Supplemental Figure 1. Motion levels before/after scrubbing and subject matching. (a) The two-way ANOVA with repeated measures on the task factor and t-test on the mean are significant (p<0.001) between healthy controls (HC) and patients with schizophrenia (SZ) for the raw frame displacement (FD) levels in the whole sample. The ANOVA and t-test for the residual FD (rFD) levels obtained after scrubbing of volumes with FD>0.5 remain significant in the whole sample.

DOI: 10.1503/jpn.150247
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sample (p<0.01). (b) Matching of subjects by keeping 30 SZ with minimal rFD and keeping 30 HC with maximal rFD. ANOVA and t-tests are not significant with regards to rFD, the number of scrubbed volumes as well as the number of unscrubbed volumes, which are used in the connectome-wide association analysis.
Supplemental Figure 2. Application of general linear models to connectomes. (a) The brain is parcellated at the group-level into functional 50 brain regions generated through a clustering algorithm. (b) Individual connectomes are 50 x 50 matrices measuring functional connectivity between and within every 50 regions for each subject. Each column/line of the symmetric matrix corresponds to the functional connectivity map for one given region. The connectivity map of the posterior cingulate cortex (PCC) is illustrated. (c) A general linear model is used to test at the group level the association between phenotypes and the connectomes of all subjects, independently at each connection. The parametric connectome for the schizophrenia variable (SZ) reveal, for all functional connections, the weights of differences between patients with schizophrenia and healthy controls, while regressing out the effects of age and sex.