

Supplementary Materials: Prevalence and Genetic Diversity of Staphylococcal Enterotoxin (-like) Genes *sey*, *selw*, *selx*, *selz*, *sel26* and *sel27* in Community-Acquired Methicillin-Resistant *Staphylococcus aureus*

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(a)

JP087- <i>sey</i> 1	MKAKLCFLLTTLAFLI AVTGSIGIAEVKAKTTGLITENSNDSLKEHYAQKFEVYTNKEVT	60
SC1133- <i>sey</i> 4	MKAKLCFLLTTLAFLI AVTGSIGIAEVKAKTTGLITENSNDSLKEHYAQKFEVYTNKEVT	60
JP096- <i>sey</i> 3	MKAKLWFLLTTLAFLI AVTGSIGIAEVKAKTTGLITENSNDSLKEHYAQKFEVYTNKEIT	60
SC570- <i>sey</i> 5	MKAKLWFLLTTLAFLI AVTGSIGIAEVKAKTTGLITENSNDSLKEHYAQKFEVYTNKEVT	60
RF122- <i>sey</i> 7	MKAKLWFLLTTLAFLI AVTESIGIAEVKAKTTGLITENSNDSLKEHYAQKFEVYTNKEVT	60
JP074- <i>sey</i> 2	MKAKLWFLLTTLAFLI AVTGSIGIAEVKAKTTGLITENSNDSLKEHYAQKFEVYTNKEVT	60
RK14- <i>sey</i> 6	MKAKLWFLLTTLAFLI AVTGSIGIAEVKAKTTGLITENSNDSLKEHYAQKFEVYTNKEVT	60

JP087- <i>sey</i> 1	GVGENYIDAKVDTYNVRTVLYNTDYLKQFKNQDKVNIWGTLYENQQSKVYRGTVVKYDPI	120
SC1133- <i>sey</i> 4	GVGENYIDAKVDTYNVRTVLYNTDYLKQFKNQDKVNIWGTLYENQQSKVYRGTVVKYDPI	120
JP096- <i>sey</i> 3	GVGENYIDAKVDTYNVRTVLYNTDYLKQFKNQDKVNIWGTLYENKQSKVYRGTVVKYDPI	120
SC570- <i>sey</i> 5	GVGENYIDAKVDTYNVRTVLYNTDYLKQFKNQDKVNIWGTLYENKQSKVYRGTVVKYDPI	120
RF122- <i>sey</i> 7	GVGENYIDTKVDTYNVRTVLYNTDYLKQFKNQDKVNIWGTLYENQQSKVYRGTVVKYDPI	120
JP074- <i>sey</i> 2	GVGENYIDTKVDTYNVRTVLYNTDYLKQFKNQDKVNIWGTLYENQQSKVYRGTVVKYDPI	120
RK14- <i>sey</i> 6	GVGENYIDVKVDTYNVRTVLYNTDYLKQFKNQDKVNIWGTLYENQQSKVYRGTVVKYDPI	120

JP087- <i>sey</i> 1	SKVTNLSYRMNLFVNGHQTKVNPDSLLEVKNKQISLKETDFRIRKYLLEKEHLYSNYNSG	180
SC1133- <i>sey</i> 4	SKVTNLSYRMNLFVNGHQTKVNPDSLLEVKNKQISLKETDFRIRKYLLEKEHLYSNYNSG	180
JP096- <i>sey</i> 3	SKVTNLSYRMNLFVNGHQTKVNPDSLLEVKNKQISLKETDFRIRKYLLEKEHLYSNYNSG	180
SC570- <i>sey</i> 5	SKVTNLSYRMNLFVNGHQTKVNPDSLLEVKNKQISLKETDFRIRKYLLEKEHLYSNYNSG	180
RF122- <i>sey</i> 7	SKVTNLSYRMNLFVNGHQTKVNPDSLLEVKNKQISLKETDFRIRKYLLEKEHLYSNYNSG	180
JP074- <i>sey</i> 2	SKVTNLSYRMNLFVNGHQTKVNPDSLLEVKNKQISLKETDFRIRKYLLEKEHLYSNYNSG	180
RK14- <i>sey</i> 6	SKVTNLSYRMNLFVNGHQTKVNPDSLLEVKNKQISLKETDFRIRKYLLEKEHLYSNYNSG	180

JP087- <i>sey</i> 1	ELIEMKNGARHKIDLGDILSDSQEKTFFDNI SHIDIYMK	221
SC1133- <i>sey</i> 4	ELIEMKNGARHKIDLGDILSDSQEKTFFDNI SHIDIYMK	221
JP096- <i>sey</i> 3	ELIEMKNGARHKIDLGDILSDSQEKTFFDNI SHIDIYMK	221
SC570- <i>sey</i> 5	ELIEMKNGARHKIDLGDILSDSQEKTFFDNI SHIDIYMK	221
RF122- <i>sey</i> 7	ELIEMKNGARHKIDLGDILSDSQEKTFFDNI SHIDIYMK	221
JP074- <i>sey</i> 2	ELIEMKNGARHKIDLGDILSDSQEKTFFDNI SHIDIYMK	221
RK14- <i>sey</i> 6	ELIEMKNGARHKIDLGDILSDSQEKTFFDNI SHIDIYMK	221
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(b)

<i>sey</i> 4	ATGAAAGCGAAACTATGTTTTTTATTGACAACCTTTGGCATTGTTTATTGTCAGTAACGGGA	60
<i>sey</i> 1	ATGAAAGCGAAACTATGTTTTTTATTGACAACCTTTGGCATTGTTTATTGTCAGTAACGGGA	60
<i>sey</i> 6	ATGAAAGCTAAATTATGGTTTTTTATTGACAACCTTTGGCATTGTTTATTGTCAGTAACGGGA	60
<i>sey</i> 2	ATGAAAGCGAAACTATGTTTTTTATTGACAACCTTTGGCATTGTTTATTGTCAGTAACGGGA	60
<i>sey</i> 7	ATGAAAGCGAAACTATGTTTTTTATTGACAACCTTTGGCATTGTTTATTGTCAGTAACGGAA	60
<i>sey</i> 5	ATGAAAGCTAAACTATGGTTTTTTATTGACAACCTTTGGCATTGTTTATTGTCAGTAACGGGA	60
<i>sey</i> 3	ATGAAAGCTAAACTATGGTTTTTTATTGACAACCTTTGGCATTGTTTATTGTCAGTAACGGGA	60
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sey4      TCTATTGGAATAGCAGAAGTAAAAGCAAAAACAACCTGGATTGATTACAGAAAATAGTAAT 120
sey1      TCTATTGGAATAGCAGAAGTAAAAGCAAAAACAACCTGGATTGATTACAGAAAATAGTAAT 120
sey6      TCTATTGGAATAGCAGAAGTAAAAGCAAAAACAACCTGGATTGATTACAGAAAATAGTAAT 120
sey2      TCTATTGGAATAGCAGAAGTAAAAGCAAAAACAACCTGGATTGATTACAGAAAATAGTAAT 120
sey7      TCTATTGGAATAGCAGAAGTAAAAGCAAAAACAACCTGGATTGATTACAGAAAATAGTAAT 120
sey5      TCTATTGGAATAGCAGAAGTAAAAGCAAAAACAACCTGGATTGATTACAGAAAATAGTAAT 120
sey3      TCTATTGGAATAGCAGAAGTAAAAGCAAAAACAACCTGGATTGATTACAGAAAATAGTAAT 120
*****

