Supplementary Data

Supplement 1. Image Processing

Independent components analysis (ICA)

Estimating the number of independent components

Determining the number of components is a challenging issue in ICA. A lesser number of components than required will result in more than one independent spatial pattern in one component network, and ICA would not be able to discriminate the independent spatial patterns accurately. Vice versa, more components than required will result in some spatial maps—for instance, RSNs—being split into more than one component network. Therefore, choosing the number of components is crucial in ICA analysis.

Previously, researchers usually chose between 20 and 25 components. Meanwhile, some articles discussed the superiority of choosing a higher number of components, and researchers used higher number of components such as 50 or 75.[1–4] To find the most likely correct number of components, both Melodic and GIFT were used to answer this question. They both estimated between 48 and 52 components for each group. Therefore, we chose the higher number of components, 52 components, for our analysis to make sure that we would not miss any network in our analysis.

Network selection

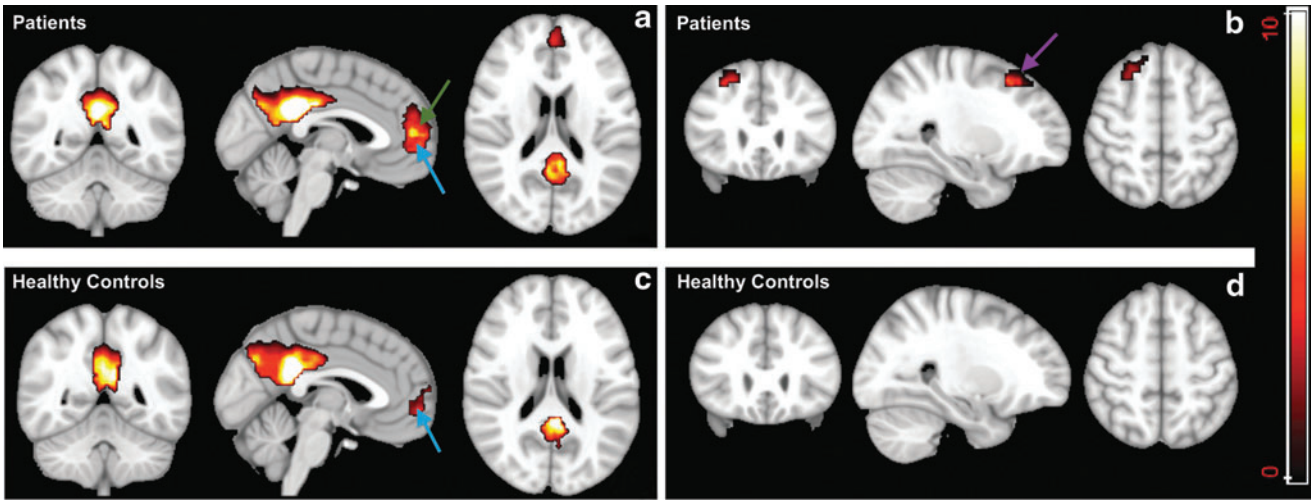
Network selection was performed automatically to eliminate human errors. Spatial correlation between ICA components and the template of desired resting-state networks—i.e., the default mode network (DMN) and basal ganglia network (BGN)—were used to determine these two networks. We chose the RSNs built by Allen and associates[5] based on 603 subjects as a resting-state template. In the chosen template, four DMNs are defined; we used the ''classic'' DMN, identified as independent component (IC) 53 on the template. The IC 21, in the template, is the BGN.

A two-step approach was adopted to select the desired networks.

1. A network—e.g., the DMN—was selected from the 75 template networks to correlate with 52 components obtained from the data. The component in our data set with the highest spatial correlation to the template DMN would be considered as a candidate DMN. In this step, IC 21 was selected for BGN and IC 50 was originally selected for DMN.
2. The components chosen as candidate networks in our dataset were further correlated with all 75 ICs of the template to check whether the selected template network is the one with the highest spatial correlation value with the DMN in our dataset. In this step, IC 21 was confirmed with highest correlation with the template. Template component IC 53, however, showed even higher correlation with our data. Indeed, the two DMN (IC 50 and IC 53) are highly spatially overlapped—in other words spatially correlated between these two DMNs in the template. To examine our result, after finding the desired network, the power spectrum of the component was calculated to make sure the selected component has the highest amplitude in resting-state band pass frequency.

Seed-based analysis (SBA)

SBA was performed by using MATLAB software (http://www.mathworks.com/). The network regions were selected by registering the data on AAL atlas,[6] to minimize operator differences



SUPPLEMENTARY FIG. S1. Functional connectivity (FC) map for the posterior cingulated cortex (PCC): One-sample *t* test ($p=0.01$). **(a, b)** Patient group and **(c, d)** healthy control group. Results show there is greater FC of PCC with BA 10 (blue arrow) in the patient group **(a)** compared with the control group **(c)**. In addition, unlike the patient group that shows significant FC of the PCC with BA 32 **(a)** (green arrow) and BA 9 **(b)** (purple arrow), the healthy control group does not show any FC of the PCC with BA 32 **(c)** and BA 9 **(d)** at $p=0.01$.

on selecting regions. Moreover, to minimize the effect of local fluctuations and increase similarity between reference time series and resting-state activities, the average of the time series of all voxels in selected network regions was recruited to generate the reference time series for each region.

Pearson correlation coefficient was used to measure functional connectivity (FC). A brain correlation map was obtained by measuring correlation coefficient value between a reference time series and time series of whole voxels of the brain. A corrected correlation map was obtained by converting correlation coefficient values (r) using the Fisher z-transformation.

FC map

For each network region, the corrected correlation map of the brain was calculated by using the correlation value between the average time series (reference course series) of all voxels in a region and whole brain voxels. Therefore, there would be one corrected correlation map of each desired area for each subject. For both healthy controls and patients groups, the FC map was calculated by performing the right-tailed one sample *t* test for correlation mean value equal to 0.25 ($m = 0.25$) and further by applying the spatial thresholding.

FC comparisons

Between-group and within-group comparisons were performed on FC. For between-group analysis, the corrected correlation map of the brain was obtained for each individual. A correlation mask was used to identify voxels that are eligible for statistical analysis. A correlation mask was a binary mask including the voxels that have correlation value more than 0.2 in at least one of the mean group correlation maps. A two-sample *t* test and spatial thresholding were performed to identify the difference between healthy controls and patients. The same procedure as between-group comparison was applied in within-group comparison.

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