

Figure S5

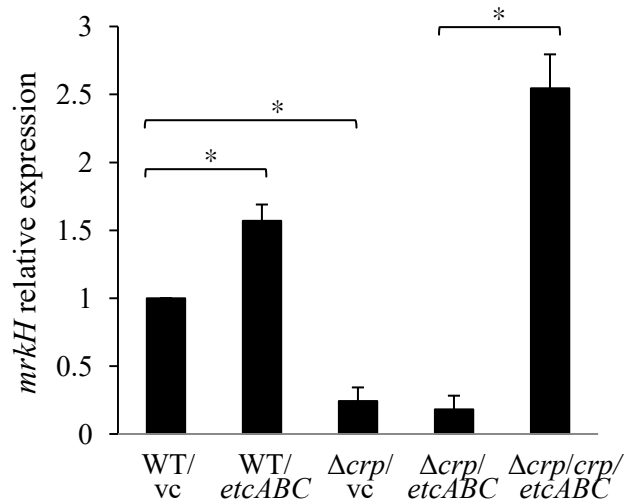


Figure S5. RT-qPCR analysis of *mrkH* transcription in each strain grown in LB. The 16S rRNA gene was used as the reference. The transcriptional level of *mrkH* in each strain was compared to WT/vc. The presented results are the means \pm standard deviations of three replicates. An asterisk (*) represents $p < 0.05$ as compared with WT/vc or Δ *crp*/*crp*/*etcABC* compared with Δ *crp*/*etcABC*. WT/vc: *K. pneumoniae* STU1 carrying pBSK-Gm as the vector control. WT/*etcABC*: *K. pneumoniae* STU1 carrying pBSK::*Gm*::*etcABC* to overexpress *etcABC*. Δ *crp*/vc: *K. pneumoniae* STU1 *crp* mutant carrying pBSK-Gm as the vector control. Δ *crp*/*etcABC*: *K. pneumoniae* STU1 *crp* mutant carrying pBSK::*Gm*::*etcABC* to overexpress *etcABC*. Δ *crp*/*crp*/*etcABC*: *K. pneumoniae* STU1 *crp* mutant carrying pBAD33::*crp* and pBSK::*Gm*::*etcABC*. The phenotype of the *crp* mutant carrying the two plasmids, pBAD33 and pBSK::*Gm*::*etcABC*, was the same as that of the *crp* mutant carrying one plasmid, pBSK::*Gm*::*etcABC*.