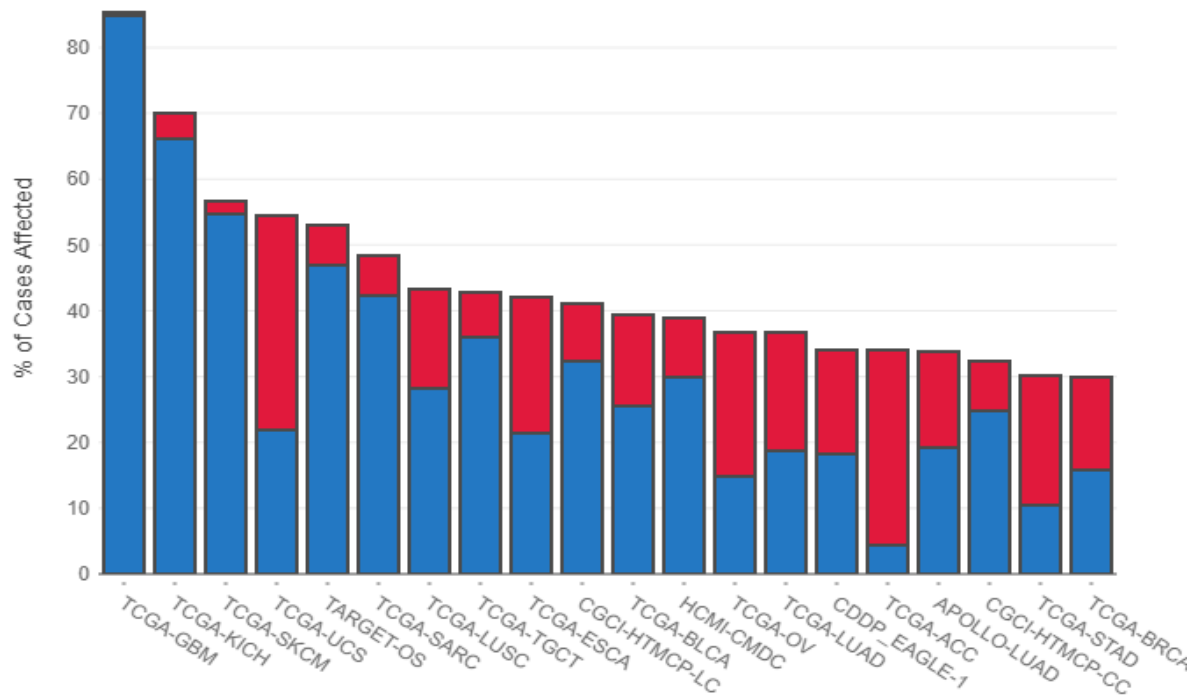# COL13A1 (Up)

Fig: Sample info from TCGA Database for tumor and normal sample
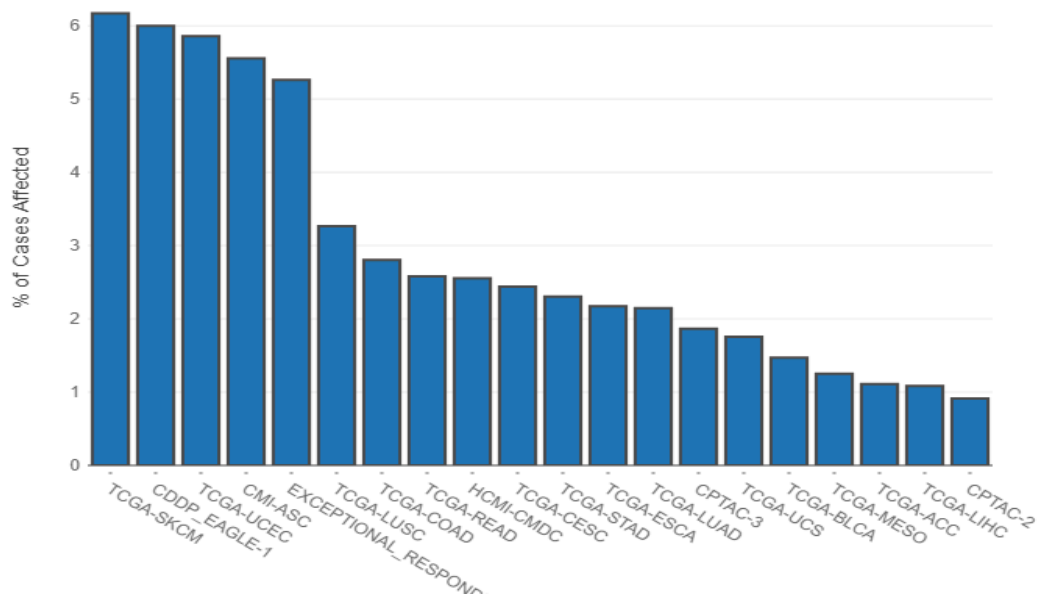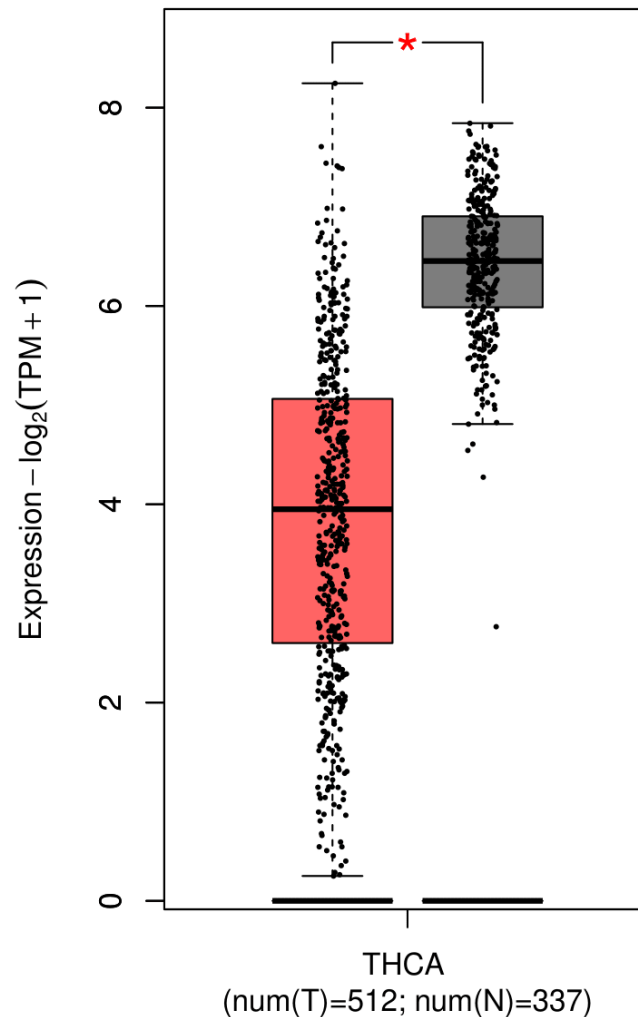

Fig: Sample info from TCGA Database for normal sample

Data exploration:

Box Plot

THCA
(num(T)=512; num(N)=337)

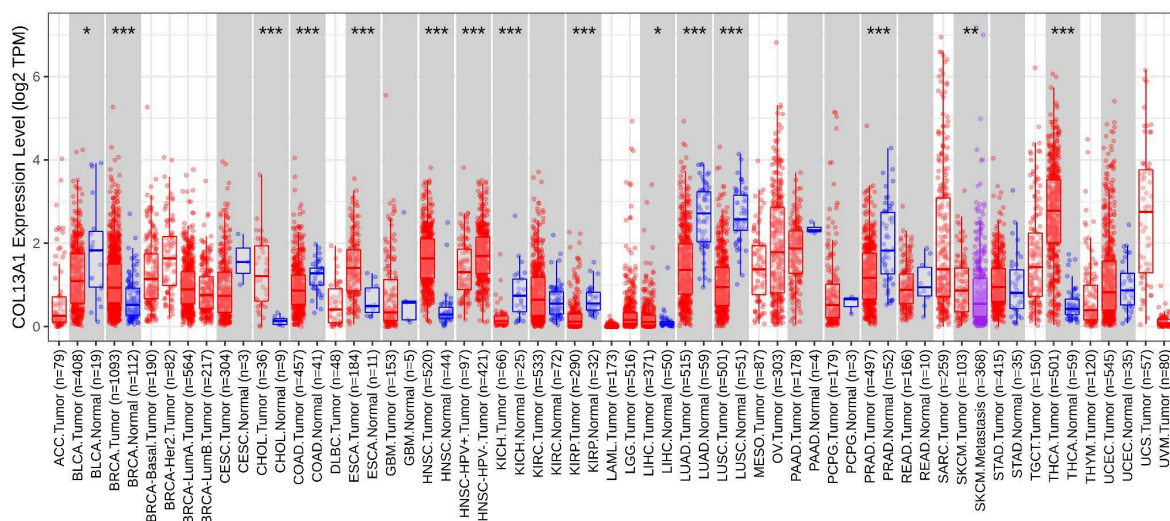The boxplot shows the expression level of THCA where the x-axis is labeled "Expression - log2(TPM+1)". Here TPM stands for Transcripts Per Million. The y-axis represents the number of samples used in normal and tumor cells. Here Red represents tumor cells and the other one is normal cells. In this plot, the IQR which is the middle part of the plot is relatively small, which suggests that the expression levels of THCA are consistent across the samples. The data suggests that THCA has low expression for COL13A1.

