digitalMLPA™ NXtec™

D006 Multiple Myeloma

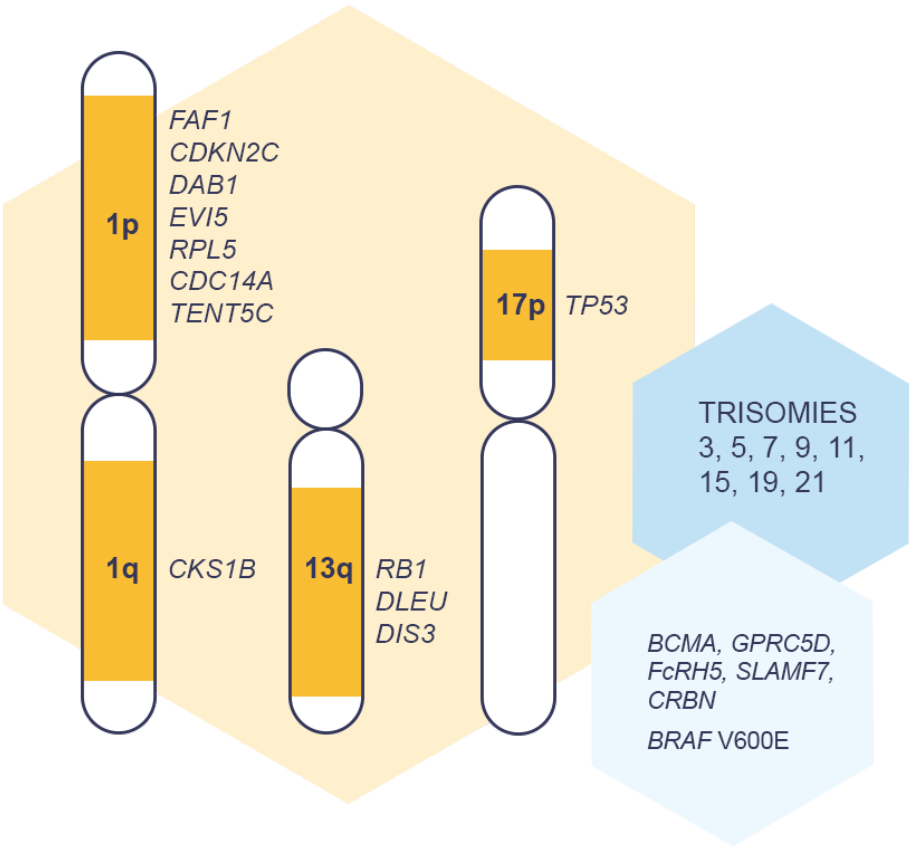
MRC Holland

✓ **Multiple Myeloma-copy number altered genes, regions and trisomies** targeted
✓ **Only 20 ng of DNA input** needed
✓ **Quick turnaround** of 48-72 hours

Multiple myeloma (MM) is a blood cancer characterized by malignant proliferation of monoclonal plasma cells. Despite common histological and morphological features, MM harbors an enormous underlying genetic complexity. Recent progress in molecular cytogenetics has led to a better understanding of multiple myeloma and provided a rationale for its molecular subclassification, spurring a demand for assays with a large genomic coverage. Using MRC Holland's digitalMLPA technology, a NXtec panel was created for targeted yet broad molecular MM copy number (CN) subtyping: **NXtec D006 Multiple Myeloma**.

This panel is the perfect time-saving complement to next generation sequencing (NGS).

