

FIG. 1A

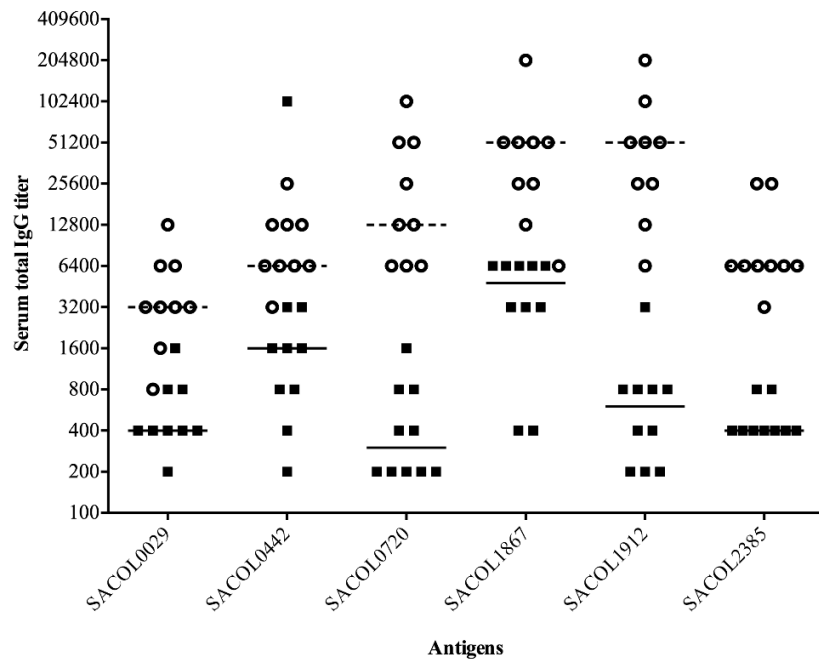


FIG. 1B

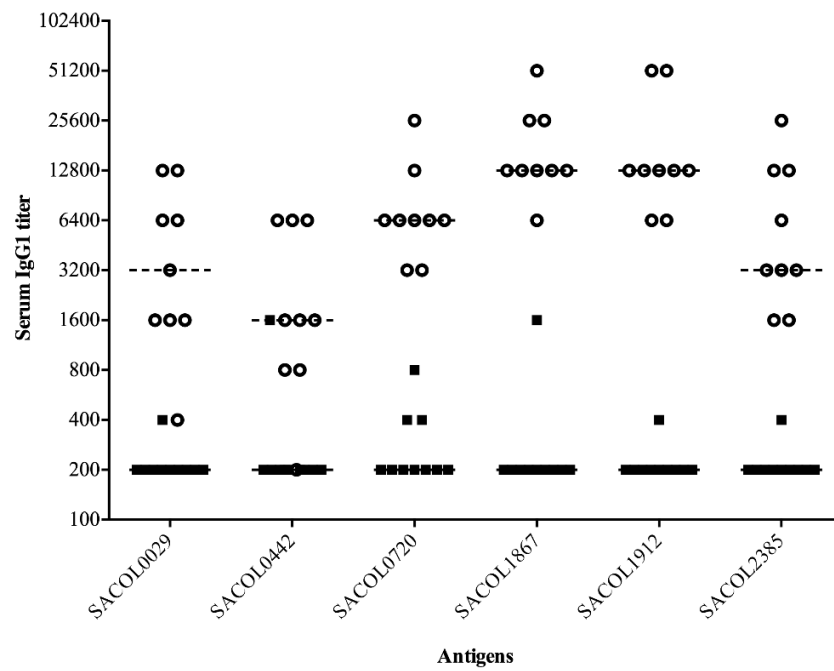


FIG. 1C

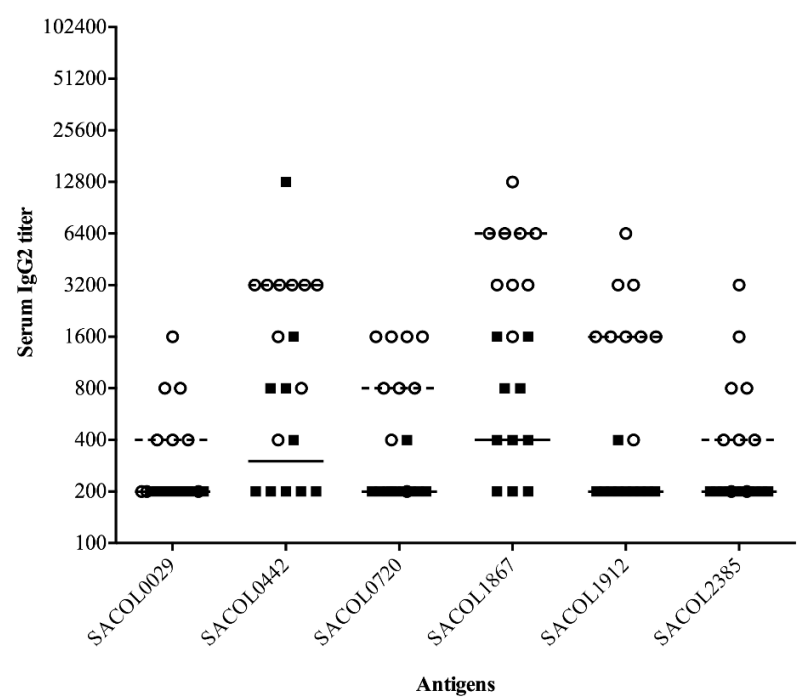
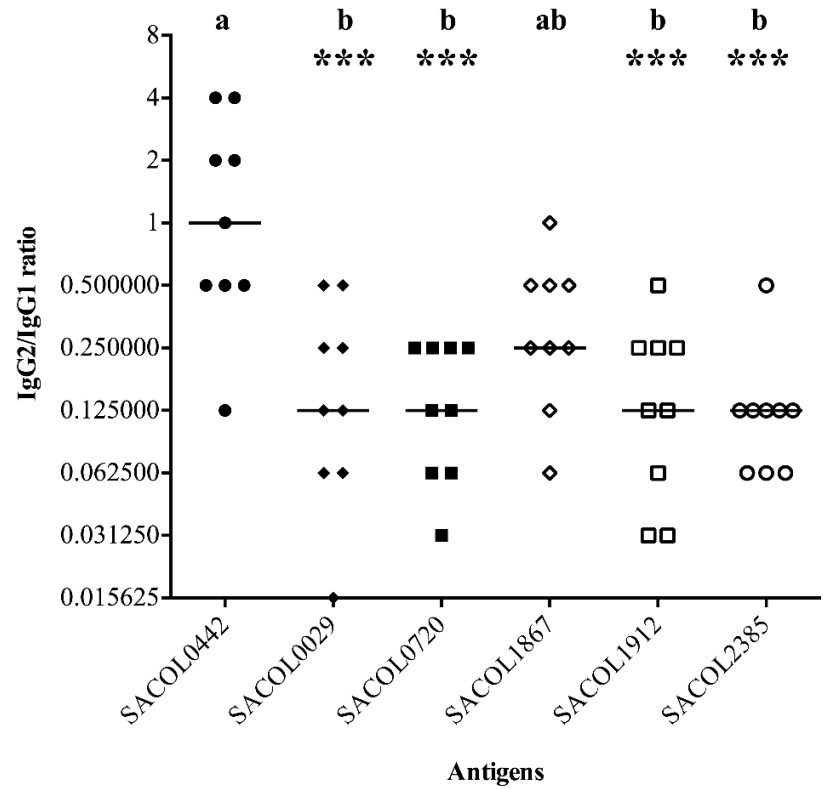


FIG. 1D



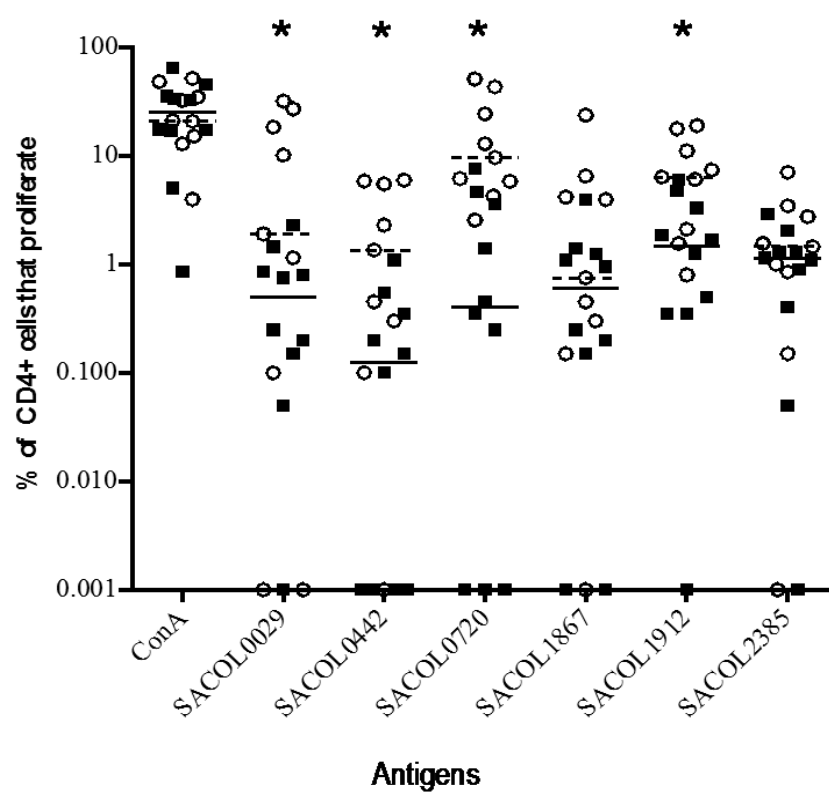


FIG. 2

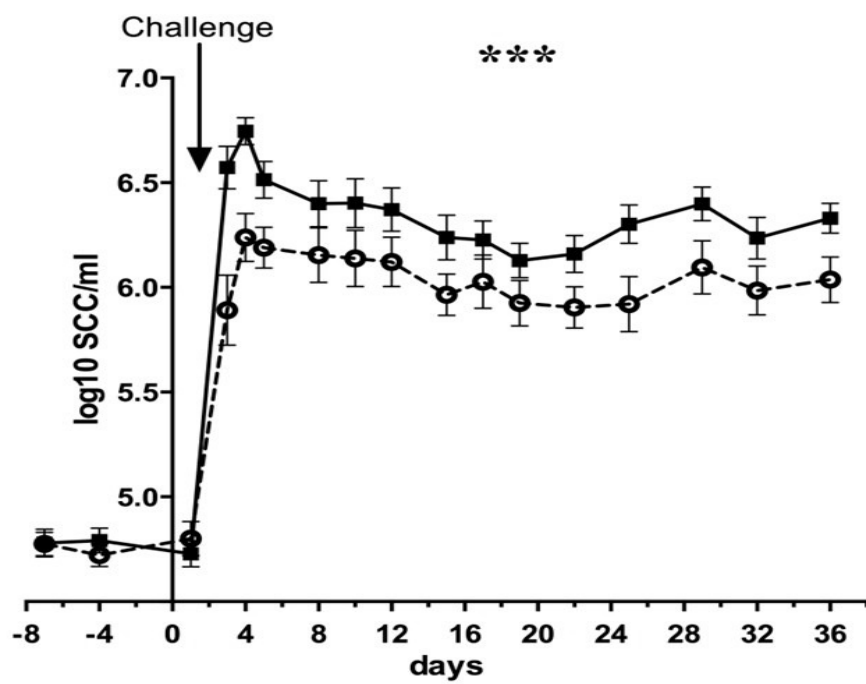


FIG. 3

FIG. 4A

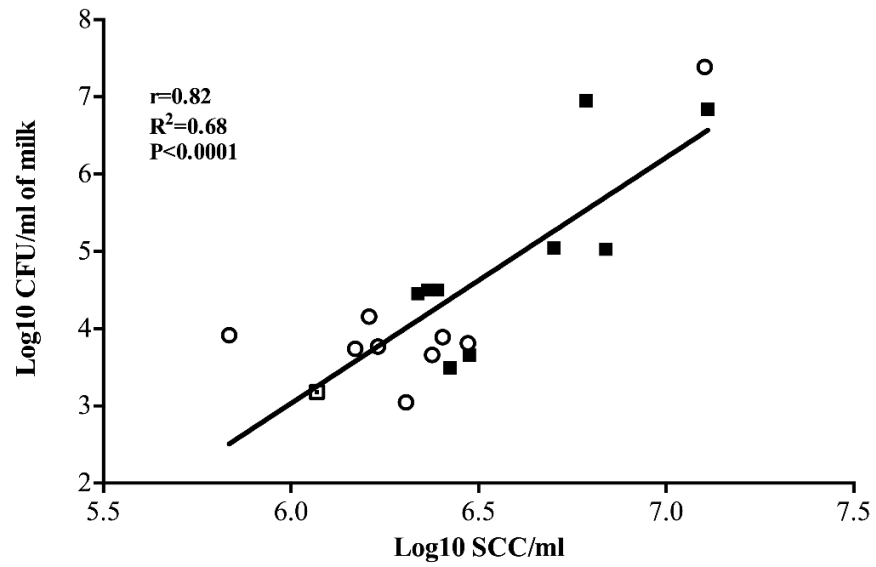


FIG. 4B

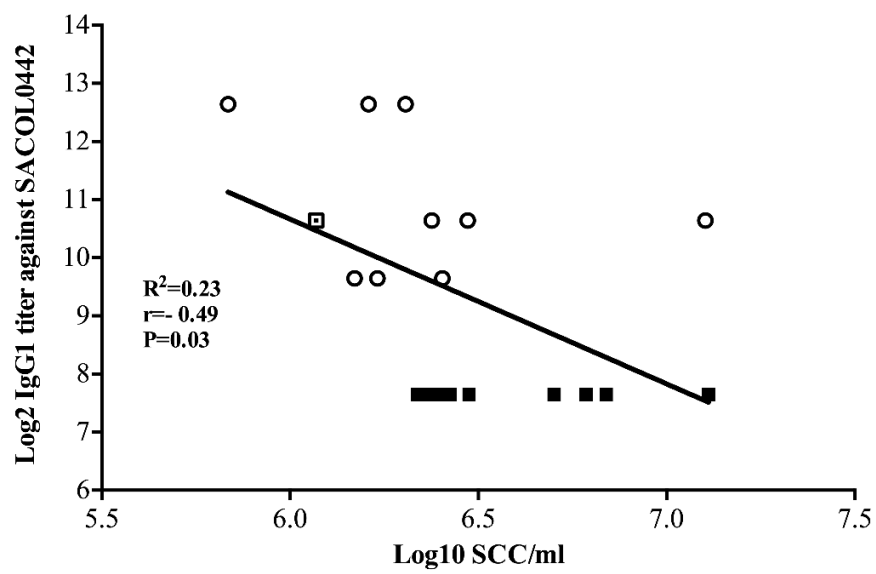


FIG. 4C

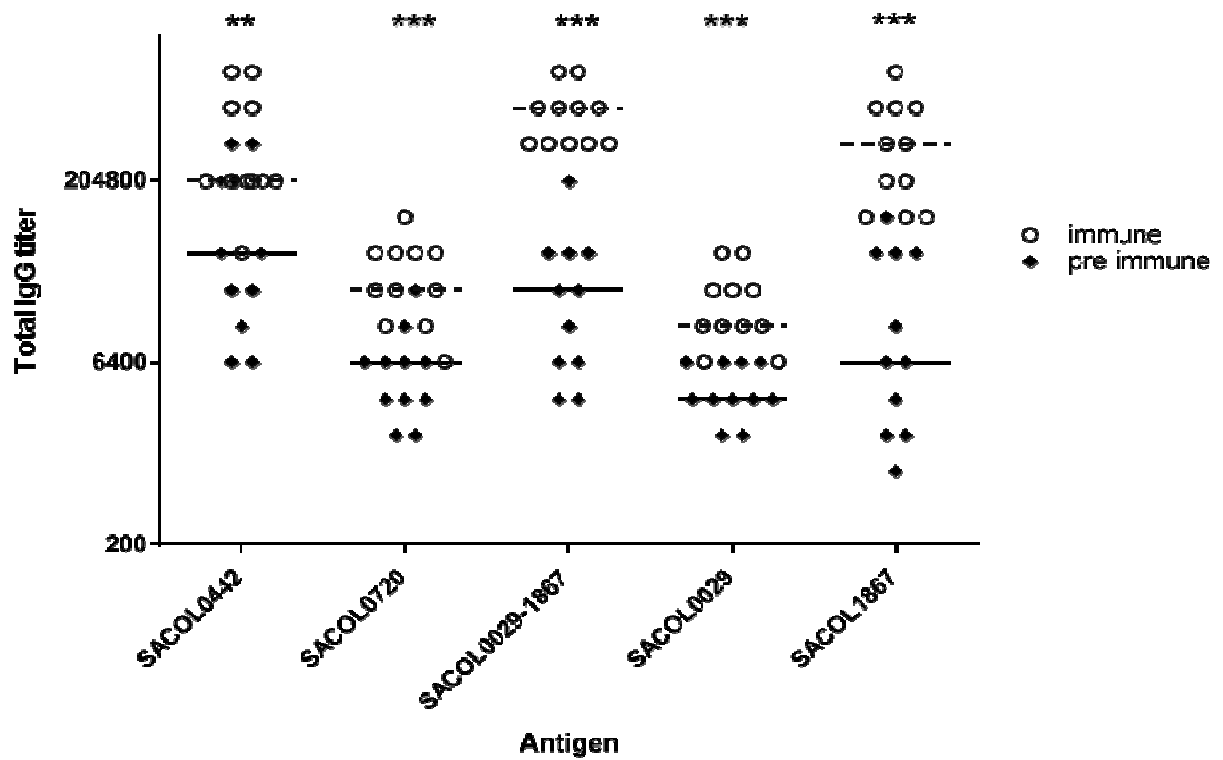
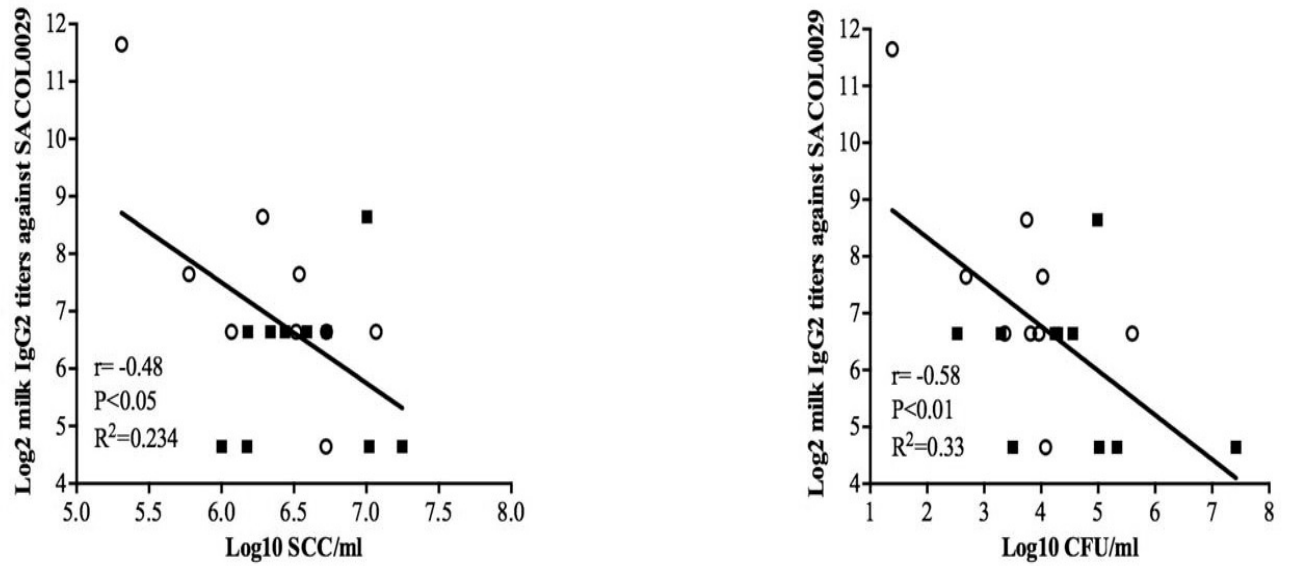


