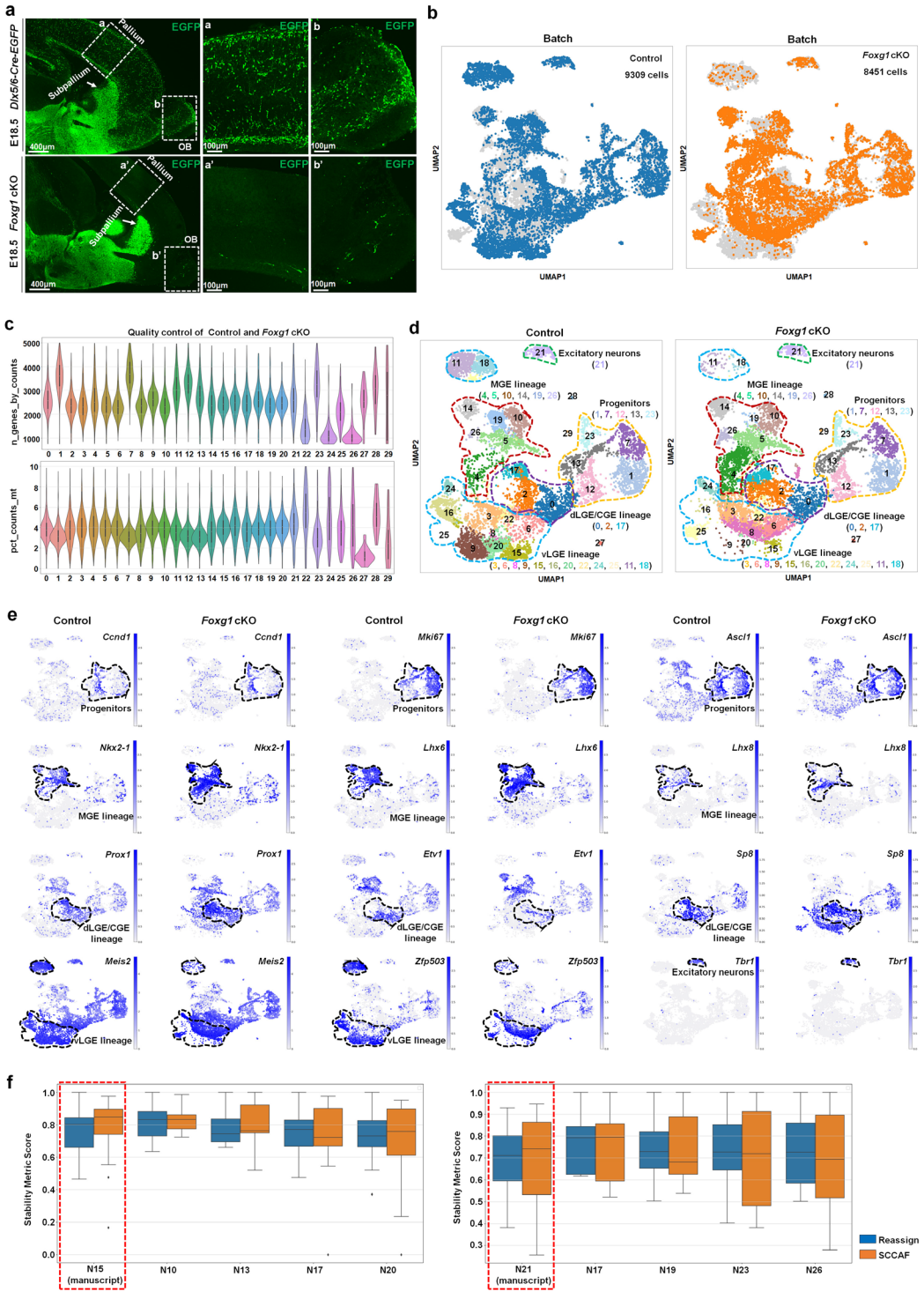
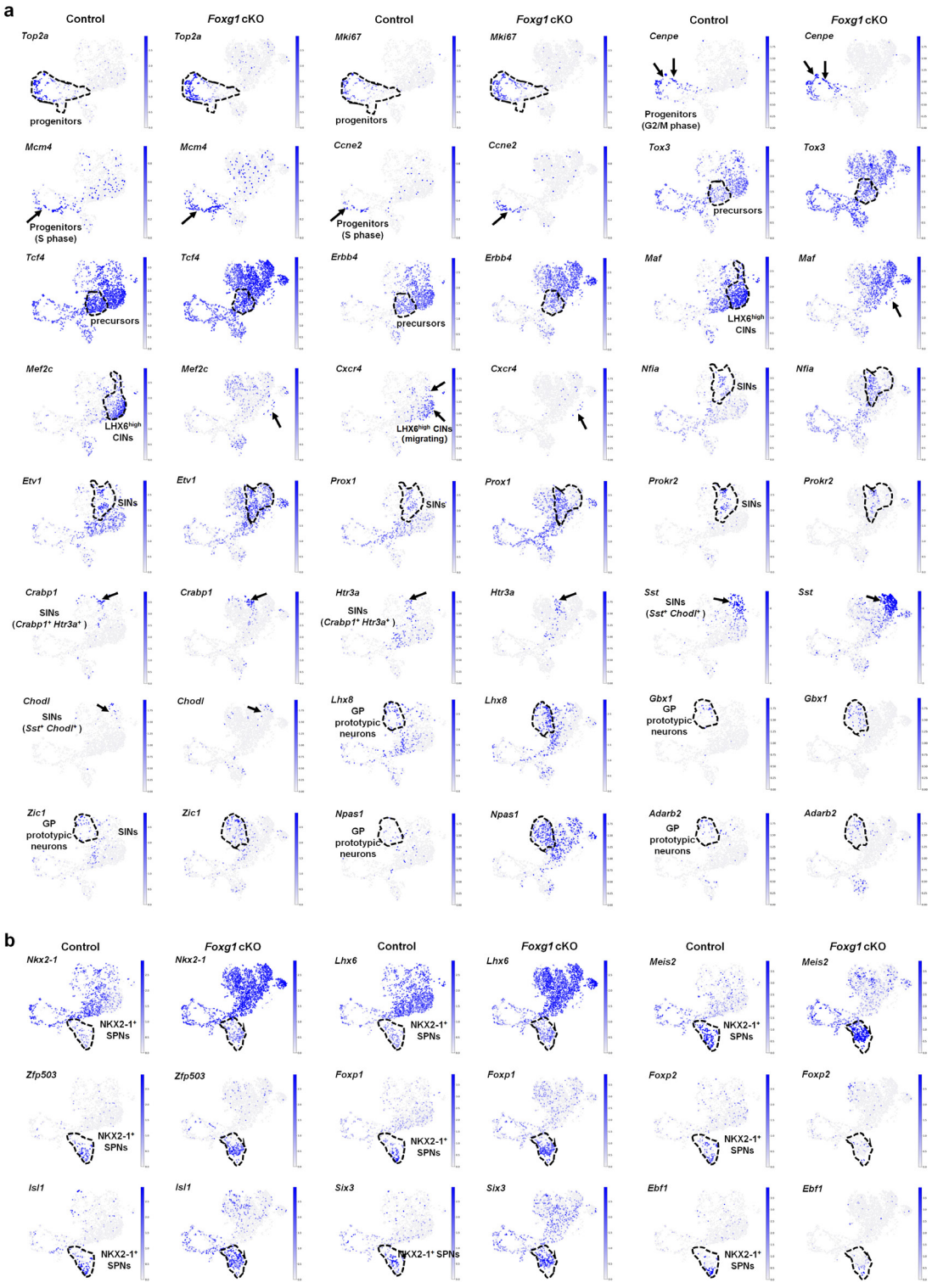
Supplementary Figures and Figure Legends



