Ensuring the virus safety profile of your product: recommendations from the proposed revision to ICH Q5A

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ICH Q5A revision



A Draft Revision of ICH Q5A is under Public Consultation

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INTERNATIONAL COUNCIL FOR HARMONISATION OF TECHNICAL REQUIREMENTS FOR PHARMACEUTICALS FOR HUMAN USE

isation for better health

ICH HARMONISED GUIDELINE

VIRAL SAFETY EVALUATION OF BIOTECHNOLOGY PRODUCTS DERIVED FROM CELL LINES OF HUMAN OR ANIMAL ORIGIN

Q5A(R2)

Draft version Endorsed on 29 September 2022

Currently under public consultation

At Step 2 of the ICH Process, a consensus draft text or guideline, agreed by the appropriate ICH Expert Working Group, is transmitted by the ICH Assembly to the regulatory authorities of the ICH regions for internal and external consultation, according to national or regional procedures. The new revision will apply to new classes of products, such as virus-like particles, viral vectored products such as vaccines and gene therapies using novel mammalian and insect-based expression systems

For some of these products, viral clearance may need to be demonstrated. These products may include:

- Adenovirus vectors
- Adeno-associated virus vectors
- Virus-like particles (VLPs)
- Baculovirus-expressed vectors, VLPs, proteins

Revision likely to be finalized late 2023/ early 2024



Viral Safety Strategy

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Safe sourcing and testing of raw materials

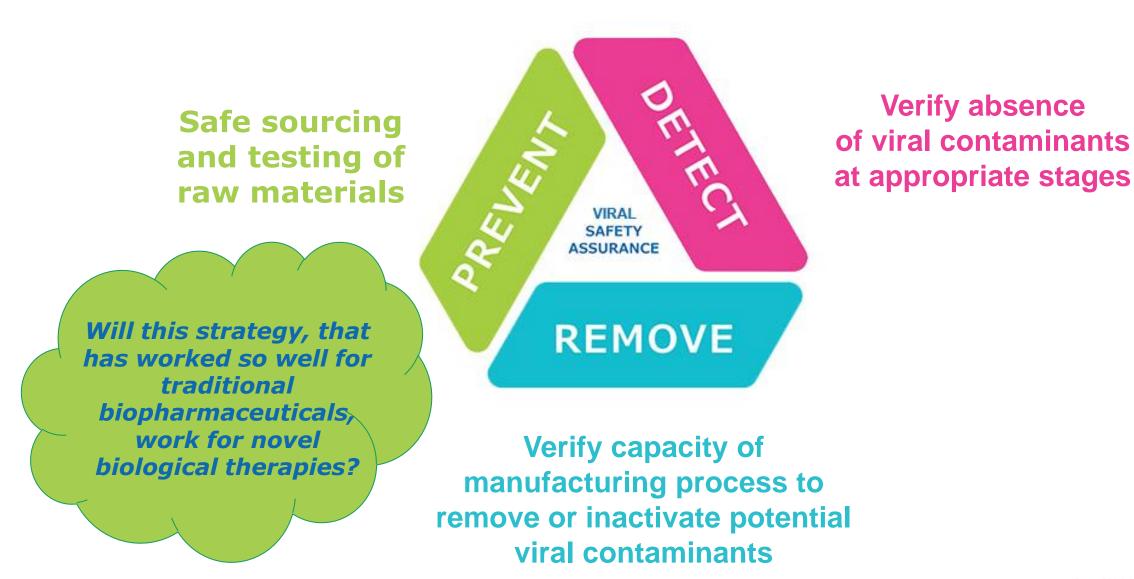


Verify absence of viral contaminants at appropriate stages

Verify capacity of manufacturing process to remove or inactivate potential viral contaminants



Viral Safety Strategy





Prevention and Detection of Viral Contamination are in Focus When Removal is not Feasible



Viral safety assurance strategies are expected to be implemented based on risk and the ability of the vector to withstand clearance methods.

