

Additional material

Supplemental table S2. Oligonucleotides used in the study.

A. Identification of transposon insertion sites in *H. arsenicoxydans* mutants.

Corresponding gene name	Primer name	Primer sequence (5'-3')
<i>aoxB</i>	aoxB forward	AAATGACAGCATCTGGTGG
	aoxB reverse	CCGTCAATCCAACATTCTG
<i>aoxS</i>	aoxS forward	TCTTCCTGGTGACTIONACTA
	aoxS reverse	CAAATTGACTCACCCATGA
<i>aoxR</i>	aoxR forward	ATTAATGGACGAGGTACCG
	aoxR reverse	CGACTACTAGAGAAGTAGC
<i>modC</i>	modC forward	CTCTGCAATATCTGAACGG
	modC reverse	ACATTGAATCCAACCGGAC
<i>modB</i>	modB forward	GAGCAAAGGCAAAGACAAC
	modB reverse	GTCCGGTTGGATTCAATGT
<i>dnaJ</i>	dnaJ forward	GAGCCAGCATAGAAGCTT
	dnaJ reverse	TTGTCTGAAGTCGCAAGAC
<i>rpoN</i>	rpoN forward	AGCAATCCCTGCAATTACGCG
	rpoN reverse	AATGGCTTGGGTGGTATACAG

B. Quantitative RT-PCR.

Primer name	Primers sequence (5'-3')
HEAR0118 forward	GATCAGCTCGGGATTGATGTAG
HEAR0118 reverse	GCATGAACAGGTGATCGTCATC
HEAR0478 forward	CCCACGTACCTTTGTAGTAAG
HEAR0478 reverse	GACGTGGTGGAAGTGTTTAATG
HEAR0482 forward	CAGGTCAATATCGTGTGCTC
HEAR0482 reverse	CAACCCGTTAGGTGGAATGC
HEAR0483 forward	GTGCGCTACGATGAAGTAAG
HEAR0483 reverse	GCTTACTGCGGGAAGTTCAC
HEAR2646 forward	GCACGCCCTTAATACCCTTG
HEAR2646 reverse	CGACTTGCACTGCGAGATTC
HEAR3109 forward	GCAGCAGGTTCAATGCAATC
HEAR3109 reverse	GCGAACACTTGCTGGAACAG
HEAR2922 forward	GGCATTCCCTCGACTCGTTTC
HEAR2922 reverse	GGAGCCAGTCCCTTTGTTTC

