

**Analytical and Bioanalytical Chemistry**

**Electronic Supplementary Material**

**Detection of methicillin-resistant *Staphylococcus aureus* using phage amplification  
combined with matrix-assisted laser desorption/ionization mass spectrometry**

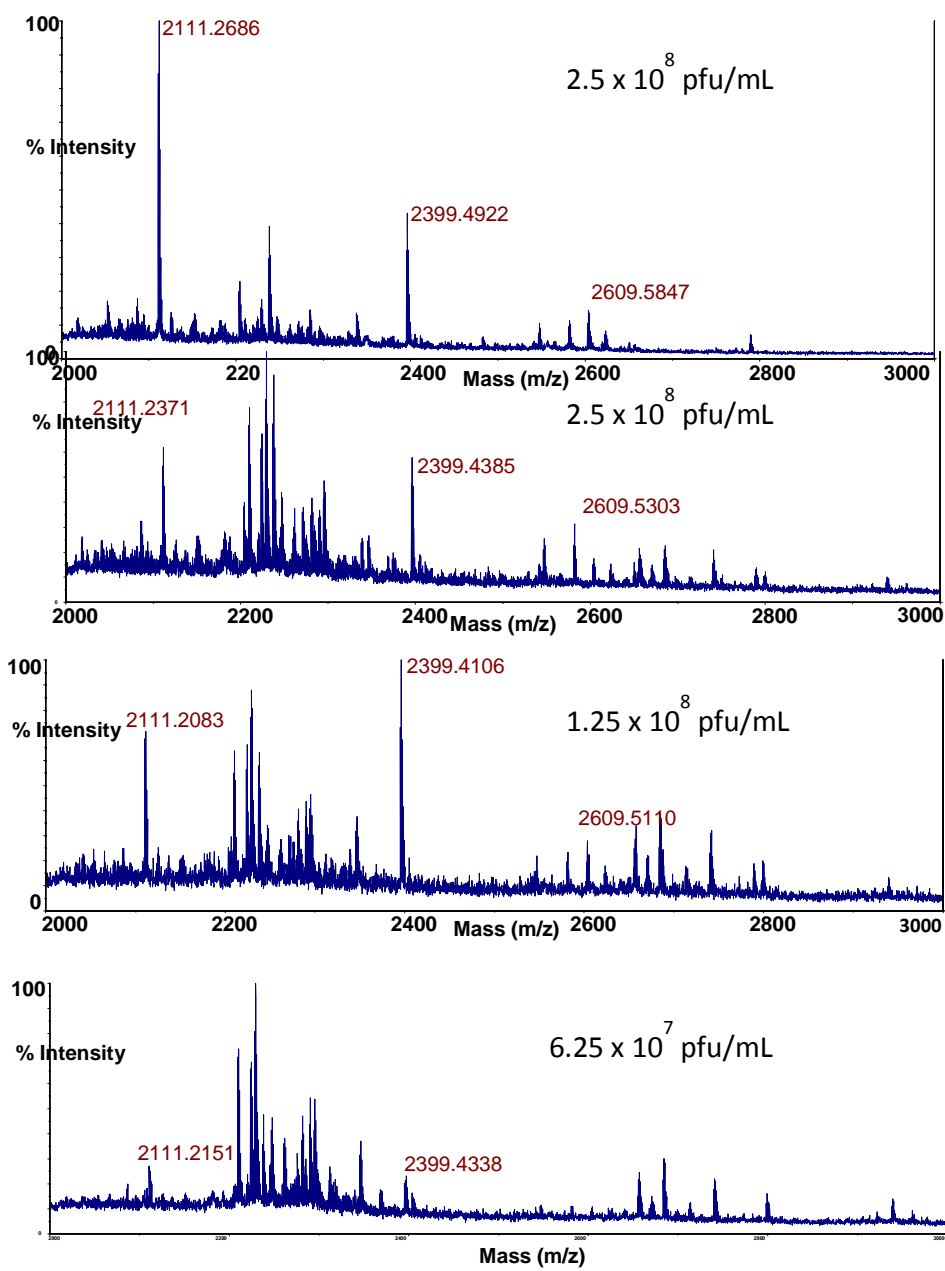
Jon C. Rees, John R. Barr

**Table S1** List of all peptide sequences found for a tryptic digest of Phage K by LC-MS/MS followed by database searching. Peptides used for MALDI-MS identification of Phage K are highlighted in yellow

