SUPPLEMENTARY MATERIAL

Rapid Detection of Colistin Resistance Protein MCR-1 by LC-MS/MS

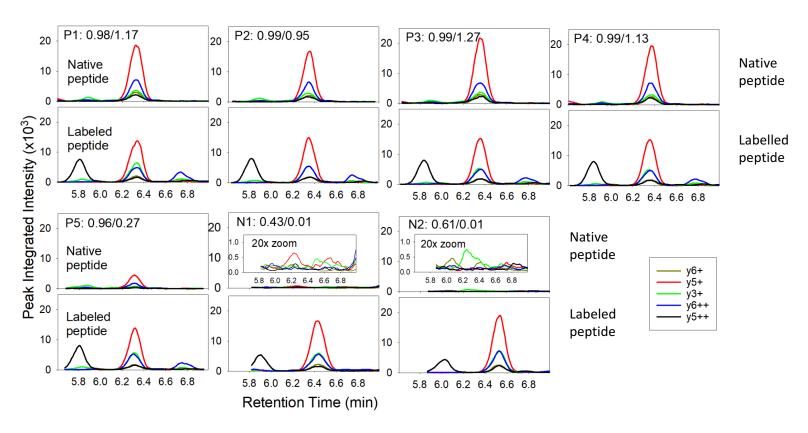
Honghui Wang, Yong Chen, Jeffrey R. Strich, Steven K. Drake, Jung-Ho Youn, Avi Z. Rosenberg, Marjan Gucek,

Patrick T. McGann, Anthony F. Suffredini, John P. Dekker

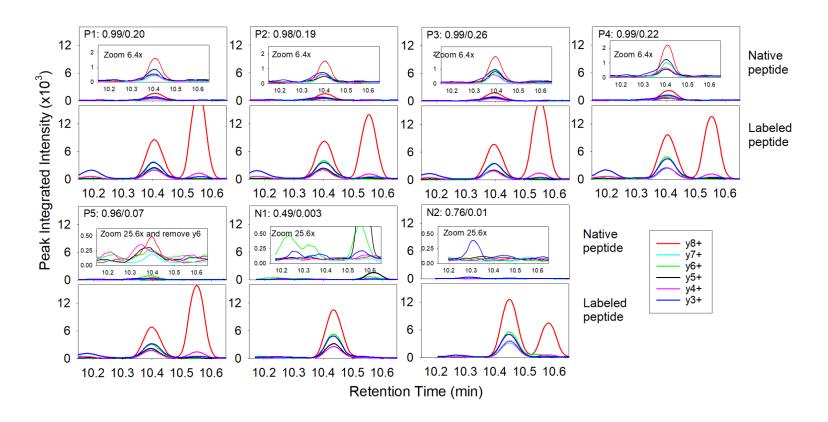
MCR1 - DTFPQLAK, Charge 2 y5 556.345 Intensity (10^3) 600 400 precursor++ 460.248 y6 703.414 /2 | b2 20217 082 | 14 15 y5++ y3y6+0 278.676 331.234211 200 459 293 0 300 400 500 600 200 700 MCR1 - SVPAFFWTDK, Charge 2 300 Intensity (10⁴³) y8++ 506.25 200 y6 843.404₉₁4.441 y8 1011.493 100 y5 696.335 b6 -18++/3 316.1<u>66</u>3.187 y4 549.267 0 500 600 700 800 900 1000 200 300 400 MCR1 - ADHVSFNGYER, Charge 2 300 y7 872.39 Intensity (10^3) 200 b3 324.13 y8 971.458 y9++ b5 554.76precursor 18++ 100 b4 b4239199 405.188 y6 785.358 b3 -1 306. 638.789 510.231 0 300 400 500 700 800 900 1000 600

Supplemental Figure 1: MS/MS spectra acquired by Orbitrap Lumos LC-MS for three peptide markers.

