

# ZytoLight® SPEC DiGeorge Triple Color Probe



## Background

The ZytoLight® SPEC DiGeorge Triple Color Probe is designed to detect deletions affecting the chromosomal regions 22q11.21 harboring the genes HIRA (a.k.a. TUPLE1) and CRKL as well as 22q11.21-q11.22 harboring the MAPK1 (a.k.a. PRKM2, ERK) gene.

The 22q11.2 deletion syndrome (22q11.2DS), also known as velocardio-facial syndrome (VCFS) and DiGeorge syndrome, is a genetic disorder caused by hemizygous microdeletions on chromosome 22q11.2, with population prevalence of about 1 in 4,000 births. The characteristic phenotype of 22q11.2DS includes cardiac defects, immune deficiency, growth restriction, and deficits in cognitive abilities.

The 22q11.2 deletion usually occurs by meiotic non-allelic homologous recombination events between low copy repeats on chromosome 22q11.2 termed LCR22. There are eight LCR22s that span the 22q11.2 region termed LCR22A through LCR22H. The majority (90%) of 22q11.2DS patients show a recurrent 3 Mb deletion between LCR22A and LCR22D while 8% harbor a nested 1.5 Mb deletion (LCR22A-B). Some rare atypical deletions of shorter size and in variable locations have also been reported (e.g., LCR22B-D and LCR22C-D). Classic FISH probes for the detection of 22q11.2DS target the HIRA gene mapping to the LCR22A-B region, and thus, miss deletions that occur outside this region. The DiGeorge Triple Color Probe additionally targets CRKL that maps to the LCR22C-D region allowing the detection of rare deletions.

### References

- Ben-Shachar S, et al. (2008) Am J Hum Genet 82: 214-21.
- Burnside RD (2015) Cytogenet Genome Res 146: 89-99.
- Michaelovsky E, et al. (2012) BMC Med Genet 13: 122.
- Morrow BE, et al. (2018) Am J Med Genet A 176: 2070-81.
- Scambler PJ, et al. (1991) Genomics 10: 201-6.

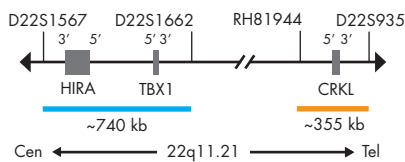
## Probe Description

The ZytoLight® SPEC DiGeorge Triple Color Probe is composed of:

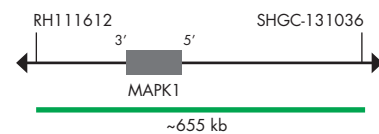
- ZyBlue (excitation 418 nm/emission 467 nm) labeled polynucleotides (~37 ng/μl), which target sequences mapping in 22q11.21\*\* (chr22:19,191,435-19,932,689) harboring the HIRA gene region.
- ZyOrange (excitation 547 nm/emission 572 nm) labeled polynucleotides (~4.5 ng/μl), which target sequences mapping in 22q11.21\*\* (chr22:21,096,895-21,454,102) harboring the CRKL gene region.
- ZyGreen (excitation 503 nm/emission 528 nm) labeled polynucleotides (~10 ng/μl), which target sequences mapping in 22q11.21-q11.22\*\* (chr22:21,931,816-22,587,439) harboring the MAPK1 gene region.
- Formamide based hybridization buffer



Ideogram of chromosome 22 indicating the hybridization locations.



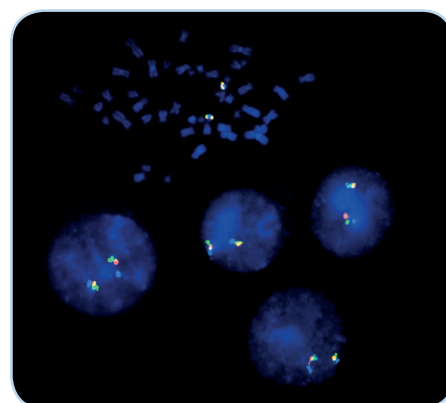
SPEC HIRA/SPEC CRKL Probe map (not to scale).



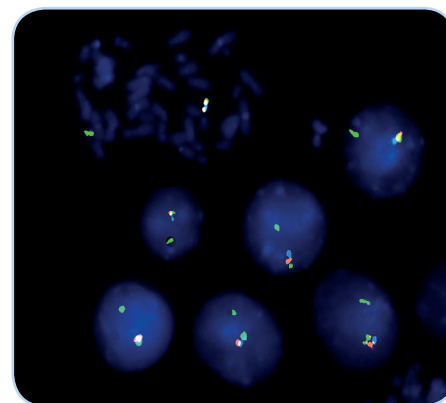
SPEC MAPK1 Probe map (not to scale).

## Results

In a normal interphase nucleus, two blue, two orange, and two green signals are expected. In a cell with deletion of the HIRA and/or the CRKL gene locus, a reduced number of blue and/or orange signals will be observed, respectively. In a cell with deletion of the MAPK1 gene locus, a reduced number of green signals will be observed.



SPEC DiGeorge Triple Color Probe hybridized to normal interphase cells as indicated by two orange, two green, and two blue signals and to metaphase chromosomes of a normal cell.



Lymphocytes and metaphase chromosomes from a DiGeorge syndrome case showing a HIRA/CRKL deletion as indicated by the loss of one blue and one orange signal.

Kindly provided by Dr. Liehr, Jena, Germany.

Prod. No.	Product	Label	Tests* (Volume)
Z-2289-50	ZytoLight SPEC DiGeorge Triple Color Probe CE IVD	●/●/●	5 (50 μl)
<b>Related Products</b>			
Z-2099-20	ZytoLight FISH-Cytology Implementation Kit CE IVD Incl. Cytology Pepsin Solution, 4 ml; 20x Wash Buffer TBS, 50 ml; 10x MgCl <sub>2</sub> , 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