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Bioinformatics Analysis of the Immune Microenvironment and Diagnostic Biomarkers in AIDS-Related Diffuse Large B-Cell Lymphoma

Shengnan Zhao[1#], Xiaojie Huang[1*]

[1] Clinical and Research Center for Infectious Diseases Beijing Youan Hospital, Capital Medical University, No.8 Xitoutiao, Youanmenwai, Feng Tai District, Beijing, 100069, P.R. China

Background

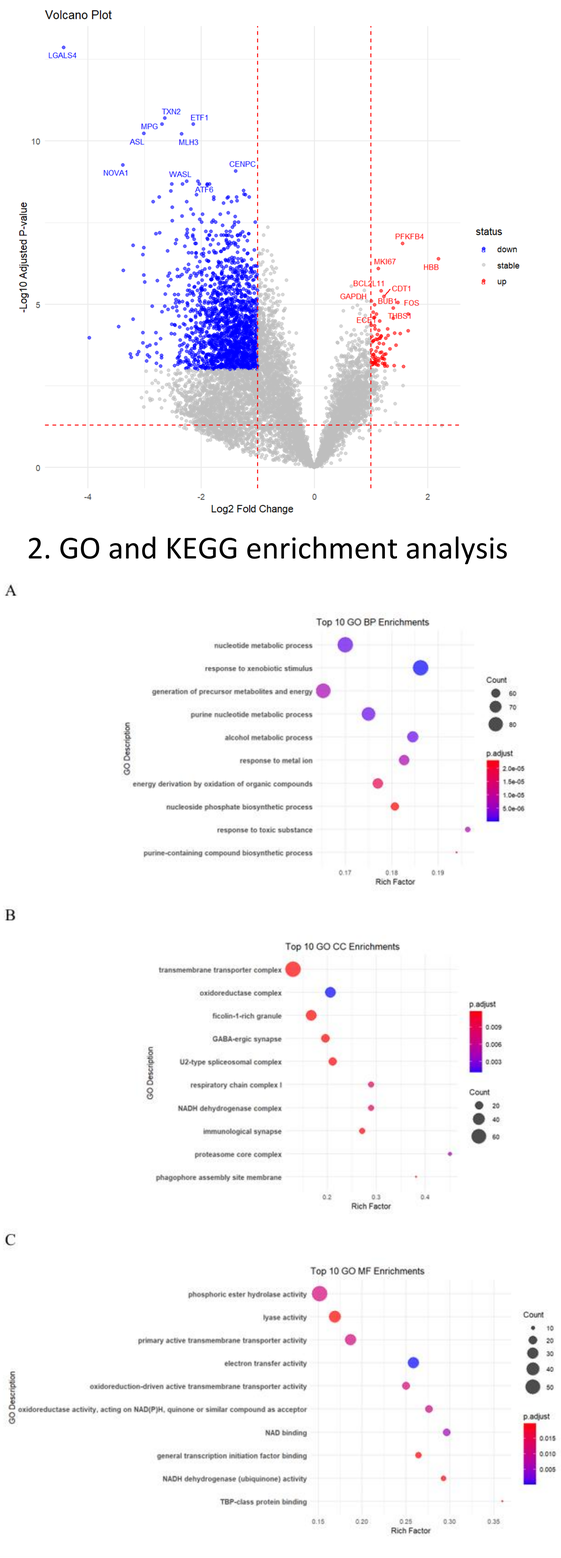
AIDS-associated diffuse large B-cell lymphoma (DLBCL) is one of the common malignancies in people living with HIV (PLWH). Despite the application of antiretroviral therapy (ART), PLWH have a significantly higher risk of developing non-Hodgkin's lymphoma, especially DLBCL, than the general population, and their prognosis remains relatively poor. If the tendency of PLWH to develop DLBCL is detected late, it is more difficult to help their recovery by means of treatment.

Methods

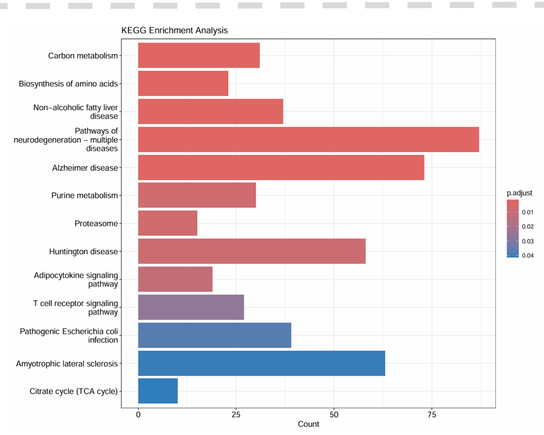
Transcriptome high-throughput sequencing data from AIDS-associated DLBCL and HIV-negative DLBCL tumor tissue samples were obtained from the GEO datasets (GSE2350 and GSE262621). A range of bioinformatics methods were used to screen for genetic markers for the diagnosis of AIDS-associated DLBCL and to characterize the AIDS-associated DLBCL immune microenvironment.

