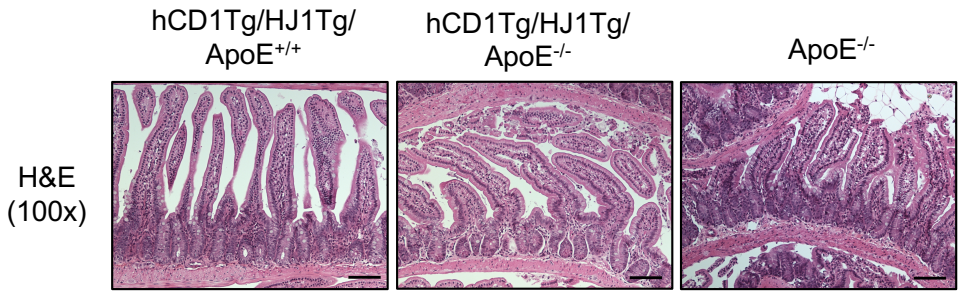
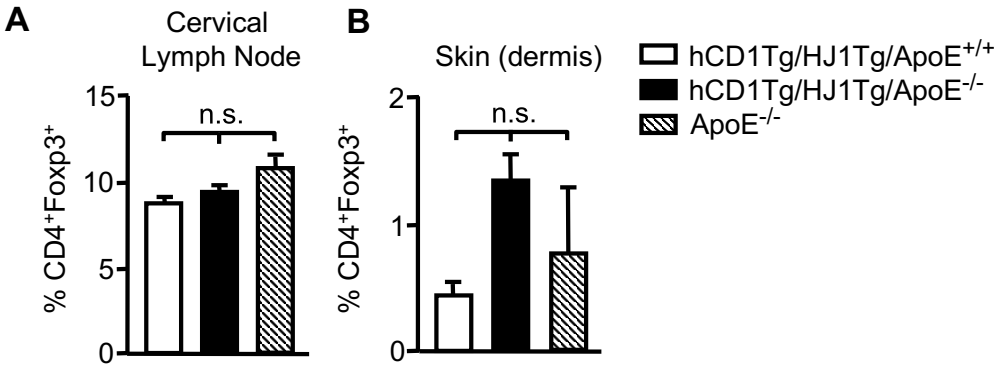
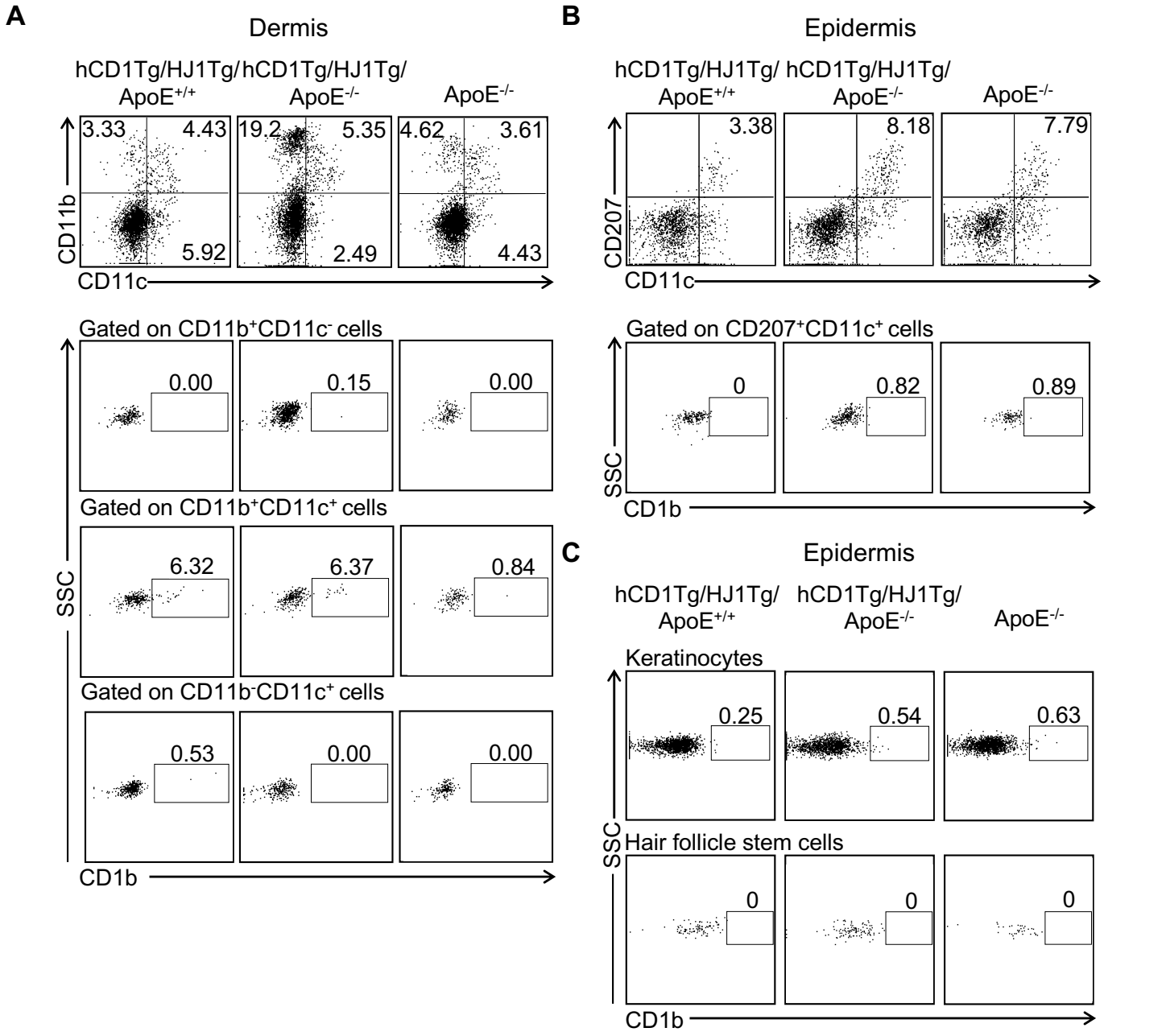


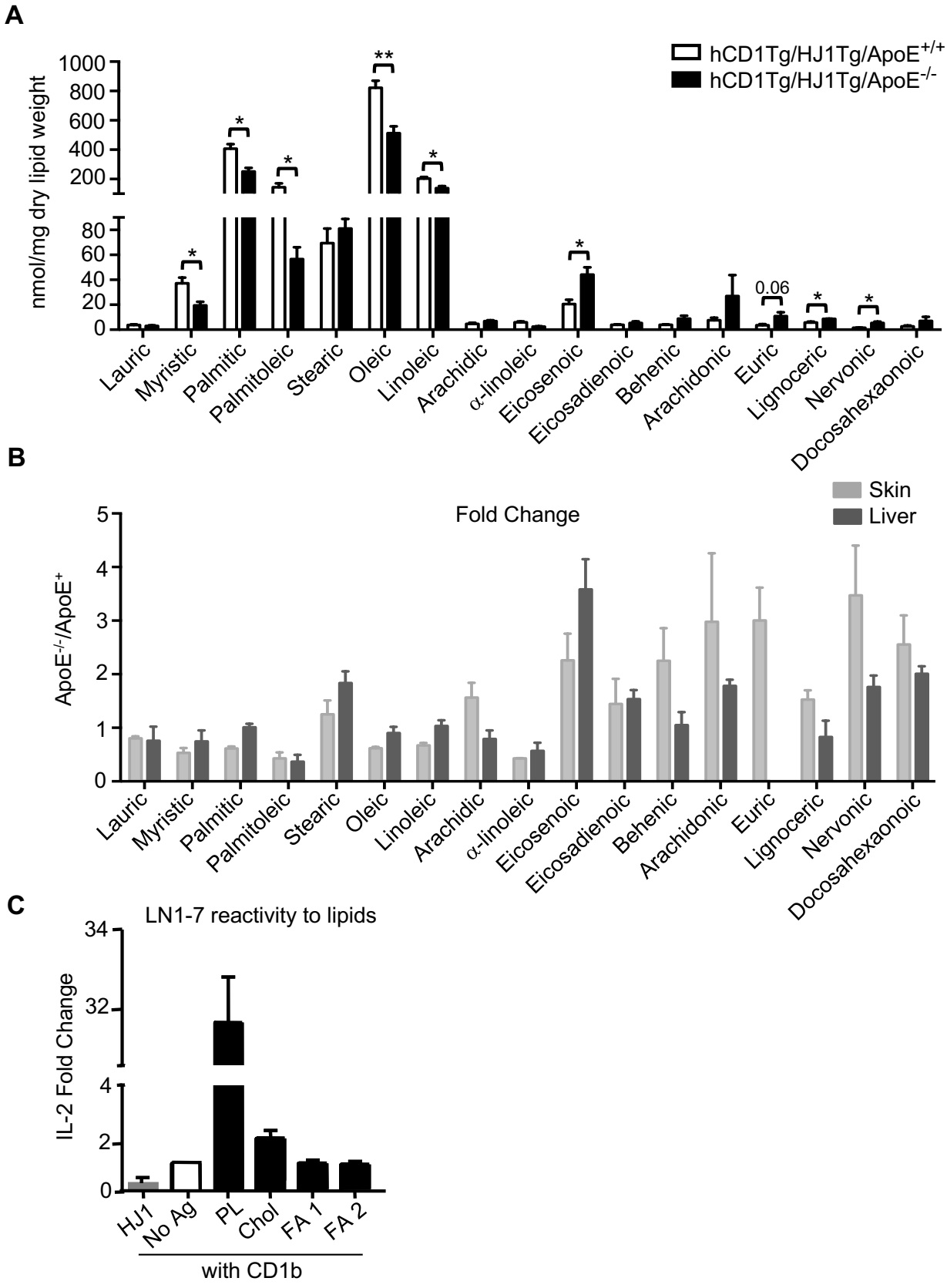
Supplementary Figure 1. No obvious pathology is observed in the colon of diseased hCD1Tg/HJ1Tg/ApoE$^{-/-}$ mice. Colon samples were fixed in 10% formalin and laid out in Swiss rolls for paraffin embedding. Paraffin sections were cut and stained with H&E to examine the tissue architecture. Scale bars represent 100 μm.



Supplementary Figure 2. hCD1Tg/HJ1Tg/ApoE$^{+/+}$ and hCD1Tg/HJ1Tg/ApoE$^{-/-}$ mice have comparable numbers of FoxP3^{+} regulatory T cells. Cells isolated