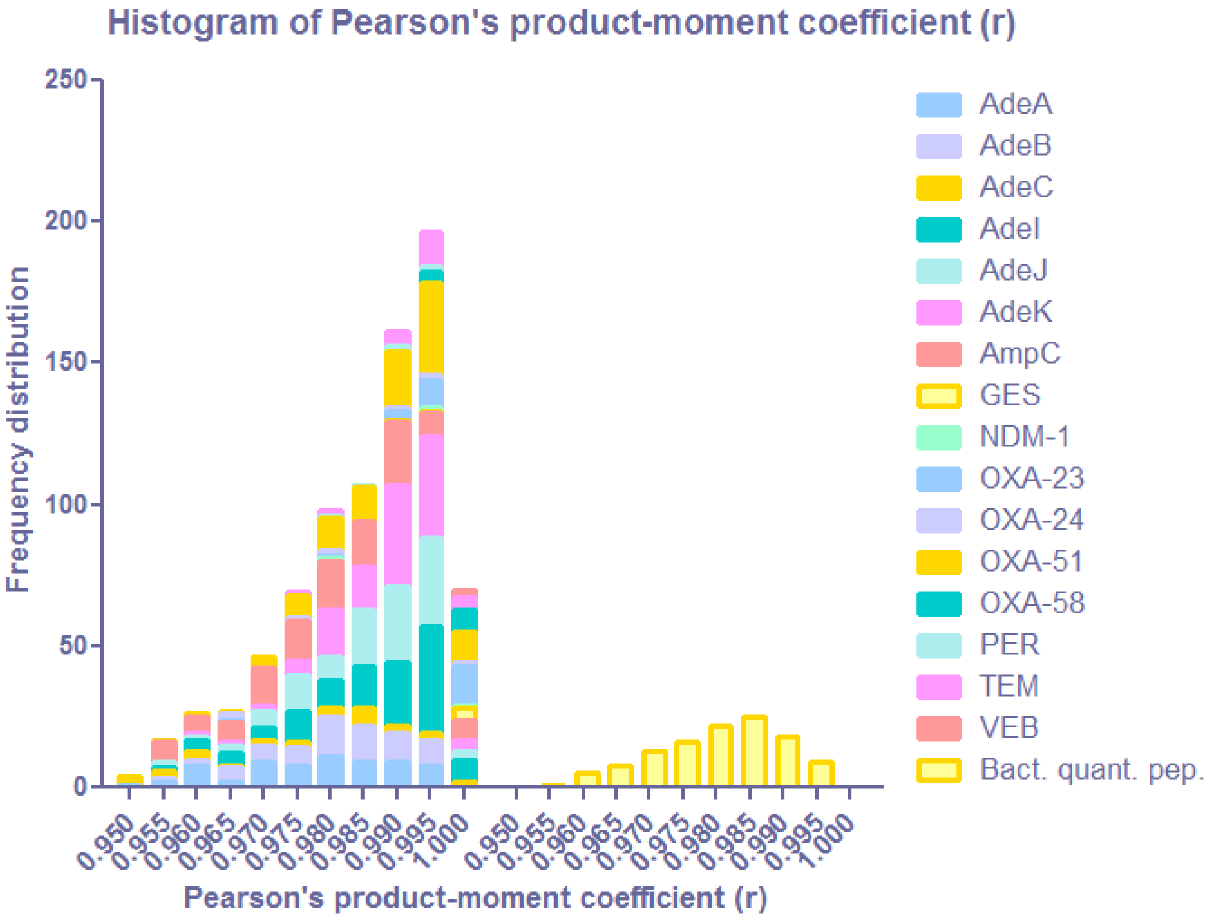
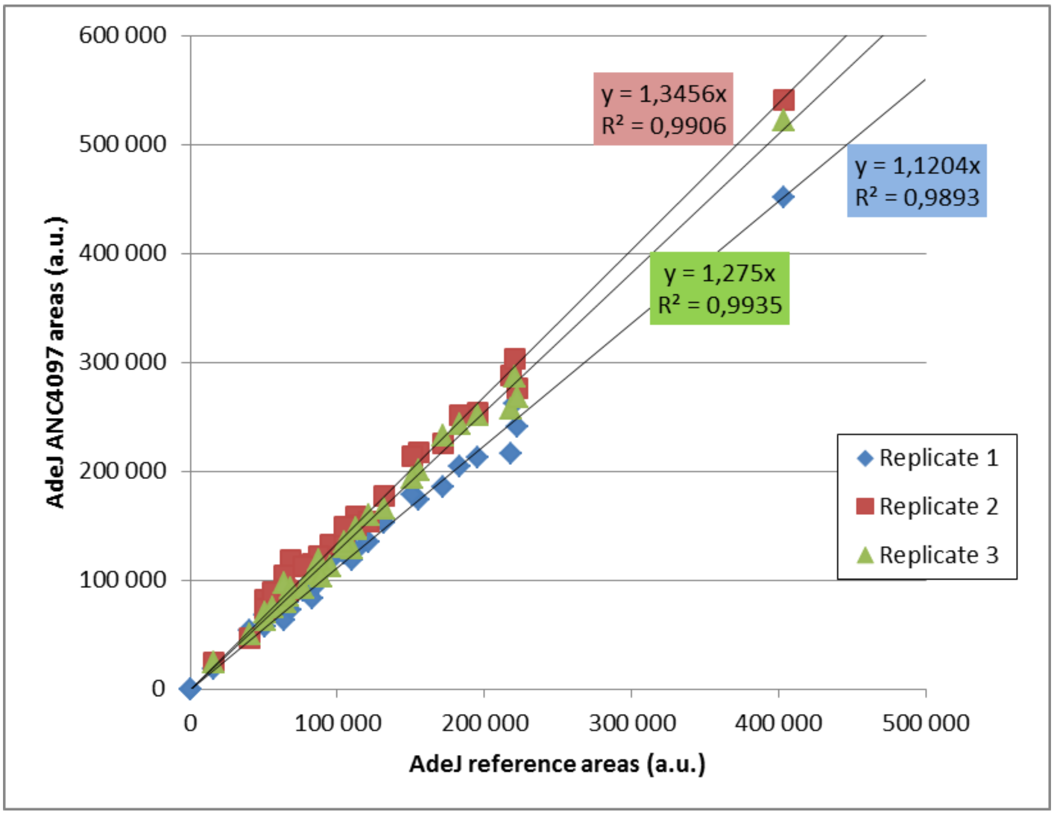
Contents of Supplemental Figures & Table

