

**Fig. S1** Effects of dietary high lipid and BAs on intestinal microbiota. **A–B**: the percentage of *Proteobacteria* and *Bacteroidetes* in the total population at phylum levels (n=6). **C**: the ratio of *Firmicutes* / *Bacteroidetes* at the phylum level. **D**: the unweighted UniFrac and principal coordinate analysis (PCoA) of intestinal microbiota. **E**: the nonmetric multidimensional scaling analysis (NMDS) of intestinal microbiota. **F**: the linear discriminant analysis (LDA) effect size (LEfSe) algorithm in groups (n=6). LEfSe is performed by combining the Kruskal-Wallis test or Wilcoxon rank-sum test with LDA scores to estimate the effect size of differentially abundant features with biological consistency and statistical significance (herein, significance value for the statistical test was set at 0.05 and threshold on the LDA score for discriminative features was more than 2.00). **G**: the heatmap with Euclidean distance to perform hierarchical clustering of the abundance of genera with significant difference (n=6). **H**: the abundance of BSH microbes, including *Bacillus*, *Bacteroides*, *Clostridium*, *Lactobacillus*, *Bifidobacterium*, *Streptococcus*, *Lactococcus*, *Ruminococcus*, *Fusobacterium*, and *Pseudomonas*. Values are presented as means with SD, where “\*” indicates significant ( $p < 0.05$ ) differences in the HD group (compared to the CD group), and “#” indicates significant ( $p < 0.05$ ) differences in the B900D group (compared to the HD group).

**Fig. S2** The relative expression of genes associated with BAs metabolism in liver (**A–H** and **M–O**) and hindgut (**I–L**). *hmgcr*: 3-hydroxy-3-methylglutaryl-CoA reductase; *cyp7b1*: oxysterol 7 $\alpha$ -hydroxylase; *cyp27a1*: sterol-27-hydroxylase; *oatp4*: organic anion transporters 4; *meh*: microsomal epoxide hydrolase; *bsep*: bile salt export pump; *mrp2*: multidrug resistance-associated protein 2; *mdr3*: multidrug resistance protein 3; *asbt*: apical sodium-dependent BAs transporter; *osta*: organic solute transporter subunit  $\alpha$ ; *fgfr4*: fibroblast growth factor receptor 4; *cyp7a1*: cholesterol 7 $\alpha$ -hydroxylase. Data are normalized to *18s* and  $\beta$ -actin as the reference genes and presented as a fold change in relation to the control group (CD, set as 1) (n=6). Values are presented as means with SD, where significant ( $p < 0.05$ ) differences between groups are indicated by different letters.