Supplementary Table S1: Overview of all bacterial strains, bacteriophages and their origin. Additionally, the strain stereotype and phage host strain information are listed.

Strain name	Origin	Isolation site	Additional information
K. pneumoniae			
390	MIT[i]	Not specified	Capsular serotype K11, susceptible to phage K11 (1)
31	IP[ii]	Clinical isolate/Not specified	Capsular serotype K31
77	UWr[iii]	Clinical isolate/Not specified	Capsular serotype K63, susceptible to phage KP34 and KP36
486	UWr[iii]	Clinical isolate/Not specified	Capsular serotype K63, susceptible to phage KP34 and KP36
271	UWr[iii]	Clinical isolate/Not specified	Capsular serotype K3, susceptible to phage KP32 (2)
968	UWr[iii]	Clinical isolate/Not specified	Capsular serotype K21 and KL163, susceptible to phage KP32 (2)
E. coli			
TOP10	Invitrogen	Laboratory strain derived from K-12	Commercial strain; F- *mcrA* Δ(*mrr-hsd*RMS-*mcr*BC) Φ80*lac*ZΔM15 Δ*lac*X74 *rec*A1 *ara*D139 Δ(*araleu*)7697 *gal*U *gal*K *rps*L (StrR) *end*A1 *nup*G
10G	LGC Genomics	Laboratory strain derived from K-12	Commercial strain; F- *mcrA*
Phages			
Klebsiella phage K11	MIT[i]	Not specified	Host *K. pneumoniae* strain 390 (1)
Klebsiella phage KP34	UWr[iii]	Sewage sample (Cesspool holding tank)	Host *K. pneumoniae* strains 77 and 486 (3, 4)

Klebsiella phage KP36	UWr[iii]	Biologically treated sewage (Communal wastewater treatment plant)	Host *K. pneumoniae* strains 77 and 486 (5)
Klebsiella phage KP32	UWr[iii]	Environmental water (Roadside ditch)	Host *K. pneumoniae* strain 271, 358, and 968 (6)

[i] Synthetic Biology Group, Massachusetts Institute of Technology (MIT), USA

[ii] Institute Pasteur (IP), France

[iii] Department of Pathogen Biology and Immunology, University of Wroclaw (UWr), Poland

Supplementary Table S2: **Components and conditions for tile sequence amplification for the VersaTile cloning step using Phusion High-Fidelity DNA polymerase.** Annealing temperature 1 (TA1) represented the optimal TA only for the matching parts of both the forward and the reverse primer. This temperature was used in the first ten cycles to ensure efficient primer annealing to the template. The Thermo Fisher Scientific TA calculator tool was used to calculate the optimal annealing temperature.

Components	Volume
5x High-Fidelity buffer (Thermo Fisher)	10 µL
10 mM dNTPs (Thermo Fisher)	1 µL
Forward primer (10 µM)	2.5 µL
Reverse primer (10 µM)	2.5 µL
Template DNA	50-100 ng
Phusion DNA polymerase (2 U/µL) (Thermo Fisher)	0.5 µL
Ultrapure water	variable
Total volume	50 µL

Conditions	Temperature (°C)	Time	Cycles
Initial denaturation	98	30 s	1
Denaturation	98	10 s	
Annealing	TA1	25 s	10
Extension	72	30 s/kb (<30s)	
Denaturation	98	10 s	
Annealing	72	25 s	20
Extension	72	30 s/kb (≥ 30 s)	
Final extension	72	10 min	1

Supplementary Table S3: **Tile repository.** Overview of all tiles created and their corresponding primers, target DNA and amplified region. The fragment length was given in bp for non-coding tiles and aa for coding tiles. Starting from the DNA ends, the following parts were attached: 1) a SapI/BpiI recognition (underlined) and restriction site for cloning in the pVTE vector; 2) a BsaI recognition site (underlined) for VersaTile assembly; 3) and a position-specific tag of two amino acids defining their order in the final construct (bold).

