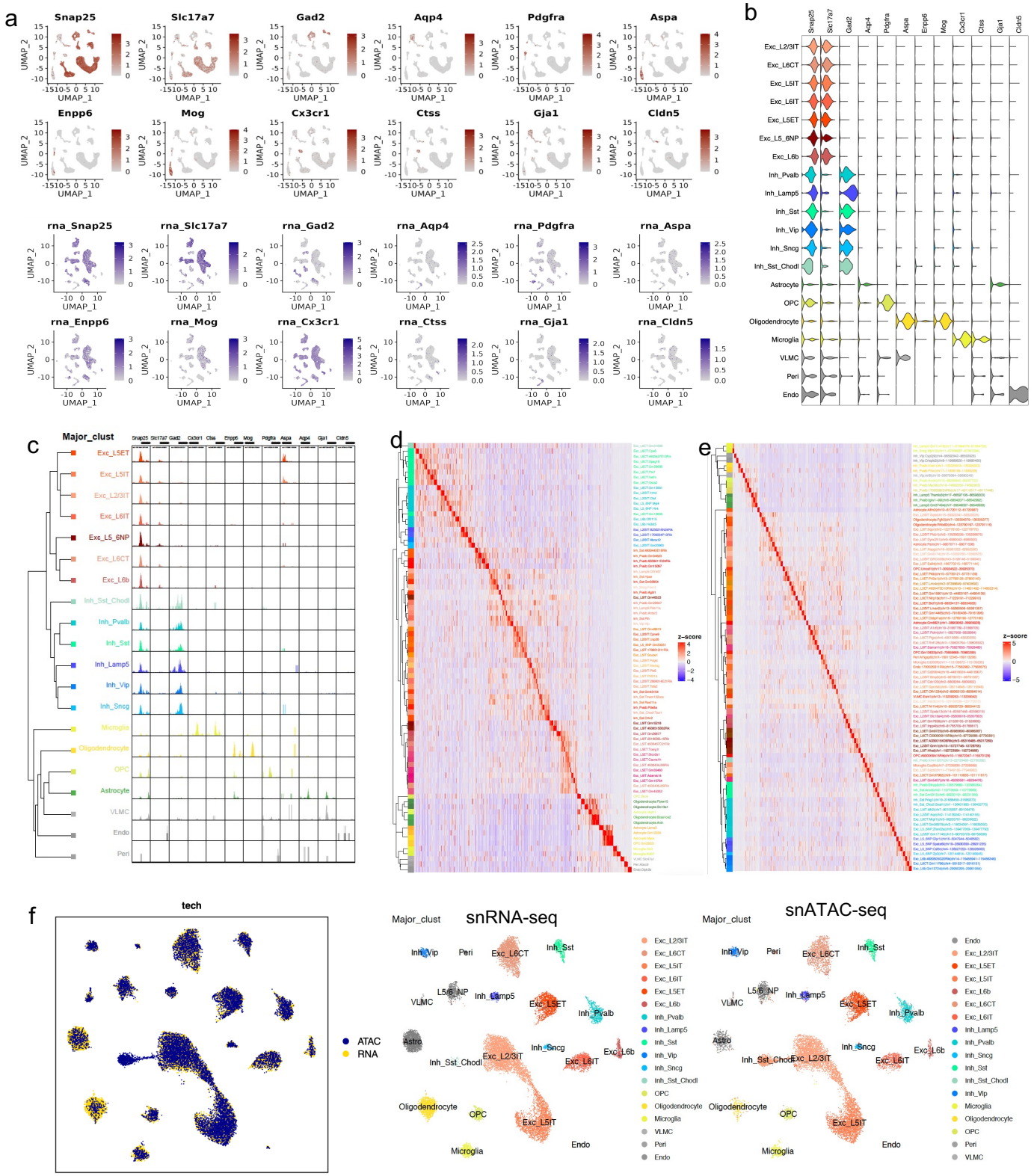
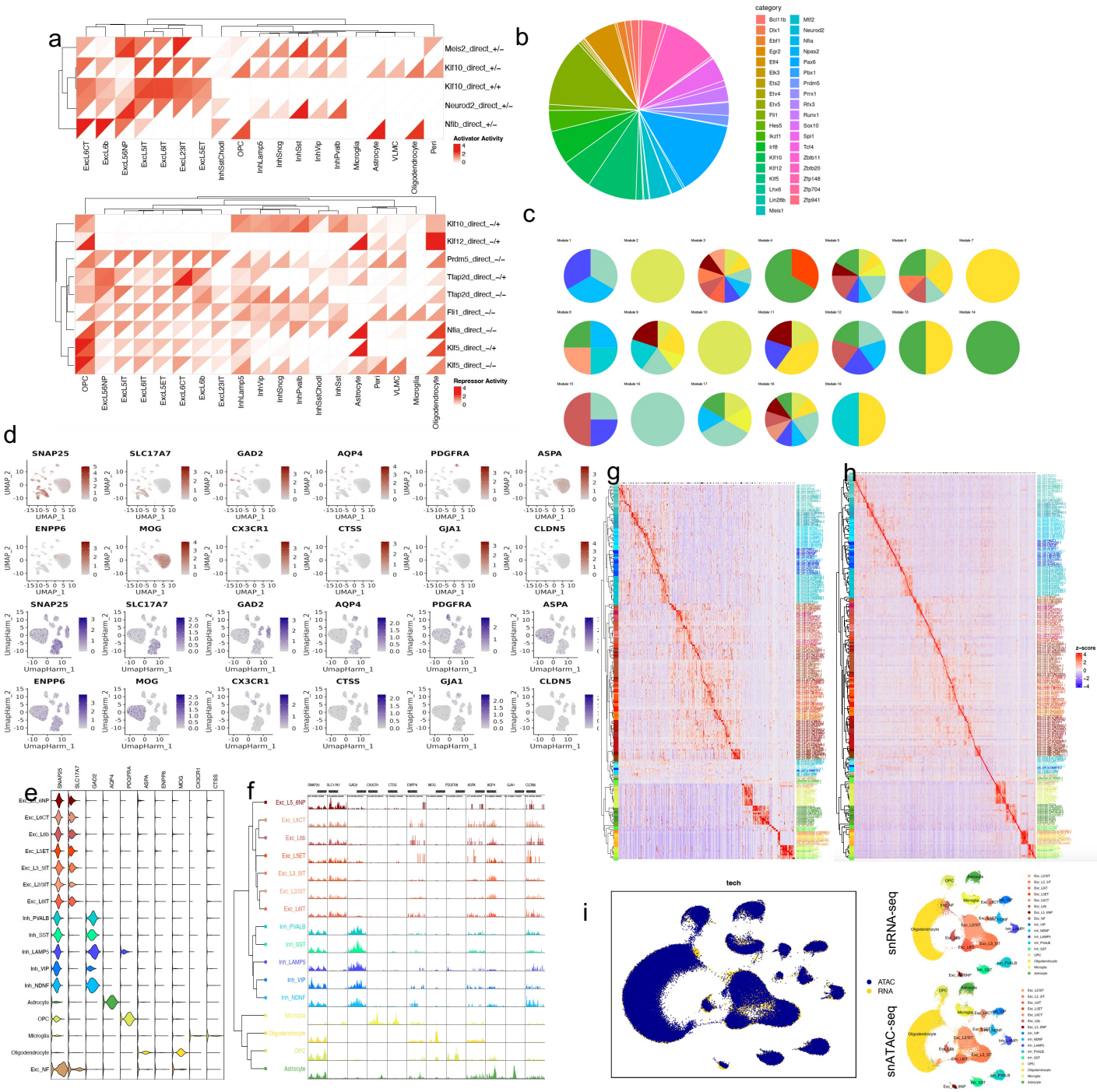
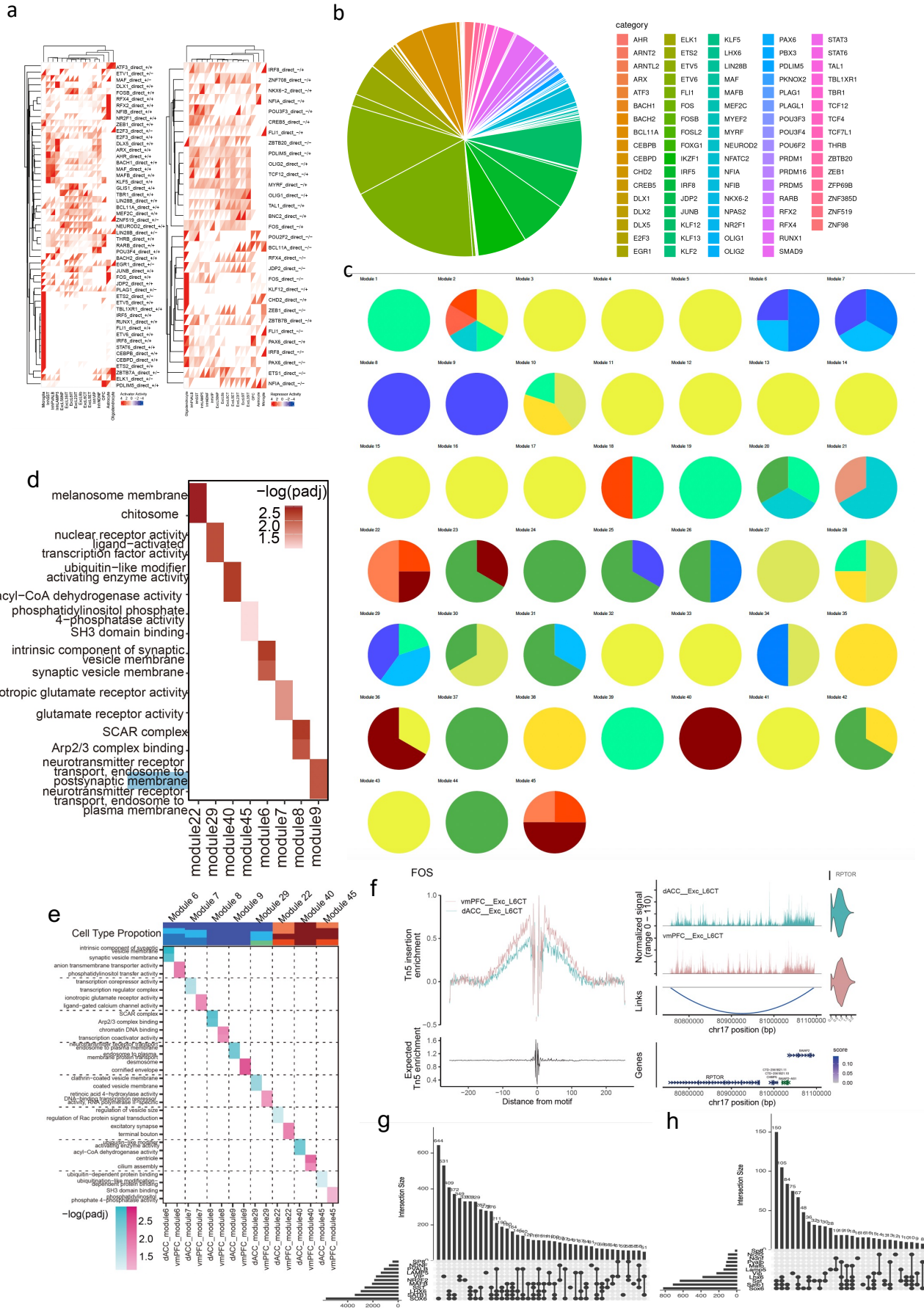


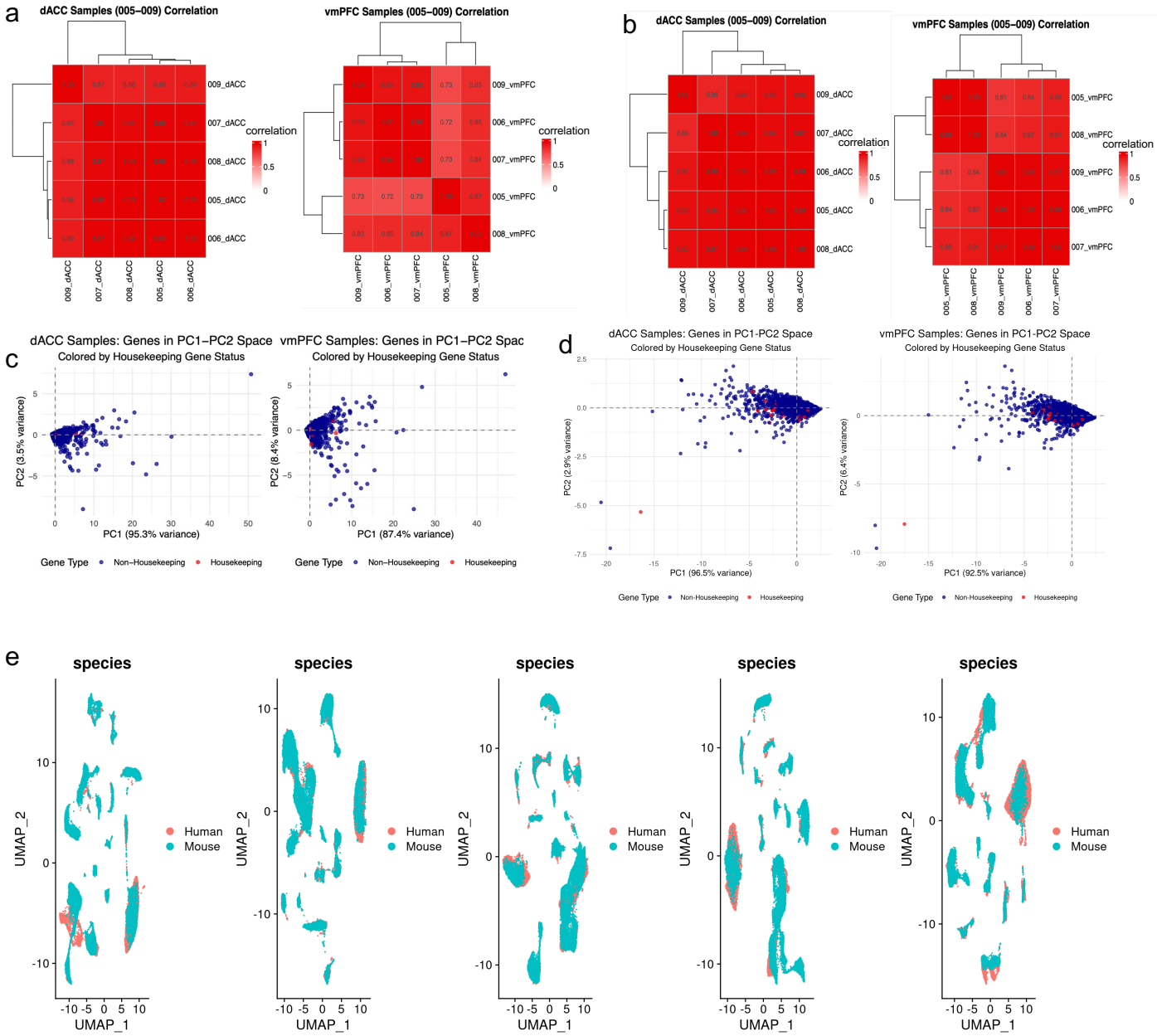
Extended Data Figure 1. **a**. Marker gene feature plot of canonical marker genes frequently used in previous researches for mouse. First two rows (in red) represents the gene expression values of snRNA-seq normalized data. Lower two rows (in blue) represent the gene accessibility level of snATAC-seq. **b-c**. ViolinPlot of gene expression and peaks showing the accessibility of snRNA-seq and snATAC-seq, respectively. **d-e**. Marker gene and marker feature for snRNA-seq and snATAC-seq in mouse. **f**. embedding of snRNA-seq and snATAC-seq of mouse. Colored by sequencing techniques (Left panel) and split by sequencing techniques (Middle and right panel).