sey4      GACAGTTTAAAAGAGCATTATGCACAAAAATTTGAAGTTTATACGAATAAAGAAGTAACA 180
sey1      GACAGTTTAAAAGAGCATTATGCACAAAAATTTGAAGTTTATACGAATAAAGAAGTAACA 180
sey6      GACAGTTTAAAAGAGCATTATGCACAAAAATTTGAAGTTTATACGAATAAAGAAGTAACA 180
sey2      GACAGTTTAAAAGAGCATTATGCACAAAAATTTGAAGTTTATACGAATAAAGAAGTAACA 180
sey7      GACAGTTTAAAAGAGCATTATGCACAAAAATTTGAAGTTTATACGAATAAAGAAGTAACA 180
sey5      GACAGTTTAAAAGAGCATTATGCACAAAAATTTGAAGTTTATACGAATAAAGAAGTAACA 180
sey3      GACAGTTTAAAAGAGCATTATGCACAAAAATTTGAAGTTTATACGAATAAAGAAGTAACA 180
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sey4      GGAGTTGGGGAAAATTATATAGACGCGAAAGTTGACACCTACAATGTACGGACAGTGCTC 240
sey1      GGAGTTGGGGAAAATTATATAGACGCGAAAGTTGACACCTACAATGTACGGACAGTGCTC 240
sey6      GGAGTTGGGGAAAATTATATAGACGCGAAAGTTGACACCTACAATGTACGGACAGTGCTC 240
sey2      GGAGTTGGGGAAAATTATATAGACGCGAAAGTTGACACCTACAATGTACGGACAGTGCTC 240
sey7      GGAGTTGGGGAAAATTATATAGACGCGAAAGTTGACACCTACAATGTACGGACAGTGCTC 240
sey5      GGAGTTGGGGAAAATTATATAGACGCGAAAGTTGACACCTACAATGTACGGACAGTGCTC 240
sey3      GGAGTTGGGGAAAATTATATAGACGCGAAAGTTGACACCTACAATGTACGGACAGTGCTC 240
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sey4      TACAACACTGATTATTTGAAACAGTTTAAAAATCAAGACAAAGTTAATATATGGGGAACA 300
sey1      TACAACACTGATTATTTGAAACAGTTTAAAAATCAAGACAAAGTTAATATATGGGGAACA 300
sey6      TACAACACTGATTATTTGAAACAGTTTAAAAATCAAGACAAAGTTAATATATGGGGAACA 300
sey2      TACAACACTGATTATTTGAAACAGTTTAAAAATCAAGACAAAGTTAATATATGGGGAACA 300
sey7      TACAACACTGATTATTTGAAACAGTTTAAAAATCAAGACAAAGTTAATATATGGGGAACA 300
sey5      TACAACACTGATTATTTGAAACAGTTTAAAAATCAAGACAAAGTTAATATATGGGGAACA 300
sey3      TACAACACTGATTATTTGAAACAGTTTAAAAATCAAGACAAAGTTAATATATGGGGAACA 300
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sey4      TTATATGAAAACCAACAATCTAAAGTATATCGTGGCACAGTAGTTAAGTATGATCCTATA 360
sey1      TTATATGAAAACCAACAATCTAAAGTATATCGTGGCACAGTAGTTAAGTATGATCCTATA 360
sey6      TTATATGAAAACCAACAATCTAAAGTATATCGTGGCACAGTAGTTAAGTATGATCCTATA 360
sey2      TTATATGAAAACCAACAATCTAAAGTATATCGTGGCACAGTAGTTAAGTATGATCCTATA 360
sey7      TTATATGAAAACCAACAATCTAAAGTATATCGTGGCACAGTAGTTAAGTATGATCCTATA 360
sey5      TTATATGAAAACCAACAATCTAAAGTATATCGTGGCACAGTAGTTAAGTATGATCCTATA 360
sey3      TTATATGAAAACCAACAATCTAAAGTATATCGTGGCACAGTAGTTAAGTATGATCCTATA 360
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sey4      TCAAAAGTAACTAECTTATCTTATAGAATGAACCTGTTTGTAAACGGTCATCAAACATAA 420
sey1      TCAAAAGTAACTAECTTATCTTATAGAATGAACCTGTTTGTAAACGGTCATCAAACATAA 420
sey6      TCAAAAGTAACTAECTTATCTTATAGAATGAACCTGTTTGTAAACGGTCATCAAACATAA 420
sey2      TCAAAAGTAACTAECTTATCTTATAGAATGAACCTGTTTGTAAACGGTCATCAAACATAA 420
sey7      TCAAAAGTAACTAECTTATCTTATAGAATGAACCTGTTTGTAAACGGTCATCAAACATAA 420
sey5      TCAAAAGTAACTAECTTATCTTATAGAATGAACCTGTTTGTAAACGGTCATCAAACATAA 420
sey3      TCAAAAGTAACTAECTTATCTTATAGAATGAACCTGTTTGTAAACGGTCATCAAACATAA 420
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sey4      GTCAATCCAGACAGTTTATTAGAAGTTAAGAATAAACAGATTTCTCTAAAAGAAACAGAT 480
sey1      GTCAATCCAGACAGTTTATTAGAAGTTAAGAATAAACAGATTTCTCTAAAAGAAACAGAT 480
sey6      GTGAATCCAGACAGTTTATTAGAAGTTAAGAATAAACAGATTTCTCTAAAAGAAACAGAT 480
sey2      GTGAATCCAGACAGTTTATTAGAAGTTAAGAATAAACAGATTTCTCTAAAAGAAACAGAT 480
sey7      GTGAATCCAGACAGTTTATTAGAAGTTAAGAATAAACAGATTTCTCTAAAAGAAACAGAT 480
sey5      GTGAATCCAGACAGTTTATTAGAAGTTAAGAATAAACAGATTTCTCTAAAAGAAACAGAT 480
sey3      GTGAATCCAGACAGTTTATTAGAAGTTAAGAATAAACAGATTTCTCTAAAAGAAACAGAT 480
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sey4      TTTAGAATTAGAAAATATTTATTAGAAAAAGAACACCTATATAGTAATTACAATTCAGGG  540
sey1      TTTAGAATTAGAAAATATTTATTAGAAAAAGAACACCTATATAGTAATTACAATTCAGGG  540
sey6      TTTAGAATTAGAAAATATTTATTAGAAAAAGAACACCTATATAGTAATTACAATTCAGGG  540
sey2      TTTAGAATTAGAAAATATTTATTAGAAAAAGAACACCTATATAGTAATTACAATTCAGGG  540
sey7      TTTAGAATTAGAAAATATTTATTAGAAAAAGAACACCTATATAGTAATTACAATTCAGGG  540
sey5      TTTAGAATTAGAAAATATTTATTAGAAAAAGAACACCTATATAGTAATTACAATTCAGGG  540
sey3      TTTAGAATTAGAAAATATTTATTAGAAAAAGAACACCTATATAGTAATTACAATTCAGGT  540
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sey4      GAACTAATTGTAGAAATGAAAAATGGAGCAAGACATAAAATAGATTTATGCGCATATTG    600
sey1      GAACTAATTGTAGAAATGAAAAATGGAGCAAGACATAAAATAGATTTAGGCGCATATTG    600
sey6      GAACTAATTATAGAAATGAAAAATGGAGCAAGACATAAAATAGATTTAGGCGCATATTG    600
sey2      GAACTAATTATAGAAATGAAAAATGGAGCAAGACATAAAATAGATTTAGGCGCATATTG    600
sey7      GAACTAATTATAGAAATGAAAAATGGAGCAAGACATAAAATAGATTTAGGCGCATATTG    600
sey5      GAACTAATTATAGAAATGAAAAATGGAGCAAGACATAAAATAGATTTAGGCGCATATTG    600
sey3      GAACTAATTATAGAAATGAAAAATGGAGCAAGACATAAAATAGATTTAGGCGCATATTG    600
          *****

sey4      AGCGACTCACAAGAAAAAACGTTTGATTTTGATAATATTAGTCATATAGATATTTATATG   660
sey1      AGCGACTCACAAGAAAAAACGTTTGATTTTGATAATATTAGTCATATAGATATTTATATG   660
sey6      AGTGACTCACAAGAAAAAACGTTTGATTTTGATAATATTAGTCATATAGATATTTATATG   660
sey2      AGTGACTCACAAGAAAAAACGTTTGATTTTGATAATATTAGTCATATAGATATTTATATG   660
sey7      AGTGACTCACAAGAAAAAACGTTTGATTTTGATAATATTAGTCATATAGATATTTATATG   660
sey5      AGTGACTCACAAGAAAAAACGTTTGATTTTGATAATATTAGTCATATAGATATTTATATG   660
sey3      AGTGACTCACAAGAAAAAACGTTTGATTTTGATAATATTAGTCATATAGATATTTATATG   660
          ** *****

sey4      AAATAG  666
sey1      AAATAG  666
sey6      AAATAG  666
sey2      AAATAG  666
sey7      AAATAG  666
sey5      AAATAA  666
sey3      AAATAG  666
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Figure S1. Alignment of amino acid (a) and nucleotide (b) sequences of SEY (sey1-sey7). Asterisk indicates identical amino acid or nucleotide. Amino acids that are different from those of SEY1 are marked in yellow.

