

Supplementary Materials

Quantitative proteomics of plasma and liver reveals the mechanism of turmeric in preventing hyperlipidemia in mice

Meiqin Wang,^{‡a} Runjing Wang,^{‡a} Lieyao Li,^a Yingfei Yan,^a Shuailong Jia,^b Hongliang Jiang^{*a} and Zhifeng Du^{*a}

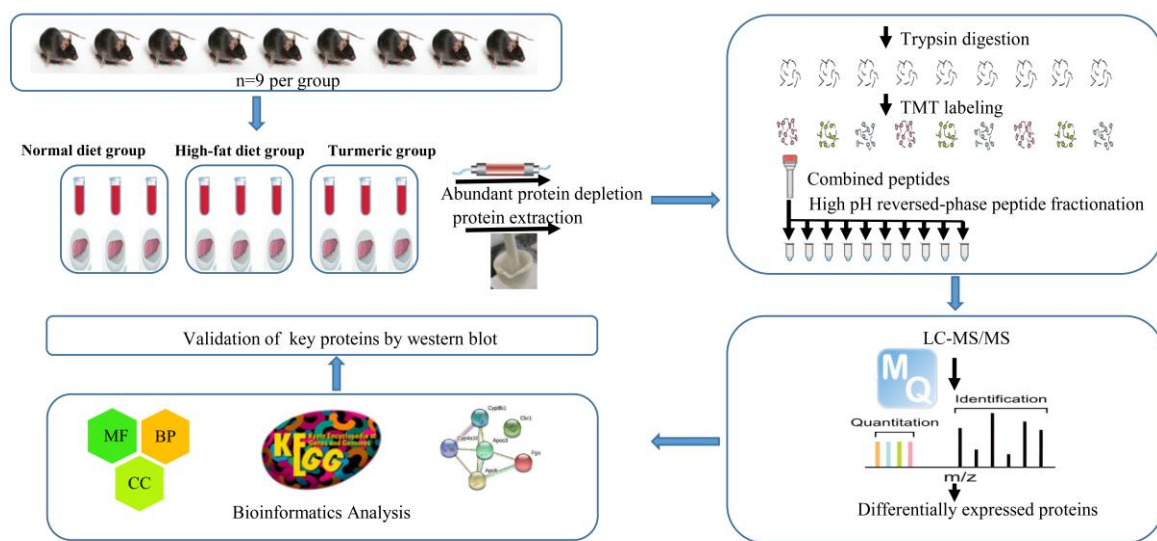
^a Tongji School of Pharmacy, Huazhong University of Science and Technology, Wuhan 430030, China;

^b Department of Pharmacy, Union Hospital, Tongji Medical College, Huazhong University of Science and Technology, Wuhan 430030, China

*Corresponding author: Hongliang Jiang; E-mail: jianghongliang@hust.edu.cn; Tel/Fax: 011-86-27-66663909.

*Corresponding author: Zhifeng Du; E-mail: duzhifeng@hust.edu.cn

[‡] These authors contributed equally to this work.



Scheme S1. The workflow for this study.

Table S1. The calibration curves of curcuminoids by HPLC-UV

Compound	Regression equation	r^2	Concentration range($\mu\text{g/mL}$)
Curcumin	$y = 1.7657x - 2.5417$	0.9996	10-120
Desmethoxycurcumin	$y = 1.4291x - 1.6144$	0.9989	4-48
Bisdesmethoxycurcumin	$y = 1.9584x - 0.5827$	0.9978	0.5-6

Table S2. Food intake and body weight of mice fed with turmeric for 8 weeks.

Groups	n	Food intake (g/mouse*day)	Initial weight (g)	Final weight (g)
ND	9	3.32 $\pm$ 0.24	23.71 $\pm$ 2.06	28.82 $\pm$ 2.15
HFD	9	3.17 $\pm$ 0.16	23.98 $\pm$ 2.11	33.14 $\pm$ 2.62***
TUR	9	3.42 $\pm$ 0.25	23.80 $\pm$ 2.08	30.13 $\pm$ 1.43 [#]

The values are display as mean $\pm$ SD in each group. Compared with ND group, *** $p < 0.001$; compared with HFD group, [#] $p < 0.05$

Table S3. Differentially expressed proteins in plasma of HFD vs ND group mice.

Protein ID	Protein name	HFD/ND Ratio	HFD/ND <i>p</i> - value
O35744	Chitinase-like protein 3	0.809	0.027
O55111	Desmoglein-2	0.81	0.035
P01592	Immunoglobulin J chain	0.676	0.014
Q3UWC2	Serum amyloid A protein	0.373	0.047
Q4FK40	Apoe protein	1.541	0.0001
P09813	Apolipoprotein A-II	1.23	0.036
Q545I9	Protein S100	1.511	0.029
P27656	Hepatic triacylglycerol lipase (HL)	1.301	0.012
P34928	Apolipoprotein C-I	1.894	0.005
P47877	Insulin-like growth factor-binding protein 2	1.299	0.014
P50543	Protein S100-A11	1.558	0.024
P51437	Cathelicidin antimicrobial peptide	1.421	0.015
P51910	Apolipoprotein D	1.615	0.001
A0A0G2JGC1	Serine/threonine-protein phosphatase	0.783	0.023
Q3TYD5	Uncharacterized protein	0.819	0.024
P97399	Dentin sialophosphoprotein	0.715	0.029
Q3V2G1	Uncharacterized protein	1.215	0.004
Q3UJG0	Apoc2 protein	1.329	0.013
Q5BKQ4	Inactive pancreatic lipase-related protein 1	0.786	0.022
Q6F3F9	Adhesion G-protein coupled receptor G6	0.793	0.042
Q80W93	Hydrocephalus-inducing protein	0.496	0.006
Q80YX1	Tenascin	0.792	0.032
Q08EE6	Tsku protein	1.299	0.044
Q8VC49	Interferon alpha-inducible protein 27-like protein 2B	1.687	0.0002
Q3UER1	Fructose-bisphosphate aldolase	1.396	0.02
Q3URM4	Thioredoxin domain-containing protein	0.716	0.002
Q9Z0K8	Pantetheinase	1.446	0.018
A0A075B5R5	Immunoglobulin heavy variable 4-1	0.716	0.018
A0A0F7R5U8	MAB 110 light chain	0.559	0.008
E9Q4Y1	Alcohol dehydrogenase 6A	0.775	0.004
B7ZNY4	ErbB2ip protein	0.466	0.026
E9PZ00	Prosaposin	1.206	0.048
G3UXD0	Trypsin 5	0.724	0.023
Q3UQS9	Uncharacterized protein	1.476	0.004
Q6NXM5	4632419I22Rik protein	1.249	0.016
Q99KA4	Igh protein	0.71	0.007

Key information about the proteins were provided as protein IDs in UniProt, protein names and fold changes exceeded 1.2 (ratio > 1.2 or < 0.83, $p < 0.05$) of proteins abundance.

