



Genome-wide SNP markers from ddRAD reveals the population structure of Italian donkey populations

Chessari G., Criscione A., Cesarani A., Ablondi M., Asti V., Bigi D., Bordonaro S., Ciampolini R., Cipolat-Gotet C., Congiu M., De Palo P., Landi V., Macciotta N. P. P., Matassino D., Portolano B., Riggio S., Sabbioni A., Sardina M. S., Senczuk G., Tumino S., Vasini M., Ciani E. and Mastrangelo S.



Overview ● ● ● ●

Origin of *Equus asinus*

Studies on mitochondrial variability suggests that current domestic donkeys derive from two maternal lines: the Nubian wild ass (*Equus africanus africanus*) and the Atlas wild ass (*Equus africanus atlanticus*).
(Cattani *et al.*, 2002; Kimura *et al.*, 2011; Todd *et al.*, 2022)

Importance

- Milk production for food and cosmetics
- Therapeutic purposes
- Exploitation of biodiversity
(150 recognized breeds worldwide)
- Cultural and genetic heritage
- Promotion of micro-economies of marginal areas through sustainable livestock production



Overview ● ● ● ●

Origin of *Equus asinus*

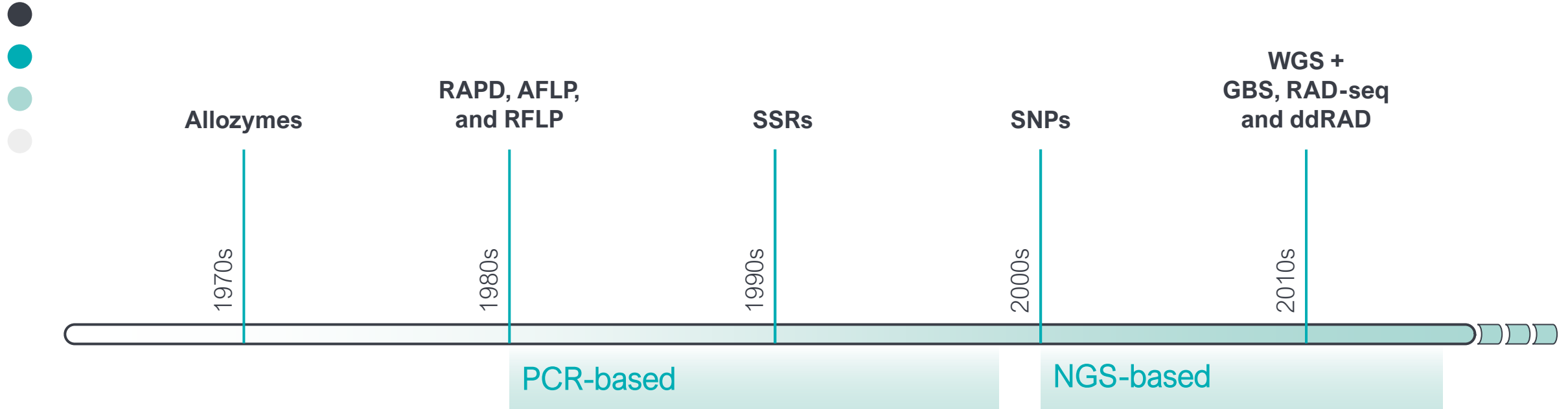
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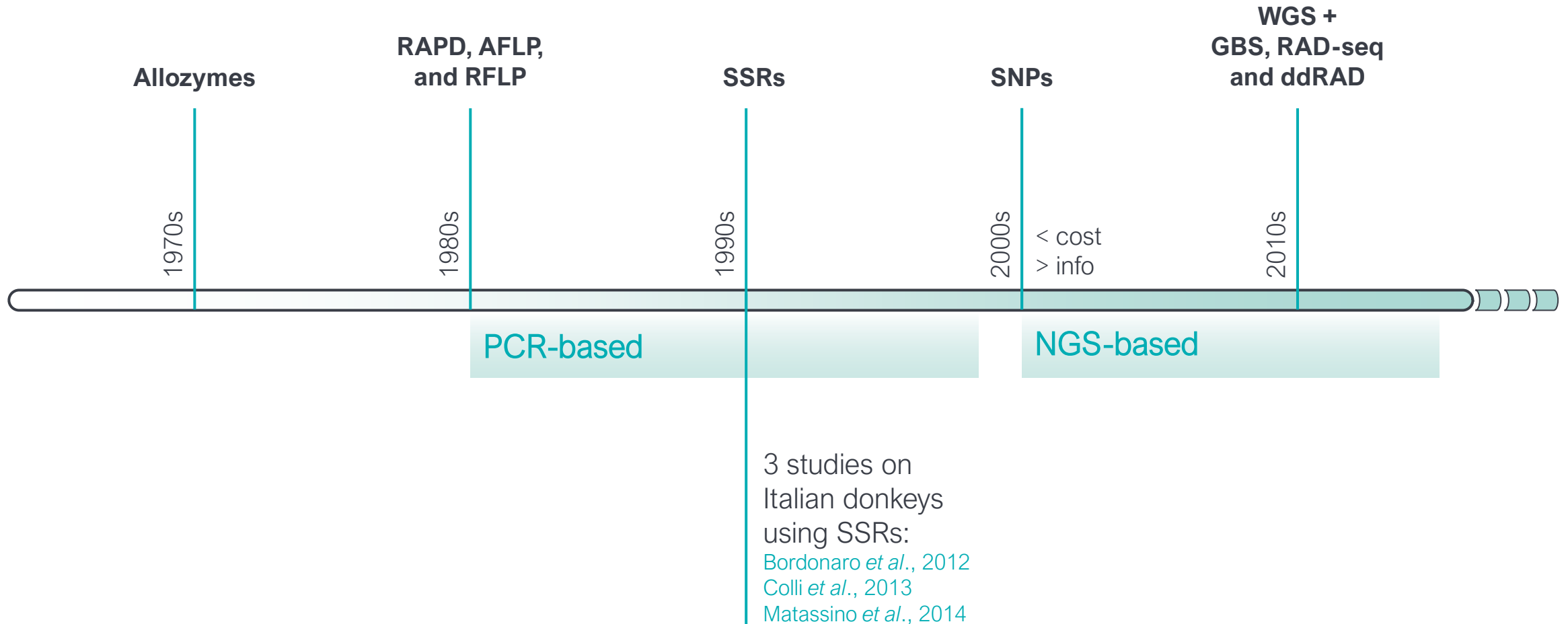
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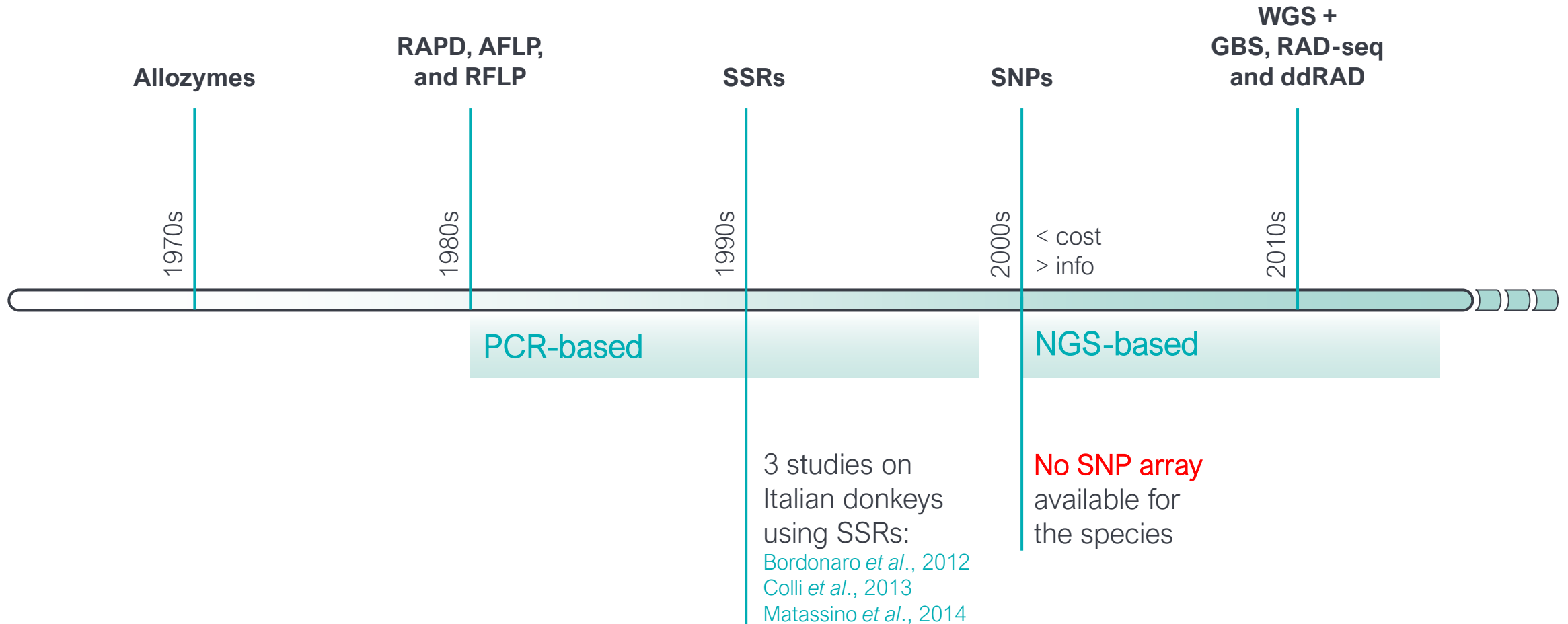
Timeline of key marker technologies in population genetics



