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**WROCLAW UNIVERSITY
OF ENVIRONMENTAL
AND LIFE SCIENCES**

Genetic basis of stillborn piglets in hyperprolific sows based on a genome-wide association study

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Hyperprolific sows

produce more piglets than they have
functional teats



Excessively numerous litters – pros or cons?

large variation in piglet birth weight due to intrauterine crowding

(Declerk et al., 2016)

piglets with low birth weight and affected by intrauterine growth retardation syndrome

(Langendijk et al., 2018)

prolonged parturition and increased perinatal piglet mortality

(Baxter et al., 2020)

Purpose of the study

Analysis of the genetic background of stillborn piglets in hyperprolific sows based on genome-wide association study:

1) identification of SNPs showing an association with the incidence of stillborn piglets in excessively large litters

2) linkage of identified SNP markers to relevant genes

3) determine the risk of stillborn piglets associated with particular genotypes within SNPs

Material

144 hyperprolific DanBred sows

72 control group

72 case group



sows that gave birth in the 1st and 2nd litters:

only live-born piglets

at least one stillborn piglet



genotyping

PoricneSNP80v1_HTS microarray (Illumina), containing **75,000 SNP**

Methods – SNP selection

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Original Research Article



Genetic basis of sow hyperprolificacy and litter size optimization based on a genome-wide association study

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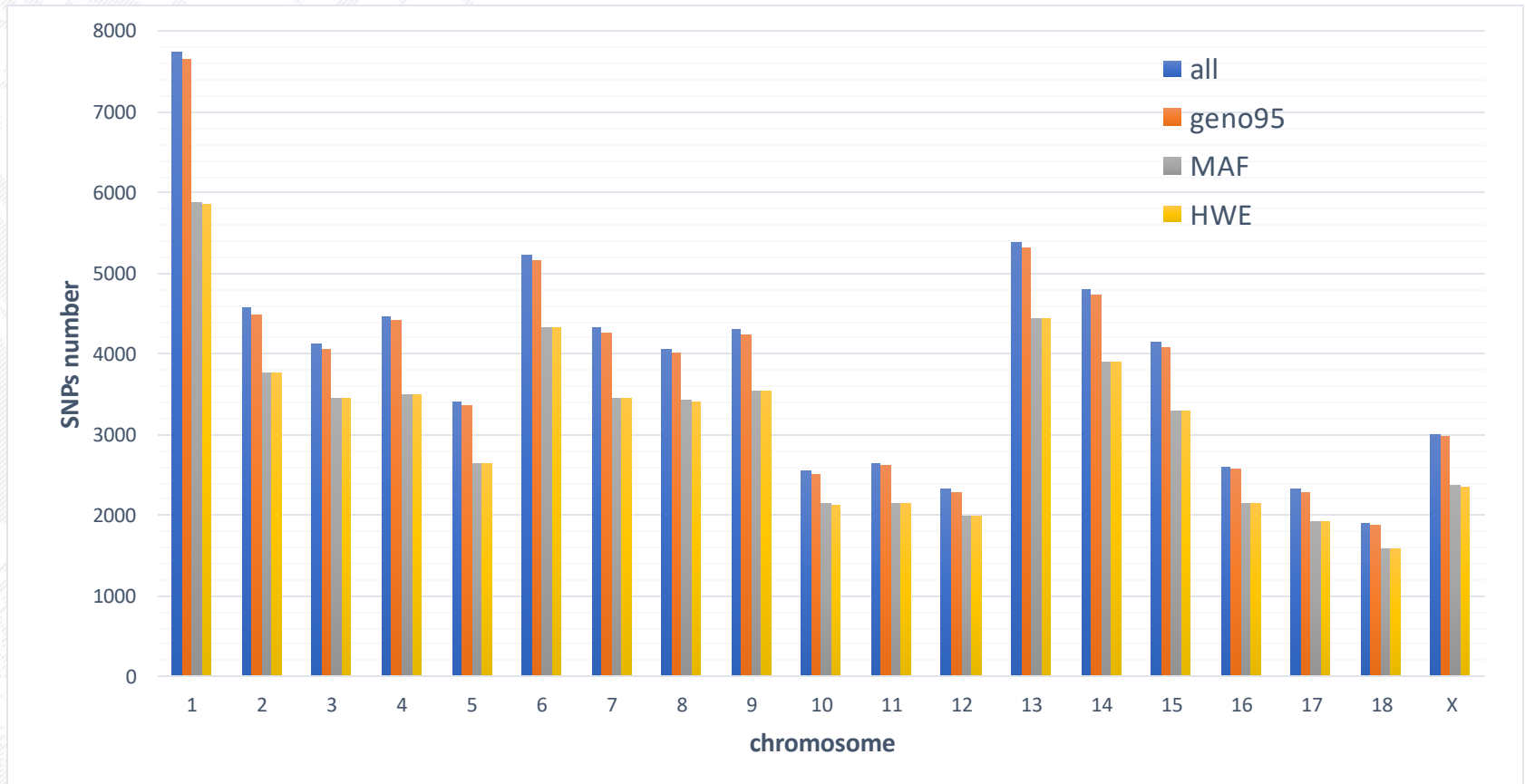
codominant model

