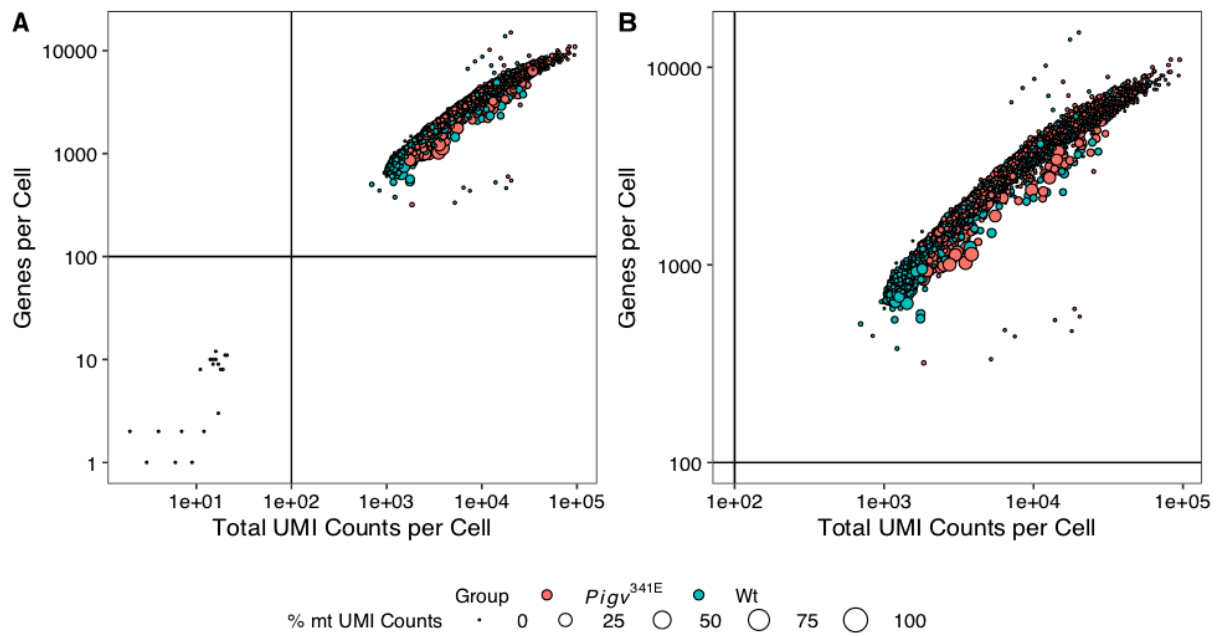