Stage Plot
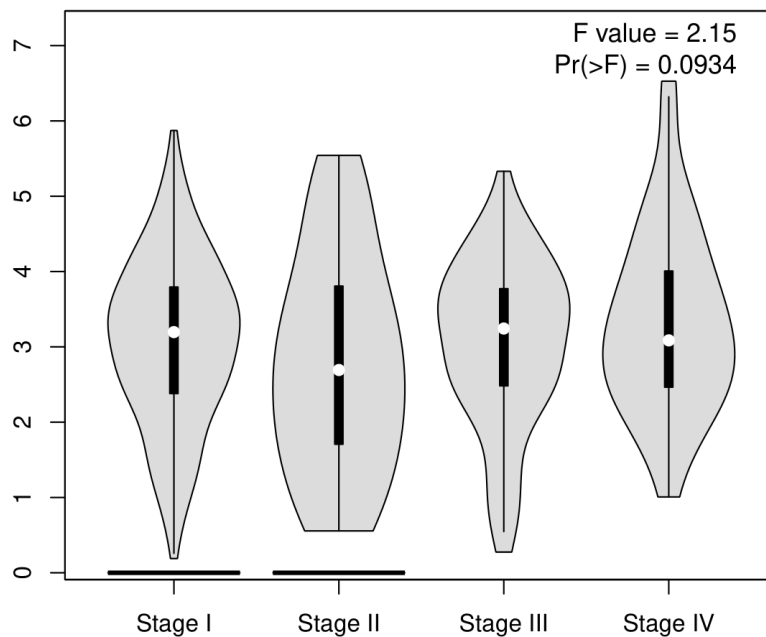
COL13A1 expression levels were compared among main pathological stages (stage I, stage II, stage III, stage IV).It also includes an F value of 2.15 and a Pr(>F) value of 0.0934. These values likely correspond to a statistical test done to compare the means between the four stages.
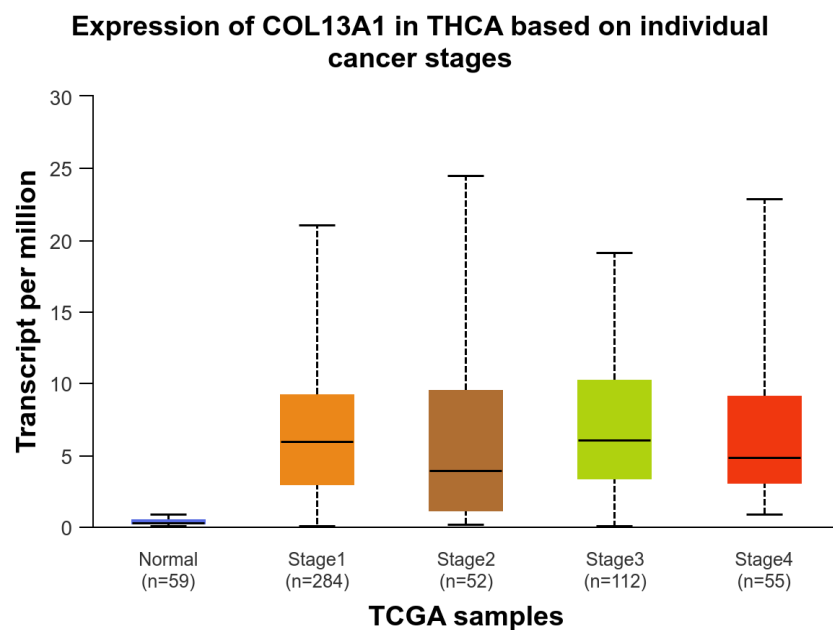
Gene Expression Analysis

The TIMER 2.0 database is used to analyze the expression level of COL13A1. Here,The expression level of COL13A1 in many cancer types is compared based on tumor and normal cells. As shown in Fig, the expression level of COL13A1 is significantly higher in tumors than in the corresponding normal tissues. The sample number of THCA tumor tissue is (n=501) and normal tissue is (n=59).
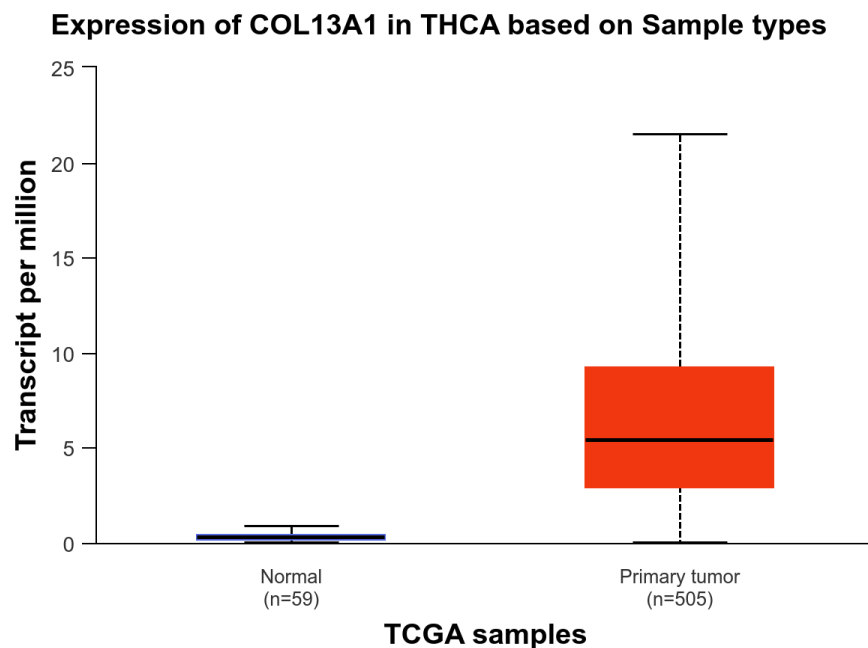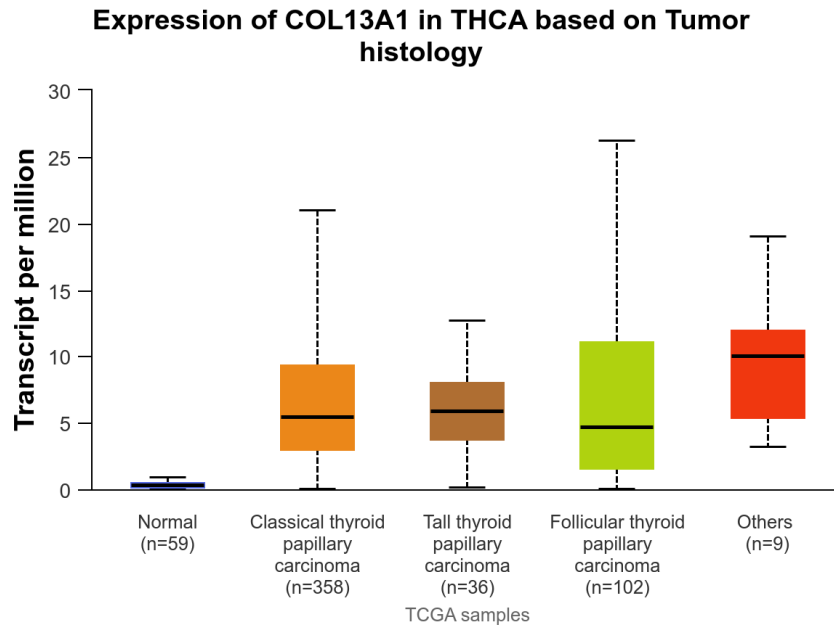
Immune Infiltration Analysis

Above shown plot is a Immune Infiltration Analysis heatmap where many cancer types are compared between these immune cell types T cell CD4+, T cell CD8+, B cell, Macrophage, Nutrophill. The sample number of THCA (Thyroid carcinoma) is (n=505). Here red represents higher expression and blue represents lower expression level.

Expression Analysis

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**

The 1st plot shows the expression levels of gene COL13A1 in tumor and normal samples from patients with thyroid carcinoma where normal cells have lower gene expression compared to primary tumor cells.

The 2nd plot shows the comparison between normal cells and different cancer stages where stage 2 has the higher expression and stage 3 has the lower expression.

