Protective Efficacy and Mechanism of Passive Immunization with Polyclonal Antibodies in a Sepsis Model of *Staphylococcus aureus* Infection

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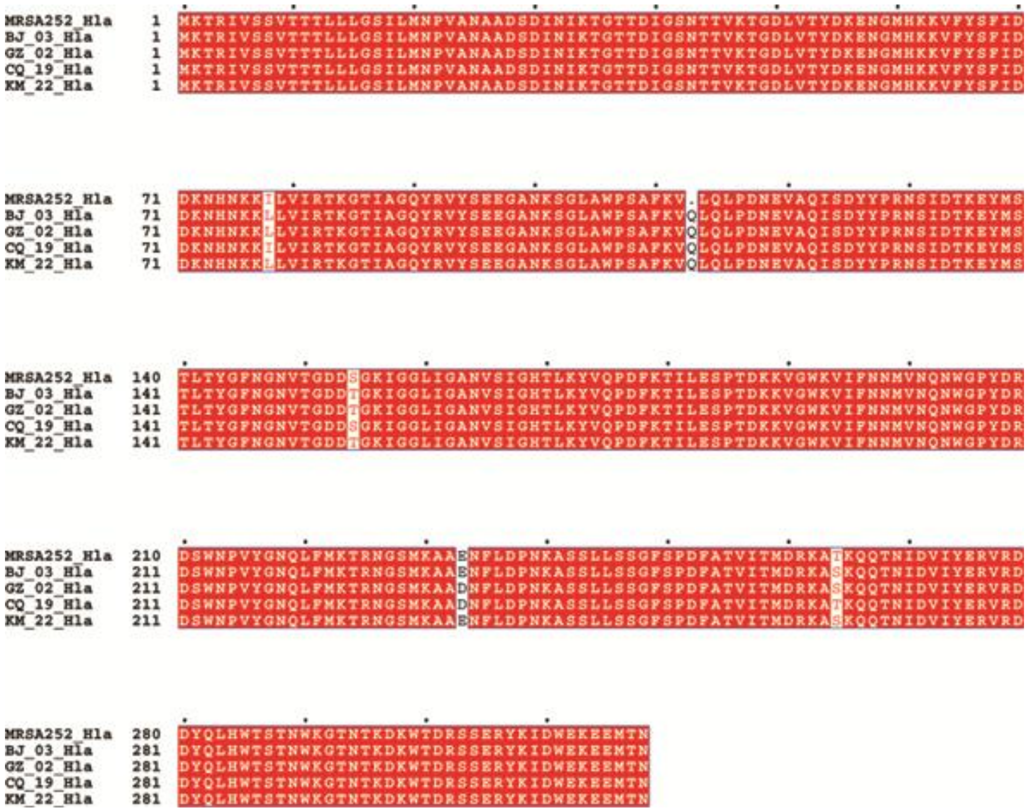
Supplementary Fig. 1 Sequence alignment of Hla from MRSA252 with those from 4 clinical strains of *S. aureus*.



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BJ_03_Hla      1  MKTRIVSSVTTTLLLGSILMNPVANAADSDINIKTGTTDIGSNTTVKTGDLVTYDKENGMHKKVFYSFID
GZ_02_Hla      1  MKTRIVSSVTTTLLLGSILMNPVANAADSDINIKTGTTDIGSNTTVKTGDLVTYDKENGMHKKVFYSFID
CQ_19_Hla      1  MKTRIVSSVTTTLLLGSILMNPVANAADSDINIKTGTTDIGSNTTVKTGDLVTYDKENGMHKKVFYSFID
KM_22_Hla      1  MKTRIVSSVTTTLLLGSILMNPVANAADSDINIKTGTTDIGSNTTVKTGDLVTYDKENGMHKKVFYSFID