Supplemental Figures

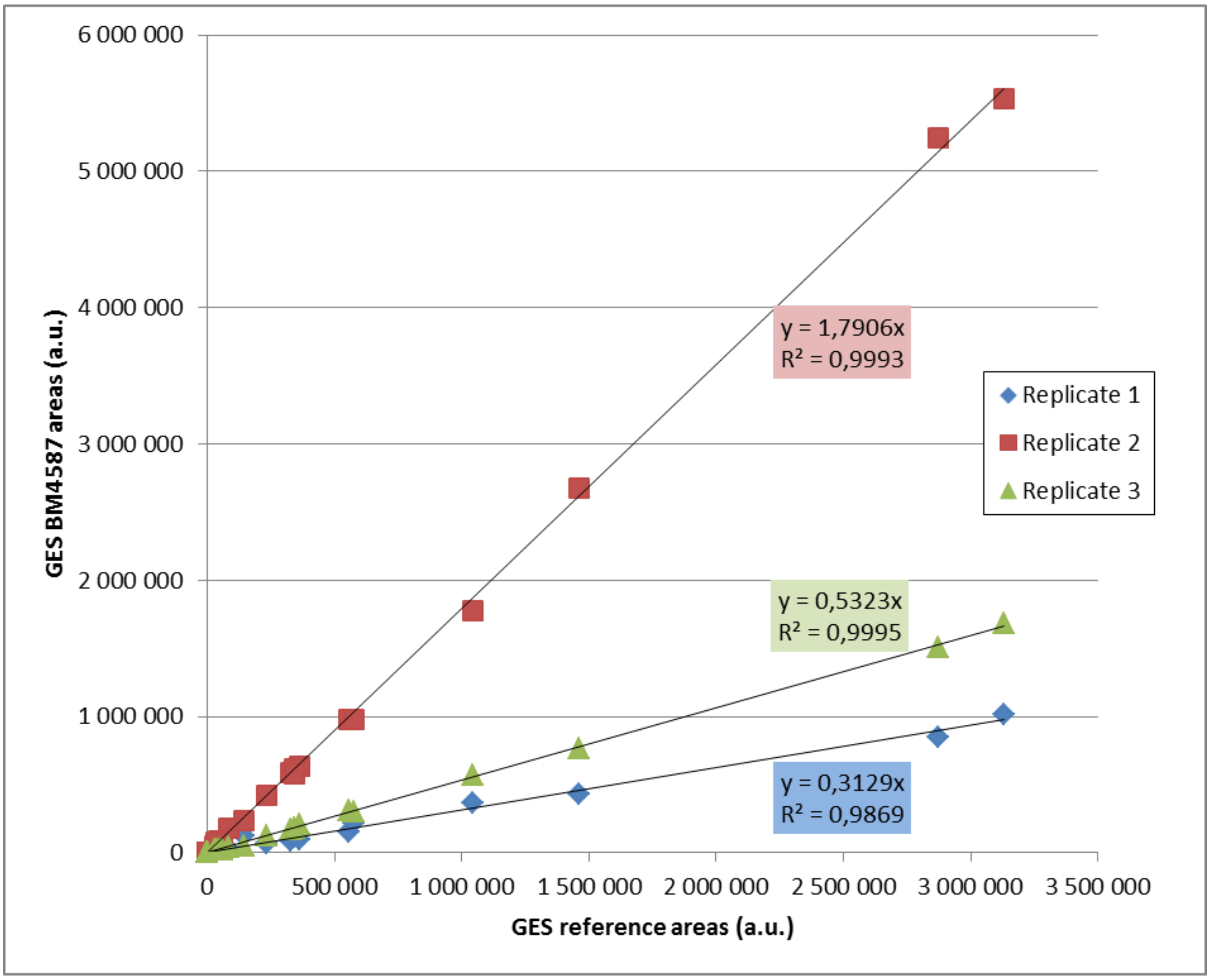


Supplemental Fig. S1: Histogram of Pearson's product-moment coefficients (r) calculated between the non-zero transition areas of each strain and reference transition areas estimated by averaging all the non-zero transition areas from the whole data set. The distribution of bacterial quantotypic peptides are on the right and the cumulative distribution of other proteins on the left.



