



# Detection of Adventitious Agents

Accelerate and de-risk your manufacturing process

Adventitious agents, such as viruses, bacteria and fungi, are microorganisms that are unintentionally introduced to the manufacturing process of a biological or medicinal product. The presence of these contaminants in biologics is a major safety concern and it often hampers the product's market approval. Timely identification of unwanted microorganisms present in your sample can therefore have a great impact on your production.

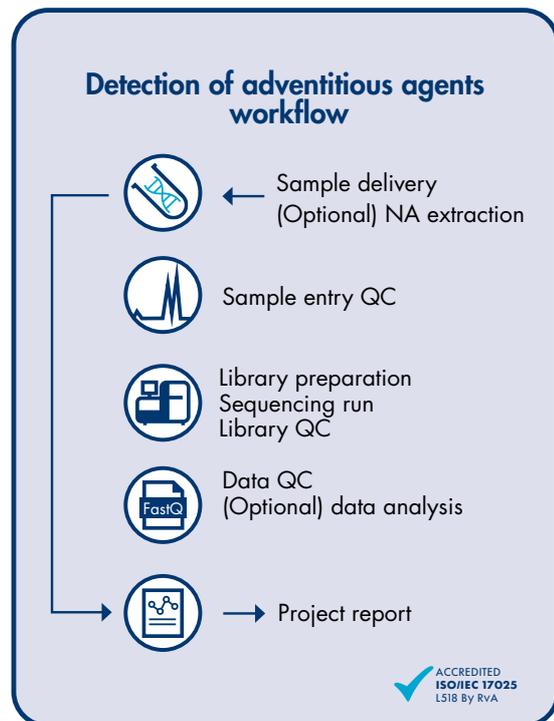
GenomeScan's Next Generation Sequencing (NGS)-based assay for detecting adventitious agents is a high-throughput sensitive and rapid method that will accelerate and de-risk your manufacturing process. We are able to detect thousands of different viral contaminants with a single assay and can provide you with the detailed taxonomic classifications of the detected adventitious agents. GenomeScan's scientists will work with you to design the most appropriate reporting set-up tailored to your specific needs.

## Key benefits

Our NGS-based solutions for detection of adventitious agents:

- Replace multiple tests with a single, comprehensive assay
- De-risk and accelerate your manufacturing processes
- Improve sensitivity and accuracy of your biosafety testing
- Reduce costs

Our proprietary RNA and DNA library preparation protocols combined with short (Illumina) or long-read (PacBio, ONT) sequencing solutions are compatible with a wide range of samples (raw materials, ancillary reagents, virus seeds, cell substrates, cell banks, pre-production cells, pre-filtered harvest, post-production cells, control cells, post-filtered harvest and final product).



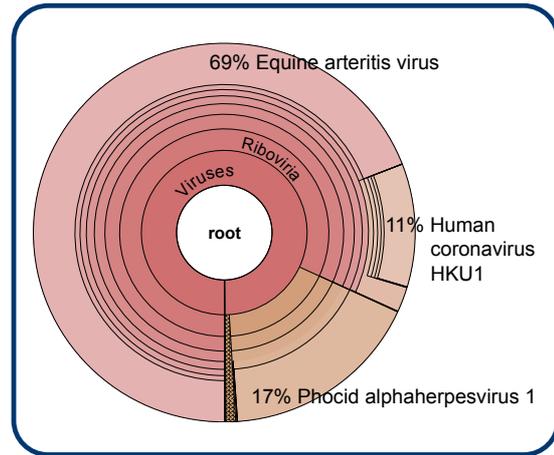
## Trustworthy results

### Data quality guarantee

Sequence quality control is an essential tool in our workflow. Using our in-house validated pipelines, we minimize intra- and inter-experiment variability, and ensure that you always receive data of the highest possible quality. In most of our workflows that include PCR amplification, we incorporated unique molecular identifiers (UMIs), which allow distinguishing PCR duplicates from true identical input molecules.

### Professional reporting

We deliver comprehensive, consistent, and transparent project reports that describe all experimental procedures and include relevant QC metrics.



Krona plot displaying species abundance in clinical sample

## Data analysis options

Our data analysis workflows are based on state-of-the-art bioinformatics tools that conduct exhaustive analyses with insightful data visualization outputs. This way, we provide you with easily comprehensible and ready-to-publish results. For example, your data analysis report can include a comprehensive table of all detected agents, their taxonomic rank, and the number of reads. You can also view your report in html format to make use of the interactive elements, such as an interactive Krona plot for sample composition visualization.

## Custom solutions

At GenomeScan, we continuously improve our services and validate new solutions. Take advantage of our pilot program in which bioinformatics pipelines can be tailored to your specific needs, allowing more in-depth mining of your dataset. In addition to that, we offer various customizable publication grade visualization options to present your results.

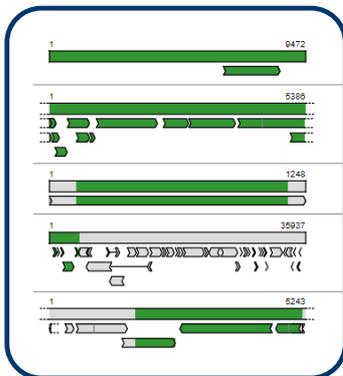
## Detection of adventitious agents insights

Our detection of adventitious agents service aids, amongst others:

- Identification of all contaminants present in the sample
- Taxonomic classification down to species, subspecies and strain level
- *De novo* assembly of putative adventitious agents
- Gene prediction and functional annotation

## About GenomeScan

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



Visualization of biological relevance of detected hits by sequence identity and coverage

Name	TaxID	TaxRank	GenomeSize	NumReads	NumReads%
Bovine coronavirus	11128	leaf	31028	1411462	73.55
Rabbit coronavirus HKU14	1160968	species	31100	434313	22.63
Homo sapiens	9606	species	2147483647	62114	3.24
Synthetic construct	32630	species	26537524	3661	0.19
Betacoronavirus HKU24	1590370	species	31249	2675	0.14
Murine hepatitis virus strain A59	11142	leaf	31357	908	0.05
Leuconostoc mesenteroides	1245	species	1966146	338	0.02

Table of seven most abundant taxonomic groups detected in the sample

