHWAY GOTERM, BP DIRECT KEGG PATHWAY GOTERM, CC DIRECT KEGG PATHWAY GOTERM, BP DIRECT GOTERM, BP DIRECT GOTERM, BP DIRECT KEGG PATHWAY GOTERM, CC DIRECT	GO:002593*plucose homestasis mmu00883.0#cml metabolism GO:000557*extracellular region GO:000557*extracellular region GO:000557*extracellular region GO:000557*extracellular region GO:0005557*extracellular region GO:0005557*extracellular region GO:0005554*response to bistosterone stimulus GO:0005654*response to stilleenoid mmu000154*rati ad degradation GO:000562*raty ad desolic process mmu000054*reti y ad desolic process mmu00054*reti y ad desolic process	7 9.3 7 9.3 15 20.0 4 5.3 5 6.7 4 5.3 5 6.7 21 28.0 3 4.0 5 6.7	10.7 10.0 3.6 4.4 41.0 16.1 22.5 11.6 2.1 42.3 8.5	4.09E-05 4.45E-05 4.47E-05 9.99E-05 2.27E-04 6.53E-04 7.15E-04 9.16E-04 2.03E-03 2.29E-03	1.23E-03 1.38E-03 2.86E-03 9.79E-04 2.76E-03 0.006 0.015 0.011 0.029 0.044 0.028	GePC, MUP2, MUP2, MUP2, MUP2, MUP3, MUP3, MUP11 (CPVAID (05TAL) (CP289, UST28), CP2AIA1, CYP2C40, BETSAT MUP2, MUP2, MUP3, MUP2, SEPHIALE, MUP10, SEPHIAE, POSFIL, MUP18, MUP15, MUP15, MUP14, MUP3, MUP11, ANGPT14 ETNPFL, ACCX1, CP249, GNE, EHHADH, CP289, UGT281, CP2C40, UP22, AK4, UP12, PUN1, CYPA410, UGT1A10, TD02, GBPC, HYKK, HMGC52, H0C, CP3A412, ACAA18 MUP1, MUP1, MUP2, MUP13, MUP13 ACCX1, EC2, EHHADH, ACAA18, SCC27A SLC07A1, MUP1, MUP3, CP289 (CPA410, ACCX1, EC2, EHHADH, ACAA18 TXNIF, MUP1, GNE, GUP24, CACA18 TXNIF, MUP1, GNE, MUP2, EHHADH, MUP2, UP12, GPCP01, INMT, STARD4, ULK1, HDC, CPNE1, CES1F, MUP18, GYS2, FABP1, YOD1, MUP9, CR48, MUP1 EC2, LIPU8, LIPU14 EC2, LIPU8, LIPU14
BOTEM, JP, DIRCET 00.005629*:joint metabolis process 9 12.0 3.6 3.04E.63 0.052 ACCM, MASCS, EHHADH, ASPC, JUNZ, GOCDD, ACARLIS, SICZPAZ, JUNI GOTEM, LC, DIRECT 00.00589*:endpotengialition of transcription, DNA-templated 11 14.7 2.9 3.91E.64 0.0058 MUPR, MISL, MUPR, M	Correm de planect Correm de planect KEGG PATHWAY GOTERM CC DIRECT KEGG PATHWAY GOTERM BP DIRECT GOTERM BP DIRECT KEGG PATHWAY GOTERM BP DIRECT KEGG PATHWAY GOTERM BP DIRECT KEGG PATHWAY GOTERM BP DIRECT GOTERM BP DIRECT GOTERM BP DIRECT	G0:004293*Pjucose homeostais mm00830.64mion metabolism G0:0005576*extracellular region mm01100.Metabolic pathways G0:0005576*extracellular region mm011394*rellular regionse to testosterone stimulus G0:0006557*extraded G0:0005654*response to stillebroid mm000171*stty add beta-oxidation G0:000563*response to stillebroid mm000171*stty add degradation G0:000562*response	7 9.3 7 9.3 15 20.0 21 28.0 4 5.3 5 6.7 4 5.3 5 6.7 21 28.0 3 4.0 5 6.7 9 12.0	10.7 10.0 3.6 2.4 4.0 16.1 22.5 11.6 2.1 42.3 8.5 3.7 6.2	4.09E-05 4.45E-05 4.47E-05 9.99E-05 2.27E-04 6.53E-04 7.15E-04 9.16E-04 2.03E-03 2.29E-03 2.33E-03 2.53E-03	1.23E-03 1.38E-03 2.86E-03 9.79E-04 2.76E-03 0.006 0.015 0.011 0.029 0.044 0.028 0.047	GerC, MUP2, MUP2, MUP2, MUP3, MUP3, MUP3, MUP3 CPRA10, UGTLAID, CP289, UGT281, CP3A415, CP2640, RETSAT MUP2, MUP3, MUP2, MUP3, MUP2, SEIPHARE, MUP10, SEIPHARE, POGFRL, MLP18, MUP17, MLP15, MUP14, MUP3, MUP11, ANGPTL4 ETNIPEL, ACXX, CP289, GNE, BHARDH, CP289, UGT281, CP3240, UP92, AKA, LPIN2, LPIN1, CPPA410, UGTLAI0, TD02, GBPC, HYKK, HMG52, HOC, CP340, ACAAL8 MUP2, UGT381, MUP3, MUP3, MUP11 ACXX, EC2, EHANDH, ACAAL8, SLC22A2 SLC01AL, MUP3, MUP3, GNE3, EHARDH, MLP2, LPIN2, GPC91, INMT, STARDA, ULK1, HDC, CPNE1, CE51F, MUP18, GY52, FABP1, YOD1, MUP9, CAR3, MUP1, MUP3, GNE3, LPIN3, EHARDH, MLP2, LPIN2, GPC91, INMT, STARDA, ULK1, HDC, CPNE1, CE51F, MUP18, GY52, FABP1, YOD1, MUP9, CAR3, MUP11 UGTLAID, CC22, LPIN2, LPIN1 UGTLAID, CC22, LPIN2, LPIN1 UGTLAID, CC22, LPIN2, LPIN1 UGTLAID, CC22, MUC52, MUC53, GAE, EHHADH, GY52, ACAAL8, SLC27A2
SOTEM & P. DIRECT 60/005822*negative regulation of transcription, DNA-templated 9 2.2 3.5 3.46:26 0.055 [MUE7, NN1D2, KET3, MUP3, MUP2, MUP13, MUP2, MUP14, MUP3, MU	KEGG PATHWAY GOTERM, CC, DIRECT KEGG PATHWAY GOTERM, CC, DIRECT KEGG PATHWAY GOTERM, BP, DIRECT GOTERM, BP, DIRECT	G0.2002593*plucose homeostasis mmu00883.0#cml metabolism G0.2005576*extracellular region mmu10103.Metabolic pathways G0.200556*extracellular region G0.2005657*fatty add beta exidation G0.2005657*fatty add beta exidation G0.200562*fatty add degradation G0.200562*fatty add catabolic process G0.200562*fatty add catabolic process G0.200562*fatty add catabolic process G0.2005615*ruty add metabolic process	7 9.3 7 9.3 15 20.0 4 5.3 5 6.7 4 5.3 5 6.7 21 28.0 3 4.0 5 6.7 9 12.0 6 8.0	10.7 10.0 3.6 2.4 4.0 16.1 22.5 11.6 2.1 42.3 8.5 3.7 6.2	4.09E-05 4.45E-05 4.47E-05 9.99E-05 2.27E-04 6.53E-04 7.15E-04 9.16E-04 2.03E-03 2.29E-03 2.33E-03 2.53E-03	1.23E-03 1.38E-03 2.86E-03 9.79E-04 2.76E-03 0.006 0.015 0.011 0.029 0.044 0.024 0.028	GBCC, MUP2, MUP2, MUP2, MUP3, MUP3, MUP3, MUP3 (CPA410, UGT1A10, CP288, UGT28, UGT28, UGT28, UGT281, CVP204, BETSAT MUP2, MUP2, MUP3, MUP3, SEPENALE, MUP10, SEPENALA, POGERL, MUP18, MUP15, MUP15, MUP14, MUP3, MUP1, ANGPTL4 EINPA, LACXI, LOV28, BARE, EHHADH, CVP28, UGT281, CVP2040, UPP2, AKA, UPIA, LPIN2, LPIN1, CVPA410, UGT1A10, TDO2, GBPC, HYKK, HMG523, HDC, CVP3ML8, ACAA18 SLC014, GD2, EHHADH, ACAA18, SLC27A2 SLC0141, MUP1, MUP3, GPT286 (CVPA410, ACXI, EG2, EHHADH, MUP2, LPIN2, GPCP01, INMT, STARD4, ULK1, HDC, CPNE1, CES1F, MUP18, GYS2, FABP1, YOD1, MUP9, GM3, MUP1, GWE, MUP3, EHHADH, MUP2, LPIN2, GPCP01, INMT, STARD4, ULK1, HDC, CPNE1, CES1F, MUP18, GYS2, FABP1, YOD1, MUP9, GM3, MUP1, GWE, MUP3, EHHADH, MUP2, LPIN2, GPCP01, INMT, STARD4, ULK1, HDC, CPNE1, CES1F, MUP18, GYS2, FABP1, YOD1, MUP9, GM3, MUP1, GWE, MUP3, EHHADH, MUP2, LPIN2, GPCP01, INMT, STARD4, ULK1, HDC, CPNE1, CES1F, MUP18, GYS2, FABP1, YOD1, MUP9, GUT1A10, CC798, UGT281, CVP3A41A, CYP2C40 UGT1A10, ACXX1, EG2, HMAD4, ACAR, SLC27A2 CVPA403, ACXX1, EG2, HMAD4, MUP2, LCAA18, SLC27A2
