Screening of *Streptococcus Suis* serotype 2 resistance genes with SNP and transcriptomic microarray

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Supplementary

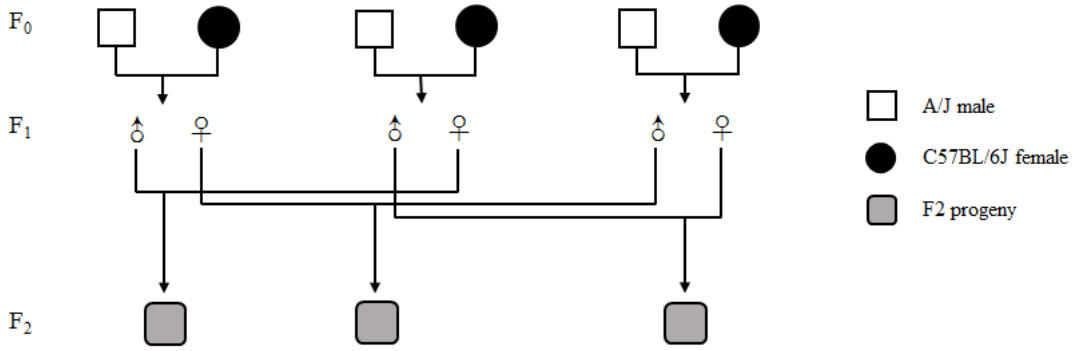

Figure S1. Breeding scheme used to generate F_2 mice. Since the fertility of C57BL/6 female mice is higher than A/J female mice, we chose C57BL/6 female mice and A/J male mice as parents to generate F_1 progeny. To avoid inbreeding, F_1 male mice were mated with F_1 female mice from a different group to generate the F_2 mice.

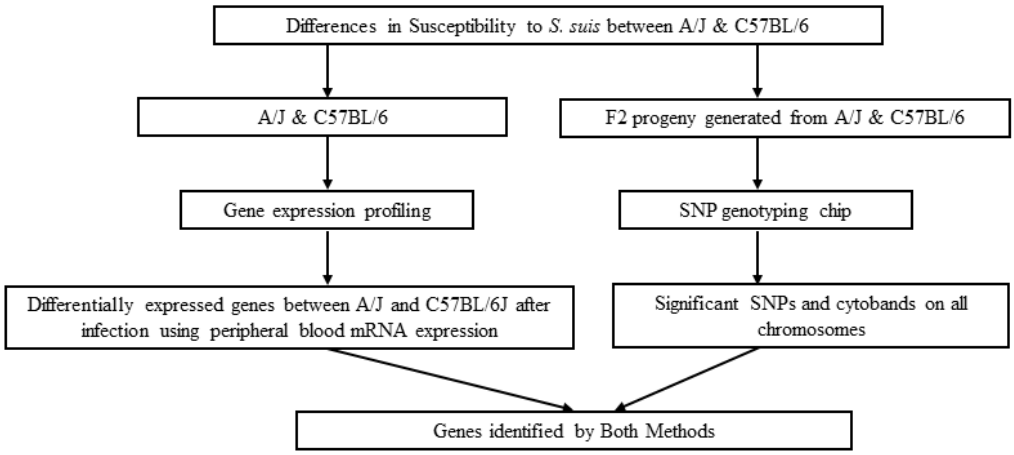

Figure S2. Overall strategy for identifying genes associated with resistance to *S. suis* in swine. Flow chart of the strategy for identifying *S. suis* resistant genes in swine through gene expression profiling and SNP genotyping chip.

