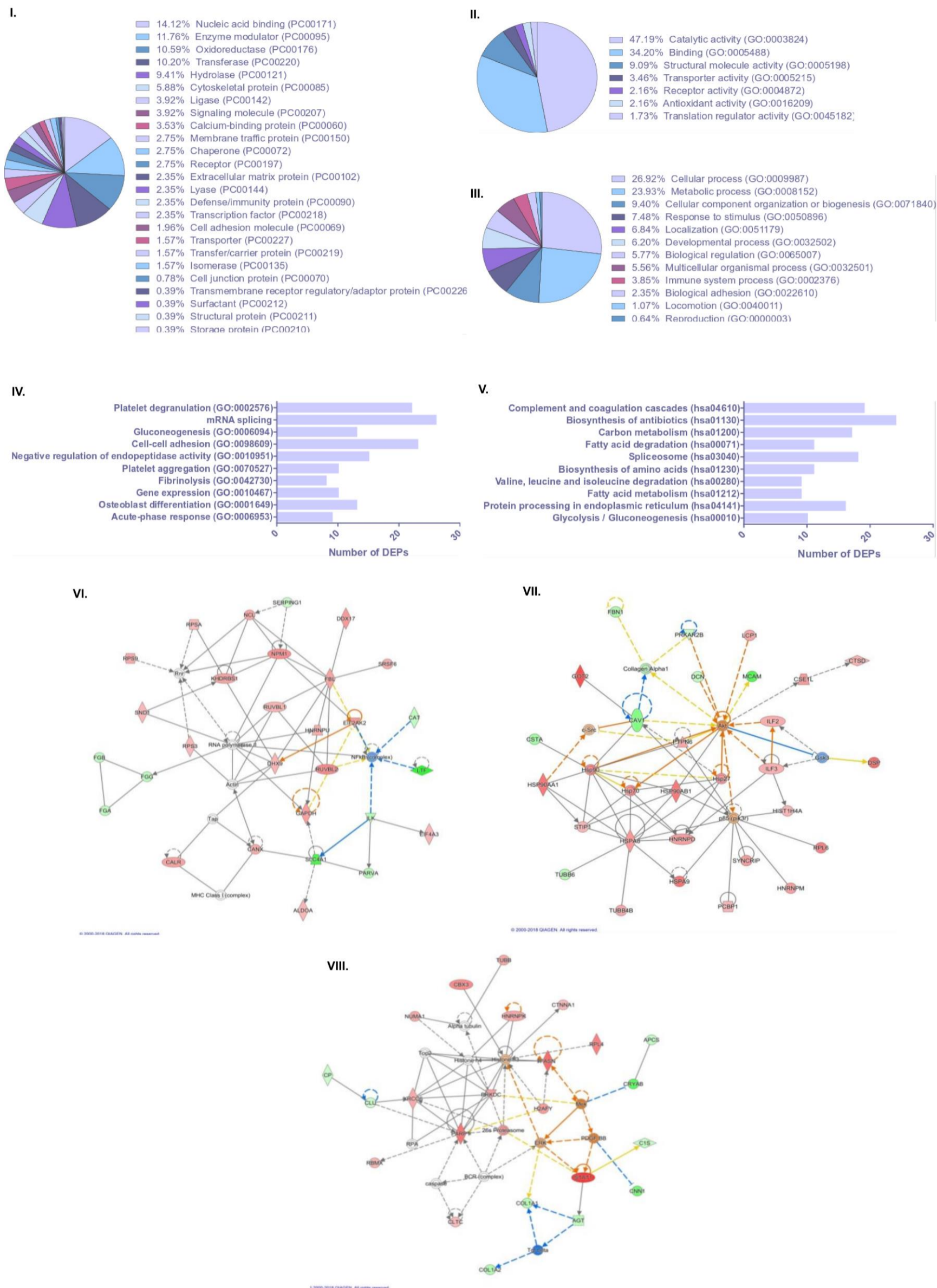# Supplementary Material to "Integrated analysis of label-free quantitative proteomics and bioinformatics reveal insights into signaling pathways in male breast cancer"

Figure S2 – Functional annotation of the differentially expressed proteins identified in the MLN x MNT tissues' comparison. According to the functional classification of the PANTHER system v. 13.1, based on the gene ontology (GO) terms: I. Protein class; II. Molecular function; III. Biological process. According to the functional enrichment analysis of the DAVID v. 6.8 database: IV. Top enriched biological processes (GO terms, p<0.05); V. Top enriched KEGG pathways (p<0.05). Predicted protein interactive networks of the differentially expressed proteins identified in the MLN x MNT tissues' comparison (VI-VIII), according to the IPA analysis.