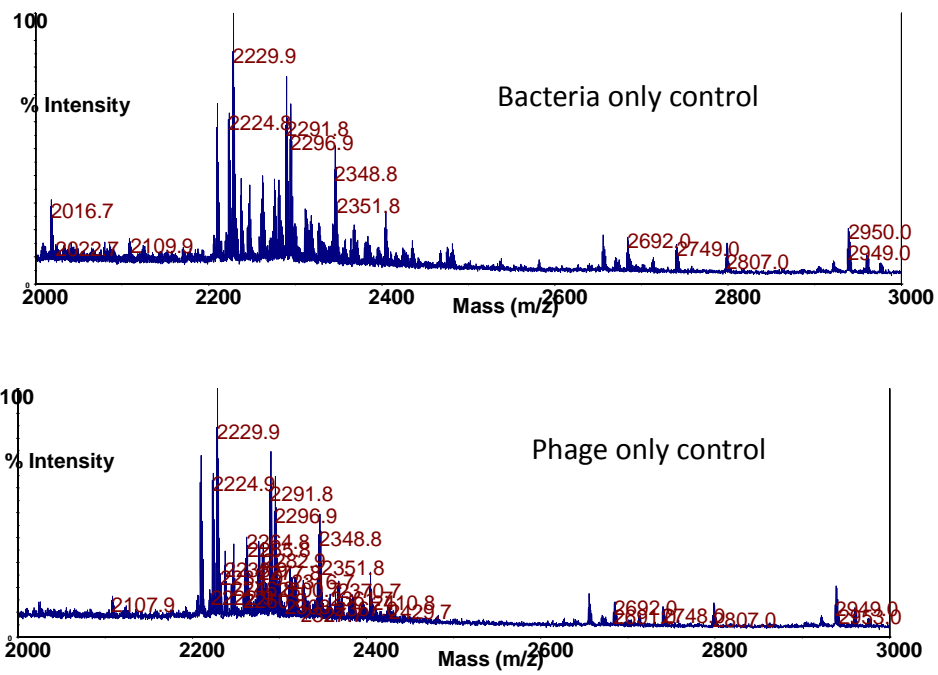
Accession gi   48696433	Description - Putative capsid protein
Sequence	Actual Mass
(K)SFQ <b>TGYG</b> ITPDTQIDAGALR(R)	<b>2,110.03</b>
(K)EIGVAPVSDPNIR(Q)	1,365.73
(K)NMSIASGLVNNIADPSQILTEDAIAVVAK(T)	2,953.55
(K)TIEWASFYGDASLTSEVEGEGLEFDGLAK(L)	3,120.45
(K)HLNEAAVR(I)	908.4836
(K)GFGTATDAYMPIGVHAD <b>FVNSILGR(Q)</b>	<b>2,608.29</b>
(K)LHGSTMENELILDES <b>LQPLNAPQPAK(V)</b>	3,040.56
(K)GAFENEEDR(A)	1,065.44
(K)LSINVNAMYQQ <b>QPQFVSIYR(Q)</b>	<b>2,398.22</b>
(K)DAQEDGTIVFVDK(N)	1,435.68
Accession gi   48696453	ORF65
Sequence	Actual Mass
(K)VLFNPDRPLQQAELNEMQSIDQYYLK(N)	3,151.58
(R)IVTPDEDASLLDQTSQVPSYFSK(G)	2,468.21
(K)DYEVTQGEGLSK(K)	1,425.66
(R)TLEEMIEFIR(I)	1,279.65
(K)GSEDGTIMTDAK(G)	1,223.54
(K)NANSTSATTYTAQGR(K)	1,541.71
(R)VTVNLVDPLAQSFQYDENR(T)	2,207.09
(K)WEPIGNYQDL <b>DVLGLAR(Q)</b>	1,957.99

Accession gi   48696481	ORF95
Sequence	Actual Mass
(K)NVNDVLQQESVTVADK(Y)	1,757.88
(K)DSLEHAHEDVIADFPASPAR(K)	2,176.02
(K)GVDSGEGQGDTSEPSAPK(N)	1,716.74
Accession gi   48696454	ORF66
Sequence	Actual Mass
(K)GAPSGEATAGFVR(L)	1,218.60
(K)ELTESTTQYATLVNPPK(E)	1,890.96
(R)EITASEITTEWK(K)	1,406.69
(K)GNGAVVYYALPK(L)	1,250.66
Accession gi   48696456	ORF68
Sequence	Actual Mass
(M)ALNFTTITENNVIR(D)	1,604.86
(R)DDGSASFLLVYTSDSK(T)	1,800.85
(K)TFQQAIIHDHIDR(T)	1,455.75
(K)ELWTGAQSFLSTGTTK(N)	1,725.86
(K)GSTWTLVDSAVQNSK(T)	1,591.79
Accession gi   48696432	ORF43
Sequence	Actual Mass
(K)EAQEQGEKVESEEEVAEGNEDEEVEK(S)	2,819.22
(K)VESEEEVAEGNEDEEVEK(S)	1,919.82

Accession gi   48696452	ORF64
Sequence	Actual Mass
(K)WVYLESSIVGDELPLGTYR(Q)	2,196.12
(K)FNLVPSEVESTGTLFFDNK(Q)	2,256.14



**Fig. S1** Dilution series of bacteriophage K as detected by MALDI-MS



**Fig. S2** Control spectra from samples containing bacteria only and phage only processed after a 5 hour incubation. Peaks associated with phage amplification cannot be found in either spectrum