CORRIGENDUM

Genome-wide quantitative assessment of variation in DNA methylation patterns

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The authors would like to apologize for an error in Figure 1D of their article. The methylation entropy for the methylation pattern shown in Figure 1D should read '*ME* = 0.25' not '*ME* = 0.1875'. The corrected figure appears below. The entropy for code bit (e) in Figure 1A is 3.321928095. This error does not affect the results and conclusion of the article.

A
$$ME = \frac{e}{b} \sum \left(-\frac{n_i}{N} Log \frac{n_i}{N} \right)$$

ME: Methylation Entropy
e: Entropy for code bit
b: Number of CpG sites
n_i: Observed occurrence of methylation pattern i
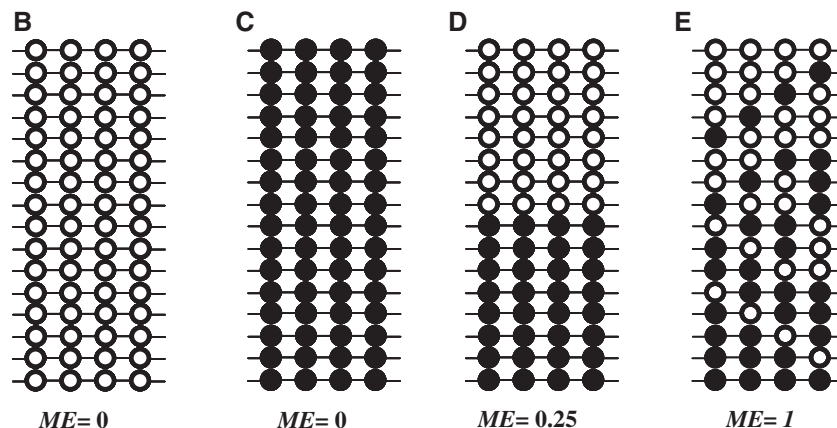N: Total number of sequence reads generated

B	**C**	**D**	**E**
ME= 0	*ME= 0*	*ME= 0.25*	*ME= 1*

Figure 1