

Genome-wide association study for daily milk yield in Istrian dairy sheep

M. Špehar¹, J. Ramljak², A. Kasap²

¹Croatian Agency for Agriculture and Food, Svetošimunska 25, 10000 Zagreb, Croatia, e-mail: marija.spehar@hapih.hr

²University of Zagreb, Faculty of Agriculture, Department of Animal Science and Technology, Svetošimunska 25, 10000 Zagreb, Croatia

AIM & CONCLUSION

Identifying associations between genetic markers and traits of economic importance provides practical benefits for the dairy sheep industry facilitating discovery of the underlying genes and mutations

The study aimed to identify genomic regions associated with daily milk yield (DMY)

None of the markers showed significant effect

Six were significant on the suggestive level (two on chromosomes 1, and 18, and one on chromosomes 6 and 13)

MATERIAL

- Istrian breed
- 38,293 test-day records
- 719 genotyped animals (Ovine SNP50 BeadChip)
- QC: SNP and individual genotype call rate > 0.9, MAF > 0.05, autosomal SNPs
- 693 animals and 43,793 SNPs

METHODS

- Estimation of DMY BVs
- Single step genomic BLUP
- GWAS analysis
- R package 'rrBLUP'
- Four models
 1. without controlling for population structure (PS)
 2. controlling for PS effect
 3. controlling for relatedness
 4. controlling for both PS and relatedness



