LEXOGEN

Enabling complete transcriptome sequencing

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QuantSeq-Pool Targeted SARS-CoV-2 Panel

- The most economical solution for SARS-CoV-2 mass screening
- Scalable to population size, analysis of up to 36,864 samples per NGS run
- High-quality results within 20 hours
- Batch processing reduces plasticware and time requirements

Introduction

The impact of the COVID-19 pandemic has called for a new, more efficient screening approach to identify and isolate infected individuals. Current testing methods are limited in throughput and do not allow upscaling to the screening level required to test repeatedly at population scale. Lexogen has therefore developed the QuantSeq-Pool Targeted SARS-CoV-2 Panel, a targeted RNA sequencing method that leverages the ultra-high throughput capacity of Next Generation Sequencing (NGS). Early sample-barcoding allows to trace individual samples throughout the workflow while triple indexing enables the analysis of millions of samples. This way, the panel allows to quickly identify and isolate infected individuals even if they are pre- or asymptomatic. These individuals are then quarantined before they can infect others, thereby stopping the spread of the disease (Fig. 1).

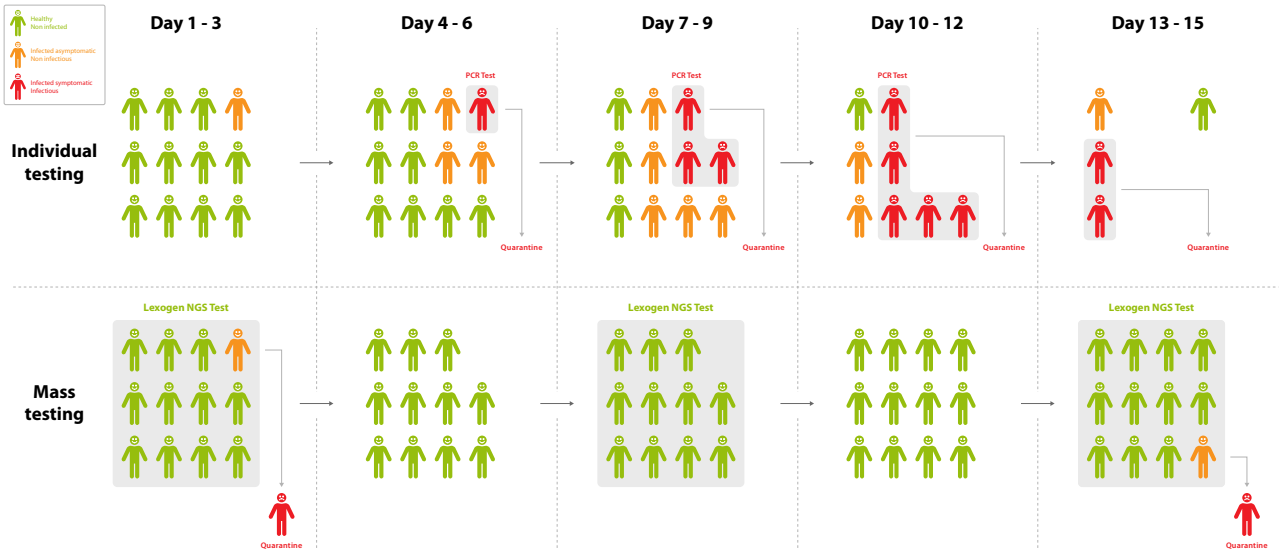

Figure 1 | Mass testing can stop the spread of COVID-19 by identifying infected persons before the onset of symptoms. TOP: In an individual testing scheme persons are tested when they already start to show symptoms. Their quarantine comes too late, since they could have already infected other people (family, colleagues, etc) when they did not yet show symptoms. BOTTOM: In contrast, regular mass testing identifies infected persons before the onset of symptoms but when they are already infectious. In many cases, these will also not show symptoms later on. Their quarantine not only prevents the spread of the infection but also enables an early treatment of the infected persons themselves, and extensive quarantine measures can be avoided.

Results in 20 hours

This new SARS-CoV-2 test works with extracted RNA, which can be extracted not only from nasopharyngeal swabs but also from convenient gargle samples, making the procedure painless and allowing for self-sampling. Lexogen's SARS-CoV-2 Rapid RNA Extraction Kit enables RNA extraction from 96 samples in 15 minutes with full automation compatibility for high-throughput processing (Fig. 2).

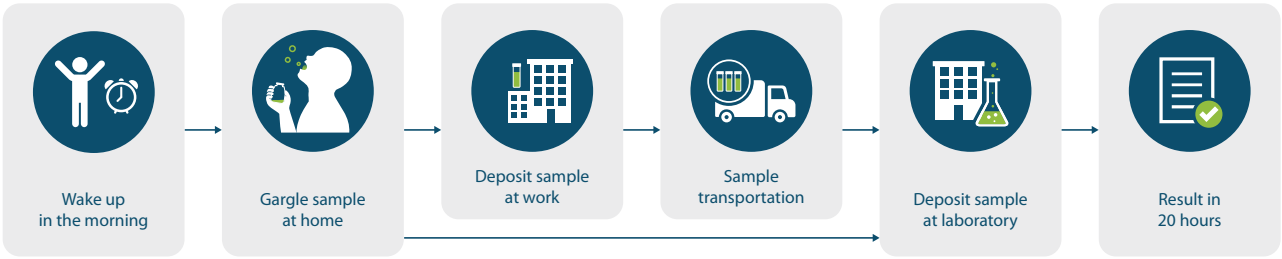

Figure 2 | Convenient gargle-based self-sampling as initial step in a mass screening workflow for the detection of of SARS-CoV-2 infections. Lexogen's SARS-CoV-2 panel enables the analysis of thousands of samples per laboratory within 20 hours.

