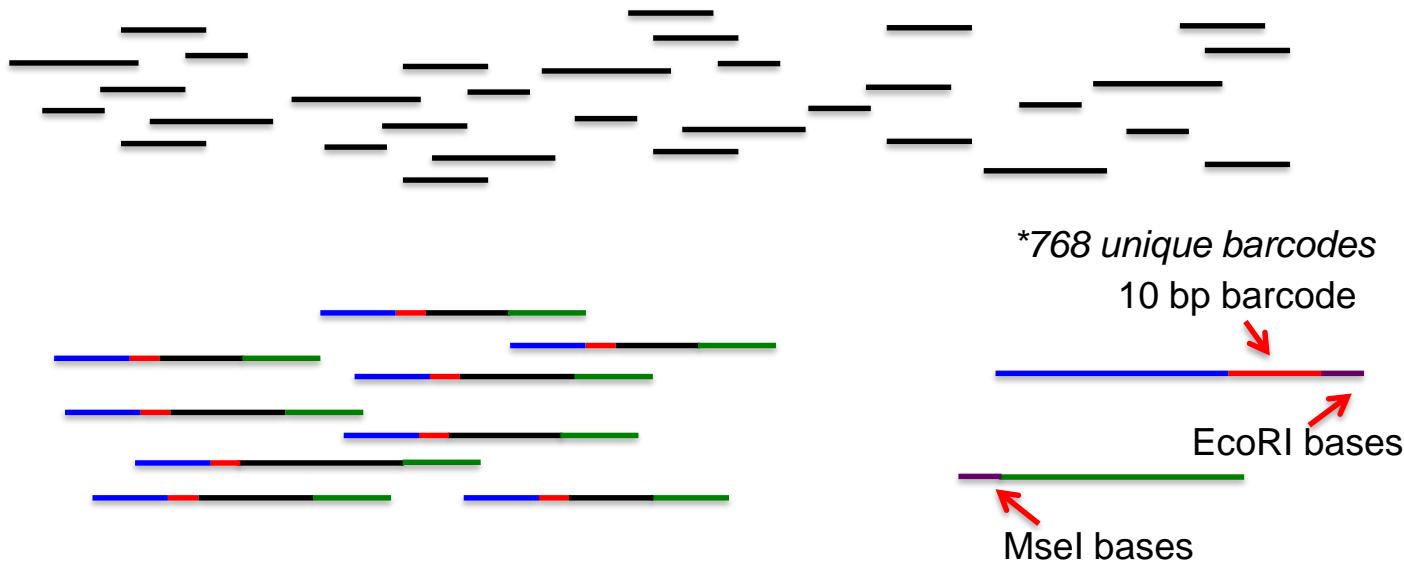




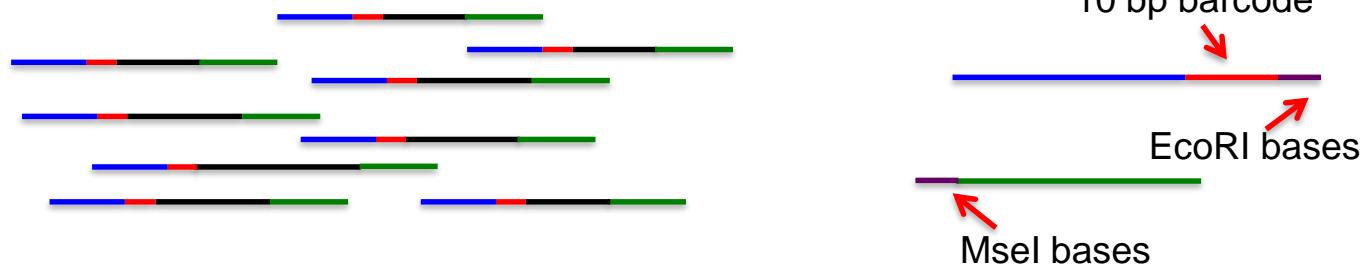
Genomic reduction and highly multiplexed library preparation

Parchman et al. 2012

1. Digest genomic DNA with EcoRI and Msel



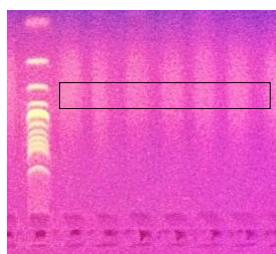
2. Ligate Illumina adaptors to fragments



