

Fig. S1: Changes in the diversity, richness, and composition of the gut microbiota in mice.

- **a** Body weights and total distances in the open field tests for mice with different ranks (Rank1, n = 7; Rank2, n = 7; Rank3, n = 6; Rank4, n = 6; Rank1 vs Rank2 vs Rank3 vs Rank4, no statistical difference in p values; data are mean \pm SEM; Kruskal-Wallis test, two-tailed)
- **b** Alpha diversity indices of gut microbiota in mice with different ranks (Rank1, n = 6; Rank2, n = 7; Rank3, n = 6; Rank4, n = 6; Rank1 vs Rank2 vs Rank3 vs Rank4, no statistical difference in p values; data are mean \pm SEM; Wilcoxon rank-sum test, two-tailed).
- **c** The overall characteristics of gut microbiota displayed using PCoA based on the abund_jaccard distance, with internal differences analyzed by PERMANOVA test (permutations = 999, p = 0.275).
- **d** Body weights and total distances in the open field tests for mice in the go-through-tube and forced loss groups (Go-through-tube, n = 7; Forced loss, n = 7; Go-through-tube vs. Forced loss, no statistical difference in p values; data are mean \pm SEM; T test, two-tailed).
- **e** Alpha diversity indices of the gut microbiota in go-through-tube mice and forced loss mice (Go-through-tube, n = 6; Forced loss, n = 6; Go-through-tube vs. Forced loss, no statistical difference in p values; data are mean \pm SEM; Wilcoxon rank-sum test, two-tailed).
- **f** DNA expression of gut microbiota genes in the control and ABX groups (Con, n = 8; ABX, n = 14; Con vs. ABX, **** p < 0.0001; data are mean \pm SEM; T test, two-tailed).
- **g** Time percentages of pushing, voluntary retreating, resistance (when pushed by an opponent), and passive retreating (when pushed by an opponent) during tube test for microbiota-depleted mice before and after go-through-tube or forced loss procedure (Go-through-tube + ABX, n = 6 mice, 18 trials; forced loss + ABX, n = 7 mice, 21 trials. *p < 0.05, **p < 0.01, ****p < 0.001, ****p < 0.0001, ns, not significant; data are mean \pm SEM; Mann-Whitney test, two-tailed).

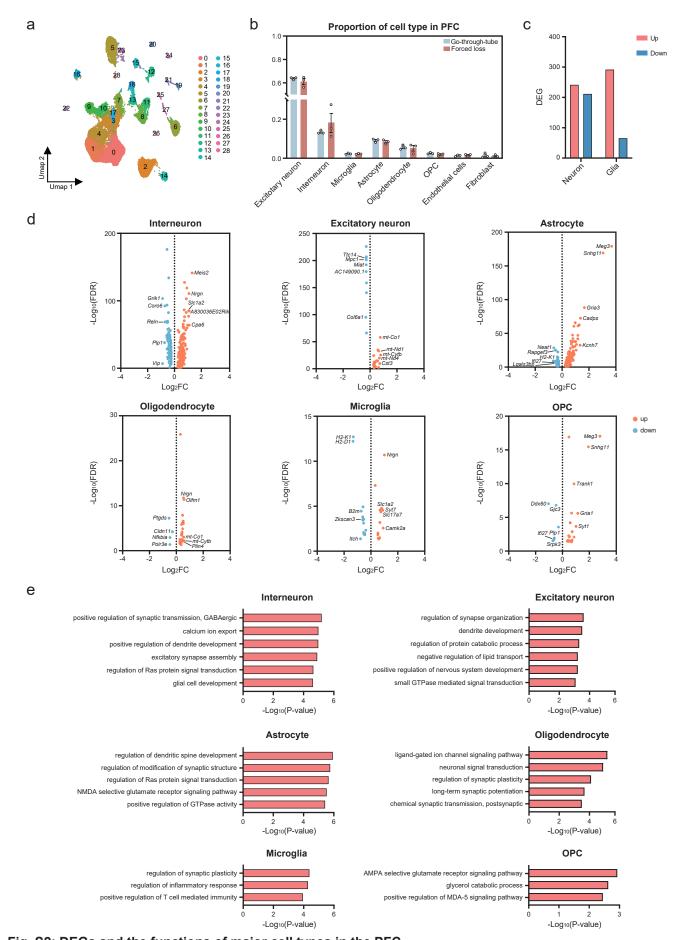
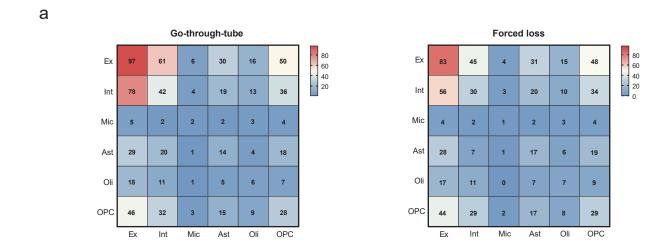


Fig. S2: DEGs and the functions of major cell types in the PFC.

