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FRANÇOIS MALLET

MICROARRAY-BASED SKETCHES OF THE HUMAN ENDOGENOUS RETROVIRUSES (HERV) TRANSCRIPTOME: FROM JUNK DNA TO BIOMARKER APPLICATION.

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SARDEGNA RICERCHE
Loc. Piscinamanna – Edificio 2 – Pula

Moderator: Prof. Enzo Tramontano, UniCa

François Mallet

Director of Joint Unit Hospice civil de LYON-bioMérieux Lyon Sud Cancer
Group leader of Cancer Biomarkers Research group

The human genome contains 25,000 genes but also 200,000 endogenous retroviral sequences (HERV) integrated during the evolution and which are nowadays organized into complex multicopy families. Improperly named junk DNA in the 80's, it has been uncovered during the last 15 years that HERV activity can be neutral, beneficial or detrimental to the host. The first example of the domestication of a retroviral envelope (ERVWE1/Synctin-1) involved in placental morphogenesis has been demonstrated by the research group of Prof. Mallet. Using custom

microarrays in Affymetrix format and a panel of normal and tumor tissues, they further proposed a first view of the HERV transcriptome landscape. They also showed that the HERV transcriptome follows tropism rules and is sensitive to the state of cell differentiation. Prof. Mallet will show how this dedicated tool allows a functional interpretation of HERV expression, notably the identification of embedded promoter functions and associated epigenetic regulation. He will also illustrate applications to biomarker discovery for diagnostic in the cancer field.

Information and registration available at www.sardegna-ricerche.it