

Supplemental Materials

File S1. Adjusted methods for measured AGE and measured BF

Age at 100 kg (AGE) and backfat thickness at 100 kg (BF) were calculated based on the National Swine Performance Recording Standards of China as follows.

1. Adjustment formula of AGE

$$AGE = DP + \frac{(100 - WP) * (DP - A)}{WP}$$

DP and WP refer to days of age and weight at performance testing, respectively.

The parameter A is 50.775 and 46.415 for males and females, respectively.

2. Adjustment formula of BF

$$BF = BP + \frac{(100 - WP) * BP}{(WP - B)}$$

BP refers to back fat alive at performance testing, and WP is the same as above.

The parameter B is equal to -7.277 and -9.440 for males and females, respectively.

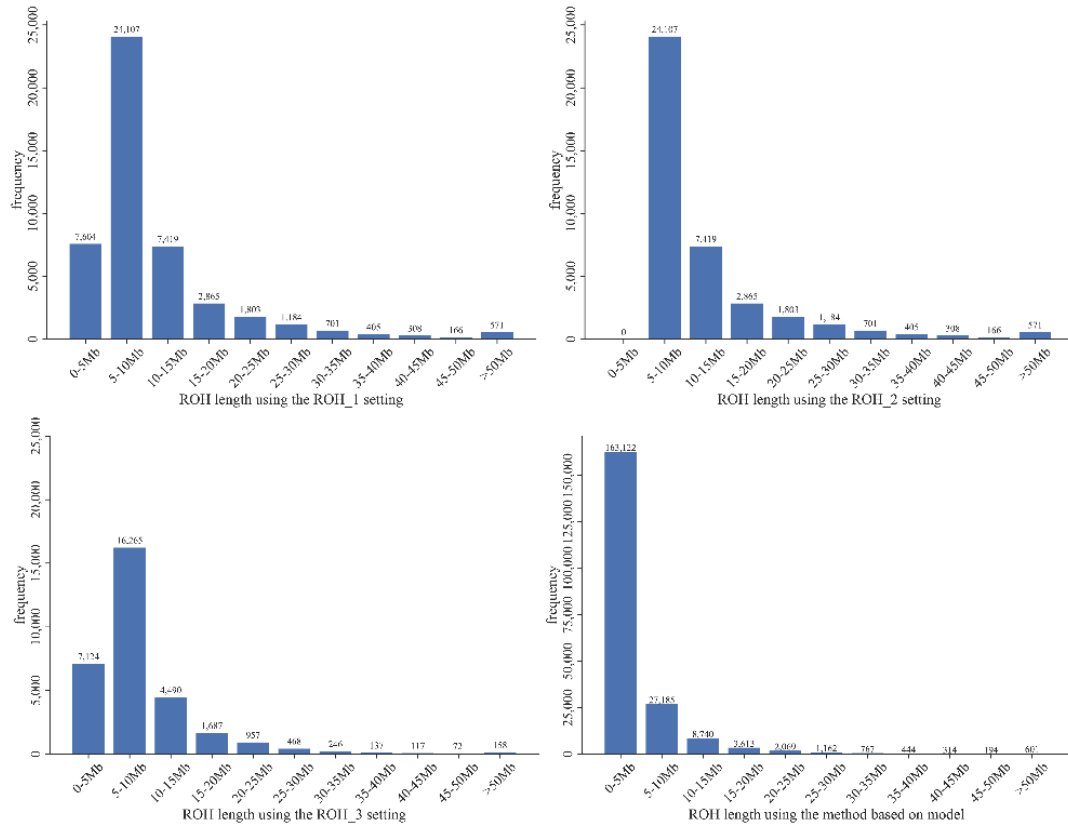


Figure S1. frequency distribution of ROH length under the ROH_1, ROH_2, ROH_3 settings and using the method based on model. ROH_1 was based on Meyermans's recommendation. More strict parameters about the length of a ROH (>5Mb) in ROH_2 and a minimum density of one SNP per ROH (<70/kb) in ROH_3 were set. ROH_model used the model-based software RZooRoH.

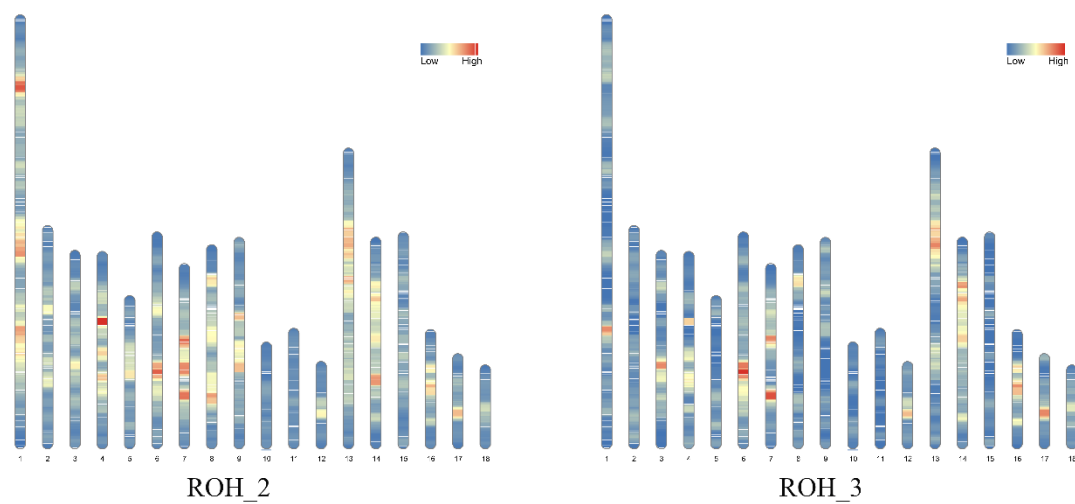


Figure S2. The distribution of ROHs in ROH_2 (the length of a ROH (>5Mb)) and ROH_3 (a minimum density of one SNP per ROH (<70/kb)) on chromosomes.