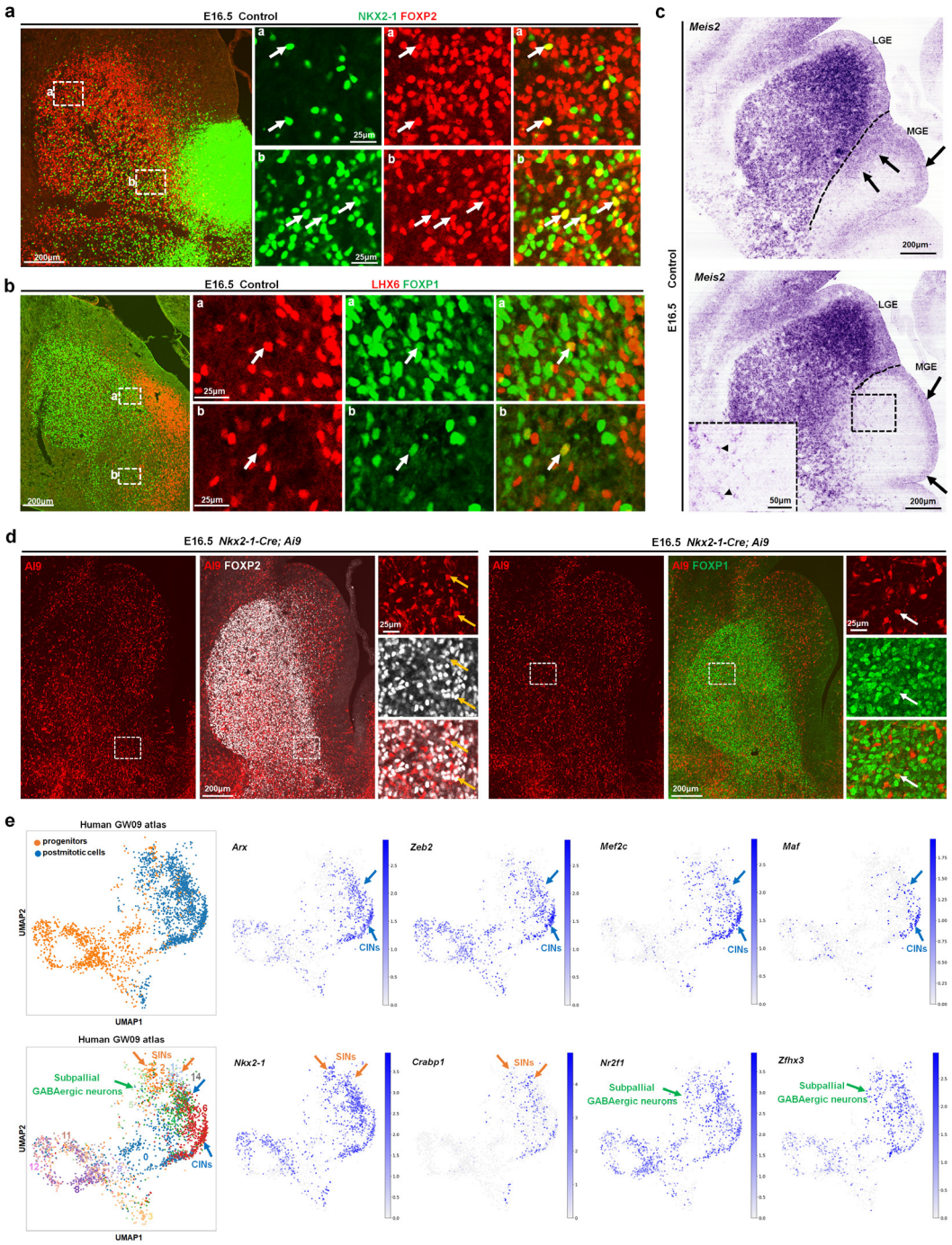
Supplementary Fig. 1 | Quality control of the scRNA-seq dataset and classification of cell types in the GE at E16.5. Related to Fig. 1. **a**, Immunostaining for anit-EGFP in control and *Foxg1* cKO mice at E18.5. **b**, UMAP plots to inspect

batch correction. Top: 9,309 cells in the control; bottom: 8,451 cells in the *Foxg1* cKO. **c**, Quality control of the integrated scRNA-seq dataset (control and *Foxg1* cKO). Top: number of genes per cell for each cluster. Bottom: percentage of mitochondrial gene counts per cell for each cluster. **d**, UMAP plots of cells from the E16.5 GEs and cell type identification in control and *Foxg1* cKO. Color: cell identity. **e**, UMAP plots showing expression maps of marker genes for GE progenitors (*Ccnd1*, *Mki67*, *Ascl1*), MGE lineage (*Nkx2-1*, *Lhx6*, *Lhx8*), dLGE/CGE lineage (*Prox1*, *Etv1, Sp8*), vLGE lineage (*Meis2, Zfp503*), and excitatory neurons (*Tbr1*) in control and *Foxg1* cKO mice. **f,** Box plots visualization of stability metric scores calculated using scTriangulate, including SCCAF and reassign scores for MGE cell populations (N=15, 10, 13, 17, 20) and dLGE/CGE cell populations (N=21, 17, 19, 23, 26).



