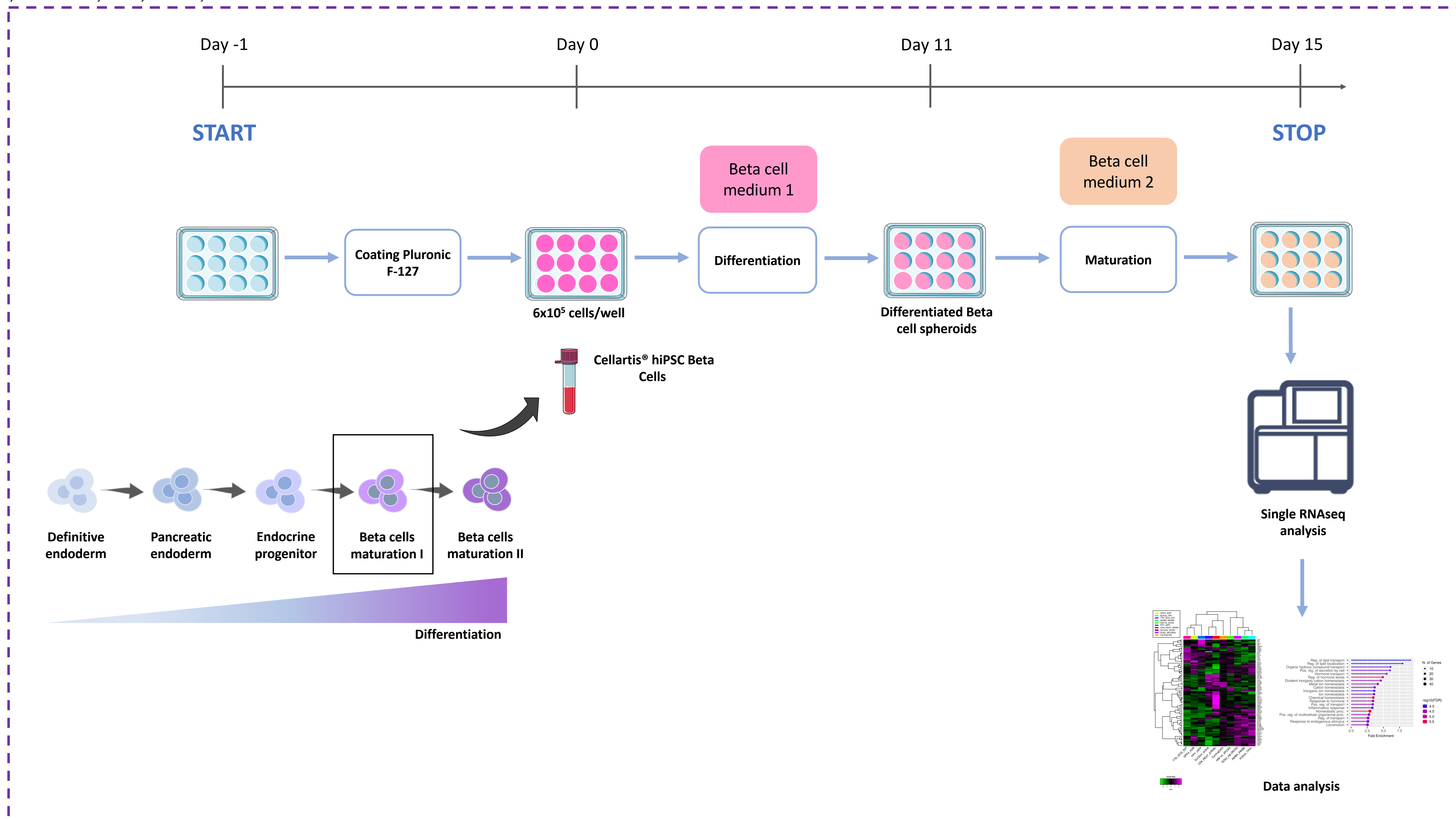
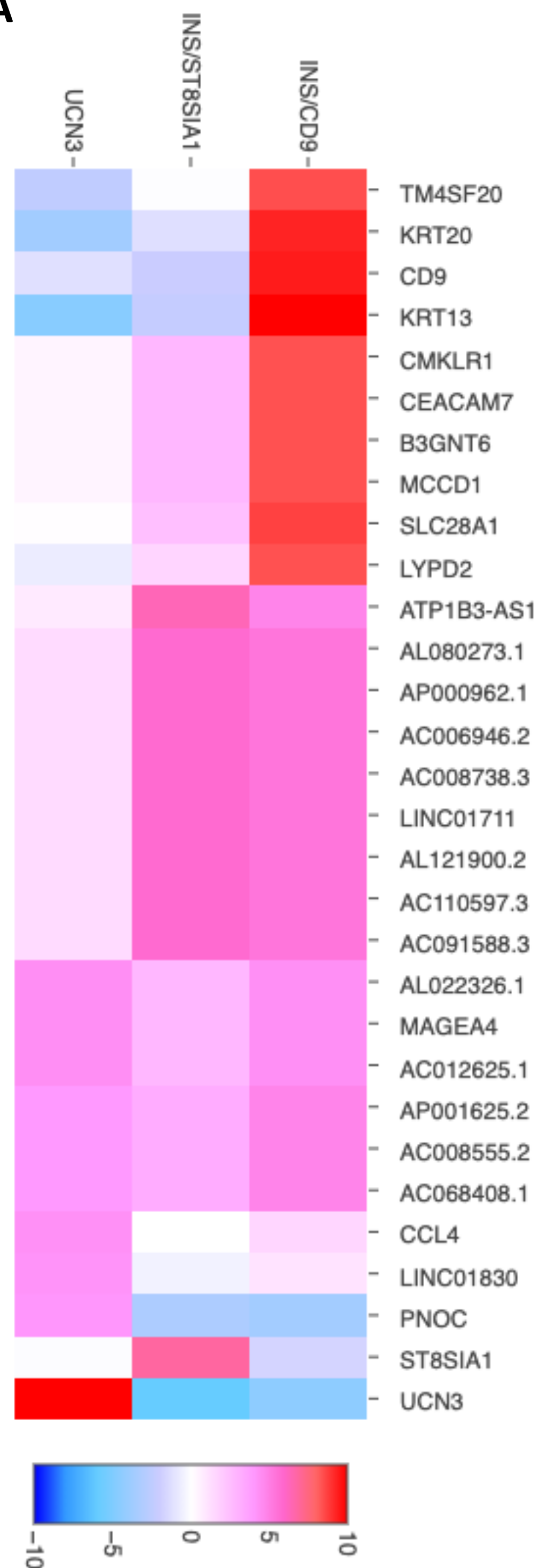


