CLAUTASTROPHE

COVERSHEET

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All gaps have been checked, in all cases at least visually and except in two cases (where there seemed to be so many stop codons that further inspection was pointless) by examining for GM CP and by BLASTx via the NCBI servers. We call one of these to your attention below.

Concern: Precise location of programmed frameshift upstream from tapemeasure. Our original proposed base for the actual shift was 10388, but attempts to modify the dnam file to reflect this (including using nearby bases) lead to products that do not validate.

Concern: Uncertain NrdH glutaredoxin function call stop 29050

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Concern: Uncertain function call feat stop 29647 (REV)

Concern: Gap centered around c.36,200bp may contain gene, but has very little CP and BLASTx results at NCBI are inconclusive—only 2 small alignments, not 1:1

Concern: uncertain function at stop 34954 (HTH dna binding)

Concern: uncertain function at stop 35166 (DNA binding or excise or both?)

Concern: uncertain func. at stop 45530 (maybe ERF-family ssDNA binding protein, maybe not)

Concern: large overlap betw. Feat stop 53825 and feat stop 54063

Concern: large overlap(31bp) downstream of start for feat with stop (reverse) at 68481. Starterator not really helpful here.

Concern: Very small feat with stop 71037, only 1BLAST hit, goes “wrong way”, retained because it does BLAST very well to Snenia

Functions not on “approved” or “standard” terminology list:

**Function stop Reverse?**

**Nucleotidyl transferase 29647 yes Is this same as “tRNA nucleotidyl transferase?**

**Lsr2 binding protein 30484 yes Is it “binding” or “bridging”?**

**Ribose phosphate pyrophosphokinase 50753 no Not on list at all**

**Nicotinate phosphoribosyl transferase 52225 no Same as nicotinate ribosyl transferase?**