

1 **Regulator RcsB Controls Prodigiosin Synthesis and Various**
2 **Cellular Processes in *Serratia marcescens* JNB5-1**

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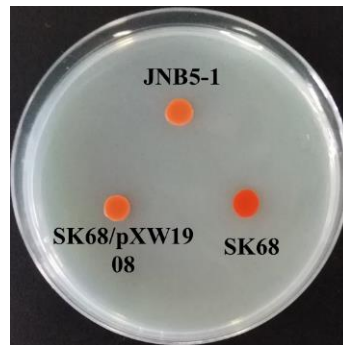
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23 **Fig. S1**



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25 **Figure S1. Spot assays on agar plate showed that RcsB was negatively regulates**
26 **prodigiosin synthesis in *S. marcescens*.** JNB5-1 is a wild-type *S. marcescens*, SK68
27 is a *rcsB* disrupted mutant, and SK68/pXW1908 is a *rcsB* complementary strain with
28 plasmid pXW1908.

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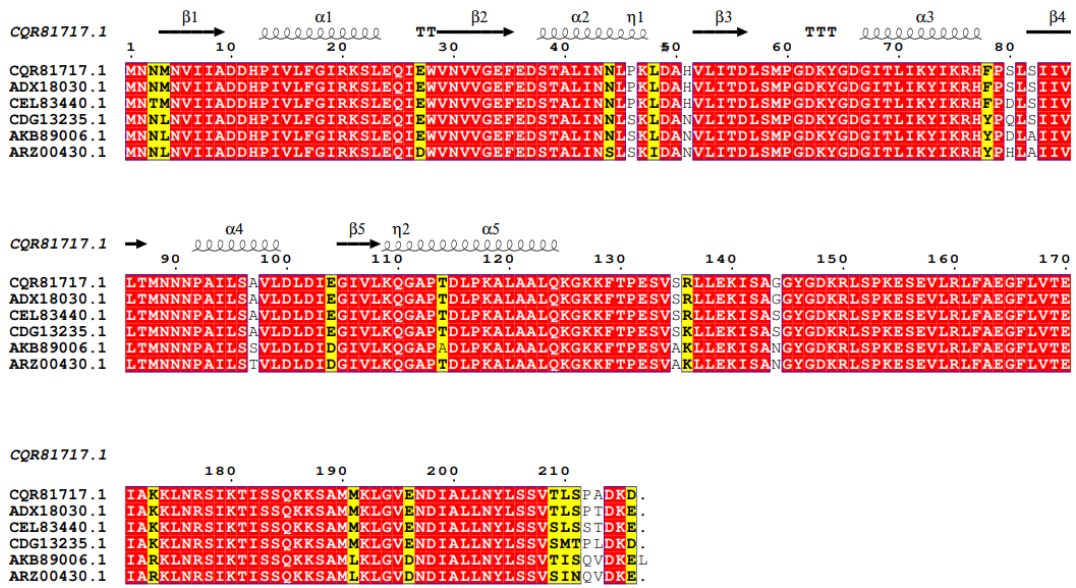
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42 **Fig. S2**



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44 **Figure S2. Multiple sequence alignment of RcsB homologies.** The sequences used
 45 for analysis were RcsB homologies from *Serratia marcescens* (CDG13235.1),
 46 *Escherichia coli* (CQR81717.1), *Klebsiella pneumoniae* (CEL83440.1), *Salmonella*
 47 *enterica subsp. enterica serovar Typhimurium* (ADX18030.1), *Yersinia pestis*
 48 (*AKB89006.1*) and *Yersinia ruckeri* (*ARZ00430.1*).

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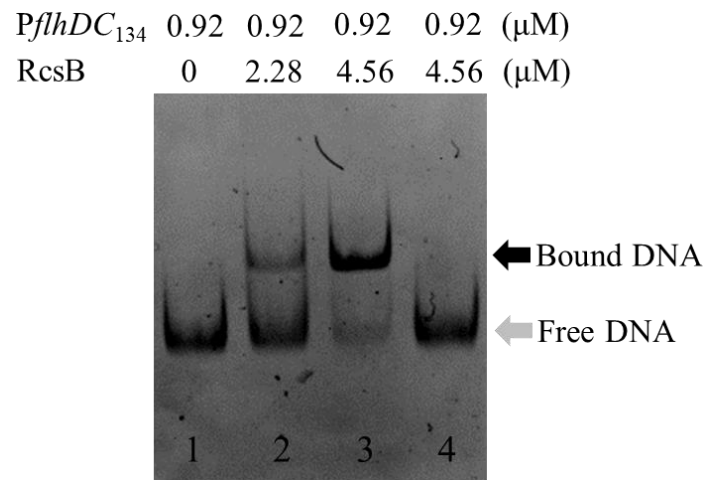
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58 **Fig. S3**



60 **Figure S3. EMSA results revealed that RcsB could specifically bind to the binding**
61 **site RcsB-2 *in vitro*.** *PflhDC*₁₃₄, 134-bp DNA fragment from -532 to -666 relative to
62 the translational start site of *flhD* gene. Lane 1: *PflhDC*₁₃₄ without protein RcsB. Lane
63 2: *PflhDC*₁₃₄ with 2.28 μ M RcsB. Lane 3: *PflhDC*₁₃₄ with 4.56 μ M RcsB. Lane 4:
64 *PflhDC*₁₃₄ carrying mutation in positions TTA with protein RcsB.

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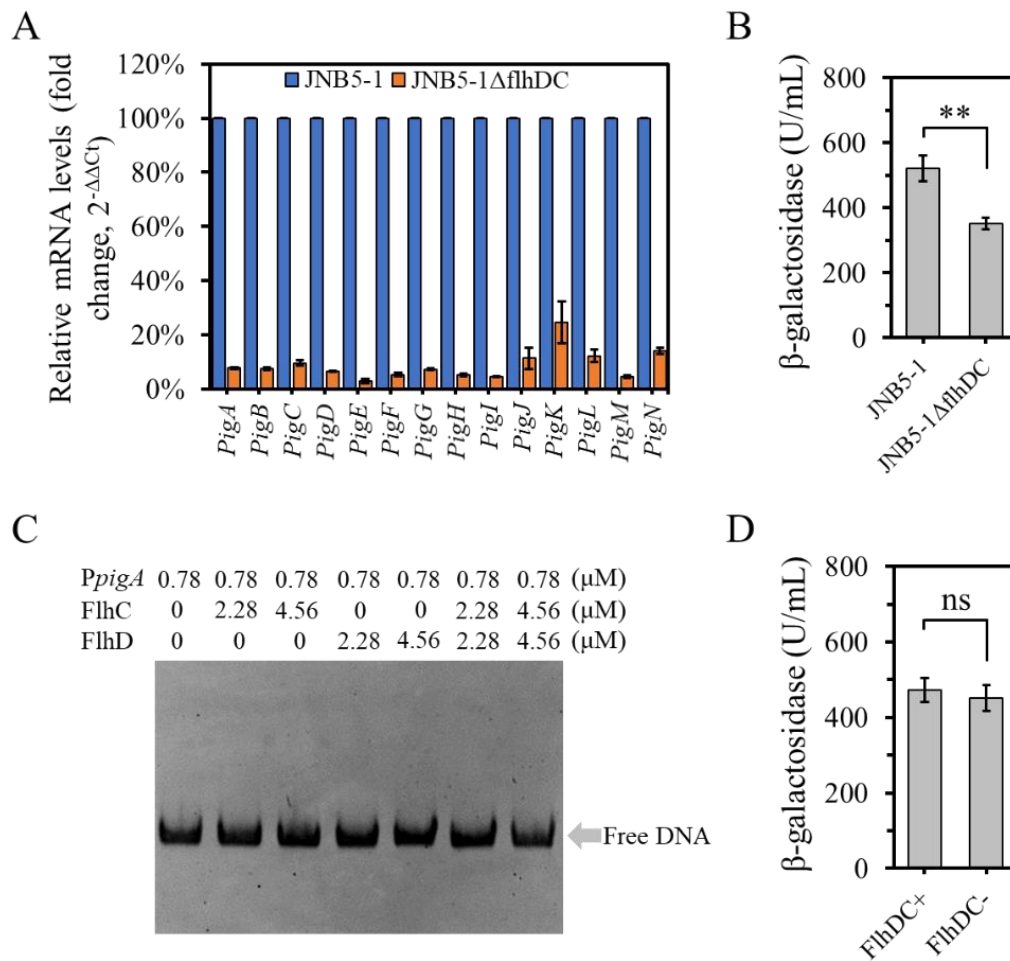
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75 **Fig. S4**



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77 **Figure S4. FlhDC regulates the prodigiosin synthesis genes indirectly.** A. RT-qPCR

78 analysis the *pig* gene cluster expression level in the strains JNB5-1 and JNB5-1ΔflhDC

79 at an OD₆₀₀ of 6.0. B. Analysis of β-galactosidase activity of strains JNB5-1 and JNB5-

80 1ΔflhDC harboring the *PpigA-lacZ* reporter fusion at an OD₆₀₀ of 5.0. C. EMSA for

81 FlhD protein or FlhC protein or FlhDC proteins binding to the promoter region of the

82 *pig* operon. D. Overexpression of FlhDC proteins has no significant effect on the

83 expression of the *pig* gene cluster in *E. coli*. The transcription fusions *PpigA-lacZ* was

84 used in the *E. coli* strains DH5α/pXW2005/pDN19lacΩ-*PpigA* (FlhDC+) and

85 DH5α/pUCP18/pDN19lacΩ-*PpigA* (FlhDC-). The plasmid pXW2005 carries the intact

86 *flhD* and *flhC* genes. The samples were collected at an OD₆₀₀ of 4.0. For B and C, the

87 experiments were performed in biological triplicates. Error bars indicate the standard
88 deviations. For B and D, student's t-test was used for statistical analysis. **, $P < 0.01$;
89 ns, no significance difference.

