The prognosis of MYC translocation positive diffuse large B-cell lymphoma depends on the second hit

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Abstract

A proportion of MYC translocation positive diffuse large B-cell lymphomas (DLBCL) harbour a BCL2 and/or BCL6 translocation, known as double-hit DLBCL, and are clinically aggressive. It is unknown whether there are other genetic abnormalities that cooperate with MYC translocation and form double-hit DLBCL, and whether there is a difference in clinical outcome between the double-hit DLBCL and those with an isolated MYC translocation. We investigated TP53 gene mutations along with BCL2 and BCL6 translocations in a total of 234 cases of DLBCL, including 81 with MYC translocation. TP53 mutations were investigated by PCR and sequencing, while BCL2 and BCL6 translocation was studied by interphase fluorescence in situ hybridization. The majority of MYC translocation positive DLBCLs (60/81 = 74%) had at least one additional genetic hit. In MYC translocation positive DLBCL treated by R-CHOP (n = 67), TP53 mutation and BCL2, but not BCL6 translocation had an adverse effect on patient overall survival. In comparison with DLBCL with an isolated MYC translocation, cases with MYC/TP53 double-hits had the worst overall survival, followed by those with MYC/BCL2 double-hits. In MYC translocation negative DLBCL treated by R-CHOP (n = 101), TP53 mutation, BCL2 and BCL6 translocation had no impact on patient survival. The prognosis of MYC translocation positive DLBCL critically depends on the second hit, with TP53 mutations and BCL2 translocation contributing to an adverse prognosis. It is pivotal to investigate both TP53 mutations and BCL2 translocations in MYC translocation positive DLBCL, and to distinguish double-hit DLBCLs from those with an isolated MYC translocation.

Keywords: DLBCL; chromosome translocation; TP53 mutation; double-hit; overall survival

Introduction

Diffuse large B-cell lymphoma (DLBCL) represents 30–45% of adult cases of non-Hodgkin lymphoma (https://www.hmrn.org/statistics) [1], accounting for more than 80% of aggressive lymphomas. The addition of rituximab has significantly improved the treatment outcome of patients with DLBCL. Nonetheless,
a significant proportion of DLBCLs show primary treatment failure (~10%), partial response (~15%) or relapse after initial response (20–30%) to R-CHOP (rituximab, cyclophosphamide, doxorubicin, vincristine and prednisone), the current first line treatment for this malignancy [2]. A number of biomarkers have been investigated with the aim of predicting treatment outcome at diagnosis and identifying those that may benefit from novel therapeutic strategies, but only a few have proven to be clinically useful due to lack of reproducibility (immunohistochemistry-based markers) and/or difficulty of routine clinical application (molecular subtypes by gene expression profiling) on formalin-fixed paraffin-embedded diagnostic tissue biopsies [3–5]. Among the many biomarkers investigated, MYC chromosome translocation is widely accepted and used in routine clinical practice.

The MYC translocation occurs in 5–15% of DLBCL, and is usually associated with a complex pattern of genomic alterations [6–12]. A proportion (21–83%) of DLBCLs with MYC translocation also harbour a BCL2 and/or BCL6 translocation, known as ‘double-hit’ or ‘triple-hit’ lymphoma. Patients with ‘double-hit’ DLBCL commonly show aggressive clinical features and respond poorly to currently available treatments, with a median survival less than 1.5 years [6]. However, it remains controversial whether DLBCL with MYC single translocation has a different prognosis from that with MYC/BCL2 double translocation. For example, the recent studies by Cucuini et al [13], Aukema et al [6] and Valera et al [14] showed a similar poor overall survival between DLBCL with MYC single translocation and those with MYC double translocations. In contrast, the studies by Johnson et al, Green et al and Landsburg et al demonstrated no adverse impact of MYC single translocation in DLBCL, while cases with MYC/BCL2 double translocations had a very poor outcome [15–17]. Although the reasons underlying the discrepancies between these studies are unclear, potential factors that may account for the discrepancies could include the small numbers of cases investigated, variations in clinicopathological parameters (age, stage, international prognostic index [IPI]) and a variable presence of additional genetic changes such as TP53 mutation that modifies the prognostic value of MYC translocation.

