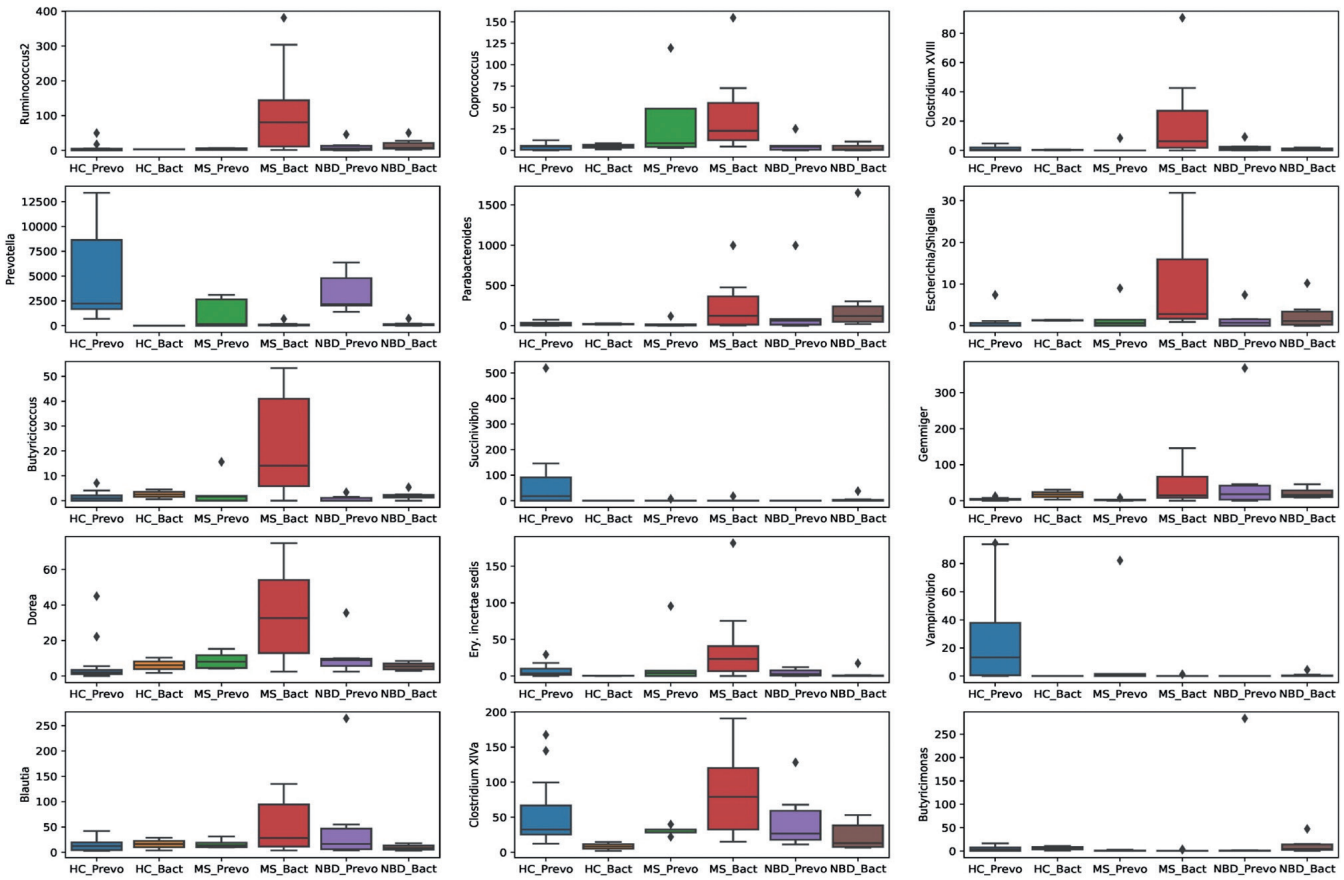
Supplementary Table 1: Best 30 descriminating individual OTUs between HC, MS, and NBD according to ANOVA analysis. Here p, c, o, f, and g are abbreviations for Phylum, Class, Order, Family, and Genus.

