

SupplementaryTable3: Number of OTUs belonging to each iBBiG module along with the major genera (relative abundance greater than 1% after removing the unclassified OTUs within each module)

iBBiG_Module	Number of OTUs	Major Genera
a	291	Lachnospiracea_incertae_sedis, Blautia, Clostridium_IV, Coprococcus, Bacteroides, Faecalibacterium, Roseburia, Oscillibacter, Gemmiger, Ruminococcus, Alistipes, Bifidobacterium, Dorea, Flavonifractor, Clostridium_XIVa, Clostridium_XI, Parabacteroides, Streptococcus
b	153	Clostridium_IV, Coprococcus, Lachnospiracea_incertae_sedis, Oscillibacter, Faecalibacterium, Sporobacter, Flavonifractor, Gemmiger, Prevotella, Acetanaerobacterium, Bacteroides, Blautia, Butyricimonas, Clostridium_XIVa, Clostridium_XIVb, Enterorhabdus, Erysipelotrichaceae_incertae_sedis, Haemophilus, Methanobrevibacter, Parasutterella, Pseudobutyrvibrio, Ruminococcus, Slackia
c	90	Clostridium_IV, Alistipes, Oscillibacter, Erysipelotrichaceae_incertae_sedis, Flavonifractor, Sporobacter, Gemmiger, Ruminococcus, Acetanaerobacterium, Anaerofilum, Asaccharobacter, Blautia, Clostridium_XIVa, Eggerthella, Gordonibacter, Pseudoflavonifractor, Roseburia
d	99	Lachnospiracea_incertae_sedis, Bacteroides, Blautia, Coprococcus, Faecalibacterium, Ruminococcus, Alistipes, Clostridium_XIVb, Gemmiger, Anaerostipes, Barnesiella, Butyricimonas, Clostridium_IV, Dorea, Haemophilus, Lactococcus, Oscillibacter, Parasutterella, Sporacetigenium
e	142	Lachnospiracea_incertae_sedis, Blautia, Roseburia, Clostridium_XIVa, Bacteroides, Dorea, Bifidobacterium, Actinomyces, Clostridium_IV, Coprococcus, Gemmiger, Streptococcus, Anaerostipes, Clostridium_XI, Clostridium_XVIII, Faecalibacterium, Flavonifractor, Ruminococcus
f	66	Lachnospiracea_incertae_sedis, Blautia, Clostridium_IV, Faecalibacterium, Ruminococcus, Actinomyces, Alistipes, Anaerostipes, Bacteroides, Clostridium_XIVa, Coprococcus, Dorea, Eggerthella, Erysipelotrichaceae_incertae_sedis, Flavonifractor, Gemmiger, Gordonibacter, Granulicatella, Rothia