Supporting information

Untargeted metabolomics of colonic digests reveals kynurenine pathway metabolites, dityrosine and 3-dehydroxycarnitine as red versus white meat discriminating metabolites

Caroline Rombouts¹, Lieselot Y. Hemeryck¹, Thomas Van Hecke², Stefaan De Smet², Winnok H. De Vos^{3,4} and Lynn Vanhaecke^{1*}

¹Ghent University, Faculty of Veterinary Medicine, Department of Veterinary Public Health and Food Safety, Laboratory of Chemical Analysis, Salisburylaan 133, B-9820 Merelbeke, Belgium

² Ghent University, Faculty of Bioscience Engineering, Department of Animal Production, Laboratory of Animal Nutrition and Animal Product Quality, Proefhoevestraat 10, B-9090 Melle, Belgium

³ Ghent University, Faculty of Bioscience Engineering, Department of Molecular Biotechnology, Laboratory of Cell Systems & Imaging, Coupure Links 653, B-9000 Ghent, Belgium

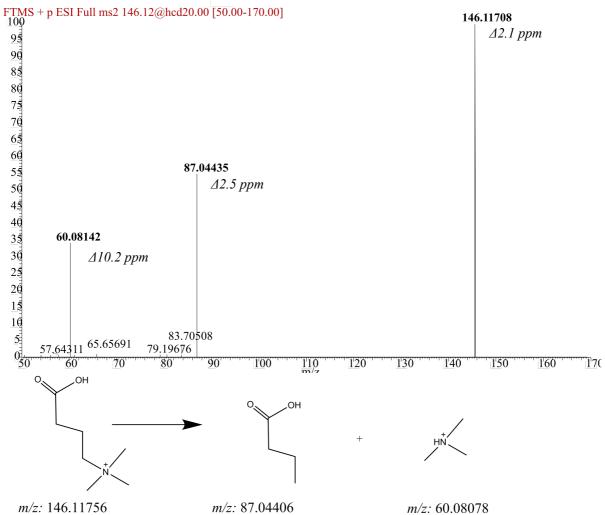
⁴ Antwerp University, Faculty of Pharmaceutical, Biomedical and Veterinary Sciences, Department of Veterinary Sciences, Laboratory of Cell Biology and Histology, Groenenborgerlaan 171, B-2020 Antwerp, Belgium

*Correspondence: Prof. Lynn Vanhaecke, Ghent University, Faculty of Veterinary Medicine, Department of Veterinary Public Health and Food Safety, Laboratory of Chemical Analysis, Salisburylaan 133, B-9820 Merelbeke, Belgium

E-mail: Lynn.Vanhaecke@ugent.be

Fax: +32-9-2647492

Figure S1. MS/MS data (+ ionization mode) used for identification of 3dehydroxycarnitine. MS/MS fragmentation data (PRM) of m/z 146.11708.



Chemical Formula: $C_7H_{16}NO_2^+$ Chemical Formula: $C_4H_7O_2$

m/z: 60.08078 Chemical Formula: C₃H₁₀N⁺

Figure S2. MS/MS data (+ ionization mode) used for identification of kynurenic acid.

MS/MS fragmentation data (PRM) of *m/z* 190.04919.

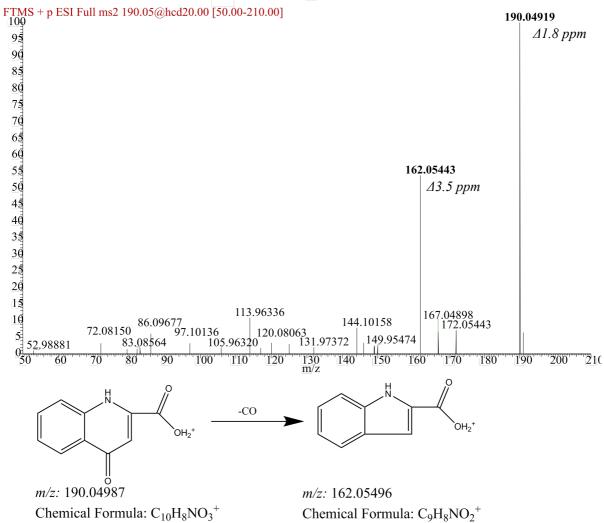


Figure S3. MS/MS data (+ ionization mode) used for identification of L-kynurenine.