Prevention

- Quality of raw/starting materials
- Containment in the facility

Detection

- Raw materials
- Entire process

Viral clearance required when there is no impact on quality



Validation of clearance is required using appropriate model viruses





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Viral Clearance

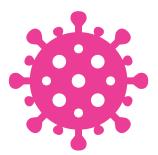


Potential for Viral Clearance

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Enveloped Viral Vectors and Cell Therapies

- Inactivation steps will denature enveloped viral vectors or cell therapies
- Due to their large size, viral filtration is not a viable clearance option
- Virus inactivation/removal measures for culture medium and supplements is recommended for these products



Non-Enveloped Viral Vectors

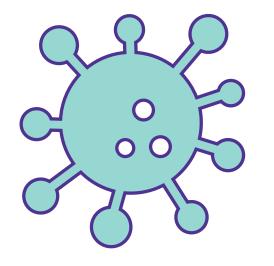
- Resistant to inactivation procedures for enveloped viral contaminants
- Potential exists to separate small nonenveloped viral vectors from larger enveloped viral contaminants by large pore virus filtration
- Chromatography steps may contribute to clearance of enveloped viral contaminants





"When possible, cell culture media or media supplement treatments such as gamma irradiation, virus filtration, high temperature short time processing or ultraviolet C irradiation can be used as additional virus risk mitigation measures."

ICH Q5A (R2)

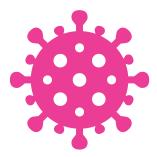




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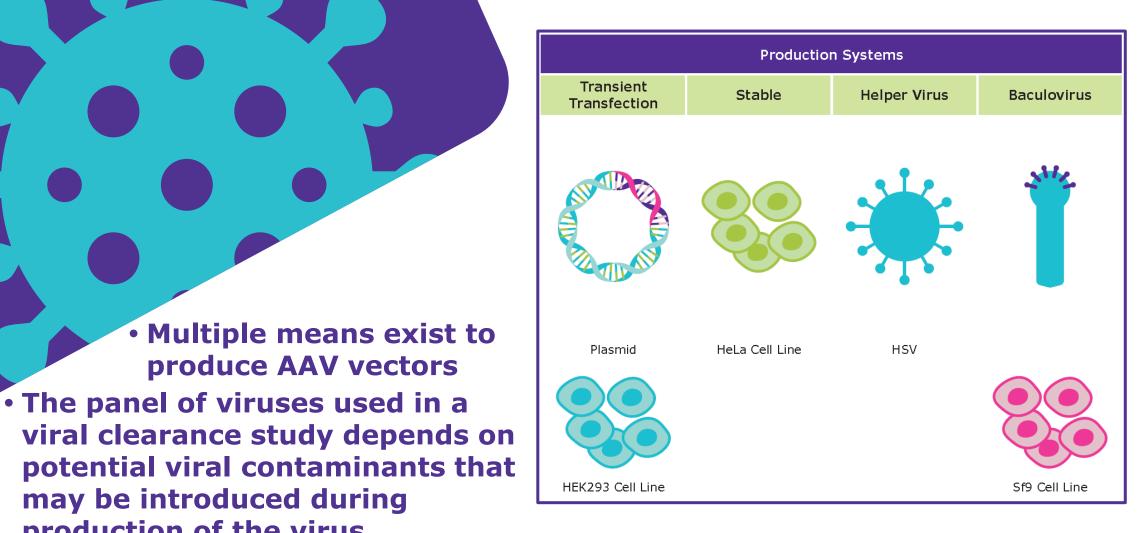
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Which viruses do I use for an AAV viral clearance study?



production of the virus

Virus panel



Virus Panel for AAV Clearance Dependent on Expression System



Considerations for Viral Clearance Studies

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Proper scale down of steps



Pre-study



Determine kinetics of inactivation

Sanitization of chromatography resins



Aged resin studies

EMEA/CHMP/BWP/268/95 Note for Guidance on Virus Validation Studies: The Design, Contribution and Interpretation of Studies Validating the Inactivation and Removal of Viruses

> ICH Topic Q5A (R2); Quality of Biotechnological Products: Viral Safety Evaluation of Biotechnology Products Derived from Cells Lines of Human or Animal Origin



Viral Safety at All Stages

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Is a virus or virus-like particle present in the cells or bulk harvest? If yes, then this represents a different risk profile than cells or bulk harvest where no virus can be detected.

