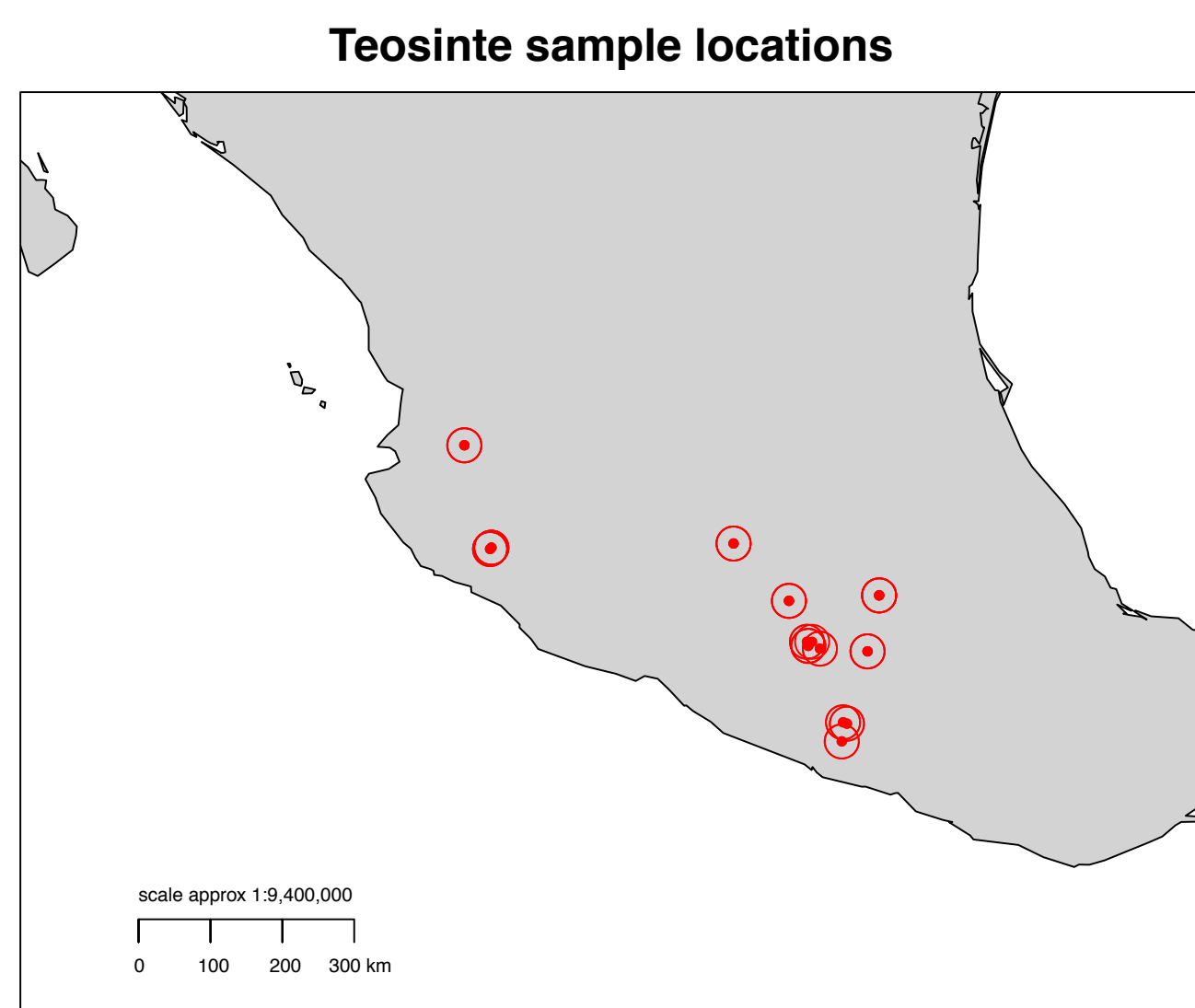
