ITALIA

Empowering Personalized Cancer Treatment

MLL Break Apart DNA-FISH Probe

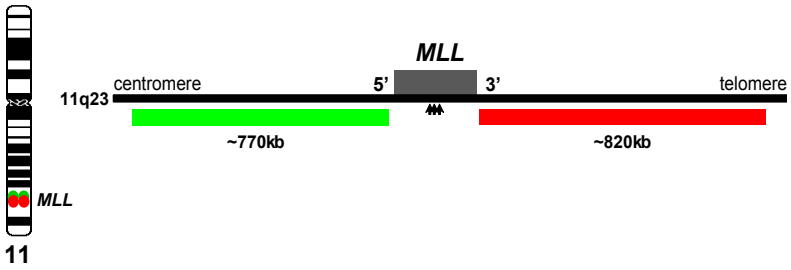
Two Color, Break Apart Probe CE

Ref: 11-002

MLL Break Apart

Intended Use

The *MLL* Break Apart probe is designed to detect the translocation involving the *MLL* gene on chromosome 11q23 using fluorescence *in situ* hybridization (FISH). At least 104 translocation partner genes have been identified.[1] Translocation of *MLL* is found in ~3-10% of acute lymphoblastic leukemia (ALL) cases, and in ~8-10% of acute myeloid leukemia (AML) cases, and is prognostically relevant in these leukemias.[2,3] However, the prognostic implication is dependent on the age and phenotype of the leukemia. *MLL* rearrangement has been observed in ~80% of infant ALL cases and is associated with a high risk in such cases and requires aggressive treatment. In AML, the prognosis is intermediate regardless of age. *MLL* translocations are also found in ~25% of patients with therapy-related leukemias, particularly following treatment with DNA topoisomerase II inhibitors and the prognosis in such patients is poor.[2,3] In addition to translocations, deletions of 3' *MLL* and amplification of *MLL* also occurs in a subset of ALL and AML cases.[4,5]



Schematic of the *MLL* Break Apart DNA-FISH Probe:

Horizontal red and green bars indicate the region covered by the probe (approximate to scale, NCBI Build 36.1/Hg18/2006). Breakpoints in *MLL* span an 8 kb region between exons 5 to 11 (arrows). The directly labeled 5' *MLL* (green) and 3' *MLL* (red) probes flank the *MLL* gene and can detect translocations, amplifications, and 3' *MLL* deletions.

Signal Interpretation

In normal diploid metaphase chromosomes and interphase nuclei, the probe generates two fusion signals (red/green or yellow) corresponding to the two normal homologous chromosomes 11 (Figure 1). In cells with chromosomal rearrangement involving the *MLL* gene, the most commonly observed pattern is one fusion, representing the normal chromosome 11, and a single red and green signal, representing the derivative chromosomes (Figure 2). Amplifications, 3' *MLL* deletions, additional copies of chromosome 11, unbalanced translocations, or multiple copies of derivatives may result in variant signal patterns and these should be confirmed by metaphase chromosome analysis whenever possible.[4,5]

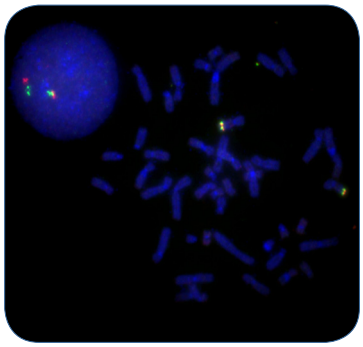


Figure 1: Normal diploid metaphase and interphase nucleus (from normal peripheral blood specimen) with 2 fusion signals (red/green or yellow).

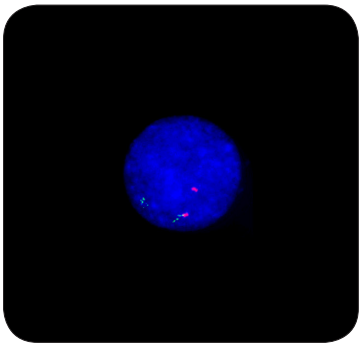


Figure 2: Interphase nuclei with 1 fusion (red/green or yellow), 1 red (3' *MLL*), and 1 green (5' *MLL*) signals.

References

1. Meyer, C., et al., Leukemia, 2009. 23: 1490-9.
2. Coenen, E.A., et al., Blood, 2011. 117(26): 7102-11.
3. Chowdhury, T., et al. Blood Cells Mol Dis, 2008. 40:192-199.
4. Barber, K. E., et al. Genes Chromosomes Cancer, 2001. 41:226-271.
5. Andersen, M. K., et al. Genes Chromosomes Cancer, 2001. 31:33-41.

Fluorescence Microscopy Filter Requirements

Fluorophore	Excitation $_{max}$	Emission $_{max}$
Green	496 nm	520 nm
Red	580 nm	603 nm
DAPI	360 nm	460 nm

Instructions for use are available at www.cancergeneticsitalia.com

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