

The interplay between retinal pathways of cholesterol output and its effects on mouse retina

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Supporting Text T1. Gene abbreviations, protein abbreviations, and functions of proteins indicated in the present work. Gene symbols are italicized and begin with an uppercase letter; protein symbols have all letters in uppercase.

Gene abbreviations

Abca1 (ATP binding cassette subfamily A member 1); *Apoa1*, *Apoa2*, *Apoa4*, *Apob*, *Apoc3*, *Apod*, *ApoE*, *ApoJ* (apolipoproteins A1, A2, A4, B, C3, D, E and J, respectively); *Ccl2* (C-C motif chemokine 2); *Cox-2* (prostaglandin G/H synthase 2); *Hmgcr* (3-hydroxy-3-methylglutaryl-CoA reductase); *Il-6* (interleukin-6); *Srebp2* (sterol regulatory element-binding protein 2); *Tnf α* (tumor necrosis factor α).

Protein abbreviations

ACAA2 (3-ketoacyl-CoA thiolase); ANK2 (ankyrin B); ANP32B (acidic leucine-rich nuclear phosphoprotein 32 family member B); APOA1, APOA2, APOA4, APOE (apolipoproteins A1, A2, A4 and E, respectively); ASAH1 (acid ceramidase); ASAP1 (arf-GAP with SH3 domain ANK repeat and PH domain-containing protein 1); ATP1A2 (sodium/potassium-transporting ATPase subunit alpha-2); BPHL (valacyclovir hydrolase); C1ORF123 (UPF0587 protein chromosome 1 open reading frame 23); CD59A (CD59A glycoprotein); CHGA (chromogranin-A), CUL1 (cullin-1); CYP27A1 (cytochrome P450 family 27 subfamily A member 1); CYP46A1 (cytochrome P450 family 46 subfamily A member 1); E2A (transcription factor 3); EEF1D (elongation factor 1-delta); EF-1 α (elongation factor 1-alpha); EGFR (epidermal growth factor receptor); EZR (ezrin); GAA (lysosomal alpha-glucosidase); GALE (UDP-galactose 4-epimerase); GAP43 (growth associated protein 43 or neuromodulin); GPM6A (neuronal membrane glycoprotein M6-a); GTF2E1 (general transcription factor IIE subunit 1); HDAC6 (histone deacetylase 6); KCTD8 (BTB/POZ domain-containing protein KCTD8); LAMTOR3 (regulator complex protein LAMTOR3); LXR (liver X receptor); mTORC1 (mammalian target of rapamycin complex 1); NF- κ B (Nuclear Factor Kappa B Subunit 1); NIPBL (nipped-B-like protein; cohesin loading factor); NR2E3 (photoreceptor-specific nuclear receptor); NRL (neural retina leucine zipper); NXF1 (nuclear RNA export factor 1); OGF (opioid growth factor); OGFR (opioid growth factor receptor); PAFAH1B2 (platelet-activating factor acetylhydrolase IB subunit beta); PDHX (pyruvate dehydrogenase protein X component); PDS5A (sister chromatid cohesion protein PDS5 homolog A); PI4KA (phosphatidylinositol 4-kinase alpha); PKR (protein kinase R); PLC (phospholipase C); PRKRA (interferon-inducible double-stranded RNA-dependent protein kinase activator A); PSAT1 (phosphoserine aminotransferase); RAB4B (ras-related protein Rab-4B2); RHOA (ras homolog gene family; member A); ROR β (nuclear receptor ROR β); RPA3 (replication protein A 14 kDa subunit); SEPT6 (septin-6); SERPINA1E (α -1-antitrypsin 1-5); SKP1 (S-phase kinase-associated protein 1); SLC14A1 (urea transporter 1); SOAT1 (sterol-O-acyltransferase or acyl-coenzyme A: cholesterol acyltransferase); SRP19 (signal recognition particle 19 kDa); STUB1 (STIP1 homology and U box-containing protein 1 or CHIP); TAGLN2 (transgelin-2); TAGLN3 (transgelin-3); TINAGL1 (tubulointerstitial nephritis antigen-like); TLR (toll-like receptor); TRAFD1 (tRAF-type zinc finger domain-containing protein 1); U2AF2 (splicing factor U2AF 65 kDa subunit); UCHL5 (ubiquitin carboxyl-terminal hydrolase isozyme L5); WDFY1 (WD repeat and FYVE domain-containing protein 1).