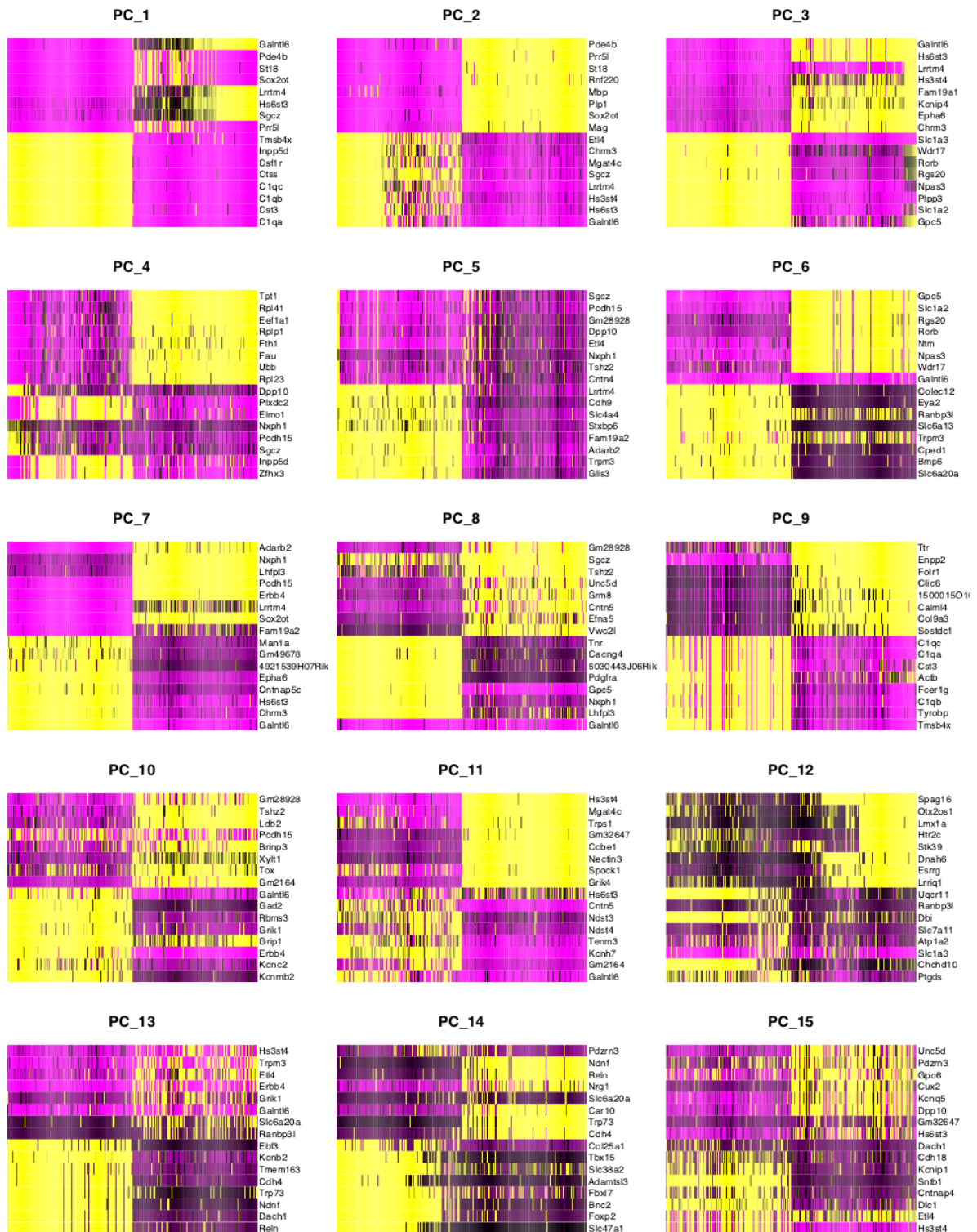


