

Supplemental Table S1. Comparison of the ingredients in #D12450J (STD) and high-fat diet (HFD).

Ingredients	STD (10% dietary fat)		HFD (60% dietary fat)	
	g	kcal	g	kcal
Casein	200	800	200	800
L-cystine	3	12	3	12
Corn starch	506.2	2024.8	0	0
Maltodextrin 10	125	500	125	500
Sucrose	72.8	291.2	72.8	291.2
Cellulose, BW200	50	0	50	0
Soybean oil	25	225	25	225
Lard	20	180	245	2205
Mineral mix s10026B	50	0	50	0
Vitamin mix V10001C	1	4	1	4
Choline bitartrate	2	0	2	0
FD&C red dye #40	0	0	0	0
FD&C yellow dye #5	0.04	0	0	0
FD&C blue dye #1	0.01	0	0.05	0
Total	1055.05	4037	773.85	4037.2

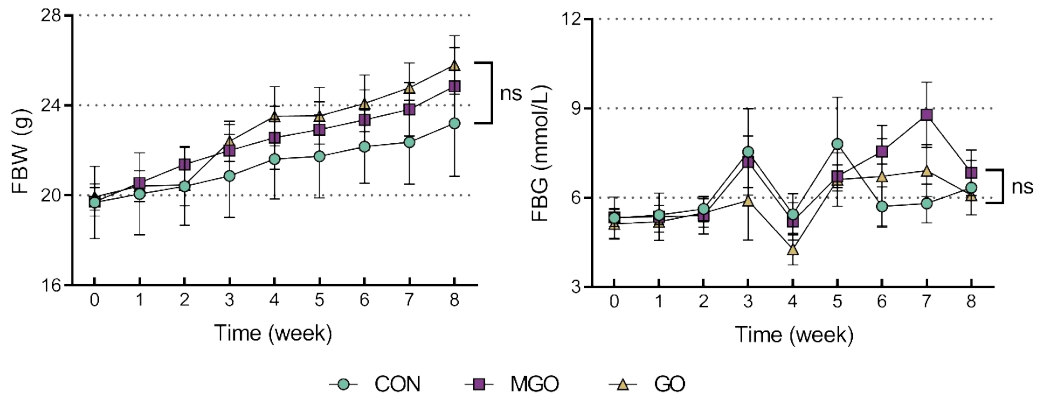
Supplemental Table S2. Selected DEGs in HF-MGO and HF-GO groups and their enriched KEGG pathways.

Group	Gene name	Log ₂ FC	p-value	KEGG pathways
HF-MGO vs HF	Gadd45g	4.86	0.000	MAPK signaling pathway, Apoptosis, FoxO signaling pathway
	Ddit4	8.01	0.000	Autophagy, PI3K-Akt signaling pathway, mTOR signaling pathway
	Fgf21	-8.93	0.001	MAPK signaling pathway, PI3K-Akt signaling pathway
	Ngf	-2.67	0.002	MAPK signaling pathway, Apoptosis, PI3K-Akt signaling pathway
	Prkacb	2.63	0.002	MAPK signaling pathway, Autophagy, Insulin signaling pathway
	Gadd45b	7.02	0.004	MAPK signaling pathway, Apoptosis, FoxO signaling pathway
	Flt1	3.64	0.006	MAPK signaling pathway, PI3K-Akt signaling pathway, HIF-1 signaling pathway
	Tgfb1	7.39	0.019	MAPK signaling pathway, NAFLD, AGE-RAGE signaling pathway in diabetic complications, FoxO signaling pathway
	Ndufv1	1.81	0.026	NAFLD, Alzheimer disease, Oxidative phosphorylation
HF-GO vs HF	Prkca	4.35	0.038	MAPK signaling pathway, AGE-RAGE signaling pathway in diabetic complications, PI3K-Akt signaling pathway
	Gadd45g	4.13	0.000	MAPK signaling pathway, Hepatocellular carcinoma, Apoptosis, FoxO signaling pathway
	Ndufb6	6.28	0.000	NAFLD, Alzheimer disease, Oxidative phosphorylation, Parkinson disease
	Tgfb1	7.30	0.000	NAFLD, AGE-RAGE signaling pathway in diabetic complications, MAPK signaling pathway, Hepatocellular carcinoma, FoxO signaling pathway
	Tgfb2	7.10	0.001	AGE-RAGE signaling pathway in diabetic complications, MAPK signaling pathway, Hepatocellular carcinoma, FoxO signaling pathway
mt-Co3	-1.76	0.007	NAFLD, Alzheimer disease, Oxidative phosphorylation, Parkinson disease	