FIG. 5

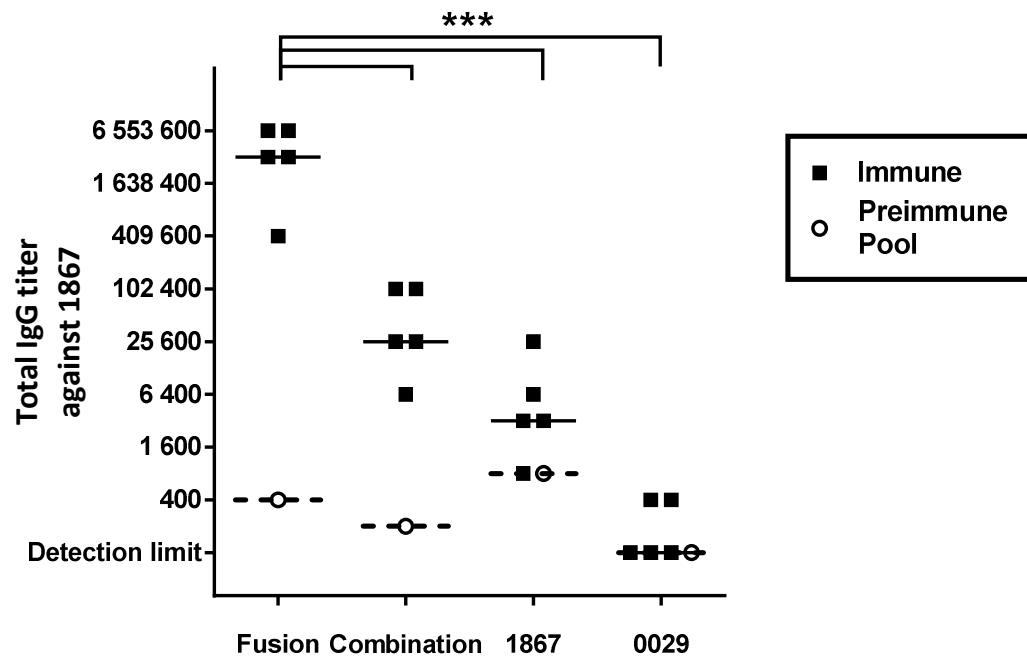


FIG. 6

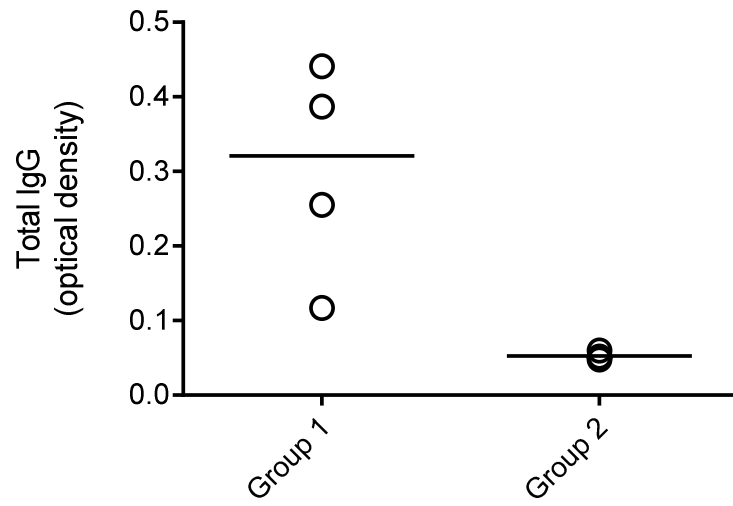


FIG. 7

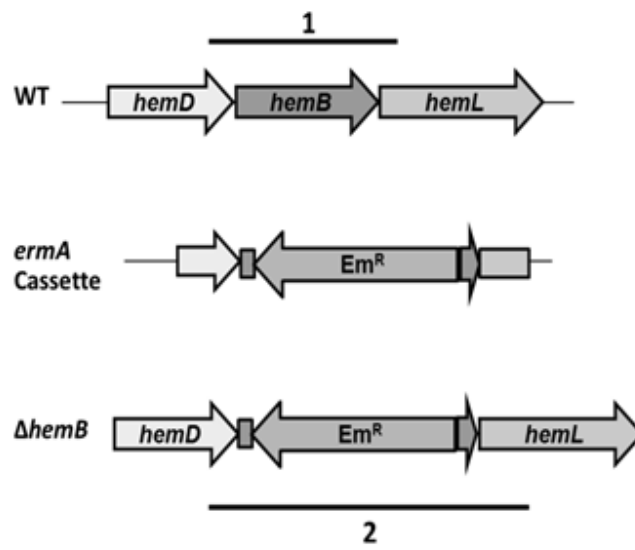


FIG. 8A

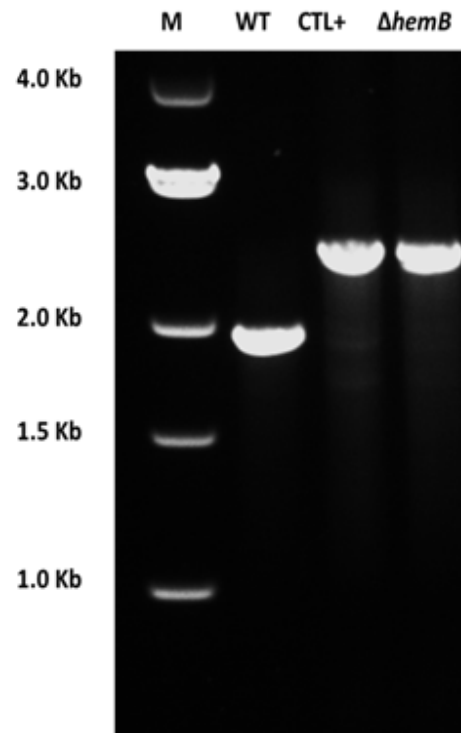


FIG. 8B

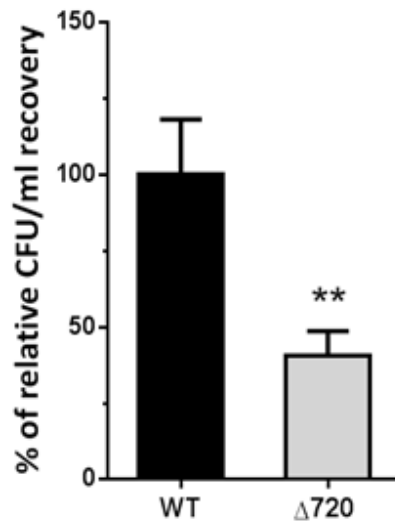


FIG. 9A

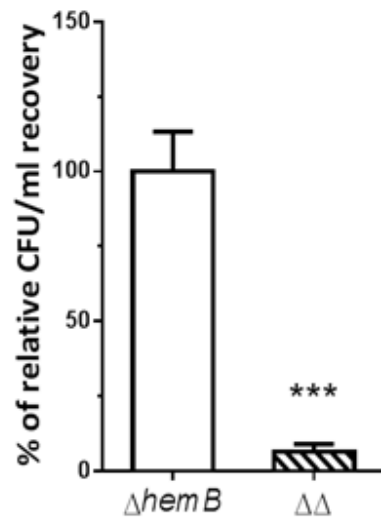


FIG. 9B

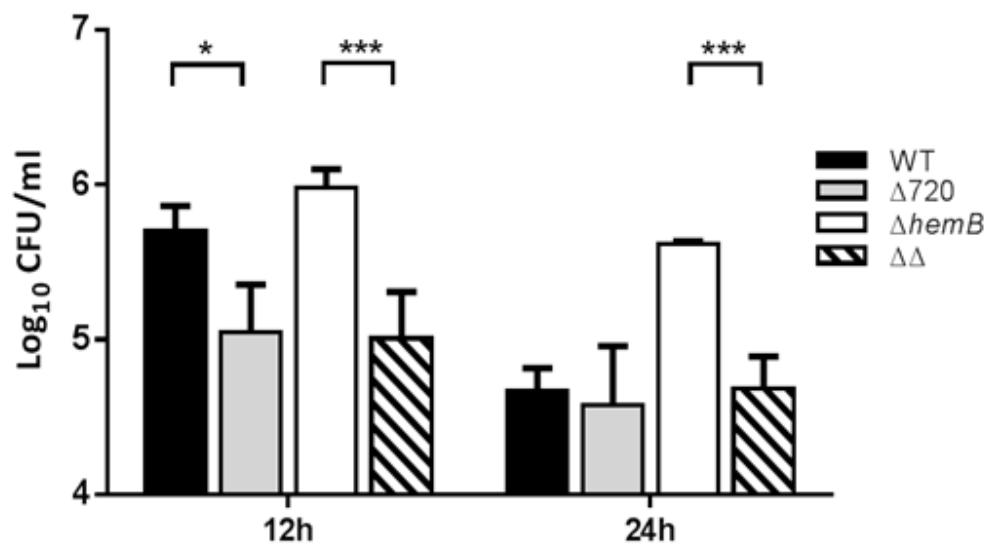


FIG. 9C

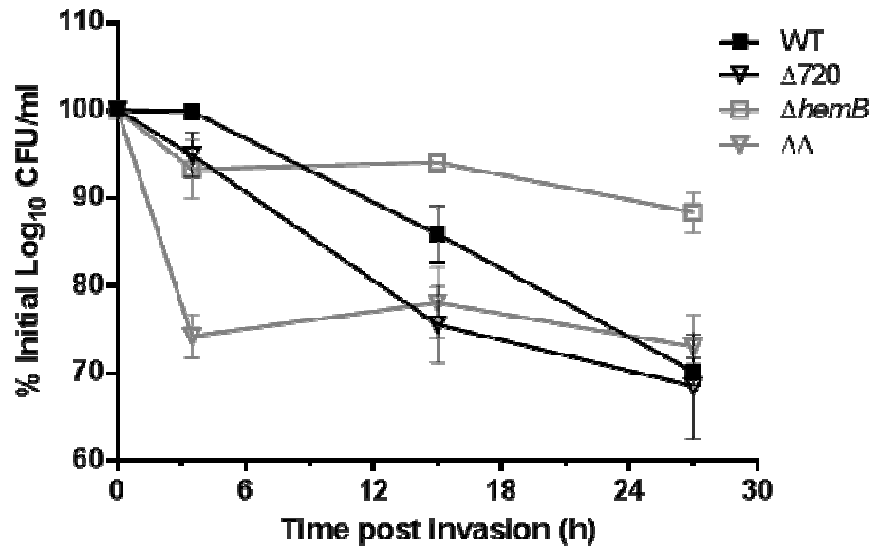


FIG. 10

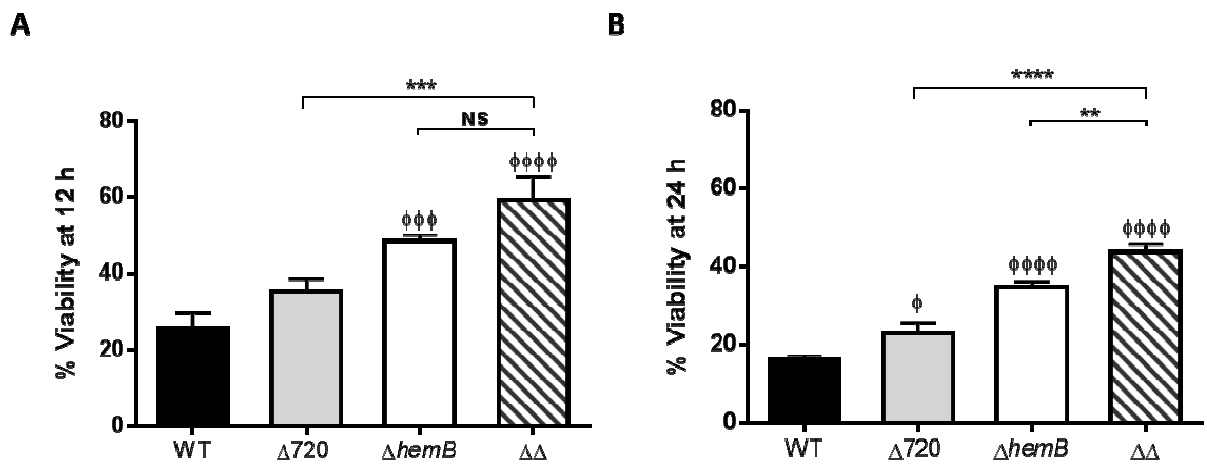


FIG. 11

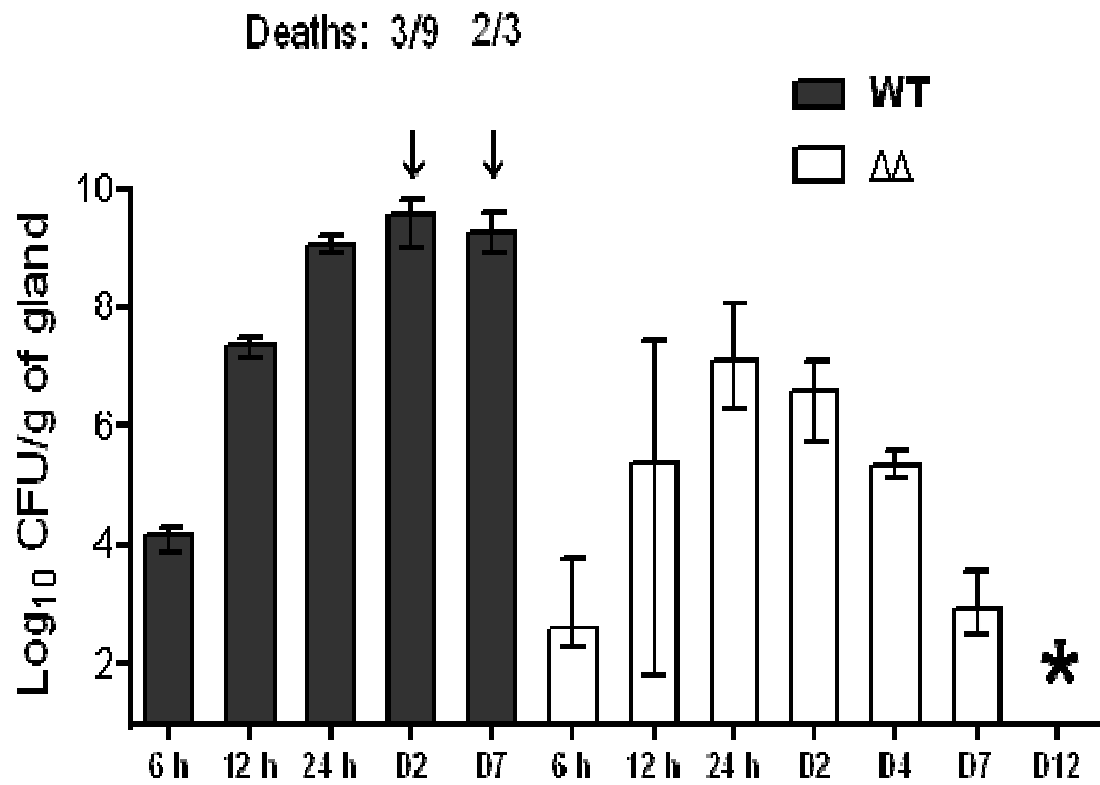


FIG. 12

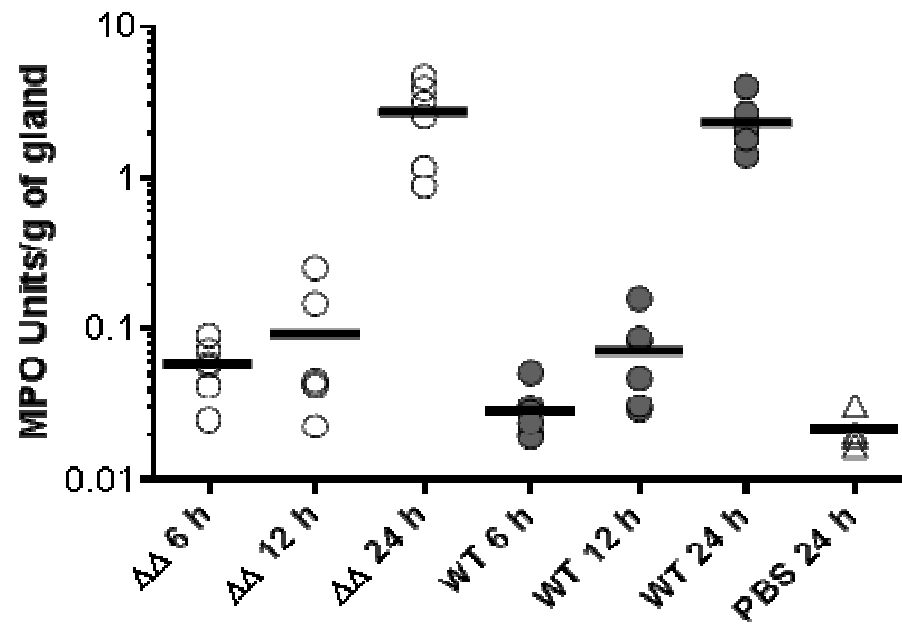


FIG. 13

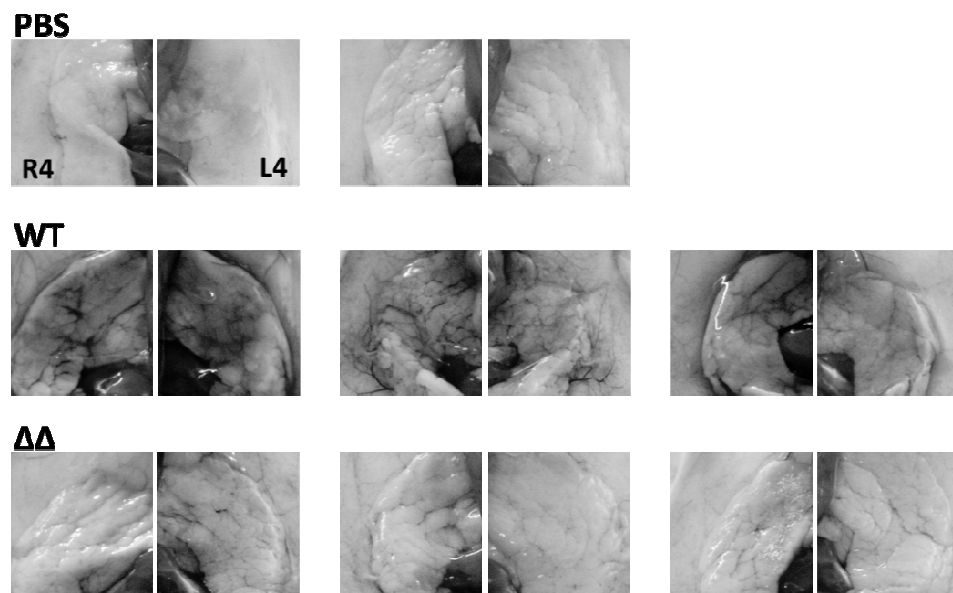


FIG. 14

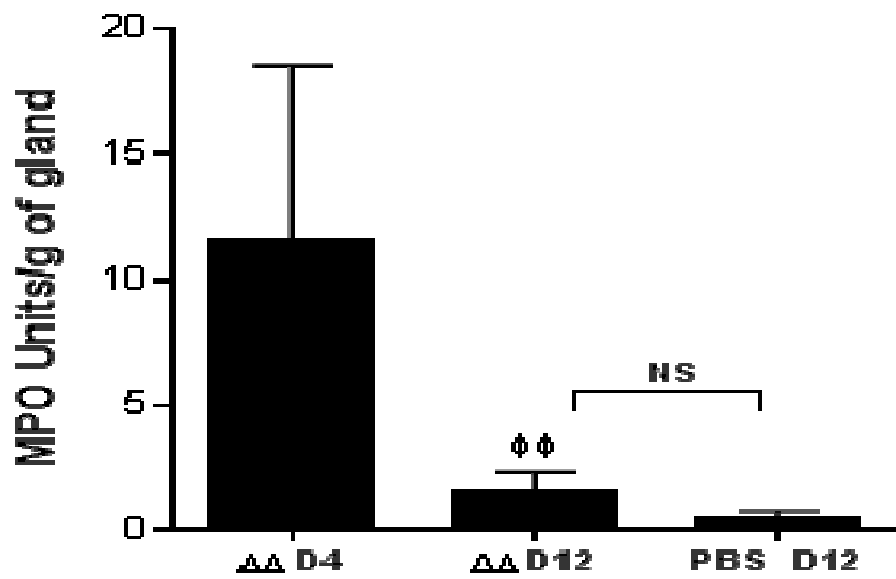


FIG. 15A

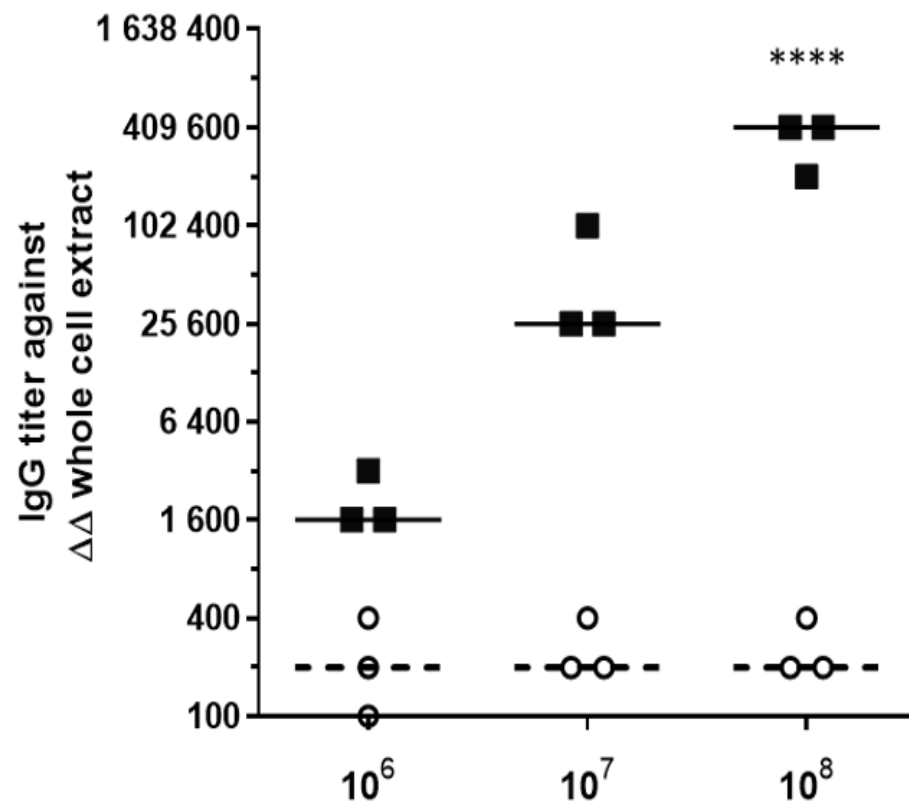


FIG. 15B

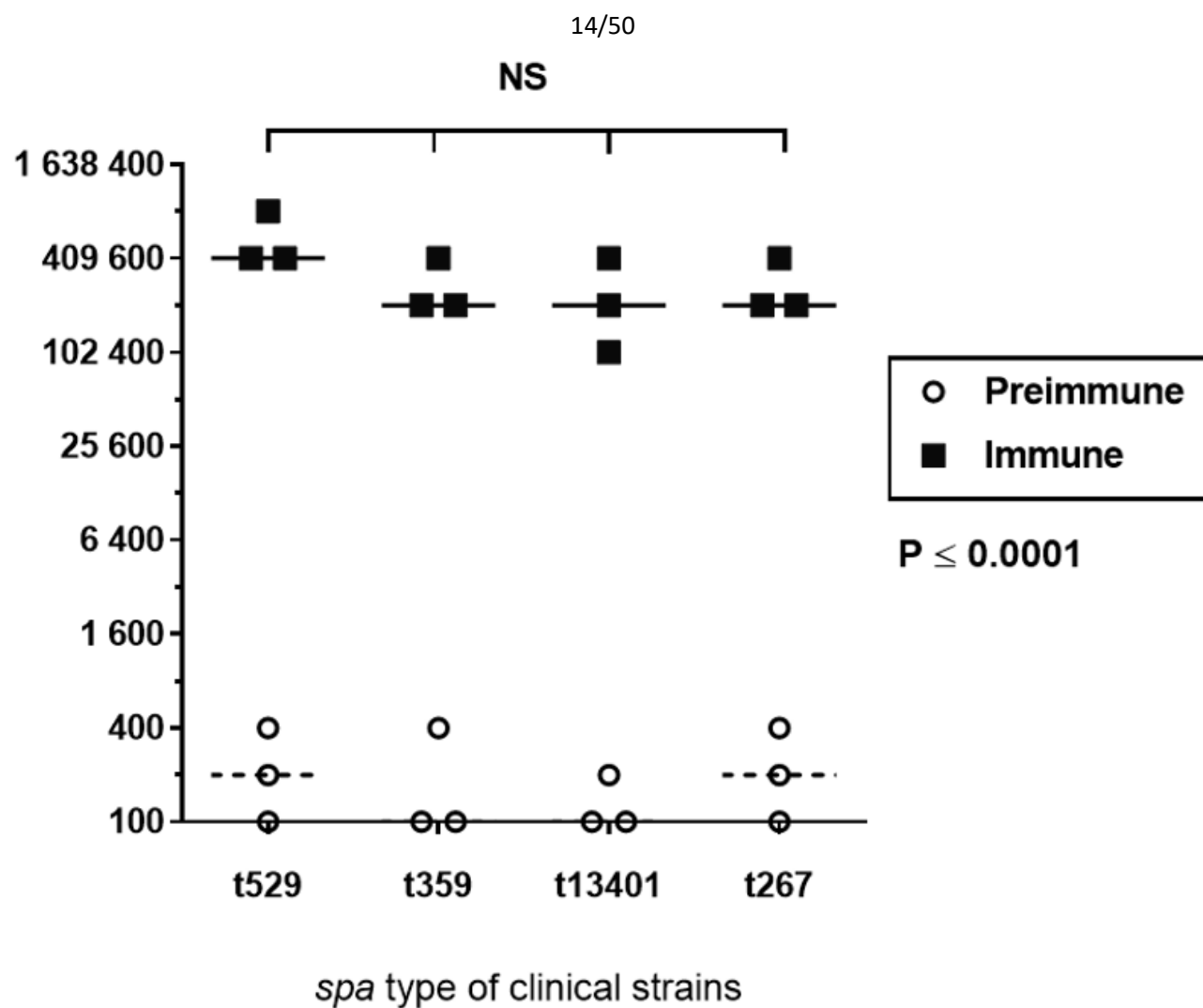


FIG. 15C



FIG. 16

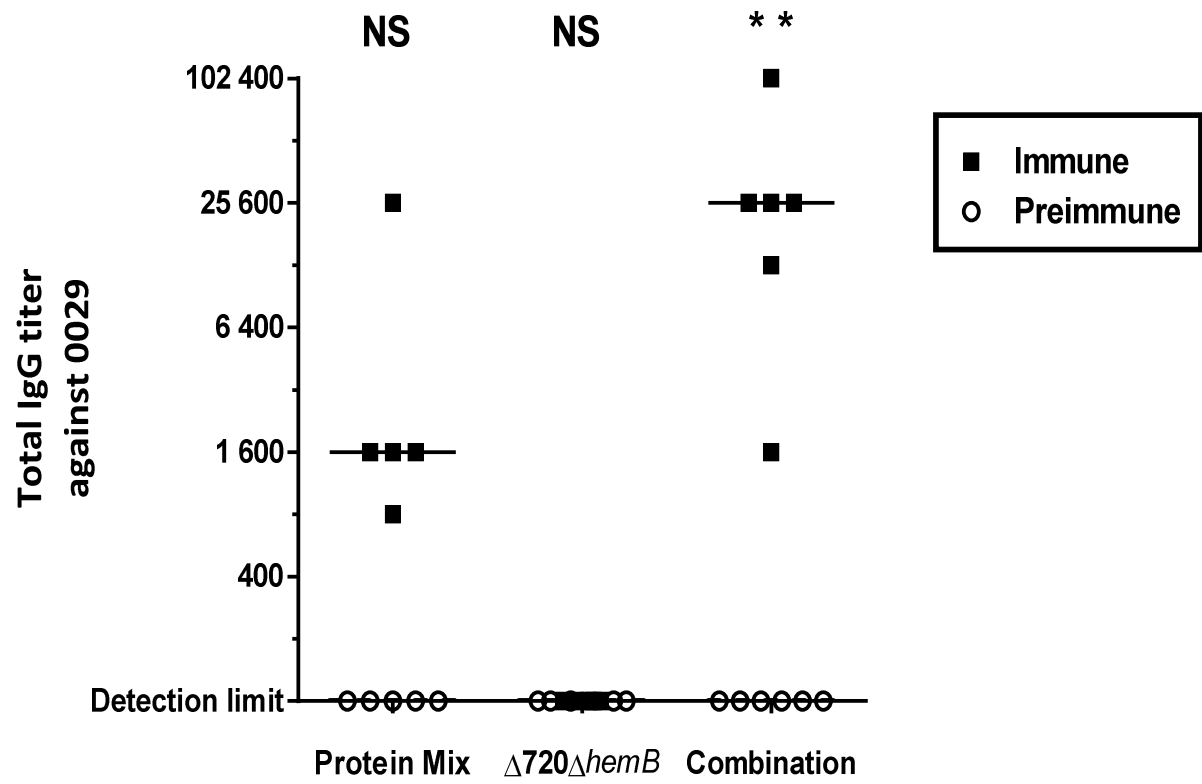


FIG. 17

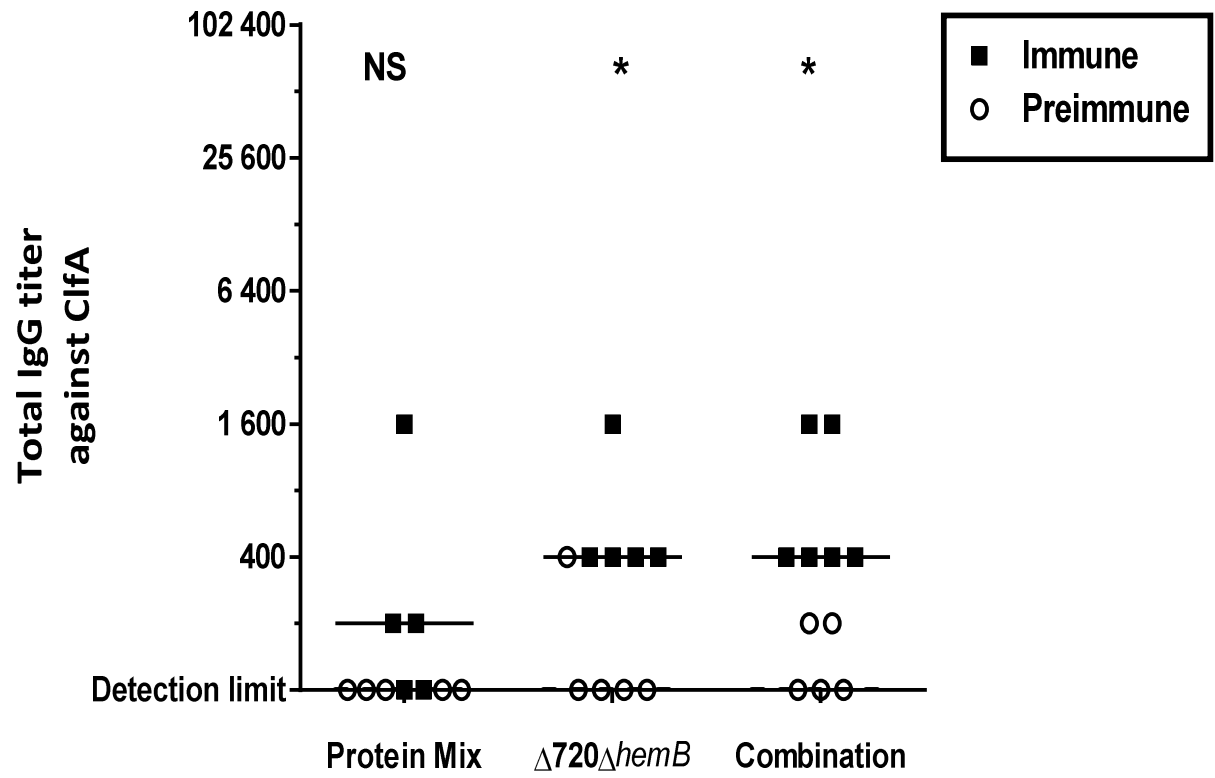


FIG. 18

18/50

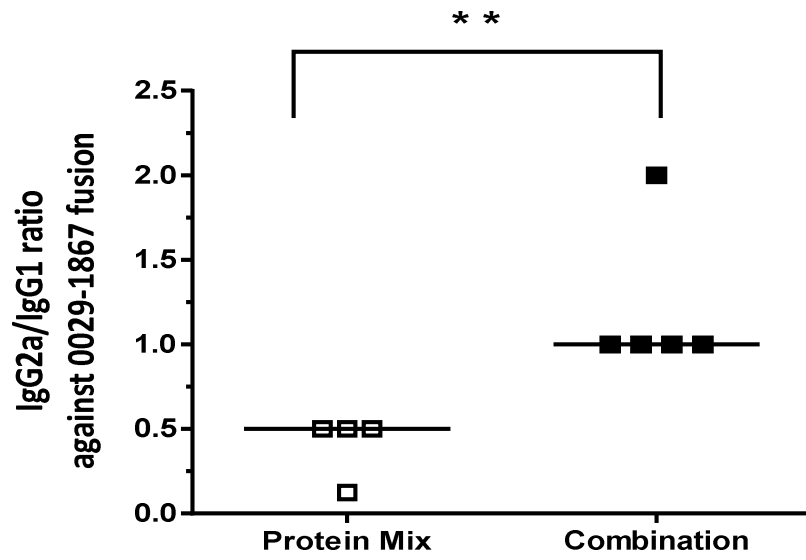


FIG. 19

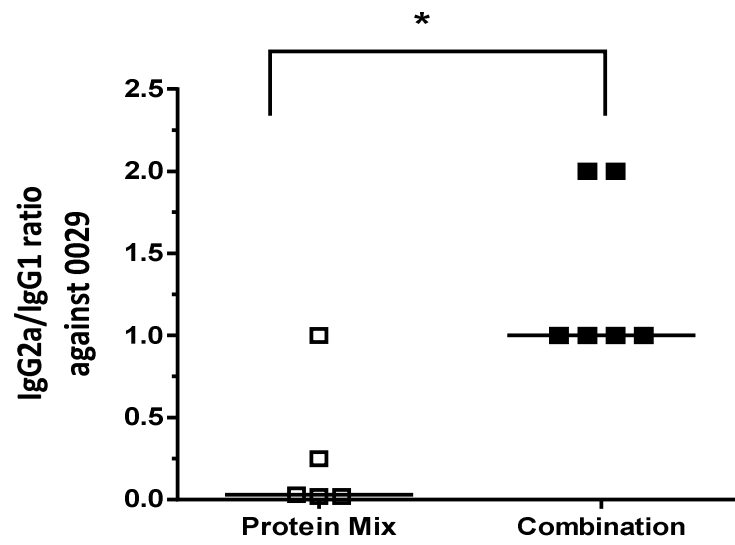


FIG. 20

I. SACOL0029

FULL LENGTH

POLYNUCLEOTIDE

>SEQ ID NO:4 (GENBANK GENE ID 3236748)

ATGCTAGAATCTAGAGAGCAATTATCAGTCGAAGAATACGAAACATTCTTTAACAGATTGATAATCAAGAATTTGATTTGGA
ACGTGAATTGACACAAGATCCATATTCAAAAGTATACTTATACAGTATAGAAGACCATATCAGAACATATAAGATAGAGAAAT
AA

POLYPEPTIDE

>SEQ ID NO: 5 (GENBANK PROTEIN ID YP_184940.1); Size: 55AA.

MLEESREQLSVEEYETFFFNRFDNQEFDFERELTQDPYSKVLYSIEDHIRTYKIEK

FRAGMENTS

>SEQ ID NO:6

CTAGAATCTAGAGAGCAATTATCAGTCGAAGAATACGAAACATTCTTTAACAGATTGATAATCAAGAATTTGATTTGGAACG
TGAATTGACACAAGATCCATATTCAAAAGTATACTTATACAGTATAGAAGACCATATCAGAACATATAAGATAGAGAAATAA

>SEQ ID NO:7; localization in full length SACOL0029: 2-55; size: 54 AA.

LESREQLSVEEYETFFFNRFDNQEFDFERELTQDPYSKVLYSIEDHIRTYKIEK

VARIANT

>SEQ ID NO:8; Comprising a SACOL0029 fragment localized in the full length SACOL0029: 2-55.
The polyhistidine is double underlined.

MHHHHHHLESREQLSVEEYETFFFNRFDNQEFDFERELTQDPYSKVLYSIEDHIRTYKIEK

>SEQ ID NO:9; Comprising a SACOL0029 fragment localized in the full length SACOL0029: 2-55.
The RGS-polyhistidine-GS tag is double underlined.

MRGSHHHHHHGSLESREQLSVEEYETFFFNRFDNQEFDFERELTQDPYSKVLYSIEDHIRTYKIEK

FIG. 21A

II. SACOL0720FULL LENGTHPOLYNUCLEOTIDE

>SEQ ID NO: 10 (GENBANK GENE ID 3236600).

ATGACCTTTAACGAGATAATATTTAAAAATTTCCGTCAAATTTATCACATTATGCCATCTATCTTTTTTCGTTAATTACGAG
 TGTAGTATTGTATTTTAGCTTTGTAGCATTAAAATACGCTCATAAACTAAACATGACAGAGTCATATCCAATTATAAAGGAAG
 GCTCACAAGTCGGAAGCTACTTTCTATTTTTCATCATAATTGCATTTTGTATATGCCAATGTGTTATTTATTAAACGACGA
 AGTTATGAGCTTGCATTATATCAAACATTAGGTTTATCTAAATTCAACATTATTTATATACTAATGCTCGAACAATTACTAAT
 ATTTATAATTACGGCAATATTAGGTATTATTATTGGTATTTTGGTTCGAACTGTTATTAATGATTGTCTTTACATTATTAG
 GAATTAAGAAAAAGGTTCCAATTATTTTATGTTTGGGGCGGTATTTGAAACATTAATGTTAATCGGTGTGCGTTATTTTTTA
 ACATCTGCTCAAAAATTTTATATTAGTGTTCAAACAATCTATTTACAGATGTCAAAGAATAACCAGGTTAAAGAAACAAATCA
 TAATAAAATTACATTTGAAGAGGTTGTTTTAGGCATCTTAGGTATAGTATTGATTACCACAGGATACTATCTATCTTTGAACA
 TTGTTCAATATTATGATTCTATCGGTACACTTATGTTTATTTTATTGTCAACTGTGATTGGGGCATACTTATTTTTTAAAGC
 TCTGTTTCTCTAGTTTTTAAAATGGTGAAGAAGTTTAGAAAAGGTGTTATAAGTGTAATGATGTCATGTTCTCATCATCTAT
 TATGTATCGTATTAAGAAAAATGCTTTTTCACTTACGGTCATGGCAATCATTTTCAGCGATTACTGTTTCAGTTCTTTGCTTTG
 CTGCTATAAGTAGAGCGTCCTTATCAAGTGAAATAAAATATACTGCACCACACGACGTTACAATTAAAGACCAACAAAAAGCT
 AATCAATTAGCAAGTGAATTAACAATCAAAAAATTCCTCATTTTTATAATTATAAAGAAAGTAATTCATACGAAATTGTATAA
 AGATAATTTATTTGATGTAAAAGCGAAAGAACCATAACAATGTAACAATTACTAGTGATAAATACATCCCTAATACTGATTTGA
 AACGTGGGCAAGCTGATTTATTTGTAGCGGAAGGTTCTATCAAAGATTTAGTGAACATAAGAAGCATGGTAAGGCAATTATA
 GGAACGAAAAAACATCATGTTAATATTAAGTTACGTAAAGATATTAATAAAATCTATTTTATGACAGATGTTGATTTAGGTGG
 ACCAACGTTTGTCTTAAATGACAAAGACTATCAAGAAATAAGAAAGTATACAAAGGCAAGCATATCGTCTCTCAATTTGGAT
 TCGATTTGAAACATAAAAAAGATGCTTTAGCATTAGAAAAAGCGAAAAATAAAGTTGATAAATCTATTGAAACAAGAAGTGAA
 GCGATAAGCTCAATATCAAGTTTAAACCGGAATATTATTATTTGTAACATCATTTTTAGGTATTACATTCTTGATTGCTGTATG
 TTGCATTATATACATAAAGCAAATAGATGAAACCGAAGATGAGTTAGAGAATTATAGTATTTTGAGAAAGCTTGGATTTACAC
 AAAAAAGATATGGCAAGGGGACTAAAGTTTAAATTATGTTTAATTTGGGTTACCTTTAGTTATTGCACTATCACATGCATAT
 TTTACATCATTAGCATATATGAAATTAATGGGTACAACGAATCAAATACCGGTTTTCATAGTAATGGGATTATACATTTGTAT
 GTATGCTGTTTTTGCAGTGACGGCTTATAATCATTCCAAGCGAACATTAGACATTCCATATAA

POLYPEPTIDE

> SEQ ID NO: 11 (GENBANK PROTEIN ID YP_185601.1); Size: 629AA.

MTFNEIIFKNFRQNLSHYAIYLFSLITSVVLYFSFVALKYAHKLNMTESYPIIKEGSQVGSYFLFFIIIAFLLYANVLFIKRR
 SYELALYQTLGLSKFNIIYILMLEQLLIFIITAILGIIIGIFGSKLLLMIVFTLLGIKEKVPIIFSLRAVFETLMLIGVAYFL
 TSAQNFIILVFKQSISSQMSKNNQVKETNHNKITFEEVVLGILGIVLITGGYYLSLNIVQYYDSIGTLMFILLSTVIGAYLFFKS
 SVSLVFKMVKKFRKGVISVNDVMFSSSIMYRIKKNASLTVMAIISAITVSVLCFAAISRASLSSEIKYTAPHDVTIKDQQKA
 NQLASELNNQKIPHFYNYKEVIHTKLYKDNLFVKAKEPYNVTITSDKYIPNTDLKRGQADLFVAEGSIKDLVKHKKHKGKAI
 GTKKHHVNIKLKDKINKIYFMTDVDLGGPTFVLNDKDYQEIRKYTKAKHIVSQFGFDLKHKKDALALEKAKNKVDKSIETRSE
 AISSISSLTGILLFVTSFLGITFLIAVCCIIYIKQIDETELENYSILRKLGFTQKDMARGLKFKIMFNFGPLPLVIALSHAY
 FTSLAYMKLMGTTNQIPVFI VMGLYICMYAVFAVTAYNHSKRTIRHSI

FIG. 21B

FRAGMENTS

>SEQ ID NO : 12 ; localization in full length SACOL0720: 309-508; size: 200 AA.