Table S4. Differentially expressed proteins in plasma of TUR vs HFD group mice.

Protein ID	Protein name	TUR/HFD Ratio	TUR/HFD <i>p</i> -value
E9PV24	Fibrinogen alpha chain	0.631	0.021
E9Q414	Apolipoprotein B-100	0.82	0.03
B7ZCG3	BPI fold-containing family A member 2	1.376	0.006
A0A494BBD8	Annexin	0.303	0.002
Q542I8	Integrin beta	0.829	0.046
P27656	Hepatic triacylglycerol lipase	0.815	0.004
A0A0R4J1N3	Apolipoprotein C-III	0.829	0.046
B1AR34	Asialoglycoprotein receptor 1	0.665	0.016
P48036	Annexin A5	0.709	0.048
Q5SS40	14_3_3 domain-containing protein	0.655	0.008
P68368	Tubulin alpha-4A chain	0.524	0.025
P68510	14-3-3 protein eta	0.39	0.021
Q3UXJ2	Transforming growth factor-beta-induced protein ig-h3	0.82	0.001
A0A494BAZ4	Peroxiredoxin	0.683	0.013
Q9CSE4	Uncharacterized protein	0.704	0.041
Q3UER0	Uncharacterized protein	0.522	0.014
Q3V3W7	TGc domain-containing protein	0.487	0.008
Q3TGR2	Fibrinogen beta chain	0.616	0.014
Q3UEM7	Fibrinogen C-terminal domain-containing protein	0.6	0.016
Q8VDD5	Myosin-9	0.776	0.0002
D6RFD9	ATP-binding cassette sub-family B member 9	0.525	0.015
D3Z6I8	Tropomyosin alpha-3 chain	0.695	0.037
Q8VDD0	Anti-MOG Z12 variable light chain	1.284	0.039
Q99KA4	Igh protein	1.273	0.016

Table S5. Differentially expressed proteins in liver of HFD vs ND group mice.

Protein ID	Protein name	HFD/ND Ratio	HFD/ND <i>p</i> - value
A2AVZ9	Solute carrier family 43 member 3	0.796	0.009
G5E8K5	Ankyrin-3	0.824	0.036
O35423	Serine--pyruvate aminotransferase, mitochondrial	0.688	0.022
O35490	Betaine--homocysteine S-methyltransferase 1	0.796	0.008
O35682	Myeloid-associated differentiation marker	0.689	0.018
O35728	Cytochrome P450 4A14	0.614	0.020
O70172	Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha	0.797	0.027
O70451	Monocarboxylate transporter 2	1.357	0.007
O70493	Sorting nexin-12	0.816	0.013
O88455	7-dehydrocholesterol reductase	0.508	0.012
O88522	NF-kappa-B essential modulator	0.799	0.010
O88531	Palmitoyl-protein thioesterase 1	1.271	0.009
O88736	3-keto-steroid reductase	0.583	0.002
O88829	Lactosylceramide alpha-2,3-sialyltransferase	0.810	0.048
O88986	2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	0.807	0.002
O89086	RNA-binding protein 3	0.787	0.008
P00186	Cytochrome P450 1A2	1.322	0.006
P01878	Ig alpha chain C region	0.810	0.011
P03893	NADH-ubiquinone oxidoreductase chain 2	0.826	0.018
P04939	Major urinary protein 3	1.263	0.006
P05063	Fructose-bisphosphate aldolase C	0.724	0.042
P05201	Aspartate aminotransferase, cytoplasmic	0.707	0.010
P06797	Cathepsin L1;Cathepsin L1 heavy chain;Cathepsin L1 light chain	0.821	0.003
P08030	Adenine phosphoribosyltransferase	0.791	0.00004
P09242	Alkaline phosphatase, tissue-nonspecific isozyme	0.798	0.024
P10648	Glutathione S-transferase A2	0.686	0.047
P11609	Antigen-presenting glycoprotein CD1d1	0.801	0.031
P13516	Acyl-CoA desaturase 1	2.597	0.008
P16460	Argininosuccinate synthase	0.780	0.030
P18581	Cationic amino acid transporter 2	0.809	0.043
P26040	Ezrin	0.768	0.034
P28700	Retinoic acid receptor RXR-alpha	1.311	0.045
P29391	Ferritin light chain 1	0.720	0.002
P29758	Ornithine aminotransferase, mitochondrial	0.792	0.002
P33587	Vitamin K-dependent protein C	1.693	0.006
P43006	Excitatory amino acid transporter 2	0.746	0.001
P46638	Ras-related protein Rab-11B	1.724	0.0001
P47740	Fatty aldehyde dehydrogenase	1.584	0.001

