

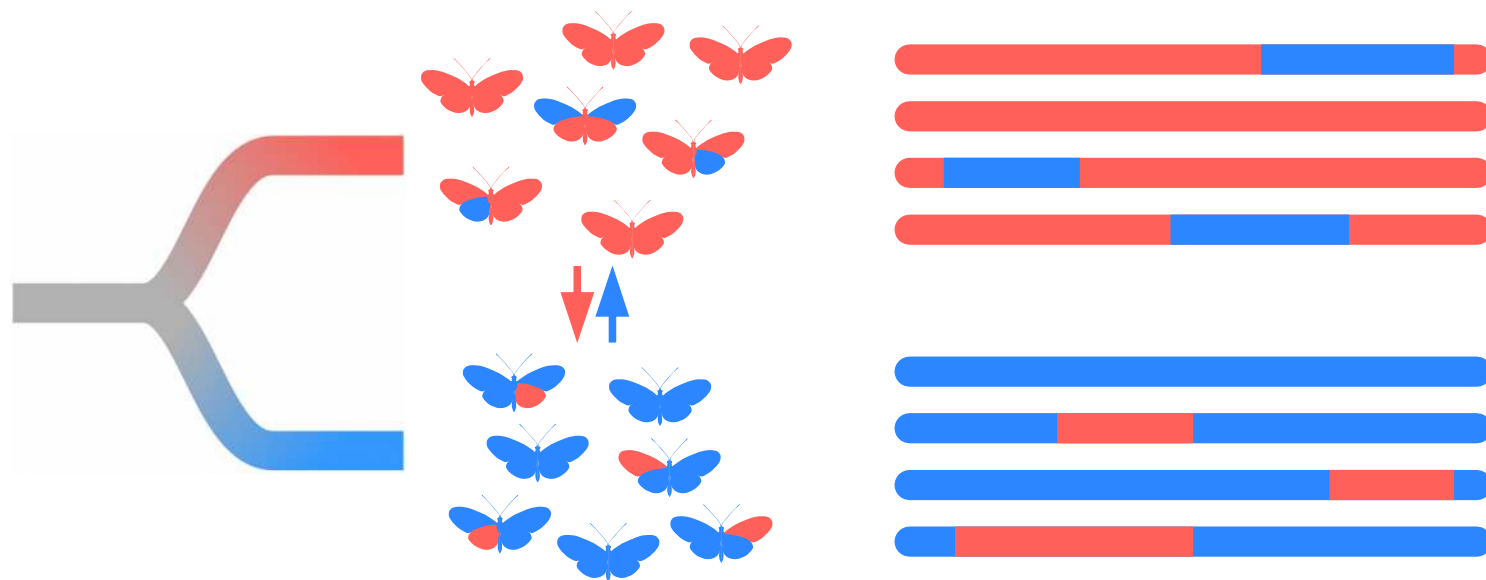
Speciation and hybridisation

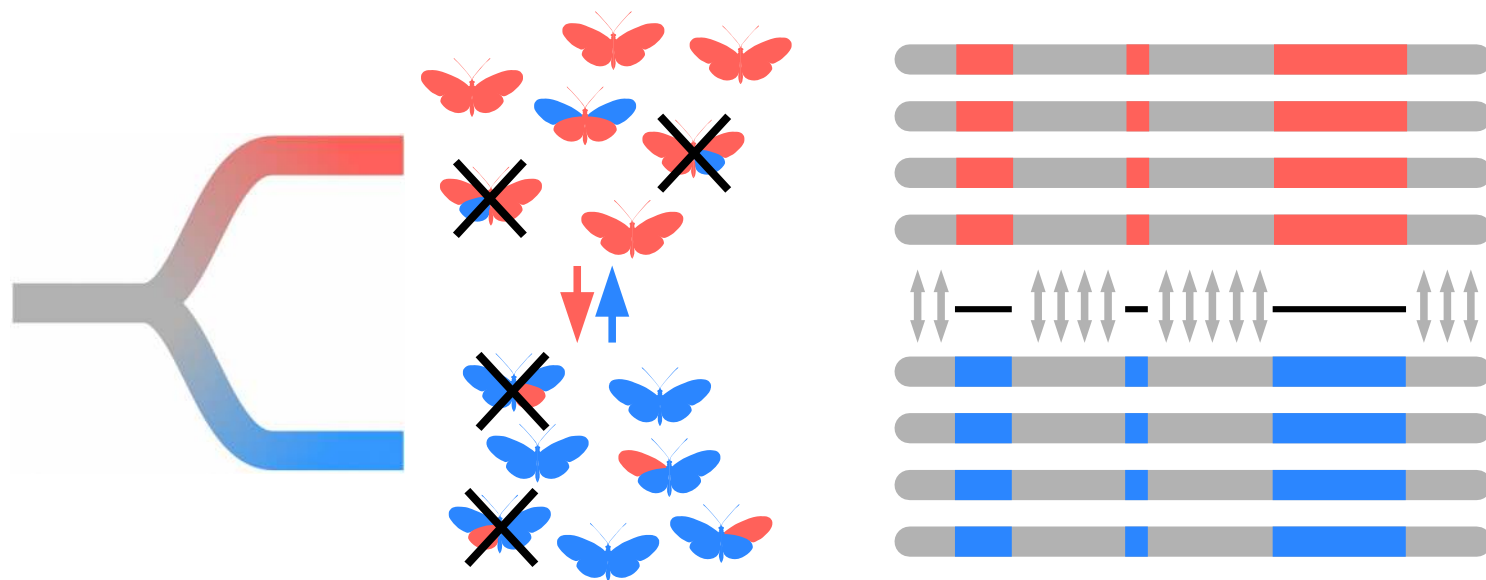
Part 2: All that is gold does not glitter

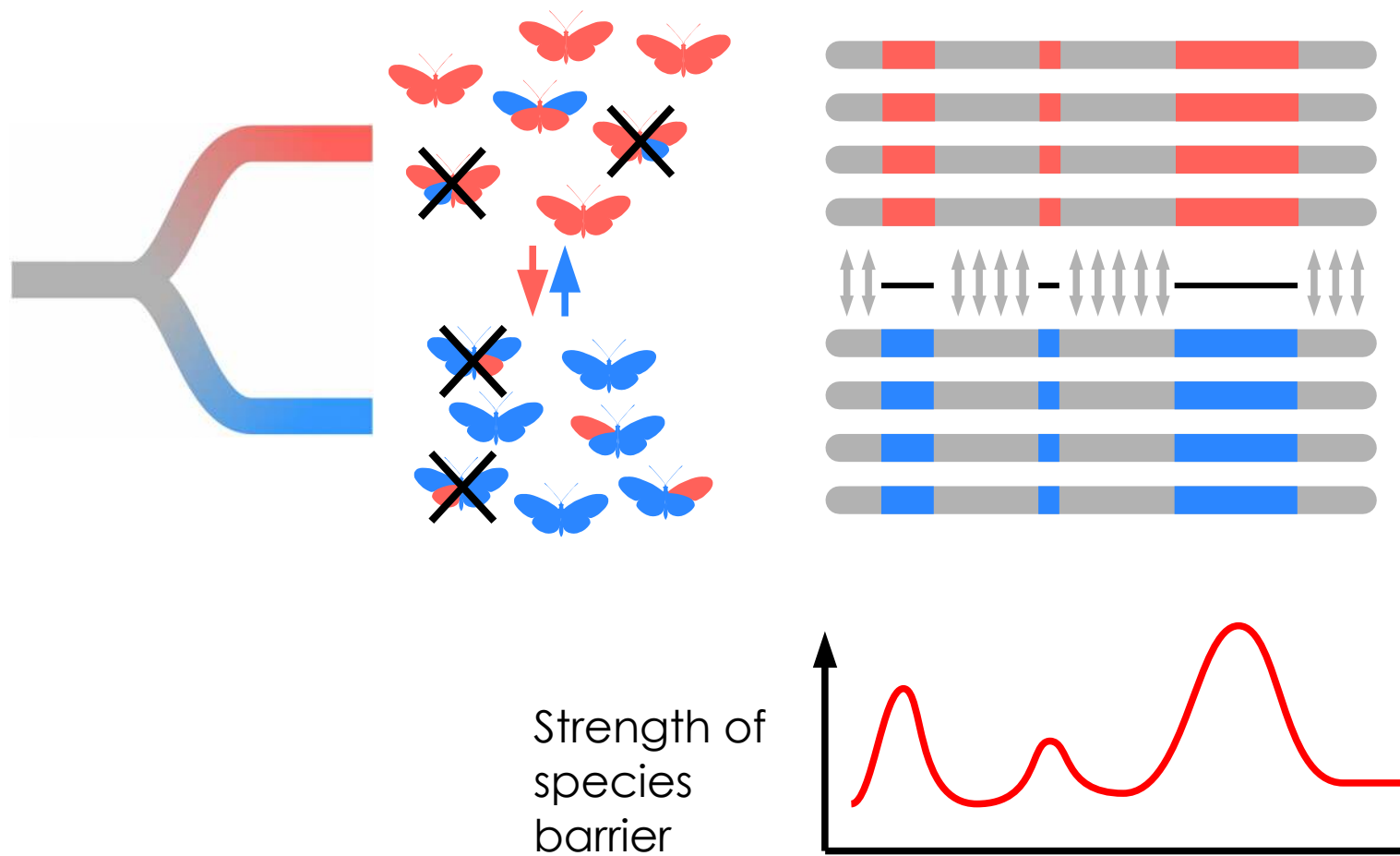
Simon Martin

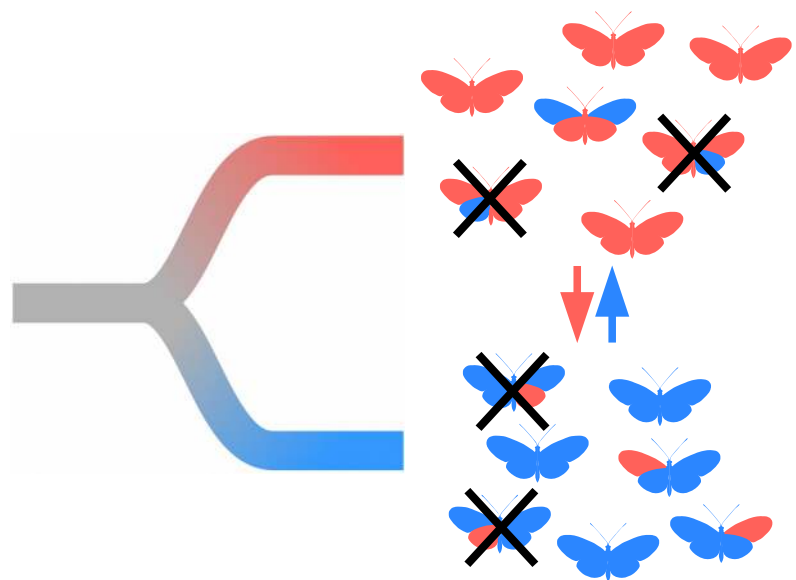
Institute of Evolutionary Biology
University of Edinburgh

January 2020

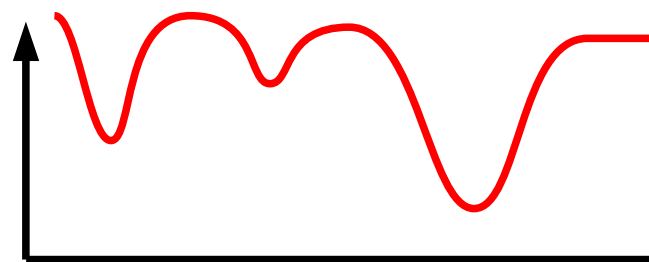
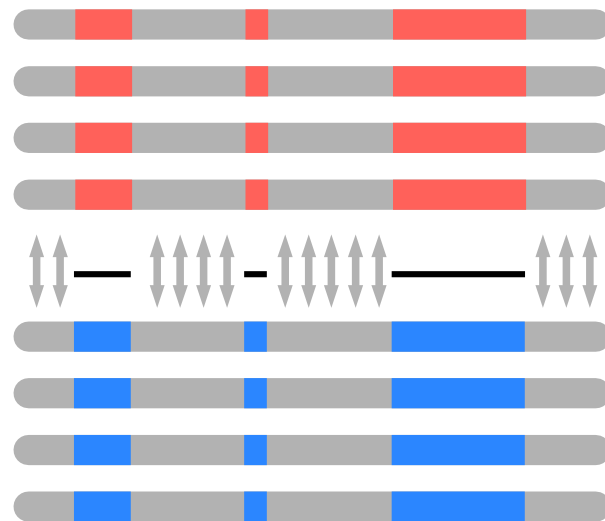


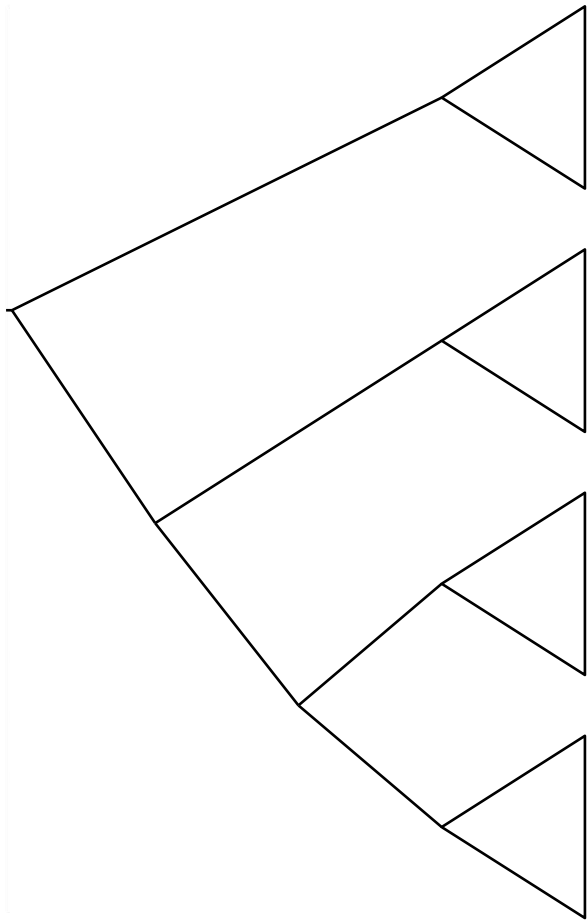




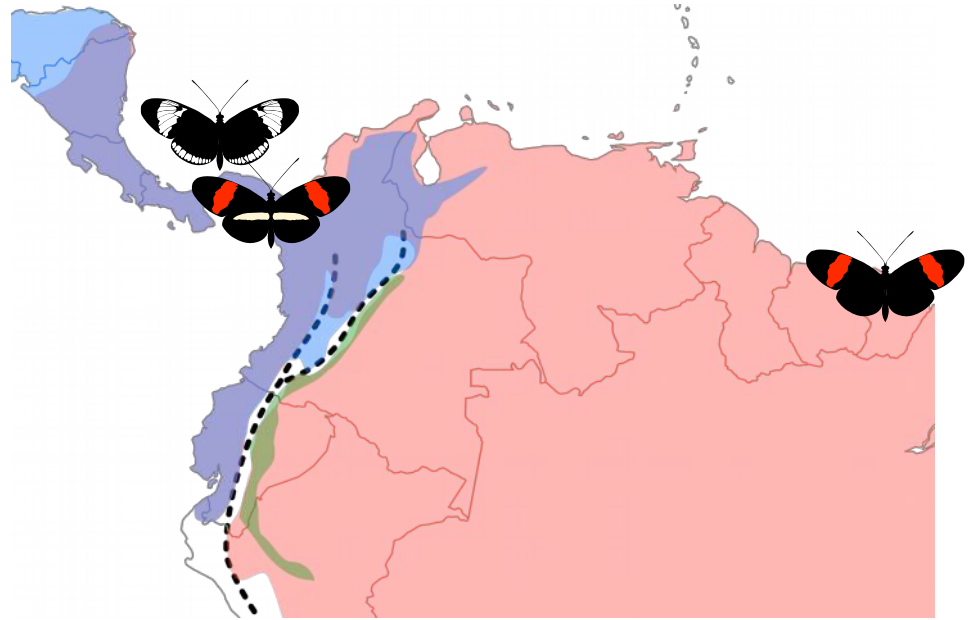


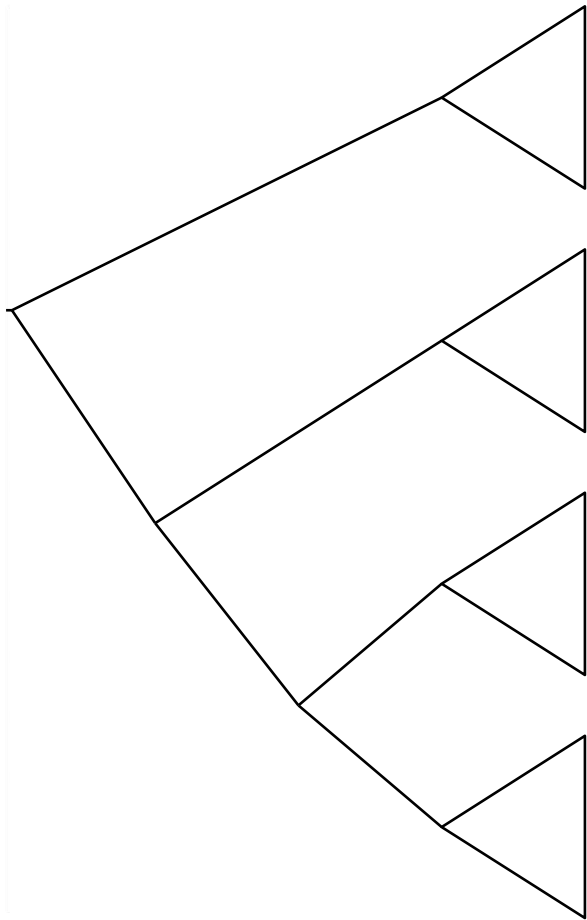
effective
migration
rate (m_e)



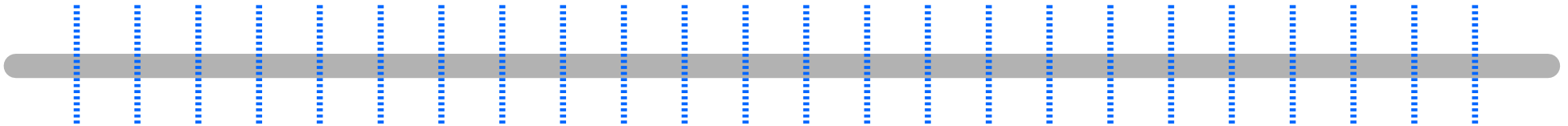
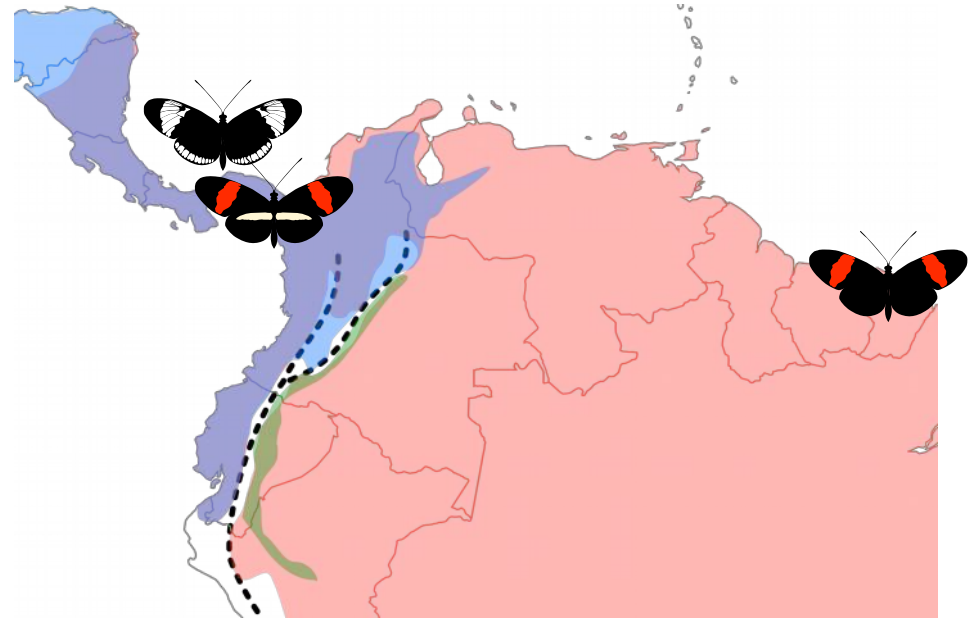


