

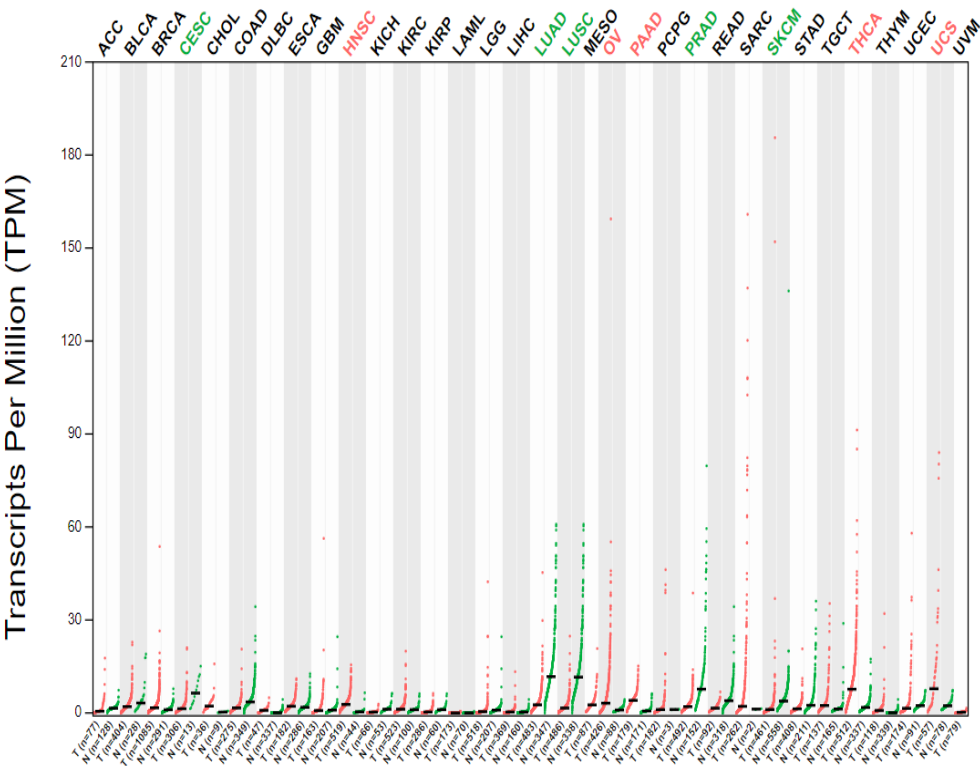
# THYROID CANCER

## (COL13A1 & COL23A1)

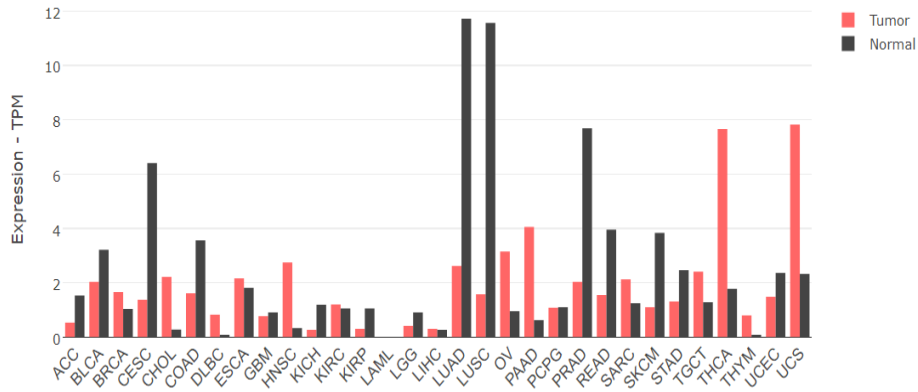
### 1.Transcriptional Analysis of Gene(GEPIA2) : COL13A1

The gene expression profile across all tumor samples and paired normal tissues.(Dot plot)

Each dots represent expression of samples.

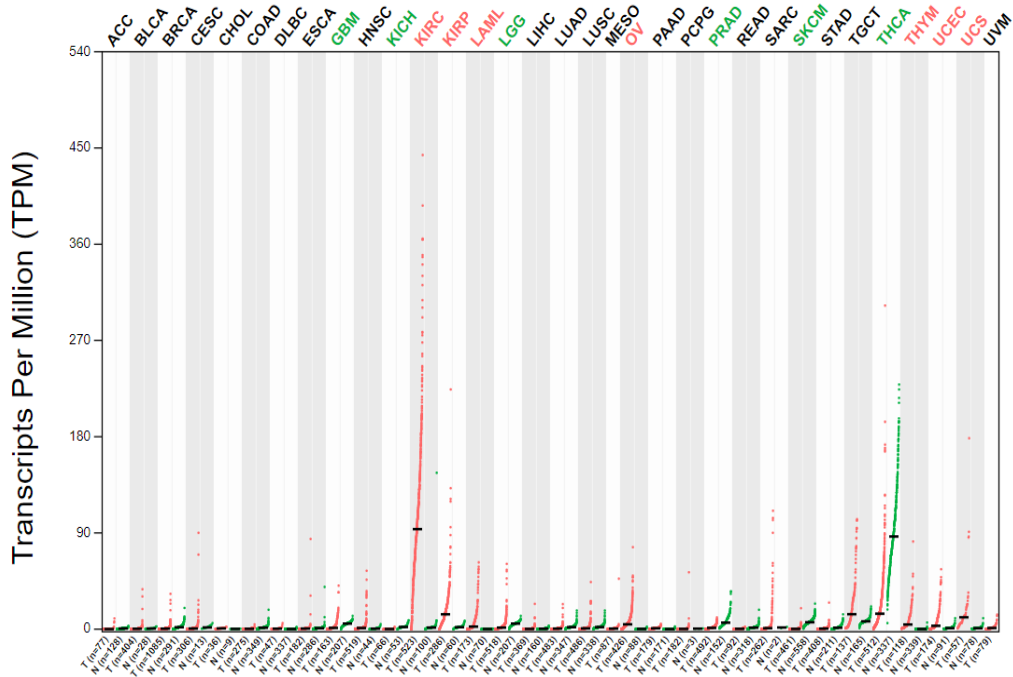


The gene expression profile across all tumor samples and paired normal tissues.(Bar plot)  
The height of bar represents the median expression of certain tumor type or normal tissue.

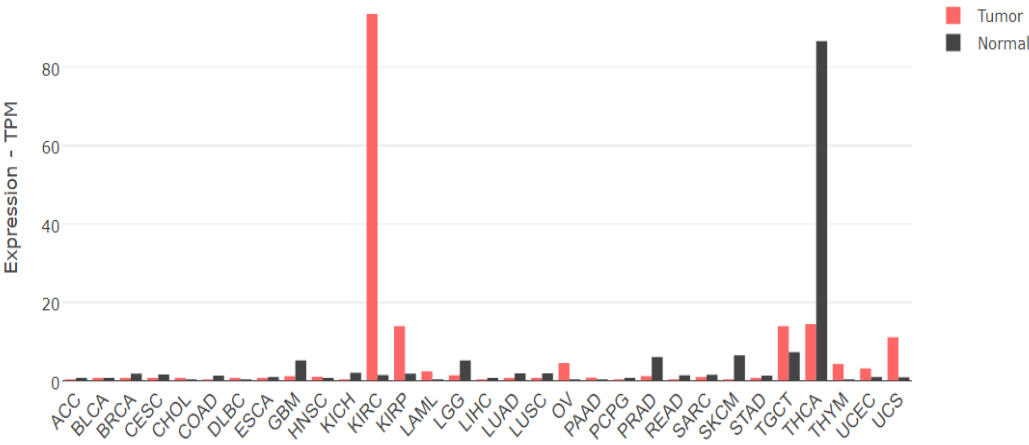


COL23A1:

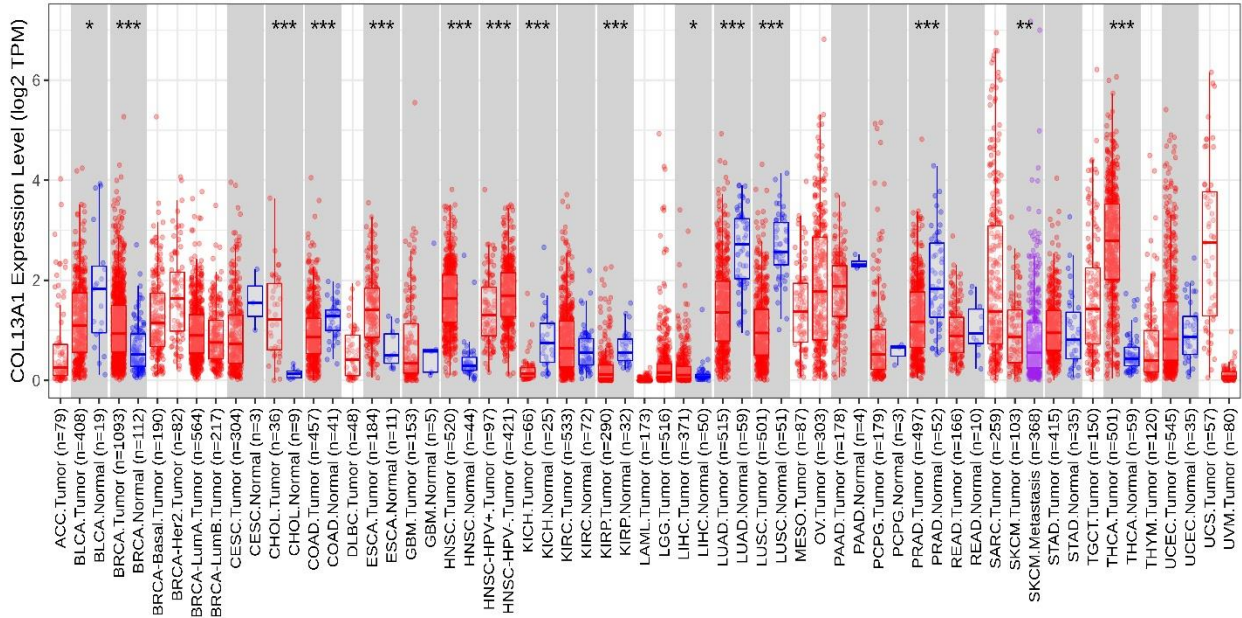
The gene expression profile across all tumor samples and paired normal tissues.(Dot plot)  
Each dots represent expression of samples.

