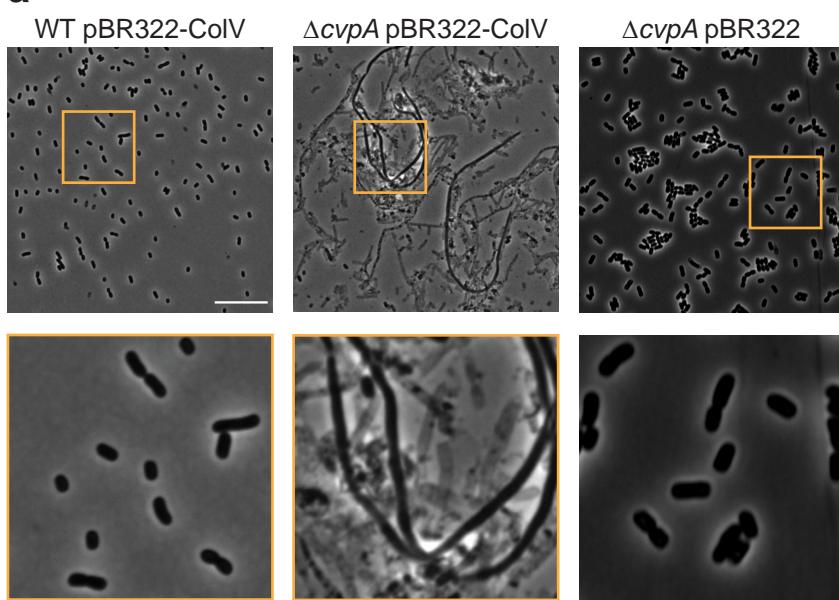
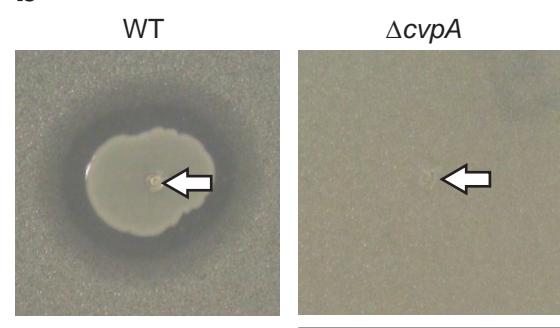


## **Supplemental Figures**

**a****b**

**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  $\mu\text{M}$ . Orange box denotes inset. b) 5  $\mu\text{L}$  jab of overnight culture of indicated strain in soft agar matrix containing 100  $\mu\text{L}$  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--IDY	YIAIIAVIAFSSLVSL	SLSLIRGVRE	EVLSLV	TWGCAFFVASH	YTYL	SVWF-	
<i>Enterobacter cloacae</i>	-	MVW--IDY	YIAIIAVIGFSC	LVSLLIRGVRE	ALSLV	TWGCAFFVASH	YTYL	SVWF-	
<i>Serratia marcescens</i>	-	MVW--IDY	VIAIVGFSALSVS	LIRGVRE	ALSLV	TWGCAFFVASH	FYSYLA	VYF-	
<i>Bradyrhizobium algeriense</i>	-	MPITI-LD	LVLGVMLISG	LLAMVRGFMR	EILSIA	AWGAALVTLYAFSKL	LPTA	KTYFN-NDT	
<i>Agrobacter tumefaciens</i>	-	MPITI-FD	GIVIAVVLFS	AILAMVRGFSR	EILSIA	SWGSVAAYYL	PVLPY	RNYT-DDD	
<i>Neisseria meningitidis</i>	-	MNLPV-A	DLLVSAIIAACIVL	SMSLRGIVIAEAG	MSMAAWVVAFFKA	LKFAPADIA	FAFQ-	PRLFALAFS	
<i>Thermodesulfobium acidiphilum</i>	-	MNL-I	LLILIVIILSYFSGY	KTGKLVFTFLFAFFL	SLYLT	PHLMNIAEAFF	SKALL-FNG	KCLISISFIFT	
<i>Leptotrichia shahii</i>	-	MI-LD	GFVVVLIIIFI	FLGYKRGLEF	NNMKYFI	IFTNYYVKFLDSL	RIKPQS	QSKLIFIVV	
<i>Granulicella tundricola</i>	MQLPPTTSYNP-FD	WFVLVVLV	LISTIAAFMGR	LIRSLLS	LGFLIAIVVASW	NLYLSFASYL	GRWIL-NFT	VAEIILAYTL	
<i>Thermovibrio ammonificans</i>	-	MGLPTMNV-LD	GLIILILGWNL	IRGFNKGLVE	ELLSLS	GMVVSLYGAYKLTP	FVAKKL	VGYA-DPTT	
<i>Bacteroides fragilis</i>	-	MTT-ID	IILIALGAGVII	GFMKFRQ	LAISLGLIV	GLLVLA	KALYTS	LLFTGAVVYTV	
<i>Fibrobacter succinogenes</i>	-	MNW-ID	ACAACLLWFGVII	IGWRGLSSV	RFLCWA	VAAILGAYFA	QAGLGDFF	DSMTV	TAHLICCTC
<i>Myxococcus xanthus</i>	-	MV-ID	LILGLVLFAMIGAI	TGASRQVANV	GLAVGYFA	SRRLLGPV	PAH	PTV	FLVPLIFLFS
<i>Tetragenococcus muriaticus</i>	-	MI-LT	WILLVLLV	GGFFIGLRRGL	QVVGVL	TGFII	ALAASLYNTL	EDFYQQIA	FCTWL
<i>Spirochaeta cellobiosiphila</i>	MNLVL-MD	LIIFLMLGGFV	FFGLRGVTE	IINMFL	TVLGGVILA	VALGLPASEYI	KGYLDWGDNTI	AFILL	FLVIRLN
<i>Flavobacterium segetis</i>	-	MGF-FD	IILCALLVFAFKG	VNVNGFIEL	ALASLIS	SILGIYFAIKFSS	FMKEL	NGFV	KWPNTVQVVA
