# Supplementary Information:

# Complex modular architecture around a simple toolkit of wing pattern genes

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# S1. Color pattern loci

**Table S 1. Summary of major loci affecting color pattern variation in *Heliconius erato* considered in this study and their original description.**

| **Locus** | **Major phenotypic effect** | **Original description of phenotype (Sheppard et al. 1985)** | **Candidate Gene** |
|---|---|---|---|
| *Sd* | Forewing band shape | Shortened: affecting shape of the forewing band | *wntA* |
| *St* | Forewing band shape | Split: breaking up forewing band in two spots | *wntA* |
| *Ly* | Forewing band shape | Linked to yellow line: breaking up forewing band in multiple spots | *wntA* |
| *Ro* | Forewing band shape | Round: affecting shape distal portion of forewing band | *vvl* or *rsp3** |
| *R* | Red pattern | Rays: red rays on hindwing | *optix* |
| *D* | Red pattern | Dennis: red patch in proximal part of forewing | *optix* |
| *Y* | Red pattern | Band: red forewing band | *optix* |
| *Cr* | Yellow hindwing band | Cream rectangles: yellow hindwing bar (and white hindwing fringes in H. e. cyrbia) | *cortex* |

*In this study we identify two likely gene candidates underlying variation at *Ro*.

## S2. Genome assembly

### S2.1. Library construction and sequencing

**Table S 2. Sequencing data for *Heliconius erato* (*demophoon*) genome assembly and linkage mapping.**

| | Insert size | Sample | Intrinsic coverage | Type | Sequencing Center | SRA accession |
|---|---|---|---|---|---|---|
| Small insert pair-end sequencing | 250 | STRI_6581 | 127 | PE 150 | BGI | SAMN05578372 |
| | 500 | STRI_6581 | 52 | PE 150 | BGI | SAMN05578373 |
| | 800 | STRI_6581 | 43 | PE 100 | BGI | SAMN05578374 |
| Small mate-pair bridging libraries and sequencing | 4.3kb | STRI_6582 | 61 | PE 100 | Duke | SAMN05578375 |
| | 6.5kb | STRI_6582 | 46 | PE 100 | Duke | SAMN05578376 |
| PacBio Long Reads | - | STRI_6591 | 25 | - | Duke | SAMN05578377 |
| Mapping Family | 250 | STRI_6405 (Father) | 30 | PE 100 | Duke | SAMN05572290 |
| | 250 | STRI_6659 (Mother) | 47 | PE 100 | Duke | SAMN05572291 |
| | 250 | STRI_6520 | 9 | PE 100 | Duke | SAMN05572292 |
| | 250 | STRI_6523 | 10 | PE 100 | Duke | SAMN05572293 |
| | 250 | STRI_6524 | 12 | PE 100 | Duke | SAMN05572294 |
| | 250 | STRI_6525 | 9 | PE 100 | Duke | SAMN05572295 |
| | 250 | STRI_6526 | 11 | PE 100 | Duke | SAMN05572296 |
| | 250 | STRI_6527 | 7 | PE 100 | Duke | SAMN05572297 |
| | 250 | STRI_6528 | 8 | PE 100 | Duke | SAMN05572298 |
| | 250 | STRI_6529 | 6 | PE 100 | Duke | SAMN05572299 |
| | 250 | STRI_6530 | 9 | PE 100 | Duke | SAMN05572300 |
| | 250 | STRI_6531 | 8 | PE 100 | Duke | SAMN05572301 |
| | 250 | STRI_6532 | 8 | PE 100 | Duke | SAMN05572302 |
| | 250 | STRI_6533 | 8 | PE 100 | Duke | SAMN05572303 |
| | 250 | STRI_6534 | 9 | PE 100 | Duke | SAMN05572304 |
| | 250 | STRI_6539 | 11 | PE 100 | Duke | SAMN05572305 |
| | 250 | STRI_6542 | 8 | PE 100 | Duke | SAMN05572306 |
| | 250 | STRI_6543 | 9 | PE 100 | Duke | SAMN05572307 |
| | 250 | STRI_6544 | 7 | PE 100 | Duke | SAMN05572308 |
| | 250 | STRI_6550 | 9 | PE 100 | Duke | SAMN05572309 |
| | 250 | STRI_6551 | 8 | PE 100 | Duke | SAMN05572310 |
| | 250 | STRI_6562 | 10 | PE 100 | Duke | SAMN05572311 |
| | 250 | STRI_6619 | 8 | PE 100 | Duke | SAMN05572312 |
| | 250 | STRI_6620 | 9 | PE 100 | Duke | SAMN05572313 |
| | 250 | STRI_6643 | 8 | PE 100 | Duke | SAMN05572314 |
| | 250 | STRI_6644 | 10 | PE 100 | Duke | SAMN05572315 |
| | 250 | STRI_6645 | 12 | PE 100 | Duke | SAMN05572316 |
| | 250 | STRI_6646 | 10 | PE 100 | Duke | SAMN05572317 |
| | 250 | STRI_6660 | 10 | PE 100 | Duke | SAMN05572318 |
| | 250 | STRI_6661 | 8 | PE 100 | Duke | SAMN05572319 |
| | 250 | STRI_6662 | 9 | PE 100 | Duke | SAMN05572320 |
| | 250 | STRI_6663 | 11 | PE 100 | Duke | SAMN05572321 |
| | 250 | STRI_6664 | 5 | PE 100 | Duke | SAMN05572322 |
| | 250 | STRI_6563 | 6 | PE 100 | Duke | SAMN05572323 |
| | 250 | STRI_6564 | 6 | PE 100 | Duke | SAMN05572324 |
| | 250 | STRI_6565 | 16 | PE 100 | Duke | SAMN05572325 |
| | 250 | STRI_6566 | 7 | PE 100 | Duke | SAMN05572326 |
| | 250 | STRI_6567 | 12 | PE 100 | Duke | SAMN05572327 |
| | 250 | STRI_6568 | 10 | PE 100 | Duke | SAMN05572328 |
| | 250 | STRI_6569 | 9 | PE 100 | Duke | SAMN05572329 |
| | 250 | STRI_6570 | 13 | PE 100 | Duke | SAMN05572330 |
| | 250 | STRI_6576 | 13 | PE 100 | Duke | SAMN05572331 |
| | 250 | STRI_6577 | 14 | PE 100 | Duke | SAMN05572332 |

| | | | | | |
|---|---|---|---|---|---|
| 250 | STRI_6578 | 11 | PE 100 | Duke | SAMN05572333 |
| 250 | STRI_6579 | 9 | PE 100 | Duke | SAMN05572334 |
| 250 | STRI_6580 | 8 | PE 100 | Duke | SAMN05572335 |
| 250 | STRI_6583 | 10 | PE 100 | Duke | SAMN05572336 |
| 250 | STRI_6584 | 8 | PE 100 | Duke | SAMN05572337 |
| 250 | STRI_6585 | 9 | PE 100 | Duke | SAMN05572338 |
| 250 | STRI_6586 | 10 | PE 100 | Duke | SAMN05572339 |
| 250 | STRI_6592 | 8 | PE 100 | Duke | SAMN05572340 |
| 250 | STRI_6593 | 8 | PE 100 | Duke | SAMN05572341 |
| 250 | STRI_6594 | 10 | PE 100 | Duke | SAMN05572342 |
| 250 | STRI_6601 | 11 | PE 100 | Duke | SAMN05572343 |
| 250 | STRI_6602 | 9 | PE 100 | Duke | SAMN05572344 |
| 250 | STRI_6606 | 9 | PE 100 | Duke | SAMN05572345 |
| 250 | STRI_6712 | 8 | PE 100 | Duke | SAMN05572346 |
| 250 | STRI_6713 | 10 | PE 100 | Duke | SAMN05572347 |
| 250 | STRI_6714 | 9 | PE 100 | Duke | SAMN05572348 |
| 250 | STRI_6715 | 9 | PE 100 | Duke | SAMN05572349 |
| 250 | STRI_6716 | 8 | PE 100 | Duke | SAMN05572350 |
| 250 | STRI_6726 | 10 | PE 100 | Duke | SAMN05572351 |
| 250 | STRI_6727 | 9 | PE 100 | Duke | SAMN05572352 |
| 250 | STRI_6728 | 10 | PE 100 | Duke | SAMN05572353 |
| 250 | STRI_6744 | 13 | PE 100 | Duke | SAMN05572354 |
| 250 | STRI_6745 | 7 | PE 100 | Duke | SAMN05572355 |
| 250 | STRI_6746 | 10 | PE 100 | Duke | SAMN05572356 |
| 250 | STRI_6751 | 9 | PE 100 | Duke | SAMN05572357 |
| 250 | STRI_6752 | 10 | PE 100 | Duke | SAMN05572358 |
| 250 | STRI_6753 | 8 | PE 100 | Duke | SAMN05572359 |
| 250 | STRI_6754 | 8 | PE 100 | Duke | SAMN05572360 |
| 250 | STRI_6755 | 8 | PE 100 | Duke | SAMN05572361 |
| 250 | STRI_6767 | 10 | PE 100 | Duke | SAMN05572364 |
| 250 | STRI_6768 | 10 | PE 100 | Duke | SAMN05572365 |
| 250 | STRI_6769 | 7 | PE 100 | Duke | SAMN05572366 |
| 250 | STRI_6782 | 9 | PE 100 | Duke | SAMN05572367 |
| 250 | STRI_6783 | 11 | PE 100 | Duke | SAMN05572368 |
| 250 | STRI_6784 | 11 | PE 100 | Duke | SAMN05572369 |
| 250 | STRI_6787 | 10 | PE 100 | Duke | SAMN05572372 |
| 250 | STRI_6816 | 7 | PE 100 | Duke | SAMN05572373 |
| 250 | STRI_6477 | 10 | PE 100 | Duke | SAMN05572374 |
| 250 | STRI_6478 | 8 | PE 100 | Duke | SAMN05572375 |
| 250 | STRI_6495 | 11 | PE 100 | Duke | SAMN05572376 |
| 250 | STRI_6501 | 10 | PE 100 | Duke | SAMN05572377 |
| 250 | STRI_6502 | 10 | PE 100 | Duke | SAMN05572378 |
| 250 | STRI_6506 | 10 | PE 100 | Duke | SAMN05572379 |
| 250 | STRI_6500 | 8 | PE 100 | Duke | SAMN05572380 |
| 250 | STRI_6503 | 10 | PE 100 | Duke | SAMN05572381 |
| 250 | STRI_6505 | 9 | PE 100 | Duke | SAMN05572382 |
| 250 | STRI_6493 | 9 | PE 100 | Duke | SAMN05572383 |
| 250 | STRI_6494 | 9 | PE 100 | Duke | SAMN05572384 |
| 250 | STRI_6496 | 12 | PE 100 | Duke | SAMN05572385 |
| 250 | STRI_6497 | 9 | PE 100 | Duke | SAMN05572386 |
| 250 | STRI_6498 | 10 | PE 100 | Duke | SAMN05572387 |
| 250 | STRI_6499 | 12 | PE 100 | Duke | SAMN05572388 |
| 250 | STRI_6610 | 9 | PE 100 | Duke | SAMN05572389 |
| 250 | STRI_6611 | 18 | PE 100 | Duke | SAMN05572390 |

## S2.2. *De novo* assemblies

**Table S 3. *De novo* genome assemblies.**

| Assembly | Data | Length | N50 | Scaffolds | %Gaps |
|---|---|---|---|---|---|
| Herato_stage1 | Illumina/Pacbio | 402,810,510 | 611,657 | 1,275 | 4.100 |
| Herato_stage2 | Linkage map corrected | 404,432,779 | 805,173 | 746 | 4.100 |
| Herato_stage3 | Discovar/Allpaths correctd | 382,844,248 | 10,745,484 | 196 | 1.400 |

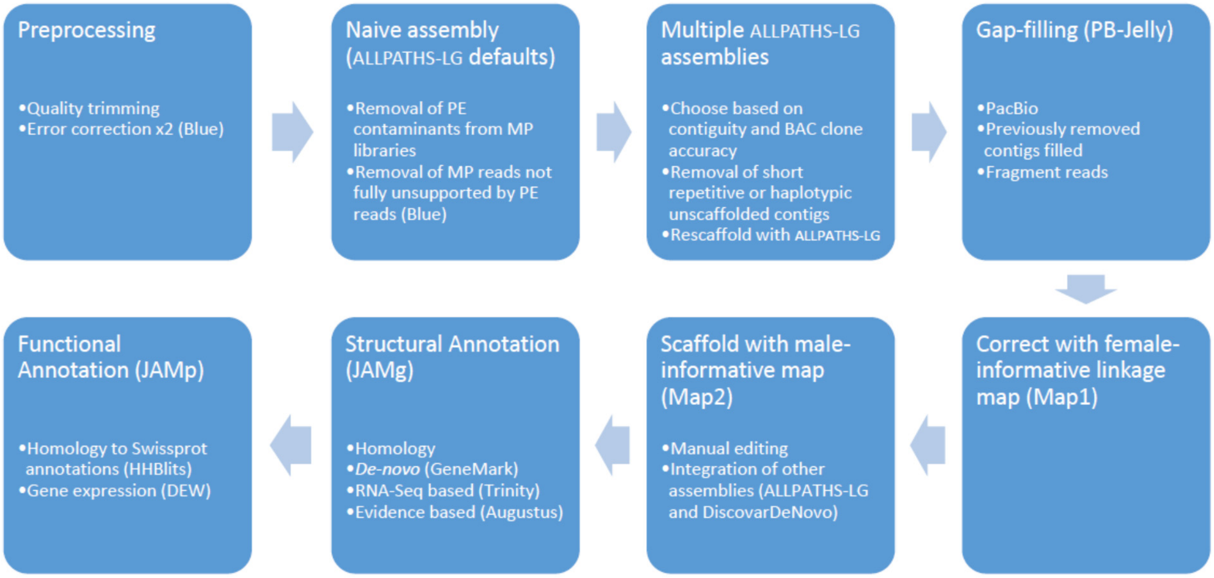


**Figure S 1. Schematic figure of *Heliconius erato* genome assembly and annotation process[1–5].**

## S2.3. Linkage mapping and assembly validation

**Table S 4. Linkage map statistics.** Two maps were constructed from markers informative only on the mother (map 1) or father (map 2). We used biphasic linkage mapping[6]: achiasmatic meiosis in Lepidoptera, the maternal map only gives information on the chromosome of markers and not the position within each chromosome.

| Chromosome | Markers in map 1 | Markers in map 2 | Map 1 length | Mb |
|---:|---:|---:|---:|---:|
| 1 | 138070 | 116509 | 49 | 23.3 |
| 2 | 106156 | 0 | 38 | 14.3 |
| 3 | 78332 | 68566 | 47 | 17.8 |
| 4 | 76837 | 71440 | 48 | 17.3 |
| 5 | 81039 | 74708 | 44 | 14.5 |
| 6 | 148236 | 65212 | 44 | 19.8 |
| 7 | 179873 | 23584 | 42 | 19.7 |
| 8 | 92129 | 41707 | 40 | 15.3 |
| 9 | 64311 | 47910 | 42 | 14.5 |
| 10 | 166114 | 120991 | 47 | 24.5 |
| 11 | 100043 | 84406 | 45 | 18.3 |
| 12 | 170326 | 109476 | 50 | 21.8 |
| 13 | 174551 | 75580 | 44 | 24.7 |
| 14 | 75735 | 69027 | 39 | 15.7 |
| 15 | 104692 | 50336 | 52 | 18 |
| 16 | 87143 | 75736 | 47 | 19 |
| 17 | 107757 | 84390 | 36 | 21.4 |
| 18 | 152173 | 94396 | 52 | 22.8 |
| 19 | 129946 | 96628 | 47 | 23.6 |
| 20 | 112258 | 81843 | 52 | 20.4 |
| Z | 32676 | 15769 | 41 | 18.4 |
| Total | 2378397 | 1468214 | 946 | 405.1* |

*The total genome length is slightly bigger than the total length of the Herato_stage2 assembly as short errors and uncertain regions are sometimes put to multiple chromosomes. The final Herato_stage3 assembly (< 400Mb) was obtained by resolving these and other uncertain regions.