HF-GO vs HF	mt-Co2	-1.54	0.008	NAFLD, Alzheimer disease, Oxidative phosphorylation, Parkinson disease
	Gadd45b	7.10	0.009	MAPK signaling pathway, Hepatocellular carcinoma, Apoptosis, FoxO signaling pathway
	mt-Cytb	-1.19	0.013	NAFLD, Alzheimer disease, Oxidative phosphorylation, Parkinson disease
	Uqcrl1	2.81	0.022	NAFLD, Alzheimer disease, Oxidative phosphorylation, Parkinson disease
	Col4a6	5.92	0.028	AGE-RAGE signaling pathway in diabetic complications, PI3K-Akt signaling pathway

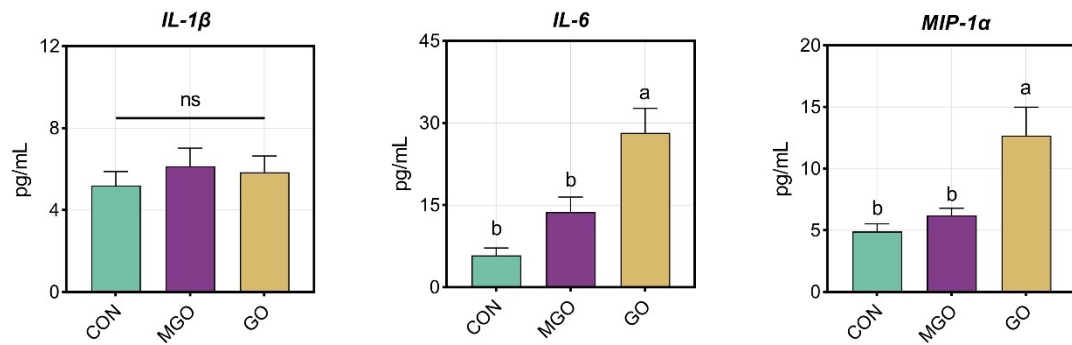
DEGs, differentially expressed genes.

Supplemental Figure S1. Changes in FBW (a) and FBG (b) levels in mice fed a normal diet interfered by α -DCs.



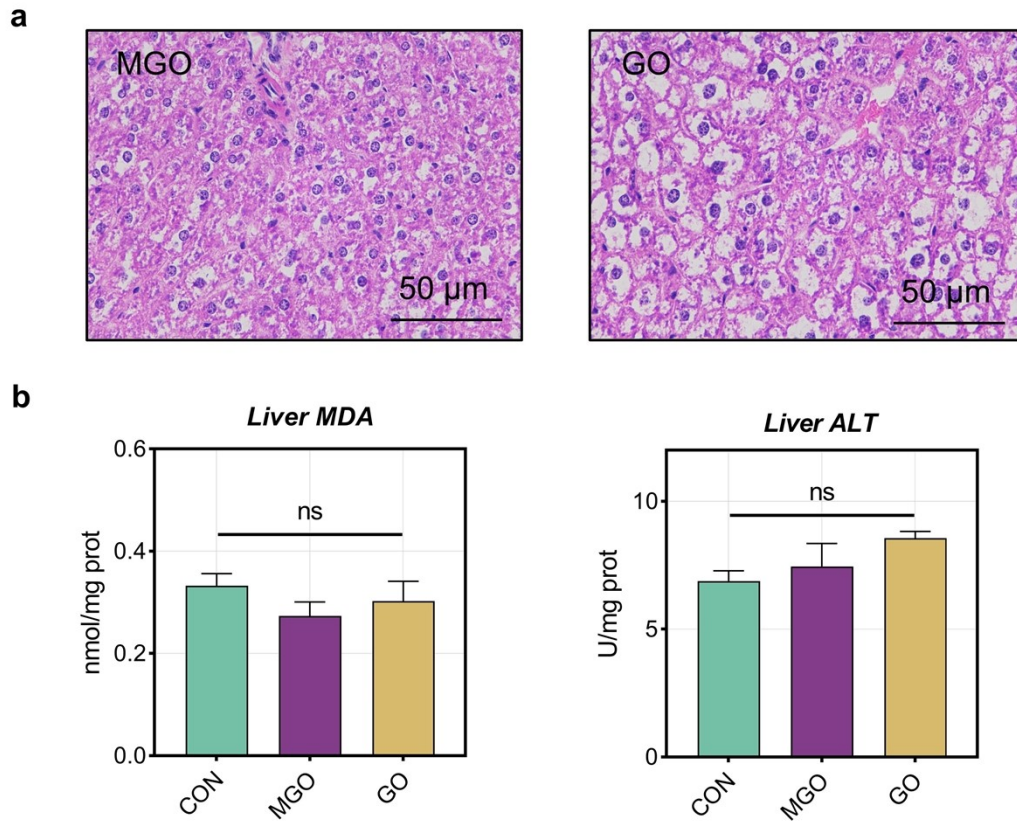
Data were presented as the mean \pm SD ($n = 6$) and values with different letters indicate statistical difference at $p < 0.05$ (Tukey's test). FBW, fasting food weight; FBG, fasting food glucose.