Tile name	Name Primer	Primer sequence (5'-3')	Target DNA	Amplified region (bp/aa)
P1P2				
Start_P1P2_K11	BB1_Scaffoldstart_K11_F	GTGGCTCTTCCAGAGGTCTC**TGACTG**GCCTGATGAACTCCACCAAG	K11	33,038-33,222bp
	phageScaffoldK11_R	ATAGCTCTTCCCTTGGTCTC**CATGGT**GACCTCCTTTAGTTGAATGAGAAG		
Start_P1P2_KP32	BB1_Scaffoldstart_KP32_F	GTGGCTCTTCCAGAGGTCTC**TGACTG**GCCTGATGAACTCCACAAAG	KP32	33,238-33,418 bp
	ScaffoldEnd_KP32_R	ATAGCTCTTCCCTTGGTCTC**CATGGT**GACCTCCTTAAGTTGAATAGGAG		
	T3_T4gp10domain_K11_Rev	ATAGCTCTTCCCTTGGTCTC**TTCAGA**GGTAACACATTCCACAAAGTCTCCAG		
P2P4				
Anchor_P2P4_1	Anchor K11 F	GTGGCTCTTCCAGAGGTCTC**ACCATG**GACCAAGACATTAAAACAGTCATTCAG	K11 *gp17*	2-256 aa
	T3_T4gp10domain_K11_Rev	ATAGCTCTTCCCTTGGTCTC**TTCAGA**GGTAACACATTCCACAAAGTCTCCAG		
Anchor_P2P4_2	Anchor KP32 F	GTGGCTCTTCCAGAGGTCTC**ACCATG**GACCAAGATATTAAAACAATCATTCAGTAC	KP32 *gp37*	2-256 aa
	T3_T4gp10domain_KP32_Rev	ATAGCTCTTCCCTTGGTCTC**TTCAGA**GGTAAGCATTACAACAAAGTCG		
P2P5				
RBP_P2P5_1	Anchor K11 F	GTGGCTCTTCCAGAGGTCTC**ACCATG**GACCAAGACATTAAAACAGTCATTCAG	K11 *gp17*	2-596 aa
	T4_RBP1_K11_R	GTGGCTCTTCCCTTGGTCTC**TTCTCC**TTATAAAACAAATGATGCTAATCTCG		
RBP_P2P5_2	Anchor KP32 F	GTGGCTCTTCCAGAGGTCTC**ACCATG**GACCAAGATATTAAAACAATCATTCAGTAC	KP32 *gp37*	2-577 aa
	T4_RBP1_KP32_R	ATAGCTCTTCCCTTGGTCTC**TTCTCC**TTATTTGTAGGTCAGGCCGAG		
P4P5				
RBP_P4P5_1	RBP1 K11 F	GTGGCTCTTCCAGAGGTCTC**TCTGAA**GGCGTACTGCCGCTGTCTAATCTTCTG	K11 *gp17*	259-875 aa
	RBP1 K11 R	GTGGCTCTTCCCTTGGTCTC**TTCTCC**TTATAAAACAAATGATGCTAATCTCG		