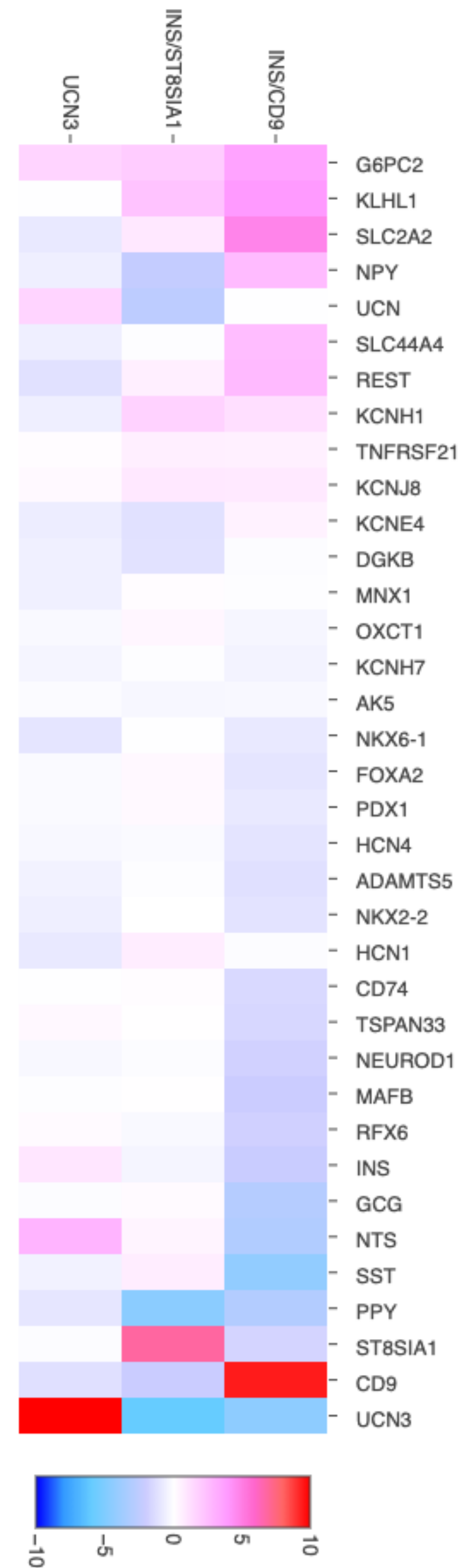


Supp Fig 1: Experimental protocol

A

