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# Investigation of microRNA-146a and microRNA-218 expression in cervical cancer



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## Background

Increasing evidence indicates that a substantial number of microRNAs (miRNAs) are aberrantly expressed in various forms of cancer. Analysis of miRNAs is becoming more effective for discovering novel tumor biomarkers suitable for clinical applications.

Cervical cancer is the second most common cancer among women worldwide. However, information about miRNAs in cervical cancer remains limited. In this study, we investigated the expression of miRNA-146a and miRNA 218 in cervical cancer on tissue microarray (TMA) samples

## Materials & Methods

Cervical cancer TMA samples (BioGenex TS-4215) were used in this study.

## Materials & Methods

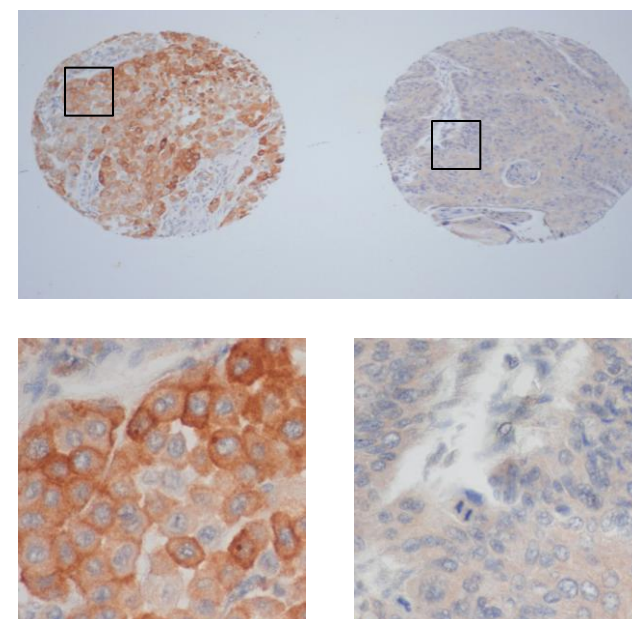
Probes for miRNA-146a and miRNA 218 were labeled with 5'-Fluorescein.

Fully automated Xmatrix system (from slides baking, denaturation, hybridization, detection, and final coverslipping) was used for the experiments. BioGenex Kit #DF-300 was used for chromogenic detection

