

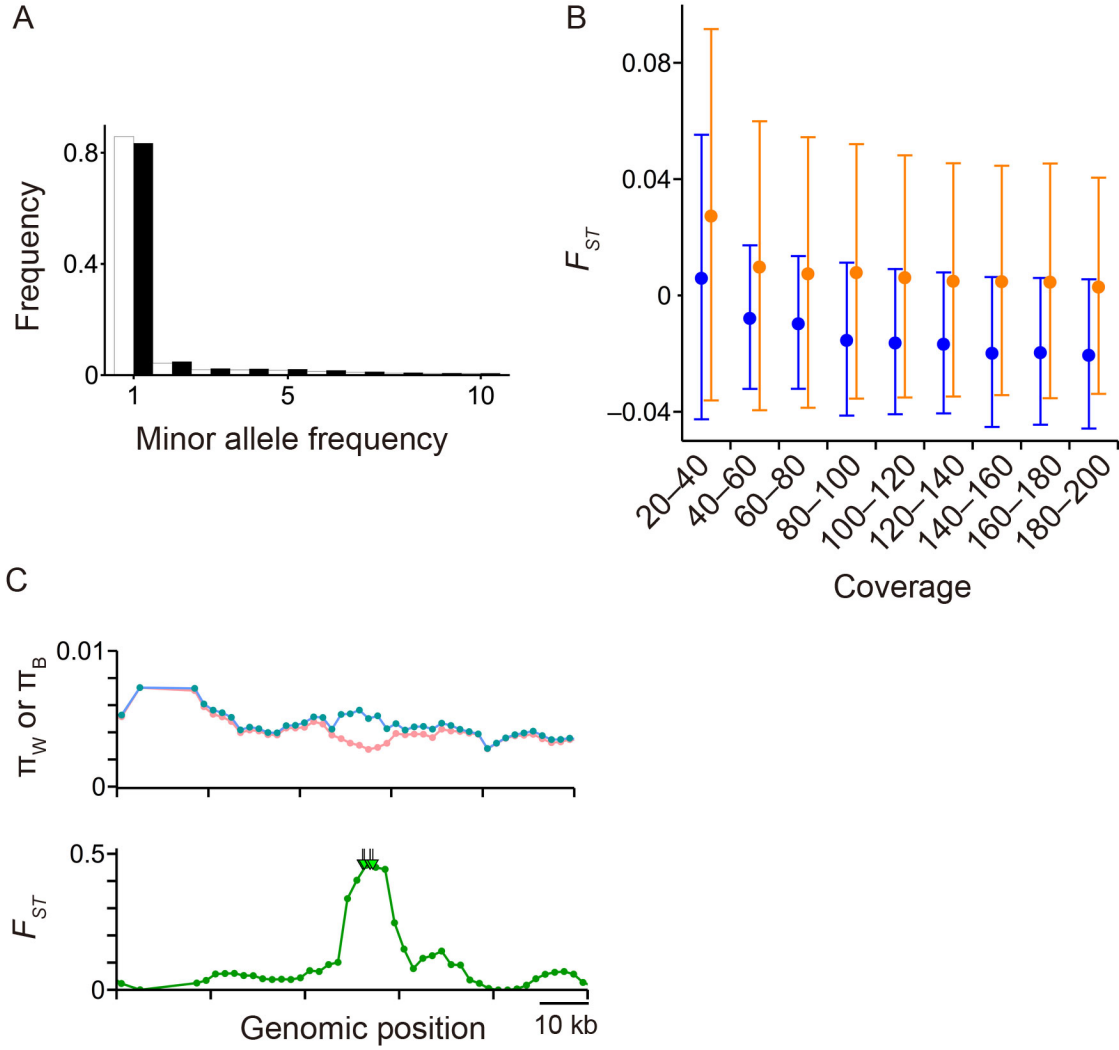


Figure S2. Population genomic analyses using only male individuals. **(A)** Site frequency spectrum in *H. pyrrhocephalus* (white bars; 126,843 SNPs) and *H. sp. 'macula'* (black bars; 146,456 SNPs). Nucleotide diversity and Tajima's D values were almost same as those in all samples. **(B)** Average F_{ST} values (± 1 SD) against coverage for Pool-seq data as in Fig. 1B (5,662,990 SNPs). The blue and orange dots represent observed and simulated values under panmixia. **(C)** The spatial patterns of average nucleotide diversity within each species (π_W ; pink), average pairwise nucleotide divergence between species (π_B ; blue), and F_{ST} (green) in and around *LWS* gene as in Fig. 2B. The green arrows represent fixed nucleotide differences between species.