overdominant model

recessive model

log-additive model

Results – SNP selection



Applying the above selection criteria reduced the number of SNPs from **74,408** to **59,967**.

Results – SNP selection

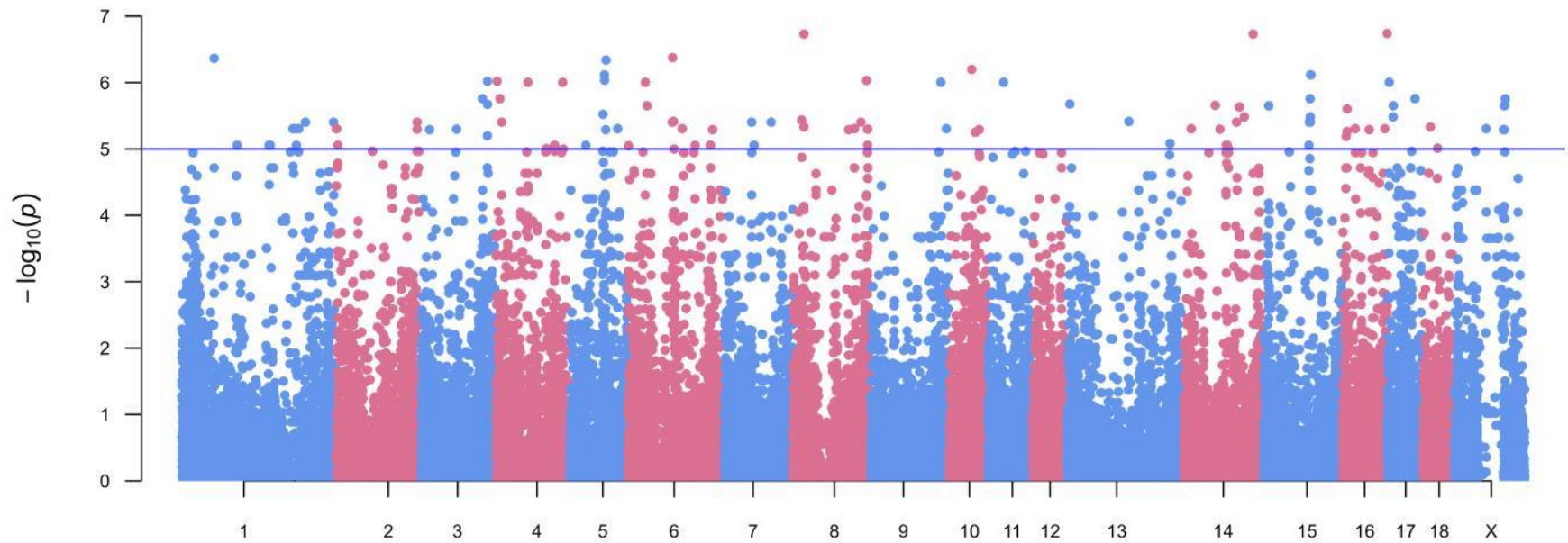
180 markers showing an association with the presence of stillborn piglets in a litter