- **a** The UMAP graph showed single-cell dimensionality reduction clusters in PFC. The UMAP graph showed that 52626 nuclei were clustered in PFC to obtain 29 pretreated cell clusters.
- **b** Proportion of cell types in PFC (Go-through-tube, n = 3; Forced loss, n = 3; Go-through-tube vs. Forced loss, no statistical difference in p values; data are mean \pm SEM; Mann-Whitney test, two-tailed).
- c The amount of DEG up-regulated and down-regulated in neurons and glial cells.
- d Volcano plots showed DEGs expressed in six major cell types in PFC (log₂FC > 0.25 or < -0.25, and FDR < 0.05).
- **e** GO enrichment analysis showed the functions of DEGs enrichment expressed in interneurons, excitatory neurons, astrocytes, oligodendrocytes, microglia and OPC (p < 0.05).



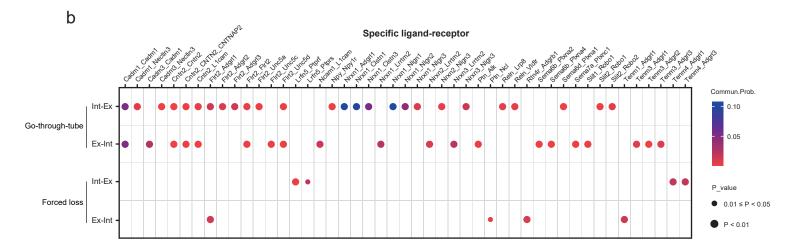


Fig. S3: The number and specific function of ligand-receptor pairs in the go-through-tube and forced loss groups. a The number of all activated ligand-receptor pairs in the go-through-tube and forced loss groups (Go-through-tube, n = 3; Forced loss, n = 3).

b Functions of specific connections in the ligand-receptor relationships between interneurons and excitatory neurons (p < 0.05).

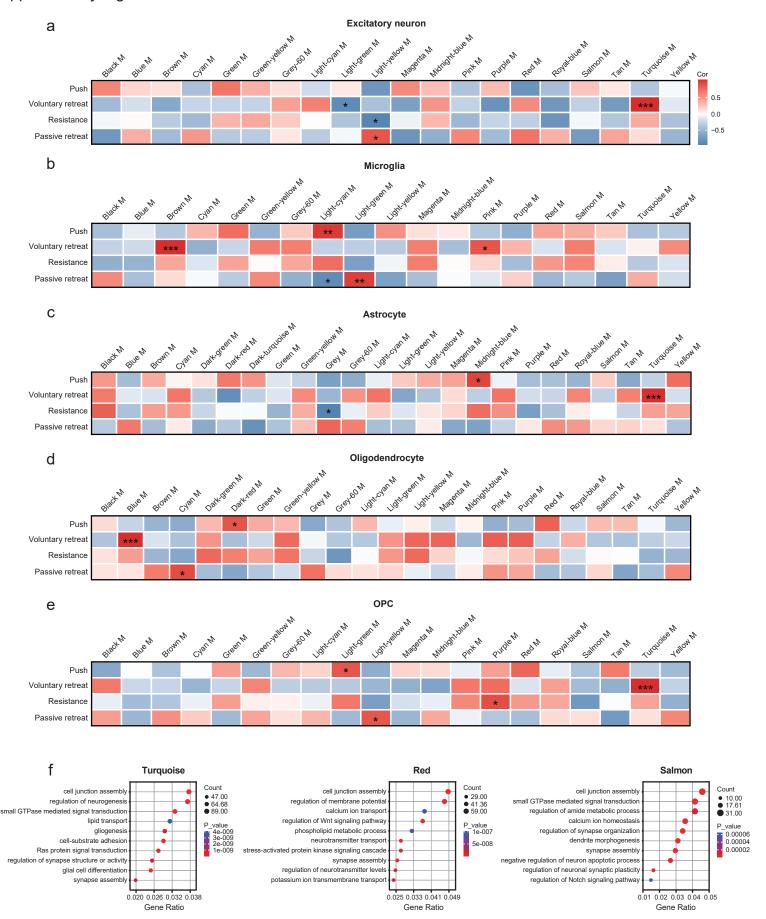


Fig. S4: Correlation between gene modules of differential cell types and forced loss related behaviors.

a-e The heatmap showed gene modules associated with four behaviors (push, voluntary retreat, resistance, passive retreat) in excitatory neurons, microglia, astrocytes, oligodendrocytes and OPC (r > 0.6 or < -0.6, *p < 0.05, **p < 0.01, ***p < 0.001, two-tailed Pearson correlation).

f GO enrichment analysis showed the functions and pathways of genes enrichment in three modules (turquoise, red, salmon) associated with voluntary retreat in interneurons (p < 0.05).