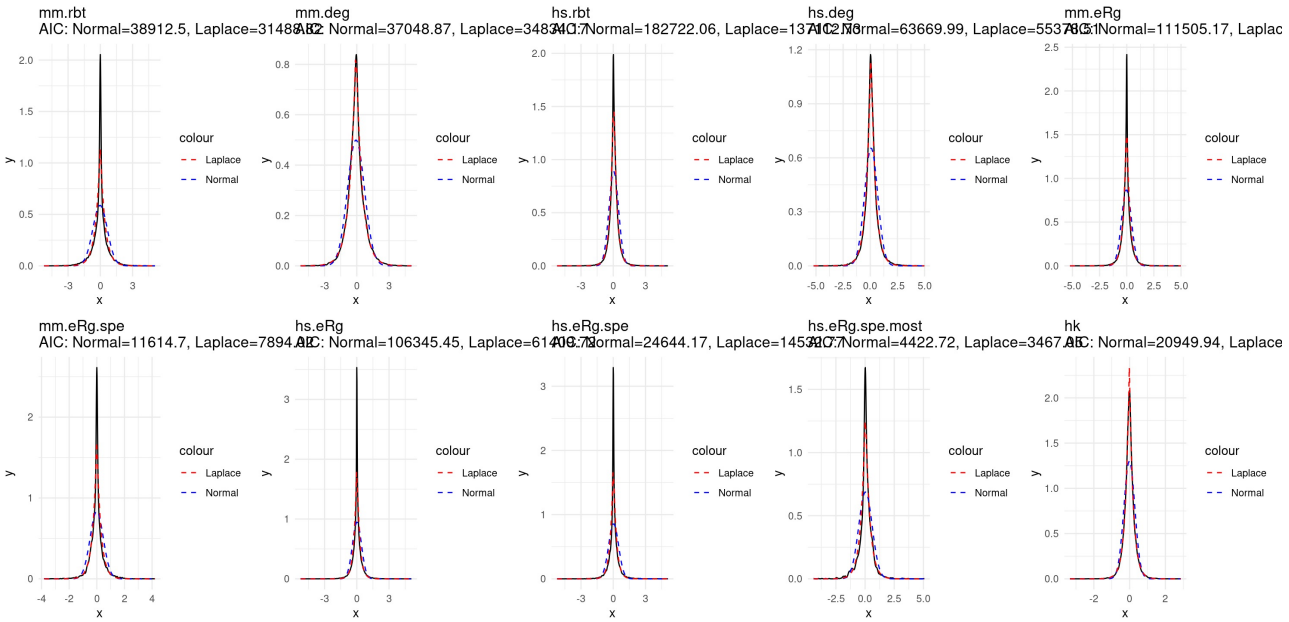
Extended Data Figure 2. **a**. RSS score for TF-centered regulon sets for mouse. Upper panel, activators, lower panel, repressors. **b**. Pie chart of the TF composition of the cell-type specific regulons found in mouse. **c**. Composition of cell types of Modules in mouse. **e-f**. Functional annotation (GO analysis) of genes regulated by neuron-associated modules, analyzed separately for dACC and vmPFC. **d**. Marker gene feature plot of canonical marker genes frequently used in previous researches for human. First two rows (in red) represents the gene expression values of snRNA-seq normalized data. Lower two rows (in blue) represent the gene accessibility level of snATAC-seq. **e-f**. ViolinPlot of gene expression and peaks showing the accessibility of snRNA-seq and snATAC-seq, respectively. **g-h**. Marker gene and marker feature for snRNA-seq and snATAC-seq in human for sub-clusters found by MultiK. **i**. embedding of snRNA-seq and snATAC-seq of mouse. Colored by sequencing techniques (Left panel) and split by sequencing techniques (upper and lower panel).



