

Limited contribution of transposable elements to regulatory adaptation in maize inbreds and hybrids



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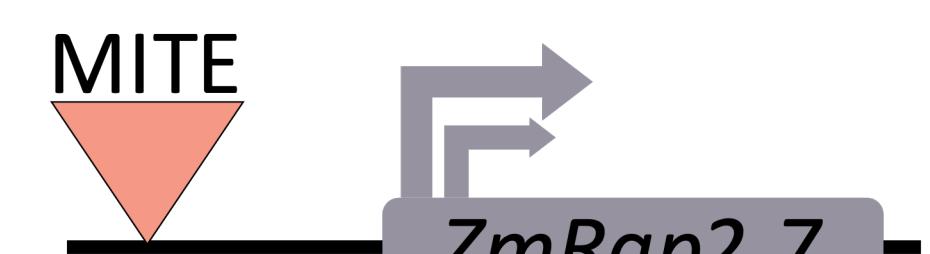
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Transposable element insertions in maize can drastically alter plant phenotypes and gene expression under stress.

Vegetative to generative transition 1

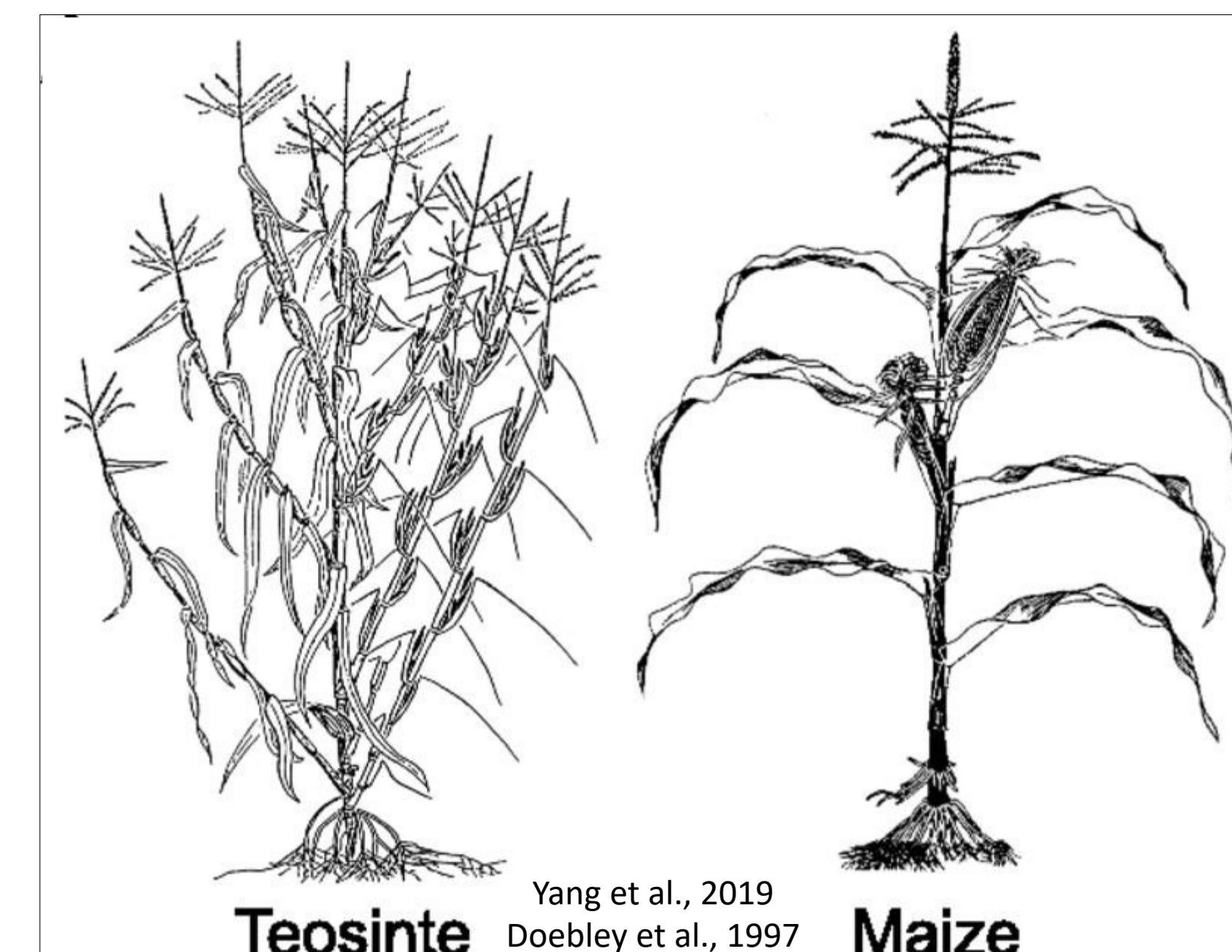
Tourist family MITE insertion in *Vgt1* 70 Kb upstream of *ZmRap2.7* leads to a ~4.5-day difference in days to silking.



