



Novel NGS-based genomic platform reveals unexploited variability of *Prunus persica* (L. batch) for future genetic breeding of peach



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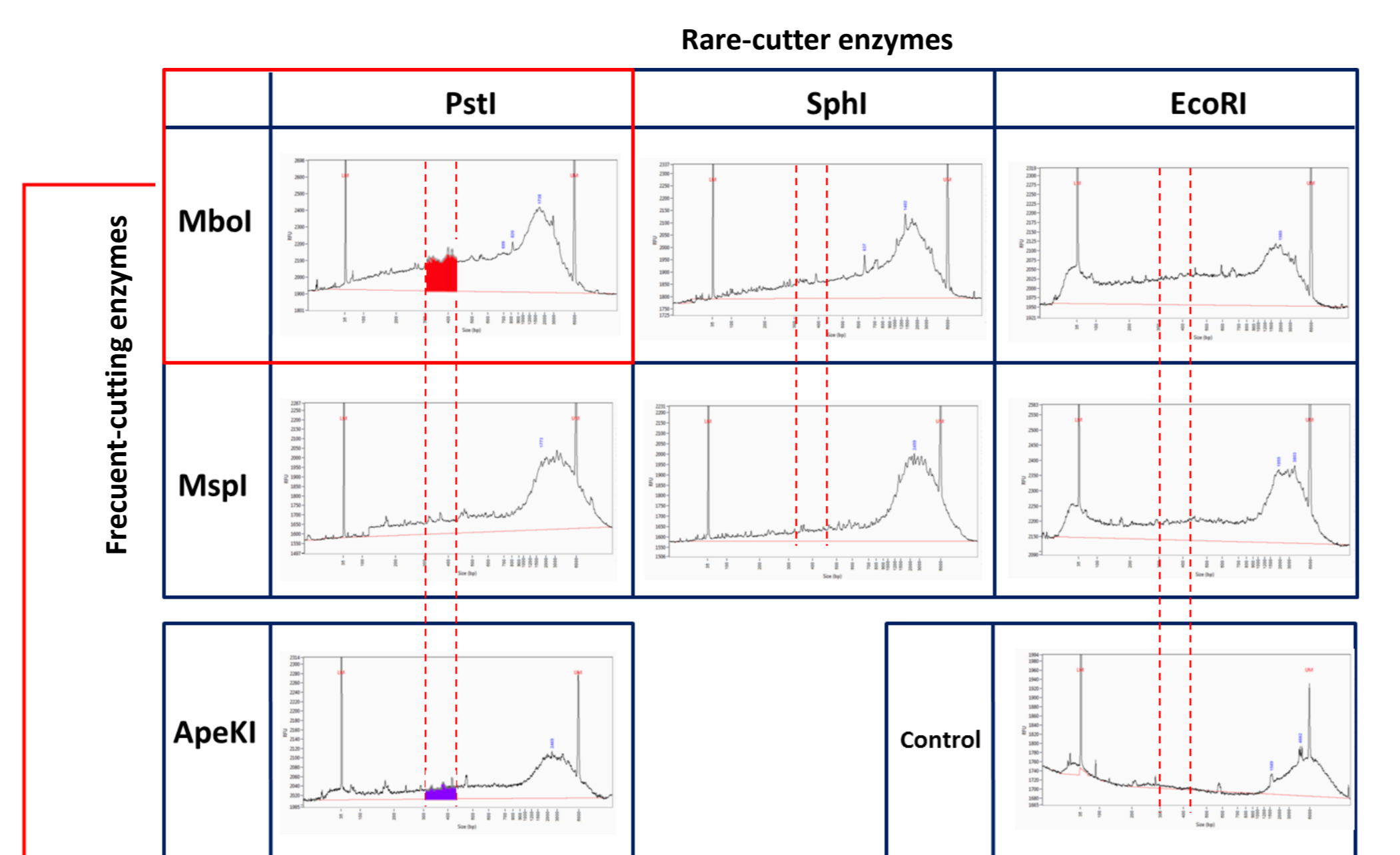
Introduction

Peach is a diploid ($2n=2x=16$, 265Mb) specie with a narrow genetic base due to its self-compatibility and long generation periods. Therefore novel germplasm are continuously pursued for breeding purposes. A novel RADseq platform, based on a double restriction and a size selection step for genome-complexity reduction, was developed. A collection, composed of 191 peaches and one plum genotype, was deeply characterized with the genomic platform. The study of the genetic relationships uncovered unexpected similarity and sources of variability that are scarcely used in breeding programs.

