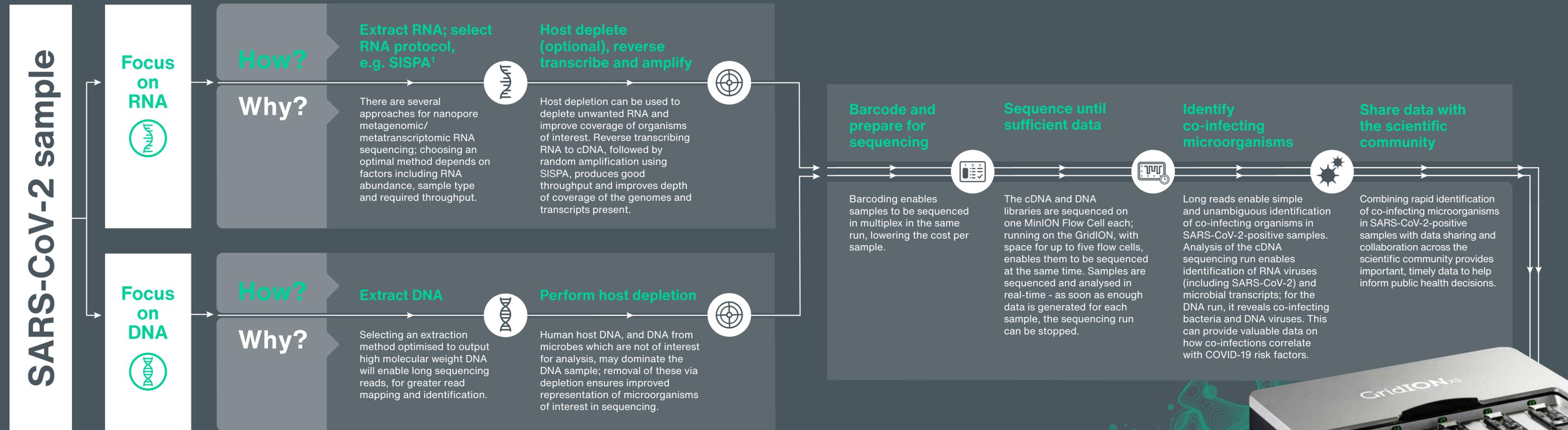


Metagenomic & metatranscriptomic sequencing of SARS-CoV-2 with Oxford Nanopore

Long-read DNA and RNA metagenomic and metatranscriptomic sequencing of SARS-CoV-2 samples enables rapid, sensitive identification of co-infecting microorganisms. This provides valuable information for research into how co-infection with certain bacteria and viruses may affect COVID-19 outcomes.



Read more about metagenomics with SISPA at nanoporetech.com/resource-centre/overview-covid-19-metagenomic-sequencing

Find out more at nanoporetech.com/covid19

1. Moreno, G. and O'Connor, D. Protocol: Sequence-Independent, Single-Primer Amplification of RNA viruses V.3. Available at: <https://www.protocols.io/view/sequence-independent-single-primer-amplification-o-bckxiuxn> [accessed 21May20]