ID: 01018
Type: Poster
Topic: Tumor biology

Staufen 1, a new class of pro-oncogenic factor in melanoma linked to dsRNA signalling

CRISTINA tejedo[1] , panagiotis karras[1] , daniela C. Cerezo[1] , Maria S. Soengas[1]

1) Melanoma Group, CNIO

Cutaneous melanoma is an increasing prevalent cancer, characterized for the extensive changes in the transcriptome. Yet, the specific contribution of RNA binding proteins (RBPs) to melanoma progression is largely unknown. Targeted therapies together with immunotherapy have arisen as promising therapeutic approaches for metastatic patients. However, there is still an important fraction of patients that do not respond. Understanding the mechanisms underlying this resistance may pave the way for new therapeutic strategies. Here we present computational analyses of large clinical datasets together with histological and functional studies, leading to the identification of the dsRNA binding protein STAU1 as a potential novel driver and immune modulator in melanoma. In particular, we have found a high upregulation of STAU1 mRNA and protein levels in human melanoma biopsies (to our knowledge the largest changes reported for an RBP in this tumor type). Mechanistically, analyses in genetically modified mouse models support a contribution of the MAPK pathway to STAU1 expression. Moreover, STAU1 depletion compromises melanoma cell proliferation and invasion in cell culture. Potential targets of STAU1 include the coding transcript for the immune checkpoint blocker PD-L1. Together these data support unanticipated roles of STAU1 in the control of aggressive features of malignant melanoma.

[files191=2;500;500][fileShow][/files]