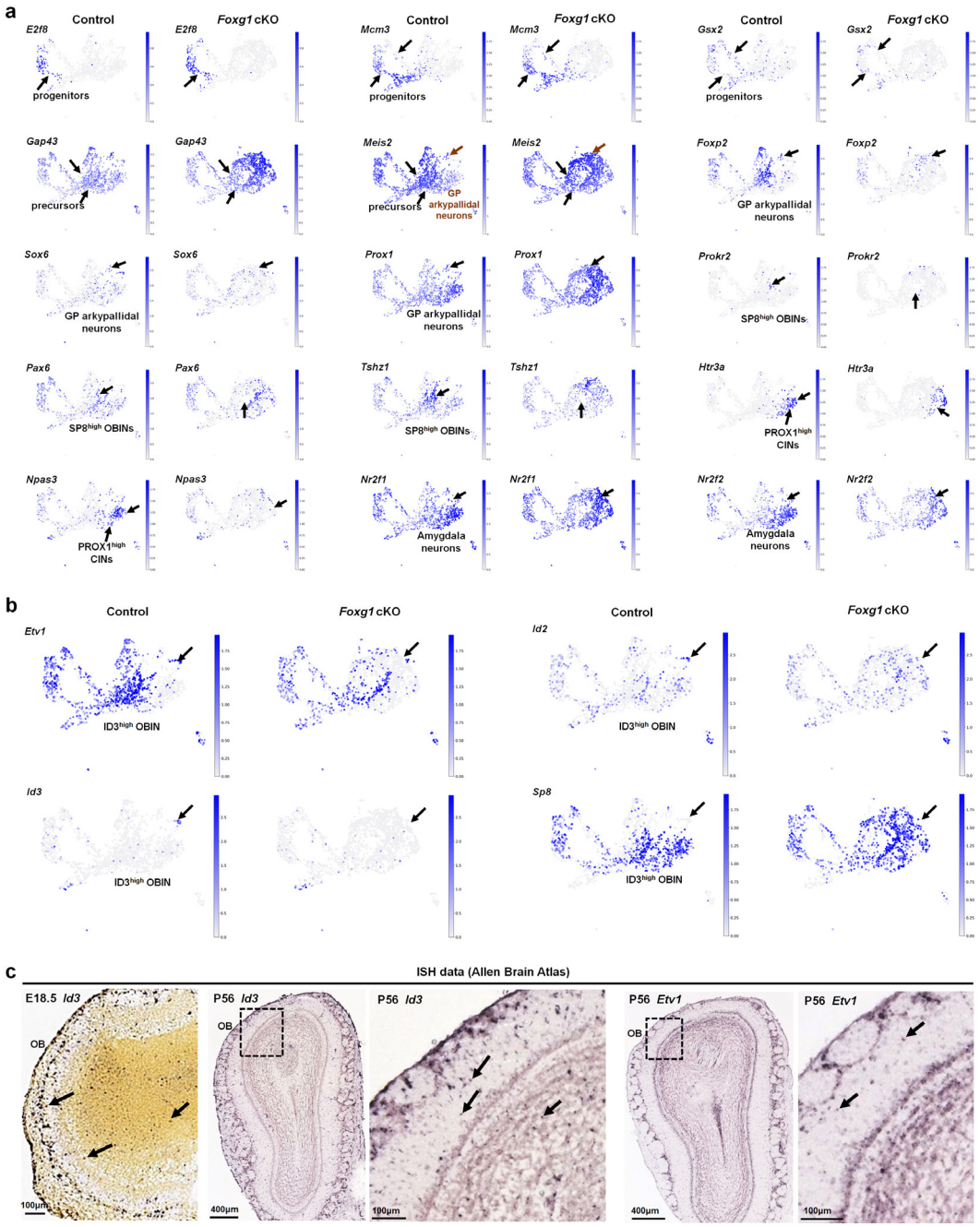
Supplementary Fig. 2 | Annotated cell types of the MGE lineage at E16.5 from the scRNA-seq dataset. Related to Fig. 1. **a**, **b**, UMAP plots showing expression maps of marker genes for the cell types of MGE lineage in control and *Foxg1* cKO mice, as follows progenitors (*Top2a*, *Mki67, Cenpe, Mcm4, Ccne2*), precursors (*Tox3*,

Tcf4, *Erbb4*), LHX6^{high} PINs (*Maf, Mef2c*, *Cxcr4)*, SINs (*Nfia*, *Etv1*, *Prox1*, *Prokr2, Crabp1, Htr3a, Sst, Chodl*), GP prototypic neurons (*Lhx8*, *Gbx1*, *Zic1, Npas1, Adarb2*), and NKX2-1^{+} SPNs (*Nkx2-1*, *Lhx6*, *Meis2*, *Zfp503*, *Foxp1*, *Foxp2*, *Isl1*, *Six3*, *Ebf1*).



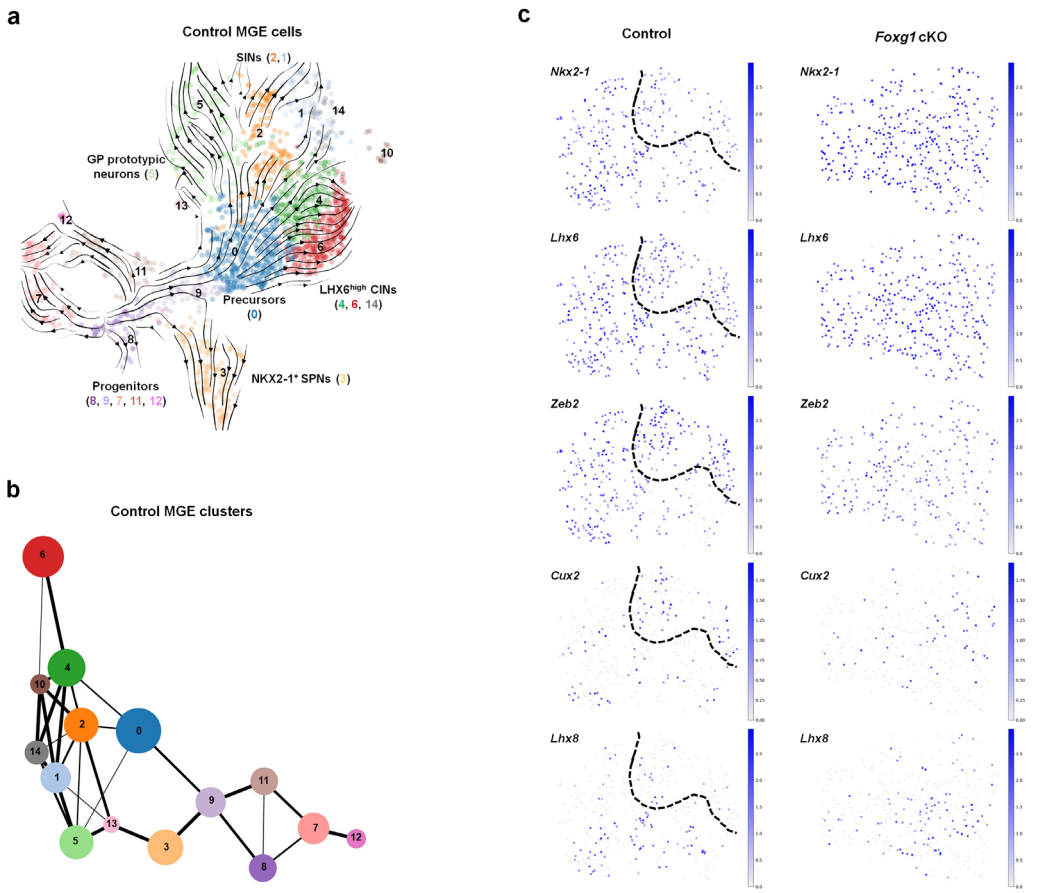
Supplementary Fig. 3 | Detected MGE-derived SPNs at E16.5. Related to Fig. 1. **a**, **b**, Double immunostaining of anti-NKX2-1 with FOXP2 and anti-LHX6 with FOXP1 in the control mice at E16.5. **c**, *In situ* hybridization of *Meis2* in the control mice at E16.5. Arrows indicate that *Meis2* is expressed at a low level in MGE progenitors. Arrowheads indicate that *Meis2*$^{+}$cells migrate towards the striatum. **d**, Double

