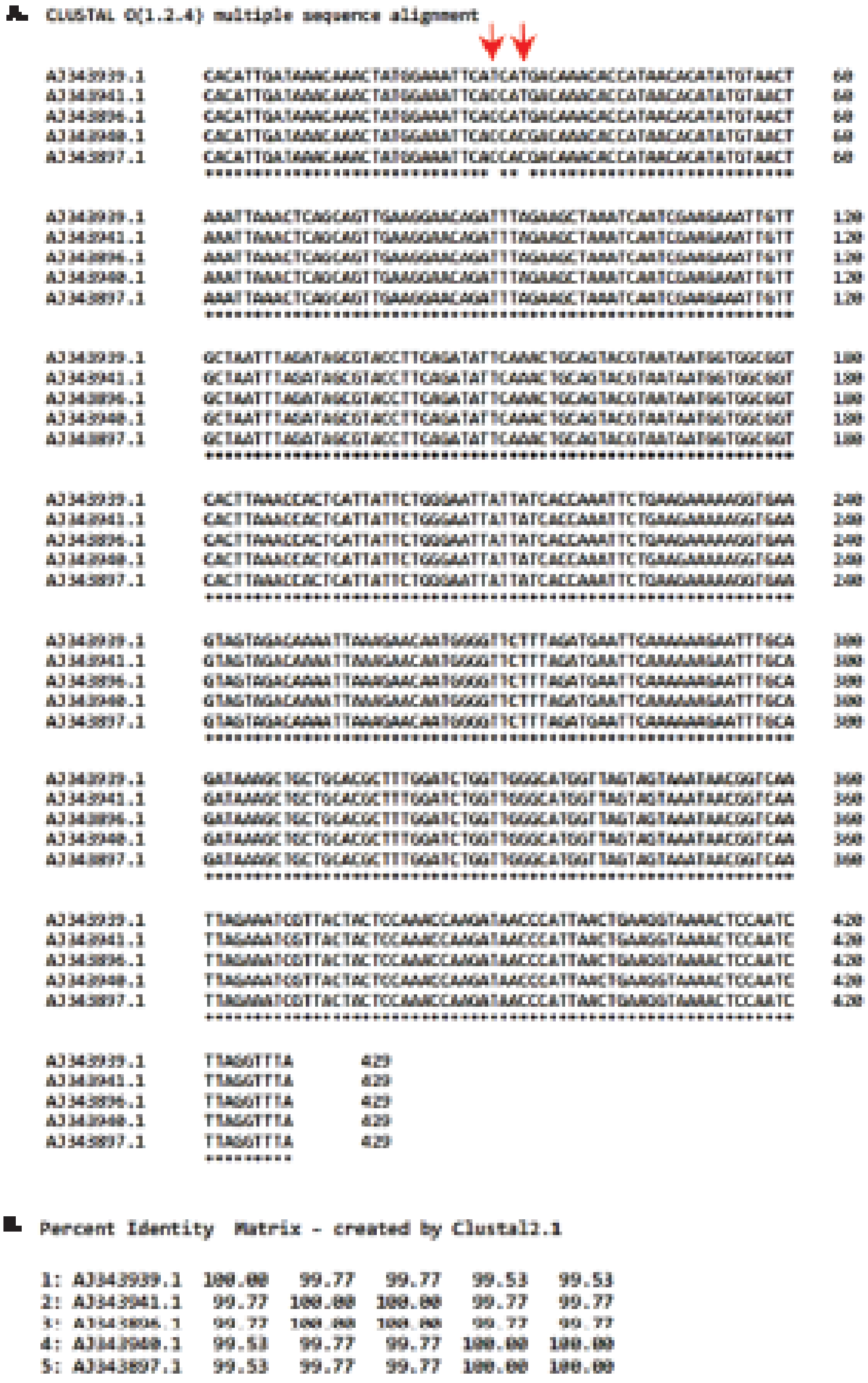
Supplementary 1.

