SUPPORTING INFORMATION FOR:

DISTINCT PROTEOMIC BRAIN STATES UNDERLYING LONG-TERM MEMORY FORMATION IN AVERSIVE OPERANT CONDITIONING

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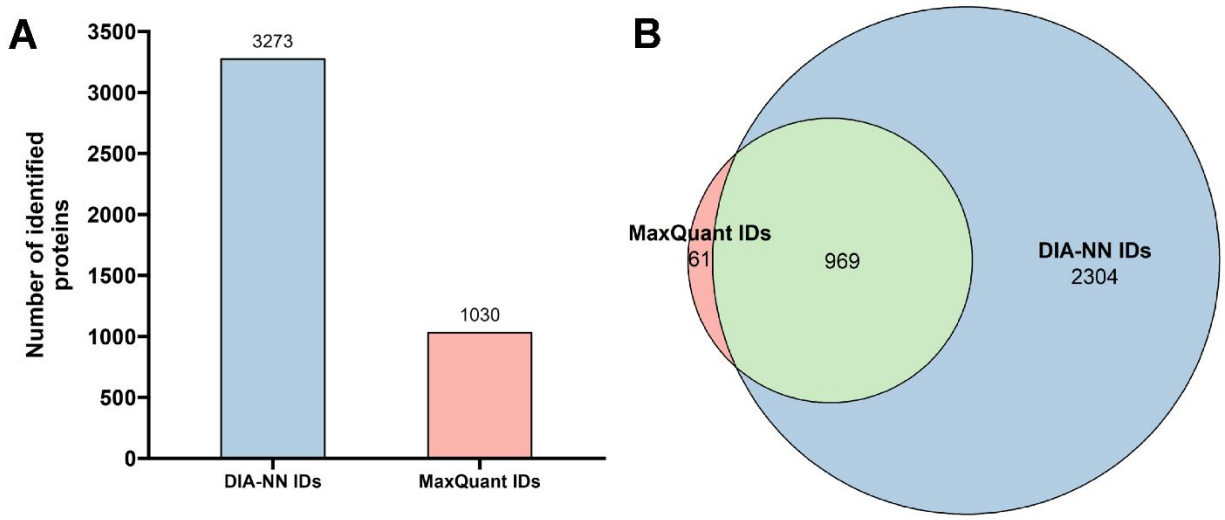
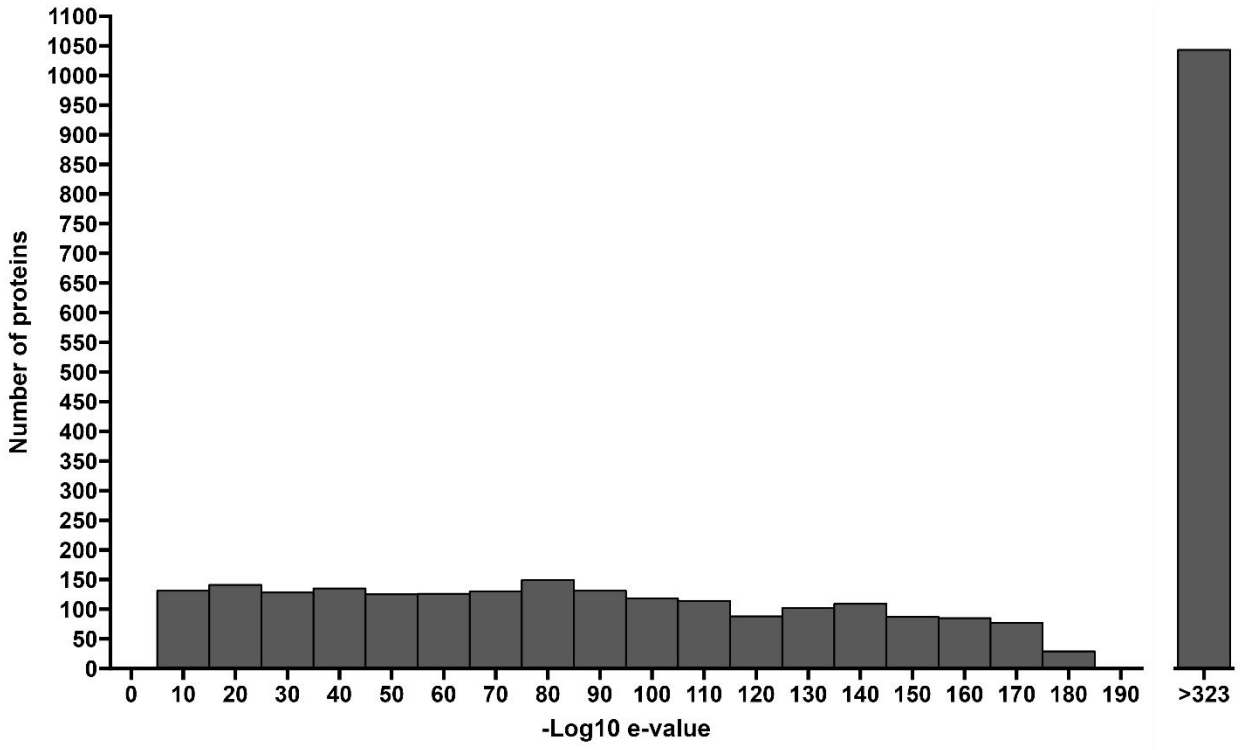
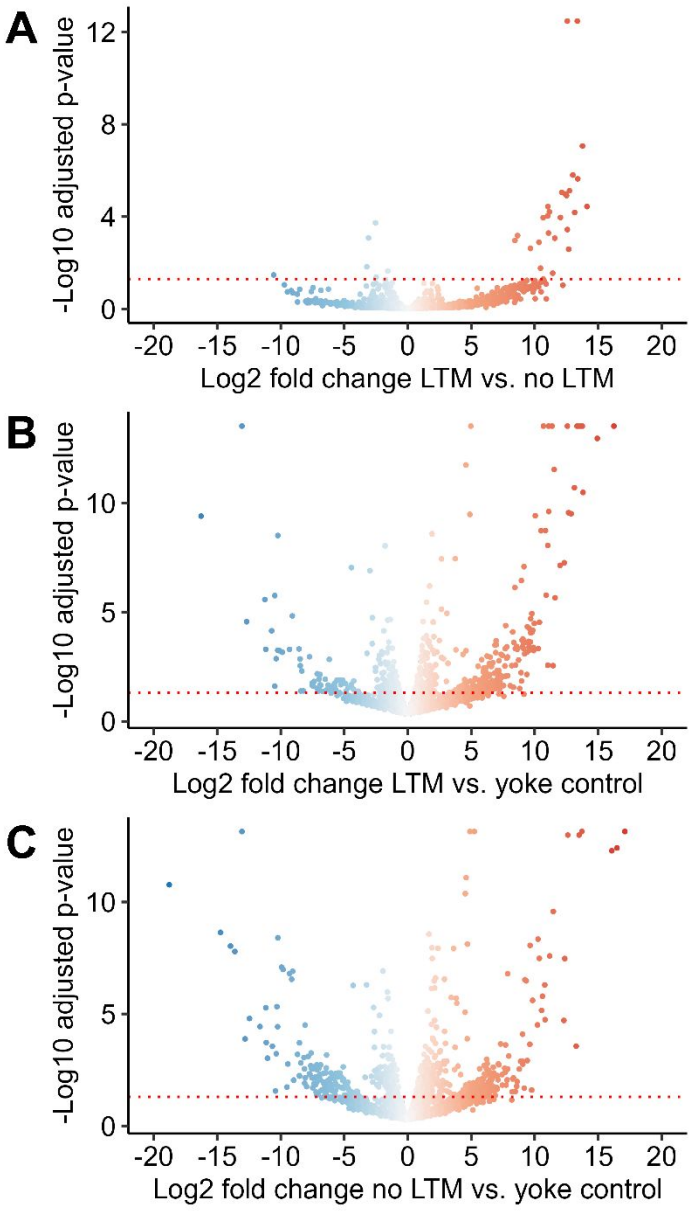