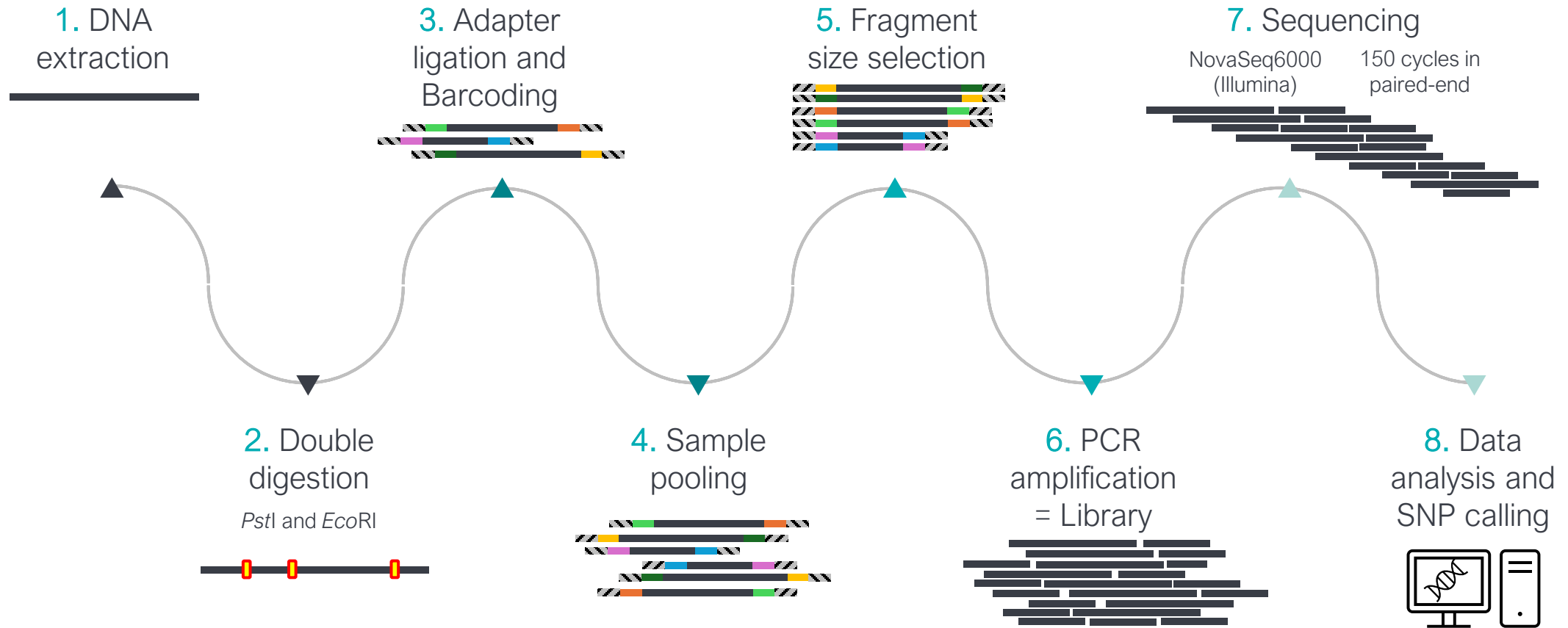
Timeline of key marker technologies in population genetics