MYC drives cell proliferation but also sensitizes cells to apoptotic stimuli, which provides a safeguard to prevent any potential MYC induced malignant transformation. The MYC mediated proapoptotic activity is largely through the activation of the p19(ARF)-MDM2-TP53 pathway and repression of the apoptosis inhibitor BCL2 [18,19]. There is extensive literature showing that MYC requires cooperating events to abrogate its proapoptotic activities to exert its full oncogenic potential, and both expression of BCL2 and loss of TP53 function cooperate with MYC translocation in lymphomagenesis [18–21]. In DLBCL, TP53 mutations are found in ~20% of cases and are significantly and independently associated with poor overall survival of both activated B-cell like (ABC) and germinal centre B-cell like (GCB) DLBCL treated with R-CHOP [22,23]. TP53 mutations have been reported in cases of DLBCL with MYC translocation [24,25], but their frequency in MYC translocation positive DLBCL and their combined clinical impact are unclear. In this study, we have investigated TP53 mutations and BCL2 translocations in a large cohort of DLBCL, and analysed their association and clinical impact in the presence and absence of MYC translocation.

Materials and Methods

Patients and tissue materials

A total of 234 cases of de novo DLBCL were investigated in this study. 168 cases were retrieved from the Haematological Malignancy Diagnostic Service (HMDS) at St James’s University Hospital, Leeds (n = 145) and Addenbrooke’s hospital, Cambridge (n = 23), based on the availability of lymphoma tissue specimens. 153 of these cases have been classified by cell of origin (COO) using the Illumina WG-DASL assay used in previous studies [7,26]. The remaining 66 cases were positive for MYC translocation by interphase fluorescence in situ hybridisation (FISH) and identified from five participating centres where the assessment of MYC translocation status is a part of the routine diagnostic workup of DLBCL [27]. The diagnosis in each case was established by two expert haematopathologists, and those defined as B-cell lymphoma, unclassifiable, with features intermediate between DLBCL and Burkitt lymphoma, in the 2008 WHO classification were included in this study [28]. Burkitt lymphoma, DLBCL potentially transformed from a low grade lymphoma, cases with HIV or primary CNS lymphoma were excluded from this study. All the laboratory investigations described below were based on the initial diagnostic lymphoma tissue specimens. Ethical guidelines were followed for the use of archival tissues for research with the approval of the ethics committees of the involved institutions.
Microdissection and DNA preparation

Haematoxylin and eosin slides were reviewed for all cases, and crude microdissection was performed where indicated to enrich tumour cells, ensuring that the tissue area containing >60% of tumour cells was used for DNA preparation. DNA was extracted using the QIAamp DNA Micro Kit (QIAGEN, Crawley, UK). The quality of the DNA samples was assessed by polymerase chain reaction (PCR) of variably sized genomic fragments [29], and those with successful amplifications of >300 bp were used for mutational screening.

PCR and Sanger sequencing

Mutations in TP53 coding exons 5–10, commonly targeted by somatic mutation in human cancer, were investigated by PCR and Sanger sequencing using primers and conditions detailed in supplementary material Table S1. In each case, sequence change was confirmed by at least two independent PCR and sequencing experiments. The somatic mutation was ascertained by excluding germline changes through SNP database search and analysis of DNA prepared from microdissected normal cells, where possible.

Interphase FISH

Chromosome translocations involving the MYC, BCL2 and BCL6 loci were investigated using dual-colour break-apart probes (Vysis/Abbott Laboratories, UK) [30]. For each probe, the mean plus three standard deviations of false positive signals in 100 nuclei from 8 to 10 reactive tonsils was used as the cut-off value for the diagnosis of chromosomal translocation. The cut-off value for MYC, BCL2 and BCL6 break-apart probes is very similar, all being <6%.

Statistical analyses

Rates of genetic alterations and molecular subtypes by COO classification were compared using difference-of-proportions tests. Survival analyses were performed using the Kaplan–Meier method with log-rank tests and by using the Cox proportional hazards model.

Results

We investigated a total of 234 cases of primary DLBCL, including 168 cases selected based on tissue availability, and 66 additional cases based on their positivity for MYC translocation. Among the 168 cases selected based on tissue availability, the frequencies of MYC (15/168 = 8.9%), BCL2 (30/168 = 17.8%) and BCL6 (49/167 = 29.3%) translocation and TP53 mutation (26/166 = 15.7%) were in line with those reported in the literature [6,22,23,31,32]. To understand the potential oncogenic cooperation of these genetic changes, we analysed associations across the entire patient group.

