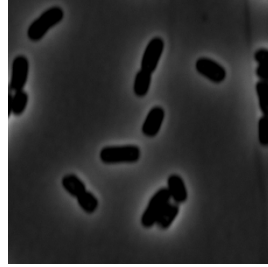
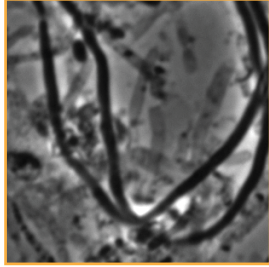
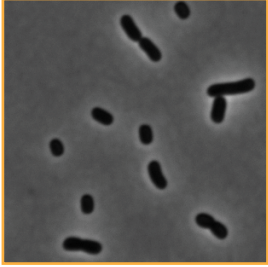
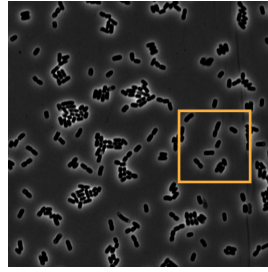
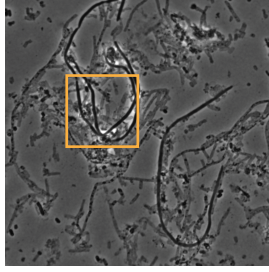
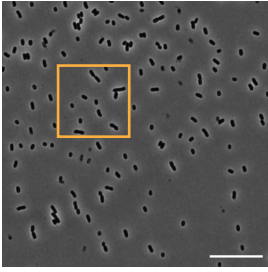


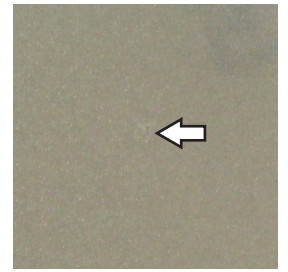
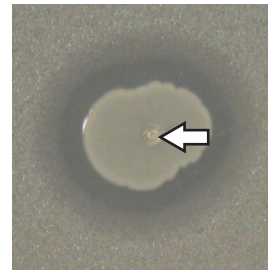
## Supplemental Figures

**a**

WT pBR322-ColV

 $\Delta cvpA$  pBR322-ColV $\Delta cvpA$  pBR322**b**

WT

 $\Delta cvpA$ 

**Figure S1:  $\Delta cvpA$  EHEC is sensitive to Colicin V production and does not appear to secrete it.** a) Micrograph of overnight culture of indicated strains expressing ColV from plasmid pBR322-ColV or carrying empty vector plasmid pBR322. Scale bar is 10  $\mu$ M. Orange box denotes inset. b) 5  $\mu$ L jab of overnight culture of indicated strain in soft agar matrix containing 100  $\mu$ L of indicator (sensitive EHEC) strain. Arrow indicates position of jab. Line represents 20 mm.

