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Identifying clusters of *cis*-regulatory elements underpinning TAD structures and lineage-specific regulatory networks

1733^{OA}

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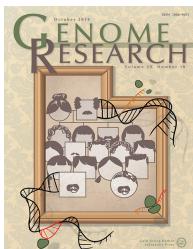
Resource

Exploration of fine-scale recombination rate variation in the domestic horse

1744

Samantha K. Beeson, James R. Mickelson, and Molly E. McCue

^{OA}Open Access paper



Cover In this issue, the first direct estimate of retrotransposition rates in a whole-genome sequenced data set of three-generation CEPH pedigrees is calculated. The cover features an old family portrait representing the multigenerational pedigrees in the CEPH reference panel. The wooden frame is in the shape of the state of Utah to represent the large number of Utah families included in CEPH, as well as to pay homage to Raymond White and his contribution to CEPH in Utah. On the outside of the frame, a mobile element is transcribed into an mRNA intermediate, reverse-transcribed, and reinserted into a new location in the genome of a descendant. (Cover artwork by Cecile Avery, cecileavery@utah.edu. [For details, see Feusier et al., pp. 1567–1577.])