Complex interactions of temperature, light and tissue damage on seagrass wasting disease in *Zostera marina*

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Supporting information

Table S1
Figure S1

Table S1. Results of three algorithms for selection of most stable expressed genes over the experimental data set.

GeNorm[1]	Normfinder[2]	Bestkeeper[3]
10kDa	APX	ubiquitin
SOD	SOD	GRFb
APX	GADPH	APX
GRFb	ubiquitin	*10kDa*
ubiquitin	10kDa	eIF4A

[1](Vandesompele et al., 2002)
[2](Andersen et al., 2004)
[3](Pfaffl *et al.*, 2004)

Andersen CL, Jensen JL, Ørntoft TF. **2004**. Normalization of real-time quantitative reverse transcription-PCR data: a model-based variance estimation approach to identify genes suited for normalization, applied to bladder and colon cancer data sets. *Cancer research* **64**: 5245–5250.

Pfaffl MW, Tichopad A, Prgomet C, Neuvians TP. **2004**. Determination of stable housekeeping genes, differentially regulated target genes and sample integrity: BestKeeper - Excel-based tool using pair-wise correlations. *Biotechnology Letters* **26**: 509–515.

Vandesompele J, De Preter K, Pattyn F, Poppe B, Van Roy N, De Paepe A, Speleman F. **2002**. Accurate normalization of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes. *Genome Biology* **3**: research0034.1.

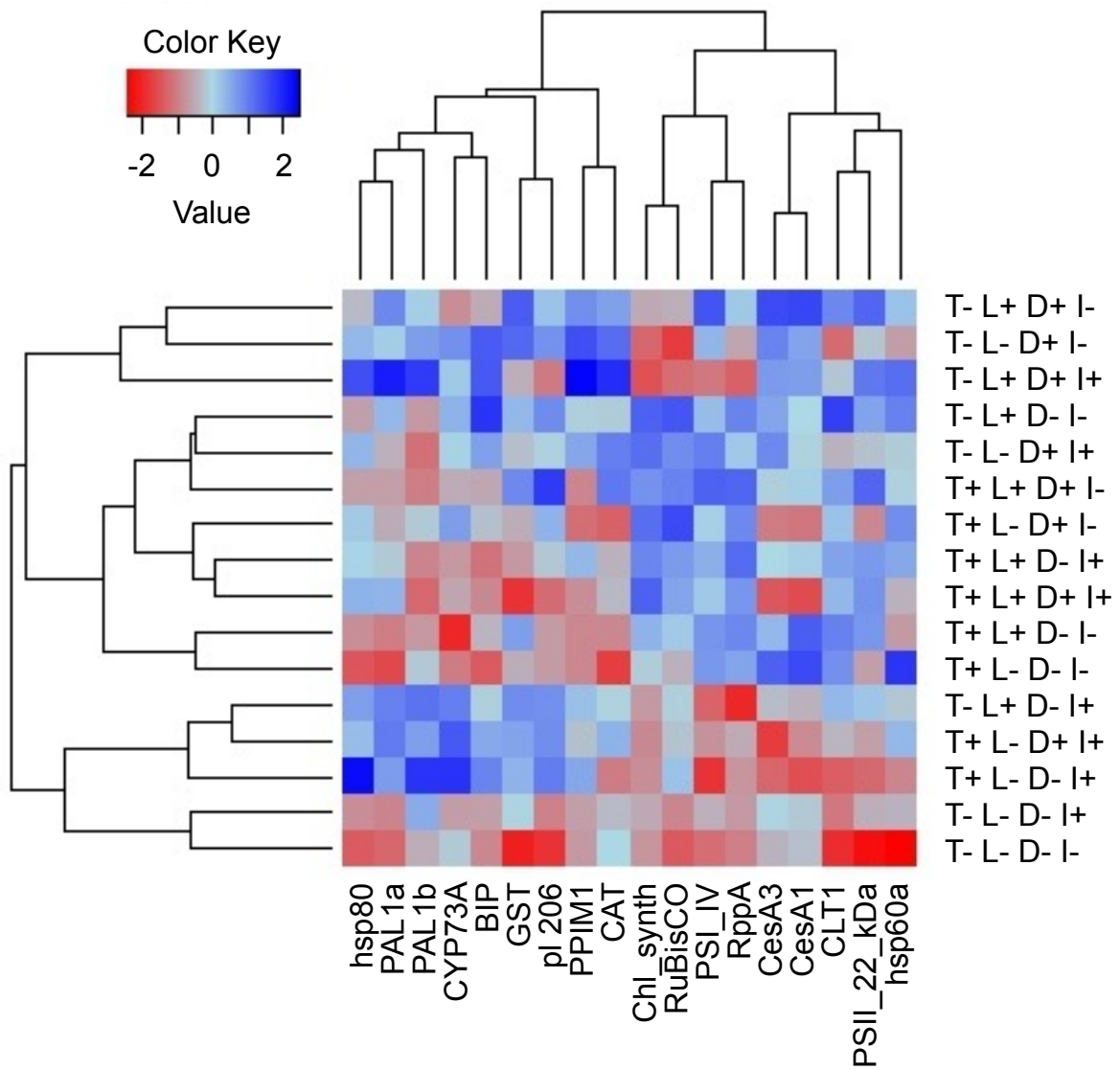

Figure S1. Heat map showing mean values on relative *Zostera marina* gene expression (-ΔCt) for 18 targeted genes following 9 days of inoculation by *Labyrinthula zosterae* under different treatment conditions. T+: increased temperature; T-: ambient temperature; L+: ambient light; L-: reduced light; D +: damaged; D- : undamaged; I+: inoculated with *L. zosterae*; I-: non-inoculated.