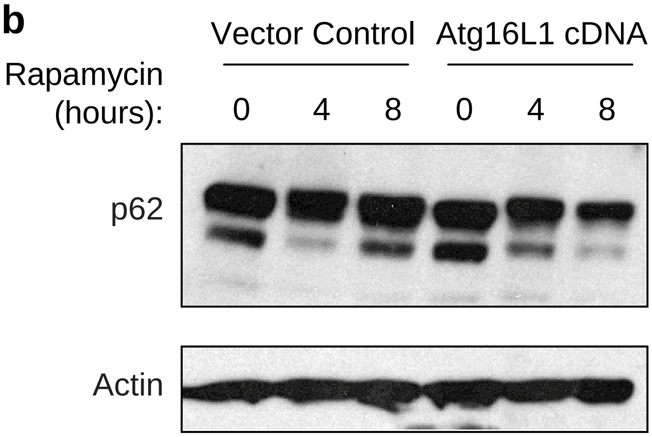
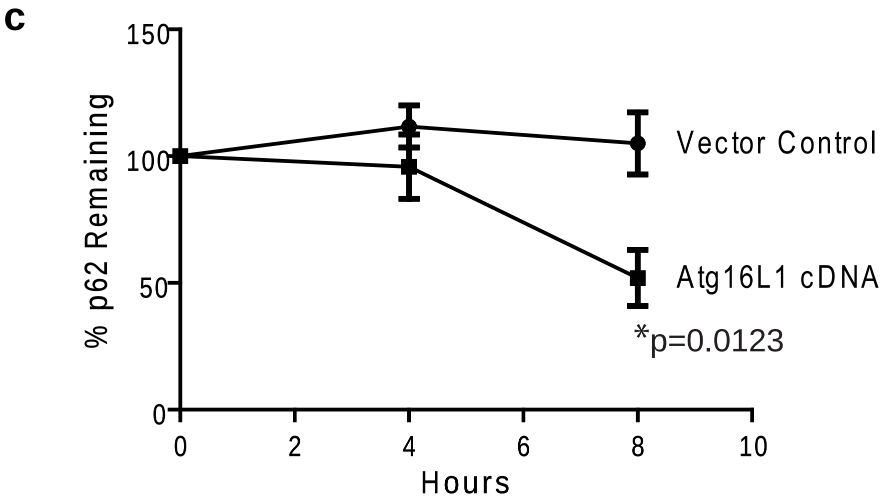
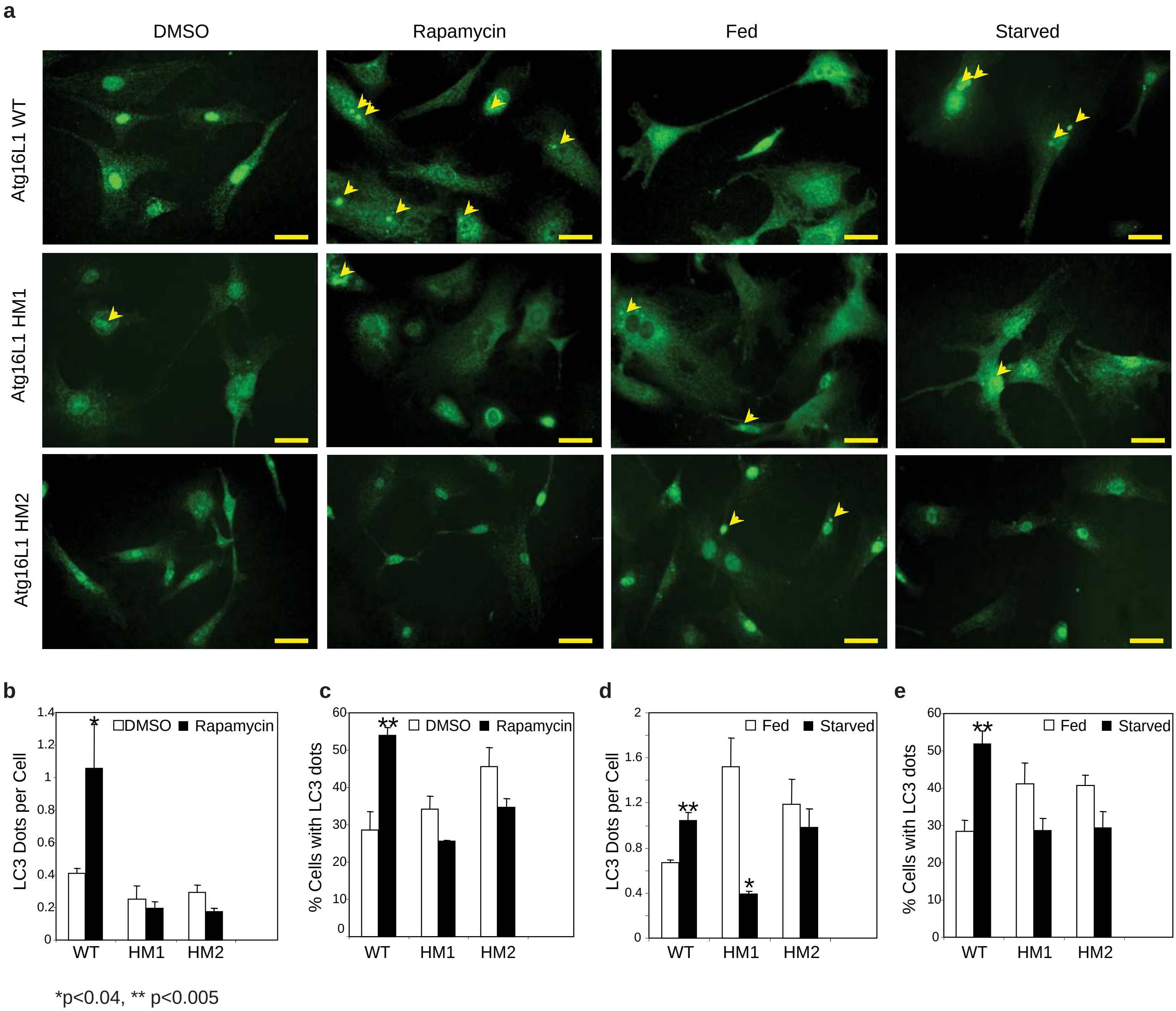
a

	wt	hm/+	hm/hm
Atg16L HM1	**21** (18.4%)	**64** (56.3%)	**30** (25.2%)
Atg16L HM2	**40** (26.7%)	**67** (41.2%)	**43** (32.1%)

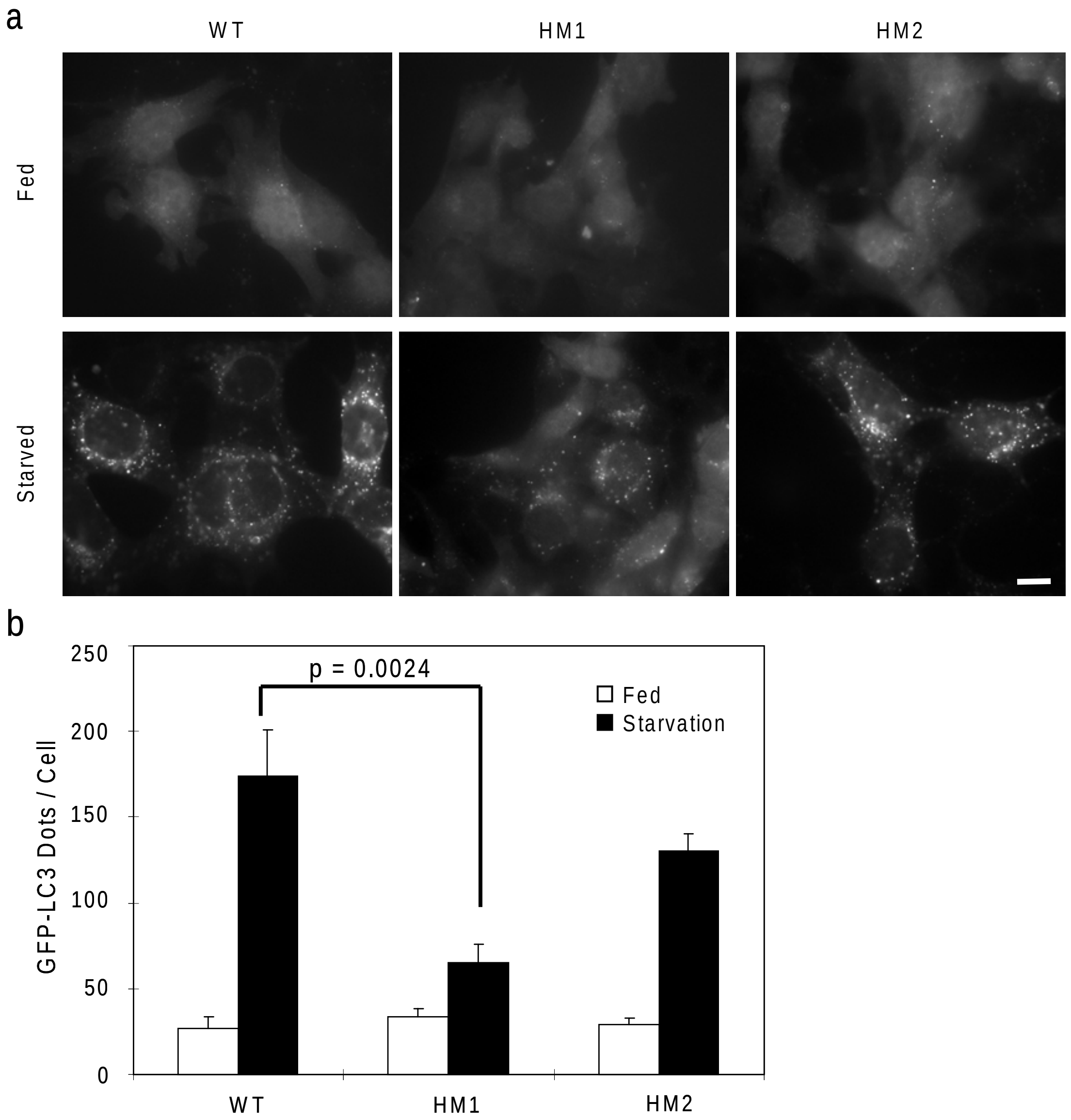




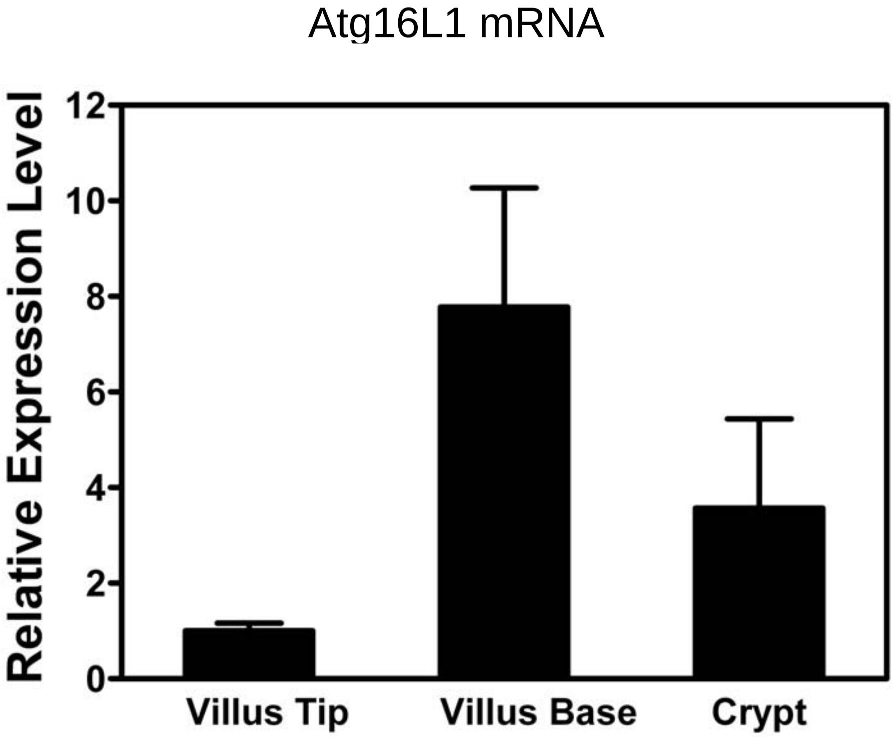
Supplementary Figure 1. **Allelic inheritance in Atg16L1^{HM} mice and rescue of autophagy deficiency in Atg16L1 deficient fibroblasts.** a, Mice heterozygous for the gene trap mutation were bred to each other and produced wild-type (wt), heterozygous (hm/+) and homozygous (hm/hm) progeny which were separated by genotype ~4 weeks after birth. Both gene trap alleles displayed Mendelian inheritance (no significant deviation by Fisher's chi-square test, p>0.2 for ATG16L1^{HM1} and p>0.3 for ATG16L1^{HM2}) b-c, Atg16L1 cDNA or vector control were reintroduced into Atg16L1^{HM1} MEFs via retroviral transduction. MEFs were selected for successful transduction with 5μg/ml puromycin, then grown in the presence of the chemical inducer of autophagy rapamycin (50μg/ml) and cyclohexamide (5μg/ml) for 0, 4, and 8 h. Western blot analysis of cell lysates show a restoration of p62 degradation in MEFs selected for Atg16L1 expression but not vector control (b) which was quantified by densitometry and normalized to actin (n = 3) (c).



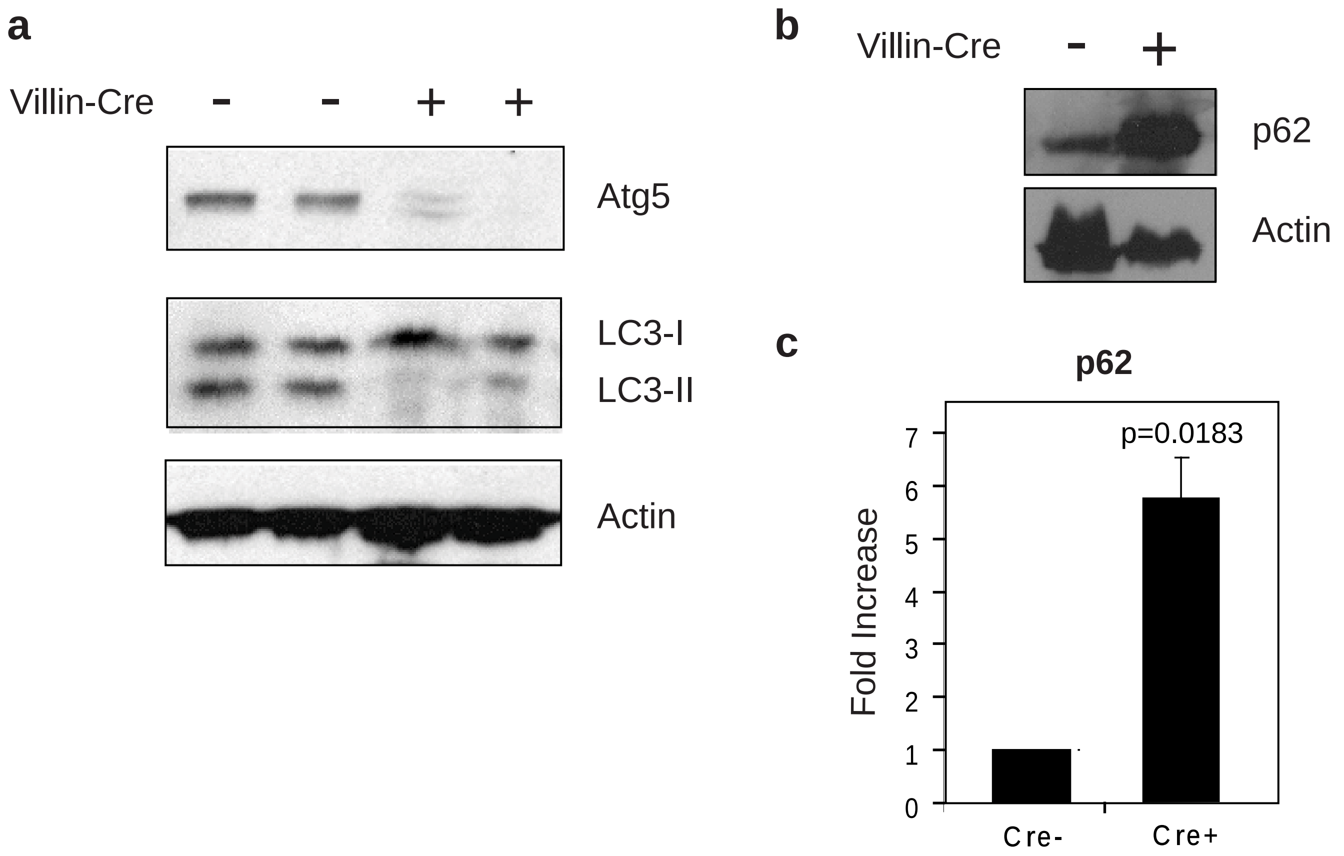
Supplementary Figure 2. MEFs derived from Atg16L1^{HM1} and Atg16L1^{HM2} lines show reduced endogenous LC3 dot formation. **a**, Representative immunofluorescence images of primary low-passage MEFs grown in 50µg/ml rapamycin for 4h or in amino acid and serum replete EBSS media for 2h to induce autophagy and stained with LC3. LC3-positive dots >0.5µm in diameter are indicated by arrow heads. Scale bar, 20µm. **b-e**, Quantification of LC3 dots revealed that both the accumulation of LC3 dots per cell (**b** and **d**) or % cells with LC3 dots (**c** and **e**) after autophagy induction were compromised in Atg16L1^{HM} cells, indicating that autophagosome formation was aberrant under these conditions (n = 3, at least 70 cells were analyzed per sample). The increase in LC3 dots was statistically significant in all WT samples. There was no statistically significant increase in Atg16L1^{HM} cells (note: Atg16L1^{HM1} cells display a statistically significant decrease in dots per cell under starvation conditions). *P* values were calculated using two-tailed student's t test. Error bars represent SEM.



