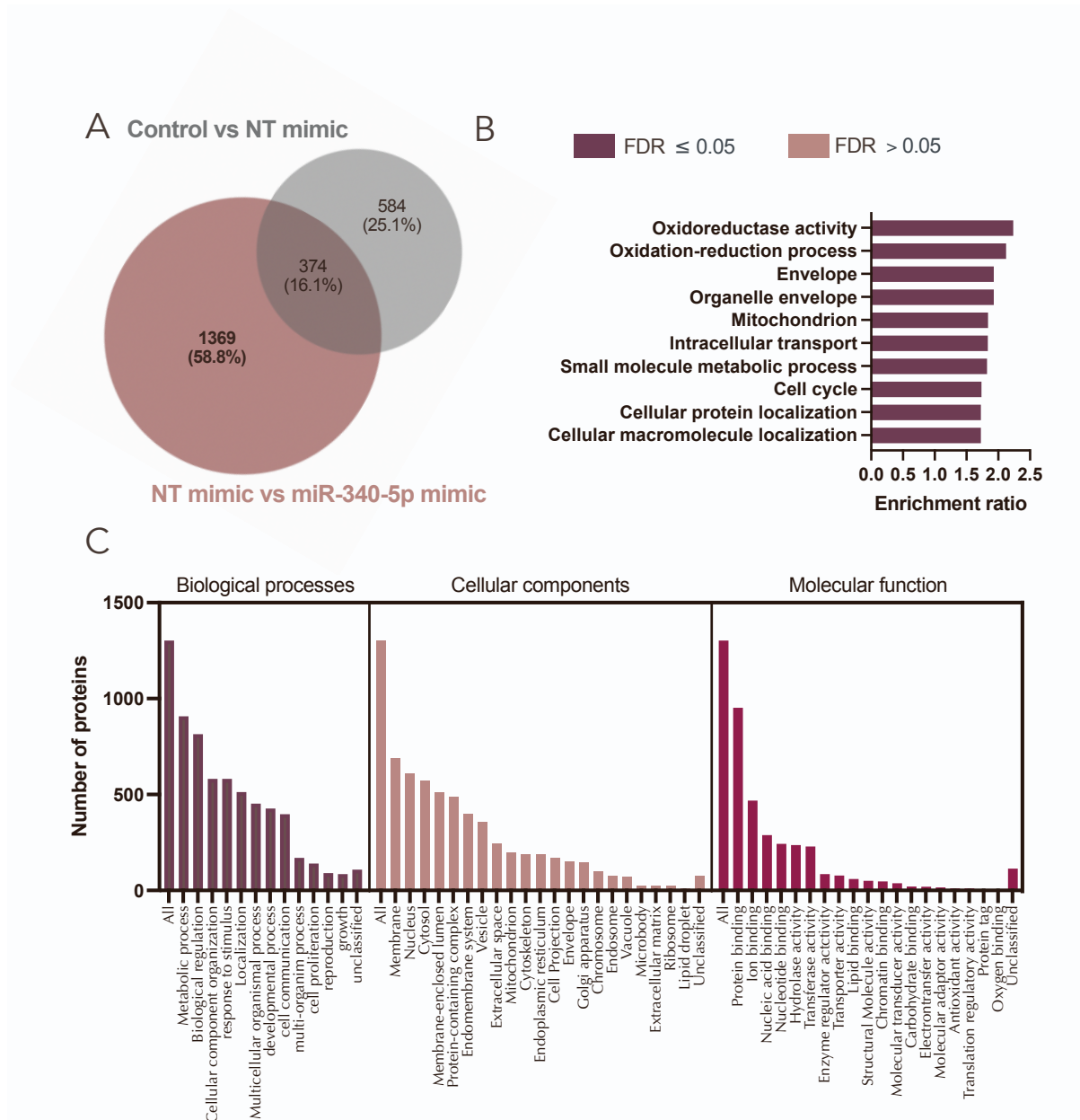


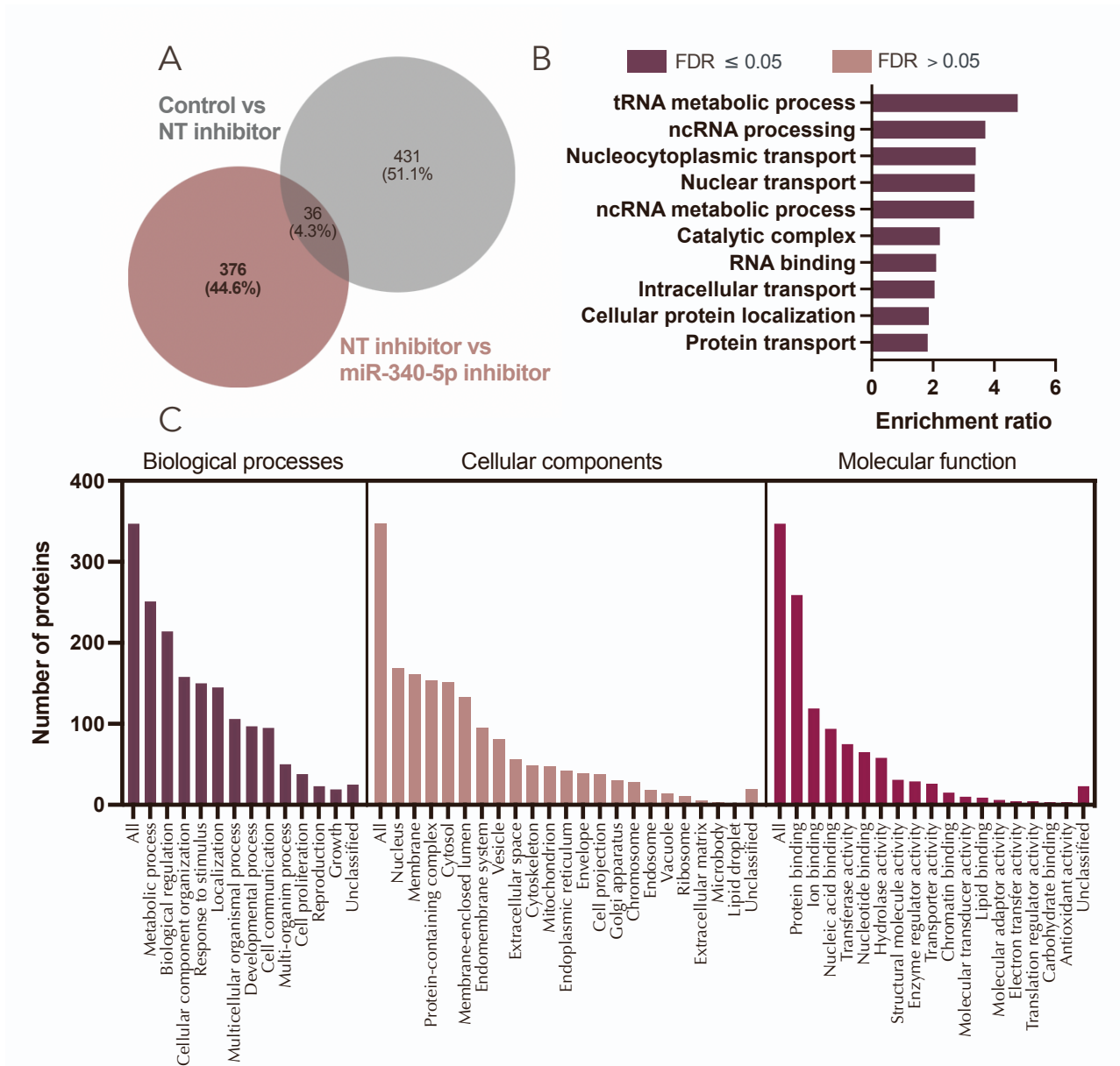
Supplemental information

**MicroRNAs emerging coordinate with placental
mammals alter pathways in endometrial epithelia
important for endometrial function**

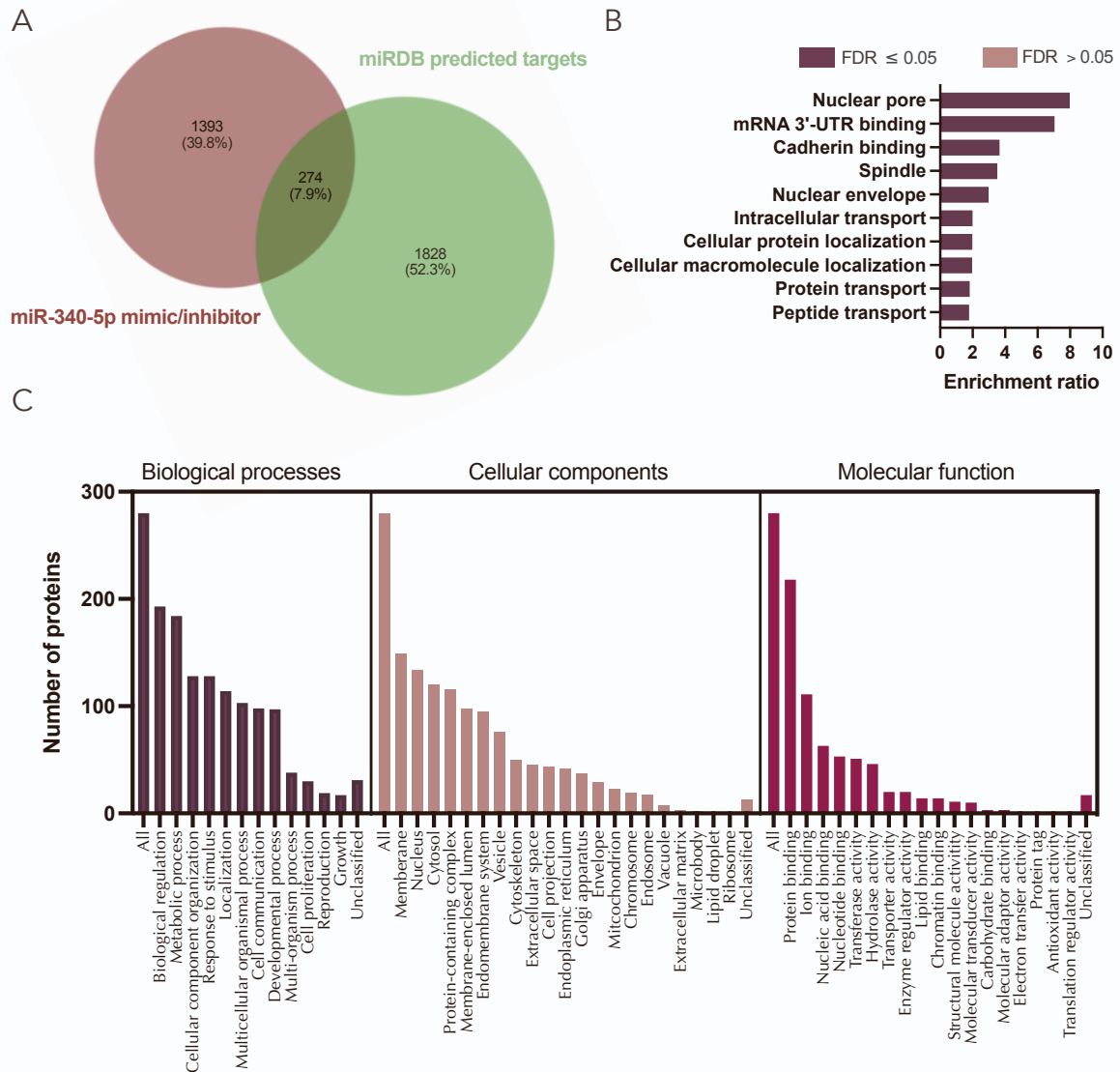
Laura Hume, Jessica C. Edge, Haidee Tinning, Dapeng Wang, Alysha S. Taylor, Vladimir Ovchinnikov, Annika V. Geijer-Simpson, Pavle Vrljicak, Jan J. Brosens, Emma S. Lucas, Nigel A.B. Simpson, Jayne Shillito, Karen Forbes, Mary J. O'Connell, and Niamh Forde



