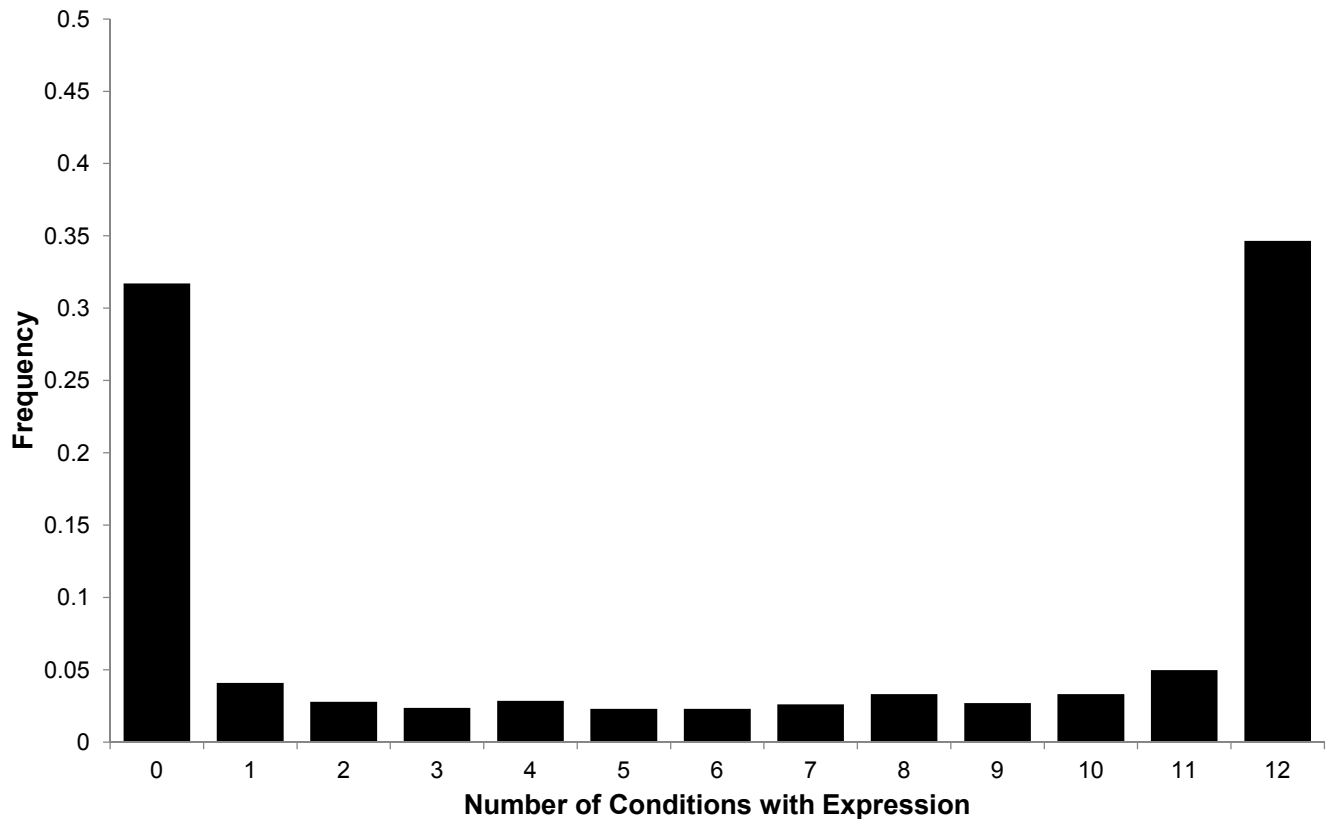
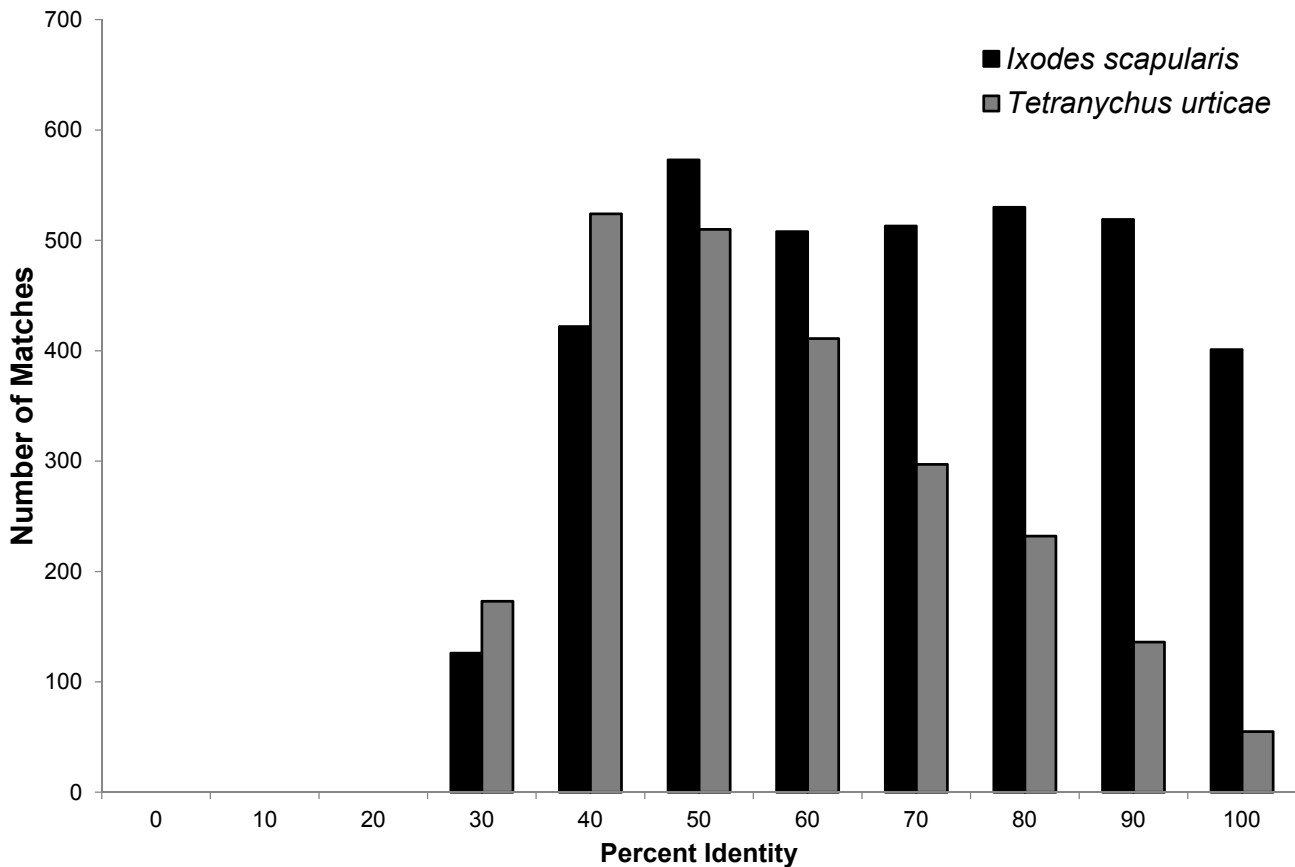
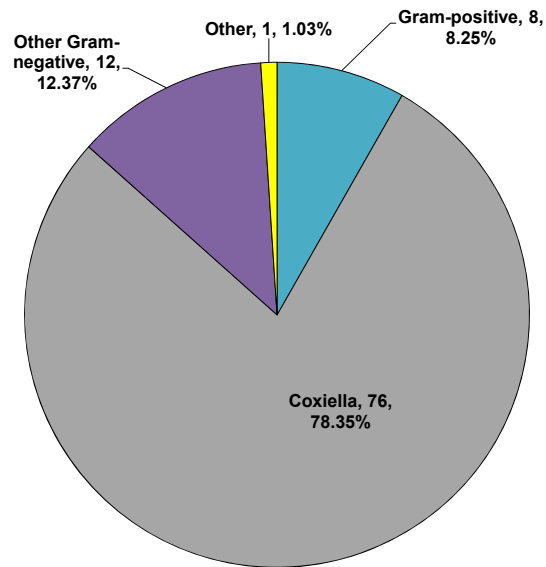




