

Complex adaptation in *Zea*

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acknowledgements



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Paul Bilinski



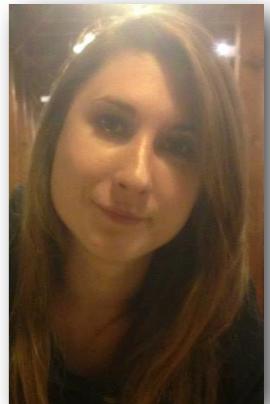
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(KWS) (Iowa State)



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(U Minnesota)

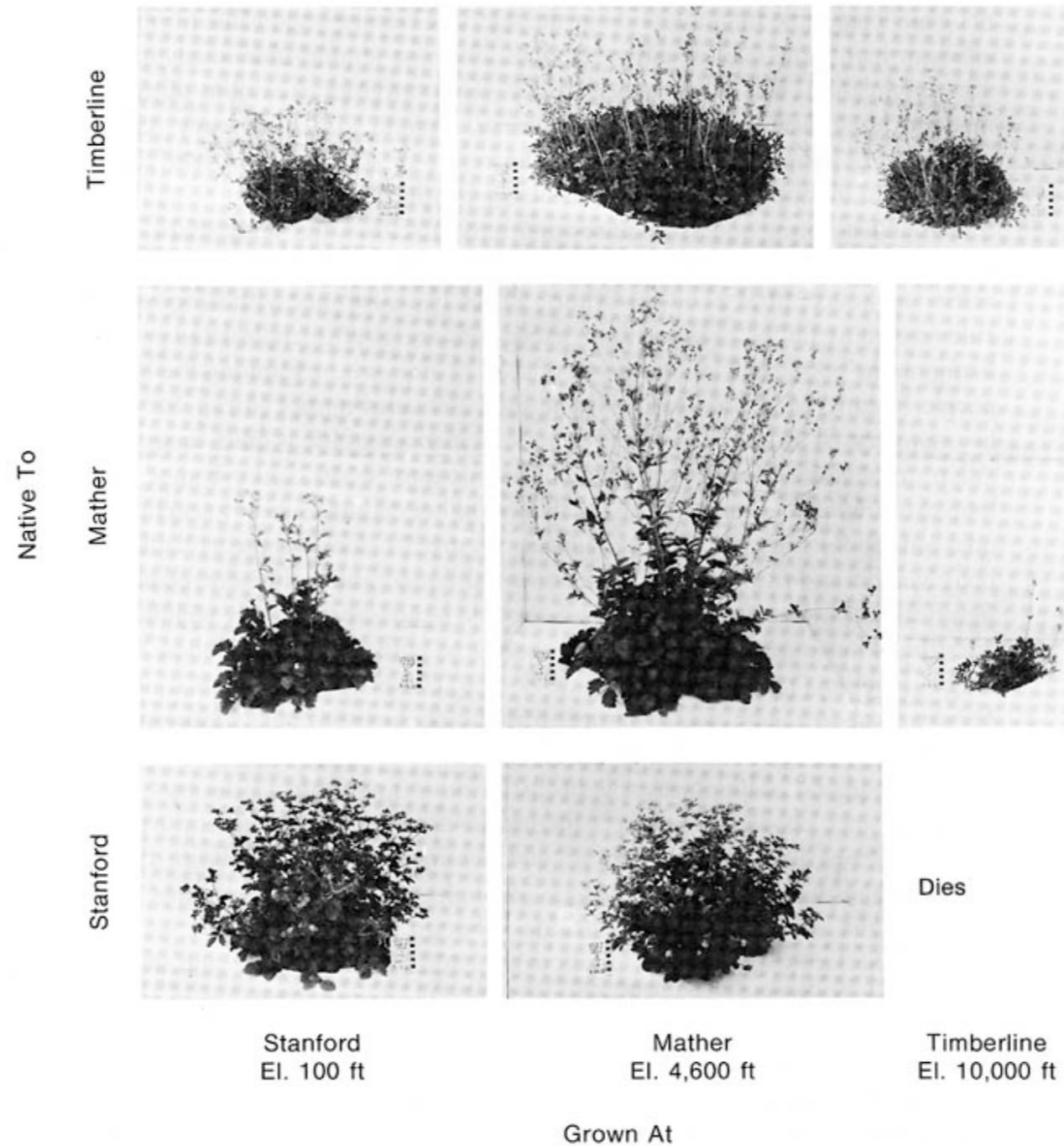


Vince Buffalo



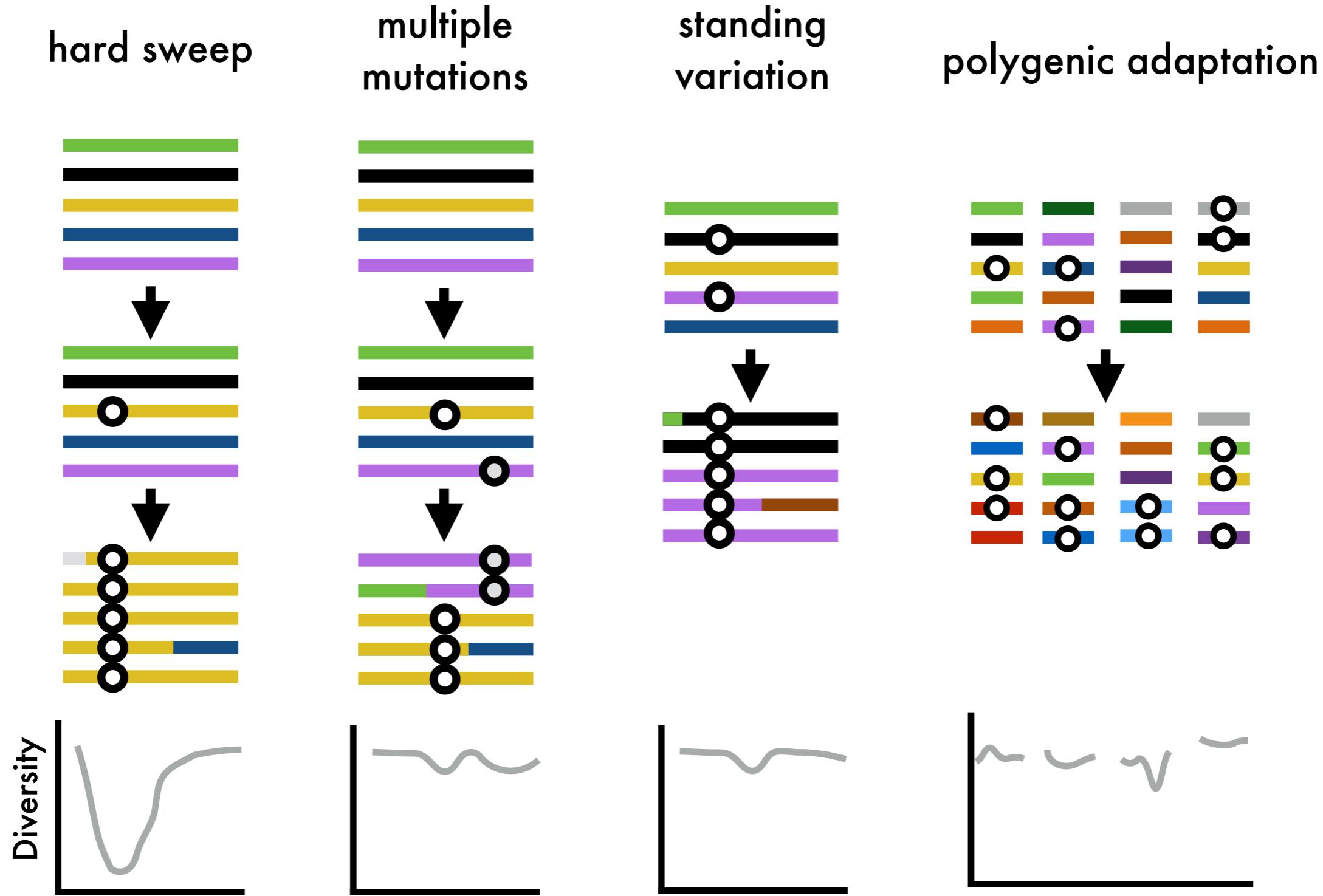
Anne Lorant

how do plants adapt?

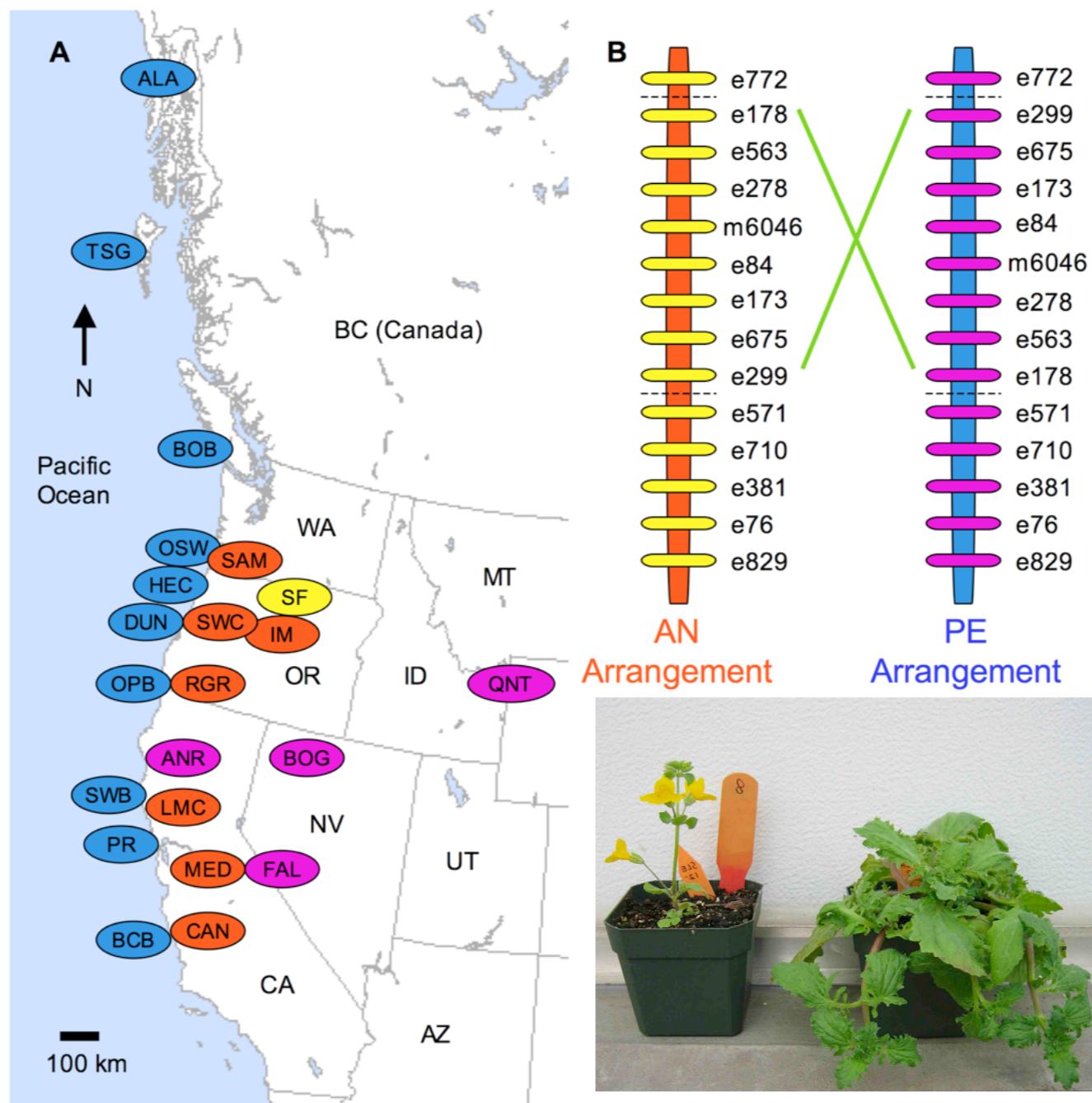


Clausen, Keck, and Hiesey 1940

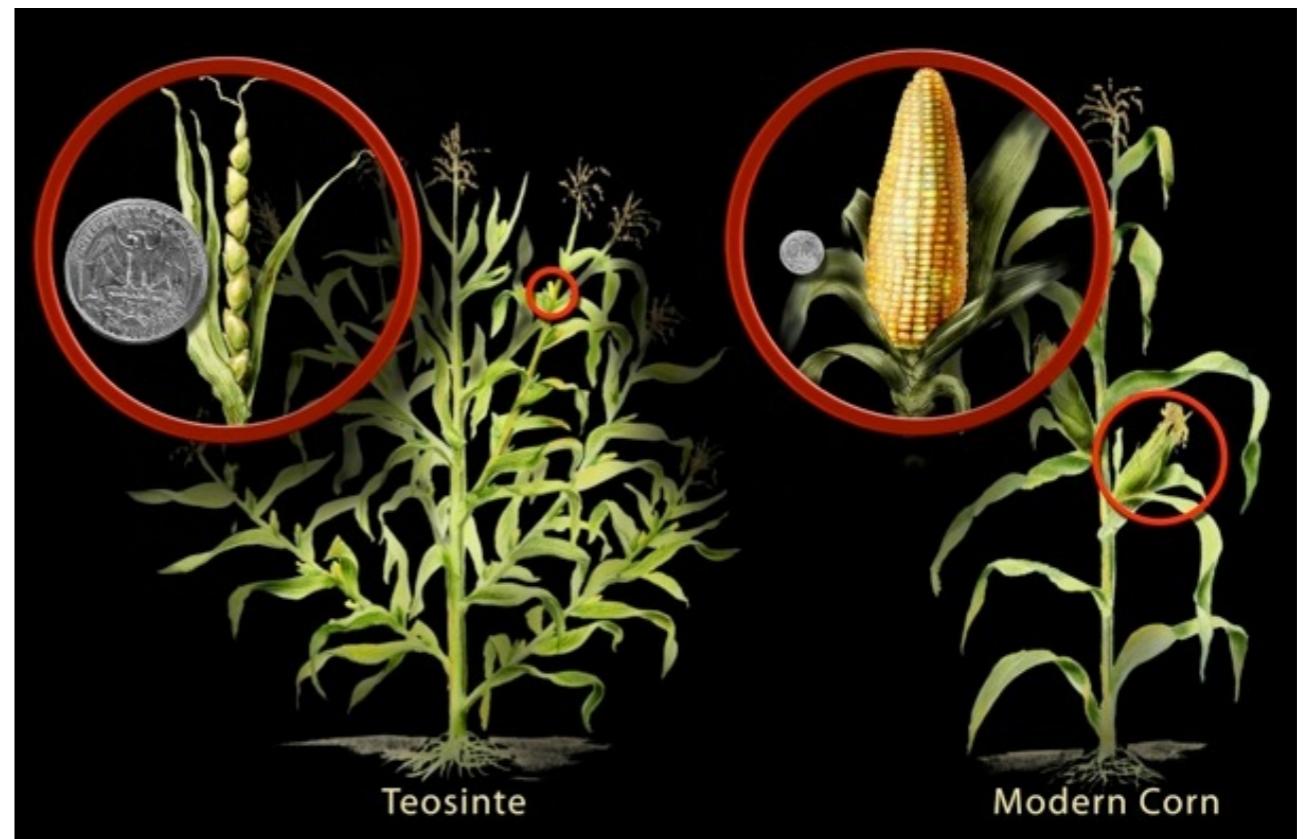
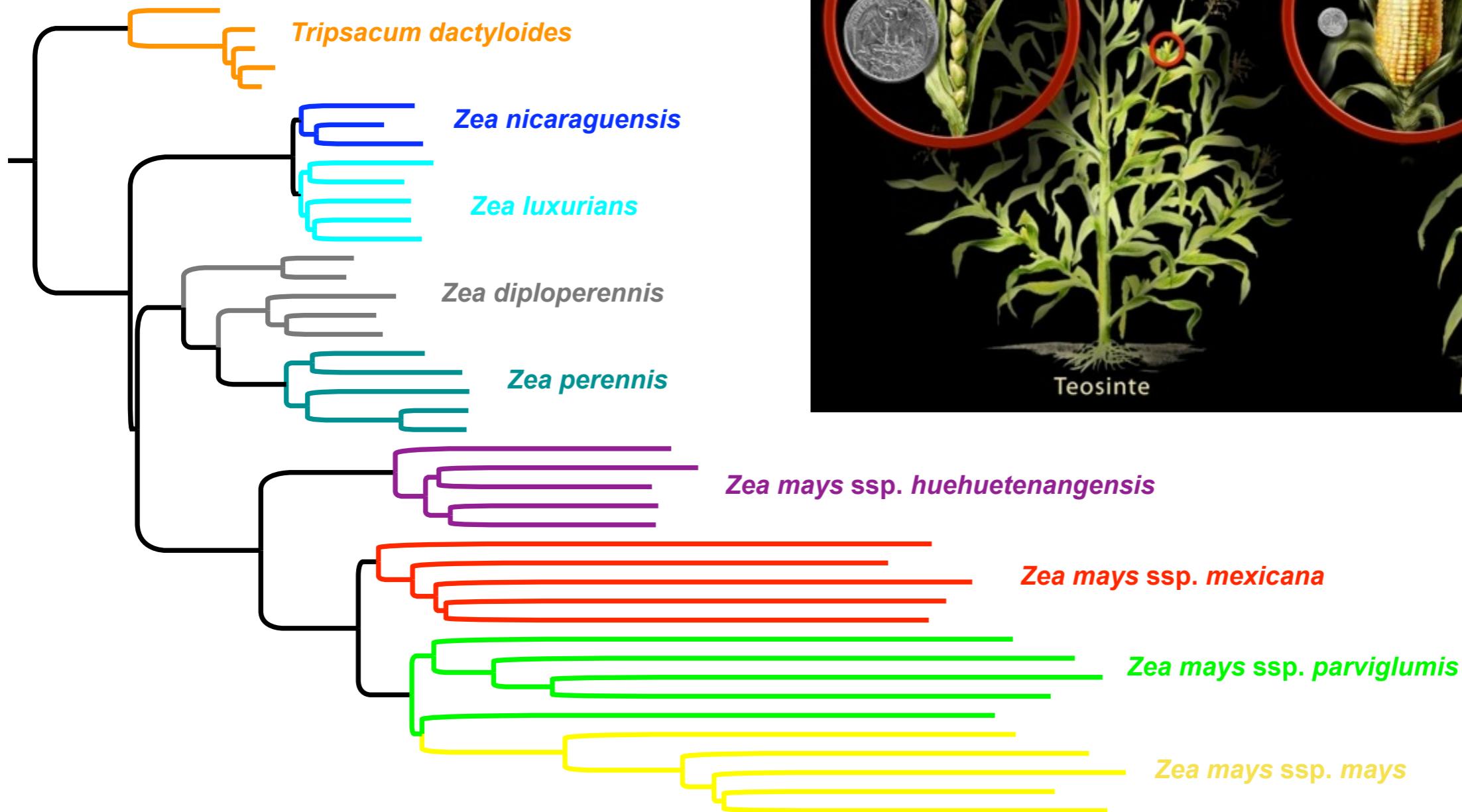
what evolutionary processes are involved?



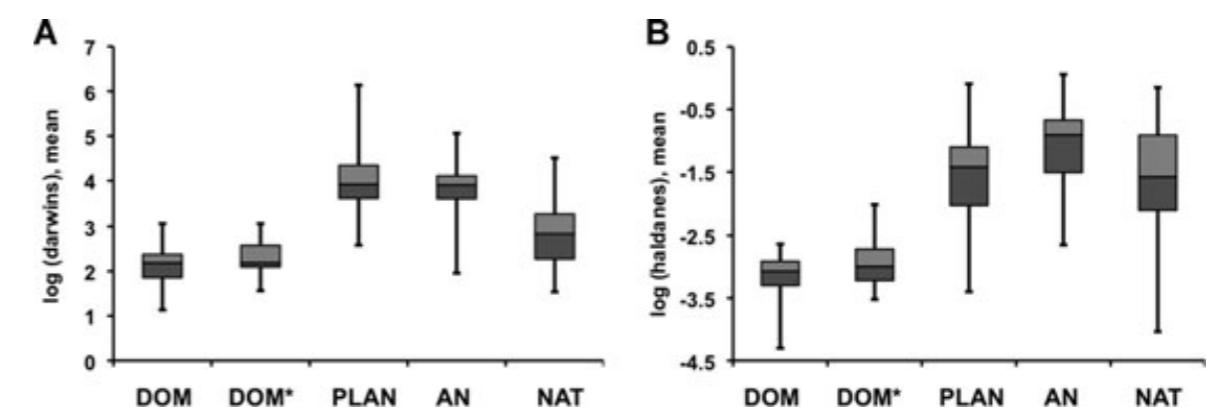
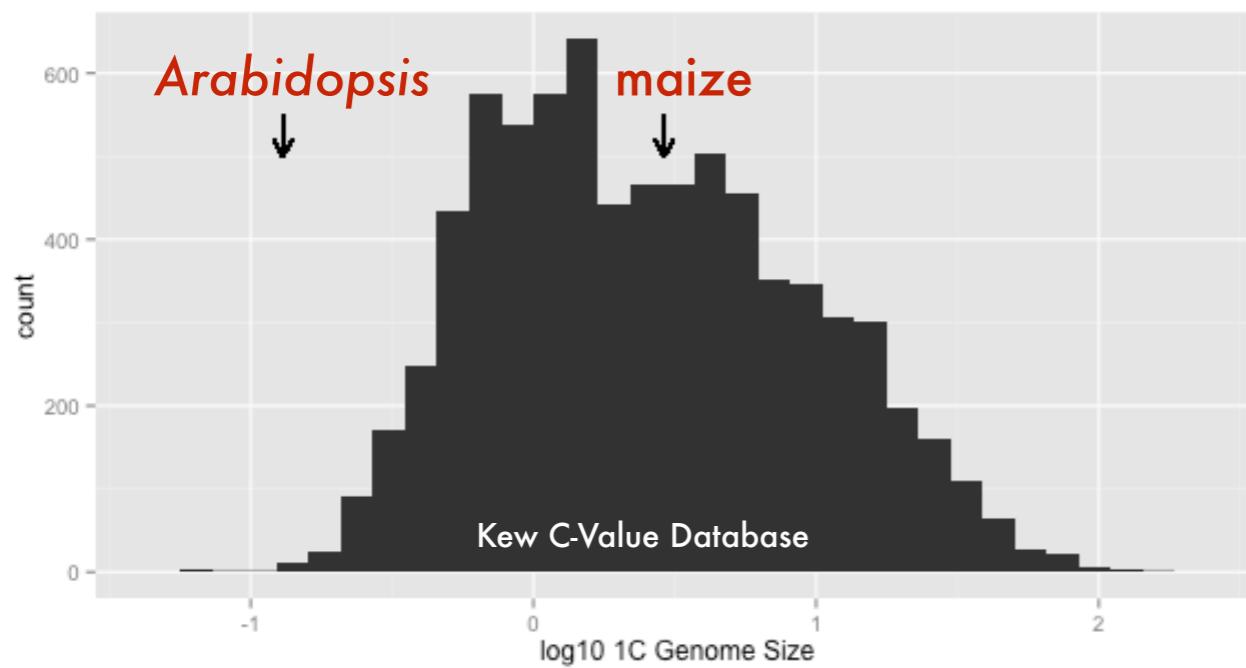
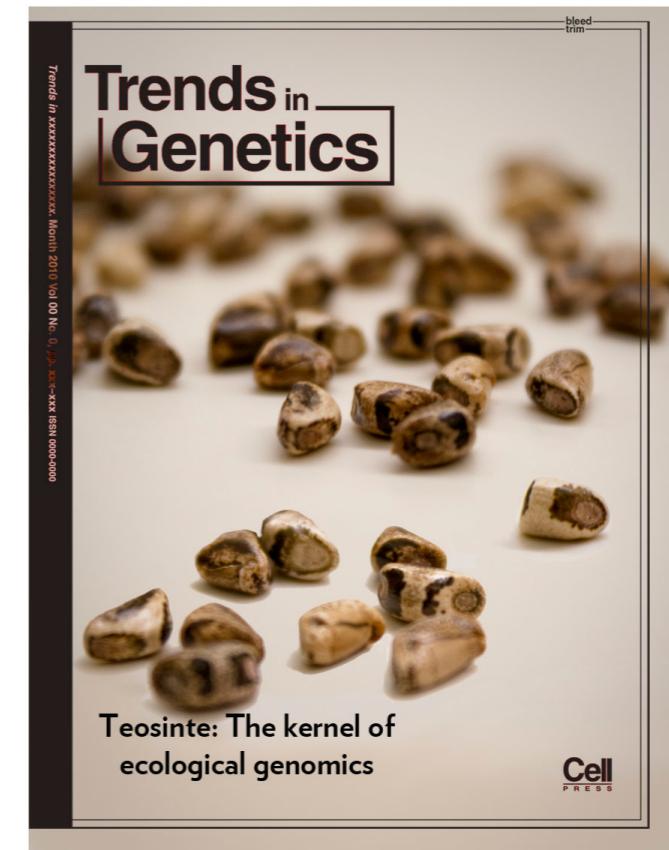
what is the genetic basis of adaptation?



