



CIBBIOTECH
FROM MANTO CELL FOR MAN



Con il patrocinio di

INTERNATIONAL WORKSHOP NO-CANCER **2024**

from cancer cell biology to personalized therapy

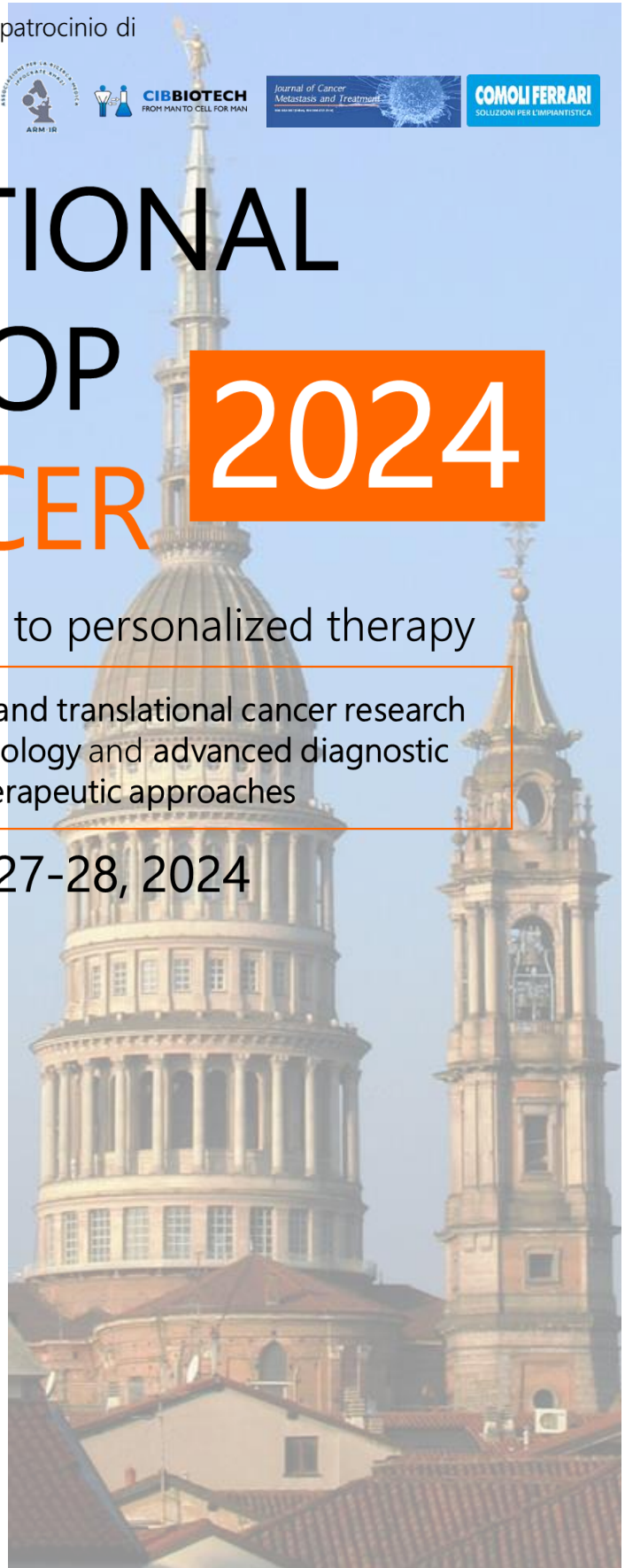
The workshop focuses on basic and translational cancer research with emphasis on cancer cell biology and advanced diagnostic and personalized therapeutic approaches

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ABSTRACT BOOK



<https://nocancercongress.uniupo.it>



Droplet Digital PCR Development to Quantify the DNA Methylation Levels of *SEPT9* and *SHOX2* in Plasma from Patients with Head and Neck Squamous Cell Carcinoma

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Methylation of septin 9 (*SEPT9*) and short stature homeobox 2 (*SHOX2*) in circulating cell-free DNA (ccfDNA) has emerged as a promising biomarker in many cancers. In head and neck squamous cell carcinoma (HNSCC), data obtained with qPCR suggested the valuable role of *SEPT9* and *SHOX2* gene methylation as non-invasive tool for diagnosis and prognosis. However, a precise method would improve detection at low circulating gene methylation levels. Therefore, we have developed highly sensitive assays using droplet digital PCR (ddPCR) for the absolute quantification of *SEPT9* and *SHOX2* methylation. The methylation-specific ddPCR (MS-ddPCR) assays were first set up using commercial methylated/unmethylated DNA set, and then used to quantify *SEPT9* and *SHOX2* methylation in the plasma of 20 HNSCC patients before treatment and longitudinally during follow-up. The MS-ddPCR efficiency was demonstrated. Methylated *SEPT9* and *SHOX2* levels were significantly reduced in patients at first follow-up time points *versus* T0. Interestingly, different trends of longitudinal DNA methylation variation were found in small groups of stratified patients. In summary, we present successful MS-ddPCR assays for detecting *SEPT9* and *SHOX2* methylation in ccfDNA; a prospective multicenter study is ongoing to validate the ability of *SEPT9/SHOX2* ccfDNA methylation for recurrence/second malignancy detection in HNSCC (IDENTIFY project).

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