SDTEML CC_DIRECT 60.0005/28P*-endplasmic reticulum membrane 11 14/2 2.9 391E-68 0.008 (CYMALD, RITT, REX0EGBABBIK, CYP226, UP284, U	KEGG PATHWAY GOTERM & P.DIRECT KEGG PATHWAY GOTERM_CC_DIRECT KEGG PATHWAY GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT GOTERM_BP_DIRECT	G0.002393*glucose homestasis mmu00883.Refution Inetabolism G0.00055*Textracellular region mmu0100.Netabolicy patways G0.00055*Textracellular regions to testosterone stimulus G0.000563*Tatty add beta-oxidation G0.00052*Textracellular response to testosterone stimulus G0.000563*Tatty add degradation mmu00021*Fatty add catabolic process mm00002*Tatty add catabolic process mm00002*Tatty add tatabolic process G0.000651*Tatty add metabolic process	7 9.3 7 9.3 15 20.0 4 5.3 5 6.7 4 5.3 5 6.7 21 28.0 3 4.0 5 6.7 9 12.0 6 8.0 3 4.0	10.7 10.0 3.6 2.4 41.0 16.1 22.5 11.6 2.1 42.3 8.5 3.7 6.2 3.7 6.2 3.7	4.09E-05 4.45E-05 4.47E-05 9.99E-05 2.27E-04 6.53E-04 7.15E-04 9.16E-04 2.03E-03 2.29E-03 2.29E-03 2.25E-03 2.53E-03 2.53E-03 2.53E-03	1.23E-03 1.38E-03 2.86E-03 9.79E-04 2.76E-03 0.006 0.015 0.011 0.029 0.044 0.028 0.047 0.047	GREC, MUP2, MUP2, MUP2, MUP3, MUP3, MUP3, MUP3 CYPAA10, UGTLA10, CYP289, UGT281, CYP3A43A, CYP2C40, RETSAT MUP7, MUP3, MUP2, MUP3, MUP2, SEIPHIAAE, MUP10, SEIPHIAAE, PDGFRL, MUP18, MUP17, MUP15, MUP14, MUP3, MUP11, ANGPTL4 ETNPFL, ACXXL, CYP28, ONE, BHAUH, CYP289, UGT281, CYP2C40, UPP2, AK4, LPIN2, LPIN1, CYPA410, UGTLA10, TDD2, GBPC, HYKK, HMG52, HDC, CYP28, ANDE, BHAUH, CYP289, UGT281, CYP2C40, UPP2, AK4, LPIN2, LPIN1, CYPA410, UGTLA10, TDD2, GBPC, HYKK, HMG52, HDC, CYP38, MUP18, MUP11 ACCXXL, EC02, EHADH, ACAN18, SIC27A2 SIC01A1, MUP1, MUP3, GYP289 CYPA410, ACCXXL, ED4HADH, ACAN18, SIC27A2 SIC01A1, MUP1, GNE, MUP3, EHHADH, MUP2, LPIN2, GCPD1, INMT, STARD4, ULK1, HDC, CPNE1, CES1F, MUP18, GNS2, FABP1, VOD1, MUP9, CA83, MUP11 UGTLA10, CCYP280, UGT281, CYP3A41, CYP2C40 UGTLA10, CCYR1, ENC, HMC52, GBE, EHHADH, GNS2, ACAN18, SIC27A2 CYP4A10, ACCXXL, ENCH, HMC52, CRE, EHHADH, GNS2, ACAN18, SIC27A2 CYP4A10, ACCXXL, ENCH, HMC52, GBE, EHHADH, GNS2, ACAN18, SIC27A2 CYP4A10, ACCXXL, ENCH, HMC52, GBE, EHHADH, GNS2, ACAN18, SIC27A2 CYP4A10, ACCXXL, ENCHADE, ACCAN18, SIC27A2 CYP4A10, ACCXXL, ENCHADE, ACCAN18, SIC27A2 CYP4A10, ACCXXL, ENCHADE, ACCAN18, SIC27A2
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SOTEM CC_DRECT 60/005777_provisione \$ 67 \$ 55 0.02 0.188 ACCV, EO2, EHADH, ACAAB, SLCZA2 SOTEM VD_DRECT 60/005177_provisione \$ 67 \$ 55 0.02 0.188 ACCV, EO2, EHADH, ACAAB, SLCZA2 SOTEM VD_DRECT 60/005177_provisione \$ 3 4.0 0.013 0.125 (2744.10, KVP280, CYP381A, CYP240, SDR97, AKRELIA, RETSAT SOTEM VD_DRECT 60/005377*provisione \$ 4 \$ 5 7.4 0.016 (VP280, CYP381A, CYP240, SDR97, AKRELIA, RETSAT GOTEM, CC_DRECT 60/005377*provisione \$ 4 \$ 5 7.4 0.015 (VP481, CYP280, CYP381A, CYP240, SDR97, AKRELIA, RETSAT GOTEM, CC_DRECT 60/005377*provisione \$ 4 \$ 5.0 0.018 (LRT1, CYP28, CYP3841A, CYP240 GOTEM, CC_DRECT 60/00537*strandplankine relabolism \$ 4 \$ 5.0 6.0 0.021 0.138 (LRT1, CYP28, CYP3841A, CYP240 GOTEM, CDRECT 60/00547*postrendpospholiphi relabolism \$ 4 \$ 5.0 0.022 0.138 (LRT1, CYP28, CYP3441A, CYP240 GOTEM, CDRECT 60/00547*postrendpospholiphi relabolism \$ 4 \$ 5.0 0.021 0.138 (LRT1, CYP28, CYP3441A, CYP240 GOTEM, MP_DRECT 60/0054	KEGG PATHWAY GOTERM, GP, DIRECT GOTERM, GC, DIRECT KEGG PATHWAY GOTERM, GC, DIRECT KEGG PATHWAY GOTERM, GP, DIRECT GOTERM, GC,	Go 2002593*plucose homestasis mmuD08308.fetuion lee tabolism mmuD08308.fetuion lee tabolism mmuD0103.Metabolis pathways Go 2007134**Calliar regione mmuD0103.Metabolis pathways Go 2007134**Calliar regiones to testosterone stimulus Go 200563**Tatty add beta-axidation Go 200563**Tatty add beta-axidation Go 200562**Tatty add betabolis process Go 200562**Tatty add betabolis process Go 200562**Tatty add betabolis process Go 200562***Tatty add betabolis process Go 200562**********************************	7 9.3 7 9.3 15 20.0 21 28.0 4 5.3 5 6.7 21 28.0 3 4.0 5 6.7 9 12.0 6 8.0 3 4.0 9 12.0 9 12.0 12.0 12.0 12.0 12.0 12.0 12.0 12.0	10.7 10.0 10.0 3.6 2.4 41.0 16.1 22.5 11.6 2.1 42.3 8.5 3.7 6.2 3.7.6 3.6 3.5 2.9 7.0	4.09E-05 4.45E-05 4.47E-05 9.99E-05 2.27E-04 6.53E-04 7.15E-04 9.16E-04 2.03E-03 2.33E-03 2.33E-03 2.53E-03 3.04E-03 3.04E-03 3.91E-03 0.005	1.23E-03 1.38E-03 2.86E-03 9.79E-04 2.76E-03 0.006 0.011 0.029 0.044 0.028 0.047 0.048 0.047 0.048 0.047 0.052 0.056	GBCC, MUP2, MUP2, MUP2, MUP3, MUP3, MUP3, GBCC, MUP2, MUP2, MUP2, MUP3,
SOTEM. C2, DIRECT 00:005777*peroxisiome \$ 6.7 5.5 0:012 0.180 ACXX, EC12, EH4ADH, ACAAB, SLCZAA2 SOTEM. MP_DIRECT 00:005177*operoxisiome 10 3 2.6 0:013 D125 (CP4A10, ACAAB, SLCZAA2 SOTEM. MP_DIRECT 00:005177*operoxisiome 3 4.0 15.1 0:014 0.194 (CP2C40 CP2BA, CP2BA10, CP2BA2, CP2BA10, CP2BA2, CP2BA10, CP2CA0 SOTEM. MC_DIRECT 00:005177*peroxisiome 4 5.3 7.4 0:016 0:138 (PT1, CP2B, CP2BA14, CP2CA0 SOTEM. MC_DIRECT 00:005787*endplasmic reticulum 14 18.7 2.0 0:013 0:181 (PT1, CP2B, CP2BA14, CP2CA0 COTEM. MC_DIRECT 00:005787*endplasmic reticulum 14 18.7 2.0 0:013 0:181 (PT1, CP2B, CP2BA14, CP2CA0 COTEM. MC_DIRECT 00:005787*endplasmic reticulum 14 18.7 0.012 0:138 (PT1, CP2B, CP2BA14, CP2CA0 COTEM. MC_DIRECT 00:00587*indgra1 (One) 4 5.3 0.022 0:138 (PT1, CP2B, CP2A14, SC2PA2, SLC2A2, S	Corrend P Direct Corrend P Direct Corrend C Direct Corrend C Direct Corrend P Direct Corren	G0.0002937-glucose homeostasis mmu00830.804-end metabolism G0.0005576*extracellular region mmu10103Metabolic pathways G0.0005576*extracellular region G0.0005576*extracellular region G0.0005576*extracellular region G0.0005576*extracellular region G0.000657 mmu00010.1016*ud degradation G0.000582*rytosol G0.000582*regiber process G0.000582*regiber process