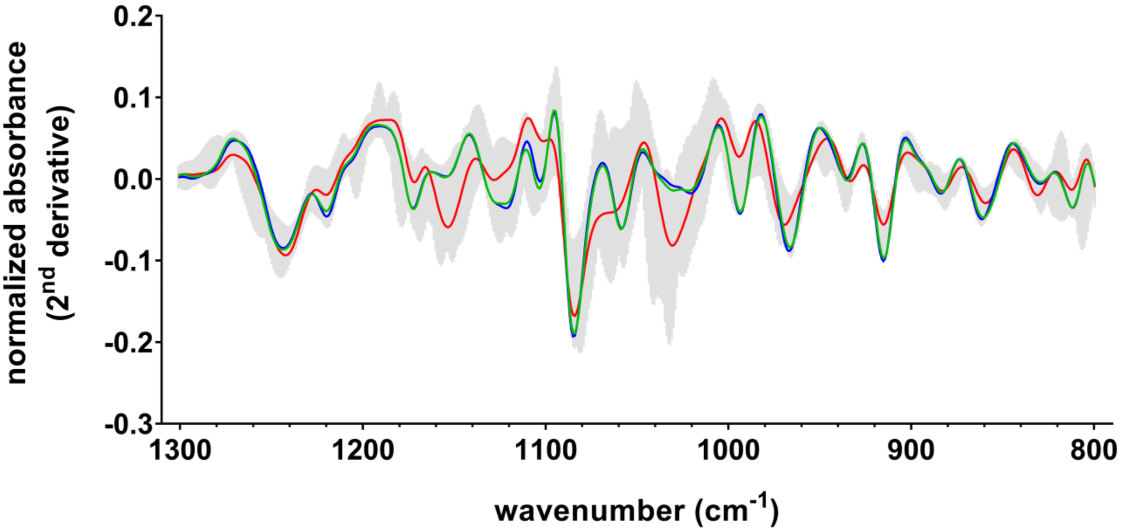
Dinkelacker et al.: “Typing and species identification of clinical *Klebsiella* isolates by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry and Fourier-transform infrared spectroscopy”

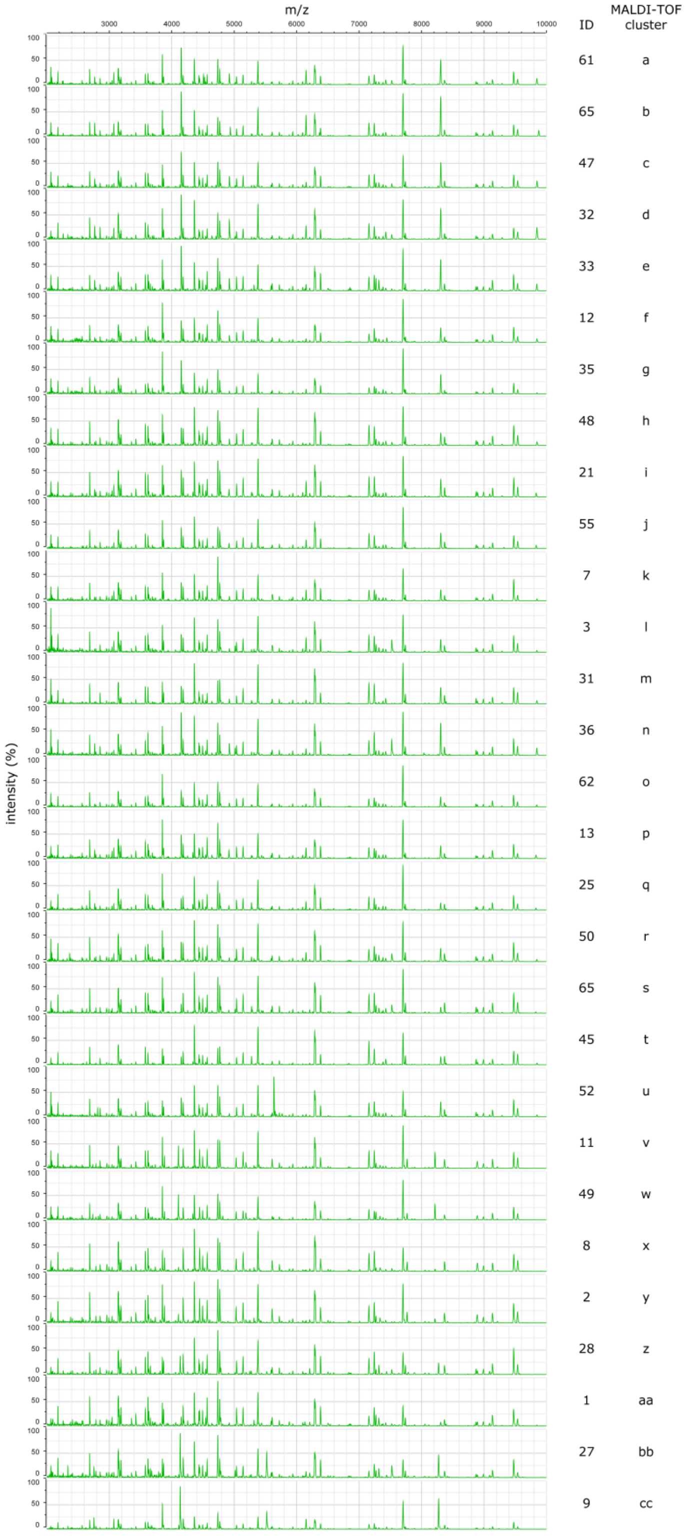
SUPPLEMENTARY MATERIAL

Figure S1



FTIR spectra. Representative isolate spectra (ID5 – green, ID6 – blue, ID30 – red) are shown. Grey shading represents the range between the minimum and maximum normalized absorbance of all 68 isolate spectra at each wavenumber.

Figure S2



MALDI-TOF spectra. The 2,000-10,000 *m*/*z* spectrum range of one representative isolate spectrum from each MALDI-TOF cluster is shown.

Table S1

Isolate #	Month and year of collection	Patient #
ID 1	12-2013	Pat 1
ID 2	01-2014	Pat 2
ID 3	01-2014	Pat 3
ID 4	01-2014	Pat 4
ID 5	01-2014	Pat 5
ID 6	01-2014	Pat 6
ID 7	01-2014	Pat 4
ID 8	01-2014	Pat 7
ID 9	01-2014	Pat 8
ID 10	01-2014	Pat 3
ID 11	01-2014	Pat 9
ID 12	02-2014	Pat 10
ID 13	02-2014	Pat 11
ID 14	02-2014	Pat 12
ID 15	02-2014	Pat 10
ID 16	02-2014	Pat 13
ID 17	02-2014	Pat 14
ID 18	03-2014	Pat 15
ID 19	03-2014	Pat 16
ID 20	03-2014	Pat 17
ID 21	03-2014	Pat 18
ID 22	03-2014	Pat 19
ID 23	03-2014	Pat 20
ID 24	03-2014	Pat 21
ID 25	03-2014	Pat 22
ID 26	04-2014	Pat 23
ID 27	04-2014	Pat 24
ID 28	04-2014	Pat 8
ID 29	04-2014	Pat 25
ID 30	05-2014	Pat 26
ID 31	05-2014	Pat 21
ID 32	06-2014	Pat 27
ID 33	06-2014	Pat 28
ID 34	06-2014	Pat 29
ID 35	06-2014	Pat 30
ID 36	06-2014	Pat 31
ID 37	06-2014	Pat 32
ID 38	06-2014	Pat 33
ID 39	06-2014	Pat 34
ID 40	06-2014	Pat 27
ID 41	06-2014	Pat 35
ID 42	06-2014	Pat 36

ID 43	06-2014	Pat 16
ID 44	06-2014	Pat 37
ID 45	07-2014	Pat 35
ID 46	07-2014	Pat 38
ID 47	08-2014	Pat 35
ID 48	08-2014	Pat 39
ID 49	08-2014	Pat 40
ID 50	08-2014	Pat 41
ID 51	08-2014	Pat 16
ID 52	08-2014	Pat 42
ID 53	09-2014	Pat 43
ID 54	09-2014	Pat 44
ID 55	09-2014	Pat 45
ID 56	09-2014	Pat 46
ID 57	09-2014	Pat 47
ID 58	09-2014	Pat 48
ID 59	10-2014	Pat 49
ID 60	10-2014	Pat 50
ID 61	10-2014	Pat 51
ID 62	10-2014	Pat 52
ID 63	10-2014	Pat 53
ID 64	10-2014	Pat 54
ID 65	10-2014	Pat 55
ID 66	10-2014	Pat 53
ID 67	10-2014	Pat 56
ID 68	11-2014	Pat 57

Isolate characteristics. Isolate numbers and corresponding collection date and patient numbers are indicated.

