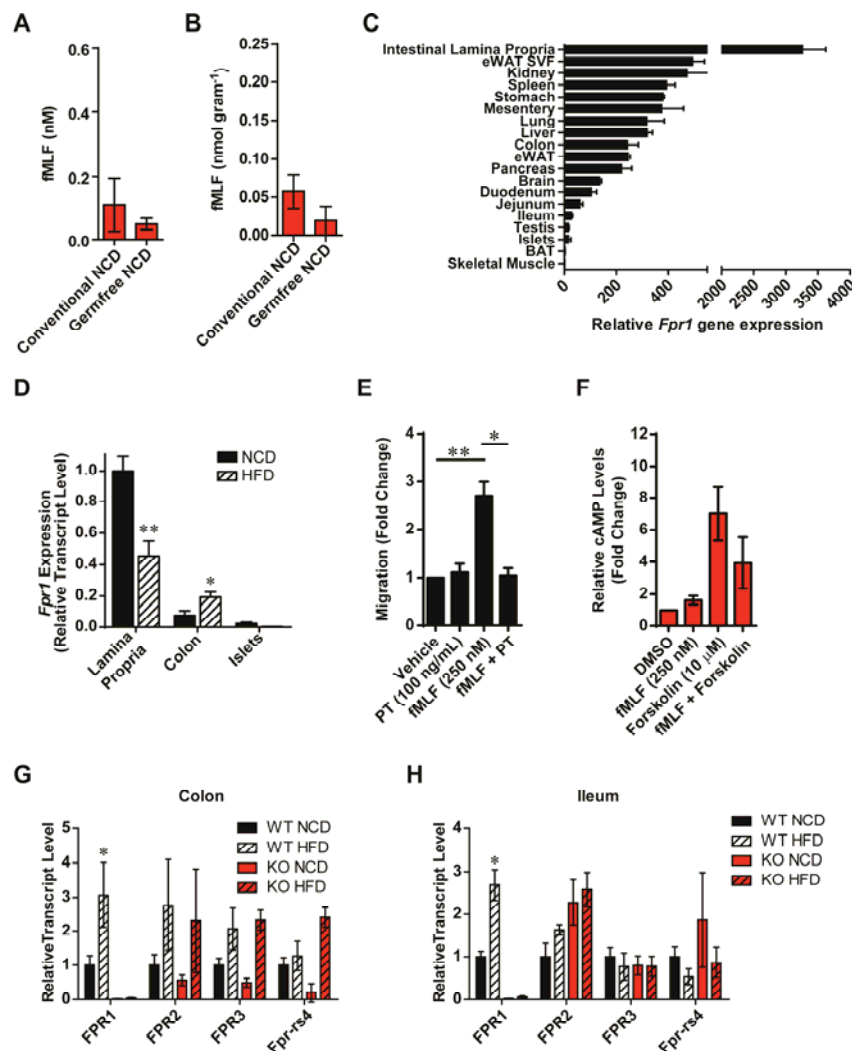


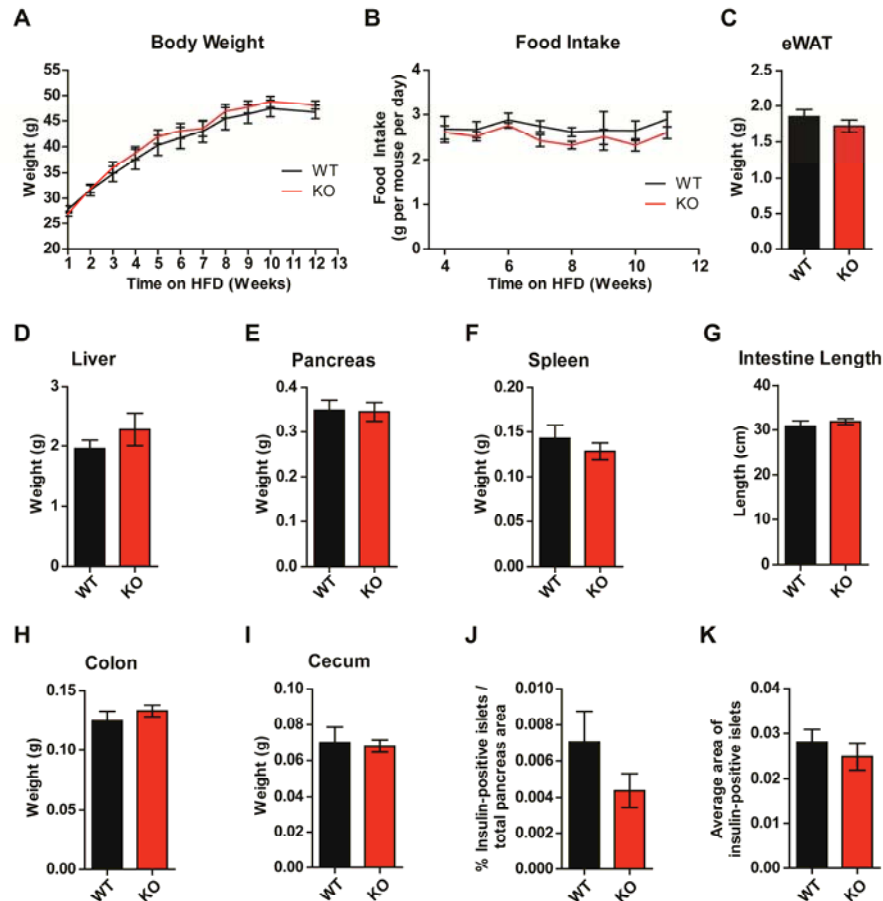
SUPPLEMENTARY DATA

Supplementary Figure 1. Fpr1 is expressed in the gastrointestinal tract and influences cAMP. (A) Levels of fMLF levels in the plasma of germfree animals on NCD ($n = 3$), compared to conventional NCD animals ($n = 3$). (B) Levels of fMLF levels in the colon of germfree animals on NCD ($n = 4$), compared to conventional NCD animals ($n = 8$). (C) Relative Fpr1 gene expression in various tissues of lean 16-week old WT NCD mice (eWAT = epididymal white adipose tissue; SVF = stromal vascular fraction; BAT = brown adipose tissue). (D) Relative Fpr1 gene expression in the small intestinal lamina propria, colon, and pancreatic islets isolated from WT animals fed either NCD or HFD ($n = 3$). (E) Chemotaxis of thioglycolate-elicited intraperitoneal macrophages (IP-Macs) in response to fMLF (250 nM) is suppressed by co-incubation with Pertussis Toxin (PT), an inhibitor of Gi-coupled signaling. (F) Relative cAMP levels in forskolin-stimulated IP-Macs are reduced by treatment with fMLF. (G) Relative transcript levels of four related Fpr genes in the colon of WT and Fpr1-KO mice on NCD and HFD ($n = 6$ mice per group). (H) Relative transcript levels of related Fpr genes in the ileum of WT and Fpr1-KO mice on NCD and HFD. Data = mean \pm SEM. ns = not significant. # = below detection limit. * $P < 0.05$, ** $P < 0.001$, *** $P < 0.0001$ by two-tailed t test (D) or One-way ANOVA and Bonferroni's post-test (E-H), comparing the indicated groups.



