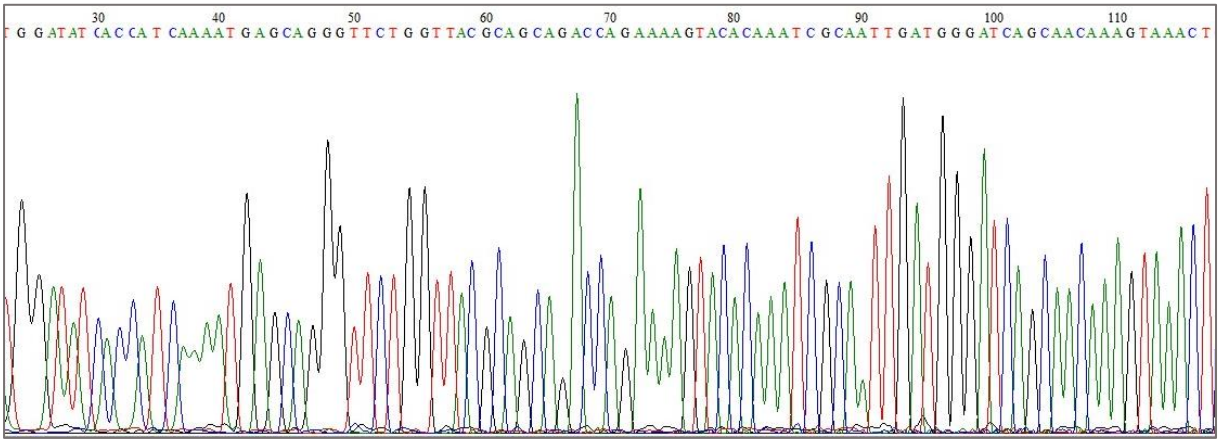
Diagnostic sequencing for Influenza A virus



In addition to PCR, sequencing is also available for the typing of diagnostically relevant pathogens.
This is particularly interesting when, in addition to a "rough division" into different genotypes or serotypes, the delimitation of gene sequence variants is important, which enables different live vaccines to be distinguished from wild-type variants or wild types among themselves.
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This is the case with **PRRSV** when, for example, the success of a vaccination regime is to be checked or the source of virus entry is to be determined.
The same is often the background of a **differentiation of PCV2** in case of positive PCR results, in order to recognise those types that can spread in the herd despite immunisation (in Germany mainly PCV2d).
In addition to this well-established diagnostic, the IVD GmbH now also offers **Sanger sequencing of the Haemagglutinin gene (HA gene) of the Influenza A virus** as a supplement to our typing-PCR for samples from pigs.
Due to high sequence variability of the influenza virus, a reliable assignment of the HA gene in particular to the respective variants of avian, human or pandemic origin is not always possible in PCR. Sequencing fills this gap and thus allows a more targeted adaptation of the vaccination.
The prerequisites for successful sequencing are a sufficiently high pathogen load in the sample (usually ct values <30 in the PCR) and good sample quality. Saliva samples in particular are less suitable, as they often contain a mixture of different pathogen types and the nucleic acid is degraded more quickly than in other sample material.
Of course, we can also carry out sequencing for other pathogens if required by prior arrangement. Please do not hesitate to contact us!

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