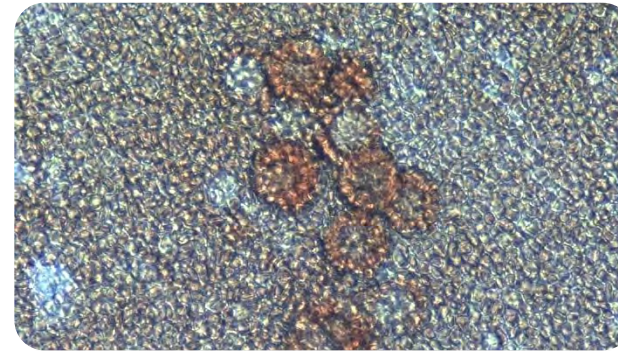
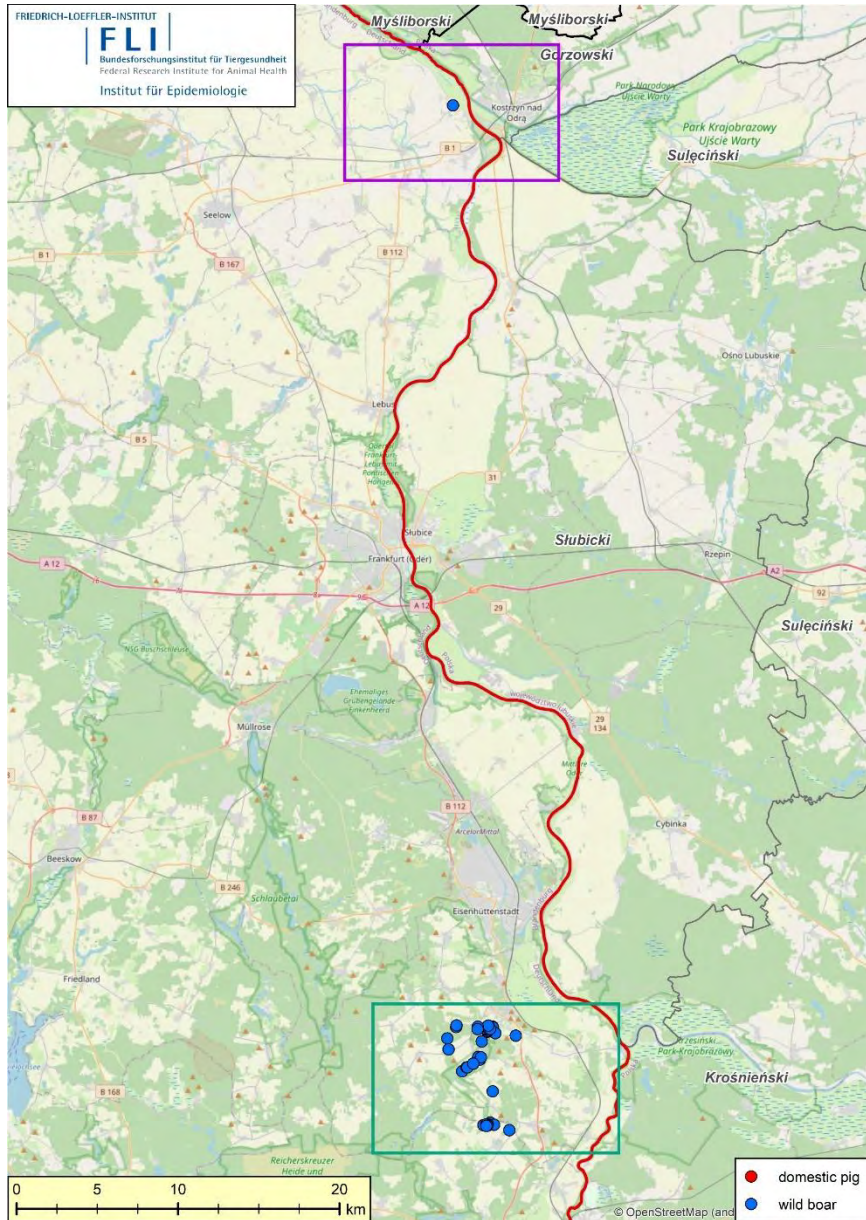


