Supporting Information

Supporting information document for "*Divergent Connectomic Organization Delineates Genetic-Evolutionary Traits in the Human Brain*" by Elisenda Bueichekú, Jose M. Gonzalez-de-Echavarri, Laura Ortiz-Teran, Victor Montal, Federico d'Oleire Uquillas, Lola De Marcos, William Orwig, Chanmie Kim, Elena Ortiz-Teran, Silvia Bassaia, Ibai Diez, Jorge Sepulcre.

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1. SUPPLEMENTARY TABLES

Supplementary table 1. Genes linked to the upper bound of the probability distribution.

SCN1A
SCN1B
GALR1
ST8SIA1
NR2C1
SCN8A
DCLK1
TTC21B
ATXN1
OR2L3
LYSMD4
NR3C2
NR3C1
OPN3
MAFB
TTC39C
TTC39B
NFIC
INA
MADCAM1
GK
KCNAB3
HIST1H1D
ARL4C
CS
IDE
HR
CFAP221
PRH2
MOGAT1
EFHA2
SORL1
ZADH2
PLA2R1
SLC5A6
IGFBP2
LY6G5B
PLEKHH3
TCHP
ST3GAL6
CORO6
AFTPH
SLC6A17
TC2N
TBR1
OSBPL6
RBM20
ABCC8
AADACL1
CD274
ATG16L1
ATP8B1
GAS2
AS3MT
USP45
GPR89B
MIAT
HS3ST1
CNNM1
LRRC37A4P
SEMA7A
SEMA6D
MAP3K13

LOC254559
ATP6V0A2
FOXO3
STAMBPL1
FOXP1
C11orf52
CCNB1IP1
EXTL2
TRPM3
TRPC3
SNRPN
STAG3L4
TAF4B
GRIN2A
SRSF1
P2RX6
A26C1B
SOHLH1
C12orf24
KIAA0802
HECW1
PARM1-AS1
TMPPE
NAP1L2
SERTAD4
PCDHB15
PCDHB10
DDX3Y
POSTN
C14orf104
PLCB4
PLCB1
ZNF792
PAIP1
ESRRG
GLCCI1
EIF4A2
CDKN1B
C4orf18
PLAGL1
ZMAT4
MCF2L
ATP4A
INTS4L1
INTS4L2
MRPS30
KIAA0240
C18orf25
EIF5A2
NCALD
ECM1
SETBP1
TSHZ1
STRBP
TTLL11
KIAA1107
BACH1
FGF5
FGF9
FHDC1
C20orf20
OSBPL1A
GABRD

VSTM2A
PRDM5
PRDM2
SLC24A2
NPM2
OXCT2
LOC100134173
CMYA5
ZNF684
ZNF35
ZNF20
RET
RAD54B
CDKL1
C10orf140
KIAA1797
GPLD1
RP11-422J8.1
IL6R
ZNF333
FMN1
ZNF358
GK3P
RNF148
RNF168
RNF157
NXPH3
SLC45A4
ERMP1
STX19
C6orf186
CCNI
VWC2
C6orf138
SPAG6
RHBDL3
CDH7
FLT3
CDS1
FGF18
FGF14
MRS2
EGR1
PDSS1
EMILIN3
PRAG1
ATP2B2
DYNC2H1
RIMS3
ATP2A2
RAB37
ZNF193
GLRB
STRC
FSTL1
ZNF225
ZNF295
RG9MTD2
PCSK1
ZNF268
HAPLN4
ELAVL4
KIAA1456

STX8
TRIM7
CACNB4
NUAK1
ARHGEF18
CACNG2
JDP2
PASK
ANKRD34C
LOC100288939
MIR31HG
JARID2
LRRN3
MSRB3
FBLN7
SLC25A37
SSX2IP
SLC25A12
NIPAL2
RSRC1
RUSC1
GRAMD1B
NAGPA
LNX2
LOC100131943
AP000926.2
STXBP5L
FASTKD1
FNDC5
ITPR1
SATB1
SATB2
SLITRK3
DSCC1
PPIEL
SPAG16
PPP3CC
ACSL3
PVALB
VAMP1
PPIL5
LOC100286909
ASPSCR1
KLF9
AGPAT9
MTBP
CADPS2
ZYX
ZDHHC5
KCNC1
KCNC3
RASGRF1
KCNA2
KCNA1
TTBK2
KCNB1
HIVEP2
CHGA
JAM2
ENPP5
EDNRA
AC013402.2
ELL2

KCNT1
KCNS1
ENTPD4
THAP10
MSL2
SETD7
RORB
RORA
CDR2L
DMKN
NFKBIZ
FAM71E1
MYO19
NKX3-1
C6orf47
STS
GRHL2
ADAM22
INPP5A
SHD
CEP152
ASB13
CRABP1
SRL
C8orf47
TNFRSF25
POU3F2
ICA1
SLC29A1
FAM131B
TEAD4
DENND5B
C17orf75
IFNE
C9orf72
C9orf45
ZBTB16
VIPR2
CCDC39
CCDC58
TMEM86B
RP11-403C10.2
CCDC136
SPTSSB
ZNF385D
ZNF385B
ZNF385A
UCHL5
LYPD5
MRPL33
STARD5
SMC1A
IL1RAP
PLXDC1
PKD1
GPR161
LGI3
LGI2
POU6F1
POU6F2
CPLX1
PKNOX2
HCN1