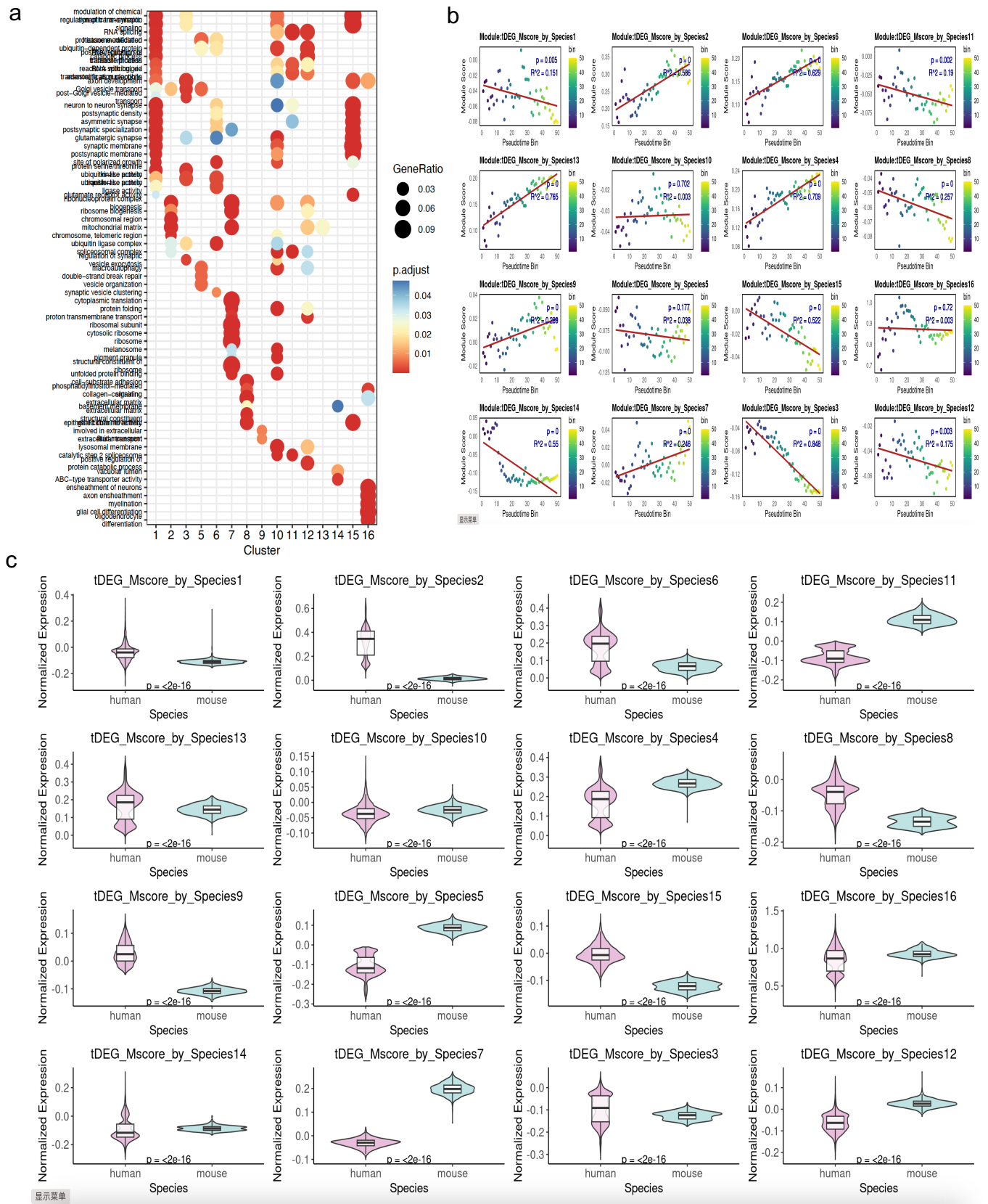
Extended Data Figure 4. **a**. RSS score for TF-centered regulon sets for human. Left panel, activators, right panel, repressors. **b**. Pie chart of the TF composition of the cell-type specific regulons found in mouse. **c**. Composition of cell types of Modules in mouse. **d-e**. Functional annotation (GO analysis) of genes regulated by neuron-associated modules, analyzed separately for dACC and vmPFC. **f.** Example activator regulon: FOS, a neuronal immediate early gene, binds an open region downstream of RPTOR (functioning as an enhancer), activating higher expression in vmPFC within the excitatory L6 CT neuron type. **g-h**. Inhibitory neuron canonical marker co-expression summary for human (f) and mouse (g), respectively.