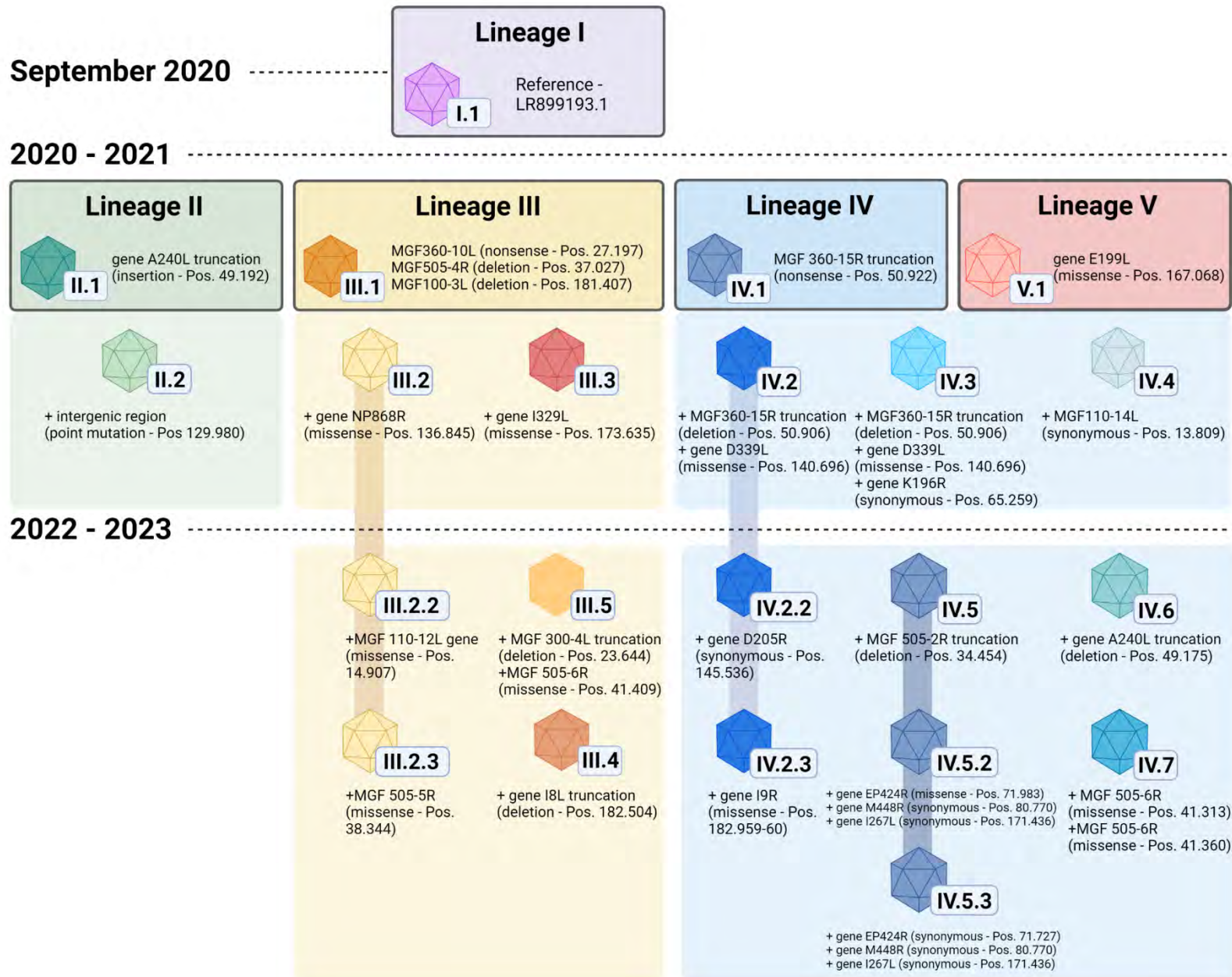
African swine fever virus variants in Germany

