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* You should state whether an appropriate sample size was computed when the study was being designed
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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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Replicate information is reported in figure legends. The authors have full intention to upload big data sets from this study to a public repository but this is not yet completed. However, source data has been provided in the form of supplementary data files for all of these datasets.

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* Statistical analysis methods should be described and justified
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* 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.

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Statistical methods, p-values, and sample sizes are reported in figure legends and supplementary data tables. Statistical analysis of mass spectrometry and CRISPRi datasets is elaborated on in the methods section. The authors have not yet reported exact p-values for Figures 5e, 5g, and 6e, but will gladly comply and provide these values.

(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.)

**Group allocation**

* 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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To the best of our understanding, group allocation did not apply to any of our presented data.

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* Include model definition files including the full list of parameters used
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Please indicate the figures or tables for which source data files have been provided:

Source data has been provided for all mass spectrometry, RNAseq, and CRISPRi experiments. The authors intend to upload all raw data from these experiments to public repositories prior to publication. The authors also intend to upload source code for the mass spectrometry data analysis to a git-hub repository.