Protein ID	Protein name	HFD/ND Ratio	HFD/ND <i>p</i> - value
P48774	Glutathione S-transferase Mu 5	0.815	0.024
P52430	Serum paraoxonase/arylesterase 1	1.333	0.0003
P55050	Fatty acid-binding protein, intestinal	1.899	0.011
P56380	Bis(5-nucleosyl)-tetraphosphatase [asymmetrical]	0.822	0.023
P58044	Isopentenyl-diphosphate Delta-isomerase 1	0.270	0.005
P60824	Cold-inducible RNA-binding protein	0.815	0.015
P61079	Ubiquitin-conjugating enzyme E2 D3	2.264	0.042
P63328	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	0.805	0.014
P97785	GDNF family receptor alpha-1	0.784	0.003
P97872	Dimethylaniline monooxygenase [N-oxide-forming] 5	1.266	0.0004
Q00977	Gap junction beta-2 protein	0.707	0.043
Q02788	Collagen alpha-2(VI) chain	0.797	0.022
Q08481	Platelet endothelial cell adhesion molecule	0.827	0.019
Q08857	Platelet glycoprotein 4	1.289	0.002
Q3U2U7	Methyltransferase-like protein 17, mitochondrial	1.270	0.044
Q3U9G9	Lamin-B receptor	0.827	0.004
Q3U9N9	Monocarboxylate transporter 10	1.883	0.018
Q3UM29	Conserved oligomeric Golgi complex subunit 7	0.824	0.002
Q3UP75	UDP-glucuronosyltransferase 3A1	1.284	0.018
Q3UVK0	Endoplasmic reticulum metalloproteinase 1	1.203	0.019
Q5SSZ5	Tensin-3	0.822	0.015
Q5SUC9	Protein SCO1 homolog, mitochondrial	1.208	0.009
Q61425	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	1.203	0.011
Q61508	Extracellular matrix protein 1	0.819	0.004
Q61559	IgG receptor FcRn large subunit p51	1.238	0.009
Q64378	Peptidyl-prolyl cis-trans isomerase FKBP5	0.790	0.008
Q64435	UDP-glucuronosyltransferase 1-6	1.228	0.009
Q64458	Cytochrome P450 2C29	1.305	0.042
Q6A009	E3 ubiquitin-protein ligase listerin	0.718	0.002
Q6DIC0	Probable global transcription activator SNF2L2	0.808	0.008
Q6P3D0	U8 snoRNA-decapping enzyme	1.216	0.008
Q71KT5	Delta(14)-sterol reductase	0.547	0.0005
Q7TNE1	Succinate--hydroxymethylglutarate CoA-transferase	1.211	0.008
Q80WS3	rRNA/tRNA 2-O-methyltransferase fibrillarin-like protein 1	1.225	0.041
Q8BGT5	Alanine aminotransferase 2	0.787	0.010
Q8BH57	WD repeat-containing protein 48	1.243	0.021
Q8BI08	Protein MAL2	1.694	0.013
Q8BK48	Pyrethroid hydrolase Ces2e	1.293	0.0002
Q8BLN5	Lanosterol synthase	0.686	0.009
Q8BNI4	Derlin-2	0.796	0.010
Q8BSM7	Large neutral amino acids transporter small subunit 3	0.764	0.001

Protein ID	Protein name	HFD/ND Ratio	HFD/ND <i>p</i> - value
Q8BUG2	Beta-Ala-His dipeptidase	1.207	0.004
Q8BZA9	Fructose-2,6-bisphosphatase TIGAR	0.819	0.037
Q8C025	Cholinephosphotransferase 1	1.427	0.008
Q8C0L9	Glycerophosphocholine phosphodiesterase GPCPD1	0.714	0.007
Q8C1Y8	Vacuolar fusion protein CCZ1 homolog	1.343	0.001
Q8CGZ0	Calcium homeostasis endoplasmic reticulum protein	0.713	0.018
Q8CIZ8	von Willebrand factor;von Willebrand antigen 2	0.805	0.042
Q8K0C4	Lanosterol 14-alpha demethylase	0.540	0.001
Q8K1B9	Polypeptide N-acetylgalactosaminyltransferase 18	1.272	0.024
Q8K211	High affinity copper uptake protein 1	1.342	0.003
Q8QZR1	Tyrosine aminotransferase	0.511	0.042
Q8R143	Pituitary tumor-transforming gene 1 protein-interacting protein	1.204	0.0003
Q8R1S9	Sodium-coupled neutral amino acid transporter 4	0.775	0.011
Q8R2Y0	Monoacylglycerol lipase ABHD6	1.228	0.005
Q8R3Q0	Store-operated calcium entry-associated regulatory factor	1.298	0.039
Q8R4R6	Nucleoporin NUP53	0.822	0.007
Q8R519	2-amino-3-carboxymuconate-6-semialdehyde decarboxylase	0.540	0.002
Q8VCH0	3-ketoacyl-CoA thiolase B, peroxisomal	1.475	0.007
Q8VCN5	Cystathionine gamma-lyase	0.761	0.015
Q8VCT4	Carboxylesterase 1D	1.352	0.016
Q8VHQ9	Acyl-coenzyme A thioesterase 11	1.201	0.026
Q91V61	Sideroflexin-3	1.243	0.037
Q91W59	RNA-binding motif, single-stranded-interacting protein 1	0.798	0.011
Q91WU0	Carboxylic ester hydrolase	1.214	0.004
Q91X83	S-adenosylmethionine synthase isoform type-1	0.735	0.009
Q91ZP3	Phosphatidate phosphatase LPIN1	0.607	0.009
Q920E5	Farnesyl pyrophosphate synthase	0.320	0.0004
Q99J47	Dehydrogenase/reductase SDR family member 7B	1.205	0.028
Q99J94	Solute carrier organic anion transporter family member 1A6	1.732	0.029
Q99JF5	Diphosphomevalonate decarboxylase	0.522	0.002
Q99JZ7	ERBB receptor feedback inhibitor 1	0.797	0.006
Q99PE8	ATP-binding cassette sub-family G member 5	1.242	0.019
Q99PT3	INO80 complex subunit B	1.333	0.021
Q9CQ88	Tetraspanin-31	0.802	0.016
Q9CSV6	Vesicle transport protein SFT2C	1.567	0.007
Q9CWI3	BRCA2 and CDKN1A-interacting protein	0.822	0.006
Q9CWS0	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	1.296	0.044
Q9CYV5	Transmembrane protein 135	1.430	0.00009
Q9CZS1	Aldehyde dehydrogenase X, mitochondrial	0.741	0.012
Q9D1L0	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2	1.238	0.037
Q9D273	Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial	0.688	0.0004