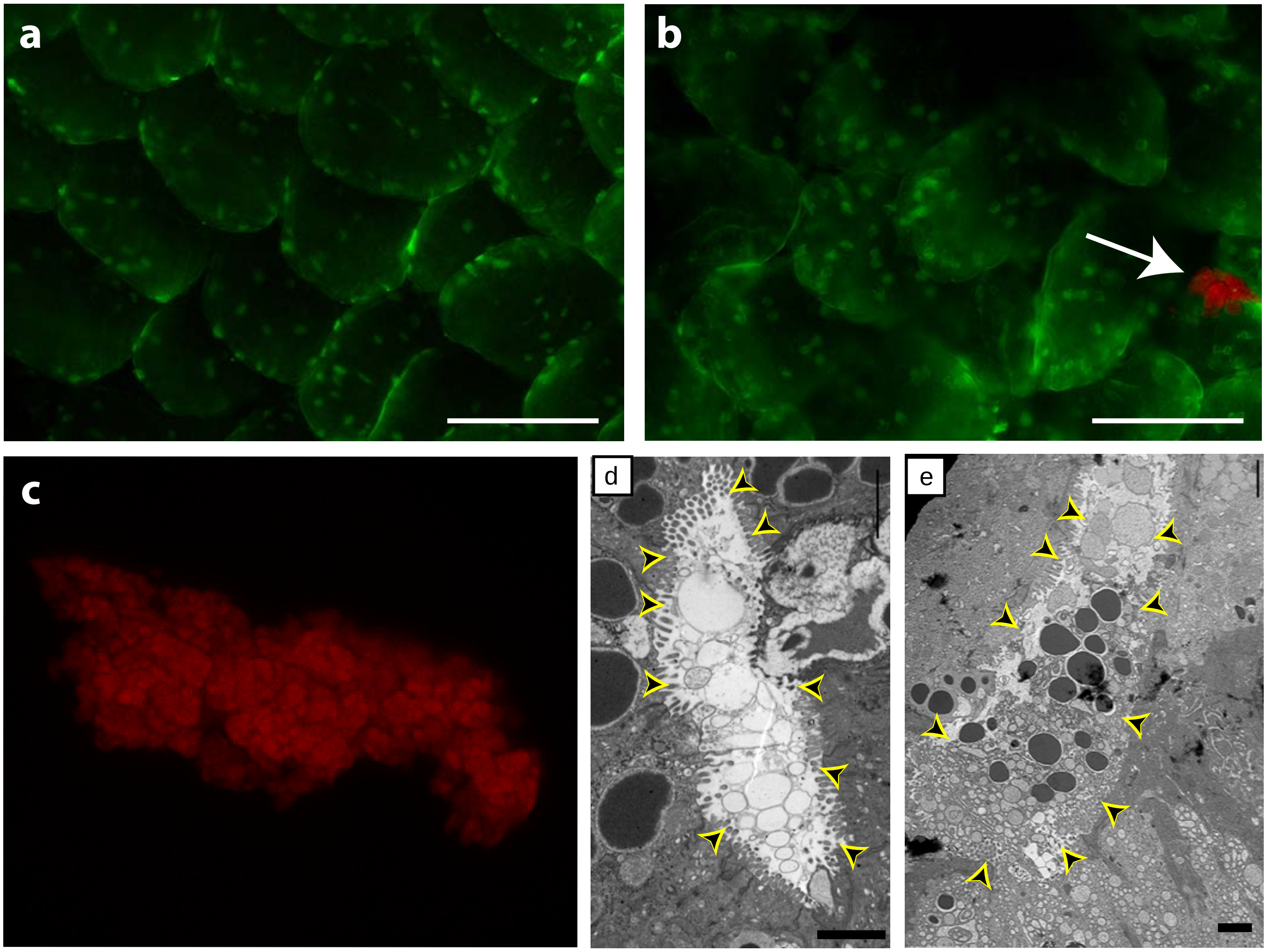
Supplementary Figure 3. GFP-LC3 dot formation is reduced in Atg16L1^{HM1} MEFs. a, Representative fluorescence images of in immortalized Atg16L1^{HM} MEFs stably expressing GFP-LC3. Cells were cultured in DMEM with 10% FBS or DMEM without amino acids and serum for 2 h. Scale bar, 10 μm. **b**, Quantification of the number of GFP-LC3 dots per cell (counted in at least 5 different images) show a significant reduction in dot formation in Atg16L1^{HM1} cells. Atg16L1^{HM2} cells did not show a statistically significant reduction in dot formation, consistent with the higher expression of Atg16L1 in these cells. *P* values were calculated using two-tailed student's t test. Error bars represent SEM.



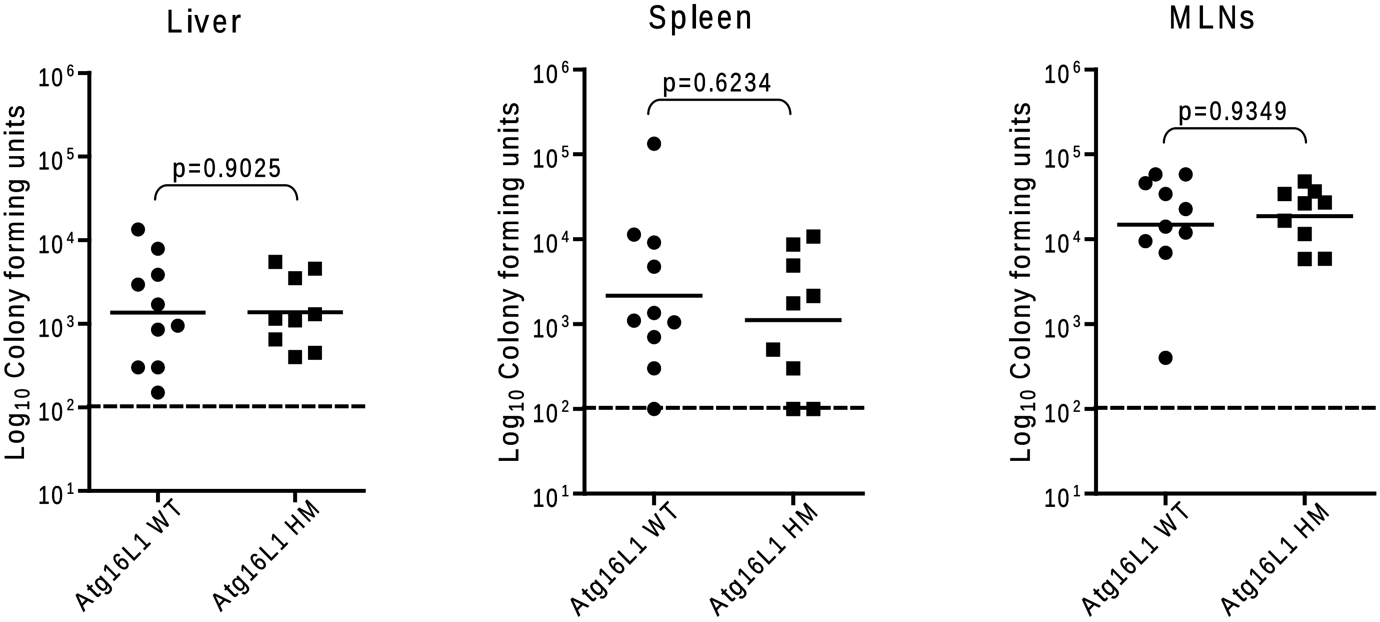
Supplementary Figure 4. **Atg16L1 is expressed throughout the ileal crypt-villus axis.** RNA was procured by LCM from the villus tip, villus base, and crypt base of the distal ileum from Atg16L1^{HM} mice. qRT-PCR analysis shows detectable Atg16L1 transcripts in all three compartments (n = 3). There was a statistically significant difference between the villus tip and the villus base ($p<0.1$) or crypt ($p<0.05$) indicating that Atg16L1 transcripts are enriched in the villus base and crypt. *P* values were calculated using two-tailed student's t test. Error bars represent SEM.



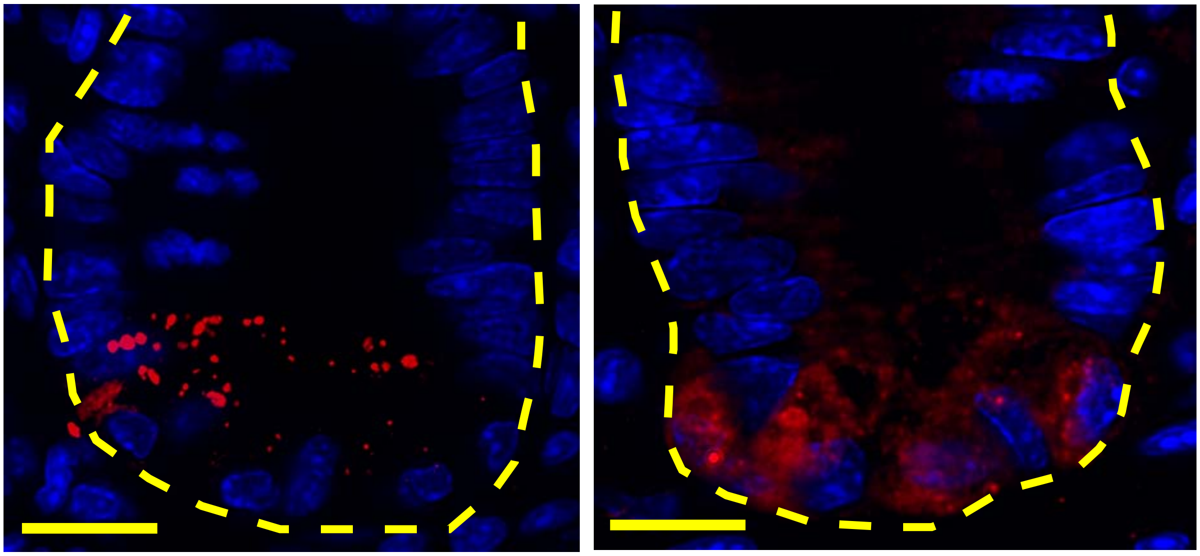
Supplementary Figure 5. **Conditional deletion of *Atg5* in the intestinal epithelium leads to reduced LC3 conversion and accumulation of p62.** **a**, Western blot analysis of ileal lysates from *Atg5*$^{flox/flox}$*villin-Cre* mice reveal decreased Atg5 expression and an increase in LC3-I to LC3-II ratio similar to Atg16L1^{HM} mice suggesting a critical role for these proteins in intestinal autophagy (n = 3 of each genotype, 2 of each shown). **b-c**, *Atg5*$^{flox/flox}$*villin-Cre* mice also display an increase in p62 protein expression in the ileal epithelium (**b**) similar to Atg16L1^{HM} mice. Quantification of p62 levels by densitometry normalized to actin revealed ~7-fold increase in *Atg5*$^{flox/flox}$*villin-Cre*+ mice (n = 3) (**c**). *P* values were calculated using two-tailed student's t test. Error bars represent SEM.



Supplementary Figure 6. Abnormal Paneth granule exocytosis in Atg16L1 deficient mice. a-c, Whole mounts of the small intestines from control (a) and Atg16L1^{HM} (b, c) mice stained with FITC-conjugated *Helix pomatia* lectin that labels goblet cell mucus (green) and antisera directed against lysozyme (red). Lectin positive goblet cells stud the surface of the villi. No accumulated mucin is shown in these fields. Strikingly, the lysozyme staining in the Atg16L1^{HM} mice is concentrated in small clusters of spherical aggregates (white arrow in b) that are present in the crypt lumen. High power view of the aggregate in (c) is 40µm in its greatest dimension. d-e, EM analysis of the Atg16L1^{HM} ileum reveals diminished microvilli on Paneth cells (d) and the adjacent crypt lumen (indicated by arrow heads) contains intact Paneth granules and cytoplasm (e). Scale bars: a, b, 200 µm; d, e, 2 µm.

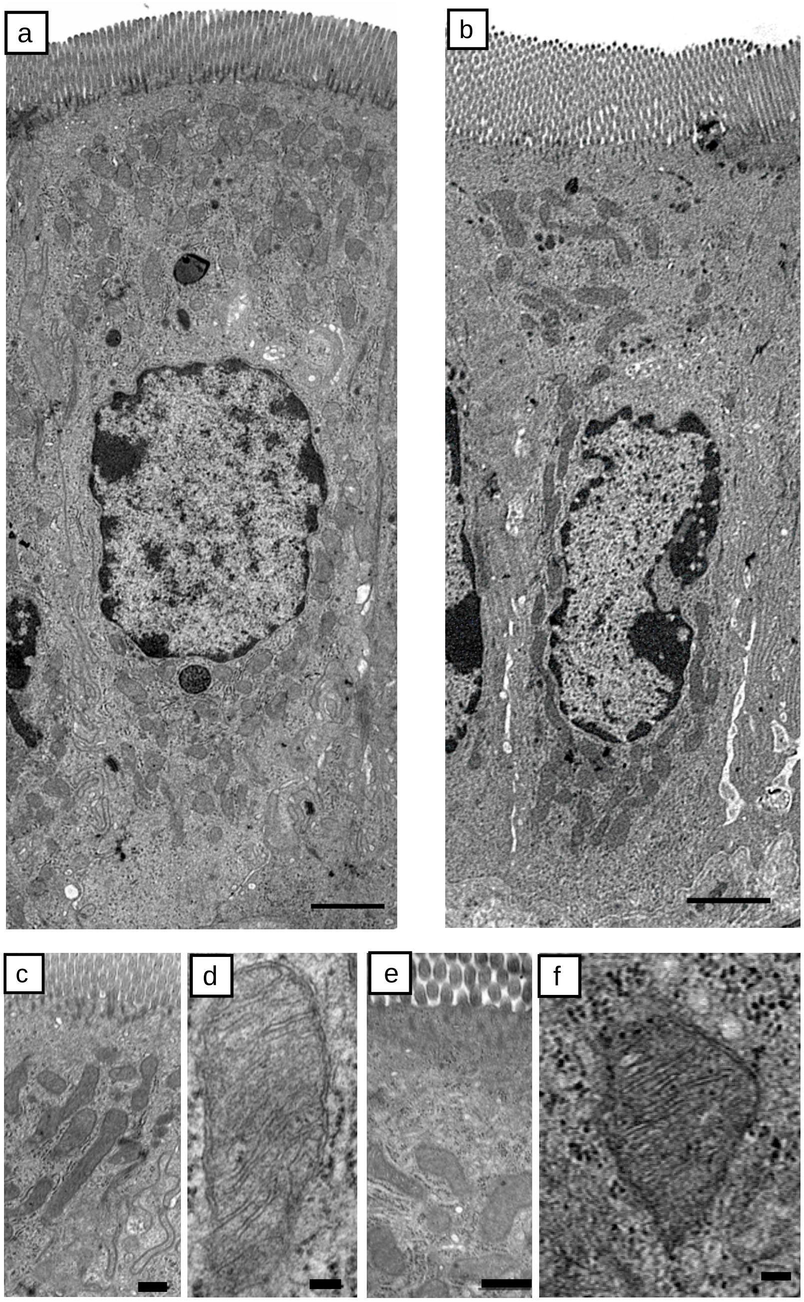


Supplementary Figure 7. **Atg16L1 mutant mice do not display increased susceptibility to oral *L. monocytogenes* infection.** Littermate WT (n = 10) and Atg16L1^{HM} (n = 5 for HM1 and n = 4 for HM2) mice were infected orally with 10^9 *L. monocytogenes* re-suspended in 200μl of 5% sodium bicarbonate by gastric gavage. The number of bacteria in liver, spleen, and mesenteric lymph nodes were determined 72 h after infection and displayed no significant differences with WT. *P* values were calculated using two-tailed Mann-Whitney test. Horizontal bars represent the geometric mean.



