

**Supplementary Table S4 Verification of expression of select genes by RT-qPCR.**

Locus	Locus Tag	Fold change		Primer F	Primer R
		Microarray	RT-qPCR		
<b>Amino acid transport and metabolisms</b>					
<i>aroA</i>	b0908	0.92 ± 0.12	1.14 ± 0.19	TTGCAAAAAGGCACCACCACG	GACAACGCCACCAGCGAGAA
<i>aroG</i>	b0754	0.91 ± 0.10	0.72 ± 0.14	TGGCATCAGGGCTTTCTTGTC	TCGCCGTTACCCTGGTATTCA
<i>tyrB</i>	b4054	0.80 ± 0.09	0.56 ± 0.10	ATTGACGAACAACACTGACGCAT	GCTCGCCGTAAAGGAGAAAA
<i>thrA</i>	b0002	0.86 ± 0.11	1.32 ± 0.25	TTACCCCCATCGCCCAGT	ACCATCCCTTTCATCCCC
<i>asd</i>	b3433	0.77 ± 0.10	0.88 ± 0.18	GCCATTTCGCCCTGTCTTC	TCCAGTAACCTTGCCATCCGCTTTC
<i>ilvD</i>	b3771	0.70 ± 0.08	0.24 ± 0.04	GTCGCCGGAGATGTGGTAGTA	CTTTGCCGAGACCCATTGATT
<i>mmuM</i>	b0261	3.16 ± 0.39	3.51 ± 0.65	CGAGATTGAGGCGTTGGC	CCGTTAAACCGTGTAATGCTG
<b>Replication, recombination and repair</b>					
<i>yagL</i>	b0278	2.45 ± 0.29	2.03 ± 0.32	ACACGCTTGTCATTCAGAT	CTTCCCTCCTTCGTCCTA
<i>fimE</i>	b4313	-2.23 ± 0.24	-3.76 ± 0.69	AGGCGGTTTGTACGGG	CACGGGTTACGCTCAT
<i>Pine</i>	b1158	-3.12 ± 0.40	-5.23 ± 1.00	GATAAGCGGCACAAAGTCC	GCACCCATCACATGAAAGAA
<i>pinR</i>	b1374	-2.03 ± 0.16	-2.32 ± 0.42	TCAACGCTGGATCAGACCAC	CAATGCCACCCAATGCTAA
<b>Cell motility</b>					
<i>fimA</i>	b4314	2.29 ± 0.30	1.79 ± 0.41	ATCGCTGGCACAGGAAG	TCTGAACTAAATGTGCGACC
<i>cpxP</i>	b3914	-2.46 ± 0.30	-3.98 ± 0.76	AGCCACGCTGCTGAAGTC	TTTCTGCGGTGACAAGGC
<i>sfmC</i>	b0531	-2.33 ± 0.22	-3.66 ± 0.71	TATCCCGCTGATGCTAAACA	CAAAACATTCTGCCGTTTC
<i>sfmH</i>	b0533	-2.37 ± 0.28	-4.19 ± 0.85	CAAACATATCCTGGGCTACTG	CCAGACTCATCGCACCTAAT
<b>Energy production and conversion</b>					
<i>betB</i>	b0312	5.13 ± 0.35	3.21 ± 0.46	CGTAGTGGCAGGGATTGG	CGGATGCTCGGTACAGATA
<b>Nucleotide transport and metabolism</b>					
<i>Coda</i>	b0337	2.34 ± 0.31	2.01 ± 0.36	CCACATATTCACCTGGACACC	GCGACTTCCTGCTTCACTT
<b>Inorganic ion transport and metabolism</b>					
<i>nikD</i>	b3479	2.33 ± 0.26	3.28 ± 0.54	ACCACCACCGACCTTGA	CATGATGCCAGCTCCATACC
<i>fhuA</i>	b0150	2.05 ± 0.11	2.59 ± 0.40	CGCAAGTTGGGAAGGATG	GGTGTAAGTATAAGAACCAGTAC
<i>feoA</i>	b3408	2.48 ± 0.23	3.57 ± 0.79	ATGCAATACACTCCAGATACTGC	GGAAACCGCTTCCACTTCTA
<b>Translation</b>					
<i>cspF</i>	b1558	-2.33 ± 0.12	-4.01 ± 0.79	CCCGTAAAATGACAGGAAT	TGAAAGGTAAACATTGGCAG
<i>marR</i>	b1530	-2.14 ± 0.22	-3.59 ± 0.63	GAAATTATTCATTGGGTCG	TGAAAGGTAAACATTGGCAG
<i>pspA</i>	b1304	-2.05 ± 0.08	-3.11 ± 0.30	CCGATCTGATTAAGTCCCTGG	GCTGTGGCTTCTGCTTCC
<i>tdcA</i>	b3118	-2.12 ± 0.11	-2.14 ± 0.33	TGGTAGCCAGTAAGTCCCG	GCATATTGTGCCACAGGTAA
<b>Signal transduction mechanisms</b>					
<i>fimZ</i>	b0535	-2.18 ± 0.13	-1.88 ± 0.36	TTTTTCATGCCGTTTCAGAT	CGTATAAATTTGGCGTAGTCG
<b>Cell wall/membrane/envelope biogenesis</b>					
<i>betT</i>	b0314	-2.47 ± 0.27	-3.04 ± 0.50	GCACGCTGGACTGGGTT	CGGCTACGGAGAAGAACAT
<i>rfaL</i>	b3622	-2.31 ± 0.33	-2.46 ± 0.38	TTGCCATTTCTGTCTAC	TCCTGTGCGGTTCTCTAC
<i>ycgH_1</i>	b1169	-2.58 ± 0.37	-3.05 ± 0.56	ACTCCGTGTTACCCATCTG	GGAGATTATCGCCATTCA
<i>ycgH_2</i>	b1170	-2.08 ± 0.25	-3.47 ± 0.31	AGAATGACGCAAATAACAACA	TGCCATTTACGCCAAGTT
<b>General function prediction only</b>					
<i>arpA</i>	b4017	-2.11 ± 0.15	-1.94 ± 0.39	ACCTCAACGCTCAGACACTC	GGAAACCAACGCCAAAGT
<b>Function unknown</b>					

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<i>emrY</i>	b2367	$-2.74 \pm 0.29$	$-4.05 \pm 0.78$	ACTGGCAGGTTGGCACA	GCCACATATCGGAGCG
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