

## Supplementary Method

### Metabolites qualitative and quantitative analysis

Based on the self-database MWDB (metware database) and the public database of metabolites information, qualitative analysis of the first-order and second-order spectra detected by mass spectrometry was carried out. Some of these substances are qualitatively analyzed, removing isotopic signals, repetitive signals containing K<sup>+</sup> ions, Na<sup>+</sup> ions, and NH<sub>4</sub><sup>+</sup> ions, as well as repeated signals of fragmented ions that themselves are of larger molecular weight. Metabolite structure resolution is referenced in MassBank, KNAPSAcK, HMDB, existing mass spectrometry public databases such as MoTo DB and METLIN.

Quantitation of metabolites was accomplished using multiple reaction monitoring (MRM) triple quadrupole mass spectrometry. In the MRM mode, the quadrupole rod first screened precursor ions (parent ions) of the target substance to exclude ions corresponding to other molecular weight substances to initially eliminate the interference; the precursor ions were induced to ionize in the collision cell to form many fragment ions, fragment ions And then through the triple quadrupole filter to select the desired one of the characteristic fragment ions, excluding non-target ion interference, making more accurate quantitative and better repeatability. After obtaining the mass spectral analysis data of different samples, the peak areas of all the mass spectral peaks are integrated, and the mass spectral peaks of the same metabolites in different samples are integrated and corrected.

From the samples, aliquots of each of the individual samples were combined to make technical replicates, which were extracted as described above. During instrumental analysis, a control sample was inserted into every 10 test samples to monitor the reproducibility of the analysis. Extracts of this pooled sample were injected to assess process variability. As an additional QC, water aliquots were extracted as part of the sample set to serve as process blanks for artifact identification. By overlapping display analysis of the total ion chromatogram (TIC) of different QC samples for mass spectrometric detection and analysis, the repeatability of the extraction and detection of metabolites can be judged, that is, technical repeatability. The high stability of the instrument provides an important guarantee for the repeatability and reliability of the data.

Figure S1

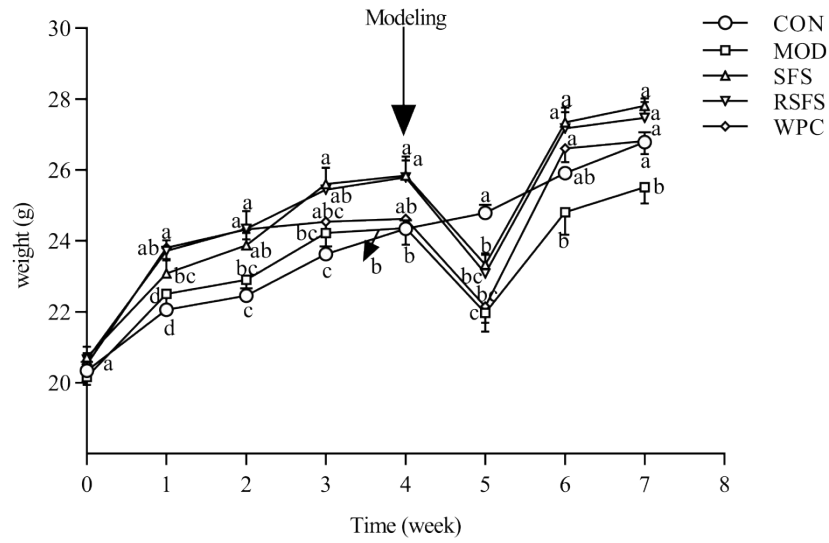


Fig. S1 Effects of deoiled sunflower seeds (SFS) on body weight. (n=10/group, Values in each column without a common lowercase letter are significantly different ( $P < 0.05$ ). The letter is the same, indicating no significant difference ( $P > 0.05$ )).

