(A) Reference metabolic Reference genomes with pathways, known uptake draft annotations transporters for vitamins (PATRIC / RAST) **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 Phenotype rules Vitamin Salvage / Uptake (B) **Phylotype Profiler RDP NCBI** 16S rRNA Filtered 16S **Phylotype OTUs with** sequences DADA2 datasets by: **Profile** abundances (HMP, AGP OIIME2 (OTUs with - read length (read counts) **Taxonomic** taxonomic samples) - sample size Classifiers assignments & relative From Metabolic Reconstruction abundances Ai) **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 $CPI = \sum_{i} A_i P_i$ for each OTU (P_i)

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.