



# Analyzing Differential Expression of p53, BCL2, and BAX in T-Cell Lymphoblastic Leukemia

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## Introduction

Acute Lymphoblastic Leukemia is a severe blood disease and it is one of the most common type of childhood leukemia. T-cell Acute Lymphoblastic Leukemia occurs in the malignant transformation of T-cells in the thymus and approximately 15-18% of childhood Acute Lymphoblastic Leukemia patients belong to T-Cell Acute Lymphoblastic Leukemia. Several genes which are involved in T-cell development have been demonstrated to have important roles in leukemogenesis. Here, we studied 30 T-ALL childhood patients for their expression levels of p53, BAX, and BCL2 by quantitative real time PCR. p53, is a tumor suppressor gene, and BAX are pro-apoptotic genes while BCL2 inhibits apoptosis. p53 was found to be significantly upregulated in patient samples when compared with control thymocytes. Upregulation of p53 might lead the cells to malignant transformation.

## Materials and Methods

Differential gene expressions were detecting by quantitative real time PCR.

- T-ALL Patient Samples (n=30)
- Healthy Thymocytes and Thymus
- RNA Isolation
- cDNA Synthesis
- Quantitative Real Time PCR (qRT-PCR) (Figure 1)

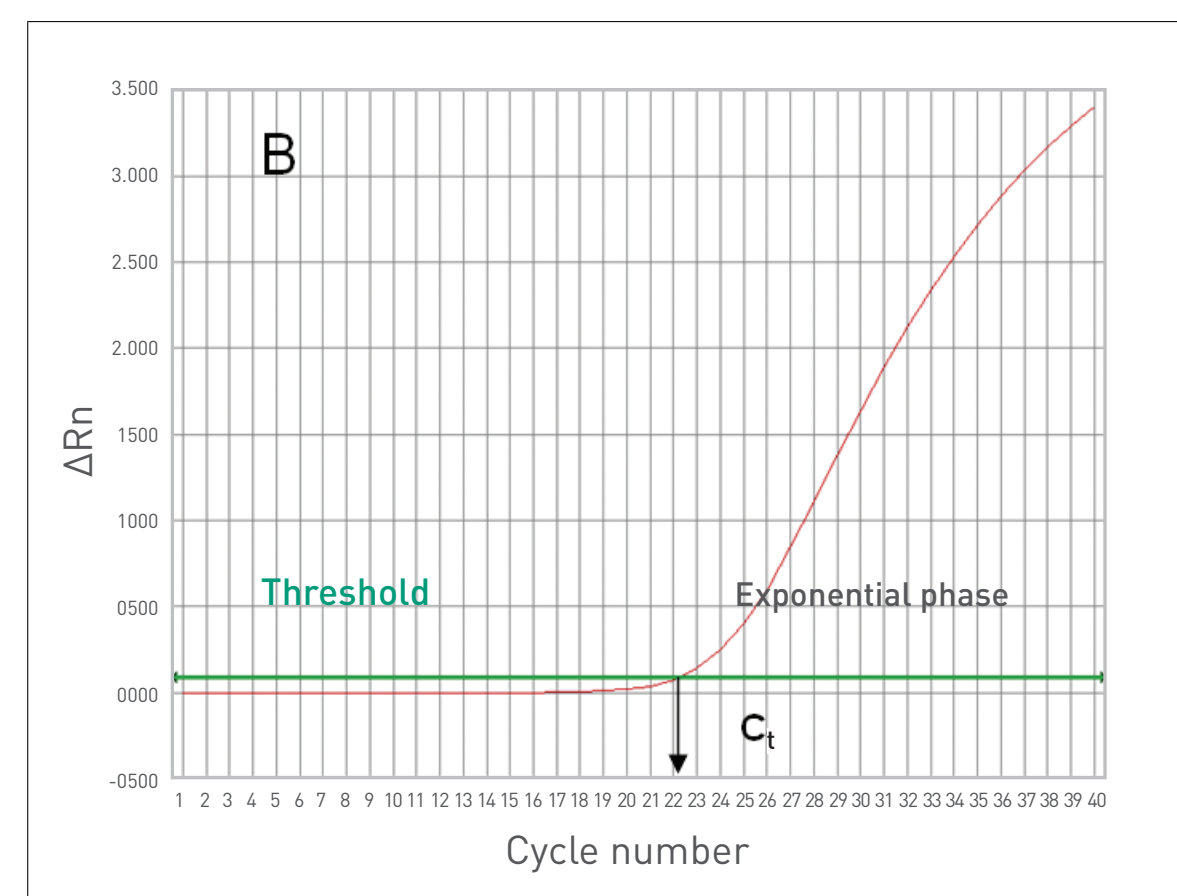


Figure 1: Ct (threshold cycle) for qRT-PCR

Relative quantification by  $\Delta Ct_{method}(Ct_{targetgene} - Ct_{housekeepinggene})$ .

