

Resilience Effects of *SGK1* and *TAP1* DNA Markers During PRRSV Outbreaks in Reproductive Sows

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Table S1. Description of primers used for the amplification of the *SGK1* and *TAP1* genes.

Locus	Region Name	Primer Sequences (5'→ 3')		PCR size (bp)	Transcript ID ¹	PCR template
		Forward	Reverse			
<i>SGK1</i>	SGK1_exon1	TCTCCCTCTGCTTTTCTGGC	AACCTGTCCTTACCCGCTTC	629	ENSSSCT00000062973.2	Genomic
	SGK1_exon2	CTTTGCAGCTTGCTCCCTTC	CCACCCGTCCTCTGAAACAT	320	ENSSSCT00000037228.1	Genomic
	SGK1_exon2	GGAGGCACCGGCTAATCTTT	ACTCCTTTTCTGCACCTCGG	815	ENSSSCT00000037646.1	Genomic
	SGK1_exon1	GCCACTTCCTCATTGTTGCG	CAACGCCACGCACACTAATC	290	ENSSSCT00000027054.3	Genomic
	SGK1_exon13	CCTGGACCTCTTGACCCTGA	AAACACCAGGCTCTGACTGA	980	ENSSSCT00000037228.1	Genomic
	SGK1_exon1-9	CTGTGAACTCCCCACTGTGG	GTAACCCAAGGCACTGGCTA	953	ENSSSCT00000062973.2	cDNA
	SGK1_exon3-9	TGAAACAGAGAAGGATGGGC	TGTGTCCCTGTGAATCTAGCA	513	ENSSSCT00000037228.1	cDNA
	SGK1_exon7-13	CGGTGGAGAGTTGTTCTACCA	TCGGTCTGCTTCCTTGACG	708	ENSSSCT00000037228.1	cDNA
<i>TAP1</i>	TAP1_exon1	TCGTTTTCCCTTTCCATAA	GTCAGAAGGAGCCAGAGGTG	778	ENSSSCT00000001630.4	Genomic
	TAP1_exon 11	GTGGAGTCGCTCCTGTATGAA	AAATACCAAGAATCCACAGGGTA	603	ENSSSCT00000001630.4	Genomic
	TAP1_exon1-7	CTCTGGCTCCTTCTGACCCT	AGGTGGACAGCAGTACCTGA	830	ENSSSCT00000001630.4	cDNA
	TAP1_exon6-11	AGCGGAAACCTCGTCACATT	AGGATGTGATTGGCCTGCTC	818	ENSSSCT00000001630.4	cDNA

¹ Based on Ensembl release 99, Sscrofa11.1 (GCA_000003025.6).

Table S2. Primers used in the high-resolution melting genotyping protocols.

Locus	Target Polymorphism	Forward Primer Sequence (5'→3')	Reverse Primer Sequence (5'→3')	Amplicon Size (bp)
<i>SGK1</i>	rs338508371	TGTTGCTCCTCGTGGACTTC	GTGTCCTGCAAGTGTACATTG	101
<i>TAP1</i>	rs1109026889	CTTCGCCCTCAGCTATGC	TGACTTCCTTGCACCCAAAG	81
<i>TAP1</i>	rs80928141	CGGAGCTTTGCCAATGAAGAG	TGAGTGTCTTCATGTCCTGCAG	70

Table S3. List of polymorphisms identified in the regulatory and coding sequences of the *SGK1* and *TAP1* genes.

Locus	Location Within Transcript ¹	Mutation Type	Gene Location	Gene Effect	Genomic Location (SScfoa11.1)	rs number
<i>SGK1</i>	c.-726T>C	SNP	Exon 1	5'UTR	1:29626049	rs31849774
	c.-708A>G	SNP	Exon 1	5'UTR	1:29626067	rs329854265
	c.1122T>C	SNP	Exon 17	Synonymous	1:29752467	rs332443855
	c.*8A>T	SNP	Exon 17	3'UTR	1:29752568	rs345836515
	c.*269indelG	indel	Exon 17	3'UTR	1:29752829	
	c.*350A>G	SNP	Exon 17	3'UTR	1:29752910	rs337827000
	c.*433G>A	SNP	Exon 17	3'UTR	1:29752993	rs332161325
	c.*510C>A	SNP	Exon 17	3'UTR	1:29753070	rs338508371
	c.+517G>A	SNP	Exon 1	Synonymous GCG/GCA A141	7:25071346	rs1109026889
	c.+729G>A	SNP	Exon 3	Synonymous GGG/GGA G243	7:25070440	
<i>TAP1</i>	c.+942G>A	SNP	Exon 4	Synonymous GGG/GGA G314	7:25068693	rs1114053665
	c.+1155G>A	SNP	Exon 5	Synonymous AAG/AAA K385	7:25068055	rs80928141
	c.+1608C>G	SNP	Exon 9	Synonymous CCC/CCG P536	7:25065461	
	c.+1707T>C	SNP	Exon 10	Synonymous TAT/TAC Y569	7:25065138	
	c.+1749C>T	SNP	Exon 10	Synonymous GCC/GCT A583	7:25065096	rs1113696702
	c.+1900C>T	SNP	Exon 11	Synonymous CTG/TTC L634	7:25064167	rs809555756

¹ Transcript used for polymorphism location: *SGK1*-ENSSSCT00000062973; *TAP1*-ENSSSCT0000001630.4; Polymorphisms genotyped in this study are highlighted in bold.