immunostaining of anti-AI9 with FOXP2 or FOXP1 in *Nkx2-1-Cre; Ai9* mice at E16.5. Arrows indicate that small portions of $AI9^{+}FOXP1^{+}$ and $AI9^{+}FOXP2^{+}$ neurons in the SPNs. **e**, Integrated human GW09 cells with control MGE cells, and visualized in UMAP. Color: cell identity. UMAP plots showing expression maps of marker genes for CINs (*Arx*, *Zeb2*, *Mef2c*, *Maf*), SINs (*Nkx2-1*, *Crabp1*), subpallial GABAergic neurons (*Nr2f1*, *Zfhx3*) in human GW09 cells.

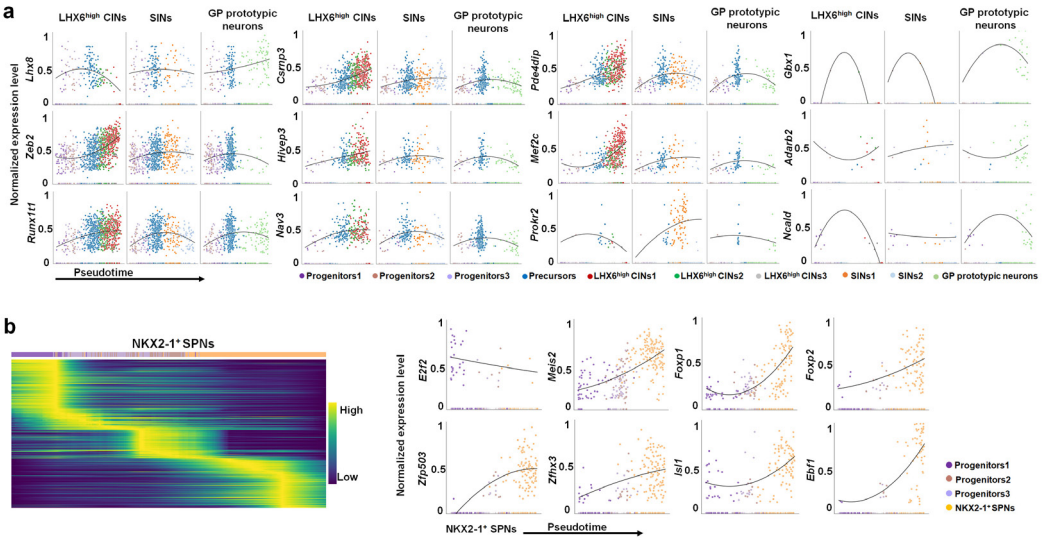


Supplementary Fig. 4 | Annotated cell types of the dLGE/CGE lineage at E16.5 from the scRNA-seq dataset. Related to Fig. 1. **a**, **b**, UMAP plots showing expression maps of marker genes for the cell types of dLGE/CGE lineage in control and *Foxg1* cKO mice, as follows progenitors (*E2f8, Mcm3, Gsx2*), precursors (*Gap43*, *Meis2*), GP arkypallidal neurons (*Meis2*, *Foxp2, Sox6*, *Prox1*), SP8^{high} OBINs (*Prokr2, Pax6*, *Tshz1, Sp8*), PROX1^{high} PINs (*Htr3a*, *Npas3),* amygdala neurons (*Nr2f1*, *Nr2f2*),

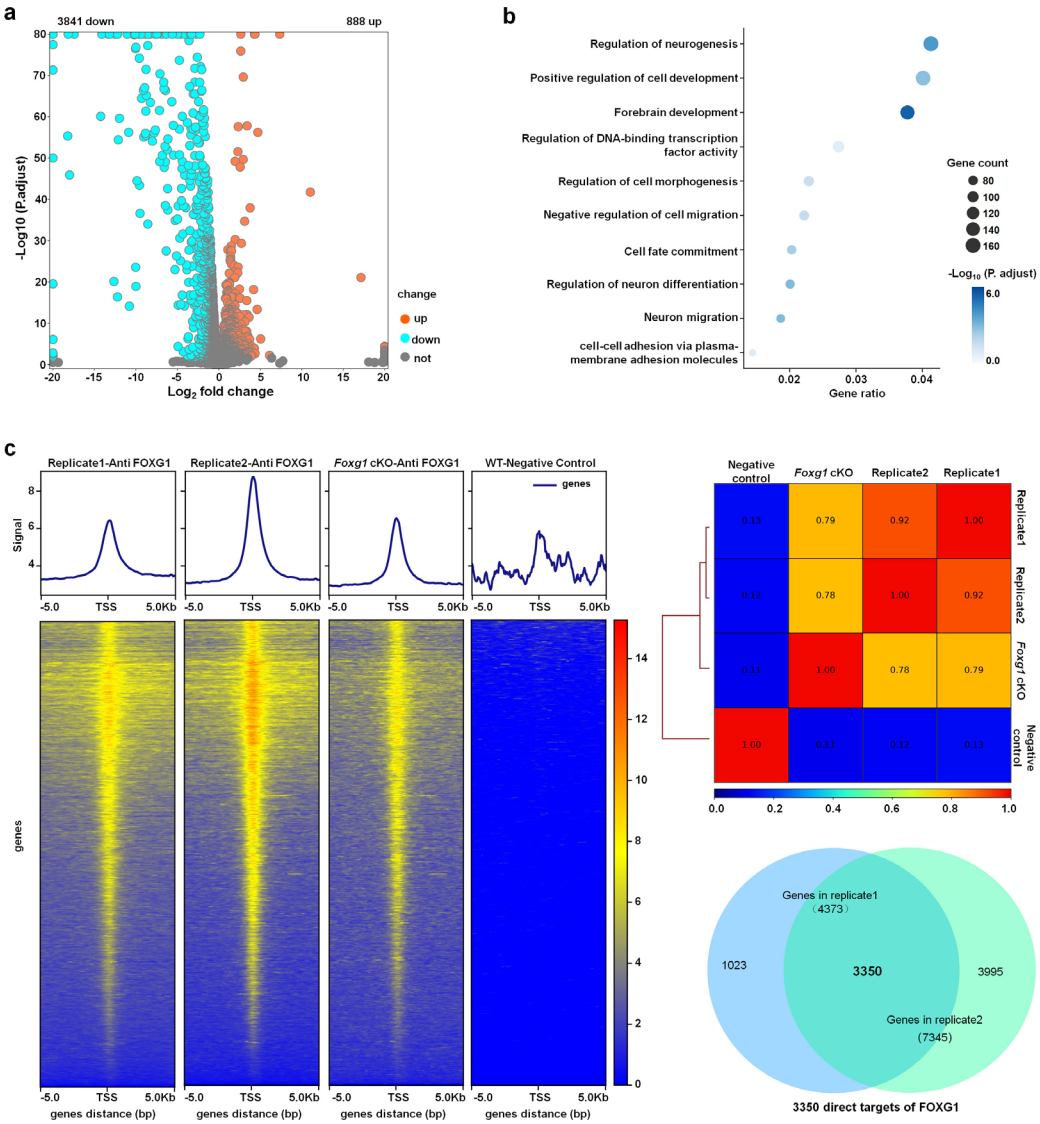
and ID3^{high} OBINs (*Etv1*, *Id2*, *Id3*). **c**, *In situ* hybridization of *Id3* at E18.5 (Allen Brain Atlas, http://developingmouse.brain-map.org/experiment/show/100076262) and P56 (Allen Brain Atlas, https://mouse.brain-map.org/experiment/show?id=74724763), and *Etv1* at P56 (Allen Brain Atlas, https://mouse.brain-map.org/experiment/show?id=72119595). Arrows indicate the scattered OBINs.