Materials and Methods



**EEA San Pedro
Germplasm collection**
-191 Peach accessions
- 1 plum accession



Results

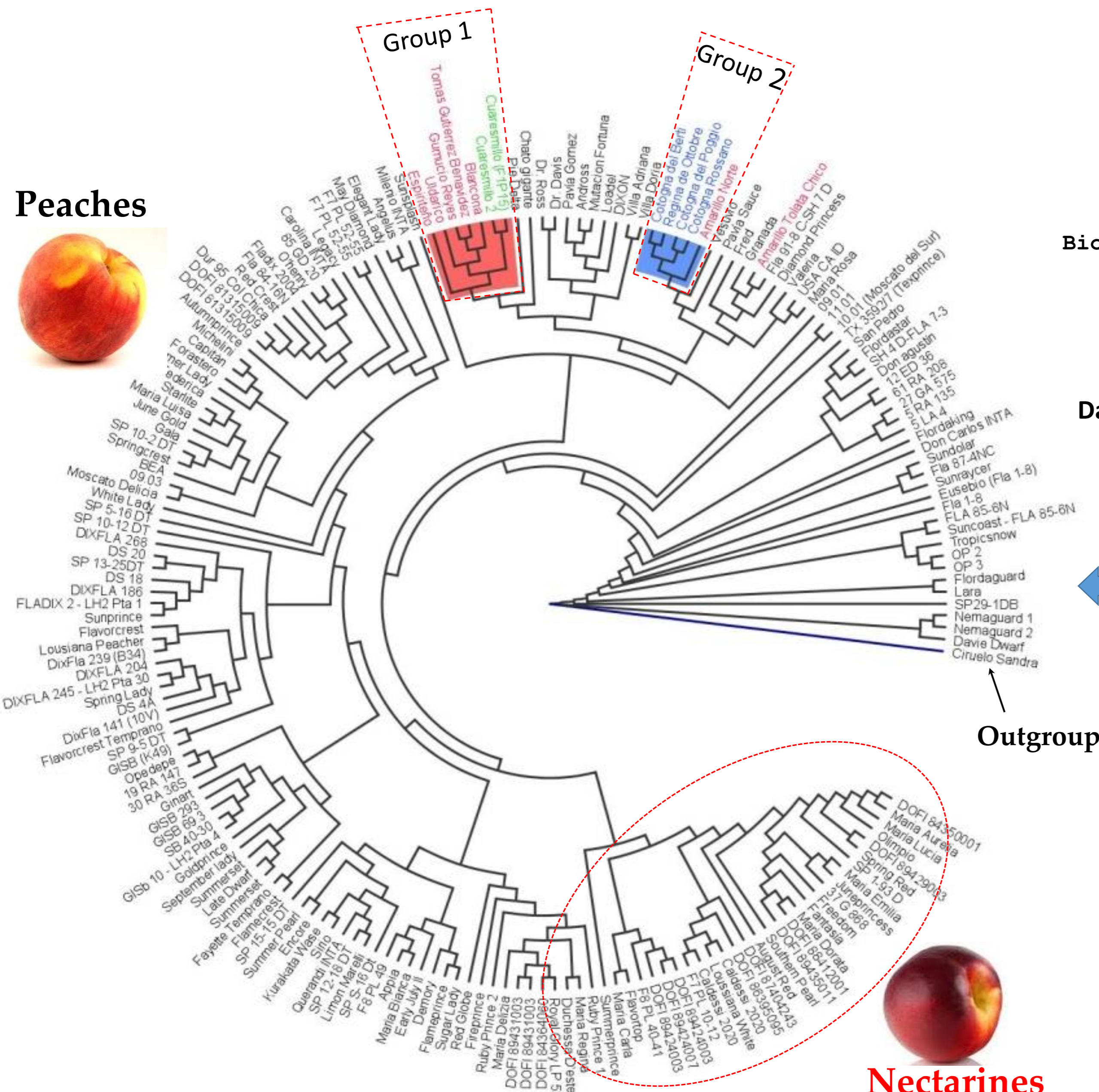


Fig. 1. UPGMA Phylogenetic Tree. Argentinean feral ("Cuaresmillo", in green) and Bolivian landraces (in red) clustered together (Group 1). One accession of Bolivian landrace (in red) clustered with Italian traditional varieties (in blue). Most of nectarines formed a group. A *Prunus salicina* accession ("ciruelo Sandra") was used as outgroup. (Data set 192 accessions, 23448 SNPs)

Conclusions:

-A novel RADseq platform was developed that allowed the identification of **113411 peach SNPs** in total.