90 **Table S1. Primers used for characterize the target site of RcsB protein within the *flhDC* promoter region in this study**

Primer	Primer sequence (5'-3')	Function
FlhDC ₂₈₈ -F	GGCAAATTAATCTCTCAAAAACGACTGC	Amplification of the DNA fragment FlhDC ₂₈₈ which containing the predicted RcsB binding site RcsB-1
FlhDC ₂₈₈ -R	GGGTGTATTTGGCTTAATTATTTTTATTTTTGTGATCTATG	
FlhDC ₁₃₄ -F	GGCAACAAACTCAGTATAAATAACCATTTGAGTTAC	Amplification of the DNA fragment FlhDC ₁₃₄ which containing the predicted RcsB binding site RcsB-2
FlhDC ₁₃₄ -R	GAAAATTAGAACAGCCTCAGGCGG	
FlhDC ₂₈₈ (C ⁻²⁴⁵ C ⁻²⁴⁶ C ⁻²⁴⁷)-F1	GGCAAATTAATCTCTCAAAAACGACTGC	Amplification of mutated DNA fragment <i>PflhDC</i> ₂₈₈ (C ⁻²⁴⁵ C ⁻²⁴⁶ C ⁻²⁴⁷)
FlhDC ₂₈₈ (C ⁻²⁴⁵ C ⁻²⁴⁶ C ⁻²⁴⁷)-R1	<u>GGGT</u> TAAATTTGTAAAAATAGTTTCATGGTGACTAAACACTATCGAA	
FlhDC ₂₈₈ (C ⁻²⁴⁵ C ⁻²⁴⁶ C ⁻²⁴⁷)-F2	TATTTTTACAAATTTA <u>ACCCG</u> ATTATTCCTAAAGCAGCGCAACTCTACC	
FlhDC ₂₈₈ (C ⁻²⁴⁵ C ⁻²⁴⁶ C ⁻²⁴⁷)-R2	GGGTGTATTTGGCTTAATTATTTTTATTTTTGTGATCTATG	
FlhDC ₂₈₈ (A ⁻²⁵⁴ A ⁻²⁵⁵ A ⁻²⁵⁶)-F1	GGCAAATTAATCTCTCAAAAACGACTGC	Amplification of mutated DNA fragment <i>PflhDC</i> ₂₈₈ (A ⁻²⁵⁴ A ⁻²⁵⁵ A ⁻²⁵⁶)
FlhDC ₂₈₈ (A ⁻²⁵⁴ A ⁻²⁵⁵ A ⁻²⁵⁶)-R1	<u>TTTATA</u> AATCTTATTAATTTGTAAAAATAGTTTCATGGTGACTAAACAC	
FlhDC ₂₈₈ (A ⁻²⁵⁴ A ⁻²⁵⁵ A ⁻²⁵⁶)-F2	AAATTTAATAAGATTATA <u>AAA</u> TAAAGCAGCGCAACTCTACCCC	
FlhDC ₂₈₈ (A ⁻²⁵⁴ A ⁻²⁵⁵ A ⁻²⁵⁶)-R2	GGGTGTATTTGGCTTAATTATTTTTATTTTTGTGATCTATG	
FlhDC ₂₈₈ (RcsB-1)-F1	GGCAAATTAATCTCTCAAAAACGACTGC	Amplification of mutated DNA fragment <i>PflhDC</i> ₂₈₈ (RcsB-1)
FlhDC ₂₈₈ (RcsB-1)-R1	TTAAATTTGTAAAAATAGTTTCATGGTGACTAAACACTATCG	
FlhDC ₂₈₈ (RcsB-1)-F2	AACTATTTTTACAAATTTAAAAGCAGCGCAACTCTACCCC	
FlhDC ₂₈₈ (RcsB-1)-R2	GGGTGTATTTGGCTTAATTATTTTTATTTTTGTGATCTATG	
FlhDC ₁₃₄ (C ⁻⁶³⁴ C ⁻⁶³⁵ C ⁻⁶³⁶)-F1	GGCAACAAACTCAGTATAAATAACCATTTGAGTTAC	Amplification of mutated DNA fragment <i>PflhDC</i> ₁₃₄ (C ⁻⁶³⁴ C ⁻⁶³⁵ C ⁻⁶³⁶)
FlhDC ₁₃₄ (C ⁻⁶³⁴ C ⁻⁶³⁵ C ⁻⁶³⁶)-R1	<u>GGGGT</u> CAAATCCGATAGCTAATAACCTTATAGTTTAC	

FlhDC ₁₃₄ (C ⁻⁶³⁴ C ⁻⁶³⁵ C ⁻⁶³⁶)-F2	TAGCTATCGGATTTGACCCCAGCCCTCCGCCTGAGGCTGTT	
FlhDC ₁₃₄ (C ⁻⁶³⁴ C ⁻⁶³⁵ C ⁻⁶³⁶)-R2	GAAAATTAGAACAGCCTCAGGCGG	
FlhDC ₅₈₁ -F	GGCAAATTAATCTCTCAAAAACGACTGC	Amplification of the DNA fragment FlhDC ₅₈₁ which containing the predicted RcsB binding site RcsB-1 and RcsB-2
FlhDC ₅₈₁ -R	GAAAATTAGAACAGCCTCAGGCGG	
FlhDC ₅₈₁ (C ⁻²⁴⁵ C ⁻²⁴⁶ C ⁻²⁴⁷)-F1	GGCAAATTAATCTCTCAAAAACGACTGC	Amplification of mutated DNA fragment <i>PflhDC</i> ₅₈₁ (C ⁻²⁴⁵ C ⁻²⁴⁶ C ⁻²⁴⁷)
FlhDC ₅₈₁ (C ⁻²⁴⁵ C ⁻²⁴⁶ C ⁻²⁴⁷)-R1	<u>GGGTTAAATTTGTA</u> AAAATAGTTTCATGGTGACTAAACACTATCGAA	
FlhDC ₅₈₁ (C ⁻²⁴⁵ C ⁻²⁴⁶ C ⁻²⁴⁷)-F2	TATTTTTACAAATTTAACCCGATTATTCCTAAAGCAGCGCAACTCTACC	
FlhDC ₅₈₁ (C ⁻²⁴⁵ C ⁻²⁴⁶ C ⁻²⁴⁷)-R2	GAAAATTAGAACAGCCTCAGGCGG	
FlhDC ₅₈₁ (A ⁻²⁵⁴ A ⁻²⁵⁵ A ⁻²⁵⁶)-F1	GGCAAATTAATCTCTCAAAAACGACTGC	Amplification of mutated DNA fragment <i>PflhDC</i> ₅₈₁ (A ⁻²⁵⁴ A ⁻²⁵⁵ A ⁻²⁵⁶)
FlhDC ₅₈₁ (A ⁻²⁵⁴ A ⁻²⁵⁵ A ⁻²⁵⁶)-R1	<u>TTTATAATCTTATTA</u> AAATTTGTA AAAATAGTTTCATGGTGACTAAACAC	
FlhDC ₅₈₁ (A ⁻²⁵⁴ A ⁻²⁵⁵ A ⁻²⁵⁶)-F2	AAATTTAATAAGATTATA <u>AAATA</u> AAAGCAGCGCAACTCTACCCC	
FlhDC ₅₈₁ (A ⁻²⁵⁴ A ⁻²⁵⁵ A ⁻²⁵⁶)-R2	GAAAATTAGAACAGCCTCAGGCGG	
FlhDC ₅₈₁ (RcsB-1 ⁻)-F1	GGCAAATTAATCTCTCAAAAACGACTGC	Amplification of mutated DNA fragment <i>PflhDC</i> ₅₈₁ (RcsB-1 ⁻)
FlhDC ₅₈₁ (RcsB-1 ⁻)-R1	TTAAATTTGTA AAAATAGTTTCATGGTGACTAAACACTATCG	
FlhDC ₅₈₁ (RcsB-1 ⁻)-F2	AACTATTTTTACAAATTTAAAAGCAGCGCAACTCTACCCC	
FlhDC ₅₈₁ (RcsB-1 ⁻)-R2	GAAAATTAGAACAGCCTCAGGCGG	
FlhDC ₅₈₁ (C ⁻⁶³⁴ C ⁻⁶³⁵ C ⁻⁶³⁶)-F1	GGCAAATTAATCTCTCAAAAACGACTGC	Amplification of mutated DNA fragment <i>PflhDC</i> ₅₈₁ (C ⁻⁶³⁴ C ⁻⁶³⁵ C ⁻⁶³⁶)
FlhDC ₅₈₁ (C ⁻⁶³⁴ C ⁻⁶³⁵ C ⁻⁶³⁶)-R1	<u>GGGGTCAAATCCG</u> ATAGCTAATAACCTTATAGTTTAC	
FlhDC ₅₈₁ (C ⁻⁶³⁴ C ⁻⁶³⁵ C ⁻⁶³⁶)-F2	TAGCTATCGGATTTGACCCCAGCCCTCCGCCTGAGGCTGTT	
FlhDC ₅₈₁ (C ⁻⁶³⁴ C ⁻⁶³⁵ C ⁻⁶³⁶)-R2	GAAAATTAGAACAGCCTCAGGCGG	
FlhDC ₅₈₁ (RcsB-2 ⁻)-F1	GGCAAATTAATCTCTCAAAAACGACTGC	Amplification of mutated DNA fragment <i>PflhDC</i> ₅₈₁ (RcsB-2 ⁻)

