



### Helbing Laboratory eDNA Technical Bulletin

All eDNA tools are validated through a rigorous multi-step evaluation protocol that includes tests of DNA target specificity and amplification sensitivity<sup>1-3</sup>.

#### General eDNA Assay Information

Target Species: Umatilla Dace (*Rhinichthys umatilla*) eDNA qPCR Tool: eRHUM4 Gene Target: MT-CTRL  
Species Code: te-RHUM eDNA qPCR Format: TaqMan Published in:

#### eDNA Assay Sensitivity Test Summary using gBlocks™ Synthetic DNA

LOD 1.6 95% CI 1.1-3.0 Copies/Rxn LOQ 6.2 95% CI 4.3-11.2 Copies/Rxn LOB 0 hits/8  
LOQ<sub>continuous</sub> 20 Copies/Rxn

Binomial-Poisson model for 8 technical replicates determined using eLowQuant R code<sup>4</sup>. When the LOQ < LOD, use the LOD for the LOQ. Enzyme: Immolase

#### eDNA Assay Specificity Test Information

Each qPCR reaction in the specificity assay contained 10 picograms of voucher target gDNA (n=25 technical replicates)

Species	Common Name ( <i>Species</i> )	Detection	# Voucher		Sample Sources/Locations
			Specimens		
ma-HOSA	Human ( <i>Homo Sapiens</i> )	No	1		Netherlands
te-CAAU	Goldfish ( <i>Carassius auratus</i> )	No	1		British Columbia
te-COCO	Slimy Sculpin ( <i>Cottus cognatus</i> )	No	1		British Columbia
te-ESLU	Northern Pike ( <i>Esox lucius</i> )	No	1		British Columbia
te-GAAC	Three Spine Stickleback ( <i>Gasterosteus aculeatus</i> )	No	1		British Columbia
te-MIDO	Smallmouth Bass ( <i>Micropterus dolomieu</i> )	No	1		British Columbia
te-MISA	Largemouth Bass ( <i>Micropterus salmoides</i> )	No	1		British Columbia
te-ONCL	Cutthroat Trout ( <i>Oncorhynchus clarkii</i> )	No	1		British Columbia
te-ONMY	Rainbow Trout ( <i>Oncorhynchus mykiss</i> )	No	1		British Columbia
te-PRCY	Round Whitefish ( <i>Prosopium cylindraceum</i> )	No	1		Yukon
te-RHUM	Umatilla Dace ( <i>Rhinichthys umatilla</i> )	Yes	5		British Columbia
te-SACO	Bull Trout ( <i>Salvelinus confluentus</i> )	No	1		British Columbia
te-SAMA	Dolly Varden ( <i>Salvelinus malma</i> )	No	1		British Columbia
te-THPA	Eulachon ( <i>Thaleichthys pacificus</i> )	No	1		British Columbia

#### References

- Hobbs, J, Adams, IT, Round, JM, Goldberg, CS, Allison, MJ, Bergman, LC, Mirabzadeh, A, Allen, H, Helbing, CC (2020) Revising the range of Rocky Mountain tailed frog, *Ascaphus montanus*, in British Columbia, Canada, using environmental DNA methods. Environmental DNA, 2: 350-361. <https://doi.org/10.1002/edn3.82>
- Hobbs, J, Round, JM, Allison, MJ, Helbing, CC (2019) Expansion of the known distribution of the coastal tailed frog, *Ascaphus truei*, in British Columbia, Canada, using robust eDNA detection methods. PLOS ONE 14(3): e0213849. <https://doi.org/10.1371/journal.pone.0213849>
- Langlois, VS, Allison, MJ, Bergman, LC, To, TA, and Helbing, CC (2020) The need for robust qPCR-based eDNA detection assays in environmental monitoring and risk assessments. Environmental DNA, 3: 519-527. doi: 10.1002/edn3.164
- Lesperance, M, Allison, MJ, Bergman, LC, Hocking, MD, and Helbing, CC (2021) A statistical model for calibration and computation of detection and quantification limits for low copy number environmental DNA samples. Environmental DNA, 3: 970-981. doi: 10.1002/edn3.220



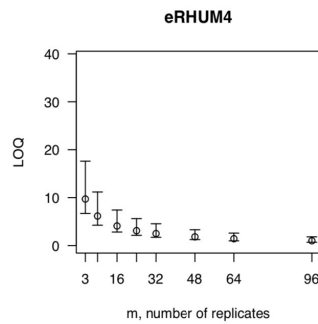
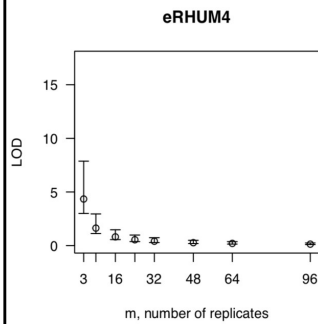
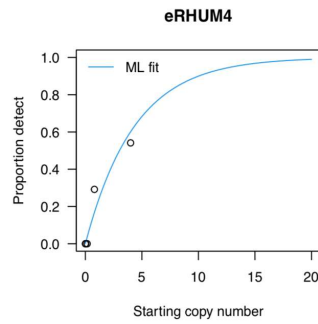
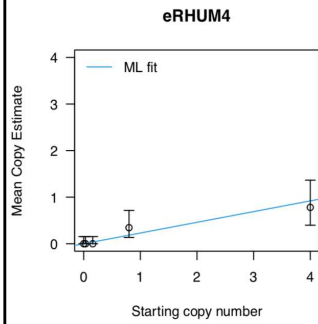
eDNA Assay Sensitivity Test Details using gBlocks™ synthetic DNA

To calculate tables for different numbers of replicates, raw csv data files can be accessed here:  
<https://onlineacademiccommunity.uvic.ca/helbinglab/edna/>

From 8 Technical Replicates

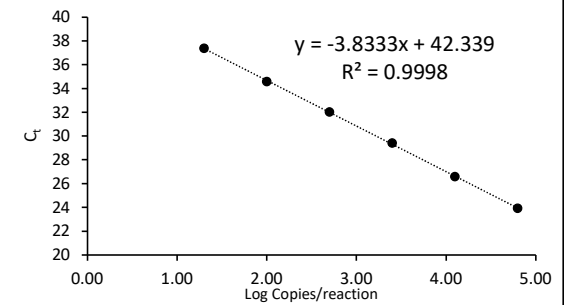
# Detects	# Copies	SE
0	0	0
1	0.58	0.6
2	1.25	0.93
3	2.04	1.28
4	3.02	1.69
5	4.27	2.21
6	6.02	2.99
7	9.04	4.56

Determined using eLowQuant R code<sup>4</sup>.



Binomial-Poisson model: No intercept  
Determined using eLowQuant R code<sup>4</sup>.  
Based on a 2 µL DNA input in a total 15 µL reaction

Applied to reactions with ≥ 95% positive hits



Efficiency 82%

Field Sample Validation

Known  
Sample Type Presence # Samples Detected Location

Abbreviations			
95% CI	95% Confidence interval	LOQ	Limit of quantification
eDNA	Environmental DNA	MT-CTRL	Mitochondrial control region gene
gDNA	Total genomic DNA extracted from voucher specimen	NTC	qPCR no template control
LOB	Limit of blank	qPCR	Quantitative real-time polymerase chain reaction
LOD	Limit of detection	SE	Standard error