

# GENOTYPING BY SEQUENCING APPROACH FOR AUTOTETRAPLOID *UROCHLOA RUZIZIENSIS* GENETIC BREEDING

R.M. Simeão<sup>3</sup>, F.B. Martins<sup>1</sup>, M.M. Vilela<sup>3</sup>, A.C.L. Moraes<sup>1</sup>, R.C.U. Ferreira<sup>1</sup>, T.G. Déo<sup>1</sup>, F.A. Moreira<sup>1</sup>, M.M. Pastina<sup>4</sup>, R.W. Noda<sup>4</sup>, A.P. Souza<sup>1,2</sup>

<sup>1</sup>Center for Molecular Biology and Genetic Engineering (CBMEG), University of Campinas (UNICAMP), Campinas, SP, Brazil.

<sup>2</sup>Plant Biology, Biology Institute, State University from Campinas, Campinas, SP, Brazil.

<sup>3</sup>Empresa Brasileira de Pesquisa Agropecuária, Campo Grande, MS, Brazil.

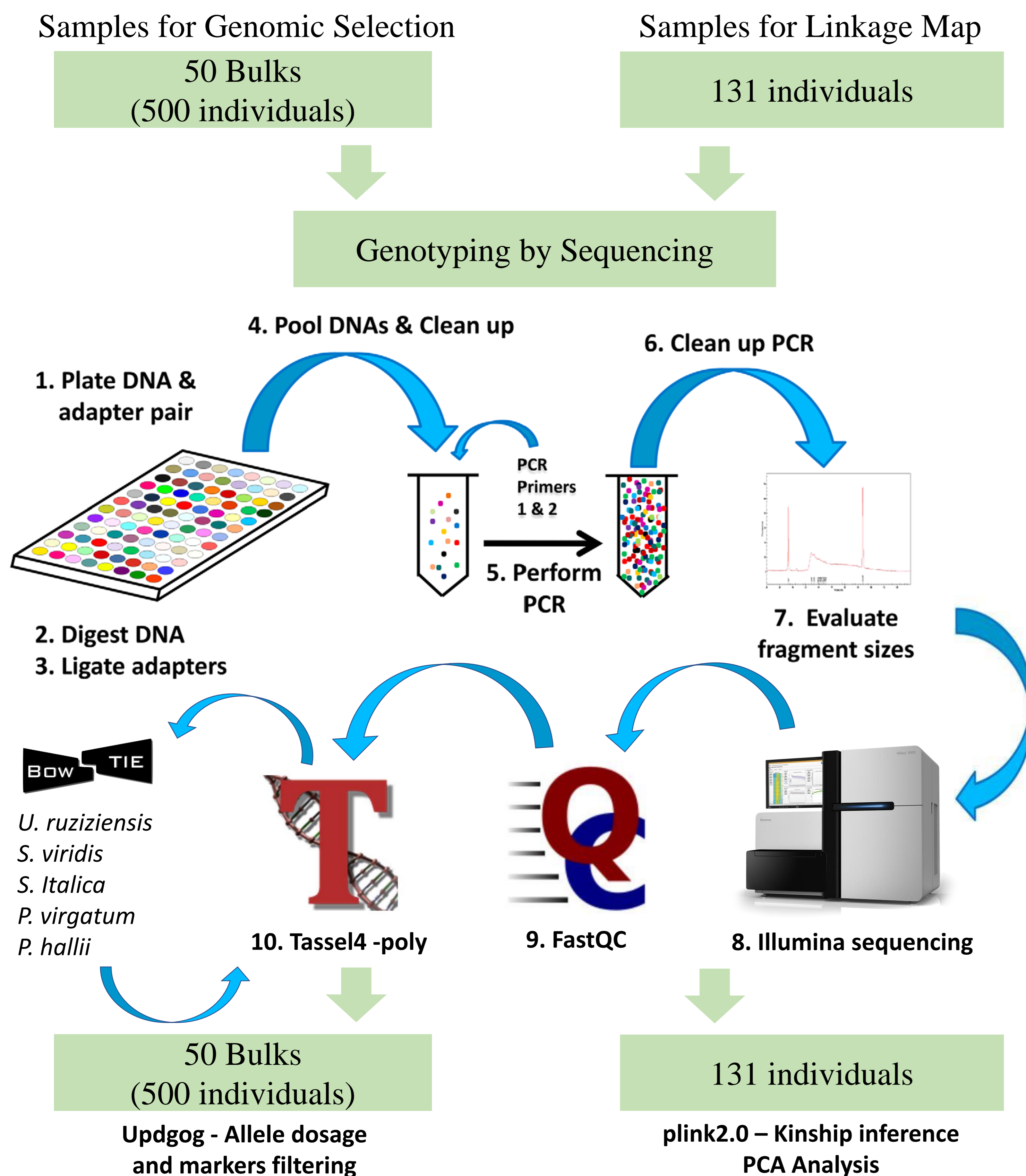
<sup>4</sup>Empresa Brasileira de Pesquisa Agropecuária, Sete Lagoas, MG, Brazil.

