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Reporting Summary

Nature Portfolio 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 Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the 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
☐	☒ A statement on 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 *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 statistical parameters 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 *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

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	Data were collected from subscribers to the commercial biometric device platform WHOOP, Inc. (Boston, MA) across a 1-year study (Sep 1, 2021 to Aug 31, 2022).
Data analysis	Data organization and analysis was performed in R (v4.2.0). The analysis code is available at https://github.com/joshleota/ERP2023. The association of exercise strain and timing with sleep and autonomic outcomes was completed with R functions ('bam'; 'emmeans') from R packages ('mgcv'; 'emmeans'). Plotting of smooth functions from resultant models was completed using the 'ggplot' function from the R package ('ggplot2').

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 and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio 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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

The dataset associated with this study comprises regularly collected physiological and healthcare data as well as demographic information and is stored in a proprietary repository. Given its sensitive nature and the potential for reidentification, access to the dataset is enforced through an application process. For inquiries regarding data access, please contact support@whoop.com. All data requests will be assessed and addressed in accordance with policies designed to safeguard participant and user confidentiality, as outlined in the terms and conditions and informed consent documentation. The timeframe for response to requests will be four weeks.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	Gender was self-reported during data collection. We provide descriptive information on gender and adjusted for gender in all models. Separate gender-based analyses were performed, but the nature of the relationships between primary variables of interest (exercise strain and timing on sleep and autonomic outcomes) did not differ between genders. These analyses are provided in the supplement.
Reporting on race, ethnicity, or other socially relevant groupings	We do not have access to race or ethnicity data given that the data reported in this manuscript were collected through a commercial device platform owned by a industry partner.
Population characteristics	The study population included 14,689 participants. Baseline characteristics (Table S1) included age (M=37.89, SD=10.81), gender (10,845[73.83%] men), weight (M=80.39 kilograms, SD=15.10), and height (1.76 meters, SD=0.94).
Recruitment	Participants were subscribers to the biometric device platform WHOOP, Inc. (Boston, MA) which may be a source of self-selection bias. Objective data were collected in real-time and are therefore not subject to recall and response bias.
Ethics oversight	Monash University Human Research Ethics Committee (#32928).

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is 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/documents/nr-reporting-summary-flat.pdf

Behavioural & social sciences study design

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

Study description	The present study is a large-cohort quantitative multi-level design
Research sample	The study population included 14,689 subscribers to the biometric device platform WHOOP, Inc. (Boston, MA). Baseline characteristics (Table S1) included age (M=37.89, SD=10.81), gender (10,845[73.83%] men), weight (M=80.39 kilograms, SD=15.10), and height (1.76 meters, SD=0.94). The sample is non-representative.
Sampling strategy	The study sample was randomly selected from a larger subscriber population based on criteria outlined in CONSORT flow diagram (Figure 3). This sample is the largest-to-date of objectively measured exercise strain, timing and sleep data. The sample size (n = 14,689; k = 4,084,354 nights) exceeds 99% statistical power.
Data collection	demographic information and written informed consent was provided during registration with WHOOP. A multi-sensor wrist-worn biometric device (WHOOP versions 3.0 or 4.0; Boston, MA) that captures continuous heart rate, accelerometer, and three-axis gyroscope data was used to derive exercise, cardiovascular, and sleep/wake metrics. This biometric device has been validated against electrocardiography and polysomnography for the assessment of heart rate (99% agreement) and 2-stage sleep categorisation (86-89% agreement), respectively. Data were collected under free-living conditions without any experimenters present.
Timing	Sep 1, 2021 to Aug 31, 2022.

Data exclusions	n = 1,261 were excluded due to insufficient exercises logged or missing/invalid data. k = 1,418,619 nights were excluded due to exercises logged falling outside of analysis window (e.g., morning exercise). k = 226,495 nights excluded due to invalid exercise type (e.g., relaxation or recovery activities, etc). Finally, of the remaining n = 18,739, n = 4,050 were excluded due to fewer than 50 exercise activities logged within analysis window. All exclusion criteria and exact numbers are reported in the manuscript, Figure 3: CONSORT flow diagram.
Non-participation	NA
Randomization	There was no randomization. Exercise activities were sorted into four groups based on exercise strain quantified using summated-heart-rate-zones scores (SHRZS).The duration (minutes) spent in each heart rate zone was multiplied by a corresponding factor for each zone (i.e., zone 1=1; zone 2=2; etc.) and then summated. SHRZS were then categorized into four groups: <116=light; 116 to <214=moderate; 214 to 461=high; >461=maximal. Covariates included weekday vs. weekend, prior night's outcome variable, participant general fitness (mean daily exercise strain), gender, and a smoothing term for age as there are nonlinear changes in sleep by age.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*