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# Supplementary Materials: "A new multiplexed magnetic-capture and droplet digital PCR (ddPCR) tool for monitoring wildlife population health and pathogen surveillance"

**Table S1**. A summary of the synthesized oligonucelotides (g-blocks) used as positive controls for each of the target pathogens.

DOUBLE-STRANDED SYNTHETIC OLIGONUCLEOTIDE SEQUENCE (5' – 3')

### *Erysipelothrix rhusiopathiae* (341 bp)

### *Francisella tularensis* (381 bp)

# Mycobacterium tuberculosis (272 bp)

# *Toxoplasma gondii* (354 bp)

# *Trichinella nativa* (231 bp)

**Table S2.** A summary of the in vitro specificity analyses performed. American Type Culture collection (ATCC), Iowa State University, Veterinary Diagnostic Laboratory (ISU-VDL), European Union Reference Laboratory for Parasites (EURLP).

Target	Pathogen (strain)	PCR	Source
Francisella tularensis	Francisella tularensis (410062; Jellison type B)	+	
	Francisella tularensis (410101; Jellison type A)	+	
	Bacillus anthracis	-	
	Bacillus subtilis (6633)	-	ATCC
	Brucella abortus	-	
	Clostridium sporogenes	-	
	Coxiella burnetii (VR- 616)	-	ATCC
	Enterobacter cloacae	-	
	Enterococcus faecalis	-	
	Escherichia coli (270011)	-	
	Escherichia coli (e23716)	-	ATCC
	Haemophilus influenzae	-	
	Hafnia alvei (45201)	-	
	Klebsiella pneumoniae (1.1526)	-	
	Legionella pneumophila	-	
	Leptospira	-	
	Listeria monocytogenes (19111)	-	ATCC
	Moraxella catarrhalis	-	
	Morganella morganii (430024)	-	
	Mycobacteria spp. (n=11)	-	
	Mycobacterium tuberculosis	-	
	Proteus mirabilis (430011)	_	
	Proteus vulgaris (430052)	_	
	Providencia stuartii (1.1209)	_	
	Pseudomonas aeruginosa (14502)	_	ATCC
	Pseudomonas psuedomallei	_	
	Salmonella typhimurium (460691)	-	
	Salmonella typhimurium (19585)	_	ATCC
	Serratia marcescens	_	
	Shigella dysenteriae (480011)	_	
	Staphylococcus aureus (6538)	_	ATCC
	Streptococci (Lancefield's serological groups B and C)	_	
	Vibrio cholerae (SM 6)	-	
	Yersinia enterocolitica (52302)	-	
	Yersinia enterocolitica (9610)	_	ATCC
	Yersinia pestis (410041)	_	
	Yersinia pestis (23053)	_	ATCC

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	Yersinia pseudotuberculosis (410051)	-	
Erysipelothrix rhusiopathiae	Erysipelothrix rhusiopathiae (2017)	+	ISU-VDL
	Erysipelothrix rhusiopathiae (422-1)	+	ISU-VDL
	Erysipelothrix rhusiopathiae (545)	+	ISU-VDL
	Erysipelothrix rhusiopathiae (Bano 36)	+	ISU-VDL
	Erysipelothrix rhusiopathiae (CJPT-97)	+	ISU-VDL
	Erysipelothrix rhusiopathiae (Doggersharbe)	+	ISU-VDL
	Erysipelothrix rhusiopathiae (HC-585)	+	ISU-VDL
	Erysipelothrix rhusiopathiae (Kaparek)	+	ISU-VDL
	Erysipelothrix rhusiopathiae (MEW 22N/5)	+	ISU-VDL
	Erysipelothrix rhusiopathiae (NF-4)	+	ISU-VDL
	Erysipelothrix rhusiopathiae (P-190)	+	ISU-VDL
	Erysipelothrix rhusiopathiae (P-92)	+	ISU-VDL
	Erysipelothrix rhusiopathiae (Pecs 3597)	+	ISU-VDL
	Erysipelothrix rhusiopathiae (Pecs 9)	+	ISU-VDL
	Erysipelothrix rhusiopathiae (Tanzania III)	+	ISU-VDL
	Erysipelothrix rhusiopathiae (Tuzok)	+	ISU-VDL
	Erysipelothrix rhusiopathiae (VI-12/8)	+	ISU-VDL
	Actinobacillus pleuropneumoniae (1359)	-	ISU-VDL
	Actinobacillus suis (1376)	-	ISU-VDL
	Arcanobacterium pyogenes (2135)	-	ISU-VDL
	Erysipelothrix sp. strain 1 (Pecs 18)	-	ISU-VDL
	Erysipelothrix sp. strain 2 (715)	-	ISU-VDL
	Erysipelothrix tonsillarum (2553)	-	ISU-VDL
	Erysipelothrix tonsillarum (Bano 107)	-	ISU-VDL
	Erysipelothrix tonsillarum (CJSF 14-2)	-	ISU-VDL
	Erysipelothrix tonsillarum (Iszap 4)	-	ISU-VDL
	Erysipelothrix tonsillarum (KS20A)	-	ISU-VDL
	Erysipelothrix tonsillarum (L136)	-	ISU-VDL
	Erysipelothrix tonsillarum (Lengyel-P)	-	ISU-VDL
	Erysipelothrix tonsillarum (P-43)	-	ISU-VDL
	Erysipelothrix tonsillarum (Wittling E1)	-	ISU-VDL
	Escherichia coli	-	ISU-VDL
	Haemophilus parasuis (1298)	-	ISU-VDL
	Listeria monocytogenes (12784)	-	ISU-VDL
	Pasteurella multocida (1861)	-	ISU-VDL
	Salmonella group E (1295)	-	ISU-VDL
	$C_{i} = 1.1$ (1.410)	_	ISU-VDL
	Staphylococcus aureus (1419)		
Mycobacterium tuberculosis complex (MTBC)	Staphylococcus aureus (1419) Streptococcus suis (39831)		ISU-VDL
		+	
	Streptococcus suis (39831)	- + +	ISU-VDL
	Streptococcus suis (39831)  Mycobacterium tuberculosis		ISU-VDL VISAVET

