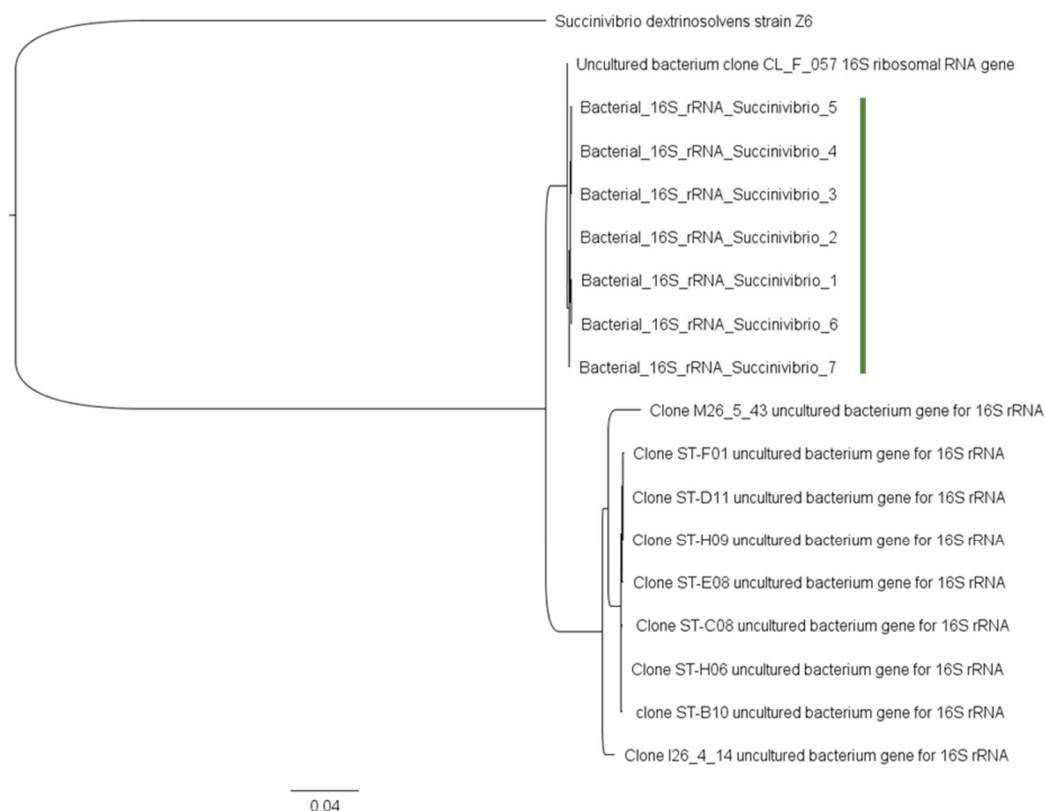
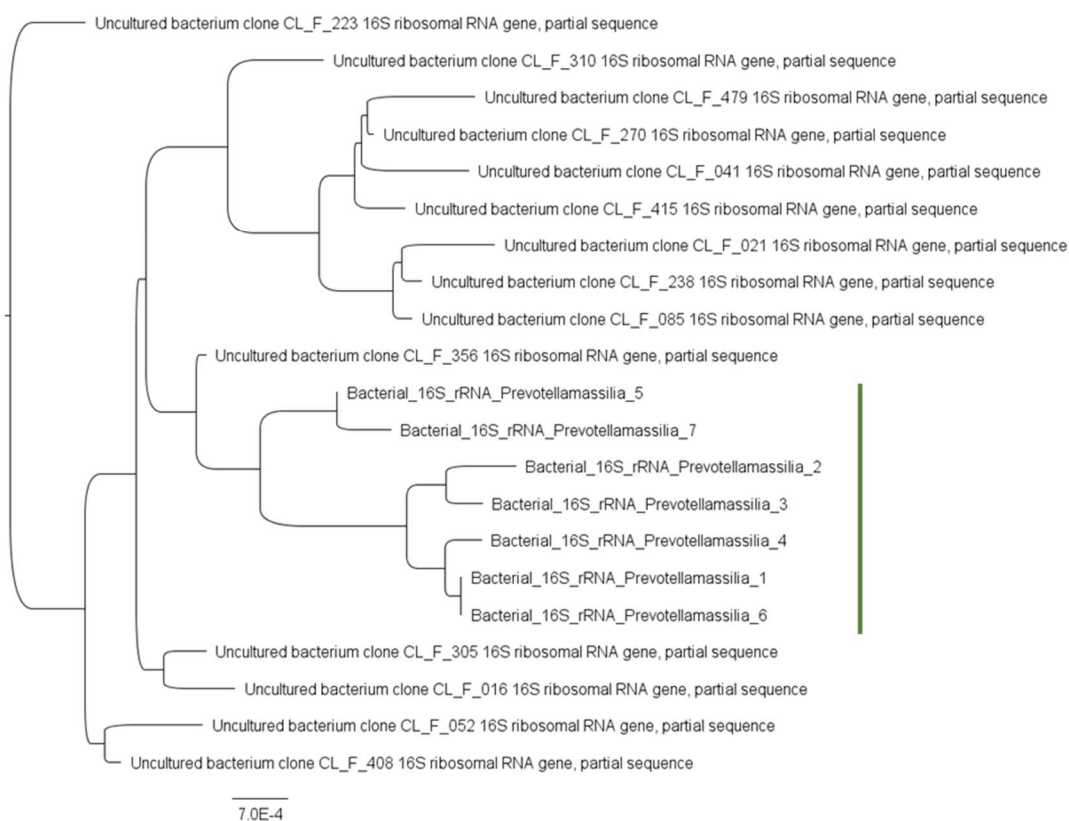


