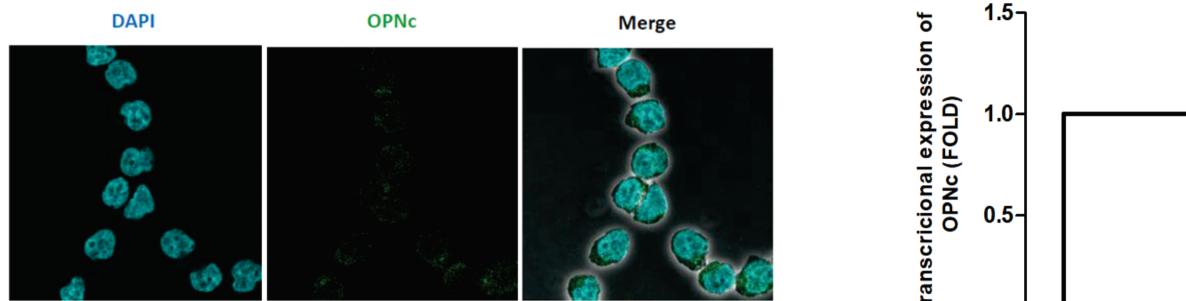
# **OSTEOPONTIN-C ACTIVATES B-CELL ACUTE** LYMPHOBLASTIC LEUKEMIA PROGRESSION FEATURES

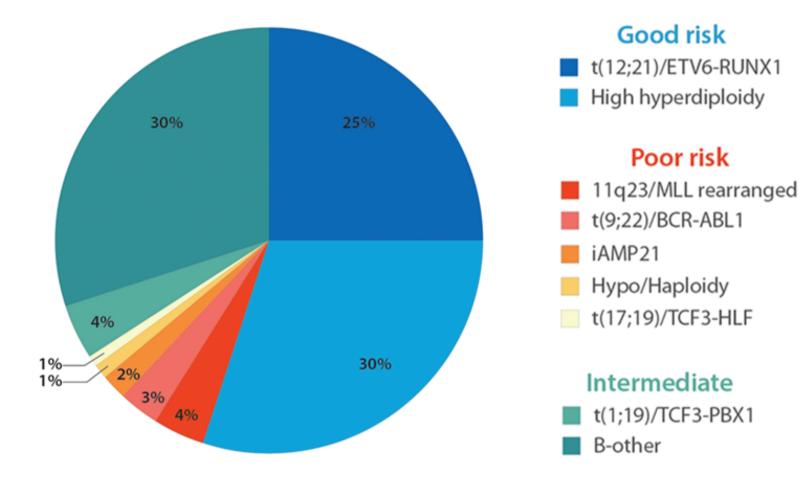
Ana Clara Santos da Fonseca Bastos<sup>1</sup>, Júlio César Santoro<sup>2</sup>, Luciana Bueno Ferreira<sup>1</sup>, Érika Elias Ferreira<sup>1</sup>, Júlio César Madureira de Freitas Júnior<sup>1</sup>, Marco Antônio Marques Pretti<sup>3</sup>, Martin Hernan Bonamino<sup>3</sup>, Mariana Emerenciano<sup>2</sup>, Etel Rodrigues Pereira Gimba<sup>1,4</sup> <sup>1</sup>Laboratório de Oncobiologia Celular e Molecular, INCa, RJ.<sup>2</sup>Laboratório de Pesquisa Clínica de Desenvolvimento Tecnológico, INCa, RJ.<sup>3</sup>Laboratório de Imunologia de Tumores, INCa, RJ. <sup>4</sup>Laboratório de Biomarcadores Neoplásicos, IHS, UFF, RJ.

## INTRODUCTION

RESULTADOS

Osteopontin (OPN) primary transcript is subject to alternative splicing, generating at least five OPN splicing isoforms (OPN-SI) named OPNa, OPNb, OPNc, OPN4, and OPN5. A hallmark of B- cell acute lymphoblastic leukemia (B-ALL) is the occurrence of specific gene rearrangements associated with prognostic risk stratification. Patients harboring the KMT2A-AFF1 gene fusion are included in the poor prognostic subgroup, with an overall survival rate of 35% and increased risk of extramedullary sites involvement. In B-ALL, it has been reported that total OPN (tOPN) supports tumor dormancy and cell survival in response to chemotherapeutic drugs. However, the putative roles of OPN-SI in B-ALL cells have not been addressed. Previous data from our group showed that OPNc is overexpressed in B-ALL patients harboring the KMT2A-AFF1 gene fusion and is correlated to poor prognostic features (Bastos et al., 2019 sob revisão).





