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* You should state whether an appropriate sample size was computed when the study was being designed
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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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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.)

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

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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.