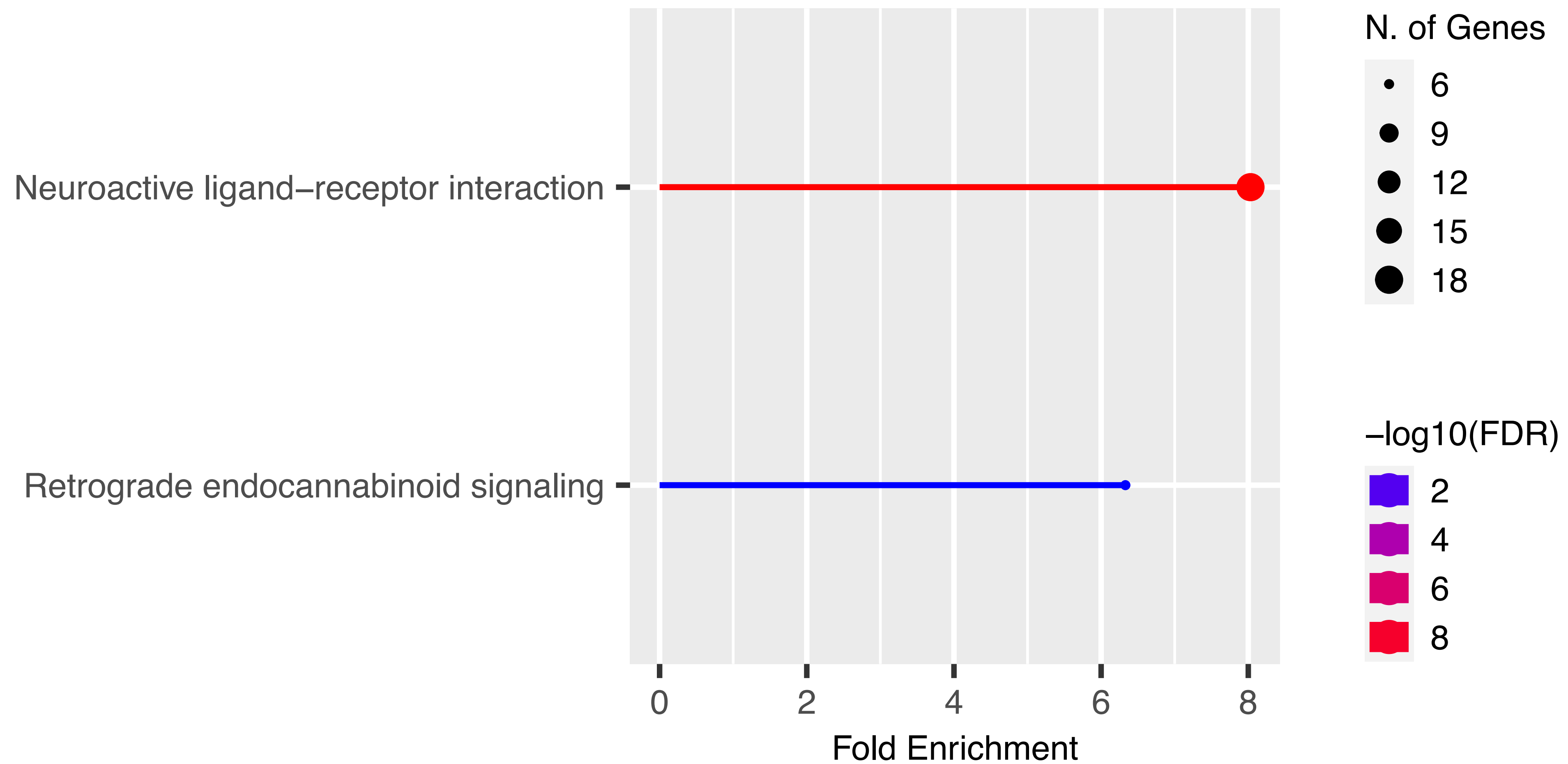


B

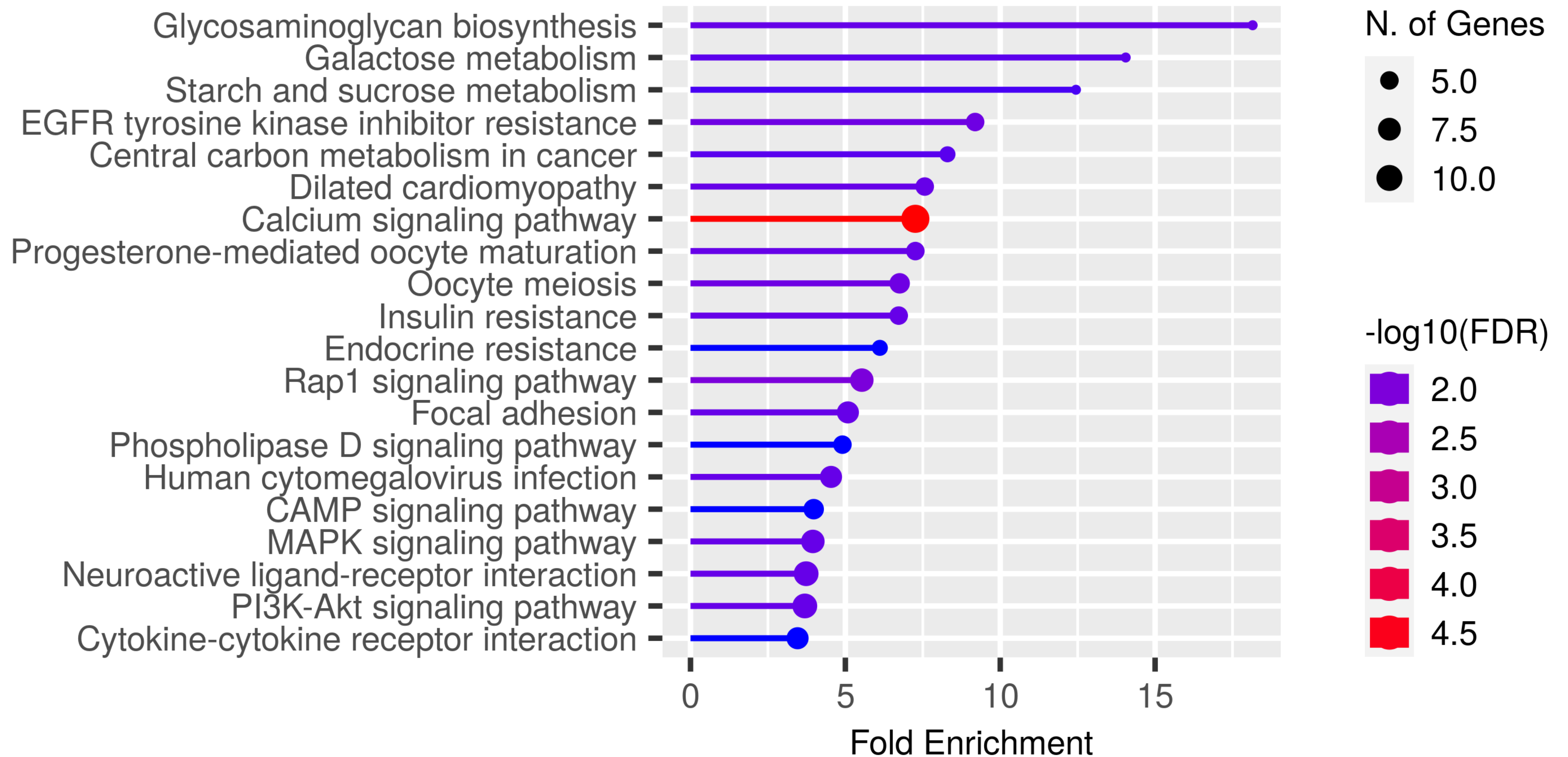


Supp Fig 2:

