



XIX CONGRESSO
NAZIONALE
SIES 2026

***NONO modula la progressione del mieloma
multiplo attraverso percorsi dipendenti ed
indipendenti dalle paraspecole***

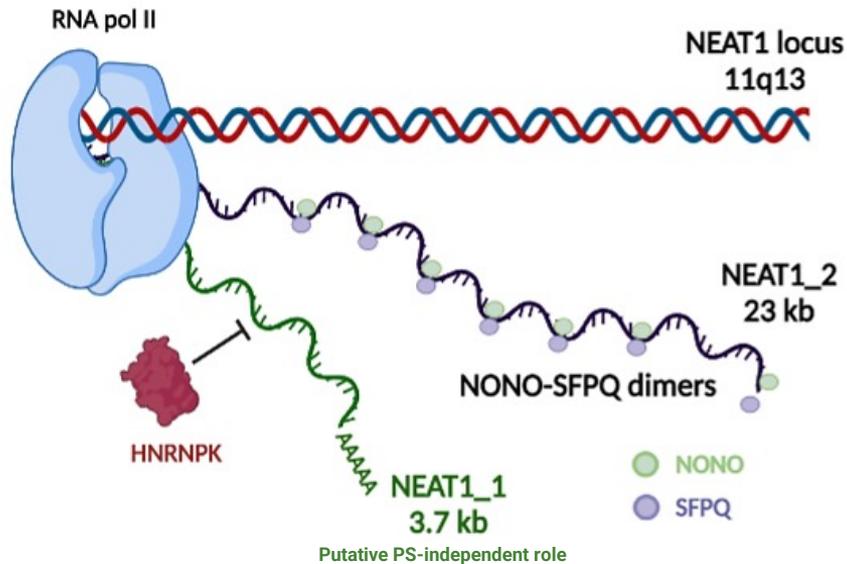
Elisa Taiana

Firenze | 4-6 marzo 2026
Palazzo degli Affari



Disclosures of Name Surname

Company name	Research support	Employee	Consultant	Stockholder	Speakers bureau	Advisory board	Other



Leukemia

Long non-coding RNA NEAT1 targeting impairs the DNA repair machinery and triggers anti-tumor activity in multiple myeloma.

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Long Non-Coding RNA NEAT1 Shows High Expression Unrelated To Molecular Features And Clinical Outcome In Multiple Myeloma

Elisa Taiana, Domenica Ronchetti, Vanessa Favasuli, Katia Todoerti, Martina Manzoni, Nicola Amodio, Pierfrancesco Tassone, Luca Agnelli, Antonino Neri

Activation of long non-coding RNA NEAT1 leads to survival advantage of multiple myeloma cells by supporting a positive regulatory loop with DNA repair proteins

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NONO/p54^{nrb} (Nuclear RNA-binding protein, 54 kDa)

- overexpressed in MM PCs as compared to healthy donors-derived PCs
- associated with poor OS and PFS
- correlated with high-risk molecular subtypes
- linked to activation of cell cycle pathways
- associated with upregulated DNA repair mechanisms
- involved in deregulated RNA processing and splicing

- a potential prognostic biomarker
- a potential therapeutic target

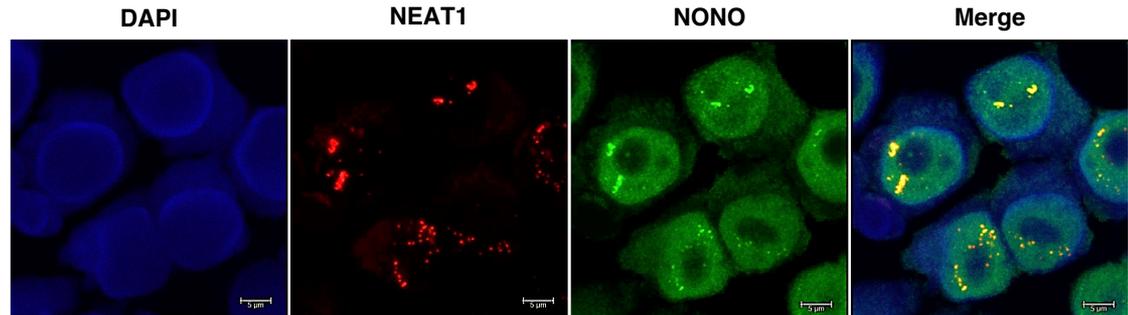
Discover Oncology



Brief Communication

Expression levels of NONO, a nuclear protein primarily involved in paraspeckles function, are associated with several deregulated molecular pathways and poor clinical outcome in multiple myeloma