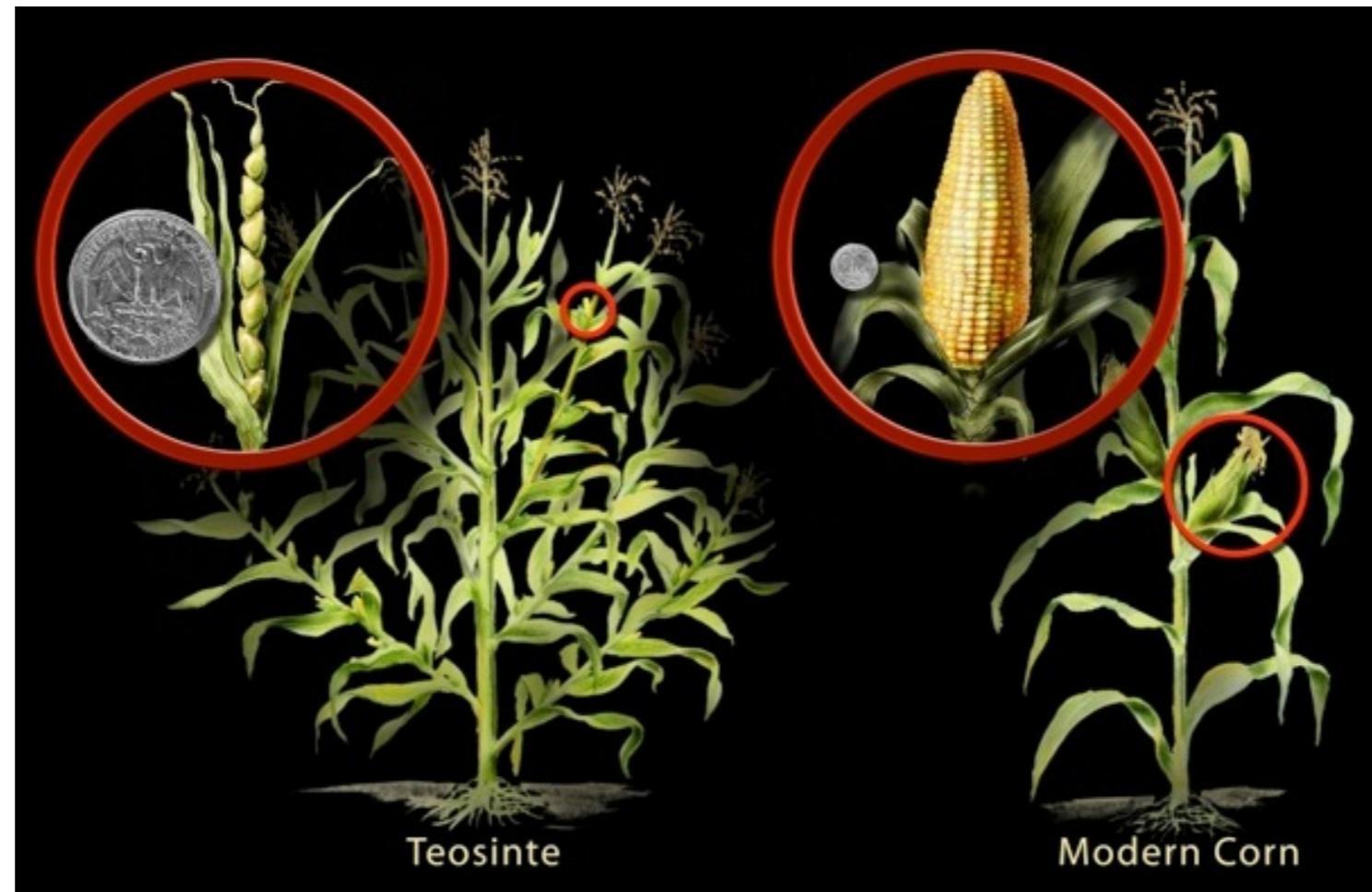
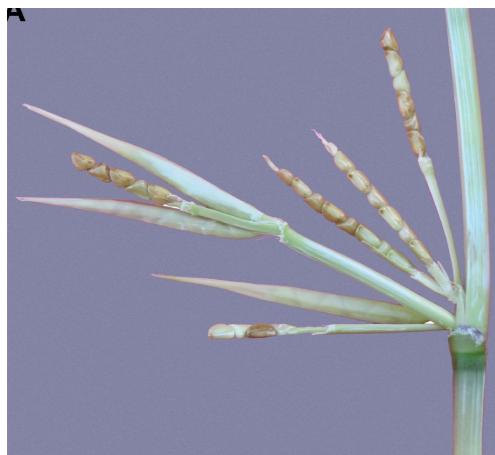
Zea: teosinte & maize



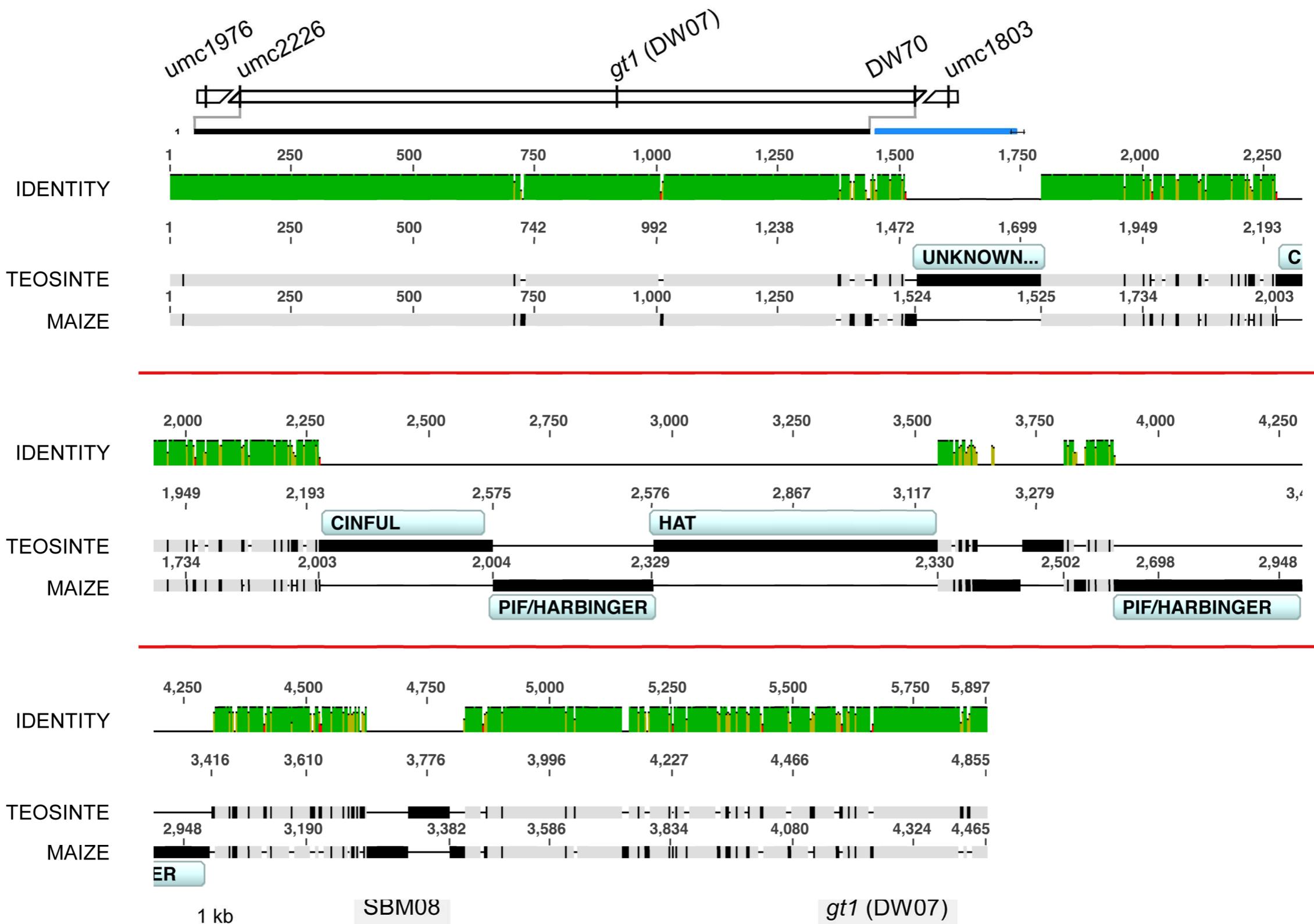
Zea as an evolutionary model



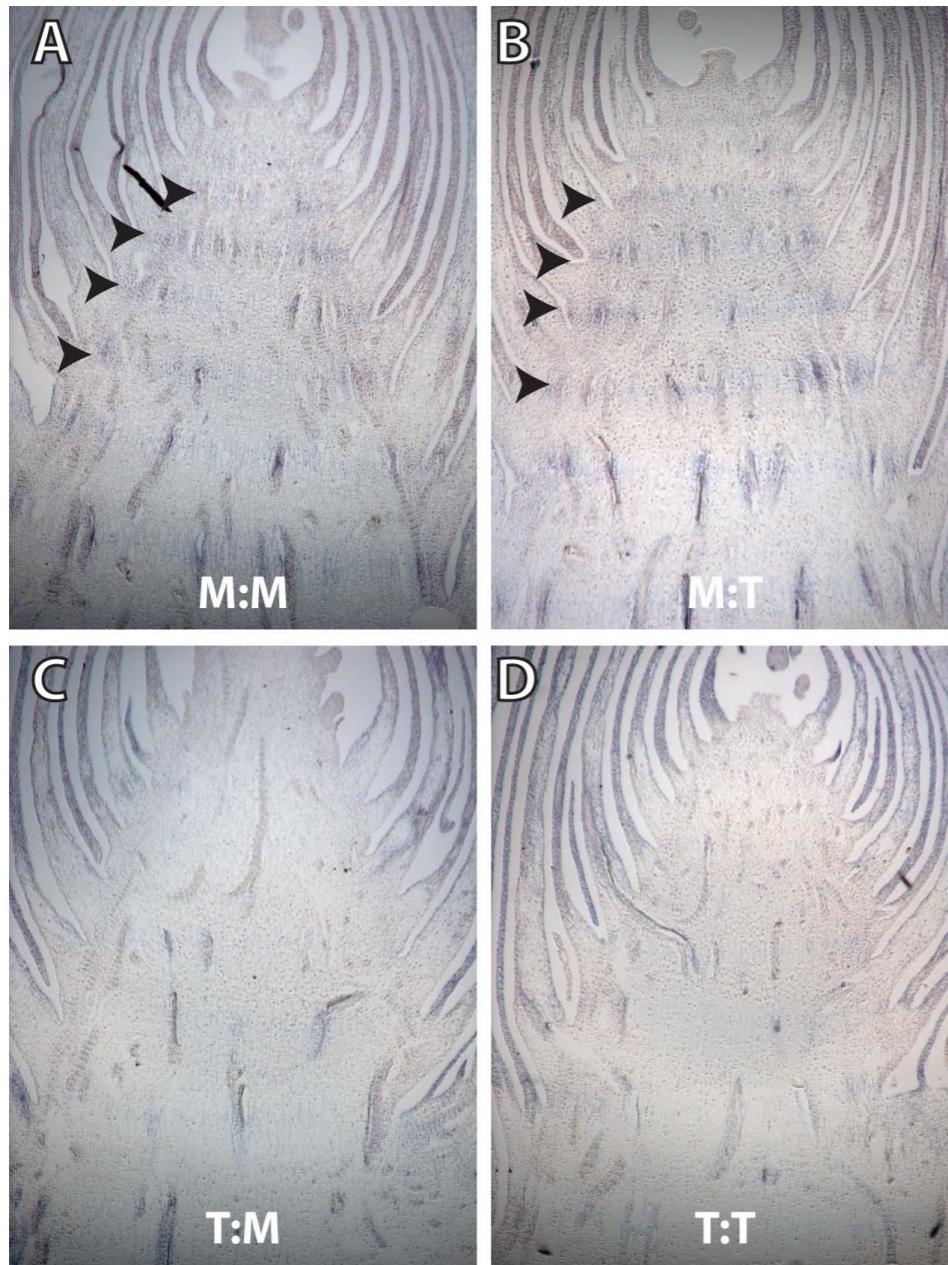
grassy tillers: evolution of plant architecture



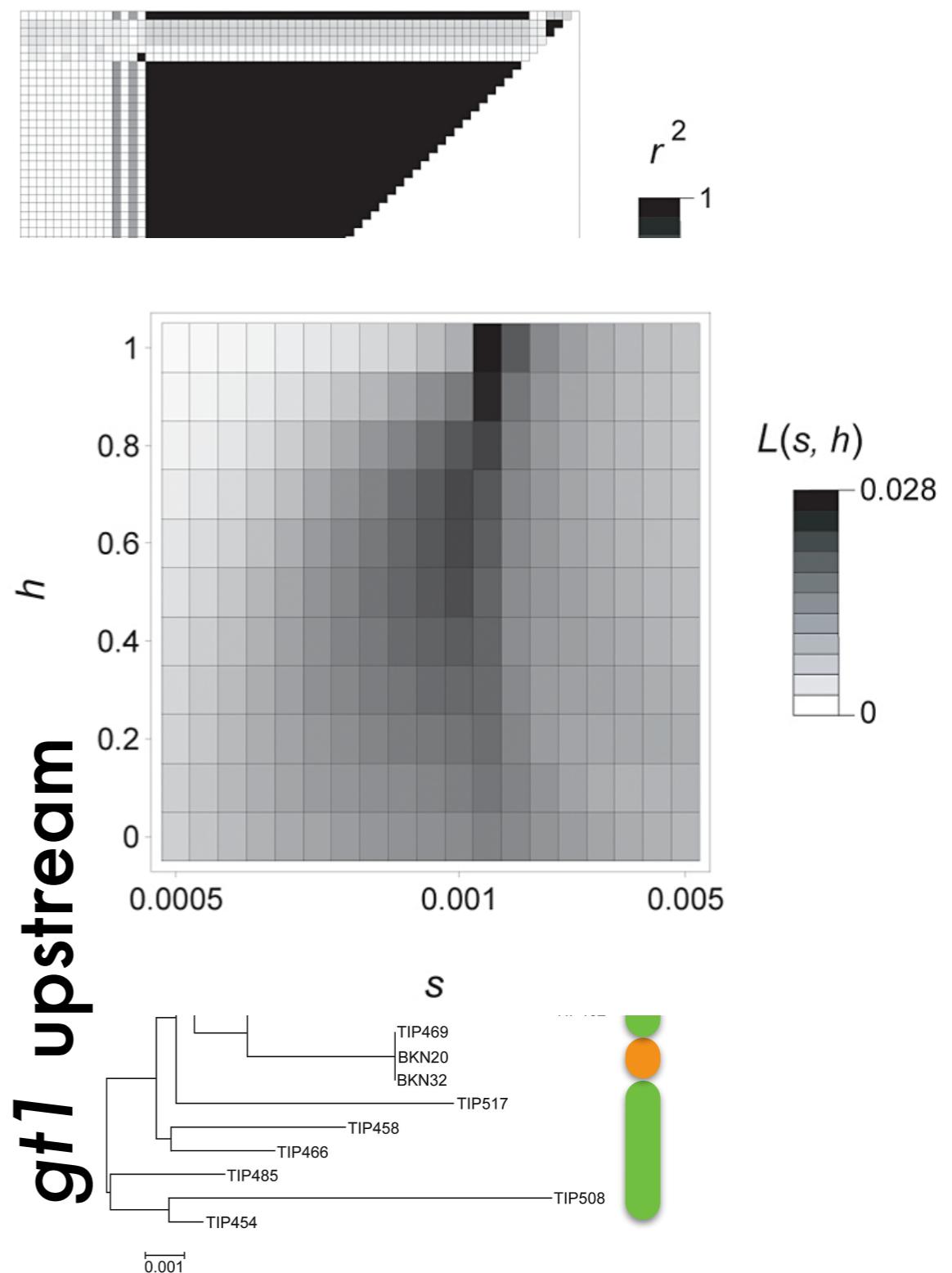
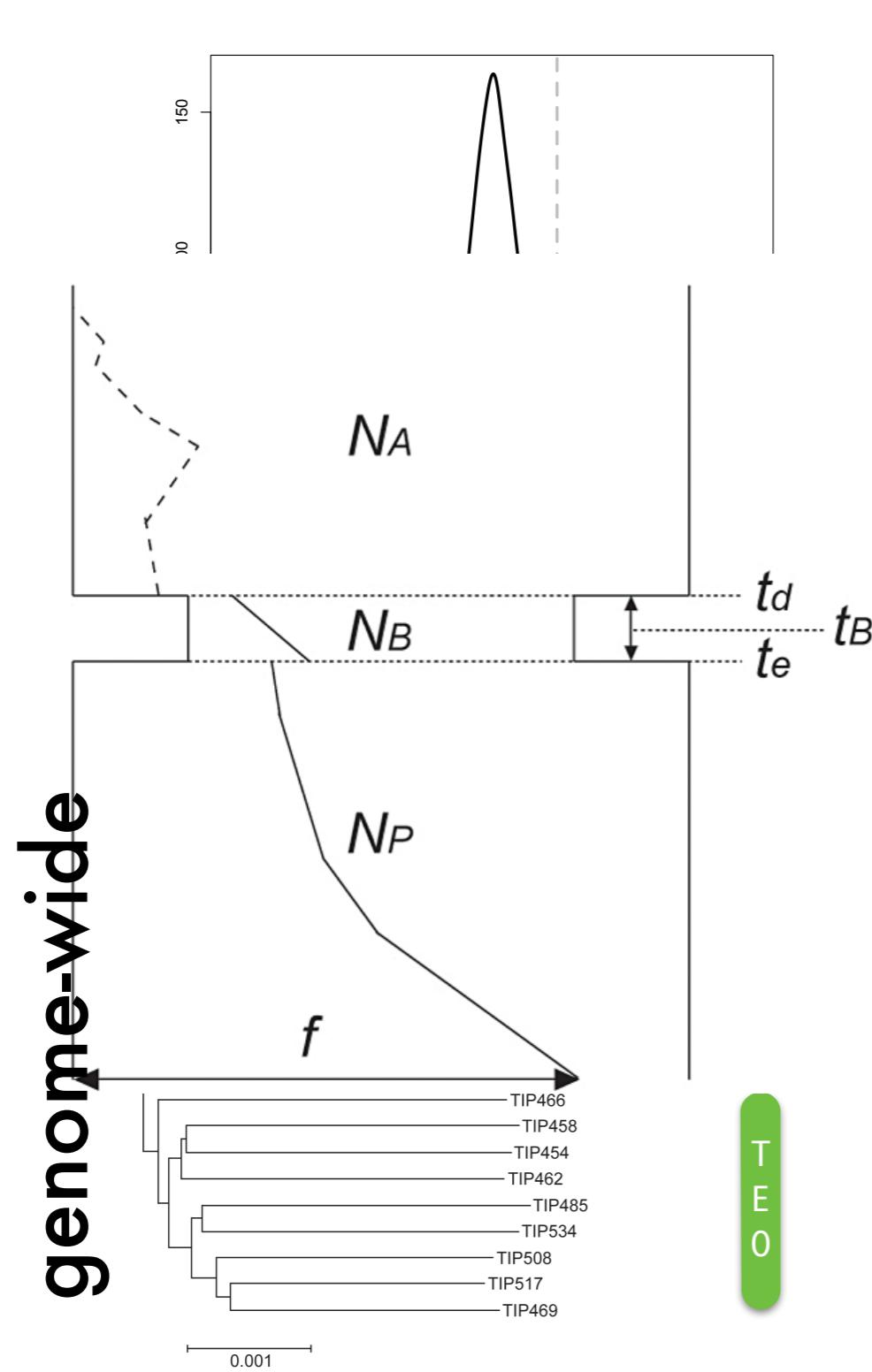
prolificacy mapped to upstream of *gt1*



