

A GWAS for additive and dominance effects of number of teats in pigs

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Background

So far the main focus of association studies has been on additive genetic effects

Objective

Simultaneously identify genomic regions with additive and dominance effects related to number of teats in pigs

Conclusion

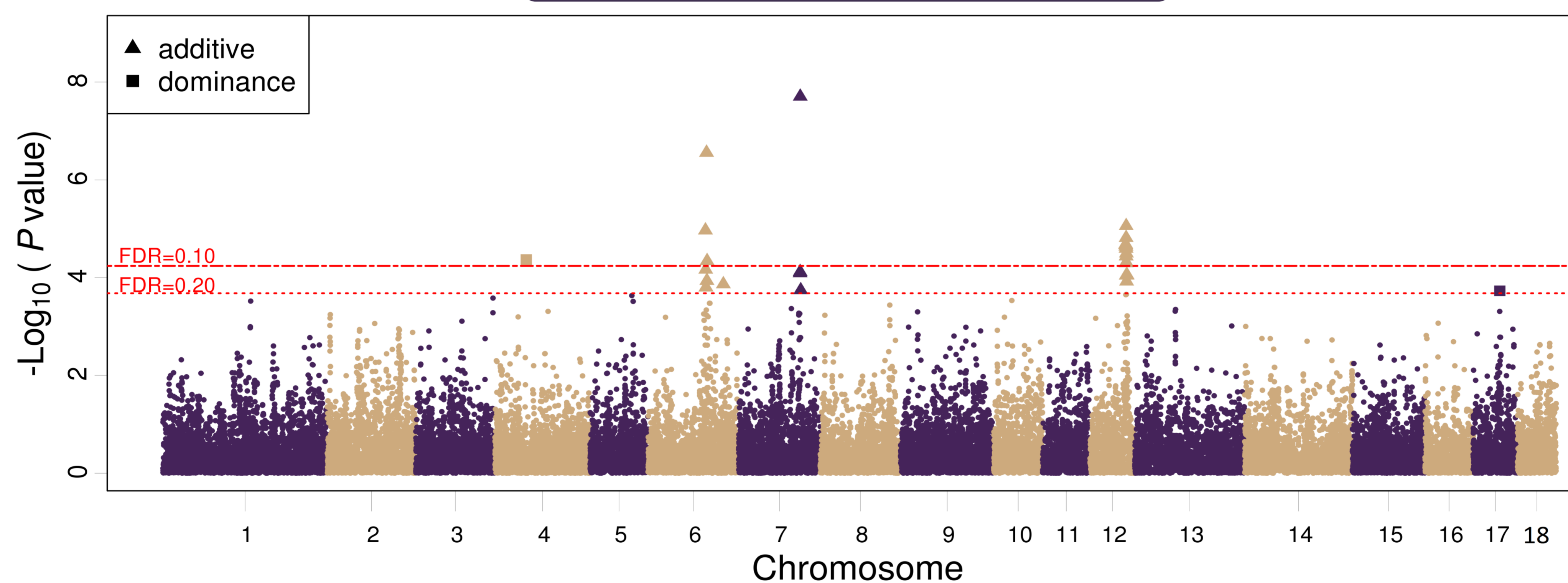
- Four QTL regions with additive and two with dominance effects were identified
- The σ_D^2 equals 1/3 of the σ_A^2 of all QTLs

Material and Methods

$$NT = \mu + \text{sex} + \text{HYS}_{\text{birth}} + \text{SNP} + \text{animal} + e$$

- 1,645 Landrace based animals genotyped for 32,929 SNPs were used
- SNP genotypes (AA, AB and BB) were fitted as a class variable in a single SNP analysis using ASReml
- Genomic relationship matrix was used to account for population stratification
- Mode of inheritance of the QTL was determined by testing contrasts of genotype class effect estimates (ASReml option !CONTRAST)

Results



Graphical summary of GWAS results. FDR (False Discovery Rate) ≤ 0.10 : significant association and $0.10 < \text{FDR} \leq 0.20$: suggestive association.

QTL region	SSC	Position (Mbp)		MAF	Contrast P-values*		Mode of inheritance	SNP effects		SNP variance (% of σ_P^2)	
		start	end		additive	dominance		a**	d	σ_A^2	σ_D^2
1	4	44.53	- 44.53	0.31	0.103	<0.001	dominance	0.02	-0.26	0.23	1.16
2	6	101.77	- 105.20	0.37	<0.001	0.059	additive	0.28	-0.19	2.21	0.70
3	6	135.09	- 135.09	0.24	<0.001	0.040	additive	0.23	-0.01	1.69	0.00
4	7	103.03	- 104.40	0.32	<0.001	0.080	additive	0.30	0.04	3.32	0.03
5	12	52.71	- 54.68	0.43	<0.001	0.658	additive	0.24	0.05	2.33	0.06
6	17	44.38	- 44.62	0.29	0.147	<0.001	dominance	0.15	-0.24	0.09	0.93
Total										9.87	2.88

*Contrasts were significant when $P < 0.01$; **Additive effects in absolute values.