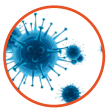
Stronger Science for Animal Health

Quantabio supports advances in animal health research by providing robust and highly sensitive amplification tools. Our PCR & qPCR ToughMix® chemistries along with sparQ NGS solutions are used in laboratories around the world to help assess animal health in livestock, poultry, aquaculture as well as veterinary diagnostics, by rapidly detecting difficult pathogens and genetic mutations.

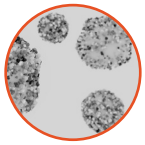
PATHOGEN DETECTION

Rapidly detect DNA and RNA viral and bacterial pathogens that pose health threats to various animal species using PCR, qPCR or NGS molecular workflow applications.



ENVIRONMENTAL SURVEILLANCE

Protect animal and public health with Quantabio solutions for environmental surveillance, enabling pathogen detection, antimicrobial resistance monitoring, and microbiome analysis in veterinary, agricultural, and wildlife settings.



ANIMAL AND MICROBIOMICS SEQUENCING

Advance animal health research with reliable solutions for whole-genome, targeted, and microbiome sequencing applications, delivering high-quality data from challenging veterinary, livestock, and environmental samples.

Learn More

ToughMix. Experience the Amplification Difference!

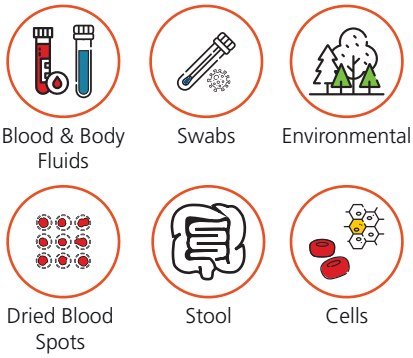
ToughMix chemistry is the trade secret difference to our mastermix formulations. For more than 20 years, it has helped scientists to amplify and analyze challenging samples by overcoming common PCR inhibitors. ToughMix formulations can be used directly from crude lysates as well as following an extraction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

What can ToughMix do?

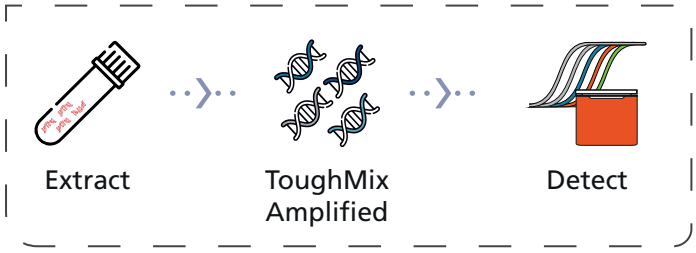
- Work directly with crude lysates
- Avoid expensive and time-consuming purification steps
- Compatible with a wide range of probe designs and detection chemistries
- High quality *Taq* polymerase – free of residual host DNA
- Neutralize problem causing inhibitors present in crude samples

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

Sample Types



Workflow



Discover the Right Product by Application

	Product	Pathogen Detection	Gene Expression Analysis	Microbiome Profiling	Infectious Disease Surveillance	16S Sequencing	Veterinary Diagnostics	Viral Load	Diagnostic Development	Monitoring Environment
PCR	repliQa HiFi ToughMix	X	X	X		X	X			X
	AccuStart II PCR ToughMix	X	X	X	X	X	X			X
qPCR	PerfeCTa SYBR Green FastMix	X	X				X			
	PerfeCTa Multiplex qPCR ToughMix	X	X	X	X		X			X
RT-qPCR	eQo 1-Step ToughMix	X	X		X		X	X	X	
	UltraPlex 1-Step ToughMix	X	X		X		X	X	X	
NGS	sparQ DNA Library Prep Kits	X	X	X			X			
	sparQ RNA Library Prep Kits	X	X				X			
	sparQ HiFi PCR MasterMix	X	X	X	X	X	X			X

ToughMix.
Designed for Diverse Animal Health PCR & qPCR Applications

Pathogen Detection

Hamond *et al.* (Scientific Reports 2022) used PerfeCTa qPCR ToughMix for detecting pathogenic *Leptospira* in wild rodent kidneys from the U.S. Virgin Islands, revealing a 43.6% infection rate and confirming rodents as key reservoirs (Figure 1).

