

A genome wide set of SNPs detects population substructure and long range linkage disequilibrium in wild sheep

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Introduction

- Single nucleotide polymorphisms (SNPs) are fast becoming the marker of choice for evolutionary and population genetic studies^{1,2}.
- Increasingly researchers are applying resources developed in domestic organisms to related wild counterparts. However, a few key questions remain:
 - How efficient are these methods at finding new markers?
 - How far phylogenetically can you go from the organism for which the technique was developed³?
- We applied the OvineSNP50 BeadChip, developed for domestic sheep⁴, to bighorn sheep (*Ovis canadensis*) and thinhorn sheep (*Ovis dalli*).

Methods and Materials

Study animals and SNP genotyping

- Fifty two bighorn sheep and two thinhorn sheep were genotyped.
 - 50 bighorn sheep from Ram Mountain Alberta, Canada.
 - ♦ The Ram Mountain population has been extensively monitored over the past 40 years⁵.
 - 2 bighorn sheep from Wyoming.
 - 2 thinhorn from Yukon-Charley Rivers National Park, Alaska.



Summary statistics and case study in bighorn sheep

- We used PLINK v. 1.07⁶ to generate taxa specific summary statistics and smartpca, part of EIGANSTRAT v. 3.0⁷, to conduct principal component analysis (PCA).
- In addition, we calculated the degree of allele sharing between individual bighorn sheep and extent of linkage disequilibrium (LD) within Ram Mountain.