<i>Flexistipes sinuarabici</i>	-	MPI-TD	IVLIIIGFFAV	GKLFKG	LINENEV	FGLLGLILG	YIPLPSKLY	IYLG	TFIIVVIA
<i>Pyramidobacter piscolens</i>	-	MTLVDGF-DL	CMLLIVVF	AVKGIFRGFS	OEGIE	FSLGLAVGIV	GQYFGFKYAD	RNFFG	SESSAIVL
<i>Sulfurcurvum kujjense</i>	-	MDLNY-FD	LVGSV	LLGKGL	NGLNSKE	FLVGLV	IVGGGVF	SHGGI	GKFL
<i>Campylobacter jejuni</i>	-	MNFYW-FD	AFILGFT	LLLGLKG	INGLKE	IGGVFIA	ASKYATQAAEF	SDVLFH	FESSAIVL

	C	TM	P
81	91	101	111
I-VNFVIGQLVEK <b>TG</b> Ls	-GTDRVL <b>G</b> VCF <b>G</b> ALRGVLIVAA	-ILFFLDSFTGV	-
I-VNYVIGQLVEK <b>TG</b> Ls	-GTDRVL <b>G</b> ICFG <b>G</b> ALRGVLIVAA	-ILFFLDTFTGF	-
I-VNYVISSLVEK <b>TG</b> Ls	-GTDRVL <b>G</b> ICFG <b>G</b> ALRGVLIVAA	-ILFFLDTFTGF	-
V-ITVRI <b>S</b> D <b>M</b> I <b>L</b> DSRIG	-ALDRT <b>L</b> GFLFGLRG <b>R</b> LLIVVV	-AFLFFSWLVPDK	-
F-ITSRI <b>A</b> D <b>F</b> I <b>L</b> DSRIG	-ALDRT <b>L</b> GFLF <b>G</b> ARG <b>L</b> LLIVVV	-AVAFWNWLVDVK	-
I-LRSLLTGAVSAVG <b>L</b> G	-FANR <b>L</b> GGVF <b>G</b> ALK <b>G</b> ILI <b>T</b> L	-LVMLASKTDL	-
K-FLLLVA <b>D</b> IL <b>G</b> ISRIS	-KNS <b>F</b> IAG <b>G</b> FL-NVLLS <b>I</b> LM <b>L</b> SL	-I <b>K</b> SLDWANMYM	-
A-ILIINREF <b>L</b> K <b>S</b> KIK	-RF <b>D</b> SS <b>G</b> MG <b>I</b> FG <b>N</b> KLFFVATIVYIVVVVG <b>I</b> SK <b>S</b> KK <b>K</b> I	-	-
M-LANLLRKTA <b>S</b> AVG <b>L</b> G	-FLDR <b>L</b> LLGA <b>A</b> FG <b>V</b> LR <b>G</b> FLAG <b>V</b> A	-AMMAIAAFSPN	-
Y-FASLIDR <b>K</b> VR <b>K</b> TALN	-FINNV <b>L</b> GFFF <b>G</b> IF <b>R</b> YFIAAV	-IVFIVAVISP <b>D</b> GY	-
L-VASVLT <b>K</b> ALE <b>A</b> V <b>S</b> LG	-WLN <b>R</b> ML <b>G</b> AG <b>L</b> GAK <b>L</b> Y <b>L</b> LLV <b>S</b> L	-VIC <b>C</b> V <b>I</b> Q <b>F</b> IDSD <b>S</b> QL	-
L-IGHIV <b>G</b> DS <b>K</b> NT <b>I</b> VG	-KT <b>N</b> R <b>I</b> LG <b>M</b> LF <b>G</b> I <b>I</b> KAV <b>L</b> VC <b>F</b>	-LLT <b>I</b> HL <b>P</b> VE <b>G</b> N <b>L</b> K	-