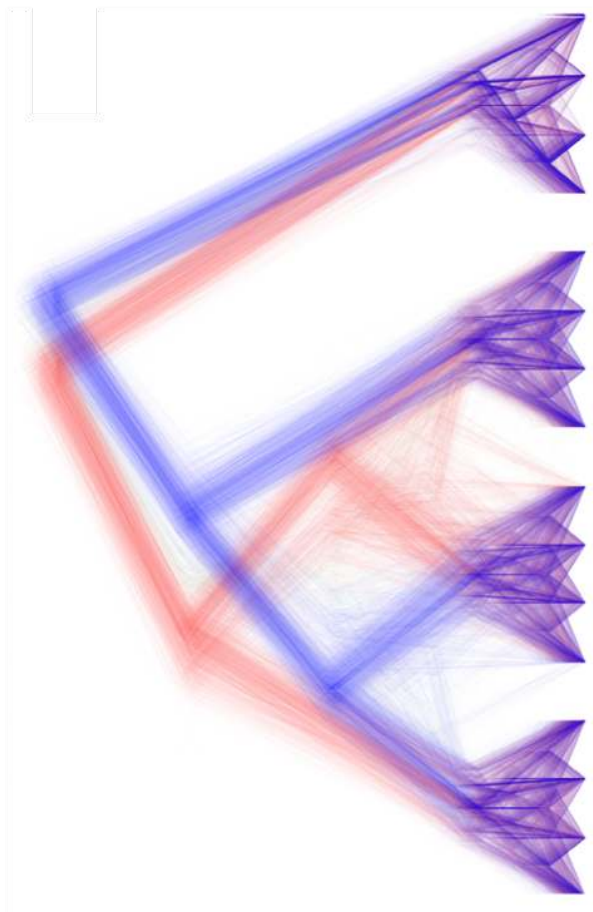
Outgroups





Outgroups



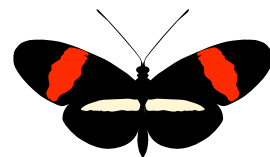


Outgroups



H. cydno

Panama



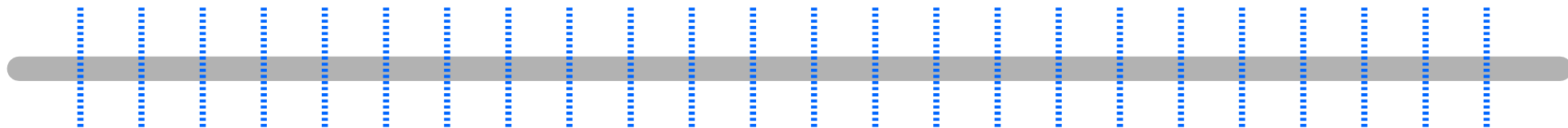
H. m. rosina

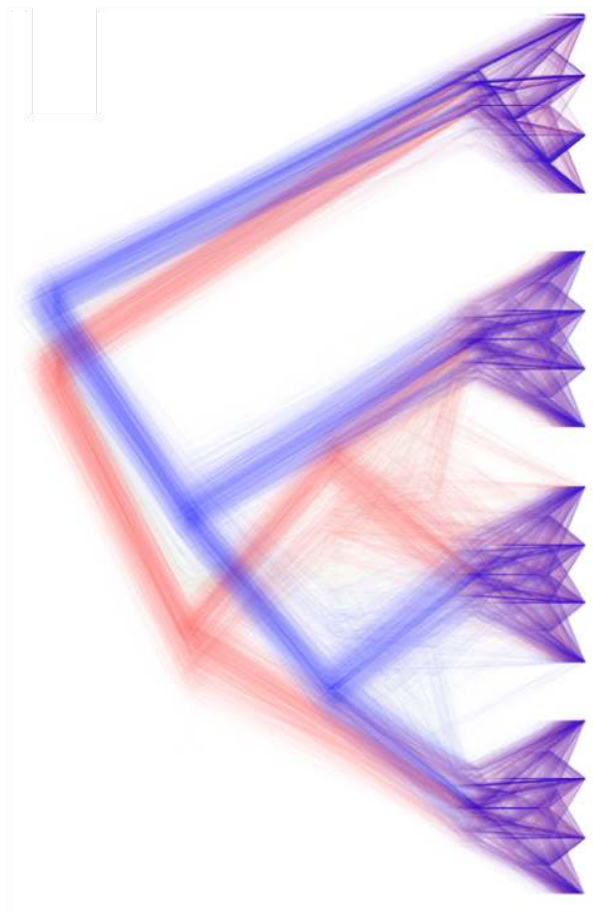
Panama



H. m. melpomene

French Guiana



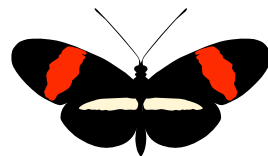


Outgroups



H. cydno

Panama



H. m. rosina

Panama



H. m. melpomene

French Guiana

"species" topology



1510 (53.0%)

"geography" topology



1201 (42.2%)

"control" topology

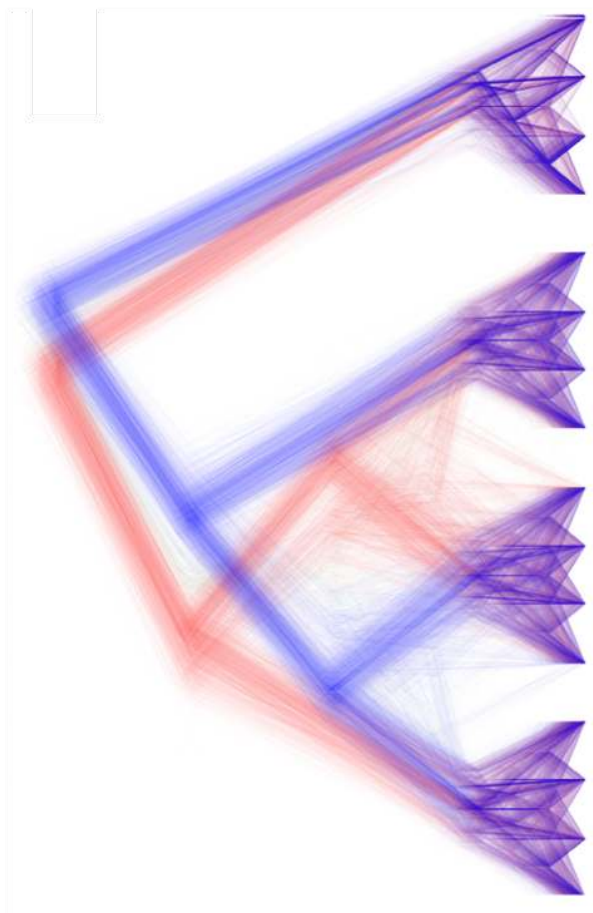


32 (1.1%)

"unresolved" topology



105 (3.7%)

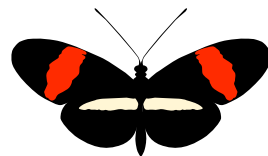


Outgroups



H. cydno

Panama



H. m. rosina

Panama



H. m. melpomene

French Guiana

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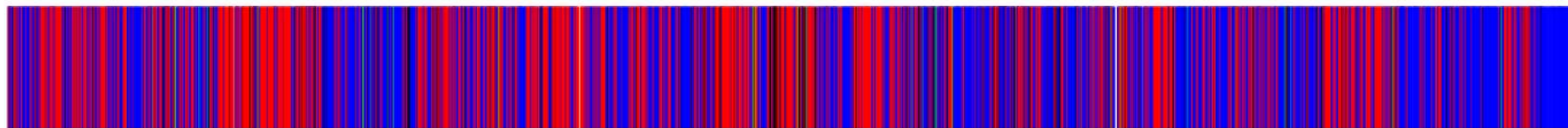


32 (1.1%)

"unresolved" topology

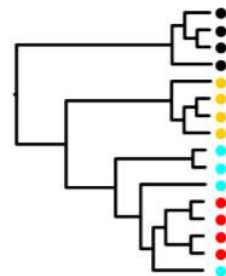
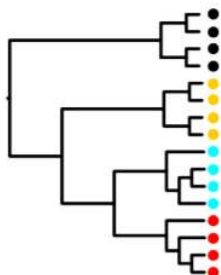
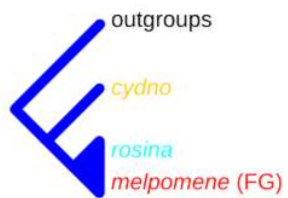


105 (3.7%)

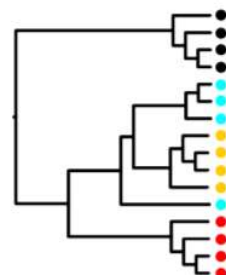
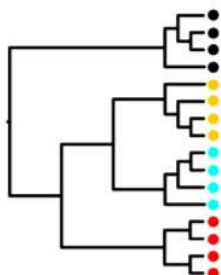
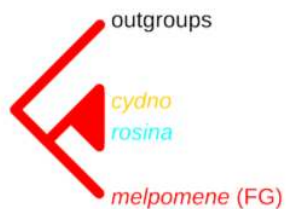


1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20Z

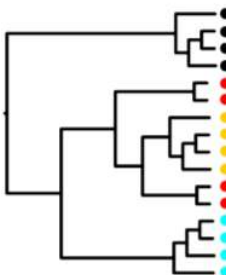
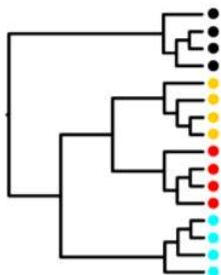
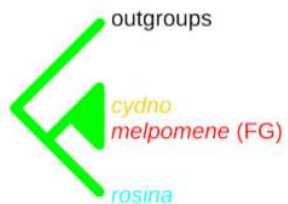
"species tree"



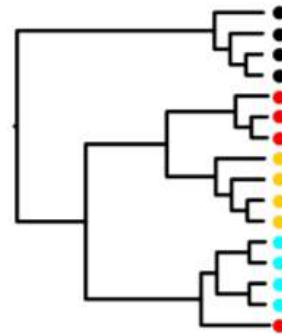
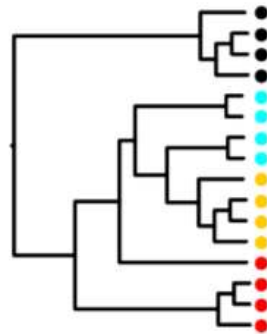
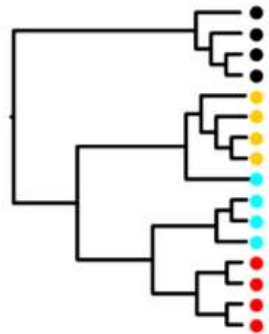
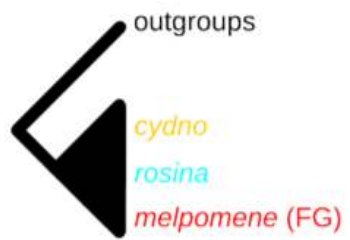
"geography tree"



"control tree"

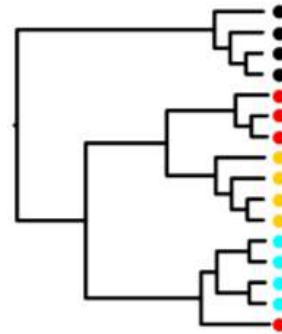
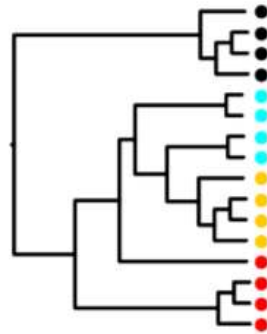
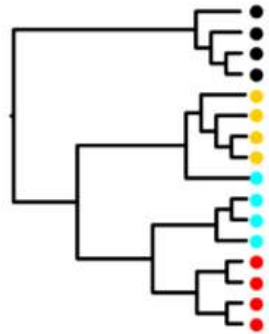
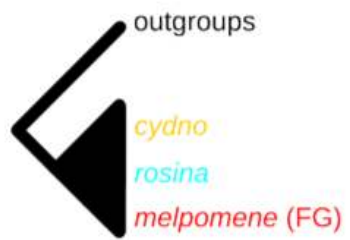


"unresolved"

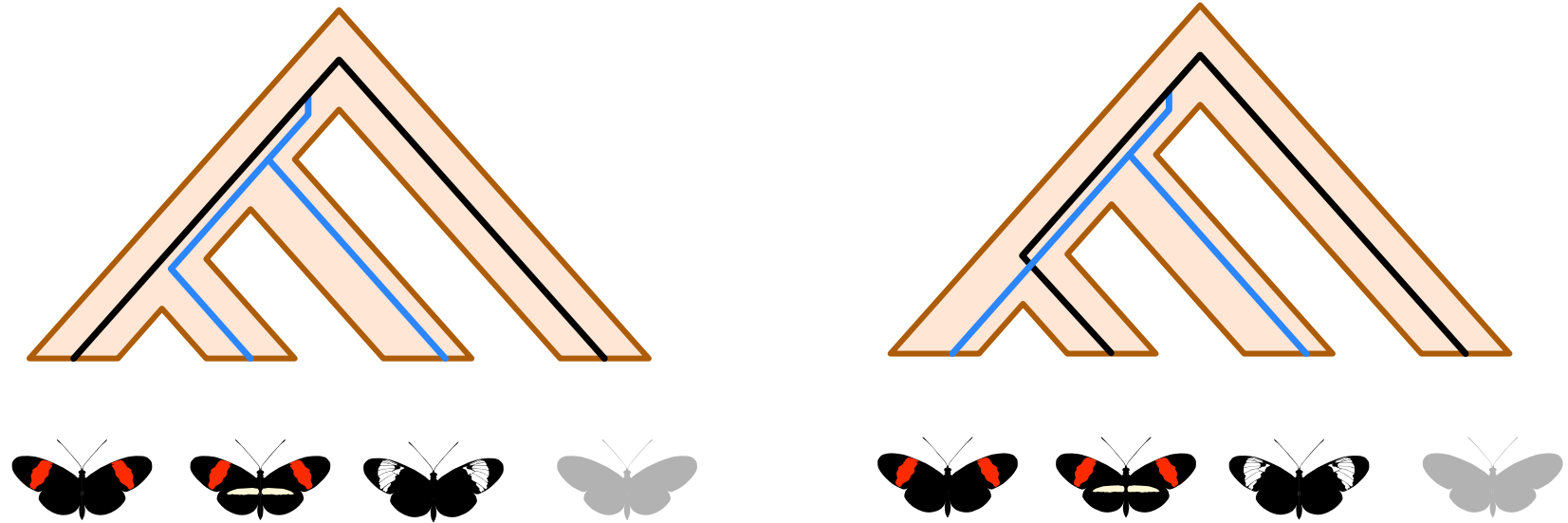


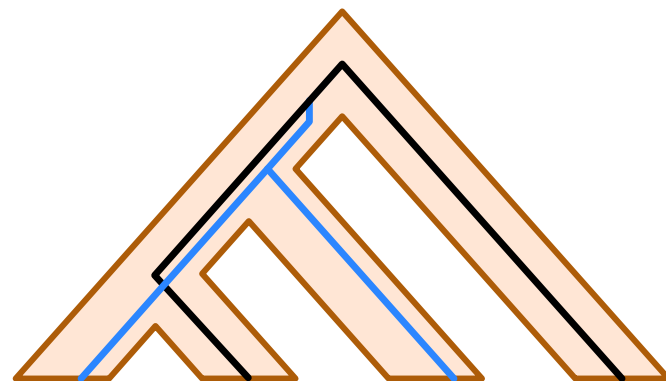
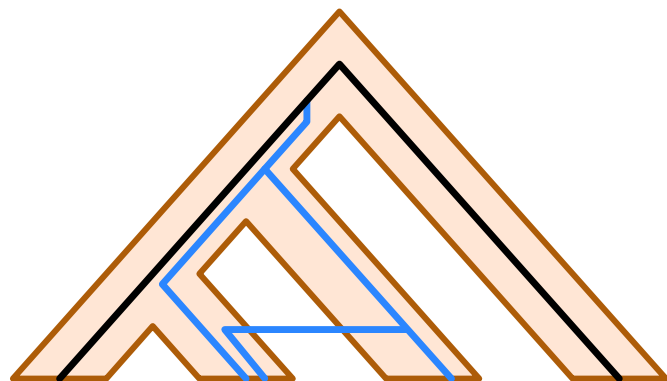
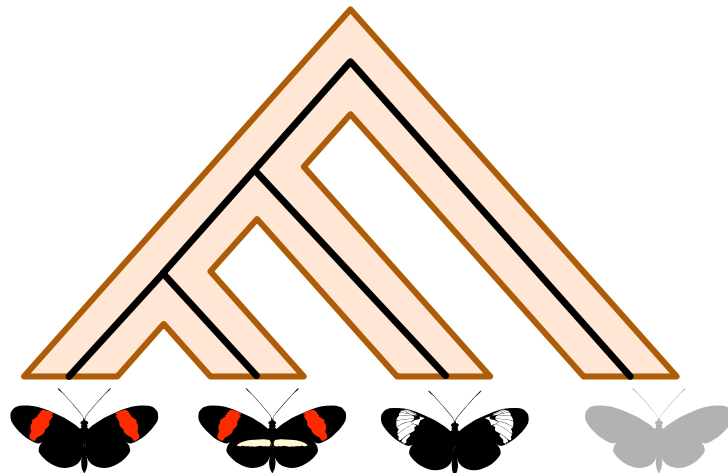
Window Size (kb)	Species topology	Geography topology	Control topology	Unsorted
10	38%	31%	2%	30%
20	45%	37%	2%	17%
50	51%	41%	1%	6%
100	53%	42%	1%	4%
200	56%	41%	1%	2%

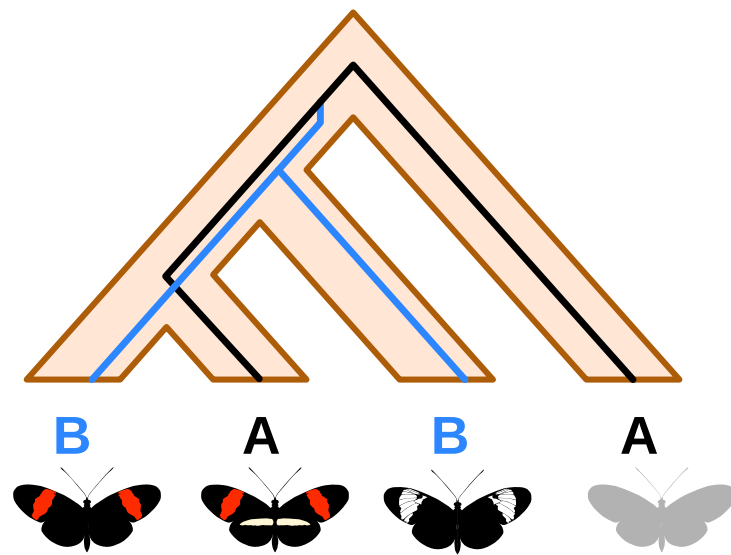
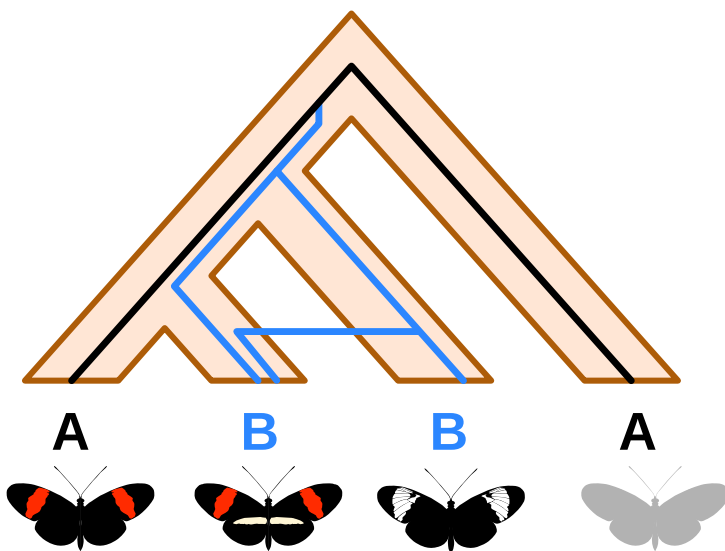
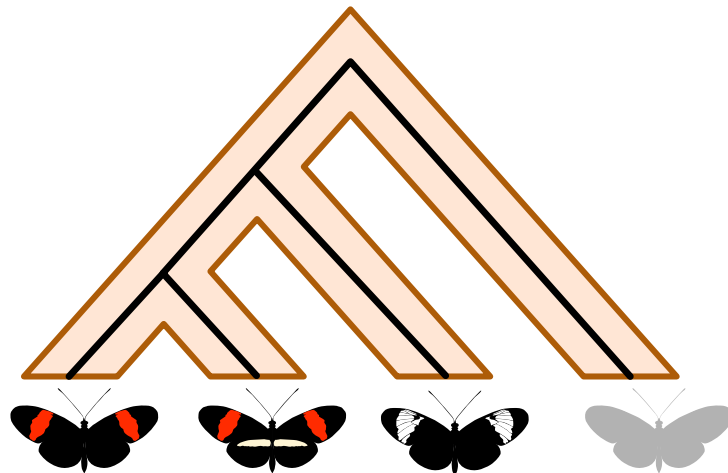
"unresolved"

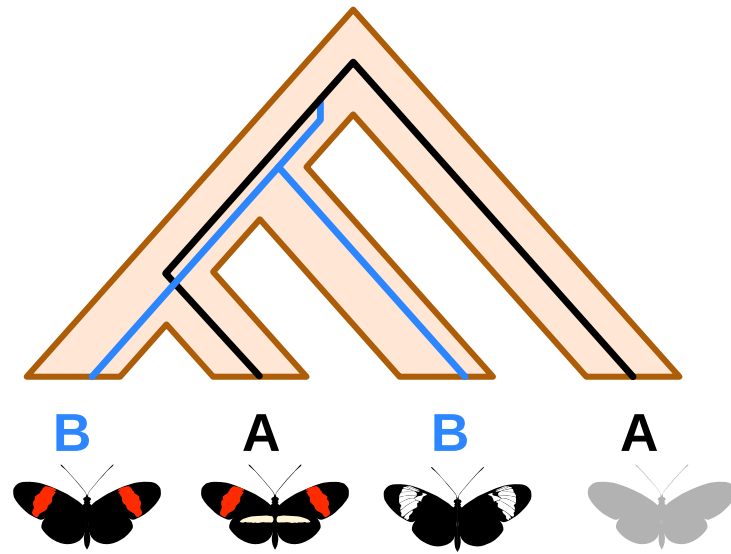
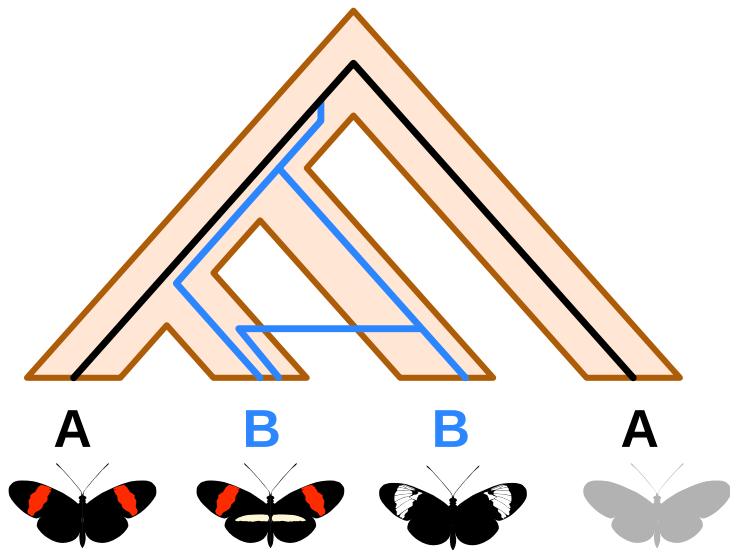


1. We need to work at much finer resolution
2. We need to **quantify** genealogy shapes

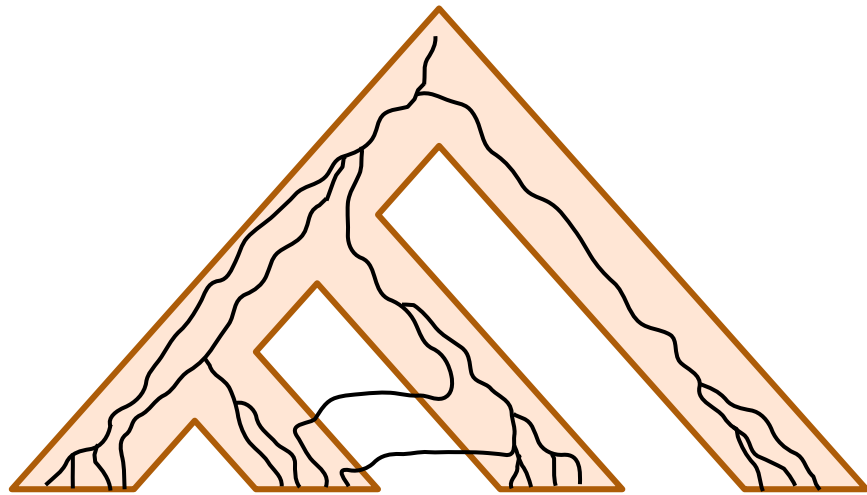








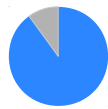
$$D(P_1, P_2, P_3, O) = \frac{\sum C_{ABBA}(i) - C_{BABA}(i)}{\sum C_{ABBA}(i) + C_{BABA}(i)}$$



