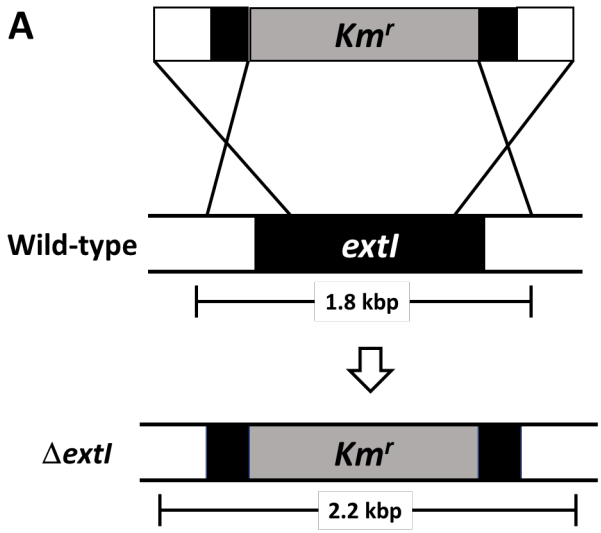
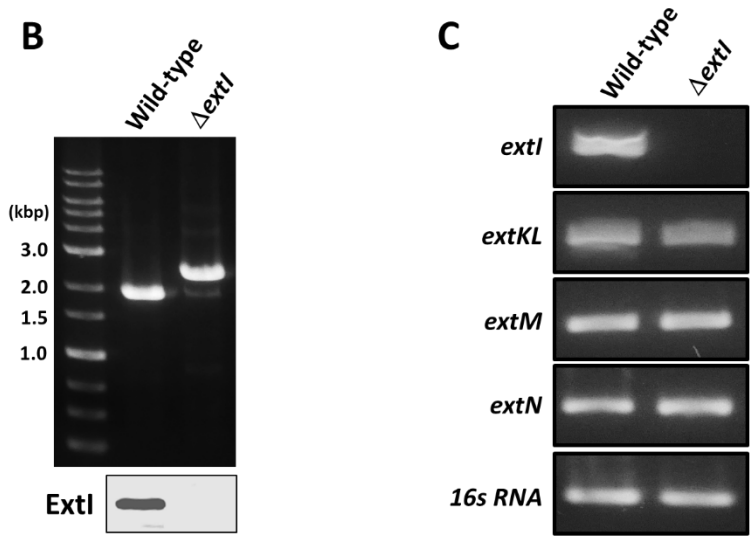
Supplementary Materials

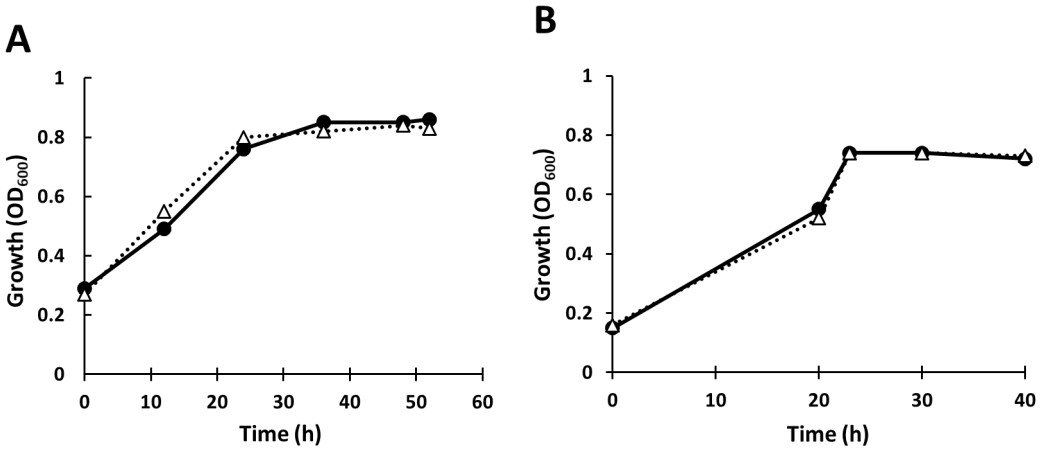
Supplementary Table S1. Primers used in this study

