

1 Supplementary material for:

2 **Class II Contact-Dependent growth Inhibition (CDI) systems**
3 **allow for broad-range cross-species toxin delivery within the**
4 ***Enterobacteriaceae* family**

5
6
7
8 Petra Virtanen^{1†}, Marcus Wäneskog^{1†} and Sanna Koskiniemi^{1*}

9
10 **Affiliations:**

11 ¹ Department of Cell and Molecular Biology, Uppsala University, 75124 Sweden.

12 * Correspondence to: sanna.koskiniemi@icm.uu.se

13 † These authors contributed equally to this work.

14
15 **This supplementary file includes:**

16 Supplementary methods

17 Supplementary data Tables S1-S3

18 Supplementary references

19 Supplementary figures S1-S8

22 **Supplementary methods:**

23 **Chromosomal and plasmid constructs**

24 *Replacement of ompC CDS on the chromosome*

25 A *cat-sacB-amilCP* selection, counter-selection and screening marker, described previously
26 (Nasvall, 2017), was amplified with primers 1190 and 1191 to introduce 40bp overlap at both
27 5' and 3' ends with homology to the 5' and 3' ends of the *ompC* CDS of MG1655. The *cat-*
28 *sacB-amilCP* cassette was then integrated onto the genome of MG1655 by lambda red
29 recombination (Datsenko et al., 2000), simultaneously knocking-out *ompC*^(MG1655) and
30 generating strain SK2754. *ompC* CDS from *S. typhimurium* LT2, *E. coli* Nissle 1917, *E. coli*
31 F11 and *E. cloacae* ATCC 13047 was amplified with primers 1192 and 1193 and the
32 subsequent PCR products was integrated on the chromosome by lambda red recombination
33 (Datsenko et al., 2000) knocking-out the *cat-sacB-amilCP* cassette and generating seamless
34 *ompC* CDS swaps (SK2777-SK2780). Positive clones were selected for sucrose tolerance and
35 screened for the lack of blue coloring (result of chromo protein AmilCP expression) and
36 chloramphenicol sensitivity. The constructs were verified by PCR using primers 631 and 632,
37 as well as primers 634 and 635, and further verified by sequencing of the PCR products
38 generated from primers 631 and 632.

39

40 *Construction of pSC101::PJ23101-ompC expressing plasmids*

41 *ompC* was amplified from *S. typhimurium* LT2, *E. coli* K12 MG1655, *E. coli* Nissle 1917, *E.*
42 *coli* F11 and *E. cloacae* ATCC 13047 using oligos 606-612 as indicated in Table S3 and
43 inserted into the pSC101 plasmid under the control of the PJ23101 promoter. The resulting
44 plasmids were verified by sequencing using oligos 482 and 483.

45

46

47 *Construction of pCloDF1::PJ23101-cdi^{EC93main} expression plasmid*

48 *cdiI* was amplified from EC93 using oligos 964 and 972 as indicated in Table S3 and cloned
49 into the pCloDF1 plasmid under the control of the PJ23101 promoter. The resulting plasmids
50 were verified by sequencing using oligos 986 and 987.

51

52 *Replacement of the cdiA receptor-binding domains on the medium-copy pcolE1-cdiBAI*
53 *plasmid*

54 To change the receptor-binding domain of *cdiA^{EC93}*, a *cat-sacB* cassette (Nasvall, 2017) with
55 homology upstream and downstream of the receptor-binding domain of *cdiA^{EC93}* was
56 amplified using oligos 583 and 613. The insert was designed to create SrfI restriction sites
57 upstream and downstream of the receptor-binding domain when inserted. The receptor-
58 binding domains from *E. cloacae* ATCC 13047 and *E. coli* CFT073 *cdiA* was amplified using
59 oligos 794, 795, 584 and 585 and cloned into pDAL660 *cdiA::cat-sacB* using SrfI restriction
60 sites. A potential class II CDI system from *S. typhi* was identified bioinformatically and the
61 receptor-binding domain was synthesized (Gene art, Thermo Scientific, USA) and cloned as
62 described for the other constructs. The resulting plasmids were transformed into *E. coli* K12
63 MG1655 *ompC::kan* and positive clones were selected for sucrose tolerance and screened for
64 Cam sensitivity, followed by PCR verification and sequencing with primers indicated in table
65 S2. The resulting plasmids carrying the *cdiBAI^{EC93}* system with the receptor binding domain
66 swaps was transformed into *E. coli* K12 MG1655 *ompC::kan*.

67

68 *sYFP2 reporter plasmid*

69 The *pJ23101-sYFP2* and *osmY-mtagBFP* reporter plasmid (SK2292), previously described in
70 (Ghosh et al., 2018) was modified to remove the ClpXP dependent degradation tags fused to
71 both sYFP2 and mtagBFP. The pSC101 plasmid was amplified with primers 1062 and 1276,

72 the resulting PCR-products were gel-purified followed by re-circularized with T4 DNA ligase
73 (Thermo Scientific, USA) and transformation into NEB5alfa (New England Biolabs, USA)
74 generating plasmid SK2876. Positive clones were verified by sequencing using the same
75 primers described before (Ghosh et al., 2018). The SK2876 plasmid was amplified with
76 primers 1050 and 1266, the resulting PCR-products were then gel-purified followed by re-
77 circularized with T4 DNA ligase (Thermo Scientific, USA) and transformation into NEB5alfa
78 (New England Biolabs, USA) generating plasmid SK2938. Positive clones were verified same
79 as above.

