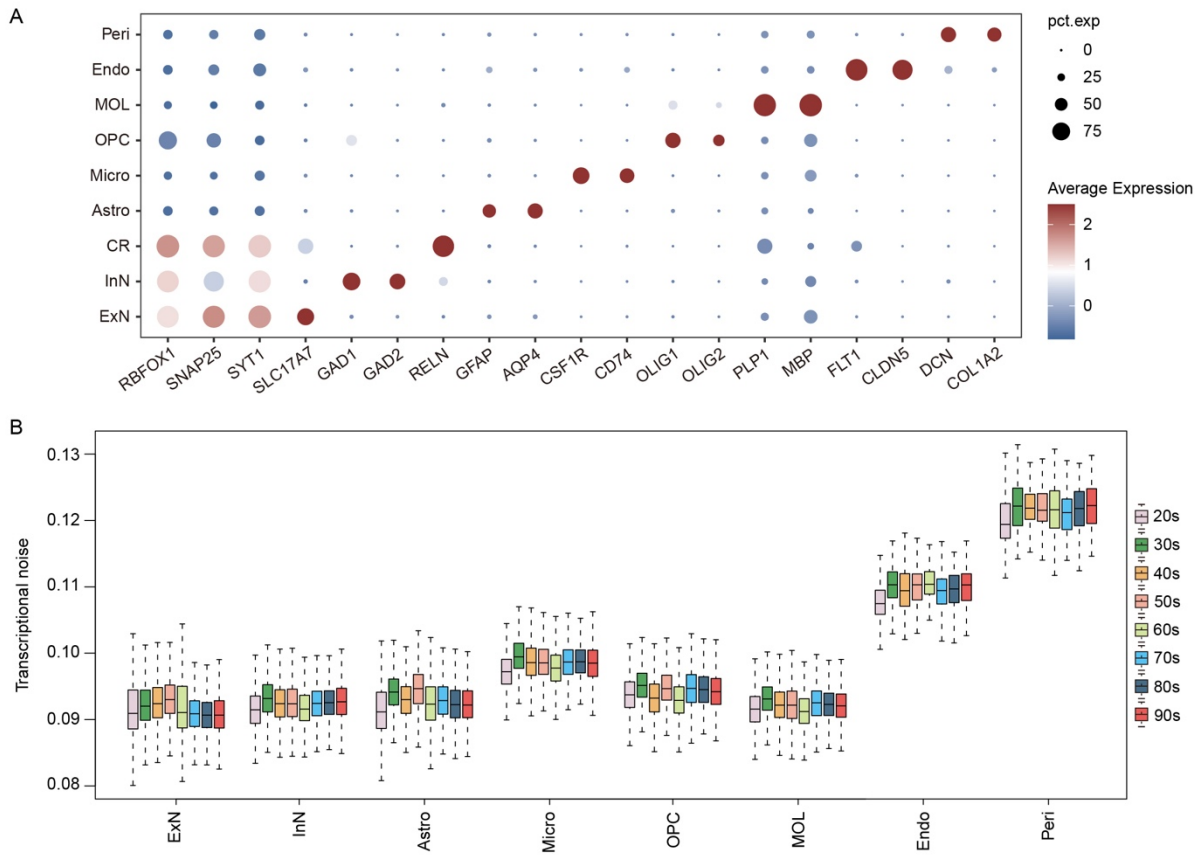
Supplementary Materials for

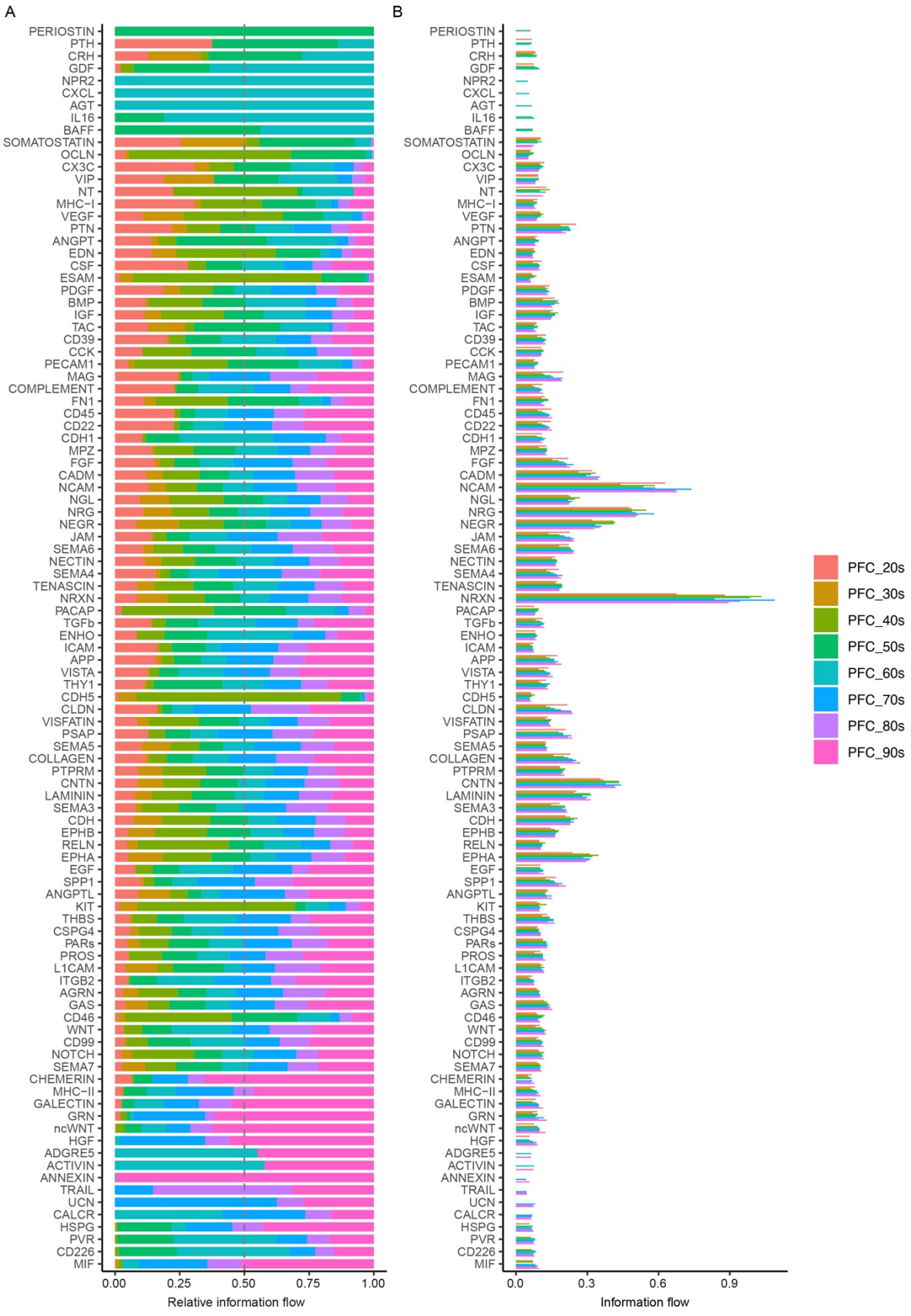
A single-cell transcriptome atlas of cell diversity in human prefrontal cortex across the postnatal lifespan

Niu et al.