FlhDC ₅₈₁ (RcsB-2)-R1	TAGCTAATAACCTTATAGTTTACATTGGTTATTTTCAGC
FlhDC ₅₈₁ (RcsB-2)-F2	AACTATAAGGTTATTAGCTAAGCCCTCCGCCTGAGGCTGTT
FlhDC ₅₈₁ (RcsB-2)-R2	GAAAATTAGAACAGCCTCAGGCGG

91 The sequences wavelined stand for the mutated bases in the predicted RcsB binding site RcsB-1 or RcsB-2.

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Table S2. Primers used for RT-qPCR analysis in this study

Primer	Primer sequence (5'-3')	Function
PigA-RT-F	ATGGCTTTATGGGCGTGTCC	qPCR primers, coding region of gene <i>pigA</i>
PigA-RT-R	GAGAGGCAATCTTTCGGGCT	
PigB-RT-F	AACCGACGACGACTTCACCC	qPCR primers, coding region of gene <i>pigB</i>
PigB-RT-R	CGGTCTGAGCGGCGTATATAAATC	
PigC-RT-F	AAGTTCACGACCCGCTACGC	qPCR primers, coding region of gene <i>pigC</i>
PigC-RT-R	GGGGCCATAGGGGTTTTTGTAC	
PigD-RT-F	TGATAGGTATTGATGACGGACAGAC	qPCR primers, coding region of gene <i>pigD</i>
PigD-RT-R	CCATCCGCAGTTGCTGAATAAA	
PigE-RT-F	GGGTGTTCTTCAGCAACTCCG	qPCR primers, coding region of gene <i>pigE</i>
PigE-RT-R	CGGCGGTGTTTGTCTCGTC	
PigF-RT-F	CTCGCCCCATAGCGGATACA	qPCR primers, coding region of gene <i>pigF</i>
PigF-RT-R	GTTGAGCGACGAACCCAGT	
PigG-RT-F	TCCTGACGCAGAAAATCCACC	qPCR primers, coding region of gene <i>pigG</i>
PigG-RT-R	TGAATGCTCAAACCCCGCTG	
PigH-RT-F	CAAACGAAGCCGCCTAACCC	qPCR primers, coding region of gene <i>pigH</i>
PigH-RT-R	CACGGCGGAACACTTCAATATG	
PigI-RT-F	CGAAGGTGCTCAGATCAAAGGC	qPCR primers, coding region of gene <i>pigI</i>

PigI-RT-R	CTTCAGGCTCCACAGGCACC	
PigJ-RT-F	ATGGCGTGAGCGGTGTAGG	qPCR primers, coding region of gene <i>pigJ</i>
PigJ-RT-R	CATCGACTATCAGCCCATCACC	
PigK-RT-F	GCCTGGTAATCGGTCGTCTCC	qPCR primers, coding region of gene <i>pigK</i>
PigK-RT-R	GCTAAAAGACATCGCCCACCG	
PigL-RT-F	ACGGTTGTCCACTCGCCTCAT	qPCR primers, coding region of gene <i>pigL</i>
PigL-RT-R	CCTCTGTCGGCGGTGAAAAA	
PigM-RT-F	GCTCGGCACTTTCGTCGTTC	qPCR primers, coding region of gene <i>pigM</i>
PigM-RT-R	CTTCAAGTGGCGTTTCATCCTC	
PigN-RT-F	AACATCGGGCGAGTGTCCTG	qPCR primers, coding region of gene <i>pigN</i>
PigN-RT-R	TTGCCCTGCTGGCGTTTATTA	
FlhD-RT-F	CATTTTGCTATCAAGCCATTTACTGC	qPCR primers, coding region of gene <i>flhD</i>
FlhD-RT-R	GGCTCTTTTCTTCGTCGGGC	
FlhC-RT-F	TCGTTCAAGAAGCCAAGGACATT	qPCR primers, coding region of gene <i>flhC</i>
FlhC-RT-R	AACGGTAACATTCCTTTTGGCG	
MotA-RT-F	TTGCTGTTCCGTCTGCTGG	qPCR primers, coding region of gene <i>motA</i>
MotA-RT-R	CAGCCGTAAATAGTCGGTAATGAA	
FlhB-RT-F	TTCTGTTCAAGCGGCAAGTCG	qPCR primers, coding region of gene <i>flhB</i>
FlhB-RT-R	GTGACCCAACCGACCAACG	
FlgE-RT-F	ACACCATCACCGCCTACGACT	qPCR primers, coding region of gene <i>flgE</i>

FlgE-RT-R	TGTCTTCGGTCTTCACAAAGTAGG	
FliF-RT-F	TGAACAATACCAGCCGAACCA	qPCR primers, coding region of gene <i>fliF</i>
FliF-RT-R	GCTTGGCGGTTTCAATCGG	
GalU-RT-F	GTCAAGGACAGGCGAAAGGG	qPCR primers, coding region of gene <i>galU</i>
GalU-RT-R	ATCATCCAATAAAACATCGGGC	
Wza-RT-F	GTGACGGGCGAAGTTACCAAA	qPCR primers, coding region of gene <i>wza</i>
Wza-RT-R	GCCAGTCGGCATTTCAGTCA	
NeuB-RT-F	CGTATTGGTGCCGCTTTGGG	qPCR primers, coding region of gene <i>neuB</i>
NeuB-RT-R	TGGGAATGGAGGCATCGTTTG	
Wzx-RT-F	CGAAACCGTCCCCATCACTG	qPCR primers, coding region of gene <i>wzx</i>
Wzx-RT-R	CGACCCGTTGGAGCAGGAGTA	
Wzy-RT-F	CCTGGCGAGAAGTGCTGGAAG	qPCR primers, coding region of gene <i>wzy</i>
Wzy-RT-R	AGACCACCCTCAACCCACCAC	
ManC-RT-F	AACCTCAAAGCGTTGTCGTCG	qPCR primers, coding region of gene <i>manC</i>
ManC-RT-R	GAGACCTAAGTGGAAGTGGCAAA	
ManB-RT-F	GCTGAAGCGGGTAAACTGGC	qPCR primers, coding region of gene <i>manB</i>
ManB-RT-R	ACGCCGCAAATACTGGAACC	
SpeA-RT-F	GAACGGGTGCCTTCGTAGTCG	qPCR primers, coding region of gene <i>speA</i>
SpeA-RT-R	GAACGGGTGCCTTCGTAGTCG	
SMDB11_RS08645-RT-F	ATTTTTATGCCCGTTTCGTGC	qPCR primers, coding region of gene <i>SMDB11_RS08645</i>

SMDB11_RS08645-RT-R	TCGGTCGCTGCTCTGAGGAT	
ArgF-RT-F	CAAGACGCCGACTTCCTCTACAC	qPCR primers, coding region of gene <i>argF</i>
ArgF-RT-R	CGTGGTTTGGTCGTCGTGG	
CadC-RT-F	CTGTGGCAACGGTGGAGTCAT	qPCR primers, coding region of gene <i>cadC</i>
CadC-RT-R	CAGCAAAGAGGCGAGTAGCGT	
16S rRNA-RT-F	CACACCGCCCGTCACACCA	qPCR primers, coding region of gene 16S rRNA
16S rRNA-RT-R	CGCAGGTTCCCCTACGGTTAC	

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111 **Table S3. Primers used for gene knockout in this study**

Primer	Primer sequence (5'-3')	Function
RcsA-D-U-F	<u>TAGGCCGAATTCGAGCTCGGTACCGTGTTTCTGTCAGCGCTGGACG</u>	The upstream fragment for knocking out the <i>rscA</i> gene
RcsA-D-U-R	<u>TTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCGCGATCGCACCCCCACTTAAATCCG</u>	
RcsA-D-D-F	<u>ATGCGAAGAATGCGATGCCGCTCGCCAGTCGATTGGCTGACCGCTGAACCACAGAGAACG</u>	The downstream fragment for knocking out the <i>rscA</i> gene
RcsA-D-D-R	<u>ATTACAGCCGGATCCCCGGGTACCTCGCCATGGCGGCTTACAT</u>	
RcsB-D-U-F	<u>TAGGCCGAATTCGAGCTCGGTACCCTCTGGTTATCGACCATGAGCCC</u>	The upstream fragment for knocking out the <i>rscB</i> gene
RcsB-D-U-R	<u>TTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCGCGGTTGTTGGCTACCTTGCTTCAGC</u>	
RcsB-D-D-F	<u>ATGCGAAGAATGCGATGCCGCTCGCCAGTCGATTGGCTGAAAAGCCCGCCTCACGGCAG</u>	The downstream fragment for knocking out the <i>rscB</i> gene
RcsB-D-D-R	<u>ATTACAGCCGGATCCCCGGGTACCTGGCGATCTGCGAGAAGTTGG</u>	
RcsC-D-U-F	<u>CCTAGGCCGAATTCGAGCTCGGTACCGGGCTGTTTGTCGATACAGTACCC</u>	The upstream fragment for knocking out the <i>rscC</i> gene
RcsC-D-U-R	<u>TTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCGCGAACGGGTACGCTACAACCG</u>	
RcsC-D-D-F	<u>ATGCGAAGAATGCGATGCCGCTCGCCAGTCGATTGGCTGATCGGATACCATACGAAAGTCAGTGAC</u>	The downstream fragment for knocking out the <i>rscC</i> gene
RcsC-D-D-R	<u>GGATTACAGCCGGATCCCCGGGTACCGTGTACCAACTGCCTGAAGCCA</u>	
RcsD-D-U-F	<u>TAGGCCGAATTCGAGCTCGGTACCGATGCCGCTGACCGGTTTCC</u>	The upstream fragment for knocking out the <i>rscD</i> gene
RcsD-D-U-R	<u>TTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCGCGAGTGGCTGCGCATTCTGAA</u>	
RcsD-D-D-F	<u>ATGCGAAGAATGCGATGCCGCTCGCCAGTCGATTGGCTGAGACTGCTGAAGCAAGGTAGCC</u>	The downstream fragment for knocking out the <i>rscD</i> gene

