

## Proposal and validation of a method to classify genetic subtypes of diffuse large B cell lymphoma

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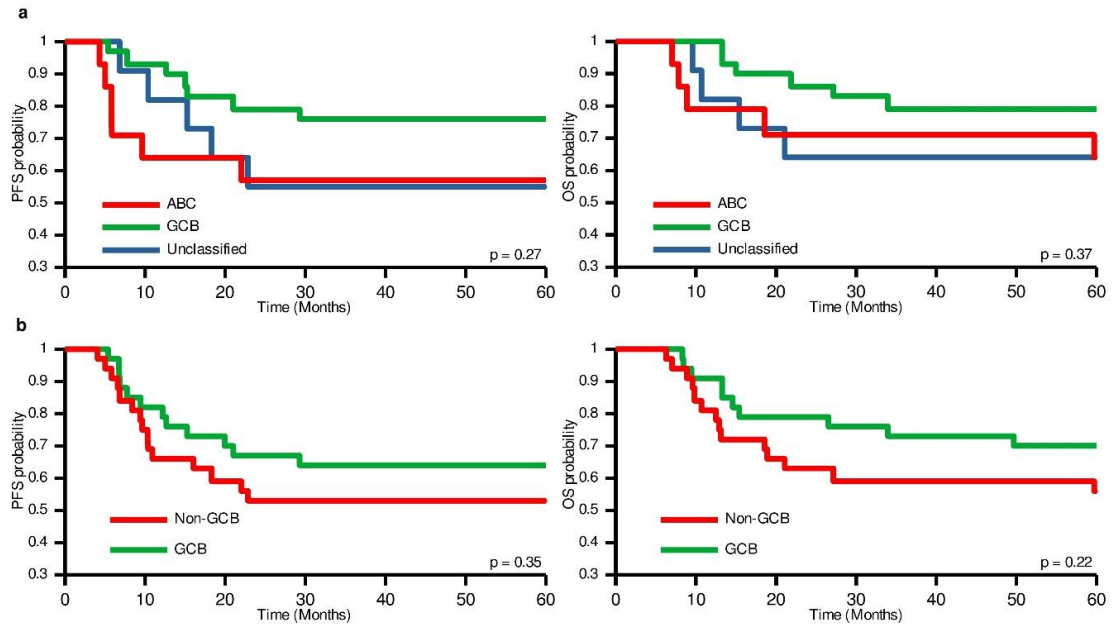
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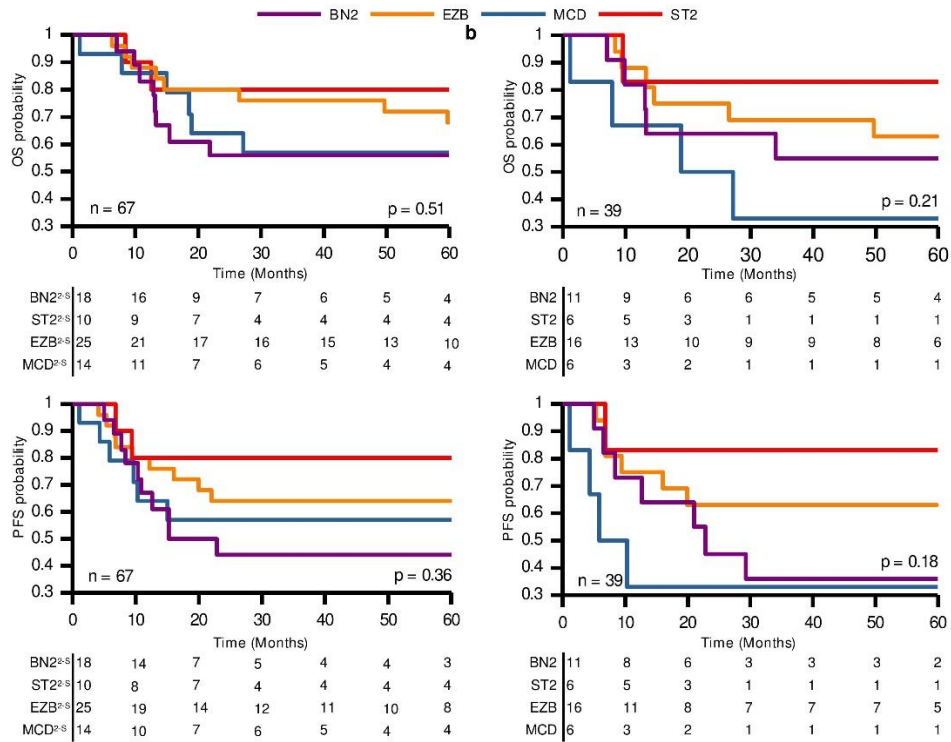
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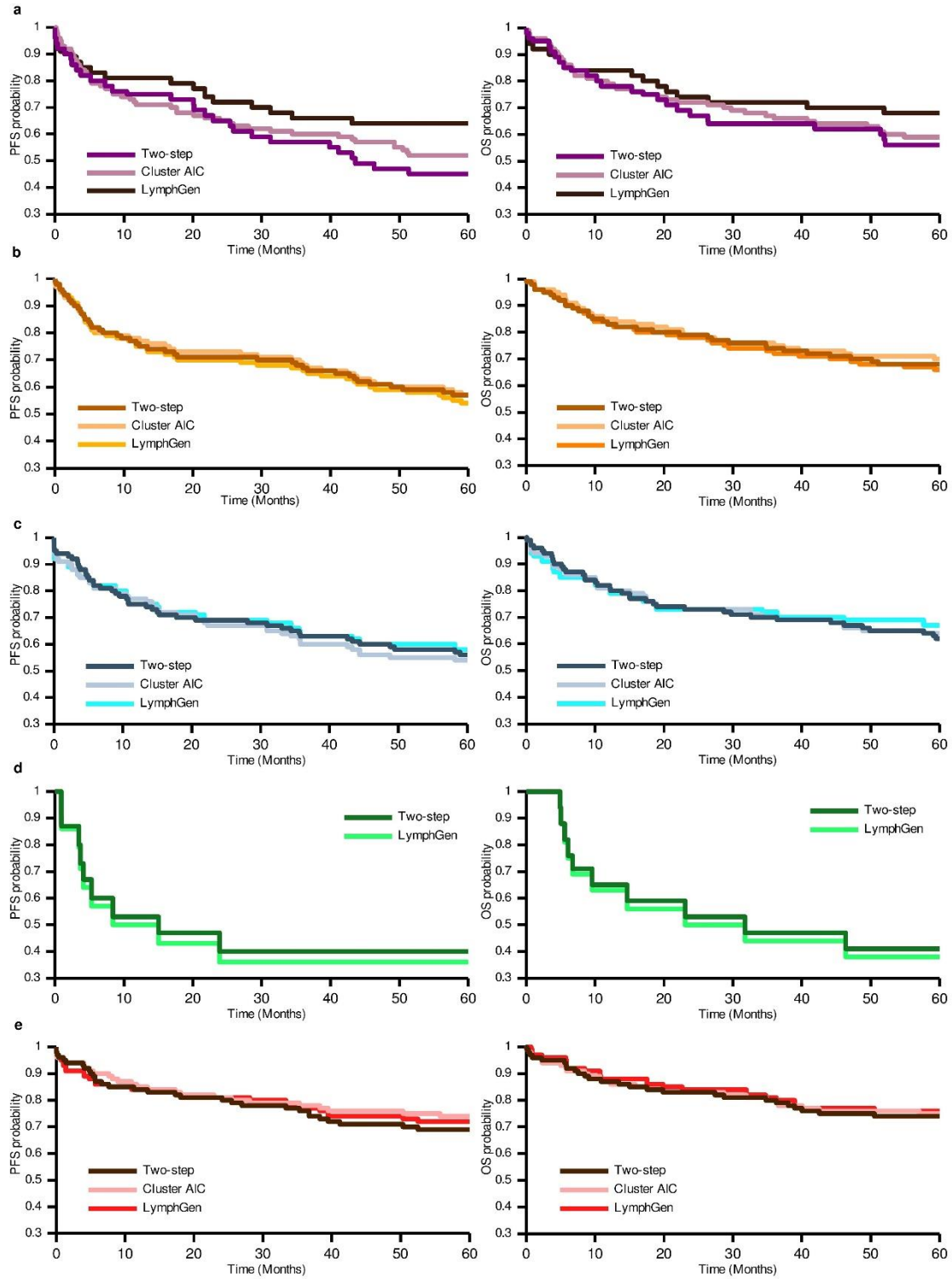
