Table S1. Number of detections per genus, per sample for the morphological approach. Total number of samples was 18 x 17 = 306.

| Phylum	Taxon	Presence	Phylum	Taxon	Presence
Annelida	Arenicola_adult	216	Arthropoda	Bathyporeia	1
	Arenicola_juvenile	89		Bodotria	1
	Aricidea	1		Carcinus	4
	Capitella	252		Crangon	75
	Eteone	94		Cumacea	1
	Glycera	1		Gammarus	4
	Hediste	45		Mysida	1
	Heteromastus	81		Praunus	2
	Lanice	7		Urothoe	172
	Magelona	8			
	Malacoceros	1	Mollusca	Cerastoderma	2
	Marenzelleria	91		Ensis	8
	Nephtys	8		Hydrobia	1
	Oligochaeta	79		Kurtiella	7
	Phyllodoce	7		Limecola	37
	Polydora	2		Mya	5
	Polynoidea sp	34		Tellina	1
	Pygospio	126			
	Scoloplos	288			
	Spio	5			
	Spiophanes	9			
	Tharyx	111			
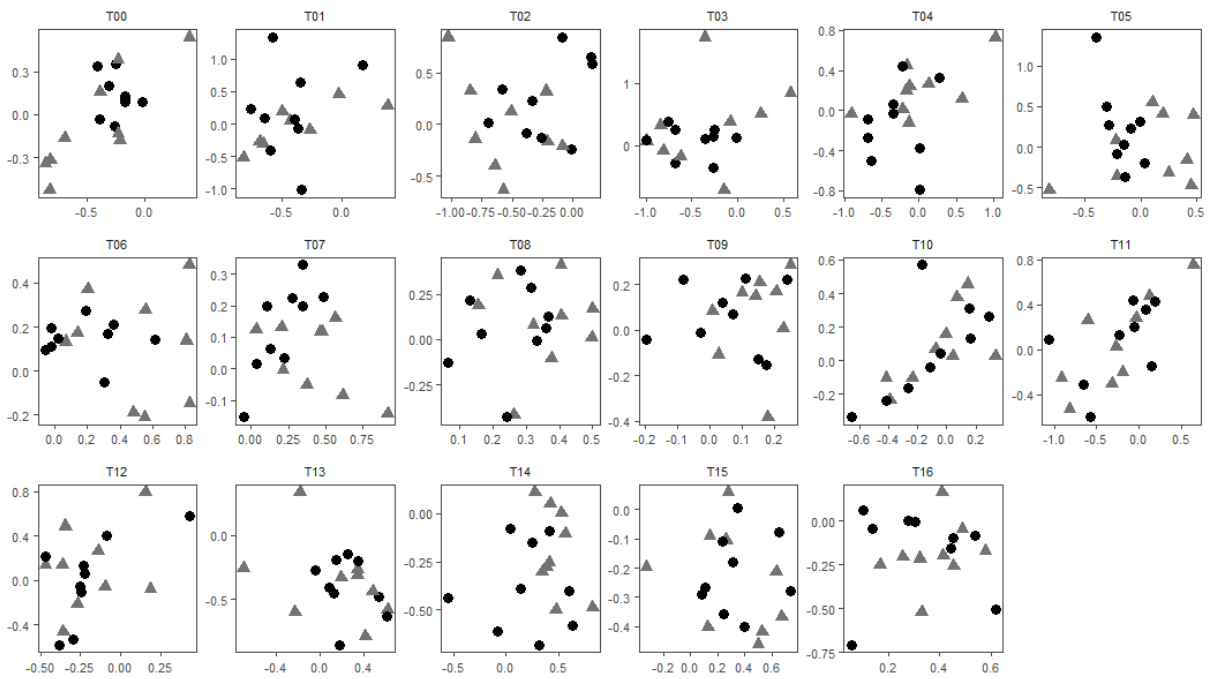
