Supplement materials

Table S1. Sequence, purity, molecular weight, source, and CMSR of cholesterol-lowering flaxseed peptides synthesized by Solid-phase peptide synthesis.

Sequence	Purity (%)	molecular weight (Da)	Source	CMSR (%)
IPPF	**98.6**	**473**	**Flaxseed (Linum usitatissimum) NADH dehydrogenase subunit F (423-426) 418LSLCGIPPFACFW430**	**93.5±2.3**
IIPAF	98.9	560	Flaxseed (*Linum usitatissimum*) NADH dehydrogenase subunit F (11-15) 1MQHXTYSYSW**IIPAF**TLLVP20	82.8±1.8
LNFF	98.6	540	Flaxseed (*Linum usitatissimum*) NADH dehydrogenase subunit F (133-136) 131KV**LNFF**GFNGQHVLRWFAKR150	77.8±0.2
LLGTL	97.0	516	Flaxseed (*Linum usitatissimum*) NADH dehydrogenase subunit F (114-119) 111QSA**FLLGTL**SLCGIPPFACF130	88.0±1.8
IIF	96.7	392	Flaxsee（*Linum usitatissimum*）LINUS Chloroplast envelope membrane protein(17-19) 11FYLTSX**IIF**LPWWIS25	80.3±1.4
LLGA	99.2	373	Flaxseed (Linum usitatissimum) NADH dehydrogenase subunit F (18-21) 12VGIITV**LLGA**TLALAQ27	87.1±1.5

Table S2. The detailed components of experimental diets.

Component	Normal diet		High cholesterol and High fat diet	
	%	kcal	%	kcal
Casein	19	800	22.3	800
L-Cystine	0.28	12	0.33	12
Corn Starch	36.6	1544.6	23.6	848
Maltodextrin	11.9	500	7.91	284
Sucrose	19	800	13.9	497.64
Cellulose	4.74	0	5.57	0
Soybean Oil	2.37	225	2.79	225
Lard	1.9	180	17.3	1395
Mineral Mix S10020	0.47	0	0.56	0
Calcium Phosphate	1.23	0	1.45	0
Calcium Carbonate	0.52	0	0.61	0
Potassium Citride,1 H_2O	1.56	0	1.84	0
Sodium Chloride	0.25	0	0.29	0
Vitamin Mix V10001C	0.095	4	0.11	4
Choline Bitartrate	0.19	0	0.22	0
Cholesterol	0	0	1.25	0
Total		4065.6		4065.64

Table S3. Primers used for real-time RT-PCR

Gene name	Forward primer	Reverse primer
Gapdh	CCTCGTCCCGTAGACAAAATG	TGAGGTCAATGAAGGGGTCGT
Srebp2	CAAGATGCACAAGTCTGGCGTT	GATGCCCTTCAGGAGCTTGTT
Cyp7a1	TCTGGGCATCTCAAGCAAACA	TGATGCTATCTAGTACTGGCAGGTT
Hmgcr	ACAGCGGAGCAGGCTAAGGT	TTTGAGGTCACGACGGGAGA
Abcg5	TGCCAGCAGAAGTGGGACAG	CTCGCAGCCATTCACAAACA
Abcg8	TGCTGGTCCTTATTTCTTTGCC	AGGAGTTGTAGAGGGCATTGCA
Lxrα	TCATCAAGGGAGCACGCTATGT	CTTGAGCCTGTTCCTCTTCTTGC
Pparα	TTTCACAAGTGCCTGTCTGTCG	TCTTCAGGTAGGCTTCGTGGAT
Srb1	AATGTCCGCATAGACCCGAG	CGTTTGGGTTGACCACTTCG
Ldlr	GTTCCTGTCCATCTTCTTCCCTA	TTCTGGTAGACTGGGTTGTCAAAG