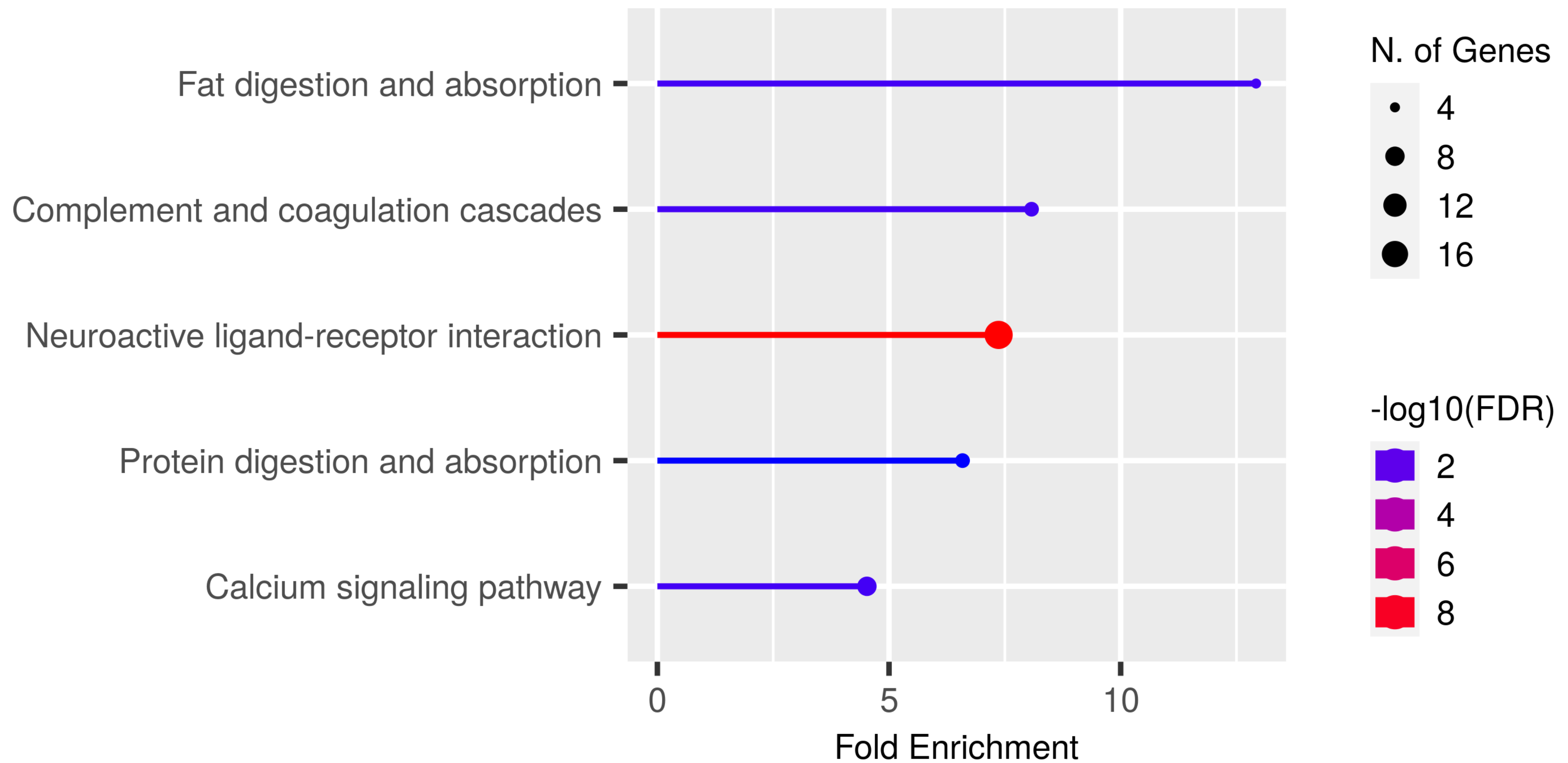
Heatmap showing the expression level of selected genes in the INS+/UCN3+ (β 1-cells), INS+/CD9+ (β 2-cells), INS+/ST8SIA1+ (β 3-cells), INS+/GRHL+, INS+/ARX/GCG+, INS+/PPY+, INS+/STT+ populations extracted from Loupe browser analysis.



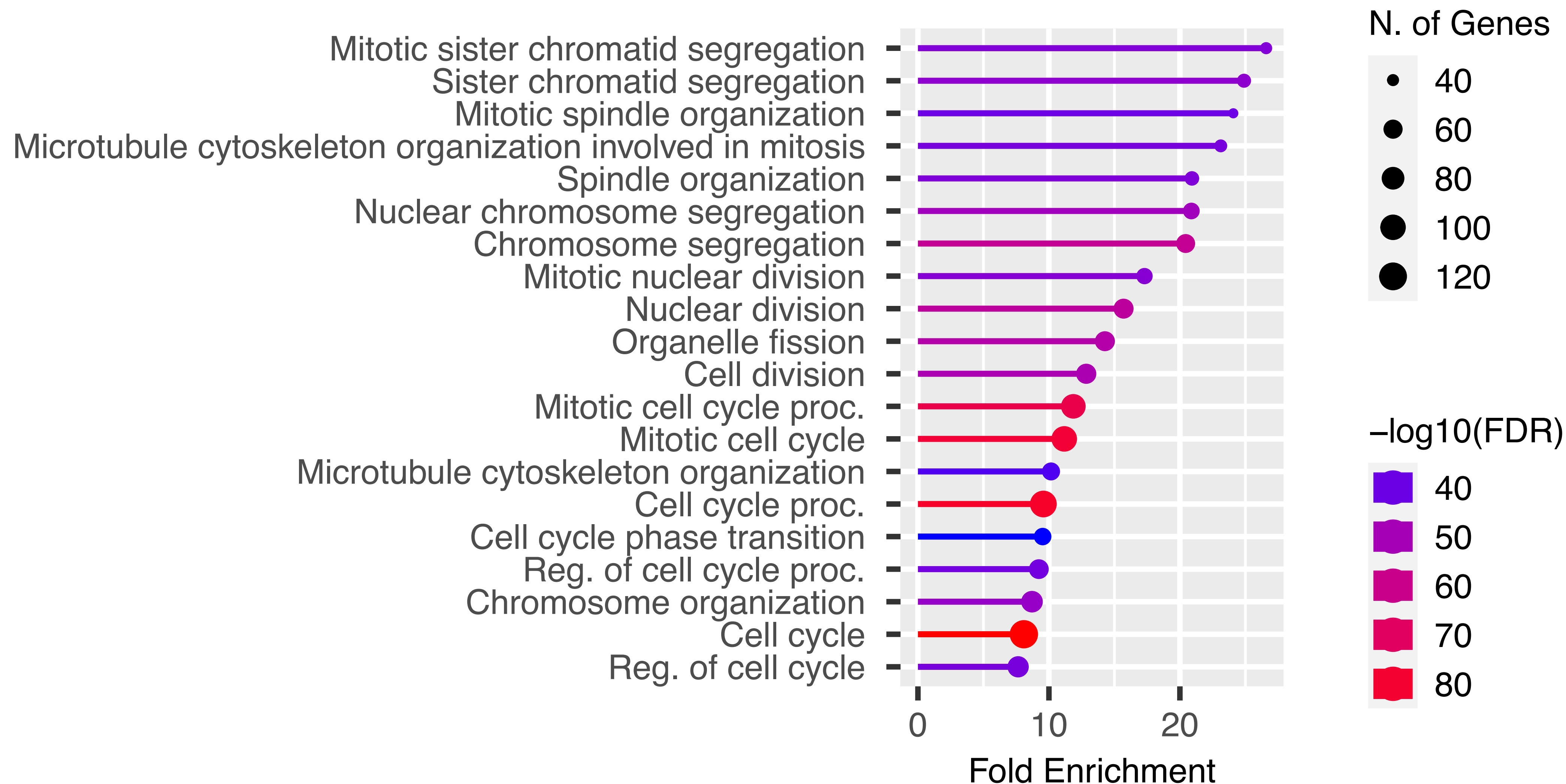
Supp Fig 4: Enriched KEGG pathways by the top 200 genes of PPY+/IAPP+ subpopulation