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



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CLUSTAL O(1.2.4) multiple sequence alignment
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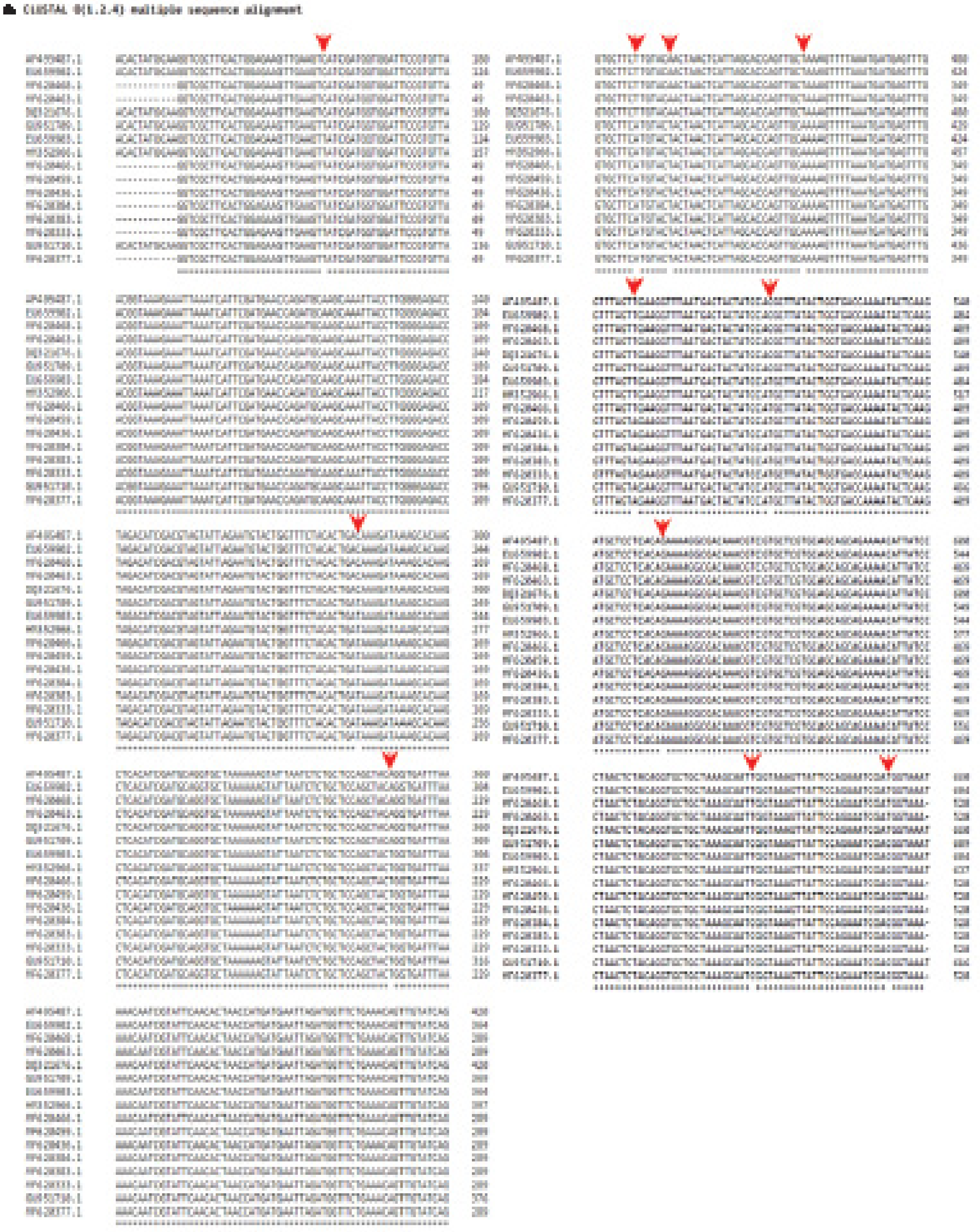
Percent Identity  Matrix - created by Clustal2.1

1: AJ343939.1  100.00   99.77   99.77   99.53   99.53
2: AJ343941.1   99.77  100.00  100.00   99.77   99.77
3: AJ343896.1   99.77  100.00  100.00   99.77   99.77
4: AJ343940.1   99.53   99.77   99.77  100.00  100.00
5: AJ343897.1   99.53   99.77   99.77  100.00  100.00
```

Supplementary 2A.

