# Immune-Cell Expression Signatures in B-cell Lymphoma

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## Abstract

Intro: B-cell lymphomas are a group of diseases that originate from the B cell compartment of your white blood cells. B-cell lymphoma and High-Grade Lymphoma are difficult to distinguish by pathologists based on morphology but have been shown to have very different expression profiles by suggesting these lymphomas come from different stages of B-cell development.

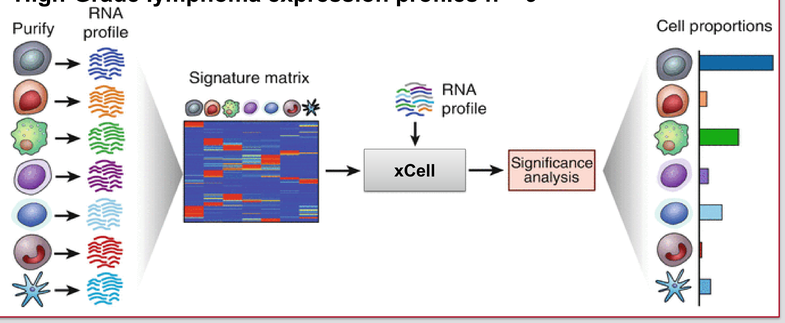
M&M: CIBERSORTx is an analytical tool to impute gene expression profiles and provide an estimation of the abundances of member cell types in a mixed cell population, using gene expression data.

Results: A program called xCell was utilized to see that High-Grade Lymphoma cases were enhanced for memory B-cell marks while Burkitt Lymphoma cases were improved for plasma cell signatures suggesting a potential difference in the normal cell counterpart. For immune-cell signatures in the microenvironment, I observed that High Grade Lymphoma samples had a statistically significant increase in T-regulatory cell signatures

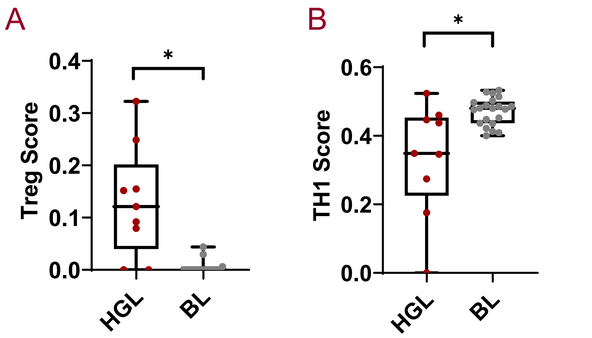
Conclusions: I observed that High Grade Lymphoma samples had a statistically significant increase in T-regulatory cell signatures while Burkitt Lymphoma samples had a statistically significant increase in T-helper 1 signatures. Taken together, these results suggest differential microenvironments in these malignancies which could be exploited in therapeutic strategies as T-regulatory and T-helper 1 subsets can influence anti-tumor responses.

## Materials and Methods

**Burkitt lymphoma expression profiles n = 21**
**High-Grade lymphoma expression profiles n = 9**




## Results



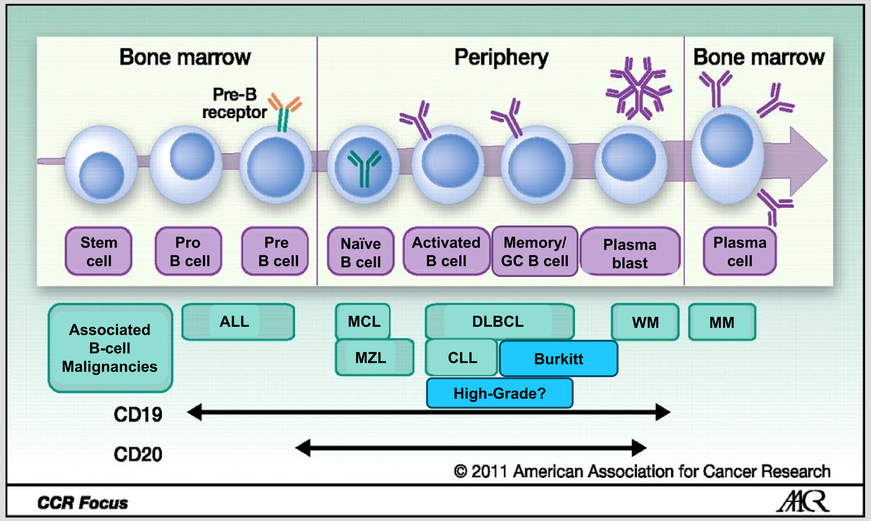




Figure 1. Schematic representation of B-cell development and its relationship to B-cell lymphomagenesis. The current study focuses on the relationship between Burkitt lymphoma and High-Grade B-cell lymphoma, which are denoted in blue.

Figure 2. Pictorial depiction of workflow for obtaining gene expression-based immune-cell estimations in B-cell lymphoma patient samples.

## Results

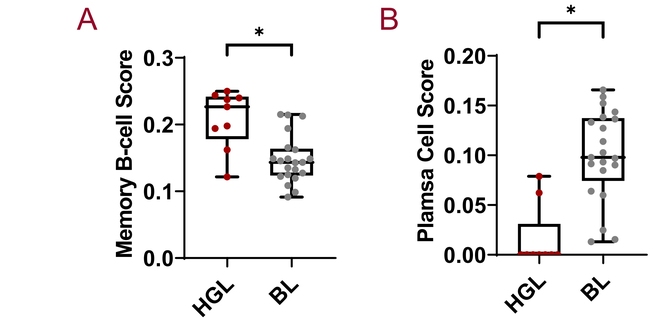



Figure 3. High-Grade B-cell lymphoma (HGL) and Burkitt lymphoma (BL) differ in malignant B-cell signatures. (A) Boxplot of Memory B-cell Score from xCell in HGL and BL patient samples. (B) Boxplot of Plasma Cell Score from xCell in HGL and BL samples. * = $p < 0.05$

Figure 4. High-Grade B-cell lymphoma (HGL) and Burkitt lymphoma (BL) differ in tumor microenvironment T-cell signatures. (A) Boxplot of T-regulatory ($T_{reg}$) Score from xCell in HGL and BL patient samples. (B) Boxplot of T-Helper 1 (TH1) Score from xCell in HGL and BL samples. * = $p < 0.05$

## Conclusions

- In the patients affected in combination with traditional chemotherapy and other novel agents play a huge role in understanding this diverse group of diseases. these results suggest differential microenvironments in these malignancies which could be exploited in therapeutic strategies as T-regulatory and T-helper 1 subsets can influence anti-tumor responses.
- Knowing this information could regulate inflammation, decreasing the potential for pro-tumor effects in patients.

## Acknowledgments

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## References

Figure 1 adapted from Digital Image. *American Association for Cancer Research.2011*
Figure 2 adapted from Digital ImageShen-Orr, S.S. & Gaujoux, R. Computational deconvolution: extracting cell type-specific information from heterogeneous samples.. *Curr. Opin. Immunol.* **25**, 571–578 (2013).