PIM1
BMP4
PION
PDIK1L
A2BP1
PIF1
DCBLD2
BTBD11
SERPINB9
PHYH
SCRT1
RPH3A
TUBE1
TUBD1
C7orf63
UPP1
LINC00473
ETV6
C20orf100
LMTK2
PPP1R28
INTS9
INTS8
PDIA5
RASSF5
RBAK
ECEL1P2
ANK1
ANKH
LOC643669
TAS2R13
ALDH1A3
TAS2R43
TAS2R31
TAS2R30
ANKRD29
SGCG
YPEL4
RTKN2
LINC00515
ARC
PCP4L1
LRRC38
LRRC49
LRRC8C
ZCCHC8
TIFA
C1orf201
GABRB2
TRIM37
GABRA1
RFX5
GABRG2
GABRG3
CDC42EP3
IQSEC1
KLF12
PENK
LEPROTL1
LAG3
NCK2
SIX4
EPB41
DPY19L2P4
IL28RA
LEPREL2
STAC2
TPTE2P6
LUZP1
PPARGC1A
SLC39A14
CUX1
C1RL
C1orf71
C19orf46
MAGI3
C1orf97
TRIP11
CABP1
C1orf172
CRHR2
STAT4
RP5-1022P6.1
DNAJC5G
CPNE9

Supplementary table 2. Genes linked to the lower bound of the probability distribution.

GDA
SCN3B
TMEFF2
RALGPS2
GHR
SPATA18
SCN9A
PHPT1
CAMK2D
PTPRF
NUTF2
HN1
GNG10
DACH2
TAF7L
RTBDN
KLHL1
SLC4A3
MAFG
ECHDC3
LOC392145
PTPRA
NFIB
SLC30A10
PEA15
OPRK1
EXOC6
NTNG2
TXLNB
S100Z
KL
C21orf62
EFHC2
STYK1
C21orf67
TG
BIRC3
TMTC1
ARL10
PLXNC1
RPS27AP11
DTNBP1
IGFBP5
SLC2A4RG
CDCA7
WNT10B
GGCT
SMARCD3
PSD3
CDC42
RASL10A
RASL11B
B9D1
PSMB2
CD244
MGST1
NECAB2
TXNL4A
PKIB
PKIA
APLN
TBCA
FIBIN
MESP1
APOE
PLD6
LOC728392
CAMKV
C11orf66
PLB1
FBXO2
SEMA3D
GOLM1
SEMA4A
ZWILCH
NIT2
LINC00086
C1S
UBL5
CXorf57
DAP
NTSR1
NTSR2
CLEC4G
CFD
AKAP14
AC006273.1
NUPR1
CALM3
ANKRD6
CALB2
LOC100292909
ARHGAP6
MAPK1
MAPK3
PMVK
AL161668.2
SLC1A4
PTCHD1
GTF3C6
C12orf73
HES5
C12orf45
C12orf53
C12orf23
DACT1
LY6H
PNCK
CORO1A
SCGN
LINC00260
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LINC00282
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PCDH17
WDR66
WDR69
HTR3A
HTR2C
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F12
UHMK1
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PLCB2
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ATOX1
SNX26
HIF3A
FAM65B
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MMD2
SLC26A4
ATOH7
ZNF831
ARHGAP18
TP53I3
GNG2
GNG4
RILPL2
C9orf9
SH3RF1
GPR88
GPR98
GNB4
KIAA1244
NCAM2
NKAIN2
NKAIN4
PRDX4
CAPSL
MDGA1
SUSD1
SLC27A5
PYGL
PTHLH
GMFB
ANXA11
SSTR2
SSTR1
CENPVL1
FGGY
PNPLA4
MOBKL1A
HRH1
TMEM200A
KIF21B
OXCT1
HIST1H2BK
RPS10
GPD2
ENOX2
GPC4
TTPAL
RASAL1
C10orf116
FAM70A
RAB27B
JUN
C17orf108
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AC093310.1
RNASEH2A
RNASEH2C
IL33
IL34
RNF150
PTPLAD2
CD63
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PYCRL
FLJ38379
CD24
C6orf118
FGFR3
CD83
DYDC2
SAP30BP
AC044839.2
LSM3
TMSB4X
CXXC11
KIAA1644
TMSB10
MRAS
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CDH9
SLIT1
SLIT3
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LYZL4
LOR
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RP11-566K11.2
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SPARC
AC005152.2
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CASK
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SEPW1
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PCSK5
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MYL12B
TRIM6
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CACNG3
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GLUD2
PGM2L1
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CTXN1
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TMEM176A
SLC25A23
SLC25A22
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C16orf55
KIRREL2
SULF2
ITPRIPL2
DDAH2
UG0898H09
AP3S1
CES7
LARGE
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VAV1
RSPO4
RSPO3
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SNCA
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NUDT11
FAM122C
GYPE
SUMO3
ENO1
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C6orf225
CCDC42B
ST6GALNAC5
PGAP1
NHLRC1
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WNT7B
PRSS23
GRAMD2
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HPCAL4
VBP1
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FKBP1B
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SNX7
RRAGB
TSKU
PRKCG
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RP11-60I3.5
UBE2S
C3orf78
KCNJ1
AP1S1