Salvi et al., 2007

Teosinte branched 1

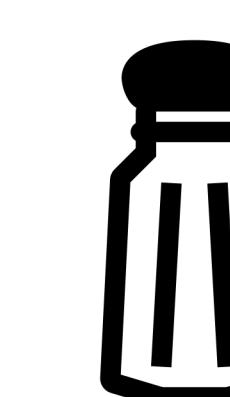
Hopscotch insertion 64 Kb upstream of *Tb1* represses growth of aerial branching.



Yang et al., 2019
Doebley et al., 1997



Heat
etug & naiba
(RLX) upregulate 173 genes



Salt
ipiki & naiba (RLX)
upregulate 201 genes



Cold
joemon & naiba
(RLX) upregulate 621 genes



UV
ipiki & joemon
(RLX) upregulate 252 genes

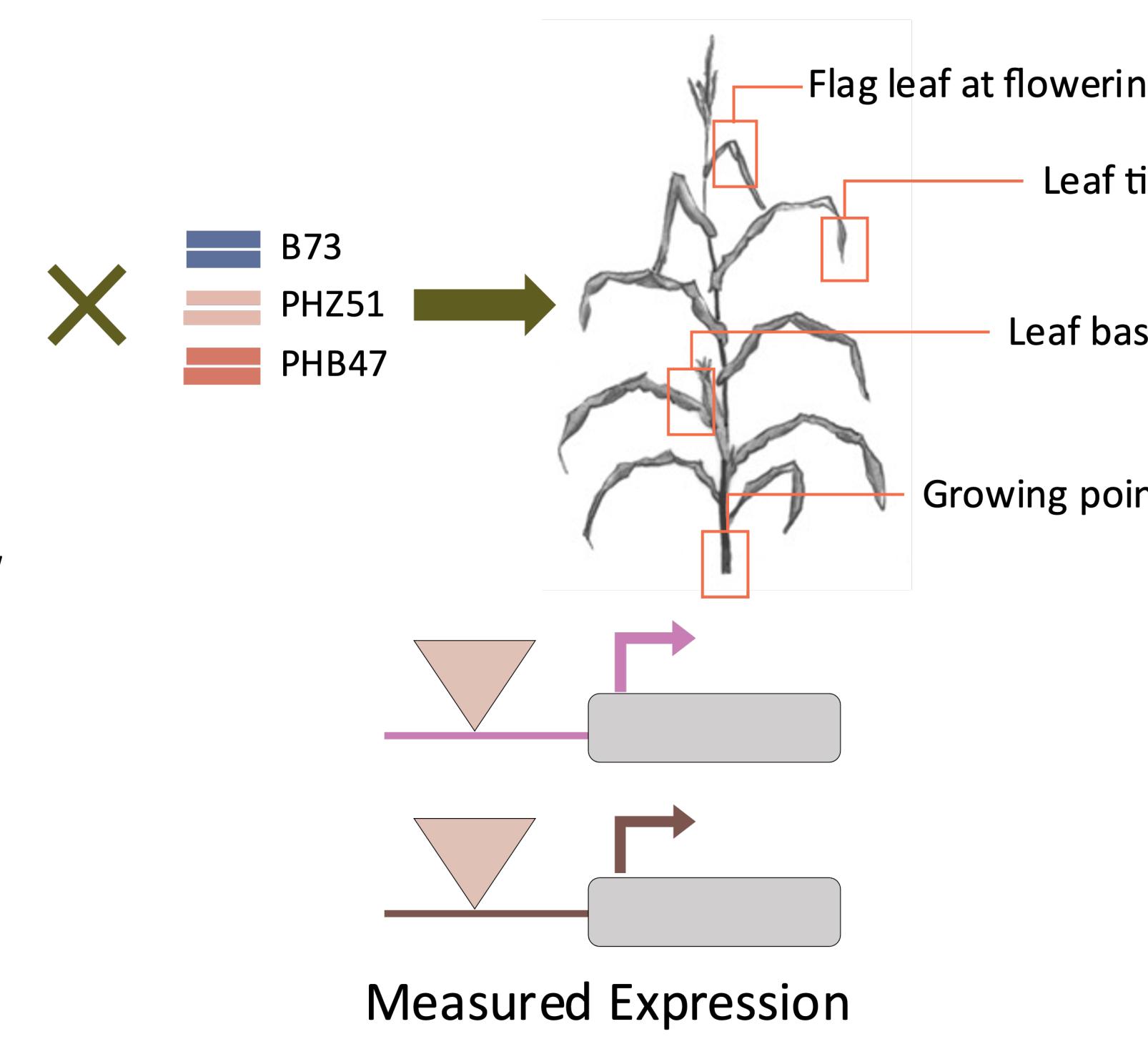
Which TEs impact gene expression during normal plant development in maize inbreds and hybrids?