Protein ID	Protein name	HFD/ND Ratio	HFD/ND <i>p</i> - value
Q9D287	Pre-mRNA-splicing factor SPF27	0.808	0.002
Q9D379	Epoxide hydrolase 1	1.333	0.003
Q9D7S7	60S ribosomal protein L22-like 1	0.801	0.005
Q9DBE0	Cysteine sulfinic acid decarboxylase	1.331	0.039
Q9DCP2	Sodium-coupled neutral amino acid transporter 3	0.760	0.004
Q9DD06	Retinoic acid receptor responder protein 2	1.212	0.036
Q9EPT5	Solute carrier organic anion transporter family member 2A1	0.681	0.013
Q9EQ06	Estradiol 17-beta-dehydrogenase 11	1.433	0.001
Q9ERY9	Probable ergosterol biosynthetic protein 28	0.770	0.005
Q9JI99	Sphingosine-1-phosphate phosphatase 1	1.222	0.002
Q9JIW9	Ras-related protein Ral-B	0.828	0.019
Q9JJZ2	Tubulin alpha-8 chain	2.132	0.006
Q9QXG4	Acetyl-coenzyme A synthetase, cytoplasmic	0.669	0.015
Q9QXM0	Abhydrolase domain-containing protein 2	0.664	0.002
Q9QYC7	Vitamin K-dependent gamma-carboxylase	1.360	0.009
Q9QYF1	Retinol dehydrogenase 11	0.679	0.001
Q9QZD8	Mitochondrial dicarboxylate carrier	1.261	0.017
Q9R008	Mevalonate kinase	0.490	0.00028
Q9R0L7	A-kinase anchor protein 8-like	0.829	0.020
Q9R1J0	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	0.437	0.001
Q9WUZ9	Ectonucleoside triphosphate diphosphohydrolase 5	1.209	0.007
Q9Z0K8	Pantetheinase	1.220	0.011
Q9Z0M5	Lysosomal acid lipase/cholesteryl ester hydrolase	1.376	0.010
Q9Z211	Peroxisomal membrane protein 11A	1.352	0.004
Q9Z2V4	Phosphoenolpyruvate carboxykinase, cytosolic [GTP]	0.778	0.008

Table S6. Differentially expressed proteins in liver of TUR vs HFD group mice.

Protein ID	Protein name	TUR/HFD Ratio	TUR/HFD <i>p</i> -value
A6H611	Mitochondrial intermediate peptidase	0.736	0.006
O35423	Serine--pyruvate aminotransferase, mitochondrial	0.798	0.019
O54754	Aldehyde oxidase 1	1.223	0.020
O55239	Nicotinamide N-methyltransferase	0.802	0.016
O70475	UDP-glucose 6-dehydrogenase	1.273	0.002
O88425	Nucleoside diphosphate kinase 6	0.730	0.033
O88829	Lactosylceramide alpha-2,3-sialyltransferase	0.747	0.041
O88833	Cytochrome P450 4A10	0.605	0.020
O88962	7-alpha-hydroxycholest-4-en-3-one 12-alpha-hydroxylase	0.819	0.048
O89086	RNA-binding protein 3	0.824	0.009
P07901	Heat shock protein HSP 90-alpha	1.203	0.008
P10649	Glutathione S-transferase Mu 1	1.541	0.003
P12791	Cytochrome P450 2B10	1.759	0.012
P14901	Heme oxygenase 1	0.773	0.001
P18581	Cationic amino acid transporter 2	0.640	0.014
P19639	Glutathione S-transferase Mu 3	1.598	0.003
P29758	Ornithine aminotransferase, mitochondrial	0.795	0.002
P33146	Cadherin-15	1.499	0.009
P33622	Apolipoprotein C-III	0.819	0.040
P35441	Thrombospondin-1	0.721	0.005
P43883	Perilipin-2	0.747	0.040
P46638	Ras-related protein Rab-11B	1.556	0.001
P48758	Carbonyl reductase [NADPH] 1	1.317	0.033
P51658	Estradiol 17-beta-dehydrogenase 2	1.243	0.014
P56375	Acylphosphatase-2	1.234	0.012
P62500	TSC22 domain family protein 1	1.227	0.014
P63254	Cysteine-rich protein 1	0.810	0.020
P70349	Histidine triad nucleotide-binding protein 1	1.236	0.011
P97494	Glutamate--cysteine ligase catalytic subunit	1.201	0.011
Q1ERP8	CMRF35-like molecule 9	0.639	0.023
Q3U2U7	Methyltransferase-like protein 17, mitochondrial	0.721	0.046
Q571F8	Glutaminase liver isoform, mitochondrial	0.809	0.005
Q60648	Ganglioside GM2 activator	1.233	0.010
Q60738	Zinc transporter 1	0.830	0.007
Q62452	UDP-glucuronosyltransferase 1A9	1.271	0.011
Q64458	Cytochrome P450 2C29	1.416	0.004
Q64505	Cholesterol 7-alpha-monooxygenase	0.824	0.047
Q64669	NAD(P)H dehydrogenase [quinone] 1	1.370	0.027
Q7TMW6	Cytosolic Fe-S cluster assembly factor NARFL	0.799	0.027
Q7TQK4	Exosome complex component RRP40	0.787	0.032
Q80WS3	rRNA/tRNA 2-O-methyltransferase fibrillarin-like protein 1	1.417	0.000