SSC	p < 0.00001					p < 0.00000005				
	model									
	C	D	R	O	L-A	C	D	R	O	L-A
1	17	17	17	16	18	0	0	0	0	0
2	7	7	7	7	7	0	0	0	0	0
3	3	6	2	2	3	0	0	0	0	0
4	8	7	4	8	8	0	0	0	0	0
5	5	8	2	4	6	0	0	0	0	0
6	9	19	8	10	9	0	0	0	0	0
7	5	5	5	5	5	0	0	0	0	0
8	15	12	17	8	9	1	0	4	0	0
9	4	4	2	5	4	0	0	0	0	0
10	1	3	0	2	2	0	0	0	0	0
11	1	1	1	1	1	0	0	0	0	0
12	0	0	0	0	0					
13	3	3	2	3	3					
14	19	20	17	19	19					
15	24	26	22	25	24					
16	8	11	6	9	9					
17	3	4	2	3	3					
18	0	2	0	1	0					
X	6	8	4	7	6	0	0	0	0	0
ALL	138	163	118	135	136	1	0	4	0	0

All of these four markers are located within the potassium voltage-gated channel interacting protein 4 (**KCNIP4**) gene.

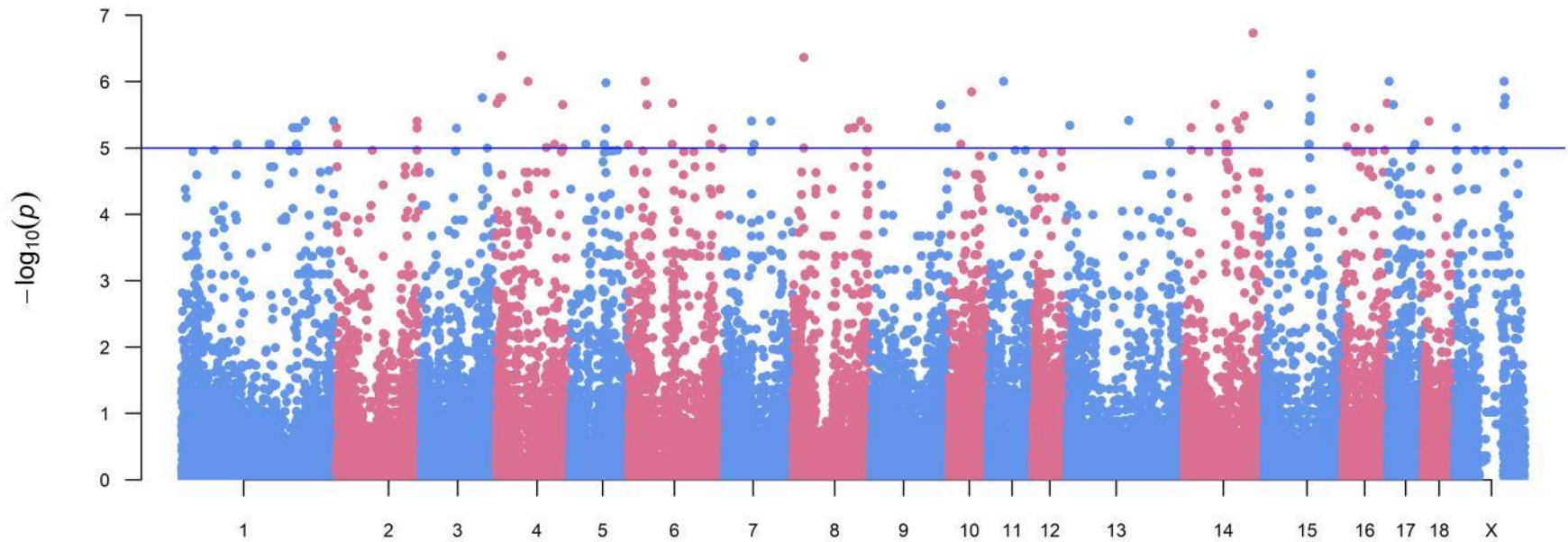
C – codominat model; D – dominant model; R – recessive model, O – overdominant model, L-A – log-additive model