Results

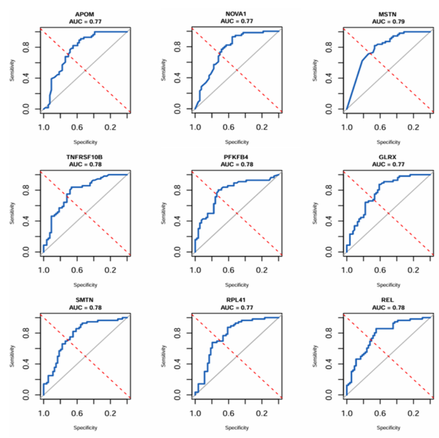
1. By differential analysis of mRNA series matrix data from 56 AIDS-associated DLBCL and 54 HIV-negative DLBCL genes, we identified a total of 1797 differential expressed genes, of which 80 were up-regulated genes (log2FC>1 and P<0.001) and 1717 were down-regulated genes (1og2FC<-1 and P<0.001).



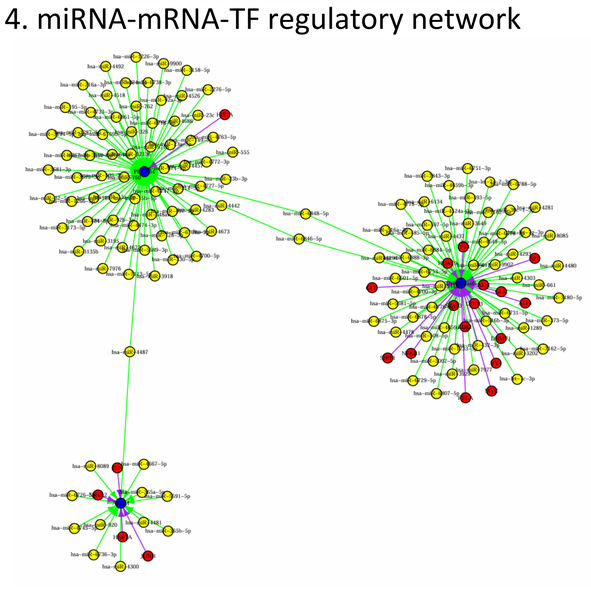
2. GO and KEGG enrichment analysis



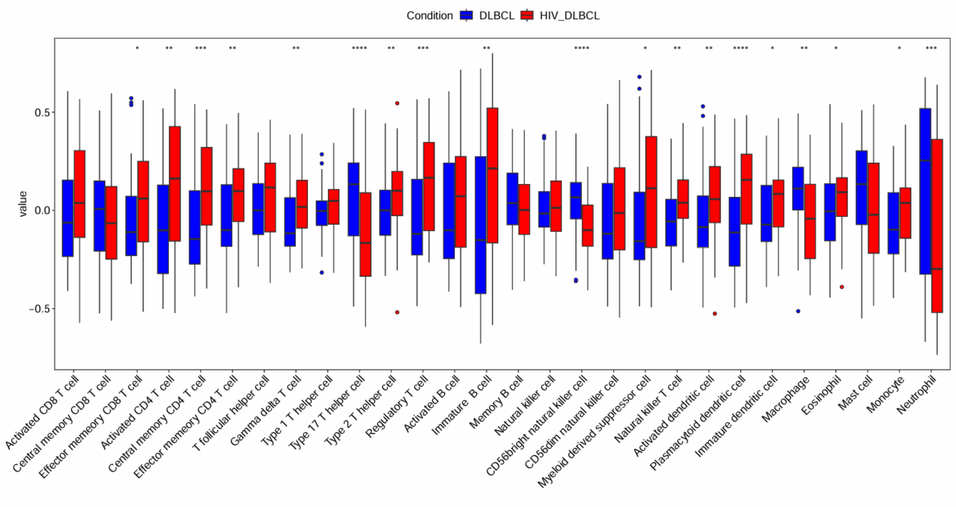
3. Gene markers validated by external datasets (GSE67763 and GSE178965)