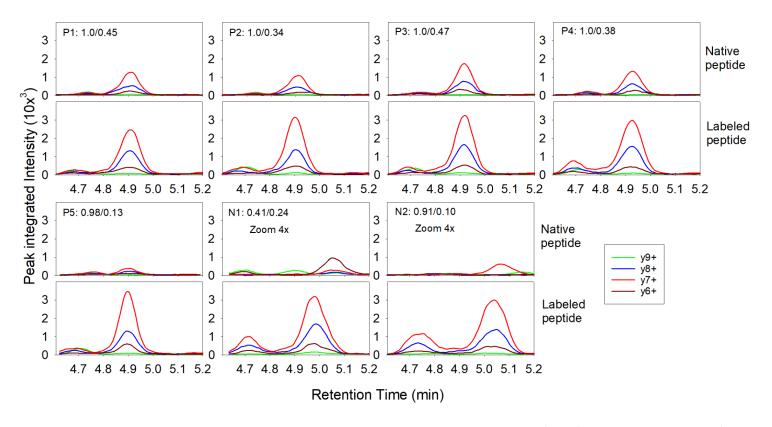
m/z



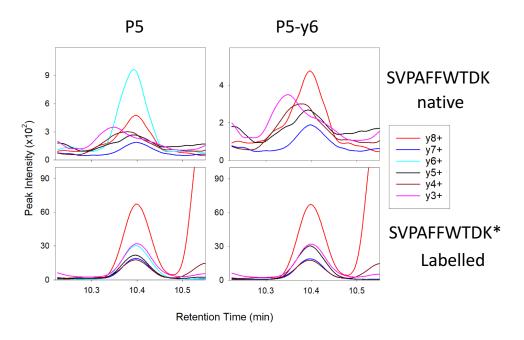
Supplemental Figure 2a: LC-MS chromatograms of DTFPQLAK for the five *mcr-1*-containing isolates (P1-P5) and two negative controls (N1 and N2) used in assay development.



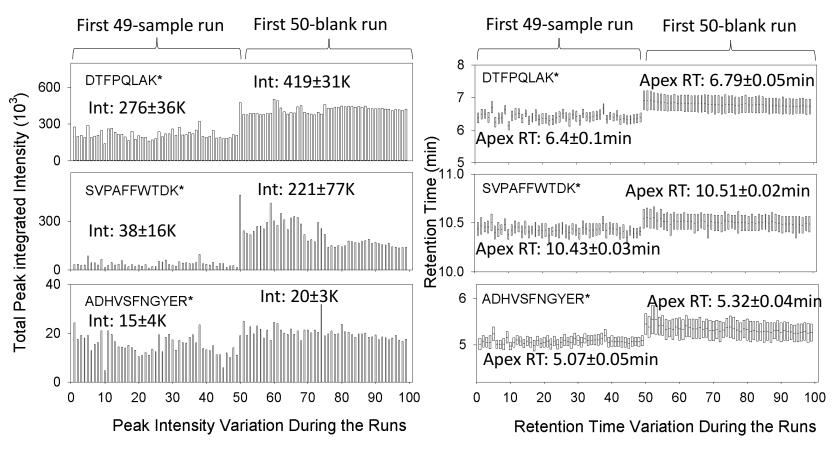
Supplemental Figure 2b: LC-MS chromatograms of SVPAFFWTDK for the five *mcr-1*-containing isolates (P1-P5) and two negative controls (N1 and N2) used in assay development.



