

Supporting Information

Development of an Integrated Pipeline for Profiling Microbial Proteins from Mouse Fecal Samples by LC-MS/MS

Jing Wu¹, Jianhui Zhu¹, Haidi Yin¹, Xinhua Liu^{1,2}, Mingrui An¹, Nicholas A. Pudlo³, Eric C. Martens³, Grace Y. Chen⁴, and David M. Lubman^{1}*

¹University of Michigan, Department of Surgery, Ann Arbor, MI 48109

²Experiment Center for Science and Technology, Shanghai University of Traditional Chinese Medicine, Shanghai 201203, China

³University of Michigan, Department of Microbiology and Immunology, Ann Arbor, MI 48109

⁴University of Michigan, Division of Hematology/Oncology, Department of Internal Medicine, Ann Arbor, MI 48109

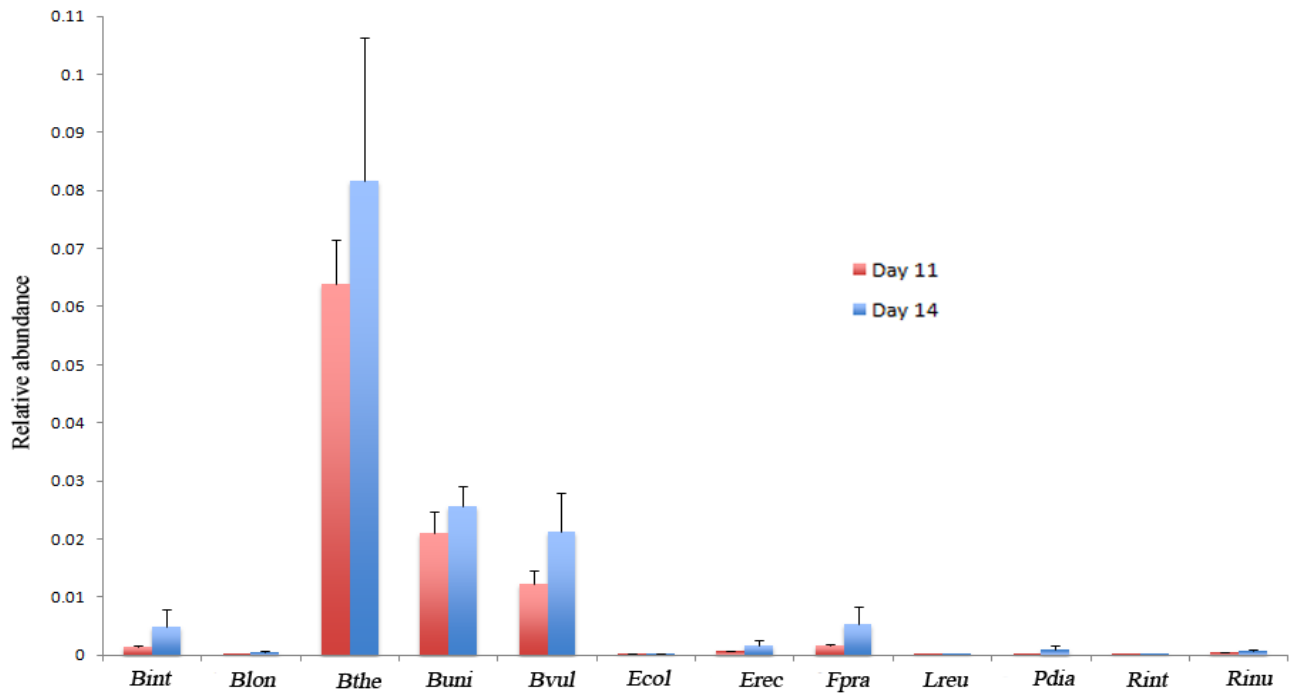
Title running head: An Effective Pipeline for Metaproteomic Characterization

* To whom correspondence should be addressed. David M. Lubman, Department of Surgery, The University of Michigan Medical Center, 1150 West Medical Center Drive, Building MSRB1 Rm A510B, Ann Arbor, MI 48109-0656. E-mail: dmlubman@umich.edu. Telephone: 734-647-8834, Fax: 734-615-2088.