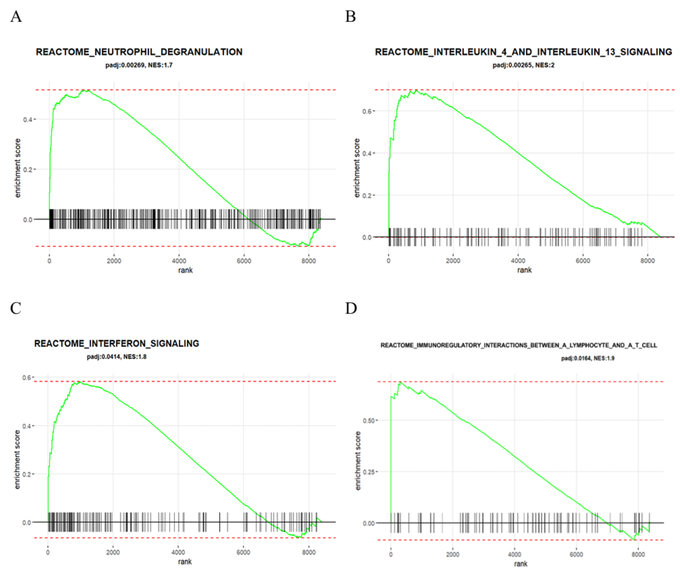
4. miRNA-mRNA-TF regulatory network



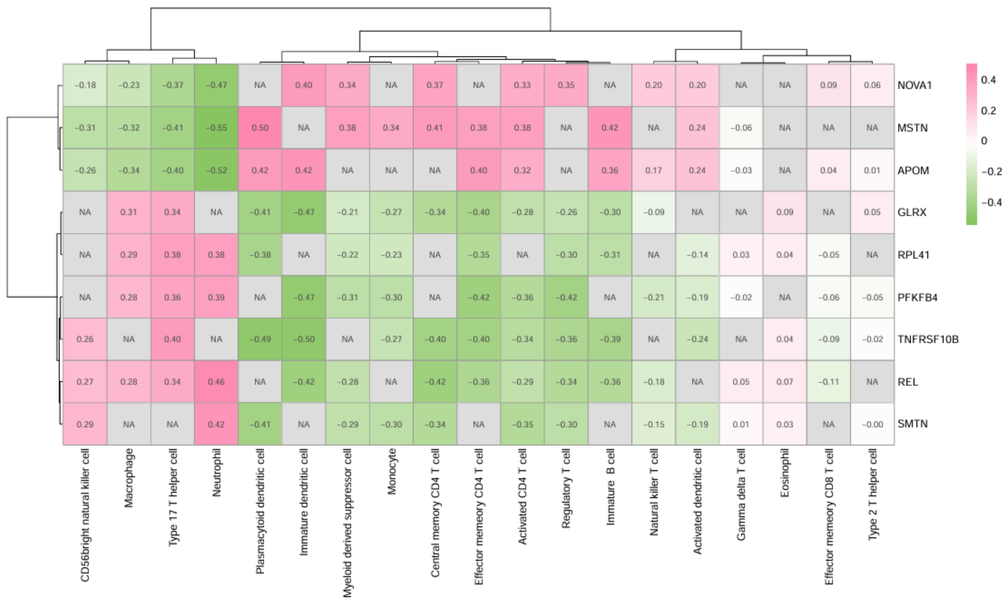
5. Characterization of the AIDS-associated DLBCL immune microenvironment



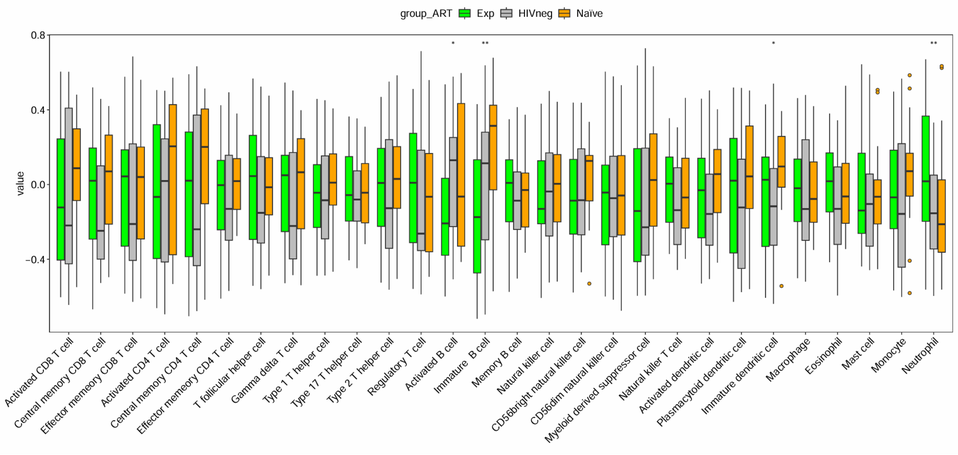
6. Gene set enrichment analysis



7. Correlation of genetic markers with differential immune cell subsets



8. The role of ART on the immune microenvironment of AIDS-associated DLBCL



Conclusion

In this study, we analyzed the characteristics of the immune microenvironment of AIDS-associated DLBCL based on the bioinformatics method and searched for potential biomarkers for determining AIDS-associated DLBCL, and found that there was a significant difference in the immune infiltration of immune system tissues (tumor tissues), and nine genes were obtained, which can provide a theoretical basis for the clinical diagnosis of AIDS-associated DLBCL. It provides a theoretical basis for the clinical diagnosis of AIDS combined DLBCL.

References

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zsn95ci@outlook.com