Supplementary files

Metabolic perturbations and health impacts from exposure to combination of mutiple harmful Maillard reaction products on Sprague-Dawley rats

Wei Quan*[a, c], Yong Lin[b], Chaoyi Xue[c], Yong Cheng[c], Jie Luo[a], Aihua Lou[a], Maomao Zeng[c], Zhiyong He[c], Qingwu Shen[a], Jie Chen*[c, d]

[a] College of Food Science and Technology, Hunan Agricultural University, Changsha, Hunan 410128, China

[b] National Research Center of Engineering Technology for Utilization of Functional Ingredients from Botanicals, Hunan Agricultural University, Changsha, Hunan 410128, China

[c] State Key Laboratory of Food Science and Technology, Jiangnan University, Wuxi, Jiangsu 214122, China

[d] International Joint Laboratory on Food Safety, Jiangnan University, Wuxi, Jiangsu 214122, China

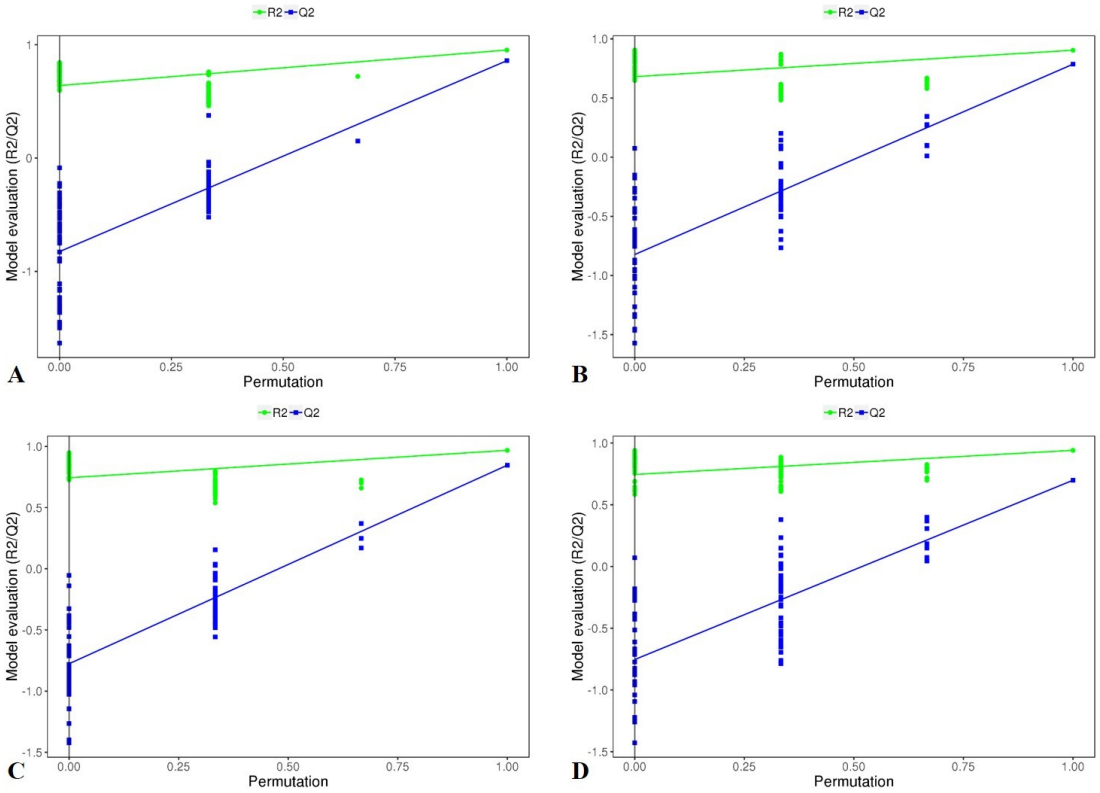
*Corresponding author: Dr. Wei Quan and Prof. Jie Chen

