Phage = **BirksAndSocks**

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1. Checked. The genome lengths match.
2. Checked. All genes were validated.
3. Checked. New DNA master file uploaded with corrected numbering
4. Checked. The genome was reblasted entirely and new results are present.
5. Checked. Locus changed.
6. Checked. Documentation recreated.
7. Checked. tRNA adjusted.
8. Checked.
9. There was some disagreements concerning the final annotation of the following genes:
* Gene 63 (52324-53856 Rev): as called there is a 61bp overlap and some coding potential is cut off. Original called start 53688 leaves a 107bp gap and has poor alignment with closest relatives
* Gene 72 (57831-58388 Rev): Original called start leaves a 220bp gap and has poor alignment, but no other starts that lessen the gap improve alignment.
* Gene 108 (74853-75068 Rev): Original called start leaves a 170bp gap and has poor alignment, but no other starts that lessen the gap improve alignment or functional call.
* Auto-annotated Gene 87 (65095-65157 Rev) was deleted because of its short length and lack of BLAST results.
* Auto-annotated Gene 97 (71566-71706): There is no coding potential for reverse gene, but there is potential for a forward gene. However, this gene was not called by Glimmer, it would be a forward gene in the middle of a group of reverse, there are no BLAST results, and 21bp is not enough for a transcription promoter. Therefore, this gene was deleted even though it will leave a large gap of 164bp.

Only one tRNA was found and trimmed.

No integrase was discovered.