Figure S1. MDS ordinations based on the benthic community composition for the morphological approach for all sampling moments. A selection was shown in figure 4 in the manuscript. The control transects are shown in dark circles, the fished transects with the lighter triangles
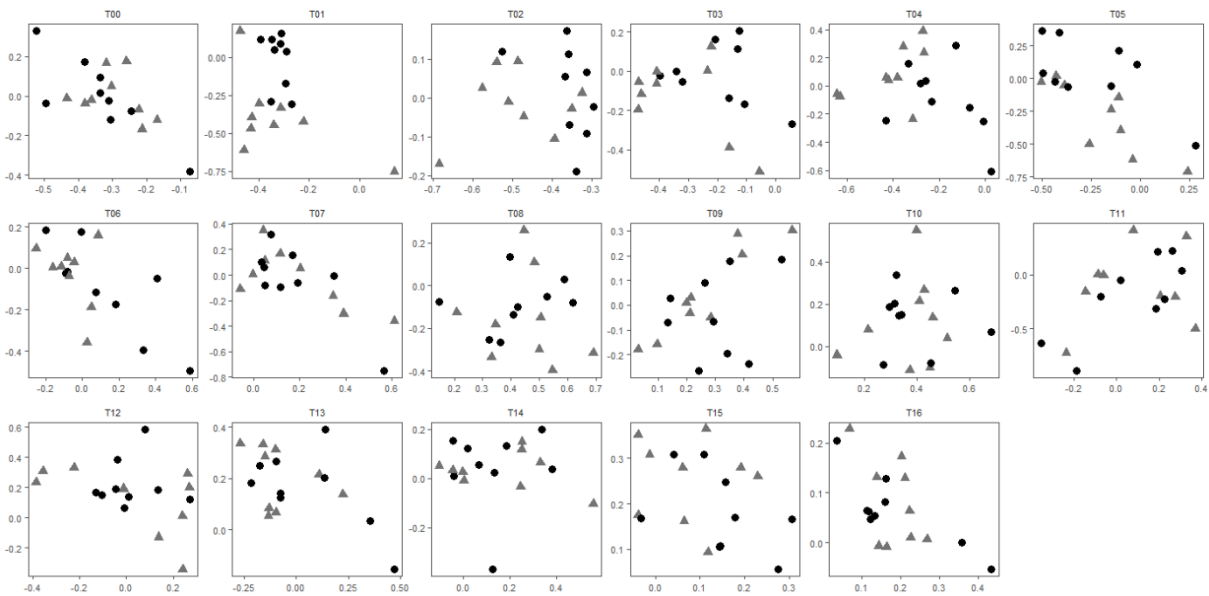

Figure S2. MDS ordinations based on the benthic community composition for the molecular approach for all sampling moments. A selection was shown in figure 4 in the manuscript. The control transects are shown in dark circles, the fished transects with the lighter triangles
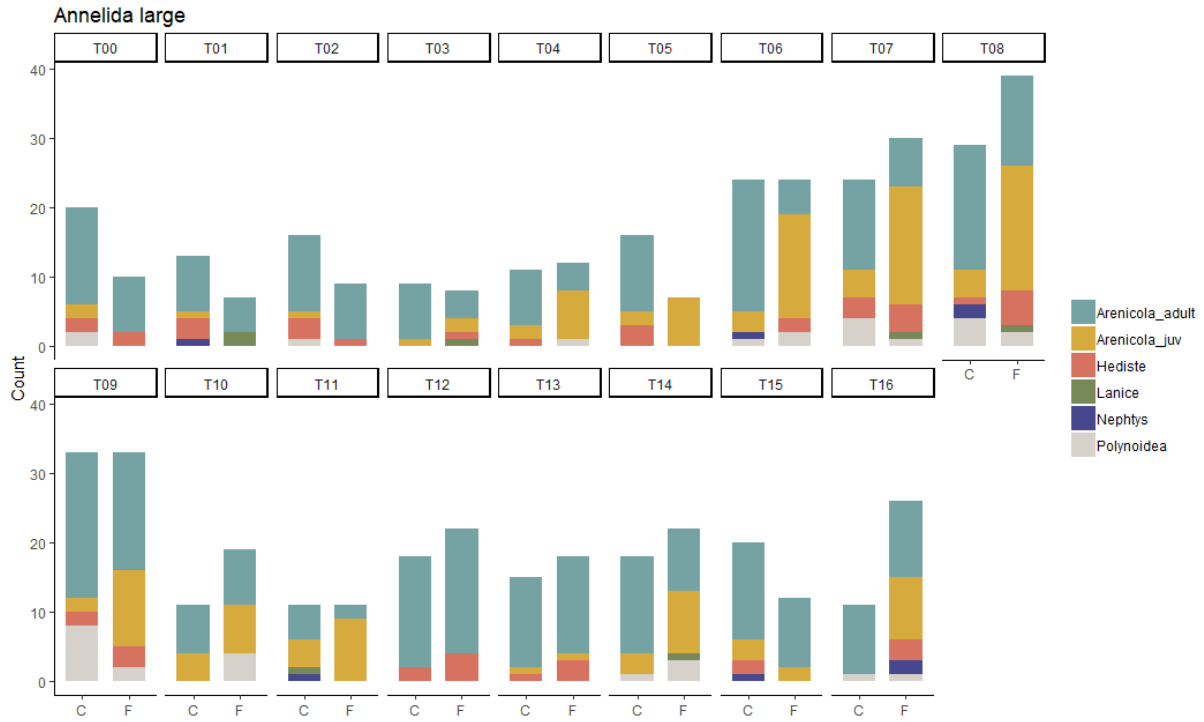
Figure S3. Morphological analysis of benthic biodiversity based on abundance data for larger Annelida for all sampling moments. A selection was shown in figure 5 in the manuscript. C = control, F = fished, TXX = sampling moment.