RBP_P4P5_2	RBP1 KP32 F RBP1 KP32 R	GTGGCTCTTCCAGAGGTCTC**TCTGAA**GGTACTCACTCATTAGCGTCCATACTG ATAGCTCTTCCCTTGGTCTC**TTCTCC**TTATTTGTAGGTCAGGCCGAG	KP32 *gp37*	259-870 aa
P5P6				
CP_P5P6_1	CP K11 F BB5 CP K11.rv	GTGGAAGACGCTAGAGGTCTC**GGAGAA**AACATGCTGAATGATTTAAACCAACC GTGGAAGACGCGCTTGGTCTC**TCCGCT**ATCAAAATCTAAAATGTTTGGTAAGGTG	K11 *gp0043*	1-36 aa
CP_P5P6_2	CP_K32_F CP_KP32_R	GTGGAAGACGCTAGAGGTCTC**GGAGAA**CCTCATGTTAGACAATTTCAATCAG ATAGAAGACGCGCTTGGTCTC**TCCGCT**GAAGGACTCAAGGCGCGGTAATG	KP32 *gp38*	1-35 aa
P5P7				
RBP_P5P7_1	fw_K11ASC0043E_1/596 rv_K11ASC0043E_1/596	GTGGCTCTTCCAGAGGTCTC**GGAGAA**AACATGCTGAATGATTTAAACC ATAGCTCTTCCCTTGGTCTC**ATTACC**TCCTTAGTTAAGGAACAGCC	K11 *gp17*	1-596 aa
RBP_P5P7_2	KP32gp38 36036 P5newFOR KP32gp38 LEC576 P7 REV	ATAGCTCTTCAAGAGGTCTC**GGAGAA**CCTC ATGTTAGACAATTTCAATCAGCC GAAAG GTAGCTCTTCACTTGGTCTC**ATTACC**TCCTTATGATACGAATGCCCTTACTCG	KP32 *gp37*	1-577 aa
P6P7				
RBP_P6P7_1	RBP2 KP32 F RBP2 KP32 R	ATAGCTCTTCCAGAGGTCTC**AGCGGA**TCCACGGCAACCGACAAGCTACG ATAGCTCTTCCCTTGGTCTC**ATTACC**TCCTTATGATACGAATGCCCTTACTC	KP32 *gp38*	36-578 aa
RBP_P6P7_2	BB6 RBP2 KP36.fw BB6 RBP2 KP36.rv	GTGGCTCTTCCAGAGGTCTC**AGCGGA**AGCGCTGCGGCTGCTGCTG GTGGCTCTTCCCTTGGTCTC**ATTACC**TCCTTATGCCGTCAAATCTTCTAACTGAAG	KP36 *gp50*	136-883 aa
RBP_P6P7_3	RBP2 K11 F RBP2 K11 R	GTGGCTCTTCCAGAGGTCTC**AGCGGA**AGCCTTAACGATGATAGCACTCG ATAGCTCTTCCCTTGGTCTC**ATTACC**TCCTTAGTTAAGGAACAGCCTAAC	K11 *gp0043*	37-596 aa
RBP_P6P7_4	fw_BB6_K11gp17E_257_875 fw_BB6_K11gp17E_257_875	GTGGCTCTTCCAGAGGTCTC**AGCGGA**GGCGTACTGCCGCTGTCTAATCTTCTG GTGGCTCTTCCCTTGGTCTC**ATTACC**TCCTTATAAAACAAATGATGCTAATCTCG	K11 *gp17*	259-875 aa
RBP_P6P7_5	fw_BB6_RBP2_KP34 rv_BB6_RBP2_KP34	GTGGCTCTTCCAGAGGTCTC**AGCGGA**GCACTCACTAAACTAGTAGATG ATAGCTCTTCCCTTGGTCTC**ATTACC**TCCCTAACCAGTGAGTTCAGATGGAG	KP34 *gp57*	2-630 aa
RBP_P6P7_6	fw_BB6_KP32gp37E_259/870 rv_BB6_KP32gp37E_259/870 RBP2 KP32 R	GTGGCTCTTCCAGAGGTCTC**AGCGGA**GGTACTCACTCATTAGCGTCCATACTG GTGGCTCTTCCCTTGGTCTC**ATTACC**TCCTTATTTGTAGGTCAGGCCGAG ATAGCTCTTCCCTTGGTCTC**ATTACC**TCCTTATGATACGAATGCCCTTACTC	KP32 *gp37*	259-869 aa

		P7P8		
End_P1P2_K11	ScaffoldEnd K11 F	GTGGAAGACGCTAGAGGTCTC**GGTAAT**ATGTTGTCCCTAGACTTCAAC	K11	37,661-37,843 bp
	ScaffoldEnd K11 R	ATAGAAGACGCGCTTGGTCTC**TTTCTT**CCAGTCAATGATTTTGTCGAC		
End_P7P8_KP32	ScaffoldEnd KP32 F	GTGGAAGACGCTAGAGGTCTC**GGTAAT**ATGTTGTCCCTAGACTTCAATAACG	KP32	37,661-37,843 bp
	ScaffoldEnd KP32 R	ATAGAAGACGCGCTTGGTCTC**TTTCTT**CCAGTCAATGATTTTATCGACTACC		
	T4_RBP1_KP32_R	ATAGCTCTTCCCTTGGTCTC**TTCTCC**TTATTTGTAGGTCAGGCCGAG		

Supplementary Table S4: Components and conditions for the restriction-ligation reaction of the VersaTile cloning step.

Components	Volume
Buffer T4 ligase (Thermo Fisher)	2 µL
T4 DNA Ligase (5 U/µL) (Thermo Fisher)	3 µL
SapI (5 U/µL) (Thermo Fisher)	1 µL
pVTE	25 nM
Tile fragment	46 nM
Ultrapure water	variable
Total volume	20 µL

Conditions	Temperature (°C)	Time	Cycles
Restriction	37	2 min	30
Ligation	22	3 min	
Ligase inactivation	50	5 min	1
Type IIs inactivation	65	20 min	1

Supplementary Table S5: Overview of all primers used for clone analysis, for removal of the BsaI recognition sites present within the DNA sequence of tiles, for sequencing and for amplification of phage scaffold fragments.