Timeline of key marker technologies in population genetics



ddRAD technology



PROS

- Relatively inexpensive
- Free of ascertainment bias

CONS

- Possible gaps in the genome
- High-quality DNA

Materials and Methods ● ● ● ●



Amiata
 $n = 22$



Viterbese
 $n = 20$



Romagnolo
 $n = 25$



Sardo
 $n = 25$



Asinara
 $n = 18$



Martina Franca
 $n = 30$



Pantesco
 $n = 23$



Grigio
 $n = 25$



Ragusano
 $n = 32$

- Total number of animals: 220
- Number of raw reads: ~420 M
- ddRAD mean coverage: 29.15x
- Raw SNP panel: 60k
- Reference genome: *E. asinus* ASM1607732v2
GenBank GCA_016077325.2

Materials and Methods

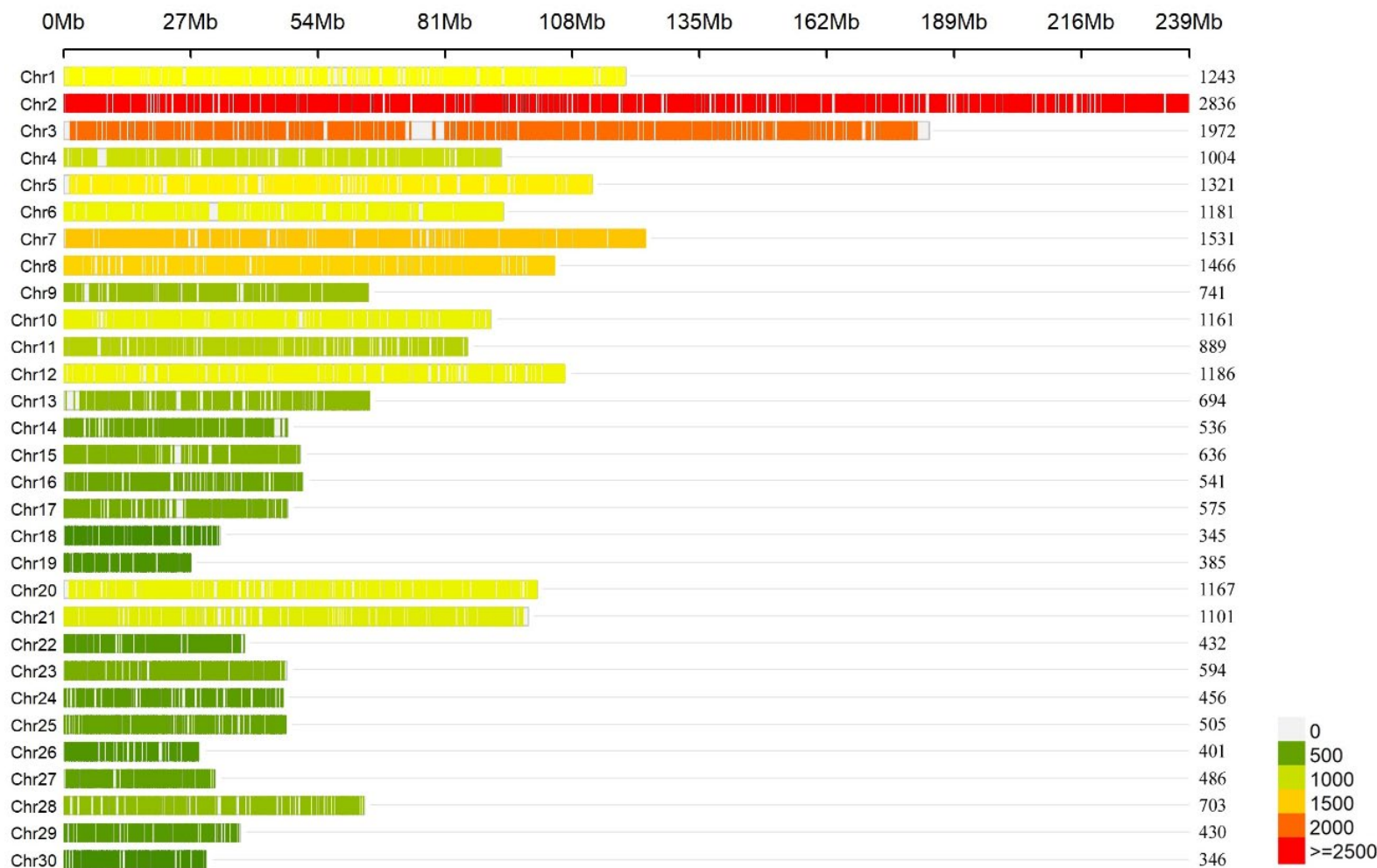
Quality Control

- Autosomes (30)
- No animals with >10% missing genotypes
- No SNP with a call rate < 90%
- No SNP with a minor allele frequency < 1%

— 197 animals and
— 26'864 SNPs

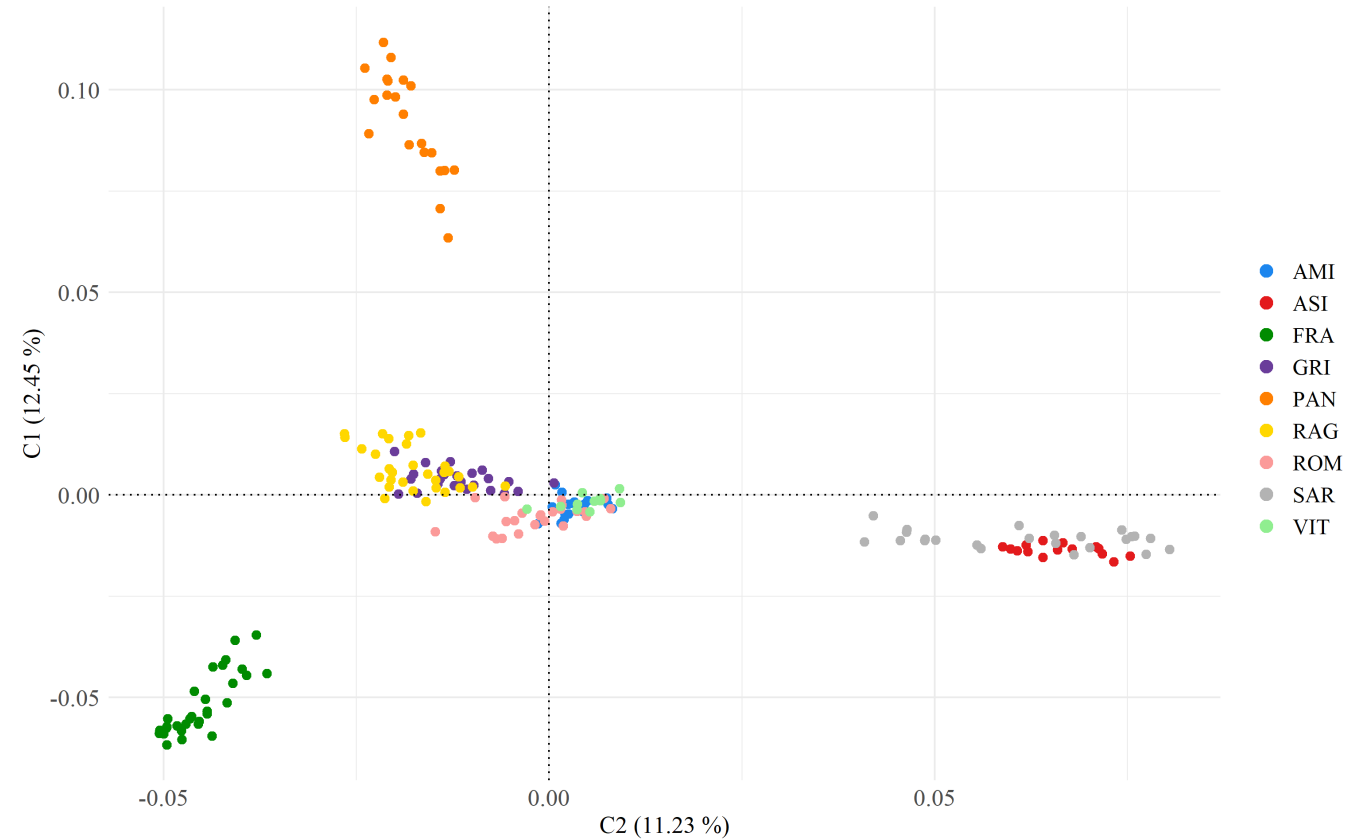
Analyses

- Genetic diversity indices
- Population structure analyses
- Runs of homozygosity in the metapopulation