	P	TM	C	TM	P	TM		
	1	11	21	31	41	51	61	71
<i>Escherichia coli</i>	---MVW---	DYAIIAVIAFSSLSVSLIRGFVRE	EVLSSLVTWGC	CAFFVASHYYTYLSVWF	---	TGFE	DELVNRNGIAIAVLF	IATLIVGA
<i>Enterobacter cloacae</i>	---MVW---	DYAIIAVIAFSSLSVSLIRGFVRE	EALSLVTWGC	CAFFVASHYYTYLSVWF	---	TGFE	DELVNRNGIAIAVLF	IATLIVGA
<i>Serratia marcescens</i>	---MVW---	DYVIAVIAFSSLSVSLIRGFVRE	EALSLVTWGC	CAFFVASHFYSLAVYF	---	TRFE	DELVNRNGIAIAILF	IATLIVGA
<i>Bradyrhizobium algieriense</i>	---MPITI---	DLVLLGVMLISGLLAMVRGFMR	EILSIAAWGAAALVTLYAF	SKLLPTA	---	KTYFN	NDTVASVVVA	GTFI
<i>Agrobacterium tumefaciens</i>	---MPITI---	DGIVIAVVLFSAILAMVRGF	REILSIAAWGAAALVTLYAF	SKLLPTA	---	RNYT	DDDKIAIAGS	AVVFLVSLIVIS
<i>Neisseria meningitidis</i>	---MNNLPV---	ADLLVSAIIAACIVLSAMR	GVIAEAGSMAAWVVAFFA	AKLFAAPFADIA	---	FASFQ	PRLFALALS	SFISLFVIACLIQK
<i>Thermodesulfobium acidiphilum</i>	---MNL---	DLILLIVIIISYFSGYKTL	GLIVVFTFLFAFFLSLYL	PLHMLNIAEAF	---	SKALL	FNGKCLIS	ISFIFTLMLNALV
<i>Leptotrichia shahii</i>	---MI---	LDIGFVLLIIFIFLGYKRG	FSLEFFNMFKYIFIFIT	NYVYKFFLDSK	---	RIKPK	SQLKIF	IIIVVIQYIIYS
<i>Granulicella tundricola</i>	MQLPPTTSYNP	FDWFLVVLIVISTIAAFMR	GLIRSLLSLVGFILAI	IVVASWNYLSFAS	---	GRWIL	NFTVAEII	IAYLTLIVITIAFS
<i>Thermovibrio ammonificans</i>	---MGLPTMNV---	LDGLIIIIILGNLIRGFN	KGLVELELLSLSGMV	SVLSYAYKLT	PFVAKKL	---	VGYA	---DPTTL
<i>Bacteroides fragilis</i>	---MTT---	DIILIALGAGVIVGF	MKGFIHQASILGLIV	GLLAAKALY	TS LAVKL	---	CPTVT	DSMTVAQILAF
<i>Fibrobacter succinogenes</i>	---MNW---	DIACAACLLVFGIIGLWR	GLSSVFRLC	AWVAAILGAY	FAQGLL	---	IHNFA	FSDFTAHLICT
<i>Mycococcus xanthus</i>	---MV---	DLIILGLVLFMGAIT	GASRQVANVGLAV	GYFASRRL	GPVAA	---	AEALG	SPLFLG
<i>Tetragenococcus muritaticus</i>	---MI---	LTWIILLVLI	GGFFIGLRR	GLVQVVG	LTFGFI	IA	AAASLY	SNTLAPYLSW
<i>Spirochaeta cellobiosiphila</i>	---MNLVLL---	MDIIFLMI	GGVFFVGGFR	GFVTEI	INFMTLV	GGV	ILAV	ALG
<i>Flavobacterium segetis</i>	---MGF---	DIILCALLVAFYKGVN	GLFIELASLISL	LIYFAIK	FSSFMKEIL	---	NGFV	KWNPNTVQV
<i>Flexistipes sinusarabici</i>	---MPI---	TDIVILIIIGFFAVK	GLFGLINEV	FGLGLI	GYILS	---	YLG	ISEE
<i>Pyramidobacter piscolenis</i>	---MTLVDGF---	LDMLLVIVVFAV	KIFRFGSE	EIFSLAGV	GGVYFK	---	RNFF	GS
<i>Sulfuricurvum kujijense</i>	---MDLNY---	FDLVGSVILL	LKGLNLGSK	EVFGLV	GGVFA	---	SDVLF	HFESSAA
<i>Campylobacter jejuni</i>	---MNFYW---	FDAFILG	FLLGLKGI	INGLIKE	IFG	---	QSTFY	KIENQSLA

	C	TM	P		
	81	91	101	111	121
	I-VNFVIGQLVEK	TGLS	---GDRVLG	VCFGALRG	VLIVAA
	I-VNYVIGQLVEK	TGLS	---GDRVLG	VCFGALRG	VLIVAA
	I-VNYVIVSSLVEK	TGLS	---GDRVLG	VCFGALRG	VLIVAA
	V-ITVRISDMILDS	RITG	---ALDRTL	GFLFLG	LRG
	F-ITSRIADDFID	SRI	---ALDRTL	GFLFLG	LRG
	I-LRSLLTGAVS	AVGLG	---FANRIL	GGVFG	ALKG
	K-FLLLVADILG	ISRTS	---KNSFI	AGFL	NVLLS
	A-ILIIINREF	LKS	IKIK	---RFDK	SSG
	M-LANLLRKT	ASAV	GLG	---FLDR	LLG
	Y-FASLIDR	KVR	KTALN	---FINN	VLF
	L-VASVLT	KALE	AVSLG	---WLN	RML
	L-I	GHIV	GDSIK	N	TIVG
	YALG	ALLR	ILST	G	QHNE
	I-LGSS	LD	FLAS	L	PLLN
	L-AQN	MLN	MVEN	L	NLE
	L-LG	KFLT	GIAN	FA	FLG
	L-SG	KLAR	FFKA	I	QLG
	L-I	GKLF	RALL	S	MSLS
	A-LG	SGFK	KL	TS	SLG
	L-V	GNF	LS	KL	IKLS

	131	141	151	161
	SKSE	DWS	KS	QLIP
	SKSE	DWS	KS	QLIP
	SQ	SAD	WK	QS
	QR	P	D	W
	TQ	PE	W	T
	P	T	E	W
	L	F	S	N
	I	R	D	K
	S	E	W	V
	L	I	K	R
	I	S	Q	T
	N	L	R	N
	D	P	K	R
	T	A	Q	E
	D	P	Q	K
	A	K	K	E
	A	F	S	K
	L	P	G	V
	N	F	E	G
	K	L	D	N

**Figure S2: MUSCLE alignment of 20 CvpA homologs from bacterial species**

**across diverse phyla.** Residues with >70% conservation across species are indicated by a colored box. Residue numbering and predicted membrane topology for the *E. coli* CvpA is shown above the alignment. The green box indicates predicted periplasmic (P) segments, the gray box indicates transmembrane (TM) segments, and the pink box represents cytoplasmic (C) segments.