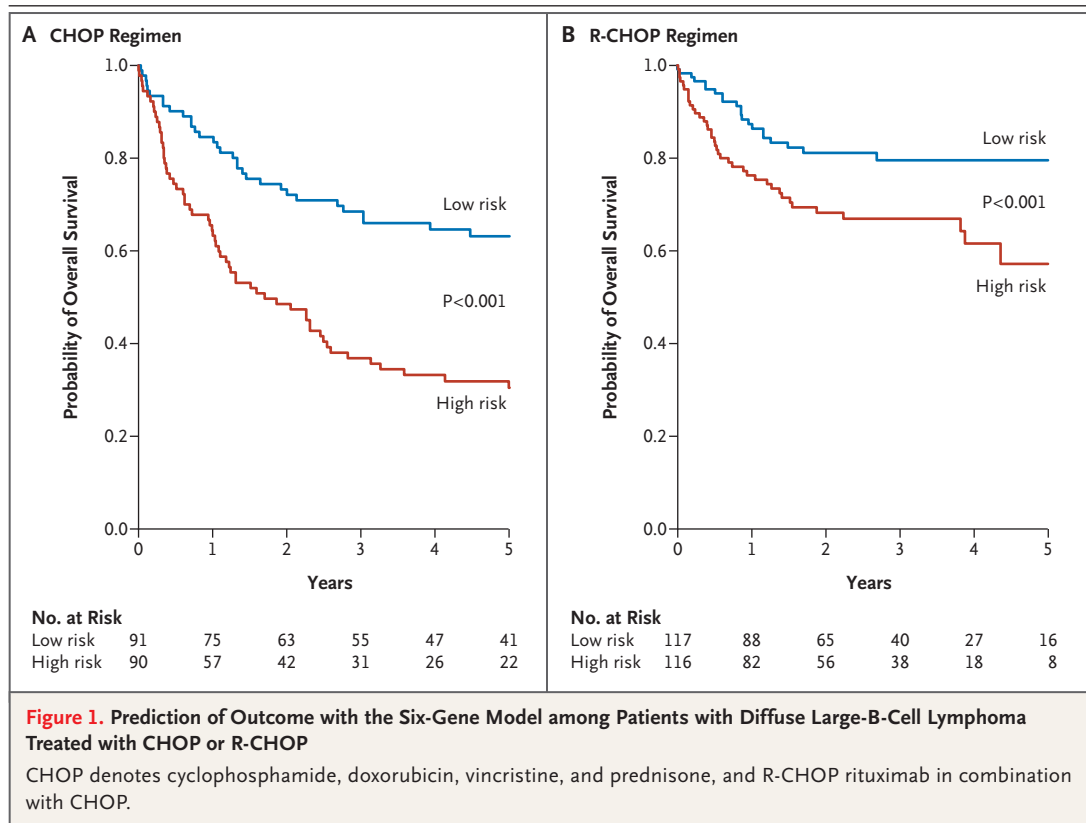


Molecular Outcome Prediction in Diffuse Large-B-Cell Lymphoma

TO THE EDITOR: Lenz et al. (Nov. 27 issue)¹ report the results of an important study of gene expression and survival in patients with diffuse large-B-cell lymphoma. We reassessed the performance of a survival predictor that we had previously reported² by applying it to the expression profiles of tumors from patients described by Lenz et al. Our model performed well in predicting overall survival in these patients, whether they were treated with cyclophosphamide, doxorubicin, vincristine, and prednisone (CHOP) or with CHOP in combination with rituximab (R-CHOP) ($P < 0.001$) (Fig. 1). Furthermore, when risk was in the model as a continuous variable, this model, which used the expression levels of only six genes, distinguished risk groups nearly as well as the survival predic-

tor proposed by Lenz et al., which incorporated stromal-cell signatures. Three of the 6 genes in our model (*LMO2* [LIM domain only 2 (rhombotin-like 1)], *BCL6* [B-cell chronic lymphocytic leukemia/lymphoma 6], and *FN1* [fibronectin 1]) are also represented in the prediction model of Lenz et al.; however, the latter requires the measurement of nearly 400 genes in fresh or frozen tumor specimens. Furthermore, our model is a robust predictor of outcomes in other cohorts of patients treated with CHOP or R-CHOP regimens, regardless of the type of diagnostic specimen obtained and the method of measurement used.³ Our prediction model is simple, robust, and applicable to routinely obtained diagnostic specimens that are formalin-fixed and paraffin-embedded.



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Drs. Alizadeh, Lossos, and Levy report holding a patent for the classification of patients with diffuse large-B-cell lymphoma

based on gene expression. No other potential conflict of interest relevant to this letter was reported.

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