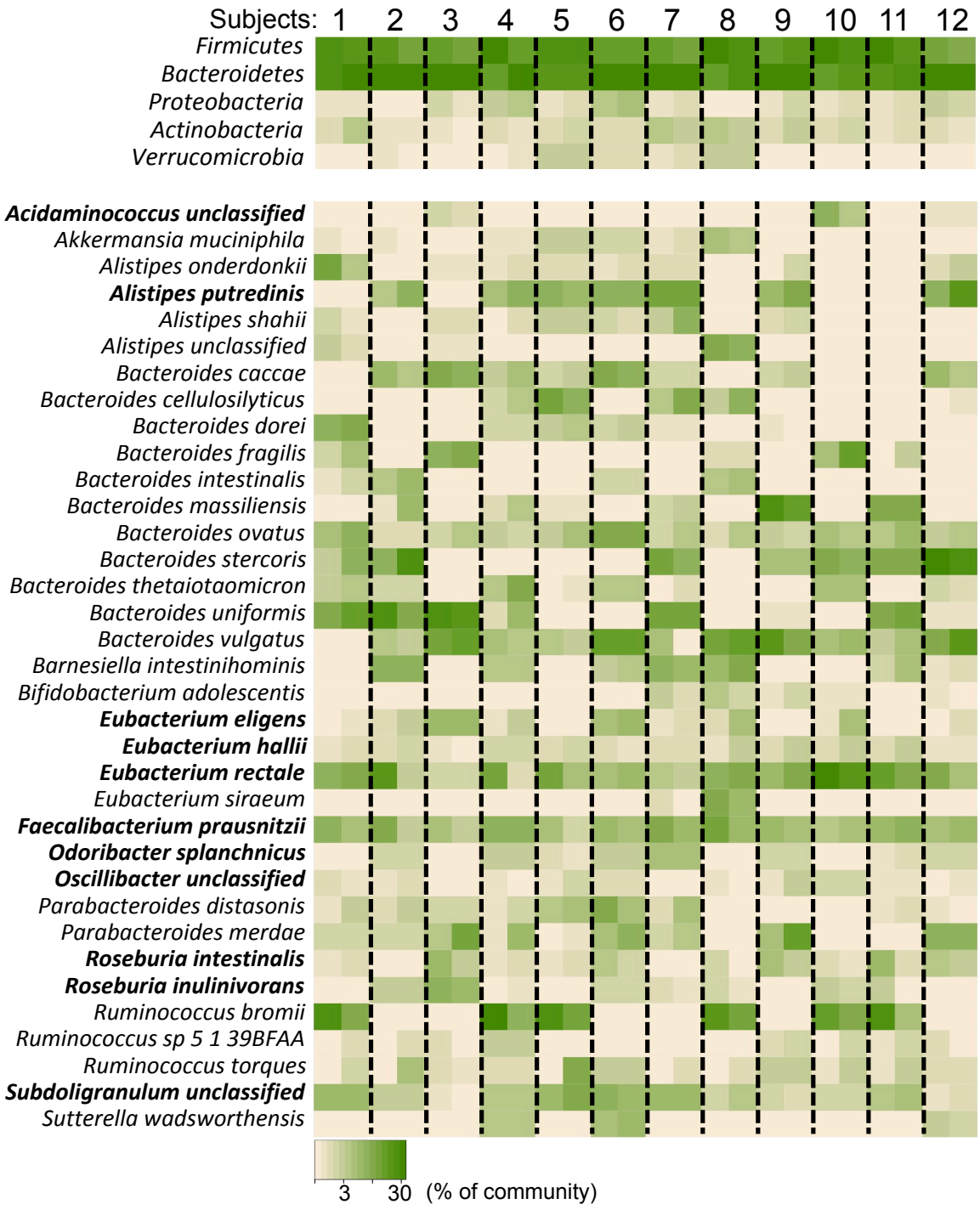

Figure S1. Taxonomic composition on phylum and species level of the 12 participants. Results of samples derived from high RS2 diets followed by those from low RS2 diets are displayed for each individual. Taxa associated with butyrate production based on Vital et al 2017, mSystems **2**:e00130-17 are shown in bold.

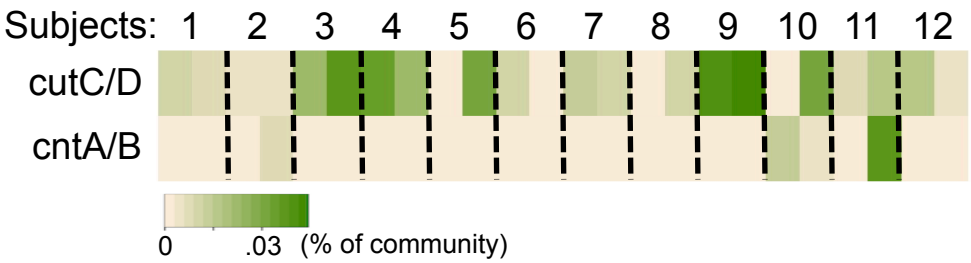

Figure S2. Abundance of major TMA-producing pathways fed by choline (cutC/D) and carnitine (cntA/B). Results of samples derived from high RS2 diets followed by those from low RS2 diets are displayed for each individual.