G0.000582*regiber process G0.000587*regiber process G0.000587*regiber process G0.000587*regiber process G0.000587*regiber process G0.000587*regiber process G0.000578*rendoglasmic reticulum membrane mmu002004.remical carcinogeneeris	7 9.3 7 9.3 15 20.0 21 28.0 4 5.3 5 6.7 21 28.0 3 4.0 5 6.7 9 12.0 6 8.0 3 4.0 9 12.0 9 12.0 12.0 12.0 12.0 12.0 12.0 12.0 12.0	10.7 10.0 10.0 3.6 2.4 41.0 16.1 22.5 11.6 2.1 42.3 8.5 3.7 6.2 3.7.6 3.6 3.5 2.9 7.0	4.09E-05 4.45E-05 4.47E-05 9.99E-05 2.27E-04 6.53E-04 7.15E-04 9.16E-04 2.03E-03 2.33E-03 2.33E-03 2.53E-03 3.04E-03 3.04E-03 3.91E-03 0.005	1.23E-03 1.38E-03 2.86E-03 9.79E-04 2.76E-03 0.006 0.015 0.011 0.029 0.044 0.028 0.047 0.048 0.047 0.052 0.056 0.0600	GREC, MUP2, MUP2, MUP2, MUP13, MUP3, MUP11 CYCHALD, UCTALD, CYP280, UCT29, VGPA41A, CYP2C40, RETSAT MUP7, MUP1, MUP3, MUP2, SERPINATE, MUP10, SERPINAG, POGFRL, MUP18, MUP17, MUP15, MUP14, MUP3, MUP1, ANGPTL4 ETMPR, ACXX, CYP20, ONE, EHHADH, CYP280, UGT281, CYP2C40, UPP2, AK4, UPIN2, UPIN1, CYPA410, UGTAL10, TDO2, G6PC, HYKK, HMKC52, HOC, CYPA41A, CACA18 MUP2, MUP18, MUP18, MUP11 ACXX1, FC2, EHHADH, ACXA18, SLC27A2 SLC01AZ, MUP1, MUP3, GYP280 CYPA410, GCX18, CC2, EHHADH, ACA18 TXNIP, MUP1, GNE, GUP14, ACA18 CIVA110, CYP28, UGT281, CYP240 UGT1A10, ACX18, EG2, HHADH, ACA18, SLC27A2 SLC01AZ, MUP1, MUP3, GYP280 CYPA410, ACX18, EG2, HHADH, ACA18 CIVA110, CYP28, UGT281, CYP2401 UGT1A10, ACX18, UG2, HHADH, ACA18, SLC27A2 SLC01AZ, SLC21H, UD1, ACA18, SLC27A2 SLC01AZ, SLC21H, UD1, ACA18, SLC27A2 UGT1A10, CYP28, UGT281, CYP2401 UGT1A10, CYP28, UGT281, CYP2404 UGT1A10, CYP28, UGT281, UD12, GACA18, SLC27A2 CIC01AZ, SLC01AZ, SLC21AZ SLC01AZ, SLC01AZ, SLC21AS, SLC27AZ UGT1A10, CYP28, UGT281, GYP240, UPIN2, GACA18, SLC27A2, UPIN1 MUP1, NIC12, LEVENT UGT1A10, CYP28, UGT28, UPIN2, GACA18, SLC27A2, UPIN1 MUP1, NIC2, RETA, G
SOTEM. JP. DIRECT 00.0055114*-oidation-reduction process 10 13.3 2.6 0.013 0.122 (PPRAID, ALCOX, TDO2, EHHADP, (VP2B9, (VP2A4), CVP2C4), SDBSC7, AKRL14, RETSAT SOTEM. JP. DIRECT 00.00337*propyname. P495 pathway 3 4 15.1 0.014 0.134 (VP226), CVP2B3, CVP2C40 SDBSC7, AKRL14, RETSAT SOTEM. JC. DIRECT 00.00337*propyname. P495 pathway 4 5.3 7.4 0.016 0.138 (VP4A10, CVP226), CVP2B3, CVP2C40 SDBSC7, AKRL14, RETSAT SOTEM. JC. DIRECT 00.00357*propynamel membrane 4 5.3 7.4 0.016 0.138 (VTP4A10, CVP2B, CVP2C40, SPBRN41E, LPN14, LPN14, LPN14, LPN14, LPN14, CVP2A10, CVP2A10, CVP2B, CVP2C40, SPBRN41E, LPN142, LPN14, CVP2A10, CVP2A10, CVP2B, CVP2A10, SPBRN41E, LPN142, LPN144, CVP2A10, CVP2B10, CVP2B, CVP2A10, SPBRN41E, LPN142, LPN144, CVP2A10, CVP2B10, CVP2B, CVP2A10, SPBRN41E, LPN144, CVP2A10, CVP2B10, CVP2B10, CVP2B, CVP2A10, SPBRN41E, LPN142, LPN144, CVP2A10, CVP2B10, CVP2B1	KEGG PATHWAY GOTERM_CC_DIRECT GOTERM_CC_DIRECT KEGG PATHWAY GOTERM_CC_DIRECT KEGG PATHWAY GOTERM_CC_DIRECT GOTERM_BP_DIRECT GOTERM_CD_R GOTR	Go 2002393*plucose homeostasis mmu008830*etmol metabolism mmu008830*etmol metabolism mmu008830*etmol metabolism mmu0100.Metabolis pathways Go 200739**Utiliar response to testosterone stimulus Go 200563**fatty add beta-axidation Go 200563**fatty add beta-axidation mmu00000**fatty add beta-axidation mmu00000**fatty add betabolis process Go 200582**protosol Go 200582**protosol Go 200582**rotosol Go 200582**rotosol Go 200582**rotosol Go 200582**rotosol Go 20058**rotosol mmu004#*rotosol mmu04#*rotosol mmu04#*rotosol mmu04#*rotosol mmu04#*rotosol mmu04#*rotosol mmu04#*rotosol mmu04#*rotosol mmu04#*rotosol Go 20058**rotosol Go 20058**	7 9.3 7 9.3 15 20.0 21 28.0 4 5.3 5 6.7 21 28.0 3 4.0 5 6.7 9 12.0 6 8.0 3 4.0 9 12.0 9 12.0 9 12.0 11 14.7 5 6.7 5 6.7	10.7 10.0	4.09E-05 4.45E-05 4.47E-05 9.99E-05 2.27E-04 6.53E-04 7.15E-04 9.16E-04 2.03E-03 2.29E-03 2.33E-03 2.33E-03 2.53E-03 3.04E-03 3.04E-03 3.04E-03 3.04E-03 3.04E-03 3.04E-03 0.0005	1.23E-03 1.38E-03 2.86E-03 9.79E-04 2.76E-03 0.006 0.015 0.011 0.029 0.044 0.047 0.048 0.047 0.056 0.049 0.056	GBCC, MUP2, MUP2, MUP2, MUP3, MUP3, MUP3, GEOC, MUP2, MUP2, MUP3, M
SOTEM. BP. DIRECT 60.001377*pcoxyeenae P450 pathway 3 4.0 1.5.1 0.014 0.149{CPP2C80 CPP2C80 SOTEM. CD. DIRECT 60.001377*pcoxyeenae P450 pathway 4 5.3 7.4 0.016 0.149{CPP2C80 CPP2C80 CPP2C80 SOTEM. CD. DIRECT 60.001377*pcoxyeenae membrane 4 18.7 2.0 0.015 0.0133 [BF17, CPP2.80, CPP22.80, CPP2.80, CPP2.40, SEP1MA1E, UP1A1.0, GPC, STARD4, CES1F, SLC27A2, RETSAT VEGE PATHWAY mmu00545% consponses membrane 7 9.3 3.1 0.022 0.138 [BF17, CPP2.80, CPP2.80, SEP1MA1E, UP1A1, CPP2.40, SEP1MA1E, UP1A1, UPTAA10, GPC, STARD4, CES1F, SLC27A2, RETSAT GOTEM. VC. DIRECT 60.005887*integral component of plasma membrane 7 9.3 3.1 0.022 0.218 [MF1, MP2, MUP2, MUP3, MUP2, MUP1, MUP3, MUP2, MUP1, MUP4, MUP4, MUP1, MUP4, MUP4, MUP1, MUP4, MU	GOTERM & DURECT GOTERM & DURECT GOTERM & DURECT GOTERM & DURECT GOTERM (C_DURECT GOTERM (C_DURECT	Go 2002593*plicose homestais mmu008836*ention letabolism Go 200357*extracellular region mmu0100.Metabolic pathways GO 200357*extracellular region GO 200357*extracellular region GO 200357*extracellular region GO 200557*extracellular region GO 200557*extracellular region GO 200557*extracellular region GO 200557*extracellular region mmu00100*extraposes to stilbenoid mmu00000*extraposes to stilbenoid mmu00000*extraposes to stilbenoid GO 200562**rative acid catabolic process GO 200562**rative acid catabolic process GO 200582**roptade hormone biosynthesis GO 200582**roptade metabolic process GO 200582**roptade metabolic	7 9.3 7 9.3 15 20.0 21 28.0 4 5.3 5 6.7 4 5.3 5 6.7 21 28.0 3 5 6.7 9 12.0 5 6.7 9 12.0 3 9 12.0 9 12.0 9 12.0 9 12.0 11 14.7 5 6.7 5 6.7 5 6.7 5 6.7	10.7 10.0 10.0 3.6 2.4 41.0 16.1 22.5 11.6 2.1 42.3 8.5 3.7 6.2 9.7.6 3.6 3.5 3.5 2.9 7.0 6.3 9.5	4.09E-05 4.45E-05 4.47E-05 9.99E-05 2.27E-04 