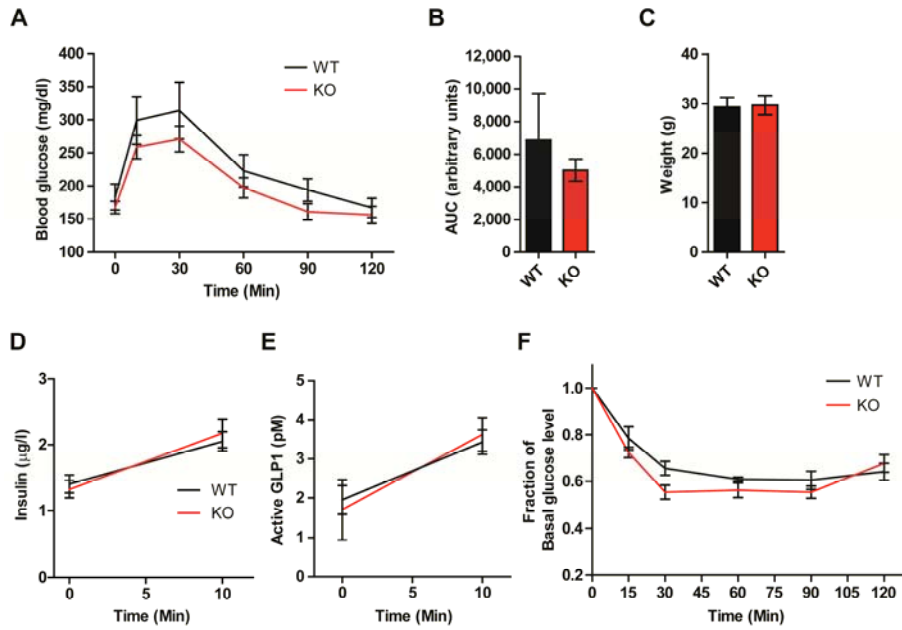
SUPPLEMENTARY DATA

Supplementary Figure 2. Obese/HFD Fpr1-KO mice do not display significant differences in weight gain or organ weight (A) Body weight gain of WT and Fpr1-KO littermates on 60% HFD ($n = 7-10$ mice per group). (B) Food intake. (C-F) Weight of epididymal white adipose tissue, liver, pancreas, and spleen of mice after 13 weeks on HFD. (G) Intestine length (H-I) weight of the colon and cecum after contents were removed. (J) Area of insulin-positive islets as a percentage of the pancreas, an estimation of beta cell mass, in HFD WT and Fpr1-KO littermates ($n = 6-7$ mice per group). (K) Average islet size ($n = 6-7$ mice per group). Data = mean \pm SEM.



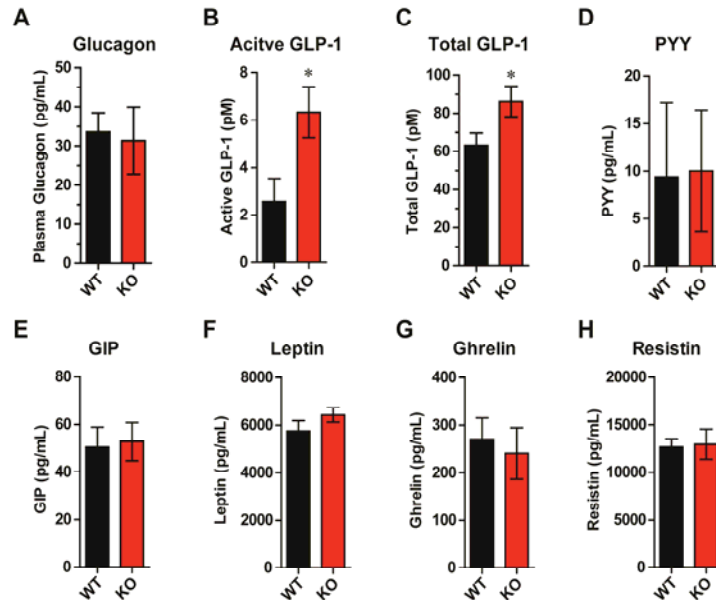
SUPPLEMENTARY DATA

Supplementary Figure 3. Loss of Fpr1 does not significantly improve glucose tolerance in lean/NCD animals. (A-B) OG-GTT of WT and Fpr1-KO littermates at 16 weeks of age, and corresponding AUC ($n = 6-10$ mice per group). (C) Body weight of the mice at the time of the OG-GTT. (D-E) Insulin levels and basal GLP-1 levels measured during the OG-GTT. (F) IP-ITT at 17 weeks of age. Data = mean \pm SEM.



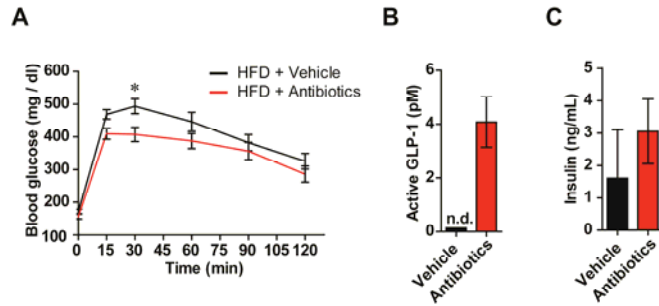
SUPPLEMENTARY DATA

Supplementary Figure 4. Analysis of basal glucagon and gastric hormone levels in obese/HFD animals. (A) Basal fasted blood plasma glucagon levels measured immediately prior to OG-GTT in HFD WT and Fpr1-KO littermates ($n = 9$ mice per group). (B-H) Active GLP-1, Total GLP-1, Peptide YY (PYY), Gastric Inhibitory Polypeptide (GIP), Leptin, Ghrelin, and Resistin levels in the basal fasted state measured immediately prior to OG-GTT ($n = 7-10$ mice per group). Data = mean \pm SEM. ns = not significant. $*P < 0.05$, by two-tailed t test.

