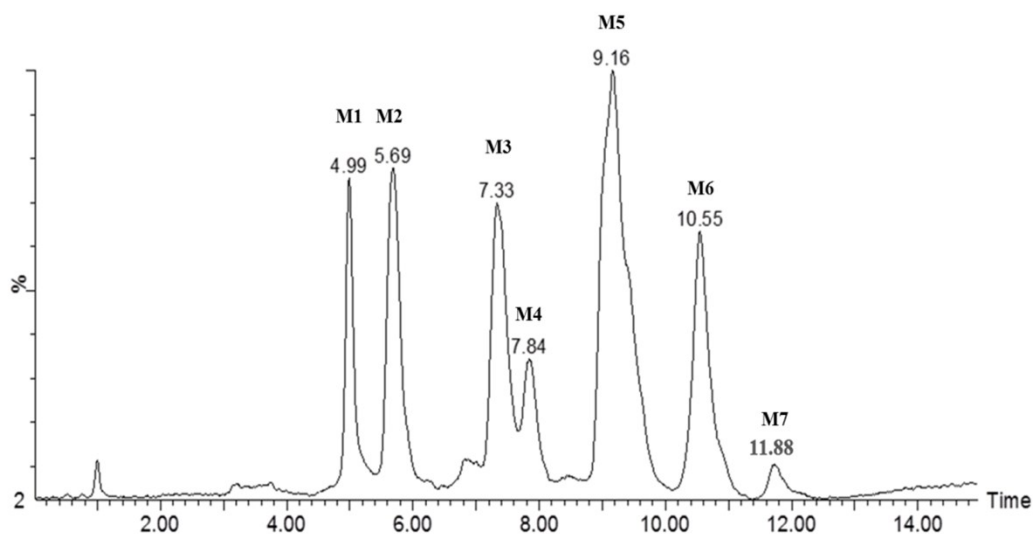


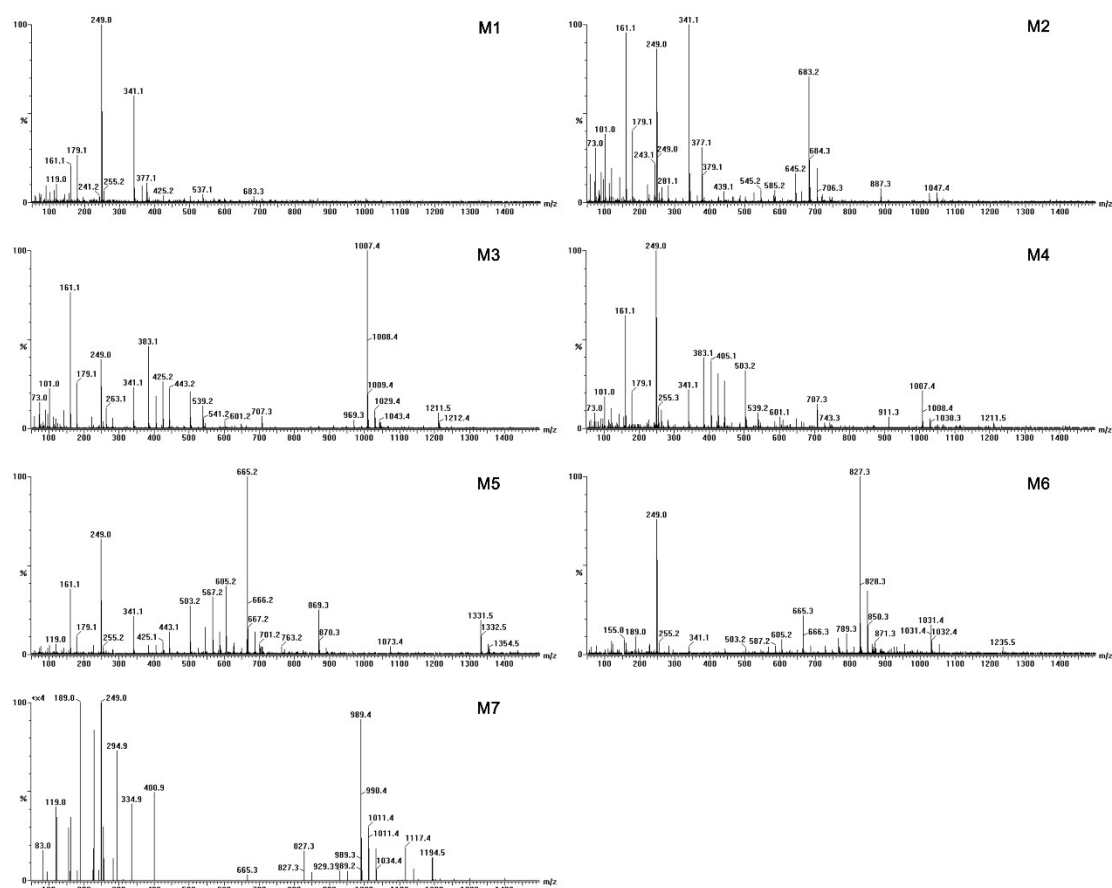
1

Supplementary Information



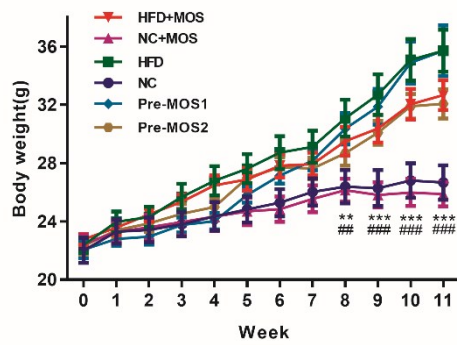
2

3 Fig. S1 HPLC chromatogram of MOS.



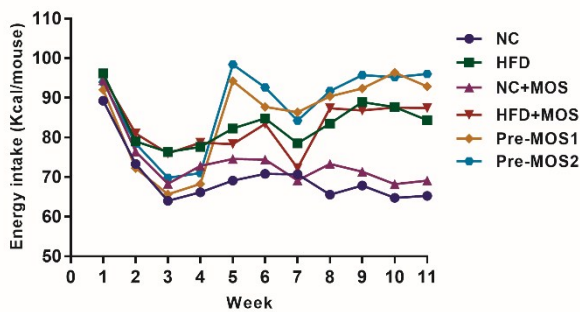
4

5 Fig. S2 ESI-MS spectrum of MOS



6

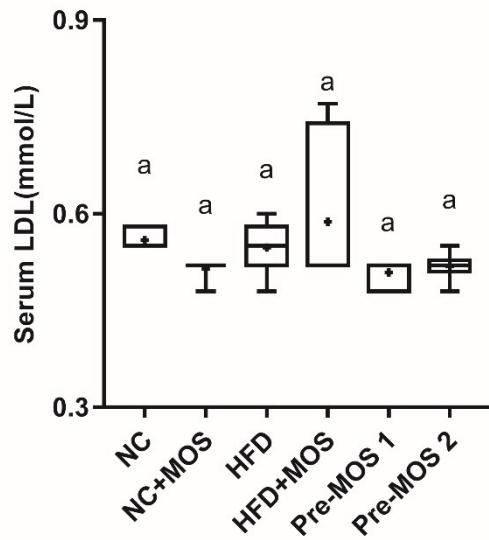
7 Fig. S3 Weight changes of different diets groups during the 11-weeks experiments. Data are shown
 8 as means±SEM. **P<0.01, ***P<0.001: NC group vs. HFD group; ###P<0.01, ####P<0.001:
 9 NC+MOS group vs. HFD group by analysis of two-way ANOVA followed by Tukey's test. n=6 for
 10 each group.



