

MRC Holland Support

[Help Centre](#) > [digitalMLPA & Coffalyser digitalMLPA](#) > [digitalMLPA Technique](#) > [How can I confirm my MLPA or digitalMLPA results?](#)

How can I confirm my MLPA or digitalMLPA results?

This article was retrieved from [MRC Holland Support \(support.mrcholland.com\)](https://support.mrcholland.com) on Wednesday, 26th August 2026.

We recommend confirming all abnormalities detected by MLPA or digitalMLPA. You can either use a different (confirmation) probemix when available or an independent technique.

Single-probe aberrations

It is essential to confirm copy number changes detected by a single probe. Single probes may more readily be affected by experimental issues or variability. In addition, a mutation or polymorphism in the probe's target sequence may lead to a reduced signal, which can even mimic a deletion. Sanger sequencing of the probe's target sequence can reveal if there are any variants in the probe's target sequence that could explain such a reduced signal.

Confirmation probemixes

If available, you can use a specifically designed confirmation probemix to confirm results from initial testing. A confirmation probemix targets locations close to the targets of the probemix intended for initial testing, but with sufficient distance between ligation sites to allow confirmation of results. You should not use confirmation probemixes for initial testing.

The existence of a confirmation probemix is clearly indicated on product pages and in product descriptions.

Note

Not all probemixes that target the same genes or regions can be used to confirm each other's results because the probes may target the same locations.

Different techniques

It may be possible to confirm results obtained with [digitalMLPA](#) with an [MLPA](#) probemix, or vice versa. If this is possible, this is usually mentioned in the product documentation.

You can also use a variety of other techniques to confirm results, including Sanger sequencing of (long-range) PCR products, qPCR, long-range PCR, array-CGH and various NGS techniques. The method that is most suitable depends on e.g. the complexity of the region, the size of the aberration, and the availability of other techniques.

- [Tags](#)
- [digitalMLPA](#)
- [MLPA](#)

Related Content

- [Do mismatches between probes and their target sequences influence MLPA and digitalMLPA results?](#)

Disclaimer

The information provided in this material is correct for the majority of our products. For certain applications, the instructions for use may differ. In the event of conflicting information, the relevant instructions for use take

precedence.