Figure S2

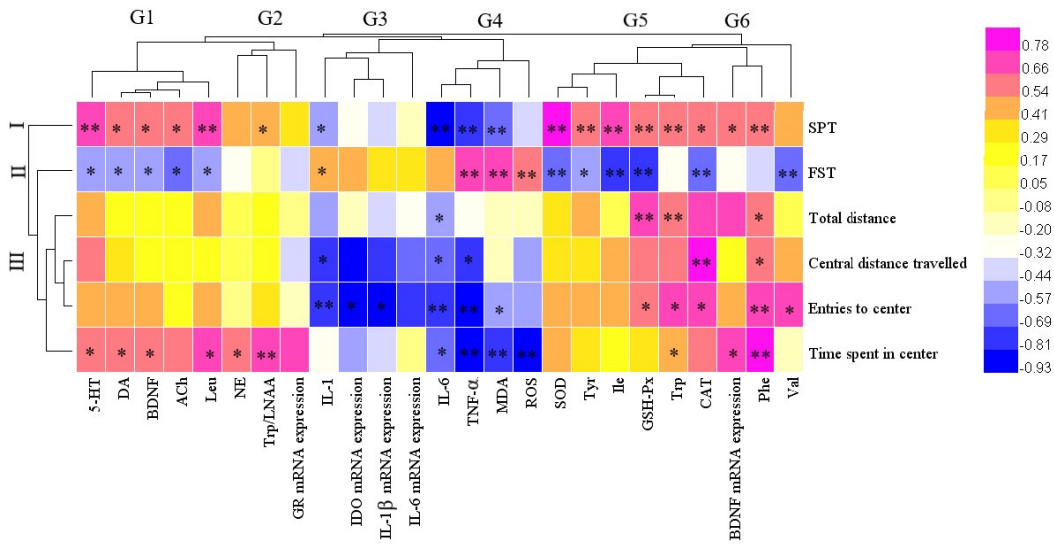


Fig. S2 Correlation heat map of behavioral indicators and biochemical indicators  
 Note: The x-axis and y-axis of the heat map are biochemical and behavioral indicators respectively, and the  $R$  value and  $P$  value are obtained by calculation. The  $R$  value is represented by different colors in figure, and the color card on the right is the color interval of different  $R$  values. \* was significantly correlated at the 0.05 level; \*\* was significantly correlated at the 0.01 level. The top represents the cluster of behavioral indicators, and the right is the cluster of biochemical indicators.

Table S1. Amino acid composition

AAs (g/100 g pro)	Soy protein	SFS/RSFS	WPC
Lys	6.40	3.35	10.25
Met + Cys	2.58	3.18	4.18
Thr	4.10	5.40	7.82
Ile	5.30	8.71	8.25
Leu	8.06	11.31	12.03
Phe + Tyr	8.61	14.15	6.65
Val	4.93	10.30	7.54
Trp	1.30	2.35	1.22
Glu	17.89	45.06	22.92
Arg	8.12	16.58	3.06
Asp	11.43	19.97	13.23
Gly	4.57	9.80	2.25
Pro	5.33	8.12	7.86
Ala	4.41	7.96	6.26
Ser	5.28	6.07	4.77
His	2.77	4.94	2.14

Note: Soy protein (Protein: 80 g /100 g); SFS, deoiled sunflower seeds (Protein: 38.2 g/100 g, chlorogenic acid: 2.04 g/100 g); RSFS, deoiled and dechlorogenic acid sunflower seeds (Protein: 38.2 g/100 g, chlorogenic acid: undetected); WPC, whey protein (Protein: 66.27 g/100 g). AAs, amino acids; Lys, lysine; Met, methionine; Cys, cysteine; Thr, threonine; Ile, isoleucine; Leu, leucine; Phe, phenylalanine; Tyr, tyrosine; Val, valine; Trp, tryptophan; Glu, glutamic acid; Arg, arginine; Asp, aspartic acid; Gly, glycine; Pro, proline; Ala, alanine; Ser, serine; His, histidine.

Table S2. Composition of animal feed (g/kg)

Composition	CON	MOD	SFS	RSFS	WPC
Protein	140	140	140	140	140
(Protein material)	(175)	(175)	(367)	(367)	(211)
Sucrose	100.3	100.3	100.3	100.3	100.3
Corn starch	548	548	460.8	460.8	534.4
Sunflower oil	85	85	0	0	82.2
Mixed minerals (AIN-93M-MX)	27.3	27.3	27.3	27.3	27.3
Mixed vitamins	10	10	10	10	10
Fiber	50	50	32.1	32.1	47.7
Choline	2.3	2.3	2.3	2.3	2.3
Total protein supply (%)	14.7	14.7	14.7	14.7	14.7
Total oil and fat supply (%)	18.1	18.1	18.1	18.1	18.1
Total carbohydrate supply (%)	75.8	75.8	75.8	75.8	75.8
Energy supply ratio (KJ/g)	21.39	21.39	21.39	21.39	21.39

Note: The mineral mixture was prepared according to AIN-93M-MX; Mixed vitamins (mg/kg): VA 4000 IU; VD3 1000 IU; VE 50 IU; VB3 30; VB5 16; VB6 7; VB1 6; VB2 6; VB11 2; VK3 2; VB12 0.01; VH 0.2 mg/kg. Protein: actual protein content per kg of diet; Protein material: actual dose of protein material added per kg of diet.

