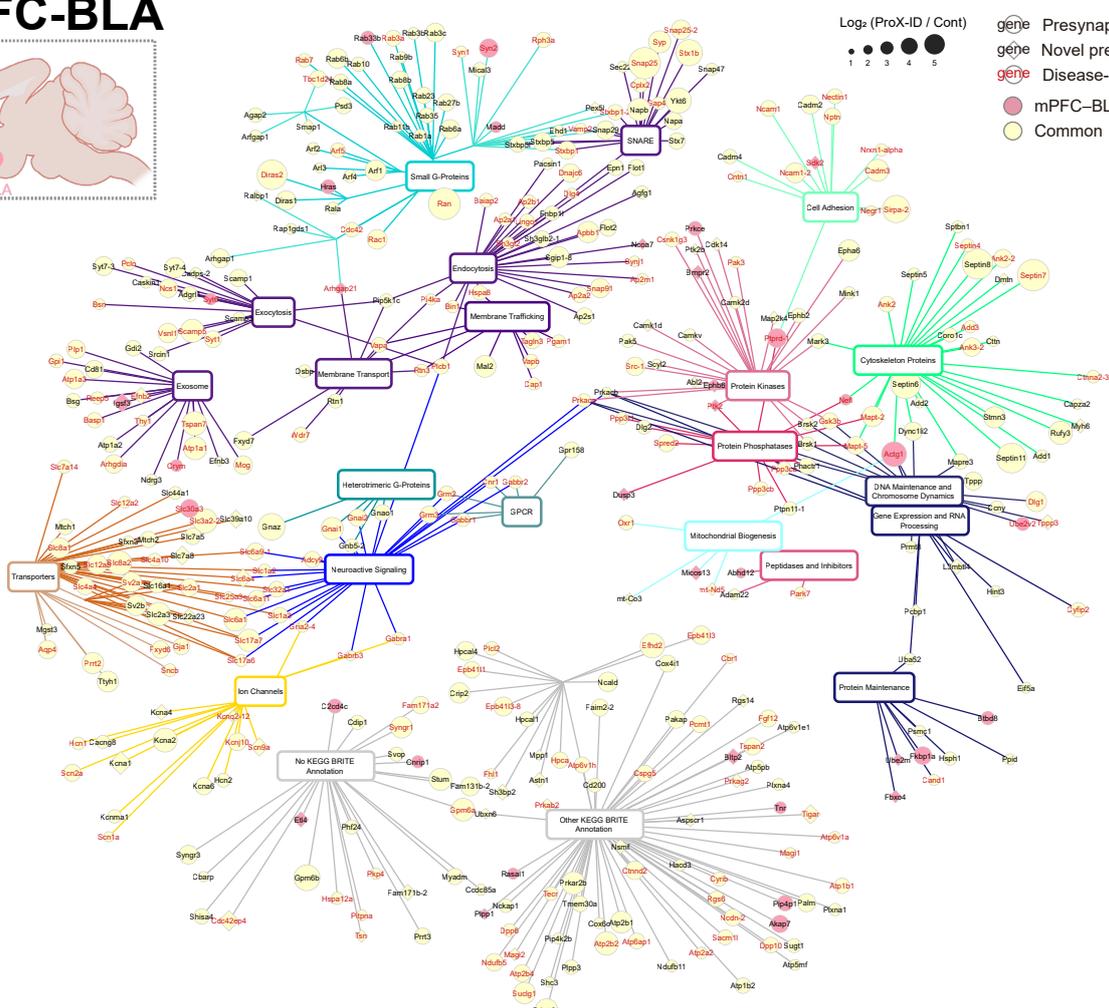
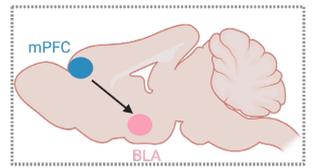


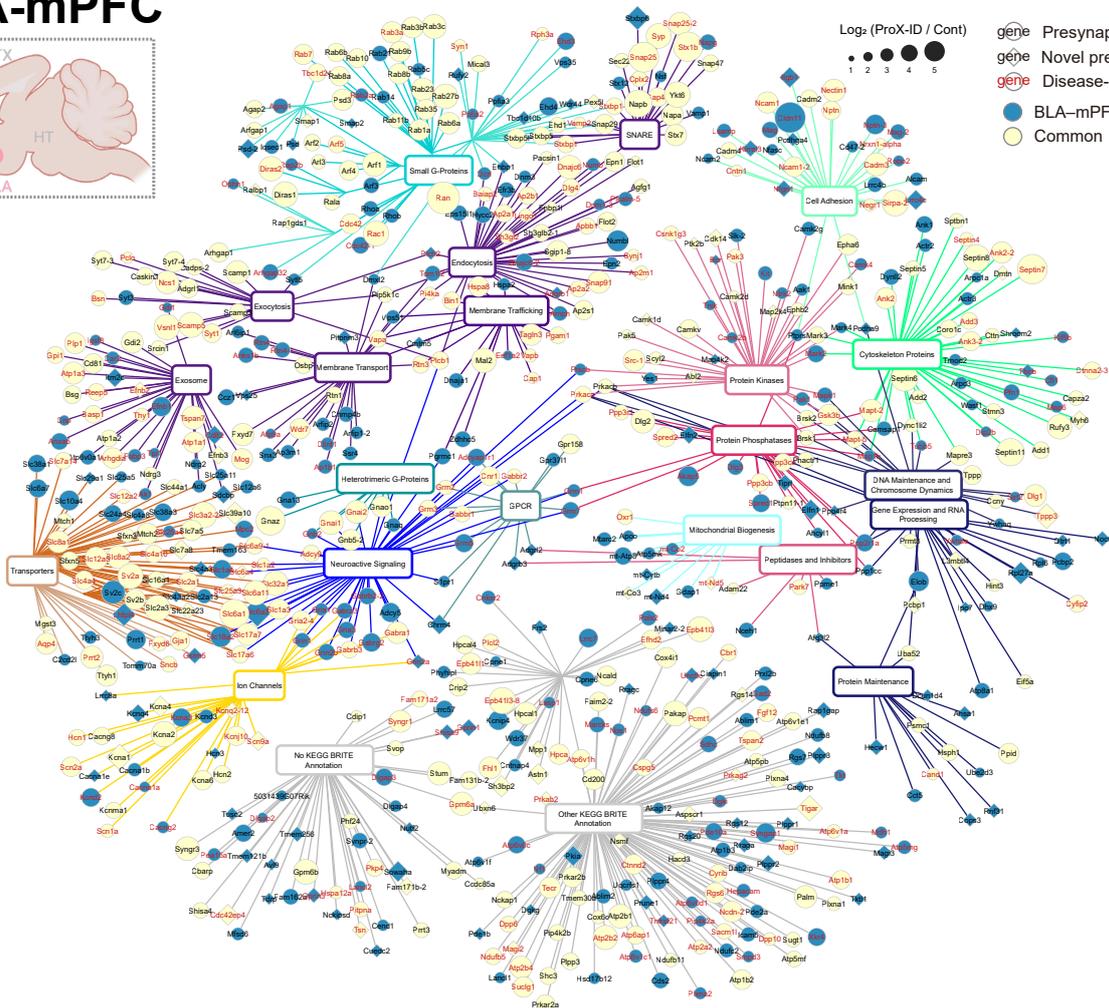
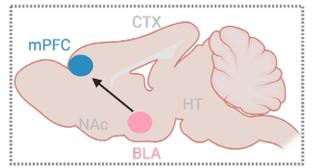
a mPFC-BLA