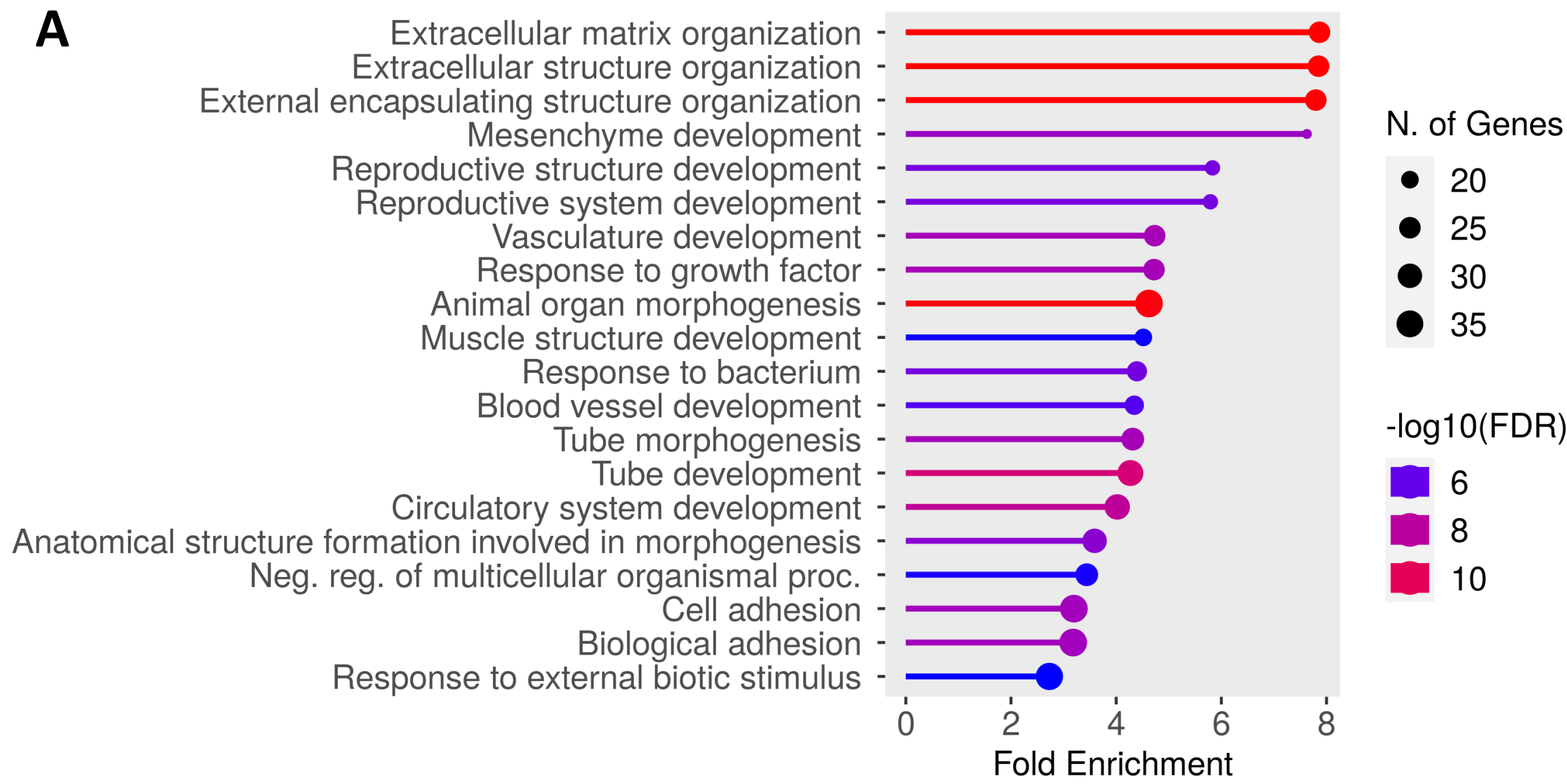
Supp Fig 5: Enriched KEGG pathways by the top 200 genes of DPP4+/KDR+ subpopulation



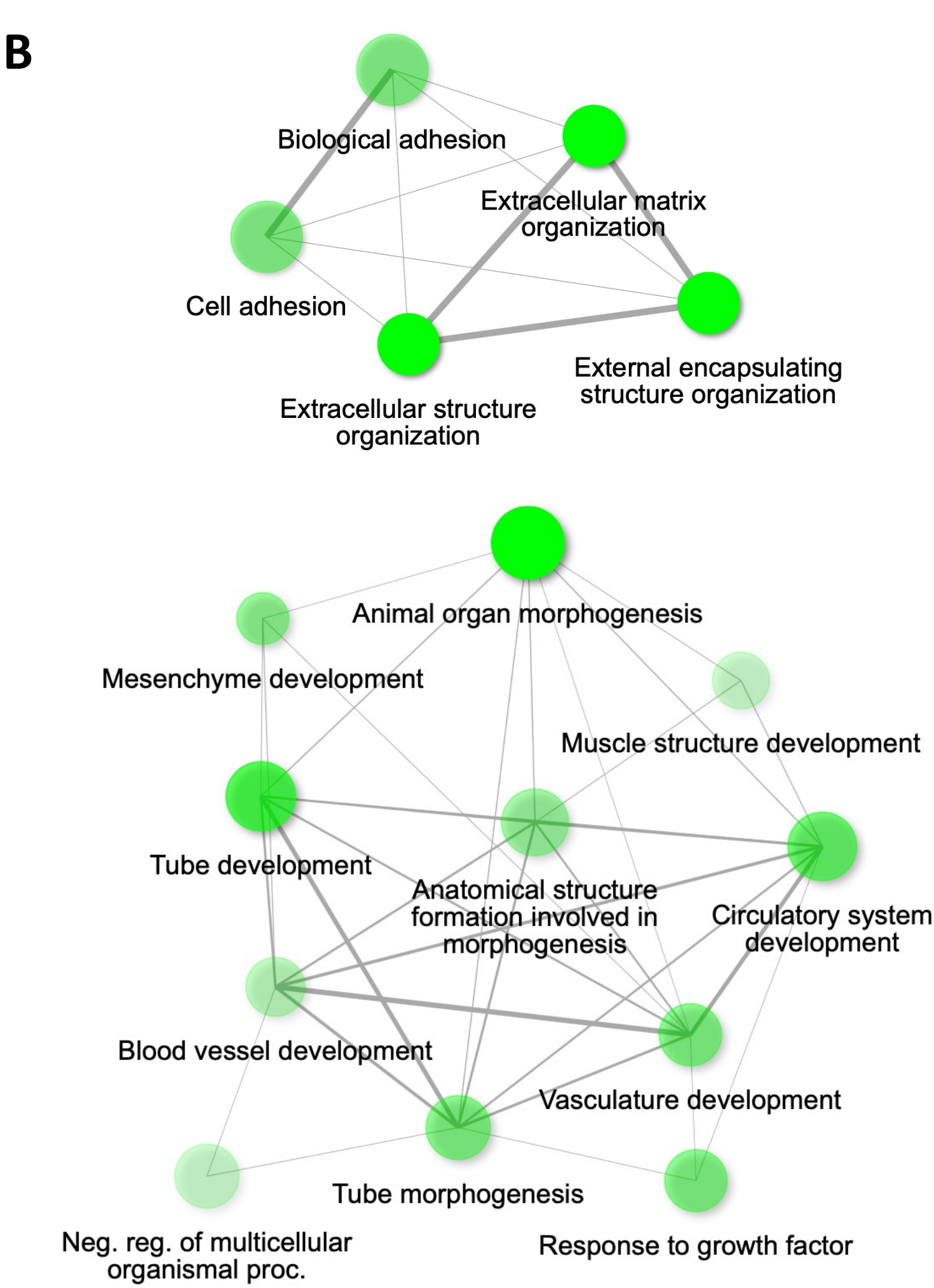
Supp Fig 6: Enriched KEGG pathways by the top 200 genes of TTR/GCG+/SST+ subpopulation