Table S2

ID	**WGS cluster**	***K. pneumoniae* HS11286**	***K. pneumoniae* NJST258_2**	***K. quasipneumoniae* ATCC700603**	***K. quasipneumoniae* HKUOPA4**	***K. variicola* GJ1**	***K. variicola* At-22**
32	**A**	99,2	99,2	94,0	94,0	94,7	94,7
48	**B**	99,2	99,1	94,0	94,0	94,7	94,7
1	**C**	99,2	99,1	94,0	94,0	94,7	94,7
26	**D**	99,2	99,2	94,0	94,0	94,7	94,7
45	**E**	99,1	99,1	94,0	94,0	94,6	94,6
46	**F**	99,1	99,0	94,0	94,0	94,7	94,6
52	**G**	99,2	99,1	94,0	94,0	94,7	94,6
3	**H**	99,1	99,1	94,0	94,0	94,7	94,7
63	**I**	99,2	99,2	94,0	94,0	94,7	94,7
56	**J**	99,2	99,1	94,0	94,0	94,7	94,7
42	**K**	99,1	99,1	94,0	94,0	94,6	94,7
31	**L**	99,3	99,3	94,0	94,0	94,7	94,7
51	**M**	99,2	99,2	94,0	94,0	94,6	94,7
12	**N**	99,2	99,2	94,0	94,0	94,7	94,7
62	**O**	99,2	99,2	93,9	94,0	94,7	94,7
50	**P**	99,1	99,1	94,0	94,0	94,7	94,7
30	**Q**	99,2	99,2	94,0	94,0	94,7	94,7
60	**R**	99,2	99,2	93,9	94,0	94,7	94,7
53	**S**	99,2	99,2	93,9	94,0	94,7	94,7
13	**T**	99,2	99,1	94,0	94,0	94,7	94,7
34	**U**	99,2	99,2	94,0	94,0	94,7	94,7
55	**V**	99,3	99,2	94,0	94,0	94,7	94,7
61	**W**	99,1	99,1	94,1	94,0	94,7	94,7
64	**X**	99,1	99,1	94,0	94,1	94,7	94,7
9	**Y**	93,8	93,8	96,7	96,7	93,6	93,6
2	**Z**	94,6	94,6	93,7	93,7	99,1	99,2
49	**AA**	94,7	94,6	93,6	93,7	99,2	99,2
16	**BB**	94,7	94,7	93,7	93,6	99,0	99,1
24	**CC**	94,6	94,6	93,6	93,6	99,1	99,1

Average nucleotide identity (ANI). Values (%) for one representative isolate of each WGS cluster (Figure 1) in comparison to each of two reference genomes of *K. pneumoniae*, *K. quasipneumoniae*, and *K. variicola*. Shading indicates ANI of ≥ 96%.

Table S3

		MALDI-TOF cluster																												
		a	b	c	d	e	f	g	h	i	j	k	l	m	n	o	p	q	r	s	t	u	v	w	x	y	z	aa	bb	cc
WGS cluster	**W**	1																												
	X		1																											
	A			2	1	2									1															
	N						1																							
	U							1			2			1	1															
	B								1																					
	H								2			1	2																	
	J								1																					
	R								1																					
	Q								1																					
	K								2																					
	T									5							1	2												
	V										4																			
	L													1																
	S													1																
	P															1														
	D															1														
	I																	1		4										
	O																		1											
	M																		1											
	F																			1										
	E																				1									
	G																					2								
	Z																						1		3	1				
	BB																						3		1					
	AA																							1						
	CC																							1						2
	Y																										1		1	
	C																											1		

Contingency table. The number of isolates assigned to the respective WGS/MALDI-TOF cluster combination is indicated.

Table S4

K. pneumoniae (ID 1)	**K. pneumoniae NJST258_2**	**K. pneumoniae HS11286**	**K. variicola (ID 2)**	**K. variicola At-22**	**K. variicola GJ1**	**Protein**	***m/z***	***m/z* (dMet)**	**≈ *m/2z***	**≈ *m/2z* (dMet)**	**Amino Acid Sequence**
X	X	X	X	X	X	L10p (P0)	17801.3	17670.1	8900.7	8835.1	MALNLQDKQAIVAEVSEVAKGALSAVVADSRGVTVDKMTELRKAGREAGVYMRVVRNTLLRRVVEGTQFECLKDTFVGPTLIAYSMEHPGAAARLFKEFAKANAKFEVKAAAFEGELIPASQIDRLATLPTYEEAIARLMATMKEASAGKLVRTLAAVRDAKEAA
X	X	X				L11p (L12e)	14876.0	14744.8	7438.0	7372.4	MAKKVQAYVKLQVAAGMANPSPPVGPALGQQGVNIMEFCKAFNAKTDSLEKGLPIPVVITVYADRSFTFVTKTPPAAVLLKKAAGIKSGSGKPNKDKVGKISRAQLQEIAQTKAADMTGADIEAMTRSIEGTARSMGLVVED
			X	X	X	L11p (L12e)	14908.1	14776.9	7454.0	7388.4	MAKKVQAYVKLQVAAGMANPSPPVGPALGQQGVNIMEFCKAFNAKTESMEKGLPIPVVITVYADRSFTFVTKTPPAAVLLKKAAGIKSGSGKPNKDKVGKISRAQLQEIAQTKAADMTGADIEAMTRSIEGTARSMGLVVED
X		X		X	X	L13p (L13Ae)	16110.3	15979.1	8055.1	7989.5	MKTFTAKPETVKRDWYVVDATGKTLGRLATELARRLRGKHKAEYTPHVDTGDYIIVLNAEKVAVTGNKREDKMYYHHTGHIGGIKEATFEEMIARRPERVIEIAVKGMLPKGPLGRAMYRKLKVYAGNEHNHAAQQPQVLDI
	X		X			L13p (L13Ae)	16653.0	16521.8	8326.5	8260.9	MGKLLMKTFTAKPETVKRDWYVVDATGKTLGRLATELARRLRGKHKAEYTPHVDTGDYIIVLNAEKVAVTGNKREDKMYYHHTGHIGGIKEATFEEMIARRPERVIEIAVKGMLPKGPLGRAMYRKLKVYAGNEHNHAAQQPQVLDI
X	X	X	X	X	X	L14p (L23e)	13555.6	13424.4	6777.8	6712.2	MIQEQTMLNVADNSGARRVMCIKVLGGSHRRYAGVGDIIKITIKEAIPRGKVKKGDVLKAVVVRTKKGVRRPDGSVIRFDGNACVILNNNSEQPIGTRIFGPVTRELRTEKFMKIISLAPEVL
X	X	X	X	X	X	L15p (L27Ae)	15135.2	15004.0	7567.6	7502.0	MRLNTLSPAEGSKKAGKRLGRGIGSGLGKTGGRGHKGQKSRSGGGVRRGFEGGQMPLYRRLPKFGFTSRKAMITAEIRLSDLAHVEGDVVDLNALKAANIIGVQIEFAKVILSGEVTRPVTVRGLRVTKGARAAIEAAGGKIEE
X	X	X	X	X	X	L16p (L10e)	15250.7	15119.5	7625.3	7559.7	MLQPKRTKFRKVHKGRNRGLAQGTDVSFGTFGLKAVGRGRLTARQIEAARRAMTRAVKRQGKIWIRVFPDKPITEKPLEVRMGKGKGNVEYWVALIQPGKVLYEMDGVPEELAREAFGLAAAKLPIKTTFVTKTVM
X	X	X	X	X	X	L17p	14446.2	14315.0	7223.1	7157.5	MRHRKSGRQLNRNSSHRQAMFRNMAGSLVRHEIIKTTLPKAKELRRVVEPLITLAKTDSVANRRLAFARTRDNEIVAKLFNELGPRFASRAGGYTRILKCGFRAGDNAPMAYIELVDRAEPKAEAAAE
X	X	X				L18p (L5e)	12770.1	12638.9	6385.0	6319.4	MDKKSARIRRATRARRKLQELGATRLVVHRTPRHIYAQVIAPNGSEVLVAASTVEKAIAEQLKYTGNKDAAAAVGKAVAERALEKGIKDVSFDRSGFQYHGRVQALADAAREAGLQF
			X	X	X	L18p (L5e)	12786.1	12654.9	6393.0	6327.4	MDKKSARIRRATRARRKLQELGATRLVVHRTPRHIYAQVIAPNGSEVLVAASTVEKAISEQLKYTGNKDAAAAVGKAVAERALEKGIKDVSFDRSGFQYHGRVQALADAAREAGLQF
X	X	X	X	X	X	L19p	13133.8	13002.6	6566.9	6501.3	MSNIIKQLEQEQMKQDVPSFRPGDTVEVKVWVVEGSKKRLQAFEGVVIAIRNRGLHSAFTVRKISNGEGVERVFQTHSPVVDSIAVKRRGAVRKAKLYYLRERTGKSARIKERLN
			X	X	X	L1p (L10Ae)	24632.4	24501.2	12316.2	12250.6	MAKLTKRMSVIRDKVDATKQYDINEAISLLKELATAKFVESVDVAVNLGIDARKSDQNVRGATVLPHGTGRSVRVAVFAQGANAEAAKAAGAELVGMEDLADQIKKGEMNFDVVIASPDAMRVVGQLGQVLGPRGLMPNPKVGTVTPNVAEAVKNAKAGQVRYRNDKNGIIHTTIGKVDFDADKLKENLEALLVALKKAKPTQAKGVYIKKVSISTTMGAGVAVDQAGLNASAN
X	X	X				L1p (L10Ae)	24745.6	24614.4	12372.8	12307.2	MAKLTKRMRVIREKVDATKQYDINEAIALLKELATAKFTESVDVAVNLGIDARKSDQNVRGATVLPHGTGRSVRVAVFTQGANAEAAKAAGAELVGMEDLAEQIKKGEMNFDVVIASPDAMRVVGQLGQVLGPRGLMPNPKVGTVTPNVAEAVKNAKAGQVRYRNDKNGIIHTTIGKVDFDADKLKENLEALLVALKKAKPTQAKGVYIKKVSISTTMGAGVAVDQAGLNASAN
X	X	X	X	X	X	L20p	13497.4	13366.2	6748.7	6683.1	MARVKRGVIARARHKKILKQAKGYYGARSRVYRVAFQAVIKAGQYAYRDRRQRKRQFRQLWIARINAAARQNGISYSKFINGLKKASVEIDRKILADIAVFDKVAFTALVEKAKAALA
X	X	X	X	X	X	L21p	11562.9	11431.7	5781.4	5715.8	MYAVFQSGGKQHRVSEGQTVRLEKLDIATGEAVEFAEVLMIANGEEIKIGVPFVEGGVIKAEVVAHGRGEKVKIVKFRRRKHYRKQQGHRQWFTDVKITGISA

