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Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, seeAuthors & Referees and theEditorial Policy Checklist.

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For	all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.
n/a	Confirmed
	$oxed{x}$ 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 Only common tests should be described solely by name; describe more complex techniques in the Methods section.
×	A description of all covariates tested
×	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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
×	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
×	\square Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated
,	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.
Sof	ftware and code

Custom code written in Matlab R2015b. Deposited in GitHub [https://github.com/Ringrose546/Beyond_memory_V2]

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Fiji (ImageJ) 2.0.0.-rc 41; ImageJ64, Huygens Essential 16.05, Adobe Photoshop 2-15.01. MetaMorph 7.1.1.0, Image studio Digits 5.2.

Data

Data collection

Data analysis

Policy information about availability of data

All manuscripts must include a <u>data availability statement</u>. 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

Policy information about availability of computer code

None used

Source data for Figure 4E are provided with this paper. The ChIP-seq data shown in Figure 5A are publically available at [http://compbio.med.harvard.edu/modencode/webpage/Chromatin.v0.6.html#ChIP-seq%20and%20ChIP-chip%20data]. H3K27me3 (track ID 3955), PSC, Posterior Sex Combs (track ID 3960), GAF, GAGA Factor (track ID 4119). The other data sets generated during the current study are available from the corresponding author on reasonable request.

Field-spe	ecific reporting				
Please select the o	ne below that is the best fit for yo	our research. If you are not sure, read the appropriate sections before making your selection.			
x Life sciences	Behavioural & socia	al sciences			
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Life scier	nces study desig	gn			
All studies must dis	sclose on these points even when	the disclosure is negative.			
Sample size	Relevant for ChIP experiments - two embryo collections, three independent IPs per sample and three qPCR replicates per IP (dilution series) were performed. Larger sample sizes were not feasible due to multiple time point embryo collections. Mean and SD of three IPs (not of PCR replicates) is shown in Fig. 4E. Sample sizes were chosen in line with standard practice in ChIP analysis.				
Data exclusions	No data were excluded unless a PCR reaction failed, visible as a missing data point in a dilution series.				
Replication	Replication was successful. Three ChIP analyses for each embryo collection, several hundred embryos for each Immunofluorescence slide, 6 to 10 eye imaginal discs for each genotype for in situ hybridisation on transgenic lines, 50 to 100 progeny for each cross for each genotype for genetic experiments, showed similar results.				
Randomization	Not relevant because randomisation is used for clinical trials with interventions. We did not perform any such trials.				
Blinding	Not relevant because blinding is used for clinical trials to prevent subjects from knowing about their treatment. We did not perform any such trials.				
We require informati system or method lis Materials & ex n/a Involved in the system of the system of the system or method lise.	ion from authors about some types of ted is relevant to your study. If you ar perimental systems ne study	naterials, systems and methods materials, experimental systems and methods used in many studies. Here, indicate whether each material, e not sure if a list item applies to your research, read the appropriate section before selecting a response. Methods n/a Involved in the study ChIP-seq R Flow cytometry			
Eukaryotic cell lines Palaeontology		RII-based neuroimaging			

Antibodies

Clinical data

✗ Animals and other organisms Human research participants

Antibodies used

▼ MRI-based neuroimaging

Primary antibodies : Antibody:Supplier/Catalog no./lot no

Mouse anti Histone H3: Active Motif/39763/5217020, Mab clone 301

Rabbit anti H3K4me1: Abcam/ab8895/gr271478-1 Rabbit anti H3K4me3: Abcam/ab8580/gr240214-3 Rabbit anti H3K27me3: Active Motif/39155/31814017 Rabbit anti H3K36me2: Abcam/ab9049/gr266894-1 Rabbit anti H3K36me3: Abcam/ab9050/gr249065-1 Mouse anti Fluorescein: Roche/11426320/Mab clone 001

Secondary Antibodies

Goat anti Rabbit IgG, Alexa Fluor 555 conjugate: Thermo Fisher Scientific/A21429/1715464 $Goat\ anti\ Mouse\ IgG,\ Alexa\ Fluor\ 488\ conjugate:\ Thermo\ Fisher\ Scientific/A11029/1705900$

Goat anti Rabbit IgG, Horse Radish Peroxidase (HRP) conjugate: Life Technologies/A16104/42-28-042114 Goat anti Mouse IgG, Horse Radish Peroxidase (HRP) conjugate: Life Technologies/A16072/46-137-05115

Goat anti Mouse IgG, Horse Radish Peroxidase (HRP) conjugate: Invitrogen /T-20912

The same information is given in supplementary Tables 4 and 5.

Validation

We performed our own validation of primary antibodies against modified histones presented in Supplementary Figure 4. The mouse anti H3 antibody is validated for ChIP, IF and Western blot on the supplier's website https://www.activemotif.com/catalog/details/39763

Animals and other organisms

Policy information about <u>studies involving animals</u>; <u>ARRIVE guidelines</u> recommended for reporting animal research

Laboratory animals Drosophila melanogaster OregonR and transgenic derivatives thereof. Males and females.

Wild animals Not applicable. We used only laboratory strains

Field-collected samples Not applicable. We used only laboratory strains

Ethics oversight The work was performed exclusively with Drosophila melanogaster, which does not require ethics documentation according to

German law.

Note that full information on the approval of the study protocol must also be provided in the manuscript.