6.53E-04 7.15E-04 9.16E-04 2.03E-03 2.33E-03 2.33E-03 2.33E-03 2.33E-03 3.46E-03 3.04E-03 3.91E-03 0.005 0.007 0.007	1.23E-03 1.38E-03 2.86E-03 9.79E-04 2.76E-03 0.006 0.015 0.011 0.029 0.044 0.028 0.047 0.048 0.047 0.048 0.049 0.055 0.057 0.850	GBCC, MUP2, MUP2, MUP2, MUP3, MUP3, MUP3, GEC GBCC, MUP2, MUP2, MUP2, MUP3, MUP3, MUP3, GERSAT MUP2, MUP2, MUP3, MUP3, SEPPINALE, MUP3D, SEPINAA, POGERI, MUP3B, MUP13, MUP3, MUP3, MUP3, MUP3, MUP3, MUP31, ANGPTL4 EINPV, ACX1, CV298, MCF3EHAAC, KP28B, UGT2B1, CVP2C40, UP22, AKA, UPIN2, UPIN1, CVPAA10, UGT3A10, TDO2, GEPC, HYKK, MMD2, MUP3, MUP3, MUP31, MUP3, MUP31 GCCX1, EC22, EHNADH, ACAA18, SLC27A2 GCCX1, EC22, EHNADH, ACAA18, SLC27A2 SLCDAL, MUP2, MUP3, MUP31 GCCX1, EC22, EENHADH, ACAA18, SLC27A2 GCCX1, EC22, EHNADH, ACAA18, SLC27A2 SLCDAL, MUP2, MUP3, MUP31 GCCX1, EC22, EHNADH, ACAA18, SLC27A2 GCCX1, EC22, EHNADH, ACAA18, SLC27A2 SLCDAL, MUP2, MUP3, GCC32, ENDE, HALDH, CYS2, GCCPD1, INMT, STARD4, ULK1, HDC, CPNE1, CES1F, MUP18, GYS2, FABP1, YOD1, MUP9, GNE3, GYS2, FABP1, YOD1, MUP9, GNE3, GYS2, FABP1, YOD1, MUP9, GNE3, GYS2, GABP1, YOD2, MUP3, GNE3, SLC27A2 GUTALAD, CP280, GUT381, CVP3A41A, CYP2C40 GUTALAD, CP280, GUT381, CVP3A41A, CYP2C40 GUTALAD, CP280, GUT381, CVP3A41A, CYP2C40 GCX2, HMC22, GEND41, SLC27A2 GLAND, ENDE, GLANDH, SLC2ALAS, SLC27A2, GUTALAD, CYP2A4, GUTALAD, SLC27A2, GUTALAD, CYP2A4, GUTALAD, SLC27A2, GUTALAD, CYP2A4, GUT341, GUT340, GUT3
SOTEM, C2, DIRECT SOU3030P*organelle membrane 4 5.3 7.4 0.016 1.38[CPRA10, CPP280, CPP3A14A, CPP240 SOTEM, C2, DIRECT SOU30P*organelle membrane 4 9.3 7.4 0.016 1.38[CPRA10, CPP280, CPP3A14A, CPP240 KEGG, PATHWAY mmu00564:Givererophospholipid metabolism 4 5.3 6.6 0.021 0.138[EP11, CPP32, CPP30, SPP30, SPE304, SPENPIA1E, LPIN1, CPPA14, UIX1A10, GPC7, STARD4, CESIF, SLC27A2, RETSAT SOTEM, C2, DIRECT SOU30587*intergal component of plasma methrane methrane 7 9.3 3.1 0.022 0.228[LO128], SLC021A, SLC27A2, SLC7A2, SLC2A5 GOTEM, LP, DIRECT SOU30587*intergal component of plasma methrane 6 8.0 3.7 0.022 0.228[LO128, SLC021A, SLC2A5, SLC7A2, SLC7A2, SLC7A2, SLC7A2, SLC7A2, SLC2A5 GOTEM, LP, DIRECT SOU30587*intergal entabolism 3 4.0 1.8 0.025 0.124[CP29, CP341A, CP24, CP341A, CP242, CP341A, CP242 GOTEM, LP, DIRECT SOU3058*intergal entabolism 3 4.0 1.1 0.025 0.026 0.026 SLC317, VIP174, VIP1744, VIP141 0.014 0.025	GOTERM & DURECT GOTERM & DURECT GOTERM & DURECT GOTERM & DURECT GOTERM (C_DURECT GOTERM (C_DURECT	Go 2002593*plicose homestais mmu008836*ention letabolism Go 200357*extracellular region mmu0100.Metabolic pathways GO 200357*extracellular region GO 200357*extracellular region GO 200357*extracellular region GO 200557*extracellular region GO 200557*extracellular region GO 200557*extracellular region GO 200557*extracellular region mmu00100*extraposes to stilbenoid mmu00000*extraposes to stilbenoid mmu00000*extraposes to stilbenoid GO 200562**rative acid catabolic process GO 200562**rative acid catabolic process GO 200582**roptade hormone biosynthesis GO 200582**roptade metabolic process GO 200582**roptade metabolic	7 9.3 7 9.3 15 20.0 4 5.3 5 6.7 4 5.3 5 6.7 9 12.0 6 8.0 9 12.0 9	10.7 10.0 3.6 2.4 41.0 11.1 22.5 11.6 21.1 42.3 3.5 8.5 3.7 6.2 3.7.6 3.5 2.9 7.0 6.3 9.5 5.5	4.09E-05 4.45E-05 4.47E-05 9.99E-05 2.27E-04 6.53E-04 7.15E-04 9.16E-04 2.03E-03 2.23E-03 2.33E-03 2.33E-03 3.04E-03 3.04E-03 3.04E-03 3.04E-03 3.04E-03 3.04E-03 3.04E-03 0.005 0.007 0.007	1.23E-03 1.38E-03 2.86E-03 9.79E-04 2.76E-03 0.006 0.015 0.011 0.029 0.044 0.028 0.047 0.048 0.047 0.048 0.049 0.055 0.057 0.850	GBCC, MUP2, MUP2, MUP2, MUP3, MUP3, MUP3, GEC GBCC, MUP2, MUP2, MUP2, MUP3, MUP3, MUP3, GERSAT MUP2, MUP2, MUP3, MUP3, SEPPINALE, MUP3D, SEPINAA, POGERI, MUP3B, MUP13, MUP3, MUP3, MUP3, MUP3, MUP3, MUP31, ANGPTL4 EINPV, ACX1, CV298, MCF3EHAAC, KP28B, UGT2B1, CVP2C40, UP22, AKA, UPIN2, UPIN1, CVPAA10, UGT3A10, TDO2, GEPC, HYKK, MMD2, MUP3, MUP3, MUP31, MUP3, MUP31 GCCX1, EC22, EHNADH, ACAA18, SLC27A2 GCCX1, EC22, EHNADH, ACAA18, SLC27A2 SLCDAL, MUP2, MUP3, MUP31 GCCX1, EC22, EENHADH, ACAA18, SLC27A2 GCCX1, EC22, EHNADH, ACAA18, SLC27A2 SLCDAL, MUP2, MUP3, MUP31 GCCX1, EC22, EHNADH, ACAA18, SLC27A2 GCCX1, EC22, EHNADH, ACAA18, SLC27A2 SLCDAL, MUP2, MUP3, GCC32, ENDE, HALDH, CYS2, GCCPD1, INMT, STARD4, ULK1, HDC, CPNE1, CES1F, MUP18, GYS2, FABP1, YOD1, MUP9, GNE3, GYS2, FABP1, YOD1, MUP9, GNE3, GYS2, FABP1, YOD1, MUP9, GNE3, GYS2, GABP1, YOD2, MUP3, GNE3, SLC27A2 GUTALAD, CP280, GUT381, CVP3A41A, CYP2C40 GUTALAD, CP280, GUT381, CVP3A41A, CYP2C40 GUTALAD, CP280, GUT381, CVP3A41A, CYP2C40 GCX2, HMC22, GEND41, SLC27A2 GLAND, ENDE, GLANDH, SLC2ALAS, SLC27A2, GUTALAD, CYP2A4, GUTALAD, SLC27A2, GUTALAD, CYP2A4, GUTALAD, SLC27A2, GUTALAD, CYP2A4, GUT341, GUT340, GUT3
GOTEM, C.C. DIRECT 60.0005783°=cndplasmic reticulum 14 18.7 2.0 0.019 0.138]RTT, (PV2B, (PV2B, (PV2B, CV2B, SEPINATE, IPN2, LPIN1, (PVAL0), GGTARD4, (ES1F, SLC2A2, RETAT KEGE, PATHWAY mmu00567/Giverophophophicid metabolism 4 5.3 6.6 0.02 0.138]RTT, (PV2B, (PV2B, CV2B, SCP01, LPIN1, (PVAL0), GGTARD4, (ES1F, SLC2A2, RETAT GOTEM, DC, DIRECT GOD008887 integral component of Jasma membrane 7 9.3 3.1 0.022 0.138[RTT, (PV2B, VP2B, CVP2D, LPIN1, (PVAL0), SCP01, LPIN1, (PVAL0), GGTARD4, SIC3A2, SLC2AA5, SLC7A2, SL	KEGG PATHWAY GOTERM, BP.DIRECT KEGG PATHWAY GOTERM, BP.DIRECT KEGG PATHWAY GOTERM, BP.DIRECT KEGG PATHWAY GOTERM, CD.DIRECT GOTERM, BP.DIRECT KEGG PATHWAY GOTERM, CD.DIRECT GOTERM, BP.DIRECT GOTERM, CD.DIRECT GOTERM, BP.DIRECT GOTERM, CD.DIRECT GOTERM, CD.DIRECT GOTERM, CD.DIRECT GOTERM, CD.DIRECT GOTERM, CD.DIRECT GOTERM, CD.DIRECT GOTERM, BP.DIRECT GOTERM, CD.DIRECT GOTERM, BP.DIRECT	Go 2002937-glucose homeostais mmu008836-encl metabolism Go 200357-enctracellular region