

**Table S2. Summary of the metabarcoding pipelines for 18S and COI.****METABARPARK 18S PIPELINE**

<b>Process</b>	<b>Software</b>	<b>Total reads</b>	<b>Number of clusters/MOTUs</b>
QC of Raw sequences	fasttqc	2 x 15,121,913	
Paired-end alignment	illumina pairedend	15,121,913	
Post-alignment QC	obiannotate score>40 obisplit	14,690,851	
Demultiplexing	ngsfilter	8,718,756	
Group the unique seqs	obiuniq	8,718,756s	440,862
Delete singletons	obigrep count>1	8,403,738	125,844
Sequence length filter 75-180 bp	obigrep seq_length>75 & seq_length<180	8,372,867	122,303
Clustering at 99%	CROP l=0.3 u=0.5 obitab RECOUNT.AFTER.CROP.R	8,372,867	7,145
Annotate with Ecotag	ecotag db_18s_r117.fasta owi_add_taxonomy	8,372,867	7,145
Blank correction	Rscript	8,356,242	7,090
Delete unassigned MOTUs with <10 reads	Metabarpark_18S.calculatio ns.R	8,351,630	5,897
Delete all MOTUs with < 5 reads		8,349,530	5,067
Delete defective samples (< 10,000 reads)		8,344,298	5,067
Abundance renormalization	owi_renormalize	8,266,952	5,067
Minimum relative abundance filter per sample = 0.01%	Rscript Remove_MOTUs_0.01	7,640,737	2,510

## METABARPARK COI PIPELINE

Process	Software	Total reads	Number of clusters/MOTUs
QC of Raw sequences	fasttqc fastx_trimmer	2 x 15,280,243	
Paired-end alignment	illuminapairedend	15,280,243	
Post-alignment QC	obiannotate obisplit	14,338,344	
Demultiplexing	ngsfilter	11,806,729	
Sequence length filter 300-320 bp	obigrep	11,302,626	
Group the unique seqs	obiuniq	11,302,626	3,735,669
Rename the identifiers	obiannotate	11,302,626	3,735,669
Chimera removal	VSEARCH uchime_denovo	11,142,197	3,609,834
Clustering at 95%	CROP l=1.5 u=2.5 z=400 obitab owi_recount_crop.R	11,142,197	63,724
Taxonomic identification	ecotag db_COI_MBPk owi_add_taxonomy	11,142,197	63,724
Blank correction and removal of Prokaryota	Rscript Metabarpark_COI.blank.R	10,266,592	52,750
Collapse duplicated species	owi_collapse	10,266,592	39,777
Delete unassigned MOTUs with <10 reads	Rscript Metabarpark_COI.calculatio	10,204,250	26,054
Delete all MOTUs with < 5 reads	ns.R	10,188,565	21,453
Delete defective samples (< 10,000 reads)		10,171,101	21,452
Abundance renormalization	owi_renormalize	10,093,453	21,452
Minimum relative abundance filter per sample = 0.01%	Rscript Remove_MOTUs_0.01	9,128,836	9,679