Protein ID	Protein name	TUR/HFD Ratio	TUR/HFD <i>p</i> -value
Q80ZJ1	Ras-related protein Rap-2a	0.752	0.041
Q8BH57	WD repeat-containing protein 48	1.252	0.029
Q8BSM7	Large neutral amino acids transporter small subunit 3	0.797	0.003
Q8BUB4	WD repeat and FYVE domain-containing protein 2	0.799	0.040
Q8BZ20	Poly [ADP-ribose] polymerase 12	0.744	0.014
Q8C4X7	Major intrinsically disordered NOTCH2-binding receptor 1-like homolog	1.382	0.027
Q8CJ61	CKLF-like MARVEL transmembrane domain-containing protein 4	0.800	0.031
Q8K354	Carbonyl reductase [NADPH] 3	1.288	0.007
Q8K3A9	7SK snRNA methylphosphate capping enzyme	0.799	0.046
Q8R0G7	Protein spinster homolog 1	0.799	0.007
Q8R1Q9	Ribokinase	1.247	0.019
Q8R5I6	Glutathione S-transferase Mu 4	1.421	0.005
Q8VC19	5-aminolevulinate synthase, nonspecific, mitochondrial	0.682	0.015
Q91V76	Ester hydrolase C11orf54 homolog	1.344	0.005
Q91W64	Cytochrome P450 2C70	1.309	0.045
Q91WC9	Sn1-specific diacylglycerol lipase beta	0.822	0.042
Q91WL5	Cytochrome P450 4A12A	1.314	0.020
Q91WP6	Serine protease inhibitor A3N	0.786	0.026
Q923D2	Flavin reductase (NADPH)	1.331	0.009
Q99JY8	Lipid phosphate phosphohydrolase 3	0.801	0.005
Q9CPP0	Nucleoplasmin-3	0.722	0.041
Q9CR88	28S ribosomal protein S14, mitochondrial	0.813	0.021
Q9CSV6	Vesicle transport protein SFT2C	1.254	0.020
Q9CXY9	GPI-anchor transamidase	0.815	0.017
Q9CYV5	Transmembrane protein 135	1.731	0.000
Q9D379	Epoxide hydrolase 1	1.235	0.002
Q9DBE0	Cysteine sulfinic acid decarboxylase	1.333	0.049
Q9DBT9	Dimethylglycine dehydrogenase, mitochondrial	0.817	0.002
Q9DC29	ATP-binding cassette sub-family B member 6, mitochondrial	0.817	0.009
Q9EQK5	Major vault protein	1.215	0.028
Q9JHK5	Pleckstrin	0.684	0.033
Q9JKW0	ADP-ribosylation factor-like protein 6-interacting protein 1	1.220	0.019
Q9QXM0	Abhydrolase domain-containing protein 2	0.658	0.003
Q9QXS8	Probable N-acetyltransferase CML5	1.243	0.035
Q9R060	Cytosolic Fe-S cluster assembly factor NUBP1	1.213	0.015

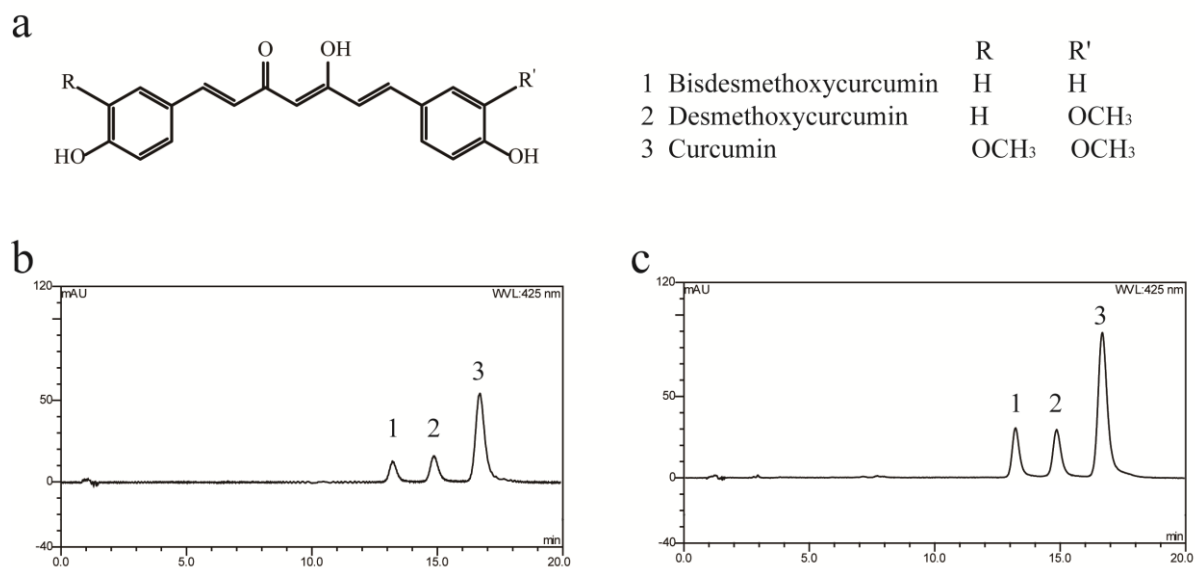


Fig. S1. Chemical structures and typical HPLC chromatograms of three kinds of curcuminoids. (a) The chemical structures of bisdesmethoxycurcumin (1), desmethoxycurcumin (2) and curcumin (3); (b) HPLC chromatograms of standard solution with 2.5 $\mu\text{g/mL}$ of bisdesmethoxycurcumin, 5 $\mu\text{g/mL}$ of desmethoxycurcumin and 15 $\mu\text{g/mL}$ of curcumin; (c) HPLC chromatograms of turmeric extract.

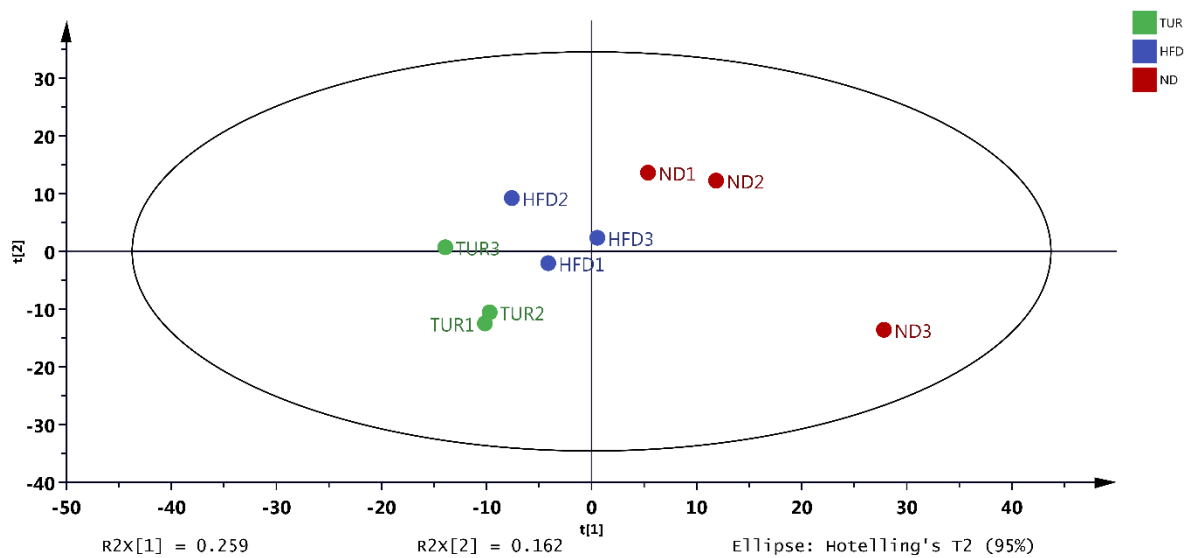


Fig. S2. PCA score plot of plasma proteins of mice in ND, HFD and TUR groups.