mmu0100.Metabolic pathways GO 200357-enctracellular region GO 200357-enctracellular region GO 200557-enctracellular region mmu00100-feetabolic process GO 2005627-tarty add tetabolic process GO 2005627-tarty add metabolic process GO 2005767-tarty add metabolism GO 200	7 9.3 7 9.3 15 20.0 4 5.3 5 6.7 4 5.3 5 6.7 21 28.0 3 4.0 5 6.7 9 12.0 6 8.0 9 12.0 9 12.0 9 12.0 9 12.0 9 11 14.7, 5 6.7 5 6.7 7 10 10 10 10 10 10 10 10 10 10 10 10 10	107 1000 3.6 4.0 151 151 152 255 255 3.6 23 3.6 2.9 3.6 3.6 3.5 5.5 5.5 5.5 5.5 5.5 5.5 5.5 5.5 5.5	4.09E-05 4.45E-05 4.47E-05 9.99E-05 2.27E-04 6.53E-04 7.15E-04 9.16E-04 2.03E-03 2.29E-03 2.29E-03 2.23E-03 2.33E-03 2.53E-03 3.04E-03 3.04E-03 3.04E-03 3.04E-03 3.04E-03 3.04E-03 0.007 0.007 0.0012 0.013 0.014	1.23E-03 1.38E-03 2.86E-03 9.79E-04 2.76E-03 0.006 0.015 0.029 0.044 0.028 0.047 0.048 0.047 0.056 0.080 0.060 0.057 0.180 0.059 0.080 0.059 0.080 0.059 0.080 0.059 0.080 0.059 0.080 0.059 0.080 0.059 0.080 0.059 0.080 0.059 0.080 0.059 0.080 0.059 0.080 0.092 0.080 0.080 0.092 0.080 0.092 0.044 0.055 0.080 0.047 0.055 0.080 0.047 0.055 0.080 0	GBCC_MUP1_MUP2_MUP1_MUP1_B_MUP1_MUP1_ CYCHALD_UCTALD_CY2PB_UCT2B_UCT2B_UCT2BALLCY2P2.04, BETSAT MUP2_MUP1_MUP1_MUP2_SEPENALG_CY2P3ALLCY2P2.04, BETSAT MUP2_MUP1_MUP1_MUP3_MUP1_SEPENALG_CY2P3ALLCY2P2.04, UPP2_AKA_UPN2_UP15_MUP15_MUP1_MUP3_MUP1_ANGPTL4 EMPPA_CACXL_CY2P3_08_ME_EHADALCY2P3ALLCY2P2.04, UPP2_AKA_UPN2_UP15_MUP15_MUP1_MUP3_MUP1_ANGPTL4 EMPVA_CACXL_CY2P3_08_ME_EHADALCY2P3.04 MUP1_UCT3L_MUP3_MUP3_AUP11 CCCV1_EC2_EHADAL_ACAA1B_ SICLOLA_MUP1_MUP3_CYP2B_ UCTALS_MUP1_SAUP1_ CCCV1_EC2_EHADAL_ACAA1B_ TXNIP_MUP1_GYL_CHADAL_ACAA1B_ UCTALS_MUP1_MUP3_GYP2B_ UCTALS_MUP1_GYL_CHADAL UCTALS_MUP1_GYL_CHADAL UCTALS_CYL_RADAL_ACAA1B_ UCTALS_MUP1_GYL_GYL_ACAA1B_ UCTALS_MUP1_GYL_GYL_ACAA1B_ UCTALS_MUP1_GYL_GYL_MUP1_GYL_GYL_GYL_GYL_GYL_GYL_ACAA1BSLC27A2 UCTALAL_GYL_MUP3_UCTAL_GYL_GYL_GYL_ACAA1BSLC27A2 UCTALAL_GYL_MUP3_UCTALBAL_S_GYL_GYL_ACAA1BSLC27A2 UCTALAL_GYL_MUP3_UCTALB_GYL_GYL_ACAA1BSLC27A2 UCTALAL_GYL_MUP3UCTALBAL_S_GYL_GYL_ACAA1BSLC27A2 UCTALAL_GYL_MUP3UCTALBGYL_GYL_ACAA1BSLC27A2 UCTALAL_GYL_MUP3UCTALBGYL_GYL_ACAA1BSLC27A2 UCTALAL_GYL_MUP3MUP3MUP3MUP3MUP3MUP3MUP3MUP3MUP3M
IEEG_PATHWAY mmu00564 Giverophospholipid metabolism 4 5.3 6.6 0.021 0.133 [TMPPL, LPN2, GPCPD, LPN1 OOTEML_CD_DURCET 00.000588*7 integral component of plasma methrane 7 9.3 0.12 0.124 [Sc1028, SIC021A, SIC2AA, SIC2AA, SIC7A2, SIC7A2	KEGG PATHWAY GOTERM, BP.DIRECT KEGG PATHWAY GOTERM, BP.DIRECT KEGG PATHWAY GOTERM, BP.DIRECT KEGG PATHWAY GOTERM, CD.DIRECT GOTERM, BP.DIRECT KEGG PATHWAY GOTERM, CD.DIRECT GOTERM, BP.DIRECT GOTERM, CD.DIRECT GOTERM, BP.DIRECT GOTERM, CD.DIRECT GOTERM, CD.DIRECT GOTERM, CD.DIRECT GOTERM, CD.DIRECT GOTERM, CD.DIRECT GOTERM, CD.DIRECT GOTERM, BP.DIRECT GOTERM, CD.DIRECT GOTERM, BP.DIRECT	Go 2002937-glucose homeostais mmu008836-encl metabolism Go 200357-enctracellular region mmu0100.Metabolic pathways GO 200357-enctracellular region GO 200357-enctracellular region GO 200557-enctracellular region mmu00100-feetabolic process GO 2005627-tarty add tetabolic process GO 2005627-tarty add metabolic process GO 2005767-tarty add metabolism GO 200	7 9.3 7 9.3 15 20.0 4 5.3 5 6.7 4 5.3 5 6.7 21 28.0 3 4.0 5 6.7 9 12.0 6 8.0 9 12.0 9 12.0 9 12.0 9 12.0 9 11 14.7, 5 6.7 5 6.7 7 10 10 10 10 10 10 10 10 10 10 10 10 10	107 1000 3.6 4.0 151 151 152 255 255 3.6 23 3.6 2.9 3.6 3.6 3.5 5.5 5.5 5.5 5.5 5.5 5.5 5.5 5.5 5.5	4.09E-05 4.45E-05 4.47E-05 9.99E-05 2.27E-04 6.53E-04 7.15E-04 9.16E-04 2.03E-03 2.29E-03 2.29E-03 2.23E-03 2.33E-03 2.53E-03 3.04E-03 3.04E-03 3.04E-03 3.04E-03 3.04E-03 3.04E-03 0.007 0.007 0.0012 0.013 0.014	1.23E-03 1.38E-03 2.86E-03 2.86E-03 0.79E-04 2.76E-03 0.005 0.0015 0.001 0.029 0.044 0.028 0.047 0.048 0.047 0.048 0.047 0.052 0.055	GREC, MUP2, MUP2, MUP2, MUP3, MUP3, MUP3, MUP3 GREC, MUP2, MUP2, MUP2, MUP3, MUP3, MUP3, SEPNIAG, PDGRL, MUP18, MUP17, MUP15, MUP3, MUP3, MUP3, ARDP11, ANGP114 MUP7, MUP3, MUP2, SERPINATE, MUP10, SEPNIAG, PDGRL, MUP18, MUP17, MUP15, MUP14, MUP3, MUP3, MUP3, MUP3, MUP11, ANGP114 MUP2, MUP3, MUP2, SERPINATE, MUP10, SEPNIAG, PDGRL, MUP18, MUP17, MUP15, MUP14, MUP3, MUP3, MUP3, MUP11, ANGP114 MUP2, MUP2, MUP2, MUP11, MUP18, MUP11, MUP18, MUP17, MUP18, MUP18, MUP11, MUP18, MUP11, MUP18, MUP11, MUP18, MUP1, MUP3, MUP3, MUP3, MUP3, MUP3, MUP14, MUP11, MUP1, MUP3, MUP3, MUP3, MUP3, MUP3, MUP14, MUP1, MUP3, MUP1, MUP3, MUP3, MUP2, MUP3, MUP2, MUP3, MUP2, MUP3,
SOTEML &P. DIRECT 50.001628* positive regulation of gene expression 6 8.0 3.7 0.02 0.278 [MJP1, MUP3, M	Cortem de Direct Gottem de Direct KEGG PATHWAY GOTEM (C. DIRECT GOTEM (C. DIRECT	G0.002593*plucose homeostasis mmu00830.80*cml on textbolism G0.000557*extracellular region mmu10010Metabolic pathways G0.000557*extracellular region G0.000557*extracellular region G0.000557*taty add beta-oxidation G0.000582*regions G0.00057*regions G0.00057*regions G0.00057*regions G0.00057*regions G0.00057*regions G0.00057*regions G0.00057*regions G0.00057*regions G0.00057*re	7 9.3 7 9.3 15 20.0 4 5.3 5 6.7 21 28.0 4 5.3 5 6.7 9 12.0 6 8.0 9 12.0 9 12.0 9 12.0 9 12.0 9 12.0 9 12.0 11 14.7 5 6.7 5 6.7 9 12.0 9 12.0 12.0 9 12.0 9 1	107 1000 3.6 4.0 151 151 152 255 116 116 116 1255 1255 1	4 408-05 4 445-05 4 445-05 4 447-05 4 47-06 4 47-06 9 999-05 2 227-04 6 532-04 9 999-05 2 227-04 6 532-04 9 999-05 2 227-04 9 999-05 2 229-03 2 336-03 3 346-03 3 346-03 3 346-03 3 346-03 3 346-03 3 346-03 3 340-007 0 0007 0 0	1.23E-03 1.38E-03 2.86E-03 2.86E-03 0.79E-04 2.76E-03 0.005 0.0015 0.001 0.029 0.044 0.028 0.047 0.048 0.047 0.048 0.047 0.052 0.055	GREC, MUP2, MUP2, MUP2, MUP3, MUP3, MUP3, MUP3 GREC, MUP2, MUP2, MUP2, MUP3, MUP3, MUP3, SEPNIAG, PDGRL, MUP18, MUP17, MUP15, MUP14, MUP3, MUP2, SREPNIAG, PMDC, MUP3, MUP2, MUP3, M