The 3rd plot depicts the comparison Between normal cells and different types of thyroid carcinoma. Where Follicular thyroid papillary carcinoma shows the higher expression and Tall thyroid papillary carcinoma shows the lower expression.
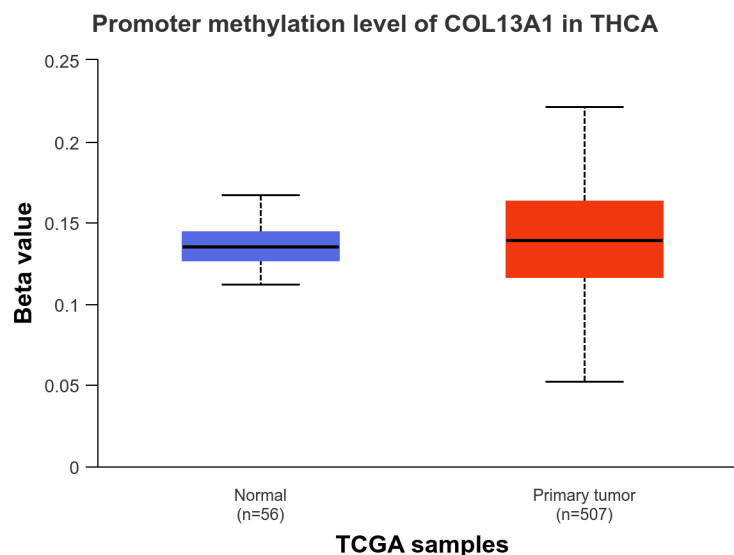
Survival Analysis
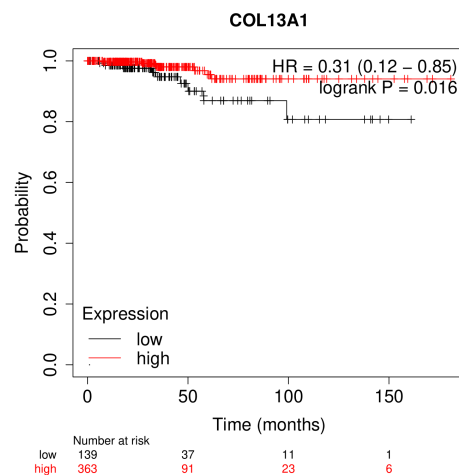
According to the expression levels of COL13A1 we divided the cancer cases into high-expression and lower-expression groups. Patients with high COL13A1 expression appear to have a better chance of survival over time compared to those with low COL13A1 expression.
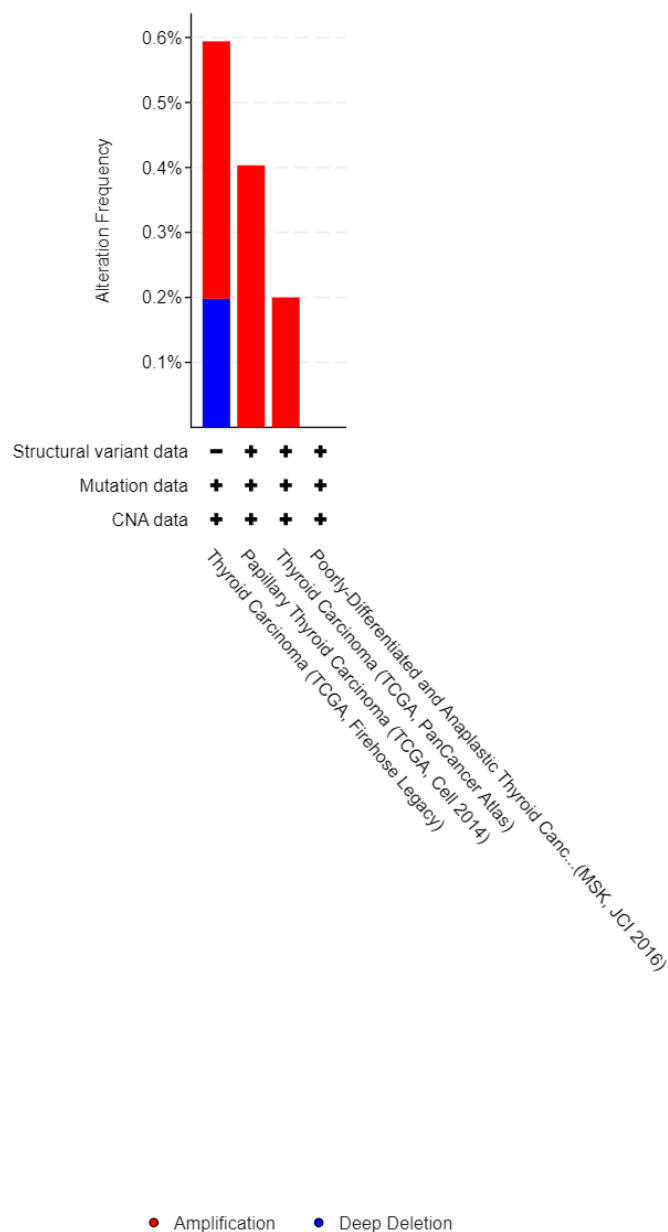
Pan Cancer View

Expression of COL13A1 across TCGA cancers (with tumor and normal samples)
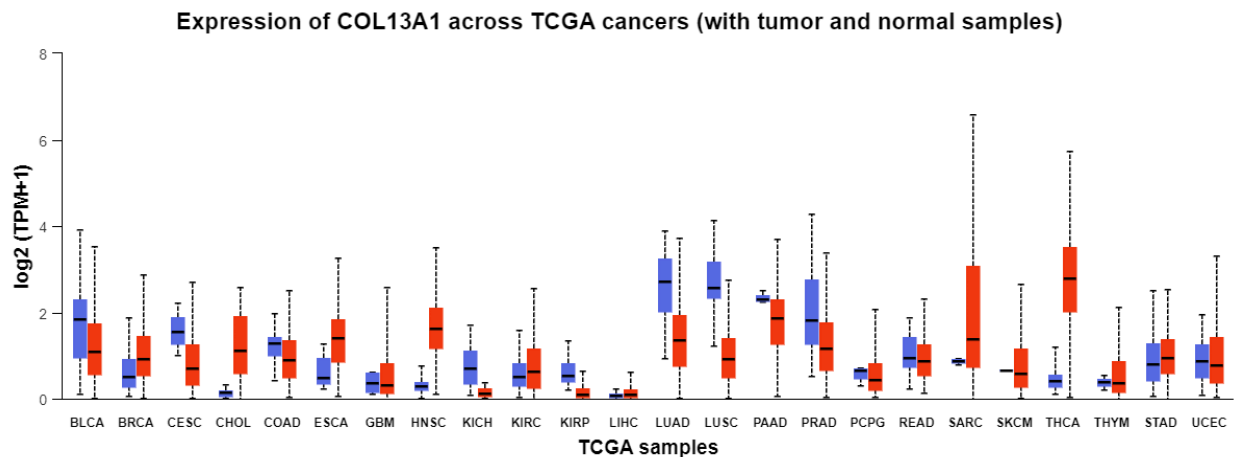
COL13A1 expression is generally higher in tumor samples compared to normal samples across most cancer types.

DNA Methylation Analysis

Promoter methylation level of COL13A1 in THCA

The graph shows the promoter methylation analysis level between normal and primary tumor cells. Where x-axis shows the number of TCGA samples and y-axis shows the Beta value where Primary tumor cells have higher Beta value and normal cells have lower Beta value.
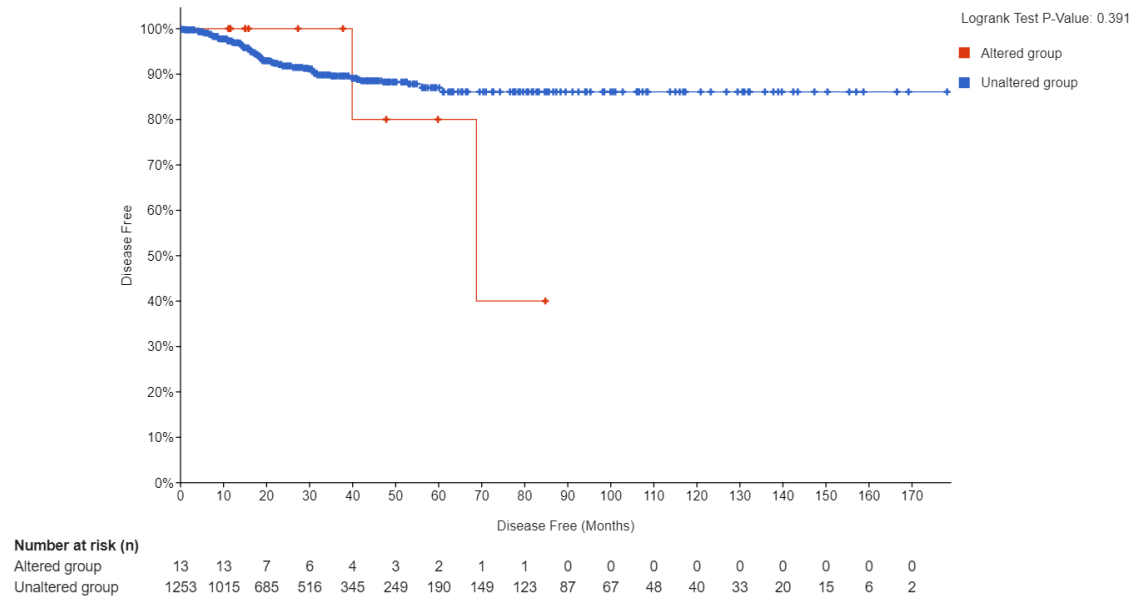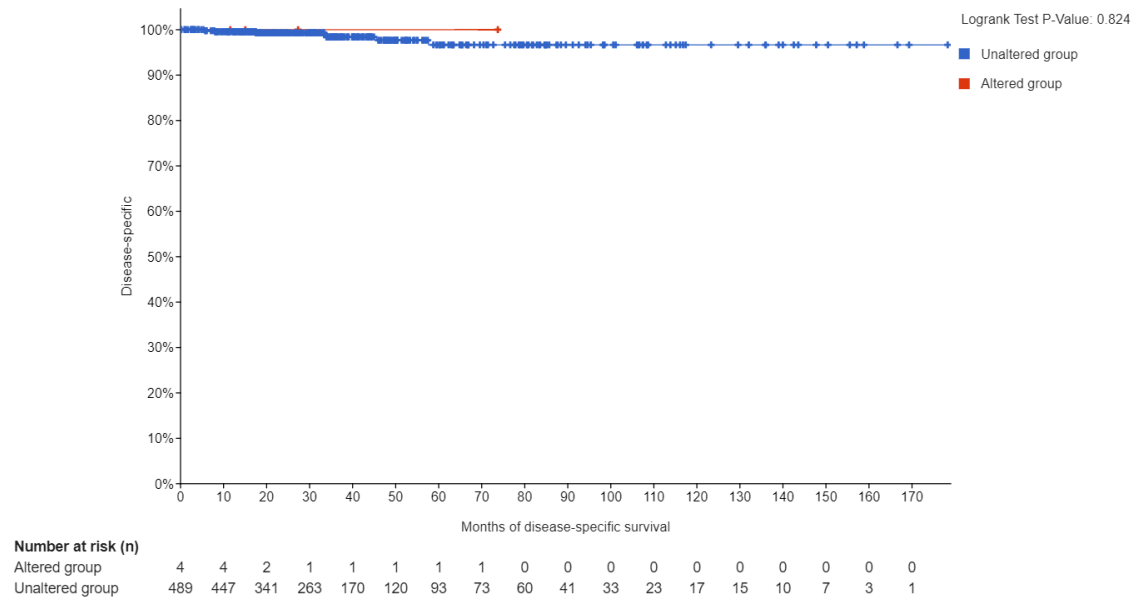
Gene Alteration Analysis

