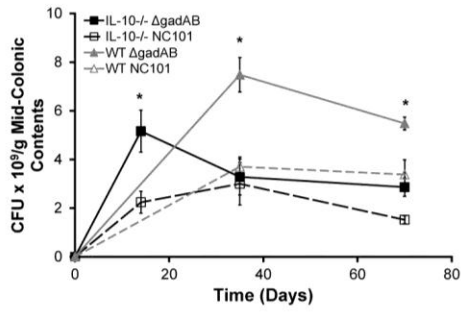
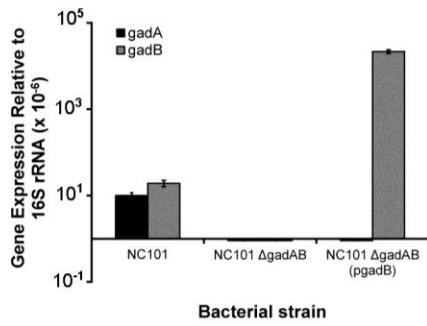


# Supplementary Figures

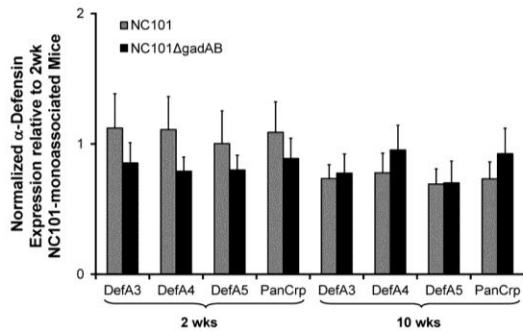
**S1**



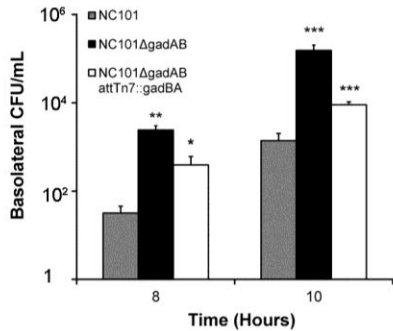
**S2**



**S3**



**S4**



## 2 SUPPLEMENTARY FIGURE LEGENDS

3 Figure S1: Luminal bacterial concentrations in mid-colonic contents from monoassociated WT  
4 and *Il-10*<sup>-/-</sup> mice. Data are presented as mean ± SEM, n=5 mice/group, \*p<.05 relative to mice  
5 with the same genetic background, but monoassociated with NC101.

6 Figure S2. *GadA* and *gadB* expression in cecal bacteria from monoassociated *Il-10*<sup>-/-</sup> mice. Real-  
7 time PCR was performed using bacterial RNA isolated from cecal contents of *Il-10*<sup>-/-</sup> mice  
8 monoassociated with the indicated bacterial strains for 5 weeks, and the specific primers *gadA2*  
9 and *gadB2* (Table S1). Results are normalized to 16S rRNA expression using the  $\Delta$ Ct method.  
10 Data are presented as mean ± SEM, n=4-6 samples per group.

11 Figure S3. DefA3, DefA4, DefA5 and Pan-Cryptdin expression in ileal tissues from  
12 monoassociated *Il-10*<sup>-/-</sup> mice. Real-time Taqman PCR was performed using RNA isolated from  
13 fragments of the ileum of *Il-10*<sup>-/-</sup> mice monoassociated with NC101 and NC101 $\Delta$ *gadAB* for 2  
14 and 10 weeks, and commercially-available  $\alpha$ -defensin TaqMan primers (Life Technologies,  
15 Grand Island, NY). Results are normalized to murine  $\beta$ -actin expression and data are presented  
16 as mean ± SEM of fold change relative to 2 week NC101 monoassociated mice.

17 Figure S4. Bacterial translocation across intestinal epithelial cell monolayers. CFU/mL measured  
18 in media from the basolateral chamber of the culture at the indicated time intervals post infection  
19 with the indicated bacterial strains. Data are presented as mean ± SEM, n=5-6 samples per group.  
20 \*p<.05, \*\*p<.01 and \*\*\*p<.001 relative to NC101 infected epithelial cells.