Log₂(ProX-ID / Cont)
 ● 1 ● 2 ● 3 ● 4 ● 5

● gene Presynaptic proteins
● gene Novel presynaptic proteins
● gene Disease-related proteins
● mPFC-BLA selective
● Common

b BLA-mPFC

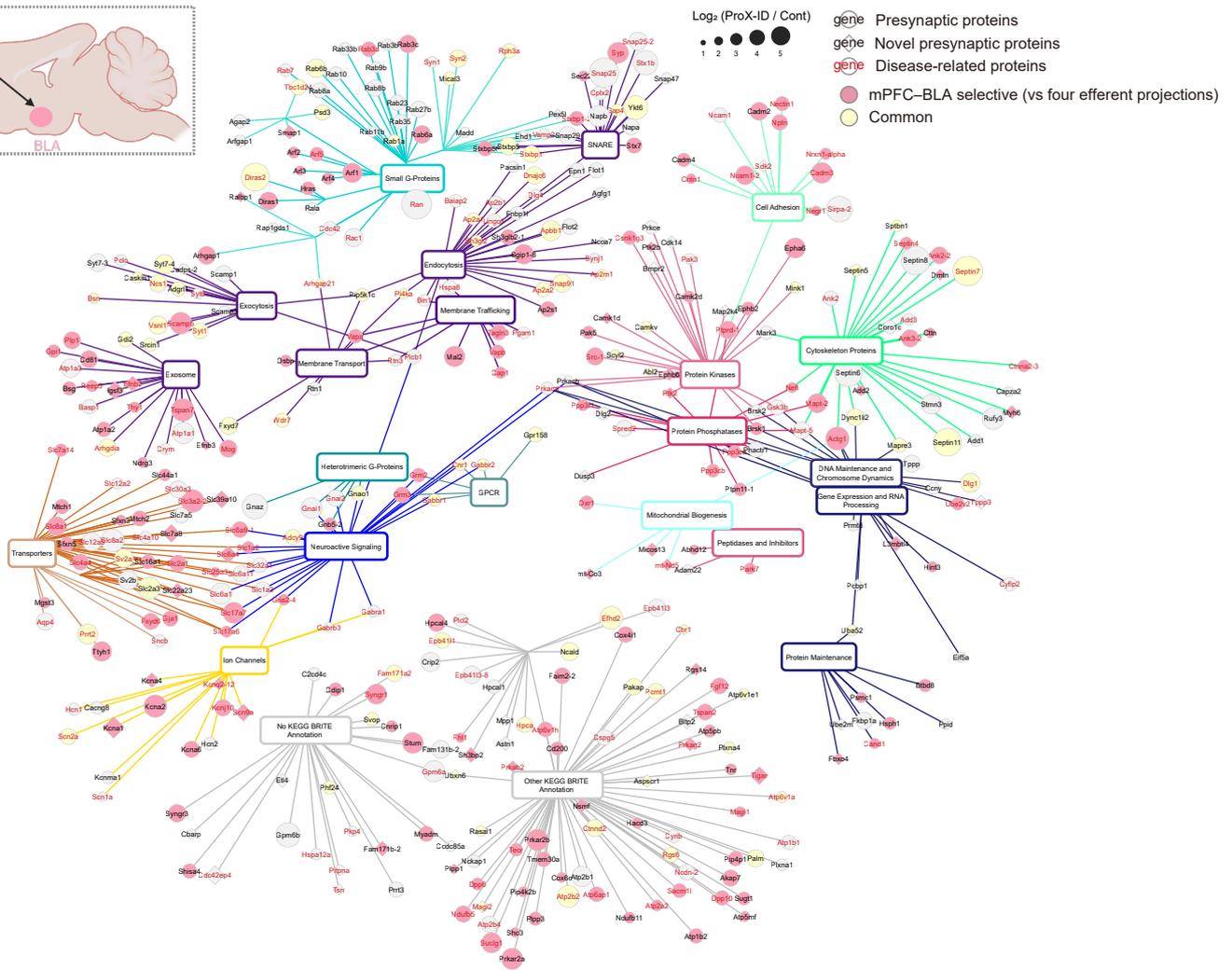
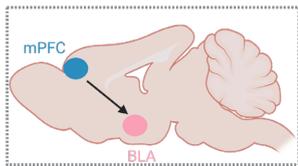


Log₂(ProX-ID / Cont)
 ● 1 ● 2 ● 3 ● 4 ● 5

● gene Presynaptic proteins
● gene Novel presynaptic proteins
● gene Disease-related proteins
● BLA-mPFC selective
● Common

Supplemental Figure 1. Protein-term network for neural pathway-enriched proteins. Protein-term networks of mPFC-BLA-enriched (a) and BLA-mPFC-enriched (b) proteins were constructed using KEGG BRITE annotations. Nodes represent proteins and functional terms, with edges indicating associations based on BRITE functional classifications. Note that mPFC-BLA-enriched proteins in this figure are defined as those uniquely identified in the mPFC-BLA neural pathway, with no overlap with proteins enriched in the BLA-mPFC neural pathway.

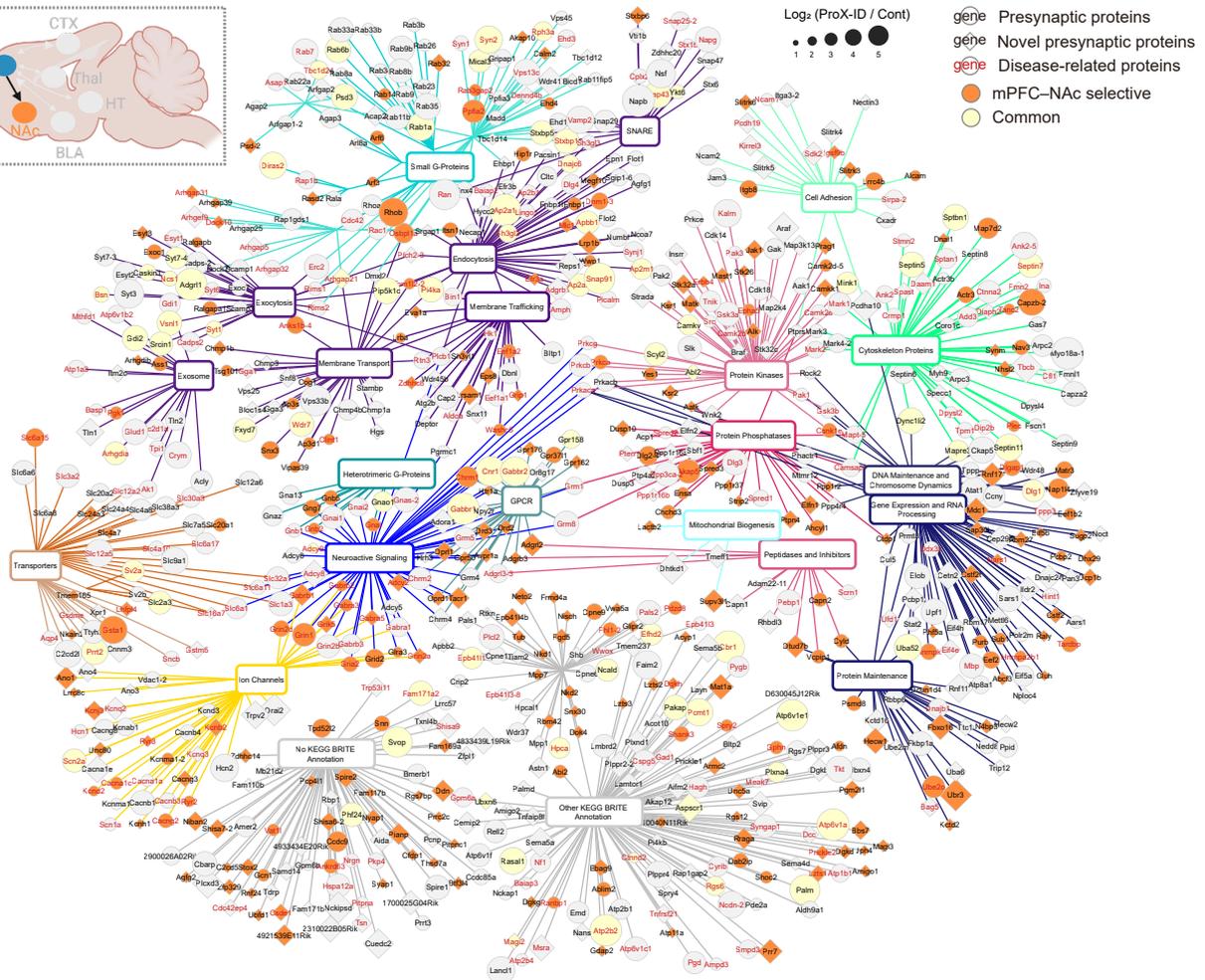
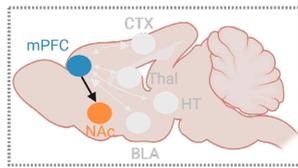
mPFC-BLA



