

**2008 AACR Annual Meeting****April 12-16, 2008****San Diego, CA**[Print this Page for Your Records](#)[Close Window](#)

**Abstract Number:** 5163

**Session Title:** Integration of Omics Technologies

**Presentation Title:** LC-MS-based quantitative proteome analysis of archival melanoma tissues reveals potential biomarkers associated with metastasis

**Presentation Start/End Time:** Wednesday, Apr 16, 2008, 8:00 AM -12:00 PM

**Location:** Exhibit Hall B-F, San Diego Convention Center

**Poster Section:** 6

**Poster Board Number:** 18

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Metastatic melanoma is usually associated with poor prognosis. Limited information is known about proteomic changes during tumor progression. To better understand the changes in protein expression involved in melanoma progression and metastasis, and to identify potential biomarkers, we conducted a global quantitative proteome analysis on melanoma metastases and primary melanomas. Proteins were extracted from microdissected formalin-fixed paraffin-embedded (FFPE) archival tissue of melanoma metastases and primary melanomas using Liquid Tissue<sup>®</sup> reagents and protocols, and analyzed by a recently developed, LC/MS-based label-free protein quantification method to profile the global protein expression. More than 1500 proteins were identified in tissue lysates prepared from approximately 30,000 microdissected cells, covering a wide variety of biological functions. The approach identified 120 significantly changing proteins, including 78 up-regulated and 42 down-regulated; these were identified from multiple peptides with high ID confidence and expressed at significantly different levels in metastases as compared with primary melanoma (q-Value < 0.05). These differentially expressed proteins were classified by their biological process and several proteins were implicated as cancer-related or metastasis-related. Of particular interest are those proteins which showed elevated expression levels in metastatic tissue and have functions related to cell adhesion and migration, cell cycle modulation, and cellular metabolism. The proteins identified represent potential biomarkers for tumor progression. Further analysis using a pathway/network software tool demonstrated significant activated biological pathways between primary and metastatic tumors. The technology described here successfully identified differentially expressed proteins between metastatic and primary melanoma in FFPE tissue samples.

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