Supplementary Figure 1: Proteins altered in Ishikawa cells following treatment with miR-340-5p mimic related to Figure 9. A) Venn diagram depicting total number of significantly differentially expressed proteins ($p < 0.05$) following transfection of Ishikawa cells ($n = 3$ biological replicates) with miR-340-5p mimic (LHS) and non-targeting (NT) mimic (RHS). **B)** Enriched KEGG pathways associated with miR-340-5p mimic regulated proteins. **C)** WebGestalt overrepresentation analysis of biological process, cellular component and molecular function categories for identified significantly differentially expressed proteins ($p < 0.05$) in response to miR-340-5p mimic.

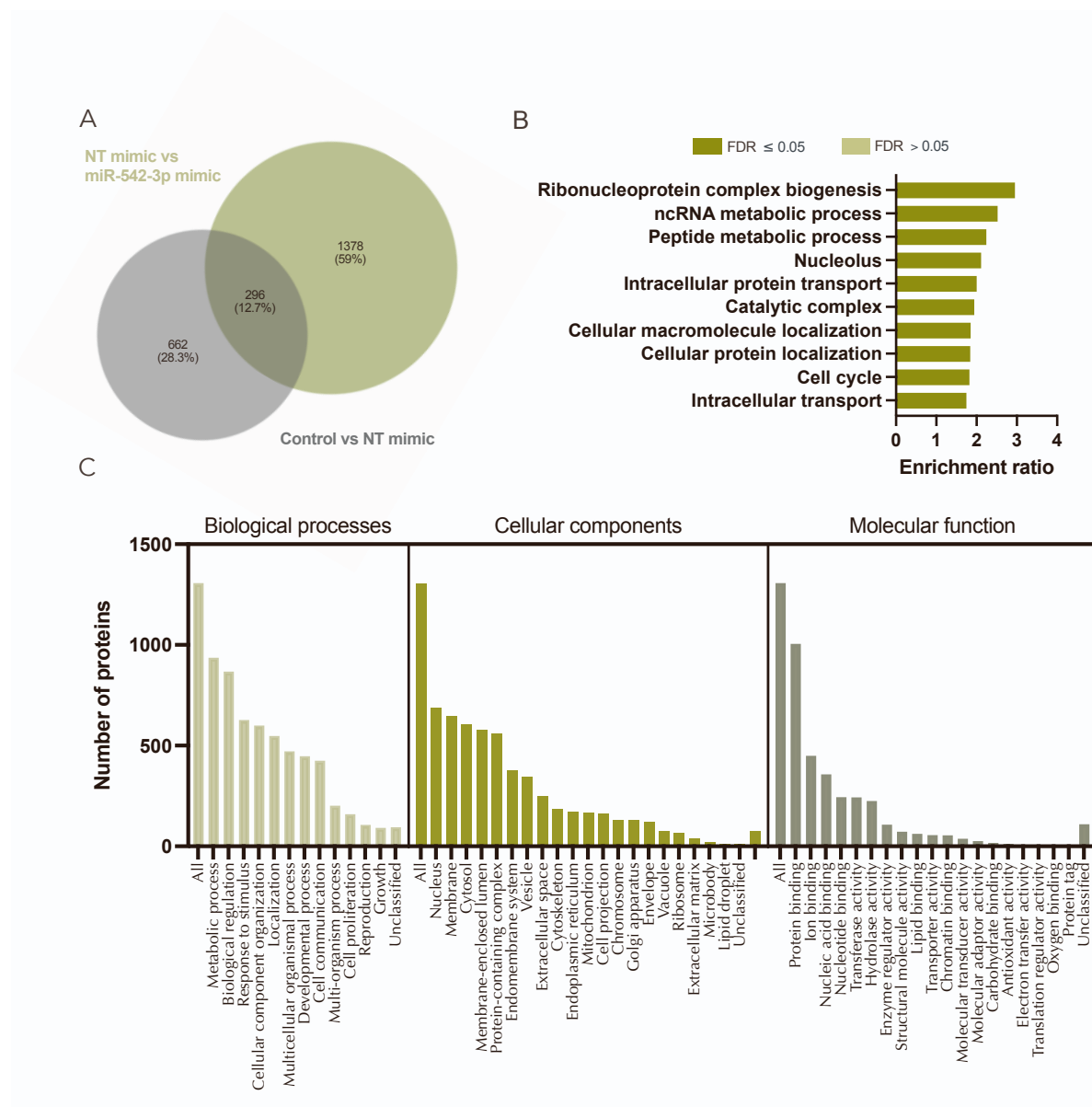


Supplementary Figure 2: Proteins altered in Ishikawa cells following treatment with miR-340-5p inhibitor related to Figure 9. A) Venn diagram depicting total number of significantly differentially expressed proteins ($p < 0.05$) following transfection of Ishikawa cells ($n = 3$ biological replicates) with miR-340-5p inhibitor (LHS) and