MRSA252_Hla   71  DKNHNKKILVIRTKGTIAGQYRVYSEEGANKSGLAWPSAFKV.LQLPDNEVAQISDYYPRNSIDTKEYMS
BJ_03_Hla     71  DKNHNKKLLVIRTKGTIAGQYRVYSEEGANKSGLAWPSAFKVQLQLPDNEVAQISDYYPRNSIDTKEYMS
GZ_02_Hla     71  DKNHNKKLLVIRTKGTIAGQYRVYSEEGANKSGLAWPSAFKVQLQLPDNEVAQISDYYPRNSIDTKEYMS
CQ_19_Hla     71  DKNHNKKILVIRTKGTIAGQYRVYSEEGANKSGLAWPSAFKVQLQLPDNEVAQISDYYPRNSIDTKEYMS
KM_22_Hla     71  DKNHNKKLLVIRTKGTIAGQYRVYSEEGANKSGLAWPSAFKVQLQLPDNEVAQISDYYPRNSIDTKEYMS

MRSA252_Hla  140  TLTYGFNGNVTGDDSGKIGGLIGANVSIGHTLKYVQPDFKTILESPTDKKVGWKVIFNNMVNQNWGPYDR
BJ_03_Hla    141  TLTYGFNGNVTGDDTGKIGGLIGANVSIGHTLKYVQPDFKTILESPTDKKVGWKVIFNNMVNQNWGPYDR
GZ_02_Hla    141  TLTYGFNGNVTGDDTGKIGGLIGANVSIGHTLKYVQPDFKTILESPTDKKVGWKVIFNNMVNQNWGPYDR
CQ_19_Hla    141  TLTYGFNGNVTGDDSGKIGGLIGANVSIGHTLKYVQPDFKTILESPTDKKVGWKVIFNNMVNQNWGPYDR
KM_22_Hla    141  TLTYGFNGNVTGDDTGKIGGLIGANVSIGHTLKYVQPDFKTILESPTDKKVGWKVIFNNMVNQNWGPYDR

MRSA252_Hla  210  DSWNPVYGNQLFMKTRNGSMKAAENFLDPNKASSLLSSGFSPDFATVITMDRKATKQQTNIDVIYERVRD
BJ_03_Hla    211  DSWNPVYGNQLFMKTRNGSMKAAENFLDPNKASSLLSSGFSPDFATVITMDRKASKQQTNIDVIYERVRD
GZ_02_Hla    211  DSWNPVYGNQLFMKTRNGSMKAADNFLDPNKASSLLSSGFSPDFATVITMDRKASKQQTNIDVIYERVRD
CQ_19_Hla    211  DSWNPVYGNQLFMKTRNGSMKAADNFLDPNKASSLLSSGFSPDFATVITMDRKATKQQTNIDVIYERVRD
KM_22_Hla    211  DSWNPVYGNQLFMKTRNGSMKAAENFLDPNKASSLLSSGFSPDFATVITMDRKASKQQTNIDVIYERVRD

