EXTENDED DATA FORMATTING GUIDE

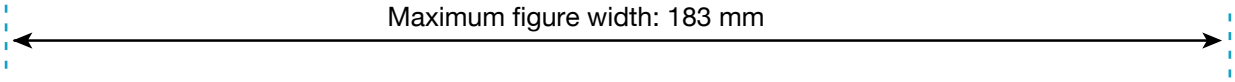
Nature allows authors to supply up to a maximum of ten Extended Data display items (figures and tables), which do not appear in the printed version of the *Nature* paper but are included online within the full-text HTML and at the end of the online PDF. Authors may combine their Extended Data figures into multi-panelled figures providing they meet the size rules below, but authors may not supply additional figures. Tabulated data can either be integrated into an Extended Data figure as a separate panel (for example, see Extended Data Figure 2, panel d) or be formatted as a separate display item: Extended Data table (for example, see Extended Data Table 1). Extended Data tables must be supplied as images (excluding title and footnote, which should be inserted at the end of the Word file containing the text of the paper), according to the rules below.

Extended Data figures and tables are cited in the text in the same way as the main (print) figures and tables. Unlike the main figures, Extended Data figures are not edited or styled by *Nature*'s art department; for this reason, authors are requested to follow *Nature* style as closely as possible when creating these figures. Extended Data tables are also not edited by *Nature*'s subediting department.

You will have one opportunity to resupply revised files later in the production process if there are inconsistencies in presentation between the Extended Data figures and the *Nature*-edited print-only figures.

Please use the following guide to ensure that your Extended Data figure files are in the correct format, and are within acceptable limits in terms of file size, dimension and resolution.

Figure sizing and positioning



- Maximum page dimension is 183 mm x 247 mm.
- Try to position the figure in the same place on the page each time (i.e., centre).

Figures should be sized such that they fit to a single page (preferably leaving enough room for the legend to be set below, across two columns). However, in exceptional circumstance (for example, if sizing to keep the image and legend to one page results in an illegible figure) the legend may continue to a second page. Supplying figures at greater dimensions will result in larger files that we may not be able to use.

Lettering

- All text should be in a sans-serif typeface, preferably Helvetica or Arial.
- Amino acid sequences should be presented in one-letter code in `Courier`.
- Separate panels in multi-panelled figures should be labelled with **8 pt bold**, upright (not italic) and lowercase **a**, **b**, **c**, etc.
- Maximum text size for all other text: 7 pt.
- Minimum text size: 5 pt.
- Use 'symbol' for glyphs and Greek alphabet.

Sans-serif body text | Bold labels | Courier one-letter code

Resolution

- All photographic images and figures can be supplied at 300 p.p.i.
- The example below shows how an image would look at 300 p.p.i.; this is sufficient for viewing online. Anything exceeding this will make the file size too large and readers may be timed out before they can view or download them.

300 p.p.i.

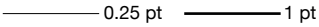
72 p.p.i.

File formats and rasterizing art

- In order to upload to the web, files must be rasterized or flattened.
- Export and save each individual figure in JPEG/TIFF/EPS format (please note that other file formats are not acceptable for Extended Data files).
- Files must be as small as possible for clear visibility and must not exceed 10 MB.

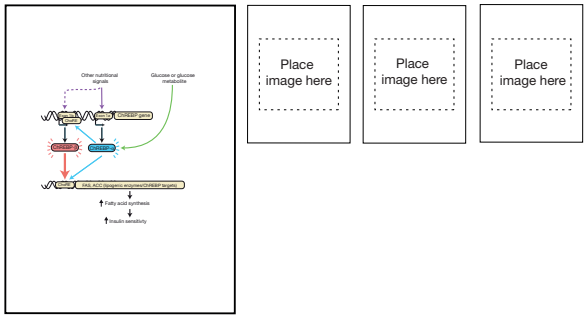
Line weights

- Lines and strokes should be set between 0.25 and 1 pt.



Arrangement

- Try to keep white space to a minimum when arranging panels within a figure.
- Place each figure on a new page when uploading online.