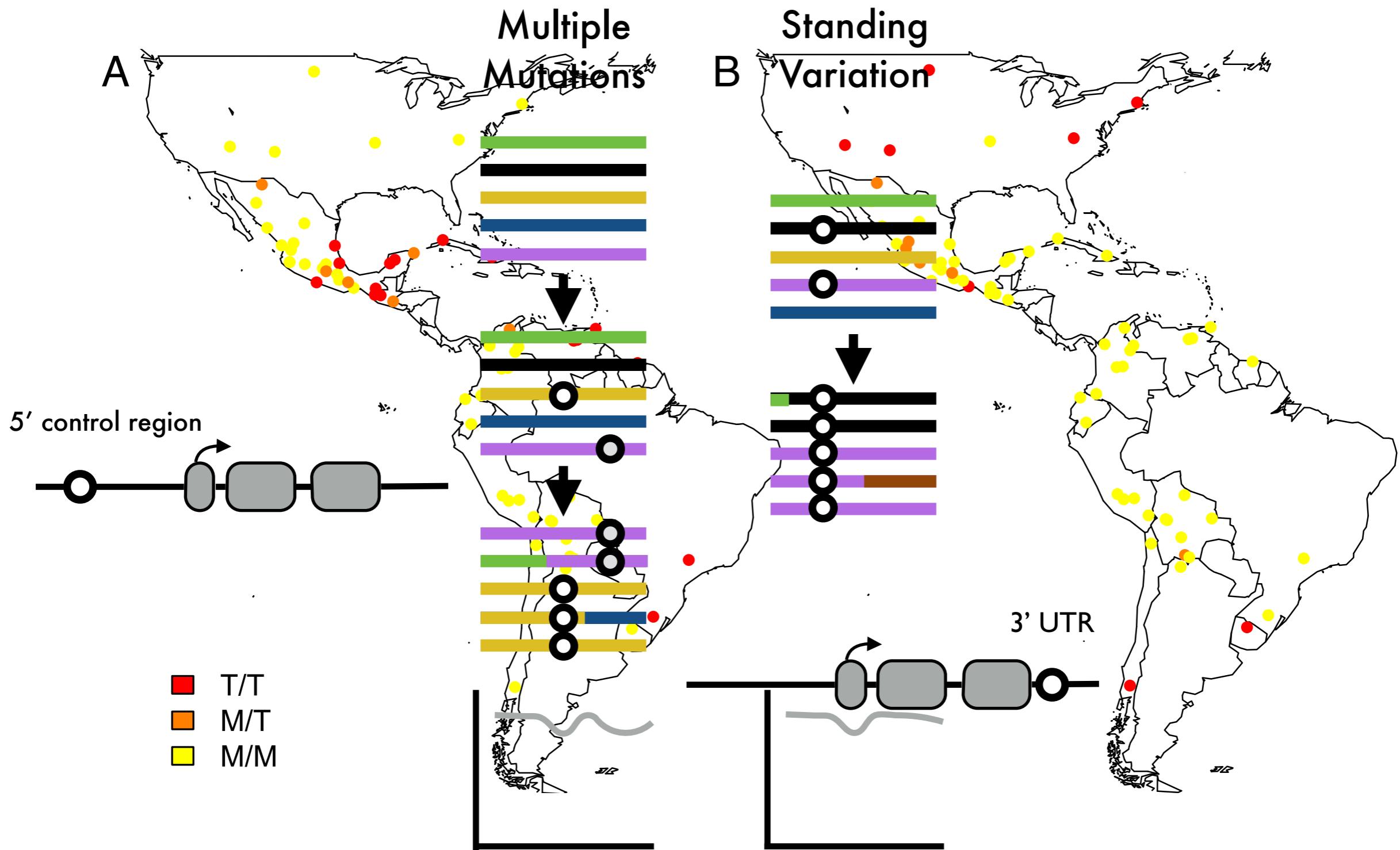
gt1 controls lateral bud formation



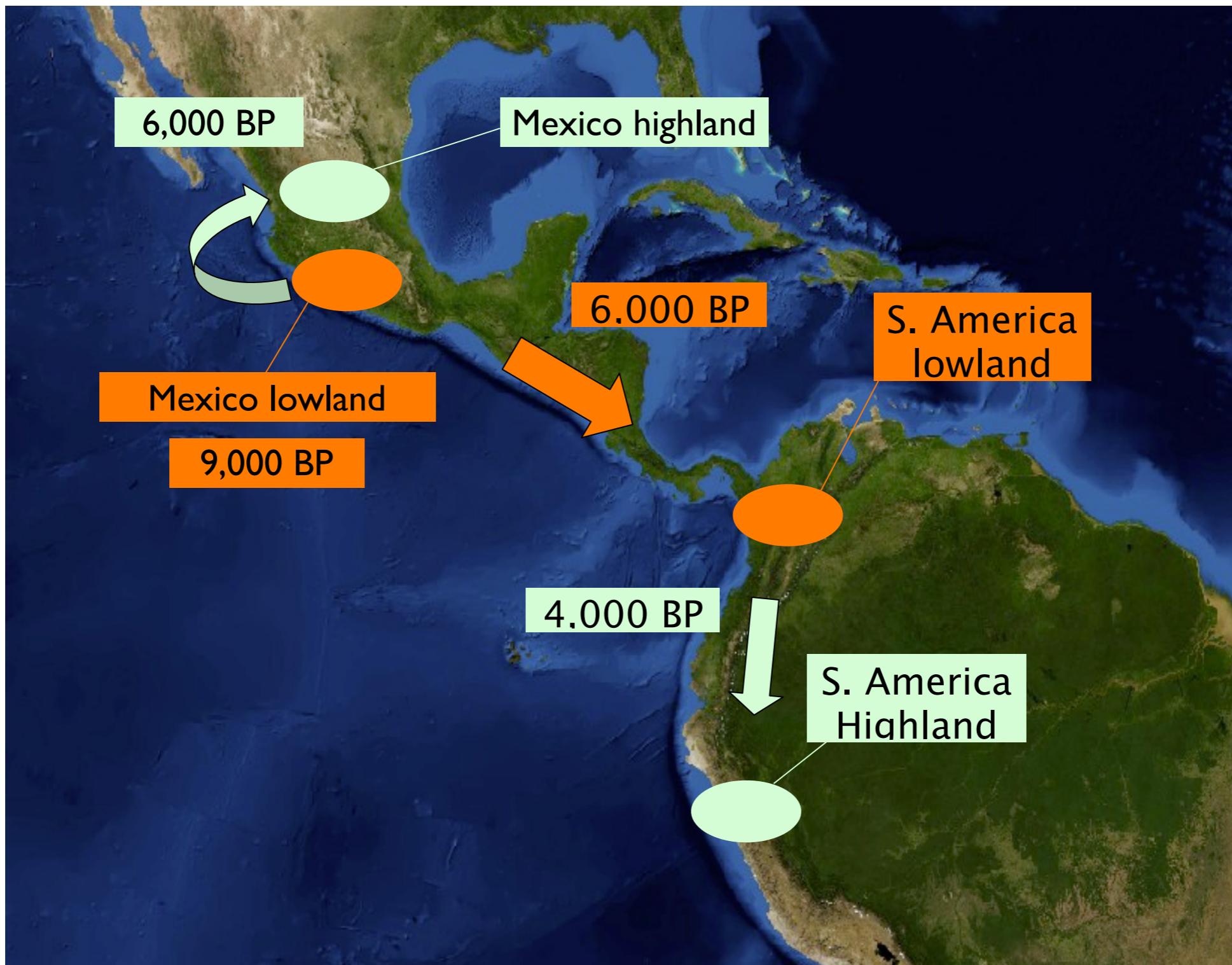
partial sweep upstream of *gt1*



convergent evolution at *gt1*

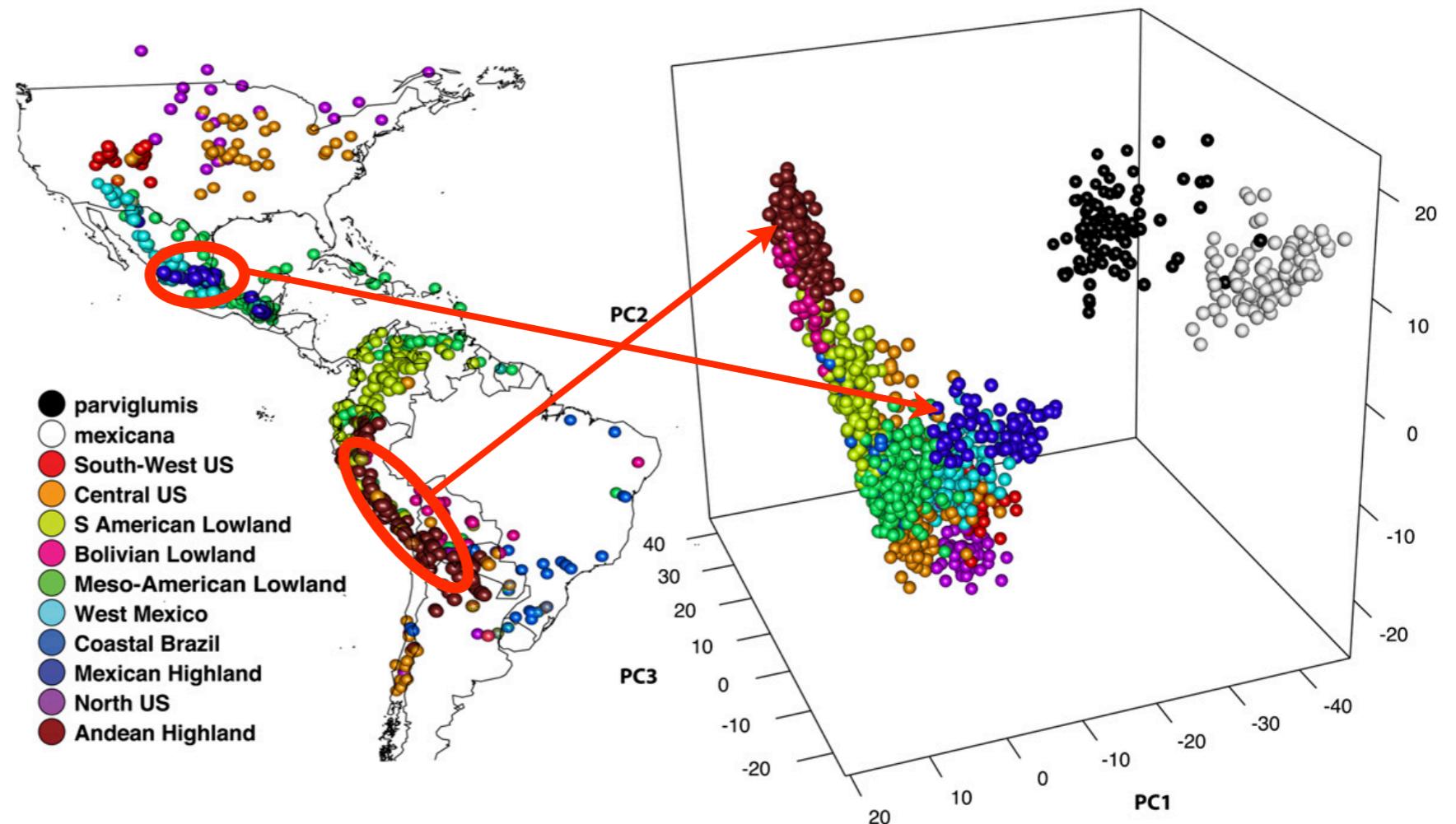


maize colonization of highlands

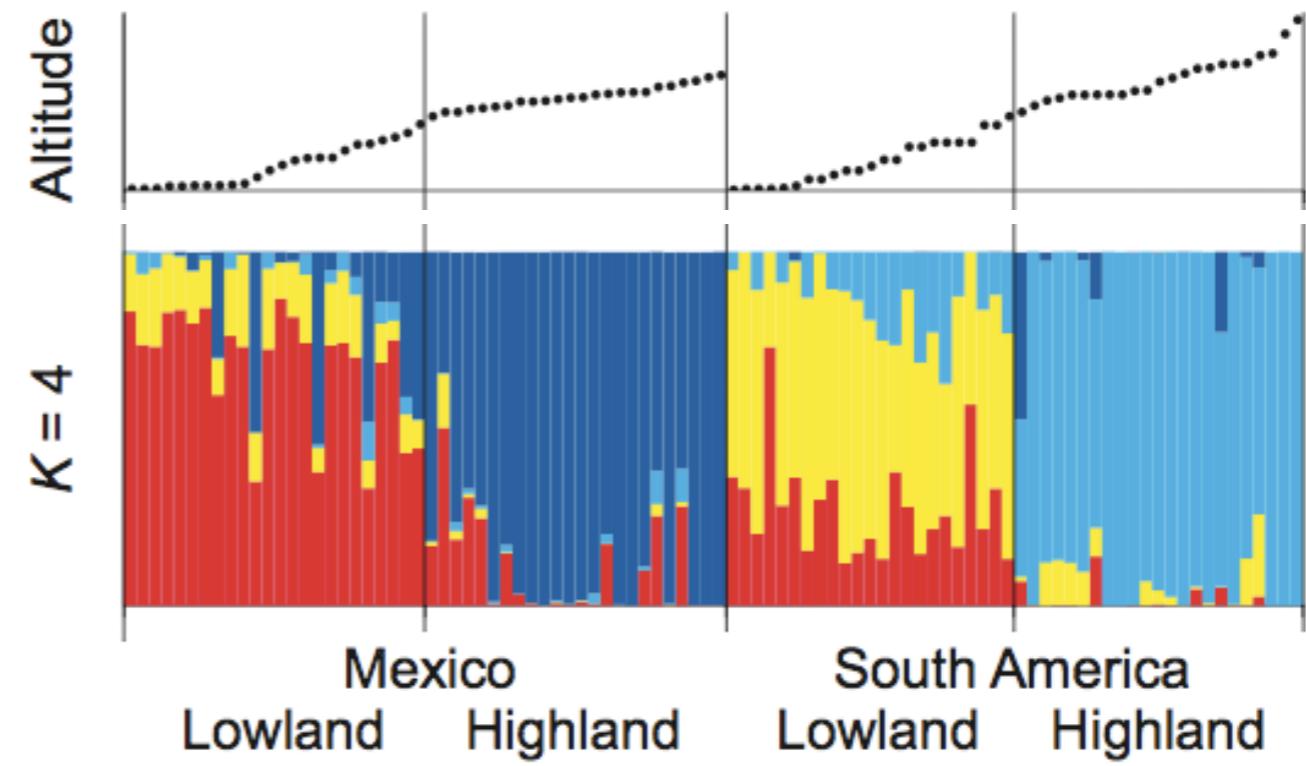
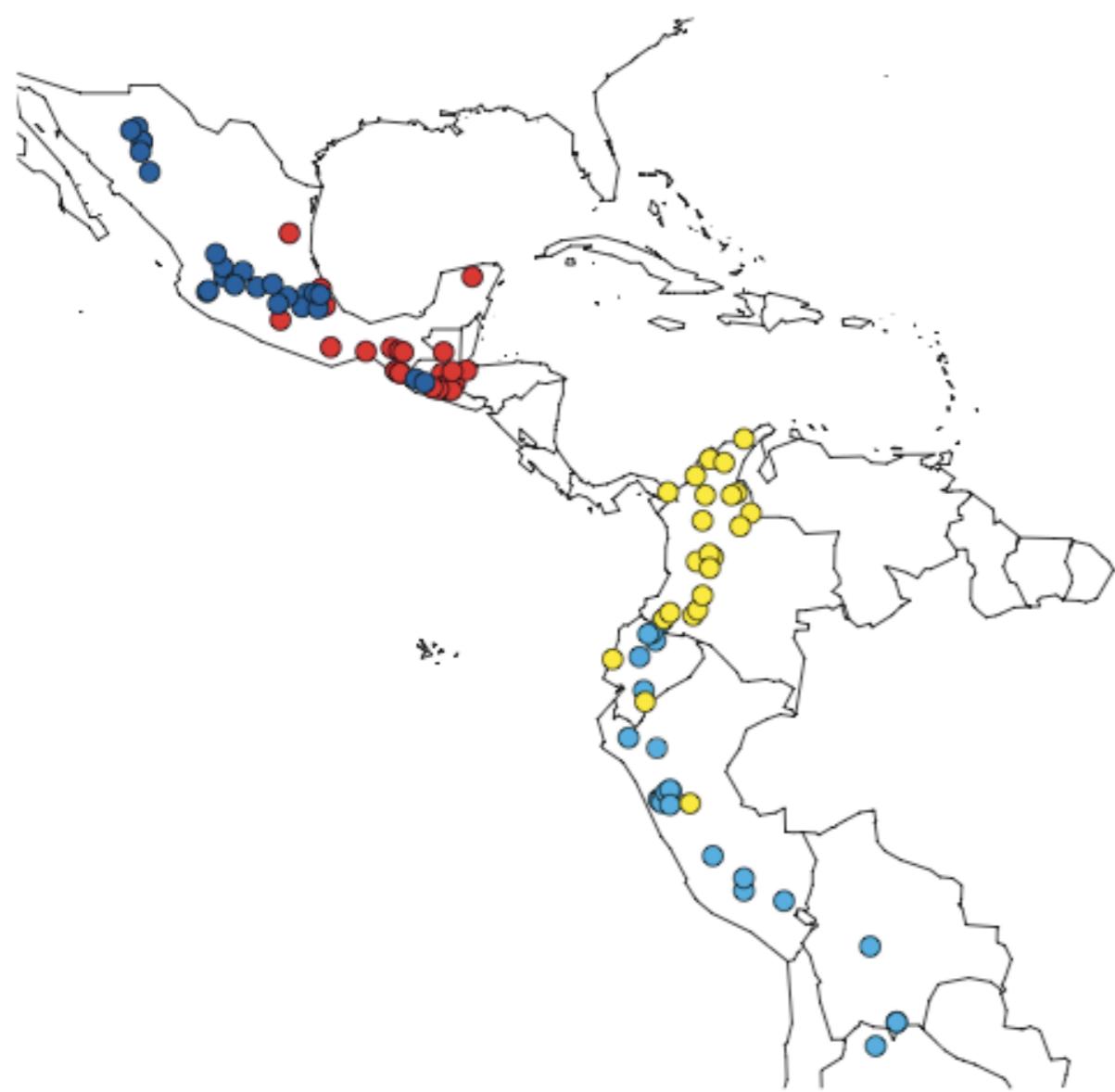


Matsuoka et al. 2002; Piperno 2006
Perry et al. 2006; Piperno et al. 2009

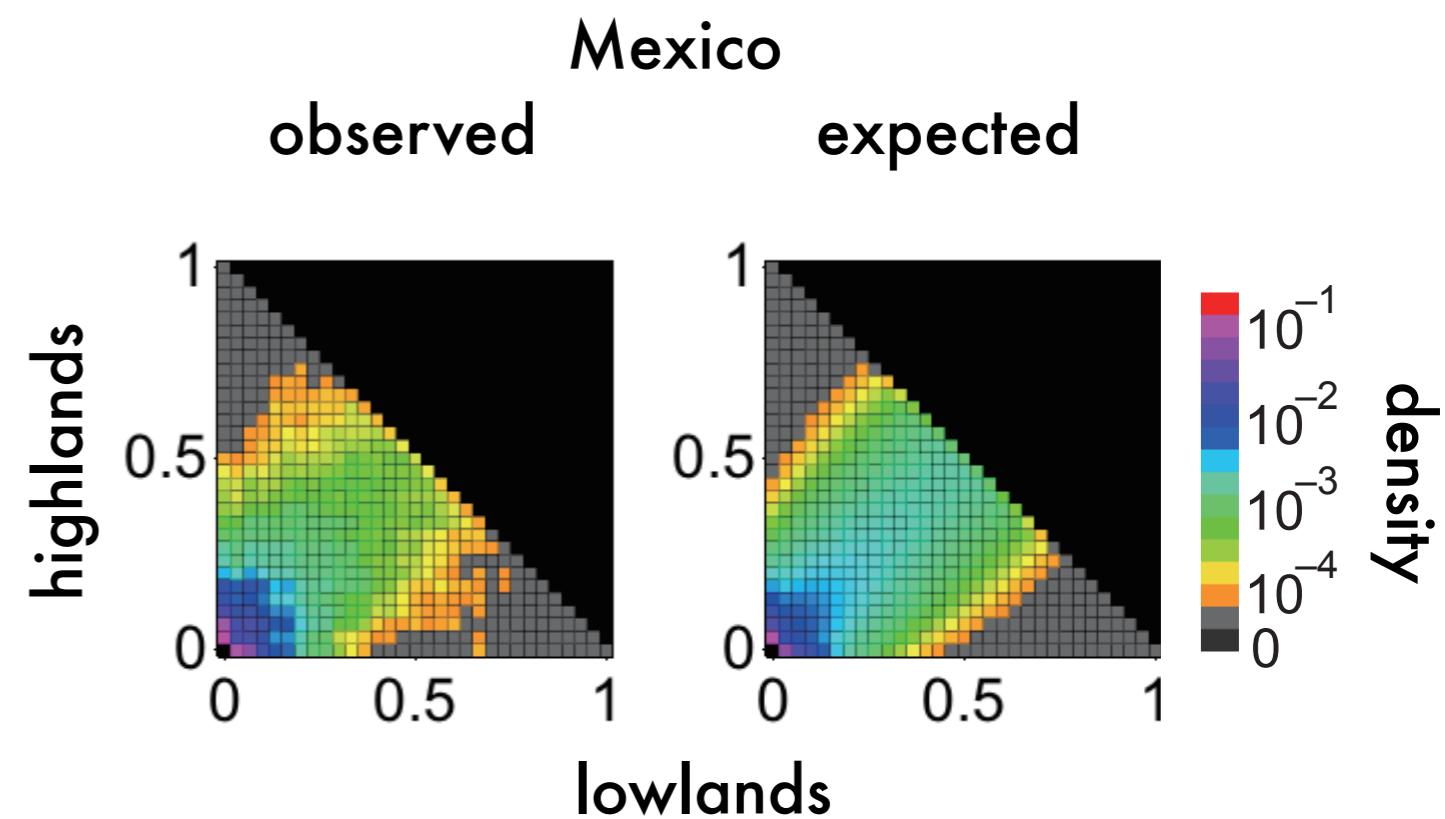
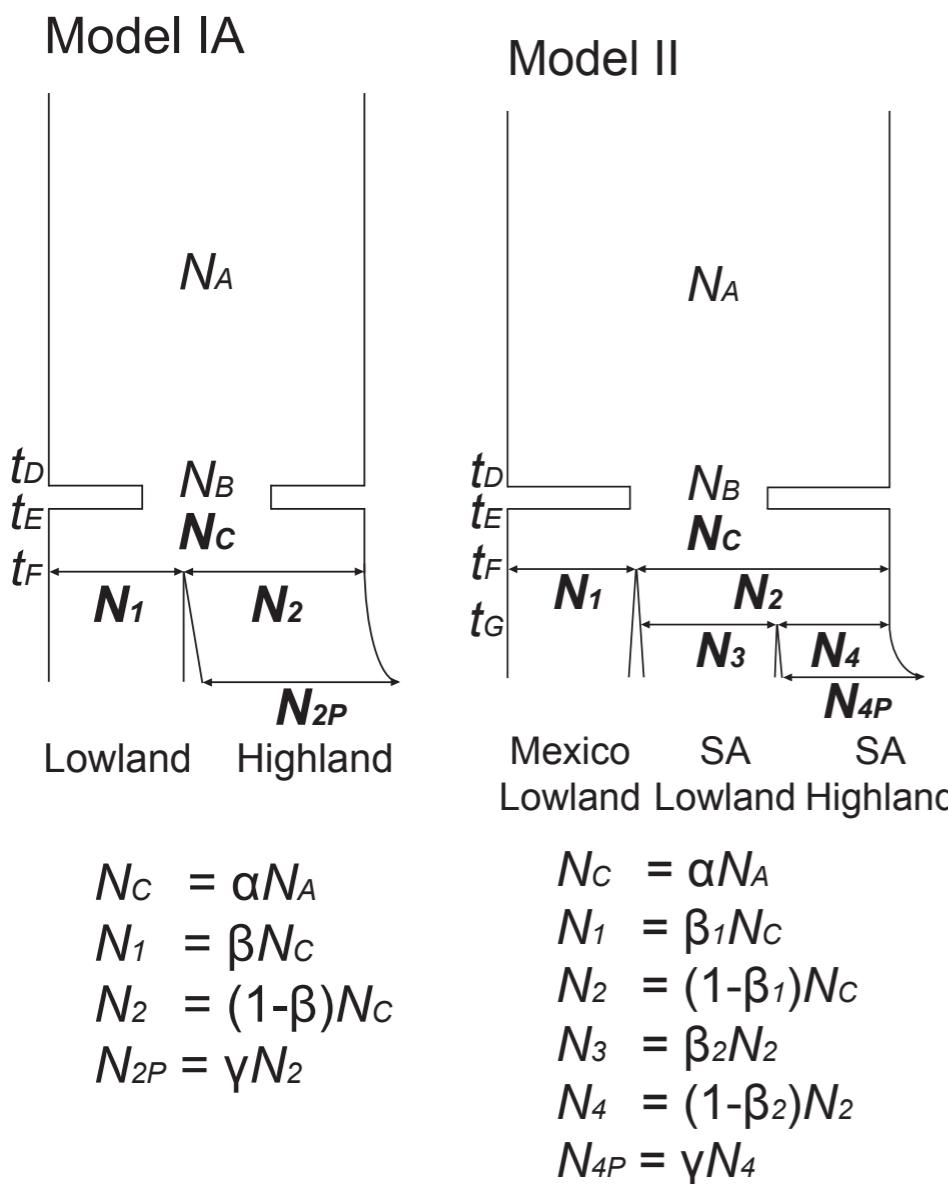
convergent phenotypic adaptation



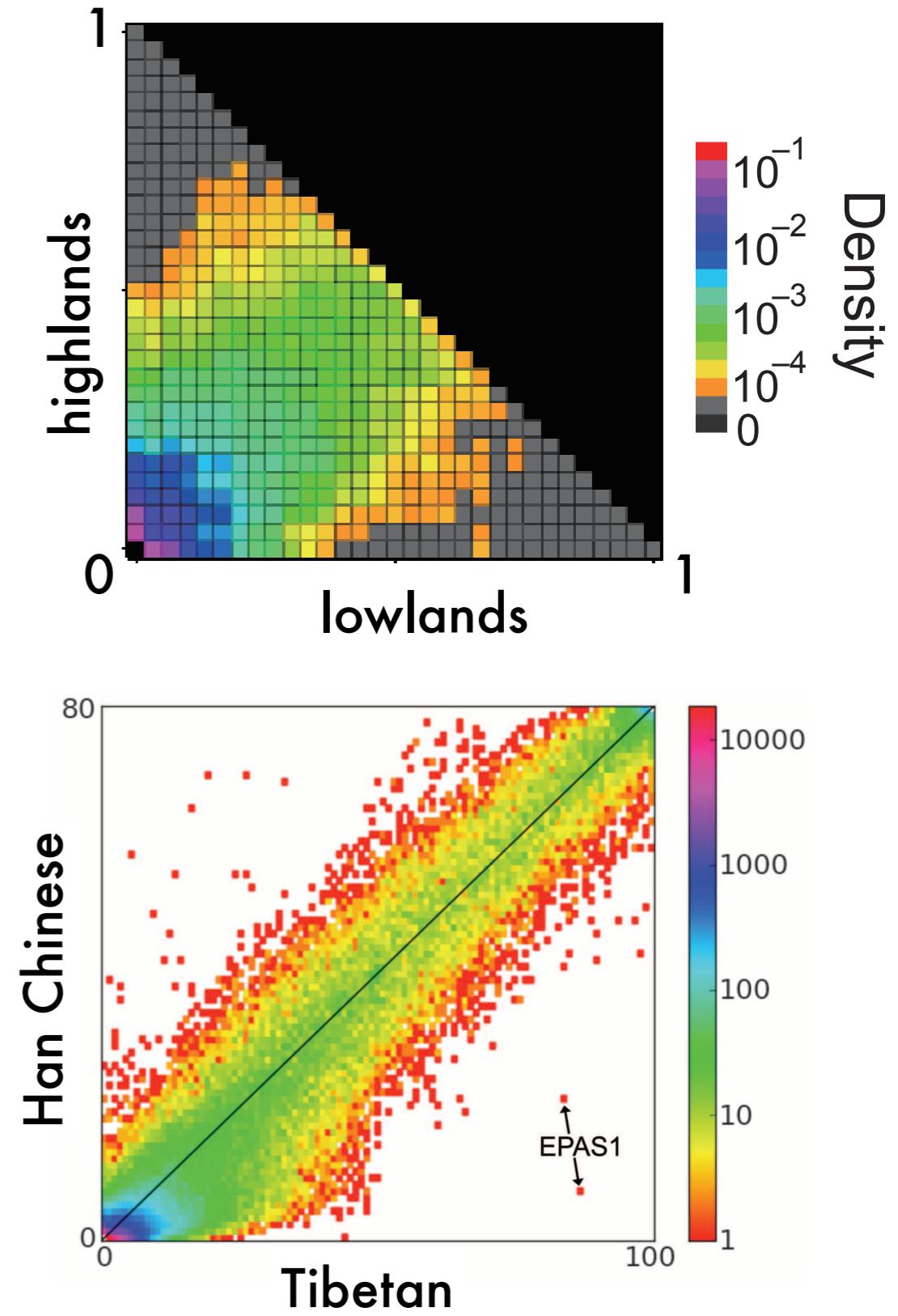
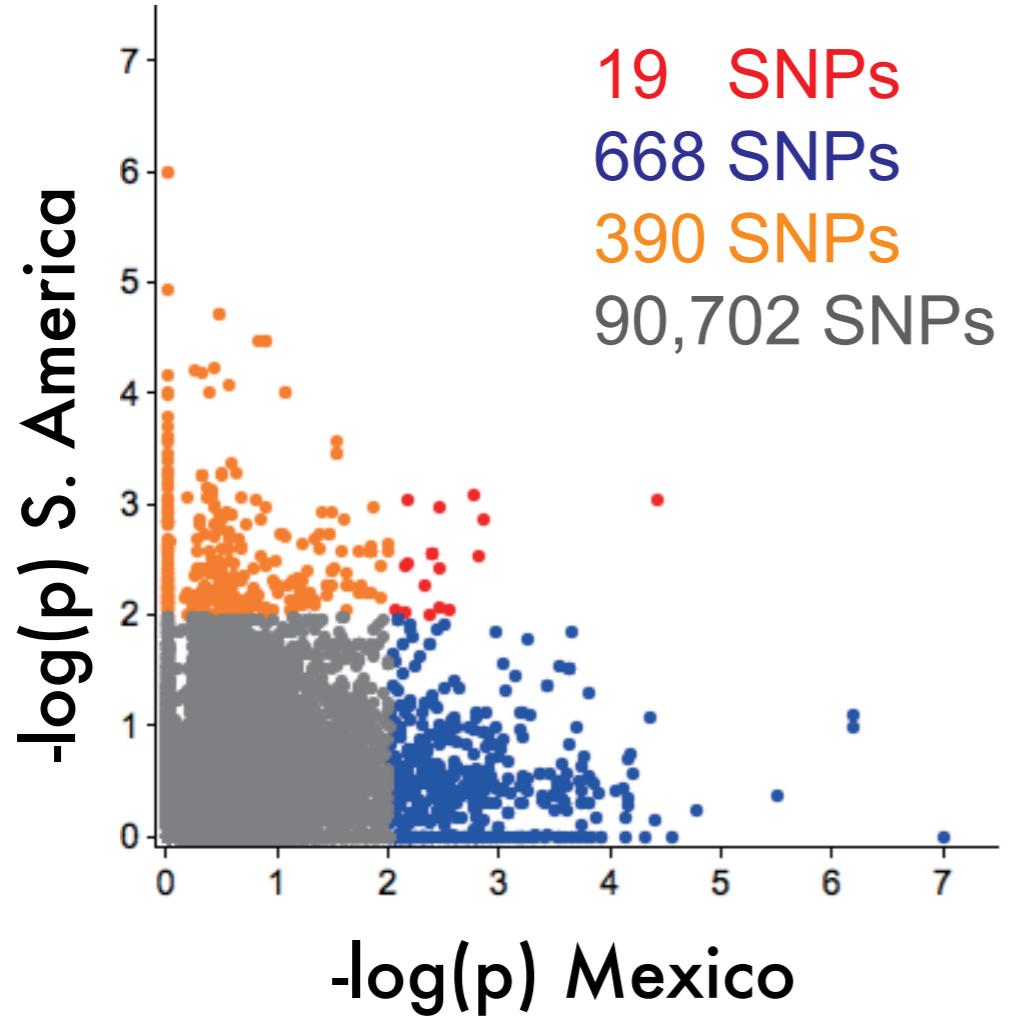
independent genetic origins



