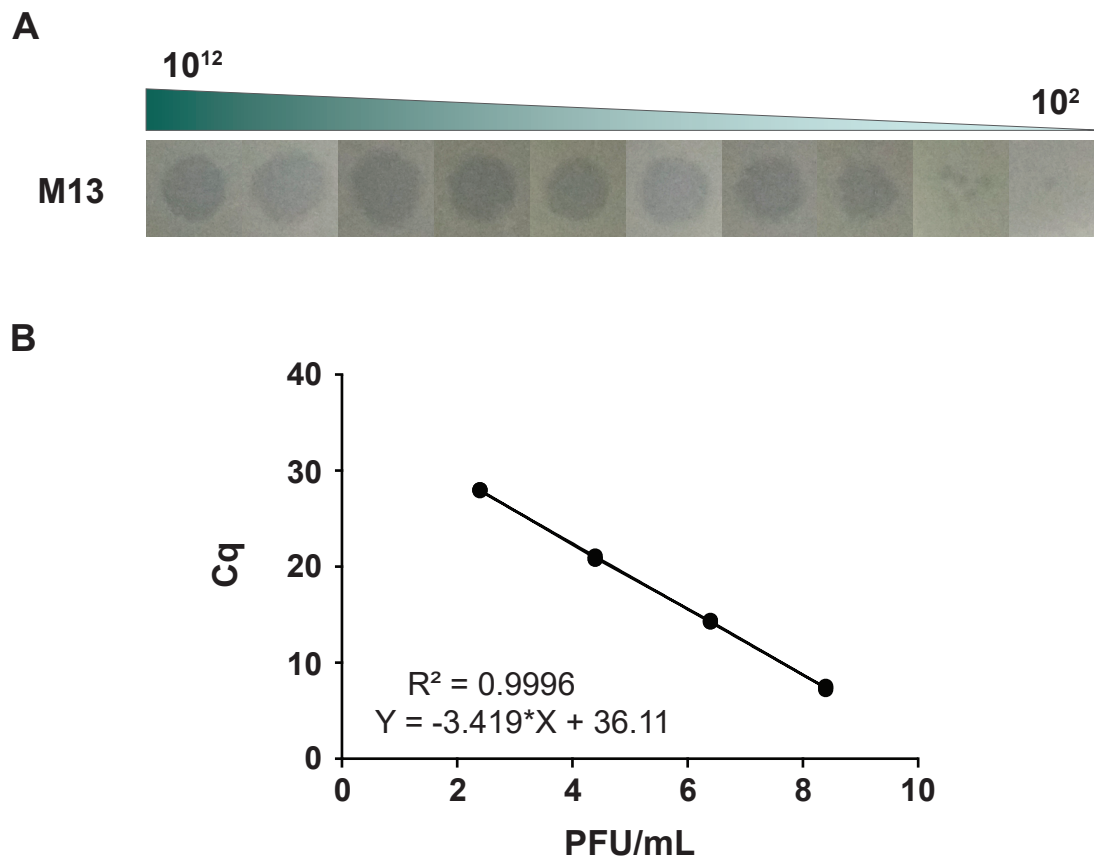


Supplementary Figure 1

CTXZOT	HHGWDICLTTPNIAKVHNMIREAAEI---GYRHFNRATVGLGA-KFTLTTHDAANSQGMDSHALTRQVKKIP	197
VFJZOT	KLGDVIFIVQNI SMVDKQAREGLAEHVVHCKRLDRMQIPFLSTIVWILTLG-----QLKIP	171
M13	KLGDIIIFLVQDLSIVDKQARSALAEHVVYCRRLDRITLPFVGTLYSLITG-----SKMP	170
cons	: ***: : . ::: *: : *.. : : : : : : : : : : : : : *	
CTXZOT	SPIFKM---Y-----ASTTTGKARDTMAGTALWKDRKILFLFGMVFLMFSYSFYGLHDNPIF	251
VFJZOT	MPKLHIGIVKYGDTINALTVDKWMLWGTDLYSSYDTKQIFQNHYPH-----GTYSVLPPWYIHGRYTPPYT	237
M13	LPKLHVGVVKYGDSQLSPTVERWLYTGKNLYNAYDTKQAFSSNYDS-----GVYSYLTPLYSHGRYFKPLN	236
cons	* ::: * : : : : : : : : : : : : : : : : : : : *	
CTXZOT	TGGNDATIESEQSEPQSKATVGNAVGSKAVAPASFGFCI-GRLCVQDGFVTVGDERYRLVDNLDIPYRGLWA	322
VFJZOT	-----ARNIMRITKILFRKYSRVAMFAVGAAF-----	264
M13	-----LGQKMRLTKIYLKKFSRVLCLAIGFAS-----	263
cons	 *	
CTXZOT	TGHHIYKDTLTVFFETESGSVPTELFASSYRYKVLPLPDFNHVVFDTF-----	372
VFJZOT	-----GAAFWHFTSPEPELIQLV-QAQNQ--MLTSESDHKLSELLGGFTIS	307
M13	-----AFTYSYITQPKPEVKKVV-SQTYDFDKFTIDSSQRLNL-----S--Y	302
cons	. : : : . * *: . : . *	
CTXZOT	-----AQALWVEVKR-----GLPIKTENDKKGLNSIF	399
VFJZOT	RYTALPDAPVTFELSNAGKRLTSYELQSMGFEIEPLSRCEIIKSGAQNETIHC--	361
M13	RY-----VFKDSKG-KLINSDDLQKQGYSLTYIDLCTVSIKKGNSNEIVKCN-	348
cons	* . : : ** . : : : .	