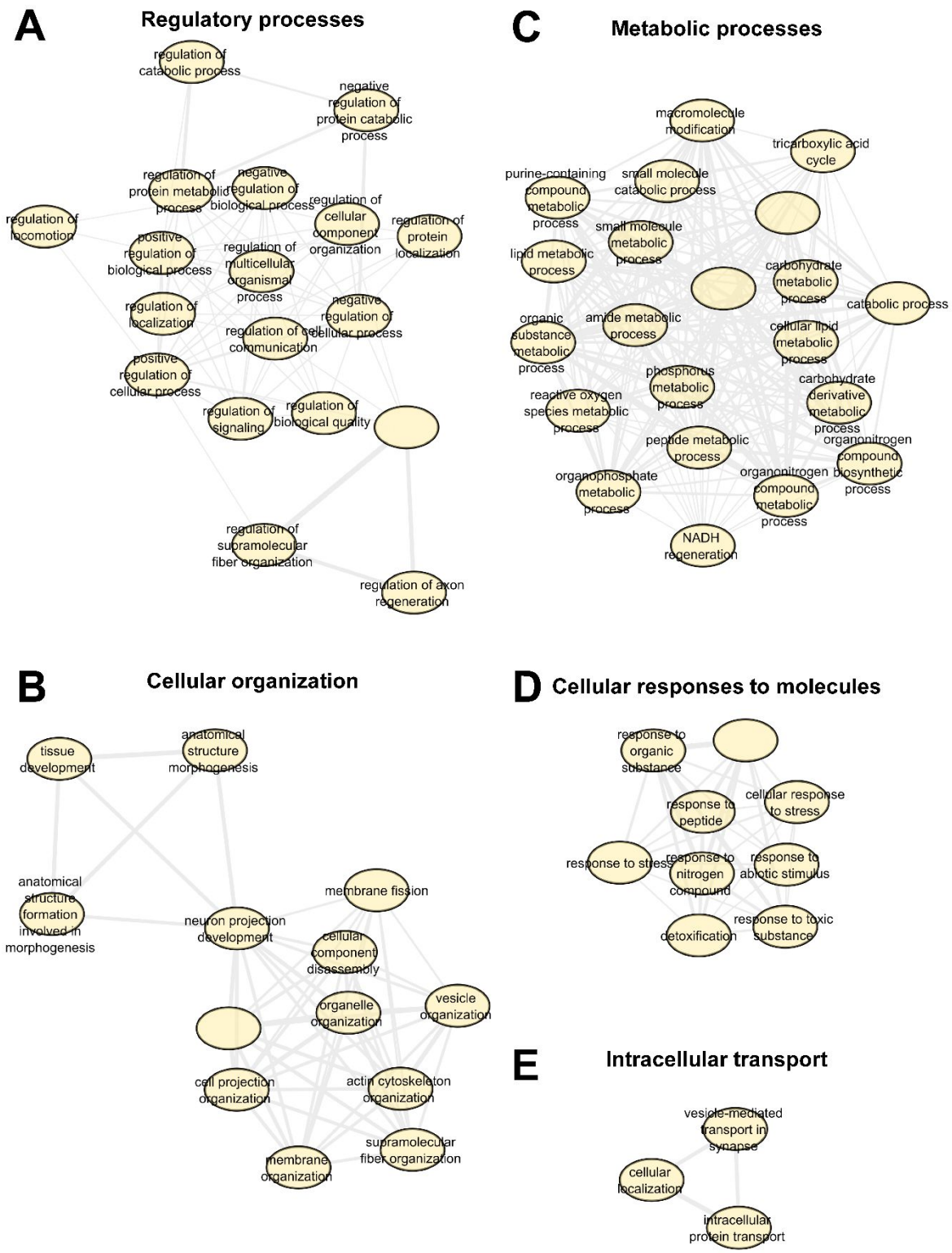
Supplementary Figure 1. Comparison of identification of *L. stagnalis* proteins from raw mass spectrometry output files between MaxQuant and DIA-NN. A) Total number of unique protein groups identified using DIA-NN and MaxQuant. B) Euler plot of unique protein groups identified using DIA-NN and MaxQuant.



