Recent DNA/RNA Shield Citations w/ Short summaries

#1
A robust and sensitive assay was developed to screen for the 18S rRNA gene of *Plasmodium falciparum* and *Plasmodium vivax* from asymptomatic and low density infections. The new RT-PCR based method could detect malaria infections that were significantly lower than the standard microscopy and rapid detection method. DNA/RNA Shield™ was used to preserve patient's blood samples in the field for 14 days at 28°C and 80% humidity.

Adams M, et. al. (2015). An ultrasensitive reverse transcription polymerase chain reaction assay to detect asymptomatic low‐density *Plasmodium falciparum* and *Plasmodium vivax* infections in small volume blood samples. Malar. J. 14:520.

#2
An RNA-based detection method was developed to detect low asymptomatic malaria infections in rural areas of Haiti. Three different detection methods were utilized--rapid diagnostic test, thick smear microscopy and a qRT-PCR assay were evaluated. The blood samples used for qRT-PCR were preserved in DNA/RNA Shield™ to maintain the sample integrity until RNA isolation. The qRT-PCR method was the most sensitive and identified significantly more samples.

Elbadry MA, et. al. (2015). High prevalence of asymptomatic malaria infections: a cross‐sectional study in rural areas in six departments in Haiti. Malar. J. 14:510.

#3
During a survey of Middle East respiratory syndrome coronavirus (MERS-CoV), nasal swabs from dromedary camels were collected into DNA/RNA Shield™. Any MERS-positive swab samples were completely inactivated in DNA/RNA Shield and were subsequently used for RNA extraction. Successful detection of MERS-CoV and phylogenetic analysis suggests local zoonotic transmission through the respiratory route onto humans.

Nowotny N, et. al. (2014). Middle east Respiratory Syndrome Coronavirus (MERS-CoV) in Dromedary Camels, Oman, 2013. Eurosurveillance. 19(16).

#4
West Nile virus positive plasma samples were inactivated in DNA/RNA Shield™ and resulting viral RNA was detected and identified by qRT-PCR. Phylogenetic comparisons between human and mosquito-derived strains were closely related but not identical which indicates co-circulation in a confined area.

Kolodziejek J, et. al. (2015). West Nile Virus Positive Blood Donation and Subsequent Entomological Investigation, Austria, 2014. PLoS One. 10(5).

#5
DNA/RNA Shield™ was used to preserve RNA in plasma samples positive for Dengue and Chikungunya virus. Extracted total RNA was used for downstream sequencing for genotyping and phylogenetic analysis. Results revealed two serotypes (DENV-2 and DENV-3) along with CHIKV infection representing the first documented co-infection.

Phommanivong V, et. al. (2016). Co-circulation of the dengue with chikungunya virus during the 2013 outbreak in the southern part of Lao PDR. Tropical Medicine and Health. 44:24.

#6
Samples taken from groundwater supplies in the city of Kabwee, Zambia were preserved and inactivated in DNA/RNA Shield™. The samples were then examined for enteric pathogens. 16S rRNA analyses of the

samples identified the presence of enteric bacteria contamination with prevalent contamination of *Citrobacter freundii* and *Vibrio cholera*.

Sorensen, JPR. (2015). Tracing enteric pathogen contamination in sub-Saharan African groundwater. Science of the Total Environment. 538: 888–895.

#7
DNA/RNA Shield™ was used to preserve biofilm samples of Xyella fastidiosa, a gram negative plant-pathogenic bacterium, until RNA isolation for RNA-Seq analyses. The authors reported that during the presence of calcium (Ca) supplementation, transcriptomic changes were observed in cells to promote biofilm growth, while non-supplementation of Ca resulted in the scattering of Xylella fastidiosa.

Parker JK, et. al. (2016). Calcium transcriptionally regulates the biofilm machinery of Xylella fastidiosa to promote continued biofilm development in batch cultures. Environmental Microbiology. 18(5): 1620–1634.

#8
DNA/RNA Shield™ was used to store water collected onto filters and total RNA was isolated. A detailed metatranscriptomic analysis of the microbial communities points towards differing metabolic cycles occurring in anoxic and saline habitats in upper and deep sea regions respectively.

Pachiadaki MG, et. al. (2014). Unveiling microbial activities along the halocline of Thetis, a deep-sea hypersaline anoxic basin. ISME J. 8(12): 2478-89.

#9
MicroRNA expression profiles of 11 African sorghum plants were analyzed under watered and drought conditions to determine the mechanisms involved in drought tolerance. The leaves from sorghum plants exposed to different growing conditions were preserved in DNA/RNA Shield™ until RNA extraction.

Hamza NB, et. al. (2016). MicroRNA expression profiles in response to drought stress in Sorghum bicolor. Gene Expression Patterns. 20: 88-98.

#10
The researchers sought to better understand the physiological importance of the non-sense-mediated mRNA decay (NMD) in murine Sertoli cells. Mice testes were preserved in DNA/RNA Shield™ and stored RNA isolation. The data revealed that the knockout of *Upf2*, which is part of the NMD pathway, resulted in testicular atrophy and sterility.

Bao J, et. al. (2015). UPF2, a nonsense-mediated mRNA decay factor, is required for prepubertal Sertoli cell development and male fertility by ensuring fidelity of the transcriptome. Development. 142: 352-362.

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