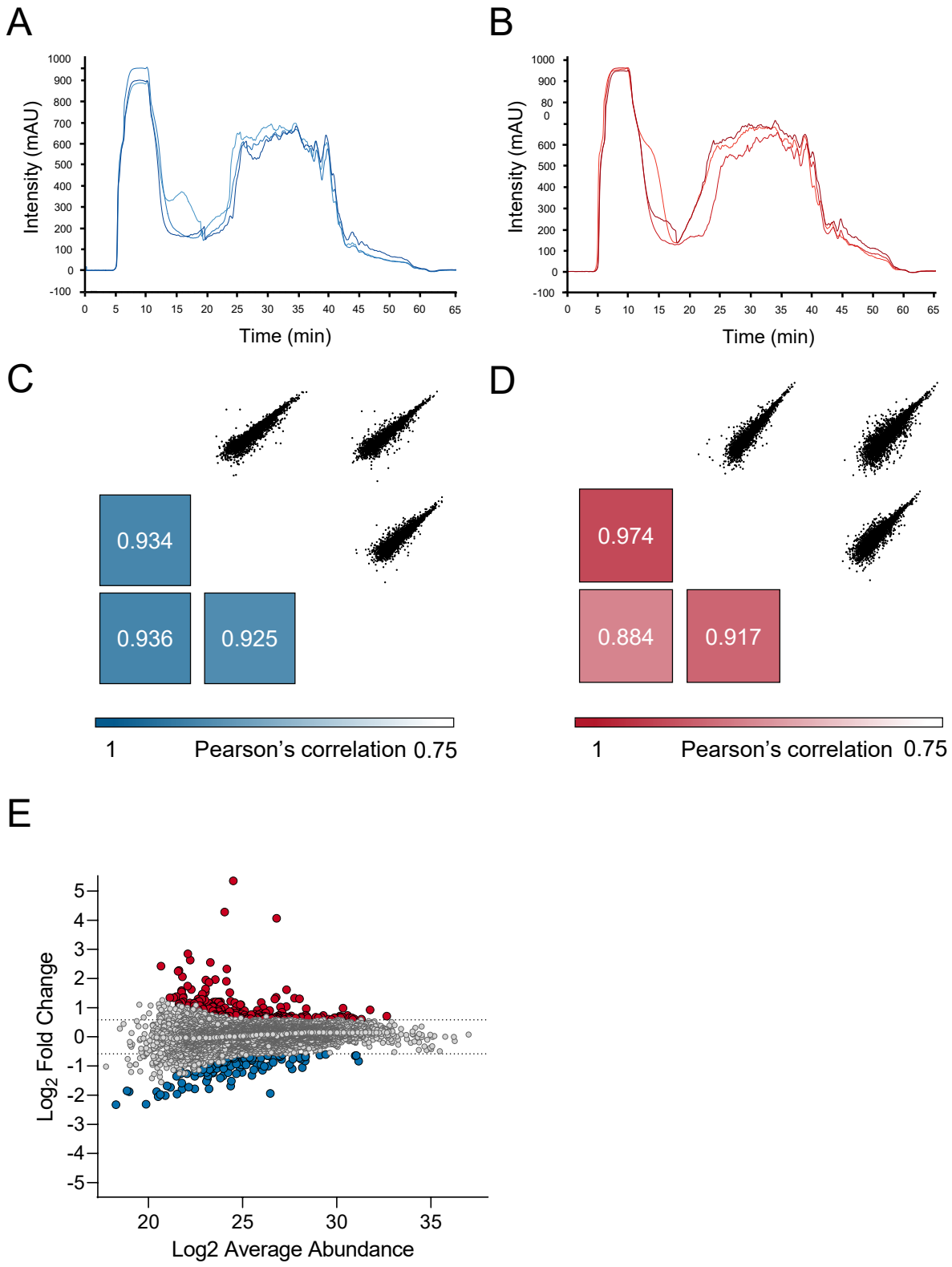
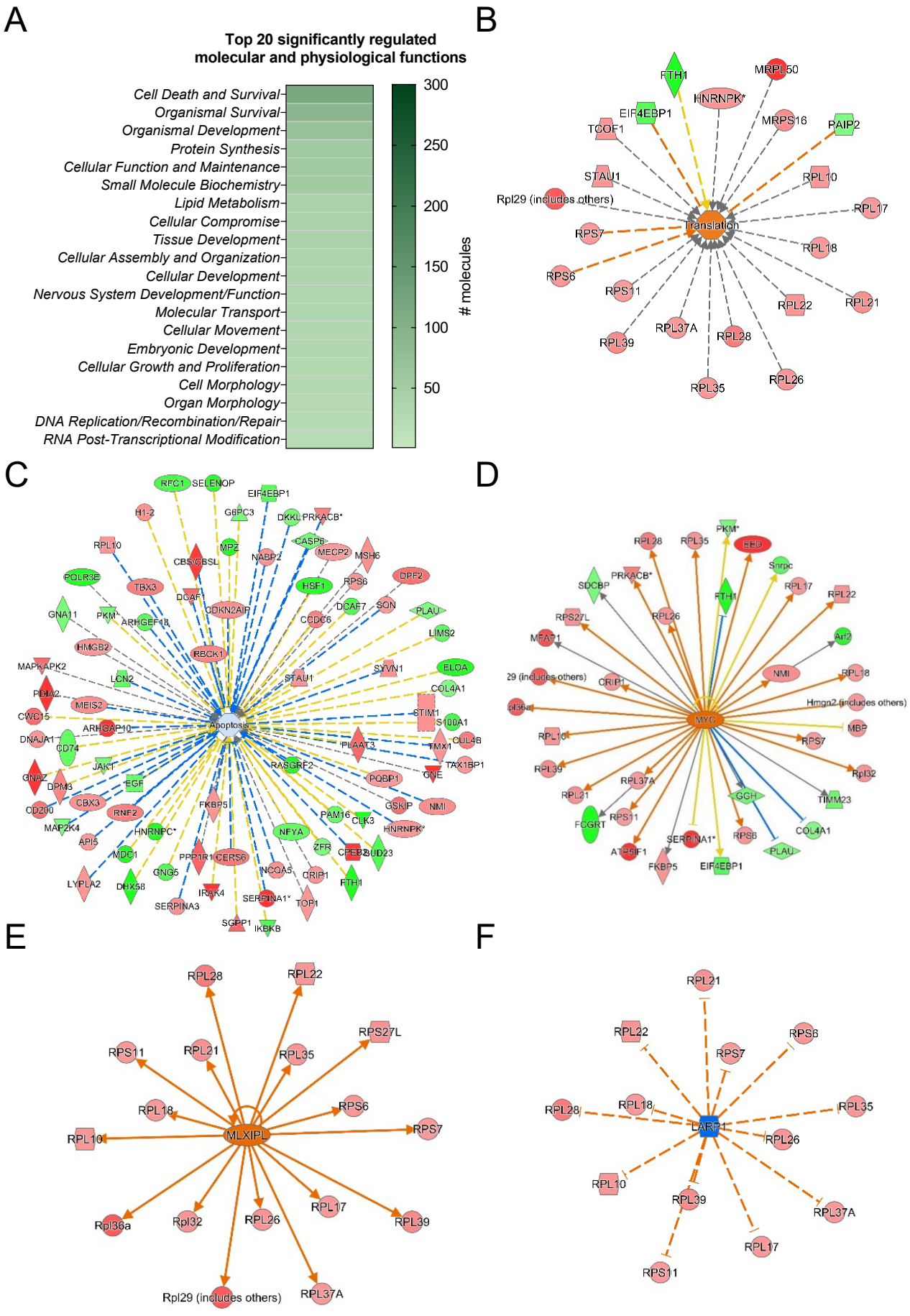
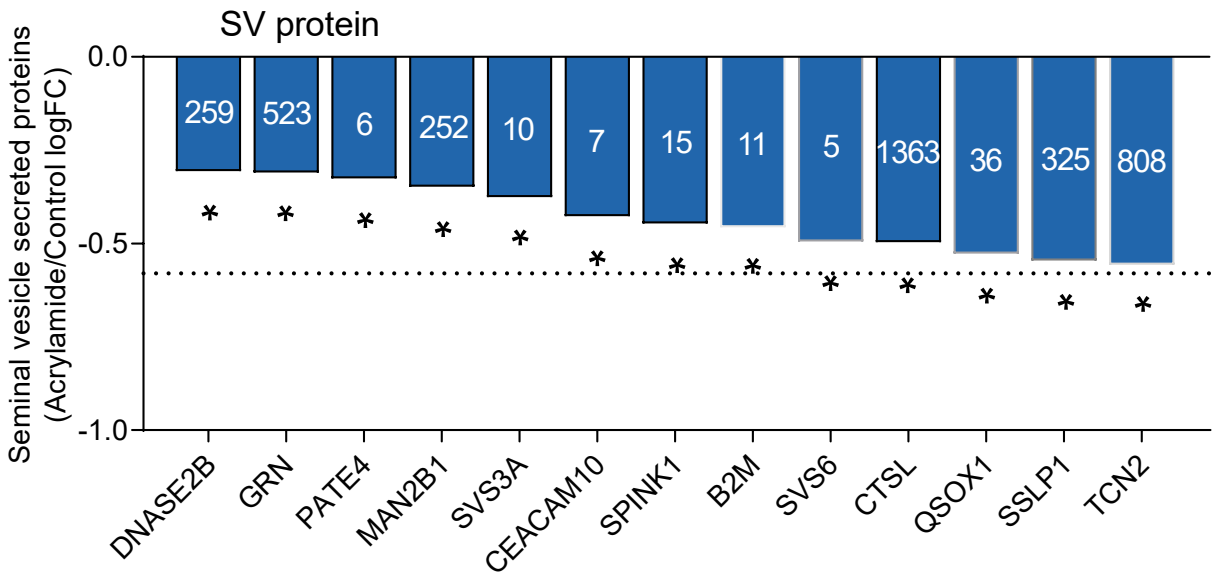


Supplemental Figure S1 Proteomic analysis of mouse seminal vesicle tissue. ***(A-B)*** Hydrophilic interaction liquid chromatography chromatograms and ***(C-D)*** scatter plots of normalized abundances for both control ***(A, C)*** and acrylamide (B, D) seminal vesicle proteomes. (E) MA plot depicting a global illustration of protein abundance compared to those proteins that were significantly different (fold-change ≥ 1.5 or ≤ -1.5 and p value ≤ 0.05).



Supplemental Figure S2. Molecular functions and upstream regulators influenced by acrylamide exposure in the mouse seminal vesicles. Ingenuity Pathway Analysis was used to predict ($p \leq 0.05$) molecular and physiological functions associated with the seminal vesicle proteins that were differentially

