Abrogate annotation cover sheet

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Most genes had a lot of blast support with other A1 phages. Gp1 was an orpham at the time we originally annotated this genome, but now there is a second pham member,

Gp 5 was not called by either program and there was no coding potential, but there was some blastp matching with A5 phages and others (only a few, though) had called a gene in this region.

The last gene, gp91, was extended and the short genes on either side were deleted. This made sense with the coding potential in this area, and there was blast support for a gene with this longer start.

Thanks