Supp Fig 7: Enriched GO_biological processes identified by the top 200 genes of the cycling cell subpopulation

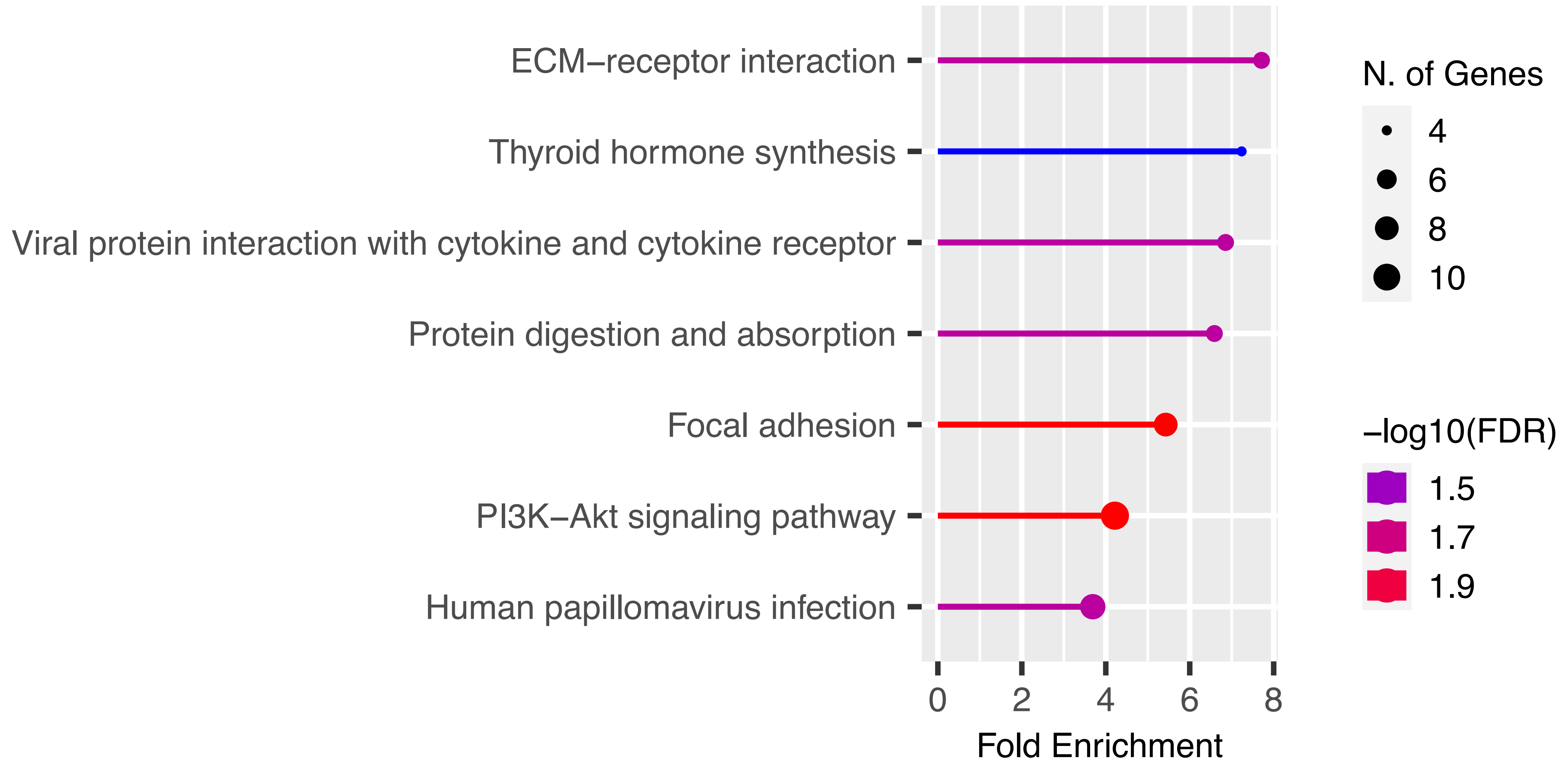


Top 200 genes of CD9+/SPARC+/REST+ cell population enriched biological process

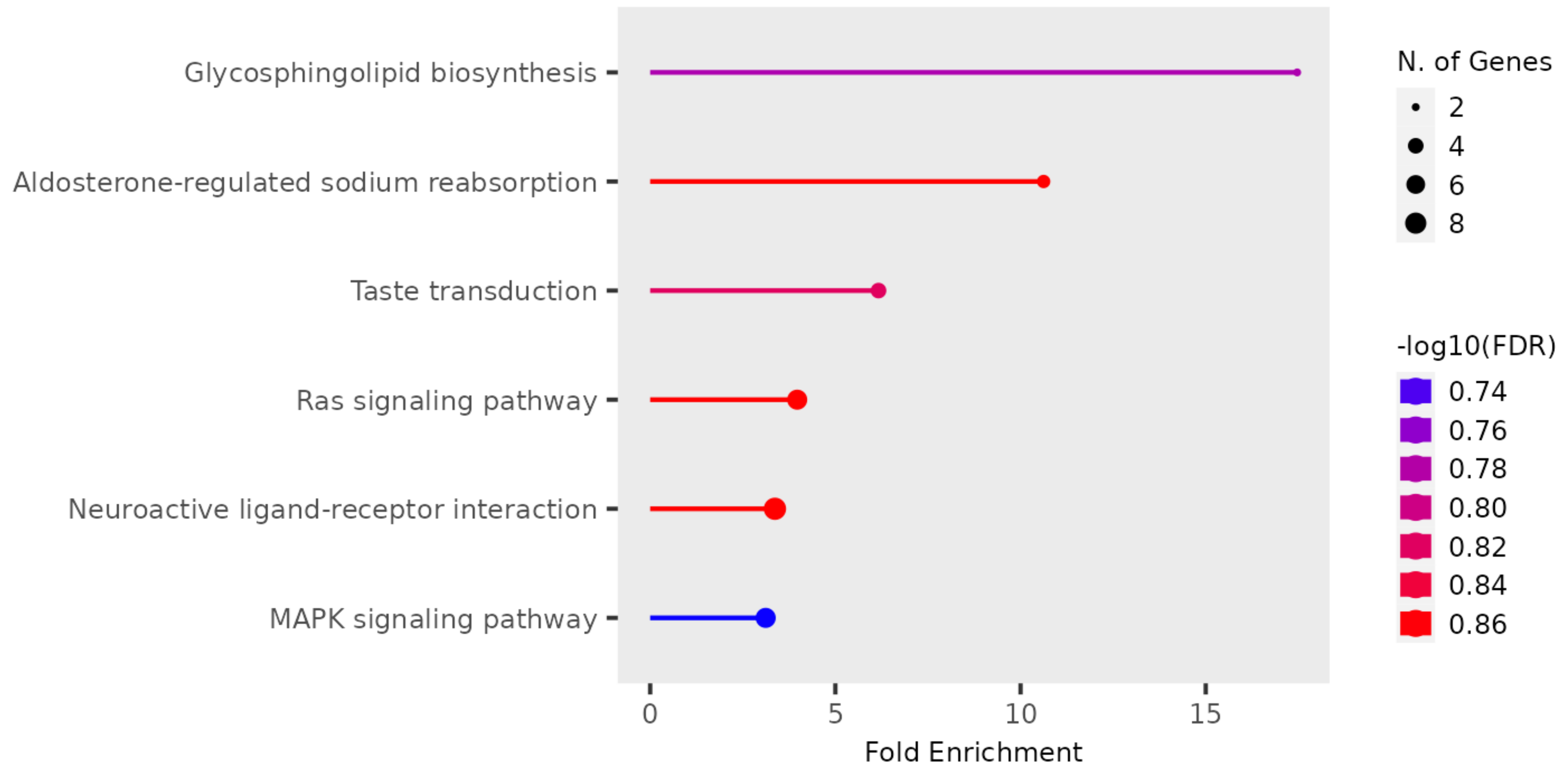


