**Supplementary Information**

Supplementary Figure S1. Table of Taxa

Supplementary Figure S2. The 105 topologies from Twisst comparison with Peruvian hybrid zone taxa (Fig 2B; Fig 3B; Fig 4B; Fig 5B; Fig 6B). Red rings show introgression topologies with optix and cortex phenotypes (1,4,9,12,13) while black rings show introgression topologies for the WntA phenotype (1,13,16,28,76).

Supplementary Figure S3. The 105 topologies from Twisst comparison with *H. e. tumatumari* and *H. m. meriana* from the Guianese hybrid zone taxa (Fig 2D). Red rings show introgression topologies with optix and cortex phenotypes.

Supplementary Figure S4. The 105 topologies from Twisst comparison with *H. e. bari* and *H. e. tumatumari* together and *H. m. thelxiope* and *H. m. meriana* together from the Guianese hybrid zone taxa (Fig 3C; Fig S10). Red/black rings show introgression topologies for optix, cortex and *WntA* phenotypes.

Supplementary Figure S5. The 105 topologies from Twisst comparison with *H. besckei* and *H. m. thelxiope* from the Guianese hybrid zone taxa (Fig 2C; Fig 4C). Red rings show introgression topologies with optix and cortex phenotypes.

Supplementary Figure S6. The 105 topologies from Twisst comparison with *H. besckei* and *H. m. thelxiope* and *H m. meriana* from the Guianese hybrid zone taxa (Fig 6C). Red rings show introgression topologies with optix and cortex phenotype.

Supplementary table S7. Table showing taxa used, and phenotypes tested in each Twisst comparison.

Supplementary table S8. Table showing taxa in each phenotype group for each ‘diagnostically fixed’ analysis.

Supplementary Figure S9 - Twisst comparison with Peruvian hybrid zone taxa across all of chromosome 18. Shading shows putative regulatory elements as determined in main manuscript Fig 2. Red circle highlights the peak at Hmel218005:227000.

Supplementary Figure S10 - Twisst comparison with Guianese hybrid zone taxa (*H. e. tumatumari* and *H. m. meriana*) across all of chromosome 18. Shading shows putative regulatory elements as determined in main manuscript Fig 2. Red circle highlights the peak at Hmel218005:227000.

Supplementary Figure S11 - Twisst comparison with *H. besckei* and Guianese hybrid zone taxa across all of chromosome 18. Shading shows putative regulatory elements as determined in main manuscript Fig 2. Red circle highlights the peak at Hmel218005:227000.

Supplementary Figure S12 - Twisst comparison with Peruvian hybrid zone taxa across all of chromosome 10. Shading shows putative regulatory elements as determined in main manuscript Fig 5.

Supplementary Figure S13 - Twisst comparison with Peruvian hybrid zone taxa across all of chromosome 15. Shading shows putative regulatory elements as determined in main manuscript Fig 6.

Supplementary Figure S14 - Twisst comparison with Guianese hybrid zone taxa (*H. e. tumatumari* together with *H. m. bari* and *H. m. meriana* together with *H. m. thelxiope*) across all of chromosome 15. Shading shows putative regulatory elements as determined in main manuscript Fig 6.

Supplementary Figure S15 - Twisst comparison with *H. besckei* and Guianese hybrid zone taxa (*H. e. tumatumari* together with *H. m. bari* and *H. m. meriana* together with *H. m. thelxiope*) across all of chromosome 15. Shading shows putative regulatory elements as determined in main manuscript Fig 6.

Supplementary Figure S16 – Species tree from all SNPs across chromosomes 10, 15 and 18 which contain the WntA, cortex and optix colour pattern loci. Bootstrap supports indicated on nodes, green diamond ≥ 75%, pink diamond ≥ 95%.

Supplementary Figure S17 - Paired phylogenetic Twisst comparison across the *WntA* region of scaffold Hmel210004. A) Twisst comparison with Guianese hybrid zone taxa. Note that there is no evidence of shared ancestry between *H. elevatus* and *H. melpomene* mimics indicating independent evolution of the broken band phenotype in these taxa leaving us unable to identify regulatory elements around *WntA* controlling this broken band phenotype.

Supplementary Figure S18 - Sequence conservation at wing patterning loci. Pairwise conservation between *H. melpomene* and other Lepidopteran species *H. erato demophoon, Junonia coenia, Bicyclus anynana, Danaus plexippus, Papilio machoan, Papilio polytes, Pieris napi, Amyelois transitella,* and *Bombyx mori are* plotted below, with regions over 70% identity shaded pink, exons shaded purple and regions corresponding to pattern elements shaded blue. A shows the optix locus, with the dennis elements in orange, *Ray* elements in blue and *Band* elements in green. B shows the *WntA* locus. The blue regions labelled 1 and 2 indicate the two elements identified herein. C shows the *Cortex* locus, with the two identified elements A and B in purple and red.

Supplementary Table S19. Scaffold names and locations identified by blast in Fig. S11 across Lepidoptera species.

Supplementary Table S20. Table showing ACT-BLAST hits for each of our defined module in *H. melpomene* and the corresponding positions in the *H. erato demophoon* genome.