RASLSSEIKYTAPHDV**TIKDQQKANQLASE**LNNQKIPHFYNYKEVIHTKLYKDNLFDVKAKEPYNVTITSDKYIPNTDLKRGQAD
LFVAEGSIKDLVKHKKHGKAIIGTKKHHVNIKL**RKDINKIYFMTD**VDLGGPTFVLNDKDYQEIRKYTKAKHIVSQFGFDLKHKKDA
LALEKAKNKVDKSIETRSEAISSISLTG

>SEQ ID NO : 13; localization in full length SACOL0720: 310-508; size: 199 AA.

ASLSSEIKYTAPHDV**TIKDQQKANQLASE**LNNQKIPHFYNYKEVIHTKLYKDNLFDVKAKEPYNVTITSDKYIPNTDLKRGQADL
FVAEGSIKDLVKHKKHGKAIIGTKKHHVNIKL**RKDINKIYFMTD**VDLGGPTFVLNDKDYQEIRKYTKAKHIVSQFGFDLKHKKDAL
ALEKAKNKVDKSIETRSEAISSISLTG

>SEQ ID NO : 14 ; localization in full length SACOL0720: 310-455; size: 146 AA.

ASLSSEIKYTAPHDV**TIKDQQKANQLASE**LNNQKIPHFYNYKEVIHTKLYKDNLFDVKAKEPYNVTITSDKYIPNTDLKRGQADL
FVAEGSIKDLVKHKKHGKAIIGTKKHHVNIKL**RKDINKIYFMTD**VDLGGPTFVLNDKDYQE

>SEQ ID NO : 15 ; localization in full length SACOL0720: 428-481; size: 54 AA.

KDINKIYFMTDVDLGGPTFVLNDKDYQEIRKYTKAKHIVSQFGFDLKHKKDALA

>SEQ ID NO : 16 ; localization in full length SACOL0720: 428-452; size: 25 AA.

KDINKIYFMTDVDLGGPTFVLNDKD

>SEQ ID NO : 17 ; localization in full length SACOL0720: 428-453; size: 26 AA.

KDINKIYFMTDVDLGGPTFVLNDKDY

>SEQ ID NO : 18 ; localization in full length SACOL0720: 467-481; size: 15 AA.

SQFGFDLKHKKDALA

>SEQ ID NO : 19 ; localization in full length SACOL0720: 428-450; size: 23 AA.

KDINKIYFMTDVDLGGPTFVLND

>SEQ ID NO : 20 ; localization in full length SACOL0720: 463-481; size: 19 AA.

KHIVSQFGFDLKHKKDALA

>SEQ ID NO : 21 ; localization in full length SACOL0720: 468-481; size: 14 AA.

QFGFDLKHKKDALA

>SEQ ID NO : 22 ; localization in full length SACOL0720: 325-337; size: 13 AA.

FIG. 21C

TIKDQQKANQLAS

>SEQ ID NO : 23 ; localization in full length SACOL0720: 428-441; size: 14 AA.

KDINKIYFMTDVDL

>SEQ ID NO : 24 ; localization in full length SACOL0720: 438-450; size: 13 AA.

DVDLGGPTFVLND

VARIANT

>SEQ ID NO: 25 with polyhistidine in N-terminus; Comprises fragment localized in full length SACOL0720 at positions 310-455. The polyhistidine is double underlined.

MHHHHHHASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNYKEVIHTKLYKDNLFDVKAKEPYNVTITSDKYIPNTDLKRGQADL
FVAEGSIKDLVKHKKHGKAIIGTKKHHVNIKLKDKINKIYFMTDVDLGGPTFVLNDKDYQE

>SEQ ID NO: 26 with polyhistidine in N-terminus; Comprises fragment localized in full length SACOL0720 at positions 310-455. The RGS-polyhistidine-GS tag is double underlined.

MRGSHHHHHHGSASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNYKEVIHTKLYKDNLFDVKAKEPYNVTITSDKYIPNTDL
KRGQADLFVAEGSIKDLVKHKKHGKAIIGTKKHHVNIKLKDKINKIYFMTDVDLGGPTFVLNDKDYQE

>SEQ ID NO: 27 Comprises fragments localized in full length SACOL0720 at positions 428-450 and 463-481. Size: 50 AA. The underlined sequence is variant vs. native sequence. The remaining portions are native.

KDINKIYFMTDVDLGGPTFVLNDKDYERKYKHHIVSQFGFDLKHKKDALA

III. SACOL0442

FULL LENGTH

POLYNUCLEOTIDE

>SEQ ID NO:28(GENBANK GENE ID 3236485).

ATGTTCAAAAAATATGACTCAAAAAATTCATCGTATTAAATCTATTCTATCGCTAGGTATCATCTATGGGGGAACATTTGGAATATATCC
AAAAGCAGACGCGTCAACACAAAATTCCTCAAGTGACAAAGATAAACAATTACAAAAAGTTGAAGAAGTACCAAATAATTCAGAAAAAGCTT
TGGTTAAAAAACTTTACGATAGATACAGCAAGGATACAATAAATGGAAAATCTAATAAATCTAGGAATTGGGTTTATTCAGAGAGACCTTTA
AATGAAAACCAAGTTCGTATACATTTAGAAGGAACATACACAGTTGCTGGCAGAGTGATACACCTAAGAGGAATATTACTCTTAATAAAGA
AGTTGTCACTTTAAAGAATTGGATCATATCATAAGATTTGCTCATATTTCTATGGCTTGATATGGGAGAACATTTGCCTAAAGGTAACA
TCGTCATAAATACAAAAGATGGTGGTAAATATACATTAGAGTCGCATAAAGAGCTACAAAAAGATAGGGAAAATGTAAAAATTAATACAGCC
GATATAAAAAATGTAACCTTCAAACCTGTGAAAAGTGTTAATGACATTGAACAAGTTTGA

POLYPEPTIDE

>SEQ ID NO: 29 (GENBANK PROTEIN ID YP_185332.1); Size:203AA.

MFKKYDSKNSIVLKSILSLGIYGGTFGIYPKADASTQNSSSVQDKQLQKVEEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPL
NENQVRIHLEGTYTVAGRVYTPKRNITLNKEVVTLLKELDHIIIRFAHISYGLYMGHELPKGNIVINTKDGGKYTLESHKELQKDRENVKINTA
DIKNVTFKLVKSVNDIEQV

FIG. 21D

FRAGMENTS

>SEQ ID NO: 30; localization in full length SACOL0442: 36-203; Size: 168 AA.

STQNSSSVQDKQLQKVEEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVAGRVYTPKRNI
TLNKEVVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKDGGKYTLESHKELQKDRENVKINTADIKNVTFLVKSVNDIE
QV

>SEQ ID NO: 31; localization in full length SACOL0442: 44-159; Size: 116 AA.

QDKQLQKVEEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVAGRVYTPKRNITLNKEVVTL
LKELDHIIIRFAHISYGLYMGEHLPKGNIVINTK

>SEQ ID NO: 33; localization in full length SACOL0442: 45-203; Size: 159 AA.

DKQLQKVEEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVAGRVYTPKRNITLNKEVVTL
KELDHIIIRFAHISYGLYMGEHLPKGNIVINTKDGGKYTLESHKELQKDRENVKINTADIKNVTFLVKSVNDIEQV

> SEQ ID NO: 34 ; localization in full length SACOL0442: 72-85; Size: 14 AA.

KDTINGKSNKSRNW

> SEQ ID NO: 1 ; localization in full length SACOL0442: 159-173; Size: 15 AA.

KDGGKYTLESHKELQ

VARIANTS

>SEQ ID NO: 35 ; Comprises fragment localized in full length SACOL0442 at positions 45-203. The polyhistidine is double underlined.

MHHHHHHDKQLQKVEEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVAGRVYTPKRNITL
NKEVVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKDGGKYTLESHKELQKDRENVKINTADIKNVTFLVKSVNDIEQV

>SEQ ID NO: 36 ; Comprises fragment localized in full length SACOL0442 at positions 45-203. The RGS-polyhistidine-GS tag is double underlined.

MRGSHHHHHHGSDKQLQKVEEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVAGRVYTPK
RNITLNKEVVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKDGGKYTLESHKELQKDRENVKINTADIKNVTFLVKSVN
DIEQV

FIG. 21E

IV. SACOL1867

FULL LENGTH

POLYNUCLEOTIDE

>SEQ ID NO: 37 (GENBANK GENE ID 3236101).

ATGAATAAAAAATATAGTCATTAAAAGCATGGCAGCATTAGCCATTCTAACCTCAGTAACTGGAATAAATGCTGCAGTCGTTGA
AGAGACACAACAAATAGCAAATGCAGAGAAGAATGTTACGCAAGTTAAAGATACAAATATTTTTCCATATAATGGCGTCGTTT
CATTTAAAGATGCGACAGGTTTTGTAATTGGAATAAATACAATTATCACCAATAAACATGTATCAAAAGATTATAAAGTTGGC
GATAGAATTACTGCCCATCCAAACGGTGACAAAGGAAATGGTGGTATATATAAAATTTAAAGCATTCTGATTATCCGGGTGA
TGAAGACATCTCTGTCATGAATATTGAAGAACAAGCAGTCGAACGTGGACCAAAAGGCTTTAATTTTAATGAAAATGTCCAAG
CATTCAATTTTGCGAAAGATGCTAAAGTTGATGACAAAATTAAGTTATTGGTTACCCATTACCTGCTCAAAATAGTTTTAA
CAGTTTGAATCTACAGGAAGTATAAAAAGAATCAAAGACAATATTTTAAATTTTATGATGCATACATTGAACCCGGGAATTCAGG
ATCACCAGTTCTAAATTCTAACAATGAGGTGATAGGTGTGGTGTATGGCGGTATTGGAAAAATTGGTTCTGAATATAATGGTG
CCGTATACTTTACGCCTCAAATCAAAGATTTTATTCAAAGCACATTGAACAATAA

POLYPEPTIDE

>SEQ ID NO: 38 (GENBANK PROTEIN ID YP_186695.1); Size: 239 AA.

MNKNIVIKSMAALAILTSVTGINAAVVEETQOIANAEKNVTQVKDTNIFPYNGVVSFKDATGFVIGKNTIITNKHVSKDYKVG
DRITAHPNGDKGNNGGIYIKSISDYPGDEDISVMNIEEQAVERGPKGFNFNENVQAFNFAKDAKVDDKIKVIGYPLPAQNSFK
QFESTGTIKRIKDNILNFDAYIEPGNSGSPVLNSNNEVIGVVYGGIGKIGSEYNGAVYFTPQIKDFIQKHIEQ

FRAGMENTS

>SEQ ID NO: 39; localization in full length SACOL1867: 41-239; Size: 199 AA.

TQVKDTNIFPYNGVVSFKDATGFVIGKNTIITNKHVSKDYKVGDRITAHPNGDKGNNGGIYIKSISDYPGDEDISVMNIEEQA
VERGPKGFNFNENVQAFNFAKDAKVDDKIKVIGYPLPAQNSFKQFESTGTIKRIKDNILNFDAYIEPGNSGSPVLNSNNEVIG
VVYGGIGKIGSEYNGAVYFTPQIKDFIQKHIEQ

VARIANT

>SEQ ID NO: 40; Comprises fragment localized in full length SACOL1867 at positions 41-239.
Polyhistidine double underlined.

MHHHHHTTQVKDTNIFPYNGVVSFKDATGFVIGKNTIITNKHVSKDYKVGDRITAHPNGDKGNNGGIYIKSISDYPGDEDISV
MNIEEQAVERGPKGFNFNENVQAFNFAKDAKVDDKIKVIGYPLPAQNSFKQFESTGTIKRIKDNILNFDAYIEPGNSGSPVLN
SNNEVIGVVYGGIGKIGSEYNGAVYFTPQIKDFIQKHIEQ

>SEQ ID NO: 41; Comprises fragment localized in full length SACOL1867 at positions 41-239. The
RGS-polyhistidine-GS tag is double underlined.

MRGSHHHHHHGSTQVKDTNIFPYNGVVSFKDATGFVIGKNTIITNKHVSKDYKVGDRITAHPNGDKGNNGGIYIKSISDYPGD
EDISVMNIEEQAVERGPKGFNFNENVQAFNFAKDAKVDDKIKVIGYPLPAQNSFKQFESTGTIKRIKDNILNFDAYIEPGNSG
SPVLNSNNEVIGVVYGGIGKIGSEYNGAVYFTPQIKDFIQKHIEQ

FIG. 21F

V. SACOL1912

FULL LENGTH

POLYNUCLEOTIDE

>SEQ ID NO: 42 (GENBANK GENE ID 3236086).

ATGGCAATGAACCTTTAAAGTCTTTGACAATAGTCAACTTGTAGCAGAATATGCTGCTGATATTATTAGAAAGCAATTTAACAA
TAATCCTACTACAATTGCAGGTTTTTCATTTAGATACAGATCAAGCGCCAGTTCTAGATGAATTAAAGAAAAATGTTGAAAAAC
ATGCTGTTGATTTTAGCCAAATAAATATTTTAGATTATGACGATAAAAAATCATATTTTGAAGCGTTAGGTGTACCAGCAGGT
CAAGTTTATCCAATTGCTTATGAAAAAGATGCAATCGAATTAATCGCTGATAAGATTAAACTAAAGAAAAATAAAGGGAAATT
AACATTACAAGTTGTTTCTATCGATGAGCAAGGTAAGTTAAATGTTAGTATTCTGCAAGGACTAATGGAAGCAAGAGAAATTT
TCTTAGTAGTGACAGGTGCTAATAAACGAGATGTAGTTGAAAAATTATATCAAGAAAAATGGTAAACAAGCTTCGAACCAGCC
GATTTAAAGCACATAGAATGGTAAATGTTATTCTTGATAAAGAAGCGGCTGCAGGTTTACCTGAAGATGTTAAAGCTTACTT
TACGTCACGCTTTGCTTAA

POLYPEPTIDE

>SEQ ID NO: 43 (GENBANK PROTEIN ID YP_186737.1); Size: 199AA.

MAMNFKVFDNSQLVAEYAADIIIRKQFNNNPPTTIAGFHLDTDQAPVLDELKKNVEKHAVDFSQINILDYDDKKS~~YFEALGVPAG~~
~~QVYP~~IAYEKDAIELIADKIKTKENKGLTLQVVSIDEQGKLNVSIRQGLMEAREIFLVVTGANKRDRVVEKLY~~QENGKTSFEPADL~~
DLKAHRMVNVILDKEAAAGLPEDVKAYFTSRFA

VARIANT

>SEQ ID NO: 44 ; Comprises full length SACOL1912. The polyhistidine is double underlined.

M~~HHHHHH~~MAMNFKVFDNSQLVAEYAADIIIRKQFNNNPPTTIAGFHLDTDQAPVLDELKKNVEKHAVDFSQINILDYDDKKS~~YFE~~
~~ALGVPAGQVYP~~IAYEKDAIELIADKIKTKENKGLTLQVVSIDEQGKLNVSIRQGLMEAREIFLVVTGANKRDRVVEKLY~~QENG~~
~~KTSFEPADL~~KAHRMVNVILDKEAAAGLPEDVKAYFTSRFA

VI. SACOL2385

FULL LENGTH

POLYNUCLEOTIDE

> SEQ ID NO: 49 (GENBANK GENE ID 3238646).

ATGATATTGAACTTCAATCAATTCGAGAATCAAACTTTTTTAACGGTAATCCAAGTGATACATTTAAAGATTTAGGTAAACA
AGTATTTAATTACTTTTCAACACCTTCATTTGTAACGAATATATATGAAACAGACGAATTATATTACTTAGAAGCTGAAGTAG
CAGGTGTAAATAAAGAAGATATTAGTATCGATTTCAATAATAATACGCTCACTATTCAAGCTACTAGAAGCGCAAAATACAAA
TCTGAACAACCTCATTTTAGATGAGCGTAACTTCGAATCATTAAATGCGTCAATTTGATTTTGAAGCTGTTGATAAGCAACATAT
TACTGCTAGTTTTGAAAAATGGGTTATTAACCATTACCTTGCCATAAATCAAACCAAGCAATGAACTACTTCATCAACATCTA
TTCCAATTTTCATAG

FIG. 21G

POLYPEPTIDE

> SEQ ID NO: 50 (GENBANK PROTEIN ID YP_187189.1); Size: 93AA.

MILNFNQFENQNFFNGNPSDTFKDLGKQVFNYFSTPSFVTNIYETDELYYLEAELAGVNKEDISIDFNNNTLTIQATRSACYK
 SEQLILDERN

VARIANT

>SEQ ID NO: 51; Comprises full length SACOL2385.

MHHHHHMHILNFNQFENQNFFNGNPSDTFKDLGKQVFNYFSTPSFVTNIYETDELYYLEAELAGVNKEDISIDFNNNTLTIQA
 TRSAKYKSEQLILDERN

VII. FUSIONS

>SACOL0029-1867 (1)

POLYNUCLEOTIDE

>SEQ ID NO: 54

CTAGAATCTAGAGAGCAATTATCAGTCGAAGAATACGAAACATTCTTTAACAGATTGATAATCAAGAATTTGATTTGGAACG
 TGAATTGACACAAGATCCATATTCAAAAGTATACTTATACAGTATAGAAGACCATATCAGAACATATAAGATAGAGAAAGGAG
 GTGGCGGTTTCAGGAGGTGGAGGATCTGGAGGCGGTGGATCA**ACGCAAGTTAAAGATACAAATATTTTCCATATAATGGCGTC**
GTTTCATTTAAAGATGCGACAGGTTTTGTAATTGGAAAAAATACAATTATCACCAATAAACATGTATCAAAAGATTATAAAGT
TGGCGATAGAATTACTGCCCATCCAAACGGTGACAAAGGAAATGGTGGTATATATAAAATTTAAAGCATTCTGATTATCCGG
GTGATGAAGACATCTCTGTCTATGAATATTGAAGAACAAGCAGTCGAACGTGGACCAAAAGGCTTTAATTTTAATGAAAATGTC
CAAGCATTCAATTTTGCAGAAAGATGCTAAAGTTGATGACAAAATTAAAGTTATTGGTTACCCATTACCTGCTCAAAATAGTTT
TAAACAGTTTGAATCTACAGGAACTATAAAAAGAATCAAAGACAATATTTTAAATTTTGTATGCATACATTGAACCCGGAATT
CAGGATCACCAGTTCTAAATTCTAACAATGAGGTCATAGGTGTGGTGTATGGCGGTATTGGAAAAATTGGTTCTGAATATAAT
GGTGCCGTATACTTTACGCCTCAAATCAAAGATTTTATTCAAAGCACATTGAACAATAA

POLYPEPTIDE

>SEQ ID NO: 55; Size: 268AA.

LESREQLSVEEYETFFNFRDNQ**EFDFERELTQDPYS**KVLYLSIEDHIRTYKIEKGGGSGGGSGGGGS**TQVKDTNIFPYNGV**
VSFKDATGFVIGKNTIITNKHVSKDYKVGDRITAHPNGDKGNGGIYKIKSISDYPGDEDISVMNIEEQAVERGPKGFNFENV
QAFNFAKDAKVDDKIKVIGYPLPAQNSFKQFESTGTIKRIKDNILNFDAYIEPGNSGSPVLNSNNEVIGVVYGGIGKIGSEYN
 GAVYFTPQIKDFIQKHIEQ

FIG. 21H

>SACOL0029-1867 (2)

POLYNUCLEOTIDE

>SEQ ID NO: 56

ATGCCACCACCACCACCACCACCCTGGAATCCCGTGAACAACCTGTCCGTGGAAGAATACGAAACCTTCTTTAACCGCTTTGATAACCAAGAATT
TGATTTTGAACGTGAACCTGACCCAGGATCCGTATTCTAAAGTGTATCTGTACAGTATCGAAGATCATATTCGCACGTACAAAATCGAAAAAG
CGGGTGGCGGTTCTGGCGGTGGCGGTAGTGGCGGTGGCGGTAGCACCCAGGTGAAAGATACGAATATCTTTCCGTATAACGGCGTGGTTTCT
TTTAAAGATGCGACCGGCTTCGTTATCGGTAAAAACACCATCATCACGAACAAACATGTGAGCAAAGATTACAAAGTTGGCGATCGTATTAC
CGCCACCCGAATGGCGATAAGGGTAACGGCGGTATCTACAAAATCAAAGCATCTCTGATTACCCGGGTGATGAAGATATCAGCGTGATGA
ATATTGAAGAACAGGCAGTTGAACGGGCCCCGAAAGGTTTTAACTTCAATGAAACGTTCAAGCGTTTTAATTCGCGAAAGATGCCAAAGTG
GATGATAAAATCAAAGTTATTGGCTATCCGCTGCCGGCCAGAACAGCTTTAAACAGTTCGAATCTACCGGTACGATCAAACGTATCAAAGA
TAACATCCTGAACCTTCGATGCATATATTGAACCGGGCAATAGTGGTAGCCCGGTGCTGAACAGTAACAATGAAGTTATTGGTGTGGTTTATG
GCGGTATCGGCAAAATTGGTAGCGAATACAACGGTGCTGTGTATTTTACGCCGCAGATCAAAGACTTCATCCAGAAACATATCGAACAA

POLYPEPTIDE

>SEQ ID NO: 57; Size: 275AA. The polyhistidine is double underlined

MHHHHHLESREQLSVEEYETTFNRFDNQEFDFERELTQDPYSKVYLYSIEDHIRTYKIEKGGGSGGGSGGGGSTQVKDTNIFPYNGVVS
FKDATGFVIGKNTIITNKHVSKDYKVGDRITAHPNGDKGNGGIYKIKSISDYPGDEDISVMNIEEQAVERGPKGFNFNENVQAFNFAKDAKV
DDKIKVIGYPLPAQNSFKQFESTGTIKRIKDNILNFDAYIEPGNSGSPVLNSNNEVIGVVYGGIGKIGSEYNGAVYFTPQIKDFIQKHIEQ

>SEQ ID NO: 58; Size: 280AA. The RGS-polyhistidine-GS tag is double underlined.

MRGSHHHHHHGSLESREQLSVEEYETTFNRFDNQEFDFERELTQDPYSKVYLYSIEDHIRTYKIEKGGGSGGGSGGGGSTQVKDTNIF
PYNGVVSFKDATGFVIGKNTIITNKHVSKDYKVGDRITAHPNGDKGNGGIYKIKSISDYPGDEDISVMNIEEQAVERGPKGFNFNENVQAFN
FAKDAKVDDKIKVIGYPLPAQNSFKQFESTGTIKRIKDNILNFDAYIEPGNSGSPVLNSNNEVIGVVYGGIGKIGSEYNGAVYFTPQIKDFIQKHIEQ

>SACOL0720-720

POLYPEPTIDE

>SEQ ID NO: 27.

KDINKIYFMTDVDLGGPTFVLNDKDYERKYKHHIVSQFGFDLKHKKDALA

>SACOL00442-720

POLYPEPTIDE

>SEQ ID NO: 3.

KDGGKYTLESHKELQEAAAKEAAAKKDINKIYFMTDVDLGGPTFVLND

FIG. 211

VIII. LINKERSUsed in exemplified fusion SACOL0029-1867.POLYNUCLEOTIDE

>SEQ ID NO: 59

GGAGGTGGCGGTTTCAGGAGGTGGAGGATCTGGAGGCGGTGGATCA

POLYPEPTIDE

>SEQ ID NO: 60.

GGGGSGGGSGGGGS

POLYPEPTIDE Used in exemplified fusion SACOL00720-720

>SEQ ID NO: 61.

ERKYKPOLYPEPTIDE Used in exemplified fusion SACOL00442-720

>SEQ ID NO: 62.

EAAAKEAAAKOther exemplary linker polypeptides

>SEQ ID NO: 63.

EAAAK

>SEQ ID NO: 64.

EAAAKEAAAKEAAAK

>SEQ ID NO: 65.

ERKYKERKYK

>SEQ ID NO: 66.

ERKYKERKYKERKYK

>SEQ ID NO: 67.

GGGGS

>SEQ ID NO: 68.

GGGSGGGGS

>SEQ ID NO: 69.

XPXPXP wherein x may be any amino acid.

>SEQ ID NO: 70.

XPXPXPXPXP, wherein x may be any amino acid.

FIG. 21J

I- SACOL0442 : Multiple polynucleotide sequences alignment

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MW0345 (MW2) ATGTTCAAAAAAATGACTCGAAAAATTC AATTCTATTAAAAATCTATTCT 50
SAS0347 (MSSA476) ATGTTCAAAAAAATGACTCGAAAAATTC AATTCTATTAAAAATCTATTCT 50
SACOL0442 (COL) ATGTTCAAAAAAATATGACTCAAAAAATTC AATCGTATTAAAAATCTATTCT 50
SAOUHSC_00354 (NCTC8325) ATGTTCAAAAAAATATGACTCAAAAAATTC AATCGTATTAAAAATCTATTCT 50
NWMN_0362 (Newman) ATGTTCAAAAAAATATGACTCAAAAAATTC AATCGTATTAAAAATCTATTCT 50
SAUSA300_0370 (USA300-FPR3757) ATGTTCAAAAAAATATGACTCAAAAAATTC AATCGTATTAAAAATCTATTCT 50
SaurJH1_0429 (JH1) ATGTTCAAAAAAATATGACTCAAAAAATTC AATCGTATTAAAAATCTATTCT 50
SAHV_0367 (Mu3) ATGTTCAAAAAAATATGACTCAAAAAATTC AATCGTATTAAAAATCTATTCT 50
SaurJH9_0419 (JH9) ATGTTCAAAAAAATATGACTCAAAAAATTC AATCGTATTAAAAATCTATTCT 50
SAV0370 (Mu50) ATGTTCAAAAAAATATGACTCAAAAAATTC AATCGTATTAAAAATCTATTCT 50
SA0357 (N315) ATGTTCAAAAAAATATGACTCAAAAAATTC AATCGTATTAAAAATCTATTCT 50
SAB0321 (RF122) ATGTTCAAAAAAATATGACTCAAAAAATTC AATCGTATTAAAAATCTATTCT 50
*****

MW0345 (MW2) ATCGCTAGGTATCATCTATG GGGGAACATTGGAATATATCCAAAAGCAG 100
SAS0347 (MSSA476) ATCGCTAGGTATCATCTATG GGGGAACATTGGAATATATCCAAAAGCAG 100
SACOL0442 (COL) ATCGCTAGGTATCATCTATG GGGGAACATTGGAATATATCCAAAAGCAG 100
SAOUHSC_00354 (NCTC8325) ATCGCTAGGTATCATCTATG GGGGAACATTGGAATATATCCAAAAGCAG 100
NWMN_0362 (Newman) ATCGCTAGGTATCATCTATG GGGGAACATTGGAATATATCCAAAAGCAG 100
SAUSA300_0370 (USA300-FPR3757) ATCGCTAGGTATCATCTATG GGGGAACATTGGAATATATCCAAAAGCAG 100
SaurJH1_0429 (JH1) ATCGCTAGGTATCATCTATG GGGGAACATTGGAATATATCCAAAAGCAG 100
SAHV_0367 (Mu3) ATCGCTAGGTATCATCTATG GGGGAACATTGGAATATATCCAAAAGCAG 100
SaurJH9_0419 (JH9) ATCGCTAGGTATCATCTATG GGGGAACATTGGAATATATCCAAAAGCAG 100
SAV0370 (Mu50) ATCGCTAGGTATCATCTATG GGGGAACATTGGAATATATCCAAAAGCAG 100
SA0357 (N315) ATCGCTAGGTATCATCTATG GGGGAACATTGGAATATATCCAAAAGCAG 100
SAB0321 (RF122) ATCGCTAGGTATCATCTATG GGGGAACATTGGAATATATCCAAAAGCAG 100
*****

MW0345 (MW2) ACGCGTCAACACAAAAATTC CCAAGTGTAACAAGATAAAC AATTCCAAAAA 150
SAS0347 (MSSA476) ACGCGTCAACACAAAAATTC CCAAGTGTAACAAGATAAAC AATTCCAAAAA 150
SACOL0442 (COL) ACGCGTCAACACAAAAATTC CCAAGTGTAACAAGATAAAC AATTCCAAAAA 150
SAOUHSC_00354 (NCTC8325) ACGCGTCAACACAAAAATTC CCAAGTGTAACAAGATAAAC AATTCCAAAAA 150
NWMN_0362 (Newman) ACGCGTCAACACAAAAATTC CCAAGTGTAACAAGATAAAC AATTCCAAAAA 150
SAUSA300_0370 (USA300-FPR3757) ACGCGTCAACACAAAAATTC CCAAGTGTAACAAGATAAAC AATTCCAAAAA 150
SaurJH1_0429 (JH1) ACGCGTCAACACAAAAATTC CCAAGTGTAACAAGATAAAC AATTCCAAAAA 150
SAHV_0367 (Mu3) ACGCGTCAACACAAAAATTC CCAAGTGTAACAAGATAAAC AATTCCAAAAA 150
SaurJH9_0419 (JH9) ACGCGTCAACACAAAAATTC CCAAGTGTAACAAGATAAAC AATTCCAAAAA 150
SAV0370 (Mu50) ACGCGTCAACACAAAAATTC CCAAGTGTAACAAGATAAAC AATTCCAAAAA 150
SA0357 (N315) ACGCGTCAACACAAAAATTC CCAAGTGTAACAAGATAAAC AATTCCAAAAA 150
SAB0321 (RF122) ACGCGTCAACACAAAAATTC CCAAGTGTAACAAGATAAAC AATTCCAAAAA 150
*****

MW0345 (MW2) GTTGAAGAAGTACCAATAATTC AGAAAAAGCTTTGGTTAAAAAACTTTA 200
SAS0347 (MSSA476) GTTGAAGAAGTACCAATAATTC AGAAAAAGCTTTGGTTAAAAAACTTTA 200
SACOL0442 (COL) GTTGAAGAAGTACCAATAATTC AGAAAAAGCTTTGGTTAAAAAACTTTA 200
SAOUHSC_00354 (NCTC8325) GTTGAAGAAGTACCAATAATTC AGAAAAAGCTTTGGTTAAAAAACTTTA 200
NWMN_0362 (Newman) GTTGAAGAAGTACCAATAATTC AGAAAAAGCTTTGGTTAAAAAACTTTA 200
SAUSA300_0370 (USA300-FPR3757) GTTGAAGAAGTACCAATAATTC AGAAAAAGCTTTGGTTAAAAAACTTTA 200
SaurJH1_0429 (JH1) GTTGAAGAAGTACCAATAATTC AGAAAAAGCTTTGGTTAAAAAACTTTA 200
SAHV_0367 (Mu3) GTTGAAGAAGTACCAATAATTC AGAAAAAGCTTTGGTTAAAAAACTTTA 200
SaurJH9_0419 (JH9) GTTGAAGAAGTACCAATAATTC AGAAAAAGCTTTGGTTAAAAAACTTTA 200
SAV0370 (Mu50) GTTGAAGAAGTACCAATAATTC AGAAAAAGCTTTGGTTAAAAAACTTTA 200
SA0357 (N315) GTTGAAGAAGTACCAATAATTC AGAAAAAGCTTTGGTTAAAAAACTTTA 200
SAB0321 (RF122) GTTGAAGAAGTACCAATAATTC AGAAAAAGCTTTGGTTAAAAAACTTTA 200
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FIG. 22A

