Illumina vs Oxford Nanopore: a multi-marker comparative study on fish eDNA metabarcoding

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Key aspects of environmental DNA metabarcoding

Markers

12S rRNA

Cytochrome Oxidase C Subunit I (COI)

Are they comparable?

Is multi-marker better?

Sequencing platform

Illumina

Nanopore

Are they comparable?

Longer amplicon = higher taxonomic resolution?

Samples (n=20)

Mock

Genomic DNA

13 species

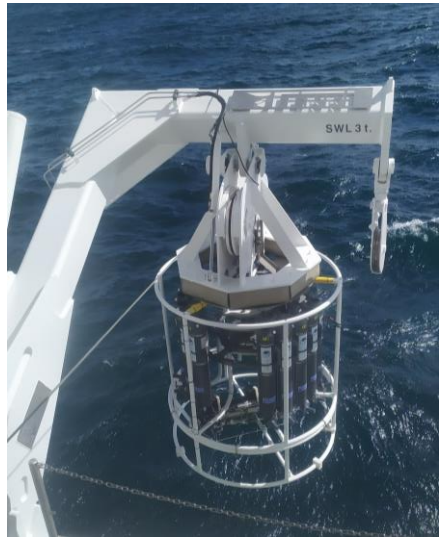
n=4

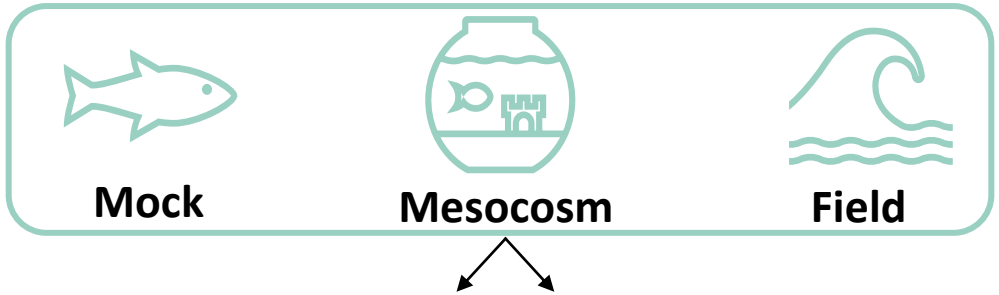
Mesocosm

Ray tank	Ocean tank
5 species	5 species
n=4	n=4

Field

Pelagic	Mesopelagic
Unknown species	
n=4	n=4





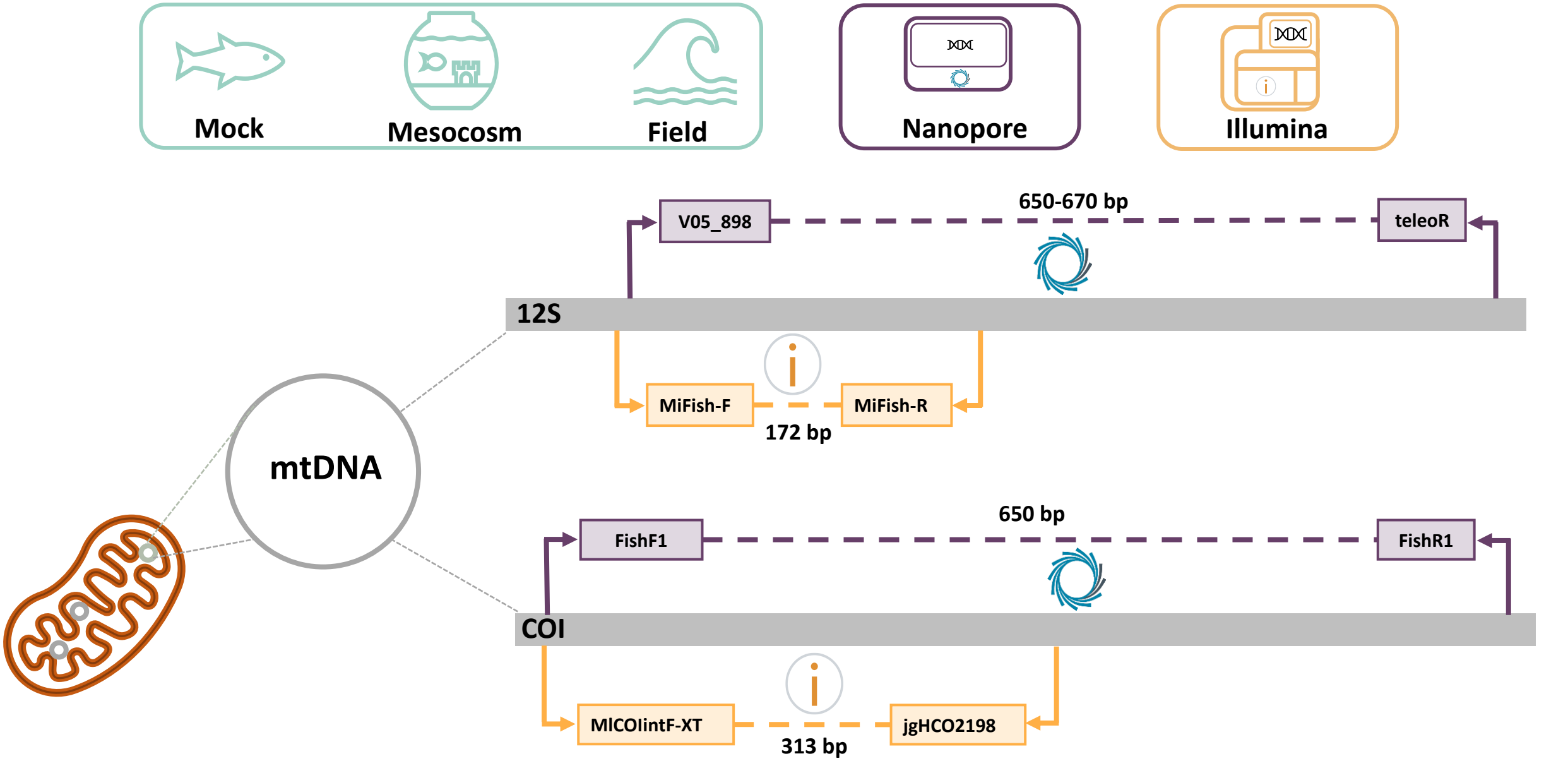
