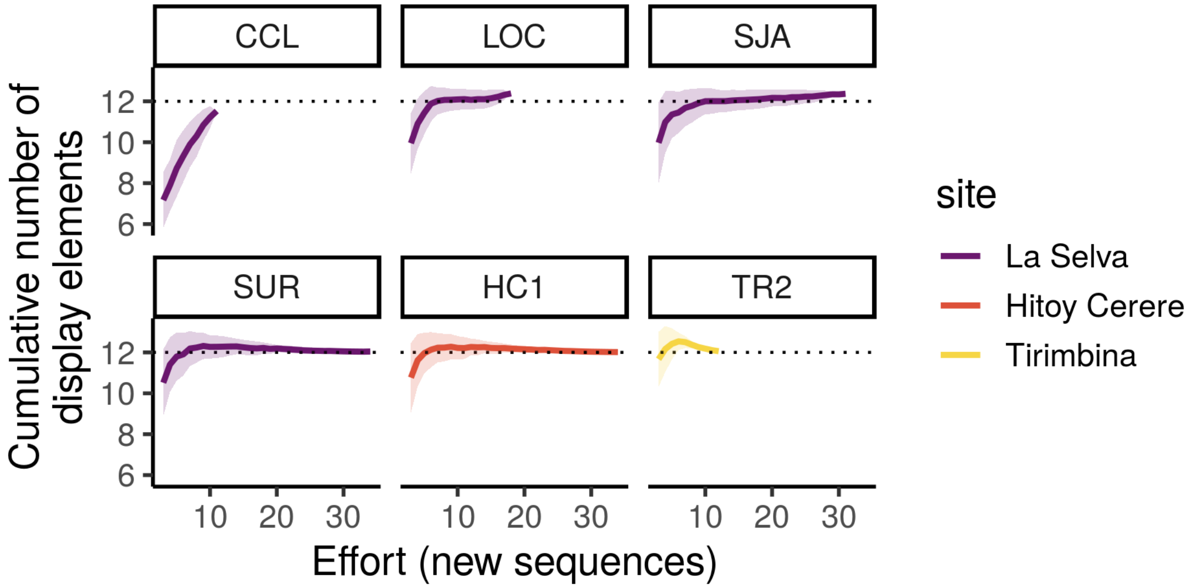

Fig S1. Accumulation curve of number of display elements by sampling effort (display sequences). Leks reached a maximum number of elements (12) after ~15 sequences were analyzed (except for lek CCL).