Nested Association Mapping (NAM) inbreds

- B97
- CML103
- CML228
- CML247
- CML777
- CML322
- CML333
- CML52
- CML69
- Hp301
- II14H
- KI11
- KI3
- Ky21
- M162W
- M37W
- Mo17
- Mo18W
- MS71
- NC350
- NC358
- Oh43
- Oh7B
- P39
- Tx303
- Tz18

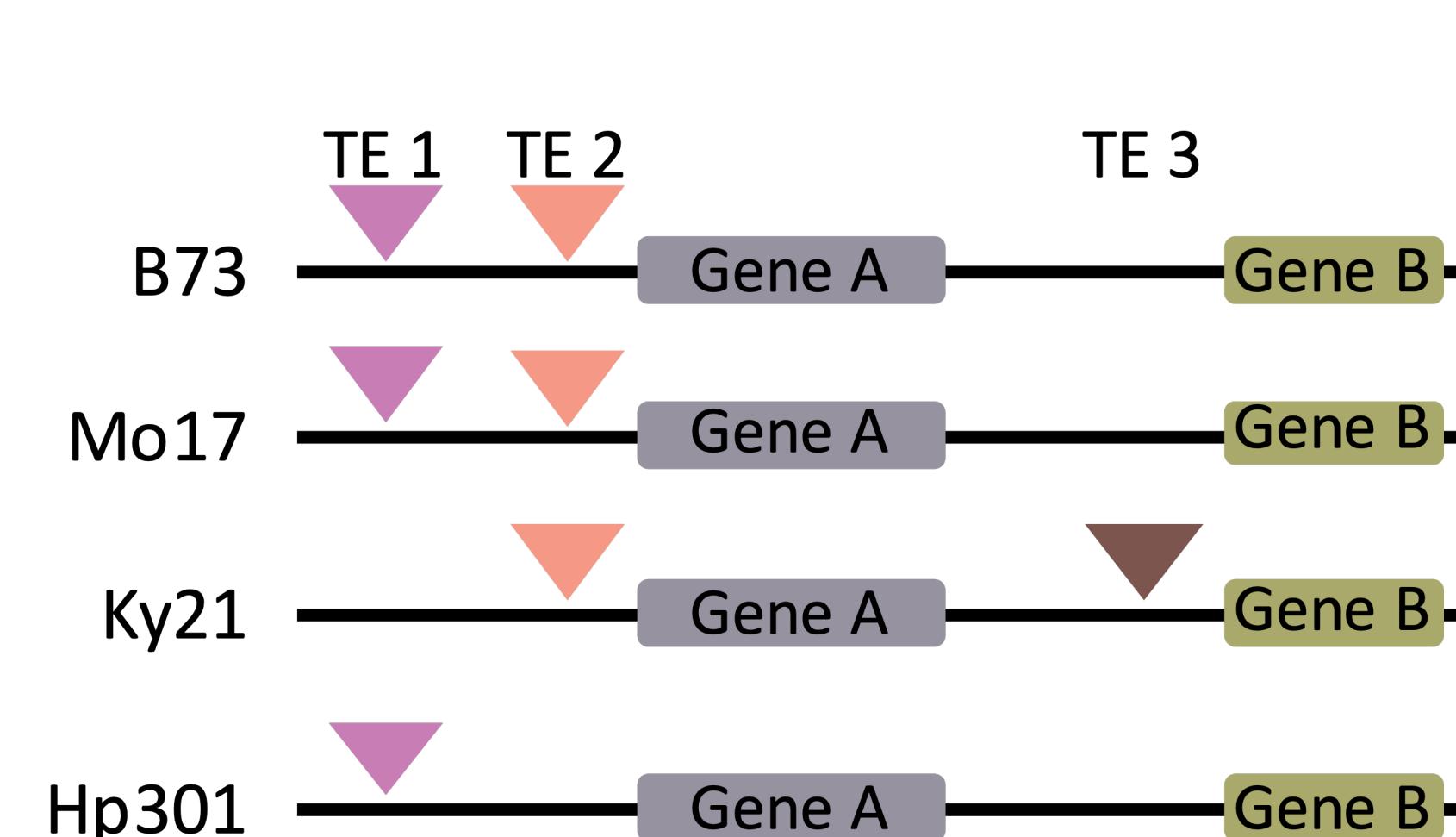
RNAseq Expression Data

Collected and sequenced 372 samples from inbred parents and hybrids.



Maize RNA Expression ~ TE Presence or Absence + Maize Kinship

TE Presence/Absence Genotypes



	Model 1	Model 2	Model 3
Taxa	Gene A TE1	Gene A TE2	Gene B TE3
B73	1	1	0
Mo17	1	1	0
Ky21	0	1	1
Hp301	1	0	0

