

Carbapenem-resistant *Klebsiella pneumonia*

B

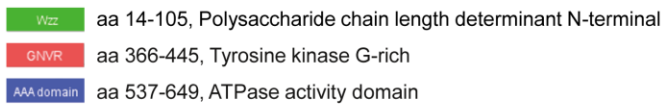
| | trunc | Non-trunc |

Figure S1 Variant classification and mutated positions of Wzc. A

Variant classification and mutated positions of 230 clinical ST11-KL47 CRKp and 2517 *K. pneumoniae* genomes from NCBI. **B** Diagram of Wzc. The predicted functional domains (Wzz, GNVR, and AAA domain) from UniProt and cellular localization of each domain, active site, and oligomer interface predicted by InterPro. **C** Sedimentation values between RmpA2-truncated harboring group (n=90) and Non-RmpA2-truncated harboring group (n=140). Each point represents the mean value of three biological replicates of one strain. $P = 0.004$. *** $P < 0.001$; Unpaired two-sided Welch's t -test.

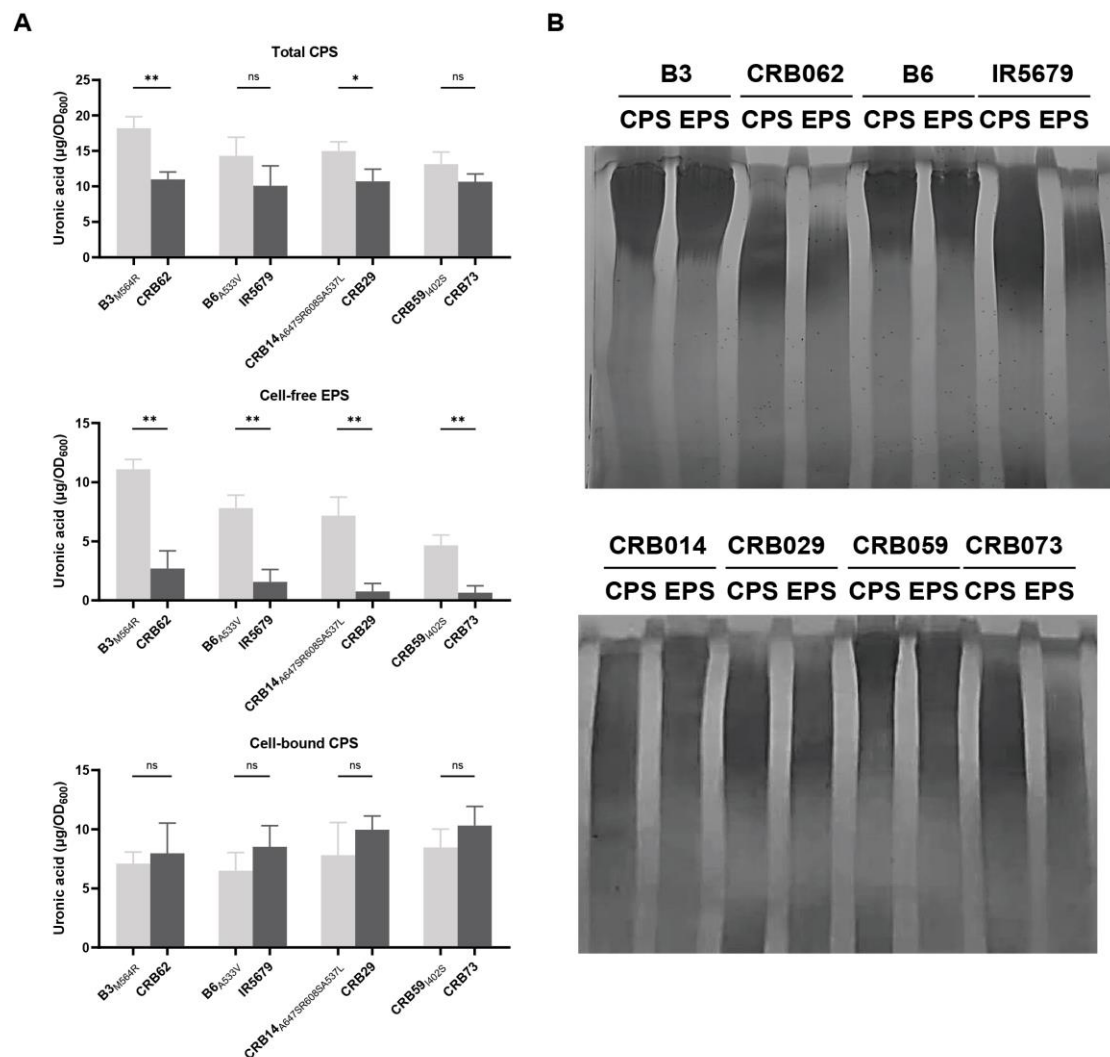
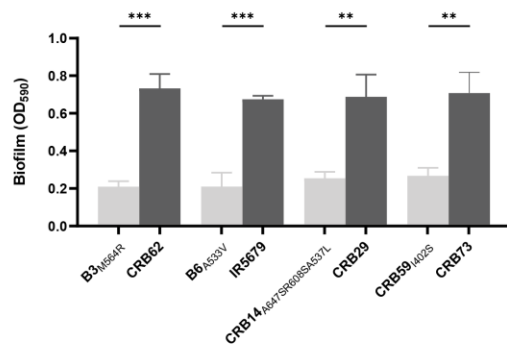
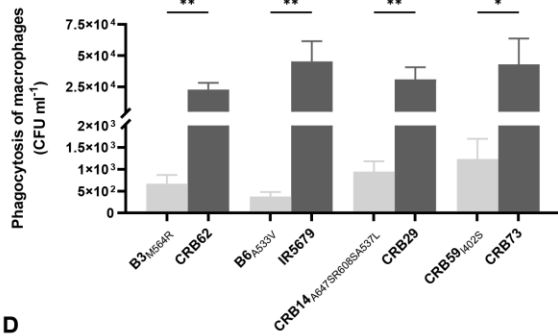


