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# INTRODUCTION

The AID (activation-induced cytidine deaminase) /APOBEC (apolipoprotein B mRNA editing) enzyme, catalytic polypeptide) family consists of proteins (AID and APOBEC1-5) that participate in a process known as DNA editing<sup>1</sup>;

## OBJECTIVE

To evaluate the contribution of APOBECs to the mutational signature of HNSCC and ESCC.



APOBECs, especially APOBEC3s, are established as potent an enzymatic source of endogenous mutations in diverse tumors<sup>1</sup>. The APOBEC signatures are present in many tumor genomes as C-to-Thypermutation and as C-to-G in TpC context, enriched in APOBEC-preferred motifs<sup>2-5</sup>;

In esophageal squamous cell carcinoma (ESCC), an APOBEC-mediated mutational signature in 50% of tumor samples suggests that APOBEC-catalyzed deamination provides a source of DNA damage<sup>°</sup>;

Head and Neck squamous cell carcinoma (HNSCC) also showed the highest APOBEC3B mRNA levels and display the putative APOBEC mutational signature';

HNSCC is the 6th most frequent type of cancer<sup>8</sup> and esophageal cancer (EC) is the 6th most frequent type of cancer among men and the 14th, among women, in Brazil<sup>9</sup>, in which ESCC is the main histological type<sup>10</sup>;

HNSCC and ESCC are tumors with similarities in morphology and etiologic factors<sup>11,12</sup>.





## **METHODOLOGY**

Through the exome sequencing data from TCGA database of HNSCC and ESCC samples, we investigated the mutational signatures profile of these tumors, using R software;

Using RNA-seq, we evaluated the mRNA expression of APOBECs in laryngeal squamous cell carcinoma (LSCC) and ESCC and matched surrounding non-tumor tissue of LSCC and ESCC patients from Instituto Nacional de Câncer, INCA/RJ;

Using RNA-seq, through R software, we performed correlation analysis for the detected expression of these genes with APOBEC mutations in ESCC patients.

#### RESULTS



The mutational signature contribution of ultraviolet light exposure, APOBEC signature and tobacco exposure in subsites of HNSCC and in ESCC through the exome sequencing data from TCGA database







5 - 0 -					I NMAM
-5-	APOBEC3H	APOBEC4	APOBECs	log2FoldChange	p Value
10 -			APOBEC2	-0.94	0.074
			APOBEC3A	3.37	3.54 <b>E-</b> 10
5 -			APOBEC3B	2.95	4.93 <b>E-</b> 17
			APOBEC3C	0.34	0.058
0 -			APOBEC3D	1.81	3.33E-08
-5 -			APOBEC3F	1.54	1.47E-10
0	NMAM tumor	NMAM tumor	APOBEC3G	1.34	4.69 <b>E-</b> 09
			APOBEC3H	0.99	0.012



Alterations in TpC context

0.30-

0.25-

Comparison of APOBECs expression in non-tumor surrounding mucosa (NMAM) and tumor tissue from 14 ESCC patients using RNAseq.

Comparison of the mutation fractions of C-to-T and C-to-G in TpC context in LSCC and ESCC samples using RNAseq.

Correlation analysis between APOBEC3H and APOBEC3D expression with total APOBEC mutations (C-to-T and C-to-G), with C-to-T APOBEC mutations and with C-to-G APOBEC mutations in ESCC patients using RNAseq

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## **CONCLUSION**

The deregulation of the APOBEC family of genes is a common feature in ESCC and LSCC, but the APOBEC signature seems to be able to distinguish these two tumors

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#### Projeto Gráfico: Serviço de Edição e Informação Técnico-Científica / INCA



\*p<0.05

