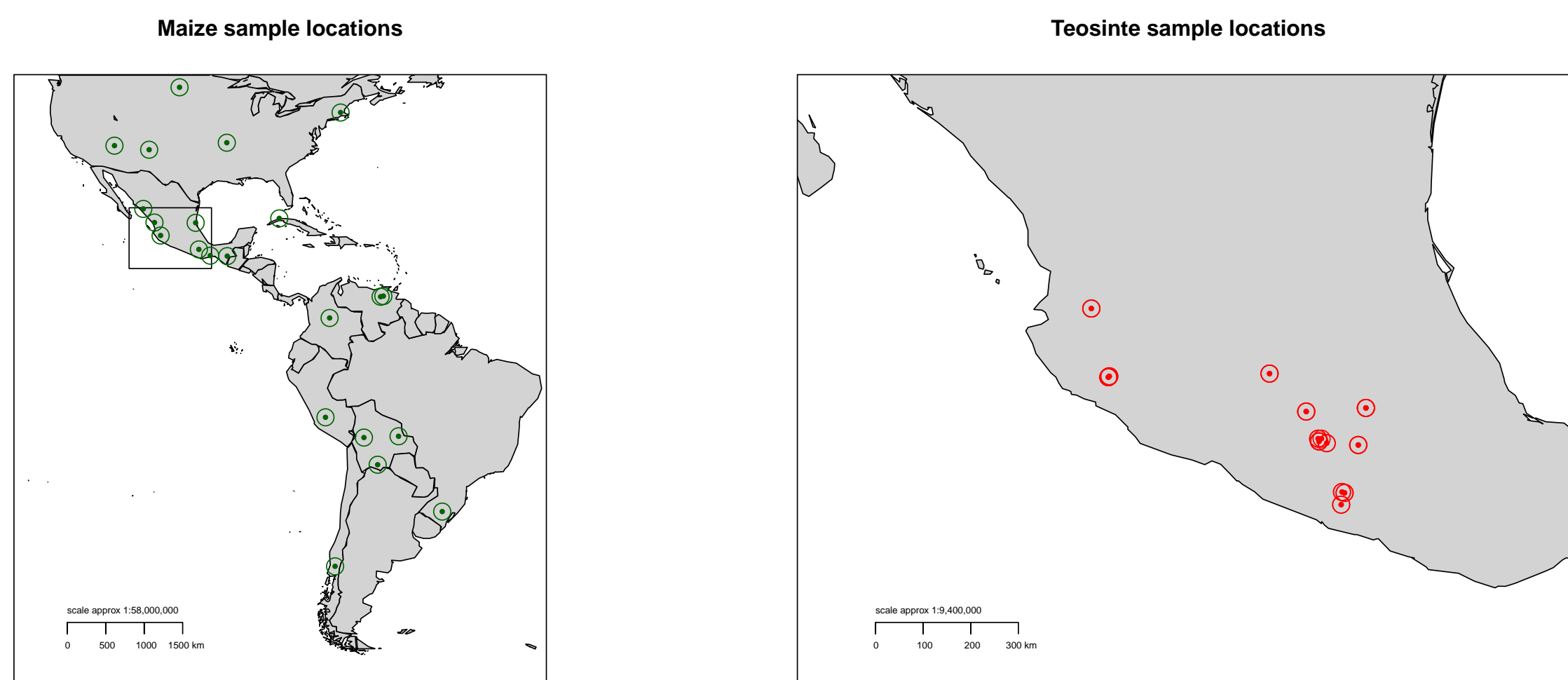


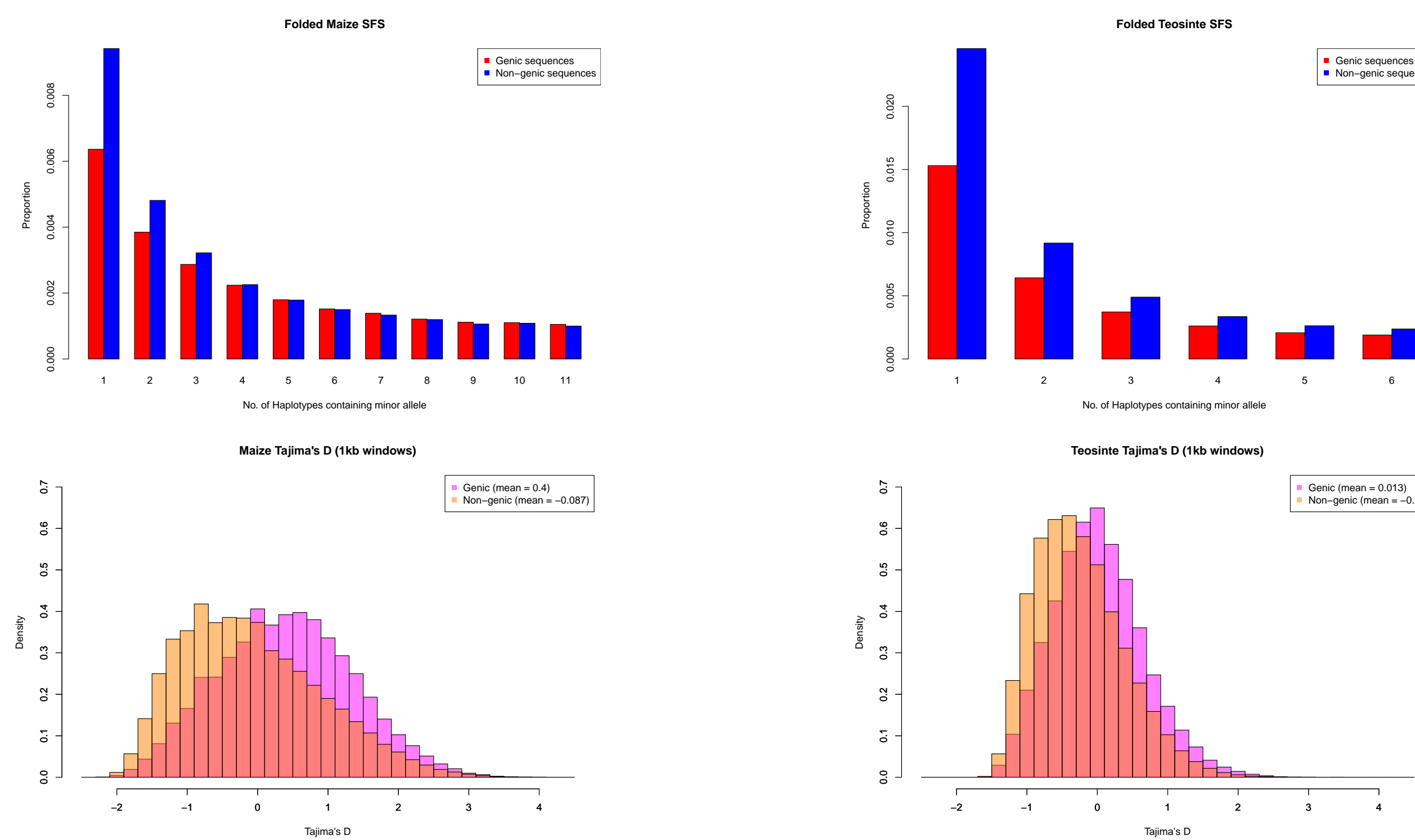
## Introduction

To better understand maize domestication, we employed whole genome sequence data from 23 maize and 13 teosinte samples from Maize HapMap2 (Chia et al., 2012) to investigate patterns of genetic variability resulting from the domestication process. Parameters of the domestication process were inferred from non-genic regions of the genome, for which selection is less likely to impact evolution. Next, diversity surrounding different classes of sites was evaluated to gauge the general selective forces governing domestication.



