Electronic Supplementary Material (ESI) for Food & Function.

Supporting Information

The effects of carbon dots produced by Maillard reaction on HepG2 cell substance and energy metabolism

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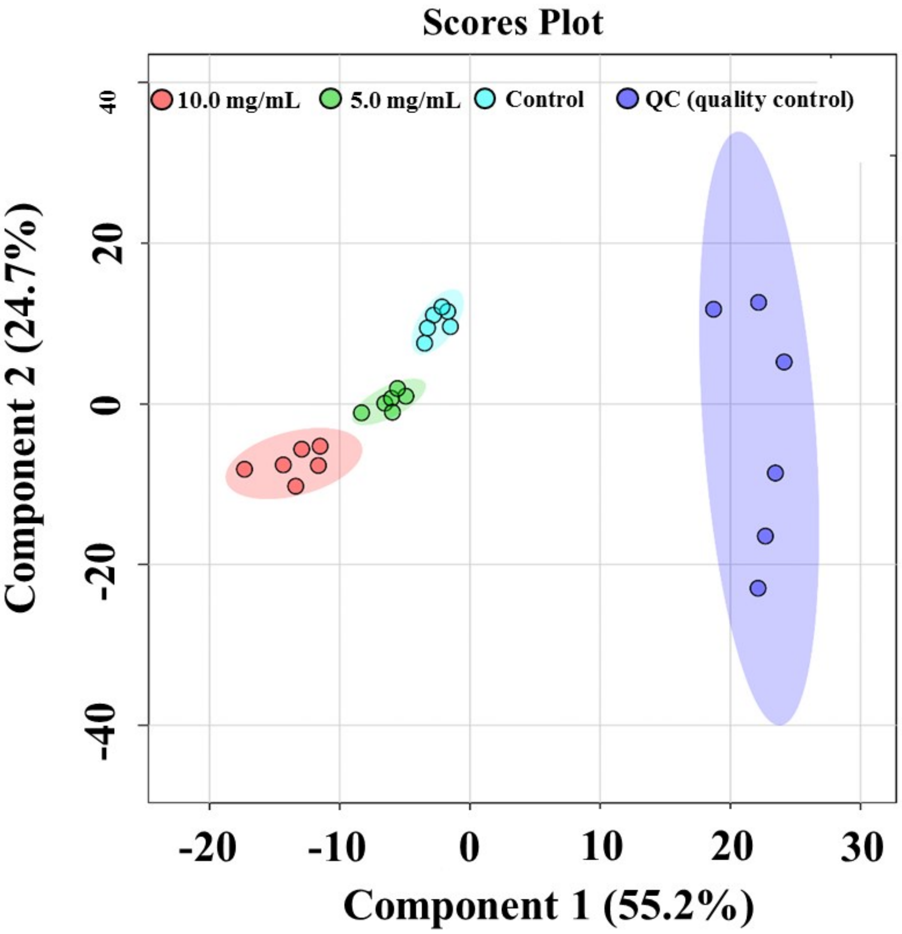

Fig. S1 PLS-DA score plot of metabolites in HepG2 cells after incubation with different concentration of CDs.

Tab.S1 Relevant pathways influenced by CDs based on the pathway analysis.

Number	Pathway Name	Match Status	-log(p)	Impact	Details
1	Glycolysis / Gluconeogenesis	5/26	20.3020	0.2135	KEGG SMP SMP
2	Citrate cycle (TCA cycle)	11/20	20.1740	0.5718	KEGG SMP
3	Pyruvate metabolism	8/22	19.8920	0.3349	KEGG SMP
4	Amino sugar and nucleotide sugar metabolism	7/37	18.3860	0.1557	KEGG SMP SMP
5	Biotin metabolism	2/10	14.7270	0.2000	KEGG SMP
6	Lysine degradation	3/25	14.2400	0.1409	KEGG SMP
7	Pentose and glucuronate interconversions	2/18	13.8940	0.2031	KEGG
8	Inositol phosphate metabolism	3/30	13.2170	0.1294	KEGG SMP
9	Galactose metabolism	3/27	13.2170	0.0361	KEGG SMP
10	Ascorbate and aldarate metabolism	4/8	13.2170	0.5000	KEGG
11	Phosphatidylinositol signaling system	1/28	13.2150	0.0374	KEGG
12	Propanoate metabolism	3/23	12.7540	0.0457	KEGG SMP
13	Selenocompound metabolism	1/20	12.6120	0.0	KEGG SMP
14	Fatty acid degradation	1/39	12.0360	0.0	KEGG SMP

