



Figure S1. Cluster Analysis of Microarray dataset. Linkage clustering analysis of statistically significant ($p < 0.05$) *P. alcaliphila* 34 genes exhibiting $\log_2\text{FC} > 1.0$ or $\log_2\text{FC} < -1.0$ at least at one time points during Cr(VI) stress exposure. Transcriptional profiles, based on the Euclidean similarity, are shown at 5, 30, 60, 90 and 120 min post-chromate addiction. Individual genes are represented by a single row and near to each gene is reporting the corresponding putative function, based on RAST annotation. Each exposure time point is represented by a single column. Red represents the level of induction, while green represents repression. The cluster analysis was performed using the software package *Multi Experiment Viewer Version 4.8.1* (<http://www.tm4.org/mev/>).