(A) Reference metabolic Reference genomes with pathways, known vitamin draft annotations (PATRIC / RAST) uptake transporters **Reconstructed metabolic subsystems Genome context analysis:** (mcSEED platform): **Chromosomal gene clusters (operons)** Co-regulated genes (TFs, riboswitches) Functional roles (enzymes, transporters, regulators) **Co-occurrence profiles Expert curation across genomes representing HGM Pathway variants: Predicted Phenotypes: Binary Phenotype Matrix Auxotrophs / Prototrophs Alternative biochemical routes** for 2,228 reference genomes **Vitamin Salvage / Uptake** Phenotype rules (B) **Phylotype Profiler RDP NCBI HMP AGP** Filtered 16S **Phylotype OTUs with Profile** datasets by: DADA2 abundances 16S rRNA gene (OTUs with QIIME2 - Read length (read counts) sequences - Sample size **Taxonomic** taxonomic Classifiers assignments & relative abundances A<sub>i</sub>) **From Metabolic Reconstruction Binary Phenotype Matrix** for 2,228 reference genomes **Phenotype Profiler Community Taxonomic map between Community Phenotype** Reference genomes and **Phenotype Phylotypes Matrix (CPM)** Index (CPI) Species, genus, family - Average phenotype **Mapping weights**  $CPI = \sum_{i} A_i P_i$ 

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.

for each OTU  $(P_i)$