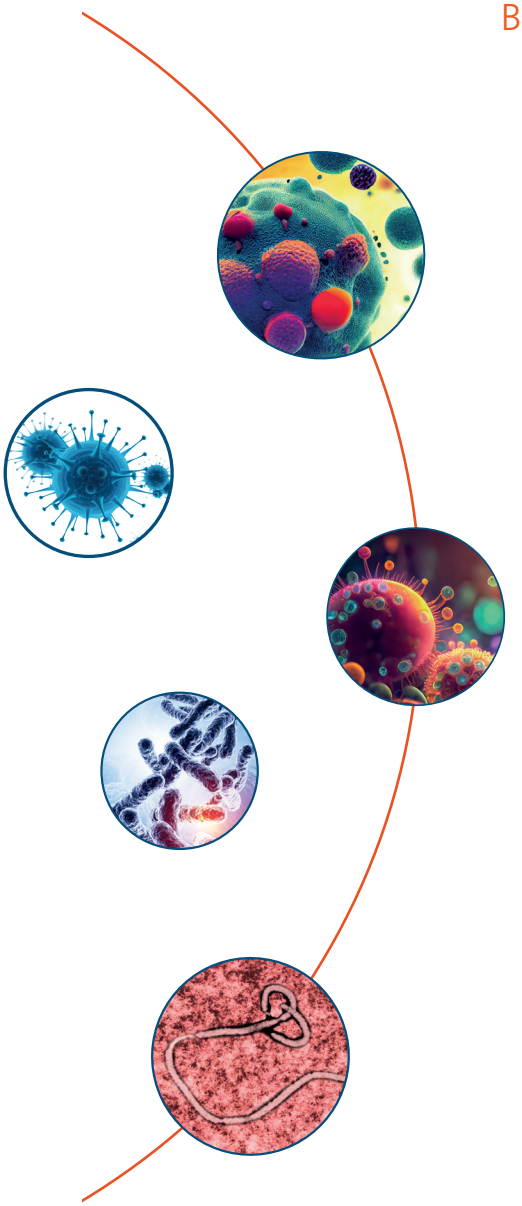
Stronger Science for Pathogen Detection

As public health labs and clinical research labs expand molecular testing for infectious diseases, the need for sensitive, resilient assays with faster turnaround times continues to grow. Quantabio's qPCR, RT-qPCR and NGS solutions provide robust amplification across inhibitor-rich samples and support confident low limits of detection for viral, bacterial and fungal pathogens.

Overcoming Molecular Testing Challenges

Clinical and environmental research samples such as swabs, blood, saliva and others often contain high levels of PCR inhibitors, which can compromise results and hinder public health outcomes. Quantabio addresses these challenges with solutions that maintain assay sensitivity and consistency across diverse, inhibitor-rich sample types to support dependable testing in high-throughput and resource-limited settings.



BACTERIAL & FUNGAL DETECTION BY qPCR

Rapid and accurate detection and quantification of bacterial and fungal DNA by qPCR is critical to determine species type, which aids in triaging infectious pathogens.

MULTIPLEX VIRUS DETECTION BY RT-qPCR

Results per sample are increased with up to 5 multiplex RNA targets in easy to use 1-step reaction setups. This enables the detection and differentiation of multiple respiratory and other RNA viruses, including COVID, Flu A/B, RSV, etc.

SURVEILLANCE & GENOTYPING BY SEQUENCING

Metagenomic sequencing using both short & long read NGS enables multiplexing identification of infectious pathogens as well as re-emergence of new strains via molecular mutations for broad community/population surveillance.