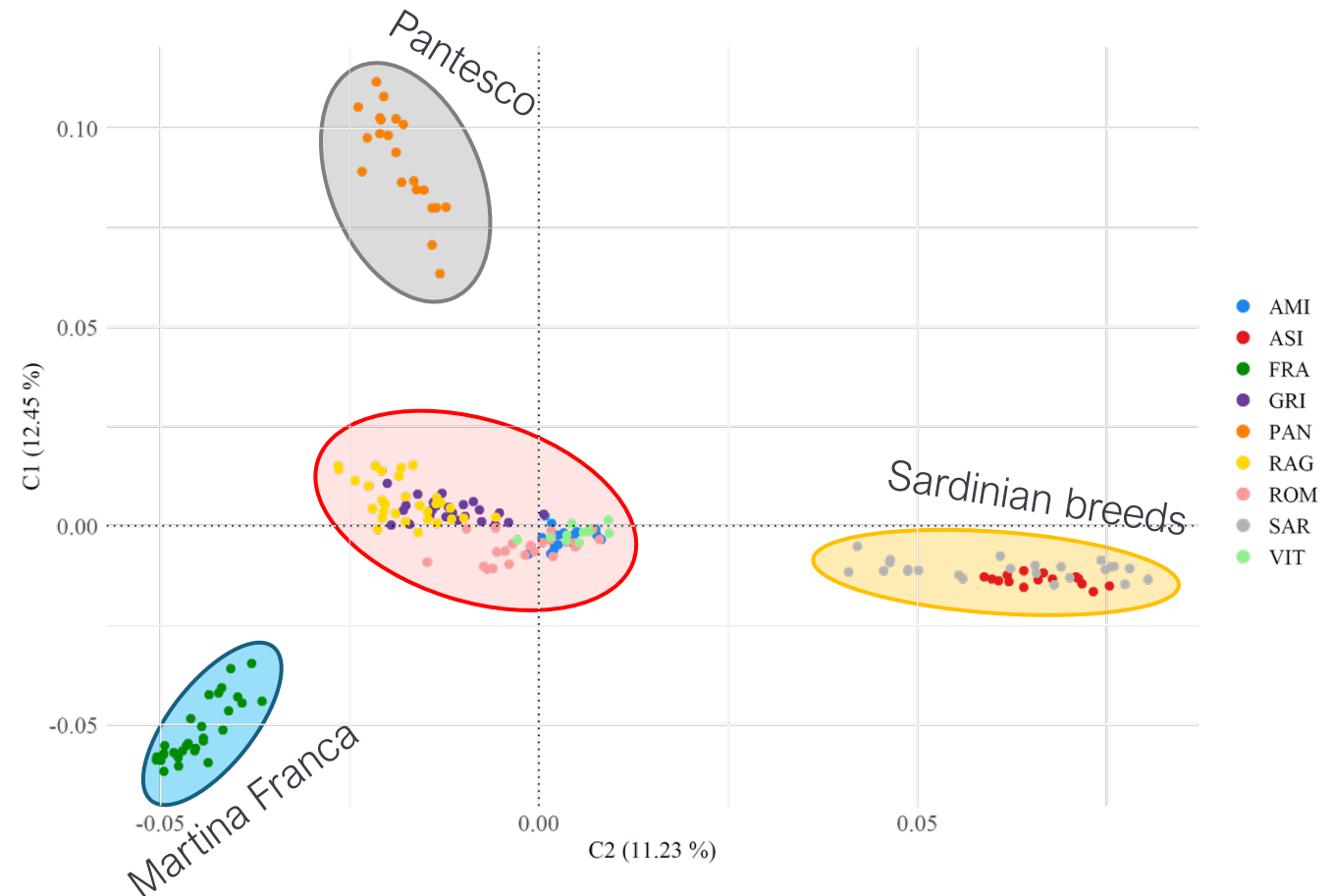
Results and Discussion ● ● ● ●

Breed	H_O	H_E	F_{IS}	N_e
Amiata	0.234	0.230	0.044	83
Asinara	0.179	0.198	0.273	47
Martina Franca	0.215	0.211	0.128	78
Grigio	0.232	0.237	0.060	111
Pantesco	0.222	0.211	0.104	50
Ragusano	0.241	0.240	0.021	127
Romagnolo	0.239	0.234	0.030	106
Sardo	0.203	0.216	0.176	83
Viterbese	0.222	0.221	0.096	57