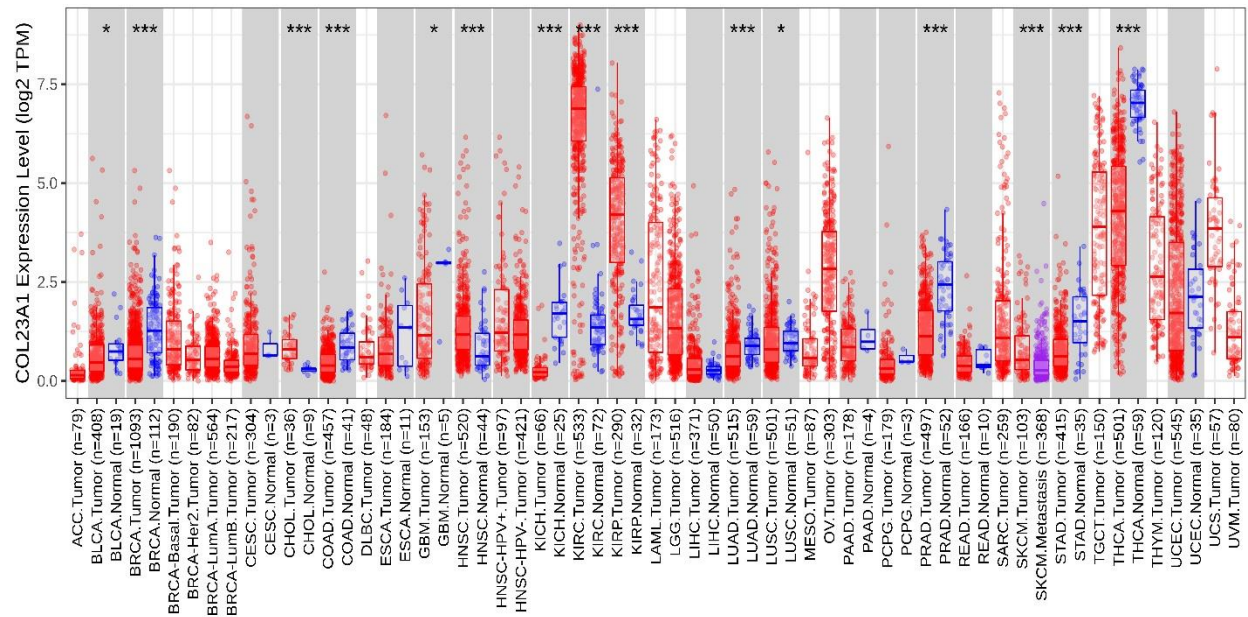


The gene expression profile across all tumor samples and paired normal tissues.(Bar plot)  
The height of bar represents the median expression of certain tumor type or normal tissue.