E-mail: Reus_quan@hunau.edu.cn and Chenjie@jiangnan.edu.cn

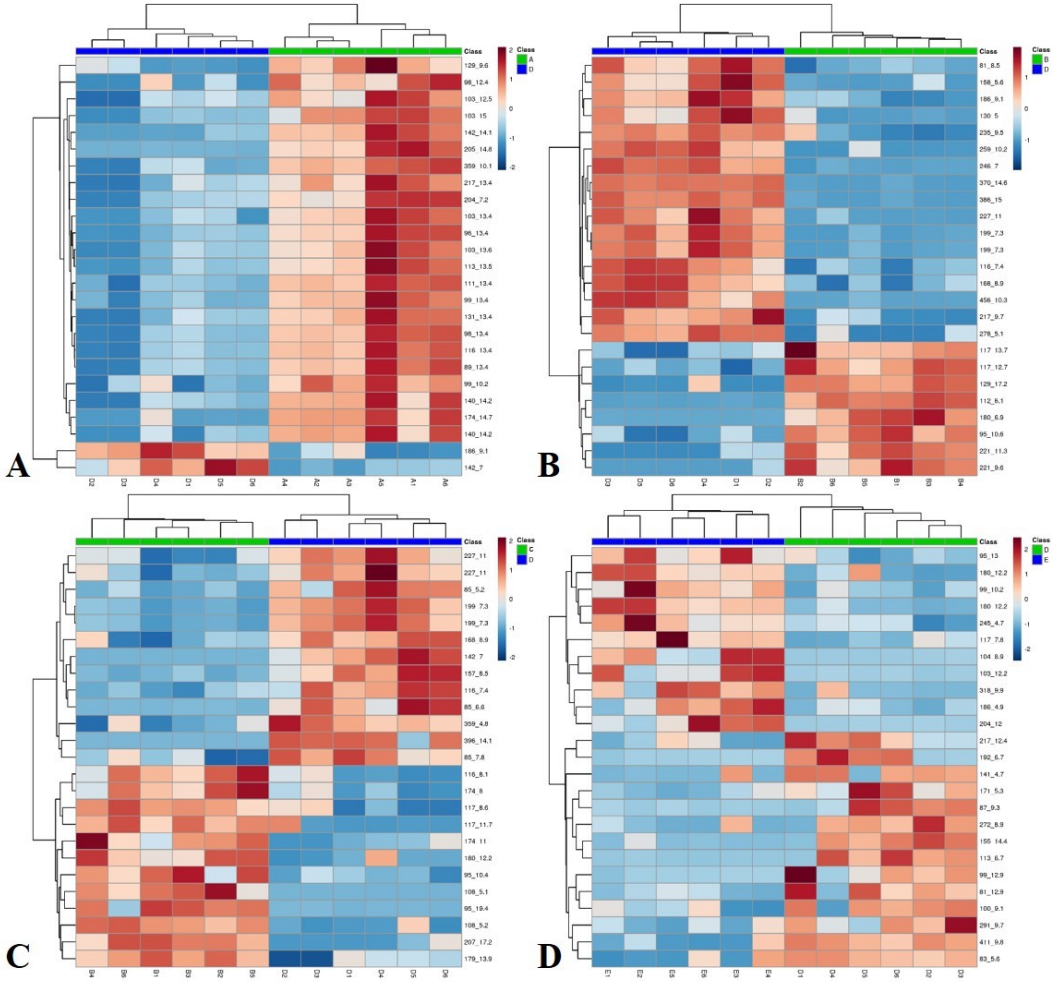
Tel.: +86 510 85919065; Fax: +86 510 85919065

Supplementary Table 1. The pathway analysis of the identified metabolites affected in the experiment groups. Based on the selected metabolites, the global metabolic disorders of the most relevant pathways induced by acrylamide, CML, harmane and co-accumulation were revealed using the MetaboAnalyst 4.0.

Group	Metabolism pathway	P	-log(p)	Holm adjust	FDR	Impact
Acrylamide	Arginine biosynthesis	0.0028	5.8875	0.2330	0.2316	0.1776
	Pentose phosphate pathway	0.0063	5.0730	0.5199	0.2316	0.0022
	Glutathione metabolism	0.0110	4.5069	0.9046	0.2316	0.0196
	Alanine, aspartate and glutamate metabolism	0.0110	4.5069	0.9046	0.2316	0.1971
	Arginine and proline metabolism	0.0199	3.9176	1	0.3341	0.1966
	Aminoacyl-tRNA biosynthesis	0.0309	3.4759	1	0.3707	0
	Nitrogen metabolism	0.0353	3.3435	1	0.3707	0
	D-Glutamine and D-glutamate metabolism	0.0353	3.3435	1	0.3707	0.5
Harmane	Arginine biosynthesis	0.0007	7.1471	0.0661	0.0661	0.2893
CML	Arginine biosynthesis	0.0004	7.6526	0.0398	0.0398	0.2893
Com	Arginine biosynthesis	0.0276	3.5902	1	0.8531	0
	Fructose and mannose metabolism	0.0354	3.3415	1	0.8531	0
	Citrate cycle (TCA cycle)	0.0392	3.2375	1	0.8531	0.0298
	Pyruvate metabolism	0.0431	3.1435	1	0.8531	0



Supplementary Figure 1. Permulation test plots based on GC-TOF-MS spectra of serum sample. (A) Acrylamide group, (B) Harmane group, (C) CML group, and (D) Co-accumulation group.



Supplementary Figure. 2 Heat map visualizing the changes in the concentration of potential biomarkers in the serum sample of all four groups. Rows: samples. Columns: biomarkers extracted from the volcano plot in the serum samples of the control group and acrylamide group (A), harmane group (B), CML group (C), and co-accumulation group (D). Color key indicates the concentration of metabolites: blue, lowest; red, highest.