

# Sample Submission Guide

| Application  | Input material   | Optimal amount (per sample)                  | Concentration range       | Turn-around time* |
|--|--|--|---------------------------|-------------------|
| All samples should be submitted in $\geq 15 \mu\text{l}$ volume  |  |  |                           |                   |
| <b>DNA</b>   |  |  |                           |                   |
| Whole Genome Sequencing (WGS)                                    | Purified gDNA  | Standard: >10 ng<br>PCR free protocol:>100ng | 5-50 ng/ $\mu\text{l}$    | 2-3 weeks         |
| Targeted Resequencing  | Purified gDNA/<br>Amplicon                             | Standard: >10 ng<br>PCR free protocol:>100ng | 5-50 ng/ $\mu\text{l}$    | 2-3 weeks         |
| Whole Exome Sequencing (WES)                                     | Purified gDNA  | 500 ng                                       | 50-200 ng/ $\mu\text{l}$  | 2-3 weeks         |
| ChIP-Sequencing/complexity reduction                             | Enriched DNA   | Standard: >10 ng<br>PCR free protocol:>100ng | >2 ng/ $\mu\text{l}$      | 2-3 weeks         |
| Whole Genome Bisulfite Sequencing (WGBS)                         | Purified gDNA  | 100 ng                                       | >10 ng/ $\mu\text{l}$     | 3-4 weeks         |
| Mitochondrial DNA (mtDNA)  | Purified gDNA  | 250-500 ng                                   | 5-50 ng/ $\mu\text{l}$    | 2-3 weeks         |
| Microbiome 16S rRNA Sequencing                                   | Purified gDNA  | 1-100 ng <sup>***</sup>                      | >2 ng/ $\mu\text{l}$      | 2-3 weeks         |
| Whole Microbiome Sequencing                                      | Purified gDNA  | 250-500 ng                                   | 5-50 ng/ $\mu\text{l}$    | 2-3 weeks         |
| Methylation EPIC BeadChip (850K)                                 | Purified gDNA  | 250 ng                                       | 25 ng/ $\mu\text{l}$      | 3-4 weeks         |
| PacBio Sequencing  | Purified gDNA/<br>Amplicon                             | 500 ng - 5 $\mu\text{g}$                     | >50 ng/ $\mu\text{l}$     | 2-6 weeks         |
| <b>RNA</b>   |  |  |                           |                   |
| RNA-Seq using Poly-A selection **<br>(Gene-expression profiling) | Purified RNA   | $\geq 100$ ng                                | 10-50 ng/ $\mu\text{l}$   | 3-4 weeks         |
| RNA-Seq using rRNA reduction **<br>(Total transcriptome)         | Purified RNA   | $\geq 30$ ng                                 | 3-50 ng/ $\mu\text{l}$    | 3-4 weeks         |
| Small RNA-Seq  | Purified RNA or<br>equivalent of enriched<br>small RNA | 1000 ng or enriched<br>equivalent            | 250-350 ng/ $\mu\text{l}$ | 3-4 weeks         |
| Low-input RNA-Seq  | Purified RNA (or cells)                                | 1 ng   | >0.1 ng/ $\mu\text{l}$    | 3-4 weeks         |
| Single cell RNA-Seq  | Methanol fixed cells                                   | 1,000 cells                                  | 1,000-10,000<br>cells     | 3-4 weeks         |

The table below specifies the input requirement for RNA samples. Be aware that these recommendations were determined using a high purity and quality reference sample. Samples of sub-optimal quality will require more material to achieve similar numbers.

| Input  | Optimal       | Recommended  | Minimum |
|--|---------------|--------------|---------|
| Poly-A selection (Gene expression profiling) | $\geq 100$ ng | $\geq 30$ ng | 1 ng    |
| rRNA depletion (Total transcriptome)         | $\geq 30$ ng  | $\geq 10$ ng | 0.5 ng  |
| Expected duplicates                          | < 30%         | 30 - 50%     | > 80%   |

\* Turnaround time (TAT) depends on project size and starts after successful sample QC

\*\* Optimal input for RNA-Seq based on 30% or less PCR duplicates

\*\*\* Depending on sample origin

# Successful Sample Submission

To optimize sample transfer and prevent any delays in shipment, please consider our checklist.



## Project Initiation

Your project will be initiated upon receipt of the completed and signed PO form. Please, do not ship samples before we have confirmed reception of your purchase order (PO) via email.



## Sample Submission Form

After your project is initiated you will receive a confirmation email with a project number and a Sample Submission Form (SSF). Return the fully completed form by email and include a copy in your sample shipment.



## Sample Identification

Each sample must be labelled with a unique GenomeScan code (GS\_ID) as indicated in the SSF. When using 96-well plates, be sure that the labels associated with positions A1-H12 correspond to the sample ID as indicated on the SSF.



## Biological Contaminants

Samples shipped to GenomeScan need to be free of biological contaminants. Our laboratory operates in compliance with BSL-1 and BSL-2 requirements and cannot handle potential hazardous materials. In general RNA/DNA samples extracted from cells or tissue do not represent a biological threat.



## Shipment of samples

### Shipping address:

GenomeScan  
Plesmanlaan 1d, 4th floor  
2333 BZ LEIDEN  
The Netherlands

Samples can be shipped in a sealed bag or box in a polystyrene container.

- Preferably deliver your samples in 96-well plates.
- To ensure optimal preservation of the sample, we recommend shipment of (g)DNA using ice packs.
- Use dry ice for sending RNA samples.

Remember that international shipment may take longer than expected. Make sure that your package contains sufficient cooling materials to preserve the quality of your samples during transport. Avoid shipment of samples on days that will require transit on a weekend or over a holiday period.

## About GenomeScan

As an ISO-accredited leading Dutch Next Generation Sequencing service provider, GenomeScan develops customizable NGS solutions for pharmaceutical and biotech companies, health care providers and academic institutions. By providing new tools to analyze genetic disorders quicker, affordably and effectively, GenomeScan fosters innovation through partnership with medical centers and research laboratories.