80

81

82 **Table S1. Bacterial strains used in this study**

| Strain number | Genotype | Origin |
|---------------|---|---------------------------|
| SK2 | <i>E. coli</i> K12 MG1655 | (Ghosh et al., 2018) |
| SK160 | <i>Enterobacter cloacae</i> ATCC 13047 | (Beck et al., 2014) |
| SK161 | <i>E. coli</i> UPEC536 | Gift from David Low |
| SK540 | <i>E. coli</i> CFT073 <i>cobUS::GFP::cat</i> | Gift from Agneta Richter |
| SK620 | <i>E. coli</i> K12 MG1655 <i>lacA-cat</i> | This study |
| SK1031 | <i>S. typhimurium</i> LT2 /pDAL7720 | This study |
| SK1323 | <i>E. coli</i> K12 MG1655 Δ <i>ompC lacA-cat</i> | This study |
| SK1360 | <i>E. coli</i> K12 MG1655 <i>ompC::kan</i> /pDAL7720 | This study |
| SK1435 | <i>E. coli</i> K12 MG1655 <i>ompC::kan</i> /pSK1435 | This study |
| SK1543 | <i>Enterobacter aerogenes</i> ATCC 13048 | This study |
| SK1735 | <i>K. pneumoniae</i> subsp. <i>Pneumoniae</i> C105 | Gift from Linus Sandegren |
| SK1736 | <i>K. pneumoniae</i> subsp. <i>Pneumoniae</i> C105 NCV (non-capsulating mutant) | Gift from Linus Sandegren |
| SK1998 | <i>E. coli</i> K12 MG1655 Δ <i>ompC lacA-cat</i> /pSC101:: <i>ompC</i> ^{Sty} | This study |
| SK1999 | <i>E. coli</i> K12 MG1655 Δ <i>ompC lacA-cat</i> /pSC101:: <i>ompC</i> ^{K12} | This study |
| SK2000 | <i>E. coli</i> K12 MG1655 Δ <i>ompC lacA-cat</i> /pSC101:: <i>ompC</i> ^{CFT073} | This study |
| SK2001 | <i>E. coli</i> K12 MG1655 Δ <i>ompC lacA-cat</i> /pSC101:: <i>ompC</i> ^{F11} | This study |
| SK2002 | <i>E. coli</i> K12 MG1655 Δ <i>ompC lacA-cat</i> /pSC101:: <i>ompC</i> ^{ECL} | This study |
| SK2020 | <i>E. coli</i> K12 MG1655 Δ <i>ompC lacA-cat</i> /pSC101:: <i>ompC</i> ^{Sty} /pSK1752 | This study |
| SK2021 | <i>E. coli</i> K12 MG1655 Δ <i>ompC lacA-cat</i> /pSC101:: <i>ompC</i> ^{K12} /pSK1752 | This study |
| SK2022 | <i>E. coli</i> K12 MG1655 Δ <i>ompC lacA-cat</i> /pSC101:: <i>ompC</i> ^{CFT073} /pSK1752 | This study |
| SK2023 | <i>E. coli</i> K12 MG1655 Δ <i>ompC lacA-cat</i> /pSC101:: <i>ompC</i> ^{F11} /pSK1752 | This study |
| SK2024 | <i>E. coli</i> K12 MG1655 Δ <i>ompC lacA-cat</i> /pSC101:: <i>ompC</i> ^{ECL} /pSK1752 | This study |
| SK2167 | <i>E. coli</i> K12 MG1655 <i>ompC::kan</i> /pSK2167 | This study |
| SK2208 | <i>E. coli</i> K12 MG1655 <i>ompC::kan</i> /pSK2208 | This Study |
| SK2211 | <i>E. coli</i> K12 MG1655 Δ <i>ompC lacA-cat</i> /pSC101:: <i>omp36</i> ^{E. aerogenes} | This Study |
| SK2338 | <i>E. coli</i> K12 MG1655 Δ <i>ompC lacA-cat</i> /pSC101:: <i>ompK36</i> ^{K. pneuminiae} | This Study |
| SK2462 | <i>S. typhimurium</i> LT2 <i>STM1553::cat</i> | Lab collection |
| SK2468 | <i>E. coli</i> K12 MG1655 Δ <i>ompC lacA-cat</i> /pSC101:: <i>omp36</i> ^{E. aerogenes} /pSK1752 | This Study |
| SK2469 | <i>E. coli</i> K12 MG1655 Δ <i>ompC lacA-cat</i> /pSC101:: <i>ompK36</i> ^{K. pneuminiae} /pSK1752 | This Study |

| | | |
|--------|--|------------|
| SK2565 | Eco MG1655 $\Delta ompC \Delta ompF$ /pDAL7720 | This study |
| SK2639 | <i>E. coli</i> K12 MG1655 $\Delta ompC lacA-cat$ /pSC101 /pSK1752 | This study |
| SK2754 | <i>E. coli</i> MG1655 $ompC::cat-sacB amilCP$ /pSIM5tet | This study |
| SK2777 | <i>E. coli</i> MG1655 $ompC^{Sly}$ | This study |
| SK2778 | <i>E. coli</i> MG1655 $ompC^{CFT073}$ | This study |
| SK2779 | <i>E. coli</i> MG1655 $ompC^{F11}$ | This study |
| SK2780 | <i>E. coli</i> MG1655 $ompC^{ECL}$ | This study |
| SK2817 | <i>E. coli</i> K12 MG1655 $ompC^{Sly} lacA-cat$ | This study |
| SK2818 | <i>E. coli</i> K12 MG1655 $ompC^{CFT073} lacA-cat$ | This study |
| SK2819 | <i>E. coli</i> K12 MG1655 $ompC^{F11} lacA-cat$ | This study |
| SK2820 | <i>E. coli</i> K12 MG1655 $ompC^{ECL} lacA-cat$ | This study |
| SK3068 | <i>E. coli</i> K12 MG1655 $lacA-cat$ /pCloDF1:: PJ23101- <i>cdi</i> ^{EC93} | This study |
| SK3287 | <i>E. coli</i> K12 MG1655 $ompF::tet lacA-cat$ | This study |
| SK3288 | <i>E. coli</i> K12 MG1655 $ompC^{Sly} lacA-cat ompF::tet$ | This study |
| SK3289 | <i>E. coli</i> K12 MG1655 $ompC^{CFT073} lacA-cat ompF::tet$ | This study |
| SK3362 | <i>E. coli</i> K12 MG1655 $ompC^{F11} lacA-cat ompF::tet$ | This study |
| SK3363 | <i>E. coli</i> K12 MG1655 $ompC^{ECL} lacA-cat ompF::tet$ | This study |
| SK3364 | <i>E. coli</i> K12 MG1655 $\Delta ompC \Delta ompF lacA-cat$ | This study |
| SK3429 | <i>E. coli</i> K12 MG1655 $\Delta ompC \Delta ompF galK::dTomato-catR$ /pDAL7720 | This study |
| SK3430 | <i>E. coli</i> K12 MG1655 $lacA-cat$ /pSK2938 | This study |
| SK3431 | <i>E. coli</i> K12 MG1655 $lacA-cat ompF::tet$ /pSK2938 | This study |
| SK3432 | <i>E. coli</i> K12 MG1655 $ompC^{ECL} lacA-cat$ /pSK2938 | This study |
| SK3433 | <i>E. coli</i> K12 MG1655 $ompC^{ECL} lacA-cat ompF::tet$ /pSK2938 | This study |
| SK3434 | <i>E. coli</i> K12 MG1655 $\Delta ompC lacA-cat$ /pSK2938 | This study |
| SK3435 | <i>E. coli</i> K12 MG1655 $\Delta ompC \Delta ompF lacA-cat$ /pSK2938 | This study |
| SK3792 | <i>E. coli</i> K12 MG1655 $ompC^{Sly} lacA-cat$ /pSK1752 | This study |
| SK3793 | <i>E. coli</i> K12 MG1655 $ompC^{CFT073} lacA-cat$ /pSK1752 | This study |
| SK3794 | <i>E. coli</i> K12 MG1655 $ompC^{F11} lacA-cat$ /pSK1752 | This study |
| SK3795 | <i>E. coli</i> K12 MG1655 $ompC^{ECL} lacA-cat$ /pSK1752 | This study |
| SK3796 | <i>K. pneumoniae</i> subsp. <i>Pneumoniae</i> C105 /pSK1752 | This study |
| SK3797 | <i>K. pneumoniae</i> subsp. <i>Pneumoniae</i> C105 NCV /pSK1752 | This study |
| SK3798 | <i>E. coli</i> UPEC536 /pSK1752 | This study |
| SK3799 | <i>E. coli</i> K12 MG1655 $\Delta ompC lacA-cat$ /pSK1752 | This study |
| SK3800 | <i>E. coli</i> K12 MG1655 $\Delta ompC galK::dTomato-catR$ | This study |
| SK3801 | <i>E. coli</i> K12 MG1655 $galK::dTomato-catR$ | This study |
| SK3802 | <i>E. coli</i> K12 MG1655 $ompC^{Sly} galK::dTomato-catR$ | This study |
| SK3803 | <i>E. coli</i> K12 MG1655 $ompC^{CFT073} galK::dTomato-catR$ | This study |
| SK3804 | <i>E. coli</i> K12 MG1655 $ompC^{F11} galK::dTomato-catR$ | This study |
| SK3805 | <i>E. coli</i> K12 MG1655 $ompC^{ECL} galK::dTomato-catR$ | This study |
| SK3806 | <i>E. coli</i> K12 MG1655 $\Delta ompC galK::sYFP2-catR$ /pDAL7720 | This study |
| SK3807 | <i>E. coli</i> CFT073 $cobUS::GFP::cat$ /pSK1752 | This study |
| SK3808 | <i>S. typhimurium</i> LT2 $STM1553::cat$ /pSK1752 | This study |
| SK3811 | <i>Enterobacter cloacae</i> ATCC 13047 /pSK1752 | This study |