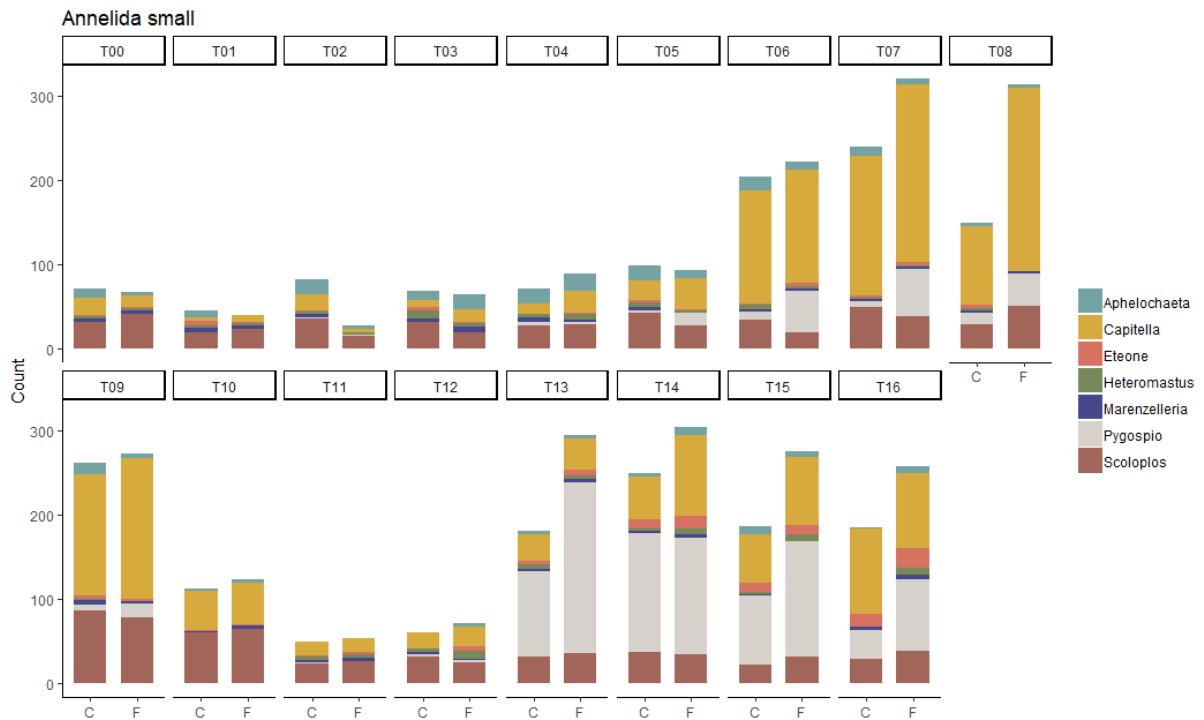

Figure S4. Morphological analysis of benthic biodiversity based on abundance data for small Annelida for all sampling moments. A selection was shown in figure 5 in the manuscript. C = control, F = fished, TXX = sampling moment.
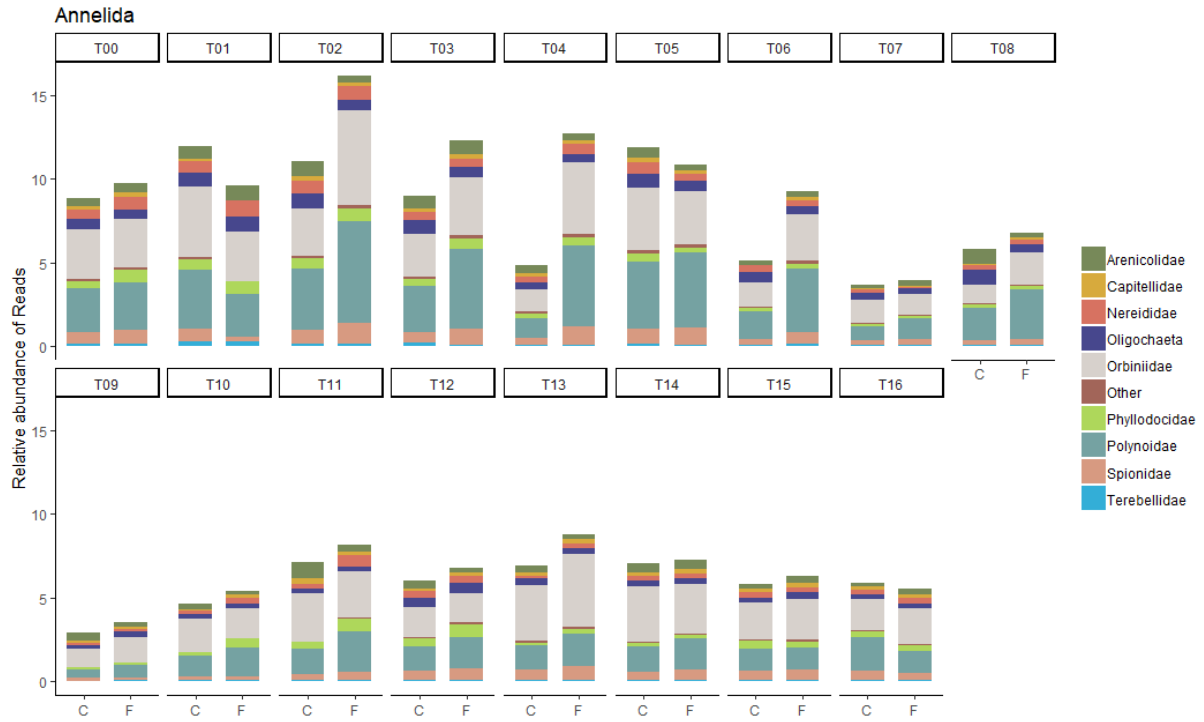
Figure S5. Molecular analysis of benthic biodiversity based on the relative read abundance for Annelida for all sampling moments. A selection was shown in figure 6 in the manuscript. C= control, F = fished, TXX = sampling moment.