$Atg5^{flox/flox}$ *$Atg5^{flox/flox}$villin-Cre*

Supplementary Figure 8. **Mice with conditional deletion of *Atg5* in the intestinal epithelium have abnormal lysozyme distribution in Paneth cells similar to observations made in Atg16L1 deficient mice.** Representative images of indirect immunofluorescence of sections stained for lysozyme (red) in *$Atg5^{flox/flox}$* control and *$Atg5^{flox/flox}$villin-Cre* mouse ileal crypts. Dotted lines denote crypt unit. Scale bars: 10 μm.



Supplementary Figure 9. Enterocytes in the ileal epithelium are similar between Atg16L1 mutant and wild-type controls by ultrastructural analysis. a-b, EM of ileal villus enterocytes from WT (**a**, **c**, **d**) and Atg16L1^{HM} (**b**, **e**, **f**) mice show similar morphology with intact mitochondria. Scale bars: **a**, **b**, 2 μm; **c**, **e**, 500 nm; **d**, **f**, 100 nm.

Gene	qRT-PCR Validation	Fold Change	Low Bound of FC
Selenoprotein P, plasma, 1	114.0 ± 10.8	1.10	1.03
Peripheral myelin protein 22	169.3 ± 10.2	1.40	1.27
Serine/cysteine peptidase inhibitor, clade B, member 1a	14.0 ± 1.1	1.38	1.20
Serum/glucocorticoid regulated kinase 1	2.8 ± 0.1	-2.05	-1.82
BTB and CNC homology 1	2.5 ± 0.4	-1.09	-0.99
Protein tyrosine phosphatase, non-receptor type 9	3.3 ± 0.7	-1.27	-1.04
Villin 1	Enterocyte marker*	1.12	1.04
Mucin 2	Goblet cell marker*	-1.13	-1.05
Chloride channel calcium activated 3	Goblet cell marker*	1.21	1.01
Chromogranin B	Enteroendocrine cell marker*	-1.25	-1.16

Supplementary Figure 10. Validation of lack of contamination of LCM procured Paneth cells with villus epithelial cells. a, We quantified 6 genes by qRT-PCR known to be enriched in villus epithelial cells[1] and not involved in fatty acid or cholesterol metabolism. We compared gene expression in LCM-procured Paneth cells versus villus epithelial cells. The fold-enrichment for villus epithelial cells is indicated for each gene (experiments were performed in triplicate). For each of these 6 genes and 4 well-characterized markers of villus epithelial cells (indicated by an asterisk), we compared the fold-change for Atg16L1^{HM} Paneth cells versus WT. Transcripts highly enriched in villus epithelial cells were not enriched in LCM procured Paneth cells.

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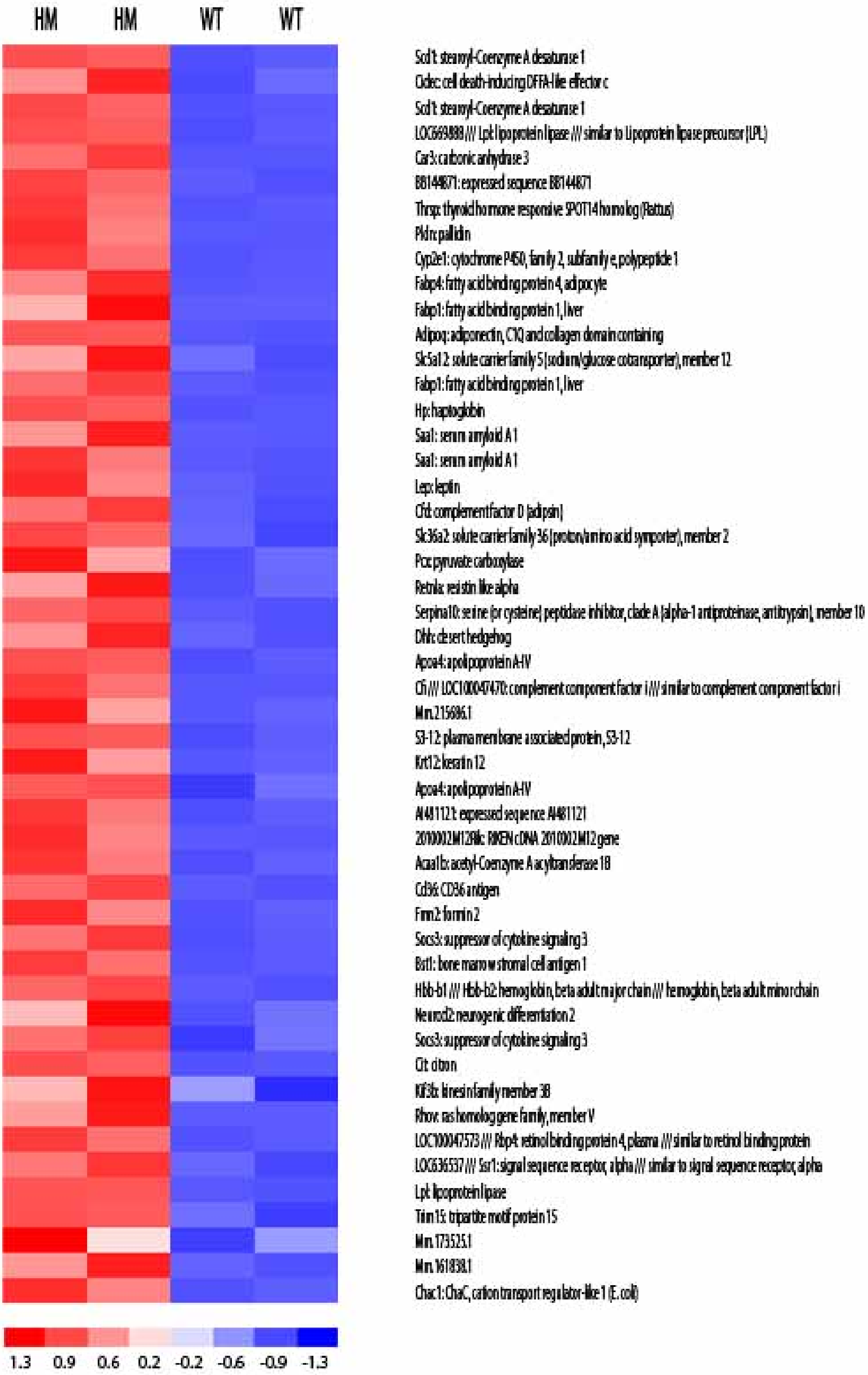
HM
HM
WT
WT
Scd1: stearoyl-Coenzyme A desaturase 1
Cidec: cell death-inducing DFFA-like effector c
Scd1: stearoyl-Coenzyme A desaturase 1
LOC669888 /// Lpl: lipoprotein lipase /// similar to Lipoprotein lipase precursor (LPL)
Car3: carbonic anhydrase 3
BB144871: expressed sequence BB144871
Thrsp: thyroid hormone responsive SPOT14 homolog (Rattus)
Pldn: pallidin
Cyp2e1: cytochrome P450, family 2, subfamily e, polypeptide 1
Fabp4: fatty acid binding protein 4, adipocyte
Fabp1: fatty acid binding protein 1, liver
Adipoq: adiponectin, C1Q and collagen domain containing
Slc5a12: solute carrier family 5 (sodium/glucose cotransporter), member 12
Fabp1: fatty acid binding protein 1, liver
Hp: haptoglobin
Saa1: serum amyloid A 1
Saa1: serum amyloid A 1
Lep: leptin
Cfd: complement factor D (adipsin)
Slc36a2: solute carrier family 36 (proton/amino acid symporter), member 2
Pcx: pyruvate carboxylase
Retnla: resistin like alpha
Serpina10: serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10
Dhh: desert hedgehog
Apoa4: apolipoprotein A-IV
Cfi /// LOC100047470: complement component factor i /// similar to complement component factor i
Mm.215686.1
S3-12: plasma membrane associated protein, S3-12
Krt12: keratin 12
Apoa4: apolipoprotein A-IV
AI481121: expressed sequence AI481121
2010002M12Rik: RIKEN cDNA 2010002M12 gene
Acaa1b: acetyl-Coenzyme A acyltransferase 1B
Cd36: CD36 antigen
Fmn2: formin 2
Socs3: suppressor of cytokine signaling 3
Bst1: bone marrow stromal cell antigen 1
Hbb-b1 /// Hbb-b2: hemoglobin, beta adult major chain /// hemoglobin, beta adult minor chain
Neurod2: neurogenic differentiation 2
Socs3: suppressor of cytokine signaling 3
Cit: citron
Kif3b: kinesin family member 3B
Rhov: ras homolog gene family, member V
LOC100047573 /// Rbp4: retinol binding protein 4, plasma /// similar to retinol binding protein
LOC636537 /// Ssr1: signal sequence receptor, alpha /// similar to signal sequence receptor, alpha
Lpl: lipoprotein lipase
Trim15: tripartite motif protein 15
Mm.173525.1
Mm.161838.1
Chac1: ChaC, cation transport regulator-like 1 (E. coli)
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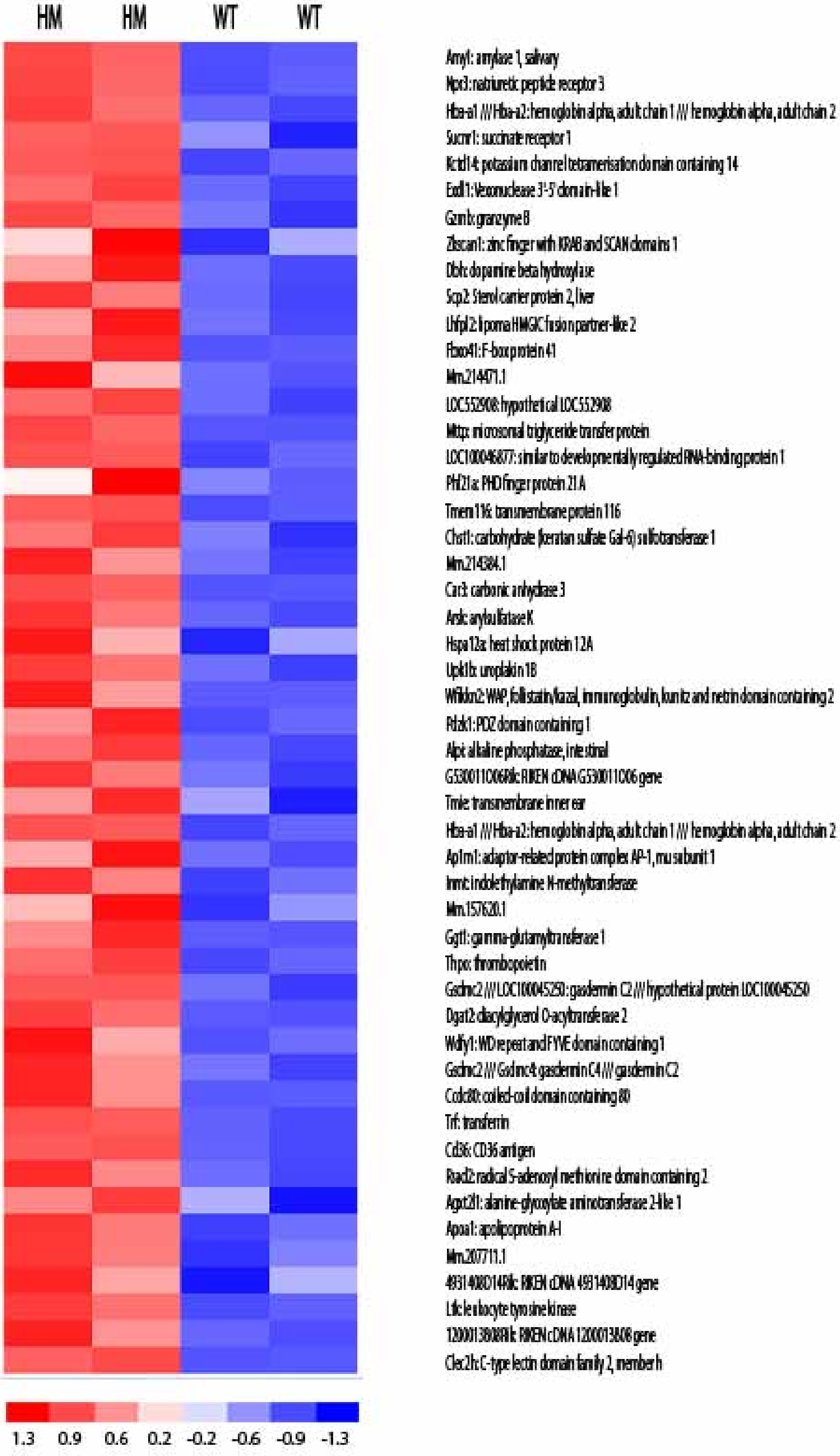
0.9
0.6
0.2
-0.2
-0.6
-0.9
-1.3


