Supplementary Figure 3. Network visualization of enriched functional categories.

Significantly enriched Gene Ontology categories (‘Biological Process’ branch) in the SREBP1 dataset are shown with their hierarchical relationships represented as a directed acyclic graph drawn using the BiNGO program (http://www.psb.ugent.be/cbd/papers/BiNGO/). Nodes are colored by \( P \)-value as indicated. Node size corresponds to the number of genes within each category. \( P \)-values are derived from a hypergeometric test followed by false discovery rate correction. A \( P \)-value cutoff of 0.05 was used to identify significantly enriched nodes. Some category labels are not shown for clarity.