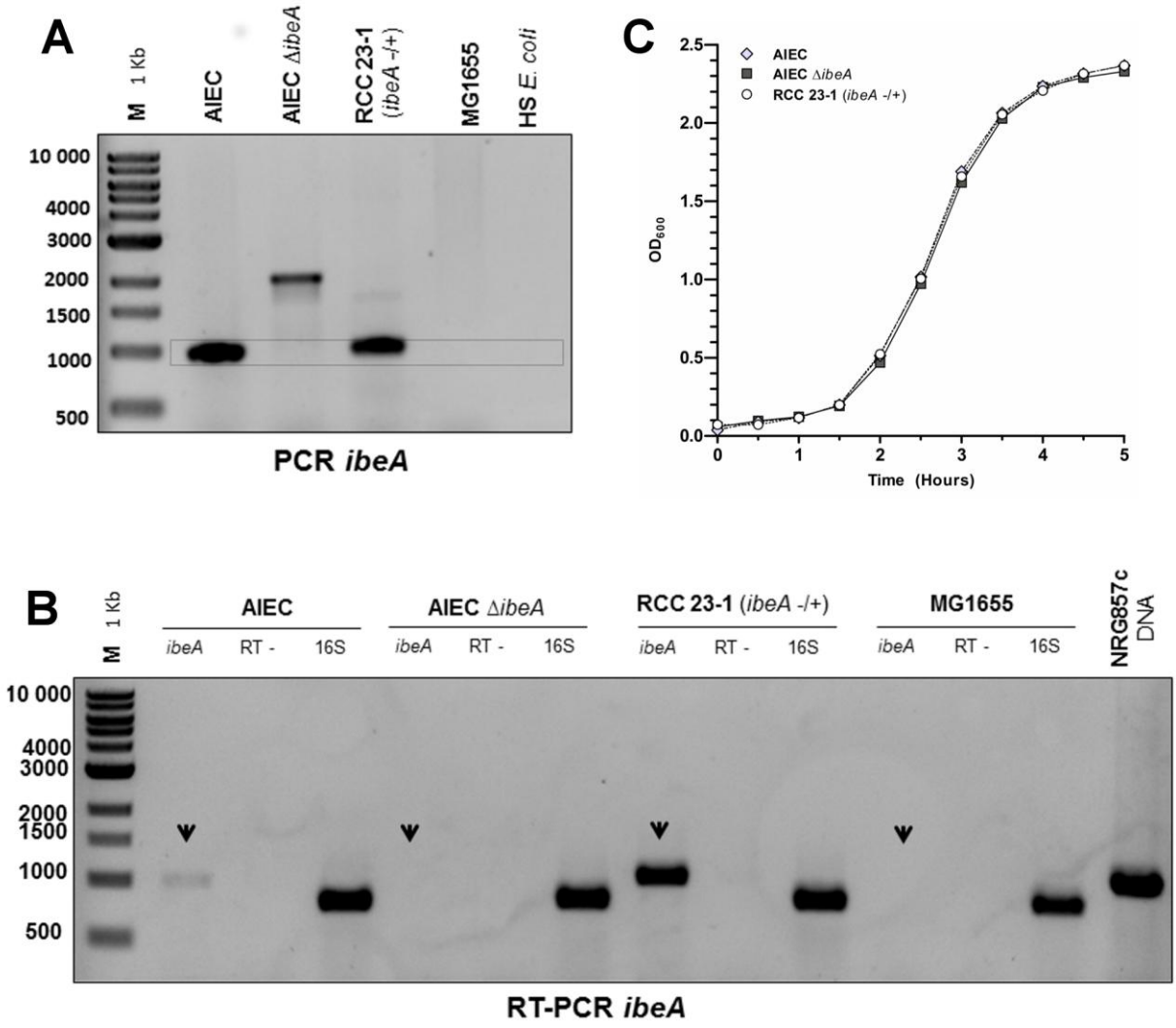
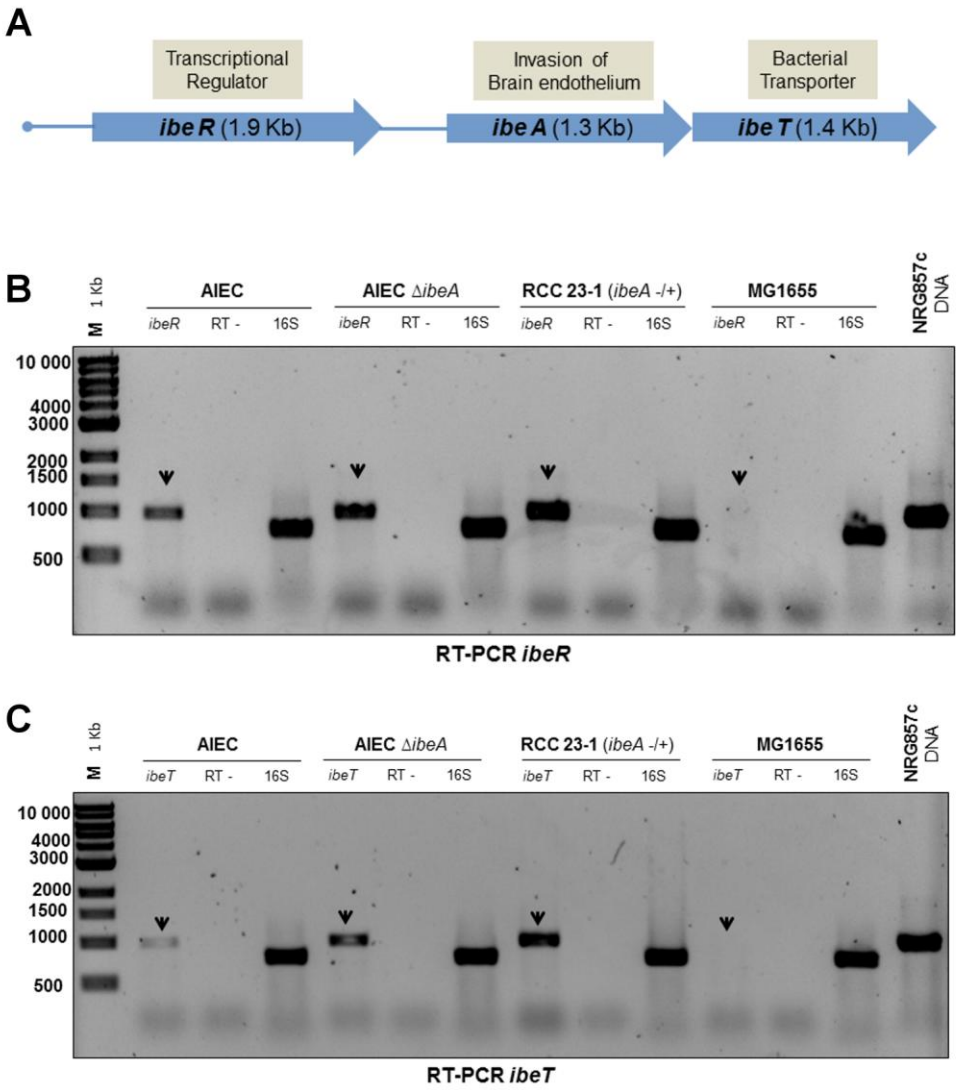
SUPPLEMENTAL TABLE 1. Bacterial shedding in feces and colonization levels of AIEC and AIECΔ*ibeA* in the mice intestine throughout infection.