-By a combination of analyses was demonstrated that "Cuaresmillo" (Argentinean feral) and Bolivian landraces shared genetic similarities that could reflect a common origin. This source of variability, poorly represented in modern improved peaches, was harnessed in a genomic-driven crosses designed to maximize segregation in the progeny.

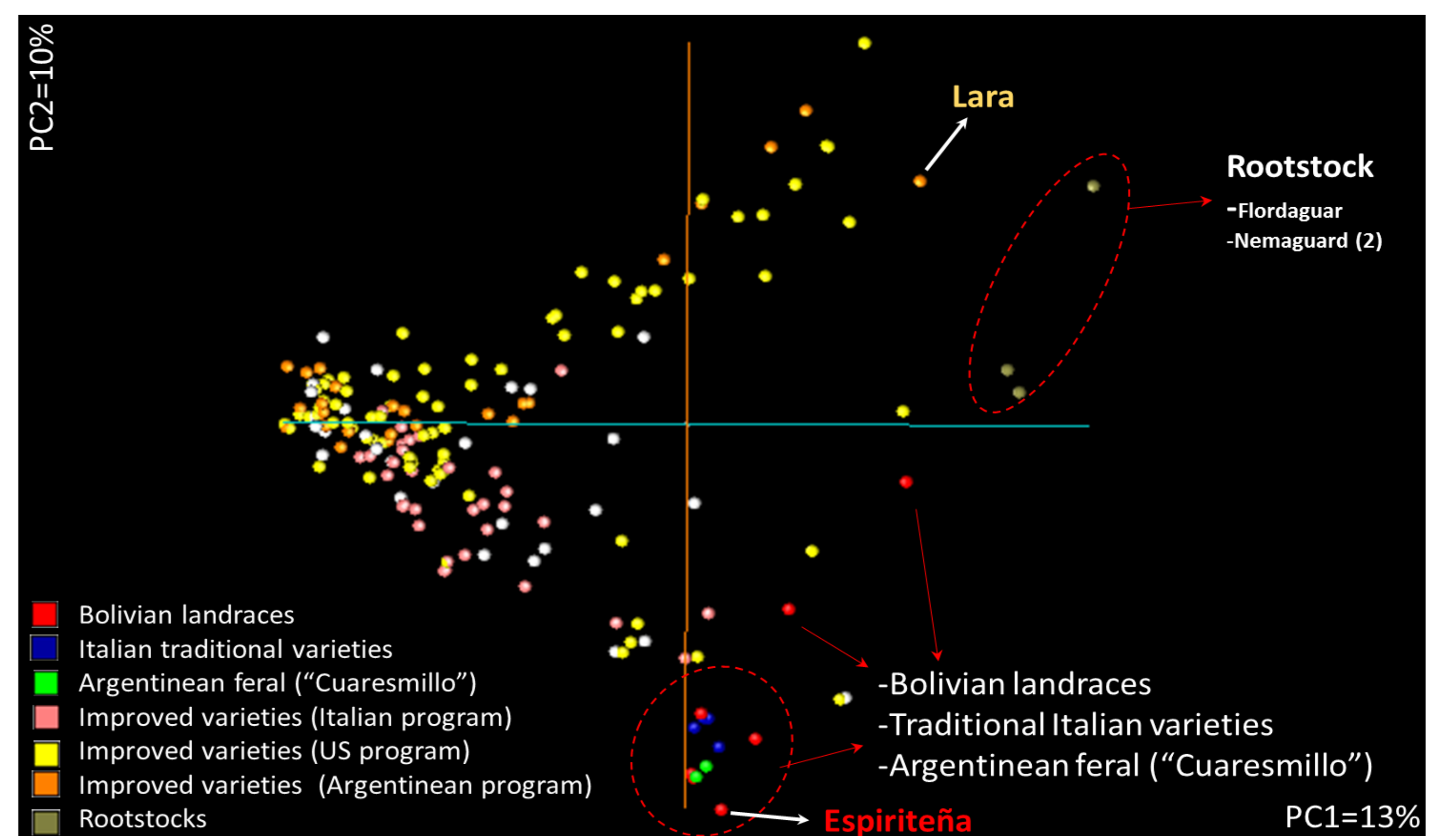


Fig. 3. Principal Component Analysis (PCA). Materials that were improved by traditional practices (Traditional Italian varieties and Bolivian landraces) and improved but scape to wild life ("Cuaresmillo" feral) showed differences with varieties improved in modern breeding programs. The genotypes selected as parental of our breeding program (Lara and Espiriteña) are pointed. (Data set 191 peach accession, 6028 SNPs)

