

1 **Table. Primer sequences for the *Sii*/SBSEC MLST scheme.**

Primer name	sequence (5'-3') ¹⁾	target gene	amplicon size [bp]
ddl-fw	CTT ACG TGA CTT ATG TTG AAG G	D-alanine-D-alanine ligase	522
ddl-rev	CCA AAG AAG TGG ATA CAT TGA C		
gki-fw2	TGA ACT GGG CAC ACA CTG	glucokinase	521
gki-rev	CTG GGT TYA AGA TGT TTG CG		
gki-fw6.2-ala ²⁾	GGG MTC WCC TGG AGC TGT		
gki-rev1.2-ala ²⁾	PGC AGC WGA HAC DCC ACC		
glnA-fw	GCT GTT GCA GGT TTG ATC TG	glutamine synthetase	478
glnA-rev	TAC AGT GCA TAC CTG AAC CG		
mutS-fw	GTG CCA GAT TAY TTC TTC CG	DNA mismatch repair ATPase	581
mutS-rev	GCT TCC ATC ATT TCC ACC AT		
mutS2-fw	CCA AAT ACT GGT GGT AAG AC	mismatch repair ATPase	529
mutS2-rev	TCA AAC GCT CTG CTT CAT TG		
pheS-fw	GCT AAA TTG GCT GAA ATG CG	phenylalanyl tRNA synthetase	557
pheS-rev	ACA CGY CCT GGT GAR ATC AT		
proS-fw	CTG CTA ACC TTG AAA TGG CA	prolyl tRNA synthetase	455
proS-rev2	AAC GTA TTC CGC TTC AAA ATC		
pyrE-fw	AGC ATC ACA AAT TGC ATC AG	orotate phosphoribosyl transferase	426
pyrE-rev	ACA TCA GCA CCT TCA CGT TC		
thrtRNA-syn-fw	CCA CCG TAA ACT TGG TAA AG	threonyl tRNA synthetase	606
thrtRNA-syn-rev	TGW GCA TTT TCC CAC ATT TC		
tpi fw3	ATC GCT GGT AAC TGG AAA ATG	triosephosphate isomerase	410
tpi-rev	CGA TAG CCC AGA TTG GTT CG		

2 ¹⁾ mixed base sites according to IUB code ²⁾ modified primers to amplify the same gene region in

3 *S. alactolyticus*.