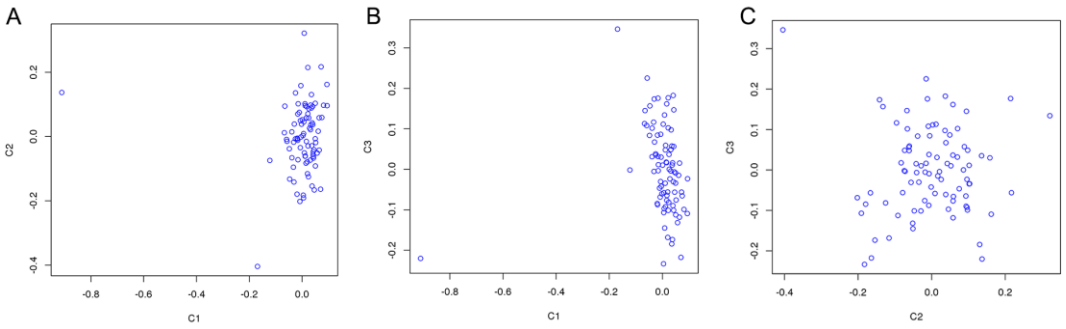

Figure S3. Population structure analyzed from PCA values. Principal component values (C1, C2 and C3) were obtained through PLINK1.09 and used to correct population structure. Each point stands for a sample in the plots. Although points are concentrated in (A) and (B), and scattered in (C), none formed into several clusters in the three plots, showing the genetic background was consistent in F_2 mice.

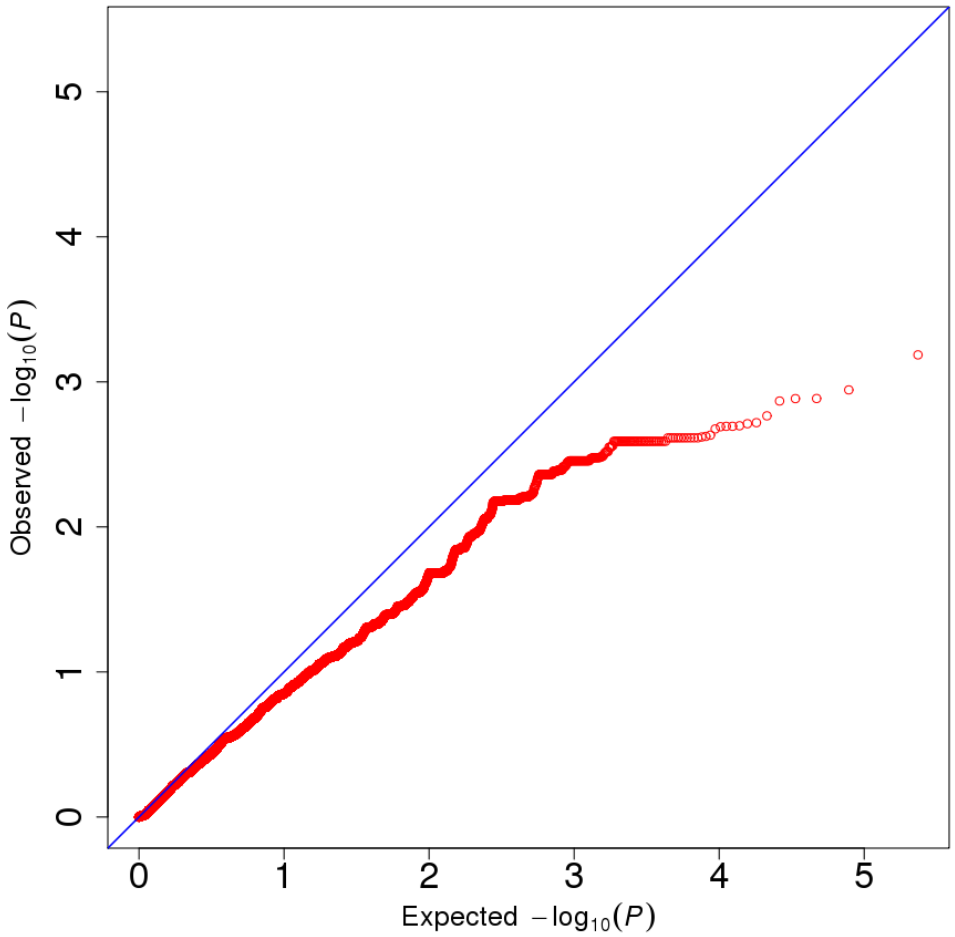

Figure S4. Q-Q plot of F_2 susceptible samples and F_2 resistant samples. The plot showed deviation between expected *P*-values and observed *P*-values. Each point stands for a SNP. Points on the diagonal of coordinate were considered as non-influential to SS2 susceptibility, while points deviating from the diagonal might be associated with the trait.