Genome-wide Associations for Coat Color Traits in a Cross of Domestic Pig Breeds

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Background

Exploitation of genetic variation through selection is important because it allows desirable alleles to be passed down to future generations, resulting in improved phenotypes. Thus, knowing how genetic variations affect phenotypic traits is beneficial for breeding because it enables artificial selection to be implemented more effectively to improve the performance of livestock populations. This study focused on coat color traits because they can be used as proxies for human skin health and to cater to diverse consumer preferences for meat that comes from different colored pigs.

Purpose

The goal of this study was to find genomic variants that affect coat color in pigs (*Sus scrofa domesticus*) and to find possible genes associated with those variants.

Methods

Pigs from a F2 Duroc × Pietrain cross were genotyped at 44911 SNP markers. Phenotypes for coat color, spot size, hair density, face color, and underbelly color were recorded.

496 pigs for coat color, size of spots, underbelly color, and hair density phenotypes and 705 pigs for the face color phenotype.

A genomic best linear unbiased prediction (GBLUP) based genome wide association study (GWAS) was done with the gwaR package in the R programming language to generate Manhattan plots.

Bioinformatic analysis was done in the R programming language to retrieve a list of genes and quantitative trait loci (QTLs) by performing a BioMart query of Ensembl and using the Pig QTL database.

