



Supplement of

Multifactorial effects of warming, low irradiance, and low salinity on Arctic kelps

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1 **Supplementary material**

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3 **RNAseq data**

4 The lists of differentially expressed genes (DEG) for *Hedophyllum nigripes* and *Saccharina*
5 *latissima* represents 6 DEG files per species, or 12 files. These can be accessed and viewed
6 accordingly by named CSV files, 1 per species. For each species, a CSV file contains the DEGs
7 by function, with associated annotation:

8 1) [https://github.com/MarcMeynadier/SaccharinaHedophyllumTranscriptomic/tree/main/DE](https://github.com/MarcMeynadier/SaccharinaHedophyllumTranscriptomic/tree/main/DESeq2/Hedophyllum)
9 [Seq2/Hedophyllum](https://github.com/MarcMeynadier/SaccharinaHedophyllumTranscriptomic/tree/main/DESeq2/Hedophyllum)

10 2) [https://github.com/MarcMeynadier/SaccharinaHedophyllumTranscriptomic/tree/main/DE](https://github.com/MarcMeynadier/SaccharinaHedophyllumTranscriptomic/tree/main/DESeq2/Saccharina)
11 [Seq2/Saccharina](https://github.com/MarcMeynadier/SaccharinaHedophyllumTranscriptomic/tree/main/DESeq2/Saccharina)

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15 **Table S1:** Tools and parameters used for transcriptomic data processing.

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Tool	Version	Arguments and parameters
FastQC	0.11.7	-o \$outputDirectory
Trimmomatic	0.39	PE -threads 10 -phred33 -trimlog LEADING:3 TRAILING:3 SLIDINGWINDOW:4:15 MINLEN:36 TruSeq3-PE.fa:2:30:10
Trinity	2.14.0	--seqType fq --max_memory 128G --samples_file \$sampleFiles --CPU 32 --output \$outputDirectory --full_cleanup
CD-HIT	4.8.1	-i \$transcriptome -o \$output -c 0.95 -n 8
rnaSPAdes	3.14.1	--pe1-1 \$seq1 --pe1-2 \$seq2 [...] --pe4-1 \$seq7 --pe4-2 \$seq8 -o \$output_directory
BUSCO	5.4.3	--in \$transcriptome --out \$output -c 24 -l /\$pathDB/eukaryota_odb10 --config \$config --mode transcriptome
Kallisto	0.46.0	quant -i \$index -o \$outputDirectory -b 100 -t 16 \$seq1 \$seq2
DESeq2	1.34.0	Counts recovery via txlImport (files=DesignFile, type='Kallisto', tx2gene=tx2geneFile) Contrasts depends on biological questions with alpha=0.05
TransDecoder	5.5.0	LongOrfs : \$transcriptome Predict : \$transcriptome
HMMER	3.3	--domtblout \$output -E 1e-10 --cpu 16 \$pfamDB \$transdecoderLongestOrf
eggNOG-mapper	2.1.10	-i \$transdecoderLongestOrf -o \$eggnogAnnot
Ontologizer	2.1	-a \$associationFile -g \$goDB -s \$studySamples -p \$populationFile -c Parent-Child-Union -o \$outputDirectory -d 0.05 -r 1000

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18 **Table S2:** Analysis of deviance (Type II Wald chi-square tests) in a linear mixed model with
19 a hierarchical structure to predict the chlorophyll a contents.

	Chisq	Df	Pr(>Chisq)
species	91.310	2	<2.2e-16 ***
treatment	98.991	4	<2.2e-16 ***
species:treatment	39.729	8	3.599e-06 ***