non-targeting (NT) inhibitor (RHS). **B)** Enriched KEGG pathways associated with miR-340-5p inhibition regulated proteins. **C)** WebGestalt overrepresentation analysis of biological process, cellular component and molecular function categories for identified significantly differentially expressed proteins ($p < 0.05$) in response to miR-340-5p inhibitor.



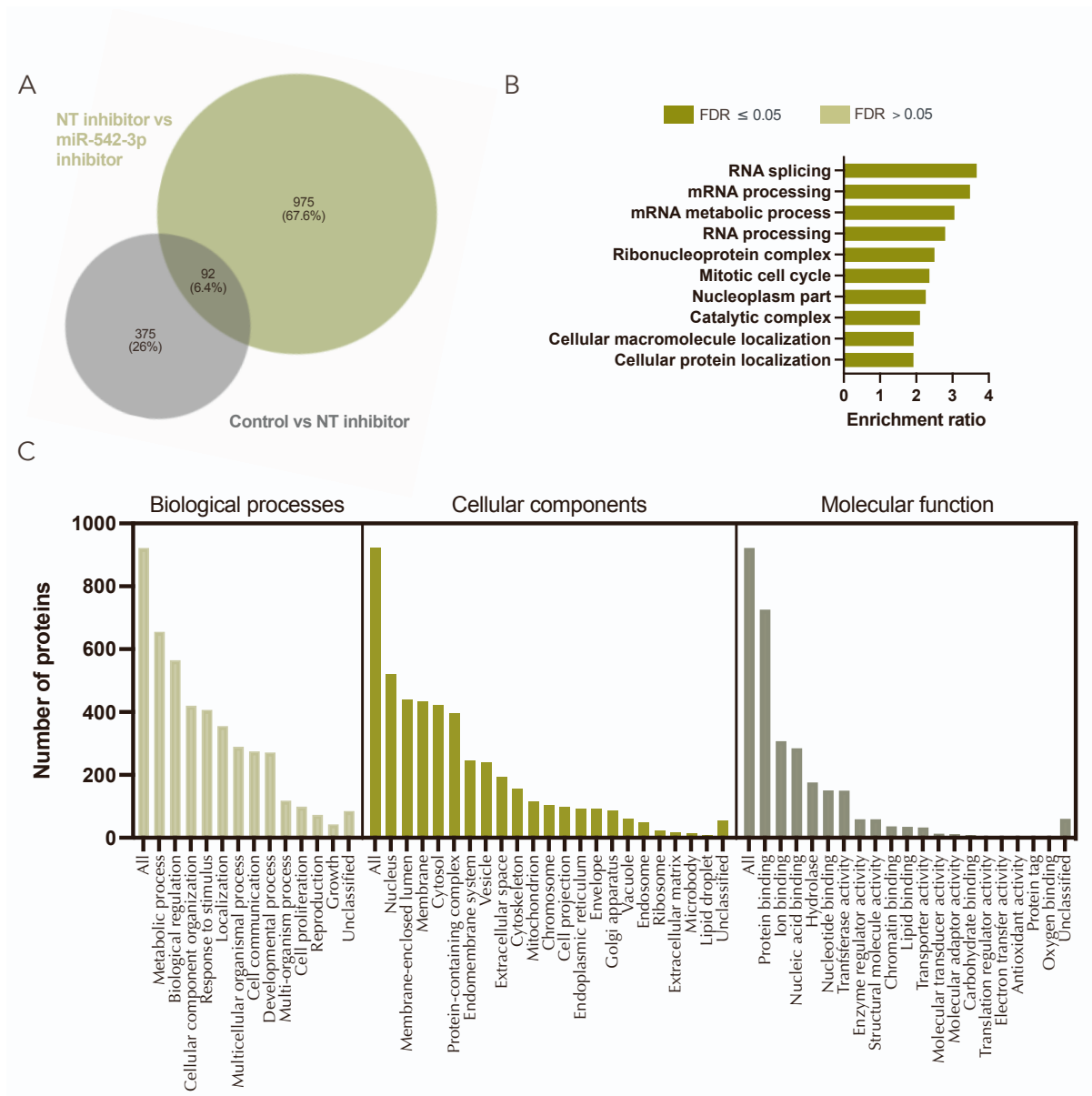
Supplementary Figure 3: Proteins altered in Ishikawa cells following treatment with miR-340-5p mimic and inhibitor compared to mirDB predicted targets related to Figure 9. A) Venn diagram depicting total number of significantly differentially expressed proteins ($p < 0.05$) following transfection of Ishikawa cells ($n = 3$ biological replicates) with miR-340-5p mimic or inhibitor vs non-targeting controls and mirDB predicted targets. **B)** Enriched KEGG pathways associated with miR-340-5p mimic and inhibition regulated proteins and predicted target overlap. **C)** WebGestalt overrepresentation analysis of biological process, cellular component