Supplementary Figure 2. Distribution of -$\log_{10}$ e-values for mouse homologues of *Lymnaea stagnalis* CNS proteins. Mouse proteins were considered homologues of *Lymnaea stagnalis* proteins for protein-protein BLAST e-value <1E-5. The majority of *Lymnaea stagnalis* e-values were calculated as 0 by BLAST, indicating an e-value of <1E-323.



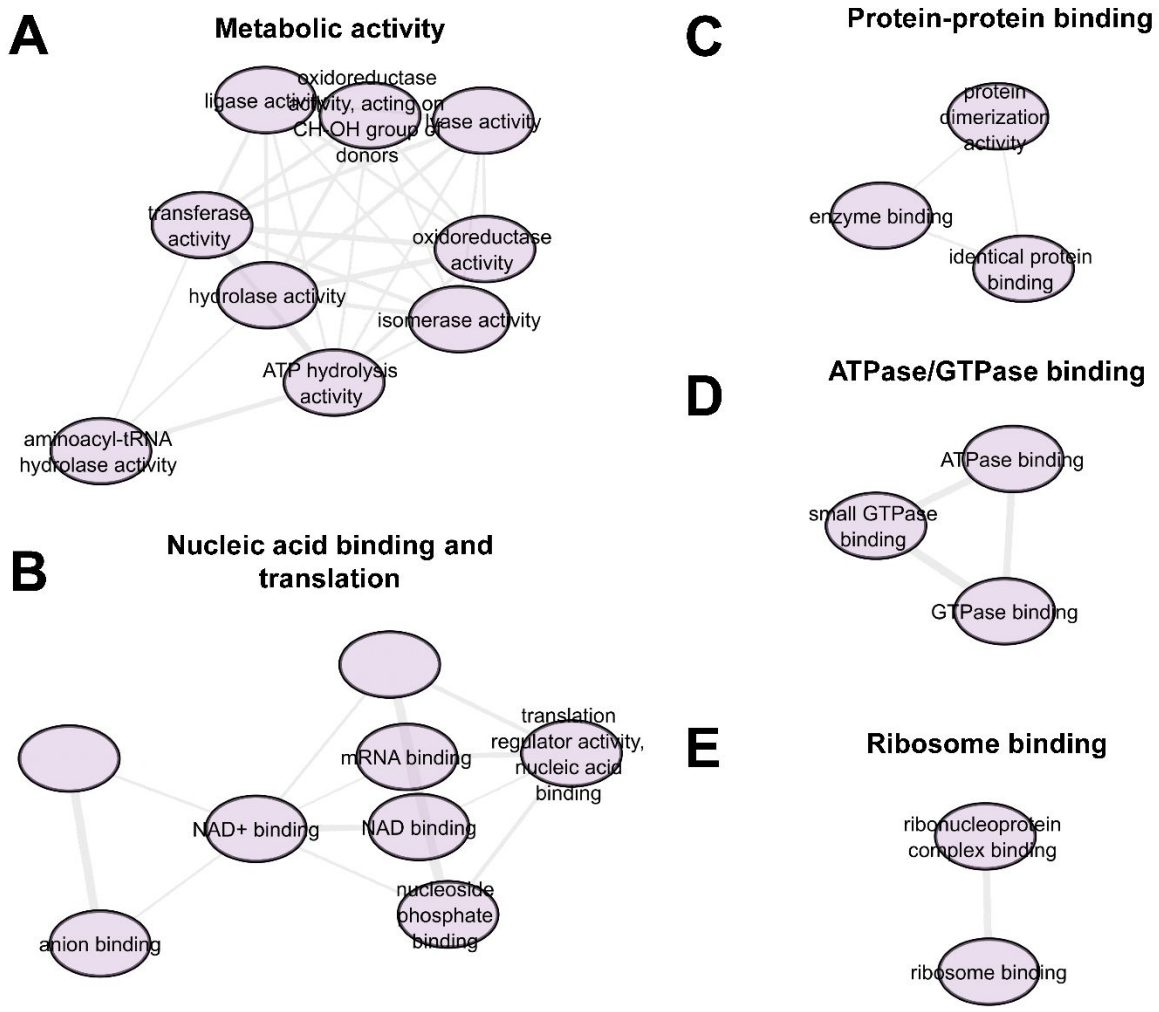
Supplementary Figure 3. **Identification of differentially expressed proteins between LTM, no LTM, and yoke control CNS.** Log2-fold changes and associated -$\log_{10}$-transformed adjusted p-values (FDR) of proteins identified in the DEP workflow[43] between LTM vs. no LTM (B), LTM vs. yoke control (C), and no LTM vs. yoke control (D). Significant differentially expressed proteins lie above the dashed red line, which corresponds to -$\log_{10}$(0.05).



