## SUPPLEMENTAL INFORMATION

**Supplemental Text 1.** Supporting Methods and Results.

**Supplemental Figure 1.** PC Analyses of population structure. A) A three-dimensional plot of PC1, 2, and 3 for all 20 sequenced isolates. Yellow spheres represent *C. immitis* isolates, blue spheres represent *C. posadasii* isolates. Orthogonal distribution of species indicates that SNP variation is dominated by fixed differences between species or species-specific variants. B) A two-dimensional plot of PC1 and PC2 for *C. immitis*. Red circles indicate isolates from central California, orange circles indicate isolates from Southern California/ Northern Mexico. C) A two-dimensional plot of PC1 and PC2 for *C. posadasii*. Blue circles represent isolates from Arizona, purple circles indicate isolates from Texas/ South America, and green circles indicate isolates from Southern/ Central Mexico.

**Supplemental Figure 2.** SNP rate from genome sequence data shows several *C. immitis* isolates with signals of introgression and variable introgression boundaries.

**Supplemental Figure 3.** Detailed profiles of the *Mep4* region showing introgression between species. PCR-based sequencing of eight amplicons in this region confirms widespread introgression of *C. posadasii* haplotype into multiple *C. immitis* isolates, but no evidence of introgression in the opposite direction. Each bar represents phylogenetic species affiliation: black for *C. immitis* grouping, white for *C. posadasii* grouping.

**Supplemental Figure 4.** Profile of copy number classes for repetitive sequence in each of the assembled genome sequences. Copy number is estimated from the number of locations that each 1kb window matches with BLASTN. *C. posadasii* isolate RMSCC_3700 is unique in the paucity of high copy number repeat sequences.

**Supplemental Figure 5.** A histogram of $-\log_{10}$ Neutrality Index (NI) values for all genes with at least 4 SNPs. The vertical red line indicates the median. The majority of genes exhibit –log10(NI) values less than one, suggesting weak purifying selection ( light blue bars). Though a substantial fraction of genes exhibit values greater than one (pink bars), possibly indicating positive selection, no genes exhibit a statistically significant MK result after correction for multiple testing.

**Supplemental Table 1**: List of genes with introgression signal by coalescent method.

**Supplemental Table 2**: Genomic regions showing introgression by strain.

**Supplemental Table 3**: List of genes disrupted by recent TE insertions.

**Supplemental Table 4**: List of genes with high promiscuous epitope density and extracellular localization.