RcsD-D-D-R	<u>ATTACAGCCGGATCCCCGGGTACCGCAGATGCAGTTCAGTGCGC</u>	
RcsF-D-U-F	<u>TAGGCCGAATTCGAGCTCGGTACCTCGCATCGTCAAAGCCGTTACC</u>	The upstream fragment for knocking out the <i>rscF</i> gene
RcsF-D-U-R	<u>TTGAATGTATTTAGAAAAATAAACAAATAGGGGTCCGCGTGAGATTCCTCTGCCTTAATGAAAGTGGC</u>	
RcsF-D-D-F	<u>ATGCGAAGAATGCGATGCCGCTCGCCAGTCGATTGGCTGACCGAATTCGTTTTCGAGCAGATCG</u>	The downstream fragment for knocking out the <i>rscF</i> gene
RcsF-D-D-R	<u>ATTACAGCCGGATCCCCGGGTACCCAACCTTCTTCAGAACGCGCAG</u>	
IgaA-D-U-F	<u>TAGGCCGAATTCGAGCTCGGTACCTGCCTCGGAAAGGAACAGCG</u>	The upstream fragment for knocking out the <i>igaA</i> gene
IgaA-D-U-R	<u>TTGAATGTATTTAGAAAAATAAACAAATAGGGGTCCGCGGCAATCCCCATCTCACACCCG</u>	
IgaA-D-D-F	<u>ATGCGAAGAATGCGATGCCGCTCGCCAGTCGATTGGCTGACGATGGCTGAACCTGACGC</u>	The downstream fragment for knocking out the <i>igaA</i> gene
IgaA-D-D-R	<u>ATTACAGCCGGATCCCCGGGTACCGCACGATCACCGTACGTTCTTCG</u>	
FlhDC-D-U-F	<u>TAGGCCGAATTCGAGCTCGGTACCGCACGTGTTCTTCCAGCTCAAC</u>	The upstream fragment for knocking out the <i>flhDC</i> gene
FlhDC-D-U-R	<u>TTGAATGTATTTAGAAAAATAAACAAATAGGGGTCCGCGCCATTGAGCCGCCACATTGC</u>	
FlhDC-D-D-F	<u>ATGCGAAGAATGCGATGCCGCTCGCCAGTCGATTGGCTGAATTCCCCATCCCGACAGACTATG</u>	The downstream fragment for knocking out the <i>flhDC</i> gene
FlhDC-D-D-R	<u>ATTACAGCCGGATCCCCGGGTACCGCTGCTTGCGTTGAAAAACCG</u>	
AacC3-D-F	CGCGGAACCCCTATTGTTTATTTTTCT	Amplification of <i>aacC3</i> gene for gene knocking out
AacC3-D-R	TCAGCCAATCGACTGGCGAGC	

112 a. The sequences underlined stand for the homologous sequence of the pUTKm plasmid.

113 b. The sequences wavelined stand for the homologous sequence of the apramycin resistance *aacC3* gene.

114 **Table S4. Genes significantly upregulated in the *rcsB* mutant relative to the wild-type strain of *S. marcescens***

GeneName	Gene sizes (bp)	JNB5-1_FPKM	SK68_FP KM	log₂FC (SK68 vs JNB5-1)	P-Value	Product	KEGG
<i>abgA</i>	1317	11.87	28.25	1.336950781	0.04955572	p-aminobenzoyl-glutamate hydrolase, A subunit	-
<i>abgT</i>	1527	11.73	28.84	1.384040849	0.041587833	p-aminobenzoyl-glutamate transporter	-
<i>agaS</i>	1167	2.6	7.15	1.539744481	0.038745116	Tagatose-6-phosphate ketose/aldose isomerase	-
<i>araB</i>	1638	24.38	58.25	1.342652462	0.045543056	L-ribulokinase	-
<i>argO</i>	618	17.39	50.27	1.61713374	0.019750919	Arginine transporter	-
<i>argT</i>	783	204.86	775.44	2.006816997	0.003111407	Lysine/arginine/ornithine transporter subunit	K10014
<i>bcsG</i>	1656	27.26	71.16	1.470286888	0.028675091	Putative endoglucanase, DUF3260 family	-
<i>bcsZ</i>	1104	48.96	128.23	1.47544421	0.028040208	Endo-1, 4-D-glucanase	K01179
<i>bglF</i>	1866	0.23	1.51	2.746044319	0.005759502	Beta-glucoside-specific PTS system IIABC component	K02755
<i>bioC</i>	768	0.14	1.57	3.407675099	0.019786881	Malonyl-CoA methyltransferase, SAM-dependent	K02169
<i>cadB</i>	1344	4.12	82.14	4.401144421	9.91E-09	Putative lysine/cadaverine transporter	-
<i>ccmD</i>	237	0	4.67	6.46403802	0.006149306	Heme exporter protein D	K02196
<i>chbA</i>	339	47.7	121.01	1.428747033	0.03577257	N, N'-diacetylchitobiose-specific enzyme IIA component of PTS	K02759
<i>chbB</i>	318	17.41	103.39	2.654019246	0.000235015	N, N'-diacetylchitobiose-specific enzyme IIB component of PTS	K02760
<i>cheA</i>	2004	167.4	464.38	1.558521484	0.019833886	Chemotaxis regulator, signal transduction histidine kinase	K03407
<i>cheR</i>	831	284.18	687.94	1.361929819	0.040855134	Chemotaxis regulator, protein-glutamate methyltransferase	K00575
<i>cheW</i>	501	444.29	1328.91	1.667124267	0.013026519	Purine-binding chemotaxis protein	K03408
<i>cheY</i>	390	53.99	175.56	1.78718798	0.009076422	Chemotaxis regulator, receiver protein	K03413
<i>chiP</i>	1404	8.12	26.93	1.815368962	0.008849746	Chitoporin	-
<i>citC</i>	1071	4.15	45.62	3.539523393	2.21E-06	[citrate [pro-3S]-lyase] ligase	K01910

<i>citD</i>	288	0	13.27	8.240875514	4.28E-06	Citrate lyase, acyl carrier gamma subunit	K01646
<i>citE</i>	921	3.54	29.91	3.162099952	2.45E-05	Citrate lyase, citryl-ACP lyase beta subunit	K01644
<i>citF</i>	1509	10.14	36.85	1.946889665	0.00478224	Citrate lyase, citrate-ACP transferase alpha subunit	K01643
<i>citG</i>	885	1.23	8.86	2.924272514	0.000423146	2-(5''-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase	K05966
<i>cysA</i>	1089	20.63	93.71	2.269336907	0.001055614	Sulfate/thiosulfate transporter subunit	K02045
<i>cysC</i>	690	1.73	11.95	2.86041216	0.000478524	Adenosine 5'-phosphosulfate kinase	K00860
<i>cysD</i>	909	29.97	158.61	2.489944651	0.000347927	Sulfate adenylyltransferase, subunit 2	K00957
<i>cysH</i>	735	36.18	253.75	2.896178213	4.19E-05	3'-phosphoadenosine 5'-phosphosulfate reductase	K00390
<i>cysI</i>	1716	45.54	191.36	2.157507756	0.001604587	Sulfite reductase, beta subunit	K00381
<i>cysJ</i>	1803	23.96	80.69	1.838145418	0.006769057	Sulfite reductase, alpha subunit	K00380
<i>cysN</i>	1428	21.74	158.42	2.951538026	3.00E-05	Sulfate adenylyltransferase, subunit 1	K00956
<i>ddpC</i>	870	6.36	18.84	1.650159691	0.01949314	D-ala-D-ala transporter subunit	K02034
<i>dhaK</i>	1071	166.19	1733.05	3.468858271	1.41E-06	Dihydroxyacetone kinase	K05878
<i>dhaL</i>	633	70.29	751.76	3.504905854	1.24E-06	Dihydroxyacetone kinase	K05879
<i>dhaM</i>	1431	193.02	1264.81	2.798603952	6.18E-05	Dihydroxyacetone-specific PTS system HPr/EI component	K05881
<i>dppF</i>	990	63.91	149.39	1.311290801	0.049857505	Dipeptide transporter	K12372
<i>entD</i>	735	0	0.96	5.821269516	0.034782609	phosphopantetheinyltransferase component of enterobactin synthase	K02362
<i>feoA</i>	225	50.65	160.87	1.752654692	0.01141805	Ferrous iron transporter, protein A	-
<i>flgB</i>	414	16.25	381.52	4.636749545	2.20E-09	Flagellar basal-body rod protein FlgB	K02387
<i>flgC</i>	405	8.84	193.39	4.532153666	6.63E-09	Flagellar basal-body rod protein FlgC	K02388
<i>flgD</i>	678	12.81	302.37	4.645817703	1.73E-09	Flagellar basal-body rod modification protein FlgD	K02389
<i>flgE</i>	1224	25.8	585.67	4.590466529	1.56E-09	Flagellar hook protein FlgE	K02390
<i>flgF</i>	756	13.06	186.45	3.919886095	1.50E-07	Flagellar basal-body rod protein FlgF	K02391
<i>flgG</i>	783	14.42	345.54	4.668080305	1.28E-09	Flagellar basal-body rod protein FlgG	K02392

