

CORRECTION

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# The majority of total nuclear-encoded non-ribosomal RNA in a human cell is 'dark matter' un-annotated RNA

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The publisher notes typographical errors which were introduced to the first paragraph of page 10 (beginning "Previously, human large intergenic non-coding (linc) RNAs were identified in normal human embryonic and stem cell lines...") during the production process. The publisher apologises for the errors caused. The online article HTML was corrected on 19 October 2011, and the article PDF on 31 October 2011; readers with previous versions of the article are advised to update to the corrected version [1].

Corrected paragraph:

"Previously, human large intergenic non-coding (linc) RNAs were identified in normal human embryonic and stem cell lines [twenty seven] and we sought to determine whether the vlinc regions were overlapping those. In fact, the majority of the vlinc transcribed regions we have identified did not overlap the known human lincRNA regions and, thus, represent novel RNAs that are also large, intergenic and non-coding, as exemplified in the four examples shown (Figure four c and four d, Figure five a and five b). These latter regions have known lincRNA regions located nearby, without overlap, while the former do not have lincRNA regions in their vicinity. Furthermore, the intergenic regions identified here achieve much greater lengths than known lincRNAs, with a median size of ~84 kb versus 21 kb for the lincRNAs (significant at  $P = 1.72 \times 10^{-53}$ , t-test). Overall, 37% (215/580) of the vlinc regions overlapped the K4-K36 domains harbouring lincRNAs as reported by Khalil et al. [twenty seven]. However, even when overlapping, the

lincRNA regions corresponded to only a fraction of our intergenic regions: the overlap of base pairs in the intergenic regions found here with the lincRNA regions was only approximately 19% (13.51/68.51 Mbp). However, the overlap between the two categories of the intergenic transcribed regions is highly significant ( $P$ -value  $< 10^{-16}$ , chi-square test)."

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