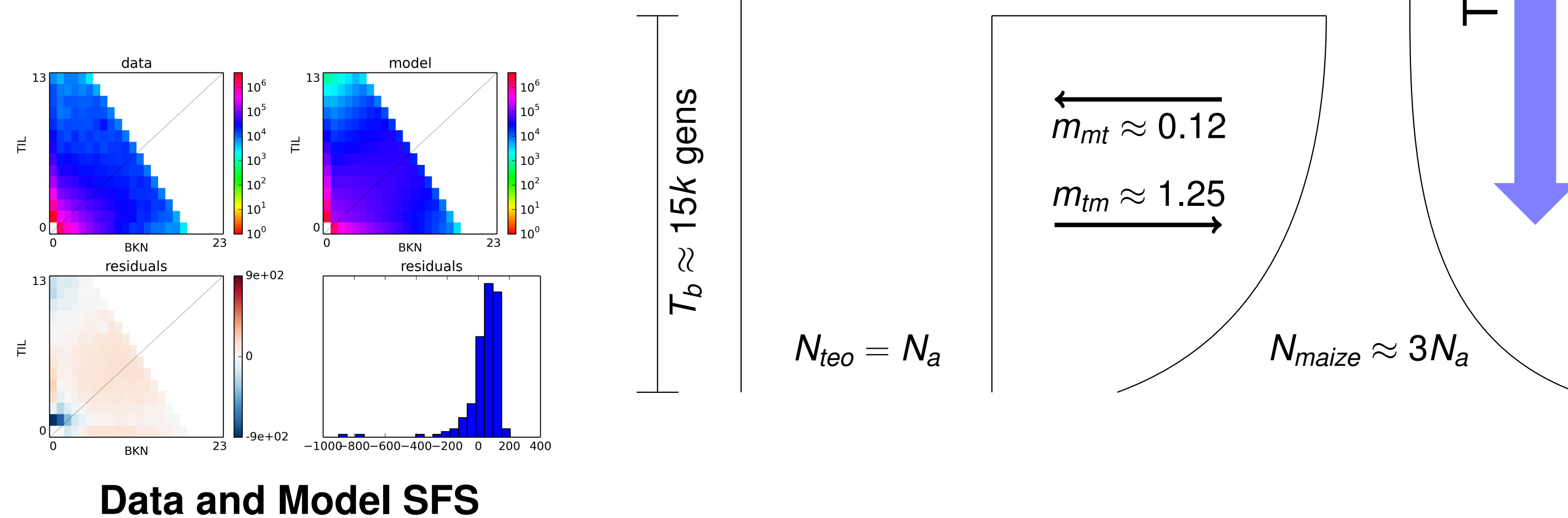
## SFS Demonstrates that genes are not evolving neutrally

By sequencing entire maize and teosinte genomes, it is possible to evaluate patterns of diversity both within, and outside of, genic regions. As depicted via the site frequency spectrum (SFS) and Tajima's D in the plots below, such an evaluation demonstrates that genic regions are not evolving neutrally. Instead, gene evolution is constrained, likely by selection, and therefore demographic patterns inferred from these sites are likely to be biased.