KCNG1
C3orf26
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MT2A
DLL3
TUBB
ORC6L
ALDH9A1
C2orf80
ZCCHC12
ZCCHC18
ZCCHC17
GNPTAB
LRP1B
ELL3
TIMM8B
SOX5
RP11-544M22.1
C3orf14
LASS1
KCNQ2
SYNPR
FAM107A
SLC17A8
KCNN3
FAM150B
TMEM120A
ELMO2
TXN
SNAP29
FAM71F1
ASCL2
IL12RB2
DMC1
CLSPN
GRIA1
C6orf52
NT5DC3
ROBLD3
KCTD4
TPO
FILIP1
PPP4R4
ETNK2
TUBB2A
DAPL1
SYTL5
GLRA2
SQLE

EFEMP2
MAN1A1
PDLIM5
RAVER2
RAPGEF4
LYRM2
DMWD
WBP1
DMRTC1B
LIX1
GPRIN2
C8orf46
TBC1D26
GUK1
ST5
SLA
SP5
LIPH
MYH7
TOX3
C17orf89
IL13RA2
DOK6
CMAS
TMEM106C
GLOD4
SYT17
GRM1
GLP2R
DISC1
DYNLL1
AC093283.3
UCHL1
CCDC103
CCDC112
MRPL49
LOC339524
TNNT1
EFCAB1
FAM149A
FAM148C
SPRR2G
TPM3
RGS14
RGS22
RGS20
DOC2A
DUSP18
DUSP13
IGFN1

AK3L1
DPYD
COCH
MILR1
HBG1
HS2ST1
RBP4
PELI1
GPR160
ZFP64
COG1
PDGFB
NPTXR
CPLX3
DNAH5
AGXT2L1
RDBP
PJA1
CCDC109B
VAT1L
STK32B
GNAO1
EFNB2
HBQ1
PID1
CNR1
LOC100287347
CNN3
LDHD
C7orf31
RAP2B
LOC100287146
DSEL
UPP2
FAM171B
ICAM5
LINC00461
MBOAT2
ROBO1
ROBO2
C20orf112
PHEX
AC078937.4
PPP1R1A
LOC100287080
TLL1
LOC648771
BATF3
C1QL1
C1QL2

TNFAIP2
ANO3
LCP1
C12ORF75
DCAKD
C6orf1
YPEL1
DTNB
ANKRD43
ANKRD50
MOXD1
AMZ1
LOC100289263
NDUFC2
PGA3
LRRC36
LRRC42
LRRC3B
LRRC56
LRRC57
RGMB
C1orf226
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TMSB15A
RPL39L
AC010980.2
SFT2D2
GABRB1
TRIM36
PACRG
GABRA2
GABRA3
GABRA5
PDCD6
EPCAM
SEL1L2
IFI27L2
GUCY1A3
CREM
PGRMC1
POLE4
DNAJC25-GNG10
LOC100131504
RHOC
PDYN
PRODH2
SNRNP27
RPL27A

MAGED4B
ODZ3
C5orf33
EXD1
LOC642852
LOC100131482
CHID1
PTRH1
DNAJA4
LUZP2
FANCL
LOC100129309
MSANTD1
LRRC16B
C1orf50
C1orf53
C19orf12
C1orf95
LOC391722
RNASET2
PDE1A
PDE2A
SLC7A4
TIMP4
TIMP2
TIMP1
DYRK3
DYRK2
DCAF15
AC024575.2
C1orf187
CABP7
ANXA8
DPYSL3
GDPD2
SLC2A12
GCNT1
DNAJC12
LOC100129291
FZD1
FZD2
SAMD3
FZD7
THRA
CPNE6
CPNE7
LOC100131283
KCTD17
KCTD12

Supplementary table 3. Cellular components linked to the upper bound of the probability distribution.

Cluster 01: Ion channel complex

	Gene Ontology (GO)	Log10 (p-value)	Fold Enrichment (FE)	Cellular Component Annotation name
1	0034702	11.39	5.55	Ion channel complex
2	1902495	10.66	5.14	Transmembrane transporter complex
3	1990351	10.43	5.02	Transporter complex
4	0034703	8.24	5.48	Cation channel complex
5	0098796	5.73	2.25	Membrane protein complex
6	0034705	4.78	6.12	Potassium channel complex
7	0098797	4.42	2.63	Plasma membrane protein complex
8	0008076	4.24	5.99	Voltage-gated potassium channel complex

Cluster 02: Integral component of plasma membrane

	Gene Ontology (GO)	Log10 (p-value)	Fold Enrichment (FE)	Cellular Component Annotation name
1	0005887	10.21	2.46	Integral component of plasma membrane
2	0031226	9.38	2.35	Intrinsic component of plasma membrane

Cluster 03: Synapse

	Gene Ontology (GO)	Log10 (p-value)	Fold Enrichment (FE)	Cellular Component Annotation name
1	0045202	10.02	2.77	Synapse
2	0098794	8.01	3.31	Postsynapse
3	0097060	7.45	3.72	Synaptic membrane
4	0045211	7.06	4.15	Postsynaptic membrane
5	0098793	4.36	2.76	Presynapse
6	0099572	4.23	3.14	Postsynaptic specialization
7	0098978	4.08	3.05	Glutamatergic synapse
8	0098590	4.03	1.99	Plasma membrane region
9	0098984	3.68	2.93	Neuron to neuron synapse
10	0014069	3.5	2.95	Postsynaptic density
11	0032279	3.45	2.92	Asymmetric synapse