Results

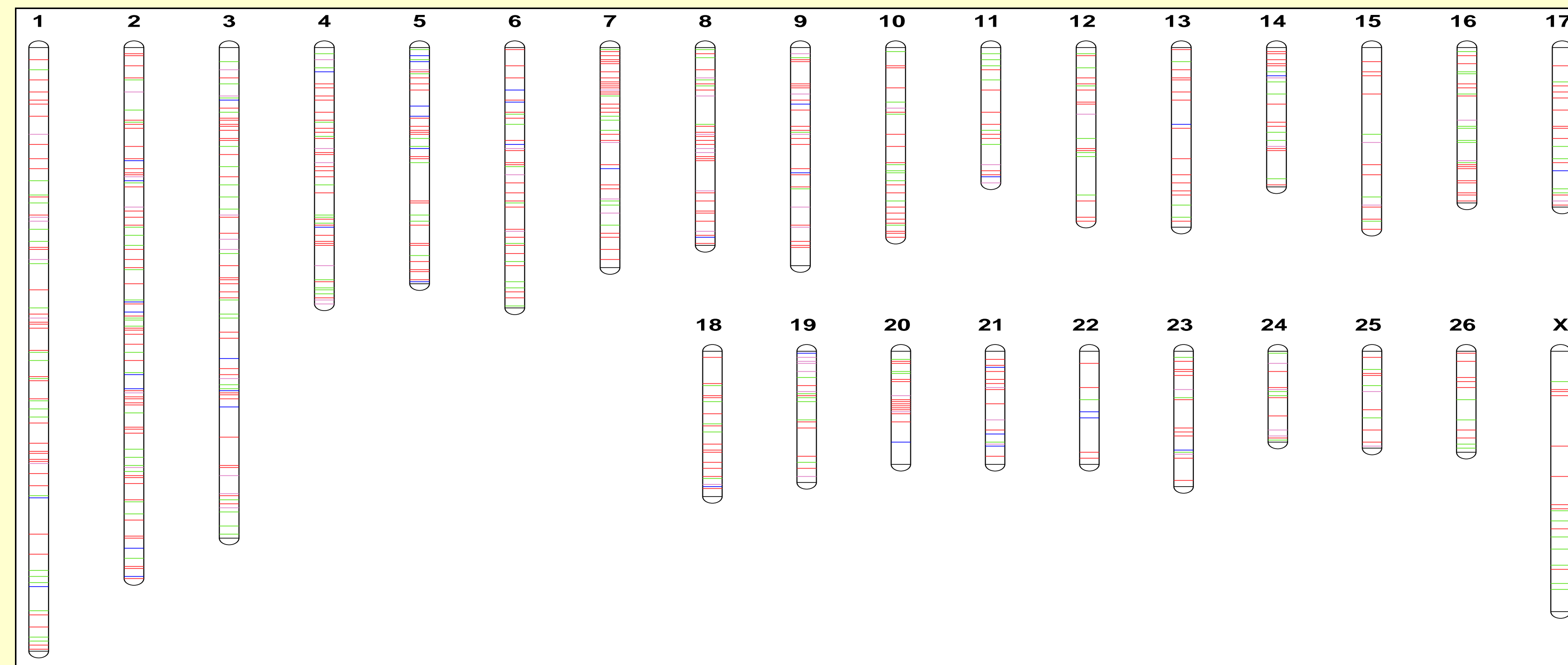


Fig 1: Chromosomal distribution of SNPs discovered with the OvineSNP50 BeadChip. Colors indicate species in which the loci are polymorphic: red = bighorn sheep, green = thinhorn sheep, purple = shared polymorphisms, and blue = fixed differences between bighorn and thinhorn sheep.

- Call-rate was high in both species (over 90%) and yielded 868 SNPs (Figure 1).
 - 484 were polymorphic only in bighorn sheep.
 - 244 were polymorphic only in thinhorn sheep.
 - 54 were fixed differences between the two species.
 - 86 were polymorphic in both species.

- We found clear distinctions between species and populations (Figure 2).
- Allele sharing within bighorn sheep elucidated substructure not seen in the PCA (Figures 3 & 4).
- Extensive LD was found within Ram Mountain (Figure 5).

