







D

Supplementary Figure 1: Bayesian and maximum likelihood estimate of phylogenetic relationships among elasmobranch species using mitochondrial protein coding genes, for *Rhinobatos punctifer* (**A**), *Torpedo sinuspersici* (**B**), *Carcharhinus sorrah* (**C**), *Mobula mobular* and *Mobula tarapacana* (**D**). The unknown sequence contig for each of the five specimens clusters with their taxonomically assigned identities and thus confirms their taxonomic classification based on morphology. Numbers at nodes are posterior probabilities for BI trees and bootstrap support values are the numbers at nodes in ML trees.



Supplementary Figure 2: A) A comparison of species occurrence across sampling loca1ons, determined by assessing the number of specimens collected at each sampling site. **B)** Percentage of species for sharks and batoids sampled in each conservation category.

В

Α



Supplementary Figure 3: Depth range of 24 species sampled and described across all four sample locations.



Supplementary Figure 4: Comparison of previously reported geographic ranges and landing site locations for three species from the current study indicated as: Okha (blue arrow), Porbandar (red arrow) and Veraval (black arrow). **A)** Geographic range of *Carcharhinus sorrah* on the IUCN Redlist Database, and landing sites for the species in Porbandar and Veraval, **B)** Geographic range of *Torpedo sinuspersici* on the IUCN Redlist Database, and landing site for the species in Porbandar, and **C)** Geographic range of *Rhinobatos punctifer* on the IUCN Redlist Database, and landing sites for the species in Okha, Porbandar and Veraval.