

## **Supplementary details about the methods and results for Lafferty et al. Detecting southern California's white sharks with environmental DNA**

### **Extraction details.**

PCR effort was equal across sites. Before extraction, the external surfaces of columns were wiped with 5% bleach solution, allowed to dry, and then re-wiped with 70% EtOH solution to aid in sterilization. Sterivex columns were placed vertically and allowed to dry with caps off for 30 min after removing the internal buffer with a lure lock syringe. Internal buffers were transferred to 2 ml microcentrifuge tubes and spun at 14000 rpm for 30 min. Liquid from this centrifuge step was discarded and the pellet was allowed to dry. Lysis mixtures were then prepared for filter and buffer extractions (720 ul buffer ATL +80 ul proteinase K for capsule and 180 ul buffer ATL plus 20 ul proteinase K) for the solution extraction along with proteinase K; Qiagen Inc.; 800 ul total volume for filters and 200 ul for buffer extractions) and upon the addition of lysis buffer, the samples were incubated at 56°C for 24 hr on a rotating incubator.

### **Primer selection details.**

Single mismatches between primer and template can result in non-binding or non-detection. Thus, primer specificity is essential to target species and mismatches from non-target organisms are critical, particularly at the 3' end of the primer (see Wilcox et al. 2013 for review of target/primer mismatch). To ensure specificity, we used Primer-BLAST (Goldberg et al. 2016) to target only white shark DNA and not the 14 other elasmobranch species found in the study region (Table 1). Primer-BLAST was developed at NCBI to make primers that are specific to the intended PCR target. It uses Primer3 (Untergasser et al. 2012) to design PCR primers and then uses BLAST and global alignment algorithm to screen primers against a user-selected database to avoid primer pairs (all combinations including forward-reverse primer pair, forward-forward as well as reverse-reverse pairs) that can cause non-specific amplifications.

### **Control details.**

Samples were replicated one time each with only multiple replication on our controls (i.e., multiple positive controls and multiple negative controls for each ddPCR run). At no time did any of these controls fail. Field samples were only repeated if they screened positively, and then were only considered positive if they repeated their positive screening a second time.