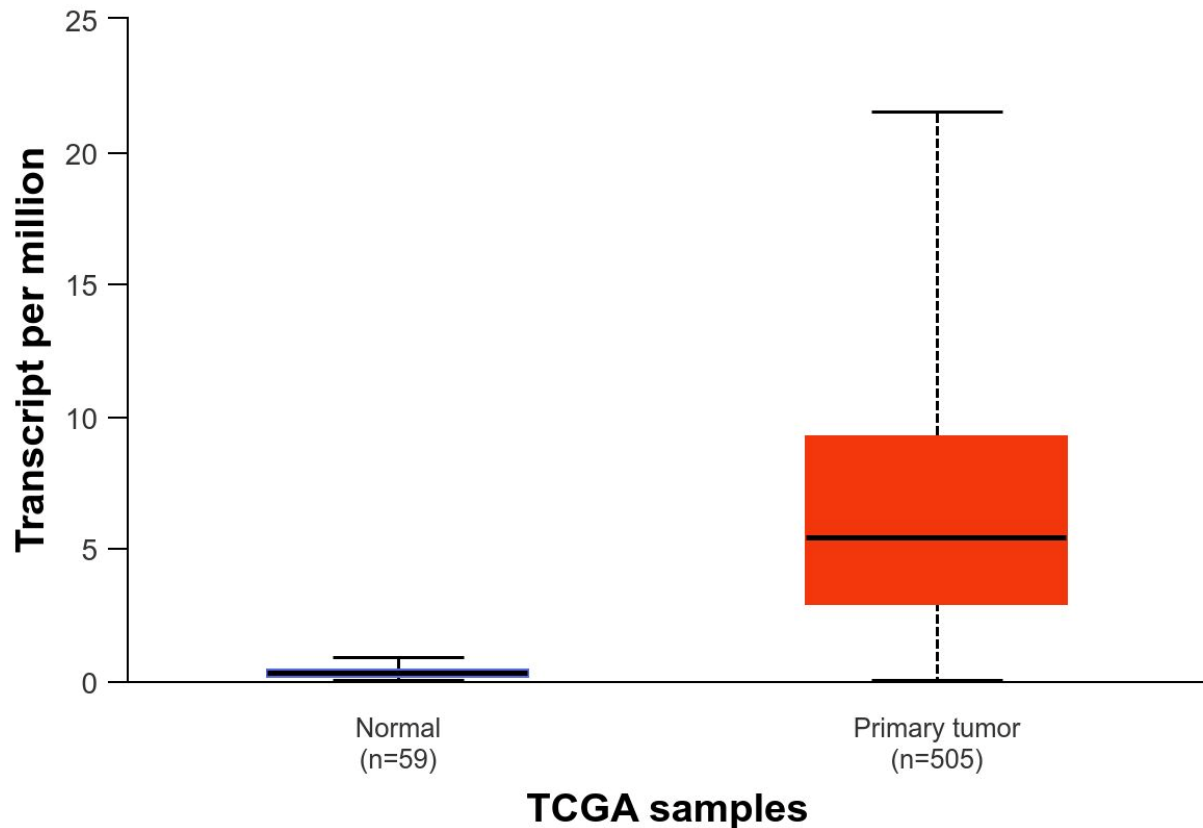
**TIMER2.0:**



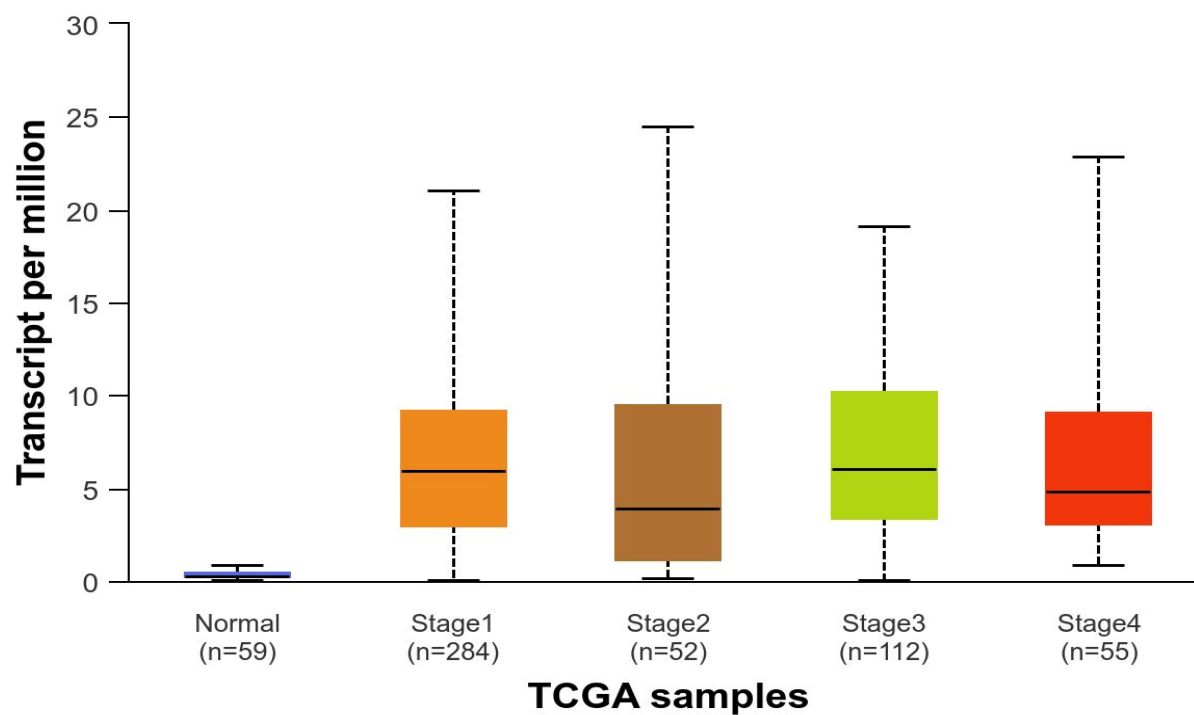


## 2.PROTEOMIC EXPRESSION ANALYSIS OF GENE(UALCAN): COL13A1 & COL23A1

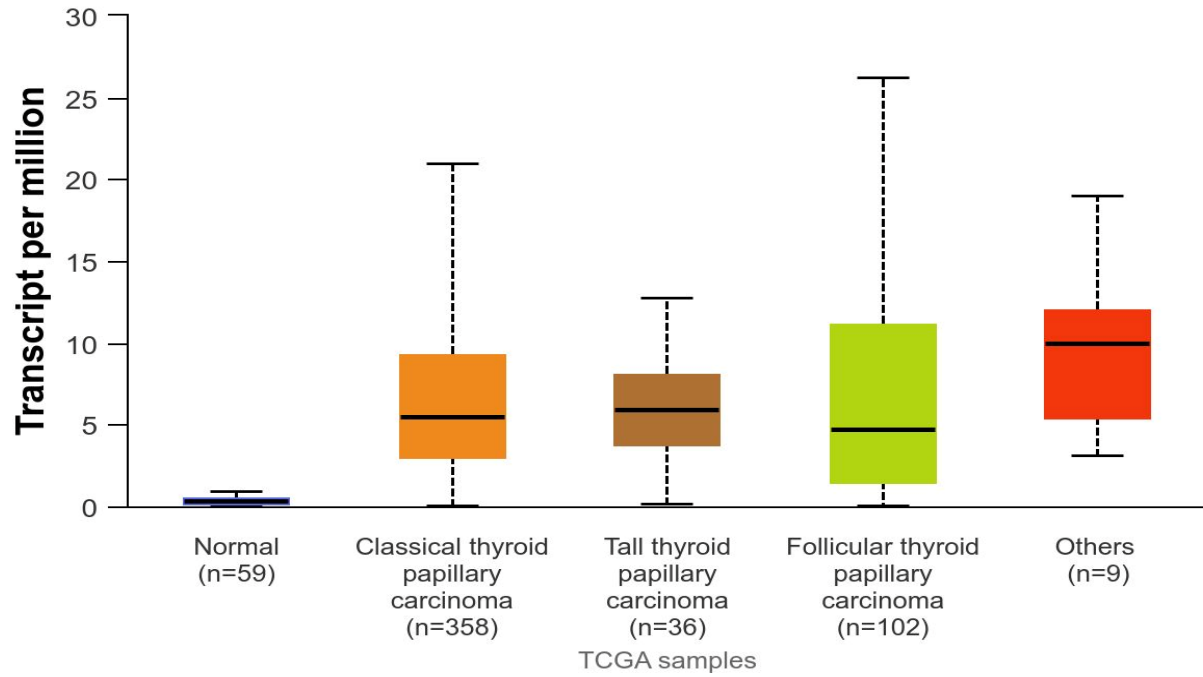
### Expression of COL13A1 in THCA based on Sample types



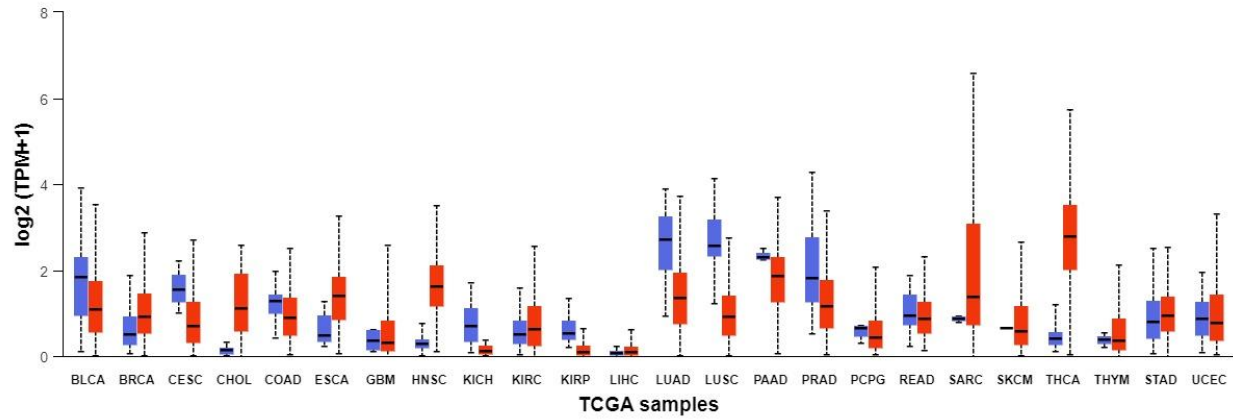
### Expression of COL13A1 in THCA based on individual cancer stages

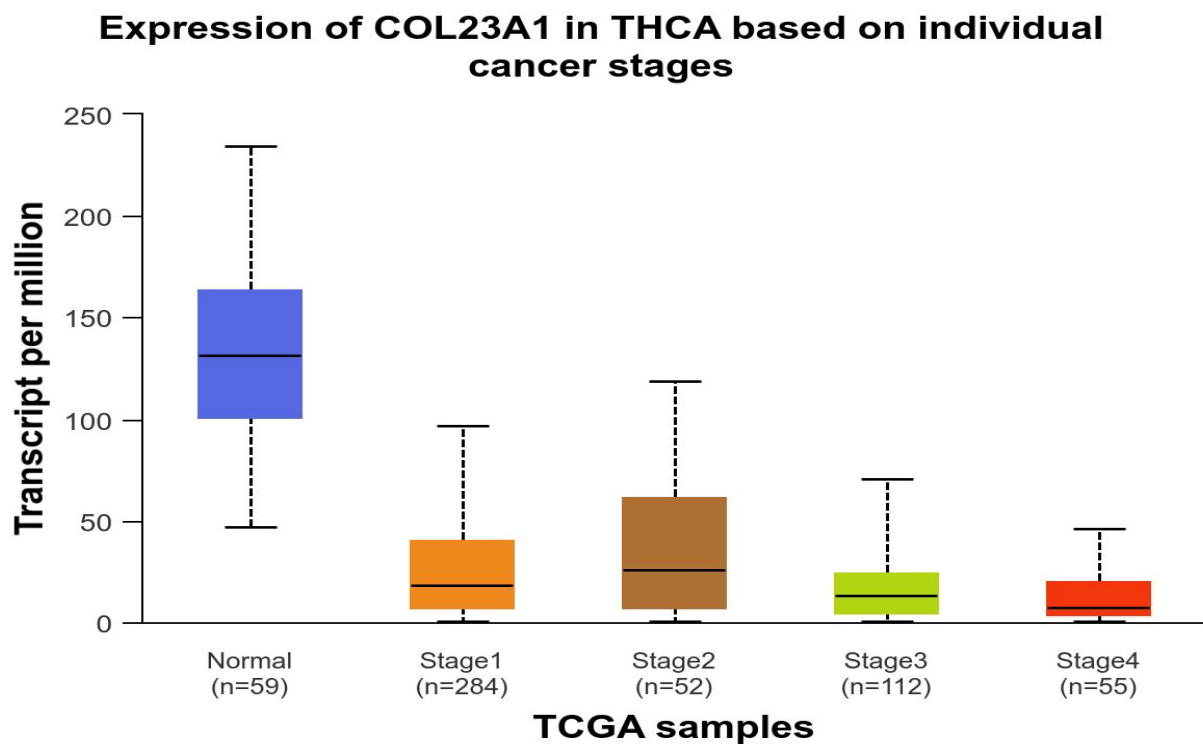
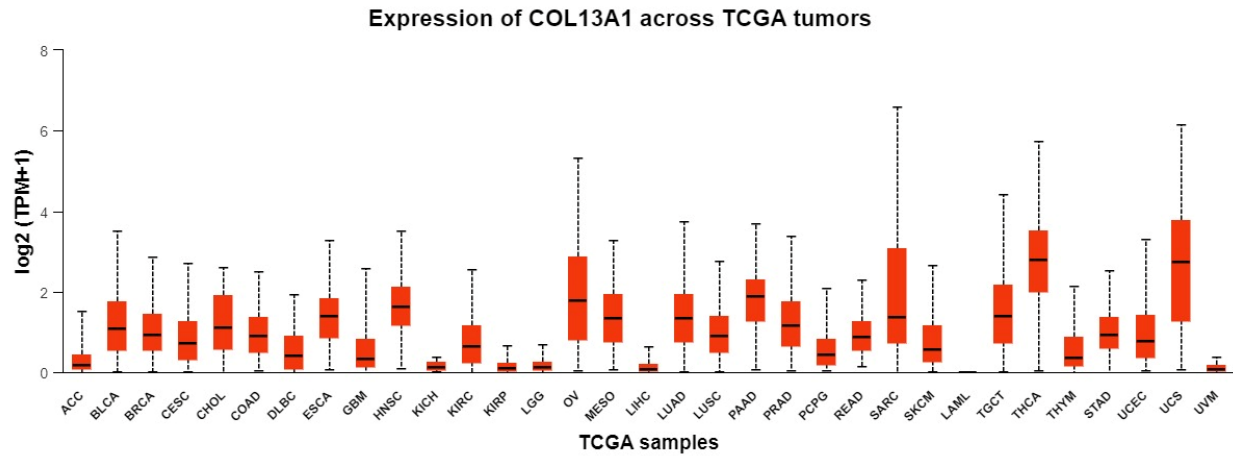