Maize Kinship Matrix

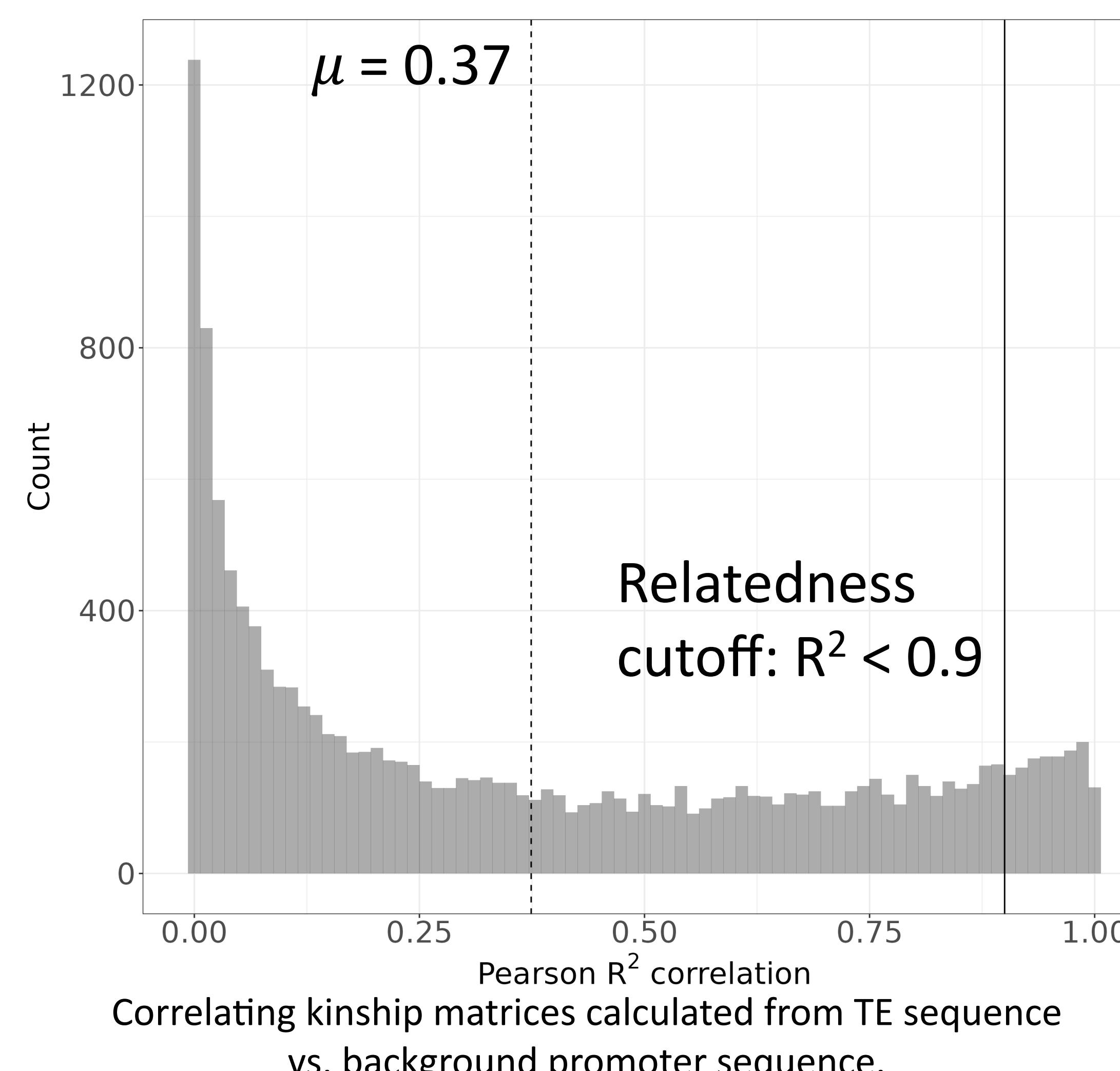
Accounts for relatedness and linkage disequilibrium between individuals.

	B73	Mo17	Ky21	Hp301
B73	1.0	0.9	0.5	0.5
Mo17	0.9	1.0	0.7	0.3
Ky21	0.5	0.7	1.0	0.0
Hp301	0.5	0.3	0.0	1.0

