

Description of Additional Supplementary Files

File name: Supplementary Data 1

Description: Heritability estimates and significance indications for all 783 imaging derived phenotypes: language network (categories L, R and inter) and hemispheric differences (edge HD).

File name: Supplementary Data 2

Description: An overview of all 14 loci discovered in a multivariate GWAS of the language network

File name: Supplementary Data 3

Description: 111 Mapped genes by FUMA based on multivariate GWAS results of the language network

File name: Supplementary Data 4

Description: Gene set preferential brain expression in Brainspan dataset for language network genes as used in figure 1C. Derived using MAGMA.

File name: Supplementary Data 5

Description: Gene set analysis of the language network results with MAGMA as implemented in FUMA. Gene sets smaller than 10 were excluded.

File name: Supplementary Data 6

Description: An overview of all underlying univariate beta weights for the lead SNPs of 14 loci discovered in a multivariate GWAS of the language network used in figure 1E and Supplementary Figure 8

File name: Supplementary Data 7

Description: Underlying univariate P-values of lead SNPs for each significant language network genomic locus

File name: Supplementary Data 8

Description: T-tests for comparison of global change in language network connectivity, left and right intrahemispheric connectivity, and intra and interhemispheric connectivity for 14 significant genomic loci

File name: Supplementary Data 9

Description: An overview of all 3 loci discovered in a multivariate GWAS of hemispheric differences of the language network

File name: Supplementary Data 10

Description: 9 Mapped genes by FUMA based on multivariate GWAS results of hemispheric differences in the language network

File name: Supplementary Data 11

Description: Gene set preferential brain expression in Brainspan dataset for language network hemispheric differences genes as used in figure 1D. Derived using MAGMA.

File name: Supplementary Data 12

Description: Gene set analysis of the hemispheric differences results with MAGMA as implemented in FUMA. Gene sets smaller than 10 were excluded.

File name: Supplementary Data 13

Description: An overview of all underlying univariate beta weights for the lead SNPs of 3 loci discovered in a multivariate GWAS of hemispheric differences in the language network used in figure 1F

File name: Supplementary Data 14

Description: An overview of all underlying univariate P-values for the lead SNPs of 3 loci discovered in a multivariate GWAS of hemispheric differences in the language network

File name: Supplementary Data 15

Description: T-test results for global left-right shift in hemispheric differences for 3 significant genomic loci

File name: Supplementary Data 16

Description: CCA loadings of individual IDPs for language network with polygenic scores used in figure 2A.

File name: Supplementary Data 17

Description: T-tests for comparison of global change in language network connectivity, left and right intrahemispheric connectivity, and intra and interhemispheric connectivity for 3 polygenic scores

File name: Supplementary Data 18

Description: CCA loadings of individual IDPs for hemispheric differences with polygenic scores used in figure 2B.

File name: Supplementary Data 19

Description: T-test results for global left-right shift in hemispheric differences for 3 polygenic scores

File name: Supplementary Data 20

Description: Gene-based associations (-log₁₀ p-value) with the language network (MINP_edges) and hemispheric differences (MINP_HDs) when applying a broad variant filter. Average (avg_LOGP) and lowest -log₁₀ p-values (MINP) are reported, as well as the univariate association driving the result. GENPOS refers to position according to positions in genome build GRCh38.

File name: Supplementary Data 21

Description: Broad variant filter gene-based SKATO associations (-log₁₀ p-value) for all edges of the language network as shown in figure 3A and 3C

File name: Supplementary Data 22

Description: Gene-based associations (-log₁₀ p-value) with the language network (MINP_edges) and hemispheric differences (MINP_HDs) when applying a strict variant filter. Average (avg_LOGP) and

lowest $-\log_{10}$ p-values (MINP) are reported, as well as the univariate association driving the result. GENPOS refers to position according to positions in GRCh38.

File name: Supplementary Data 23

Description: Strict variant filter gene-based SKATO associations ($-\log_{10}$ p-value) for all edges of the language network hemispheric differences as shown in figure 3B and 3D

File name: Supplementary Data 24

Description: Variant-based associations ($-\log_{10}$ P values) with the language network (MINP_edges) and hemispheric differences (MINP_HDs) for the exome-wide significant genes.

File name: Supplementary Data 25

Description: Univariate z-statistics from a gene-based burden test (broad filter) for all 629 heritable imaging derived phenotypes of the language network

File name: Supplementary Data 26

Description: T-tests for comparison of global change in language network connectivity, left and right intrahemispheric connectivity, and intra and interhemispheric connectivity for 5 significant genes

File name: Supplementary Data 27

Description: Univariate z-statistics from a gene-based burden test (strict filter) for all 103 heritable imaging derived phenotypes of hemispheric differences in the language network

File name: Supplementary Data 28

Description: T-test results for global left-right shift in hemispheric difference for 2 significant genes

File name: Supplementary Data 29

Description: Brainspan RNA-seq RKPM expression levels for significant genes in rare variant analysis that are available in the rare variant analysis used in figure 3E