regulated following acrylamide treatment. Data are presented as a heat map based on –log10 p values, and show the top 20: (A) molecular and physiological functions associated with differentially expressed proteins. (B-C) Molecular and physiological functions predicted to be activated ((B) translation, orange), or inhibited ((C) apoptosis, blue) are presented as interaction networks with differentially regulated proteins (red = up-regulated, green = down-regulated) in the dataset. (D-F) Upstream regulators including: (E) Myc proto-oncogene protein (MYC) and (F) MLX-interacting protein-like (MLXIPL), which were predicted to be activated (orange), or (F) La-related protein 1 (LARP1), which was predicted to be inhibited (blue), are presented as interaction networks with proteins differentially regulated by acrylamide (red = up-regulated, green = down-regulated). Connecting lines indicate several predicted relationships that lead to activation (orange), inhibition (blue), relationship inconsistent with that documented in the literature (yellow), and relationship is known but effects on function is yet to be completely characterized (grey).



Supplemental Figure S3. Proteins secreted by mouse seminal vesicles are influence by acrylamide. Expression of seminal vesicle secreted proteins (n = 3 individual mice per treatment group) identified by proteomics of mouse seminal vesicle fluid as statistically significant ($p \leq 0.05$ indicated by *) but not matching our expression change criteria (fold-change ≥ 1.5 or ≤ -1.5 and $p \leq 0.05$) in our proteomic analysis. Data are presented as column graphs of log fold-change (logFC) with the order of abundance within the core proteome protein shown within the columns.