



**Figure S1. N-acetylglucosamine utilization pathway mutants.** Mutations in the predicted NagA deacetylase gene (FTN\_1149) prevented N-acetylglucosamine utilization, as expected. Three additional gene functions were needed for growth on N-acetylglucosamine: a predicted sugar porter FTN\_1079 (here named “*nagP*”), glucokinase (*glk*) and a putative transaminase FTN\_1080 (“*nagB*”). The FTN\_1080 (*nagB*) product was annotated as a “phosphosugar binding protein” and appears to encode a glutamine fructose-6-phosphate transaminase related to GlmS (FTN\_0485). Mutations in a predicted efflux gene (FTN\_1685) also blocked growth on N-acetylglucosamine. NAG, N-acetylglucosamine; NAG-6P, N-acetylglucosamine 6-phosphate