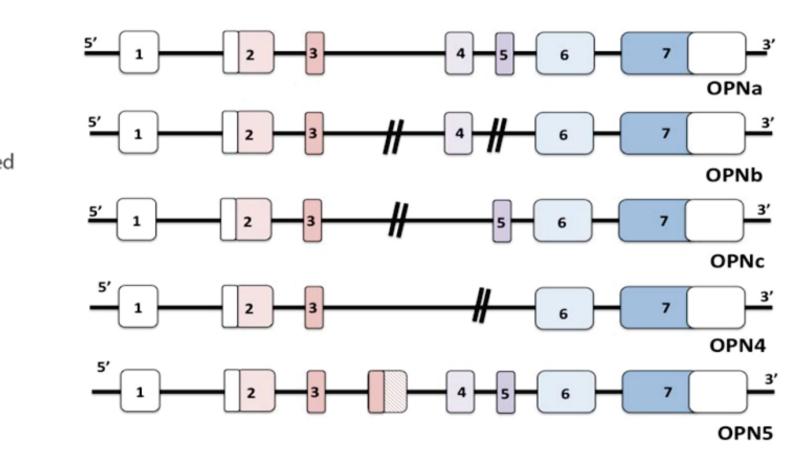


Figure 1: Frequency of molecular-cytogenetic abnormalities in B-ALL. Rearrangements of the KMT2A (also known as mixed lineage leukemia (MLL) gene located on chromosome 11q23 are observed in 4% of ALL patients and are related to poor prognosis. (Adapted from Schwab & Harrison, 2018)

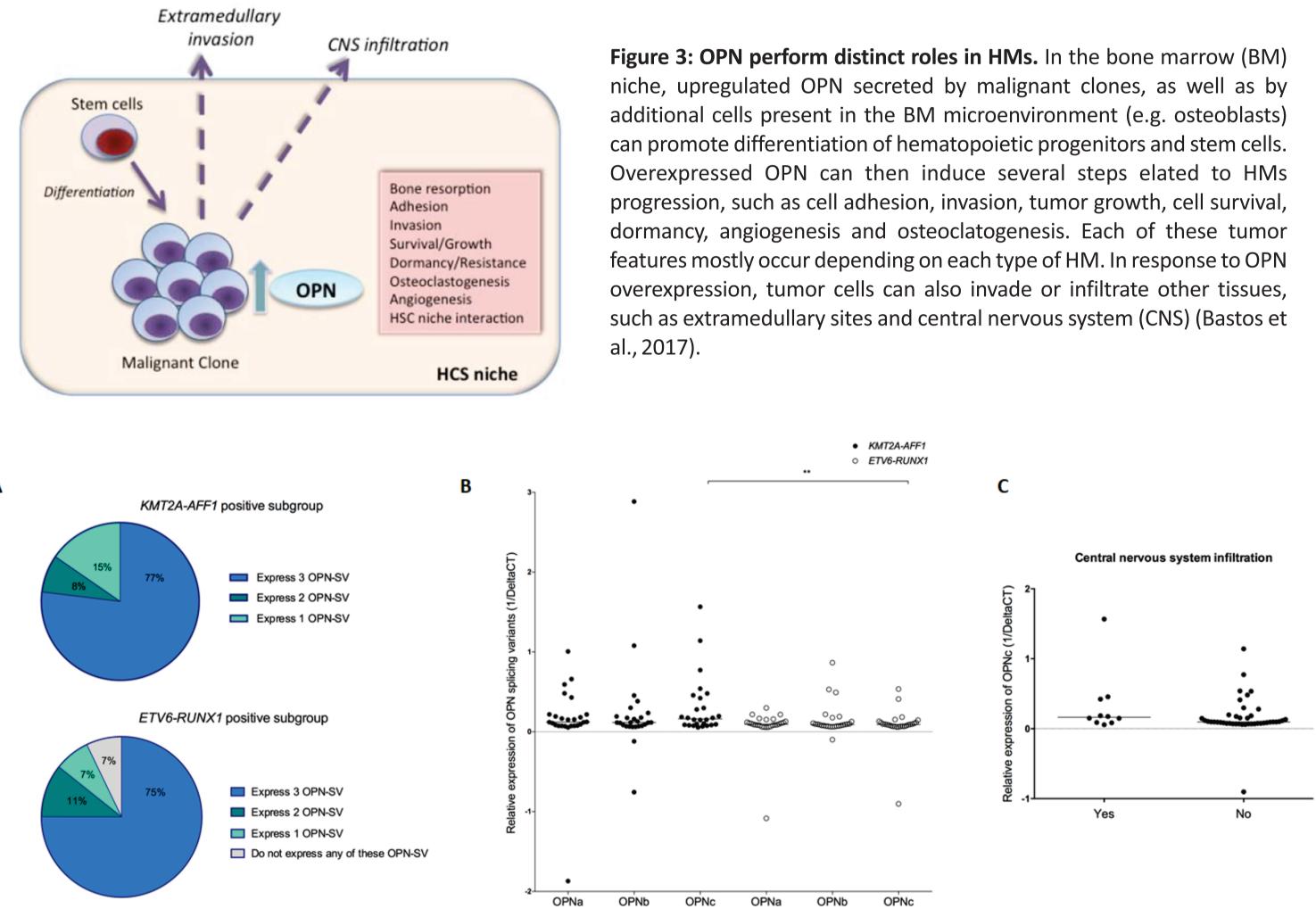
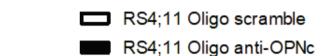