## Expression of COL13A1 in THCA based on Tumor histology

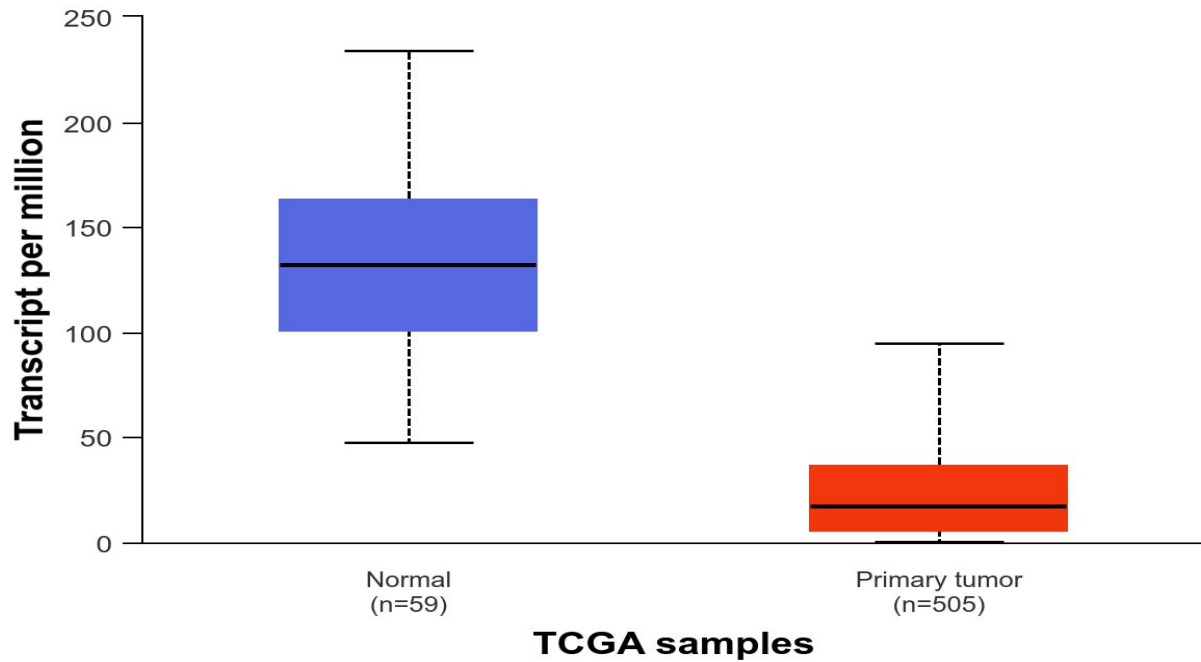


## Expression of COL13A1 across TCGA cancers (with tumor and normal samples)

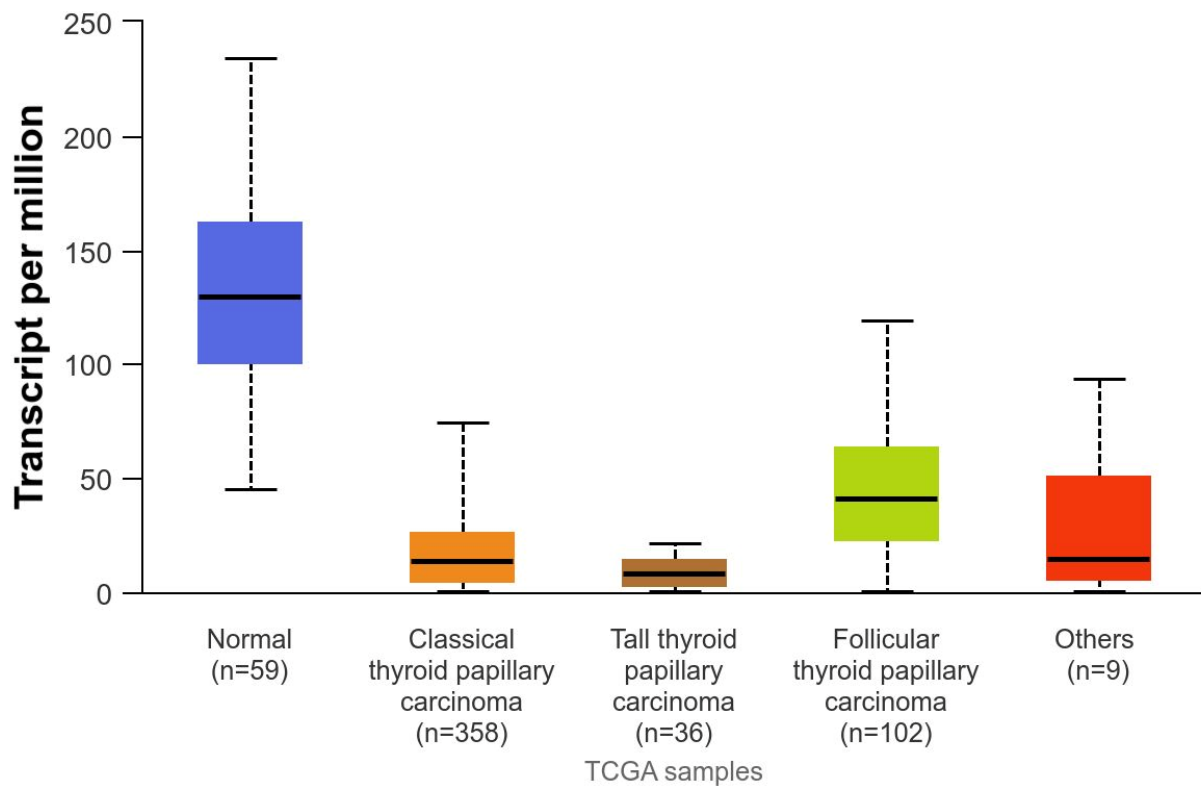




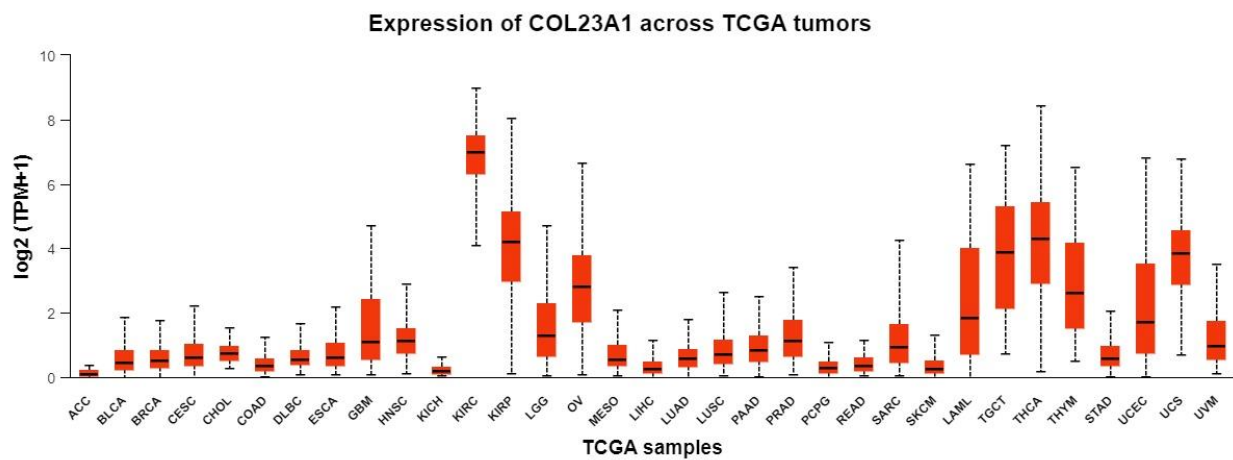
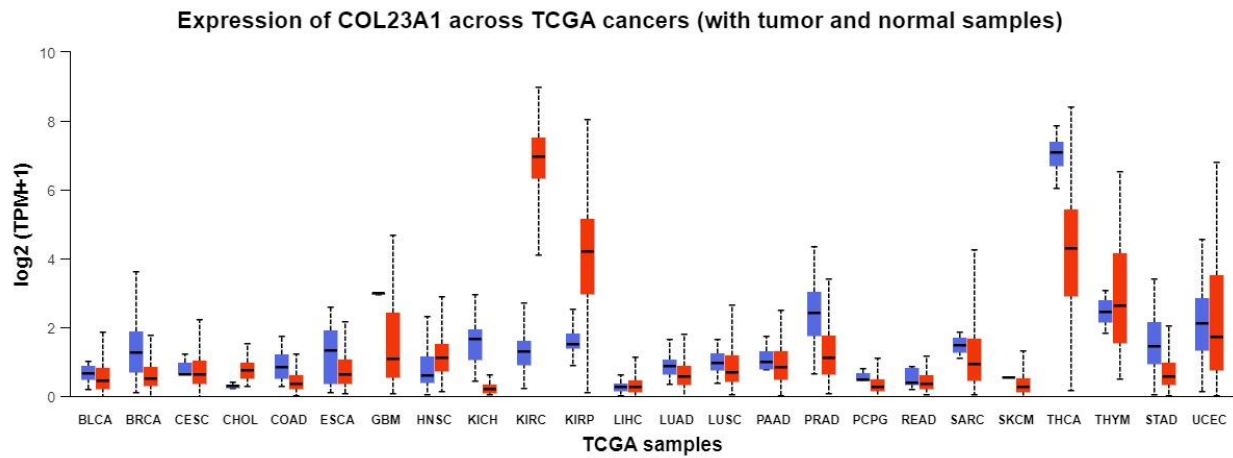
**Expression of COL23A1 in THCA based on Sample types**



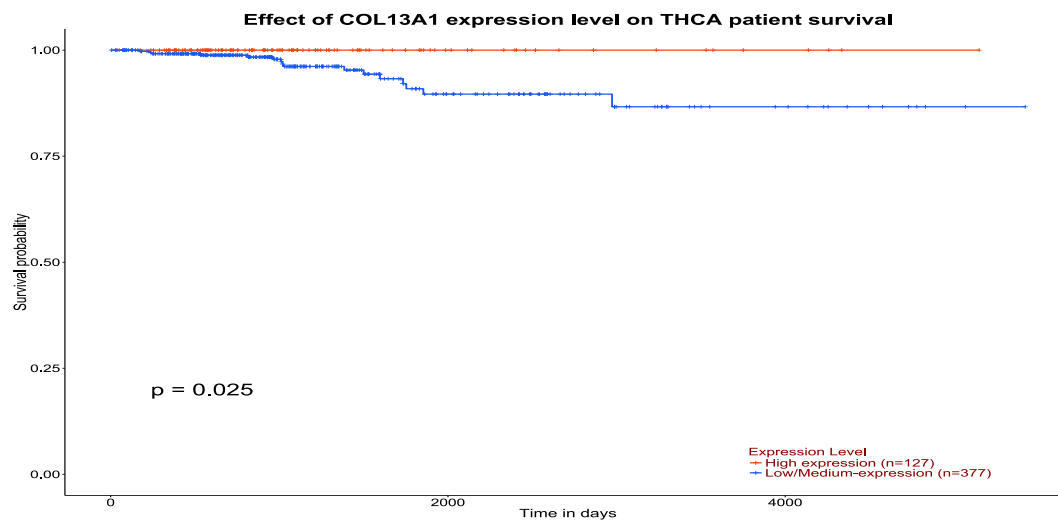
**Expression of COL23A1 in THCA based on Tumor histology**