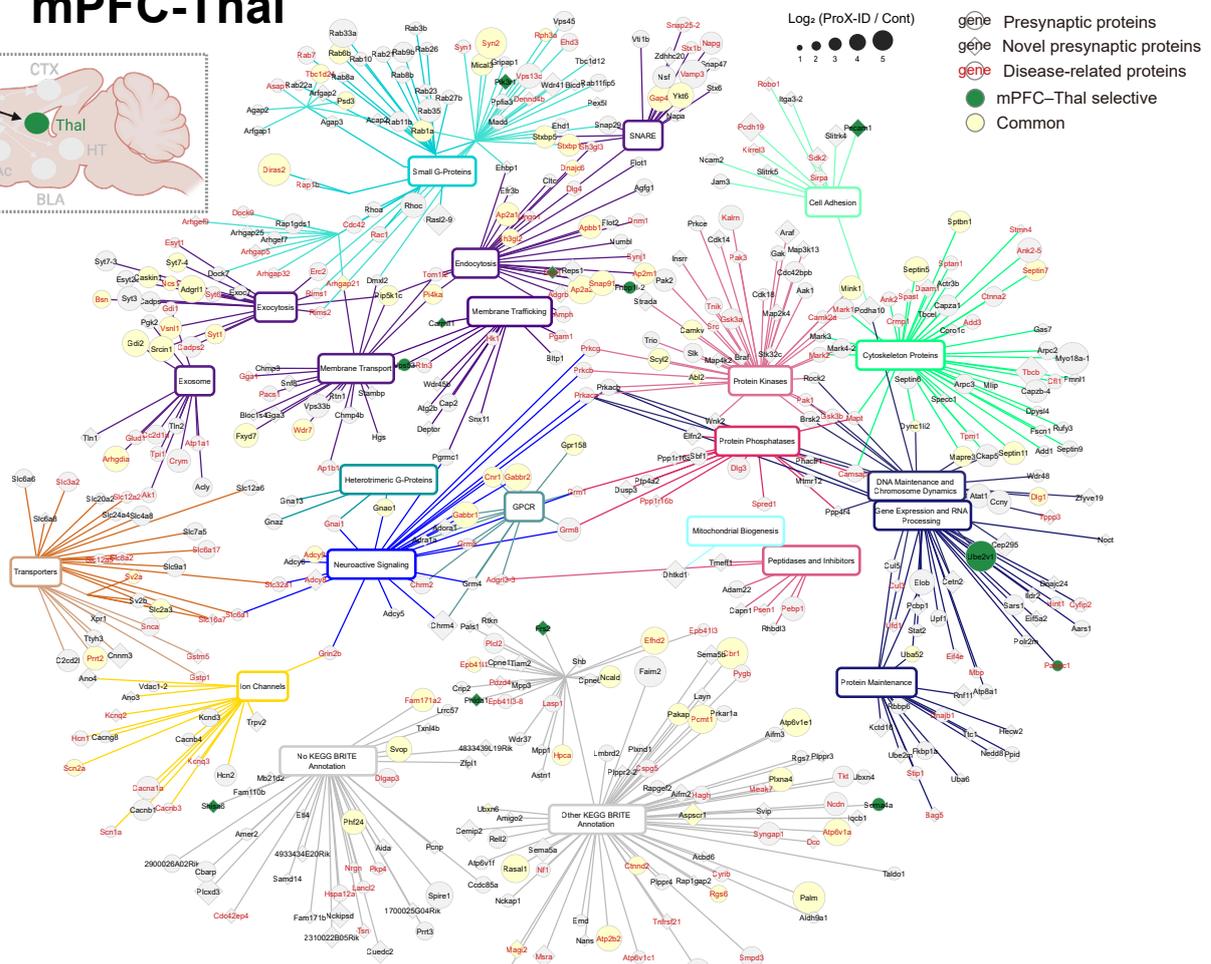
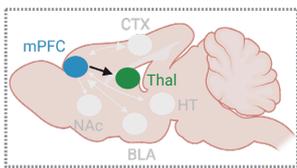
Supplemental Figure 2. Protein-term network for mPFC-BLA neural pathway-enriched proteins.

Protein-term networks were constructed using KEGG BRITe annotations. Nodes represent proteins and functional terms, with edges indicating associations based on BRITe functional classifications. Note that the mPFC-BLA-enriched proteins in this figure are defined as those uniquely identified in the mPFC-BLA neural pathway, with no overlap with proteins from the other four mPFC neural pathways.

a mPFC-NAc

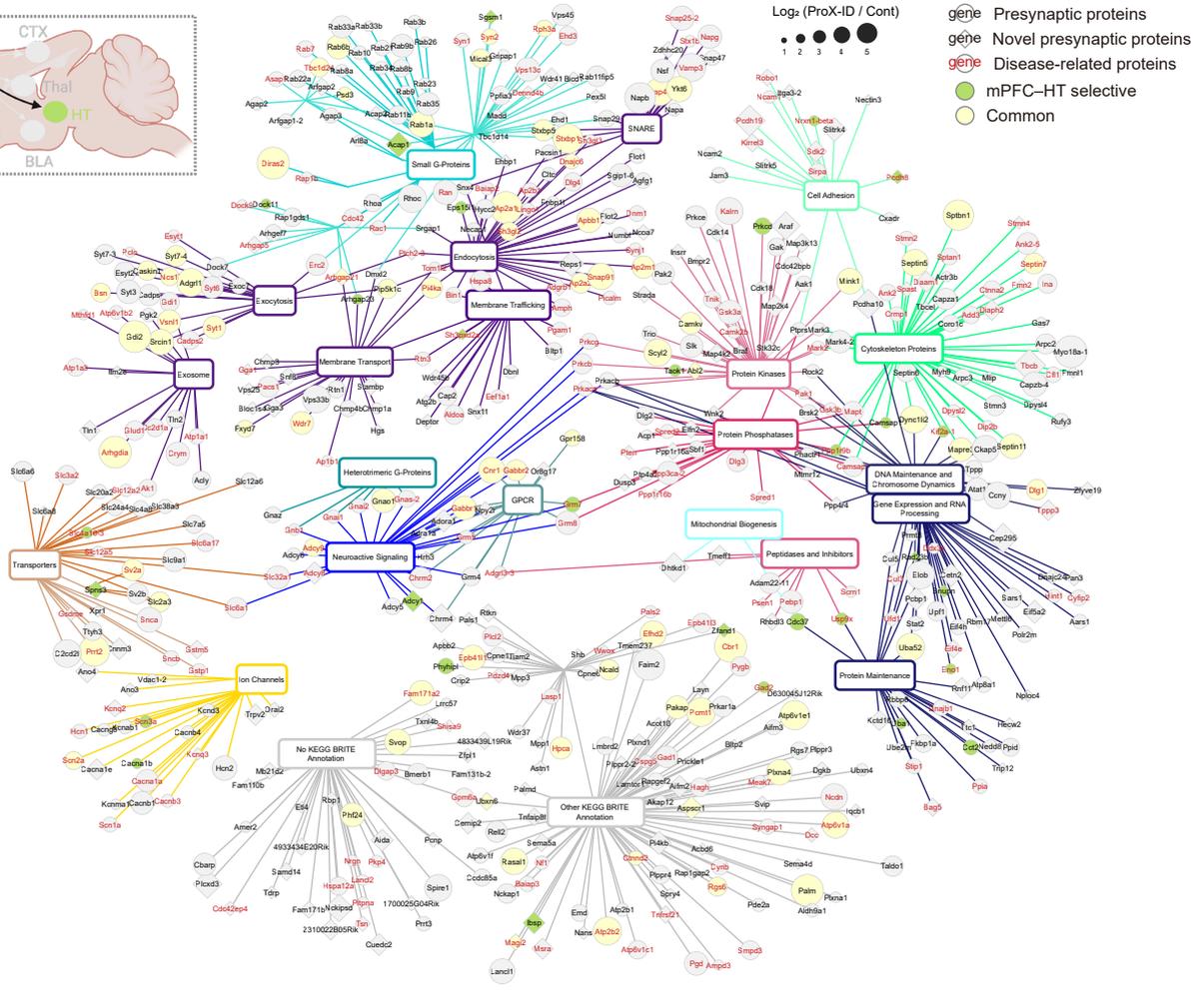
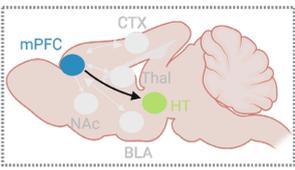


