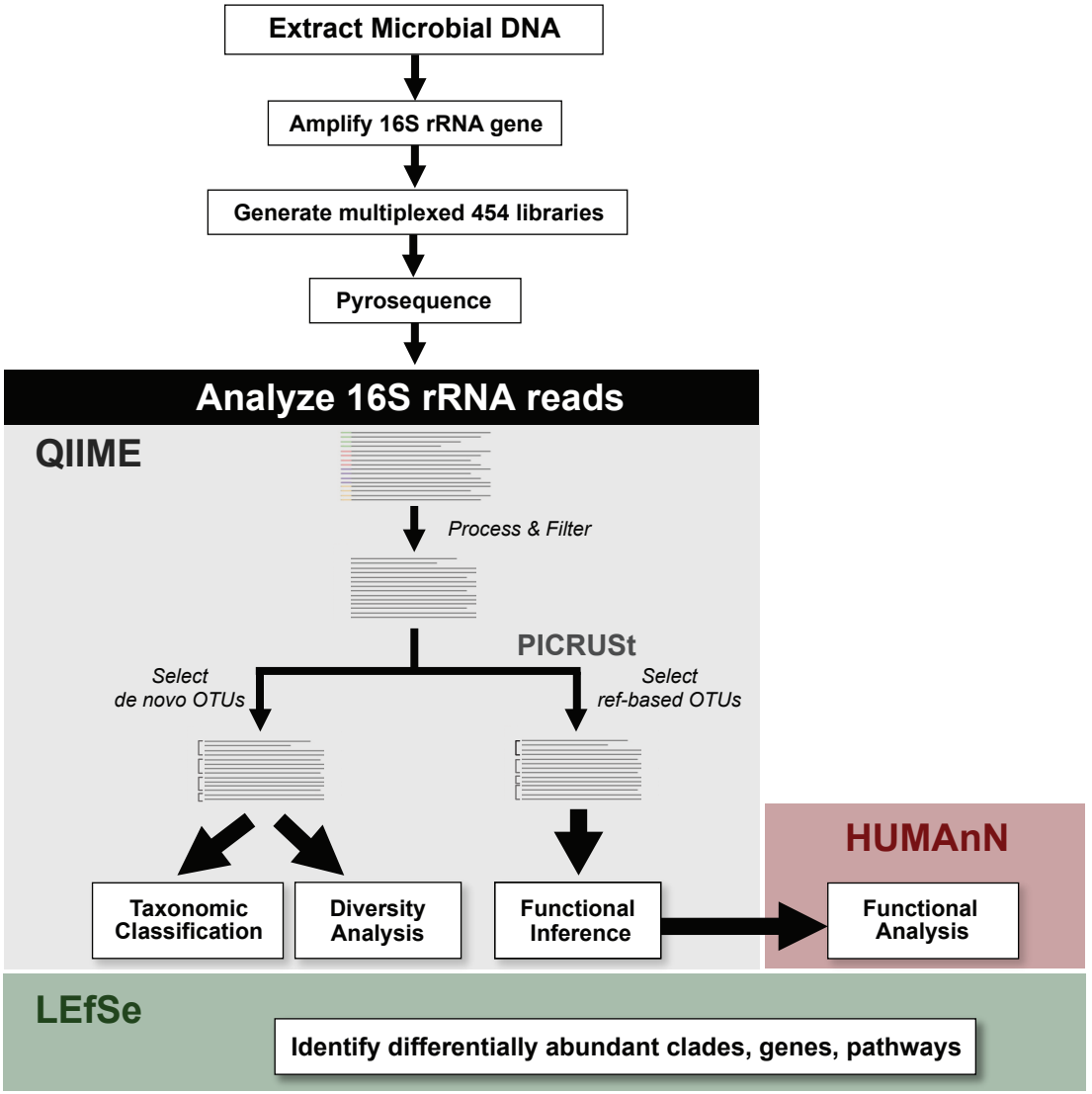
Figure S1


Extract Microbial DNA
Amplify 16S rRNA gene
Generate multiplexed 454 libraries
Pyrosequence
Analyze 16S rRNA reads
QIIME
Process & Filter
PICRUSt
Select de novo OTUs
Select ref-based OTUs
Taxonomic Classification
Diversity Analysis
Functional Inference
HUMAnN
Functional Analysis
LEfSe
Identify differentially abundant clades, genes, pathways