A_B



AB



A_B



A



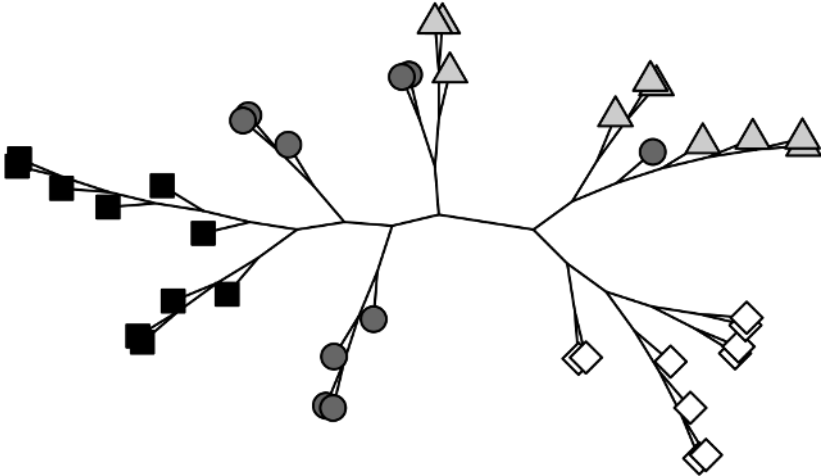
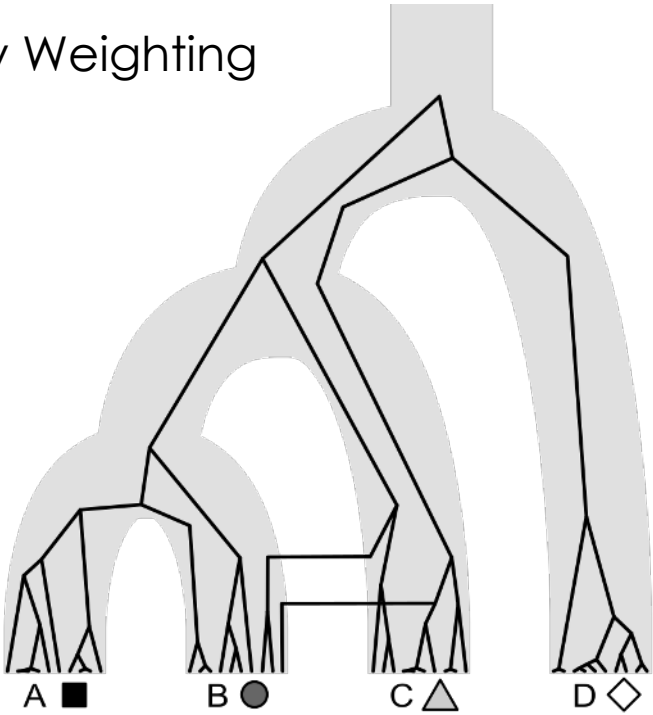
$$D(P_1, P_2, P_3, O) = \frac{\sum C_{ABBA}(i) - C_{BABA}(i)}{\sum C_{ABBA}(i) + C_{BABA}(i)}$$

$$C_{ABBA}(i) = (1 - \hat{p}_{i1})\hat{p}_{i2}\hat{p}_{i3}(1 - \hat{p}_{i4})$$

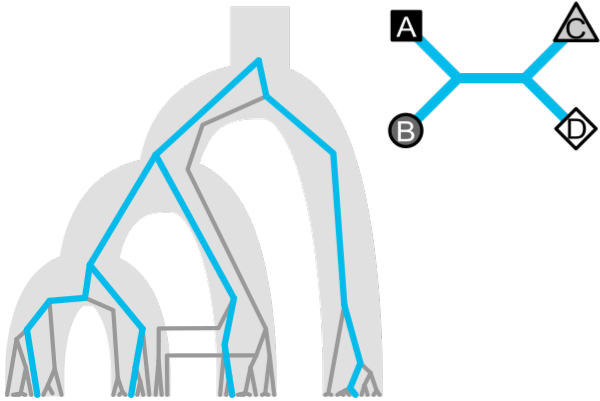
$$C_{BABA}(i) = \hat{p}_{i1}(1 - \hat{p}_{i2})\hat{p}_{i3}(1 - \hat{p}_{i4})$$

Can we quantify the shape of **trees** in the same way?

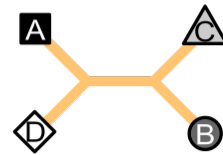
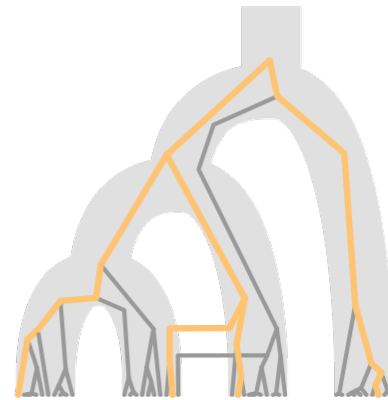
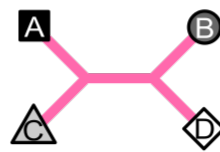
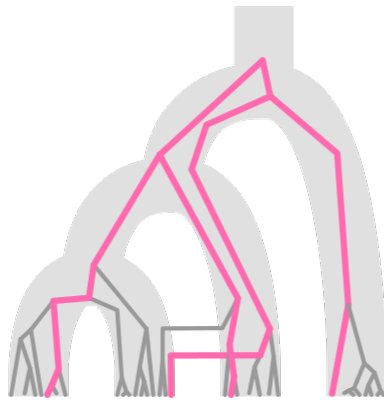
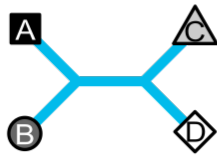
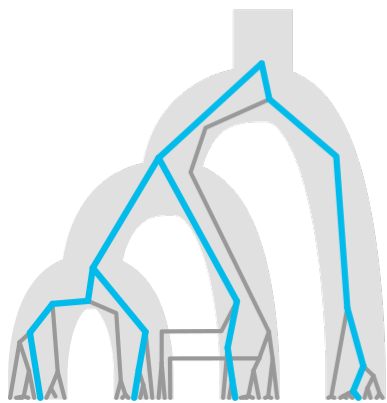
Topology Weighting



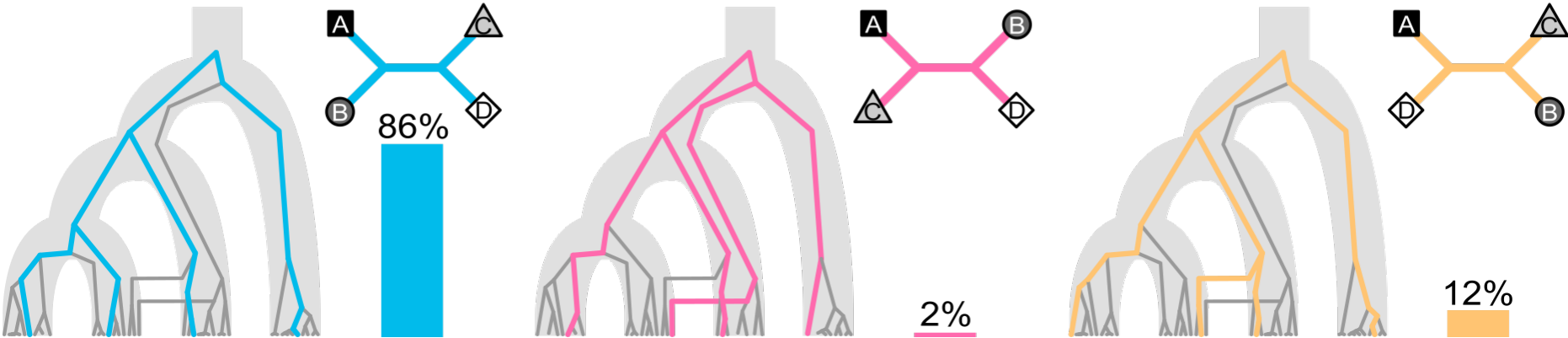
Topology Weighting

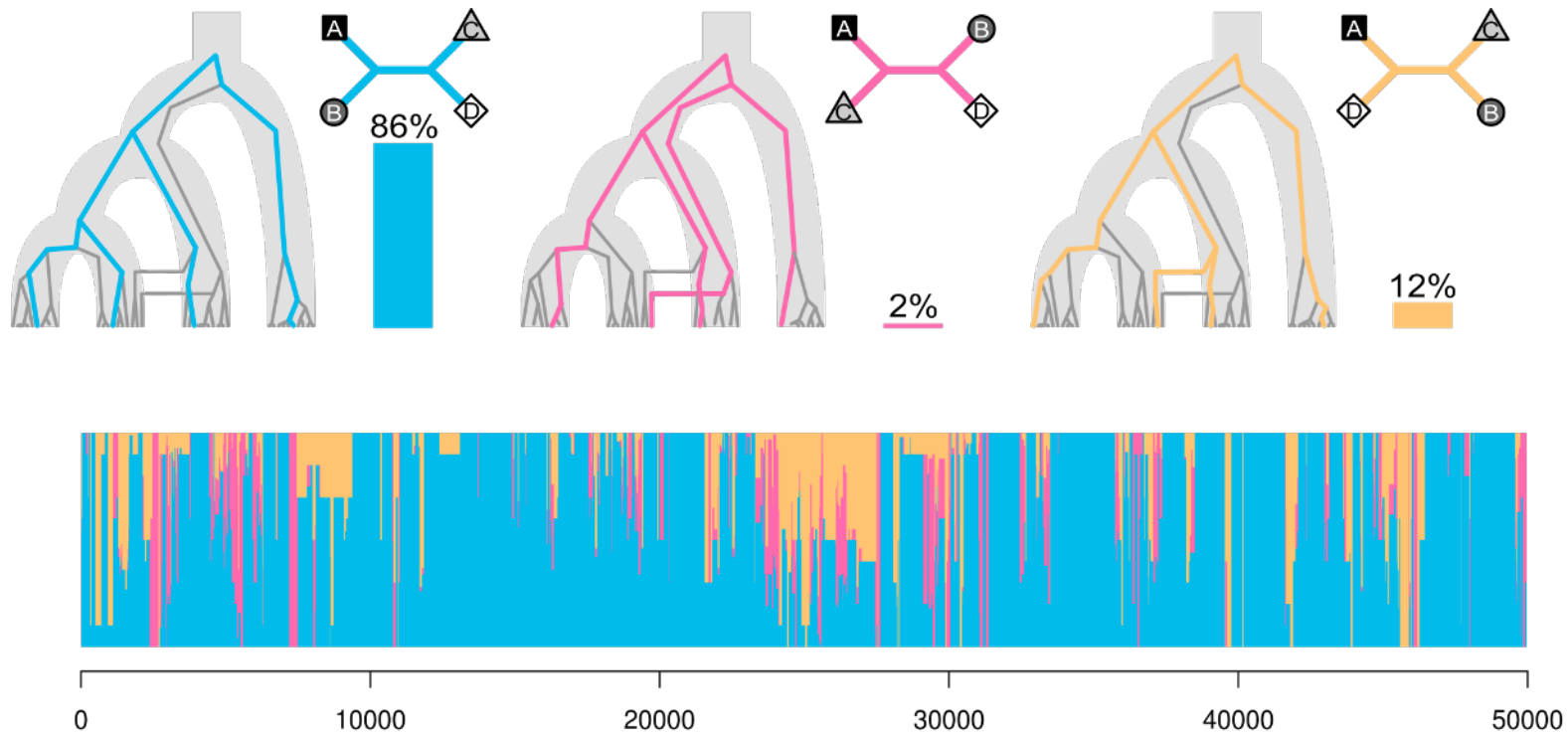


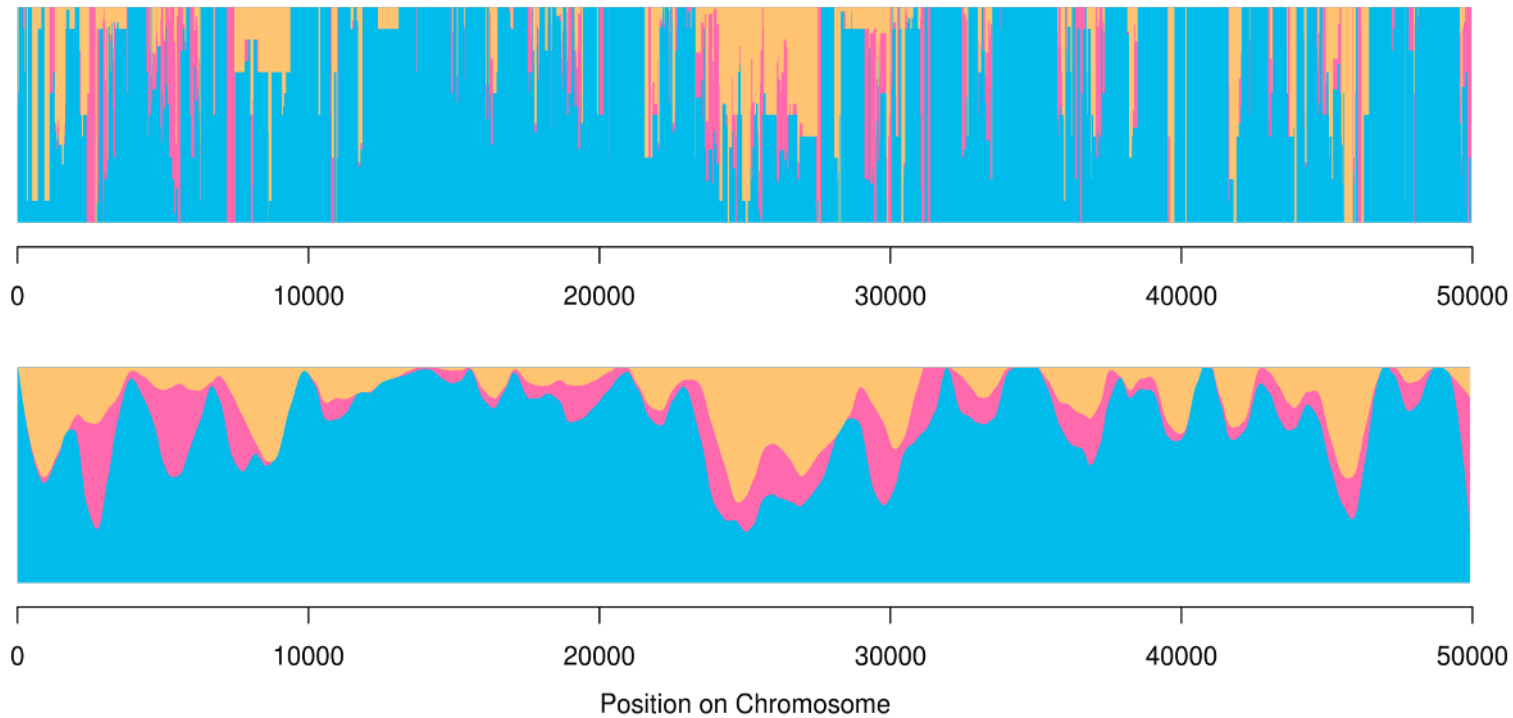
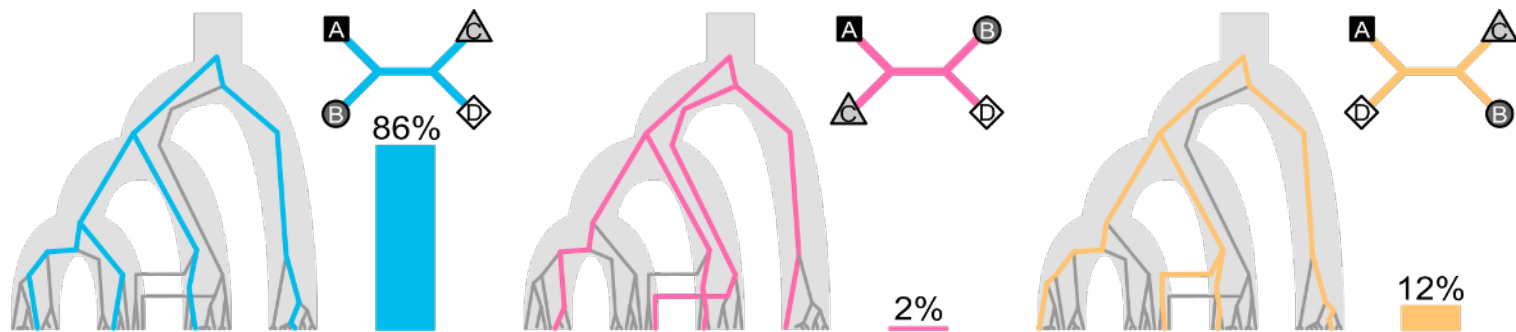
Topology Weighting

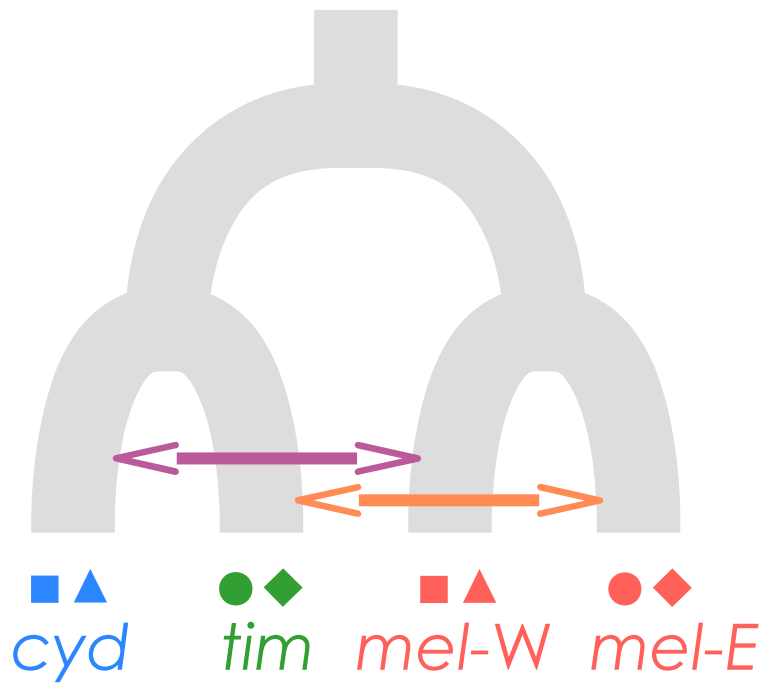
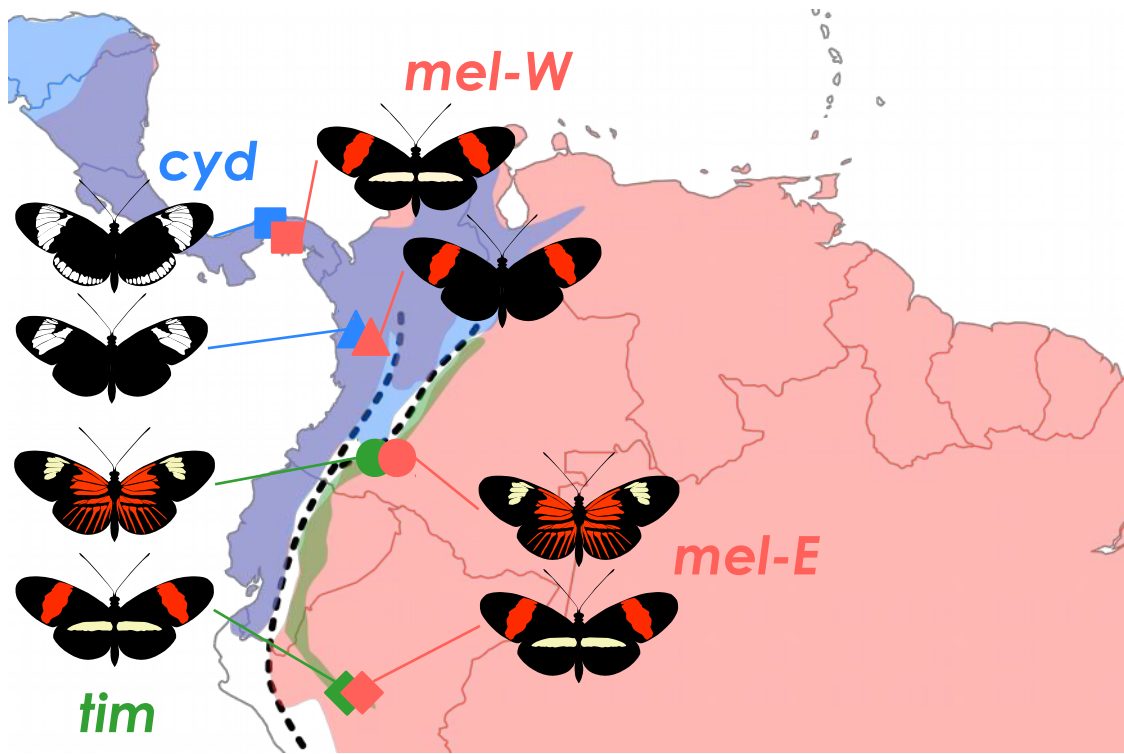