Here the y- axis shows the alteration frequency and the x- axis shows the structural variant data, mutation data, CNA data across different types of THCA samples from the cBioportal website. The red part shows the amplification and the blue part shows deep deletion.

Mutation

The gene COL13A1 belongs to the collagen family. No mutation is observed.

Survival Stage

Logrank Test P-Value: 0.824

■ Unaltered group
■ Altered group

Number at risk (n)

Altered group	4	4	2	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
Unaltered group	489	447	341	263	170	120	93	73	60	41	33	23	17	15	10	7	3	1

Logrank Test P-Value: 0.391

■ Altered group
■ Unaltered group

Number at risk (n)

|																		
Altered group	13	13	7	6	4	3	2	1	1	0	0	0	0	0	0	0	0	0
Unaltered group	1253	1015	685	516	345	249	190	149	123	87	67	48	40	33	20	15	6	2

Four stages; Progress free survival, Disease free survival, Months of disease-specific survival, Overall survival are shown. Red color depicts the altered group and blue depicts the unaltered group.

The probability of survival is generally higher for the unaltered group compared to the altered group.

PPI Analysis
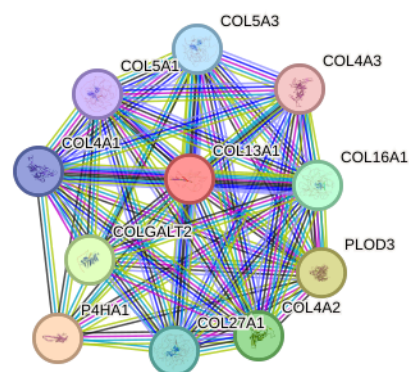
Here the protein protein interaction structure has been shown for COL13A1 where the other collagen family members' genes are connected with each other.
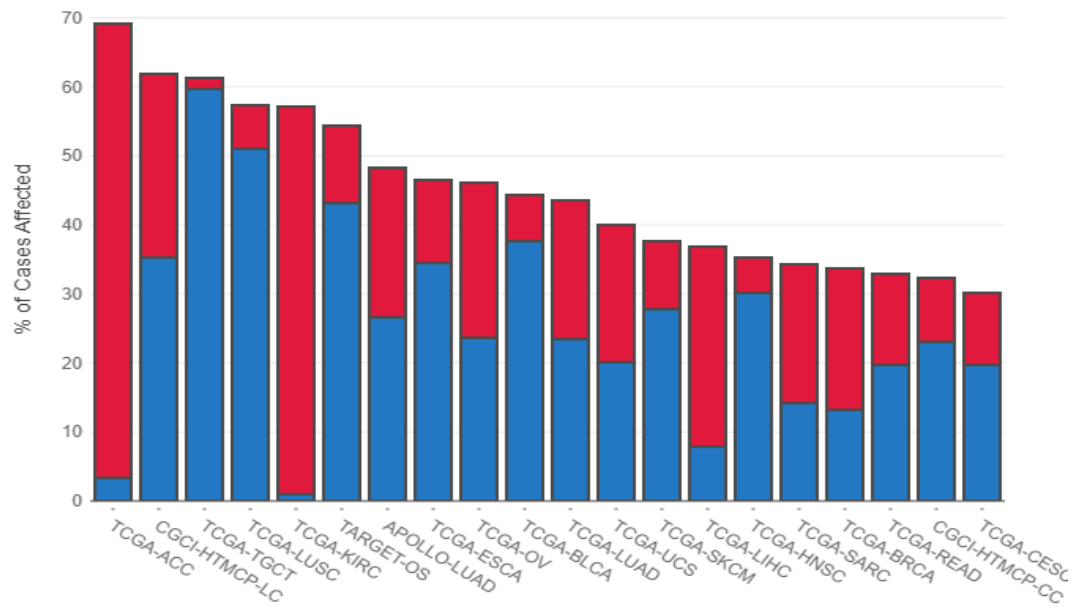
COL23A1 (Down)

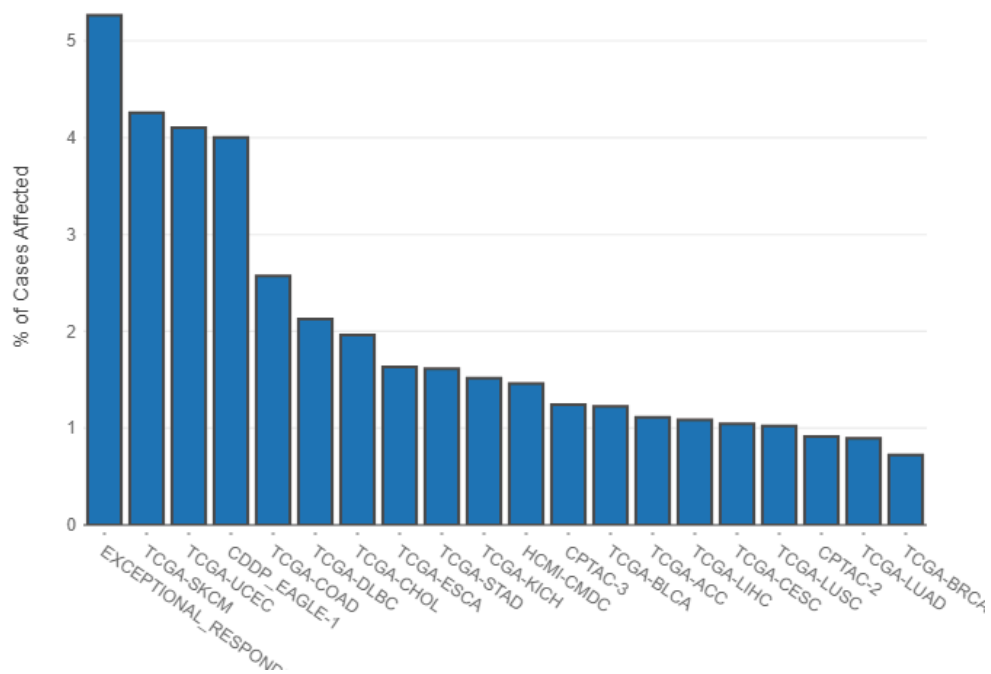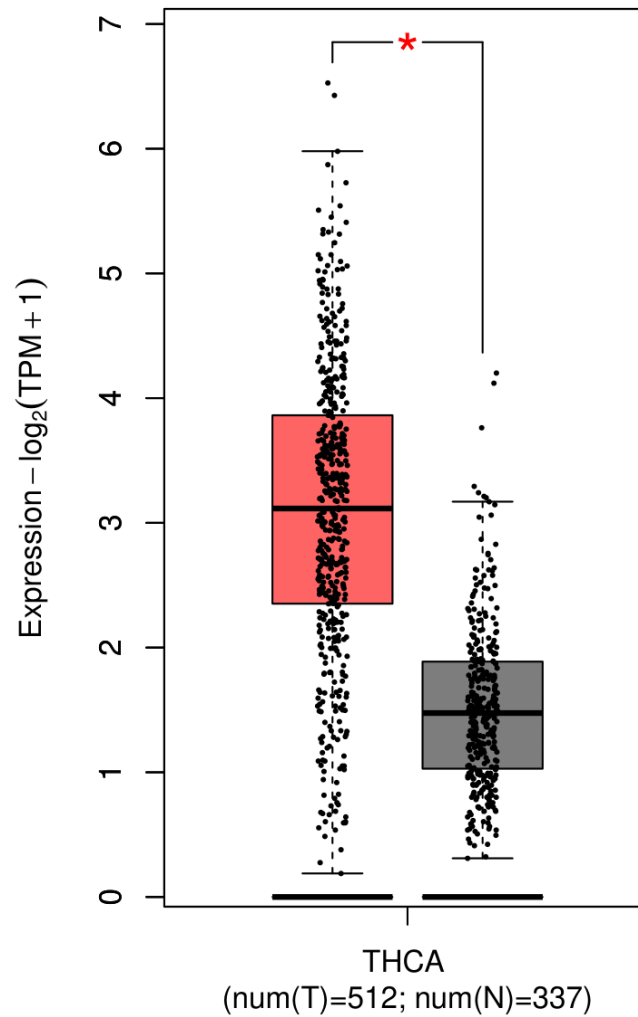Fig: Sample info from TCGA Database for tumor and normal sample

