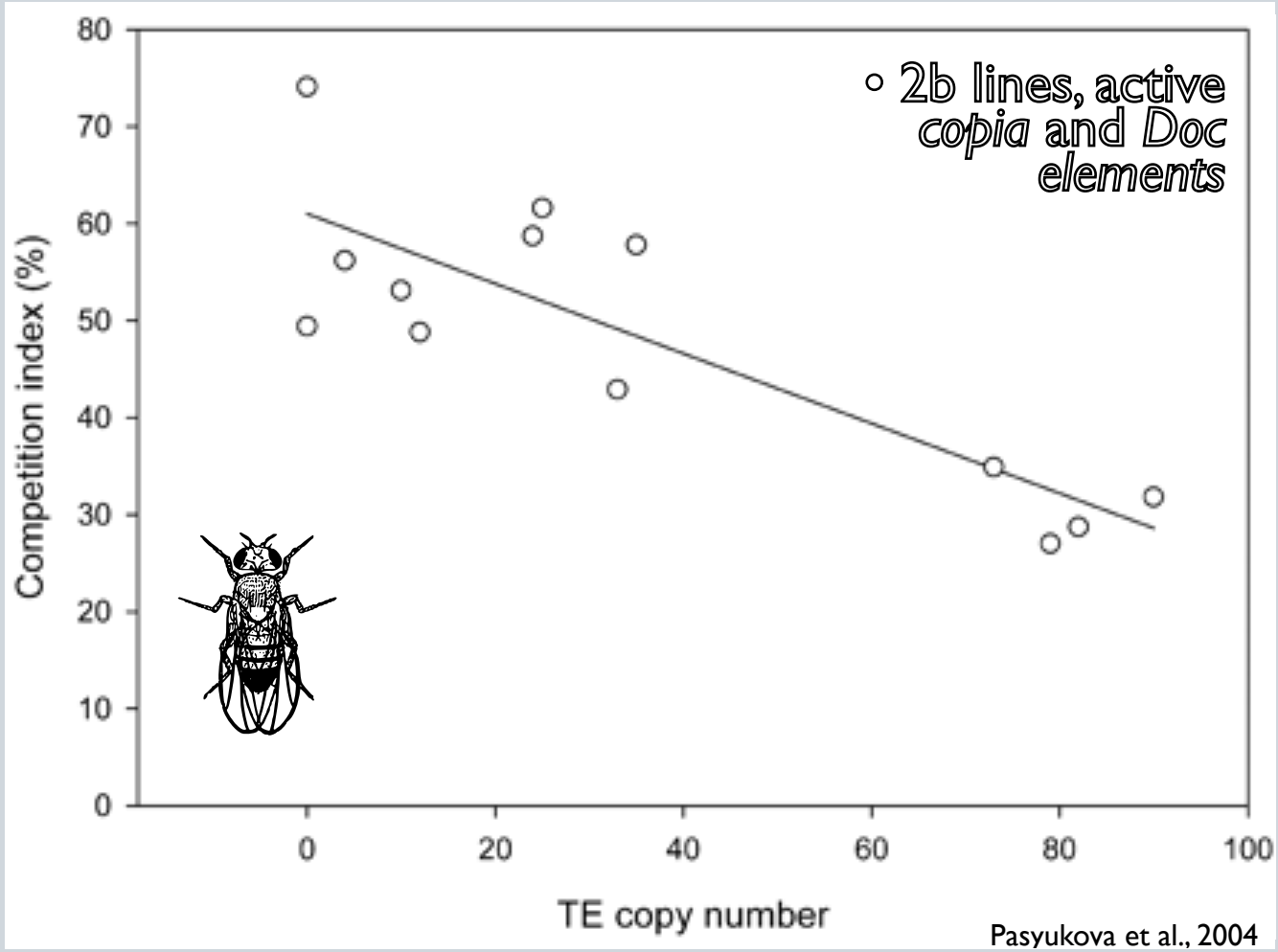


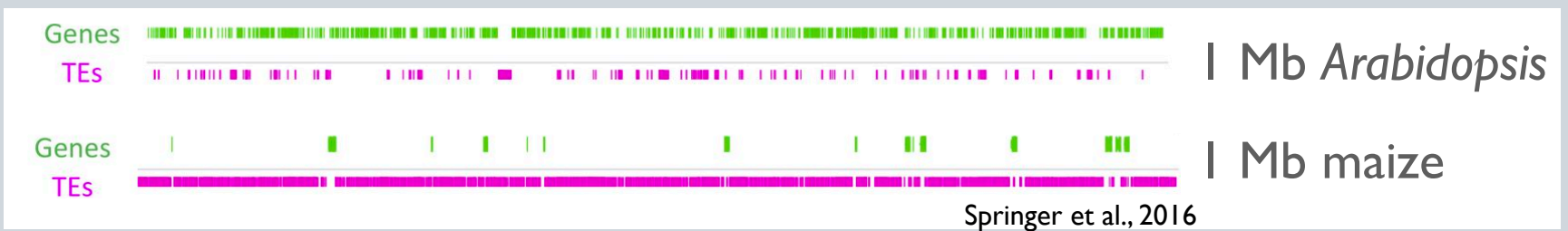
# Transposable element accumulation reduces fitness in maize

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Increased TE copy number decreases fitness in other organisms (that have smaller genomes)