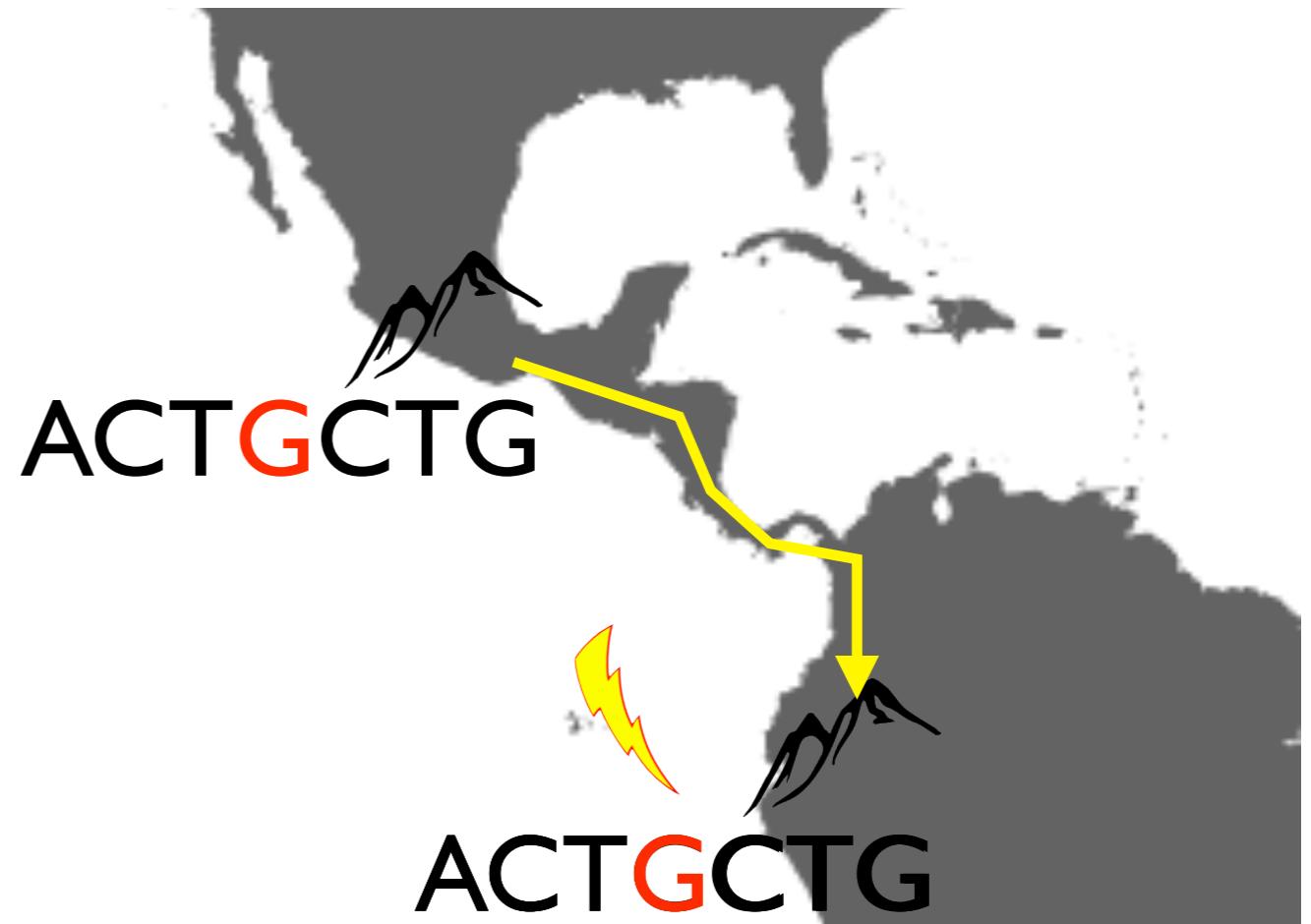
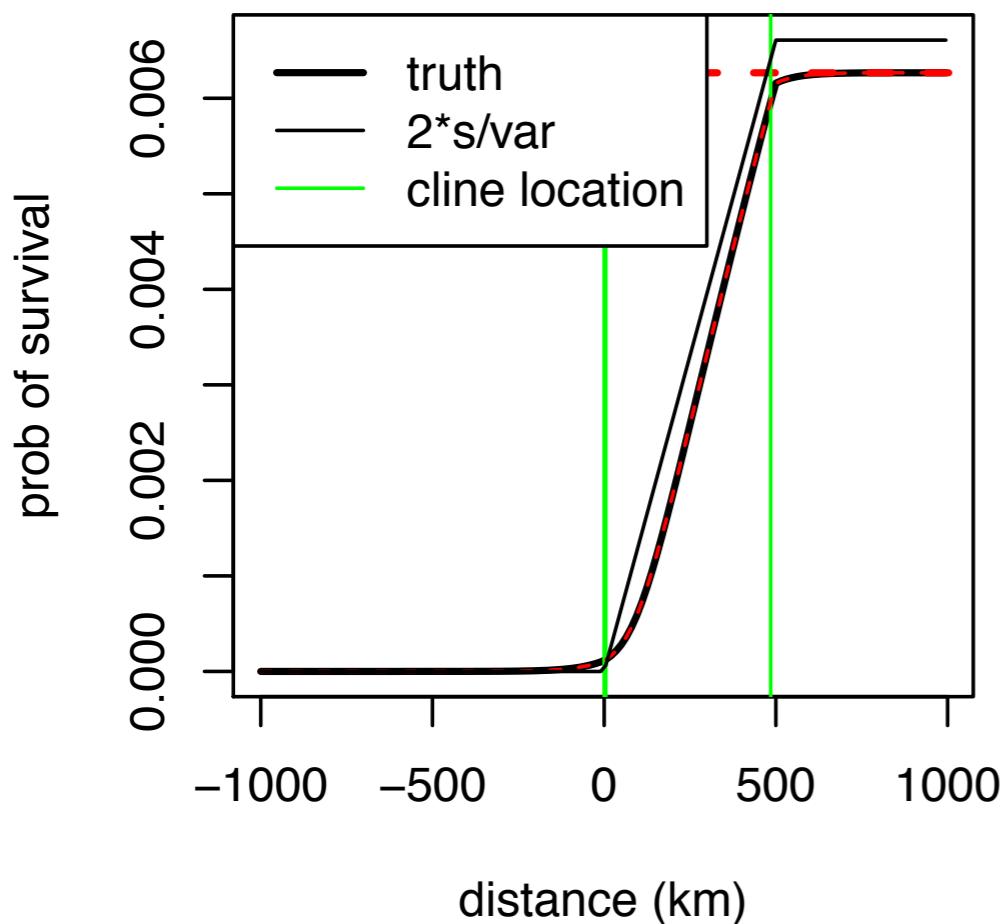
demography explains most differentiation



little evidence for convergent sweeps



theory predicts little convergence



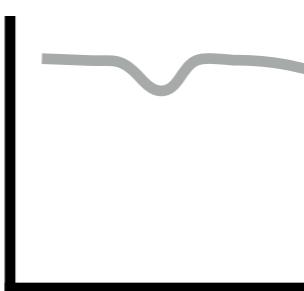
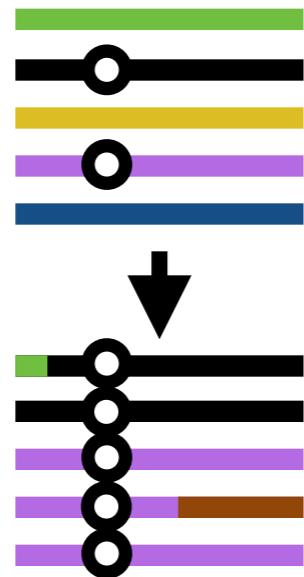
Peter Ralph
(USC)

$$T_{\text{mut}} = 1/\lambda_{\text{mut}} = \frac{2\mu\rho As_b}{\xi^2} \approx 10^4 \text{ gens}$$

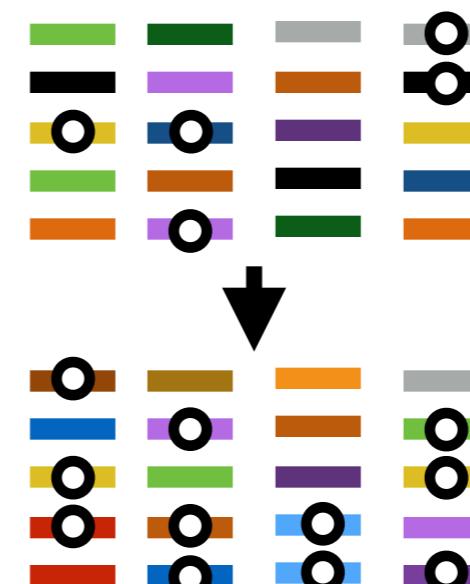
$$T_{\text{mig}} = (2/N) \exp(R\sqrt{2s_m}/\sigma) \approx 5 \times 10^{34} \text{ gens}$$

theory predicts little convergence

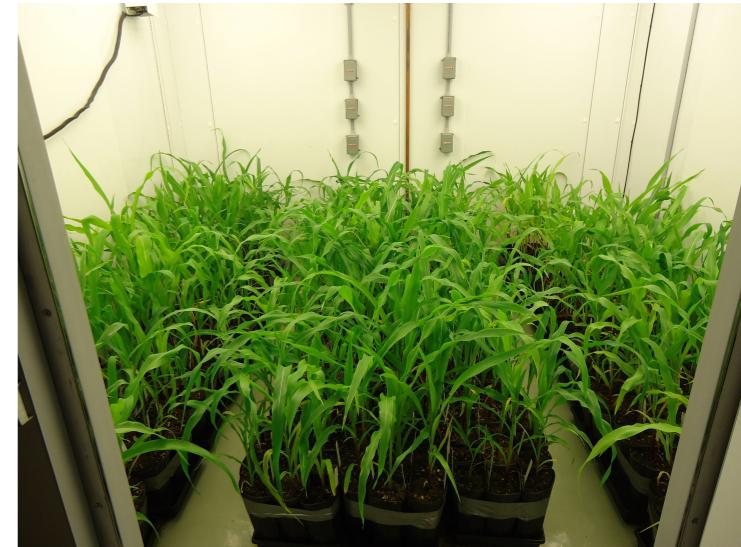
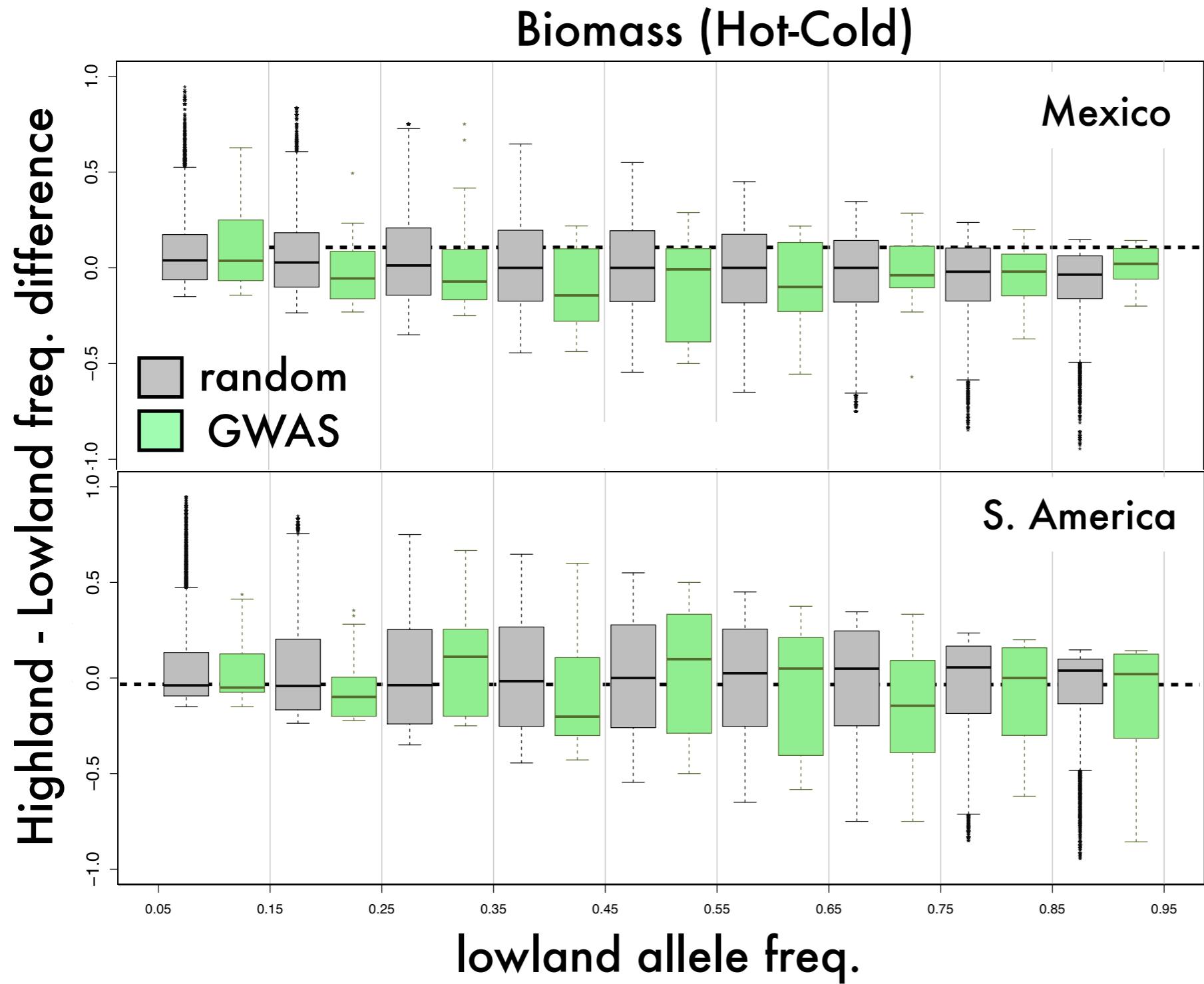
standing
variation



