

## Supplementary Data

### Materials and Methods

#### Statistical analysis

For the whole-brain two-way ANOVA, we performed 6670 separate statistical tests. Multiple comparisons were corrected using the degree-based correction. Methodologically similar to the network-based statistics (Zalesky et al., 2010) and cluster correction in voxel-based task fMRI analysis (Forman et al., 1995), our multiple comparisons were corrected based on nonrandom data distribution patterns. We would like to use the following graphs to schematically illustrate the principles of our approach using a  $15 \times 14$  matrix as an example (with 105 independent elements below the diagonal line). As shown in Figure a, at a  $p < 0.05$  threshold, it is possible that all five identified elements are all false positives (because  $5 < 0.05 \times 105$ ). For the same reason, if we identify only four (or any number  $< 5$ ) elements, it is very likely that they are all false positives. On the other hand, as shown in Figure b, if the five elements form a special distribution pattern (in this case, all of them are within the same column, i.e., degree=5), then the statistical probability that this particular column (indicated by the red arrow) purely reflects the false positive is very low ( $< 0.05$ , according to Monte Carlo simulations). As shown in Figure c, even if there are only four active elements that are identified, the statistical probability that this particular column (indicated by the red arrow) purely reflects the false positive is still very low ( $< 0.05$ ) because of the unique and nonrandom data distribution pattern.

The number of functional links connected to a single region (i.e., the degree) that is required to correct for multiple comparisons at  $p < 0.05$  is a function of the alpha level and the number of brain regions parceled. Based on our 10,000 Monte Carlo simulations, the number of functional links connected to a single region (i.e., the degree) should be at least 15 for matrix-based fMRI analysis of a  $116 \times 116$  matrix size (i.e., with 6670 separate statistical tests) to correct for multiple comparisons at  $p < 0.05$ . The following table summarizes the degree required for corrections of multiple comparisons at  $p < 0.05$  with various alpha levels and matrix sizes:

<i>Alpha level</i>	<i>Degree</i>
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116 × 116 matrix	
0.05	15
0.01	7
0.005	5
0.001	3
90 × 90 matrix	
0.05	12
0.01	6
0.005	5
0.001	3

