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* You should state whether an appropriate sample size was computed when the study was being designed
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Figure legends list the minimum cell count used in demographs

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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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Materials and Methods and raw sequencing reads available at <http://www.ncbi.nlm.nih.gov/bioproject/610521>. All codes referenced in the manuscript are available at https://github.com/jsher-Bernhardtlab/cofA).

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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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* 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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Figure 2 – source data 1. All codes referenced in the manuscript are available at https://github.com/jsher-Bernhardtlab/cofA).