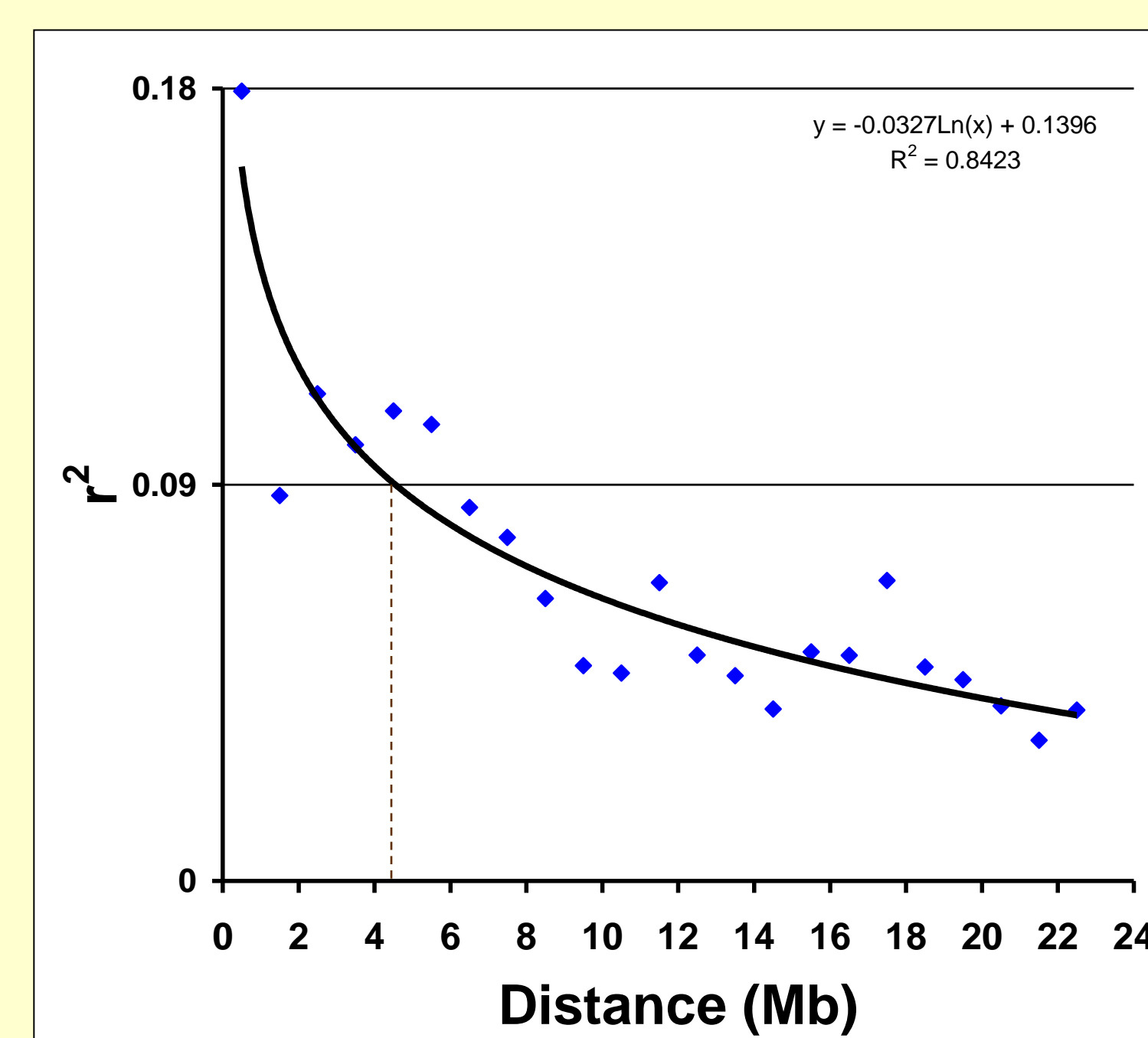


Fig 5: Genome wide half-length measured by r^2 plotted as a function of intermarker distance. A logistic fitted line is shown.

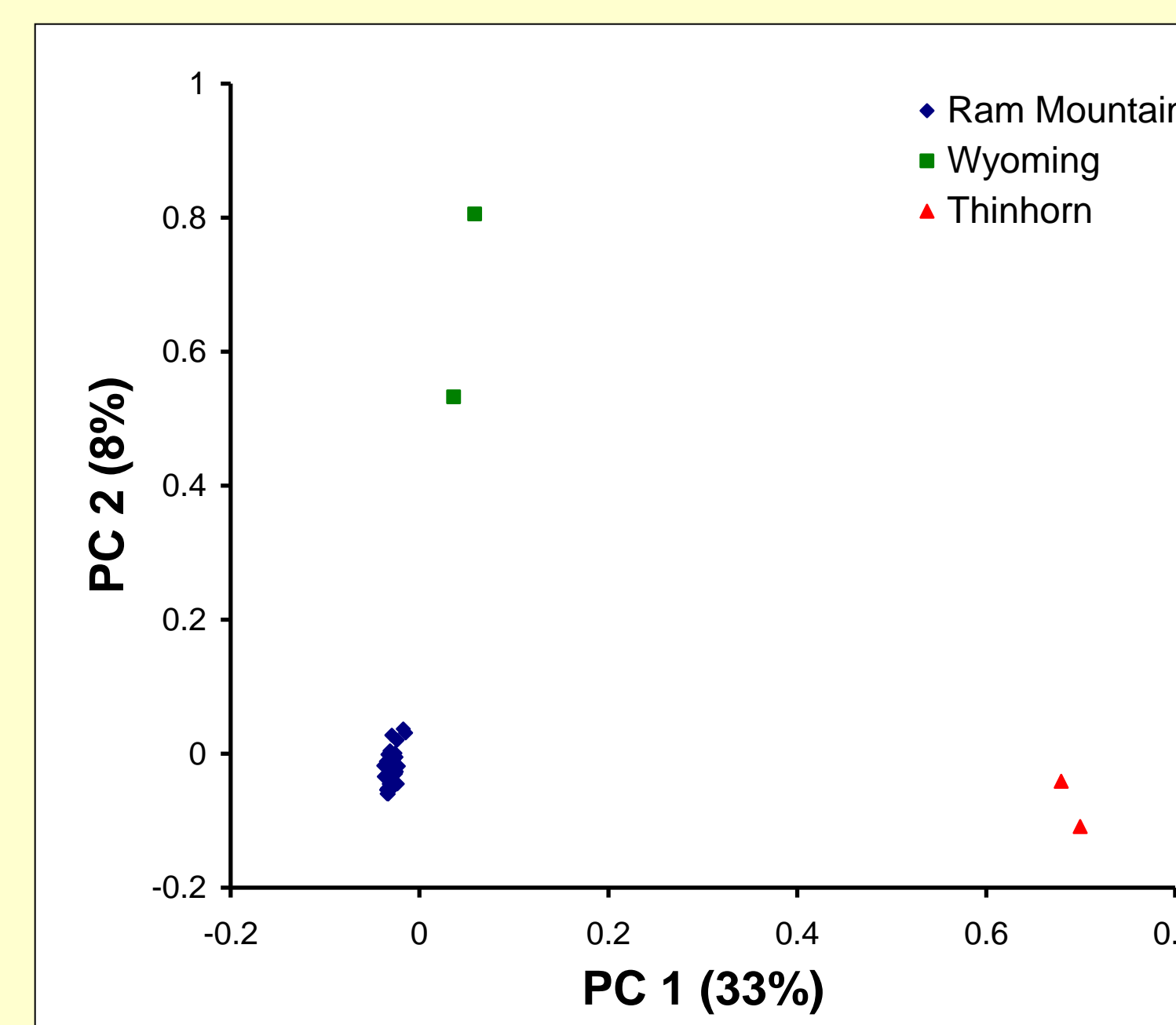


Fig 2: Plot of the first two principal components for both species.