(a)

SC761-coaVa-ST121	MILGEFEVKYLTGFILILLLEGILTNASASAI EYSDLHHKSKLNSKRLSNAKMSFINPTQL	60
SC1133-coaVa-ST121	MILGEFEVKYLTGFILILLLEGILTNASASAI EYSDLHHKSKLNSKRLSNAKMSFINPTQL	60
SC1137-coaVa-ST121	MILGEFEVKYLTGFILILLLEGILTNASASAI EYSDLHHKSKLNSKRLSNAKMSFINPTQL	60
SC732-coaVa-ST121	MILGEFEVKYLTGFILILLLEGILTNASASAI EYSDLHHKSKLNSKRLSNAKMSFINPTQL	60
SC533-coaVIIb-ST45	MILGEFEVKYLTGFILILLLEGILTNASASAI EYSDLHHKSKFNSKRLSNAKMSFANPTDL	60
SC465-coaIIa-ST764	--MGEFEVKYLTGFILILLLEGIFTNSASAI EYSDLHHKSKFDSKRLSNAKMSFINPTQL	58
SC792-coaIIa-ST5	--MGEFEVKYLTGFILILLLEGIFTNSASAI EYSDLHHKSKFDSKRLSNAKMSFINPTQL	58
SC936-coaIIa-ST5	--MGEFEVKYLTGFILILLLEGIFTNSASAI EYSDLHHKSKFDSKRLSNAKMSFINPTQL	58
SC955-coaIIa-ST5	--MGEFEVKYLTGFILILLLEGIFTNSASAI EYSDLHHKSKFDSKRLSNAKMSFINPTQL	58
SC1096-coaVb-ST5425	MILGEFEVKYLTGFILILLLEGIFTNSASAI EYSDLHHKSKFDSKRLSNAKMSFINPTQL	60
SC519-coaIVa-ST30	--MGEFEVKYLTGFILILLLEGIFTNSASAI EYSDLHHKSKLDSKRLYNKVSFANPTDL	58
SC1130-coaIIIa-ST8	--MGEFEVKYLTGFILILLLEGIFTNSASAI EYSDLHHKSKFDSKRLSNAKMSFINPTQL	58
SC526-coaIIIa-ST8	--MGEFEVKYLTGFILILLLEGIFTNSASAI EYSDLHHKSKFDSKRLSNAKMSFINPTQL	58
SC625-coaIIIa-ST8	--MGEFEVKYLTGFILILLLEGIFTNSASAI EYSDLHHKSKFDSKRLSNAKMSFINPTQL	58
SC546-coaIIIa-ST8	--MGEFEVKYLTGFILILLLEGIFTNSASAI EYSDLHHKSKFDSKRLSNAKMSFINPTQL	58
SC1019-coaIIIa-ST8	--MGEFEVKYLTGFILILLLEGIFTNSASAI EYSDLHHKSKFDSKRLSNAKMSFINPTQL	58
SC635-coaVIIa-ST1	--MGEFEVKYLTGFILILLLEGIFTNSASAI EYSDLHHKSKFDSKRLSNAKMSFINPTQL	58
SC458-coaVIIa-ST1	--MGEFEVKYLTGFILILLLEEILTNASASAI EYSDLHHKSKFDSKRLSNAKMSFINPTQL	58
SC470-coaVIIa-ST1	--MGEFEVKYLTGFILILLLEEILTNASASAI EYSDLHHKSKFDSKRLSNAKMSFINPTQL	58
SC560-coaVIIa-ST1	--MGEFEVKYLTGFILILLLEEILTNASASAI EYSDLHHKSKFDSKRLSNAKMSFINPTQL	58
SC735-coaIa-ST89	--MGEFEVKYLTGFILILLLEGIFTNSASAI EYSDLHHKSELDSKRLYNKVSFANPTQL	58
SC756-coaIa-ST89	--MGEFEVKYLTGFILILLLEGIFTNSASAI EYSDLHHKSELDSKRLYNKVSFANPTQL	58
SC778-coaIa-ST89	--MGEFEVKYLTGFILILLLEGIFTNSASAI EYSDLHHKSELDSKRLYNKVSFANPTQL	58
SC912-coaVIIb-ST45	--MGEFEVKYLTGFILILLLEGIFTNSASAI EYSDLHHKSKLDSKRLYNKVSFANPTDL	58

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SC761-coaVa-ST121	ENKKTNDRLLLTHDLLFHDMLNDASKKDFKVEFENEALSNEFINKNIDIYAGSYSYEGCHG	120
SC1133-coaVa-ST121	ENKKTNDRLLLTHDLLFHDMLNDASKKDFKVEFENEALSNEFINKNIDIYAGSYSYEGCHG	120
SC1137-coaVa-ST121	ENKKTNDRLLLTHDLLFHDMLNDASKKDFKVEFENEALSNEFINKNIDIYAGSYSYEGCHG	120
SC732-coaVa-ST121	ENKKTNDRLLLTHDLLFHDMLNDASKKDFKVEFENEALSNEFINKNIDIYAGSYSYEGCHG	120
SC533-coaVIIb-ST45	ENKKTNDRLLLTHDLLFHDMLNDASKKDFKVEFENEALSNEFINKNIDIYAGSYSYEGCHG	120
SC465-coaIIa-ST764	ENKNTNDRLLLKHDLLFHDMLVNDASKKDFKVEFENEALSNEFINKNIDIYAGSYSYEGCHG	118
SC792-coaIIa-ST5	ENKNTNDRLLLKHDLLFHDMLVNDASKKDFKVEFENEALSNEFINKNIDIYAGSYSYEGCHG	118
SC936-coaIIa-ST5	ENKNTNDRLLLKHDLLFHDMLVNDASKKDFKVEFENEALSNEFINKNIDIYAGSYSYEGCHG	118
SC955-coaIIa-ST5	ENKNTNDRLLLKHDLLFHDMLVNDASKKDFKVEFENEALSNEFINKNIDIYAGSYSYEGCHG	118
SC1096-coaVb-ST5425	ENKNTNDRLLLKHDLLFHDMLVNDASKKDFKVEFENEALSNEFINKNIDIYAGSYSYEGCHG	120
SC519-coaIVa-ST30	ENKKTNDRLLLKHDLLFHDMLNDASKKDFKVEFENEALSNEFINKNIDVYAGSYSYEGCHG	118
SC1130-coaIIIa-ST8	ENKNTNDRLLLKHDLLFHDMLVNDASKKDFKVEFENEALSNEFINKNIDIFAGNYGYGCHG	118
SC526-coaIIIa-ST8	ENKNTNDRLLLKHDLLFHDMLVNDASKKDFKVEFENEALSNEFINKNIDIFAGNYGYGCHG	118
SC625-coaIIIa-ST8	ENKNTNDRLLLKHDLLFHDMLVNDASKKDFKVEFENEALSNEFINKNIDIFAGNYGYGCHG	118
SC546-coaIIIa-ST8	ENKNTNDRLLLKHDLLFHDMLVNDASKKDFKVEFENEALSNEFINKNIDIFAGNYGYGCHG	118
SC1019-coaIIIa-ST8	ENKNTNDRLLLKHDLLFHDMLVNDASKKDFKVEFENEALSNEFINKNIDIFAGNYGYGCHG	118
SC635-coaVIIa-ST1	ENKNTNDRLLLKHDLLFHDMLVNDASKKDFKVEFENEALSNEFINKNIDIFAGNYGYGCHG	118
SC458-coaVIIa-ST1	ENKNTNDRLLLKHDLLFHDMLVNDASKKDFKVEFENEALSNEFINKNIDIFAGNYGYGCHG	118
SC470-coaVIIa-ST1	ENKNTNDRLLLKHDLLFHDMLVNDASKKDFKVEFENEALSNEFINKNIDIFAGNYGYGCHG	118
SC560-coaVIIa-ST1	ENKNTNDRLLLKHDLLFHDMLVNDASKKDFKVEFENEALSNEFINKNIDIFAGNYGYGCHG	118
SC735-coaIa-ST89	ENKKTNDRLLLKHDLLFHDMLVNDASKKDFKVEFENEALSNEFINKNIDIFAGNYGYGCHG	118
SC756-coaIa-ST89	ENKKTNDRLLLKHDLLFHDMLVNDASKKDFKVEFENEALSNEFINKNIDIFAGNYGYGCHG	118
SC778-coaIa-ST89	ENKKTNDRLLLKHDLLFHDMLVNDASKKDFKVEFENEALSNEFINKNIDIFAGNYGYGCHG	118
SC912-coaVIIb-ST45	ENKKTNDRLLLKHDLLFHDMLVNDASKKDFKVEFENEALSNEFINKNIDIFAGNYGYGCHG	118