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GOTERM &P DIRECT GOODSS088*lipid homeostasis 3 4.0 11.7 0.026 0.038 ACOX1, G&PC, NR102 GOTERM CD, DIRECT GOODSG15*estracellular space 10 13.3 2.3 0.027 0.137/MUP1, SKPINK6, MUP3, MUP2, MUP18, CES1F, SERPINA1E, MUP9, ANGPTL4, MUP11 GOTERM MP, DIRECT GOODSG814*sodium ion transport 2 7 56.4 0.034 0.373/INP12, CPNE1 GOTERM MP, DIRECT GOODSG814*sodium ion transport 3 4.0 9.7 0.037 0.338 SLC38A2, SLC17A2, SLC2A5 KEGG PATHWAY mmu03803(Tryptophan metabolism 3 4.0 9.0 0.048 0.028 (TOX), MUP11 GOTEMM MP, DIRECT GOODS(5)*bestravior 2 2 7.4 0.049 0.0471/MUP13, MUP11	Corrent Control of Con	Go 2002393*glucose homeostasis mmu008836*denio metabolism GO 200557*extracellular region mmu01003.Metabolic pathways GO 200557*extracellular region GO 200568*fatty add beta oxidation GO 200568*fatty add betabolic process GO 200568*fatty add catabolic process GO 200558*fatty add catabolic process GO 200558*regroups GO 200558*regroups GO 200558*regroups GO 200588*regroups GO 200588*regroups GO 200588*regroups GO 200578*recreation	7 9.3 7 9.3 15 20.0 21 28.0 4 5.3 5 6.7 21 28.0 4 5.3 5 6.7 9 12.0 6 8.0 9 12.0 9 12.0 9 12.0 9 12.0 9 12.0 9 12.0 9 12.0 9 12.0 9 12.0 9 12.0 9 12.0 9 12.0 9 12.0 9 12.0 9 12.0 11 14.7 5 6.7 10 13.3 4 5.3 4 5.3 7 9.3	107 1000 3.6 4.0 151 151 152 255 116 153 8.5 3 6 2 3 7 6 2 3 6 3 6 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	4.096.05 4.45F.05 4.47E.05 9.996.05 9.996.05 9.227E-04 6.533E-04 7.15E-04 9.16E-04 2.03E-03 2.29E-03 2.29E-03 2.29E-03 2.235E-03 2.045E-	123E-03 138E-03 2.86E-03 2.79E-04 2.76E-03 0.000 0.015 0.011 0.029 0.044 0.047 0.047 0.047 0.047 0.047 0.047 0.047 0.047 0.049 0.049 0.056 0.060 0.056 0.060 0.055 0.080 0.055 0.080 0.055 0.080 0.055 0.080 0.055 0.080 0.055 0.080 0.055 0.080 0.055 0.080 0.055 0.080 0.055 0.080 0.055 0.080 0.055 0.080 0.085 0.080 0.055 0.080 0.085 0.080 0.085	GREC_MUP1_MUP2_MUP2_MUP13_MUP14 CPCAALQ LOFTALD CP289, UCT281, CP2841A, CP224QR, RETSAT MUP2_MUP1_MUP1_MUP2_SEPENATE. MUP10_SEPENATE.POSERL_MUP12_MUP17_MUP15_MUP14_MUP3_MUP11_ANGPTL4 EMPP4_ACXX_LP293, GNE_EHAAD, CP283B, UCT281, CP224Q, RETSAT MUP2_MUP1_MUP3_MUP13_MUP13_ ACX01_EQ2_EHAADH, ACAA18 MUP1_MUP1_MUP3_MUP13_FAUP11 ACX01_EQ2_EHAADH, ACAA18 MUP2_MUP1_MUP3_MUP3_CP28B COPA4LQ_ACX14_B MUP1_MUP3_MUP3_CP28B COPA4LQ_ACX14_EC2_EHAADH, ACAA18 MUP2_MUP3_MUP3_CP28B COPA4LQ_ACX14_EC2_EHAADH, ACAA18 MUP3_MUP3_CP28B COPA4LQ_ACX14_EC2_EHAADH, ACAA18 MUP3_MUP3_CP28B COPA4LQ_ACX14_EC2_EHAADH, ACAA18 MUP3_MUP3_CP28B COPA4LQ_ACX14_EC2_EHAADH, ACAA18 MUP3_MUP3_CP28B COPA4LQ_ACX14_EC2_EHAADH, ACAA18 MUP3_MUP3_CP28B_CC2A2 MUP3_MUP3_MUP3_MUP3_MUP3_MUP3_MUP3_MUP3_
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GOTERM &P DIRECT GO:1901223"negative regulation of NIK/NF-kappa8 signaling 2 2.7 56.4 0.034 0.373 NLRP12, CPNE1 GOTERM &P DIRECT GO:0005814"sodium ion transport 3 4.0 9.7 0.333 0.333 0.333 0.333 0.228 CPNE1 GOTERM &P DIRECT GO:0005814"sodium ion transport 3 4.0 9.7 0.333 0.333 0.333 0.228 COTEM PLADET 0.004 0.208 CO2E CO2E DOLOG TO/DE APORTO 0.417 MUP13 0.417 MUP13	Contemporation of the provided and provided	Go 2002393*plucose homeostasis mmu00883.0Featuraetilular region mmu01003.Metabolic pathways GO 200357*or extracellular region mmu01003.Metabolic pathways GO 200368*Tatty add beta couldation GO 200368*Tatty add catabolic process GO 200368*Tatty add netabolic process GO 200368*Tatty add netabolic process GO 200352*Tatty add netabolic process GO 200357*Derevisione Mmu00304.0fencial carinogenesis Mmu00304.0fencial carinogenesis Mmu00304.0fencial carinogenesis Mmu00304.0fencial carinogenesis Mmu00304.0fencial carinogenesis Mmu00304.0fencial carinogenesis Mmu0304.0fencial carinogenesis Mmu0304.0fencialcarinogenesis Mmu0304.0fencialcarinogenesis Mmu0304.0fencialcarinogenesis	7 9.3 7 9.3 15 20.0 4 5.3 5 6.7 21 28.0 3 4.0 5 6.7 21 28.0 6 7.0 21 28.0 6 8.0 9 12.0 6 8.0 9 12.0 11 14.7 5 6.7 10 13.3 3 4.0 4 5.3 5 6.7 10 13.3 3 4.0 4 5.3 7 9.3 4 5.3 7 9.3 7 9.3 4 0.0 3 4.0	107 1000 36 44.00 151 151 152 55 36 36 36 36 36 36 36 36 36 36 36 36 36	4.096.05 4.45F.05 4.47E.05 9.99F.05 9.99F.05 9.99F.05 2.27E.040 7.15F.04 2.03E.03 2.29F.03F.03 2.29F.03 2.29F.03 2.29F.03 2.29F.03 2.29F.0	1 238-03 1 386-03 2.866-03 9.796-04 2.766-03 0.006 0.015 0.011 0.028 0.044 0.028 0.044 0.028 0.044 0.049 0.049 0.062 0.057 0.080 0.057 0.080 0.057 0.189 0.080 0.192 0.052 0.080 0.057 0.189 0.080 0.057 0.189 0.189 0.133 0.184 0.133 0.184 0.286 0.133 0.184 0.286 0.133 0.184 0.133 0.184 0.286 0.133 0.184 0.286 0.133 0.184 0.133 0.184 0.134 0.134 0.144 0.286 0.134 0.144 0.286 0.144 0.286 0.144 0.286 0.157 0.144 0.286 0.157 0.157 0.157 0.157 0.157 0.157 0.157 0.057 0	GREC, MUPJ, MUPJ, MUPJ, MUPJ, MUPJ, MUPJ CYPAILD (GTALID, CYPBB, UGT22), CYPAILA, CYPACQA, RETSAT MUPJ, MUPJ, MUPJ, SUPJ, SEPHNALE, MUPJD, SEPHNAR, POGFRL, MUPJZ, MUPJZ, MUPJA, MUPJ, MUPJ, ANGPTLA ETNPPL, ACCAL, CYPJAGA, ACAALB MUPJ, MUPJ, MUPJ, GNE, EHHADH, CYP2B, UGT2BJ, CYP2C40, UFP2, AK4, UPIN2, LPIN1, CYPALD, UGTJALD, TOD2, GGPC, HYKK, HMGCS2, HOC, CYP3AGA, ACAALB MUPJ, MUPJ, MUPJ, MUPJ, MUPJ, MUPJ SLCOLAT, MUPJ, MUPJ, MUPJ, MUPJ SLCOLAT, MUPJ, MUPJ, MUPJ, MUPJ SLCOLAT, MUPJ, MUPJ, GNE, DEMADH, CYP2B, UGT2BJ, CPD2J, INMT, STARDA, ULK1, HDC, CPNEJ, CESIF, MUPJB, GYS2, FABPJ, YODJ, MUPJ, GNEAR, UPINZ, GYS2, FABPJ, YODJ, MUPJ, GNEAR, UPINZ, UPINZ, GPCDJ, INMT, STARDA, ULK1, HDC, CPNEJ, CESIF, MUPJB, GYS2, FABPJ, YODJ, MUPJ, GNEAR, UPINZ, UPINZ, UPINZ, UPINZ, UPINZ, UPINZ, UPINZ, UPINZ, GPCDJ, INMT, STARDA, ULK1, HDC, CPNEJ, CESIF, MUPJB, GYS2, FABPJ, YODJ, MUPJ, GNEAR, UPINZ, UPINZ, UPINZ, GPCDJ, INMT, STARDA, ULK1, HDC, CPNEJ, CESIF, MUPJB, GYS2, FABPJ, YODJ, MUPJ, GNEAR, UPINZ, GNEAR, MUPJE COLTALD, CYP2B, UGT2BL, CYP3AHA, CYP2CAO UGTALAD, CYP2B, UGT2BL, CYP3AHA, CYP2CAO UGTALAD, CYP2B, UGT2BL, CYP3AHA, CYP2CAO UGTALAD, CYP2B, UGT2BL, CYP3AHA, CYP2CAO UGTALAD, CYP2B, UGT2BL, CYP3AHA, CYP2CAO, UPINZ, GMA951, SIC27A2, UPINJ, RETSAT UGTALAD, CYP2B, CYP3AHA, CYP2CAO, UPINZ, GMA951, SIC27A2, UPINJ, RETSAT UGTALAD, CYP2B, UGT2BL, CYP3AHA, CYP2CAO, LPINZ, GMA951, SIC27A2, UPINJ, RETSAT UGTALAD, CY
