frontiers

*Supplementary Material*

# The *Staphylococcus aureus* Two-Component System AgrAC Displays Four Distinct Genomic Arrangements That Delineate Genomic Virulence Factor Signatures

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## SUPPLEMENTARY FIGURE

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CLUSTAL O(1.2.4) multiple sequence alignment


1368166.3_typeI       METLNSYNFVLFVVTQMILMFTIPALISGIKYSKLDYFFIIVITSLSLFLYKMFDSASLI  60
1280.10759_typeI      METLNSYNFVLFVVTQMILMFTIPALISGIKYSKLDYFFIIVITSLSLFLYKMFDSASLI  60
1118959.3_typeI       METLNSYNFVLFVVTQMILMFTIPALISGIKYSKLDYFFIIVITSLSLFLYKMFDSASLI  60
685039.3_typeI        METLNSYNFVLFVVTQMILMFTIPALISGIKYSKLDYFFIIVITSLSLFLYKMFDSASLI  60
1201010.3_typeI       METLNSYNFVLFVVTQMILMFTIPALISGIKYSKLDYFFIIVITSLSLFLYKMFDSASLI  60
1194085.3_typeI       METLNSYNFVLFVVTQMILMFTIPALISGIKYSKLDYFFIIVITSLSLFLYKMFDSASLI  60
1280.3367_typeI       MELLNSYNFVLFVLTQMILMFTIPAIISGIKYSKLDYFFIIGITTLSLFLFKMFDSASLI  60
1280.5205_typeI       MELLNSYNFVLFVLTQMILMFTIPAIISGIKYSKLDYFFIIGITTLSLFLFKMFDSASLI  60
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46170.148_typeI        MELLNSYNFVLFVLTQMILMFTIPAIISGIKYSKLDYFFIIVISTLSLFLFKMFDSASLI  60
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1280.10152_typeI       MELLNSYNFVLFVLTQMILMFTIPAIISGIKYSKLDYFFIIVISTLSLFLFKMFDSASLI  60
46170.86_typeI         MELLNSYNFVLFVLTQMILMFTIPAIISGIKYSKLDYFFIIVISTLSLFLFKMFDSASLI  60
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1280.4805_typeI       MELLNSYNFVLFVLTQMILMFTIPAIISGIKYSKLDYFFIIVISTLSLFLFKMFDSASLI  60
93061.5_typeI         MELLNSYNFVLFVLTQMILMFTIPAIISGIKYSKLDYFFIIVISTLSLFLFKMFDSASLI  60
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685039.3_typeI        ILTSFIIILYFVKIKWYSILLIMASQIILYCANYMYIVIYAYVTKISDSILVIFPSFLAI  120
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523796.5_typeI        ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1280.4850_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1280.4852_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1155084.3_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
46170.288_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1229492.3_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1280.4851_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1006543.3_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
46170.245_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
46170.187_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1280.5203_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
46170.186_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1193576.3_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1280.8873_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
46170.185_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1280.7175_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
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46170.155_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
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1280.7245_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1406863.3_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
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451515.3_typeI        ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1458279.3_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
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46170.148_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1280.5204_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1280.4800_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1280.2216_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
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1280.3352_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
46170.149_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
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426430.8_typeI        ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1305598.3_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
46170.182_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
46170.290_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1280.4809_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
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46170.181_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
46170.183_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1321369.3_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1280.10152_typeI      ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
46170.86_typeI        ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1280.4826_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
46170.184_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
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1280.3589_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1241616.6_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
546342.4_typeI        ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
1280.4805_typeI       ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
93061.5_typeI         ILTSFIIIMYFVKIKWYSILLIMTSQIILYCANYMYIVIYAYITKISDSIFVIFPSFFVV  120
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1280.10759_typeI      YVTISLLFSYIINRVLKKISTSYLILNKGFLIVISTILLLTFSLFFFYSQINSD------  174
1118959.3_typeI       YVTISLLFSYIINRVLKKISTSYLILNKGFLIVISTILLLTFSLFFFYSQINSD------  174
685039.3_typeI        YVTISLLFSYIINRVLKKISTSYLILNKGFLIVISTILLLTFSLFFFYSQINSD------  174
1201010.3_typeI       YVTISLLFSYIINRVLKKISTSYLILNKGFLIVISTILLLTFSLFFFYSQINSD------  174
1194085.3_typeI       YVTISLLFSYIINRVLKKISTSYLILNKGFLIVISTILLLTFSLFFFYSQINSD------  174
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93061.5_typeI         ------------------------------------------------------------  175