Fig: Sample info from TCGA Database for normal sample

Data exploration:

Box Plot

The boxplot shows the expression level of THCA where the x-axis is labeled "Expression - log2(TPM+1)". Here TPM stands for Transcripts Per Million. The y-axis represents the number of samples used in normal and tumor cells. Here Red represents tumor cells and the other one is normal cells. In this plot, the IQR which is the middle part of the plot is relatively high, which suggests that the expression levels of THCA are getting high across the samples. The data suggests that THCA has high expression for COL23A1.

Stage Plot
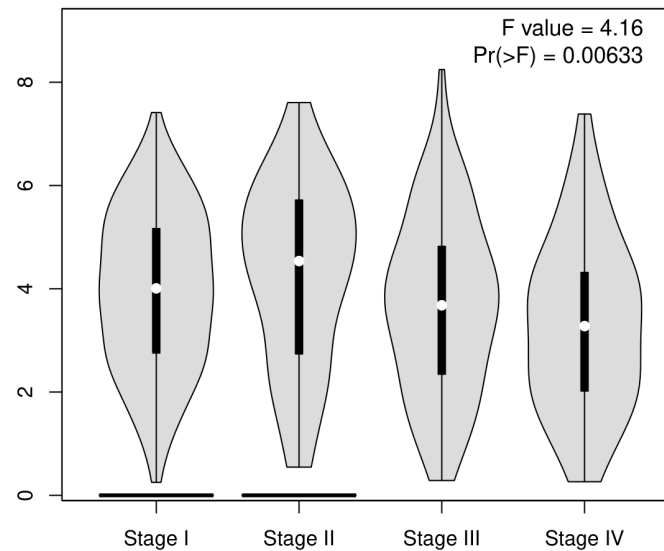
COL23A1 expression levels were compared among main pathological stages (stage I, stage II, stage III, stage IV). It also includes an F value of 4.16 and a Pr(>F) value of 0.00633. These values likely correspond to a statistical test done to compare the means between the four stages.
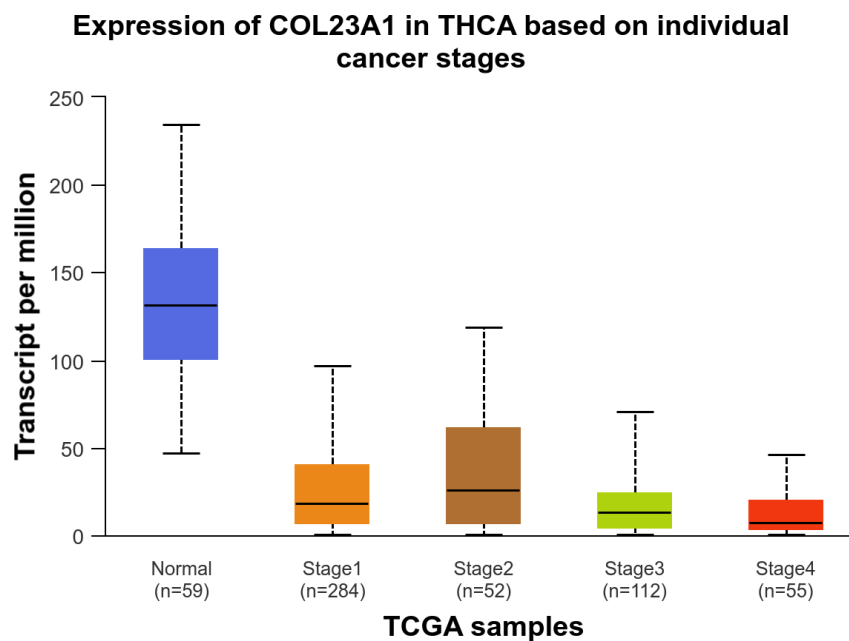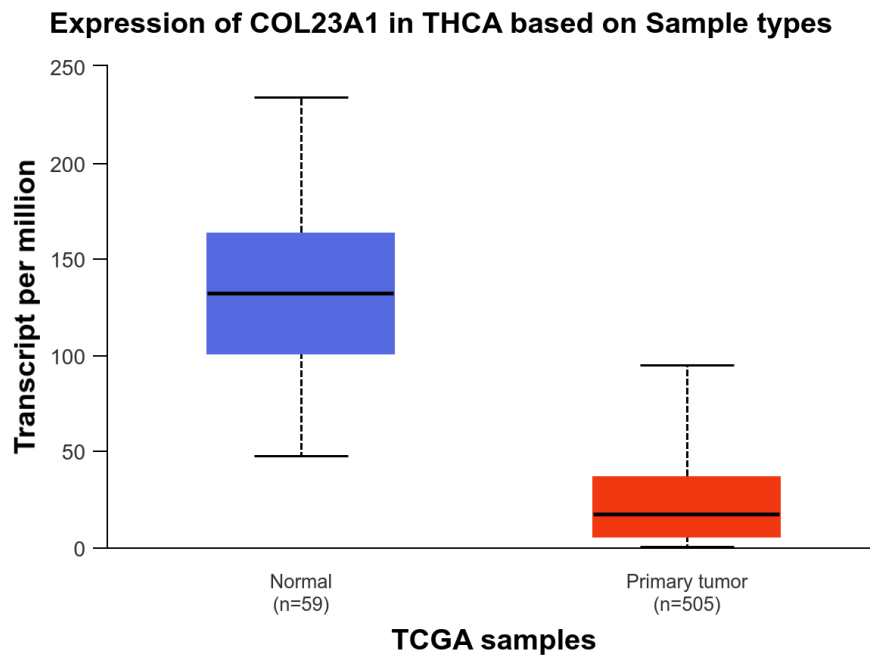
Gene Expression Analysis
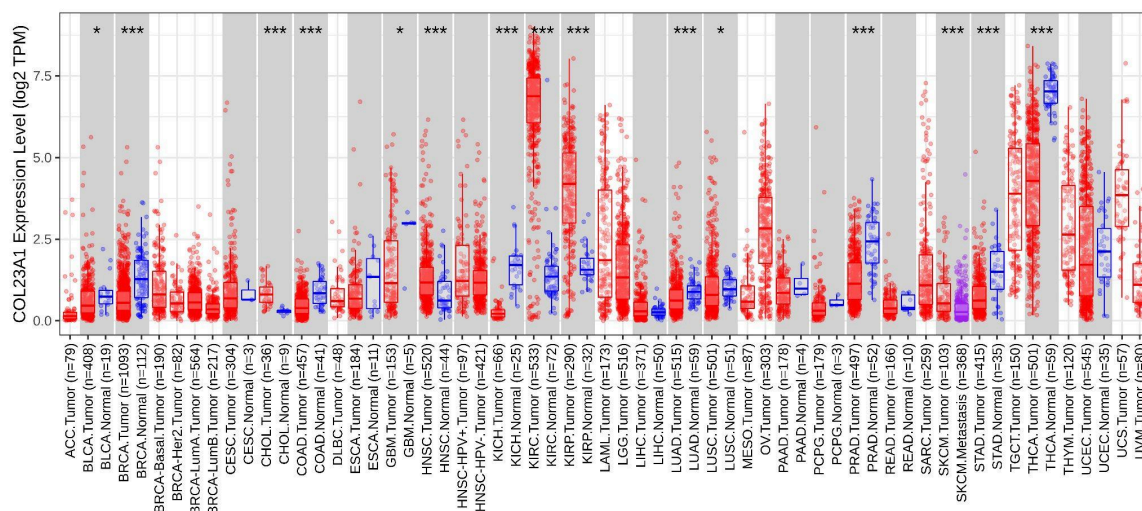
The TIMER 2.0 database is used to analyze the expression level of COL23A1. Here the expression level of COL23A1 in many cancer types is compared based on normal cells and tumor cells. As shown in Fig, the expression level of COL23A1 was significantly lower in tumors than in the corresponding normal tissues. The sample number of THCA tumor tissue is (n=501) and normal tissue is (n=59).
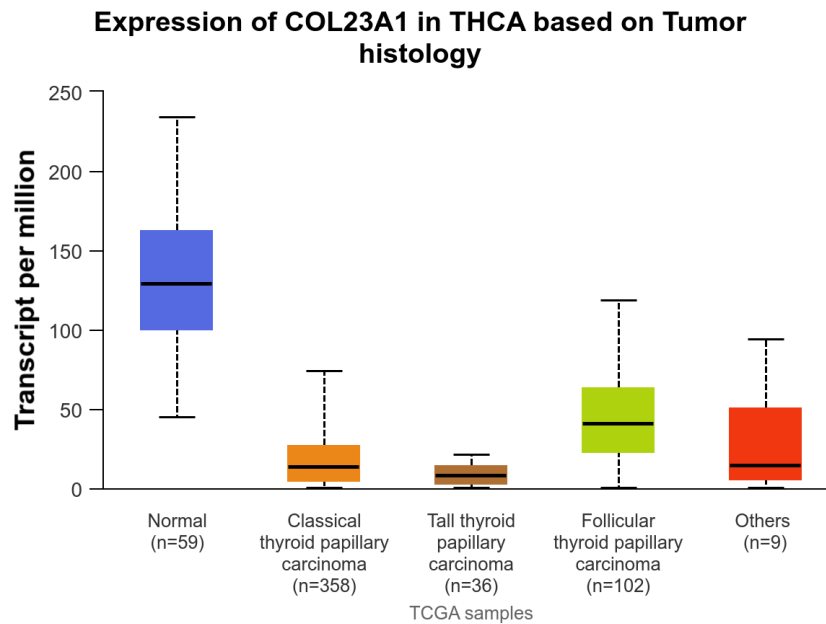
Immune Infiltration Analysis
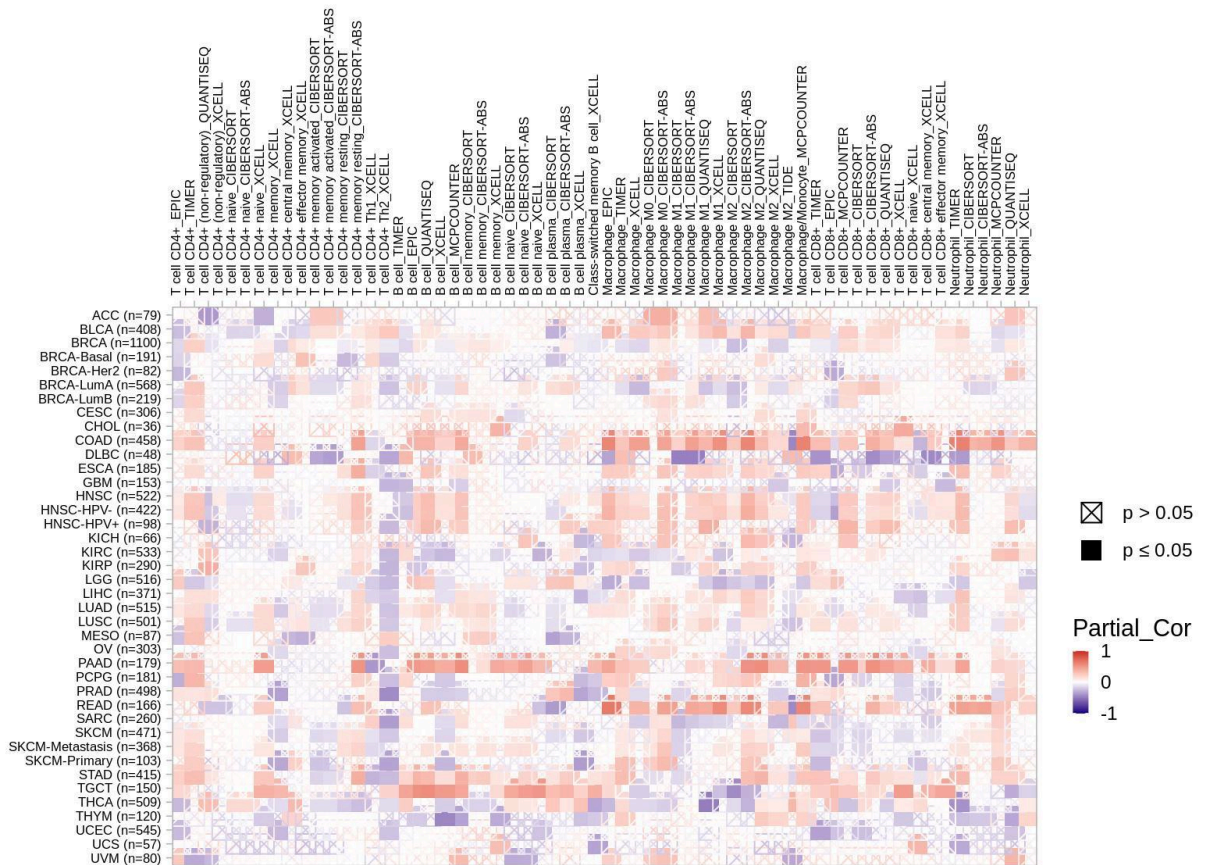
Above shown plot is a Immune Infiltration Analysis heatmap where many cancer types are compared between these immune cell types T cell CD4+, T cell CD8+, B cell, Macrophage, Nutrophill. The sample number of THCA (Thyroid carcinoma) is (n=509). Here red represents higher expression and blue represents lower expression level.