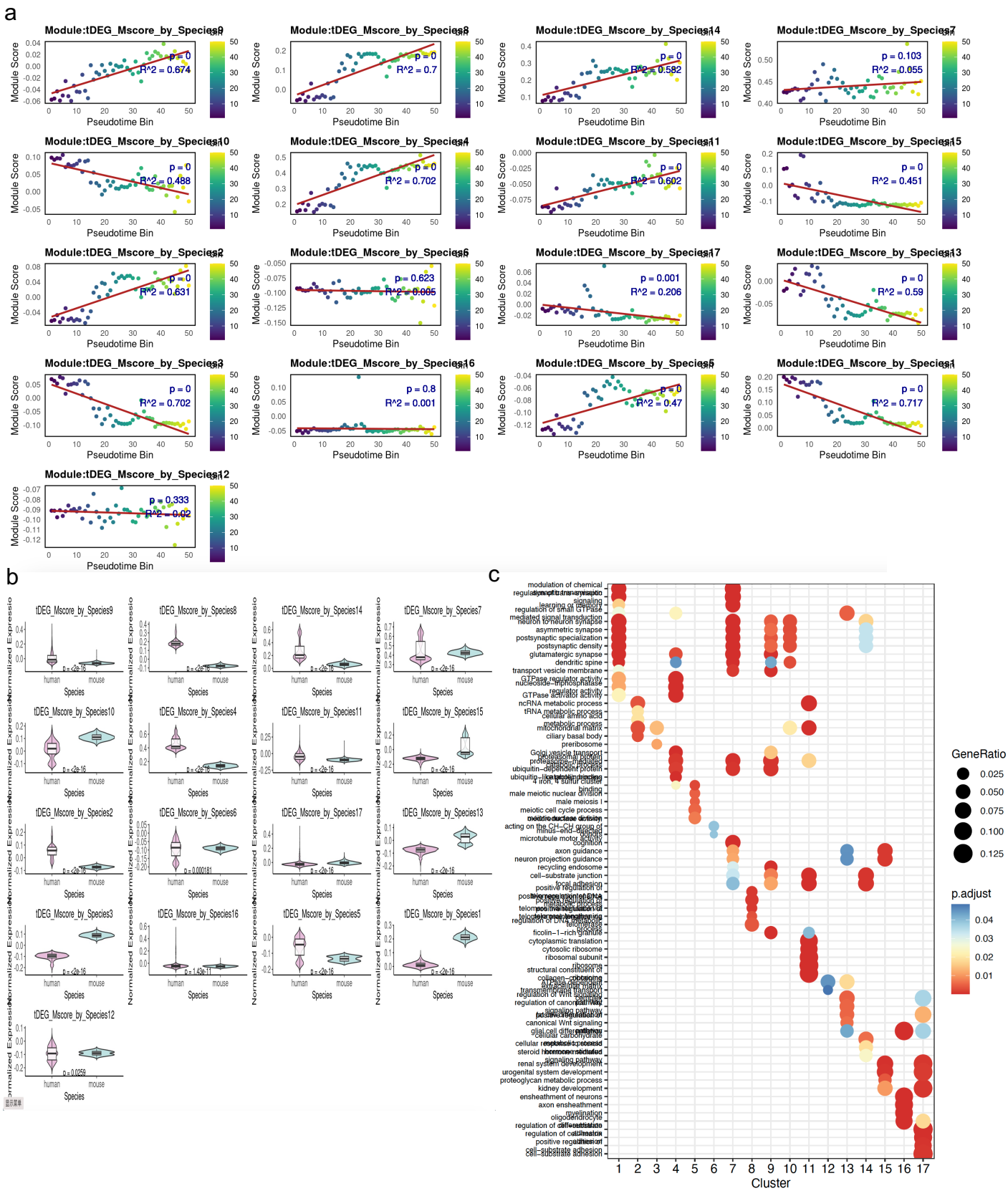
Extended Data Figure 4. **a-b**, Consistency of human donors measured by Pearson's correlation for snRNA-seq (a) and snATAC-seq (b), respectively. **c-d**, PCA reduction of 3,000 HVGs (Highly variable genes) in 5 human samples for snRNA-seq (c) and snATAC-seq (d), respectively. Each dot represent a gene. PCs are calculated based on samples (human donor). Housekeeping genes are marked as red points as anchors due to the consistency of expression across batches.



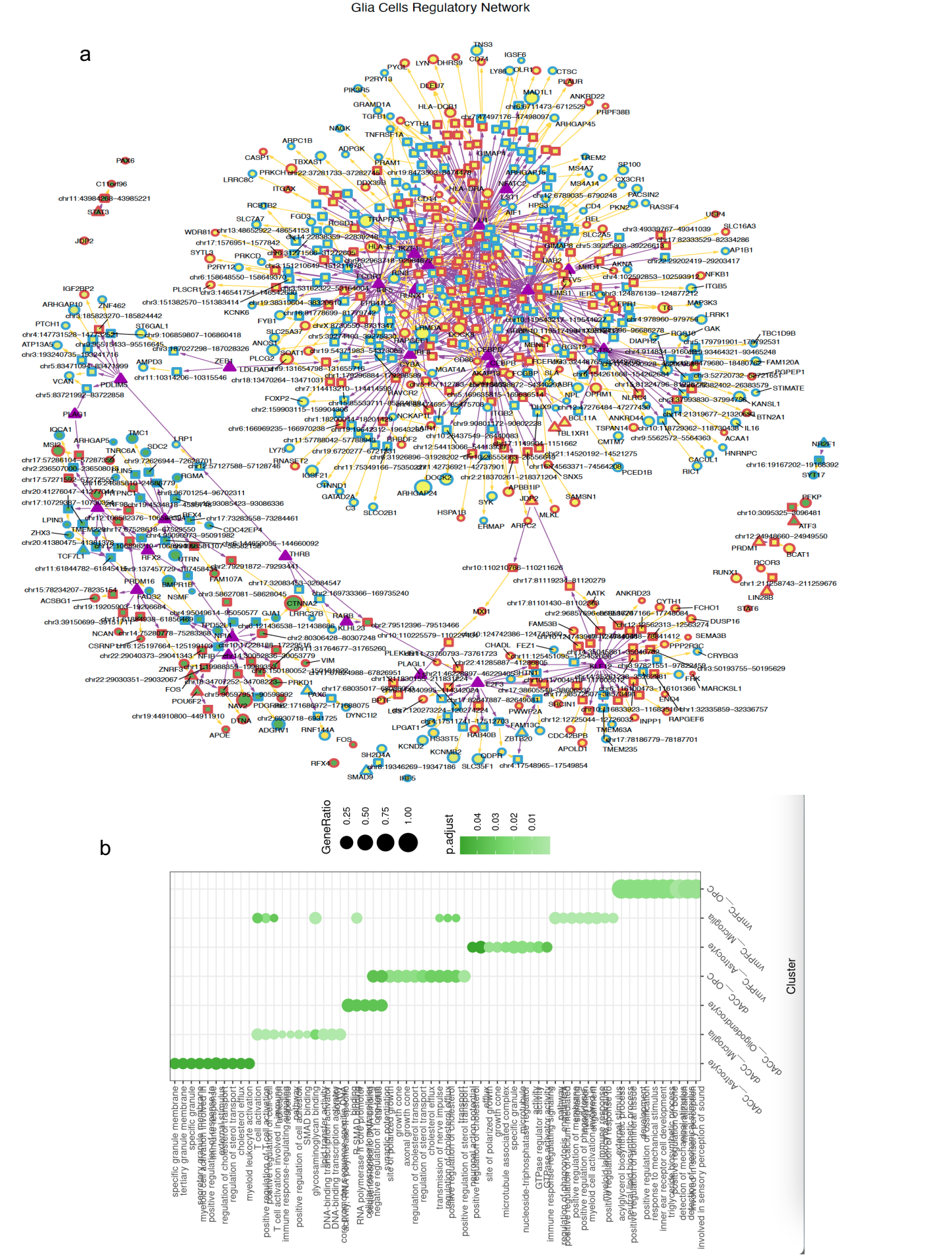
Extended Data Figure 5. DS for each element and the fitted normal distribution and Laplace distribution.



