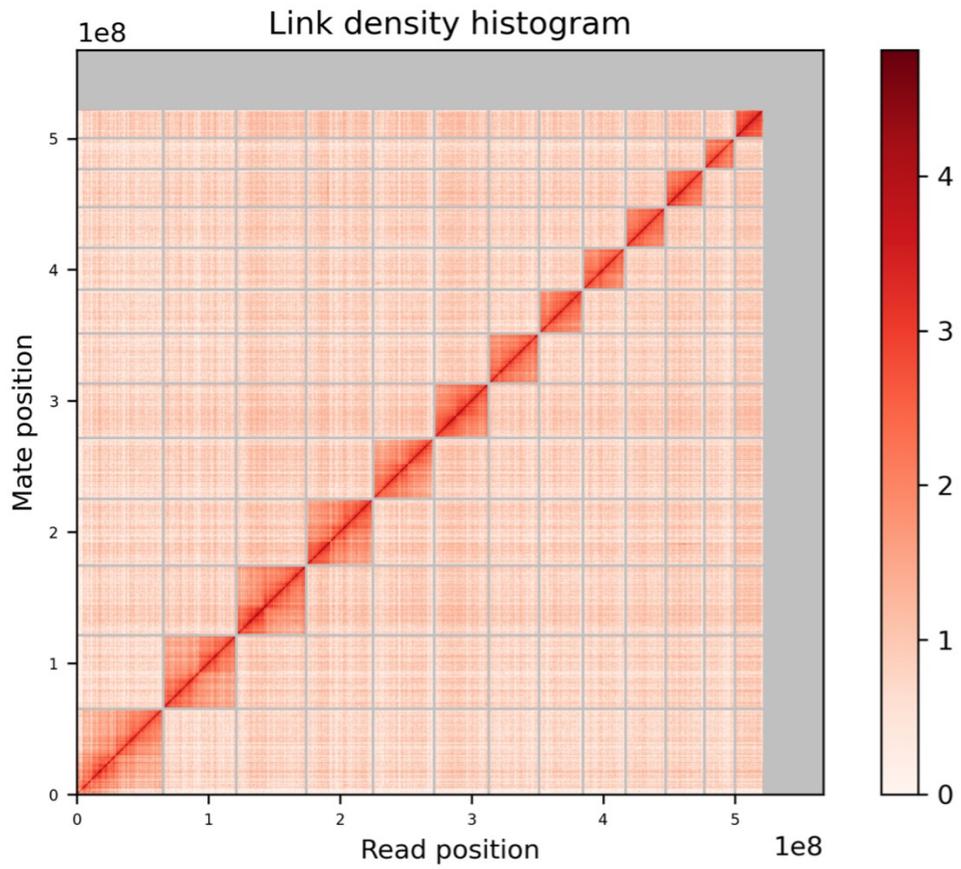
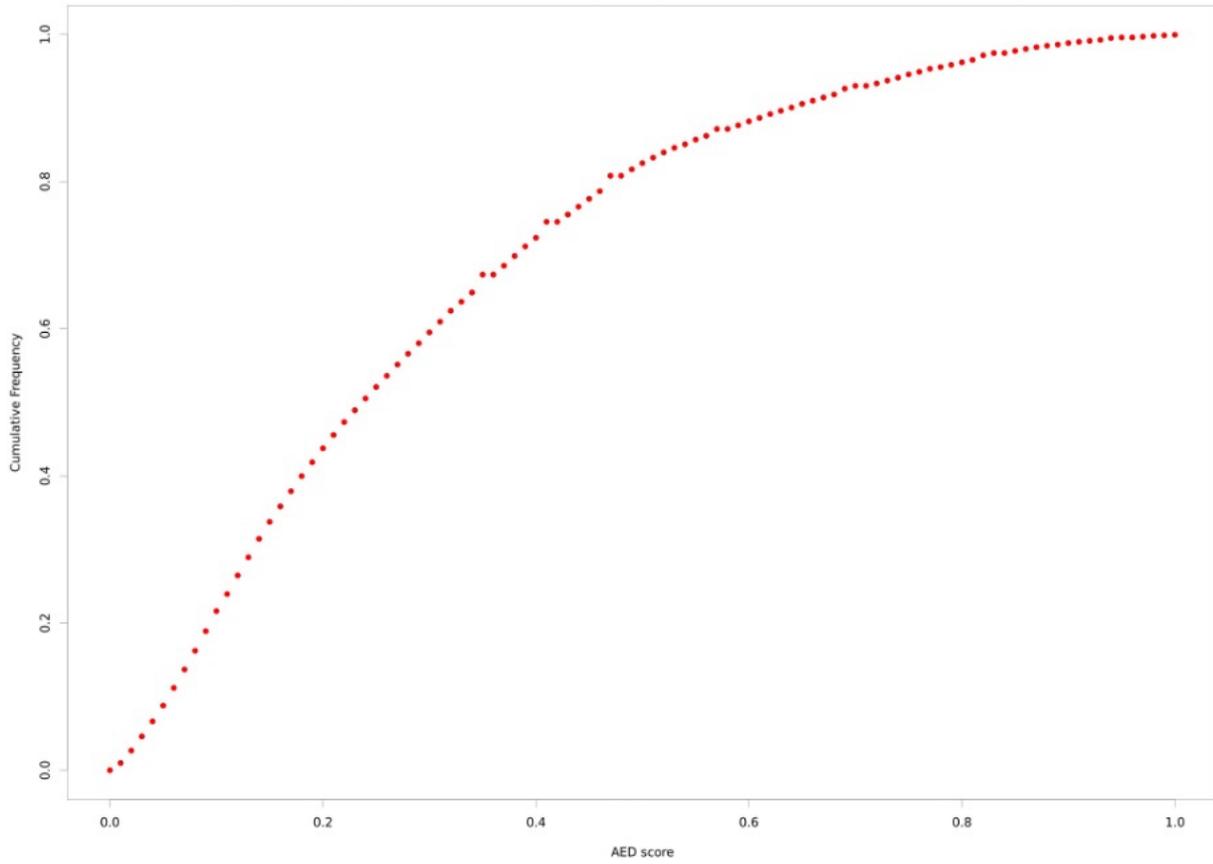


