**ANANSI\_ 2** (before renumbering) was deleted because it was a reverse gene that completely overlapped and was surrounded by forward genes. Also, it was not marked by GeneMark, and showed no results in Blast.

**ANANSI\_ 85** (before renumbering) was deleted because it was a reverse gene that completely overlapped and was surrounded by forward genes. Also, it was not marked by GeneMark, and showed no results in Blast.

**All tRNAs (ANANSI\_12, 13, 14, 15, 16, 50, 58 and 59)** ends were trimmed to match web-based Aragorn. All were detected by Aragorn, except for **ANANSI\_ 50**.

**ANANSI\_ 69** showed Glimmer and GeneMark with different start site calls. However, there was not enough evidence to change the start site.

We list **ANANSI\_ 56** as a DNA binding protein as its function. The gene does show strong hits to transposase genes as well.

Phamerator map name was **Jesse** due to a contamination.

**Additional Notes: Several reverse genes near the end of the genome were given functions in DNA replication via HHPred analysis with probability scores less than our normal cutoff of 95%. The scores for several of the genes were between 85-95% but were located within a presumed operon that contains GREAT hits to DNA replication genes.**

**The reported SD scores are those that represent the Final SD scores for each gene, not the raw SD score. Sometimes the raw and final SD scores were the highest possible within a potential ORF but sometimes not.**

**Lastly, as noted with several of the other related genomes (Gorgeous, Sorjuana and Rings) the reverse genes called in DNA Master were in a different reading frame from the GeneMark Smeg Output.**