Is it possible to use DNA extracted from formalin-fixed paraffin-embedded (FFPE) tissue for (digital)MLPA?

It is possible to use DNA extracted from FFPE tissue for a limited number of conventional MLPA and digitalMLPA probemixes. When a probemix has been optimized for use with DNA from FFPE tissue this is mentioned in the relevant product description.

As the purity and quality of FFPE-derived DNA is often low, reactions are usually more variable than reactions on DNA from other sources. This variability is usually worse for probemixes that have not been optimized for DNA from FFPE tissue.

Note
We offer the SALSA FFPE Solution (SFS) together with an extraction protocol that was developed by us, and that produces crude tissue lysates suitable for direct use in conventional MLPA reactions. This protocol does not include a deparaffinization step with xylene, can be performed in one tube, and uses low-cost reagents. More information.

Background

DNA extracted from FFPE tissue often contains impurities, and is frequently fragmented and damaged by depurination, cross-links, and other base modifications. This often results in a higher standard deviation. The quality of FFPE-derived DNA is variable, and depends on the fixation protocol and the extraction method, among other things. Therefore, we recommend comparing test samples to samples from similarly treated, healthy tissue to exclude that findings on test samples are due to the effects of the FFPE treatment. It may not be possible to obtain reliable results if the sample DNA has accumulated too much damage.

Some extraction protocols include a deparaffinization step using xylene to dewax the samples. If traces of xylene remain, this can greatly reduce the quality of MLPA reactions. Xylene is sometimes washed away with ethanol, but ethanol can also inhibit MLPA reactions if it is not sufficiently removed. This is why the protocol that comes with our SALSA FFPE Solution (SFS) does not include a deparaffinization step.

When using FFPE samples derived from tumour material, please also keep the following in mind:

- Analysis on tumour samples provides information on the *average* situation in the cells from which the DNA sample was purified.
- Gains or losses of genomic regions or genes may not be (reliably) detected if the percentage of tumour cells in the sample is low, or if the tumour has subclonal

aberrations.

- Reference probes may not always be suitable, as they may target regions with frequent copy number variations in a particular tumour type.

Tags

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