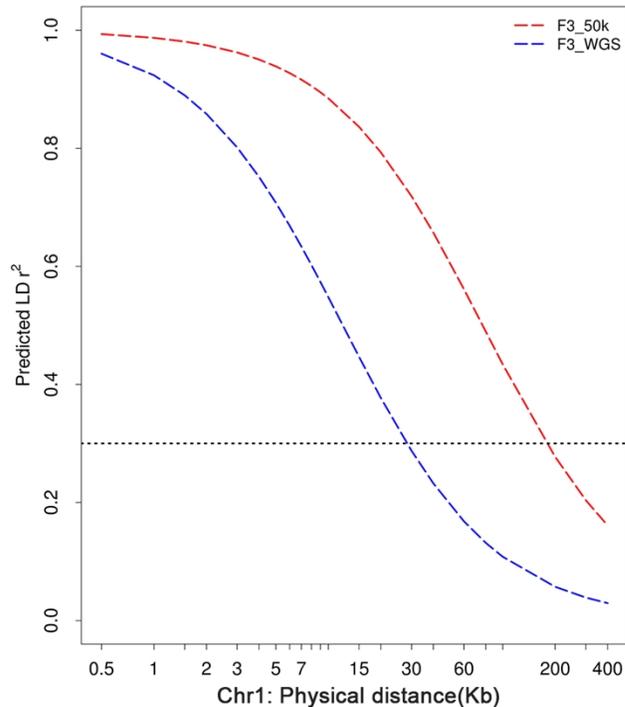# SUPPLEMENTARY MATERIAL:

Title: Rediscover and Refine QTLs for Pig Scrotal Hernia by Increasing a Specially Designed F₃ Population and Using Whole Genome Sequence Imputation Technology

Wenwu Xu, Dong Chen, Guorong Yan, Shijun Xiao, Tao Huang, Zhiyan Zhang[†] and lusheng Huang[†]