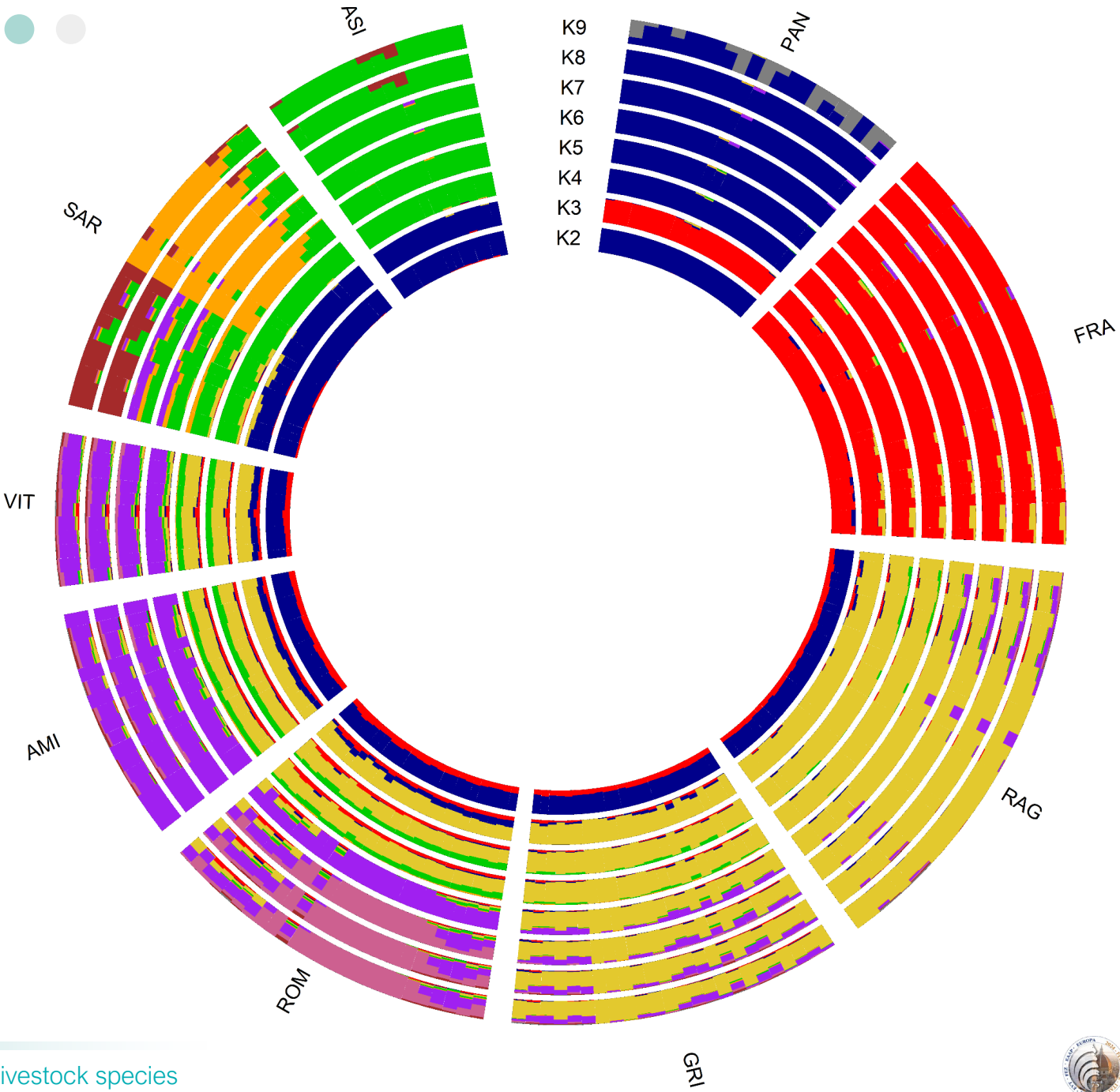
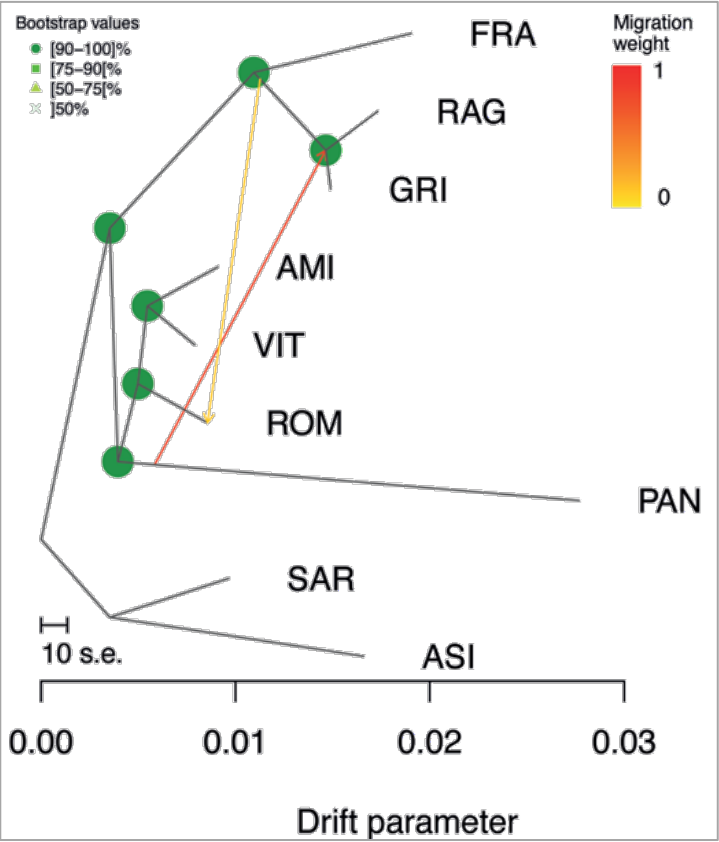


Results and Discussion ● ● ● ●

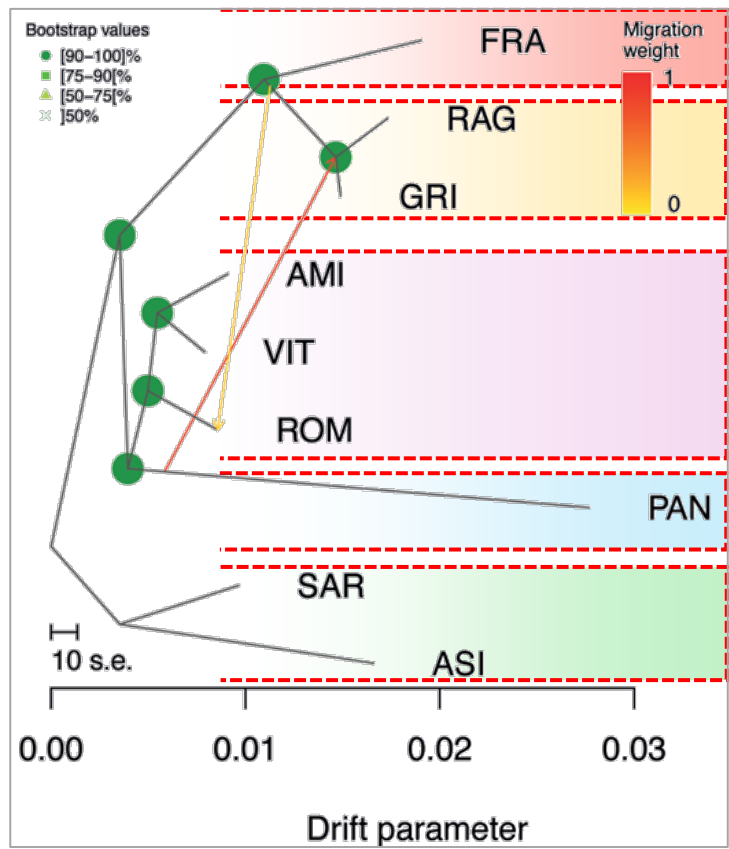
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Results and Discussion