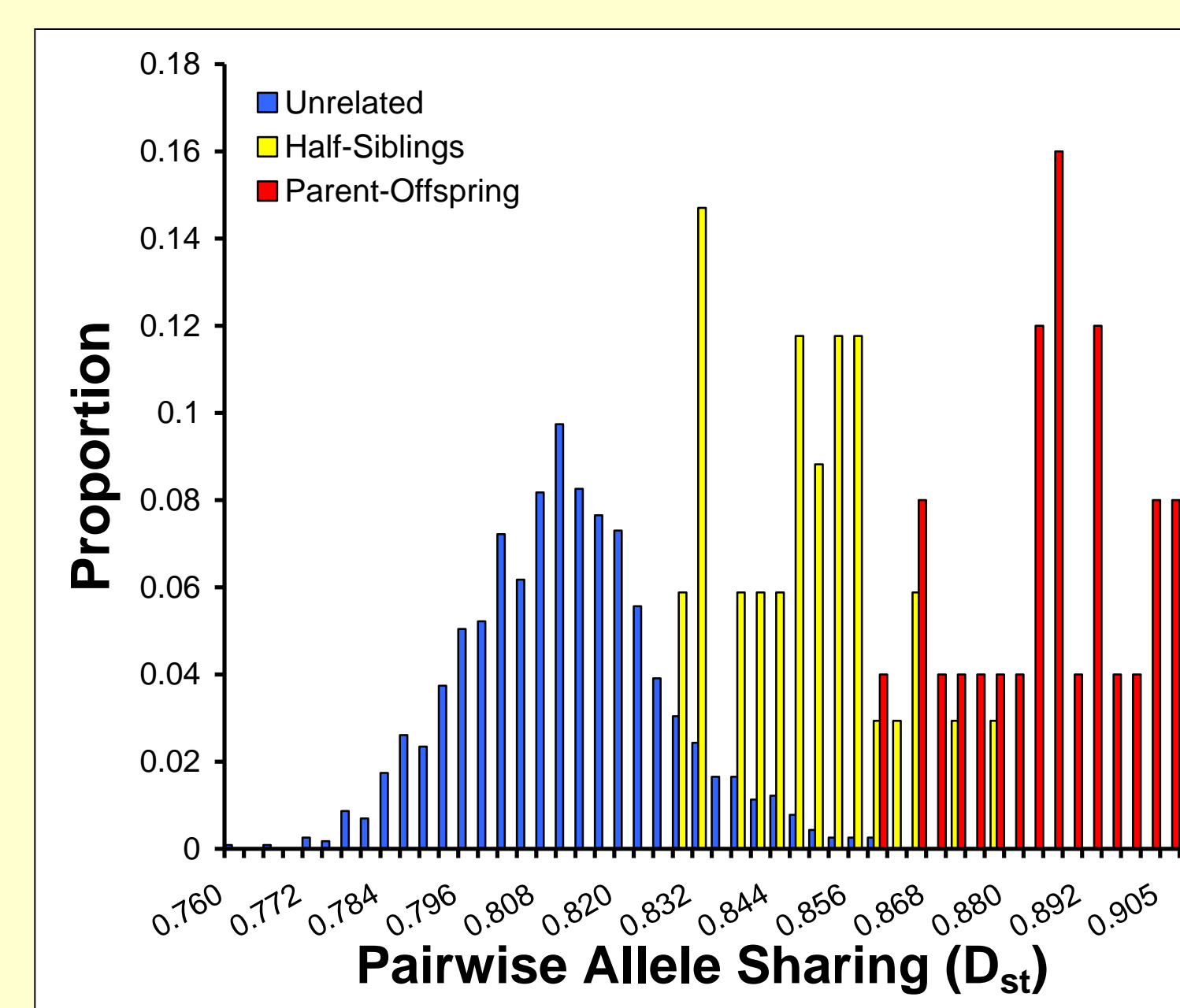


Fig 3: Distribution of genetic distances (D_{ST}) between individuals of different relationship classes within Ram Mountain bighorn sheep

