Hatful Laboratory June, 2014

376 Crawford Hall

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Pittsburgh, PA 15260

Dear Hatfull Lab,

 Please see the attached EvilGenius\_Final.dnam5 genome file and .csv author list also attached to this email. We are not confident in a couple areas of our annotation. They are as follows:

1. Gap from 1427- 1670, between ORF’s 2+3, with GeneMark- smeg coding potential. No significant BLAST matches or HHPRED data. ORF 3 has the potential to cover the gap and the coding potential (Start 1331 instead of 1670) but there would be a 96bp overlap.
2. ORF 12 (Start: 6871 Stop: 7812 (FWD)) Does not include all GeneMark-smeg coding potential. A longer ORF is possible but would produce a 133bp overlap.
3. ORF (16113 to 16226 (REV)) deleted. No coding potential seen on GeneMark Smeg output. Called by Glimmer not GeneMark, no BLAST matches, and no significant HHPRED data. Also, single gene called going in Rev direction in the middle of FWD genes with no gap for promoter. It’s possible that there is GeneMark-TB coding potential but unable to obtain the data.
4. Frameshift introduced for ORF’s 26+27 (16210 to 17042).
5. ORF added Start: 40802 Stop: 40698 (REV). Includes all GeneMark smeg coding potential. Not called by GeneMark or Glimmer and no BLAST matches or HHPRED data. Not called by phamerator. ORF contained in other A2 phage including Turbido.
6. An ORF (Start: 50143 Stop: 50075 (REV)) was deleted though called by Glimmer. Reasoning included low BLAST matches, lack of GeneMark-smeg coding potential, and ORF length (69nt).

Thank you,

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