Nucleic Acids Research (ISSN 0305-1048) is published twice monthly by Oxford University Press and is distributed by Central Mailing Services c/o UKP Worldwide, 3390 Rand Road, South Plainfield, NJ 07080, USA. Periodicals Postage Paid at South Plainfield, NJ and additional mailing offices. Issue Date: July 2, 2018.

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Printed by Bell & Bain, Glasgow, UK.

Cover: Image produced by Galaxy HiCEXplorer (https://hicexplorer.usegalaxy.eu). Definition of a Topologically Associating Domains (TAD) and its boundaries. Starting from the top:

- Contact matrix heatmap (first track) visualizing low (blue), medium (yellow) or red (high) interaction frequencies between genomic regions.
- Topologically associated domains (TADs, second track) were annotated using the TAD-separation score (third track).
- TAD separation z-scores (third track) of different window sizes (10-40 kb, grey line) and the mean z-score score (blue line with error bars) are plotted.
- The chromatin state track (fourth track) shows annotated promoters (red), strong and weak enhancers, (orange, yellow) as well as transcribed (green), polycomb-repressed (black) heterochromatin (brown) and undefined (gray) regions.
- Principal component analysis reveals A (PC1 > 0) and B (PC1 < 0) compartments (track five). A compartments are associated with active and B compartments with inactive chromatin as indicated by H3K27ac enrichment (track six) and chromatin state annotation.

Raw data were taken from Nothjuinge et al. 2017 (Nature Communications, 8:1667, doi: 10.1038/s41467-017-01724-9).

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