3. Amplify with Illumina PCR primers



4. Gel purify product to desired size range (350-450bp)



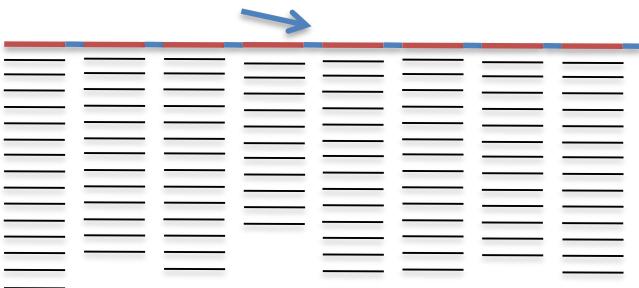
Illumina sequencing

Illumina sequencing

De novo assembly

Assemble reads onto reference

Artificial reference



Illumina reads

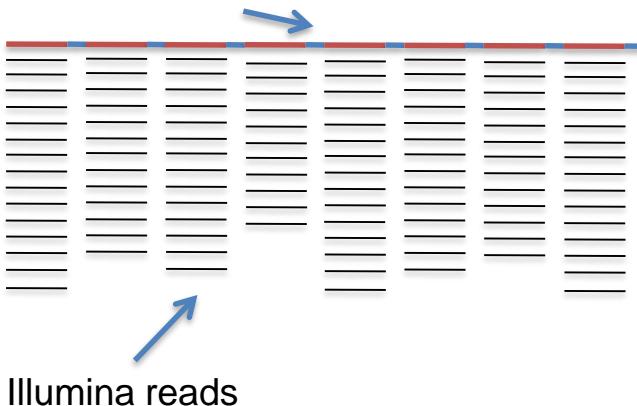
Call SNPs (SAMtools)

Illumina sequencing

De novo assembly

Assemble reads onto reference

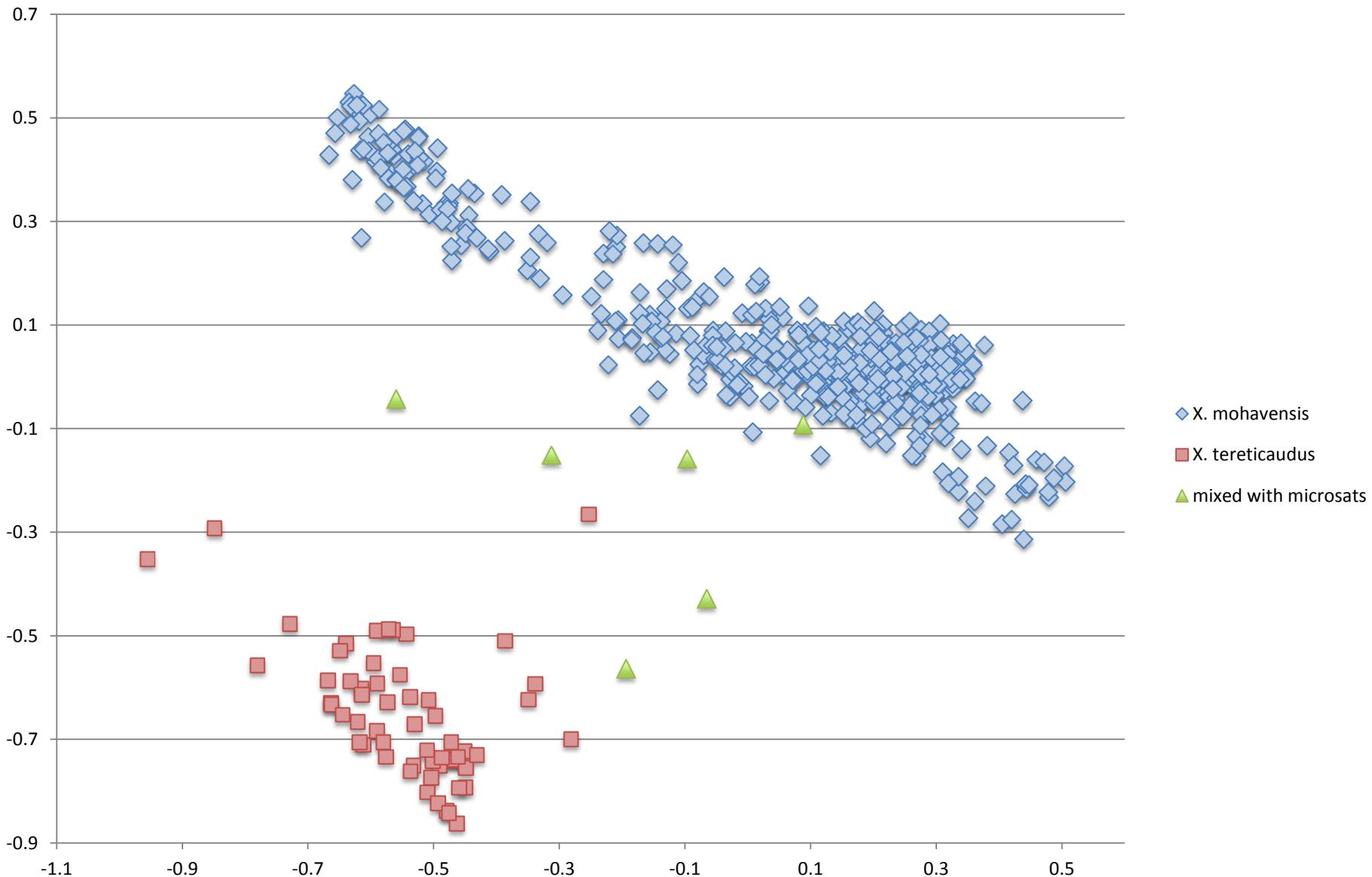
Artificial reference



Call SNPs (SAMtools)

- 800,000,000 sequences
 - 450,000 SNPs
 - 25,550 SNPs in 608 individuals

25,550 SNPs in 608 individuals



25,550 SNPs in 608 individuals

