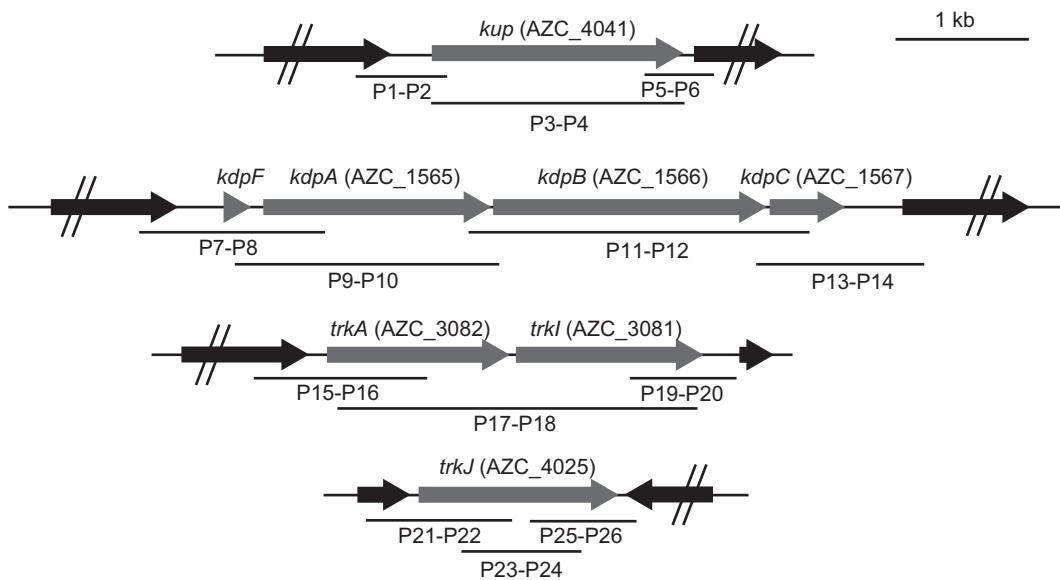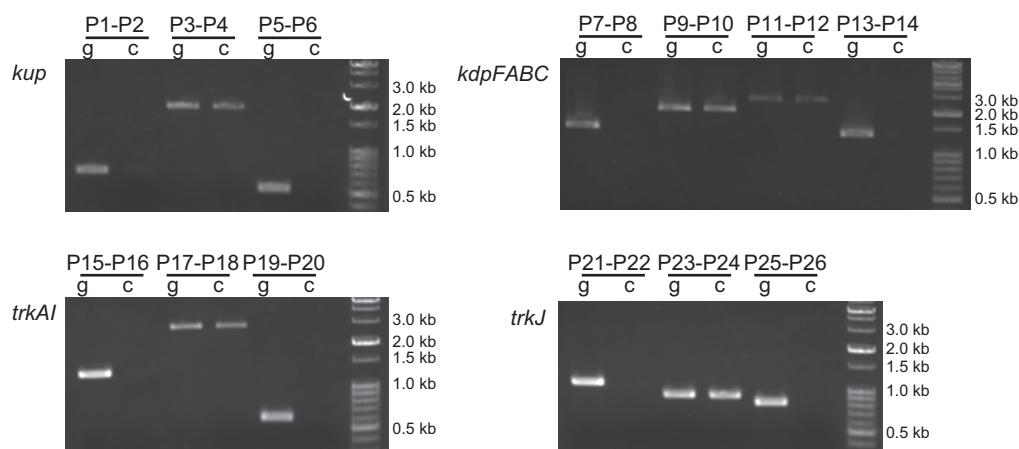**Fig. S1.** Determination of transcription units of K$^+$ uptake system genes of *A. caulinodans* (**A**) Maps of the *kdpFABC*, *kup*, *trkAI*, and *trkJ* with target regions for RT-PCR analyses. (**B**) RT-PCR analyses to determine transcription units of *kdpFABC*, *kup*, *trkAI*, and *trkJ*. cDNA was synthesized using total RNA (0.5 µg) from WT strain grown in a medium containing 0.5 mM K$^+$ at 38°C. Subsequent PCRs were performed using the cDNAs (c) and WT genomic DNA (1 × 10^{-1} ng µl^{-1}; g) as templates with the indicated primer pairs.

Table S1. Features of the predicted amino acid sequences encoded by K$^+$ uptake system genes of *A. caulinodans* ORS571.

K+ uptake system genes of *A. caulinodans* name	locus tag	Sequence identity based on blastp program	number of transmembrane regions based on SOSUI program
kup	AZC_4041	40% with *E. coli* Kup (E-value: 3e-148)	12
kdpF	not assigned	69% with *Methylobacterium extorquens* DM4 KdpF (E-value: 1e−04) 62% with *Rhizobium* sp. AP16 KdpF (E-value: 2e−04) 62% with *Agrobacterium* sp. ATCC 31749 KdpF (E-value: 2e−04)	1
kdpA	AZC_1565	53% with *E. coli* KdpA (E-value: 2e-158)	10
kdpB	AZC_1566	61% with *E. coli* KdpB (E-value: 0.0)	7
kdpC	AZC_1567	47% with *E. coli* KdpC (E-value: 1e-32)	1
trkA	AZC_3082	40% with *E. coli* TrkA (E-value: 6e−104)	0
trkI	AZC_3081	24% with *E. coli* TrkG (E-value: 9e−11) 26% with *E. coli* TrkH (E-value: 3e−16)	11
trkJ	AZC_4025	35% with *E. coli* TrkG (E-value: 3e−76) 34% with *E. coli* TrkH (E-value: 1e−73)	11