GARCIA *ET AL.* SUPPLEMENTAL TABLE LEGENDS

Supplemental Table 1. SAM output data that shows unique BioIDs whose expression was changed two-fold or more in the indicated comparison. Gene ID indicates the Stanford unique BioSequence ID. Gene Name is the available information on each gene. Score(d) is the T-statistic value. Numerator (r) is the numerator of the T-statistics. Denominator ($s+s_0$) is the denominator of the T statistics. Fold change is the fold change from the indicated comparison group. The q-value is the lowest false discovery rate at which a gene is called significant.

Supplemental Table 2. Supplemental Table 2 contains all of the genes whose expression changed three-fold or more in the CP9 vs. CP9*cnf1* and/or CP9 vs. CP9Δ$hlyA_1$ comparisons. Gene names and fold-changes are from Supplemental Table 1. Protein names and Biological Processes are from UniProt and Gene Ontology.