X	X	X	X	X	X	L22p (L17e)	12196.6	12065.4	6098.3	6032.7	METLAQHRHARSSAQKVRLVADLIRGKKVSQALDILTYTNKKAAVLVKKVLESAIANAEHNDGADIDDLKVAKIFVDEGPSMKRIMPRAKGRADRILKRTSHITVVVSDR
X	X	X	X	X	X	L23p (L23Ae)	11213.6	11082.4	5606.8	5541.2	MIREERLLKVLRAPHVSEKASTAMEKTNTIVLKVAKDATKAEIKAAVQKLFEVEVEVVNTLVVKGKVKRHGQRIGRRSDWKKAYVTLKEGQNLDFVGGAE
X	X	X				L24p (L26e)	11316.7	11185.5	5658.3	5592.7	MAAKIRRDDEVIVLTGKDKGKRGKVKNVLSSGKVIVEGINLVKKHQKPVPALNQPGGIVEKEAAIQVSNVAIFNAATGKADRVGFRFEDGKKVRFFKSNSETIK
			X	X	X	L24p (L26e)	11344.7	11213.5	5672.4	5606.8	MAAKIRRDDEVIVLTGKDKGKRGKVKNVLSSGKVIVEGINLVKKHQKPVPALNQPGGIVEKEAAIQISNLAIFNAATGKADRVGFRFEDGKKVRFFKSNSETIK
X		X	X	X	X	L25p	10618.7	10487.5	5309.3	5243.7	MFTINAEVRKEQGKGASRRLRAANKFPAIIYGGEAAPVAIELDHDKLWNIQDKAEFYGEVVTLVIDGKEEKVKVQAVQRHAFKPKLTHIDFVRA
	X					L25p	14811.6	14680.4	7405.8	7340.2	MIARVSFGGYNAARFCIRKADNPPVAGSPVAGFIYRETSMFTINAEVRKEQGKGASRRLRAANKFPAIIYGGEAAPVAIELDHDKVWNMQDKAEFYSEVLTVVVDGKEEKVKVQAVQRHAFKPKLTHIDFVRA
X	X	X	X	X	X	L27p	9123.9	8992.7	4562.0	4496.4	MAHKKAGGSTRNGRDSEAKRLGVKRFGGEAVLAGSIIVRQRGTKFHAGTNVGCGRDHTLFALTDGKVKFEVKGPKNRKFISIVAE
X	X	X				L28p @ LSU	9006.8	**8875.6**	4503.4	**4437.8**	MSRVCQVTGKRPVTGNNRSHALNATKRRFLPNLHSHRFWVESEKRFVTLRVSAKGMRVIDKKGIDTVLAELRARGEKY
			X	X	X	L28p @ LSU	9022.8	**8891.6**	4511.4	**4445.8**	MSRVCQVTGKRPVTGNNRSHALNATKRRFLPNLHSHRFWVESEKRFVTLRVSAKGMRVIDKKGIDTVLSELRARGEKY
X	X	X	X	X	X	L29p (L35e)	7243.7	7112.5	3621.9	3556.3	MKAKELREKSVEELNAELLNLLREQFNLRMQAASGQLQQTHLLKQVRRDVARVKTLLTQKAGA
X	X	X	X	X	X	L2p (L8e)	29835.6	29704.4	14917.8	14852.2	MAVVKCKPTSPGRRHVVKVVNPELHKGKPFAPLLEKNSKSGGRNNNGRITTRHIGGGHKQAYRIVDFKRNKDGIPAVVERLEYDPNRSANIALVLYKDGERRYILAPKGLKAGDQIQSGVDAAIKAGNTLPMRNIPVGSTVHNVEMKPGKGGQLARSAGTYVQIVARDGAYVTLRLRSGEMRKVEADCRATLGEVGNAEHMLRVLGKAGAARWRGVRPTVRGTAMNPVDHPHGGGEGRNFGKHPVSPWGLQTKGKKTRSNKRTDKFIVRRRSK
X	X	X	X	X	X	L30p (L7e)	6514.0	6382.8	3257.0	3191.4	MAKTIKITQTRSAIGRLPKHKATLLGLGLRRIGHTVEREDTPAVRGMVNAVSFMVKVEE
X	X	X				L31p @ LSU	**7742.2**	7611.0	**3871.1**	3805.5	MKKGIHPNYDEITATCSCGNVMKIRSTVGHDLNLDVCGKCHPFFTGKQRDVATGGRVDRFNKRFSIPGSK
			X	X	X	L31p @ LSU	**7770.3**	7639.1	**3885.2**	3819.6	MKKGIHPKYEEITATCSCGNVMKIRSTVGHDLNLDVCGKCHPFFTGKQRDVATGGRVDRFNKRFSIPGSK
X	X	X				L31p @ LSU	9944.6	9813.4	4972.3	4906.7	MKAHIHPPYRTVVFHDTSANEYFKVGSTIRTDRVIELDGETFPYVTIDVSSKSHPYYTGKQKTFANEGSAARFRQRFGGFIDAKRKA
			X	X	X	L31p @ LSU	9945.6	9814.4	4972.8	4907.2	MKAHIHPPYRTVVFHDTSVNEYFKVGSTIRTDRVIELDGETFPYVTIDVSSKSHPYYTGKQKTFASEGSAARFRQRFGGFIDAKRKA
			X	X	X	L32p	19341.6	19210.4	9670.8	9605.2	MQKVKLPLTLDPVRTAQKRLDYEGIYARDQVERVADSVVSVDSDVECSMSFAIDNQRLAVITGDAKVTVTLECQRCGKPFPHHVHTTYCFSPVRNDEQAEALPEAYEPIEVNEFGEIDLQAMVEDEIILSLPVVPVHDSEHCEVSDADMVFGELPEEAQKPNPFAVLASLKRK
X	X	X				L32p	19361.6	19230.4	9680.8	9615.2	MQKVKLPLTLDPVRTAQKRLDYEGIYARDQVERVTDSVVSVDSDVECSMSFAIDNQRLAVITGDAKVTVTLECQRCGKPFSHHVHTTYCFSPVRNDEQAEALPEAYEPIEVNEFGEIDLQAMVEDEIILSLPVVPVHDSEHCEVSDADMVFGELPEEAQKPNPFAVLASLKRK
X	X	X	X	X	X	L32p @ LSU	6430.6	6299.4	3215.3	3149.7	MAVQQNKPTRSKRGMRRSHDALTAVTSLSVDKTSGEKHLRHHITADGFYRGRKVIAK
X	X	X	X	X	X	L33p @ LSU	6405.9	6274.7	3202.9	3137.3	MAKGIREKIKLVSSAGTGHFYTTTKNKRTKPEKMELKKYDPVVRQHVIYKEAKIK
X	X	X	X	X		L34p	5380.6	5249.4	2690.3	2624.7	MKRTFQPSVLKRNRSHGFRARMATKNGRQVLARRRAKGRARLTVSK
X	X	X	X	X	X	L35p	7289.2	7158.0	3644.6	3579.0	MPKIKTVRGAAKRFKKTGKGGFKHKHANLRHILTKKATKRKRHLRPKAMVSKGDLGLVIACLPYA
			X		X	L36p @ LSU	4364.5	4233.3	2182.2	2116.6	MKVRASVKKLCRNCKIVKRDGVIRVICSAEPKHKQRQG
X	X		X	X	X	L36p @ LSU	5465.8	5334.6	2732.9	2667.3	MQVVNSLRSAKQRHPDCQLVKRKGRLYVICKSNPRFKAVQGRKKRR
		X				L36p @ LSU	6690.1	6558.9	3345.0	3279.4	MQVVNSLRSAKQRHPDCQLVKRKGRLYVICKSNPRFKAVQGRKNAVNGNSPASGAVGRRR
X	X	X	X	X	X	L3p (L3e)	22239.5	22108.3	11119.7	11054.1	MIGLVGKKVGMTRIFTEDGVSIPVTVIEVEANRVTQVKDLANDGYRAIQVTTGAKKANRVTKPEAGHFAKAGVEAGRGLWEFRLADGEEFTVGQNISVELFADVKKVDVTGTSKGKGFAGTVKRWNFRTQDATHGNSLSHRVPGSIGQNQTPGKVFKGKKMAGQLGNERVTVQSLDVVRVDAERNLLLVKGAVPGATGSDLIVKPAVKA
X	X	X	X	X	X	L4p (L1e)	22114.4	21983.2	11057.2	10991.6	MELVLKDAQSALTVSETTFGRDFNEALVHQVVVAYAAGARQGTRAQKTRAEITGSGKKPWRQKGTGRARSGSIKSPIWRSGGVTFAARPQDHSQKVNKKMYRGALKSILSELVRQDRLIVVEKFSVEAPKTKLLAQKLKDMALEDVLIITGELDENLFLAARNLHKVDVRDANGIDPVSLIAFDKVVMTADAVKQVEEMLA
			X	X	X	L5p (L11e)	20275.2	20144.0	10137.6	10072.0	MAKLHDYYKDEVVAKLMTEFNYNSVMQVPRVEKITLNMGVGEAIADKKLLDNAAADLTAISGQKPLITKARKSVAGFKIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKSFDGRGNYSMGVREQIIFPEIDYDKVDRVRGLDITITTTAKSDEEGRALLAAFDFPFRK