High frequencies of TP53 mutation and BCL2 translocation in MYC translocation positive DLBCL

The frequency of TP53 mutation was significantly higher in cases with MYC translocation than in those without the translocation (27/81 = 33.3% versus 23/151 = 15.2%, p = 0.001, Figure 1A,B). However, there was no significant difference in the frequency of TP53 mutation between DLBCL with an isolated MYC translocation and those with double translocations (MYC plus BCL2 or BCL6) (14/35 = 40% versus 13/46 = 28.3%, p = 0.38). Five cases (6% within the MYC translocation positive series) were found to have concurrent translocations of MYC, BCL2 and BCL6, and none of these had a TP53 mutation (Figure 1A). In addition, no differences in the spectrum of TP53 mutations were observed between DLBCL with MYC translocation and those without (supplementary material Figure S1).

The frequency of BCL2 translocation was also significantly higher in DLBCL with MYC translocation than in those without (36/81 = 44.4% versus 20/153 = 13.1%, p = 8.74 × 10−8, Figure 1B). In contrast, the frequency of BCL6 translocation was lower in DLBCL with MYC translocation than in those without (15/79 = 18.9% versus 46/152 = 30.0%, p = 0.065, Figure 1B).

In cases with MYC translocation, there was no evidence of correlation among TP53 mutation, BCL2 and BCL6 translocation (supplementary material Table S2). In cases without MYC translocation, there was a positive correlation between BCL2 translocation and TP53 mutation (p = 0.048), and a negative correlation between BCL2 and BCL6 translocation (p = 0.034) (supplementary material Table S2).

Among the 234 cases of DLBCL investigated, 153 had data on COO-classification by Illumina WG-DASL array from a previous study and 140 of these cases were MYC translocation negative [4]. We, thus, correlated COO subtypes with genetic abnormalities in cases without MYC translocation. As expected [33], BCL2 translocation was significantly associated with GCB-DLBCL (p = 0.004), although no significant association was seen between BCL6 translocation and COO subtype (p = 0.079, supplementary
material Table S2). There was no correlation between TP53 mutation and COO molecular subtype.

Distinct impact of TP53 mutations, BCL2 and BCL6 translocations on prognosis of MYC translocation positive DLBCL

Of the 81 MYC translocation positive DLBCLs investigated, 60 (74.1%) had at least one additional genetic abnormality, namely TP53 mutation, BCL2 or BCL6 translocation. Of these 60 cases, 18 had three abnormalities, including nine cases with MYC/BCL2 double translocation and TP53 mutation, four cases with MYC/BCL6 double translocation and TP53 mutation, and a further five cases with triple translocations (Figure 1A). The remaining 42 cases with a single additional genetic abnormality included 22 with BCL2 translocation, 14 with TP53 mutation, and six with BCL6 translocation (Figure 1A).

To investigate whether the prognosis of these MYC translocation positive DLBCLs was affected by the number and nature of additional genetic abnormalities, we performed a series of survival analyses. These were carried out exclusively on cases treated with R-CHOP or equivalent regimens with a curative intent, and included 67 cases with MYC translocation and 101 cases without MYC translocation.

We first focused on the MYC translocation positive DLBCL, subdivided according to the number (1 or 2) of additional genetic abnormalities regardless of their nature, and examined whether the number of additional genetic abnormalities impacted on patient survival. To our surprise, cases with one, but not those with two additional genetic abnormalities, showed a worse survival than those with an isolated MYC translocation. Such difference might be due to an insufficient number of the cases with two additional genetic abnormalities for comparison. Alternatively,
the findings suggest that the nature rather than the number of the additional genetic abnormalities may be more important in influencing the prognosis of MYC translocation positive DLBCL.

We next examined the survival of patients with MYC translocation positive DLBCL purely according to the status of TP53 mutation, BCL2 and BCL6 translocation. The MYC translocation positive DLBCL with TP53 mutation had a significantly worse overall survival than those without TP53 mutation by multivariate Cox regression analysis adjusted for age (p = 0.036, supplementary material Figure S2C). Similarly, MYC translocation positive DLBCL with BCL2 translocation showed a worse survival, albeit not statistically significant, than those lacking the translocation (supplementary material Figure S2A). In contrast, MYC translocation positive DLBCL with BCL6 translocation had a significantly better overall survival than those without BCL6 translocation by multivariate Cox regression analysis adjusted for age (p = 0.035, supplementary material Figure S2B). Despite that the reference subgroup in each of the above analyses comprised of mixed cases that included not only those with isolated MYC translocation but also cases with other second hit, the analyses, nonetheless, suggested that TP53 mutation and possibly BCL2, but not BCL6 translocation may have an adverse effect on patients survival. In view of this and the small number of cases with only MYC and BCL6 translocation, our subsequent analyses focused on TP53 mutation and BCL2 translocation.