	CFU x g^{-1} (feces)		
	NRG857c	**NRG857c Δ*ibeA***	**MG1655 (K12 *E. coli*)**
Day 1	**1.72E+09** ± 3.31E+08	**7.61E+08** ± 2.50E+08^{ns}	**3.17E+08** ± 2.15E+08**
Day 2	**2.69E+09** ± 7.37E+08	**4.03E+08** ± 1.52E+08^{ns}	**3.64E+06** ± 2.76E+06***
Day 3	**8.97E+07** ± 3.20E+07	**2.46E+07** ± 1.17E+07^{ns}	**1.63E+04** ± 1.10E+04***
Day 4	**1.74E+07** ± 1.61E+07	**8.40E+06** ± 4.64E+06^{ns}	**1.74E+04** ± 1.69E+04*
Day 6	**6.73E+03** ± 4.52E+03	**4.24E+04** ± 2.62E+04^{ns}	**1.84E+01** ± 1.84E+01^{ns}
Day 8	**1.56E+03** ± 1.01E+03	**4.96E+04** ± 3.97E+04^{ns}	**ND**^{ns}
Day 10	**9.74E+02** ± 9.08E+02	**1.60E+04** ± 1.41E+04^{ns}	**ND**^{ns}
Day 12	**6.08E+03** ± 6.07E+03	**5.77E+03** ± 3.99E+03^{ns}	**ND**^{ns}
Day 14	**1.31E+03** ± 9.38E+02	**2.63E+03** ± 1.65E+03^{ns}	**ND**^{ns}
	CFU x g^{-1} (organ)		
	NRG857c	**NRG857c Δ*ibeA***	**MG1655 (K12 *E. coli*)**
Day 4 (Ileum)	**8.08E+03** ± 4.02E+03	**9.06E+02** ± 4.19E+02^{ns}	**ND****
Day 4 (Cecum)	**5.03E+05** ± 2.95E+05	**3.95E+06** ± 2.54E+06^{ns}	**2.79E+03** ± 2.65E+03*
Day 4 (Colon)	**3.27E+05** ± 2.81E+05	**3.42E+05** ± 3.12E+05^{ns}	**6.36E+03** ± 6.17E+03*
Day 14 (Ileum)	**1.29E+02** ± 1.05E+02	**2.44E+04** ± 2.17E+04^{ns}	**ND**^{ns}
Day 14 (Cecum)	**7.08E+02** ± 5.17E+02	**3.11E+03** ± 2.41E+03^{ns}	**ND**^{ns}
Day 14 (Colon)	**4.19E+02** ± 3.10E+02	**4.14E+02** ± 3.56E+02^{ns}	**ND**^{ns}
	Values represent the mean ± SE at each time point		
	* $P \leq 0.05$, ** $P \leq 0.01$, *** $P \leq 0.001$ denote statistical significance when compared to NRG857c		
	ND = non detectable levels of bacteria		