Learn More

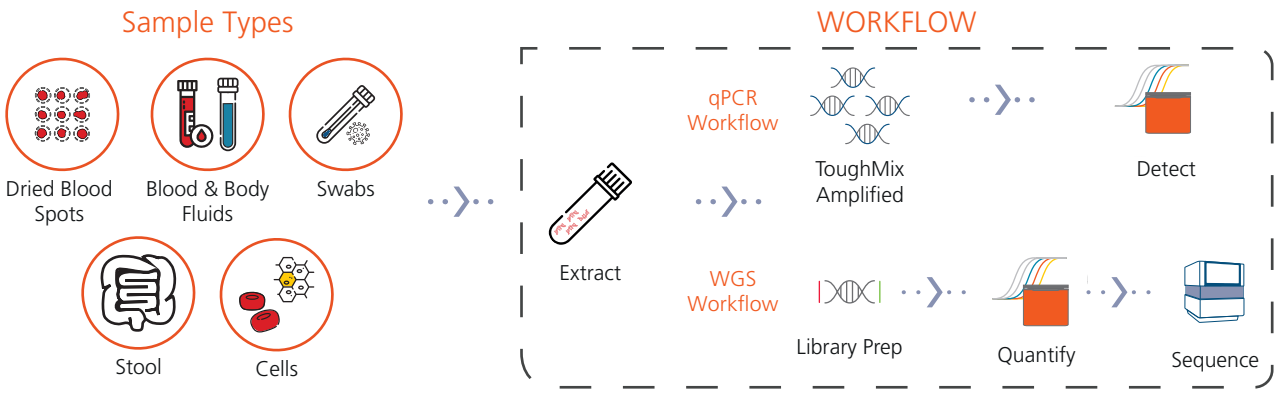
ToughMix. Experience the Amplification Difference!

ToughMix chemistry is the trade secret difference to our mastermix formulations. For more than 20 years, it has helped scientists amplify and analyze challenging samples by overcoming common PCR inhibitors. ToughMix formulations can be used directly from crude lysates as well as from purified, extracted samples.

What can ToughMix do?

- Work directly with crude lysates
- Avoid expensive and time-consuming purification steps
- Compatible with a wide range of probe designs and detection chemistries
- High quality *Taq* polymerase – free of residual host DNA
- Neutralize problem causing inhibitors present in crude samples

Inhibitor	Common sources	Reagent performance	
		Competitor	ToughMix
Hematin	Blood Dried blood spots	–	✓
Hemoglobin	Blood	✓	✓
Polysaccharides	Feces Plant tissues	–	✓
Melanin	Hair Skin	–	✓



Discover the Right Product by Application

Product	qPCR Applications			Sequencing Applications				
	Bacterial/ Fungal Pathogen Detection/ Quantification	Viral Pathogen Detection/ Quantification	Genotyping	16S/ 18S/ ITS Amplicon Sequencing	AMR Testing and Tracking	Whole Genome Sequencing	Whole Viral RNA Sequencing	Long Read Sequencing
PerfeCTa qPCR ToughMix/ Multiplex ToughMix	X		X					
UltraPlex 1-Step ToughMix		X	X					
qScript XLT 1-Step ToughMix		X	X					
eQo 1-Step ToughMix		X	X					
qScript Ultra Flex Kit			X				X	X
repliQa HiFi ToughMix				X	X		X	X
sparQ DNA Library Prep Kits					X	X	X	

ToughMix
Designed for Diverse Pathogen PCR & qPCR Applications

Pathogen Detection and Quantification

Inhibitor-tolerant qPCR detection and quantification enables faster time to result and can reduce the need for laborious extraction methods in resource-limited settings. Byrnes *et al.* (2021) aimed to examine the impact of an extraction-free method applied to samples stored in Viral Transport Media (VTM) on amplification and detection of SARS-CoV-2. This group found that both UltraPlex 1-Step ToughMix and qScript XLT 1-Step ToughMix were the most inhibitor-tolerant of the mixes tested, allowing for confident detection of virus from extraction-free samples (Figure 1).