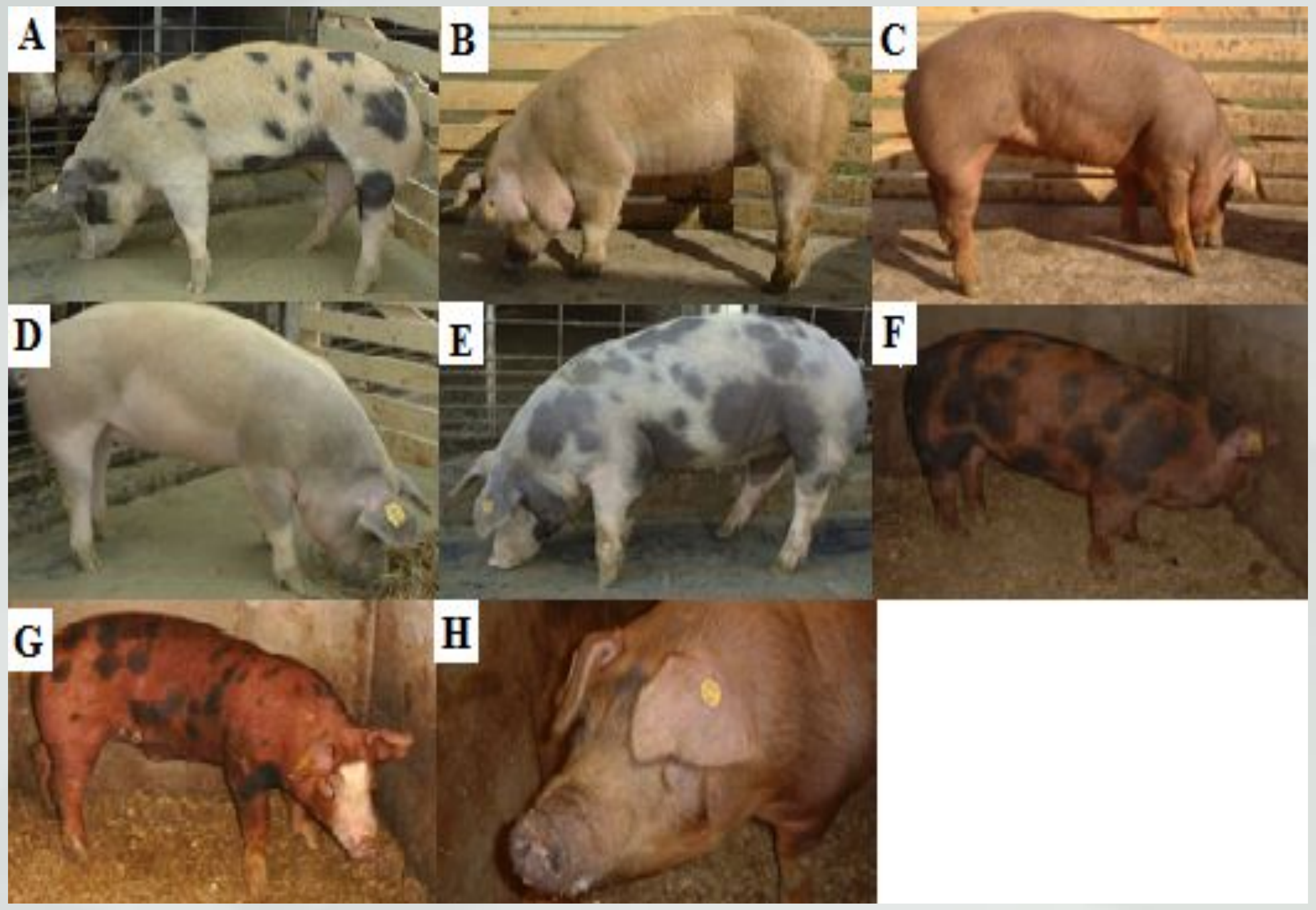
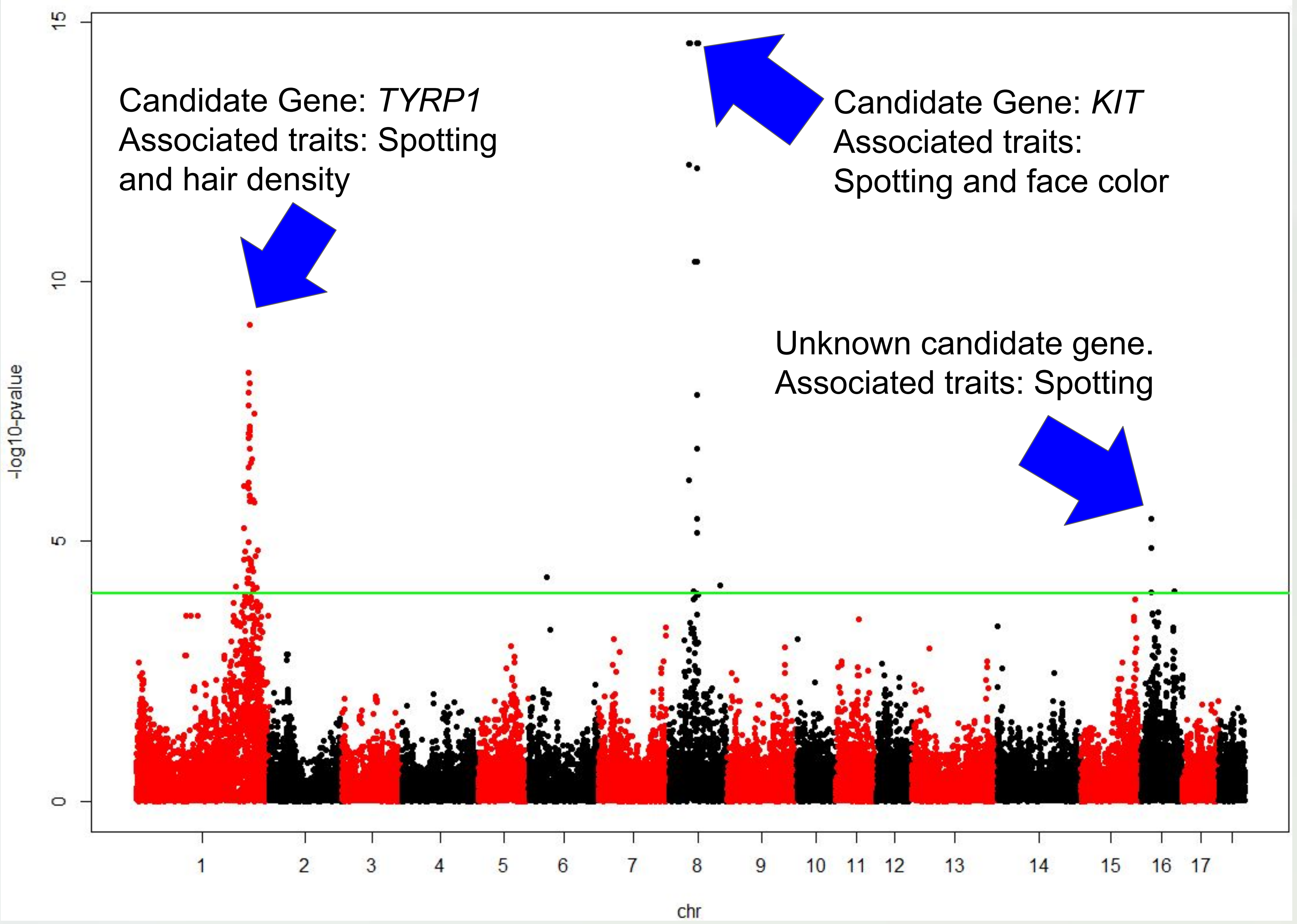


Figure 1: The pigs from the F2 Duroc x Pietrain cross. A. Fawn, medium spots, extreme underbelly shading. B, Light red, no spots, intermediate underbelly shading. C, Red, small spots, intermediate underbelly shading. D, Mouse, no spots, extreme underbelly shading. E, White, medium spots, no underbelly shading. F, Dark red, large spots, no underbelly shading. G, White head spot, red medium spots, no underbelly shading. H, No spots.