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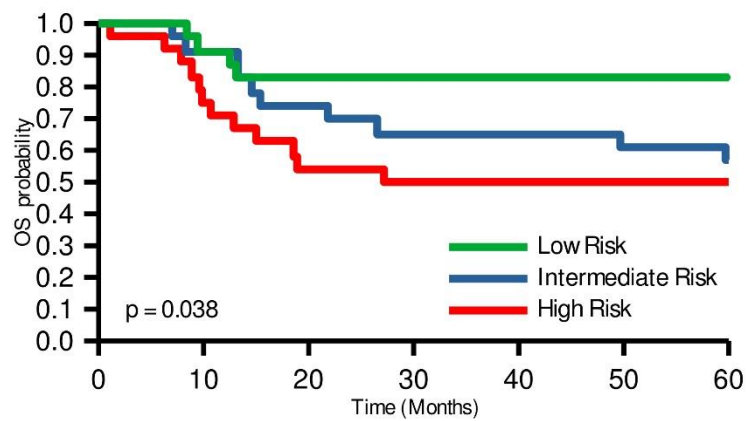
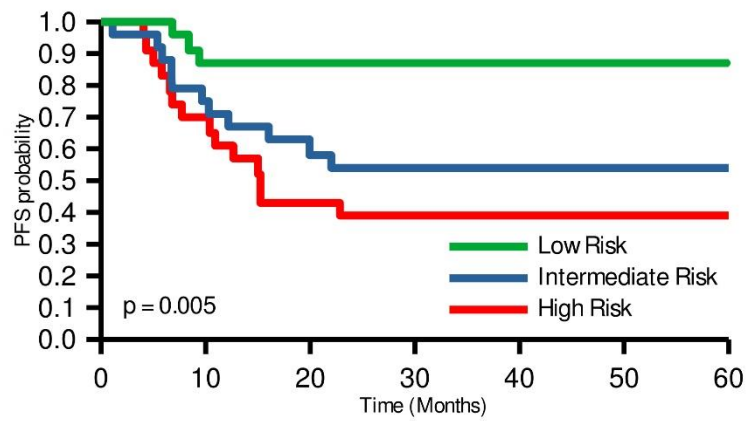
**Figure S1. Progression-free survival (PFS) and overall survival (OS) Kaplan-Meier analysis of cell-of-origin (COO) classification in the PdH cohort. A) Lymph2Cx classification; B) Hans classification. ABC: activated B-cell; GCB: germinal center B-cell.**