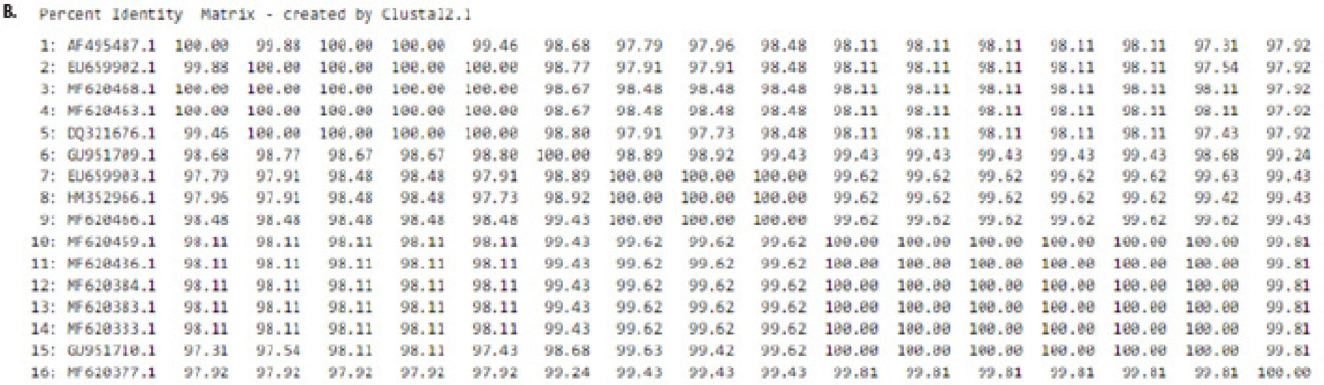
Multiple alignments of *S. capitis gap* gene generated by Clustal Omega. Red arrows show the SNPs.



CLUSTAL O(1.2.4) multiple sequence alignment

Supplementary 2B.

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



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B.  Percent Identity  Matrix - created by Clustal2.1

     1: AF495487.1  100.00   99.88  100.00  100.00   99.46   98.68   97.79   97.96   98.48   98.11   98.11   98.11   98.11   98.11   97.31   97.92
     2: EU659902.1   99.88  100.00  100.00  100.00  100.00   98.77   97.91   97.91   98.48   98.11   98.11   98.11   98.11   98.11   97.54   97.92
     3: MF620468.1  100.00  100.00  100.00  100.00  100.00   98.67   98.48   98.48   98.48   98.11   98.11   98.11   98.11   98.11   98.11   97.92
     4: MF620463.1  100.00  100.00  100.00  100.00  100.00   98.67   98.48   98.48   98.48   98.11   98.11   98.11   98.11   98.11   98.11   97.92
     5: DQ321676.1   99.46  100.00  100.00  100.00  100.00   98.80   97.91   97.73   98.48   98.11   98.11   98.11   98.11   98.11   97.43   97.92
     6: GU951709.1   98.68   98.77   98.67   98.67   98.80  100.00   98.89   98.92   99.43   99.43   99.43   99.43   99.43   99.43   98.68   99.24
     7: EU659903.1   97.79   97.91   98.48   98.48   97.91   98.89  100.00  100.00  100.00   99.62   99.62   99.62   99.62   99.62   99.63   99.43
     8: HM352966.1   97.96   97.91   98.48   98.48   97.73   98.92  100.00  100.00  100.00   99.62   99.62   99.62   99.62   99.62   99.42   99.43
     9: MF620466.1   98.48   98.48   98.48   98.48   98.48   99.43  100.00  100.00  100.00   99.62   99.62   99.62   99.62   99.62   99.62   99.43
    10: MF620459.1   98.11   98.11   98.11   98.11   98.11   99.43   99.62   99.62   99.62  100.00  100.00  100.00  100.00  100.00  100.00   99.81
    11: MF620436.1   98.11   98.11   98.11   98.11   98.11   99.43   99.62   99.62   99.62  100.00  100.00  100.00  100.00  100.00  100.00   99.81
