

Figure S1. Rates of chromate removal from LB medium by wild-type *S. oneidensis* MR-1 (●) cell suspensions and the LB broth-only abiotic control (○) in the presence of 1 mM K₂CrO₄. Graphed values represent the mean concentration ± standard error (bars) of three independent measurements performed in triplicate.

Figure S2. Cluster Analysis of Microarray dataset. Complete linkage clustering analysis of 910 *S. oneidensis* MR-1 genes exhibiting altered mRNA expression levels in response to 1 mM potassium chromate (K₂CrO₄) exposure over time. Transcriptional profiles, based on the Euclidean similarity/distance measure, are shown at 5, 30, 60, and 90 min post- chromate shock. Individual genes are represented by a single row and each exposure time point is represented by a single column. Red represents the level of induction, while green represents repression. Genes grouped within three primary clusters (I, II, III) and individual genes that belong to subgroups A-H are described in Table S1. The cluster analysis was performed using the software package *Hierarchical Clustering Explorer Version 3.0* (<http://www.cs.umd.edu/hcil/multi-cluster>)

Figure S3. Comparison of gene expression measurements by microarray hybridization and real-time quantitative RT-PCR. The gene expression ratios for wild-type *S. oneidensis* MR-1 shocked with 1 mM chromate for 5, 30, 60, and 90 min under aerobic growth conditions were log transformed (in base 10). The real-time RT-PCR log₁₀ ratio values were plotted against the microarray data log₁₀ values. Comparison of the two methods indicated a high level of concordance ($r^2 = 0.81$).