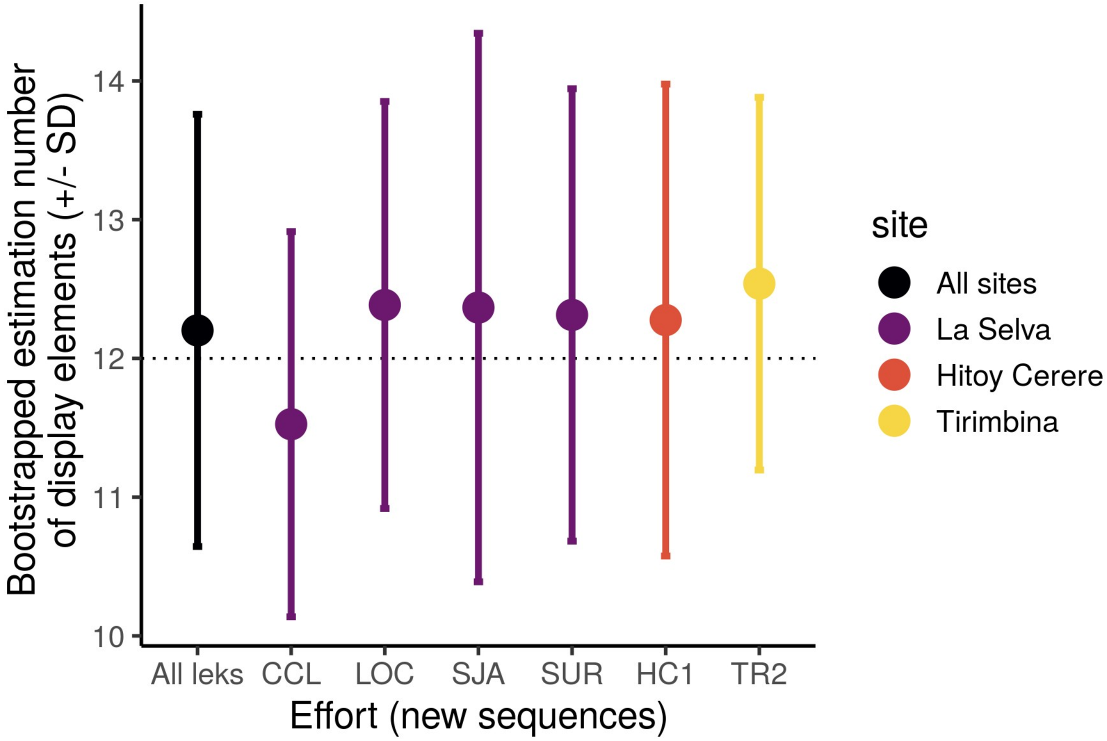

Fig S2. Bootstrap extrapolated number of display elements (± 95% CI) by sampling effort (display sequences). Values did not differ from 12 display elements in any lek (including CCL) as well as for all leks combined.

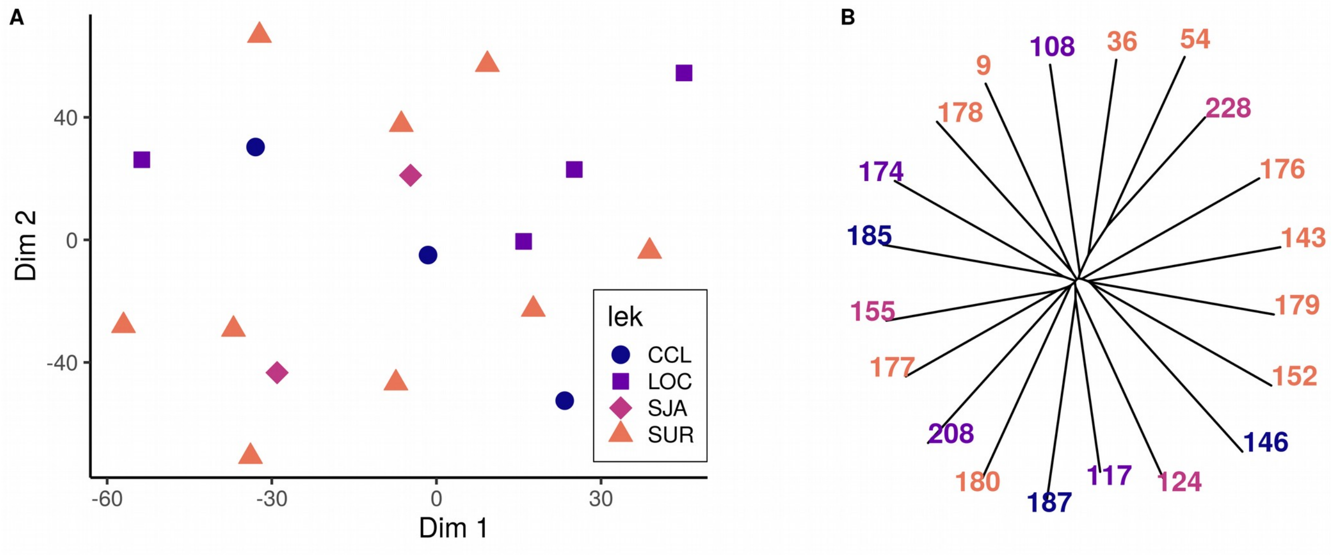

Fig S3. Genomic clustering of long-billed hermit males from four leks at La Selva Biological Station. (a) Scatter plot of the two dimensions obtained by t-SNE (t-distributed Stochastic Neighbor Embedding, a non-parametric dimensionality reduction method, van der Maaten & Hinton 2008) and (b) neighbor joining tree, both based on the genetic distance between males. The lack of defined groups in the scatter plot and the star-shape of the tree both indicate little genomic structure and no clustering associated to lek membership.