Expression Analysis

Expression of COL23A1 in THCA based on Sample types

Expression of COL23A1 in THCA based on individual cancer stages

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

The 1st plot shows the expression levels of gene COL23A1 in tumor and normal samples from patients with thyroid carcinoma where normal cells have higher gene expression compared to primary tumor cells.

The 2nd plot shows the comparison between normal cells and different cancer stages where stage 2 has the higher expression and stage 3 has the lower expression.

The 3rd plot depicts the comparison Between normal cells and different types of thyroid carcinoma. Where Follicular thyroid papillary carcinoma shows the higher expression and Tall thyroid papillary carcinoma shows the lower expression.

Survival Analysis
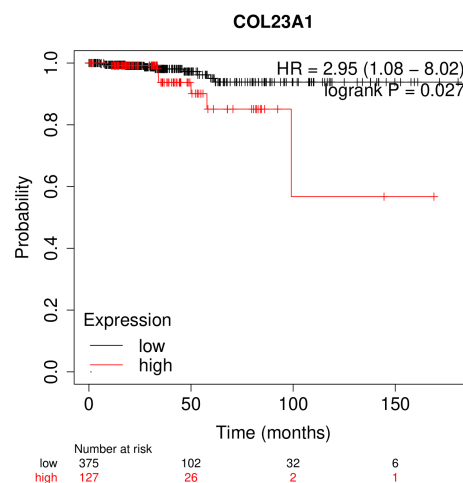
According to the expression levels of COL23A1 we divided the cancer cases into high-expression and lower-expression groups. Patients with low COL23A1 expression appear to have a better chance of survival over time compared to those with high COL23A1 expression.

Pan Cancer View

Expression of COL23A1 across TCGA cancers (with tumor and normal samples)
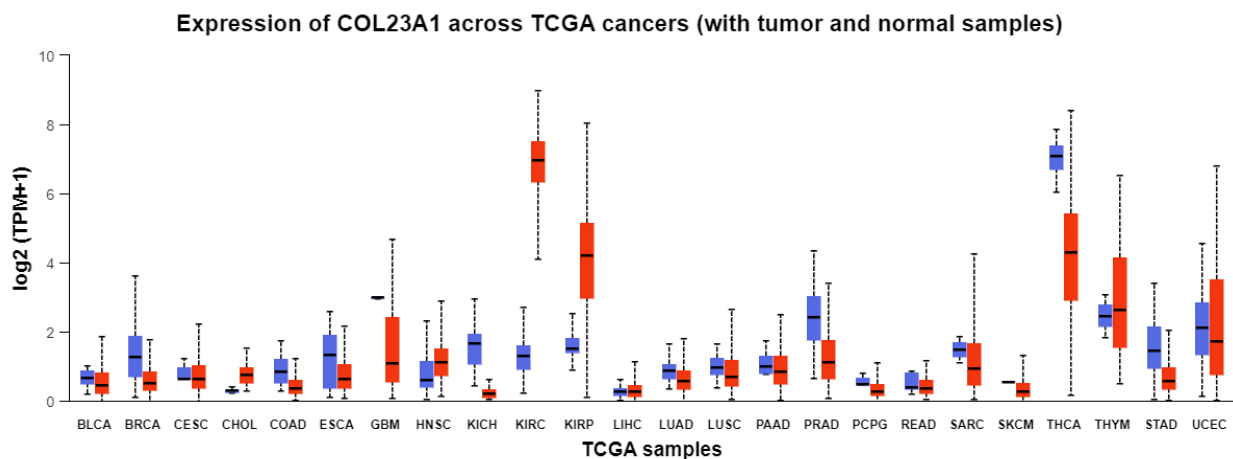
COL23A1 expression is higher in some tumor samples than in normal samples. There is also a wide range of expression levels in both tumor and normal samples. It depicts that COL23A1 expression may vary depending on the specific cancer type.THCA (Thyroid Carcinoma) tumors have a higher expression of COL23A1 compared to normal samples.