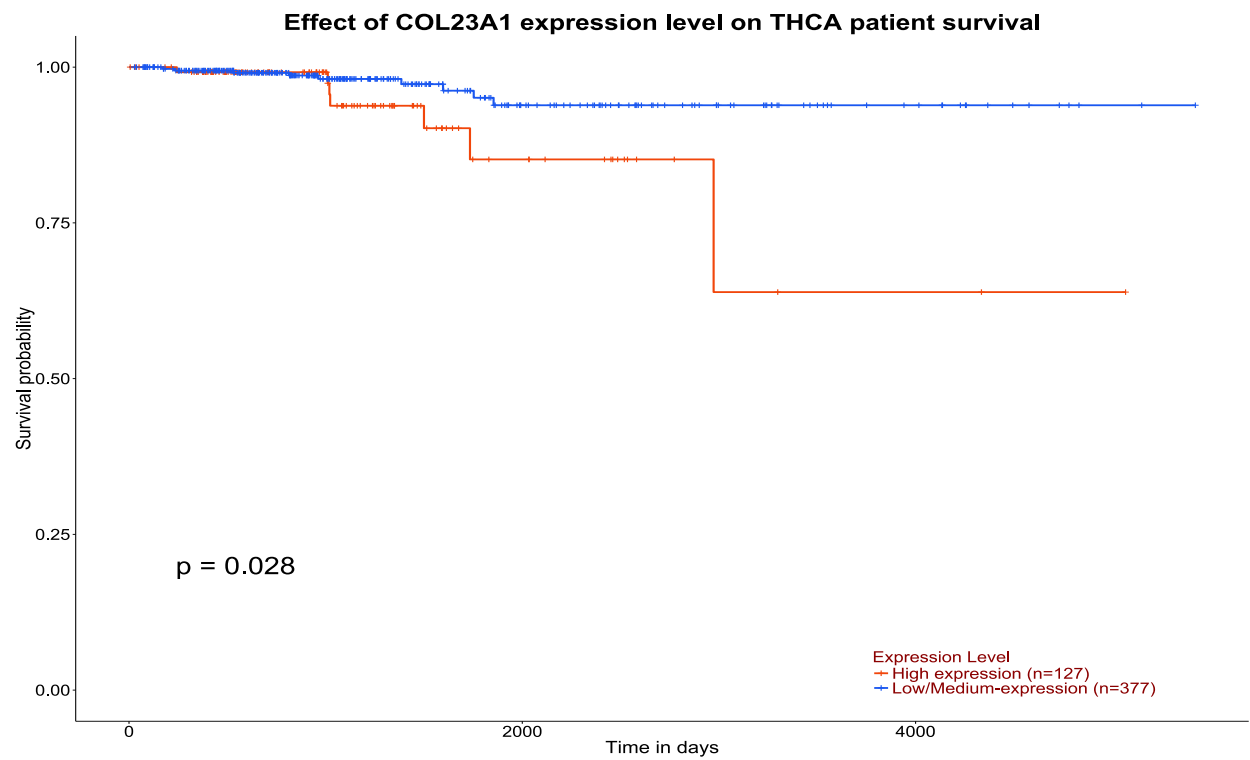
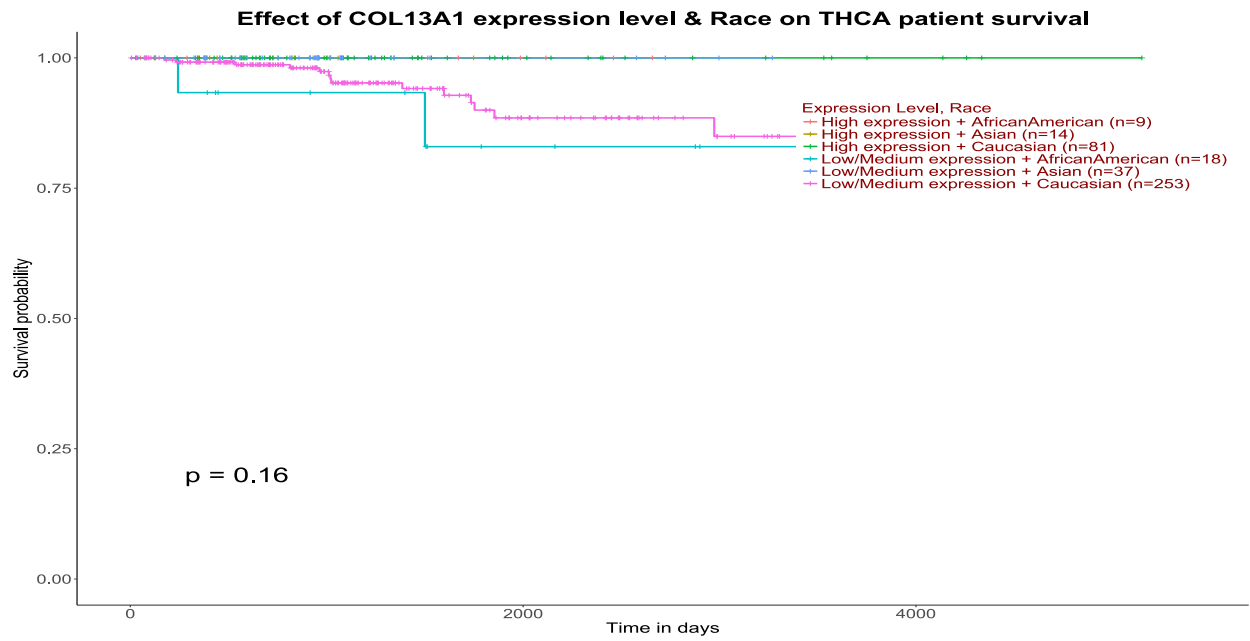


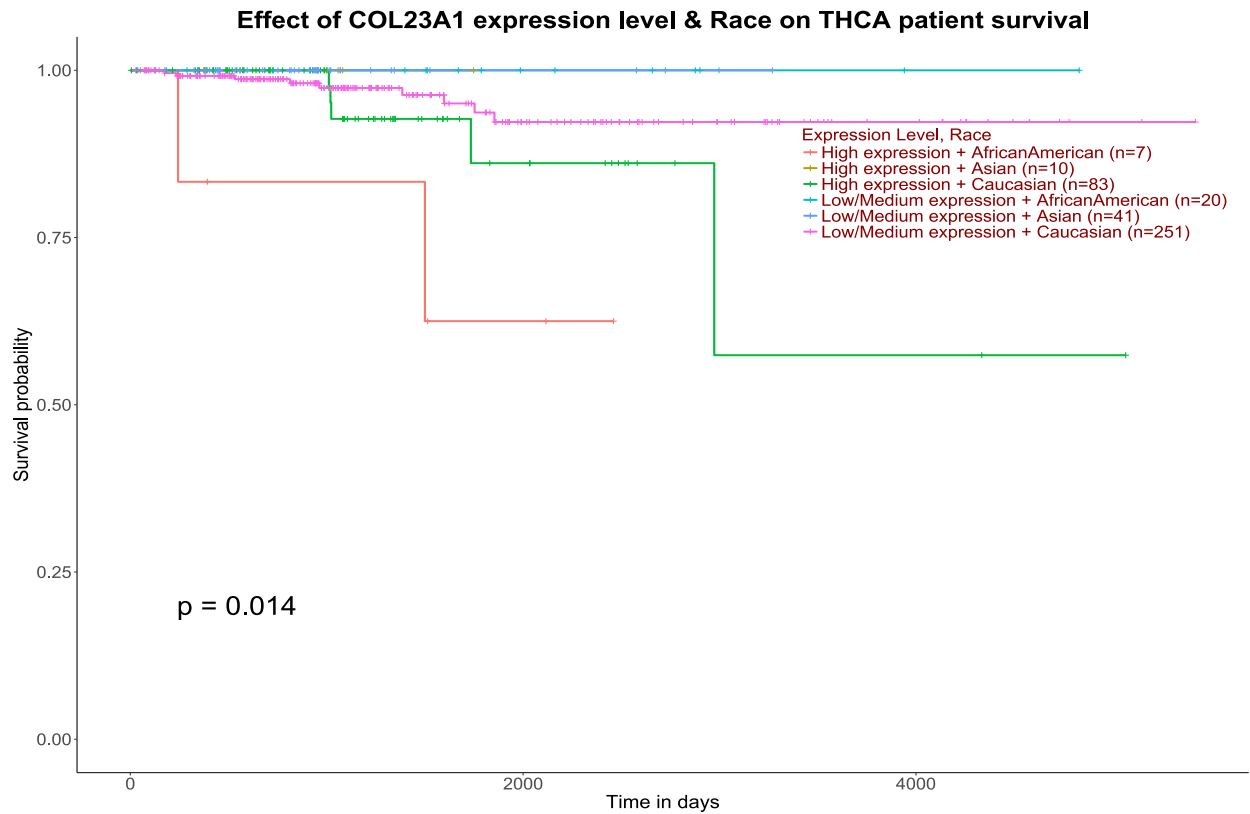




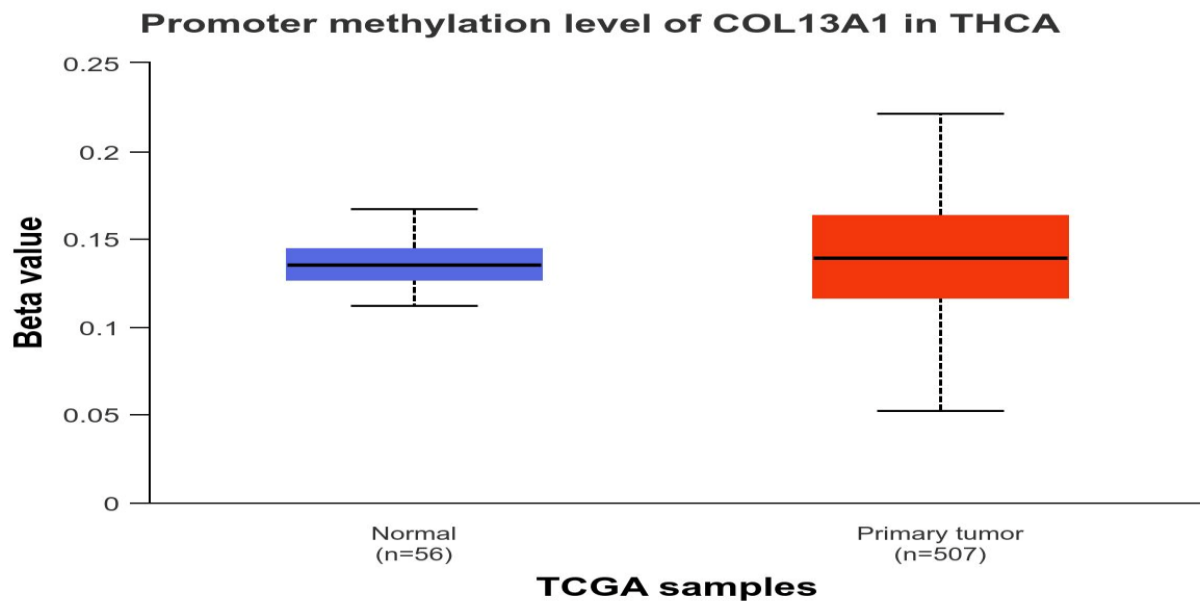
### 3.Survival Analysis :