Supplementary Figure 11



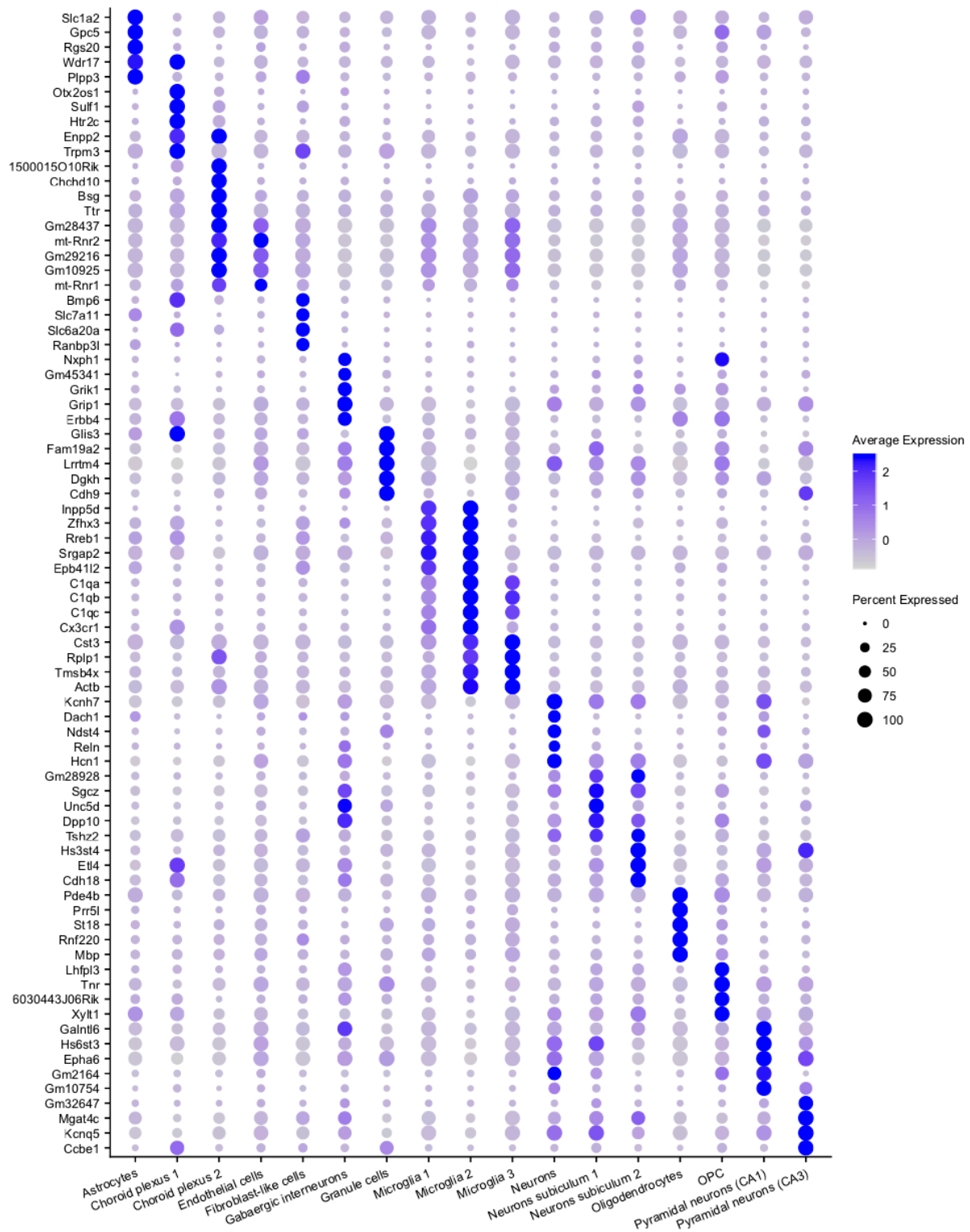
Filtering removes outlying barcodes. Keeping only cellular barcodes with more than 100 genes per cell, more than 100 UMI counts per cell and less than 30 % UMI counts mapping to mitochondrial genes from the full preprocessed data set comprising 15,949 barcodes (A) removes 19 outlying barcodes, resulting in the filtered data set comprising 15,930 barcodes (B).

