**Supplemental Materials:** 

A refined cell-of-origin classifier with targeted NGS and Artificial Intelligence shows robust predictive value in DLBCL

## Supplemental Data File with two worksheets.xlsx

QC Metrics	Acceptance Criteria
RNA integrity	28s:18s rRNA ratio (Agillent 4200 tape station) (RIN): from 2 to 5
Total number of reads (limit of detection, LoD)	> 5 million reads
Base Quality	> 80% of bases with QS above $> Q30$
Percent Mapped to coding	> 60%
Mean Insert size	130-160 (bp)
Coverage	> 10 ×
% Cluster passing	The percent cluster passing filter (Cluster $PF$ ) > 80%
% Reads passing filter	The percent reads passing filter (Reads PF) > 80%
Positive Run Control	Mean expression level of the Universal Human Control =220 $\pm$ 18 (Mean $\pm$ 2SD)
Limit of Blank (LoD)	< 1 ng at library preparation
% of duplicate reads	< 40%

Supplemental Table S1. RNA quality control metrics

Biomarker enriched in GCB or ABC	<b>P</b> value	
Higher frequency in GCB vs ABC		
BCL2 gene rearrangement	P < 0.0001	
MYC/BCL2 genetic double-hit	P = 0.009	
BCL6+ expression	P < 0.0001	
CD10+ expression	P < 0.0001	
CTLA-4+ cell % in T cells	P = 0.005	
GCET1+ expression	<i>P</i> < 0.0001	
PTEN gene deletion	P = 0.01	
CDKN2A p16+ expression	P = 0.014	
SSBP2+ expression	<i>P</i> < 0.0001	
Higher frequency in ABC vs GCB		
BCL2+ expression	P = 0.002	
BCL6 gene rearrangement	P = 0.002	
CXCR4+ expression	P = 0.014	
CD5+ expression	P < 0.0001	
CD37+ expression	P = 0.039	
FOXP1 high expression	P < 0.0001	
IgM+ expression	P < 0.0001	
JUNB high expression	P = 0.002	
MUM1+ expression	P < 0.0001	
MYC+/BCL2+ double expression	P = 0.006	
NFKB1 p50+ expression	P = 0.001	
CDKN1A/p21+ expression	P = 0.003	
PD-L1 positive expression in B cells	<i>P</i> < 0.0001	
High PD-L1+ cell % in B cells	P = 0.007	
PD-L1 expression (by PD-L1+%) in CD4+ T cells	P = 0.001	
PD-L1 expression (by PD-L1+%) in CD8+ T cells	<i>P</i> < 0.0001	
PD-L1 expression (by PD-L1+%) in NK cells	P = 0.001	
PRDM1+ expression	<i>P</i> < 0.0001	
STAT3 high expression	P = 0.001	

**Supplemental Table S2.** Biomarkers showing differential distribution in the new GCB/ABC groups defined in the current study

**Supplemental Figure S1.** A flow chart for the current study applying NGS and Artificial Intelligence (AI) in DLBCL model construction



(Top 7 contributing variables: *TP53* mutation and expression levels of *CDK8*, *LMO2*, *BCR*, *TGFBR2*, *CHD2*, & *ETS1*)