

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

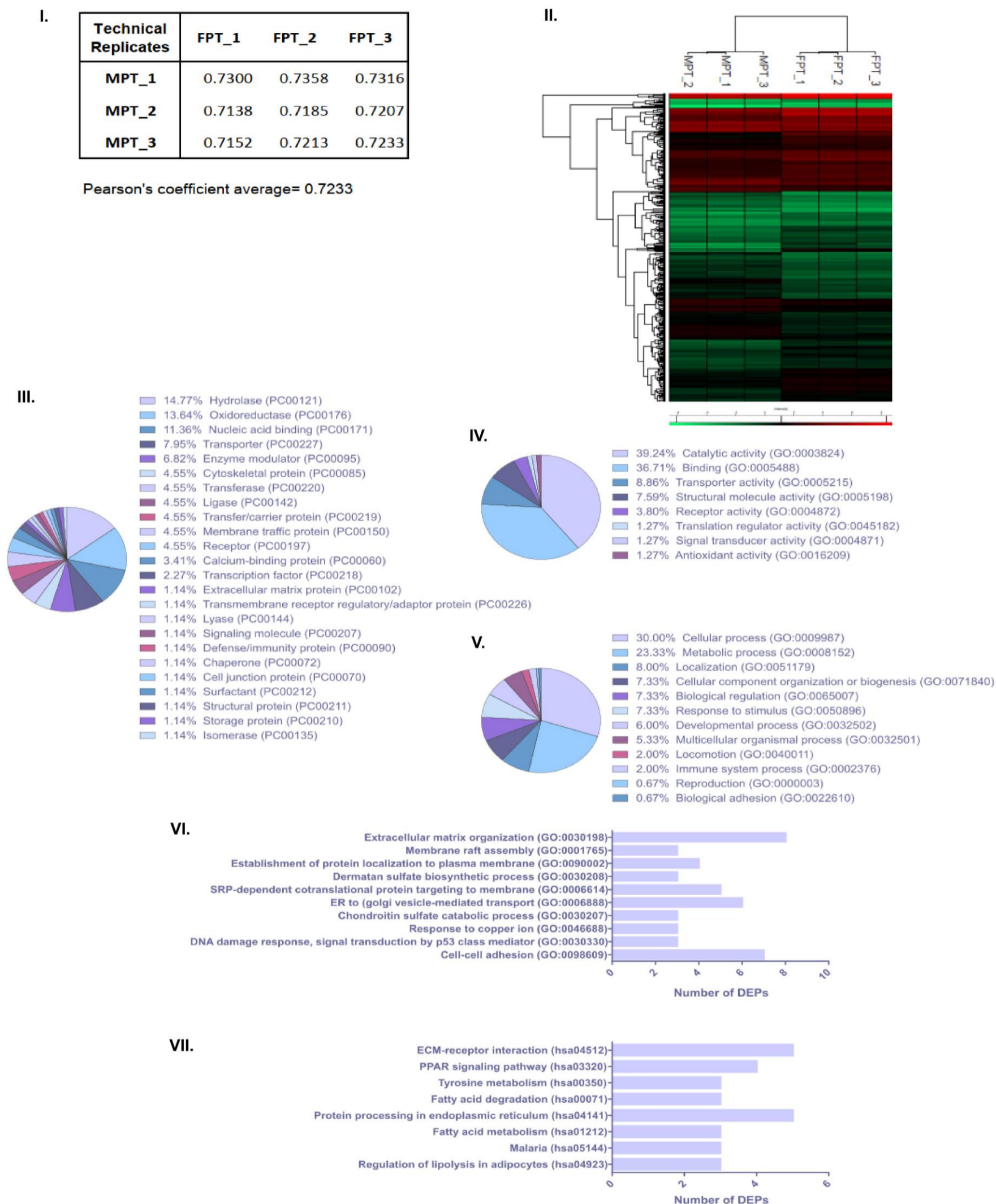


Figure S5 – Technical replicates and the differentially expressed proteins from the MPT x FPT tissues comparison. I. Pearson correlation analysis between the MPT x FPT tissues based on LFQ intensity values of the 1,340 identified proteins. II. Hierarchical clustering analysis from the 447 DEPs between the MPT x FPT tissues. Functional annotation of the differentially expressed proteins identified in the MPT x FPT tissues comparison: According to the functional classification of the PANTHER system v.13.1, based on gene ontology (GO) terms: III. Protein class; IV. Molecular function; V. Biological process. According to the functional enrichment analysis of the DAVID v. 6.8 database: VI. Top enriched biological processes (GO terms, $p < 0.05$); VII. Top enriched KEGG pathways ($p < 0.05$).