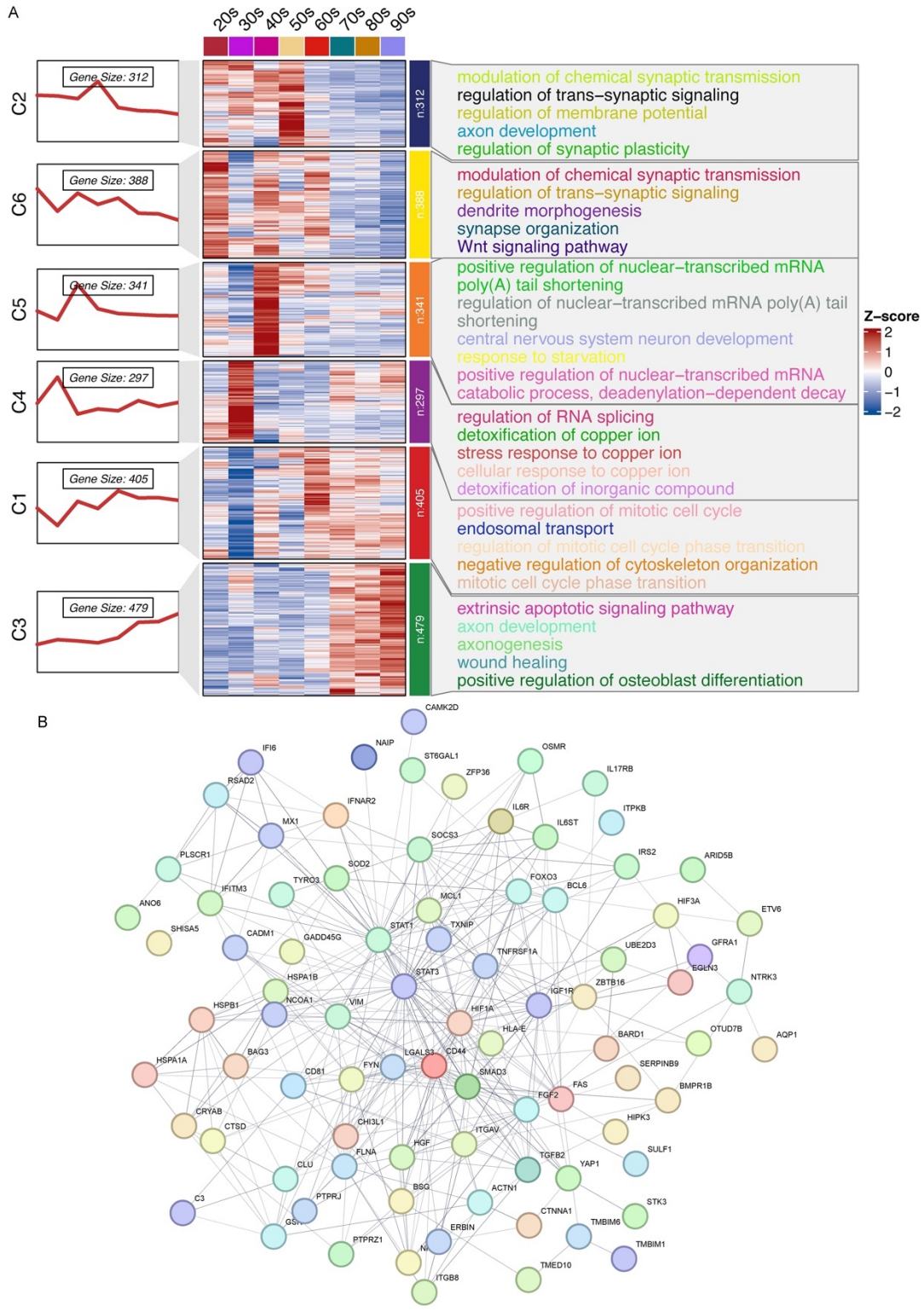
This PDF file includes:



Supplementary Figure. 1 Cell-specific markers and transcriptional noise analysis. A. Dot plot demonstrating subtype-specific marker expression patterns. B. Boxplot showing transcriptional noise in different cell types of PFC across the postnatal lifespanin

