

**Table S2 - Features of BCL2 mutations in DLBCL**

<b>Features</b>	<b>BCL2 translocation -</b>	<b>BCL2 translocation +</b>
<b>Single bp substitutions</b>	113	955
<b>Deletions, duplications, insertions</b>	11	30
<b>Transitions</b>		
<b>G → A</b>	18 (16.5)	143 (15.6)
<b>A → G</b>	13 (11.9)	118 (12.9)
<b>T → C</b>	12 (9.9)	106 (10.3)
<b>C → T</b>	30 (25.8)	142 (14.5)
<b>Transversions</b>		
<b>C → G</b>	4 (3.4)	64 (6.6)
<b>C → A</b>	4 (3.4)	27 (2.8)
<b>G → T</b>	5 (4.6)	29 (3.2)
<b>G → C</b>	10 (9.2)	78 (8.5)
<b>A → T</b>	6 (5.5)	59 (6.4)
<b>A → C</b>	7 (6.4)	69 (7.5)
<b>T → G</b>	2 (1.6)	60 (5.9)
<b>T → A</b>	2 (1.6)	60 (5.9)
<b>Transitions/Transversions ratio</b>	1.95	1.14
<b>% Mutations at G/C</b>	63	51.1
<b>% Mutations at A/T</b>	37	48.9
<b>RGYW / WRCY BIAS<sup>1</sup></b>		
<b>G within RGYW / WRCY</b>	+	+
<b>any bp within RGYW / WRCY</b>	+	+
<b>DGYW / WRCH BIAS<sup>2</sup></b>		
<b>G within DGYW / WRCH</b>	+	+
<b>any bp within DGYW / WRCH</b>	+	+

The frequency of substitutions affecting each base was corrected for the base composition of the unmutated sequences (Gojobory et al, J Mol Evol, 1982;18:414-23). The bias at RGYW and DGYW motifs was determined by a binomial test.

<sup>1</sup>Neuberger MS et al, Immunol Rev 1998;162:107-116

<sup>2</sup>Rogozin IB, Diaz M J Immunol 2004;172:3382-84