| | | |
|--------|--|------------|
| SK3812 | <i>Enterobacter cloacae</i> ATCC 13047 <i>vasK::kan</i> | This study |
| SK3813 | <i>Enterobacter cloacae</i> ATCC 13047 <i>vasK::kan</i> /pSK1752 | This study |
| SK3876 | <i>Enterobacter aerogenes</i> ATCC 13048 /pSK1752 | This study |

83

84
85**Table S2. Plasmids used in this study**

| Plasmid | Genotype | Origin |
|--------------|---|----------------------|
| pDAL660Δ1-39 | pWEB:: <i>cdiBAI</i> ^{EC93} | (Aoki et al., 2005) |
| pDAL878 | pDAL660 derivative, deletion of main CdiA-CT/I | Gift from David Low |
| pDAL7720 | pDAL660Δ1-39 derivative that expresses chimeric CdiA ^{EC93} with residues Ser1347 to Gly2205 replaced with residues Ala1345 to Gly2310 from CdiA ^{EC536} ; Amp ^r | (Ruhe, 2017) |
| pCloDF1 | Empty vector | |
| pSC101 | Empty vector | |
| pSK1435 | pDAL660Δ1-39 derivative that expresses chimeric CdiA ^{EC93} with residues 1208 to 2266 replaced with residues 1225 to 2391 from CdiA ^{Eco Nissle} ; Amp ^r | This study |
| pSK1752 | pCloDF1:: PJ23101- <i>cdiI</i> ^{EC93} | This study |
| SK1978 | pMA-T::Salmonella <i>cdiA</i> BD part 1 | This study |
| SK1979 | pMK-RQ::Salmonella <i>cdiA</i> BD part 2 | This study |
| pSK1998 | pSC101:: PJ23101- <i>ompC</i> (<i>S. typhimurium</i>) | This study |
| pSK1999 | pSC101:: PJ23101- <i>ompC</i> (<i>E. coli</i> K12 MG1655) | This study |
| pSK2000 | pSC101:: PJ23101- <i>ompC</i> (<i>E. coli</i> Nissle 1917) | This study |
| pSK2001 | pSC101:: PJ23101- <i>ompC</i> (<i>E. coli</i> F11) | This study |
| pSK2002 | pSC101:: PJ23101- <i>ompC</i> (<i>E. cloacae</i>) | This study |
| pSK2167 | pDAL660Δ1-39 derivative that expresses chimeric CdiA ^{EC93} with residues 1208 to 2266 replaced with residues 1224 to 2389 from CdiA ^{S.typhi} ; Amp ^r | This study |
| pSK2208 | pDAL660Δ1-39 derivative that expresses chimeric CdiA ^{EC93} with residues 1208 to 2266 replaced with residues 1326 to 2438 from CdiA ^{E.cloacae} ; Amp ^r | This study |
| pSK2292 | pSC101(pJ23101:sYFP2(deg-tag) pOsmY:mtagBFP2(deg-tag)) | (Ghosh et al., 2018) |
| pSK2876 | pSC101(pJ23101:sYFP2(deg-tag) pOsmY:mtagBFP) | This study |
| pSK2938 | pSC101(pJ23101:sYFP2 pOsmY:mtagBFP) | This study |

86

87

Table S3. Oligos used in this study

| Oligo | Sequence (5' to 3') | Comment |
|-------|--|---|
| 482 | GTCTAAGAAACCATTATTAT CATGAC | Forward primer used for sequencing of pSC101 constructs |
| 483 | CCAGAACAGCCCGTTTGC | Forward primer used for sequencing of pSC101 constructs |
| 578 | CCTGAAGCTGTTTACAGACC GTCTG | Forward primer binding in the binding domain of <i>cdiA</i> (EC93) |
| 579 | TCCTTCAGCGTATCCGGCAG | Reverse primer binding in the binding domain of <i>cdiA</i> (EC93) |
| 580 | GGTGAATACTGTCAACGGCG GAC | Forward primer binding up-stream of the binding domain of <i>cdiA</i> (EC93) |
| 581 | GGCTGTCGCTGGTTTCTTTCG | Reverse primer binding down-stream of the binding domain of <i>cdiA</i> (EC93) |
| 582 | GTGGCCACCGGTGATGTCAC ACTGAACTGATTGCTGCCC gggcatagCAGGAGCTAAGGAA GCTAAAATG | Forward primer to amplify <i>cat-sacB</i> cassette with homology upstream and downstream of the <i>cdiA</i> receptor binding domain |
| 584 | TCACGAATCATGGTACCCTG GC | Forward primer used to amplify the <i>cdiA</i> binding domain from <i>E. coli</i> CFT073 |
| 585 | CGGGTCAACCACCACACTGT C | Reverse primer used to amplify the <i>cdiA</i> binding domain from <i>E. coli</i> CFT073 |
| 606 | ATAggatccCAGAGGGTTAATA ACATGAA | Forward primer used to amplify <i>ompC</i> from <i>E. coli</i> MG1655, <i>S. Typhimurium</i> LT2, <i>E. coli</i> F11 or <i>E. coli</i> CFT073 and <i>E. cloacae</i> ATCC 13047 introducing restriction site for BamHI at the 5' end |
| 608 | GCGgtcgacCAATCGAGATTAG AACTGG | Reverse primer to amplify <i>ompC</i> from <i>E. coli</i> MG1655, introducing restriction site for Sall at the 3' end |
| 609 | GCGgtcgacCTGATTAGAACTG GTAAACC | Reverse primer to amplify <i>ompC</i> from <i>S. Typhimurium</i> LT2, introducing restriction site for Sall at the 3' end |
| 610 | GCGgtcgacAAAGCGATTAGAA CTGGT | Reverse primer to amplify <i>ompC</i> from <i>E. cloacae</i> ATCC 13047, introducing restriction site for Sall at the 3' end |
| 611 | GCGgtcgacCGAGATTAGAACT GGTAAAC | Reverse primer to amplify <i>ompC</i> from <i>E. coli</i> F11, introducing restriction site for |
| 612 | GCGgtcgacGAGATTAGAACTG GTAAACC | Reverse primer to amplify <i>ompC</i> from <i>E. coli</i> CFT073, introducing restriction site for Sall at the 3' end |
| 613 | GTGGCCACCGGTGATGTCAC ACTGAACTGATTGCTGCCC gggcatagTGTAGGCTGGAGCTG CTTCGA | Forward primer to amplify <i>cat-sacB</i> cassette with homology upstream and downstream of the <i>cdiA</i> receptor binding domain |
| 631 | CGTGATTATCCTCATGC | Forward primer binding up-stream of <i>ompC</i> of MG1655 |

