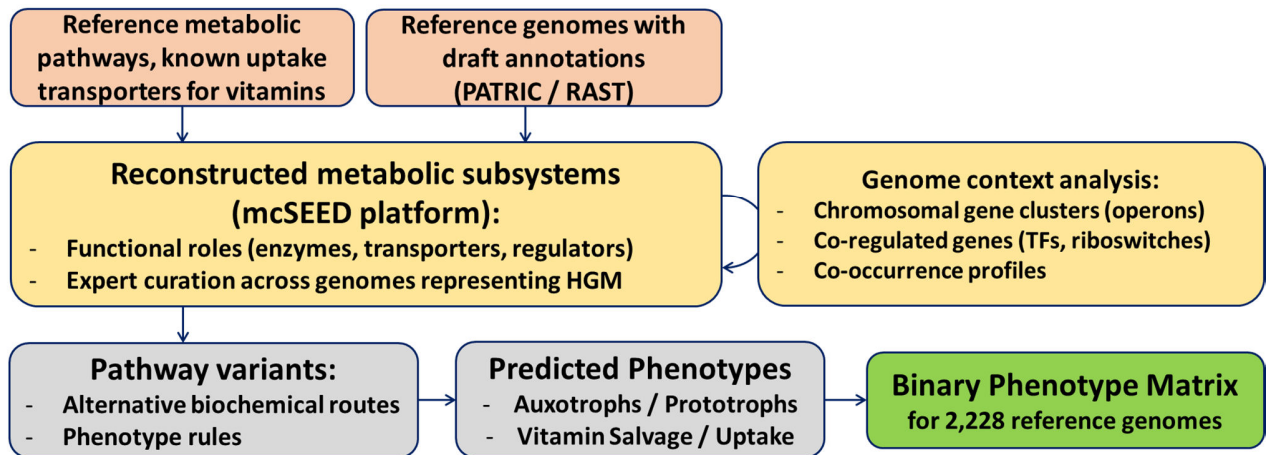


(A)



(B)

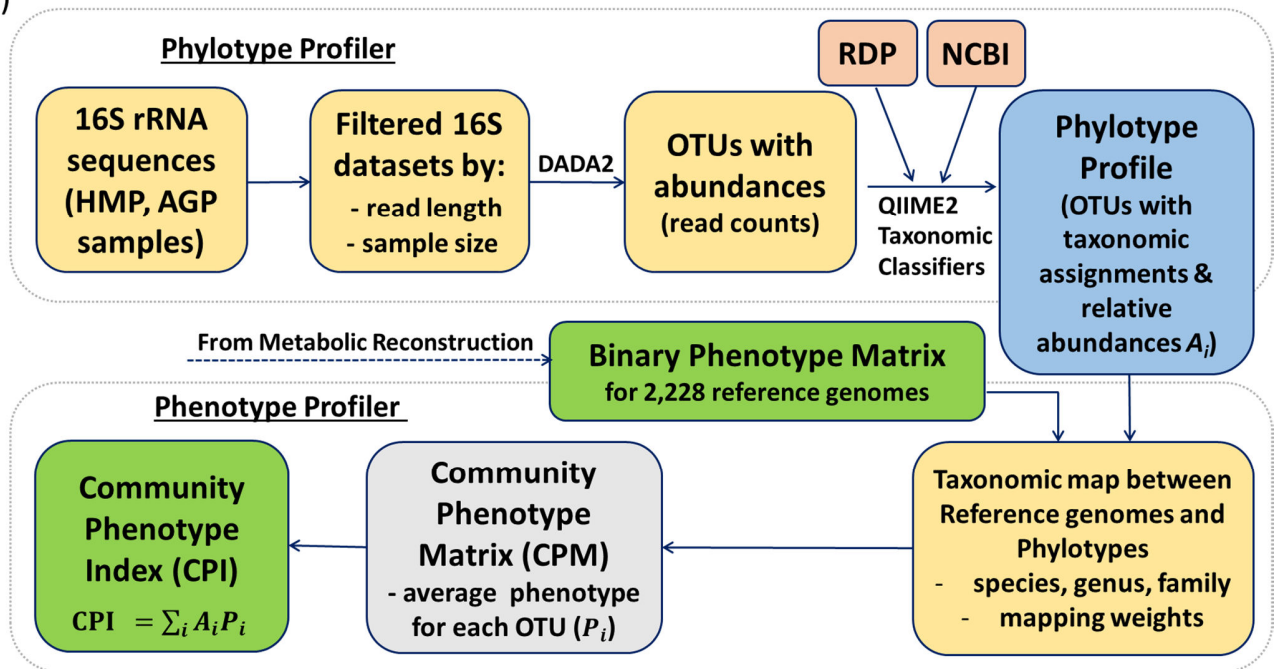


Figure S2. Workflows used for (A) comparative genomics reconstruction of metabolic pathways and phenotype assignments in reference genomes, and (B) predictive phenotype profiling of 16S communities.