

Fine mapping of quantitative trait loci for androstenone and skatole levels in a French commercial Large White pig population

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Objectives

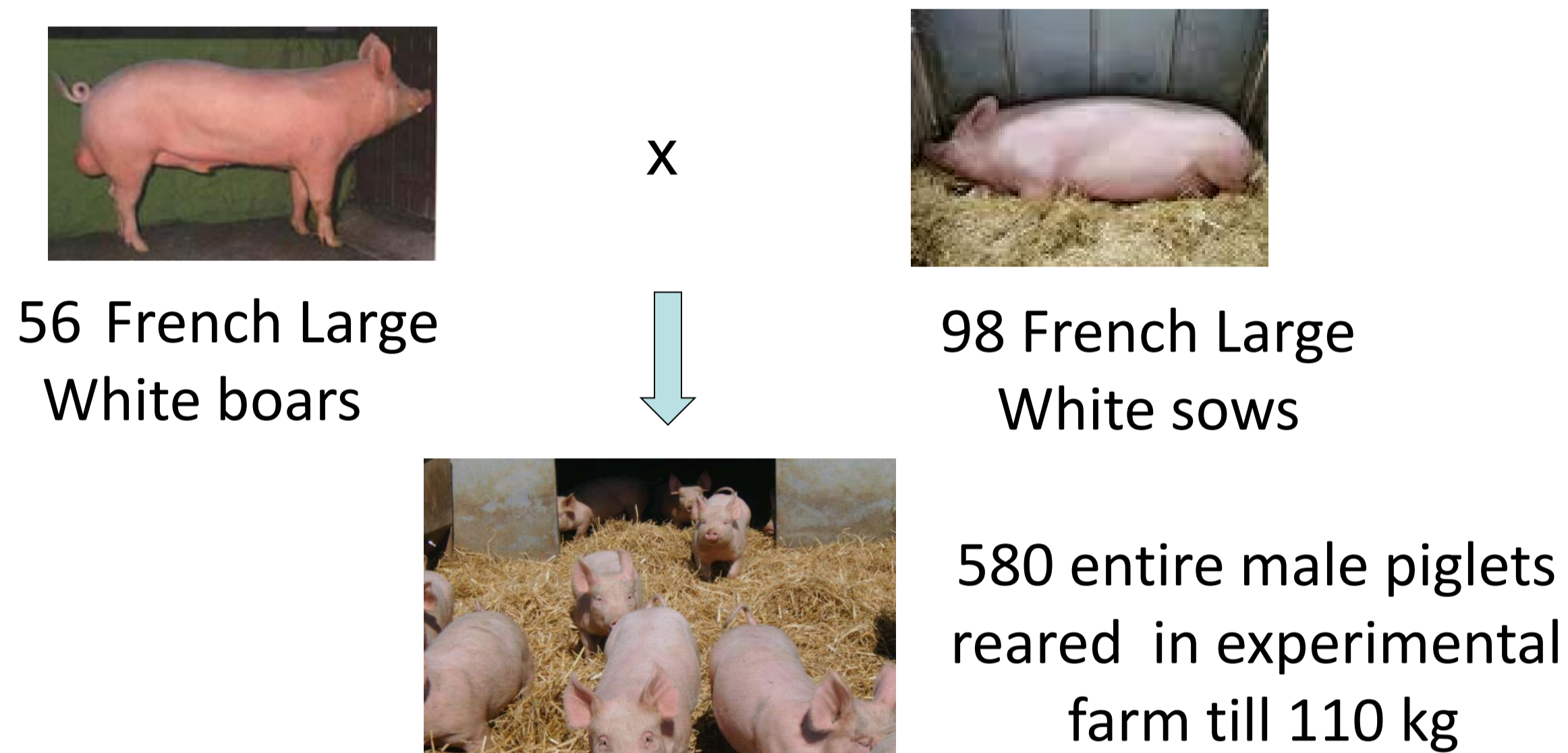
In Europe, male piglets are commonly castrated to reduce androstenone and skatole compounds mostly responsible for boar taint. Understanding genetic components of boar taint is the first step before raising intact males and the planned prohibition of castration.

The objective of this study was to map boar taint QTLs in a French commercial population of Large White pigs using the Illumina PorcineSNP60 BeadChip whole genome single nucleotide polymorphism (SNP) assay.