Nanopore Sequencing

Kit 110	Kit 114
long 12S n=20	long 12S n=20
long COI n=20	long COI n=20

Illumina Sequencing

NovaSeq PE250

short 12S n=20	short COI n=20

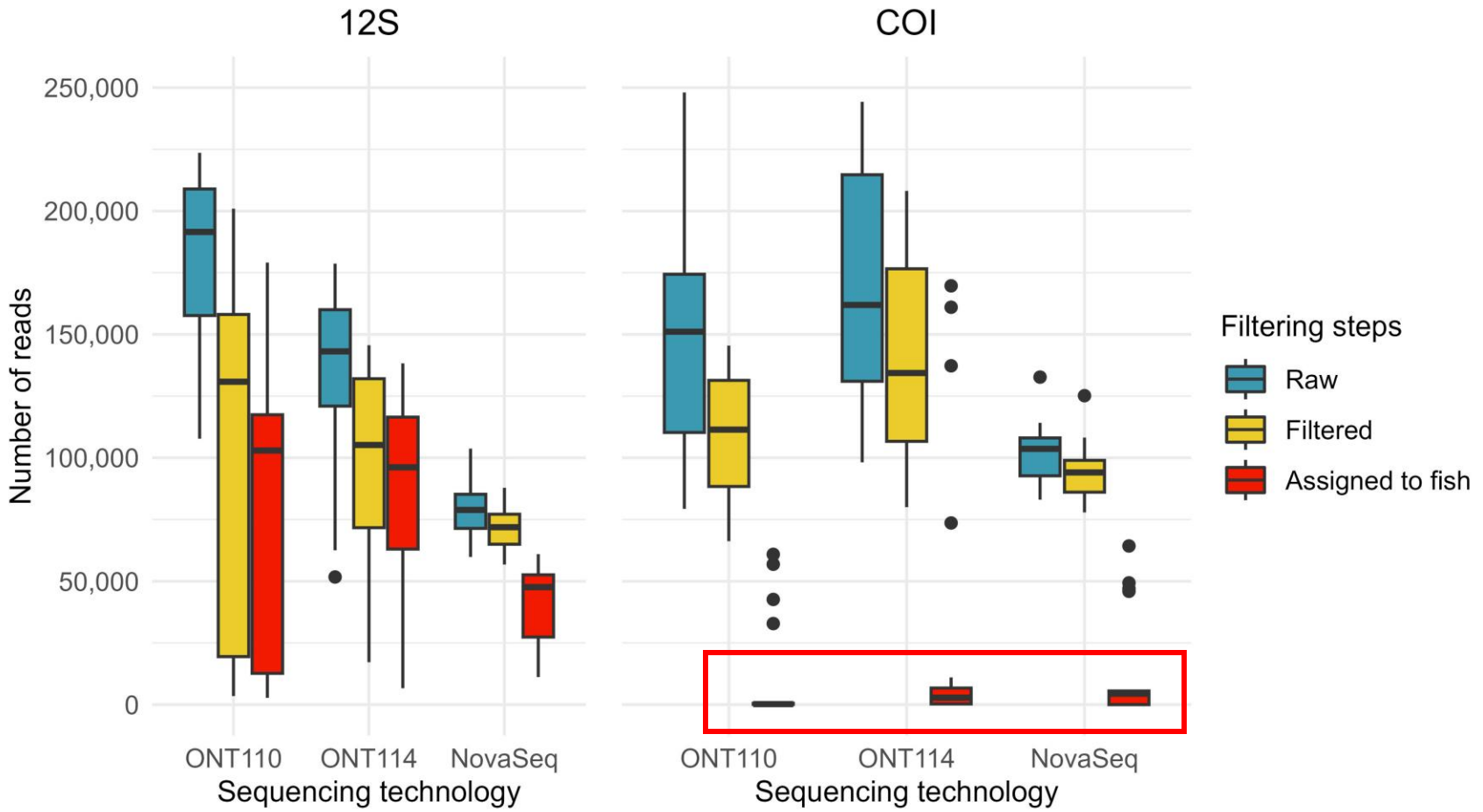

Mock
Mesocosm
Field
Nanopore
Illumina
mtDNA
12S
V05_898
teleoR
650-670 bp
MiFish-F
MiFish-R
172 bp
COI
FishF1
FishR1
650 bp
MlCOIintF-XT
jgHCO2198
313 bp

