

S22 Fig. Summary and selection statistics across colour pattern regions for all populations analysed in the *Heliconius erato*-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 (Herato1001 = *WntA* scaffold, Herato1505 = *cortex* scaffold, Herato1801 = *optix* scaffold). The 18 single figures have been uploaded to GitHub:
https://github.com/markusmoest/SelectionHeliconius/tree/master/S22_Fig_H_erato