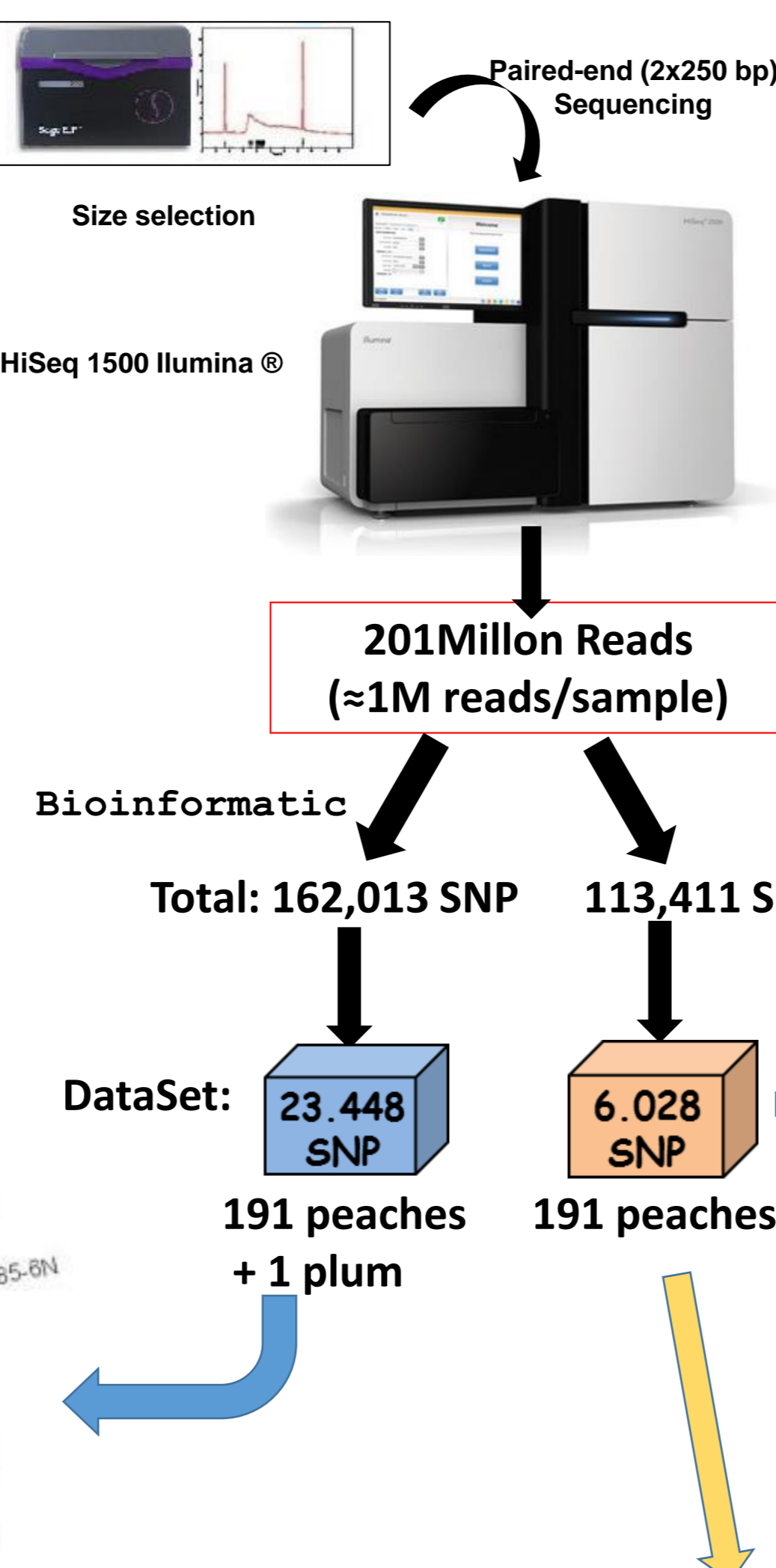


Fig. 4. Genomic-driven selection of A parentals to maximize loci segregation. "Lara" and "Espiriteña" genotypes were selected as parental since they have a high percentage of heterozygous SNP (A), and low Identity-By-State (IBS, B) between them. It is anticipated that 10607 SNPs, covering the 8 chromosomes, will segregate (C). Heterozygous SNPs (segregating) are indicated with grey in the bars representing chromosomes (Ch1 to Ch8). Green indicates homozygous SNP in Espiriteña (E). Pink indicates homozygous SNP in Lara (L).