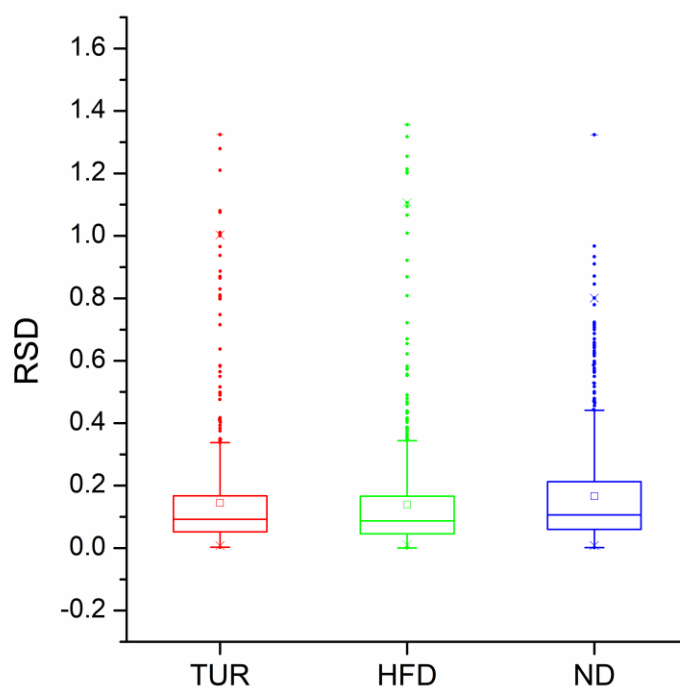


Fig. S3. Box plot of distributions of RSD from quantitative result of plasma proteins.

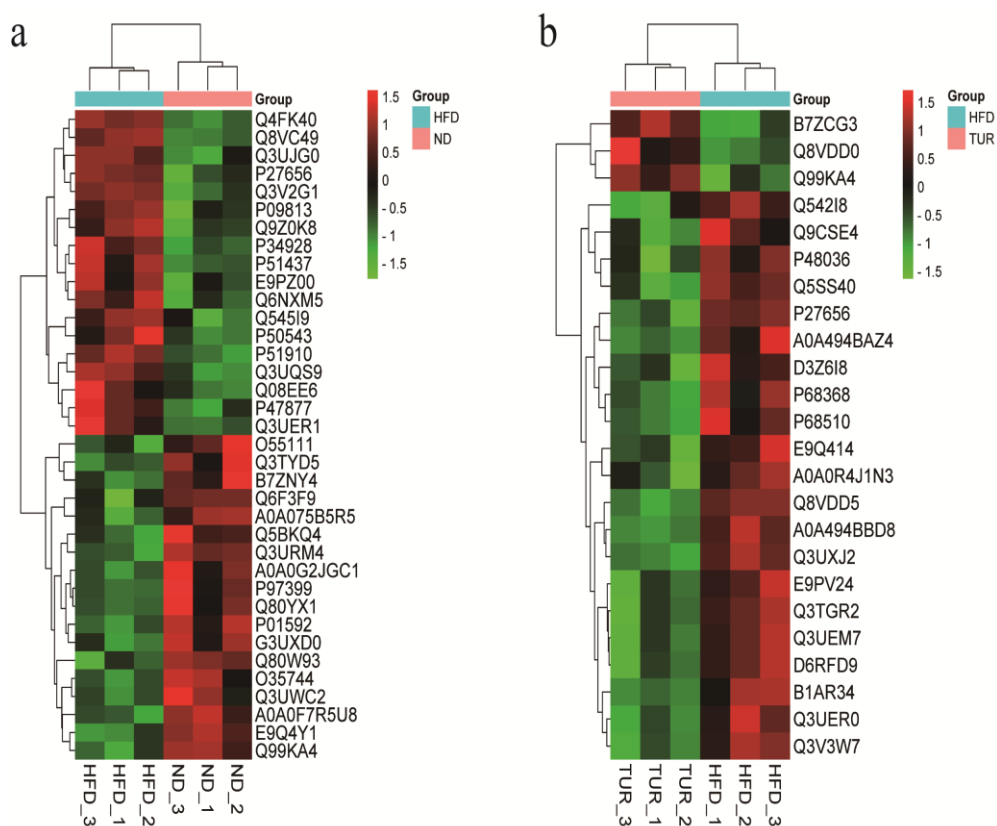


Fig. S4. Heatmap with hierarchical clustering analysis of DEPs of plasma proteomics. (a) Heatmap of DEPs in plasma of HFD vs ND group mice. (b) Heatmap of DEPs in plasma of HFD vs TUR group mice. The color scale indicates the protein expression value; green is the lowest and red is the highest.