## Results

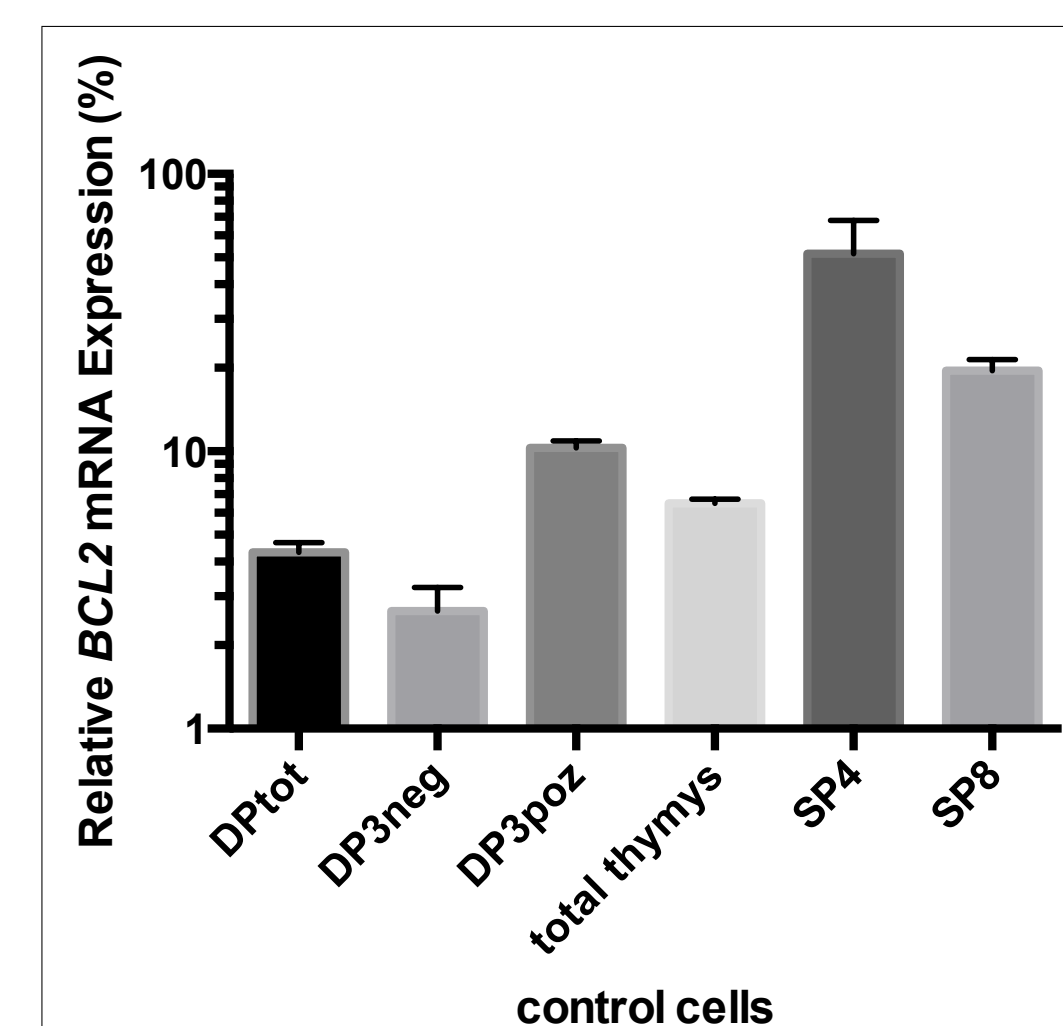