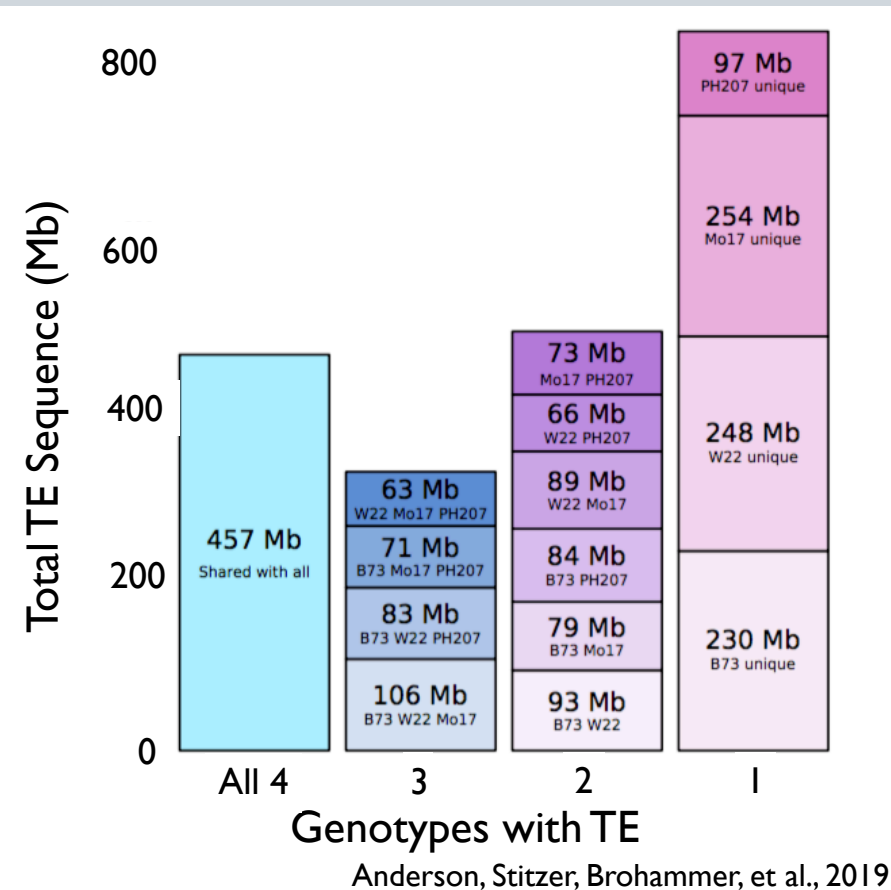


The maize genome has hundreds of thousands of TEs



TEs are polymorphic between maize individuals

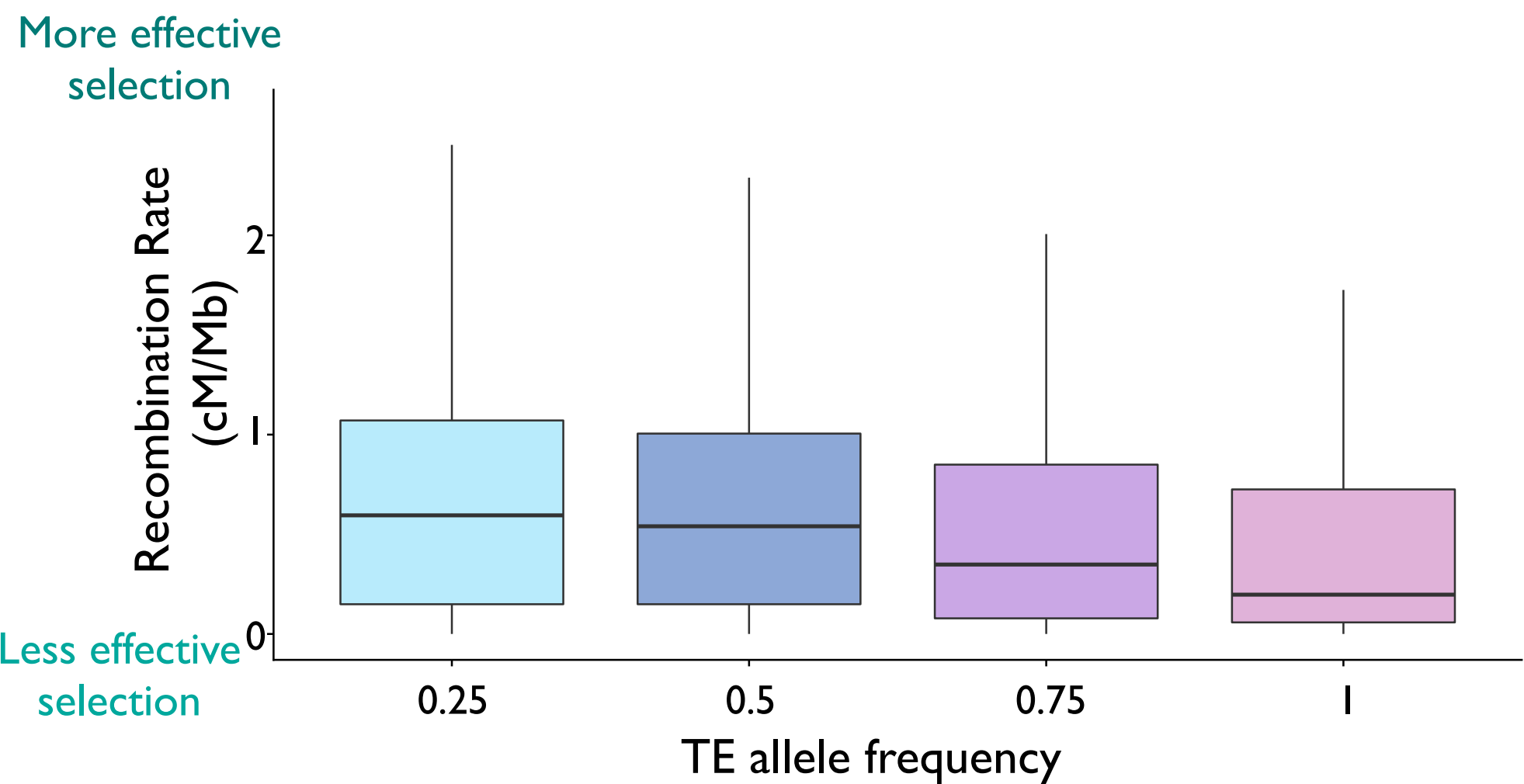
Most TE copies are absent in at least one inbred line, as shown by identifying orthologous TE insertion loci across four inbred lines, B73, W22, MoI7, and PH207.



