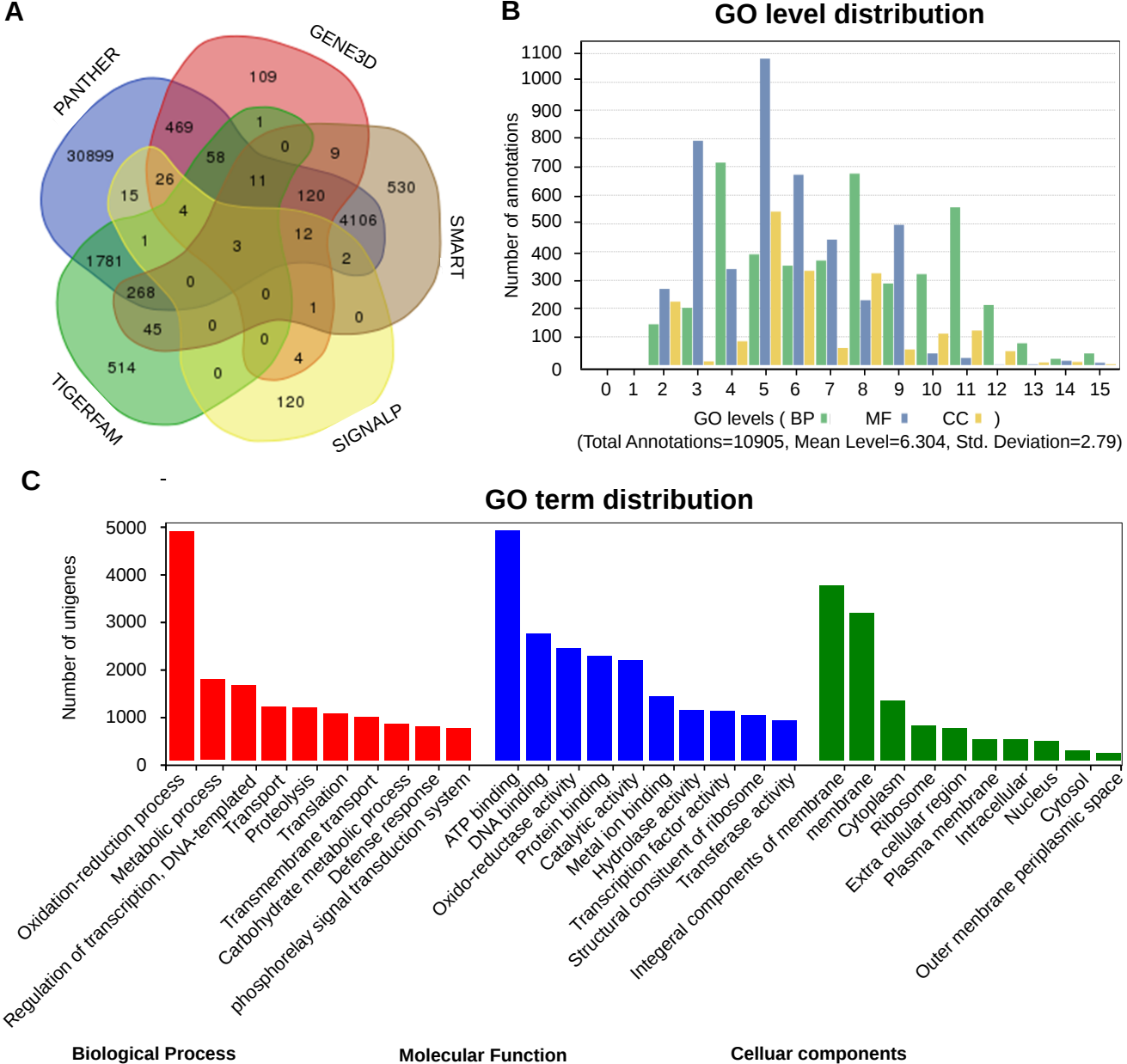




Supplementary Figure 1 A) Association of protein signatures for a specific transcript among PANTHER, GENE3D SMART, TIGERFAM and SIGNALP protein databases. **B)** Distribution of gene ontologies annotation from GO-levels 2 to 15 for each category of biological process (BP) molecular function (MF) and cellular components (CC). **C)** Gene ontology distribution among three main categories of molecular function (MF), biological process (BP), and cellular components (CC). Y-axis represents the number of genes for their respective function/process/component as on X-axis.