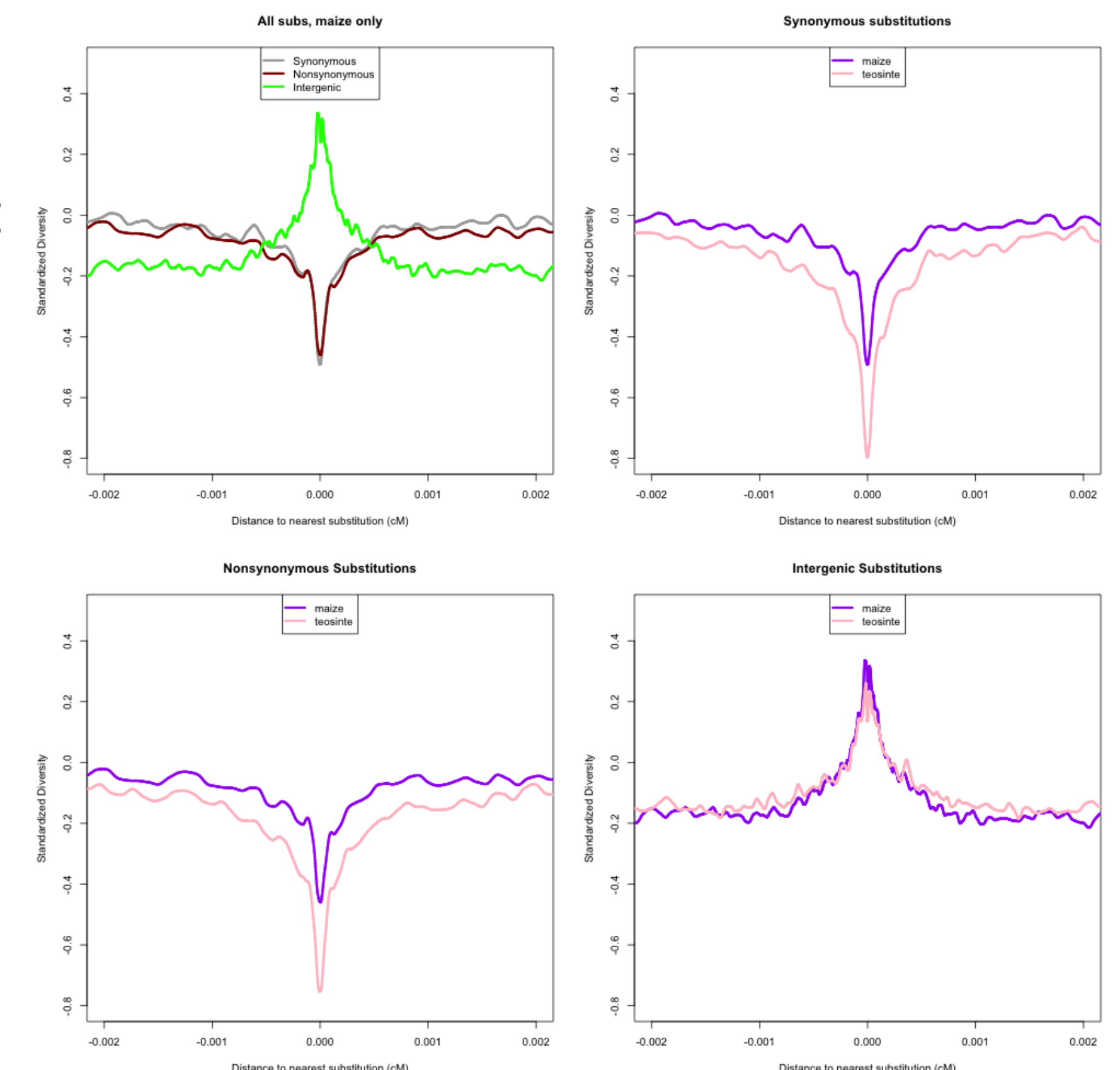
## Diffusion approximation to estimate demographic parameters

- ▶ Model estimated with  $\delta a \delta i$  (Gutenkunst et al., 2009).
- ▶ Estimated demographic parameters with nongenic DNA.
- ▶ 412 million positions sequenced.
- ▶ Modern  $N_{maize}$  likely an underestimate.