febimartins@gmail.com

## INTRODUCTION

Although Brazil is the major producer and exporter of beef in the world, its rangelands are cultivated with varieties obtained by selection on germplasm and conventional breeding. *Urochloa ruziziensis* is a sexual autotetraploidized forage that meets its importance in integrated systems and is essential as a female parent in other *Urochloa* spp. breeding programs. Thus, this work intends to use the Genotyping by Sequencing (GBS) approach to identify SNP markers to construct the first map of the species and estimate breeding values for Genomic Selection.

## MATERIALS AND METHODS



## RESULTS

The SNP calling found 150.000 markers in the Linkage Map sample and 185.000 in the Genomic Selection sample using *U. ruziziensis* as reference. The sum of the markers found in the Genomic Selection sample using all references was 314.000 markers (Fig. 1). The allele dosage estimation and markers filtration retained 3722 for a mean dept of 50 reads and 1847 markers for a mean dept of 60 reads (Fig. 2).

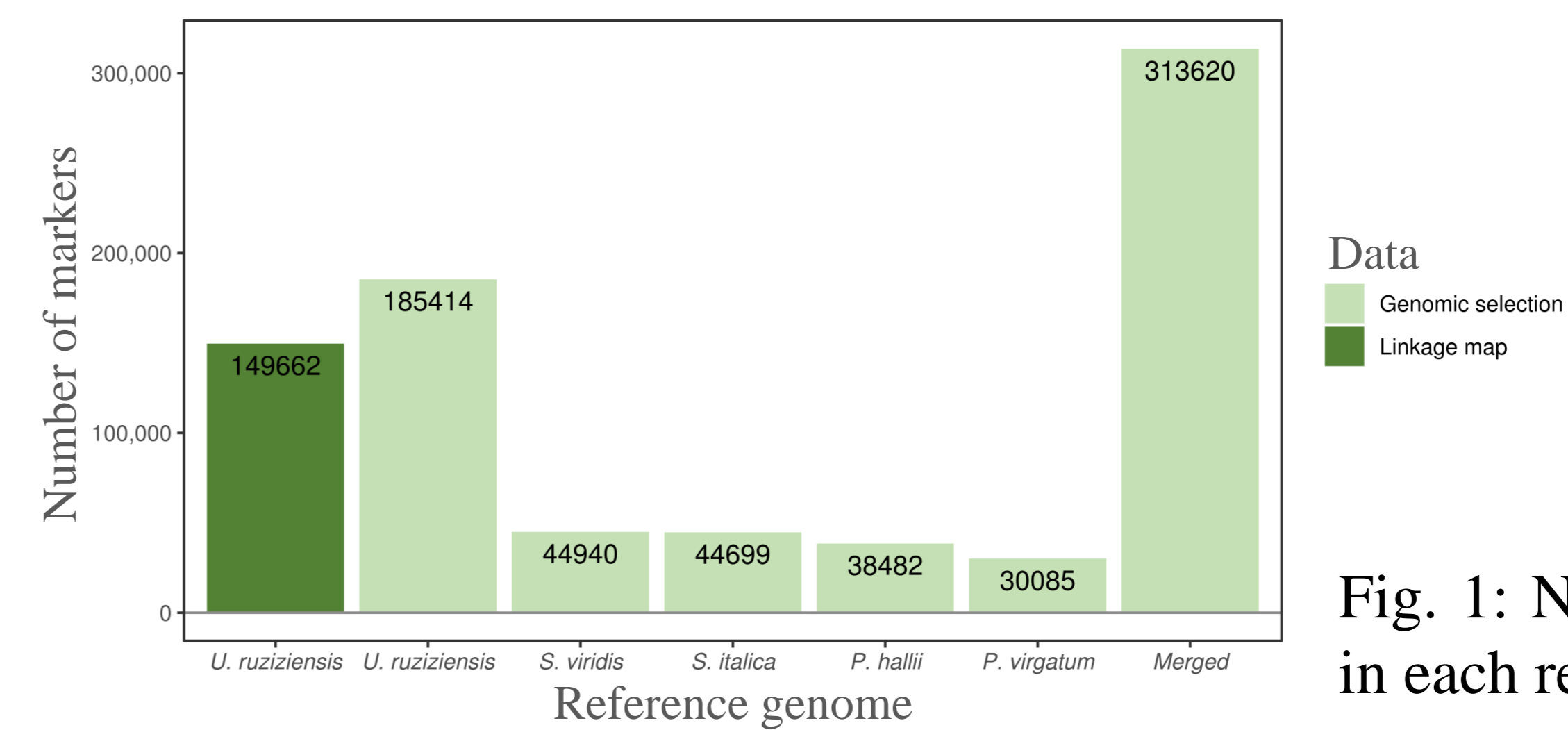


Fig. 1: Number of markers discovered in each reference.

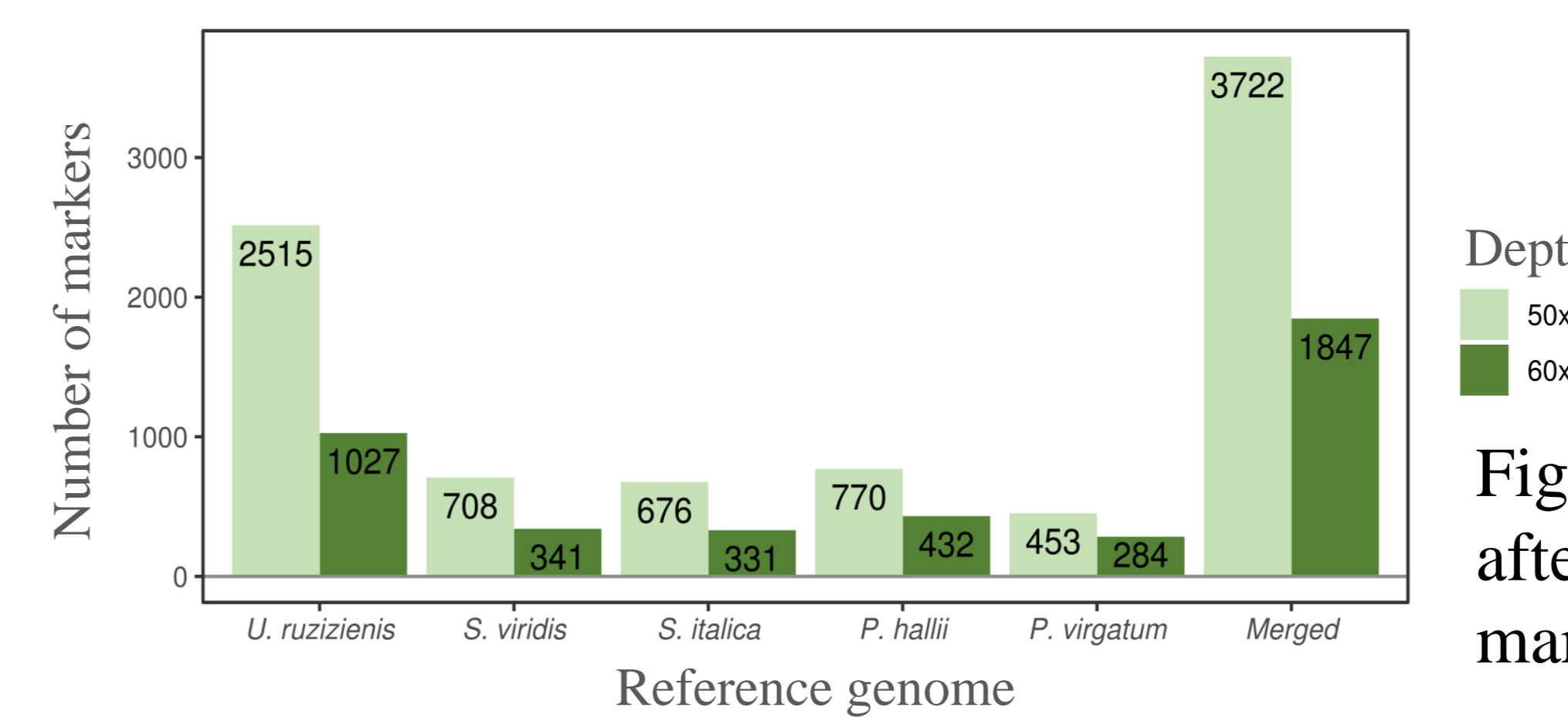


Fig. 2: Number of markers retained after the allele dosage estimation and markers filtering.