## Does genetic load contributed by TEs reduce maize fitness?

Over evolutionary time scales, TEs are deleterious

For example, TEs that are fixed across B73, W22, MoI7, and PH207 are found in regions of lower recombination, where natural selection is less effective.



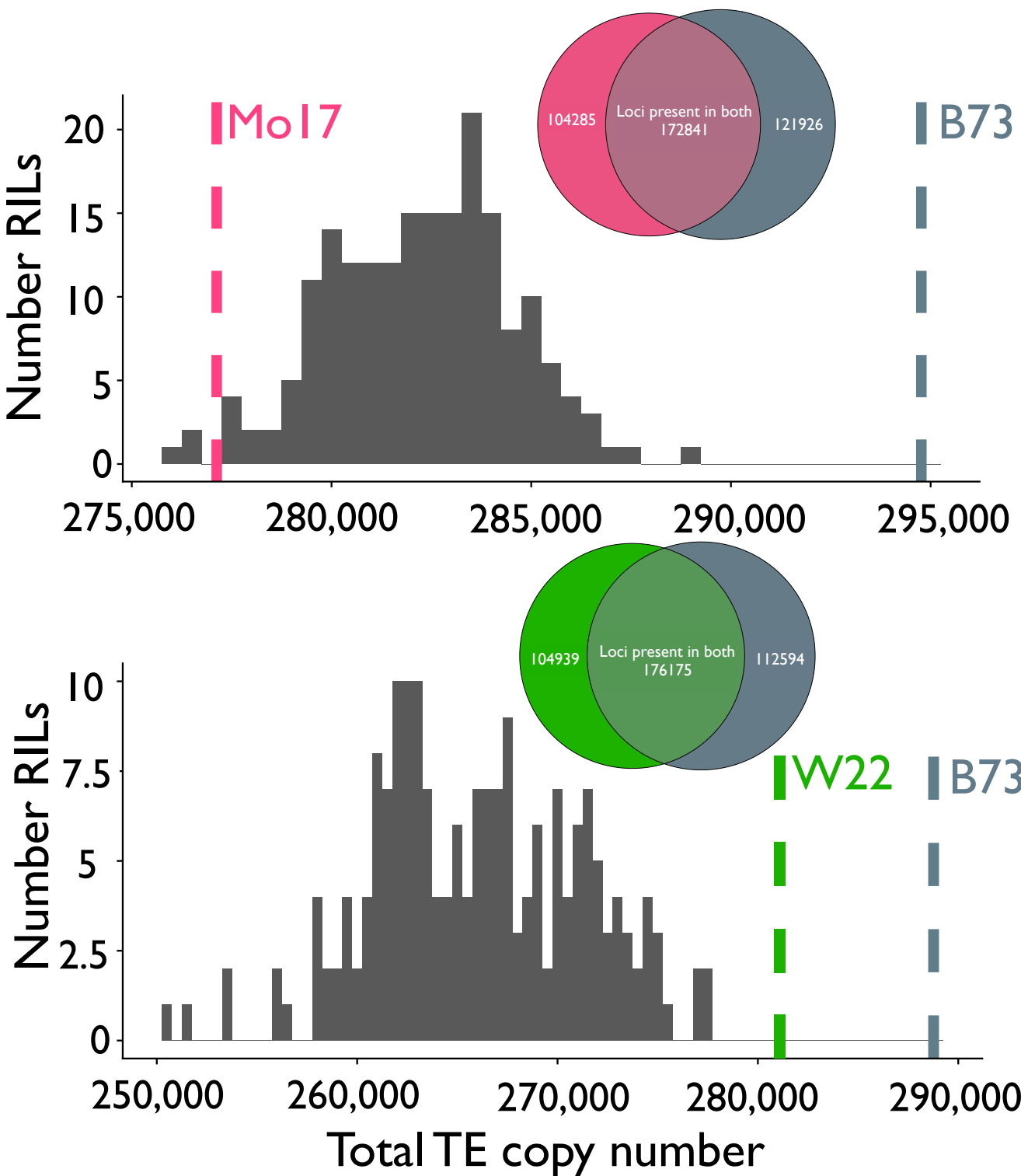
Over shorter time scales, we can project TE copy number to RILs to explore fitness costs

We impute TE copy number from parental genomes onto two genotyped populations of Recombinant Inbred Lines (RILs)

- B73 x MoI7 (IBM)
- B73 x W22

RIL TE copy number shows different relationships to parental copy number in each population.