DNA Methylation Analysis
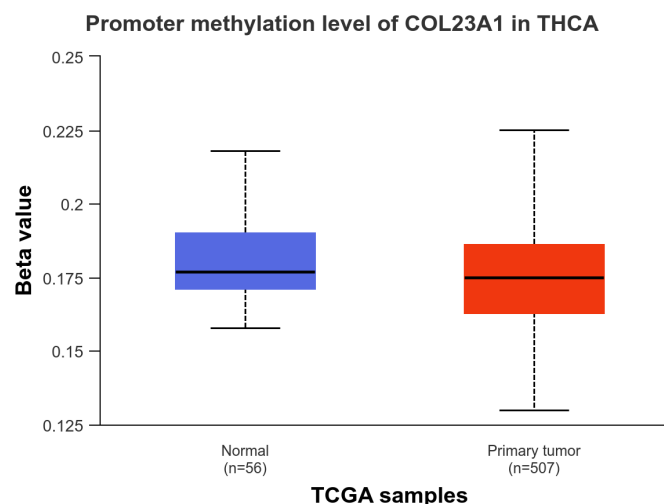
Promoter methylation level of COL23A1 in THCA

The graph shows the promoter methylation analysis level between normal and primary tumor cells. Where x-axis shows the number of TCGA samples and y-axis shows the Beta value where Primary tumor cells have higher Beta value and normal cells have lower Beta value.
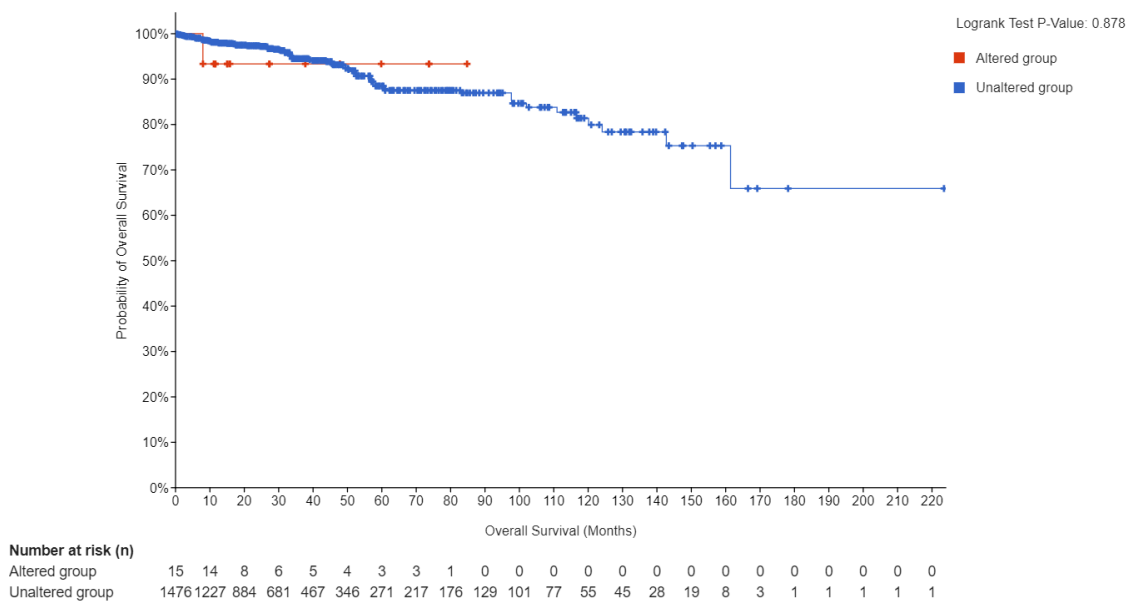
Gene Alteration Analysis
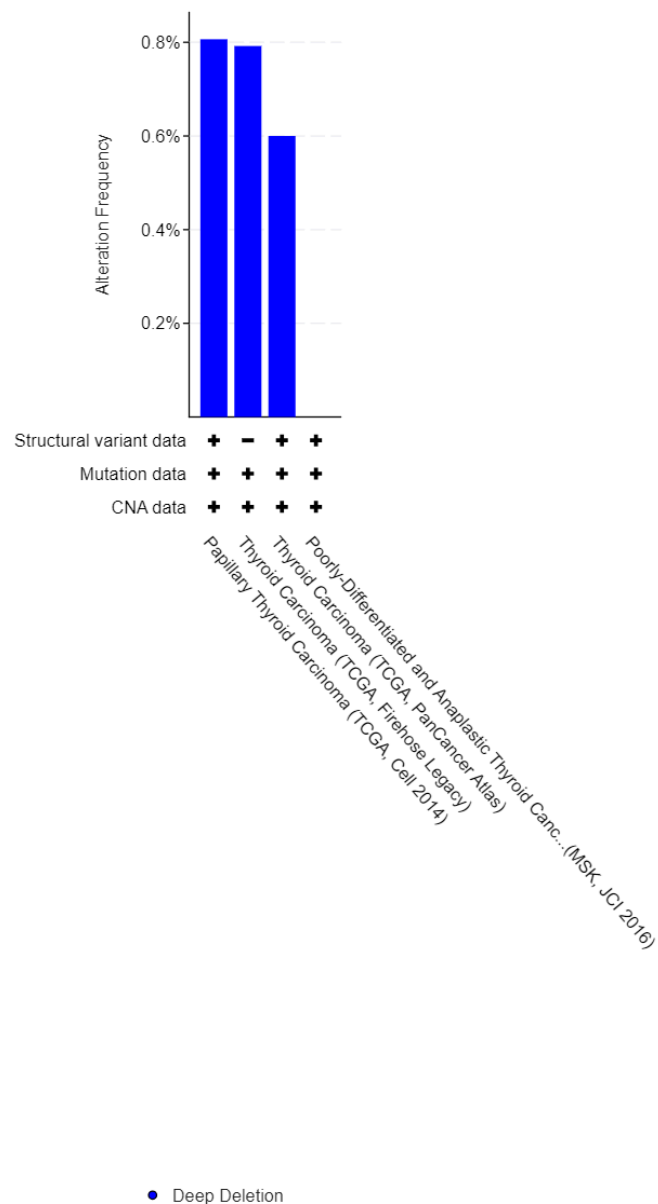
Here the y- axis shows the alteration frequency and the x- axis shows the structural variant data, mutation data, CNA data across different types of THCA samples from the cBioportal website. The blue part shows deep deletion.
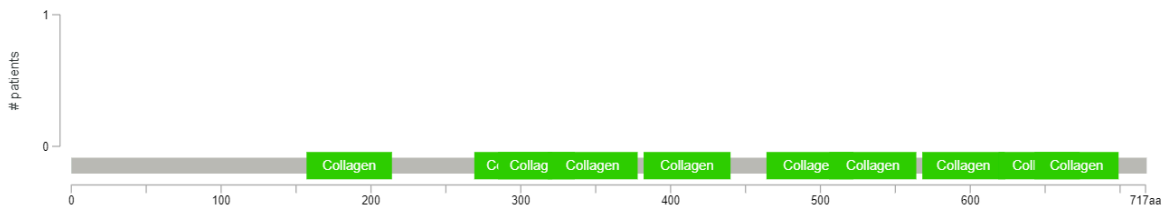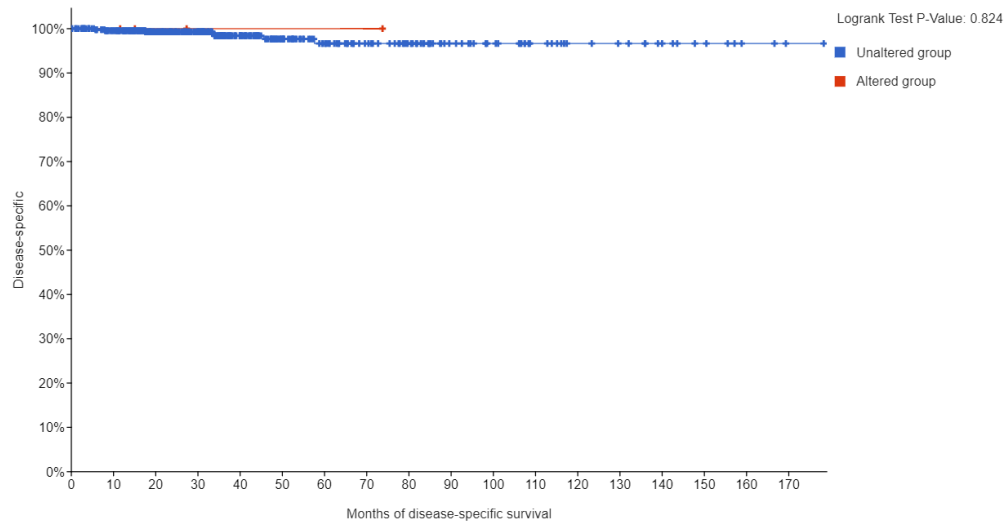
Mutation