We divided MYC translocation positive DLBCL into the following subgroups according to TP53 mutation and BCL2 translocation status: MYC/BCL2 double translocation with TP53 mutation, MYC single translocation with TP53 mutation, MYC/BCL2 double translocation, and isolated MYC translocation. In comparison with the subgroup with isolated MYC translocation, all other three subgroups had a significantly worse overall survival than by logrank test (Figure 2A). Interestingly, the patients with MYC/BCL2/TP53 triple hit and the cases with MYC/TP53 double-hit appeared to be separated from those with the MYC/BCL2 double-hit (Figure 2A). In view of these findings, we combined all cases with TP53 mutation irrespective of the BCL2 translocation status, and these cases had the worst overall survival (Figure 2B, supplementary material Table S3). Further univariate and multivariate Cox regression analyses adjusted for age confirmed the significant worse overall survival of patients with MYC/TP53 (n = 22, p = 0.0095 and p = 0.0059 respectively) and cases with MYC/BCL2 (n = 25, p = 0.03 and p = 0.019, respectively) double-hit in comparison with those with isolated MYC translocation (n = 20) Figure 2B, Table 1).

Figure 2. Impact of TP53 mutation and BCL2 translocation on overall survival of patients with MYC translocation positive DLBCL. (A) MYC translocation positive DLBCL are divided into four subgroups: MYC/BCL2 translocation/TP53 mutation, MYC translocation/TP53 mutation, MYC/BCL2 translocation, and MYC translocation only. The cases with the MYC/BCL2 TP53 triple-hit show the worst overall survival, followed by cases with the MYC/TP53 and those with the MYC/BCL2 double-hit. The significant difference in overall survival between cases with the MYC/BCL2 TP53 triple-hit and those with isolated MYC translocation is also shown by Cox proportional hazards regression adjusted for age. (B) The cases with TP53 mutation are combined together irrespective of their BCL2 translocation status. The cases with TP53 mutation show a worse overall survival than those with an isolated MYC translocation, being statistically significant by Cox regression model adjusted for age (p = 0.0059, Table 1). The cases with BCL2 translocation also show a significantly worse overall survival than those with isolated MYC translocation by Cox regression model adjusted for age (p = 0.019, Table 1).
Hospital, Leeds and Addenbrooke’s hospital, Cambridge, and 101 of these cases treated with R-CHOP had clinical follow up data. As expected, COO-classification clearly separated these cases into distinct prognostic groups with the ABC-DLBCL showing a worse overall survival by logrank test \((p = 0.011\), supplementary material Figure S3D). To our surprise, neither isolated \(TP53\) mutation nor single \(BCL2\) translocation had a significant impact on overall survival (supplementary material Figure S3A,C). \(BCL6\) translocation appeared to be associated with a worse overall survival; however, this was not statistically significant by Cox regression analysis after age adjustment (supplementary material Figure S3B).

**Discussion**

This is the first study combining chromosome translocations and \(TP53\) mutation analysis in a large cohort of DLBCL. We have demonstrated that \(MYC\) translocation positive DLBCL had a significantly higher frequency of \(TP53\) mutation and \(BCL2\) translocation [7], and that DLBCL with \(MYC\) translocation and \(TP53\) mutation had the worst overall survival, followed by cases with \(MYC/BCL2\) double-hits. These findings have significant implications for using these biomarkers in the prognostic evaluation of patients with DLBCL.

By investigating retrospectively a large cohort of \(MYC\) translocation positive DLBCL, we showed that the prognostic value of \(MYC\) translocation was critically influenced by the presence of the second hit, essentially its oncogenic cooperating events. The patients with \(MYC/TP53\) abnormalities irrespective of \(BCL2\) translocation status had a significantly worse overall survival than those with an isolated \(MYC\) translocation. The cases with \(MYC/BCL2\) double translocations but wild type \(TP53\) showed an intermediate overall survival, appearing better than those with \(MYC/TP53\) abnormalities, but worse than those with an isolated \(MYC\) translocation (Figure 2B).