X	X	X				L5p (L11e)	20302.3	20171.1	10151.1	10085.5	MAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEKITLNMGVGEAIADKKLLDNAAADLAAISGQKPLITKARKSVAGFKIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKSFDGRGNYSMGVREQIIFPEIDYDKVDRVRGLDITITTTAKSDEEGRALLAAFDFPFRK
X	X	X				L6p (L9e)	18844.5	18713.3	9422.3	9356.7	MSRVAKAPVVVPAGVDVKINGQVITIKGKNGELTRTLNDAVEVKHADNALTFGPRDGYADGWAQAGTARALLNSMVIGVTEGFTKKLQLVGVGYRAAVKGNVVNLALGFSHPVDHQLPAGITAECPTQTEIVLKGADKQVIGQVAADLRAYRRPEPYKGKGVRYADEVVRTKEAKKK
			X	X	X	L6p (L9e)	18873.6	18742.4	9436.8	9371.2	MSRVAKAPVVVPAGVDVKVNGQVITIKGKNGELTRTLNDAVEVKHADNALTFGPRDGYVDGWAQAGTARALLNSMVIGVTEGFTKKLQLVGVGYRAAVKGDVVNLALGFSHPVEHKLPAGITAECPTQTEIVLKGADKQVIGQVAADLRAYRRPEPYKGKGVRYADEVVRTKEAKKK
X	X	X	X	X	X	L7p/L12p (P1/P2)	12341.7	12210.5	6170.8	6105.2	MSITKDQIIEAVSAMSVMDVVELISAMEEKFGVSAAAAVAVAAGPVEAAEEKTEFDVILKAAGANKVAVIKAVRGATGLGLKEAKDLVESAPAALKEGISKDDAEALKKSLEEAGAEVEVK
			X	X	X	L9p	15752.7	15621.5	7876.3	7810.7	MQVILLDKVANLGSLGDQVNVKAGYARNFLVPQGKAVPATKKNVEFFEARRAELEAKLADVLSAAEARAAQINALESVTIASKAGDEGKLFGSIGTRDIADAVTAAGVKVAKSEVRLPNGVLRNVGEHEVDFQVHSEVFAKVIINVVAE
X	X	X				L9p	15793.7	15662.5	7896.9	7831.3	MQVILLDKVANLGSLGDQVNVKAGYARNFLVPQGKAVPATKKNVEFFEARRAELEAKLADVLAAAEARAEQINALESVTIASKAGDEGKLFGSIGTRDIADAVTAAGVKVAKSEVRLPNGVLRNVGEHEVNFQVHSEVFAKVIINVVAE
X	X	X	X	X	X	S10p (S20e)	11767.0	11635.8	5883.5	5817.9	MQNQRIRIRLKAFDHRLIDQSTAEIVETAKRTGAQVRGPIPLPTRKERFTVLISPHVNKDARDQYEIRTHKRLVDIVEPTEKTVDALMRLDLAAGVDVQISLG
X	X	X			X	S11p (S14e)	4880.9	4749.7	2440.5	2374.9	MVKGPGPGRESTIRALNAAGFRITNITDVTPIPHNGCRPPKKRRV
			X			S11p (S14e)	11741.9	11610.7	5870.9	5805.3	MAHIHASFNNTIVTITDRQGNALGWATAGGSGFRGSRKSTPFAAQVAAERCAEAVKEYGIKNLEVMVKGPGPGRESTIRALNAAGFRITNITDVTPIPHNGCRPPKKRRV
X	X	X	X	X	X	S12p (S23e)	13751.6	13620.4	6875.8	6810.2	MATINQLVRKPRARKVAKSNVPALEACPQKRGVCTRVYTTTPKKPNSALRKVCRVRLTNGFEVTSYIGGEGHNLQEHSVILIRGGRVKDLPGVRYHTVRGALDCSGVKDRKQARSKYGVKRPKA
X	X	X	X	X	X	S13p (S18e)	13211.0	13079.8	6605.5	6539.9	MARIAGINIPDHKHTVIALTAIFGIGKTRSKAICAETGIAENVKISELSEEQIDILREAVGKFVVEGDLRREITLSIKRLMDLGCYRGLRHRRGLPVRGQRTKTNARTRKGPRKPIKK
X	X	X	X	X	X	S14p (S29e) @ SSU	11578.9	11447.7	5789.4	5723.8	MAKQSMKAREVKRVALADKFFAKRAELKAIISDVNATDEDRWNAVLKLQTLPRDSSPSRQRNRCRQTGRPHGFLRKFGLSRIKVREAAMRGEIPGLKKASW
			X	X	X	S15p (S13e)	10193.1	**10061.9**	5096.6	**5031.0**	MSLSVEAKAKIVSEFGRGENDSGSTEVQVALLTAQINHLQGHFAEHKKDHHSRRGLLRMVSQRRKLLDYLKRKDVARYAALIERLGLRR
X	X	X				S15p (S13e)	10209.1	**10077.9**	5104.6	**5039.0**	MSLSVEAKAKIVSEFGRGENDSGSTEVQVALLTAQINHLQGHFAEHKKDHHSRRGLLRMVSQRRKLLDYLKRKDVARYSALIERLGLRR
			X	X	X	S16p	9048.7	8917.5	4524.4	4458.8	MVTIRLARHGAKKRPFYQVVVTDSRNARNGRFIERVGFFNPIASGAEEETRLDLDRIAHWVGLGATVSDRVAALIKAANKAA
X	X	X				S16p	9090.7	8959.5	4545.4	4479.8	MVTIRLARHGAKKRPFYQVVVTDSRNARNGRFIERVGFFNPIANGAEEETRLDLDRIAHWVGQGATVSDRVAALIKAANKAA
			X	X	X	S17p (S11e)	9674.8	9543.6	4837.4	4771.8	MTDKIRTLQGRVVSDKMEKSIVVAIERMVKHPVYGKFIKRTTKLHVHDENNECGIGDVVEIRECRPLSKTKSWTLVRVVEKAVL
X	X	X				S17p (S11e)	9703.9	9572.7	4851.9	4786.3	MTDKIRTLQGRVVSDKMEKSIVVAIERMVKHPVYGKFIKRTTKLHVHDENNECGIGDKVEIRECRPLSKTKSWTLVRVVEKAVL
X	X	X	X	X	X	S18p @ SSU	8986.7	8855.5	4493.4	4427.8	MARYFRRRKFCRFTAEGVQEIDYKDIATLKNYITESGKIVPSRITGTRAKYQRQLARAIKRARYLSLLPYTDRHQ
X	X	X	X	X	X	S19p (S15e)	10416.7	10285.5	5208.3	5142.7	MPRSLKKGPFIDLHLLKKVEKAVESGDKKPLRTWSRRSTIFPNMIGLTIAVHNGRQHVPVFVSDEMVGHKLGEFAPTRTYRGHAADKKAKKK
X	X	X	X	X	X	S1p	61179.4	61048.2	30589.7	30524.1	MTESFAQLFEESLKEIETRPGSIVRGVVVAIDKDVVLVDAGLKSESAIPAEQFKNAQGELEIQVGDEVDVALDAVEDGFGETLLSREKAKRHEAWITLEKAYEDAETVTGVINGKVKGGFTVELNGIRAFLPGSLVDVRPVRDTLHLEGKELEFKVIKLDQKRNNVVVSRRAVIESENSAERDQLLENLQEGMEVKGIVKNLTDYGAFVDLGGVDGLLHITDMAWKRVKHPSEIVNVGDEITVKVLKFDRERTRVSLGLKQLGEDPWVAIAKRYPEGTKLTGRVTNLTDYGCFVEIEEGVEGLVHVSEMDWTNKNIHPSKVVNVGDVVEVMVLDIDEERRRISLGLKQCKSNPWQQFAETHNKGDRVEGKIKSITDFGIFIGLDGGIDGLVHLSDISWNVAGEEAVREYKKGDEIAAVVLQVDAERERISLGVKQLAEDPFNNYVALNKKGAIVVGKVTAVDAKGATVELADGVEGYLRASEASRDRVEDATLVLSVGDEVEAKFTGVDRKNRVVSLSVRAKDEAEEKDAIATVNKQEDANFSNNAMAEAFKAAKGE
	X		X	X	X	S20p	6735.2	6604.0	3367.6	3302.0	MMRTFIKKVYAAIEAGDKAAAQKAFNEMQPIVDRQAAKGLIHKNKAARHKANLTAQINKLA
X	X	X	X	X	X	S21p	8500.2	8369.0	4250.1	4184.5	MPVIKVRENEPFDVALRRFKRSCEKAGVLAEVRRREFYEKPTTERKRAKASAVKRHAKKLARENARRTRLY
X	X	X				S2p (SAe)	26700.6	26569.4	13350.3	13284.7	MATVSMRDMLKAGVHFGHQTRYWNPKMKPFIFGARNKVHIINLEKTVPMFNEALAELNKIAARKGKILFVGTKRAASEAVKDAALSCDQFFVNHRWLGGMLTNWKTVRQSIKRLKDLETQSQDGTFDKLTKKEALMRTRELDKLENSLGGIKDMGGLPDALFVIDADHEHIAIKEANNLGIPVFAIVDTNSDPDGVDFVIPGNDDAIRAVSLYLGAVAATVREGRSQDLASQAEESFVEAE
			X	X	X	S2p (SAe)	26731.5	26600.3	13365.8	13300.2	MATVSMRDMLKAGVHFGHQTRYWNPKMKPFIFGARNKVHIINLEKTVPMFNEALAELNKISARKGKILFVGTKRAASEAVKEAANSCDQFFVNHRWLGGMLTNWKTVRQSIKRLKDLETQSQDGTFDKLTKKEALMRTRELDKLENSLGGIKDMGGLPDALFVIDADHEHIAIKEANNLGIPVFAIVDTNSDPDGVDFVIPGNDDAIRAVSLYLGAVAATVREGRSQDLASQAEESFVEAE