Number	Primer name	Sequence (5′ – 3′)
#1	Up-Fwd	ACCATCAGCACCACGATCTTGCCCAGCGG
#2	Up-Rev	CTGGTATGCCAAGGCCGGTTACATGCTCCC
#3	Down-Fwd	ACTCCGAGGGTACCCACGTTGGGATCTTCG
#4	Down-Rev	TCGTCGCCTTTCACCTCGACAATGGTCGGC
#5	Km^r-Fwd	CGAAGATCCCAACGTGGGTACCCTCGGAGTGGATGAATGTCAGC TAC
#6	Km^r-Rev	GGGAGCATGTAACCGGCCTTGGCATACCAGAGAAGGCGGCGGT GGAATCG
#7	Del_check_Fwd	CTTGACGGCATCGCCTACTACAACTCCAAC
#8	Del_check_Rev	CGATGCAGGAGCTGGAATCATACATCTTTG
#9	GSU2939_F	TCGATCCCGAGAAGGATTAC
#10	GSU2939_R	TGTCCACATTGGTGGATACG
#11	GSU2937_F	GAGAAAAACGGCTGGTATGC
#12	GSU2937_R	TGATGAACGTGGTGAAGTCC
#13	16S RNA_F	TGAGACACGGTCCAGACTCCTAC
#14	16S RNA_R	TCATTTCTTCCCTCCCGACA
#15	GSU2935_F	AATGCTACGGCTGTCATACGAAATA
#16	GSU2935_R	TTTCCCCTTGAAGGTAGAGACGTAG
#17	GSU2934_F	CCAGTTCATCCTTTACCATTCGGATTT
#18	GSU2934_R	GGTCCCAGAAGGAATCGAGAGAAAG