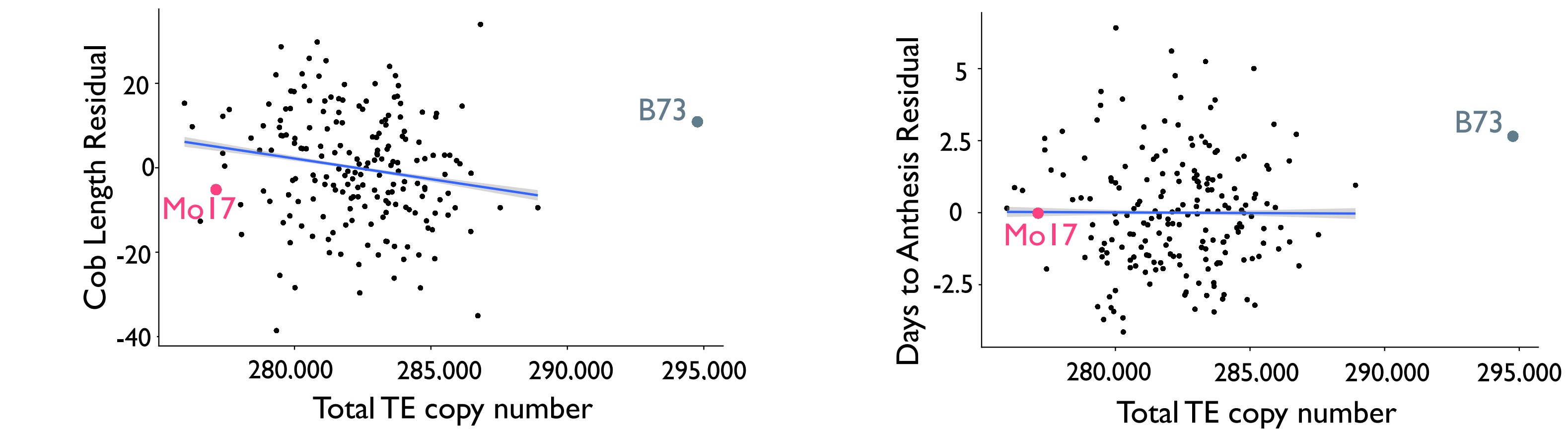
Recently released genomes of parents of 25 mapping populations (the maize Nested Association Mapping panel) will allow us to explore the generality of transgressive copy number in RILs.