| | | |
|-----|--|---|
| 632 | TTAGTATCATATTCGTGTTGG | Reverse primer binding down-stream of <i>ompC</i> of MG1655 |
| 634 | GAAACTCAGGTTACTGACCA GC | Forward primer binding in the <i>ompC</i> of MG1655 |
| 635 | GAACTGGTACTGAGCAACAG C | Reverse primer binding in the <i>ompC</i> of MG1655 |
| 665 | CGGAACAACCACTGCACA | Primer to be used for sequencing of <i>S. Typhi</i> , <i>E. coli</i> CFT073 and F11 <i>cdiA</i> binding domain swaps |
| 666 | CTGAATGCGGGGCTGATAAG | Primer to be used for sequencing of <i>S. Typhi</i> , <i>E. coli</i> CFT073 and F11 <i>cdiA</i> binding domain swaps |
| 667 | GAGACAGTCCGTCAGCAG | Primer to be used for sequencing of <i>S. Typhi</i> , <i>E. coli</i> CFT073 and F11 <i>cdiA</i> binding domain swaps |
| 679 | CAACGGACTGGGTTTCAGACA C | Primer to be used for sequencing of <i>S. Typhi</i> , <i>E. coli</i> CFT073 and F11 <i>cdiA</i> binding domain swaps |
| 779 | GACCTGCTGGTGAATTAC | Forward primer that binds upstream of the binding domain in <i>cdiA</i> EC93 (pDAL660) |
| 780 | GTATCTGATTACGGTGAACC | Forward primer that binds in conserved region in <i>cdiA</i> binding domain from <i>E. coli</i> CFT073, F11 and <i>E. cloacae</i> ATCC 13047. |
| 781 | GGTTCACCGTAATCAGATAC | Reverse primer that binds in conserved region in <i>cdiA</i> binding domain from <i>E. coli</i> CFT073, F11 and <i>E. cloacae</i> ATCC 13047. |
| 786 | CATCTGTTCCGTGTCTGAAC CCA | Reverse primer used together with 584 to amplify first part of synthesized <i>S. Typhi cdiA</i> binding-domain |
| 787 | TGGGTTTCAGACACGGAACAG ATG | Forward primer used together with 585 to amplify second part of synthesized <i>S. Typhi cdiA</i> binding-domain |
| 794 | TCGTTAACACCGGCACCCT | Forward primer to amplify <i>cdiA</i> binding domain from <i>E. cloacae</i> ATCC 13047 |
| 795 | TGGCTCAATCACCACGCTG | Reverse primer to amplify <i>cdiA</i> binding domain from <i>E. cloacae</i> ATCC 13047 |
| 796 | AGCAAATGGGAGCCTCTGAC | Forward primer for sequencing of <i>E. cloacae cdiA</i> binding domain |
| 835 | GCATTCAGACTCAGGTCGTT | Reverse primer for sequencing of <i>S. Typhi cdiA</i> binding domain |
| 838 | GTCAGAGGCTCCCATTTGCT | Reverse primer primer for sequencing of <i>E. cloacae cdiA</i> binding domain |
| 839 | AACGAGATTGTGACCAGCGA | Forward primer for sequencing of <i>E. cloacae cdiA</i> binding domain |
| 964 | ATATGTCGACGGTAATAAGG AAGGGGC | Forward primer to amplify <i>cdiI</i> ^{EC93main} with Sall restriction-site |
| 972 | TTAAGTCGACCTATTTTCTGT CTAAGATACTAAGGC | Reverse primer to amplify <i>cdiI</i> ^{EC93main} with Sall restriction-site |

| | | |
|------|--|---|
| 986 | ATCACCACCACCATCACGTG G | Primer to be used for sequencing of pCloDF:: <i>cdiI</i> ^{EC93main} plasmid |
| 987 | GTGACCGTGTGCTTCTCAA TGC | Primer to be used for sequencing of pCloDF:: <i>cdiI</i> ^{EC93main} plasmid |
| 1050 | CCCTAGACCTAGGGTACGG | Forward primer for amplifying pSC101 plasmid backbone |
| 1062 | CTGCTCGAGGTGAAGACGAA AGGG | Reverse primer for amplifying pSC101 plasmid backbone |
| 1190 | GCAAATAAAGGCATATAACA GAGGGTTAATAACATGAAAG GATCTATCAACAGGAGTCCA AGC | Forward primer used to amplify <i>cat-sacB-amilCP</i> cassette with homology to upstream sequence of <i>ompC</i> CDS of MG1655 |
| 1191 | TGTTTCGATATCAATCGAGAT TAGAACTGGTAAACCAGACC GTGTAGGCTGGAGCTGCTTC | Reverse primer used to amplify <i>cat-sacB-amilCP</i> cassette with homology to downstream sequence of <i>ompC</i> CDS of MG1655 |
| 1192 | GCAAATAAAGGCATATAACA GAGGGTTAATAACATGAAAG | Forward primer used to amplify <i>ompC</i> CDS from <i>S. Typhimurium</i> LT2, <i>E. coli</i> F11, <i>E. coli</i> CFT073 and <i>E. cloacae</i> ATCC 13047 |
| 1193 | TGTTTCGATATCAATCGAGAT TAGAACTGGTAAACCAGACC | Reverse primer used to amplify <i>ompC</i> CDS from <i>S. Typhimurium</i> LT2, <i>E. coli</i> F11, <i>E. coli</i> CFT073 and <i>E. cloacae</i> ATCC 13047 |
| 1262 | GGTGAATTACCACACATTCA GC | Forward primer used to amplify <i>cdiA</i> BD ^{UPEC536} |
| 1263 | TCGTCTCAGACTTCGACTGC | Forward primer used to amplify <i>cdiA</i> BD ^{UPEC536} |
| 1264 | GCAGGCAACCTGCTGCTTGA CGCTCAGGACTTCAGTGGTC CATATGAATATCCTCCTTAG TTCC | Forward primer used to amplify <i>cat-sacB-amilCP</i> cassette with homology to upstream sequence of <i>cdiA</i> BD ^{EC93} |
| 1265 | GGTGACCGCATTATTGATGG CACTACCCACCGCACCGGAC GTAGGCTGGAGCTGCTTC | Reverse primer used to amplify <i>cat-sacB-amilCP</i> cassette with homology to upstream sequence of <i>cdiA</i> BD ^{EC93} |
| 1266 | TTATTTATACAGCTCATCCAT ACCC | Reverse primer to amplify sYFP2 without degradation tag |
| 1276 | TTAATTCAGTTTATGACCCA GCTTGCTAG | Forward primer to amplify mtagBFP without degradation tag |