11

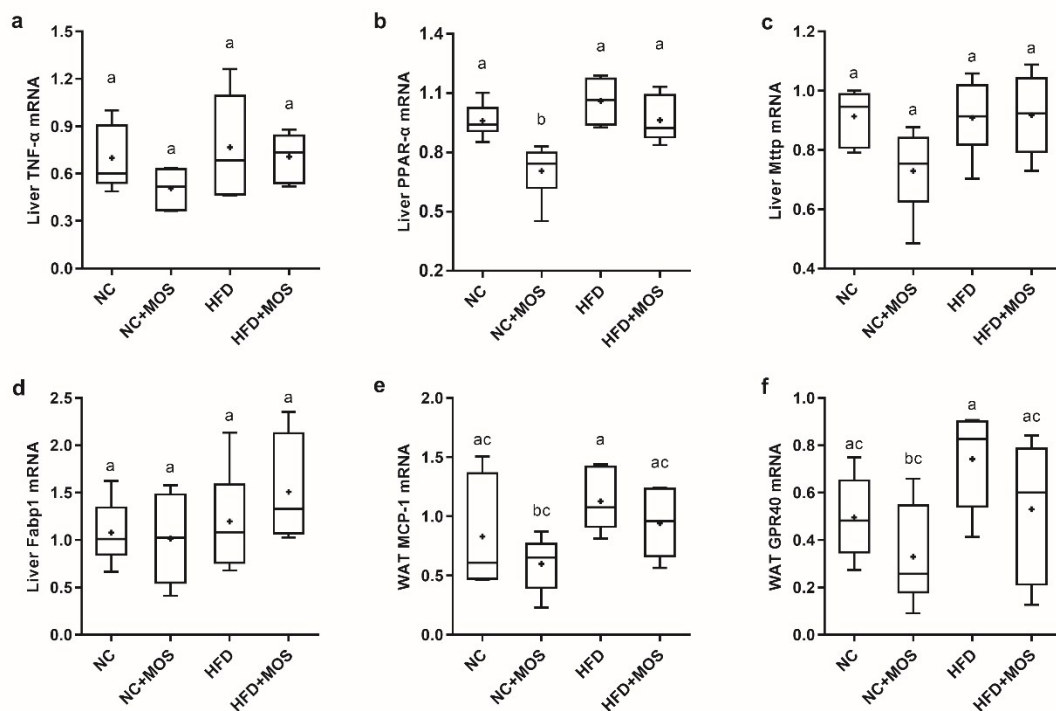
12 Fig. S4 Energy intake of different diets mice during the experiments.