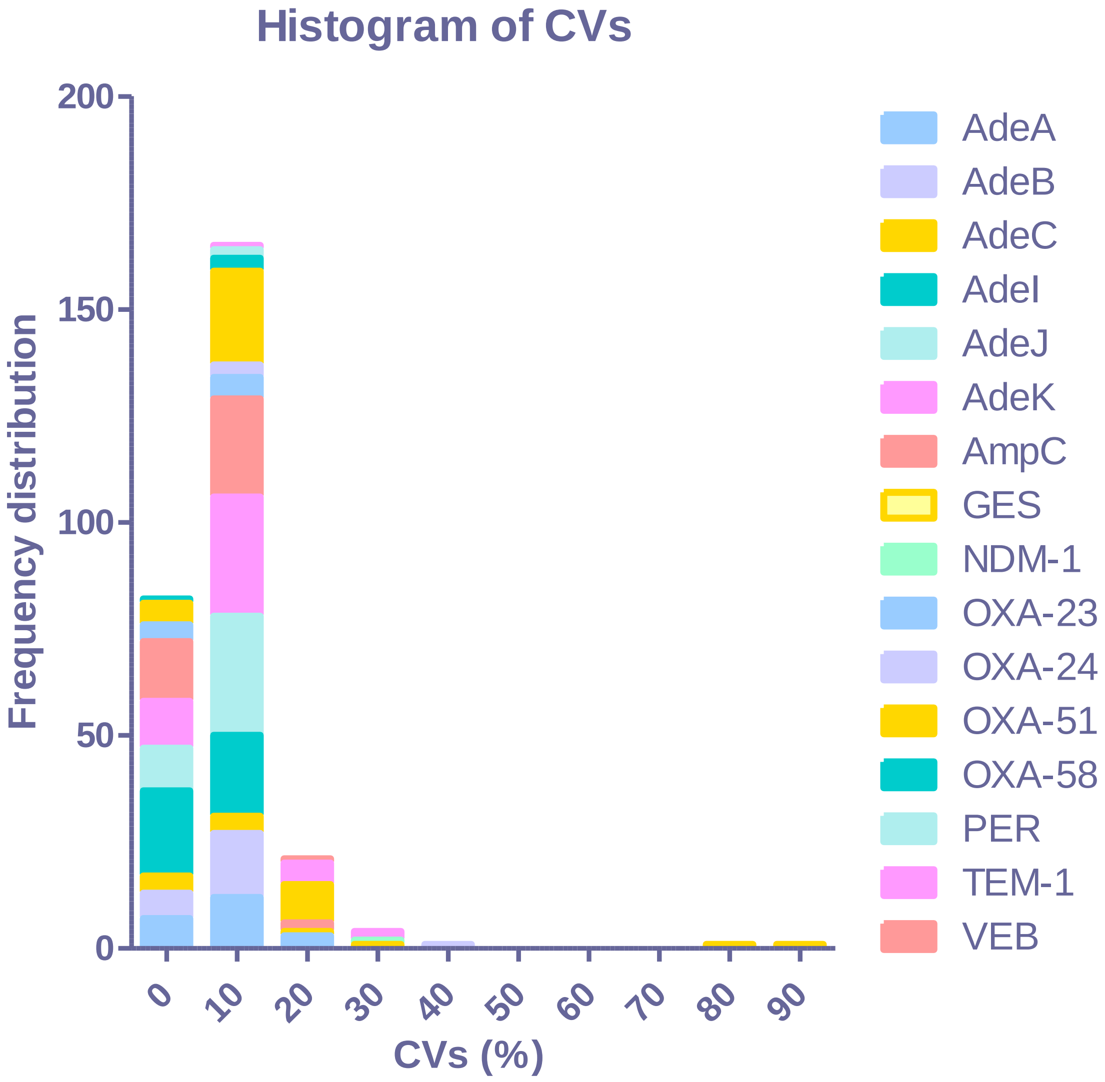
Supplemental Fig. S2a: correlation curves for AdeJ measurement via SRM in ANC4097 sample, relative protein quantitation 2.4/4.9%.