Name primer	Primer sequence (5'-3')	Target DNA	Goal
pVTE.fw	GAGCGTCGATTTTTGTGATGCTCG	pVTE	Primer pair pVTE
pVTE.rv	CAGCGTTTCTGGGTGAGC		Clone analysis tile in pVTE, Sanger Sequencing
pVTD23.fw	GAGTGGAGGAGTCGATACG	pVTD23	Primer pair pVTD23
pVTD23.rv	CGTATCACGAGGCCCTTTCG		Clone analysis RBPC in pVTD23, Sanger Sequencing
Gibson_ScaffoldStartFw	GCCTGATGAACTCCACCAAGG	Klebsiella phage K11	K11 primer pair 2
Gibson_ScaffoldEndRev	CCAGTCAATGATTTTGTCGAC	genome	Clone analysis RBPC in pVTD23, Sanger Sequencing
fw_K11gp17E_471-490	TGTGGTGGCCATAGGTAACG	Klebsiella phage K11	K11 primer pair 3
K11_CP.rv	GACTCAAGGCGCGGTAATGAG	genome	Clone analysis RBPC in pVTD23, Sanger Sequencing
KP32scaf 33250 FOR	GAACTCCACAAAGGAGCTTGTGCCAAA	Klebsiella phage KP32	KP32 primer pair 2
KP32scaf 37960 REV	GTCAATGATTTTATCGACTACCTTGGC	genome	Clone analysis RBPC in pVTD23, Sanger Sequencing
KP32scaf 33250 FOR	GAACTCCACAAAGGAGCTTGTGCCAAA	Klebsiella phage KP32	KP32 primer pair 3
KP32_CP.rv	GACTCAAGGCGCGGTAATGAG	genome	Clone analysis RBPC in pVTD23, Sanger Sequencing
K11T4gp10.rv	TCAGAGGTAACACATTCCACAAAGTCT	K11 *gp17*	Clone analysis RBPC in pVTD23, Sanger Sequencing
KP32_33908.rv	CTCAGACAGAATACCACCAG	KP32 *gp38*	Clone analysis RBPC in pVTD23, Sanger Sequencing
fw_K11gp17E_471-490	TGTGGTGGCCATAGGTAACG	K11 *gp17*	Sanger Sequencing
rv_K11gp17E_1353-1334	GATGTTCCACCCACGGTTCT	K11 *gp17*	Sanger Sequencing
fw_K11ASC0043E_456-13	GCTGGTCAACCTCTCGTTCA	K11 *gp0043*	Sanger Sequencing
rv_K11ASC0043E_1363-1	TGGAAACAATGGAGCCGTCA	K11 *gp0043*	Sanger Sequencing
2A 745-764 sequencing	GCATCCTGTGCCGTAACACC	KP32 *gp37*	Sanger Sequencing
KP32_33908.rv	CTCAGACAGAATACCACCAG	KP32 *gp38*	Sanger Sequencing
fw_KP32gp38_538	ATGTCTGGCCCTTGGATTGG	KP32 *gp38*	Sanger Sequencing

