

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, see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

Statistics

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

- | | | |
|-------------------------------------|-------------------------------------|--|
| ☐ | ☒ | 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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☒ | ☐ | 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. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P 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 |
| ☒ | ☐ | Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated |

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection FEI EPU 1.10;

Data analysis Warp 1.0.6; RELION 3.0; Gautomatch v0.56, Gctf v1.06, CryoSPARC v2; COOT v. 0.8.9.1; PHENIX v. 1.14; Pymol v. 2.2.3; Chimera v. 1.13 ; Molprobability 4.5 server; 3DFSC server; ImageJ 1.52k; Microsoft Excel 14.7.7; XSCALE BUILT=20170601; PHASER 1.2;

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.

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

The electron density reconstructions and corresponding models were deposited with the Electron Microscopy Data Base (EMD-10390, EMD-10391, EMD-10392, EMD-10393, EMD-10394) and with the Protein Data Bank (6T78, 6T79, 6T7A, 6T7B, 6T7C, 6T7D). Source data is relevant for Fig. 2, ED Figures 2,4,5,6,10,13

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.

x

Life sciences study design

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

Sample size	Numbers of particles used for cryo-EM reconstructions are listed in Extended Table 1. Sample sizes were estimated on the basis of previous studies using similar methods and analyses that are widely published.
Data exclusions	No data were excluded from the analysis.
Replication	All attempts at replication were successful and reproducible. At least two independent biological repeats per experiment performed and showed similar results. Structure determination does not require replication.
Randomization	Samples were not allocated into groups. Randomization is not relevant to this study.
Blinding	Blinding was not relevant to this study because there was no group allocation.

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

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

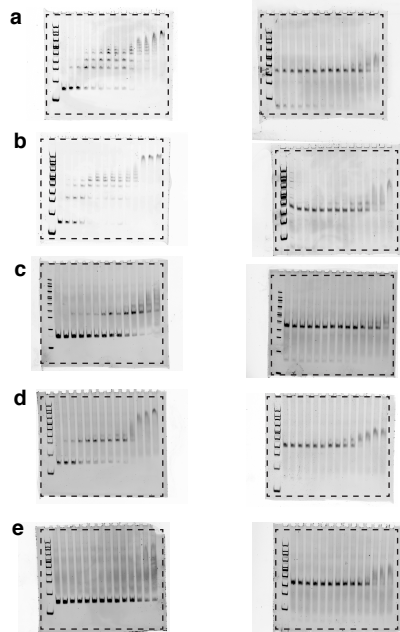
Supplementary information

**Nucleosome-bound SOX2 and SOX11
structures elucidate pioneer factor function**

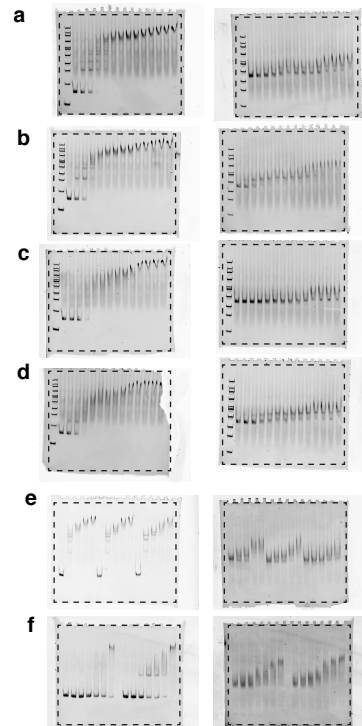
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authors and unedited

Svetlana O. Dodonova, Fangjie Zhu, Christian Dienemann, Jussi Taipale & Patrick Cramer✉

Extended Figure 3



Extended Figure 6



Extended Figure 7