and molecular function categories for identified significantly differentially expressed proteins ($p < 0.05$) in response to miR-340-5p mimic and inhibition and predicted targets.



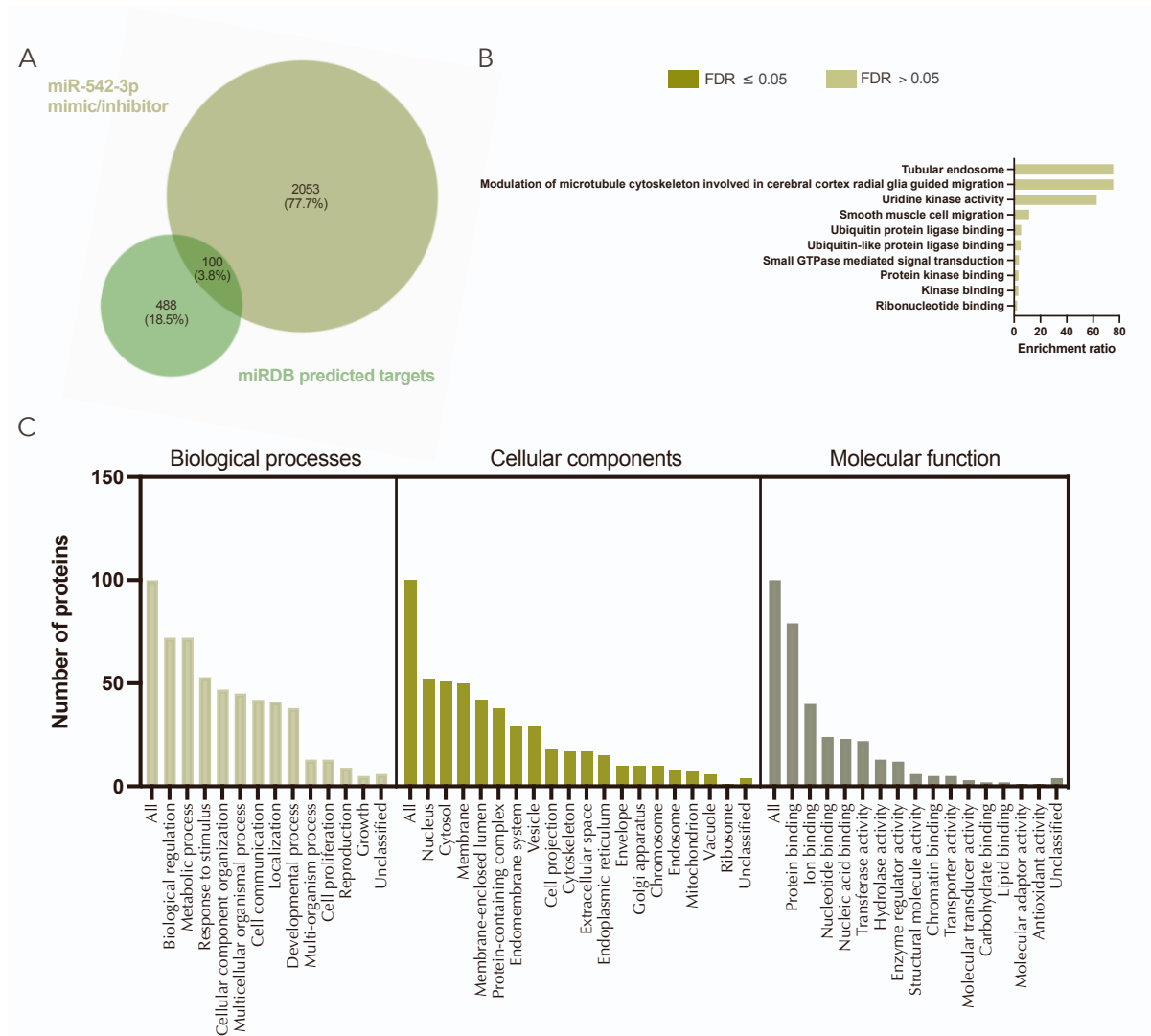
Supplementary Figure 4: Proteins altered in Ishikawa cells following treatment with miR-542-3p mimic related to Figure 11. A) Venn diagram depicting total number of significantly differentially expressed proteins ($p < 0.05$) following transfection of Ishikawa cells ($n=3$ biological replicates) with miR-542-3p mimic (RHS) and non-targeting (NT) mimic (LHS). **B)** Enriched KEGG pathways associated with miR-542-3p mimic regulated proteins. **C)** WebGestalt overrepresentation analysis of biological process, cellular component, and

molecular function categories for identified significantly differentially expressed proteins ($p < 0.05$) in response to miR-542-3p mimic.



