Erratum to: Genome-wide incorporation dynamics reveal distinct categories of turnover for the histone variant H3.3

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After the publication of this work [1] an error was noticed in Fig. 1d. In the DAPI columns the same image was used accidentally for the 48 h and 72 h timepoints. The corrected figure is shown below. We apologize for this error.

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Received: 25 January 2016 Accepted: 25 January 2016 Published: 4 February 2016

References
1. Kraushaar DC, Jin W, Maunakea A, Abraham B, Ha M, Zhao K. Genome-wide incorporation dynamics reveal distinct categories of turnover for the histone variant H3.3. Genome Biol. 2013;14:R121.
Fig. 1 A versatile system to study replication-independent nucleosome dynamics in mammals. (a) Schematic of TET-inducible expression system to study H3.3 turnover. CMV, cytomegalovirus; rtTA, reverse tetracycline-controlled transactivator; TRE, tetracycline responsive elements. (b) Western blot showing protein levels of transgenic HA/FLAG-H3.3 compared to endogenous H3.3. HA/FLAG-H3.3 expression 24 hours after DOX addition. The band marked with an asterisk is non-specific. The arrow marks transgenic HA/FLAG-H3.3. (c) Time course western blots of HA/FLAG-H3.3 expression. (d) Bromodeoxyuridine (BrdU) immunostaining of NIH/3 T3 cells treated with DNA polymerase inhibitor aphidicolin and DOX across time points of H3.3 induction. DMSO, dimethylsulfoxide. (e) Cell cycle analysis of cells treated with aphidicolin/DOX. Cells were stained with propidium iodide and analyzed by flow cytometry.