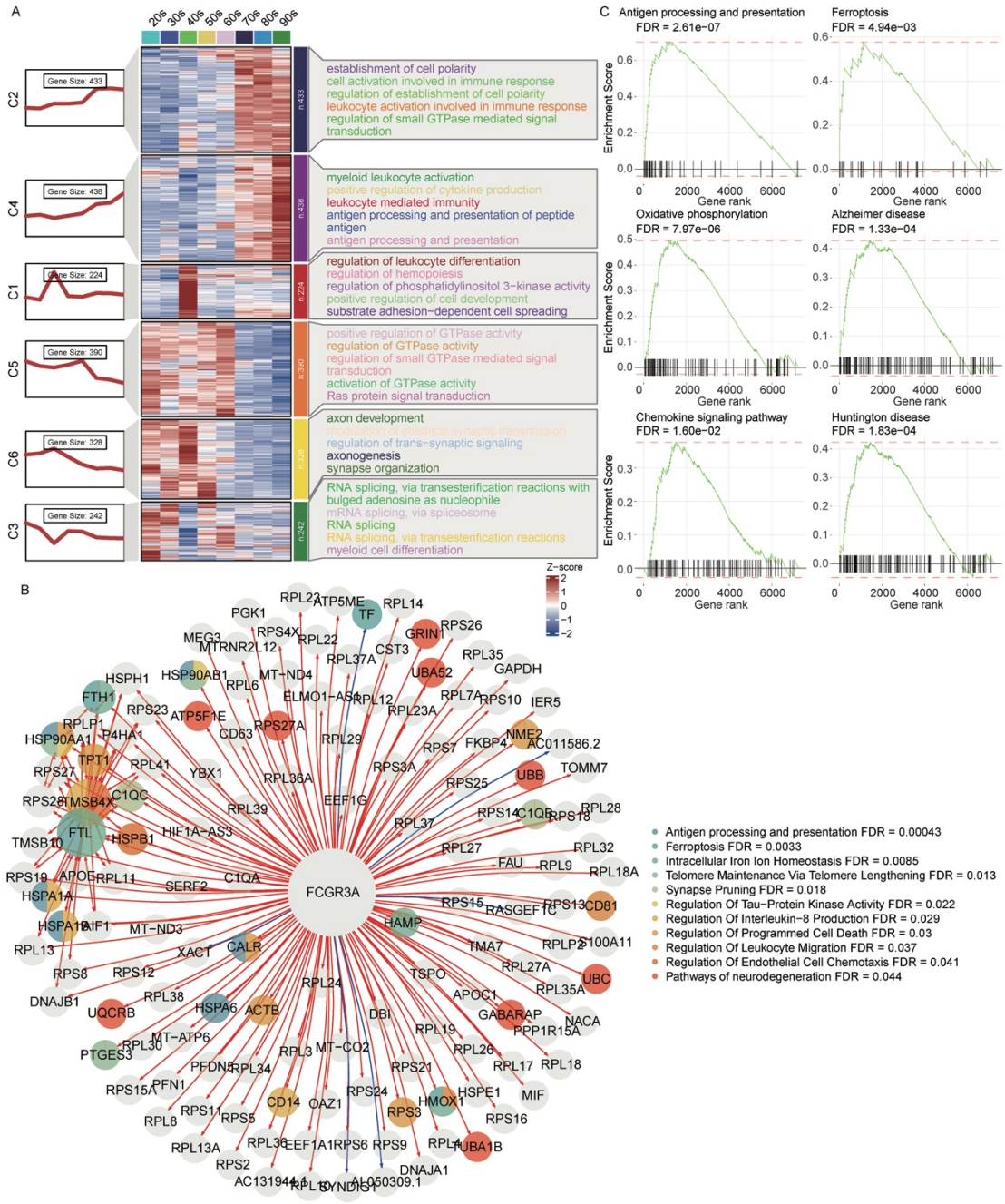

A
B
PERIOSTIN
PTH
CRH
GDF
NPR2
CXCL
AGT
IL16
BAFF
SOMATOSTATIN
OCLN
CX3C
VIP
NT
MHC−I
VEGF
PTN
ANGPT
EDN
CSF
ESAM
PDGF
BMP
IGF
TAC
CD39
CCK
PECAM1
MAG
COMPLEMENT
FN1
CD45
CD22
CDH1
MPZ
FGF
CADM
NCAM
NGL
NRG
NEGR
JAM
SEMA6
NECTIN
SEMA4
TENASCIN
NRXN
PACAP
TGFb
ENHO
ICAM
APP
VISTA
THY1
CDH5
CLDN
VISFATIN
PSAP
SEMA5
COLLAGEN
PTPRM
CNTN
LAMININ
SEMA3
CDH
EPHB
RELN
EPHA
EGF
SPP1
ANGPTL
KIT
THBS
CSPG4
PARs
PROS
L1CAM
ITGB2
AGRN
GAS
CD46
WNT
CD99
NOTCH
SEMA7
CHEMERIN
MHC−II
GALECTIN
GRN
ncWNT
HGF
ADGRE5
ACTIVIN
ANNEXIN
TRAIL
UCN
CALCR
HSPG
PVR
CD226
MIF
0.00
0.25
0.50
0.75
1.00
Relative information flow
0.0
0.3
0.6
0.9
Information flow
PFC_20s
PFC_30s
PFC_40s
PFC_50s
PFC_60s
PFC_70s
PFC_80s
PFC_90s

Supplementary Figure. 2 Comparison of cell communication and signaling pathway across age. A. The bar chart shows the relative information flow of intercellular interactions in the PFC across various age groups. B. The bar chart presents the strength of information flow of intercellular interactions in the PFC at different ages