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MW0345 (MW2) CGATAGATACAGCCAAAATACAATAAACGGAAAAATCTAATAAAATCTAGGA 250
SAS0347 (MSSA476) CGATAGATACAGCCAAAATACAATAAACGGAAAAATCTAATAAAATCTAGGA 250
SACOL0442 (COL) CGATAGATACAGCAAGGATACAATAAAATGGAAAAATCTAATAAAATCTAGGA 250
SAOUHSC_00354 (NCTC8325) CGATAGATACAGCAAGGATACAATAAAATGGAAAAATCTAATAAAATCTAGGA 250
NWMN_0362 (Newman) CGATAGATACAGCAAGGATACAATAAAATGGAAAAATCTAATAAAATCTAGGA 250
SAUSA300_0370 (USA300-FPR3757) CGATAGATACAGCAAGGATACAATAAAATGGAAAAATCTAATAAAATCTAGGA 250
SaurJH1_0429 (JH1) CGATAGATACAGCAAGGATACAATAAAATGGAAAAATCTAATAAAATCTAGGA 250
SAHV_0367 (Mu3) CGATAGATACAGCAAGGATACAATAAAATGGAAAAATCTAATAAAATCTAGGA 250
SaurJH9_0419 (JH9) CGATAGATACAGCAAGGATACAATAAAATGGAAAAATCTAATAAAATCTAGGA 250
SAV0370 (Mu50) CGATAGATACAGCAAGGATACAATAAAATGGAAAAATCTAATAAAATCTAGGA 250
SA0357 (N315) CGATAGATACAGCAAGGATACAATAAAATGGAAAAATCTAATAAAATCTAGGA 250
SAB0321 (RF122) CGATAGATACAGCCAAAATACAATAAACGGAAAAATCTAATAAAGCTAGGA 250
***** * ***** ***** ***** *****

MW0345 (MW2) ATTGGGTTTATTCAGAGAGACCTTTAAATGAAAACCAAGTTCGTATAAAT 300
SAS0347 (MSSA476) ATTGGGTTTATTCAGAGAGACCTTTAAATGAAAACCAAGTTCGTATAAAT 300
SACOL0442 (COL) ATTGGGTTTATTCAGAGAGACCTTTAAATGAAAACCAAGTTCGTATACAT 300
SAOUHSC_00354 (NCTC8325) ATTGGGTTTATTCAGAGAGACCTTTAAATGAAAACCAAGTTCGTATACAT 300
NWMN_0362 (Newman) ATTGGGTTTATTCAGAGAGACCTTTAAATGAAAACCAAGTTCGTATACAT 300
SAUSA300_0370 (USA300-FPR3757) ATTGGGTTTATTCAGAGAGACCTTTAAATGAAAACCAAGTTCGTATACAT 300
SaurJH1_0429 (JH1) ATTGGGTTTATTCAGAGAGACCTTTAAATGAAAACCAAGTTCGTATACAT 300
SAHV_0367 (Mu3) ATTGGGTTTATTCAGAGAGACCTTTAAATGAAAACCAAGTTCGTATACAT 300
SaurJH9_0419 (JH9) ATTGGGTTTATTCAGAGAGACCTTTAAATGAAAACCAAGTTCGTATACAT 300
SAV0370 (Mu50) ATTGGGTTTATTCAGAGAGACCTTTAAATGAAAACCAAGTTCGTATACAT 300
SA0357 (N315) ATTGGGTTTATTCAGAGAGACCTTTAAATGAAAACCAAGTTCGTATACAT 300
SAB0321 (RF122) ATTGGGTTTATTCAGAGAGACCTTTAAATGAAAATCAAGTTCGTATACAT 300
***** ***** ***** ***** *****

MW0345 (MW2) TTAGAAGGAACATACAGAGTTGCTGATAGAGTATATACACCTAAGAGAAA 350
SAS0347 (MSSA476) TTAGAAGGAACATACAGAGTTGCTGATAGAGTATATACACCTAAGAGAAA 350
SACOL0442 (COL) TTAGAAGGAACATACACAGTTGCTGGCAGAGTGTATACACCTAAGAGGAA 350
SAOUHSC_00354 (NCTC8325) TTAGAAGGAACATACACAGTTGCTGGCAGAGTGTATACACCTAAGAGGAA 350
NWMN_0362 (Newman) TTAGAAGGAACATACACAGTTGCTGGCAGAGTGTATACACCTAAGAGGAA 350
SAUSA300_0370 (USA300-FPR3757) TTAGAAGGAACATACACAGTTGCTGGCAGAGTGTATACACCTAAGAGGAA 350
SaurJH1_0429 (JH1) TTAGAAGGAACATACACAGTTGCTGATAGAGTATATACACCTAAGAGAAA 350
SAHV_0367 (Mu3) TTAGAAGGAACATACACAGTTGCTGATAGAGTATATACACCTAAGAGAAA 350
SaurJH9_0419 (JH9) TTAGAAGGAACATACACAGTTGCTGATAGAGTATATACACCTAAGAGAAA 350
SAV0370 (Mu50) TTAGAAGGAACATACACAGTTGCTGATAGAGTATATACACCTAAGAGAAA 350
SA0357 (N315) TTAGAAGGAACATACACAGTTGCTGATAGAGTATATACACCTAAGAGAAA 350
SAB0321 (RF122) TTAGAAGGTATACATACAGAGTTGCTGATAGAGTGTATACACCTAAGAGGAA 350
***** ***** ***** ***** *****

MW0345 (MW2) TATTACTCTTAATAAAGAAGTTGTCACCTTTAAAGGAATTGGATCATATCA 400
SAS0347 (MSSA476) TATTACTCTTAATAAAGAAGTTGTCACCTTTAAAGGAATTGGATCATATCA 400
SACOL0442 (COL) TATTACTCTTAATAAAGAAGTTGTCACCTTTAAAGGAATTGGATCATATCA 400
SAOUHSC_00354 (NCTC8325) TATTACTCTTAATAAAGAAGTTGTCACCTTTAAAGGAATTGGATCATATCA 400
NWMN_0362 (Newman) TATTACTCTTAATAAAGAAGTTGTCACCTTTAAAGGAATTGGATCATATCA 400
SAUSA300_0370 (USA300-FPR3757) TATTACTCTTAATAAAGAAGTTGTCACCTTTAAAGGAATTGGATCATATCA 400
SaurJH1_0429 (JH1) TATTACTCTTAATAAAGAAGTTGTCACCTTTAAAGGAATTGGATCATATCA 400
SAHV_0367 (Mu3) TATTACTCTTAATAAAGAAGTTGTCACCTTTAAAGGAATTGGATCATATCA 400
SaurJH9_0419 (JH9) TATTACTCTTAATAAAGAAGTTGTCACCTTTAAAGGAATTGGATCATATCA 400
SAV0370 (Mu50) TATTACTCTTAATAAAGAAGTTGTCACCTTTAAAGGAATTGGATCATATCA 400
SA0357 (N315) TATTACTCTTAATAAAGAAGTTGTCACCTTTAAAGGAATTGGATCATATCA 400
SAB0321 (RF122) TATTACTCTTAATAAAGAAGTTGTCACCTTTAAAGGAATTGGATCATATCA 400
***** ***** ***** ***** *****

MW0345 (MW2) TAAGATTGCTCATATTTCTTATGGCTTATATATGGGAGAACATTTGCCT 450
SAS0347 (MSSA476) TAAGATTGCTCATATTTCTTATGGCTTATATATGGGAGAACATTTGCCT 450
SACOL0442 (COL) TAAGATTGCTCATATTTCTTATGGCTTGTATATGGGAGAACATTTGCCT 450
SAOUHSC_00354 (NCTC8325) TAAGATTGCTCATATTTCTTATGGCTTGTATATGGGAGAACATTTGCCT 450
NWMN_0362 (Newman) TAAGATTGCTCATATTTCTTATGGCTTGTATATGGGAGAACATTTGCCT 450
SAUSA300_0370 (USA300-FPR3757) TAAGATTGCTCATATTTCTTATGGCTTGTATATGGGAGAACATTTGCCT 450
SaurJH1_0429 (JH1) TAAGATTGCTCATATTTCTTATGGCTTATATATGGGAGAACATTTGCCT 450
SAHV_0367 (Mu3) TAAGATTGCTCATATTTCTTATGGCTTATATATGGGAGAACATTTGCCT 450
SaurJH9_0419 (JH9) TAAGATTGCTCATATTTCTTATGGCTTATATATGGGAGAACATTTGCCT 450
SAV0370 (Mu50) TAAGATTGCTCATATTTCTTATGGCTTATATATGGGAGAACATTTGCCT 450
SA0357 (N315) TAAGATTGCTCATATTTCTTATGGCTTATATATGGGAGAACATTTGCCT 450
SAB0321 (RF122) TAAGATTGCTCATATTTCTTATGGCTTATATATGGGAGAACATTTGCCT 450
***** ***** ***** ***** *****

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FIG. 22B

MW0345 (MW2)	AAAGGTAACATCGTCATAAATACAAAAGATGGCGGTAATATACATTAGA	500
SAS0347 (MSSA476)	AAAGGTAACATCGTCATAAATACAAAAGATGGCGGTAATATACATTAGA	500
SACOL0442 (COL)	AAAGGTAACATCGTCATAAATACAAAAGATGGTGGTAAATATACATTAGA	500
SAOUHSC_00354 (NCTC8325)	AAAGGTAACATCGTCATAAATACAAAAGATGGTGGTAAATATACATTAGA	500
NWMN_0362 (Newman)	AAAGGTAACATCGTCATAAATACAAAAGATGGTGGTAAATATACATTAGA	500
SAUSA300_0370 (USA300-FPR3757)	AAAGGTAACATCGTCATAAATACAAAAGATGGTGGTAAATATACATTAGA	500
SaurJH1_0429 (JH1)	AAAGGTAACATCGTCATAAATACAAAAGATGGCGGTAATATACATTAGA	500
SAHV_0367 (Mu3)	AAAGGTAACATCGTCATAAATACAAAAGATGGCGGTAATATACATTAGA	500
SaurJH9_0419 (JH9)	AAAGGTAACATCGTCATAAATACAAAAGATGGCGGTAATATACATTAGA	500
SAV0370 (Mu50)	AAAGGTAACATCGTCATAAATACAAAAGATGGCGGTAATATACATTAGA	500
SA0357 (N315)	AAAGGTAACATCGTCATAAATACAAAAGATGGCGGTAATATACATTAGA	500
SAB0321 (RF122)	AAAGGTAACATCGTCATAAATACAAAAGATGGCGGTAATATACATTAGA	500

MW0345 (MW2)	GTTCGCATAAAGAGCTACAAAAAGATAGGGAAAATGTAAAAATTAATACAG	550
SAS0347 (MSSA476)	GTTCGCATAAAGAGCTACAAAAAGATAGGGAAAATGTAAAAATTAATACAG	550
SACOL0442 (COL)	GTTCGCATAAAGAGCTACAAAAAGATAGGGAAAATGTAAAAATTAATACAG	550
SAOUHSC_00354 (NCTC8325)	GTTCGCATAAAGAGCTACAAAAAGATAGGGAAAATGTAAAAATTAATACAG	550
NWMN_0362 (Newman)	GTTCGCATAAAGAGCTACAAAAAGATAGGGAAAATGTAAAAATTAATACAG	550
SAUSA300_0370 (USA300-FPR3757)	GTTCGCATAAAGAGCTACAAAAAGATAGGGAAAATGTAAAAATTAATACAG	550
SaurJH1_0429 (JH1)	GTTCGCATAAAGAGCTACAAAAAGATAGGGAAAATGTAAAAATTAATACAG	550
SAHV_0367 (Mu3)	GTTCGCATAAAGAGCTACAAAAAGATAGGGAAAATGTAAAAATTAATACAG	550
SaurJH9_0419 (JH9)	GTTCGCATAAAGAGCTACAAAAAGATAGGGAAAATGTAAAAATTAATACAG	550
SAV0370 (Mu50)	GTTCGCATAAAGAGCTACAAAAAGATAGGGAAAATGTAAAAATTAATACAG	550
SA0357 (N315)	GTTCGCATAAAGAGCTACAAAAAGATAGGGAAAATGTAAAAATTAATACAG	550
SAB0321 (RF122)	GTTCGCATAAAGAGCTACAAAAAGATAGGGAAAATGTAGAAATTAATACTG	550

MW0345 (MW2)	CCGATATAAAAAATGTAACTTTCAAACCTTGTGAAAAGTGTTAATGACATT	600
SAS0347 (MSSA476)	CCGATATAAAAAATGTAACTTTCAAACCTTGTGAAAAGTGTTAATGACATT	600
SACOL0442 (COL)	CCGATATAAAAAATGTAACTTTCAAACCTTGTGAAAAGTGTTAATGACATT	600
SAOUHSC_00354 (NCTC8325)	CCGATATAAAAAATGTAACTTTCAAACCTTGTGAAAAGTGTTAATGACATT	600
NWMN_0362 (Newman)	CCGATATAAAAAATGTAACTTTCAAACCTTGTGAAAAGTGTTAATGACATT	600
SAUSA300_0370 (USA300-FPR3757)	CCGATATAAAAAATGTAACTTTCAAACCTTGTGAAAAGTGTTAATGACATT	600
SaurJH1_0429 (JH1)	CCGATATAAAAAATGTAACTTTCAAACCTTGTGAAAAGTGTTAATGACATT	600
SAHV_0367 (Mu3)	CCGATATAAAAAATGTAACTTTCAAACCTTGTGAAAAGTGTTAATGACATT	600
SaurJH9_0419 (JH9)	CCGATATAAAAAATGTAACTTTCAAACCTTGTGAAAAGTGTTAATGACATT	600
SAV0370 (Mu50)	CCGATATAAAAAATGTAACTTTCAAACCTTGTGAAAAGTGTTAATGACATT	600
SA0357 (N315)	CCGATATAAAAAATGTAACTTTCAAACCTTGTGAAAAGTGTTAATGACATT	600
SAB0321 (RF122)	ATGATATAAAAAATGTAACTTTCGAAGCTTGTGAAAAGTGTTAATGACATT	600

MW0345 (MW2)	GAACAAGTTTGA	612
SAS0347 (MSSA476)	GAACAAGTTTGA	612
SACOL0442 (COL)	GAACAAGTTTGA	612
SAOUHSC_00354 (NCTC8325)	GAACAAGTTTGA	612
NWMN_0362 (Newman)	GAACAAGTTTGA	612
SAUSA300_0370 (USA300-FPR3757)	GAACAAGTTTGA	612
SaurJH1_0429 (JH1)	GAACAAGTTTGA	612
SAHV_0367 (Mu3)	GAACAAGTTTGA	612
SaurJH9_0419 (JH9)	GAACAAGTTTGA	612
SAV0370 (Mu50)	GAACAAGTTTGA	612
SA0357 (N315)	GAACAAGTTTGA	612
SAB0321 (RF122)	GAACAAGTTTGA	612

FIG. 22C

II-SACOL0442 : Multiple polypeptide sequences alignment : selected epitopes shaded

SACOL0442 (COL)	MFKKYDSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQLQK	50
SAOUHSC_00354 (NCTC8325)	MFKKYDSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQLQK	50
NWMN_0362 (Newman)	MFKKYDSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQLQK	50
SAUSA300_0370 (USA300-FPR3757)	MFKKYDSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQLQK	50
SaurJH1_0429 (JH1)	MFKKYDSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQLQK	50
SAHV_0367 (Mu3)	MFKKYDSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQLQK	50
SaurJH9_0419 (JH9)	MFKKYDSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQLQK	50
SAV0370 (Mu50)	MFKKYDSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQLQK	50
SA0357 (N315)	MFKKYDSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQLQK	50
SAS0347 (MSSA476)	MFKKNDKSNISLLKSILSLGIIYGGTFGIYPKADASTQNSPSVQDKQFQK	50
SAB0321 (RF122)	MFKKYDSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQFQK	50
	**** *::*****:*****:****:*	
Consensus	MFKKXDSKNSIXLKSILSLGIIYGGTFGIYPKADASTQNSXSVDKQXQK	
SACOL0442 (COL)	VEEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIH	100
SAOUHSC_00354 (NCTC8325)	VEEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIH	100
NWMN_0362 (Newman)	VEEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIH	100
SAUSA300_0370 (USA300-FPR3757)	VEEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIH	100
SaurJH1_0429 (JH1)	VEEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIH	100
SAHV_0367 (Mu3)	VEEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIH	100
SaurJH9_0419 (JH9)	VEEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIH	100
SAV0370 (Mu50)	VEEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIH	100
SA0357 (N315)	VEEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIH	100
SAS0347 (MSSA476)	VEEVPNNSEKALVKKLYDRYSQNTINGKSNKSRNWVYSERPLNENQVRIN	100
SAB0321 (RF122)	VEEVPNNSEKALVKKLYDRYSQNTINGKSNKARNWVYSERPLNENQVRIH	100
	*****::*****:*****:*****:	
Consensus	VEEVPNNSEKALVKKLYDRYSXTINGKSNKKRNWVYSERPLNENQVRIX	
SACOL0442 (COL)	LEGTYTVAGRVYTPKRNIITLNKEVVTLKELDHIIRFAHISYGLYMGEHL	150
SAOUHSC_00354 (NCTC8325)	LEGTYTVAGRVYTPKRNIITLNKEVVTLKELDHIIRFAHISYGLYMGEHL	150
NWMN_0362 (Newman)	LEGTYTVAGRVYTPKRNIITLNKEVVTLKELDHIIRFAHISYGLYMGEHL	150
SAUSA300_0370 (USA300-FPR3757)	LEGTYTVAGRVYTPKRNIITLNKEVVTLKELDHIIRFAHISYGLYMGEHL	150
SaurJH1_0429 (JH1)	LEGTYTVADRVTYTPKRNIITLNKEVVTLKELDHIIRFAHISYGLYMGEHL	150
SAHV_0367 (Mu3)	LEGTYTVADRVTYTPKRNIITLNKEVVTLKELDHIIRFAHISYGLYMGEHL	150
SaurJH9_0419 (JH9)	LEGTYTVADRVTYTPKRNIITLNKEVVTLKELDHIIRFAHISYGLYMGEHL	150
SAV0370 (Mu50)	LEGTYTVADRVTYTPKRNIITLNKEVVTLKELDHIIRFAHISYGLYMGEHL	150
SA0357 (N315)	LEGTYTVADRVTYTPKRNIITLNKEVVTLKELDHIIRFAHISYGLYMGEHL	150
SAS0347 (MSSA476)	LEGTyrVADRVTYTPKRNIITLNKEVVTLKELDHIIRFAHISYGLYMGEHL	150
SAB0321 (RF122)	LEGTyrVADRVTYTPKRNIITLNKEVVTLKELDHIIRFAHISYGLYMGEHL	150
	**** *.*****:*****:*****:*****	
Consensus	LEGTYXVAXRVYTPKRNIITLNKEVVTLKELDHIIRFAHISYGLYMGEHL	
SACOL0442 (COL)	KGNIVINTKDGGKYTLESHKELQKDRENVKINTADIKNVTFLVKSVNDI	200
SAOUHSC_00354 (NCTC8325)	KGNIVINTKDGGKYTLESHKELQKDRENVKINTADIKNVTFLVKSVNDI	200
NWMN_0362 (Newman)	KGNIVINTKDGGKYTLESHKELQKDRENVKINTADIKNVTFLVKSVNDI	200
SAUSA300_0370 (USA300-FPR3757)	KGNIVINTKDGGKYTLESHKELQKDRENVKINTADIKNVTFLVKSVNDI	200
SaurJH1_0429 (JH1)	KGNIVINTKDGGKYTLESHKELQKDRENVKINTADIKNVTFLVKSVNDI	200
SAHV_0367 (Mu3)	KGNIVINTKDGGKYTLESHKELQKDRENVKINTADIKNVTFLVKSVNDI	200
SaurJH9_0419 (JH9)	KGNIVINTKDGGKYTLESHKELQKDRENVKINTADIKNVTFLVKSVNDI	200
SAV0370 (Mu50)	KGNIVINTKDGGKYTLESHKELQKDRENVKINTADIKNVTFLVKSVNDI	200
SA0357 (N315)	KGNIVINTKDGGKYTLESHKELQKDRENVKINTADIKNVTFLVKSVNDI	200
SAS0347 (MSSA476)	KGNIVINTKDGGKYTLESHKELQKDRENVKINTADIKNVTFLVKSVNDI	200
SAB0321 (RF122)	KGNIVINTKNNGKYTLESHKELQKNRENVEINTDDIKNVTFLVKSVNDI	200
	*****:*****:*****:***:*** *****:*****	
Consensus	KGNIVINTKXGGKYTLESHKELQKXRENVXINTXDIKNVTFLVKSVNDI	
SACOL0442 (COL)	EQV 203	
SAOUHSC_00354 (NCTC8325)	EQV 203	
NWMN_0362 (Newman)	EQV 203	
SAUSA300_0370 (USA300-FPR3757)	EQV 203	
SaurJH1_0429 (JH1)	EQV 203	
SAHV_0367 (Mu3)	EQV 203	
SaurJH9_0419 (JH9)	EQV 203	
SAV0370 (Mu50)	EQV 203	
SA0357 (N315)	EQV 203	
SAS0347 (MSSA476)	EQV 203	
SAB0321 (RF122)	EQV 203	

Consensus	XXX	

FIG. 22D

I- SACOL0720 : Multiple polynucleotide sequences alignment

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SaurJH1_0700 (JH1) -----
SaurJH9_0685 (JH9) -----
SAHV_0659 (Mu3) -----
SAV0662 (Mu50) ATGACCTTTAACGAGATAATATTTAAAAATTCCGTCAAAATTTATCACA 50
SA0617 (N315) ATGACCTTTAACGAGATAATATTTAAAAATTCCGTCAAAATTTATCACA 50
MW0624 (MW2) ATGACCTTTAACGAGATAATATTTAAAAATTCCGTCAAAATTTATCACA 50
SAS0627 (MSSA476) ATGACCTTTAACGAGATAATATTTAAAAATTCCGTCAAAATTTATCACA 50
SACOL0720_ ATGACCTTTAACGAGATAATATTTAAAAATTCCGTCAAAATTTATCACA 50
SAUSA300_0648 (USA300-FPR3757) ATGACCTTTAACGAGATAATATTTAAAAATTCCGTCAAAATTTATCACA 50
SAOUHSC_00668 (NCTC8325) -----
NWMN_0631 (Newman) -----
SAB0611 (RF122) ATGACCTTTAACGAGATAATATTTAAAAATTCCGTCAAAATTTATCACA 50

SaurJH1_0700 (JH1) -----
SaurJH9_0685 (JH9) -----
SAHV_0659 (Mu3) -----
SAV0662 (Mu50) TTATGCCATCTATCTTTTTTCATTAATTACGAGTGTAGTATTGTATTTTA 100
SA0617 (N315) TTATGCCATCTATCTTTTTTCATTAATTACGAGTGTAGTATTGTATTTTA 100
MW0624 (MW2) TTATGCCATCTATCTTTTTTCATTAATTACGAGTGTAGTATTGTATTTTA 100
SAS0627 (MSSA476) TTATGCCATCTATCTTTTTTCATTAATTACGAGTGTAGTATTGTATTTTA 100
SACOL0720_ TTATGCCATCTATCTTTTTTCGTTAATTACGAGTGTAGTATTGTATTTTA 100
SAUSA300_0648 (USA300-FPR3757) TTATGCCATCTATCTTTTTTCGTTAATTACGAGTGTAGTATTGTATTTTA 100
SAOUHSC_00668 (NCTC8325) -----TTGTATTTTA 10
NWMN_0631 (Newman) -----
SAB0611 (RF122) TTATGCCATCTATCTTTTTTCATTAATTACGAGTGTAGTATTGTATTTTA 100

SaurJH1_0700 (JH1) -----ATGACAGAGTCATAT 15
SaurJH9_0685 (JH9) -----ATGACAGAGTCATAT 15
SAHV_0659 (Mu3) -----ATGACAGAGTCATAT 15
SAV0662 (Mu50) GCTTTGTAGCATTTAAATACGCGCATAAACTAAACATGACAGAGTCATAT 150
SA0617 (N315) GCTTTGTAGCATTTAAATACGCGCATAAACTAAACATGACAGAGTCATAT 150
MW0624 (MW2) GCTTTGTAGCATTTAAATACGCGCATAAACTAAACATGACAGAGTCATAT 150
SAS0627 (MSSA476) GCTTTGTAGCATTTAAATACGCGCATAAACTAAACATGACAGAGTCATAT 150
SACOL0720_ GCTTTGTAGCATTTAAATACGCTCATAAACTAAACATGACAGAGTCATAT 150
SAUSA300_0648 (USA300-FPR3757) GCTTTGTAGCATTTAAATACGCTCATAAACTAAACATGACAGAGTCATAT 150
SAOUHSC_00668 (NCTC8325) GCTTTGTAGCATTTAAATACGCTCATAAACTAAACATGACAGAGTCATAT 60
NWMN_0631 (Newman) -----ATGACAGAGTCATAT 15
SAB0611 (RF122) GCTTTGTAGCATTTAAATACGCTCATAAACTAAACATGACAGAGTCATAT 150
*****

SaurJH1_0700 (JH1) CCAATTATTAAGGAAGGCTCACAAGTCGGAAGCTACTTTCTATTTTTTCAT 65
SaurJH9_0685 (JH9) CCAATTATTAAGGAAGGCTCACAAGTCGGAAGCTACTTTCTATTTTTTCAT 65
SAHV_0659 (Mu3) CCAATTATTAAGGAAGGCTCACAAGTCGGAAGCTACTTTCTATTTTTTCAT 65
SAV0662 (Mu50) CCAATTATTAAGGAAGGCTCACAAGTCGGAAGCTACTTTCTATTTTTTCAT 200
SA0617 (N315) CCAATTATTAAGGAAGGCTCACAAGTCGGAAGCTACTTTCTATTTTTTCAT 200
MW0624 (MW2) CCAATTATTAAGGAAGGCTCACAAGTCGGAAGCTACTTTCTATTTTTTCAT 200
SAS0627 (MSSA476) CCAATTATTAAGGAAGGCTCACAAGTCGGAAGCTACTTTCTATTTTTTCAT 200
SACOL0720_ CCAATTATTAAGGAAGGCTCACAAGTCGGAAGCTACTTTCTATTTTTTCAT 200
SAUSA300_0648 (USA300-FPR3757) CCAATTATTAAGGAAGGCTCACAAGTCGGAAGCTACTTTCTATTTTTTCAT 200
SAOUHSC_00668 (NCTC8325) CCAATTATTAAGGAAGGCTCACAAGTCGGAAGCTACTTTCTATTTTTTCAT 110
NWMN_0631 (Newman) CCAATTATTAAGGAAGGCTCACAAGTCGGAAGCTACTTTCTATTTTTTCAT 65
SAB0611 (RF122) CCAATTATTAAGGAAGGCTCACAAGTCGGAAGCTACTTTCTATTTTTTCAT 200
*****

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FIG. 23A

SaurJH1_0700 (JH1)	CATAATTGCATTTTTGTTATATGCCAATGTGTTATTTATTAACGACGAA	115
SaurJH9_0685 (JH9)	CATAATTGCATTTTTGTTATATGCCAATGTGTTATTTATTAACGACGAA	115
SAHV_0659 (Mu3)	CATAATTGCATTTTTGTTATATGCCAATGTGTTATTTATTAACGACGAA	115
SAV0662 (Mu50)	CATAATTGCATTTTTGTTATATGCCAATGTGTTATTTATTAACGACGAA	250
SA0617 (N315)	CATAATTGCATTTTTGTTATATGCCAATGTGTTATTTATTAACGACGAA	250
MW0624 (MW2)	CATAATTGCATTTTTGTTATATGCCAATGTGTTATTTATTAACGACGAA	250
SAS0627 (MSSA476)	CATAATTGCATTTTTGTTATATGCCAATGTGTTATTTATTAACGACGAA	250
SACOL0720_	CATAATTGCATTTTTGTTATATGCCAATGTGTTATTTATTAACGACGAA	250
SAUSA300_0648 (USA300-FPR3757)	CATAATTGCATTTTTGTTATATGCCAATGTGTTATTTATTAACGACGAA	250
SAOUHSC_00668 (NCTC8325)	CATAATTGCATTTTTGTTATATGCCAATGTGTTATTTATTAACGACGAA	160
NWMN_0631 (Newman)	CATAATTGCATTTTTGTTATATGCCAATGTGTTATTTATTAACGACGAA	115
SAB0611 (RF122)	CATAATTGCATTTTTGTTATATGCCAATGTGTTATTTATTAACGACGAA	250

SaurJH1_0700 (JH1)	GTTATGAGCTTGCAATTATATCAAACATTAGGTTTATCTAAATTCACATT	165
SaurJH9_0685 (JH9)	GTTATGAGCTTGCAATTATATCAAACATTAGGTTTATCTAAATTCACATT	165
SAHV_0659 (Mu3)	GTTATGAGCTTGCAATTATATCAAACATTAGGTTTATCTAAATTCACATT	165
SAV0662 (Mu50)	GTTATGAGCTTGCAATTATATCAAACATTAGGTTTATCTAAATTCACATT	300
SA0617 (N315)	GTTATGAGCTTGCAATTATATCAAACATTAGGTTTATCTAAATTCACATT	300
MW0624 (MW2)	GTTATGAGCTTGCAATTATATCAAACATTAGGTTTATCTAAATTCACATT	300
SAS0627 (MSSA476)	GTTATGAGCTTGCAATTATATCAAACATTAGGTTTATCTAAATTCACATT	300
SACOL0720_	GTTATGAGCTTGCAATTATATCAAACATTAGGTTTATCTAAATTCACATT	300
SAUSA300_0648 (USA300-FPR3757)	GTTATGAGCTTGCAATTATATCAAACATTAGGTTTATCTAAATTCACATT	300
SAOUHSC_00668 (NCTC8325)	GTTATGAGCTTGCAATTATATCAAACATTAGGTTTATCTAAATTCACATT	210
NWMN_0631 (Newman)	GTTATGAGCTTGCAATTATATCAAACATTAGGTTTATCTAAATTCACATT	165
SAB0611 (RF122)	GTTATGAGCTTGCAATTATATCAAACATTAGGTTTATCTAAATTCACATT	300

SaurJH1_0700 (JH1)	ATTTATATACTAATGCTCGAACAATTACTAATATTTATAAATTACGGCAAT	215
SaurJH9_0685 (JH9)	ATTTATATACTAATGCTCGAACAATTACTAATATTTATAAATTACGGCAAT	215
SAHV_0659 (Mu3)	ATTTATATACTAATGCTCGAACAATTACTAATATTTATAAATTACGGCAAT	215
SAV0662 (Mu50)	ATTTATATACTAATGCTCGAACAATTACTAATATTTATAAATTACGGCAAT	350
SA0617 (N315)	ATTTATATACTAATGCTCGAACAATTACTAATATTTATAAATTACGGCAAT	350
MW0624 (MW2)	ATTTATATACTAATGCTCGAACAATTACTAATATTTATAAATTACGGCAAT	350
SAS0627 (MSSA476)	ATTTATATACTAATGCTCGAACAATTACTAATATTTATAAATTACGGCAAT	350
SACOL0720_	ATTTATATACTAATGCTCGAACAATTACTAATATTTATAAATTACGGCAAT	350
SAUSA300_0648 (USA300-FPR3757)	ATTTATATACTAATGCTCGAACAATTACTAATATTTATAAATTACGGCAAT	350
SAOUHSC_00668 (NCTC8325)	ATTTATATACTAATGCTCGAACAATTACTAATATTTATAAATTACGGCAAT	260
NWMN_0631 (Newman)	ATTTATATACTAATGCTCGAACAATTACTAATATTTATAAATTACGGCAAT	215
SAB0611 (RF122)	ATTTATATACTAATGCTCGAACAATTACTAATATTTATAAATTACGGCAAT	350