HM
HM
WT
WT
Amy1: amylase 1, salivary
Npr3: natriuretic peptide receptor 3
Hba-a1 /// Hba-a2: hemoglobin alpha, adult chain 1 /// hemoglobin alpha, adult chain 2
Sucnr1: succinate receptor 1
Kctd14: potassium channel tetramerisation domain containing 14
Exdl1: Vexonuclease 3'-5' domain-like 1
Gzmb: granzyme B
Zkscan1: zinc finger with KRAB and SCAN domains 1
Dbh: dopamine beta hydroxylase
Scp2: Sterol carrier protein 2, liver
Lhfpl2: lipoma HMGIC fusion partner-like 2
Fbxo41: F-box protein 41
Mm.214471.1
LOC552908: hypothetical LOC552908
Mttp: microsomal triglyceride transfer protein
LOC100046877: similar to developmentally regulated RNA-binding protein 1
Phf21a: PHD finger protein 21A
Tmem116: transmembrane protein 116
Chst1: carbohydrate (keratan sulfate Gal-6) sulfotransferase 1
Mm.214384.1
Car3: carbonic anhydrase 3
Arsk: arylsulfatase K
Hspa12a: heat shock protein 12A
Upk1b: uroplakin 1B
Wfikkn2: WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2
Pdzk1: PDZ domain containing 1
Alpi: alkaline phosphatase, intestinal
G530011O06Rik: RIKEN cDNA G530011O06 gene
Tmie: transmembrane inner ear
Hba-a1 /// Hba-a2: hemoglobin alpha, adult chain 1 /// hemoglobin alpha, adult chain 2
Ap1m1: adaptor-related protein complex AP-1, mu subunit 1
Inmt: indolethylamine N-methyltransferase
Mm.157620.1
Ggt1: gamma-glutamyltransferase 1
Thpo: thrombopoietin
Gsdmc2 /// LOC100045250: gasdermin C2 /// hypothetical protein LOC100045250
Dgat2: diacylglycerol O-acyltransferase 2
Wdfy1: WD repeat and FYVE domain containing 1
Gsdmc2 /// Gsdmc4: gasdermin C4 /// gasdermin C2
Ccdc80: coiled-coil domain containing 80
Trf: transferrin
Cd36: CD36 antigen
Rsad2: radical S-adenosyl methionine domain containing 2
Agxt2l1: alanine-glyoxylate aminotransferase 2-like 1
Apoa1: apolipoprotein A-I
Mm.207711.1
4931408D14Rik: RIKEN cDNA 4931408D14 gene
Ltk: leukocyte tyrosine kinase
1200013B08Rik: RIKEN cDNA 1200013B08 gene
Clec2h: C-type lectin domain family 2, member h
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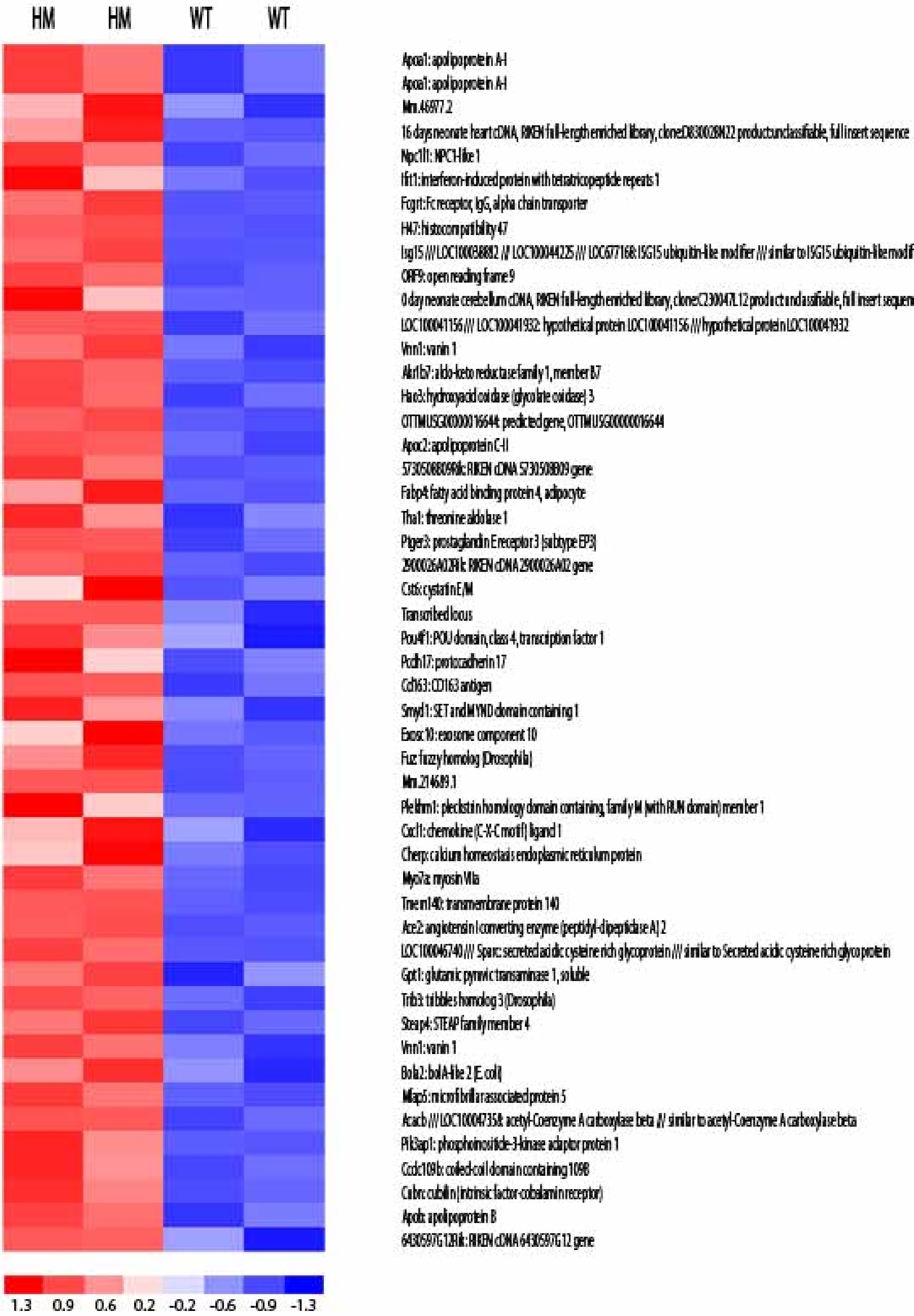
0.6
0.2
-0.2
-0.6
-0.9
-1.3


HM
HM
WT
WT
Apoa1: apolipoprotein A-I
Apoa1: apolipoprotein A-I
Mm.46977.2
16 days neonate heart cDNA, RIKEN full-length enriched library, clone:D830028M22 product:unclassifiable, full insert sequence
Npc1l1: NPC1-like 1
Ifit1: interferon-induced protein with tetratricopeptide repeats 1
Fcgrt: Fc receptor, IgG, alpha chain transporter
H47: histocompatibility 47
Isg15 /// LOC100038882 /// LOC100044225 /// LOC677168: ISG15 ubiquitin-like modifier /// similar to ISG15 ubiquitin-like modif
ORF9: open reading frame 9
0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230047L12 product:unclassifiable, full insert sequen
LOC100041156 /// LOC100041932: hypothetical protein LOC100041156 /// hypothetical protein LOC100041932
Vnn1: vanin 1
Akr1b7: aldo-keto reductase family 1, member B7
Hao3: hydroxyacid oxidase (glycolate oxidase) 3
OTTMUSG00000016644: predicted gene, OTTMUSG00000016644
Apoc2: apolipoprotein C-II
5730508B09Rik: RIKEN cDNA 5730508B09 gene
Fabp4: fatty acid binding protein 4, adipocyte
Tha1: threonine aldolase 1
Ptger3: prostaglandin E receptor 3 (subtype EP3)
2900026A02Rik: RIKEN cDNA 2900026A02 gene
Cst6: cystatin E/M
Transcribed locus
Pou4f1: POU domain, class 4, transcription factor 1
Pcdh17: protocadherin 17
Cd163: CD163 antigen
Smyd1: SET and MYND domain containing 1
Exosc10: exosome component 10
Fuz: fuzzy homolog (Drosophila)
Mm.214689.1
Plekhm1: pleckstrin homology domain containing, family M (with RUN domain) member 1
Cxcl1: chemokine (C-X-C motif) ligand 1
Cherp: calcium homeostasis endoplasmic reticulum protein
Myo7a: myosin VIIa
Tmem140: transmembrane protein 140
Ace2: angiotensin I converting enzyme (peptidyl-dipeptidase A) 2
LOC100046740 /// Sparc: secreted acidic cysteine rich glycoprotein /// similar to Secreted acidic cysteine rich glycoprotein
Gpt1: glutamic pyruvic transaminase 1, soluble
Trib3: tribbles homolog 3 (Drosophila)
Steap4: STEAP family member 4
Vnn1: vanin 1
Bola2: bolA-like 2 (E. coli)
Mfap5: microfibrillar associated protein 5
Acacb /// LOC100047358: acetyl-Coenzyme A carboxylase beta /// similar to acetyl-Coenzyme A carboxylase beta
Pik3ap1: phosphoinositide-3-kinase adaptor protein 1
Ccdc109b: coiled-coil domain containing 109B
Cubn: cubilin (intrinsic factor-cobalamin receptor)
Apob: apolipoprotein B
6430597G12Rik: RIKEN cDNA 6430597G12 gene
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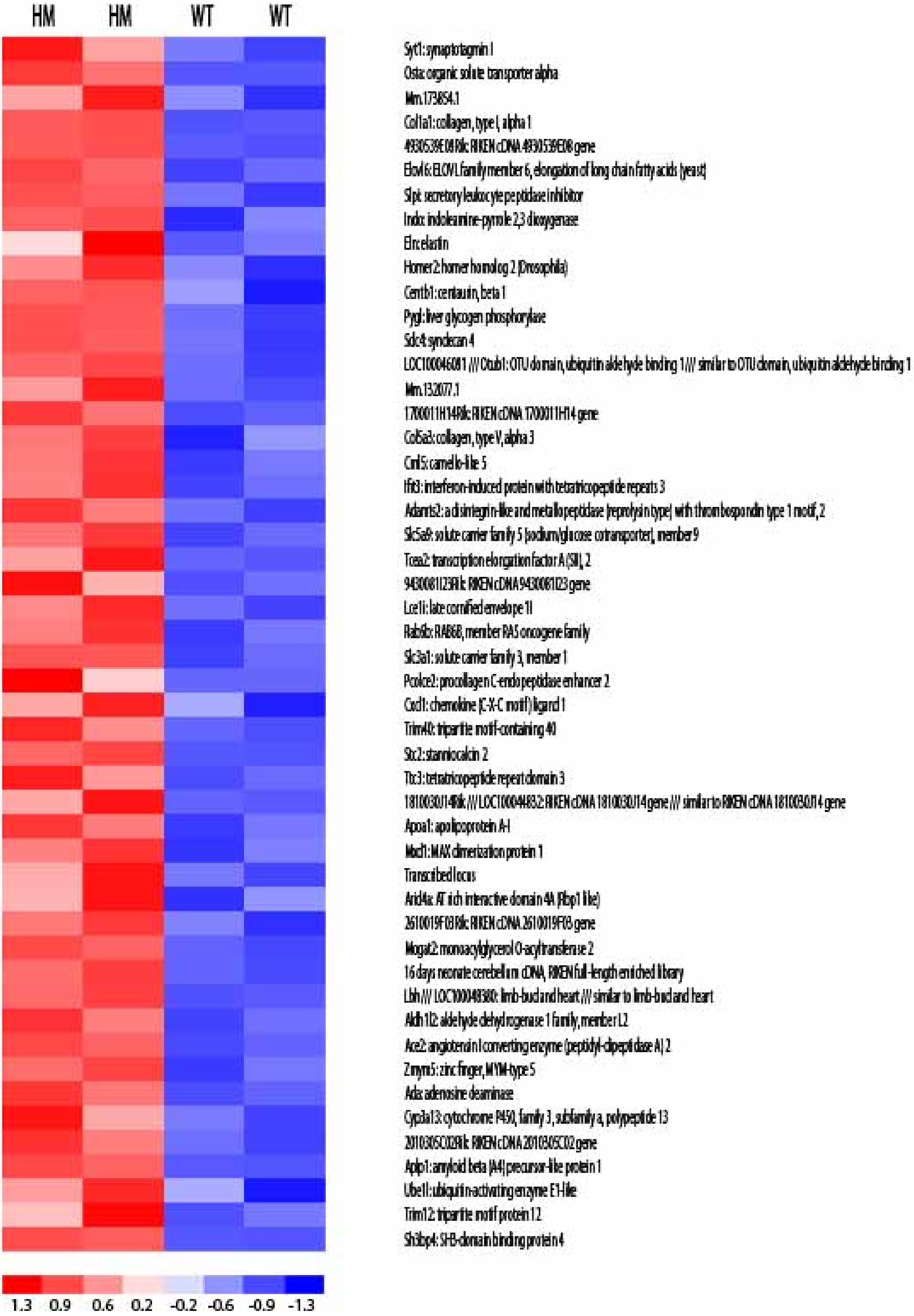
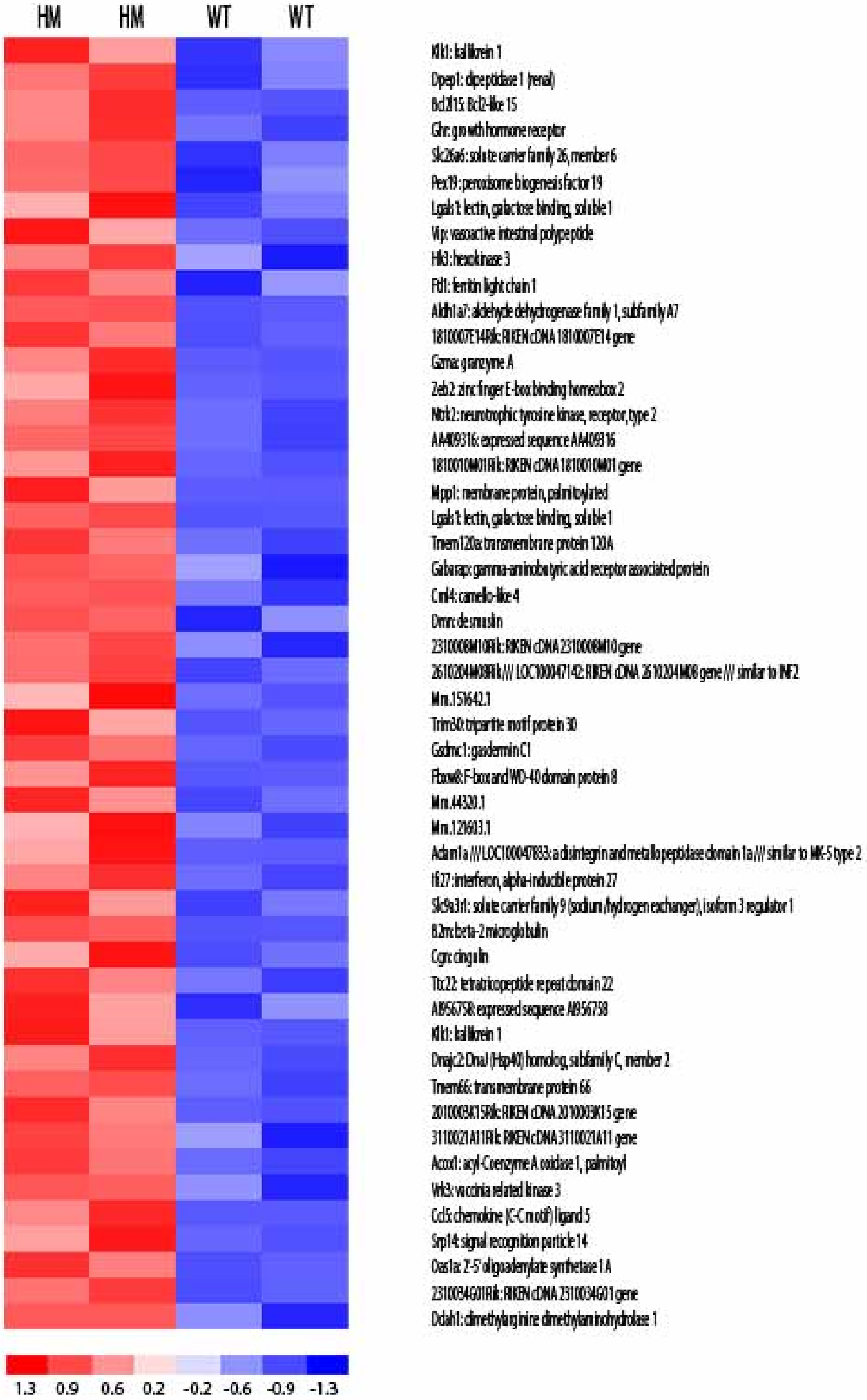
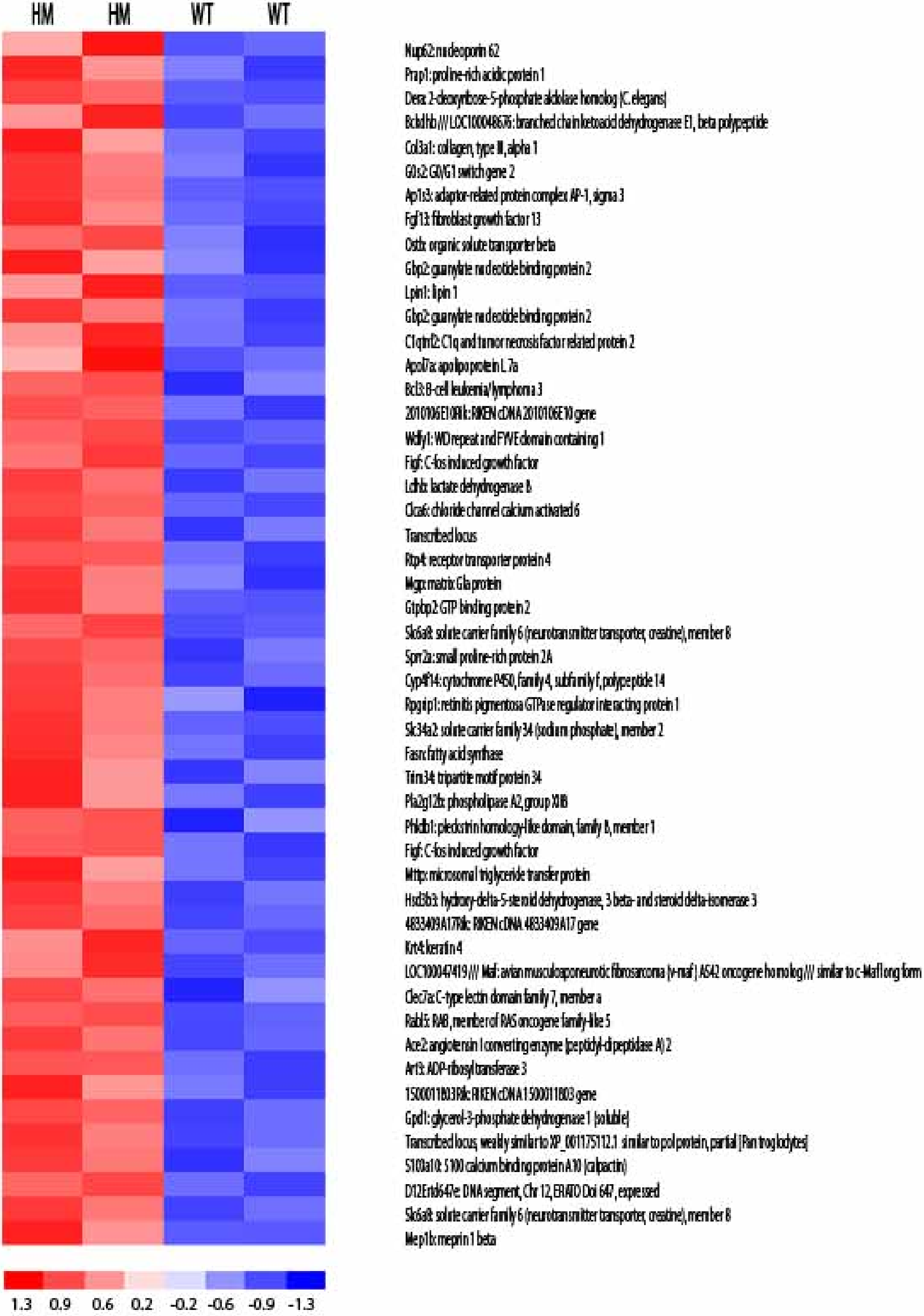
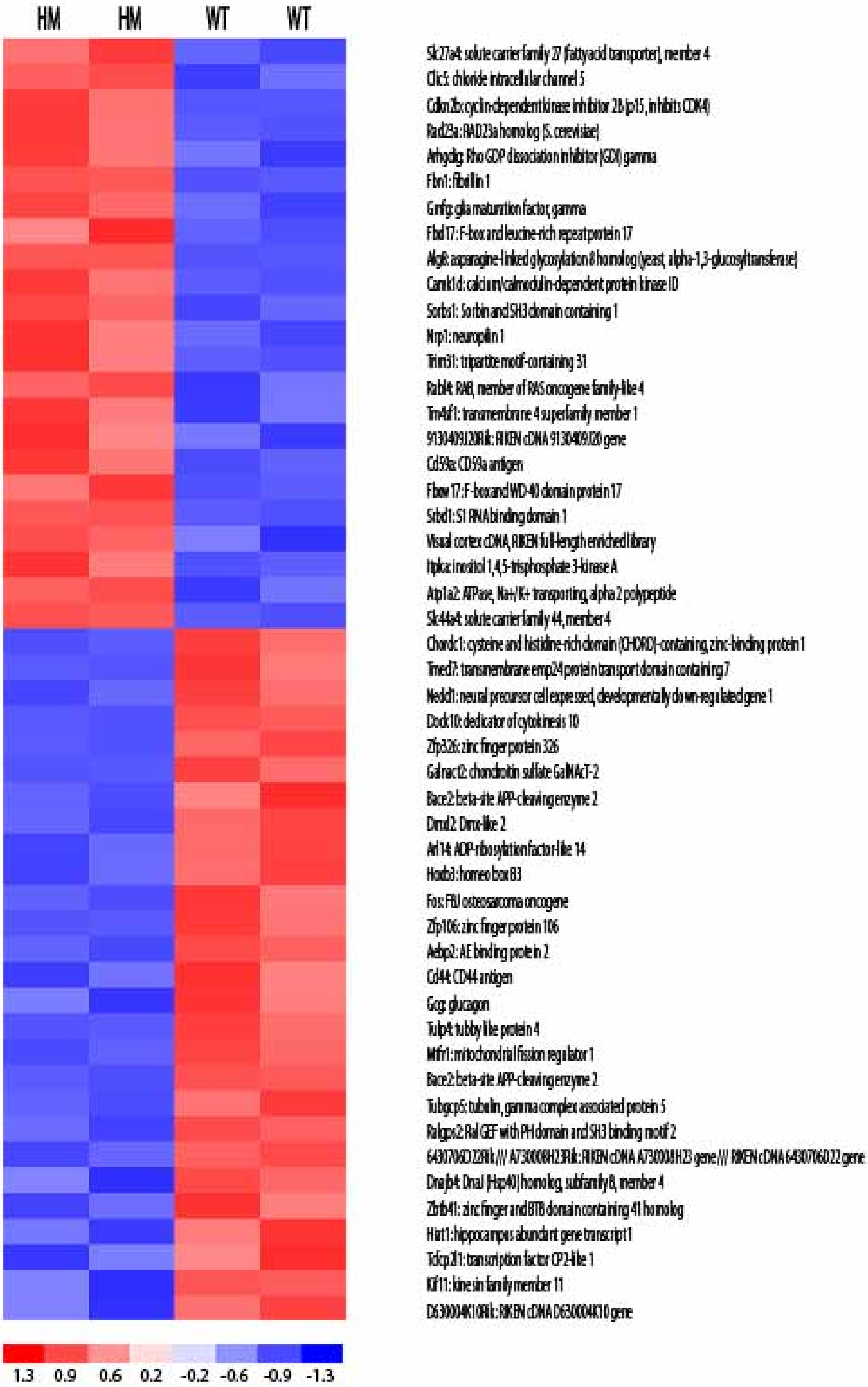
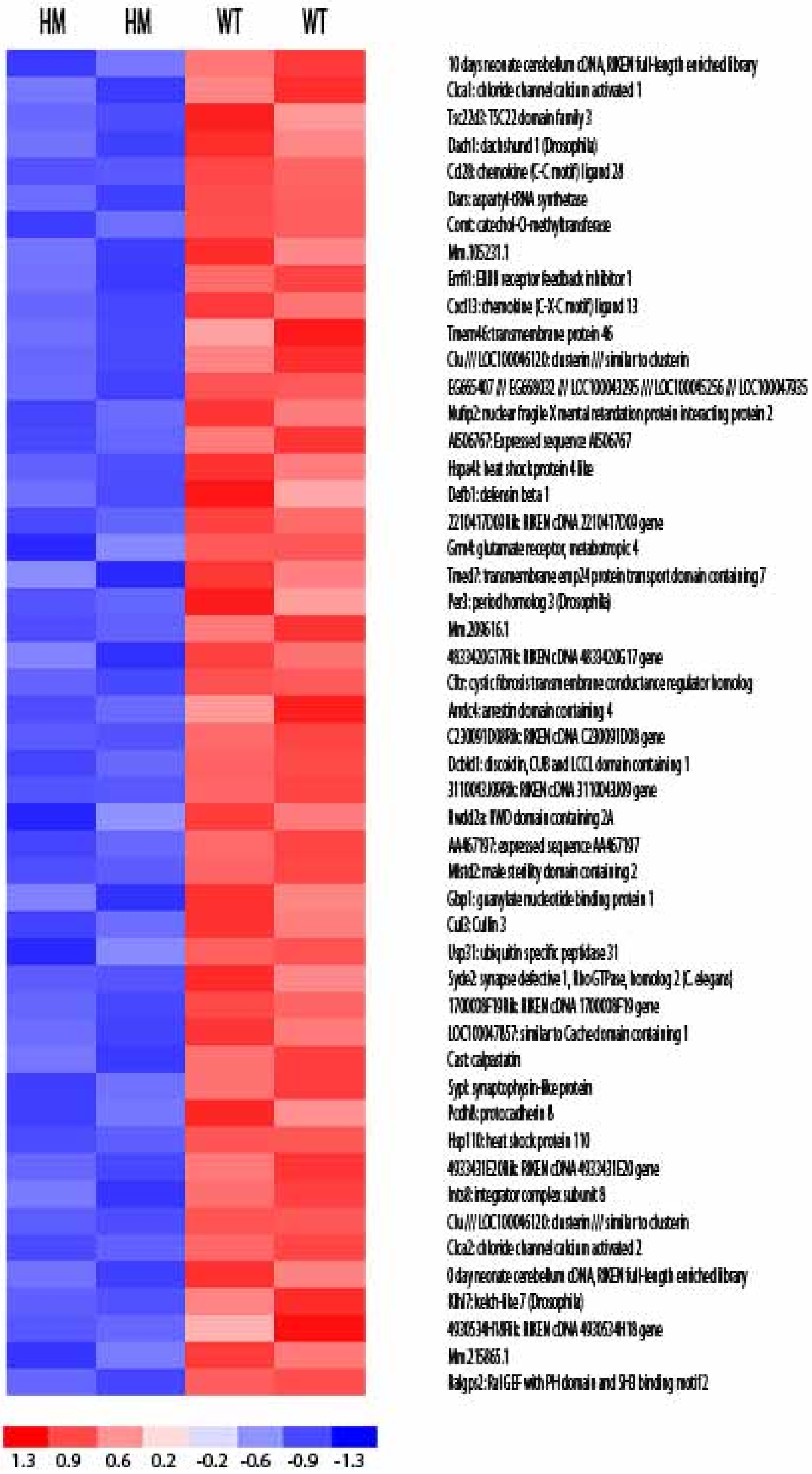
0.6
0.2
-0.2
-0.6
-0.9
-1.3