X	X	X	X	X	X	S3p (S3e)	25840.1	25708.9	12920.0	12854.4	MGQKVHPNGIRLGIVKPWNSTWFANTKEFADNLDSDFKVRQFLTKELAKASVSRIVIERPAKSIRVTIHTARPGIVIGKKGEDVEKLRKVVADIAGVPAQINIAEVRKPELDAKLVADSITSQLERRVMFRRAMKRAVQNAMRLGAKGIKVEVSGRLGGAEIARTEWYREGRVPLHTLRADIDYNTSEAHTTYGVIGVKVWIFKGEILGGMAAVEQPEPAAQPKKQQRKGRK
X	X	X	X	X	X	S4p (S9e) @ SSU	23503.0	23371.8	11751.5	11685.9	MARYLGPKLKLSRREGTDLFLKSGVRAIDTKCKIEQAPGQHGARKPRLSDYGVQLREKQKVRRMYGVLERQFRNYYKEAARLKGNTGENLLALLEGRLDNVVYRMGFGATRAEARQLVSHKAIMVNGRVVNIASYQVKANDVVSIREKAKKQSRVKAALELAEQREKPTWLEVDAGKMEGTFKRQPERSDLSADINEHLIVELYSK
			X	X	X	S5p (S2e)	17604.2	17473.0	8802.1	8736.5	MAHIEKQAGELQEKLIAVNRVSKTVKGGRIFSFTALTVVGDGNGRVGFGYGKAREVPAAIQKAMEKARRNMINVALNNGTLQHPVKGVHTGSRVFMQPASEGTGIIAGGAMRAVLEVAGVHNVLAKAYGSTNPINVVRATIDGLENMNSPEMVAAKRGKSVEEILGK
X	X	X				S5p (S2e)	17648.3	17517.1	8824.1	8758.5	MAHIEKQAGELQEKLIAVNRVSKTVKGGRIFSFTALTVVGDGNGRVGFGYGKAREVPAAIQKAMEKARRNMINVALNHGTLQHPVKGTHTGSRVFMQPASEGTGIIAGGAMRAVLEVAGVRNVLAKAYGSTNPINVVRATIDGLENMKSPDMVAAKRGKSVEEILGK
			X	X	X	S6p	15099.4	14968.2	7549.7	7484.1	MRHYEIVFMVHPDQSEQVPGMIERYTGAITAAAGTIHRLEDWGRRQLAYPINKLHKAHYVLLNVEAPQEAIDELETNFRFNDAVIRSMVMRTKHAVTEASPMVKAKDERRERREDFANETADDSEAGDSEE
X	X	X				S6p	15117.5	14986.3	7558.7	7493.1	MRHYEIVFMVHPDQSEQVPGMIERYTGAITAAAGTIHRLEDWGRRQLAYPINKLHKAHYVLMNVEAPQEAIDELETNFRFNDAVIRSMVMRTKHAVTEASPMVKAKDERRERREDFANETADDSEAGDSEE
			X	X	X	S7p (S5e)	17602.0	17470.8	8801.0	8735.4	MPRRRVIGQRKILPDPKFGSELLAKFVNILMVDGKKSTAEAIVYSALETLAQRSGKNELEAFEVALDNVRPTVEVKSRRVGGSTYQVPVEVRPVRRNALAMRWIVEAARKRGDKSMALRLANELTDAADNKGTAVKKREDVHRMAEANKAFAHYRW
X	X	X				S7p (S5e)	17619.0	17487.8	8809.5	8743.9	MPRRRVIGQRKILPDPKFGSELLAKFVNILMVDGKKSTAETIVYSALETLAQRSGKSELEAFEVALENVRPTVEVKSRRVGGSTYQVPVEVRPVRRNALAMRWIVEAARKRGDKSMALRLANELTDAADNKGTAVKKREDVHRMAEANKAFAHYRW
X	X	X				S8p (S15Ae)	14099.1	13967.9	7049.5	6983.9	MSMQDPIADMLTRIRNGQAANKAAVTMPSSKLKVAIANVLKEEGFIEDFKVEGDTKPELELTLKYFQGKAVVESIQRVSRPGLRIYKKKDELPKVMAGLGIAVVSTSKGVMTDRAARQAGLGGEIICYVA
			X	X	X	S8p (S15Ae)	14139.1	14007.9	7069.6	7004.0	MSMQDPIADMLTRIRNGQAANKAAVTMPSSKLKVAIANVLKEEGFIEDFKVEGDIKPELELTLKYFQGKAVVESIQRVSRPGLRIYKRKDELPKVMAGLGIAVVSTSKGVMTDRAARQAGLGGEIICYVA
			X	X	X	S9p (S16e)	14826.7	14695.5	7413.4	7347.8	MAENQYYGTGRRKSSAARVFIKPGNGKIVINQRSLEQYFGRETARMVVRQPLELVDMVEKLDLYITVKGGGISGQAGAIRHGITRALMEYDESLRGELRKAGFVTRDARQVERKKVGLRKARRRPQFSKR
X	X	X				S9p (S16e)	14856.8	14725.6	7428.4	7362.8	MAENQYYGTGRRKSSAARVFIKPGNGKIVINQRSLEQYFGRETARMVVRQPLELVDMVEKLDLYITVKGGGISGQAGAIRHGITRALMEYDESLRSELRKAGFVTRDARQVERKKVGLRKARRRPQFSKR

Characteristics of ribosomal proteins. Calculated mass peak positions of native and de-methionated (dMet) form of single (*m/z*) charged ribosomal proteins extracted from the annotated genome sequences of *K. pneumoniae* (ID 1) and *K. variicola* (ID 2) isolates and references. Half of *m*/*z* values were used as an approximation for double charged (*m*/2*z*) ions. “X” denotes the presence of the gene in an isolate or reference genome, which encodes the ribosomal protein with the amino acid sequence shown. Peak positions in the shaded boxes correspond to the observed specific MALDI-TOF mass peaks.

