The effect of community complexity on AGS estimation error. a) Low, medium, and high complexity mock microbial community were constructed. 20 communities of each type were constructed. Each community contained 20 randomly selected prokaryotic genomes. 100-bp metagenomes were simulated from each community. b) AGS was estimated for each of the metagenomes described in (a). Shown are distributions of unsigned estimation error for each community type. Unsigned estimation error is lower for higher complexity communities, likely because signed errors cancel out for each of the individual taxa present in the community.