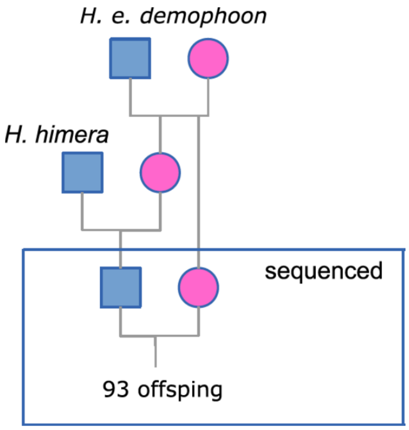
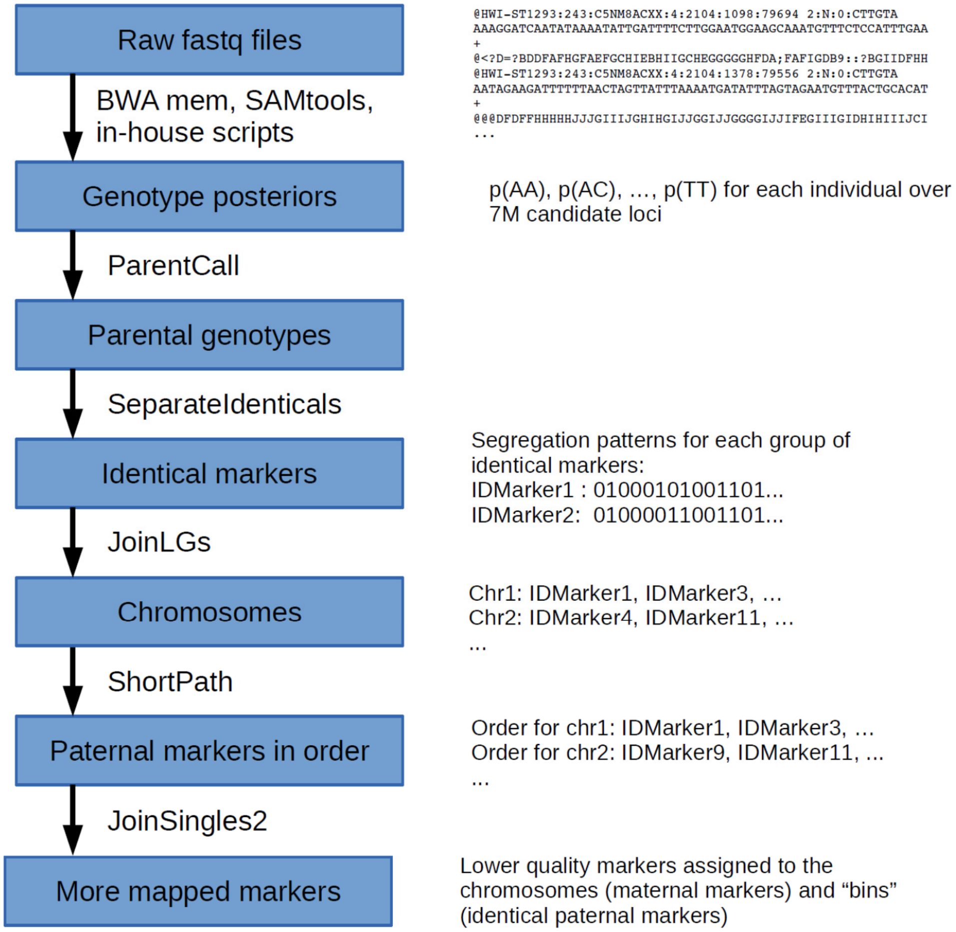
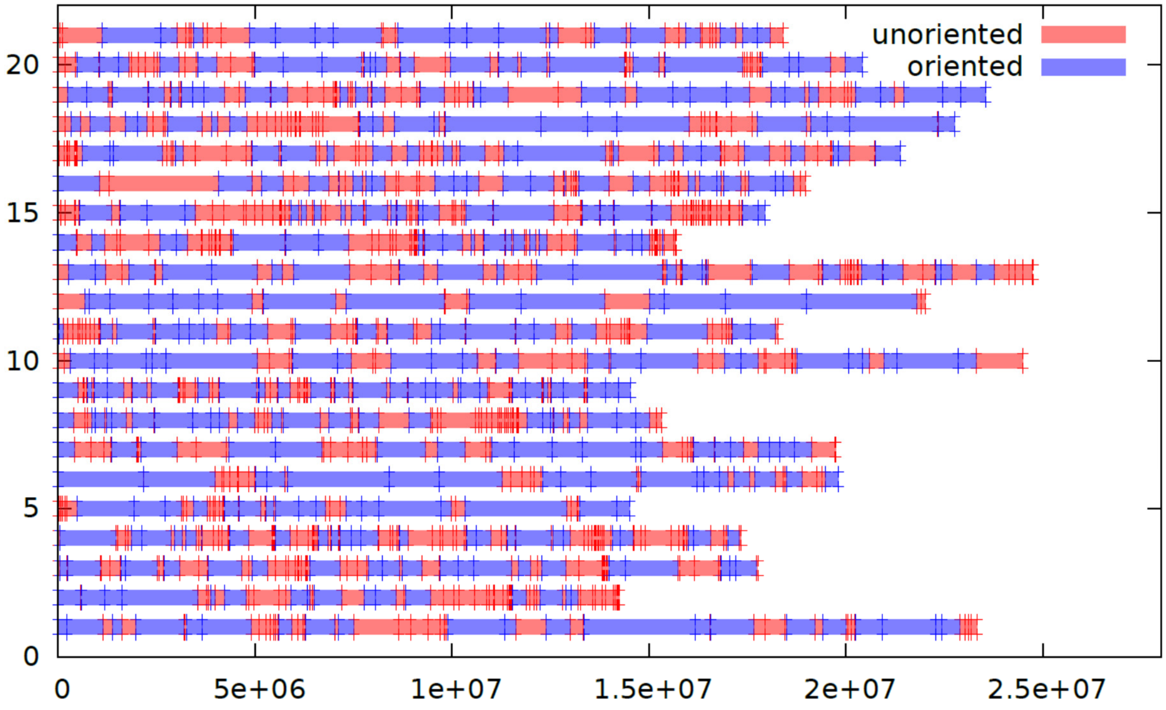


Figure S 2. Backcross for linkage mapping.



```
@HWI-ST1293:243:C5NM8ACXX:4:2104:1098:79694 2:N:0:CTTGTA
AAAGGATCAATATAAAATATTGATTTTCTTGGAATGGAAGCAAATGTTTCTCCATTTGAA
+
@<?D=?BDDFAFHGFAEFGCHIEBHIIGCHEGGGGGHFDA;FAFIGDB9::?BGIIDFHH
@HWI-ST1293:243:C5NM8ACXX:4:2104:1378:79556 2:N:0:CTTGTA
AATAGAAGATTTTTTAACTAGTTATTTAAAATGATATTTAGTAGAATGTTTACTGCACAT
+
@@@DFDFFHHHHHJJJGIIIJGHIHGIJJGGIJJGGGGIJJIFEGIIIGIDHIHIIIJCI
...
```

Figure S 3. Schematic figure of linkage mapping process using Lep-Map3.



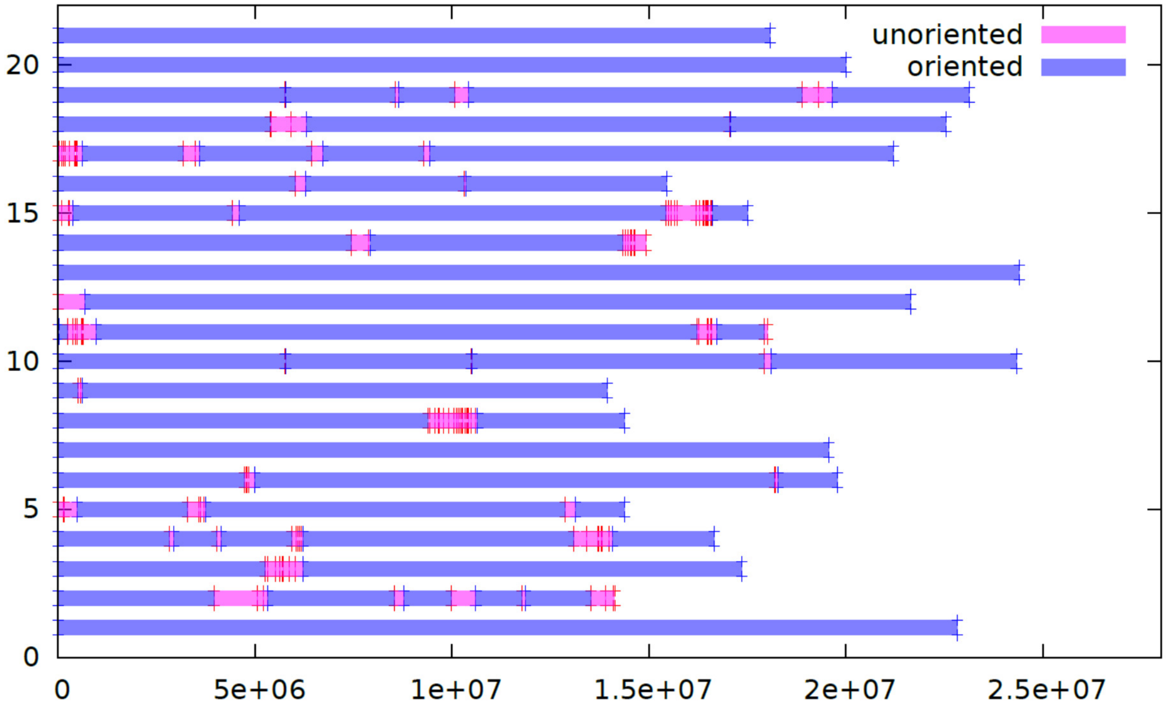


**Figure S 4. Genome assembly results.** Upper figure shows the completeness of the chromosomes in the assembly after made error-free based on the linkage maps (Herato_stage2). Below is the final assembly after removing haplotypic scaffolds and joining scaffold based on secondary genome assemblies and PacBio data (Herato_stage3).

## S2.4. *H. erato* and Lepidoptera genome assembly statistics

Assembly statistics for the *Heliconius erato* and other Lepidoptera genomes were computed using summarizeAssembly.py in PBSuite 14.9.9 [7]. Assembly completeness was assessed against a benchmarked set of 2,675 single-copy orthologs using BUSCO [8].

**Table S 5. Lepidoptera genome assembly statistics. Assembly size and scaffold statistics**

| | Scaffolds | Total length | Mean scaffold size | Maximum scaffold size |
|---|---|---|---|---|
| ***Heliconius erato*** | **196** | **382,844,248** | **1,953,287** | **23,854,410** |
| *Heliconius melpomene* v1 | 4,309 | 273,786,188 | 63,538 | 1,451,426 |
| *Heliconius melpomene* v2 | 795 | 275,198,613 | 346,161 | 9,352,983 |
| *Bombyx mori* | 43,462 | 481,803,763 | 11,085 | 16,203,812 |
| *Danaus plexippus* | 5,397 | 248,564,116 | 46,055 | 6,243,218 |
| *Lerema accius* | 29,988 | 298,173,436 | 9,943 | 3,082,282 |
| *Melitaea cinxia* | 8,261 | 389,907,520 | 47,198 | 668,473 |
| *Papilio glaucus* | 68,029 | 375,987,417 | 5,526 | 1,977,235 |
| *Papilio polytes* | 3,873 | 227,005,758 | 58,612 | 9,881,032 |
| *Papilio xuthus* | 5,572 | 243,890,167 | 43,770 | 16,292,344 |
| *Plutella xylostella* | 1,819 | 394,062,517 | 216,636 | 3,493,687 |
| *Bicyclus anynana* | 15,180 | 458,610,584 | 30,211 | 2,943,548 |
| *Chilo suppressalis* | 80,479 | 372,375,373 | 4,626 | 111,673 |
| *Manduca sexta* | 20,871 | 419,424,771 | 20,096 | 3,253,989 |
| *Plodia interpunctella* | 10,542 | 381,952,380 | 36,231 | 7,207,896 |

**Table S 6. Lepidoptera genome assembly statistics. Scaffold statistics.**

| | Scaffold N50 | Scaffold N90 | Scaffold N95 | Scaffold L50 | Scaffold L90 | Scaffold L95 |
|---|---|---|---|---|---|---|
| ***Heliconius erato*** | **10,745,484** | **2,677,609** | **1,104,102** | **12** | **40** | **52** |
| *Heliconius melpomene* v1 | 194,302 | 38,051 | 21,864 | 345 | 1,634 | 2,105 |
| *Heliconius melpomene* v2 | 2,102,720 | 273,111 | 124,798 | 34 | 176 | 251 |
| *Bombyx mori* | 4,008,358 | 61,147 | 928 | 38 | 258 | 5,679 |
| *Danaus plexippus* | 715,606 | 160,499 | 68,064 | 101 | 366 | 483 |
| *Lerema accius* | 525,349 | 60,308 | 1,913 | 160 | 689 | 3,385 |
| *Melitaea cinxia* | 119,328 | 29,598 | 16,097 | 970 | 3,396 | 4,263 |
| *Papilio glaucus* | 230,299 | 2,022 | 945 | 421 | 7,589 | 21,037 |
| *Papilio polytes* | 3,672,263 | 930,396 | 417,439 | 21 | 63 | 81 |
| *Papilio xuthus* | 6,198,915 | 533,617 | 160,478 | 16 | 48 | 91 |
| *Plutella xylostella* | 737,182 | 152,088 | 72,492 | 155 | 575 | 753 |
| *Bicyclus anynana* | 364,913 | 55,873 | 22,189 | 303 | 1,523 | 2,131 |
| *Chilo suppressalis* | 5,215 | 2,401 | 2,191 | 19,910 | 63,459 | 71,579 |
| *Manduca sexta* | 664,006 | 46,417 | 4,807 | 169 | 1,025 | 2,265 |
| *Plodia interpunctella* | 1,270,674 | 18,727 | 8,920 | 76 | 713 | 2,348 |

**Table S 7. Lepidoptera genome assembly statistics. Contigs and gabs.**

| | Contigs | Mean contig size | Contig N50 | Gaps | Total gap length | Gap % |
|---|---:|---:|---:|---:|---:|---:|
| ***Heliconius erato*** | *5,851* | 64,539 | 169,806 | 5,655 | 5,223,833 | 1.4 |
| *Heliconius melpomene* v1 | 11,607 | 23,231 | 51,611 | 7,298 | 4,132,701 | 1.5 |
| *Heliconius melpomene* v2 | 3,105 | 88,314 | 330,037 | 2,310 | 981,612 | 0.4 |
| *Bombyx mori* | 87,972 | 4,907 | 15,765 | 44,510 | 50,083,569 | 10.4 |
| *Danaus plexippus* | 10,545 | 22,939 | 113,903 | 5,148 | 6,664,276 | 2.7 |
| *Lerema accius* | 52,985 | 5,466 | 18,018 | 22,997 | 8,535,705 | 2.9 |
| *Melitaea cinxia* | 45,618 | 7,914 | 15,003 | 37,357 | 28,877,732 | 7.4 |
| *Papilio glaucus* | 96,532 | 3,754 | 12,958 | 28,503 | 13,599,067 | 3.6 |
| *Papilio polytes* | 13,441 | 16,239 | 51,561 | 9,568 | 8,725,522 | 3.8 |
| *Papilio xuthus* | 10,483 | 22,697 | 133,779 | 4,911 | 5,949,704 | 2.4 |
| *Plutella xylostella* | 15,764 | 24,557 | 59,184 | 13,945 | 6,937,203 | 1.8 |
| *Bicyclus anynana* | 28,866 | 15,650 | 60,000 | 13,686 | 6,852,021 | 1.5 |
| *Chilo suppressalis* | 331,320 | 983 | 2,183 | 250,841 | 46,484,604 | 12.5 |
| *Manduca sexta* | 35,212 | 11,351 | 51,909 | 14,341 | 19,705,457 | 4.7 |
| *Plodia interpunctella* | 17,231 | 21,160 | 338,910 | 6,689 | 17,329,456 | 4.5 |

**Table S 8. Lepidoptera genome assembly statistics. BUSCO results.**

| | Complete Single-Copy BUSCOs % | Complete Duplicated BUSCOs % | Fragmented BUSCOs % | Missing BUSCOs % |
|---|---:|---:|---:|---:|
| ***Heliconius erato*** | **82** | **2.3** | **11** | **6.3** |
| *Heliconius melpomene* v1 | 81 | 2.8 | 11 | 7.2 |
| *Heliconius melpomene* v2 | 85 | 3.1 | 9.4 | 5 |
| *Bombyx mori* | 75 | 2.2 | 16 | 8.4 |
| *Danaus plexippus* | 87 | 3.5 | 10 | 2.7 |
| *Lerema accius* | 77 | 2.6 | 13 | 8.3 |
| *Melitaea cinxia* | 55 | 1.6 | 20 | 23 |
| *Papilio glaucus* | 75 | 2.7 | 14 | 9.6 |
| *Papilio polytes* | 76 | 2.4 | 12 | 11 |
| *Papilio xuthus* | 84 | 3 | 8.2 | 7.4 |
| *Plutella xylostella* | 74 | 20 | 11 | 13 |
| *Bicyclus anynana* | 81 | 3 | 12 | 6.5 |
| *Chilo suppressalis* | 33 | 0.7 | 17 | 48 |
| *Manduca sexta* | 81 | 4.4 | 11 | 6.4 |
| *Plodia interpunctella* | 85 | 3.4 | 9.4 | 4.7 |

# S3. RNAseq for genome annotation

**Table S 9. Tissue and developmental stages for which RNA was sequenced for genome annotation.**

| Label | Developmental stage | Tissue | Sex | Race | SRA accession |
|---|---|---|---|---|---|
| emma_1d_pupae_hindwing_1 | 1d_pupae | hindwing | unknown | *emma* | SRR616680 |
| emma_1d_pupae_hindwing_2 | 1d_pupae | hindwing | unknown | *emma* | SRR616681 |
| emma_1d_pupae_hindwing_3 | 1d_pupae | hindwing | unknown | *emma* | SRR616682 |
| emma_3d_pupae_hindwing_1 | 3d_pupae | hindwing | unknown | *emma* | SRR616686 |
| emma_3d_pupae_hindwing_2 | 3d_pupae | hindwing | unknown | *emma* | SRR616687 |
| emma_3d_pupae_hindwing_3 | 3d_pupae | hindwing | unknown | *emma* | SRR616688 |
| emma_5th_instar_hindwing_1 | 5th_instar | hindwing | unknown | *emma* | SRR616278 |
| emma_5th_instar_hindwing_2 | 5th_instar | hindwing | unknown | *emma* | SRR616674 |
| emma_5th_instar_hindwing_3 | 5th_instar | hindwing | unknown | *emma* | SRR616675 |
| favorinus_1d_pupae_hindwing_1 | 1d_pupae | hindwing | unknown | *favorinus* | SRR616683 |
| favorinus_1d_pupae_hindwing_2 | 1d_pupae | hindwing | unknown | *favorinus* | SRR616684 |
| favorinus_1d_pupae_hindwing_3 | 1d_pupae | hindwing | unknown | *favorinus* | SRR616685 |
| favorinus_3d_pupae_hindwing_1 | 3d_pupae | hindwing | unknown | *favorinus* | SRR616689 |
| favorinus_3d_pupae_hindwing_2 | 3d_pupae | hindwing | unknown | *favorinus* | SRR616690 |
| favorinus_3d_pupae_hindwing_3 | 3d_pupae | hindwing | unknown | *favorinus* | SRR616691 |
| favorinus_5th_instar_hindwing_1 | 5th_instar | hindwing | unknown | *favorinus* | SRR616677 |
| favorinus_5th_instar_hindwing_2 | 5th_instar | hindwing | unknown | *favorinus* | SRR616678 |
| favorinus_5th_instar_hindwing_3 | 5th_instar | hindwing | unknown | *favorinus* | SRR616679 |
| hyd_36h_larval_hw_prox | 36h_larva | hindwing_proximal | unknown | *hydara* | SAMN05578182 |
| hyd_prepupae_wing | prepupae | wing | unknown | *hydara* | SAMN05578183 |
| pet_1d_pupa | 1d_pupae | body | unknown | *petiverana* | SAMN05578184 |
| pet_1instar | 1st_instar | whole | unknown | *petiverana* | SAMN05578185 |
| pet_24h_eggs | 24h_egg | eggs | unknown | *petiverana* | SAMN05578186 |
| pet_2instar | 2nd_instar | body | unknown | *petiverana* | SAMN05578187 |
| pet_3.5d_pupa | 3.5d_pupae | body | unknown | *petiverana* | SAMN05578188 |
| pet_36h_larval_hw_distal | 36h_larva | hindwing_distal | unknown | *petiverana* | SAMN05578189 |
| pet_36h_larval_hw_prox | 36h_larva | hindwing_proximal | unknown | *petiverana* | SAMN05578190 |
| pet_3instar | 3rd_instar | whole | unknown | *petiverana* | SAMN05578191 |
| pet_48h_eggs | 48h_egg | eggs | unknown | *petiverana* | SAMN05578192 |
| pet_4instar | 4th_instar | body | unknown | *petiverana* | SAMN05578193 |
| pet_4instar_gut | 4th_instar | gut | unknown | *petiverana* | SAMN05578194 |
| pet_5d_pupa | 5d_pupae | body | unknown | *petiverana* | SAMN05578195 |
| pet_5instar | 5th_instar | body | unknown | *petiverana* | SAMN05578196 |
| pet_9d_pupa | 9d_pupae | body | unknown | *petiverana* | SAMN05578197 |
| pet_eggs_12h | 12h_egg | eggs | unknown | *petiverana* | SAMN05578198 |
| pet_female_abdomen | adult | abdomen | female | *petiverana* | SAMN05578199 |
| pet_female_eye | adult | eye | female | *petiverana* | SAMN05578200 |
| pet_female_head | adult | head | female | *petiverana* | SAMN05578201 |
| pet_female_thorax | adult | thorax | female | *petiverana* | SAMN05578202 |
| pet_male_abdomen | adult | abdomen | male | *petiverana* | SAMN05578203 |
| pet_male_head | adult | head | male | *petiverana* | SAMN05578204 |
| pet_male_thorax | adult | thorax | male | *petiverana* | SAMN05578205 |
| pet_prepupae_wing | prepupae | wing | unknown | *petiverana* | SAMN05578206 |

# S4. Population genomics

## S4.1. Sampling and sequencing

To determine the pattern of genome wide differences across the *H. erato* radiation, we sequenced the genomes of 101 individuals to 15-30x coverage, effectively genotyping an average of 62 % of the genome for each individual (Table S 10). Additionally, we sequenced the genomes of 15 individuals from 8 outgroup species to 15-30x coverage (Table S 11).