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1280.4851_typeI         ---------------------------------EARVIRQYSFIFIGITIFLSILTFVIS  201
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1241616.6_typeI       QFLLKEMKYKRNQEEIETYYEYTLKIEAINNEMRKFRHDYVNILTTLSEYIREDDMPGLR  261
546342.4_typeI        QFLLKEMKYKRNQEEIETYYEYTLKIEAINNEMRKFRHDYVNILTTLSEYIREDDMPGLR  261
1280.4805_typeI       QFLLKEMKYKRNQEEIETYYEYTLKIEAINNEMRKFRHDYVNILTTLSEYIREDDMPGLR  261
93061.5_typeI         QFLLKEMKYKRNQEEIETYYEYTLKIEAINNEMRKFRHDYVNILTTLSEYIREDDMPGLR  261
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1368166.3_typeI       DYFNKNIVPMKDNLQMNAIKLNGIENLKVREIKGLITAKILRAQEMSIPISIEIPDEVTH  321
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685039.3_typeI        DYFNKNIVPMKDNLQMNAIKLNGIENLKVREIKGLITAKILRAQEMSIPISIEIPDEVTH  321
1201010.3_typeI       DYFNKNIVPMKDNLQMNAIKLNGIENLKVREIKGLITAKILRAQEMSIPISIEIPDEVTH  321
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1280.3367_typeI       DYFNKNIVPMKDNLQMNAIKLNGIENLKVREIKGLITAKILRAQEMSIPISIEIPDEVTR  321
1280.5205_typeI       DYFNKNIVPMKDNLQMNAIKLNGIENLKVREIKGLITAKILRAQEMSIPISIEIPDEVTR  321
523796.5_typeI        DYFNKNIVPMKDNLQMNAIKLNGIENLKVREIKGLITAKILRAQEMNIPISIEIPDEVTR  321
1280.4850_typeI       DYFNKNIVPMKDNLQMNAIKLNGIENLKVREIKGLITAKILRAQEMNIPISIEIPDEVTR  321
1280.4852_typeI       DYFNKNIVPMKDNLQMNAIKLNGIENLKVREIKGLITAKILRAQEMNIPISIEIPDEVTR  321
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46170.288_typeI       DYFNKNIVPMKDNLQMNAIKLNGIENLKVREIKGLITAKILRAQEMNIPISIEIPDEVTR  321
1229492.3_typeI       DYFNKNIVPMKDNLQMNAIKLNGIENLKVREIKGLITAKILRAQEMNIPISIEIPDEVTR  321
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46170.245_typeI       AYFNKNIVPMKDNLQMNAIKLNGIENLKVREIKGLITAKILRAQEMNIPISIEIPDEVSS  321
46170.187_typeI       AYFNKNIVPMKDNLQMNAIKLNGIENLKVREIKGLITAKILRAQEMNIPISIEIPDEVSS  321
1280.5203_typeI       AYFNKNIVPMKDNLQMNAIKLNGIENLKVREIKGLITAKILRAQEMNIPISIEIPDEVSS  321
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1193576.3_typeI       AYFNKNIVPMKDNLQMNAIKLNGIENLKVREIKGLITAKILRAQEMNIPISIEIPDEVSS  321
1280.8873_typeI       AYFNKNIVPMKDNLQMNAIKLNGIENLKVREIKGLITAKILRAQEMNIPISIEIPDEVSS  321
46170.185_typeI       DYFNKNIVPMKDNLQMNAIKLNGIENLKVREIKGLITAKILRAQEMNIPISIEIPDEVSS  720
1280.7175_typeI       DYFNKNIVPMKDNLQMNAIKLNGIENLKVREIKGLITAKILRAQEMNIPISIEIPDEVSS  321
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546342.4_typeI        DYFNKNIVPMKDNLQMNAIKLNGIENLKVREIKGLITAKILRAQEMNIPISIEIPDEVSS  321
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93061.5_typeI         DYFNKNIVPMKDNLQMNAIKLNGIENLKVREIKGLITAKILRAQEMNIPISIEIPDEVSS  321
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| 1118959.3_typeI | INLNMIDLSRSIGIILDNAIEASTEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |
| 685039.3_typeI | INLNMIDLSRSIGIILDNAIEASTEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |
| 1201010.3_typeI | INLNMIDLSRSIGIILDNAIEASTEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |
| 1194085.3_typeI | INLNMIDLSRSIGIILDNAIEASTEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |
| 1280.3367_typeI | INLNMIDLSRSIGIILDNAIEASTEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |
| 1280.5205_typeI | INLNMIDLSRSIGIILDNAIEASTEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |
| 523796.5_typeI | INLNMIDLSRSIGIILDNAIEASSEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |
| 1280.4850_typeI | INLNMIDLSRSIGIILDNAIEASSEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |
| 1280.4852_typeI | INLNMIDLSRSIGIILDNAIEASSEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |
| 1155084.3_typeI | INLNMIDLSRSIGIILDNAIEASSEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |
| 46170.288_typeI | INLNMIDLSRSIGIILDNAIEASSEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |
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| 1006543.3_typeI | INLNMIDLSRSIGIILDNAIEASTEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 732 |
| 46170.245_typeI | INLNMIDLSRSIGIILDNAIEASTEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |
| 46170.187_typeI | INLNMIDLSRSIGIILDNAIEASTEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |
| 1280.5203_typeI | INLNMIDLSRSIGIILDNAIEASTEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |
| 46170.186_typeI | INLNMIDLSRSIGIILDNAIEASTEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |
| 1193576.3_typeI | INLNMIDLSRSIGIILDNAIEASTEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |
| 1280.8873_typeI | INLNMIDLSRSIGIILDNAIEASTEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |
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| 1280.7175_typeI | INLNMIDLSRSIGIILDNAIEASTEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |
| 1280.7179_typeI | INLNMIDLSRSIGIILDNAIEASTEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |
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| 46170.246_typeI | INLNMIDLSRSIGIILDNAIEASTEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |
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| 46170.247_typeI | INLNMIDLSRSIGIILDNAIEASTEIDDPIIRVAFIESENSVTFIVMNKCADDIPRIHEL | 381 |

