

S11 Fig. Summary and selection statistics across colour pattern regions for all populations analysed in the *Heliconius melpomene*-clade. For each population genotyping coverage (calculated as proportion of retained genotypes after quality filtering in 500 bp windows), nucleotide diversity, Kelly's Z_{ns} , Tajima's D , pooled integrated haplotype homozygosity score, and SweepFinder2's [74,76] composite likelihood ratio statistics across each colour pattern region are shown (top to bottom). File names contain population and colour pattern region identifiers (Hmel201011 = *aristaleless* scaffold, Hmel210004 = *WntA* scaffold, Hmel215006 = *cortex* scaffold, Hmel218003 = *optix* scaffold). The 120 single figures have been uploaded to GitHub:

https://github.com/markusmoest/SelectionHeliconius/tree/master/S11_Fig_H_melpomene