90

91

92 **References:**

- 93 Aoki, S. K., Pamma, R., Hernday, A. D., Bickham, J. E., Braaten, B. A., & Low, D. A.
94 (2005). Contact-dependent inhibition of growth in *Escherichia coli*. *Science*,
95 309(5738), 1245-1248. doi:10.1126/science.1115109
- 96 Beck, C. M., Morse, R. P., Cunningham, D. A., Iniguez, A., Low, D. A., Goulding, C. W., &
97 Hayes, C. S. (2014). CdiA from *Enterobacter cloacae* delivers a toxic ribosomal
98 RNase into target bacteria. *Structure*, 22(5), 707-718. doi:10.1016/j.str.2014.02.012
- 99 Datsenko, K. A., & Wanner, B. L. (2000). One-step inactivation of chromosomal genes in
100 *Escherichia coli* K-12 using PCR products. *Proceedings of the National Academy of*
101 *Sciences of the United States of America*, 97(12), 6640-6645.
102 doi:10.1073/pnas.120163297
- 103 Ghosh, A., Baltekin, O., Waneskog, M., Elkhalfi, D., Hammarlof, D. L., Elf, J., &
104 Koskiniemi, S. (2018). Contact-dependent growth inhibition induces high levels of
105 antibiotic-tolerant persister cells in clonal bacterial populations. *EMBO J*.
106 doi:10.15252/embj.201798026
- 107 Nasvall, J. (2017). Direct and Inverted Repeat stimulated excision (DIRex): Simple, single-
108 step, and scar-free mutagenesis of bacterial genes. *PLoS One*, 12(8), e0184126.
109 doi:10.1371/journal.pone.0184126
- 110 Ruhe, Z. C., Nguyen, J. Y., Xiao, J., Koskiniemi, S., Beck, C. M., Perkins, B., Low, D. A.,
111 Hayes, C. S. (2017). CdiA effectors use modular receptor-binding domains to
112 recognize target bacteria. *Submitted manuscript*.

114

115 **Supplementary figures:**

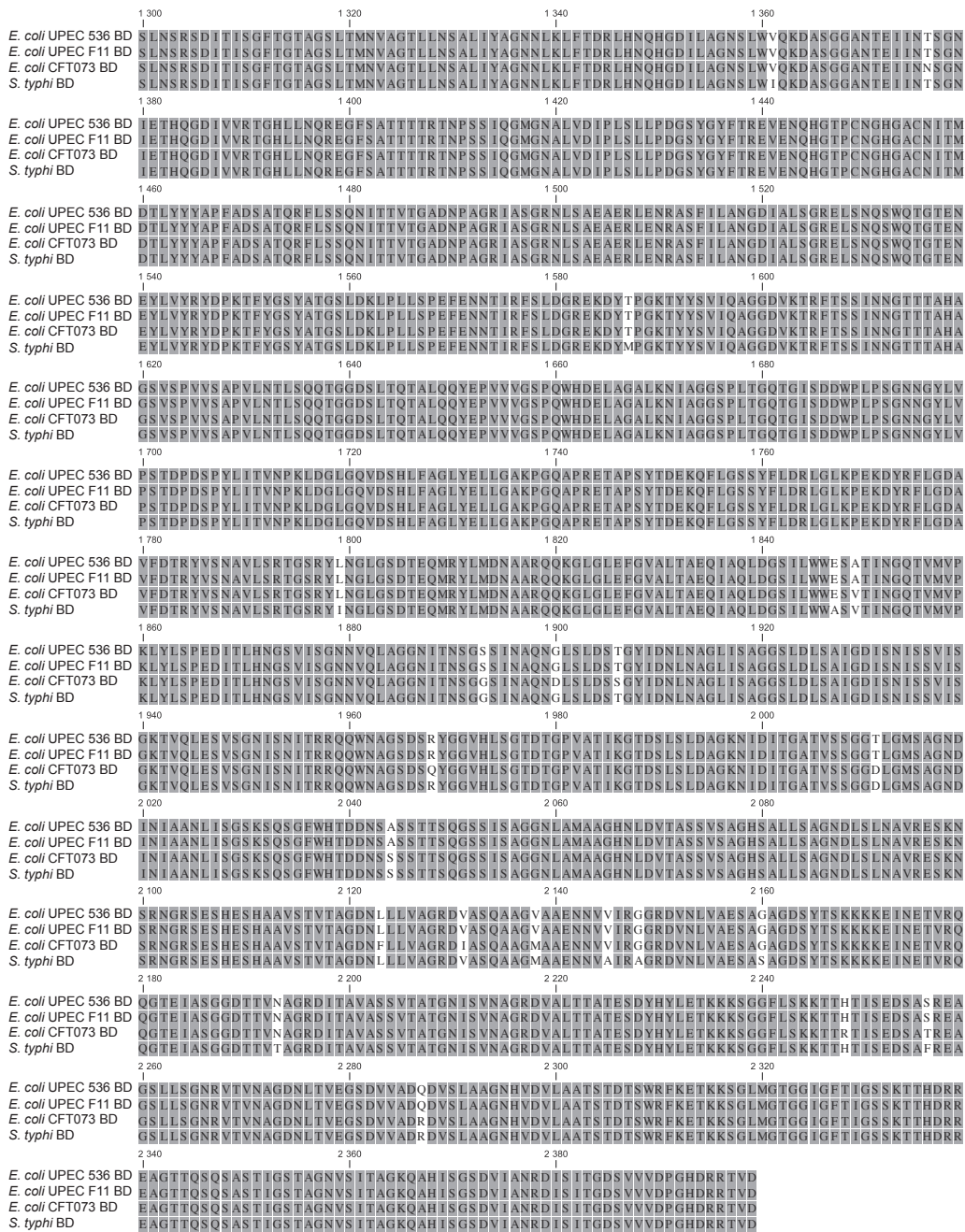
116 **Figure S1. Alignment of CdiA receptor binding domains from *Escherichia coli* strains**