polygenic adaptation



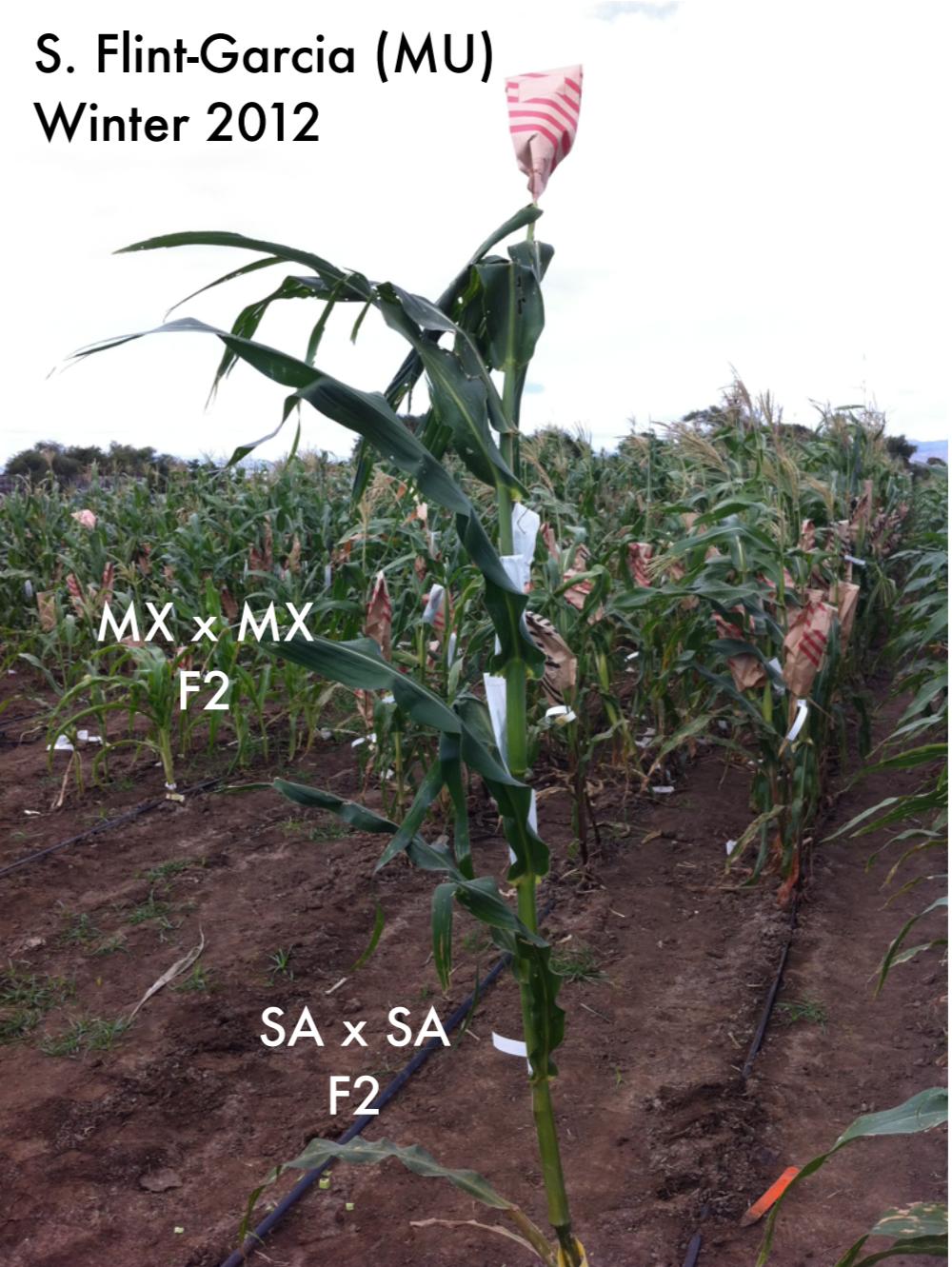
no change in frequency for growth SNPs



in progress: mapping pops

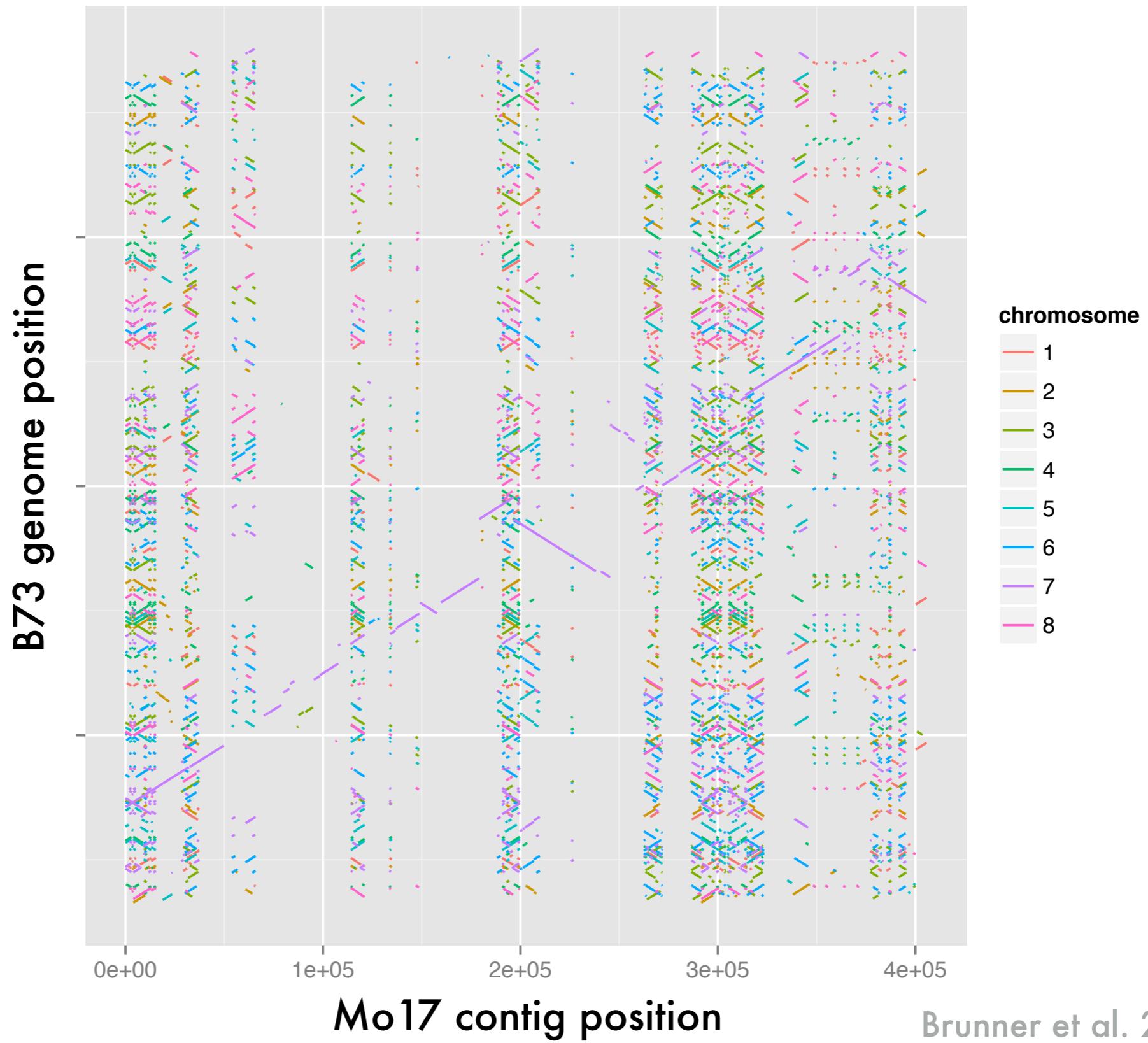


Highland Landrace (PT) x
B73 BC2 NILs

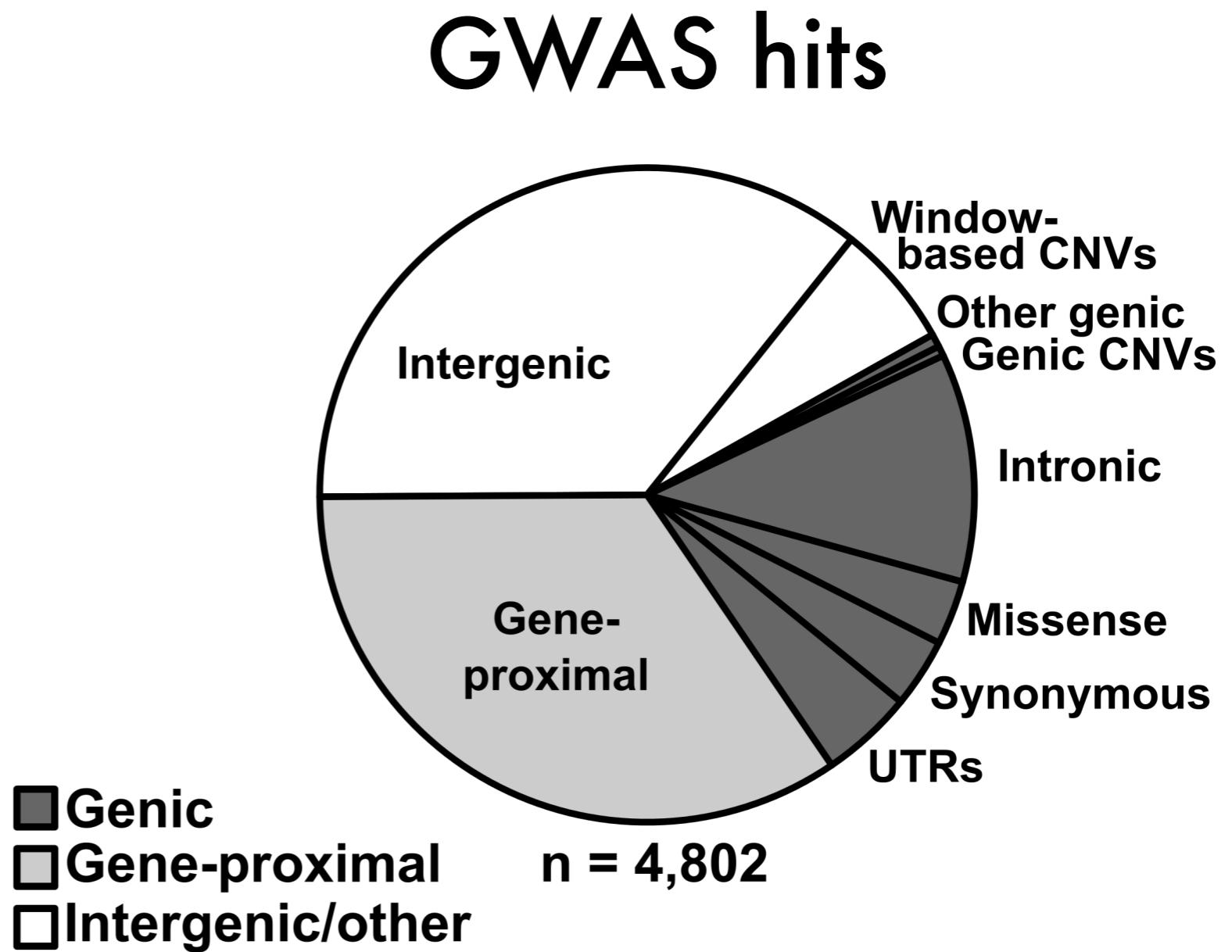
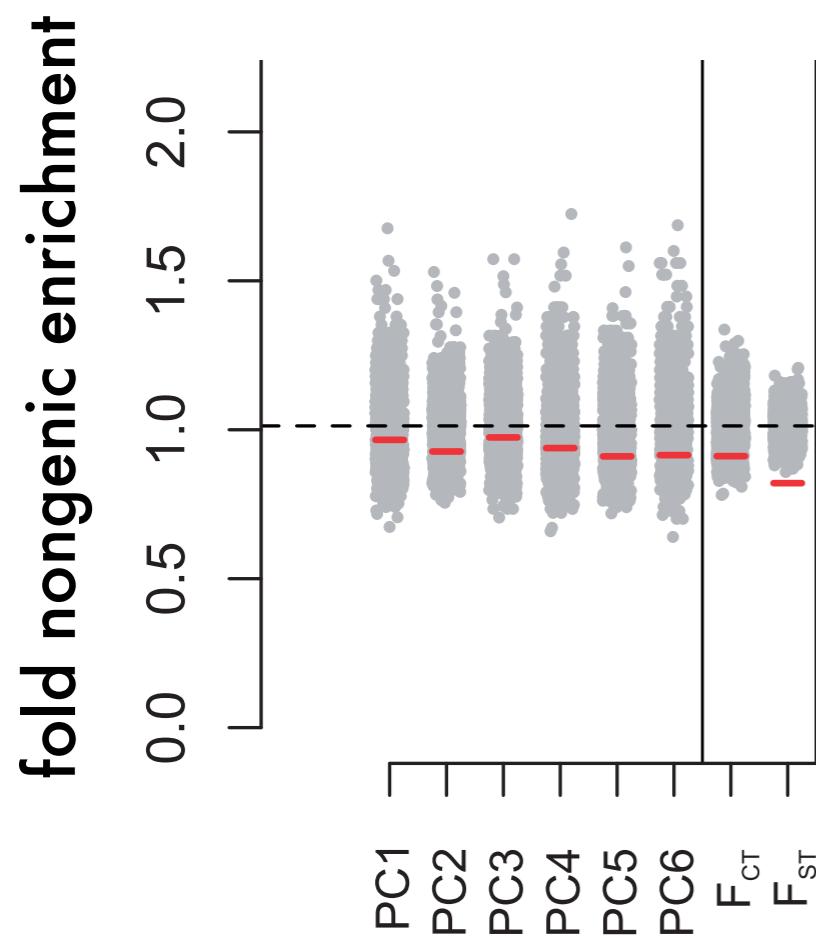


Highland x Lowland Landrace
F2 populations

the genome's a mess



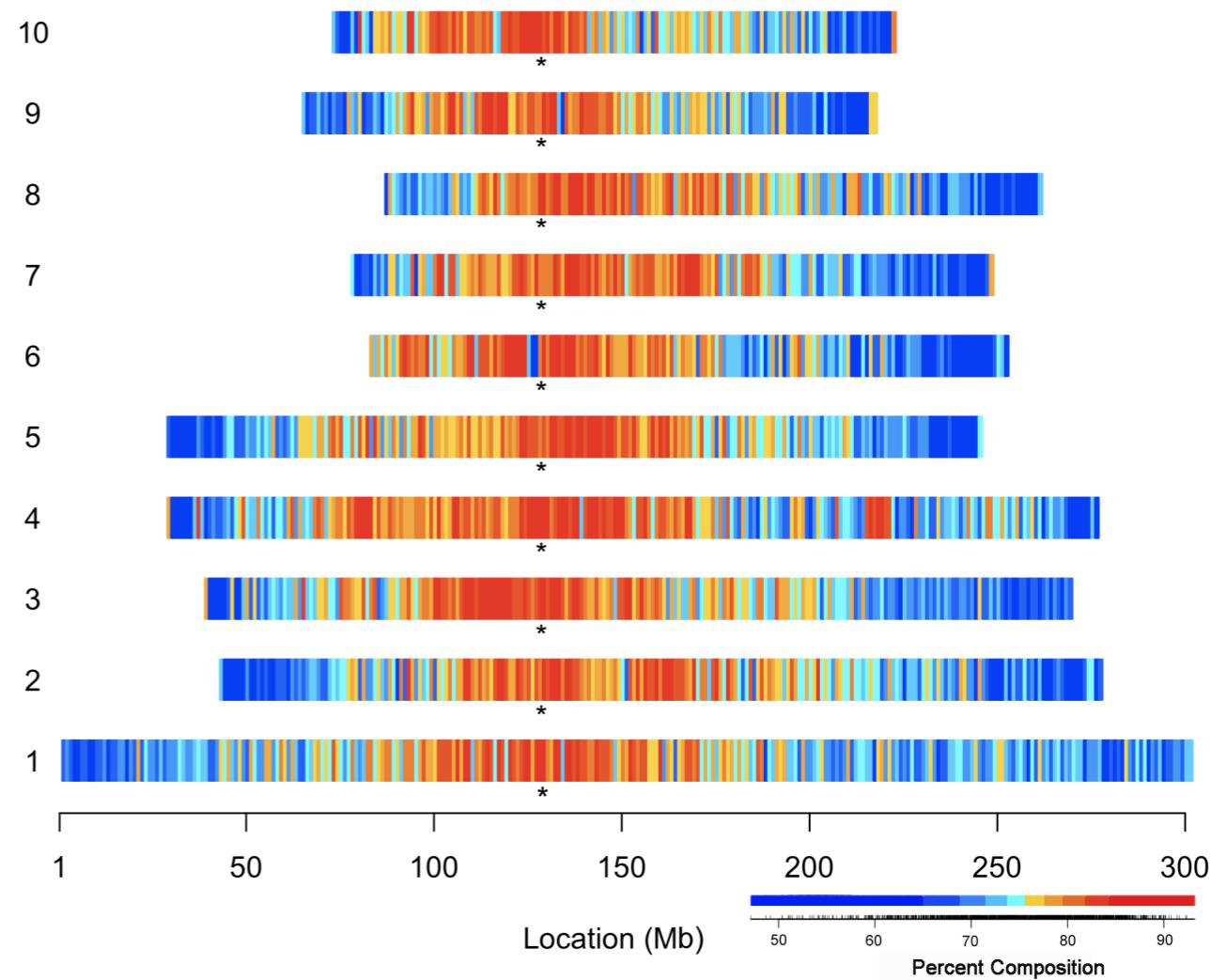
...and that mess is important



transposable elements: 85% of maize



Damon Lisch

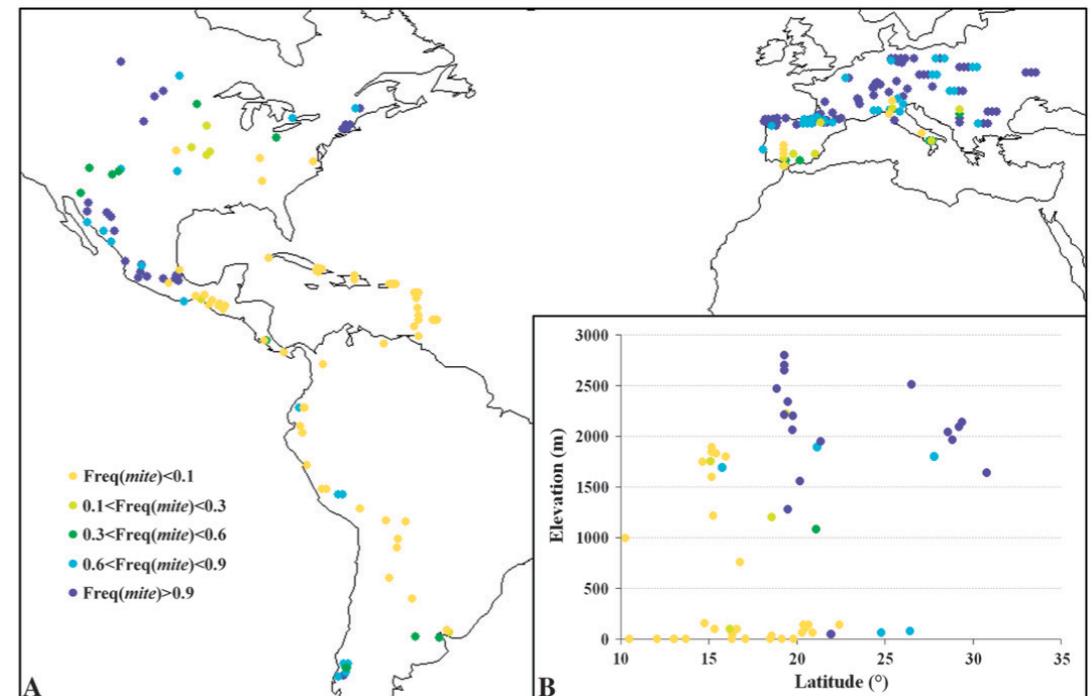


McClintock 1984 Science
Baucom et al. 2009 PLoS Genetics

TEs impact morphology, flowering time



tb1

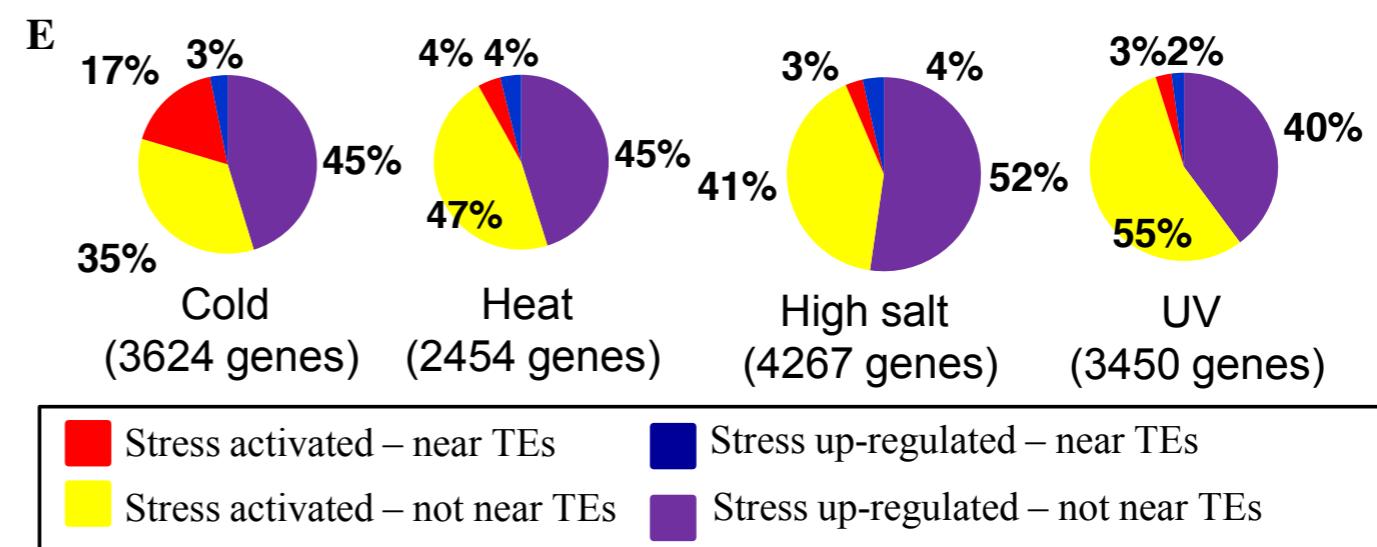
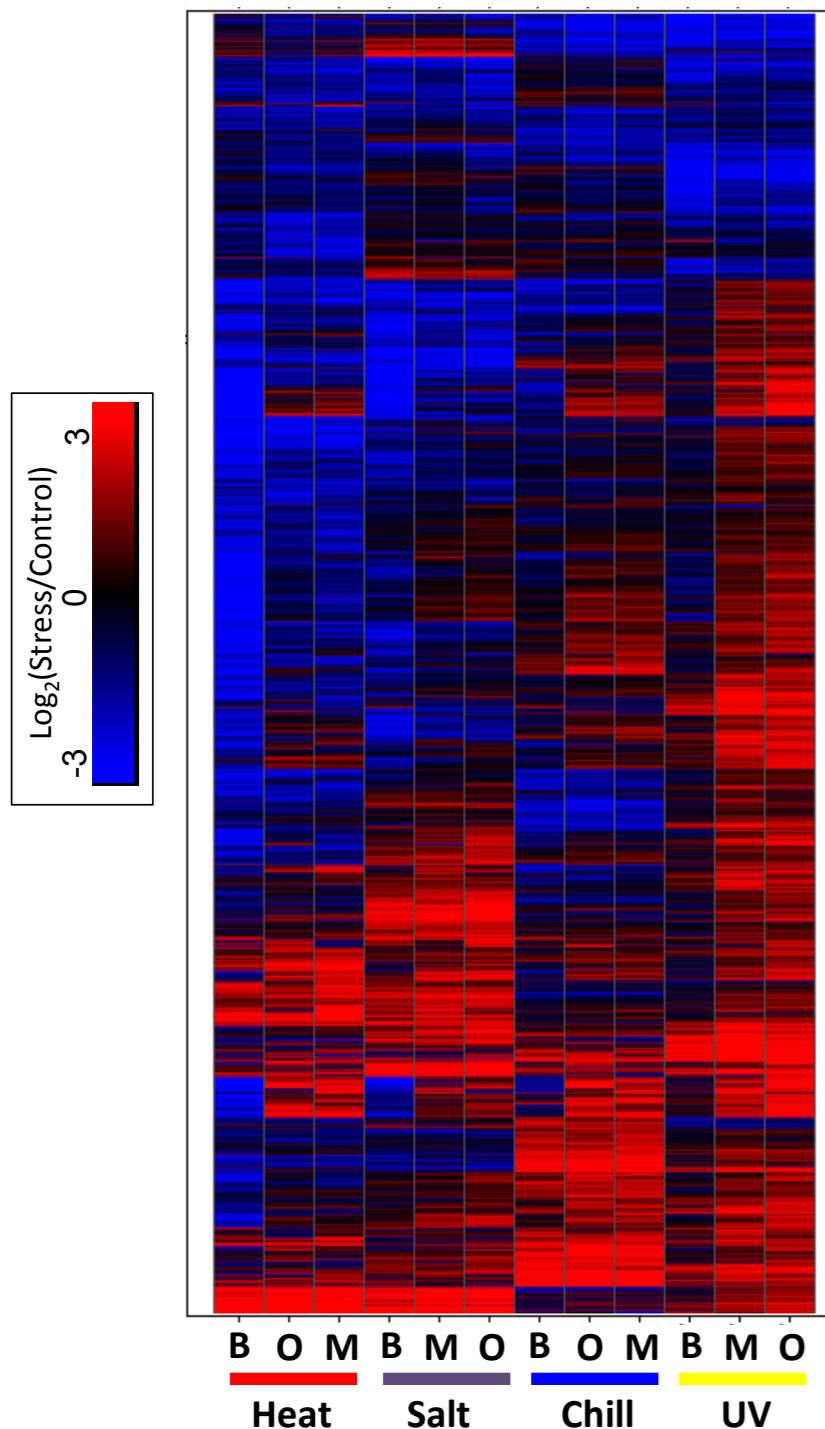


