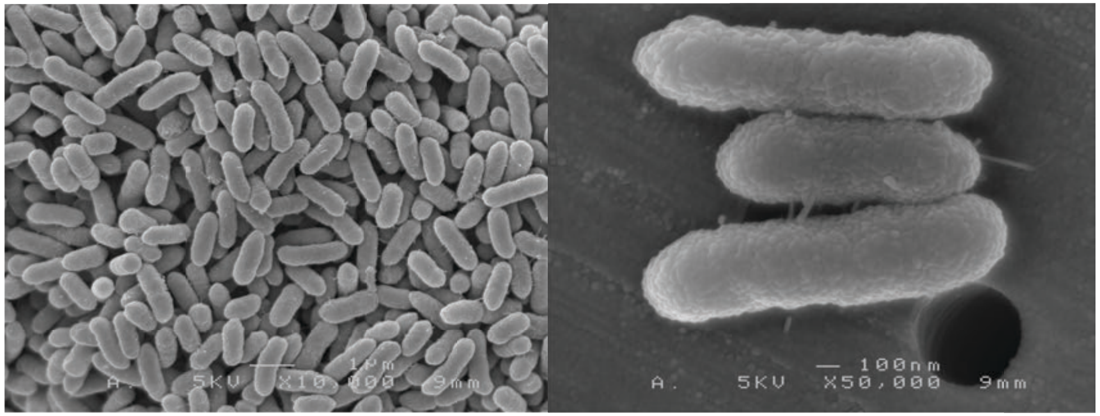

**Figure S1**. SEM images of *Citrobacter freundii* IFO 13545, which is a Gram-negative rod-shaped bacterium that is phylogenetically very close to *Escherichia coli*.

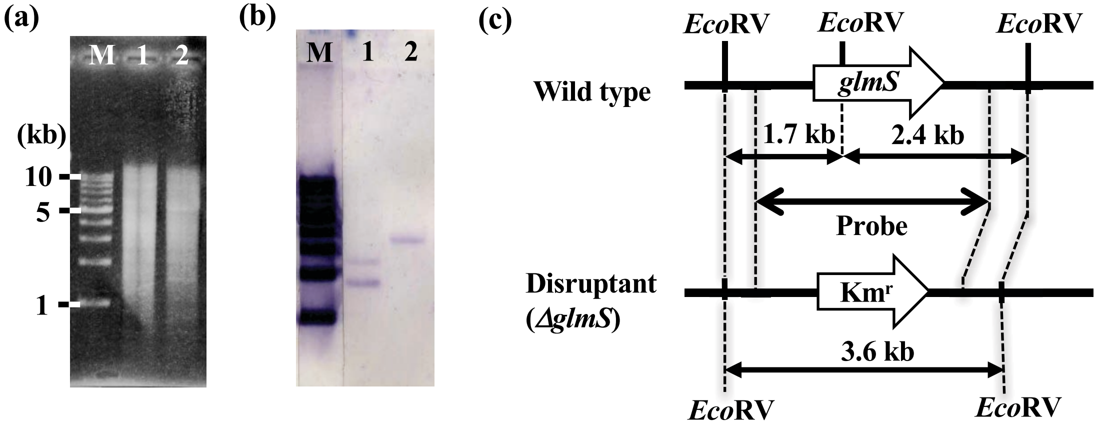

**Figure S2**. Electrophoresis of *Eco*RV-digested total DNA of *C. freundii* IFO 13545 and its *glmS*-disrupted mutant (*ΔglmS*) (a), corresponding Southern blots (b), and restriction maps of the regions around *glmS* in the genomes of IFO 13545 and the disruptant (c). Lane M: 1-kb DNA ladder (size marker); Lane 1: IFO 13545 (wild type); Lane 2: *ΔglmS*.

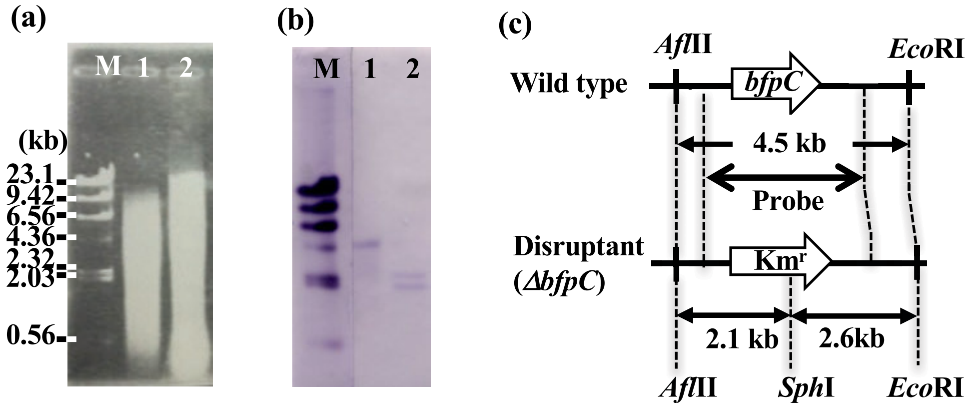

**Figure S3**. Electrophoresis of *Afl*II-*Eco*RI-*Sph*I-digested total DNA of *C. freundii* IFO 13545 and its *bfpC*-disruptant (*ΔbfpC*) (a), corresponding Southern blots (b), and restriction maps of the regions around *bfpC* in the genomes of IFO 13545 and the disruptant (c). Lane M: λDNA *Hin*dIII digest (size marker); Lane 1: IFO 13545 (wild type); Lane 2: *ΔbfpC*.