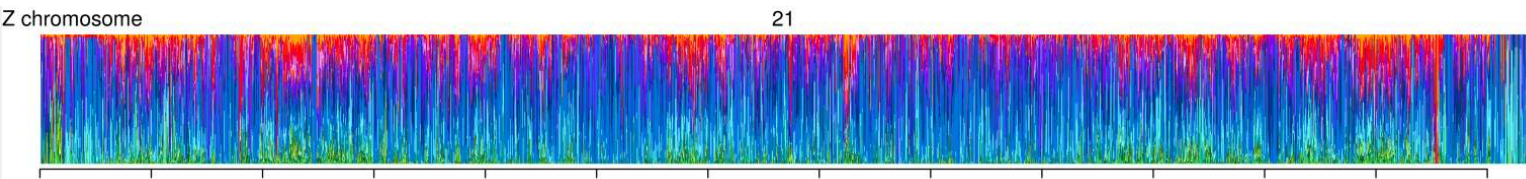
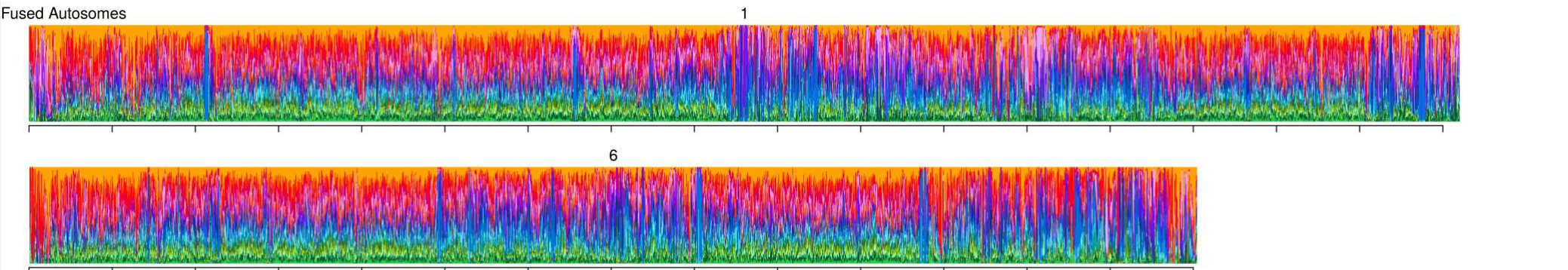
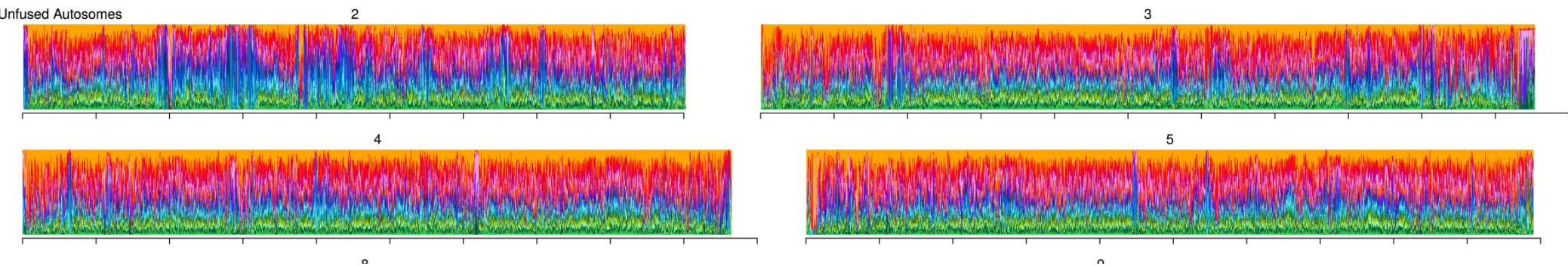
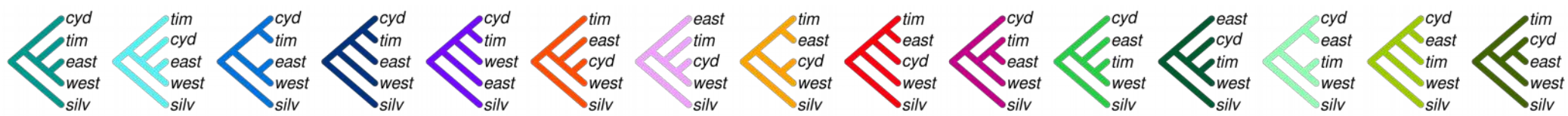
Topology Weighting

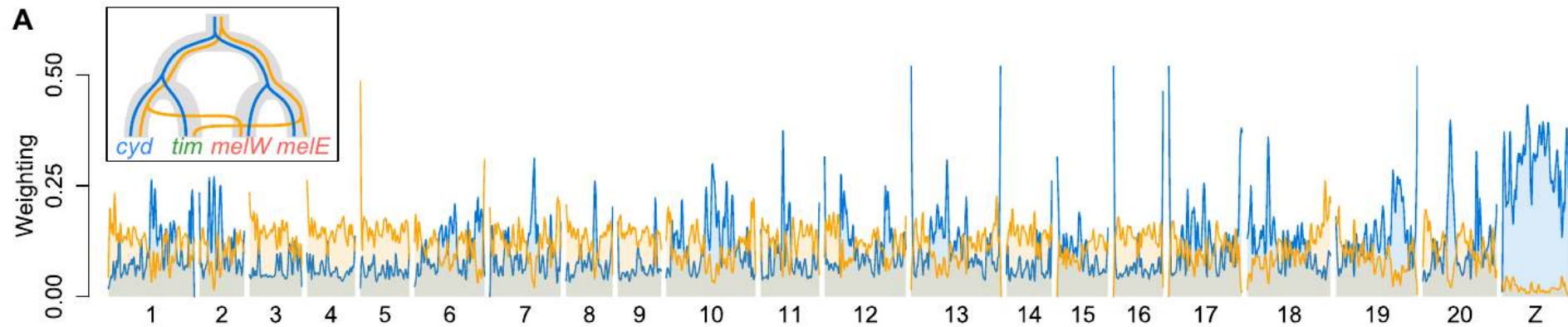


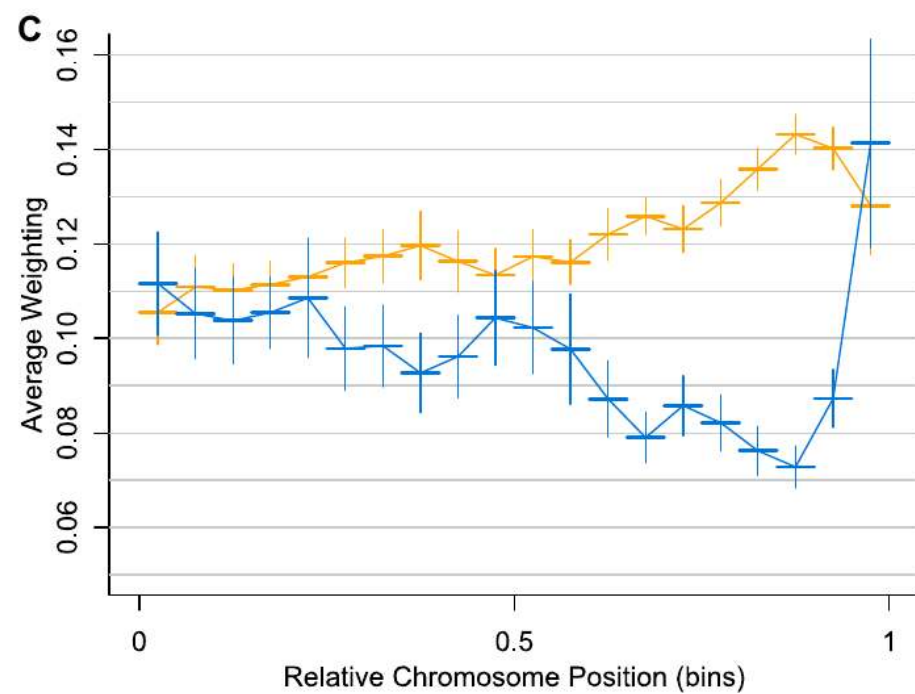
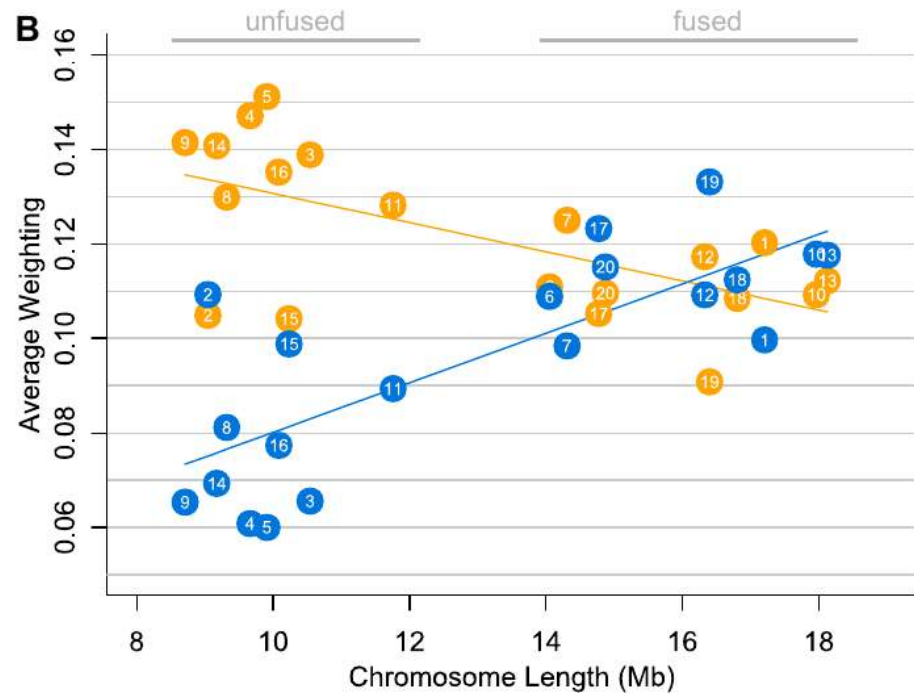
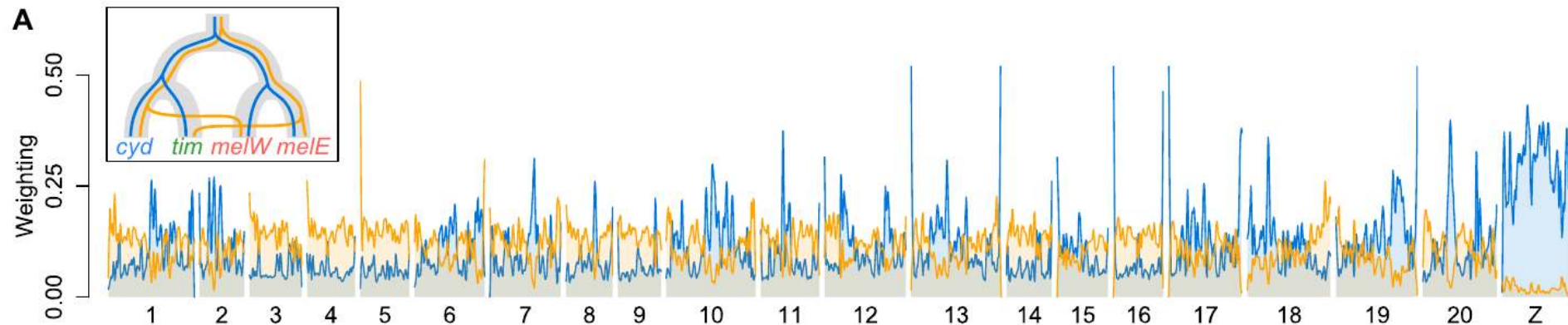


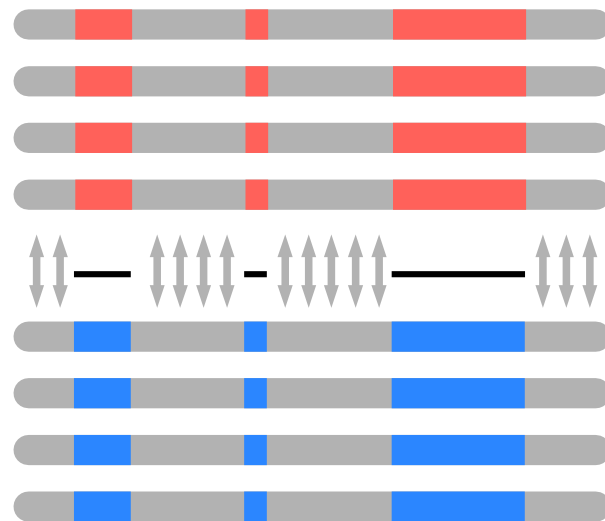
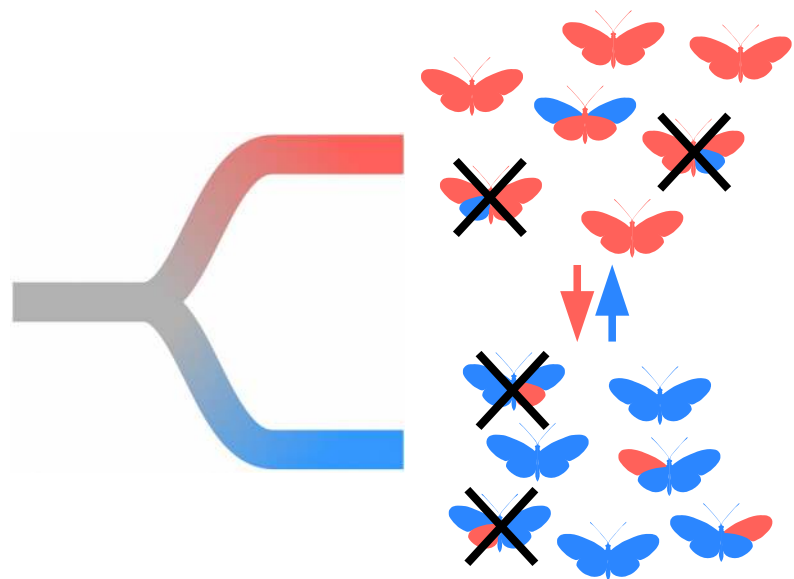




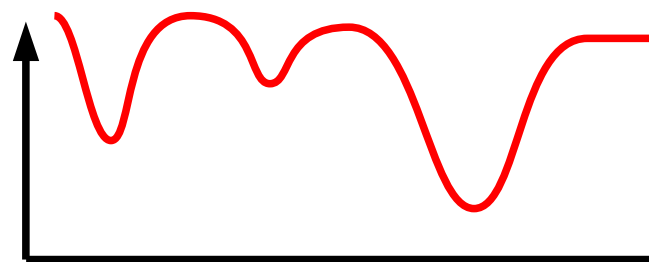


A





effective
migration
rate (m_e)



We want a measure that is:

Proportional to the effective migration rate

Unaffected by confounding factors like N_e and mutation rate

We want a measure that is:

Proportional to the effective migration rate

Unaffected by confounding factors like N_e and mutation rate

$$D(P_1, P_2, P_3, O) = \frac{\sum C_{ABBA}(i) - C_{BABA}(i)}{\sum C_{ABBA}(i) + C_{BABA}(i)}$$

We want a measure that is:

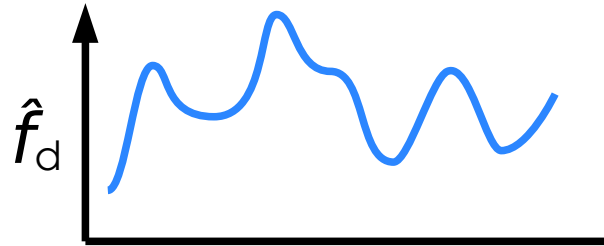
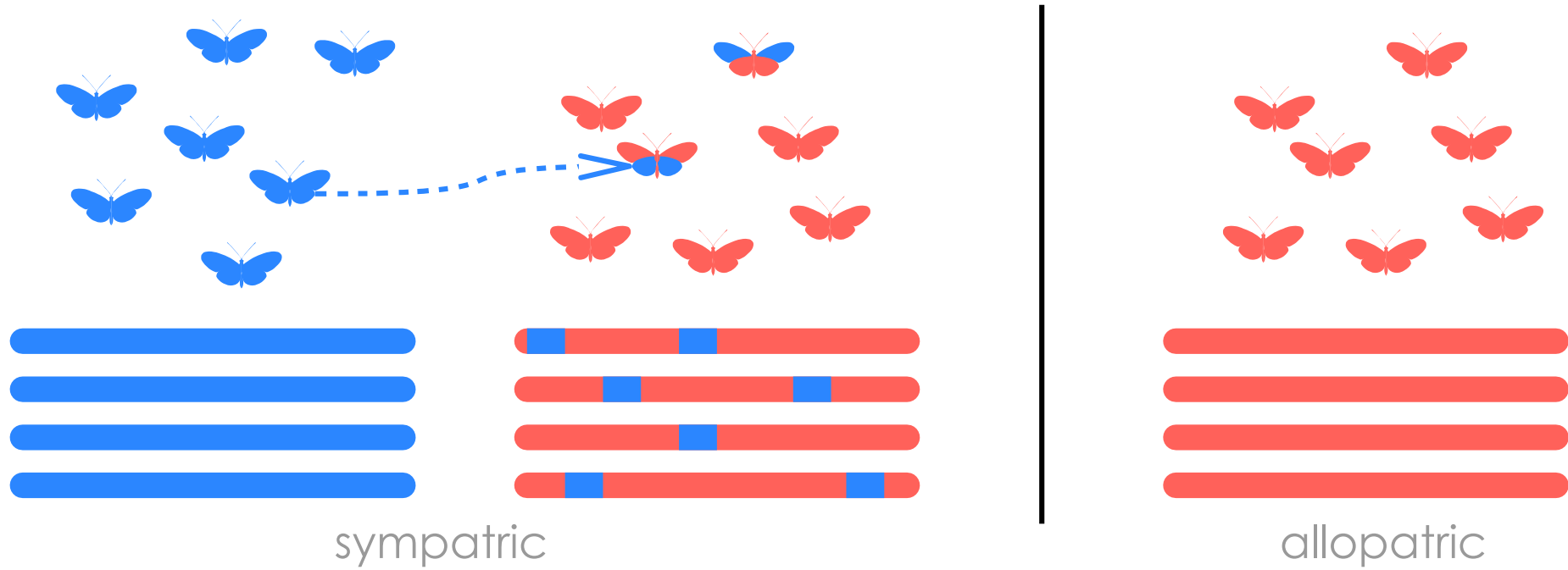
Proportional to the effective migration rate

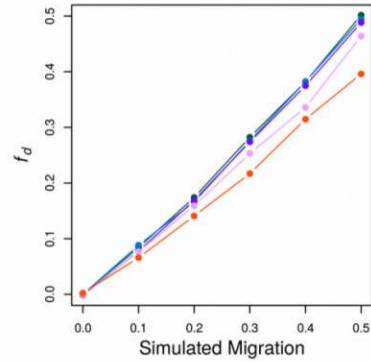
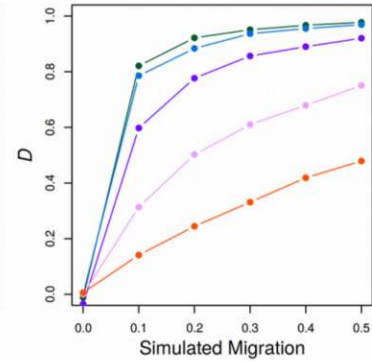
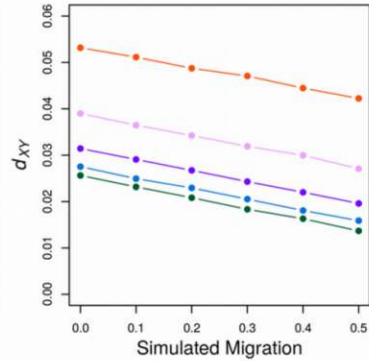
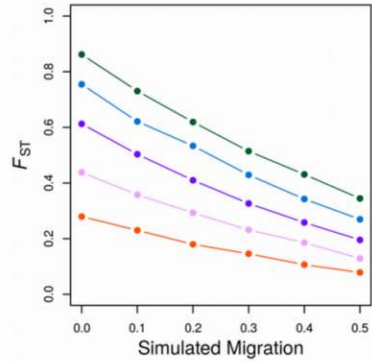
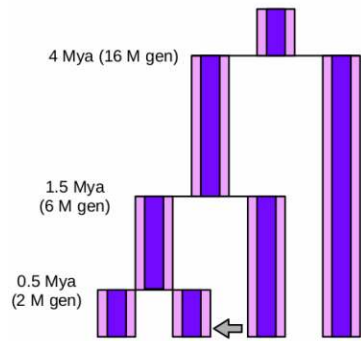
Unaffected by confounding factors like N_e and mutation rate

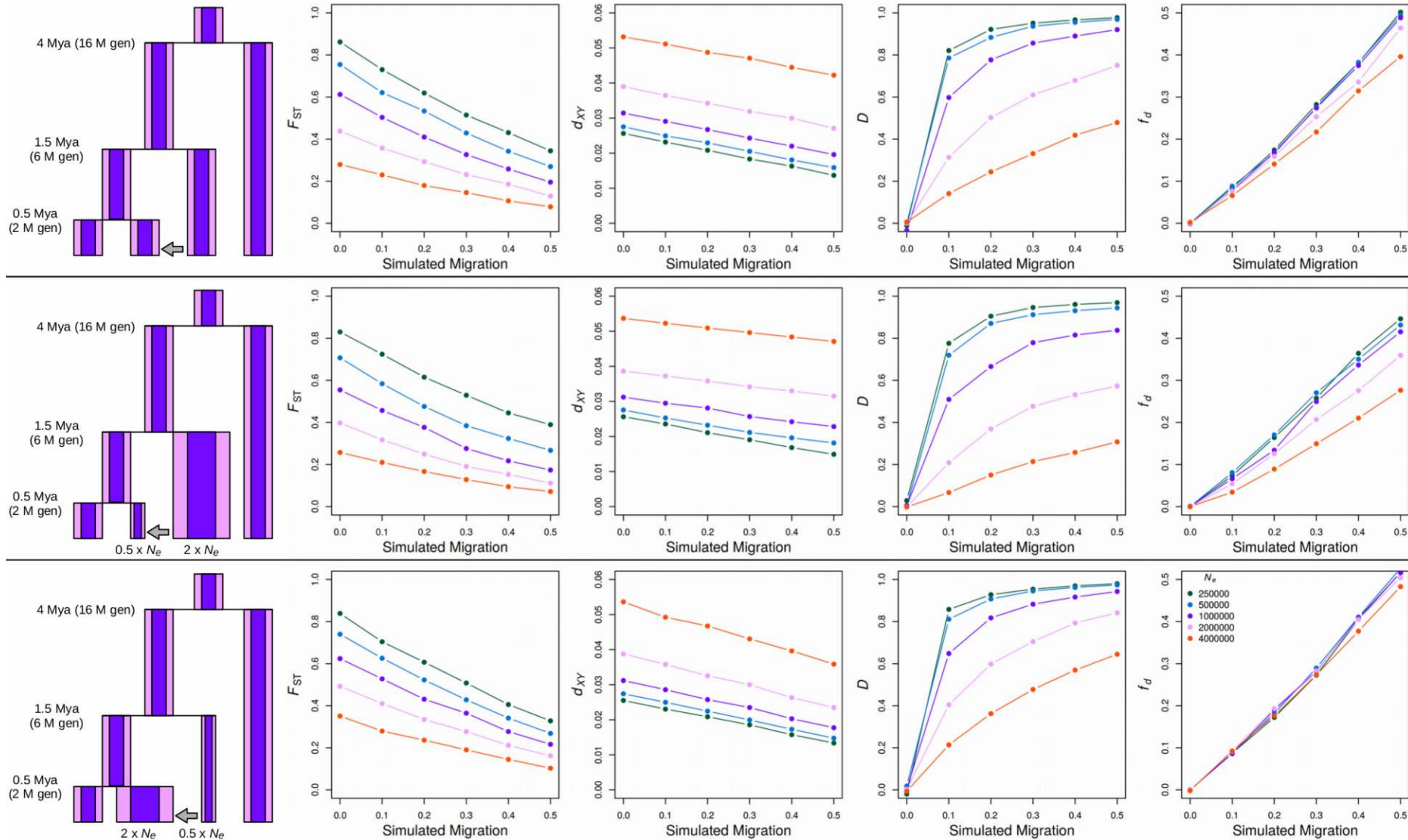
$$f_d \times D(P_1, P_2, P_3, O) = \frac{\sum C_{ABBA}(i) - C_{BABA}(i)}{\sum C_{ABBA}(i) + C_{BABA}(i)}$$