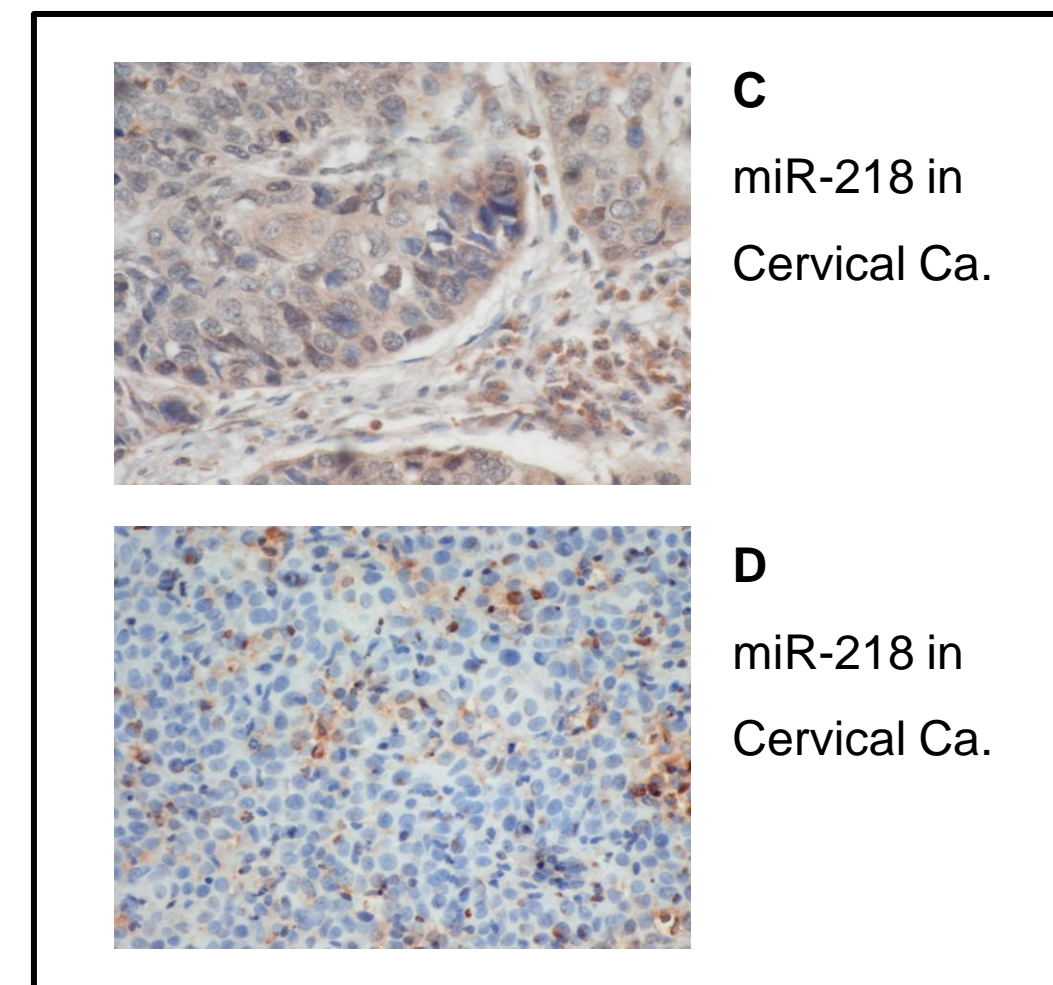
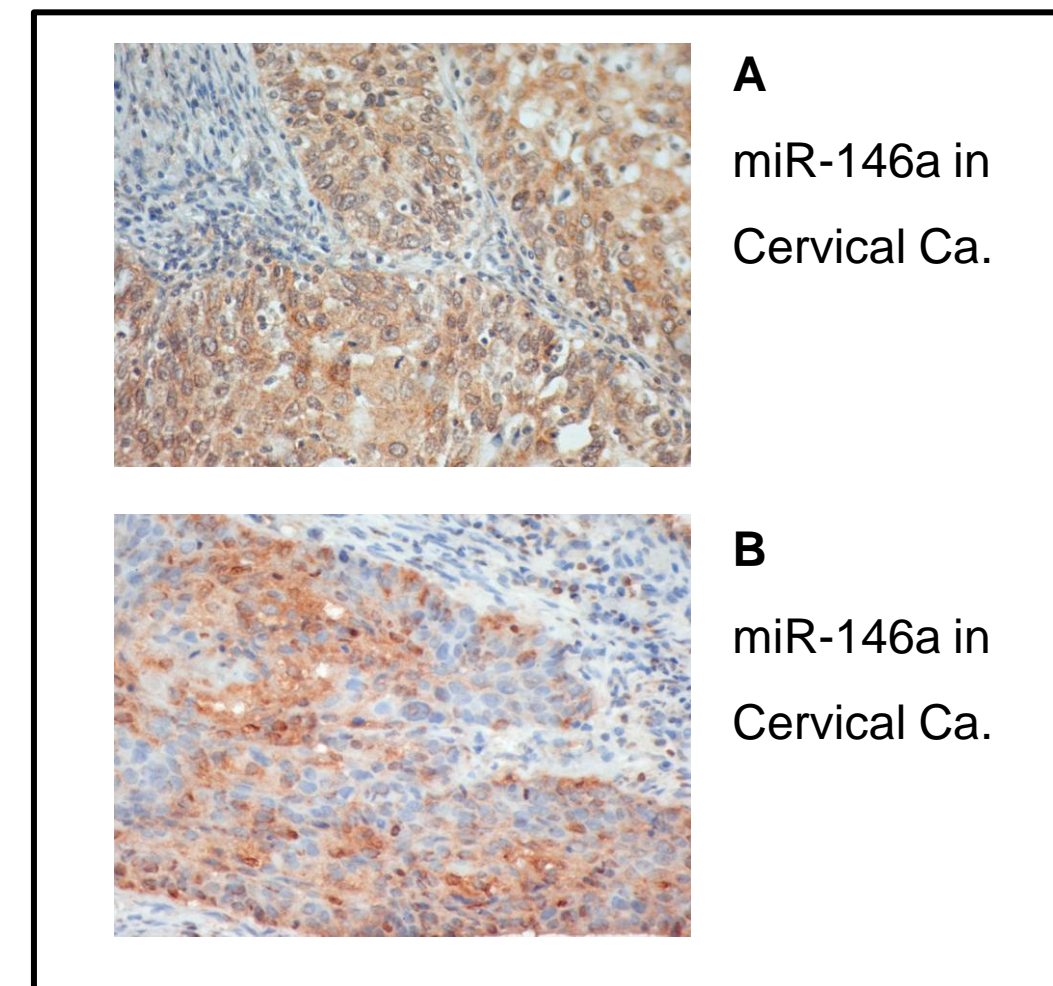


## Results

miR-146a in Cervical Cancer



## Results



## Results

Among the 33 cervical cancer TMA samples, upregulated cytoplasmic expression of miR-146a in cancer cells was observed in 22 tissue samples (66.7%). There were 11 cervical cancer samples that exhibited basal level expression (33.3%).

Only 8 out of 33 cervical cancer samples demonstrated elevated levels of miR-218 (24.2%), 19/33 (58%) showed basal level expression, and there were 6/33 samples (18%) displayed low expression level.

## Conclusions

- 1) miR-146a expression is upregulated in cervical cancer. This may be used as a biomarker for the molecular diagnosis of cervical cancer.
- 2) Future determination of the expression level and clinical prognosis is of importance for developing miR-146a as a potential novel therapeutic agent against cervical cancer.