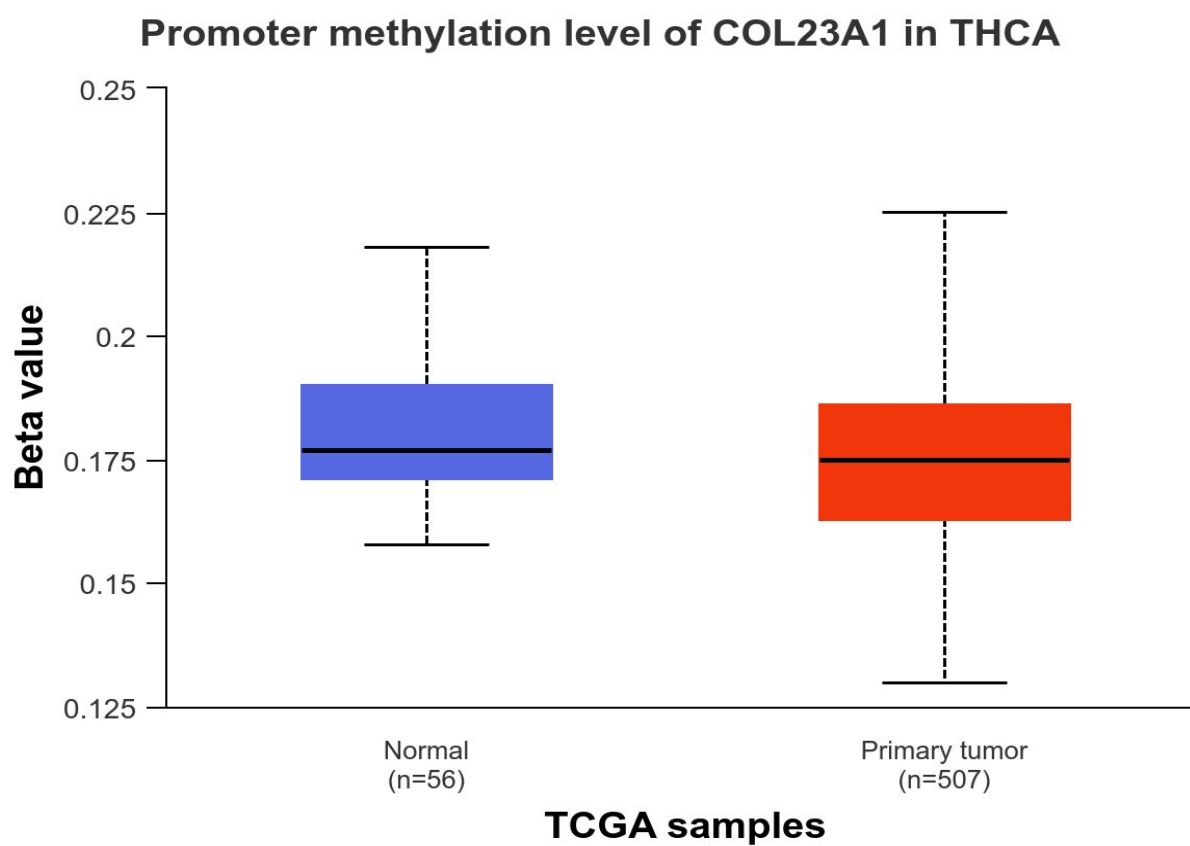
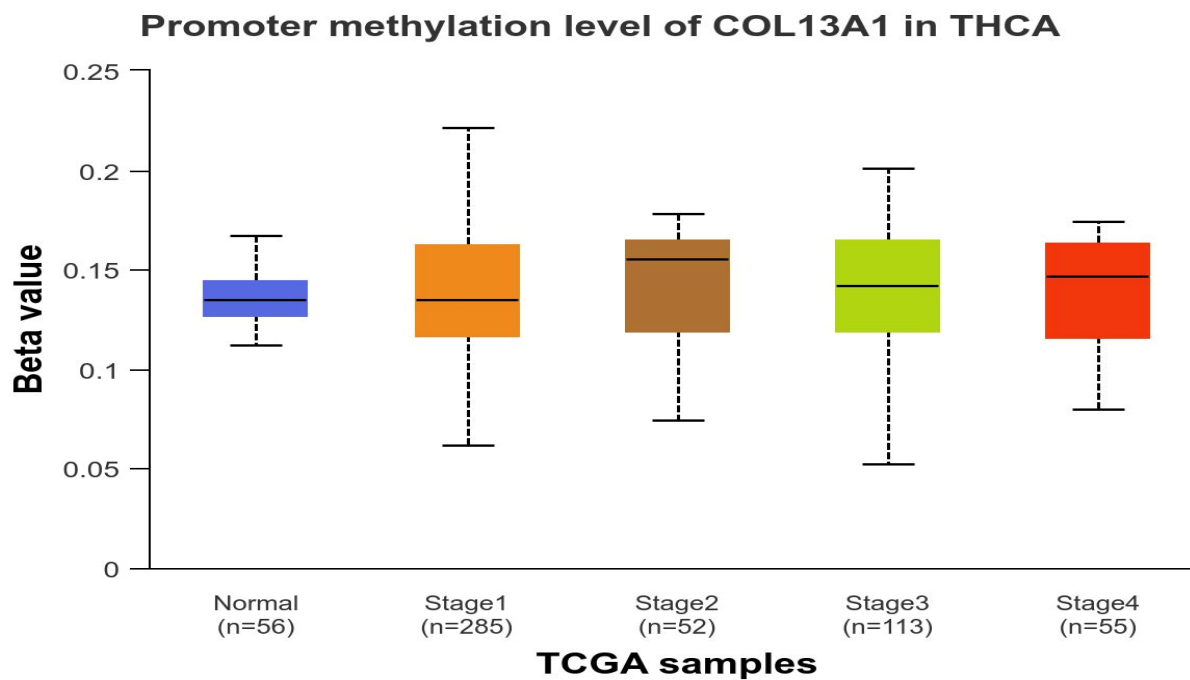


