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Dear Annotation Quality Control Team,

We are submitting a completed annotation for the phage LittleB. It belongs to Subcluster A4, has a genome length of 51,373bp, and is Siphoviridae morphotype. This phage was sequenced in Pittsburgh Bacteriophage Institute. Upon completion of annotation, we documented 89 genes. We suggest special attention should be given to the following genes for the reasons listed below:

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| Gene | Reason |
| 23 | This gene is the first of a transcriptional frameshift. We are fairly certain that we identified the slippery sequence but we kindly request confirmation. |
| 45 | We were uncertain whether to denote this gene “DNA Polymerase” or “DNA Primase/Polymerase” (the latter was most suitable term found in the seaphages.org Functional Assignment document); we had a similar concern about nomenclature for gene 55 |
| 46 | We named this gene “HTH DNA Binding Protein” (not helix-turn-helix DNA binding domain or HTH DNA Binding Protein, MerR-like) because it had matches with HTH Binding Protein with other phages. However, on the seaphages.org Functional Assignment document we only saw “HTH DNA Binding Protein, MerR-like” as a most suitable name; because we did not find matches that had “MerR-like,” we kept the name “HTH DNA Binding Protein,” but we were not sure if the name we listed was allowed. |
| 53 | Based on genome comparisons of related phages, there might seem to be a gene missing between gene 53 and 54. We checked against Obama12, Iracema64, and BellusTerra, and there is a small reverse gene in those phages between LittleB gene 53 and the next homologous downstream gene (LittleB gene 54), but there is no indication that a reverse gene is present in LittleB in either of the remaining reverse frames. |
| 54, 55 | Both of these genes had matches to DNA Primases, but only gene 54 matched to topisomerase primase. Thus, we listed gene 54 as “DnaG DNA Primase” and gene 55 “DNA Primase.” |
| 62 | Best matches were with “Phosphoribosyl Transferase,” but most suitable name on the seaphages.org Functional Assignment document was “Nucleotidyl Transferase,” which is what we chose. |
| 77-78 | A member of the SeaPhages Annotation QC Team informed us that there is a probably DNA Methylase frameshift here. We have indicated this in the notes but were unable to annotate it as a frameshift in DNAMaster.  |
| 89 | Called by Glimmer but had no Coding Potential present. |

 Thank you for your time and consideration of our completed annotation of LittleB. Please feel free to contact Peter Park (peter.park@nyack.edu) regarding any comments or concerns.

 Sincerely,

 Peter J. Park, PhD