Supplementary figure 12



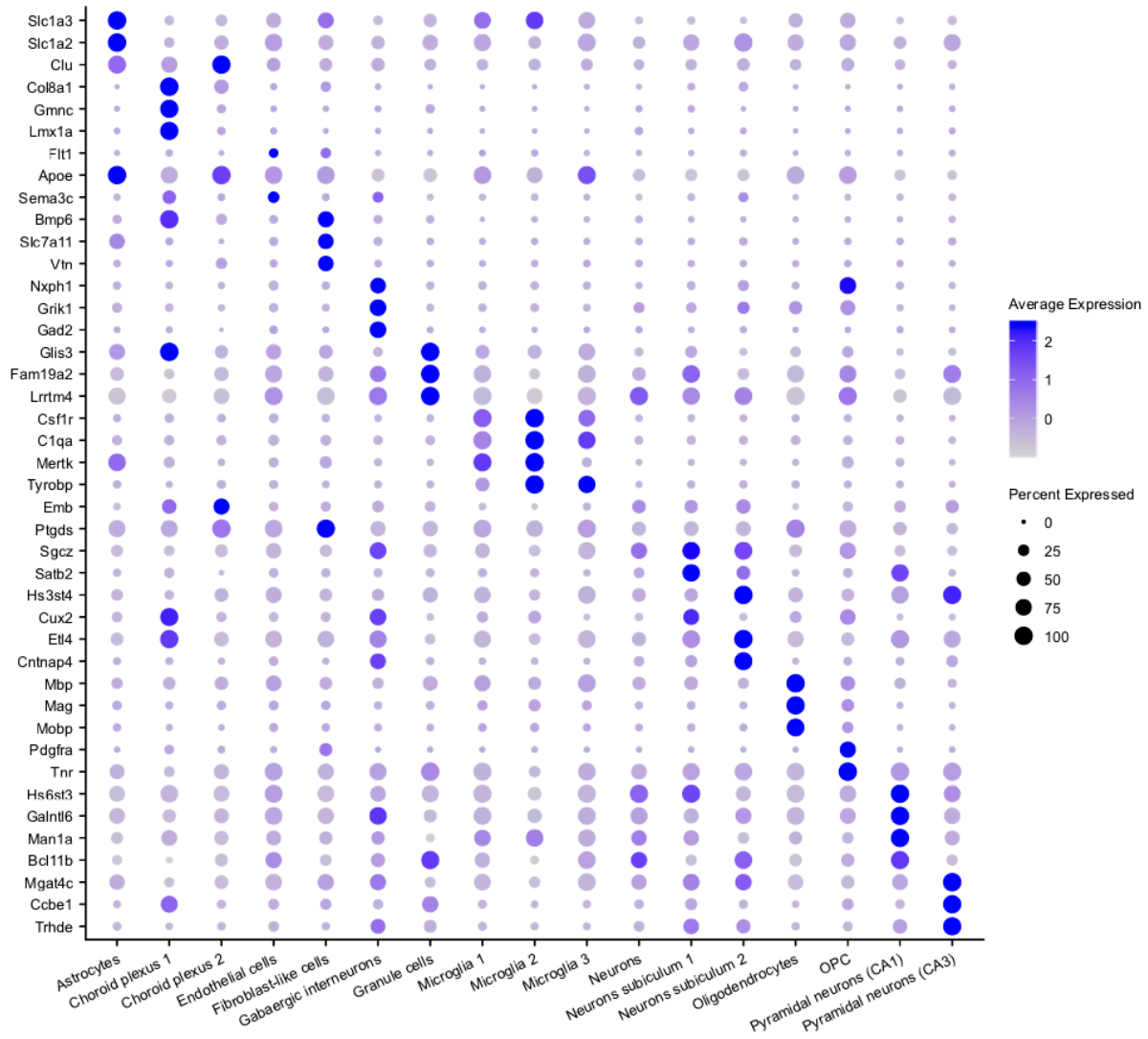
Dimensional reduction heat maps. Heat maps on the 15 most influential genes and 250 cells sorted by principal component score for each of the first 15 principal components support the selection of the top 11 principal components for further non-parametric dimensionality reduction and downstream analysis.