21

22

23 **SUPPLEMENTARY TABLE**

24 Table S1. Sequences of oligonucleotides used in PCR reactions.

Primer Name	Organism	Sequence (5' → 3')
gadA2F	<i>Escherichia coli</i> NC101	GAAGCTGTTAACGGATTTCC
gadA2R	<i>Escherichia coli</i> NC101	GCGGAAATCGTTTTGACTCC
gadB2F	<i>Escherichia coli</i> NC101	GGTGTTC AACGTTGACTACC
gadB2R	<i>Escherichia coli</i> NC101	CCGGGCGGGAGAAGTTGA
gadAkoF	<i>Escherichia coli</i> NC101	TTTTTTATTGCCTTCAAATAAATTTAAGGAGTT CGAAATGGTGTAGGCTGGAGCTGCTTC
gadAkoR	<i>Escherichia coli</i> NC101	TTTTTACAACGTGATGTTATCAGGTGTGTTAA AGCTGTTATGGGAATTAGCCATGGTCC
gadBkoF	<i>Escherichia coli</i> NC101	TTTTTTAATGCGATCCAATCATTTTAAGGAGTT TAAAATGGTGTAGGCTGGAGCTGCTTC
gadBkoR	<i>Escherichia coli</i> NC101	CCGTTACCGTTAAACGTTATCAGGTGTGTTA AAGCTGTTATGGGAATTAGCCATGGTCC
gadB3Fnd	<i>Escherichia coli</i> NC101	AACATATGATCACAGCCCCGTCAACACATC
gadB3Rnh	<i>Escherichia coli</i> NC101	AAGCTAGCCCCCTAAAACGGTATTCCTGTC
gadA5Fm	<i>Escherichia coli</i> NC101	AACAATTGTTAATTTGATCGCCCGAACAG
gadA5Rn	<i>Escherichia coli</i> NC101	AAAGCGCCGCTCAACACGATGAATAGACAG GT
gadB4Fk	<i>Escherichia coli</i> NC101	AAGGTACCATCACAGCCCCGTCAACAC
gadB5Rm	<i>Escherichia coli</i> NC101	AACAATTGCCCTAAAACGGTATTCCTGTC
16SF	<i>Escherichia coli</i> NC101	GAATGCCACGGTGAATACGTT
16SR	<i>Escherichia coli</i> NC101	ACCCACTCCCATGGTGTGA
GAPDHF	<i>Mus musculus</i>	CCTGCTCCCCCTACACACA
GAPDHR	<i>Mus musculus</i>	CCTGTTCTTCTCGGGCAAAA

25

26

## 27 SUPPLEMENTARY METHODS

### 28 Construction of NC101 $\Delta$ *gadAB*

29 NC101 $\Delta$ *gadAB* was constructed using the  $\lambda$ -*red* recombinase method as described elsewhere  
30 (Datsenko and Wanner, 2000). Briefly, the FRT-flanked kanamycin cassette in pKD4 was  
31 amplified using primers *gadAkoF*, *gadAkoR*, *gadBkoF* and *gadBkoR* (Table S1) each of which  
32 contains 60 nucleotides that are homologous to the 5' and 3' regions of the *gadA* and the *gadB*  
33 coding region in NC101, respectively. The PCR product was gel-purified, digested with DpnI,  
34 and transformed into NC101, which had previously been transformed with pKD46. A kanamycin  
35 resistant clone in which the *gadAB* genes were replaced by the kanamycin resistance cassette was  
36 transformed with pCP20 in order to remove the kanamycin resistance cassette. Loss of pCP20  
37 and pKD46 from the resultant colonies was confirmed by replicate plating onto kanamycin and  
38 carbenicillin agar plates. The *gadAB* gene regions on the NC101 chromosome were sequenced to  
39 confirm deletion of the coding region.

### 40 41 Construction of NC101 $\Delta$ *gadAB* (*pgadB*)

42 The *gadB*-complemented strain of NC101 was constructed using standard molecular biology  
43 protocols. Briefly, the NC101 *gadB* gene and its native promoter were PCR-amplified as one  
44 DNA fragment using purified *E. coli* NC101 chromosomal DNA template, forward *gadB3Fnd*,  
45 and reverse *gadB3Rnh* primers (Table S1), containing at the 5' end the *NdeI* and *NheI* restriction  
46 sites, respectively. Amplification was performed using Phusion DNA Polymerase (New England  
47 BioLab, Ipswich, MA) according to manufacturer's instructions and using the following  
48 conditions: 98°C for 30 seconds; 30 cycles of 98°C for 10 seconds, 67°C for 15 seconds, 72°C for  
49 30 seconds; and 72°C for 5 minutes. The amplicon was digested with *NdeI* and *NheI*, and

50 subcloned into the multiple cloning site of pGEN-MCS (kind gift from M. Chelsea Lane, UNC  
51 Chapel Hill) to generate pGEN-gadB, which contains the *hok sok* postsegregation killing system  
52 and two *par* loci to enhance plasmid stability over multiple generations (Lane et al., 2007).  
53 Integrity of the *gadB* gene was confirmed by sequencing after which electro-competent  
54 NC101 $\Delta$ *gadAB* cells were transformed with pGEN-*gadB* using electroporation to obtain the  
55 plasmid-complemented NC101 $\Delta$ *gadAB* (NC101  $\Delta$ *gadAB* (p*gadB*)) strain. *GadB* expression was  
56 confirmed by PCR.