MRSA252_Hla  280  DYQLHWTSTNWKGTNTKDKWTDRSSERYKIDWEKEEMTN
BJ_03_Hla    281  DYQLHWTSTNWKGTNTKDKWTDRSSERYKIDWEKEEMTN
GZ_02_Hla    281  DYQLHWTSTNWKGTNTKDKWTDRSSERYKIDWEKEEMTN
CQ_19_Hla    281  DYQLHWTSTNWKGTNTKDKWTDRSSERYKIDWEKEEMTN
KM_22_Hla    281  DYQLHWTSTNWKGTNTKDKWTDRSSERYKIDWEKEEMTN
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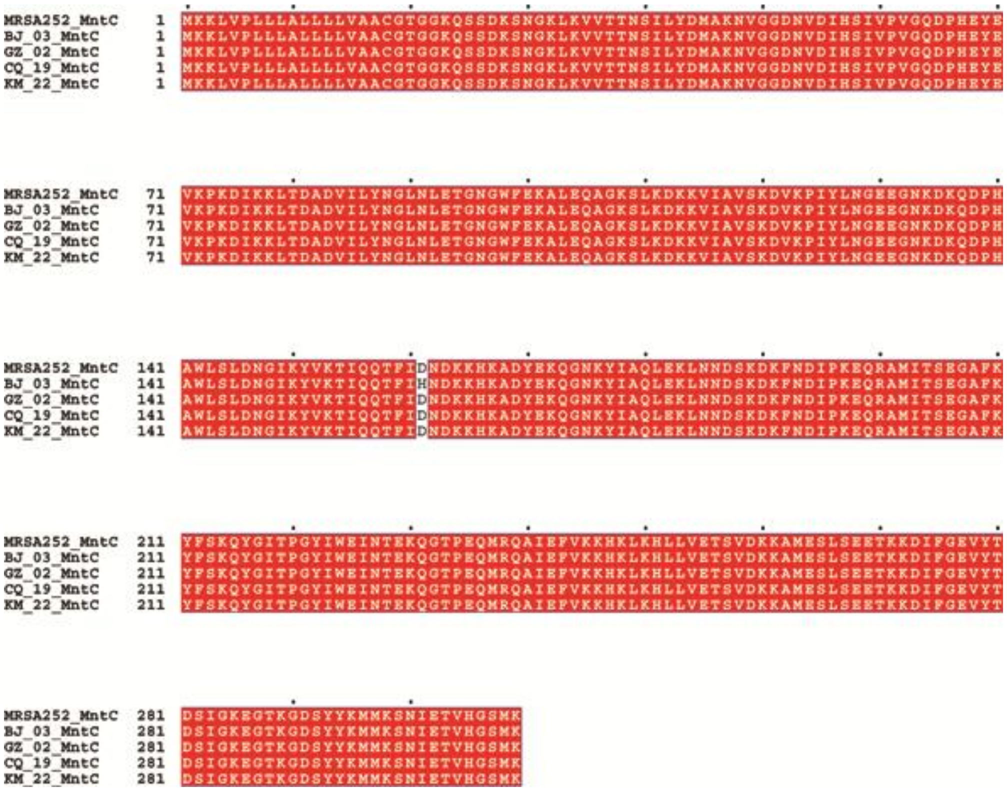
Supplementary Fig. 2 Sequence alignment of MntC from MRSA252 with those from 4 clinical strains of *S. aureus*.



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MRSA252_MntC   1 MKKLVPLLLALLLLVAACGTGGKQSSDKSNGKLKVVTTNSILYDMAKNVGGDNVDIHSIVPVGQDPHEYE
BJ_03_MntC     1 MKKLVPLLLALLLLVAACGTGGKQSSDKSNGKLKVVTTNSILYDMAKNVGGDNVDIHSIVPVGQDPHEYE
GZ_02_MntC     1 MKKLVPLLLALLLLVAACGTGGKQSSDKSNGKLKVVTTNSILYDMAKNVGGDNVDIHSIVPVGQDPHEYE
CQ_19_MntC     1 MKKLVPLLLALLLLVAACGTGGKQSSDKSNGKLKVVTTNSILYDMAKNVGGDNVDIHSIVPVGQDPHEYE
KM_22_MntC     1 MKKLVPLLLALLLLVAACGTGGKQSSDKSNGKLKVVTTNSILYDMAKNVGGDNVDIHSIVPVGQDPHEYE

MRSA252_MntC  71 VKPKDIKKLTDADVILYNGLNLETGNGWFEKALEQAGKSLKDKKVIAVSKDVKPIYLNGEEGNKDKQDPH
BJ_03_MntC    71 VKPKDIKKLTDADVILYNGLNLETGNGWFEKALEQAGKSLKDKKVIAVSKDVKPIYLNGEEGNKDKQDPH
GZ_02_MntC    71 VKPKDIKKLTDADVILYNGLNLETGNGWFEKALEQAGKSLKDKKVIAVSKDVKPIYLNGEEGNKDKQDPH
CQ_19_MntC    71 VKPKDIKKLTDADVILYNGLNLETGNGWFEKALEQAGKSLKDKKVIAVSKDVKPIYLNGEEGNKDKQDPH
KM_22_MntC    71 VKPKDIKKLTDADVILYNGLNLETGNGWFEKALEQAGKSLKDKKVIAVSKDVKPIYLNGEEGNKDKQDPH