Protein functions

Cytoskeletal organization, vesicular, and secretory pathway

ASAP1, a phosphatidylinositol 4,5-bisphosphate-dependent Arf GTPase-activating protein involved in vesicular transport of rhodopsin from the Golgi complex to cilia in photoreceptor cells [1,2].

ATP1A2, the catalytic α 2 subunit of the Na⁺/K⁺ pump responsible for establishing and maintaining the electrochemical gradients of Na⁺ and K⁺ ions across the plasma membrane. In the photoreceptors, Na⁺/K⁺ pump interacts with membrane cytoskeleton via ankyrin that tethers the pump to spectrin and actin cytoskeleton [3].

HDAC6, a tubulin-specific deacetylase, which is a critical component for the cilia disassembly *via* tubulin deacetylation. HDAC6 also deacetylates actin-regulatory protein cortactin, thereby stimulating actin polymerization. The latter contributes to cilia disassembly and membrane ruffle (protrusion) formation [4-6]. HDAC6 was found in extracellular vesicles derived from oxidatively stressed RPE [7]. HDAC6 inhibition can protect retinal cells from oxidative stress as well as from ischemia and reperfusion injury [8,9].

CHGA, a neuroendocrine secretory protein, which is required for secretory granule formation and positively controls a number of formed granules [10].

PAFAH1B2, a catalytic subunit 2 of Platelet Activating Factor Acetylhydrolase (PAFAH) Ib having the phospholipase A2 activity. Activity of this complex is required for endosome membrane tube formation and integrity of Golgi complex, thereby contributing to cargo recycling *via* endosomal route and maintaining secretion, respectively [11-13].

PI4KA, a phosphatidylinositol (PI) 4-kinase, which catalyzes the first step in the biosynthesis of phosphatidylinositol 4,5-bisphosphate. It is mostly membrane-bound and located at the endoplasmic reticulum. PI4KA is involved in membrane traffic and phototransduction [14-17].

SEPT6, a member of the filament-forming GTP-binding proteins implicated in cytoskeleton and membrane organization; SEPT6 binds to F-actin and is required for multivesicular body maturation from early endosomes. SEPT6 also triggers filopodia formation by increasing the recruitment of cortactin, a regulator of actin polymerization [18,19].

SRP19, an essential protein for the assembly of the signal recognition particle, a conserved ribonucleoprotein complex that mediates the translation and targeting of secretory and membrane proteins to endoplasmic reticulum for the further incorporation into the secretory pathway [20,21].

TAGLN2 and TAGLN3, members of the actin-binding protein family. TAGLN2 and TAGLN3 stimulate G-actin polymerization that can enhance formation of the filopodia-like membrane protrusion and processes [22-25].

TINAGL1, a secreted extracellular protein and a ligand for integrins; regulates cell adhesion [26,27].

Energy homeostasis

ACAA2, a mitochondrial enzyme, which catalyzes the last step of the mitochondrial fatty acid β -oxidation. The oxidation of fatty acids in the brain is limited by the activity of the ACAA2 [28].

ASAH1, a lysosomal ceramidase that hydrolyzes ceramides into sphingosine and free fatty acids [29]. Deficiency in ASAH1 leads to retinal inflammation and severe visual impairment [30]. Induction of ASAH1 could rescue retinal pigment epithelium from oxidative stress by hydrolyzing ceramide excess, which is accumulated in response to oxidative stress and could induce cell death [31].

BPHL, a mitochondrial serine hydrolase, which can hydrolyze a highly toxic homocysteine thiolactone, a byproduct of protein biosynthesis, to homocysteine [32,33].

GAA, a lysosomal α -glucosidase, which cleaves glycogen to glucose in lysosomes. Deficiency of GAA leads to Pompe disease, characterized by accumulation of glycogen in the lysosomes [34].

GALE, a cytosolic enzyme, which catalyzes the reversible epimerization of UDP-galactose and UDP-glucose. GALE plays a critical role in the Leloir pathway of galactose catabolism, in which galactose is converted to glucose 1-phosphate, a precursor of glucose 6-phosphate [35].

LAMTOR3, a part of the Ragulator complex, which along with V-ATPase (a proton pump) is involved in amino acid sensing in the lysosomes [36].

PDHX, a component X of the pyruvate dehydrogenase complex, which catalyzes the irreversible oxidation of pyruvate to acetyl CoA. This reaction is rate-limiting under aerobic conditions for the oxidative removal of glucose and pyruvate [37].

