**Supplementary Figure 1:** Technical validation of Notch Signaling Pathway DNA Methylation PCR Array. Upper panel: Determination of promoter methylation by QMSP; Lower panel: Normalized beta-value from methylation array. Zero values cannot be plotted correctly on a log scale. It is not expected that the bar graph will show same level of methylation values as the analysis procedures are different for both the techniques. In general, QMSP and NOTCH methylation array findings are consistent after dicotomization of methylation (negative or positive).

#### Supplementary Figure 2: Promoter methylation is inversely associated with gene expression: A) Upper panel: Promoter demethylation of CTBP1 and NCSTN gene after arsenic treatment. β-value from Notch methylation array, in which 0% means completely unmethylated and 100% means completely methylated; Lower panel: Expression of CTBP1 and NCSTN genes determined by Q-RT-PCR assay. Methylation status of these two demethylated genes are generally associated with expression data. B) Upper panel: Promoter methylation of ERBB2 and NFKB2 gene after arsenic treatment. β-value from Notch methylation array, in which 0% means completely unmethylated and 100% means completely methylated; Lower panel: Expression status of ERBB2 and NFKB2 genes determined by Q-RT-PCR assay. Methylation status of these two genes are associtaed with expression.

**Supplementary Figure 3:** Association of miRNA expression with water arsenic concentration and creatinine adjusted urine arsenic concentration (Mann–Whitney U test). Water arsenic was categorized into 3 groups [a: < 10µg/L (n=28), b: 10-50µg/L (n=22), c: >50µg/L (n=21)]. No significant differences were observed for miR-200a and miR-205 expressions; however statistically significant decrease level of miR-200c and miR-200 expression were observed in the urine creatinine group ≥ 200µg/L compared to urine creatinine group ≤100µg/g (p=0.005 and 0.009 respectively). Creatinine adjusted urine arsenic concentration was defined as urinary arsenic concentration (µg/L) divided by urinary creatinine (mg/dL), multiplied by 100 for easier tabulation, and categorized into 3 groups (a: < 100µg/g (n=35), b: 100-200µg/L (n=38), c: >200µg/L (n=37)). This value indirectly reflects blood arsenic concentration adjusted by renal function.

**Supplementary Figure 4:** ROC curves for individual micro RNA expression in 177 normal and 32 bladder cancer urine samples were shown. Y axis denotes sensitivity and X-axis denotes 1-specificity. AUC and the most effective cutoff values were determine by maximizing the sensitivity and specificity. The curve of miR-205 showed the high AUC value (0.845) and promising sensitivity (93.8%) and specificity (76.8%).