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SC761-coaVa-ST121	GETNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELDVQ	180
SC1133-coaVa-ST121	GETNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELDVQ	180
SC1137-coaVa-ST121	GETNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELDVQ	180
SC732-coaVa-ST121	GETNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELDVQ	180
SC533-coaVIIb-ST45	GATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEKELTAVKTKKKIVTIQELDVQ	180
SC465-coaIIa-ST764	GATNKTQCSYGGVTLSDNNK-----	138
SC792-coaIIa-ST5	GATNKTQCSYGGVTLSDNNK-----	138
SC936-coaIIa-ST5	GATNKTQCSYGGVTLSDNNK-----	138
SC955-coaIIa-ST5	GATNKTQCSYGGVTLSDNNK-----	138
SC1096-coaVb- ST5425	GATNKTQCSYGGVTLSDNNK-----	140
SC519-coaIVa-ST30	GETNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKK-----	167
SC1130-coaIIIa-ST8	GATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELELVQ	178
SC526-coaIIIa-ST8	GATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELELVQ	178
SC625-coaIIIa-ST8	GATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELELVQ	178
SC546-coaIIIa-ST8	GATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELELVQ	178
SC1019-coaIIIa-ST8	GATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELELVQ	178
SC635-coaVIIa-ST1	GATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELELVQ	178
SC458-coaVIIa-ST1	GATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELDVQ	178
SC470-coaVIIa-ST1	GATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELDVQ	178
SC560-coaVIIa-ST1	GATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELDVQ	178
SC735-coaIa-ST89	GETNKTLCYGGVTLSDNNKYDDYKNIPCNLWIDGHQTGIELTAVKTKKKIVTIQELDVQ	178
SC756-coaIa-ST89	GETNKTLCYGGVTLSDNNKYDDYKNIPCNLWIDGHQTGIELTAVKTKKKIVTIQELDVQ	178
SC778-coaIa-ST89	GETNKTLCYGGVTLSDNNKYDDYKNIPCNLWIDGHQTGIELTAVKTKKKIVTIQELDVQ	178
SC912-coaVIIb-ST45	GETNKTQCSYGGVTLSDNNKYDNDKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELDVQ	178

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SC761-coaVa-ST121	LRNYLSEKYKLYEKGGDIVKGYVKYHNDDEKNVEYDFYNLNGEYGHVLEKMYADNKTINS	240
SC1133-coaVa-ST121	LRNYLSEKYKLYEKGGDIVKGYVKYHNDDEKNVEYDFYNLNGEYGHVLEKMYADNKTINS	240
SC1137-coaVa-ST121	LRNYLSEKYKLYEKGGDIVKGYVKYHNDDEKNVEYDFYNLNGEYGHVLEKMYADNKTINS	240
SC732-coaVa-ST121	LRNYLSEKYKLYEKGGDIVKGYVKYHNDDEKNVEYDFYNLNGEYGHVLEKMYADNKTINS	240
SC533-coaVIIb-ST45	LRNYLSEKYKLYEKGGDIVKGYVKYHNDDEKNVEYDFYNLNGEYGHVLEKMYADNKTINS	240
SC465-coaIIa-ST764	-----	138
SC792-coaIIa-ST5	-----	138
SC936-coaIIa-ST5	-----	138
SC955-coaIIa-ST5	-----	138
SC1096-coaVb- ST5425	-----	140
SC519-coaIVa-ST30	-----	167
SC1130-coaIIIa-ST8	LRNYLSEKYKLYEKGGDIVKGYVKYHNDDEKNVEYDFYNLNGEYGHVLEKMYADNKTINS	238
SC526-coaIIIa-ST8	LRNYLSEKYKLYEKGGDIVKGYVKYHNDDEKNVEYDFYNLNGEYGHVLEKMYADNKTINS	238
SC625-coaIIIa-ST8	LRNYLSEKYKLYEKGGDIVKGYVKYHNDDEKNVEYDFYNLNGEYGHVLEKMYADNKTINS	238
SC546-coaIIIa-ST8	LRNYLSEKYKLYEKGGDIVKGYVKYHNDDEKNVEYDFYNLNGEYGHVLEKMYADNKTINS	238
SC1019-coaIIIa-ST8	LRNYLSEKYKLYEKGGDIVKGYVKYHNDDEKNVEYDFYNLNGEYGHVLEKMYADNKTINS	238
SC635-coaVIIa-ST1	LRNYLSEKYKLYEKGGDIVKGYVKYHNDDEKNVEYDFYNLNGEYGHVLEKMYADNKTINS	238
SC458-coaVIIa-ST1	LRNYLSEKYKLYEKGGDIVKGYVKYHNDDEKNVEYDFYNLNGEYGHVLEKMYADNKTINS	238
SC470-coaVIIa-ST1	LRNYLSEKYKLYEKGGDIVKGYVKYHNDDEKNVEYDFYNLNGEYGHVLEKMYADNKTINS	238
SC560-coaVIIa-ST1	LRNYLSEKYKLYEKGGDIVKGYVKYHNDDEKNVEYDFYNLNGEYGHVLEKMYADNKTINS	238
SC735-coaIa-ST89	LRNYLSEKYKLYELGGDIVKGYVKYHNDDEKNVEYDFYNLNGEYGHVLEKMYADNKTINS	238
SC756-coaIa-ST89	LRNYLSEKYKLYELGGDIVKGYVKYHNDDEKNVEYDFYNLNGEYGHVLEKMYADNKTINS	238
SC778-coaIa-ST89	LRNYLSEKYKLYELGGDIVKGYVKYHNDDEKNVEYDFYNLNGEYGHVLEKMYADNKTINS	238
SC912-coaVIIb-ST45	LRNYLSEKYKLYEKGGDIVKGYVKYHNDDEKNVEYDFYNLNGEYGHVLEKMYADNKTINS	238

SC761-coaVa-ST121	DKLHLDIYLFKS	252
SC1133-coaVa-ST121	DKLHLDIYLFKS	252
SC1137-coaVa-ST121	DKLHLDIYLFKS	252
SC732-coaVa-ST121	DKLHLDIYLFKS	252
SC533-coaVIIb-ST45	DKLHLDIYLFKS	252
SC465-coaIIa-ST764	-----	138
SC792-coaIIa-ST5	-----	138
SC936-coaIIa-ST5	-----	138
SC955-coaIIa-ST5	-----	138
SC1096-coaVb-ST5425	-----	140
SC519-coaIVa-ST30	-----	167
SC1130-coaIIIa-ST8	DKLHLDIYLFKS	250
SC526-coaIIIa-ST8	DKLHLDIYLFKS	250
SC625-coaIIIa-ST8	DKLHLDIYLFKS	250
SC546-coaIIIa-ST8	DKLHLDIYLFKS	250
SC1019-coaIIIa-ST8	DKLHLDIYLFKS	250
SC635-coaVIIa-ST1	DKLHLDIYLFKS	250
SC458-coaVIIa-ST1	DKLHLDIYLFKS	250
SC470-coaVIIa-ST1	DKLHLDIYLFKS	250
SC560-coaVIIa-ST1	DKLHLDIYLFKS	250
SC735-coaIa-ST89	DKLHLDIYLFKS	250
SC756-coaIa-ST89	DKLHLDIYLFKS	250
SC778-coaIa-ST89	DKLHLDIYLFKS	250
SC912-coaVIIb-ST45	DKLHLDIYLFKS	250

(b)

SC761-selw7	MILGEFEVKYLTGFILILLLEGILTNSASAIEYSDLHHKSKLNSKRLSNAKMSFINPTQL	60
TD101-selw10	-----MLEEILTNSVSAIEYSDLHHKSKLNSKRLYNKVSFANPTDL	42
K17-selw9	-----MLEGIFTNSASAIEYSDLHHKSKLNSKRLYNKVSFANPTDL	42
SC465-selw4	--MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQL	58
N315-selw4	--MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQL	58
TD3-selw5	--MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQL	58
MW2-selw3	-----MTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQL	37
TD21-selw3	-----MLEEILTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQL	42
SC458-selw3	--MGEFEVKYLTGFILILLLEEILTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQL	58
TD115-selw3	-----MLEEILTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQL	42
SC1130-selw2	--MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQL	58
COL-selw2	--MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQL	58
TD8-selw6	--MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKFDSKRLSNAKMSFINPTQL	58
RF122-selw1c	--MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKLDSKGLYNKVSFANPTDL	58
SC519-selw8	--MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKLDSKRLYNKVSFANPTDL	58
TCH60-selw8	--MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKLDSKRLYNKVSFANPTDL	58
SC756-selw1a	--MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSELDSKRLYNKVSFANPTQL	58
Tager104-selw1c	MILGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKLDSKGLYNKVSFANPTDL	60
TD123-selw1b	--MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKLDSKRLYNKVSFANPTDL	58
ISU926-selw1d	--MGEFEVKYLTGFILILLLEGIFTNSASAIEYSDLHHKSKLDSKRLYNKVSFANPTDL	58