b mPFC-Thal

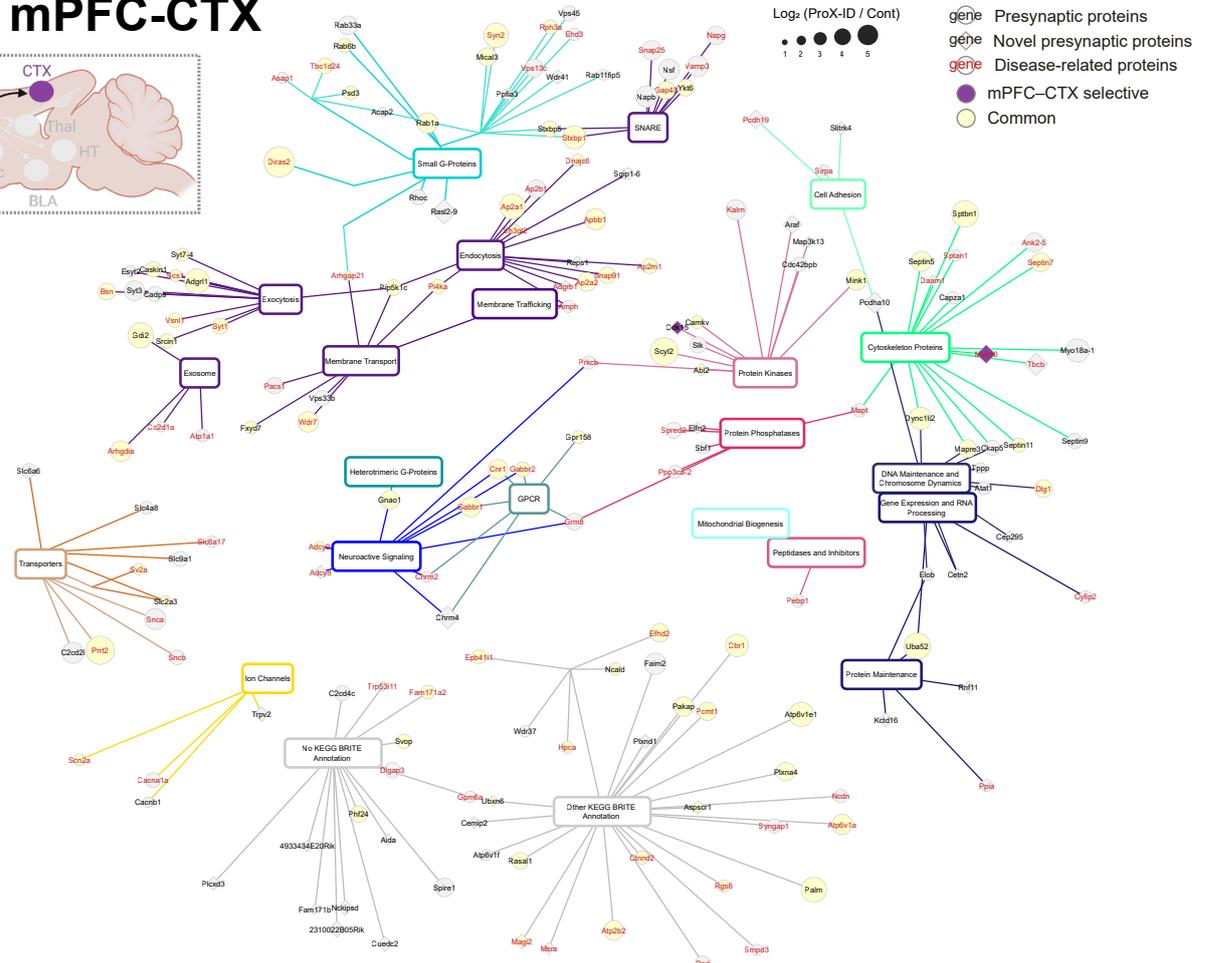
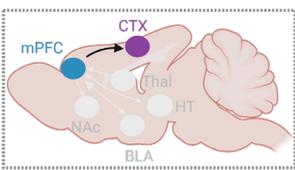


Supplemental Figure 3. Protein-term network for neural pathway-enriched proteins. Protein-term networks for mPFC-NAc-enriched (a) and mPFC-Thal-enriched (b) proteins were constructed using KEGG BRITE annotations. Nodes represent proteins and functional terms, with edges indicating associations based on BRITE functional classifications.