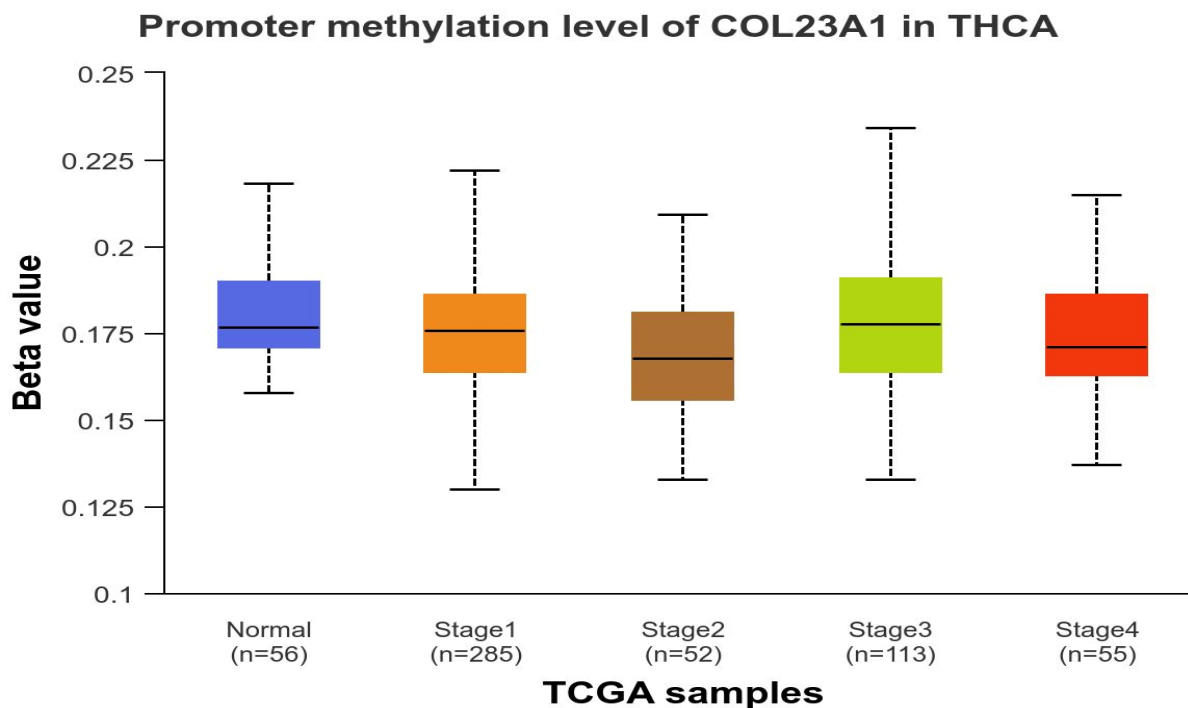




#### 4.DNA METHYLATION ANALYSIS:



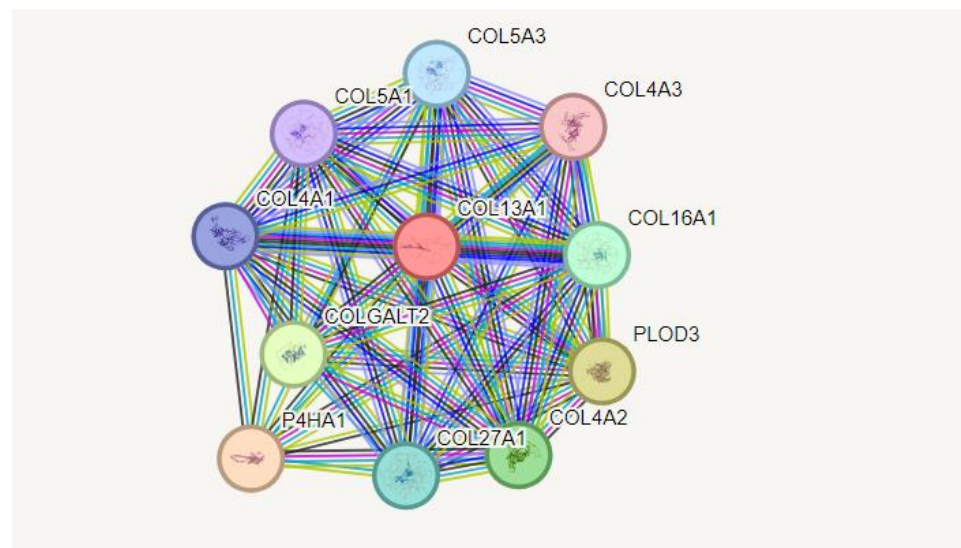




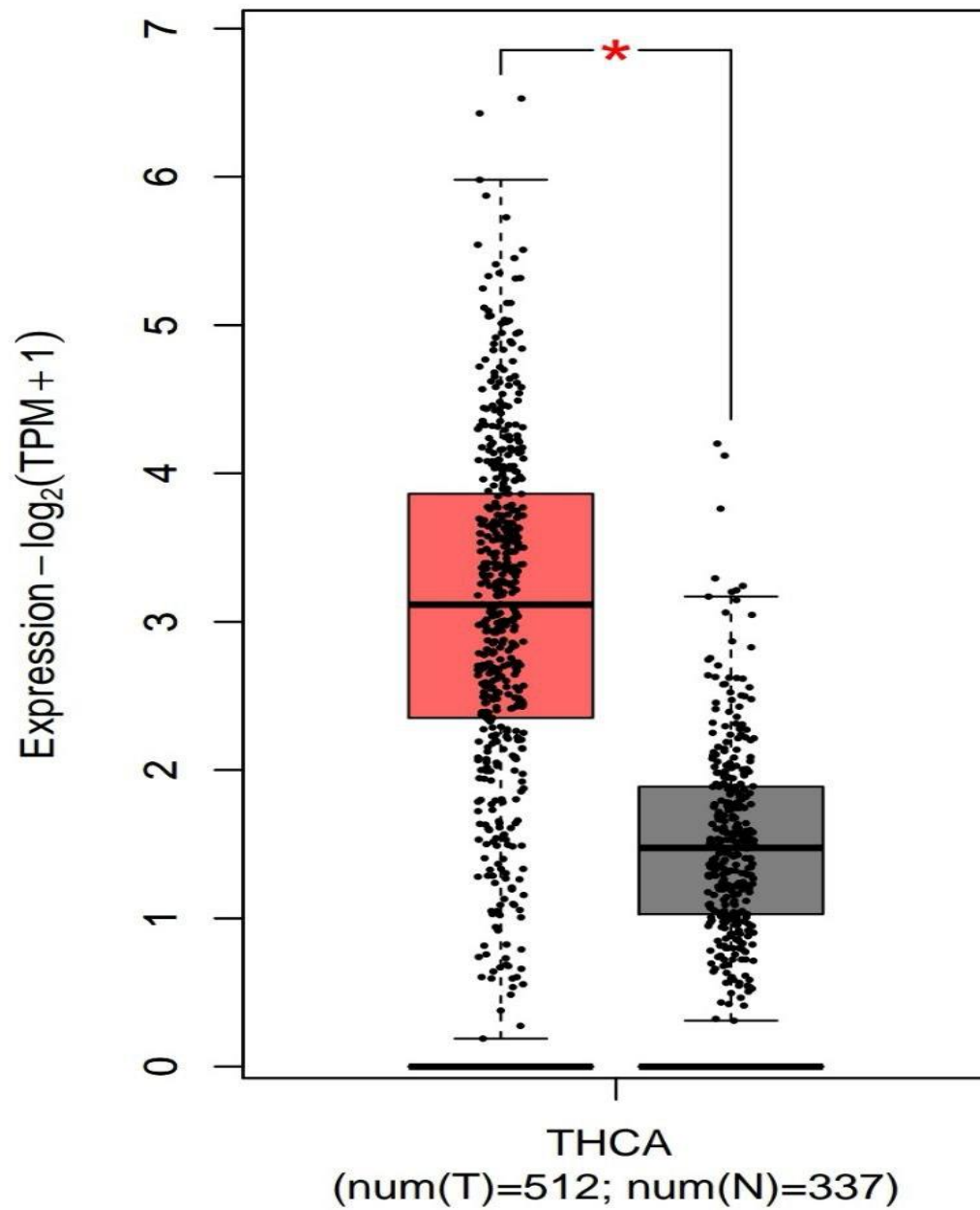
## 5.PPI :

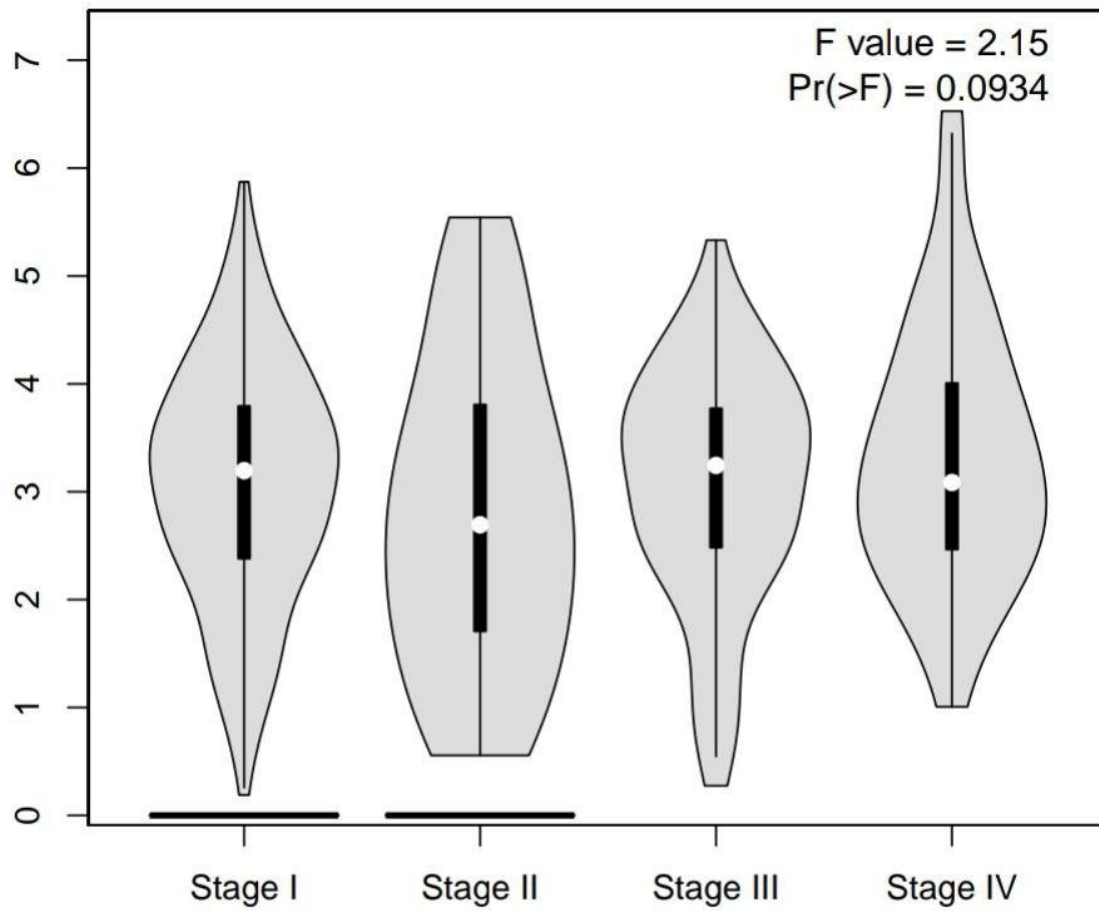
number of nodes: 11  
 number of edges: 54  
 average node degree: 9.8  
 avg. local clustering coefficient: 0.982  
 expected number of edges: 10  
 PPI enrichment p-value:  $< 1.0e-16$