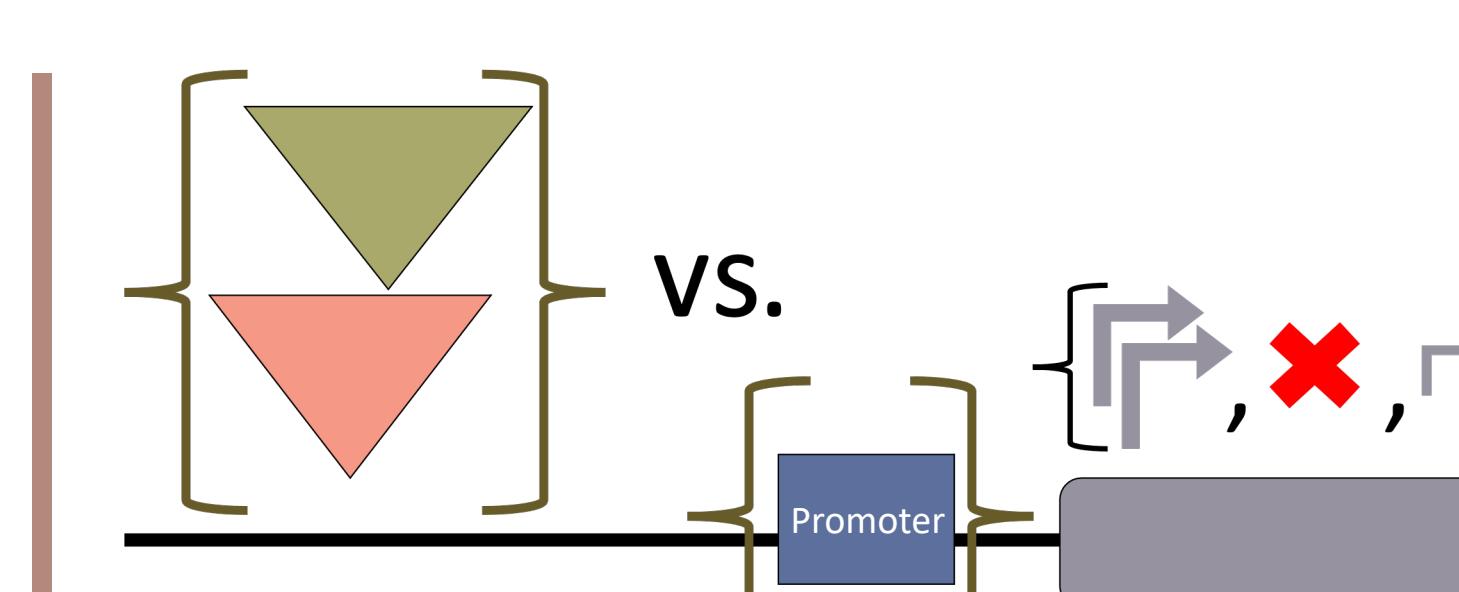
