

Table S1. The influence of sex on the objects of study of the genetics damage and histone methylation in Controls ($\bar{x}\pm SD$, adjusted $\bar{x}\pm SE$)

Variables	Controls(n=97)		P-value	Test statistic
	male(n=28)	female(n=69)		
Genetic damage				
Micronucleus (‰)	1.21±1.13	1.18±0.92	0.874 ^a	t=0.158
Micronucleus age adjusted (‰)	1.19±0.18	1.19±0.12	0.992 ^b	F=0.001
Olive tail Moment	2.12±5.48	3.43±6.56	0.492 ^a	t=1.322
Olive tail Moment age adjusted	2.10±2.74	3.45±1.33	0.220 ^b	F=1.545
Tail DNA%	2.07±1.83	4.20±6.58	0.240 ^a	t=1.190
Tail DNA% age adjusted	2.17±1.53	3.88±1.15	0.269 ^b	F=1.250
Histone modifications (µg/mL)				
H3K9me2	0.59±0.23	0.55±0.23	0.634 ^a	t=0.478
H3K9me2 age adjusted	0.59±0.05	0.55±0.03	0.688 ^b	F=0.163
H3K36me3	0.50±0.18	0.55±0.35	0.224 ^a	t=1.225
H3K36me3 age adjusted	0.51±0.06	0.59±0.04	0.838 ^b	F=0.042
H3K79me2	0.15±0.12	0.16±0.14	0.555 ^a	t=0.593
H3K79me2 age adjusted	0.15±0.02	0.16±0.01	0.574 ^b	F=0.319
H4K20me1	0.49±0.21	0.52±0.29	0.725 ^a	t=0.353
H4K20me1 age adjusted	0.50±0.06	0.52±0.04	0.747 ^b	F=0.105
H4K20me2	1.01±0.42	0.89±0.36	0.503 ^a	t=0.977
H4K20me2 age adjusted	1.01±0.08	0.89±0.08	0.363 ^b	F=0.541
H4K20me3	1.08±0.31	1.21±0.78	0.503 ^a	t=0.674
H4K20me3 age adjusted	1.09±0.16	1.21±0.10	0.506 ^b	F=0.448

a Independent-sample t-test; b General linear model (univariate analysis)

Table S2. The influence of sex on the objects of study of the genetics damage and histone methylation in Arsenic poisoning group

($\bar{x} \pm SD$, adjusted $\bar{x} \pm SE$)

Variables	Arsenic poisoning group(n=162)		P-value	Test statistic
	male(n=91)	female(n=71)		
Genetic damage (mean \pm SD)				
Micronucleus (‰)	2.26 \pm 1.58	2.03 \pm 1.49	0.364 ^a	t=0.911
Micronucleus age adjusted (‰)	2.28 \pm 0.16	2.01 \pm 0.19	0.285 ^b	F=1.153
Olive tail Moment	15.35 \pm 13.57	15.87 \pm 13.57	0.829 ^a	t=0.217
Olive tail Moment age adjusted	15.39 \pm 1.76	15.82 \pm 1.82	0.855 ^b	F=0.034
Tail DNA%	12.56 \pm 9.70	13.41 \pm 10.16	0.628 ^a	t=0.486
Tail DNA% age adjusted	12.58 \pm 1.12	13.38 \pm 1.34	0.649 ^b	F=0.209
Histone modifications (μg/mL)				
H3K9me2	0.34 \pm 0.27	0.33 \pm 0.26	0.783 ^a	t=0.276
H3K9me2 age adjusted	0.34 \pm 0.03	0.33 \pm 0.03	0.790 ^b	F=0.074
H3K36me3	0.99 \pm 0.80	1.07 \pm 0.78	0.848 ^a	t=0.192
H3K36me3 age adjusted	1.00 \pm 0.08	1.07 \pm 0.10	0.838 ^b	F=0.042
H3K79me2	0.23 \pm 0.31	0.26 \pm 0.48	0.357 ^a	t=0.924
H3K79me2 age adjusted	0.23 \pm 0.03	0.26 \pm 0.04	0.345 ^b	F=0.896
H4K20me1	0.59 \pm 0.30	0.57 \pm 0.24	0.612 ^a	t=0.509
H4K20me1 age adjusted	0.59 \pm 0.04	0.58 \pm 0.04	0.256 ^b	F=0.019
H4K20me2	0.77 \pm 0.28	0.70 \pm 0.23	0.456 ^a	t=0.748
H4K20me2 age adjusted	0.77 \pm 0.04	0.70 \pm 0.04	0.392 ^b	F=0.740
H4K20me3	1.19 \pm 0.53	1.13 \pm 0.42	0.562 ^a	t=0.581
H4K20me3 age adjusted	1.19 \pm 0.06	1.14 \pm 0.07	0.594 ^b	F=0.285

a Independent-sample t-test; b General linear model (univariate analysis)

Table S3. The influence of age on the objects of study of the genetics damage and histone methylation in controls

Variables	Controls(n=97)			P-value	Test statistic
	≤40(n=50)	40<age≤51(n=28)	>51(n=19)		
Genetic damage (mean ± SD)					
Micronucleus (‰)	1.02±0.88	1.18±0.92	1.47±1.08	0.106 ^a	t=1.975
Olive tail Moment	5.50±10.22	1.75±2.50	1.24±0.80	0.120 ^a	t=2.218
Tail DNA%	5.26±8.71	2.54±2.50	2.73±2.02	0.274 ^a	t=1.330
Histone modifications (mean ± SD, µg/mL)					
H3K9me2	0.53±0.26	0.57±0.31	0.600±0.20	0.292 ^a	t=1.246
H3K36me3	0.61±0.28	0.49±0.36	0.54±0.31	0.318 ^a	t=1.161
H3K79me2	0.15±0.12	0.14±0.11	0.13±0.09	0.815 ^a	t=0.205
H4K20me1	0.51±0.26	0.59±0.31	0.41±0.19	0.265 ^a	t=1.360
H4K20me2	0.92±0.39	1.03±0.37	0.89±0.46	0.433 ^a	t=0.849
H4K20me3	1.13±0.69	1.26±0.74	1.18±0.58	0.805 ^a	t=0.217

^a one-way analysis of variance

Table S4. The influence of age on the objects of study of the genetics damage and histone methylation in Arsenic poisoning group

Variables	Arsenic poisoning group(n=162)			P-value	Test statistic
	≤40(n=50)	40<age≤51(n=28)	>51(n=19)		
Genetic damage (mean ± SD)					
Micronucleus (‰)	1.98±1.12	2.30±1.40	2.41±1.70	0.198 ^a	t=1.870
Olive tail Moment	16.64±13.16	11.60±9.37	16.00±14.61	0.357 ^a	t=1.039
Tail DNA%	13.95±9.90	10.22±7.29	12.94±10.50	0.361 ^a	t=1.026
Histone modifications (mean ± SD, µg/mL)					
H3K9me2	0.32±0.28	0.34±0.27	0.40±0.29	0.318 ^a	t=1.155
H3K36me3	1.01±0.93	0.99±0.67	0.91±0.67	0.830 ^a	t=0.186
H3K79me2	0.25±0.12	0.23±0.33	0.22±0.36	0.140 ^a	t=1.994
H4K20me1	0.56±0.23	0.66±0.27	0.54±0.28	0.100 ^a	t=2.357
H4K20me2	0.73±0.18	0.77±0.30	0.71±0.26	0.823 ^a	t=0.195
H4K20me3	1.21±0.55	1.15±0.41	1.14±0.52	0.854 ^a	t=0.159

^a one-way analysis of variance