

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Significant loci following MOST GWAS for the Dorsal Attention Network

File Name: Supplementary Data 2

Description: Significant loci following MOST GWAS for the Default Mode Network

File Name: Supplementary Data 3

Description: Significant loci following MOST GWAS for the Frontal Parietal Network

File Name: Supplementary Data 4

Description: Significant loci following MOST GWAS for the Limbic Network

File Name: Supplementary Data 5

Description: Significant loci following MOST GWAS for the Somatosensory Network

File Name: Supplementary Data 6

Description: Significant loci following MOST GWAS for the Ventral Attention Network

File Name: Supplementary Data 7

Description: Significant loci following MOST GWAS for the Visual Network

File Name: Supplementary Data 8

Description: Results from the MOST GWAS for each rfMRI network

File Name: Supplementary Data 9

Description: List of LD-blocks based on Berisa & Prickell (2016) segmentation with at least 1 GWAS significant hit in any network or mental disorder investigated at $p < 1 \times 10^{-5}$

File Name: Supplementary Data 10

Description: MAGMA Gene-Level Multi-Model P-values for the Dorsal Attention Network. Only genes surpassing the genome-wide significant p-value threshold are shown.

File Name: Supplementary Data 11

Description: MAGMA Gene-Level Multi-Model P-values for the Default Mode Network. Only genes surpassing the genome-wide significant p-value threshold are shown.

File Name: Supplementary Data 12

Description: MAGMA Gene-Level Multi-Model P-values for the Frontoparietal network. Only genes surpassing the genome-wide significant p-value threshold are shown.

File Name: Supplementary Data 13

Description: MAGMA Gene-Level Multi-Model P-values for Somatosensory Network. Only genes surpassing the genome-wide significant p-value threshold are shown.

File Name: Supplementary Data 14

Description: MAGMA Gene-Level Multi-Model P-values for the Ventral Attention Network. Only genes surpassing the genome-wide significant p-value threshold are shown.

File Name: Supplementary Data 15

Description: Gene Ontology Enrichment Analyses (for simplicity only gene sets where the FDR corrected p value is smaller or equal 1% are shown)