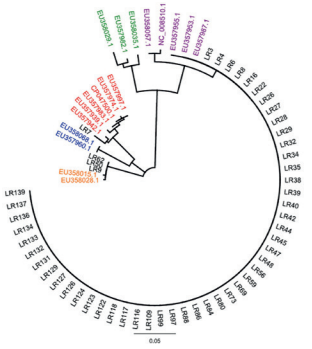


Figure 1 Phylogeny of *Leptospira* isolates based on secY gene sequence (522 bp) analysis using the neighbor-joining method. U.S. Virgin Islands isolates of *Leptospira* from rodents are annotated as LR and colored black. Figure from Hamond *et al.* Assessing rodents as carriers of pathogenic *Leptospira* species in the U.S. Virgin Islands and their risk to animal and public health, 2022.

Hill *et al.* (PLOS Pathogens, 2022) used qScript XLT One-Step RT-qPCR ToughMix to detect and quantify influenza A virus RNA from wild bird samples, revealing species-specific roles in avian influenza spread. This study highlights the importance of long-term surveillance in understanding viral transmission dynamics (Figure 2).

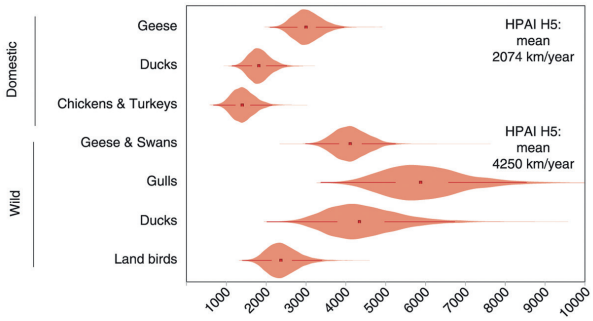
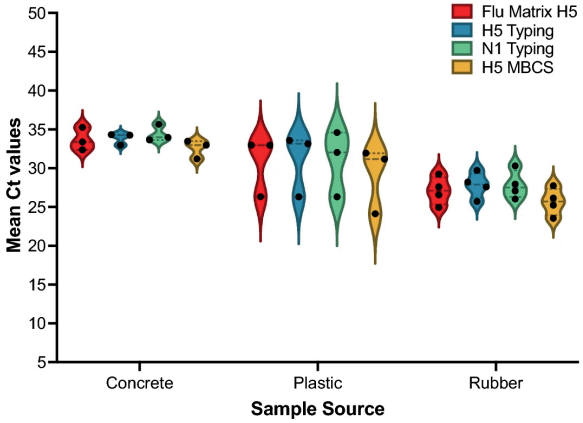


Figure 2 Ecologically divergent hosts contribute to the diffusion and geographic expansion of influenza A virus. The diffusion rates of highly pathogenic avian influenza (HPAI) H5 (red). Figure from Hill *et al.* Ecological divergence of wild birds drives avian influenza spillover and global spread, 2022.

Environmental Surveillance



Researchers at Kansas State University (2024) used qScript XLT One-Step RT-qPCR ToughMix to detect H5N1 HPAIV in environmental swabs from a dairy farm, confirming contamination on multiple surfaces. Genomic analysis identified mutations linked to mammalian adaptation, highlighting an evolving public and animal health risk (Figure 3).

Figure 3 Characterization of samples for H5N1 HPAIV using RT-qPCR assays. The Violin graph shows mean Ct values on the x-axis, sample swab sourceon the y-axis, grouped with four different RT-qPCR assays for H5N1 HPAIV characterization and detection. Figure from Singh *et al.* Detection and characterization of H5N1 HPAIV in environmental samples from a dairy farm, 2024.

eQo 1-Step ToughMix delivers highly sensitive detection of RNA pathogens like H5N1 avian influenza virus, validated with Twist synthetic controls from 20,000 to 2 copies (Figure 4). This robust lyophilized RT-qPCR solution performs well with inhibitor-rich samples and is ideal for veterinary diagnostics and environmental surveillance workflows in animal health.