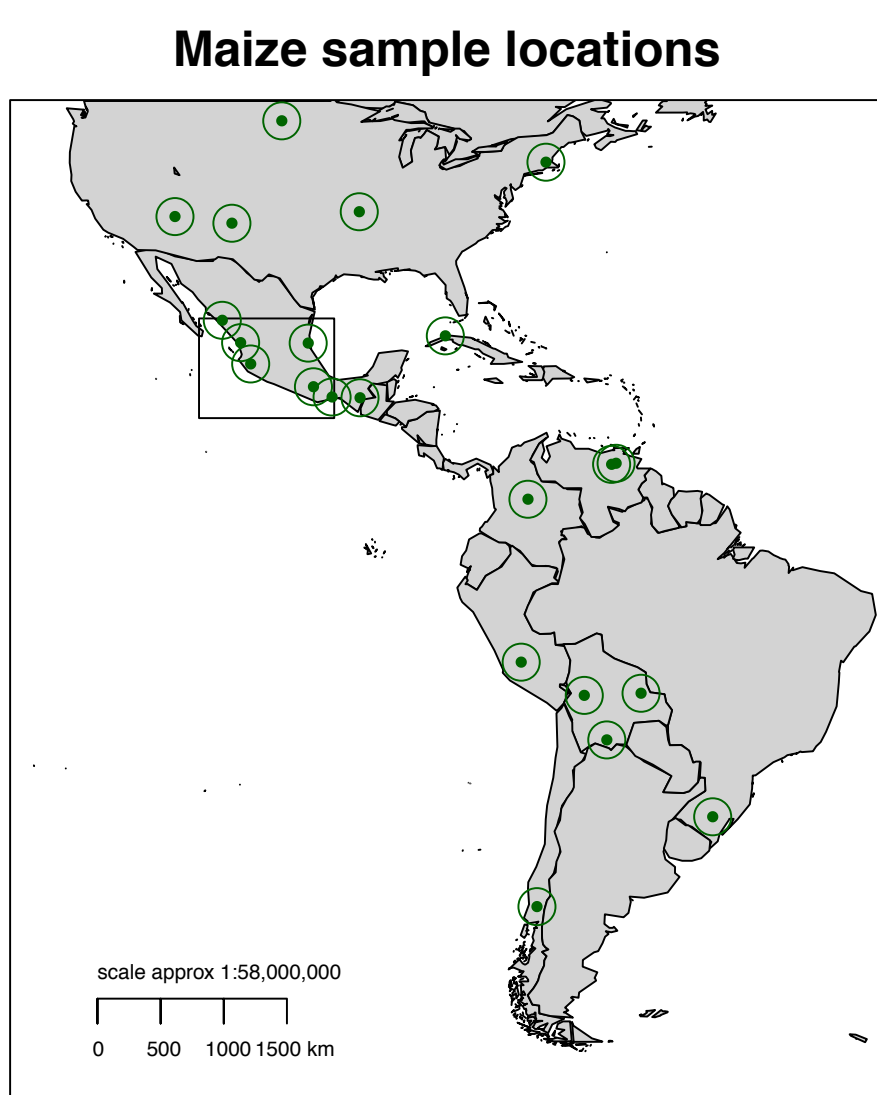


