ZytoLight® SPEC NUP214 Dual Color Break Apart Probe

CE IVD

Background

The ZytoLight® SPEC NUP214 Dual Color Break Apart Probe is designed for the detection of translocations involving the chromosomal region 9q34.13 harboring the NUP214 (nucleoporin 214, a.k.a. CAN, CAIN) gene.

Rearrangements of the NUP214 gene have been implicated in the pathogenesis of several types of hematologic malignancies, including T-cell acute lymphoblastic leukemia (T-ALL), acute myeloid leukemia (AML), and also myelodysplastic syndrome (MDS). Several fusion partners have been identified for NUP214. The most common are the DEK, SET, and the tyrosine kinase encoding gene ABL1.

The translocation t(6;9)(p22.3;q34.1) results in a DEK-NUP214 fusion and defines a specific subcategory of AML according to the World Health Organization 2008 classification.

The SET-NUP214 fusion is associated with T-ALL, less frequently with AML, and acute undifferentiated leukemia and can result from either a translocation or a deletion.

NUP214-ABL1 fusions are exclusively associated with T-ALL patients. These patients may be considered for a targeted therapy with specific tyrosine kinase inhibitors. The fusion is often located on amplified episomes and is cytogenetically cryptic but can be detected by FISH.

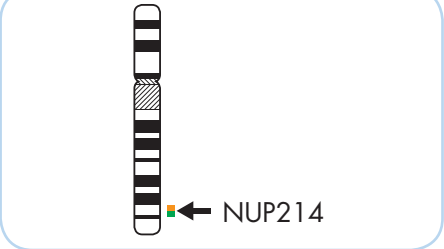
Malignancies with NUP214 rearrangements are associated with a poor prognosis indicating the usefulness of NUP214 also as a prognostic biomarker.

References
Fahrenkrog B (2014) New J Sci 2014: 468306.
Takeda A & Yaseen NR (2014) Semin Cancer Biol 27: 3-10.
von Lindern M, et al. (1992) Baillieres Clin Haematol 5: 857-79.
Zhou MH & Yang QM (2014) Oncol Lett 8: 959-62.

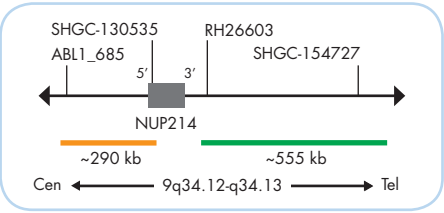
Probe Description

The ZytoLight® SPEC NUP214 Dual Color Break Apart Probe is composed of:

- ZyGreen (excitation 503 nm/emission 528 nm) labeled polynucleotides (~10.0 ng/µl), which target sequences mapping in 9q34.13** (chr9:134,153,663-134,706,700) distal to the NUP214 breakpoint region.
- ZyOrange (excitation 547 nm/emission 572 nm) labeled polynucleotides (~4.5 ng/µl), which target sequences mapping in 9q34.12-q34.13** (chr9:133,739,333-134,028,546) proximal to the NUP214 breakpoint region.
- Formamid based hybridization buffer



Ideogram of chromosome 9 indicating the hybridization locations.

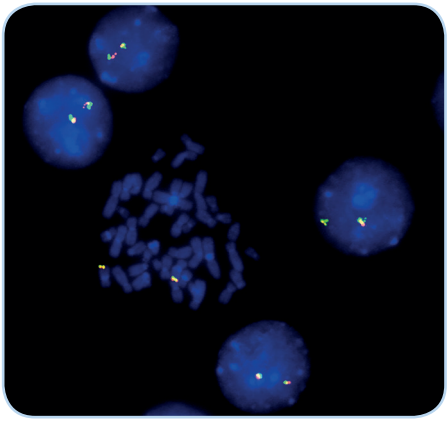


SPEC NUP214 Probe map (not to scale).

Results

In an interphase nucleus lacking a rearrangement involving the 9q34.12-q34.13 band, two orange/green fusion signals are expected representing two normal (non-rearranged) 9q34.12-q34.13 loci. A signal pattern consisting of one orange/green fusion signal, one orange signal, and a separate green signal indicates one normal 9q34.12-q34.13 locus and one 9q34.12-q34.13 locus affected by a translocation.

Isolated green signals are the result of deletions proximal to the NUP214 breakpoint region.



SPEC NUP214 Dual Color Break Apart Probe hybridized to normal interphase cells as indicated by two orange/green fusion signals per nucleus and to metaphase chromosomes of a normal cell.

Prod. No.	Product	Label	Tests* (Volume)
Z-2265-50	ZytoLight SPEC NUP214 Dual Color Break Apart Probe CE IVD	●/●	5 (50 µl)
Related Products			
Z-2099-20	ZytoLight FISH-Cytology Implementation Kit CE IVD Incl. Cytology Pepsin Solution, 4 ml; 20x Wash Buffer TBS, 50 ml; 10x $MgCl_2$, 50 ml; 10x PBS, 50 ml; Cytology Stringency Wash Buffer SSC, 500 ml; Cytology Wash Buffer SSC, 500 ml; DAPI/DuraTect-Solution, 0.8 ml		20

** Using 10 µl probe solution per test. IVD labeled products are only available in certain countries. All other countries research use only! Please contact your local dealer for more information.*

***According to Human Genome Assembly GRCh37/hg19*