117 **UPEC 536, UPEC F11, CFT073 and *Salmonella typhi*.** The receptor binding domains

118 located between amino acids 1300-2390 in CdiA are shown. Homologous residues are shown

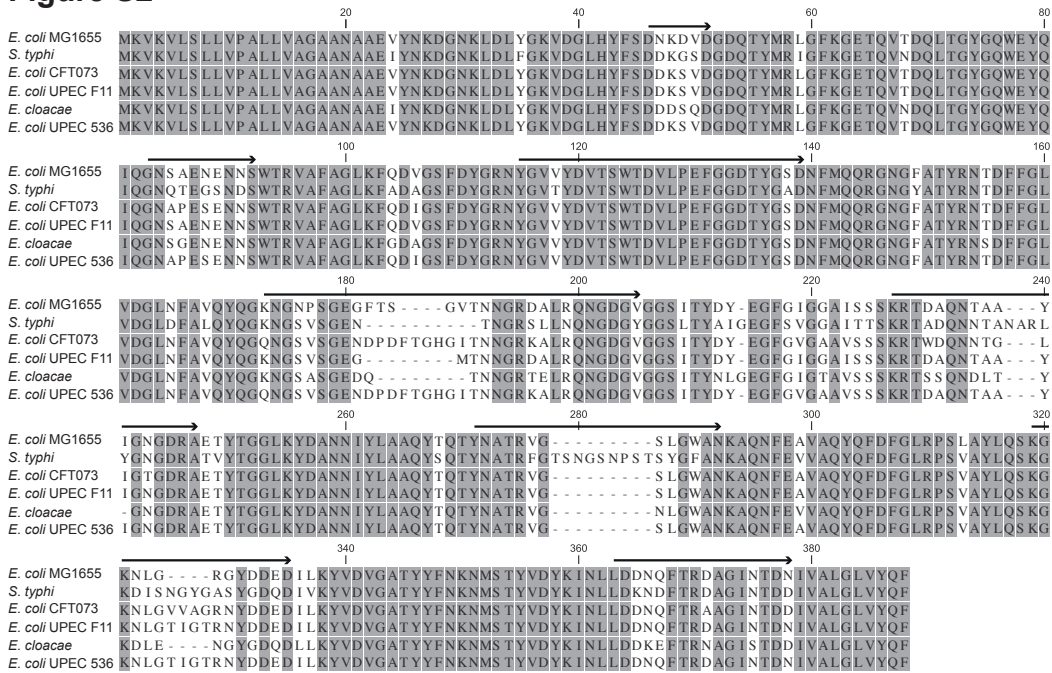
119 in grey and non-homologous residues are white.

Figure S1



121 **Figure S2. Alignment of OmpC proteins from *Escherichia coli* strains K12 MG1655,**
 122 **UPEC 536, UPEC F11, CFT073 and *Enterobacter cloacae* and *Salmonella typhi*.**
 123 Homologous residues are shown in grey and non-homologous residues are white. The
 124 location of the 8 extracellular loops in OmpC are marked with a black arrow above the
 125 sequence.

Figure S2



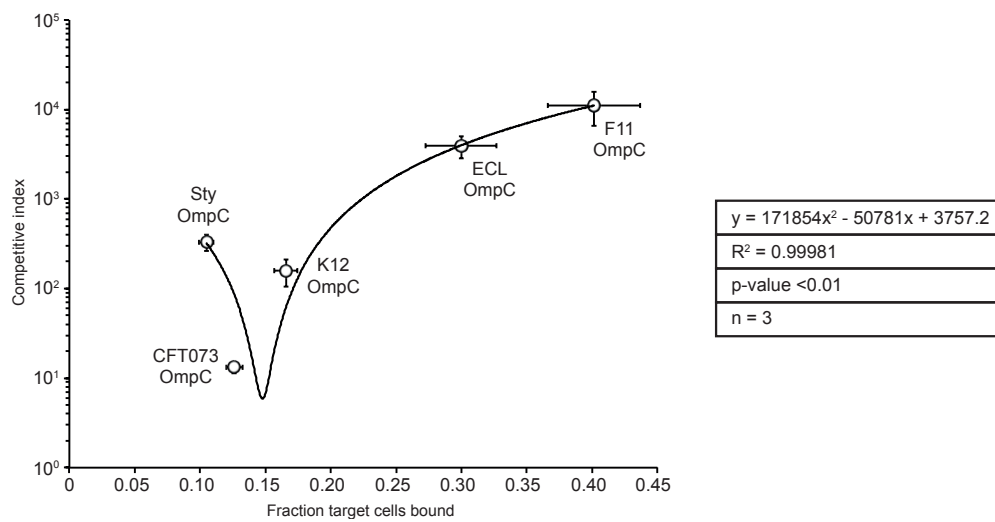
126

127

128

129 **Figure S3. Correlation of cell-cell binding with growth inhibition.** Fraction of target cells,
130 expressing different OmpC's, bound to inhibitor cells expressing CdiA^{F11} was correlated
131 against the measured competitive index of the same strains when co-cultured in LB (n=3
132 biological replicates). Statistical significance was determined using Pearson correlation tables
133 for R² values.