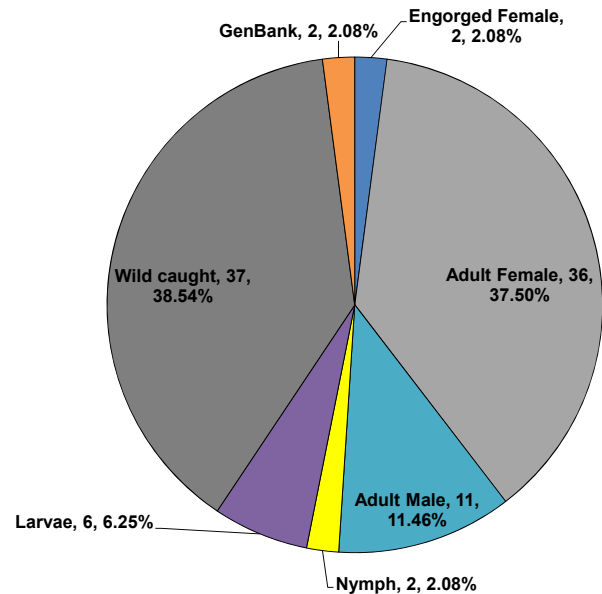
Supplemental Figure 1: Frequency distribution of expression of 13,962 microarray probes in 12 conditions. Microarray probes were derived from the *Amblyomma americanum* transcriptome. Histogram indicates the proportion of total probes that had detectable levels of transcription in zero to 12 of the conditions, based upon a 0.5% false discovery rate. Sequences expressed in zero or one conditions (N=5000) were classified as non-functional.