Results – dominant model



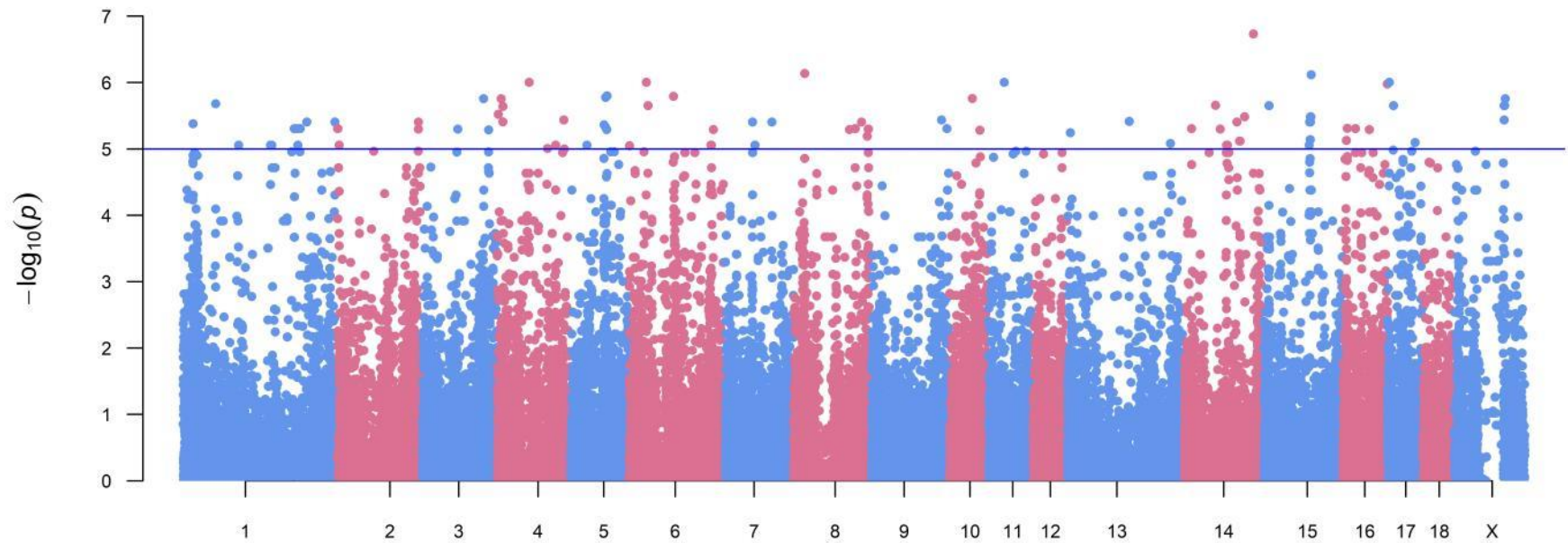
Horizontal blue line represents genome-wide significance threshold of 10^{-5}