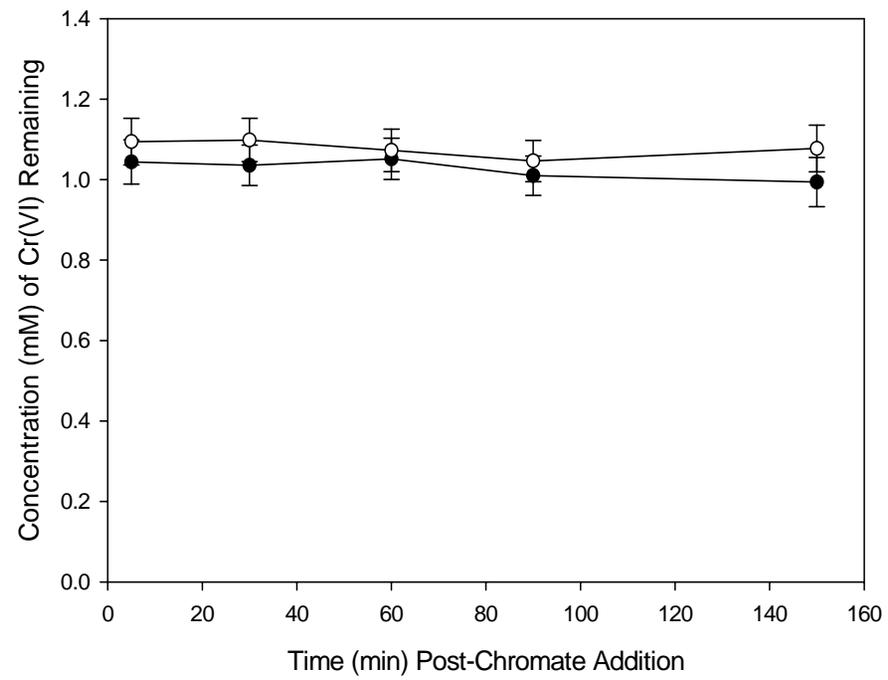


Figure S1

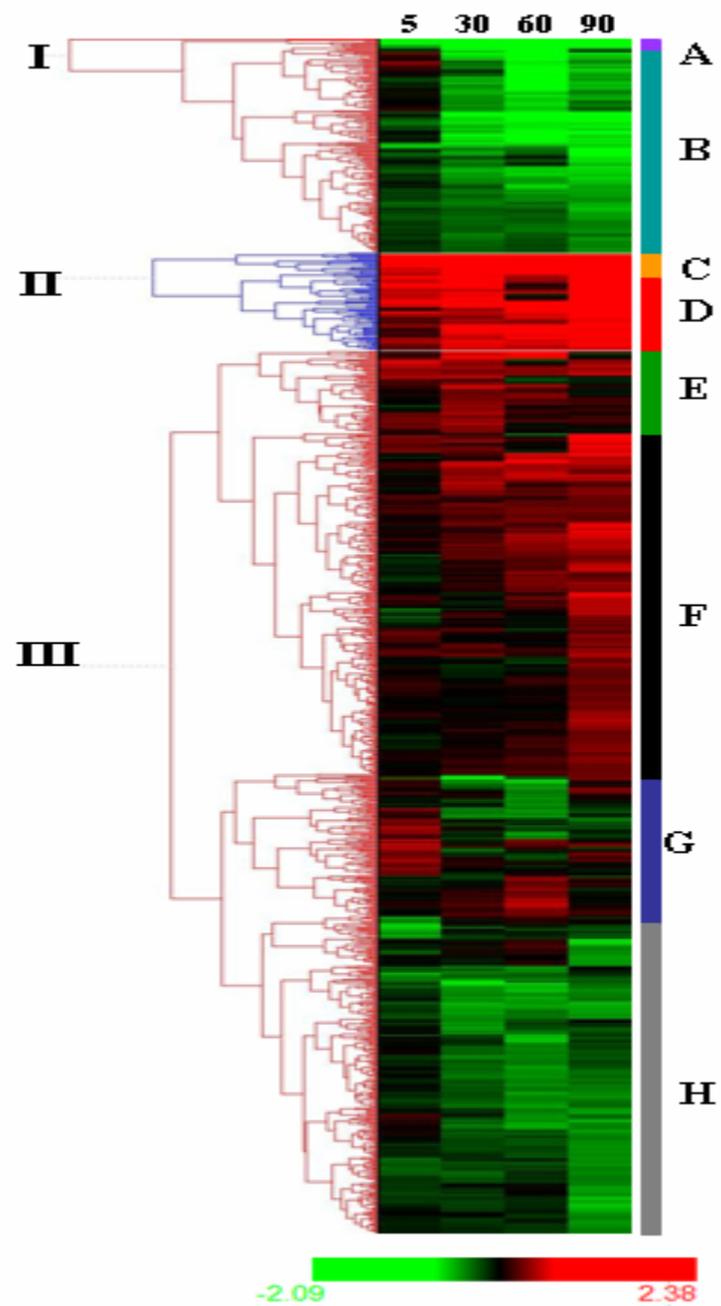


Figure S2

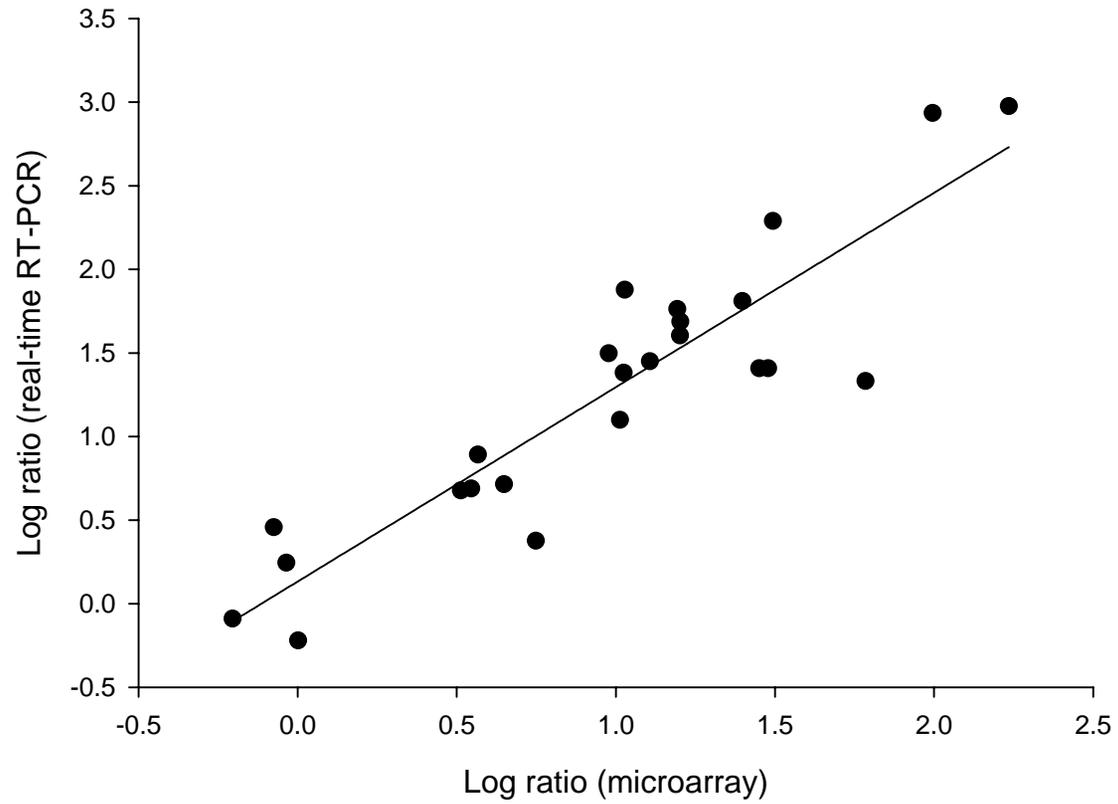


Figure S3