Correction to: Novel genetic tools for probing individual H3 molecules in each nucleosome

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In the original publication, Fig. 1 was incorrectly published. The amino acid sequence was shifted to the left relative to the rest of the diagram in the published version and the corrected Fig. 1 is given here.

The original article can be found online at <https://doi.org/10.1007/s00294-018-0910-0>.

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Fig. 1 Design of an asymmetric H3–H3 interface. (Left) Nucleosome structure with histone H3 in blue (PDB ID: 1KX5). The red circle indicates the histone H3–H3 interface. (Right upper) Secondary structure and sequences of the C-terminal domains of wild type H3 (blue), H3X (green) and H3Y (yellow). Red residues indicate the asymmetric alterations and the substituted amino acids are shown

below. (Right lower) Schematic of the experimental strategy. The H3 N-terminal tail is indicated as a wavy line extending from the H3 globular histone fold domain. The H3X/H3Y pair makes an asymmetrical heterodimer, whereas H3X–H3X or H3Y–H3Y pairs cannot homodimerize, as indicated