Results – overdominant model



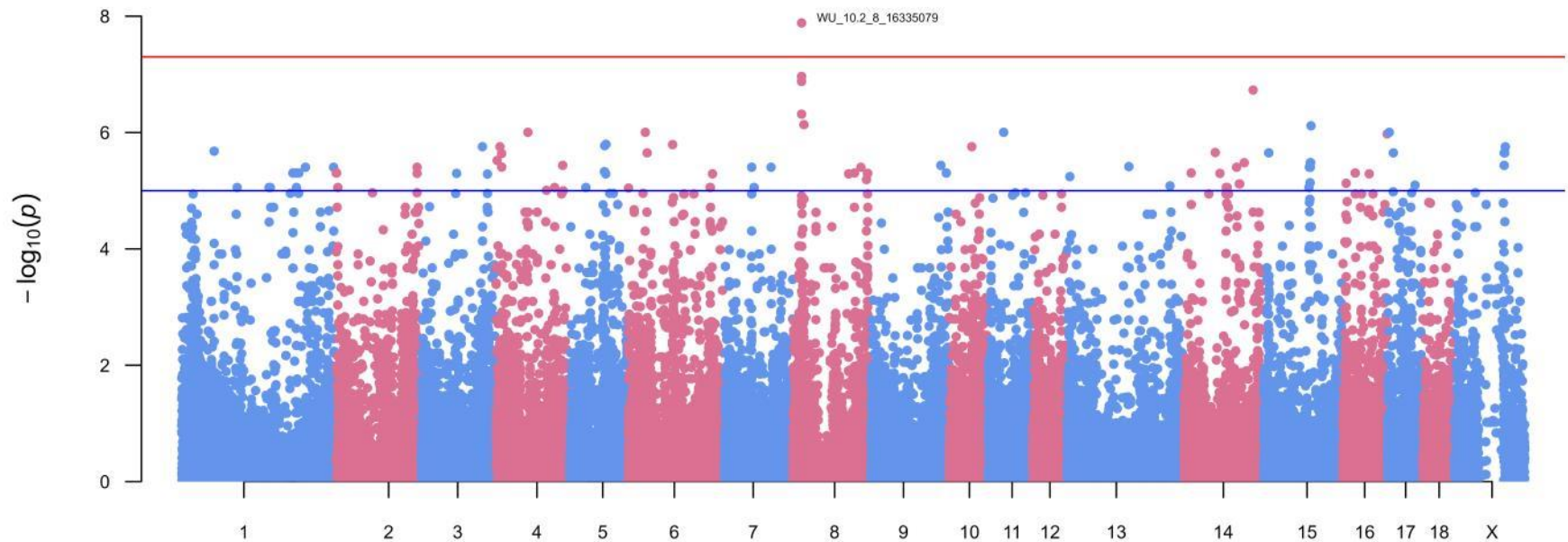
Horizontal blue line represents genome-wide significance threshold of 10^{-5}