The gene COL23A1 belongs to the collagen family. No mutation is observed.
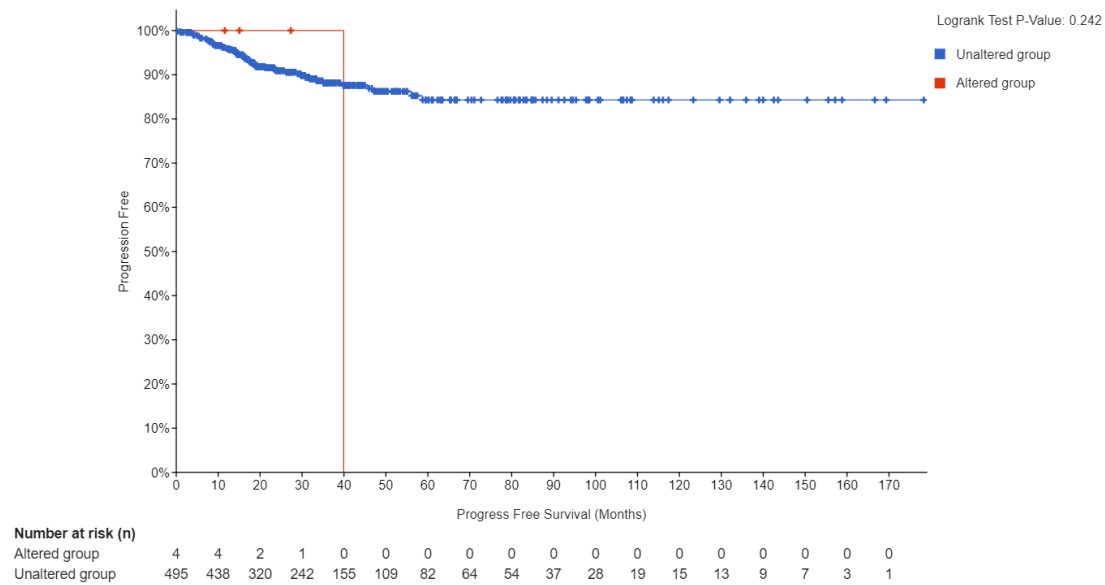
Survival Stage

Logrank Test P-Value: 0.824

- Unaltered group
- Altered group

Disease-specific

Months of disease-specific survival

Number at risk (n)

Altered group	4	4	2	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
Unaltered group	489	447	341	263	170	120	93	73	60	41	33	23	17	15	10	7	3	1

Logrank Test P-Value: 0.391

- Altered group
- Unaltered group

Disease Free

Disease Free (Months)
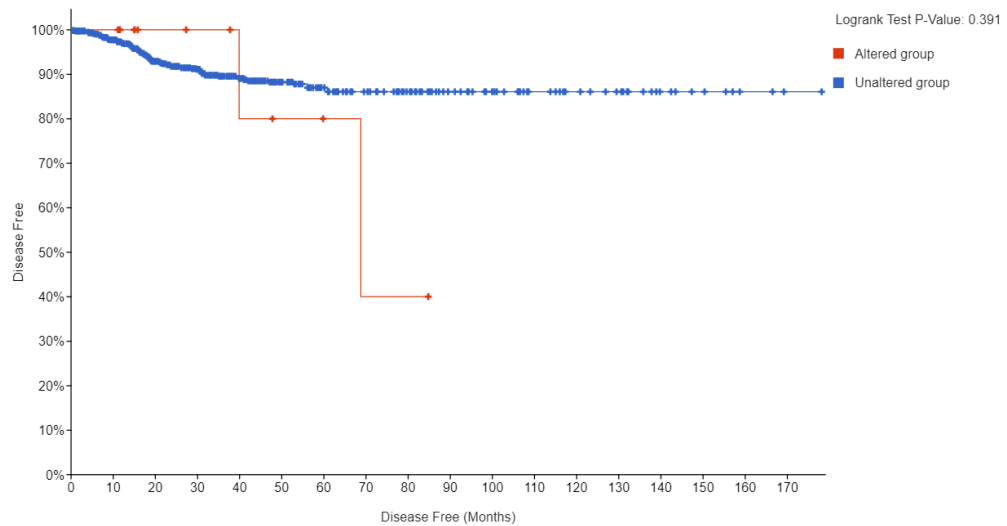
Number at risk (n)

Altered group	13	13	7	6	4	3	2	1	1	0	0	0	0	0	0	0	0	0
Unaltered group	1253	1015	685	516	345	249	190	149	123	87	67	48	40	33	20	15	6	2

Four stages; Progress free survival, Disease free, Months of disease-specific survival, Overall survival are shown. Red color depicts the altered group and blue depicts the unaltered group.
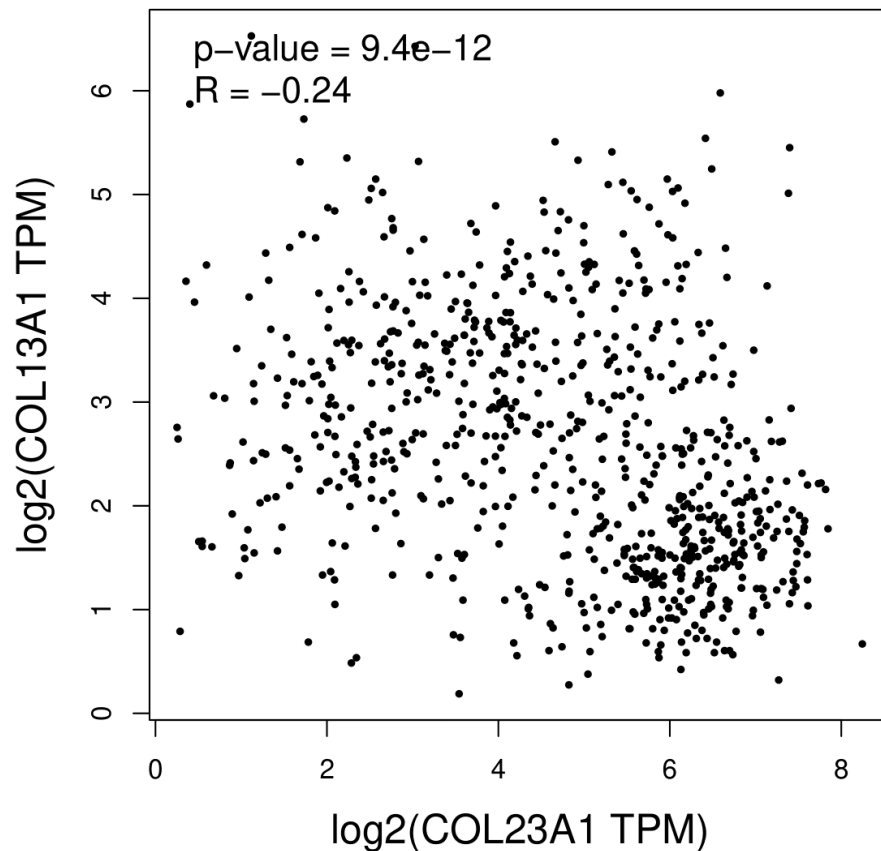
The probability of survival is generally higher for the unaltered group compared to the altered group.

PPI Analysis
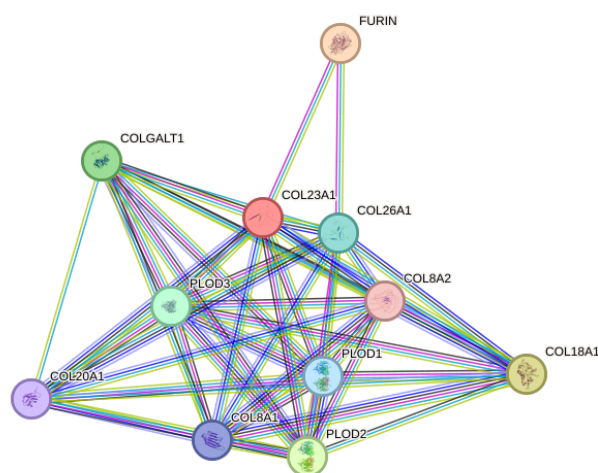
Here the protein protein interaction structure has been shown for COL23A1 where the other collagen family members' genes are connected with each other.

Correlation between COL13A1 and COL23A1

A scatter plot showing the correlation between COL13A1 and COL23A1 gene. The x-axis shows the values for Col13A1 gene expression, after it's been log2 transformed the y-axis shows the values for Col23A1 gene expression, also log2 transformed. There is a positive correlation. This means that as the log2(COL13A1 TPM) value increases, the log2(COL23A1 TPM) value also tends to increase. This plot suggests that there is a weak positive correlation between Col13A1 and COL23A1 gene expression. This means that there is a slight tendency for these two genes to be expressed together.