Cluster 04: GABA-ergic synapse

	Gene Ontology (GO)	Log10 (p-value)	Fold Enrichment (FE)	Cellular Component Annotation name
1	0098982	6.77	8.89	GABA-ergic synapse

Cluster 05: Cell junction

	Gene Ontology (GO)	Log10 (p-value)	Fold Enrichment (FE)	Cellular Component Annotation name
1	0030054	6.36	2.26	Cell junction

Cluster 06: Neuron projection

	Gene Ontology (GO)	Log10 (p-value)	Fold Enrichment (FE)	Cellular Component Annotation name
1	0043005	6.21	2.23	Neuron projection
2	0030425	4.79	2.63	Dendrite
3	0097447	4.76	2.62	Dendritic tree
4	0036477	4.28	2.26	Somatodendritic compartment
5	0030424	3.43	2.35	Axon
6	0043025	3.38	2.47	Neuronal cell body
7	0044297	2.71	2.18	Cell body

Cluster 07: Integral component of synaptic membrane

	Gene Ontology (GO)	Log10 (p-value)	Fold Enrichment (FE)	Cellular Component Annotation name
1	0099699	5.43	5.19	Integral component of synaptic membrane
2	0099240	5.1	4.82	Intrinsic component of synaptic membrane
3	0099055	4.97	5.7	Integral component of postsynaptic membrane
4	0098936	4.81	5.46	Intrinsic component of postsynaptic membrane
5	0099634	4.64	5.88	Postsynaptic specialization membrane
6	0099060	3.92	6.3	Integral component of postsynaptic specialization membrane
7	0098948	3.81	6.06	Intrinsic component of postsynaptic specialization membrane
8	0098839	3.04	5.33	Postsynaptic density membrane
9	0042734	2.52	3.31	Presynaptic membrane
10	0099061	2.15	5.23	Integral component of postsynaptic density membrane
11	0099146	2.06	4.94	Intrinsic component of postsynaptic density membrane

Cluster 08: GABA-A receptor complex

	Gene Ontology (GO)	Log10 (p-value)	Fold Enrichment (FE)	Cellular Component Annotation name
1	1902711	5.14	17.54	GABA-A receptor complex
2	1902710	5.03	16.66	GABA receptor complex
3	0034707	4.06	8.16	Chloride channel complex

Cluster 09: Main axon

	Gene Ontology (GO)	Log10 (p-value)	Fold Enrichment (FE)	Cellular Component Annotation name
1	0044304	5.06	7.73	Main axon
2	0033268	2.88	13.33	Node of Ranvier
3	0043194	2.5	10	Axon initial segment

Cluster 10: Neuron projection membrane

	Gene Ontology (GO)	Log10 (p-value)	Fold Enrichment (FE)	Cellular Component Annotation name
1	0032589	4.66	8.19	Neuron projection membrane
2	0032590	4.57	10	Dendrite membrane
3	0032809	3.18	9.87	Neuronal cell body membrane
4	0044298	3.18	9.87	Cell body membrane
5	0031256	2.39	3.16	Leading edge membrane
6	0031253	2.31	2.39	Cell projection membrane

Supplementary table 4. Cellular components linked to the lower bound of the probability distribution.

Cluster 01: Neuron projection

	Gene Ontology (GO)	Log10 (p-value)	Fold Enrichment (FE)	Cellular Component Annotation name
1	0043005	16.90	3.93	Neuron projection
2	0030424	9.94	4.37	Axon
3	0036477	9.81	3.79	Somatodendritic compartment
4	0030425	8.57	4.06	Dendrite
5	0097447	8.53	4.04	Dendritic tree
6	0044297	6.49	3.75	Cell body
7	0043025	5.13	3.57	Neuronal cell body
8	0150034	3.69	3.81	Distal axon
9	0044306	2.67	4.32	Neuron projection terminus
10	0043679	2.48	4.41	Axon terminus
11	0030426	2.20	3.66	Growth cone
12	0030427	2.16	3.61	Site of polarized growth

Cluster 02: synapse

	Gene Ontology (GO)	Log10 (p-value)	Fold Enrichment (FE)	Cellular Component Annotation name
1	0045202	14.46	3.87	Synapse
2	0097060	9.59	4.96	Synaptic membrane
3	0098590	6.59	2.89	Plasma membrane region
4	0045211	6.14	4.57	Postsynaptic membrane
5	0030054	5.91	2.73	Cell junction
6	0098794	5.01	3.31	Postsynapse
7	0098978	4.47	3.81	Glutamatergic synapse
8	0099572	3.21	3.33	Postsynaptic specialization
9	0098984	2.59	3.13	Neuron to neuron synapse
10	0005911	2.29	2.72	Cell-cell junction
11	0014069	2.17	2.95	Postsynaptic density
12	0032279	2.14	2.92	Asymmetric synapse