13



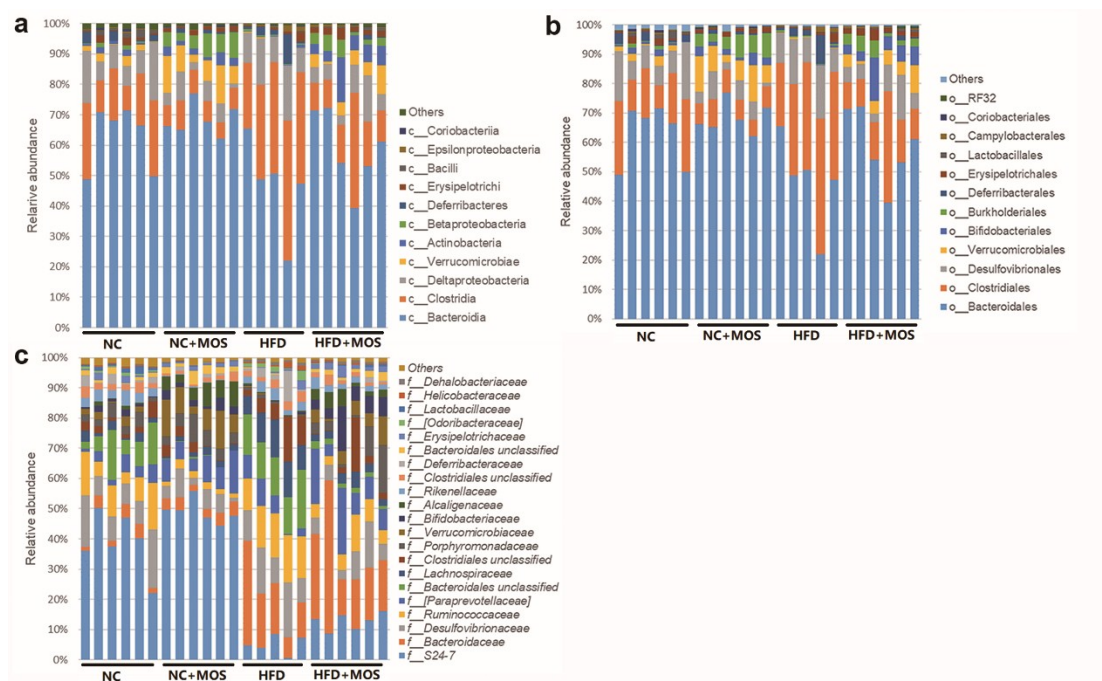
14

15 Fig. S5 Serum LDL of different diets mice. For the box plots, the bottom and top of the box are the
 16 first and third quartiles, and the band inside the box is the second quartile (the median), the ends of
 17 the whiskers represent the minimum and maximum of all of the data, “+” in the box represent the
 18 mean value of each group. Values of each group with different letters are significantly different by
 19 analysis of one-way ANOVA followed by Tukey’s test. n=6 for each group.