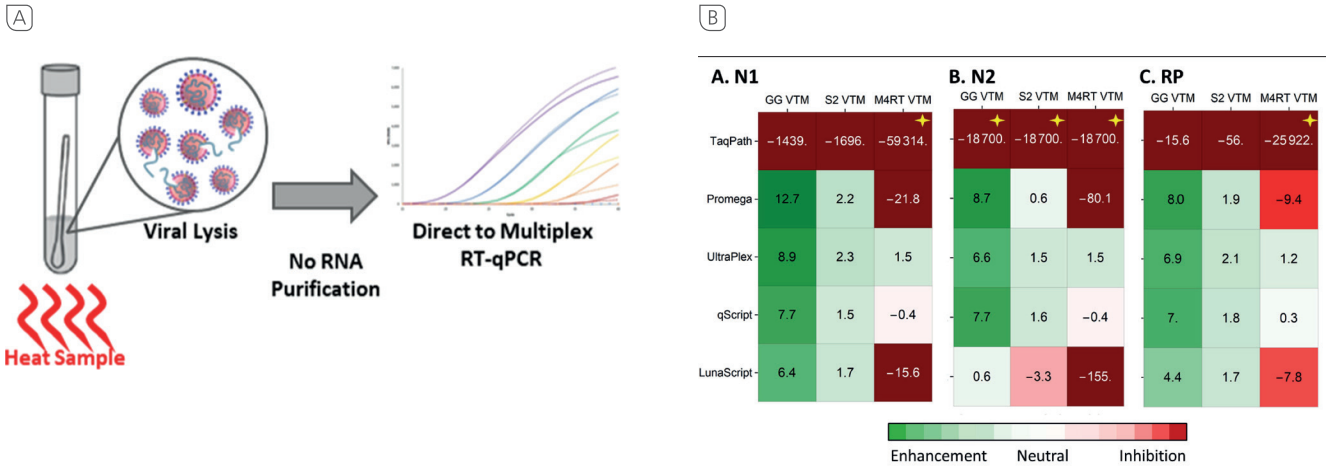
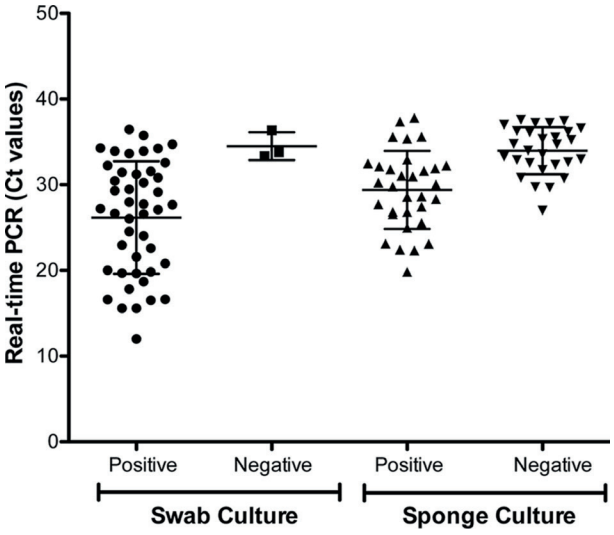


Figure 1 **Extraction-free detection of SARS-CoV-2. (A)** Workflow for extraction-free detection from samples stored in Viral Transport Media (VTM). **(B)** Calculated impact of VTM on CDC SARS-CoV-2 detection test. UltraPlex 1-Step ToughMix and qScript XLT 1-Step ToughMix were found to be the most inhibitor tolerant of the mixes tested and even showed some amplification enhancement of the qPCR signal. Figure from Byrnes *et al.* Multiplexed and Extraction-Free Amplification for Simplified SARS-CoV-2 RT-PCR Tests, 2021.



Environmental Surveillance

Environmental surveillance is key for rapid screening and prevention of spread due to emerging pathogens. For example, *Candida auris* is an emerging fungal pathogen of concern for hospital-acquired infections with many isolates showing multidrug resistance. Leach *et al.* (2018) developed an qPCR assay for rapid *C. auris* detection using PerfeCTa Multiplex qPCR ToughMix for superior detection and faster time to results vs. traditional culture-based detection methods (Figure 2).

