Supplementary data

Table S1. Genetic changes present in the *K. pneumoniae* 7De mutant. No mutations were detected in the strain's plasmids.

Position in the bacterial chromosome	Reference nucleotide	Alteration nucleotide	Type of mutation	Gene	Product
1729903	AT	C	frameshift variant, start lost	*wbaP*	undecaprenyl-phosphate galactose phosphotransferase WbaP
2437981	G	C	synonymous variant	*ydcP_2*	putative protease YdcP
2797478	A	G	-	intergenic region	possible promoter of putative L-galactonate transporter
3080156	G	A	synonymous variant	*sapA*	peptide transport periplasmic protein SapA
3095136	C	A	synonymous variant	hypothetical gene	putative kinase
5018734	G	A	-	intergenic region	-

Table S2. ^{1}H and ^{13}C NMR chemical shifts and inter-residue connectivities of the O-specific polysaccharides from *K. pneumoniae* Kp486 (O1v1).

Residue	Atom chemical shift (ppm)						Connectivities to		Inter-Residue Atoms/Residues
	H1/C1	H2/C2	H3/C3	H4/C4	H5/C5	H6,6′/C6 (CH_3)	δ_H	δ_C	
A →3)-β-D-Gal*f*-(1→	5.22 110.5	4.35 81.4	4.09 85.3	4.31 80.5	3.86 71.0	3.69 63.8	3.92	77.7	H-3, C-3 of **C**
B →3)-α-D-Gal*p*-(1→	5.19 95.8	4.05 68.1	4.16 80.0	4.29 70.0	4.24 71.3	3.76 61.9	4.15	80.0	H-3, C-3 of **E**
C →3,4)-α-D-Gal*p*-(1→	5.10 100.8	4.10 68.7	3.92 77.7	4.18 79.1	4.24 71.4	3.79 60.9	4.09	85.3	H-3, C-3 of **A**
D →D-Gal*p*-(1→	5.01 101.2	3.83 69.9	3.92 70.0	4.07 69.5	4.24 71.4	3.79 60.9	4.18	79.1	H-4, C-4 of **C**
E →3)-β-D-Gal*p*-(1→	4.69 105.2	3.75 70.5	3.81 77.7	4.19 65.6	3.68 75.6	3.76 61.9	4.16	80.0	H-3, C-3 of **B**

Spectra were recorded for $^{2}H_2O$ solution at 298 K. Acetone (δ_H/δ_C 2.225/31.05 ppm) was used as an internal reference.

Table S3. Characteristics of the four *Klebsiella*-specific phages used in this study.

	vB_KpnS_KP36 [phage KP36]	**vB_KpnP_KP34 [phage KP34]**	**vB_KpnM_KP27 [phage KP27]**	**vB_KpnM_KP15 [phage KP15]**
Genus	*Webervirus*	*Drulisvirus*	*Slopekvirus*	*Slopekvirus*
Host strain	Kp486	Kp486	KpATCC 700603 Kp767	KpATCC 700603 Kp767
Capsular-type specificity	K63	K63	KL53 KL10	KL53 KL10
GenBank accession number	NC_029099.1	NC_013649.2	NC_020080.1	NC_014036.1

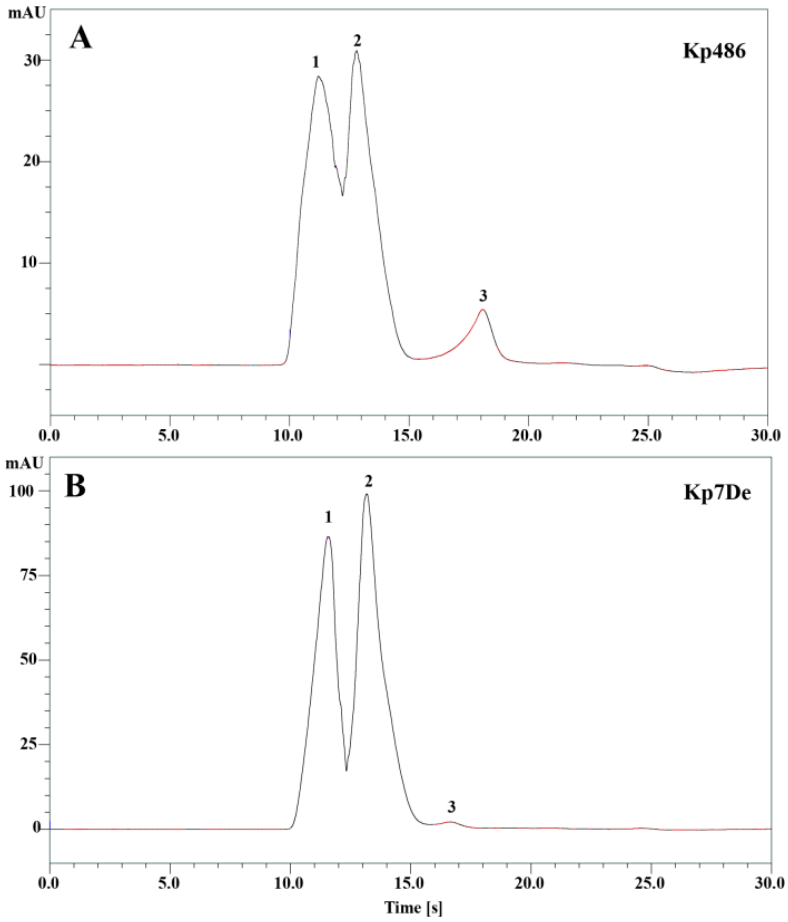

Figure S1. Comparison of elution profiles for poly- and oligosaccharides isolated by mild acid hydrolysis of Kp486 (A) and Kp7De (B) LPS. Numbers indicate fractions (1, 2, 3). Three fractions were eluted and checked by ^{1}H NMR spectroscopy. Fractions 1 did not contain sugar constituents, fractions 2 were identified as O-specific polysaccharide (O-PS), and fractions 3 as unsubstituted core oligosaccharides of LPS.