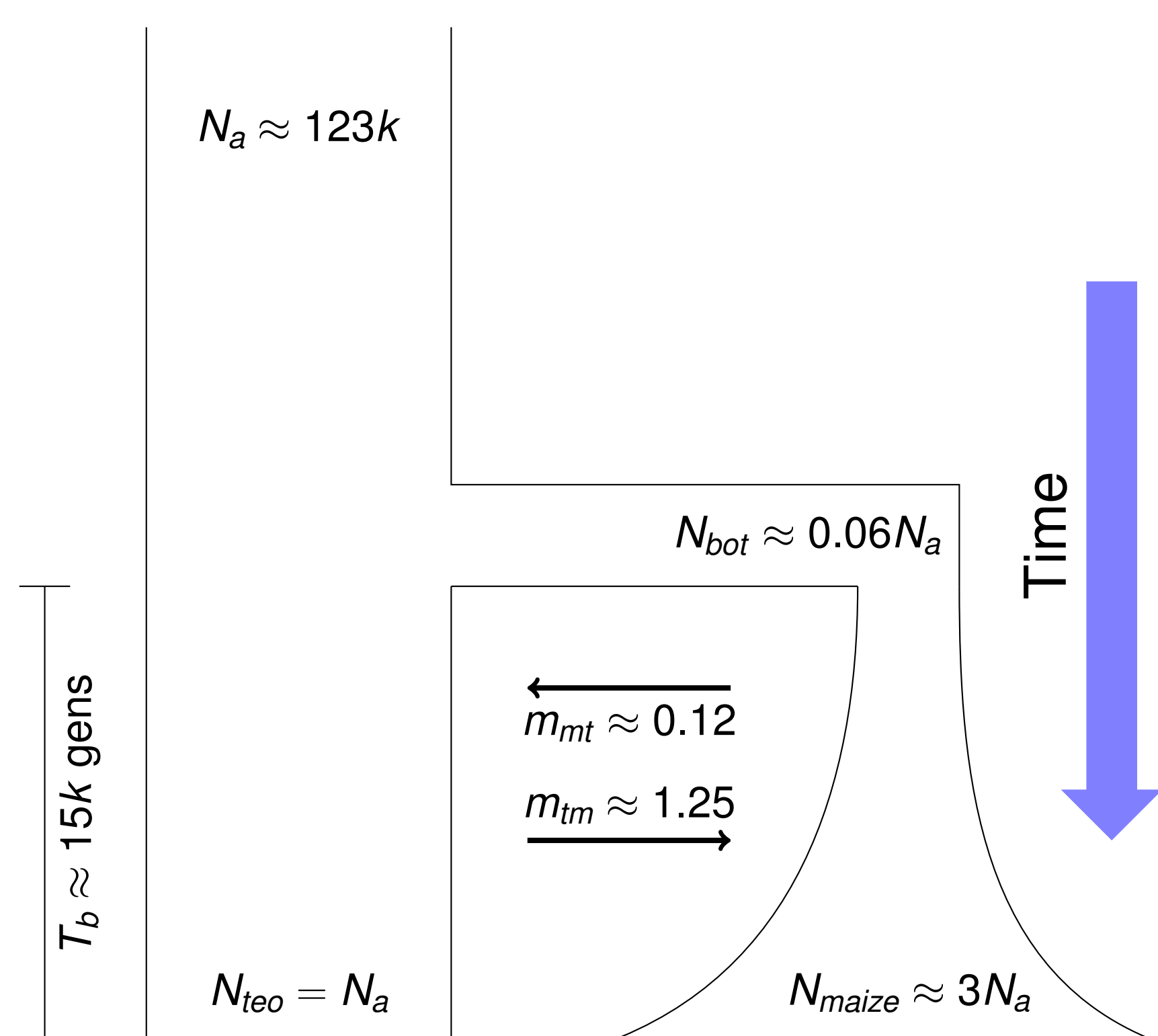
Introduction

The demographic history and selective patterns experienced by a population govern genetic diversity within that population. This is especially true for domesticated species, which tend to have encountered vastly different demographic and selective forces than their wild progenitors. In the case of maize, a more complete understanding of modern genetic variability can be achieved by evaluating this variability in the context of its wild ancestor teosinte. We employed whole genome sequence data from 23 maize and 13 teosinte samples from Maize HapMap2 [1] to investigate genetic patterns resulting from the domestication process. Parameters of domestication 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.

