

Figure S1. Reducing redundancy in the mosquito repeats families lists.
(A) Top: Diagram of the pipeline to condense the *AnGam* repeats families list, with critical parameters for the BLAT algorithm in the red box. Bottom: Benchmarking results from reducing the *AnGam* repeats list to 555 repeats families. (B) Top: Diagram of the pipeline to condense *AeAeg* repeats families list, with the critical parameters for the MeShClust algorithm in the red box. Bottom: Benchmarking results for reducing the *AeAeg* repeats list to 1,242 repeats families. (C) and (D) The ideogram represents the similar pipeline as the *AeAeg* pipeline and benchmarking results from reducing repeats families in *CuQuin* and *AeAlbo* genomes.

E

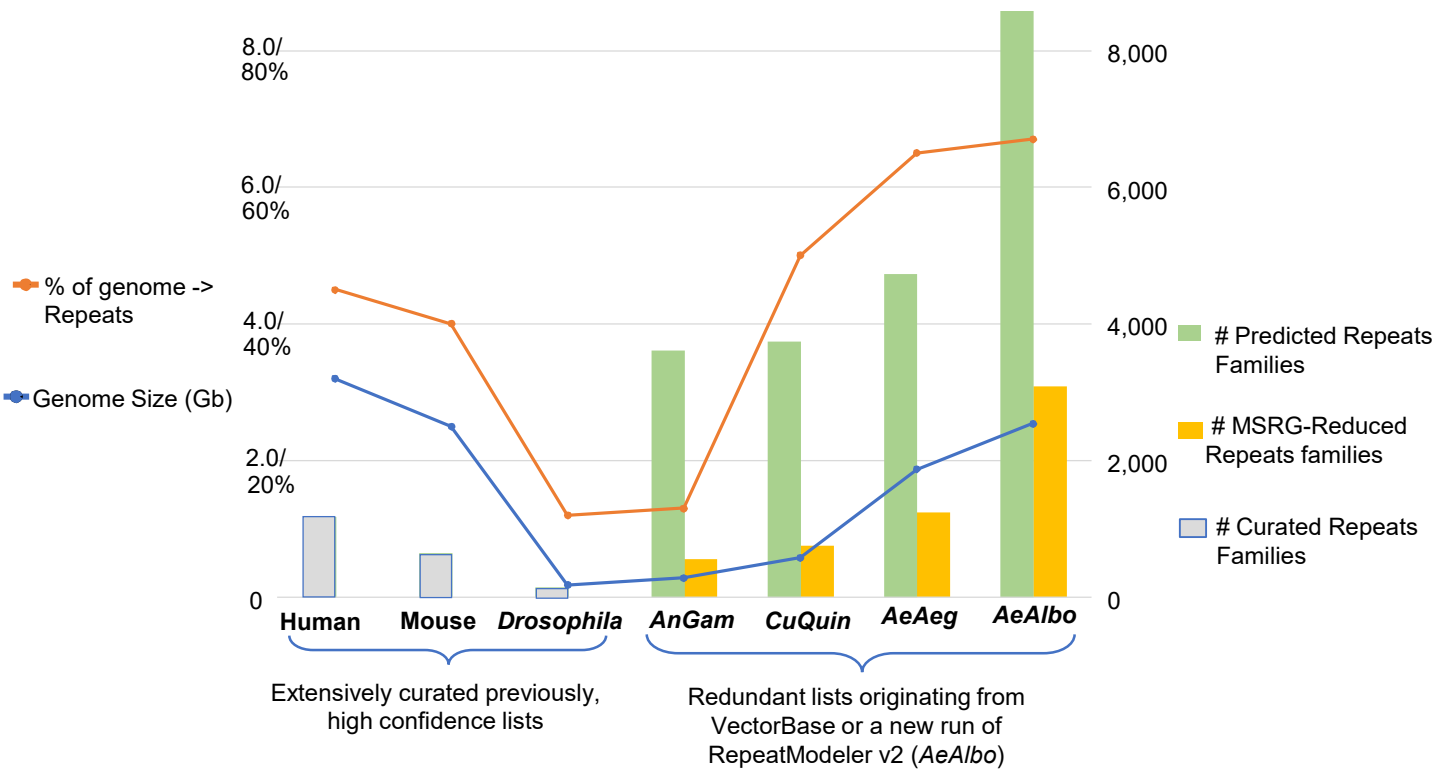


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(E) Diagram showing relationship of different animal genomes' sizes, the percentage of the genome is comprised of repeats, and the number of predicted, MSRG-Reduced, and manually curated repeats consensus sequence families in each of the animals' sequenced genomes.