Executive Summary

The past SARS-CoV-2 pandemic demonstrated the value of molecular epidemiology and genomic data sharing to monitor pathogens evolution. Around the globe, SARS-CoV-2 genomic surveillance has been used to follow emerging, new and concerning variants and to estimate the impact of public health counter measures. During the pandemic, large sequencing capacities have been formed in Switzerland, allowing now to provide pathogen surveillance of highly virulent and resistant bacterial pathogens with an unprecedented and high spatiotemporal resolution. These data are of invaluable interest for public and individual health, to inform experts and the public on contagious threats, and to promote the general well-being of the Swiss population. Also, at the European level, there is an increasing demand for the use of sequence-based surveillance and for data exchanges with the goal to improve food safety and public health in a One Health context of rising antimicrobial resistance. To efficiently access the available data and fulfill Swiss and European risk assessments, an independent Swiss data sharing platform is urgently necessary for bacteria and viruses. The platform will allow us to standardize data exchange, automate the technical process, run comparative validated bioinformatic analyses, and allow us to generate structured reports for different stakeholders across Switzerland and European partners.

The Swiss Pathogen Surveillance Platform (SPSP, www.spsp.ch) addresses exactly these open points, closing the gaps while delivering an affordable and sustainable solution. During the pandemic, SPSP processed all SARS-CoV-2 sequencing data within the national genomic surveillance program and Switzerland was amongst the global top data providers. However, while many European countries continued to invest into building a sustainable data environment for future pandemic threats and antimicrobial resistant bacteria, Switzerland, to this date, has no sustainable and functional data sharing platform for genome sequencing.

We have formulated **four driving questions** to further build and expand SPSP 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?