Scalability by Sample-barcoding and Early Pooling

In the first step, extracted RNA is added to primers provided dried in 96-well plates for robust and easy handling. The primer plate also contains a synthetic positive control to validate functionality of the test for each individual sample. In the subsequent cDNA synthesis, four regions of the viral RNA genome are reverse transcribed, and samples are barcoded individually. The cDNAs are then pooled and transferred to a single well in another 96-well plate for second strand synthesis and PCR amplification. In this amplification, each cDNA pool obtains one of 384 Unique Dual Indices (UDIs), enabling multiplexing of up to 36,864 samples for analysis in a single NGS run (Fig. 3).

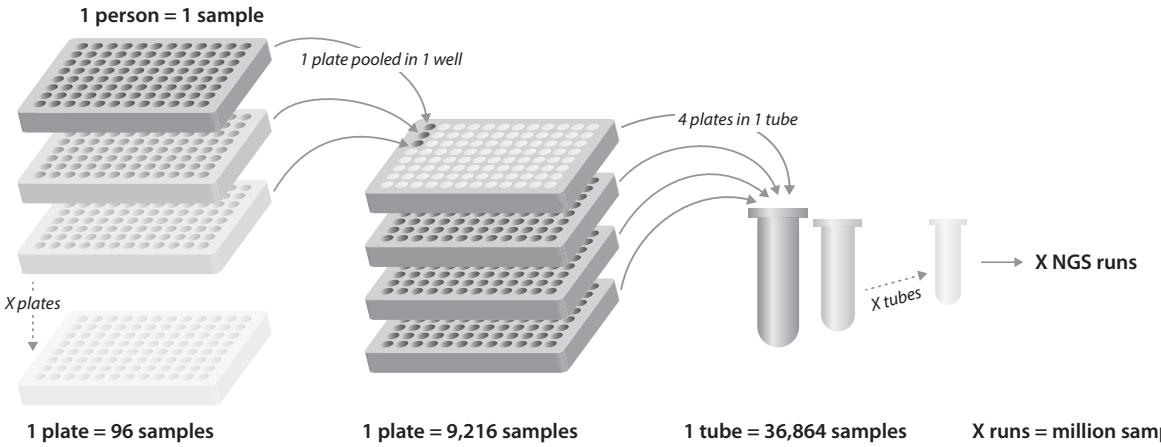

Figure 3 | Pooling strategy for the QuantSeq-Pool Targeted SARS-CoV-2 Panel. Each sample is barcoded during reverse transcription in a 96-well plate. These 96 cDNA samples are then pooled into a single well of another set of plates for PCR amplification which adds another layer of barcoding by introducing one of 384 UDIs. Thereby, up to 36,864 samples can be multiplexed in a single NGS run, allowing for the analysis of millions of samples in parallel setups.

High Cost Efficiency by Batch Processing, Ultra-plexing, and Automation

Early pooling and batch processing significantly decrease overall and hands-on time and reduce the need for plasticware, not only driving down costs but also alleviating the pressure on supply chains in a highly volatile pandemic period. Massive savings are further leveraged by ultra-high multiplexing and the possibility to perform the NGS run economically in single-read mode with read lengths starting already at 50 bp. The complete workflow is bead-based providing for automation and parallel preparations at lowest cost.

Ordering Information

140 (QuantSeq-Pool Targeted SARS-CoV-2 Panel for Illumina)
164 (QuantSeq-Pool Targeted SARS-CoV-2 Panel with Rapid RNA Extraction)

Benefits

- **Scalable to ultra-high throughput:** Triple indexing for currently up to 36,864 samples per NGS run for millions of samples in parallel settings. Automation compatible for ultra-high throughput.
- **Cost-efficient:** Early pooling and batch processing reduce hands-on time and limit plasticware usage. Short, single-read, and highly multiplexed NGS runs significantly save sequencing costs.
- **Maintaining sample identity:** Sample-barcoding prior to pooling makes every sample fully traceable.
- **Confidence:** Reverse transcription primers and positive controls are dried in 96-well plates minimizing the risk of cross-contamination.
- **Fast protocol:** 768 samples can be prepared in 3.5 hours, and high-throughput results can be obtained in less than 20 hours.
- **Fast data analysis:** The straightforward, comprehensive analysis pipeline is based on efficient tag counting and available on github.
- **State-of-the-art indexing:** Minimal risk of sample misassignment due to Lexogen's patent-applied 12 nt UDIs and sample-barcodes.

Associated Products

107-111, 120 (Lexogen UDI 12 nt Unique Dual Indexing Add-on Kits)
142 (SARS-CoV-2 Rapid RNA Extraction Kit)