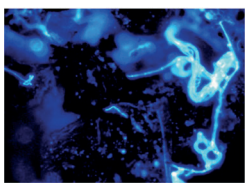
Centre the figure

Extended Data table formatting

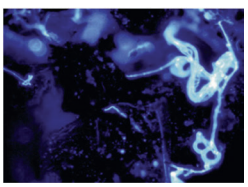
- Add a horizontal rule above and below column headings and at the bottom of the Table.
- Tables can be set at one-column (8.9 cm) or two-column (18 cm) width.
- Use spaces rather than rules to separate blocks of data, but horizontal rules can be used to improve clarity in certain cases.
- Colour is to be avoided unless scientifically necessary.
- Footnotes can be used in Tables. Footnote symbols are used in the order * † ‡ § || ¶ # ☆, then doubled.
- All text should be in a sans-serif typeface, preferably Helvetica or Arial.
- Use 7 pt text size.
- For file formats and resolution, follow the same guidelines as for Extended Data figures.
- Tables should not exceed a single page (leaving enough room for the legend/footnote to be set below).

Colours

- Files must be saved in RGB for maximum colour saturation and smaller file size for optimized viewing online.



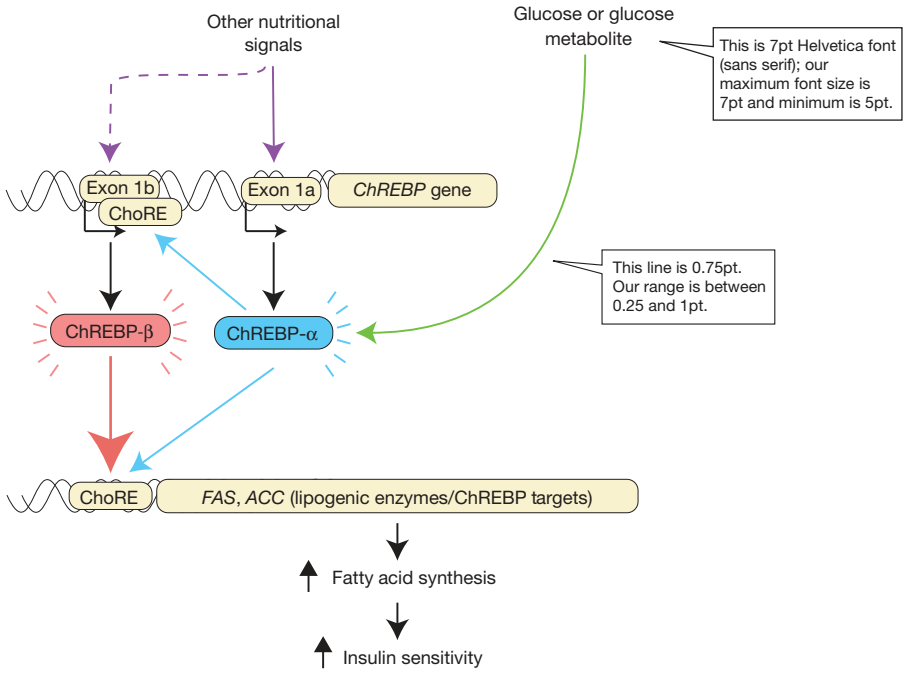
RGB (optimised for web)