**Table S 10. *Heliconius erato* sampling. If individuals are sampled near hybrid zones, the hybridizing race is indicated.**

| Sample ID | Genus | Species | Race | location | country | Hybrid zone | SRA accession |
|---|---|---|---|---|---|---|---|
| BC2115 | *Heliconius* | *erato* | *amalfreda* | Brokopondo | Suriname | *erato + hydara* | SAMN05224103 |
| BC2124 | *Heliconius* | *erato* | *amalfreda* | Brokopondo | Suriname | *erato + hydara* | SAMN05224104 |
| STRIWOM5779 | *Heliconius* | *erato* | *amalfreda* | Brokopondo | Suriname | *erato + hydara* | SAMN05224208 |
| STRIWOM5780 | *Heliconius* | *erato* | *amalfreda* | Brokopondo | Suriname | *erato + hydara* | SAMN05224209 |
| STRIWOM5781 | *Heliconius* | *erato* | *amalfreda* | Brokopondo | Suriname | *erato + hydara* | SAMN05224210 |
| M3661 | *Heliconius* | *erato* | *chestertonii* | Rio Calima | Colombia | - | SAMN05224096 |
| M3662 | *Heliconius* | *erato* | *chestertonii* | Rio Calima | Colombia | - | SAMN05224097 |
| M3663 | *Heliconius* | *erato* | *chestertonii* | Rio Calima | Colombia | - | SAMN05224098 |
| M3664 | *Heliconius* | *erato* | *chestertonii* | Rio Calima | Colombia | - | SAMN05224099 |
| STRIWOM0057 | *Heliconius* | *erato* | *chestertonii* | Rio Calima | Colombia | - | SAMN05224192 |
| STRIWOM0058 | *Heliconius* | *erato* | *chestertonii* | Rio Calima | Colombia | - | SAMN05224193 |
| STRIWOM0059 | *Heliconius* | *erato* | *chestertonii* | Rio Calima | Colombia | - | SAMN05224194 |
| cyrbia004 | *Heliconius* | *erato* | *cyrbia* | Balsas | Ecuador | - | SAMN05224122 |
| cyrbia005 | *Heliconius* | *erato* | *cyrbia* | Balsas | Ecuador | - | SAMN05224123 |
| cyrbia023 | *Heliconius* | *erato* | *cyrbia* | Balsas | Ecuador | - | SAMN05224124 |
| cyrbia024 | *Heliconius* | *erato* | *cyrbia* | Balsas | Ecuador | - | SAMN05224125 |
| PetED3 | *Heliconius* | *erato* | *demophoon* | Gamboa | Panama | *hydara + demophoon* | SAMN05224182 |
| PetED4 | *Heliconius* | *erato* | *demophoon* | Gamboa | Panama | *hydara + demophoon* | SAMN05224183 |
| PetED5 | *Heliconius* | *erato* | *demophoon* | Gamboa | Panama | *hydara + demophoon* | SAMN05224184 |
| PetED6 | *Heliconius* | *erato* | *demophoon* | Gamboa | Panama | *hydara + demophoon* | SAMN05224185 |
| STRIWOM0033 | *Heliconius* | *erato* | *demophoon* | Lago Bayano | Panama | *hydara + demophoon* | SAMN05224188 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| STRIWOM0082 | *Heliconius* | *erato* | *demophoon* | Lago Bayano | Panama | *hydara + demophoon* | SAMN05224195 |
| STRIWOM0087 | *Heliconius* | *erato* | *demophoon* | Lago Bayano | Panama | *hydara + demophoon* | SAMN05224196 |
| STRIWOM1284 | *Heliconius* | *erato* | *demophoon* | Lago Bayano | Panama | *hydara + demophoon* | SAMN05224198 |
| STRIWOM5353 | *Heliconius* | *erato* | *demophoon* | Lago Bayano | Panama | *hydara + demophoon* | SAMN05224202 |
| STRIWOM5362 | *Heliconius* | *erato* | *demophoon* | Lago Bayano | Panama | *hydara + demophoon* | SAMN05224203 |
| GS020redo | *Heliconius* | *erato* | *emma* | San Cristobal | Peru | *favorinus + emma* | SAMN05224127 |
| GS021redo | *Heliconius* | *erato* | *emma* | San Cristobal | Peru | *favorinus + emma* | SAMN05224128 |
| NCS1671 | *Heliconius* | *erato* | *emma* | San Cristobal | Peru | *favorinus + emma* | SAMN05224154 |
| NCS1672 | *Heliconius* | *erato* | *emma* | San Cristobal | Peru | *favorinus + emma* | SAMN05224155 |
| NCS1673 | *Heliconius* | *erato* | *emma* | San Cristobal | Peru | *favorinus + emma* | SAMN05224156 |
| NCS1674 | *Heliconius* | *erato* | *emma* | San Cristobal | Peru | *favorinus + emma* | SAMN05224157 |
| NCS1675 | *Heliconius* | *erato* | *emma* | San Cristobal | Peru | *favorinus + emma* | SAMN05224158 |
| NCS2005 | *Heliconius* | *erato* | *erato* | Kaw | French Guiana | *hydara + erato* | SAMN05224160 |
| NCS2012 | *Heliconius* | *erato* | *erato* | Kaw | French Guiana | *hydara + erato* | SAMN05224161 |
| NCS2020 | *Heliconius* | *erato* | *erato* | Kaw | French Guiana | *hydara + erato* | SAMN05224162 |
| NCS2023 | *Heliconius* | *erato* | *erato* | Kaw | French Guiana | *hydara + erato* | SAMN05224163 |
| NCS2025 | *Heliconius* | *erato* | *erato* | Kaw | French Guiana | *hydara + erato* | SAMN05224164 |
| NCS2556 | *Heliconius* | *erato* | *erato* | Kaw | French Guiana | *hydara + erato* | SAMN05224174 |
| BC3277 | *Heliconius* | *erato* | *etylus* | Huamboya | Ecuador | *notabilis + etylus* | SAMN05224110 |
| BC3278 | *Heliconius* | *erato* | *etylus* | Huamboya | Ecuador | *notabilis + etylus* | SAMN05224111 |
| BC3280 | *Heliconius* | *erato* | *etylus* | Huamboya | Ecuador | *notabilis + etylus* | SAMN05224112 |
| BC3281 | *Heliconius* | *erato* | *etylus* | Huamboya | Ecuador | *notabilis + etylus* | SAMN05224113 |
| BC3282 | *Heliconius* | *erato* | *etylus* | Huamboya | Ecuador | *notabilis + etylus* | SAMN05224114 |
| GS012redo | *Heliconius* | *erato* | *favorinus* | ,Urahuasha | Peru | *favorinus + emma* | SAMN05224126 |
| NCS0471 | *Heliconius* | *erato* | *favorinus* | Urahuasha | Peru | *favorinus + emma* | SAMN05224148 |
| NCS0473 | *Heliconius* | *erato* | *favorinus* | Urahuasha | Peru | *favorinus + emma* | SAMN05224149 |
| NCS0476 | *Heliconius* | *erato* | *favorinus* | Urahuasha | Peru | *favorinus + emma* | SAMN05224150 |
| NCS0478 | *Heliconius* | *erato* | *favorinus* | Urahuasha | Peru | *favorinus + emma* | SAMN05224151 |
| NCS0479 | *Heliconius* | *erato* | *favorinus* | Urahuasha | Peru | *favorinus + emma* | SAMN05224152 |
| NCS2554 | *Heliconius* | *erato* | *favorinus* | Urahuasha | Peru | *favorinus + emma* | SAMN05224172 |
| NCS2555 | *Heliconius* | *erato* | *favorinus* | Urahuasha | Peru | *favorinus + emma* | SAMN05224173 |
| himera001 | *Heliconius* | *himera* | - | Vilcabamba | Ecuador | - | SAMN05224132 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| himera002 | *Heliconius* | *himera* | - | Vilcabamba | Ecuador | - | SAMN05224133 |
| himera003 | *Heliconius* | *himera* | - | Vilcabamba | Ecuador | - | SAMN05224134 |
| himera006 | *Heliconius* | *himera* | - | Vilcabamba | Ecuador | - | SAMN05224135 |
| himera030 | *Heliconius* | *himera* | - | Vilcabamba | Ecuador | - | SAMN05224136 |
| NCS1179 | *Heliconius* | *erato* | *hydara* | Kaw | French Guiana | *hydara* + *erato* | SAMN05224153 |
| NCS1979 | *Heliconius* | *erato* | *hydara* | Kaw | French Guiana | *hydara* + *erato* | SAMN05224159 |
| NCS2080 | *Heliconius* | *erato* | *hydara* | Kaw | French Guiana | *hydara* + *erato* | SAMN05224165 |
| NCS2211 | *Heliconius* | *erato* | *hydara* | Kaw | French Guiana | *hydara* + *erato* | SAMN05224166 |
| NCS2217 | *Heliconius* | *erato* | *hydara* | Kaw | French Guiana | *hydara* + *erato* | SAMN05224167 |
| NCS2574 | *Heliconius* | *erato* | *hydara* | Kaw | French Guiana | *hydara* + *erato* | SAMN05224175 |
| NCS2581 | *Heliconius* | *erato* | *hydara* | Kaw | French Guiana | *hydara* + *erato* | SAMN05224176 |
| NCS2609 | *Heliconius* | *erato* | *hydara* | Kaw | French Guiana | *hydara* + *erato* | SAMN05224177 |
| STRIWOM0039 | *Heliconius* | *erato* | *hydara* | Lago Bayano | Panama | *hydara* + *demophoon* | SAMN05224189 |
| STRIWOM0040 | *Heliconius* | *erato* | *hydara* | Lago Bayano | Panama | *hydara* + *demophoon* | SAMN05224190 |
| STRIWOM0088 | *Heliconius* | *erato* | *hydara* | Lago Bayano | Panama | *hydara* + *demophoon* | SAMN05224197 |
| STRIWOM5193 | *Heliconius* | *erato* | *hydara* | Lago Bayano | Panama | *hydara* + *demophoon* | SAMN05224200 |
| STRIWOM5351 | *Heliconius* | *erato* | *hydara* | Lago Bayano | Panama | *hydara* + *demophoon* | SAMN05224201 |
| STRIWOM0042 | *Heliconius* | *erato* | *hydara* | Lago Bayano | Panama | *hydara* + *demophoon* | SAMN05224191 |
| BC0411 | *Heliconius* | *erato* | *lativitta* | Ahuano | Ecuador | *notabilis* + *lativitta* | SAMN05224101 |
| lativitta01 | *Heliconius* | *erato* | *lativitta* | Ahuano | Ecuador | *notabilis* + *lativitta* | SAMN05224137 |
| lativitta02 | *Heliconius* | *erato* | *lativitta* | Ahuano | Ecuador | *notabilis* + *lativitta* | SAMN05224138 |
| lativitta03 | *Heliconius* | *erato* | *lativitta* | Ahuano | Ecuador | *notabilis* + *lativitta* | SAMN05224139 |
| lativitta04 | *Heliconius* | *erato* | *lativitta* | Jondachi | Ecuador | *notabilis* + *lativitta* | SAMN05224140 |
| BC3223 | *Heliconius* | *erato* | *notabilis* | Huamboya | Ecuador | *notabilis* + *etylus* | SAMN05224105 |
| BC3224 | *Heliconius* | *erato* | *notabilis* | Huamboya | Ecuador | *notabilis* + *etylus* | SAMN05224106 |
| BC3225 | *Heliconius* | *erato* | *notabilis* | Huamboya | Ecuador | *notabilis* + *etylus* | SAMN05224107 |
| BC3227 | *Heliconius* | *erato* | *notabilis* | Huamboya | Ecuador | *notabilis* + *etylus* | SAMN05224108 |
| BC3228 | *Heliconius* | *erato* | *notabilis* | Huamboya | Ecuador | *notabilis* + *etylus* | SAMN05224109 |
| BC0410 | *Heliconius* | *erato* | *notabilis* | Mera | Ecuador | *notabilis* + *lativitta* | SAMN05224100 |
| notabilis01 | *Heliconius* | *erato* | *notabilis* | Mera | Ecuador | *notabilis* + *lativitta* | SAMN05224178 |
| notabilis02 | *Heliconius* | *erato* | *notabilis* | Mera | Ecuador | *notabilis* + *lativitta* | SAMN05224179 |
| notabilis03 | *Heliconius* | *erato* | *notabilis* | Mera | Ecuador | *notabilis* + *lativitta* | SAMN05224180 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| notabilis04 | *Heliconius* | *erato* | *notabilis* | Mera | Ecuador | *notabilis + lativitta* | SAMN05224181 |
| CA51 | *Heliconius* | *erato* | *petiverana* | Campeche | Mexico | - | SAMN05224115 |
| CA53 | *Heliconius* | *erato* | *petiverana* | Campeche | Mexico | - | SAMN05224116 |
| CA54 | *Heliconius* | *erato* | *petiverana* | Campeche | Mexico | - | SAMN05224117 |
| CA55 | *Heliconius* | *erato* | *petiverana* | Campeche | Mexico | - | SAMN05224118 |
| CA56 | *Heliconius* | *erato* | *petiverana* | Campeche | Mexico | - | SAMN05224119 |
| MRK_MX09_01 | *Heliconius* | *erato* | *cruentus* | Puerto Vallarta | Mexico | - | SAMN05224147 |
| 5732 | *Heliconius* | *erato* | *phyllis* | Samaipata | Bolivia | - | SAMN05224204 |
| 5742 | *Heliconius* | *erato* | *phyllis* | Samaipata | Bolivia | - | SAMN05224205 |
| 5765 | *Heliconius* | *erato* | *phyllis* | Samaipata | Bolivia | - | SAMN05224206 |
| 5766 | *Heliconius* | *erato* | *phyllis* | Samaipata | Bolivia | - | SAMN05224207 |
| M3654 | *Heliconius* | *erato* | *venus* | Queremal | Colombia | - | SAMN05224141 |
| M3655 | *Heliconius* | *erato* | *venus* | Queremal | Colombia | - | SAMN05224142 |
| M3656 | *Heliconius* | *erato* | *venus* | Queremal | Colombia | - | SAMN05224143 |
| M3657 | *Heliconius* | *erato* | *venus* | Queremal | Colombia | - | SAMN05224144 |
| M3659 | *Heliconius* | *erato* | *venus* | Queremal | Colombia | - | SAMN05224145 |

**Table S 11. Outgroup sampling.**

| Sample ID | Genus | Species | location | country | Hybrid Zone | SRA accession |
|---|---|---|---|---|---|---|
| char001 | *Heliconius* | *charithonia* | Cambalache, Yauco | Puerto Rico | - | SAMN05224120 |
| char002 | *Heliconius* | *charithonia* | Cambalache, Yauco | Puerto Rico | - | SAMN05224121 |
| NCS2511 | *Heliconius* | *clysonimus* | Mina Negra | Peru | - | SAMN05224168 |
| NCS2512 | *Heliconius* | *clysonimus* | Mina Negra | Peru | - | SAMN05224169 |
| STRIWOM2312 | *Heliconius* | *hecalesia* | Boquete | Panama | - | SAMN05224199 |
| LMCI94-13 | *Heliconius* | *hermathena* | Santarém, Pará | Brazil | - | SAMN05224129 |
| LMCI94-14 | *Heliconius* | *hermathena* | Santarém, Pará | Brazil | - | SAMN05224130 |
| LMCI94-15 | *Heliconius* | *hermathena* | Santarém, Pará | Brazil | - | SAMN05224131 |
| MRKhort2 | *Heliconius* | *hortense* | Buttterfly Farm | El Salvador | - | SAMN05224146 |
| STRIWOM5792 | *Heliconius* | *ricini* | Brokopondo | Suriname | - | SAMN05224211 |
| BC2004 | *Heliconius* | *sara* | Brokopondo | Suriname | - | SAMN05224102 |
| MRK_EC_08_025 | *Heliconius* | *sara* | Mindo | Ecuador | - | SAMN05224186 |
| sar08025 | *Heliconius* | *sara* | Unknown | Unknown | - | SAMN04412545 |
| NCS2541 | *Heliconius* | *telesiphe* | Puente Chalayaco | Peru | - | SAMN05224170 |
| NCS2550 | *Heliconius* | *telesiphe* | Mina Negra | Peru | - | SAMN05224171 |