Using CHO-derived recombinant proteins as a model, viral clearance data may be expected as part of an IND/IMP application

Are you using a plasmid transfection system, with no animal-derived products, and you determine the risk of viral transmission to be low? Discuss with regulators. A viral clearance study may not be required before an IND/IMP application.

Note that ICH Q5A outlines the data that should be submitted in marketing applications and registration packages



Baculovirus expressed virus/virus-like product

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Drococc Stop	Log ₁₀ Reduction				
Process Step	BACV	VSV			
Inactivation	≥5.15	≥ 4.41			
Chromatography	1.82	3.84			
Virus Reduction Filtration (Large Pore)	≥ 4.91	≥ 4.83			
Overall Reduction	≥ 11.88	≥ 13.08			

BACV expression system small, non-enveloped virus product

BACV expression system small, non-enveloped virus product

Drococc Stop	Log ₁₀ Reduction				
Process Step	BACV	VSV			
Inactivation	≥5.05	≥ 4.37			
Chromatography	4.13	3.70			
Virus Reduction Filtration (Large Pore)	≥ 5.08	≥ 4.65			
Overall Reduction	≥ 14.26	≥ 12.72			



Virus/virus-like product expressed in human cell line

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Human cell line Small, non- enveloped virus product		Log ₁₀ Virus Reduction						
		Envelo	ped Model Vi	Non-Enveloped Viruses				
		XMuLV	BVDV	PRV	ЕМС	PPV		
	Inactivation	≥4.62	4.13	≥5.02	ND	ND		
	Chromatography	3.84	3.28	3.24	2.19	4.09		
	Overall Reduction	≥8.46	7.41	≥8.26	2.19	4.09		

ND – clearance not evaluated

	Log ₁₀ Reduction						
Process Step	Envelo	oped	Non-Enveloped				
	BVDV	PRV	EMC	PPV			
Inactivation	≥ 5.63	≥ 5.71	ND	ND			
Chromatography	NR	≥ 5.51	NR	1.90			
Overall Reduction	≥ 5.63	≥11.22	NR	1.90			

Human cell line Small, non-enveloped virus product



17 ND – clearance not evaluated NR – no reduction

How much clearance?

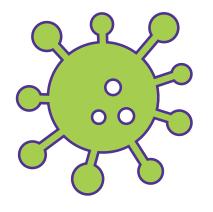
- The revision of ICH Q5A does not define viral clearance specification for viral vectors, VLPs or other novel products
- AAV can be produced in a variety of systems, and the potential and known contaminants is dependent on the expression system
- It is probable, however, that any expression system that includes a helper virus or an insect virus will be expected to demonstrate the capacity of the manufacturing process to clear in excess of the amount of virus used in that system.





"Some virus clearance steps used during production of genetically engineered viral vectors and viral vector-derived products may not be as effective as when used for recombinant proteins. In such cases, <u>considerations for</u> <u>further risk reduction</u> (e.g., treatment of raw materials, extensive testing for broad virus detection) should be applied."

ICH Q5A (R2)





Viral clearance for non-enveloped viral vectors and VLPs

- The recent revision of ICH Q5A requires viral clearance studies for nonenveloped viral vectors and virus-like particles
- The design of viral clearance studies for non-enveloped viral vectors is similar to the design of a study for a recombinant protein or monoclonal antibody
- The virus panel used in clearance studies may be unique to each vector product, its expression system and potential contaminants
- Our scientists will help you design a clearance study for your non-enveloped gene therapy vector





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Adventitious Agent Detection using Next Generation Sequencing



NGS is key to replacement of traditional methods in a comprehensive biosafety testing strategy

NGS applications as part of a comprehensive biosafety strategy

Characterize and demonstrate the safety of biological products as part of a comprehensive biosafety strategy, including:



Cell line characterization



Virus seed characterization



Virus identification during contamination events

Raw material testing



NGS as an appropriate replacement for traditional methods

Sequence-agnostic, broad-range virus detection makes NGS an ideal replacement for current virus testing methodology by:

