Multimodal Precision Liquid Biopsy to Predict Risk of Melanoma Recurrence in Early Stage IIB/IIC Disease

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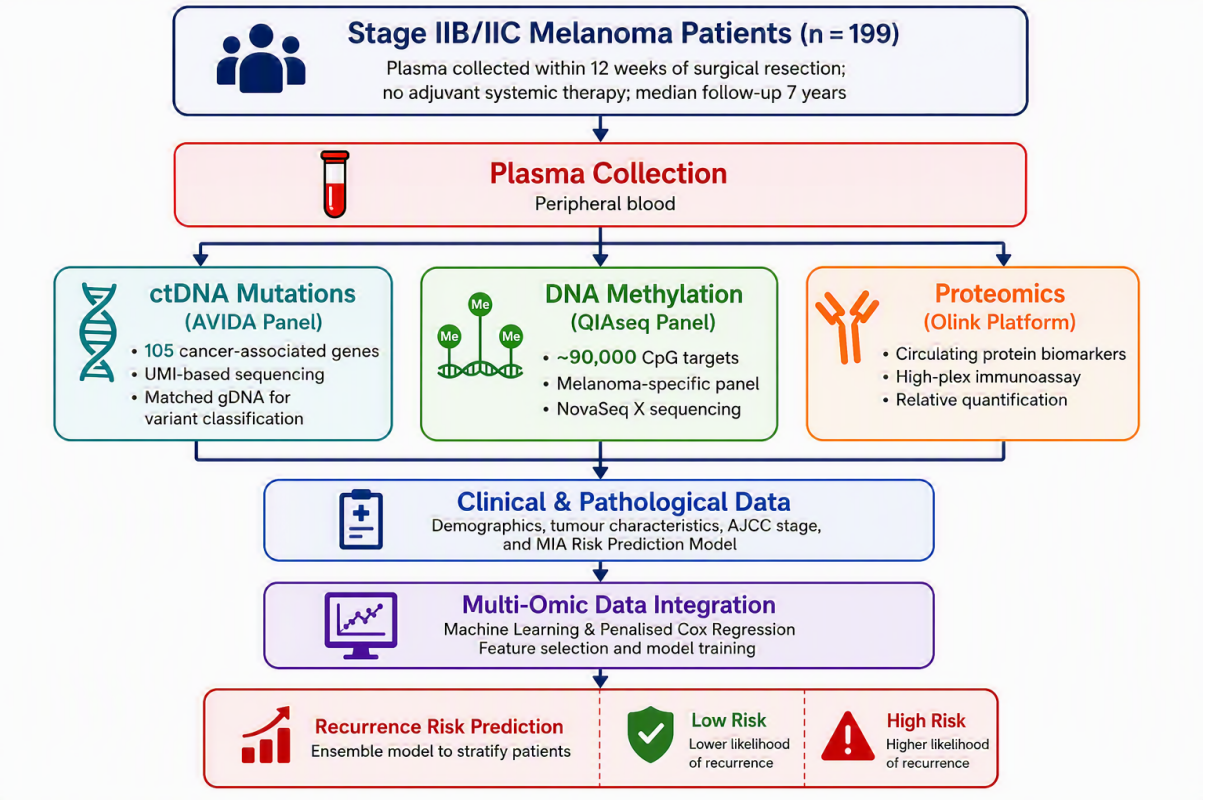
Background: Despite surgical resection, patients with Stage IIB/IIC melanoma remain at substantial risk of recurrence, while current risk assessment relies largely on clinicopathological features. More accurate risk stratification could guide adjuvant therapy while reducing unnecessary treatment and toxicity.

Aim: Develop and integrate ctDNA mutation, ctDNA methylation and circulating protein signatures with clinicopathological factors to build a multi-omic model predicting recurrence risk.



Key Updates:

Component	Status
Methylation and Protein Profiling	Completed
ctDNA Sequencing	Completed
Matched gDNA Sequencing	Completed
Multi-omic model development	Ongoing

Discussion and Conclusions:

Proteomic, methylation and ctDNA datasets have been generated from a well-characterised Stage IIB/IIC melanoma cohort. Preliminary analyses suggest that protein and methylation biomarkers, combined with clinicopathological factors, are associated with recurrence risk. Matched genomic DNA sequencing, co-funded by the Multi-omics Research Centre, will support somatic variant identification and multi-omic data integration. The resulting model aims to identify patients at high risk of recurrence, guide adjuvant therapy and reduce overtreatment.

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