Corrigendum

TriTag: an integrative tool to correlate chromatin dynamics and gene expression in living cells

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Nucleic Acids Research, gkaa906, https://doi.org/10.1093/nar/gkaa906

Objects hidden behind the images in the submitted version of Figure 4 appear on top of the images in the published figure. The Author wish to replace Figure 4 with a clean version as shown below.

The published article has been updated. This error does not affect the conclusions of the article.

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**Figure 4.** TriTag monitors allele-specific transcriptional bursting across the cell cycle. (A) Fluorescent images of a cell showing DNA labeling of two LMNA alleles labeled by dCas9-GFP14X and their transcriptional kinetics indicated by stdMCP-tdTomato at multiple time points. See Movie S3 for dynamics. (B, C) Line scan of intensity profiles illustrating dynamic labeling of DNA (green) and nascent RNAs (red) of locus 1 (B) and locus 2 (C) indicated in (A). (D) Representative images revealing three distinct transcriptional states of sister chromatid pairs identified by co-labeling of dCas9-GFP14X and stdMCPtdTomato. (E) Line scan of intensity profiles showing dynamic labeling of DNA and nascent RNAs at corresponding sister chromatid points by arrows in (D). (F) Sister chromatids of the same allele have correlated transcription activity. Intensities of both transcription sites were plotted, with each dot representing a different pair of sister chromatids, n = 240 pairs. Green line denotes the linear fit. $R^2$ represents the coefficient of determination. (G) Bar graph showing transcription states of two LMNA alleles in the same cell (case in A, n = 284 cells) or pairs of sister chromatids (case in D, n = 229 cells). (H) Snapshots of the transcription activity of LMNA gene in HeLa cells at indicated time points through mitosis. See Movie S4 and S5 for dynamics. (I) Transcriptional activity of the mother cell and its daughter cells at LMNA loci was quantified to generate the scatter plot. Each dot represents a pair of the mother cell and one of its daughter cells, n = 90 pairs. Green line denotes the linear fit. $R^2$ represents the coefficient of determination. (J) Bar graph showing quantifications of transcriptional activity in daughter cells derived from three groups of mother cells with no, low and high transcription of LMNA gene, respectively. n ≥ 52 cells. All scale bars: 5 μm.