**Table S 12. *Heliconius erato* mapping and genotyping results.**

| Sample ID | Genus | Species | Race | Reads | Mapped (%) | Properly paired (%) | Genotyped (%) | Homozygous (%) | Heterozygous (%) |
|---|---|---|---|---:|---:|---:|---:|---:|---:|
| BC2115 | *Heliconius* | *erato* | *amalfreda* | 124725685 | 92.98 | 66.70 | 63.54 | 96.75 | 3.25 |
| BC2124 | *Heliconius* | *erato* | *amalfreda* | 134483280 | 93.03 | 66.66 | 64.32 | 96.73 | 3.27 |
| STRIWOM5779 | *Heliconius* | *erato* | *amalfreda* | 146432487 | 95.04 | 73.42 | 65.14 | 96.75 | 3.25 |
| STRIWOM5780 | *Heliconius* | *erato* | *amalfreda* | 121593810 | 94.40 | 71.28 | 62.69 | 96.89 | 3.11 |
| STRIWOM5781 | *Heliconius* | *erato* | *amalfreda* | 108858237 | 94.82 | 72.88 | 60.90 | 96.90 | 3.10 |
| M3661 | *Heliconius* | *erato* | *chestertonii* | 99124314 | 96.36 | 70.01 | 65.48 | 98.83 | 1.17 |
| M3662 | *Heliconius* | *erato* | *chestertonii* | 131202069 | 94.61 | 69.20 | 67.16 | 98.97 | 1.03 |
| M3663 | *Heliconius* | *erato* | *chestertonii* | 124765688 | 96.60 | 75.24 | 67.00 | 98.97 | 1.03 |
| M3664 | *Heliconius* | *erato* | *chestertonii* | 158840593 | 97.28 | 74.82 | 68.42 | 98.89 | 1.11 |
| STRIWOM0057 | *Heliconius* | *erato* | *chestertonii* | 115608137 | 94.16 | 74.69 | 60.63 | 98.99 | 1.01 |
| STRIWOM0058 | *Heliconius* | *erato* | *chestertonii* | 115958053 | 95.81 | 75.97 | 60.70 | 98.97 | 1.03 |
| STRIWOM0059 | *Heliconius* | *erato* | *chestertonii* | 135669920 | 96.03 | 76.76 | 65.17 | 99.00 | 1.00 |
| cyrbia004 | *Heliconius* | *erato* | *cyrbia* | 118648654 | 95.50 | 76.08 | 61.46 | 97.77 | 2.23 |
| cyrbia005 | *Heliconius* | *erato* | *cyrbia* | 108428572 | 95.55 | 76.07 | 60.08 | 97.89 | 2.11 |
| cyrbia023 | *Heliconius* | *erato* | *cyrbia* | 107602073 | 95.33 | 75.84 | 63.66 | 97.84 | 2.16 |
| cyrbia024 | *Heliconius* | *erato* | *cyrbia* | 106407244 | 95.75 | 76.70 | 59.91 | 97.85 | 2.15 |
| PetED3 | *Heliconius* | *erato* | *demophoon* | 147571378 | 97.61 | 84.17 | 65.27 | 97.08 | 2.92 |
| PetED4 | *Heliconius* | *erato* | *demophoon* | 147831384 | 96.32 | 83.27 | 64.26 | 97.05 | 2.95 |
| PetED5 | *Heliconius* | *erato* | *demophoon* | 124430446 | 97.27 | 83.64 | 60.84 | 97.09 | 2.91 |
| PetED6 | *Heliconius* | *erato* | *demophoon* | 147157885 | 97.66 | 84.25 | 64.75 | 97.06 | 2.94 |
| STRIWOM0033 | *Heliconius* | *erato* | *demophoon* | 103265835 | 96.40 | 78.96 | 61.15 | 97.01 | 2.99 |
| STRIWOM0082 | *Heliconius* | *erato* | *demophoon* | 132459907 | 94.90 | 74.73 | 61.73 | 96.85 | 3.15 |
| STRIWOM0087 | *Heliconius* | *erato* | *demophoon* | 254747400 | 95.40 | 73.43 | 67.96 | 96.97 | 3.03 |
| STRIWOM1284 | *Heliconius* | *erato* | *demophoon* | 144143162 | 94.62 | 71.57 | 70.29 | 97.18 | 2.82 |
| STRIWOM5353 | *Heliconius* | *erato* | *demophoon* | 137933040 | 94.75 | 73.14 | 66.47 | 96.95 | 3.05 |
| STRIWOM5362 | *Heliconius* | *erato* | *demophoon* | 132459907 | 94.90 | 74.73 | 65.53 | 97.00 | 3.00 |
| GS020redo | *Heliconius* | *erato* | *emma* | 127435592 | 94.02 | 75.37 | 56.28 | 96.84 | 3.16 |
| GS021redo | *Heliconius* | *erato* | *emma* | 110321776 | 92.25 | 73.90 | 53.05 | 97.36 | 2.64 |
| NCS1671 | *Heliconius* | *erato* | *emma* | 138212409 | 94.87 | 74.80 | 63.79 | 96.69 | 3.31 |

|  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|
| NCS1672 | *Heliconius* | *erato* | *emma* | 124260648 | 95.30 | 74.38 | 61.98 | 96.72 | 3.28 |
| NCS1673 | *Heliconius* | *erato* | *emma* | 134588320 | 94.75 | 74.33 | 63.06 | 96.70 | 3.30 |
| NCS1674 | *Heliconius* | *erato* | *emma* | 123541303 | 94.85 | 73.93 | 62.17 | 96.69 | 3.31 |
| NCS1675 | *Heliconius* | *erato* | *emma* | 88975238 | 95.26 | 75.48 | 51.91 | 96.84 | 3.16 |
| NCS2005 | *Heliconius* | *erato* | *erato* | 131970196 | 94.20 | 74.50 | 61.65 | 96.85 | 3.15 |
| NCS2012 | *Heliconius* | *erato* | *erato* | 149713935 | 92.69 | 74.01 | 61.89 | 96.92 | 3.08 |
| NCS2020 | *Heliconius* | *erato* | *erato* | 128119208 | 94.95 | 75.68 | 61.73 | 96.86 | 3.14 |
| NCS2023 | *Heliconius* | *erato* | *erato* | 157127558 | 92.47 | 74.64 | 64.40 | 96.82 | 3.18 |
| NCS2025 | *Heliconius* | *erato* | *erato* | 131170024 | 94.16 | 75.42 | 61.59 | 96.86 | 3.14 |
| NCS2556 | *Heliconius* | *erato* | *erato* | 104241150 | 94.18 | 74.39 | 60.36 | 96.84 | 3.16 |
| BC3277 | *Heliconius* | *erato* | *etylus* | 86701039 | 94.39 | 67.40 | 57.11 | 96.76 | 3.24 |
| BC3278 | *Heliconius* | *erato* | *etylus* | 98511471 | 94.63 | 67.34 | 58.65 | 96.80 | 3.20 |
| BC3280 | *Heliconius* | *erato* | *etylus* | 89246745 | 93.49 | 66.23 | 55.80 | 96.78 | 3.22 |
| BC3281 | *Heliconius* | *erato* | *etylus* | 102130480 | 94.55 | 68.05 | 61.00 | 96.71 | 3.29 |
| BC3282 | *Heliconius* | *erato* | *etylus* | 103368694 | 94.50 | 67.47 | 59.72 | 96.78 | 3.22 |
| GS012redo | *Heliconius* | *erato* | *favorinus* | 140981241 | 94.98 | 76.95 | 61.22 | 96.87 | 3.13 |
| NCS0471 | *Heliconius* | *erato* | *favorinus* | 107620175 | 93.25 | 73.57 | 60.09 | 96.83 | 3.17 |
| NCS0473 | *Heliconius* | *erato* | *favorinus* | 101638593 | 94.31 | 74.54 | 58.62 | 96.84 | 3.16 |
| NCS0476 | *Heliconius* | *erato* | *favorinus* | 122366761 | 93.19 | 73.12 | 65.12 | 96.76 | 3.24 |
| NCS0478 | *Heliconius* | *erato* | *favorinus* | 144088132 | 95.29 | 73.92 | 65.90 | 96.82 | 3.18 |
| NCS0479 | *Heliconius* | *erato* | *favorinus* | 116707167 | 93.72 | 72.92 | 64.61 | 96.74 | 3.26 |
| NCS2554 | *Heliconius* | *erato* | *favorinus* | 104925650 | 94.64 | 74.75 | 62.35 | 97.13 | 2.87 |
| NCS2555 | *Heliconius* | *erato* | *favorinus* | 135257331 | 95.51 | 75.92 | 66.13 | 97.31 | 2.69 |
| himera001 | *Heliconius* | *himera* |  | 98013649 | 95.55 | 75.60 | 59.50 | 98.70 | 1.30 |
| himera002 | *Heliconius* | *himera* |  | 106525064 | 95.19 | 75.01 | 61.14 | 98.69 | 1.31 |
| himera003 | *Heliconius* | *himera* |  | 110558877 | 95.47 | 75.20 | 61.51 | 98.64 | 1.36 |
| himera006 | *Heliconius* | *himera* |  | 79235786 | 94.77 | 74.00 | 53.26 | 98.73 | 1.27 |
| himera030 | *Heliconius* | *himera* |  | 75307798 | 95.00 | 74.46 | 52.29 | 98.77 | 1.23 |
| NCS1179 | *Heliconius* | *erato* | *hydara* | 96419175 | 95.25 | 75.09 | 57.84 | 96.94 | 3.06 |
| NCS1979 | *Heliconius* | *erato* | *hydara* | 110070137 | 95.22 | 74.91 | 60.46 | 96.87 | 3.13 |
| NCS2080 | *Heliconius* | *erato* | *hydara* | 107728439 | 95.79 | 75.31 | 59.48 | 96.98 | 3.02 |
| NCS2211 | *Heliconius* | *erato* | *hydara* | 126470247 | 94.52 | 74.48 | 63.23 | 96.85 | 3.15 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| NCS2217 | *Heliconius* | *erato* | *hydara* | 142163032 | 95.26 | 74.81 | 65.09 | 96.83 | 3.17 |
| NCS2574 | *Heliconius* | *erato* | *hydara* | 61179802 | 94.03 | 74.34 | 42.84 | 98.16 | 1.84 |
| NCS2581 | *Heliconius* | *erato* | *hydara* | 141887122 | 95.44 | 76.47 | 63.43 | 97.03 | 2.97 |
| NCS2609 | *Heliconius* | *erato* | *hydara* | 147479030 | 95.86 | 76.74 | 63.30 | 97.19 | 2.81 |
| STRIWOM0039 | *Heliconius* | *erato* | *hydara* | 109671810 | 96.47 | 78.71 | 61.63 | 97.00 | 3.00 |
| STRIWOM0040 | *Heliconius* | *erato* | *hydara* | 112212395 | 96.01 | 78.33 | 62.74 | 96.98 | 3.02 |
| STRIWOM0088 | *Heliconius* | *erato* | *hydara* | 56427236 | 94.78 | 71.99 | 68.49 | 96.77 | 3.23 |
| STRIWOM5193 | *Heliconius* | *erato* | *hydara* | 159885870 | 95.32 | 72.08 | 65.96 | 96.79 | 3.21 |
| STRIWOM5351 | *Heliconius* | *erato* | *hydara* | 247932516 | 95.42 | 71.66 | 63.25 | 96.79 | 3.21 |
| STRIWOM0042 | *Heliconius* | *erato* | *hydara* | 113978486 | 95.56 | 77.63 | 60.65 | 97.05 | 2.95 |
| BC0411 | *Heliconius* | *erato* | *lativitta* | 167711422 | 90.91 | 72.37 | 64.95 | 96.82 | 3.18 |
| lativitta01 | *Heliconius* | *erato* | *lativitta* | 112167739 | 94.35 | 75.00 | 58.21 | 98.01 | 1.99 |
| lativitta02 | *Heliconius* | *erato* | *lativitta* | 143079745 | 94.85 | 75.78 | 61.23 | 96.97 | 3.03 |
| lativitta03 | *Heliconius* | *erato* | *lativitta* | 163526599 | 95.72 | 76.15 | 63.04 | 96.84 | 3.16 |
| lativitta04 | *Heliconius* | *erato* | *lativitta* | 171477845 | 93.92 | 74.37 | 63.87 | 96.91 | 3.09 |
| BC0410 | *Heliconius* | *erato* | *notabilis* | 160272309 | 95.12 | 76.27 | 65.52 | 96.81 | 3.19 |
| BC3223 | *Heliconius* | *erato* | *notabilis* | 89779257 | 94.47 | 67.80 | 57.70 | 96.73 | 3.27 |
| BC3224 | *Heliconius* | *erato* | *notabilis* | 91802518 | 94.41 | 67.99 | 57.13 | 96.78 | 3.22 |
| BC3225 | *Heliconius* | *erato* | *notabilis* | 96513836 | 94.51 | 67.81 | 57.97 | 96.77 | 3.23 |
| BC3227 | *Heliconius* | *erato* | *notabilis* | 91732038 | 93.23 | 66.62 | 56.51 | 96.86 | 3.14 |
| BC3228 | *Heliconius* | *erato* | *notabilis* | 76146914 | 94.39 | 68.31 | 51.89 | 96.81 | 3.19 |
| notabilis01 | *Heliconius* | *erato* | *notabilis* | 115174166 | 94.54 | 74.33 | 59.26 | 96.90 | 3.10 |
| notabilis02 | *Heliconius* | *erato* | *notabilis* | 120120673 | 92.65 | 72.79 | 60.73 | 96.85 | 3.15 |
| notabilis03 | *Heliconius* | *erato* | *notabilis* | 132385897 | 93.92 | 73.73 | 62.06 | 96.96 | 3.04 |
| notabilis04 | *Heliconius* | *erato* | *notabilis* | 122086027 | 95.33 | 74.95 | 61.54 | 96.92 | 3.08 |
| CA51 | *Heliconius* | *erato* | *petiverana* | 84636118 | 96.48 | 75.30 | 63.25 | 98.68 | 1.32 |
| CA53 | *Heliconius* | *erato* | *petiverana* | 100757305 | 95.01 | 73.41 | 65.97 | 98.65 | 1.35 |
| CA54 | *Heliconius* | *erato* | *petiverana* | 127961432 | 95.31 | 74.76 | 67.80 | 98.63 | 1.37 |
| CA55 | *Heliconius* | *erato* | *petiverana* | 97940026 | 96.32 | 75.62 | 64.96 | 98.67 | 1.33 |
| CA56 | *Heliconius* | *erato* | *petiverana* | 114976134 | 96.09 | 74.38 | 67.12 | 98.65 | 1.35 |
| MRK_MX09_01 | *Heliconius* | *erato* | *cruentus* | 133056919 | 93.89 | 68.99 | 64.44 | 99.35 | 0.65 |
| 5732 | *Heliconius* | *erato* | *phyllis* | 113500563 | 94.79 | 68.00 | 60.68 | 96.64 | 3.36 |

|  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|
| 5742 | *Heliconius* | *erato* | *phyllis* | 134943613 | 92.91 | 69.17 | 63.59 | 96.63 | 3.37 |
| 5765 | *Heliconius* | *erato* | *phyllis* | 130522327 | 95.32 | 72.98 | 63.21 | 96.64 | 3.36 |
| 5766 | *Heliconius* | *erato* | *phyllis* | 93584774 | 95.13 | 67.84 | 61.26 | 96.53 | 3.47 |
| M3654 | *Heliconius* | *erato* | *venus* | 128044805 | 94.78 | 74.26 | 65.31 | 97.63 | 2.37 |
| M3655 | *Heliconius* | *erato* | *venus* | 154784987 | 94.33 | 73.43 | 66.63 | 97.66 | 2.34 |
| M3656 | *Heliconius* | *erato* | *venus* | 130613531 | 94.55 | 74.40 | 65.31 | 97.67 | 2.33 |
| M3657 | *Heliconius* | *erato* | *venus* | 140573742 | 94.75 | 75.51 | 64.74 | 97.70 | 2.30 |
| M3659 | *Heliconius* | *erato* | *venus* | 142004452 | 94.02 | 73.57 | 66.27 | 98.12 | 1.88 |

**Table S 13. Outgroup mapping and genotyping results.**

| Sample ID | Genus | Species | Reads | Mapped (%) | Properly paired (%) | Genotyped (%) | Homozygous (%) | Heterozygous (%) |
|---|---|---|---|---|---|---|---|---|
| char001 | *Heliconius* | *charithonia* | 140245309 | 77.91 | 47.78 | 40.45 | 99.53 | 0.47 |
| char002 | *Heliconius* | *charithonia* | 79721501 | 79.07 | 44.26 | 30.40 | 98.91 | 1.09 |
| NCS2511 | *Heliconius* | *clysonimus* | 92849122 | 88.31 | 60.67 | 39.26 | 98.81 | 1.19 |
| NCS2512 | *Heliconius* | *clysonimus* | 112450950 | 89.29 | 62.08 | 41.37 | 98.78 | 1.22 |
| STRIWOM2312 | *Heliconius* | *hecalesia* | 152544131 | 89.95 | 62.79 | 49.41 | 98.90 | 1.10 |
| LMCI94-13 | *Heliconius* | *hermathena* | 145055665 | 89.08 | 61.96 | 55.52 | 99.77 | 0.23 |
| LMCI94-14 | *Heliconius* | *hermathena* | 173637812 | 88.76 | 61.05 | 57.12 | 99.77 | 0.23 |
| LMCI94-15 | *Heliconius* | *hermathena* | 209772280 | 88.98 | 62.84 | 57.77 | 99.76 | 0.24 |
| MRKhort2 | *Heliconius* | *hortense* | 141576626 | 85.68 | 57.42 | 48.57 | 98.98 | 1.02 |
| STRIWOM5792 | *Heliconius* | *ricini* | 238855233 | 79.26 | 52.89 | 41.20 | 99.47 | 0.53 |
| BC2004 | *Heliconius* | *sara* | 133231891 | 80.00 | 49.41 | 40.83 | 98.61 | 1.39 |
| MRK_EC_08_025 | *Heliconius* | *sara* | 135516002 | 81.31 | 51.76 | 39.99 | 98.85 | 1.15 |
| sar08025 | *Heliconius* | *sara* | 70726663 | 79.63 | 46.34 | 32.59 | 98.90 | 1.10 |
| NCS2541 | *Heliconius* | *telesiphe* | 110690751 | 89.07 | 61.13 | 42.14 | 98.94 | 1.06 |
| NCS2550 | *Heliconius* | *telesiphe* | 122493430 | 88.96 | 59.24 | 44.65 | 98.89 | 1.11 |