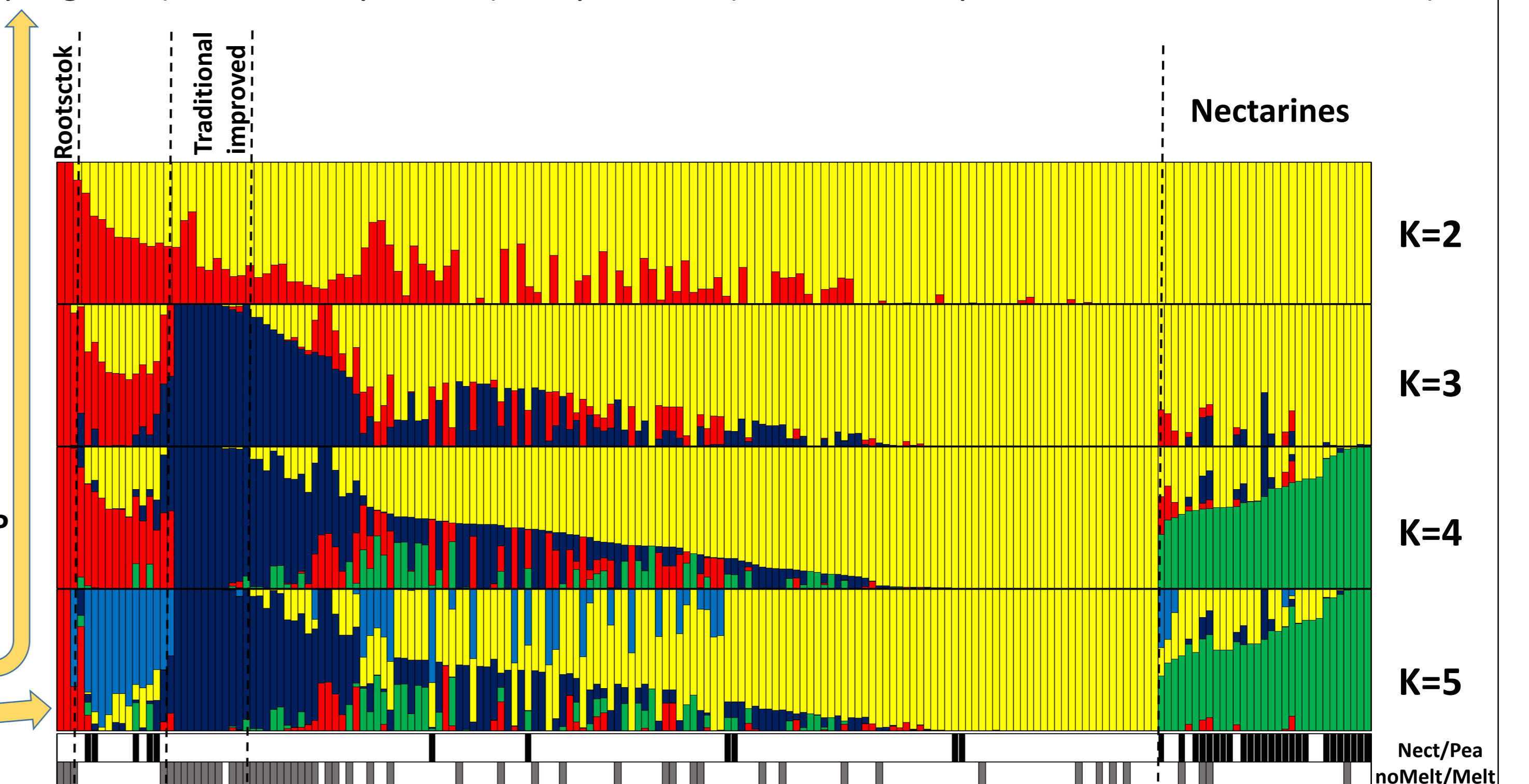


Fig. 2. Genetic structure. Traditional improved (Italian + Bolivian) germplasm belong to the same subpopulation. Nect=Nectarine (black box), Pea=Peach (white box), noMelt=no Melting (grey box), Melt=Melting (white box). (Data set 191 peach accessions, 6028 SNPs).