These findings suggest that \(TP53\) mutation may have a more adverse impact on prognosis than \(BCL2\) translocation in \(MYC\) translocation positive DLBCL. The importance of the second hit in prognosis of \(MYC\) translocation positive DLBCL is further emphasized by the observation that cases with an isolated \(MYC\) translocation appeared to have an overall survival similar to those without \(MYC\) translocation (supplementary material Figure S4). No adverse impact of \(MYC\) single translocation in DLBCL was also reported in some previous studies [15–17], but not supported by others [6,13,14]. However, these previous studies did not investigate \(TP53\) mutation and it is unknown whether the discrepancy was caused by a variable presence of \(TP53\) mutation in cases with single \(MYC\) translocation among these studies. In view of the retrospective nature of the current study, it remains necessary to confirm these findings in a prospective study containing a large cohort of \(MYC\) translocation positive DLBCL.

Both \(TP53\) mutation and \(BCL2\) translocation are known to cooperate with \(MYC\) translocation in lymphomagenesis by impeding the proapoptotic activities of \(MYC\). In \(E\mu-Myc\) transgenic animals, lymphoma development requires the acquisition of additional genetic alterations, which commonly comprise of disruption of the p19\(^{ARF}\)-Mdm2-p53 pathway or overexpression of Bcl2 [34,35]. In addition, \(E\mu-Myc\) mice with lymphoma showing a loss of p53 function have a significantly worse survival than those with lymphoma overexpressing Bcl2 [36]. These findings together with our observations in this study indicate that there is a strong selection of genetic events that cooperates with \(MYC\) translocation during lymphoma development, and these cooperating events are a major determining factor in modulating the prognostic impact of \(MYC\) translocation in DLBCL.

The prognostic value of \(BCL6\) translocation in \(MYC\) translocation positive DLBCL is unclear. The majority of DLBCL with \(MYC\) and \(BCL6\) translocation also had \(BCL2\) translocation or \(TP53\) mutation, and the number of cases with only \(MYC\) and \(BCL6\) translocation is small for assessing the prognostic impact of \(BCL6\) translocation in \(MYC\) translocation

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**Table 1.** Impact of \(TP53\) mutation and \(BCL2\) translocation on overall survival of patients with \(MYC\) translocation positive DLBCL by Cox proportional hazards regression.

|                         | Univariate analysis* | Multivariate analysis adjusted for age |
|-------------------------|----------------------|--------------------------------------|
|                         | HR 95% CI  \(p\)     | HR 95% CI  \(p\)                     |
| \(MYC + BCL2\) translocation \((n=25)\) | 5.11 1.15-22.7 0.03 | 6.17 1.34-28.3 0.019 |
| \(MYC\) translocation + \(TP53\) mutation \(\text{irrespective of BCL2 translocation status}(n=22)\) | 7.26 1.62-32.5 0.0095 | 8.74 1.87-40.8 0.0059 |

*In comparison with DLBCL with isolated \(MYC\) translocation; HR: Hazard ratio; CI: confidence interval.
positive DLBCL. There was no association between MYC and BCL2 translocation in DLBCL. In addition, there is no direct evidence supporting critical oncogenic cooperation between MYC and BCL6 translocation in lymphoma development. Findings from the present and a previous study [37] suggest that BCL6 translocation appears to be associated with a better prognosis in MYC translocation positive DLBCL, although this differs from that observed by Pillai et al [38]. There are several potential reasons that might account for the discrepancy among these studies, and these include small numbers of cases with MYC/BCL6 translocation, difference/potential bias in case selection, variations in clinicopathological features (age, stage, IPI) and treatment, and potential differences in the genetic abnormalities associated with MYC translocation among these studies. Therefore, it is important to investigate the prognostic value of BCL6 translocation in MYC translocation positive DLBCL in a prospective study.

The term ‘double-hit’ lymphoma was originally used to describe aggressive DLBCL with MYC and BCL2 translocation, then subsequently extended to include those with MYC and BCL6 translocation. In light of the findings in this study and the discussion above, the term ‘double-hit’ lymphoma should be extended to include those with MYC translocation and TP53 mutation. Our data clearly highlight the prognostic significance of TP53 mutation, even more so than BCL2 translocation, in MYC translocation positive DLBCL. It is therefore pivotal to confirm these findings in a prospective study and investigate TP53 mutation status in routine clinical practice for cases of MYC translocation positive DLBCL, in addition to the current standard investigation for BCL2 translocation.