Results – log-additive model



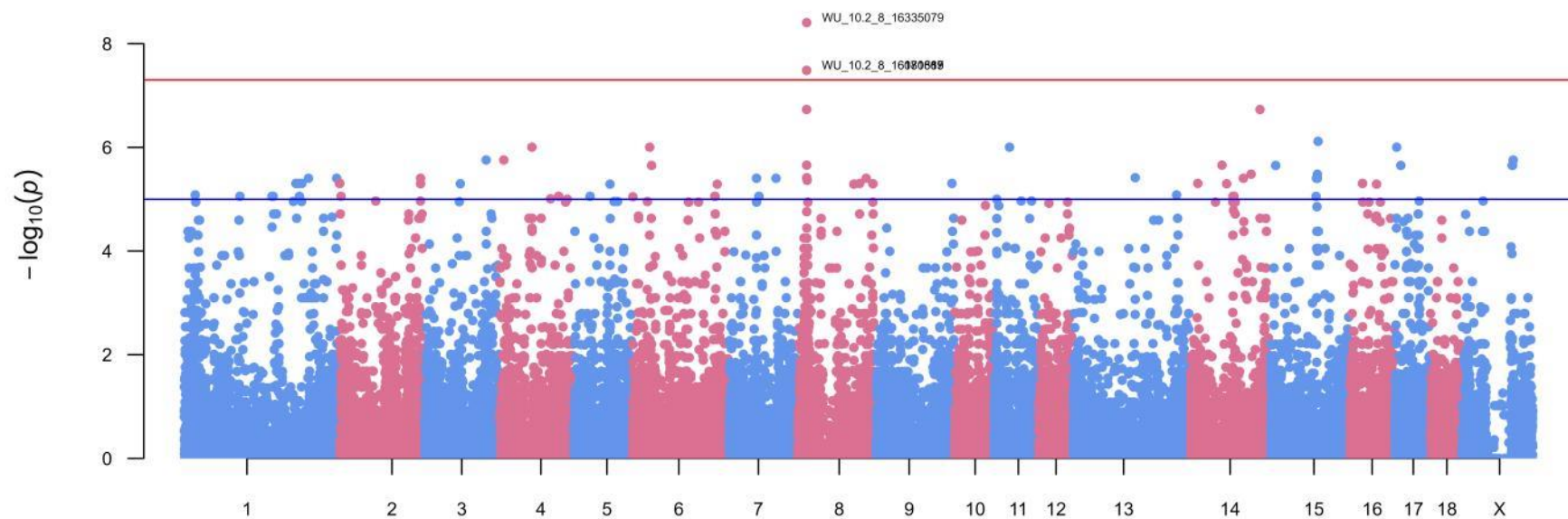
Horizontal blue line represents genome-wide significance threshold of 10^{-5}

Results – codominant model



Horizontal blue line represents genome-wide significance threshold of 10^{-5} , while the red line threshold of 10^{-8}

Results – recessive model



Horizontal blue line represents genome-wide significance threshold of 10^{-5} , while the red line threshold of 10^{-8}

SNP markers for stillborn piglets in hyperprolific sows

Table 1. The risk of stillborn associated with particular genotypes within SNPs for codominant model

CHR	SNP	genotype	genotype number (percentage)		OR	95% CI	p-value
			control	case			
8	WU_10.2_8_16335079	A/A	16 (22.2%)	18 (25.0%)	1.00		
		G/A	27 (37.5%)	52 (72.2%)	1.71	(0.76 ; 3.88)	1.304×10 ⁻⁸
		G/G	29 (40.3%)	2 (2.8%)	0.06	(0.01 ; 0.30)	

CHR = chromosome, OR = odds ratio, CI = confidence interval

Table 2. The risk of stillborn associated with particular genotypes within SNPs for recessive model

CHR	SNP	genotype	genotype number (percentage)		OR (95% CI)	p-value
			control	case		
8	WU_10.2_8_16181667	G/G-A/G	43 (59.7%)	69 (95.8%)	0.06	3.27×10 ⁻⁸
		A/A	29 (40.3%)	3 (4.2%)	(0.02 ; 0.22)	
	WU_10.2_8_16071319	A/A-C/A	43 (59.7%)	69 (95.8%)	0.06	3.27×10 ⁻⁸
		C/C	29 (40.3%)	3 (4.2%)	(0.02 ; 0.22)	
	WU_10.2_8_16130585	G/G-A/G	43 (59.7%)	69 (95.8%)	0.06	3.27×10 ⁻⁸
		A/A	29 (40.3%)	3 (4.2%)	(0.02 ; 0.22)	
	WU_10.2_8_16335079	A/A-G/A	43 (59.7%)	70 (97.2%)	0.04	3.93×10 ⁻⁹
		G/G	29 (40.3%)	2 (2.8%)	(0.01 ; 0.19)	

CHR = chromosome, OR = odds ratio, CI = confidence interval. Odds ratio refers to the genotype in bold.

What's next?

Linkage disequilibrium analysis and search for haplotypes associated with stillborn piglets in litters of hyperprolific SOWS.

Expand the study to include more individuals and breeds.

Thank you for your attention!

