Potential problem areas:

gp14 could be longer; a start at 9311 would produce a better, but not perfect, alignment with the same gene in Send513, but it would lower SD score and eliminate 1:1 alignment with gene in Papyrus. However there is a large gap with the gene called as is as is.

gp17 has a DNA binding domain – should this be listed as function? It is listed as the function of the same gene in Papyrus.

For the most part, when all other factors were about equal, we considered a start that produces a 1:1 alignment with the corresponding gene in Sen513 and Papyrus the best start, even if there was a start that produced a longer ORF. However in some cases, an TTG start would produce both a higher SD score and longer ORF. For example:

gp 23 has potential TTG starts at 14412 and 14409. Both these starts would produce a longer ORF and have a higher SD score than the start called by DNA Master. However, the start called by DNA Master produces a 1:1 alignment with genes in Send and Papyrus. There is a similar situation with gp68, gp78 gp82, and gp92.

gp 65: we are not sure if gp 65 should actually be called as a gene. It is only 78 bp long, and is much shorter than the homologous gene in Papyrus. It was not called in Send513.

There was a gene called in both Papyrus and Send513as gp 42 in the reverse direction in those genomes that we did not call. The sequence is present in Weiss13, but DNA Master never called it, and there is no coding potential in that region in that reading frame. So we are not sure why it was called in Papyrus and Send513. The coordinates of the gene would be 36821-37057 in Weiss13.

gp8: There is a single nucleotide insertion at position33 in this gene that changes the amino acid sequence downstream of the insertion relative to the amino acid sequence in the homologous genes in Send513 and Papryrus. Thus the first 11 amino acids in the Weiss13 gene match those in Send513 and Papyrus, but the rest do not, and the gene in Weiss is much shorter. This is shown as an orpham on Phamerator but we not sure that is correct.

This is my first time submitting a genome so I’d appreciate any feedback on our annotation and these submission notes.

Thanks,

Mandy Butler