rv_KP32gp38_1070	ACCGAAGTTGTCTCACCGTC	KP32 *gp38*	Sanger Sequencing
2B 742-758 sequencing	GGTCGGTAGTGTACGGC	KP34 *gp57*	Sanger Sequencing
2C 861-878 sequencing	GCCCCTCACATTCAAGCC	KP36 *gp50*	Sanger Sequencing
K11 T4gp10domain BsaI Fw	TTTGCTCTTCAGAAACCTCCATCCTGATTACC	K11 *gp17*	Silent point mutation of BsaI recognition site present in the Tile
K11 T4gp10domain BsaI Rev	ATAGCTCTTCATTCGCCACCATTGGCCGAC	K11 *gp17*	Silent point mutation of BsaI recognition site present in the Tile
K11 RBP2 BsaI Fw	ATAGCTCTTCAGGACTCTCGTTCCAAGGTGAG	K11 *gp0043*	Silent point mutation of BsaI recognition site present in the Tile
K11 RBP2 BsaI Rev	GTGGCTCTTCATCCGTCAATGCGGCCTCC	K11 *gp0043*	Silent point mutation of BsaI recognition site present in the Tile
KP32scaf 33119 FOR seq	GCTGGTAACTTAGGGTCTCAGGTCC	Klebsiella phage KP32 genome	Amplification the RBPC from the (engineered) K11 phage genome; used for sequencing
KP32scaf38079 REV seq	GCTGAGGGGTTCGCTTCTCGTTATTC	Klebsiella phage KP32 genome	Amplification the RBPC from the (engineered) K11 phage genome; used for sequencing
K11 scaf 32917 FOR seq	CTTGCGGGTAACTTAGGGTCTCAGG	Klebsiella phage K11 genome	Amplification the RBPC from the (engineered) KP32 phage genome; used for sequencing
K11 scaf 37996 REV seq	CGCTCCAGTAGTTTACCAATGGCGTTG	Klebsiella phage K11 genome	Amplification the RBPC from the (engineered) KP32 phage genome; used for sequencing
Fragment1_Fw_Gibson	CTCACAGTTTACACTTTT	Klebsiella phage K11 genome	Fragment 1_K11 (1-11,055 bp)
Fragment1_Rev_Gibson	AAAGTAATCTCCGTTGGTGTGGTC		
Fragment2_Fw_Gibson	CAATTACGTTTCCCTGTTGTCACA	Klebsiella phage K11 genome	Fragment 2_K11 (10,931-21,463 bp)
Fragment2_Rev_Gibson	ATTACGCTGACCAAACGGGC		
Fragment3_Fw_Gibson	CCATCAGACTGAACACGGTGAC	Klebsiella phage K11 genome	Fragment 3_K11 (21,271-33,219 bp)
Fragment4a_Rev_Gibson	ACCTCCTTTAGTTGAATGAGAAGG		
Gibson_ScaffoldStartFw	GCCTGATGAACTCCACCAAGG	Klebsiella phage K11 genome	Fragment 4 RBPC_K11 (33,044-37,843 bp)
Gibson_ScaffoldEndRev	CCAGTCAATGATTTTGTCGAC		
Fragment4b_Fw_Gibson	ATGTTGTCCCTAGACTTCAACAACG	Klebsiella phage K11 genome	Fragment 5_K11 (37,661-41,181 bp)
Fragment4b_Rev_Gibson	GACATCAACATATAGTGTCCTCAGGT		

KP32scaf 2 FOR	CTCACAGTTTAAACTTTTGGTTATCCCCC	Klebsiella phage KP32 genome	Fragment 1_KP32 (1-11,015 bp)
KP32-4 aga	GAAGGATAGCGCCCACAAGCCTAACAG		
KP32scaf 10899 FOR	CAATTACGTTTCCCTGTTGTCGCTTG	Klebsiella phage KP32 genome	Fragment 2_KP32 (10,899-21,702 bp)
KP32scaf 21702 REV	GCTCACCTTGCATGTTAGCCATGTTG		
KP32scaf 21566 FOR	GACCCCAGCGCAACTGTAAG	Klebsiella phage KP32 genome	Fragment 3_KP32 (21,566-33,356 bp)
KP32scaf 33356 REV	GTTGGGTCTAGGCTGCTGCTTTATGGTG		
KP32scaf 33250 FOR	GAACTCCACAAAGGAGCTTGTGCCAAA	Klebsiella phage KP32 genome	Fragment 4 RBPC_KP32 (33250-37960 bp)
KP32scaf 37960 REV	GTCAATGATTTTATCGACTACCTTGGC		
KP32-21	GGAGGTAATATGTTGTCCCTAGACTTC	Klebsiella phage Kp32 genome	Fragment 5_KP32 (37770-156 bp)
KP32scaf 156 REV	GGGACACAGAGACATCAACATATA		

Supplementary Table S6: Components and conditions for the restriction-ligation reaction of the two-step VersaTile technique.

