**Table S4 Characteristic genera in the gut bacterial community of mammal hosts grouped by diet and habitat.**

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| --- | --- | --- | --- | --- |
| **Group** | **Phylum** | **Genus** | **Average abundance** | **Contribution to total (%)** |
| **Terrestrial herbivores**  | *Firmicutes* | *Oscillibacter* | 2.4 | 10.4 |
| *Firmicutes* | *Coprococcus* | 2.0 | 9.4 |
| *Bacteroidetes* | *Rikenella* | 1.6 | 6.8 |
| *Firmicutes* | *Papillibacter* | 1.5 | 6.4 |
| *Firmicutes* | *Robinsoniella* | 1.3 | 4.9 |
| *Firmicutes* | *Acetivibrio* | 1.3 | 4.7 |
| *Firmicutes* | *Sporobacter* | 1.2 | 4.6 |
| *Firmicutes* | *Ruminococcus* | 1.3 | 4.5 |
| *Firmicutes* | *Ethanoligenens* | 1.0 | 3.2 |
| *Firmicutes* | *Anaerotruncus* | 0.9 | 3.0 |
| **Terrestrial omnivores** | *Bacteroidetes* | *Prevotella* | 2.2 | 11.9 |
| *Firmicutes* | *Coprococcus* | 1.7 | 10.9 |
| *Firmicutes* | *Blautia* | 1.9 | 10.4 |
| *Firmicutes* | *Streptococcus* | 1.5 | 4.8 |
| *Firmicutes* | *Oscillibacter* | 1.2 | 4.6 |
| *Bacteroidetes* | *Bacteroides* | 1.5 | 4.5 |
| *Firmicutes* | *Robinsoniella* | 0.9 | 3.8 |
| *Firmicutes* | *Faecalibacterium* | 1.0 | 3.6 |
| *Bacteroidetes* | *Barnesiella* | 0.9 | 3.5 |
| *Proteobacteria* | *Hallella* | 0.7 | 3.3 |
| **Terrestrial carnivores**  | *Firmicutes* | *Peptostreptococcus* | 3.1 | 19.3 |
| *Firmicutes* | *Clostridium* | 2.7 | 16.6 |
| *Firmicutes* | *Sporacetigenium* | 2.1 | 11.7 |
| *Firmicutes* | *Blautia* | 2.4 | 11.5 |
| *Firmicutes* | *Coprococcus* | 1.5 | 7.8 |
| *Actinobacteria* | *Collinsella* | 1.5 | 5.7 |
| *Firmicutes* | *Lactobacillus* | 1.8 | 5.6 |
| *Proteobacteria* | *Escherichia / Shigella* | 1.2 | 5.0 |
| *Firmicutes* | *Robinsoniella* | 0.8 | 2.6 |
| *Firmicutes* | *Enterococcus* | 0.8 | 2.5 |
| **Marine carnivores** | *Fusobacteria* | *Fusobacterium* | 3.0 | 16.8 |
| *Firmicutes* | *Faecalibacterium* | 1.9 | 9.8 |
| *Fusobacteria* | *Cetobacterium* | 1.9 | 8.9 |
| *Firmicutes* | *Oscillibacter* | 1.6 | 7.4 |
| *Proteobacteria* | *Psychrobacter* | 1.9 | 6.2 |
| *Bacteroidetes* | *Bacteroides* | 1.5 | 5.5 |
| *Firmicutes* | *Butyricicoccus* | 0.9 | 3.6 |
| *Firmicutes* | *Sporanaerobacter* | 1.0 | 3.2 |
| *Firmicutes* | *Sporobacter* | 0.7 | 3.0 |
| *Bacteroidetes* | *Porphyromonas* | 1.1 | 2.9 |
| **Marine herbivore** | *Firmicutes* | *Clostridium* | 10.0 | 11.1 |
| *Firmicutes* | *Coprococcus* | 7.0 | 7.8 |
| *Bacteroidetes* | *Bacteroides* | 6.0 | 6.7 |
| *Bacteroidetes* | *Prevotella* | 6.0 | 6.7 |
| *Firmicutes* | *Oscillibacter* | 5.0 | 5.6 |
| *Verrucomicrobia* | *Akkermansia* | 4.0 | 4.4 |
| *Firmicutes* | *Anaerotruncus* | 4.0 | 4.4 |
| *Bacteroidetes* | *Alistipes* | 3.0 | 3.3 |
| *Firmicutes* | *Roseburia* | 3.0 | 3.3 |
| *Firmicutes* | *Ruminococcus* | 3.0 | 3.3 |

The foremost ten characteristic genera in the gut bacterial community of hosts identified using SIMPER analysis. Hosts are grouped based on diet and habitat.