Supplementary Figure 13



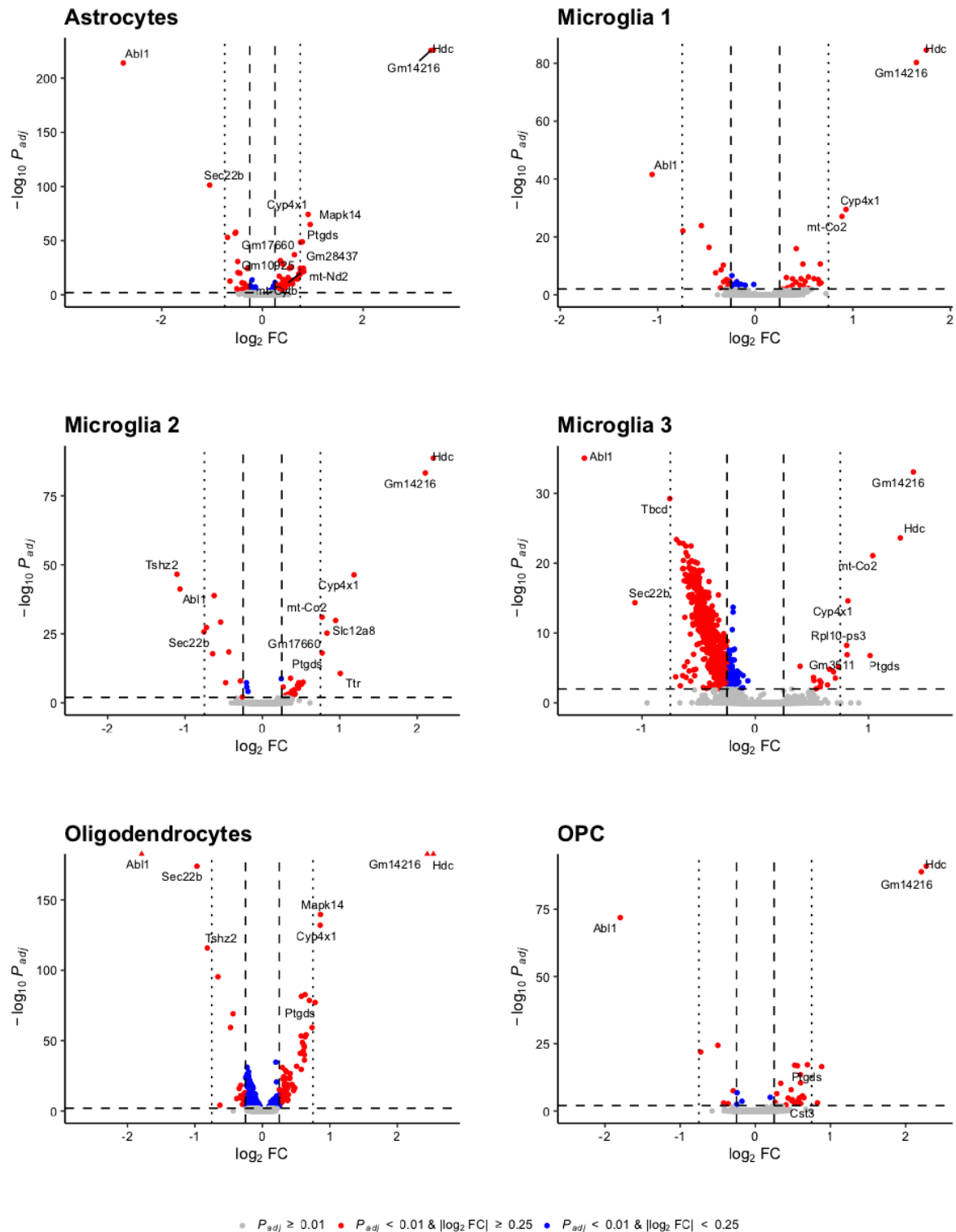
Expression of marker genes in cellular subgroups. For each of the 17 cellular subgroups, the 5 differentially expressed genes with highest average fold change in comparison to all remaining cells are depicted. The dot size represents the percentage of cells within a cluster with non-zero expression of the respective gene.