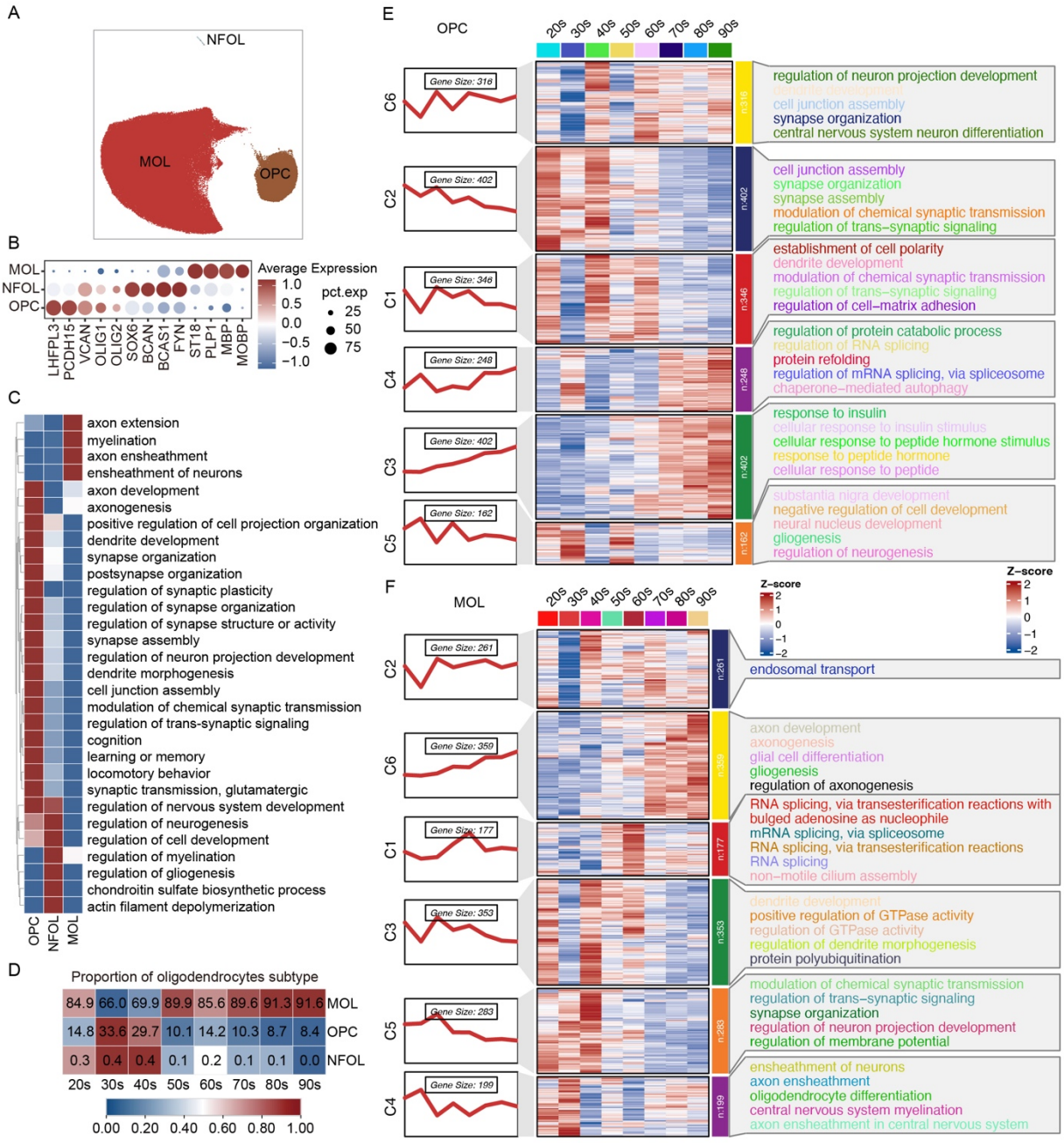


Supplementary Figure. 3 Temporal analysis of Astro's DEGs. A. Temporal analysis of Astro's DEGs throughout the life course. The line graph on the left represents the average expression levels

and trends of DEGs based on clustering in each age group, the heatmap in the middle represents the expression levels of DEGs in each cell, and the right side shows the functional enrichment annotations corresponding to the gene clusters (top 5 are displayed). B. PPI network of the C3 gene cluster.