Picture 1. Flock of Istrian sheep

RESULTS

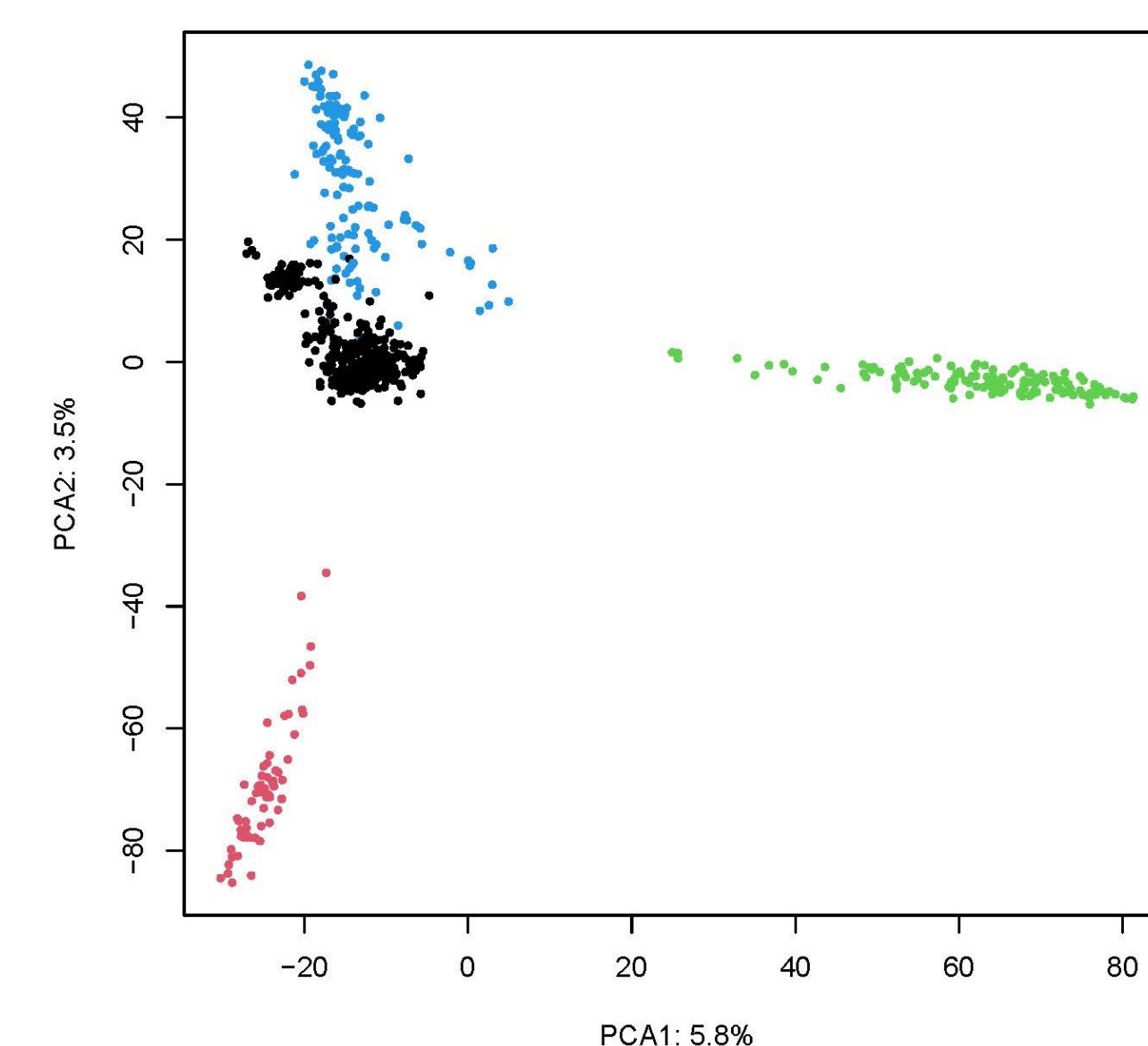


Figure 1. First and second principal component analysis