We performed a genome wide association study (GWAS) using a family-based association test for quantitative traits to detect SNP associations, then we combined linkage disequilibrium with linkage analysis (LDLA) using the same whole data set.

Material & Methods

Experimental design



Phenotypes:

Androstenone level in backfat; Skatole level in backfat

Genotypes: Illumina PorcineSNP60 BeadChip, 36188 SNPs passed the quality control

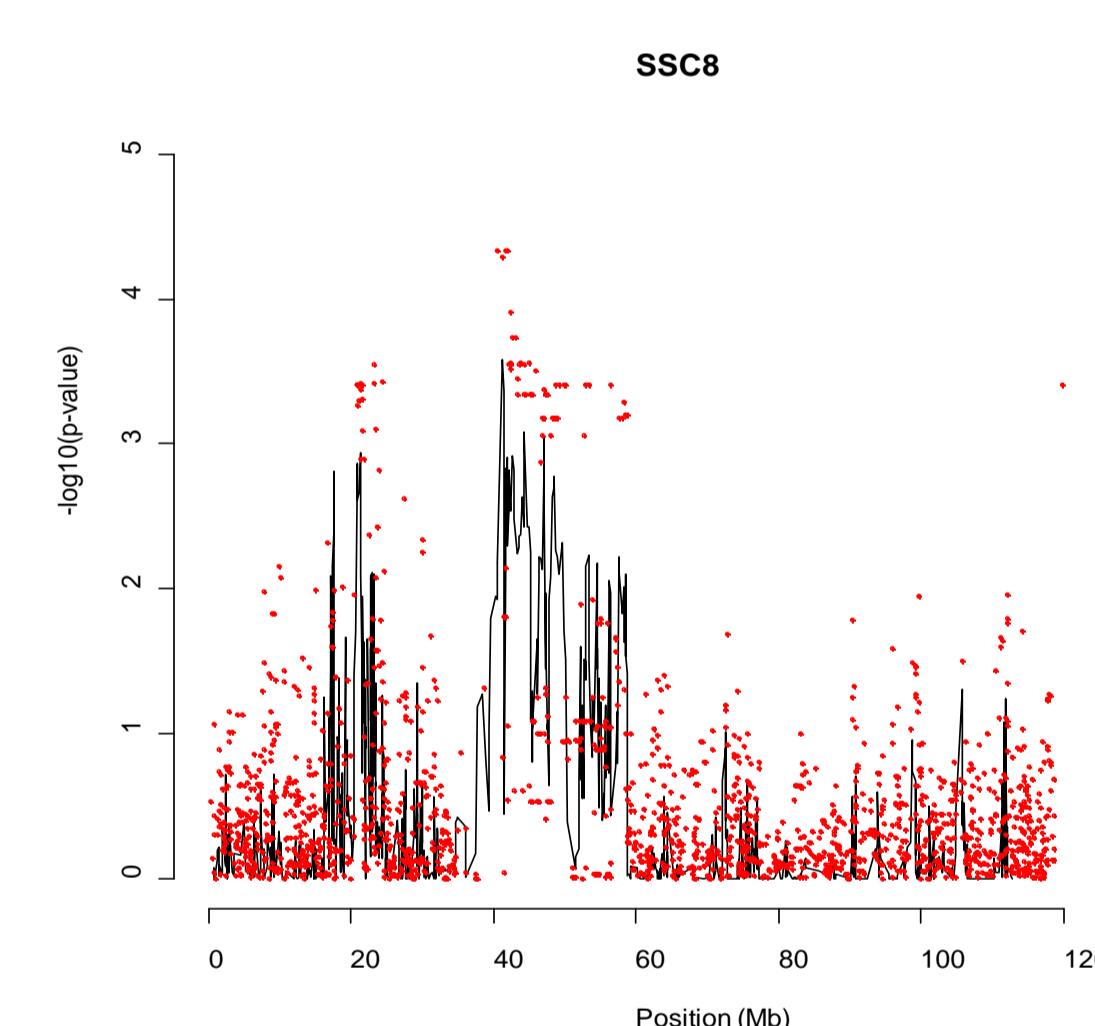
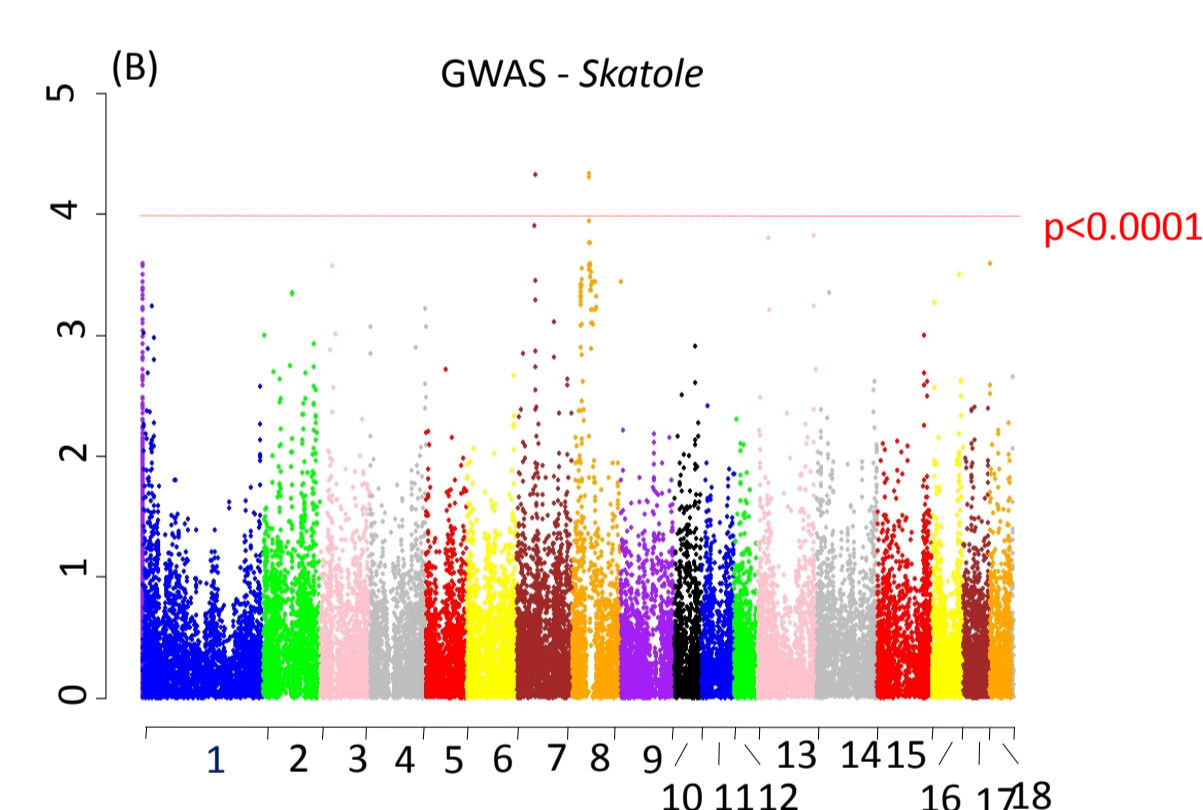
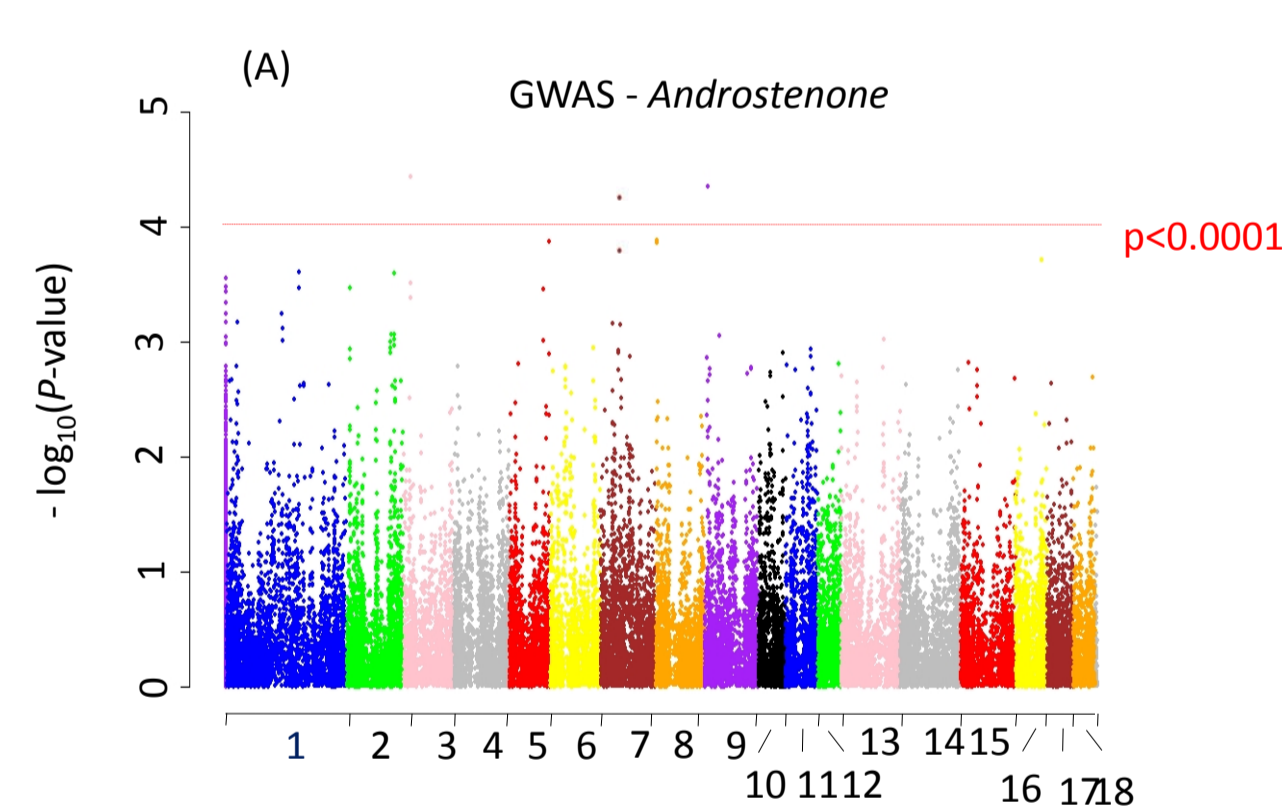
Statistical analyses