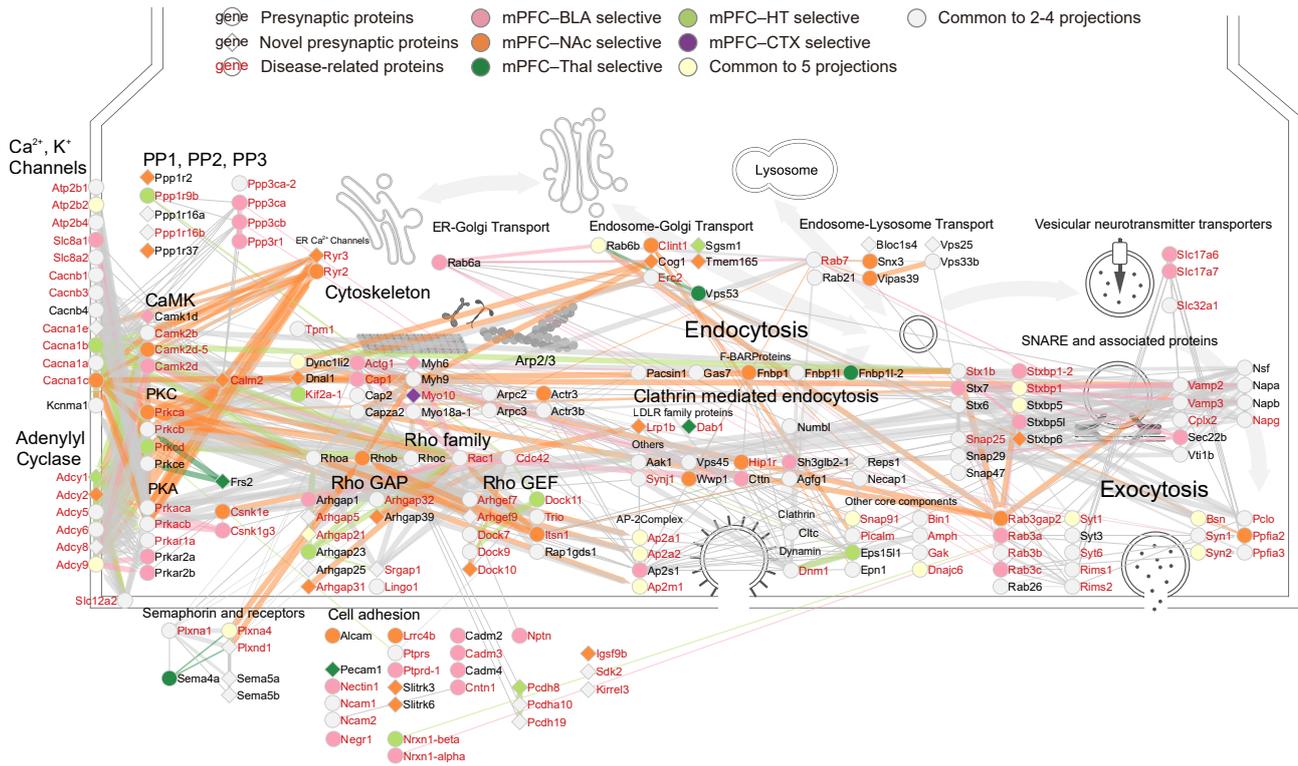
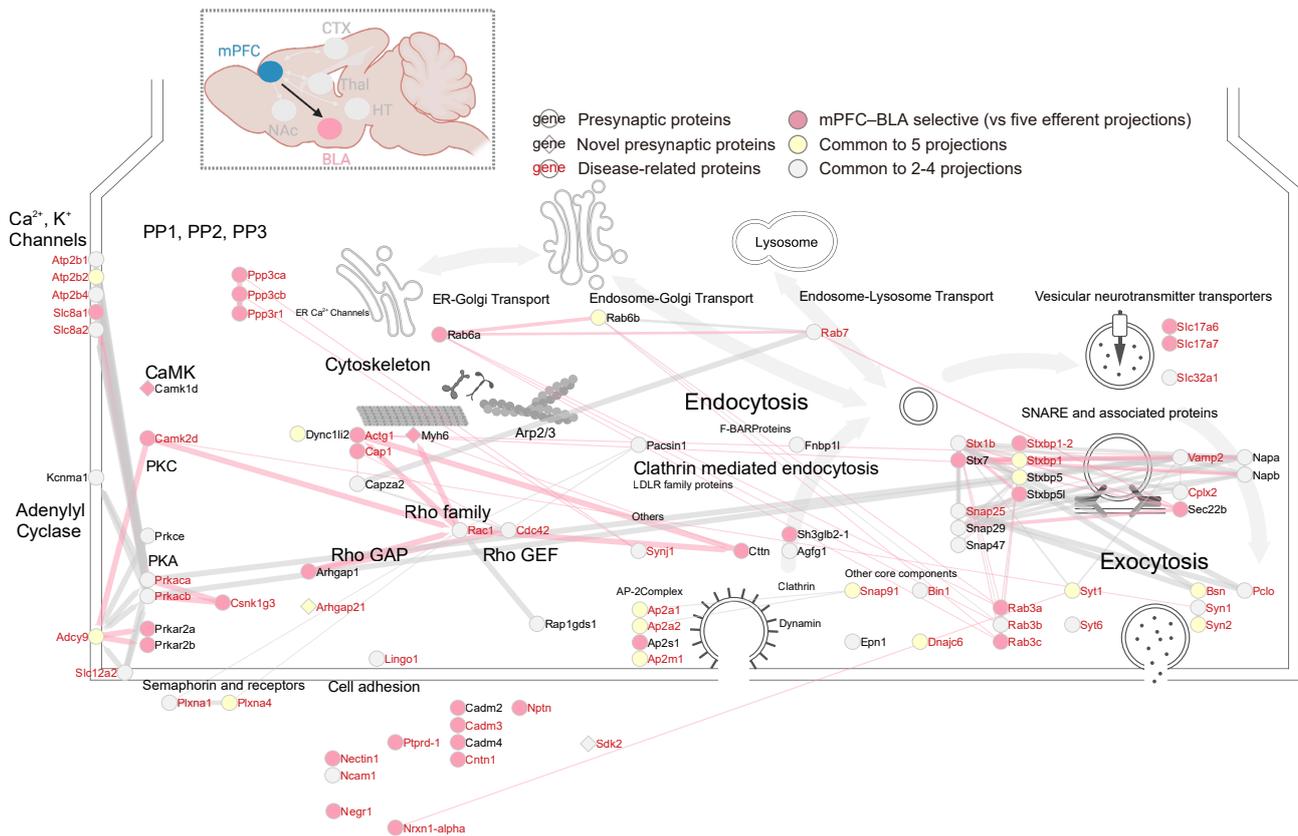
a mPFC-HT



b mPFC-CTX

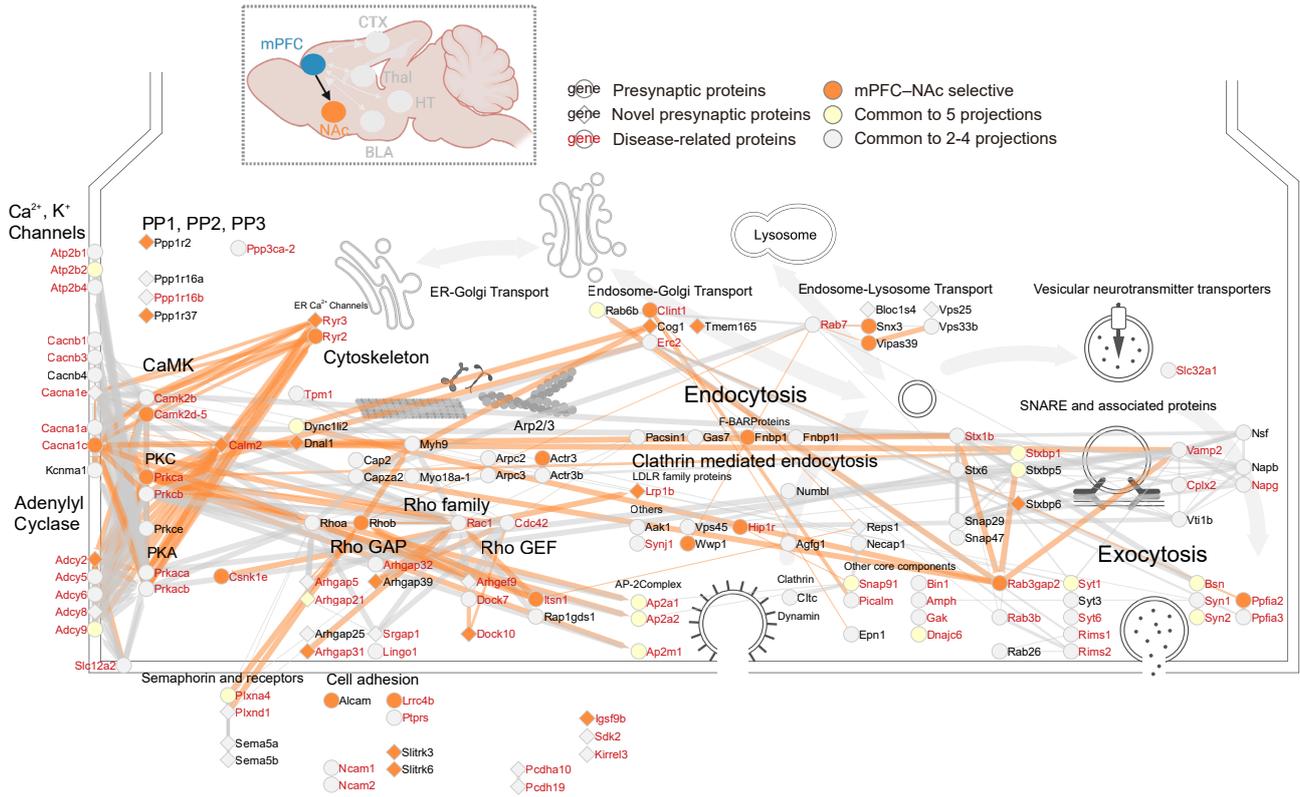


Supplemental Figure 4. Protein-term network for neural pathway-enriched proteins. Protein-term networks for mPFC-HT-enriched (a) and mPFC-CTX-enriched (b) proteins were constructed using KEGG BRITE annotations. Nodes represent proteins and functional terms, with edges indicating associations based on BRITE functional classifications.