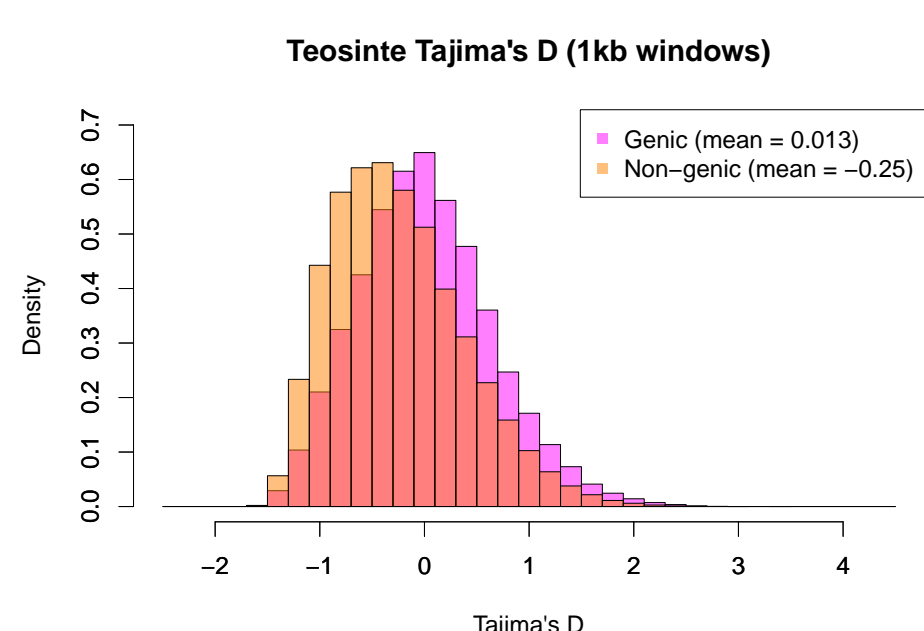
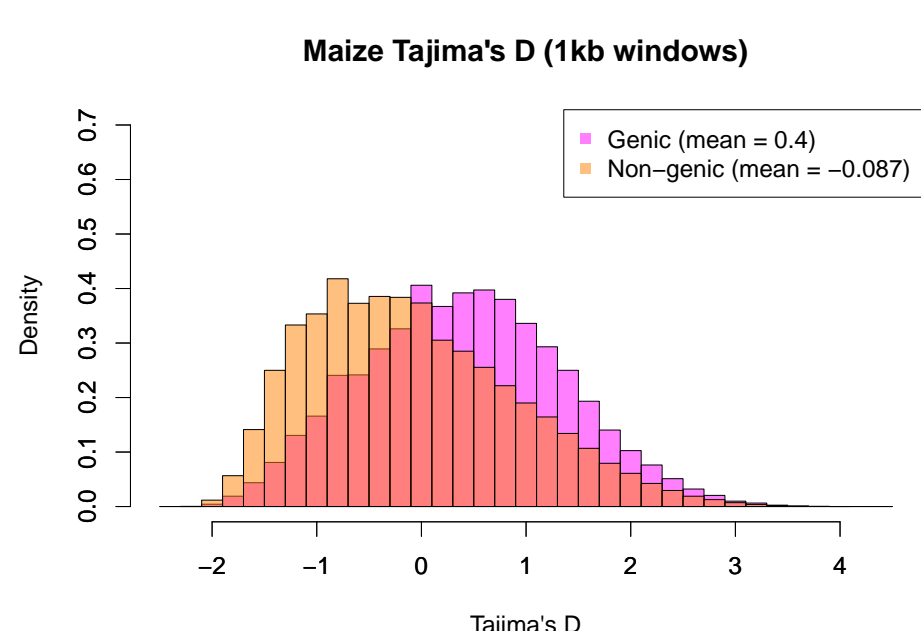
