

Supplementary Table S1: Fold change of transcription measured by microarray expression profiling for selected genes.

CH34 <sup>a</sup>	NA4 <sup>a</sup>	Function	Ident % <sup>b</sup>	Transcription (fold change) <sup>c</sup>						
				Non-selective condition <sup>d</sup>				1 μM AgNO <sub>3</sub>		
				CH34S1	CH34S2	AE104S	NA4S	CH34S1 <sup>e</sup>	CH34S2 <sup>e</sup>	CH34 <sup>f</sup>
<b>0477</b>	40157	Conserved hypothetical, CopQ-like	100	9.0	9.1	3.9	15.8	10.0	11.0	(0.9)
<b>3571</b>	10101	Conserved hypothetical, CopQ-like, PsrQ1	100	23.8	22.0	21.2	2.9	20.2	26.0	(0.7)
<b>4461</b>	570171	Conserved hypothetical, CopQ-like, PsrQ2	100	81	88.6	106.6	26.2	53.8	ND	(0.7)
<b>4464</b>	570173	Conserved hypothetical, Czcl	98	5.1	4.9	2.1	2.8	5.4	5.1	(1.1)
<b>4595</b>	570182	Conserved hypothetical, Czcl2	100	7.7	8.2	3.1	2.7	5.6	6.2	1.9
<b>5118</b>	400150	Outer membrane protein (porin), OmpC family	100	8.6	9.0	5.8	3.6	6.2	5.6	(1.2)
<b>1748</b>	170093	Outer membrane lipoprotein, AgrC	100	(1.2)	13.5	10.4	1.6	1.4	19.4	(1.0)
<b>1749</b>	170094	Membrane fusion protein, AgrB	100	(1.3)	22.7	7.9	(1.3)	1.3	24.2	(0.9)
<b>1750</b>	170095	Cation/multidrug efflux pump, AgrA	100	2.1	8.3	5.3	(1.4)	2.2	8.7	(1.0)
<b>1751</b>	170096	DNA-binding response regulator, AgrR	100	78.5	65.4	81.0	54.2	83.9	83.1	(0.8)
<b>1752</b>	170097	Histidine kinase, AgrS	100	44.4	38.0	30.4	16.2	46.5	46.1	(1.0)
<b>3523</b>	10050	Transcriptional regulator, CupR	100	(1.7)	1.5	(0.8)	4.4	1.5	(1.0)	16.3
<b>3524</b>	10051	P-type ATPase, CupA	100	(0.7)	0.7	(0.8)	3.7	(0.9)	(0.8)	43.4
<b>3525</b>	10052	Copper chaperone, CupC	100	(1.7)	1.6	(0.7)	7.1	0.8	(1.0)	15.7
<b>5030</b>	400053	Protein involved in copper and silver resistance, CusD	100	(0.9)	0.8	(0.9)	1.4	1.3	1.2	5.0
<b>5031</b>	400054	Outer membrane porin, CusC	100	(0.7)	0.7	(1.1)	(0.9)	(1.0)	(1.0)	43.4
<b>5032</b>	400055	Membrane fusion protein, CusB	100	(1.0)	(1.0)	1.3	1.6	(1.1)	(0.9)	33.8
<b>5033</b>	400056	Efflux pump, CusA	100	(1.1)	(1.1)	(1.1)	(1.3)	0.8	0.8	43.1
<b>5034</b>	400057	Periplasmic copper-binding protein, CusF	100	(1.0)	(1.0)	(1.1)	0.8	0.6	0.7	13.5
<b>6133</b>	350004	Transmembrane protein, SilD	100	(0.9)	(1.1)	(1.0)	2.3	(1.0)	(1.1)	(1.1)
<b>6134</b>	350003	Outer membrane porin, SilC	100	(0.6)	0.7	ND	(1.4)	1.6	1.4	5.5
<b>6135</b>	350002	Membrane fusion protein, SilB	100	1.6	1.6	1.5	2.1	1.5	(1.4)	2.6
<b>6136</b>	350001	Efflux pump, SilA	100	(0.5)	0.5	(1.0)	2.6	1.7	1.7	3.2

<sup>a</sup>CH34 (Rmet\_) and NA4 (CmetNA4v1\_) locus tag based on MaGe annotation v1 (Supplementary Table S3 and S4); <sup>b</sup>% protein identity between CH34 and NA4 copy;

<sup>c</sup>Fold change of gene expression measured by microarray expression profiling; <sup>d</sup>Mutant compared to its parental strain in non-selective growth conditions;

<sup>e</sup>Comparison of CH34S1 and CH34S2 to CH34 when exposed to 1 μM AgNO<sub>3</sub> (i.e. a fold change around 1 indicates a similar induction by AgNO<sub>3</sub> for the mutant and parental strain, whereas a fold change similar to that in non-selective condition indicates no induction by AgNO<sub>3</sub>); <sup>f</sup>Exposure of CH34 to 1 μM AgNO<sub>3</sub> (data derived from Monsieurs et al. 2011); Non-significant values (P-value > 0.05) are shown between brackets.