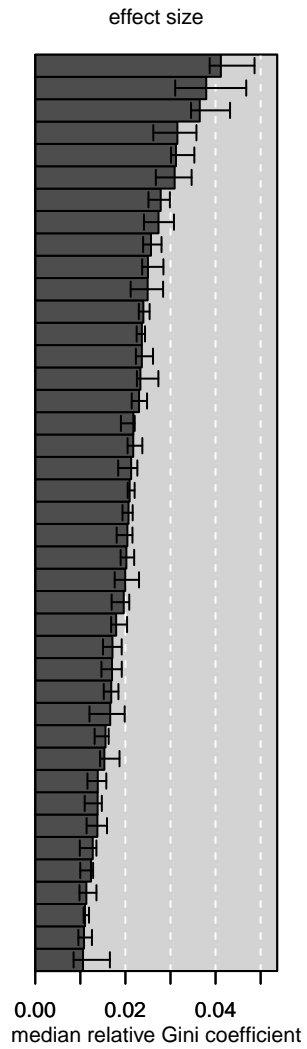
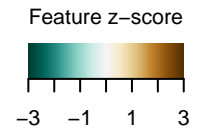
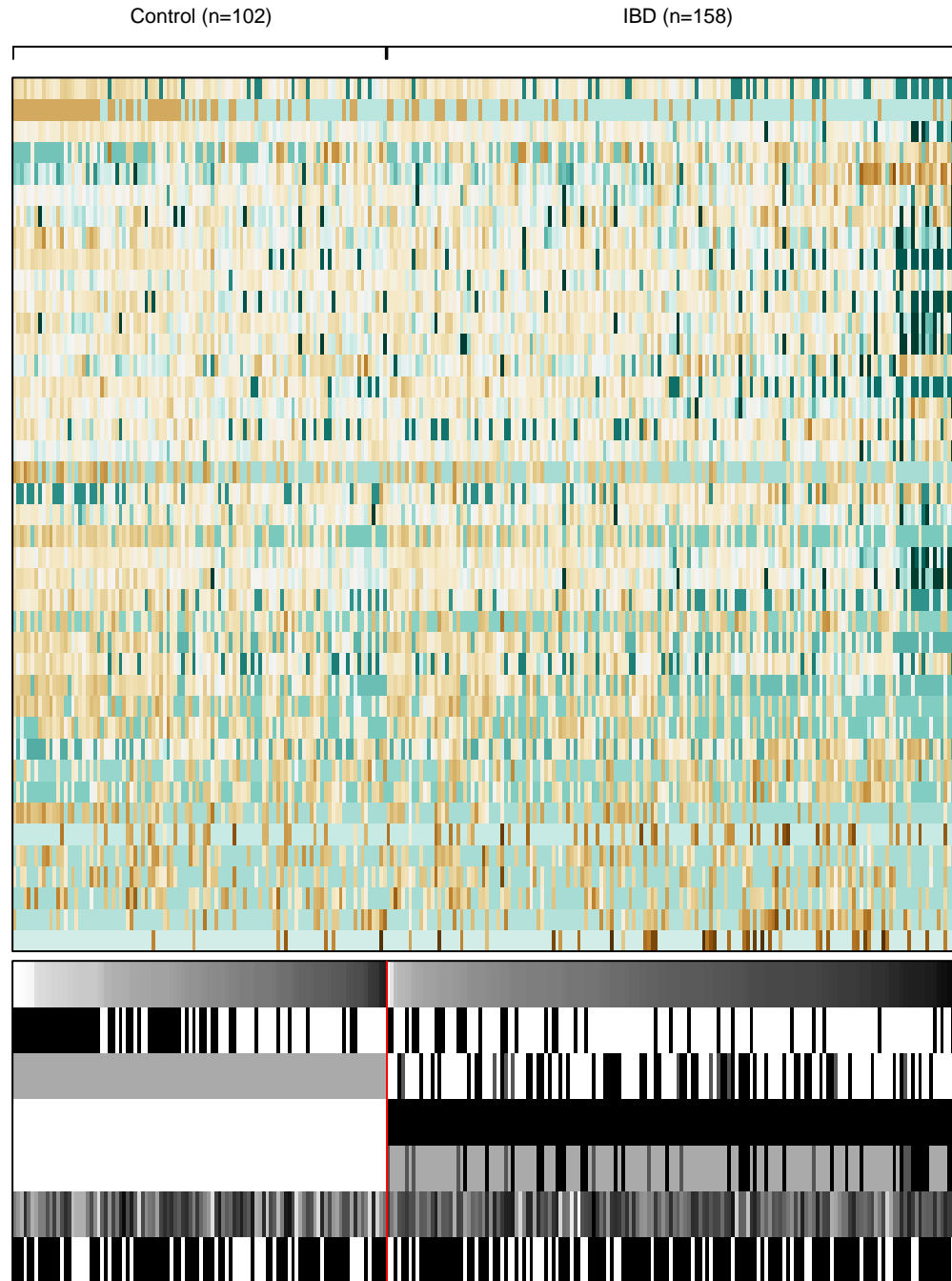


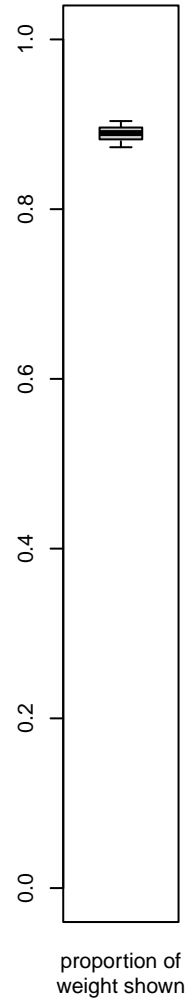
Feature Weights



Metagenomic Features



randomForest model
(|W| = 41)



- Oribacterium
- META_DIARRHOEA
- Veillonella
- Corynebacterium
- Streptococcus
- Gemella
- Capnocytophaga
- Leptotrichia
- Lachnoanaerobaculum
- Haemophilus
- Campylobacter
- Porphyromonas
- Alloprevotella
- Rothia
- Solobacterium
- Actinomyces
- Bergeyella
- Granulicatella
- Catonella
- Lautropia
- Neisseria
- Stomatobaculum
- Prevotella
- Fusobacterium
- Atopobium
- Saccharibacteria (TM7) [G-6]
- Peptostreptococcus
- Saccharibacteria (TM7) [G-1]
- Peptostreptococcaceae [X][G-1]
- Saccharibacteria (TM7) [G-3]
- Megasphaera
- Abiotrophia
- Kingella
- Aggregatibacter
- Ruminococcaceae [G-2]
- Dialister
- Ruminococcaceae [G-1]
- Selenomonas
- Parvimonas
- Cardiobacterium
- Ottowia