



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 sensitivity¹⁻³.

General eDNA Assay Information

Target Species: *Heteromastus filobranchus*
Species Code: an-HEFI

eDNA qPCR Tool: eHEFI7
eDNA qPCR Format: TaqMan

Gene Target: MT-CYB
Published in:

eDNA Assay Sensitivity Test Summary using gBlocks™ Synthetic DNA

| | | | | | | | | | | | | |
|-----|------------|--------|----------------|--------|-----|------------|--------|----------------|--------|-----|----------|--------|
| LOD | <u>0.3</u> | 95% CI | <u>0.2-0.5</u> | Copies | LOQ | <u>1.1</u> | 95% CI | <u>0.8-1.9</u> | Copies | LOB | <u>0</u> | hits/8 |
|-----|------------|--------|----------------|--------|-----|------------|--------|----------------|--------|-----|----------|--------|

LOQ_{continuous} 4 Copies/Rxn

Binomial-Poisson model for 8 technical replicates determined using eLowQuant R code⁴. 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)

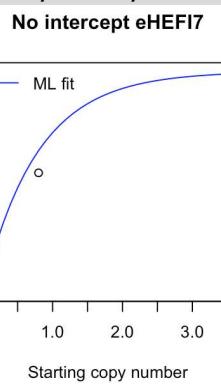
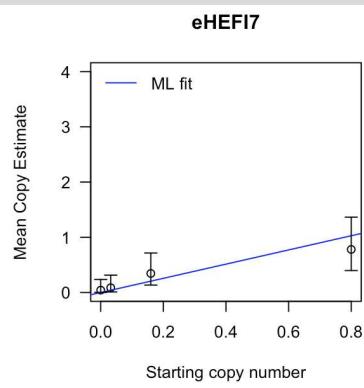
Voucher

| Species | Common Name (<i>Species</i>) | Detection | Specimens | Sample Sources/Locations |
|-----------|--|-----------|-----------|--------------------------|
| an-CACA | <i>Capitella capitata</i> | No | 3 | British Columbia |
| an-DEGR | <i>Decamastus gracilis</i> | No | 4 | British Columbia |
| an-GLNA | <i>Glycera nana</i> | No | 2 | British Columbia |
| an-HEFI | <i>Heteromastus filobranchus</i> | Yes | 4 | British Columbia |
| an-NOHE | <i>Notomastus hemipodus</i> | No | 2 | British Columbia |
| an-PRJU | <i>Prionospio (Prionospio) jubata</i> | No | 2 | British Columbia |
| an-PRLI | <i>Prionospio (Minuspio) lighti</i> | No | 4 | British Columbia |
| an-PRMU | <i>Prionospio (Minuspio) multibranchiata</i> | No | 1 | British Columbia |
| an-RIP1 | Hydrothermal vent worm (<i>Ridgeia piscesae</i>) | No | 3 | British Columbia |
| ma-CALUfa | Domestic dog (<i>Canis lupus familiaris</i>) | No | 1 | British Columbia |
| ma-FECA | Domestic cat (<i>Felis catus</i>) | No | 1 | British Columbia |
| ma-HOSA | Human (<i>Homo sapiens</i>) | No | 1 | Netherlands |

References

1. 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. 2020; 2: 350-361. <https://doi.org/10.1002/edn3.82>
2. 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>
3. 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
4. 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



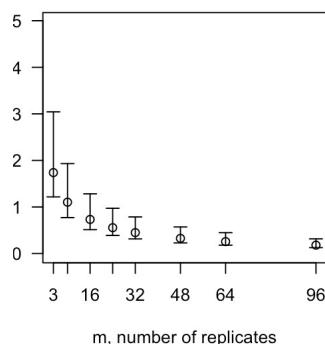
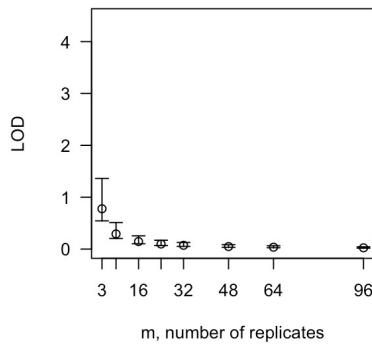
To calculate tables for different numbers of replicates, raw csv data files can be accessed here:
<https://onlineacademiccommunity.uvic.ca/helbinglab/edna/>

From 8 Technical Replicates

| # Detects | # Copies | SE |
|-----------|----------|------|
| 0 | 0 | 0 |
| 1 | 0.1 | 0.11 |
| 2 | 0.22 | 0.17 |
| 3 | 0.37 | 0.23 |
| 4 | 0.54 | 0.3 |
| 5 | 0.76 | 0.39 |
| 6 | 1.08 | 0.53 |
| 7 | 1.62 | 0.81 |

Determined using eLowQuant R code⁴.

Limits detect - no intercept eHEFI7 Limits quant - no intercept eHEFI7

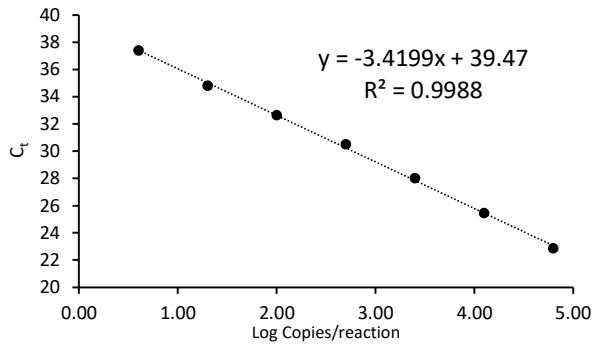


Binomial-Poisson model: No-Intercept

Determined using eLowQuant R code⁴.

Based on a 2 µL DNA input in a total 15 µL reaction

Applied to reactions with 100% positive hits



Efficiency

96%

Field Sample Validation

Known

Sample Type Presence # Samples Detected Location

Abbreviations

| | | | |
|--------|---|--------|--|
| 95% CI | 95% Confidence interval | LOQ | Limit of quantification |
| eDNA | Environmental DNA | MT-CYB | Mitochondrial cytochrome b 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 |