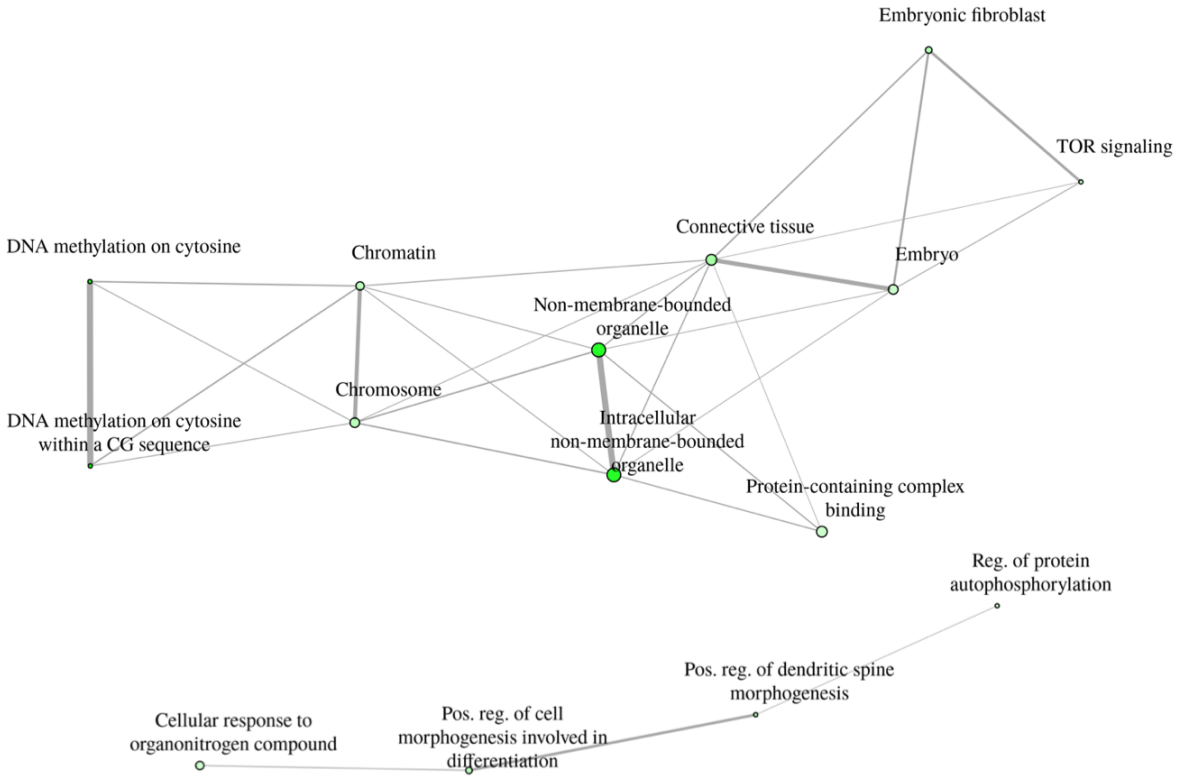


Figure S1. The enrichment plot network analysis comparing 353/11_TM and 353/11 illustrates the top 15 identified terms across different functional, using an edge cut-off of 0.3. Nodes correspond to the enriched terms, with edges representing their interactions. The thickness of the edges reflects the degree of gene overlap, while node size indicates the number of genes associated with each term (Table S10).