**Patients - eligibility**

For this analysis, adult patients (≥18years) with relapsed or refractory aggressive lymphoma (DLBCL, follicular lymphoma IIIB or transformed indolent lymphoma) were eligible. Patients with transformed lymphoma were limited to a quorum of 25%. Histology had to be proven by central pathology review, with CD20 negativity excluded.

Patients had to have had at least one prior line of treatment, excluding prior exposition to Obinutuzumab or Pixantrone. Primary refractoriness was not an exlusion criterion. Further inclusion criteria included: Eastern Cooperative Group (ECOG) performance status of ≤ 2, at least 1 measurable tumor lesion (>1.5 cm x >1.0 cm), adequate hematopoietic reserve (platelets ≥ 100.000/μl, absolute neutrophil count ≥ 1000/μl) as well as an appropriate liver (alanine aminotransferase (ALT) < 2.5 x upper limit of normal (ULN); aspartate aminotransferase (AST) < 2.5 x ULN, total bilirubin < 1.5 x ULN except Gilbert´s Syndrome) and renal function (calculated creatinine clearance > 30 mL/min). Pregnant or lactating women were excluded and, if applicable, effective birth control was mandatory.

**Central pathology and determination of Cell of origin**

A central review of all available samples was performed at a lymphoma reference laboratory (Institute of Pathology of the University of Würzburg), including thorough histological review. Gene expression profiling was performed to determine the Cell of origin (COO), if sufficient material was available. The COO was determined using the NanoString platform as previously described (21).

Formalin‐fixed and paraffin‐embedded (FFPE) -derived RNA samples were analysed for COO assignment using the NanoString nCounter FLEX gene expression profiling (GEP) system with DX enablement (Division of Translational Pathology, Gerhard-Domagk-Institute of Pathology, Münster University Hospital). The NanoString Lymphoma Subtyping Test (LST) algorithm is based on the multiplex Lymph2Cx GEP assay, providing the Linear Predictor Score (LPS) and the COO molecular subtype of DLBCL: germinal center B‑cell like (GCB), activated B-cell like (ABC), or Unclassified (22, 23). The LST CodeSet contains capture and reporter probes for 20 genes within the LST signature, including 7 genes overexpressed in GCB-DLBCL (*ASB13, ITPKB, MAML3, MME, MYBL1, S1PR2, SERPINA9*), 8 genes overexpressed in ABC‑DLBCL (*CCDC50, CREB3L2, CYB5R2, IRF4, LIMD1, PIM2, RAB7L1, TNFRSF13B*), and 5 housekeeping genes (*ISY1, R3HDM1, TRIM56, UBXN4, WDR55*). Total RNA was extracted using the Qiagen RNeasy FFPE Kit (Qiagen, cat. no. 73504), and sample quality/quantity assurance was assessed by spectrophotometry (NanoDrop, Thermo Fisher Scientific). The LST CodeSet was hybridized to 500 ng of total RNA for 18 hours at 65 °C on a thermal cycler. Hybridized RNA samples were loaded into the nCounter Prep Station for post‐hybridization processing. Expression of target mRNA was assessed with the nCounter Digital Analyzer.

Analyses were performed irrespective of whether primary DLBCL or transformed lymphoma had been diagnosed, however, sensitivity analyses were included for the entire cohort vs. the DLBCL-only cohort.