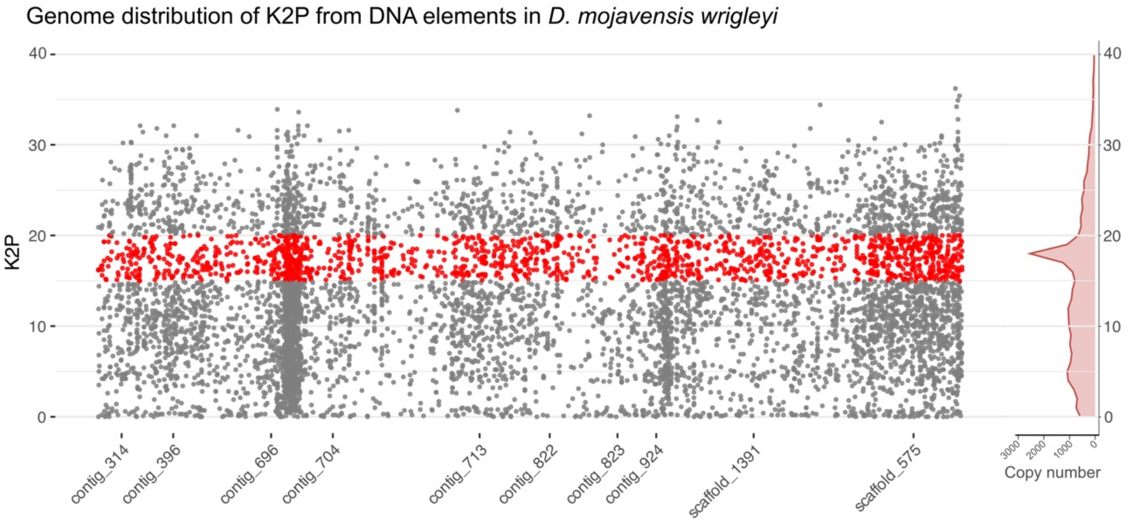

Sup. Figure 3: Genome distribution of Kimura 2-Parameters divergence from DNA elements across the 10 longest scaffolds/contigs in the *D. m. wrigleyi*. These 10 scaffolds/contigs sum up 144.7Mb, comprising 81.6% of the genome assembly. Low K2P means young insertions, while high K2P means old, relative to the consensus sequence. Red dots are insertions with K2P >= 15 and <= 20, which have a peak in copy number in the *D. m. wrigleyi* genome. The result demonstrate even genome distribution from insertions with 15-20 K2P in the genome, rather than local accumulation.