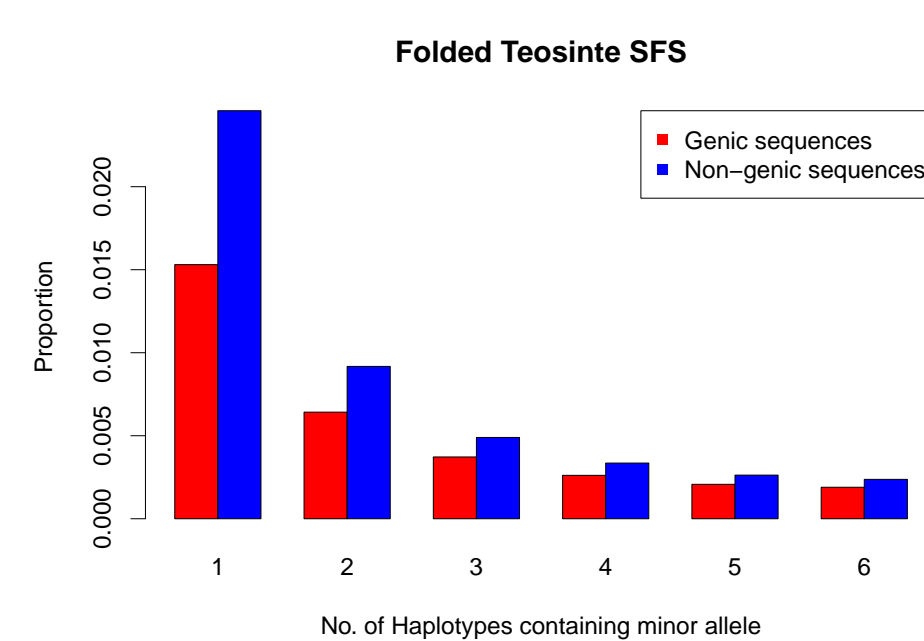
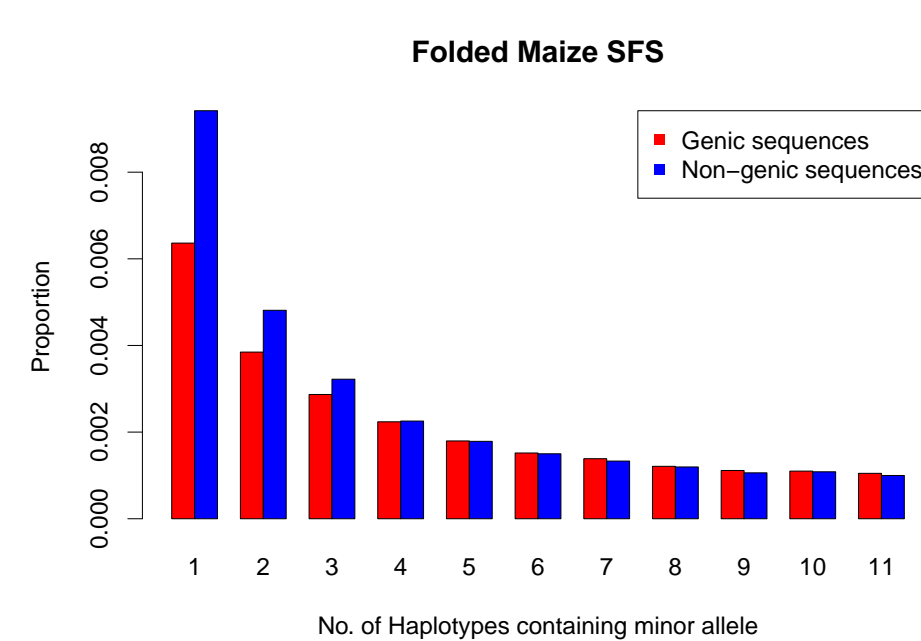