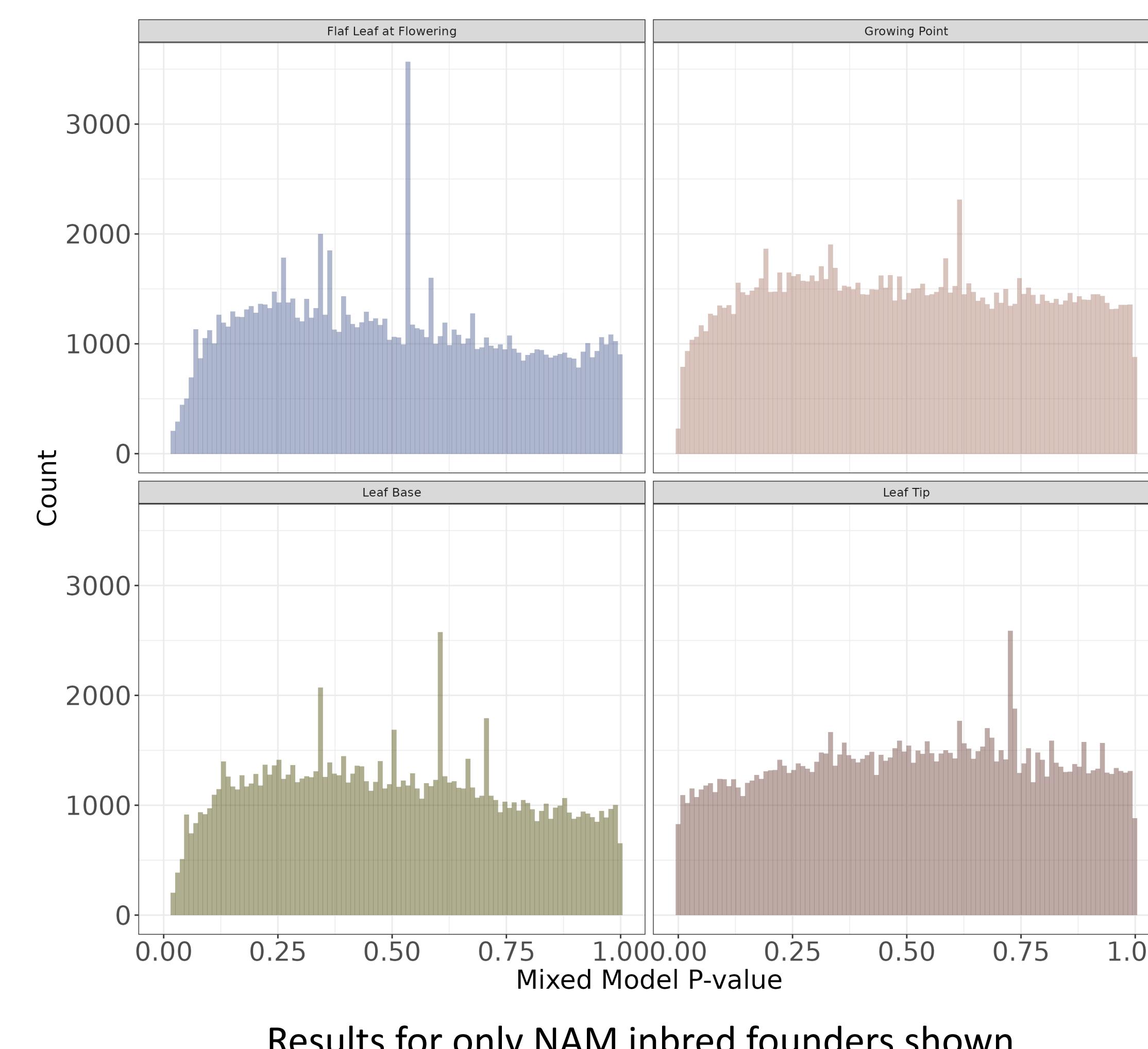
Lowly related Highly related