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21 **Table S3:** Pairwise comparisons of the chlorophyll *a* values calculated by the method of
 22 Tukey on a linear mixed model with a hierarchical structure (fixed factors: treatment and
 23 species, random factor: mesocosm). The *p*-values in bold (< 0.05) support the hypothesis that
 24 there is a significant difference in the pair. AE: *Alaria esculenta*, LD: *Laminaria digitata*, SL:
 25 *Saccharina latissima*.
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Species	Treatment	vs.	Species	Treatment	estimate	SE	df	t.ratio	p.value
AE	t0	-	LD	t0	124.75	18.6	117.0	6.708	<.0001
AE	t0	-	SL	t0	104.37	18.6	117.0	5.612	<.0001
AE	t0	-	AE	Ctrl	136.06	19.0	22.9	7.146	<.0001
AE	t0	-	AE	T1	167.96	19.3	25.6	8.706	<.0001
AE	t0	-	AE	T2	48.68	20.4	30.6	2.388	0.5405
AE	t0	-	AE	T3	155.52	21.2	33.5	7.325	<.0001
LD	t0	-	SL	t0	-20.38	18.6	117.0	-1.096	0.9988
LD	t0	-	LD	Ctrl	49.65	27.8	69.5	1.783	0.8967
LD	t0	-	LD	T1	54.29	24.0	38.6	2.260	0.6231
LD	t0	-	LD	T2	56.08	27.8	69.5	2.014	0.7829
LD	t0	-	LD	T3	60.95	23.5	43.6	2.588	0.4048
SL	t0	-	LD	Ctrl	70.03	27.8	69.5	2.515	0.4437
SL	t0	-	SL	Ctrl	79.06	18.0	20.0	4.396	0.0158
SL	t0	-	SL	T1	90.64	18.5	22.2	4.887	0.0044
SL	t0	-	SL	T2	89.20	18.0	19.9	4.953	0.0049
SL	t0	-	SL	T3	93.45	18.6	21.9	5.019	0.0034
AE	Ctrl	-	LD	Ctrl	38.33	27.2	117.8	1.409	0.9850
AE	Ctrl	-	SL	Ctrl	47.36	17.0	118.9	2.779	0.2727
AE	Ctrl	-	AE	T1	31.89	18.4	118.7	1.733	0.9184

AE	Ctrl	-	AE	T2	-87.38	19.4	117.9	-4.497	0.0015
AE	Ctrl	-	AE	T3	19.46	20.3	118.6	0.958	0.9997
LD	Ctrl	-	SL	Ctrl	9.04	26.5	117.2	0.341	1.0000
LD	Ctrl	-	LD	T1	4.64	30.9	119.0	0.150	1.0000
LD	Ctrl	-	LD	T2	6.43	34.0	117.0	0.190	1.0000
LD	Ctrl	-	LD	T3	11.30	30.5	118.0	0.370	1.0000
SL	Ctrl	-	LD	T1	-4.40	22.6	115.7	-0.194	1.0000
SL	Ctrl	-	SL	T1	11.58	16.5	118.4	0.702	1.0000
SL	Ctrl	-	SL	T2	10.14	15.7	117.4	0.644	1.0000
SL	Ctrl	-	SL	T3	14.39	16.4	117.3	0.878	0.9999
AE	T1	-	LD	T1	11.08	23.6	117.3	0.469	1.0000
AE	T1	-	SL	T1	27.05	17.9	118.0	1.511	0.9722
AE	T1	-	AE	T2	-119.27	19.7	117.2	-6.040	<.0001
AE	T1	-	AE	T3	-12.43	20.7	118.6	-0.600	1.0000
LD	T1	-	SL	T1	15.98	22.6	119.0	0.707	1.0000
LD	T1	-	LD	T2	1.79	30.9	119.0	0.058	1.0000
LD	T1	-	LD	T3	6.66	26.4	118.0	0.252	1.0000
SL	T1	-	SL	T2	-1.44	16.6	118.8	-0.087	1.0000
SL	T1	-	SL	T3	2.81	17.2	118.9	0.163	1.0000
AE	T2	-	LD	T2	132.14	28.2	117.1	4.691	0.0007
AE	T2	-	SL	T2	144.88	18.4	117.1	7.856	<.0001
AE	T2	-	AE	T3	106.84	21.7	118.4	4.920	0.0003
LD	T2	-	SL	T2	12.74	26.5	117.3	0.481	1.0000
LD	T2	-	LD	T3	4.87	30.5	118.0	0.159	1.0000
SL	T2	-	SL	T3	4.25	16.4	117.6	0.259	1.0000

AE	T3	-	LD	T3	30.17	24.5	118.1	1.231	0.9959
AE	T3	-	SL	T3	42.29	20.2	119.0	2.091	0.7381
LD	T3	-	SL	T3	12.12	22.6	119.0	0.537	1.0000