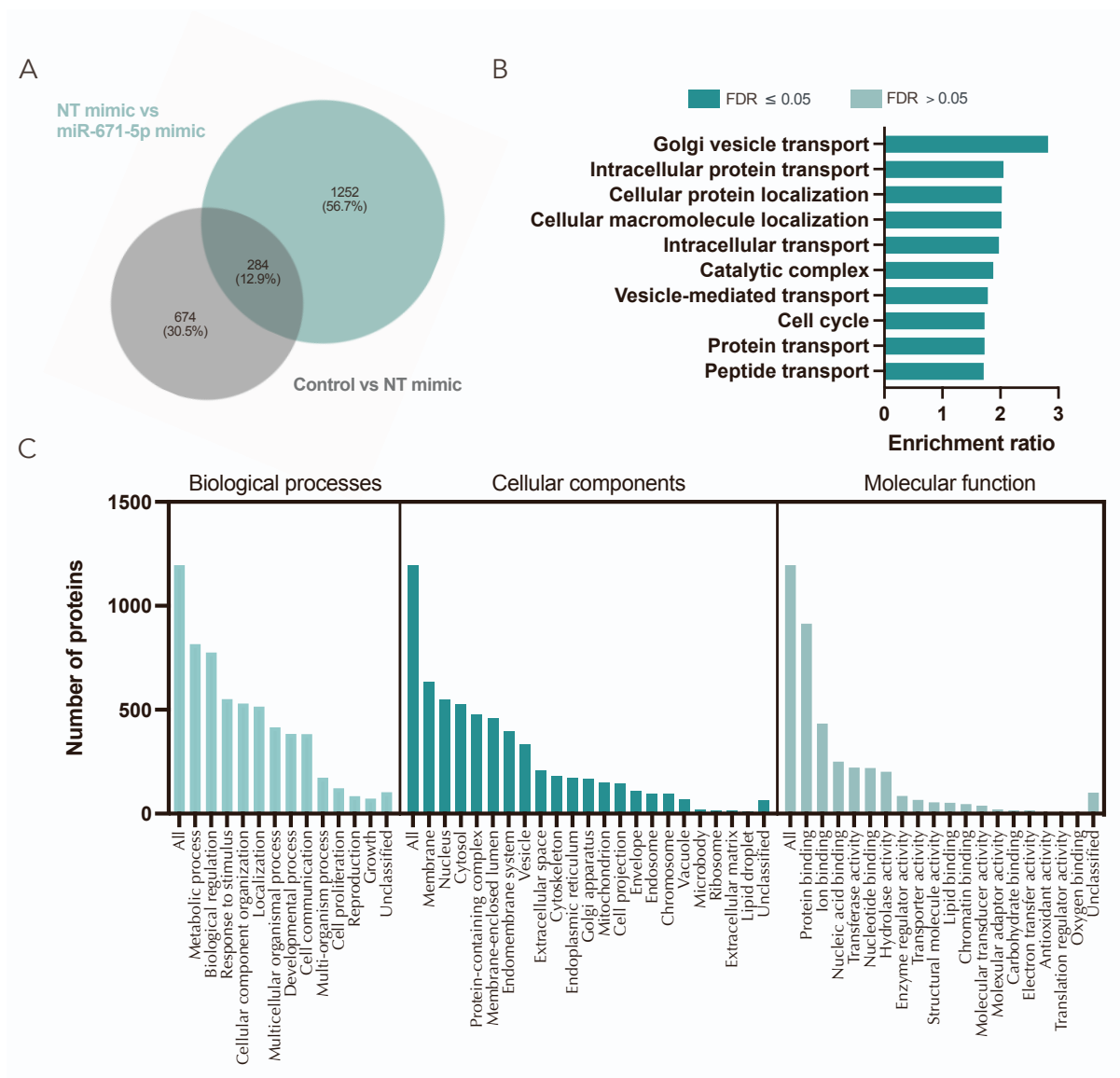
Supplementary Figure 5: Proteins altered in Ishikawa cells following treatment with miR-542-3p inhibitor related to Figure 11. A) Venn diagram depicting total number of significantly differentially expressed proteins ($p < 0.05$) following transfection of Ishikawa cells ($n = 3$ biological replicates) with miR-542-3p inhibitor (RHS) and non-targeting (NT) inhibitor (LHS). **B)** Enriched KEGG pathways associated with miR-542-3p inhibition regulated proteins. **C)**

WebGestalt overrepresentation analysis of biological process, cellular component, and molecular function categories for identified significantly differentially expressed proteins ($p < 0.05$) in response to miR-542-3p inhibitor.



