

THE LONG NON-CODING RNAS LINC01405-210, CCDC26-315, AND TCL6-206 ASSOCIATED WITH A GENETIC SIGNATURE IN PRIMARY AND METASTATIC CERVICAL CANCER

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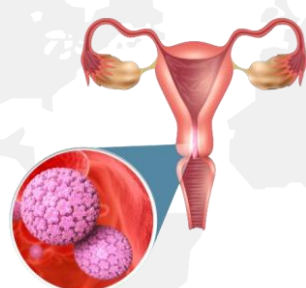
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INTRODUCTION

Cervical cancer (CC): 4th most common

WHO 2022:
660.000 cases
and 350.000
deaths

Treatment:
surgery,
chemotherapy,
and radiotherapy



Access and tracking limitations:
low/middle-income
countries

LncRNAs as biomarkers:
body fluids and
fundamental
processes of cancer

Differential expression: primary vs metastatic
tumors - genetic signatures - personalized medicine

OBJECTIVE

Identify and characterize differentially expressed lncRNAs (DETs) in CC patients and evaluate their role in molecular processes such as epithelial-mesenchymal transition (EMT) and metastasis.

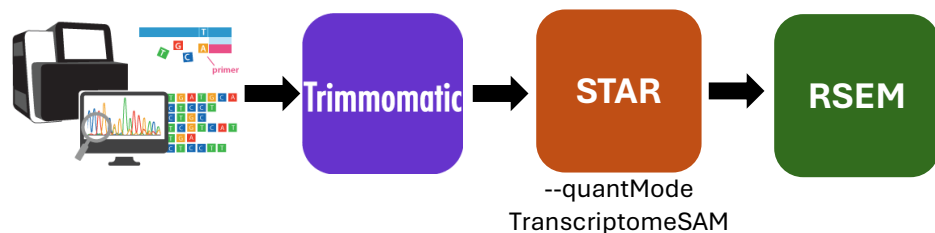
METHODOLOGY

Samples:

24 patients with CC classified as: 13 metastatic (M) and 11 primary (P)

Processing

Mapping and quantification



Differential expression analysis



$\log_2FC \geq 1$ or ≤ -1 ; $padj \leq 0,05$

Annotation and interactions

NONCODE

AnnoLnc2

LncBase
Diana Tools

LNCipedia
version 5.2

RESULTS AND DISCUSSION

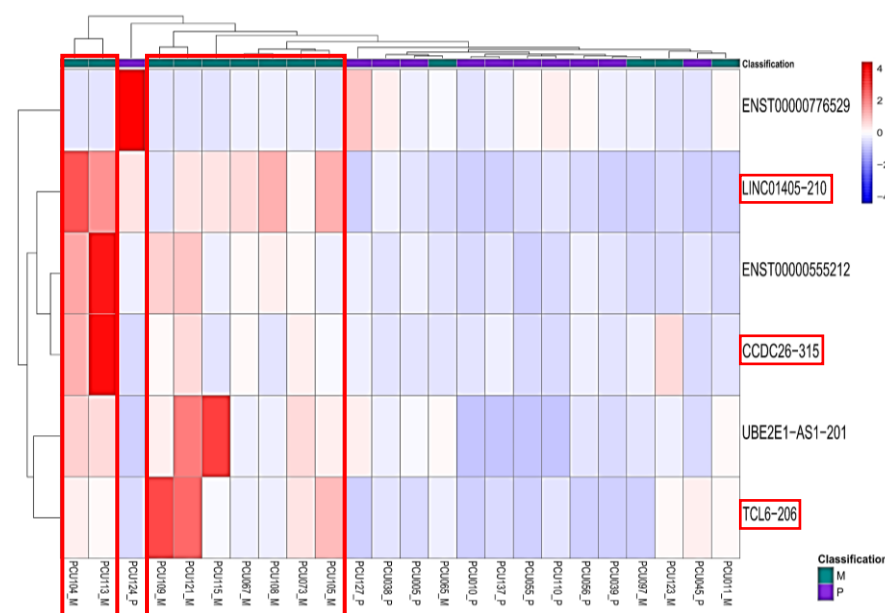
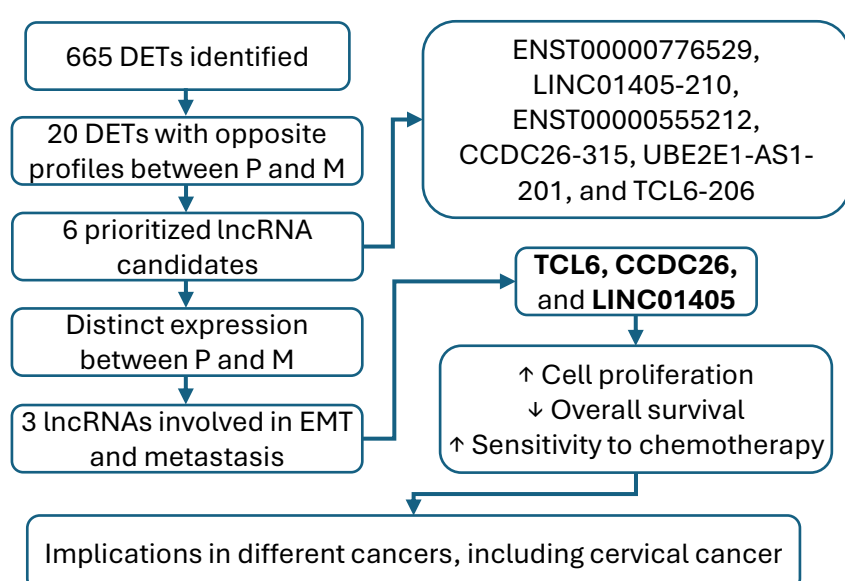


Figure 1: Heatmap of the 6 lncRNAs differentially expressed between patients classified with M and primary P tumors.

CONCLUSION

The lncRNAs LINC01405-210, CCDC26-315, and TCL6-206 were highlighted as potential biomarkers for diagnosing, prognosis, and monitoring CC. Functional studies and validations are needed to confirm their clinical role.

ACKNOWLEDGEMENTS

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REFERENCES



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