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eLife's transparent reporting form

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. If you have any questions, please contact us: editorial@elifesciences.org.

Sample-size estimation

- You should state whether an appropriate sample size was computed when the study was being designed
- You should state the statistical method of sample size computation and any required assumptions
- If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., page numbers or figure legends), or explain why this information doesn't apply to your submission:

The reproducibility of promoter activity measurements was assessed based on 2 biological replicates of the *D. melanogaster* time series (please see first section of Results & Figure 1).

Throughout the manuscript, quantitative comparisons are made across groups of promoters (or groups of genes), rather than across samples/conditions. For instance, comparisons are made between mRNA and lncRNA promoters (see Fig. 6). Therefore, sample sizes were mostly defined by the number of promoters/genes in the genome that belong to each category of interest. We further filtered promoters/genes based on their maximal expression level throughout the time series, aiming for a trade-off between measurement reproducibility and statistical power. Detailed explanations are provided where appropriate throughout the main text, figure legends, and supplementary material.

All necessary p-values and sample sizes, as well as detailed descriptions of statistical tests and multiple testing corrections, are available where appropriate throughout the main text, figure legends, and supplementary material.

Replicates

- You should report how often each experiment was performed
- You should include a definition of biological versus technical replication

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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
- If you encountered any outliers, you should describe how these were handled
- 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)

Please outline where this information can be found within the submission (e.g., page numbers or figure legends), or explain why this information doesn't apply to your submission:

For experimental design and rationale, please see the section above, as well as the Methods section and the first paragraph of Results.

The primary data for this study is available through the GEO database, under accession numbers GSE36212 and GSE89335. GSE36212 is public, and reviewers can access GSE89335 here: https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?token=onklcqcedfohvkt&acc=GSE89335

Statistical reporting

- Statistical analysis methods should be described and justified
- Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
- For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
- Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

Please outline where this information can be found within the submission (e.g., page numbers or figure legends), or explain why this information doesn't apply to your submission:

All necessary measures of center and dispersion, as well as p-values and sample sizes, along with detailed descriptions of statistical tests and multiple testing corrections, are available where appropriate throughout the main text, figure legends, and supplementary material.

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to page numbers in the manuscript.)

Additional data files ("source data")

- We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
- Where provided, these should be in the most useful format, and they can be uploaded as "Source data" files linked to a main figure or table
- Include model definition files including the full list of parameters used
- Include code used for data analysis (e.g., R, MatLab)
- Avoid stating that data files are "available upon request"

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

Raw and processed data files are available at GEO under accession numbers GSE36212 and GSE89335. GSE36212 is public, and reviewers can access GSE89335 here: https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?token=onklcqcedfohvkt&acc=GSE89335