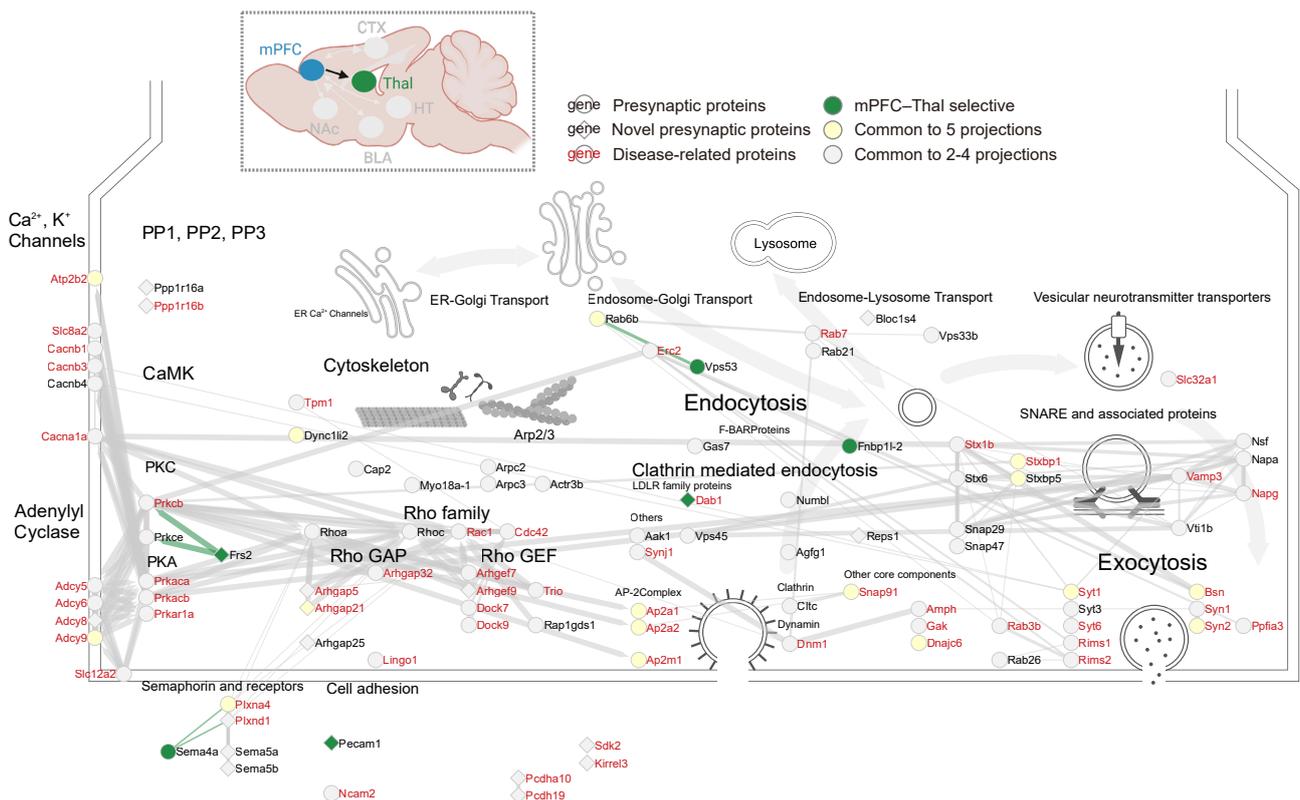
a**b****mPFC-BLA****Supplemental Figure 5. Neural pathway-enriched proteins involved in representative presynaptic events.**

Proteins enriched in at least one of the five mPFC efferent pathways (a) and mPFC-BLA-enriched proteins (b) involved in representative presynaptic events. Edges represent protein-protein interactions (PPIs) retrieved using the Reactome FI plugin in Cytoscape. Edge thickness and transparency reflect FI scores, which range from 0.89 to 1. For visualization, the edge thickness and transparency of PPIs annotated as "complex" were displayed using the same line style as those with an FI score of 0.1.