Figure S2 The capsule-traits of ST11-KL47 CRKp. A Uronic acid measure for capsule polysaccharide (CPS) quantification. $n = 3$ biological replicates, bars indicate mean $\pm$ SD. P values from left to right: 0.0031, 0.1286, 0.0254, 0.1027, 0.0010, 0.0020, 0.0029, 0.0026, 0.3383, 0.4094, 0.2187, 0.7118. ns, not significant; $*P < 0.05$, $**P < 0.01$; two-tailed Student's t -test. **B** Silver staining of CPS and EPS resolved on SDS-PAGE. Images are representatives of three independent experiments.

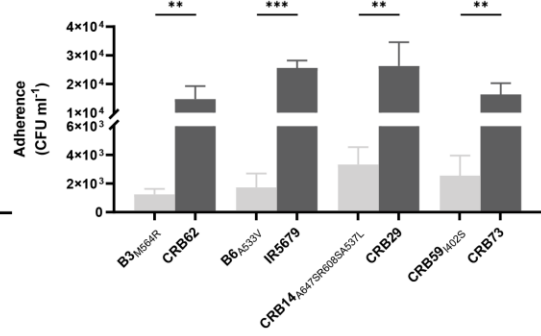
A



B



C



D

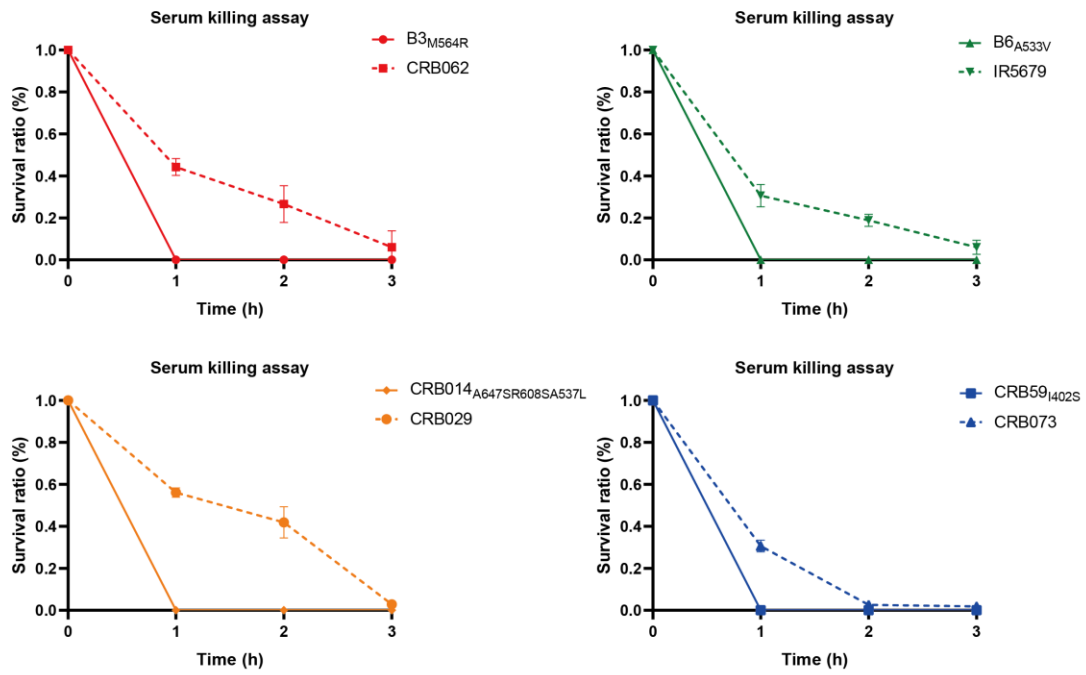


Figure S3. The fitness-traits of ST11-KL47 CRKp. A Biofilm

formation. $n = 3$ biological replicates, bars indicate mean $\pm$ SD. P values from left to right: 0.0004, 0.0005, 0.0036, 0.0029. $*P < 0.05$, $**P < 0.01$. $**P < 0.01$, $***P < 0.001$; two-tailed Student's t -test. **B**