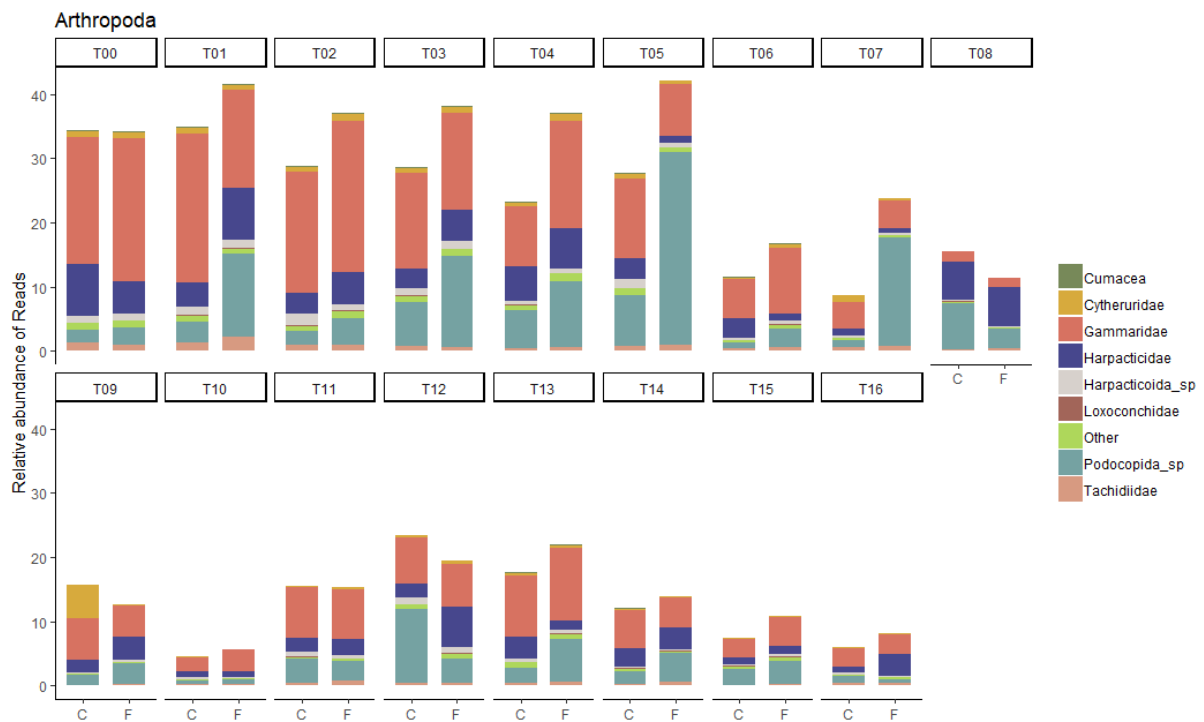

Figure S6 | Molecular analysis of benthic biodiversity based on the relative read abundance for Arthropoda for all sampling moments. A selection was shown in figure 6 in the manuscript. C= control, F = fished, TXX = sampling moment.

Figure S7 | Molecular analysis of benthic biodiversity based on the relative read abundance for Nematoda for all sampling moments. A selection was shown in figure 6 in the manuscript. C= control, F = fished, TXX = sampling moment.