a mPFC-NAc

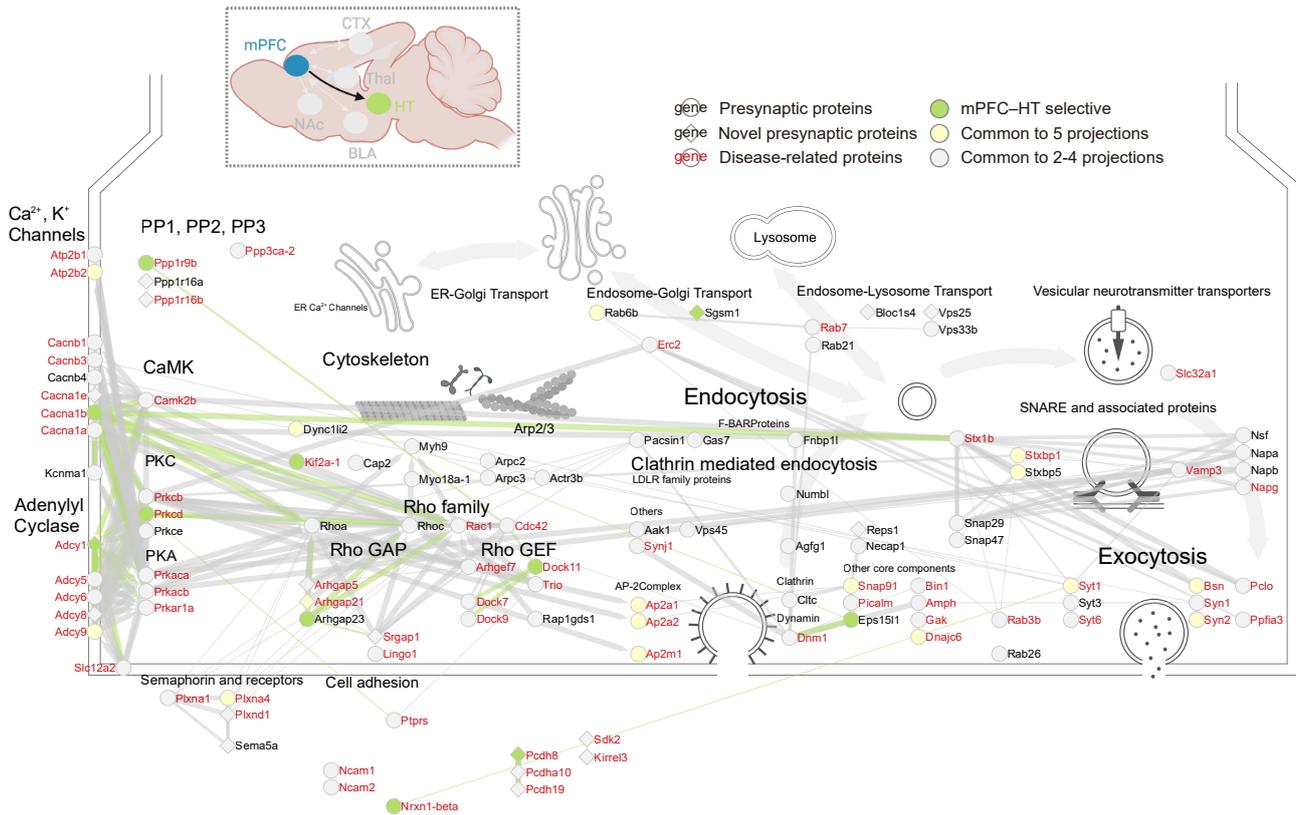


b mPFC-Thal

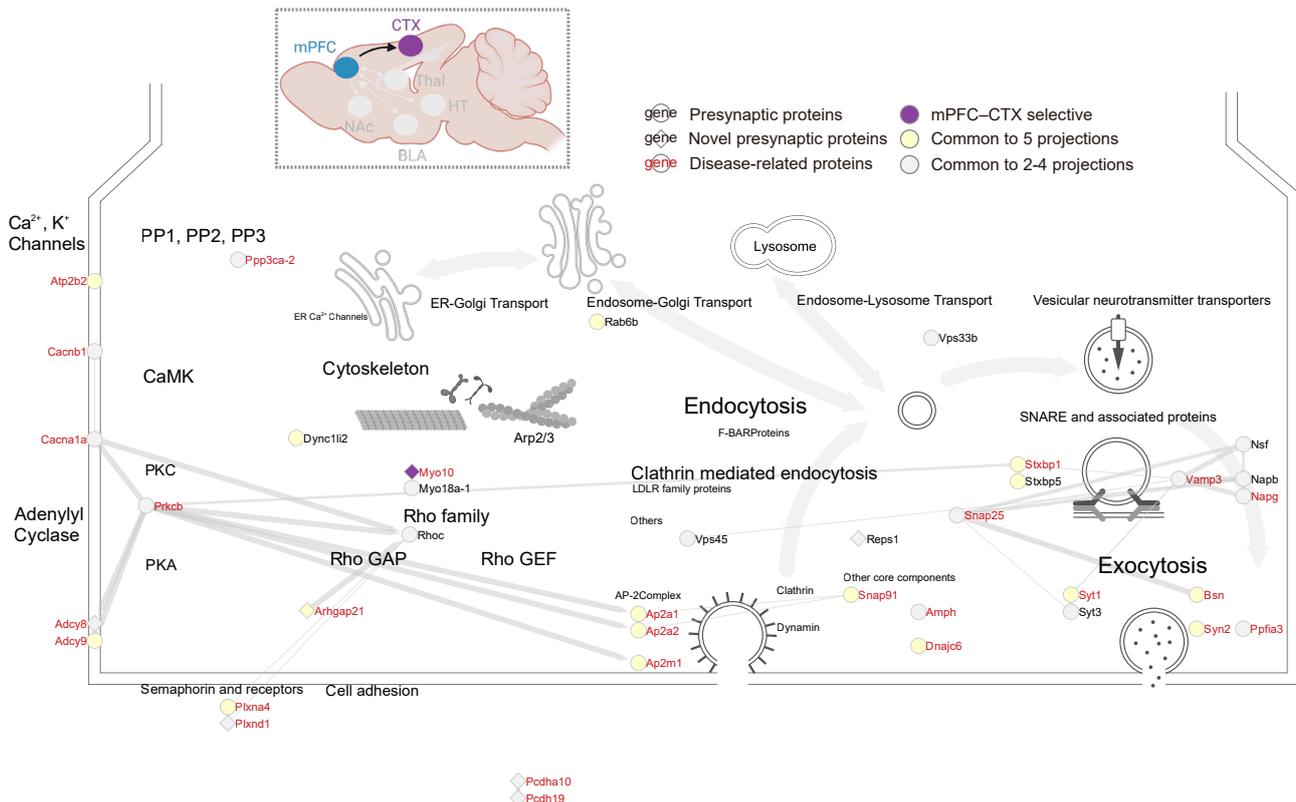


Supplemental Figure 6. Neural pathway-enriched proteins involved in representative presynaptic events. mPFC-NAc-enriched (a) and mPFC-Thal-enriched (b) proteins involved in representative presynaptic events. Edges represent protein-protein interactions (PPIs) retrieved using the Reactome FI plugin in Cytoscape. Edge thickness and transparency indicate FI scores, which range from 0.89 to 1. For visualization, the edge thickness and transparency of PPIs annotated as "complex" were displayed using the same line style as those with an FI score of 0.1.

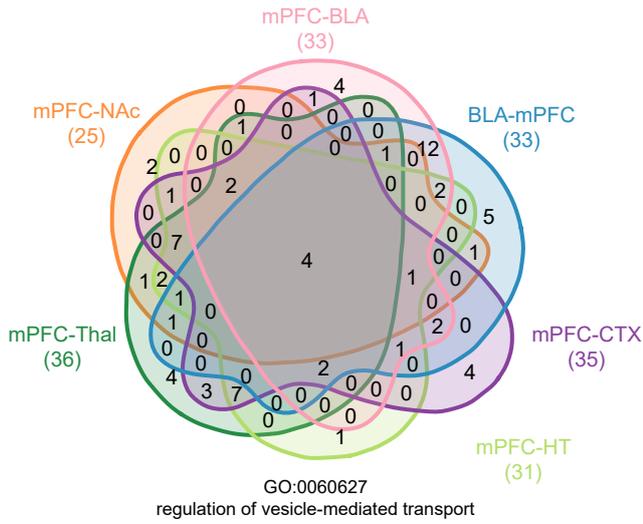
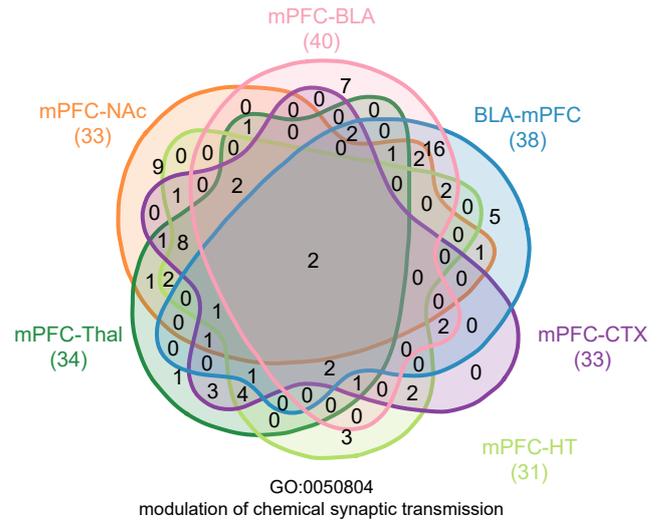
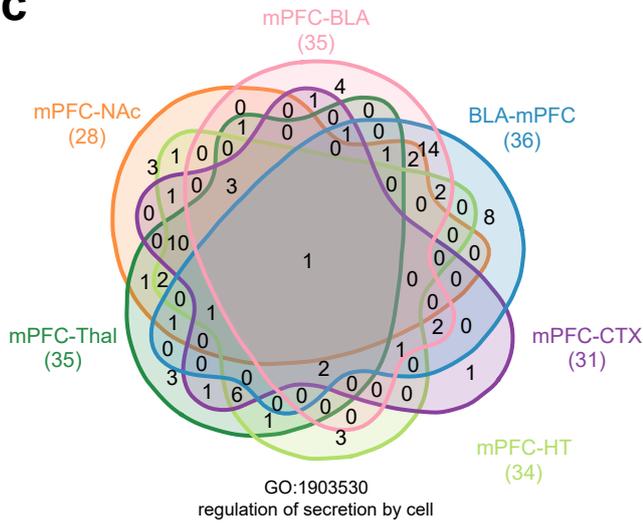
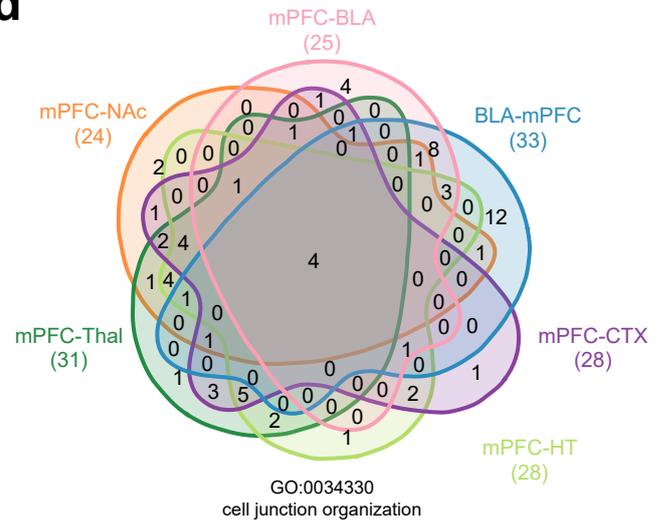
a mPFC-HT