Supplemental Figure 2: Frequency distribution of the percent identities of matches of *Amblyomma americanum* ESTs with representative *Ixodes scapularis* and *Tetranychus urticae* datasets. Matches were obtained by BLAST searches of *A. americanum* ESTs against the *I. scapularis* predicted peptides (available at VectorBase) or against the *T. urticae* predicted peptides (available at BOGAS). An e-value and match length cutoff of $1e-5$ and 33 amino acids, respectively, were applied for all BLAST results. A total of 3,592 matches were obtained against *I. scapularis* and 2,338 against *T. urticae*.



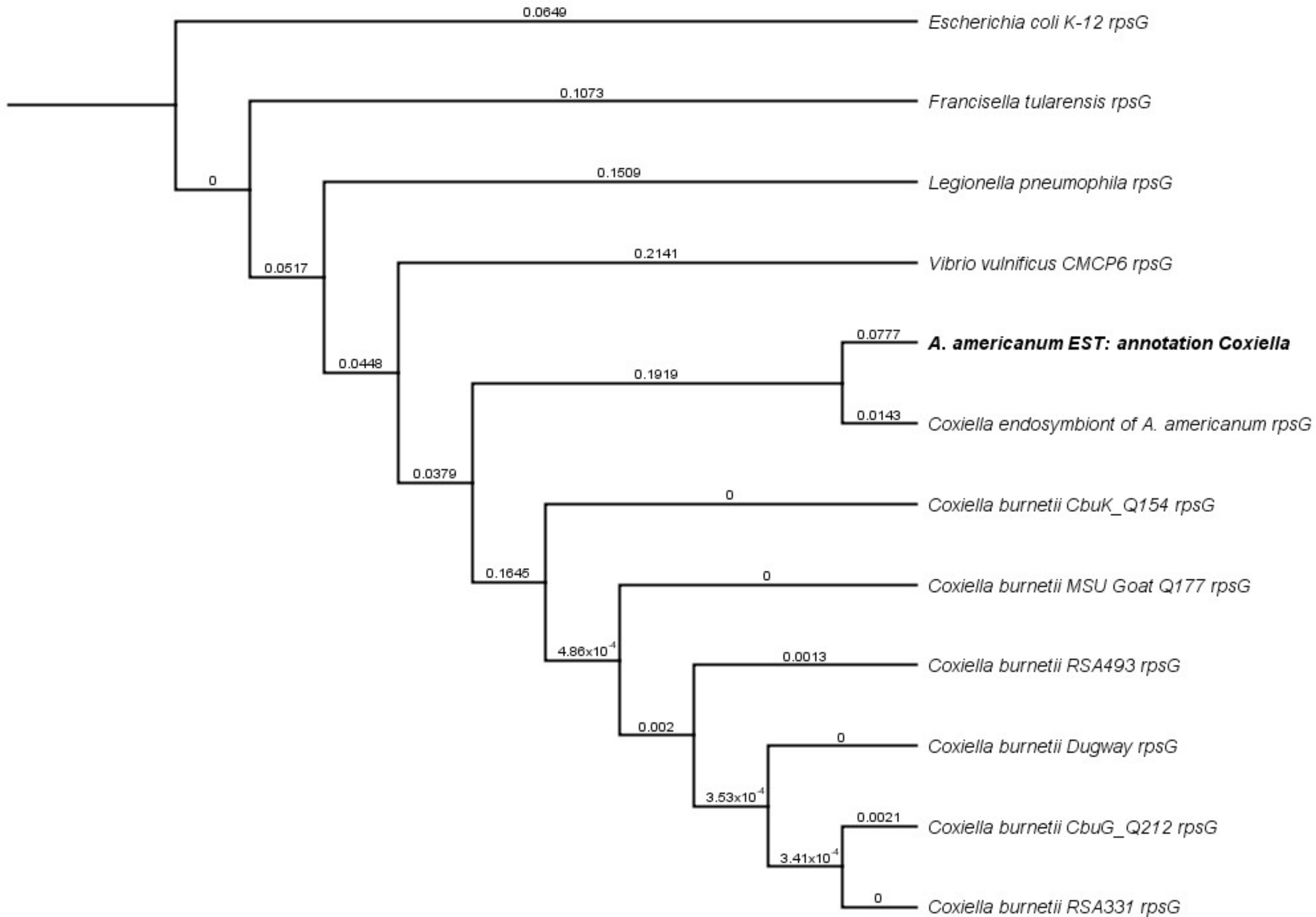
A



B

Supplemental Figure 3: Description of the *Amblyomma americanum* microbial community.

(A) The taxonomic distribution of 97 UniProtKB microbial protein matches. (B) The distribution across individual tick libraries of 76 sequences (13 contigs, 63 singletons) matching Coxiellaceae proteins.



Supplemental Figure 4: Phylogenetic reconstruction of *Amblyomma americanum* *Coxiella* EST sequences. Representative *Coxiella* EST sequence derived from *A. americanum* transcriptome groups with sequences of the *A. americanum* *Coxiella* endosymbiont rather than with *C. burnetii* sequences. This reconstruction includes six *C. burnetii* rpsG sequences, one rpsG sequence from the *Coxiella* endosymbiont of *A. americanum*, and rpsG sequences from four other gamme-proteobacteria. *A. americanum* EST annotation *Coxiella* (bolded) is a *Coxiella* endosymbiont EST generated by this study (seq_B02_wt_63_007.abi). Phylogenetic reconstruction is a Neighbor-Joining tree employing the Jukes-Cantor Genetic Distance Model set at 70% similarity. Branch labels indicate calculated substitutions per site in the aligned sequences.