Supplemental Figures

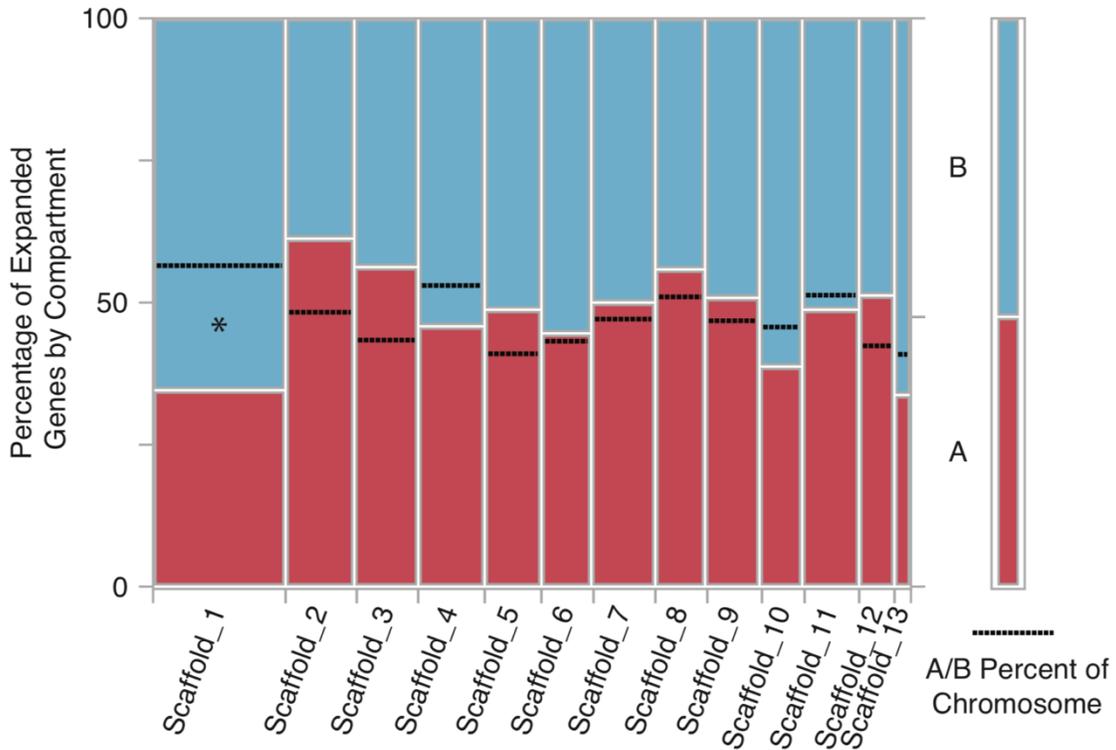
Supplemental Figure 1. *Bactericera cockerelli*'s putative chromosome regions identified by the TAD analysis pipeline.