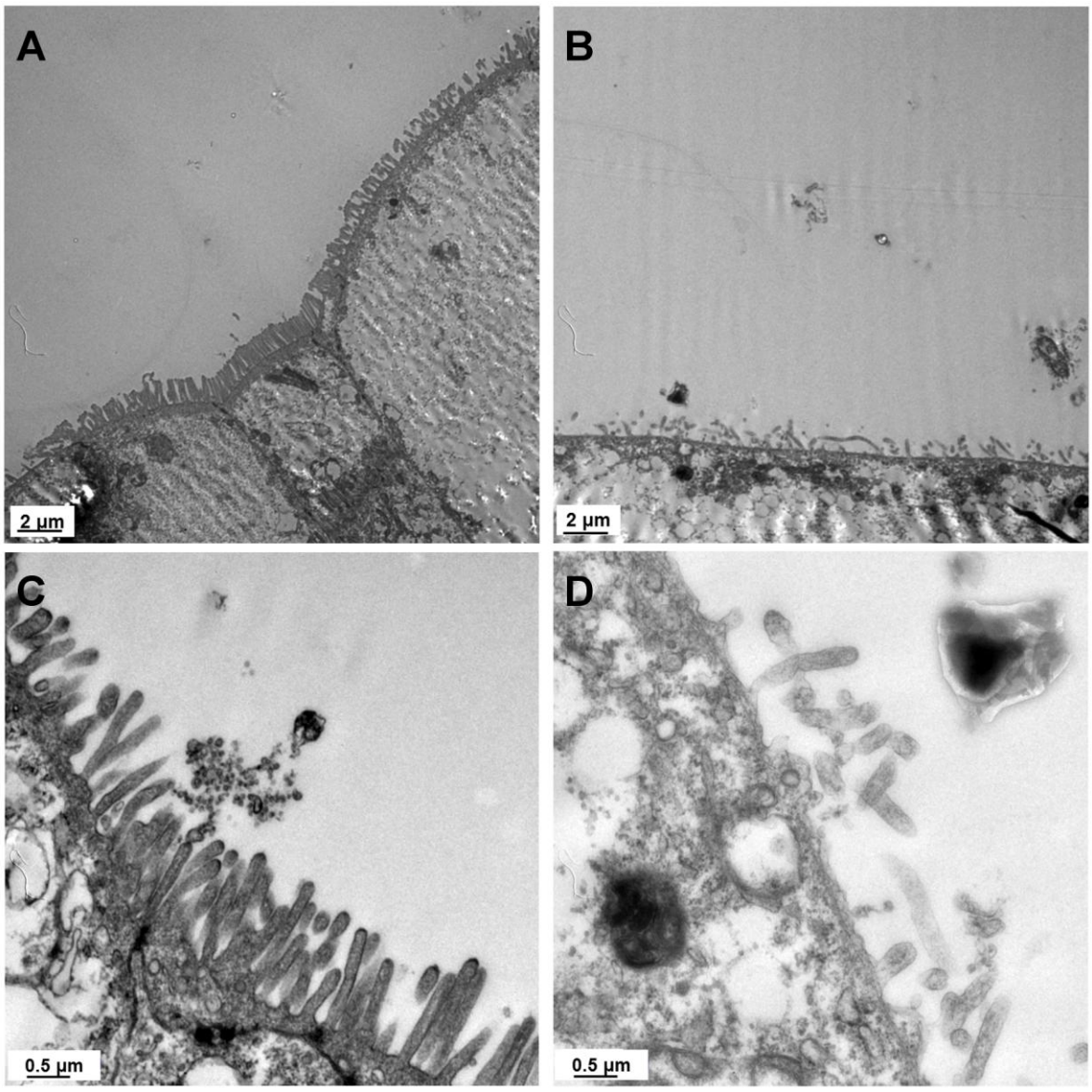
Supplemental Figures



SUPPLEMENTAL FIGURE 1. Deletion of *ibeA* at genomic and transcriptional levels. Genomic DNA from AIEC strain NRG857c, AIECcΔ*ibeA* (NRG857cΔ*ibeA*) and the complemented RCC23-1 strain (*ibeA*-/+), were used to test for the presence of *ibeA*. As negative controls the strains MG1655 and *E. coli* HS were used **(A)**. RNA was also extracted and RT-PCR performed on the same strains. 16S ribosomal RNA was used as an internal expression control. The absence of *ibeA* can be oserved in AIECcΔ*ibeA*, while a transcript is observed the wild type strain **(B)**. The growth of the strains was monitored in LB broth up to 5 h **(C)**.



SUPPLEMENTAL FIGURE 2. Effect of *ibeA* deletion in the other members of the *ibeRAT* operon. An schematic model of the *ibeRAT* operon is depicted, with the putative roles of each gene product **(A)**.. RNA was extracted and the effect on the two other members of the operon was evaluated by RT-PCR for *ibeR* **(B)** and *ibeT* **(C)**. The non pathogenic *E. coli* K12 strain MG1655 was used as a negative control. 16S ribosomal RNA was used as internal expression control.



SUPPLEMENTAL FIGURE 3. Generation of M-like cells. Fourteen days after polarization, Caco-2 cells were co-cultured with Raji B cells to generate M-like cells. Representative TEM of Caco-2 monolayers **(A)** and M-like cells **(B)** are shown with magnified images of selected areas underneath **(C and D).** Regions devoid of microvilli are observed in M-like cells. These regions were not observed in Caco-2 mono-cultures.