Executive Summary

The SARS-CoV-2 pandemic highlighted the importance of molecular epidemiology and genomic data sharing for monitoring pathogens evolution and informing public health responses. Building on these insights, there is a unique opportunity to apply such approaches in a sustainable One Health context, with a particular focus on food-borne pathogens across human, animal, and environmental interfaces. High-resolution genomic data can improve early detection of outbreaks, enhance food safety, and support coordinated responses to emerging threats. At the European level, there is a growing demand for sequence-based surveillance and an international data exchange to improve food safety and protect public health. To fully realize this potential and support Swiss and European risk assessments, a centralized Swiss data sharing platform for bacteria and viruses is essential. Such a platform will enable standardized data exchange, automated workflows, validated bioinformatic analyses, and allow us to generate tailored reports for stakeholders across Switzerland and for European partners.

The Swiss Pathogen Surveillance Platform (SPSP, www.spsp.ch) is uniquely positioned to translate these insights. As a nationwide consortium, SPSP enables centralized integration and analysis of genomic data across human, animal, and environmental sectors, creating the foundation to systematically address key One Health research questions. By analyzing data across compartments and over time, the platform supports a deeper understanding of pathogen emergence, transmission dynamics, and the relationship between genomic traits and observed characteristics. This integrated approach generates actionable knowledge to improve food safety, support targeted interventions, and strengthen evidence-based decision-making across the One Health system.

SPSP has formulated **four driving questions** to further build and expand the platform following these highly relevant One Health-related research questions:

I. How much sequencing is needed to capture outbreaks across compartments (humans, animals, and the environment)?
II. What genomic virulence factors and antibiotic resistance markers can be detected over time?
III. How does resistance evolve and transmit over time and compartments?
IV. How do genotypic and phenotypic resistances correlate