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# Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see Authors & Referees and the Editorial Policy Checklist.

## Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. figure legend, table legend, main text, or Methods section).

| n/a | Confirmed | |
|---|---|---|
| ☐ | ☒ | The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement |
| ☐ | ☒ | An indication of whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| ☐ | ☒ | The statistical test(s) used AND whether they are one- or two-sided<br>*Only common tests should be described solely by name; describe more complex techniques in the Methods section.* |
| ☐ | ☒ | A description of all covariates tested |
| ☐ | ☒ | A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| ☐ | ☒ | A full description of the statistics including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals) |
| ☐ | ☒ | For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted<br>*Give P values as exact values whenever suitable.* |
| ☒ | ☐ | For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| ☐ | ☒ | For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| ☐ | ☒ | Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated |
| ☐ | ☒ | Clearly defined error bars<br>*State explicitly what error bars represent (e.g. SD, SE, CI)* |

*Our web collection on statistics for biologists may be useful.*

## Software and code

Policy information about availability of computer code

| | |
|---|---|
| Data collection | Physiological data Experiment 1 were collected using software from Quark b2, version 8.2 (COSMED, Rome, Italy). |
| Data analysis | Data were analyzed using Stata SE 15.0. |

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

## Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

Data set is available on the Open Science Framework at the following link: https://osf.io/gz57m/?view_only=71292e851b754bacbd89dc07c8113829.

# Field-specific reporting

Please select the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/authors/policies/ReportingSummary-flat.pdf

# Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

| | |
|---|---|
| Sample size | Participants from the San Francisco Bay Area were recruited over the course of 1 year. In both experiments, we set out to recruit 120 participants such that we had approximately n=20 participants in each cell for the 3 (actual genotype: high-risk, moderate-risk, protective) x 2 (perceived genotype: high-risk, protective) design. This sample size yielded approximately 80% power to detect medium effect size differences between those informed of high-risk and those informed that they have the protective genotype. |
| Data exclusions | Only data from participants who completed the full study were analyzed and no data were excluded from the analyses. |
| Replication | Experiment 2 provides a conceptual replication of Experiment 1. |
| Randomization | As described in the paper, all participants in both experiments were randomly assigned to receive either high-risk or protective genetic test results using a 1:1 ratio, so that approximately equal numbers of each of the three actual genotypes (high-risk, moderate-risk, and protective) received high-risk and protective genetic test results. |
| Blinding | In both experiments, experimenters were blind to participants' actual genotype and outcomes from participants' baseline session. Experimenters were also blind to participants' randomly assigned genotype until participants received their genetic test report and pamphlets at the genetic risk session (thereafter, blinding of randomly assigned genotype was not possible given that participants' results were open on the table and many participants asked a question or made a comment to the experimenter which revealed their randomly assigned genotype). Individuals who processed and analyzed the physiological data were blind to participants' actual and assigned genetic risk level. |

# Reporting for specific materials, systems and methods

## Materials & experimental systems

| n/a | Involved in the study |
|---|---|
| ☒ | ☐ Unique biological materials |
| ☒ | ☐ Antibodies |
| ☒ | ☐ Eukaryotic cell lines |
| ☒ | ☐ Palaeontology |
| ☒ | ☐ Animals and other organisms |
| ☐ | ☒ Human research participants |

## Methods

| n/a | Involved in the study |
|---|---|
| ☒ | ☐ ChIP-seq |
| ☒ | ☐ Flow cytometry |
| ☒ | ☐ MRI-based neuroimaging |

## Human research participants

Policy information about studies involving human research participants

| | |
|---|---|
| Population characteristics | Participants were individuals from the San Francisco Bay Area, age 18-50, in good health, and not pregnant or diabetic. For the 116 participants in Experiment 1 [(42.2% male (N=49), 57.8% female (N=67)], the mean age was 24.7 (SD=5.2; range 18-41) and mean BMI was 23.3 (SD=3.6; range 17.2–37.0). The population was 26.7% Asian, 3.4% Black, 6.9% Latino, 51.7% White, and 11.2% multiracial or other, and 63.8% had completed at least a bachelor's degree. For the 107 participants in Experiment 2 [(31.8% male (N=34), 68.2% female (N=73)], the mean age was 26.1 (SD=6.8; range 18-49) and mean BMI was 23.8 (SD=4.0; range 17.8–43.4). The population was 17.8% Asian, 1.9% Black, 7.5% Latino, 58.9% White, and 10.3% multiracial or other, and 65.4% had completed at least a bachelor's degree. |
| Recruitment | Participants were recruited via flyer that advertised a study that was recruiting participants to "help scientists create personalized nutrition and exercise programs," and that "by participating in this experiment, [participants] will help develop nutrition and exercise regimens to optimize personal health and fitness." Participants were under the impression that they would be genotyped to learn exactly which diets and exercises are best suited for them and were aware that they would be paid $85 for participation. This recruited population was likely biased towards people who are |

interested in learning about their genetic risks and how to use genetic information to inform health behaviors and decisions.