XL TCL1 BA

Break Apart Probe

Order No.:
D-5142-100-OG

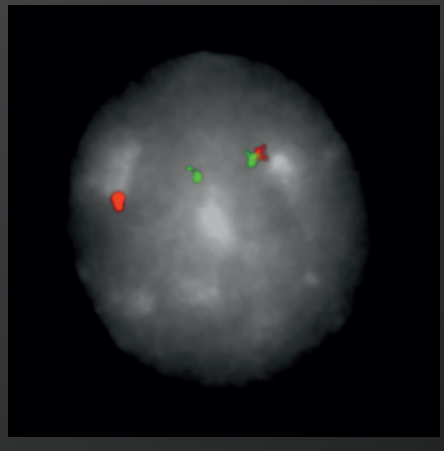
Description

XL TCL1 BA consists of an orange-labeled probe hybridizing proximal to the TCL1A/TCL1B gene region at 14q32.1 and a green-labeled probe hybridizing distal to the TCL1A/TCL1B gene region at 14q32.1-14q32.2.

Clinical Details

The gene TCL1A (TCL1 family AKT coactivator A, previously known as T-cell leukaemia/lymphoma 1A), has been described first in the early 1990s. It belongs to the TCL1 gene family including TCL1A (14q32.13), TCL1B (14q32.13) and MTCP1 (Xq28). Physiologically, the TCL1-encoded protein is expressed in fetal tissues and during early developmental stages of lymphocytes. It regulates many proteins responsible for cellular proliferation, survival and epigenetic modifications through multiple signalling pathways.

Dysregulated TCL1 expression levels have been detected in chronic lymphocytic leukaemia (CLL), various lymphomas and in T-cell prolymphocytic leukaemia (T-PLL). In T-cells, TCL1 dysregulation is caused by chromosomal rearrangement events bringing TCL1 under the control of T-cell receptor (TCR) enhancer elements. Two distinct breakpoint clusters have been described, which are located on both sides of a 160kb region flanking the TCL1A/TCL1B/TCL6 gene cluster. The rearrangements leading to TCL1A translocations with TCRα/TCRδ and TCRβ gene loci have been characterized precisely. The underlying chromosomal rearrangements are inv(14)(q11q32), being the most common aberration, t(14;14)(q11;q32.1) and t(7;14)(q35;q32.1). Phage display technology- and structure-based drug design approaches are used to target TCL1, due to its major role in the activation of different survival and proliferation maintaining pathways.



XL TCL1 BA hybridized to lymphocytes. One aberrant interphase nucleus with one fusion signal, and one separate orange and green signal is shown, representing a rearrangement with involvement of the TCL1 gene cluster.

Clinical Applications

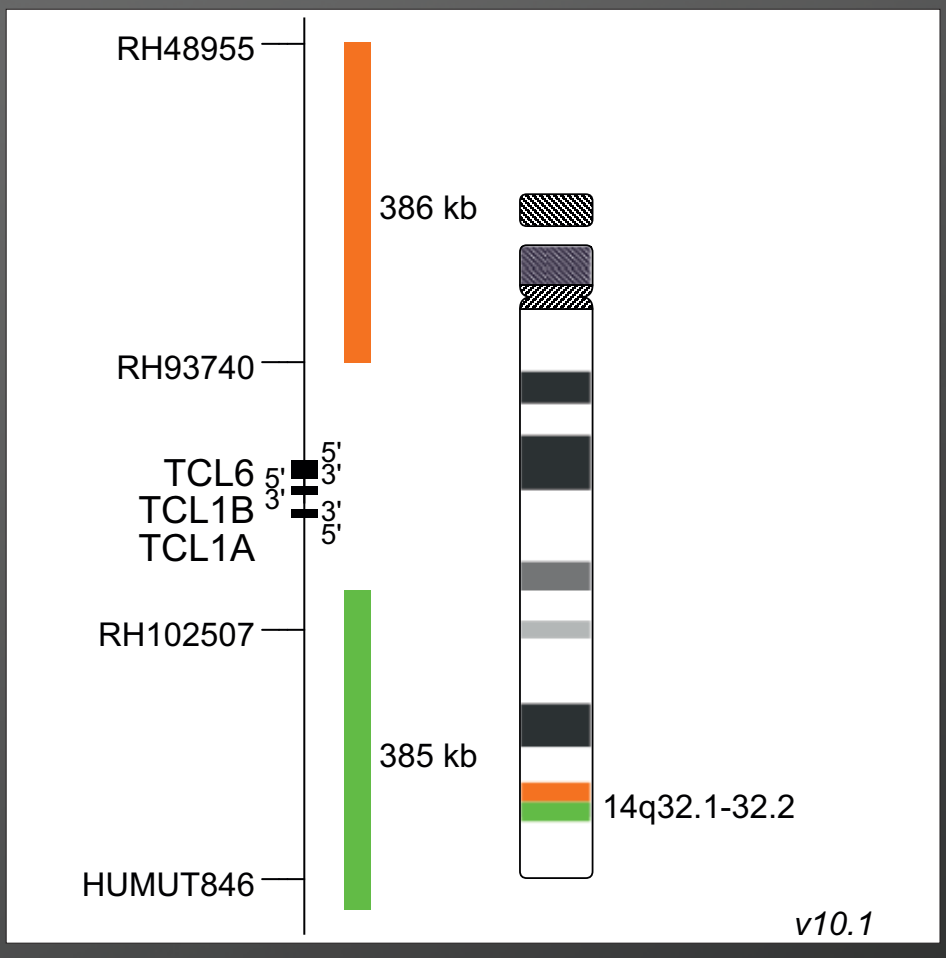
- T-PLL

Literature

- Virgilio et al (1994) PNAS 91: 12530-12534
- Saitou et al (2000) Oncogene 19: 2796-2802
- Paduano et al (2018) Front Oncol doi:10.3389/fonc.2018.00317

FACTSHEET

MetaSystems
Probes



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.	

MetaSystems Probes

EUROPE

Germany, Altlussheim
info@metasystems-probes.com

Italy, Milano
info@metasystems-italy.com

AMERICAS

USA, Medford
info@metasystems.org

Argentina, Buenos Aires
info@metasystems-latam.com

ASIA & INDIA

China, Hong Kong
info@metasystems-asia.com

China, Taizhou
info@metasystems-china.com

India, Bangalore
info@metasystems-india.com

Document No. PFS-MP-D5142-EN-2022-05-02-W

FACTSHEET

MetaSystems Probes

info@metasystems-probes.com
www.metasystems-probes.com