**Table S1.** Oligonucleotide primers used in this study.

| Primer name | Sequence |
|---|---|
| acs-up | F : 5'-GTTCAGCGTGAACTGCAGAG-3'<br>R : 5'-AAGCAGCTCCAGCCTACACAAAATGTAGGGGCTTTGAGAG-3' |
| acs-down | F : 5'-CTAAGGAGGATATTCATATGTAACTGTGAAATGCCCGATG-3'<br>R : 5'-TGTAGATTCCGGTCAGGATG-3' |
| aceA-up | F : 5'-CGGCACATGGATTGCTCATC-3'<br>R : 5'-AAGCAGCTCCAGCCTACACAGCAGGGTCAAGAAATCGATC-3' |
| aceA-down | F : 5'-CTAAGGAGGATATTCATATGTGTAGGCCGGATAAGCGAAC-3'<br>R : 5'-TCGCTAAGGACGCGAGTTAG-3' |
| glmS-up | F : 5'-TCTGGGTAAAGGCTCCAAAG-3'<br>R : 5'-AAGCAGCTCCAGCCTACACAGACCTGTATTTGCCCATTTC-3' |
| glmS-down | F : 5'-CTAAGGAGGATATTCATATGTGTTAGCTTGTAGATTGAGC-3'<br>R : 5'-CGTACTGTCAATCACTTCAC-3' |
| cpsA-up | F : 5'AAGTGACCCGGGTATTCATC3'<br>R: 5'AAGCAGCTCCAGCCTACACACACAAGGGTAGATTGTCAGC3' |
| cpsA-down | F : 5'CTAAGGAGGATATTCATATGCCGGAATTGTGATATCGCAG3'<br>R: 5'ACAACGCCAGTTCCGCTTTC3' |
| bfpC-up | F : 5'TTTGAAGATGCGTCACCG-3'<br>R : 5'AAGCAGCTCCAGCCTACACATAAAGAT GACAGCCACGC-3' |
| bfpC-down | F : 5'-CTAAGGAGGATATTCATATGATGCTTAA ACGCAAACGC-3'<br>R : 5'-TATCCACGACATTGCCTCC-3' |
| nagA-Km | F : 5'-GGCGGCATTTTTTGAAATCGGGGGTCGGAATGTATGCTTTAACCCAGGGCTGTGTAGGCTGGAGCTGCTT-3'<br>R: 5'-CTCAGTAACGACCTCGTTGCCATTAACGATGGTCTTGATAATTTTAAAGTC ATATGAATATCCTCCTTAG-3' |
| pkD4-Km | F : 5'-TGTGTAGGCTGGAGCTGCTT-3'<br>R : 5'-CATATGAATATCCTCCTTAG-3' |
| aceA-RT | F : 5'-TCATATGGGCGGCAAAGTTC-3'<br>R : 5'-TAGAACCCTTCGCTGGTACG-3' |
| ack-RT | F : 5'-TCTTACCTCTACGCCCTGCC-3'<br>R : 5'-AGACCCATGGAGGTATCAAC-3' |
| acs-RT | F : 5'-AGCCGAAAGGCGTACTGCAC-3'<br>R : 5'-ACATACGCGCCGGGGTAGGC-3' |
| bfpC-RT | F : 5'-AATCCGCGTATTCGAACCCG-3'<br>R : 5'-TATCTTCAGTGATCATGTCCG-3' |
| fba-RT | F : 5'-AGCAGGCGTTCAATATGGGC-3'<br>R : 5'-AACATGGTAATCCACGCCATC-3' |
| fbp-RT | F : 5'-TTAACGTCTCTGTCGGTACG-3'<br>R : 5'-GTTAATGGAGTACGTGCTGC-3' |
| glmS-RT | F : 5'-TACAACTCCGGTATGGTGTCCT-3'<br>R : 5'-GCCCAGCTCTTTAGATAAGCG-3' |
| icd-RT | F : 5'-GCAACATCATGAAGTTCACCG-3'<br>R : 5'-CGCAGCAGGATCTGTTGTAGG-3' |
| pfkA-RT | F : 5'-CGAAACGCCTGACTGAAATG-3'<br>R : 5'-ACCACTACGAACTCACAACC-3' |
| pck-RT | F : 5'-AACTGTCTAAAGATGCCGAGC-3'<br>R : 5'-CAGTCAGGAAGATCACTTTGG-3' |
| ptsG-RT | F : 5'-ATTCAGACGTTCTCCCAGTG-3'<br>R : 5'-AGAGTGCCAGATAGCGATAG-3' |
| yjcG-RT | F : 5'-CGCTCTGTCGTTAGGTCTTGG-3'<br>R : 5'-AAGCCGATGATAAAGGTCAGG-3' |
| 16S-RT | F : 5'-CAGGCTAGAGTCTTGTAGAG-3'<br>R : 5'-TCGACTTAACGCGTTAGCTC-3' |