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# Author Correction: Genomewide Study of Epigenetic Biomarkers of Opioid Dependence in European-American Women

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This Article contains an error in the Figure legends of Figure 3 and Figure 4. The legends of these Figures were inadvertently switched.

The legend of Figure 3:

“Association between genotype data at rs2611513 and DNA methylation levels at GWS CpG site cg17426237. rs2611513 associated with DNA methylation levels at cg17426237; C allele associated with lower DNA methylation in (A) all sample ( $n = 141$ ,  $p = 0.025$ ), and (B) OD cases ( $n = 112$ ;  $p = 0.042$ ). No association was obtained in (C) opioid-exposed controls ( $n = 29$ ; NS). \*Represents  $p < 0.05$ .”

should read:

“Association between genome-wide significant (GWS) CpG sites and opioid dependence (OD)-related traits. DNA methylation (beta values) of GWS CpG sites associated with OD-related traits are shown: (A–C) OD symptoms, (D–F) age of onset (years), (G–I) duration of opioid use (years), (J–L) longest duration of chronic opioid use (years). Significant threshold is set at  $p < 0.05$ .”

The legend of Figure 4:

“Association between genome-wide significant (GWS) CpG sites and opioid dependence (OD)-related traits. DNA methylation (beta values) of GWS CpG sites associated with OD-related traits are shown: (A–C) OD symptoms, (D–F) age of onset (years), (G–I) duration of opioid use (years), (J–L) longest duration of chronic opioid use (years). Significant threshold is set at  $p < 0.05$ .”

should read:

“Association between genotype data at rs2611513 and DNA methylation levels at GWS CpG site cg17426237. rs2611513 associated with DNA methylation levels at cg17426237; C allele associated with lower DNA methylation in (A) all sample ( $n = 141$ ,  $p = 0.025$ ), and (B) OD cases ( $n = 112$ ;  $p = 0.042$ ). No association was obtained in (C) opioid-exposed controls ( $n = 29$ ; NS). \*Represents  $p < 0.05$ .”

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