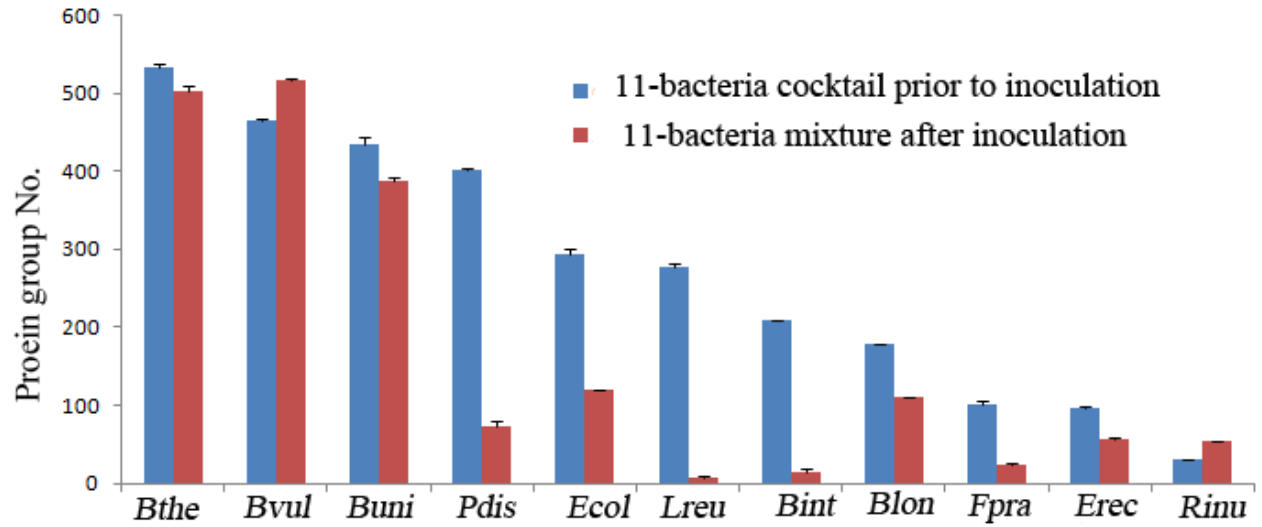
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Supplemental Figure S1. Level of colonization by 11 bacterial species on days 11 and 14 after gavage of germfree mice (N=6). Bacterial DNA was isolated using the Mobio DNA extraction kit followed by qPCR using bacterial specific primers. Bars represent mean abundance of each bacteria strain relative to total bacteria as assessed by a universal bacterial primer. Error bars indicate standard deviation.



Supplemental Figure S2. The number of proteins identified from the 11-bacteria cocktail before and after inoculation to the mice. *Error bar* indicates standard deviation.



Supplemental Table S1. The bacterial-specific primers were used for qPCR

Name	Forward and reverse primer sequence (5'-3')
<i>Bint</i>	TATTGGCACAAGCCATCGTA CACTTTGGCTACGGCTTTGT
<i>Buni</i>	CTGATTGGGTGGACGCTATT CACCTTCACGTTTGCATAA
<i>Rint</i>	TAGTTCGGCAGAAAACCAC TCTTACCGTCCCCGATGTAG
<i>Bthe</i>	TGGTACTTTTGGGGCGAATAGC CTCTGTTGTACCCCTTTTTGTTGTGA
<i>Erec</i>	ATCCGACACAGAAGCCAGAA GGTAGTTCGGATCCACAGA
<i>Lreu</i>	CGCTAGTGAAGGGTCAGGAG AATTACTTGGAGCGCGTTTG
<i>Rinu</i>	ATTCCGGGGATAAAGCAAAG CAATACTGGCAACCTGCTCA
<i>Blon</i>	GACAACCCGCAGTTCATCTT CGTCGATGGTGATGATCTTG
<i>Bvul</i>	AGCAAGCAACTCCCGAAGTA TTCCAATACTGGCACCAA
<i>Fpra</i>	AGGCCAGTGGAACATCTAGG AGTAGGGCATGATGGACTCG
<i>Ecol</i>	TTGTTATAACCGGAGTGCTG CCCCGTTTCTCTCCATTTTT
<i>Pdis</i>	CCGACGTGTTGAATGAGTTG GCTGTACGGCGTCTTTCTTC