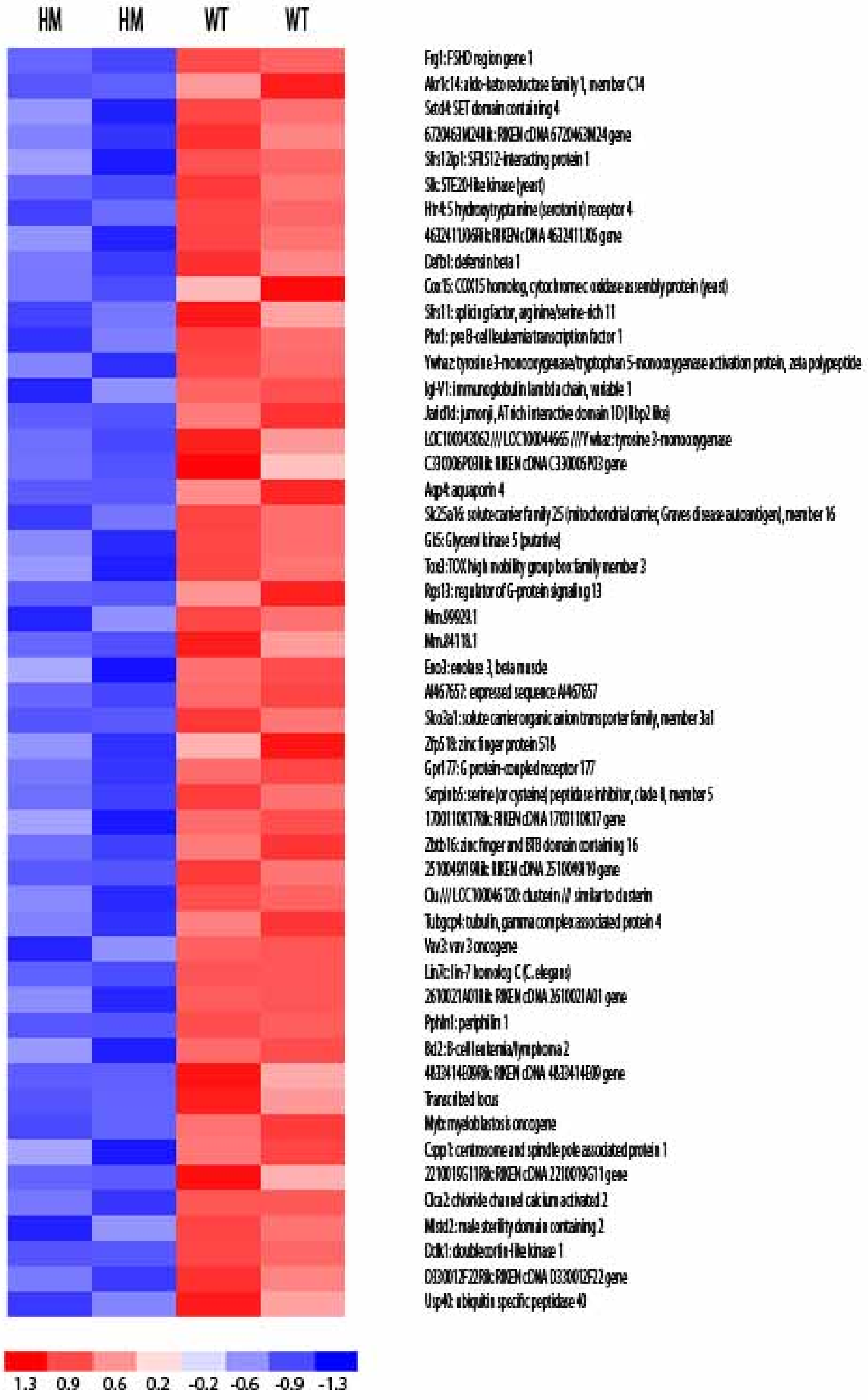

HM
HM
WT
WT
Syt1: synaptotagmin I
Osta: organic solute transporter alpha
Mm.173854.1
Col1a1: collagen, type I, alpha 1
4930539E08Rik: RIKEN cDNA 4930539E08 gene
Elovl6: ELOVL family member 6, elongation of long chain fatty acids (yeast)
Slpi: secretory leukocyte peptidase inhibitor
Indo: indoleamine-pyrrole 2,3 dioxygenase
Eln: elastin
Homer2: homer homolog 2 (Drosophila)
Centb1: centaurin, beta 1
Pygl: liver glycogen phosphorylase
Sdc4: syndecan 4
LOC100046081 /// Otub1: OTU domain, ubiquitin aldehyde binding 1 /// similar to OTU domain, ubiquitin aldehyde binding 1
Mm.132077.1
1700011H14Rik: RIKEN cDNA 1700011H14 gene
Col5a3: collagen, type V, alpha 3
Crnl5: camello-like 5
Ifit3: interferon-induced protein with tetratricopeptide repeats 3
Adamts2: a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 2
Slc5a9: solute carrier family 5 (sodium/glucose cotransporter), member 9
Tcea2: transcription elongation factor A (SII), 2
9430081I23Rik: RIKEN cDNA 9430081I23 gene
Lce1i: late cornified envelope 1I
Rab6b: RAB6B, member RAS oncogene family
Slc3a1: solute carrier family 3, member 1
Pcolce2: procollagen C-endopeptidase enhancer 2
Cxcl1: chemokine (C-X-C motif) ligand 1
Trim40: tripartite motif-containing 40
Stc2: stanniocalcin 2
Ttc3: tetratricopeptide repeat domain 3
1810030J14Rik /// LOC100044832: RIKEN cDNA 1810030J14 gene /// similar to RIKEN cDNA 1810030J14 gene
Apoa1: apolipoprotein A-I
Mxd1: MAX dimerization protein 1
Transcribed locus
Arid4a: AT rich interactive domain 4A (Rbp1 like)
2610019F03Rik: RIKEN cDNA 2610019F03 gene
Mogat2: monoacylglycerol O-acyltransferase 2
16 days neonate cerebellum cDNA, RIKEN full-length enriched library
Lbh /// LOC100048380: limb-bud and heart /// similar to limb-bud and heart
Aldh1l2: aldehyde dehydrogenase 1 family, member L2
Ace2: angiotensin I converting enzyme (peptidyl-dipeptidase A) 2
Zmym5: zinc finger, MYM-type 5
Ada: adenosine deaminase
Cyp3a13: cytochrome P450, family 3, subfamily a, polypeptide 13
2010305C02Rik: RIKEN cDNA 2010305C02 gene
Aplp1: amyloid beta (A4) precursor-like protein 1
Ube1l: ubiquitin-activating enzyme E1-like
Trim12: tripartite motif protein 12
Sh3bp4: SH3-domain binding protein 4
1.3
0.9
0.6
0.2
-0.2
-0.6
-0.9
-1.3

