**Seume\_3** start site was changed from 471 to 444 to reduce gap, give better SD score, and to include all coding potential. The new start site also provided a better blast alignment.

**Seume\_8** and **Seume\_10** had functions solely based off of homologous phages genes.

**Seume\_19** start site was changed start site from 12670 to 12682 to align 1:1 with Toulouse and a 1:1 alignment with blast results.

**Seume\_24** was deleted because it was a single reverse gene surrounded by forward genes, and completely overlapped **Seume\_23**.