Supplemental Table S21. Summary and annotation of SNPs in 1,737 missing genes for Chinese wild boars (*n* = 6) and domestic pigs (*n* = 41).

Category		Number of SNP							
		Chinese wild boar (*n* = 6)	**Bamaxiang (*n* = 6)**	**Erhualian (*n* = 5)**	**Hetao (*n* = 6)**	**Laiwu (*n* = 6)**	**Luchuan (*n* = 6)**	**Min (*n* = 6)**	**Wuzhishan (*n* = 6)**
Total		535,770	354,351	274,944	345,074	325,882	349,101	309,446	402,760
Intronic		502,184	330,246	256,336	321,658	301,284	323,969	287,545	375,954
Splicing		1,014	434	231	459	554	708	467	558
Exonic (i.e. CDS)	**Missense**	17,275	11,927	8,281	11,634	12,965	13,050	10,960	13,360
	Stop gain (i.e. nonsense)	339	247	163	240	302	247	242	242
	Stop loss	36	29	18	30	37	32	31	26
	Synonymous	13,150	10,590	9,025	10,058	9,859	10,169	9,417	11,482
	Unknown	1,772	878	890	995	881	926	784	1,138

The package ANNOVAR[45] was used to identify whether a SNP causes protein coding changes and the amino acids that are affected. 'Stop gain' means that a nonsynonymous SNP leads to the creation of a stop codon at the variant site. 'Stop loss' means that a nonsynonymous SNP leads to the elimination of a stop codon at the variant site. 'Unknown' means unknown function (due to various errors in the gene structure definition in the database file). 'Splicing' means that a variant is within 2 bp of a splice junction. The major allele of the wild boar population was used as the reference allele.