Markers

12S > COI

Significantly more species recovered

Increased species richness with **multi-marker** approach



Sequencing platforms

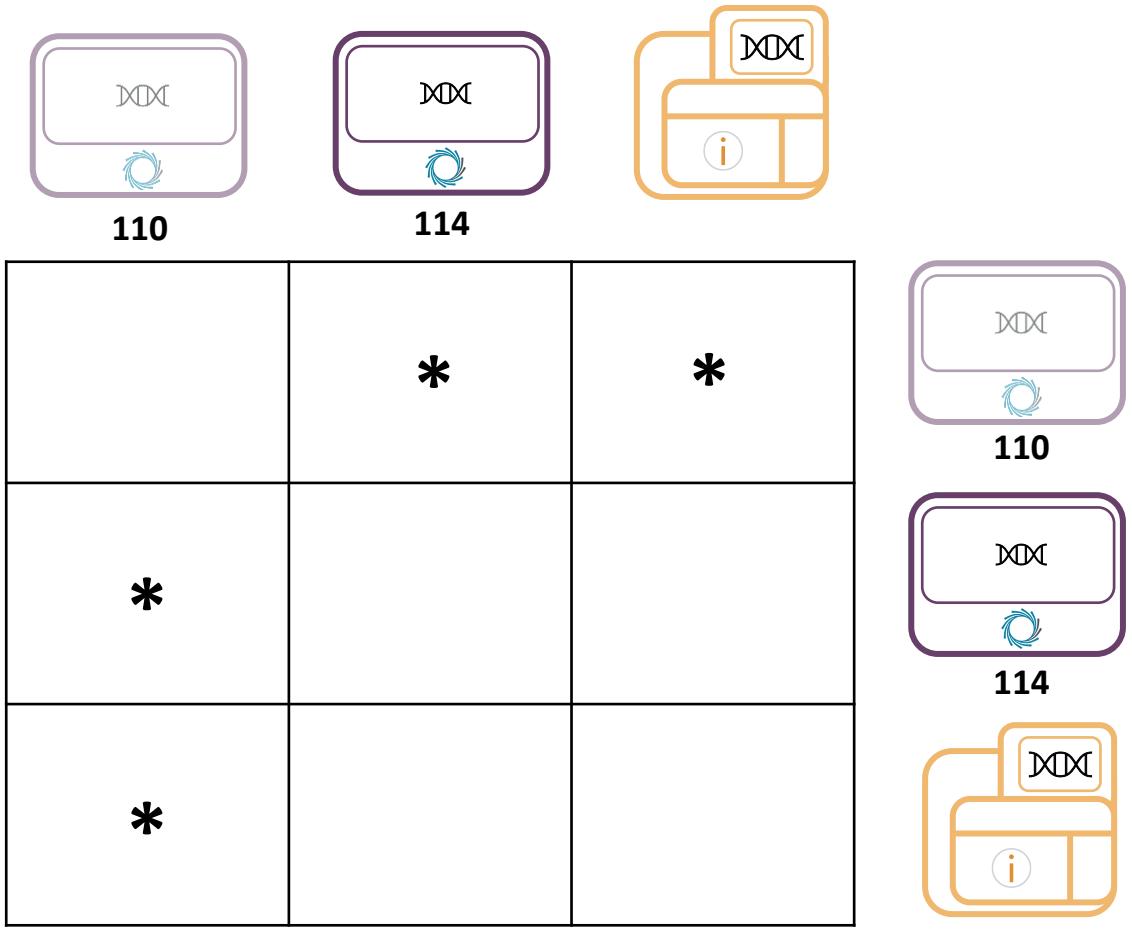
110

114

	110	114	
q-score	≈10	≈10	>30

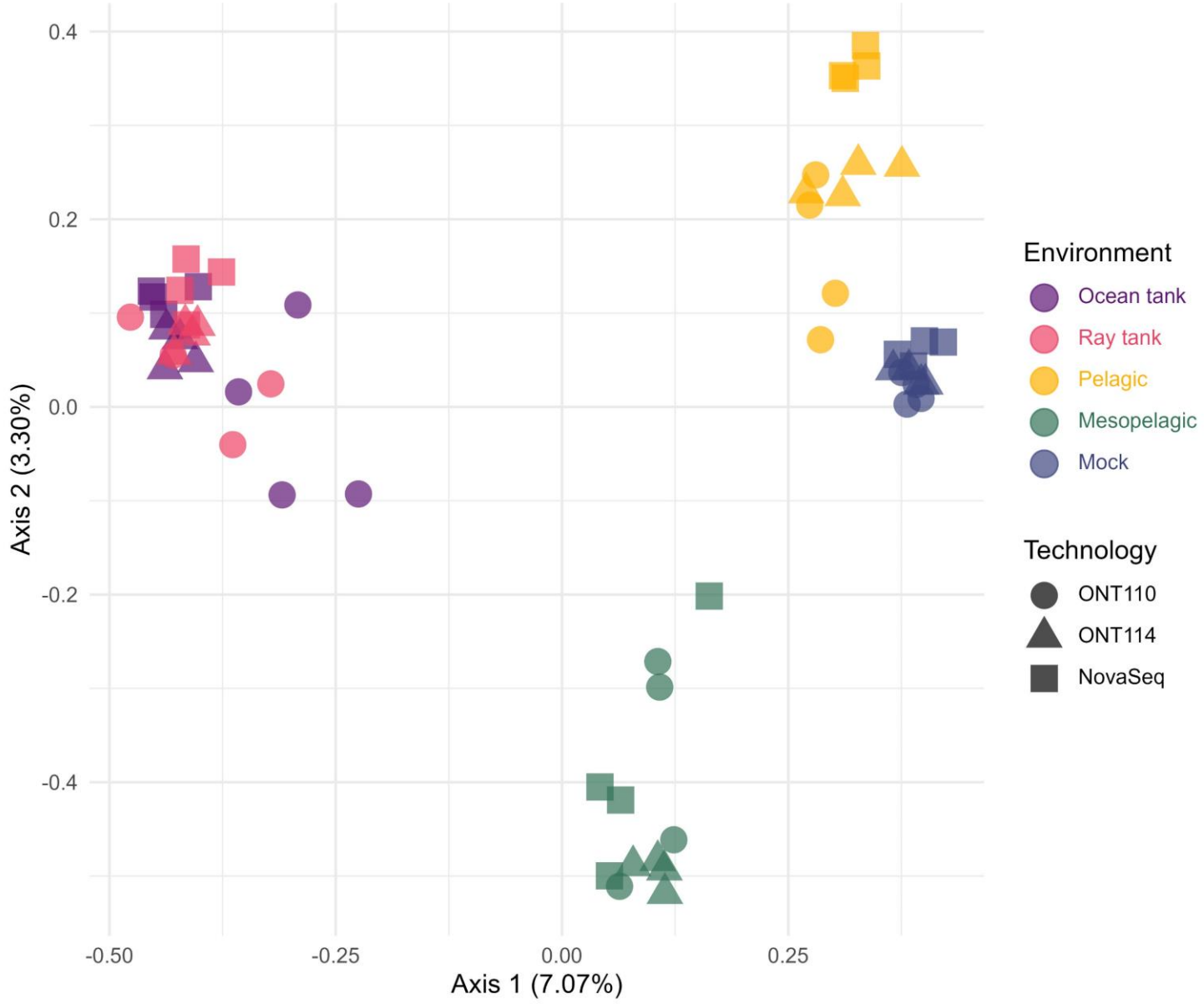
Sequencing platforms

Species richness (12S+COI)