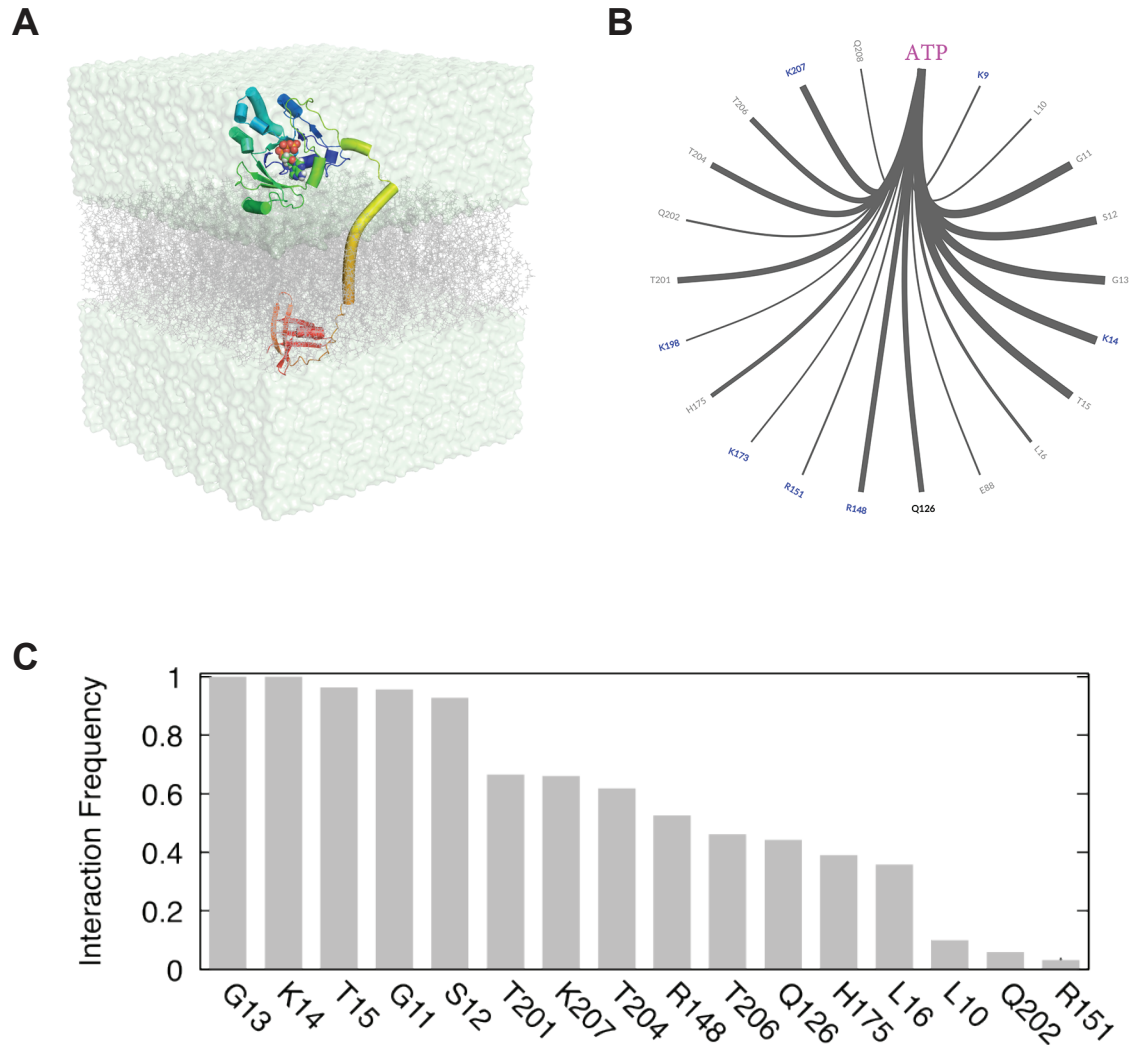
Supplementary Figure 1: Amino acid sequence alignment of the C-terminus of CTX-ZOT, VFJ-ZOT and M13 gene1. Alignment was conducted using tCoffee (Notredame, et. al. JMB, 2000). Colours indicate similarity: **BAD** **AVG** **GOOD**

