

Supporting Information

Characterization of The Functional Changes in Mouse Gut Microbiome Associated with Increased *Akkermansia muciniphila* Population Modulated by Dietary Black Raspberries

Pengcheng Tu¹, Xiaoming Bian², Liang Chi¹, Bei Gao², Hongyu Ru¹, Thomas J Knobloch^{3,4},
Christopher M. Weghorst^{3,4*}, and Kun Lu^{1*}

1. Department of Environmental Sciences and Engineering,
University of North Carolina at Chapel Hill, Chapel Hill, NC, 27519, United States
2. Department of Environmental Health Science,
University of Georgia, Athens, GA, 30602, United States
3. Division of Environmental Health Sciences,
College of Public Health, Ohio State University, Columbus, OH, 43210, United States
4. Comprehensive Cancer Center, The Ohio State University, Columbus, OH, 43210, United States

* Corresponding Authors

Kun Lu, PhD

Department of Environmental Sciences and Engineering

University of North Carolina at Chapel Hill, Chapel Hill, NC, 27599, United States

Tel: 919-966-7337

Email: kunlu@unc.edu

and

Christopher M. Weghorst, PhD

Division of Environmental Health Sciences,

College of Public Health, Ohio State University, Columbus, OH, 43210, United States

Phone: 614-247-4942

Email: weghorst.2@osu.edu

Supplementary figures

Figure S1. Gut microbial comparisons at phylum level in the BRB diet and control groups.

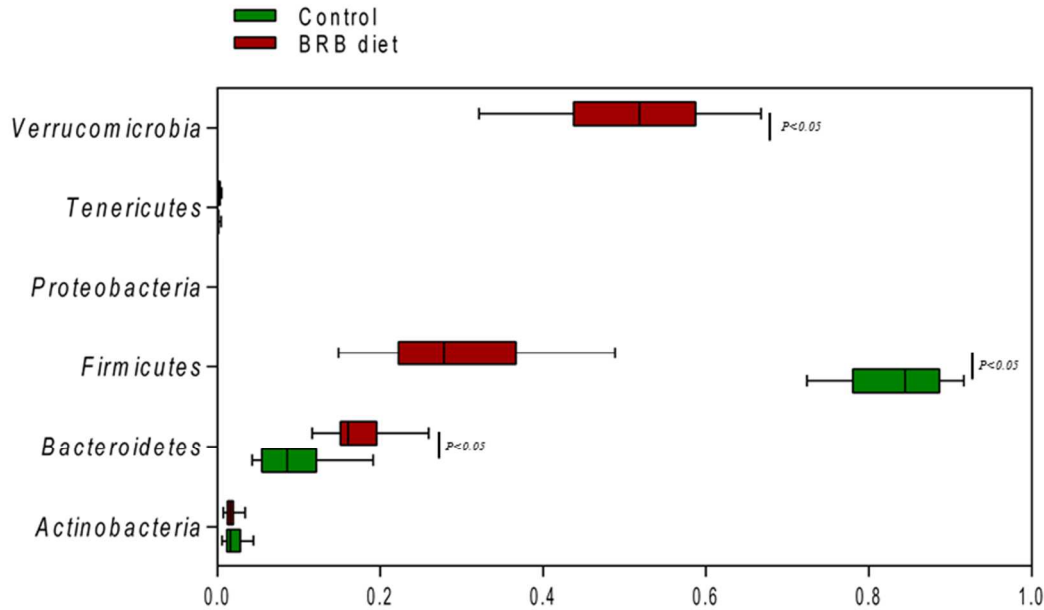


Figure S2. The fold changes of significantly altered gut bacterial genera in the BRB diet group compared to the control group, with 7 increased bacterial genera and 10 decreased genera.

