(A)

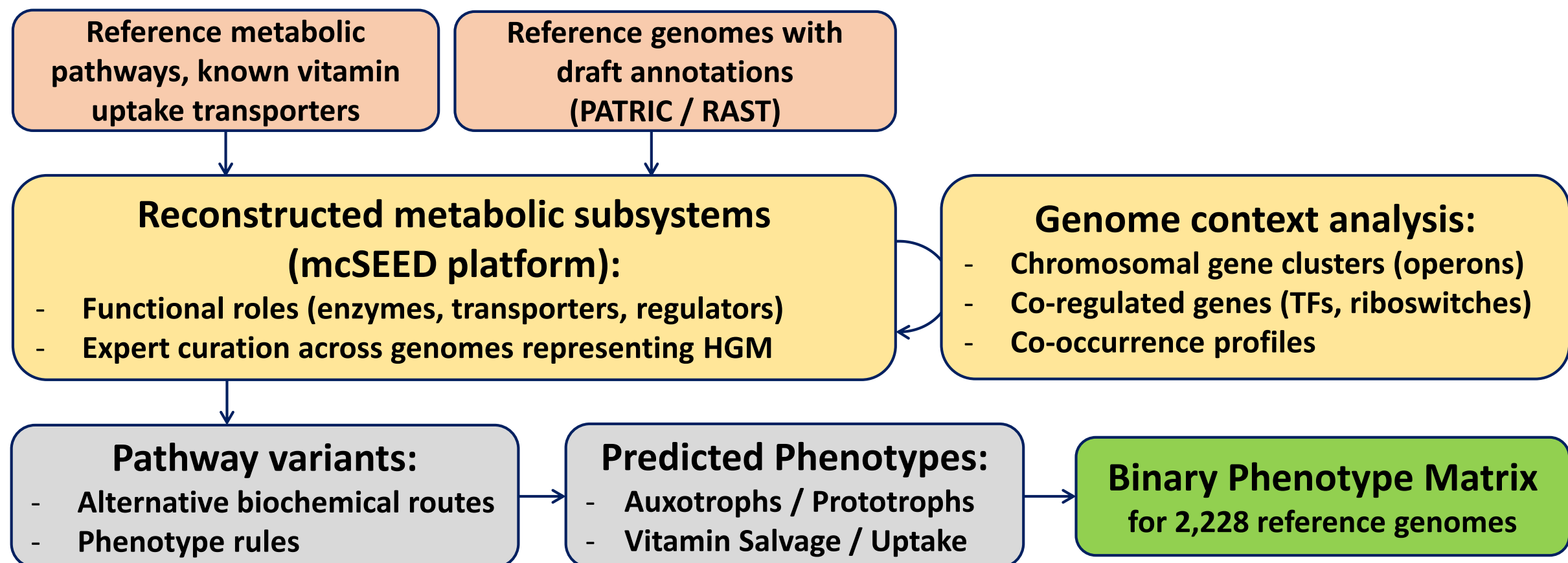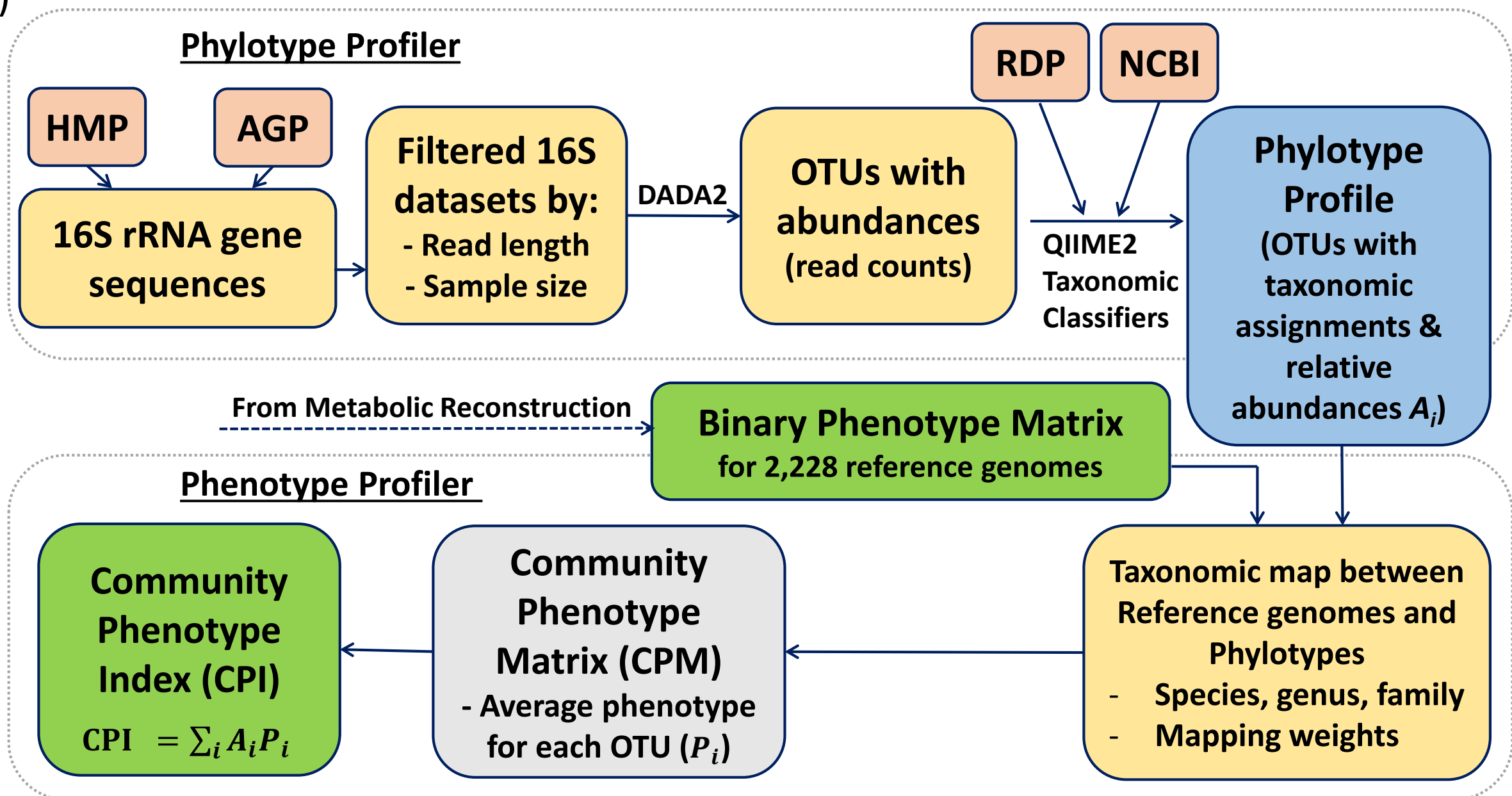## (B)

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