vgt1

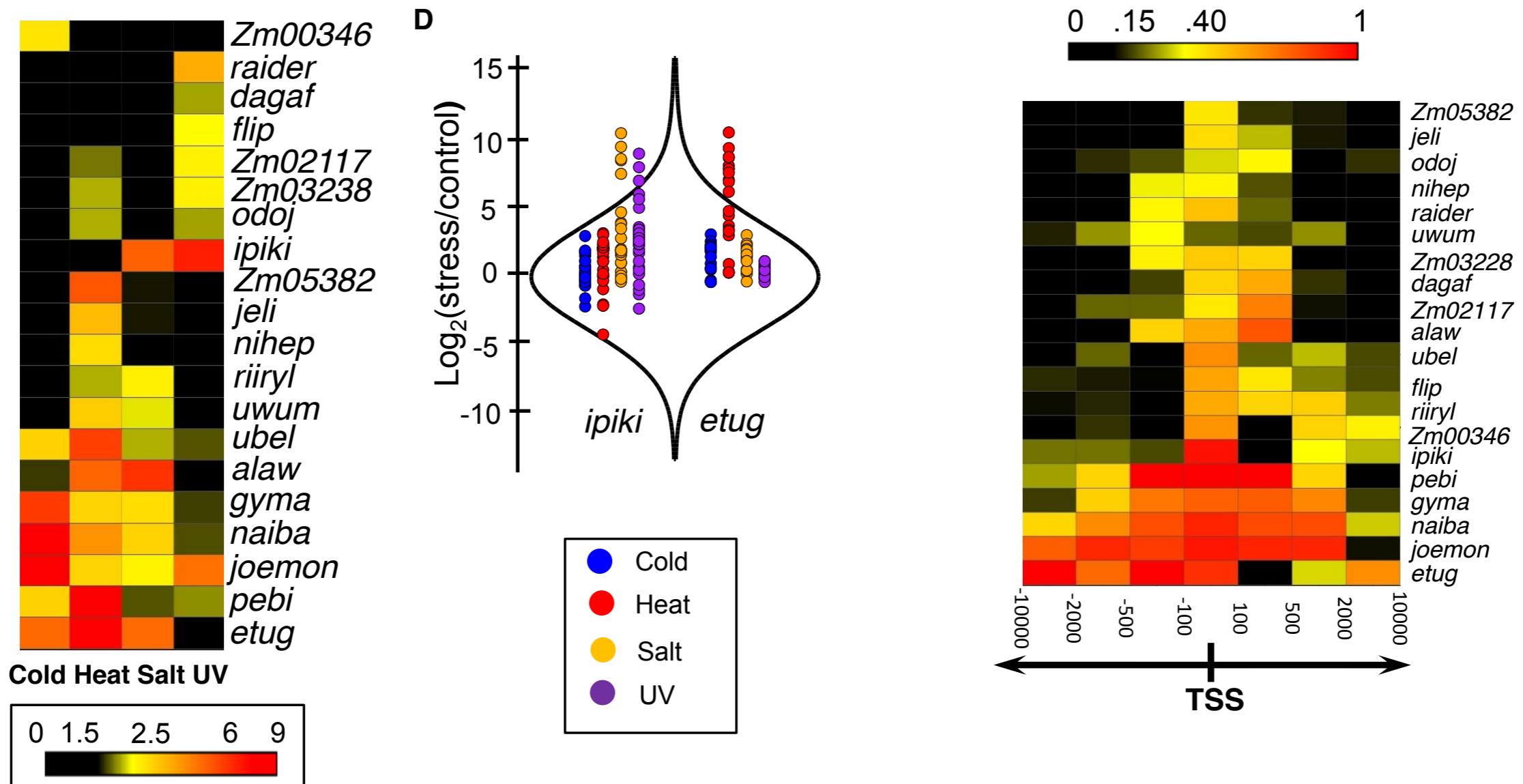


ZmCCT

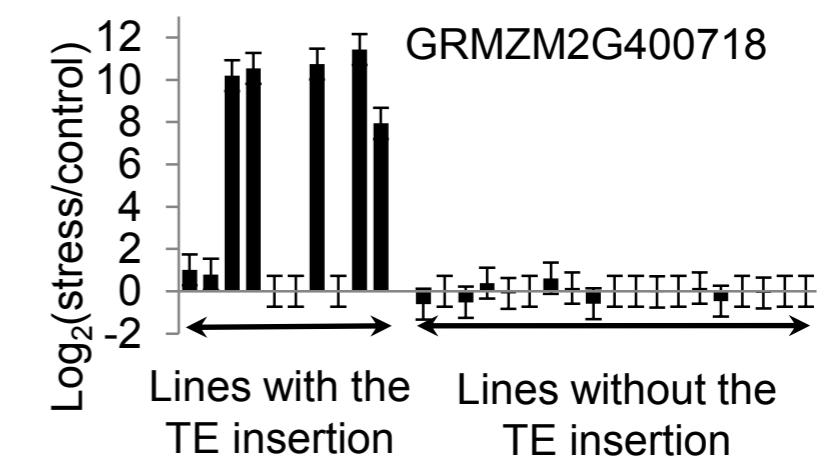
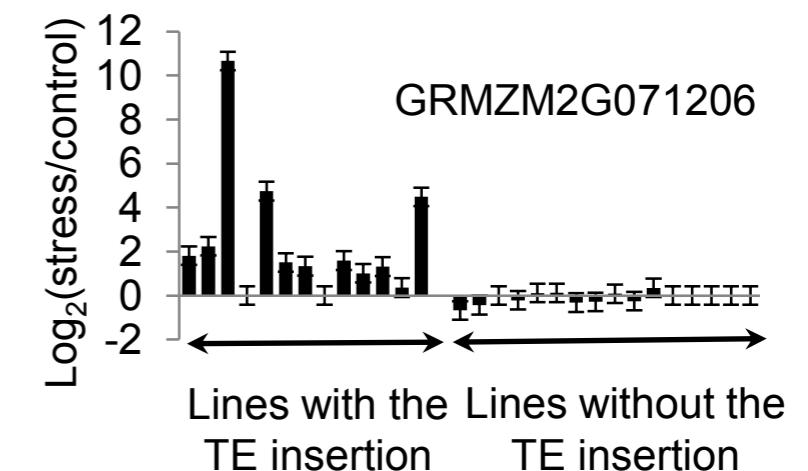
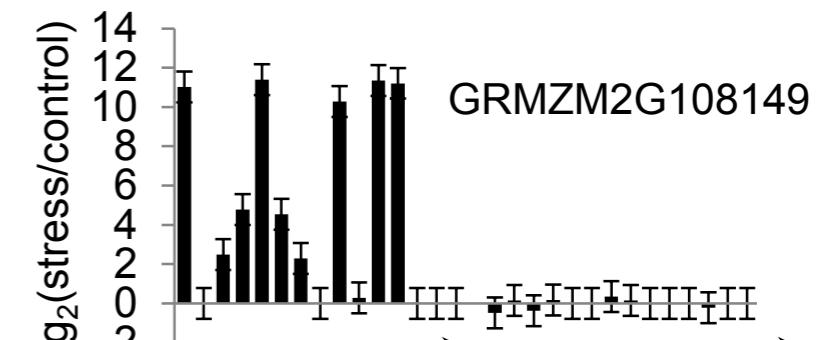
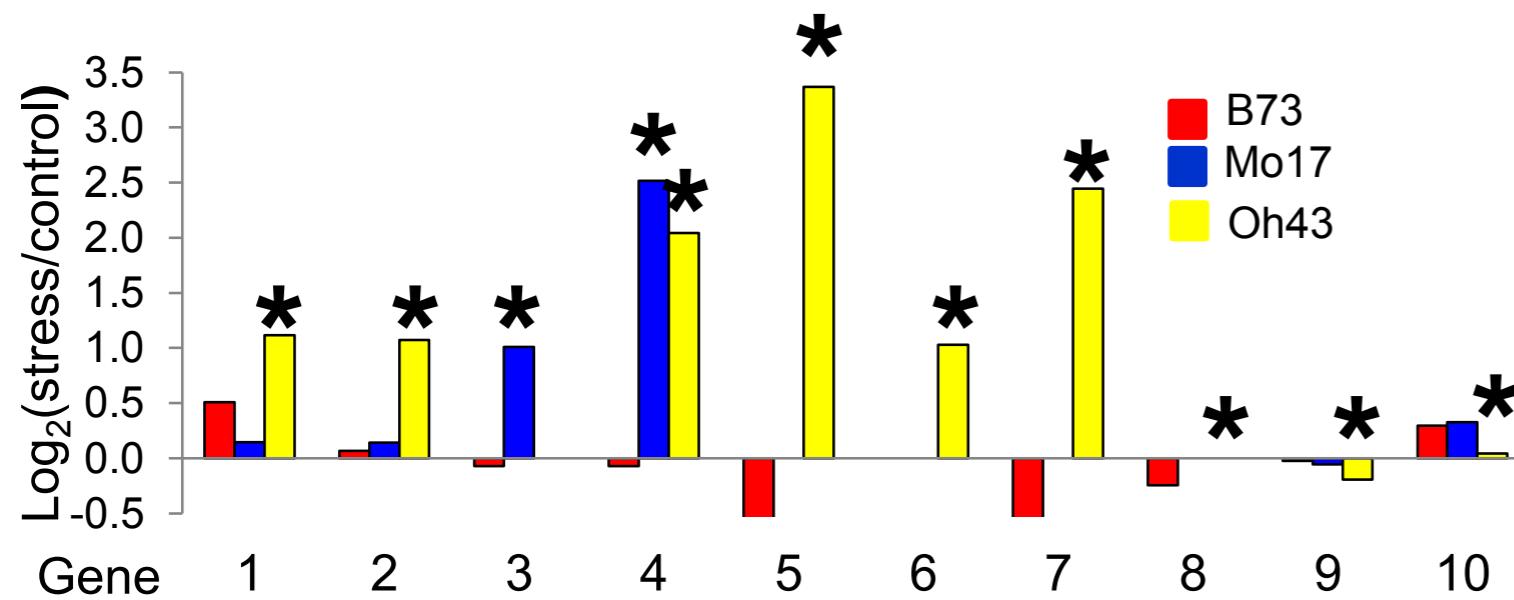
stress response associated with TEs



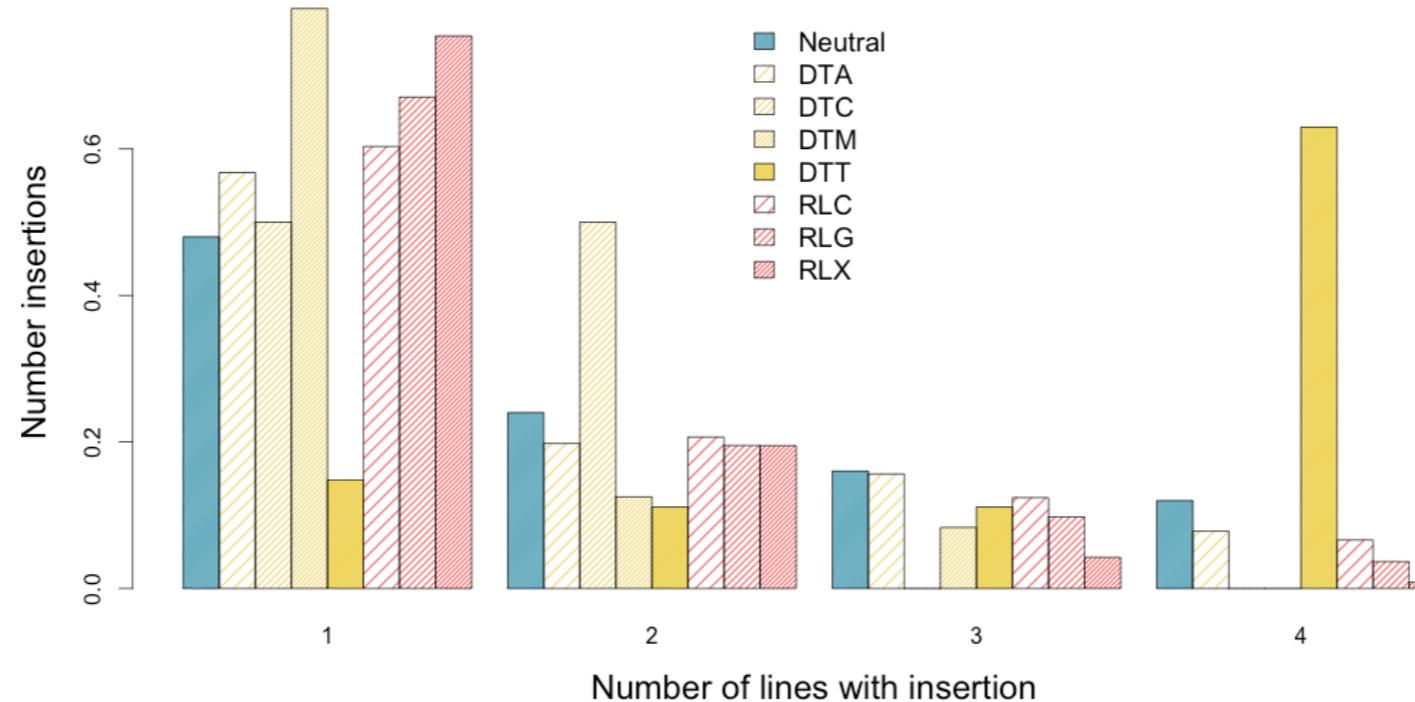
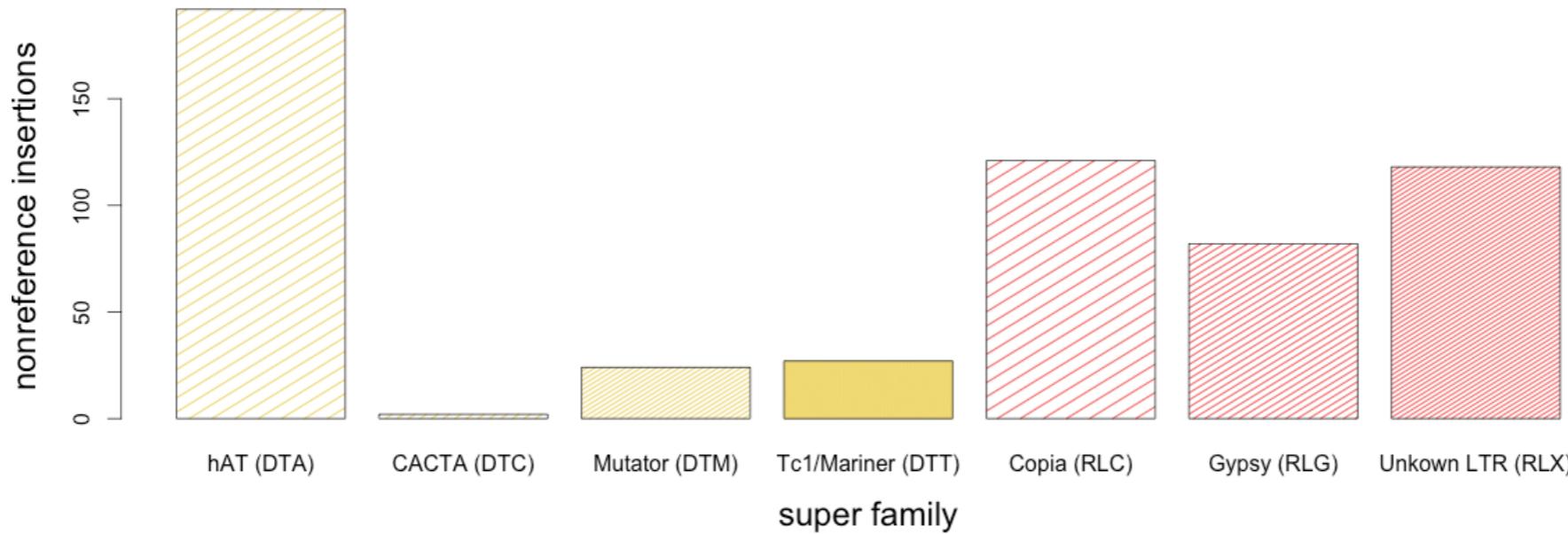
enrichment of specific TEs near genes



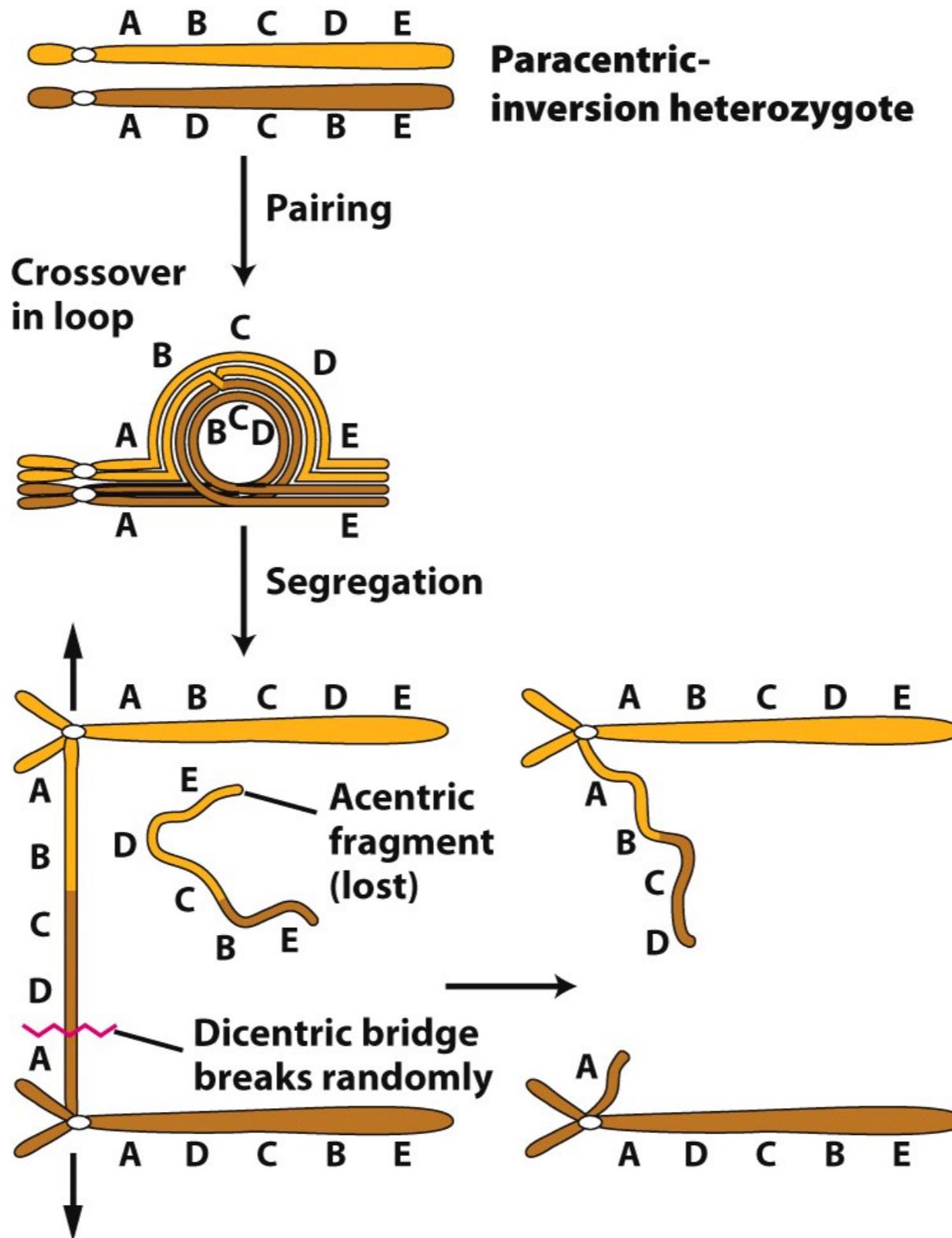
new insertions activate expression



evolutionary patterns differ among TEs

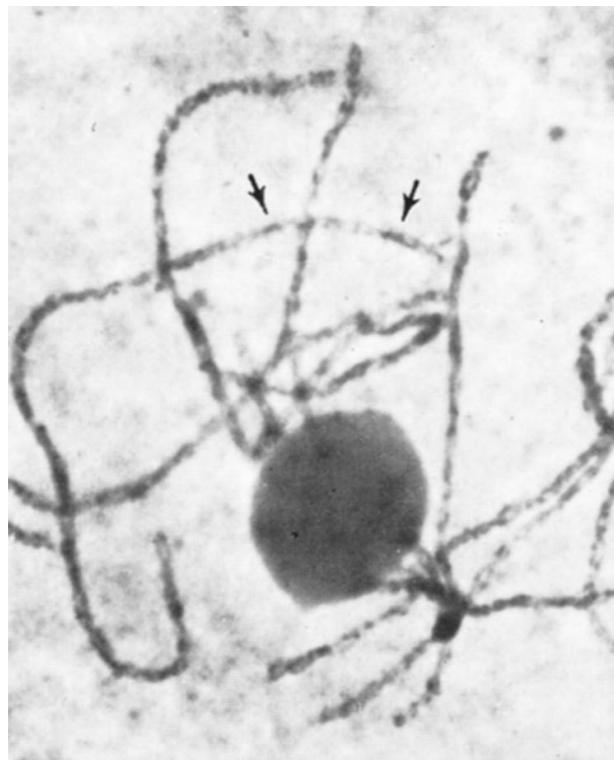


fitness cost of inversions

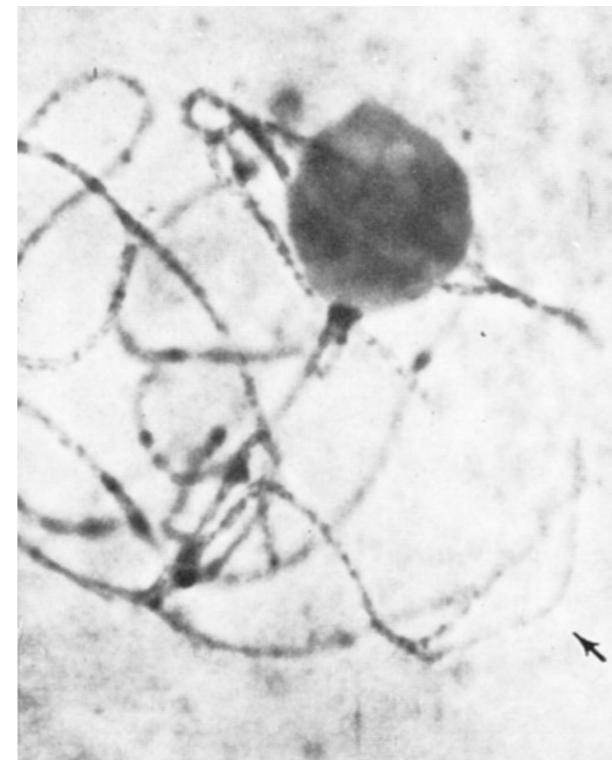


limited underdominance in maize

46%



20%



34%

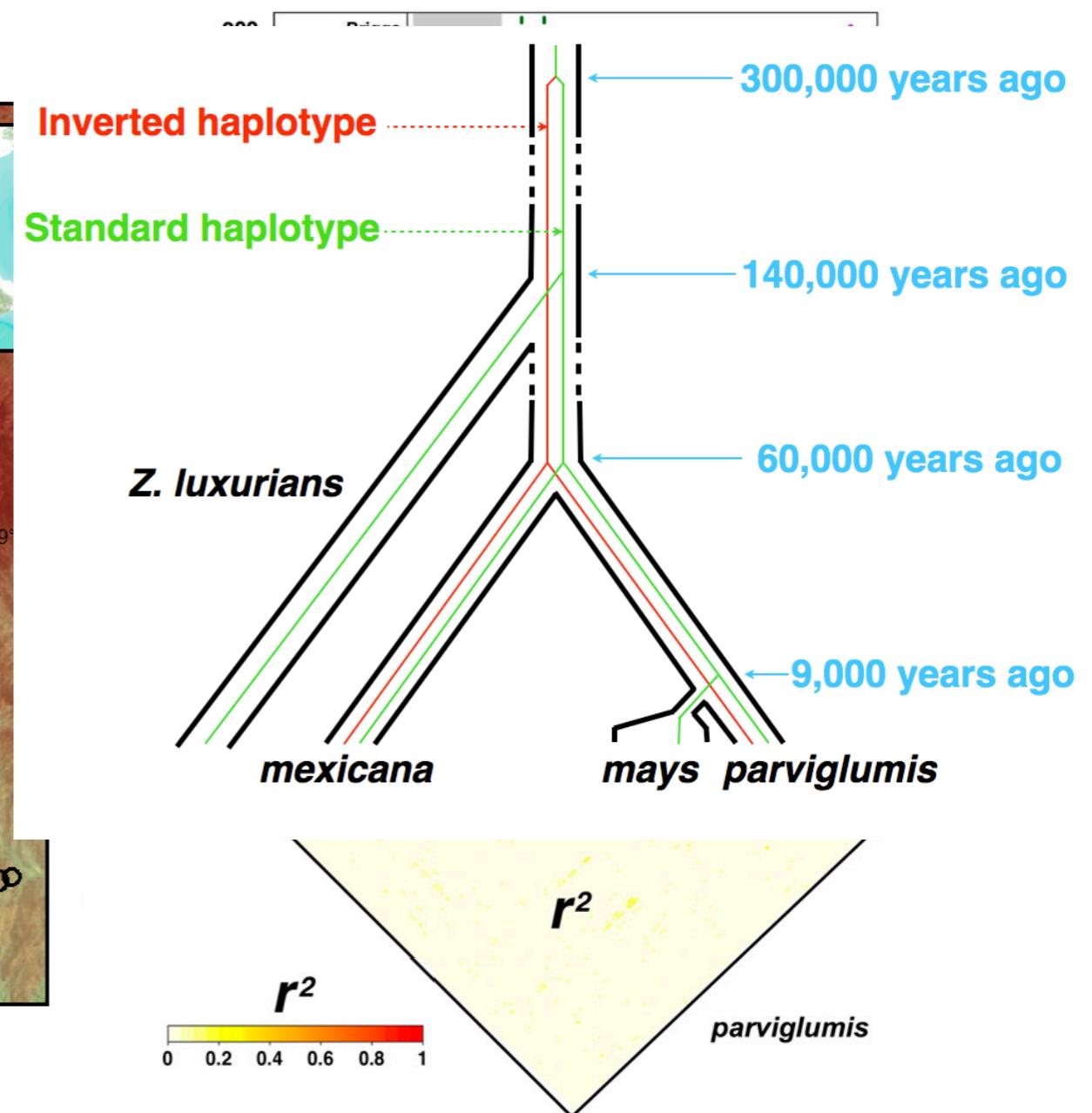
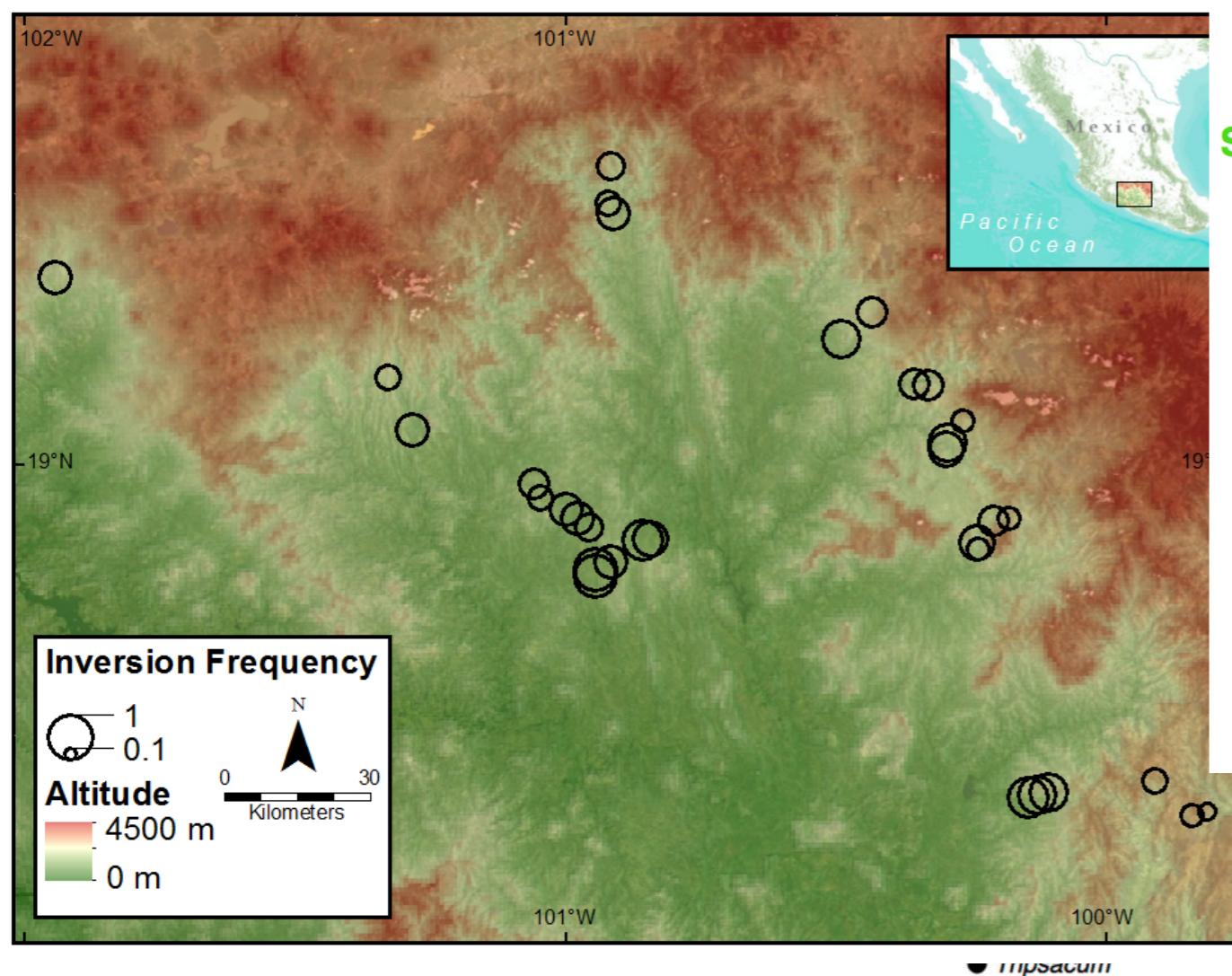


