Statistics
For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

- The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- The statistical test(s) used AND whether they are one- or two-sided
- A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- For null hypothesis testing, the test statistic (e.g. F, t, r) with confidence intervals, effect sizes, degrees of freedom and P value noted. Give P values as exact values whenever suitable.
- For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- Estimates of effect sizes (e.g. Cohen’s d, Pearson’s r), indicating how they were calculated

Software and code
Policy information about availability of computer code

Data collection
All publicly available data used in the study is referenced by accession number or the applicable manuscript directly.

Data analysis
All R packages used in the analysis and presentation of data are publicly available and referenced in the methods section. Functions relevant to each analysis are referenced in the methods with non-default parameters noted. Scripts used in generating individual figures as well as rate fitting are available upon request.

Data
Policy information about availability of data
All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:
- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

Raw and processed sequencing data has been deposited in the Gene Expression Omnibus (GEO) database under the accession number GSE129470. All publicly available data sets used are referenced in the relevant methods section.
GEO link: https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE129470
Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

- Life sciences
- Behavioural & social sciences
- Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

- Sample size: No sample-size calculation was performed. Experiments were performed in triplicate to assess reproducibility of measurements.
- Data exclusions: No data were excluded from the analyses.
- Replication: Time course measurements were performed in triplicate to assure reproducibility.
- Randomization: No randomization was performed.
- Blinding: Not applicable.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

| Materials & experimental systems | Methods |
|---------------------------------|---------|
| n/a                             | Involved in the study |
| □ Eukaryotic cell lines         | □ ChIP-seq |
| □ Palaeontology                 | □ Flow cytometry |
| □ Animals and other organisms   | □ MRI-based neuroimaging |
| □ Human research participants   |         |
| □ Clinical data                 |         |

Antibodies

Antibodies used: Slot blotting was carried out using an antibody against 5hmC (#39769, Active Motif) and 5mC(Bi-MECY-1000, Eurogentec). Western blot antibodies used are DNMT3A (Novus 64B1446), DNMT3B (Imgenex #MG-1844A), DNMT1 (AbCam ab188453), UHRF1 (MBL D289-3) and LAMINB1 (AbCam ab16048).

Validation: Antibodies were validated by mixing genomic DNA from unperturbed cell lines with discrete amounts of DNA from a published mouse stem cell line devoid of DNA methylation (see Supplementary Figure 1b). DNMT3 and DNMT1 antibodies were tested in a knockout background.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s): ES cell lines conditionally deficient for Dnmt3a and Dnmt3b were derived by outgrowth of blastocyst embryos obtained by crossing mice doubly homozygous for floxed alleles of Dnmt3a and Dnmt3b (reference 50). The mouse strain was maintained on a C57BL/6J background.

Authentication: Mice were genotyped by PCR and ESCs derived from a homozygous clone. Conditional deletion of Dnmt3 alleles was carried out using TaqMan PCR as outlined in methods.

Mycoplasma contamination: Cell lines used in this study tested negative for mycoplasma contamination

Commonly misidentified lines: Name any commonly misidentified cell lines used in the study and provide a rationale for their use.