28 **Table S4:** C:N ratios (**A**), carbon contents (**B**), and nitrogen contents as a function of the
 29 treatment were investigated with an analysis of deviance (Type II Wald chi-square tests) in a
 30 linear mixed model with a hierarchical structure.
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A	Chisq	Df	Pr(>Chisq)
species	61.003	2	5.667e-14 ***
treatment	29.275	4	6.872e-06 ***
species:treatment	11.285	8	0.1861

B	Chisq	Df	Pr(>Chisq)
species	23.8694	2	6.559e-06 ***
treatment	3.8547	4	0.4260
species:treatment	6.0497	8	0.6417

C	Chisq	Df	Pr(>Chisq)
species	51.647	2	6.096e-12 ***
treatment	25.979	4	3.196e-05 ***
species:treatment	14.373	8	0.07254

33 **Table S5:** Pairwise comparisons of **A)** the C:N ratios, **B)** the carbon contents, **C)** the nitrogen
 34 contents calculated by the method of Tukey on a linear mixed model with a hierarchical
 35 structure (fixed factors: treatment and species, random factor: mesocosm). The *p*-values in
 36 bold (*p* < 0.05) indicates a significant difference in the pair. AE: *Alaria esculenta*, LD:
 37 *Laminaria digitata*, SL: *Saccharina latissima*.
 38

A	Species	Treatment	vs.	Species	Treatment	estimate	SE	df	t.ratio	p.value
	AE	to	-	LD	to	-0.1152	2.63	125.0	-0.044	1.0000
	AE	to	-	SL	to	-6.7996	2.56	125.0	-2.654	0.3458
	AE	to	-	AE	Ctrl	-0.4640	2.47	41.0	-0.187	1.0000
	AE	to	-	AE	T1	5.2689	2.51	45.0	2.100	0.7276
	AE	to	-	AE	T2	6.7233	2.83	58.0	2.378	0.5403
	AE	to	-	AE	T3	5.8060	2.56	47.8	2.264	0.6201
	LD	to	-	SL	to	-6.6845	2.56	125.0	-2.609	0.3746
	LD	to	-	LD	Ctrl	9.4646	3.72	98.2	2.546	0.4190
	LD	to	-	LD	T1	5.3231	2.99	58.9	1.783	0.8955
	LD	to	-	LD	T2	7.2351	3.72	98.2	1.946	0.8236
	LD	to	-	LD	T3	4.4934	3.14	69.9	1.431	0.9814
	SL	to	-	SL	Ctrl	2.9358	2.36	36.1	1.246	0.9937
	SL	to	-	SL	T1	3.6898	2.22	31.4	1.659	0.9302
	SL	to	-	SL	T2	8.5439	2.32	34.5	3.686	0.0453
	SL	to	-	SL	T3	1.5997	2.36	35.2	0.677	1.0000
	AE	Ctrl	-	LD	Ctrl	9.8134	3.61	125.6	2.718	0.3066
	AE	Ctrl	-	SL	Ctrl	-3.3998	2.28	126.8	-1.490	0.9755
	AE	Ctrl	-	AE	T1	5.7328	2.34	126.1	2.449	0.4841
	AE	Ctrl	-	AE	T2	7.1873	2.67	126.2	2.694	0.3206
	AE	Ctrl	-	AE	T3	6.2700	2.41	126.7	2.599	0.3810