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	Mycobacterium caprae	+	VISAVET
	Mycobacterium microti	+	VISAVET
	Mycobacterium pinnipedii	+	VISAVET
	Brucella abortus	-	VISAVET
	Brucella mellitensis	-	VISAVET
	Corynebacterium pseudotuberculosis	-	VISAVET
	Enterococcus hirae	-	VISAVET
	Lysteria monocytogenes	-	VISAVET
	Mycobacterium avium group X (n=10)	-	VISAVET
	Mycobacterium avium subsp. avium (n=3)	-	VISAVET
	Mycobacterium avium subsp. hominissuis (n=7)	-	VISAVET
	Mycobacterium chitae	-	VISAVET
	Mycobacterium colombiense	-	VISAVET
	Mycobacterium europeum	-	VISAVET
	Mycobacterium flavescens	-	VISAVET
	Mycobacterium fortuitum (n=3)	-	VISAVET
	Mycobacterium gordonae	-	VISAVET
	Mycobacterium hibernae	-	VISAVET
	Mycobacterium intracellulare	-	VISAVET
	Mycobacterium kansasii (n=9)	-	VISAVET
	Mycobacterium marinum (n=2)	-	VISAVET
	Mycobacterium neoaurum	-	VISAVET
	Mycobacterium nonchromogenicum (n=4)	-	VISAVET
	Mycobacterium parascrofulaceum	-	VISAVET
	Mycobacterium peregrinum (n=2)	-	VISAVET
	Mycobacterium phlei (n=2)	-	VISAVET
	Mycobacterium scrofulaceum	-	VISAVET
	Mycobacterium seoulense	-	VISAVET
	Mycobacterium shimodei	-	VISAVET
	Mycobacterium smegmatis (n=2)	-	VISAVET
	Mycobacterium terrae	-	VISAVET
	Mycobacterium thermoresistible	-	VISAVET
	Mycobacterium vaccae	-	VISAVET
	Nocardia sp.	-	VISAVET
	Rhodococcus equi	-	VISAVET
	Salmonella enterica Sv. Typhimurium	-	VISAVET
	Serratia maucencens	-	VISAVET
	Streptomyces sp.	-	VISAVET
Trichinella spp.	Trichinella britovi	+	EURLP
	Trichinella murreli	+	EURLP
	Trichinella nativa	+	EURLP
	Trichinella nelsoni	+	EURLP
	Trichinella papuae	+	EURLP
	Trichinella pseudospiralis	+	EURLP

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	Trichinella spiralis	+ EURLP	
	Trichinella zimbabwensis	+ EURLP	
	Ancylostoma caninum	-	
	Ascaris suum	-	
	Dipylidium caninum	-	
	Echinococcus granulosus	-	
	Sarcocystis cruzi	-	
	Spirometra erinacei	-	
	Taenia hydatigena	-	
	Taenia solium	-	
	Toxocara canis	-	
	Trichuris suis	-	
	Cat	-	
	Fox	-	
	Pig	-	
	Saltwater crocodile	-	
	Tasmanian devil		
Toxoplasma gondii	Toxoplasma gondii (n=12)	+	
	Clinically negative samples (n=160)	-	

Bacterial genera (n=118)

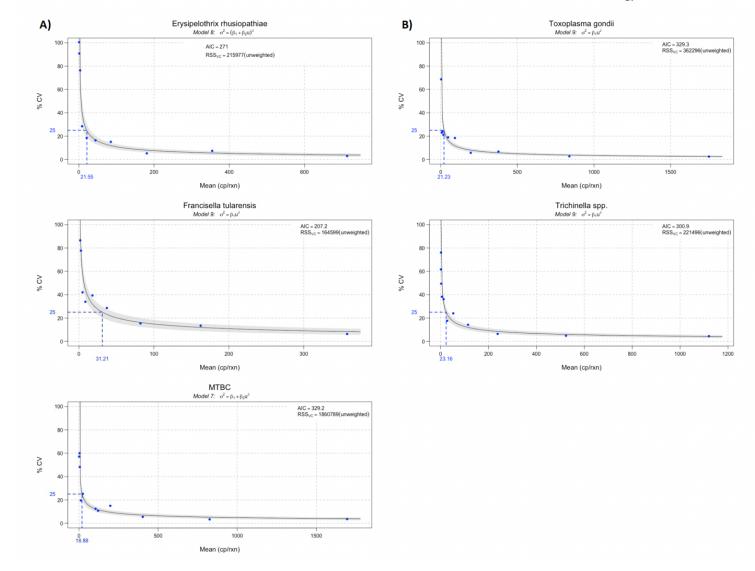


Figure S1. The precision profile of each of the pathogenic targets (A) the triplex assay targets B) the duplex assay targets) fit to their regression model of best fit. The LOQ was assessed as the copy numbers per  $\mu$ L where the percent coefficient variation met our precision goal of  $\leq 25\%$ .