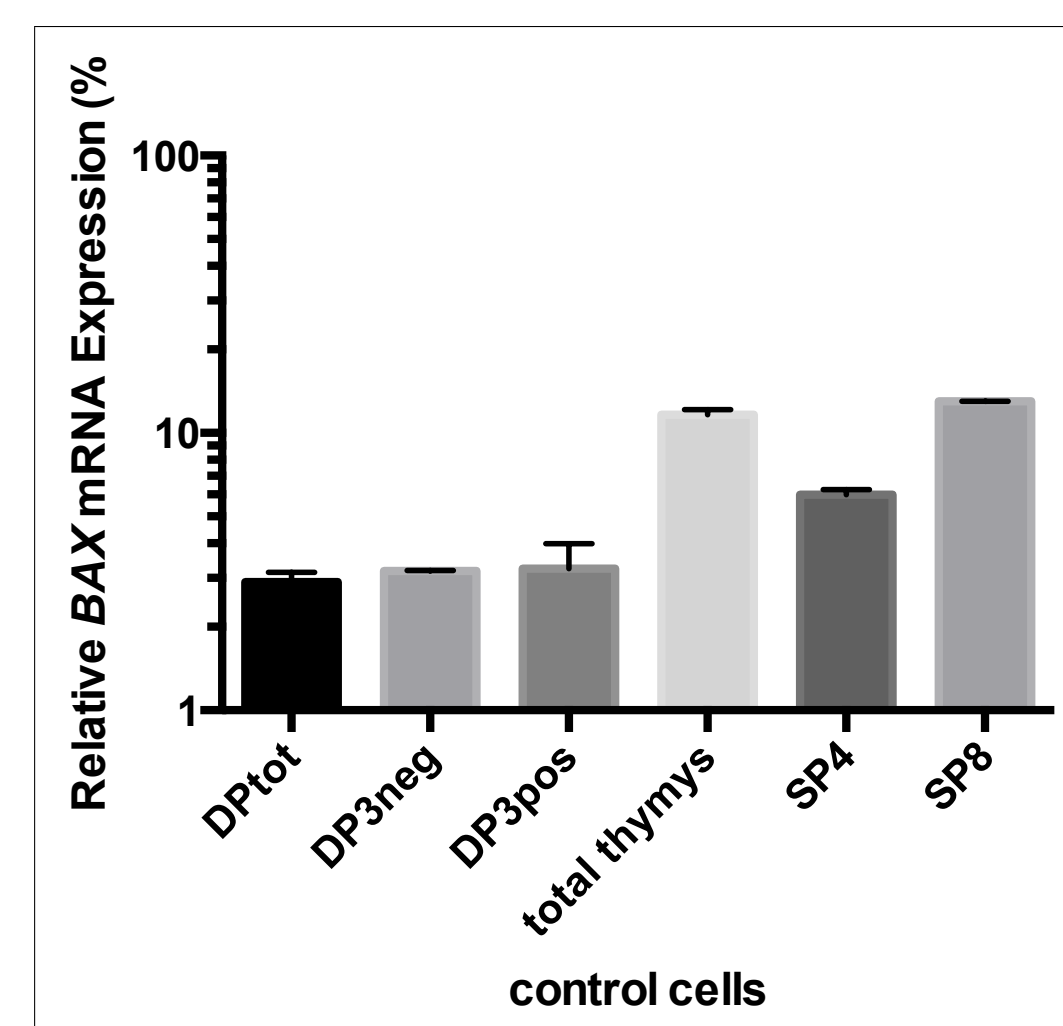
