

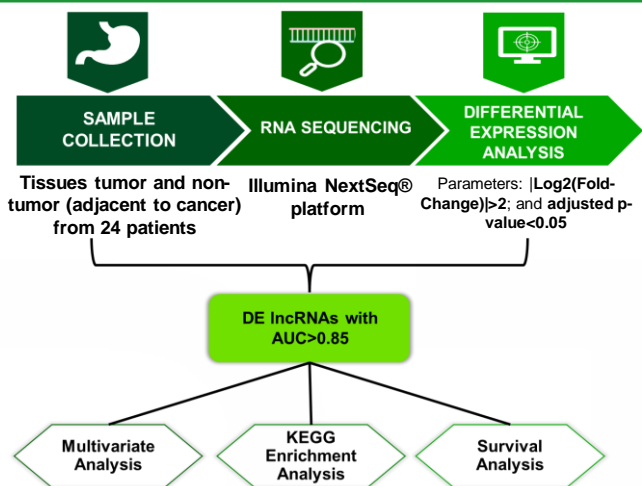
COMPREHENSIVE ANALYSIS OF LONG NON-CODING RNA EXPRESSION IN GASTRIC CANCER

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INTRODUCTION

The complexity of Gastric Cancer (GC), which includes tumor heterogeneity, constitutes a barrier to diagnosis and access to therapies. Thus, investigations are needed to search for precision biomarkers. Recently, long non-coding RNAs (lncRNAs) have emerged as a class of regulatory molecules that play crucial roles in various aspects of carcinogenesis and progression of GC, including proliferation, metastasis, and resistance to therapies. The aim of this study was to analyze the expression profiles of lncRNAs in GC.

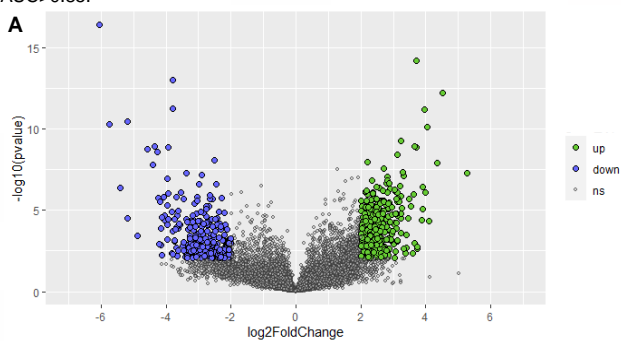
METHODS



RESULTS

DIFFERENTIAL EXPRESSION ANALYSIS

Figure 1. 716 Differentially expressed (DE) lncRNAs among tumor and non-tumor samples. A) Volcano plot B) Top 9 DE lncRNAs with AUC>0.85.

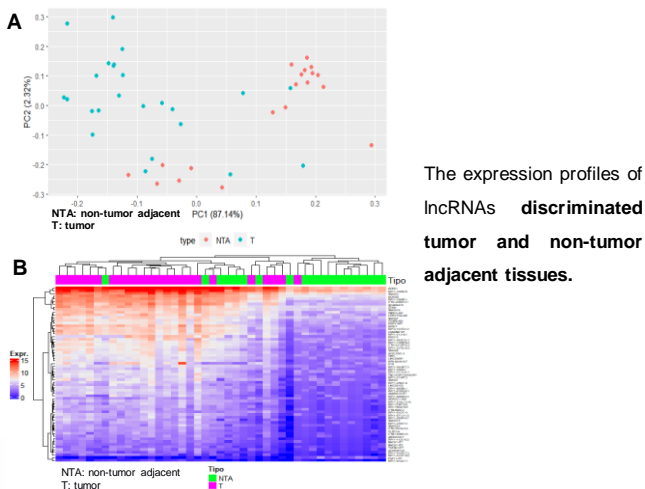


lncRNA	AUC	Log2FoldChange	p-adj
H19	0,89	4,51	1E-09
SNHG5	0,83	4,34	5E-06
FGF14-IT1	0,87	-4,26	1E-06
RP11-283C24.1	0,88	4,04	6E-08
AC007128.1	0,81	4,00	1E-04
RP11-25K21.6	0,90	3,95	9E-09

RESULTS

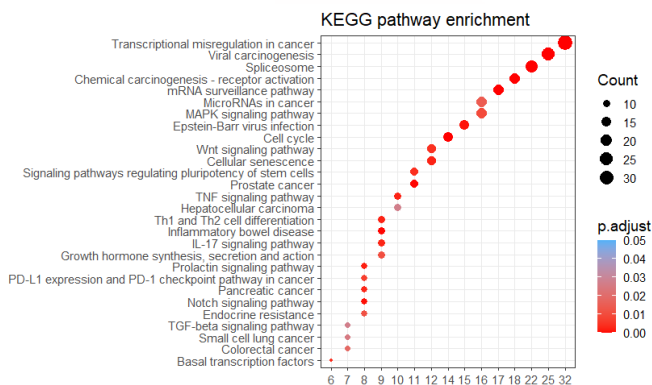
MULTIVARIATE ANALYSIS

Figure 2. Multivariate analysis based on DE lncRNAs with AUC>0.85. A) Principal Component Analysis B) Hierarchical clustering heatmap.



KEGG ENRICHMENT ANALYSIS

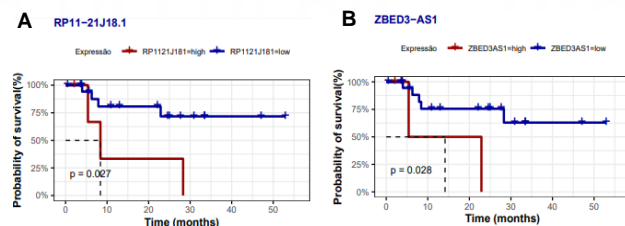
Figure 3. KEGG pathway analysis of proteins that interact with DE lncRNAs.



DE lncRNAs interact with enriched proteins in signaling pathways associated with the development and progression of GC, including microRNAs in cancer, PD-L1 expression and PD-1 checkpoint pathway, Wnt, TGF- β , Notch, and cell cycle.

SURVIVAL ANALYSIS

Figure 4. Kaplan-Meier curves based on the expression of DE lncRNAs significantly associated with overall survival. A) RP11-21J18.1 e B) ZBED3-AS1.



Low expression levels of RP11-21J18.1, ZBED3-AS1, and THAP9-AS1 were strongly related to better survival outcomes ($p < 0.05$).

CONCLUSIONS

lncRNAs exhibit a tumor-specific expression profile and interact with essential proteins enriched in pathways implicated in tumor development and progression. Moreover, the expression of DE lncRNAs affects the overall survival of GC patients. Despite additional validations are still necessary for a better understanding of the dynamics of lncRNAs in GC, this study highlights the functional relevance of these transcripts, which might help guide future investigations for the establishment of precision biomarkers and development of personalized therapeutic strategies.

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