1 Supplementary figures

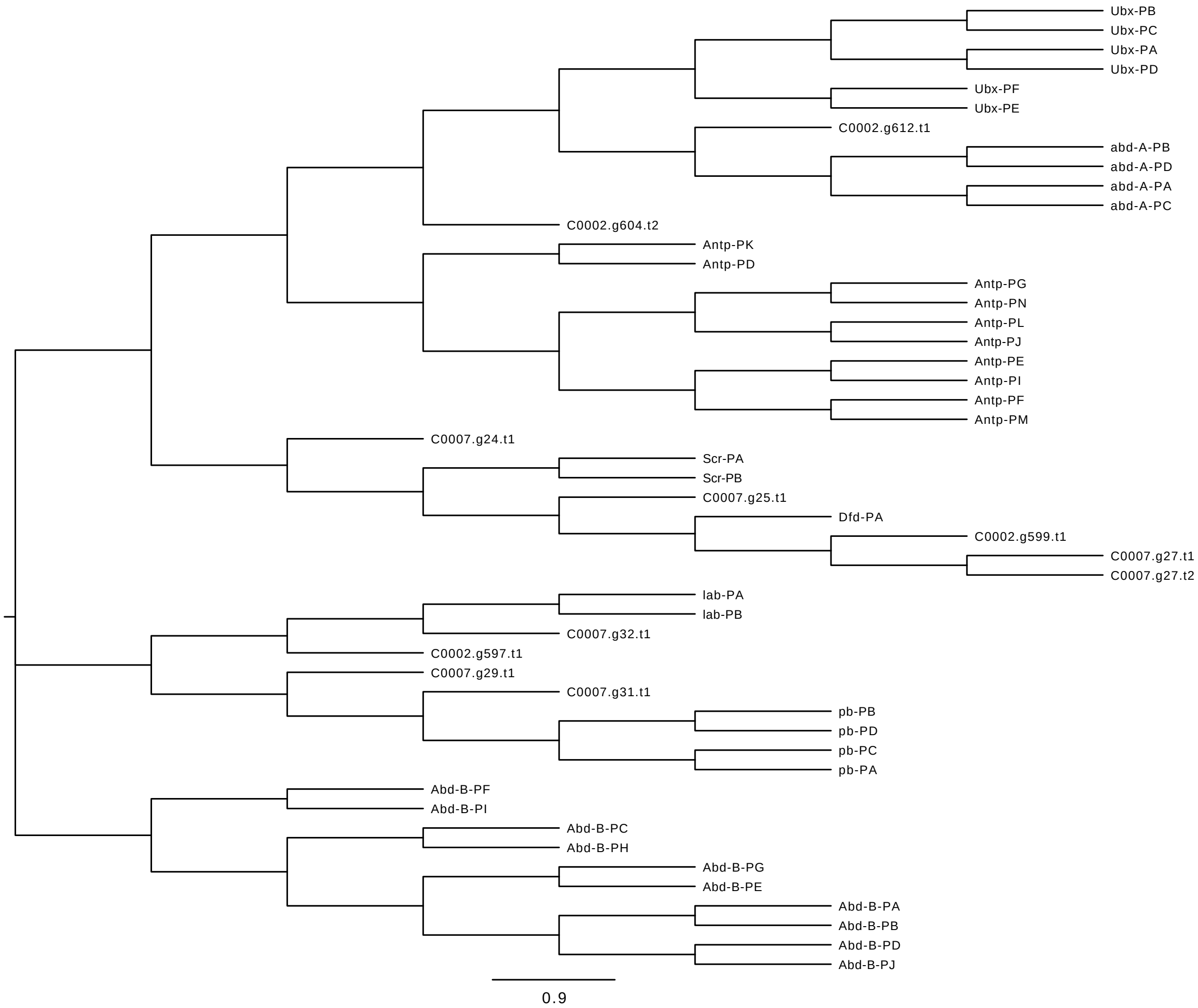

Figure 1: A bootstrap consensus maximum likelihood tree, generated using 300 bootstrap iterations in MEGA, comparing the predicted translations of putative clam shrimp HOX genes to *D. melanogaster* HOX genes. Clam shrimp genes are assumed to be orthologous to *D. melanogaster* genes that are sister to them.

