The viral disease African swine fever (ASF) has spread in Eastern Europe over the last years. The virus causes up to 100% mortality in domestic pigs and is a potential threat to the European pork industry. Efforts to eradicate or cure the disease with vaccines or antiviral therapy have been unsuccessful. Therefore, new approaches to treat the disease are frequently sought. Genome editing applying the CRISPR/Cas9 system has become a standardized tool in research and also qualifies to address ASF. By integrating Cas9 into the porcine genome; Cas9 may act upon infection and inhibit virus replication. Previous in vitro experiments in wild boar lung cells targeting the p30 gene showed resistance towards a European strain of ASF. p30 is expressed by CP204L and is critical for virus replication. However, due to variation in the CP204L sequence no resistance was found towards a Kenyan strain (Hübner et al., 2018). The study aims to further explore the feasibility to integrate Cas9 into the porcine genome with a variety of guide sequences to address the variation between ASF strains. Offspring will be generated through somatic cell nuclear transfer and if identified as positive carriers of Cas9 will be tested for resistance.

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