Sandra Blome & Sten Calvelage

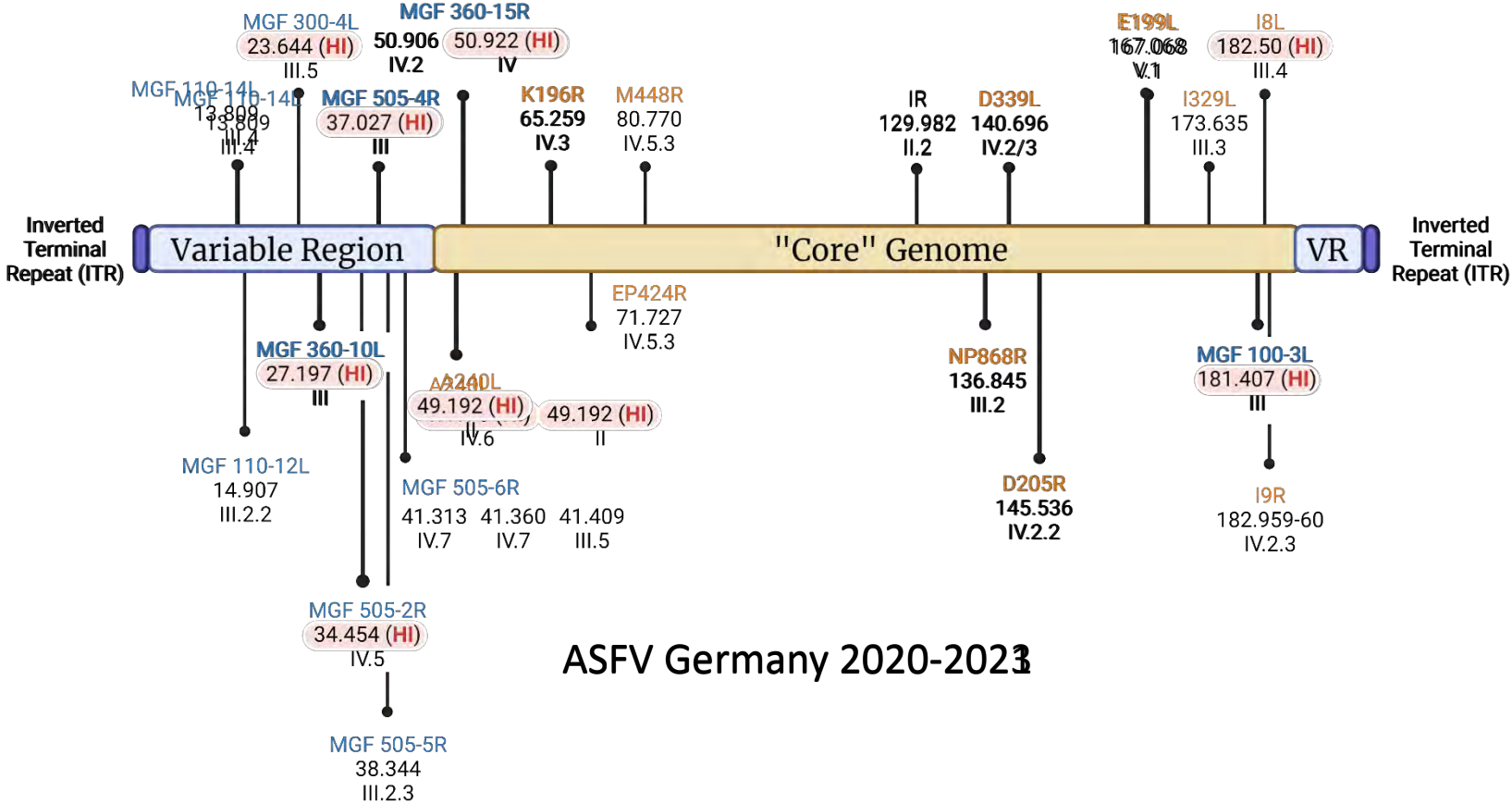
ASFV in Germany 2020



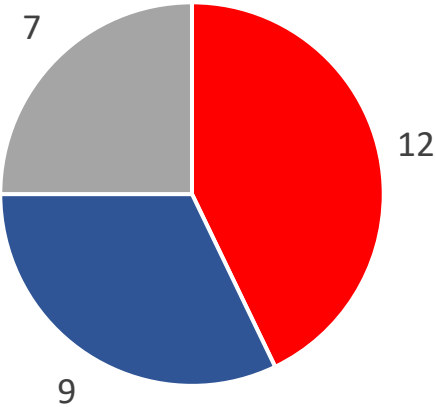
NGS Monitoring 2020 - 2023



ASFV - Variant-specific mutations



- Samples from September 2020 – June 2023
- Total of 28 characteristic mutations identified
- Classification into 5 lineages and 22 variants



