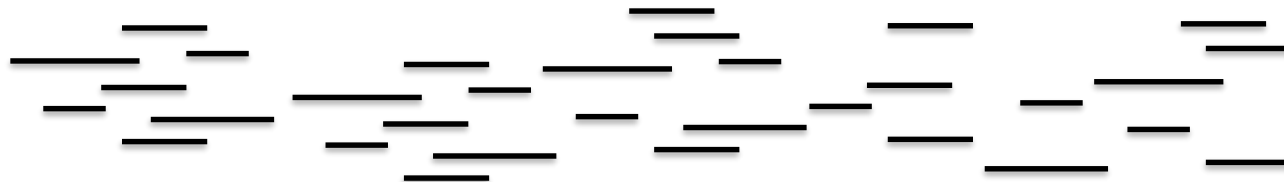




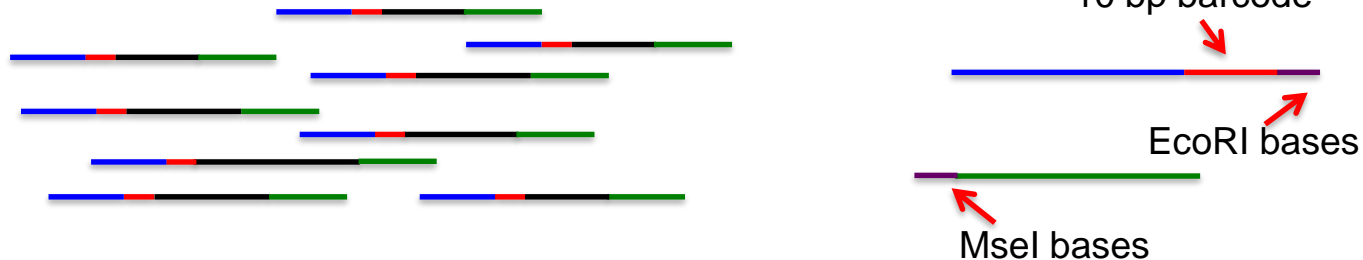
Genomic reduction and highly multiplexed library preparation

Parchman *et al.* 2012

1. Digest genomic DNA with EcoRI and MseI



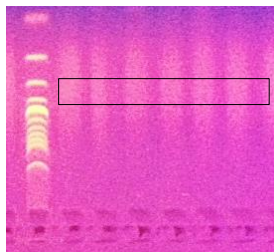
2. Ligate Illumina adaptors to fragments