    12: MF620384.1   98.11   98.11   98.11   98.11   98.11   99.43   99.62   99.62   99.62  100.00  100.00  100.00  100.00  100.00  100.00   99.81
    13: MF620383.1   98.11   98.11   98.11   98.11   98.11   99.43   99.62   99.62   99.62  100.00  100.00  100.00  100.00  100.00  100.00   99.81
    14: MF620333.1   98.11   98.11   98.11   98.11   98.11   99.43   99.62   99.62   99.62  100.00  100.00  100.00  100.00  100.00  100.00   99.81
    15: GU951710.1   97.31   97.54   98.11   98.11   97.43   98.68   99.63   99.42   99.62  100.00  100.00  100.00  100.00  100.00  100.00   99.81
    16: MF620377.1   97.92   97.92   97.92   97.92   97.92   99.24   99.43   99.43   99.43   99.81   99.81   99.81   99.81   99.81   99.81  100.00
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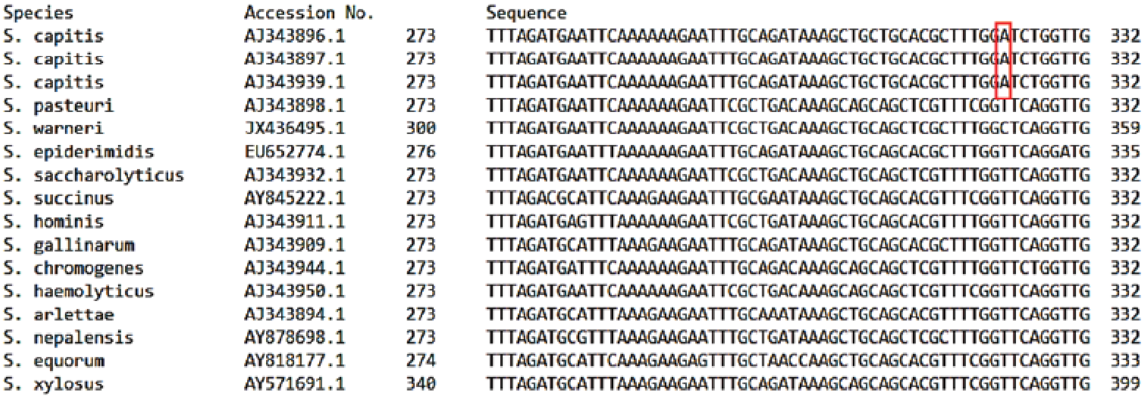
Supplementary 3.

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



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Species              Accession No.         Sequence
S. capitis           AJ343896.1     273    TTTAGATGAATTCAAAAAAGAATTTGCAGATAAAGCTGCTGCACGCTTTGGATCTGGTTG   332
S. capitis           AJ343897.1     273    TTTAGATGAATTCAAAAAAGAATTTGCAGATAAAGCTGCTGCACGCTTTGGATCTGGTTG   332
S. capitis           AJ343939.1     273    TTTAGATGAATTCAAAAAAGAATTTGCAGATAAAGCTGCTGCACGCTTTGGATCTGGTTG   332
S. pasteuri          AJ343898.1     273    TTTAGATGAATTCAAAAAAGAATTCGCTGACAAAGCAGCAGCTCGTTTCGGTTCAGGTTG   332
S. warneri           JX436495.1     300    TTTAGATGAATTCAAAAAAGAATTCGCTGACAAAGCTGCAGCTCGCTTTGGCTCAGGTTG   359
S. epiderimidis      EU652774.1     276    TTTAGATGAATTTAAAAAAGAATTTGCAGATAAAGCTGCAGCACGCTTTGGTTCAGGATG   335
S. saccharolyticus   AJ343932.1     273    TTTAGATGAATTCAAAAAAGAATTCGCTGACAAAGCTGCAGCTCGTTTTGGTTCAGGTTG   332
S. succinus          AY845222.1     273    TTTAGACGCATTCAAAGAAGAATTTGCGAATAAAGCTGCAGCACGTTTCGGTTCAGGTTG   332
S. hominis           AJ343911.1     273    TTTAGATGAGTTTAAAAAAGAATTCGCTGATAAAGCTGCAGCACGTTTTGGTTCAGGTTG   332
