CeGaT offers you SARS-CoV-2 genome sequencing (WGS SARS-CoV-2) and immediate classification of the virus. To help fighting the COVID-19 pandemic, it is essential to provide high-quality SARS-CoV-2 genome sequence data. These data can provide valuable information about viral spread and evolution. Routine analysis of the SARS-CoV-2 genome data will enable to identify virus variants and will help to understand which virus variants have a higher potential to infect humans.

SARS-CoV-2 is a positive-sense single-stranded RNA virus with a genome size of 29.8 to 29.9 kb. Although it has a lower mutation rate than most RNA viruses, mutations certainly accumulate and result in genomic diversity both between and within individually infected patients. Since the first entry into the human host, SARS-CoV-2 has acquired several polymorphic nucleotide positions in the genome. Some of these new virus variants are even more infectious than the virus that was first detected in Wuhan, China.

Upon isolation of SARS-CoV-2 RNA from human samples, the virus RNA may be mixed with the host RNA, making it challenging to reconstruct the viral genome. Therefore, we specifically enrich the virus genome by using primer pools that utilize designs from ARTIC primers and cover the entire SARS-CoV-2 genome. The amplicons are sequenced on our Illumina platforms.

You will receive raw sequencing data. Additionally, we offer a bioinformatic service, for immediate classification of the SARS-CoV-2 sequences. We are using CoVpipe for data analyses, a pipeline recommended and maintained by the Robert Koch Institute (RKI) for the reference-based reconstruction of NGS-based SARS-CoV-2 genome data. The sequences are assigned to official Pango lineages (cluster of sequences that are associated with an epidemiological event) including, e.g. B.1.1.7, B.1.351, P.1, B.1.617.2, A.23.1 and B.1.525.

Potential applications of SARS-CoV-2 sequencing:
- Detection and tracing of novel genetic variants
- Assessment of the impact of mutations on the performance of diagnostic methods, antiviral drugs, or vaccines
- Exploration of transmissibility and infectivity of virus variants
- Investigation of virus transmission dynamics

We need:
- Isolated high quality RNA (> 25 µl)
- Cycle threshold (Ct) value < 30

You receive:
- Ready-to use SARS-CoV-2 sequencing data and a project report

Optional bioinformatics:
- A report including mapping data, statistics and variants
- Consensus sequence of the SARS-CoV-2 genome sequence
- Classification of SARS-CoV-2 genome sequence according to official Pango lineages