Removing subjectivity 🧭

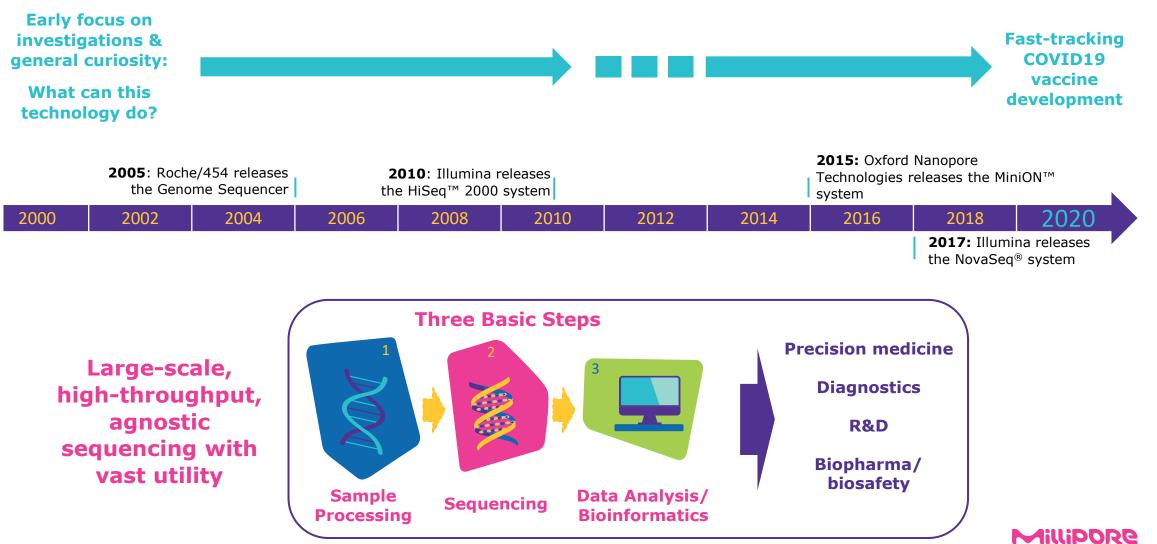
Providing a faster alternative

Supporting 3R principles to replace animal use



Evolution of NGS over the years





How does NGS contribute to the overall safety profile?



- NGS generates genomic sequence data for all sequences present in a test agent (unbiased method)
- Sequences generated are queried against an appropriate database (generally viral) in a BROAD SCREEN.
- Sequence profile of suspect viral agents are revealed and qualified.
- NGS only identifies the presence of sequence signatures but does not provide information about whether it is infectious.
- Positive hits in NGS typically require follow-up/investigation (e.g. With *in vitro* culture-based methods)
- Can be used on a wide variety of samples and intermediaries:
 - Virus, Cells
 - Bulk harvest
 - Final product



When is it appropriate to use NGS technology?

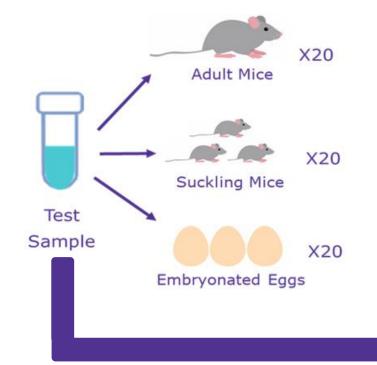
- Infectious products or intermediates where a neutralizing antibody is unavailable for culture-based methods
- Cell line screening in lieu of animal studies and in vivo testing
- Broad virus screening assay to complement or round out the safety profile of the test agent
- Product release testing as an alternative method to confirm safety profile
- Instances where traditional assays would not be expected to identify a potential contaminant of interest or no traditional assay exists.
- Replacement for *in vivo* and *in vitro* methods (with appropriate qualification/validation testing).
 - Consistent with 3R Principles to reduce animal use
 - Provides faster alternative to traditional testing
 - Consistent with proposed revisions to ICH Q5A



NGS supplies an appropriate replacement for the *in vivo* adventitious virus test