Figure S3



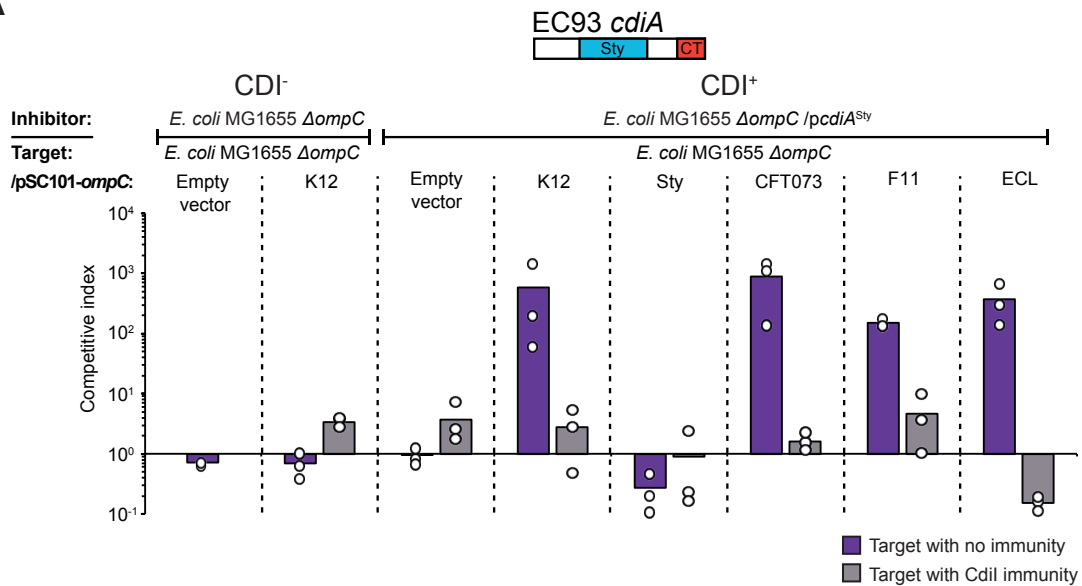
134

135

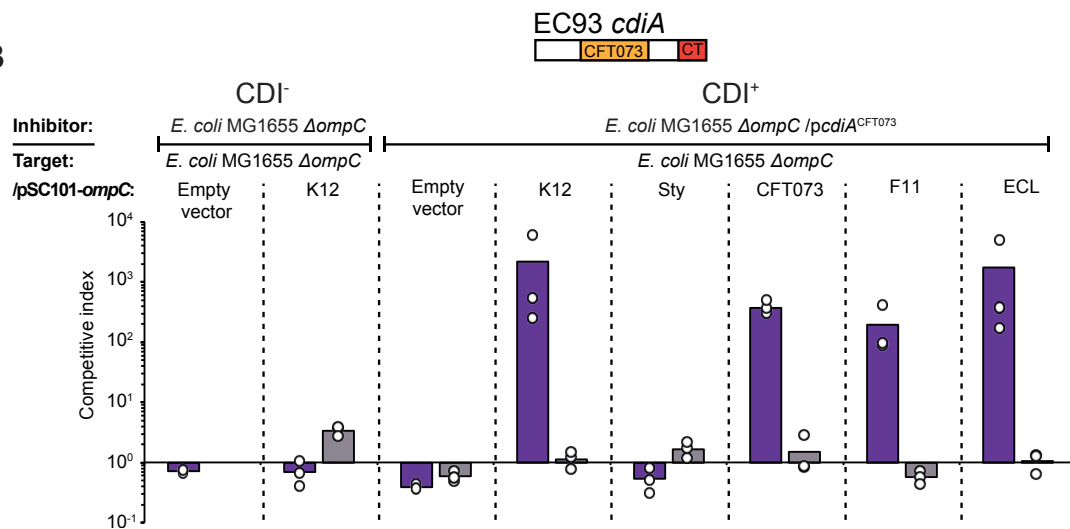
136 **Figure S4. Other Class II CdiA RBD is able to deliver effectors to cells expressing the**
 137 **OmpC receptor from other strains and species on solid media. A & B) Average**
 138 competitive index of cells expressing CdiA^{Sty} (A) or CdiA^{CFT073} (B) after co-culturing with
 139 MG1655 cells expressing different OmpC's from a low-copy (pSC101) plasmid with (light
 140 grey bars) or without (dark purple bars) CdiI expressed from plasmid (n=3 biological
 141 replicates). Cells were co-cultured for 24h on solid M9Glu media. Individual data points of
 142 the biological replicates are shown as black and white circles.

Figure S4

A



B

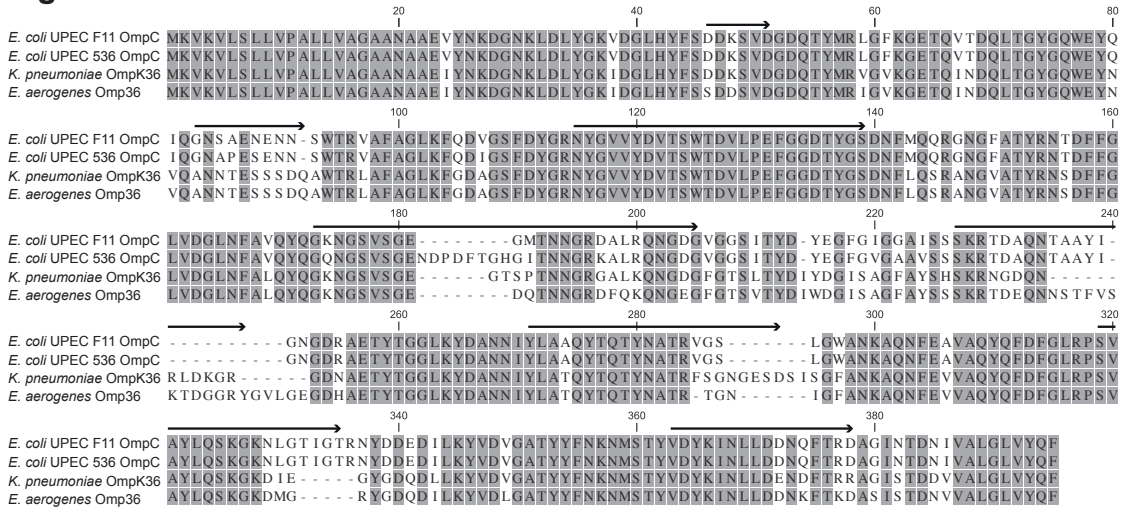


143

144

145 **Figure S5. Alignment of OmpC homologs from *Klebsiella pneumoniae* and *Enterobacter***
 146 ***aerogenes*.** Homologous residues are shown in grey and non-homologous residues are white.

Figure S5

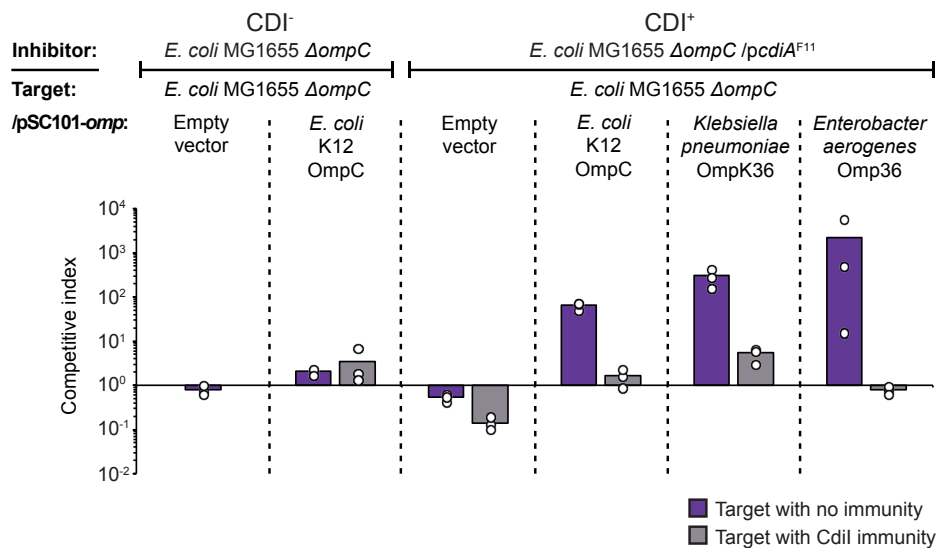


147

148

149 **Figure S6. Expression of OmpC homologs from *Klebsiella pneumoniae* and *Enterobacter***
 150 ***aerogenes* allow effector delivery into MG1655 cells.** Average competitive index of cells
 151 expressing CdiA^{F11} (after co-culturing with MG1655 cells expressing different OmpC's from
 152 a low-copy (pSC101) plasmid with (light grey bars) or without (dark purple bars) CdiI
 153 expressed from plasmid (n=3 biological replicates). Cells were co-cultured for 24h on solid
 154 M9Glu media. Individual data points of the biological replicates are shown as black and white
 155 circles.