Demography of maize domestication

- Model estimated with $\delta a d i$ [2] using nongenic SNPs.
- Bottleneck involved N_e only $\sim 6\%$ of teosinte.
- Current maize N_e much larger than teosinte, and likely an underestimate.



Genes are not evolving neutrally

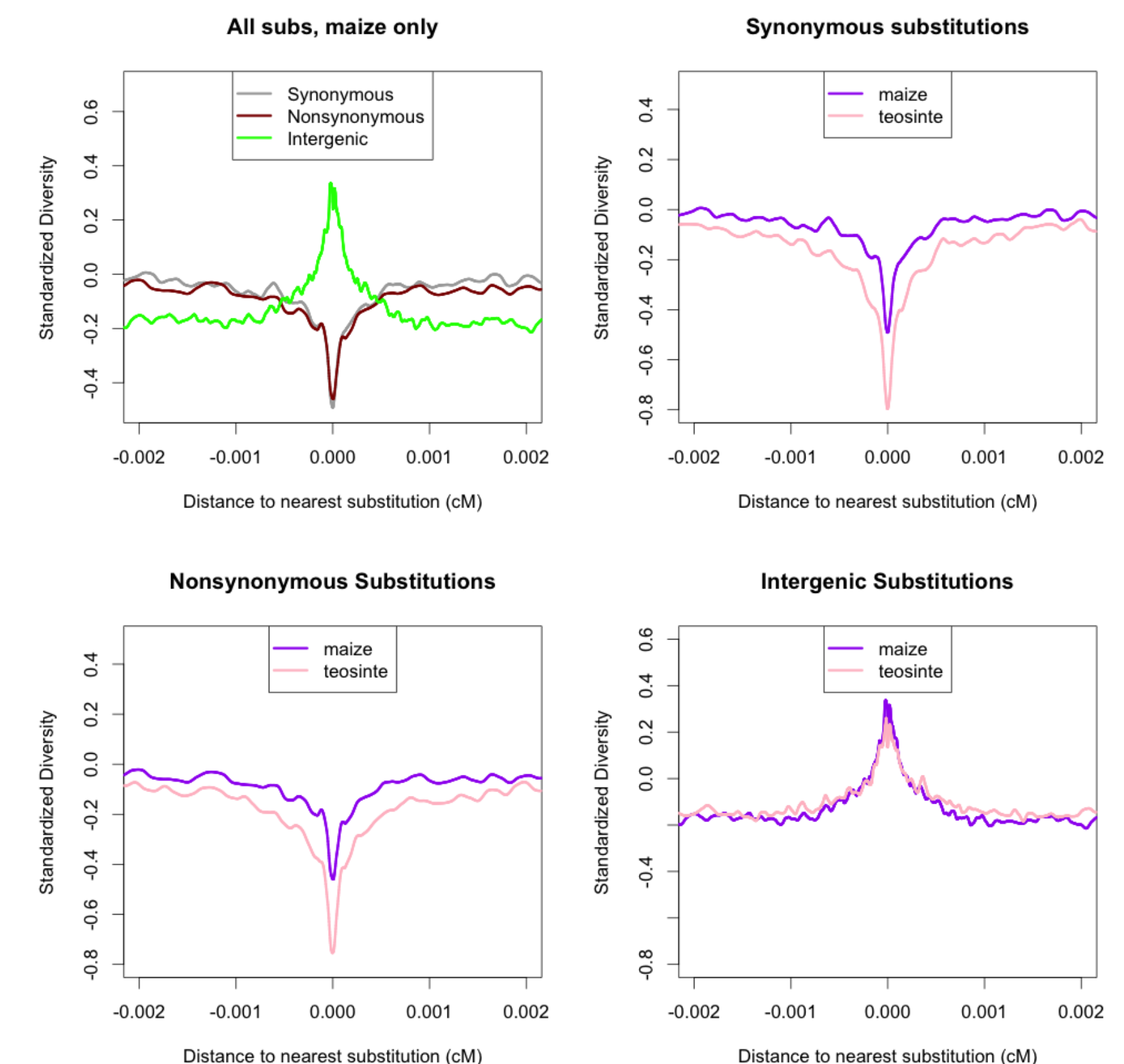


Genome-wide site frequency spectra show a paucity of low frequency alleles in genes compared to nongenic regions. Because demographic processes should impact the whole genome similarly, this suggests the action of purifying selection removing diversity in genes.