57

### 58 **Construction of NC101 $\Delta$ *gadAB attTn7::gadBA***

59 The chromosomal *gadAB*-complemented strain of NC101 was constructed using the mini-Tn7  
60 insertion method as described elsewhere (Choi et al., 2005). Briefly, NC101 *gadA* and *gadB*  
61 genes and their native promoters were PCR-amplified as one DNA fragment respectively, using  
62 purified *E. coli* NC101 chromosomal DNA template and the following primer sets which contain  
63 distinct restriction sites at the 5' ends: forward *gadA*5Fm, reverse *gadA*5Rn, and forward  
64 *gadB*4Fk and reverse *gadB*5Rm. Amplifications were performed using Phusion DNA  
65 Polymerase (New England BioLab, Ipswich, MA) and the following conditions: 98°C for 30  
66 seconds; 35 cycles of 98°C for 10 seconds, 65°C for 20 seconds, 72°C for 55 seconds; and 72°C  
67 for 5 minutes. The *gadA* amplicon was digested with *MfeI* and *NotI*; the *gadB* amplicon with  
68 *KpnI* and *MfeI*. Both *gadA* and *gadB* were then subcloned into the MCL2868 plasmid (kind gift  
69 from M. Chelsea Lane) to generate MCL2868-*gadA* and MCL2868-*gadB*, respectively. The  
70 *gadA* fragment was digested from MCL2868-*gadA* with *MfeI* and *NotI* and subcloned into  
71 MCL2868-*gadB* to generate MCL2868-*gadBA*. MCL2868-*gadBA* includes mini-Tn7 elements,  
72 an ampicillin resistance gene, and pTNS2, a mobilizable helper plasmid containing specific

73 *tnsABC* + *tnsE* genes to promote transposition to *attTn7* sites. Electro-competent NC101 $\Delta$ *gadAB*  
74 cells were transformed with MCL2868-*gadBA* using electroporation and selected by replicate  
75 plating onto carbenicillin agar plates to obtain the chromosomal-complemented NC101 $\Delta$ *gadAB*  
76 *attTn7::gadBA* strain. *GadAB* expression was confirmed by PCR.

77

#### 78 **DNA isolation from cecal tissue biopsies**

79 Approximately 50 mg of snap frozen tissue was suspended in 750  $\mu$ l of sterile bacterial lysis  
80 buffer (200 mM NaCl, 100 mM Tris (pH 8.0), 20 mM EDTA, and 20 mg/ml lysozyme) and  
81 incubated at 37°C for 30 min. Then 40  $\mu$ l of proteinase K (20 mg/ml) and 85  $\mu$ l of 10% SDS  
82 were added to the mixture. After 30 min of incubation at 65°C, 500  $\mu$ L of phenol:chloroform:  
83 isoamyl alcohol (25:24:1) and 300 mg of 0.1-mm zirconium beads (BioSpec Products,  
84 Bartlesville, OK) were added, and the mixture was homogenized in a bead beater (Precellys 48,  
85 Bertin Technologies, Rockville, MD) for 3 min. The homogenized mixture was cooled on ice  
86 and then centrifuged at 14,000 rpm for 5 min. The supernatant was transferred to a new 1.5-ml  
87 microfuge tube, and DNA was further extracted by phenol-chloroform-isoamyl alcohol (25:24:1)  
88 and then by chloroform-isoamyl alcohol (24:1). After extraction, the supernatant was  
89 precipitated with 1/10 volume of 3M sodium acetate (pH5.2) and 2.5 volumes of absolute  
90 ethanol at -20°C for 1h. The precipitated DNA was suspended in DNase-free H<sub>2</sub>O and then  
91 cleaned using the DNeasy blood and tissue extraction kit according to the manufacturer's  
92 instructions.

93

#### 94 **RNA isolation from ileal tissue**

95 Approximately 20 mg of frozen ileal tissue was thawed into 0.4mL of RLT Lysis buffer  
96 containing 1% of 2-Mercaptoethanol (RNeasy Mini Kit, Qiagen, Germantown, MD), physically

97 disrupted using a T25 basic tissue homogenizer (IKA Labortechnik, Wilmington, NC) at medium  
98 speed and RNA was purified using the RNeasy Mini Kit.

99

100 **SUPPLEMENTARY REFERENCES**

101 Datsenko, K.A., and Wanner, B.L. (2000). One-step inactivation of chromosomal genes in  
102 *Escherichia coli* K-12 using PCR products. *Proc Natl Acad Sci USA* 97, 6640-6645.

103

104 Lane, M.C., Alteri, C.J., Smith, S.N., and Mobley, H.L. (2007). Expression of flagella is  
105 coincident with uropathogenic *Escherichia coli* ascension to the upper urinary tract. *Proc Natl*  
106 *Acad Sci USA* 104, 16669-16674.

107

108 Choi, K.H., Gaynor, J.B., White, K.G., Lopez, C., Bosio, C.M., Karkhoff-Schweizer, R.R., and  
109 Schweizer, H.P. (2005). A Tn7-based broad-range bacterial cloning and expression system. *Nat*  
110 *Methods*, 443-448.

111

112