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SC761-selw7	ENKKTNDRLRLTHDLLFHDMFLNDASKKDFKVEFENEALSNEFINKNIDYAGSYSYECHG	120
TD101-selw10	ENKNTNDRLRLKHDLLFHDMFVNVASKKDFKVEFENEALSNEFINKNIDYAGNYGYGCHG	102
K17-selw9	ENKNTNDRLRLKHDLLFHDMFVNVASKKDFKVEFENEALSNEFINKNIDYAGSYSYECHG	102
SC465-selw4	ENKNTNDRLRLKHDLLFHDMFVNVASKKDFKVEFENEALSNEFINKNIDYAGSYSYECHG	118
N315-selw4	ENKNTNDRLRLKHDLLFHDMFVNVASKKDFKVEFENEALSNEFINKNIDYAGSYSYECHG	118
TD3-selw5	ENKNTNDRLRLKHDLLFHDMFVNVASKKDFKVEFENEALSNEFINKNIDYAGSYSYECHG	118
MW2-selw3	ENKNTNDRLRLKHDLLFHDMFVNVASKKDFKVEFENEALSNEFINKNIDYAGNYGYGCHG	97
TD21-selw3	ENKNTNDRLRLKHDLLFHDMFVNVASKKDFKVEFENEALSNEFINKNIDYAGNYGYGCHG	102
SC458-selw3	ENKNTNDRLRLKHDLLFHDMFVNVASKKDFKVEFENEALSNEFINKNIDYAGNYGYGCHG	118
TD115-selw3	ENKNTNDRLRLKHDLLFHDMFVNVASKKDFKVEFENEALSNEFINKNIDYAGNYGYGCHG	102
SC1130-selw2	ENKNTNDRLRLKHDLLFHDMFVNVASKKDFKVEFENEALSNEFINKNIDYAGNYGYGCHG	118
COL-selw2	ENKNTNDRLRLKHDLLFHDMFVNVASKKDFKVEFENEALSNEFINKNIDYAGNYGYGCHG	118
TD8-selw6	ENKNTNDRLRLKHDLLFHDMFVNVASKKDFKVEFENEALSNEFINKNIDYAGNYGYGCHG	118
RF122-selw1c	ENKKTNDRLRLKHDLLFHDMFVNVASKKDFKVEFENEALSNEFINKNIDYAGNYGYECHG	118
SC519-selw8	ENKKTNDRLRLKHDLLFHDMFLNDAWKDLKVEFENEALSNEFINKNIDVYAGSYSYECHG	118
TCH60-selw8	ENKKTNDRLRLKHDLLFHDMFLNDAWKDLKVEFENEALSNEFINKNIDVYAGSYSYECHG	118
SC756-selw1a	ENKKTNDRLRLKHDLLFHDMFVNVASKKDFKVEFENEALSNEFINKNIDYAGNYGYGCHG	118
Tager104-selw1c	ENKKTNDRLRLKHDLLFHDMFVNVASKKDFKVEFENEALSNEFINKNIDYAGNYGYGCHG	120
TD123-selw1b	ENKKTNDRLRLKHDLLFHDMFVNVASKKDFKVEFENEALSNEFINKNIDYAGNYGYGCHG	118
ISU926-selw1d	ENKKTNDRLRLKHDLLFHDMFVNVASKKDFKVEFENEALSNEFINKNIDYAGNYGYGCHG	118

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SC761-selw7	GETNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELDVQ	180
TD101-selw10	GATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELEVVQ	162
K17-selw9	GATNKTQCSYGGVTLSDNNK-----	122
SC465-selw4	GATNKTQCSYGGVTLSDNNK-----	138
N315-selw4	GATNKTQCSYGGVTLSDNNK-----	138
TD3-selw5	GATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELDVQ	178
MW2-selw3	GATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELDVQ	157
TD21-selw3	GATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELDVQ	162
SC458-selw3	GATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELDVQ	178
TD115-selw3	GATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELDVQ	162
SC1130-selw2	GATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELEVVQ	178
COL-selw2	GATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELEVVQ	178
TD8-selw6	GATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQAEIELTAVKTKKKIVTIQELDVQ	178
RF122-selw1c	GRNQ-----	122
SC519-selw8	GETNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKK-----	167
TCH60-selw8	GETNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKK-----	167
SC756-selw1a	GETNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELDVQ	178
Tager104-selw1c	GATNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELDVQ	180
TD123-selw1b	GETNKTQCSYGGVTLSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELDVQ	178
ISU926-selw1d	GEANKTQCSYGGVTFSDNNKYDDYKNIPCNLWIDGHQTEIELTAVKTKKKIVTIQELDVQ	178

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SC761-selw7	LRNYLSEKYKLYEKGDDIVKGYVKYHNDDEKNVEYDFYLNNGEYGHEVLKMYADNKTINS	240
TD101-selw10	LRNYLNEKYKLYEQGGDIVKGYVKYHNDDEQNVEYDFYLNNGEYGREVLKMYADNKTINS	222
K17-selw9	-----	122
SC465-selw4	-----	138
N315-selw4	-----	138
TD3-selw5	LRNYLNEKYKLYEQQGDIVKGYVKYHNDDEQNIEYNFYLNNGEYGYEVLKMYADNKTINS	238
MW2-selw3	LRNYLNEKYKLYEQQGDIVKGYVKYHNDDEQNIEYNFYLNNGEYGYEVLKMYADNKTINS	217
TD21-selw3	LRNYLNEKYKLYEQQGDIVKGYVKYHNDDEQNIEYNFYLNNGEYGYEILKMYADNKTINS	222
SC458-selw3	LRNYLNEKYKLYEQQGDIVKGYVKYHNDDEQNIEYNFYLNNGEYGYEVLKMYADNKTINS	238
TD115-selw3	LRNYLNEKYKLYEQQGDIVKGYVKYHNDDEQNIEYNFYLNNGEYGYEVLKMYADNKTINS	222
SC1130-selw2	LRNYLNEKYKLYEQQGDIVKGYVKYHNDDEQNVEYDFYLNNGEYGREVLKMYADNKTINS	238
COL-selw2	LRNYLNEKYKLYEQQGDIVKGYVKYHNDDEQNVEYDFYLNNGEYGREVLKMYADNKTINS	238
TD8-selw6	LRNYLNEKYKLYEQQGDIVKGYVKYHNDDEQNVEYDFYLNNGEYGREVLKMYADNKTINS	238
RF122-selw1c	-----	122
SC519-selw8	-----	167
TCH60-selw8	-----	167
SC756-selw1a	LRNYLNEKYKLYELGGDIVKGYVKYHNDDEKNVEYDFYLNNGEYGHEVLKMYADNKTINS	238
Tager104-selw1c	LRNYLNEKYKLYEQQGDIVKGYVKYHNDDEKNVEYDFYLNNGEYGHEVLKIYADNKTINS	240
TD123-selw1b	LRNYLNEKYKLYEQQGDIVKGYVKYHND-EKNVEYDFYLNNGEYGHEVLKMYADNKTINS	237
ISU926-selw1d	LRNYLNEKYKLYEQQGDIVKGYVKYHNDDEKNVEYDFYLNNGEYGHEVLKMYADNKTINS	238
SC761-selw7	DKLHLDIYLFKS	252
TD101-selw10	DKLHLDIYLFKS	234
K17-selw9	-----	122
SC465-selw4	-----	138
N315-selw4	-----	138
TD3-selw5	DKLHLDIYLFKS	250
MW2-selw3	DKLHLDIYLFKS	229
TD21-selw3	DKLHLDIYLFKS	234
SC458-selw3	DKLHLDIYLFKS	250
TD115-selw3	DKLHLDIYLFKS	234
SC1130-selw2	DKLHLDIYLFKS	250
COL-selw2	DKLHLDIYLFKS	250
TD8-selw6	DKLHLDIYLFKS	250
RF122-selw1c	-----	122
SC519-selw8	-----	167
TCH60-selw8	-----	167
SC756-selw1a	DKLHLDIYLFKS	250
Tager104-selw1c	DKLHLDIYLFKS	252
TD123-selw1b	DKLHLDIYLFKS	249
ISU926-selw1d	DKLHLDIYLFKS	250

Figure S2. Alignment of SEIW amino acid sequences of all the MRSA isolates analyzed in the present study (a) and representative strains of all the *selw* phylogenetic groups (b). Asterisk indicates identical amino acid. Dash denotes gap.