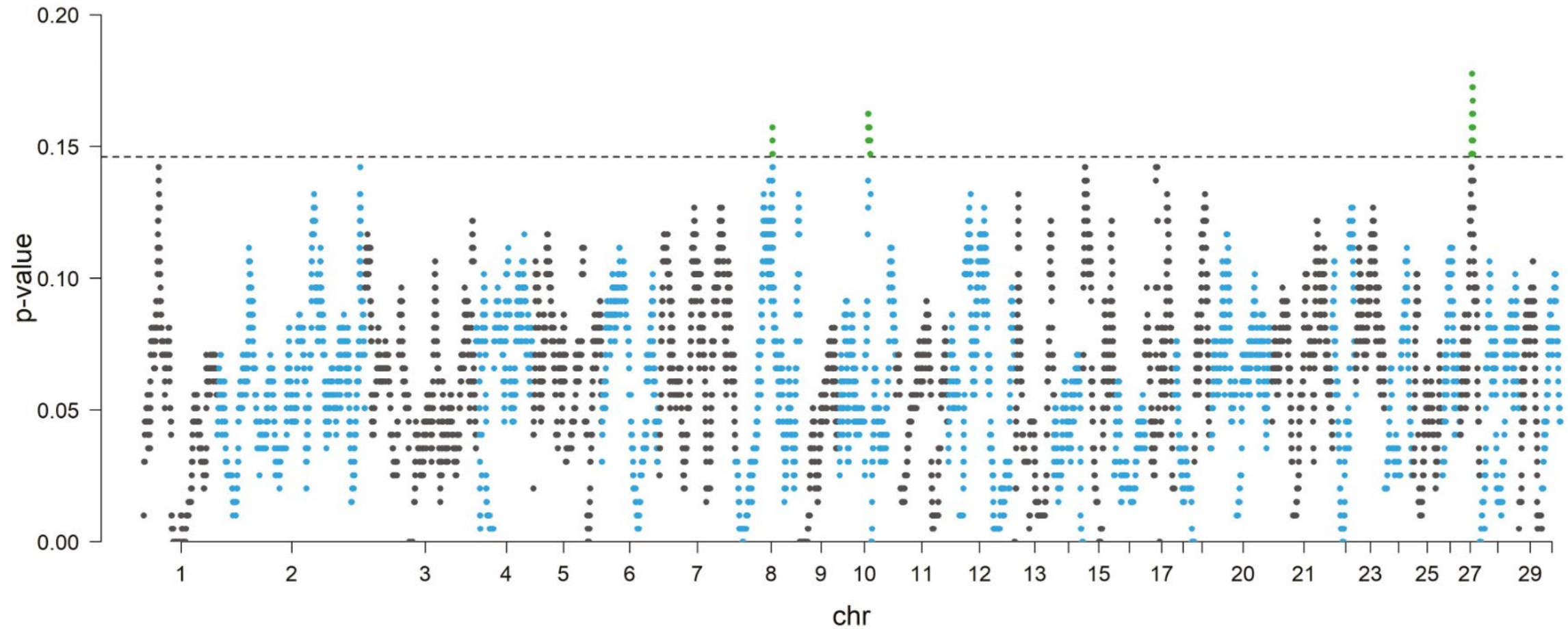


Results and Discussion



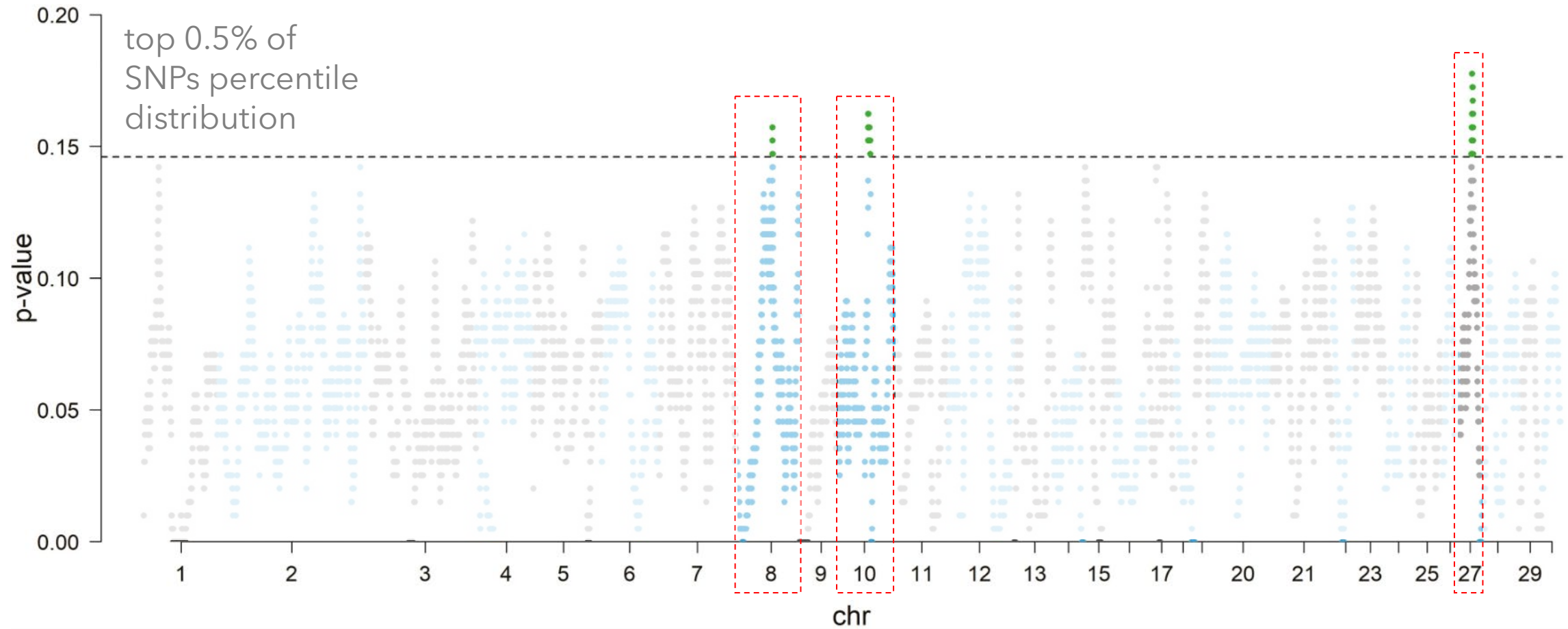
Runs of homozygosity

in all 197 individuals



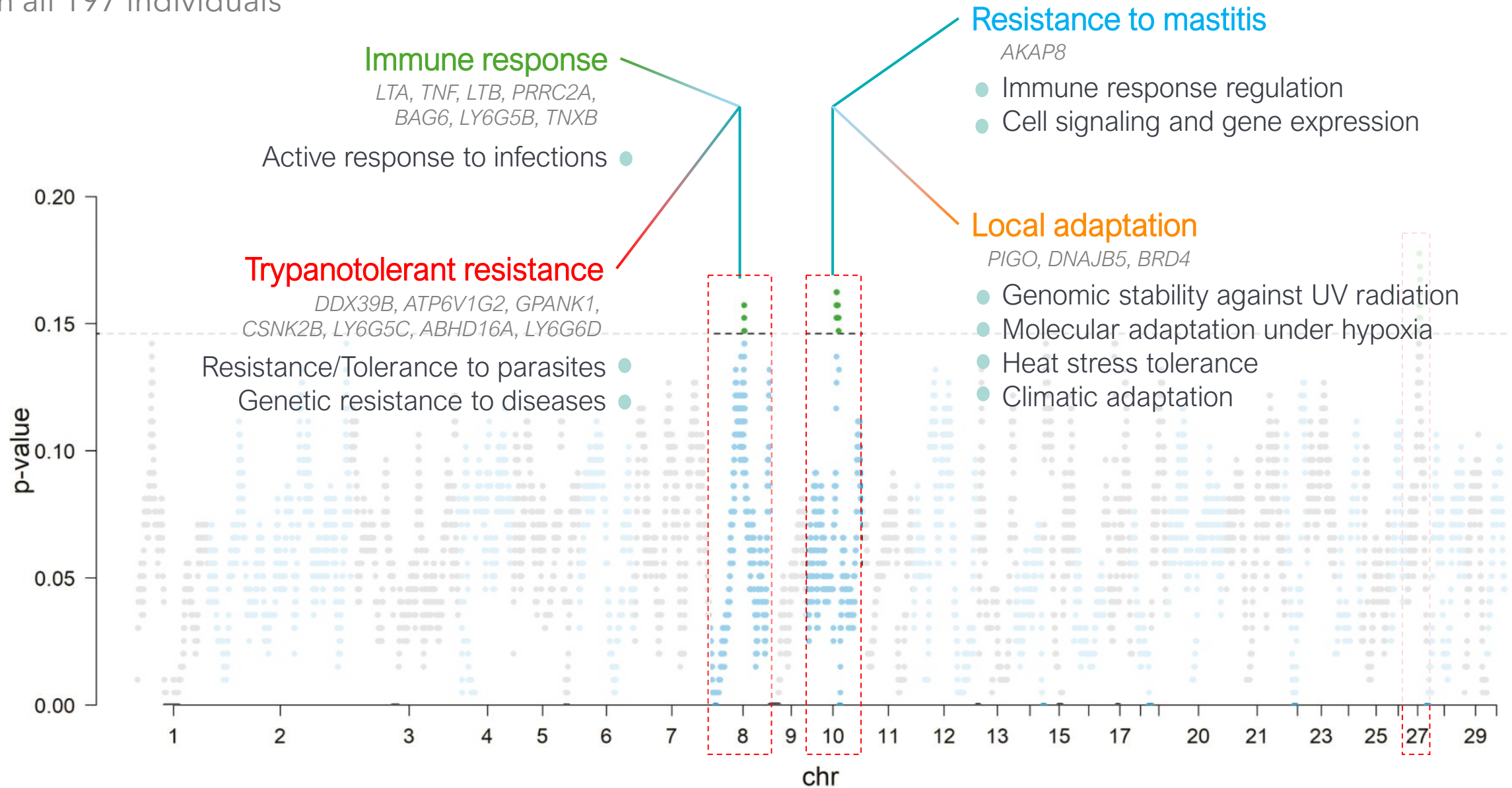
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Conclusion

1 Population structure investigation in donkey species

2 Application of a new approach in biodiversity studies

3 Starting point for further investigations



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Thanks for the attention



Any questions?



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