OTU	Taxonomy
OTU_125	*p Firmicutes; c Clostridia; o Clostridiales; f unclassified_Clostridiales; g unclassified_Clostridiales*
OTU_10	*p Bacteroidetes; c Bacteroidia;o Bacteroidales; f Prevotellaceae; g Prevotella*
OTU_1	*p Bacteroidetes; c Bacteroidia;o Bacteroidales; f Prevotellaceae; g Prevotella*
OTU_43	*p Proteobacteria; c Deltaproteobacteria;o Bdellovibrionales; f Bdellovibrionaceae; g Vampirovibrio*
OTU_36	*p Proteobacteria; c Gammaproteobacteria; o Aeromonadales; f Succinivibrionaceae; g Succinivibrio*
OTU_94	*p Bacteroidetes; c Bacteroidia; o Bacteroidales; f Prevotellaceae; g Prevotella*
OTU_170	*p Proteobacteria; c Betaproteobacteria; o Burkholderiales; f unclassified_Burkholderiales*
OTU_3	*p Bacteroidetes; c Bacteroidia; o Bacteroidales; f Prevotellaceae; g Prevotella*
OTU_47	*p Firmicutes; c Clostridia; o Clostridiales; f Lachnospiraceae; g Coprococcus*
OTU_148	*p Proteobacteria; c Betaproteobacteria; o Burkholderiales; f unclassified_Burkholderiales*
OTU_87	*p Firmicutes; c Clostridia; o Clostridiales; f Lachnospiraceae; g Coprococcus*
OTU_34	*p Firmicutes; c Clostridia; o Clostridiales; f Lachnospiraceae; g unclassified_Lachnospiraceae*
OTU_69	*p Firmicutes; c Clostridia; o Clostridiales; f Lachnospiraceae; g unclassified_Lachnospiraceae*
OTU_9	*p Bacteroidetes; c Bacteroidia; o Bacteroidales; f Prevotellaceae; g Prevotella*
OTU_49	*p Firmicutes; c unclassified_Firmicutes*
OTU_89	*p Bacteroidetes; c Bacteroidia; o Bacteroidales; f Prevotellaceae; g Prevotella*
OTU_225	*p Firmicutes; c Clostridia; o Clostridiales; f Lachnospiraceae; g unclassified_Lachnospiraceae*
OTU_42	*p Firmicutes; c Clostridia; o Clostridiales; f unclassified_Clostridiales; g unclassified_Clostridiales*
OTU_20	*p Firmicutes; c Clostridia; o Clostridiales; f Ruminococcaceae; g unclassified_Ruminococcaceae*
OTU_140	*p Actinobacteria; c Actinobacteria; o Coriobacteriales;f Coriobacteriaceae; g unclassified_Coriobacteriaceae*
OTU_14	*p Bacteroidetes; c Bacteroidia; o Bacteroidales; f Porphyromonadaceae; g Parabacteroides*
OTU_13	*p Bacteroidetes; c Bacteroidia; o Bacteroidales; f Rikenellaceae; g Alistipes*
OTU_52	*p Firmicutes; c Clostridia; o Clostridiales; f unclassified_Clostridiales; g unclassified_Clostridiales*
OTU_126	*p Firmicutes; c Clostridia; o Clostridiales; f Lachnospiraceae; g Lachnospiracea_incertae_sedis*
OTU_211	*p Firmicutes; c Clostridia; o Clostridiales; f Peptococcaceae 1; g Peptococcus*
OTU_182	*p Firmicutes; c Clostridia; o Clostridiales; f Ruminococcaceae; g unclassified_Ruminococcaceae*
OTU_45	*p Firmicutes; c Clostridia; o Clostridiales; f Ruminococcaceae; g unclassified_Ruminococcaceae*
OTU_334	*p unclassified_Bacteria*
OTU_78	*p Firmicutes; c Clostridia; o Clostridiales; f Ruminococcaceae; g unclassified_Ruminococcaceae*
OTU_25	*p Firmicutes; c Clostridia; o Clostridiales; f Lachnospiraceae; g Lachnospiracea_incertae_sedis*



Supplementary Fig. 1: Box-polts of the DESeq2 scaled abundances of the named significantly different genera mentioned in Table II, Table III, and Table IV. The box indicates the 1st and 3rd quartiles and the horizontal line in the box indicates the mean value.