Additional File 6. Phylogenetic 16S rRNA gene tree of HQ MAGs. The phylogenetic trees were computed using MOLE-BLAST against nt/nr database and including uncultured and environmental taxa. The 16S rRNA genes from our HQ MAGs are indicated with a green line. A) *Succinivibrio*: Uncultured bacterium clone CL_F_057 16S from wild wolves' feces [1]; B) *Prevotellamassilia*: Uncultured bacterium clone with codes CL_F from wild wolves' feces [1]; C) *Phascolarctobacterium*: Uncultured bacterium clone C2-26 from canine GI tract [2]; D) *Catenibacterium*: Uncultured organism clone ELU0052-T330-S-NIPCRAMgANa_000116 from the human GI microbiome [3]; and E) *Blautia* sp900541345 : *Ruminococcus* sp. WAL 17306 from the human GI microbiome (FJ687607.1).

A) *Succinivibrio* HQ MAG

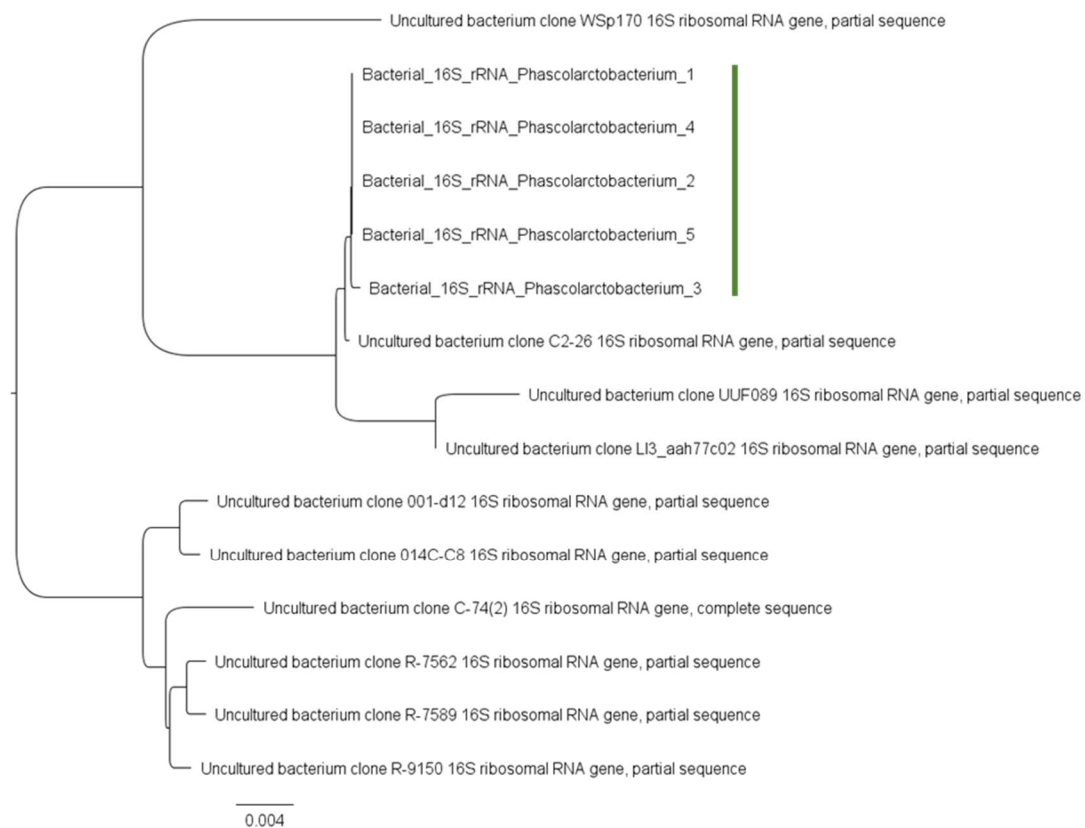


B) *Prevotellamassilia* HQ MAG

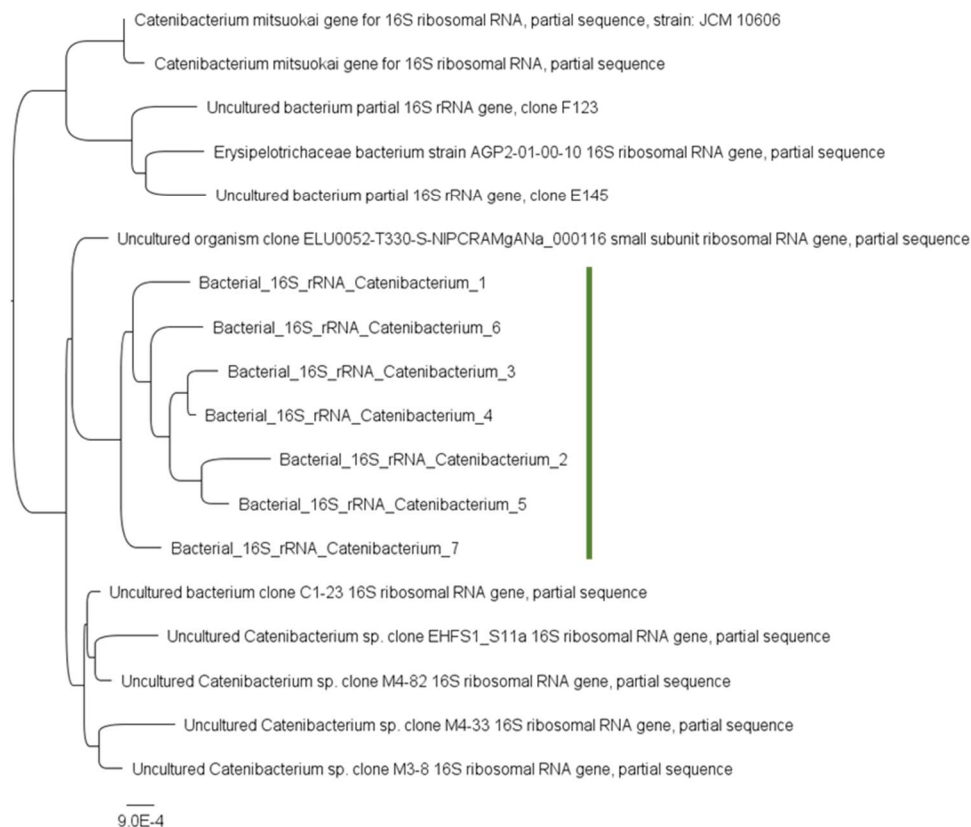


Additional File 6. Phylogenetic 16S rRNA gene tree of HQ MAGs (Cont.)