Table S5

Isolate	Protein	MW	Amino Acid Sequence
K. pneumoniae (ID 1)	Transposase, IS3/IS911 family	8000.56	MPIVKDVCREAGISEASYNNWREKFGGMEACDIKKMKDFEDENRRLKQMFAELSLECRALKDIIEKKL
K. variicola (ID 2)	hypothetical protein	8014.55	MYNFFHNDMYSETVYFFVLILFIDFKGIFDFINLYKKAVLCRMRIQGNQTGDNDADPIGIRALSVYVT
K. pneumoniae (ID 1)	hypothetical protein	8015.47	MIPKTYQQWYRCITEECGIPLTQAFIASRLAVLESQDHQETRRFVSLYGQQHLNSVVQWFKKAGEELL
K. pneumoniae (ID 1)	Prophage P2 OGR protein	8024.46	MMNCPKCGHAAHTRSSFRVTDQTKERYCQCQNINCGTTFITHETVVRYIMTPGVIDNAPPHPTAAGQGHMNF
K. pneumoniae (ID 1)	Multiple antibiotic resistance protein MarB	8025.18	MKLFAAAAIVLLSLASSLSYAEQNTTPVRQNQRDTMIIPSEHNDSPFDFNHMAAGNDKSDELGVPYYQQHDL
K. variicola (ID 2)	FIG00731318: hypothetical protein	8032.79	MLAVLEFTNDRIKQNSILFIYKSRHIKDIASIDPILCILATNDNLYPPLRMKPLISRANLCMKIITSNNT
K. variicola (ID 2)	hypothetical protein	8053.49	MEKQPFTGGFRFCMLIKLRNEFYQVQCDAFGDLATDLLDIRPKILRAMSPDAKKSANSNAWFYGDETGVQG
K. variicola (ID 2)	Uncharacterized protein YtfK	8053.99	MKIFQRYNPLQVAKYVKILFRGRLYIKDVGAFEFDKGKILIPKVKDKLHLSVMSEVNRQVLRLQTEMA
K. pneumoniae (ID 1)	Uncharacterized protein YtfK	8053.99	MKIFQRYNPLQVAKYVKILFRGRLYIKDVGAFEFDKGKILIPKVKDKLHLSVMSEVNRQVLRLQTEMA
K. pneumoniae (ID 1)	possible secretory protein	8061.8	MTLERISAFITYCIAVLLAWMGDLSLKDVSTVGGVLIGVLMLAINWYYKHKTYQLLRGGKITQGEYESFNR
K. pneumoniae (ID 1)	FIG00731318: hypothetical protein	8075.78	MLAVLEFTNDRIKQNSILFIYKSRHIHDIASIDPIFCILATNDNLYPPLRMKPLISRANLCMKIITSNNT
K. pneumoniae (ID 1)	Putative cytoplasmic protein USSDB7A	8088.32	MYQILDAGVESEYFNIILENVKVTGITPNLFPDSGTGTHSETIQLRYEAITWKHCDGNIIYKDSWNHRATA
K. pneumoniae (ID 1)	FIG00732958: hypothetical protein	8106.59	MTHYRFPNVRRENSRLSYTKLRHQARLYGNFFHLFCLYGNDCVAALSITKTLNLLIWKGYDSTRSSIF
K. variicola (ID 2)	hypothetical protein	8113.93	MPGMLYRRNAREKCYFAIGNLKIFHDAKYTFLFCGFIFDLFRVYLTDKDGFLFIVMAWRNKALAGKCR
K. pneumoniae (ID 1)	hypothetical protein	8119.19	MKIKCIKDTEGYWTEGEMYPARVVAGGFVQVGDDDDPNGEGWSAAPMEYREDGSIVYQVGGIEGDVLFEEASHD
K. variicola (ID 2)	Integrase, catalytic region	8122.42	MNKRGNCQDNAVAELFFSSLKKERISKRIYKNRDLARADVFDYIKVFYNRARRHSHPGGVSPEAFEQASS
K. variicola (ID 2)	Integrase, catalytic region	8123.36	MNKRGNCQDNAVAELFFSSLKKERISKRIYKNRDLARADVFDYIEVFYNRARRHSHPGGVSPEAFEQASS
K. variicola (ID 2)	Uncharacterized protein YbfA	8129.88	MMALYKAYPAHIILLRRAFAVVAGVAALPVMLFWKDRARYYSWLHRVWSKTSEQPVWMAQAEKAAHDFY
K. pneumoniae (ID 1)	Uncharacterized protein YbfA	8129.88	MMALYKAYPAHIILLRRAFAVVAGVAALPVMLFWKDRARYYSWLHRVWSKTSEQPVWMAQAEKAAHDFY
K. pneumoniae (ID 1)	Prevent host death protein, Phd antitoxin	8133.39	MRTVNYSEARQNLADVLESAVTGVPVTITRRGHKSAVIISAEEFERYQAARIDDEFAAIMAVHGDEIRELADK
K. variicola (ID 2)	FIG00798715: hypothetical protein	8133.83	KRQFLASGYMHLPGKKIVSVTASHDELTPLARKLAQSLFRQAKKHFDRLHAQDQIKRKARRERLRELKV
K. pneumoniae (ID 1)	hypothetical protein	8140.55	MRASVIAFGSLLIQQYAHNQQYGHAHRHNTDINNHSVRQKLQLNGYGGQVKAHLIVVKECTLPTSIEQTFID
K. variicola (ID 2)	hypothetical protein	8158.69	MSSYDSRVQLTSKSSVIYKFLVHADSPQGARVKVQNHLRKLGDFDFSEICISSMEVRGDVLLLNPDGTKCLII
K. variicola (ID 2)	Prevent host death protein, Phd antitoxin	8165.45	MRTVNYSEARQNLADVLESAVTGIPVTITRRGHKSAVIISAEEFERYQAARMDDEFAAIMAVHGDEIRELADK
K. variicola (ID 2)	FIG00732852: hypothetical protein	8165.61	MMQRCLNDDDREWIRHHRNQCLKKAQRPPAPKEEFADLHQAAKETQYRMGIAKPYGEAFRLPGKGKTAAE
K. pneumoniae (ID 1)	hypothetical protein	8172.51	RGPGAAESGAARPVGFVGRLLDDPTGIVAARSLSPVRVQARRNEAEDPLADAIREIDAPIWIGDRHWGAIRMGYRP
K. pneumoniae (ID 1)	FIG00732852: hypothetical protein	8180.62	MMQRCLDDEDREWIRHHRNQCLKKAQRPPAPKEEFADLHQAAKETQYRMGIAKPYGEAFRLPGKGKTAAE