Figure 2 **Real-time qPCR data for *C. auris* detection from swab and sponge collection of surfaces.** The qPCR assay was able to detect *C. auris* in several samples that were negative by culture, showcasing superior detection. Figure from Leach *et al.* Development and Validation of a Real-Time PCR Assay for Rapid Detection of *Candida auris* from Surveillance Samples, 2018.

sparQ
Designed for Diverse Pathogen Sequencing Applications

Pathogen Surveillance

Next-generation sequencing is a powerful tool for the surveillance of new and evolving pathogens. In particular, metagenomic sequencing can be used to identify co-infections or novel divergent viruses that may be missed by lower throughput methods like qPCR analysis. Orf *et al.* utilized the sparQ DNA Frag & Library Prep Kit for high-depth sequencing to confirm the divergent results from a broad low-pass sequencing method, allowing for greater understanding of viral evolution and detection of previously uncharacterized pathogens in a viral surveillance program (Figure 3).

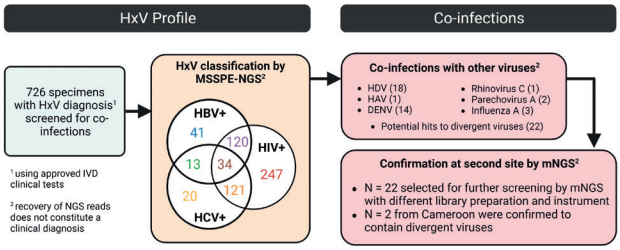
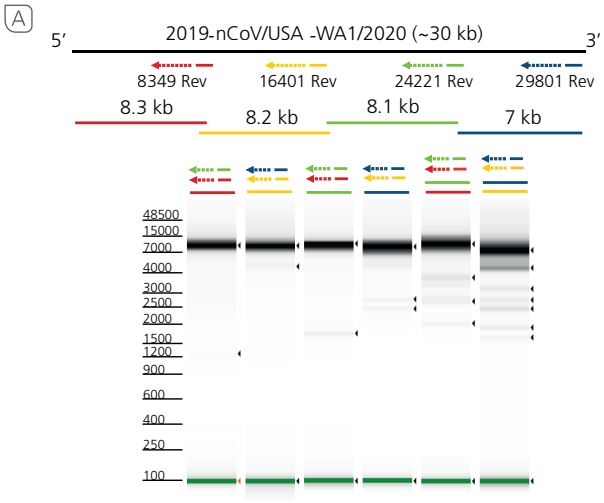


Figure 3 Surveillance and screening workflow utilized as part of blood-borne surveillance program. The sparQ DNA Frag & Library Prep Kit was used for confirmational testing of samples selected for further screening. Testing confirmed co-infections of known pathogens as well as the divergent viral sequences noted from an alternative library prep method. Figure from Orf *et al.* Metagenomic Detection of Divergent Insect- and Bat-Associated Viruses in Plasma from Two African Individuals Enrolled in Blood-Borne Surveillance, 2023.

Viral Whole Genome Sequencing

With improvements to sequencing costs and throughput, viral whole genome sequencing is essential to fully understand the rise and fall of infectious viral pathogens. Nagy *et al.* (2025) utilized repliQa HiFi ToughMix to amplify complex, overlapping ~10 kb segments of the human monkeypox (mpox) virus prior to nanopore sequencing for a better understanding of an early isolate of the 2022 multi-country outbreak of mpox. Quantabio developed a similar strategy for short read sequencing by pairing the qScript Ultra Flex kit for fast cDNA synthesis with repliQa HiFi ToughMix for amplification, followed by library preparation with the sparQ DNA Frag & Library Prep Kit. This strategy was applied for full-length SARS-CoV-2 analysis (Figure 4).



Mapped reads (%)	99	98.9	98.3	97.8	98.7	97.4
Duplication rate (%)	3.6	3.6	3.3	4.6	3	3.5

Figure 4 Library preparation and sequencing of full-length SARS-CoV-2 viral RNA. (A) After cDNA synthesis using qScript Ultra Flex Kit, 7-8.5 kb fragments were amplified using repliQa HiFi ToughMix as seen by TapeStation gDNA ScreenTape. **(B)** Library preparation was completed using the sparQ DNA Frag & Library Prep Kit using the large amplicons as input. Sequencing results showed high specificity of mapped reads and low duplication rates. Figure from Speed with precision: Faster and longer cDNA synthesis accompanied by rapid high-fidelity PCR enabling long-range sequencing of RNA viruses, presented at AGBT 2022.

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