	Protein class	Protein Name	Peptide	Transitions	Retention Time(min)	Quantotypic and Proteotypic	Used for quantitation
247	Efflux pump	AdeJ	GEDLLDATLHAAK	AdeJ.GEDLLDATLHAAK.+2y8	15,44	Used	
248	Efflux pump	AdeJ	GEDLLDATLHAAK	AdeJ.GEDLLDATLHAAK.+3y7	15,44	Used	
249	Efflux pump	AdeJ	GEDLLDATLHAAK	AdeJ.GEDLLDATLHAAK.+3y8	15,44	Used	
250	Efflux pump	AdeJ	GMALNMIIK	AdeJ.GMALNMIIK.+2y5	16,8	Used	
251	Efflux pump	AdeJ	GMALNMIIK	AdeJ.GMALNMIIK.+2y6	16,8	Used	
252	Efflux pump	AdeJ	GMALNMIIK	AdeJ.GMALNMIIK.+2y7	16,8	Used	
253	Efflux pump	AdeJ	IATGANALDTAEAVEQR	AdeJ.IATGANALDTAEAVEQR.+3y4	13	Used	
254	Efflux pump	AdeJ	IATGANALDTAEAVEQR	AdeJ.IATGANALDTAEAVEQR.+3y5	13	Used	
255	Efflux pump	AdeJ	IATGANALDTAEAVEQR	AdeJ.IATGANALDTAEAVEQR.+3y6	13	Used	
256	Efflux pump	AdeJ	IAWGGSYINDFVDR	AdeJ.IAWGGSYINDFVDR.+2y6	18,5	Used	
257	Efflux pump	AdeJ	IAWGGSYINDFVDR	AdeJ.IAWGGSYINDFVDR.+2y7	18,5	Used	
258	Efflux pump	AdeJ	IAWGGSYINDFVDR	AdeJ.IAWGGSYINDFVDR.+3y6	18,5	Used	
259	Efflux pump	AdeJ	IWLDPAK	AdeJ.IWLDPAK.+2y3	13,56	Used	TopTra2TopPep3
260	Efflux pump	AdeJ	IWLDPAK	AdeJ.IWLDPAK.+2y5	13,56	Used	TopTra2TopPep3
261	Efflux pump	AdeJ	IWLDPAK	AdeJ.IWLDPAK.+2y6	13,56	Used	
265	Efflux pump	AdeJ	NYPTGLADK	AdeJ.NYPTGLADK.+2y5	9	Used	
266	Efflux pump	AdeJ	NYPTGLADK	AdeJ.NYPTGLADK.+2y6	9	Used	TopTra2TopPep3
267	Efflux pump	AdeJ	NYPTGLADK	AdeJ.NYPTGLADK.+2y7	9	Used	TopTra2TopPep3
268	Efflux pump	AdeJ	SFNNGFDR	AdeJ.SFNNGFDR.+2y4	9,4	Used	
269	Efflux pump	AdeJ	SFNNGFDR	AdeJ.SFNNGFDR.+2y5	9,4	Used	
270	Efflux pump	AdeJ	SFNNGFDR	AdeJ.SFNNGFDR.+2y6	9,4	Used	
271	Efflux pump	AdeJ	TTPETQIGSLIQR	AdeJ.TTPETQIGSLIQR.+2y6	14,9	Used	
272	Efflux pump	AdeJ	TTPETQIGSLIQR	AdeJ.TTPETQIGSLIQR.+2y7	14,9	Used	
273	Efflux pump	AdeJ	TTPETQIGSLIQR	AdeJ.TTPETQIGSLIQR.+3y6	14,9	Used	
274	Efflux pump	AdeJ	VELGSDNYQFDSK	AdeJ.VELGSDNYQFDSK.+2y3	12,14	Used	
275	Efflux pump	AdeJ	VELGSDNYQFDSK	AdeJ.VELGSDNYQFDSK.+2y4	12,14	Used	
276	Efflux pump	AdeJ	VELGSDNYQFDSK	AdeJ.VELGSDNYQFDSK.+2y7	12,14	Used	
277	Efflux pump	AdeJ	VMSEDHTDPVTATSR	AdeJ.VMSEDHTDPVTATSR.+3y4	8	Used	
278	Efflux pump	AdeJ	VMSEDHTDPVTATSR	AdeJ.VMSEDHTDPVTATSR.+3y5	8	Used	
279	Efflux pump	AdeJ	VMSEDHTDPVTATSR	AdeJ.VMSEDHTDPVTATSR.+3y7	8	Used	
280	Efflux pump	AdeJ	VYVQGDAGSR	AdeJ.VYVQGDAGSR.+2y6	5,6	Used	TopTra2TopPep3
281	Efflux pump	AdeJ	VYVQGDAGSR	AdeJ.VYVQGDAGSR.+2y7	5,6	Used	TopTra2TopPep3
282	Efflux pump	AdeJ	VYVQGDAGSR	AdeJ.VYVQGDAGSR.+2y8	5,6	Used	