K. variicola (ID 2)	hypothetical protein	8186.54	MKQQFSTASNYSEACDMLRSGYVKHVRLNWNIGSDEFFRIASDWCDTGAKIKKDEDGFIISLKGFPIPRQH
K. pneumoniae (ID 1)	hypothetical protein	8186.54	MKQQFSTASNYSEACDMLRSGYVKHVRLNWNIGSDEFFRIASDWCDTGAKIKKDEDGFIISLKGFPIPRQH
K. variicola (ID 2)	hypothetical protein	8187.79	MCTPKIINQLLNKSYDNSLYLTTSYVNETIQHRREYHERCIGHTKIDMHQVLSRIFSAKPISVGIKKPAR
K. variicola (ID 2)	hypothetical protein	8189.73	MHHHPVKSSRIISVAYDDASATLEIYFYHQPPLQYTGVPPRIFRDFLQVVSKGRFYDGVIKGKFPERKPR
K. variicola (ID 2)	hypothetical protein	8190.17	MIAKQGKNQKWHFSHSTEVKGVCSELTLQHIKKYIKVKIQEKNTLLFLIFCKVRSKGSLTSKISLVVGLFVA
K. variicola (ID 2)	hypothetical protein	8192.81	MQTDHRIYPIAPLFCRVALHLPDQADAPTVKKDSRWLSFLFGDGMSRCRVIFIQHGSRICAGWRLTPYPAY
K. variicola (ID 2)	hypothetical protein	8196.74	MSTPDFSTAENNQELAQEVSCLKAMITLMLQAMGQADAGRVIIKMEKQIAQMEDEAQAAVFSSTVKQIKQAYRQ
K. variicola (ID 2)	hypothetical protein	8197.7	MKKSWFLHEQLSEAEATELVERYRKNNCVVEKSLSRDFASWEIRVLLPESKKPPRIDRTYIQKMWRD
K. pneumoniae (ID 1)	Putative inner membrane protein STM3160	8199.96	MNLLFCTSAPPIQAKILPGPRLAAFLLRKRKENKRDLLHSVNTNENHYQFDVVLILLWADFVIIVVEIERG
K. pneumoniae (ID 1)	hypothetical protein	8200.68	MDLSAGQTPGFGALVDELPPATQPLSNPASTSAIAPCLNVIFAILIVISQEISADFQIISKGYNIPARHQAIKSPPAAGS
K. pneumoniae (ID 1)	hypothetical protein	8202.73	MHHHPVKSSRIISVAYDDASATLEIYFYHQPPLQYTGVPPRIFHDFLQVVSKGRYYDGVIKGKFPERKLR
K. variicola (ID 2)	UPF0370 protein YpfN	8212.75	MEWLIKHWWILVLVFLVGVIINVIKDLNRVDHKKFLNNKPDLPPHRDFNDKWDDDDDWPKHDQSKKP
K. pneumoniae (ID 1)	UPF0370 protein YpfN	8212.75	MEWLIKHWWILVLVFLVGVIINVIKDLNRVDHKKFLNNKPDLPPHRDFNDKWDDDDDWPKHDQSKKP
K. variicola (ID 2)	hypothetical protein	8212.91	MKIEFNDKGVIATATITSTVFEFRLHNRAVDTALFLAPSVRAKRSGFFILKTVITGKTSHVLRAYKAIKAEASR
K. variicola (ID 2)	UPF0337 protein YjbJ	8216.46	MNKDEIGGNWKQLKGKAKEQWGKLTDDDMTVIEGKRDQLVGKIQERYGYAKDQAEKEVSDWEHKNDYRW
K. variicola (ID 2)	IS1 protein InsA	8218.84	MRNGKSTAGHQRYLCSHCRKTWQLTFTYAASQPGTHQKIIDMAMNGVGCRATARLMGVGLNTILRHLKNSGRSQ
K. variicola (ID 2)	Hnh endonuclease	8225.84	MSKQDYFENSLDVEENIISLCCNCHKQIHLGKGFEDMLRKIYAERKDVLKKAGIEILLEDLILFYKMEGN
K. pneumoniae (ID 1)	hypothetical protein	8226.85	MSTPDFSTAENKQELAQEVSCLKAMITLMLQAMGQADAGRVIIKMEKKISQMEDEAQAAVFSSTVKQIKQAYRQ
K. variicola (ID 2)	hypothetical protein	8228.67	MREIPDCPICGSAAEFYFRDYQAGACSGALRCPYGHLRVQDSYWAGGKSKSKIRLIEKWSQQVEQKKGEVKNG
K. variicola (ID 2)	Protein nifT	8228.7	MPIVIFRERGEALYAYIAKQDLEARVLQVEHDETDRWGGAIALEGGRRYYVNPQPGRPVFPISLRATRSTLL
K. variicola (ID 2)	Putative outer membrane lipoprotein STM0080	8234.52	MRNNILVASALAATAIMFVAGCSSNQSIKTTDGKTIVTSGKPQVDDDTGLVSYKNAETGRVEQINRDQVKSMDELDN
K. pneumoniae (ID 1)	Putative outer membrane lipoprotein STM0080	8234.52	MRNNILVASALAATAIMFVAGCSSNQSIKTTDGKTIVTSGKPQVDDDTGLVSYKNAETGRVEQINRDQVKSMDELDN
K. variicola (ID 2)	hypothetical protein	8236.82	MGIVKISDLLHDDIRDASKAMSRSVNAQAEYWIRLGMMSELYPELNHQQIKLLMLKSGSDRLLEVINAINNH
K. pneumoniae (ID 1)	hypothetical protein	8236.82	MGIVKISDLLHDDIRDASKAMSRSVNAQAEYWIRLGMMSELYPELNHQQIKLLMLKSGSDRLLEVINAINNH
K. variicola (ID 2)	Uncharacterized protein YncJ	8239.47	MSALLLLCALFSGHLLAHRQGHDYFPVQSLEQQLLHEADSDELRSQCEEAAADLNEHHRWQDARKPRAPHCP
K. variicola (ID 2)	Uncharacterized protein YpeB	8244	MDKAQLVEIANTEMPFGKYKGRRLIDVPEEYLLWFARKDQFPAGHLGELMALTLLIKTEGLSDLVQPLKKAR
K. pneumoniae (ID 1)	Uncharacterized protein YpeB	8244	MDKAQLVEIANTEMPFGKYKGRRLIDVPEEYLLWFARKDQFPAGHLGELMALTLLIKTEGLSDLVQPLKKAR
K. variicola (ID 2)	Phage protein	8245.68	MPFLDVTDVLLDPDFVDLSLVCYRQVQTVDEDNFPTNTAQAIPFSGVVTVDRSLEAKRMAAGQNINGAILIVTQF
K. variicola (ID 2)	Phage protein	8245.68	MPFLDVTDVLLDPDFVDLSLVCYRQVQTVDEDNFPTNTAQAIPFSGVVTVDRSLEAKRMAAGQNINGAILIVTQF
K. pneumoniae (ID 1)	Uncharacterized protein YodD	8248.22	MMKHQLTGQTGDDLDVNVDALLAAINEISESEVHRTLDDPQRASIDGRGSHTWRELAEAFELDIHDFSASEANR

K. variicola (ID 2)	Translation initiation factor 1	8249.89	MAKEDNIEMQGTVLETLPNTMFRVELENGHVVTAHISGKMRKNYIRILTGDKVTVELTPYDLSKGRIVFRSR
K. pneumoniae (ID 1)	Translation initiation factor 1	8249.89	MAKEDNIEMQGTVLETLPNTMFRVELENGHVVTAHISGKMRKNYIRILTGDKVTVELTPYDLSKGRIVFRSR
K. pneumoniae (ID 1)	Hypothetical Zinc-finger containing protein	8253.8	MADSMDLVQQRVEEERQRHIHTARSKAPGVSRVLCIECDAPIPPARRRAIPGAQCCVTCQEIAELKGKHYNGGAV
K. pneumoniae (ID 1)	hypothetical protein	8254.6	MMKKEINQNNTAEYLSVKQVTKGKDDCISNDYIIDCEMDINLNGGVKESVEINSSFTNDEGTVLFAYKLDVLVG
K. variicola (ID 2)	ATP synthase F0 sector subunit c (EC 3	8256.41	MENLNMDLLYMAAAVMMGLAAIGAAIGIGILGGKFLEGAARQPDLIPLLRTQFFIVMGLVDAIPMIAVGLGLYVMFAVA
K. pneumoniae (ID 1)	ATP synthase F0 sector subunit c (EC 3	8256.41	MENLNMDLLYMAAAVMMGLAAIGAAIGIGILGGKFLEGAARQPDLIPLLRTQFFIVMGLVDAIPMIAVGLGLYVMFAVA
K. variicola (ID 2)	mobilization protein mbeD	8261.55	MTELEKQLLSALEQLQQDYSKRLDEWENAFAEWRTMSGLMQRENAALSERVTGLSRQVQSLSEQLSWLSKG
K. pneumoniae (ID 1)	hypothetical protein	8263.19	MGAVFTRRVVAMKRSRTEVGRWRMLRQVNRRKARWLEAQSRRNMRILAIRKGLVKRQRHALLFIFPDS
K. variicola (ID 2)	hypothetical protein	8264.15	MHEHHKSSLLLVENQHWRRGMPQKYLLFGLVVICFTILLLTWMVRDSLCELQVRQGNIELVAFLACDIKQ
K. variicola (ID 2)	UPF0270 protein YheU	8278.65	MIIPWQDLDPETLDNLIESFVLREGTDYGEHERSLADKVADVKQQLKRGEAVLVWSELHETVNIMPRALFNG
K. variicola (ID 2)	Uncharacterized lipoprotein YgdI	8283.69	MKMTKAAAIISACMLTLGLSACSSNYVMHTNDGRTIVTDGKPQTDNDTGMISYKDAWGNKQQINRSDVKQLGELDE
K. pneumoniae (ID 1)	Uncharacterized lipoprotein YgdI	8283.69	MKMTKAAAIISACMLTLGLSACSSNYVMHTNDGRTIVTDGKPQTDNDTGMISYKDAWGNKQQINRSDVKQLGELDE
K. variicola (ID 2)	Putative outer membrane lipoprotein	8291.87	MRILSIIAMALLLSGCGSIISRTVPGQGHGNQYYPGVQWDVRDSAWRYLTVLDLPFSLVFDTLLLPLDASHGPYN
K. pneumoniae (ID 1)	UPF0270 protein YheU	8304.68	MIIPWQDLDPETLDNLIESFVLREGTDYGEYERSLADKVADVKQQLKRGEAVLVWSELHETVNIMPRALFNG
K. pneumoniae (ID 1)	UPF0337 protein YjbJ	8308.52	MNKDEIGGNWKQFKGKAKEQWGKLTDDDMTVIEGKRDQLVGKIQERYGYEKDQAEKEVSDWEHKNDYRW
K. pneumoniae (ID 1)	Putative outer membrane lipoprotein	8315.93	MRILPIIAMALLLSGCGSIISRTVPGQGHGNQYYPGVQWDVRDSAWRYLTILDLPFSLVFDTLLLPLDASHGPYN
K. variicola (ID 2)	hypothetical protein	8325.81	MEELKLHCHGCGGSFARDELQYRPSGRGAYRRDIYFCPVCNEKEKQKIALSAAASSFRKTLPSRPGHLANKRW
K. variicola (ID 2)	hypothetical protein	8329.14	MIVLKNFKMTLCLCSKKLLKRLLKQFDKWSLVRHRTGFDVLSVHGDEKEAKKKVEEILQQTRGSADDWFY
K. variicola (ID 2)	hypothetical protein	8349.25	MRDAFFIKALYFKENSFHTRGMDNEQIRFIKELPNQYTDWLRVKVRFCVVGIIFLFMMLSVFYLPLFI
K. variicola (ID 2)	hypothetical protein	8351.31	MEAVFTRRVVAMKRSRTEVGRWRMLRQVNRRKARWLEAQSRRNMRILAIRKGLVKRQRHALLFIFPDC
K. variicola (ID 2)	Protein SlyX	8355.82	MHDSTLETRLAELESRLAFQEITIEDLNKTVTAHEIEMAKMREHMRLMIEKLKATQPSHIASQAEETPPPHY
K. pneumoniae (ID 1)	Protein SlyX	8355.82	MHDSTLETRLAELESRLAFQEITIEDLNKTVTAHEIEMAKMREHMRLMIEKLKATQPSHIASQAEETPPPHY
K. pneumoniae (ID 1)	Ferrous iron transport protein A	8359.08	MQFTPDSAWKITGFSRDISPAYRQKLLSLGMLPGSSFHVVRVAPLGDPVHIETRRVSLVLRKKDLALIELEAVAQ
K. pneumoniae (ID 1)	Uncharacterized protein YdiE	8360.13	MIIIVALIFILRAMTRMDNTATAEKPKDNAPYPVATDREISSRVLLGSEGRVVIEHGGQRYLLRQTHAGKLILTK
K. variicola (ID 2)	Cytochrome c-type biogenesis protein CcmD, interacts with CcmCE	8363.85	MSPAFSSFAAFLNMGGYAVYVWLAVAVAVAAFGLLTVHTLWARRALFHEVRRQQARERRIAAAREHDKEAADASAS
K. variicola (ID 2)	Major outer membrane lipoprotein Lpp	8368.65	MNRTKLVLGAVILGSTLLAGCSSNAKIDQLSSDVQTLNAKVDQLSNDVNAIRSDVQAAKDDAARANQRLDNQAHSYRK
K. variicola (ID 2)	Uncharacterized protein YobH	8371.2	MRLIIRTIVVVAILWIGVLLSGYGVLFHSEENVGGLGLKCQYLTARGVSTALYVHSNSGVIGVSNCPILRKSATVVDNG
K. pneumoniae (ID 1)	Major outer membrane lipoprotein Lpp	8386.69	MNRTKLVLGAVILGSTLLAGCSSNAKIDQLSSDVQTLNAKVDQLSNDVNAMRSDVQAAKDDAARANQRLDNQAHSYRK
K. pneumoniae (ID 1)	Cardiolipin synthetase (EC 2	8387.41	SVSDSESLSDSESLSESDSLSESESLSESDSLSESESLSESESLSESESLSESESLSESESLSESESLSESESLSESESQ
K. variicola (ID 2)	hypothetical protein	8391.6	MLQRALGSGWGVVVPGVLIAALGYAGVSADVWRALVTVGMLMSAAMIWHRQLRHFILLPSCVALIGGIMLMILDFKLGG