from the (A) cervical lymph nodes and (B) dermis were stained intracellularly with Foxp3 and gated on CD45^{+}TCRb^{+}. Subsequently, the CD4 and Foxp3 positive Treg cell population was examined (n=3-5). ***P < 0.005; **P < 0.01; *P< 0.05; n.s. = not significant. Statistical analysis was performed using One-Way ANOVA followed by Bonferroni post-hoc test.



Supplementary Figure 3. CD1b is expressed on a subset of dermal dendritic cells. (A) Dermal cells were isolated and stained with mAbs against CD45, CD11b, CD11c, and CD1b. CD1b expression on $CD11b^+CD11c^-$, $CD11b^+CD11c^+$ and $CD11b^-CD11c^+$ populations were analyzed by flow cytometry. (B) Epidermal cells were isolated and stained with mAbs against CD45, CD207, CD11c and CD1b. CD1b expression on $CD207^+CD11c^+$ population (Langerhans cells) was analyzed by flow cytometry by gating on $CD45^+$ cells. (C) CD1b expression on hair follicle stem cells and keratinocytes was determined by gating on $CD45^-$ cells and then on integrin $\alpha 6$ and $\beta 1$ double positive cells. Subsequently, $CD34^+$ $Sca\text{-}1^-$ hair follicle stem cells or $CD34^-$ $Sca\text{-}1^+$ epidermal keratinocytes were output for CD1b expression. Data shown are representative of at least 2 experiments for all figure panels.