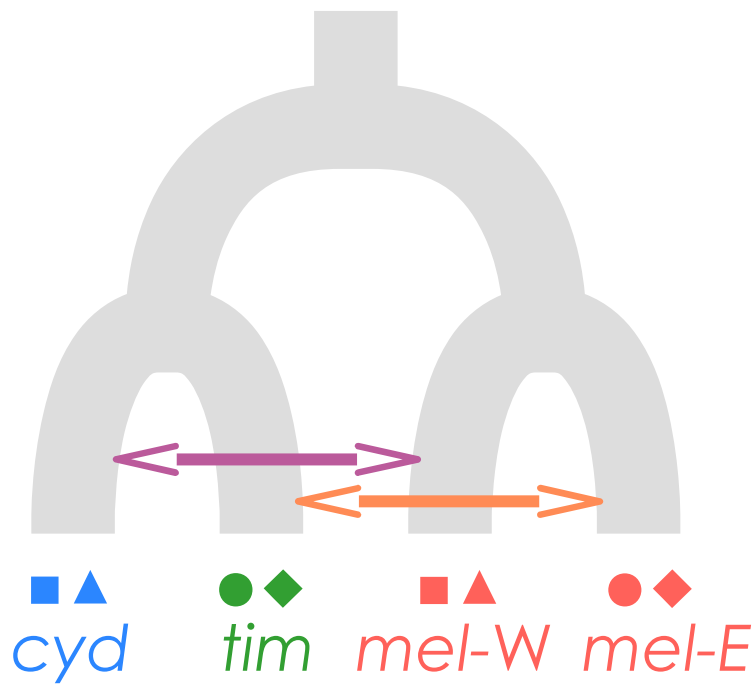
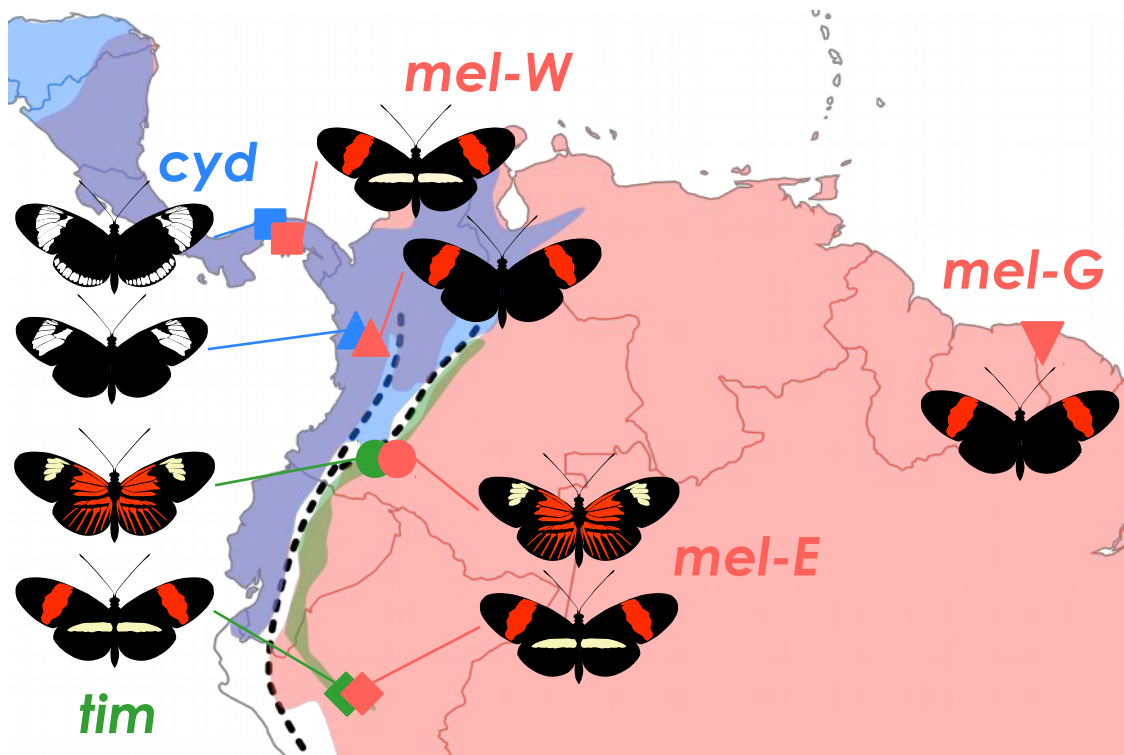
replace denominator with
maximum possible value of
numerator

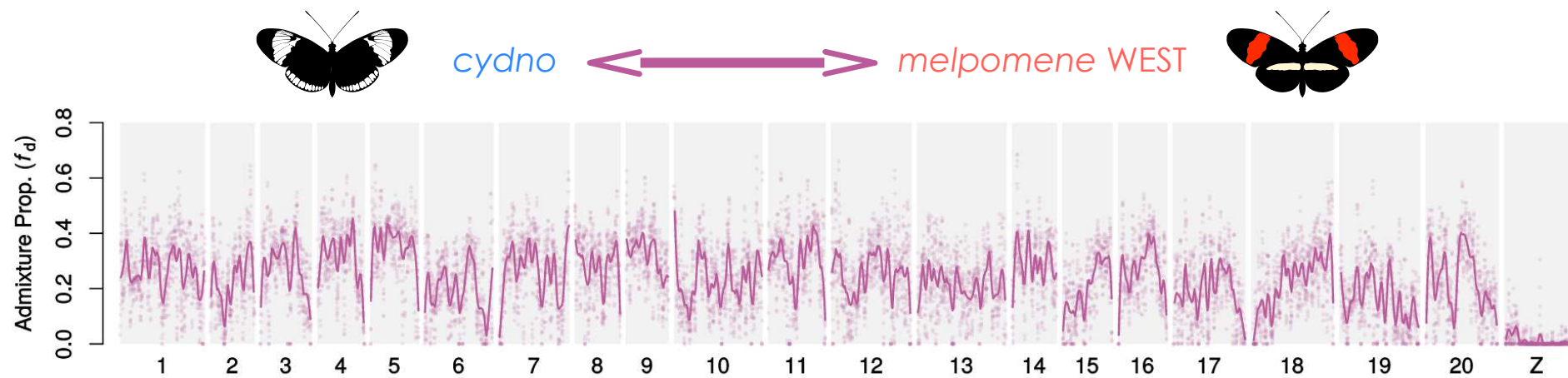
$\hat{f}_d$: estimated admixture proportion

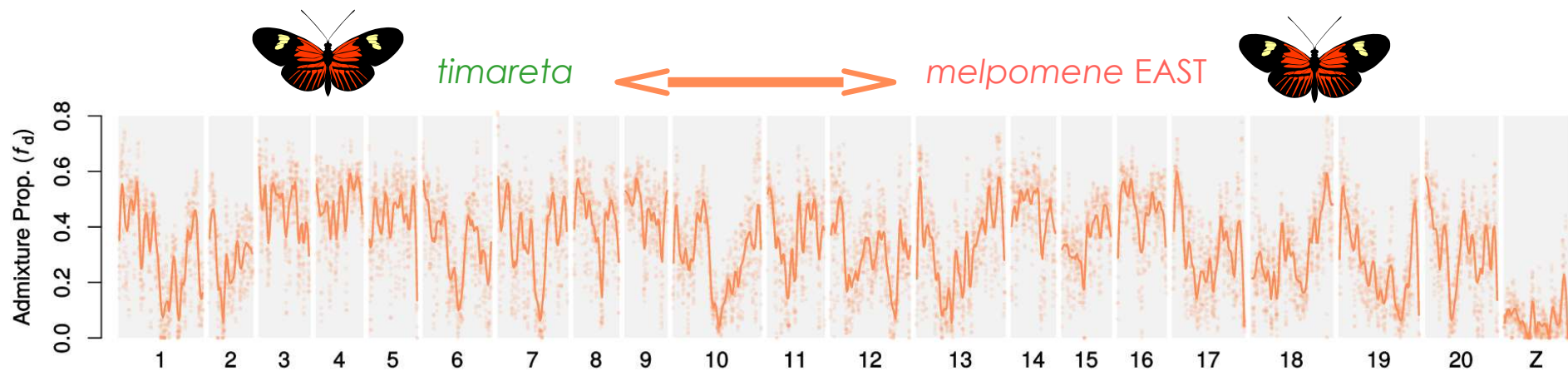
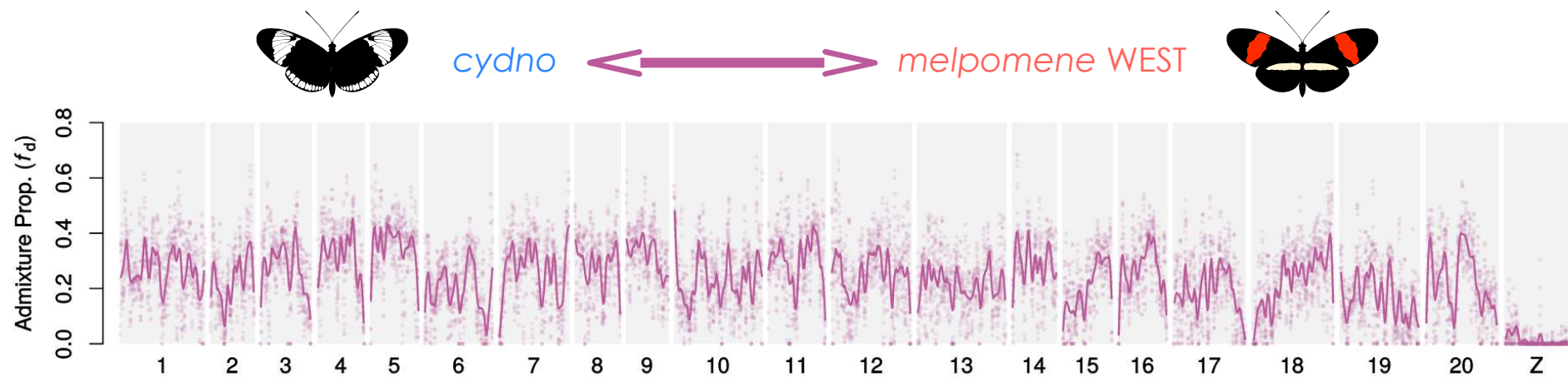










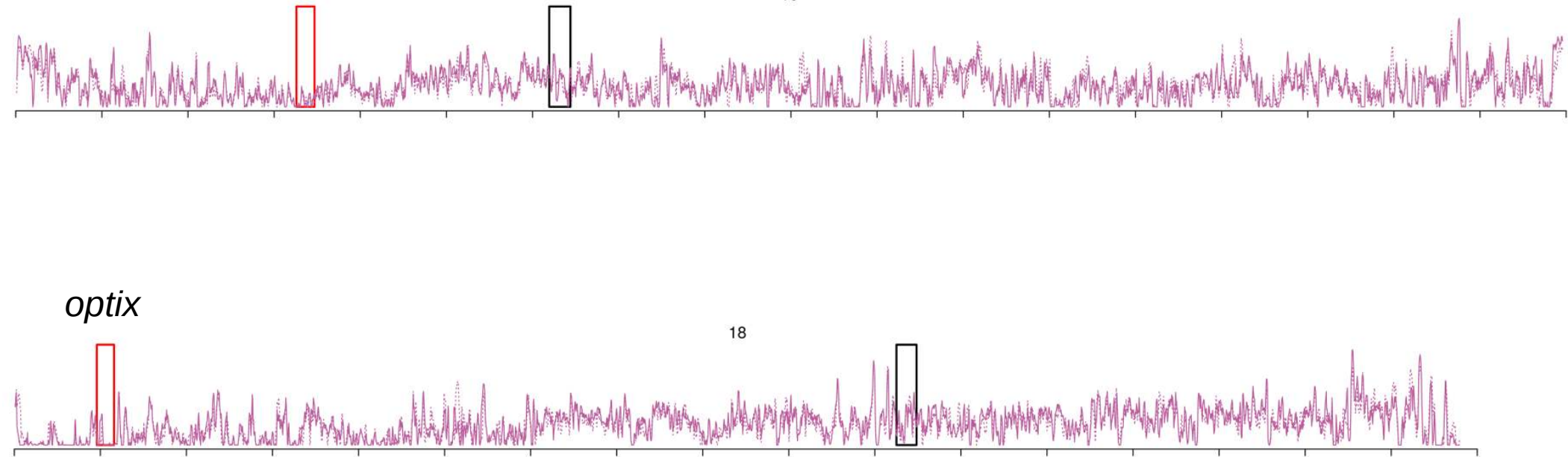


Wnt-A

10

optix

18



Wnt-A

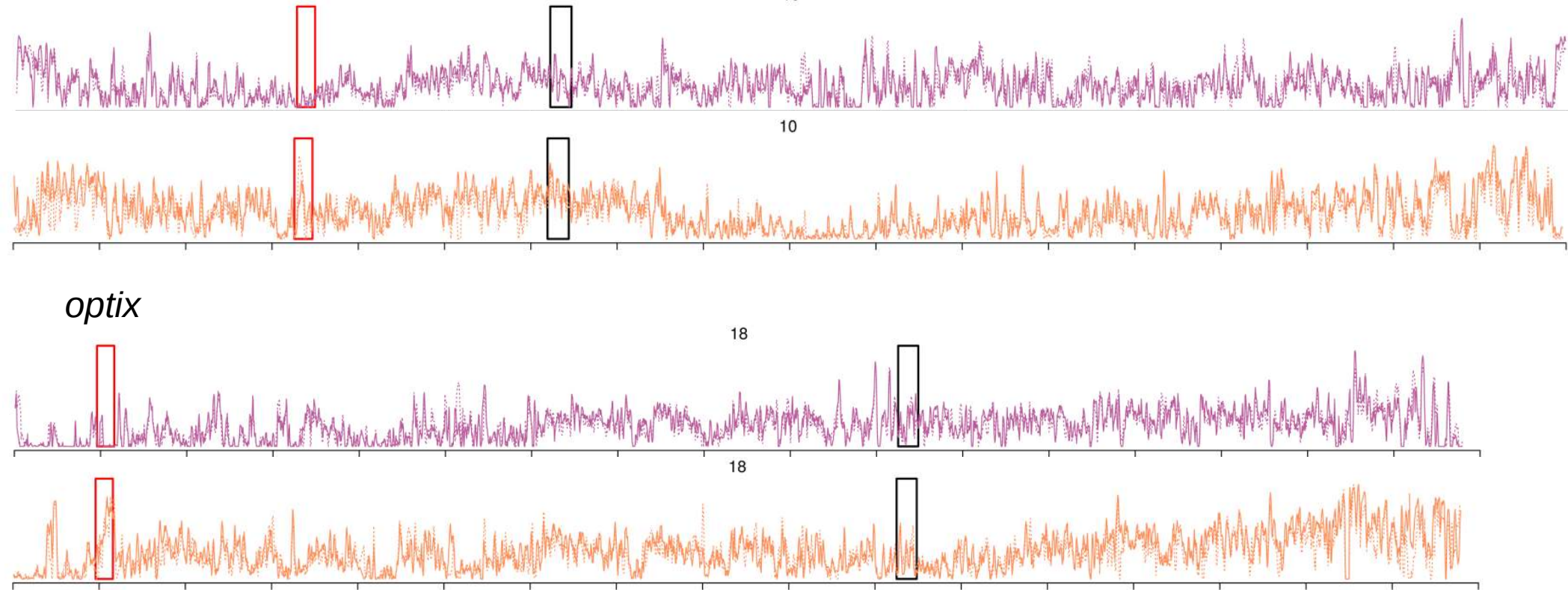
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10

optix

18

18



Wnt-A

10

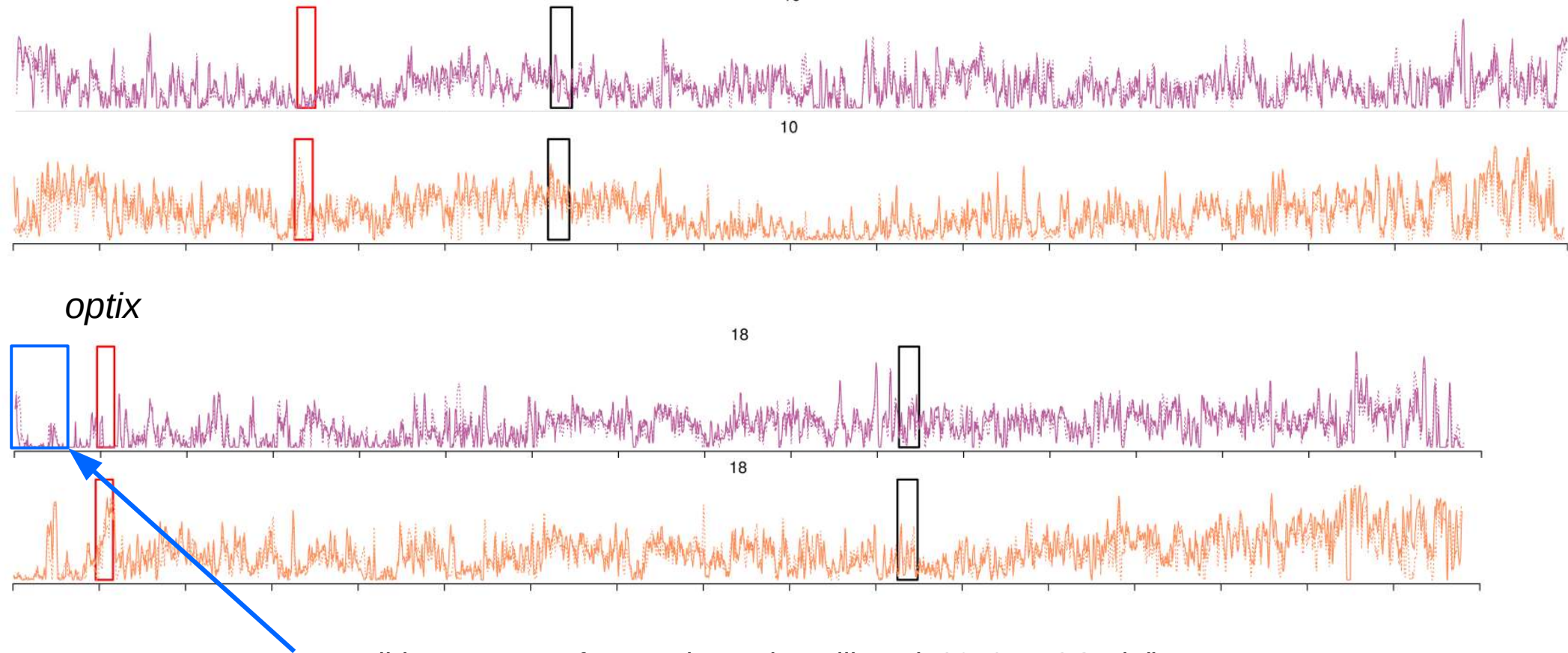
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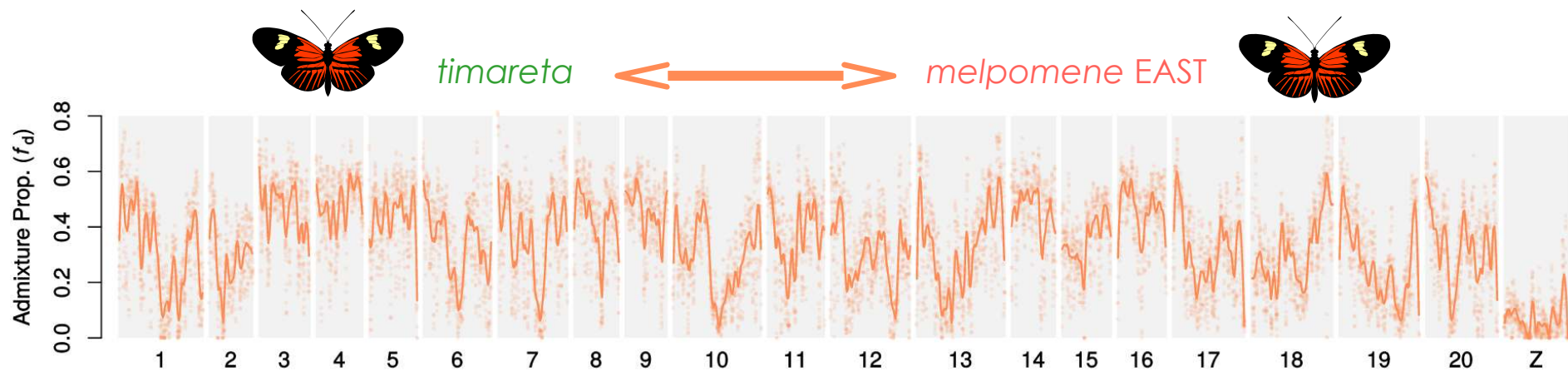
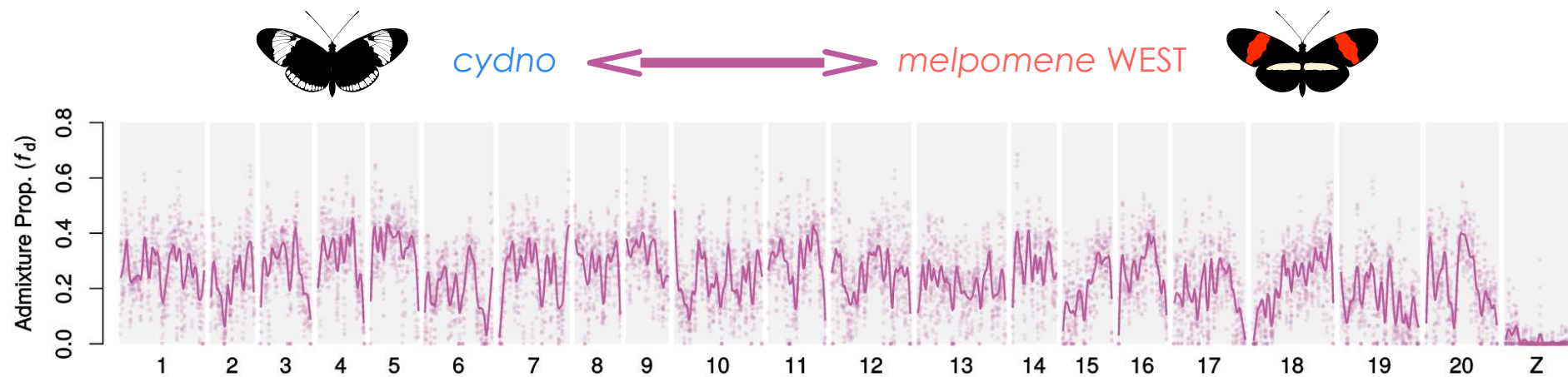
optix