## S4.2. Whole genome phylogeny

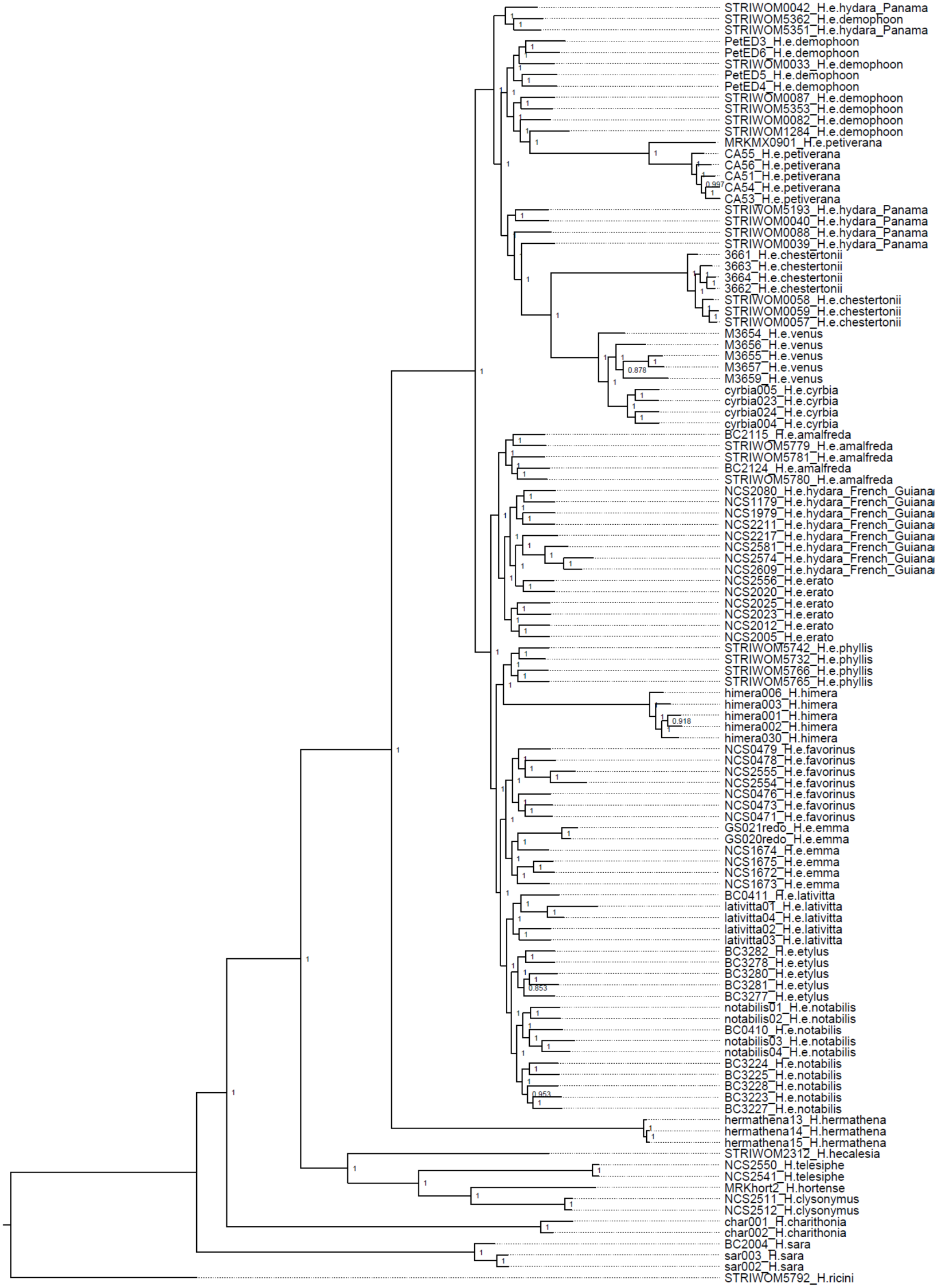


**Figure S 5. Whole genome phylogeny.** Tip labels represent sample ID and species. Node labels represent local support based on the Shimodaira-Hasegawa test.

## S4.3. Whole genome population genetic statistics for hybridizing taxa

Genome wide comparisons of genomic divergence and diversity reveal narrow peaks only near pattern loci and a few other regions of the genome. Similar to $F_{ST}$, $d_{XY}$, an absolute measure of genetic divergence, revealed peaks near the color pattern loci (chromosomes 10, 13, 15 and 18), as well as on chromosomes 2 and 3, which are not known to house color pattern loci. On chromosome 2 a large region showed elevated divergence between rayed and postman races in Peru and the Guiana shield. The elevated divergence appears to expand nearly the entire chromosome, except the end regions, which likely results from structural differences that have prevented recombination and gene flow between the races. On chromosome 3, a narrow peak of divergence is consistently found between all hybridizing races, except the postman-like races in Panama (*H. e. demophoon* and *H. e. hydara*). This region also shows elevated levels of nucleotide diversity, which may be the result of incomplete sorting of ancestral variation or balancing selection. $F_{ST}$ showed elevated levels of divergence on the Z chromosome relative to autosomes, however absolute divergence and nucleotide diversity were on average lower on the Z. Comparisons between *H. e. favorinus* and *H. e. emma* in Peru did reveal additional peaks of divergence that were not replicated in any other comparisons. Among all the hybridizing races, these two races in Peru are the only that differ at each major color pattern locus and hybridization has been shown to be associated with other environmental variables, such as rainfall[9], which could contribute to the greater number of divergent peaks across their genomes. Importantly, the only regions of the genome in which we found fixed allelic differences were at the color pattern loci, between hybridizing races that were divergently colored.

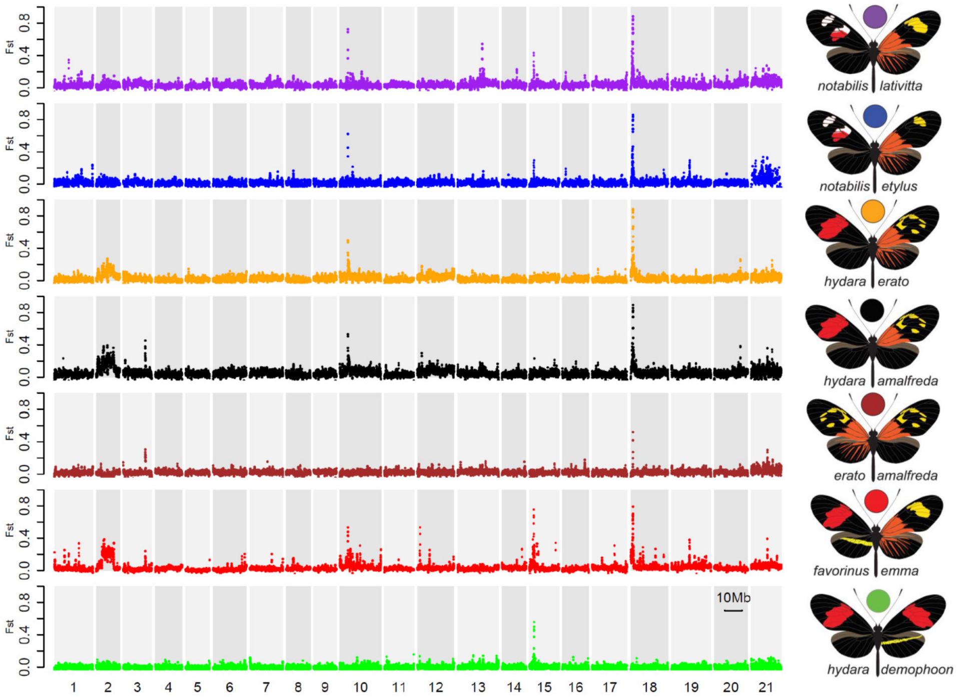


**Figure S 6. $F_{ST}$ across *Heliconius erato* phenotypic transition zones.**

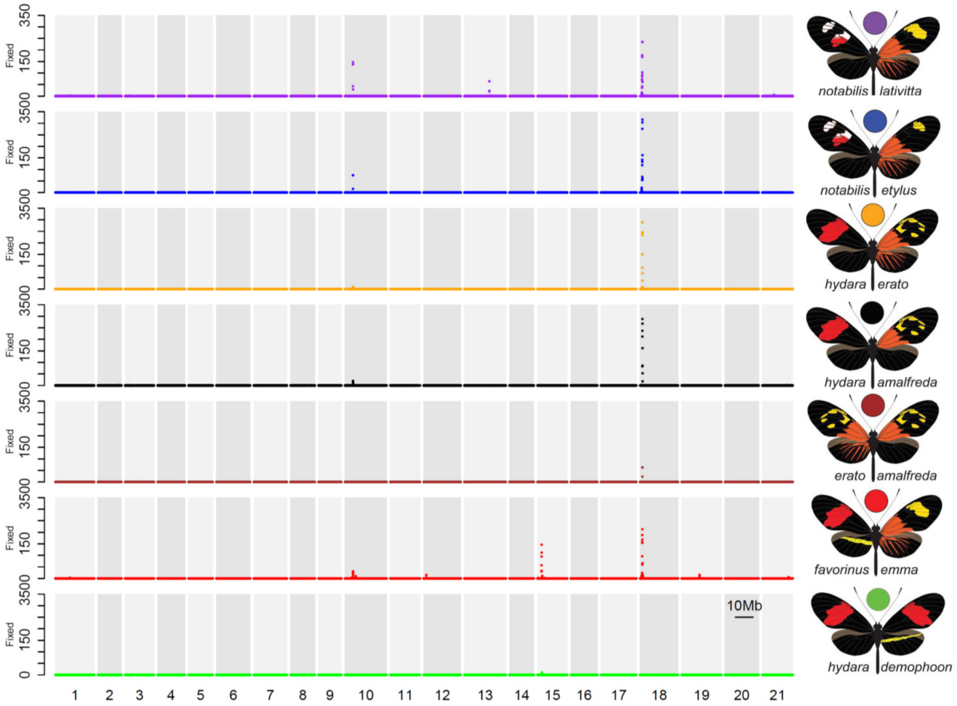


**Figure S 7. Fixed differences across *Heliconius erato* phenotypic transition zones.**

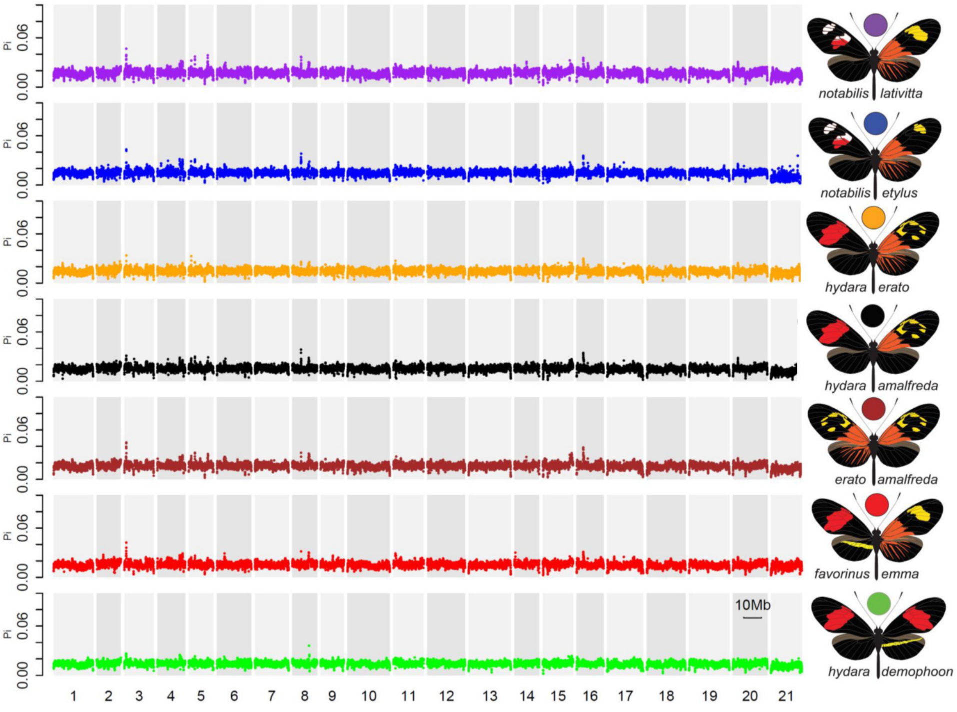


**Figure S 8. Nucleotide diversity (*Pi*) in *Heliconius erato* phenotypic transition zones.**

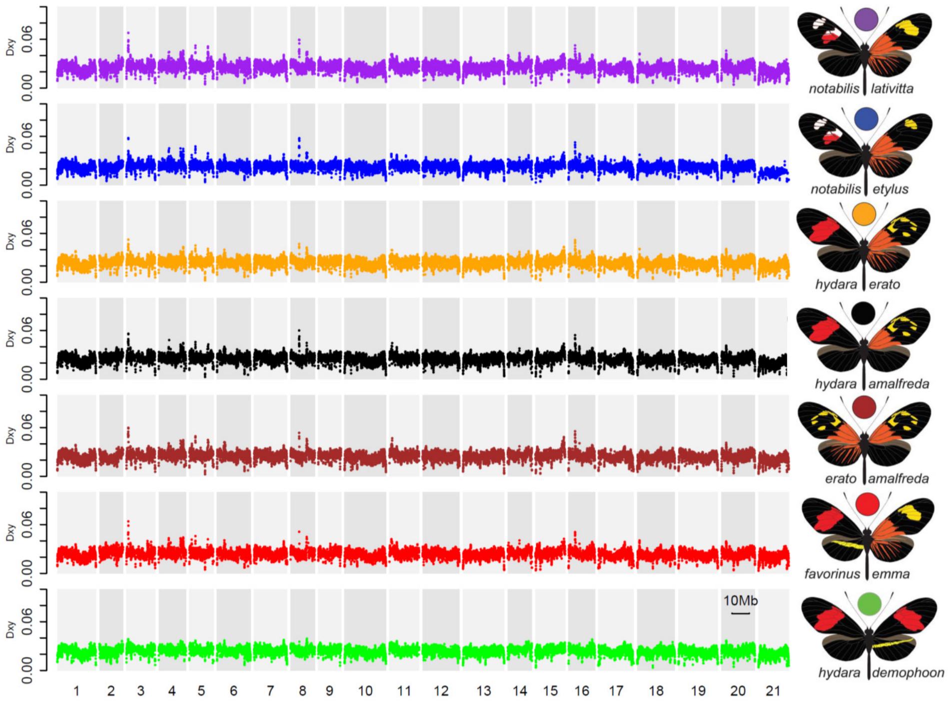


**Figure S 9. Average pairwise differences ($d_{XY}$) across *Heliconius erato* phenotypic transition zones.**

# S5. Patterns at color pattern loci

Comparisons of hybridizing races that differ in wing color patterns proved to be extremely powerful for resolving putative regulatory regions of known color patterning genes. At each of the three major color pattern loci, not only were narrow peaks of divergence and genotype by phenotype associations identified between divergently colored races, but also these peaks were absent between hybridizing races that shared similar color pattern phenotypes. For example, between the hybridizing races *H. e. demophoon* and *H. e. hydara*, which do not differ in red pattern or forewing band shape, there were no peaks of divergence found near *optix* or *wntA*, as expected. Similarly, between the *H. e. hydara* and *H. e. erato/amalfreda,* none of which vary in yellow on the hindwing, there was no peak of divergence or fixed differences across the *Cr* locus (*cortex*). These negative results further support the potential functional roles in driving color pattern differences between the divergently colored hybridizing races.

## S5.1. *wntA*

### S5.1.1. Sliding window population statistics near *wntA*

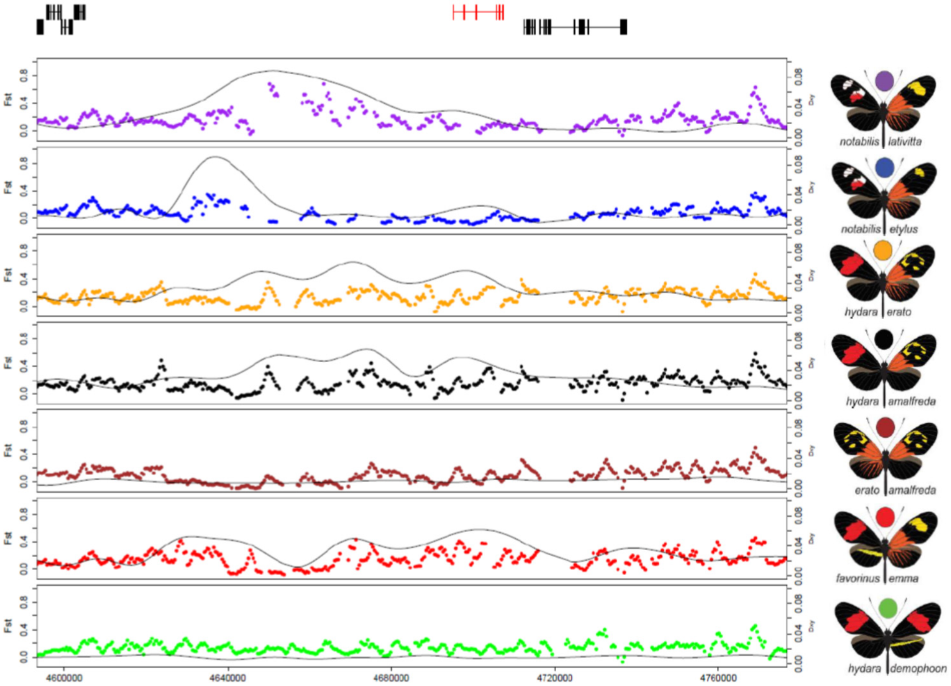


**Figure S 10. Sliding window $F_{ST}$ (black line) and $d_{XY}$ (points) near the *wntA* gene (red) on chromosome 10 across *Heliconius erato* phenotypic transition zones.** Values were calculated for 2 kb windows sliding in increments of 400 bp.

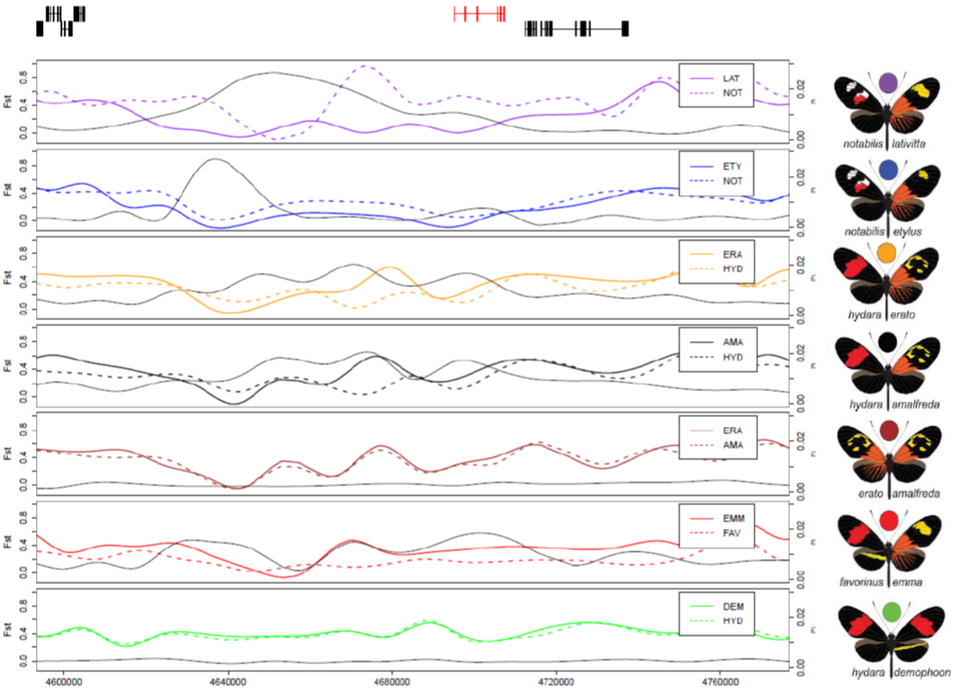


**Figure S 11. Sliding window $F_{ST}$ (black line) and nucleotide diversity (*Pi*) (colored lines) near the *wntA* gene (red) on chromosome 10 across *Heliconius erato* phenotypic transition zones.** Values were calculated for 2 kb windows sliding in increments of 400 bp.