SELX14 MFKKHHSKNSILLKSLSLGIIYSGIFGINSKADASIQDSSSVHDKQFQKVEEVPNNSEK 60
SELX6 MFKKHHSKNSILLKSLSLGIIYSGSFGIYKAGASTQNSSSLQDKQFQKVEEVPNNSEK 60
SELX11 MFKKHHSKNSILLKSLSLGIIYSGSLGIYSKANASTQNSSSVHDKQLQKVEEVPNNSEK 60
SELX4 MFKKYDSKNSILLKSLSLGIIYGGTFGIYPKADASTQNSSSVQDKQFQKVEEVPNNSEK 60
SC533 (SELX16) MFKKHHSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQFQKVEEVPNNSEK 60
TIGER104 (SELX15) MFKKYESKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQFQKVEEVPNNSEK 60
SELX5 MFKKNSDKNSILLKSLSLGIIYGGTFGIYPKADASTQNSSSVQDKQFQKVEEVPNNSEK 60
SELX9 MFKKNSDKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQLQKVEEVPNNSEK 60
SELX1 MFKKYDSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQLQKVEEVPNNSEK 60
SELX2 MFKKYDSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQLQKVEEVPNNSEK 60
SELX-BOV2 MFKKHHSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQLQKVEEVPNNSEK 60
SELX0V MFKKYDSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQLQKVEEVPNNSEK 60
SELX7 MFKKYDSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQLQKVEEVPNNSEK 60
SELX12 MFKKYDSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQLQKVEEVPNNSEK 60
SELX10 MFKKYDSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQFQKVEEVPNNSEK 60
SELX-BOV1 MFKKYDSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQFQKVEEVPNNSEK 60
SELX3 MFKKYDSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQLQKVEEVPNNSEK 60
SELX8 MFKKYDSKNSIVLKSILSLGIIYSGSFGIYPKADASTQNSSSVQDKQLQKVEEVPNNSEK 60
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SELX14 ALVKKLYDRYSQNTINGKSNKSRNWVYSERPLNENQVR IHLEGTYTVAGR VYTPKRNI TL 120
SELX6 ALVKKLYDRYSQNTINGKSNKSRNWVYSERPLNENQVR IHLEGTYTVADR VYTPKRNI TL 120
SELX11 ALVKKLYDRYSKNTINGKSNKSRNWVYSERPLNGNQVR IHLEGTYTVAGR VYTPKRNI TL 120
SELX4 TLVKKLYDRYSKNTINGKSNKSRNWVYSERPLNENQVR IHLEGTYRVADR VYTPKRNI TL 120
SC533 (SELX16) ALVKKLYDRYSKNTINGKSNKSRNWVYSERPLNGNQVR IHLEGTYTVAGR VYTPKRNI TL 120
TIGER104 (SELX15) ALVKKLYDRYSQNTINGKSNKARNWVYSERPLNENQVR IHLEGTYTVAGR VYTPKRNI TL 120
SELX5 ALVKKLYDRYSQNTINGKSNKSRNWVYSERPLNENQVR INLEGTYRVADR VYTPKRNI TL 120
SELX9 ALVKKLYDRYSQNTINGKSNKSRNWVYSERPLNENQVR IHLEGTYRVADR VYTPKRNI TL 120
SELX1 ALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVR IHLEGTYTVADR VYTPKRNI TL 120
SELX2 ALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVR IHLEGTYTVAGR VYTPKRNI TL 120
SELX-BOV2 ALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVR IHLEGTYRVADR VYTPKRNI TL 120
SELX0V ALVKKLYDRYSKDTINGKSNKARNWVYSERPLNENQVR IHLEGTYRVADR VYTPKRNI TL 120
SELX7 ALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVR IHLEGTYRVADR VYTPKRNI TL 120
SELX12 ALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVR IHLEGTYRVADR VYTPKRNI TL 120
SELX10 ALVKKLYDRYSQNTINGKSNKSRNWVYSERPLNENQVR IHLEGTYTVAGR VYTPKRNI TL 120
SELX-BOV1 ALVKKLYDRYSQNTINGKSNKARNWVYSERPLNENQVR IHLEGTYRVADR VYTPKRNI TL 120
SELX3 ALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVR IHLEGTYTVAGR VYTPKRNI TL 120
SELX8 ALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVR IHLEGTYTVAGR VYTPKRNI TL 120
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SELX14 NKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKDG GK Y T L E S H K E L Q K D R E N V E 180
SELX6 NKEVITLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKDG GK Y T L E S H K E L Q K D R E N V K 180
SELX11 NKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKNGG K Y T L E S H K E L Q K D R E N V K 180
SELX4 NKEVVTLKELNHIIRFAHISYGLYMGEHLSKGDIVINTKDG GK Y T L E S H K E L Q K N R E N V K 180
SC533 (SELX16) NKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKNGG K Y T L E S H K E L Q K N R E N V E 180
TIGER104 (SELX15) NKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKNGG K Y T L E S H K E L Q K N R E N V E 180
SELX5 NKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKDG GK Y T L E S H K E L Q K D R E N V K 180
SELX9 NKEVITLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKNGG K Y T L E S H K E L Q K D R E N V K 180
SELX1 NKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKDG GK Y T L E S H K E L Q K D R E N V K 180
SELX2 NKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKDG GK Y T L E S H K E L Q K D R E N V K 180
SELX-BOV2 NKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKNGG K Y T L E S H K E L Q K D R E N V K 180
SELX0V NKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKNGG K Y T L E S H K E L Q K D R E N V K 180
SELX7 NKEVITLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKNGG K Y T L E S H K E L Q K D R E N V K 180
SELX12 NKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKDG GK Y T L E S H K E L Q K D R E N V K 180
SELX10 NKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKNGG K Y T L E S H K E L Q K D R E N V K 180
SELX-BOV1 NKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKNGG K Y T L E S H K E L Q K N R E N V E 180
SELX3 NKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKNGG K Y T L E S H K E L Q K N R E N V E 180
SELX8 NKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKNGG K Y T L E S H K E L Q K N R E N V E 180
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SELX14	INTADIKNVTFELVKSVDIEQV	203
SELX6	INTADIKNVTFDLVKSVDIEQV	203
SELX11	INTDDIKNVTFELVKSVDIEQV	203
SELX4	INTADVKNVTFELVKSVDIEQV	203
SC533 (SELX16)	INTADVENVTFDLVKSVDIEQV	203
TIGER104 (SELX15)	INTADVENVTFDLVKSVDIEQV	203
SELX5	INTADIKNVTFKLVKSVDIEQV	203
SELX9	INTDDIKNVTFELVKSVDIEQV	203
SELX1	INTADIKNVTFKLVKSVDIEQV	203
SELX2	INTADIKNVTFKLVKSVDIEQV	203
SELX-BOV2	INTDDIKNVTFELVKSVDIEQV	203
SELX0V	NNTDDIKNVTFELVKSVDIEQV	203
SELX7	INTDDIKNVTFELVKSVDIEQV	203
SELX12	INTDDIKNVTFELVKSVDIEQV	203
SELX10	IKTDDIKNVTFELVKSVDIEQV	203
SELX-BOV1	INTDDIKNVTFELVKSVDIEQV	203
SELX3	INTDDIKNVTFELVKSVDIEQV	203
SELX8	INTDDIKNVTFELVKSVDIEQV	203
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Figure S3. Alignment of SEIX amino acid sequences representing subtypes SEIX1-SEIX16. Asterisk indicates identical amino acid. Among the 17 *selx* alleles described by Wilson et al [21], sequence data were available for 14 subtypes (*selx1-selx14*). Therefore, SEIX sequences of TIGER104 and SC533 which were distinct from SEIX1-SEIX14 were tentatively assigned as SEIX15 and SEIX16. Putative cleavage site of signal peptide is shown by triangle. Sialic acid-binding region reported previously [22,23] is shown in yellow.