Cluster 03: Presynapse

	Gene Ontology (GO)	Log10 (p-value)	Fold Enrichment (FE)	Cellular Component Annotation name
1	0098793	8.92	4.55	Presynapse
2	0030658	4.88	5.05	Transport vesicle membrane
3	0030133	4.56	3.74	Transport vesicle
4	0030672	4.37	6.53	Synaptic vesicle membrane
5	0099501	4.37	6.53	Exocytic vesicle membrane
6	0070382	4.29	4.74	Exocytic vesicle
7	0098563	3.50	8.69	Intrinsic component of synaptic vesicle membrane
8	0008021	2.94	4.07	Synaptic vesicle
9	0030285	2.37	8.08	Integral component of synaptic vesicle membrane

Cluster 04: Secretory vesicle

	Gene Ontology (GO)	Log10 (p-value)	Fold Enrichment (FE)	Cellular Component Annotation name
1	0099503	8.28	3.35	Secretory vesicle
2	0030659	5.41	3.13	Cytoplasmic vesicle membrane
3	0030141	5.16	2.97	Secretory granule
4	0012506	5.06	3.04	Vesicle membrane
5	0030667	2.03	2.96	Secretory granule membrane

Cluster 05: Intrinsic component of presynaptic membrane

	Gene Ontology (GO)	Log10 (p-value)	Fold Enrichment (FE)	Cellular Component Annotation name
1	0098889	6.91	9.52	Intrinsic component of presynaptic membrane
2	0099240	6.55	6.42	Intrinsic component of synaptic membrane
3	0042734	5.99	6.21	Presynaptic membrane
4	0099699	4.80	5.63	Integral component of synaptic membrane
5	0099056	4.69	8.00	Integral component of presynaptic membrane
6	0099055	3.87	5.70	Integral component of postsynaptic membrane
7	0098936	3.72	5.46	Intrinsic component of postsynaptic membrane
8	0098945	3.29	14.03	Intrinsic component of presynaptic active zone membrane
9	0048787	2.47	8.60	Presynaptic active zone membrane
10	0099060	2.41	5.40	Integral component of postsynaptic specialization membrane
11	0098948	2.33	5.19	Intrinsic component of postsynaptic specialization membrane
12	0099634	2.32	4.57	Postsynaptic specialization membrane

Cluster 06: Intrinsic component of plasma membrane

	Gene Ontology (GO)	Log10 (p-value)	Fold Enrichment (FE)	Cellular Component Annotation name
1	0031226	6.46	2.59	Intrinsic component of plasma membrane
2	0005887	4.84	2.42	Integral component of plasma membrane

Cluster 07: Cytoplasmic region

	Gene Ontology (GO)	Log10 (p-value)	Fold Enrichment (FE)	Cellular Component Annotation name
1	0099568	4.78	3.48	Cytoplasmic region
2	0032838	4.31	4.76	Plasma membrane bounded cell projection cytoplasm
3	0120111	3.63	6.58	Neuron projection cytoplasm
4	1904115	3.16	7.55	Axon cytoplasm

Cluster 08: GABA-ergic synapse

	Gene Ontology (GO)	Log10 (p-value)	Fold Enrichment (FE)	Cellular Component Annotation name
1	0098982	3.86	7.11	GABA-ergic synapse

Cluster 09: Ion channel complex

	Gene Ontology (GO)	Log10 (p-value)	Fold Enrichment (FE)	Cellular Component Annotation name
1	0034702	3.84	3.78	Ion channel complex
2	1990351	3.80	3.61	Transporter complex
3	1902495	3.45	3.50	Transmembrane transporter complex
4	0034703	2.75	3.65	Cation channel complex
5	0098796	2.03	2.08	Membrane protein complex
6	0034704	2.02	5.21	Calcium channel complex

Cluster 10: Anchored component of plasma membrane

	Gene Ontology (GO)	Log10 (p-value)	Fold Enrichment (FE)	Cellular Component Annotation name
1	0046658	3.78	8.04	Anchored component of plasma membrane
2	0031225	2.15	3.59	Anchored component of membrane

Supplementary table 5. Specific genes related to the cellular components linked to the upper bound of the probability distribution.

Cluster 01: Ion channel complex	Cluster 02: Integral component of plasma membrane	Cluster 03: Synapse	Cluster 04: GABA-ergic synapse	Cluster 05: Cell junction
GABRA1	ATP2A2	ANK1	ATP2B2	ATP2A2
GABRB2	ATP2B2	ATP2A2	GABRA1	ATP2B2
GABRD	ATP4A	ATP2B2	GABRB2	CDH7
GABRG2	CRHR2	CRHR2	GABRD	EPB41
GABRG3	EDNRA	SLC29A1	GABRG2	GABRA1
GLRB	SLC29A1	EPB41	GABRG3	GABRB2
GRIN2A	FLT3	GABRA1	GLRB	GABRD
KCNA1		GABRB2	SLITRK3	GABRG2
KCNA2		GABRD	PLCB1	GABRG3
KCNB1		GABRG2	SLC6A17	GLRB
KCNC1		GABRG3		GRIN2A
KCNC3		GLRB		ICA1
KCNS1		GRIN2A		
PKD1		ICA1		
SCN1A		IL1RAP		
SCN1B				
SCN8A				
ABCC8				
TRPC3				
CACNG2				
LRRC8C				
LRRC38				
HCN1				
VWC2				

Supplementary table 6. Specific genes related to the cellular components linked to the lower bound of the probability distribution.