<i>flgH</i>	654	6.31	114.38	4.263021176	3.07E-08	Flagellar L-ring protein precursor FlgH	K02393
<i>flgI</i>	1101	3.35	75.34	4.57200154	5.01E-09	Flagellar P-ring protein precursor FlgI	K02394
<i>flgJ</i>	945	3.22	45.96	3.917824413	3.58E-07	Flagellar protein FlgJ	-
<i>flgK</i>	1650	564.28	1552.97	1.547054342	0.020637594	Flagellar hook-associated protein 1 FlgK	K02396
<i>flgL</i>	960	922.83	2822.49	1.699343238	0.011363383	Flagellar protein FlgJ	K02397
<i>flgM</i>	312	110.62	458.24	2.136632824	0.00187321	Negative regulator of flagellin synthesis FlgM	K02398
<i>flgN</i>	435	282.17	1014.66	1.93274979	0.004334402	Flagella synthesis protein FlgN	K02399
<i>flhA</i>	2079	6.11	28.92	2.328657621	0.000883119	Flagellar biosynthesis protein FlhA	K02400
<i>flhB</i>	1152	3.01	16.5	2.533870281	0.000591373	Flagellar biosynthesis protein FlhB	K02401
<i>flhC</i>	582	61.72	198.66	1.772593089	0.00905084	DNA-binding transcriptional dual regulator with FlhD	K02402
<i>flhD</i>	351	27.21	161.27	2.652095918	0.000198995	DNA-binding transcriptional dual regulator with FlhC	K02403
<i>fliA</i>	723	5.25	28.92	2.543174035	0.000523713	RNA polymerase, sigma 28 factor	K02405
<i>fliC</i>	1083	8584.86	38929.48	2.267521215	0.000915221	Flagellar filament structural protein	K02406
<i>fliD</i>	1401	1147.72	3968.41	1.876307006	0.005433606	Flagellar filament capping protein	K02407
<i>fliF</i>	1695	3.84	44.37	3.613513617	1.23E-06	Flagellar M-ring protein FliF	K02409
<i>fliG</i>	993	5.9	56.5	3.342495827	5.58E-06	Flagellar motor switch protein FliG	K02410
<i>fliH</i>	705	3.69	67.31	4.266877209	5.29E-08	Flagellar assembly protein FliH	K02411
<i>fliI</i>	1362	1.51	43.11	4.909070144	1.39E-09	Flagellum-specific ATP synthase	K02412
<i>fliJ</i>	447	2.91	48.36	4.125492386	4.52E-07	Flagellar FliJ protein	K02413
<i>fliK</i>	1230	0.88	7.85	3.223396364	9.67E-05	Flagellar hook-length control protein FliK	K02414
<i>fliL</i>	486	3.13	46.96	3.983519884	7.43E-07	Flagellar FliL protein	-
<i>fliM</i>	1005	3.78	88.94	4.638104558	3.17E-09	Flagellar motor switch protein FliM	K02416
<i>fliN</i>	417	12.49	112.6	3.255228733	9.87E-06	Flagellar motor switch protein FliN	K02417
<i>fliO</i>	405	0.54	33.27	5.956925925	7.07E-09	Flagellar biosynthesis protein FliO	K02418

<i>fliP</i>	762	2.71	26.26	3.356472288	1.53E-05	Flagellar biosynthetic protein FliP	K02419
<i>fliQ</i>	270	0	2.61	5.821269516	0.034782609	Flagellar biosynthesis protein FliQ	K02420
<i>fliR</i>	783	0	5.14	8.314637628	2.94E-06	Flagellar biosynthesis protein FliR	K02421
<i>fliS</i>	411	392.13	1354.01	1.874277292	0.005554555	Flagellar protein potentiates polymerization	K02422
<i>fliT</i>	369	261.47	1116.31	2.180400268	0.0014271	Putative chaperone	K02423
<i>fliZ</i>	510	2.98	37.06	3.711726306	3.59E-06	RpoS antagonist	K02425
<i>galK</i>	1152	8.38	292.2	5.207641002	4.20E-11	Galactokinase	K00849
<i>galM</i>	1044	3.33	114.7	5.188776511	1.02E-10	Galactose-1-epimerase	K01785
<i>galS</i>	1038	10.98	39.13	1.91895809	0.005737694	DNA-binding transcriptional repressor	-
<i>galT</i>	1053	5.26	221.04	5.477191515	9.37E-12	Galactose-1-phosphate uridylyltransferase	K00965
<i>gldA</i>	1101	386.7	3359.96	3.205645127	6.45E-06	Glycerol dehydrogenase, NAD	K00005
<i>gltI</i>	897	486.62	1655.85	1.853190172	0.006021482	Glutamate, aspartate binding protein, periplasmic	K10001
<i>gntK</i>	540	0	2.61	6.808455209	0.001996045	Gluconate kinase 2	K00851
<i>gntU</i>	1338	0.08	1.95	4.515055775	0.000385253	Gluconate transporter, low affinity GNT 1 system	-
<i>gpr</i>	990	14.69	142.79	3.366331391	3.39E-06	L-glyceraldehyde 3-phosphate reductase	-
<i>gutM</i>	357	7.3	20.28	1.55629709	0.040272556	DNA-binding transcriptional activator of glucitol operon	-
<i>hcaD</i>	1212	16.57	40.07	1.360152357	0.045485375	Phenylpropionate dioxygenase, ferredoxin reductase subunit	K00529
<i>kdpB</i>	2070	2.31	6.02	1.468415634	0.039702125	Potassium translocating ATPase, subunit B	K01547
<i>lamB</i>	1290	54.52	280.19	2.447945139	0.000395265	Maltose outer membrane porin (maltoporin)	-
<i>mglA</i>	1509	7.41	255.58	5.193442982	4.24E-11	Galactose/methyl galactoside transporter ATP-binding protein	K10542
<i>mglB</i>	993	463.29	1464.08	1.746486554	0.009402528	Methyl-galactoside transporter subunit	K10540
<i>mglC</i>	1011	15.89	266.42	4.153129904	2.88E-08	Methyl-galactoside transporter subunit	K10541
<i>moaB</i>	516	15.77	39.94	1.425409835	0.042368924	Molybdopterin biosynthesis protein B	K03638
<i>motA</i>	891	191.96	483.19	1.418190733	0.033561049	Chemotaxis protein MotA	K02556

<i>motB</i>	1065	108.12	270.85	1.411262616	0.034593317	Chemotaxis protein MotB	K02557
<i>mrjD3</i>	765	0	2.5	7.245636611	0.000390825	Fimbrial chaperone MrjD	-
<i>potE</i>	1317	276.8	795.78	1.610013977	0.016252005	Putrescine/proton symporter: putrescine/ornithine antiporter	-
<i>prpR</i>	1587	11.69	36.55	1.730089025	0.011317118	Propionate catabolism operon regulatory protein	-
<i>ribB</i>	654	444.07	1818.51	2.120371123	0.001845285	3, 4-dihydroxy-2-butanone-4-phosphate synthase	K02858
<i>SMWW4_v1c00170</i>	840	48.19	123.76	1.446929556	0.031382738	Extracellular solute-binding protein	-
<i>SMWW4_v1c00690</i>	1929	409.13	1381.1	1.841686126	0.006307713	Methyl-accepting chemotaxis sensory transducer	K05875
<i>SMWW4_v1c01070</i>	393	0	2.56	6.328167771	0.009223959	Hypothetical protein	-
<i>SMWW4_v1c01540</i>	204	3.19	17.25	2.496245653	0.00638213	Cellulose biosynthesis protein BcsF	-
<i>SMWW4_v1c01560</i>	192	14.13	60.74	2.184799464	0.003483529	Hypothetical protein	-
<i>SMWW4_v1c04050</i>	1554	35.76	125.77	1.900801243	0.005120754	Methyl-accepting chemotaxis sensory transducer	K05877
<i>SMWW4_v1c04440</i>	228	2.38	16.76	2.871686585	0.002125618	Hypothetical protein	-
<i>SMWW4_v1c04520</i>	2163	228.4	1176.42	2.451290427	0.000373522	Ornithine decarboxylase	K01581
<i>SMWW4_v1c05190</i>	204	31.39	80.83	1.449233476	0.041355343	Hypothetical protein	-
<i>SMWW4_v1c05260</i>	396	0	7.62	7.901109759	2.25E-05	Hypothetical protein	-
<i>SMWW4_v1c05480</i>	747	0.15	1.35	3.147636445	0.039970491	TonB family protein	-
<i>SMWW4_v1c05490</i>	2244	1.74	4.48	1.447033168	0.046500719	TonB-dependent receptor	-
<i>SMWW4_v1c05500</i>	651	0.17	2.16	3.627923883	0.010215054	MotA/TolQ/ExbB proton channel	-
<i>SMWW4_v1c05600</i>	1302	0.83	2.86	1.850900243	0.029463659	FAD dependent oxidoreductase	K09471
<i>SMWW4_v1c05630</i>	1113	9.46	31.62	1.826219497	0.008684979	Histone deacetylase superfamily protein	-
<i>SMWW4_v1c05950</i>	846	5.26	19.61	1.981760562	0.005798082	Hypothetical protein	K16856
<i>SMWW4_v1c05960</i>	1278	6.28	20.77	1.809458899	0.010083535	Mandelate racemase/muconate lactonizing protein	K18334
<i>SMWW4_v1c06050</i>	1080	8.04	31.56	2.057760184	0.003484959	Diguanylate cyclase	-
<i>SMWW4_v1c07960</i>	1431	7.96	19.32	1.36424545	0.047544446	Uroporphyrin-III C-methyltransferase	K02302