Table S3. Primer sequences of the genes

Gene	Forward primer (5'→3')	Reverse primer Primer R (5'→3')
β-actin	GGCTGTATTCCCCTCCATCG	CCAGTTGGTAACAATGCCATGT
BDNF	TTATTTCATACTTCGGTTGC	TGTCAGCCAGTGATGTCG
GR	AGCTCCCCCTGGTAGAGAC	GGTGAAGACGCAGAAACCTT
IDO	GCTTTGCTCTACCACATCCAC	CAGGCGCTGTAACCTGTGT
IL-1β	GCAACTGTTCTGAACTCAACT	ATCTTTTGGGGTCCGTCAACT
IL-6	TGGAGTCACAGAAGGAGTGGCTAA	TCTGACCACAGTGAGGAATGTCCA
	G	C

Abbreviations: BDNF, brain-derived neurotrophic factor; GR, glucocorticoid receptor; IDO, indoleamine 2,3-dioxygenase; IL-1β, interleukin 1β; IL-6, interleukin 6.

Table S4. Identified differential metabolites in hippocampus

Compounds ID	MOD vs CON				SFS vs MOD				RSFS vs MOD				WPC vs MOD			
	VIP	FC	P	Type	VIP	FC	P	Type	VIP	FC	P	Type	VIP	FC	P	Type
Lysopc 16:0	5.07	0.63	<0.01	Down	6.20	1.70	<0.01	Up	4.58	1.51	<0.01	Up	4.90	1.40	0.014	Up
Lysopc 18:0	5.40	0.58	<0.01	Down	6.56	1.88	<0.01	Up	5.38	1.78	<0.01	Up				
Lysopc 18:1	4.85	0.51	<0.01	Down	5.46	2.02	<0.01	Up	4.34	1.83	<0.01	Up				
Lysopc 18:3	2.72	0.64	<0.01	Down	3.65	1.76	<0.01	Up	2.83	1.59	<0.01	Up	2.79	1.42	0.043	Up
Lysopc 16:0	3.21	0.61	<0.01	Down	3.54	1.70	<0.01	Up	3.03	1.59	<0.01	Up				
Lysopc 18:0	4.10	0.65	<0.01	Down	4.45	1.61	<0.01	Up	4.04	1.59	<0.01	Up				
Lysopc 18:1	2.26	0.64	<0.01	Down	2.38	1.71	0.05	Up	2.35	1.67	<0.01	Up				
PAF C-16	5.57	0.59	<0.01	Down	6.88	1.87	<0.01	Up	5.67	1.77	<0.01	Up				
Cis-3-Hexenyl acetate	6.11	1.55	<0.01	Up	5.56	0.74	<0.01	Down	5.93	0.68	<0.01	Down	5.22	0.78	<0.01	Down
Ethyl dodecanoate	1.29	1.62	<0.01	Up	1.15	0.73	<0.01	Down	1.15	0.67	<0.01	Down	1.17	0.76	<0.01	Down
Butyl Isovalerate	1.85	1.82	<0.01	Up	1.47	0.70	<0.01	Down	1.62	0.66	<0.01	Down	1.79	0.65	<0.01	Down
Butanoic acid	2.60	1.73	<0.01	Up	2.24	0.71	0.042	Down	2.29	0.66	0.039	Down	2.65	0.58	0.02	Down
Undecylenic acid													1.06	0.47	<0.01	Down
Cholesterol									1.01	0.59	<0.01	Down	1.30	0.54	<0.01	Down
2-Nonanone	6.03	1.51	<0.01	Up	5.64	0.74	<0.01	Down	6.00	0.69	<0.01	Down	5.67	0.76	<0.01	Down
L-Dihydroorotic Acid	5.65	1.61	<0.01	Up	4.63	0.75	0.011	Down	5	0.67	<0.01	Down	3.79	0.82	0.034	Down
6-Methylmercaptapurine	4.90	1.43	<0.01	Up	4.47	0.78	<0.01	Down	4.85	0.72	<0.01	Down	4.72	0.77	<0.01	Down
Phosphocholine	1.35	1.47	0.023	Up	1.48	0.71	<0.01	Down	1.43	0.69	0.004	Down	2.04	0.54	<0.01	Down
2,6-Dihydroxypurine	1.78	0.67	0.012	Down												
D-Fructose	1.06	1.25	<0.01	Up												
6-phosphogluconic acid trisodium salt	2.45	1.42	<0.01	Up	1.92	0.84	0.024	Down	2.84	0.66	<0.01	Down	3.25	0.64	<0.01	Down
L-Lysine									1.53	1.41	0.037	Up				
L-Leucine													3.96	1.47	0.012	Up

L-Proline													1.03	1.33	<0.01	Up
DL-stachydrine	1.28	1.55	0.018	Up	1.42	0.67	0.03	Down	1.37	0.65	0.017	Down	1.50	0.64	0.041	Down
Creatine													1.11	1.24	0.015	Up
Pantetheine	1.64	1.58	<0.01	Up	1.15	0.80	0.014	Down	1.36	1.29	<0.01	Up				
2-Acetylfuran	2.09	1.50	<0.01	Up	2.07	0.72	0.017	Down	2.45	0.60	<0.01	Down	2.26	0.66	0.015	Down

---