

Table S1 PCR primers used in this study^a

Primer	Sequence (5'→3')	Purpose
2937N-F 2937N-R	GTGAGCTCTACCGAGCATCG CTGGTACCAGTGGAACGGTG	pΔ2937 construction
2937C-F 2937C-R	GGGGTACCATCGAAAACCTG CATTCTAGAAGTTCCTGCAGG	pΔ2937 construction
HemAN-F HemAN-R	GAAGAGCTCATCGACAGCGAA CGGGTACC GAA ACCATCCAG	pΔHemA construction
HemPN-F HemPN-R	CTCAAGCTTAAGTACGACCAGGGCATCC GTTTCTAGACGCAGCAGTACAGGTTGAGCA	pΔHemP & pΔHemA construction
0796N-F 0796N-R	GCGGTACCTCGAATGGTCGT CGTCTAGAGGGTTCGACAGAC	pΔHemP & pΔ0796 construction
0797N-F 0797N-R	CACTCTAGACGCCAGTCTGTCGACCCTGTCCT CGTGAGCTCGACCACGATGACCACTTCACTG	pΔ0796 & pΔ0797 construction
0797C-F 0797C-R	CAAGAGCTCGGAAAAGGCCAGTAGATCC GCAGAATTCGTGAAGCTGGTGATGGTGTTTC	pΔ0797 construction
2355N-F 2355N-R	GTGGTCGCCAATCTTGATG CTGGTATCGGCCACTTCAAT	pΔ2355 construction
2356N-F 2356N-R	CAGGTACCACGACTGATCCA CATCTAGACCAGCAACATCGT	pΔ2355 & pΔ2356 construction
2357N-F 2357N-R	CGTCTAGATTCGTTGGCCTGGT AGAAGCTTGCCCAACAGGCT	pΔ2356 & pΔ2357 construction
2357C-F 2357C-R	GTGCTGCACGACCTCAATC CACCGTCGCTACTGGAATG	pΔ2357 construction
HemA-F HemA-R	CATCTAGAAGCTGATCCTGA GCTCATGAGCTCACCAGGAA	pHemA construction
0797-C	CTCGACCACGATGACCACTTCACTG	RT-PCR
HemPQ95-F HemPQ95-R	GAATGCTCAACCTGTACTGCTG CTTCGCTGTCGATGACCTCT	RT-PCR
HemAQ93-F HemAQ93-R	CCTGCTCAGCAAACCTGGTCT AGCACATTGGTATCGGTGGT	RT-PCR
0796Q120-F 0796Q120-R	ACCGTGTTGTGCCTGTACCA AAGGAAGCACAGGCTTTC	RT-PCR
0797Q108-F 0797Q108-R	GTGCACCTGAAGACCAGGAT GTCGTCGATCTGCTTGTCTCT	RT-PCR
2937m-F 2937m-R	GACCAGTTGGCCACTCAGTT AGTCCAGCAGTTCCTGCAGG	KJΔ2937 mutant check

HemAm-F	<u>GAAGAGCTCATCGACAGCGAA</u>	KJΔHemA mutant check
HemAm-R	<u>CGTCTAGAGGGTCGACAGAC</u>	
HemPm-F	<u>AAGTACGACCAGGGCATCC</u>	KJΔHemP mutant check
HemPm-R	<u>CGGATGCGGAAACCATCCAG</u>	
0796m-F	<u>GCTACATCGAATGGTCGTC</u>	KJΔ0796 mutant check
0796m-R	<u>CGGTGTACTCACCTGCAT</u>	
0797m-F	<u>CGCCAGTCTGTGACCCTGTCCT</u>	KJΔ0797 mutant check
0797m-R	<u>GTGAAGCTGGTGATGGTGTC</u>	
2355m-F	<u>ATCACCCCGAAGCAGTAAGTC</u>	KJΔ2355 mutant check
2355m-R	<u>GGAATACGCAGCTGCCAGAC</u>	
2356m-F	<u>CTTGCAGCTGAAGTACACC</u>	KJΔ2356 mutant check
2356m-R	<u>CCACCTCATGCAGCTTCAAC</u>	
2357m-F	<u>CGTTCTTCCTCTGGCTGGT</u>	KJΔ2357 mutant check
2357m-R	<u>GACCAGCGAGGCGTTCTC</u>	