LD	Ctrl	-	SL	Ctrl	-13.2133	3.58	125.5	-3.692	0.0247
LD	Ctrl	-	LD	T1	-4.1415	3.98	126.7	-1.041	0.9993
LD	Ctrl	-	LD	T2	-2.2295	4.55	125.0	-0.490	1.0000
LD	Ctrl	-	LD	T3	-4.9712	4.09	126.2	-1.214	0.9965
SL	Ctrl	-	SL	T1	0.7539	2.07	126.7	0.363	1.0000
SL	Ctrl	-	SL	T2	5.6081	2.17	126.8	2.581	0.3927
SL	Ctrl	-	SL	T3	-1.3361	2.21	126.6	-0.606	1.0000
AE	T1	-	LD	T1	-0.0609	2.90	126.3	-0.021	1.0000
AE	T1	-	SL	T1	-8.3787	2.16	125.5	-3.875	0.0136
AE	T1	-	AE	T2	1.4545	2.72	126.7	0.535	1.0000
AE	T1	-	AE	T3	0.5372	2.44	125.2	0.220	1.0000
LD	T1	-	SL	T1	-8.3178	2.69	126.9	-3.086	0.1367
LD	T1	-	LD	T2	1.9120	3.98	126.7	0.481	1.0000
LD	T1	-	LD	T3	-0.8297	3.38	125.1	-0.246	1.0000
SL	T1	-	SL	T2	4.8542	2.02	126.2	2.398	0.5214
SL	T1	-	SL	T3	-2.0900	2.08	127.0	-1.004	0.9995
AE	T2	-	LD	T2	0.3966	3.86	125.7	0.103	1.0000
AE	T2	-	SL	T2	-4.9791	2.61	126.9	-1.907	0.8453
AE	T2	-	AE	T3	-0.9173	2.78	126.8	-0.330	1.0000
LD	T2	-	SL	T2	-5.3757	3.55	125.4	-1.513	0.9721
LD	T2	-	LD	T3	-2.7417	4.09	126.2	-0.670	1.0000
SL	T2	-	SL	T3	-6.9442	2.15	125.7	-3.223	0.0967
AE	T3	-	LD	T3	-1.4278	3.09	126.9	-0.462	1.0000
AE	T3	-	SL	T3	-11.0059	2.36	126.1	-4.669	0.0007
LD	T3	-	SL	T3	-9.5782	3.02	125.3	-3.173	0.1101

B	Species	Treatment	vs.	Species	Treatment	estimate	SE	df	t.ratio	p.value
	AE	to	-	LD	to	5.634	14.1	125.0	0.400	1.0000
	AE	to	-	SL	to	-6.839	13.7	125.0	-0.498	1.0000
	AE	to	-	AE	Ctrl	3.002	13.3	41.0	0.226	1.0000
	AE	to	-	AE	T1	8.934	13.4	45.0	0.664	1.0000
	AE	to	-	AE	T2	10.408	15.2	58.0	0.687	1.0000
	AE	to	-	AE	T3	1.157	13.7	47.8	0.084	1.0000
	LD	to	-	SL	to	-12.473	13.7	125.0	-0.908	0.9999
	LD	to	-	LD	Ctrl	21.981	19.9	98.2	1.103	0.9987
	LD	to	-	SL	Ctrl	-7.587	13.0	39.6	-0.583	1.0000
	LD	to	-	LD	T1	24.351	16.0	58.9	1.521	0.9679
	LD	to	-	LD	T2	25.098	19.9	98.2	1.259	0.9947
	LD	to	-	LD	T3	28.694	16.8	69.9	1.705	0.9244
	SL	to	-	SL	Ctrl	4.886	12.6	36.1	0.387	1.0000
	SL	to	-	SL	T1	0.176	11.9	31.4	0.015	1.0000
	SL	to	-	SL	T2	-0.691	12.4	34.5	-0.056	1.0000
	SL	to	-	SL	T3	-18.336	12.7	35.2	-1.447	0.9761
	AE	Ctrl	-	LD	Ctrl	24.612	19.4	125.6	1.272	0.9944
	AE	Ctrl	-	SL	Ctrl	-4.956	12.2	126.8	-0.405	1.0000
	AE	Ctrl	-	AE	T1	5.932	12.5	126.1	0.473	1.0000
	AE	Ctrl	-	AE	T2	7.406	14.3	126.2	0.518	1.0000
	AE	Ctrl	-	LD	T2	27.730	19.4	125.6	1.433	0.9827
	AE	Ctrl	-	AE	T3	-1.845	12.9	126.7	-0.143	1.0000
	LD	Ctrl	-	SL	Ctrl	-29.568	19.2	125.5	-1.541	0.9674