Figure 2: OPN gene structure, described splice variants and their respective exon arrangements. The full length isoform, named OPNa, contains 7 exons represented by white (non-coding) and colored (coding) boxes. While OPNb and OPNc lack exons 5 and 4, respectively (Bastos et al., 2017).

Figure 6: OPNc expression levels in RS4;11 cell line. The expression of OPN-c in RS4;11 cell line was analyzed by immunofluorescence assay. Cells were incubated in the presence of OPNc antibody conjugated with FITC and DAPI. Imagens were analyzed using confocal laser microscopy.



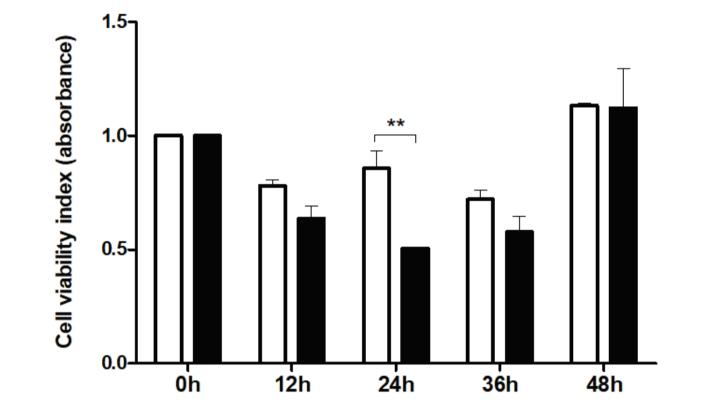
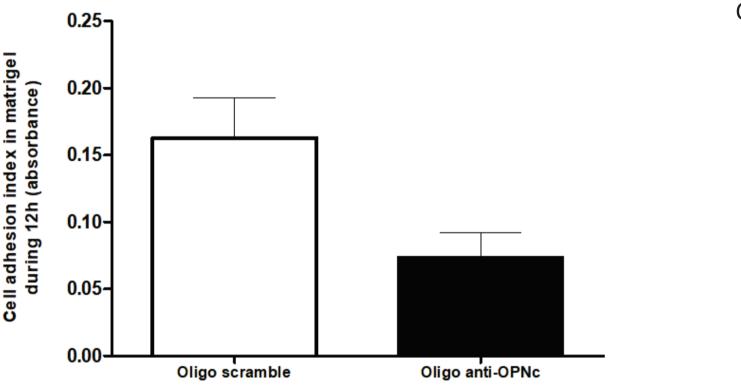


Figure 8: OPNc knock-down inhibit RS4;11 B-ALL cell viability rates. Curve graphs represent viability rates according to MTT analysis every 12 hours in cells transfected with 50nM of anti-OPNc or scrambled DNA oligomers at 0-48h time range. Cell viability rates were evaluated by absorbance measurement at 650nm (p=0.009).