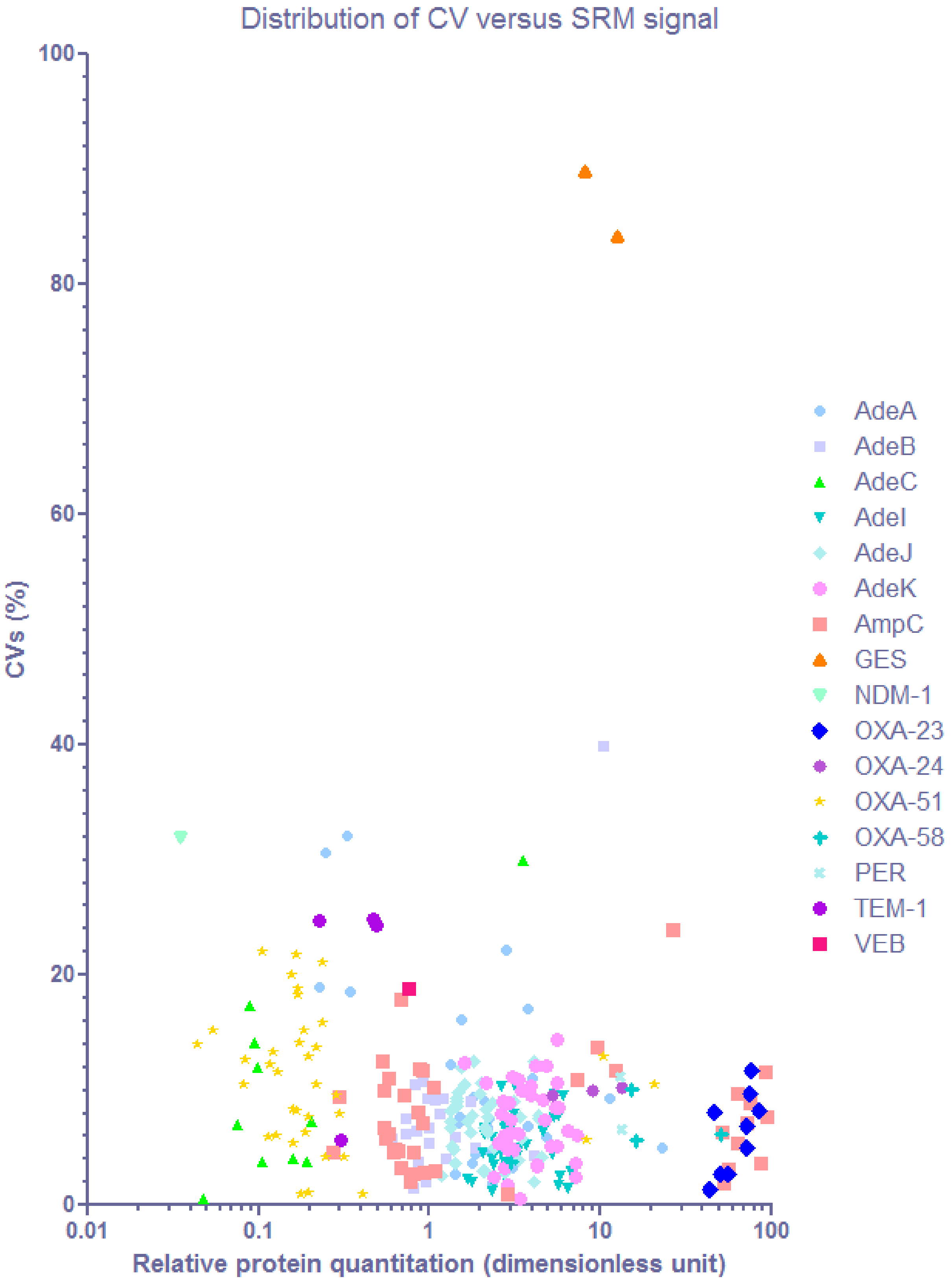


Supplemental Fig. S2b: correlation curves for GES measurement via SRM in BM4701 sample, relative protein quantitation 8.1/89.8%.

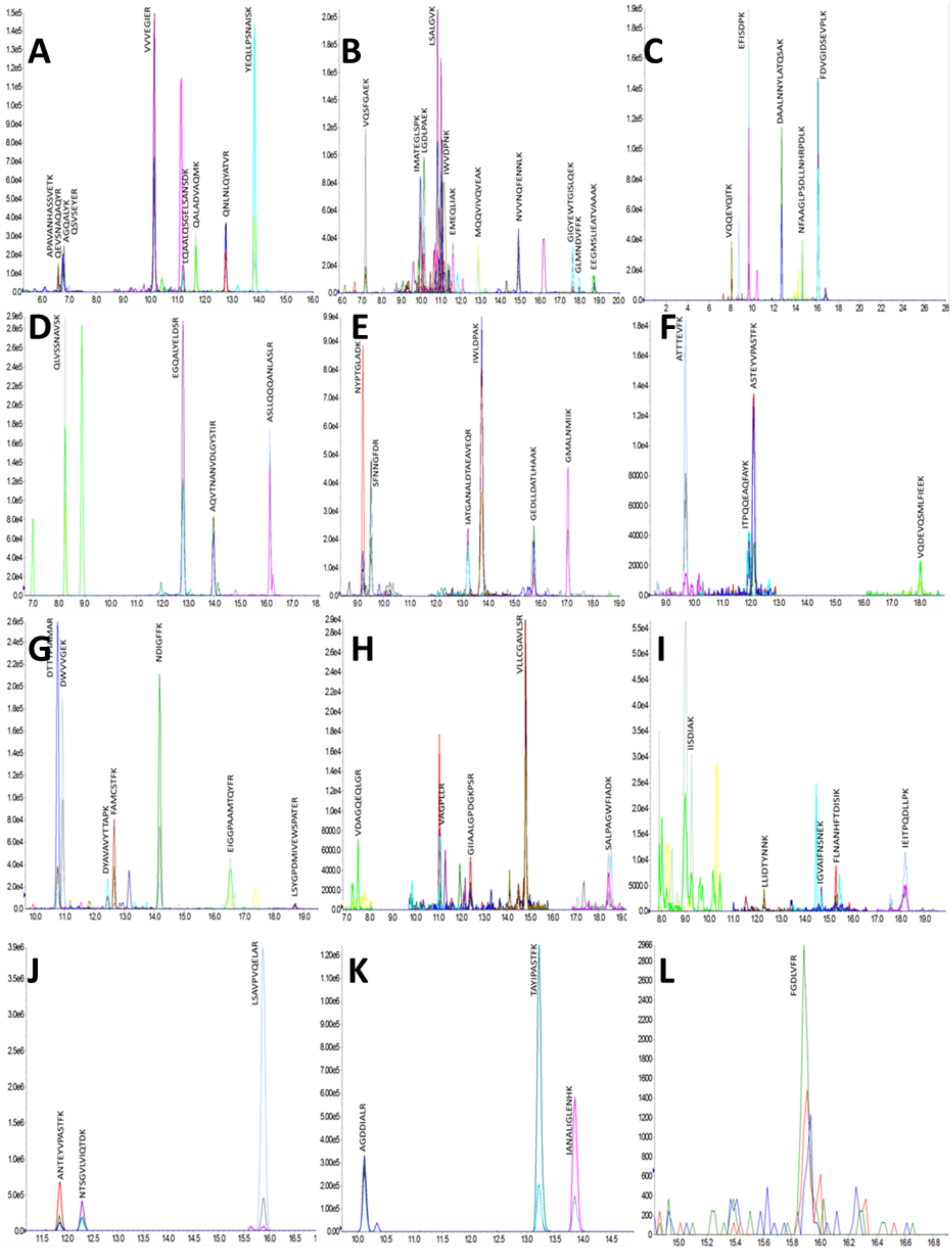
	Protein class	Protein Name	Peptide	Transitions	Retention Time(min)	Quantotypic and Proteotypic	Used for quantitation
343	Wide-Spectrum β-lactamase	GES	AAEIGVAIVDPQGEIVAGHR	GES.AAEIGVAIVDPQGEIVAGHR.+3y13+2	15,5	Used	
344	Wide-Spectrum β-lactamase	GES	AAEIGVAIVDPQGEIVAGHR	GES.AAEIGVAIVDPQGEIVAGHR.+3y14+2	15,5	Used	
345	Wide-Spectrum β-lactamase	GES	AAEIGVAIVDPQGEIVAGHR	GES.AAEIGVAIVDPQGEIVAGHR.+3y16+2	15,5	Used	
346	Wide-Spectrum β-lactamase	GES	AAQIGVAIVDPQGEIVAGHR	GES.AAQIGVAIVDPQGEIVAGHR.+3y13+2	15,5	Used	
347	Wide-Spectrum β-lactamase	GES	AAQIGVAIVDPQGEIVAGHR	GES.AAQIGVAIVDPQGEIVAGHR.+3y14+2	15,5	Used	TopTra2TopPep3
348	Wide-Spectrum β-lactamase	GES	AAQIGVAIVDPQGEIVAGHR	GES.AAQIGVAIVDPQGEIVAGHR.+3y16+2	15,5	Used	TopTra2TopPep3