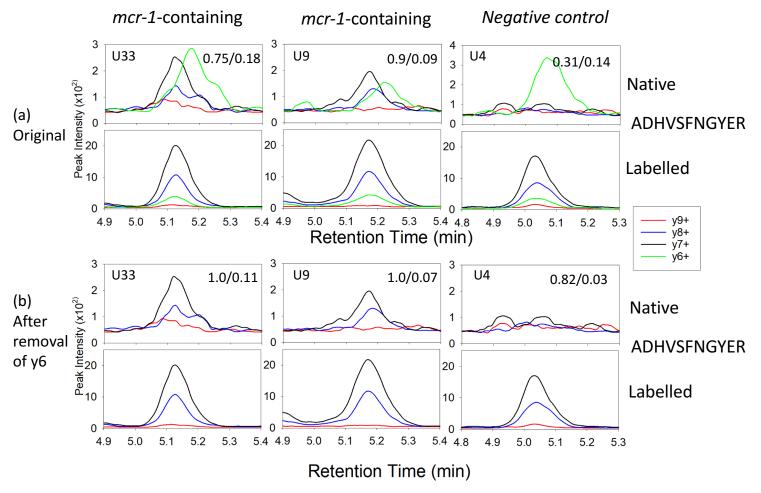
Supplemental Figure 2c: LC-MS chromatograms of ADHVSFNGYER for the five *mcr-1*-containing isolates (P1-P5) and two negative controls (N1 and N2) used in assay development.



Supplemental Figure 3: For *mcr-1*-containing isolate P5 used in assay development, distortion in the y3 transition, likely due to interference, as well as a fully interfering transition (y6) were observed. Left: original LC-MS chromatogram; Right: LC-MS chromatogram after removal of the interfering transition y6.



Supplemental Figure 4: Left panel shows peak intensity variation during the first 49-sample and 50 no-matrix blank runs. Right panel shows retention time variation during the first 49-sample and 50 no-matrix blank runs. The no-matrix blank run contained labelled peptides only were run between the samples and were used to monitor instrument performance. Strong matrix effect was observed for SVPAFFWTDK*



Supplemental Figure 5: y6 interferences were observed in native ADHVSFNGYER peptide. Removal of the y6 transition increased the rdotp value for *mcr-1*-containing isolates. Ratios are given as rdopt/R ratio.

Supplemental Table 1: Core peptides for 12 MCR-1 variants and calcuated ESPPredictor values (ESP)					
In silico digested tryptic peptide	# variants containing peptide	aa position	Unique to MCR-1	Note	ESP
DAVQATKPDMR	12	225-235	yes	Detected (not used)	0.40
ADHVSFNGYER	12	250-260	yes	Detected	0.28
DTFPQLAK	12	261-268	yes	Detected	0.76
SVPAFFWTDK	12	491-500	yes	Detected	0.42
SYVNPIMPIYSVGK	12		yes	Not detected	0.53
VDYPTWGK	12		yes	Not detected	0.32
DVGMLVGLDDFVAANNGK	12		yes	Not detected	0.30
SATNNAICNTNPYNECR	12		yes	Not detected	0.29
IIGLGVLPSLLVAFVK	12		yes	Not detected	0.24
DLLNAAFIMR	12		yes	Not detected	0.23
QTGITPMATDTVLTHDAITPTLLK	12		yes	Not detected	0.15
LGLIVASLALILLPVVAFSSHYASFFR	12		yes	Not detected	0.08
SVSPFVLVASVAVFLTATANLTFFDK	12		yes	Not detected	0.06
LFDVTADK	12		no	MCR-2.1	0.59
AQFADYK	12		no		0.19
DMLIMLHQMGNHGPAYFK	12		no	MCR-2	0.09
DNNSDSK	12		no		0.05
DTIYHAK	12		no		0.07
FTPVCEGNELAK	12		no	MCR-2	0.87
LASIEYK	12		no		0.28
LVVFVVGETAR	12		no		0.32
VHKPLR	12		no		0.11
LGVSILWR	11		yes		0.27
YQENVLDTLDR	11		no	MCR-2	0.61
MMQHTSVWYR	8		yes		0.12
DHTAFIR	1		no		0.22
HTSVWYR	1		yes		0.11
LGVSFLWR	1		yes		0.24
MMLHTSVWYR	1		yes		0.14
MMQHTSVCYR	1		yes		0.18
MQHTSVWYR	1		yes		0.10
VLDTSDR	1		no		0.09