expected number of edges: 10  
 PPI enrichment p-value:  $< 1.0e-16$

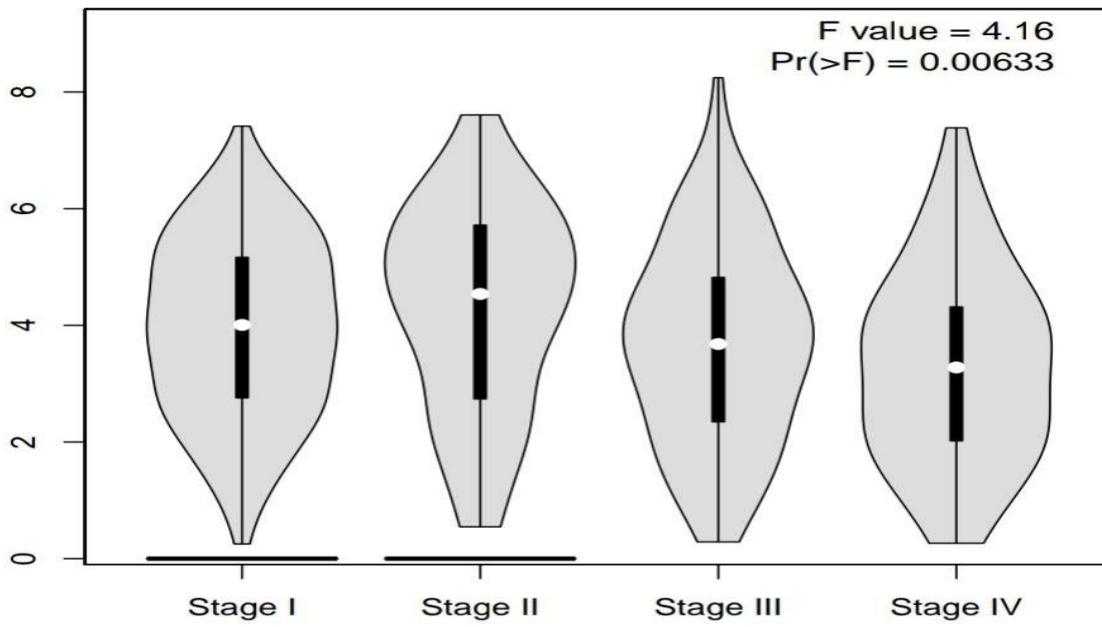
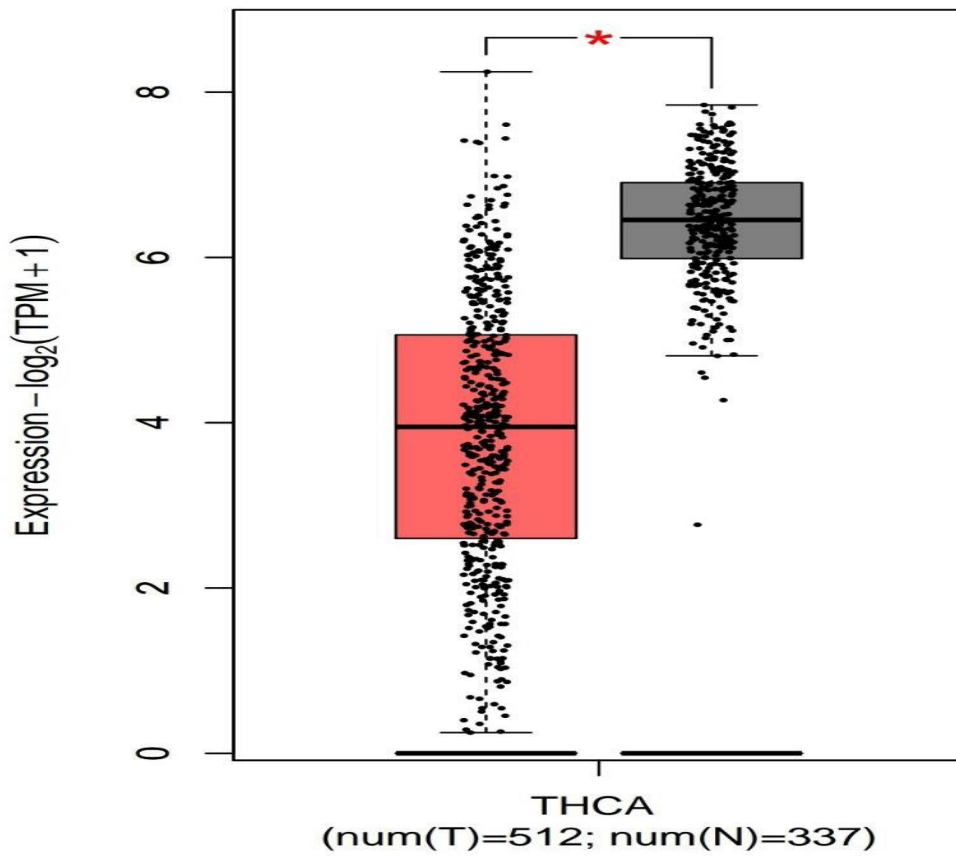


# STAGE PLOT & BOX PLOT (COL13A1):



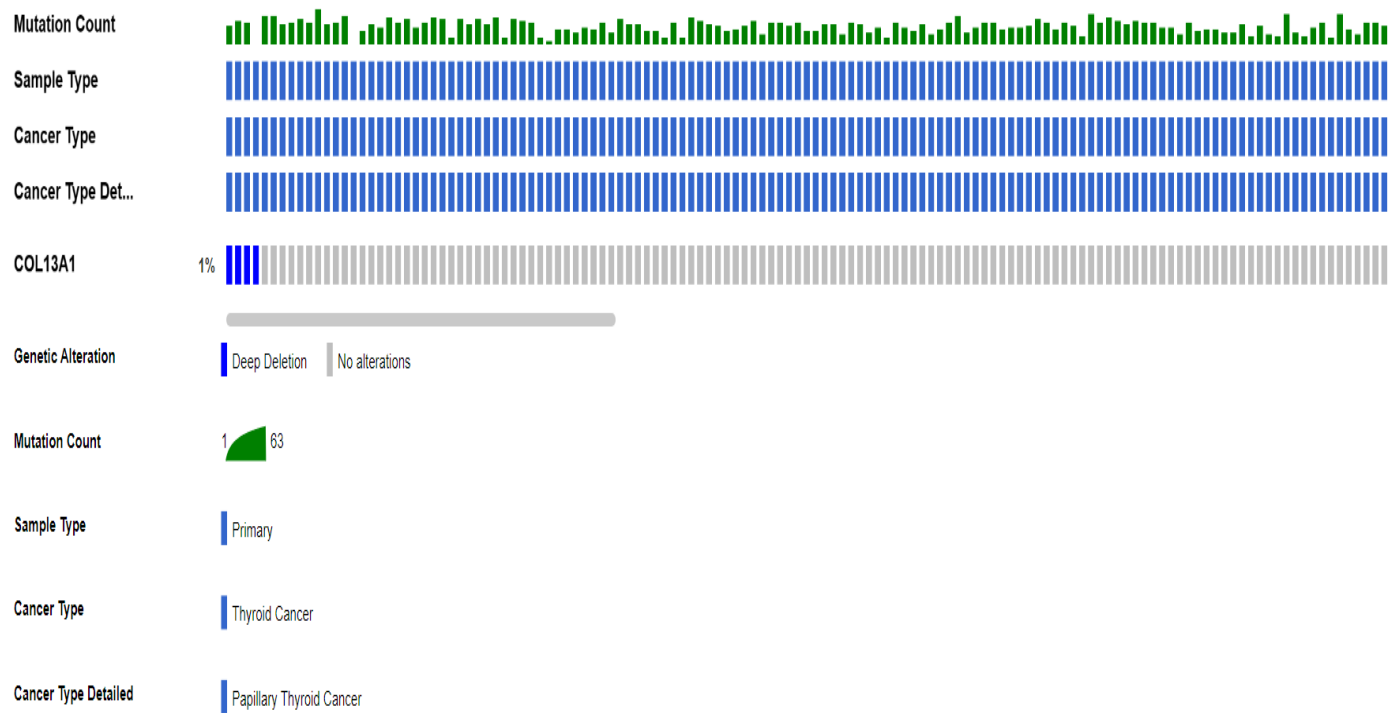


STAGE PLOT & BOX PLOT (COL23A1):

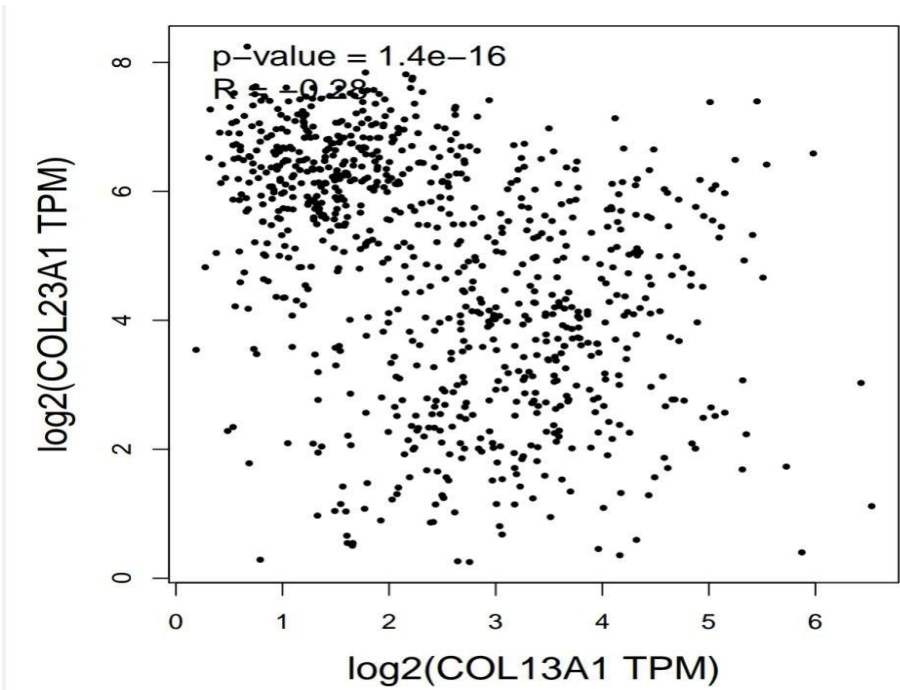




MUTATION OF GENE:



CORRELATION:



## INTERPRETATION:

The expression of the COL13A1 gene is UP regulated in Thyroid cancer, suggesting a possible tumor suppressor role of this gene. The role and regulation of COL13A1 in thyroid cancer have not been examined. In this study, we explored that tumor behaviors in thyroid carcinoma because of COL13A1. We used DNA methylation to examine the promoter methylation and expression of COL13A1 and tumor characteristics. We found methylation expression of COL13A1 of the PTC tissue samples vs 100% of the matched normal thyroid tissue samples. In contrast, an opposite distribution pattern of COL23A1 gene(Down regulation) methylation was observed; specifically, the Thyroid Cancer tissue samples vs 0% of the matched normal thyroid tissue samples of COL23A1 methylation. A correlation between COL13A1 and COL23A1 in Thyroid Cancer tissue samples was also observed. the correlation between COL13A1 and COL23A1 gene are showing a scatter. The value of  $p=1.4e-16$  and the value of  $R = -0.28$ . There is a correlation between Col13A1 and COL23A1 gene expression. This means that there is a slight tendency for these two genes to be expressed together. These data demonstrate that the COL13A1 gene is a potential tumor suppressor gene in thyroid cancer and that aberrant promoter methylation is an important mechanism for its up-regulation, which may play a role in the tumorigenesis and aggressiveness of Thyroid Cancer.