GOTEM MP DIRECT GOOD083M*sodium ion transport 3 4.0 9.7 0.037 0.383 LsC28A2, SLC1A2, SLC2AS KEGG PATHWAY mmu00380.Tryptophan metabolism 3 4.0 9.0 0.041 0.020 ETD02, EHHADH, INNT GOTEM MP DIRECT GODOG/Str/behavior 2 2.7 45.1 0.041 0.041 FMUP18, MUP11	Contemportation of the provided and provi	G0.002593*plucose homeostais mmu00883.0#cml metabolism G0.002557*extracellular region mmu10107.Metabolic pathways G0.002557*extracellular region G0.002557*extracellular region to teststerone stimulus G0.002562*extracellular regions to teststerone stimulus G0.002562*extracellular regions to teststerone stimulus G0.002562*response to stilloenoid mmu00017.1#xt ad degradation G0.000562*response to stilloenoid mmu000152*rest ad degradation G0.000562*response to stilloenoid G0.000567*response to stilloenoid G0.000567*response G0.000567*response G0.000567*response G0.00057*response G0.00057*responsione G0.00057*responsione G0.00057*responsione G0.00057*responsione G0.00057*responsione G0.000057*responophysispluing metabolism	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	107 1000 1000 24 400 151 161 212 225 225 225 225 225 225 326 336 335 355 299 70 63 36 355 299 205 205 205 205 205 205 205 205	4.096.05 4.455.05 4.447E.05 9.996.05 9.996.05 9.996.05 9.996.05 9.127E.04 9.166.04 9.166.04 2.33E.03 2.33E.03 2.33E.03 3.04E.03 3.04E.03 3.04E.03 3.04E.03 3.04E.03 3.04E.03 3.04E.03 3.04E.03 0.007 0.0017 0.0012 0.0022 0.0222 0.0222	1 238-03 1 386-03 2.866-03 9.796-04 2.766-03 0.006 0.015 0.011 0.028 0.044 0.028 0.044 0.028 0.044 0.049 0.049 0.062 0.057 0.080 0.057 0.080 0.057 0.189 0.080 0.192 0.052 0.080 0.057 0.189 0.080 0.057 0.189 0.189 0.133 0.184 0.133 0.184 0.286 0.133 0.184 0.286 0.133 0.184 0.133 0.184 0.286 0.133 0.184 0.286 0.133 0.184 0.133 0.184 0.134 0.134 0.144 0.286 0.134 0.144 0.286 0.144 0.286 0.144 0.286 0.157 0.144 0.286 0.157 0.157 0.157 0.157 0.157 0.157 0.157 0.057 0	GREC, MUPJ, MUPJ, MUPJ, MUPJ, MUPJ, MUPJ CYPAILD (GTALID, CYPBB, UGT22), CYPAILA, CYPACQA, RETSAT MUPJ, MUPJ, MUPJ, SUPJ, SEPHNALE, MUPJD, SEPHNAR, POGFRL, MUPJZ, MUPJZ, MUPJA, MUPJ, MUPJ, ANGPTLA ETNPPL, ACCAL, CYPJAGA, ACAALB MUPJ, MUPJ, MUPJ, GNE, EHHADH, CYP2B, UGT2BJ, CYP2C40, UFP2, AK4, UPIN2, LPIN1, CYPALD, UGTJALD, TOD2, GGPC, HYKK, HMGCS2, HOC, CYP3AGA, ACAALB MUPJ, MUPJ, MUPJ, MUPJ, MUPJ, MUPJ SLCOLAT, MUPJ, MUPJ, MUPJ, MUPJ SLCOLAT, MUPJ, MUPJ, MUPJ, MUPJ SLCOLAT, MUPJ, MUPJ, GNE, DEMADH, CYP2B, UGT2BJ, CPD2J, INMT, STARDA, ULK1, HDC, CPNEJ, CESIF, MUPJB, GYS2, FABPJ, YODJ, MUPJ, GNEAR, UPINZ, GYS2, FABPJ, YODJ, MUPJ, GNEAR, UPINZ, UPINZ, GPCDJ, INMT, STARDA, ULK1, HDC, CPNEJ, CESIF, MUPJB, GYS2, FABPJ, YODJ, MUPJ, GNEAR, UPINZ, UPINZ, UPINZ, UPINZ, UPINZ, UPINZ, UPINZ, UPINZ, GPCDJ, INMT, STARDA, ULK1, HDC, CPNEJ, CESIF, MUPJB, GYS2, FABPJ, YODJ, MUPJ, GNEAR, UPINZ, UPINZ, UPINZ, GPCDJ, INMT, STARDA, ULK1, HDC, CPNEJ, CESIF, MUPJB, GYS2, FABPJ, YODJ, MUPJ, GNEAR, UPINZ, GNEAR, MUPJE COLTALD, CYP2B, UGT2BL, CYP3AHA, CYP2CAO UGTALAD, CYP2B, UGT2BL, CYP3AHA, CYP2CAO UGTALAD, CYP2B, UGT2BL, CYP3AHA, CYP2CAO UGTALAD, CYP2B, UGT2BL, CYP3AHA, CYP2CAO UGTALAD, CYP2B, UGT2BL, CYP3AHA, CYP2CAO, UPINZ, GMA951, SIC27A2, UPINJ, RETSAT UGTALAD, CYP2B, CYP3AHA, CYP2CAO, UPINZ, GMA951, SIC27A2, UPINJ, RETSAT UGTALAD, CYP2B, UGT2BL, CYP3AHA, CYP2CAO, LPINZ, GMA951, SIC27A2, UPINJ, RETSAT UGTALAD, CY
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GOTERM_BP_DIRECT GO:0007610"behavior 2 2.7 45.1 0.043 0.417 MUP18, MUP11	Base State Stat	Go 2002393*plucose homeostasis mmu00883.0Featuraetilular region mmu01003.Metabolic pathways GO 200357*or extracellular region mmu01003.Metabolic pathways GO 2003684**Taty add beta couldation GO 2003684***Taty add beta couldation GO 2003684************************************	7 9.3 7 9.3 15 20.0 21 28.0 4 5.3 5 6.7 21 28.0 3 4.0 3 4.0 3 4.0 9 12.0 6 8.0 9 12.0 11 14.7 5 6.7 5 6.7 10 13.3 4 5.3 4 5.3 4 5.3 6 8.0 3 4.0 4 5.3 5 6.7 10 13.3 4 5.3 4 5.3 6 8.0 3 4.0 3 4.0 10 13.3 2 2.7 3 4.0	107 1000 1	4.096.05 4.455.05 0 4.	128-00 128-00 286-03 286-03 286-03 286-03 0.066 0.057 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0	GBCC_MUP1_MUP2_MUP1_MUP1_MUP1_MUP1_ CPCAALD_UCTALD_CP28B_UCT2B_UP2ALAL_CP22CQ_RETSAT MUP2_MUP1_MUP3_MUP2_SEPENALE_MUP10_SEPENALE_POGEN_MUP12_MUP15_MUP15_MUP14_MUP9_MUP1_ANOPTL4 EMPPL_ACXEL_CP28B_UCT2BL_CP28ALA_CP22CQ_RETSAT MUP2_MUP1_MUP1_MUP13_MUP13_EXCP28ALG_CP28ALG_CP22CQ_UP22_AK4_EPIX2_MUP15_MUP15_MUP14_AMUP9_MUP1_ANOPTL4 EMPPL_ACXEL_CP22_SIGN_EFIADAC_CP28ALG_CP28ALG_CP22CQ_UP22_AK4_EPIX2_MUP15_MUP13_MUP13_ANOPTL4 ACXM_ED2_EPIXABA_CACA1B_S MUP1_UCT28A_MUP1A_MUP3_AMUP13 ACXX_ED2_EPIXABA_ACCA1B_S_CC22A2 COTALA_UP2_AMUP3_CP28B CPMADIA_CCXL_ED2_EPIXABA_ACCA1B_S_CC2A2 MUP1_MUP3_CP28_MUP3_CP28B CPMADIA_CCXL_ED2_EPIXABA_ACCA2AS MUP3_ACCXL_ED2_EPIXABA_ACCA2AS CPMADIA_CCXL_ED2_EPIXABA_ACCA2AS CPMADIA_CCXL_ED2_EPIXABA_ACCA2AS MUP3_MUP3_CC22AS MUP3_MUP3_CC22AS MUP3_MUP3_MUP3_MUP3_MUP3_MUP3_MUP3_MUP3 MUP3_MUP3_MUP3_MUP3_MUP3_MUP3_MUP3_MUP3_