Genome-Wide Association Study (GWAS): We used methods accounting for close relatedness as implemented in GRAMMAR procedure in GenABEL.

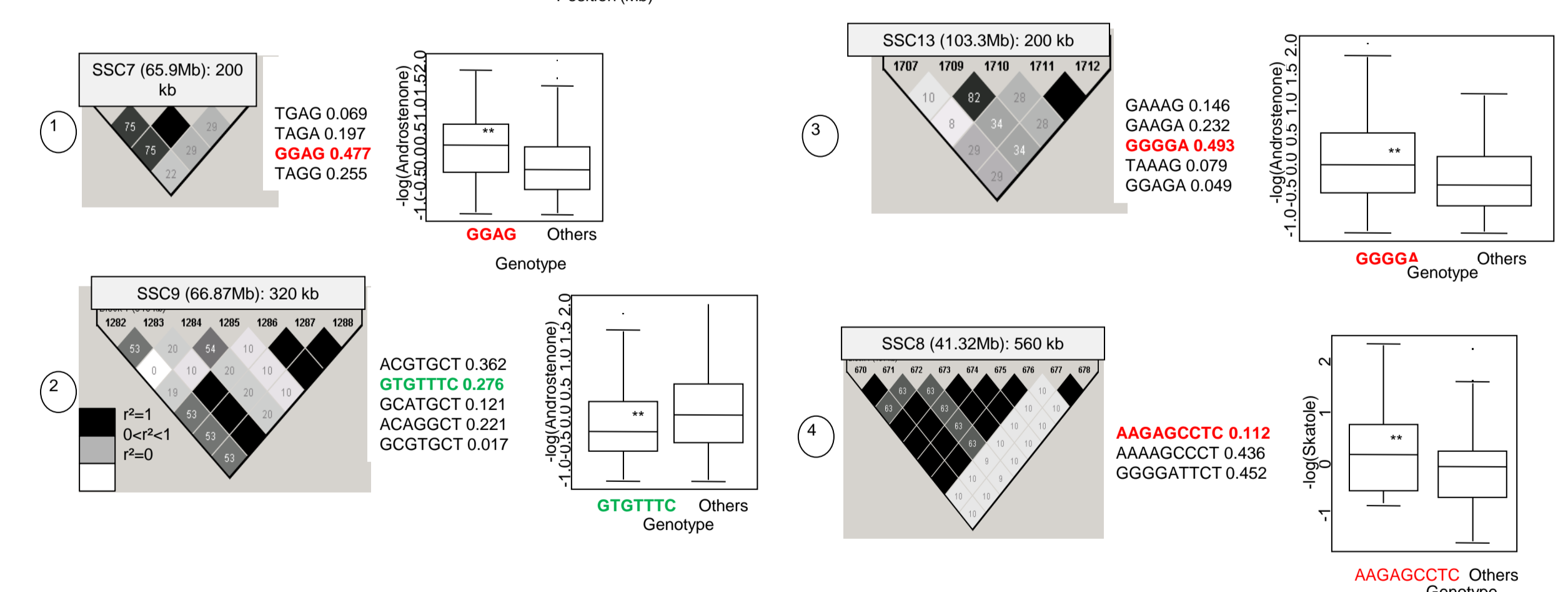
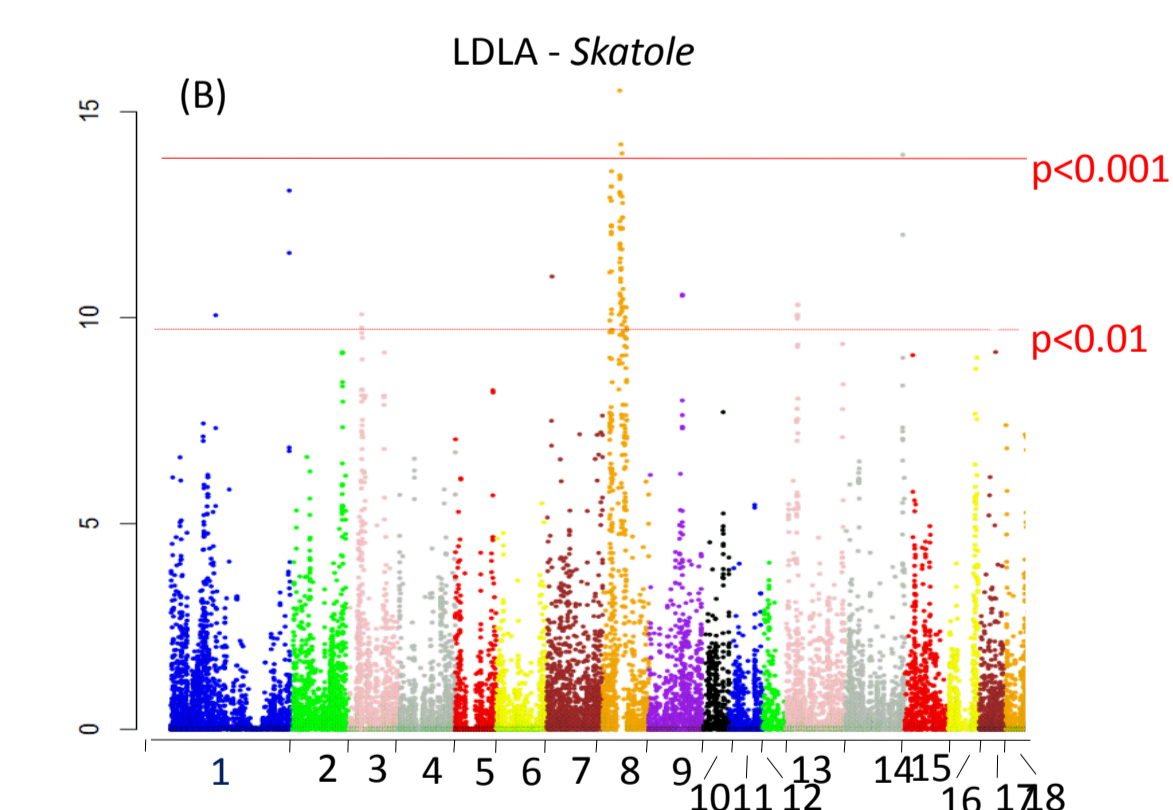
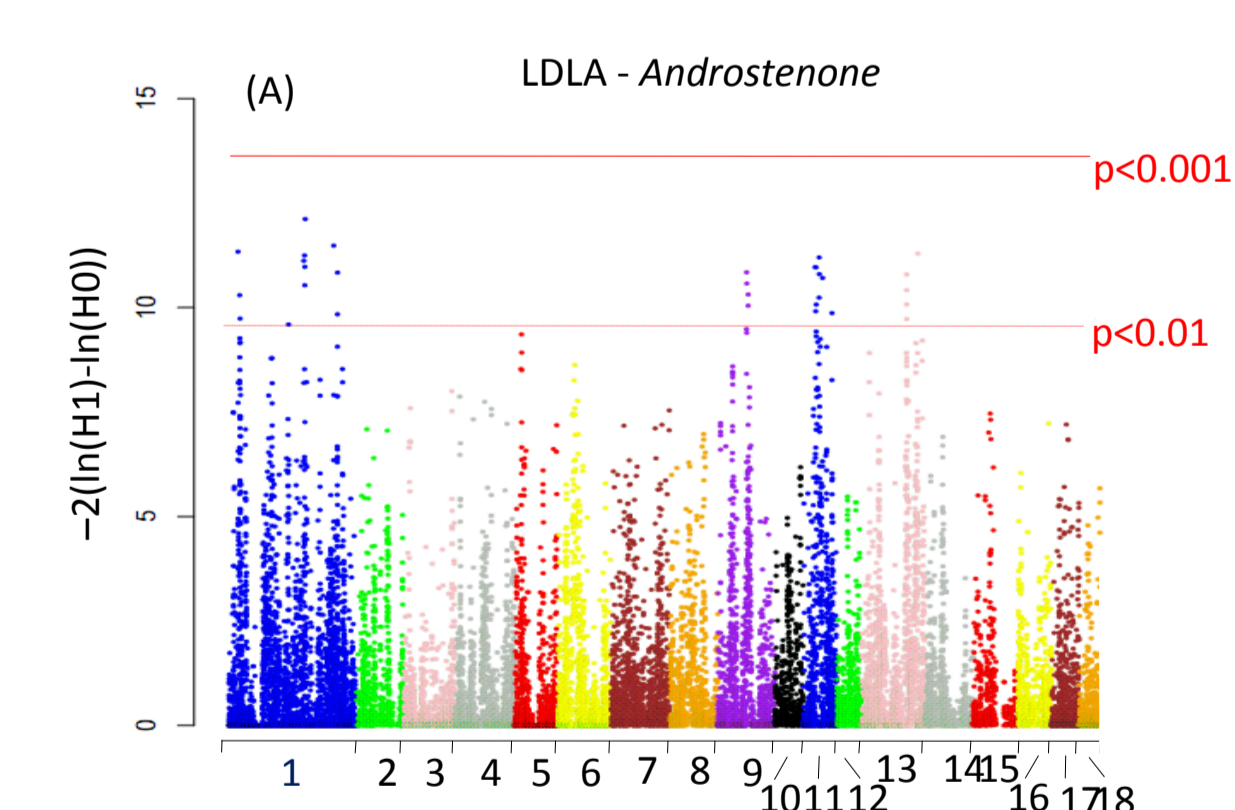
LDLA: A strategy to combine LD and LA information on the basis of their variance components. We used a window of 6 SNPs to calculate Identity By Descent (IBD) probabilities and haplotypes with IBD probability greater than 0.5, were considered to carry same QTL allele and were grouped in same cluster.

Haplotype analysis: After GWAS the top most significant peaks were checked for pairwise SNP correlation (r^2) and haplotypes possible in that region as implemented in Haploview.

Results



Only one common QTL between the two methods (SSC8 for skatole).



GWAS: 4 QTL detected

2 for androstenone SSC3, SSC7

2 for skatole SSC7, SSC8

LDLA: 14 QTL detected (7 for androstenone, 8 for skatole)

We characterized four highly significant haplotypes specifically associated with the levels of either androstenone (1, 2 and 3) or skatole (4). The three androstenone haplotypes and the skatole haplotype explained 39.6% and 11% of trait genetic variance, respectively.

Conclusion

We finally identified 18 QTLs involved in variations in androstenone or skatole levels in a French commercial Large White pig population.

The most significant skatole QTL was located on SSC8.

The most promising haplotype to reduce androstenone in French LW pigs was located in the *CYP11A1* region (SSC7).