Phagocytosis of B1230, IR5061, and corresponding mutants by RAW 264.7 macrophages. $n = 3$ biological replicates, bars indicate mean $\pm$ SD. P values from left to right: 0.0021, 0.0085, 0.0057, 0.0249. $*P < 0.05$, $**P < 0.01$; two-tailed Student's t -test. **C** Cell adhesion of B1230, IR5061, and corresponding mutants to A549 lung epithelial cells. $n = 3$ biological replicates, bars indicate mean $\pm$ SD. P values from left to right: 0.0069, 0.0001, 0.0090, 0.0045. $**P < 0.01$, $***P < 0.001$; two-tailed Student's t -test. **D** Survival in human serum.

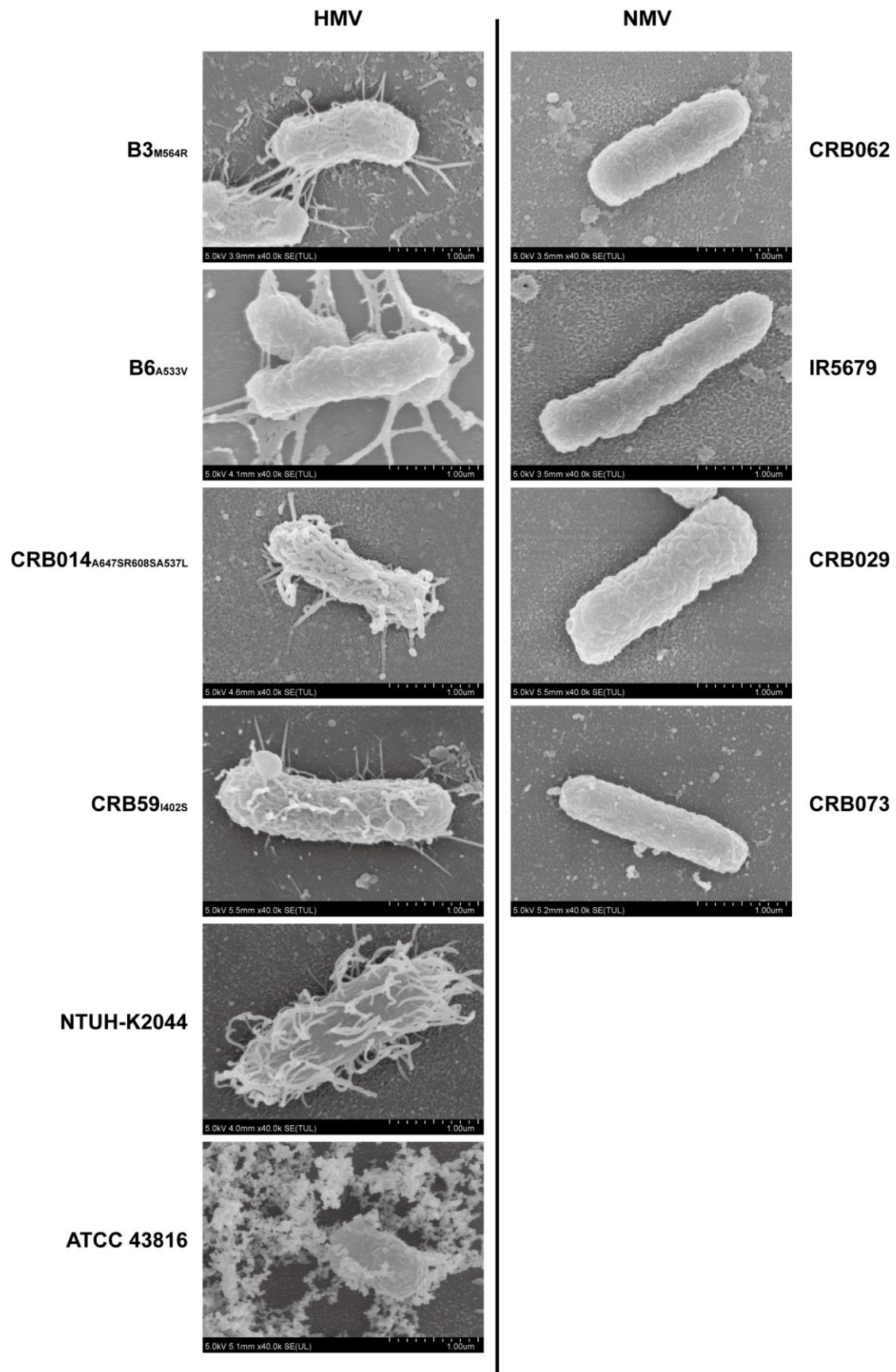


Figure S4 Representative SEM images of SEM of four pairs ST11-

KL47 CRKp, NTUH-K2044, and ATCC 43816. Images are representatives of three independent experiments.