TE and promoter regulatory effects can be separated in a subset of genes. Within those genes, very few TEs impact gene expression.

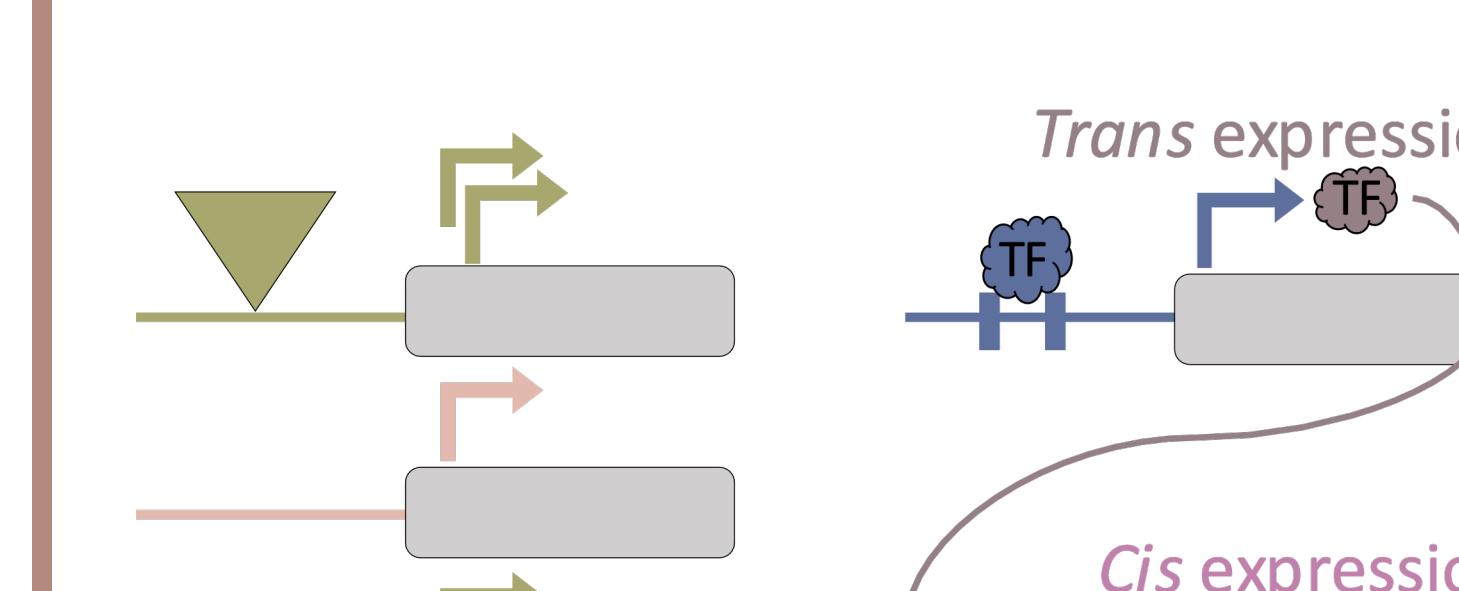
For 66% of genes (12,668) TE effects are statistically indistinguishable from background SNP and promoter effects due to LD.



