



Figure S1. Physical map of the *vb_Kpn_1825* plasmid prophage and comparison with closely related elements. The circles, from the outermost to the innermost, show: (i) coding DNA sequences (CDS) encoded on the plus and minus DNA strands; (ii) sequence alignment with the *K. pneumoniae* prophage ST13-OXA48phi12.3; (iii) sequence alignment with the *S. enterica* phage SSU5. Genes encoding proteins of known functions are in different colors, as detailed in the legend.

KPC-3	<u>MSLYRRLLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGATVSYR</u>	60
KPC-2	MSLYRRLLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGATVSYR	60
KPC-40	MSLYRRLLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGATVSYR	60
KPC-53	MSLYRRLLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGATVSYR	60
KPC-25	MSLYRRLLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGATVSYR	60

KPC-3	AERFPLCSSFKGFLLAAVLAARSQQQAGLLDTPIRYGKNALVPWSPISEKYLTGTMVAE	120
KPC-2	AERFPLCSSFKGFLLAAVLAARSQQQAGLLDTPIRYGKNALVPWSPISEKYLTGTMVAE	120
KPC-40	AERFPLCSSFKGFLLAAVLAARSQQQAGLLDTPIRYGKNALVPWSPISEKYLTGTMVAE	120
KPC-53	AERFPLCSSFKGFLLAAVLAARSQQQAGLLDTPIRYGKNALVPWSPISEKYLTGTMVAE	120
KPC-25	AERFPLCSSFKGFLLAAVLAARSQQQAGLLDTPIRYGKNALVPWSPISEKYLTGTMVAE	120

KPC-3	LSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGD ^T FRLLDRWELE--LNSAIPGDARD	178
KPC-2	LSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGD ^T FRLLDRWELE--LNSAIPGDARD	178
KPC-40	LSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGD ^T FRLLDRWELELELNSAIPGDARD	180
KPC-53	LSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGD ^T FRLLDRWELELELNSAIPGDARD	180
KPC-25	LSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGD ^T FRLLDRWELELELNSAIPGDARD	180

KPC-3	TSSPRAVTESLQKLT ^L GSALAAPQRQQFVDWLKGNTTGNHRIRA ^A VPADWAVGDKTGT ^C G	238
KPC-2	TSSPRAVTESLQKLT ^L GSALAAPQRQQFVDWLKGNTTGNHRIRA ^A VPADWAVGDKTGT ^C G	238
KPC-40	TSSPRAVTESLQKLT ^L GSALAAPQRQQFVDWLKGNTTGNHRIRA ^A VPADWAVGDKTGT ^C G	240
KPC-53	TSSPRAVTESLQKLT ^L GSALAAPQRQQFVDWLKGNTTGNHRIRA ^A VPADWAVGDKTGT ^C G	240
KPC-25	TSSPRAVTESLQKLT ^L GSALAAPQRQQFVDWLKGNTTGNHRIRA ^A VPADWAVGDKTGT ^C G	240

KPC-3	VYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDK ^Y SEAVIAAAARLAL ^E GLGVNGQ	293
KPC-2	VYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDK ^H SEAVIAAAARLAL ^E GLGVNGQ	293
KPC-40	VYGSANDYAVVWPTGRAPIVLAVYTRAPNKDDK ^Y SEAVIAAAARLAL ^E GLGVNGQ	295
KPC-53	VYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDK ^Y SEAVIAAAARLAL ^E GLGVNGQ	295
KPC-25	VYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDK ^H SEAVIAAAARLAL ^E GLGVNGQ	295
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Figure S2. Alignment of relevant KPC variants. KPC-40 confers reduced susceptibility to CZA and susceptibility to meropenem. The phenotype conferred by KPC-25 is not known. The signal peptide is underlined and the Ω -loop region is boxed, as well as other observed differences in the aminoacidic sequences of related KPC enzymes.