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GENOME RESEARCH

Erratum

Genome Res. 2011 21: 146

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Genome Research 20: 1719–1729 (2010)

Evaluation of affinity-based genome-wide DNA methylation data: Effects of CpG density, amplification bias, and copy number variation

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Panels A and B in Figure 7 were incorrectly reversed in the text and the figure legend. The corrected text and legend are as follows:

The first full sentence in the top left column of page 1725 should read as follows:

Figure 7B illustrates changes in MBDCap-seq read counts along chromosome 13. As expected, they are correlated with changes in copy number (Fig. 7A) for the same regions.

The corrected figure legend should read as follows:

Figure 7. Effects of copy number changes on differential methylation detection. (*A*) Smoothed Affymetrix SNP 6.0 array data showing corresponding changes in copy number for human chromosome 13. (*B*) Differential methylation *Z*-score between LNCaP and PrEC cells, using MBD-SF-seq. (*C*) Genome-wide distributions of *Z*-scores, stratified by the change-in-copy-number status of the corresponding regions.

The authors apologize for any confusion this may have caused.

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