Supplementary Figure 2



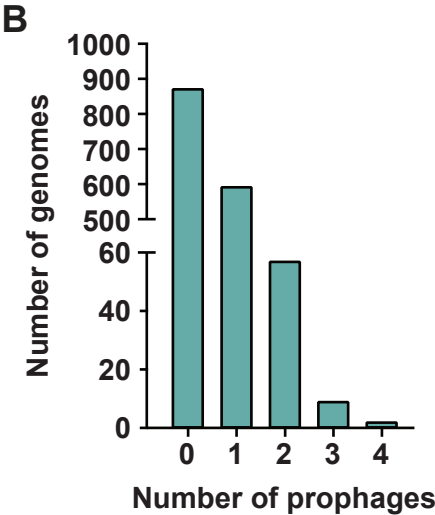
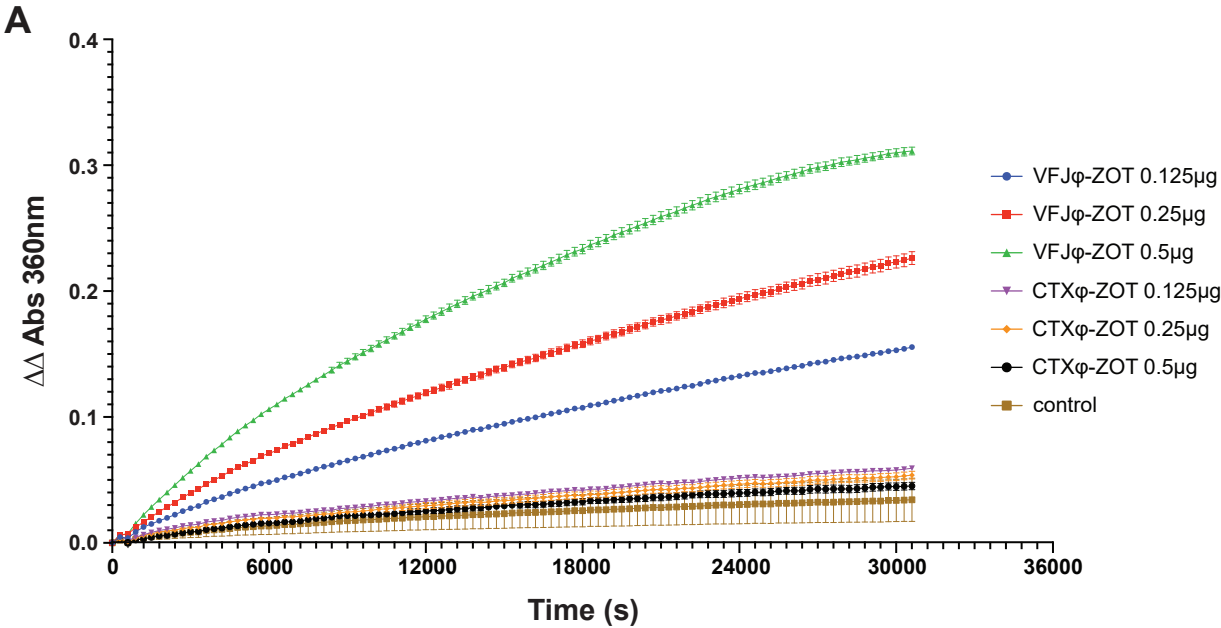
Supplementary Figure 2: M13 was used to determine whether plaque forming units correlate to qPCR results. A) Number of phage determined by top agar overlay method. B) Amplification of gene3 from M13.

Supplementary Figure 3



Supplementary Figure 3: MD simulation of the ATP bound M13 gp1p. A) Panel shows the explicit solvent all-atom model of M13 gp1p. The protein is in cartoon representation, the ATP molecule is represented by spheres, the lipid bilayer is shown in grey lines and the water solvent by transparent surface. B) The residue pairs interacting with ATP which are connected by black lines whose thickness linearly scales with the frequency observed in MD simulations. C) The frequency of the residues interacting with ATP.

Supplementary Figure 4



Supplementary Figure 4: A) ATPase activity of VFJ ϕ -ZOT and CTX ϕ -ZOT at varying concentrations over time. Control: parent plasmid without Zot gene. B) Number of *Vibrio* genomes that contain filamentous prophages.