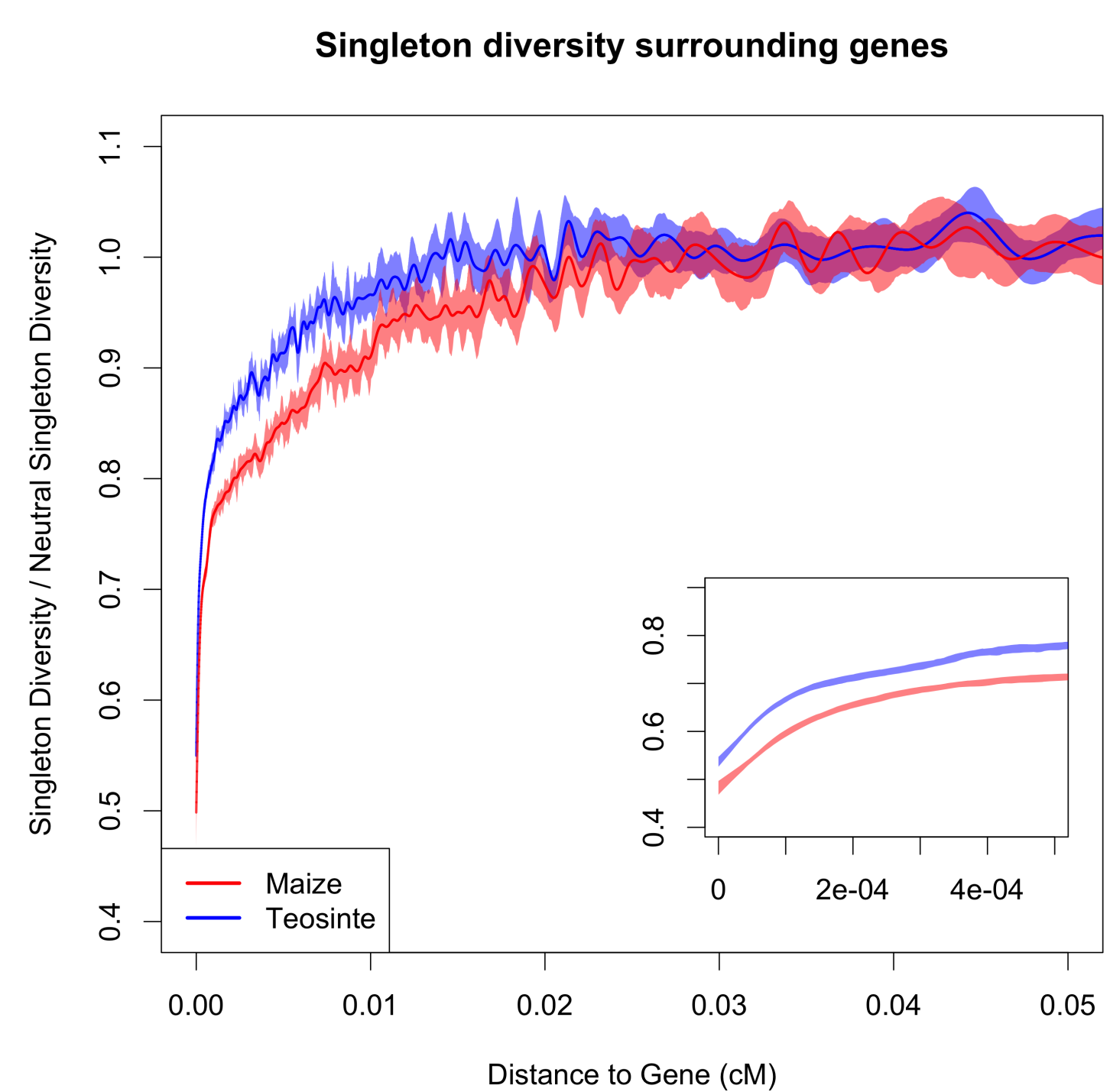
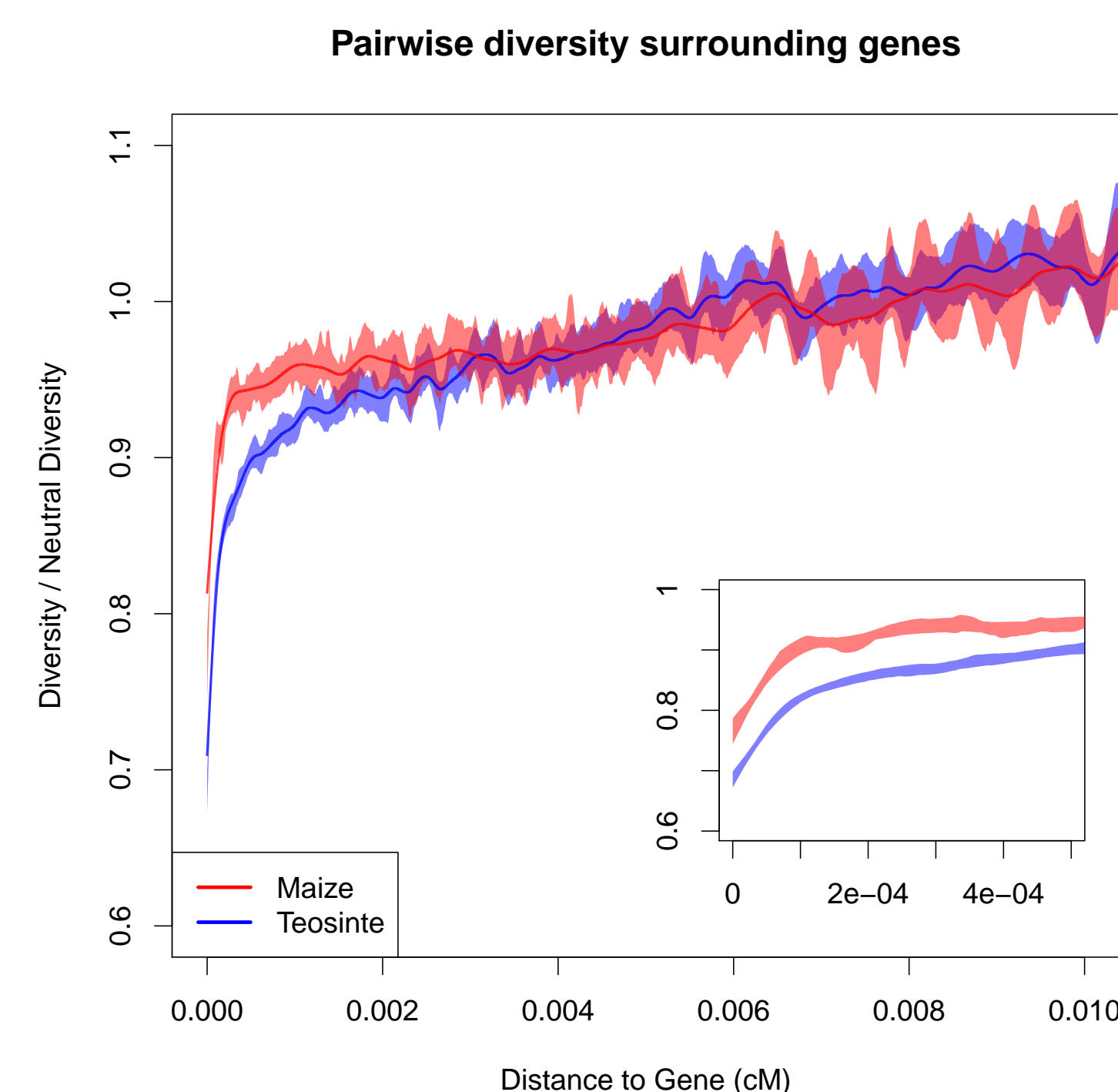
Few classical hard sweeps in *Zea mays*

- Synonymous and nonsynonymous substitutions show similar reductions in diversity.

- Diversity around both classes of substitution shows greater reduction in teosinte than maize.



Demography changes strength of purifying selection.



- Purifying selection reduces genetic diversity in and near genes.
- Teosinte displays a greater reduction of pairwise diversity near genes than does maize (top), reflecting long-term differences in N_e .
- Maize displays a greater reduction in singleton diversity near genes than does teosinte (bottom), reflecting larger recent N_e in maize.
- Maize domestication bottleneck reduced efficacy of purifying selection, but large N_e post-expansion leads to stronger purifying selection on recent mutations.

References and acknowledgements

- [1] Chia et al., Maize HapMap2 identifies extant variation from a genome in flux. *Nature Genetics*, 2012.
- [2] 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).