

Table S1. qPCR primer sequences.

Gene	Sequence 5'- 3'
GAPDH	FW: CCATCACCATCTTCCAGGAG RV: CCTGCTTCACCACCTTCTTG
TNF- α	FW: CACCACGCTCTTCTGTCTACT RV: CCACTTGGTGGTTTGTGAGTG
IL-1 β	FW: GTGTCTTCCCGTGGACCTT RV: AATGGGAACGTCACACACCA
IL-10	FW: GCGCTGTCATCGATTTCTC RV: ATGGCCTGTAGACACCTTGG
MCP-1	FW: CTGCATCTGCCCTAAGGTCT RV: AGTGCTTGAGGTGGTTGTGG
PAI-1	FW: TGGAAGGGCAACATGACCAG RV: TCAGGCATGCCCAACTTCTC
IFN- γ	FW: GCGTCATTGAATCACACCTGA RV: CTGGACCTGTGGGTTGTTGA
CD36	FW: GAAGAAGGAACCACTGC RV: CTACAGCCAGATTCAGAAC
Fasn	FW: TGGAGGAGGTGGTGATAG RV: AGTGAGGCTGGGTTGATA
PPAP- γ	FW: CCACCAACTTCGGAATC RV: GCTCTTGTGAATGGAATGTC

Table S2. The tissue weights and intestinal length of mice

	HFD	HFD+CPO	CHOW	CHOW+CPO
Intestinal length (cm)	44.26 ± 2.01	43.85 ± 1.81	42.29 ± 3.26	42.59 ± 1.79
Liver (g)	1.11 ± 0.13	1.01 ± 0.11 [#]	1.00 ± 0.19 ^{**}	1.01 ± 0.08
Heart(g)	0.11 ± 0.01	0.11 ± 0.01	0.11 ± 0.01	0.11 ± 0.01
Spleen(g)	0.06 ± 0.01	0.07 ± 0.02	0.06 ± 0.02	0.06 ± 0.01
Kidney(g)	0.34 ± 0.02	0.33 ± 0.02	0.30 ± 0.04 [*]	0.30 ± 0.02
Pancreas(g)	0.21 ± 0.04	0.17 ± 0.03	0.18 ± 0.04	0.17 ± 0.03

Values are means ± SD., n = 10. ^{**}*P* < 0.01 for CHOW vs. HFD; [#]*P* < 0.05 for HFD+CPO vs. HFD.

Table S3. The sequencing reads statistics of samples in different groups.

Samples	Sequencing reads
HFD1	73386
HFD2	75241
HFD3	79644
HFD4	75501
HFD5	76722
HFD6	71467
Mean	75327
HFD+CPO1	75222
HFD+CPO2	72680
HFD+CPO3	78270
HFD+CPO4	77946
HFD+CPO5	71473
HFD+CPO6	73230
Mean	74804
CHOW1	75207
CHOW2	75760
CHOW3	76709
CHOW4	80116
CHOW5	74061
CHOW6	78414
Mean	76711

Table S4. Potentiale biomarkers associated with CPO treatment in mouse plasma

	Metabolites	KEGG ID	HMDB ID	Formula	tR/min	Mass(m/z)	FCs	FCT	HFD vs CHOW	HFD+CPO vs HFD	pathway
1	2-methylhistamine	C17928	--	C6H11N3	0.77	125.09	1.51	0.52	Up	Down	
2	3-dehydrocarnitine	C02636	HMDB0012154	C7H13NO3	0.79	159.09	0.62	1.69	Down	Up	
3	4-methylphenol	C01468	HMDB0001858	C7H8O	3.74	108.06	0.42	2.24	Down	Up	a
4	8'-hydroxyabscisate	C15514	--	C15H20O5	4.17	280.13	1.72	0.56	Up	Down	b
5	albuterol	C11770	HMDB0001937	C13H21NO3	4.46	239.15	3.54	0.50	Up	Down	
6	beta-ionone	C12287	HMDB0036565	C13H20O	4.52	192.15	0.57	1.64	Down	Up	
7	boschnaloside	C11652	--	C16H24O8	3.68	344.15	2.07	0.41	Up	Down	
8	capsi-amide	C17515	HMDB0040940	C17H35NO	7.75	269.27	0.34	1.68	Down	Up	
9	cortisol	C00735	HMDB0000063	C21H30O5	4.16	362.21	1.94	0.47	Up	Down	c,d
10	decylubiquinol	C15495	--	C19H32O4	5.47	324.23	0.42	1.55	Down	Up	

11	elaecanane c	C10592	--	C12H21NO2	3.65	211.16	0.56	2.23	Down	Up	
12	fusidic acid	C06694	HMDB0015570	C31H48O6	5.87	516.34	1.58	0.54	Up	Down	
13	isodomedin	C09115	--	C22H32O6	4.38	392.22	1.51	0.56	Up	Down	
14	L-kynurenine	C00328	HMDB0000684	C10H12N2O3	2.96	208.08	1.75	0.57	Up	Down	e
15	oleamide	C19670	HMDB0002117	C18H35NO	7.62	281.27	1.61	0.65	Up	Down	
16	palmitoyl ethanolamide	C16512	HMDB0002100	C18H37NO2	5.06	299.28	13.58	0.12	Up	Down	f
17	piperidine	C01746	HMDB0034301	C5H11N	1.90	85.09	0.65	1.61	Down	Up	
18	pseudouridine	C02067	HMDB0000767	C9H12N2O6	1.23	244.07	0.65	1.76	Down	Up	g
19	sulcatone	C07287	HMDB0035915	C8H14O	3.52	126.10	2.27	0.67	Up	Down	
20	taurochenodeoxycholic acid	C05465	HMDB0000951	C26H45NO6S	4.60	516.32	0.11	12.22	Down	Up	h,i,j

a: Protein digestion and absorption; b: Carotenoid biosynthesis; c: Bile secretion; d: Neuroactive ligand-receptor interaction; e: Tryptophan metabolism; f: Neuroactive ligand-receptor interaction; g: Pyrimidine metabolism; h: Primary bile acid biosynthesis; i: Secondary bile acid biosynthesis; j: Cholesterol metabolism