<i>SMWW4_v1c09380</i>	405	33.23	95.82	1.613534545	0.018821985	Entry exclusion protein 2	-
<i>SMWW4_v1c09590</i>	453	5.03	13.54	1.509150281	0.047647683	Thiol-disulfide oxidoreductase DCC	-
<i>SMWW4_v1c09630</i>	804	18.09	45.14	1.405179799	0.039711158	XRE family transcriptional regulator	-
<i>SMWW4_v1c14030</i>	570	0	1.94	6.46403802	0.006149306	D-amino acid aminotransferase	-
<i>SMWW4_v1c14570</i>	1305	44.41	183.75	2.135063453	0.001796588	Methyl-accepting chemotaxis transducer/sensory box protein	K03406
<i>SMWW4_v1c14880</i>	612	1.06	4.27	2.069193026	0.028123146	Thiosulfate reductase cytochrome subunit B	-
<i>SMWW4_v1c15130</i>	498	0.44	3.43	2.987599272	0.012766938	Cell division protein ZipA	-
<i>SMWW4_v1c15760</i>	1947	837.07	2588.93	1.715457701	0.010633868	Surface layer protein	-
<i>SMWW4_v1c16110</i>	1146	89.97	238.28	1.491607242	0.025865665	Cystathionine gamma-synthase	K01758
<i>SMWW4_v1c18240</i>	435	0.5	3.24	2.709764564	0.029588432	Hypothetical protein	-
<i>SMWW4_v1c18740</i>	366	1.19	5.49	2.26320099	0.029323086	Alpha/beta hydrolase	-
<i>SMWW4_v1c19630</i>	219	0	10.56	7.519616802	0.000125561	Hypothetical protein	-
<i>SMWW4_v1c19920</i>	750	0	1.07	6.010721672	0.021900161	Gram-negative pili assembly chaperone	-
<i>SMWW4_v1c19930</i>	1341	0	0.75	6.328167771	0.009223959	Hypothetical protein	-
<i>SMWW4_v1c20390</i>	555	0.2	3.26	3.987630815	0.003042849	S-type pyocin domain-containing protein	-
<i>SMWW4_v1c21100</i>	1620	183.43	791.92	2.196627397	0.001292975	Phosphoenolpyruvate carboxykinase	K01610
<i>SMWW4_v1c21110</i>	1344	22.45	277.61	3.714301489	3.71E-07	Citrate carrier protein	K11616
<i>SMWW4_v1c21220</i>	765	52.77	126.04	1.342181562	0.045553947	Putative chaperone protein	-
<i>SMWW4_v1c21230</i>	555	34.61	99.09	1.603358212	0.018341349	Spore coat U domain-containing protein	-
<i>SMWW4_v1c21240</i>	459	57.93	141.94	1.379007292	0.04099466	Spore coat U domain protein	-
<i>SMWW4_v1c22860</i>	1155	0.75	2.96	2.046860068	0.020165681	Beta-lactamase	-
<i>SMWW4_v1c25010</i>	816	1.2	5.67	2.31409184	0.006447493	Alpha/beta hydrolase	-
<i>SMWW4_v1c25080</i>	93	2.33	14.05	2.603839127	0.039696281	Hypothetical protein	-
<i>SMWW4_v1c25960</i>	249	2.62	11.31	2.175611044	0.01990983	Hypothetical protein	-

<i>SMWW4_v1c26990</i>	555	15.45	61.41	2.075879276	0.003234492	Hypothetical protein	-
<i>SMWW4_v1c27020</i>	1506	12.83	82.65	2.773449081	8.36E-05	Sugar ABC transporter ATP-binding protein	K17207
<i>SMWW4_v1c27030</i>	1038	13.07	60.25	2.290093156	0.001038141	Sugar ABC transporter permease	K17206
<i>SMWW4_v1c27040</i>	1008	39.08	184.63	2.326113537	0.000750124	Sugar ABC transporter periplasmic protein	K17205
<i>SMWW4_v1c28020</i>	405	0.54	3.48	2.709764564	0.029588432	Hypothetical protein	-
<i>SMWW4_v1c29060</i>	672	6.3	23.34	1.972830863	0.006192488	ABC transporter-like protein	K02032
<i>SMWW4_v1c29070</i>	843	10.17	31.61	1.720736071	0.013998183	ABC transporter-like protein	K02031
<i>SMWW4_v1c29100</i>	1569	46	187.11	2.110579955	0.002007458	ABC transporter periplasmic protein	K02035
<i>SMWW4_v1c29800</i>	405	10.99	95.82	3.20726482	1.44E-05	Hypothetical protein	-
<i>SMWW4_v1c30870</i>	90	0	14.52	6.702529772	0.002863891	Hypothetical protein	-
<i>SMWW4_v1c31740</i>	768	0.71	4.19	2.624652974	0.005619692	ABC transporter	K15599
<i>SMWW4_v1c32210</i>	3090	10.89	96.9	3.239732351	6.06E-06	Beta-D-galactosidase	K01190
<i>SMWW4_v1c33380</i>	309	450.97	5410.69	3.671100444	4.25E-07	Hypothetical protein	-
<i>SMWW4_v1c33680</i>	468	1.86	7.95	2.168418532	0.01320914	TetR family transcriptional regulator	-
<i>SMWW4_v1c34300</i>	282	0.77	246.36	8.322285499	1.50E-15	PTS family sugar porter component IIB	K02822
<i>SMWW4_v1c34320</i>	1020	15.11	83.39	2.549967155	0.000281616	Purine operon repressor	-
<i>SMWW4_v1c35180</i>	96	0	16.76	6.999490466	0.001006409	Hypothetical protein	-
<i>SMWW4_v1c35460</i>	780	1.95	6.19	1.744916129	0.029826037	Alpha-acetolactate decarboxylase	K01575
<i>SMWW4_v1c35510</i>	468	51.25	287.87	2.575685839	0.000231096	Hypothetical protein	-
<i>SMWW4_v1c36450</i>	1638	0.27	2.82	3.459719534	0.000295197	Hypothetical protein	-
<i>SMWW4_v1c37810</i>	756	92.02	840.37	3.277294275	4.51E-06	Ankyrin	-
<i>SMWW4_v1c37820</i>	960	150.47	1236.66	3.125307671	1.03E-05	Phospholipase	-
<i>SMWW4_v1c38400</i>	381	0	3.17	6.588206425	0.004165659	Putative cytoplasmic protein	-
<i>SMWW4_v1c38530</i>	1356	12.65	53.16	2.157415084	0.001822705	Citrate carrier protein	-

<i>SMWW4_v1c38880</i>	2139	3.25	14.52	2.245503956	0.001667577	Lysine decarboxylase	K01582
<i>SMWW4_v1c39550</i>	303	0.72	9.95	3.802419114	0.000608346	XRE family transcriptional regulator	-
<i>SMWW4_v1c40650</i>	1641	8.13	152.25	4.311379937	1.15E-08	Acetolactate synthase	K01652
<i>SMWW4_v1c40660</i>	1470	12.77	199.37	4.049925347	5.19E-08	Aldehyde dehydrogenase	K00130
<i>SMWW4_v1c40670</i>	795	3.14	62.22	4.387811248	2.67E-08	L-aspartate dehydrogenase	K06989
<i>SMWW4_v1c40680</i>	795	2.87	64.25	4.564477896	1.02E-08	Short-chain dehydrogenase	-
<i>SMWW4_v1c40690</i>	819	6.23	89.49	3.927879678	1.97E-07	Putative alpha/beta hydrolase	-
<i>SMWW4_v1c40700</i>	525	7.44	155.5	4.466919726	9.13E-09	Cupin	-
<i>SMWW4_v1c40710</i>	1257	3.8	16.16	2.171865074	0.002528126	Major facilitator superfamily transporter	-
<i>SMWW4_v1c40730</i>	942	11.52	27.96	1.364717697	0.048032886	Glyoxalase/bleomycin resistance protein/dioxygenase	-
<i>SMWW4_v1c40780</i>	318	0.68	13.6	4.319967473	5.78E-05	Rieske (2Fe-2S) domain-containing protein	-
<i>SMWW4_v1c42100</i>	1524	9.33	27.97	1.669806066	0.014934254	Alkaline phosphatase	K01077
<i>SMWW4_v1c43430</i>	777	4.75	13.46	1.585717802	0.029686015	Permease	-
<i>SMWW4_v1c43450</i>	366	1.19	6.04	2.399882993	0.019112419	Transcriptional regulator	-
<i>SMWW4_v1c43810</i>	1068	266.95	720.45	1.518809367	0.023078189	Hypothetical protein	-
<i>SMWW4_v1c43830</i>	2232	112.81	289.87	1.448010999	0.030017945	Hypothetical protein	-
<i>SMWW4_v1c43840</i>	1206	70.46	274.78	2.049703283	0.002607293	Permease	-
<i>SMWW4_v1c44490</i>	1680	19.7	101.86	2.456114923	0.000407683	Hemolysin activator HlyB domain-containing protein	K11017
<i>SMWW4_v1c44500</i>	4824	17.57	151.62	3.195593292	7.12E-06	Filamentous hemagglutinin outer membrane protein	K11016
<i>SMWW4_v1c44730</i>	1122	1.35	4.21	1.714622861	0.032991148	Hypothetical protein	-
<i>SMWW4_v1c46340</i>	1239	4.91	48.04	3.375459774	4.50E-06	Virulence factor	-
<i>SMWW4_v1c46350</i>	2949	4.75	58.03	3.696753596	4.94E-07	Virulence protein SrfB	-
<i>SMWW4_v1c46360</i>	2190	6.69	80.57	3.675463584	5.50E-07	Putative virulence factor	-
<i>SMWW4_v1c46520</i>	987	46.73	135.58	1.622936147	0.016280328	Carbohydrate ABC transporter periplasmic-binding protein	-