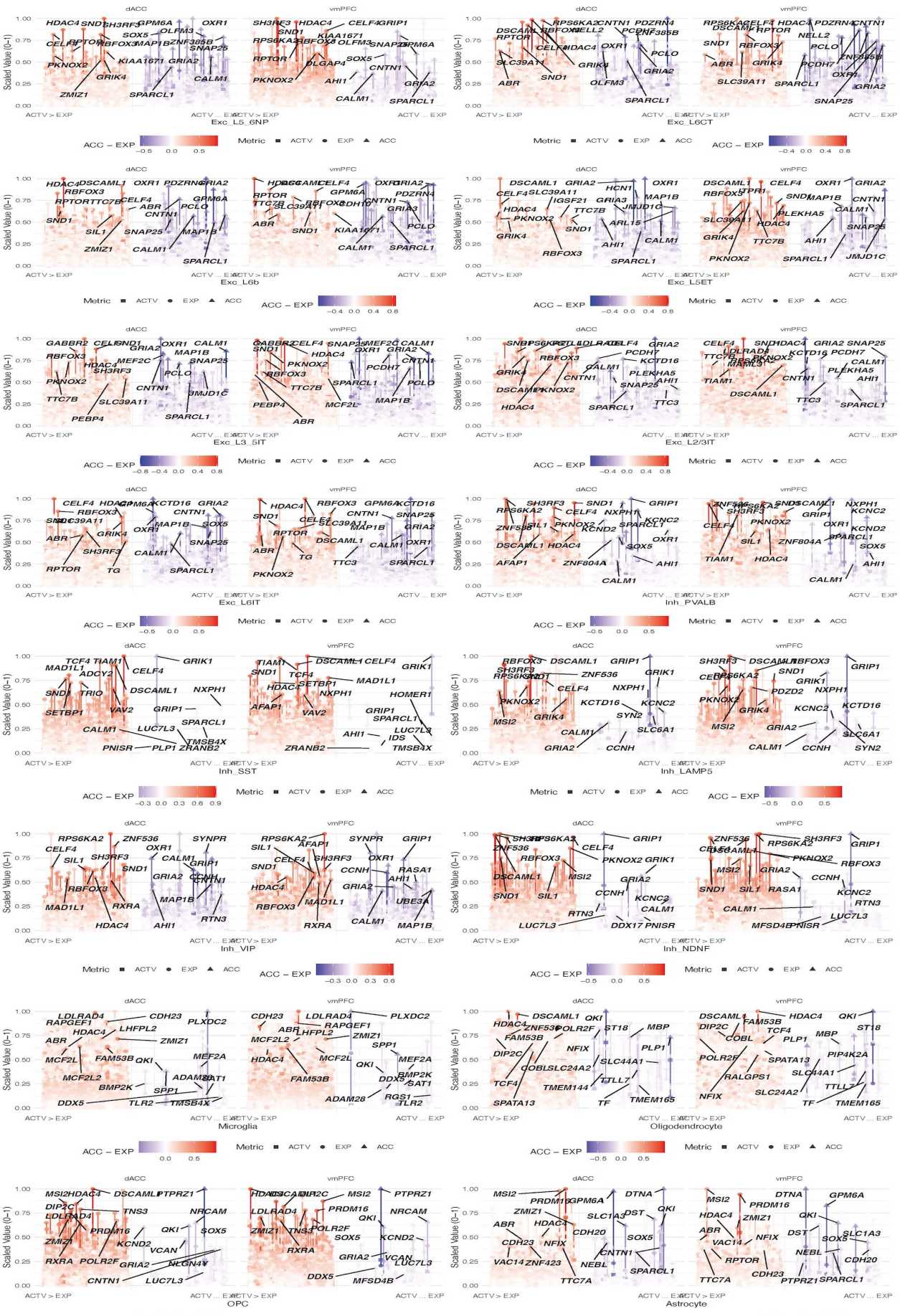
Extended Data Figure 6. Trajectory analysis in dACC. a. Function analysis of each module found for the genes vary along the trajectory. p values are indicated using color while ratio enriched in a term is represented by the size of the dot. b. Module scores along the gradient from bin1 to bin50 and the linear fitting, p value and R^2. c. Module score in mouse and human cells. Wilcox-tests are utilized for significant tests.