SaurJH1_0700 (JH1)	ATTAGGTATTATTATTGGTATTTTTGGTTCAAAACTGTTATTAATGATTG	265
SaurJH9_0685 (JH9)	ATTAGGTATTATTATTGGTATTTTTGGTTCAAAACTGTTATTAATGATTG	265
SAHV_0659 (Mu3)	ATTAGGTATTATTATTGGTATTTTTGGTTCAAAACTGTTATTAATGATTG	265
SAV0662 (Mu50)	ATTAGGTATTATTATTGGTATTTTTGGTTCAAAACTGTTATTAATGATTG	400
SA0617 (N315)	ATTAGGTATTATTATTGGTATTTTTGGTTCAAAACTGTTATTAATGATTG	400
MW0624 (MW2)	ATTAGGTATTATTATTGGTATTTTTGGTTCAAAACTGTTATTAATGATTG	400
SAS0627 (MSSA476)	ATTAGGTATTATTATTGGTATTTTTGGTTCAAAACTGTTATTAATGATTG	400
SACOL0720_	ATTAGGTATTATTATTGGTATTTTTGGTTCAAAACTGTTATTAATGATTG	400
SAUSA300_0648 (USA300-FPR3757)	ATTAGGTATTATTATTGGTATTTTTGGTTCAAAACTGTTATTAATGATTG	400
SAOUHSC_00668 (NCTC8325)	ATTAGGTATTATTATTGGTATTTTTGGTTCAAAACTGTTATTAATGATTG	310
NWMN_0631 (Newman)	ATTAGGTATTATTATTGGTATTTTTGGTTCAAAACTGTTATTAATGATTG	265
SAB0611 (RF122)	ATTAGGTATTATTATTGGTATTTTTGGTTCAAAACTGTTATTAATGATTG	400

SaurJH1_0700 (JH1)	TCTTTACATTATTAGGAATTAAGAAAAGGTTCCAATTATTTTTAGTTTG	315
SaurJH9_0685 (JH9)	TCTTTACATTATTAGGAATTAAGAAAAGGTTCCAATTATTTTTAGTTTG	315
SAHV_0659 (Mu3)	TCTTTACATTATTAGGAATTAAGAAAAGGTTCCAATTATTTTTAGTTTG	315
SAV0662 (Mu50)	TCTTTACATTATTAGGAATTAAGAAAAGGTTCCAATTATTTTTAGTTTG	450
SA0617 (N315)	TCTTTACATTATTAGGAATTAAGAAAAGGTTCCAATTATTTTTAGTTTG	450
MW0624 (MW2)	TCTTTACATTATTAGGAATTAAGAAAAGGTTCCAATTATTTTTAGTTTG	450
SAS0627 (MSSA476)	TCTTTACATTATTAGGAATTAAGAAAAGGTTCCAATTATTTTTAGTTTG	450
SACOL0720_	TCTTTACATTATTAGGAATTAAGAAAAGGTTCCAATTATTTTTAGTTTG	450
SAUSA300_0648 (USA300-FPR3757)	TCTTTACATTATTAGGAATTAAGAAAAGGTTCCAATTATTTTTAGTTTG	450
SAOUHSC_00668 (NCTC8325)	TCTTTACATTATTAGGAATTAAGAAAAGGTTCCAATTATTTTTAGTTTG	360
NWMN_0631 (Newman)	TCTTTACATTATTAGGAATTAAGAAAAGGTTCCAATTATTTTTAGTTTG	315
SAB0611 (RF122)	TCTTTACATTATTAGGAATTAAGAAAAGGTTCCAATTATTTTTAGTTTG	450

FIG. 23B

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SaurJH1_0700 (JH1) AGGGCGGTATTTGAAACATTAATGTTAATCGGTGTCGCTTATTTTTTAAC 365
SaurJH9_0685 (JH9) AGGGCGGTATTTGAAACATTAATGTTAATCGGTGTCGCTTATTTTTTAAC 365
SAHV_0659 (Mu3) AGGGCGGTATTTGAAACATTAATGTTAATCGGTGTCGCTTATTTTTTAAC 365
SAV0662 (Mu50) AGGGCGGTATTTGAAACATTAATGTTAATCGGTGTCGCTTATTTTTTAAC 500
SA0617 (N315) AGGGCGGTATTTGAAACATTAATGTTAATCGGTGTCGCTTATTTTTTAAC 500
MW0624 (MW2) AGGGCGGTATTTGAAACATTAATGTTAATCGGTGTCGCTTATTTTTTAAC 500
SAS0627 (MSSA476) AGGGCGGTATTTGAAACATTAATGTTAATCGGTGTCGCTTATTTTTTAAC 500
SACOL0720_ AGGGCGGTATTTGAAACATTAATGTTAATCGGTGTCGCTTATTTTTTAAC 500
SAUSA300_0648 (USA300-FPR3757) AGGGCGGTATTTGAAACATTAATGTTAATCGGTGTCGCTTATTTTTTAAC 500
SAOUHSC_00668 (NCTC8325) AGGGCGGTATTTGAAACATTAATGTTAATCGGTGTCGCTTATTTTTTAAC 410
NWMN_0631 (Newman) AGGGCGGTATTTGAAACATTAATGTTAATCGGTGTCGCTTATTTTTTAAC 365
SAB0611 (RF122) AGGGCGGTATTTGAAACATTAATGTTAATCGGTGTCGCTTATTTTTTAAC 500
*****

SaurJH1_0700 (JH1) CTCTGCTCAAAATTTTATATTAGTGTTCAAACAATCTATTTTCACAGATGT 415
SaurJH9_0685 (JH9) CTCTGCTCAAAATTTTATATTAGTGTTCAAACAATCTATTTTCACAGATGT 415
SAHV_0659 (Mu3) CTCTGCTCAAAATTTTATATTAGTGTTCAAACAATCTATTTTCACAGATGT 415
SAV0662 (Mu50) CTCTGCTCAAAATTTTATATTAGTGTTCAAACAATCTATTTTCACAGATGT 550
SA0617 (N315) CTCTGCTCAAAATTTTATATTAGTGTTCAAACAATCTATTTTCACAGATGT 550
MW0624 (MW2) CTCTGCTCAAAATTTTATATTAGTGTTCAAACAATCTATTTTCACAGATGT 550
SAS0627 (MSSA476) CTCTGCTCAAAATTTTATATTAGTGTTCAAACAATCTATTTTCACAGATGT 550
SACOL0720_ CTCTGCTCAAAATTTTATATTAGTGTTCAAACAATCTATTTTCACAGATGT 550
SAUSA300_0648 (USA300-FPR3757) ATCTGCTCAAAATTTTATATTAGTGTTCAAACAATCTATTTTCACAGATGT 550
SAOUHSC_00668 (NCTC8325) ATCTGCTCAAAATTTTATATTAGTGTTCAAACAATCTATTTTCACAGATGT 460
NWMN_0631 (Newman) ATCTGCTCAAAATTTTATATTAGTGTTCAAACAATCTATTTTCACAGATGT 415
SAB0611 (RF122) ATCTGCTCAAAATTTTATATTAGTGTTCAAACAATCTATTTTCACAGATGT 550
*****

SaurJH1_0700 (JH1) CAAAGAATAACCAGGTTAAAGAAACAAATCATAATAAAATTACATTTGAA 465
SaurJH9_0685 (JH9) CAAAGAATAACCAGGTTAAAGAAACAAATCATAATAAAATTACATTTGAA 465
SAHV_0659 (Mu3) CAAAGAATAACCAGGTTAAAGAAACAAATCATAATAAAATTACATTTGAA 465
SAV0662 (Mu50) CAAAGAATAACCAGGTTAAAGAAACAAATCATAATAAAATTACATTTGAA 600
SA0617 (N315) CAAAGAATAACCAGGTTAAAGAAACAAATCATAATAAAATTACATTTGAA 600
MW0624 (MW2) CAAAGAATAACCAGGTTAAAGAAACAAATCATAATAAAATTACATTTGAA 600
SAS0627 (MSSA476) CAAAGAATAACCAGGTTAAAGAAACAAATCATAATAAAATTACATTTGAA 600
SACOL0720_ CAAAGAATAACCAGGTTAAAGAAACAAATCATAATAAAATTACATTTGAA 600
SAUSA300_0648 (USA300-FPR3757) CAAAGAATAACCAGGTTAAAGAAACAAATCATAATAAAATTACATTTGAA 600
SAOUHSC_00668 (NCTC8325) CAAAGAATAACCAGGTTAAAGAAACAAATCATAATAAAATTACATTTGAA 510
NWMN_0631 (Newman) CAAAGAATAACCAGGTTAAAGAAACAAATCATAATAAAATTACATTTGAA 465
SAB0611 (RF122) CAAAGAATAACCAGGTTAAAGAAACAAATCATAATAAAATTACATTTGAA 600
*****

SaurJH1_0700 (JH1) GAGGTTGTTTTAGGCATCTTAGGTATAGTATTGATTATCACAGGATACTA 515
SaurJH9_0685 (JH9) GAGGTTGTTTTAGGCATCTTAGGTATAGTATTGATTATCACAGGATACTA 515
SAHV_0659 (Mu3) GAGGTTGTTTTAGGCATCTTAGGTATAGTATTGATTATCACAGGATACTA 515
SAV0662 (Mu50) GAGGTTGTTTTAGGCATCTTAGGTATAGTATTGATTATCACAGGATACTA 650
SA0617 (N315) GAGGTTGTTTTAGGCATCTTAGGTATAGTATTGATTATCACAGGATACTA 650
MW0624 (MW2) GAGGTTGTTTTAGGCATCTTAGGTATAGTATTGATTATCACAGGATACTA 650
SAS0627 (MSSA476) GAGGTTGTTTTAGGCATCTTAGGTATAGTATTGATTATCACAGGATACTA 650
SACOL0720_ GAGGTTGTTTTAGGCATCTTAGGTATAGTATTGATTATCACAGGATACTA 650
SAUSA300_0648 (USA300-FPR3757) GAGGTTGTTTTAGGCATCTTAGGTATAGTATTGATTATCACAGGATACTA 650
SAOUHSC_00668 (NCTC8325) GAGGTTGTTTTAGGCATCTTAGGTATAGTATTGATTATCACAGGATACTA 560
NWMN_0631 (Newman) GAGGTTGTTTTAGGCATCTTAGGTATAGTATTGATTATCACAGGATACTA 515
SAB0611 (RF122) GAGGTTGTTTTAGGCATCTTAGGTATAGTATTGATTATCACAGGATACTA 650
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SaurJH1_0700 (JH1) TCTATCTTTGAACATTGTTCAATATTATGATTCTATCGGTATACTTATGT 565
SaurJH9_0685 (JH9) TCTATCTTTGAACATTGTTCAATATTATGATTCTATCGGTATACTTATGT 565
SAHV_0659 (Mu3) TCTATCTTTGAACATTGTTCAATATTATGATTCTATCGGTATACTTATGT 565
SAV0662 (Mu50) TCTATCTTTGAACATTGTTCAATATTATGATTCTATCGGTATACTTATGT 700
SA0617 (N315) TCTATCTTTGAACATTGTTCAATATTATGATTCTATCGGTATACTTATGT 700
MW0624 (MW2) TCTATCTTTGAACATTGTTCAATATTATGATTCTATCGGTATACTTATGT 700
SAS0627 (MSSA476) TCTATCTTTGAACATTGTTCAATATTATGATTCTATCGGTATACTTATGT 700
SACOL0720_ TCTATCTTTGAACATTGTTCAATATTATGATTCTATCGGTATACTTATGT 700
SAUSA300_0648 (USA300-FPR3757) TCTATCTTTGAACATTGTTCAATATTATGATTCTATCGGTATACTTATGT 700
SAOUHSC_00668 (NCTC8325) TCTATCTTTGAACATTGTTCAATATTATGATTCTATCGGTATACTTATGT 610
NWMN_0631 (Newman) TCTATCTTTGAACATTGTTCAATATTATGATTCTATCGGTATACTTATGT 565
SAB0611 (RF122) TCTATCTTTGAACATTGTTCAATATTATGATTCTATCGGTATACTTATGT 700
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FIG. 23C

SaurJH1_0700 (JH1)	TTATTTTATTGTCAACTGTGATTGGGGCATACTTATTTTTTAAAAGCTCT	615
SaurJH9_0685 (JH9)	TTATTTTATTGTCAACTGTGATTGGGGCATACTTATTTTTTAAAAGCTCT	615
SAHV_0659 (Mu3)	TTATTTTATTGTCAACTGTGATTGGGGCATACTTATTTTTTAAAAGCTCT	615
SAV0662 (Mu50)	TTATTTTATTGTCAACTGTGATTGGGGCATACTTATTTTTTAAAAGCTCT	750
SA0617 (N315)	TTATTTTATTGTCAACTGTGATTGGGGCATACTTATTTTTTAAAAGCTCT	750
MW0624 (MW2)	TTATTTTATTGTCAACTGTGATTGGGGCATACTTATTTTTTAAAAGCTCT	750
SAS0627 (MSSA476)	TTATTTTATTGTCAACTGTGATTGGGGCATACTTATTTTTTAAAAGCTCT	750
SACOL0720_	TTATTTTATTGTCAACTGTGATTGGGGCATACTTATTTTTTAAAAGCTCT	750
SAUSA300_0648 (USA300-FPR3757)	TTATTTTATTGTCAACTGTGATTGGGGCATACTTATTTTTTAAAAGCTCT	750
SAOUHSC_00668 (NCTC8325)	TTATTTTATTGTCAACTGTGATTGGGGCATACTTATTTTTTAAAAGCTCT	660
NWMN_0631 (Newman)	TTATTTTATTGTCAACTGTGATTGGGGCATACTTATTTTTTAAAAGCTCT	615
SAB0611 (RF122)	TTATTTTATTGTCAACTGTGATTGGGGCATACTTATTTTTTAAAAGCTCT	750

SaurJH1_0700 (JH1)	GTTTCTCTAGTTTTTAAAATGGTGAAGAAGTTTAGAAAAGGTGTTATAAG	665
SaurJH9_0685 (JH9)	GTTTCTCTAGTTTTTAAAATGGTGAAGAAGTTTAGAAAAGGTGTTATAAG	665
SAHV_0659 (Mu3)	GTTTCTCTAGTTTTTAAAATGGTGAAGAAGTTTAGAAAAGGTGTTATAAG	665
SAV0662 (Mu50)	GTTTCTCTAGTTTTTAAAATGGTGAAGAAGTTTAGAAAAGGTGTTATAAG	800
SA0617 (N315)	GTTTCTCTAGTTTTTAAAATGGTGAAGAAGTTTAGAAAAGGTGTTATAAG	800
MW0624 (MW2)	GTTTCTCTAGTTTTTAAAATGGTGAAGAAGTTTAGAAAAGGTGTTATAAG	800
SAS0627 (MSSA476)	GTTTCTCTAGTTTTTAAAATGGTGAAGAAGTTTAGAAAAGGTGTTATAAG	800
SACOL0720_	GTTTCTCTAGTTTTTAAAATGGTGAAGAAGTTTAGAAAAGGTGTTATAAG	800
SAUSA300_0648 (USA300-FPR3757)	GTTTCTCTAGTTTTTAAAATGGTGAAGAAGTTTAGAAAAGGTGTTATAAG	800
SAOUHSC_00668 (NCTC8325)	GTTTCTCTAGTTTTTAAAATGGTGAAGAAGTTTAGAAAAGGTGTTATAAG	710
NWMN_0631 (Newman)	GTTTCTCTAGTTTTTAAAATGGTGAAGAAGTTTAGAAAAGGTGTTATAAG	665
SAB0611 (RF122)	GTTTCTCTAGTTTTTAAAATGGTGAAGAAGTTTAGAAAAGGTGTTATAAG	800

SaurJH1_0700 (JH1)	TGTAATGATGTCATGTTCTCATCATCTATTATGTATCGTATTAAGAAAA	715
SaurJH9_0685 (JH9)	TGTAATGATGTCATGTTCTCATCATCTATTATGTATCGTATTAAGAAAA	715
SAHV_0659 (Mu3)	TGTAATGATGTCATGTTCTCATCATCTATTATGTATCGTATTAAGAAAA	715
SAV0662 (Mu50)	TGTAATGATGTCATGTTCTCATCATCTATTATGTATCGTATTAAGAAAA	850
SA0617 (N315)	TGTAATGATGTCATGTTCTCATCATCTATTATGTATCGTATTAAGAAAA	850
MW0624 (MW2)	TGTAATGATGTCATGTTCTCATCATCTATTATGTATCGTATTAAGAAAA	850
SAS0627 (MSSA476)	TGTAATGATGTCATGTTCTCATCATCTATTATGTATCGTATTAAGAAAA	850
SACOL0720_	TGTAATGATGTCATGTTCTCATCATCTATTATGTATCGTATTAAGAAAA	850
SAUSA300_0648 (USA300-FPR3757)	TGTAATGATGTCATGTTCTCATCATCTATTATGTATCGTATTAAGAAAA	850
SAOUHSC_00668 (NCTC8325)	TGTAATGATGTCATGTTCTCATCATCTATTATGTATCGTATTAAGAAAA	760
NWMN_0631 (Newman)	TGTAATGATGTCATGTTCTCATCATCTATTATGTATCGTATTAAGAAAA	715
SAB0611 (RF122)	TGTAATGATGTCATGTTCTCATCATCTATTATGTATCGTATTAAGAAAA	850

SaurJH1_0700 (JH1)	ATGCTTTTTCACTTACGGTCATGGCAATCATTTACGCGATTACTGTTTCA	765
SaurJH9_0685 (JH9)	ATGCTTTTTCACTTACGGTCATGGCAATCATTTACGCGATTACTGTTTCA	765
SAHV_0659 (Mu3)	ATGCTTTTTCACTTACGGTCATGGCAATCATTTACGCGATTACTGTTTCA	765
SAV0662 (Mu50)	ATGCTTTTTCACTTACGGTCATGGCAATCATTTACGCGATTACTGTTTCA	900
SA0617 (N315)	ATGCTTTTTCACTTACGGTCATGGCAATCATTTACGCGATTACTGTTTCA	900
MW0624 (MW2)	ATGCTTTTTCACTTACGGTCATGGCAATCATTTACGCGATTACTGTTTCA	900
SAS0627 (MSSA476)	ATGCTTTTTCACTTACGGTCATGGCAATCATTTACGCGATTACTGTTTCA	900
SACOL0720_	ATGCTTTTTCACTTACGGTCATGGCAATCATTTACGCGATTACTGTTTCA	900
SAUSA300_0648 (USA300-FPR3757)	ATGCTTTTTCACTTACGGTCATGGCAATCATTTACGCGATTACTGTTTCA	900
SAOUHSC_00668 (NCTC8325)	ATGCTTTTTCACTTACGGTCATGGCAATCATTTACGCGATTACTGTTTCA	810
NWMN_0631 (Newman)	ATGCTTTTTCACTTACGGTCATGGCAATCATTTACGCGATTACTGTTTCA	765
SAB0611 (RF122)	ATGCTTTTTCACTTACGGTCATGGCAATCATTTACGCGATTACTGTTTCA	900

SaurJH1_0700 (JH1)	GTTCTTTGCTTTTGCTGCTATAAGTAGAGCGTCCTTATCAAGTGAATAAAA	815
SaurJH9_0685 (JH9)	GTTCTTTGCTTTTGCTGCTATAAGTAGAGCGTCCTTATCAAGTGAATAAAA	815
SAHV_0659 (Mu3)	GTTCTTTGCTTTTGCTGCTATAAGTAGAGCGTCCTTATCAAGTGAATAAAA	815
SAV0662 (Mu50)	GTTCTTTGCTTTTGCTGCTATAAGTAGAGCGTCCTTATCAAGTGAATAAAA	950
SA0617 (N315)	GTTCTTTGCTTTTGCTGCTATAAGTAGAGCGTCCTTATCAAGTGAATAAAA	950
MW0624 (MW2)	GTTCTTTGCTTTTGCTGCTATAAGTAGAGCGTCCTTATCAAGTGAATAAAA	950
SAS0627 (MSSA476)	GTTCTTTGCTTTTGCTGCTATAAGTAGAGCGTCCTTATCAAGTGAATAAAA	950
SACOL0720_	GTTCTTTGCTTTTGCTGCTATAAGTAGAGCGTCCTTATCAAGTGAATAAAA	950
SAUSA300_0648 (USA300-FPR3757)	GTTCTTTGCTTTTGCTGCTATAAGTAGAGCGTCCTTATCAAGTGAATAAAA	950
SAOUHSC_00668 (NCTC8325)	GTTCTTTGCTTTTGCTGCTATAAGTAGAGCGTCCTTATCAAGTGAATAAAA	860
NWMN_0631 (Newman)	GTTCTTTGCTTTTGCTGCTATAAGTAGAGCGTCCTTATCAAGTGAATAAAA	815
SAB0611 (RF122)	GTTCTTTGCTTTTGCTGCTATAAGTAGAGCGTCCTTATCAAGTGAATAAAA	950

FIG. 23D

SaurJH1_0700 (JH1)	ATATACTGCACCACACGACGTTACAATTAAGACCAACAAAAAGCTAATC	865
SaurJH9_0685 (JH9)	ATATACTGCACCACACGACGTTACAATTAAGACCAACAAAAAGCTAATC	865
SAHV_0659 (Mu3)	ATATACTGCACCACACGACGTTACAATTAAGACCAACAAAAAGCTAATC	865
SAV0662 (Mu50)	ATATACTGCACCACACGACGTTACAATTAAGACCAACAAAAAGCTAATC	1000
SA0617 (N315)	ATATACTGCACCACACGACGTTACAATTAAGACCAACAAAAAGCTAATC	1000
MW0624 (MW2)	ATATACTGCACCACACGACGTTACAATTAAGACCAACAAAAAGCTAATC	1000
SAS0627 (MSSA476)	ATATACTGCACCACACGACGTTACAATTAAGACCAACAAAAAGCTAATC	1000
SACOL0720_	ATATACTGCACCACACGACGTTACAATTAAGACCAACAAAAAGCTAATC	1000
SAUSA300_0648 (USA300-FPR3757)	ATATACTGCACCACACGACGTTACAATTAAGACCAACAAAAAGCTAATC	1000
SAOUHSC_00668 (NCTC8325)	ATATACTGCACCACACGACGTTACAATTAAGACCAACAAAAAGCTAATC	910
NWMN_0631 (Newman)	ATATACTGCACCACACGACGTTACAATTAAGACCAACAAAAAGCTAATC	865
SAB0611 (RF122)	ATATACTGCACCACACGACGTTACAATTAAGACCAACAAAAAGCTAATC	1000

SaurJH1_0700 (JH1)	AATTAGCAAGTGAATTAACAATCAAAAAATTCCTCATTTTTATAATTAT	915
SaurJH9_0685 (JH9)	AATTAGCAAGTGAATTAACAATCAAAAAATTCCTCATTTTTATAATTAT	915
SAHV_0659 (Mu3)	AATTAGCAAGTGAATTAACAATCAAAAAATTCCTCATTTTTATAATTAT	915
SAV0662 (Mu50)	AATTAGCAAGTGAATTAACAATCAAAAAATTCCTCATTTTTATAATTAT	1050
SA0617 (N315)	AATTAGCAAGTGAATTAACAATCAAAAAATTCCTCATTTTTATAATTAT	1050
MW0624 (MW2)	AATTAGCAAGTGAATTAACAATCAAAAAATTCCTCATTTTTATAATTAT	1050
SAS0627 (MSSA476)	AATTAGCAAGTGAATTAACAATCAAAAAATTCCTCATTTTTATAATTAT	1050
SACOL0720_	AATTAGCAAGTGAATTAACAATCAAAAAATTCCTCATTTTTATAATTAT	1050
SAUSA300_0648 (USA300-FPR3757)	AATTAGCAAGTGAATTAACAATCAAAAAATTCCTCATTTTTATAATTAT	1050
SAOUHSC_00668 (NCTC8325)	AATTAGCAAGTGAATTAACAATCAAAAAATTCCTCATTTTTATAATTAT	960
NWMN_0631 (Newman)	AATTAGCAAGTGAATTAACAATCAAAAAATTCCTCATTTTTATAATTAT	915
SAB0611 (RF122)	AATTAGCAAGTGAATTAACAATCAAAAAATTCCTCATTTTTATAATTAT	1050

SaurJH1_0700 (JH1)	AAAGAAGTAATTCATACGAAATTGTATAAAGATAATTTATTTGATGTAAA	965
SaurJH9_0685 (JH9)	AAAGAAGTAATTCATACGAAATTGTATAAAGATAATTTATTTGATGTAAA	965
SAHV_0659 (Mu3)	AAAGAAGTAATTCATACGAAATTGTATAAAGATAATTTATTTGATGTAAA	965
SAV0662 (Mu50)	AAAGAAGTAATTCATACGAAATTGTATAAAGATAATTTATTTGATGTAAA	1100
SA0617 (N315)	AAAGAAGTAATTCATACGAAATTGTATAAAGATAATTTATTTGATGTAAA	1100
MW0624 (MW2)	AAAGAAGTAATTCATACGAAATTGTATAAAGATAATTTATTTGATGTAAA	1100
SAS0627 (MSSA476)	AAAGAAGTAATTCATACGAAATTGTATAAAGATAATTTATTTGATGTAAA	1100
SACOL0720_	AAAGAAGTAATTCATACGAAATTGTATAAAGATAATTTATTTGATGTAAA	1100
SAUSA300_0648 (USA300-FPR3757)	AAAGAAGTAATTCATACGAAATTGTATAAAGATAATTTATTTGATGTAAA	1100
SAOUHSC_00668 (NCTC8325)	AAAGAAGTAATTCATACGAAATTGTATAAAGATAATTTATTTGATGTAAA	1010
NWMN_0631 (Newman)	AAAGAAGTAATTCATACGAAATTGTATAAAGATAATTTATTTGATGTAAA	965
SAB0611 (RF122)	AAAGAAGTAATTCATACGAAATTGTATAAAGATAATTTATTTGATGTAAA	1100

SaurJH1_0700 (JH1)	AGCGAAAGAACCATAACAATGTAACAATTACTAGTGATAAATATATCCCTA	1015
SaurJH9_0685 (JH9)	AGCGAAAGAACCATAACAATGTAACAATTACTAGTGATAAATATATCCCTA	1015
SAHV_0659 (Mu3)	AGCGAAAGAACCATAACAATGTAACAATTACTAGTGATAAATATATCCCTA	1015
SAV0662 (Mu50)	AGCGAAAGAACCATAACAATGTAACAATTACTAGTGATAAATATATCCCTA	1150
SA0617 (N315)	AGCGAAAGAACCATAACAATGTAACAATTACTAGTGATAAATATATCCCTA	1150
MW0624 (MW2)	AGCGAAAGAACCATAACAATGTAACAATTACTAGTGATAAATATATCCCTA	1150
SAS0627 (MSSA476)	AGCGAAAGAACCATAACAATGTAACAATTACTAGTGATAAATATATCCCTA	1150
SACOL0720_	AGCGAAAGAACCATAACAATGTAACAATTACTAGTGATAAATATATCCCTA	1150
SAUSA300_0648 (USA300-FPR3757)	AGCGAAAGAACCATAACAATGTAACAATTACTAGTGATAAATATATCCCTA	1150
SAOUHSC_00668 (NCTC8325)	AGCGAAAGAACCATAACAATGTAACAATTACTAGTGATAAATATATCCCTA	1060
NWMN_0631 (Newman)	AGCGAAAGAACCATAACAATGTAACAATTACTAGTGATAAATATATCCCTA	1015
SAB0611 (RF122)	ATCGAAACAACCATAACAATGTAACAATTACTAGTGATAAATATATCCCTA	1150
	* *****	
SaurJH1_0700 (JH1)	ATACTGATTTGAAACGTGGACAAGCTGATTTGTTTGTAGCGGAAGGTTCT	1065
SaurJH9_0685 (JH9)	ATACTGATTTGAAACGTGGACAAGCTGATTTGTTTGTAGCGGAAGGTTCT	1065
SAHV_0659 (Mu3)	ATACTGATTTGAAACGTGGACAAGCTGATTTGTTTGTAGCGGAAGGTTCT	1065
SAV0662 (Mu50)	ATACTGATTTGAAACGTGGACAAGCTGATTTGTTTGTAGCGGAAGGTTCT	1200
SA0617 (N315)	ATACTGATTTGAAACGTGGACAAGCTGATTTGTTTGTAGCGGAAGGTTCT	1200
MW0624 (MW2)	ATACTGATTTGAAACGTGGACAAGCTGATTTGTTTGTAGCGGAAGGTTCT	1200
SAS0627 (MSSA476)	ATACTGATTTGAAACGTGGACAAGCTGATTTGTTTGTAGCGGAAGGTTCT	1200
SACOL0720_	ATACTGATTTGAAACGTGGGCAAGCTGATTTATTGTAGCGGAAGGTTCT	1200
SAUSA300_0648 (USA300-FPR3757)	ATACTGATTTGAAACGTGGGCAAGCTGATTTATTGTAGCGGAAGGTTCT	1200
SAOUHSC_00668 (NCTC8325)	ATACTGATTTGAAACGTGGGCAAGCTGATTTATTGTAGCGGAAGGTTCT	1110
NWMN_0631 (Newman)	ATACTGATTTGAAACGTGGGCAAGCTGATTTATTGTAGCGGAAGGTTCT	1065
SAB0611 (RF122)	GTACTGATTTGAAACGTGGGCAAGCTGATTTGTTTGTAGCGGAAGGTTCT	1200

FIG. 23E

SaurJH1_0700 (JH1)	ATCAAAGATTTAGTGAAACATAAGAAGCATGGTAAGGCAATTATAGGAAC	1115
SaurJH9_0685 (JH9)	ATCAAAGATTTAGTGAAACATAAGAAGCATGGTAAGGCAATTATAGGAAC	1115
SAHV_0659 (Mu3)	ATCAAAGATTTAGTGAAACATAAGAAGCATGGTAAGGCAATTATAGGAAC	1115
SAV0662 (Mu50)	ATCAAAGATTTAGTGAAACATAAGAAGCATGGTAAGGCAATTATAGGAAC	1250
SA0617 (N315)	ATCAAAGATTTAGTGAAACATAAGAAGCATGGTAAGGCAATTATAGGAAC	1250
MW0624 (MW2)	ATCAAAGATTTAGTGAAACATAAGAAGCATGGTAAGGCAATTATAGGAAC	1250
SAS0627 (MSSA476)	ATCAAAGATTTAGTGAAACATAAGAAGCATGGTAAGGCAATTATAGGAAC	1250
SACOL0720_	ATCAAAGATTTAGTGAAACATAAGAAGCATGGTAAGGCAATTATAGGAAC	1250
SAUSA300_0648 (USA300-FPR3757)	ATCAAAGATTTAGTGAAACATAAGAAGCATGGTAAGGCAATTATAGGAAC	1250
SAOUHSC_00668 (NCTC8325)	ATCAAAGATTTAGTGAAACATAAGAAGCATGGTAAGGCAATTATAGGAAC	1160
NWMN_0631 (Newman)	ATCAAAGATTTAGTGAAACATAAGAAGCATGGTAAGGCAATTATAGGAAC	1115
SAB0611 (RF122)	ATCAAAGATTTAGTGAAACATAAGAAGCATGGTAAGGCAATTATAGGAAC	1250