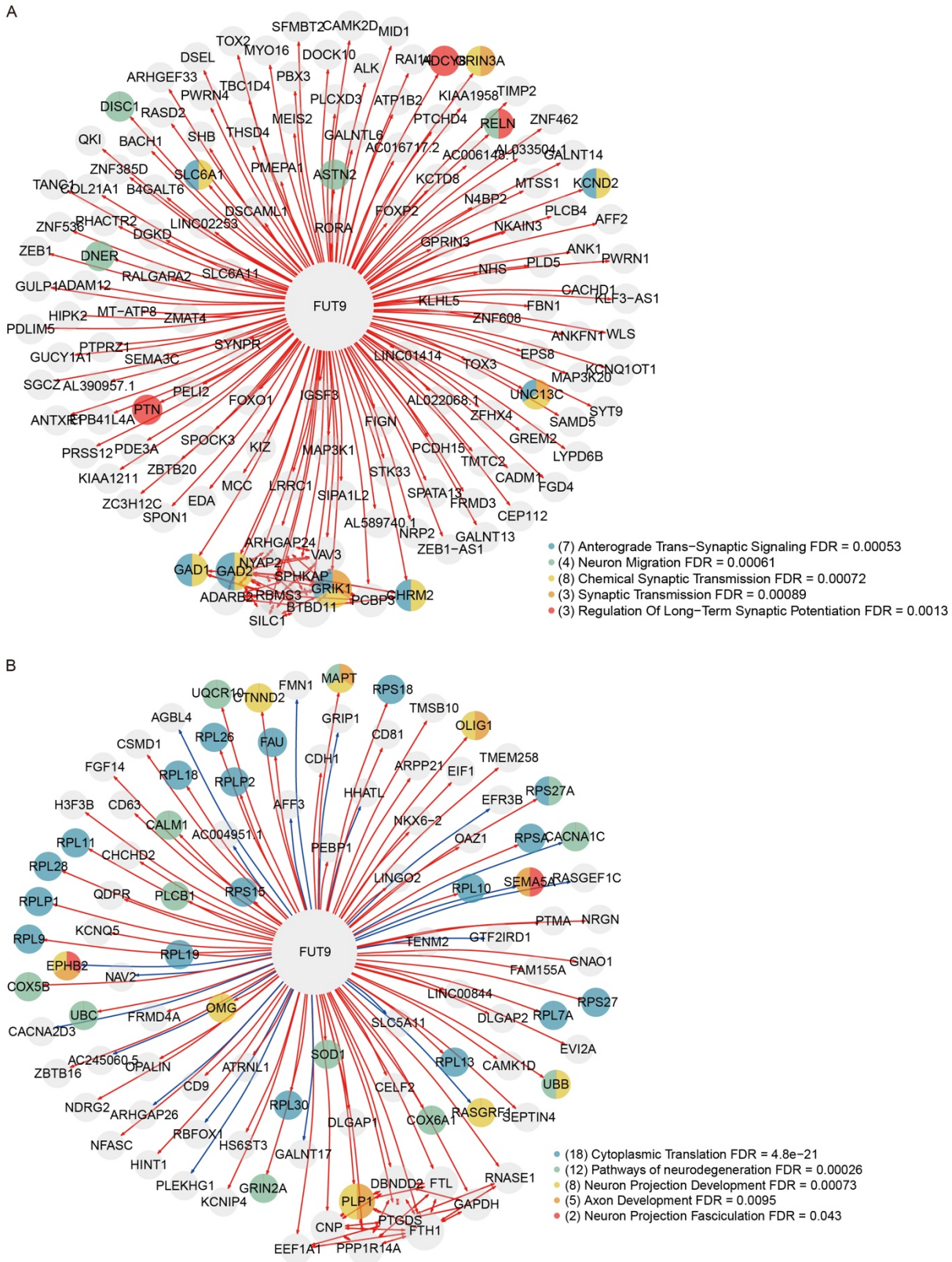


Supplementary Figure. 4 Temporal analysis of DEGs in Micro. A. Temporal analysis of DEGs in Micro throughout the life course. The left line graph represents the average expression levels and trends of DEGs based on clustering in each age group, the middle heatmap represents the expression levels of DEGs in each cell, and the right side shows the functional enrichment annotations corresponding to the gene clusters (top 5 are displayed). B. The ego-centered graph shows the connections between the KO gene (*FCGR3A*) and significantly perturbed genes (FDR < 0.05). Nodes are color-coded based on the membership of each gene in the enriched functional groups, and only those functional enrichments related to Mendelian disease phenotypes are displayed. C. GSEA analysis identified important gene sets related to perturbed genes.



Supplementary Figure. 5 Temporal analysis of DEGs in OPC and MOL. A. UMAP visualization of oligodendrocyte lineage. B. Dot plot showing the expression of marker genes in oligodendrocyte lineage subpopulations. C. The biological functions of different oligodendrocyte lineage cells. D. Proportion of oligodendrocyte lineage subpopulations in different groups. E and F respectively present the temporal analysis of DEGs in OPC and MOL throughout the life course. The left line graph represents the average expression level and trend of DEGs based on clustering in each age group, the middle heatmap represents the expression level of DEGs in each cell, and

the right side shows the functional enrichment annotations corresponding to the gene clusters (top 5 are displayed).


