Review Statement 2 for Noguigurus

Significance

The goal stated in the introduction was not included in the pipeline; examining host-effect on the evolution of organisms needs to connect to examining SNPs and/or be identified as a future goal from your work if you aren’t including specific steps to address that aim. Needs to include more detail about why you chose the species that you did. There were a lot of individual points that seemed promising, but weren’t well connected to each other or elaborated upon enough. Refining the writing here would fix this.

Investigators

Conflict management was not included. The tasks of writing the proposal and final report were not assigned. Great job identifying individual strengths.

Innovation

Again, this is vague. How will this experiment lead to you better understanding host effects on evolution? Mapping the metagenome is innovative, so make sure you go into a little more detail as to why it is important and highlight this aspect of your approach.

Approach

Very nice organization. Outputs and pipeline steps were thorough. Be sure to include numbers such as genome size. Again, the significance and the approach of this project are contradictory; pipeline stops at SNP/indel output but does not mention methods to parse out host-effect on evolution from your data. All the language in the introduction suggests a lot of dissimilarities and varying “genome capabilities” (should define these ideas: does this mean different metabolic genes, regulatory differences?) between your Buchnera species. This creates a lot of doubt about the appropriateness of your data sets, but methods suggested a high degree of mapping expected. Including a metric for relatedness (looking at a conserved gene?) would help resolve these contradictions. Some potential downsides to a metagenomic analysis were identified in the methods, but there was no mention in Expected Outcomes. It is encouraging that your members have experience that might help troubleshooting, but there should be some specific examples of steps you could take to remedy chimeric mapping or false positives since this was an anticipated result in your methods. The TA-content was mentioned as an intrinsic aid to eukaryotic-prokaryotic data sets, but your intro mentions the potential for secondary endosymbionts: what tools could help you separate prokaryotic data sets?