***eLife’s* transparent reporting form**

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* You should state whether an appropriate sample size was computed when the study was being designed
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No explicit power analysis was performed, since the experiments shown are performed as stand-alone proof-of-concept for HyDrop.

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* You should report how often each experiment was performed
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* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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No replicates were performed on the same sample, since the experiments shown are performed as stand-alone proof-of-concept for HyDrop.

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All data analysis and figure generation is documented in open-source notebooks. These notebooks, in tandem with our GEO repository (GSE175684), can be used to replicate our figures 1:1.

(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 sections in the manuscript.)

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* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
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* 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
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All figures involving sequencing data can be replicated 1:1 using the notebooks in our github repository (<https://github.com/aertslab/hydrop_data_analysis>) combined with data in our GEO repository (GSE175684, both raw FASTQ and processed gene expression and fragments files available). In addition, summary figure source data has been added to the manuscript for figures (4a, 5b,c,d, 8a, b, c + supplementary fig. 2 and 10b). Summary figure source data was not provided for figure 5a, as the underlying table has a size of > 60 gb, and it can be readily regenerated using the GEO and github resources. Dimension-reduced expression or chromatin accessibility data is available in SCope, our tool specially designed for viewing this type of data ([https://scope.aertslab.org/#/HyDrop/\*/welcome](https://scope.aertslab.org/#/HyDrop/*/welcome)). Unedited .tiff files have been provided for all microscopy images used in the manuscript, and are also publicly available in the github repository, as well as the source code for the python program used to analyse them.