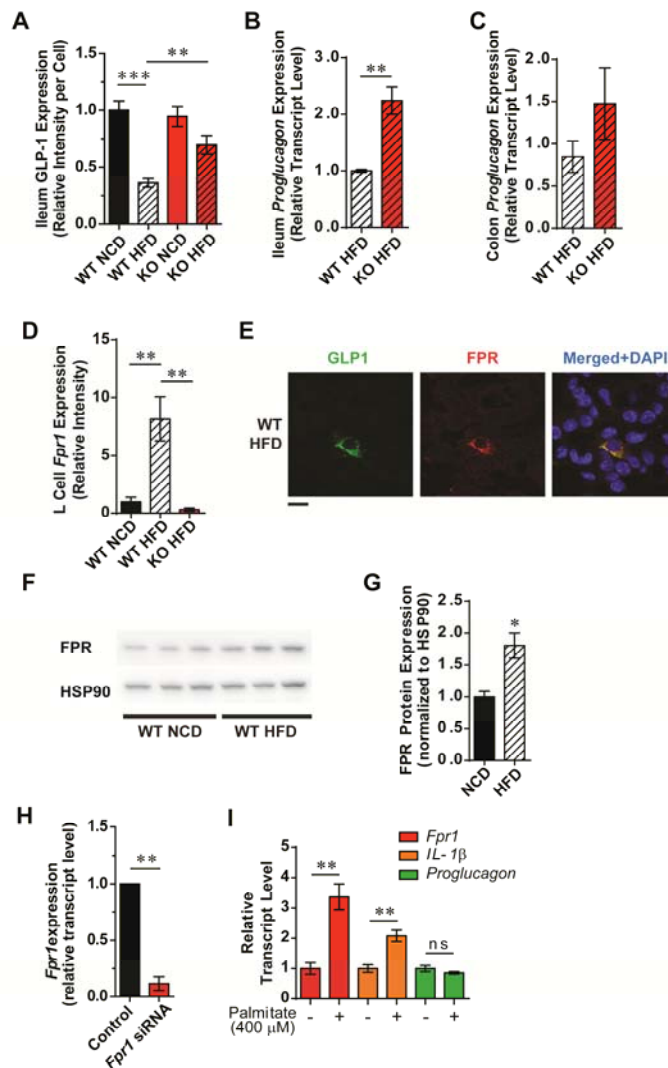


SUPPLEMENTARY DATA

Supplementary Figure 5. Oral treatment with broad-spectrum antibiotics improves glucose tolerance and increases GLP-1 levels. (A) OG-GTT of WT HFD animals after daily oral gavage of broad-spectrum antibiotics for two weeks ($n = 8$ mice per group). (B) Basal active GLP-1 levels measured immediately prior to OG-GTT. (C) Basal insulin levels prior to OG-GTT. Error bars = s.e.m. n.d. = not detectable. $*P < 0.05$ by One-way ANOVA with Bonferroni's post-test.