Domenica Ronchetti^{1,2} · Vanessa Katia Favasuli^{1,2} · Ilaria Silvestris^{1,2} · Katia Todoerti^{1,5} · Federica Torricelli³ · Niccolò Bolli^{1,2} · Alessia Ciarrocchi³ · Elisa Taiana¹ · Antonino Neri⁴



NEAT1-specific RNA-FISH

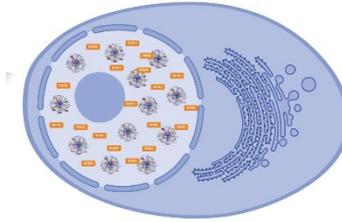
NONO IF

Aim of the study

To define how NONO shapes the transcriptomic landscape of MM plasma cells, both through its PS-associated and independent mechanisms



Experimental design

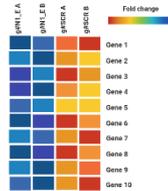
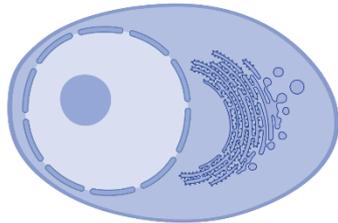


NONO within PSs

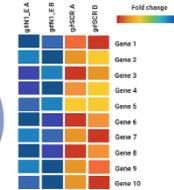
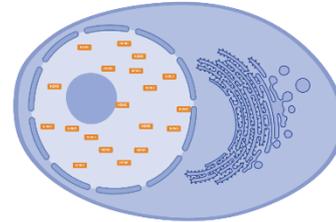
NONO out side PSs



NONO



GLOBAL transcriptional signature of NONO

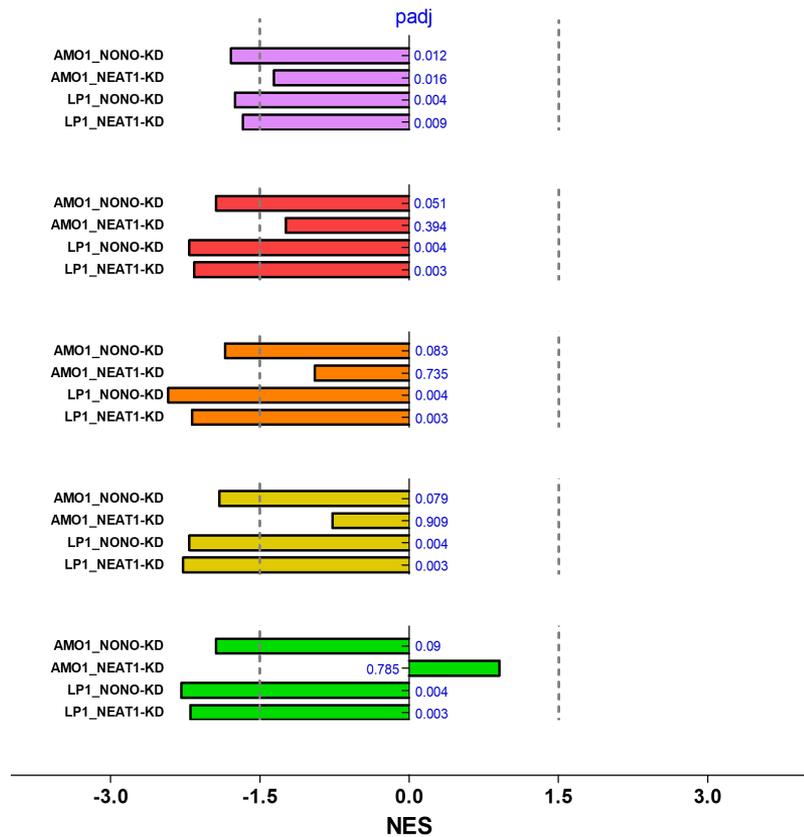


PSSs-DEPENDENT transcriptional signature of NONO

Shared pathways between NONO-KD and NEAT1-KD samples will shed light on NONO's functions related to PS