STEP 1	
Components	**Volume**
Tile (46 nM)	1 µL/Tile
10X ligation buffer (Thermo Fisher)	2 µL
BsaI (10 U/µL) (Thermo Fisher)	1.5 µL
T4 DNA ligase (5 U/µL) (Thermo Fisher)	0.7 µL
Ultrapure water	variable
Total volume	20 µL

Conditions	**Temperature (°C)**	**Time**	**Cycles**
Restriction	37	5 min	30
Ligation	22	5 min	

STEP 2	
Components	**Volume**
VersaTile assembly mixture	20 µL
pVTD23 (25 nM)	1 µL
10X ligation buffer (Thermo Fisher)	2 µL
BsaI (10 U/µL) (Thermo Fisher)	0.8 µL
T4 DNA ligase (5 U/µL) (Thermo Fisher)	0.5 µL
Ultrapure water	variable
Total volume	25 µL

Conditions	**Temperature (°C)**	**Time**	**Cycles**
Restriction	37	5 min	30
Ligation	22	5 min	
Ligase inactivation	50	5 min	1
BsaI inactivation	80	5 min	1

Supplementary Table S7: Overview of all constructed chimeric RBPCs . All tiles used for the assembly and the capsular serotype of RBP1 and RBP2 are listed. Names of the engineered K11, KP32 phages are marked in yellow and blue respectively.

Engineered phage	Tile 1 P1P2	Tile 2 P2P4	Tile 4 P4P5	Tile 5 P5P6	Tile 6 P6P7	Tile 7 P7P8	Capsular serotype RBP1	Capsular serotype RBP2
KP32gp38_RBD2::KP32gp38_RBD2	Start_P1P2_KP32	RBP_P2P5_2		CP_P5P6_2	RBP_P6P7_1	End_P7P8_KP32	K3	K21
K11gp17_RBD1::K11gp17_RBD1	Start_P1P2_K11	Anchor_P2P4_1	RBP_P4P5_1	RBP_P5P7_1		End_P7P8_K11	K11	K31
K11gp0043_RBD2::K11gp0043_RBD2	Start_P1P2_K11	RBP_P2P5_1		CP_P5P6_1	RBP_P6P7_3	End_P7P8_K11	K11	K31
KP32gp37_RBD1::K11gp17_RBD1	Start_P1P2_KP32	Anchor_P2P4_2	RBP_P4P5_1	RBP_P5P7_2		End_P7P8_KP32	K11	K31
KP32gp38_RBD2::K11gp0043_RBD2	Start_P1P2_KP32	RBP_P2P5_2		CP_P5P6_2	RBP_P6P7_3	End_P7P8_KP32	K3	K31
K11gp0043::KP32gp38	Start_P1P2_K11	RBP_P2P5_1		RBP_P5P7_2		End_P7P8_K11	K11	K21
KP32gp38_RBD2::K11gp17_RBD1	Start_P1P2_KP32	RBP_P2P5_2		CP_P5P6_2	RBP_P6P7_4	End_P7P8_KP32	K3	K11
K11gp0043_RBD2::KP32gp37_RBD1	Start_P1P2_K11	RBP_P2P5_1		CP_P5P6_1	RBP_P6P7_6	End_P7P8_K11	K11	K3
KP32gp37::K11gp17 & KP32gp38_RBD2::KP32gp37_RBD1	Start_P1P2_KP32	Anchor_P2P4_1	RBP_P4P5_2	CP_P5P6_2	RBP_P6P7_6	End_P7P8_KP32	K11	K3
KP32gp38_RBD2::KP34gp57	Start_P1P2_KP32	RBP_P2P5_2		CP_P5P6_2	RBP_P6P7_5	End_P7P8_KP32	K3	K63
K32gp38_RBD2::KP36gp50_RBD	Start_P1P2_KP32	RBP_P2P5_2		CP_P5P6_2	RBP_P6P7_2	End_P7P8_KP32	K11	K63
K11gp0043::KP34gp57	Start_P1P2_K11	RBP_P2P5_1		CP_P5P6_1	RBP_P6P7_5	End_P7P8_K11	K11	K63

Supplementary Table S9: **Components and conditions for clone analysis using DreamTaq polymerase.** Clone analysis was conducted to verify the correct assembly of all tiles and RBPCs into pVTD23. Template DNA was prepared by picking a single colony with a toothpick, resuspending it in 30 µL of ultrapure water, and streaking the same toothpick on an LB agar plate with the appropriate antibiotic. Plates were incubated at 37 °C.