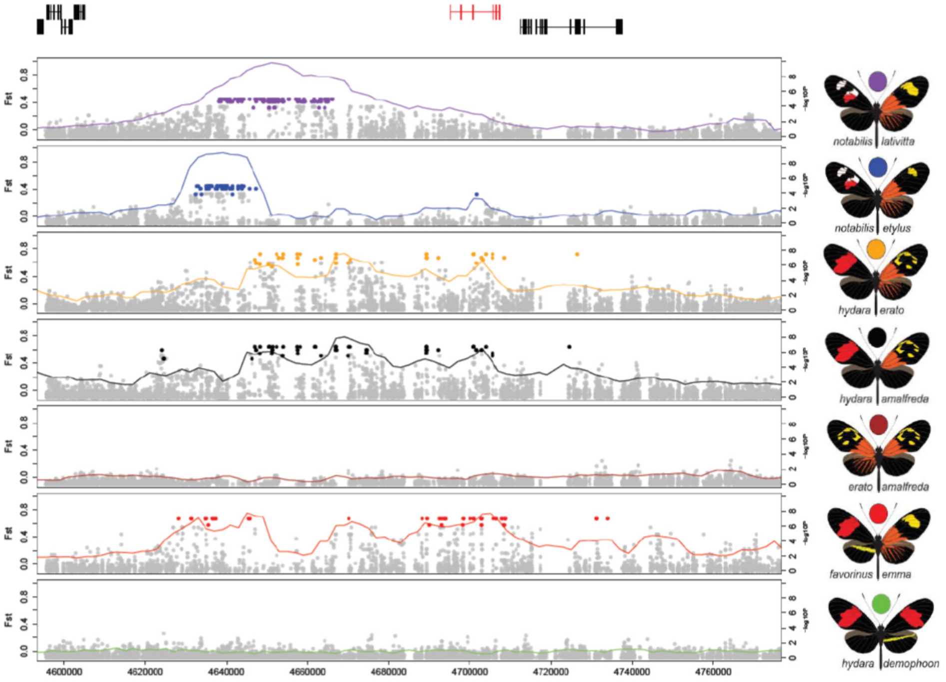


**Figure S 12. $F_{ST}$ (lines; 20 kb window, 5 kb step size) and association analysis (points) near the *wntA* gene on chromosome 10.** Colored points represent associations estimated from fixed SNPs.

## S5.1.2. Maximum likelihood trees for identified color pattern modules near *wntA*

**Figure S 13. Maximum likelihood tree for the *Sd* element near *wntA* on chromosome 10 (Herato1001 position 4624122-4647331) for all *H. erato* samples and closely related outgroup species.**

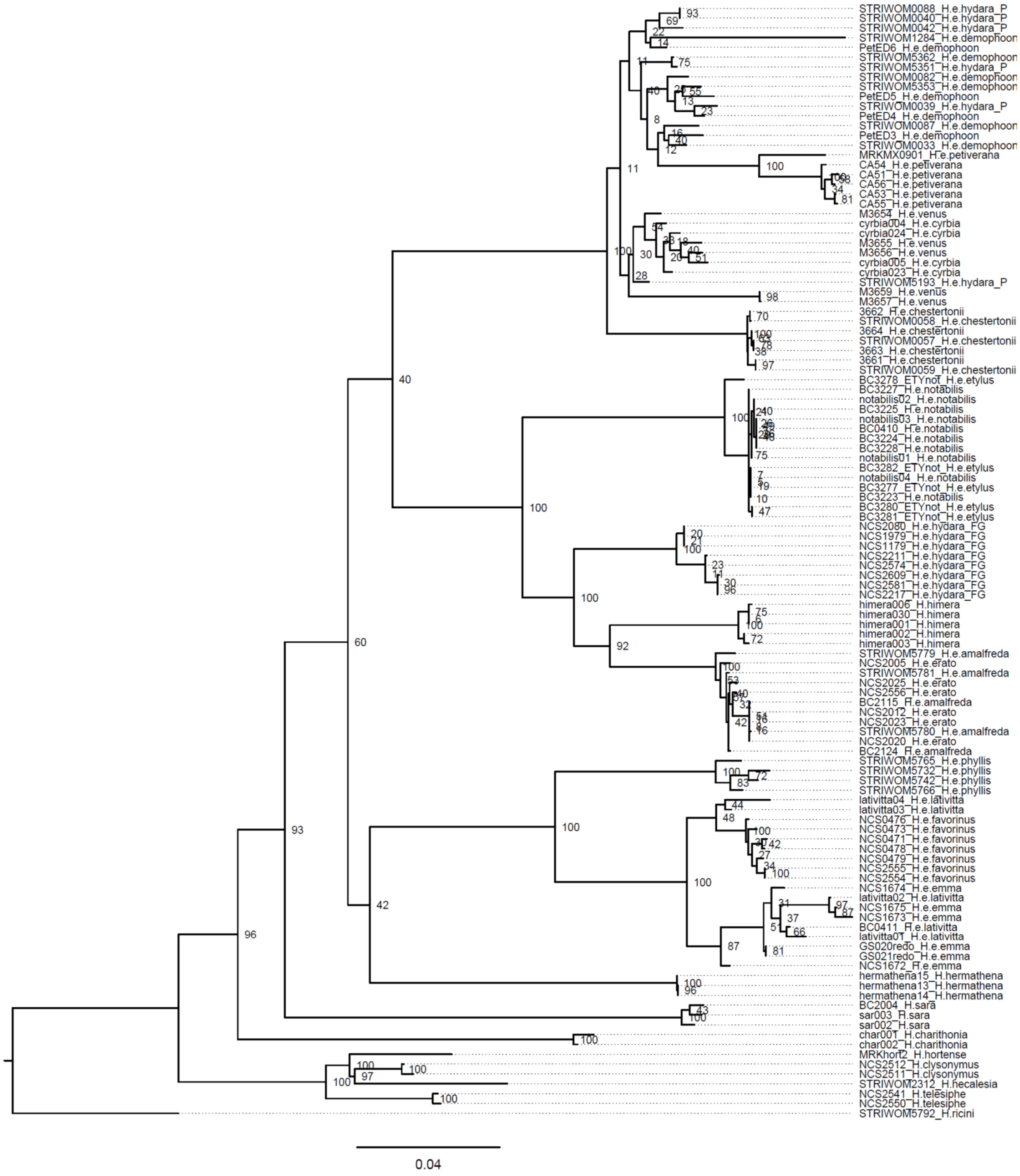


**Figure S 14. Maximum likelihood tree for the *St* element near *wntA* on chromosome 10 (Herato1001 position 4647332-4674571) for all *H. erato* samples and closely related outgroup species.**

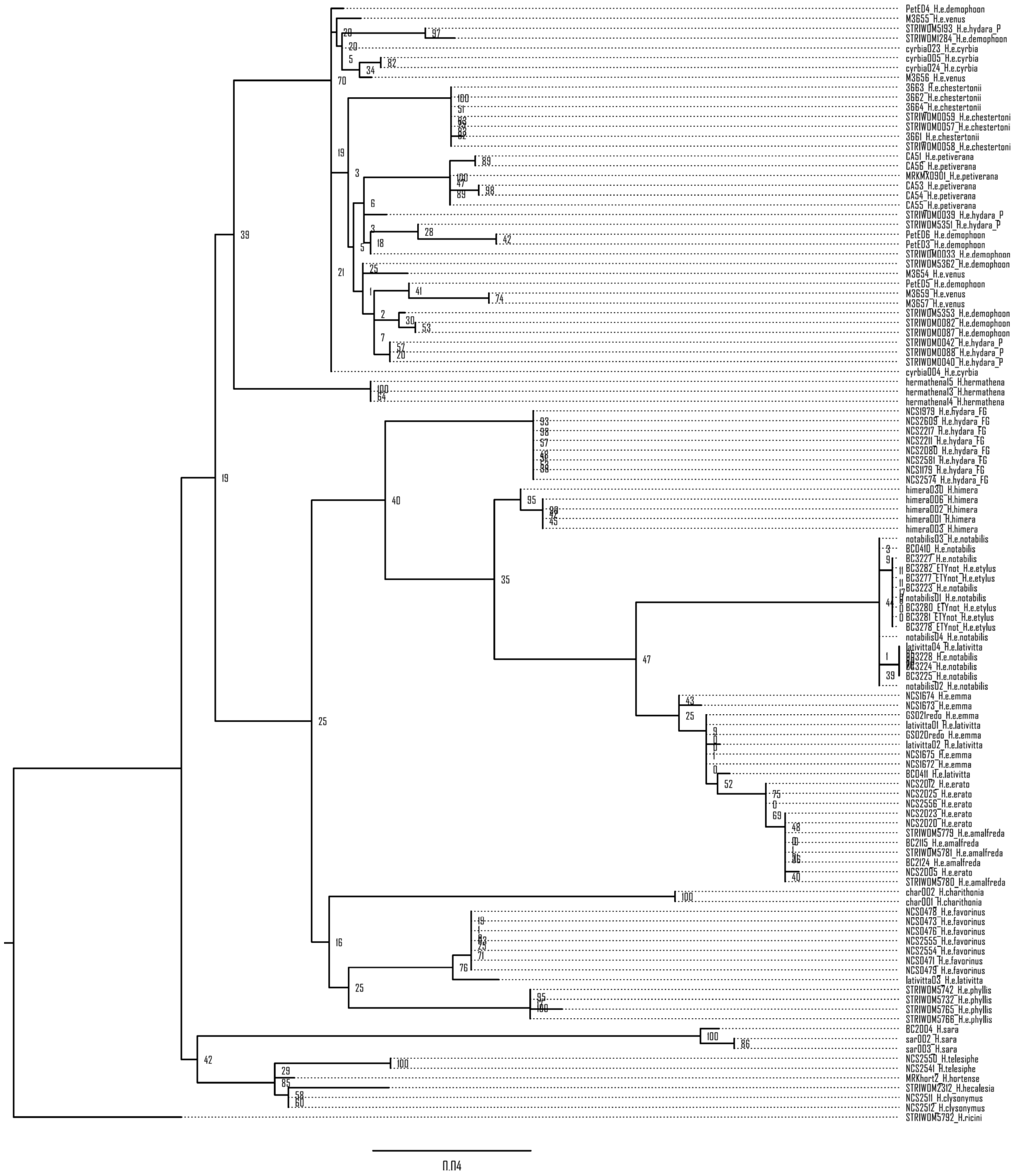


**Figure S 15. Maximum likelihood tree for the *Ly1* element near *wntA* on chromosome 10 (Herato1001 position 4666909-4670474) for all *H. erato* samples and closely related outgroup species.**

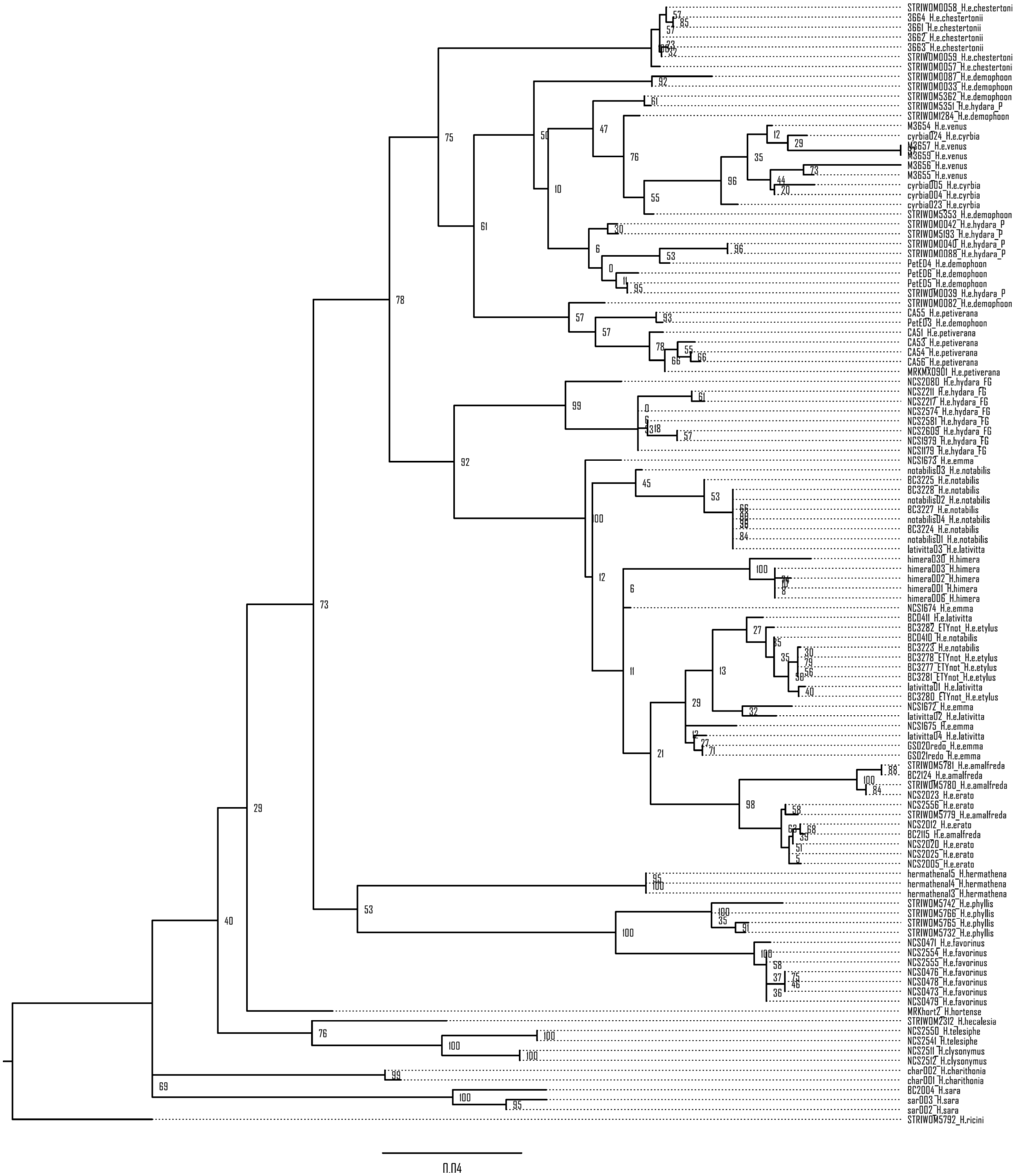


**Figure S 16. Maximum likelihood tree for the *Ly2* element near *wntA* on chromosome 10 (Herato1001 position 4700932-4708441) for all *H. erato* samples and closely related outgroup species.**

## S5.2. Ro

### S5.2.1. Sliding window population statistics near *Ro*

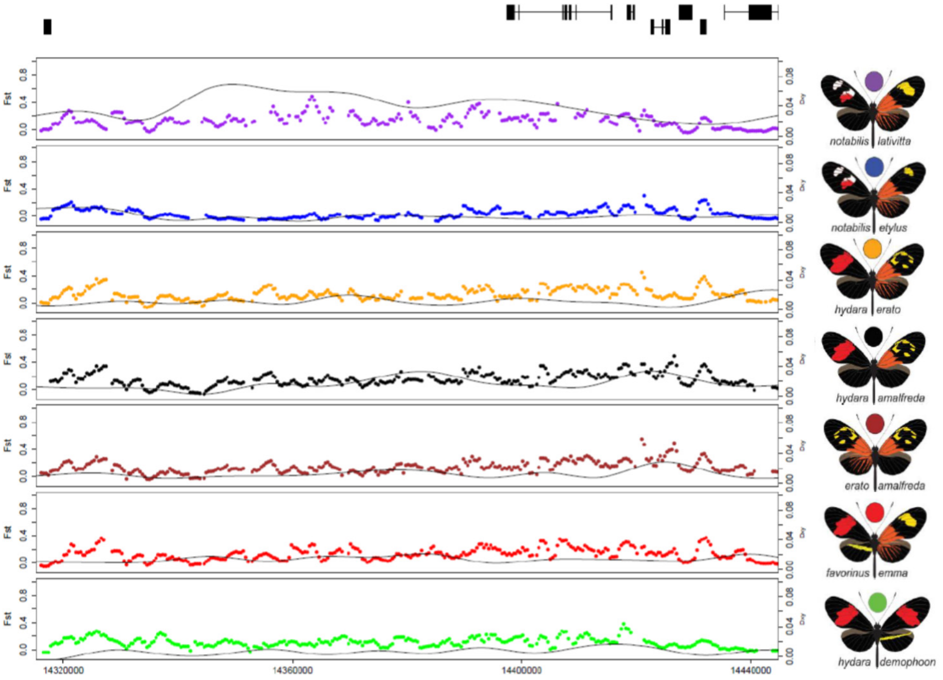


**Figure S 17. Sliding window $F_{ST}$ (black line) and $d_{XY}$ (points) near the *Ro* locus on chromosome 13 across *Heliconius erato* phenotypic transition zones.** Values were calculated for 2 kb windows sliding in increments of 400 bp.

