Supporting Information for:

Identification of Novel Gene Targets and Putative Regulators of Arsenic-Associated DNA Methylation in Human Urothelial Cells and Bladder Cancer

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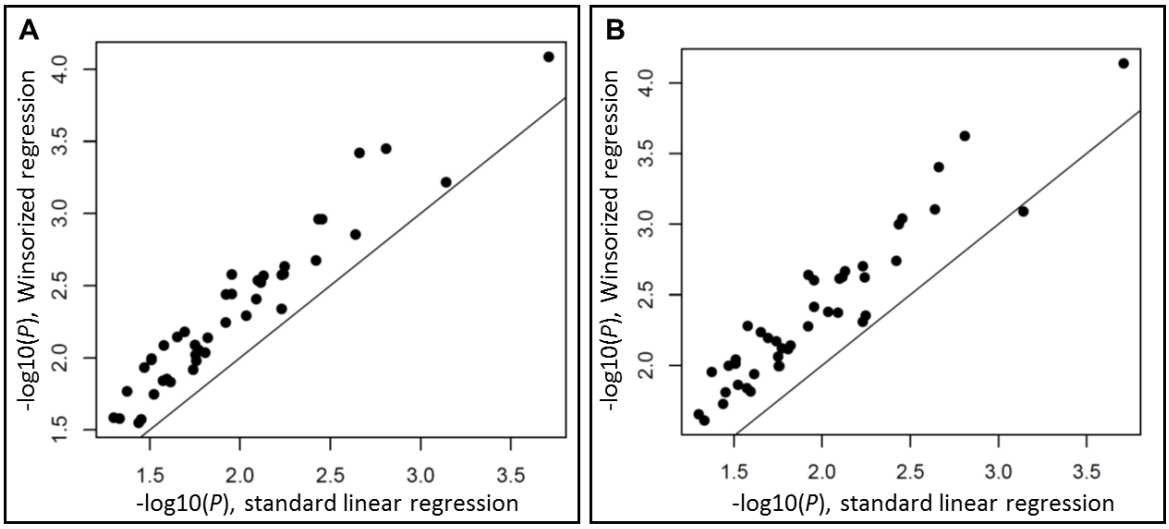
SUPPORTING INFORMATION AVAILABLE

Supporting Information, Figures S1, S2, and S3 are available in this document: (Figure S1) Comparison of p-values for association of tAs with methylation for each of 43 differentially methylated genes associated with EUC tAs, using Winsorized regression versus standard linear regression, (Figure S2) Molecular network involving genes with promoter DNA methylation levels associated with EUC arsenicals, (Figure S3) Quantitative real time PCR (qPCR) validation of CpG DNA methylation levels for *PSMB2* and *SLC12A7*.

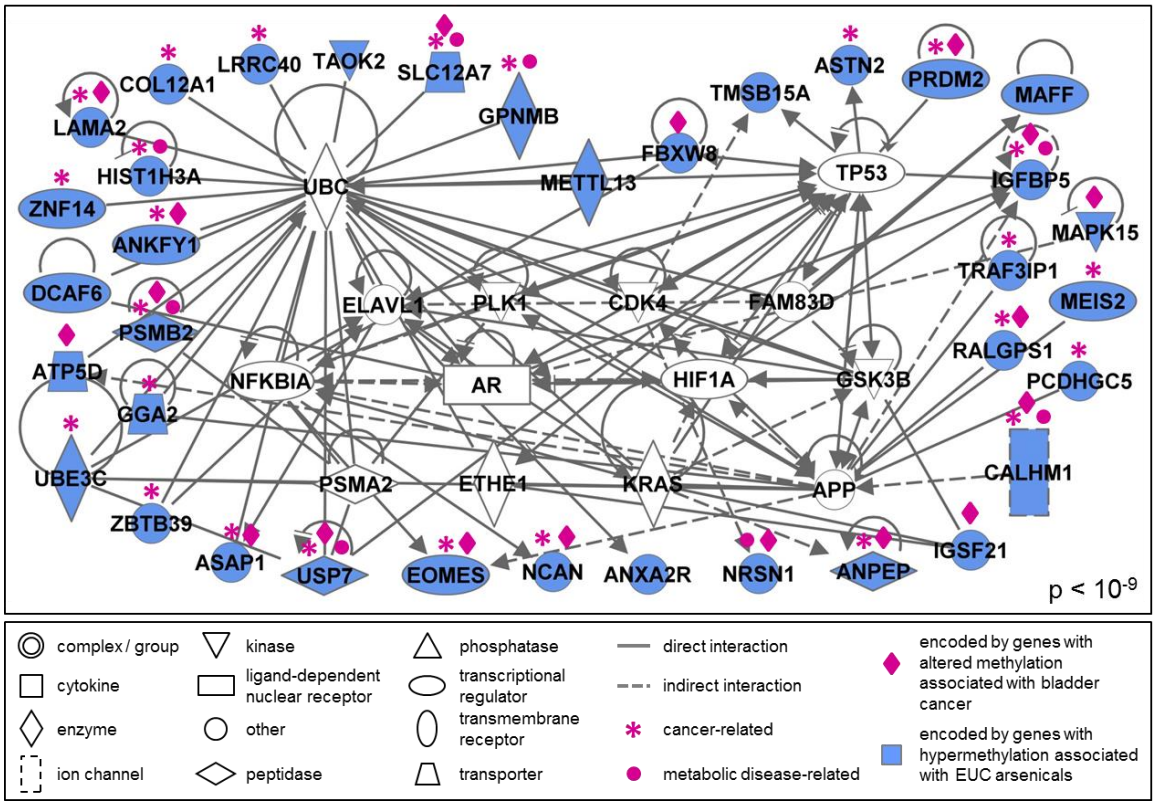
Supporting Information, Tables S1 through S5 are available in a separate excel workbook. These include the following tables: (Table S1) The correlation between arsenic species in exfoliated urothelial cells (EUCs) and arsenic species in urine, and between arsenic species in EUCs, (Table S2) Genes with differential methylation associated with arsenic species in human exfoliated urothelial cells, (Table S3) Exfoliated urothelial cell (EUC) arsenical measures, urinary arsenical measures, and DNA methylation levels of 49 genes significantly associated with EUC arsenical(s) across all 46 subjects, (Table S4) Comparative Toxicogenomics Database (CTD) results, (Table S5) Genes with differential methylation associated with bladder cancer using The Cancer Genome Atlas (TCGA) repository, (Table S6) Transcription factor (TF) families with binding sites enriched for either exfoliated urothelial cell (EUC) arsenic-associated hypermethylated genes and/or bladder cancer-associated hypermethylated genes. This information is available free of charge via the Internet at http://pubs.acs.org/.