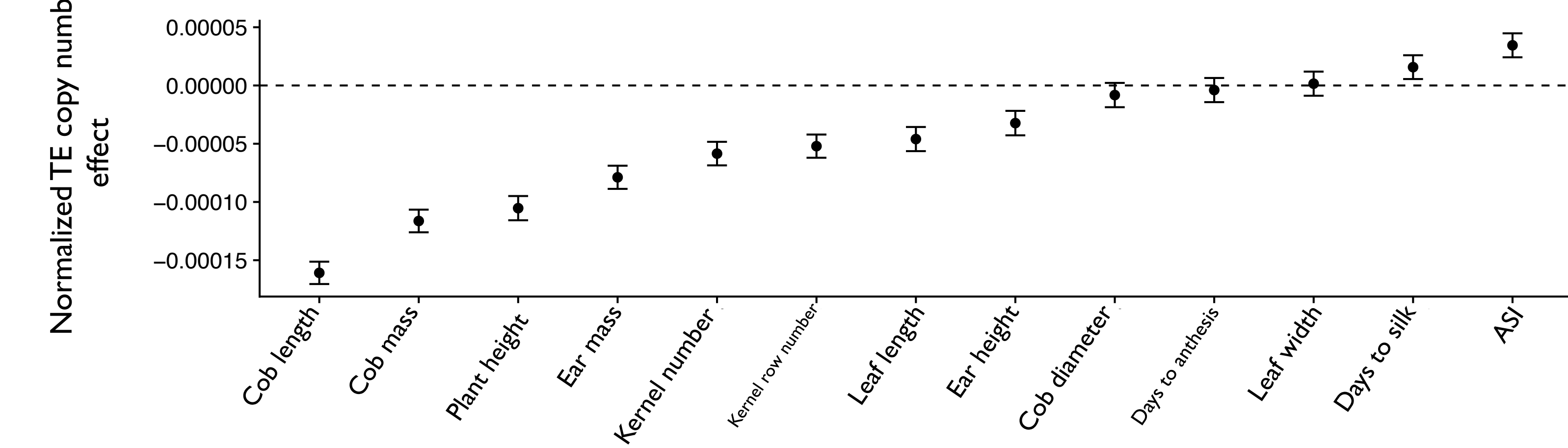
## Higher TE copy number is associated with lower fitness

Individuals with more TEs have lower values of fitness related phenotypes

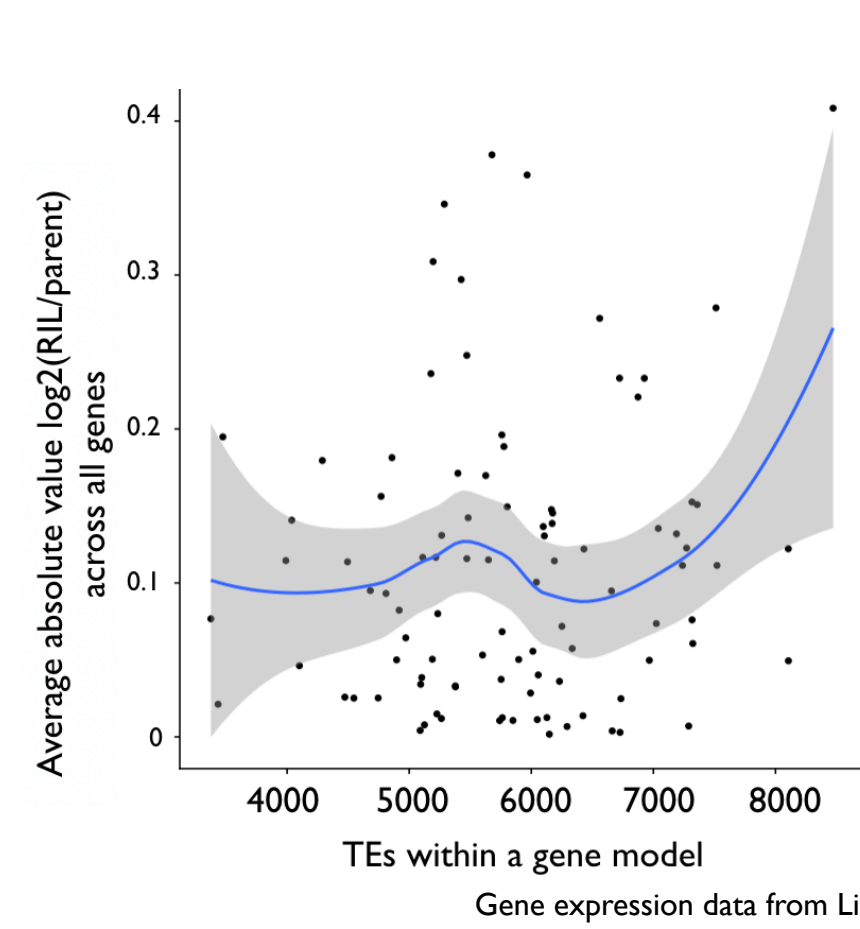
We correct for proportion B73 parentage in each RIL, and associate residual values with phenotypes.