Cluster 01: Neuron projection	Cluster 02: Synapse	Cluster 03: Presynapse	Cluster 04: Secretory vesicle	Cluster 05: Intrinsic component of presynaptic membrane
APOE	APOE	ATP2B4	ANXA11	ATP2B4
RHOC	ATP2B4	CALB2	CD63	CDH9
ATP2B4	CALB2	CDH9	CDC42	CDH10
CALB2	CDC42	CDH10	CFD	CNR1
CAMK2D	CDH9	AP1S1	DPYSL3	EFNB2
CDC42	CDH10	CNR1	FABP5	GPC4
AP1S1	AP1S1	EFNB2	GABRA2	GABRA5
AP3S1	CNN3	GPC4	GRIA1	HTR3A
CNN3	CNR1	GABRA2	CXCL1	OPRK1
CNR1	DPYSL3	GABRA5	LOXL1	PCDH17
DMWD	EFNB2	GRIA1	MGST1	NTNG2
DPYSL3	FABP5	HTR3A	MIF	CPLX3
GABRA2	GPC4	NTSR1	NDUFC2	
GABRA3	GABRA2	OPRK1	HN1	
GABRA5	GABRA3	PDE2A	OPRK1	
GABRB1	GABRA5	PDYN	PCSK5	
GLRA2	GABRB1	PRKCG	PDGFB	
GNAO1	GLRA2	RAB27B	PRKCD	
GRIA1	GRIA1	SNCA	MAPK1	
GRM1	GRM1	DOC2A	KLK7	
HRH1	GUCY1A3	CASK	PYGL	
HTR1A	HTR3A	SNAP29	RAB27B	
HTR2C	NTSR1	SCGN	RAP2B	
HTR3A	OPRK1	C1QL1	SNCA	
KCNN3	PDE2A	PCDH17	SPARC	
KCNQ2	PDYN	SYT17	TIMP1	
NCAM2	PRKCG	SVOP	TIMP2	
NFIB	MAPK1	DTNBP1	TMSB4X	
NOV	PTPRA	NTNG2	DOC2A	
NTSR1	RAB27B	KCTD12	RNASET2	
OPRK1	SNCA	SYNPR	DYNLL1	
PDYN	SPARC	SLC17A8	SNAP29	
PRKCG	DOC2A	CPLX3	CAP1	
MAPK1	CASK		PRDX4	
PTPRF	SNAP29		PGRMC1	
RAB27B	MAPK8IP1		C9orf9	
ROBO1	CACNG3		MOXD1	
ROBO2	SCGN		ROBLD3	
SCN9A	PDLIM5		SYT17	
SLC1A4	RGS14		TRIM36	
SNCA	PGRMC1		SVOP	
SNCG	C1QL1		NIT2	
TIMP2	RAPGEF4		DTNBP1	
UCHL1	CORO1A		SYTL5	
DOC2A	FAM107A		LYZL4	
DYNLL1	LPHN3		SYNPR	
CPNE6	PSD3		TUBB	
MAPK8IP1	NPTXR		SLC17A8	
FAM65B	CADM1		CPLX3	
ODZ3	FBXO2			
CACNG3	DISC1			
SCGN	PCDH17			
PDLIM5	DACT1			
RGS14	SYT17			
PGRMC1	SVOP			
C1QL1	PCDH15			
CORO1A	TMEM108			
FAM107A	CAMKV			
KIF21B	GPR98			

LPHN3	DTNBP1
NPTXR	NTNG2
FBXO2	KCTD12
EXOC6	SNX26
NECAB2	SYNPR
KLHL1	SLC17A8
PCDH15	MDGA1
TMEM108	CPLX3
GPR98	
DTNBP1	
NTNG2	
SNX26	
UHMK1	
SYNPR	
PACRG	
SLC17A8	
CPLX3	

Supplementary table 7. Original curve fitting model analysis results and permutation analysis results. The regression analysis was performed between the mean dN/dS ratio and the evolutionary divergence times of the *Homo Sapiens*. The mean dN/dS ratio is an evolutionary measurement that captures the rate in which biological features are conserved in the species during evolutionary adaptive periods. The mean dN/dS ratios were obtained for each cellular component (*i.e.,* products of the genes with significant cortical expression within the phenotypic segregation-integration map) in the homologue-orthologue comparison between humans *vs.* non-human primates (*i.e.,* the chimpanzee, the gorilla, the orangutan, the macaque, the olive baboon, the vervet AGM, and the marmoset). Then, the mean dN/dS ratios were used to investigate the relationship between the S-I connectivity map and the *Homo Sapiens* evolutionary pathway. The cellular components linked to the upper bound of the probability distribution appear in Section A, and in Section B the ones linked to the lower bound of the probability distribution. The table contains the original curve fitting results (R^2, F-statistic and *p*-value), and the corrected *p*-value was obtained from the permutation analysis, which was done for testing the robustness of the original analysis.