LD	Ctrl	-	LD	T1	2.370	21.3	126.7	0.111	1.0000
LD	Ctrl	-	SL	T1	-34.278	18.7	125.0	-1.831	0.8810
LD	Ctrl	-	LD	T2	3.117	24.4	125.0	0.128	1.0000
LD	Ctrl	-	LD	T3	6.713	22.0	126.2	0.306	1.0000
SL	Ctrl	-	SL	T1	-4.710	11.1	126.7	-0.424	1.0000
SL	Ctrl	-	SL	T2	-5.577	11.6	126.8	-0.479	1.0000
SL	Ctrl	-	SL	T3	-23.222	11.8	126.6	-1.963	0.8153
AE	T1	-	LD	T1	21.051	15.5	126.3	1.355	0.9896
AE	T1	-	SL	T1	-15.598	11.6	125.5	-1.345	0.9903
AE	T1	-	AE	T2	1.474	14.6	126.7	0.101	1.0000
AE	T1	-	AE	T3	-7.777	13.1	125.2	-0.595	1.0000
LD	T1	-	SL	T1	-36.648	14.4	126.9	-2.537	0.4227
LD	T1	-	LD	T2	0.747	21.3	126.7	0.035	1.0000
LD	T1	-	LD	T3	4.343	18.1	125.1	0.240	1.0000
SL	T1	-	LD	T2	37.396	18.7	125.0	1.997	0.7962
SL	T1	-	SL	T2	-0.867	10.9	126.2	-0.080	1.0000
SL	T1	-	SL	T3	-18.512	11.2	127.0	-1.658	0.9414
AE	T2	-	AE	T3	-9.251	14.9	126.8	-0.621	1.0000
LD	T2	-	SL	T2	-38.262	19.1	125.4	-2.008	0.7896
LD	T2	-	LD	T3	3.596	22.0	126.2	0.164	1.0000
SL	T2	-	SL	T3	-17.645	11.6	125.7	-1.528	0.9697
AE	T3	-	LD	T3	33.171	16.6	126.9	2.001	0.7940
AE	T3	-	SL	T3	-26.332	12.6	126.1	-2.084	0.7429
LD	T3	-	SL	T3	-59.503	16.2	125.3	-3.677	0.0259

C	Species	Treatment	vs.	Species	Treatment	estimate	SE	df	t.ratio	p.value
	AE	to	-	LD	to	0.2529	1.44	125.0	0.176	1.0000
	AE	to	-	SL	to	3.5217	1.40	125.0	2.508	0.4423
	AE	to	-	AE	Ctrl	0.0322	1.36	41.0	0.024	1.0000
	AE	to	-	AE	T1	-2.8539	1.37	45.0	-2.077	0.7425
	AE	to	-	AE	T2	-3.8535	1.55	58.0	-2.487	0.4650
	AE	to	-	AE	T3	-3.8036	1.41	47.8	-2.707	0.3318
	LD	to	-	SL	to	3.2689	1.40	125.0	2.328	0.5718
	LD	to	-	LD	Ctrl	-5.7111	2.04	98.2	-2.804	0.2626
	LD	to	-	LD	T1	-1.4098	1.64	58.9	-0.862	0.9999
	LD	to	-	LD	T2	-3.1407	2.04	98.2	-1.542	0.9665
	LD	to	-	LD	T3	-1.0560	1.72	69.9	-0.614	1.0000
	SL	to	-	SL	Ctrl	-1.1248	1.29	36.1	-0.871	0.9999
	SL	to	-	SL	T1	-1.8877	1.22	31.4	-1.550	0.9576
	SL	to	-	SL	T2	-4.5131	1.27	34.5	-3.554	0.0622
	SL	to	-	SL	T3	-1.3004	1.30	35.2	-1.004	0.9993
	AE	Ctrl	-	LD	Ctrl	-5.4905	1.98	125.6	-2.776	0.2740
	AE	Ctrl	-	SL	Ctrl	2.3647	1.25	126.8	1.892	0.8529
	AE	Ctrl	-	AE	T1	-2.8861	1.28	126.1	-2.251	0.6282
	AE	Ctrl	-	AE	T2	-3.8856	1.46	126.2	-2.659	0.3426
	AE	Ctrl	-	AE	T3	-3.8358	1.32	126.7	-2.902	0.2102
	LD	Ctrl	-	SL	Ctrl	7.8552	1.96	125.5	4.006	0.0087
	LD	Ctrl	-	LD	T1	4.3014	2.18	126.7	1.973	0.8098
	LD	Ctrl	-	LD	T2	2.5704	2.49	125.0	1.030	0.9994
	LD	Ctrl	-	LD	T3	4.6552	2.24	126.2	2.075	0.7485

