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

**I.**

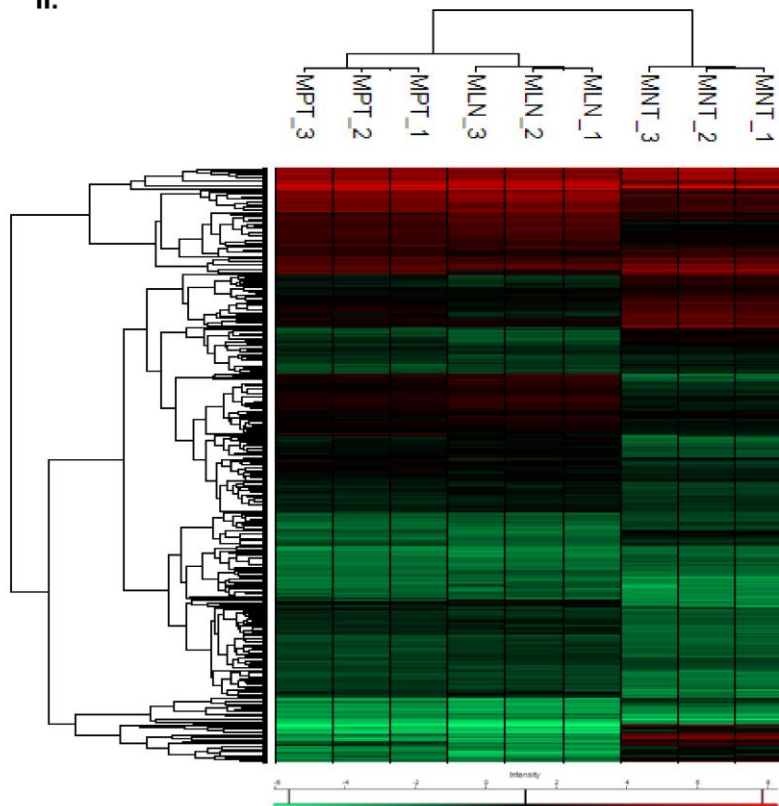| Technical Replicates | MNT_1 | MNT_2 | MNT_3 | MPT_1 | MPT_2 | MPT_3 | MLN_1 | MLN_2 | MLN_3 |
|---|---|---|---|---|---|---|---|---|---|
| MNT_1 | - | 0.9611 | 0.9630 | 0.6567 | 0.6534 | 0.6549 | 0.5590 | 0.5509 | 0.5601 |
| MNT_2 | 0.9611 | - | 0.9616 | 0.6499 | 0.6470 | 0.6512 | 0.5542 | 0.5423 | 0.5542 |
| MNT_3 | 0.9630 | 0.9616 | - | 0.6512 | 0.6497 | 0.6518 | 0.5534 | 0.5426 | 0.5571 |
| MPT_1 | 0.6567 | 0.6499 | 0.6512 | - | 0.9862 | 0.9851 | 0.9475 | 0.9453 | 0.9383 |
| MPT_2 | 0.6534 | 0.6470 | 0.6497 | 0.9862 | - | 0.9858 | 0.9414 | 0.9400 | 0.9345 |
| MPT_3 | 0.6549 | 0.6512 | 0.6518 | 0.9851 | 0.9858 | - | 0.9437 | 0.9427 | 0.9362 |
| MLN_1 | 0.5590 | 0.5542 | 0.5534 | 0.9475 | 0.9414 | 0.9437 | - | 0.9906 | 0.9759 |
| MLN_2 | 0.5509 | 0.5423 | 0.5426 | 0.9453 | 0.9400 | 0.9427 | 0.9906 | - | 0.9755 |
| MLN_3 | 0.5601 | 0.5542 | 0.5571 | 0.9383 | 0.9345 | 0.9362 | 0.9759 | 0.9755 | - |

Intensity

low          high

**II.**



**Figure S1** – Technical replicates and the differentially expressed proteins from the MBC case. I. Pearson correlation analysis among the MBC tissues based on LFQ intensity values of the 962 identified proteins. II. Hierarchical clustering analysis from the 675 DEPs among the MCB tissues.