Categorize samples into MAB, SNE, GOM etc regions. Tally the most abundant fishes in each region.

Categorize fishes into deep sea and shallow. Calculate the percentage of deep sea species at surface depth vs at deep depth.

Compare eDNA with BTS

Deep vs demersal vs pelagic vs mesopelagic (took all surface vs >200m samples and run indicator species analysis)

Vertical structure: thermocline vs chlorophyll max, which matters to fish