Supplementary Fig. 5 | Developmental trajectories of MGE cells and subtypes of MGE precursors. Related to Fig. 2. **a**, Development trajectories of control MGE cells calculated using the CellRank framework. Streamlines of pseudotime order indicate the forward developmental direction of MGE lineage. Color: cell identity. **b**, Abstracted PAGA graph showing the structure connectivity among cell clusters in control MGE lineages. Colored nodes represent the cell clusters and weighted edges reflect the PAGA connectivity between these clusters. **c**, UMAP plots showing the subtypes of MGE precursors (Cluster 0) and the expression levels (normalized) of genes specific for Pre-CINs (*Lhx6*, *Zeb2,* and *Cux2*) and Pre-SINs/GP prototypic neurons (*Nkx2-1*, *Lhx6,* and *Lhx8*) in control and *Foxg1* cKO mice.

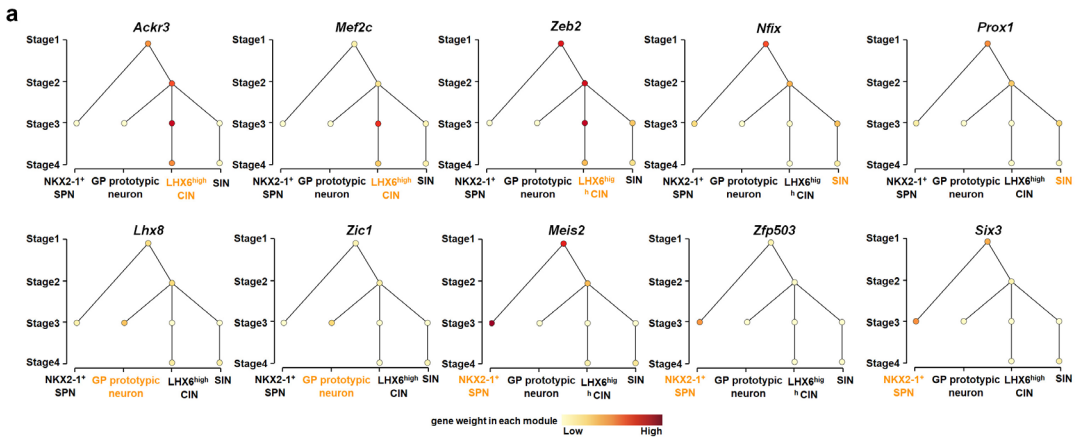


Supplementary Fig. 6 | The expression levels of representative genes along the developmental trajectories of the MGE lineage. Related to Fig. 3. **a**, Scatterplots showing the expression levels of representative genes along the developmental trajectories of LHX6^{high} CINs, SINs, and GP prototypic neurons in the control mice. Dots: single cells. Vertical axis: normalized gene expression. Horizontal axis: cellular pseudotime of each trajectory. Color: cell identity. **b**, Heatmap of the top 500 most dynamic genes cascades for the NKX2-1^{+} SPN trajectory in the control mice. Cells are ordered in columns based on their pseudotime. Color of top bars: cell identity. Color bar: smoothened spliced mRNA counts. Scatterplots showing the expression levels of representative genes along the NKX2-1^{+} SPN developmental trajectory in the control mice.

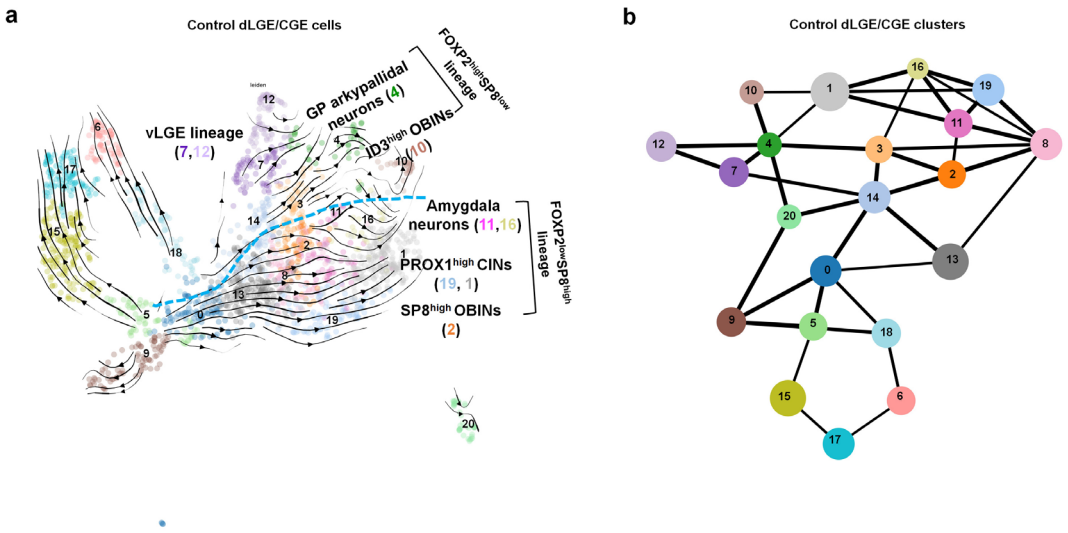


Supplementary Fig. 7 | Identification of the FOXG1-driven transcriptional programs in the MGE lineage. Related to Fig. 3. **a**, Volcano plot showing the MGE DEGs between the two genotypes. **b**, Bubble plot showing GO terms enriched in the MGE DEGs. **c**, Analyses of CUT&Tag-seq in wild-type and *Foxg1* cKO mice GE cells at E16.5. Heatmaps showing the CUT&Tag signals 5.0 kb upstream and 5.0 kb downstream of the transcription start sites in wild-type replicates 1&2 and *Foxg1* cKO (FOXG1 antibody was used), and negative control (no antibody). Hierarchically

