Author Correction: A functional Cis-eQTL locus in lncRNA ZNRD1-AS1 contributes to the susceptibility of endometrial cancer

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The authors state that "to compare the results with those of bladder cancer in the literature we reported the study by Li D, Song L, Wen Z, Li X, Jie J, Wang Y, Peng L. Strong evidence for LncRNA ZNRD1-AS1, and its functional Cis- eQTL locus contributing more to the susceptibility of lung cancer. Oncotarget 2016; 7: 35813-35817. In particular, we referred to their table format, but we misused the reference table as the official table in the manuscript".

In addition to Table I, the authors make the following corrections:

- in the abstract results change "(OR: 1.33; 95% CI: 1.09-1.61; $p = 0.004$)" to "(OR: 1.31; 95% CI: 1.08-1.6; $p=0.007$)."
- in the "Association of tagSNPs of the Cis-eQTL for ZNRD1 in ZNRD1-AS1 Gene Region With EC Susceptibility" paragraph change "(OR: 1.33; 95% CI: 1.09-1.61; $p = 0.004$)" to "(OR: 1.31; 95% CI: 1.08-1.6; $p=0.007$), "1.71 (95% CI: 1.11-2.64)" to "1.67 (95% CI: 1.07-2.59)", and "($0.004 \times 3 = 0.012 < 0.05$)" to "(0.007*3=0.021<0.05)".

The Publisher apologizes for any inconvenience this may cause.

The correct sections are reproduced below.

RESULTS: Higher expression of ZNRD1-AS1 and lower expression of ZNRD1 were detected in the EC tissues, compared to the normal tissues. Minor allele of rs9261204 was significantly associated with increased risk of EC (OR: 1.31; 95% CI: 1.08-1.6; *p*=0.007). Furthermore, *in vitro* experiments confirmed that Ishikawa cells with rs9261204 G allele had lower mRNA level of ZNRD1, compared to the A allele.

Association of tagSNPs of the Cis-eQTL for ZNRD1 in ZNRD1-AS1 Gene Region With EC Susceptibility

As shown in Table I, the genotype distributions of the three tagSNPs of the Cis- eQTL for ZNRD1 in ZNRD1-AS1 gene region (rs3757328, rs6940552, and rs9261204) in EC cases and healthy control subjects were displayed. We found G allele of rs9261204 was significantly associated with an increased risk of EC when compared with A allele (OR: 1.31; 95% CI: 1.08-1.6; $p=0.007$). The adjusted OR for the carriers with the GG genotype was 1.67 (95% CI: 1.07-2.59) and for those with the AG genotype was 1.29 (95% CI: 0.99-1.7) compared with the AA genotype. After adjusted for Bonferroni correction, the trend was still significant (0.007*3=0.021<0.05)'.

Table I. Association between 3 eQTLs SNPs in ZNRD1-AS1 and endometrial cancer susceptibility.

Genotype	Cases	Controls (n=396)	OR (95% CI) (n=595)
rs3757328			
GG	269	408	1.00 (reference)
AG	116	175	1.01 (0.76-1.33)
AA	11	12	1.39 (0.61-3.19)
Additive			1.05 (0.83-1.33)
p trend			0.684
rs6940552			
GG	217	345	1.00 (reference)
AG	138	201	1.09 (0.83-1.44)
AA	41	49	1.33 (0.85-2.08)
Additive			1.15 (0.94-1.4)
p trend			0.188
rs9261204			
AA	192	334	1.00 (reference)
AG	159	214	1.29 (0.99-1.7)
GG	45	47	1.67 (1.07-2.59)
Additive			1.31 (1.08-1.6)
p trend			**0.007**