Sequencing platforms

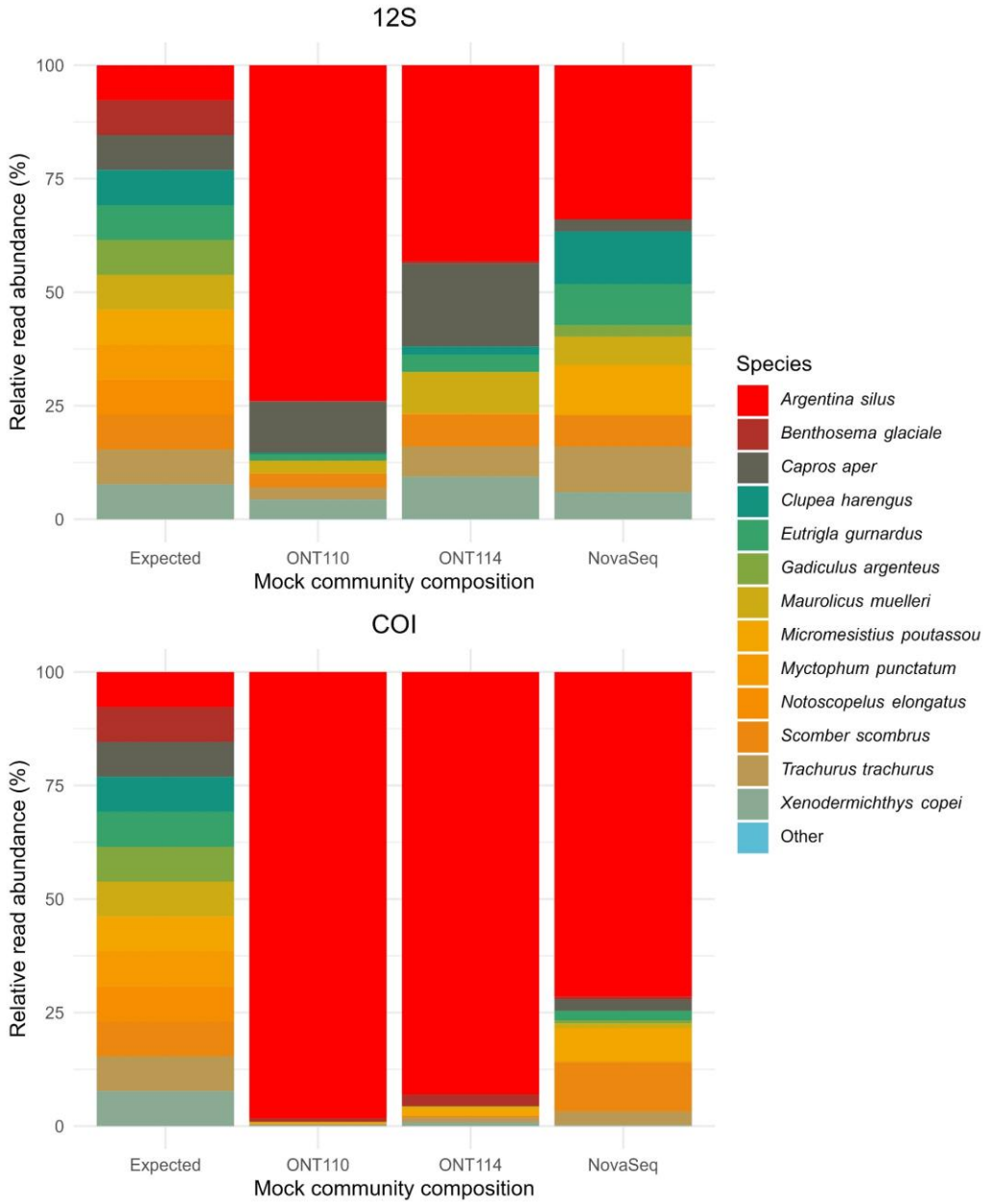
Pres./abs. matrices (12S+COI)



