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Genome Biology

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Publisher Correction: Co-opted transposons help perpetuate conserved higher-order chromosomal structures

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Following publication of the original paper [1], an error was reported in the processing of Fig. 2. The correct Fig. 2 is supplied below and the original article [1] has been corrected. The publishers apologize for the error.

Authors' information

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Reference

1. Choudhary MN, Friedman RZ, Wang JT, et al. Co-opted transposons help perpetuate conserved higher-order chromosomal structures. Genome Biol. 2020;21:16 https://doi.org/10.1186/s13059-019-1916-8.

Publisher's Note

The original article can be found online at https://doi.org/10.1186/s13059-019-1916-8

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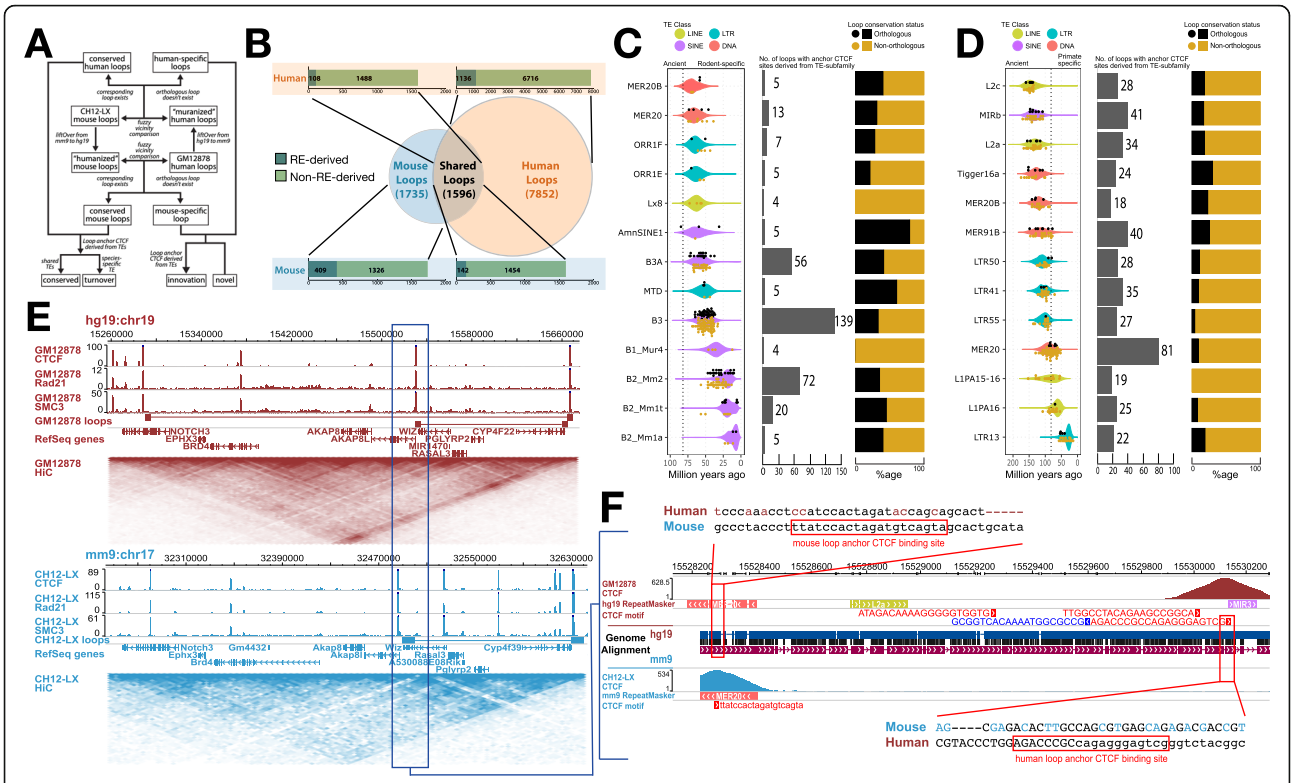

Fig. 2 Contribution of TEs to the conservation landscape of human and mouse loops. **a** Flowchart describing the methodology used to annotate loop orthology. **b** Venn diagram representing the various classes of chromatin loops based on their orthology and bar plots showing the contribution of REs to anchor CTCFs of each class of loops. **c** Age distribution and age of individual TEs that contribute loop anchor CTCF sites (black dots for orthologous loops; gold dots for non-orthologous loops) (left), total contribution to loop anchor CTCF sites (middle), distribution of orthologous and non-orthologous loops (right) derived from the top 13 TE subfamilies in mouse and **d** humans. Estimated primate/rodent divergence time (82 million years ago) is from Meredith et al. [47]. **e** Contact maps representing a conserved chromatin loop in a syntenic region between human and mouse. **f** A MER20 transposon insertion provides a redundant CTCF motif that helps in maintaining the conserved 3D structure in mouse via CTCF binding site turnover with remnants of the ancestral CTCF motif, well conserved in most non-rodent mammals (Additional file 1: Figure S2), still seen in the mouse genome