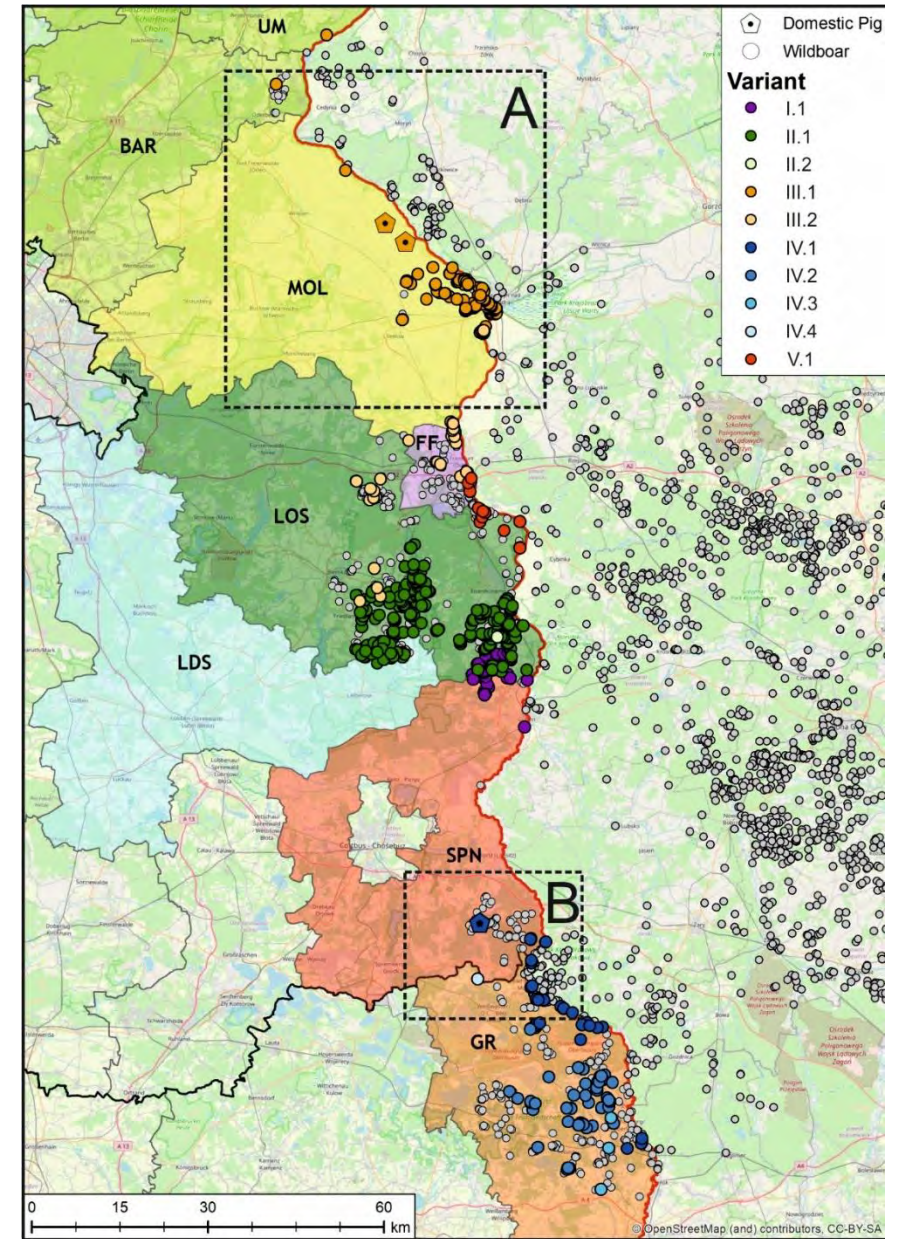
■ High Impact ■ Missense ■ Synonymous

ASFV Germany – 2020 - 2021

- Complete genome sequencing enables differentiation of 5 genetic lineages and 10 virus variants
- Spatial distribution of ASF cases shows the formation of variant-specific clusters
- Domestic pig outbreaks often caused by ASFV variants that also circulate regionally in wild boar