K. variicola (ID 2)	Tautomerase PptA	8391.93	MPHVDIKCFPRELTDEQKTALAADITEVLIRHLNSKESAVSVALTQVEPDAWQAVWDSEIAPQMAQLIKKPGYSM
K. pneumoniae (ID 1)	Tautomerase PptA	8391.93	MPHVDIKCFPRELTDEQKTALAADITEVLIRHLNSKESAVSVALTQVEPDAWQAVWDSEIAPQMAQLIKKPGYSM
K. pneumoniae (ID 1)	Cytochrome c-type biogenesis protein CcmD, interacts with CcmCE	8393.88	MSPAFSSFAAFLNMGGYAVYVWLAVAVTVAAFGLLTVHTLWARRALFHEVRRQQARERRIAAAREHDKEAADASAS
K. variicola (ID 2)	hypothetical protein	8396.68	MSRDPPQRRGAARETAVPLTARRSLAGVQGAQGTARQGGASGTEAASLPLTLRHGMEARQGGDSLAGSVHDSPPGRPLQDLK
K. pneumoniae (ID 1)	Uncharacterized protein YobH	8403.22	MRLIIRTIILVAILWIGVLLSGYGVLFHSEENVGGLGLKCQYLTARGVSTALYVHSDSGVIGVSSCPLLRKSTTVVDNG
K. variicola (ID 2)	hypothetical protein	8403.89	MADITQEDEWVMEKGIVAKMYMTPRQIKSYREGRWIEGVHYKKHSPDPEASEGRVTLLYNYTRINRLVGET
K. variicola (ID 2)	hypothetical protein	8405.26	MQGCEQAMAVMQAKLPTRPFAGMTQIRFKGFGLRHLSPHGTPLGSAMLYDIHLLNTITALSCIAMAFFCDSQHFFV
K. variicola (ID 2)	hypothetical protein	8413.07	MKKECRVVIYKEGLLGSLFFGEAKADPDKMSQFLSSYTREGWEVKTMSVERRRTALFWSREAYLFVLERPL
K. variicola (ID 2)	Uncharacterized protein YoaF	8417.09	MKKLLAILPLVLAGCAQPQSTAPTKTIGMANPASVYCQQSGGTRVPVQTPQGVSTQCKLPSGETLDEWALWRRDHPAKS
K. variicola (ID 2)	Phage protein	8424.11	MKIEFKDQGSDSVITVTSTVFEFRRHNRAVDVALLLTTEMTSQRSGFFIMKTILSGKTHHVLRAYKHLLREAK
K. pneumoniae (ID 1)	FIG00731545: hypothetical protein	8428.98	MSRIAINHNRQCHSSSLLAMFCDQTNALRRGRRDGVQNSVMETTIAARATRIVTRPSVNMAPRFAVAQDCARRGAI
K. pneumoniae (ID 1)	FIG00731353: hypothetical protein	8432.01	MHIKNTIPAEFVFNSALMKNIENTLIKQHRTVNNERMITEIQHRLQTESNEILSDLYLQALDMLYSKKPHH
K. variicola (ID 2)	FIG00731353: hypothetical protein	8434.99	MHIKNTIPAEFVFNSALMKNIENTLMKQHSTINNERMITEIQHRLQTESNEILSDLYLQALDMLYSKKHHH
K. pneumoniae (ID 1)	Uncharacterized protein YoaF	8437.17	MKKLLAILPLVLAGCAQPQPTAPTKTIGMPNPAAVYCQQSGGTRVPVQTPQGVSTQCKLPSGETLDEWALWRRDHPAKS
K. pneumoniae (ID 1)	FIG00731602: hypothetical protein	8444.5	MTKGIKIFITVVFVILALLSGMMSFMIVGMGVSGSGCGQECFDNMDSAKFISIIFWILAIISGIFAFMDNGNPKKNPQ
K. variicola (ID 2)	hypothetical protein	8466.26	MNLYAFNPLKQNDKQEVLTPVAFNLVLSLPEQLLKRLDKVGYELVKRYGIAGCSDKQRHHIAIVHLLEKHTLR
K. variicola (ID 2)	hypothetical protein	8466.99	MTFYETIMLWFSTIVSALYLIAGGWVKIRDYIKAKAQAKSDAIEEEVQTRLKAAQAASADAPAATATSVAGPVAESKTAA
K. pneumoniae (ID 1)	putative ATP/GTP-binding protein remnant	8467.93	MRKPVYYAYVAQESHPDSQGEKNTWWTKVGVAFPHHGKSGLNIVLTPGIAVSGKLVLLEPREENNPPQNTGPIETVS
K. pneumoniae (ID 1)	hypothetical protein	8469.28	MHVNVYVEKSGRCFTDLLKKLYLFRFQVLLPSTLLVSSRLLTSEYKLRDLDQVLSLLIPFSWLLFDRFDQV
K. variicola (ID 2)	hypothetical protein	8472.42	MSPGFRSVLRFARIPVDSSELVRRKFGSRLIGIVTLCLLPLLVFDVPQWVFILSQVIWGAGVYIGLSVAGDKTRPR
K. variicola (ID 2)	FIG00732217: hypothetical protein	8472.75	MPFPVIFMGVTERDGDTTLRGYGMGTGREHFGEQCTGLSALGNLQRRAHTCAAGTDNNSIKLSDWQFHYTPHTTTNP
K. variicola (ID 2)	hypothetical protein	8485.92	MNYAGHEKLRAEVAGLANNMCDLRATLNNMEHRYRFDSDVLAERLTRQTLFRINALFMAAYNDILELDACFKD
K. variicola (ID 2)	hypothetical protein	8488.31	MIVTIVSPSAEAVKPRRHPRIFRADIPAPEIDPALKAFGRHIARSHRKGRGVHIPAMKNAAFGQVLRTLELKRAFN
K. variicola (ID 2)	putative DNA-binding protein	8497.9	MTDEEESSLQAVTASKTVLNQKQLELLEVFDQLPEVEQDRFIELARTRLEELDRFMAEFLSKRKIPPPFEKD

Annotated gene products. Calculated molecular weight (MW) and amino acid sequence of annotated proteins from *K. pneumoniae* (ID 1) and *K. variicola* (ID 2) within the 8,000–8,500 Da range. Tentative peak matching proteins are shown in the shaded rows.