18

18

candidate mate preference locus (Merrill et al. 2019 PLOS Biol)





THE QTN PROGRAM AND THE ALLELES THAT MATTER FOR EVOLUTION: ALL THAT'S GOLD DOES NOT GLITTER

Matthew V. Rockman^{1,2}

¹*Department of Biology and Center for Genomics and Systems Biology, New York University, 12 Waverly Place, New York, NY 10003*

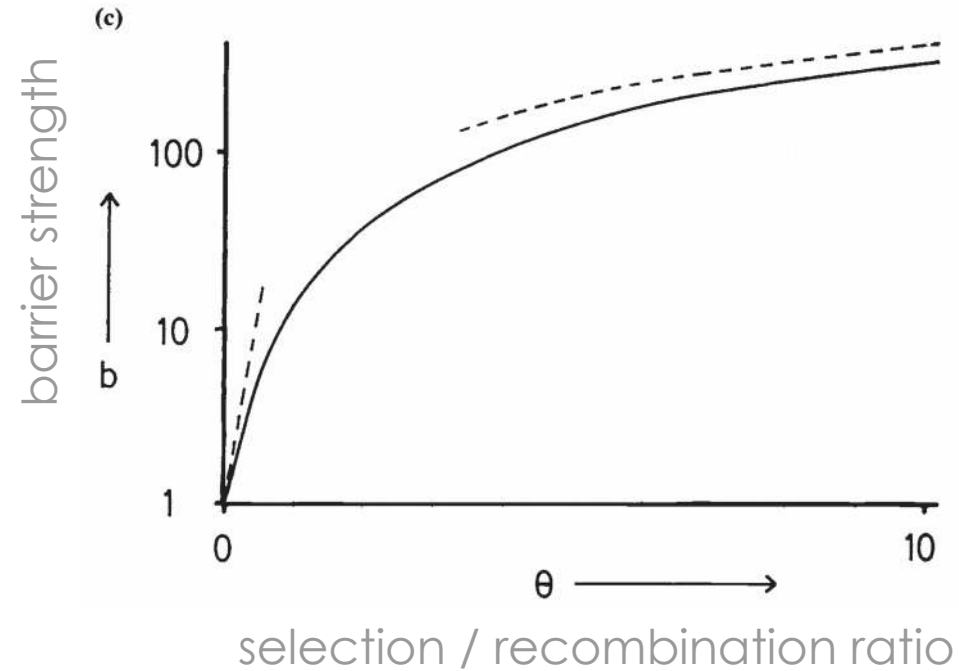
²*E-mail: mrockman@nyu.edu*

Received April 20, 2011

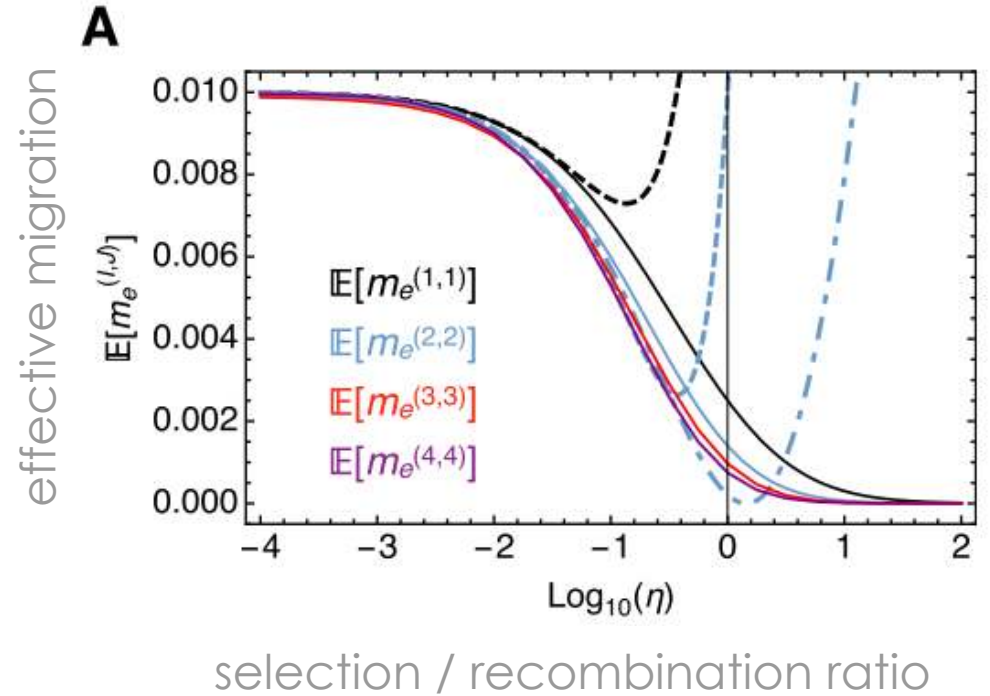
Accepted September 30, 2011

The search for the alleles that matter, the quantitative trait nucleotides (QTNs) that underlie heritable variation within populations and divergence among them, is a popular pursuit. But what is the question to which QTNs are the answer? Although their pursuit is often invoked as a means of addressing the molecular basis of phenotypic evolution or of estimating the roles of evolutionary forces, the QTNs that are accessible to experimentalists, QTNs of relatively large effect, may be uninformative about these issues if large-effect variants are unrepresentative of the alleles that matter. Although 20th century evolutionary biology generally viewed large-effect variants as atypical, the field has recently undergone a quiet realignment toward a view of readily discoverable large-effect alleles as the primary molecular substrates for evolution. I argue that neither theory nor data justify this realignment. Models and experimental findings covering broad swaths of evolutionary phenomena suggest that evolution often acts via large numbers of small-effect polygenes, individually undetectable. Moreover, these small-effect variants are different in kind, at the molecular level, from the large-effect alleles accessible to experimentalists. Although discoverable QTNs address some fundamental evolutionary questions, they are essentially misleading about many others.

Recombination predicts barrier strength

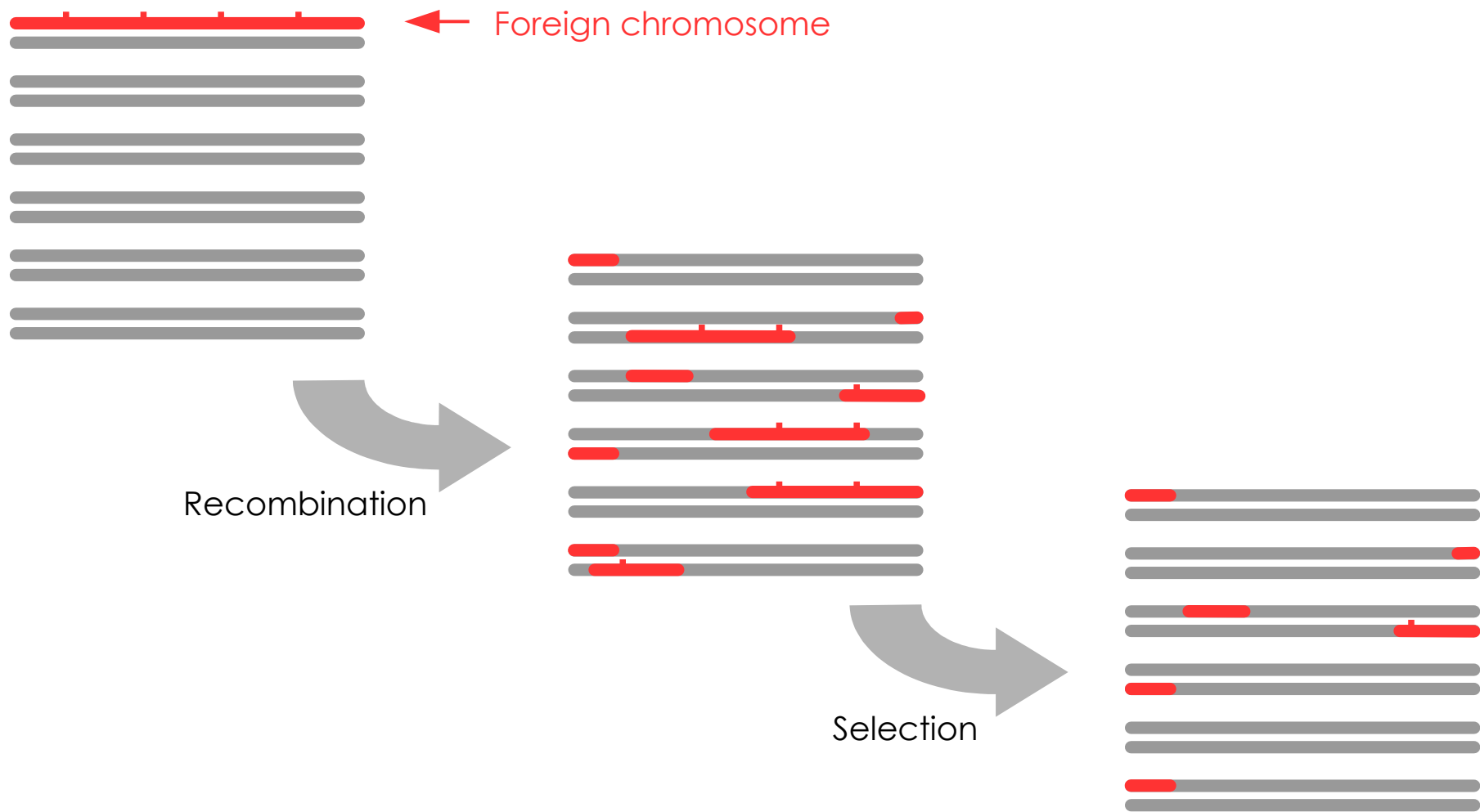


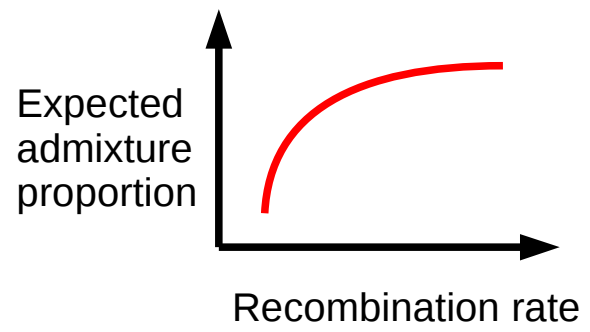
Barton & Bengtsson 1986

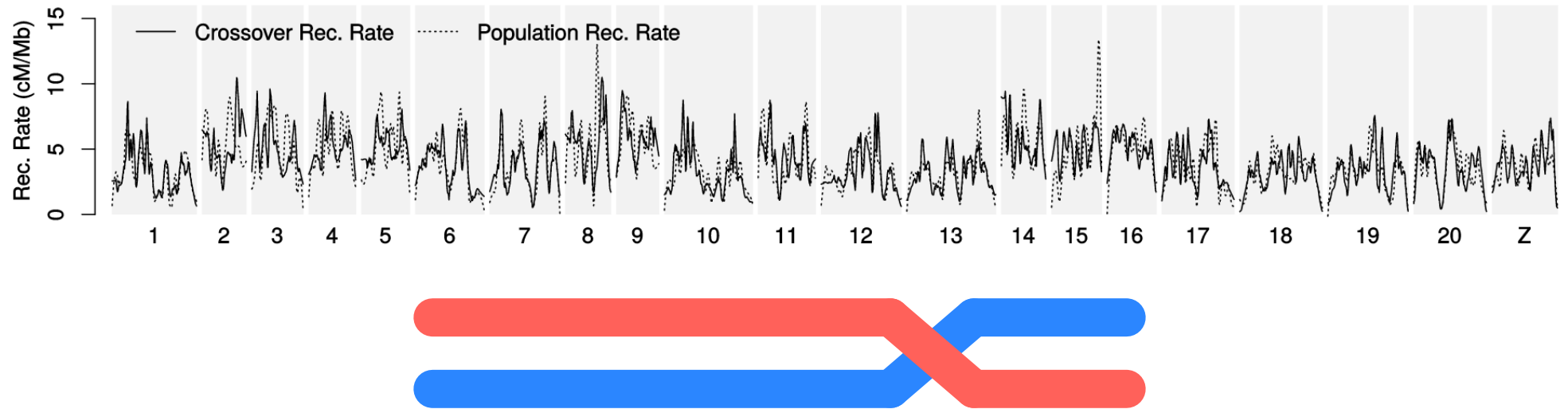
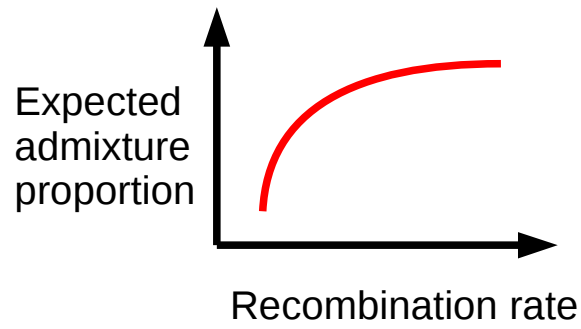


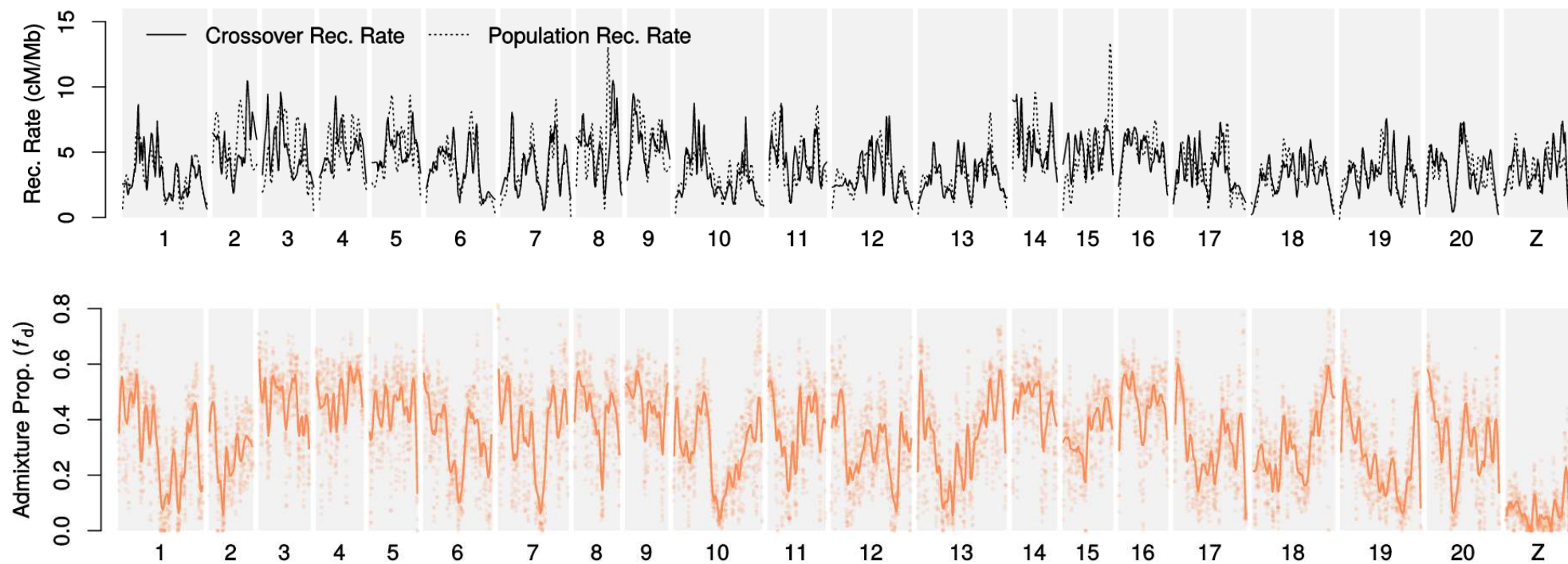
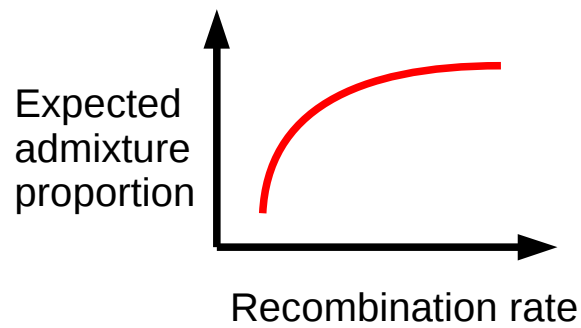
Aeschbacher et al. 2017

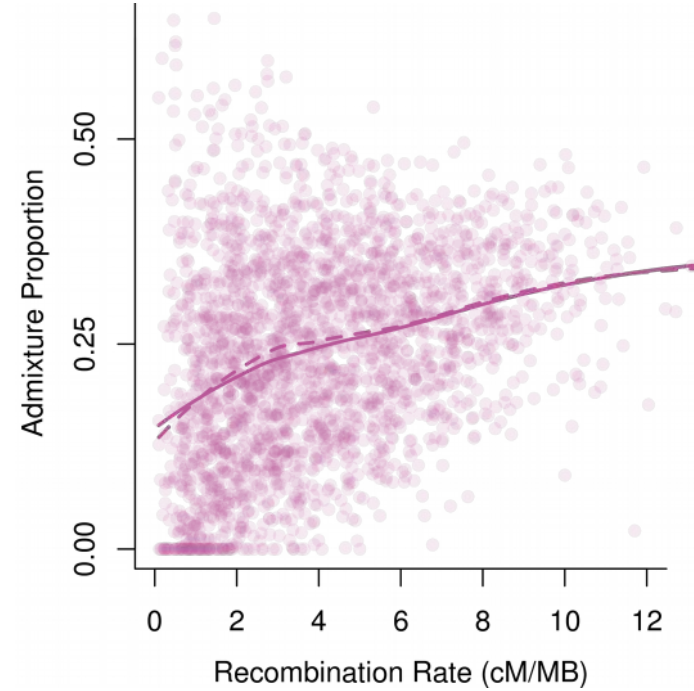
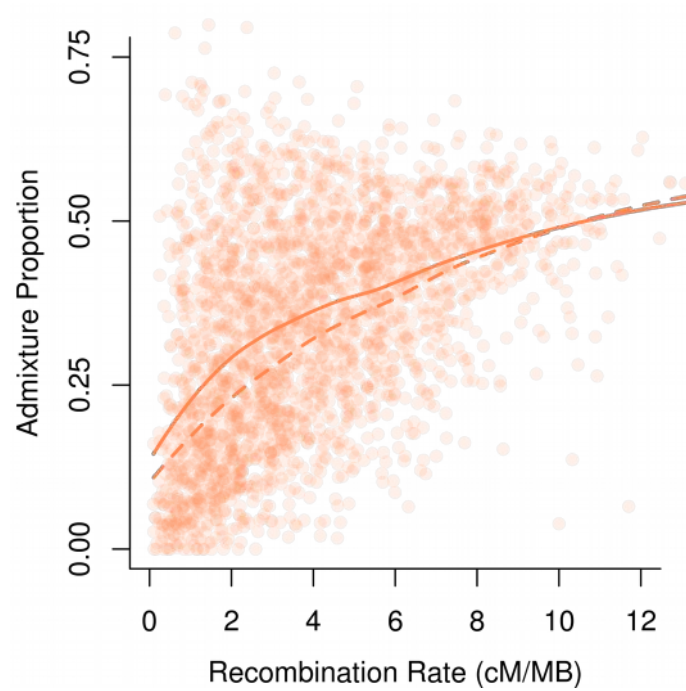
A simple simulation example





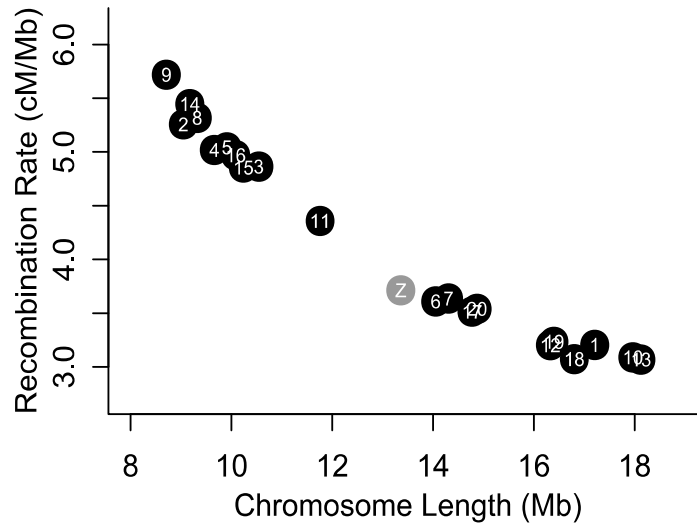
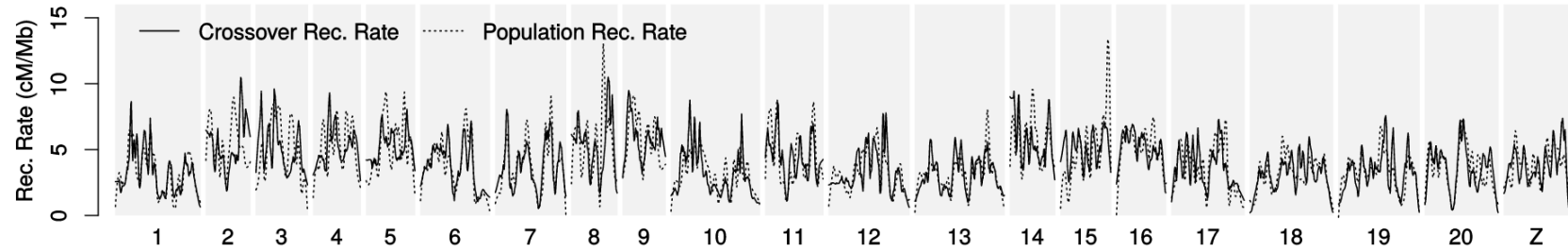