Supporting Information, Figure S1.



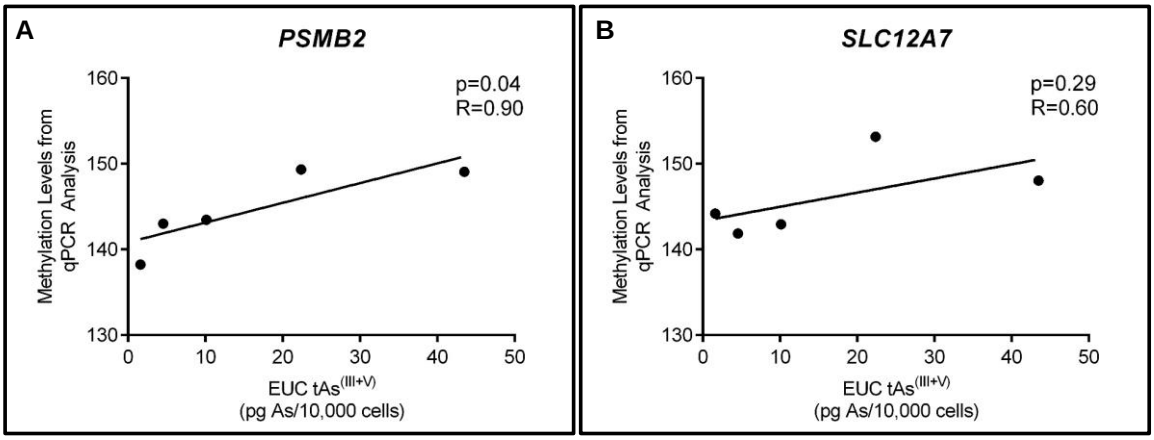
Supporting Information, Figure S1. Comparison of p-values for association of tAs with methylation for each of 43 differentially methylated genes associated with EUC tAs, using Winsorized regression versus standard linear regression. The results are generally more significant using robust regression. (**A**) Results using the model tAs~methylation+age+BMI. (**B**) Results using the model tAs~methylation, where both variables were pre-residualized for the covariates.

Supporting Information, Figure S2.



Supporting Information, Figure S2. Molecular network involving genes with promoter DNA methylation levels associated with EUC arsenicals. The network displays interactions between proteins encoded by differentially methylated genes associated with one or more EUC arsenicals (blue) and proteins associated with arsenic-related signaling (white).

Supporting Information, Figure S3.



Supporting Information, Figure S3. Quantitative real time PCR (qPCR) validation of CpG DNA methylation levels for (A) *PSMB2* and (B) *SLC12A7*. CpG promoter methylation levels are shown for the qPCR analysis results using DNA samples from five subjects within the study cohort. Methylation levels are plotted against total arsenic (tAs) levels measured in exfoliated urothelial cells (EUC).