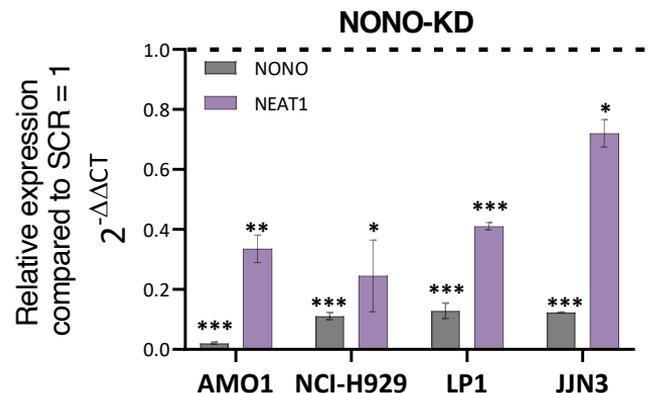
NONO-KD specific pathways will be suggestive of its PS-independent role.

NONO's involvement in PS-associated pathways



- REACTOME_SIGNALING_BY_NOTCH
- REACTOME_RUNX1_REGULATES_GENES_INVOLVED_IN_MEGAKARYOCYTE_DIFFERENTIATION_AND_PLATELET_FUNCTION
- REACTOME_HDACS_DEACETYLATE_HISTONES
- REACTOME_FORMATION_OF_THE_BETA_CATENIN_TCF_TRANSACTIVATING_COMPLEX
- REACTOME_DNA_METHYLATION