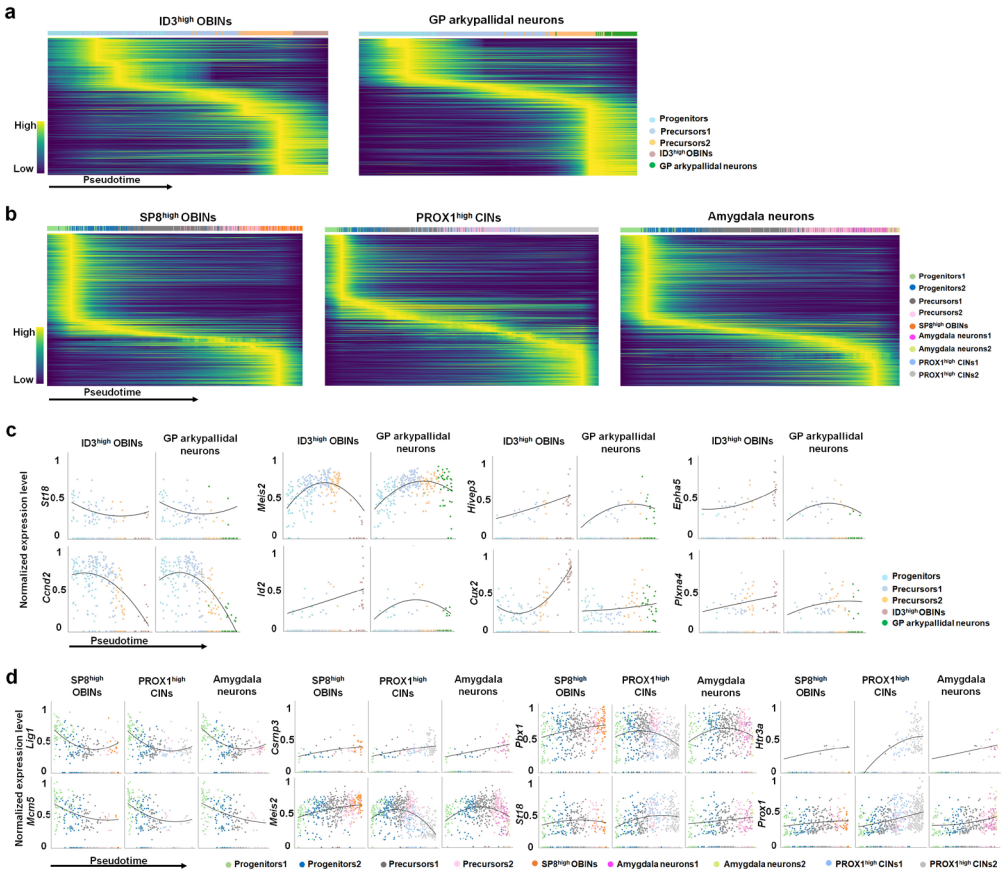
clustered correlation matrix of the negative control, *Foxg1* cKO, replicate 1&2. Venn plot: the number of shared genes and unique genes of replicates 1&2.



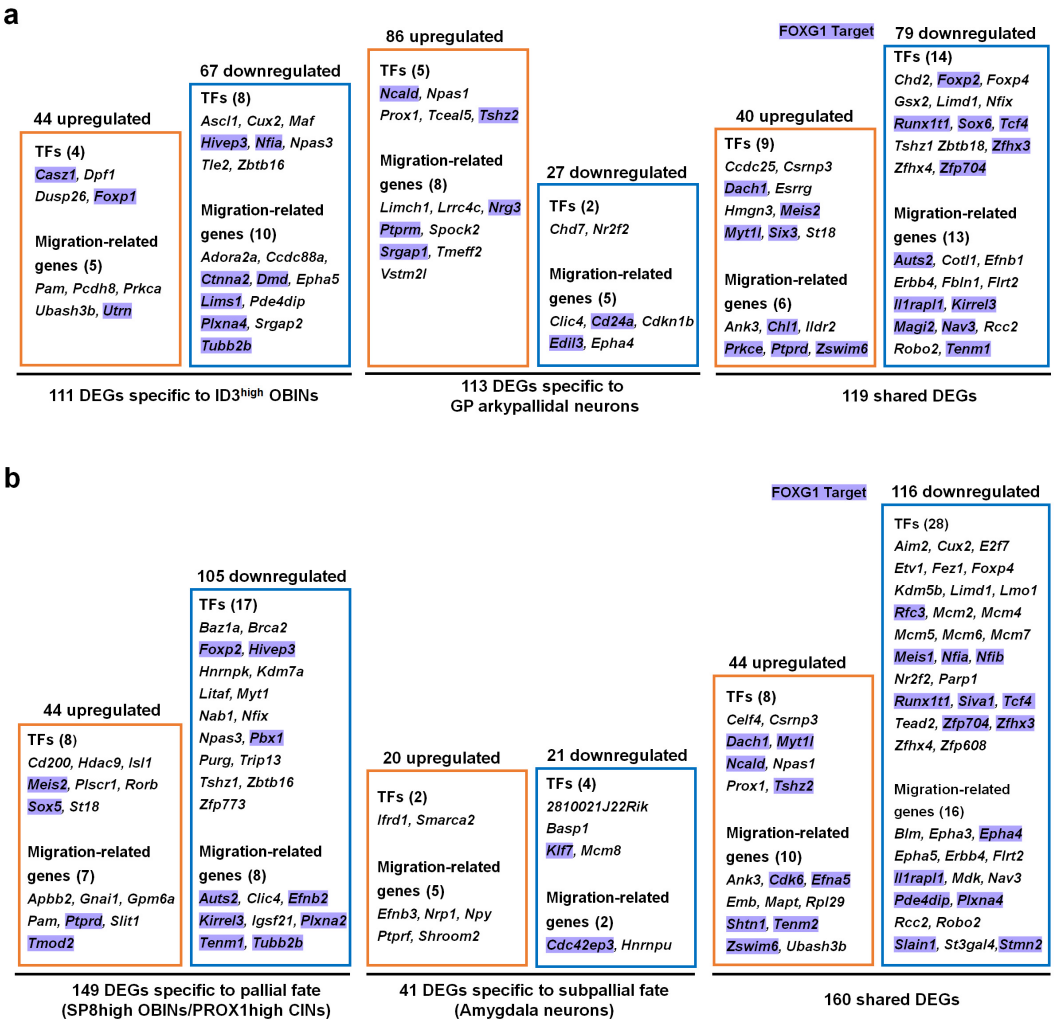
Supplementary Fig. 8 | Annotated gene programs of connected modules in the MGE lineage. Related to Fig. 3. **a**, Gene programs of connected modules in MGE lineage. Gene programs and corresponding neurons were annotated according to the weight of marker genes, as follows LHX6^{high} PIN (*Ackr3*, *Mef2c, Zeb2*), SINs (*Nfix*, *Prox1*), GP prototypic neurons (*Lhx8*, *Zic1*), and NKX2-1^{+} SPN (*Meis2*, *Zfp503*, *Six3*). Dots: gene modules, dot colors: the weights of the genes in each module, lines: connections between modules.