Supplemental Figure S2. Serum levels of IL-1 β , IL-6, and MIP-1 α in mice fed a normal diet interfered by α -DCs.



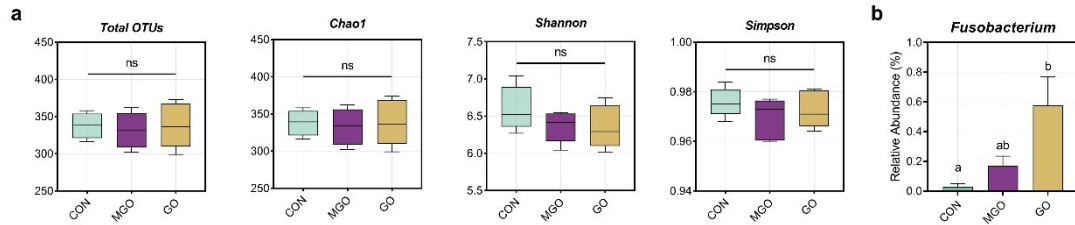
Data were presented as the mean \pm SD ($n = 5$) and values with different letters indicate statistical difference at $p < 0.05$ (Tukey's test). IL-1 β , interleukin-1 β ; IL-6, interleukin-6; MIP-1 α , macrophage inflammatory protein-1 α .

Supplemental Figure S3. Morphological changes (a), hepatic MDA and ALT levels (b) in mice fed a normal diet interfered by α -DCs.



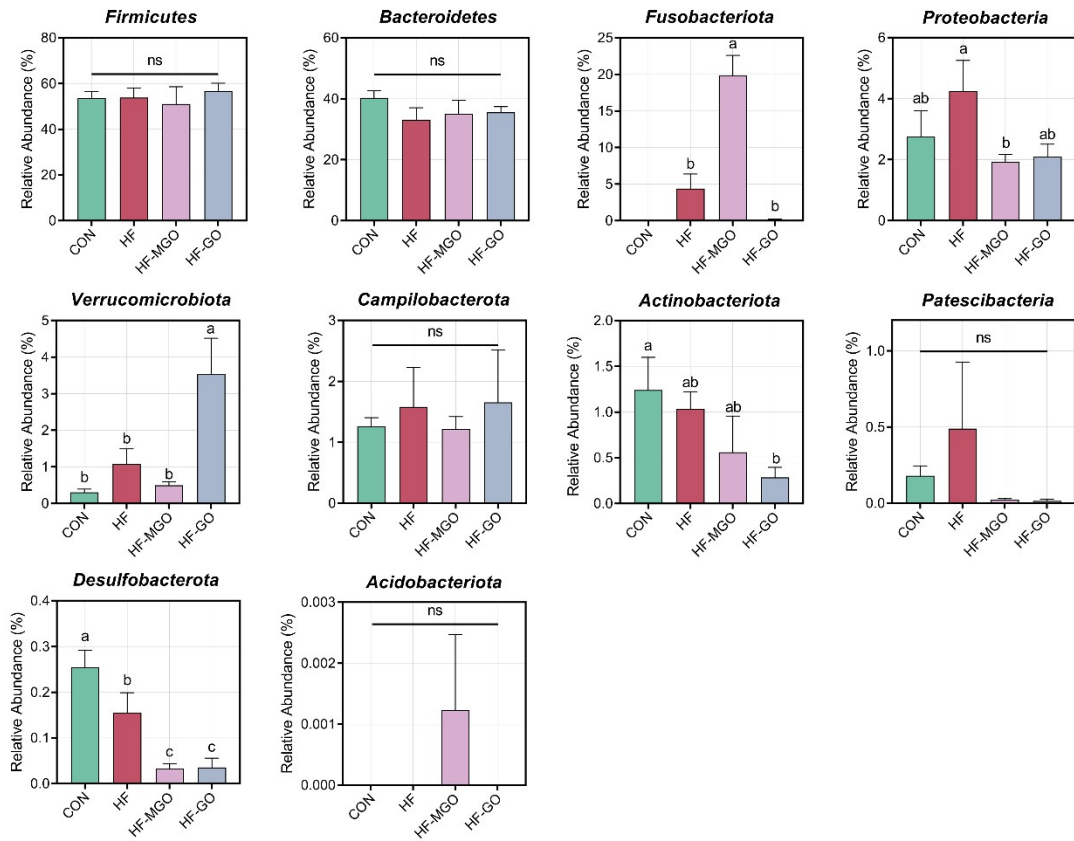
Data were presented as the mean \pm SD ($n = 6$) and values with different letters indicate statistical difference at $p < 0.05$ (Tukey's test). MDA, malondialdehyde; ALT alanine transaminase.

