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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)

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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)

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* Statistical analysis methods should be described and justified
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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).

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No ‘group allocation’ was utilized in this manuscript.

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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.

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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.