PSAT1, a member of the class-V pyridoxal-phosphate-dependent aminotransferase family. PSAT1 catalyzes the reversible conversion of 3-phosphohydroxypyruvate to phosphoserine, which is important for serine biosynthesis [38].

SLC14A1, a membrane urea transporter, whose elevated levels can represent a response to the elevated urea content inside cells [39,40].

Transcription factors

NR2E3, a photoreceptor-specific nuclear receptor, which plays a key role in photoreceptor development and regulates the expression of genes involved in phototransduction in mature retina [41,42].

ROR β , an orphan nuclear receptor β , which is expressed in throughout the retina during embryogenesis with a peak expression at neonatal stages. ROR β may play a role in the differentiation of many retinal cells; its role in cone and rod differentiation is documented [43,44].

Inflammation

ANP32B, a multifunctional protein, is involved in immunomodulation, regulation of transcription and apoptosis. ANP32B has pro-survival activity which correlates with its ability to inhibit caspase 3 [45-47].

CD59A, a potent membrane-bound inhibitor of the complement membrane attack complex. This complex can activate NF- κ B signaling and increases inflammation [48]. Deficiency in CD59A can increase accumulation of subretinal macrophages and/or microglia during aging [49]. CD59A can protect retinal cells from degeneration induced by ischemia reperfusion injury and could also counteract laser-induced choroidal neovascularization [50-52].

OGFR, the opioid growth factor receptor localized to the outer nuclear membrane. This receptor plays an immunomodulatory role, and its activation can inhibit astrocyte proliferation and astrogliosis, which can enhance inflammation [53,54].

PRKRA, an interferon-inducible double-stranded RNA-dependent protein kinase activator A. Activation of this kinase can stimulate NF- κ B-dependent pathways leading to induction of pro-inflammatory cytokines [55].

SERPINA1E, a serine peptidase inhibitor, which has anti-inflammatory properties [56]. SERPINA1E can attenuate microglia-mediated neuroinflammation and retinal degeneration in Rd1 mice, a mouse model of retinitis pigmentosa [57]. Also, SERPINA1E reduced inflammation and delayed ganglion cell loss and retinal thinning in a mouse model of diabetic retinopathy [58].

TRAFD1, an interferon and LPS-inducible gene, is a negative feedback regulator of the toll receptor (TLR) and NF- κ B signaling. TRAFD1 can limit immune response [59,60].

WDFY1, a crucial adaptor protein in the TLR3/4 signaling pathway. Overexpression of WDFY1 potentiates TLR3- and TLR4-mediated activation of NF- κ B, interferon regulatory factor 3, and production of type I interferons as well as inflammatory cytokines [61,62].

Synaptic function

GAP43, a synaptic protein and indicator of neurite elongation (axonal growth) and synapse formation. GAP43 is highly expressed during embryogenesis [63] and is upregulated during axonal regeneration, suggesting a role in regenerative responses [64].

GPM6A, a neuronal transmembrane protein which promotes various cellular protrusion formation such as neurites, filopodia and dendrite spines in an actin-independent manner [65,66]. GPM6A resides in lipid rafts and induces the clustering of lipid rafts [67]. The association of GPM6A with lipid rafts is important for its role in filopodia formation [68]. GPM6A is required for synaptic spine formation, axonal outgrowth, and synaptogenesis [69].

KCTD8, an auxiliary GABA(B) receptor subunit that modulates the receptor response, basal activity of the receptor, and its agonist-dependent desensitization [70,71].

RAB4B, a small GTPase that participates in sorting of cargo from early to recycling endosomes; the membrane material is then recycled back to the plasma membrane [72,73]. Also, RAB4B is required for synaptic spine

maintenance, and decreased expression of RAB4B correlates with reduced dendrite branching in neurons [74,75]. RAB4 can also be involved in axonal growth [76].

Ubiquitin proteasome system and protein folding

CUL1, a core component of multiple cullin-RING-based SCF (SKP1-CUL1-F-box protein) E3 ubiquitin-protein ligase complexes. These complexes can protect cells from apoptosis and neurodegeneration [77,78]. CUL1 can directly interact with STUB1 in the E3 ligase complex [79]

STUB1, an E3 ubiquitin-protein ligase CHIP, which targets misfolded chaperone substrates towards proteasomal degradation. STUB1 can protect neurons from neurodegeneration induced by misfolded proteins, mitochondrial dysfunction induced by oxygen and glucose deprivation, and death induced by oxidative stress [80-83].