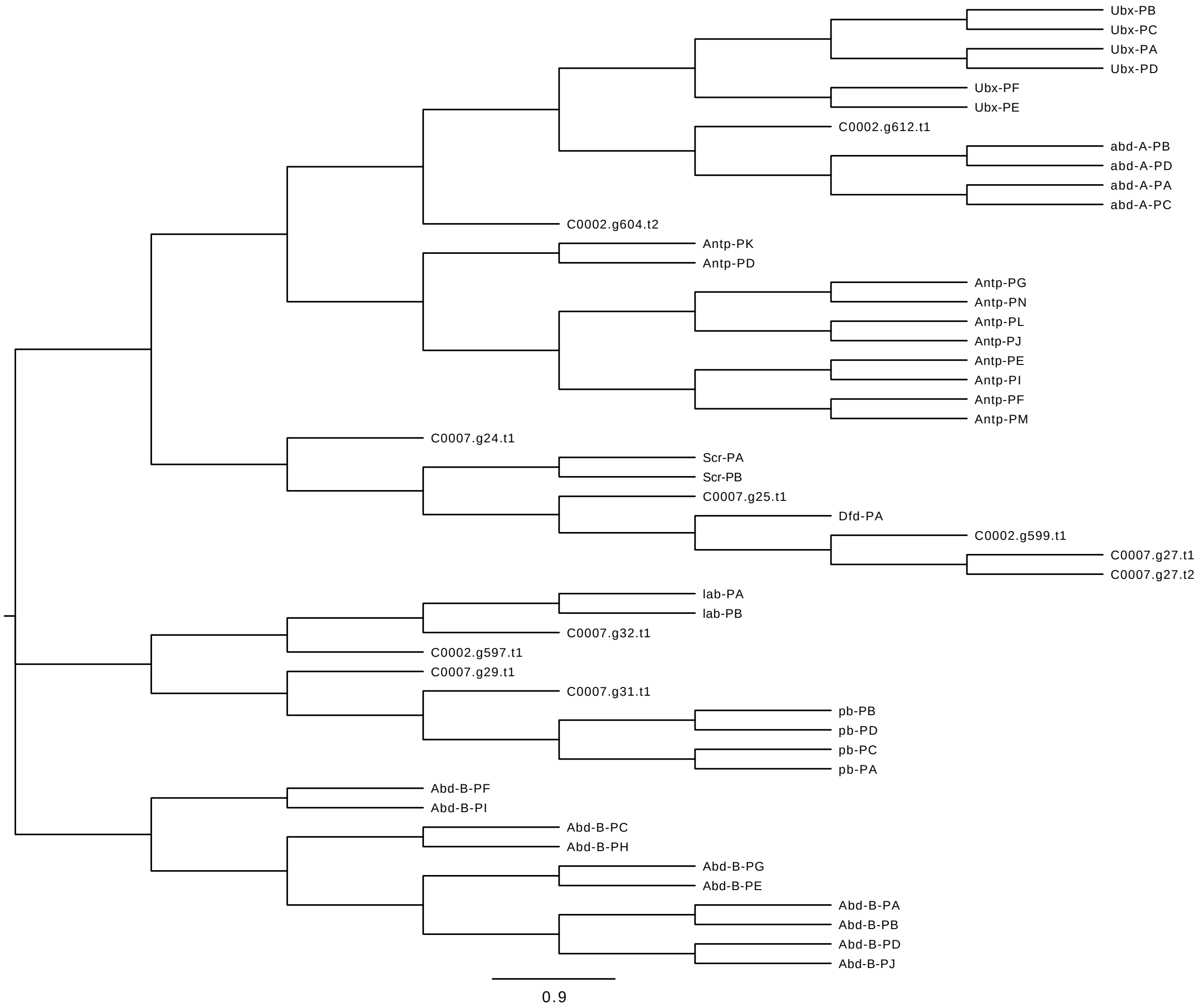

Figure 2: A bootstrap consensus maximum likelihood tree, generated using 300 bootstrap iterations in MEGA, comparing the CDS sequences putative clam shrimp HOX genes to *D. melanogaster* HOX genes. Because of the degree of divergence between sequences, this tree had to be created using an approach that allows the usage of information at sites that are missing in some sequences. Thus, it is less trustworthy than the protein tree, and was not used to call orthologs. The exception to this is the two unannotated genes: their genomic sequences were included in this tree, and they were found to be orthologous to *D. melanogaster Scr*.

