Methods

Participants

One hundred and ninety-two adults aged from 21 to 69 years have participated in this study. We recruited participants twice as independent group (group 01: 92 participants; group 02: 100 participants). Participants received cash payment and a postcard for their involvement in this study. All participants were normal or corrected-to-normal vision and no reported history of CNS-affecting drugs or neurological disease or diabetes. Before starting the experiment, all participants provided written informed consent. This study was approved by the ethical committee at Advanced Telecommunication Research Institute International (ATR) following the Declaration of Helsinki.

MRI Data acquisition

Images were acquired with 3T MRI scanners, MAGNETOM Trio Tim (Trio), MAGNETOM Verio (Verio), and MAGNETOM Prisma or Verio (Siemens Medical Systems, Erlangen, Germany) installed in Brain Activity Imaging Center (BAIC) in ATR. Due to upgrade the MRI of Trio during group 01 and 02, we used Trio and Verio for the group 01, and Prisma and Verio for the group 02. High-resolution

T1-weighted structural images were acquired for normalization to standard brain for echo planar image (EPI) registration purposes and the VBM analysis (TR = 2300 ms, TE = 2.98 ms, flip angle = 9 degree, TI = 900 ms, matrix = 256 x 256, field of view = 256 mm, slice thickness = 1 mm, iso-voxel). Functional images were acquired with an EPI sequence (TR = 2500 ms, TE = 30 ms, flip angle = 80 degrees, matrix = 64 x 64, field of view = 212 mm, slice thickness = 3.2 mm, gap: 0.8 mm, 40 slices (Trio/Prisma) or 39 slices (Verio), scan sequences: ascending) of 244 volumes at rest for 10 min. During the resting-state scan, the participants were instructed to keep looking at a central fixation point, to keep still, to stay awake, and not to think about specific things.

Resting-state fMRI data preprocessing

The data were processed with SPM 8 (Wellcome Trust Centre for Neuroimaging). The first 4 volumes were discarded to allow for T1 equilibration. The remaining data were corrected for slice timing, realigned to the mean image of that sequence to compensate for head motion. Next, the structural image was co-registered to the mean functional image and segmented into three tissue classes in the MNI space. Using associated parameters, the functional images were

normalized and resampled in a 2 x 2 x 2 mm^3 grid. Finally, they were spatially smoothed with an isotropic Gaussian kernel of 8 mm full-width at half maximum.

Calculation of ROI-to-ROI functional connectivity

For each participant, a correlation matrix was produced by extracting the averaged BOLD time course within a region of interests (ROI) based on an automated anatomical parcellation (AAL, 116 ROIs; Tzourio-Mazoyer et al., Neuroimage, 2002) and the functional brain atlas (shen 2013, 278 ROIs; Shen et al., Neuroimage, 2013). To remove several sources of spurious variance along with their temporal derivatives, linear regression was performed, including (i) six motion parameters in addition to averaged signal over (ii) gray matter, (iii) white matter, and (iv) CSF. Furthermore, to reduce spurious changes in functional connectivity by head motion, the data were checked by the method reduce motion-related artifacts. Specifically, we calculated frame-wise displacement (FD) and DVARS (D: temporal derivative of time-courses, VAR: root mean square variance over voxels) and removed volume with FD > 0.5 mm or DVARS > 0.5%, as proposed by the original article. A band-pass filter (transmission range, 0.008 - 0.1 Hz) was applied to these sets of time courses prior to the following

regression procedure. Subjects were excluded from further analysis if the number of excluded volumes was more than 20% of the total volumes. For each participant, a pair-wise, interregional functional connectivity (FC) was calculated among 116 ROIs (AAL) and 278 ROIs (shen 2013) by evaluating pair-wise temporal Pearson correlations of BOLD time courses. We finally obtained two types of FC matrices (AAL: 116 x 116; shen 2013: 278 x 278) for each participant.

References

Shen, X., Tokoglu, F., Papademetris, X., and Constable, R. T. (2013). Groupwise whole-brain parcellation from resting-state fMRI data for network node identification. *Neuroimage*, 15 (82), 403-15.

Tzourio-Mazoyer, N., Landeau, B., Papathanassiou, D., Crivello, F., Etard, O., Delcroix, N., Mazoyer, B., and Joliot, M. (2002). Automated anatomical labeling of activations in SPM using a macroscopic anatomical parcellation of the MNI MRI single-subject brain. *Neuroimage*, 15 (1), 273-89.