Online Supporting Material

1. butyrate-producing bacterium ART55/1
2. *Prevotella copri*
3. *Bacteroides uniformis*
4. Clostridiaceae bacterium DJF LS40
5. Clostridiaceae bacterium FH042
6. *Faecalibacterium prausnitzii*
7. human intestinal firmicute CO35
8. *Clostridium clostridioforme*

\[ P < 0.01 \text{ WG versus RG} \]
Supplemental Figure 2. Differences in operational taxonomic units (OTU) prevalence between whole-grain (WG) and refined-grain (RG) groups during the baseline (top 2 panels) and final (bottom 2 panels) time periods. Heat map of selected OTU at the 98% similarity level by participant showing significantly affected OTU as a result of diet group (WG, n=27; RG, n=30). Each row represents data from a single participant in WG or RG. Columns represent the OTU (see legend) with the percent similarity of the representative sequence to the database match listed at the top of each column. Cell shade signifies the sum of the proportion of an OTU in the participant shown and the proportion of that OTU in all participants with darker shades representing a greater value. Numbers within cells correspond to the number of sequence reads for an OTU within the corresponding participant.