SaurJH1_0700 (JH1)	GAAAAAACATCATGTTAATATTAAGTTACGGAAAGATATTAATAAAATCT	1165
SaurJH9_0685 (JH9)	GAAAAAACATCATGTTAATATTAAGTTACGGAAAGATATTAATAAAATCT	1165
SAHV_0659 (Mu3)	GAAAAAACATCATGTTAATATTAAGTTACGGAAAGATATTAATAAAATCT	1165
SAV0662 (Mu50)	GAAAAAACATCATGTTAATATTAAGTTACGGAAAGATATTAATAAAATCT	1300
SA0617 (N315)	GAAAAAACATCATGTTAATATTAAGTTACGGAAAGATATTAATAAAATCT	1300
MW0624 (MW2)	GAAAAAACATCATGTTAATATTAAGTTGCGGAAAGATATTAATAAAATCT	1300
SAS0627 (MSSA476)	GAAAAAACATCATGTTAATATTAAGTTGCGGAAAGATATTAATAAAATCT	1300
SACOL0720_	GAAAAAACATCATGTTAATATTAAGTTACGTAAGATATTAATAAAATCT	1300
SAUSA300_0648 (USA300-FPR3757)	GAAAAAACATCATGTTAATATTAAGTTACGTAAGATATTAATAAAATCT	1300
SAOUHSC_00668 (NCTC8325)	GAAAAAACATCATGTTAATATTAAGTTACGTAAGATATTAATAAAATCT	1210
NWMN_0631 (Newman)	GAAAAAACATCATGTTAATATTAAGTTACGTAAGATATTAATAAAATCT	1165
SAB0611 (RF122)	GAAAAAACATCATGTTAATATTAAGTTACGTAAGATATTAATAAAATCT	1300

SaurJH1_0700 (JH1)	ATTTTATGACAGATGTTGATTAGGTGGACCAACGTTTGTCTTAAATGAC	1215
SaurJH9_0685 (JH9)	ATTTTATGACAGATGTTGATTAGGTGGACCAACGTTTGTCTTAAATGAC	1215
SAHV_0659 (Mu3)	ATTTTATGACAGATGTTGATTAGGTGGACCAACGTTTGTCTTAAATGAC	1215
SAV0662 (Mu50)	ATTTTATGACAGATGTTGATTAGGTGGACCAACGTTTGTCTTAAATGAC	1350
SA0617 (N315)	ATTTTATGACAGATGTTGATTAGGTGGACCAACGTTTGTCTTAAATGAC	1350
MW0624 (MW2)	ATTTTATGACAGATGTTGATTAGGTGGACCAACGTTTGTCTTAAATGAC	1350
SAS0627 (MSSA476)	ATTTTATGACAGATGTTGATTAGGTGGACCAACGTTTGTCTTAAATGAC	1350
SACOL0720_	ATTTTATGACAGATGTTGATTAGGTGGACCAACGTTTGTCTTAAATGAC	1350
SAUSA300_0648 (USA300-FPR3757)	ATTTTATGACAGATGTTGATTAGGTGGACCAACGTTTGTCTTAAATGAC	1350
SAOUHSC_00668 (NCTC8325)	ATTTTATGACAGATGTTGATTAGGTGGACCAACGTTTGTCTTAAATGAC	1260
NWMN_0631 (Newman)	ATTTTATGACAGATGTTGATTAGGTGGACCAACGTTTGTCTTAAATGAC	1215
SAB0611 (RF122)	ATTTTATGACAGATGTTGATTAGGTGGACCAACGTTTGTCTTAAATGAC	1350

SaurJH1_0700 (JH1)	AAAGACTATCAAGAAATAAGAAAGTATACAAAAGCAAAGCATATCGTCTC	1265
SaurJH9_0685 (JH9)	AAAGACTATCAAGAAATAAGAAAGTATACAAAAGCAAAGCATATCGTCTC	1265
SAHV_0659 (Mu3)	AAAGACTATCAAGAAATAAGAAAGTATACAAAAGCAAAGCATATCGTCTC	1265
SAV0662 (Mu50)	AAAGACTATCAAGAAATAAGAAAGTATACAAAAGCAAAGCATATCGTCTC	1400
SA0617 (N315)	AAAGACTATCAAGAAATAAGAAAGTATACAAAAGCAAAGCATATCGTCTC	1400
MW0624 (MW2)	AAAGACTATCAAGAAATAAGAAAGTATACAAAAGCAAAGCATATCGTCTC	1400
SAS0627 (MSSA476)	AAAGACTATCAAGAAATAAGAAAGTATACAAAAGCAAAGCATATCGTCTC	1400
SACOL0720_	AAAGACTATCAAGAAATAAGAAAGTATACAAAGGCAAAGCATATCGTCTC	1400
SAUSA300_0648 (USA300-FPR3757)	AAAGACTATCAAGAAATAAGAAAGTATACAAAGGCAAAGCATATCGTCTC	1400
SAOUHSC_00668 (NCTC8325)	AAAGACTATCAAGAAATAAGAAAGTATACAAAGGCAAAGCATATCGTCTC	1310
NWMN_0631 (Newman)	AAAGACTATCAAGAAATAAGAAAGTATACAAAGGCAAAGCATATCGTCTC	1265
SAB0611 (RF122)	AAAGACTATCAAGAAATAAGAAAGTATACAAAGGCAAAGCATATCGTCTC	1400

SaurJH1_0700 (JH1)	TCAATTTGGATTTCGATTTGAAACATAAAAAAGATGCTTTAGCATTAGAAA	1315
SaurJH9_0685 (JH9)	TCAATTTGGATTTCGATTTGAAACATAAAAAAGATGCTTTAGCATTAGAAA	1315
SAHV_0659 (Mu3)	TCAATTTGGATTTCGATTTGAAACATAAAAAAGATGCTTTAGCATTAGAAA	1315
SAV0662 (Mu50)	TCAATTTGGATTTCGATTTGAAACATAAAAAAGATGCTTTAGCATTAGAAA	1450
SA0617 (N315)	TCAATTTGGATTTCGATTTGAAACATAAAAAAGATGCTTTAGCATTAGAAA	1450
MW0624 (MW2)	TCAATTTGGATTTCGATTTGAAACATAAAAAAGATGCTTTAGCATTAGAAA	1450
SAS0627 (MSSA476)	TCAATTTGGATTTCGATTTGAAACATAAAAAAGATGCTTTAGCATTAGAAA	1450
SACOL0720_	TCAATTTGGATTTCGATTTGAAACATAAAAAAGATGCTTTAGCATTAGAAA	1450
SAUSA300_0648 (USA300-FPR3757)	TCAATTTGGATTTCGATTTGAAACATAAAAAAGATGCTTTAGCATTAGAAA	1450
SAOUHSC_00668 (NCTC8325)	TCAATTTGGATTTCGATTTGAAACATAAAAAAGATGCTTTAGCATTAGAAA	1360
NWMN_0631 (Newman)	TCAATTTGGATTTCGATTTGAAACATAAAAAAGATGCTTTAGCATTAGAAA	1315
SAB0611 (RF122)	TCAATTTGGATTTCGATTTGAAACATAAAAAAGATGCTTTAGCATTAGAAA	1450

FIG. 23F

SaurJH1_0700 (JH1)	AAGTGA AAAAATAAAGTTGATAAAATCTATTAAAAACAAGAAGTGAAGCGATA	1365
SaurJH9_0685 (JH9)	AAGTGA AAAAATAAAGTTGATAAAATCTATTAAAAACAAGAAGTGAAGCGATA	1365
SAHV_0659 (Mu3)	AAGTGA AAAAATAAAGTTGATAAAATCTATTAAAAACAAGAAGTGAAGCGATA	1365
SAV0662 (Mu50)	AAGTGA AAAAATAAAGTTGATAAAATCTATTAAAAACAAGAAGTGAAGCGATA	1500
SA0617 (N315)	AAGTGA AAAAATAAAGTTGATAAAATCTATTAAAAACAAGAAGTGAAGCGATA	1500
MW0624 (MW2)	AAGTGA AAAAATAAAGTTGATAAAATCTATTAAAAACAAGAAGTGAAGCGATA	1500
SAS0627 (MSSA476)	AAGTGA AAAAATAAAGTTGATAAAATCTATTAAAAACAAGAAGTGAAGCGATA	1500
SACOL0720_	AAGCGA AAAAATAAAGTTGATAAAATCTATTGAAACAAGAAGTGAAGCGATA	1500
SAUSA300_0648 (USA300-FPR3757)	AAGCGA AAAAATAAAGTTGATAAAATCTATTGAAACAAGAAGTGAAGCGATA	1500
SAOUHSC_00668 (NCTC8325)	AAGCGA AAAAATAAAGTTGATAAAATCTATTGAAACAAGAAGTGAAGCGATA	1410
NWMN_0631 (Newman)	AAGCGA AAAAATAAAGTTGATAAAATCTATTGAAACAAGAAGTGAAGCGATA	1365
SAB0611 (RF122)	AAGCGA AAAAATAAAGTTGATAAAATCTATTGAGACAAGAAGTGAAGCGATA	1500
	*** ***** * *****	
SaurJH1_0700 (JH1)	AGCTCAATATCAAGTTTAACCGGAATATTATTATTGTAACATCATTTTTT	1415
SaurJH9_0685 (JH9)	AGCTCAATATCAAGTTTAACCGGAATATTATTATTGTAACATCATTTTTT	1415
SAHV_0659 (Mu3)	AGCTCAATATCAAGTTTAACCGGAATATTATTATTGTAACATCATTTTTT	1415
SAV0662 (Mu50)	AGCTCAATATCAAGTTTAACCGGAATATTATTATTGTAACATCATTTTTT	1550
SA0617 (N315)	AGCTCAATATCAAGTTTAACCGGAATATTATTATTGTAACATCATTTTTT	1550
MW0624 (MW2)	AGCTCAATATCAAGTTTAACCGGAATATTATTATTGTAACATCATTTTTT	1550
SAS0627 (MSSA476)	AGCTCAATATCAAGTTTAACCGGAATATTATTATTGTAACATCATTTTTT	1550
SACOL0720_	AGCTCAATATCAAGTTTAACCGGAATATTATTATTGTAACATCATTTTTT	1550
SAUSA300_0648 (USA300-FPR3757)	AGCTCAATATCAAGTTTAACCGGAATATTATTATTGTAACATCATTTTTT	1550
SAOUHSC_00668 (NCTC8325)	AGCTCAATATCAAGTTTAACCGGAATATTATTATTGTAACATCATTTTTT	1460
NWMN_0631 (Newman)	AGCTCAATATCAAGTTTAACCGGAATATTATTATTGTAACATCATTTTTT	1415
SAB0611 (RF122)	AGCTCAATATCAAGTTTAACCGGAATATTATTATTGTAACATCATTTTTT	1550

SaurJH1_0700 (JH1)	AGGTATTACATTCTTGATTGCTGTATGTTGCATTATATACATTAAGCAAA	1465
SaurJH9_0685 (JH9)	AGGTATTACATTCTTGATTGCTGTATGTTGCATTATATACATTAAGCAAA	1465
SAHV_0659 (Mu3)	AGGTATTACATTCTTGATTGCTGTATGTTGCATTATATACATTAAGCAAA	1465
SAV0662 (Mu50)	AGGTATTACATTCTTGATTGCTGTATGTTGCATTATATACATTAAGCAAA	1600
SA0617 (N315)	AGGTATTACATTCTTGATTGCTGTATGTTGCATTATATACATTAAGCAAA	1600
MW0624 (MW2)	AGGTATTACATTCTTGATTGCTGTATGTTGCATTATATACATTAAGCAAA	1600
SAS0627 (MSSA476)	AGGTATTACATTCTTGATTGCTGTATGTTGCATTATATACATTAAGCAAA	1600
SACOL0720_	AGGTATTACATTCTTGATTGCTGTATGTTGCATTATATACATTAAGCAAA	1600
SAUSA300_0648 (USA300-FPR3757)	AGGTATTACATTCTTGATTGCTGTATGTTGCATTATATACATTAAGCAAA	1600
SAOUHSC_00668 (NCTC8325)	AGGTATTACATTCTTGATTGCTGTATGTTGCATTATATACATTAAGCAAA	1510
NWMN_0631 (Newman)	AGGTATTACATTCTTGATTGCTGTATGTTGCATTATATACATTAAGCAAA	1465
SAB0611 (RF122)	AGGTATTACATTCTTGATTGCTGTATGTTGCATTATATACATTAAGCAAA	1600

SaurJH1_0700 (JH1)	TAGATGAAACCGAAGATGAGTTAGAGAATTATAGTATATTGAGAAAGCTT	1515
SaurJH9_0685 (JH9)	TAGATGAAACCGAAGATGAGTTAGAGAATTATAGTATATTGAGAAAGCTT	1515
SAHV_0659 (Mu3)	TAGATGAAACCGAAGATGAGTTAGAGAATTATAGTATATTGAGAAAGCTT	1515
SAV0662 (Mu50)	TAGATGAAACCGAAGATGAGTTAGAGAATTATAGTATATTGAGAAAGCTT	1650
SA0617 (N315)	TAGATGAAACCGAAGATGAGTTAGAGAATTATAGTATATTGAGAAAGCTT	1650
MW0624 (MW2)	TAGATGAAACCGAAGATGAGTTAGAGAATTATAGTATTTTGAGAAAGCTT	1650
SAS0627 (MSSA476)	TAGATGAAACCGAAGATGAGTTAGAGAATTATAGTATTTTGAGAAAGCTT	1650
SACOL0720_	TAGATGAAACCGAAGATGAGTTAGAGAATTATAGTATTTTGAGAAAGCTT	1650
SAUSA300_0648 (USA300-FPR3757)	TAGATGAAACCGAAGATGAGTTAGAGAATTATAGTATTTTGAGAAAGCTT	1650
SAOUHSC_00668 (NCTC8325)	TAGATGAAACCGAAGATGAGTTAGAGAATTATAGTATTTTGAGAAAGCTT	1560
NWMN_0631 (Newman)	TAGATGAAACCGAAGATGAGTTAGAGAATTATAGTATTTTGAGAAAGCTT	1515
SAB0611 (RF122)	TAGATGAAACCGAAGATGAGTTAGAGAATTATAGTATATTGAGAAAGCTT	1650

SaurJH1_0700 (JH1)	GGATTTACACAAAAAGATATGGCAAGGGGACTAAAGTTTAAAAATTATGTT	1565
SaurJH9_0685 (JH9)	GGATTTACACAAAAAGATATGGCAAGGGGACTAAAGTTTAAAAATTATGTT	1565
SAHV_0659 (Mu3)	GGATTTACACAAAAAGATATGGCAAGGGGACTAAAGTTTAAAAATTATGTT	1565
SAV0662 (Mu50)	GGATTTACACAAAAAGATATGGCAAGGGGACTAAAGTTTAAAAATTATGTT	1700
SA0617 (N315)	GGATTTACACAAAAAGATATGGCAAGGGGACTAAAGTTTAAAAATTATGTT	1700
MW0624 (MW2)	GGATTTACACAAAAAGATATGGCAAGGGGACTAAAGTTTAAAAATTATGTT	1700
SAS0627 (MSSA476)	GGATTTACACAAAAAGATATGGCAAGGGGACTAAAGTTTAAAAATTATGTT	1700
SACOL0720_	GGATTTACACAAAAAGATATGGCAAGGGGACTAAAGTTTAAAAATTATGTT	1700
SAUSA300_0648 (USA300-FPR3757)	GGATTTACACAAAAAGATATGGCAAGGGGACTAAAGTTTAAAAATTATGTT	1700
SAOUHSC_00668 (NCTC8325)	GGATTTACACAAAAAGATATGGCAAGGGGACTAAAGTTTAAAAATTATGTT	1610
NWMN_0631 (Newman)	GGATTTACACAAAAAGATATGGCAAGGGGACTAAAGTTTAAAAATTATGTT	1565
SAB0611 (RF122)	GGATTTACACAAAAAGATATGGCAAGGGGACTAAAGTTTAAAAATTATGTT	1700

FIG. 23G

SaurJH1_0700 (JH1)	TAATTTTGGGTTACCTTTAGTTATTGCACTATCACATGCATATTTTACAT	1615
SaurJH9_0685 (JH9)	TAATTTTGGGTTACCTTTAGTTATTGCACTATCACATGCATATTTTACAT	1615
SAHV_0659 (Mu3)	TAATTTTGGGTTACCTTTAGTTATTGCACTATCACATGCATATTTTACAT	1615
SAV0662 (Mu50)	TAATTTTGGGTTACCTTTAGTTATTGCACTATCACATGCATATTTTACAT	1750
SA0617 (N315)	TAATTTTGGGTTACCTTTAGTTATTGCACTATCACATGCATATTTTACAT	1750
MW0624 (MW2)	TAATTTTGGGTTACCTTTAGTTATTGCACTATCACATGCATATTTTACAT	1750
SAS0627 (MSSA476)	TAATTTTGGGTTACCTTTAGTTATTGCACTATCACATGCATATTTTACAT	1750
SACOL0720_	TAATTTTGGGTTACCTTTAGTTATTGCACTATCACATGCATATTTTACAT	1750
SAUSA300_0648 (USA300-FPR3757)	TAATTTTGGGTTACCTTTAGTTATTGCACTATCACATGCATATTTTACAT	1750
SAOUHSC_00668 (NCTC8325)	TAATTTTGGGTTACCTTTAGTTATTGCACTATCACATGCATATTTTACAT	1660
NWMN_0631 (Newman)	TAATTTTGGGTTACCTTTAGTTATTGCACTATCACATGCATATTTTACAT	1615
SAB0611 (RF122)	TAATTTTGGGTTACCTTTAGTTATTGCACTATCACATGCATATTTTACAT	1750

SaurJH1_0700 (JH1)	CATTAGCATATATGAAATTAATGGGTACAACGAATCAAATACCGGTTTTTC	1665
SaurJH9_0685 (JH9)	CATTAGCATATATGAAATTAATGGGTACAACGAATCAAATACCGGTTTTTC	1665
SAHV_0659 (Mu3)	CATTAGCATATATGAAATTAATGGGTACAACGAATCAAATACCGGTTTTTC	1665
SAV0662 (Mu50)	CATTAGCATATATGAAATTAATGGGTACAACGAATCAAATACCGGTTTTTC	1800
SA0617 (N315)	CATTAGCATATATGAAATTAATGGGTACAACGAATCAAATACCGGTTTTTC	1800
MW0624 (MW2)	CATTAGCATATATGAAATTAATGGGTACAACGAATCAAATACCGGTTTTTC	1800
SAS0627 (MSSA476)	CATTAGCATATATGAAATTAATGGGTACAACGAATCAAATACCGGTTTTTC	1800
SACOL0720_	CATTAGCATATATGAAATTAATGGGTACAACGAATCAAATACCGGTTTTTC	1800
SAUSA300_0648 (USA300-FPR3757)	CATTAGCATATATGAAATTAATGGGTACAACGAATCAAATACCGGTTTTTC	1800
SAOUHSC_00668 (NCTC8325)	CATTAGCATATATGAAATTAATGGGTACAACGAATCAAATACCGGTTTTTC	1710
NWMN_0631 (Newman)	CATTAGCATATATGAAATTAATGGGTACAACGAATCAAATACCGGTTTTTC	1665
SAB0611 (RF122)	CATTAGCATATATGAAATTAATGGGTACAACGAATCAAATACCGGTTTTTC	1800

SaurJH1_0700 (JH1)	ATAGTAATGGGATTATACATTTGTATGTATGCTGTTTTTGCAGTGACGGC	1715
SaurJH9_0685 (JH9)	ATAGTAATGGGATTATACATTTGTATGTATGCTGTTTTTGCAGTGACGGC	1715
SAHV_0659 (Mu3)	ATAGTAATGGGATTATACATTTGTATGTATGCTGTTTTTGCAGTGACGGC	1715
SAV0662 (Mu50)	ATAGTAATGGGATTATACATTTGTATGTATGCTGTTTTTGCAGTGACGGC	1850
SA0617 (N315)	ATAGTAATGGGATTATACATTTGTATGTATGCTGTTTTTGCAGTGACGGC	1850
MW0624 (MW2)	ATAGTAATGGGATTATACATTTGTATGTATGCTGTTTTTGCAGTGACGGC	1850
SAS0627 (MSSA476)	ATAGTAATGGGATTATACATTTGTATGTATGCTGTTTTTGCAGTGACGGC	1850
SACOL0720_	ATAGTAATGGGATTATACATTTGTATGTATGCTGTTTTTGCAGTGACGGC	1850
SAUSA300_0648 (USA300-FPR3757)	ATAGTAATGGGATTATACATTTGTATGTATGCTGTTTTTGCAGTGACGGC	1850
SAOUHSC_00668 (NCTC8325)	ATAGTAATGGGATTATACATTTGTATGTATGCTGTTTTTGCAGTGACGGC	1760
NWMN_0631 (Newman)	ATAGTAATGGGATTATACATTTGTATGTATGCTGTTTTTGCAGTGACGGC	1715
SAB0611 (RF122)	ATAGTAATGGGATTATACATTTGTATGTATGCTGTTTTTGCAGTGACGGC	1850

SaurJH1_0700 (JH1)	TTATAATCATTTCCAAGCGAACAATTAGACATTCCATATAA	1755
SaurJH9_0685 (JH9)	TTATAATCATTTCCAAGCGAACAATTAGACATTCCATATAA	1755
SAHV_0659 (Mu3)	TTATAATCATTTCCAAGCGAACAATTAGACATTCCATATAA	1755
SAV0662 (Mu50)	TTATAATCATTTCCAAGCGAACAATTAGACATTCCATATAA	1890
SA0617 (N315)	TTATAATCATTTCCAAGCGAACAATTAGACATTCCATATAA	1890
MW0624 (MW2)	TTATAATCATTTCCAAGCGAACAATTAGACATTCCATATAA	1890
SAS0627 (MSSA476)	TTATAATCATTTCCAAGCGAACAATTAGACATTCCATATAA	1890
SACOL0720_	TTATAATCATTTCCAAGCGAACAATTAGACATTCCATATAA	1890
SAUSA300_0648 (USA300-FPR3757)	TTATAATCATTTCCAAGCGAACAATTAGACATTCCATATAA	1890
SAOUHSC_00668 (NCTC8325)	TTATAATCATTTCCAAGCGAACAATTAGACATTCCATATAA	1800
NWMN_0631 (Newman)	TTATAATCATTTCCAAGCGAACAATTAGACATTCCATATAA	1755
SAB0611 (RF122)	TTATAATCATTTCCAAGCGAACAATTAGACATTCCATATAA	1890

FIG. 23H

II- SACOL0720 : Multiple polypeptide sequences alignment:selected epitopes shaded

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SACOL0720_      MTFNEIIFKNFRQNLSHYAIYLFSLITSVVLYFSFVALKYAHKLNMTESY 50
SAUSA300_0648 (USA300-FPR3757) MTFNEIIFKNFRQNLSHYAIYLFSLITSVVLYFSFVALKYAHKLNMTESY 50
SAOUHSC_00668 (NCTC8325) -----MYFSFVALKYAHKLNMTESY 20
NWMN_0631 (Newman) -----MTESY 5
SaurJH1_0700 (JH1) -----MTESY 5
SaurJH9_0685 (JH9) -----MTESY 5
SAHV_0659 (Mu3) -----MTESY 5
SAV0662 (Mu50) MTFNEIIFKNFRQNLSHYAIYLFSLITSVVLYFSFVALKYAHKLNMTESY 50
SA0617 (N315) MTFNEIIFKNFRQNLSHYAIYLFSLITSVVLYFSFVALKYAHKLNMTESY 50
MW0624 (MW2) MTFNEIIFKNFRQNLSHYAIYLFSLITSVVLYFSFVALKYAHKLNMTESY 50
SAS0627 (MSSA476) MTFNEIIFKNFRQNLSHYAIYLFSLITSVVLYFSFVALKYAHKLNMTESY 50
SAB0611 (RF122) MTFNEIIFKNFRQNLSHYAIYLFSLITSVVLYFSFVALKYAHKLNMTESY 50
*****

Consensus      XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXMTESY

SACOL0720_      PIIKEGSQVGSYFLFFIIIAFLLYANVLFIKRRSYELALYQTLGLSKFNI 100
SAUSA300_0648 (USA300-FPR3757) PIIKEGSQVGSYFLFFIIIAFLLYANVLFIKRRSYELALYQTLGLSKFNI 100
SAOUHSC_00668 (NCTC8325) PIIKEGSQVGSYFLFFIIIAFLLYANVLFIKRRSYELALYQTLGLSKFNI 70
NWMN_0631 (Newman) PIIKEGSQVGSYFLFFIIIAFLLYANVLFIKRRSYELALYQTLGLSKFNI 55
SaurJH1_0700 (JH1) PIIKEGSQVGSYFLFFIIIAFLLYANVLFIKRRSYELALYQTLGLSKFNI 55
SaurJH9_0685 (JH9) PIIKEGSQVGSYFLFFIIIAFLLYANVLFIKRRSYELALYQTLGLSKFNI 55
SAHV_0659 (Mu3) PIIKEGSQVGSYFLFFIIIAFLLYANVLFIKRRSYELALYQTLGLSKFNI 55
SAV0662 (Mu50) PIIKEGSQVGSYFLFFIIIAFLLYANVLFIKRRSYELALYQTLGLSKFNI 100
SA0617 (N315) PIIKEGSQVGSYFLFFIIIAFLLYANVLFIKRRSYELALYQTLGLSKFNI 100
MW0624 (MW2) PIIKEGSQVGSYFLFFIIIAFLLYANVLFIKRRSYELALYQTLGLSKFNI 100
SAS0627 (MSSA476) PIIKEGSQVGSYFLFFIIIAFLLYANVLFIKRRSYELALYQTLGLSKFNI 100
SAB0611 (RF122) PIIKEGSQVGSYFLFFIIIAFLLYANVLFIKRRSYELALYQTLGLSKFNI 100
*****

Consensus      PIIKEGSQVGSYFLFFIIIAFLLYANVLFIKRRSYELALYQTLGLSKFNI

SACOL0720_      IYILMLEQLLIFIITAILGIIIGIFGSKLLLMIVFTLLGIKEKVPIIFSL 150
SAUSA300_0648 (USA300-FPR3757) IYILMLEQLLIFIITAILGIIIGIFGSKLLLMIVFTLLGIKEKVPIIFSL 150
SAOUHSC_00668 (NCTC8325) IYILMLEQLLIFIITAILGIIIGIFGSKLLLMIVFTLLGIKEKVPIIFSL 120
NWMN_0631 (Newman) IYILMLEQLLIFIITAILGIIIGIFGSKLLLMIVFTLLGIKEKVPIIFSL 105
SaurJH1_0700 (JH1) IYILMLEQLLIFIITAILGIIIGIFGSKLLLMIVFTLLGIKEKVPIIFSL 105
SaurJH9_0685 (JH9) IYILMLEQLLIFIITAILGIIIGIFGSKLLLMIVFTLLGIKEKVPIIFSL 105
SAHV_0659 (Mu3) IYILMLEQLLIFIITAILGIIIGIFGSKLLLMIVFTLLGIKEKVPIIFSL 105
SAV0662 (Mu50) IYILMLEQLLIFIITAILGIIIGIFGSKLLLMIVFTLLGIKEKVPIIFSL 150
SA0617 (N315) IYILMLEQLLIFIITAILGIIIGIFGSKLLLMIVFTLLGIKEKVPIIFSL 150
MW0624 (MW2) IYILMLEQLLIFIITAILGIIIGIFGSKLLLMIVFTLLGIKEKVPIIFSL 150
SAS0627 (MSSA476) IYILMLEQLLIFIITAILGIIIGIFGSKLLLMIVFTLLGIKEKVPIIFSL 150
SAB0611 (RF122) IYILMLEQLLIFIITAILGIIIGIFGSKLLLMIVFTLLGIKEKVPIIFSL 150
*****

Consensus      IYILMLEQLLIFIITAILGIIIGIFGSKLLLMIVFTLLGIKEKVPIIFSL

SACOL0720_      RAVFETLMLIGVAYFLTSAQNFILVFKQSIQMSKNNQVKETNHNKITFE 200
SAUSA300_0648 (USA300-FPR3757) RAVFETLMLIGVAYFLTSAQNFILVFKQSIQMSKNNQVKETNHNKITFE 200
SAOUHSC_00668 (NCTC8325) RAVFETLMLIGVAYFLTSAQNFILVFKQSIQMSKNNQVKETNHNKITFE 170
NWMN_0631 (Newman) RAVFETLMLIGVAYFLTSAQNFILVFKQSIQMSKNNQVKETNHNKITFE 155
SaurJH1_0700 (JH1) RAVFETLMLIGVAYFLTSAQNFILVFKQSIQMSKNNQVKETNHNKITFE 155
SaurJH9_0685 (JH9) RAVFETLMLIGVAYFLTSAQNFILVFKQSIQMSKNNQVKETNHNKITFE 155
SAHV_0659 (Mu3) RAVFETLMLIGVAYFLTSAQNFILVFKQSIQMSKNNQVKETNHNKITFE 155
SAV0662 (Mu50) RAVFETLMLIGVAYFLTSAQNFILVFKQSIQMSKNNQVKETNHNKITFE 200
SA0617 (N315) RAVFETLMLIGVAYFLTSAQNFILVFKQSIQMSKNNQVKETNHNKITFE 200
MW0624 (MW2) RAVFETLMLIGVAYFLTSAQNFILVFKQSIQMSKNNQVKETNHNKITFE 200
SAS0627 (MSSA476) RAVFETLMLIGVAYFLTSAQNFILVFKQSIQMSKNNQVKETNHNKITFE 200
SAB0611 (RF122) RAVFETLMLIGVAYFLTSAQNFILVFKQSIQMSKNNQVKETNHNKITFE 200
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Consensus      RAVFETLMLIGVAYFLTSAQNFILVFKQSIQMSKNNQVKETNHNKITFE

