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Supplementary Material

Therapeutic potential of a designed CSαβ peptide ID13 in *Staphylococcus aureus*-induced endometritis of mice

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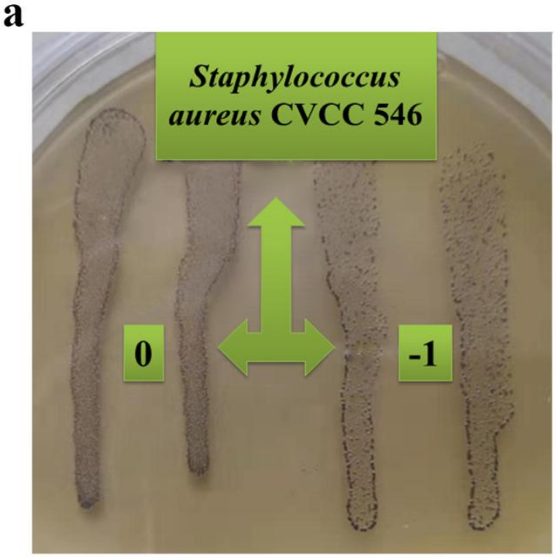
Supplementary Figures

Fig. S1 Photos of uteri morphology changes in mice between the blank and negative control.



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Taxonomy	Number of hits	Number of organisms
⊟ root	1060	74
. ⊟ Bacteria	987	73
. . ⊟ Bacilli	950	70
. . . ⊟ Bacillales	948	69
. . . . ⊟ *Staphylococcus*	947	68
. . . . . ⊟ *Staphylococcus aureus*	755	51

Fig. S2 Pathogens isolation and identification. **(a)** Homogenate of uterus (0) and 10 times dilutions (-1) were dropped on BP agar supplemented with potassium tellurite egg-yolk reagent for *S. aureus* CVCC 546. **(b)** 16S rRNA gene sequence of *S. aureus* CVCC 546. **(c)** The taxonomy report of *S. aureus* CVCC 546 via 16S rRNA gene sequence BLAST on NCBI (https://blast.ncbi.nlm.nih.gov/Blast.cgi).

Supplementary Tables

Table S1. Selected DEGs of ID13 treated-*S. aureus* CVCC546 related to membrame potential.

Gene name	Gene product	log2.fold change	qvalue	Protein type
mnhA	Na(+)/H(+) antiporter subunit A1	-1.6	7.3E-194	ion binding and transport
mnhB	Na(+)/H(+) antiporter subunit B1	-1.5	2.2E-13	
mnhC	Na(+)/H(+) antiporter subunit C1	-1.6	2.3E-10	
mnhD	Na(+)/H(+) antiporter subunit D1	-1.5	1.3E-100	
mnhE	Na(+)/H(+) antiporter subunit E1	-1.1	5.3E-16	
mnhF	Na(+)/H(+) antiporter subunit F1	-1.8	9.2E-04	
fabD	Malonyl CoA-acyl carrier protein transacylase	-1.0	6.2E-40	
ebh	Extracellular matrix-binding protein ebh	2.2	1.3E-03	
mtlA	PTS system mannitol-specific EIICB component	1.8	8.0E-04	
sdrC	Serine-aspartate repeat-containing protein C	3.6	1.2E-03	
sdrD	Serine-aspartate repeat-containing protein D	6.2	3.7E-21	
sdrE	Serine-aspartate repeat-containing protein E	2.5	5.8E-11	
copA	Copper-exporting P-type ATPase A	1.4	2.2E-19	
hutG	Formimidoylglutamase	2.1	5.7E-34	
zinT	Zinc-binding lipoprotein	1.7	6.0E-05	
lytM	Glycyl-glycine endopeptidase	-3.2	6.2E-72	
ureF	Urease accessory protein UreF	-1.3	2.9E-03	
ipdC	Indole-3-pyruvate decarboxylase	-1.4	0.0E+00	
nreB	Oxygen sensor histidine kinase NreB	1.7	3.8E-04	energy metabolism
ftnA	Bacterial non-heme ferritin	1.3	7.5E-11	
narG	Nitrate reductase alpha chain	6.2	1.2E-87	
narH	Nitrate reductase beta chain	6.0	2.5E-21	
narT	Probable nitrate transporter NarT	7.8	1.2E-94	
nasD	Nitrite reductase [NAD(P)H]	5.2	5.8E-46	
pflA	Pyruvate formate-lyase-activating enzyme	4.2	5.5E-209	
pflB	Formate acetyltransferase	4.1	0.0E+00	
trxA	Thioredoxin	-1.3	0.0E+00	
trxB	Thioredoxin reductase	-1.5	2.4E-12	
glpD	Aerobic glycerol-3-phosphate dehydrogenase	-3.6	0.0E+00	
Adh1	Alcohol dehydrogenase	5.6	2.1E-196	
ldhA	L-lactate dehydrogenase	3.3	8.4E-125	
ldhB	L-lactate dehydrogenase	2.0	3.1E-11	
natA	ABC transporter ATP-binding protein	3.9	3.2E-121	
fda	Fructose-bisphosphate aldolase class 1	-1.6	0.0E+00	
pgk	Phosphoglycerate kinase	-2.3	0.0E+00	
eno	Enolase	-1.4	0.0E+00	