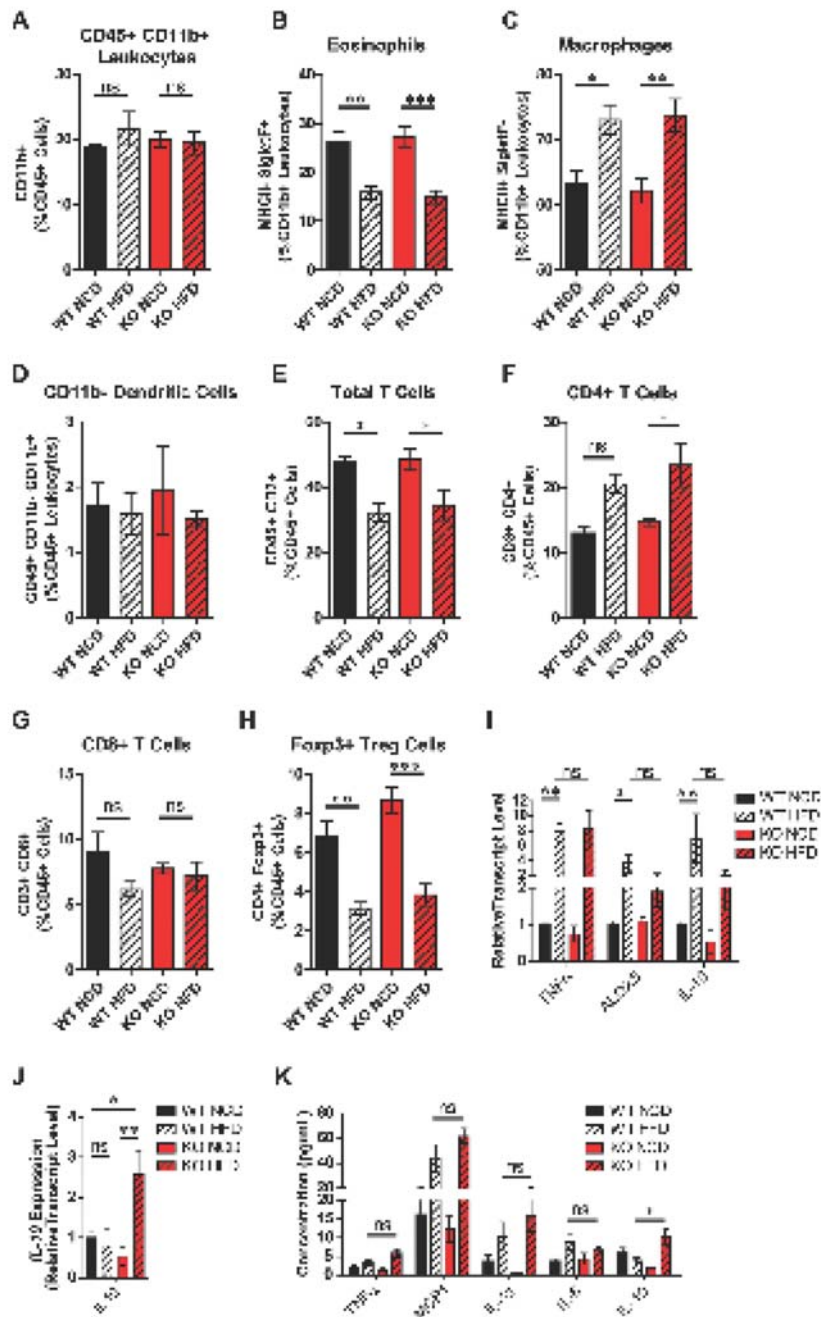
Supplementary Figure 6. fMLF Acts upon Fpr1 on L-cells to modulate GLP-1 secretion in obese/HFD animals. (A) Quantification of GLP-1 immunofluorescence labeling in the ileum of WT and Fpr1-KO animals on NCD and HFD ($n = 8$). (B) Ileum *proglucagon* transcript levels in Fpr1-KO HFD animals relative to WT HFD ($n = 8$). (C) Relative mRNA levels of *proglucagon* in the colon of WT and Fpr1-KO HFD mice. (D) Relative *Fpr1* mRNA expression in *Proglucagon*-positive L-cells as detected by RNA-fluorescence *in situ* hybridization in colon sections from NCD and HFD animals ($n = 4$). (E) Immunofluorescence staining of GLP-1 and FPR in L-cells of WT HFD colon sections (representative images, scale bars = 10 μ m). (F) Western immunoblot of FPR and HSP90 in colon tissue lysates of WT NCD versus HFD animals, normalized densitometry quantification shown in (G) ($n = 3$ per group). (H) siRNA knockdown of *fpr1* transcript levels in mGLUTag cells ($n = 5$). (I) mRNA transcript levels of *fpr1*, *il-1 β* and *proglucagon* in mGLUTag cells treated with or without 400 μ M palmitate for 24 hours ($n = 3$). Data = mean \pm SEM., ns = not significant. * $P < 0.05$, ** $P < 0.001$, *** $P < 0.0001$ by One-way ANOVA with Bonferroni's post-test (A and D) or two-tailed t test.