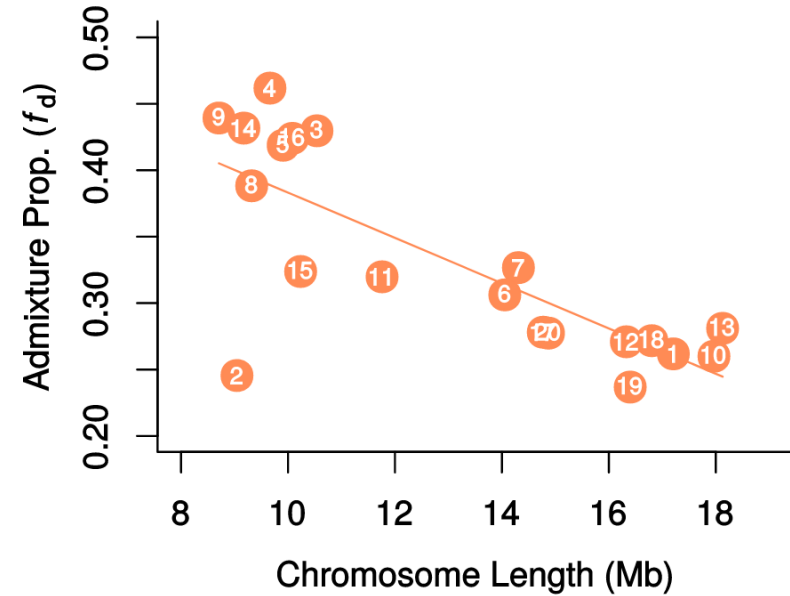
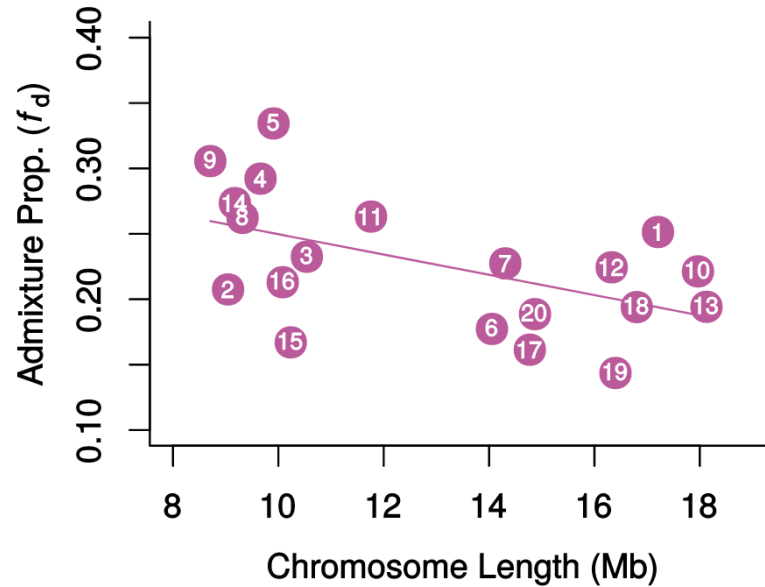


The species barrier is more porous where recombination rates are higher

Recombination also varies at the chromosome scale



Longer chromosomes form stronger barriers

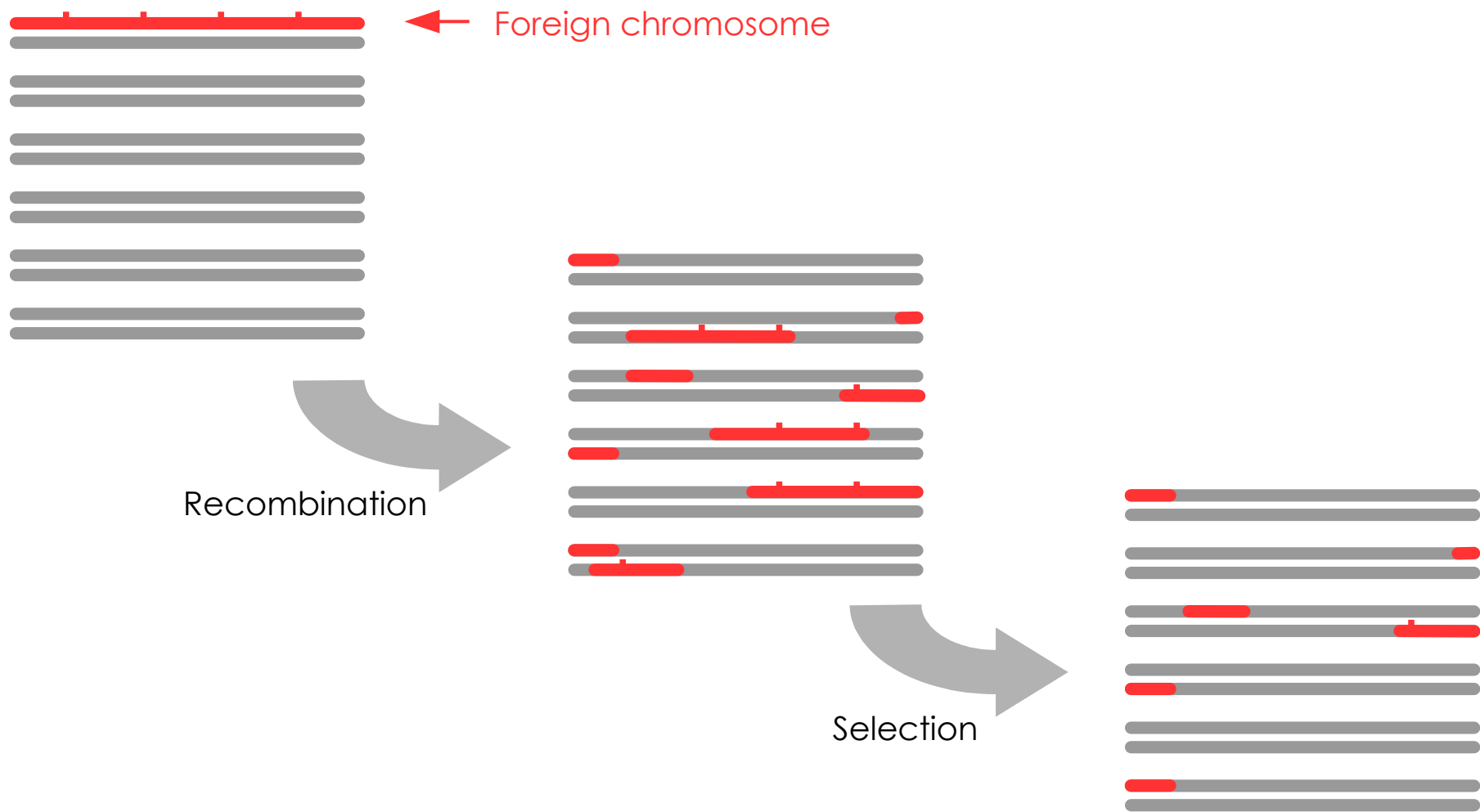




10 Chromosome
fusions in 6 million
years

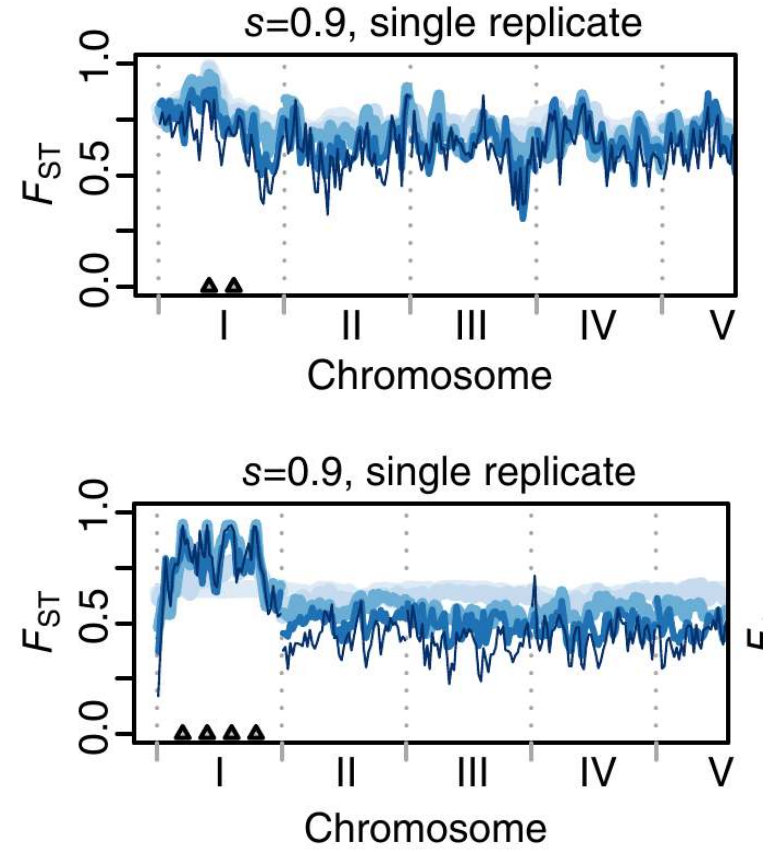
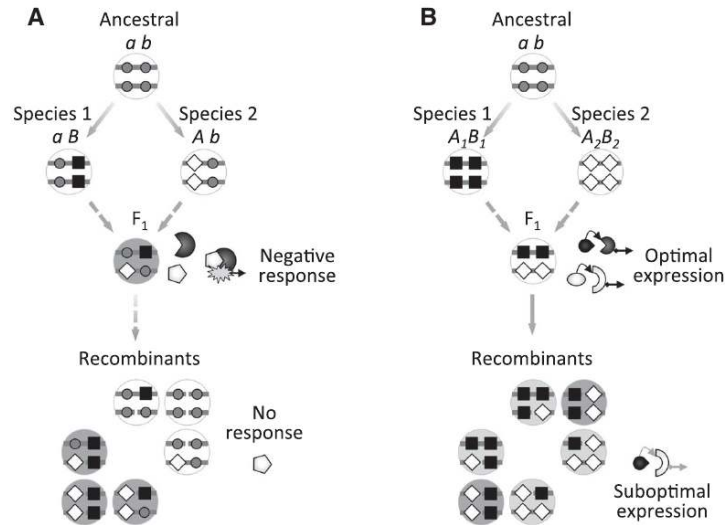


But what about incompatibilities?



The genetic architecture of hybrid incompatibilities and their effect on barriers to introgression in secondary contact

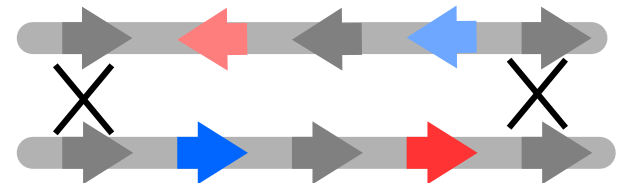
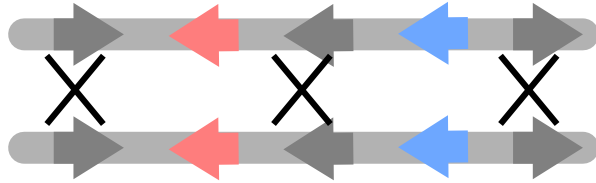
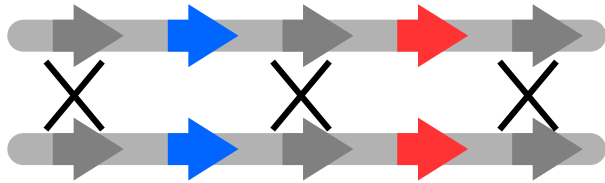
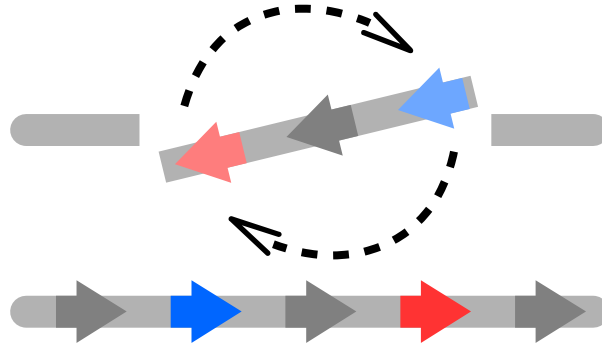
Dorothea Lindtke^{1,2,3} and C. Alex Buerkle¹

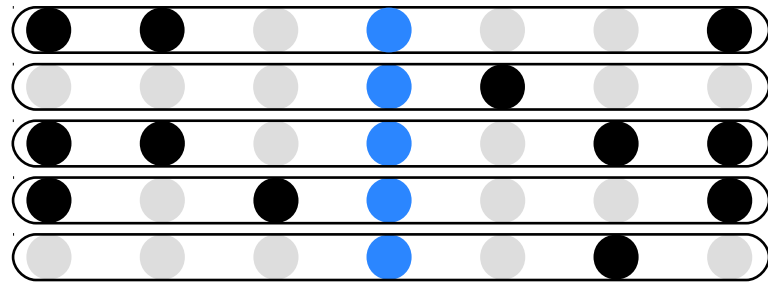
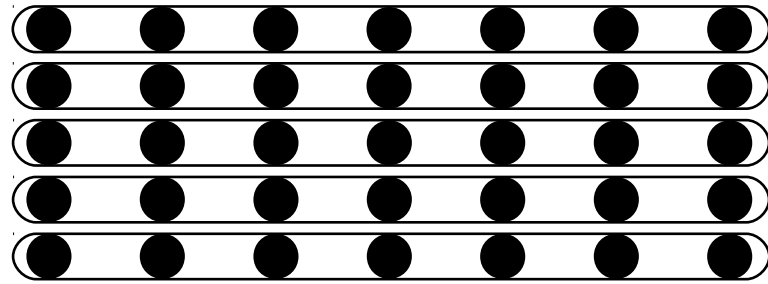


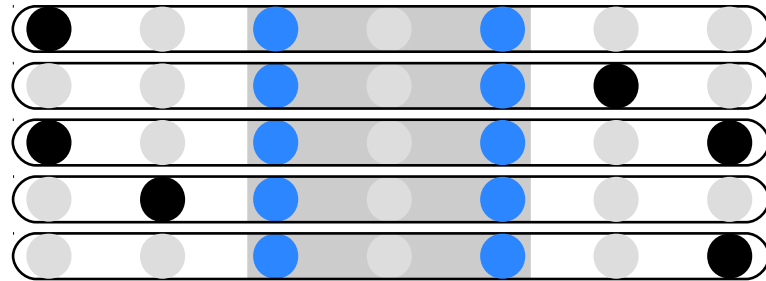
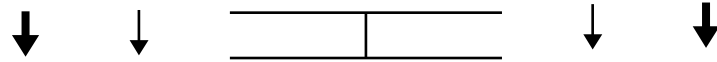
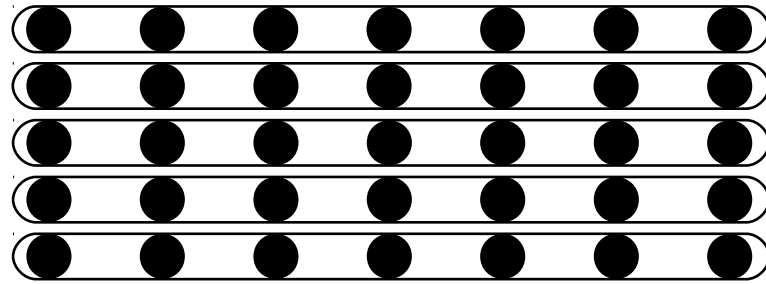
Sometimes gold does glitter

A pleasing ending

Localised recombination suppression

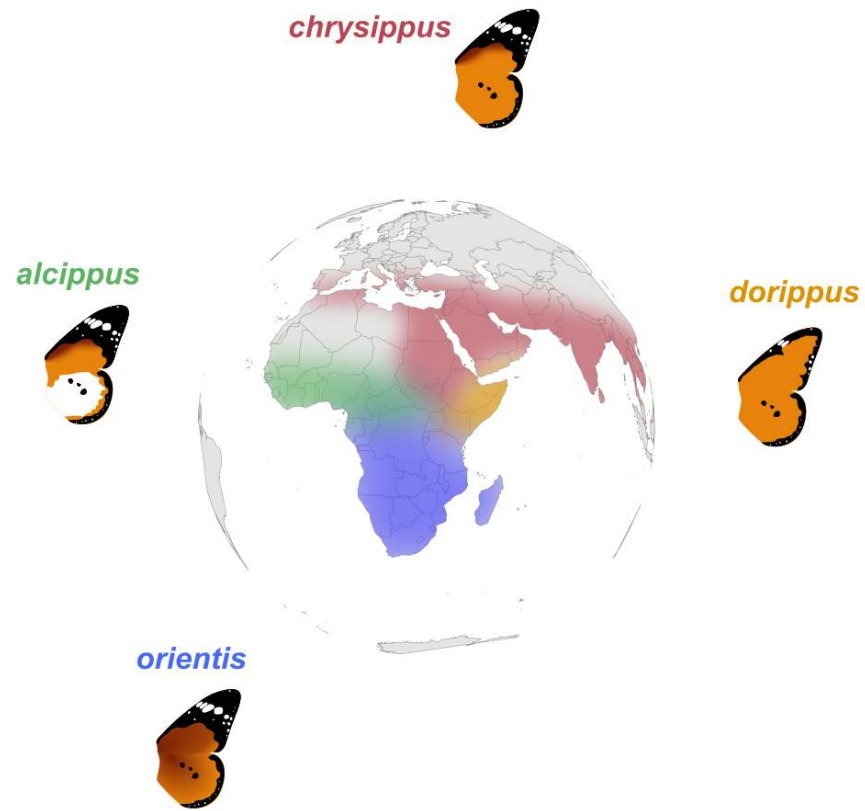






Danaus chrysippus







EASTERN DRC
| POPULATIONS.