^aThe restriction enzyme sites were underlined

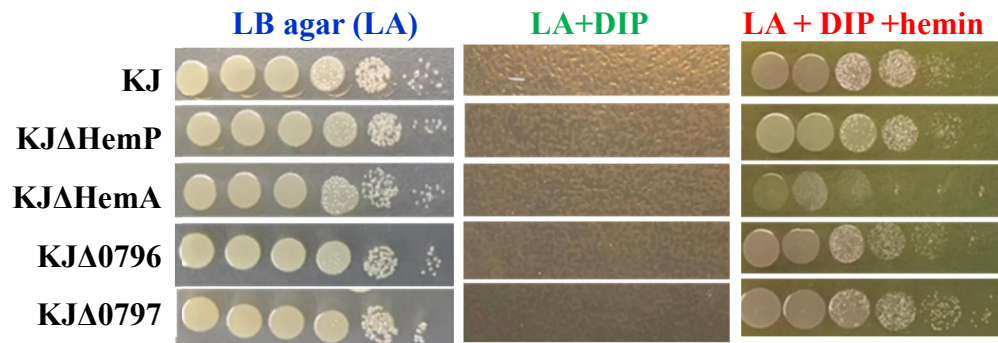


Fig. S1. The impact of hemin uptake system on a siderophore-proficient strain. The logarithmic-phase bacterial cells tested of 2×10^5 CFU/ μ l were 10-fold serially diluted. Five microliters of bacterial suspension were spotted onto the LB agar plates as indicated. The growth of bacterial cells was recorded after 24-h incubation at 37°C. The concentrations of DIP and hemin added are 50 μ g/ml and 150 μ M, respectively.

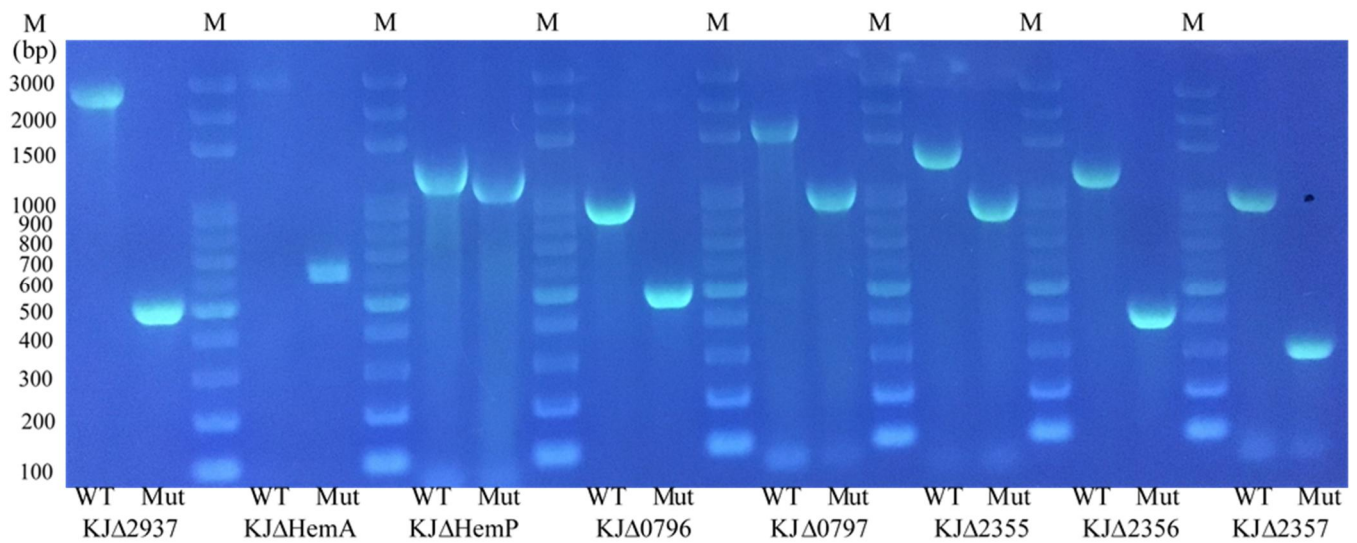


Fig. S2. Confirmation of single in-frame deletion mutants by PCR. The deletion regions of in-frame deletion mutants of *S. maltophilia* KJ were checked by colony PCR using the primer pairs, which targeted onto the upstream and downstream the deleted region, respectively. In the meanwhile, the wild-type KJ was also included for comparison. The primers used were listed in the Table S1. The PCR amplicons were separated by agarose gel electrophoresis and visible by ethidium bromide staining. Abbreviations: WT, wild-type; Mut, deletion mutant; M, DNA ladder.