SUPPLEMENTARY DATA

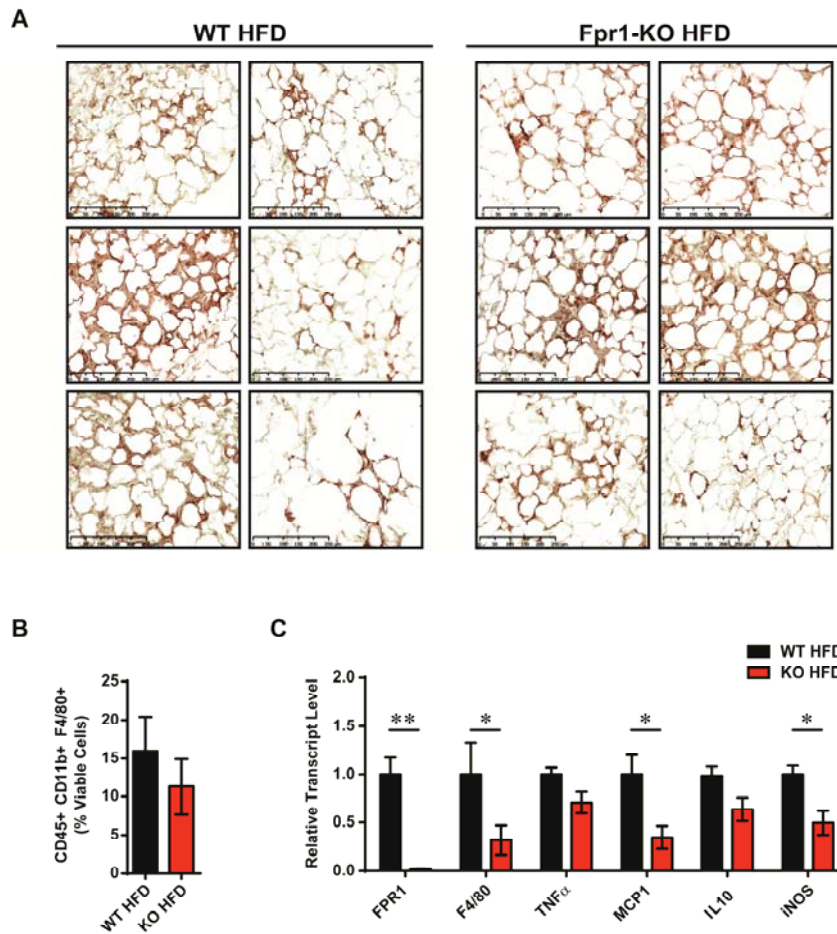
Supplementary Figure 7. Intestinal leukocyte composition and inflammatory gene expression in WT and Fpr1-KO mice. (A) Total CD11b⁺ leukocytes in the small intestinal lamina propria isolated from WT and Fpr1-KO littermates on NCD and HFD (percentage of CD45⁺ cells) ($n = 6$ mice per group). (B) MHCII⁻ SigletF⁺ eosinophils (C) MHCII⁺ SigletF⁻ macrophages (D) CD11b⁻ CD11c⁺ dendritic cells (E) CD45⁺ CD3⁺ T cells (F) CD8⁺ T cells (G) CD4⁺ T cells (H) CD4⁺ Foxp3⁺ Treg cells. (I) mRNA transcript levels of pro-inflammatory *TNF* α , *ALOX5*, and *IL1* β in immune cells of the small intestinal lamina propria from WT and Fpr1-KO littermates ($n = 4-6$ mice per group). (J) mRNA transcript levels of IL-10 ($n = 4-6$ mice per group). (K) Levels of circulating chemokines and cytokines in the blood plasma of WT and Fpr1-KO mice ($n = 8-9$ mice per group). Data = mean \pm SEM. ns = not significant. * $P < 0.05$, ** $P < 0.001$, *** $P < 0.0001$ by One-way ANOVA and Bonferroni's post-test.

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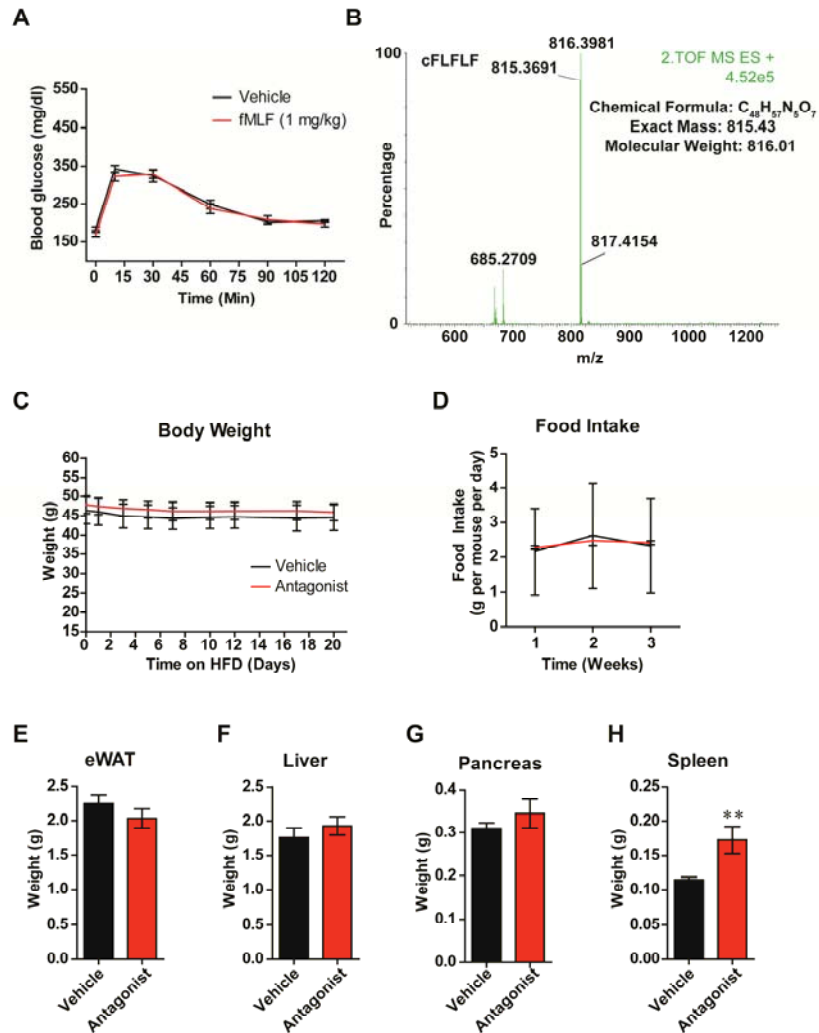
SUPPLEMENTARY DATA

