Dear Editor,

Please find attached our re-formatted manuscript, "SuperPhy: Predictive genomics for the bacterial pathogen *Escherichia coli*", by Matthew D Whiteside, Chad R Laing, Akiff Manji, Peter Kruczkiewicz, Eduardo N Taboada, and Victor PJ Gannon. We believe that we have adequately addressed the editorial concerns of our original submission, MCRO-D-15-00360. Specifically "Editor's comments: The manuscript lack references (citations appear as "?") and figures appear to lack required resolution. The manuscript appears to have been rendered in a fashion that did not transfer well to the PDF copy for review."

We have addressed the latex conversion issue by converting our manuscript to the Microsoft Word .docx format. Additionally, all figures are now at least 300dpi in resolution, and not greater than 170mm in width or 225mm in height.

We believe out manuscript aligns well with the aims of BMC Microbiology to provide analytical studies on prokaryotic organisms, as well as serving the biological research community in the rapidly changing landscape of genomics and software for performing genomic studies.

We describe an online software platform for "predictive genomics" of *Escherichia coli*, that provides pre-computed genomic analyses and phenotypic metadata, and allows users to perform phylogenetic comparisons, geospatial analyses, analysis of virulence factors and anti-microbial resistance genes, and to identify group-specific genomic markers based on the presence / absence of genomic regions, and single-nucleotide polymorphisms. The platform therefore fits well with the aims of a software article within BMC Microbiology where software tools, bioinformatics, evolution, and applications to molecular biology can all be reported. The platform is dynamic, continuously updated from public data in GenBank, and allows users to upload their own genomes under both public and private data-sharing settings.

Further, all aspects of the platform, manuscript and data are fully open access and hosted on a publicly accessible GitHub account, with all public genomes referenced via their accession numbers. Thank you for taking the time to consider our manuscript, and we look forward to your evaluation.

Sincerely,

The Authors