CD9+/SPARC+/REST+ cell population network of enriched biological process

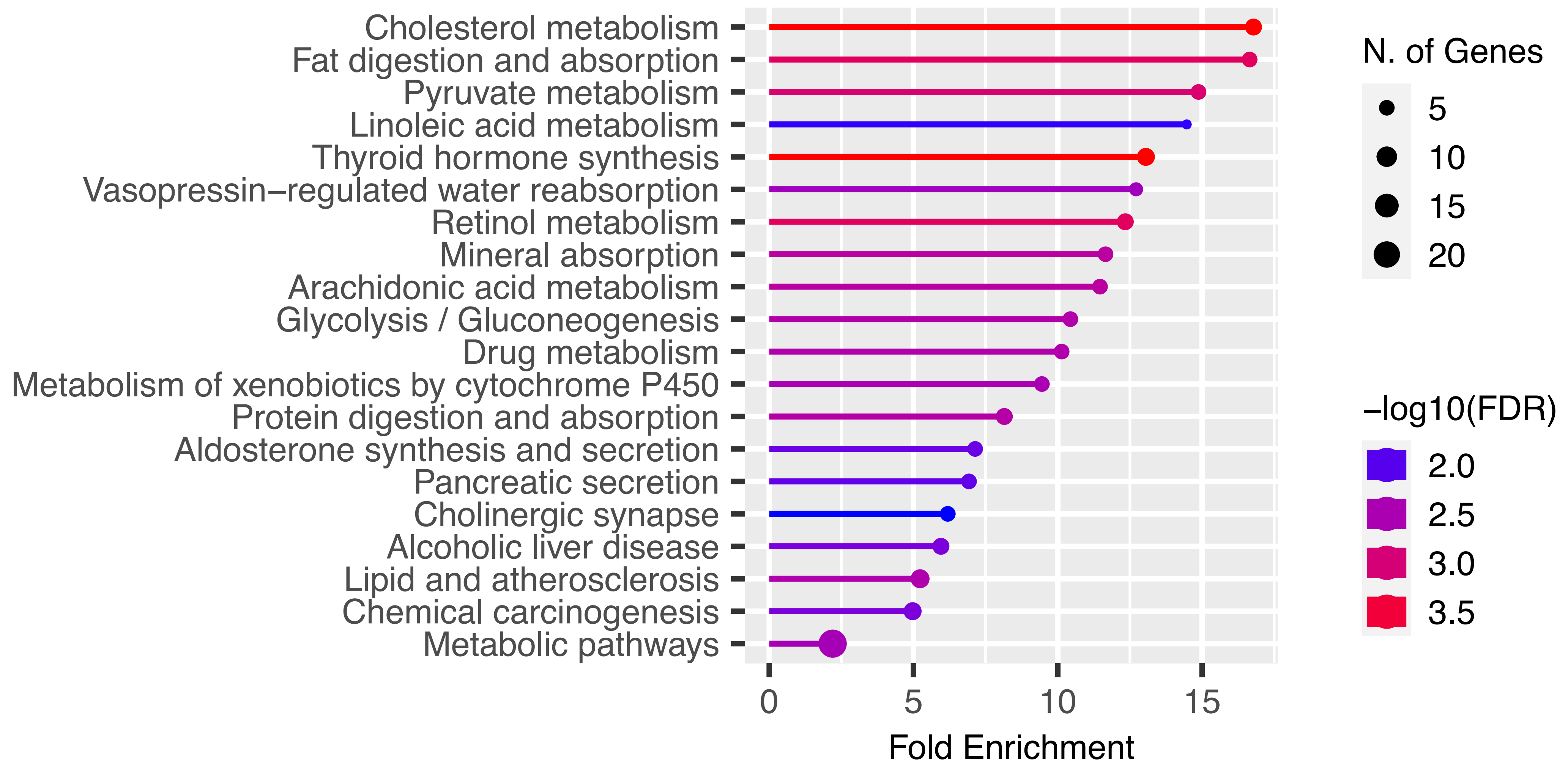
Supp Fig 8: (A) Enriched GO biological processes characterized by the top 200 representative genes in the CD9+/SPARC+/REST+ subpopulation; (B) Network of enriched biological processes in the CD9+/SPARC+/REST+ subpopulation.