nonhomologous

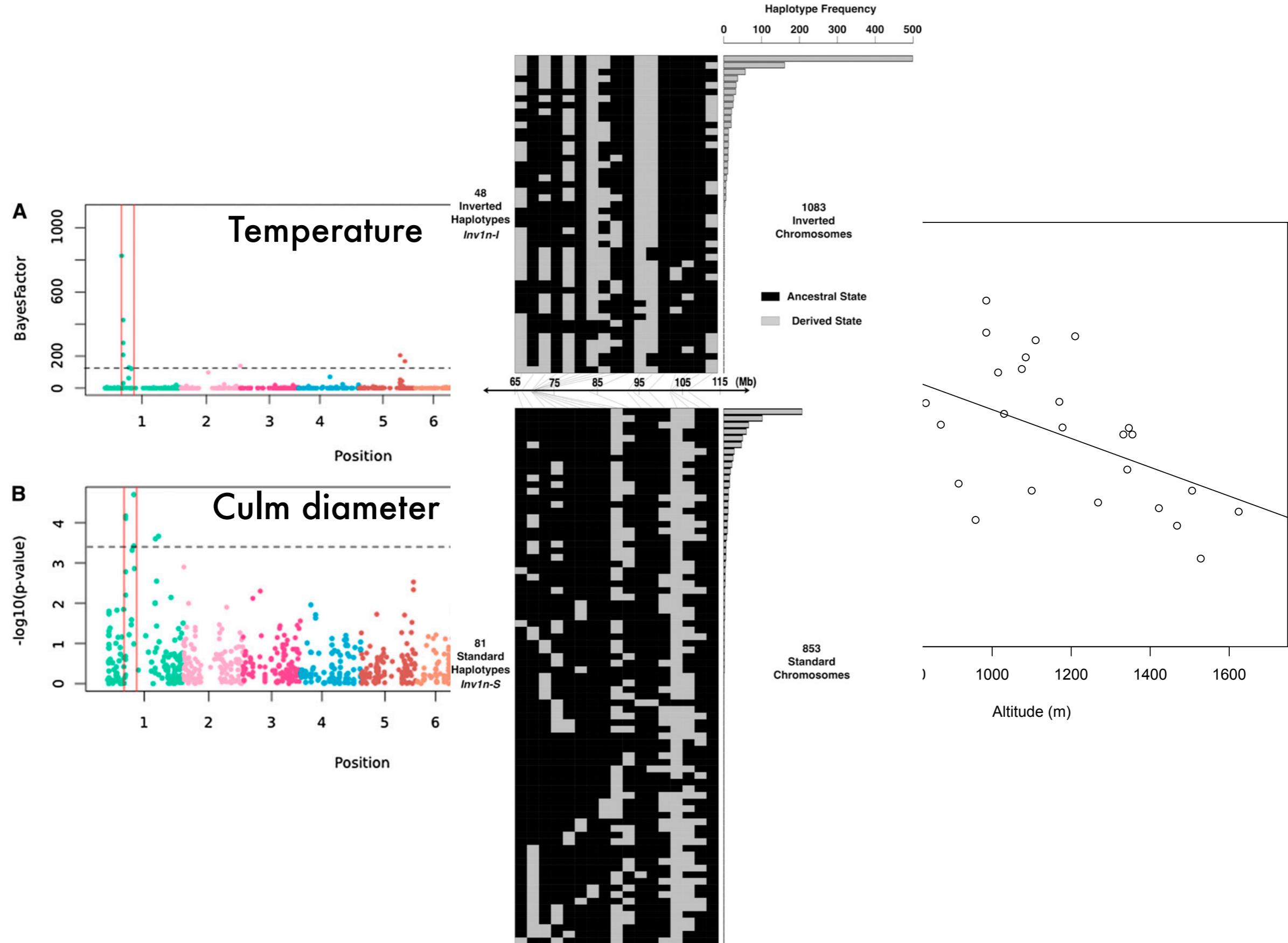
none

loop

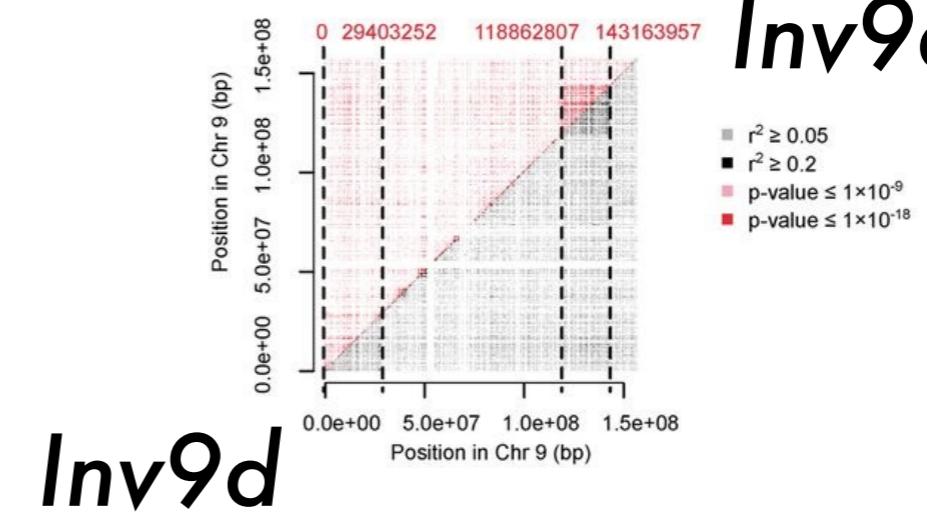
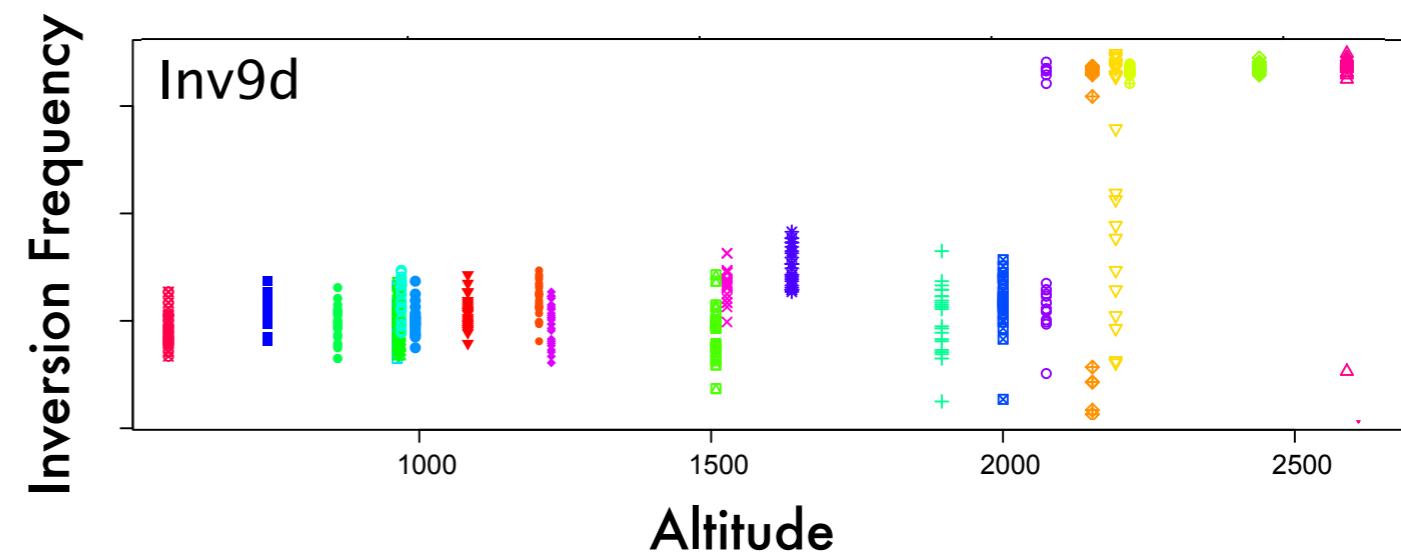
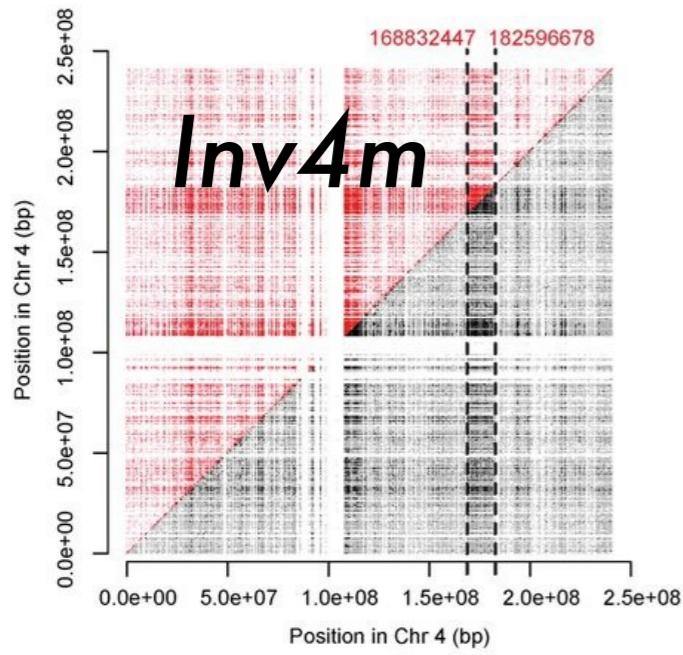
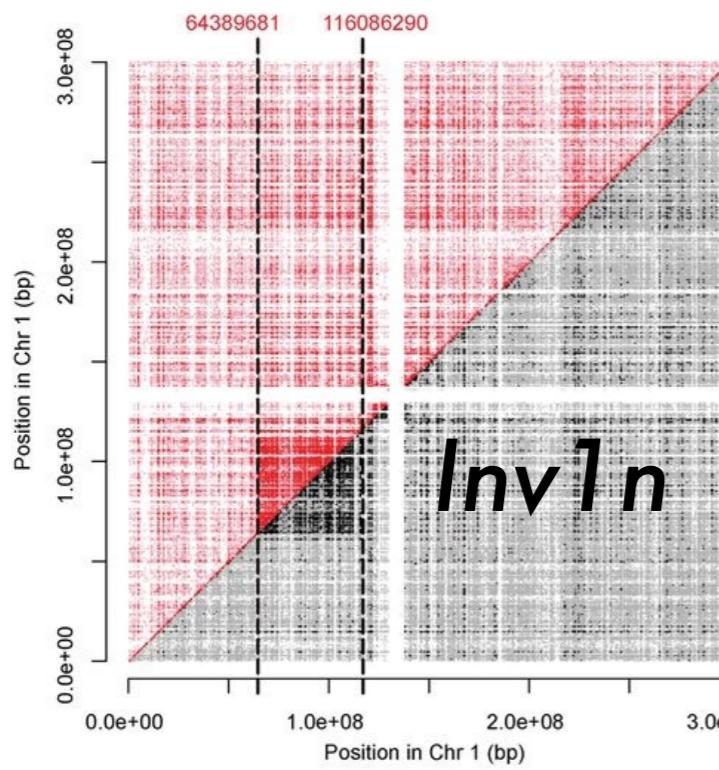
Inversion common and old