Figure S6
A



156

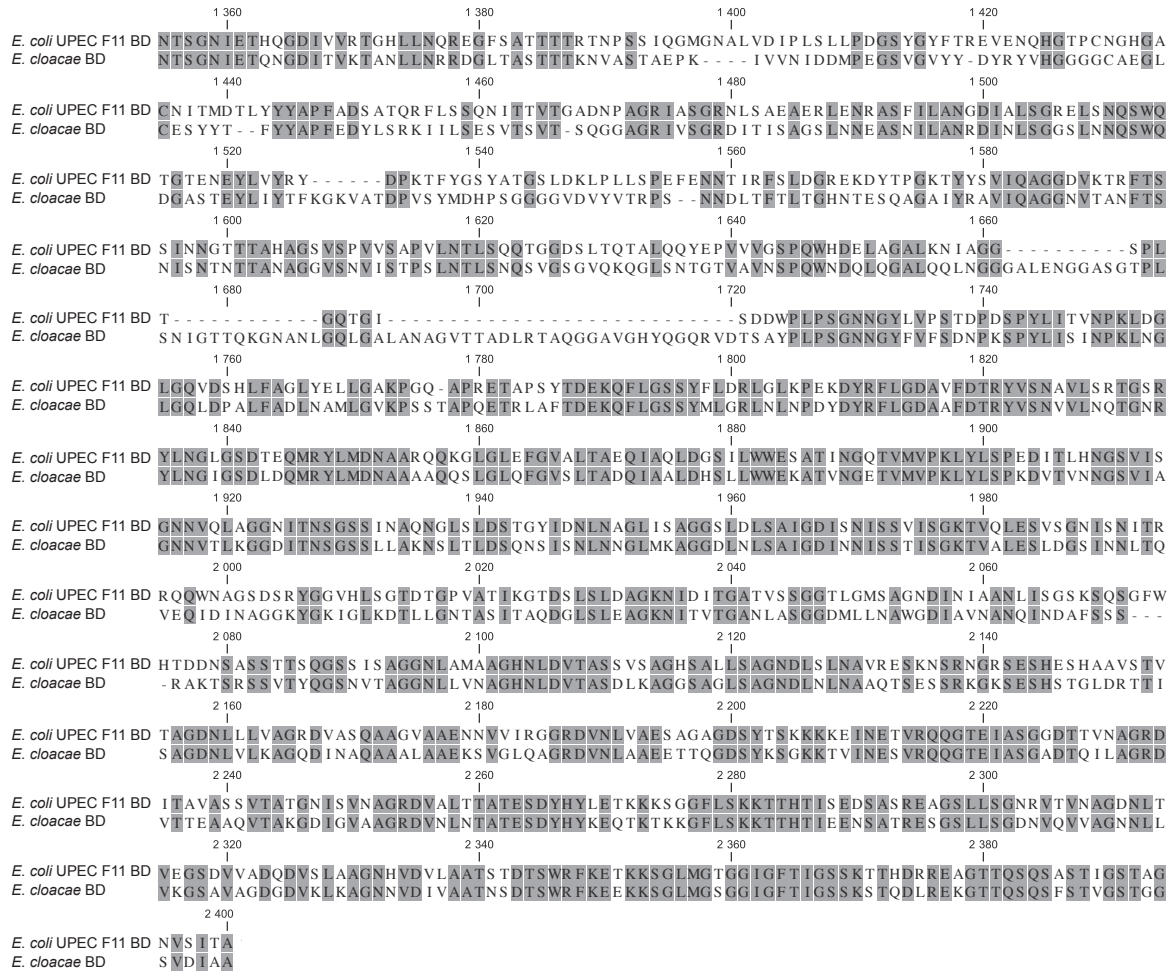
157

158 **Figure S7. Alignment of CdiA receptor-binding domains from *Escherichia coli* UPEC**

159 **F11 and *Enterobacter cloacae*.** Homologous residues are shown in grey and non-

160 homologous residues are white.

Figure S7



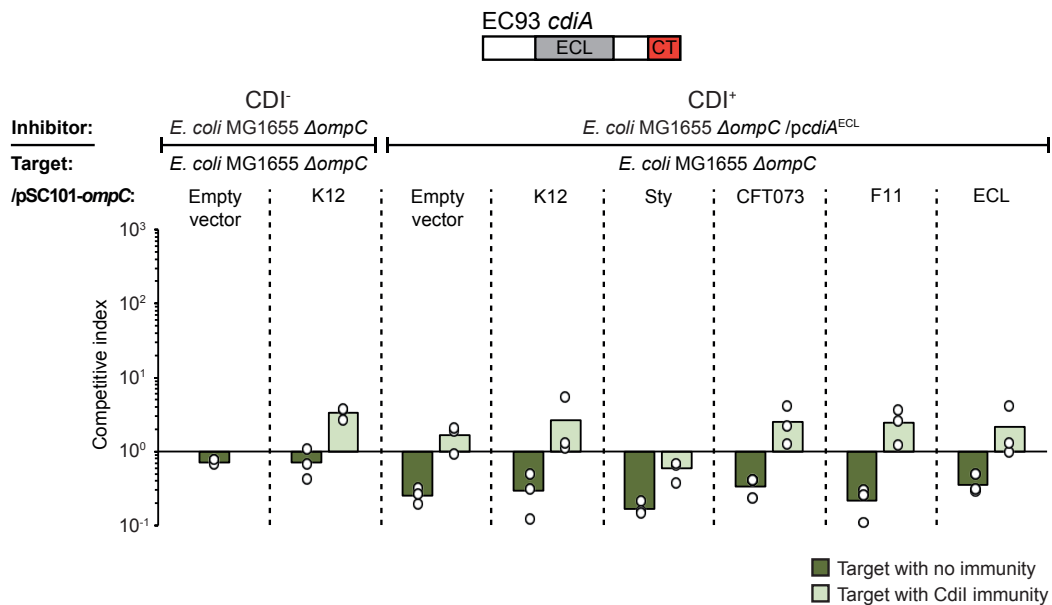
161

162

163 **Figure S8. The CdiA protein of *E. cloacae* does not inhibit *E. coli* MG1655 expressing**
 164 **different OmpC's in liquid media.**

165 Average competitive index of cells expressing CdiA^{ECL} after co-culturing with MG1655 cells
 166 expressing different OmpC's from a constitutive PJ23101 promoter on a low-copy (pSC101)
 167 plasmid. Co-culturing was for 5h in liquid LB media with (light green bars) or without (dark
 168 green bars) CdiI expressed from plasmid (n=3 biological replicates). Individual data points of
 169 the biological replicates are shown as black and white circles.

Figure S8



170