

**Supplementary Table 1. Primers used in this study.**

Purpose	Primer	Sequence (5'--3') <sup>a</sup>
Construction of D7471 mutant	7471 upstream-1	CCGGA <u>AATTC</u> CACTTGGCCGTCAGCAG ( <i>EcoRI</i> )
	7471 upstream-2	CACCTTCAGCTCCGTCGCCACTCCTTGGCGTTCCC
	7471 downstream-1	GGGAACGCCAAGGAGTGGCGACGGAGCTGAAGGGTG
	7471 downstream-2	GGA <u>AGATCT</u> CAGGACGACGACGGATT ( <i>BglII</i> )
	7471 v1	TACTGGAAGCGGACGGCG
	7471 v2	GCGCCCGGTGTCTTCAC
Over-expression of SAV7471	E7471 forward	CCGGA <u>AATTC</u> CACTTGGCCGTCAGCAG ( <i>EcoRI</i> )
	E7471 reverse	GGA <u>AGATCT</u> CACCCTTCAGTCCGTCG ( <i>BglII</i> )
Construction of His <sub>6</sub> -tagged SAV7471	His <sub>6</sub> -7471 forward	GAGATCGCAGTCGCCCC
	His <sub>6</sub> -7471 reverse	CCG <u>TCTCGAG</u> GCGCAGGCCTCCAGG ( <i>XhoI</i> )
Bacterial one-hybrid assay	B7471 forward	CGGGGTACCATGGAGATCGCAGTCGC ( <i>KpnI</i> )
	B7471 reverse	GGA <u>AGATCT</u> CACCCTTCAGTCCGTCG ( <i>BglII</i> )
	7471p forward	ATT <u>TGCGGCCG</u> CCCAGTGGATGTCGCGTCG ( <i>NotI</i> )
	7471p reverse	CCGGA <u>AATTC</u> GGGATGCCTCTCCGTCG ( <i>EcoRI</i> )
RT-PCR	hrdB forward	TACTGCGCAGCCTCAACCAG
	hrdB reverse	GCCGATCTGCTTGAGGTAGTC
	aveR forward	TGGGCTGTGGAAGAGTACG
	aveR reverse	TGACGGTCAGGCAGTAGTCC
	aveA1 forward	ACGCTCCGACGTCTTCCG
	aveA1 reverse	TTGTCCTCGGTCCACGGAG
	SAV7472 forward	ATGACCGACGACCGCCC
	SAV7472 reverse	CTCCCGCTCCTCGATCCG
	SAV7473 forward	CGTGACTGAACAGGCCGAG
	SAV7473 reverse	GCCGTCGAGCAGATCCAG
EMSA and footprinting assay	Probe 1 forward	GAACGGGCCACTCCTTG
	Probe 1 reverse	GGGATGCCTCTCCGTCG
	Probe 2 forward	CCAGTGGATGTCGCGTCG
	Probe 2 reverse	GGGATGCCTCTCCGTCG
	Probe 3 forward	GAACGGGCCACTCCTTG
	Probe 3 reverse	GCCGTGAGCAGTCCACG
	Probe 4 forward	CCAGTGGATGTCGCGTCG
	Probe 4 reverse	ATGGAGATCGCAGTCGCCC
	Probe 5 forward	ATGACCGACGACCGCCC
	Probe 5 reverse	GCCGTGAGCAGTCCACG
	Probe 6 forward	AAGCTGGTAGAGCCGTTGA (5'FAM labeled)
	Probe 6 reverse	TCCTGGCACTCGTACTGGAAG
5'-RACE	SP1-7471	GAACCACTGTCGACCCAG
	SP2-7471	CCGGTGGTGGTCGACGTG
	SP3-7471	CGACCAGCTGTTCTTGCC
	SP1-7472	CCACTTGGCCGTCAGCAG
	SP2-7472	CGAGTAGGCGAGCGAGACC
	SP3-7472	CCGGTCTC GGGTGTCCAG

<sup>a</sup>The restriction enzyme sites are underlined.