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* You should state whether an appropriate sample size was computed when the study was being designed
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**Sample size for proteome analysis:** Explicated within the main text (first mention is line 67), Figure 1 caption, Methods.

**Sample size for biological benchmarks:** Explicated in Figure 3-source data 1, Figure 3-source data 1 (available for download from **github.com/arjunsraman/Zaydman\_et\_al**). All benchmarks are explicated in Methods; section titled ‘Assembling benchmarks described in **Figure 3A**’.

**Sample size for training RF models:** Explicated in Methods (line 657)

**Replicates**

* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
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Information regarding replicates for experiments involving *Pseudomonas aeruginosa* can be found in Supplementary File 7 (available for download from **github.com/arjunsraman/Zaydman\_et\_al** as .zip file)

**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.

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Each p-value reported within the manuscript is followed by a description of the statistical test used to generate the p-value with the exception of p-values related to gene-set enrichment analyses.

p-values related to Gene Set Enrichment analyses are reported as output by DAVID analysis (v6.8), explicated in Methods (line 618). All p-values related to Gene Set Enrichment analyses generated by DAVID are found in Supplemenary Files 1 to 5 (available for download from **github.com/arjunsraman/Zaydman\_et\_al** as .zip file).

(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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No ‘group allocation’ was utilized in this manuscript.

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

Source data related to Figure 1A found in Figure 1-source data 1.

Source data related to Figure 3A found in Figure 3-source data 1; Figure 3-source data 2.

Source data related to Figure 6A found in Supplementary File 1.

Source data related to Figure 6—figure supplement 2 found in Supplementary File 2.

Source data related to Figure 6—figure supplement 3 found in Supplementary File 3.

Source data related to Figure 6—figure supplement 4 found in Supplementary File 4.

Source data related to Figure 7A,B; Figure 7—figure supplement 1 found in Supplementary File 5.

Source data related to Figure 7C found in Supplementary File 7.

Source data related to Figure 8; Figure 8—figure supplement 3 found in Figure 8-source data 1.

All tables are available for download as .zip files from **github.com/arjunsraman/Zaydman\_et\_al.**

All code used in the manuscript was written in Matlab v2020a; code for generating figures in the manuscript is available for download as .m scripts and .mat workspaces at **github.com/arjunsraman/Zaydman\_et\_al**. Instructions are in the Readme.m file included in the github repository.