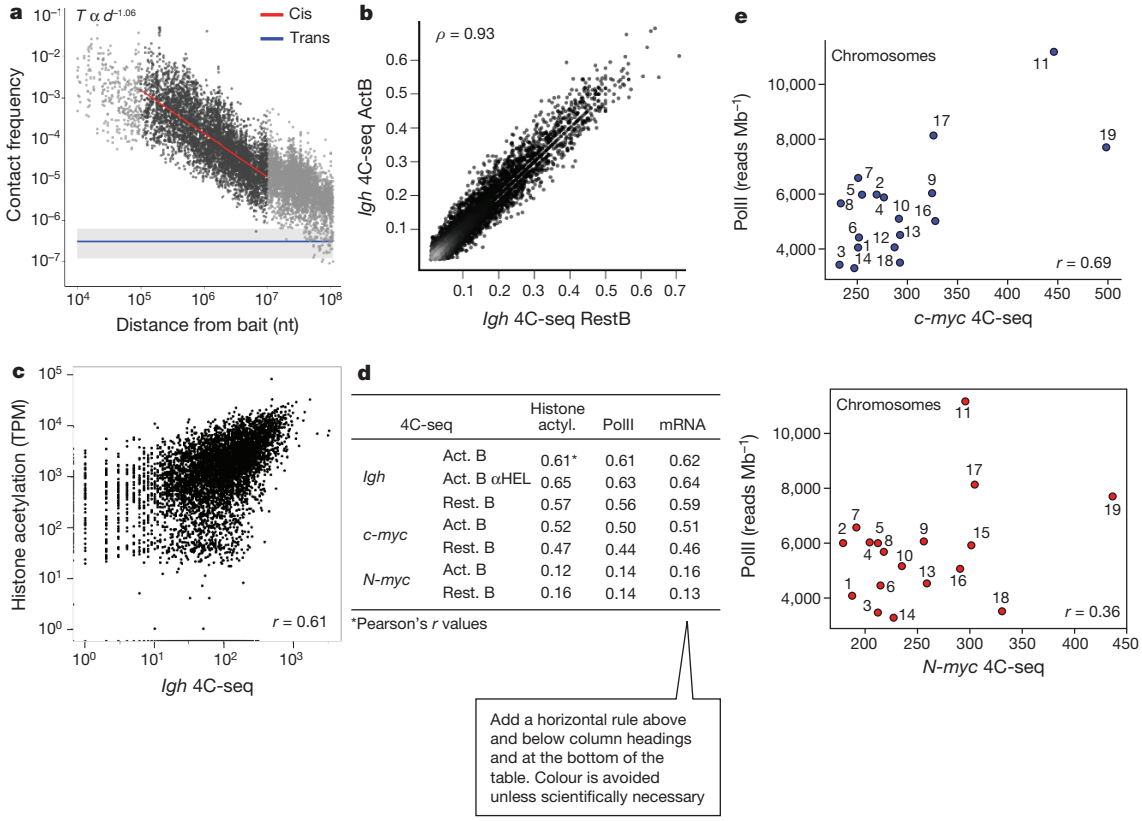
CMYK (optimised for print)

Example layouts of Extended Data figures and tables, with accompanying legends, are provided in the following pages.

- For further help and advice, e-mail our art editors at **art@nature.com**



Extended Data Figure 1 | Glucose-mediated activation of ChREBP-α induces expression of ChREBP-β. Glucose or a glucose metabolite stimulates the transcriptional activity of ChREBP-α which binds to ChoREs in its lipogenic targets and in ChREBP-β, resulting in increased gene expression. The increased ChREBP-β protein further activates expression of ChREBP lipogenic target genes by binding to ChoREs. Whereas glucose regulates ChREBP-α transcriptional activity, other nutritional signals regulate ChREBP-α expression. Other nutritional signals may also regulate ChREBP-β expression. The activation of ChREBP-α and induction of ChREBP-β expression increase fatty acid synthesis in adipose tissue, which improves systemic insulin sensitivity.