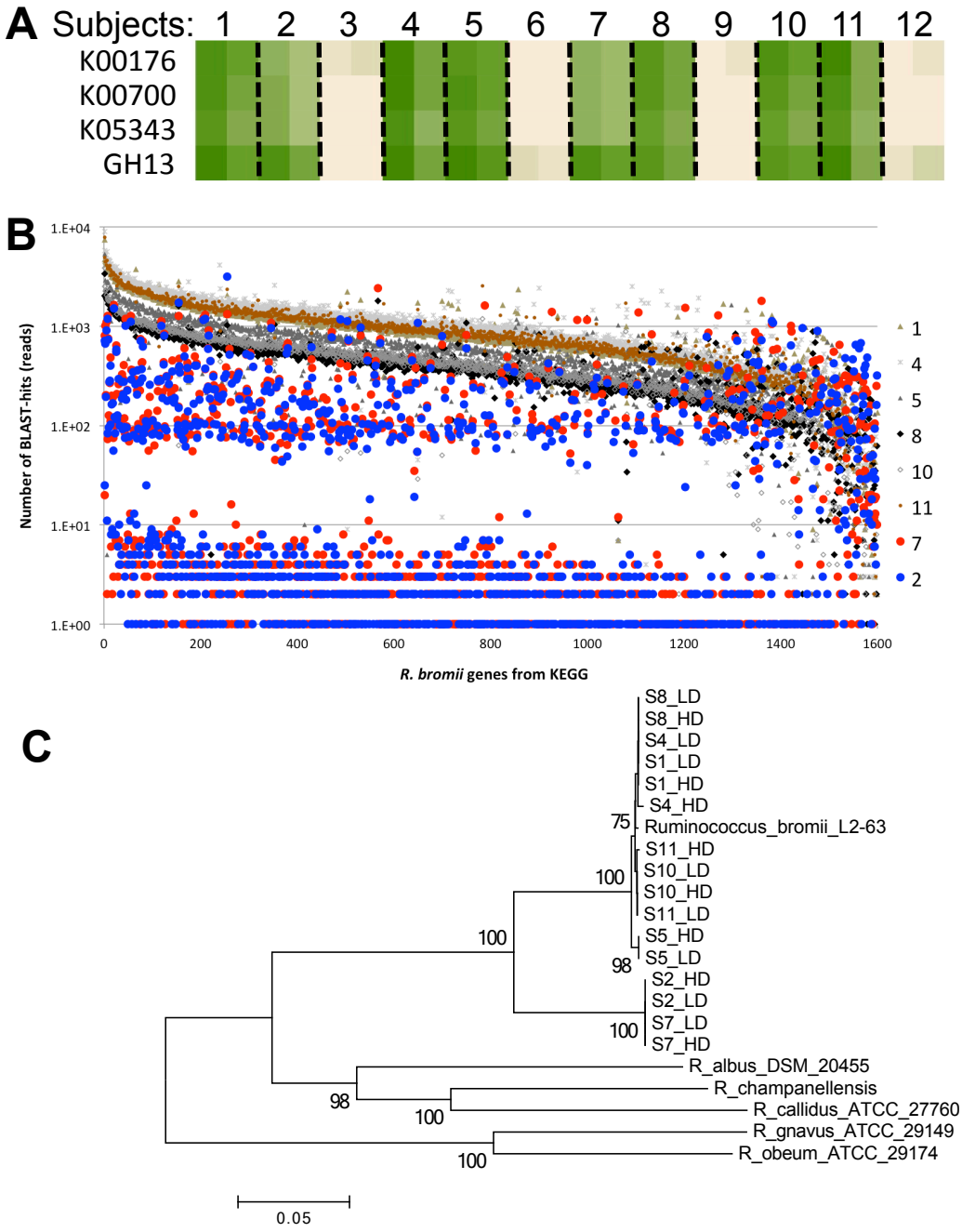

Figure S3. Specific analyses on *Ruminococcus bromii.* Abundance of major starch degrading enzymes associated with that taxon are shown in panel A, where results of samples derived from high RS2 diets followed by those from low RS2 diets are displayed for each individual. Panel B shows number of reads mapped to *R. bromii* genes based on BLASTing (blastn) reads against

the entire KEEG database (recording the top hit only). All genes that received a hit are displayed and ordered according to number of reads recruited. Only samples derived from high RS2 diets and from individuals exhibiting the taxon at high concentrations (panel A) are given. Coverage patterns of samples from subjects 1,4,5,8,10,11 follow a regular shape, whereas results from subjects 2 and 7 are highly scattered. Panel C displays a neighbor-joining tree based on full-length *rplB* nucleotide sequences related to *R. bromii* obtained with Xander from our metagenomes along with gene-sequences from other *Ruminococcus* species. Sequences from all individuals exhibiting the taxon at high concentrations (panel A) are given where H and L represent *rplB*-sequences obtained from samples given the high and low dose of RS2, respectively. Sequences from subjects 2 and 7 form a separate clade showing lower nucleotide similarity (<90%) to the *R. bromii* reference compared with sequences obtained from other individuals.