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Is it possible to detect point mutations with (digital)MLPA?

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It is possible to detect *known* point mutations with conventional MLPA and digitalMLPA, but these techniques are not suitable for the detection of *unknown* point mutations. Both conventional and digitalMLPA are primarily used to identify deletions and duplications.

Background

The conventional MLPA and digitalMLPA techniques involve the ligation of two probe oligos that are hybridised to immediately adjacent locations on the sample DNA. This ligation step is highly specific and will be inhibited if there is a mismatch around the ligation site. This allows the design of probes that are specific for either the SNP/point mutation of interest, or for the reference (wild-type) sequence at the location of a known mutation.

This principle is used to add probes for common mutations to some (digital)MLPA probemixes. However, this method is not suitable for the detection of a large number of different mutations, as this would require the design of specific probes for each individual mutation.

Note

Read more about the principle of the [MLPA](#) and [digitalMLPA](#) techniques.

Tags

digitalMLPA

MLPA

Related Pages

- [Do mismatches in probes influence \(digital\)MLPA results?](#)
- [What is MLPA, and how does it work?](#)

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