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JKD6159-selz7      MRKVLILITLLFGYSSYLLLEAKAETQNDPNI SELNKASQYTGSWHNIWYLYNSDPVKAK 60
M-selz8           MRKVFILITLLFGYSSYLLLEAKAETQNDPNI SELNKSSQYTGSWHNIWYLYNSDPVNAK 60
SC532-selz6      MRKVFILITLLFGYSSYLLSEAKAETQNDLNI SELNKSSQYTGSWHNIWYLYNSDPVNAK 60
NCTC6131-selz9   MRKVFILITLLFGYSSYLLQAKAETQNDPNI SELNKSSQYTGSWHNIWYLYNSDPVNAK 60
WA-MRSA-59-selz4 MRKVFILITLLFGYSSYLLLEARAETQNDPNI SELNKSSQYTGSWHNIWYLYNSDPVNAK 60
MOK042-selz2     MRKIFILITLLFGYSSYLLLEARAETQNDPNI SELNKSSQYTGSWHNIWYLYNSDPVNAK 60
15584-selz5      MRKVFILITLLFGYSSYLLLEARAETQNDPNI SELNKSSQYTGSLHNIWYLYNSDPVNAK 60
SC457-selz1      MRKVFILITLLFGYSSYLLLEARAETQNDPNI SELNKSSQYTGSWHNIWYLYNSDPVNAK 60
SC635-selz3      MRKVFILITLLFGYSSYLLLEARAETQNDPNI SELNKSSQYTGSWHNIWYLYNSDPVNAK 60
*****:*****. * * *:***** *****:***** *****:*****

JKD6159-selz7      KTKLSDKFLSHDFIVPINSPGHYDYVKTELKDSTMASFDFGKEVDIFGVNYFHQCYSNE 120
M-selz8           KIKLSDKFLSHDFIVPINNPSHYDYVKTELKDSTMASFDFGKEVDIFGVNYFDQCYSNE 120
SC532-selz6      KIKLSDKFLSHDFIVPINSPGHYDYVKTELKDSTMASFDFGKEVDIFGVNYFDQCYSNE 120
NCTC6131-selz9   KIKLSDKFLSHDFIVPINSPGHYDYVKTELKDSTMASFDFGKEVDIFGVNYFDQCYSNE 120
WA-MRSA-59-selz4 KIKVSDKFLSHDFIVPINNPGHYDYVKTELKDSTMASFDFGKEVDIFGVNYFDQCYSNE 120
MOK042-selz2     KIKLSDKFLSHDFIVPINNPGHYDYVKTELKDSTMASFDFGKEVDIFGVNYFDQCYSNE 120
15584-selz5      KIKLSDKFLSHDFIVPINNPGHYDYVKTELKDSTMASFDFGKEVDIFGVNYFDQCYSNE 120
SC457-selz1      KIKLSDKFLSHDFIVPINNPGHYDYVKTELKDSTMASFDFGKEVDIFGVNYFDQCYSNE 120
SC635-selz3      KIKLSDKFLSHDFIVPINNPGHYDYVKTELKDSTMASFDFGKEVDIFGVNYFDQCYSNE 120
* *:*****:*****. * *:*****:*****:*****:*****:*****:*****

JKD6159-selz7      NIQCDSNQGAGSKKTCMYGGITLNNNTNRIQPIVVKVYENDSVTLSFDINIDKETVTI 180
M-selz8           NIQCDSNQGAGSKKTCMYGGITLNNNTNRIQPIVVKVYENDSVTLSFDINIDKETVTI 180
SC532-selz6      NIQCDSNQGAGSKKTCMYGGITLNNNTNRIQPIVVKVYENDSVTLSFDINIDKETVTI 180
NCTC6131-selz9   NIQCDSNQGAGSKKTCMYGGITLNNNTNRIQPIVVKVYENDSVTLSFDINIDKETVTI 180
WA-MRSA-59-selz4 NIQCDSNQGAGSKKTCMYGGITLNNNTNRIQPIVVKVYENDSVTLSFDINIDKETVTI 180
MOK042-selz2     NIQCDSNQGAGSKKTCMYGGITLNNNTNRIQPIVVKVYENDSVTLSFDINIDKETVTI 180
15584-selz5      NIQCDSNQGAGSKKTCMYGGITLNNNTNRIQPIVVKVYENDSVTLSFDINIDKETVTI 180
SC457-selz1      NIQCDSNQGAGSKKTCMYGGITLNNNTNRIQPIVVKVYENDSVTLSFDINIDKETVTI 180
SC635-selz3      NIQCDSNQGAGSKKTCMYGGITLNNNTNRIQPIVVKVYENDSVTLSFDINIDKETVTI 180
*****. *****:*****:*****:*****:*****:*****:*****

JKD6159-selz7      QELDYKVRNKLISKINLYHLGGTSYETGYIKFIENANRYWYDMMPPDPGFTQSKYLM IYR 240
M-selz8           QELDYKVRNKLISKINLYHLGGTSYETGYIKFIENGNRYWYDMMPPDPGFTQSKYLM IYR 240
SC532-selz6      QELDYKVRNKLISKINLYHLGGTSYETGYIKFIENGNRYWYDMMPPDPGFTQSKYLM IYR 240
NCTC6131-selz9   QELDYKVRNKLISKINLYHLGGTSYETGYIKFIENGNRYWYDMMPPDPGFTQSKYLM IYR 240
WA-MRSA-59-selz4 QELDYKVRNKLISKINLYHLGGTSYETGYIKFIENGNRYWYDMMPPDPGFTQSKYLM IYR 240
MOK042-selz2     QELDYKVRNKLISKINLYHLGGTSYETGYIKFIENGNRYWYDMMPPDPGFTQSKYLM IYR 240
15584-selz5      QELDYKVRNKLISKINLYHLGGTSYETGYIKFIENGNRYWYDMMPPDPGFTQSKYLM IYR 240
SC457-selz1      QELDYKVRNKLISKINLYHLGGTSYETGYIKFIENGNRYWYDMMPPDPGFTQSKYLM IYR 240
SC635-selz3      QELDYKVRNKLISKINLYHLGGTSYETGYIKFIENGNRYWYDMMPPDPGFTQSKYLM IYR 240
*****:*****:*****:*****:*****:*****:*****

JKD6159-selz7      GNETVESAKTEIEVHLTKK      259
M-selz8           GNETVESAKTEIEVHLTKK      259
SC532-selz6      GNETVESAKTEIEVHLTKK      259
NCTC6131-selz9   GNETVESAKTEIEVHLTKK      259
WA-MRSA-59-selz4 GNETVESAKTEIEVHLTKK      259
MOK042-selz2     GNETVESAKTEIEVHLTKK      259
15584-selz5      GNETVESAKTEIEVHLTKK      259
SC457-selz1      GNETVESAKTEIEVHLTKK      259
SC635-selz3      GNETVESAKTEIEVHLTKK      259
*****:*****:*****:*****:*****:*****:*****

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Figure S4. Alignment of SEIZ amino acid sequences representing subtypes SEIZ1-SEIZ9. Asterisk indicates identical amino acid.

Table S4. Nucleotide Sequence identities (percentage) of *selz* gene among selected *S. aureus* isolates and those of reported *S. argenteus* strain.

Strain	species	genotype	<i>selz</i> subtype	Identity with strain			
				SC635	SC561	Tokyo 12480	SG01
SC485	<i>S.aureus</i>	<i>coaIIa</i> -ST764	<i>selz</i> 1	99.5	98.5	96.5	99.6
SC635	<i>S.aureus</i>	<i>coaVIIa</i> -ST12	<i>selz</i> 3		98.7	96.8	99.6
SC561	<i>S.aureus</i>	<i>coaIa</i> -ST89	<i>selz</i> 6			96.5	98.3
Tokyo 12480 (AP019712)	<i>S.aureus</i>		<i>selz</i> 7				96.2
SG01 (MN166481)	<i>S.argenteus</i>	<i>coaXI</i> d, ST2250					

Table S5. Primers used in the present study.