S. gallinarum        AJ343909.1     273    TTTAGATGCATTTAAAGAAGAATTTGCAGATAAAGCTGCAGCACGCTTTGGTTCAGGTTG   332
S. chromogenes       AJ343944.1     273    TTTAGATGATTTCAAAAAAGAATTTGCAGACAAAGCAGCAGCTCGTTTTGGTTCTGGTTG   332
S. haemolyticus      AJ343950.1     273    TTTAGATGAATTCAAAAAAGAATTCGCTGACAAAGCAGCAGCTCGTTTCGGTTCAGGTTG   332
S. arlettae          AJ343894.1     273    TTTAGATGCATTTAAAGAAGAATTTGCAAATAAAGCTGCAGCACGTTTTGGTTCAGGTTG   332
S. nepalensis        AY878698.1     273    TTTAGATGCGTTTAAAGAAGAATTTGCTGATAAAGCTGCAGCTCGCTTTGGTTCAGGTTG   332
S. equorum           AY818177.1     274    TTTAGATGCATTCAAAGAAGAGTTTGCTAACCAAGCTGCAGCACGTTTCGGTTCAGGTTG   333
S. xylosus           AY571691.1     340    TTTAGATGCATTTAAAGAAGAATTTGCAGATAAAGCAGCAGCACGTTTCGGTTCAGGTTG   399
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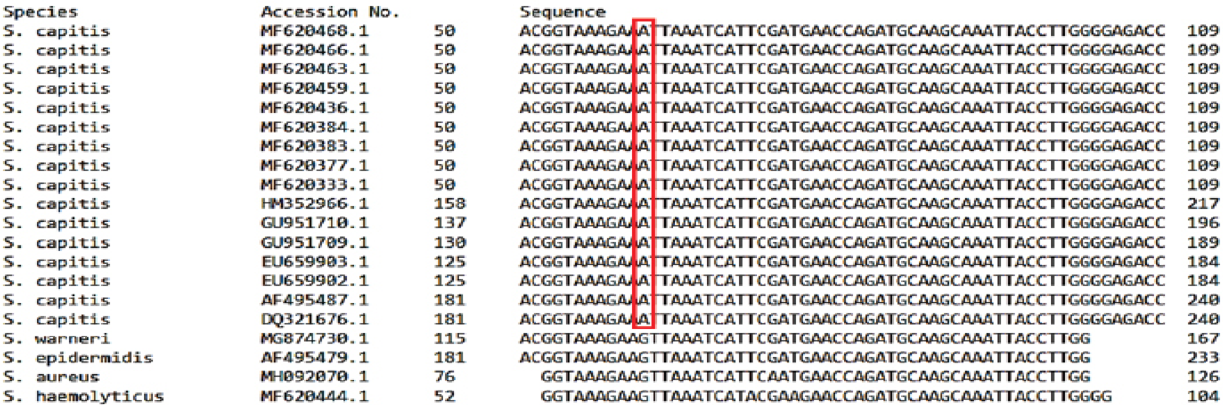
Supplementary 4.

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



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Species              Accession No.         Sequence
S. capitis           MF620468.1     50     ACGGTAAAGAAATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC   109
S. capitis           MF620466.1     50     ACGGTAAAGAAATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC   109
S. capitis           MF620463.1     50     ACGGTAAAGAAATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC   109
S. capitis           MF620459.1     50     ACGGTAAAGAAATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC   109
S. capitis           MF620436.1     50     ACGGTAAAGAAATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC   109
S. capitis           MF620384.1     50     ACGGTAAAGAAATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC   109
S. capitis           MF620383.1     50     ACGGTAAAGAAATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC   109
S. capitis           MF620377.1     50     ACGGTAAAGAAATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC   109
