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A comprehensive proteomic and epigenomic analysis of FFPE patient melanoma

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Molecular pathways regulating melanoma initiation and progression are potential targets of therapeutic development for this aggressive cancer. We present the most comprehensive analysis of formalin-fixed paraffin-embedded human melanoma tissues using quantitative proteomics. From 61 patient samples, we identified 171 proteins varying in abundance among benign nevi, primary melanoma, and metastatic melanoma. Seventy-three percent of these proteins were validated by immunohistochemistry staining of malignant melanoma tissues from the Human Protein Atlas database. Our results reveal that molecular pathways involved with tumor cell proliferation, motility, and apoptosis are mis-regulated in melanoma. These data provide the most comprehensive proteome resource on patient melanoma and reveal insight into the molecular mechanisms driving melanoma progression. Furthermore, we have used this quantitative mass spectrometry approach to uncover a panel of histone post-translational modifications that are differentially regulated in metastatic melanoma. This has allowed us to explore epigenomic mechanisms that regulate melanoma progression.

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