SL	Ctrl	-	SL	T1	-0.7629	1.14	126.7	-0.671	1.0000
SL	Ctrl	-	SL	T2	-3.3883	1.19	126.8	-2.846	0.2368
SL	Ctrl	-	SL	T3	-0.1756	1.21	126.6	-0.145	1.0000
AE	T1	-	LD	T1	1.6970	1.59	126.3	1.069	0.9991
AE	T1	-	SL	T1	4.4880	1.18	125.5	3.788	0.0181
AE	T1	-	AE	T2	-0.9995	1.49	126.7	-0.670	1.0000
AE	T1	-	AE	T3	-0.9497	1.34	125.2	-0.711	1.0000
LD	T1	-	SL	T1	2.7910	1.48	126.9	1.890	0.8536
LD	T1	-	AE	T2	-2.6966	1.72	126.8	-1.568	0.9623
LD	T1	-	LD	T2	-1.7310	2.18	126.7	-0.794	1.0000
LD	T1	-	LD	T3	0.3538	1.85	125.1	0.191	1.0000
SL	T1	-	SL	T2	-2.6254	1.11	126.2	-2.367	0.5439
SL	T1	-	SL	T3	0.5873	1.14	127.0	0.515	1.0000
AE	T2	-	LD	T2	0.9656	2.12	125.7	0.456	1.0000
AE	T2	-	SL	T2	2.8621	1.43	126.9	2.001	0.7942
AE	T2	-	AE	T3	0.0498	1.52	126.8	0.033	1.0000
LD	T2	-	SL	T2	1.8965	1.95	125.4	0.974	0.9997
LD	T2	-	LD	T3	2.0848	2.24	126.2	0.929	0.9998
SL	T2	-	SL	T3	3.2127	1.18	125.7	2.721	0.3047
AE	T3	-	LD	T3	3.0005	1.69	126.9	1.771	0.9051
AE	T3	-	SL	T3	6.0250	1.29	126.1	4.665	0.0007
LD	T3	-	SL	T3	3.0244	1.65	125.3	1.829	0.8818

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45 **Table S6:** Analysis of deviance (Type II Wald chi-square tests) in a generalized linear mixed
46 model to predict the growth rate.
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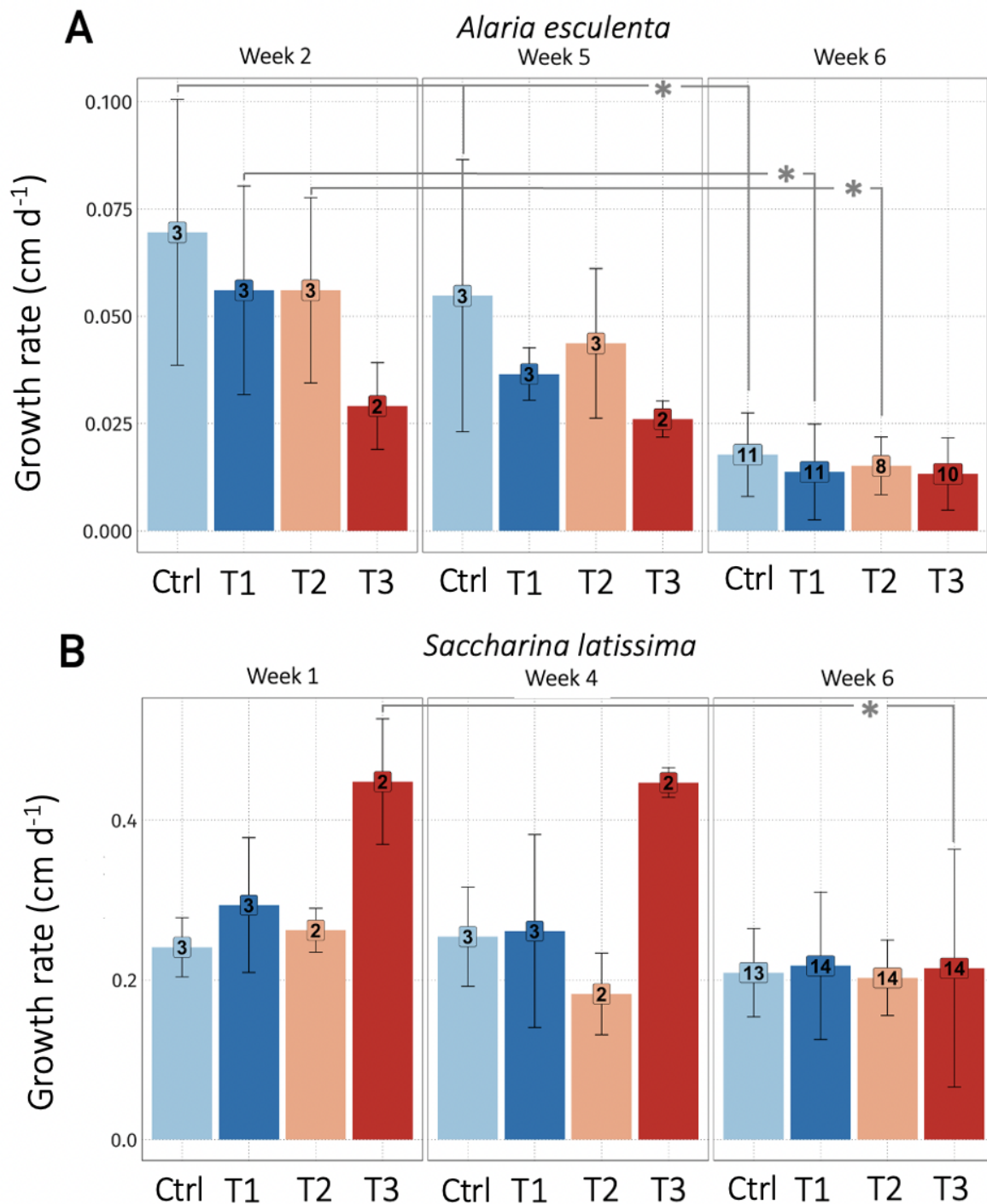
A	Chisq	Df	Pr(>Chisq)
species	91.310	2	<2.2e-16 ***
treatment	98.991	4	<2.2e-16 ***
species:treatment	39.729	8	3.599e-16 ***