Figure S1 Linkage disequilibrium (LD) decay for F3 individuals in chromosome 1. LD decay was calculated for F3 using 50K genotype (*red line*) and whole-genome imputed data (*blue line*). X-axis indicates the physical distance (kb) between two markers, and if distances between two markers is greater than 400kb, the LD will not be calculated. Y-axis indicates the predicted LD by non-linear fit.
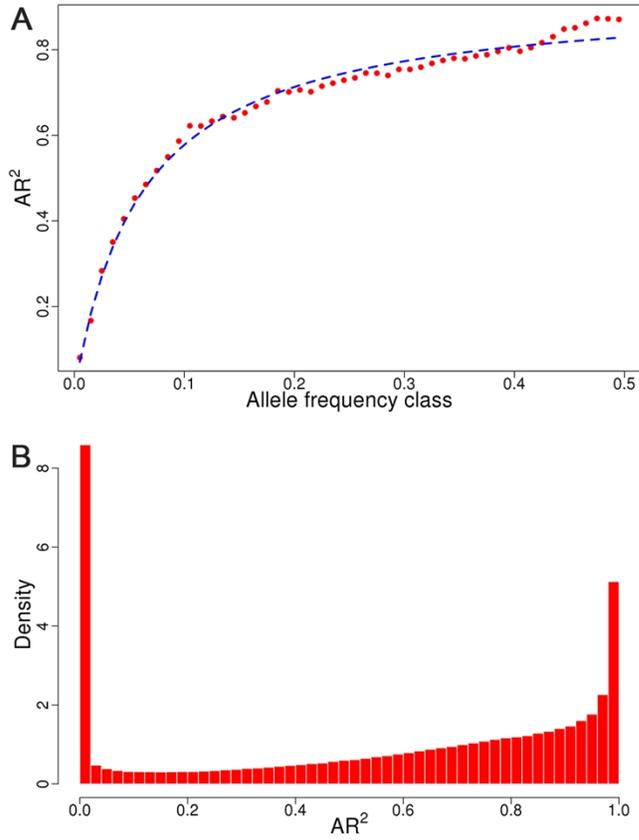
Figure S2 imputation accuracy. (A) The squared correlation between sequenced and imputed individuals, the x-axis is the MAF range from 0 to 0.5, and the y-axis is imputation accuracy denoted by the AR2. And the blue line indicates the predicted AR2 by non-linear fit. (B) the histogram of AR2.
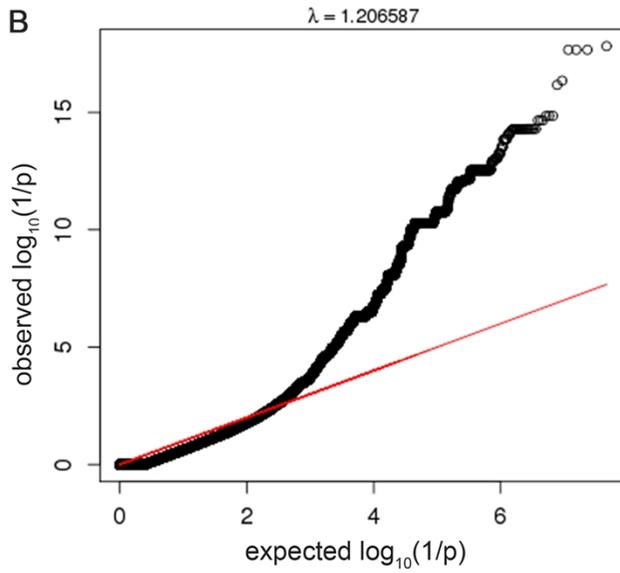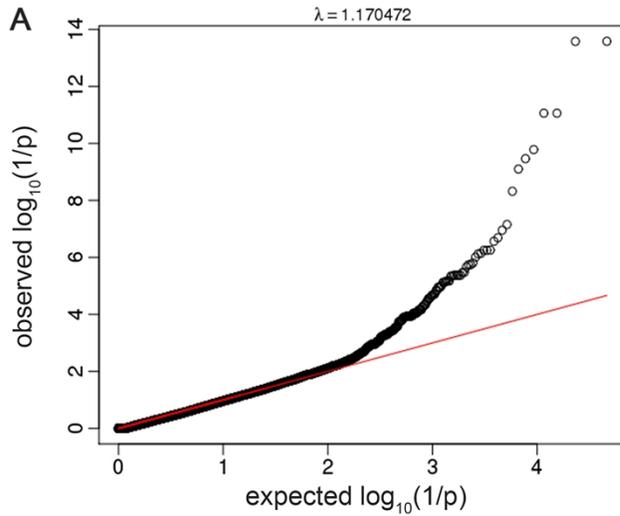
Figure S3 Quantile-quantile (Q-Q) plots for influence of population stratification on GWAS. The y-axis and x-axis represent the expected and observed negative $\log_{10}$ *P*-value, respectively.
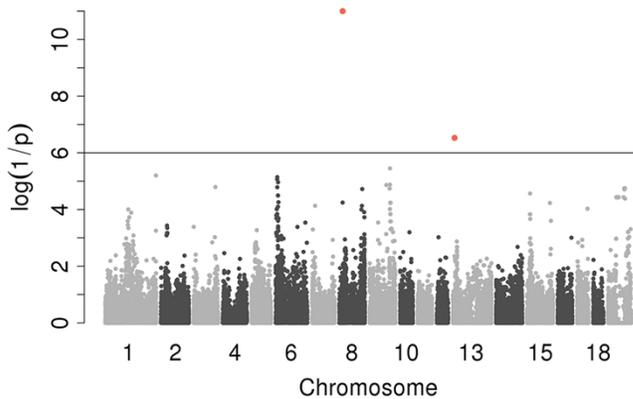
Figure S4 Manhattan plot of conditional GWAS for F$_3$ populations. Log(1/p) of SNPs were plotted against their genomic position, the solid line indicates the 5% genome-wide significant threshold. SNPs surpassing the genome-wide threshold are highlighted in pink.

Table S1 Haplotypes of the region between flanked by markers rs341392224 and rs326688253 on chromosome 8 are shown (quantity greater than 10), and the chi-square result of it.

Haplotype	case	control	*P*-value
CACGT	12	17	1.02E-12
CATAC	4	76	0.35
CATAT	1	144	2E-4
CGTGC	2	31	0.74
TGCAC	11	35	9.5E-06
TGTAC	6	150	0.035