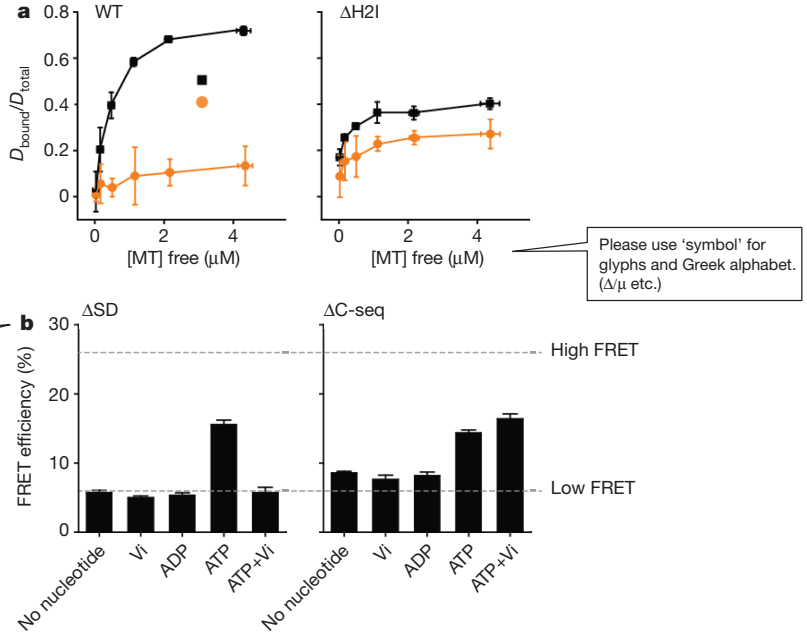
d

4C-seq		Histone actyl.	PolII	mRNA
Igh	Act. B	0.61*	0.61	0.62
	Act. B αHEL	0.65	0.63	0.64
	Rest. B	0.57	0.56	0.59
c-myc	Act. B	0.52	0.50	0.51
	Rest. B	0.47	0.44	0.46
N-myc	Act. B	0.12	0.14	0.16
	Rest. B	0.16	0.14	0.13

*Pearson's *r* values

Add a horizontal rule above and below column headings and at the bottom of the table. Colour is avoided unless scientifically necessary

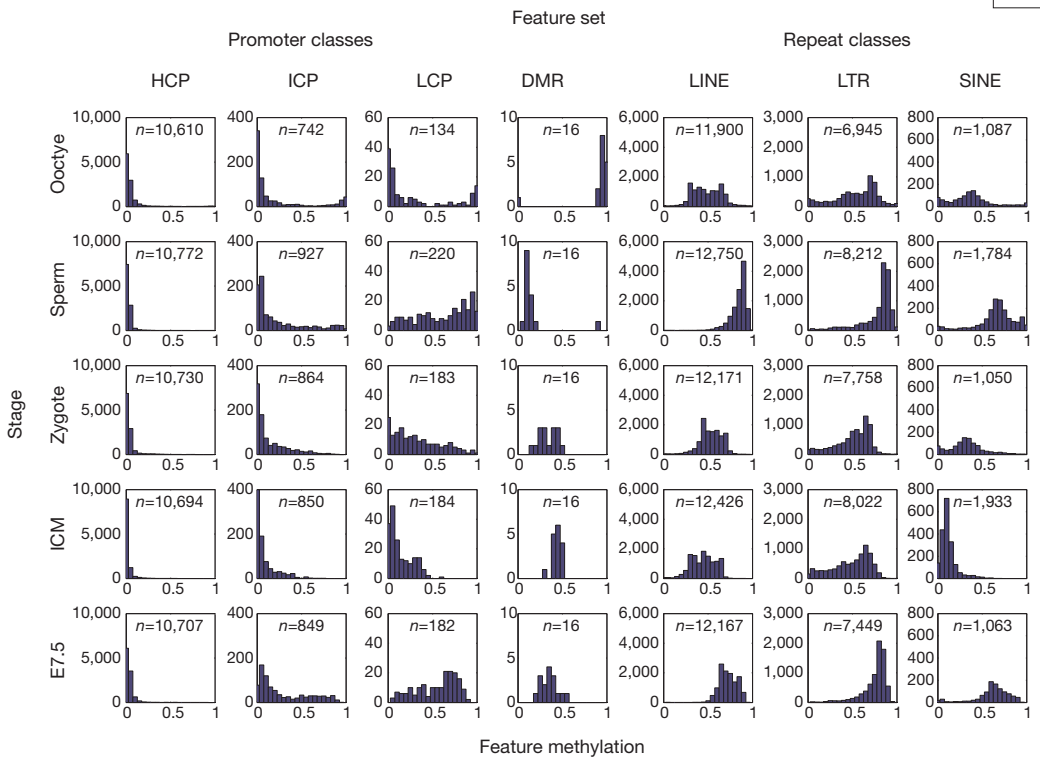
Extended Data Figure 2 | Summary of 4C-seq data. a, Scatter graph shows that contact probability in the cis-chromosome decreases as a function of distance. Between 100 kb to 10 Mb from the bait, 4C-seq reads show a power law scaling with an exponent of −1.06, R2 = 0.55 (red line depicts its average). The blue line represents the average contact probability of all baits with trans-chromosomes, from centromere (left) to telomere (right). The grey area represents the average maximum and minimum values. **b**, Scatter plot showing histone acetylation and *Igh* nuclear contacts as determined by ChIP-seq and 4C-seq, respectively. The correlation between the two data sets was calculated by Spearman's ρ. **c**, Scatter plot comparing 4C-seq data obtained using *Igh* as bait in resting (*x* axis) and activated (*y* axis) B cells. The correlation between the two data sets (0.97) was calculated using Pearson's product correlation coefficient *r*. **d**, Table showing Pearson's *r* coefficient values for the relationship between 4C-seq samples and histone acetylation, PolII, or mRNA. **e**, Scatter plots showing total 4C-seq reads per chromosome and PolII reads per megabase for *c-myc* (top, $P = 0.0013$) or *N-myc* (bottom, $P = 0.14$).



