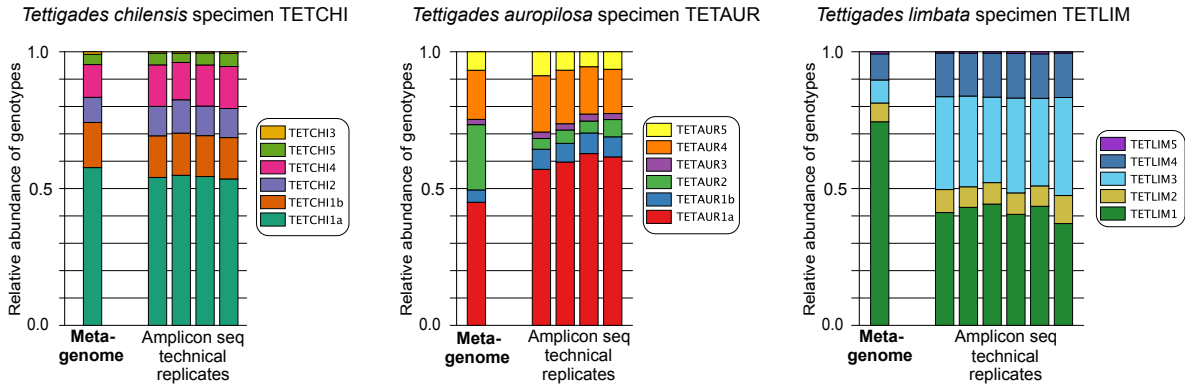A. Cicada specimens with metagenomes sequenced: genotype abundance estimated by read mapping vs amplicon sequencing

Tettigades chilensis specimen TETCHI

Tettigades auropilosa specimen TETAUR

Tettigades limbata specimen TETLIM

B. *Tettigades chilensis,* Peñalolen population - amplicon sequencing data for distinct bacteriome lobes of the same specimens
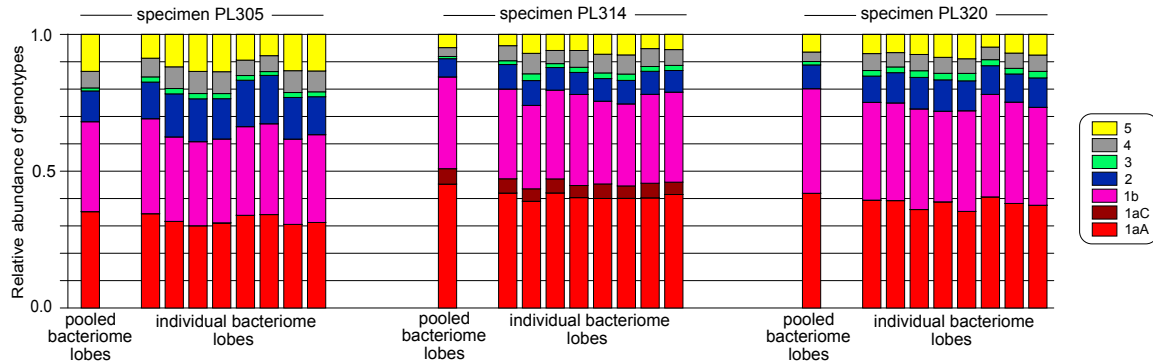
Figure S1. Testing the bias in amplicon sequencing experiments. (A) Technical replicates: the relative abundance of rpoB genotypes in replicate amplicon libraries prepared from DNA samples that had previously been used for metagenomic sequencing, compared to metagenomics-based estimates. In the case of *T. limbata*, the metagenomic library was prepared using a PCR-free protocol. (B) Biological replicates: the relative abundance of *Hodgkinia* rpoB genotypes in individual bacteriome lobes, versus all remaining lobes pooled together, in three *Tettigades chilensis* specimens from a single population.
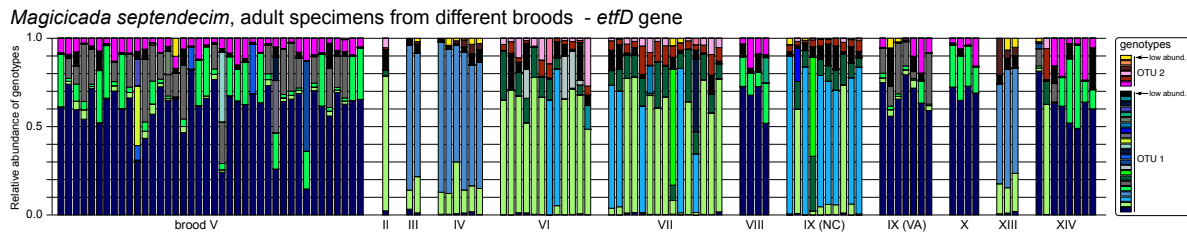
Figure S2. The relative abundances of *Hodgkinia* genotypes among adult *Magicicada septendecim* specimens from different broods, based on etfD amplicon data. Only the genotypes represented by at least 1% of reads in at least one library were used for the relative abundance calculations. Bars indicated as "low abund." represent the cumulative abundance of genotypes in each of the two OTUs that were represented by more than 1% of reads in at least one library but never by more than 10% of reads.