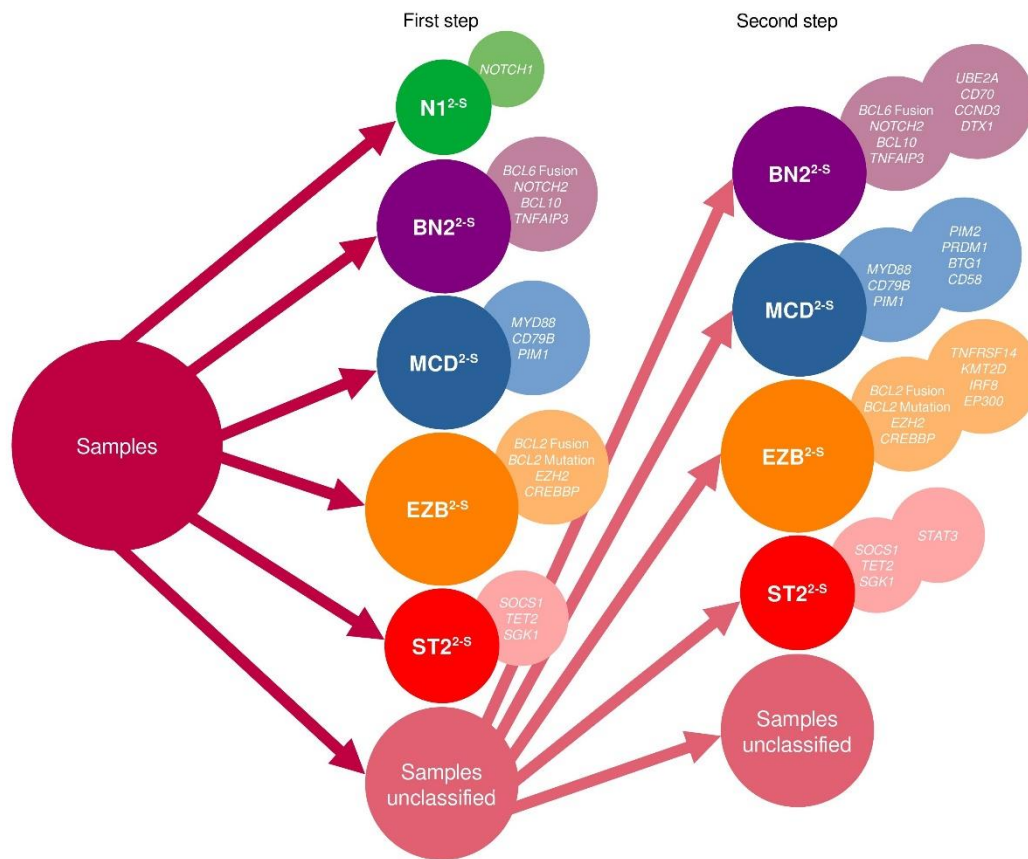
**Figure S2. Genetic subtypes from two-step and LymphGen methods in the PdH cohort.** Kaplan–Meier analysis of **A)** two-step and **B)** LymphGen genetic subtypes for overall survival (OS) and progression-free survival (PFS).



**Figure S3. Comparison between the classifiers.** Progression-free survival (PFS) and overall survival (OS) Kaplan-Meier analysis of **A)** BN2<sup>2-S</sup>/BN2/NOTCH2, **B)** EZB<sup>2-S</sup>/EZB/BCL2, **C)** MCD<sup>2-S</sup>/MCD/MYD88, **D)** N1<sup>2-S</sup>/N1 and **E)** ST2<sup>2-S</sup>/ST2/SGK1-TET2-SOCS1 in the HMRN cohort.



**Figure S4. Combinational model of IPI and genetic subtypes from two-step method in the PdH cohort.** Kaplan-Meier analysis of risk groups created by the Cox proportional-hazards multivariate model with IPI and genetic subtypes for progression-free survival (PFS) and overall survival (OS) status in the HMRN cohort and validated in the PdH cohort.



**Figure S5. Schematic representation of the two-step classifier for assigning subtypes to a sample.**