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☐ Initial submission ☐ Revised version ☒ Final submission

Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form is intended for publication with all accepted life science papers and provides structure for consistency and transparency in reporting. Every life science submission will use this form; some list items might not apply to an individual manuscript, but all fields must be completed for clarity.

For further information on the points included in this form, see Reporting Life Sciences Research. For further information on Nature Research policies, including our data availability policy, see Authors & Referees and the Editorial Policy Checklist.

Experimental design

1. Sample size

Describe how sample size was determined.

The total sample size of fMRI measurement was determined based on our previous study.

2. Data exclusions

Describe any data exclusions.

We only considered prosocial and individualistic participants determined by the Triple-Dominance task.

3. Replication

Describe whether the experimental findings were reliably reproduced.

Prosocial's Inequity-correlated activity in the amygdala has been reproduced in our and other group's studies. We confirmed the replication of depression index prediction results by sampling subpopulations.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

Training and test participants were allocated by the leave-one-out cross validation.

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

We were blind to Training and test participants separation since it was randomly and systematically determined by the cross validation.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
☐	☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☒	☐ A statement indicating how many times each experiment was replicated
☐	☒ The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
☐	☒ A description of any assumptions or corrections, such as an adjustment for multiple comparisons
☐	☒ The test results (e.g. *P* values) given as exact values whenever possible and with confidence intervals noted
☐	☒ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
☐	☒ Clearly defined error bars

See the web collection on statistics for biologists for further resources and guidance.

Software

Policy information about availability of computer code

7. Software

Describe the software used to analyze the data in this study.	R and matlab.

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* guidance for providing algorithms and software for publication provides further information on this topic.

Materials and reagents

Policy information about availability of materials

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.	All materials were available from us or companies.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).	NA.

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.	NA.
b. Describe the method of cell line authentication used.	NA.
c. Report whether the cell lines were tested for mycoplasma contamination.	NA.
d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.	NA.

Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.	We used human participants.

Policy information about studies involving human research participants

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.	Three hundred and forty three Japanese students (181 males, age = 19.0±0.096, and 162 females, age = 19.2±0.11) who did not declare any history of neurological or psychiatric disorders participated in the behavioral experiment using the Triple-Dominance measure task and BDI-II (BDI, hereafter) questionnaire. We identified 174 prosocials (88 males and 86 females) and 59 individualists (40 males and 19 females). We invited all these prosocials and individualists to the fMRI experiments. As a result of matching their availability and scanning slots, 94 participants (56 males: age = 19.4±0.17, 32 prosocials and 24 individualists; and 38 females: age = 19.5±0.24, 27 prosocials and 11 individualists.

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Date: 5th August 2017

Reporting Summary for MRI studies

Form fields will expand as needed. Please do not leave fields blank.

Experimental design

1. Describe the experimental design.	Event-related.
2. Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.	56 trials, 21±2 sec/trial, interval between trials = 9±2 sec.
3. Describe how behavioral performance was measured.	Button press & response time were recorded. Button press during a short time window (1.5s) for economic choices

Acquisition

4. Imaging	
a. Specify the type(s) of imaging.	Functional imaging.
b. Specify the field strength (in Tesla).	3 Tesla.
c. Provide the essential sequence imaging parameters.	Gradient echo, EPI, field of view =192mm, matrix size = 64 x 64, slice thickness = 3mm, TE = 2.5msec, TR =2sec, flip angle =90.
d. For diffusion MRI, provide full detail on imaging parameters.	NA.
5. State area of acquisition	Whole brain scan.

Preprocessing

6. Describe the software used for preprocessing.	spm12 for realignment, co-registration to Ta&T2 structural images, segmentation, normalization and smoothing.
7. Normalization	
a. If data were normalized/standardized, describe the approach(es).	non-linear
b. Describe the template used for normalization/transformation.	ICBM152
8. Describe your procedure for artifact and structured noise removal.	6-dimensional motion parameters
9. Define your software and/or method and criteria for volume censoring and state the extent of such censoring.	spm12. We also censored volumes during scanning.

Statistical modeling & inference

10. Define your model type and settings.	type:GLM and multivariate pattern analysis setting: SPM12 and Sparse Bayese Toolbox ver 2.0

11. Specify the precise effect tested.	the effects of social value orientation and socio-economic status on the activity induced by reward differences were tested. The factorial design was used. We measure prediction goodness of BDI scores based on the multi-variate pattern analysis of beta values obtained by the SPM GLM analysis. Evaluation was done based on the one-leave-out cross validation procedure.
12. Analysis	
a. Specify whether analysis is whole brain or ROI-based.	whole brain analysis (for key results) and ROI based small volume correction.
b. If ROI-based, describe how anatomical locations were determined.	We used the ROIs defined by Shen et al, (2013).
13. State the statistic type for inference. (See Eklund et al. 2016.)	voxel wise statistics and the one-leave-out cross validation procedure.
14. Describe the type of correction and how it is obtained for multiple comparisons.	FWE, Bonferroni method was used for multi-clusters in small volume corrected and whole-rain corrected results.
15. Connectivity	
a. For functional and/or effective connectivity, report the measures of dependence used and the model details.	NA.
b. For graph analysis, report the dependent variable and functional connectivity measure.	NA.
16. For multivariate modeling and predictive analysis, specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.	Prediction was done for each participant's depression index (BDI). Features are a vector of beta values which were obtained through a standard SPM GLM analysis. For dimension reduction, we applied PCA, and evaluation was done based on the one-leave-out cross validation procedure.