Supplemental Table S8. Summary and annotation of SNPs.

Category		Number of SNPs										
		Hampshire	Piétrain	Berkshire	Landrace	Large White	Bamei	Jinhua	Meishan	Rongchang	Tibetan wild boar	Total
Number of total SNP		8,856,625	9,357,538	9,461,325	9,616,285	10,135,196	15,140,764	15,304,203	15,318,619	15,696,859	15,949,092	33,596,930
Upstream		72,404	75,023	76,501	78,128	82,584	114,955	115,274	115,292	119,640	119,305	252,954
Exonic	**Missense**	27,715	28,066	28,782	29,134	30,064	38,132	38,318	37,756	38,995	39,811	83,385
	Synonymous	34,542	35,562	36,843	37,470	39,489	55,722	55,731	55,987	57,677	58,535	122,441
	Stop gain	354	374	371	417	410	481	480	468	480	500	1,047
	Stop loss	40	43	42	46	46	56	57	56	51	59	92
Intronic		1,840,581	1,945,180	1,980,405	2,003,636	2,116,130	3,253,709	3,247,880	3,269,520	3,372,262	3,424,873	7,179,103
Splicing		465	484	486	522	509	626	648	621	636	640	1,180
Downstream		68,544	69,447	71,188	73,522	77,900	106,796	106,479	107,675	111,240	112,528	233,788
Upstream / Downstream		719	794	839	853	1,026	1,187	1,214	1,123	1,255	1,214	2,696
Intergenic		6,811,261	7,202,565	7,265,868	7,392,557	7,787,038	11,569,100	11,738,122	11,730,121	11,994,623	12,191,627	25,720,244

The package ANNOVAR[45] was used to identify whether a SNP causes protein coding changes and the amino acids that are affected. ‘Upstream’ refers to a variant that overlaps with the 1 kb region upstream of the gene start site. ‘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. ‘Downstream’ means that a variant overlap with the 1 kb region downstream of the gene end site. ‘Upstream/Downstream’ means that a variant is located in downstream and upstream regions (possibly for two different genes). Total: the SNPs identified from the ten pig genomes were merged into a non-redundant set.