False-negative rates for *MYC* fluorescence *in situ* hybridization probes in B-cell neoplasms

Rebecca L. King,[1] Ellen D. McPhail,[1] Reid G. Meyer,[2] George Vasmatzis,[3] Kathryn Pearce,[2] James B. Smadbeck,[3] Rhett P. Ketterling,[1,2] Stephanie A. Smoley,[2] Patricia T. Greipp,[2] Nicole L. Hoppman,[2] Jess F. Peterson[2] and Linda B. Baughn[2*]*

[1]Division of Hematopathology, Department of Laboratory Medicine and Pathology; [2]Division of Laboratory Genetics, Department of Laboratory Medicine and Pathology and [3]Center for Individualized Medicine-Biomarker Discovery, Mayo Clinic, Rochester, MN, USA

**JFP and LBB contributed equally to this work.*

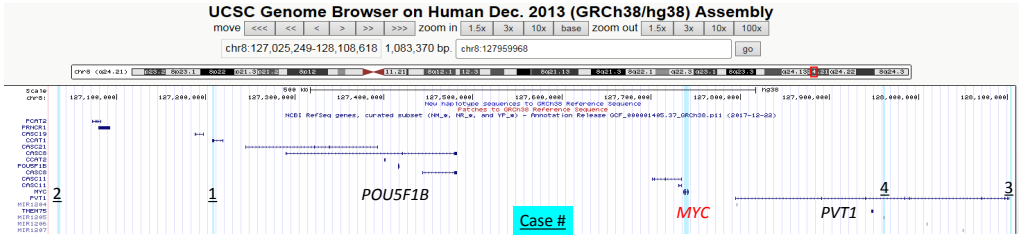
Correspondence: REBECCA L. KING.
rebecca.king98@gmail.com
doi:10.3324/haematol.2018.207290

Supplemental Data

MYC FISH laboratory reference ranges are as follows:
FFPET: abnormal cutoff for *MYC* BAP probe set: ≥7% of 100 tumor nuclei; abnormal cutoff for *MYC/IGH* D-FISH probe set: ≥5% of 100 tumor nuclei
Liquid/fresh specimens: abnormal cutoff for *MYC* BAP probe set: ≥6.5% of 200 interphase cells; abnormal cutoff for *MYC/IGH* D-FISH probe set: ≥0.6% of 500 interphase cells*.
*Cases in which the *MYC-IGH* D-FISH was positive, but below the level of sensitivity of the *MYC* BAP were excluded from analysis to ensure that false negatives due to sensitivity issues were not skewing our data.

Mate pair sequencing supplemental information:
DNA was processed using Illumina Nextera Mate Pair library preparation kit (Illumina, San Diego, CA) and sequenced on the Illumina HiSeq 2500 using 101-basepair reads and paired-end sequencing. Data was aligned to the reference genome (GRCh38) using BIMAv3, and abnormalities were identified and visualized using SVAtools and Ingenium, both in-house developed bioinformatics tools (12, 13).

Case #	Orientation of breakpoint relative to MYC	Distance from MYC	Breakpoint (GRCh38)
Case 1	centromeric of MYC within CCAT1	528513	127207556
Case 2	centromeric of MYC	700907	127035162
Case 3	telomeric of PVT1	361582	128103016
Case 4	telomeric of MYC within PVT1	218534	127959968



MYC footprint (NM_002467) chr8:127736069-127741434

Legend: Visualization of the genomic breakpoints near the *MYC* gene. The breakpoints (in GRCh38) near the *MYC* gene of each of the four cases with mate pair data are indicated. Breakpoints for each case are visualized in the UCSC genome browser as a teal colored curtain. The *MYC* gene is also highlighted in teal.