S. capitis           MF620333.1     50     ACGGTAAAGAAATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC   109
S. capitis           HM352966.1     158    ACGGTAAAGAAATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC   217
S. capitis           GU951710.1     137    ACGGTAAAGAAATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC   196
S. capitis           GU951709.1     130    ACGGTAAAGAAATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC   189
S. capitis           EU659903.1     125    ACGGTAAAGAAATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC   184
S. capitis           EU659902.1     125    ACGGTAAAGAAATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC   184
S. capitis           AF495487.1     181    ACGGTAAAGAAATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC   240
S. capitis           DQ321676.1     181    ACGGTAAAGAAATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC   240
S. warneri           MG874730.1     115    ACGGTAAAGAAGTTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGG          167
S. epidermidis       AF495479.1     181    ACGGTAAAGAAGTTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGG          233
S. aureus            MH092070.1     76       GGTAAAGAAGTTAAATCATTCAATGAACCAGATGCAAGCAAATTACCTTGG          126
S. haemolyticus      MF620444.1     52       GGTAAAGAAGTTAAATCATACGAAGAACCAGATGCAAGCAAATTACCTTGGGG        104
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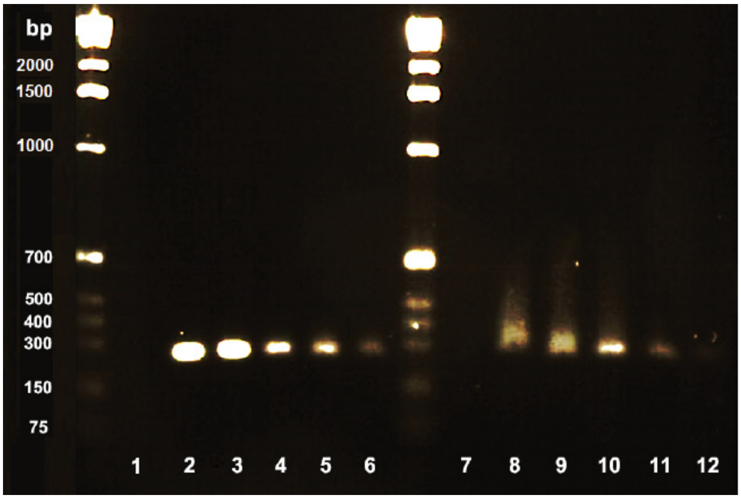
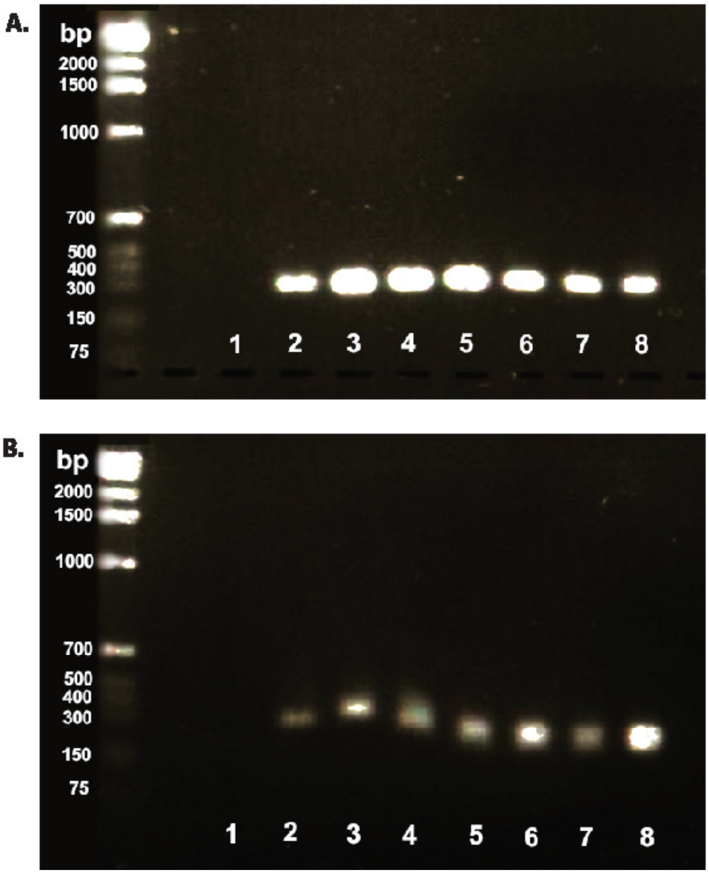
Supplementary 5.



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 (ddH$_2$O); 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.



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 (ddH$_2$O); Lane 2: annealing temperature of 50^{o}C; Lane 3: annealing temperature of 52^{o}C; Lane 4: annealing temperature of 55^{o}C; Lane 5: annealing temperature of 57^{o}C; Lane 6: annealing temperature of 59^{o}C; Lane 7: annealing temperature of 61^{o}C, Lane 8: annealing temperature of 62^{o}C.