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79 **Table S7:** Pairwise comparisons of the growth rates calculated by the method of Tukey
80 generalized linear mixed model. The *p*-values in bold ($p < 0.05$) support the hypothesis that
81 there is a significant difference in the pair. AE: *Alaria esculenta*, LD: *Laminaria digitata*, SL:
82 *Saccharina latissima*.
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A	Species	Treatment	vs.	Species	Treatment	estimate	SE	df	t.ratio	p.value
	AE	Ctrl	-	LD	Ctrl	-6.78e-03	0.0327	115	-0.207	1.0000
	AE	Ctrl	-	SL	Ctrl	-1.87e-01	0.0264	115	-7.09	<.0001
	AE	Ctrl	-	AE	T1	4.08e-03	0.0275	115	0.148	1.0000
	AE	Ctrl	-	AE	T2	2.62e-03	0.0299	115	0.088	1.0000
	AE	Ctrl	-	AE	T3	4.49e-03	0.0282	115	0.159	1.0000
	LD	Ctrl	-	SL	Ctrl	-1.80e-01	0.0318	115	-5.672	<.0001
	LD	Ctrl	-	LD	T1	-2.73e-03	0.034	115	-0.08	1.0000
	LD	Ctrl	-	LD	T2	3.85e-03	0.0358	115	0.107	1.0000
	LD	Ctrl	-	LD	T3	9.32e-03	0.034	115	0.275	1.0000
	SL	Ctrl	-	SL	T1	-1.54e-02	0.0248	115	-0.622	1.0000
	SL	Ctrl	-	SL	T2	4.00e-03	0.0244	115	0.164	1.0000
	SL	Ctrl	-	SL	T3	-9.63e-03	0.0248	115	-0.388	1.0000
	AE	T1	-	LD	T1	-1.36e-02	0.029	115	-0.469	1.0000
	AE	T1	-	SL	T1	-2.07e-01	0.026	115	-7.961	<.0001
	AE	T1	-	AE	T2	-1.45e-03	0.0299	115	-0.049	1.0000
	AE	T1	-	AE	T3	4.14e-04	0.0282	115	0.015	1.0000
	LD	T1	-	SL	T1	-1.93e-01	0.0275	115	-7.014	<.0001
	LD	T1	-	LD	T2	6.57e-03	0.0325	115	0.202	1.0000
	LD	T1	-	SL	T2	-1.74e-01	0.0272	115	-6.392	<.0001
	LD	T1	-	LD	T3	1.20e-02	0.0304	115	0.397	1.0000
	LD	T1	-	SL	T3	-1.87e-01	0.0275	115	-6.803	<.0001