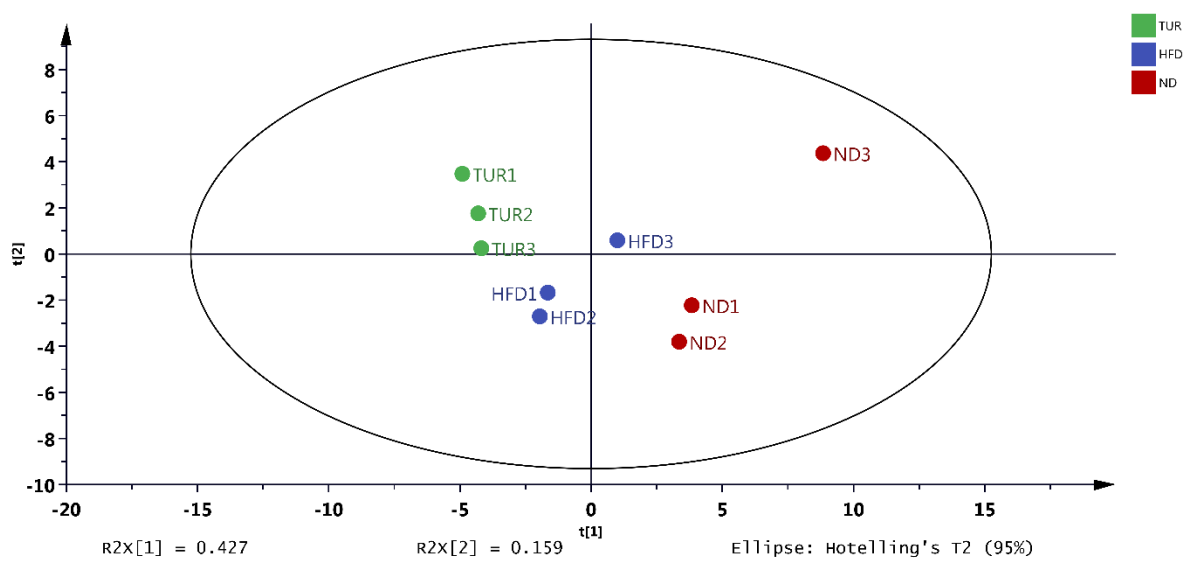


Fig. S7. PCA score plot of mice in ND, HFD and TUR groups of liver proteins.

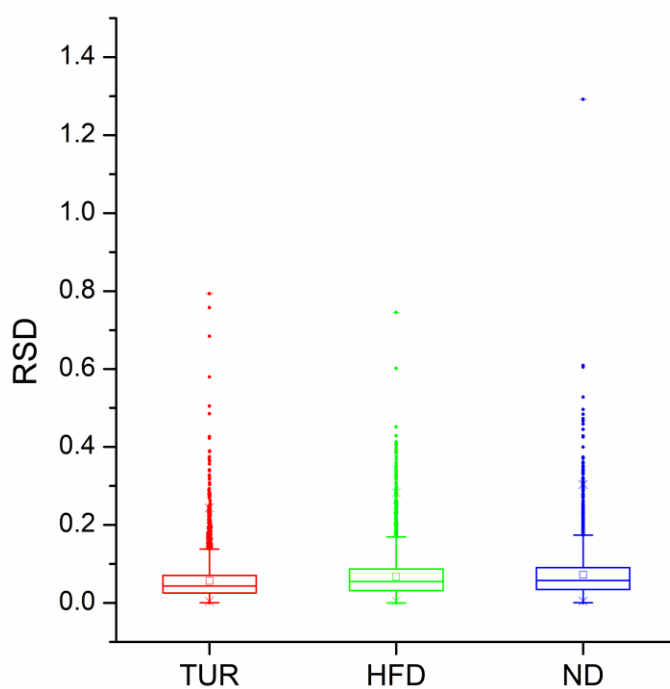


Fig. S8. Box plot of distributions of RSD from quantitative result of liver proteins.

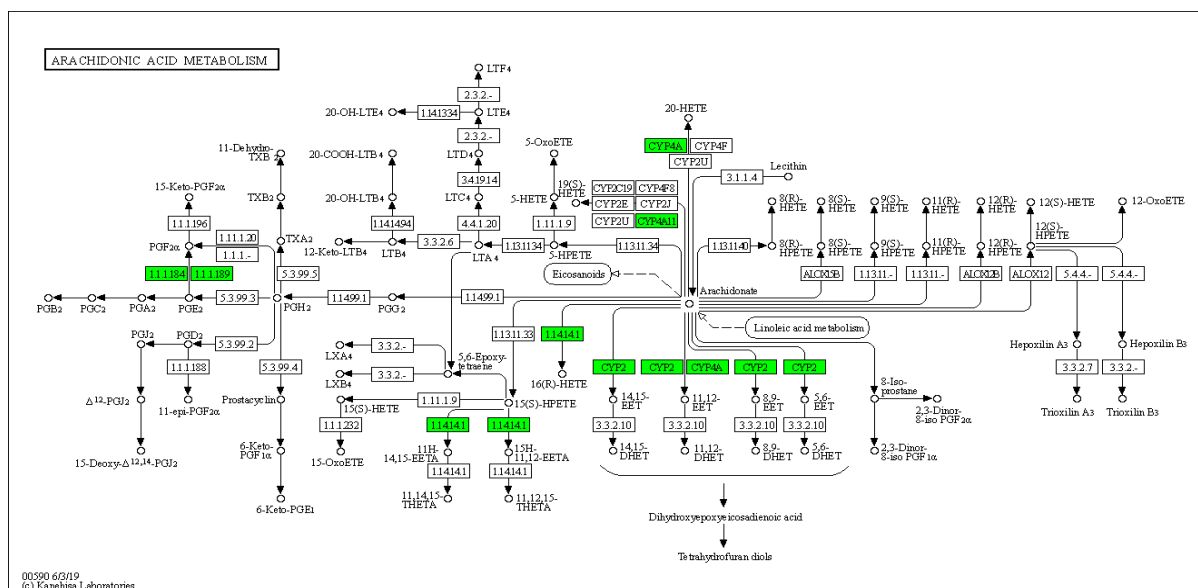


Fig. S10. The KEGG mapping of DEPs in arachidonic acid metabolism pathway. The green legends represent the DEPs.