Please use 'symbol' for glyphs and Greek alphabet. (Δ/μ etc.)

Ensure that multi-panelled figures are labelled with **8pt bold** upright (not italic) and lowercase **a**, **b**, **c**, etc.

Extended Data Figure 3 | Functional analyses of ΔH2I, ΔSD and ΔC-seq. a, MT binding activity of ΔH2I in the presence or absence of ATP. Each symbol is mean ± s.d. (n = 3). The ΔH2I mutation, disrupting the ATPase-driven linker swing actions, did not abolish ATP-induced change in the affinity for MTs, although the affinity change was smaller than that of wild type (WT). **b**, FRET efficiency between BFP and GFP moieties in ΔSD and ΔC-seq in the presence of 200 μM of indicated nucleotide. For ΔSD in the presence of ATP, the FRET efficiency was measured with 2.5 mM ATP to avoid depletion of ATP due to its very high ATPase activity. Mean ± s.d. (n = 3) are shown. The dotted lines indicate the high and low FRET values of wild type representing the linker positions at the primed (pre-powerstroke) and unprimed (post-powerstroke) states, respectively[12,15]. The ΔSD and ΔC-seq mutations, disrupting the coupling between MTBD and the AAA1 ATPase, did not block ATP-induced changes in FRET but altered the FRET efficiency and nucleotide dependence. The results suggest that the two structural units are not essential for the linker swing, but are relevant to the proper positioning of the linker and/or normal kinetics of the ATPase-driven swing actions.



Extended Data Figure 4 | Methylation histograms for genomic feature annotations throughout pre-implantation development. Notable dynamics at fertilization, across pre-implantation and upon specification of the embryo proper occur across multiple genomic feature sets. *n* indicates the number of genomic features captured at each time point.

Extended Data Table 1 | Phosphate release rates from the wild type and the double Walker-B mutants

	–MT		+MT	
Dynein	k_{obs}(burst) (s^{-1})	k_{steady} (s^{-1})	k_{obs}(burst) (s^{-1})	k_{steady} (s^{-1})
Wild-type HFB380	59.3 ± 4.9	3.9 ± 0.3	nm	31.6 ± 3.1
E2027Q/E2745Q/E3075Q	nm	nm	nm	nm
E2745Q/E3075Q	6.0 ± 0.8	1.2 ± 0.1	9.4 ± 1.8	2.8 ± 0.3
E2027Q/E3075Q	67.6 ± 8.5	0.16 ± 0.02	52.6 ± 2.3	0.20 ± 0.07
E2027Q/E2745Q	52.5 ± 4.5	0.6 ± 0.2	48.4 ± 6.4	0.77 ± 0.05

The apparent phosphate burst rate constants (k_{obs}(burst)) and steady-state rate constants (k_{steady}) in the presence (+MT) or absence (–MT) of 20 μM MTs are shown as mean ± s.d. of three independent measurements. nm, not measurable.

For tables please use a sans-serif font such as Helvetica or Arial at 7pt.

Add a horizontal rule above and below column headings and at the bottom of the table. Colour is avoided unless scientifically necessary.