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* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

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This information is provided in the Materials and methods section (under “Statistical analysis”).

**Replicates**

* You should report how often each experiment was performed
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* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
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* Criteria for exclusion/inclusion of data should be clearly stated
* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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* Statistical analysis methods should be described and justified
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* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
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These procedures are not applicable to the data types in this work.

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Please indicate the figures or tables for which source data files have been provided:

Additional data files include source data files for Figure 4, supplementary files for quantitative data corresponding to heat-map representations in Figure 1, Figure 1 – figure supplements 1-4 and Figure 2. TaDa sequencing data and experimental information have been deposited in the ArrayExpress database at EMBL-EBI ([www.ebi.ac.uk/arrayexpress](https://www.ebi.ac.uk/arrayexpress/)) and will be available under accession number E-MTAB-8935. Processed data and intermediate files, including the read coverage at GATC motifs, are available at GitLab (<https://gitlab.com/roman.arguello/ir_tada>), as described in the “Data availability” section.