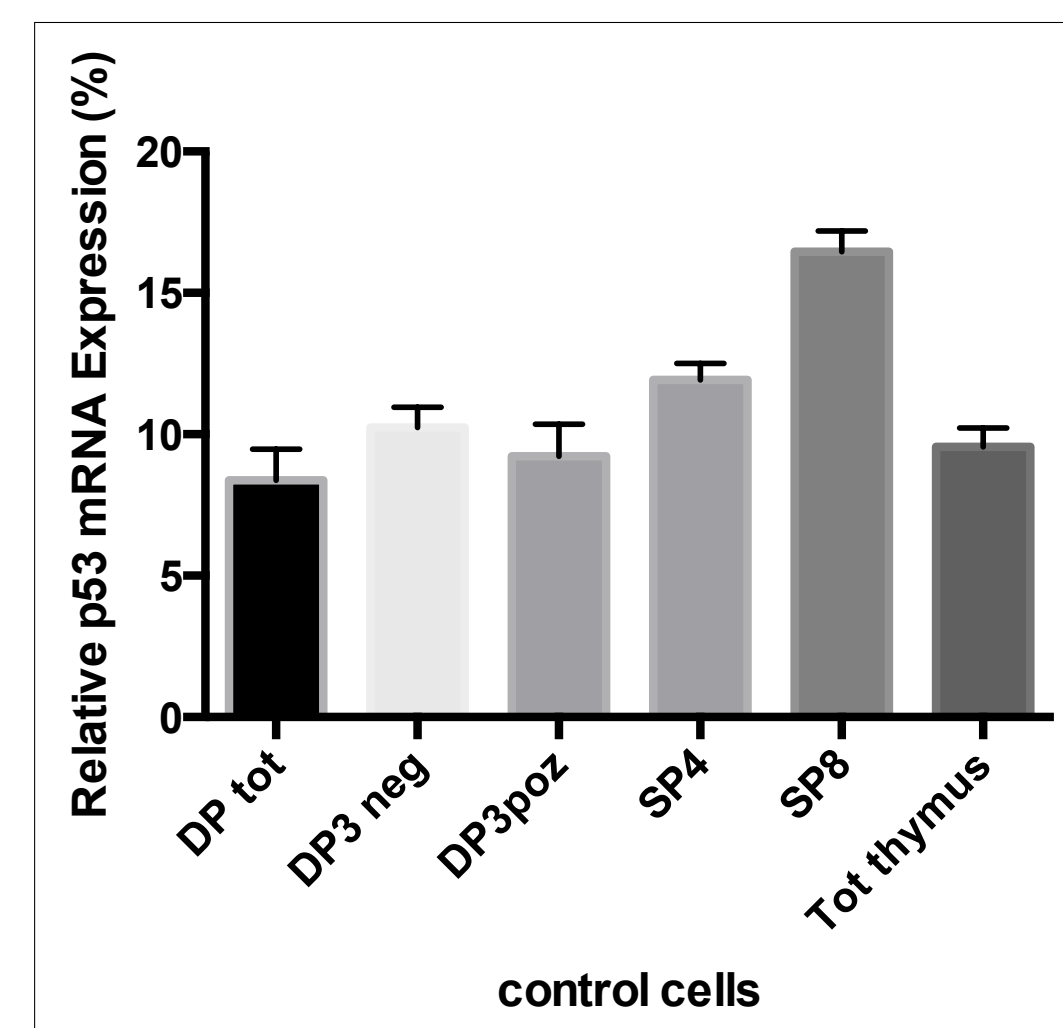