YALGALLR <b>L</b> LT <b>G</b> QH <b>N</b> EN <b>R</b> GV <b>D</b> RL <b>G</b> FL <b>V</b> LG <b>G</b> AK <b>M</b> II <b>A</b> W <b>V</b>	-V <b>L</b> SA <b>I</b> AFF <b>E</b> Q <b>H</b> V <b>V</b> IA <b>G</b> RR <b>V</b> GL <b>S</b> P <b>K</b> ES <b>L</b> <b>S</b> <b>I</b> EV <b>A</b> RR <b>Y</b> N <b>L</b> F <b>E</b> MT <b>Q</b> <b>F</b> <b>A</b> P <b>V</b> <b>K</b> <b>N</b> <b>L</b> <b>V</b> <b>E</b> <b>A</b> <b>K</b> <b>A</b> <b>G</b>	-	-
I-LGSSLD <b>F</b> ASL <b>P</b> LN	-IV <b>N</b> R <b>W</b> L <b>G</b> GA <b>F</b> G <b>I</b> V <b>K</b> <b>V</b> I <b>A</b> V <b>F</b>	-LLNL <b>V</b> AF <b>V</b> P <b>N</b> A	-
L-AQNMI <b>L</b> N <b>M</b> V <b>E</b> N <b>L</b> N <b>E</b>	-GLD <b>R</b> I <b>G</b> ILT <b>G</b> ALE <b>E</b> GLIV <b>I</b> FL	-VIM <b>V</b> IE <b>I</b> Q <b>P</b> LF	-
L-LGKF <b>L</b> T <b>G</b> IAN <b>F</b> AF <b>L</b> G	-WL <b>N</b> KG <b>I</b> GG <b>F</b> FR <b>V</b> LK <b>T</b> I <b>L</b> LS <b>I</b>	-V <b>F</b> S <b>I</b> E <b>K</b> IN <b>Y</b> NN <b>N</b> FL	-
L-S <b>G</b> K <b>L</b> LA <b>R</b> FF <b>K</b> I <b>Q</b> <b>L</b> G	-WAD <b>K</b> S <b>G</b> GG <b>F</b> A <b>G</b> FK <b>S</b> AV <b>I</b> T <b>G</b> L	-ALS <b>F</b> LL <b>T</b> LP <b>D</b> NS	-
L-I <b>G</b> K <b>L</b> F <b>R</b> ALL <b>S</b> M <b>V</b> S <b>L</b> S	-ALD <b>R</b> LC <b>G</b> FL <b>V</b> GG <b>V</b> KA <b>A</b> IV <b>I</b> L	-VV <b>V</b> VAL <b>Q</b> HA <b>E</b> RF	-
A-L <b>G</b> S <b>G</b> K <b>K</b> L <b>T</b> L <b>S</b> L <b>G</b> L	-PLD <b>R</b> VL <b>G</b> FL <b>V</b> LG <b>S</b> SS <b>K</b> FFF <b>I</b> VS <b>I</b>	-IV <b>Y</b> AL <b>F</b> SV <b>T</b> AI <b>R</b> E	-
L-VGNFL <b>S</b> K <b>L</b> IK <b>L</b> S <b>G</b> L	-FLD <b>R</b> IG <b>G</b> GI <b>F</b> GA <b>K</b> I <b>F</b> LI <b>F</b> AI	-LV <b>F</b> CV <b>A</b> RI <b>D</b> FL <b>N</b> D	-

131	141	151	161	
- SKS EDW S K S Q L I P Q F S I I R W F -		- FD Y L Q S S S S F L P R A -		
- S K S E D W Q K S Q L I P E F S I I R W F -		- FD Y L Q S S S S F L P R V -		
- S Q S A D W K Q S Q L I P Q F S Y V I R W F -		- FD Y L Q S T S S S F L P T Q L P G R -		
