BITS :: Call for Abstracts 2024 - Oral communication

Type	Oral communication
Session	Translational, Clinical and Industry Bioinformatics
Title	Validation of a non-invasive low-volume transcriptomic analysis to predict cervical cancer progression in HPV positive patients
All Authors	Martina Betti (1,2), Francesca De Nicola (3), Ludovica Ciuffreda (3), Margherita Ferretti (3), Sara Baldinelli (1), Alessandra Logoteta (5), Enrico Vizza (4), Matteo Pallocca (5), Maurizio Fanciulli (3), Valentina Bruno (4)

Martina Betti (1,2), Francesca De Nicola (3), Ludovica Ciuffreda (3), Margherita Ferretti (3), Sara Baldinelli (1), Alessandra Logoteta (5), Enrico Vizza (4), Matteo Pallocca (5), Maurizio Fanciulli (3), Valentina Bruno (4)

Affiliation

(1) Biostatistics, Bioinformatics and Clinical Trial Center, IRCCS Regina Elena National Cancer Institute, Rome, Italy.

(2) Department of Computer, Control and Management Engineering, La Sapienza University of Rome, Rome, Italy

(3) UOSD SAFU, IRCCS Regina Elena National Cancer Institute, Rome, Italy.

(4) Gynecologic Oncology Unit, Department of Experimental Clinical Oncology, IRCCS Regina Elena National Cancer Institute, Rome, Italy.

(5) Institute of Experimental Endocrinology and Oncology, National Research Council, Naples, Italy.

Motivation

HPV promotes its own DNA integration and persistence through oncoproteins E6 and E7, by influencing the host immune system through immune evasion mechanisms, leading to the so-called PIM. PIM supports viral persistence, propagation, and promoting CIN parthenogenesis first and invasive carcinoma then. Our aim is to describe, by non-invasive samples low-volume transcriptomics analysis, the HPV infection immunologic signatures at different stages of CC progression from dysplasia to full-blown cancer, with the intent to evaluate their functional role in immune escape and potentially identifying their correlation with CC prognosis.

Methods

A preliminary analysis has seen the comparisons of samples conserved at different temperatures and the benchmarking of low-input samples with their respective bulk counterpart. Tissue expression validation has been performed through the TIGER resource. Variant calling has been performed with nf-core/sarek and nf-core/hlatyping on both thin-prep and bulk sample to validate thin-prep RNA quality. Finally CibersortX has been used for TIME deconvolution and results have been compared to TCGA-CESC. A trajectory analysis of immune cell populations abundances from healthy to cancer condition passing through dysplasia has been performed to highlight the populations that play a major role in the host response to HPV and will be explore in further analysis. Upon the achievement of a reasonable number of samples, a predictive model will be developed to identify high-risk dysplasia patients.

Results

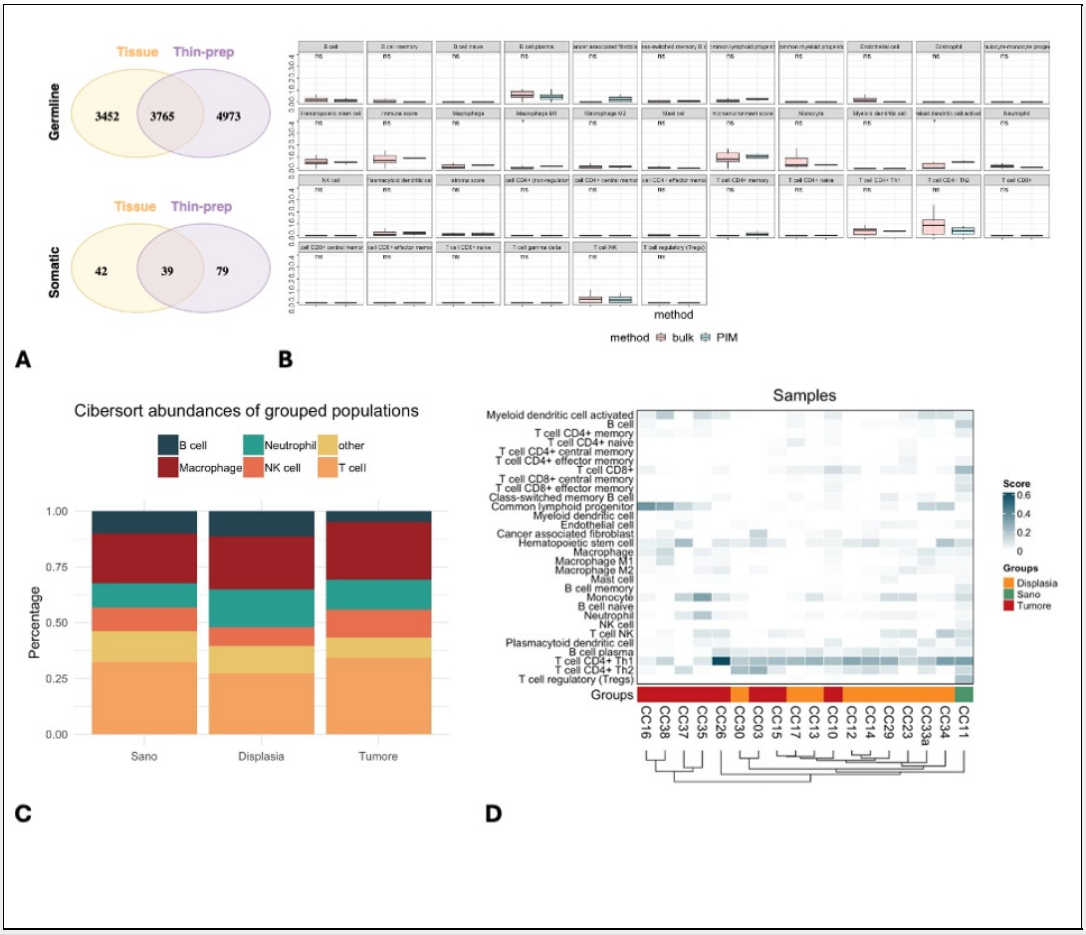
Enriched genes of all thin-prep samples have been found to be characteristics of cervical-like tissues, moreover dysplasia and cancer samples exhibited an intense inflammatory activity. Further validation for RNA quality has showed a high level of agreement. Finally, CibersortX estimates of immune cell abundances observed in our cancer cohort have been compared to the TCGA cervical cancer one, obtaining comparable results.

Info

-

filename	Slide1.png

Figure



Availability	-

Dissemination Material

Social

-

Summary

-

Corresponding Author

Name, Surname	Martina, Betti
Email	martinabetti0908@gmail.com
Submitted on	15.04.2024