

1 Supporting Information 2

2 2A) Compilation of the Literature Database

3 We compiled a literature database of published single-species eDNA assays, excluding work
4 on microbial eDNA, metabarcoding and dietary studies. First, every paper listed on the
5 “Environmental DNA: Tools and Resources” homepage of Washington State University
6 (<https://labs.wsu.edu/edna/edna-assays>) as of 10 April 2019 was checked for suitability and
7 added to the literature database. Afterwards, a literature search on Web of Science
8 (<http://apps.webofknowledge.com/>) was conducted on 11 April 2019 using the following search
9 criteria:

10 TS=("environmental DNA" OR "eDNA") NOT TS=("biofilm" OR "biofilms" OR "microbial" OR
11 "bacterial" OR "microorganism" OR "microorganisms" OR "metabarcoding" OR
12 "metagenomics" OR "next generation sequencing"); Databases= WOS, KJD, MEDLINE, RSCI,
13 SCIELO; Timespan=2008-2019; Search language=English; Research Domain: science and
14 technology; Document type: article, correction, book.

15 A list of 660 Web of Science entries was returned. Each of the publications was manually
16 checked for suitability based on the exclusion criteria above, resulting in a set of 319 papers.
17 During the assay validation process, it was necessary to include additional papers that
18 originally published a primer set or that contained other information vital to the assay validation
19 process. The final literature database contained 327 papers
20 (<https://doi.org/10.6084/m9.figshare.12184860.v1>).

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22 2B) R packages used for analysis

23 The following R packages were used for data analysis: “ggplot2” (Wickham, 2016),
24 “RColorBrewer”(Neuwirth, 2014), “scales” (Wickham & Seidel, 2019), “viridis” (Garnier, 2018),
25 “rpart” (Therneau & Atkinson, 2019), “rpart.plot” (Milborrow, 2019), and “gridExtra” (Auguie,
26 2017), “dplyr” (Wickham, François, Henry, & Müller, 2019) and “hrbrthemes” (Rudis, 2019).

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29 **References**

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