

A prognostic gene signature for predicting survival outcome in Diffuse Large B-Cell Lymphoma (DLBCL)

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The Innovation:

A prognostic gene signature consisting of 33 genes that can stratify DLBCL patients receiving R-CHOP therapy into high or low risk groups that have significantly different Overall Survival (OS). This gene signature can be utilized to identify individuals that are at high risk of poor survival outcomes with DLBCL that could be candidates for experimental medicine and clinical trials and who should be more closely monitored clinically.

Background:

Diffuse large B-cell lymphoma (DLBCL) is an heterogenous cancer that can have profound differences in survival outcomes. Molecular profiling has allowed for the identification of DLBCL subclasses and together with clinical prognostic factors, such as the International Prognostic Index, have improved clinical care and survival. Despite these advances, a gene signature that is associated with overall survival (OS) and is reproducible across different DLBCL studies could better classify risk and predict OS.

The Innovation:

Gene expression and clinical parameters in the Lymphoma/Leukemia Molecular Profiling Project from individuals that received R-CHOP therapy were used to identify genes whose expression is associated with overall survival. This was further refined to develop a prognostic gene signature of 33 genes that could be used to calculate risk scores for each individual and predict overall survival. This prognostic gene signature was validated in 3 additional data sets and determined significant differences in overall survival in individuals with high or low risk scores.

Advantages and Potential Applications:

- The unique molecular prognostic signature is useful for predicting DLBCL prognosis, regardless of subtype
- The gene signature can be utilized to identify individuals that are at high risk of poor survival outcomes with DLBCL who could be candidates for experimental medicine and clinical trials and should be more closely monitored clinically
- The 33-gene panel can also be used over time to provide an indication of disease progression and/or response to treatment

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Publications:

“A prognostic gene signature for predicting survival outcome in diffuse large B-cell lymphoma” *Cancer Genetics*, 252-253 (2021) 87-95

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