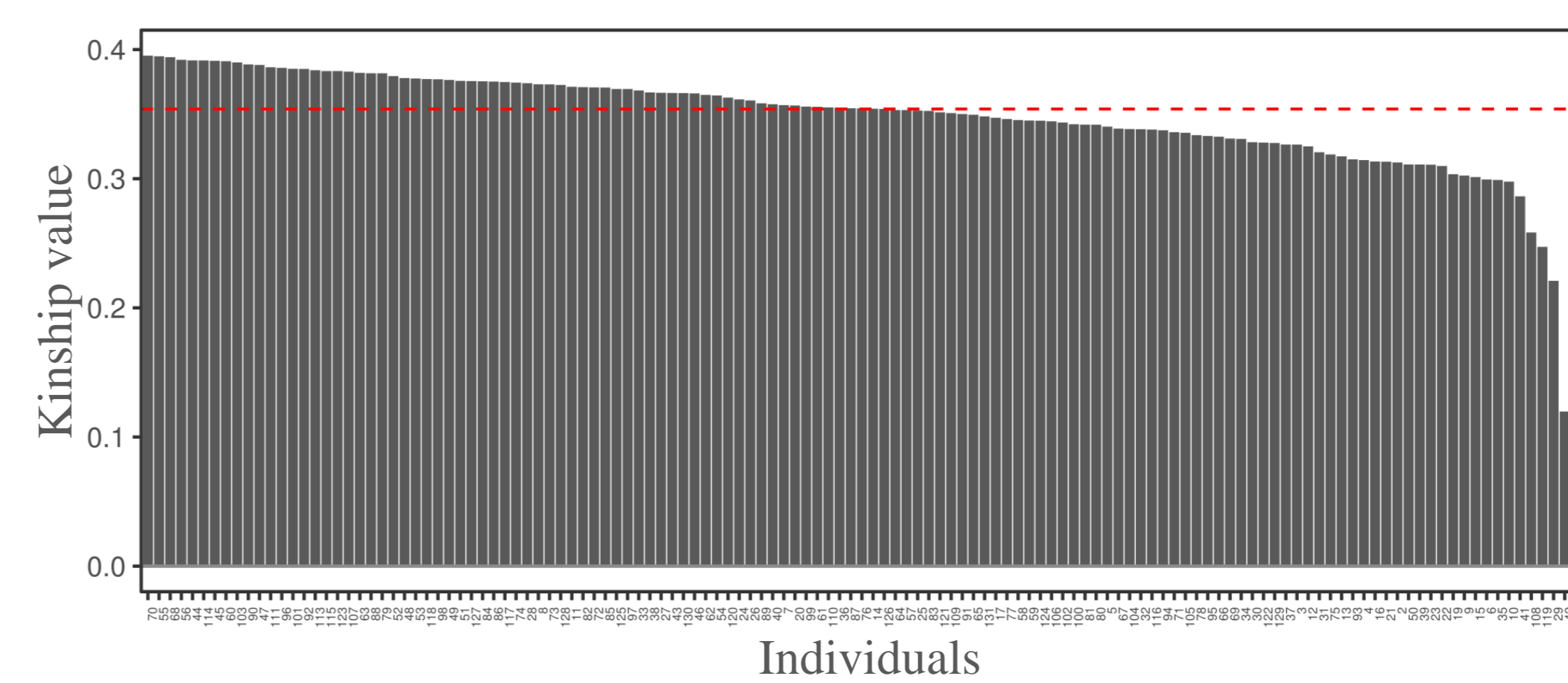


Fig. 3: Kinship analysis comparing the female progenitor against the progeny, values above 0.354 were considered clones.