<i>SMWW4_v1c46570</i>	600	13.75	52.62	2.021165259	0.004185292	Sugar isomerase (SIS)	-
<i>SMWW4_v1c47610</i>	978	2.11	8.53	2.096162672	0.006550552	Glycosyl transferase, group 2 family protein	-
<i>SMWW4_v1c48010</i>	123	8.82	31.88	1.926597925	0.022886106	Hypothetical protein	-
<i>SMWW4_v1r120</i>	1530	0	0.79	6.588206425	0.004165659	16S ribosomal RNA	K01977
<i>SMWW4_v1t280</i>	77	22.55	62.68	1.553854798	0.04970526	tRNA-Arg	K14219
<i>SMWW4_v1t370</i>	75	1.45	13.41	3.147636445	0.039970491	tRNA-Gln	K14223
<i>SMWW4_v1t440</i>	76	11.42	44.98	2.046860068	0.020165681	tRNA-Gly	K14225
<i>ssuE</i>	579	0	1.91	6.46403802	0.006149306	NAD(P)H-dependent FMN reductase	K00299
<i>tap</i>	1626	405.68	1007.58	1.398986995	0.035652998	Methyl-accepting protein IV	K05877
<i>tauC</i>	837	0.91	4.44	2.35792198	0.008158301	Taurine ABC transporter permease	K15552
<i>tauD</i>	849	1.53	10.66	2.870326025	0.000390157	Taurine dioxygenase, 2-oxoglutarate-dependent	K03119
<i>tsr</i>	1671	216.6	512.88	1.330056025	0.045524428	Methyl-accepting chemotaxis protein I, serine sensor receptor	K05874
<i>ulaA</i>	1380	51.9	2005.73	5.358374908	9.47E-12	L-ascorbate-specific enzyme IIC component of PTS	K03475
<i>ulaC</i>	444	11.98	891.51	6.300816391	3.93E-14	L-ascorbate-specific enzyme IIA component of PTS	K02821
<i>urtB</i>	1581	0	0.64	6.328167771	0.009223959	Urea ABC transporter, permease protein UrtB	K11960
<i>xylB</i>	1518	25.17	135.58	2.515689067	0.000295631	Xylulokinase	K00854
<i>ydjJ</i>	1035	121.01	690.19	2.598306531	0.000179671	Putative Zn-dependent and NAD(P)-binding oxidoreductase	K05351
<i>yhdT</i>	243	6.25	21.93	1.887517621	0.01821108	Inner membrane protein	-
<i>yhjH</i>	792	72.08	237.01	1.803589114	0.007697076	Cyclic-di-GMP phosphodiesterase, FlhDC-regulated	-
<i>yjcH</i>	312	20.18	67.03	1.816496724	0.009977559	Inner membrane protein, DUF485 family	-
<i>yjdL</i>	1452	0.3	1.59	2.463656002	0.015514096	Putative dipeptide and tripeptide permease	-
<i>ykgB</i>	465	0	1.51	5.821269516	0.034782609	Inner membrane protein, DUF417 family	-

116 **Table S5. Genes significantly downregulated in the *rcsB* mutant relative to the wild-type strain of *S. marcescens***

Gene Name	Gene sizes (bp)	JNB5-1_FPKM	SK68_FP KM	log₂FC (SK68 vs JNB5-1)	P-Value	Product	KEGG
<i>cadC1</i>	438	21.31	6.43	-1.638264464	0.02893868	Transcriptional regulator CadC	-
<i>caiD</i>	720	2.26	0.42	-2.298189371	0.049335813	Carnitiny-CoA dehydratase	K01692
<i>cynT</i>	654	10.45	2.92	-1.746406096	0.025029639	Carbonic anhydrase	K01673
<i>nemA</i>	1104	186.98	69.85	-1.333831267	0.045833215	FMN-linked N-ethylmaleimide reductase	K10680
<i>paaA</i>	939	70.16	9.42	-2.80810654	8.49E-05	Phenylacetate-CoA oxygenase subunit PaaA	K02609
<i>paaB</i>	288	27.13	1.4	-4.151408434	1.09E-05	Phenylacetate-CoA oxygenase subunit PaaB	K02610
<i>paaC</i>	1533	34.76	12.07	-1.43914916	0.033713497	3-hydroxy-acyl-CoA dehydrogenase	K00074
<i>paaD</i>	441	43.81	6.38	-2.686659399	0.00035573	Phenylacetic acid degradation protein PaaD	K02614
<i>paaF</i>	774	23.42	3.9	-2.495591756	0.000835449	Enoyl-CoA hydratase/isomerase	K01692
<i>paaG</i>	792	40.29	12.95	-1.549829261	0.024849694	Enoyl-CoA hydratase	K15866
<i>paaI</i>	759	25.31	7.82	-1.606649686	0.022400251	Phenylacetate-CoA oxygenase subunit PaaI	K02611
<i>paaJ</i>	1206	35.01	8.75	-1.911865442	0.005892683	Beta-ketoadipyl CoA thiolase	K02615
<i>paaJ2</i>	498	14.6	1.41	-3.259413293	0.000189466	Phenylacetate-CoA oxygenase subunit PaaJ	K02612
<i>paaK2</i>	1059	36.59	7.41	-2.216305289	0.00163565	Phenylacetate-CoA oxygenase subunit PaaK	K02613
<i>paaN</i>	2067	30.72	9.24	-1.645541775	0.015566613	Phenylacetic acid degradation protein PaaN	K02618
<i>phnK</i>	789	2.2	0	-7.023061828	0.001006409	Phosphonate transport system ATP-binding protein PhnK	-
<i>puuE</i>	1266	272.52	33.83	-2.923032701	3.38E-05	GABA aminotransferase, PLP-dependent	K00823
<i>puuR</i>	558	88.88	31.89	-1.391564748	0.040949264	DNA-binding transcriptional repressor for the puu divergon	-
<i>rcsB</i>	651	822.88	2.47	-8.281599096	3.50E-19	DNA-binding response regulator RcsB	K07687
<i>rffH</i>	882	0.86	0	-5.844608271	0.034782609	Glucose-1-phosphate thymidyltransferase	K00973

<i>scsC</i>	717	12.56	3.93	-1.587114199	0.034451952	Suppressor for copper-sensitivity C	-
<i>SMWW4_v1c00880</i>	441	3.69	0.46	-2.854359234	0.022208097	Hypothetical protein	-
<i>SMWW4_v1c01470</i>	1692	63.37	17.23	-1.791767829	0.008514062	Chitinase A	K01183
<i>SMWW4_v1c02160</i>	1464	1679.97	470.84	-1.748573057	0.009305008	Metalloprotease	K01406
<i>SMWW4_v1c08030</i>	771	10.84	2.09	-2.281543612	0.003839201	Amino acid-binding protein	-
<i>SMWW4_v1c10480</i>	1041	69.95	17.48	-1.91334091	0.005219833	Pyridoxal-phosphate dependent enzyme	K01738
<i>SMWW4_v1c11910</i>	1443	148.92	30.94	-2.180305234	0.001473592	Chitinase C1	K01183
<i>SMWW4_v1c12640</i>	996	1.42	0.2	-2.649726556	0.039696281	ABC transporter substrate-binding protein	K02016
<i>SMWW4_v1c12660</i>	1026	2.43	0.1	-4.383828647	0.000797167	ABC transporter permease protein	K02015
<i>SMWW4_v1c13060</i>	1032	1167.94	397.59	-1.468071746	0.027799325	Iron(III) transport system substrate-binding protein	K02012
<i>SMWW4_v1c13920</i>	714	2.74	0	-7.191753823	0.000530405	GntR family transcriptional regulator	-
<i>SMWW4_v1c14020</i>	1236	3.95	0.81	-2.179581003	0.011034893	Monooxygenase FAD-binding protein	-
<i>SMWW4_v1c14130</i>	1131	239.51	68.01	-1.729675788	0.010352973	Oxidoreductase	-
<i>SMWW4_v1c14710</i>	981	11.51	3.69	-1.550947155	0.034943366	Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	-
<i>SMWW4_v1c16240</i>	1389	0.63	0	-6.03411172	0.021900161	FKBP-type peptidyl-prolyl isomerase domain-containing protein	-
<i>SMWW4_v1c17610</i>	801	86.99	14.43	-2.503393313	0.00037907	Extracellular endonuclease	-
<i>SMWW4_v1c18120</i>	132	6.58	0	-6.03411172	0.021900161	Hypothetical protein	-
<i>SMWW4_v1c18870</i>	537	245.55	20.41	-3.500791855	1.67E-06	Hypothetical protein	-
<i>SMWW4_v1c18990</i>	747	3.05	0	-7.412735803	0.00021796	Amidohydrolase	-
<i>SMWW4_v1c19750</i>	1485	126	42.18	-1.492023135	0.026216833	ABC transporter-like protein	K17215
<i>SMWW4_v1c20330</i>	1131	4.89	1.51	-1.601564724	0.047493615	Klebicin C phage associated protein	-
<i>SMWW4_v1c22380</i>	1845	707.64	213.94	-1.639228629	0.01448166	Extracellular lipase	-
<i>SMWW4_v1c22960</i>	1797	340.8	79.06	-2.021359415	0.00291792	Glycoside hydrolase	K01207
<i>SMWW4_v1c23680</i>	213	23.44	0	-8.539371466	1.03E-06	Hypothetical protein	-