Components	Volume
10X DreamTaq Green Buffer	2 µL
10 mM dNTPs	2 µL
Forward primer (10 µM)	2 µL
Reverse primer (10 µM)	2 µL
Template DNA	2µL
DreamTaq DNA polymerase (5 U/µL) (Thermo Fisher)	0.1 µL
Ultrapure water	variable
Total volume	20 µL

Conditions	Temperature (°C)	Time	Cycles
Initial denaturation	95	5 min	1
Denaturation	95	30 s	10
Annealing	55	30 s	
Extension	72	1 min/kb	
Final extension	72	5 min	1

Supplementary Table S10: **Components and conditions for touchdown PCR amplification of the five K11 phage scaffold fragments using Q5 High-Fidelity polymerase.**

Components	Volume
5X Q5 High-Fidelity (Bioké)	0.5 µL
5X Q5 Reaction Buffer	10 µL
5X Q5 High GC Enhancer	10 µL
Forward primer (10 µM)	2.5 µL
Reverse primer (10 µM)	2.5 µL
dNTPs (10 µM)	1 µL
Template DNA	1 µL (30-50 ng)
Ultrapure water	variable
Total volume	50 µL

Conditions	Temperature (°C)	Time	Cycles
Initial denaturation	98	30 sec	1
Denaturation	98	10 s	
Annealing	70 → 62	25 s	9
Extension	72	5 min	
Denaturation	98	10 s	
Annealing	61	30 s	25
Extension	72	30 s	
Final extension	72	2 min	1

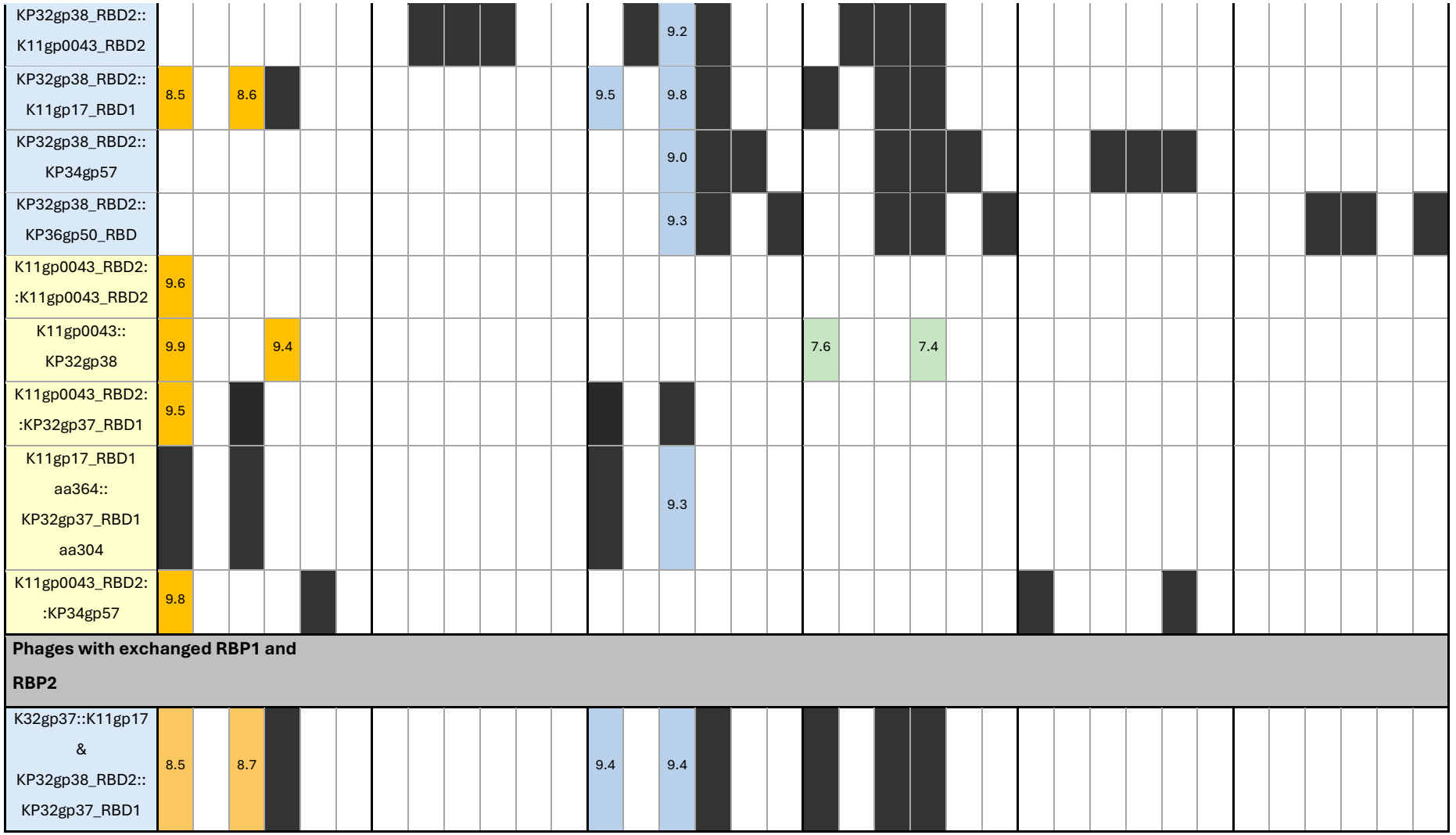
Supplementary Table S11: Components and conditions for PCR amplification of the five KP32 phage scaffold fragments using PrimeSTAR HS polymerase.