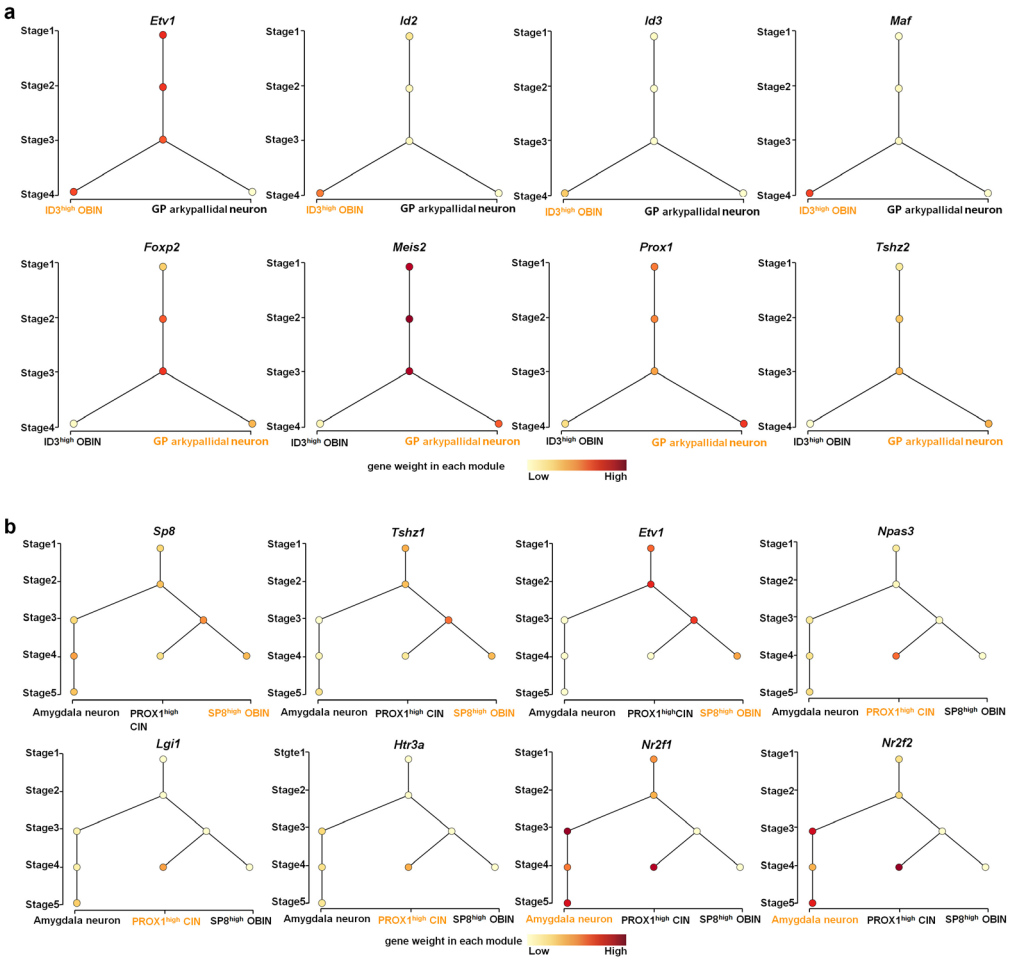
Supplementary Fig. 9 | Developmental trajectories of dLGE/CGE cells. Related to Fig. 4. **a**, Development trajectories of control dLGE/CGE cells calculated using the CellRank framework. Streamlines of pseudotime order indicate the forward developmental direction of MGE lineage. **b**, Abstracted PAGA graph showing the structure connectivity among the cell clusters in the control dLGE/CGE lineages. Colored nodes represent the cell clusters and weighted edges reflect the PAGA connectivity between these clusters.



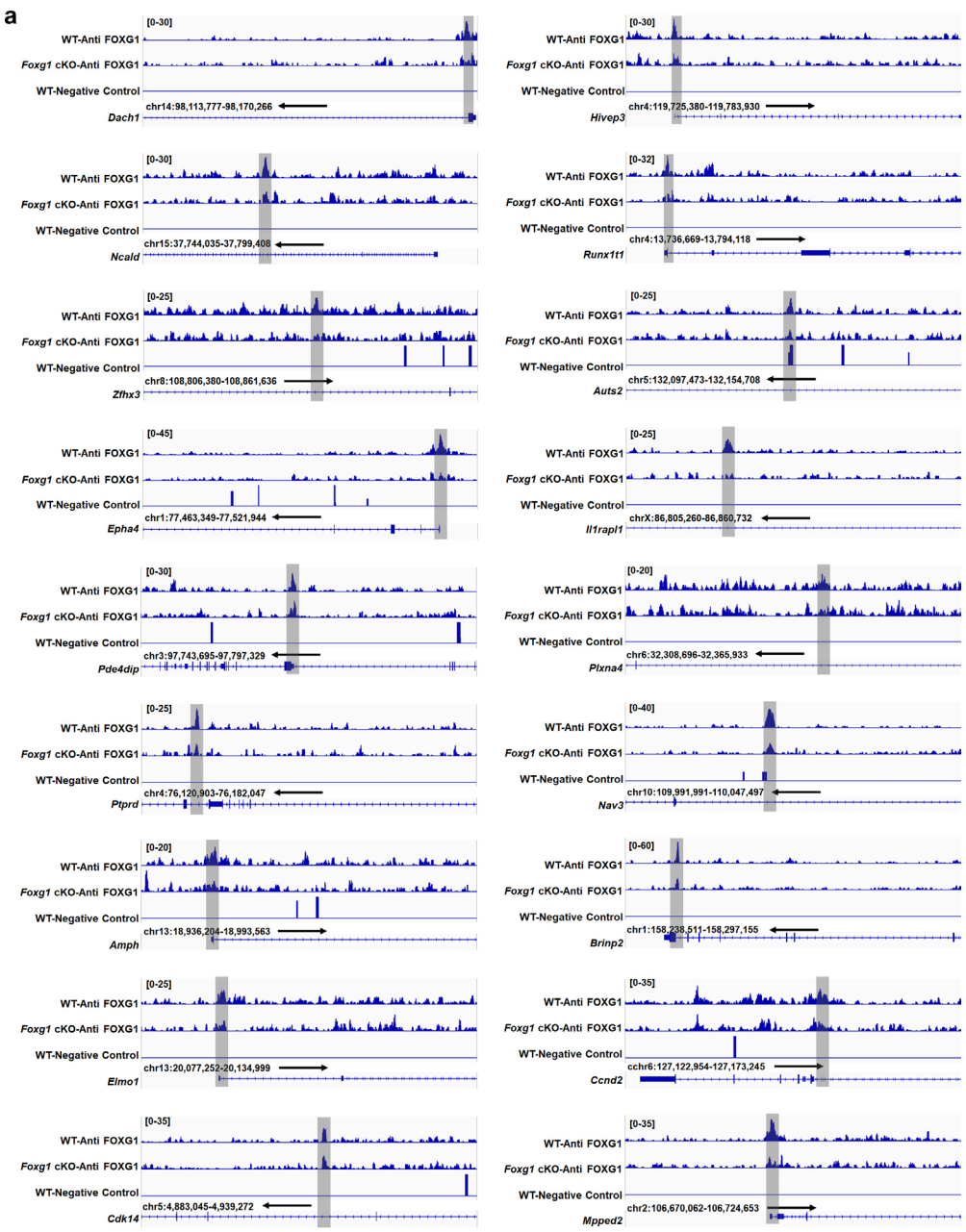
Supplementary Fig. 10 | The expression levels of representative genes along the developmental trajectories for FOXP2^{high}SP8^{low} and FOXP2^{low}SP8^{high} dLGE/CGE lineages. Related to Fig. 5. **a**, **b**, Heatmap of the top 500 most dynamic genes cascades for the FOXP2^{high}SP8^{low} and FOXP2^{low}SP8^{high} dLGE/CGE lineage trajectories in control mice. Cells are ordered in columns based on their pseudotime. Color of top bars: cell identity. Color bar: smoothened spliced mRNA counts. **c**, **d**, Scatterplots showing the expression levels of representative genes along the developmental trajectories of the FOXP2^{high}SP8^{low} and FOXP2^{low}SP8^{high} dLGE/CGE lineage in the control mice. Dots: single cells. Vertical axis: normalized gene expression. Horizontal axis: cellular pseudotime of each trajectory. Color: cell identity.



