Part 1b - Depth transect - Vector Pacific

[A] LIBRARY PREP:

12S: 1x MiSeq V3 run using MiFish-U 12S primers

COI: 1x MiSeq V3 run using Leray COI primers

[B] DATA FILE OVERVIEW:

1. METADATA

Vector\_metadata\_MAL\_Feb3,2023.csv -> Metadata for all samples and controls included in the sequencing run

2. 12S

sequence\_table.12S.merged.w\_ASV\_names.length\_var.txt -> 12S ASV table (not filtered, not QCed, with all ASVs including non-fish)

12S\_ASV\_sequences.length\_var.fasta -> List of all 12S ASV sequences

taxonomy\_table.12S.NCBI\_NT.96sim.LCA\_only.txt -> Annotation of 12S ASVs using LCA (this is a good place to start

taxonomy\_table.12S.NCBI\_NT.96sim.LCA+besthit.txt -> Annotation of 12S ASVs using hybrid approach of LCA + best hit

12S\_ASV\_sequences.length\_var.blast.out -> Full blast output from all 12S ASVs

vector2021\_Run20230121.12S.tar.gz -> Full, raw, bioinformatics output from Evan

3. COI

sequence\_table.CO1.merged.w\_ASV\_names.txt -> 12S ASV table (raw, not filtered, not QCed)

CO1\_ASV\_sequences.fasta -> List of all COI ASV sequences

taxonomy\_table.CO1.NCBI\_NT+customDB.iterative\_blast.txt -> Annotation of COI ASVs using hybrid approach of LCA + best hit

CO1\_ASV\_sequences.blast\_87.out -> Full blast output from all COI ASVs (minimum identity = 87%)

CO1\_ASV\_sequences.blast\_96.out ->Full blast output from all COI ASVs (minimum identity = 96%)

vectorPacific\_Re-Run20220916.CO1.tar.gz -> Full, raw, bioinformatics output from Evan