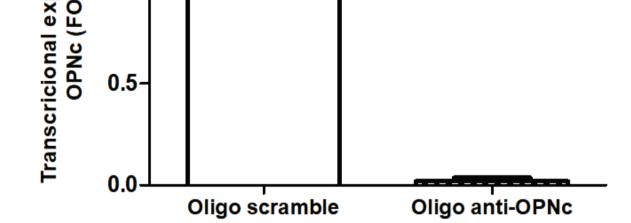


Figure 7: OPNc was efficiently knocked-down using anti-OPNc antisense DNA oligomers modified with phosphorothiotates. The RS4;11 B-ALL cell line was transfected using 50 nM anti-OPNc or scrambled DNA oligomers by the 4D-Nucleofector.

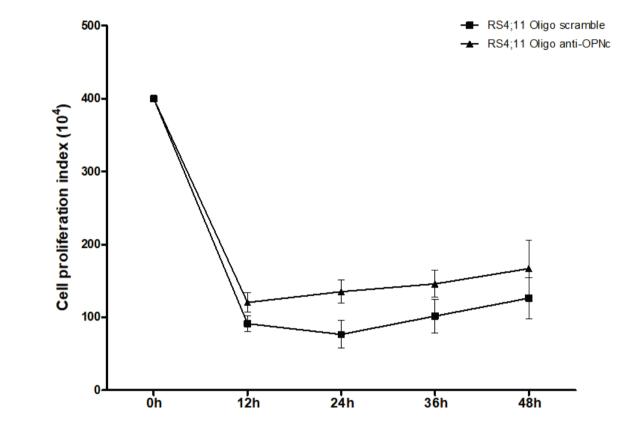


Figure 9: OPNc knock-down inhibit RS4;11 B-ALL cell proliferation rates. The RS4;11 B-ALL cell line exhibit increased proliferation rates in response to OPNc silencing at 12-48 h post transfection with anti-OPNc oligomers. Curve graphs represent proliferation rates according to trypan blue cell counting analysis every 12 h in cells transfected with 50nM of anti-OPNc or scrambled DNA oligomers at 0-48 h time range. Cell number were determined by Trypan blue.

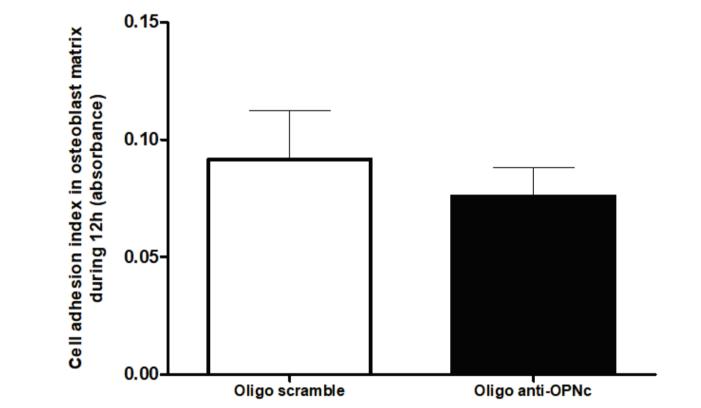


Figure 4: Frequency and expression levels of OPN-SIs in B-ALL patient samples. (A) Frequency of OPN-SIs expression levels in B-ALL patient samples. The frequency of OPN-SIs expression levels in B-ALL patients subgroups with *KMT2A-AFF1* fusion gene or ETV6-RUNX1 rearrangement, as a comparative group. (B) The mRNA expression levels of OPN-SIs in B- ALL patient samples were analyzed using real-time RT- PCR. Dot-plot graph represents OPN-SI relative expression levels as demonstrated by 1/Delta CT. Actin gene has been used as the reference gene. OPNc and OPNa isoforms are expressed in higher levels in patients samples harbouring either *KMT2A-AFF1* or ETV6-RUNX1 rearrangements. Additionally, patients harbouring KMT2A- AFF1 fusion exhibit higher OPNc transcriptional levels those harbouring ETV6-RUNX1 rearrangement (p=0.0056). (C) Dot-plot graph represent OPNc relative expression levels as demonstrated by 1/Delta CT. Patients *KMT2A-AFF1* positive with CNS infiltration present higher median OPNc transcriptional expression levels than those patient samples without CNS infiltration.