Figure 2: Relative mRNA Expressions in Normal Thymocytes

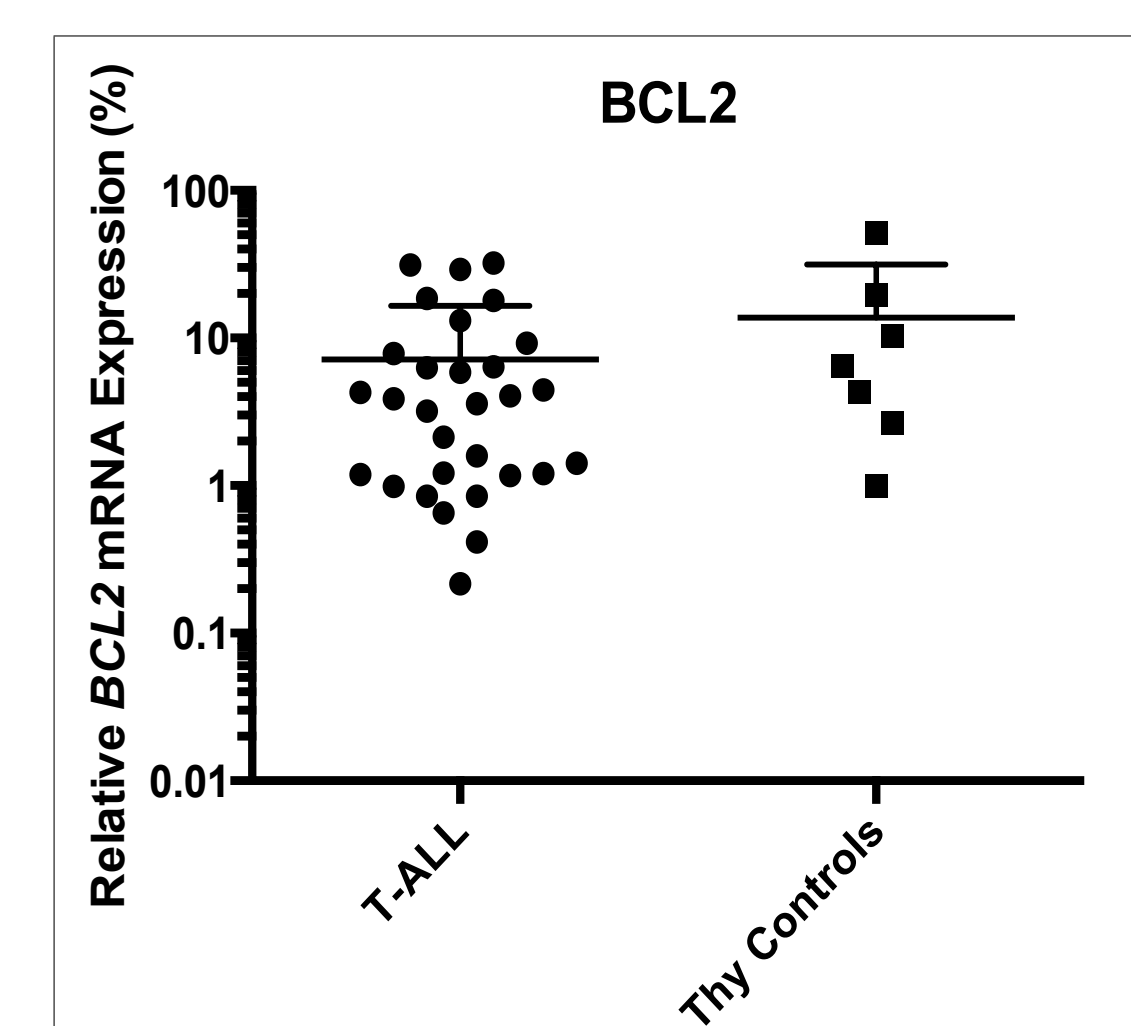
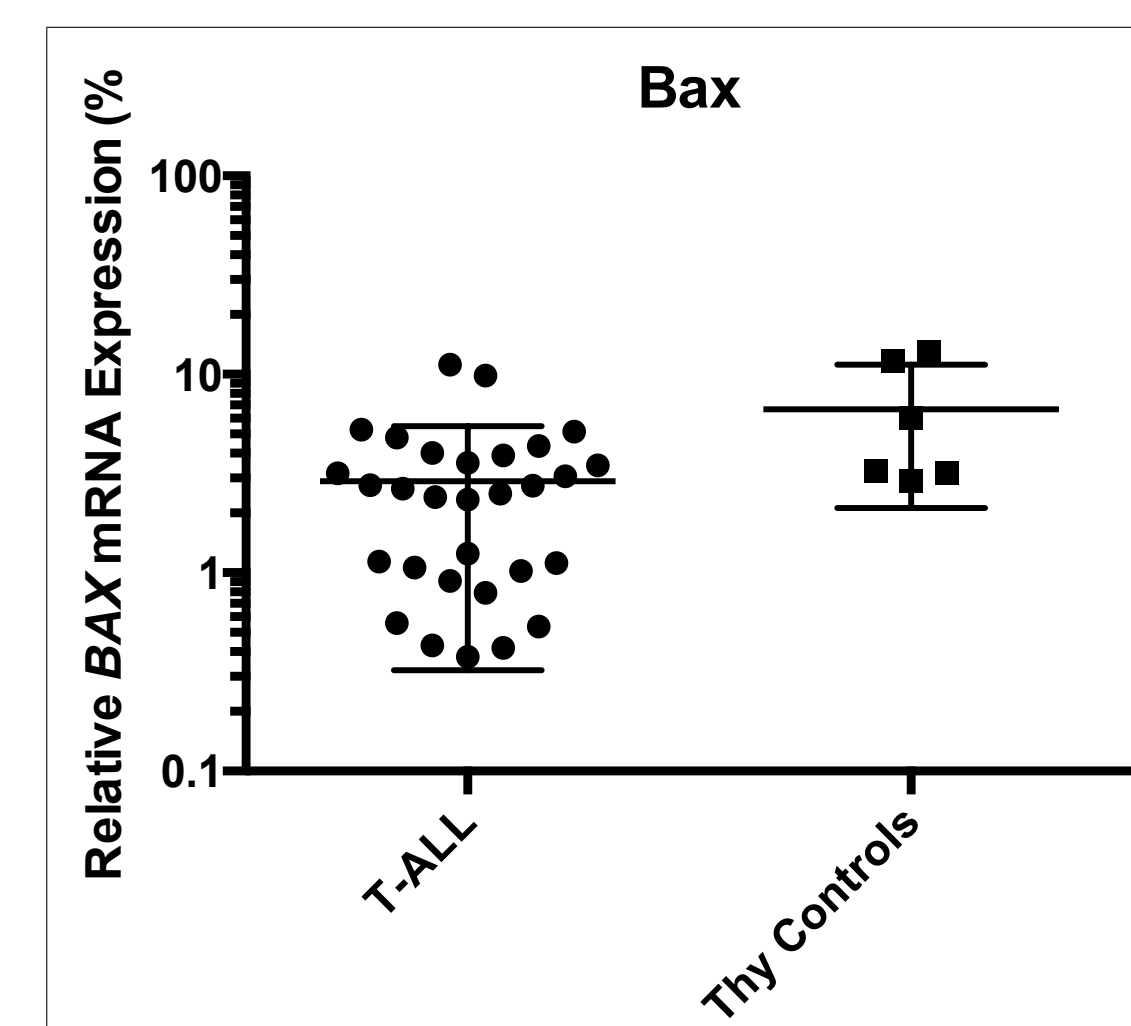
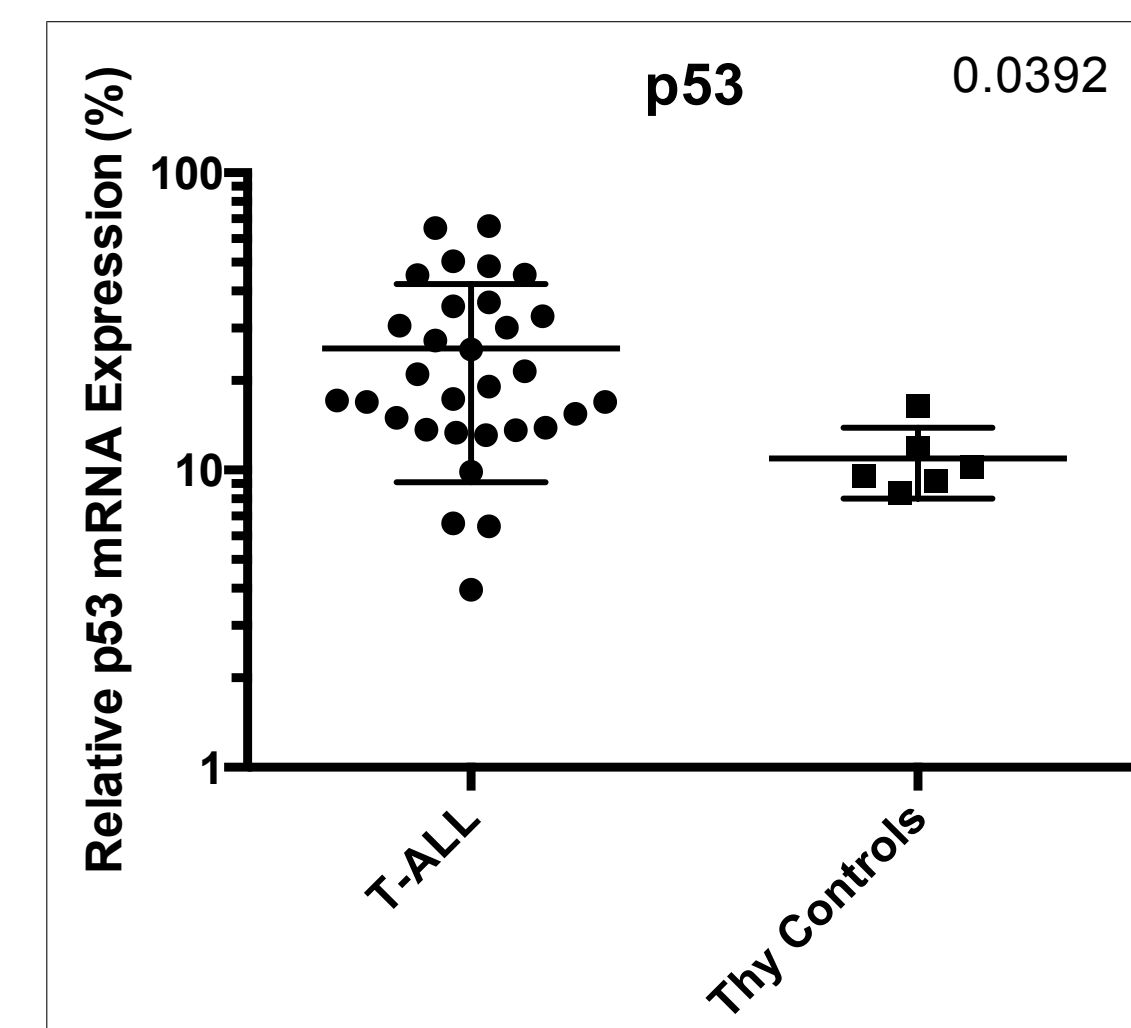


Figure 3: Relative mRNA expressions in T-ALL Patient Samples

## Conclusions

Here in this project, the differential expression of p53, BAX, and BCL2 genes were studied. p53 expression is significantly upregulated in T-ALL patient samples when compared with healthy samples ( $p=0.0392$ ). The lowest expression level for p53 is observed in double positive (DP) stage among normal thymocytes samples and it is upregulated during T-cell development. Expression of BAX gene is regulated by p53. However there is no significant difference in the expression of BAX observed by q-RT-PCR data. Significant expression difference for BCL2 in T-ALL patients is also not observed. In the T-cell development stages expression of all three genes reaches maximum level in SP stage, last stage of the development. Analyzing other members of the apoptosis pathway, whole genome analysis with more patient samples, detecting protein products of our target genes by immunohistochemistry or western blot, studying epigenetic mechanisms that control gene expression can be as a future aim of the project.

## References

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- Dik WA, Pike-Overzet K, Weerkamp F, de Ridder D, de Haas EF, and Baert MR et al. New insight on human t cell development by quantitative t cell receptor gene rearrangement studies and gene expression profiling. J Exp Med., 201:1715–1723, 2005.

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## For Further Information

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