Supplementary Material Table 1: Location of gene promoters and regions that were amplified and the CpG dinucleotide positions within the regions where DNA methylation was quantified.

Gene	Chromosome	Promoter		Amplicon		CpGs
		Start	*End*	*Start*	*End*	
P16	9	21964701	21965538	21965321	21965395	21965350 (position 1)
						21965355 (position 2)
						21965357 (position 3)
						21965361 (position 4)
						21965365 (position 5)
						21965368 (position 6)
						21965374 (position 7)
P53	17	7531143	7531743	7531409	7531628	7531486 (position 1)
						7531473 (position 2)
						7531469 (position 3)
						7531458 (position 4)

Supplementary Material Table 2: Primers used for DNA methylation analysis

ID	Forward Primer (5' to 3')	Reverse Primer (5' to 3')	Sequencing Primer (5' to 3')	Sequence analyzed[a]
Global methylation analysis				
Alu	Biotin-TTTTTATTAAAAATATAAAAATT	CCCAAACTAAAATACAATAA	AATAACTAAAATTACAAAC	G/AC/TG/AC/TG/ACCACCA
LINE-1	TTTTGAGTTAGGTGTGGGATATA	Biotin-AAAATCAAAAAATTCCCTTTC	AGTTAGGTGTGGGATATAGT	TTC/TGTGGTGC/TGTC/TG
Gene-specific methylation analysis				
p16	AGGGGTTGGTTGGTTATTAG	Biotin - CTACCTACTCTCCCCCTCTC	GGTTGGTTATTAGAGGGT	GGGGC/TGGATC/TGC/TGTGC/TGTTC/TGGC/TGGTTGC/TG
p53	Biotin - TTAGGAGTTTATTTAATTTAGGGAAG	TATCCAACTTTATACCAAAAACCTC	TCCAAAAAACAAATAACTACTAAACTC	CG/AAAAACACTTTACG/ATTCG/AAAACTAAAAACG/ATACTTT

[a]Nucleotides at which DNA methylation was measured are underlined

Supplementary Material Table 3. Estimates and 95% confidence intervals from general linear regression models that compared DNA methylation (%mC) in umbilical cord blood and maternal blood according to tertiles of total urinary arsenic (µg/L). Models are adjusted for maternal BMI and creatinine. Additionally, cord blood models are adjusted for fetal age.

		Cord Blood			Maternal Blood		
		β	95% CI	p-value	β	95% CI	p-value
LINE-1	High	0.95	-0.09, 1.99	0.07	0.06	-1.17, 1.30	0.92
	Med	0.32	-0.53, 1.17	0.46	0.05	-0.99, 1.10	0.92
	Low	Ref.	-	-	Ref.	-	-
Alu	High	0.14	-0.30, 0.58	0.52	-0.12	-0.54, 0.31	0.59
	Med	0.02	-0.34, 0.38	0.92	0.24	-0.12, 0.60	0.19
	Low	Ref.	-	-	Ref.	-	-
P16 pos 1	High	0.42	-0.37, 1.21	0.29	0.27	-0.64, 1.18	0.55
	Med	0.04	-0.62, 0.69	0.91	-0.01	-0.79, 0.76	0.97
	Low	Ref.	-	-	Ref.	-	-
P16 pos 2	High	0.64	-0.06, 1.35	0.07	0.47	-0.52, 1.46	0.5
	Med	-0.03	-0.62, 0.55	0.91	0.17	-0.67, 1.02	0.74
	Low	Ref.	-	-	Ref.	-	-
P16 pos 3	High	0.22	-0.21, 0.64	0.32	0.27	-0.10, 0.64	0.15
	Med	-0.02	-0.38, 0.33	0.89	-0.02	-0.33, 0.29	0.9
	Low	Ref.	-	-	Ref.	-	-
P16 pos 4	High	0.4	0.13, 0.92	0.14	0.38	-0.22, 0.98	0.98
	Med	-0.09	0.52, 0.35	0.7	0.35	-0.15, 0.86	0.86
	Low	Ref.	-	-	Ref.	-	-
P16 pos 5	High	0.22	-0.27, 0.71	0.38	0.09	-0.33, 0.52	0.66
	Med	-0.23	-0.64, 0.17	0.26	0.13	-0.24, 0.49	0.49
	Low	Ref.	-	-	Ref.	-	-
P16 pos 6	High	0.16	-0.26, 0.58	0.44	0.22	-0.17, 0.62	0.26
	Med	-0.23	-0.58, 0.12	0.2	0.07	-0.26, 0.40	0.67
	Low	Ref.	-	-	Ref.	-	-
P16 pos 7	High	0.37	-0.23, 0.97	0.22	0.55	-0.70, 1,80	0.39
	Med	-0.31	-0.81, 0.19	0.22	0.41	-0.66, 1.48	0.45
	Low	Ref.	-	-	Ref.	-	-
P53 pos 1	High	0.29	-0.24, 0.82	0.28	-0.05	-1.09, 1.00	0.93
	Med	-0.10	-0.55, 0.35	0.66	-0.58	1.52, 0.36	0.22
	Low	Ref.	-	-	Ref.	-	-
P53 pos 2	High	-0.32	-1.96, 1.33	0.7	-0.06	-1.67, 1.56	0.94
	Med	0.39	-1.78, 1.00	0.58	-0.50	-.95, 0.95	0.5
	Low	Ref.	-	-	Ref.	-	-
P53 pos 3	High	0.19	-0.57, 0.96	0.62	-0.09	-0.70, 0.52	0.77
	Med	0.17	-0.48, 0.82	0.6	-0.11	-0.66, 0.43	0.68
	Low	Ref.	-	-	Ref.	-	-
p53 pos 4	High	-0.27	-1.16, 0.63	0.55	0.27	-0.64, 1.17	0.56
	Med	-0.42	-1.18, 0.33	0.27	0.38	-0.43, 1.19	0.36
	Low	Ref.	-	-	Ref.	-	-