NONO's involvement in PS-unrelated pathways

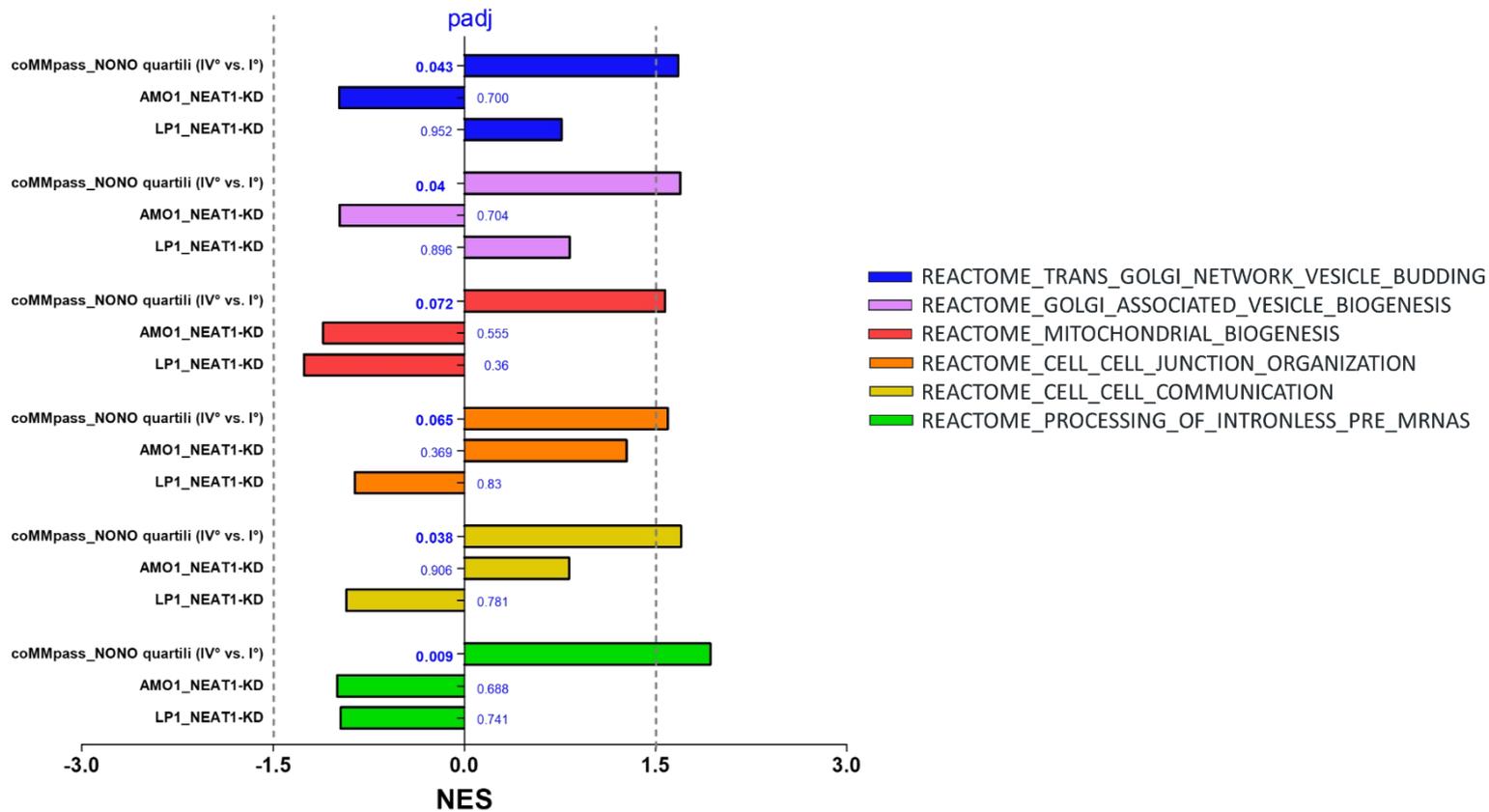


The transcriptomic alterations observed upon NONO silencing could be, at least partially, driven by NEAT1 downregulation, thereby reflecting PS-dependent effects



Highest vs. lowest quartiles of NONO expression (CoMMpass dataset)
→ identification of distinct pathways not shared with NEAT1-KD HMCLs

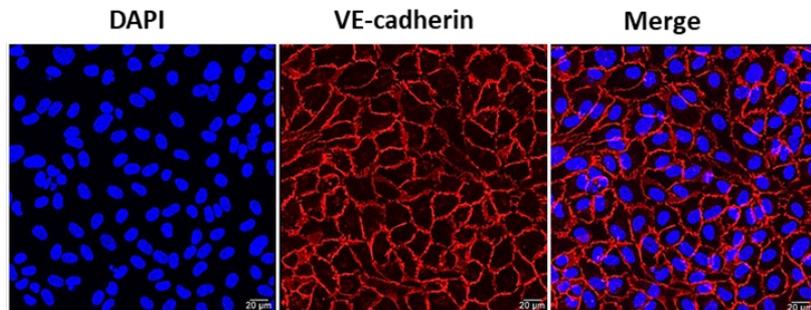
NONO's involvement in PS-unrelated pathways



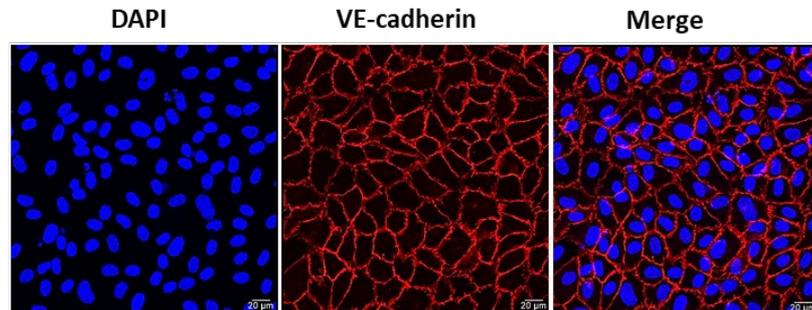


HUVEC cells cultured with conditioned medium from

NCI-H929
SCR



AMO-1
SCR



Take-Home Messages

- The comparison of NONO-related and NEAT1-related signatures reveals substantial overlap linked to PSs biology, while also identifying PS-independent roles of NONO.
- The observed dysregulation of cell-cell adhesion pathways following NONO-KD highlights a previously underappreciated role for NONO in modulating the tumour microenvironment.

Conclusions

This study highlights the potential of NONO as a therapeutic target in MM by elucidating its role in transcriptional regulation, particularly within pathways essential to disease progression.

Acknowledgments

**Department of Oncology and Hemato-oncology,
Università degli Studi di Milano**

**Hematology Unit - Fondazione IRCCS Ca' Granda
Ospedale Maggiore Policlinico, Milano**



Sistema Socio Sanitario



Domenica Ronchetti

Ilaria Silvestris

Valentina Traini

Giusi Fabbiano

Francesca Lazzaroni

Prof. Niccolò Bolli

Prof. Francesco Passamonti



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PER LA RICERCA SUL CANCRO

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**Oncology Department, Computational Oncology Unit
Mario Negri IRCCS**

Ilaria Craparotta

Marco Bolis

**Laboratory of Translational Research
Azienda USL-IRCCS di Reggio Emilia**

Noemi Puccio

Federica Torricelli

Alessia Ciarrocchi

Prof. Antonino Neri