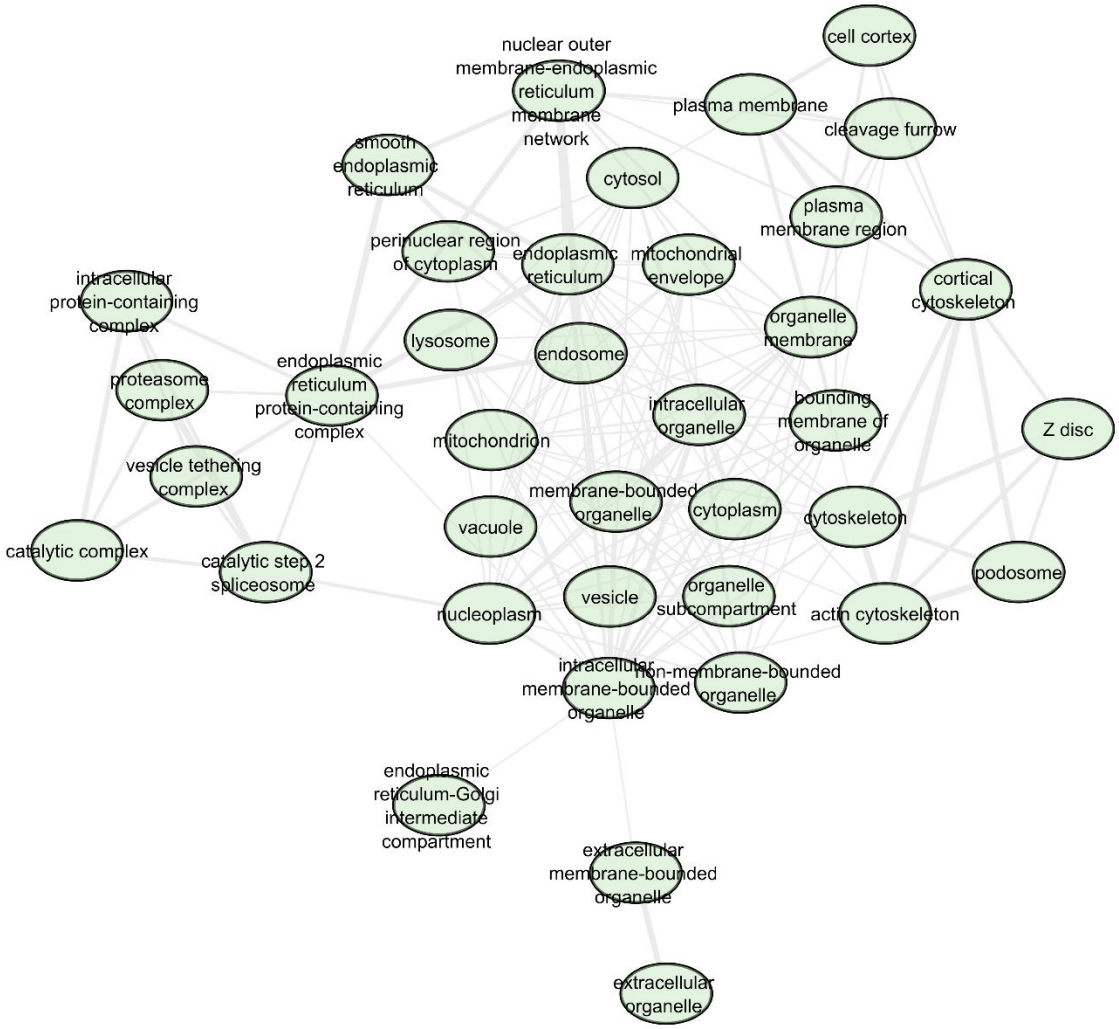
Supplementary Figure 4. Biological process GO terms in LTM-associated differentially regulated protein set.

Graphs of related biological process GO terms reduced and clustered using ReViGO, forming clusters related to

regulatory processes (A), cellular organization (B), metabolic processes (C), cellular responses to molecules (D), and transport (E). Labels are not visible for terms with dispensability >0.4 as determined via the SimRel semantic similarity scoring algorithm.



Supplementary Figure 5. Molecular function GO terms in LTM-associated differentially regulated protein set. Graphs of related molecular function GO terms reduced and clustered using ReViGO, forming clusters related to enzymatic activity (A), mRNA binding and translation (B), enzyme binding (C), ATPase/GTPase binding (D), and ribosome binding (E). Labels are not visible for terms with dispensability >0.4 as determined via the SimRel semantic similarity scoring algorithm.



Supplementary Figure 6. Cellular component GO terms in LTM-associated differentially regulated protein set. Graph of related cellular GO terms reduced and clustered using ReViGO. Labels are not visible for terms with dispensability >0.4 as determined via the SimRel semantic similarity scoring algorithm.