Traditional in vivo method

- Well-established method utilizing animals to detect adventitious virus in a biological material
- Viral contaminant indicated by the impact of infection on the host animal
- No direct identification of a contaminant without further testing by *in vitro* or molecular methodologies



NGS Alternative

- ✓ Broad spectrum virus detection
- Ability to demonstrate comparable or better virus detection
- Reduction in use of animals for virus detection methods

Suitability of *in vivo* replacement supported by:

- Peer-reviewed studies demonstrating ability of other methods to provide more reliable virus detection
- Industry trend to reduce the number of animals used in testing



Acceptability by Agencies Adventitious Agent Testing

- Lots of progress in this area within the past several years (driven by COVID).
- Recent release of proposed revisions to ICHQ5A focus on NGS as a replacement for *in vivo* testing.
- Experience working with clients and regulators on NGS AAT testing strategies for:
 - Drug Substance/Drug product testing
 - In Vivo replacement (e.g. ICH Q5A revisions)
 - In Vitro replacement (in special circumstances)
 - Vaccine products
 - Master cell bank testing
- Industry drive towards NGS
 - Removes subjectivity
 - Faster alternative
 - Consistent with 3R principles to reduce animal model use
- Spiking studies available, as requested by the agencies
- Successful implementation in testing program for preclinical through commercial products

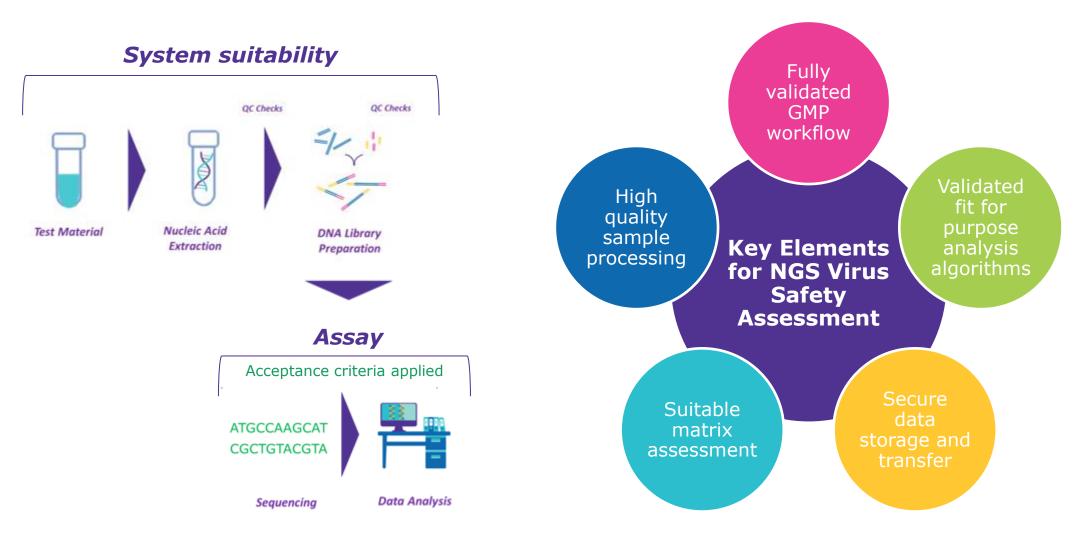


Assay Overview and Details Adventitious Agent Testing

- Provides assessment of "unknown virus" sequences in the client's test sample.
- Queries all sequences generated against proprietary viral database.
- Two main offerings for this
 - AAT for cell lines/crude harvest samples
 - AAT for virus-based samples
- Information provided:
 - Viral sequence hits and qualification of hits
 - Summary of expected sequences (based on test system- e.g. ERV's)
 - Focuses on viruses that impact the test system as well as human health
- Assay are run on the NextSeq2000 to maximize number of reads
- TAT: 42 Days (without forecast)
- Specification: **REPORT RESULTS**
- What it does not do: Does not tell you if a virus is infectious (limitation of short read technology)
- Spiking Studies required for late phase products (aka: PSQ's)



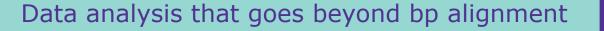
The cell-based NGS method addresses all key elements recommended by industry guidance