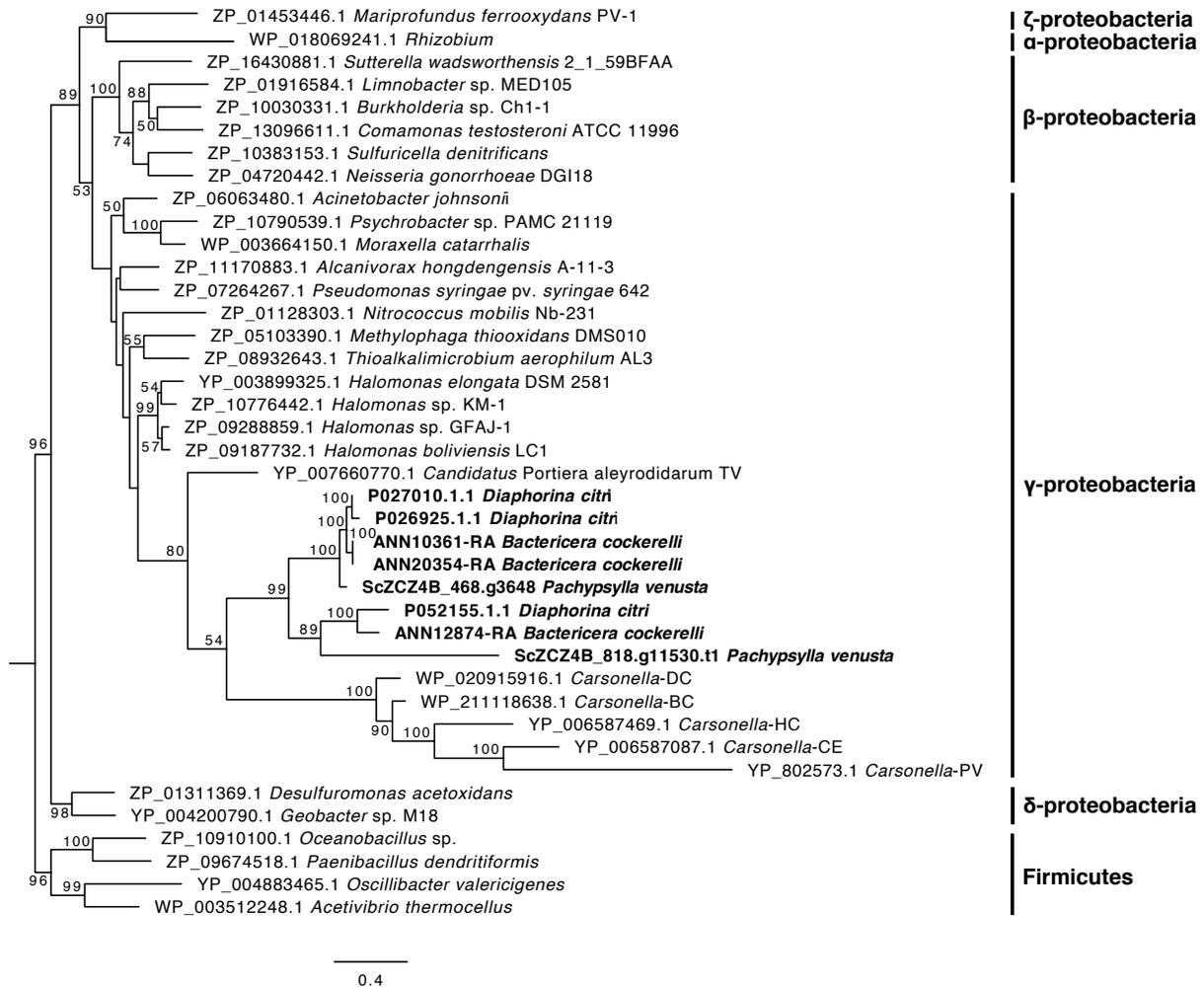
Supplemental Figure 2. Cumulative frequency graph of AED scores calculated for each annotated gene of *Bactericera cockerelli* (22,280 genes). The AED score ranges from 0 to 1 and a lower score represents more evidence support for the gene.