	Mean	SD	Min	Max
$F_{\text{PED}(\text{total})}$	0.01	0.02	0.00	0.26
F_{PED}	0.01	0.02	0.00	0.25
F_{PH}	0.64	0.02	0.59	0.75
F_{HOM}	-0.01	0.05	-0.04	0.30
$F_{\text{HOM}(\text{pruned})}$	-0.01	0.03	-0.03	0.24
F_{GRM1}	-0.01	0.07	-0.12	1.07
F_{GRM2}	-0.01	0.06	-0.13	0.75
F_{ROH1}	0.13	0.03	0.06	0.38
$F_{\text{ROH1(N)}}$	0.13	0.03	0.06	0.38
F_{ROH2}	0.12	0.03	0.05	0.37
F_{ROH3}	0.07	0.02	0.00	0.24
$F_{\text{ROH}(\text{model})}$	0.24	0.03	0.16	0.46

Table S1. Descriptive statistics of inbreeding coefficients estimated with different methods for data sets. $F_{\text{PED}(\text{total})}$ was estimated from the total animals of 27341, and F_{PED} only included 1599 animals with both genotypes and pedigrees. F_{PH} = the proportion of homozygous genotypes of all genotypes; F_{GRM} = inbreeding from genomic relationship matrix, F_{GRM1} and F_{GRM2} were from pruning data for MAF (0.01) and for MAF (0.05); F_{HOM} = inbreeding coefficients based on the observed versus expected number of homozygous genotypes, $F_{\text{HOM}(\text{pruned})}$ was from SNP pruned data based on linkage disequilibrium; Under the different settings (ROH_1, ROH_2, ROH_3), F_{ROH} was estimated based on runs of homozygosity; $F_{\text{ROH(N)}}$ was determined as the sum of SNPs in the ROHs divided by the total number of SNPs; $F_{\text{ROH}(\text{model})}$ was estimated using the model-based software RZooRoH.

	Mean	SD	Min	Max
AGE/d	161.17	14.94	107.90	308.68
BF/mm	13.76	2.89	5.84	30.40
TNB	15.34	3.81	0.00	26.00
NBA	13.64	3.71	0.00	25.00
litter weight at birth/kg	17.97	4.93	0.00	43.49

Table S2. Descriptive statistics of phenotypes of growth and reproductive traits for total animals

	AGE/d	BF/mm	TNB	NBA	litter weight at birth/kg
$F_{\text{PED(total)}}$	26.47*** (5.39)	-1.57 (1.08)	-5.10** (2.18)	-4.87* (2.13)	-2.08 (2.88)
F_{PED}	17.14 (16.17)	1.98 (4.34)	4.08 (3.68)	0.75 (3.49)	2.34 (4.90)
F_{PH}	30.49* (15.68)	0.93 (4.23)	-13.59*** (4.13)	-12.99*** (3.91)	-16.59** (5.47)
F_{HOM}	10.90* (5.60)	0.33 (1.51)	-4.86*** (1.48)	-4.64*** (1.40)	-5.93** (1.96)
$F_{\text{HOM(pruned)}}$	17.76** (7.61)	1.49 (2.06)	-2.93 (1.96)	-3.41* (1.86)	-5.88* (2.60)
F_{GRM1}	7.66* (3.35)	-1.05 (0.90)	-5.92*** (1.76)	-5.33*** (1.67)	-6.15** (2.33)
F_{GRM2}	10.40** (4.05)	-1.11 (1.09)	-5.60*** (1.67)	-5.15*** (1.58)	-6.08** (2.21)
F_{ROH1}	12.52 (7.94)	2.82 (2.13)	-6.03** (2.05)	-5.58** (1.94)	-6.83** (2.71)
$F_{\text{ROH(model)}}$	17.98* (8.38)	0.77 (2.26)	-6.71** (2.27)	-5.98** (2.16)	-7.63** (3.01)

Table S3. Estimates of inbreeding depression (standard error in brackets) for growth and reproductive traits. *p-value < .05, **p-value < .01, ***p-value < .001 Inbreeding depression with $F_{\text{PED(total)}}$ was estimated from the total animals with pedigrees, and F_{PED} only included animals with both genotypes and pedigrees. F_{PH} = the proportion of homozygous genotypes of all genotypes; F_{GRM} =inbreeding from genomic relationship matrix, F_{GRM1} and F_{GRM2} were from pruning data for MAF (0.01) and for MAF (0.05);

F_{HOM} = inbreeding coefficients based on the observed versus expected number of homozygous genotypes, $F_{\text{HOM}(\text{pruned})}$ was from SNP pruned data based on linkage disequilibrium; Under ROH_1, F_{ROH} was estimated based on runs of homozygosity; $F_{\text{ROH}(\text{model})}$ was estimated using the model-based software RZooRoH.