Target gene	Primer	Nucleotide sequence	Product size	Aim	Reference
<i>selx</i>	<i>selx</i> -1	(+) AGCAGACGCGTCAACACAAA	513 bp (+ <i>selx</i> -2)	Detection	Wilson et al., 2011
	<i>selx</i> -2	(-) ACTTGTCAATGTCATTAACACTTTTCAC		Detection	
	<i>selx</i> -F1	(+) GTCCAATTATGTGTAGACGA	ca. 900 bp (+ <i>selx</i> -R1)	Sequencing	Aung et al., 2019
	<i>selx</i> -R1	(-) GAATTTTCTATATGATGGTGCT		Sequencing	
<i>sey</i>	<i>sey</i> -F	(+) CAATGTACGGACAGTGTCTACAA	189 bp (+ <i>sey</i> -R)	Detection	Ono et al., 2015
	<i>sey</i> -R	(-) TGACCGTTAACAAACAAGTTCATTC		Detection	
	<i>sey</i> -1	(+) GAAATATTGATATATAGATCATT	843 bp (+ <i>sey</i> -2)	Sequencing	Aung et al., 2019
	<i>sey</i> -2	(-) CCTAAGAACTTAATKTCCTAAGC		Sequencing	
<i>selw</i>	<i>selw</i> -F2	(+) GGAATTTTTACAAATTCAGCG	323bp (+ <i>selw</i> -R2)	Detection	Aung et al., 2019
	<i>selw</i> -R2	(-) CTACATTGCGTTTTATTGGTTG		Detection	
	<i>selw</i> -F3	(+) TTGTTTTGGGGGAGTTTGAAG	ca.800 bp (+ <i>selw</i> -R4/R3)	Sequencing	Aung et al., 2019
	<i>selw</i> -R4	(-) ACTTTATATTTCACTGTCAAAG		Sequencing	
	<i>selw</i> -R3	(-) GTCAAAGATTATTAATGATTAAC		Sequencing	
<i>selz</i>	<i>selz</i> -F1	(+) GGTTACAGTAGCTATICTTTTGTG	ca.500 bp (+ <i>selz</i> -R1)	Detection	Aung et al., 2019
	<i>selz</i> -R1	(-) GTAAACTTTTACAACAATAGGCTG		Detection	
	<i>selz</i> -F2	(+) GTTATAAAATAGCAATGGTTG	ca.1 kb (+ <i>selz</i> -R2)	Sequencing	Aung et al., 2019
	<i>selz</i> -R2	(-) GAGCAACTTTTCCAAGTCGC		Sequencing	
	<i>selz</i> -R3	(-) CATTGAAAAATAGCATTGATC		Sequencing	
<i>selz</i> -R4	(-) GATAAGTTGCTCTATGTCTA	ca.800 bp (+ <i>selz</i> -F2)	Sequencing		
<i>sel26</i>	<i>sel26</i> -F1	(+) CTTATGCTGATGTAGGTGTTT	ca. 300 bp (+ <i>sel27</i> -R1)	Detection	Aung et al., 2019
	<i>sel26</i> -R1	(-) CATTATCCAAAAGATTTATCGG		Detection	
	<i>sel26</i> -5p-F1	(+) GAAGAAAAACACGATAACGGTG	ca.1.4 kb (+ <i>sel28</i> -3p-R1)	Sequencing	
<i>sel27</i>	<i>sel27</i> -F1	(+) TGAAGGCGCTCTATGAATCAG	ca. 500bp (+ <i>sel28</i> -R1)	Detection	Aung et al., 2019
	<i>sel27</i> -R1	(-) TACTCTGCGTAAAAATTTGGG		Detection	
	<i>sel27</i> -3p-R1	(-) ACAGGCTATCGTAAATCGCT		Sequencing	

Table 6. GenBank accession numbers assigned to *selx*, *sey*, *selw* and *selz* detected in the present study.

<i>selx</i>			<i>sey</i>			<i>selw</i>			<i>selz</i>		
Specimen ID	genotype	Accession No	Specimen ID	genotype	Accession No	Specimen ID	genotype	Accession No	Specimen ID	genotype	Accession No
SC460	<i>coa</i> Ia-ST89	MN257075	SC612	<i>coa</i> Ia-ST89	MN257099	SC735	<i>coa</i> Ia-ST89	MN257123	SC532	<i>coa</i> Ia-ST89	MN257147
SC654	<i>coa</i> Ia-ST89	MN257076	SC575	<i>coa</i> Ia-ST89	MN257100	SC756	<i>coa</i> Ia-ST89	MN257124	SC561	<i>coa</i> Ia-ST89	MN257148
SC735	<i>coa</i> Ia-ST89	MN257077	SC588	<i>coa</i> Ia-ST89	MN257101	SC778	<i>coa</i> Ia-ST89	MN257125	SC1103	<i>coa</i> Ia-ST89	MN257149
SC698	<i>coa</i> IIa-ST5	MN257078	SC823	<i>coa</i> IIa-ST5	MN257102	SC465	<i>coa</i> IIa-ST764	MN257126	SC485	<i>coa</i> IIa-ST764	MN257150
SC714	<i>coa</i> IIa-ST764	MN257079	SC610	<i>coa</i> IIa-ST764	MN257103	SC792	<i>coa</i> IIa-ST5	MN257127	SC585	<i>coa</i> IIa-ST5	MN257151
SC1100	<i>coa</i> IIa-ST5	MN257080	SC1097	<i>coa</i> IIa-ST5	MN257104	SC936	<i>coa</i> IIa-ST5	MN257128	SC1097	<i>coa</i> IIa-ST5	MN257152
SC825	<i>coa</i> IIa-ST764	MN257081	SC630	<i>coa</i> IIa-ST5	MN257105	SC955	<i>coa</i> IIa-ST5	MN257129	SC457	<i>coa</i> Va-ST121	MN257153
SC709	<i>coa</i> IIa-ST764	MN257082	SC1100	<i>coa</i> IIa-ST764	MN257106	SC526	<i>coa</i> IIIa-ST8	MN257130	SC732	<i>coa</i> Va-ST121	MN257154
SC822	<i>coa</i> IIa-ST5	MN257083	SC582	<i>coa</i> IIIa-ST8	MN257107	SC546	<i>coa</i> IIIa-ST8	MN257131	SC703	<i>coa</i> Va-ST121	MN257155
SC978	<i>coa</i> IIIa-ST8	MN257084	SC569	<i>coa</i> IIIa-ST8	MN257108	SC625	<i>coa</i> IIIa-ST8	MN257132	SC595	<i>coa</i> Va-ST121	MN257156
SC699	<i>coa</i> IIIa-ST8	MN257085	SC625	<i>coa</i> IIIa-ST8	MN257109	SC1019	<i>coa</i> IIIa-ST8	MN257133	SC584	<i>coa</i> Va-ST121	MN257157
SC706	<i>coa</i> IIIa-ST8	MN257086	SC628	<i>coa</i> IIIa-ST8	MN257110	SC1130	<i>coa</i> IIIa-ST8	MN257134	SC568	<i>coa</i> Va-ST121	MN257158
SC526	<i>coa</i> IIIa-ST8	MN257087	SC633	<i>coa</i> IIIa-ST8	MN257111	SC519	<i>coa</i> IVa-ST30	MN257135	SC462	<i>coa</i> Va-ST121	MN257159
SC1019	<i>coa</i> IIIa-ST8	MN257088	SC910	<i>coa</i> Va-ST121	MN257112	SC761	<i>coa</i> Va-ST121	MN257136	SC635	<i>coa</i> VIIa-ST12	MN257160
SC1060	<i>coa</i> IIIa-ST8	MN257089	SC736	<i>coa</i> Va-ST121	MN257113	SC732	<i>coa</i> Va-ST121	MN257137			
SC1137	<i>coa</i> Va-ST121	MN257090	SC1133	<i>coa</i> Va-ST121	MN257114	SC1133	<i>coa</i> Va-ST121	MN257138			
SC798	<i>coa</i> Va-ST121	MN257091	SC798	<i>coa</i> Va-ST121	MN257115	SC1137	<i>coa</i> Va-ST121	MN257139			
SC910	<i>coa</i> Va-ST121	MN257092	SC578	<i>coa</i> Va-ST121	MN257116	SC1096	<i>coa</i> Vb-ST5425 (ST5 SLV)	MN257140			
SC1096	<i>coa</i> Vb-ST5425 (ST5 SLV)	MN257093	SC635	<i>coa</i> VIIa-ST12	MN257117	SC458	<i>coa</i> VIIa-ST1	MN257141			
SC958	<i>coa</i> VIIa-ST1	MN257094	SC598	<i>coa</i> VIIa-ST1	MN257118	SC470	<i>coa</i> VIIa-ST1	MN257142			
SC1065	<i>coa</i> VIIa-ST1	MN257095	SC634	<i>coa</i> VIIa-ST1	MN257119	SC560	<i>coa</i> VIIa-ST1	MN257143			
SC1071	<i>coa</i> VIIa-ST1	MN257096	SC626	<i>coa</i> VIIa-ST1	MN257120	SC635	<i>coa</i> VIIa-ST12	MN257144			
SC650	<i>coa</i> VIIa-ST1	MN257097	SC614	<i>coa</i> VIIa-ST1	MN257121	SC533	<i>coa</i> VIIb-ST45	MN257145			
SC533	<i>coa</i> VIIb-ST45	MN257098	SC533	<i>coa</i> VIIb-ST45	MN257122	SC912	<i>coa</i> VIIb-ST45	MN257146			