Supplementary 1.

Multiple alignments of *S. capitis* sodA gene (A) and percent identity matrix between sequences (B) generated by Clustal Omega. Red arrows show the SNPs.
Supplementary 2A.

Multiple alignments of *S. capititis* gap gene generated by Clustal Omega. Red arrows show the SNPs.
Supplementary 2B.

Percent identity matrix between sequences of *S. capitis* gap gene generated by Clustal Omega.

Supplementary 3.

Multiple alignment of *sodA* sequences among *Staphylococcus* species performed by BLAST. The red square shows the region of *sodA* specific for *S. capitis*.

Supplementary 4.

Multiple alignment of *gap* sequences among *Staphylococcus* species performed by BLAST. The red square shows the region of *gap* specific for *S. capitis*. 

S3
Supplementary 5.

Agarose gel image of PCR products from optimisation of DNA-template dilution. Lane 1-6 show the products of gap, while lane 7-11 show the products of sodA. The DNA template used for the optimisation was extracted from clinical isolate of S. capitis no. 58. Lane 1 and 7: negative control (ddH₂O); Lane 2 and 8: undiluted DNA template; Lane 3 and 9: diluted template 1:10; Lane 4 and 10: diluted template 1:100; Lane 5 and 11: diluted template 1:1,000; Lane 6 and 12: diluted template 1:10,000.

Supplementary 6.

A.

Agarose gel image of PCR products of gap (A) and sodA (B) from optimisation of annealing temperature. DNA template used for the optimisation was extracted from clinical isolate of S. capitis no. 58 and diluted 1:10. Lane 1: negative control (ddH₂O); Lane 2: annealing temperature of 50°C; Lane 3: annealing temperature of 52°C; Lane 4: annealing temperature of 55°C; Lane 5: annealing temperature of 57°C; Lane 6: annealing temperature of 59°C; Lane 7: annealing temperature of 61°C, Lane 8: annealing temperature of 62°C.