#### **OBJECTIVES**

This study aimed to investigate the putative roles of OPNc on modulating cellular and molecular aspects of B-ALL cells with KMT2A-AFF1.

Figure 10: OPNc knock-down inhibit RS4;11 B-ALL cell adhesion rates over matrigel. Bar graphs represent cell adhesion rates over matrigel Cells were transfected with 50nM of anti-OPNc or scrambled DNA oligomers. Cell adhesion rates were evaluated by absorbance measurements at 650nm

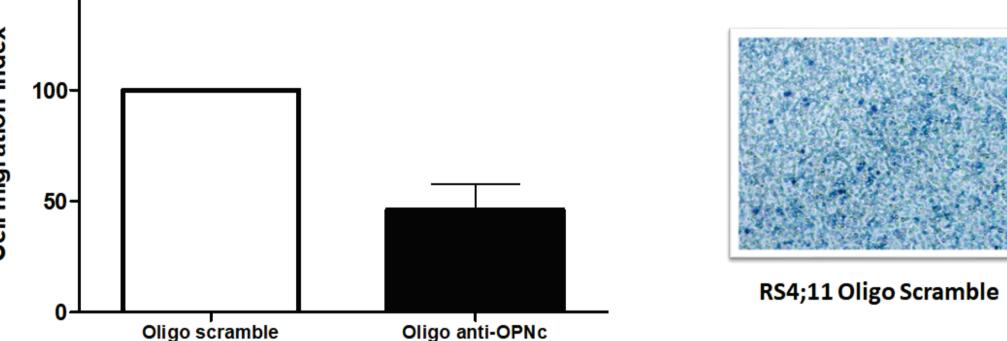


Figure 11: OPNc knock-down inhibit RS4;11 B-ALL cell adhesion rates over osteoblastic cell matrix. Bar graphs represent cell adhesion rates over extracelular matrix produced by MC3T3-E1 cell line. Cells were transfected with 50nM of anti-OPNc or scrambled DNA oligomers. Cell adhesion rates were evaluated by absorbance measurements at 650nm.

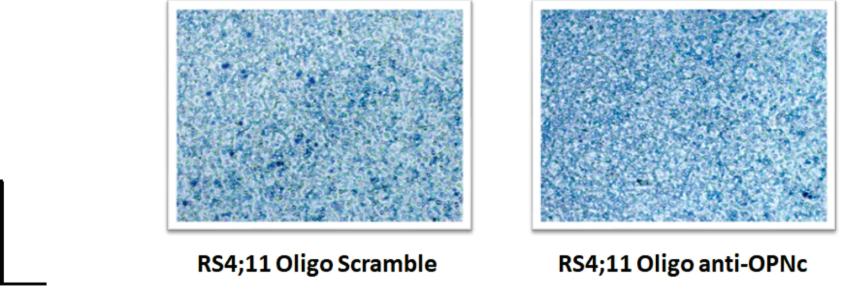
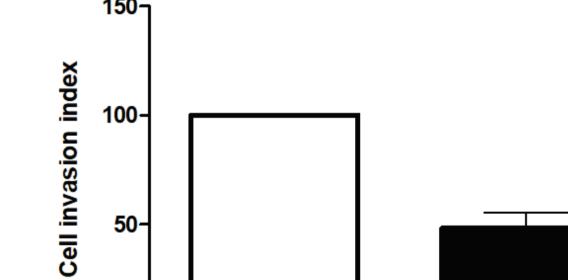
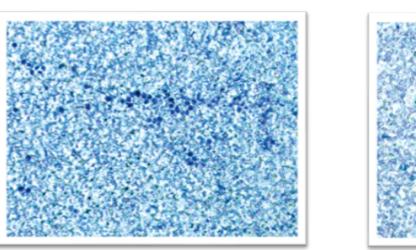
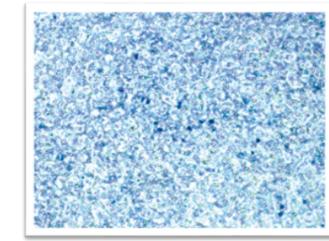