<i>SMWW4_v1c24900</i>	642	6.76	1.72	-1.874281115	0.028732664	TetR family transcriptional regulator	-
<i>SMWW4_v1c25120</i>	1503	15.81	4.15	-1.842233075	0.008729496	Ferric iron ABC transporter, permease protein	K02011
<i>SMWW4_v1c25200</i>	903	2.4	0	-7.342769752	0.000290613	Putative alpha/beta hydrolase	-
<i>SMWW4_v1c25800</i>	1158	2.81	0.69	-1.914045028	0.036252813	Multidrug resistance protein D	-
<i>SMWW4_v1c26220</i>	2307	63.41	20.74	-1.525293273	0.023350561	Oxidoreductase alpha (molybdopterin) subunit	-
<i>SMWW4_v1c28430</i>	237	25.19	3.39	-2.785812889	0.001378134	Hypothetical protein	-
<i>SMWW4_v1c28820</i>	1008	1.51	0.1	-3.672585238	0.010215054	Beta-ketoacyl-acyl-carrier-protein synthase I	K00648
<i>SMWW4_v1c28900</i>	906	2.52	0.44	-2.379810664	0.023630413	Glycosyl transferase family protein	-
<i>SMWW4_v1c30350</i>	1311	5.22	1.38	-1.823880565	0.019867521	Major facilitator superfamily transporter	-
<i>SMWW4_v1c30360</i>	765	11.35	3.68	-1.534083547	0.04110275	Short chain dehydrogenase/reductase family protein	K00059
<i>SMWW4_v1c30380</i>	1350	141.41	24.06	-2.468443791	0.000373896	Colicin-like protein	-
<i>SMWW4_v1c30820</i>	1053	5.26	1.62	-1.601564724	0.047493615	NAD-dependent epimerase/dehydratase	-
<i>SMWW4_v1c31750</i>	936	12.64	4.08	-1.540875373	0.035428277	NMT1/THI5-like domain-containing protein	K15598
<i>SMWW4_v1c33120</i>	1329	154.5	55.53	-1.389662465	0.037682998	Glutamine synthetase	K09470
<i>SMWW4_v1c33200</i>	1101	18.14	3.1	-2.455488513	0.00091773	Diguanylate cyclase	-
<i>SMWW4_v1c35030</i>	972	9.04	2.07	-2.034821226	0.008374124	Hypothetical protein	-
<i>SMWW4_v1c35350</i>	411	39.34	3.67	-3.325162486	2.99E-05	Hypothetical protein	-
<i>SMWW4_v1c35860</i>	381	9.68	0.79	-3.472137931	0.000814859	Hypothetical protein	-
<i>SMWW4_v1c35880</i>	327	13.28	3.38	-1.874281115	0.028732664	Phage holin	-
<i>SMWW4_v1c37730</i>	837	31.9	9.37	-1.679265489	0.015853579	Hypothetical protein	-
<i>SMWW4_v1c37880</i>	108	15.07	1.86	-2.854359234	0.022208097	Hypothetical protein	-
<i>SMWW4_v1c38360</i>	339	96.04	13.94	-2.694718032	0.000227592	Hypothetical protein	-
<i>SMWW4_v1c38430</i>	1431	0.68	0	-6.201588493	0.014078675	GntR family transcriptional regulator	-
<i>SMWW4_v1c38520</i>	972	102.39	22.24	-2.115690177	0.002113013	Patatin	-

<i>SMWW4_v1c41490</i>	483	8.54	0.21	-5.10513788	3.23E-05	Type VI secretion system effector	K11903
<i>SMWW4_v1c41500</i>	483	18.43	2.08	-3.04349036	0.000252713	Type VI secretion system effector	K11903
<i>SMWW4_v1c41510</i>	546	32.8	4.97	-2.629555303	0.000484226	Hypothetical protein	-
<i>SMWW4_v1c42460</i>	1212	0.9	0	-6.351630009	0.009223959	Phage major capsid protein	-
<i>SMWW4_v1c42680</i>	1149	60.92	8.14	-2.816075565	8.04E-05	Aromatic amino acid permease	-
<i>SMWW4_v1c42690</i>	1455	137.39	12.37	-3.386078766	2.91E-06	Succinic semialdehyde dehydrogenase	K00135
<i>SMWW4_v1c43610</i>	345	197.24	68.48	-1.439071916	0.033411576	Hypothetical protein	-
<i>SMWW4_v1c43640</i>	1683	22.18	4.18	-2.318661957	0.001046084	O-antigen polymerase	-
<i>SMWW4_v1c44200</i>	219	562.96	192.82	-1.458981699	0.030220457	Phage shock protein G	-
<i>SMWW4_v1c45410</i>	279	2.72	0	-5.844608271	0.034782609	Addiction module antitoxin	-
<i>SMWW4_v1c46070</i>	897	211.73	69.94	-1.511303343	0.024423444	Inosose dehydratase	K03335
<i>SMWW4_v1c46080</i>	885	982.03	362.97	-1.349346979	0.042588033	Xylose isomerase domain-containing protein	-
<i>SMWW4_v1c46090</i>	1014	1166.09	345.95	-1.666500507	0.013006588	Inositol 2-dehydrogenase	K00010
<i>SMWW4_v1c46100</i>	1941	795.71	193.31	-1.954735509	0.003882767	Thiamine pyrophosphate protein central region	K03336
<i>SMWW4_v1c46110</i>	1932	763.35	149.51	-2.265514781	0.000931697	Ribokinase-like domain-containing protein	K03338
<i>SMWW4_v1c46150</i>	822	368.63	83.3	-2.059124837	0.002513992	Myo-inositol catabolism IolB domain-containing protein	K03337
<i>SMWW4_v1c46160</i>	1506	797.1	140.53	-2.417274989	0.00044546	Methylmalonate-semialdehyde dehydrogenase	K00140
<i>SMWW4_v1c46230</i>	414	8.65	0.73	-3.429228026	0.000977184	Hypothetical protein	-
<i>SMWW4_v1c46240</i>	531	522.2	174.95	-1.49098728	0.025944656	Fimbrial protein	-
<i>SMWW4_v1c46250</i>	552	34.21	7.1	-2.177669731	0.002943482	Fimbrial protein	-
<i>SMWW4_v1c46260</i>	2502	11.84	3.3	-1.757399999	0.011626696	Fimbrial biogenesis outer membrane usher protein	-
<i>SMWW4_v1c46270</i>	747	33.85	7.27	-2.13045841	0.003005462	Pili assembly chaperone	-
<i>SMWW4_v1c46280</i>	612	12.59	2.79	-2.0779007	0.008149164	Fimbrial protein	-
<i>SMWW4_v1c46290</i>	1005	20.09	3	-2.650936951	0.000384034	Type I pilus assembly protein FimE	-

<i>SMWW4_v1c46300</i>	540	10.65	3.17	-1.656927816	0.039747057	Fimbrial protein	-
<i>SMWW4_v1c46310</i>	624	19.13	2.58	-2.79542091	0.000390798	LuxR family transcriptional regulator	-
<i>SMWW4_v1c46330</i>	918	9.69	2.63	-1.790968414	0.018376695	Hypothetical protein	-
<i>SMWW4_v1t340</i>	75	11.58	0	-6.03411172	0.021900161	tRNA-Gln	K14223
<i>srlB</i>	363	92.68	33.24	-1.392051761	0.042106722	Glucitol/sorbitol-specific enzyme IIA component of PTS	K02781
<i>srlE</i>	981	31.75	9.43	-1.663748555	0.016441846	Glucitol/sorbitol-specific enzyme IIB component of PTS	K02782
<i>xylA</i>	837	477.03	112.91	-1.992191723	0.003350782	Xylose isomerase	K06606
<i>xylE</i>	1443	512.71	69.74	-2.791295125	6.53E-05	D-xylose transporter	-
<i>ycho</i>	1512	42.28	9.77	-2.025274259	0.003416133	Putative invasin	-
<i>ydcS</i>	1155	173.27	60.24	-1.437584486	0.031772775	Spermidine/putrescine ABC transporter solute-binding protein	K02055
<i>yebE</i>	657	84.08	30.76	-1.363672699	0.043817554	Inner membrane protein, DUF533 family	-
<i>yedA</i>	924	20.2	6.42	-1.565338244	0.02602133	Amino acid exporter for phenylalanine	-
<i>yhdV</i>	222	24.93	7.7	-1.601564724	0.047493615	Putative outer membrane protein	-
<i>ytfF</i>	969	151.42	42.96	-1.730841153	0.010630564	Inner membrane protein	-

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