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523796.5_typeI        FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     430
1280.4850_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     430
1280.4852_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     430
1155084.3_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     430
46170.288_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     430
1229492.3_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     430
1280.4851_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     430
1006543.3_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     781
46170.245_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     430
46170.187_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     430
1280.5203_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     430
46170.186_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     430
1193576.3_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     430
1280.8873_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     430
46170.185_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     829
1280.7175_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     430
1280.7179_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     430
1280.7178_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     430
1280.4824_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     430
1323661.3_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     430
46170.155_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     430
1280.3356_typeI       FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN     430
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663951.4_typeI          FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.7246_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.7245_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1406863.3_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.3350_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
93062.19_typeI          FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1074252.3_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
46170.102_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.3366_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.2220_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.2217_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.2218_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.3574_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
451515.3_typeI          FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1458279.3_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.2215_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
46170.148_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.5204_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.4800_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.2216_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
46170.246_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.3352_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
46170.149_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.2219_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
46170.247_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.3566_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.3583_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
451516.9_typeI          FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
46170.289_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
426430.8_typeI          FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1305598.3_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
46170.182_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
46170.290_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.4809_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.3359_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
46170.181_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
46170.183_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1321369.3_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.10152_typeI        FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
46170.86_typeI          FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.4826_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
46170.184_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1028799.3_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.4849_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.3589_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1241616.6_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
546342.4_typeI          FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
1280.4805_typeI         FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
93061.5_typeI           FQESFSTKGEGRGLGLSTLKEIADNADNVLLDTIIENGFFIQKVEIINN      430
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**Figure 9: Multiple sequence alignment of canonical type I AgrC proteins and two non-canonical type I AgrC having transposase insertion (*S. aureus* strain T0131 and *S. aureus* strain HC1335) using EMBL-EBI Clustal Omega.** Strain IDs are from Patric database and their types are mentioned after the underscore.

The highlighted strains have transposase insertion, and with the alignment it is clear that transposase truncates AgrC (region from residue 175-550) in these two strains which inhibit the gene and subsequently the regulation of *agr* locus.