C) *Phascolarctobacterium* HQ MAG

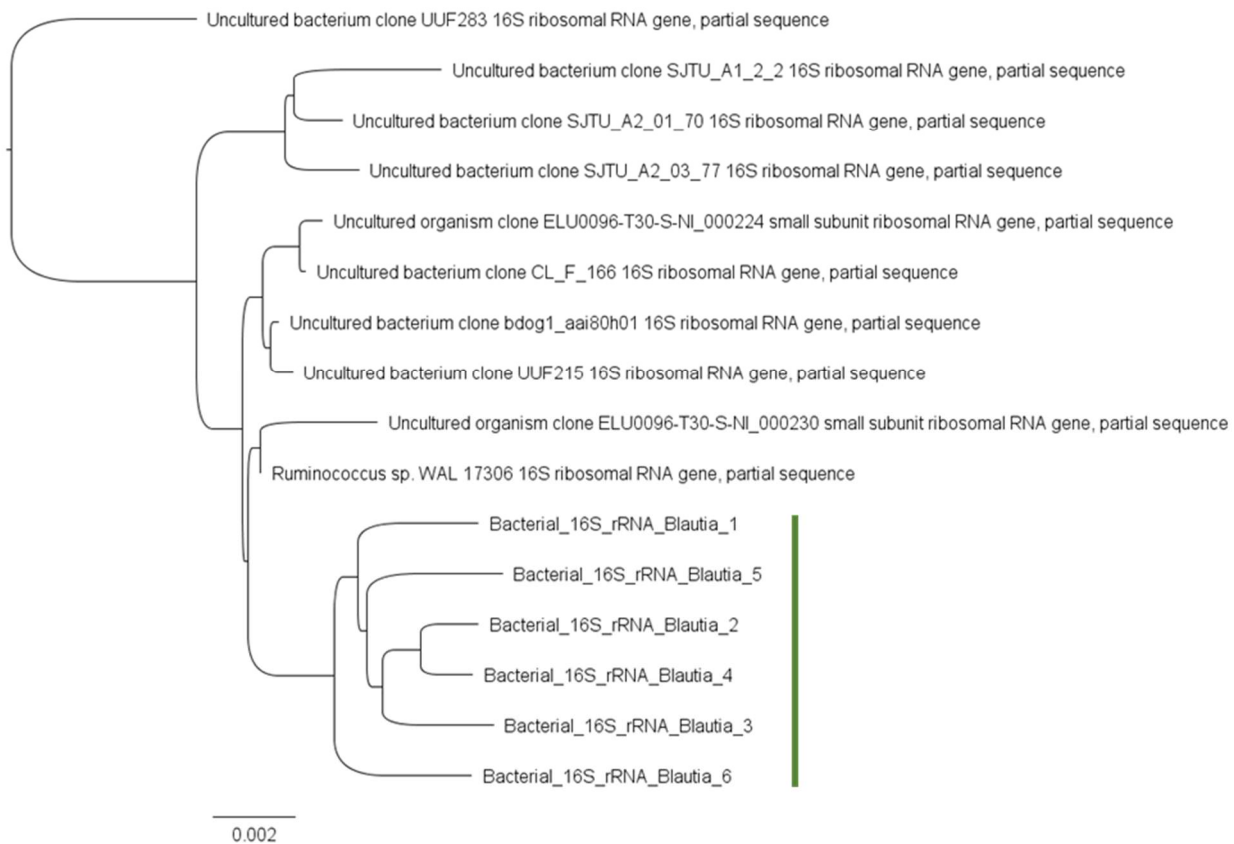


D) *Catenibacterium* HQ MAG



Additional File 6. Phylogenetic 16S rRNA gene tree of HQ MAGs (Cont.)

E) *Blautia* sp900541345 HQ MAG



References:

1. Zhang H, Chen L. Phylogenetic analysis of 16S rRNA gene sequences reveals distal gut bacterial diversity in wild wolves (*Canis lupus*). *Mol Biol Rep*. 2010;37:4013–22.
2. Suchodolski JS, Camacho J, Steiner JM. Analysis of bacterial diversity in the canine duodenum, jejunum, ileum, and colon by comparative 16S rRNA gene analysis. *FEMS Microbiol Ecol*. 2008;66:567–78.
3. Li E, Hamm CM, Gulati AS, Sartor RB, Chen H, Wu X, et al. Inflammatory Bowel Diseases Phenotype, *C. difficile* and NOD2 Genotype Are Associated with Shifts in Human Ileum Associated Microbial Composition. *PLOS ONE*. 2012;7:e26284.