

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

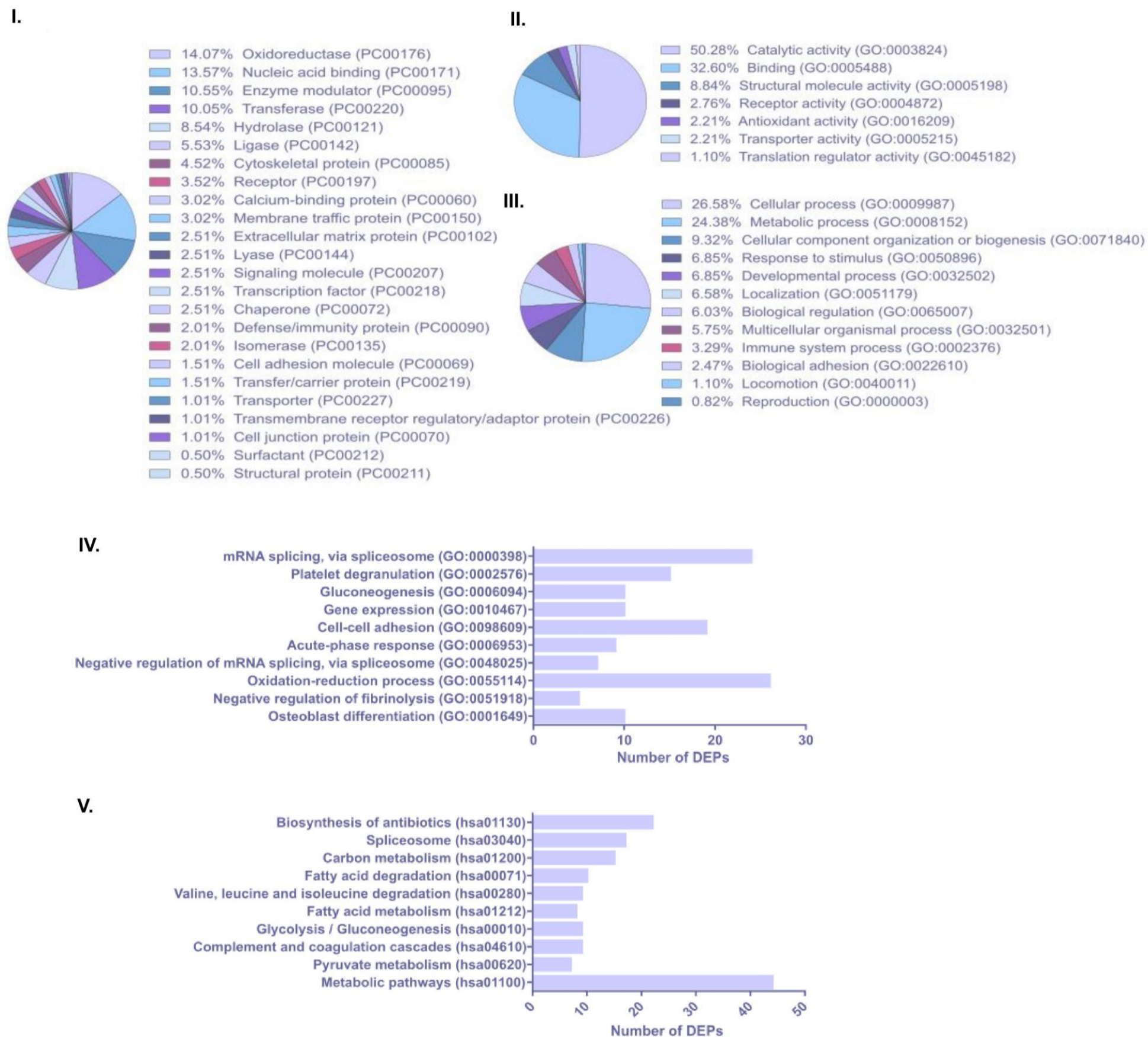


Figure S3 – Functional annotation of the differentially expressed proteins identified in the MPT x MNT tissues' comparison. According to the functional classification of the PANTHER system v. 13.1, based on the gene ontology (GO) terms: I. Protein class; II. Molecular function; III. Biological process. 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 ($p < 0.05$).