Supplementary figure 14



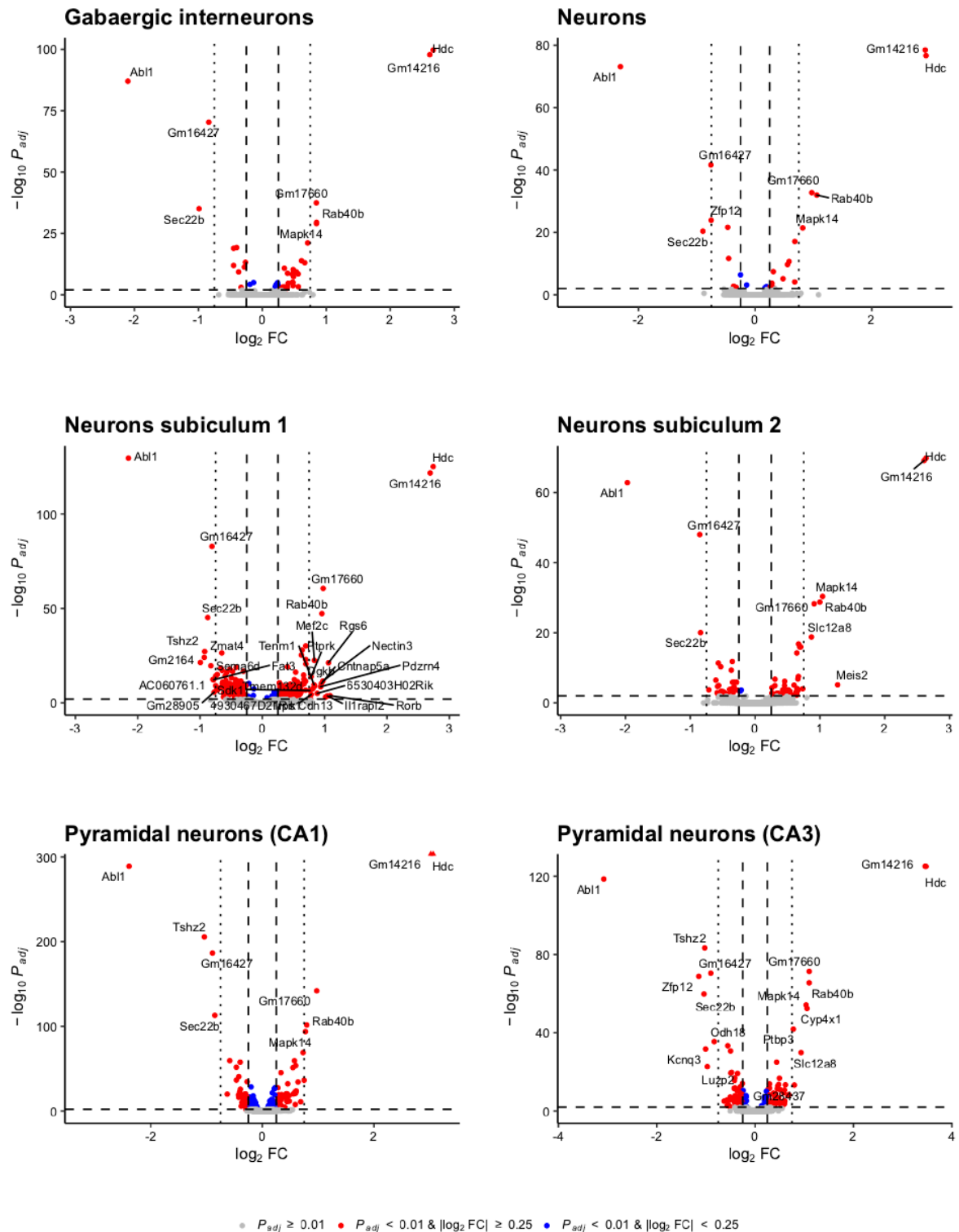
Expression of selected genes in cellular subgroups. For each of the 17 cellular subgroups, the average expression of selected genes that supported assignment of cellular subgroup identities are depicted. The dot size represents the percentage of cells within a cluster with non-zero expression of the respective gene.