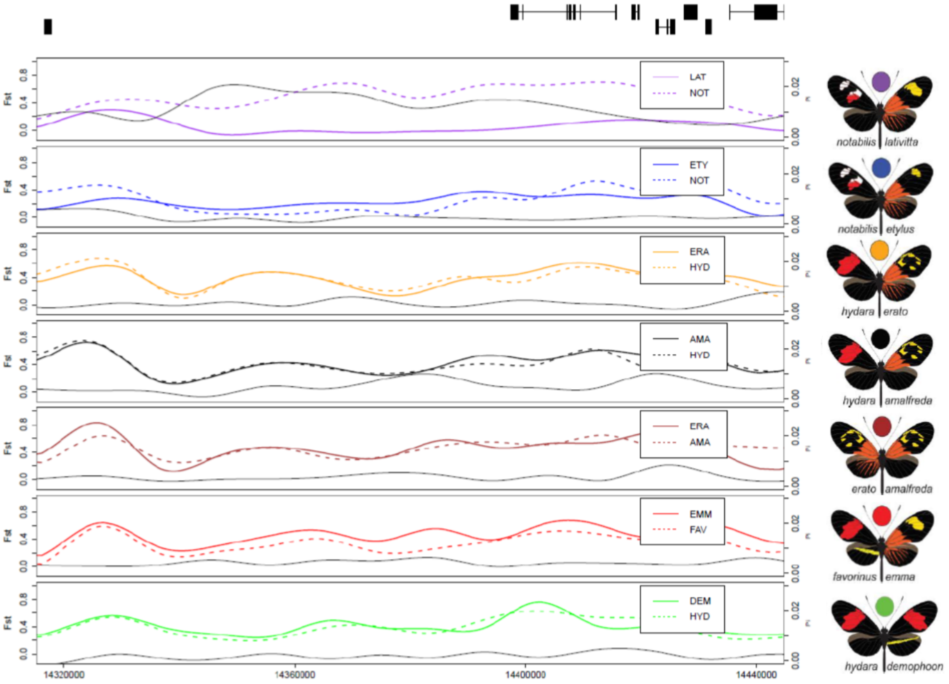


**Figure S 18. Sliding window $F_{ST}$ (black line) and nucleotide diversity (*Pi*) (colored lines) near the *Ro* locus on chromosome 13 across *Heliconius erato* phenotypic transition zones.** Values were calculated for 2 kb windows sliding in increments of 400 bp.

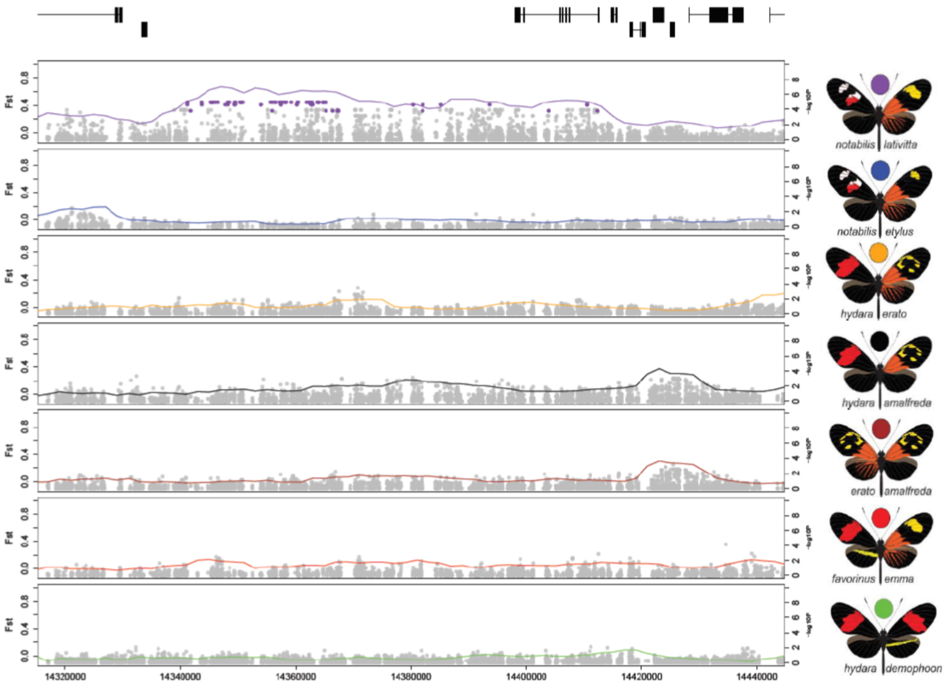


**Figure S 19. $F_{ST}$ (lines; 20 kb window, 5 kb step size) and association (points) analysis near the *Ro* locus on chromosome 13.** Colored points represent associations estimated from fixed SNPs.

### S5.2.2. Maximum likelihood tree for identified color pattern module near *Ro*

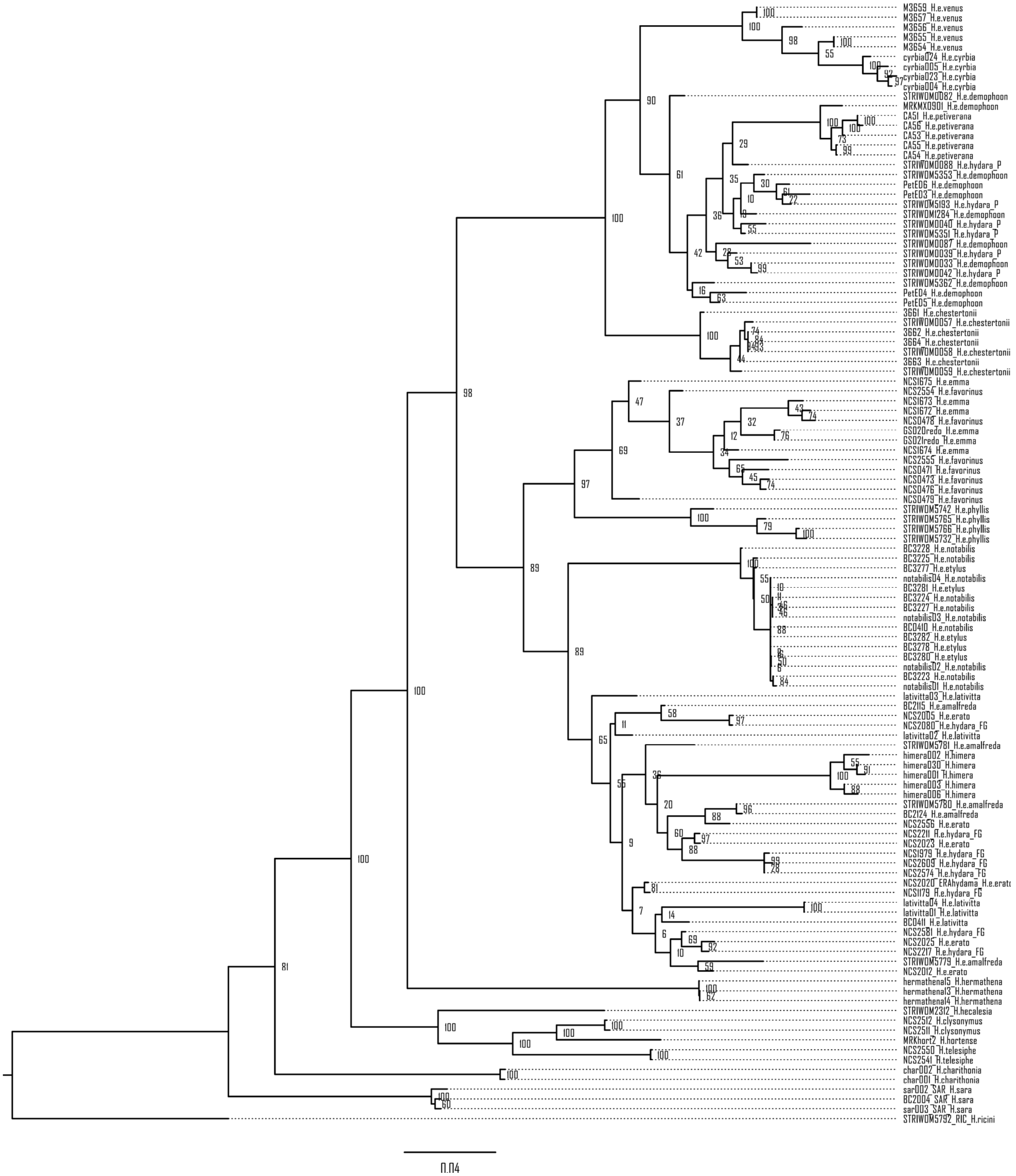


**Figure S 20. Maximum likelihood tree for the *Ro* element on chromosome 13 (Herato1301 position 14341251-14367418) for all *H. erato* samples and closely related outgroup species.**

## S5.3. *Optix*

### S5.3.1. Sliding window population statistics near *optix*

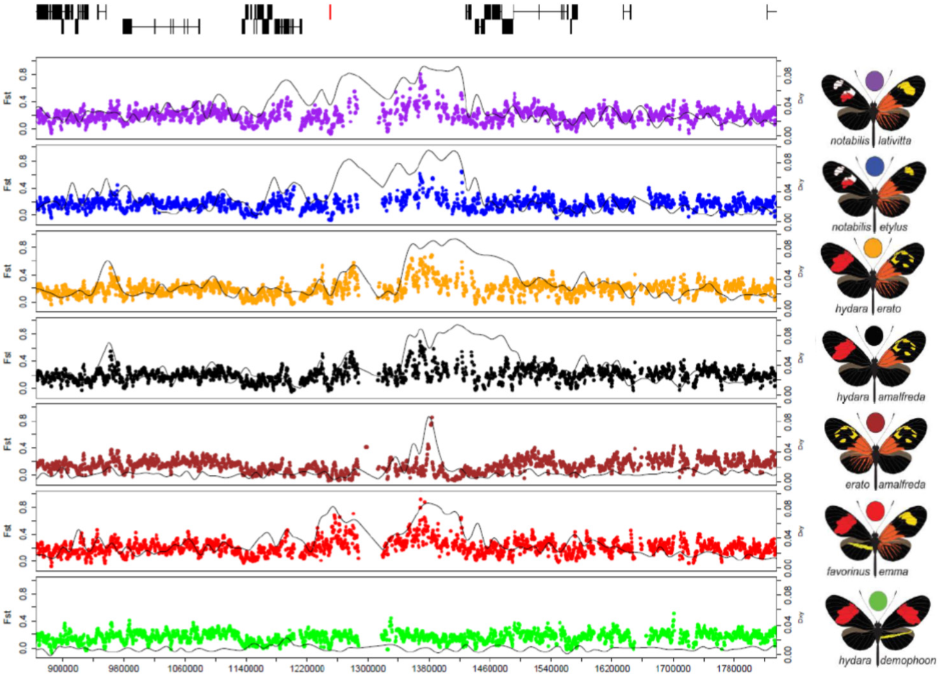


**Figure S 21. Sliding window $F_{ST}$ (black line) and $d_{XY}$ (points) near the *optix* gene on chromosome 10 across *Heliconius erato* phenotypic transition zones.** Values were calculated for 2 kb windows sliding in increments of 400 bp.

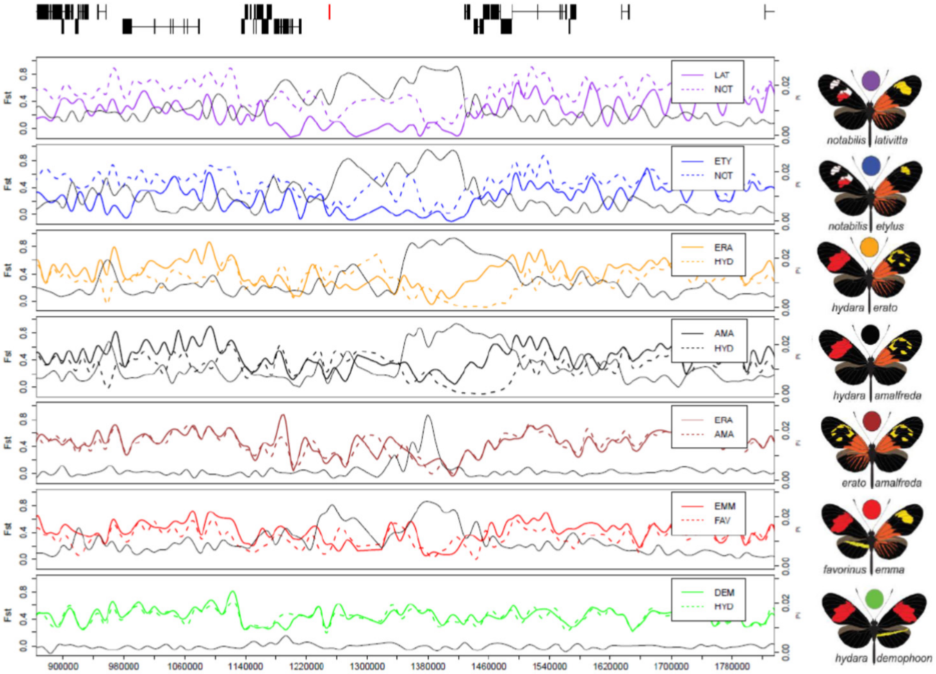


**Figure S 22. Sliding window $F_{ST}$ (black line) and nucleotide diversity (*Pi*) (colored lines) near the *optix* gene on chromosome 18 across *Heliconius erato* phenotypic transition zones.** Values were calculated for 2 kb windows sliding in increments of 400 bp.

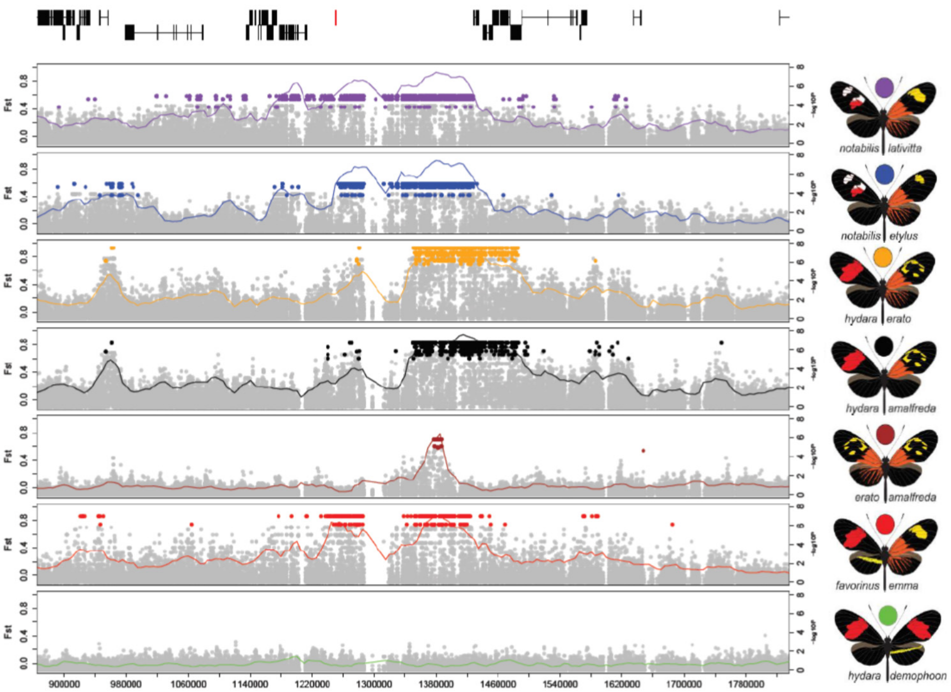


**Figure S 23. *$F_{ST}$* (lines; 20 kb window, 5 kb step size) and association (points) analysis near the *optix* gene on chromosome 18.** Colored points represent associations estimated from fixed SNPs.

## S5.3.2. Maximum likelihood trees for identified color pattern modules near *optix*

**Figure S 24. Maximum likelihood tree for the *R* element near *optix* on chromosome 18 (Herato1801 position 1377801-1384841) for all *H. erato* samples and closely related outgroup species.**

**Figure S 25. Maximum likelihood tree for the *Y1* element near *optix* on chromosome 18 (Herato1801 position 1403328-1403791) for all *H. erato* samples and closely related outgroup species.**

**Figure S 26. Maximum likelihood tree for the *Y2* element near *optix* on chromosome 18 (Herato1801 position 1420912-1422355) for all *H. erato* samples and closely related outgroup species.**

**Figure S 27. Maximum likelihood tree for the *D1* element near *optix* on chromosome 18 (Herato1801 position 1412888-1419375) for all *H. erato* samples and closely related outgroup species.**

**Figure S 28. Maximum likelihood tree for the *D2* element near *optix* on chromosome 18 (Herato1801 position 1422585-1428307) for all *H. erato* samples and closely related outgroup species.**

### S5.3.3. Comparison of the *optix* locus between *H. erato* and *H. melpomene*

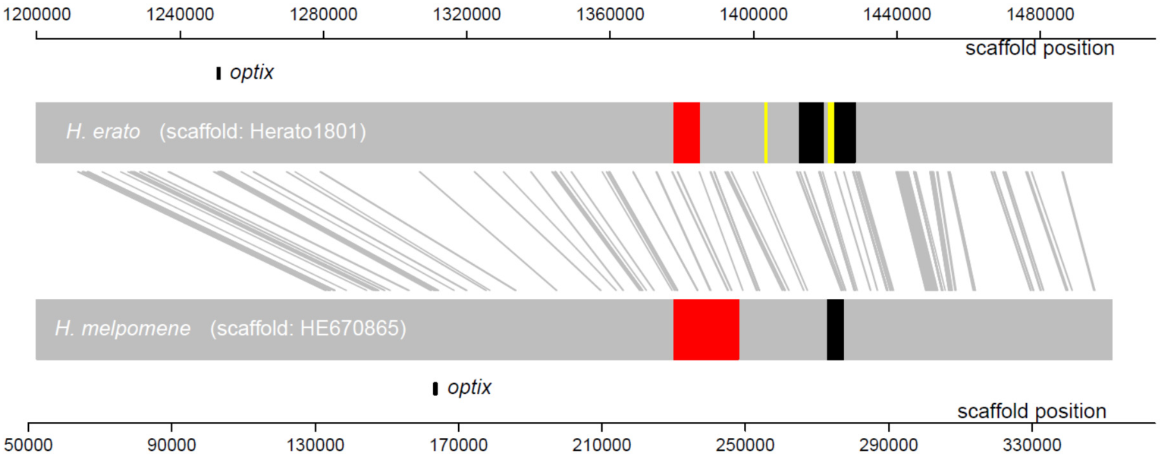


**Figure S 29. Comparison of the R (rays; red), Y (band; yellow) and D (dennis; black) regions of *Heliconius erato* to *Heliconius melpomene* near the optix gene on chromosome 18.** The *H. erato* and *H. melpomene* scaffold including the *optix* gene and the genomic intervals associated with R (Rays) and D (Dennis) were aligned using PROmer selecting for alignments with at least 85 % sequence identity (*3*). The alignment suggests that *H. erato* and *H. melpomene* have independent (non-overlapping) modules that regulate red color pattern variation.