MYC and BCL2 translocations are commonly investigated by interphase FISH, while TP53 mutation can be readily screened for by PCR and Sanger sequencing, or a next generation sequencing-based approach. Alternatively, DLBCL with MYC/BCL2 or MYC/TP53 double-hit might be screened by combined immunohistochemistry for MYC, BCL2 and TP53 [15,16,23,31,32]. The challenges for such an immunohistochemistry-based approach are reproducibility, accurate assessment of the extent and percentage of staining positivity, and the identification of the best cut-off value for dichotomy between positive and negative staining results. In addition, combined MYC and BCL2 immunohistochemistry also identifies ~20% of DLBCL that show concurrent MYC and BCL2 protein expression, but no evidence of their involvement in translocation. This group of DLBCL appears to show an overall survival better than the cases with MYC/BCL2 translocation, but worse than those without these translocations [15,16,32], and thus, should be regarded as a separate prognostic group. In contrast, combined MYC and TP53 immunohistochemistry would under-detect DLBCL with MYC translocation and TP53 mutation, as a high proportion (~17%) of TP53 mutations such as frameshift and nonsense mutations result in a truncated protein product that is unlikely to be detectable by immunohistochemistry [23].

Our findings also highlight the importance of separating MYC translocation positive DLBCL from negative cases in biomarker validation, particularly the genetic events associated with MYC translocation, to avoid the confounding effect of MYC translocation. TP53 mutations have been shown to be significantly associated with poor overall survival in both ABC and GCB-DLBCL treated with R-CHOP [22,23]. In line with this, we also found a significant association of TP53 mutation with poor overall survival in DLBCL when MYC translocation positive cases were included (based on unselected cases from HMDS, Leeds /Addenbrooke’s Hospital). However, this significant association disappeared after excluding the MYC translocation positive cases, indicating a confounding effect of the translocation. Nonetheless, the number of MYC translocation negative cases investigated in this study is relatively small and the prognostic value of TP53 mutation in MYC translocation negative DLBCL remains to be elucidated.

In summary, we have shown that MYC translocation positive DLBCL has a significantly higher frequency of TP53 mutation and BCL2 translocation, and that the cases with MYC translocation and TP53 mutation had the worst overall survival, followed by cases with MYC/BCL2 double-hits. It is critical to investigate both TP53 mutation and BCL2 rearrangement in MYC translocation positive DLBCL, and to distinguish double-hit DLBCLs from those with an isolated MYC translocation in routine clinical practice.

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Author contributions

AC, SB, NZ, HL, SK, MW & YH collected and analyzed laboratory data; SC performed statistical analyses; NFG collected clinical data; LW assisted with sample preparation; JG, JB, MN, PF, BW, JWG, PW, HED, GAF, ER, PWMJ, AJW and AJ provided cases, diagnosis and clinical follow up data. MQD supervised and coordinated the study and wrote the manuscript. All authors have commented on the manuscript and approved its final version for submission. The authors declare no conflict of interest.

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SUPPLEMENTARY MATERIAL ON THE INTERNET

Additional Supporting Information may be found in the online version of this article.

Figure S1. Nature and distribution of TP53 mutations in primary DLBCL with and without MYC translocation. All mutations are reported in the COSMIC somatic mutation database, with the exception of c.672+1G>T, c.783-1G>A and R333C. There is no apparent difference in the nature and distribution of TP53 mutation found in primary DLBCL with and without MYC translocation. trans+ve: translocation positive; trans-ve: translocation negative; Mutations seen in the same case are indicated by the same colour scheme with the exception of those in black.

Figure S2. Impact of TP53 mutation, BCL2 and BCL6 translocation on overall survival of patients with MYC translocation positive DLBCL, trans+ve: translocation positive; trans-ve: translocation negative.

Figure S3. Impact of TP53 mutation, BCL2 and BCL6 translocation, and COO molecular subtype on the overall survival of patients with MYC translocation negative DLBCL. These cases are from the Haematological Malignancy Diagnostic Service (HMDS) at St James’s University Hospital, Leeds, and Addenbrooke’s hospital, Cambridge, retrieved based on the availability of lymphoma tissue specimens. All cases included in the survival analysis were treated with R-CHOP or a rituximab-containing equivalent regimen. trans+ve: translocation positive; trans-ve: translocation negative; COO: cell of origin

Figure S4. Comparison of overall survival between DLBCL with isolated MYC translocation (absence of TP53 mutation, BCL2 and BCL6 translocation) and those without MYC translocation. These cases are selected based on the availability of lymphoma tissue specimens from the Haematological Malignancy Diagnostic Service (HMDS) at St James’s University Hospital, Leeds, and Addenbrooke’s hospital, Cambridge, and all cases included in this figure were treated with R-CHOP or equivalent regimens. Dotted lines indicate 95% confidence intervals.