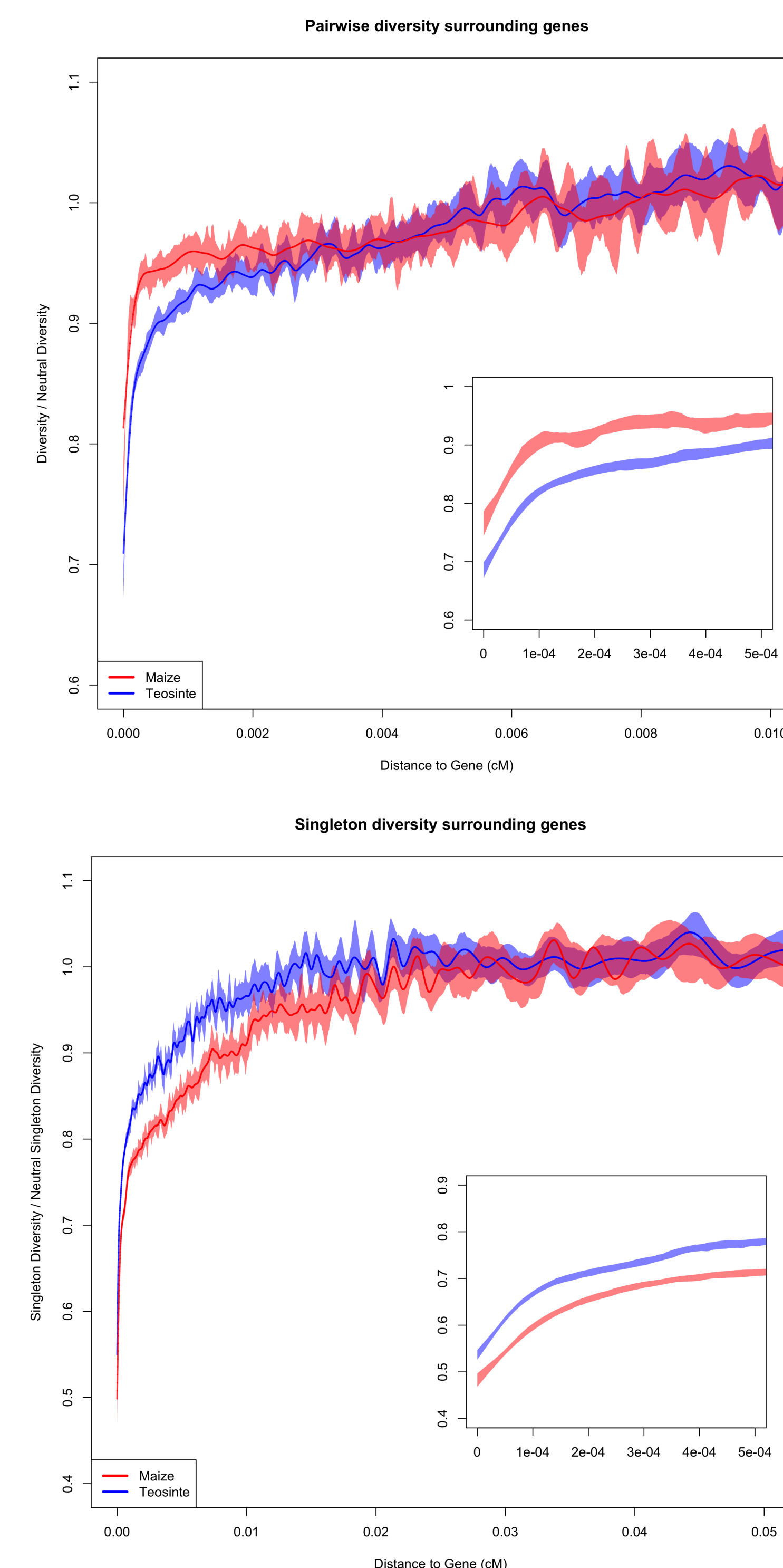


## Evaluating the abundance of hard sweeps

- ▶ Reduced diversity surrounding synonymous and nonsynonymous substitutions provides insight into hard sweeps.
- ▶ Comparable reductions for both classes suggest hard sweeps were not frequent during domestication
- ▶ Trend observed for both maize and teosinte
- ▶ For both classes of substitution, teosinte variability further reduced than maize, relative to total diversity.



## Intensity of purifying selection at different time-scales



- ▶ Purifying selection reduces genetic diversity in and near genes.
- ▶ Teosinte displays a greater reduction of pairwise diversity near genes than does maize (top).
- ▶ Suggests stronger effect of purifying selection over a long time-frame.
- ▶ Maize displays a greater reduction in singleton diversity near genes than does teosinte (bottom).
- ▶ Suggests stronger effect of purifying selection in the recent past.
- ▶ Results demonstrate that purifying selection plays a substantial roll in the evolution of both taxa.
- ▶ Observations consistent with a reduced efficiency of selection during maize bottleneck, when maize population size was small, followed by increased efficiency of purifying selection after population expanded.

## References and acknowledgements

- ▶ Chia et al., Maize HapMap2 identifies extant variation from a genome in flux. Nature Genetics, 2012.
- ▶ Gutenkunst et al., Inferring the joint demographic history of multiple populations from multidimensional SNP data. PLoS Genetics, 2009.
- ▶ We acknowledge and are grateful for funding from NSF (Proposal #1238014).