Components	Volume
PrimeSTAR HS (premix; Takara)	25 µL
Forward primer (10 µM)	1 µL
Reverse primer (10 µM)	1 µL
Template DNA	1 µL (30-50 ng)
Ultrapure water	variable
Total volume	50 µL

Conditions	Temperature (°C)	Time	Cycles
Initial denaturation	98	1 min	1
Denaturation	98	10 s	
Annealing	70	15 s	25
Extension	72	12 min	
Final extension	72	10 min	1

Supplementary Table S12: **Overview of the host specificity and phage infectivity of all engineered K11 and KP32 phages.** Propagation hosts used for the three rounds of liquid phage propagation and plating hosts for the spotting assay are indicated for each (engineered) phage with a black square. If successful propagation was observed compared to the start culture (culture before propagation), the corresponding square is colored according to the capsular serotype and the propagation efficacy is presented in $\log_{10}$(PFU/mL). Names of the (engineered) K11, KP32, KP34 and KP36 phages are marked in yellow, blue, red and red respectively.

	KP390 (K11)						KP31 (K31)						KP271 (K3)						KP968 (K21)						KP77 (K63)						KP486 (K63)					
Three-steps propagation on *K. pneumoniae* strain	KP390	KP31	KP271	KP968	KP77	KP486	KP390	KP31	KP271	KP968	KP77	KP486	KP390	KP31	KP271	KP968	KP77	KP486	KP390	KP31	KP271	KP968	KP77	KP486	KP390	KP31	KP271	KP968	KP77	KP486	KP390	KP31	KP271	KP968	KP77	KP486
Wild-type phages																																				
K11	9.5	■	■	■			■	■	■	■			■	■	■	■			■	■	■	■														
K11	9.9				■																				■				■							
KP32	■		■	■	■	■							■		9.6	9.7	■	■			8.4	8.7	■	■	■		■	■	■	■	■		■	■	■	■
KP34															■	■	■				■	■	■				■	■	8.7							
KP36															■	■	■				■	■	■										■	■		9.8
Phages with exchanged RBP1																																				
KP32gp37_RBD1:: K11gp17_RBD1	9.5		■	10.3									■		■	■			8.5		■	9.7														
K11gp17_RBD1:: K11gp17_RBD1	10.0																																			
Phages with exchanged RBP2																																				
KP32gp38_RBD2:: KP32gp38_RBD2															9.7	10.0					8.8	9.0														


KP32gp38_RBD2::
K11gp0043_RBD2
9.2
KP32gp38_RBD2::
K11gp17_RBD1
8.5
8.6
9.5
9.8
KP32gp38_RBD2::
KP34gp57
9.0
KP32gp38_RBD2::
KP36gp50_RBD
9.3
K11gp0043_RBD2:
:K11gp0043_RBD2
9.6
K11gp0043::
KP32gp38
9.9
9.4
7.6
7.4
K11gp0043_RBD2:
:KP32gp37_RBD1
9.5
K11gp17_RBD1
aa364::
KP32gp37_RBD1
aa304
9.3
K11gp0043_RBD2:
:KP34gp57
9.8
Phages with exchanged RBP1 and
RBP2
K32gp37::K11gp17
&
KP32gp38_RBD2::
KP32gp37_RBD1
8.5
8.7
9.4
9.4

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