Table S2. Selected DEGs of ID13 treated-*S. aureus* CVCC546 related to infections.

Gene name	Gene product	log2.fold change	qvalue	Protein type
clfB	Clumping factor B	2.1	1.5E-12	Colonization factors and toxins
fnbA	Fibronectin-binding protein A	-1.9	3.9E-03	
eno	Enolase	-1.4	0.0E+00	
spa	Immunoglobulin G-binding protein A	5.8	0.0E+00	
agrA	Accessory gene regulator protein A	2.2	5.1E-208	
agrB	Accessory gene regulator protein B	2.7	0.0E+00	
agrC	Accessory gene regulator protein C	1.8	1.1E-119	
sdrC	Serine-aspartate repeat-containing protein C	3.6	1.2E-03	
sdrD	Serine-aspartate repeat-containing protein D	6.2	3.7E-21	
sdrE	Serine-aspartate repeat-containing protein E	2.5	5.8E-11	
ebh	Extracellular matrix-binding protein ebh	2.2	1.3E-03	
sarA	Transcriptional regulator SarA	1.2	5.2E-32	
sarS	HTH-type transcriptional regulator SarS	3.2	2.2E-73	
sarV	HTH-type transcriptional regulator SarV	2.9	1.1E-36	
sar1418	TelA-like protein SAR1418	-1.4	6.2E-105	
sar0193	PTS system EIIBC component SAR0193	2.9	2.4E-47	
secA	Protein translocase subunit SecA	1.3	4.5E-07	
hly	Alpha-hemolysin	4.7	0.0E+00	Autolysis and biofilm-related proteins
cidA	Holin-like protein CidA	-4.2	6.2E-10	
cidB	Holin-like protein CidB	2.7	6.1E-167	
lrgB	Antiholin-like protein LrgB	2.5	1.5E-06	
lytR	Transcriptional regulator LytR	-1.3	4.0E-193	
lytM	Glycyl-glycine endopeptidase LytM	-3.2	6.2E-72	
capA	Capsular polysaccharide synthesis protein cap5A	-2.8	5.4E-63	
capB	Putative tyrosine-protein kinase CapB	-3.5	1.1E-20	
capC	Putative tyrosine-protein phosphatase CapC	-3.5	4.1E-38	
capD	UDP-glucose 4-epimerase	-2.6	6.7E-28	
capG	UDP-N-acetylglucosamine 2-epimerase	-3.5	3.2E-50	
capL	Probable glycosyltransferase	-3.6	2.5E-47	
capM	Uncharacterized sugar transferase	-2.3	5.2E-14	
capN	UDP-glucose 4-epimerase	-2.9	5.3E-28	

Table S3. Changes of different white blood cells in mice between negative and blank control (n=5).

Group	WBC[a] (10^9 cell/L)	NEU[b] (10^9 cell/L)	LYM[c] (10^9 cell/L)	NEUT%	LYM%
BC[d]	5.14±1.22	2.24±0.34	2.03±0.40	47.80±5.13	39.73±1.75
NC[e]	14.56±3.00**	9.65±2.00***	3.25±0.83*	66.24±1.51***	22.24±2.33****

[a]WBC: white blood cells; [b]NEU: neutrophils; [c]LYM: lymphocytes; [d] BC: blank control; [e]NC: negative control, *$p<0.05$, **$p<0.01$, ***$p<0.001$, ****$p<0.0001$.