Table S1: RNA-seq expression data from wild-type, ∆*rpoE1* and ∆*lovhK* strains exposed to hydrogen peroxide for 10 minutes. *Data is in a separate spreadsheet document with 4 worksheets in individual tabs. Legend for each tab is below.*

(a) FPKM_values: Transcript levels for each gene are presented as Fragments Per Kilobase of transcript per Million reads mapped (FPKM) averaged from two independent experiments for each strain.

(b) DEG_rpoE1: List of Differentially Expressed Genes between the ∆*rpoE1* and wild-type cultures. A fold change of greater than 1.5-fold and false-discovery rate cutoff of 0.05 was used to determine significant differential expression between two different conditions.

(c) DEG_lovhK: List of Differentially Expressed Genes between the ∆*lovhK* and wild-type cultures.

(d) DEG_rpoE1_lovhK: List of Differentially Expressed Genes between the ∆*rpoE1* and ∆*lovhK* cultures.