Results

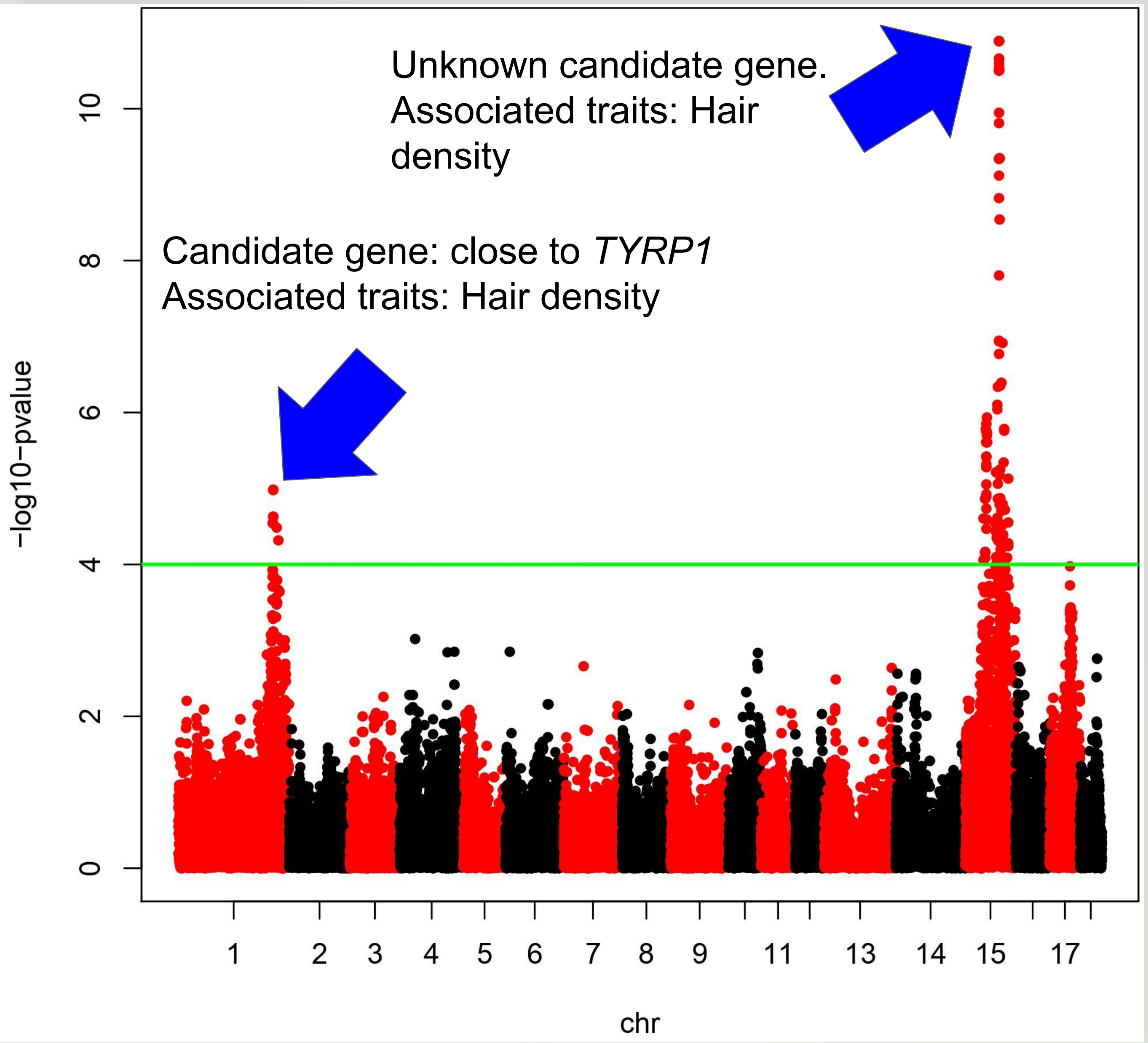


Candidate Gene: *TYRP1*
Associated traits: Spotting and hair density

Candidate Gene: *KIT*
Associated traits: Spotting and face color

Unknown candidate gene.
Associated traits: Spotting

Figure 2: Manhattan plot for GWAS of **coat color** trait "color white". The y-axis represents the -log10(P-value), the x-axis displays the chromosome number, and the green line indicates significance for the genome wide threshold.



Unknown candidate gene.
Associated traits: Hair density

Candidate gene: close to *TYRP1*
Associated traits: Hair density

Figure 3: Manhattan plot for GWAS of the "hair density" trait. The y-axis represents the -log10(P-value), the x-axis displays the chromosome number, and the green line indicates significance for the genome wide threshold.

- A QTL was found in chromosome 1 between positions 235,825,912-252,150,964 which was associated spot size, coat color, and hair density.
- A QTL was found in chromosome 6 around position 4,992,522, which was associated with spotting (presence and size) and underbelly color.
- A QTL was found in chromosome 8 around positions 37,505,202 and 73,962,803, which was associated face color and spot color.

Discussion

- Two novel QTL were detected for hair density and coat color in chromosomes 1 and 16, respectively.
  - Hair density is associated to chromosome 1 QTL close to *TYRP1*.
  - Unknown QTL in chromosome 16 for coat color.
- Several known color QTL were confirmed: *TYRP1* in chromosome 1, *MC1R* in chromosome 6, and *KIT* in chromosome 8.