**Collagen family proteins, thrombospondin 1 and lumican are differentially expressed across breast cancer subtypes by functional proteomics: a preliminary study with bioinformatics analysis**

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**Abstract**

Most multi-gene signatures for breast cancer prognostication are mRNA (gene expression)-based, and few take protein expression as a biomarker. Candidate proteins were identified using nanoscale liquid chromatography with tandem mass spectrometry (NanoLC-MS/MS) from 61 Taiwanese breast cancers. Seventeen proteins were highly differential expression from analysis of variance (ANOVA) across four distinct immunohistochemistry subtypes and protein-protein interaction (PPI) network found the strong networks including COL2A1, COL11A1, COL6A1, COL6A2, THBS1 and LUM. Using public domain databases, we found that RNASeq expression values of *COL2A1*, *COL11A1*, *COL6A1*, *COL6A2* and *LUM* were higher in tumor than in normal tissue, and all six genes were differentially expressed across four molecular subtypes. In addition, disease-specific survival discrepancy was observed comparing breast cancer patients of the upper and lower quartile of the collage family, *THBS1* and *LUM* gene expression signature. Functional proteomics with LC-MS/MS is capable for target protein identification.

**Keywords:** breast cancer subtypes; functional proteomics; protein-protein interaction; collagen family protein; thrombospondin 1; lumican