Data analysis is performed with a robust, validated bioinformatic algorithm and curated database

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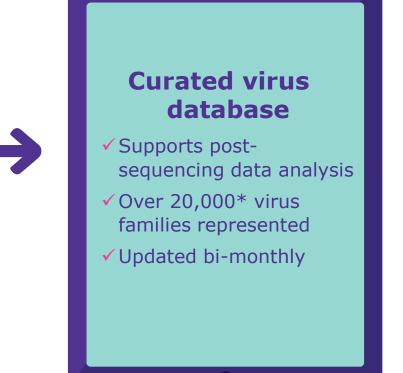


Analysis algorithm removes false positive signals based on specific criteria



Potential positive signals are challenged by sequence alignment to virus-specific databases

Expert scientific review confirms positive signals and provides context for results based on sample type



*Depending on classification of sub-families



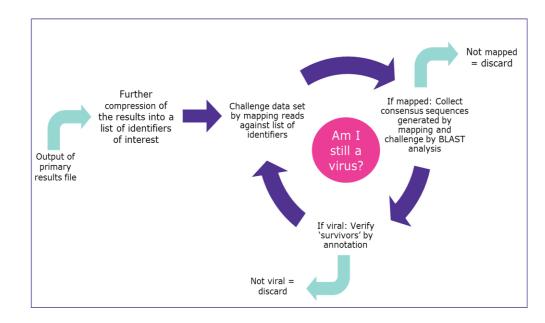
Sample results for 293 cells with scientific annotation

	ASSAY NUMBER	SPECIFICATION	RESULT	
	706522GMP.BSV	Report Result	See Appendix	
FINAL RESULT:		VIRAL SEQUENCES DETECTED ¹		Explanation of
No exogenous transcripts were		onsor's test sample, an HEK293 derived ad in the sample based on this analysis e.		human endogenous retrovirus sequences
detected in the sample based on analysis against viral database	this analysis, with mapping of the ra NC_022518 and X82272) revealing that chimeric HERV-cellular sequen that observation (Sokol <i>et al.</i> , 2016) human cell lines, no infectious parti	IERVs; multiple GenBank accession nu aw sequence reads against select HER nearly 100% sequence coverage with inces are a feature of HERVs and this m . Furthermore, while expression of HE cle has ever been recorded and most s re, these sequences do not represent "	V reference genomes (<i>e.g.</i> high sequence identity. It is known happing profile is consistent with RV sequences is a feature of all sequences are highly defective	found, consistent with sequence signatures found in HEK293 cells and do not represent contaminating viral
	near 100% sequence match to the Given the test sample origin, this is generated by transfection with sh chromosome 19 (Graham <i>et al.</i> , 19	es were also identified within the test sa first ~4.3 kb of human adenovirus typ s expected and consistent with this ce heared adenovirus 5 and is known t 77). Therefore, the presence of these sample, but are associated with the test	be 5 (Genbank accno AC_000008). Ell line as the HEK293 cell line was o contain these sequences within sequences does <i>not</i> constitute viral	sequences
		0-50-r		virus 5
	No other viral sequences of signific ¹ Note that due to the nature of this technology (e.g. represent intact, infectious or replicating viruses. T Sokol M, Jessen KM, and Pedersen FS. Utility of ri-	extgen be contained constitu	entified, which are in HEK293 cells and ite viral contamination	d do not
	2:14572-9. Epub 2004 Aug 13.	99. Doi: : Iman genome: new perspectives on an old relation. Pro Characteristics of a Human Cell Line Transformed by D		



Validation of NGS Methodology

System Suitability Assay ac checks ac checks QC checks Acceptance Criteria Applied Image: Checks Image: Checks<



NGS Assay is validated in a Modular Fashion

- Extraction
- Library
- Sequencing
- Bioinformatics

This approach **confirms that each portion of the assay behaves as-expected**.

Limits of detection for client-specific matrices are established through end-to-end analysis with known spikes (per ICH Q5A recommendations).