chrysippus



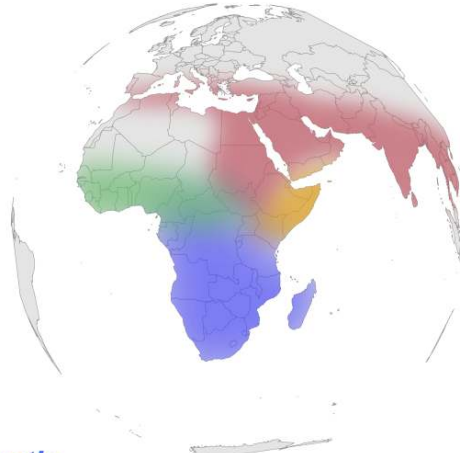
alcippus



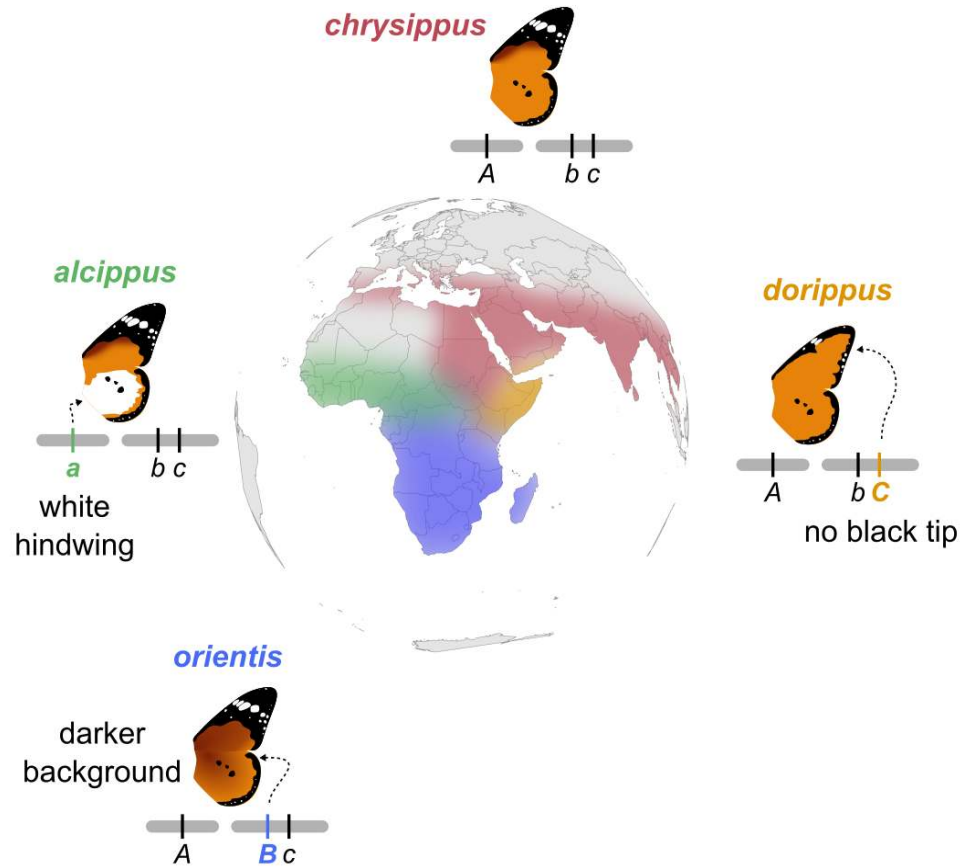
dorippus



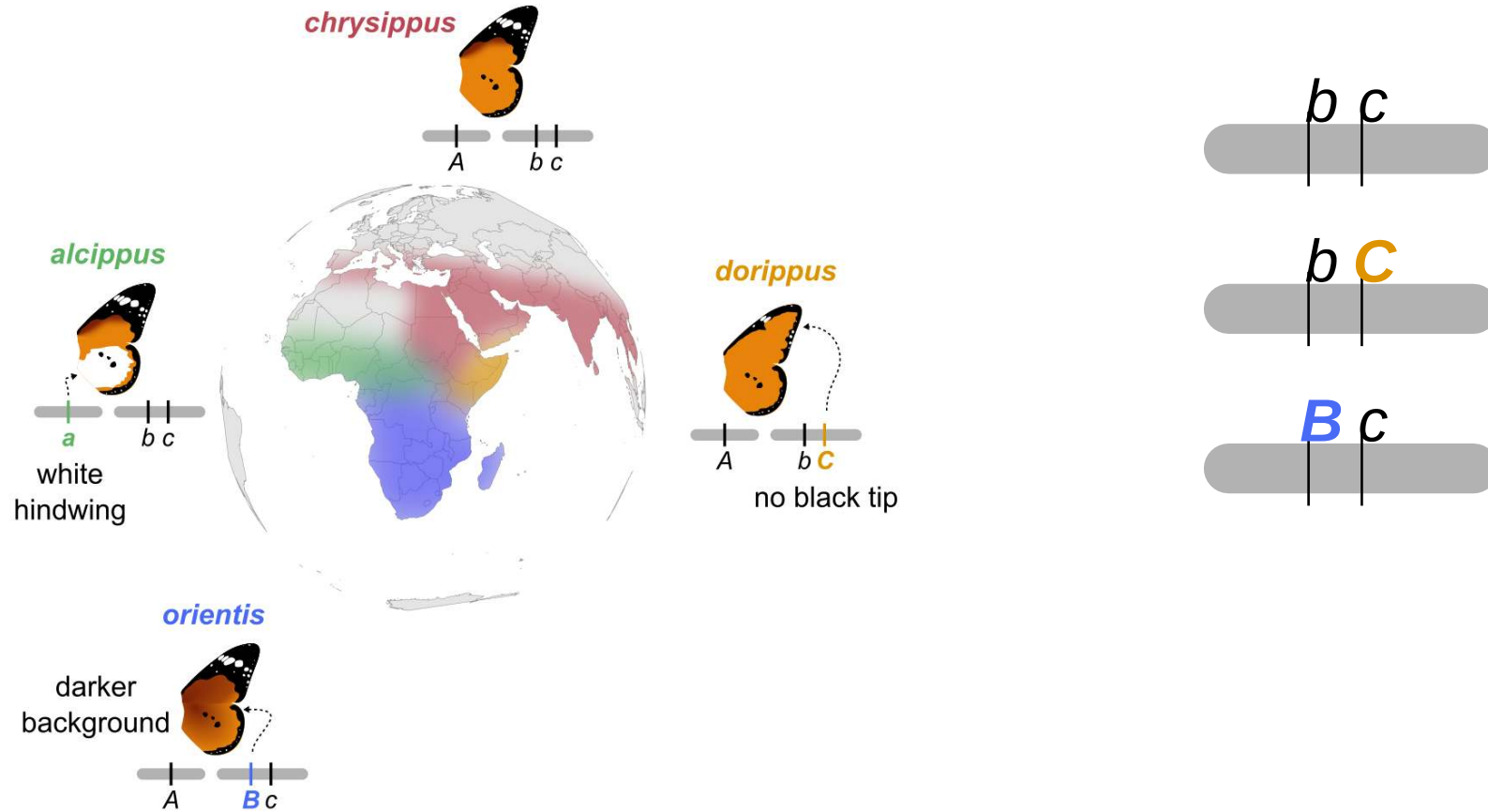
orientis

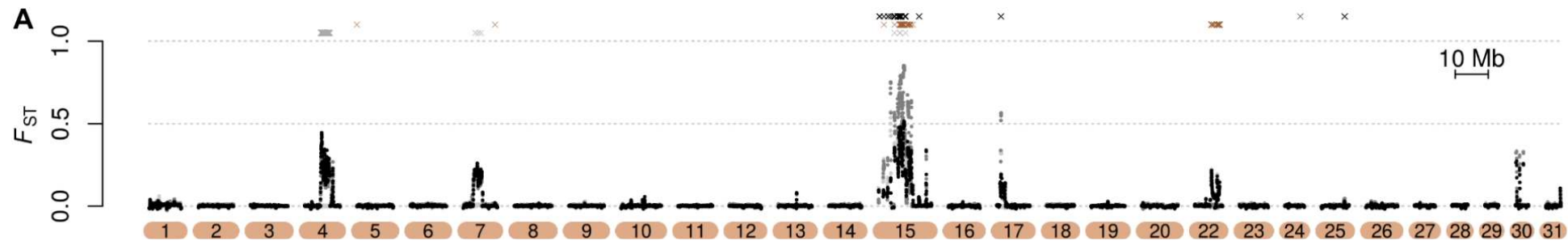


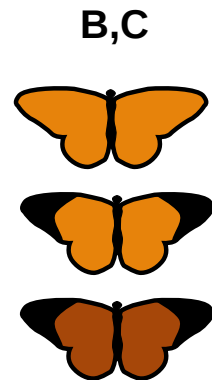
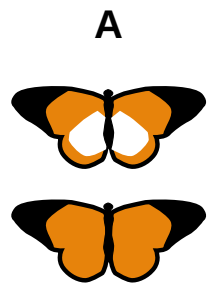
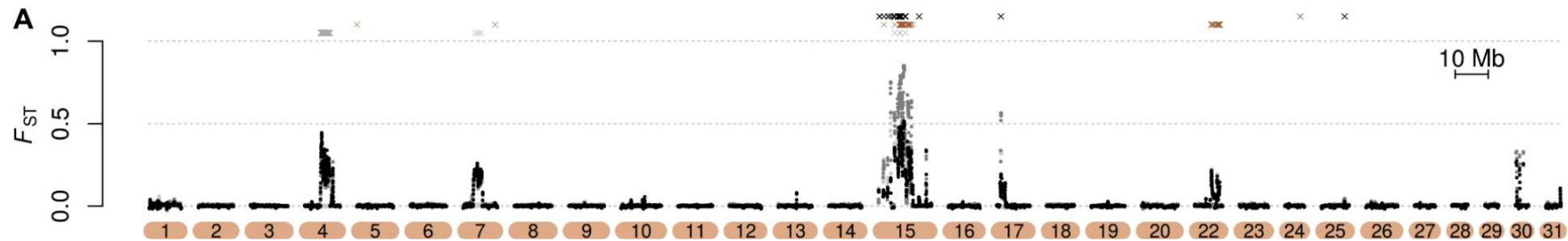
Large effect genes control differences

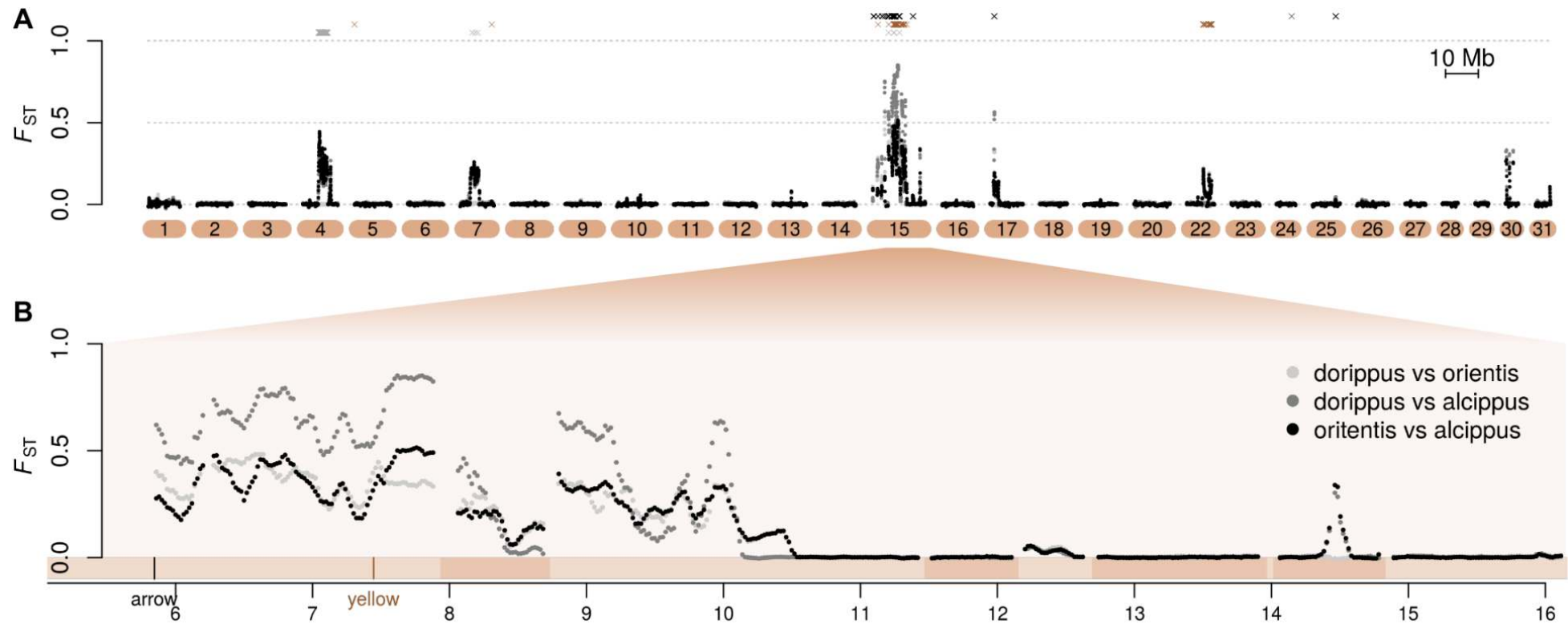


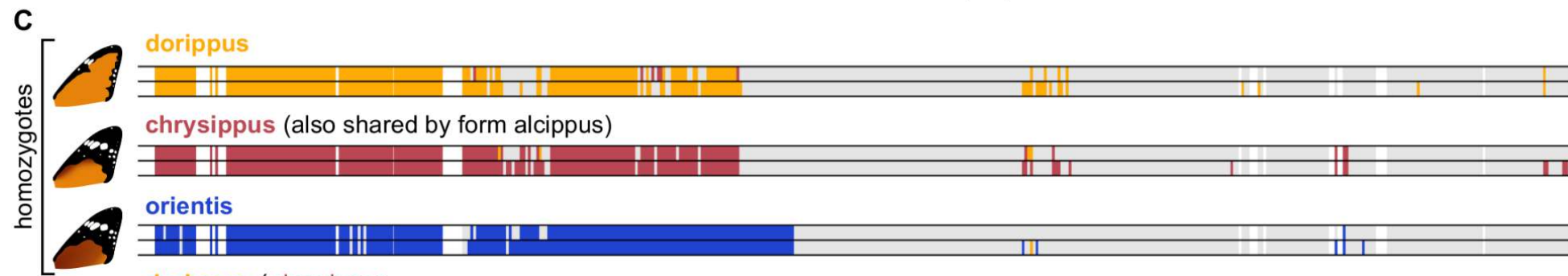
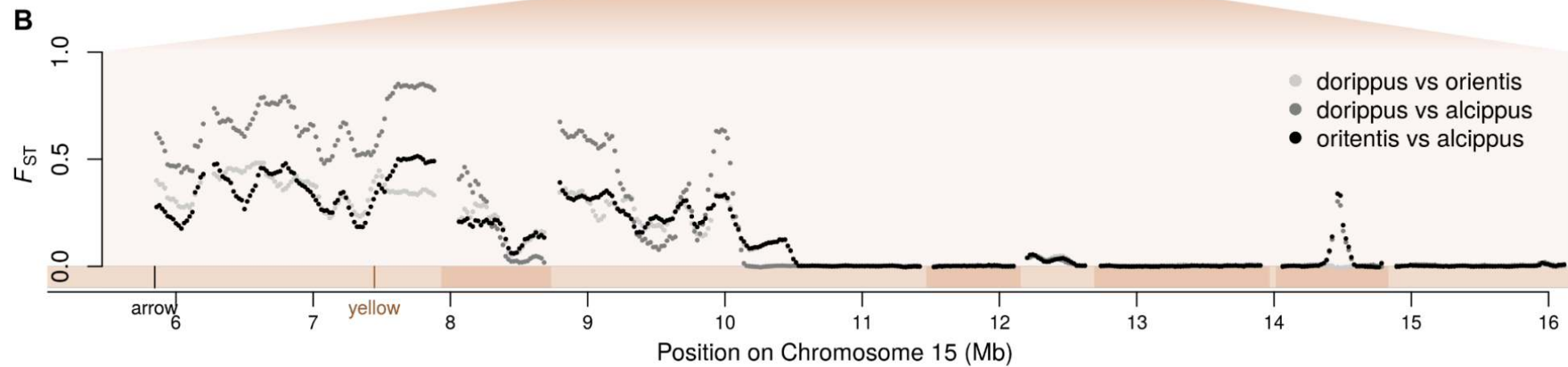
A supergene?

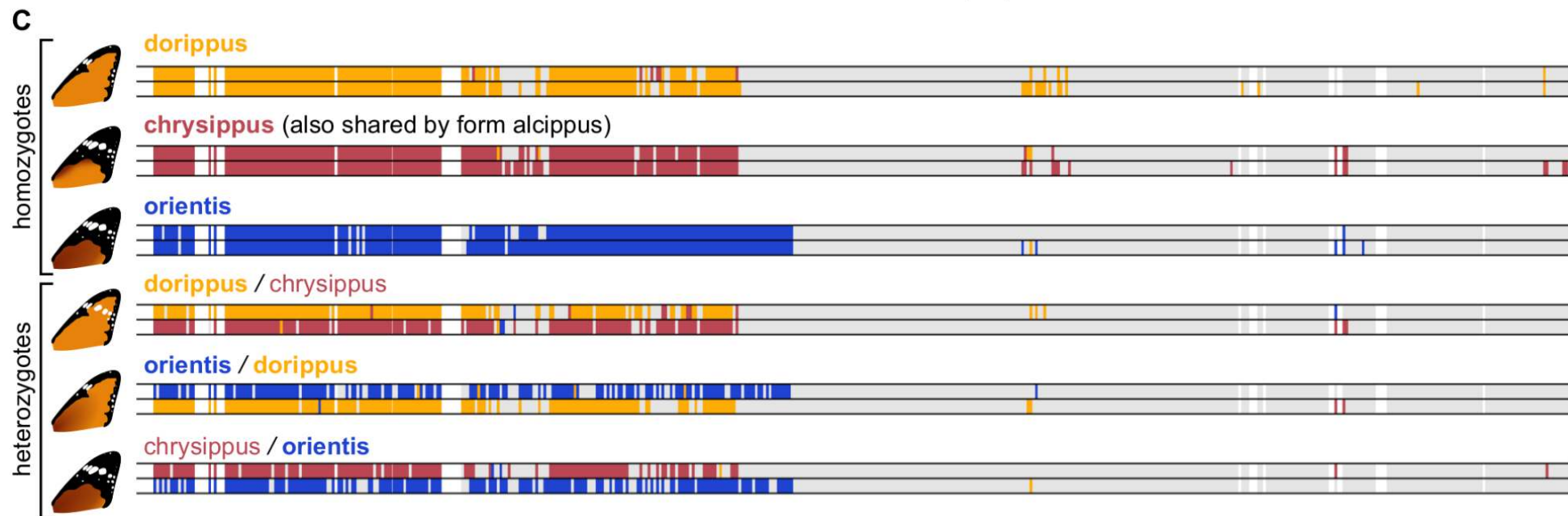
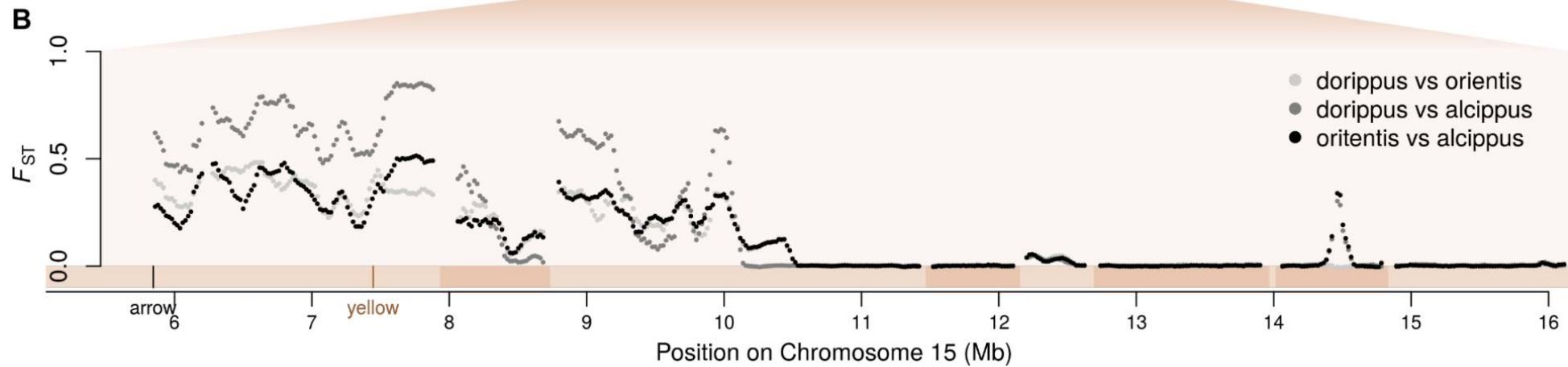




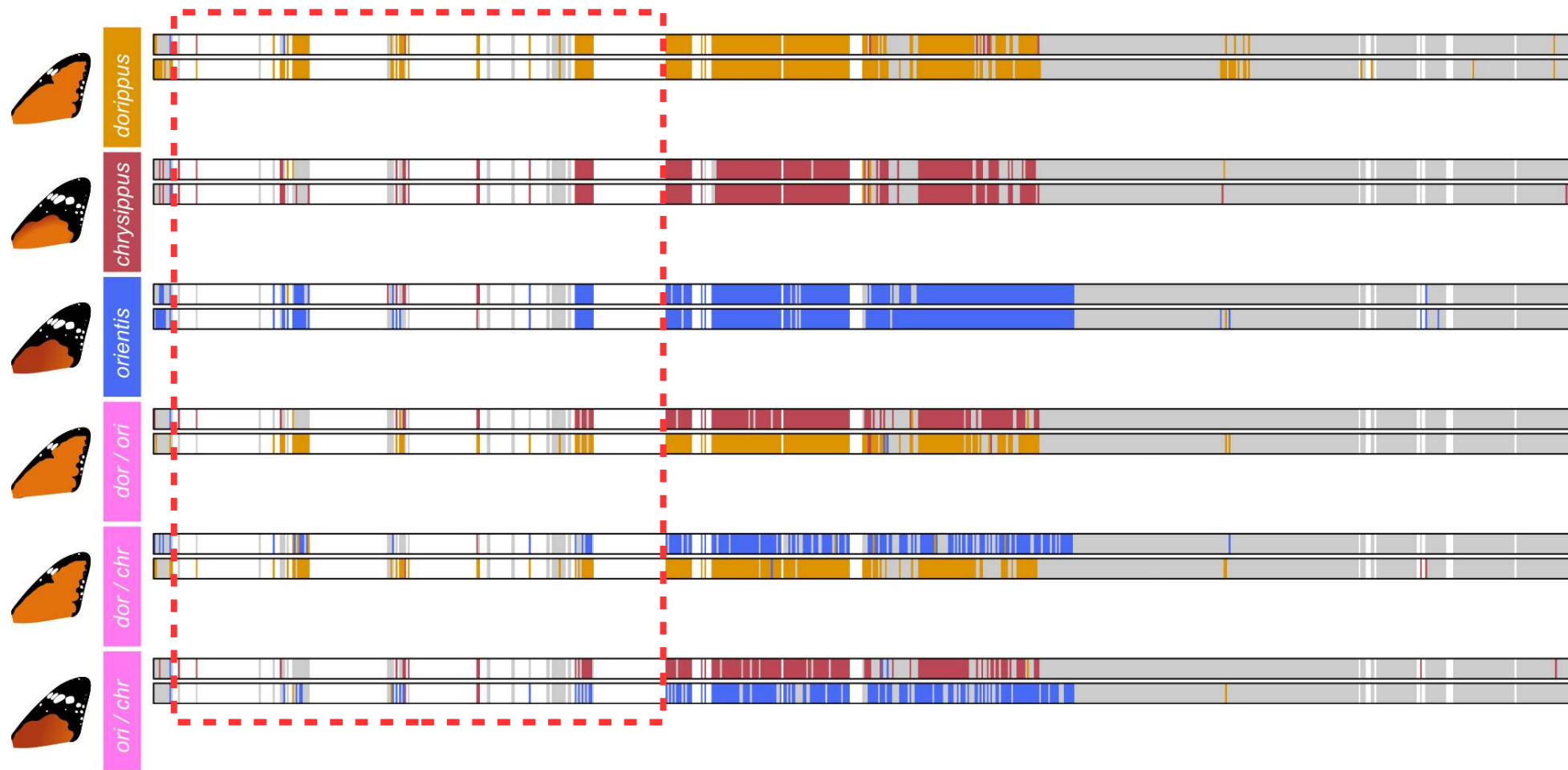




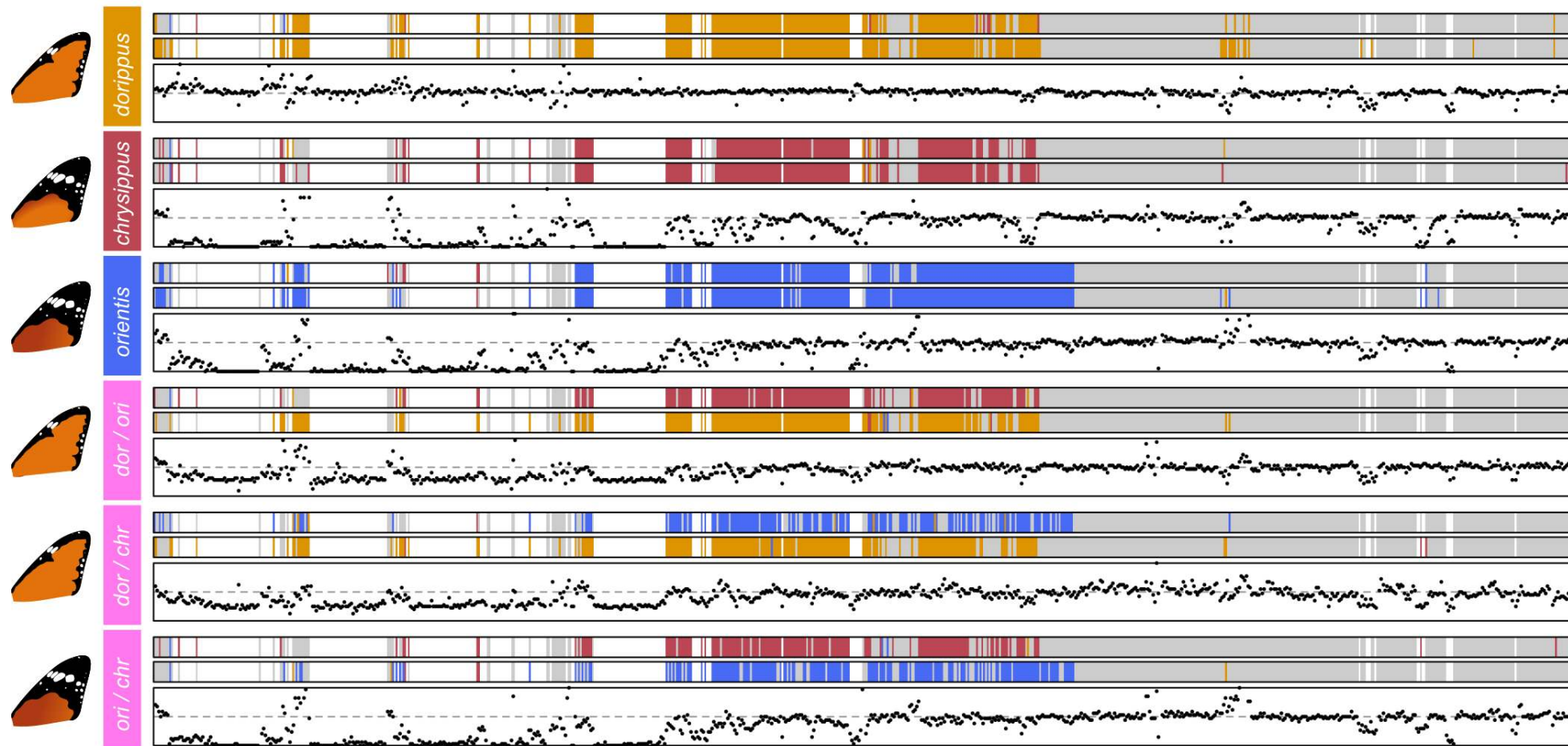




Lots of sequencing “gaps” on one end...



Missing sequences in *chrysippus* and *orientis* alleles



Tandem duplications specific to the *dorippus* allele