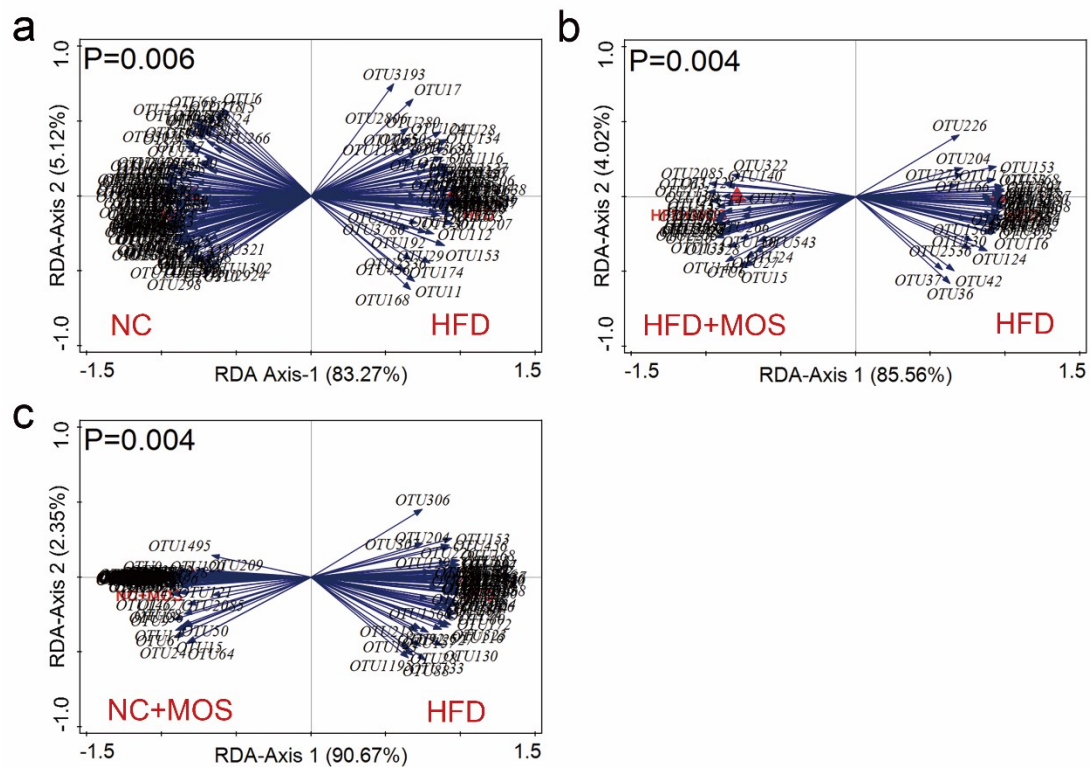


20

21 Fig. S6 Lipid metabolism related genes transcriptional level in liver or WAT. Gene transcriptional
 22 levels of TNF- α (a), PPAR- α (b), and Mttp (c) and Fabp1 (d) in liver; Gene expression levels of
 23 MCP-1 (e) and GPR40 (f) in WAT. For the box plots, the bottom and top of the box are the first and
 24 third quartiles, and the band inside the box is the second quartile (the median), the ends of the
 25 whiskers represent the minimum and maximum of all of the data, “+” in the box represent the mean
 26 value of each group. Values of each group with different letters are significantly different by analysis
 27 of one-way ANOVA followed by Tukey’s test. n=6 for each group.



29 Fig. S7 Microbiota modulated by MOS in different taxa levels. (a) Relative abundance of fecal
 30 microbiota at class level. (b) Relative abundance of fecal microbiota at order level. (c) Relative
 31 abundance of fecal microbiota at family level. n=6 for NC, NC+MOS and HFD+MOS group, n=5
 32 for HFD group.



33

34 Fig. S8 Biplots of altered OTUs from RDA analysis. RDA analysis was performed to compare

35 OTUs of HF-fed mice with NC-fed mice (a), HFD+MOS (b) and NC+MOS (c). OTUs were

36 converted to log10-transformed values. Mouse groups are indicated in red. OTUs that were

37 significantly different (Tukey's HSD test, $P < 0.05$) between the two groups are highlighted by blue

38 arrows. P values calculated with the Monte Carlo permutation procedure (MCPP) are shown in the

39 up left corner.

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47 Table S1 Primers used for qPCR in this study

Mouse Genes	Direction	Sequences (5'-3')
GAPDH	Forward	GTGTTCTACCCCAATGTGT
	Reverse	ATTGTCATACCAGGAAATGAGCTT
leptin	Forward	CCTGTGGCTTTGGTCCTATCTG
	Reverse	AGGCAAGCTGGTGAGGATCTG
adiponectin	Forward	AGGTTGGATGGCAGGC
	Reverse	GTCTCACCTTAGGACCAAGAA
TNF- α	Forward	ACGGCATGGATCTCAAAGAC
	Reverse	AGATAGCAAATCGGCTGACG
CD11c	Forward	CTGGATAGCCTTTCTTCTGCTG
	Reverse	GCACACTGTGTCCGAATC
TLR-4	Forward	GAAACGGCAACTTGGACCTG
	Reverse	TTCTTTTCCCGAGTTAGGTA
GPR43	Forward	TGTTTCAGTTCCCTCAATGCCA
	Reverse	CAGGATTGCGGATCAGTAGCA
PPAR- γ	Forward	CAGGCTTGCTGAACGTGAAG
	Reverse	GGAGCACCTTGGCGAACA
PPAR- α	Forward	CAGTGCCCTGAACATCGAGTGT
	Reverse	TTCGCCGAAAGAA GCCCTT
Mtp	Forward	ATACAAGCTCACGTACTCCACT
	Reverse	TCCACAGTAACACAACGTCCA
Fabp1	Forward	AAAGGAAACCTCATTGCCACCA
	Reverse	AATGTCGCCCCAATGTCATGGTA
MCP-1	Forward	TTAAAAACCTGGATCGGAACCAA
	Reverse	GCATTAGCTTCAGATTTACGGGT
GPR40	Forward	TGGCTAGTTTCATAAACCCGG
	Reverse	TCCCAAGTAGCCATGGACCAGT