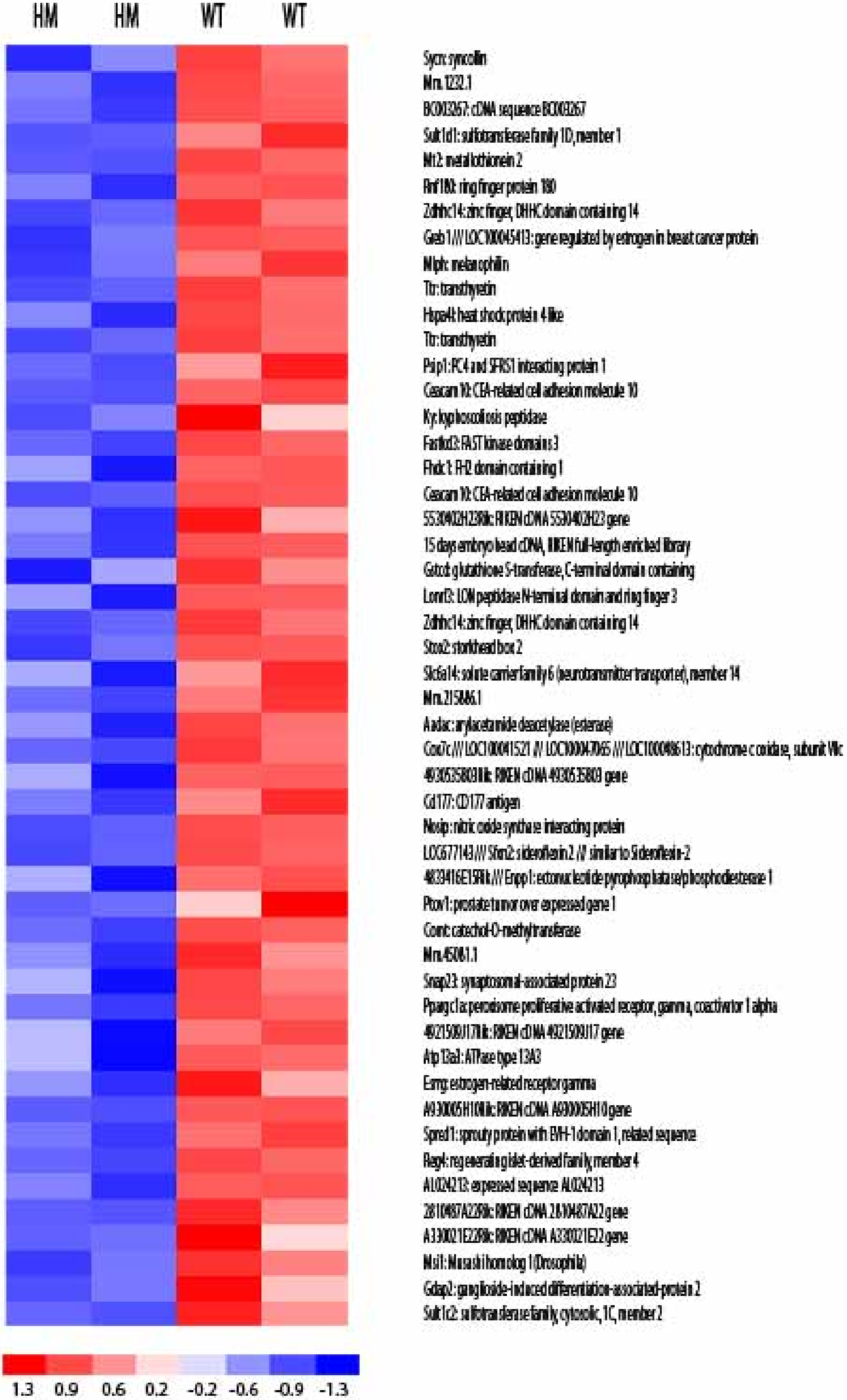

HM
HM
WT
WT
Klk1: kallikrein 1
Dpep1: dipeptidase 1 (renal)
Bcl2l15: Bcl2-like 15
Ghr: growth hormone receptor
Slc26a6: solute carrier family 26, member 6
Pex19: peroxisome biogenesis factor 19
Lgals1: lectin, galactose binding, soluble 1
Vip: vasoactive intestinal polypeptide
Hk3: hexokinase 3
Ftl1: ferritin light chain 1
Aldh1a7: aldehyde dehydrogenase family 1, subfamily A7
1810007E14Rik: RIKEN cDNA 1810007E14 gene
Gzma: granzyme A
Zeb2: zinc finger E-box binding homeobox 2
Ntrk2: neurotrophic tyrosine kinase, receptor, type 2
AA409316: expressed sequence AA409316
1810010M01Rik: RIKEN cDNA 1810010M01 gene
Mpp1: membrane protein, palmitoylated
Lgals1: lectin, galactose binding, soluble 1
Tmem120a: transmembrane protein 120A
Gabarap: gamma-aminobutyric acid receptor associated protein
Cml4: camello-like 4
Dmn: desmuslin
2310008M10Rik: RIKEN cDNA 2310008M10 gene
2610204M08Rik /// LOC100047142: RIKEN cDNA 2610204M08 gene /// similar to INF2
Mm.151642.1
Trim30: tripartite motif protein 30
Gsdmc1: gasdermin C1
Fbxw8: F-box and WD-40 domain protein 8
Mm.44320.1
Mm.121603.1
Adam1a /// LOC100047833: a disintegrin and metallopeptidase domain 1a /// similar to MK-5 type 2
Ifi27: interferon, alpha-inducible protein 27
Slc9a3r1: solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1
B2m: beta-2 microglobulin
Cgn: cingulin
Ttc22: tetratricopeptide repeat domain 22
AI956758: expressed sequence AI956758
Klk1: kallikrein 1
Dnajc2: DnaJ (Hsp40) homolog, subfamily C, member 2
Tmem66: transmembrane protein 66
2010003K15Rik: RIKEN cDNA 2010003K15 gene
3110021A11Rik: RIKEN cDNA 3110021A11 gene
Acox1: acyl-Coenzyme A oxidase 1, palmitoyl
Vrk3: vaccinia related kinase 3
Ccl5: chemokine (C-C motif) ligand 5
Srp14: signal recognition particle 14
Oas1a: 2'-5' oligoadenylate synthetase 1A
2310034G01Rik: RIKEN cDNA 2310034G01 gene
Ddah1: dimethylarginine dimethylaminohydrolase 1
1.3
0.9
0.6
0.2
-0.2
-0.6
-0.9
-1.3

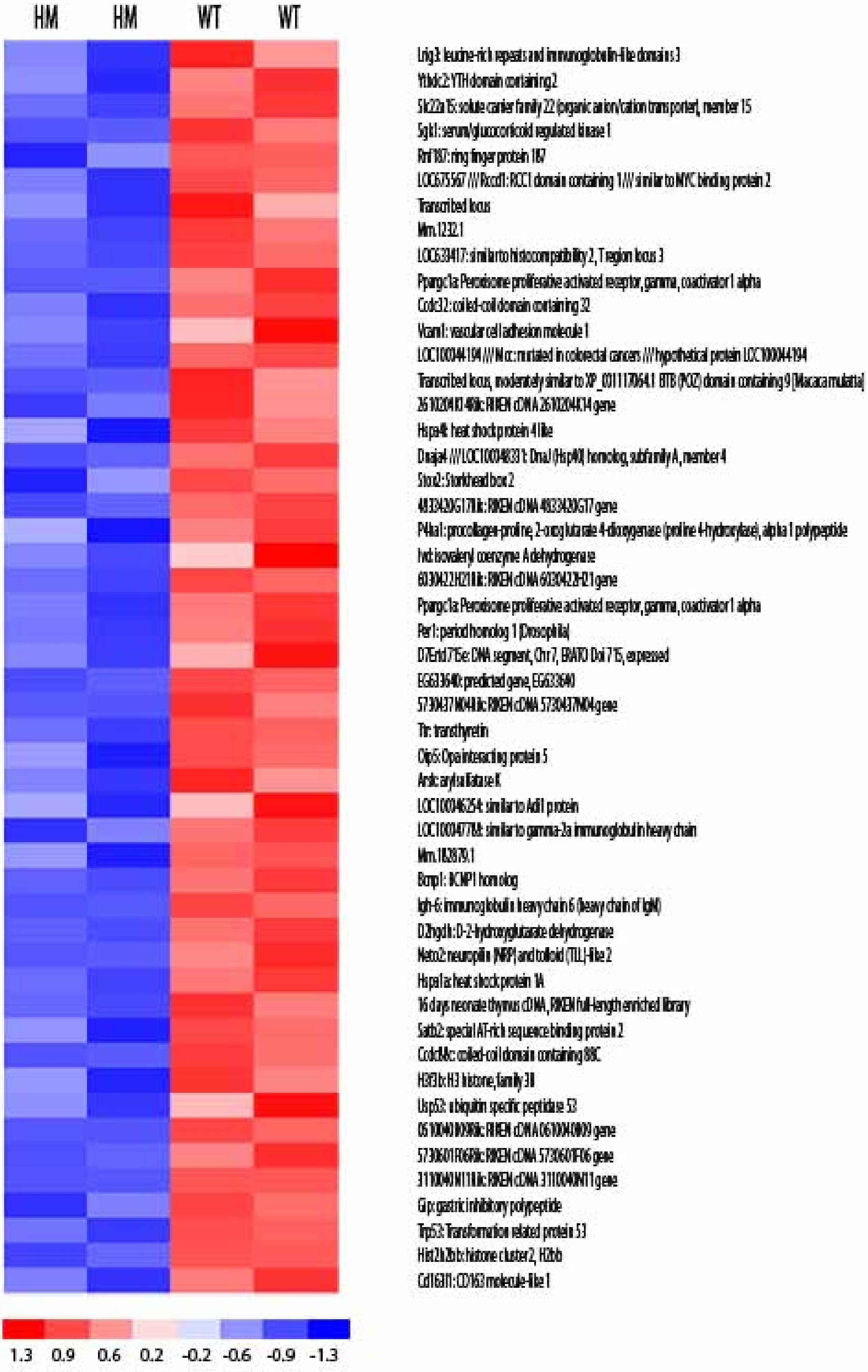

HM
HM
WT
WT
Nup62: nucleoporin 62
Prap1: proline-rich acidic protein 1
Dera: 2-deoxyribose-5-phosphate aldolase homolog (C. elegans)
Bckdhb /// LOC100048676: branched chain ketoacid dehydrogenase E1, beta polypeptide
Col3a1: collagen, type III, alpha 1
G0s2: G0/G1 switch gene 2
Ap1s3: adaptor-related protein complex AP-1, sigma 3
Fgf13: fibroblast growth factor 13
Ostb: organic solute transporter beta
Gbp2: guanylate nucleotide binding protein 2
Lpin1: lipin 1
Gbp2: guanylate nucleotide binding protein 2
C1qtnf2: C1q and tumor necrosis factor related protein 2
Apol7a: apolipoprotein L 7a
Bcl3: B-cell leukemia/lymphoma 3
2010106E10Rik: RIKEN cDNA 2010106E10 gene
Wdfy1: WD repeat and FYVE domain containing 1
Figf: C-fos induced growth factor
Ldhb: lactate dehydrogenase B
Clca6: chloride channel calcium activated 6
Transcribed locus
Rtp4: receptor transporter protein 4
Mgp: matrix Gla protein
Gtpbp2: GTP binding protein 2
Slc6a8: solute carrier family 6 (neurotransmitter transporter, creatine), member 8
Sprr2a: small proline-rich protein 2A
Cyp4f14: cytochrome P450, family 4, subfamily f, polypeptide 14
Rpgrip1: retinitis pigmentosa GTPase regulator interacting protein 1
Slc34a2: solute carrier family 34 (sodium phosphate), member 2
Fasn: fatty acid synthase
Trim34: tripartite motif protein 34
Pla2g12b: phospholipase A2, group XIIB
Phldb1: pleckstrin homology-like domain, family B, member 1
Figf: C-fos induced growth factor
Mttp: microsomal triglyceride transfer protein
Hsd3b3: hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 3
4833409A17Rik: RIKEN cDNA 4833409A17 gene
Krt4: keratin 4
LOC100047419 /// Maf: avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog /// similar to c-Maf long form
Clec7a: C-type lectin domain family 7, member a
Rabl5: RAB, member of RAS oncogene family-like 5
Ace2: angiotensin I converting enzyme (peptidyl-dipeptidase A) 2
Art3: ADP-ribosyltransferase 3
1500011B03Rik: RIKEN cDNA 1500011B03 gene
Gpd1: glycerol-3-phosphate dehydrogenase 1 (soluble)
Transcribed locus, weakly similar to XP_001175112.1 similar to pol protein, partial [Pan troglodytes]
S100a10: S100 calcium binding protein A10 (calpactin)
D12Ertd647e: DNA segment, Chr 12, ERATO Doi 647, expressed
Slc6a8: solute carrier family 6 (neurotransmitter transporter, creatine), member 8
Mep1b: meprin 1 beta
1.3
0.9
0.6
0.2
-0.2
-0.6
-0.9
-1.3