Figure 12: OPNc knock-down inhibit RS4;11 B-ALL cell migration rates. Bar graphs represent cell migration rates in boyden chamber assays. Cells were transfected with 50nM of anti-OPNc or scrambled DNA oligomers. Cell migration rates were evaluate in boyden chamber after 4h of cell plating







#### METHODOLOGY

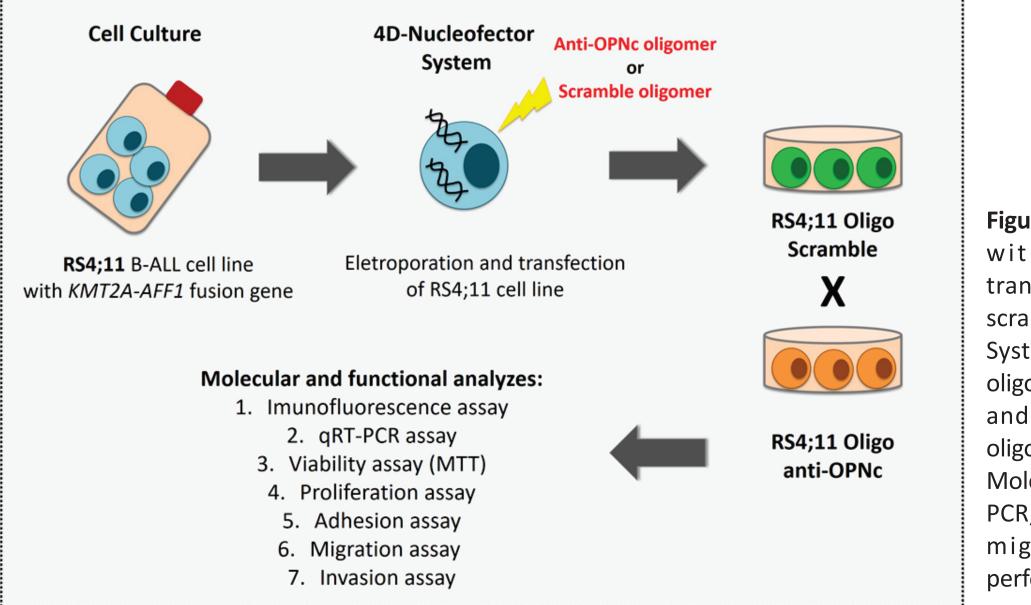
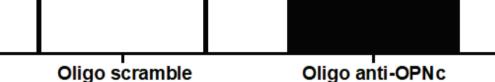


Figure 5: Methodology. RS4;11 B-ALL cell line with KMT2A-AFF1 fusion gene was transfected with anti-OPNc oligomers or scramble oligomers using 4D-Nucleofector System. Cells transfected with anti-OPNc oligomer was named RS4;11 Oligo anti-OPNc and cell transfected with the scramble oligomer was named RS4;11 Oligo scramble. Molecular and functional analysis such as qRT-PCR, cell viability, proliferation, adhesion, migration and invasion assays were performed in response to OPNc silencing.



#### RS4;11 Oligo Scramble

RS4;11 Oligo anti-OPNc

Figure 13: OPNc knock-down inhibit RS4;11 B-ALL cell invasion rates. Bar graphs represent cell invasion rates in boyden chamber coated with matrigel. Cells were electroporated with 50nM of DNA oligomers specifically targeting OPNc (anti-OPNc) ou scrambled DNA oligomers . Cell invasion rates were evaluate in boyden chamber coated with matrigel at 24h time point.

### CONCLUSIONS

In summary, these data provide evidence that OPNc splice variant may control the leukemic cell's ability to detach from the bone marrow matrix and could also be a negative modulator of cell proliferation, while inducing cell invasion properties. These features could then favor central nervous system infiltration, contributing to a more aggressive B-ALL phenotype.

Projeto Gráfico: Área de Edição e Produção de Materiais Técnico-Científicos / INCA