A
FUT9
SFMBT2
CAMK2D
MID1
TOX2
MYO16
DOCK10
DSEL
ALK
RAI14
ADCY8
BRIN3A
ARHGEF33
PBX3
TBC1D4
PWRN4
PLCXD3
ATP1B2
KIAA1958
TIMP2
DISC1
RASD2
MEIS2
PTCHD4
RELN
ZNF462
QKI
BACH1
SHB
THSD4
GALNTL6
AC016717.2
AC006148.1
AL033504.1
GALNT14
ZNF385D
SLC6A1
PMEPA1
ASTN2
KCTD8
MTSS1
KCND2
TANC1
CDL21A1
B4GALT6
N4BP2
PLCB4
DSCAML1
FOXP2
AFF2
ZNF536
RHACTR2
LINC02253
RORA
NKAIN3
DGKD
GPRIN3
ANK1
ZEB1
DNER
PLD5
PWRN1
RALGAPA2
SLC6A11
NHS
GULP1
ADAM12
CACHD1
KLF3-AS1
KLHL5
FBN1
HIPK2
MT-ATP8
ZMAT4
ZNF608
PDLIM5
ANKFN1
WLS
PTPRZ1
SYNPR
EPS8
GUCY1A1
SEMA3C
LINC01414
TOX3
KCNQ1OT1
MAP3K20
SGCZ
AL390957.1
PELI2
UNC13C
FOXO1
IGSF3
AL022068.1
SYT9
PTN
ZFHX4
SAMD5
ANTXR1
EPB41L4A
FIGN
GREM2
SPOCK3
KIZ
PCDH15
LYPD6B
PRSS12
PDE3A
MAP3K1
TMTC2
ZBTB20
STK33
CADM1
KIAA1211
MCC
LRRC1
SPATA13
FGD4
ZC3H12C
EDA
SIPA1L2
FRMD3
CEP112
SPON1
AL589740.1
NRP2
GALNT13
ARHGAP24
ZEB1-AS1
VAV3
NYAP2
GAD1
GAD2
SPHKAP
GRIK1
ADARB2
RBMS3
PCBP3
CHRM2
BTBD11
SILC1
(7) Anterograde Trans−Synaptic Signaling FDR = 0.00053
(4) Neuron Migration FDR = 0.00061
(8) Chemical Synaptic Transmission FDR = 0.00072
(3) Synaptic Transmission FDR = 0.00089
(3) Regulation Of Long−Term Synaptic Potentiation FDR = 0.0013
B
FUT9
MAPT
FMN1
UQCR10
CTNND2
RPS18
TMSB10
AGBL4
GRIP1
OLIG1
CD81
RPL26
FAU
CSMD1
CDH1
TMEM258
ARPP21
EIF1
FGF14
RPL18
RPLP2
HHATL
RPS27A
EFR3B
H3F3B
CD63
AFF3
NKX6-2
CALM1
AC004951.1
OAZ1
RPSA
CACNA1C
RPL11
PEBP1
CHCHD2
RPL28
LINGO2
RASGEF1C
SEMA5A
RPL10
QDPR
PLCB1
RPS15
RPLP1
PTMA
NRGN
KCNQ5
GTF2IRD1
RPL9
TENM2
RPL19
GNAO1
EPHB2
FAM155A
NAV2
COX5B
LINC00844
RPS27
UBC
FRMD4A
OMG
DLGAP2
RPL7A
CACNA2D3
SLC5A11
EVI2A
AC245060.5
SOD1
RPL13
CAMK1D
ZBTB16
OPALIN
ATRNL1
UBB
CD9
CELF2
NDRG2
RPL30
ARHGAP26
RASGRF2
SEPTIN4
DLGAP1
COX6A1
RBFOX1
NFASC
HS6ST3
GALNT17
HINT1
PLEKHG1
GRIN2A
DBNDD2
FTL
RNASE1
KCNIP4
PLP1
GAPDH
PTGDS
CNP
FTH1
EEF1A1
PPP1R14A
(18) Cytoplasmic Translation FDR = 4.8e−21
(12) Pathways of neurodegeneration FDR = 0.00026
(8) Neuron Projection Development FDR = 0.00073
(5) Axon Development FDR = 0.0095
(2) Neuron Projection Fasciculation FDR = 0.043

Supplementary Figure. 6 Virtual KO analysis of FUT9 in ExN and MOL . A, B. The ego-centered graph shows the connections between the KO gene (*FUT9*) and significantly perturbed genes (FDR < 0.05) in ExN (A) and MOL (B). Nodes are color-coded based on the membership of each gene in the enriched functional groups, and only those functional enrichments related to Mendelian disease phenotypes are displayed. C. GSEA analysis identified important gene sets related to perturbed genes.

Supplementary Tables

Supplementary Table 1
Sample database source and basic information.

Supplementary Table 2
The number of cell for cell type.

Supplementary Table 3
The number of DEG for cell types (|logFC|≧0.25, FDR<0.05).

Supplementary Table 4
Genes perturbed by the virtual-KO of FCGR3A in aging Micro (FDR < 0.05).

Supplementary Table 5
Genes perturbed by the virtual-KO of FUT9 in aging ExN and MOL (FDR < 0.05).