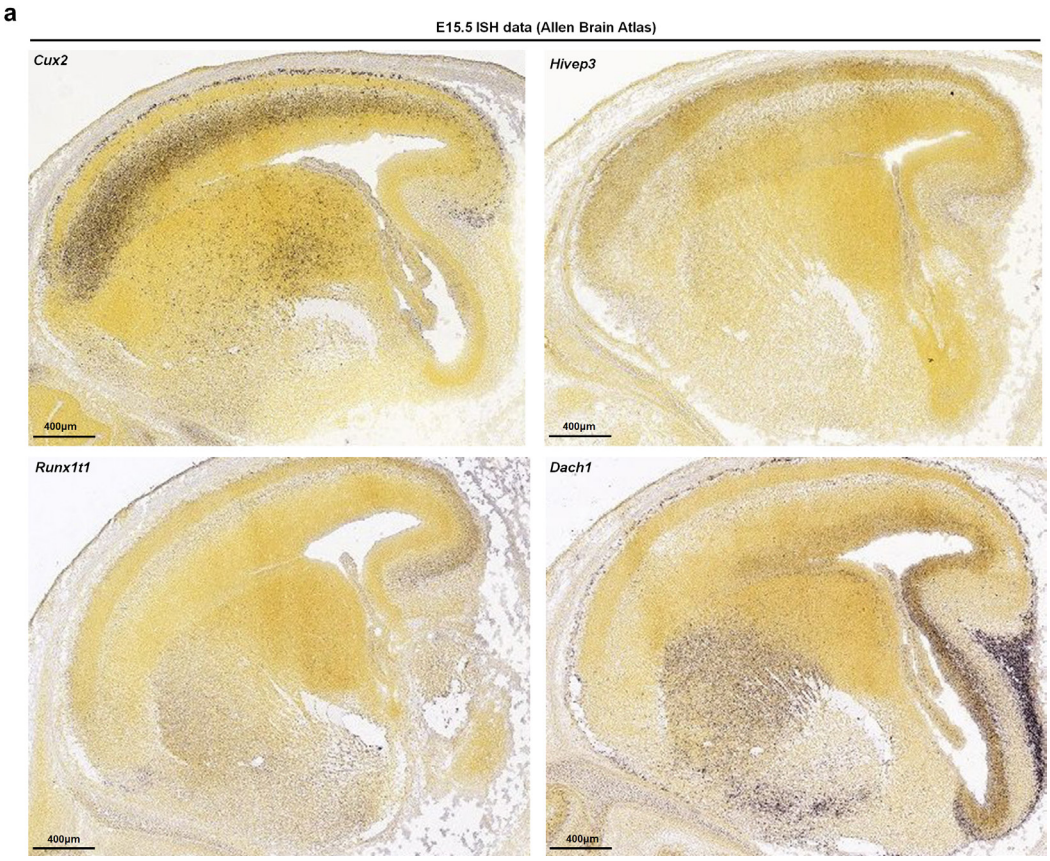
Supplementary Fig. 11 | Identification of the three category DEGs of FOXP2^{high}SP8^{low} and FOXP2^{low}SP8^{high} dLGE/CGE lineages. Related to Fig. 5. **a**, **b**, Bar chart showing the identification of the three category DEGs of FOXP2^{high}SP8^{low} and FOXP2^{low}SP8^{high} dLGE/CGE lineages. Highlighted genes are direct targets of FOXG1 (refer to Supplementary Data 5, 8, 9).



Supplementary Fig. 12 | Annotated gene programs of connected modules in FOXP2^{high}SP8^{low} and FOXP2^{low}SP8^{high} dLGE/CGE lineages. Related to Fig. 5. **a**, **b**, Gene programs of connected modules in the FOXP2^{high}SP8^{low} and FOXP2^{low}SP8^{high} dLGE/CGE lineages. Gene programs and corresponding neurons were annotated according to the weight of marker genes, as follows ID3^{high} OBIN (*Etv1, Id2, Id3, Maf),* GP arkypallidal neurons (*Foxp2*, *Meis2*, *Prox1, Tshz2*), SP8^{high} OBIN (*Sp8*, *Tshz1*, *Etv1*), PROX1^{high} CIN (*Npas3*, *Lgi1*, *Htr3a*), and amygdala neurons (*Nr2f1, Nr2f2*). Dots: gene modules, dot color: the weights of the genes in each module, lines: connections between modules.



Supplementary Fig. 13 | FOXG1 directly regulate the 19 genes among the 40 overlapping genes. Related to Fig. 6. **a**, The IGV diagram showing FOXG1 binding position on the 18 genes from CUT&Tag data. The binding signal of FOXG1 was significantly enriched at the promoter or the intron regions of the of the 18 genes in WT GE cells, while the binding signal of FOXG1 was decreased in *Foxg1* cKO GE cells.



Supplementary Fig. 14 | The expression patterns of FOXG1 drives common molecular determinants. Related to Fig. 7. **a**, *In situ* hybridization of *Cux2*, *Hivep3, Runx1t1,* and *Dach1* at E15.5 control brains (Allen Brain Atlas, *Cux2*: http://developingmouse.brain-map.org/experiment/show/100046728; *Hivep3*: http://developingmouse.brain-map.org/experiment/show/100085249; *Runx1t1*: http://developingmouse.brain-map.org/experiment/show/100057664; *Dach1*: http://developingmouse.brain-map.org/experiment/show/100057508).