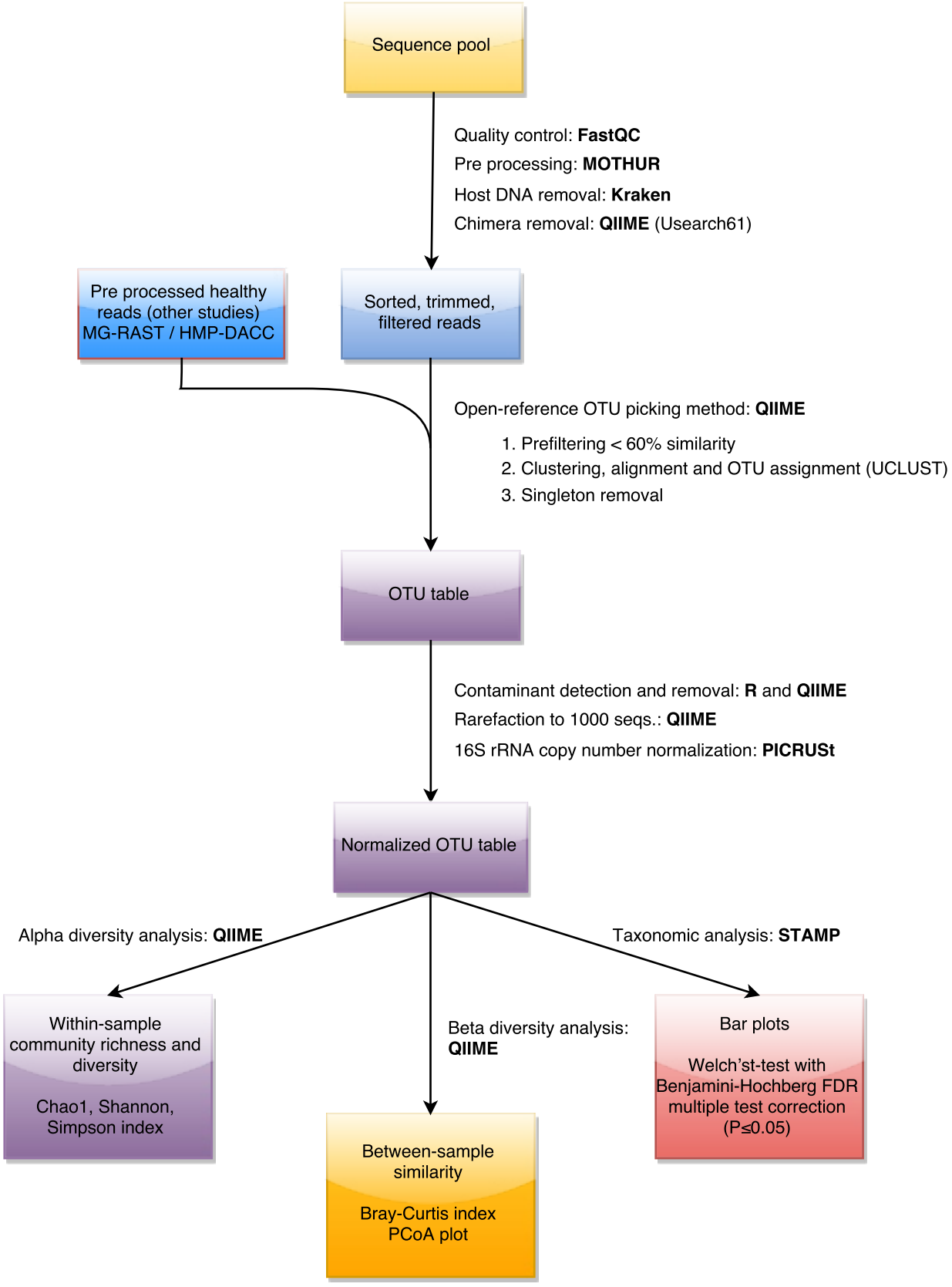
Sequence pool
Quality control: FastQC
Pre processing: MOTHUR
Host DNA removal: Kraken
Chimera removal: QIIME (Usearch61)
Pre processed healthy reads (other studies) MG-RAST / HMP-DACC
Sorted, trimmed, filtered reads
Open-reference OTU picking method: QIIME
1. Prefiltering < 60% similarity
2. Clustering, alignment and OTU assignment (UCLUST)
3. Singleton removal
OTU table
Contaminant detection and removal: R and QIIME
Rarefaction to 1000 seqs.: QIIME
16S rRNA copy number normalization: PICRUSt
Normalized OTU table
Alpha diversity analysis: QIIME
Taxonomic analysis: STAMP
Within-sample community richness and diversity
Chao1, Shannon, Simpson index
Beta diversity analysis: QIIME
Bar plots
Welch'st-test with Benjamini-Hochberg FDR multiple test correction (P≤0.05)
Between-sample similarity
Bray-Curtis index
PCoA plot