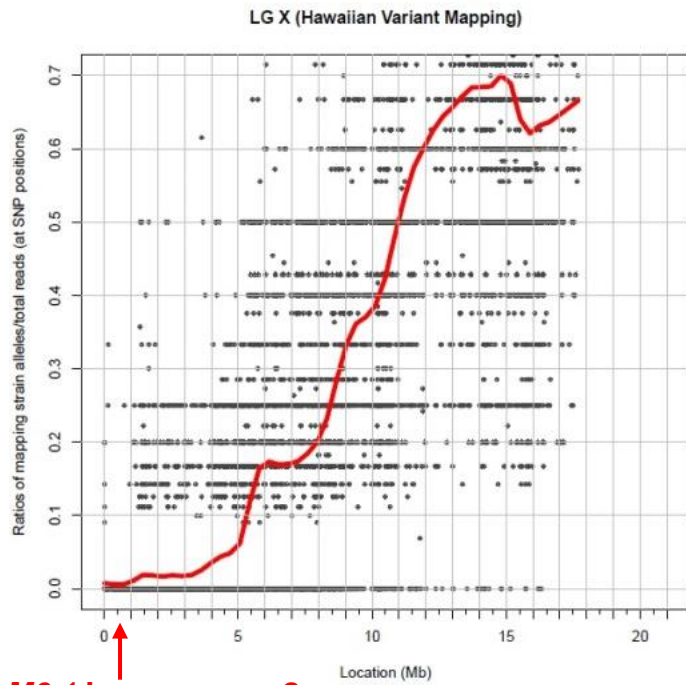


A



B

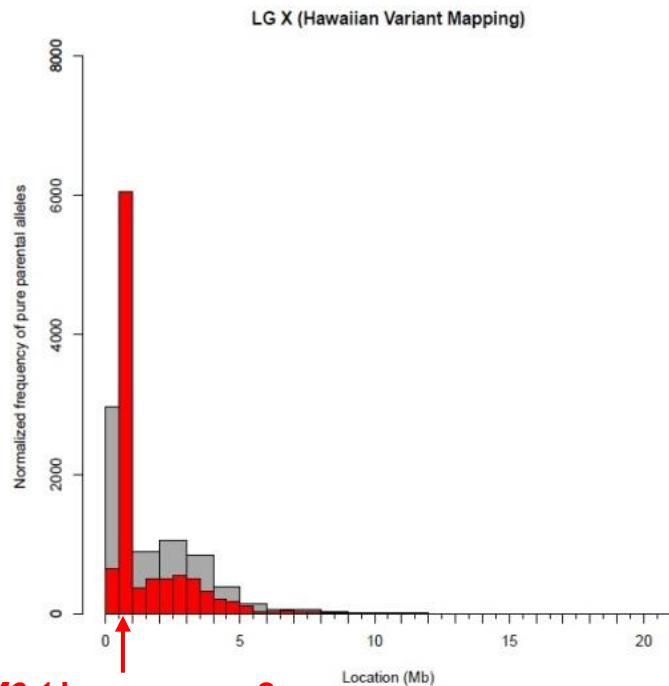


Figure S2. Cloudmapping data output of *exc-2* whole-genome sequencing.

- (A) Ratio of mapping-strain reads of CB4856 (Hawaiian wild-type) SNPs to total SNPs in populations of F2 progeny selected for homozygous Exc phenotype. CB4856 was crossed to *exc-2* mutant animals (in Bristol background) and F1 progeny allowed to self-cross. Upon selection for Exc animals, the locus of the *exc-2* mutation is located where the ratio of CB4856 to N2 reads equals zero (i.e. 100% SNP composition of the Bristol background of *exc-2*).
- (B) Data from panel A normalized via LOESS regression. The highest peak shows where pure parental (*exc-2*) SNP is located along the X-chromosome.