

**Table S1** The number of genome-wide effective SNPs in each chromosome and the chromosome-wide significant threshold

Chromosome	effective SNPs	<i>P</i> -value
1	1268	$3.94 \times 10^{-5}$
2	436	0.000115
3	580	$8.62 \times 10^{-5}$
4	823	$6.08 \times 10^{-5}$
5	650	$7.69 \times 10^{-5}$
6	563	$8.88 \times 10^{-5}$
7	812	$6.16 \times 10^{-5}$
8	585	$8.55 \times 10^{-5}$
9	654	$7.65 \times 10^{-5}$
10	481	0.000104
11	545	$9.17 \times 10^{-5}$
12	409	0.000122
13	812	$6.16 \times 10^{-5}$
14	819	$6.11 \times 10^{-5}$
15	694	$7.20 \times 10^{-5}$
16	458	0.000109
17	517	$9.67 \times 10^{-5}$
18	383	0.000131
X	550	$9.09 \times 10^{-5}$
Total	12039	

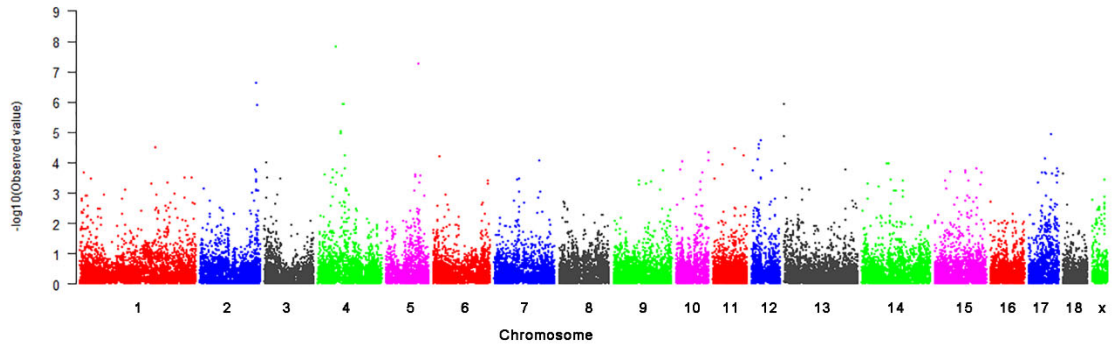
**Table S2** The primers for candidate casual mutations of *NR6A1* and *VRTN* and *TGF $\beta$ 3* resequencing

SNP		Primer (5'-3')	Amplificated region
NR6A1 c.748 C > T	F	AAAGAATAGACTCAGGGACA	
	R	GAAGGAGCAAGAGCACAA	
VRTN g.19034 A>C	F	GGAATGGGACCAGCACCTA	
	R	GCATGGACCGTCTACAGC	
VRTN g.20311_20312ins291	F	CCACAGTCTTAGCCAGTCTTC	
	R	CGTCAACCCACTGAGCAA	
TGF $\beta$ 3-1	F	AGCGGCGTTTGGCAATAT	5'UTR
	R	TGGGATGGGAGTTTAGCAG	
TGF $\beta$ 3-2	F	AGCGGCGTTTGGCAATAT	Exon1
	R	TGGGATGGGAGTTTAGCAG	
TGF $\beta$ 3-3	F	AGAACGCAGATGGAGTGG	Exon2
	R	GCAGGAGCAAATGAGGAC	
TGF $\beta$ 3-4	F	GCTCCTGCTGACCTCG	Exon3
	R	GACCAAAAGCCCCATG	
TGF $\beta$ 3-5	F	TCCTCGCCCAACCAA	Exon4
	R	AGGCAAGGCAGAACCC	
TGF $\beta$ 3-6	F	CGAAGACTGCTCCATCC	Exon5
	R	GGTGCTCCCAGAACAAC	
TGF $\beta$ 3-7	F	ACGATGACCAGTAAAGACG	Exon6
	R	TTCAGAACCCTCACAAA	
TGF $\beta$ 3-8	F	CTGAGGCGGCATTGGT	Exon7
	R	CCTCTGATTAGTAGATGCGAAC	
TGF $\beta$ 3-9	F	CTGAGGCGGCATTGGT	3'UTR
	R	CCTCTGATTAGTAGATGCGAAC	

**Table S3** Genotype frequencies of F<sub>0</sub> animals for mutations in *VRTN*, *TGFF $\beta$ 3*, and *NR6A1*

SNP	Breed	N	Genotype frequency <sup>1</sup>		
			AA	AB	BB
VRTN19034A>C	Minzhu	16	68.75% (AA)	25.00% (AC)	6.25% (CC)
	Large White	4	0.00% (AA)	25.00% (AC)	75.00% (CC)
TGF $\beta$ 3c.1749G>A	Minzhu	16	62.50% (AA)	31.25% (AG)	6.25% (GG)
	Large White	4	0.00% (AA)	0.00% (AG)	100% (GG)
NR6A1748CT	Minzhu	16	18.75% (CC)	43.75% (CT)	37.50% (TT)
	Large White	4	0.00% (CC)	0.00% (CT)	100% (TT)

Note: <sup>1</sup>Genotypes of mutations was shown in parentheses.



**Fig. S1** The Manhattan plot obtained from GWAS using VRTN19034A>C as a fixed effect. Chromosomes 1–18, and X are shown in different colors. The genome-wide significance level was  $4.15 \times 10^{-6}$ .