352	Wide-Spectrum β-lactamase	GES	DWVVGEK	GES.DWVVGEK.+2y4	11,2	Used	TopTra2TopPep3
353	Wide-Spectrum β-lactamase	GES	DWVVGEK	GES.DWVVGEK.+2y5	11,2	Used	TopTra2TopPep3
354	Wide-Spectrum β-lactamase	GES	DWVVGEK	GES.DWVVGEK.+2y6	11,2	Used	
355	Wide-Spectrum β-lactamase	GES	DYAVAVYTTAPK	GES.DYAVAVYTTAPK.+2y6	12,5	Used	
356	Wide-Spectrum β-lactamase	GES	DYAVAVYTTAPK	GES.DYAVAVYTTAPK.+2y7	12,5	Used	
357	Wide-Spectrum β-lactamase	GES	DYAVAVYTTAPK	GES.DYAVAVYTTAPK.+2y8	12,5	Used	
370	Wide-Spectrum β-lactamase	GES	LSYGPDMIVEWSPATER	GES.LSYGPDMIVEWSPATER.+3y5	19,1	Used	
371	Wide-Spectrum β-lactamase	GES	LSYGPDMIVEWSPATER	GES.LSYGPDMIVEWSPATER.+3y6	19,1	Used	
372	Wide-Spectrum β-lactamase	GES	LSYGPDMIVEWSPATER	GES.LSYGPDMIVEWSPATER.+3y7	19,1	Used	
373	Wide-Spectrum β-lactamase	GES	NDIGFFK	GES.NDIGFFK.+2y4	14,4	Used	TopTra2TopPep3
374	Wide-Spectrum β-lactamase	GES	NDIGFFK	GES.NDIGFFK.+2y5	14,4	Used	TopTra2TopPep3
375	Wide-Spectrum β-lactamase	GES	NDIGFFK	GES.NDIGFFK.+2y6	14,4	Used	