ASFV Germany – 2022 - 2023

- Continuous genetic diversification of ASFV (22 virus variants)
- Lineage III (north) and IV (south) displace other lineages
- First virus without O174L mutation detected in point entry to Baden-Württemberg (-> not from outbreak region East Germany)



ASFV Cluster 2020 - 2021

NGS Case Report Mecklenburg Western Pomarania & Hesse 2024

ASP-Fall	Zeitraum	Bundesland	Landkreis	Betroffener Wirt	Deutschland und West-Polen	Lineage III spezifisch			MV 2021 spezifisch	Lineage IV spezifisch
					O174L	MGE 360-10L	MGE 505-4R	MGE 100-3I	I329I	MGE 360-15R SNP
2024ASP01578	Juni 2024	Hessen	Groß-Gerau	Wildschwein	-	-	-	-	-	-
Fehlende O174L Mutation weist auf Eintrag außerhalb von Deutschland und West-Polen hin, da bislang bei allen deutschen Fällen diese Mutation nachgewiesen werden konnte (Ausnahme: Baden-Württemberg 2022)										
2024ASP01426	Juni 2024	Mecklenburg-Vorpommern	Vorpommern-Greifswald	Hausschwein	x	x	x	x	-	-
Nachweis der Lineage III-bekanntem Mutationen, genetisch nächstverwandt mit Viren aus Ausbruchsgeschehen in Hausschweinen aus Uckermark und Emsland und Wildschwein aus der Region Uckermark (2022ASP01516)										



Mecklenburg-Vorpommern

2021ASP05548	November 2021	Mecklenburg-Vorpommern	Rostock	Hausschwein	x	x	x	x	x	-
2021ASP05776	November 2021	Mecklenburg-Vorpommern	Ludwigslust-Parchim	Wildschwein	x	x	x	x	x	-

Bislang wurden ausschließlich Viren der Lineage III in Mecklenburg-Vorpommern nachgewiesen



Niedersachsen

2022ASP01930	Juli 2022	Niedersachsen	Emsland	Hausschwein	x	x	x	x	-	-
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Hohe genetische Übereinstimmung mit 2022ASP01938



Sachsen

2021ASP05067	Oktober 2021	Sachsen	Meißen	Wildschwein	x	-	-	-	-	x
2021ASP05402	November 2021	Sachsen	Görlitz	Wildschwein	x	-	-	-	-	x
2022ASP00073	Januar 2022	Sachsen	Meißen	Wildschwein	x	-	-	-	-	x
2022ASP00337	Februar 2022	Sachsen	Görlitz	Wildschwein	x	-	-	-	-	x