Supplementary Figure 8. Analysis of inflammation in epididymal white adipose tissue of WT and Fpr1-KO mice on HFD. (A) Mac-2 staining of eWAT sections (representative images, $n = 8$ mice per group, scale bar = 250 μm). (B) FACS analysis of F4/80+ macrophages isolated from eWAT tissue. (C) mRNA transcript levels of pro-inflammatory “M1-type” genes in eWAT. (D) mRNA transcript levels of IL-10. Data = mean \pm SEM. * $P < 0.05$, ** $P < 0.001$, *** $P < 0.0001$ by two-tailed t test.



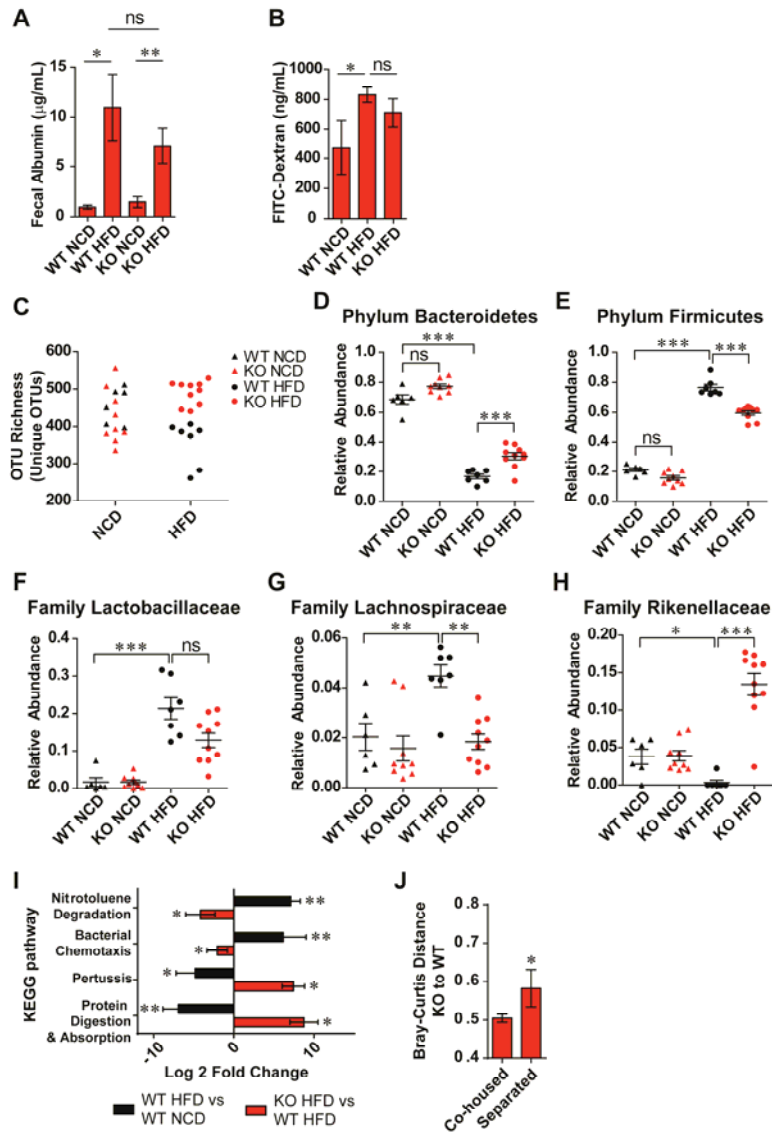
SUPPLEMENTARY DATA

Supplementary Figure 9. (A) OG-GTT of WT NCD animals after daily oral gavage with the Fpr1 agonist fMLF for 2 weeks (1 mg/kg) ($n = 8$ mice per group). (B) Matrix-assisted laser desorption-time of flight (MALDI-TOF) mass spectra of synthesized Fpr1 antagonist cFLFLF, positive ion mode. (C) Body weight of WT HFD mice during daily oral gavage treatment with the Fpr1 antagonist cFLFLF (0.5 mg/kg) or vehicle for three weeks ($n = 8$ mice per group). (D) Food intake during antagonist treatment. (E-H) Weight of epididymal white adipose tissue, liver, pancreas, and spleen upon sacrifice. Data = mean \pm SEM. ns = not significant. * $P < 0.05$, ** $P < 0.001$ by two-tailed t test.



Supplementary Figure 10. Analysis of intestinal permeability and microbiome composition in WT and Fpr1-KO littermates. (A) Analysis of fecal albumin levels in WT and Fpr1-KO littermates ($n = 12-18$ mice per group). (B) Blood plasma FITC-Dextran levels in lean/NCD and obese/HFD mice ($n = 4-6$ mice per group). (C) A second measure of alpha diversity, OTU richness, confirms that Fpr1-KO mice on HFD have significantly increased microbiome diversity within each sample compared to WT animals on HFD. Legend also applies to (D-H). ($n = 6-10$ mice per group). (D) Mean relative abundance of members of the Phylum Bacteroidetes within each sample. (E) Mean relative abundance of members of the Phylum Firmicutes within each sample. (F) Mean relative abundance of members of the Family Lactobacillaceae within each sample. (G) Mean relative abundance of members of the Family Lachnospiraceae within each sample. WT animals on HFD display increased abundance of