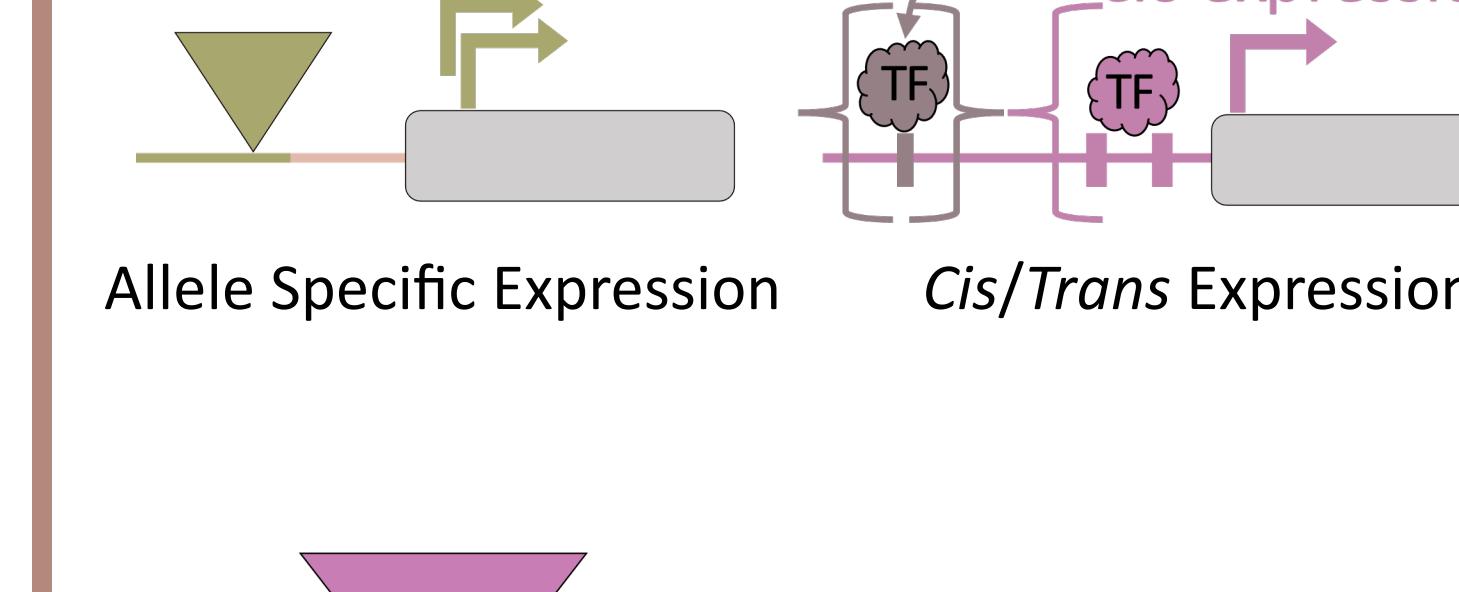
For the 34% of genes whose TE effects are not confounded by LD, 5,418 genes and 11,811 associated TEs show some effect on measured expression.



Able to separate TE from maize effects in 34% of genes.



We will investigate different types of expression estimates in future models.



Plan on identifying biological features contributing to TE-induced gene expression differences.

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This work was conducted on the traditional homelands of the Gayogohó:ngó? (the Cayuga Nation). The Gayogohó:ngó? are members of the Haudenosaunee Confederacy, an alliance of six sovereign Nations with a historic and contemporary presence on this land. The Confederacy precedes the establishment of Cornell University, New York state, and the United States of America.