Bislang wurden ausschließlich Viren der Lineage IV in Sachsen nachgewiesen



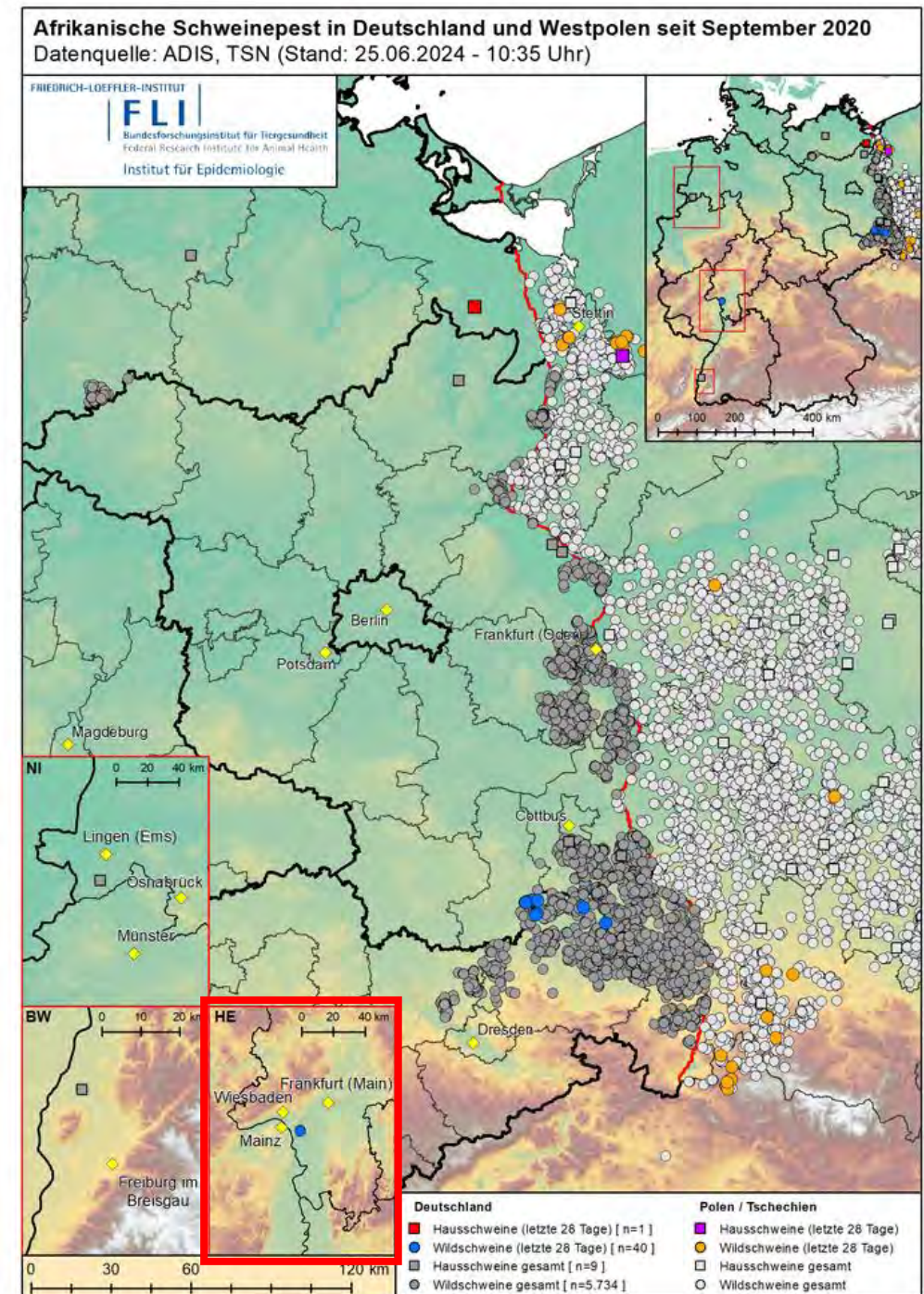
Brandenburg

2021ASP04812	September 2021	Brandenburg	Oder-Spree	Wildschwein	x	x	x	x	-	-
2022ASP01516	April 2022	Brandenburg	Uckermark	Wildschwein	x	x	x	x	-	-
2022ASP01938	Juli 2022	Brandenburg	Uckermark	Hausschwein	x	x	x	x	-	-
2022ASP03268	Oktober 2022	Brandenburg	Oder-Spree	Wildschwein	x	x	x	x	-	-
2023ASP00680	Februar 2023	Brandenburg	Cottbus	Hausschwein	x	-	-	-	-	x
2023ASP00554	Februar 2023	Brandenburg	Spree-Neiße	Wildschwein	x	-	-	-	-	x