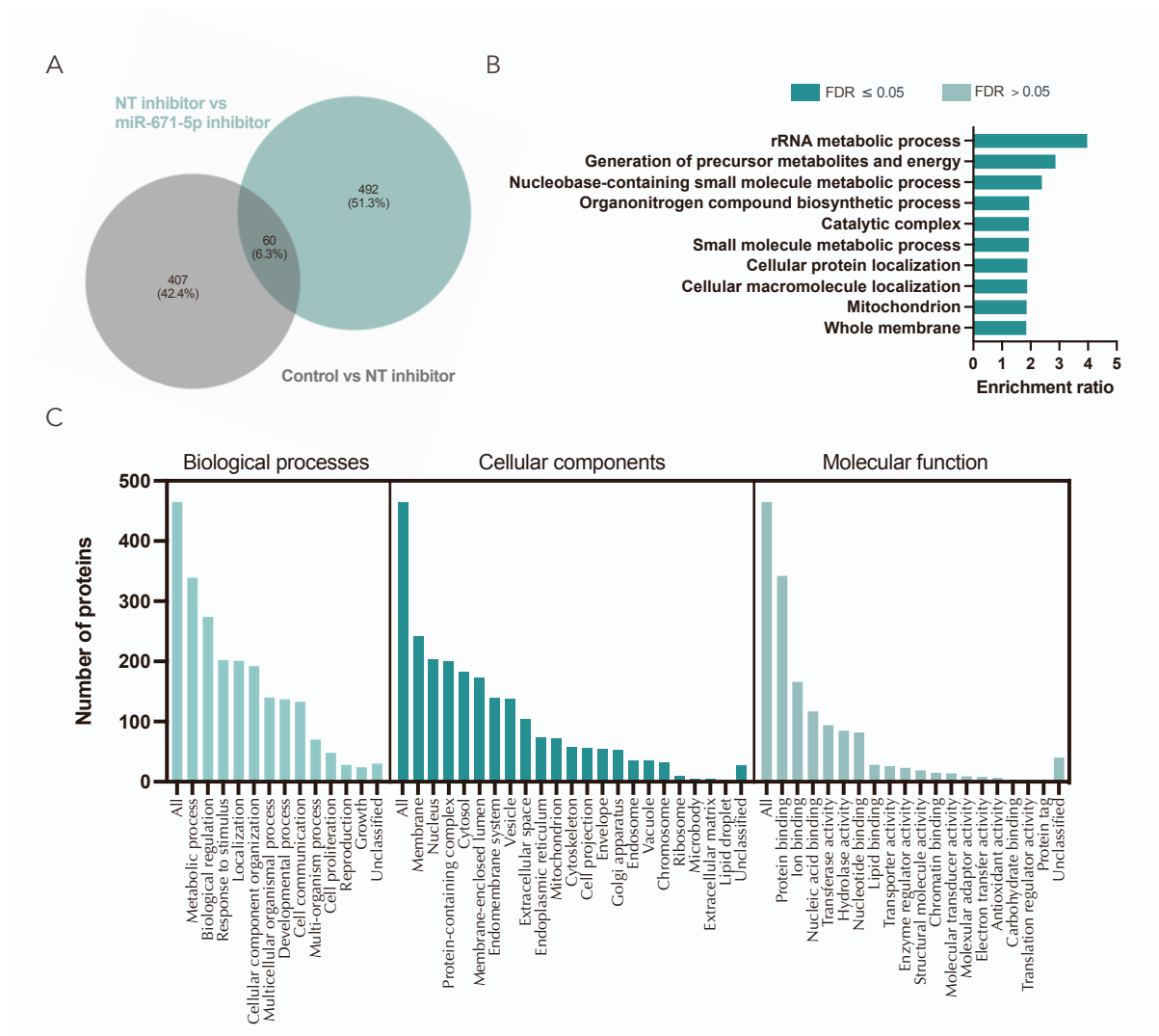
Supplementary Figure 6: Proteins altered in Ishikawa cells following treatment with miR-542-3p mimic and inhibitor compared to miRDB predicted targets related to Figure 11. A) Venn diagram depicting total number of significantly differentially expressed proteins ($p < 0.05$) following transfection of Ishikawa cells ($n = 3$ biological replicates) with miR-542-3p mimic or inhibitor vs non-targeting controls and miRDB predicted targets. **B)** Enriched KEGG pathways associated with miR-542-3p mimic and inhibition regulated proteins and predicted target

overlap. **C)** WebGestalt overrepresentation analysis of biological process, cellular component and molecular function categories for identified significantly differentially expressed proteins ($p < 0.05$) in response to miR-542-3p mimic and inhibition and predicted targets.