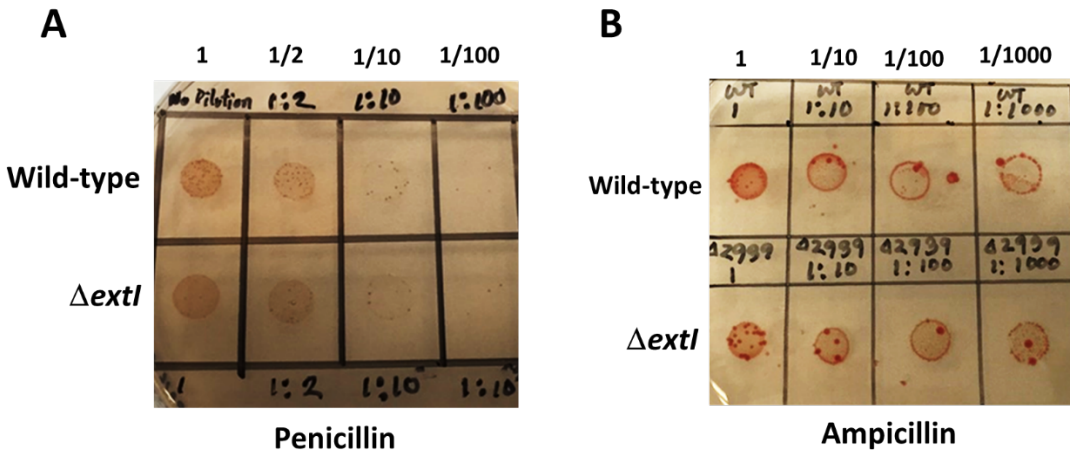




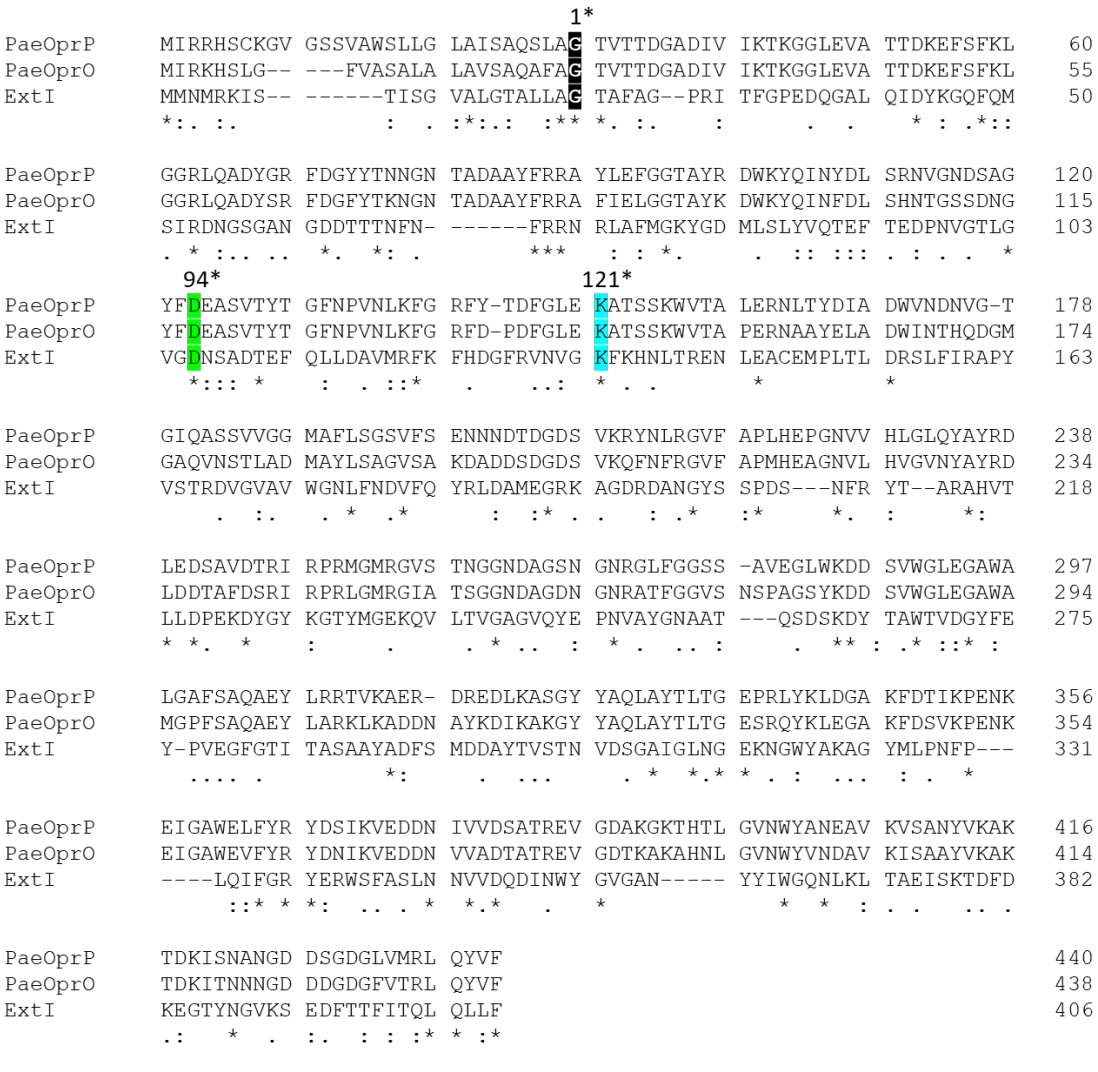
Supplementary Figure S1. Construction of an *extI*-deletion mutant (*ΔextI*). (**A**) Homologous recombination scheme for gene disruption. The *extI* gene was disrupted with a kanamycin resistance gene (*Km*^{r}) in wild-type *G. sulfurreducens* as described in the *Materials and Methods*. (**B**) The knockout mutation in the genome was confirmed by PCR (upper panel) using the genomic DNA and primers #7 and #8 shown in Supplementary Table S1 and Western blotting (lower panel) using an ExtI-specific antibody. (**C**) The mRNA levels of *extI*, *extKL*, *extM*, *extN*, and *16S rRNA* in the wild-type and the *ΔextI* strains were analyzed by semi-quantitative RT-PCR using each primer set shown in Supplementary Table S1.



Supplementary Figure S2. Effect of *extI* deficiency on cell growth. Wild-type (circle and solid line) and Δ*extI* (triangle and dotted line) were anaerobically cultured in (**A**) NBAFYE medium containing 40 mM fumarate and (**B**) FWA medium containing 20 mM fumarate. Growth was measured by determining the optical density at 600 nm (OD_{600}).



Supplementary Figure S3. Antibiotic susceptibility and permeability assay. Wild-type and Δ*extI* were anaerobically cultured in NBAFYE medium, and cells were diluted with saline and spotted onto the NBAFYE agar plate containing 1.25 μg/mL of (**A**) penicillin and (**B**) ampicillin and then cultured for 3 days.



Supplementary Figure S4. Comparison of the amino acid sequence of ExtI with those of the phosphate-selective porins. The multiple alignment of *G. sulfurreducens* ExtI, *P. aeruginosa* OprP, and *P. aeruginosa* OprO was constructed using a ClustalW program. The first amino acid (G, 1*) of the mature proteins, which are assumed to be formed after cleavage of the potential signal peptides, are highlighted in black, and the conserved D (94*) and K (121*) are highlighted in green and blue, respectively. Amino acid sequences were obtained from the KEGG databases (PaeOprP, PA3279; PaeOprO, PA3280).