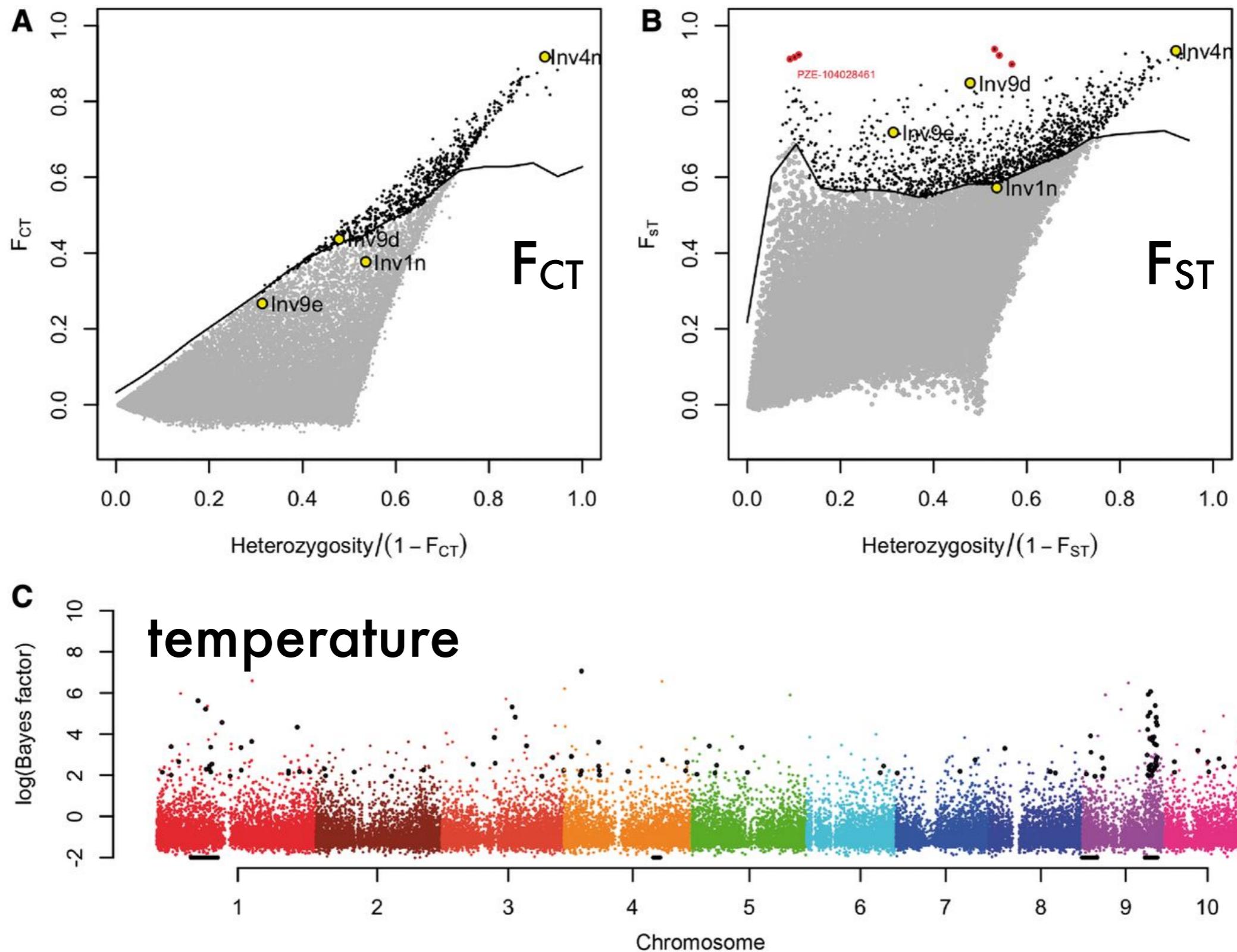
Inv1n: selection and associations



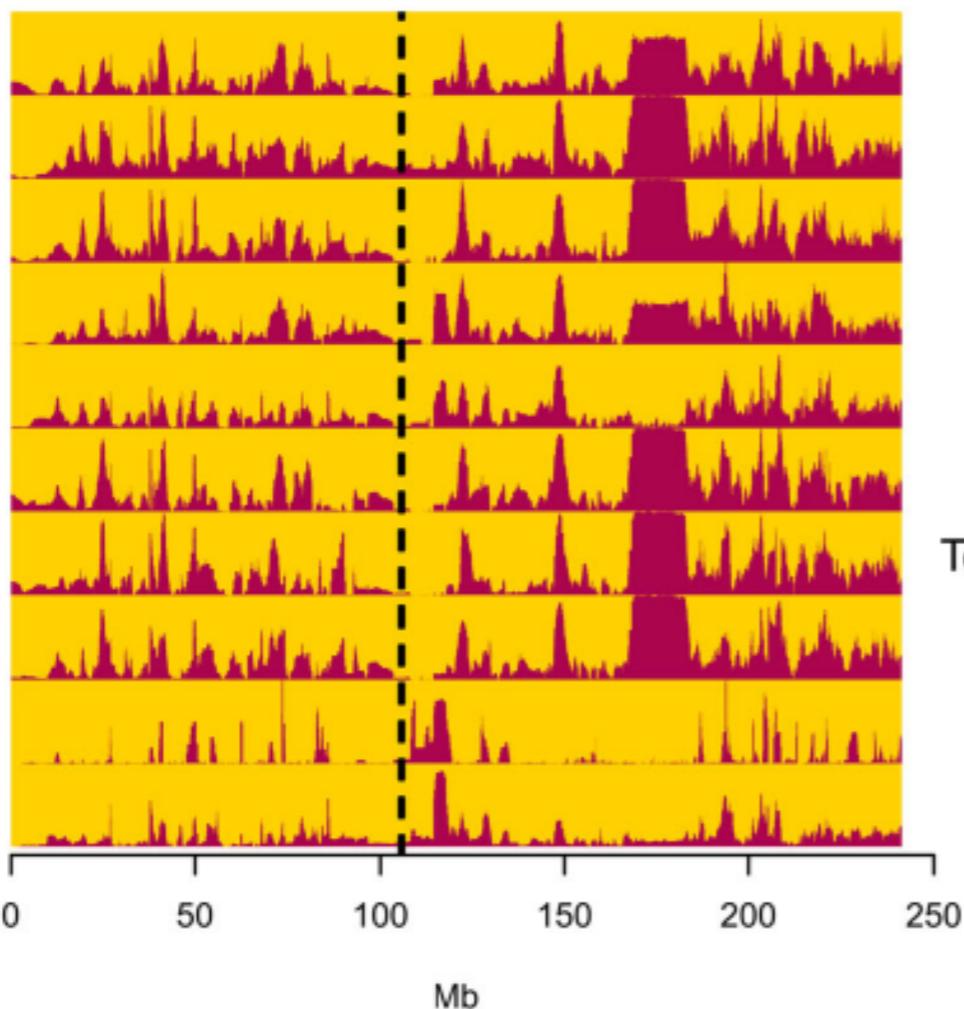
large inversions common, clinal



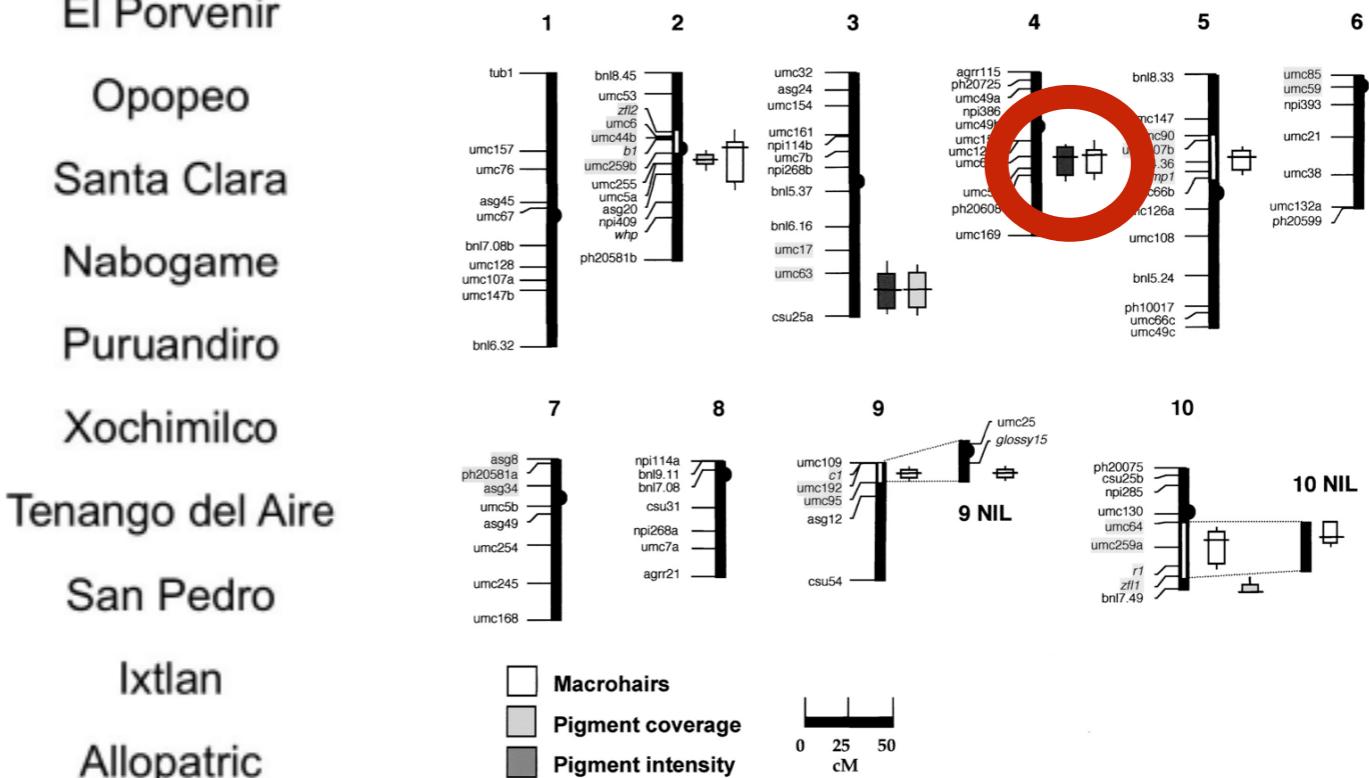
all inversions show signs of selection



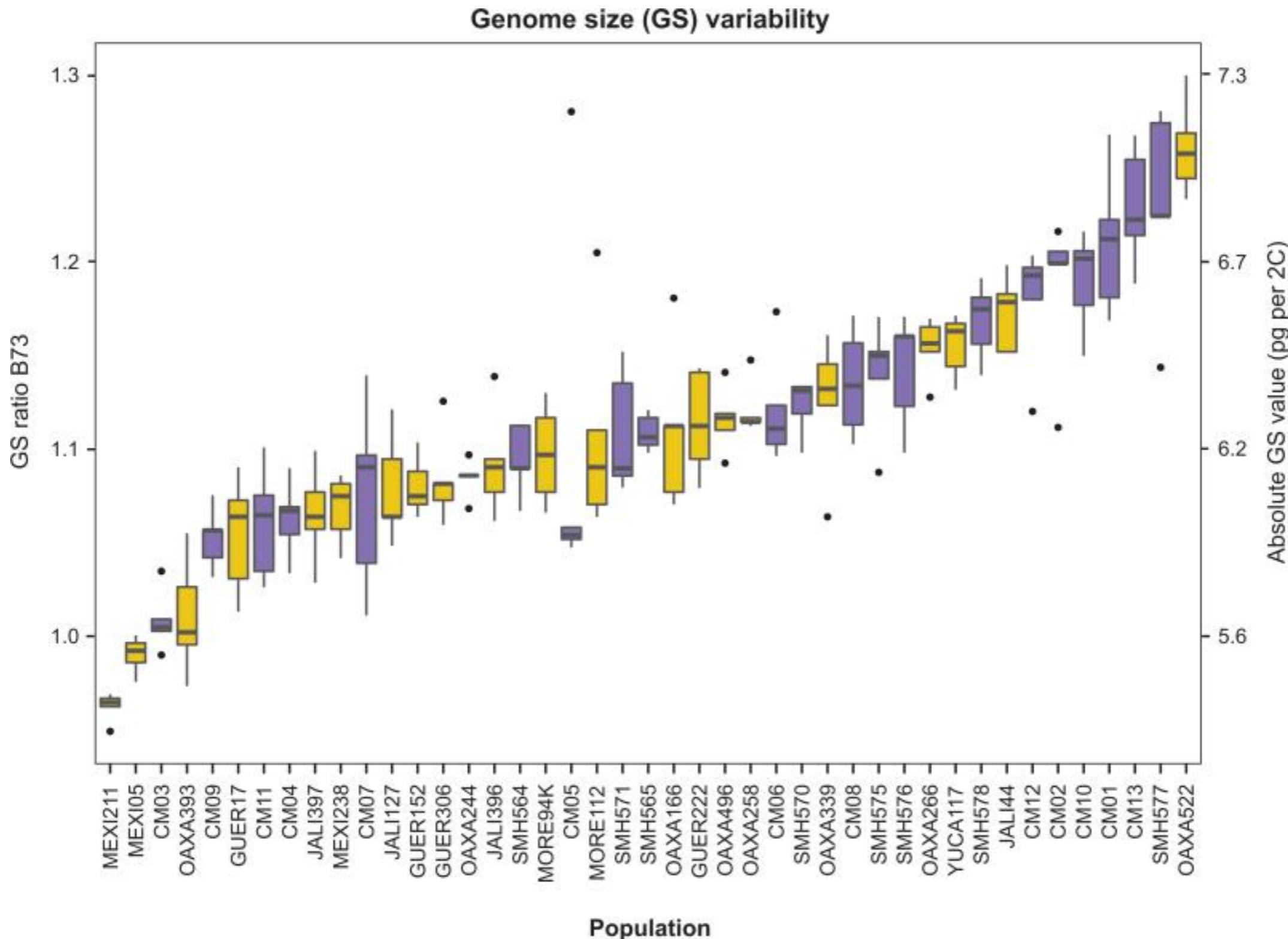
adaptive introgression of *Inv4m*



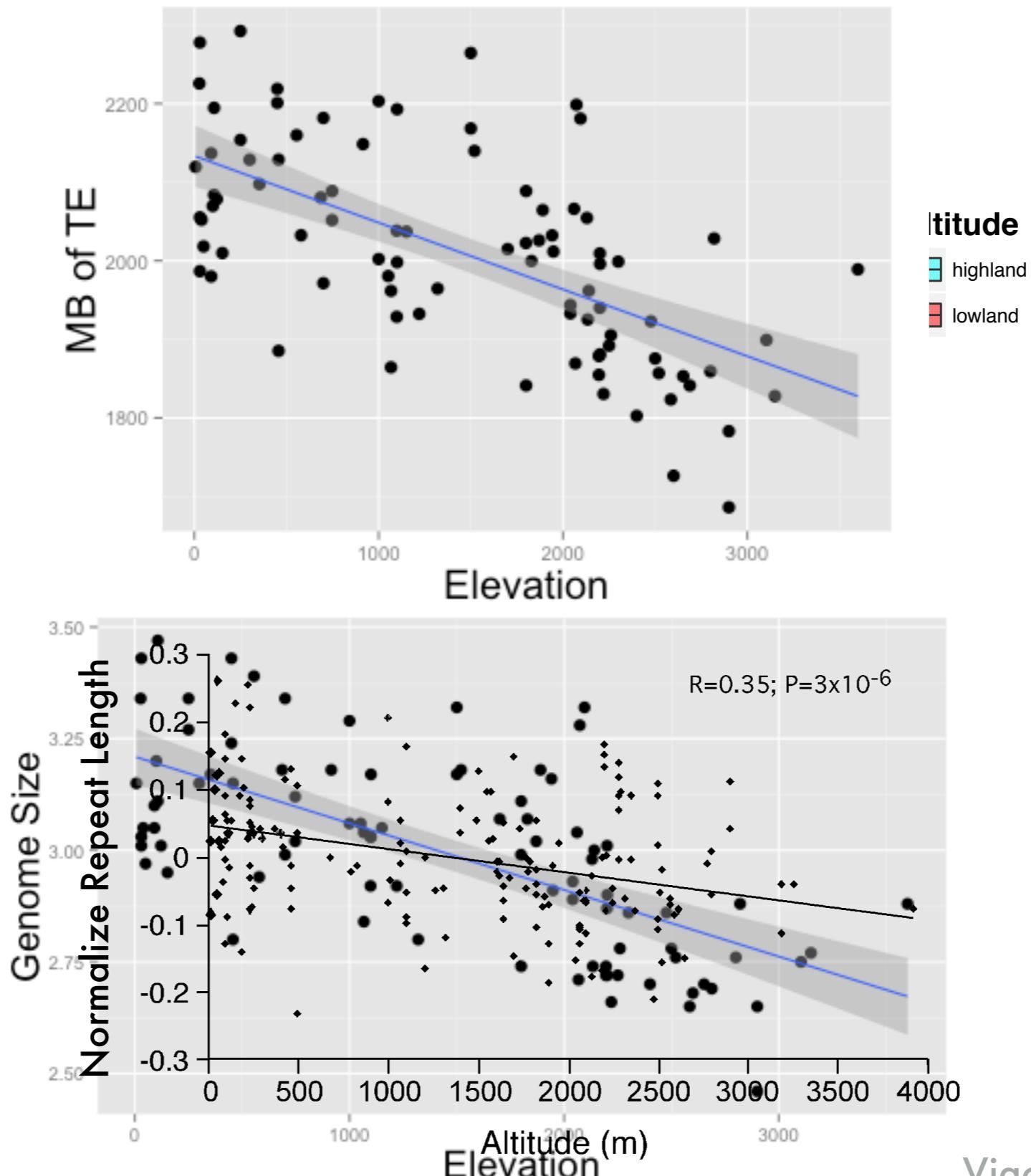
El Porvenir
Opopeo
Santa Clara
Nabogame
Puruandiro
Xochimilco
Tenango del Aire
San Pedro
Ixtlan
Allopatric



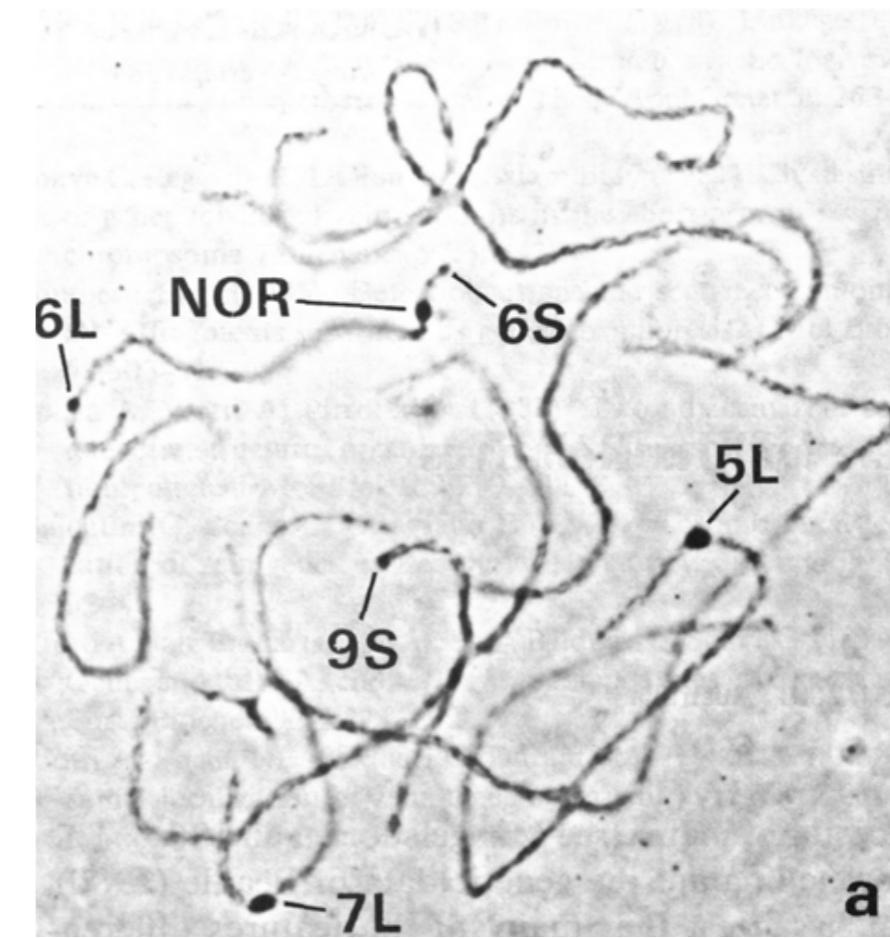
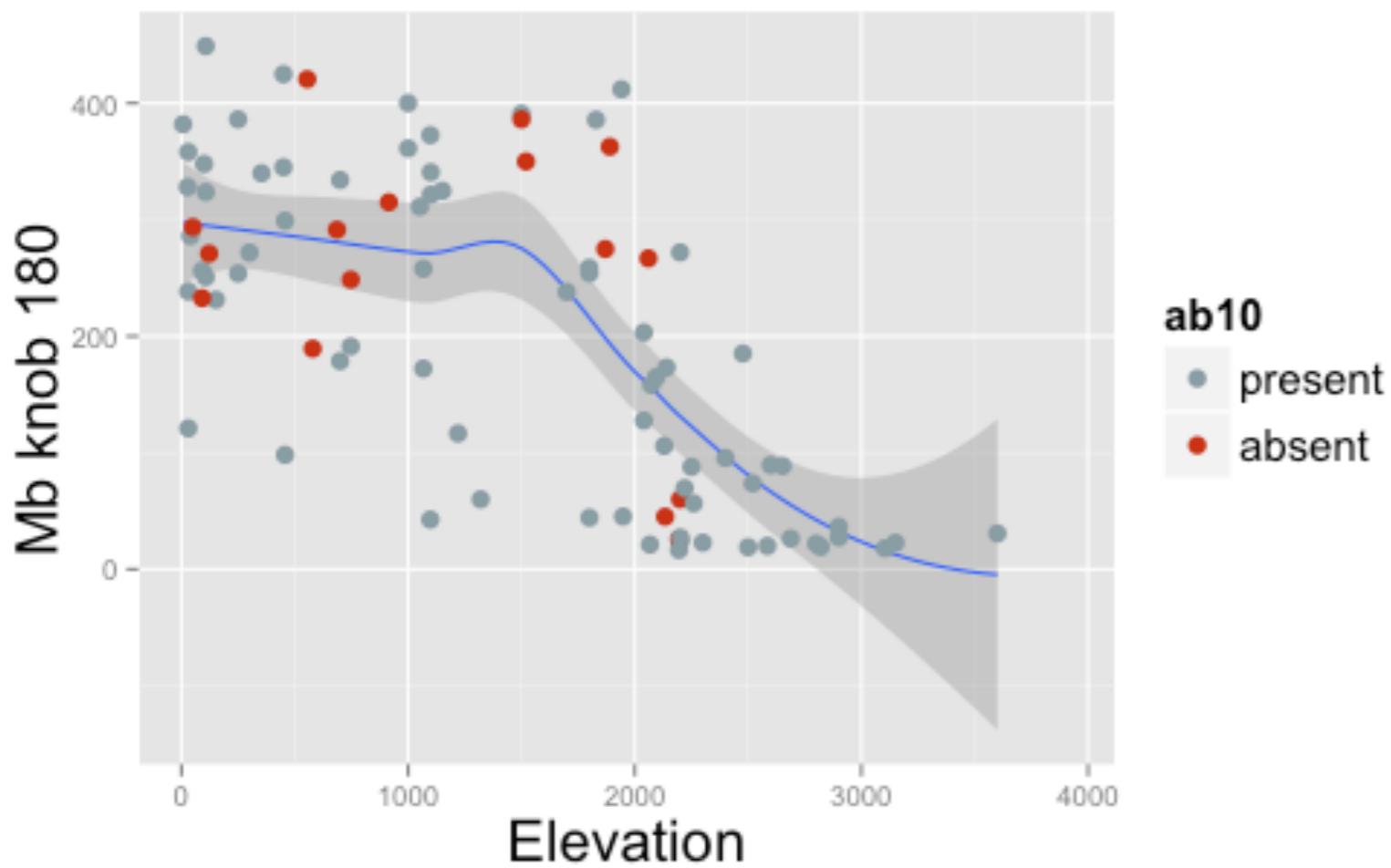
extensive variation in genome size



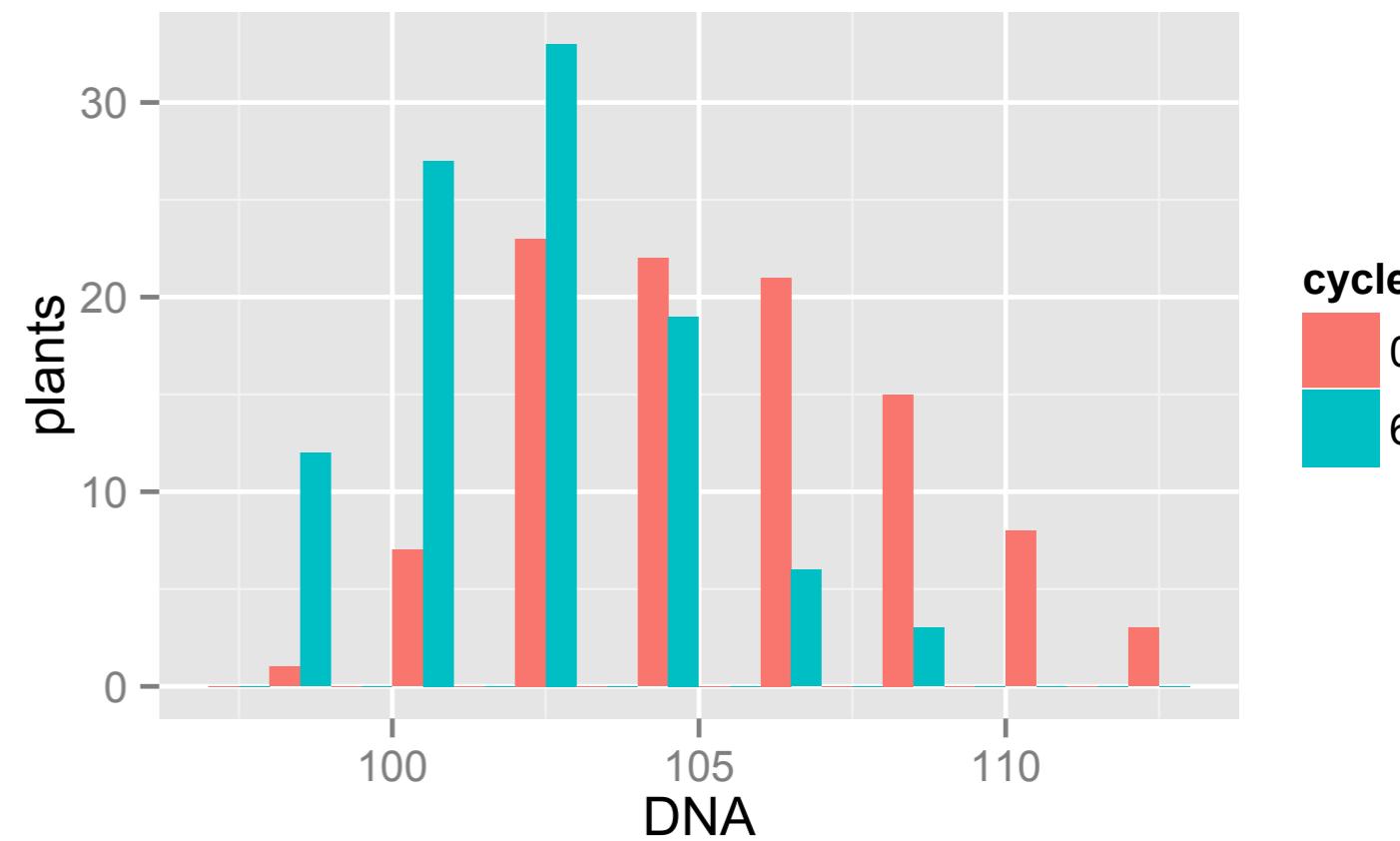
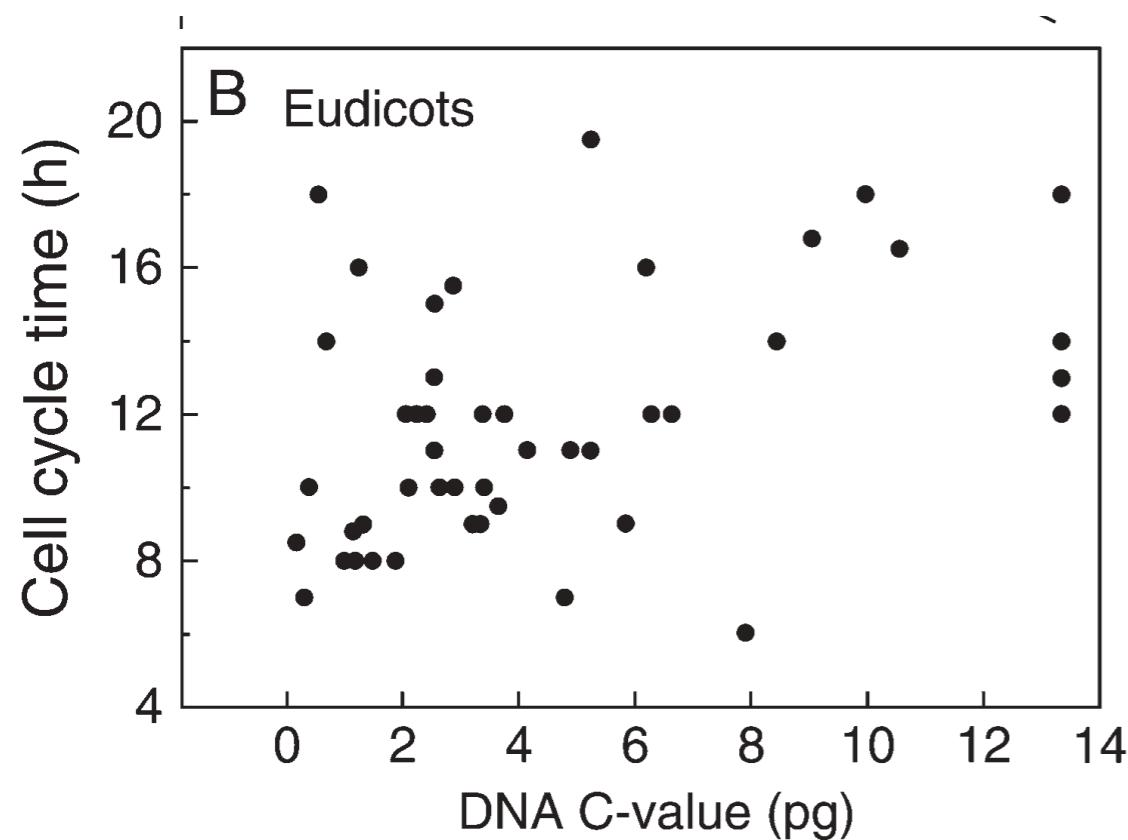
altitudinal cline in genome size in *Zea*



elevation cline at knobs

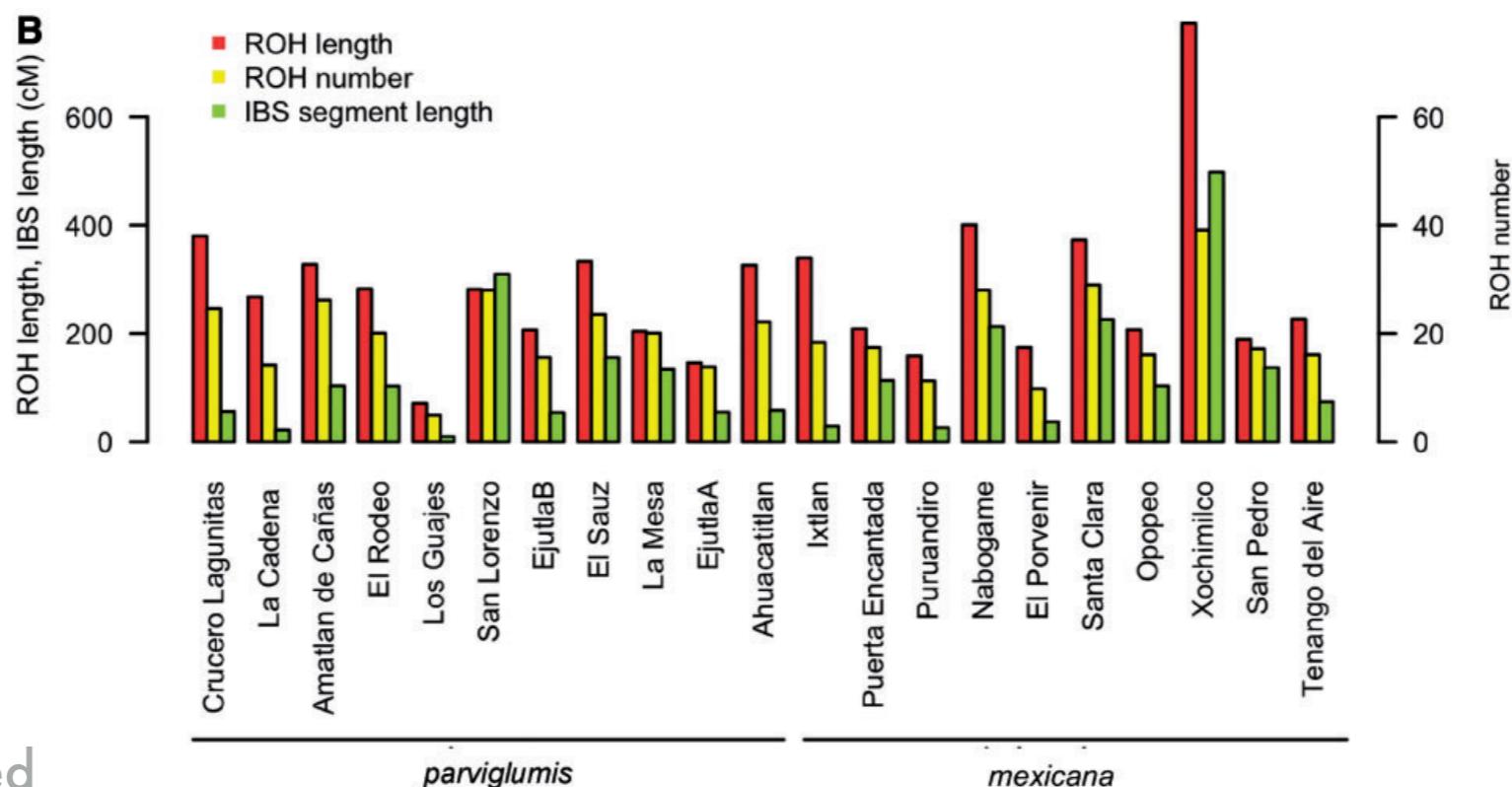
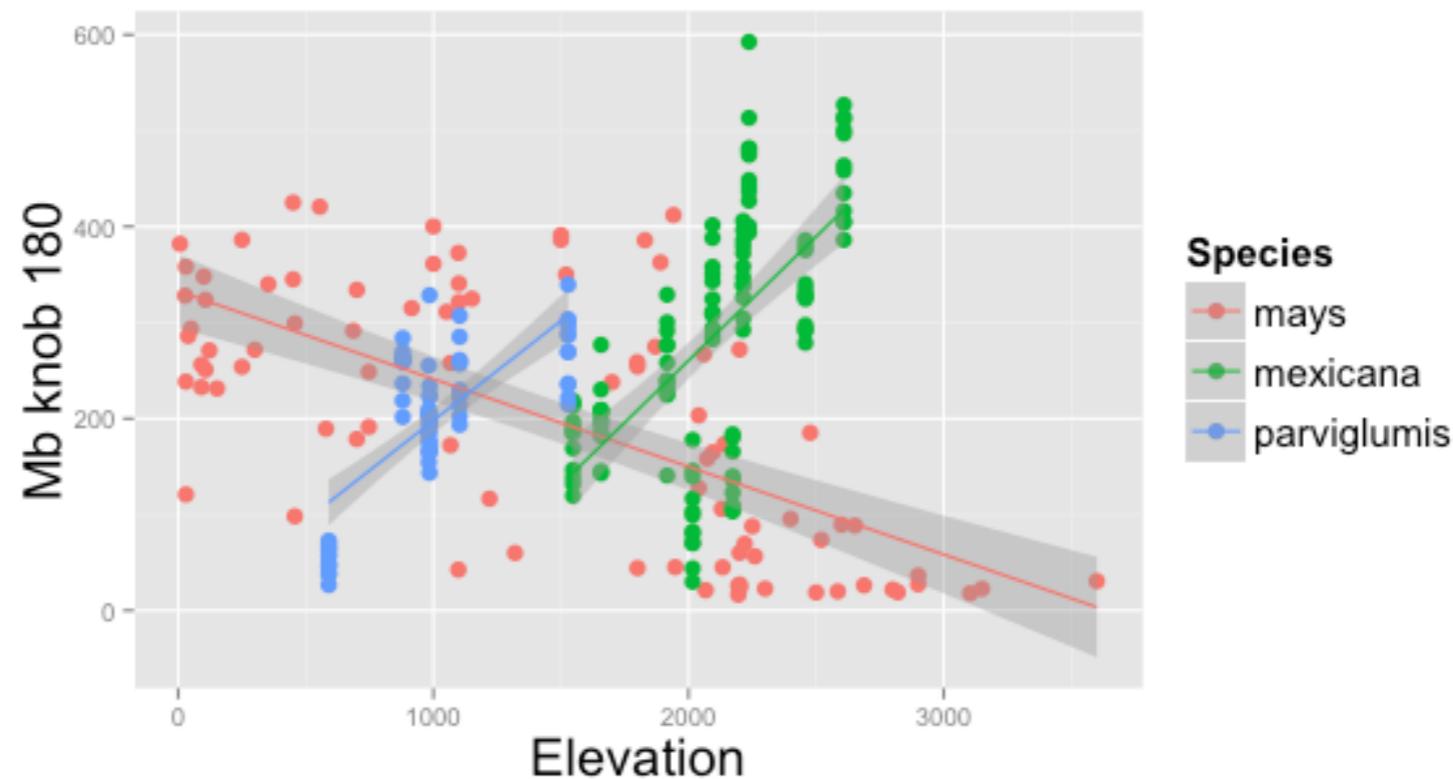


mechanism: cell cycle, flowering time?



Rayburn et al. 1994 Plant Breeding
Francis et al. 2008. Ann. Bot.

opposing clines in teosinte genome size



concluding thoughts

- simple scenarios of strong selection on new protein-coding mutations are probably rare
- much adaptation occurs via selection on quantitative traits, standing variation, and/or multiple mutations
- noncoding, structural variation likely play important roles in adaptation