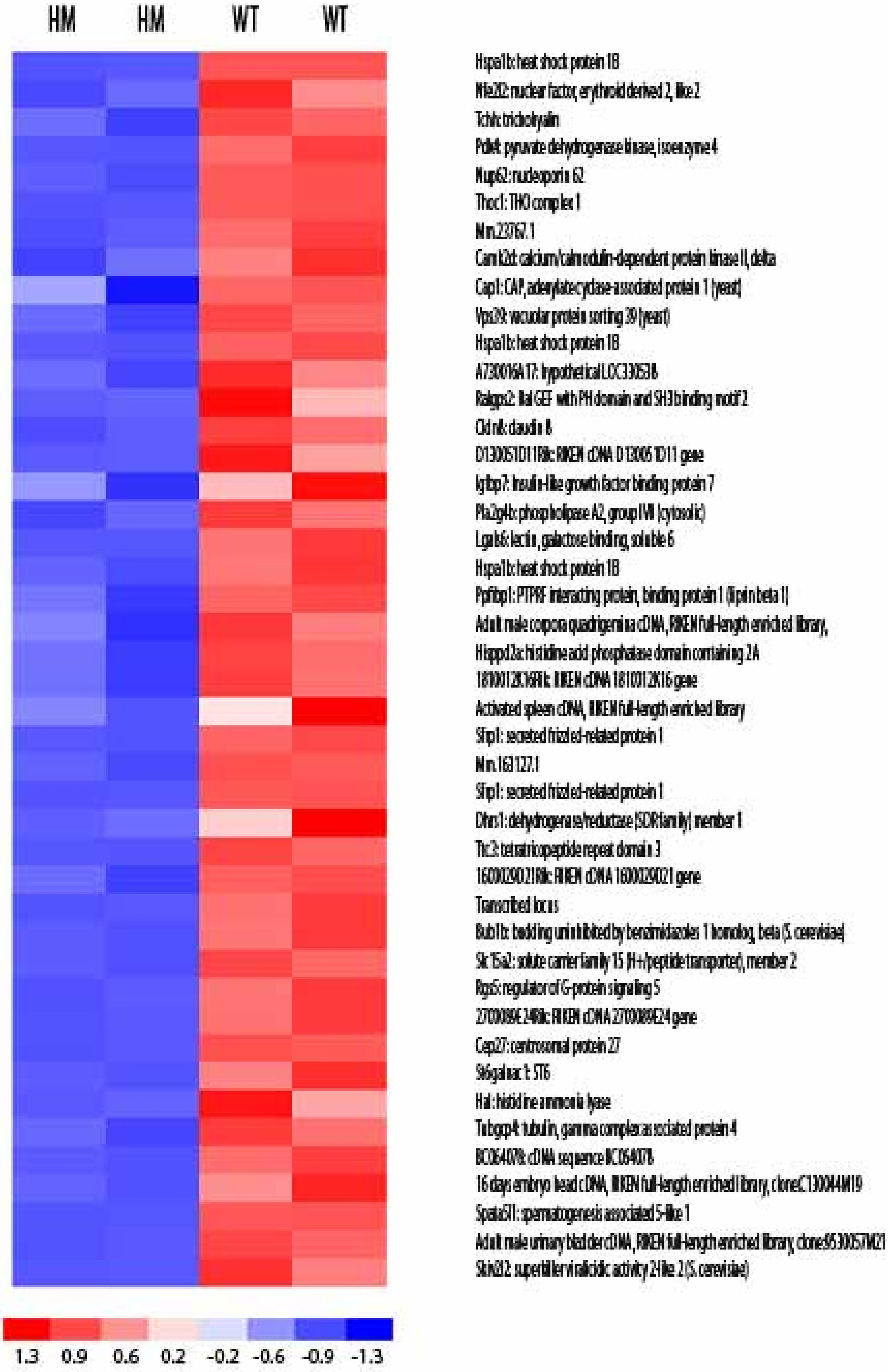

HM
HM
WT
WT
Slc27a4: solute carrier family 27 (fatty acid transporter), member 4
Clic5: chloride intracellular channel 5
Cdkn2b: cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)
Rad23a: RAD23a homolog (S. cerevisiae)
Arhgdig: Rho GDP dissociation inhibitor (GDI) gamma
Fbn1: fibrillin 1
Gmfg: glia maturation factor, gamma
Fbxl17: F-box and leucine-rich repeat protein 17
Alg8: asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glucosyltransferase)
Camk1d: calcium/calmodulin-dependent protein kinase ID
Sorbs1: Sorbin and SH3 domain containing 1
Nrp1: neuropilin 1
Trim31: tripartite motif-containing 31
Rabl4: RAB, member of RAS oncogene family-like 4
Tm4sf1: transmembrane 4 superfamily member 1
9130409J20Rik: RIKEN cDNA 9130409J20 gene
Cd59a: CD59a antigen
Fbxw17: F-box and WD-40 domain protein 17
Srbd1: S1 RNA binding domain 1
Visual cortex cDNA, RIKEN full-length enriched library
Itpka: inositol 1,4,5-trisphosphate 3-kinase A
Atp1a2: ATPase, Na+/K+ transporting, alpha 2 polypeptide
Slc44a4: solute carrier family 44, member 4
Chordc1: cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1
Tmed7: transmembrane emp24 protein transport domain containing 7
Nedd1: neural precursor cell expressed, developmentally down-regulated gene 1
Dock10: dedicator of cytokinesis 10
Zfp326: zinc finger protein 326
Galnact2: chondroitin sulfate GalNAcT-2
Bace2: beta-site APP-cleaving enzyme 2
Dmxl2: Dmx-like 2
Arl14: ADP-ribosylation factor-like 14
Hoxb3: homeo box B3
Fos: FBJ osteosarcoma oncogene
Zfp106: zinc finger protein 106
Aebp2: AE binding protein 2
Cd44: CD44 antigen
Gcg: glucagon
Tulp4: tubby like protein 4
Mtfr1: mitochondrial fission regulator 1
Bace2: beta-site APP-cleaving enzyme 2
Tubgcp5: tubulin, gamma complex associated protein 5
Ralgps2: Ral GEF with PH domain and SH3 binding motif 2
6430706D22Rik /// A730008H23Rik: RIKEN cDNA A730008H23 gene /// RIKEN cDNA 6430706D22 gene
Dnajb4: DnaJ (Hsp40) homolog, subfamily B, member 4
Zbtb41: zinc finger and BTB domain containing 41 homolog
Hiat1: hippocampus abundant gene transcript 1
Tcfcp2l1: transcription factor CP2-like 1
Kif11: kinesin family member 11
D630004K10Rik: RIKEN cDNA D630004K10 gene
1.3
0.9
0.6
0.2
-0.2
-0.6
-0.9
-1.3


HM
HM
WT
WT
10 days neonate cerebellum cDNA, RIKEN full-length enriched library
Clca1: chloride channel calcium activated 1
Tsc22d3: TSC22 domain family 3
Dach1: dachshund 1 (Drosophila)
Ccl28: chemokine (C-C motif) ligand 28
Dars: aspartyl-tRNA synthetase
Comt: catechol-O-methyltransferase
Mm.105231.1
Errfi1: ERBB receptor feedback inhibitor 1
Cxcl13: chemokine (C-X-C motif) ligand 13
Tmem46: transmembrane protein 46
Clu /// LOC100046120: clusterin /// similar to clusterin
EG665407 /// EG668032 /// LOC100043295 /// LOC100045256 /// LOC100047935
Nufip2: nuclear fragile X mental retardation protein interacting protein 2
AI506767: Expressed sequence AI506767
Hspa4l: heat shock protein 4 like
Defb1: defensin beta 1
2210417D09Rik: RIKEN cDNA 2210417D09 gene
Grm4: glutamate receptor, metabotropic 4
Tmed7: transmembrane emp24 protein transport domain containing 7
Per3: period homolog 3 (Drosophila)
Mm.200616.1
4833420G17Rik: RIKEN cDNA 4833420G17 gene
Cftr: cystic fibrosis transmembrane conductance regulator homolog
Arrdc4: arrestin domain containing 4
C230091D08Rik: RIKEN cDNA C230091D08 gene
Dcbld1: discoidin, CUB and LCCL domain containing 1
3110043J09Rik: RIKEN cDNA 3110043J09 gene
Iwd2a: IWD domain containing 2A
AA467197: expressed sequence AA467197
Mstd2: male sterility domain containing 2
Gbp1: guanylate nucleotide binding protein 1
Cul3: Cullin 3
Usp31: ubiquitin specific peptidase 31
Syde2: synapse defective 1, Rho GTPase, homolog 2 (C. elegans)
1700008F19Rik: RIKEN cDNA 1700008F19 gene
LOC100047857: similar to Cache domain containing 1
Cast: calpastatin
Sypl: synaptophysin-like protein
Pcdh8: protocadherin 8
Hsp110: heat shock protein 110
4933431E20Rik: RIKEN cDNA 4933431E20 gene
Ints8: integrator complex subunit 8
Clu /// LOC100046120: clusterin /// similar to clusterin
Clca2: chloride channel calcium activated 2
0 day neonate cerebellum cDNA, RIKEN full-length enriched library
Klhl7: kelch-like 7 (Drosophila)
4930534H18Rik: RIKEN cDNA 4930534H18 gene
Mm.215865.1
Ralgps2: Ral GEF with PH domain and SH3 binding motif 2
1.3
0.9
0.6
0.2
-0.2
-0.6
-0.9
-1.3


HM
HM
WT
WT
Frg1: FSHD region gene 1
Akr1c14: aldo-keto reductase family 1, member C14
Setd4: SET domain containing 4
6720463M24Rik: RIKEN cDNA 6720463M24 gene
Sfrs12ip1: SFRS12-interacting protein 1
Slk: STE20-like kinase (yeast)
Htr4: 5 hydroxytryptamine (serotonin) receptor 4
4632411J06Rik: RIKEN cDNA 4632411J06 gene
Defb1: defensin beta 1
Cox15: COX15 homolog, cytochrome c oxidase assembly protein (yeast)
Sfrs11: splicing factor, arginine/serine-rich 11
Pbx1: pre B-cell leukemia transcription factor 1
Ywhaz: tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
Igl-V1: immunoglobulin lambda chain, variable 1
Jarid1d: jumonji, AT rich interactive domain 1D (Rbp2 like)
LOC100043062 /// LOC100044665 /// Ywhaz: tyrosine 3-monooxygenase
C330006P03Rik: RIKEN cDNA C330006P03 gene
Aqp4: aquaporin 4
Slc25a16: solute carrier family 25 (mitochondrial carrier, Graves disease autoantigen), member 16
Gk5: Glycerol kinase 5 (putative)
Tox3: TOX high mobility group box family member 3
Rgs13: regulator of G-protein signaling 13
Mm.99029.1
Mm.84118.1
Eno3: enolase 3, beta muscle
AI467657: expressed sequence AI467657
Slco3a1: solute carrier organic anion transporter family, member 3a1
Zfp518: zinc finger protein 518
Gpr177: G protein-coupled receptor 177
Serpinb5: serine (or cysteine) peptidase inhibitor, clade B, member 5
1700110K17Rik: RIKEN cDNA 1700110K17 gene
Zbtb16: zinc finger and BTB domain containing 16
2510049I19Rik: RIKEN cDNA 2510049I19 gene
Clu /// LOC100046120: clusterin /// similar to clusterin
Tubgcp4: tubulin, gamma complex associated protein 4
Vav3: vav 3 oncogene
Lin7c: lin-7 homolog C (C. elegans)
2610021A01Rik: RIKEN cDNA 2610021A01 gene
Pphln1: periphilin 1
Bcl2: B-cell leukemia/lymphoma 2
4833414E09Rik: RIKEN cDNA 4833414E09 gene
Transcribed locus
Myb: myeloblastosis oncogene
Cspp1: centrosome and spindle pole associated protein 1
2210019G11Rik: RIKEN cDNA 2210019G11 gene
Clca2: chloride channel calcium activated 2
Mstd2: male sterility domain containing 2
Dclk1: doublecortin-like kinase 1
D330012F22Rik: RIKEN cDNA D330012F22 gene
Usp40: ubiquitin specific peptidase 40
1.3
0.9
0.6
0.2
-0.2
-0.6
-0.9
-1.3


HM
HM
WT
WT
Sycn: syncollin
Mm.1232.1
BC003267: cDNA sequence BC003267
Sult1d1: sulfotransferase family 1D, member 1
Mt2: metallothionein 2
Rnf180: ring finger protein 180
Zdhhc14: zinc finger, DHHC domain containing 14
Greb1 /// LOC100045413: gene regulated by estrogen in breast cancer protein
Mlph: melanophilin
Ttr: transthyretin
Hspa4l: heat shock protein 4 like
Ttr: transthyretin
Psip1: PC4 and SFRS1 interacting protein 1
Ceacam10: CEA-related cell adhesion molecule 10
Ky: kyphoscoliosis peptidase
Fastkd3: FAST kinase domains 3
Fhdc1: FH2 domain containing 1
Ceacam10: CEA-related cell adhesion molecule 10
5530402H23Rik: RIKEN cDNA 5530402H23 gene
15 days embryo head cDNA, RIKEN full-length enriched library
Gstcd: glutathione S-transferase, C-terminal domain containing
Lonrf3: LON peptidase N-terminal domain and ring finger 3
Zdhhc14: zinc finger, DHHC domain containing 14
Stox2: storkhead box 2
Slc6a14: solute carrier family 6 (neurotransmitter transporter), member 14
Mm.215846.1
Aadac: arylacetamide deacetylase (esterase)
Cox7c /// LOC100041521 /// LOC100047065 /// LOC100048613: cytochrome c oxidase, subunit VIIc
4930535B03Rik: RIKEN cDNA 4930535B03 gene
Cd177: CD177 antigen
Nosip: nitric oxide synthase interacting protein
LOC677143 /// Sfxn2: sideroflexin 2 /// similar to Sideroflexin-2
4833416E15Rik /// Enpp1: ectonucleotide pyrophosphatase/phosphodiesterase 1
Ptov1: prostate tumor over expressed gene 1
Comt: catechol-O-methyltransferase
Mm.45081.1
Snap23: synaptosomal-associated protein 23
Ppargc1a: peroxisome proliferative activated receptor, gamma, coactivator 1 alpha
4921508J17Rik: RIKEN cDNA 4921508J17 gene
Atp13a3: ATPase type 13A3
Esrrg: estrogen-related receptor gamma
A930005H10Rik: RIKEN cDNA A930005H10 gene
Spred1: sprouty protein with EVH-1 domain 1, related sequence
Reg4: regenerating islet-derived family, member 4
AI024213: expressed sequence AI024213
2810487A22Rik: RIKEN cDNA 2810487A22 gene
A330021E22Rik: RIKEN cDNA A330021E22 gene
Msi1: Musashi homolog 1 (Drosophila)
Gdap2: ganglioside-induced differentiation-associated-protein 2
Sult1c2: sulfotransferase family, cytosolic, 1C, member 2
1.3
0.9
0.6
0.2
-0.2
-0.6
-0.9
-1.3


HM
HM
WT
WT
Lrig3: leucine-rich repeats and immunoglobulin-like domains 3
Ythdc2: YTH domain containing 2
Slc22a15: solute carrier family 22 (organic anion/cation transporter), member 15
Sgk1: serum/glucocorticoid regulated kinase 1
Rnf187: ring finger protein 187
LOC675567 /// Rccd1: RCC1 domain containing 1 /// similar to MYC binding protein 2
Transcribed locus
Mm.1232.1
LOC639417: similar to histocompatibility 2, T region locus 3
Ppargc1a: Peroxisome proliferative activated receptor, gamma, coactivator 1 alpha
Ccdc32: coiled-coil domain containing 32
Vcam1: vascular cell adhesion molecule 1
LOC100044194 /// Mcc: mutated in colorectal cancers /// hypothetical protein LOC100044194
Transcribed locus, moderately similar to XP_001117064.1 BTB (POZ) domain containing 9 [Macaca mulatta]
2610204K14Rik: RIKEN cDNA 2610204K14 gene
Hspa4l: heat shock protein 4 like
Dnaja4 /// LOC100048331: DnaJ (Hsp40) homolog, subfamily A, member 4
Stox2: Storkhead box 2
4833420G17Rik: RIKEN cDNA 4833420G17 gene
P4ha1: procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide
Ivd: isovaleryl coenzyme A dehydrogenase
6030422H21Rik: RIKEN cDNA 6030422H21 gene
Ppargc1a: Peroxisome proliferative activated receptor, gamma, coactivator 1 alpha
Per1: period homolog 1 (Drosophila)
D7Ertd715e: DNA segment, Chr 7, ERATO Doi 715, expressed
EG633640: predicted gene, EG633640
5730437N04Rik: RIKEN cDNA 5730437N04 gene
Ttr: transthyretin
Oip5: Opa interacting protein 5
Arsk: arylsulfatase K
LOC100046254: similar to Adi1 protein
LOC100047788: similar to gamma-2a immunoglobulin heavy chain
Mm.182879.1
Bcmp1: BCMP1 homolog
Igh-6: immunoglobulin heavy chain 6 (heavy chain of IgM)
D2hgdh: D-2-hydroxyglutarate dehydrogenase
Neto2: neuropilin (NRP) and tolloid (TLL)-like 2
Hspa1a: heat shock protein 1A
16 days neonate thymus cDNA, RIKEN full-length enriched library
Satb2: special AT-rich sequence binding protein 2
Ccdc88c: coiled-coil domain containing 88C
H3f3b: H3 histone, family 3B
Usp53: ubiquitin specific peptidase 53
0610040B09Rik: RIKEN cDNA 0610040B09 gene
5730601F06Rik: RIKEN cDNA 5730601F06 gene
3110040N11Rik: RIKEN cDNA 3110040N11 gene
Gip: gastric inhibitory polypeptide
Trp53: Transformation related protein 53
Hist2h2bb: histone cluster 2, H2bb
Cd163l1: CD163 molecule-like 1
1.3
0.9
0.6
0.2
-0.2
-0.6
-0.9
-1.3