Traits like flowering time are not strongly correlated to TE copy number, while traits related to grain yield (fitness) are negatively correlated with TE copy number

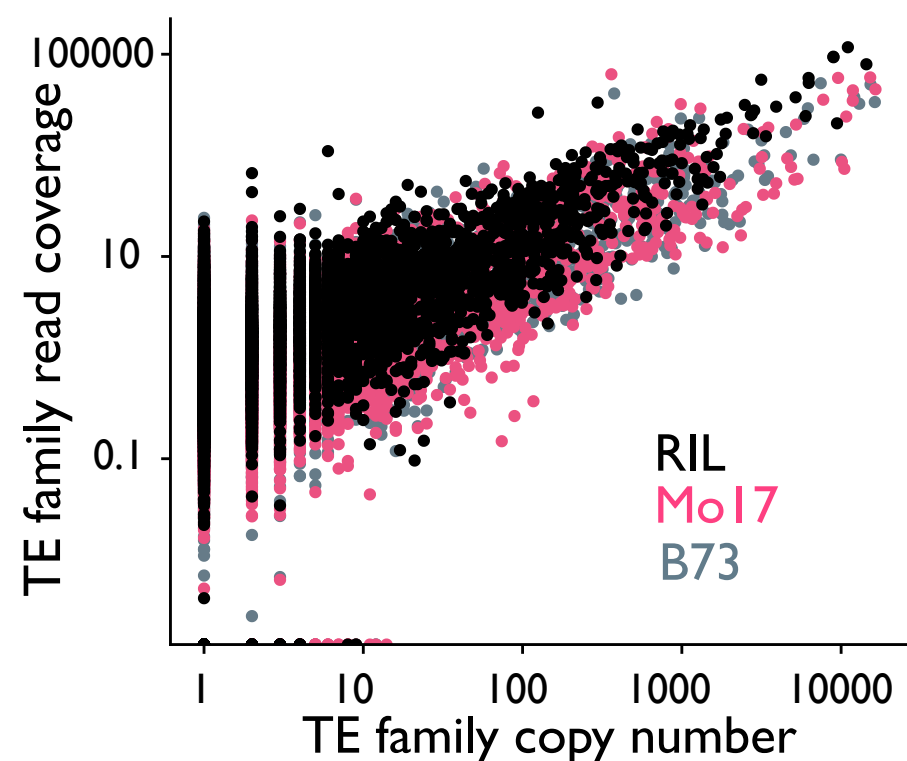


Individuals with more TEs may have expression levels more divergent from their parents



We calculate how divergent gene expression is in RILs as compared to parents, using seedling gene expression data from Li et al., 2013. RILs with more TEs in genes show higher deviation in expression from their parents.

Some of these effects may be due to new transposition



By mapping whole genome resequencing of 2 RILs, we identify TE families with higher coverage than expected from their imputed copy number, which may suggest new transposition during RIL construction.

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### References:

Anderson, Stitzer, Brohammer, Zhou, Noshay, O'Connor, Hirsch, Ross-Ibarra, Hirsch, and Springer (2019) The Plant Journal: Transposable Elements Contribute to Dynamic Genome Content in Maize; Li, Petsch, Shimizu, Liu, Xu, Ying, Yu, Scanlon, Schnable, Timmermans, Springer, and Muehlbauer (2013) PLoS Genetics: Mendelian and Non-Mendelian Regulation of Gene Expression in Maize; Pasyukova, Nuzhdin, Morozova, Mackay (2004) Journal of Heredity: Accumulation of Transposable Elements in the Genome of Drosophila melanogaster is Associated with a Decrease in Fitness; Springer, Lisch, Li (2016) The Plant Cell: Creating Order from Chaos: Epigenome Dynamics in Plants with Complex Genomes

### Acknowledgements:

This material is based upon work supported by the NSF Postdoctoral Research Fellowship in Biology under Grant No. 1907343.