Full validation package consists of the following:

Generic Validation + Spiking Studies



Our NGS solution offers robust detection with any cell species

Three (3) RNA viruses from the WHO-recommended reference virus panel were used to assess LOD:

- Respiratory Syncytia Virus (RSV)
- Feline Leukemia Virus (FeLV)
- Reovirus (Reo)

Matrix-specific limit of detection (LOD) for representative cell lines

	Cell Matrix						
	СНО	HeLa	Vero	SF9			
LOD*	1.00E+04	1.00E+04	1.00E+04	1.00E+04			

*LOD indicates lowest concentration detected for all 3 viruses, expressed as Viral Gene Copies (VGC) / 1.00E+06 cells

All spike-in RNA viruses were detected up to the viral 1e4 dilution in 1e6 cells, indicating an LOD of 1 VGC / 100 cells



Cell-based AAT by NGS

- Detection and identification of virus contaminants
- Can be used with any cell bank regardless of cell species
- Transcriptome analysis can detect RNA viruses and mRNA from DNA viruses

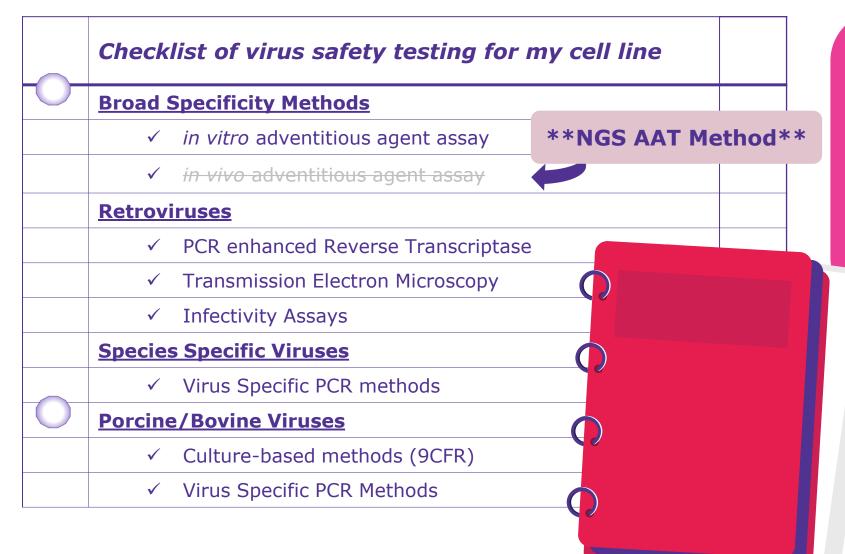


What does a Spiking Study need to look like?

-	entative uses 1e6 1e5	Test Matrix		Data An • Use esta order to	ablished mimic	d criter	ia for	detect	ability	in		
RSV FELV EBV	1e4 1e3 1e2	\rightarrow \Box $-$	→ G	- Specif - Homo - Fragm - Numb • Determ • Determ	logý ient Ler er of re ine repr	ads rec oducib	ility v	ia repl				
 Use client Pre-Study 3-5 repres 	lar validated matrix = re assessmen sentative vir ntrations (d	d methodology presentative material t of Nuclease treatment	Sample + 1e4	Exampl	Sam EBV RSV + + + + + + + + 4/4 4/4	piking ple + 1e6 FLV PC + + + + + + 4/4 4/ ple + 1e3	Spikes	dy re		ble + 1	e2 Spikes	
	*	concentration		Additional Virus + + + + <tr td=""></tr>	EBV RSV + + + + + + + + + + + + 8/8 8/8	FLV PC + + - + + + + + - + + - 8/8 2/	· ·	Additional Virus + + + + - + + + 7/8	EBV RSV + + + + + - + 4/8 5/8	FLV FLV FLV FLV FLV FLV FLV FLV FLV FLV	PCV REO + 1/8 0/8	Additional Virus - + + -



NGS AAT can be incorporated into a comprehensive virus BioReliance. BioReliance.