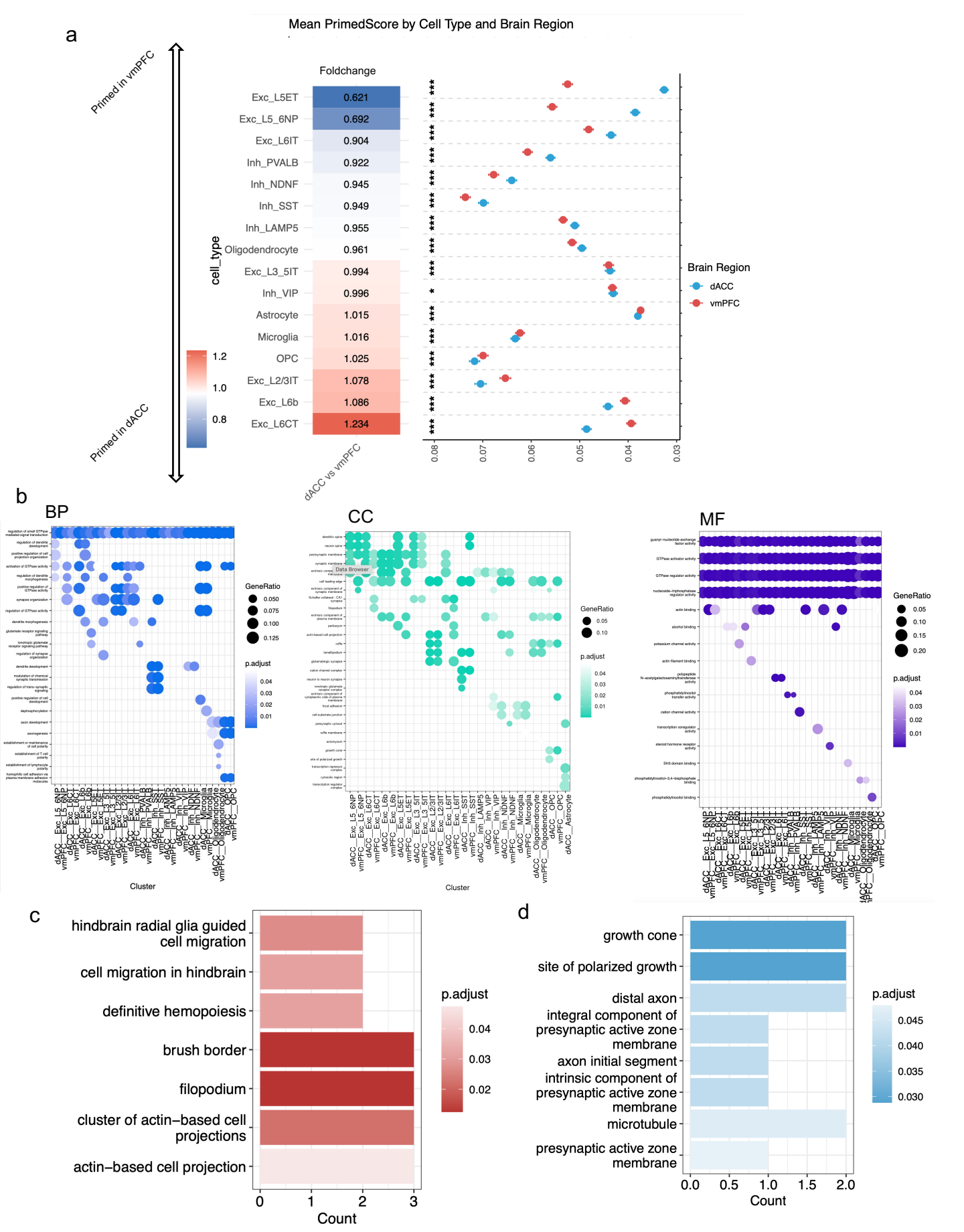
Extended Data Figure 7. Trajectory analysis in vmPFC. a. Function analysis of each module found for the genes vary along the trajectory. p values are indicated using color while ratio enriched in a term is represented by the size of the dot. b. Module scores along the gradient from bin1 to bin50 and the linear fitting, p value and R^2. c. Module score in mouse and human cells. Wilcox-tests are utilized for significant tests.



Extended Data Figure 8. a. Regulation map of PTSD SNP anchored genes in glia cells. b. Bubble plot of GO enrichment for genes significantly associated with PTSD risk within each cell type for glias.



Extended Data Figure 9. For each cell type, the profiling of gene's accessibility, TF binding region accessibility and gene expression (all scaled). Each vertical column represents three attributes of a single gene: overall chromatin accessibility (ACTV, circles), gene expression level (EXP, triangles), and enhancer accessibility (ACC, squares). For every cell type, the values of these three attributes are min–max scaled to a 0–1 range. Genes are divided into two groups according to the relative values of ACTV and EXP: genes with ACTV > EXP are placed in group 1, whereas genes with ACTV < EXP are placed in group 2. Consequently, genes in group 1 are considered candidate chromatin-primed genes (CPGs). Columns are colour-coded by the scaled difference (ACTV − EXP); deeper red indicates a higher degree of chromatin priming.



Extended Data Figure 10. a, Function annotation of CPGs, divided by biological process (BP), cellular component (CC) and molecular function (MF). **b**, Function annotation of genes primed in naïve and up-regulated in patient. **c,** Function annotation of consistently highly expressed genes. **d**, Primed Score difference in vmPFC and dACC for each cell type.