GOTERM BP DIRECT GO:0050727*regulation of inflammatory response 3 4.0 8.9 0.043 0.408 NR1D2, SLC7A2, BCL6	Test See See See See See See See See See Se	Go 2002393*plucose homeostasis mmu00883.0Featuraetilular region mmu01003.Metabolic pathways GO 200357*or extracellular region mmu01003.Metabolic pathways GO 2003684**Taty add beta couldation GO 2003684***Taty add beta couldation GO 2003684************************************	7 9.3 7 9.3 15 20.0 21 28.0 4 5.3 5 6.7 21 28.0 3 4.0 3 4.0 3 4.0 9 12.0 6 8.0 9 12.0 11 14.7 5 6.7 5 6.7 10 13.3 4 5.3 4 5.3 4 5.3 6 8.0 3 4.0 4 5.3 5 6.7 10 13.3 4 5.3 4 5.3 6 8.0 3 4.0 3 4.0 10 13.3 2 2.7 3 4.0	107 1000 1	4.096.05 4.455.05 0 4.	128-00 128-00 286-03 286-03 286-03 286-03 0.066 0.057 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.	GBCC_MUP1_MUP2_MUP2_MUP13_MUP3_MUP11 CYCHALD_UCTALD_CY2P80_UCT281_CY2PAALA_CY2P2C40_RETSAT MUP2_MUP1_MUP3_MUP2_SEPENALE_MUP10_ESEPENAL6_PDGFRL_MUP12_MUP15_MUP15_MUP1_MUP3_MUP1_ANGPTL4 EMPP4_ACXX1_CY2P38_OK_EFBAALG_CY2PAALA_CY2P2C40_RETSAT MUP2_MUP1_MUP13_MUP13_AUP11 ACX01_EO2_EHHADH, ACAA18_SLC2PA2 MUP1_MUP1_MUP13_MUP13_RETSAT MUP1_MUP1_MUP13_MUP13_RETSAT ACX01_EO2_EHHADH, ACAA18_SLC2PA2 CVPAAL0_ACX1_RETSAT MUP3_MUP1_OTESA_MUP1_ANDP3_CP38B CVPAAL0_ACX1_RETSAT CVPAAL0_ACX1_RETSAT MUP3_MUP3_CP38B CVPAAL0_ACX1_RETSAT MUP3_MUP3_CP38B CVPAAL0_ACX1_RETSAT MUP3_MUP3_CP38B CVPAAL0_ACX1_RETSAT MUP3_MUP3_CP38B CVPAAL0_ACX1_RETSAT MUP3_MUP3_CP38B CVPAAL0_ACX1_RETSAT MUP3_MUP3_CP38B CVPAAL0_ACX1_RETSAT MUP3_MUP3_MUP3_MUP3_MUP3_MUP3_MUP3_MUP3_
	GOTERM, BP, DIRECT GOTERM, CD, DIRECT GOTERM, BP, DIRECT GOTERM, CD, DIRECT GOTERM, BP, DIRECT GOTERM, CD, DIRECT GOTERM, BP, DIRECT GOTERM, CD, DIRECT GOTERM, BP, DIREC	Go 2002393*glucose homeostasis mmu00883.0*enio metabolism mmu00883.0*enio metabolism Go 200355*forextracellular region Go 200355*forextracellular region Go 2003564*forextracellular regiones to testosterone stimulus Go 2003564*forextradellar regiones to association mmu000071.fatty acid netabolic process Go 200852*forextradellar process Go 200852*forextradellar regiones to association transport Go 200852*forextradellar regiones and transport Go 200852*forextradellar regiones and transport Go 200852*forextradellar regiones and transport Go 200557*forextradellar regiones and transport Go 20057*forextradellar regiones and transport mmu0057*forextradellar regiones and transport go 20057*forextradellar regiones and transport go 20057*forextradellar regiones and transport go 20057*forextradellar regiones and transport mmu00587*forextendellar regiones and transport mmu0587*forextendellar regiones	$\begin{array}{c} 1 & 9.3 \\ 7 & 9.3 \\ 15 \\ 200 \\ 21 \\ 200 \\ 20$	107 1000 1000 1000 1000 1000 1000 1100 1	4.096.05 445E.05 447E.05 447E.05 999E.05 075 705 705 705 705 705 705 705 705 7	128:00 286:03 286:03 0050 0050 0050 0050 0050 0050 0050 0	GBCC_MUP1_MUP2_MUP2_MUP13 MUP2_MUP14 GBCC_MUP1_MUP1_MUP1_MUP13 MUP2_MUP13_MUP2_SEPENALS MUP2_MUP1_MUP1_MUP13_MUP13_SEPENALS SEPENALS MUP1_MUP1_MUP1_MUP13_MUP13_MUP13_MUP13_MUP13_MUP13_MUP13_MUP13_MUP1_MUP1_MUP1_MUP1_MUP14_MUP1_MUP1_MUP1_MUP1_MUP1_MUP1_MUP1_MUP1

Supplementary Table 2: Enriched GO terms and corresponding genes from RNA sequencing performed on microdissected (xMD) BECs

Gene symbol	Accession number	Forward	Reverse
18S	NM_003278	5' - AACTTTCgATggTAgTCgCCgT - 3'	5' - TCCTTggATgTggTAgCCgTTT - 3'
Acta2	NM_007392.3	5' - AACAgCATCATgAAgTgTgATATTgACATC - 3'	5' - gCTgATCCACATCTgCTggAAgg - 3'
Afp	NM_007423.4	5' - TgACAACAAggAggAgTgCTTCCA - 3'	5' - AATggTTgTTgCCTggAggTTTCg - 3'
Angpt2	NM_007426.4	5' - AgCCCCTACATgTCCAATgC - 3'	5' - TTgTgCTgCTgTCTggTTCA - 3'
Ccl2	NM_011333.3	5' - TCTGGACCCATTCCTTCTTGG - 3'	5' - TCAGCCAGATGCAGTTAACGC - 3'
Cd133	NM_008935.2	5' - CCCTCCAgCAAACAAgCAAC - 3'	5' - ACAgCCggAAgTAAgAgCAC - 3'
Col1a1	NM_007742	5' - gAAACCgCAggTATgCTTgA - 3'	5' - gACCAggAggACCAggAAgT - 3'
Col3a1	NM_009930.2	5' - TAggACTgACCAAggTggCT - 3'	5' - ggAACCTggTTTCTTCTCACC - 3'
Col5a2	NM_007737.2	5' - CATggAgAAggTTTCCAAATg - 3'	5' - AAAgCCCAggAACAAgAgAA - 3'
Cyp7a1	NM_007824.2	5' - ATTCCATACCTgggCTgTgC - 3'	5' - CTgTgTCCAAATgCCTTCgC - 3'
Cyp8b1	NM_010012.3	5' - TCCTCAgggTggTACAggAg - 3'	5' - CgggTTgAggAACCgATCAT - 3'
Eln	NM_007925.4	5' - ATAAAACgAggCgCTgAgAg - 3'	5' - CTCCAggACCTgCTCCAAAC - 3'
Entpd2	NM_009849.2	5' - ATgCgCCTACTCAACCTgAC - 3'	5' - AgCAggTAgTTggCAgTCAC - 3'
Fxr	NM_001163700.1	5' - ggCTgCAAAggTTTCTTCCg - 3'	5' - ACACTggATTTCAgTTAACAAACC - 3'
Fn1	NM_010233.2	5' - gACCCTTACACggTTTCCCA - 3'	5' - ACgTTgCTTCATggggATCA - 3'
Gpbar1 (TGR5)	NM_174985.1	5' - CgATgTACCCTCAACCCTgg - 3'	5' - ACgCTCATAggCCAAgACTg - 3'
Hif1a	NM_001313919.1	5' - TggACTTgTCTCTTTCTCCgC - 3'	5' - TTTTCTTCTCgTTCTCgCCg - 3'
ll1b	NM_008361	5' - CTCCACCTCAATggACAgAA - 3'	5' - gCCgTCTTTCATTACACAgg - 3'
116	NM_013693	5' - gAACAACgATgATgCACTTgC - 3'	5' - TCCAggTAgCTATggTACTCC - 3'
lfng	NM_008337	5' - ggCCATCAgCAACAACATAAgCgT - 3'	5' - TgggTTgTTgACCTCAAACTTggC - 3'
ltgb1	NM_010578.2	5' - ggACgCTgCgAAAAgATgAA - 3'	5' - CCACAATTTggCCCTgCTTg - 3'
ltgb5	NM_001145884.1	5' - gCCCgTTATgAAATggCCTC - 3'	5' - CTACCAggTCCCTTAgggCT - 3'
ltgb6	NM_021359.3	5' - ACggCTTCCAgCTTTggTC - 3'	5' - ACAggTgggTgAAATTCTCCTg - 3'
ltgb8	NM_177290.3	5' - ACTgggCCAAAgTgAACACA - 3'	5' - ACTgAgACTTCTCCCggTgT - 3'
Lta	NM_010735.2	5' - AgCAgCATCTTCTAAgCCCT - 3'	5' - gTCATgTggAgAACCTgCTgTg - 3'
Ltb	NM_008518.2	5' - CAgCTgCggATTCTACACCA - 3'	5' - CATCCAAgCgCCTATgAggT - 3'
Osm	NM_001013365.2	5' - gAgCCCTATATCCgCCTCCA - 3'	5' - AgCTTTggAAAAgCCggAGT - 3'
Pkm2	NM_001253883.1	5' - CCCgCAACACTggCATCATTTgTA - 3'	5' - TgCAAAgCTTTCTgTggCTTCACg - 3'
Tgfb1	NM_011577	5' - TgCgCTTgCAgAgATTAAAA - 3'	5' - CTgCCgTACAACTCCAgTgA - 3'
Tgfb2	NM_009367.3	5' - TCCCCTCCgAAAATgCCATC - 3'	5' - TgCTATCgATgTAgCgCTgg - 3'
Thy1	NM_009382.3	5' - AACCAAAACCTTCgCCTggAC - 3'	5' - AAgCTCACAAAAgTAgTCgCCC - 3'
Tnfa	NM_013693	5' - AATggCCTCCCTCTCATCAgTT - 3'	5' - CCACTTggTggTTTgCTACgA - 3'
Tweak (Tnfsf12)	NM_011614.3	5' - AATCAACAgCTCCAgCCCTC - 3'	5' - gATCCgAAgggAAgACCCTg - 3'

Supplementary Table 3: Oligonucleotides used for quantitative RT-PCR