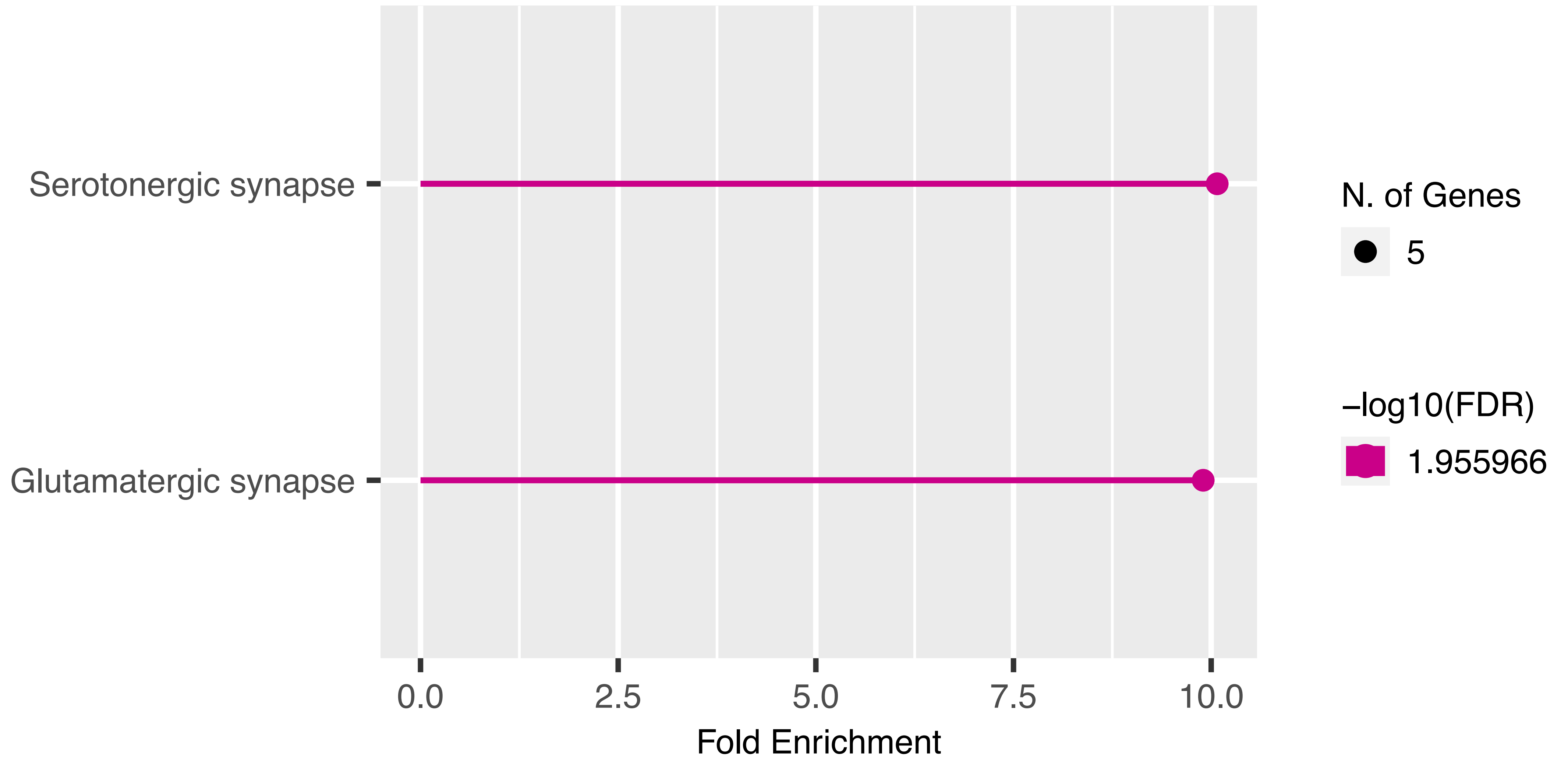
Supp Fig 9: Enriched KEGG pathways by the top 200 genes of CD9+/SPARC+/REST+ cell subpopulation



Supp Fig 10: Enriched KEGG pathways by the top 200 genes of SOX2+/NEUROG3+ subpopulation



Supp Fig 11: Enriched KEGG pathways by the top 200 genes of HNF1A+/APOA2+ subpopulation



Supp Fig 12: Enriched KEGG pathways by the top 200 genes of KCNJ3+/TPH1+/MYH4+ subpopulation

NO specific enriched KEGG pathways by the top 200 genes of INHBA+/INHBB+ subpopulation

NO specific enriched KEGG pathways by the top 200 genes of SLC2A4+/GCK+ subpopulation