

Supplementary Table 1. Oligonucleotide primers, product size and annealing temperatures used for virulence gene detection.

Gene	Primer name	Sequence (5'→3')	Accession number	Product Size (bp)	Annealing temperature (°C)	Reference
<i>se-int</i>	se-int-F	5' CTG TTT CGT ATG GCG ATC CT 3'	ADX77197	497	60	This study
	se-int-R	5' AGG TTT GAT GGG GAA TGT GA 3'				
<i>sec</i>	sec-F	5' CTC AAG AAC TAG ACA TAA AAG CTA GG 3'	-	271	55	22
	sec-R	5' TCA AAA TCG GAT TAA CAT TAT CC 3'				
<i>seh</i>	seh-F	5' CAA CTG CTG ATT TAG CTC AG 3'	-	360	45	23
	seh-R	5' GTC GAA TGA GTA ATC TCT AGG 3'				
<i>ebpS</i>	ebpS-F	5' TGA CGA GGA CGA GAC AAC TG 3'	ADX76580	592	60	This study
	ebpS-R	5' TTT GTT CCC TTG AGG TTT GC 3'				
<i>spsD</i>	spsD-F	5' ATG GCG CGA TGA AGA TCA CA 3'	ADX76659	667	60	This study
	spsD-R	5' CAC CTT TTC ACC TGG GAG CA 3'				
<i>spsL</i>	spsL-F	5' CTG TTG AAA GAA CCG CAC CG 3'	ADX75396	738	60	This study
	spsL-R	5' TCA ACT CAC CGC TTC CAC TC 3'				
<i>spsO</i>	spsO-F	5' AGT ATG CGG TGG GGC TAT TG 3'	ADX77254	873	60	This study
	spsO-R	5' AGT GAG AAA GAA AGC GCC GA 3'				
<i>lukS</i>	lukS pseud F	5' TGT AAG CAG CAG AAA ATG GGG 3'	-	503	57	24
	lukS pseud R	5' GCCCGATAGGACTTCTTACAA 3'				
	lukF pseud F	5' CCTGTCTATGCCGCTAATCAA 3'				
<i>lukF</i>	lukF pseud R	5' AGGTCATGGAAGCTATCTCGA 3'	-	572	57	24
	bap-6m	5' CCC TAT ATC GAA GGT GTA GAA TTG CAC 3'				
<i>bap</i>	bap-7c	5' GCT GTT GAA GTT AAT ACT GTA CCT GC 3'	-	971	58	25
	<i>icaA</i>	icaA-F	5' TTT CGG GGA CAA GCA TCC AA 3'	ADX75478	506	60
icaA-R		5' TGA CAA CTC GGC AGA AAT GC 3'				
<i>icaB</i>	icaB-F	5' GGT CCA TAA GCC TGA GCG TT 3'	ADX75476	417	60	This study
	icaB-R	5' GAT GAC GGC GAT AAA ACC GC 3'				
<i>icaC</i>	icaC-F	5' AGA CAG AGG CTT AGC AAC AAC A 3'	ADX75475	237	60	This study

	<i>icaC</i> -R	5' CAC ATG TAT GCT CGG CTG GA 3'				
<i>icaD</i>	<i>icaD</i> -F	5' ACC ATC GTT AAT GCC TTC TTT CT 3'	ADX75477	174	60	This study
	<i>icaD</i> -R	5' CGT ATT AGC GCA CAT TCG GTG 3'				
<i>siet</i>	<i>siet</i> 1 tox	5' ATG GAA AAT TTA GCG GCA TCT GG 3'	-	359	56	26
	<i>siet</i> 2 tox	5' CCA TTA CTT TTC GCT TGT TGT GC 3'				
<i>speta</i>	<i>speta</i> -F	5' CAA AAA GCG CCT TTA GCA AC 3'	-	438	60	This study
	<i>speta</i> -R	5' CAC TGG TGC AGT CAA TCC AG 3'				
<i>expA</i>	<i>expA</i> -1	5' GTT TTA ATT GGT AAA AAT ACA 3'	-	413	42	27
	<i>expA</i> -2	5' ATA CCT GAT CCT GAA TTA CC 3'				
<i>expB</i>	<i>expB</i> -1	5' CGC CTG GCG TAT ATG CTA AAA C 3'	AB569087	408	60	This study
	<i>expB</i> -2	5' CTG CCG CTT TGC CAT CTT TA 3'				

Supplementary Table 2. Summary of total reads and total mapped reads using different reference genomes.

Sequenced sample	Total reads (bp)	Total mapped reads with reference ED99 (bp)	Total mapped reads with reference HKU10-30 (bp)	Total mapped reads with reference E140 (bp)
MSSP	3.014.639	2.567.304	2.174.112	2.797.893
MRSP	2.576.240	2.241.214	1.617.578	2.196.676