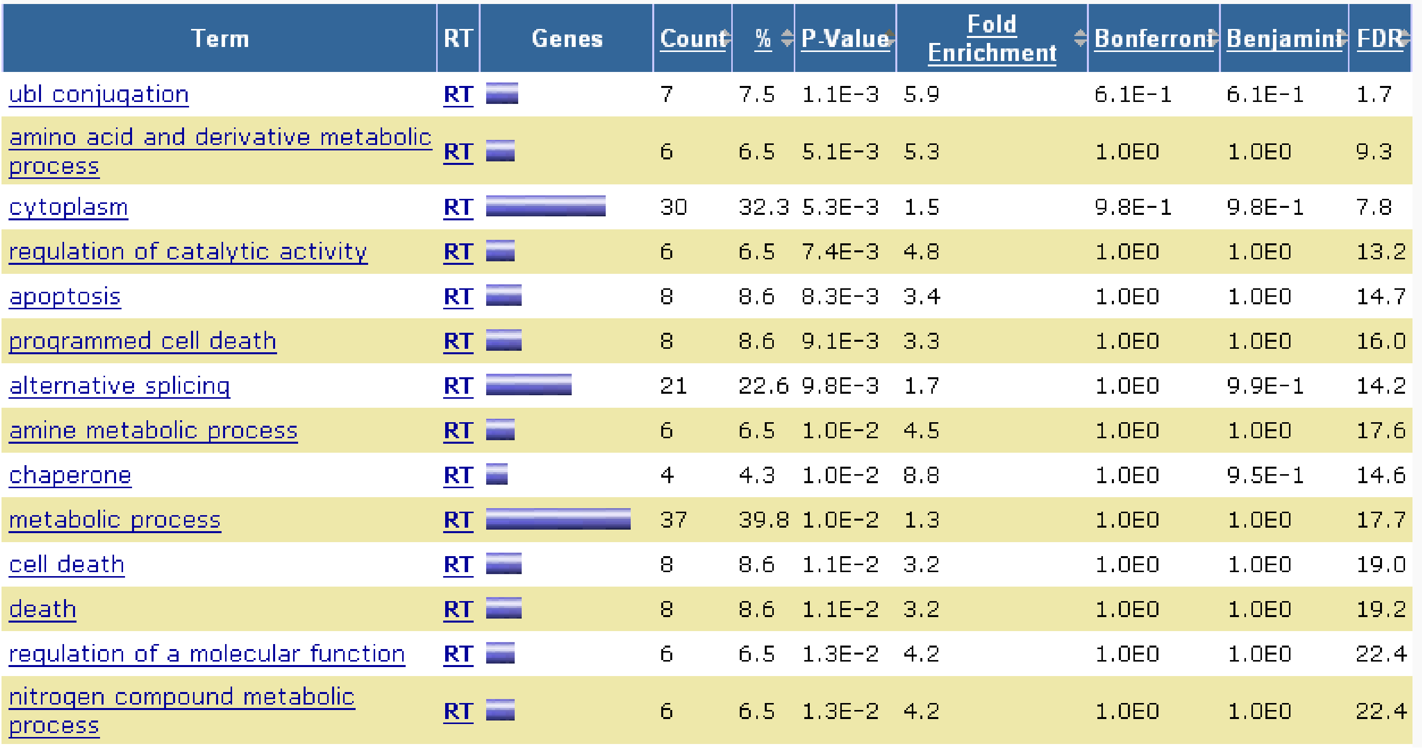

HM
HM
WT
WT
Hspa1b: heat shock protein 1B
Nfe2l2: nuclear factor, erythroid derived 2, like 2
Tchh: trichohyalin
Pdk4: pyruvate dehydrogenase kinase, isoenzyme 4
Nup62: nucleoporin 62
Thoc1: THO complex 1
Mm.23767.1
Camk2d: calcium/calmodulin-dependent protein kinase II, delta
Cap1: CAP, adenylate cyclase-associated protein 1 (yeast)
Vps39: vacuolar protein sorting 39 (yeast)
Hspa1b: heat shock protein 1B
A730016A17: hypothetical LOC330538
Ralgps2: Ral GEF with PH domain and SH3 binding motif 2
Cldn8: claudin 8
D130051D11Rik: RIKEN cDNA D130051D11 gene
Igfbp7: insulin-like growth factor binding protein 7
Pla2g4b: phospholipase A2, group IVB (cytosolic)
Lgals6: lectin, galactose binding, soluble 6
Hspa1b: heat shock protein 1B
Ppfibp1: PTPRF interacting protein, binding protein 1 (liprin beta 1)
Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library,
Hisppd2a: histidine acid phosphatase domain containing 2A
1810012K16Rik: RIKEN cDNA 1810012K16 gene
Activated spleen cDNA, RIKEN full-length enriched library
Sfrp1: secreted frizzled-related protein 1
Mm.163127.1
Sfrp1: secreted frizzled-related protein 1
Dhrs1: dehydrogenase/reductase (SDR family) member 1
Ttc3: tetratricopeptide repeat domain 3
1600029021Rik: RIKEN cDNA 1600029021 gene
Transcribed locus
Bub1b: budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae)
Slc15a2: solute carrier family 15 (H+/peptide transporter), member 2
Rgs5: regulator of G-protein signaling 5
2700089E24Rik: RIKEN cDNA 2700089E24 gene
Cep27: centrosomal protein 27
St6galnac1: ST6
Hal: histidine ammonia lyase
Tubgcp4: tubulin, gamma complex associated protein 4
BC064078: cDNA sequence BC064078
16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130044M19
Spata5l1: spermatogenesis associated 5-like 1
Adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530057M21
Skiv2l2: superkiller viralicidic activity 2-like 2 (S. cerevisiae)
1.3
0.9
0.6
0.2
-0.2
-0.6
-0.9
-1.3

Supplement Figure 11. Heat map for mRNAs that are significantly enriched or diminished in Atg16L1^{HM} thymocytes relative to control. A 1.3-fold difference and a 90% lower bound cut-off were used.

a

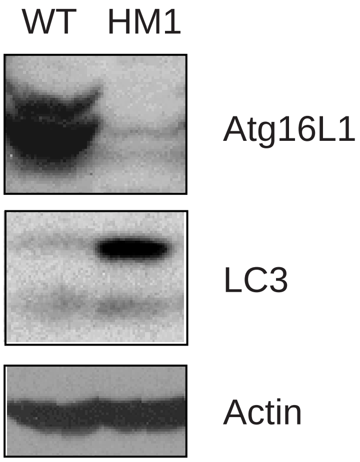
Term	RT	Genes	Count	%	P-Value	Fold Enrichment	Bonferroni	Benjamini	FDR
PPAR signaling pathway	RT	▬	8	6.0	2.0E-6	12.4	3.9E-4	3.9E-4	0.0
lipid metabolic process	RT	▬	16	12.0	6.7E-6	4.1	3.4E-2	3.4E-2	0.0
lipid transporter activity	RT	▬	6	4.5	1.4E-5	19.1	3.8E-2	3.8E-2	0.0
extracellular space	RT	▬	29	21.8	1.9E-5	2.3	1.5E-2	1.5E-2	0.0
cellular lipid metabolic process	RT	▬	14	10.5	3.0E-5	4.1	1.4E-1	7.4E-2	0.1
extracellular region part	RT	▬	29	21.8	5.8E-5	2.2	4.4E-2	2.2E-2	0.1
inflammatory response	RT	▬	9	6.8	6.1E-5	6.6	2.7E-1	9.9E-2	0.1
signal	RT	▬	32	24.1	9.4E-5	2.0	7.8E-2	7.8E-2	0.1
response to wounding	RT	▬	10	7.5	1.1E-4	5.2	4.4E-1	1.4E-1	0.2
acute inflammatory response	RT	▬	6	4.5	1.3E-4	12.2	4.8E-1	1.2E-1	0.2
lipid binding	RT	▬	11	8.3	1.5E-4	4.5	3.3E-1	1.8E-1	0.3
carboxylic acid metabolic process	RT	▬	12	9.0	2.0E-4	3.9	6.4E-1	1.6E-1	0.4
organic acid metabolic process	RT	▬	12	9.0	2.0E-4	3.9	6.5E-1	1.4E-1	0.4
regulation of cholesterol absorption	RT	▬	3	2.3	2.1E-4	124.8	6.6E-1	1.3E-1	0.4
lipid transport	RT	▬	6	4.5	2.2E-4	10.9	6.8E-1	1.2E-1	0.4
extracellular region	RT	▬	29	21.8	2.3E-4	2.0	1.7E-1	5.9E-2	0.4
alcohol metabolic process	RT	▬	9	6.8	2.7E-4	5.3	7.5E-1	1.3E-1	0.5
cholesterol absorption	RT	▬	3	2.3	3.5E-4	99.8	8.3E-1	1.5E-1	0.7
Secreted	RT	▬	19	14.3	3.5E-4	2.5	2.6E-1	1.4E-1	0.5
monocarboxylic acid metabolic process	RT	▬	8	6.0	4.1E-4	5.8	8.8E-1	1.6E-1	0.8
signal peptide	RT	▬	29	21.8	4.3E-4	1.9	1.0E0	1.0E0	0.9
lipid digestion	RT	▬	3	2.3	5.2E-4	83.2	9.3E-1	1.9E-1	1.0
acute-phase response	RT	▬	4	3.0	5.4E-4	24.7	9.4E-1	1.8E-1	1.0
lipoprotein	RT	▬	12	9.0	6.1E-4	3.5	4.1E-1	1.6E-1	0.9
response to external stimulus	RT	▬	11	8.3	7.1E-4	3.7	9.7E-1	2.2E-1	1.3

b

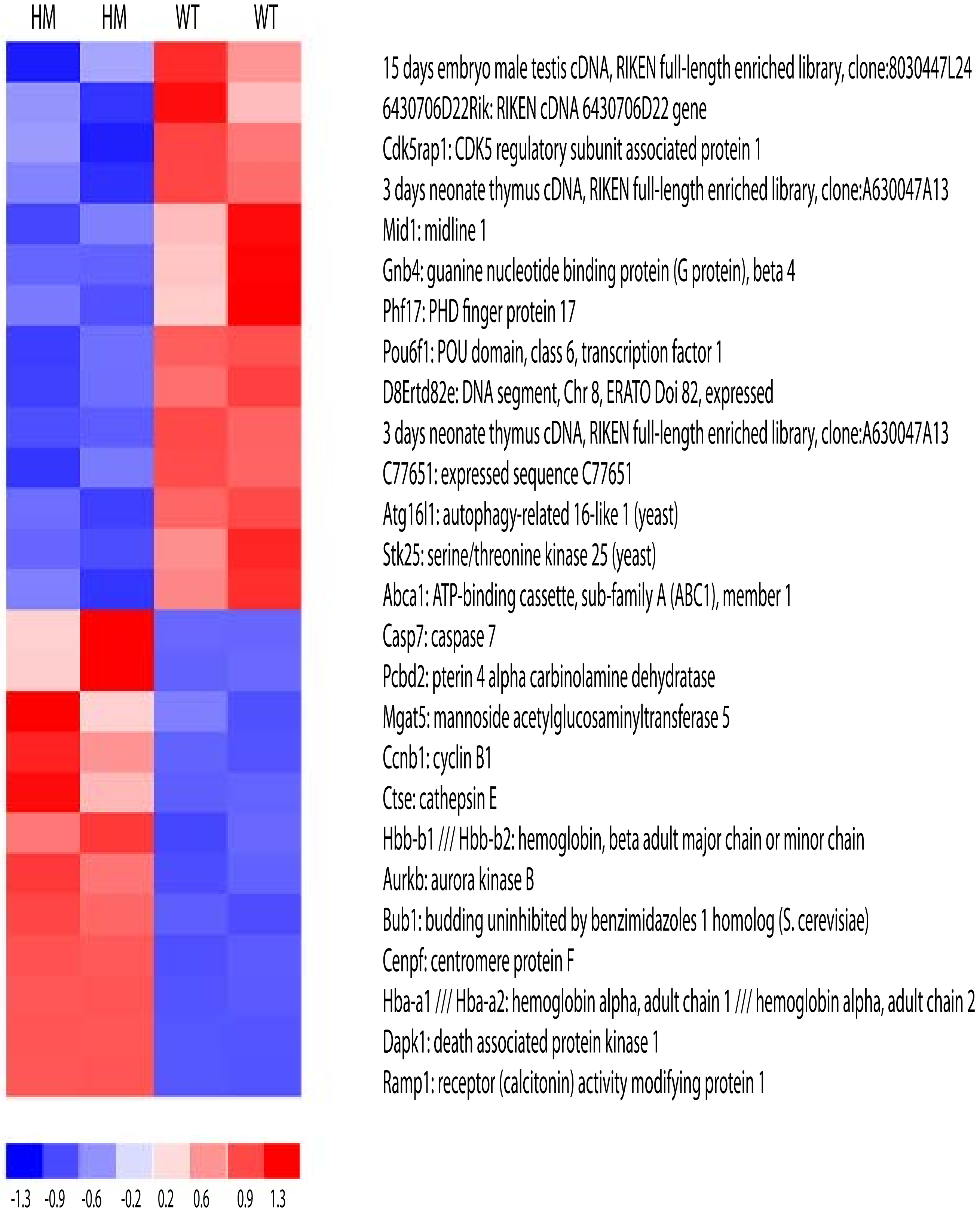


Term	RT	Genes	Count	%	P-Value	Fold Enrichment	Bonferroni	Benjamini	FDR
ubl conjugation	RT	▬	7	7.5	1.1E-3	5.9	6.1E-1	6.1E-1	1.7
amino acid and derivative metabolic process	RT	▬	6	6.5	5.1E-3	5.3	1.0E0	1.0E0	9.3
cytoplasm	RT	▬	30	32.3	5.3E-3	1.5	9.8E-1	9.8E-1	7.8
regulation of catalytic activity	RT	▬	6	6.5	7.4E-3	4.8	1.0E0	1.0E0	13.2
apoptosis	RT	▬	8	8.6	8.3E-3	3.4	1.0E0	1.0E0	14.7
programmed cell death	RT	▬	8	8.6	9.1E-3	3.3	1.0E0	1.0E0	16.0
alternative splicing	RT	▬	21	22.6	9.8E-3	1.7	1.0E0	9.9E-1	14.2
amine metabolic process	RT	▬	6	6.5	1.0E-2	4.5	1.0E0	1.0E0	17.6
chaperone	RT	▬	4	4.3	1.0E-2	8.8	1.0E0	9.5E-1	14.6
metabolic process	RT	▬	37	39.8	1.0E-2	1.3	1.0E0	1.0E0	17.7
cell death	RT	▬	8	8.6	1.1E-2	3.2	1.0E0	1.0E0	19.0
death	RT	▬	8	8.6	1.1E-2	3.2	1.0E0	1.0E0	19.2
regulation of a molecular function	RT	▬	6	6.5	1.3E-2	4.2	1.0E0	1.0E0	22.4
nitrogen compound metabolic process	RT	▬	6	6.5	1.3E-2	4.2	1.0E0	1.0E0	22.4

Supplementary Figure 12. Functional analysis of enriched and diminished transcripts of Atg16L1-deficient Paneth cells. a-b, The Functional Classification Tool from the DAVID Bioinformatics Resource[2] (NIAID, NIH) was used to determine the enriched functional categories of the two gene lists in Supplementary Table 1 comparing the transcriptome of Atg16L1^{HM} versus WT Paneth cells (enriched (**a**) or diminished (**b**) in Atg16L1^{HM} mice). In both cases, the highest statistically significant gene ontology (GO) terms that were represented within the gene list are indicated. We used medium stringency to cluster the genes. Count = number of genes in the list with a given GO term; % = fractional representation of a GO term within the list. Various statistical methods are available to determine significance (p-value, fold-enrichment, Bonferoni, Benjamini, and false-discovery rate, FDR). Functional groups were sorted by p-value in these tables. The statistical significance of the clustering for the top rated GO terms is much higher in the gene list for the enriched transcripts.



Supplementary Figure 13. Thymocytes from Atg16L1^{HM} mice have reduced Atg16L1 expression and conversion of LC3-I to LC3-II. Western blot analysis of whole cell thymocyte lysates from Atg16L1^{HM} mice reveal decreased Atg16L1 expression and an increase in LC3-I to LC3-II ratio compared to WT control.


HM
HM
WT
WT
15 days embryo male testis cDNA, RIKEN full-length enriched library, clone:8030447L24
6430706D22Rik: RIKEN cDNA 6430706D22 gene
Cdk5rap1: CDK5 regulatory subunit associated protein 1
3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630047A13
Mid1: midline 1
Gnb4: guanine nucleotide binding protein (G protein), beta 4
Phf17: PHD finger protein 17
Pou6f1: POU domain, class 6, transcription factor 1
D8Ertd82e: DNA segment, Chr 8, ERATO Doi 82, expressed
3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630047A13
C77651: expressed sequence C77651
Atg16l1: autophagy-related 16-like 1 (yeast)
Stk25: serine/threonine kinase 25 (yeast)
Abca1: ATP-binding cassette, sub-family A (ABC1), member 1
Casp7: caspase 7
Pcbd2: pterin 4 alpha carbinolamine dehydratase
Mgat5: mannoside acetylglucosaminyltransferase 5
Ccnb1: cyclin B1
Ctse: cathepsin E
Hbb-b1 /// Hbb-b2: hemoglobin, beta adult major chain or minor chain
Aurkb: aurora kinase B
Bub1: budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)
Cenpf: centromere protein F
Hba-a1 /// Hba-a2: hemoglobin alpha, adult chain 1 /// hemoglobin alpha, adult chain 2
Dapk1: death associated protein kinase 1
Ramp1: receptor (calcitonin) activity modifying protein 1
-1.3
-0.9
-0.6
-0.2
0.2
0.6
0.9
1.3

Supplement Figure 14. Heat map for mRNAs that are significantly enriched or diminished in Atg16L1^{HM} Paneth cells relative to control. A 1.3-fold difference and a 90% lower bound cut-off were used.