Table S1. Primers used in this study.	
Primers	Sequence (5'→3')
01	cgcGGATCCACGCTGAGCCAGGTACTAGT
04	acgcGTCGACCCGGATCAGTGACAGCCAAA
F0	TCGTGATGTCGAATCTGGGC
R0	CACCACGCCGTTTAAGATGC

Table S3. The genomic characterization of CRKp B1230 and IR5061.						
Isolates	ST	K locus	L locus	Genome Size (bp)	Drug Resistance genes	Virulence genes
B1230	ST11	KL47	OL101	5872290	<i>aac(3)-IId</i> , <i>aph(3'')-Ib</i> , <i>aph(6)-Id</i> , <i>bla_{CMY-2}</i> , <i>bla_{CTX-M-14}</i> , <i>bla_{CTX-M-55}</i> , <i>bla_{KPC-2}</i> , <i>bla_{SHV-182}</i> , <i>bla_{TEM-104}</i> , <i>bla_{TEM-105}</i> , <i>dfrA1</i> , <i>dfrA25</i> , <i>floR</i> , <i>fosA6</i> , <i>mdf(A)</i> , <i>ompA</i> , <i>xcpR</i> , <i>ecpABCDER</i> , <i>mph(A)</i> , <i>qnrS1</i> , <i>sul1</i> , <i>sul2</i> , <i>tet(A)</i> , <i>tet(D)</i>	<i>entABES</i> , <i>fepABCDG</i> , <i>fimAE</i> , <i>fyuA</i> , <i>irp1</i> , <i>irp2</i> , <i>iucABCD</i> , <i>iutA</i> , <i>mgtC</i> , <i>ybtAEPQSTUX</i>
IR5061	ST11	KL47	OL101	5882101		

Table S4. Thirty-two nonsynonymous SNPs between B1230 and IR5061.

<i>GENE</i>	NT_POS	AA_POS	Description
<i>hycE</i>	1367/1710	456/569	Formate hydrogenlyase subunit 5
<i>modA</i>	78/774	26/257	Molybdate-binding protein ModA
<i>glpA</i>	268/1623	90/540	Anaerobic glycerol-3-phosphate dehydrogenase subunit A
<i>ackA</i>	701/1203	234/400	Acetate kinase
<i>fadJ</i>	734/2145	245/714	Fatty acid oxidation complex subunit alpha
<i>yecM</i>	409/411	137/136	Protein YecM
<i>dhaD</i>	866/1098	289/365	Glycerol dehydrogenase
<i>prs</i>	730/948	244/315	Ribose-phosphate pyrophosphokinase
<i>mdtH_1</i>	1027/1233	343/410	Multidrug resistance protein MdtH
<i>maeA</i>	547/1698	183/565	NAD-dependent malic enzyme
<i>bcsA</i>	941/2619	314/872	Cellulose synthase catalytic subunit [UDP-forming]
<i>lacI_1</i>	934/1071	312/356	Lactose operon repressor
<i>mdoH</i>	432/2529	144/842	Glucans biosynthesis glucosyltransferase H
<i>cadC</i>	357/1569	119/522	Transcriptional activator CadC
<i>lapA</i>	223/225	75/74	Lipopolysaccharide assembly protein A
<i>ttuB_3</i>	296/1311	99/436	Putative tartrate transporter
<i>chbR</i>	173/825	58/274	HTH-type transcriptional regulator ChbR
<i>yphA</i>	103/468	35/155	Inner membrane protein YphA
<i>dld_1</i>	1215/1746	405/581	Quinone-dependent D-lactate dehydrogenase
<i>rlhA_2</i>	982/1362	328/453	23S rRNA 5-hydroxycytidine synthase
<i>xerC_4</i>	7/903	3/300	Tyrosine recombinase XerC
<i>ytbE</i>	247/870	83/289	putative oxidoreductase YtbE
<i>gntR</i>	550/945	184/314	HTH-type transcriptional regulator
<i>mukB</i>	314/4449	105/1482	Chromosome partition protein MukB
<i>nfi</i>	166/672	56/223	Endonuclease V
<i>wzc</i>	1598/2169	533/722	Putative tyrosine-protein kinase in cps region
<i>traC_5</i>	221/2628	74/875	Protein TraC