MRSA252_MntC 141 AWLSLDNGIKYVKTIQQTFIDNDKKHKADYEKQGNKYIAQLEKLNNDSKDKFNDIPKEQRAMITSEGAFK
BJ_03_MntC   141 AWLSLDNGIKYVKTIQQTFIHNDKKHKADYEKQGNKYIAQLEKLNNDSKDKFNDIPKEQRAMITSEGAFK
GZ_02_MntC   141 AWLSLDNGIKYVKTIQQTFIDNDKKHKADYEKQGNKYIAQLEKLNNDSKDKFNDIPKEQRAMITSEGAFK
CQ_19_MntC   141 AWLSLDNGIKYVKTIQQTFIDNDKKHKADYEKQGNKYIAQLEKLNNDSKDKFNDIPKEQRAMITSEGAFK
KM_22_MntC   141 AWLSLDNGIKYVKTIQQTFIDNDKKHKADYEKQGNKYIAQLEKLNNDSKDKFNDIPKEQRAMITSEGAFK

MRSA252_MntC 211 YFSKQYGITPGYIWEINTEKQGTPEQMRQAIEFVKKHKLKHLLVETSVDKKAMESLSEETKKDIFGEVYT
BJ_03_MntC   211 YFSKQYGITPGYIWEINTEKQGTPEQMRQAIEFVKKHKLKHLLVETSVDKKAMESLSEETKKDIFGEVYT
GZ_02_MntC   211 YFSKQYGITPGYIWEINTEKQGTPEQMRQAIEFVKKHKLKHLLVETSVDKKAMESLSEETKKDIFGEVYT
CQ_19_MntC   211 YFSKQYGITPGYIWEINTEKQGTPEQMRQAIEFVKKHKLKHLLVETSVDKKAMESLSEETKKDIFGEVYT
KM_22_MntC   211 YFSKQYGITPGYIWEINTEKQGTPEQMRQAIEFVKKHKLKHLLVETSVDKKAMESLSEETKKDIFGEVYT

MRSA252_MntC 281 DSIGKEGTKGDSYYKMMKSNIETVHGSMK
BJ_03_MntC   281 DSIGKEGTKGDSYYKMMKSNIETVHGSMK
GZ_02_MntC   281 DSIGKEGTKGDSYYKMMKSNIETVHGSMK
CQ_19_MntC   281 DSIGKEGTKGDSYYKMMKSNIETVHGSMK
KM_22_MntC   281 DSIGKEGTKGDSYYKMMKSNIETVHGSMK
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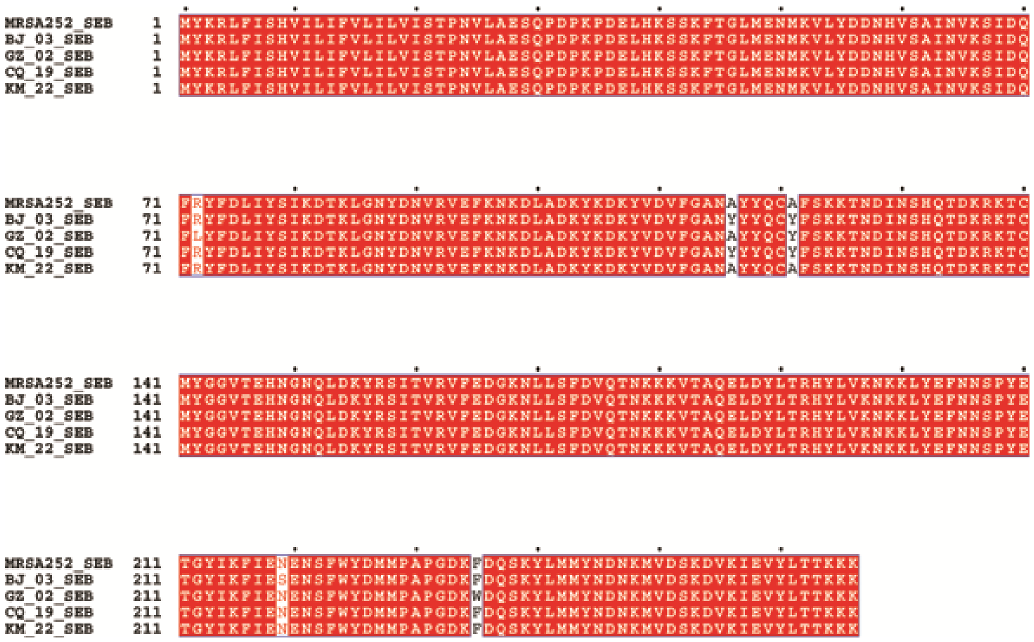
Supplementary Fig. 3 Sequence alignment of SEB from MRSA252 with those from 4 clinical strains of *S. aureus*.