MS/MS fragmentation data (PRM) of m/z 209.09186.

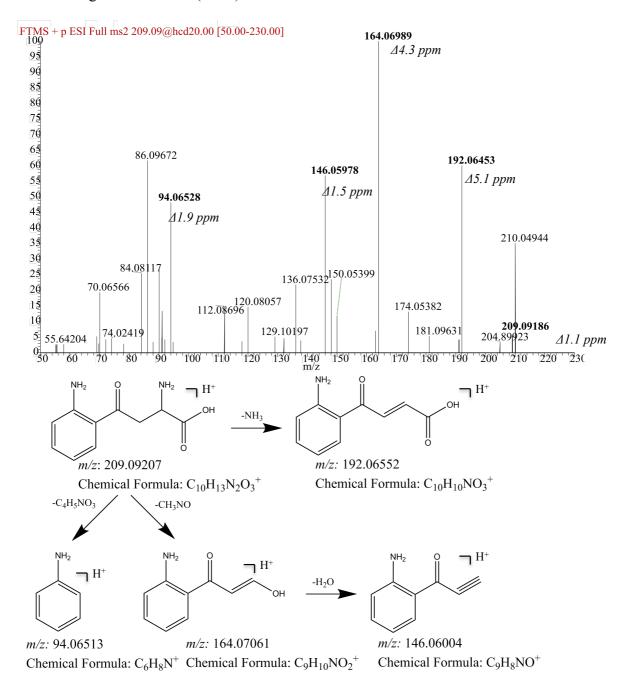


Figure S4. MS/MS data (+ ionization mode) used for identification of N'-

formylkynurenine. MS/MS fragmentation data (PRM) of *m/z* 237.08652.

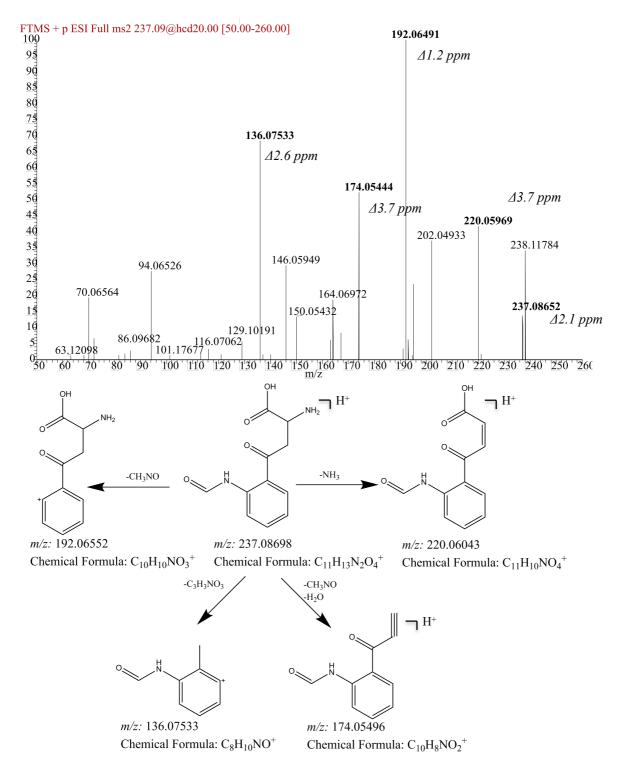


Figure S5. MS/MS data (- ionization mode) used for identification of dityrosine.

MS/MS fragmentation data (PRM) of *m/z* 359.12482.