- NGS replaces the *in vivo* adventitious agent test
- Supplements virus safety testing data
- Part of a comprehensive testing package defined by regulatory guidance and risk mitigation assessment



Select a service provider offering more than just raw data

Trusted GMP services



- Validated workflows, from sample receipt to final report (per GMP guidelines)
- Assay validation data is part of an FDA Biologics Master File (BMF)

Industry-leading footprint



- Global availability
- Facilities in the US & UK
- Increasing capacity to support growing demand

Secure data, reliable results



- Dependable bioinformatic algorithms
- Dedicated bioinformaticians
- Electronic data delivery
- Secure data management

Expert analysis and QA review



- Expert-delivered data analysis
- QA review & approval
- Detailed reports and raw data available

Support when you need it

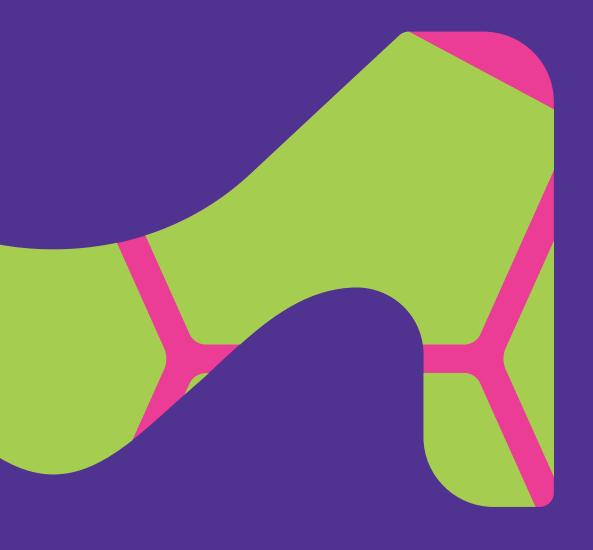


- Industry-leading scientific support
- Regulatory support
- Method customization when needed





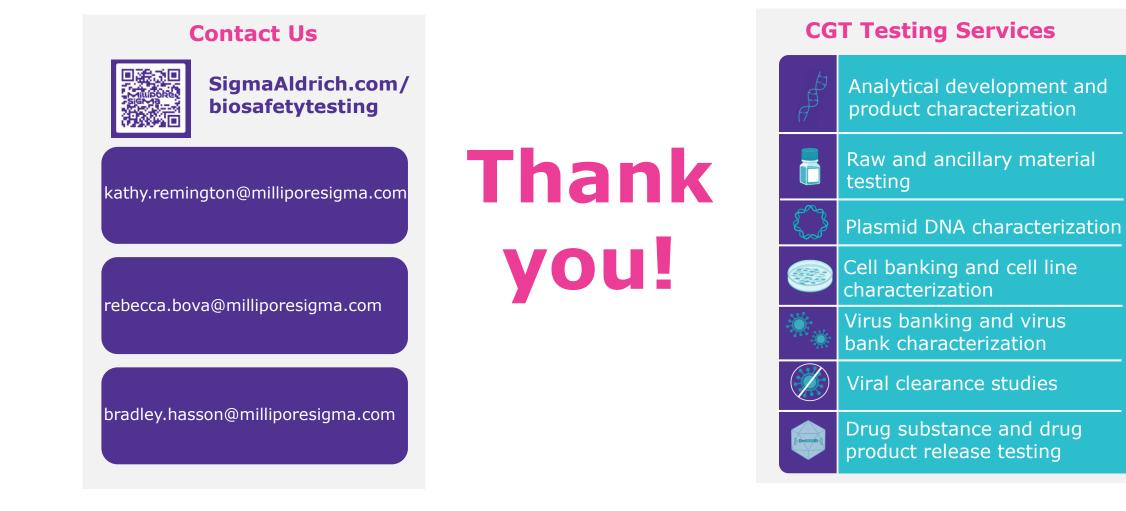
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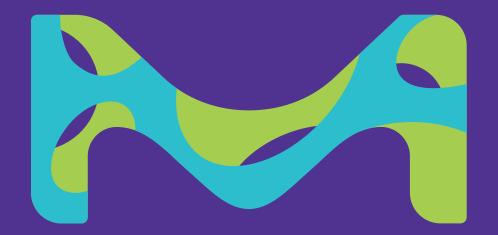
Thank you!

Millipore Sigma

Come see us at our booth or send a message







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