Section A

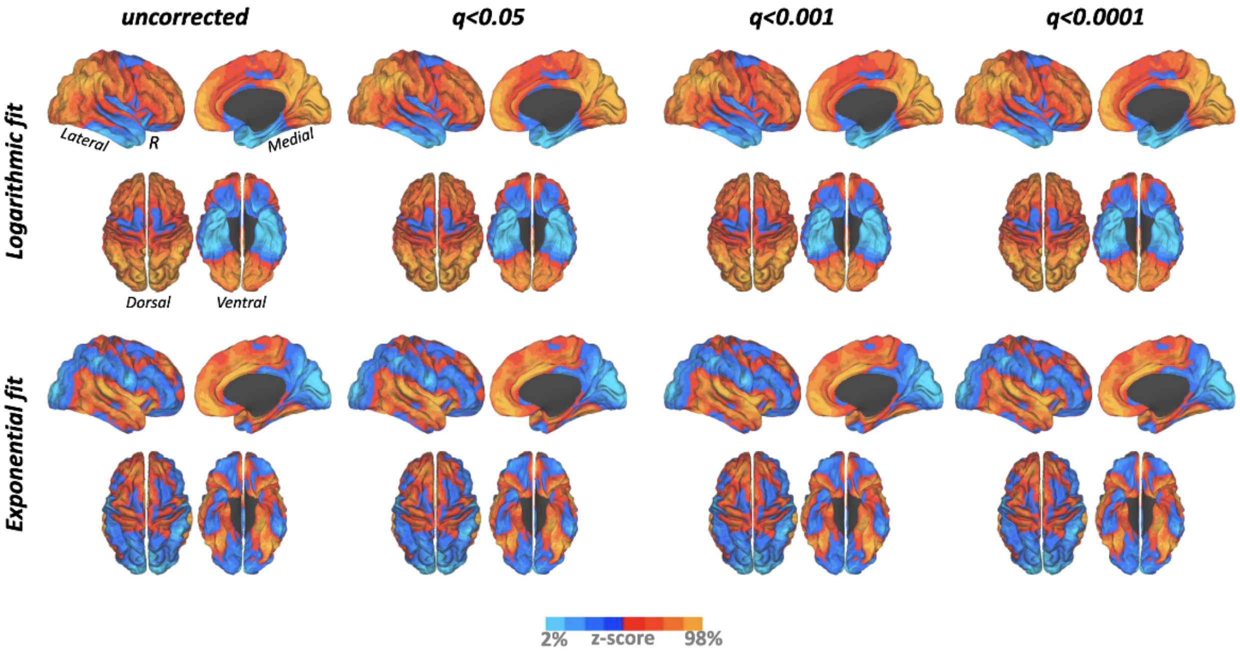
	Original analysis results			**Permutation analysis results**
Cellular components	**R^2 value**	**F-value**	***p*-value**	**Corrected *p*-value**
Ion channel complex	0.880	14.73	0.01	0.001
Integral component of plasma membrane	0.767	6.600	0.05	<0.001
Synapse	0.332	2.489	0.18	-
GABA-ergic synapse	0.325	2.407	0.18	-
Cell junction	0.284	1.979	0.22	-

Section B

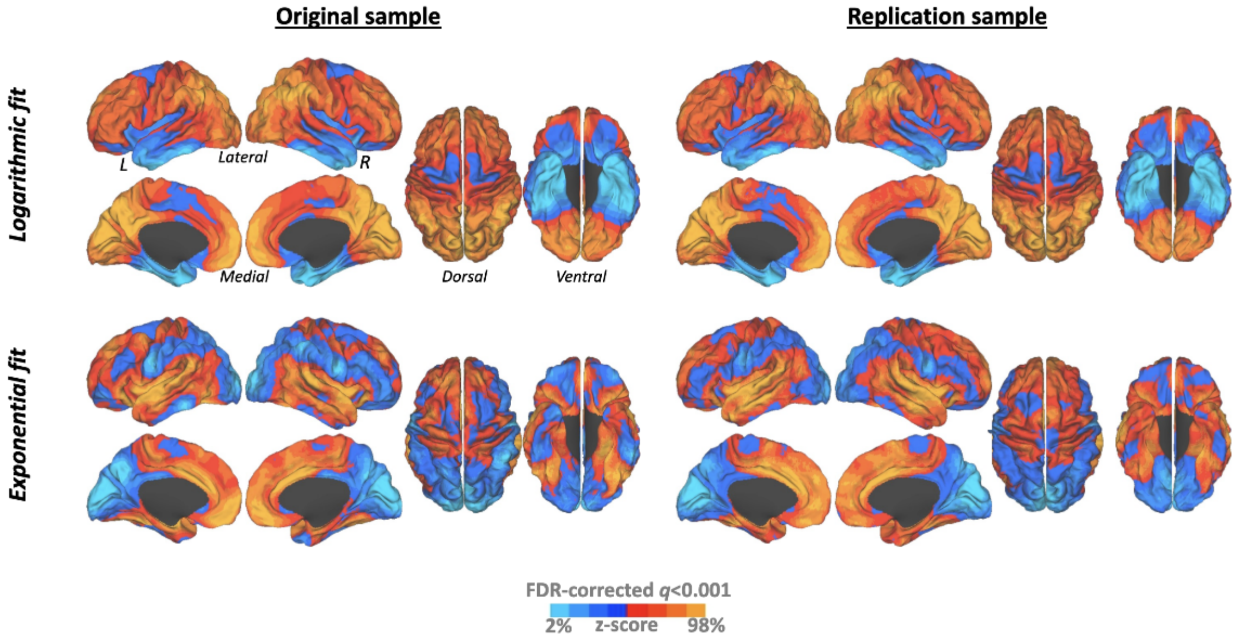
	Original analysis results			**Permutation analysis results**
Cellullar components	**R^2 value**	**F-value**	***p*-value**	**Corrected *p*-value**
Neuron projection	0.861	30.99	0.003	<0.001
Synapse	0.859	30.53	0.003	0.004
Presynapse	0.617	8.04	0.036	0.407
Secretory vesicle	0.647	9.16	0.029	0.388
Intrinsic component of presynaptic membrane	0.390	18.7	0.019	0.498