Supplemental Fig. S3a : histogram of CV distributions. CVs were calculated using SRM measurements from three biological replicates.



Supplemental Fig. S3b : CV *versus* average of relative protein quantitation.
CVs and averages were calculated using SRM measurements from three biological replicates.

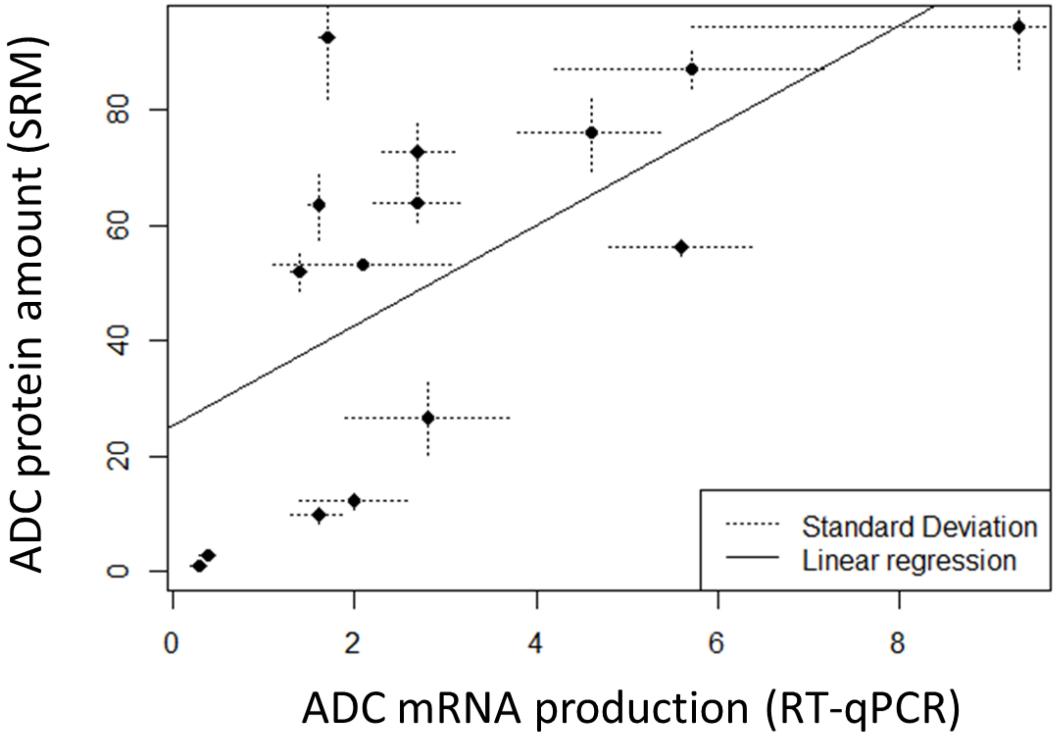


Supplemental Fig. S4 : characteristic peptide peaks by SRM (in replicate 1), from top to bottom, left to right. **A**: AdeA in BM4704 (4.8/5.9%); **B**: AdeB in CIP 70.34^T (4.1/4.3%); **C**: AdeC in NIPH 290 (3.5/3.0); **D**: AdeI in NIPH 335 (5.7 /1.8%); **E**: AdeJ in NIPH 527 (1.8/12.5%); **F**: OXA-51 like in NIPH 190 (0.3/7.9%); **G**: GES in BM4701 (8.1/89.8%); **H**: TEM-1 in ANC 4097 (0.49/24.3%); **I**: VEB in AYE (0.76/18.8%); **J**: OXA-23 in ANC 4097 (46.1/2.7%); **K**: OXA-58 in NIPH 1362: 15.1/10%; **L**: NDM-1 in ANC 4097 (0.04/31.9%). Peaks were detected using MultiQuant^{TM} 2.1 and areas under 3,000 Sciex arbitrary unit (a.u.) were set to null.

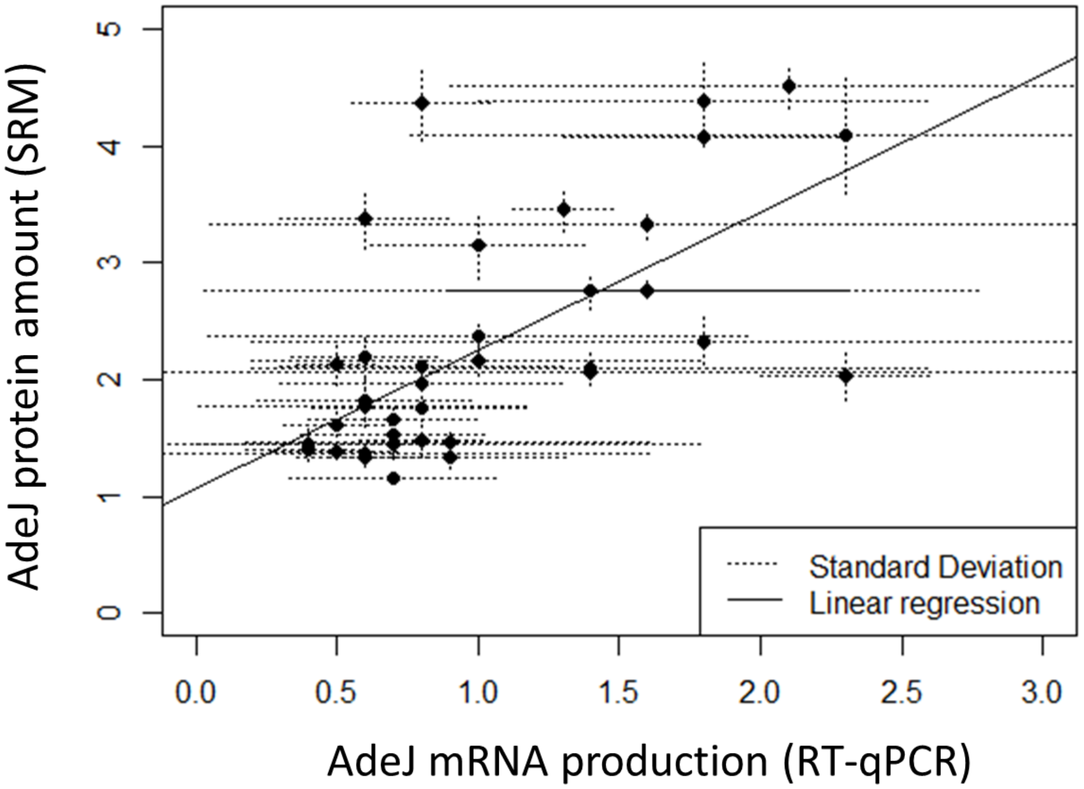
```
>acin_baum_NIPH_1362_redo

MKLLKILSLVCLSISIGACAEHSMSRAKTSTIPQVNNSIIDQNVQALFNEISADAVFVTYDGQNIKKYGTHLDRAKTAYI
PASTFKIANALIGLENHKATSTEIFKWDGKPRFFKAWDKDFTLGEAMQASTVPVYQELARRIGPSLMQSELQRIGYG
NMQIGTEVDQFWLKGPLTITPIQEVKFVYDLAQGQLPFKPEVQQQVKEMLYVERRGENRLYAKSGWGMAVDPQ
VGWYVGFVEKADGQVVAFALNMQMKAGDDIALRKQLSLDVLDKLGVFHYL
```

Supplemental Fig. S5 : OXA-58 gene identified in NIPH 1362 by new WGS.