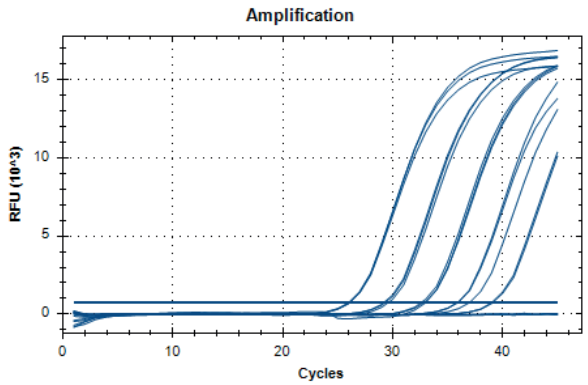


Figure 4 A representative amplification plot was generated by diluting synthetic H5N1 RNA from 20,000 to 2 copies. A strong amplification curve was observed even with two copies of the target in the reaction.

sparQ & repliQa.
Designed for Diverse Animal Health Sequencing Applications

Microbiome Analysis

The sparQ NGS library prep portfolio offers fast, efficient solutions for diverse animal health applications, including whole genome, targeted, and metagenomic sequencing. Optimized for high-quality data from challenging veterinary and environmental samples.

16S Metagenomics

Filatov *et al.* (Infection, Genetics and Evolution, 2024) used repliQa HiFi ToughMix for high-fidelity amplification of mitochondrial genomes from soft ticks, uncovering the distribution and genetic diversity of *Borrelia caucasica* vectors. Whereas, Ezzat *et al.* (Animal Microbiome, 2020) utilized AccuStart II ToughMix for 16S rRNA gene sequencing to investigate how parrotfish predation influences coral microbiomes. Their findings revealed that predation significantly alters microbial community composition and increases diversity in reef-building corals (Figure 5).

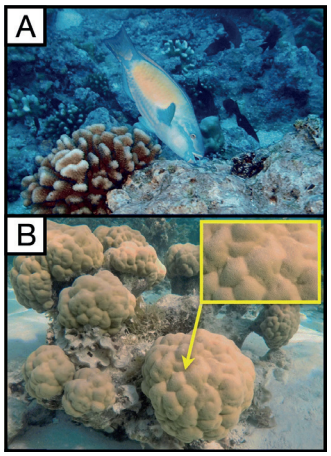


Figure 5 A **Bullethead parrotfish *Chlorurus spilurus*.** B **Unbitten colonies of *Porites lobata* in the back reef area of Mo'orea, French Polynesia.** Figure from Ezzat *et al.* Parrotfish predation drives distinct microbial communities in reef-building corals, 2020.

Whole Genome Sequencing

A cross-sectional study (Front. Microbiol. 2020) analyzed dairy cattle metagenomes to assess antimicrobial resistance (AMR) in animals farmed in a heavy metal–contaminated environment. Researchers used the sparQ DNA Library Prep Kit for Illumina® to prepare metagenomic libraries, enabling comprehensive sequencing of microbial communities. The study revealed elevated AMR gene levels, linking environmental contamination to increased resistance traits in livestock microbiomes (Figure 6).

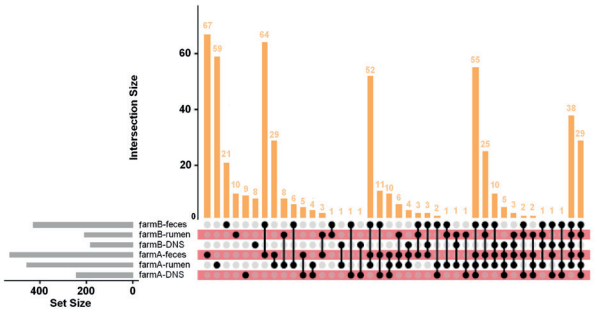


Figure 6 **AMR gene distribution across farms and anatomical sites.** Of the 549 AMR genes detected, 67 are found only in farm A fecal samples, and 59 are only in farm A rumen fluid samples. The intersections of gene combinations are shown in the dot matrix and vertical bar plot. Figure from Gaeta *et al.* A Cross-Sectional Study of Dairy Cattle Metagenomes Reveals Increased Antimicrobial Resistance in Animals Farmed in a Heavy Metal Contaminated Environment, 2020. Heavy Metal Contaminated Environment, 2020.

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