Applied Microbiology and Biotechnology

Supplementary Figures

Smokeless tobacco products harbor diverse bacterial microbiota that differ across products and brands

Eoghan M. Smyth^{1,2}, Prachi Kulkarni², Emma Claye², Stephen Stanfill³, Robert Tyx³, Cynthia Maddox¹, Emmanuel F. Mongodin¹, Amy R. Sapkota²

¹Institute for Genome Sciences, University of Maryland School of Medicine, 801 West Baltimore St., Baltimore, MD 21201; ²Maryland Institute for Applied Environmental Health, University of Maryland School of Public Health, 4200 Valley Drive, Bldg #255, College Park, MD 20742; ³Division of Laboratory Sciences, Centers for Disease Control and Prevention, 1600 Clifton Road, Atlanta, GA 30329

Corresponding Author:

Amy R. Sapkota, Ph.D, M.P.H. Maryland Institute for Applied Environmental Health University of Maryland School of Public Health 4200 Valley Drive, Bldg #255, Room 2234P College Park, MD 20742 E-mail: <u>ars@umd.edu</u> Telephone: 301-405-1772 Fax: 301-314-1012

Supplementary Figure Legends:

Figure S1: Scatterplot of Good's coverage to sequencing counts per sample. Solid curved red line represents the LOESS fit model and solid black line represents the cutoff point.

Figure S2: Ordination plot derived from nonmetric multidimensional scaling (NMDS) using *Bray*-Curtis distance of bacterial community composition. Colors, and shapes represent the different lots within a product brand. Toombak and the alkalinizing agent do not have different lots.

Figure S3: Abundance of predicted Kyoto Encyclopedia of Genes and Genomes modules in smokeless tobacco product types. Colors designate product type. Bars represent mean relative abundance of predicted modules per product type, and error bars represent the standard error of mean.

Figure S4: Abundance of predicted hydrocarbon degradation pathways across smokeless tobacco product types.

Figure S5: Abundance of predicted antibiotic biosynthesis pathways across smokeless tobacco product types.