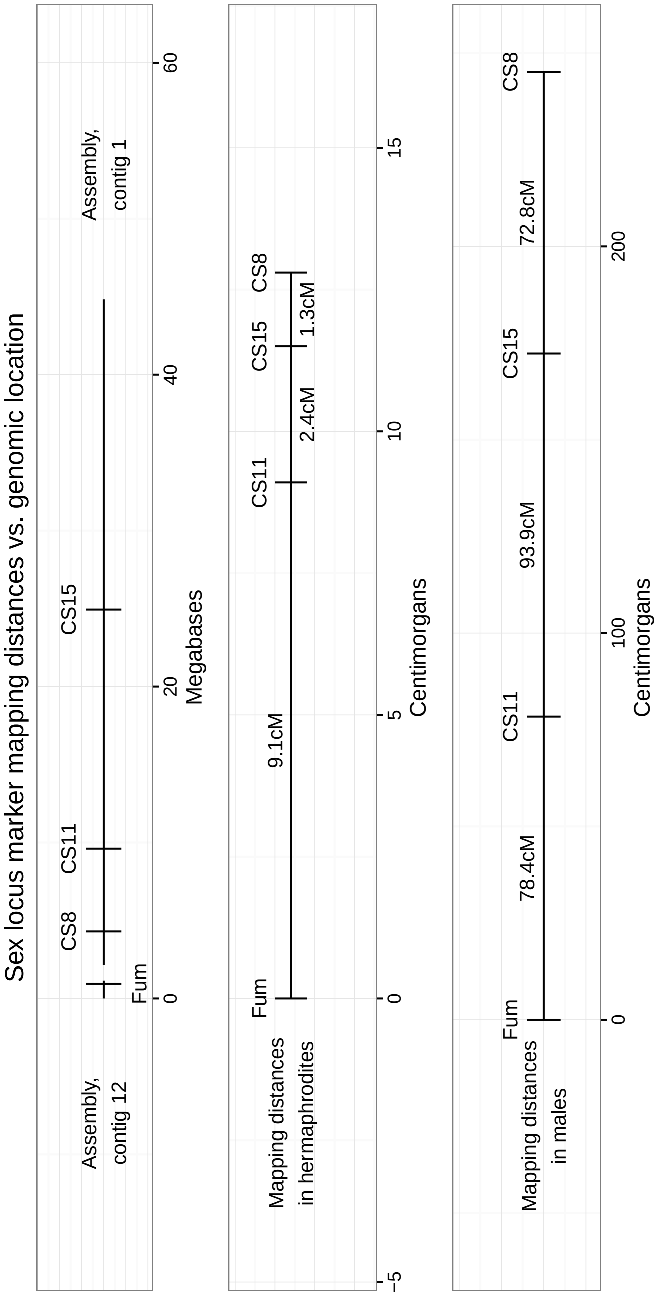

Figure 3: A diagram of the positions of sex markers according to different mapping schemes.

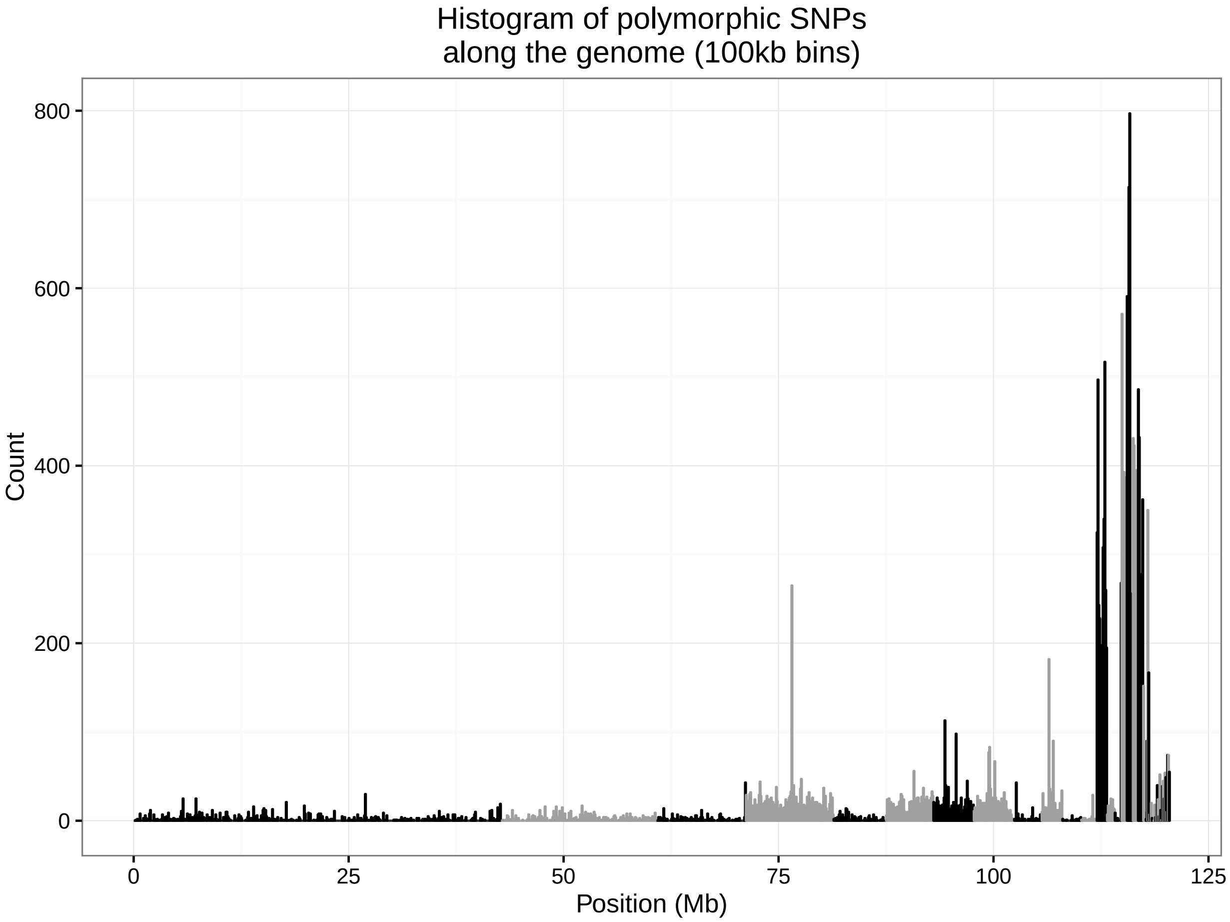

Figure 4: A Manhattan histogram of polymorphism in the inbred clam shrimp strain.