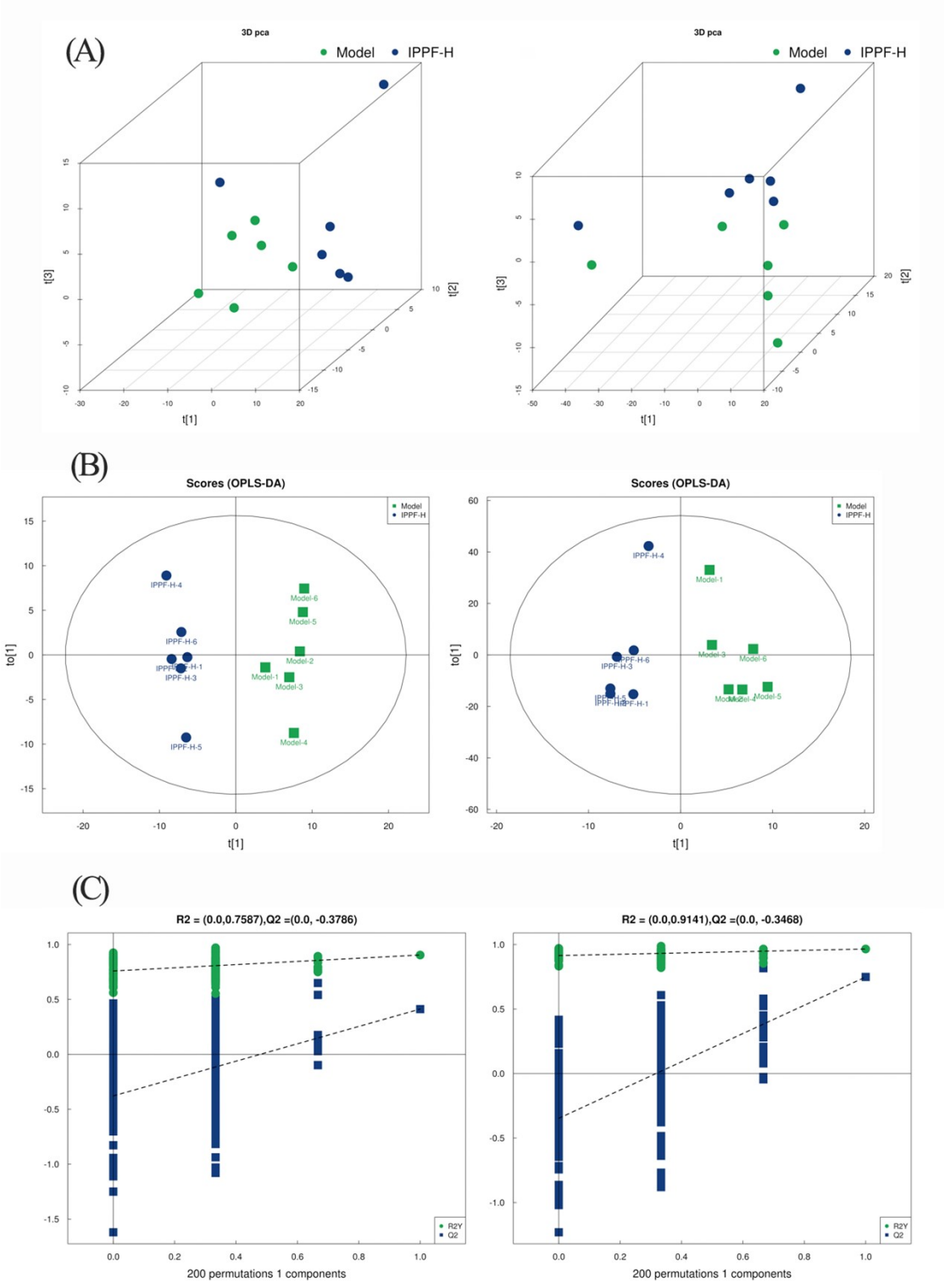

Figure S1 Principal component analysis (A), OPLS-DA score (B) and OPLS-DA permutation test (C) of Model group vs IPPF-H group under positive and negative ion mode