Supplemental Fig. S6a : ADC protein *versus* mRNA production. Correlation between mRNA synthesis (RT-qPCR) expression and protein quantitation (SRM). For SRM, 3 samples were analyzed from 3 different biological cultures. For RT-qPCR, at least 2 samples were analyzed from the same biological culture. Pearson's product-moment correlation p-values was 0.01057.



Supplemental Fig. S6b : AdeJ protein *versus* mRNA production. Correlation between AdeJ mRNA synthesis (RT-qPCR) expression and protein quantitation (SRM). For SRM, 3 samples were analyzed from 3 different biological cultures. For RT-qPCR, at least 2 samples were analyzed from the same biological culture. Pearson's product-moment correlation p-values was 1.379 x 10^{-5}.

Supplemental Tables

Sample Name	Reference (PMID numbers)	DNA Purity from NanoDrop A(260)/A(280)	DNA quantity from QuBit (ng/uL)
NIPH1362	Nemec 2004, Diancourt 2010	1.83	83.6
BM4701	Jeannot 2014	1.89	16.8
BM4702	Jeannot 2014	1.85	46.3
BM4703	Jeannot 2014	1.93	58.1
BM4704	Jeannot 2014	1.94	48.5
BM4705	Jeannot 2014	1.93	70.1
BM4706	Jeannot 2014	1.84	37.3
BM4707	Jeannot 2014	1.86	77.2
BM4708	Jeannot 2014	1.86	53.6
BM4709	Jeannot 2014	1.88	34.6
BM4710	Jeannot 2014	1.85	85.4
BM4711	Jeannot 2014	1.87	24.7
BM4712	Jeannot 2014	1.89	105.0
BM4713	Jeannot 2014	1.83	58.3

Supplemental Table S1 : strains sequenced in this study.

Supplemental Table S2 to S4 : see specific files.

OXA-23
>tr|A0A0E1PW85|A0A0E1PW85_ACIBA OXA-23 protein OS=Acinetobacter baumannii NCGM 237 GN=blaOXA-23 PE=4 SV=1
MNKYFTCYVVASLFLSGCTVQHNLINETPSQIVQGHNQVIHQYFDEKNTSGVLVIQTDKKINLYGNALS
RANTEYVPASTFKMLNALIGLENQKTDINEIFKWKGEKRSFTAWEKDMTLGEAMKLSAVPVYQELARR
IGLDLMQKEVKRIGFGNAEIGQQVDNFWLVGPLKVTPIQEVEFVSQLAHTQLPFSEKVQANVKNMLLL
EESNGYKIFGKTGWAMDIKPQVGWLTGWVEQPDGK
IVAFALNMEMRSEMPASIRNELLMKSLKQLNII

OXA-24
>tr|Q8RLA6|Q8RLA6_ACIBA Beta-lactamase OS=Acinetobacter baumannii GN=blaOXA-33 PE=1 SV=1
MKKFILPIFSISILVSLSACSSIKTKSEDNFHISSQQHEKAIKSYFDEAQTQGVIIIKEGKNLSTYGNALARA
NKEYVPASTFKMLNALIGLENHKATTNEIFKWDGKKRTYPMWEKDMTLGEAMALSAVPVYQELARR
TGLELMQKEVKRVNFGNTNIGTQVDNFWLVGPLKITPVQEVNFADDLAHNRLPFKLETQEEVKKMLLI
KEVNGSKIYAKSGWGMGVTPQVGWLTGWVEQANGKKIPFSLNLEMKEGMSGSIRNEITYKSLENLGII

OXA-51
>tr|Q5QT35|Q5QT35_ACIBA Beta-lactamase OS=Acinetobacter baumannii GN=oxa-51 PE=1 SV=1
MNIKTLLLITSAIFISACSPYIVTANPNHSASKSDEKAEKIKNLFNEVHTTGVLVIQQGQTQQSYGNDLAR
ASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEKDMTLGDAMKASAIPVYQDLARRI
GLELMSKEVKRVGYGNADIGTQVDNFWLVGPLKITPQQEAQFAYKLANKTLPFSPKVQDEVQSMLFIE
EKNGNKIYAKSGWGWDVDPQVGWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

OXA-58
>tr|Q2TR58|Q2TR58_ACIBA Beta-lactamase OS=Acinetobacter baumannii GN=blaOXA-58 PE=1 SV=1
MKLLKILSLVCLSISIGACAEHSMSRAKTSTIPQVNNSIIDQNVQALFNEISADAVFVTYDGQNIKKYGTH
LDRAKTAYIPASTFKIANALIGLENHKATSTEIFKWDGKPRFFKAWDKDFTLGEAMQASTVPVYQELAR
RIGPSLMQSELQRIGYGNMQIGTEVDQFWLKGPLTITPIQEVKFVYDLAQGQLPFKPEVQQQVKEMLYV
ERRGENRLYAKSGWGMAVDPQVGWYVGFVEKADGQVVAFALNMQMKAGDDIALRKQLSLDVLDKL
GVFHYL

Supplemental Table S5 : specificity of peptides used for OXA quantitation.
Peptides in green and yellow are unique and therefore specific. Sequence LSAVPVYQELAR (in blue) is shared by OXA-23 and OXA-24 but cannot by detected in OXA-24 digested using trypsin, because of upstream sequence alteration (DMTLGEAMK *versus* DMTLGEAMAL).