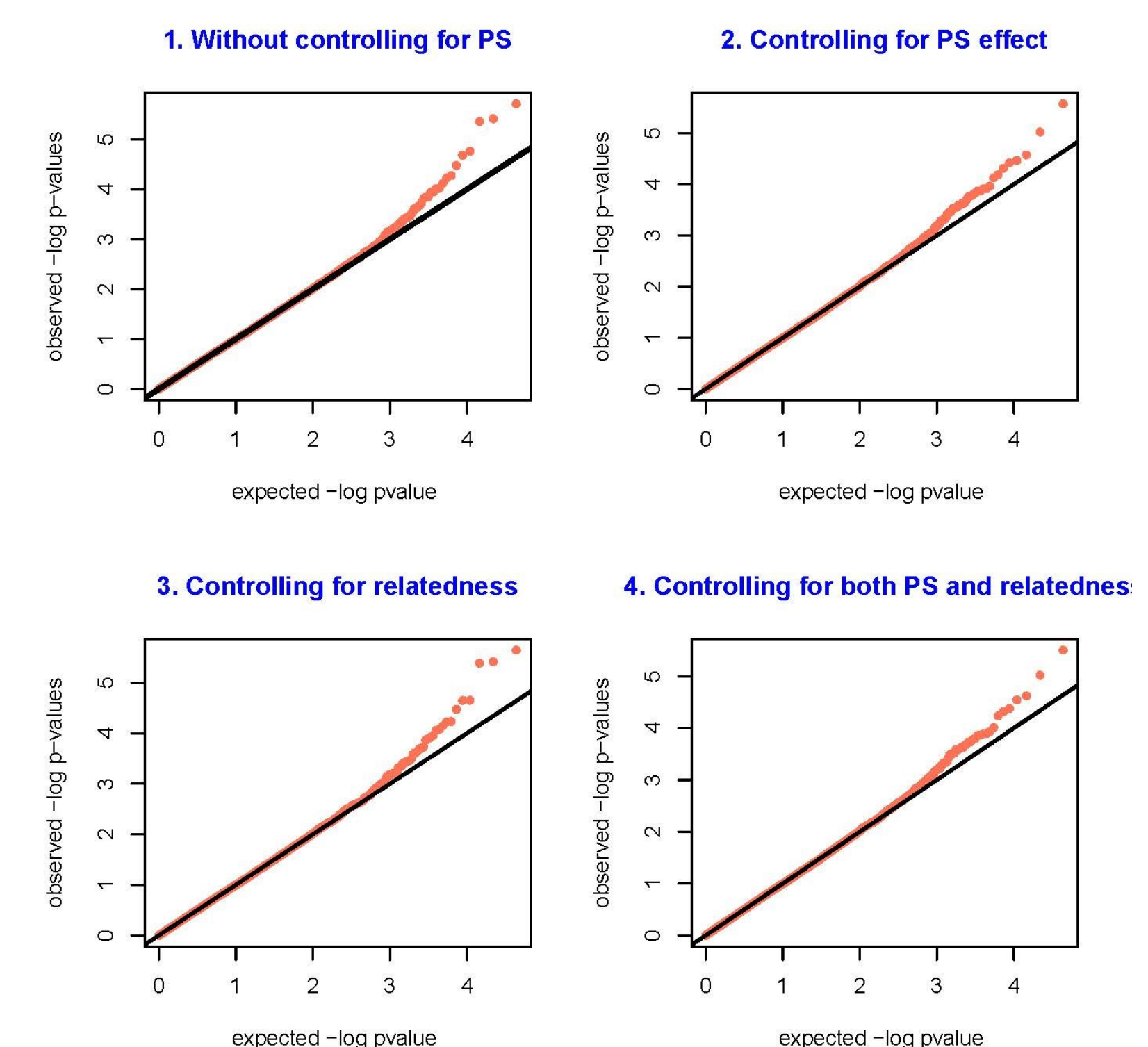


Figure 2. Q-Q plot of the different models

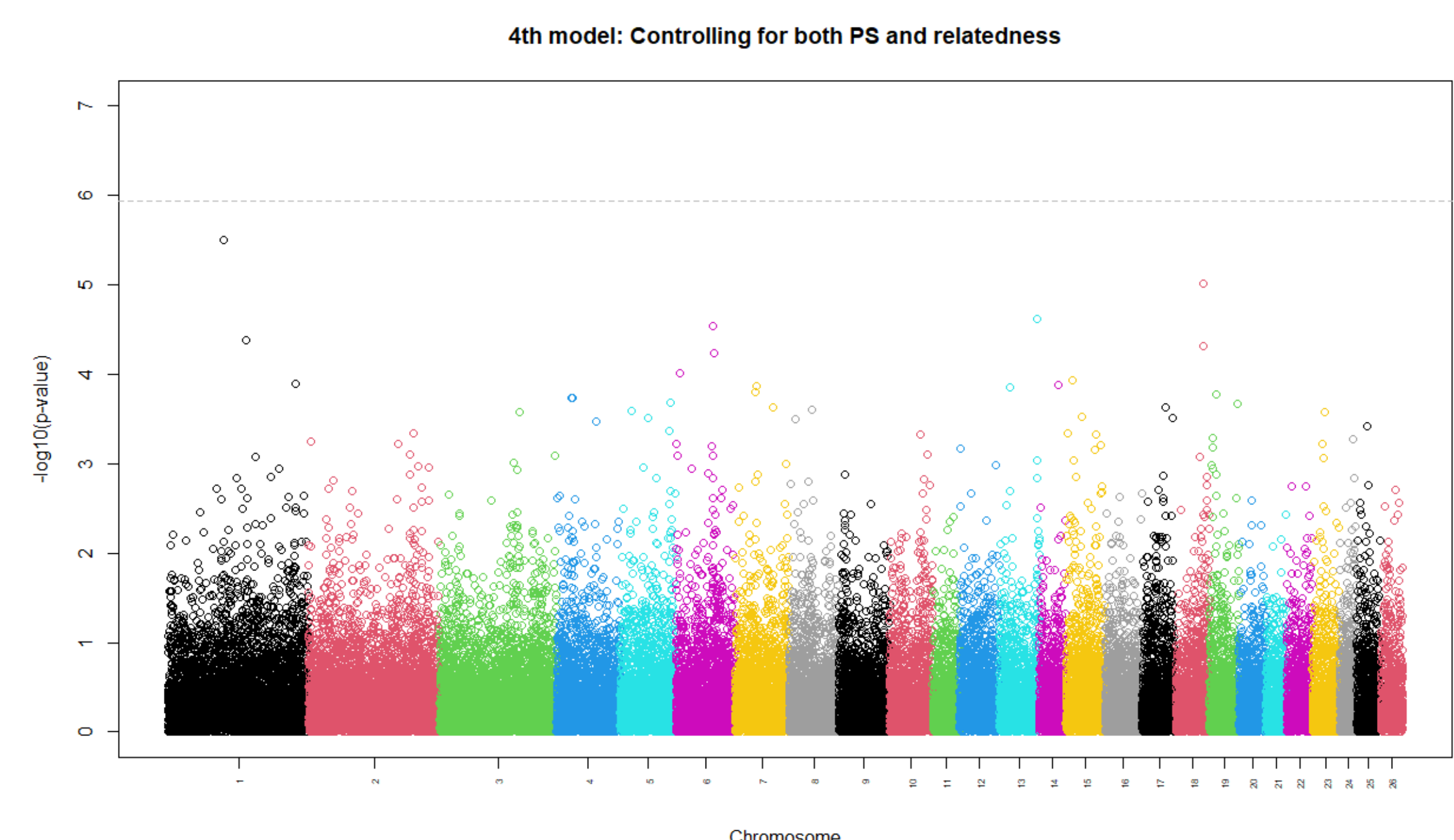


Figure 3. Manhattan plot of the 4th model