15	Pentose phosphate pathway	4/22	11.0040	0.1693	KEGG SMP
16	Glycerolipid metabolism	3/16	10.9720	0.1371	KEGG SMP
17	Ether lipid metabolism	1/20	10.2570	0.0	KEGG
18	Fructose and mannose metabolism	1/20	9.5681	0.0031	KEGG SMP
19	Valine, leucine and isoleucine degradation	4/40	9.1341	0.0642	KEGG SMP
20	Aminoacyl-tRNA biosynthesis	18/48	7.2985	0.1667	KEGG
21	Glycine, serine and threonine metabolism	17/33	6.7021	0.8007	KEGG SMP
22	Phenylalanine, tyrosine and tryptophan biosynthesis	4/4	4.9411	1.0000	KEGG SMP
23	Phenylalanine metabolism	4/10	4.9411	0.6190	KEGG SMP
24	Sphingolipid metabolism	1/21	4.8967	0.0	KEGG SMP
25	Glycerophospholipid metabolism	8/36	4.5530	0.2429	KEGG
26	Tryptophan metabolism	3/41	4.5022	0.2392	KEGG SMP
27	Cysteine and methionine metabolism	12/33	4.3868	0.6339	KEGG SMP
28	Alanine, aspartate and glutamate metabolism	15/28	4.2250	0.7628	KEGG SMP SMP
29	Glyoxylate and dicarboxylate metabolism	12/32	3.7380	0.5820	KEGG
30	Steroid hormone biosynthesis	1/85	3.6886	0.0	KEGG SMP
31	Purine metabolism	21/65	2.7576	0.4073	KEGG SMP

32	Pyrimidine metabolism	13/39	2.7543	0.4936	KEGG SMP
33	Arginine biosynthesis	11/14	2.6734	0.6853	KEGG
34	Nitrogen metabolism	3/6	2.5293	0.0	KEGG SMP
35	D-Glutamine and D-glutamate metabolism	3/6	2.5292	0.5000	KEGG SMP
36	Tyrosine metabolism	6/42	2.5059	0.2483	KEGG SMP
37	Ubiquinone and other terpenoid-quinone biosynthesis	2/9	2.4286	1.0000	KEGG SMP
38	Starch and sucrose metabolism	3/18	2.2060	0.1665	KEGG SMP
39	Riboflavin metabolism	2/4	2.0740	0.5000	KEGG SMP
40	Pantothenate and CoA biosynthesis	5/19	2.0577	0.0071	KEGG SMP
41	One carbon pool by folate	1/9	1.9952	0.0000	KEGG SMP
42	Folate biosynthesis	1/27	1.9952	0.0000	KEGG SMP
43	Thiamine metabolism	3/7	1.8411	0.6667	KEGG SMP
44	Valine, leucine and isoleucine biosynthesis	3/8	1.7828	0.0000	KEGG SMP
45	beta-Alanine metabolism	5/21	1.7497	0.0560	KEGG SMP
46	Vitamin B6 metabolism	3/9	1.6208	0.1569	KEGG SMP
47	Histidine metabolism	5/16	1.2283	0.2213	KEGG SMP
48	Arginine and proline metabolism	15/38	0.60345	0.5223	KEGG SMP

49	Neomycin, kanamycin and gentamicin biosynthesis	1/2	0.6006	0.0	KEGG
50	Butanoate metabolism	5/15	0.4512	0.1429	KEGG SMP
51	Primary bile acid biosynthesis	3/46	0.4324	0.0152	KEGG SMP
52	Glutathione metabolism	8/28	0.4165	0.1531	KEGG SMP
53	Porphyrin and chlorophyll metabolism	2/30	0.4077	0.0	KEGG
54	Taurine and hypotaurine metabolism	2/8	0.2440	0.4286	KEGG SMP
55	Nicotinate and nicotinamide metabolism	5/15	0.0731	0.2259	KEGG SMP
56	Synthesis and degradation of ketone bodies	1/5	0.0639	0.6000	KEGG SMP