3. Amplify with Illumina PCR primers



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



Illumina sequencing

Illumina sequencing

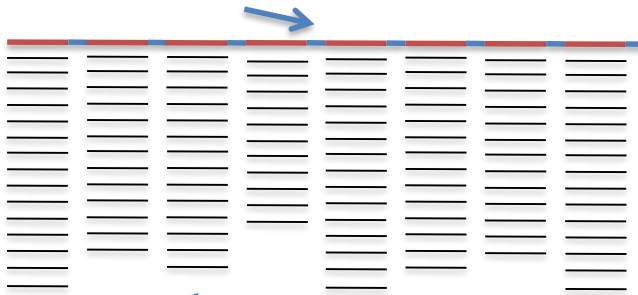


De novo assembly

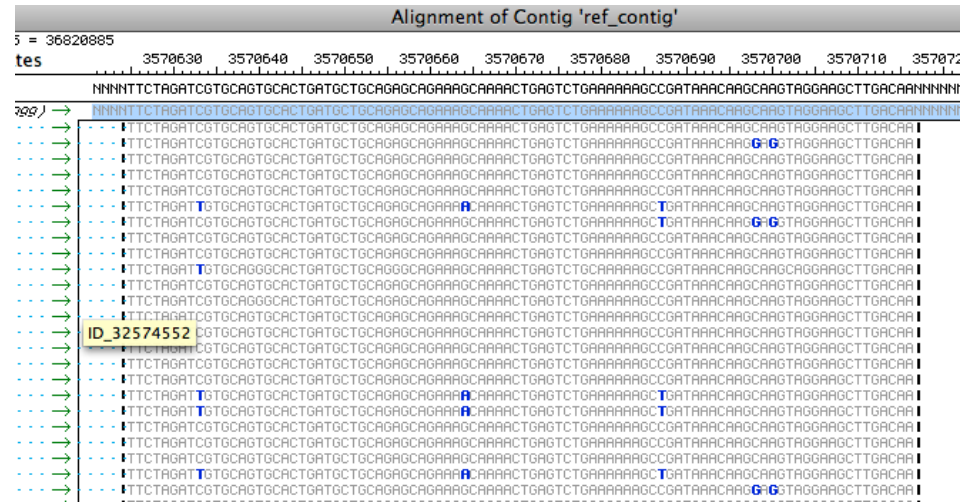


Assemble reads onto reference

Artificial reference



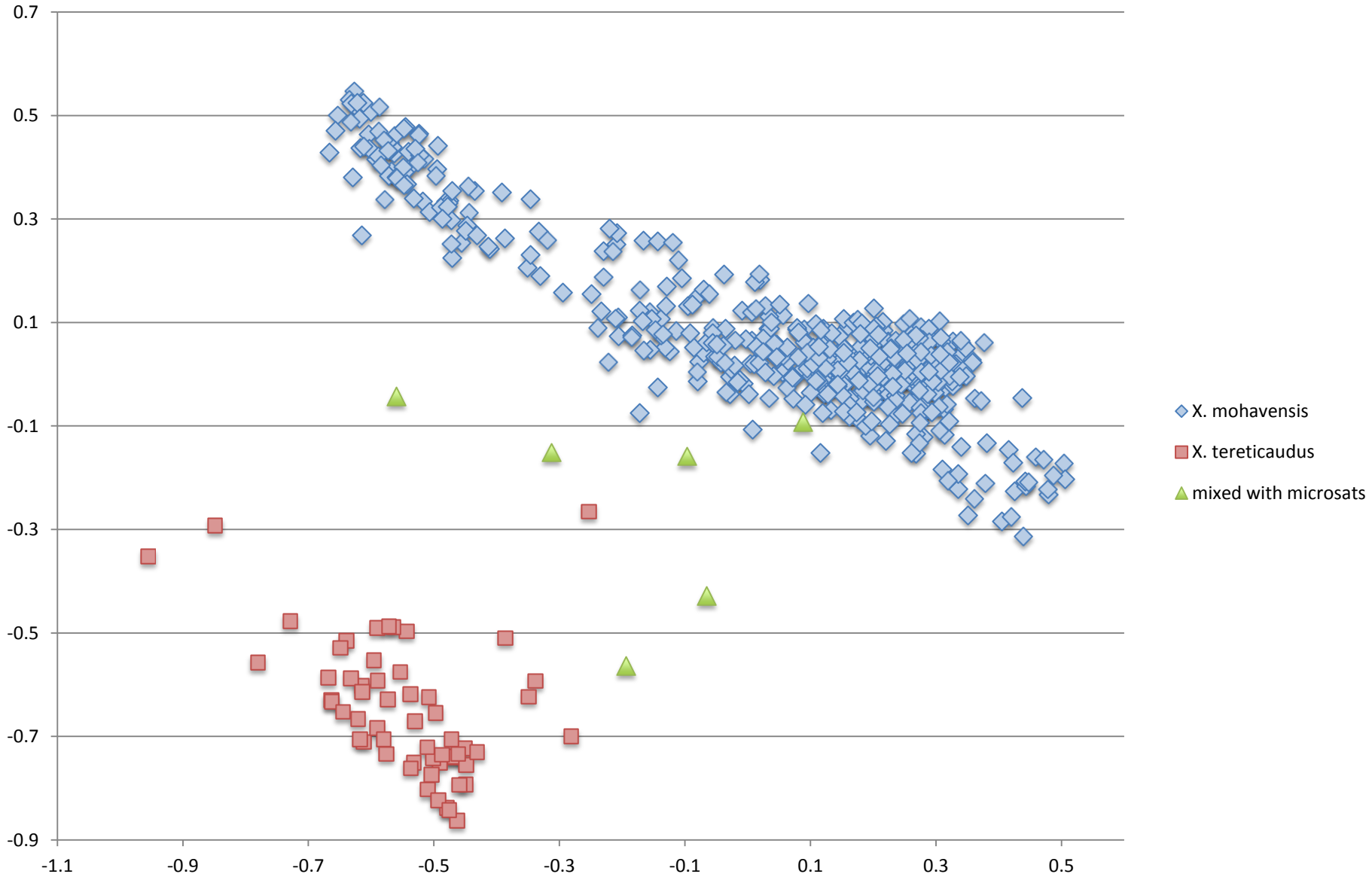
Illumina reads



Call SNPs (SAMtools)

- 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

