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Corrigendum

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Corrigendum: A genome-wide analysis of common fragile sites: What features determine chromosomal instability in the human genome?

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The authors found that the genomic coordinates for several fragile sites were accidentally truncated during conversion from cytogenetic bands. The errors shift the genomic coordinates at five out of a total of 76 aphidicolin-induced common fragile sites (aCFSs) and at 11 nonfragile regions. Seven nonfragile regions had to be removed because their coordinates now overlap with aCFSs, reducing the number of control regions from 131 to 124. These changes affected Figures 1 and 2, and Supplemental Tables S1 and S2. Upon reanalysis, the list of significant genomic features, their directional effects on fragility, and relative contributions did not change.

However, correcting of genomic coordinates resulted in the numerical changes of the regression models' attributes (coefficient, variance inflation factor, *P*-value, and relative contribution) throughout the manuscript. These changes affected Figure 3, Supplemental Figures S2 and S3, and Supplemental Tables S4–S7, S9, and S10. Additionally they include:

1. The pseudo R-squared of logistic regressions in Tables 2 and 3 are about 5% higher than previously published. This makes our models stronger. There are also small numerical changes in Table 4.
2. The logistic regression models that include CpG islands have R-squared values (Tables 2, 3) and correct prediction rates (Table S10) that are both higher than the corresponding values in the models including Twist.
3. The transcription start site density is no longer a significant predictor that can distinguish aCFSs from non-fragile regions (it was significant before Bonferroni correction); however, it is still a significant predictor in models explaining the level of fragility.

These corrections do not affect the conclusions of the article. The authors apologize for making this mistake and for any confusion this may have caused.

The article has already been corrected in both the PDF and full-text HTML files online.

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