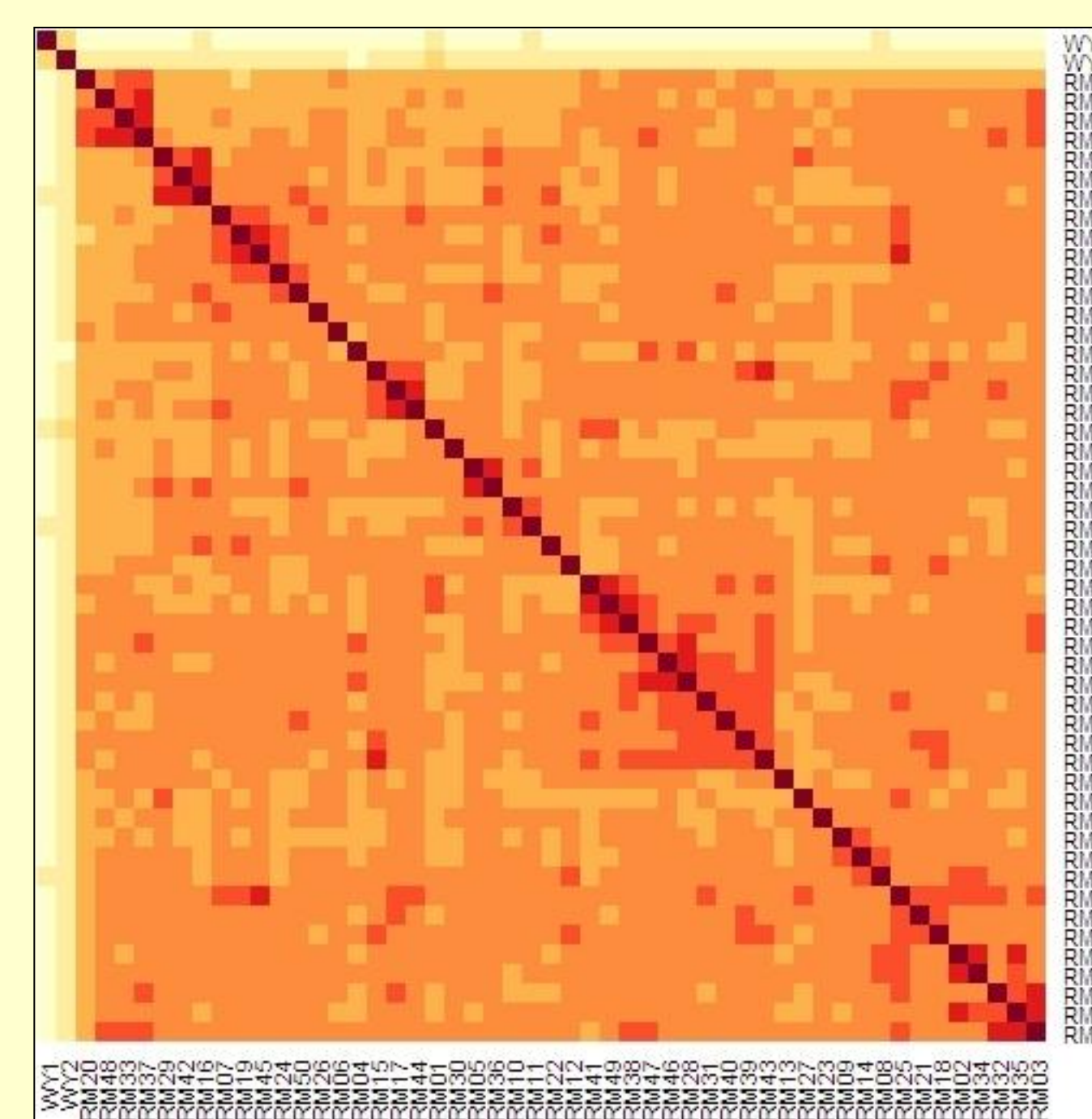


Fig 4: Heatmap of genetic similarity between individual bighorn sheep. Dark squares indicate high allele sharing, light squares indicate low allele sharing.

Discussion and Conclusion

- Application of the OvineSNP50 BeadChip can quickly provide genomic markers without the need for cloning or resequencing.
- Persistent LD observed in the Ram Mountain population is consistent with aspects of bighorn sheep biology.
- Efficiency and efficacy of marker discovery will likely be dependant on divergence between the taxa and domestic sheep.
- This new genomic resource provides excellent tool for future studies such as:
 - Candidate gene association studies
 - Linkage mapping
 - Population genomics

Acknowledgements

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