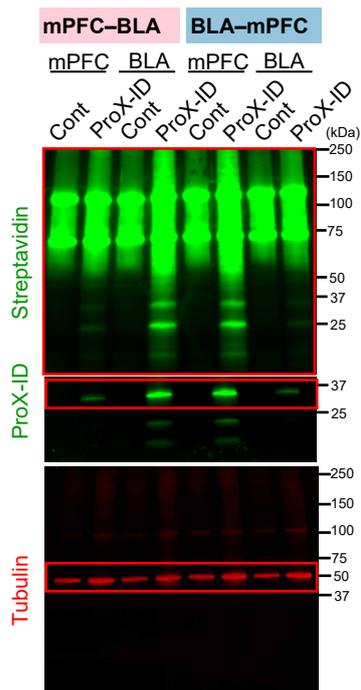
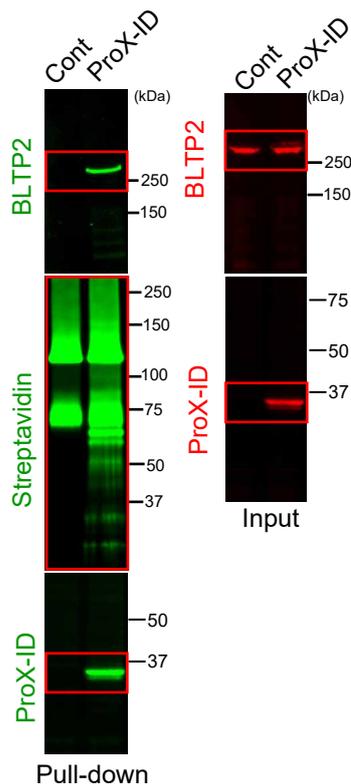
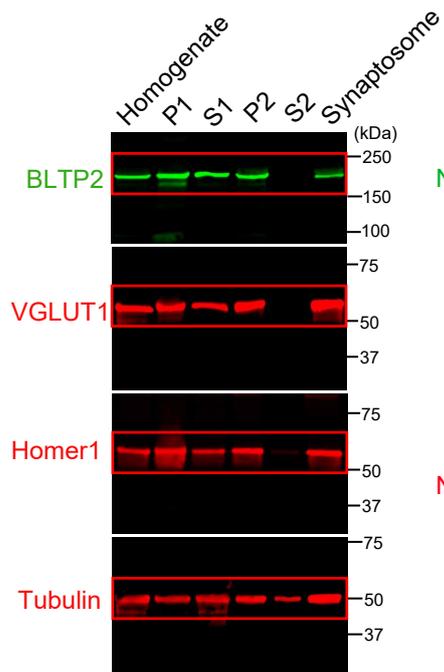
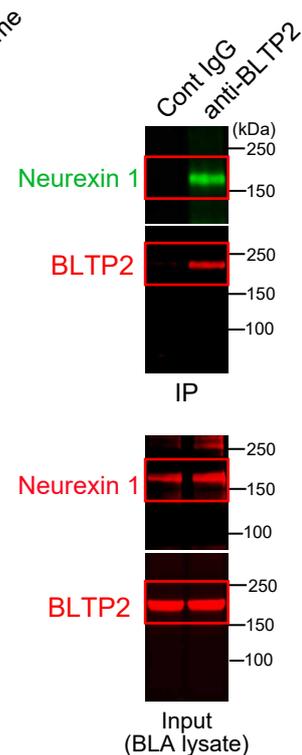
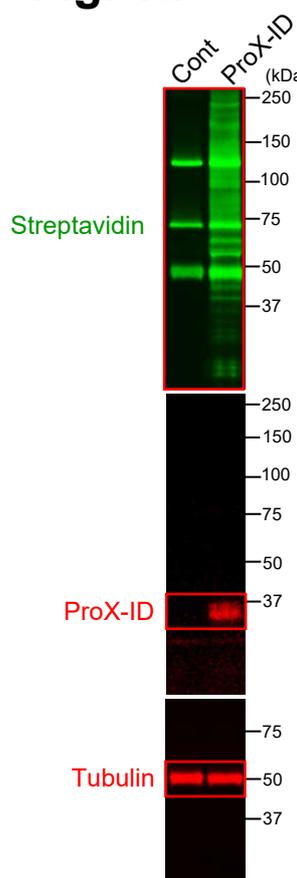
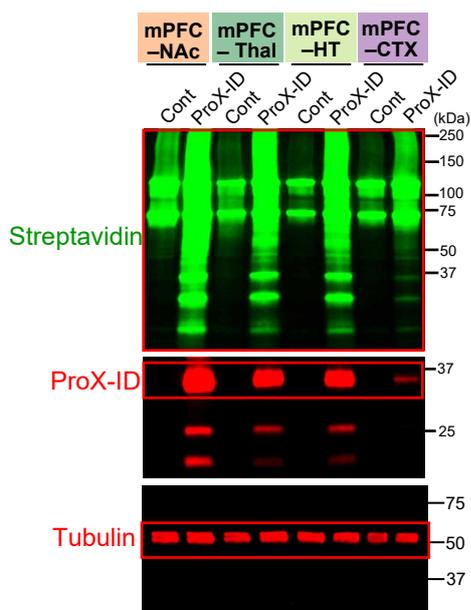
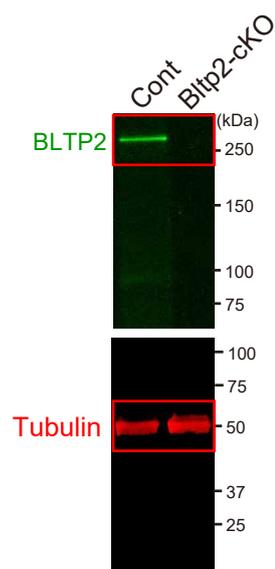
b mPFC-CTX



Supplemental Figure 7. Neural pathway-enriched proteins involved in representative presynaptic events. mPFC-HT-enriched (a) and mPFC-CTX-enriched (b) proteins involved in representative presynaptic events. Edges represent protein-protein interactions (PPIs) retrieved using the Reactome FI plugin in Cytoscape. Edge thickness and transparency indicate FI scores, which range from 0.89 to 1. For visualization, the edge thickness and transparency of PPIs annotated as "complex" were displayed using the same line style as those with an FI score of 0.1.

a**b****c****d****Supplemental Figure 8.**

a–d, Venn diagrams showing the overlap of neural pathway-enriched proteins among the six neural pathways for representative GO terms. Numbers indicate the number of proteins in each intersection. The numbers in parentheses below each projection indicate the number of proteins annotated in the GO terms.

Fig. 1c**Fig. 4b****Fig. 4f****Fig. 5s****Extended Data Fig. 1a****Extended Data Fig. 4a****Extended Data Fig. 7a****Extended Data Fig. 7c**