Mock communities

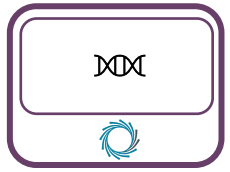
Species detected

	12S	COI	12S+COI
110	11/13	6/13	11/13
114	12/13	9/13	12/13
	10/13	11/13	12/13

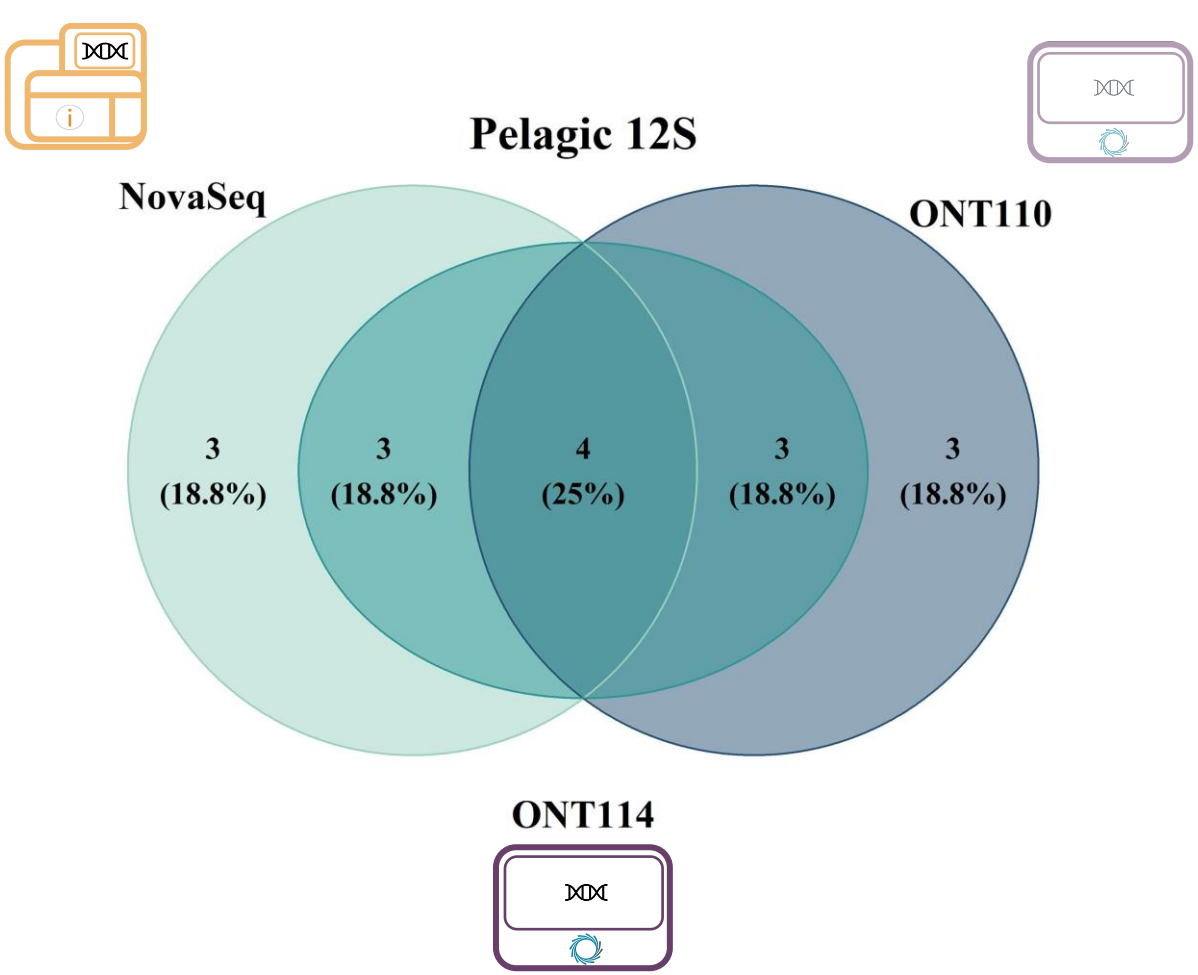


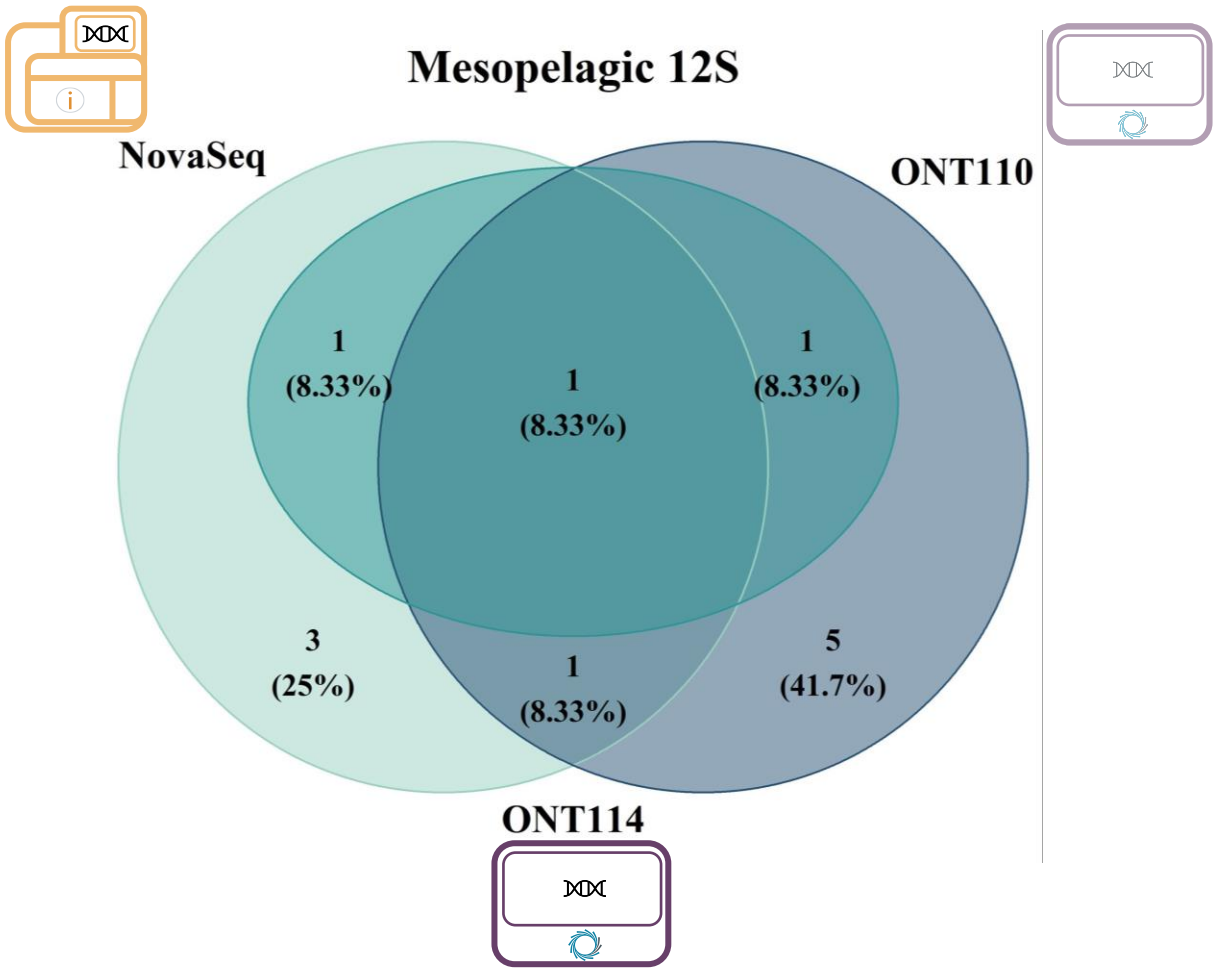
Aquarium tanks

Species detected

	12S	COI	12S+COI
 110	9/10	5/10	10/10
 114	9/10	5/10	10/10
	8/10	10/10	10/10

Field samples





Conclusions

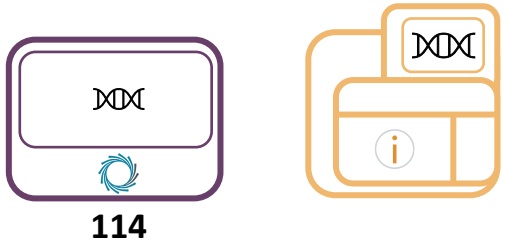
Markers

12S > COI but multi-marker preferable

high non-target amplification with COI

Long fragments =
higher taxonomic resolution

Sequencing platforms



Equivalent for species
richness recovered

Most suited for field-based studies

Travel grant

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Thank you for your attention!

Questions?

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