SL	T1	-	SL	T2	1.94e-02	0.0239	115	0.812	0.9996
SL	T1	-	SL	T3	5.81e-03	0.0244	115	0.239	1.0000
AE	T2	-	LD	T2	-5.56e-03	0.0333	115	-0.167	1.0000
AE	T2	-	SL	T2	-1.86e-01	0.0282	115	-6.586	<.0001
AE	T2	-	AE	T3	1.87e-03	0.0306	115	0.061	1.0000
LD	T2	-	SL	T2	-1.80e-01	0.0295	115	-6.111	<.0001
LD	T2	-	LD	T3	5.48e-03	0.0325	115	0.169	1.0000
SL	T2	-	SL	T3	-1.36e-02	0.0239	115	-0.569	1.0000
AE	T3	-	LD	T3	-1.95e-03	0.0296	115	-0.066	1.0000
AE	T3	-	SL	T3	-2.01e-01	0.0267	115	-7.545	<.0001
LD	T3	-	SL	T3	-1.99e-01	0.0275	115	-7.241	<.0001



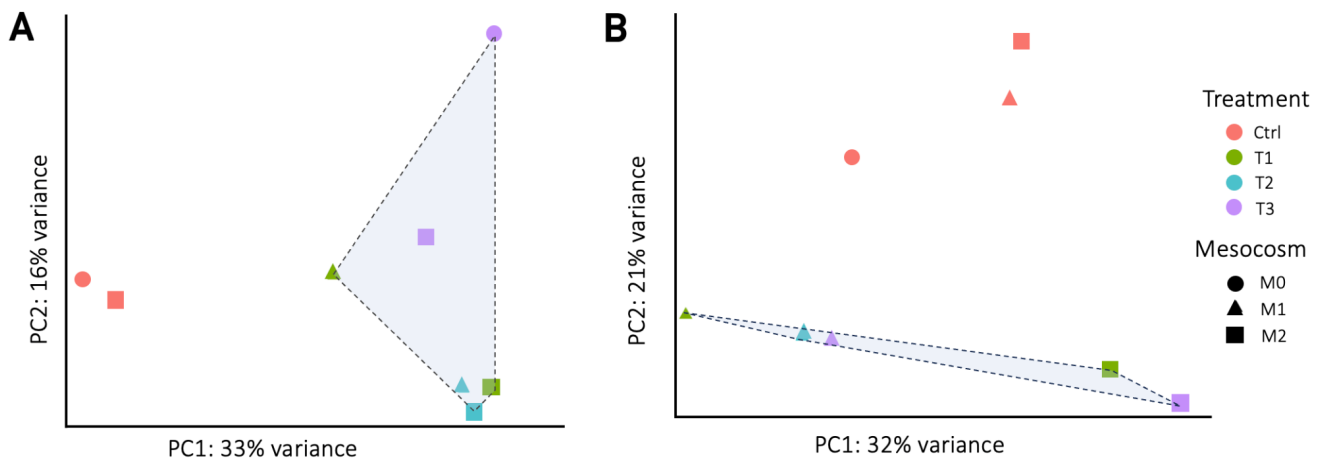
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85 **Figure S1:** Growth rate calculated at different intervals during the experiment within
 86 treatments for **A)** *Alaria esculenta* (Week 0 to 2, 2 to 5, and 5 to 6), and **B)** *Saccharina latissima*
 87 (Weeks 0 to 1, 1 to 4, and 4 to 6). The number on each barplot corresponds to the sample size.
 88 *Laminaria digitata* was not represented due to its low sample size in week 3. Values from t_0 to
 89 week 6 are represented in Figure 5. A generalized linear mixed model (GLMM) with a
 90 Gaussian distribution was used to test for the effects of the species, treatment, time, and

91 mesocosm replica. No significant differences were found between mesocosm replicas.

92 Statistically significant differences are shown with an asterisk ($p < 0.05$).

93



94 **Fig. S2:** Principal Component Analysis of the expressed genes in the control and treatments of
 95 **A) *Hedophyllum nigripes*** and **B) *Saccharina latissima***. Treatments T1, T2, and T3 are grouped
 96 in the blue geometrical figures.
 97