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FIG. 23I

SACOL0720_		EVVLGILGIVLITTTGYLSSLNIVQYYDSIGTLMFILLSTVIGAYLFFKSS	250
SAUSA300_0648 (USA300-FPR3757)		EVVLGILGIVLITTTGYLSSLNIVQYYDSIGTLMFILLSTVIGAYLFFKSS	250
SAOUHSC_00668 (NCTC8325)		EVVLGILGIVLITTTGYLSSLNIVQYYDSIGTLMFILLSTVIGAYLFFKSS	220
NWMN_0631 (Newman)		EVVLGILGIVLITTTGYLSSLNIVQYYDSIGTLMFILLSTVIGAYLFFKSS	205
SaurJH1_0700 (JH1)		EVVLGILGIVLITTTGYLSSLNIVQYYDSIGTLMFILLSTVIGAYLFFKSS	205
SaurJH9_0685 (JH9)		EVVLGILGIVLITTTGYLSSLNIVQYYDSIGTLMFILLSTVIGAYLFFKSS	205
SAHV_0659 (Mu3)		EVVLGILGIVLITTTGYLSSLNIVQYYDSIGTLMFILLSTVIGAYLFFKSS	205
SAV0662 (Mu50)		EVVLGILGIVLITTTGYLSSLNIVQYYDSIGTLMFILLSTVIGAYLFFKSS	250
SA0617 (N315)		EVVLGILGIVLITTTGYLSSLNIVQYYDSIGTLMFILLSTVIGAYLFFKSS	250
MW0624 (MW2)		EVVLGILGIVLITTTGYLSSLNIVQYYDSIGTLMFILLSTVIGAYLFFKSS	250
SAS0627 (MSSA476)		EVVLGILGIVLITTTGYLSSLNIVQYYDSIGTLMFILLSTVIGAYLFFKSS	250
SAB0611 (RF122)		EVVLGILGIVLITTTGYLSSLNIVQYYDSIGTLMFILLSTVIGAYLFFKSS	250
Consensus		EVVLGILGIVLITTTGYLSSLNIVQYYDSIGTLMFILLSTVIGAYLFFKSS	
SACOL0720_		VSLVFKMVKKFRKGVISVNDVMFSSSIMYRIKKNAFSLTVMIAISAITVS	300
SAUSA300_0648 (USA300-FPR3757)		VSLVFKMVKKFRKGVISVNDVMFSSSIMYRIKKNAFSLTVMIAISAITVS	300
SAOUHSC_00668 (NCTC8325)		VSLVFKMVKKFRKGVISVNDVMFSSSIMYRIKKNAFSLTVMIAISAITVS	270
NWMN_0631 (Newman)		VSLVFKMVKKFRKGVISVNDVMFSSSIMYRIKKNAFSLTVMIAISAITVS	255
SaurJH1_0700 (JH1)		VSLVFKMVKKFRKGVISVNDVMFSSSIMYRIKKNAFSLTVMIAISAITVS	255
SaurJH9_0685 (JH9)		VSLVFKMVKKFRKGVISVNDVMFSSSIMYRIKKNAFSLTVMIAISAITVS	255
SAHV_0659 (Mu3)		VSLVFKMVKKFRKGVISVNDVMFSSSIMYRIKKNAFSLTVMIAISAITVS	255
SAV0662 (Mu50)		VSLVFKMVKKFRKGVISVNDVMFSSSIMYRIKKNAFSLTVMIAISAITVS	300
SA0617 (N315)		VSLVFKMVKKFRKGVISVNDVMFSSSIMYRIKKNAFSLTVMIAISAITVS	300
MW0624 (MW2)		VSLVFKMVKKFRKGVISVNDVMFSSSIMYRIKKNAFSLTVMIAISAITVS	300
SAS0627 (MSSA476)		VSLVFKMVKKFRKGVISVNDVMFSSSIMYRIKKNAFSLTVMIAISAITVS	300
SAB0611 (RF122)		VSLVFKMVKKFRKGVISVNDVMFSSSIMYRIKKNAFSLTVMIAISAITVS	300
Consensus		VSLVFKMVKKFRKGVISVNDVMFSSSIMYRIKKNAFSLTVMIAISAITVS	
SACOL0720		VLCFAAISRASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNY	350
SAUSA300_0648 (USA300-FPR3757)		VLCFAAISRASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNY	350
SAOUHSC_00668 (NCTC8325)		VLCFAAISRASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNY	320
NWMN_0631 (Newman)		VLCFAAISRASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNY	305
SaurJH1_0700 (JH1)		VLCFAAISRASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNY	305
SaurJH9_0685 (JH9)		VLCFAAISRASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNY	305
SAHV_0659 (Mu3)		VLCFAAISRASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNY	305
SAV0662 (Mu50)		VLCFAAISRASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNY	350
SA0617 (N315)		VLCFAAISRASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNY	350
MW0624 (MW2)		VLCFAAISRASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNY	350
SAS0627 (MSSA476)		VLCFAAISRASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNY	350
SAB0611 (RF122)		VLCFAAISRASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNY	350
Consensus		VLCFAAISRASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNY	
SACOL0720_		KEVIHTKLYKDNLFVDVKAKEPYNVTITSDKYIPNTDLKRGQADLFVAEGS	400
SAUSA300_0648 (USA300-FPR3757)		KEVIHTKLYKDNLFVDVKAKEPYNVTITSDKYIPNTDLKRGQADLFVAEGS	400
SAOUHSC_00668 (NCTC8325)		KEVIHTKLYKDNLFVDVKAKEPYNVTITSDKYIPNTDLKRGQADLFVAEGS	370
NWMN_0631 (Newman)		KEVIHTKLYKDNLFVDVKAKEPYNVTITSDKYIPNTDLKRGQADLFVAEGS	355
SaurJH1_0700 (JH1)		KEVIHTKLYKDNLFVDVKAKEPYNVTITSDKYIPNTDLKRGQADLFVAEGS	355
SaurJH9_0685 (JH9)		KEVIHTKLYKDNLFVDVKAKEPYNVTITSDKYIPNTDLKRGQADLFVAEGS	355
SAHV_0659 (Mu3)		KEVIHTKLYKDNLFVDVKAKEPYNVTITSDKYIPNTDLKRGQADLFVAEGS	355
SAV0662 (Mu50)		KEVIHTKLYKDNLFVDVKAKEPYNVTITSDKYIPNTDLKRGQADLFVAEGS	400
SA0617 (N315)		KEVIHTKLYKDNLFVDVKAKEPYNVTITSDKYIPNTDLKRGQADLFVAEGS	400
MW0624 (MW2)		KEVIHTKLYKDNLFVDVKAKEPYNVTITSDKYIPNTDLKRGQADLFVAEGS	400
SAS0627 (MSSA476)		KEVIHTKLYKDNLFVDVKAKEPYNVTITSDKYIPNTDLKRGQADLFVAEGS	400
SAB0611 (RF122)		KEVIHTKLYKDNLFVDVKSQPYNVTITSDKYIPNTDLKRGQADLFVAEGS	400
Consensus		KEVIHTKLYKDNLFVDVKKXPYNVTITSDKYIPNTDLKRGQADLFVAEGS	
SACOL0720_		IKDLVKHKKHKGKAIIGTKKHHVNIKLKRDINKIYFMTDVDLGGPTFVLND	450
SAUSA300_0648 (USA300-FPR3757)		IKDLVKHKKHKGKAIIGTKKHHVNIKLKRDINKIYFMTDVDLGGPTFVLND	450
SAOUHSC_00668 (NCTC8325)		IKDLVKHKKHKGKAIIGTKKHHVNIKLKRDINKIYFMTDVDLGGPTFVLND	420
NWMN_0631 (Newman)		IKDLVKHKKHKGKAIIGTKKHHVNIKLKRDINKIYFMTDVDLGGPTFVLND	405
SaurJH1_0700 (JH1)		IKDLVKHKKHKGKAIIGTKKHHVNIKLKRDINKIYFMTDVDLGGPTFVLND	405
SaurJH9_0685 (JH9)		IKDLVKHKKHKGKAIIGTKKHHVNIKLKRDINKIYFMTDVDLGGPTFVLND	405
SAHV_0659 (Mu3)		IKDLVKHKKHKGKAIIGTKKHHVNIKLKRDINKIYFMTDVDLGGPTFVLND	405
SAV0662 (Mu50)		IKDLVKHKKHKGKAIIGTKKHHVNIKLKRDINKIYFMTDVDLGGPTFVLND	450
SA0617 (N315)		IKDLVKHKKHKGKAIIGTKKHHVNIKLKRDINKIYFMTDVDLGGPTFVLND	450
MW0624 (MW2)		IKDLVKHKKHKGKAIIGTKKHHVNIKLKRDINKIYFMTDVDLGGPTFVLND	450
SAS0627 (MSSA476)		IKDLVKHKKHKGKAVIGTKKHHVNIKLKRDINKIYFMTDVDLGGPTFVLND	450
SAB0611 (RF122)		IKDLVKHKKHKGKAVIGTKKHHVNIKLKRDINKIYFMTDVDLGGPTFVLND	450
Consensus		IKDLVKHKKHKGKAXIGTKKHHVNIKLKRDINKIYFMTDVDLGGPTFVLND	

FIG. 23J

SACOL0720_	KDYQEIRKYTKAKHIVS	QFGFDLKHKKDALALEKAKNKVDKSIETRSEAI	500
SAUSA300_0648 (USA300-FPR3757)	KDYQEIRKYTKAKHIVS	QFGFDLKHKKDALALEKAKNKVDKSIETRSEAI	500
SAOUHSC_00668 (NCTC8325)	KDYQEIRKYTKAKHIVS	QFGFDLKHKKDALALEKAKNKVDKSIETRSEAI	470
NWMN_0631 (Newman)	KDYQEIRKYTKAKHIVS	QFGFDLKHKKDALALEKAKNKVDKSIETRSEAI	455
SaurJH1_0700 (JH1)	KDYQEIRKYTKAKHIVS	QFGFDLKHKKDALALEKAKNKVDKSIETRSEAI	455
SaurJH9_0685 (JH9)	KDYQEIRKYTKAKHIVS	QFGFDLKHKKDALALEKAKNKVDKSIETRSEAI	455
SAHV_0659 (Mu3)	KDYQEIRKYTKAKHIVS	QFGFDLKHKKDALALEKAKNKVDKSIETRSEAI	455
SAV0662 (Mu50)	KDYQEIRKYTKAKHIVS	QFGFDLKHKKDALALEKAKNKVDKSIETRSEAI	500
SA0617 (N315)	KDYQEIRKYTKAKHIVS	QFGFDLKHKKDALALEKAKNKVDKSIETRSEAI	500
MW0624 (MW2)	KDYQEIRKYTKAKHIVS	QFGFDLKHKKDALALEKAKNKVDKSIETRSEAI	500
SAS0627 (MSSA476)	KDYQEIRKYTKAKHIVS	QFGFDLKHKKDALALEKAKNKVDKSIETRSEAI	500
SAB0611 (RF122)	KDYQEIRKYTKAKHIVS	QFGFDLKHKKDALALEKAKNKVDKSIETRSEAI	500
Consensus	KDYQEIRKYTKAKHIVS	QFGFDLKHKKDALALEKAXNKVDKSIETRSEAI	
SACOL0720_	SSISSLTGILLFVTSFLGITFLIAVCCIIYIKQIDETEDENYSILRKL		550
SAUSA300_0648 (USA300-FPR3757)	SSISSLTGILLFVTSFLGITFLIAVCCIIYIKQIDETEDENYSILRKL		550
SAOUHSC_00668 (NCTC8325)	SSISSLTGILLFVTSFLGITFLIAVCCIIYIKQIDETEDENYSILRKL		520
NWMN_0631 (Newman)	SSISSLTGILLFVTSFLGITFLIAVCCIIYIKQIDETEDENYSILRKL		505
SaurJH1_0700 (JH1)	SSISSLTGILLFVTSFLGITFLIAVCCIIYIKQIDETEDENYSILRKL		505
SaurJH9_0685 (JH9)	SSISSLTGILLFVTSFLGITFLIAVCCIIYIKQIDETEDENYSILRKL		505
SAHV_0659 (Mu3)	SSISSLTGILLFVTSFLGITFLIAVCCIIYIKQIDETEDENYSILRKL		505
SAV0662 (Mu50)	SSISSLTGILLFVTSFLGITFLIAVCCIIYIKQIDETEDENYSILRKL		550
SA0617 (N315)	SSISSLTGILLFVTSFLGITFLIAVCCIIYIKQIDETEDENYSILRKL		550
MW0624 (MW2)	SSISSLTGILLFVTSFLGITFLIAVCCIIYIKQIDETEDENYSILRKL		550
SAS0627 (MSSA476)	SSISSLTGILLFVTSFLGITFLIAVCCIIYIKQIDETEDENYSILRKL		550
SAB0611 (RF122)	SSISSLTGILLFVTSFLGITFLIAVCCIIYIKQIDETEDENYSILRKL		550
Consensus	SSISSLTGILLFVTSFLGITFLIAVCCIIYIKQIDETEDENYSILRKL		
SACOL0720_	GFTQKDMARGLKFKIMFNFGFLPLVIALSHAYFTSLAYMKLMGTTNQIPVF		600
SAUSA300_0648 (USA300-FPR3757)	GFTQKDMARGLKFKIMFNFGFLPLVIALSHAYFTSLAYMKLMGTTNQIPVF		600
SAOUHSC_00668 (NCTC8325)	GFTQKDMARGLKFKIMFNFGFLPLVIALSHAYFTSLAYMKLMGTTNQIPVF		570
NWMN_0631 (Newman)	GFTQKDMARGLKFKIMFNFGFLPLVIALSHAYFTSLAYMKLMGTTNQIPVF		555
SaurJH1_0700 (JH1)	GFTQKDMARGLKFKIMFNFGFLPLVIALSHAYFTSLAYMKLMGTTNQIPVF		555
SaurJH9_0685 (JH9)	GFTQKDMARGLKFKIMFNFGFLPLVIALSHAYFTSLAYMKLMGTTNQIPVF		555
SAHV_0659 (Mu3)	GFTQKDMARGLKFKIMFNFGFLPLVIALSHAYFTSLAYMKLMGTTNQIPVF		555
SAV0662 (Mu50)	GFTQKDMARGLKFKIMFNFGFLPLVIALSHAYFTSLAYMKLMGTTNQIPVF		600
SA0617 (N315)	GFTQKDMARGLKFKIMFNFGFLPLVIALSHAYFTSLAYMKLMGTTNQIPVF		600
MW0624 (MW2)	GFTQKDMARGLKFKIMFNFGFLPLVIALSHAYFTSLAYMKLMGTTNQIPVF		600
SAS0627 (MSSA476)	GFTQKDMARGLKFKIMFNFGFLPLVIALSHAYFTSLAYMKLMGTTNQIPVF		600
SAB0611 (RF122)	GFTQKDMARGLKFKIMFNFGFLPLVIALSHAYFTSLAYMKLMGTTNQIPVF		600
Consensus	GFTQKDMARGLKFKIMFNFGFLPLVIXLSHAYFTSLAYMKLMGTTNQIPVF		
SACOL0720_	IVMGLYICMYAVFAVTAYNHSKRTIRHSI		629
SAUSA300_0648 (USA300-FPR3757)	IVMGLYICMYAVFAVTAYNHSKRTIRHSI		629
SAOUHSC_00668 (NCTC8325)	IVMGLYICMYAVFAVTAYNHSKRTIRHSI		599
NWMN_0631 (Newman)	IVMGLYICMYAVFAVTAYNHSKRTIRHSI		584
SaurJH1_0700 (JH1)	IVMGLYICMYAVFAVTAYNHSKRTIRHSI		584
SaurJH9_0685 (JH9)	IVMGLYICMYAVFAVTAYNHSKRTIRHSI		584
SAHV_0659 (Mu3)	IVMGLYICMYAVFAVTAYNHSKRTIRHSI		584
SAV0662 (Mu50)	IVMGLYICMYAVFAVTAYNHSKRTIRHSI		629
SA0617 (N315)	IVMGLYICMYAVFAVTAYNHSKRTIRHSI		629
MW0624 (MW2)	IVMGLYICMYAVFAVTAYNHSKRTIRHSI		629
SAS0627 (MSSA476)	IVMGLYICMYAVFAVTAYNHSKRTIRHSI		629
SAB0611 (RF122)	IVMGLYICMYAVFAVTAYNHSKRTIRHSI		629
Consensus	IVMGLYICMYAVFAVTAYNHSKRTIRHSI		

FIG. 23K

SACOL0029: Multiple polypeptide sequences alignment: hypothetical epitope shaded

SACOL0029 (COL)	-----MLESREQLSVEEYETFFNRFDNQ EFDF
MW0028 (MW2)	-----MLESREQLSVEEYETFFNRFDNQ EFDF
SAUSA300_0029 (USA300-FPR3757)	-----MLESREQLSVEEYETFFNRFDNQ EFDF
SAHV_0037 (Mu3)	CLFSYSGS GAVGEIFSGSIVKGYDKALDKEKHLNMLESREQLSVEEYETFFNRFDNQ EFDF
SAV0038 (Mu)	CLFSYSGS GAVGEIFSGSIVKGYDKALDKEKHLNMLESREQLSVEEYETFFNRFDNQ EFDF
SA0035	CLFSYSGS GAVGEIFSGSIVKGYDKALDKEKHLNMLESREQLSVEEYETFFNRFDNQ EFDF
SAB2420	-----GEFYSATLVEGYKDHLDDAAHKALLNNRTEVSVDAYETFFKRFDV DFDE
SHY97-3906	GLFSYSGS GSVGEFY SATLVEGYKDHLDDAAHKALLNNRTEVSVDAYETFFKRFDV DFDE
SACOL2561	-----GEFYSATLVEGYKDHLDDAAHKALLNNRTEVSVDAYETFFKRFDV DFDE
CLJ08-1290	GLFSYSGS GSVGEFY SATLVEGYKDHLDDAAHKALLNNRTEVSVDAYETFFKRFDV DFDE
CLJ08-3	GLFSYSGS GSVGEFY SATLVEGYKDHLDDAAHKALLNNRTEVSVDAYETFFKRFDV DFDE
	:*:* :***: *****:***: :*
Consensus	XXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXRXXSVXXYETFFXRFDXXXFDX
SACOL0029 (COL)	ERELTQDPY SKVYLYSIEDHIRTYKIEK
MW0028 (MW2)	ERELTQDPY SKVYLYSIEDHIRTYKIEK
SAUSA300_0029 (USA300-FPR3757)	ERELTQDPY SKVYLYSIEDHIRTYKIEK
SAHV_0037 (Mu3)	ERELTQDPY SKVYLYSIEDHIRTYKIEK
SAV0038 (Mu)	ERELTQDPY SKVYLYSIEDHIRTYKIEK
SA0035	ERELTQDPY SKVYLYSIEDHIRTYKIEK
SAB2420	QQDAVHEDRRIFYLSNIENNVREYHRPE
SHY97-3906	QQDAVHEDRRIFYLSNIENNVREYHRPE
SACOL2561	EQDAVHEDRHIFYLSNIENNVREYHRPE
CLJ08-1290	EQDAVHEDRHIFYLSNIENNVREYHRPE
CLJ08-3	EQDAVHEDRHIFYLSNIENNVREYHRPE
	::: .:: .** .**.:* *: :
Consensus	XXXXXXXXXXYLXXIEXXRXYXXXX

FIG. 24

I SACOL1867 : Multiple polynucleotide sequences alignment

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MW1753 (MW2)                TTATTGTTCAATGTGCTTTTGAATAAAATCTTTGATTGAGGCGTAAAGTATACGGCACC 60
SAS1734 (MSSA476)          TTATTGTTCAATGTGCTTTTGAATAAAATCTTTGATTGAGGCGTAAAGTATACGGCACC 60
SACOL1867 (COL)            TTATTGTTCAATGTGCTTTTGAATAAAATCTTTGATTGAGGCGTAAAGTATACGGCACC 60
SAOUHSC_01939 (NCTC8325)  TTATTGTTCAATGTGCTTTTGAATAAAATCTTTGATTGAGGCGTAAAGTATACGGCACC 60
NWMN_1704 (Newman)         TTATTGTTCAATGTGCTTTTGAATAAAATCTTTGATTGAGGCGTAAAGTATACGGCACC 60
SAUSA300_1756 (USA300-FPR3757) TTATTGTTCAATGTGCTTTTGAATAAAATCTTTGATTGAGGCGTAAAGTATACGGCACC 60
SaurJH1_1897 (JH1)        TTATTGTTCAATGTGCTTTTGAATAAAATCTTTGATTGAGGCGTAAAGTATACGGCACC 60
SAHV_1796 (Mu3)           TTATTGTTCAATGTGCTTTTGAATAAAATCTTTGATTGAGGCGTAAAGTATACGGCACC 60
SaurJH9_1862 (JH9)        TTATTGTTCAATGTGCTTTTGAATAAAATCTTTGATTGAGGCGTAAAGTATACGGCACC 60
SAV1811 (Mu50)            TTATTGTTCAATGTGCTTTTGAATAAAATCTTTGATTGAGGCGTAAAGTATACGGCACC 60
SA1629 (N315)             TTATTGTTCAATGTGCTTTTGAATAAAATCTTTGATTGAGGCGTAAAGTATACGGCACC 60
SAB1671c (RF122)          TTATTGTTCAATGTGCTTTTGAATAAAATCTTTGATTGAGGCGTAAAGTAAACTGCACC 60
*****

MW1753 (MW2)                ATTATATTCAGAACCAATTTTCCAATACCGCCATACACCACACCTATGACCTCATTGTT 120
SAS1734 (MSSA476)          ATTATATTCAGAACCAATTTTCCAATACCGCCATACACCACACCTATGACCTCATTGTT 120
SACOL1867 (COL)            ATTATATTCAGAACCAATTTTCCAATACCGCCATACACCACACCTATGACCTCATTGTT 120
SAOUHSC_01939 (NCTC8325)  ATTATATTCAGAACCAATTTTCCAATACCGCCATACACCACACCTATGACCTCATTGTT 120
NWMN_1704 (Newman)         ATTATATTCAGAACCAATTTTCCAATACCGCCATACACCACACCTATGACCTCATTGTT 120
SAUSA300_1756 (USA300-FPR3757) ATTATATTCAGAACCAATTTTCCAATACCGCCATACACCACACCTATGACCTCATTGTT 120
SaurJH1_1897 (JH1)        ATTATATTCAGAACCAATTTTCCAATACCGCCATACACCACACCTATGACCTCATTGTT 120
SAHV_1796 (Mu3)           ATTATATTCAGAACCAATTTTCCAATACCGCCATACACCACACCTATGACCTCATTGTT 120
SaurJH9_1862 (JH9)        ATTATATTCAGAACCAATTTTCCAATACCGCCATACACCACACCTATGACCTCATTGTT 120
SAV1811 (Mu50)            ATTATATTCAGAACCAATTTTCCAATACCGCCATACACCACACCTATGACCTCATTGTT 120
SA1629 (N315)             ATTATATTCAGAACCAATTTTCCAATACCGCCATACACCACACCTATGACCTCATTGTT 120
SAB1671c (RF122)          ATTGTATTCTGATCCGATTTTCCAATACCTCCATACACAACCTCCTACGACTTCATTATT 120
*****

MW1753 (MW2)                AGAATTTAGAACTGGTGATCCTGAATTCCTGGGTTCAATGTATGCATCAAAATTTAAAT 180
SAS1734 (MSSA476)          AGAATTTAGAACTGGTGATCCTGAATTCCTGGGTTCAATGTATGCATCAAAATTTAAAT 180
SACOL1867 (COL)            AGAATTTAGAACTGGTGATCCTGAATTCCTGGGTTCAATGTATGCATCAAAATTTAAAT 180
SAOUHSC_01939 (NCTC8325)  AGAATTTAGAACTGGTGATCCTGAATTCCTGGGTTCAATGTATGCATCAAAATTTAAAT 180
NWMN_1704 (Newman)         AGAATTTAGAACTGGTGATCCTGAATTCCTGGGTTCAATGTATGCATCAAAATTTAAAT 180
SAUSA300_1756 (USA300-FPR3757) AGAATTTAGAACTGGTGATCCTGAATTCCTGGGTTCAATGTATGCATCAAAATTTAAAT 180
SaurJH1_1897 (JH1)        AGAATTTAGAACTGGTGATCCTGAATTCCTGGGTTCAATGTATGCATCAAAATTTAAAT 180
SAHV_1796 (Mu3)           AGAATTTAGAACTGGTGATCCTGAATTCCTGGGTTCAATGTATGCATCAAAATTTAAAT 180
SaurJH9_1862 (JH9)        AGAATTTAGAACTGGTGATCCTGAATTCCTGGGTTCAATGTATGCATCAAAATTTAAAT 180
SAV1811 (Mu50)            AGAATTTAGAACTGGTGATCCTGAATTCCTGGGTTCAATGTATGCATCAAAATTTAAAT 180
SA1629 (N315)             AGAATTTAGAACTGGTGATCCTGAATTCCTGGGTTCAATGTATGCATCAAAATTTAAAT 180
SAB1671c (RF122)          TAAATTTAAACTGGGGATCCTGAATTCAGGCTCGATATATGCATCAAAATTTAAAT 180
*****

MW1753 (MW2)                ATTGCTTTGATTCTTTTATAGTTCCTGTAGATTCAAACCTGTTTAAAACTATTTTGAGC 240
SAS1734 (MSSA476)          ATTGCTTTGATTCTTTTATAGTTCCTGTAGATTCAAACCTGTTTAAAACTATTTTGAGC 240
SACOL1867 (COL)            ATTGCTTTGATTCTTTTATAGTTCCTGTAGATTCAAACCTGTTTAAAACTATTTTGAGC 240
SAOUHSC_01939 (NCTC8325)  ATTGCTTTGATTCTTTTATAGTTCCTGTAGATTCAAACCTGTTTAAAACTATTTTGAGC 240
NWMN_1704 (Newman)         ATTGCTTTGATTCTTTTATAGTTCCTGTAGATTCAAACCTGTTTAAAACTATTTTGAGC 240
SAUSA300_1756 (USA300-FPR3757) ATTGCTTTGATTCTTTTATAGTTCCTGTAGATTCAAACCTGTTTAAAACTATTTTGAGC 240
SaurJH1_1897 (JH1)        ATTGCTTTGATTCTTTTATAGTTCCTGTAGATTCAAACCTGTTTAAAACTATTTTGAGC 240
SAHV_1796 (Mu3)           ATTGCTTTGATTCTTTTATAGTTCCTGTAGATTCAAACCTGTTTAAAACTATTTTGAGC 240
SaurJH9_1862 (JH9)        ATTGCTTTGATTCTTTTATAGTTCCTGTAGATTCAAACCTGTTTAAAACTATTTTGAGC 240
SAV1811 (Mu50)            ATTGCTTTGATTCTTTTATAGTTCCTGTAGATTCAAACCTGTTTAAAACTATTTTGAGC 240
SA1629 (N315)             ATTGCTTTGATTCTTTTATAGTTCCTGTAGATTCAAACCTGTTTAAAACTATTTTGAGC 240
SAB1671c (RF122)          ATTATCTTTAATACCTTTTACAGTCCAGTTGATTCAAATGTTTGAATGTATTTTGAGC 240
*****

MW1753 (MW2)                AGGTAATGGGTAACCAATAAAGTTAATTTTGTGCATCAACTTTAGCATCTTTTCGCAAAAT 300
SAS1734 (MSSA476)          AGGTAATGGGTAACCAATAAAGTTAATTTTGTGCATCAACTTTAGCATCTTTTCGCAAAAT 300
SACOL1867 (COL)            AGGTAATGGGTAACCAATAAAGTTAATTTTGTGCATCAACTTTAGCATCTTTTCGCAAAAT 300
SAOUHSC_01939 (NCTC8325)  AGGTAATGGGTAACCAATAAAGTTAATTTTGTGCATCAACTTTAGCATCTTTTCGCAAAAT 300
NWMN_1704 (Newman)         AGGTAATGGGTAACCAATAAAGTTAATTTTGTGCATCAACTTTAGCATCTTTTCGCAAAAT 300
SAUSA300_1756 (USA300-FPR3757) AGGTAATGGGTAACCAATAAAGTTAATTTTGTGCATCAACTTTAGCATCTTTTCGCAAAAT 300
SaurJH1_1897 (JH1)        AGGTAATGGGTAACCAATAAAGTTAATTTTGTGCATCAACTTTAGCATCTTTTCGCAAAAT 300
SAHV_1796 (Mu3)           AGGTAATGGGTAACCAATAAAGTTAATTTTGTGCATCAACTTTAGCATCTTTTCGCAAAAT 300
SaurJH9_1862 (JH9)        AGGTAATGGGTAACCAATAAAGTTAATTTTGTGCATCAACTTTAGCATCTTTTCGCAAAAT 300
SAV1811 (Mu50)            AGGTAATGGGTAACCAATAAAGTTAATTTTGTGCATCAACTTTAGCATCTTTTCGCAAAAT 300
SA1629 (N315)             AGGTAATGGGTAACCAATAAAGTTAATTTTGTGCATCAACTTTAGCATCTTTTCGCAAAAT 300
SAB1671c (RF122)          TGGTAAAGGGTATCCAATAAAGTTAATTTTGTGCATCAACTTTAGCATCTTTTCGCAAAAT 300
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FIG. 25A

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MW1753 (MW2)          TAATGCTTGGACATTTTCATTAAAAATTAAAGCCTTTTGGTCCACGTTCAACTGCTTGTTTC 360
SAS1734 (MSSA476)     TAATGCTTGGACATTTTCATTAAAAATTAAAGCCTTTTGGTCCACGTTCAACTGCTTGTTTC 360
SACOL1867 (COL)       GAATGCTTGGACATTTTCATTAAAAATTAAAGCCTTTTGGTCCACGTTTCGACTGCTTGTTTC 360
SAOUHSC_01939 (NCTC8325) GAATGCTTGGACATTTTCATTAAAAATTAAAGCCTTTTGGTCCACGTTTCGACTGCTTGTTTC 360
NWMN_1704 (Newman)     TAATGCTTGGACATTTTCATTAAAAATTAAAGCCTTTTGGTCCACGTTTCGACTGCTTGTTTC 360
SAUSA300_1756 (USA300-FPR3757) GAATGCTTGGACATTTTCATTAAAAATTAAAGCCTTTTGGTCCACGTTTCGACTGCTTGTTTC 360
SaurJH1_1897 (JH1)     GAATGCTTGGACATTTTCATTAAAAATTAAAGCCTTTTGGTCCACGTTTCGACTGCTTGTTTC 360
SAHV_1796 (Mu3)        GAATGCTTGGACATTTTCATTAAAAATTAAAGCCTTTTGGTCCACGTTTCGACTGCTTGTTTC 360
SaurJH9_1862 (JH9)     GAATGCTTGGACATTTTCATTAAAAATTAAAGCCTTTTGGTCCACGTTTCGACTGCTTGTTTC 360
SAV1811 (Mu50)         GAATGCTTGGACATTTTCATTAAAAATTAAAGCCTTTTGGTCCACGTTTCGACTGCTTGTTTC 360
SA1629 (N315)          GAATGCTTGGACATTTTCATTAAAAATTAAAGCCTTTTGGTCCACGTTTCGACTGCTTGTTTC 360
SAB1671c (RF122)       GAATGCTTGGACATTTTCATTAAAAATTATAACCATTTTGCTCCACGTTCAACAGCATTTTTC 360
***** * * * *