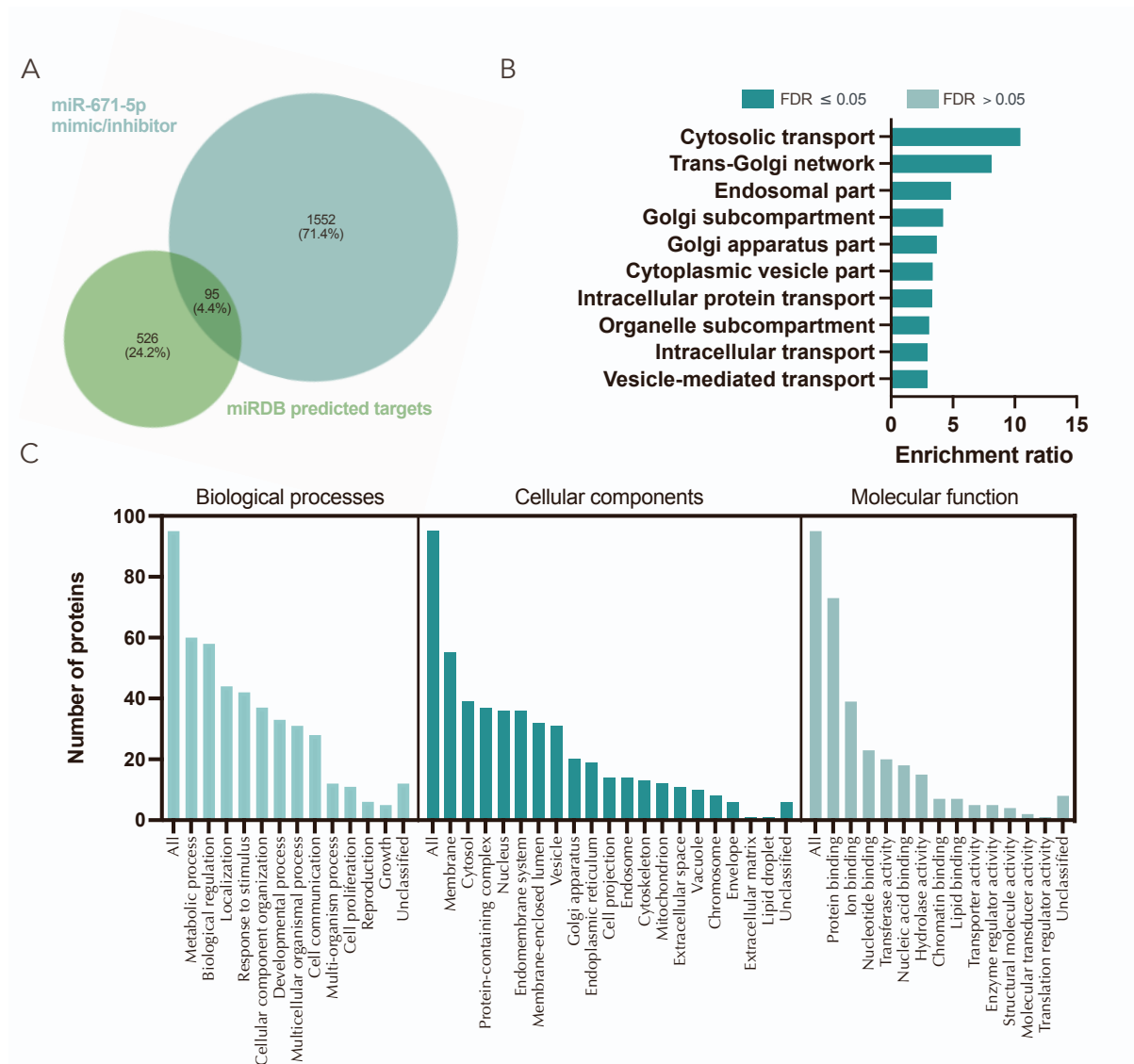
Supplementary Figure 7: Proteins altered in Ishikawa cells following treatment with miR-671-5p mimic related to Figure 13. A) Venn diagram depicting total number of significantly differentially expressed proteins ($p < 0.05$) following transfection of Ishikawa cells ($n = 3$ biological replicates) with miR-671-5p mimic (RHS) and non-targeting (NT) mimic (LHS). **B)** Enriched KEGG pathways associated with miR-671-5p mimic regulated proteins. **C)**

WebGestalt overrepresentation analysis of biological process, cellular component and molecular function categories for identified significantly differentially expressed proteins ($p < 0.05$) in response to miR-671-5p mimic.



Supplementary Figure 8: Proteins altered in Ishikawa cells following treatment with miR-671-5p inhibitor related to Figure 13. A) Venn diagram depicting total number of significantly differentially expressed proteins ($p < 0.05$) following transfection of Ishikawa cells ($n = 3$ biological replicates) with miR-671-5p inhibitor (RHS) and non-targeting (NT) mimic (LHS). **B)** Enriched KEGG pathways associated with miR-671-5p inhibitor regulated proteins. **C)** WebGestalt overrepresentation analysis of biological process, cellular component and

molecular function categories for identified significantly differentially expressed proteins ($p < 0.05$) in response to miR-671-5p inhibitor.



Supplementary Figure 9: Proteins altered in Ishikawa cells following treatment with miR-671-5p mimic and inhibitor compared to mirDB predicted targets related to Figure 13. A) Venn diagram depicting total number of significantly differentially expressed proteins ($p < 0.05$) following transfection of Ishikawa cells ($n=3$ biological replicates) with miR-671-5p mimic or inhibitor vs non-targeting controls and mirDB predicted targets. **B)** Enriched KEGG pathways associated with miR-671-5p mimic and inhibition regulated proteins and predicted target

overlap. **C)** WebGestalt overrepresentation analysis of biological process, cellular component and molecular function categories for identified significantly differentially expressed proteins ($p < 0.05$) in response to miR-671-5p mimic and inhibition and predicted targets.