Supplementary Figure 15



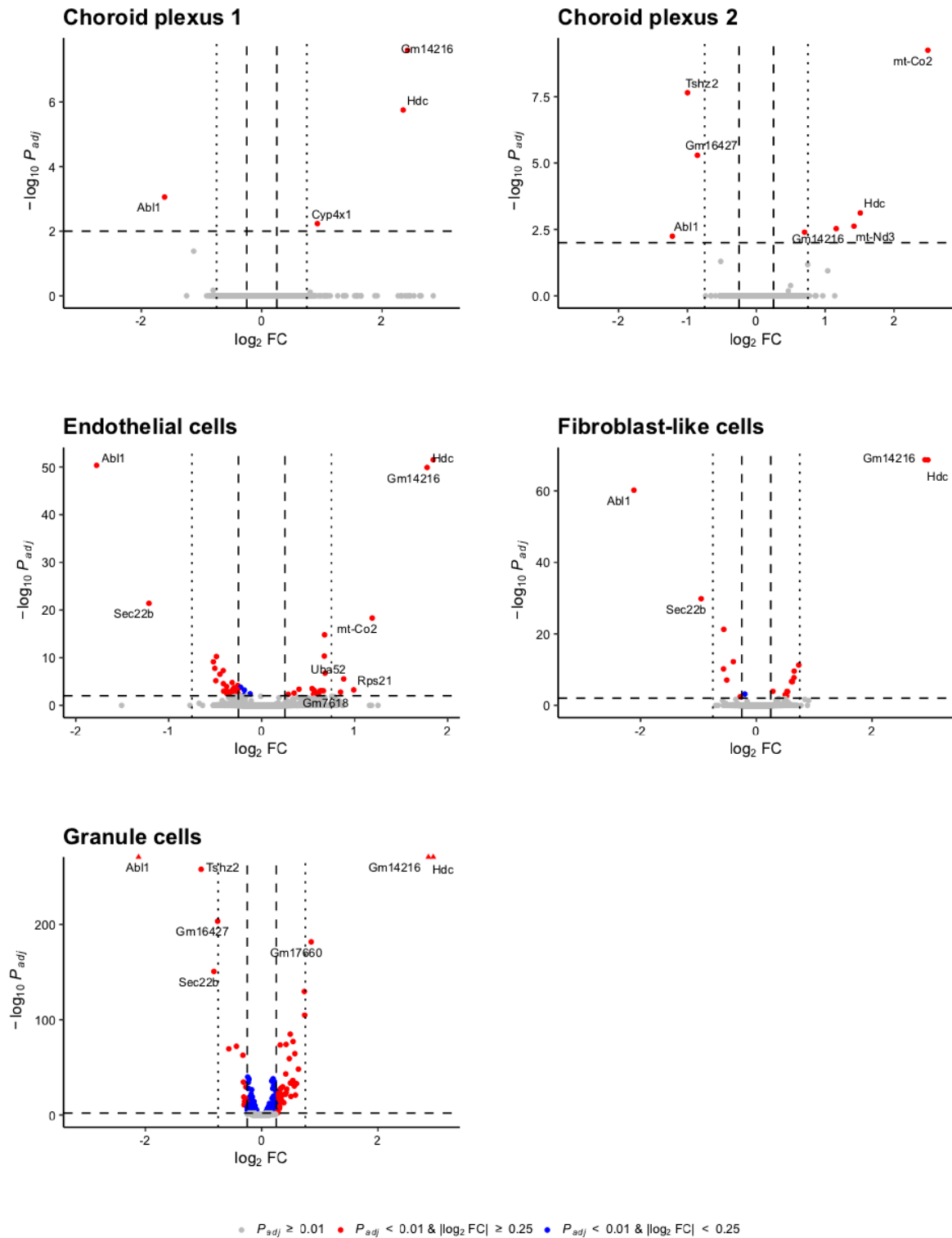
Volcano plots resulting from comparison of *Pigv*^{341E} cells and wild-type cells within glial cellular subgroups. Dashed horizontal lines are located at an adjusted p-value of 0.01, dashed vertical lines at an absolute \log_2 fold change of 0.25 and dotted vertical lines at an absolute \log_2 fold change of 0.75. For genes with an adjusted p-value below 0.01 and a minimum absolute \log_2 fold change of 0.75, gene symbols are depicted.

Supplementary Figure 16



Volcano plots resulting from comparison of *Pigv*^{341E} cells and wild-type cells within neuronal cellular subgroups. Dashed horizontal lines are located at an adjusted p-value of 0.01, dashed vertical lines at an absolute log₂ fold change of 0.25 and dotted vertical lines at an absolute log₂ fold change of 0.75. For genes with an adjusted p-value below 0.01 and a minimum absolute log₂ fold change of 0.75, gene symbols are depicted.

Supplementary Figure 17



Volcano plots resulting from comparison of *Pigv*^{341E} cells and wild-type cells within other cellular subgroups. Dashed horizontal lines are located at an adjusted p-value of 0.01, dashed vertical lines at an absolute log₂ fold change of 0.25 and dotted vertical lines at an absolute log₂ fold change of 0.75. For genes with an adjusted p-value below 0.01 and a minimum absolute log₂ fold change of 0.75, gene symbols are depicted.