UCHL5, a deubiquitinating enzyme. Inhibition of UCHL5 can induce proteotoxic stress and apoptosis [84-86]. It associates with synaptic proteasomes and participates in synaptic plasticity [87,88].

Supplemental Table S1. List of primers for quantitative real-time PCR.

Gene	Forward primer	Reverse primer
<i>Abca1</i>	5'-CAGGAAGCACGTGTCTGAAG-3'	5'-GTGGTCTCCGAGATGCCATA-3'
<i>Apoa1</i>	5'-GGGTTCAACCGTTAGTCAGC-3'	5'-TGGAATTCGTCCAGGTAGGG-3'
<i>Apoa2</i>	5'-CTGTAGCCTGGAAGGAGCTT-3'	5'-AGGTCTTGGCCTTCTCCATC-3'
<i>Apoa4</i>	5'-GAGCCCATGGGAGAGATGTT-3'	5'-TCTCCAGGAAGCTCAAGTGG-3'
<i>Apob</i>	5'-ACCAACCAGATCGTGGGAAT-3'	5'-GCCATCTTGCAGGTCAGAAG-3'
<i>Apoc3</i>	5'-CACCGGCTTCTGGGATTCTA-3'	5'-GAACAGGCACATCTGCAACA-3'
<i>Apod</i>	5'-TGAAGCCAAACAGAGCAACGT-3'	5'-GGCATCAACGGGAAGAACTG-3'
<i>ApoE</i>	5'-AACAGACCCAGCAAATACGC-3'	5'-TGTTGTTGCAGGACAGGAGA-3'
<i>ApoJ</i>	5'-ATGATCCACCAGGCTCAACA-3'	5'-GTGCGGTCATCTTCACCTTC-3'
<i>β-Actin</i>	5'-TGTTACCAACTGGGACGACATG-3'	5'-TTGTAGAAGGTGTGGTGCCAGA-3'
<i>Ccl2</i>	5'-TCACTGAAGCCAGCTCTCTCTTC-3'	5'-GTGAACAGCAGGCCCCAGAA-3'
<i>Cox-2</i>	5'-TCCTCCACTCATGAGCAGTC-3'	5'-AACCTGGTTCGGTTTGATGT-3'
<i>Hmgcr</i>	5'-TTGGTCCTTGTTACGCTCAT-3'	5'-TTCGTCCAGACCCAAGGAAAC-3'
<i>Il-6</i>	5'-AGTGGCTAAGGACCAAGACC-3'	5'-ACCACAGTGAGGAATGTCCA-3'
<i>Srebp2</i>	5'-CAGCTGGATCCTCCCAAAGA-3'	5'-CTCAGAACGCCAGACTTGTG-3'
<i>Tnfα</i>	5'-CTCATGCACCACCATCAAGG-3'	5'-ACCTGACCACTCTCCCTTTG-3'

Supplemental Table S2. Statistical analyses by two-way ANOVA with Bonferroni correction of the serum total cholesterol content in different genotypes. F, female; M, male; MB, mixed (C57BL/6J;129S6/SvEv) background; N/A, non applicable; ns, non significant; WT wild type. * $P \leq 0.05$, ** $P \leq 0.01$, *** $P \leq 0.001$