- Q R P D W I T G A K S R V V L Q G T D W L M S L L P D D P E N T I L K R F K K N K P E D D Q T D A D Q A A P A S G D G Y S K P A R D S L K K L I E K P A A R -				
- T Q P E W V T Q A K S K P F L D G L V G K L E A V L P D D I - E P Q I R A R I L G K P Q E P T T T Q A P A E D V P A T N P P A T N N -				
- P D T E E W R Q S Y T L P F F V S L S E A V -		- L N H S - G G T A E T P E D D -		
- L F S N Q W K N S S L T T H Y L E I N S N F -		- F K H L P F N F - F L P W K N -		
- I R D K S F C V K I M T E Y A L R V T D T F P R F I K N D V E R Y V I S Q R E K E V I N D V L N D Y E N P K P D E F E K S K D I N -				
- S E W K P N S Q L T P Y F L E G A H V -		- S F V V V P P R F E Q Q I A Q G A T H L L Q Q T P D L L K S H P R K N D R D -		
- L I K R S S L G G M T V P L I N K A L E Y P L D M N K K V L R N W R I A E G Y L V R N W Y R L I G K A R E E A P R L K S R L K E E K K L -				
- I S Q T K K E Q S S L L Y Y P M E S F A G I F -		- F P A A K E V T Q Q Y I F K -		
- N L R R N N A I A Y S V K C S S L K T M G Y S S N E V D L R K L A T E K A S E L T K S F S T D K A I N S T E Q A A D S A K A A V K N A A D S V T T K V T E T A E K A K D A A I A A K D A A I A K T F E N G K S S A S K D S S N T K R D P K R A G R L Q D D P A Y K A L R K D P R F Q R L L Q D P K L K Q A L Q R G D T A A L L R H D G V L Q L I Q D P D V A A R L G A A R A S E R E P -				
- T A Q E T V S D S T L A Q T I V Q D -		- T P V L S E K V E E L -		
- D P Q K L L G E S V F Y E R I S P Y -		- L P Q G Q S L F E E G V K K L N V -		
- A K K E T L D N S I F Y N P I Q K I A A Y V -		- F P S I K K G Y E E M K K K A -		
- A F S K I R N S A I S K R L K I T P Y V F D M -		- L N K L P E V R K E N P F S R E -		
- L P G V E L K D S S R T V L L V N T I -		- L P D I K N S L D A F F P K Q I V -		
- N F E G K M A D S F F Y K P M F A T G N F I -		- L H I E T D D I K S L S D E N A T D T N S S D K D H -		
- K L D N F A K N S Y T L N L I K E T O S F I M N O P L T E N S L D H A S E K L O D I V S D I N N T O K G E -				

**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.