this Family compared to NCD, whereas Fpr1-KO animals on HFD have significantly lower levels, resembling NCD. (H) Mean relative abundance of members of the Family Rikenellaceae within each sample. WT animals on HFD have reduced abundances compared to NCD, whereas Fpr1-KO animals on HFD have significantly elevated levels compared to WT ($n = 6-10$ mice per group). (I) Log 2-fold change of bacterial pathways predicted altered by inferred metagenomics content analysis, according to Kyoto Encyclopedia of Genes and Genomes (KEGG) orthology ($n = 6-10$ mice per group). (J) Analysis of Bray-Curtis dissimilarity distances between Fpr1-KO and WT HFD microbiome samples, from 3 cohorts of HFD microbiome samples, comparing mice housed separately or co-housed. Data = mean \pm SEM. ns = not significant. * $P < 0.05$, ** $P < 0.001$, *** $P < 0.0001$ by One-way ANOVA and Bonferroni's post-test (A-B) or PERMANOVA and DESeq 2 (D-H, J).

SUPPLEMENTARY DATA



Supplementary Figure 11. Model of microbiota-produced fMLF action upon GLP-1 secretion and glucose tolerance in diet-induced obesity. (A) In lean NCD conditions, a healthy intestinal microbiota produces low levels of *N*-formyl peptides including fMLF. After a meal, glucose in the intestine is taken up by L-cells in the intestinal epithelium, stimulating production and secretion of extra-pancreatic GLP-1 by these cells into systemic circulation, which promotes glucose tolerance through both insulin-dependent and independent mechanisms, including suppression of gastric emptying, reduced glucagon production, CNS effects and neuronal signaling from the gut to the brain. In this paradigm, the effects of GLP-1 from either α -cells or L-cells to stimulate insulin secretion would represent only one arm of GLP-1 regulation of glucose homeostasis. (B) In obese HFD conditions, intestinal dysbiosis leads to increased *N*-formyl peptide levels, and L-cells express higher levels of FPR1. Increased intestinal permeability in HFD animals also leads to elevated levels of *N*-formyl peptides entering circulation. In the gut, *N*-formyl peptides activate FPR1 on L-cells to suppress GLP-1 secretion, leading to reduced glucose tolerance.