MW1753 (MW2)          TTCAATATTTCATGACAGAGATGTCTTCATCACCCGGATAATCAGAAATGCTTTTAAATTTT 420
SAS1734 (MSSA476)     TTCAATATTTCATGACAGAGATGTCTTCATCACCCGGATAATCAGAAATGCTTTTAAATTTT 420
SACOL1867 (COL)       TTCAATATTTCATGACAGAGATGTCTTCATCACCCGGATAATCAGAAATGCTTTTAAATTTT 420
SAOUHSC_01939 (NCTC8325) TTCAATATTTCATGACAGAGATGTCTTCATCACCCGGATAATCAGAAATGCTTTTAAATTTT 420
NWMN_1704 (Newman)     TTCAATATTTCATGACAGAGATGTCTTCATCACCCGGATAATCAGAAATGCTTTTAAATTTT 420
SAUSA300_1756 (USA300-FPR3757) TTCAATATTTCATGACAGAGATGTCTTCATCACCCGGATAATCAGAAATGCTTTTAAATTTT 420
SaurJH1_1897 (JH1)     TTCAATATTTCATGACAGAGATGTCTTCATCACCCGGATAATCAGAAATGCTTTTAAATTTT 420
SAHV_1796 (Mu3)        TTCAATATTTCATGACAGAGATGTCTTCATCACCCGGATAATCAGAAATGCTTTTAAATTTT 420
SaurJH9_1862 (JH9)     TTCAATATTTCATGACAGAGATGTCTTCATCACCCGGATAATCAGAAATGCTTTTAAATTTT 420
SAV1811 (Mu50)         TTCAATATTTCATGACAGAGATGTCTTCATCACCCGGATAATCAGAAATGCTTTTAAATTTT 420
SA1629 (N315)          TTCAATATTTCATGACAGAGATGTCTTCATCACCCGGATAATCAGAAATGCTTTTAAATTTT 420
SAB1671c (RF122)       TTCAACGTTTCATTACTGATATATCCTCATTACCTGGATAATCAGAAATATTTTAAATTTT 420
***** * * * *

MW1753 (MW2)          ATATATACCACCATTTCCTTTGTCCACCGTCTGGATGGGCAGTAATTCTATCGCCAACTTT 480
SAS1734 (MSSA476)     ATATATACCACCATTTCCTTTGTCCACCGTCTGGATGGGCAGTAATTCTATCGCCAACTTT 480
SACOL1867 (COL)       ATATATACCACCATTTCCTTTGTCCACCGTCTGGATGGGCAGTAATTCTATCGCCAACTTT 480
SAOUHSC_01939 (NCTC8325) ATATATACCACCATTTCCTTTGTCCACCGTCTGGATGGGCAGTAATTCTATCGCCAACTTT 480
NWMN_1704 (Newman)     ATATATACCACCATTTCCTTTGTCCACCGTCTGGATGGGCAGTAATTCTATCGCCAACTTT 480
SAUSA300_1756 (USA300-FPR3757) ATATATACCACCATTTCCTTTGTCCACCGTCTGGATGGGCAGTAATTCTATCGCCAACTTT 480
SaurJH1_1897 (JH1)     ATATATACCACCATTTCCTTTGTCCACCGTCTGGATGGGCAGTAATTCTATCGCCAACTTT 480
SAHV_1796 (Mu3)        ATATATACCACCATTTCCTTTGTCCACCGTCTGGATGGGCAGTAATTCTATCGCCAACTTT 480
SaurJH9_1862 (JH9)     ATATATACCACCATTTCCTTTGTCCACCGTCTGGATGGGCAGTAATTCTATCGCCAACTTT 480
SAV1811 (Mu50)         ATATATACCACCATTTCCTTTGTCCACCGTCTGGATGGGCAGTAATTCTATCGCCAACTTT 480
SA1629 (N315)          ATATATACCACCATTTCCTTTGTCCACCGTCTGGATGGGCAGTAATTCTATCGCCAACTTT 480
SAB1671c (RF122)       ATAAATCCACCGTTGCCTTTGTCCACCATTTGGGTGGGCAGTAATTCTATCGCCAACTTT 480
*** * * * *

MW1753 (MW2)          ATAATCTTTTGATACATGTTTATTGGTGATAATTGTATTTTTTCCAATTACAAAACCTGT 540
SAS1734 (MSSA476)     ATAATCTTTTGATACATGTTTATTGGTGATAATTGTATTTTTTCCAATTACAAAACCTGT 540
SACOL1867 (COL)       ATAATCTTTTGATACATGTTTATTGGTGATAATTGTATTTTTTCCAATTACAAAACCTGT 540
SAOUHSC_01939 (NCTC8325) ATAATCTTTTGATACATGTTTATTGGTGATAATTGTATTTTTTCCAATTACAAAACCTGT 540
NWMN_1704 (Newman)     ATAATCTTTTGATACATGTTTATTGGTGATAATTGTATTTTTTCCAATTACAAAACCTGT 540
SAUSA300_1756 (USA300-FPR3757) ATAATCTTTTGATACATGTTTATTGGTGATAATTGTATTTTTTCCAATTACAAAACCTGT 540
SaurJH1_1897 (JH1)     ATAATCTTTTGATACATGTTTATTGGTGATAATTGTATTTTTTCCAATTACAAAACCTGT 540
SAHV_1796 (Mu3)        ATAATCTTTTGATACATGTTTATTGGTGATAATTGTATTTTTTCCAATTACAAAACCTGT 540
SaurJH9_1862 (JH9)     ATAATCTTTTGATACATGTTTATTGGTGATAATTGTATTTTTTCCAATTACAAAACCTGT 540
SAV1811 (Mu50)         ATAATCTTTTGATACATGTTTATTGGTGATAATTGTATTTTTTCCAATTACAAAACCTGT 540
SA1629 (N315)          ATAATCTTTTGATACATGTTTATTGGTGATAATTGTATTTTTTCCAATTACAAAACCTGT 540
SAB1671c (RF122)       ATAGTCCTTTTGATACATGTTTATTGGTGATAATTGTATTTTTTCCAATTGCAAAAACCTGT 540
*** * * * *

MW1753 (MW2)          CGCATCTTTAAATGAAACGACGCCATTATATGGAAAAATATTGTATCTTTAACTTGCGGT 600
SAS1734 (MSSA476)     CGCATCTTTAAATGAAACGACGCCATTATATGGAAAAATATTGTATCTTTAACTTGCGGT 600
SACOL1867 (COL)       CGCATCTTTAAATGAAACGACGCCATTATATGGAAAAATATTGTATCTTTAACTTGCGGT 600
SAOUHSC_01939 (NCTC8325) CGCATCTTTAAATGAAACGACGCCATTATATGGAAAAATATTGTATCTTTAACTTGCGGT 600
NWMN_1704 (Newman)     CGCATCTTTAAATGAAACGACGCCATTATATGGAAAAATATTGTATCTTTAACTTGCGGT 600
SAUSA300_1756 (USA300-FPR3757) CGCATCTTTAAATGAAACGACGCCATTATATGGAAAAATATTGTATCTTTAACTTGCGGT 600
SaurJH1_1897 (JH1)     CGCATCTTTAAATGAAACGACGCCATTATATGGAAAAATATTGTATCTTTAACTTGCGGT 600
SAHV_1796 (Mu3)        CGCATCTTTAAATGAAACGACGCCATTATATGGAAAAATATTGTATCTTTAACTTGCGGT 600
SaurJH9_1862 (JH9)     CGCATCTTTAAATGAAACGACGCCATTATATGGAAAAATATTGTATCTTTAACTTGCGGT 600
SAV1811 (Mu50)         CGCATCTTTAAATGAAACGACGCCATTATATGGAAAAATATTGTATCTTTAACTTGCGGT 600
SA1629 (N315)          CGCATCTTTAAATGAAACGACGCCATTATATGGAAAAATATTGTATCTTTAACTTGCGGT 600
SAB1671c (RF122)       CGCATCTTTAAATGAAACGACGCCATTATATGGAAAAACATTTGTATCTTTAACTTGCGGT 600
***** * * * *

MW1753 (MW2)          AACATTCTTCTCTGCATTGTCTATTGTTGTGTCTCTTCAACGACTGCAGCATTTATTCC 660
SAS1734 (MSSA476)     AACATTCTTCTCTGCATTGTCTATTGTTGTGTCTCTTCAACGACTGCAGCATTTATTCC 660
SACOL1867 (COL)       AACATTCTTCTCTGCATTGTCTATTGTTGTGTCTCTTCAACGACTGCAGCATTTATTCC 660
SAOUHSC_01939 (NCTC8325) AACATTCTTCTCTGCATTGTCTATTGTTGTGTCTCTTCAACGACTGCAGCATTTATTCC 660
NWMN_1704 (Newman)     AACATTCTTCTCTGCATTGTCTATTGTTGTGTCTCTTCAACGACTGCAGCATTTATTCC 660
SAUSA300_1756 (USA300-FPR3757) AACATTCTTCTCTGCATTGTCTATTGTTGTGTCTCTTCAACGACTGCAGCATTTATTCC 660
SaurJH1_1897 (JH1)     AACATTCTTCTCTGCATTGTCTATTGTTGTGTCTCTTCAACGACTGCAGCATTTATTCC 660
SAHV_1796 (Mu3)        AACATTCTTCTCTGCATTGTCTATTGTTGTGTCTCTTCAACGACTGCAGCATTTATTCC 660
SaurJH9_1862 (JH9)     AACATTCTTCTCTGCATTGTCTATTGTTGTGTCTCTTCAACGACTGCAGCATTTATTCC 660
SAV1811 (Mu50)         AACATTCTTCTCTGCATTGTCTATTGTTGTGTCTCTTCAACGACTGCAGCATTTATTCC 660
SA1629 (N315)          AACATTCTTCTCTGCATTGTCTATTGTTGTGTCTCTTCAACGACTGCAGCATTTATTCC 660
SAB1671c (RF122)       AACATTCTTCTCTGCATTGTCTATTGTTGTGTCTCATCAACGACTGCAGCATTTATTCC 660
***** * * * *

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FIG. 25B

MW1753 (MW2)	AGTTACTGAGGTTAGAATGGCTAATGCTGCCATGCTTTTAATGACTATATTTTATTCAT	720
SAS1734 (MSSA476)	AGTTGCTGAGGTTAGAATGGCTAATGCTGCCATGCTTTTAATGACTATATTTTATTCAT	720
SACOL1867 (COL)	AGTTACTGAGGTTAGAATGGCTAATGCTGCCATGCTTTTAATGACTATATTTTATTCAT	720
SAOUHSC_01939 (NCTC8325)	AGTTACTGAGGTTAGAATGGCTAATGCTGCCATGCTTTTAATGACTATATTTTATTCAT	720
NWMN_1704 (Newman)	AGTTACTGAGGTTAGAATGGCTAATGCTGCCATGCTTTTAATGACTATATTTTATTCAT	720
SAUSA300_1756 (USA300-FPR3757)	AGTTACTGAGGTTAGAATGGCTAATGCTGCCATGCTTTTAATGACTATATTTTATTCAT	720
SaurJH1_1897 (JH1)	AGTTACTGAGGTTAGAATGGCTAATGCTGCCATGCTTTTAATGACTATATTTTATTCAT	720
SAHV_1796 (Mu3)	AGTTACTGAGGTTAGAATGGCTAATGCTGCCATGCTTTTAATGACTATATTTTATTCAT	720
SaurJH9_1862 (JH9)	AGTTACTGAGGTTAGAATGGCTAATGCTGCCATGCTTTTAATGACTATATTTTATTCAT	720
SAV1811 (Mu50)	AGTTACTGAGGTTAGAATGGCTAATGCTGCCATGCTTTTAATGACTATATTTTATTCAT	720
SA1629 (N315)	AGTTACTGAGGTTAGAATGGCTAATGCTGCCATGCTTTTAATGACTATATTTTATTCAT	720
SAB1671c (RF122)	AGTTACTGAGGTTAGAATGGCTAATGCTGCCATGCTTTTAATGACTATATTTTATTCAT	720
	**** *	
MW1753 (MW2)	-----	
SAS1734 (MSSA476)	-----	
SACOL1867 (COL)	AAAAGCACATTGAACAATAA	740
SAOUHSC_01939 (NCTC8325)	-----	
NWMN_1704 (Newman)	-----	
SAUSA300_1756 (USA300-FPR3757)	-----	
SaurJH1_1897 (JH1)	-----	
SAHV_1796 (Mu3)	-----	
SaurJH9_1862 (JH9)	-----	
SAV1811 (Mu50)	-----	
SA1629 (N315)	-----	
SAB1671c (RF122)	-----	

FIG. 25C

II- SACOL1867: Multiple polypeptide sequences alignment: hypothetical epitopes shaded

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MW1753 (MW2)                MNKNIVIKSMAALAILTSVTGINAAVVEETQQIANAENKVTQVKDTNIFPYNGVVSFKDA 60
SAS1734 (MSSA476)          MNKNIVIKSMAALAILTSATGINAAVVEETQQIANAENKVTQVKDTNIFPYNGVVSFKDA 60
SACOL1867 (COL)            MNKNIVIKSMAALAILTSVTGINAAVVEETQQIANAENKVTQVKDTNIFPYNGVVSFKDA 60
SAOUHSC_01939 (NCTC8325)  MNKNIVIKSMAALAILTSVTGINAAVVEETQQIANAENKVTQVKDTNIFPYNGVVSFKDA 60
NWMN_1704 (Newman)         MNKNIVIKSMAALAILTSVTGINAAVVEETQQIANAENKVTQVKDTNIFPYNGVVSFKDA 60
SAUSA300_1756 (USA300-FPR3757) MNKNIVIKSMAALAILTSVTGINAAVVEETQQIANAENKVTQVKDTNIFPYNGVVSFKDA 60
SaurJH1_1897 (JH1)        MNKNIVIKSMAALAILTSVTGINAAVVEETQQIANAENKVTQVKDTNIFPYNGVVSFKDA 60
SAHV_1796 (Mu3)           MNKNIVIKSMAALAILTSVTGINAAVVEETQQIANAENKVTQVKDTNIFPYNGVVSFKDA 60
SaurJH9_1862 (JH9)        MNKNIVIKSMAALAILTSVTGINAAVVEETQQIANAENKVTQVKDTNIFPYNGVVSFKDA 60
SAV1811 (Mu50)            MNKNIVIKSMAALAILTSVTGINAAVVEETQQIANAENKVTQVKDTNIFPYNGVVSFKDA 60
SA1629 (N315)            MNKNIVIKSMAALAILTSVTGINAAVVEETQQIANAENKVTQVKDTNIFPYNGVVSFKDA 60
SAB1671c (RF122)         MNKNIVIKSMAALAILTSVTGINAAVDETTQIANAENKVTQVKDTNIFPYNGVVSFKDA 60
*****.*****:*****:***** *****
Consensus                 MNKNIVIKSMAALAILTSXTGINAAVXETQQIANAENKVTQVKDTNXFPYNGVVSFKDA

MW1753 (MW2)                TGFVIGKNTIITNKHVSKDYKVGDRITAHDPDGDKGNGGIYKIKSISDYPGDEDISVMNIE 120
SAS1734 (MSSA476)          TGFVIGKNTIITNKHVSKDYKVGDRITAHDPDGDKGNGGIYKIKSISDYPGDEDISVMNIE 120
SACOL1867 (COL)            TGFVIGKNTIITNKHVSKDYKVGDRITAHDPNGDKGNGGIYKIKSISDYPGDEDISVMNIE 120
SAOUHSC_01939 (NCTC8325)  TGFVIGKNTIITNKHVSKDYKVGDRITAHDPNGDKGNGGIYKIKSISDYPGDEDISVMNIE 120
NWMN_1704 (Newman)         TGFVIGKNTIITNKHVSKDYKVGDRITAHDPNGDKGNGGIYKIKSISDYPGDEDISVMNIE 120
SAUSA300_1756 (USA300-FPR3757) TGFVIGKNTIITNKHVSKDYKVGDRITAHDPNGDKGNGGIYKIKSISDYPGDEDISVMNIE 120
SaurJH1_1897 (JH1)        TGFVIGKNTIITNKHVSKDYKVGDRITAHDPNGDKGNGGIYKIKSISDYPGDEDISVMNIE 120
SAHV_1796 (Mu3)           TGFVIGKNTIITNKHVSKDYKVGDRITAHDPNGDKGNGGIYKIKSISDYPGDEDISVMNIE 120
SaurJH9_1862 (JH9)        TGFVIGKNTIITNKHVSKDYKVGDRITAHDPNGDKGNGGIYKIKSISDYPGDEDISVMNIE 120
SAV1811 (Mu50)            TGFVIGKNTIITNKHVSKDYKVGDRITAHDPNGDKGNGGIYKIKSISDYPGDEDISVMNIE 120
SA1629 (N315)            TGFVIGKNTIITNKHVSKDYKVGDRITAHDPNGDKGNGGIYKIKSISDYPGDEDISVMNIE 120
SAB1671c (RF122)         TGFVIGKNTIITNKHVSKDYKVGDRITAHDPNGDKGNGGIYKIKSISDYPGDEDISVMNIE 120
***.* *****.*****:*****:***** *****
Consensus                 TGFVIGKNTIITNKHVSKDYKVGDRITAHDPNGDKGNGGIYKIKSISDYPGXEDISVMNIE

MW1753 (MW2)                EQAVERGPKGFNFNENVQALNFAKDAKVDKIKVIGYPLPAQNSFKQFESTGTIKRIKDN 180
SAS1734 (MSSA476)          EQAVERGPKGFNFNENVQALNFAKDAKVDKIKVIGYPLPAQNSFKQFESTGTIKRIKDN 180
SACOL1867 (COL)            EQAVERGPKGFNFNENVQAFNFAKDAKVDKIKVIGYPLPAQNSFKQFESTGTIKRIKDN 180
SAOUHSC_01939 (NCTC8325)  EQAVERGPKGFNFNENVQAFNFAKDAKVDKIKVIGYPLPAQNSFKQFESTGTIKRIKDN 180
NWMN_1704 (Newman)         EQAVERGPKGFNFNENVQAFNFAKDAKVDKIKVIGYPLPAQNSFKQFESTGTIKRIKDN 180
SAUSA300_1756 (USA300-FPR3757) EQAVERGPKGFNFNENVQAFNFAKDAKVDKIKVIGYPLPAQNSFKQFESTGTIKRIKDN 180
SaurJH1_1897 (JH1)        EQAVERGPKGFNFNENVQAFNFAKDAKVDKIKVIGYPLPAQNSFKQFESTGTIKRIKDN 180
SAHV_1796 (Mu3)           EQAVERGPKGFNFNENVQAFNFAKDAKVDKIKVIGYPLPAQNSFKQFESTGTIKRIKDN 180
SaurJH9_1862 (JH9)        EQAVERGPKGFNFNENVQAFNFAKDAKVDKIKVIGYPLPAQNSFKQFESTGTIKRIKDN 180
SAV1811 (Mu50)            EQAVERGPKGFNFNENVQAFNFAKDAKVDKIKVIGYPLPAQNSFKQFESTGTIKRIKDN 180
SA1629 (N315)            EQAVERGPKGFNFNENVQAFNFAKDAKVDKIKVIGYPLPAQNSFKQFESTGTIKRIKDN 180
SAB1671c (RF122)         ENAVERGANGYFNENVQAFNFAKDAKVDKIKVIGYPLPAQNTFKQFESTGTIVKSIKDN 180
*:****.*:*****:*****:*****:*****:*****:*****:*****
EXAVERGXGXGNFNENVQAXNFAKDAKVDKIKVIGYPLPAQNXFKQFESTGTIXKIKDN

MW1753 (MW2)                ILNFDAYIEPGNSGSPVLNSNNEVIGVVYGGIGKIGSEYNGAVYFTPQIKDFIQKHIEQ 239
SAS1734 (MSSA476)          ILNFDAYIEPGNSGSPVLNSNNEVIGVVYGGIGKIGSEYNGAVYFTPQIKDFIQKHIEQ 239
SACOL1867 (COL)            ILNFDAYIEPGNSGSPVLNSNNEVIGVVYGGIGKIGSEYNGAVYFTPQIKDFIQKHIEQ 239
SAOUHSC_01939 (NCTC8325)  ILNFDAYIEPGNSGSPVLNSNNEVIGVVYGGIGKIGSEYNGAVYFTPQIKDFIQKHIEQ 239
NWMN_1704 (Newman)         ILNFDAYIEPGNSGSPVLNSNNEVIGVVYGGIGKIGSEYNGAVYFTPQIKDFIQKHIEQ 239
SAUSA300_1756 (USA300-FPR3757) ILNFDAYIEPGNSGSPVLNSNNEVIGVVYGGIGKIGSEYNGAVYFTPQIKDFIQKHIEQ 239
SaurJH1_1897 (JH1)        ILNFDAYIEPGNSGSPVLNSNNEVIGVVYGGIGKIGSEYNGAVYFTPQIKDFIQKHIEQ 239
SAHV_1796 (Mu3)           ILNFDAYIEPGNSGSPVLNSNNEVIGVVYGGIGKIGSEYNGAVYFTPQIKDFIQKHIEQ 239
SaurJH9_1862 (JH9)        ILNFDAYIEPGNSGSPVLNSNNEVIGVVYGGIGKIGSEYNGAVYFTPQIKDFIQKHIEQ 239
SAV1811 (Mu50)            ILNFDAYIEPGNSGSPVLNSNNEVIGVVYGGIGKIGSEYNGAVYFTPQIKDFIQKHIEQ 239
SA1629 (N315)            ILNFDAYIEPGNSGSPVLNSNNEVIGVVYGGIGKIGSEYNGAVYFTPQIKDFIQKHIEQ 239
SAB1671c (RF122)         ILNFDAYIEPGNSGSPVLNLSNNEVIGVVYGGIGKIGSEYNGAVYFTPQIKDFIQKHIEQ 239
*****.*****:*****:*****:*****:*****:*****
Consensus                 XLNFDAYIEPGNSGSPVLNLSNNEVIGVVYGGIGKIGSEYNGAVYFTPQIKXFIQKHIEQ

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FIG. 25D

I- SACOL1715 (hemB) : Nucleotide sequence (SEQ ID NO: 181)

atgaaatgtgatagacatagaagattgagatcatcagcgacaatgagagatatggttaga
gagaatcatgtaagaaaagaagatttaatatatccaatgttagttgaaaaagacgat
gtgaaaaaagaaattaagtcattgccaggtgtataccaaatcagtttgaatttacttgaa
agtgaattaaaagaagcttatgacttaggcatacgtgccattatgttttcggtgttcca
aactcaaaagatgatataggtactggtgcatacattcacgatggtgttattcaacaggca
acacgtatttgctaaaaaatgtatgatgacttattaattgttgacagacacttgtttatgt
gaataactgatcatggtcattgtggcgtgattgatgaccatacacatgacgttgacaat
gataaatcattgccactacttggttaaacagcaatttctcaagtggagctggtgctgat
attattgcgccaagtaatatgatggatgggtttgttgctgaaattcgtcgtggattagat
gaagccggctattacaatatctctataatgagttatggtgtcaagtatgcatcaagtttc
tttgaccttttagagatgcagcagattcagcgccatcatttggggatagaaaaacgat
cagatggaccctgctaaccggttggaagcacttcgtgaattagaaagtgatcttaaagaa
gggtgcgacatgatgattgttaaacctgctctaagttatttagatatagttcgagatgtt
aaaaatcacatgaatgttcagttgttgcatataatgtgagtggagaatatagtatgact
aaagcagcggcacaaaaatgggtggatagatgaagaacgtgtcgttatggaacaaatgggt
tcaatgaaacgtgcaggtgctgatatgattattacgtatgttgcaaaggacatttgcgc
tatttagataaataa

II- hemB: amino acid sequence (SEQ ID NO: 182)

MKFDRHRRRLRSSATMRDMVRENHVRKEDLIYPIFVVEKDDVKKEIKSLPGVYQISLNLLE
SELKEAYDLGIRAIMFFGVPNSKDDIGTGAYIHDGVIQQATRIAKKMYDDLIVADTCLC
EYTDHGHCGVIDDHTDVDNDKSLPLLVKTAISQVEAGADI IAPSNMMDGFVAEIRRGLD
EAGYYNIPIMSYGVKYASSFFGPFRDAADSAPSFGRKTYQMDPANRLEALRELESDLKE
GCDMMIVKPALS YLDIVRDVKNHTNVPV VAYNVSGEYSMTKAAAQNGWIDEERVVMEQMV
SMKRAGADMIITYFAKDICYLDK

FIG. 26

>ClfA (NWMN_0756, newman) (SEQ ID NO: 183)

ATGTAATATGAAGAAAAAGAAAGAAACACGCAATTTCGGAAAAAATCGATTGGCGTGGCTTCAGTGCTTGTAGGTACGTTAATCGG
TTTTGGACTACTCAGCAGTAAAGAAGCAGATGCAAGTGAAAAATAGTGTTACGCAATCTGATAGCGCAAGTAACGAAAGCAAAA
GTAATGATTCAAGTAGCGTTAGTGCTGCACCTAAAAACAGACGACACAAACGTGAGTGATACTAAAAACATCGTCAAACACTAAT
AATGGCGAAACGAGTGTGGCGCAAAATCCAGCACAAACAGGAAACGACACAATCATCATCAACAAATGCAACTACGGAAGAAAC
GCCGGTAACTGGTGAAGCTACTACTACGACAACGAATCAAGCTAATACACCGGCAACAACCTCAATCAAGCAATACAAATGCGG
AGGAATTAGTGAATCAAACAAGTAATGAAACGACTTTAATGATACTAATACAGTATCATCTGTAAATTCACCTCAAATTTCT
ACAAATGCGGAAAATGTTTCAACAACGCAAGATACTTCAACTGAAGCAACACCTTCAAACAATGAATCAGCTCCACAGAGTAC
AGATGCAAGTAATAAAGATGTAGTTAATCAAGCGGTAAATACAAGTGCGCCTAGAATGAGAGCATTAGTTTAGCGGCAGTAG
CTGCAGATGCACCGGCAGCTGGCACAGATATTACGAATCAGTTGACGAATGTGACAGTTGGTATTGACTCTGGTACGACTGTG
TATCCGCACCAAGCAGGTTATGTCAAACCTGAATTATGGTTTTTCAGTGCCTAATTCTGCTGTTAAAGGTGACACATTCAAAAT
AACTGTACCTAAAGAATTAACCTTAAATGGTGTAACTTCAACTGCTAAAGTGCCACCAATTATGGCTGGAGATCAAGTATTGG
CAAATGGTGTAAATCGATAGTGATGGTAATGTTATTATACATTTACAGACTATGTAATACTAAAGATGATGTAAAAGCAACT
TTGACCATGCCCGCTTATATTGACCCTGAAAATGTTAAAAAGACAGGTAATGTGACATTGGCTACTGGCATAGGTAGTACAAC
AGCAAAACAAAACAGTATTAGTAGATTATGAAAAATATGGTAAGTTTTATAACTTATCTATTAAAGGTACAATTGACCAAATCG
ATAAAACAAATAATACGTATCGTCAGACAATTTATGTCAATCCAAGTGGAGATAACGTTATTGCGCCGGTTTTAACAGGTAAT
TTAAAAACCAAATACGGATAGTAATGCATTAATAGATCAGCAAAATACAAGTATTAAAGTATATAAAAGTAGATAATGCAGCTGA
TTTATCTGAAAGTTACTTTGTGAATCCAGAAAACCTTTGAGGATGTCTACTAATAGTGTGAATATTACATTCCCAAATCCAAATC
AATATAAAAGTAGAGTTTTAATACGCCTGATGATCAAATTACAACACCGTATATAGTAGTTGTTAATGGTCATATTGATCCGAAT
AGCAAAGGTGATTTAGCTTTACGTTCAACTTTATATGGGTATAACTCGAATATAATTTGGCGCTCTATGTCTATGGGACAACGA
AGTAGCATTTAATAACGGATCAGGTTCTGGTGACGGTATCGATAAACCAGTTGTTCTGAACAACCTGATGAGCCTGGTGAAA
TTGAACCAATTCCAGAGGATTCAGATTCTGACCCAGGTTTCAGATTCTGGCAGCGATTCTAATTCAGATAGCGGTTTCAGATTCTG
GGTAGTGATTCTACATCAGATAGTGGTTCAGATTTCAGCGAGTGATTTCAGATTTCAGCAAGTGATTTCAGACTCAGCGAGTGATT
AGATTTCAGCAAGCGATTCCGACTCAGCGAGCGATTCCGACTCAGACAATGACTCGGATTTCAGATAGCGATTCTGACTCAGACA
GTGACTCAGATTCCGACAGTGACTCAGATTTCAGATAGCGATTCTGACTCAGACAGTGACTCAGATTTCAGATAGCGATTTCAGAT
TCAGATAGCGATTTCAGATTCCGACAGTGATTCCGACTCAGACAGCGATTCTGACTCCGACAGTGATTCCGACTCAGACAGCGA
TTCAGATTCCGACAGTGATTCCGACTCAGATAGCGATTCCGACTCAGATAGCGACTCAGATTTCAGACAGCGATTTCAGATTTCAG
ACAGCGATTTCAGATTTCAGATAGCGATTTCAGATTCCGACAGTGACTCAGATTCCGACAGTGACTCGGATTTCAGATAGCGATTTC
GATTCCGACAGTGACTCAGATTCCGACAGTGACTCAGACTCAGACAGTGATTTCGGATTTCAGCGAGTGATTTCGGATTTCAGATAG
TGATTCCGACTCCGACAGTGACTCGGATTTCAGATAGCGACTCAGACTCGGATAGCGACTCGGATTTCAGATAGCGATTTCGGACT
CAGATAGCGATTTCAGAATCAGACAGCGATTTCAGAATCAGACAGCGATTTCAGATTTCAGACAGCGACTCAGACAGTGACTCAGAT
TCAGATAGTGACTCGGATTTCAGCGAGTGATTTCAGACTCAGGTAGTGACTCCGATTTCATCAAGTGATTCCGACTCAGAAAGTGA
TTCAAATAGCGATTCCGAGTCAGGTTCTAACAATAATGTAGTTCGCGCTAATTCACCTAAAAATGGTACTAATGCTTCTAATA
AAAAATGAGGCTAAAGATAGTAAAGAACCATTACCAGATACAGGTTCTGAAGATGAAGCAAATACGTCATAAATTTGGGGATTA
TTAGCATCAATAGGTTTCATTACTACTTTTTCAGAAGAAAAAAGAAAAATAAAGATAAGAAATAA

>ClfA (NWMN_0756, newman) (SEQ ID NO: 184)

MMNMKKKEKHAIRKKSIGVASVLVGLTIGFGLSSKEADASENSVTQSDSASNESKSNDSSSVSAAPKTDDTNVSDTKTSSNTN
NGETSAQNPAQQETTQSSSTNATTEETPVTGEATTTTTNQANTPATTQSSNTNAEELVNQTSNETTFNDTNTVSSVNSPQNS
TNAENVSTTQDTSTEATPSNNESAPQSTDASNKDQVNVQAVNTSAPRMRAFLAAVAADAPAAAGTDITNQLTNVTVGIDSGTTV
YPHQAGYVKLNYGFSVPNSAVKGDFTKITYPKELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYFTFDYVNTKDDVKAT
LTMPAYIDPENVKKTGNVTLATGIGSTTANKTVLVDYEKYKGFYNLSIKGTIDQIDKTNNTYRQTIYVNPSPGDNVIAPVLTGN
LKPNTDSNALIDQQNTSIKVYKVDNAADLSESYFVNPENFEDVTNSVNIITFPNPNQYKVEFNTPDQIITTPYIVVNGHIDPN
SKGDLALRSTLYGYNSNIIWRMSWDNEVAFNNGSGSGDGIDKPVVPEQPDEPGEIEPIPEDSDSDPGSDSGSDSNSDSDSGSDS
GSDSTSDSGSDSASDSDSASDSDSASDSDSASDSDSASDSDSDNDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDS
SDS
DSDSDSDSDSDSDSDSDSDSASDSESDSDSESDSDSDSDSDSDSD
SDSDSDSASDSDSGSDSDSSDSDSESDSNSDSESGSNNNVPPNSPKNGTNASNKNEAKDSKEPLPDTGSEDEANTSLIWGL
LASIGSLLLFRRKKENKDKK

FIG. 27