Genotype	C57BL/6J, F	C57BL/6J, M	<i>Soat1</i> ^{-/-} , F	<i>Soat1</i> ^{-/-} , M	<i>ApoE</i> ^{-/-} , F	<i>ApoE</i> ^{-/-} , M	MB WT, F	MB WT, M	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , F	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , M	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} <i>Soat1</i> ^{-/-} , F	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} <i>Soat1</i> ^{-/-} , M	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} <i>ApoE</i> ^{-/-} , F	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} <i>ApoE</i> ^{-/-} , M
C57BL/6J, F	N/A	ns	ns	*	***	***	ns	ns	ns	ns	ns	***	***	***
C57BL/6J, M	ns	N/A	ns	ns	ns	***	ns	ns	ns	ns	ns	ns	ns	***
<i>Soat1</i> ^{-/-} , F	ns	ns	N/A	ns	***	***	ns	ns	ns	ns	ns	ns	***	***
<i>Soat1</i> ^{-/-} , M	*	ns	ns	N/A	ns	***	ns	ns	ns	ns	ns	ns	ns	***
<i>ApoE</i> ^{-/-} , F	***	***	***	***	N/A	***	***	***	ns	***	ns	**	ns	***
<i>ApoE</i> ^{-/-} , M	***	***	***	***	***	N/A	ns	***	ns	ns	ns	ns	ns	ns
MB WT, F	ns	ns	ns	*	***	***	N/A	ns	ns	ns	ns	**	ns	***
MB WT, M	ns	ns	ns	ns	***	***	ns	N/A	ns	ns	ns	ns	ns	ns
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , F	ns	ns	ns	ns	***	***	ns	ns	N/A	ns	ns	*	***	***
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , M	ns	ns	ns	ns	***	***	ns	ns	ns	N/A	ns	ns	ns	***
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} <i>Soat1</i> ^{-/-} , F	ns	ns	ns	ns	***	***	ns	ns	ns	ns	N/A	ns	***	***
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} <i>Soat1</i> ^{-/-} , M	***	ns	ns	ns	**	***	**	ns	*	ns	ns	N/A	ns	***
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} <i>ApoE</i> ^{-/-} , F	***	***	***	***	ns	***	***	***	***	***	***	**	N/A	***
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} <i>ApoE</i> ^{-/-} , M	***	***	***	***	***	ns	***	***	***	***	***	***	***	N/A

Supplemental Table S3. Statistical analyses by two-way ANOVA with Bonferroni correction of the retinal total cholesterol content in different genotypes. F, female; M, male; MB, mixed (C57BL/6J;129S6/SvEv) background; N/A, non applicable; ns, non significant; WT wild type. * $P \leq 0.05$, ** $P \leq 0.01$, *** $P \leq 0.001$.

Genotype	C57BL/6J, F	C57BL/6J, M	<i>Soat1</i> ^{-/-} , F	<i>Soat1</i> ^{-/-} , M	<i>ApoE</i> ^{-/-} , F	<i>ApoE</i> ^{-/-} , M	MB WT, F	MB WT, M	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , F	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , M	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , F	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , M	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , F	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , M
C57BL/6J, F	N/A	ns	ns	ns	***	***	ns	ns	**	***	ns	ns	***	***
C57BL/6J, M	ns	N/A	ns	ns	***	***	ns	ns	**	***	ns	ns	***	***
<i>Soat1</i> ^{-/-} , F	ns	ns	N/A	ns	***	***	ns	ns	***	***	ns	ns	***	***
<i>Soat1</i> ^{-/-} , M	ns	ns	ns	N/A	***	***	ns	ns	***	***	ns	ns	***	***
<i>ApoE</i> ^{-/-} , F	***	***	***	***	N/A	ns	***	***	***	***	***	***	***	ns
<i>ApoE</i> ^{-/-} , M	***	***	***	***	ns	N/A	***	***	***	***	***	***	***	ns
MB WT, F	ns	ns	ns	ns	***	***	N/A	ns	***	***	ns	ns	***	***
MB WT, M	ns	ns	ns	ns	***	***	ns	N/A	***	***	ns	ns	***	***
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , F	**	**	***	***	***	***	***	***	N/A	ns	***	**	***	***
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , M	***	***	***	***	***	***	***	***	ns	N/A	***	***	ns	***
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} <i>Soat1</i> ^{-/-} , F	ns	ns	ns	ns	***	***	ns	ns	***	***	N/A	ns	***	***
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} <i>Soat1</i> ^{-/-} , M	ns	ns	ns	ns	***	***	ns	ns	**	***	ns	N/A	***	***
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} <i>ApoE</i> ^{-/-} , F	***	***	***	***	***	***	***	***	***	ns	***	***	N/A	ns
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} <i>ApoE</i> ^{-/-} , M	***	***	***	***	ns	ns	***	***	***	***	***	***	ns	N/A

Supplemental Table S4. Statistical analyses by two-way ANOVA with Bonferroni correction of the retinal free lathosterol content in different genotypes. F, female; M, male; MB, mixed (C57BL/6J;129S6/SvEv) background; N/A, non applicable; ns, non significant; WT wild type. * $P \leq 0.05$, ** $P \leq 0.01$, *** $P \leq 0.001$.