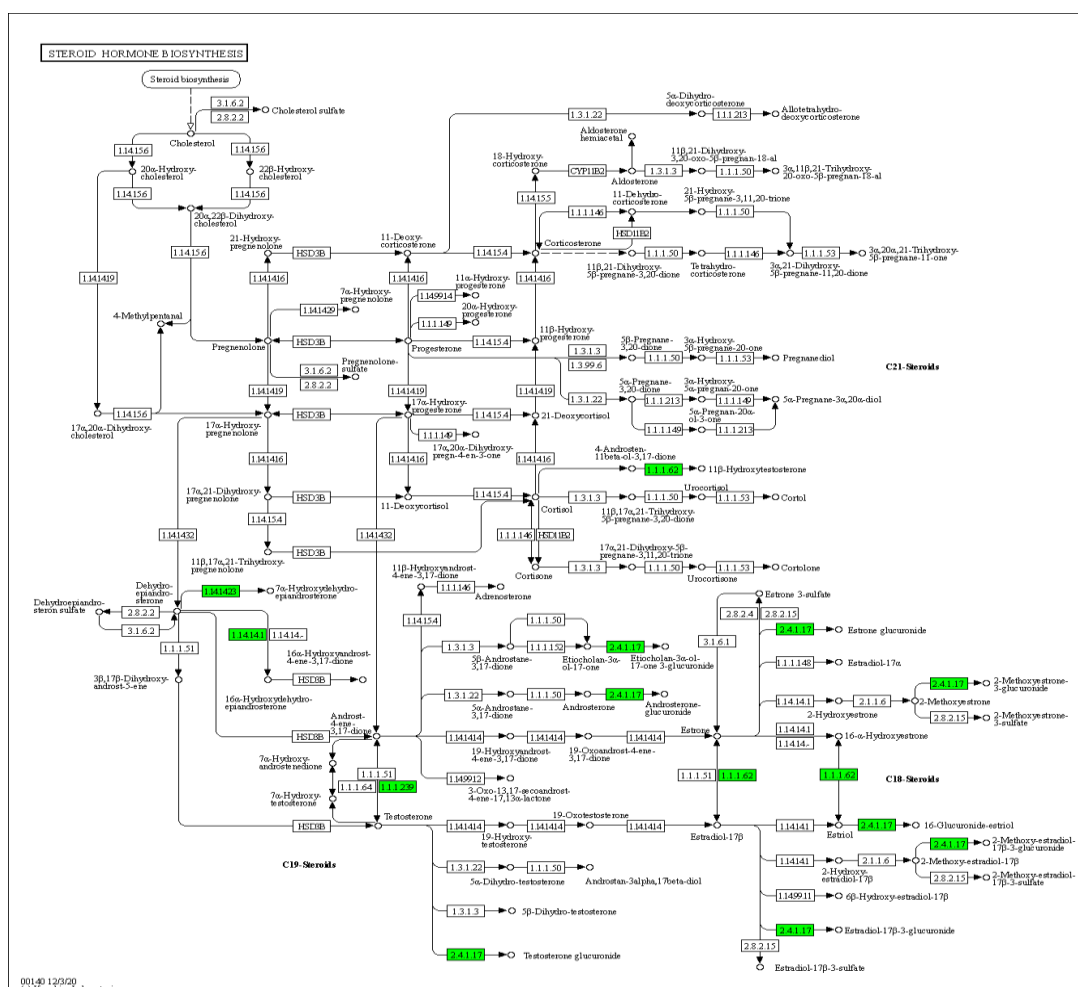


Fig. S11. The KEGG mapping of DEPs in steroid hormone biosynthesis pathway. The green legends represent the DEPs.

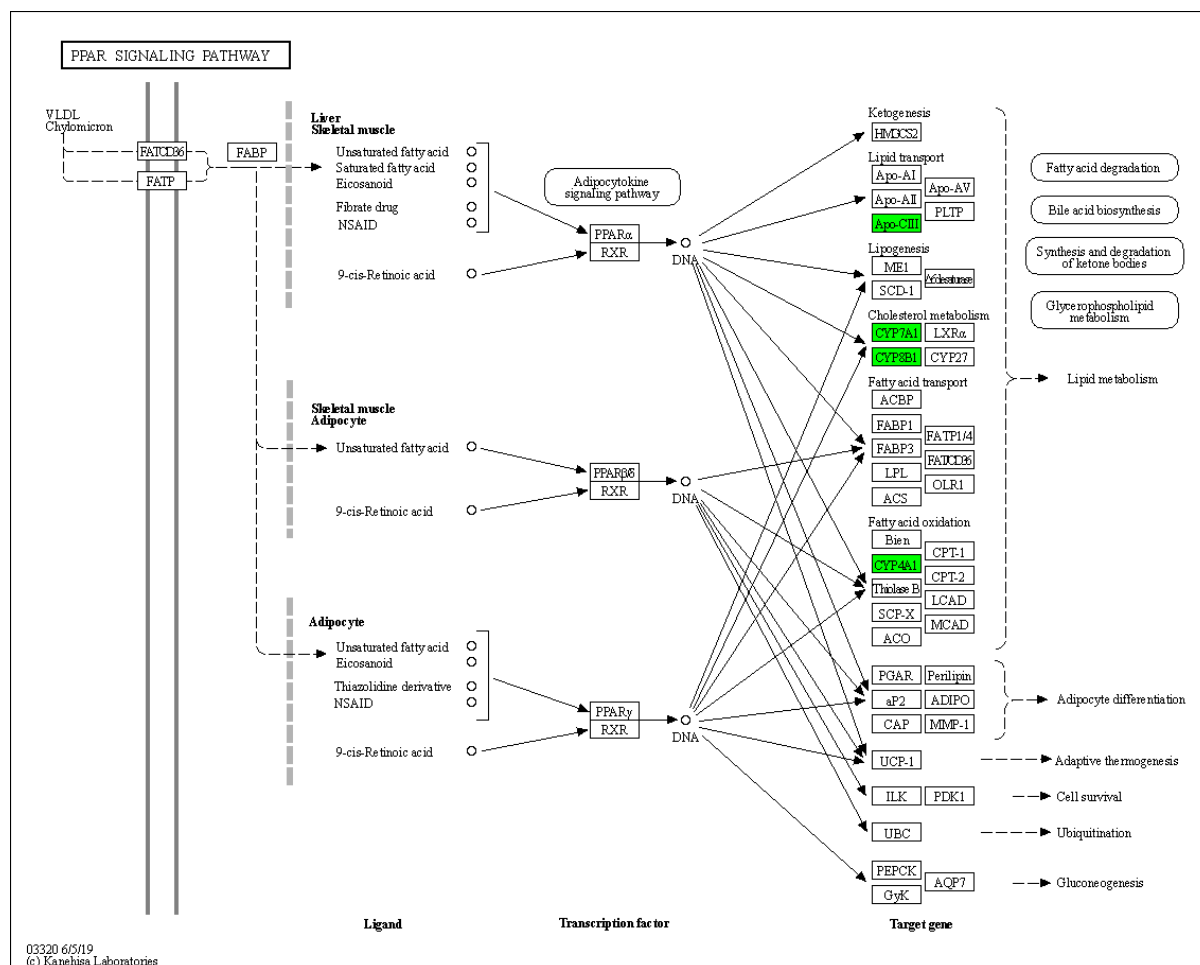


Fig. S12. The KEGG mapping of DEPs in PPAR signaling pathway. The green legends represent the DEPs.