Supplementary Materials

Oligonucleotide Binding to Non-B-DNA in *MYC*

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Supplementary table 1: Summary of BL subgroups [5-7]

Endemic	Sporadic	Immunodeficiency-associated
African children, 4-7 years Associated with EBV Involves: bones of the jaw and other facial bones, kidneys, gastrointestinal tract, ovaries, breast and other extranodal sites The break point in *MYC* is < 100 kb upstream from exon 1, and the break point in the *IgH* is in the joining segment.	Worldwide, children and adults Associated with EBV in 15-30% cases. Involves: abdomen (ileocecal area), ovaries, kidneys, omentum, Waldeyer's ring, breasts, lymph nodes, pleural effusions or ascites The break point in *MYC* is located between exon 1 and 2, and the break point in *IgH* is in the switch region.	Worldwide, young adults. Very often present with HIV, also occurs in immuno-suppressed transplant recipients. Involves: lymph nodes, bone marrow, extranodal sites most often in abdomen. The break point in *MYC* is between exon 1 and 2, and the break point in *IgH* is in the switch region.

Supplementary table 2: plasmids pMycNHE+ and pMycNHE- and non-B- DNA and target sequence, respectively[2].

Plasmid	Sequence 5′-3′
pMycNHE+	tctcctccccaccttccccaccctccccaccctcccc**ataagcgcccctcccgggttcccaaagcagagggcgtgggggaaaagaaaaaaga**tcct
pMycNHE-	gtgtacggtgggaggtctatataagcagagctggtttagtgaaccgtcagatccgctagcaaa**gcagagggcgtgggggaaaagaaaaaaga**tcca

[2] Non-B-DNA forming sequence is underlined and ON target sequence is marked with bold. pMycNHE- has a pEGFPLuc backbone. The target sequence is cloned downstream of CMV promoter. pMycNHE+ has a pBV-Luc backbone with inserted Myc promoter (pDel-1) [40]. The $NHEIII_1$ and the target sequence are cloned upstream of minP promoter.

CAGCAAATTGGGGGACTCAGTCTGGGTGGAAGGT|ATCCAATCCAGATAGCTGTGCATACATAATGCATAATA
CA

P0 ↱

TGACTCCCCCCAACAAA**T**GCAATGGGAGTTTATTCATAA|CGCGCTCTCCAAGTATACGTGGCAATGCGTTGC
TG

GGTTATTTTAATCATTCTAGGCATCGTTTTCCTCCTTATGCCTCTATCATTCCTCCCTATCTACACTAACATCCC

ACGCTCTGAACGCGCGCCCATTAATACCCTTCTTTCCTCCACT|CTCCCTGGGACTCTTGATCAAAGCGCGGC
CC

TTTCCCCAGCCTTAGCGAGGCGCCCTGCAGCCT|GGTACGCGCGTGG|CGTGGCGGTGGGCGCGCAGTGCG
TTCT

CGGTGTGGAGGGCAG|CTGTTCCGCCTGCGATGATTTATACTCACAGGACAAGGATGCGGTTTGTC|AAAC|A
GT

A|CTGCTA|CGGAGGAG|CAGCAGAGAAAGGG|A|GAGGGTTTGAG|AGGGAGCAAAAGAAAATGGTAGGCGCG
C

GTAGTTAATTCATGCGGCTC|TCTTACTCTGTTTACATCCTAGAGC|TAGAGTGCTC|GGCTGC|CCGGCTGAGT

C|TCCTCCCCACCTTCCCCACCCTCCCCACCCTCCCCATAAGCGCCCCTCCCGGGTTCCCAAAGCAGAGGG
CGTG

GGGGAAAAGAAAAAAGATCCTCTCT|CGCTAATCTCCGCCCACCGGCCCTTTATA|ATGCGAGGGT|CTGGAC
GG

P1 ↱

CTGAGG**A**CCCCCG|AGC|TGTGCT|GCTCGCGGCCGCCACCGCCGGGCCCCGGCC|GTCCCTGGCTCCCCT|
CCT

GCCTCGAGAAGGGCAGGGCTTCTCAGAGGCTTGGCGGGAAAAAGAACGGAGGGAGGGATCGCGCTGAGTA
TAAAA

P2 ↱

GCCGGTTTTCGGGGCTTTATCTA**A**CTCG

NNN = Tandem H-DNA or G-quadruplex forming sequence
| = Translocation point
↱ = promoter initiating site, base indicated in bold

Supplementary Figure 1. 127735336 to 127736236 Homo sapiens chromosome 8. [17,59]