### S5.4. ***Cortex***

The *Cr* locus has been found to control variation in yellow/white patterns across several regions of the hindwing [13]. For instance, in *H. e. cyrbia* and *H. e. venus* the hindwing bar is only present on the ventral side, unlike in several other postman *H. erato* races with yellow bars on the ventral and dorsal side. Genomic comparisons of *H. e. venus* and *H. e. cyrbia* to *H. e. hydara*, which lacks any yellow hindwing bar, revealed elevated divergence across large regions across the *Cr* locus and much of the rest of the genome (Figure S 33). This pattern of high divergence limited our ability to resolve an interval at the *Cr* locus associated with a yellow bar that is expressed exclusively on the ventral hindwing. Similarly, *H. e. cyrbia*, which possesses a unique white fringe among hindwing margin not found in any other *H. erato* races, has previously been shown to be controlled by the *Cr* locus. Although comparisons of *H. e. cyrbia* and the neighboring *H. e. venus*, which does not have a white hindwing fringe identified a few narrow regions of divergence across the *Cr* locus, many other narrow peaks of divergence were identified near the Cr locus as well as across most of the genome (Figure S 33). Again, this limited our ability to identify specific intervals associated with the presence of the white hindwing fringe. The phylogenetic weighting approach had limited ability to resolve putative regulatory intervals at the *Cr* locus, due to a lack of geographically isolated populations that shared similar *Cr* phenotypes.

### S5.4.1. Sliding window population statistics near *cortex*

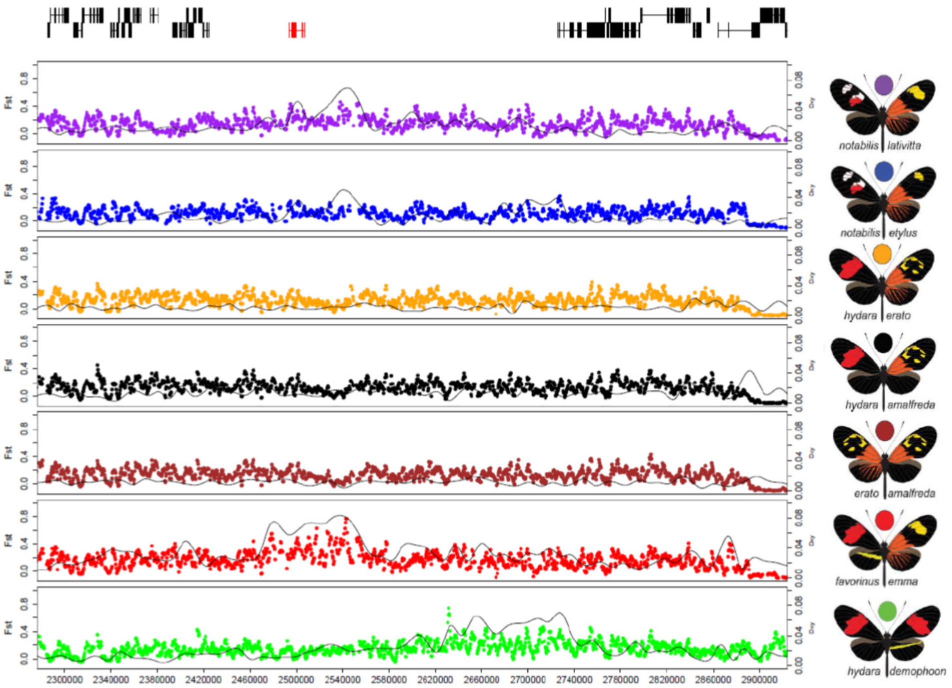


**Figure S 30. Sliding window $F_{ST}$ (black line) and $D_{XY}$ (points) near the *cortex* gene on chromosome 15 across *Heliconius erato* phenotypic transition zones.** Values were calculated for 2 kb windows sliding in increments of 400 bp.

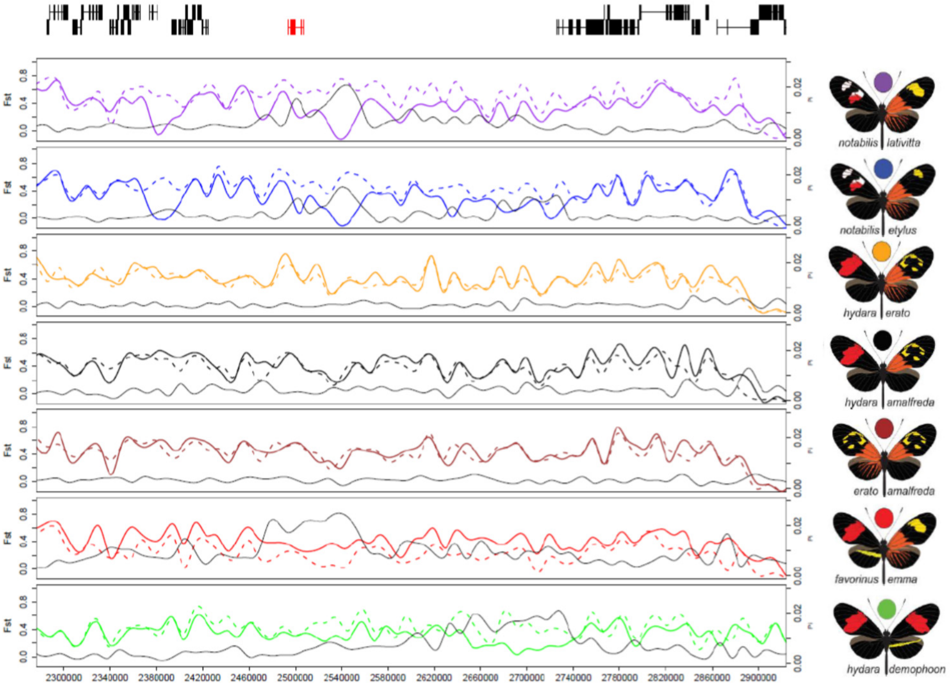


**Figure S 31. Sliding window $F_{ST}$ (black line) and nucleotide diversity (*Pi*) (colored lines) near the *cortex* gene on chromosome 15 across *Heliconius erato* phenotypic transition zones.** Values were calculated for 2 kb windows sliding in increments of 400 bp.

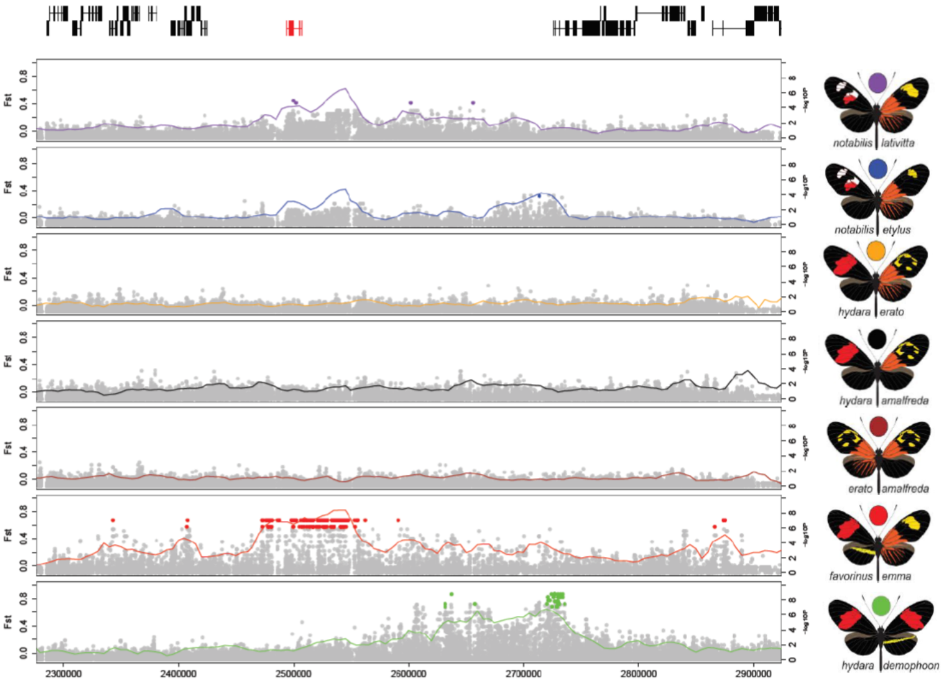


**Figure S 32.** ***$F_{ST}$*** **(lines; 20 kb window, 5 kb step size) and association (points) analysis near the *cortex* gene on chromosome 15.**Colored points represent associations estimated from fixed SNPs.

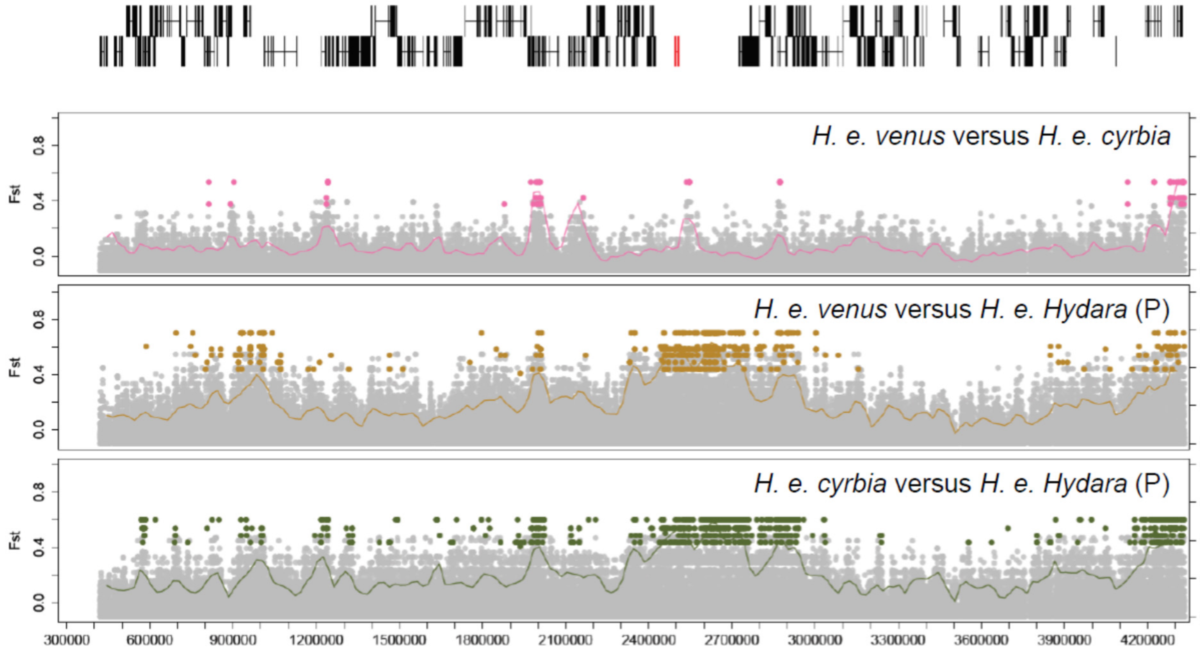


**Figure S 33.** ***$F_{ST}$*** **(lines; 20 kb window, 5 kb step size) and association (points) analysis near the *cortex* gene on chromosome 15 for comparisons between *H. e. venus*, *H. e. cyrbia* and *H. e. hydara* (Panama).**Colored points represent associations estimated from fixed SNPs.

## S5.4.2. Maximum likelihood trees for identified color pattern modules near *cortex*

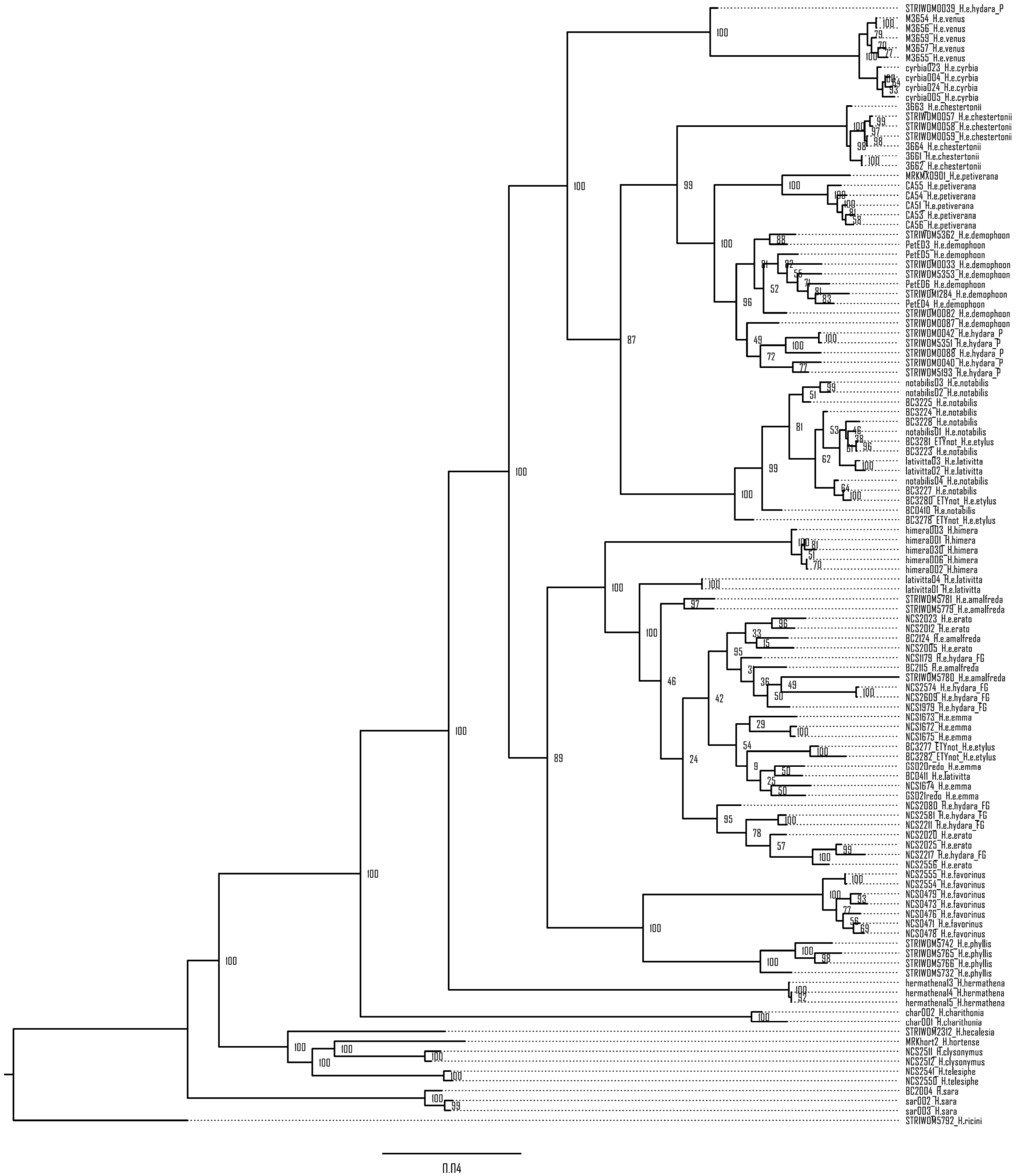


**Figure S 34. Maximum likelihood tree for the *Cr1* element near *cortex* on chromosome 15 (Herato1505 position 2053037-2171230) for all *H. erato* samples and closely related outgroup species.**

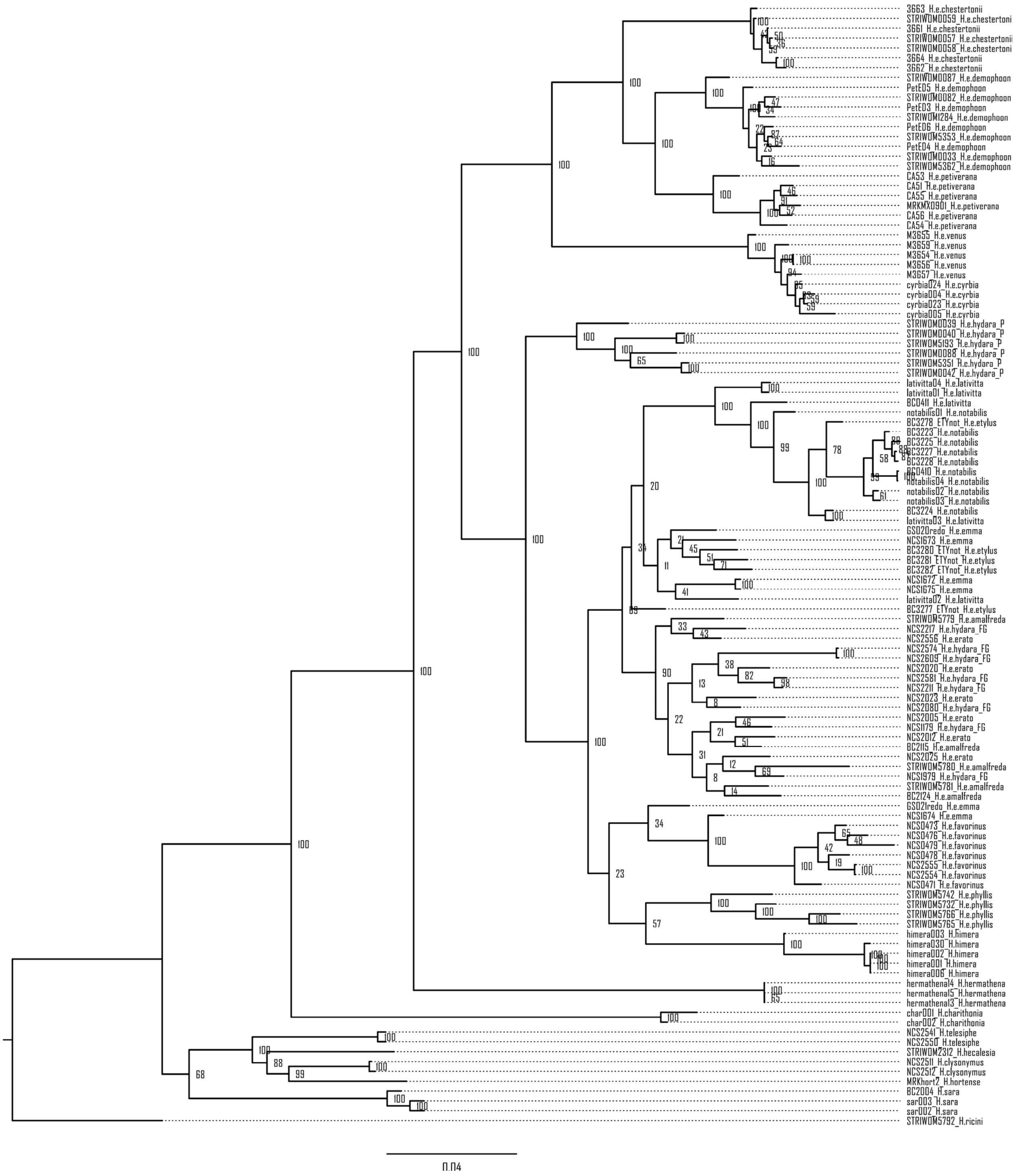


**Figure S 35. Maximum likelihood tree for the *Cr1* element near *cortex* on chromosome 15 (Herato1505 position 2211881-2315926) for all *H. erato* samples and closely related outgroup species.**

# S6. References

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