Genotype	C57BL/6J, F	C57BL/6J, M	<i>Soat1</i> ^{-/-} , F	<i>Soat1</i> ^{-/-} , M	<i>ApoE</i> ^{-/-} , F	<i>ApoE</i> ^{-/-} , M	MIX WT, F	MIX WT, M	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , F	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , M	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , F	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , M	<i>ApoE</i> ^{-/-} , F	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , M
C57BL/6J, F	N/A	ns	ns	ns	***	***	ns	ns	ns	ns	***	***	***	***
C57BL/6J, M	ns	N/A	ns	ns	***	***	ns	ns	ns	ns	***	***	***	***
<i>Soat1</i> ^{-/-} , F	ns	ns	N/A	ns	***	***	ns	ns	ns	ns	**	*	***	***
<i>Soat1</i> ^{-/-} , M	ns	***	ns	N/A	***	***	ns	ns	ns	ns	**	*	***	***
<i>ApoE</i> ^{-/-} , F	***	***	***	***	N/A	ns	***	***	***	***	***	***	***	***
<i>ApoE</i> ^{-/-} , M	***	ns	***	***	ns	N/A	***	***	***	***	***	***	***	***
MIX WT, F	ns	ns	ns	ns	***	***	N/A	ns	ns	ns	***	*	***	***
MIX WT, M	ns	ns	ns	ns	***	***	ns	N/A	ns	ns	***	*	***	***
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , F	ns	ns	ns	ns	***	***	ns	ns	N/A	ns	***	***	***	***
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , M	ns	ns	ns	ns	***	***	ns	ns	ns	N/A	**	ns	***	***
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} <i>Soat1</i> ^{-/-} , F	***	***	**	**	***	***	***	***	***	**	N/A	ns	***	***
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} <i>Soat1</i> ^{-/-} , M	***	***	*	*	***	***	*	*	***	ns	ns	N/A	***	***
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} <i>ApoE</i> ^{-/-} , F	***	***	***	***	***	***	***	***	***	***	***	***	N/A	ns
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} <i>ApoE</i> ^{-/-} , M	***	***	***	***	***	***	***	***	***	***	***	***	ns	N/A

Supplemental Table S5. Statistical analyses by two-way ANOVA with Bonferroni correction of the retinal free desmosterol content in different genotypes. F, female; M, male; MB, mixed (C57BL/6J;129S6/SvEv) background; N/A, non applicable; ns, non significant; WT wild type. * $P \leq 0.05$, ** $P \leq 0.01$, *** $P \leq 0.001$.

Genotype	C57BL/6J, F	C57BL/6J, M	<i>Soat1</i> ^{-/-} , F	<i>Soat1</i> ^{-/-} , M	<i>ApoE</i> ^{-/-} , F	<i>ApoE</i> ^{-/-} , M	MIX WT, F	MIX WT, M	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , F	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , M	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , F	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , M	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , F	<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , M
C57BL/6J, F	N/A	ns	ns	ns	***	***	ns	ns	ns	**	ns	ns	**	***
C57BL/6J, M	ns	N/A	ns	ns	***	***	ns	ns	ns	ns	ns	ns	***	***
<i>Soat1</i> ^{-/-} , F	ns	ns	N/A	ns	***	***	ns	ns	ns	**	ns	ns	**	***
<i>Soat1</i> ^{-/-} , M	ns	ns	ns	N/A	***	***	ns	ns	ns	*	ns	ns	**	***
<i>ApoE</i> ^{-/-} , F	***	***	***	***	N/A	**	***	***	***	***	***	***	***	***
<i>ApoE</i> ^{-/-} , M	***	***	***	***	**	N/A	***	***	***	***	***	***	***	***
MIX WT, F	ns	ns	ns	ns	***	***	N/A	ns	ns	*	ns	ns	***	***
MIX WT, M	ns	ns	ns	ns	***	***	ns	N/A	ns	ns	ns	ns	***	***
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , F	ns	ns	ns	ns	***	***	ns	ns	N/A	ns	ns	ns	***	***
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} , M	**	ns	**	*	***	***	*	ns	ns	N/A	ns	ns	***	***
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} <i>Soat1</i> ^{-/-} , F	ns	ns	ns	ns	***	***	ns	ns	ns	ns	N/A	ns	***	***
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} <i>Soat1</i> ^{-/-} , M	ns	ns	ns	ns	***	***	ns	ns	ns	ns	ns	N/A	***	***
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} <i>ApoE</i> ^{-/-} , F	**	***	**	**	***	***	***	***	***	***	***	***	N/A	ns
<i>Cyp27a1</i> ^{-/-} <i>Cyp46a1</i> ^{-/-} <i>ApoE</i> ^{-/-} , M	***	***	***	***	***	***	***	***	***	***	***	***	ns	N/A

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