Supplemental Figure S4. Total OTUs, α -diversity indices (a), and relative abundance of *Fusobacterium* (b) in mice fed a normal diet interfered by α -DCs.



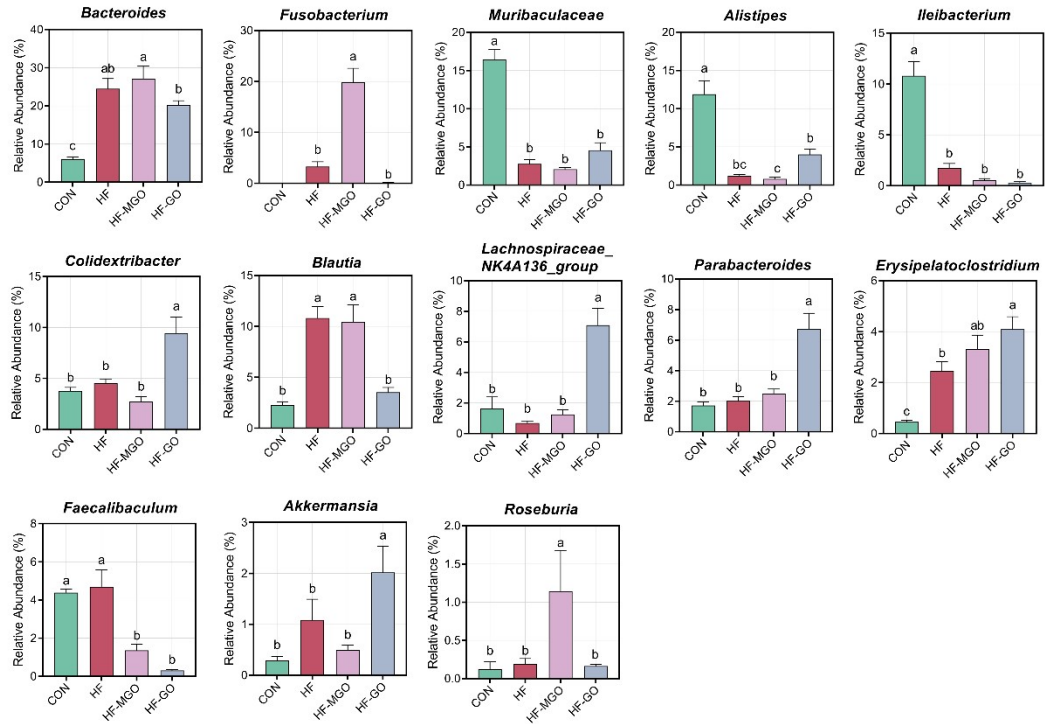
Data were presented as the mean \pm SD ($n = 5$) and values with different letters indicate statistical difference at $p < 0.05$ (Tukey's test).

Supplemental Figure S5. Relative abundance of dominant bacteria at the phylum level.



Data were presented as the mean \pm SD (n = 5) and values with different letters indicate statistical difference at $p < 0.05$ (Tukey's test).

Supplemental Figure S6. Relative abundance of dominant bacteria at the genus level.



Data were presented as the mean \pm SD (n = 5) and values with different letters indicate statistical difference at $p < 0.05$ (Tukey's test)