2. SUPPLEMENTARY FIGURES

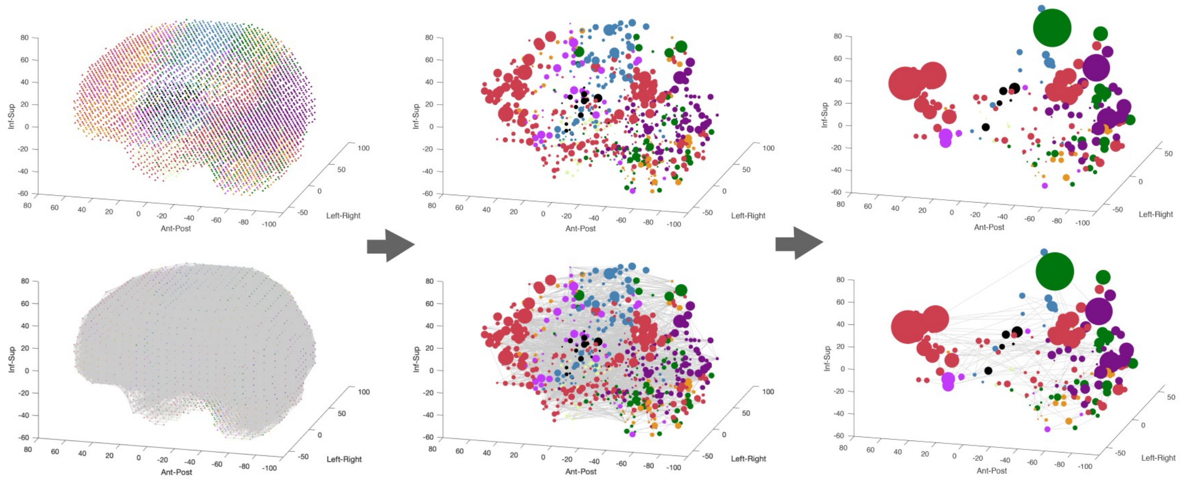
Supplementary Figure 1. Validation of the main connectomics results. The aim of the analysis was to test the robustness of the connectomics results by modifying different thresholds for the multiple-comparison correction. Brain maps appearing on the upper row were obtained after applying a logarithmic fit, which correspond to the *early trajectory mergers*. Similarly, on the lower row are showed the brain maps resulting after applying an exponential fit, which correspond to the *late trajectory mergers*. From left to right, the projections correspond to: uncorrected results; FDR-correction *q*<0.05; FDR-correction *q*<0.001; and, FDR-correction *q*<0.0001. **Note:** Brain maps are projected using CARET software. The color scale represents the 2-98% of the normalized connectivity data. **Abbreviations:** R = right hemisphere.



Supplementary Figure 2. Replication of the main connectomics results. The aim of the analysis was to test the robustness of the connectomics results using the resting-state functional MRI data of an independent sample. The results corresponding to the original sample appear on the left, while the results of the replication sample appear on the right. The brain maps related to the early trajectory mergers appear for both samples on the upper row, while the late trajectory mergers maps appear on the lower row. **Note:** Brain maps are projected using CARET software. The color scale represents the 2-98% of the normalized connectivity data. **Abbreviations:** L=left hemisphere; R = right hemisphere.



Supplementary Figure 3. Illustration of the merging process. The first row represents the nodes that are being progressively merged, while in the second row the links connecting the nodes have been plotted (upper 10% links). The left panels represent each node positioned in its MNI coordinate (upper) and the links connecting the nodes (lower). The middle and right panels represent two different moments of the merging process: two nodes were merged when they have similar connectivity and the MNI coordinates of the node with highest weighted degree was used to position "merged nodes" in the brain space. In this figure, node size represents the number of nodes that have been merged, thus, the more nodes where merged, the bigger the node size plotted. The original color palette used in Yeo et al. (Yeo et al. 2011, *J Neurophysiol, 106*(3):1125-65) was adopted in this illustration, therefore, nodes could be associated with known functional connectivity human brain networks. **Abbreviations:** Inf-Sup: inferior – superior axis; Ant-Post: anterior – posterior axis.



Supplementary Figure 4. Comparison of the merging process to a random assignation process. The left panel of the figure represents the normalized cumulative links using our merging rule, while the right panel represents the results of the process using a random merging rule. In this merging process, implementing our merging rule results in merging first segregated connections, while the integration is more predominant towards the end of merging process. Contrarily, using a random merging rule to classify the links leads to indistinctive assignations to segregation or integration. The Y axis represents the cumulative number of links, which has been normalized to account for the different number of links in segregation and integration. The X axis represents the merging time.