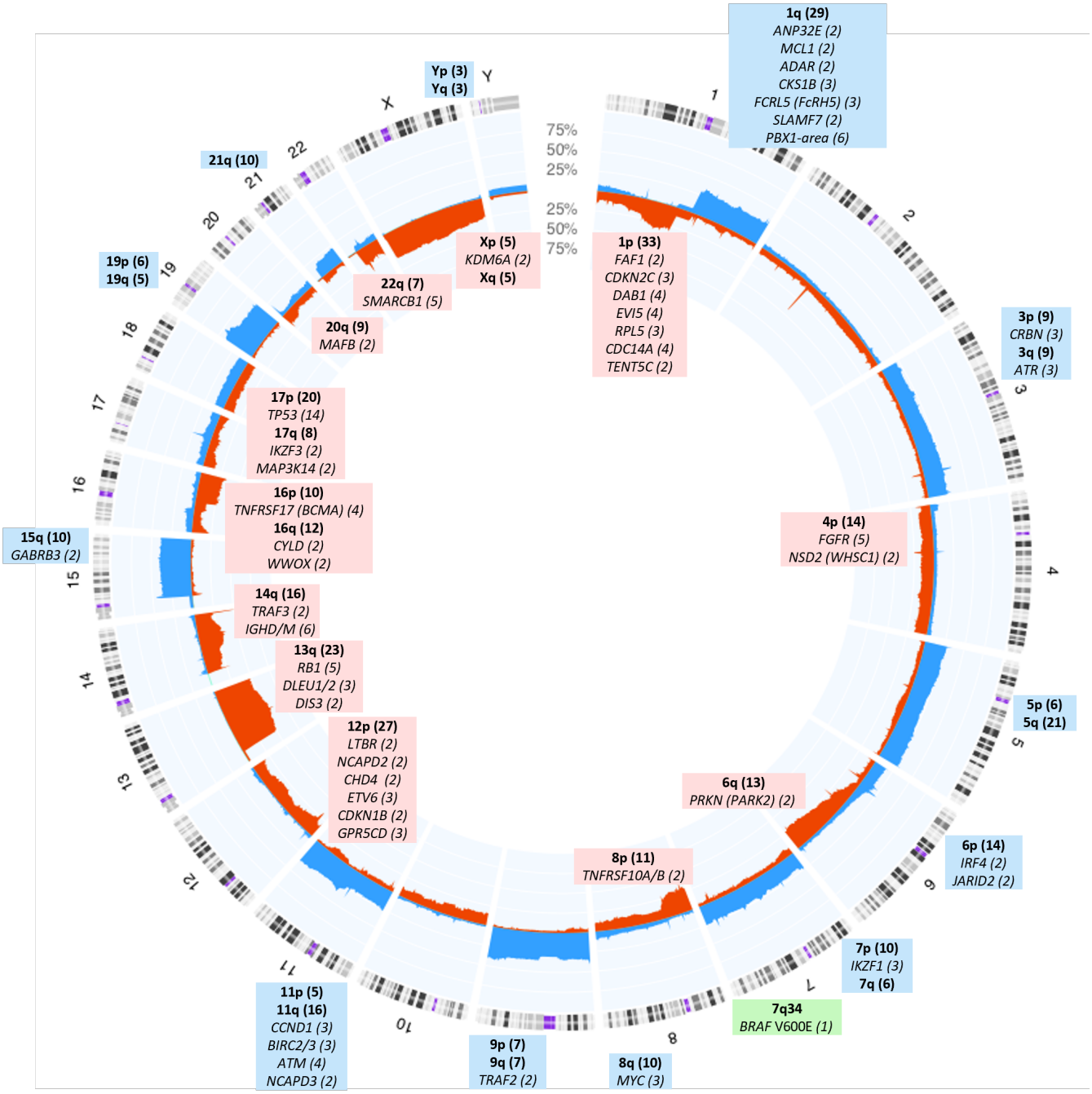
digitalMLPA ensures a high level of confidence in CN calling, even with low DNA input. Also, digitalMLPA allows to combine different NGS library types on the same flow cell. Analysis is done using free, easy-to-use Coffalyser digitalMLPA™ software – no bioinformatic skills are needed.



NXtec D006 Multiple Myeloma contains probes targeting:

1. Chromosomal arms with recurrent copy number alterations:
   - 1p (33 probes)
   - 1q (29 probes)
   - 13q (23 probes)
   - 17p (20 probes, 14 of which target *TP53*)
2. Subtelomeric and pericentromeric and middle regions of each chromosomal arm to detect larger CN alterations
3. Genes of emerging significance, including *including TNFRSF17* (*BCMA*), *CRBN*, *GPRC5D*, *FCRL5* (*FcRH5*), *IKZF1/3*, *IRF4*, *MYC*, *RPL5* and *SLAMF7*
4. *BRAF* V600E point mutation

Target genes and regions



Target genes and regions included in NXtec D006 Multiple Myeloma. Circos plot shows CNA frequencies reported in the MM patient population according to the Progenetix database. Inner circle: losses (red) and gains (blue). Outer circle: chromosomal locations. Red and blue boxes: deletions and respectively gains detected by ≥2 digitalMLPA probes. Green boxes: mutation-specific probes.(n): number of probes per targeted region.

Required materials

- 20 ng tumour-derived DNA input
- Thermocycler with heated lid
- Illumina sequencing platform (all devices), flow cell and reagents
- digitalMLPA NXtec probemix, reagents and barcode plates

References

Croft J et al. (2021). *Leukemia*. 35:2043-53

Kosztolanyi S et al. (2018). *J Mol Diagn*. 20:777-88.

Menezes K et al. (2020). *J Mol Diagn*. 22:1179-88.

MRC Holland

Confidence in Copy Number Determination

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