Bislang wurde Viren der Lineage III und IV in Brandenburg nachgewiesen

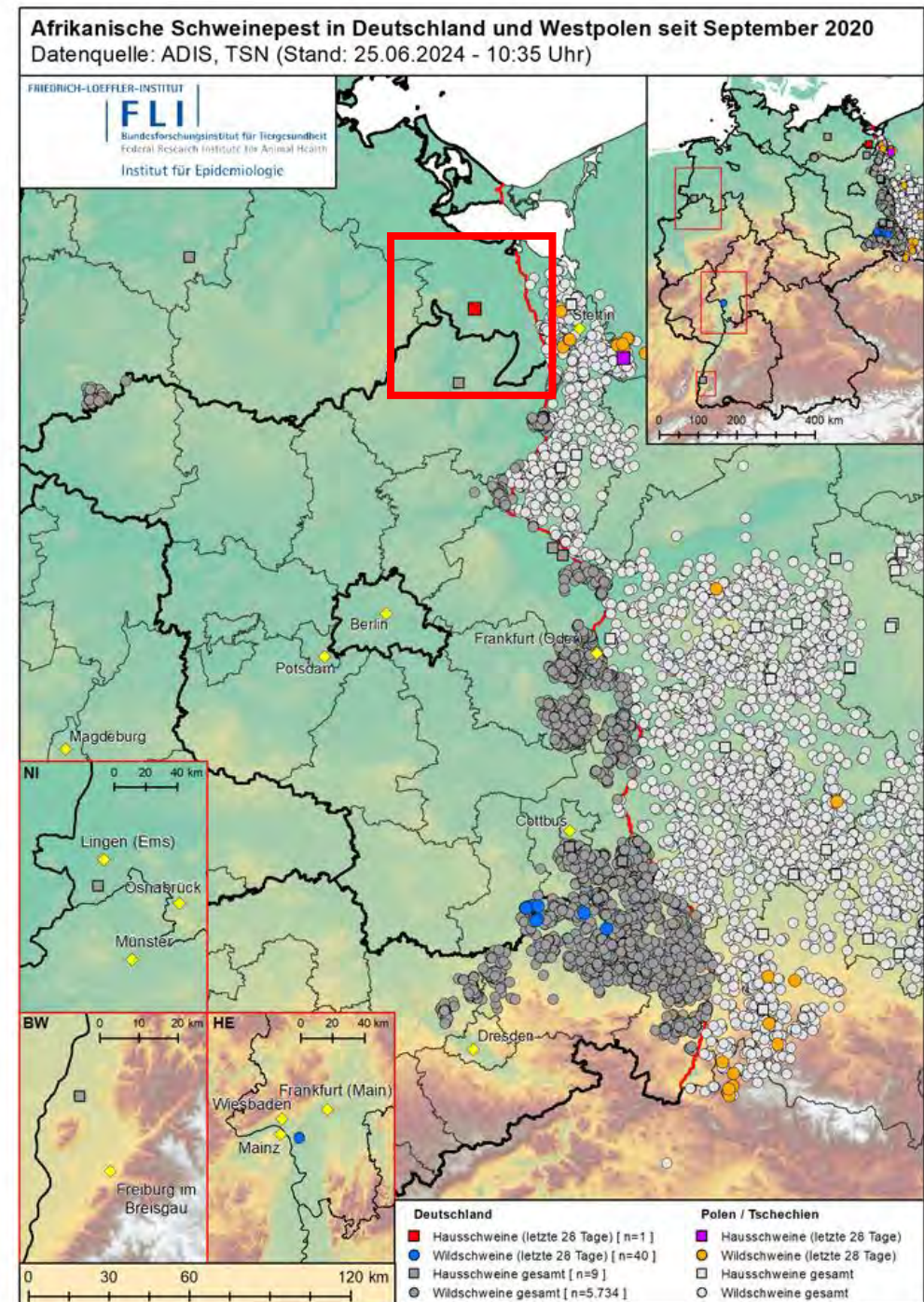
NGS Case Report Hesse 2024

- The viral complete genome was successfully sequenced (2024ASP01578)
- None of the “German” mutations (markers) detected -> **entry from eastern German outbreak regions (especially Brandenburg and Saxony) almost excluded**
- Comparison of the genome with other published ASFV sequences: highest identity with outbreak samples from the Czech Republic (2017), Belgium (2018) and Moldova (2017) -> **spread from Eastern European countries is likely**



NGS Case Report Mecklenburg Western Pomerania 2024

- The viral complete genome was successfully sequenced (2024ASP01426)
- Mutations in the genes MGF 360-10L, MGF 505-4R and MGF 100-3L assign the virus to lineage III -> **lineage III previously detected in MV and northern Brandenburg**
- Characteristic mutation in MGF 505-6R also identified in the domestic pig outbreak in Prenzlau/Emsbüren and a wild boar from the Uckermark -> **Regional entry probable**
- No mutation in the I329L gene present, which was characteristic of domestic and wild boar outbreaks in MV 2021-> **Independent outbreak events**



Thanks for your attention!