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MRSA252_SEB    1   MYKRLFISHVILIFVLILVISTPNVLAESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQ
BJ_03_SEB      1   MYKRLFISHVILIFVLILVISTPNVLAESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQ
GZ_02_SEB      1   MYKRLFISHVILIFVLILVISTPNVLAESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQ
CQ_19_SEB      1   MYKRLFISHVILIFVLILVISTPNVLAESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQ
KM_22_SEB      1   MYKRLFISHVILIFVLILVISTPNVLAESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQ

MRSA252_SEB   71   FRYFDLIYSIKDTKLGNYDNVRVEFKNKDLADKYKDKYVDVFGANAYYQCAFSKKTNDINSHQTDKRKTC
BJ_03_SEB     71   FRYFDLIYSIKDTKLGNYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTC
GZ_02_SEB     71   FLYFDLIYSIKDTKLGNYDNVRVEFKNKDLADKYKDKYVDVFGANAYYQCYFSKKTNDINSHQTDKRKTC
CQ_19_SEB     71   FRYFDLIYSIKDTKLGNYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTC
KM_22_SEB     71   FRYFDLIYSIKDTKLGNYDNVRVEFKNKDLADKYKDKYVDVFGANAYYQCAFSKKTNDINSHQTDKRKTC

MRSA252_SEB  141   MYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNSPYE
BJ_03_SEB    141   MYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNSPYE
GZ_02_SEB    141   MYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNSPYE
CQ_19_SEB    141   MYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNSPYE
KM_22_SEB    141   MYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNSPYE

MRSA252_SEB  211   TGYIKFIENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTTKKK
BJ_03_SEB    211   TGYIKFIESENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTTKKK
GZ_02_SEB    211   TGYIKFIENENSFWYDMMPAPGDKWDQSKYLMMYNDNKMVDSKDVKIEVYLTTKKK
CQ_19_SEB    211   TGYIKFIENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTTKKK
KM_22_SEB    211   TGYIKFIENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTTKKK
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Supplementary Table 1. The information of *S. aureus* clinical strains used in this study.

Strain name	Source of strain	Department	Patient's name	Gender	Age	Source of sample	Nuc gene[#]	mecA gene[*]	Genotyping[&]
BJ-02	Beijing 263 hospital	Respiratory	Zhang××	Female	69	Sputum	+	+	ST239-t437-SCCmecIII
CQ-19	Chongqing southwest hospital	ICU	Liu×	Female	22	Blood	+	+	ST398-t030-SCCmecIII
GZ-02	Guangzhou nanfang hospital	Traumatic fracture	Zhang×	male	21	Puncture fluid	+	+	ST5-t037-SCCmecIV
KM-22	Kunming medical college	Burns surgery	Lu××	male	4	Secretions	+	-	ST121-t030

[#] nuc gene, which encode the thermonuclease, has been widely used as a specific marker to detect *S. aureus* by PCR-based methods.

[*] The product of mecA gene is penicillin-binding protein, which resulting in multiple drug resistance.

[&] Three Genotyping methods were used in this study, including the multiple locus sequence typing (ST), Staphylococal Protein A genetic polymorphism analysis (t) and classification of Staphylococcal cassette chromosome mec (SCCmec).