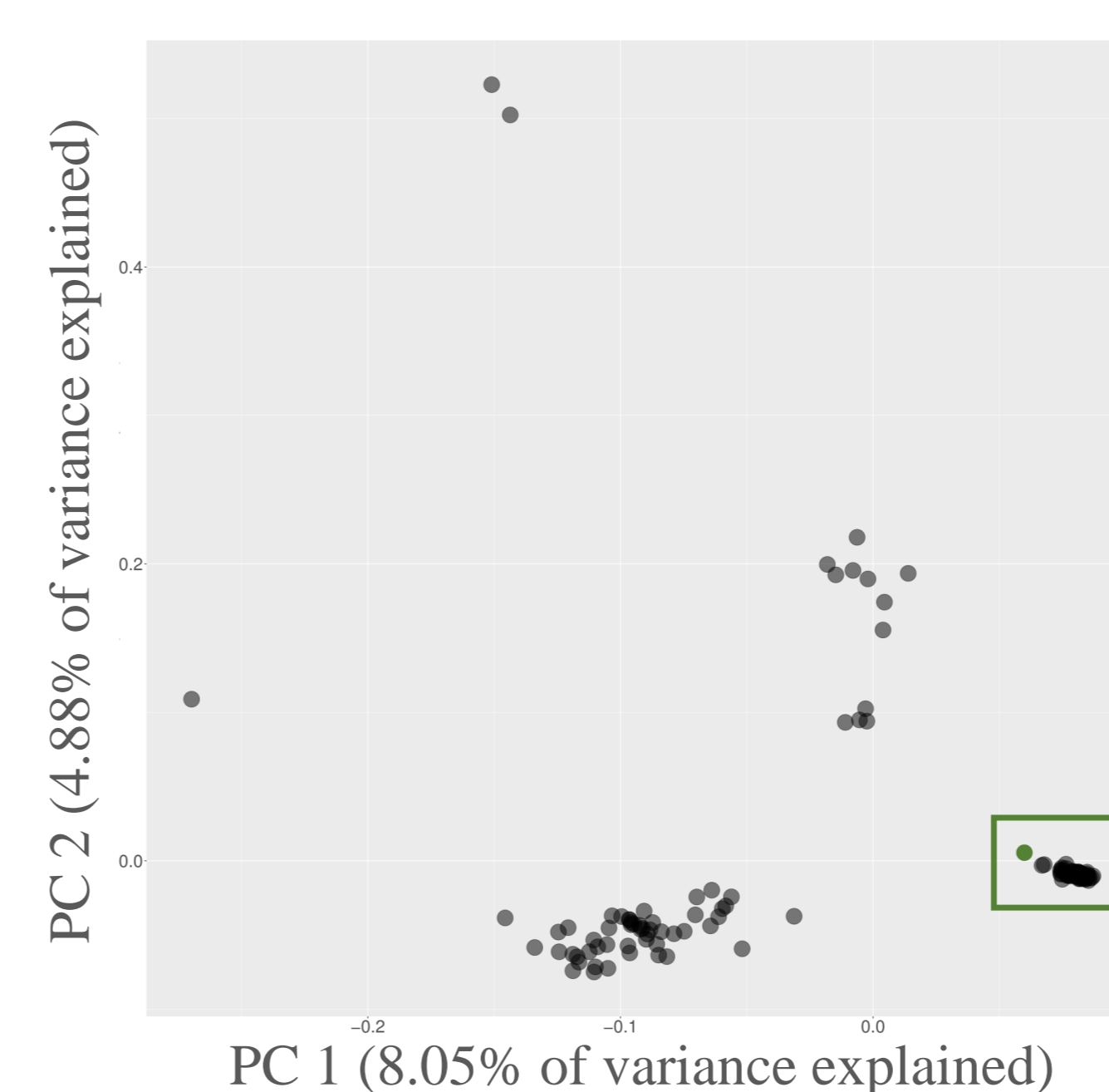


Fig. 4: Principal Component Analysis showing the progeny structure. Inside the green square are the female progenitor and the probable clones from apomixis.

A Kinship and PCA analysis were made using all markers of the Linkage Map sample, we found that 59 individuals were clones of the female progenitor and there were probably two groups from male progenitors (Fig. 3 and Fig. 4).

## CONCLUSION

The set of SNP markers found in this work seems to be very reliable, since it passed through a consolidated pipeline. However, we did not expect that the female progenitor of the Linkage Map sample was apomictic, compromising the construction of the map. Now we intend to genotype more individuals to group with this data and use it as a panel in a Genome-Wide Association Study investigating the apomictic trait. Despite the low number of markers that remained from the allele dosage estimation, it is enough to use in the next steps to estimate the bulks breeding values.