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Erratum

Erratum: Deep experimental profiling of microRNA diversity, deployment, and evolution across the *Drosophila* genus 881

Jaaved Mohammed, Alex S. Flynt, Alexandra M. Panzarino, Md Mosharrof Hossain Mondal, Matthew DeCruz, Adam Siepel, and Eric C. Lai

^{OA}Open Access paper



Cover Each of the cartoon characters in the swimming pool (except the frog) represents a molecule involved in the coordinated changes of DNA (de)methylation, nucleosome positioning, and chromatin binding. In this issue, the DNA modification landscape in mouse embryonic stem cells carrying a double knockout of the *Tet1* and *Tet2* dioxygenases (mice in TET caps) is studied. While DNA methylation (5mC) is established and maintained by DNMT enzymes (mice in DNMT caps), TET enzymes are responsible for the conversion of 5mC (red buoys) into its hydroxymethylated (blue buoys), formylated (black buoys), or carboxylated forms (white buoys represent unmodified CpG). Some CTCF molecules (octopuses with 11-zinc finger “legs”) act as bifurcation points defining the differential methylation landscape. CTCF loss from such sites is found to be correlated with DNA (de)methylation spreading and can be linked to deregulation of neighboring genes. (Cover artwork © Yana Savinich and the Teif Lab. [For details, see Wiehle et al., pp. 750–761.]