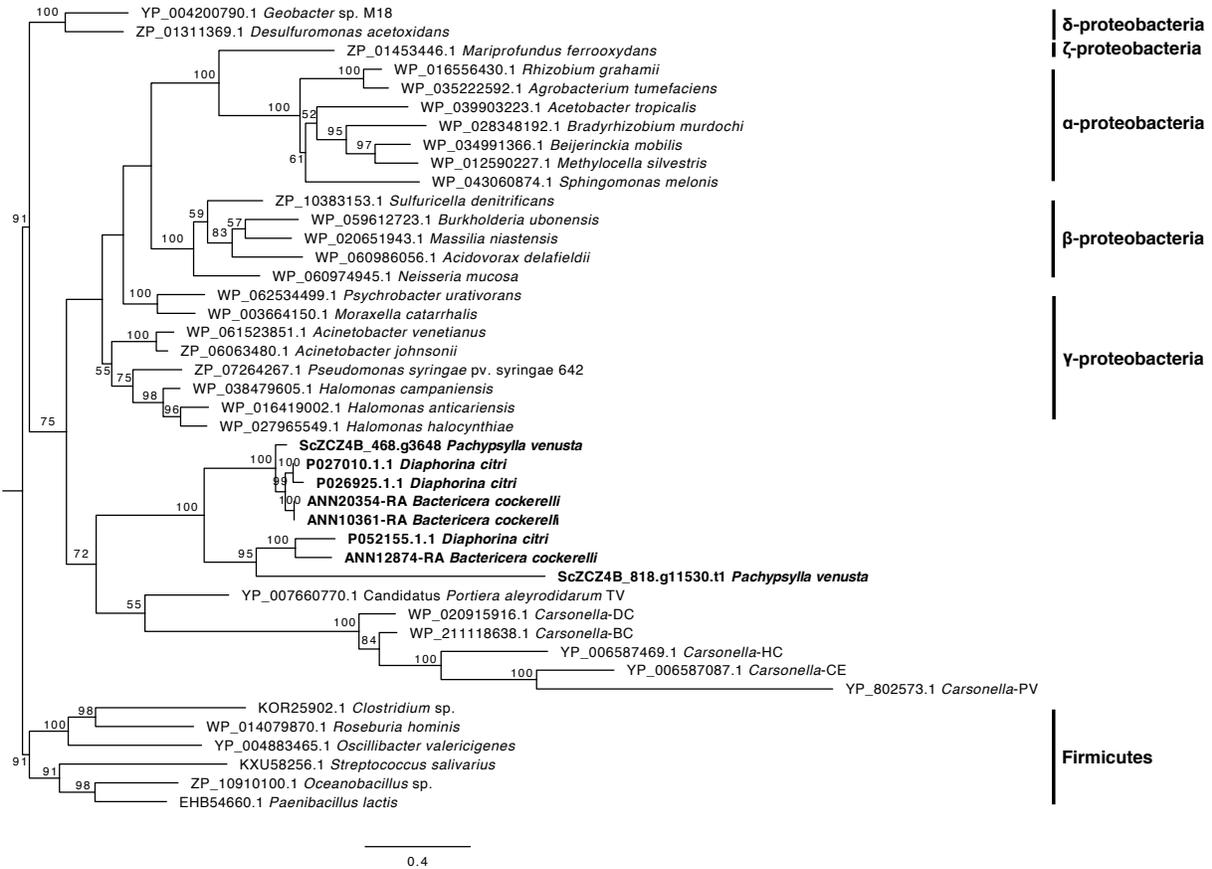
Supplemental Figure 3. Recently expanded repeat family genes are distributed across euchromatic (A) and heterochromatic (B) compartments. Mosaic plot represents chromosomal compartment locations of expanded Type I and Type II repeat family proteins ($n=2,214$) and compared to the predicted proportion of A and B compartments within the corresponding chromosome (dashed black lines). Asterisk indicates the single chromosome (Scaffold_1) showing a significant bias with more repeated detected in the heterochromatic compartment than expected by chance (Proportion test, d.f. = 1, $P = 0.001376$).



Supplemental Figure 4. Phylogenetic analysis of ASL genes in *P. venusta*, *D. citri*, and *B. cockerelli* using the same representative taxa from Sloan et al. (2014). Bootstrap values are only indicated for nodes with >50 % support.



Supplemental Figure 5. Phylogenetic analysis of ASL genes in *P. venusta*, *D. citri*, and *B. cockerelli* using different representative taxa from Supplemental Figure 4. Bootstrap values are only indicated for nodes with >50 % support.



Supplemental Figure 6. Phylogenetic analysis of CM genes in *P. venusta*, *D. citri*, and *B. cockerelli*. Bootstrap values are only indicated for nodes with >50 % support.

