XL ABL1 BA

Break Apart Probe

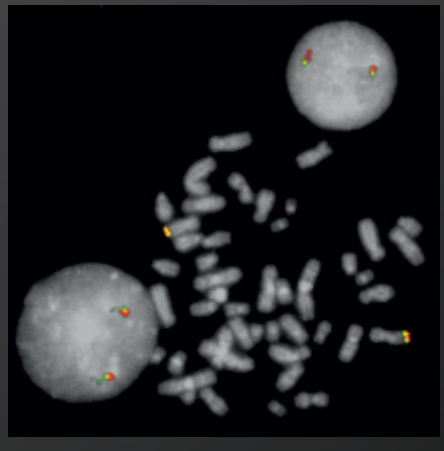
Order No.:
D-5148-100-OG

Description

XL ABL1 BA is designed as a break apart probe. The orange labeled probe hybridizes distal to the ABL1 gene region at 9q34.1 and extends into the gene up to intron 3, the green labeled probe hybridizes proximal to ABL1 and extends into the gene up to intron 1 (GRCh37/hg19).

Clinical Details

Acute lymphoblastic leukemia (ALL) is the most common malignancy in children with a prevalence of approximately 1:1500. Children with Down syndrome have a 10- to 20-fold increased risk of developing acute leukemia (B-cell precursor-ALL and acute myeloid leukemia, particularly acute megakaryoblastic leukemia). In 2017, the WHO recognized BCR-ABL1-like ALL, a subtype of B-lymphoblastic leukemia/lymphoma, as new entity. BCR-ABL1-like ALL, also known as Philadelphia chromosome (Ph)-like ALL, is found in 10 - 20 % of childhood and in 20 - 30 % of all adult B-cell dependent ALL cases. BCR-ABL1-like ALL is characterized by a gene expression profile sharing significant overlap with that of Ph-positive (Ph+) ALL. In contrast to Ph+ ALL, defined by the presence of the BCR-ABL1 fusion resulting from t(9;22)(q34;q11), BCR-ABL1-like cases include a variety of genomic alterations enhancing kinase and cytokine receptor signaling. Prominent genes involved in the pathogenesis of BCR-ABL1-like ALL are CRLF2, EPOR, JAK2, ABL1, ABL2, CSF1R and PDGFRB. The already known heterogenous 5' fusion partners of ABL1 are CENPC, ETV6, FOXP1, LSM14A, NUP153, NUP214, RANBP2, RCSD1, SFPQ, SNX1, SNX2, SPTAN1 and ZMIZ1. The kinase domain of ABL1 is present in all identified chimeric fusion proteins.



XL ABL1 BA hybridized to lymphocytes. Two normal interphases and one metaphase are shown.

Clinical Applications

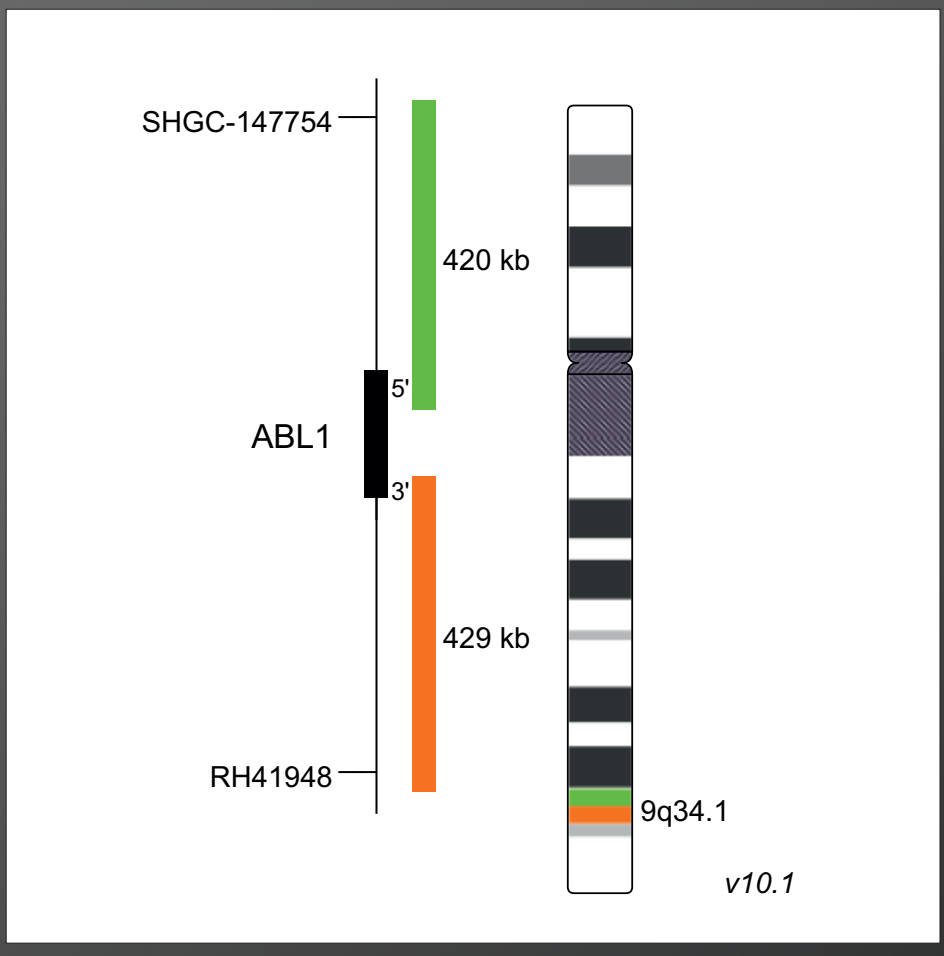
- ALL
- AML
- CML/MPN

Literature

- Tasian et al (2017) Blood 130:2064-2072
- Conant and Czuchlewski (2019) Int J Lab Hematol 41 Suppl 1:126-130
- Jain and Abraham (2019) Arch Pathol Lab Med:doi:10.5858/arpa.2019-0194-RA

FACTSHEET

MetaSystems
Probes



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Normal cell: Two green-orange colocalization/fusion signals (2GO).	
Aberrant Cell (typical results): One green-orange colocalization/fusion signal (1GO), one separate green (1G) and orange (1O) signal each resulting from a chromosome break in the respective locus.	

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