Supplementary Figure 4. Fatty acids do not show preferential accumulation in the skin of hCD1Tg/HJ1Tg/ApoE$^{-/-}$ mice and reactivity of lipids to a second mouse CD1b-autoreactive hybridoma. Total lipid was extracted from skin and liver tissues of indicated mice, weighed and analyzed by gas chromatography. (A) Fatty acid species in the skin of diseased hCD1Tg/HJ1Tg/ApoE$^{-/-}$ and healthy hCD1Tg/HJ1Tg/ApoE$^{+/+}$ mice (n=3) were quantified. (B) Ratio of fatty acids from diseased over healthy mice in the skin and liver. (C) Polar phospholipids (PL), cholesterol (Chol) and fatty acid mixtures (FA1: saturated and monounsaturated and FA2: polyunsaturated) were loaded on to CD1b protein and incubated with LN1-7 T cell hybridoma for 24 h. IL-2 in the supernatant was measured by ELISA. Data are representative of at least 2 experiments. $^{**}P < 0.01$; $^{*}P < 0.05$. Statistical analysis was performed using Student's t-test.

Supplementary table 1: Oligonucleotide primers used in the study

Name	**Sequence (5'-3')**
For genotyping	
HJ1α F	TGACACCTGCTCAGTTCTTGTGC
HJ1α R	TAGCTTGTTCCCTGCACTTGG
CD1c F	CAGAAACTGCAGAAACAGCA
CD1c R	GATGGGTGAAAAGAGGTGAAA
ApoE WT	TGTGACTTGGGAGCTCTGCAGC
ApoE Common	GCCTAGCCGAGGGAGAGCCG
ApoE Mutant	GCCGCCCCGACTGCATCT
For RT-PCR	
IL-18Rα F	TCACCGATCACAAATTCATGTGG
IL-18Rα R	TGGTGGCTGTTTCATTCCTGT
IL-12Rβ1 F	TGCCGCTACTTCTCCTCAG
IL-12Rβ1 R	ACTTCATGGTTCGGTTCCCAA
TLR9 F	ATGGTTCTCCGTCGAAGGACT
TLR9 R	GAGGCTTCAGCTCACAGGG
S100a7 F	GTA CTC AGG TCA TGG TTC TG
S100a7 R	GGT ATT CAA GCA AGG TAT CAC
S100a8 F	GGA GTT CCT TGC GAT GGT GAT
S100a8 R	TCC TTG TGG CTG TCT TTG TGA
β-actin F	CTT CTT TGC AGC TCC TTC GTT
β-actin R	AGG AGT CCT TCT GAC CCA TTC
IL-17F F	TGC TAC TGT TGA TGT TGG GAC
IL-17F R	AAT GCC CTG GTT TTG GTT GAA
IL-17A F	ACT TTC AGG GTC GAG AAG A
IL-17A R	TTC TGA ATC TGC CTC TGA AT
IL-22 F	ATG AGT TTT TCC CTT ATG GGG AC
IL-22 R	GCT GGA AGT TGG ACA CCT CAA
GM-CSF F	GGC CTT GGC AGC ATG TAG AGC
GM-CSF R	GGA GAA CTC GTT AGA GAC GAC TT
TNF-α F	CCA CCA CGC TCT TCT GTC T
TNF-α R	GGC ACC ACT AGT TGG TTG T
IL-6 F	CTT GGG ACT GAT GCT GGT GAC A
IL-6 R	GCC TCC GAC TTG TGA AGT GGT A
TGβ1 F	CTC CCG TGG CTT CTA GTG C
TGβ1 R	GGCC TTA GTT TGG ACA GGA TCT G
IL-4 F	AAC TCC ATG CTT GAA GAA GAA CTC
IL-4 R	CCA GGA AGT CTT TCA GTG ATG TG
IL-23 F	CCA TTA GGA CTT GTG CTG TTC T
IL-23 R	CCA AGG GCT CGA GAC TTT ATT C
IFN-γ F	TCA AGT GGC ATA GAT GTG GAA GAA
IFN-γ R	TGG CTC TGC AGG ATT TTC ATG
HJ1Vβ F	ATC TCT TCC CGG TGC TGA TT
HJ1Vβ R	TCT GGT TCC TGA GCC AAA AT