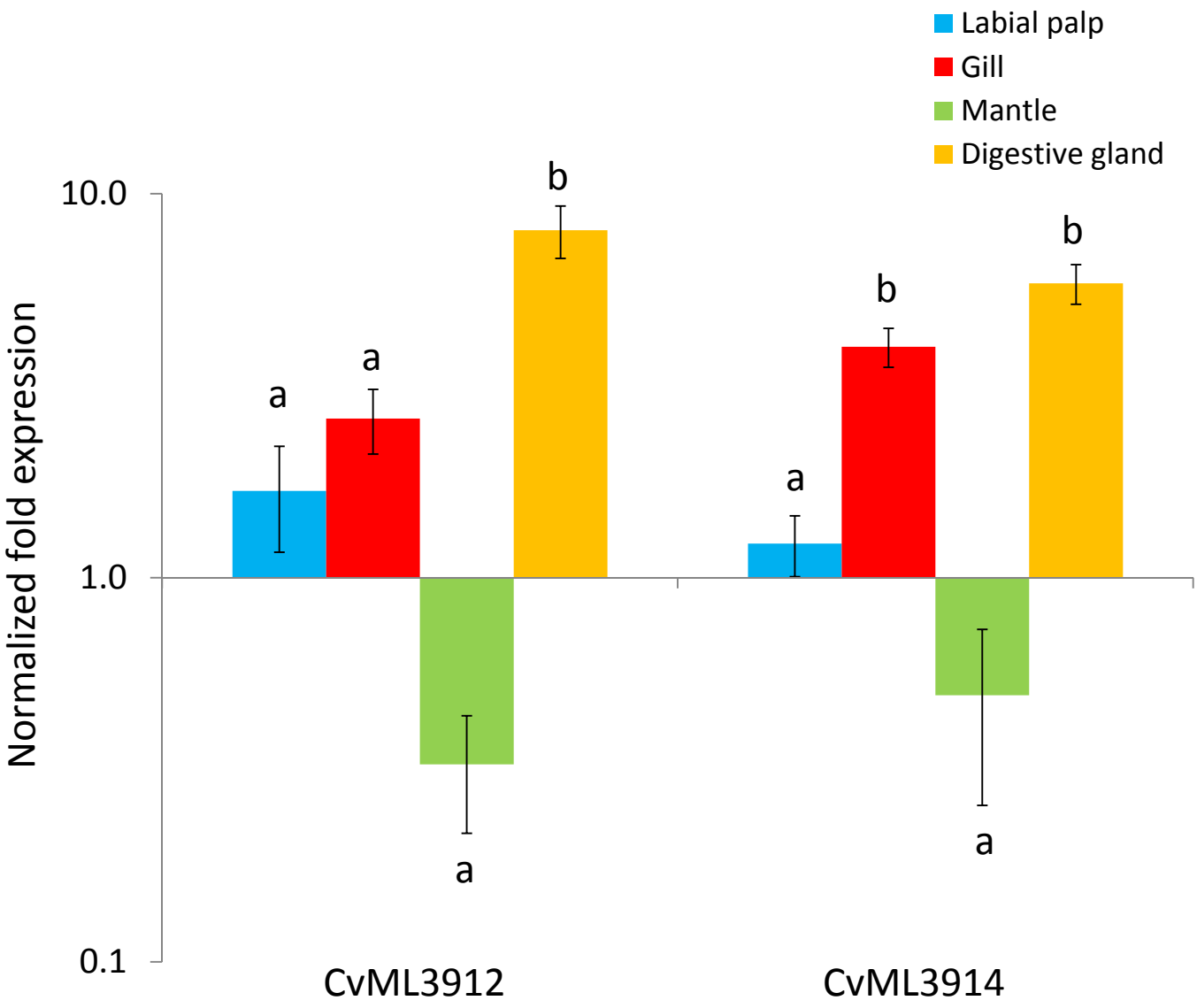

Figure S1. Relative expression of CvML3912 and CvML3914 in oyster tissues determined by quantitative real-time PCR. Expression levels were normalized to 18S RNA and are presented as relative expression (mean ± SEM, n=8 oysters). Different letters indicate significant differences between tissues (ANOVA, SNK, $p < 0.05$).

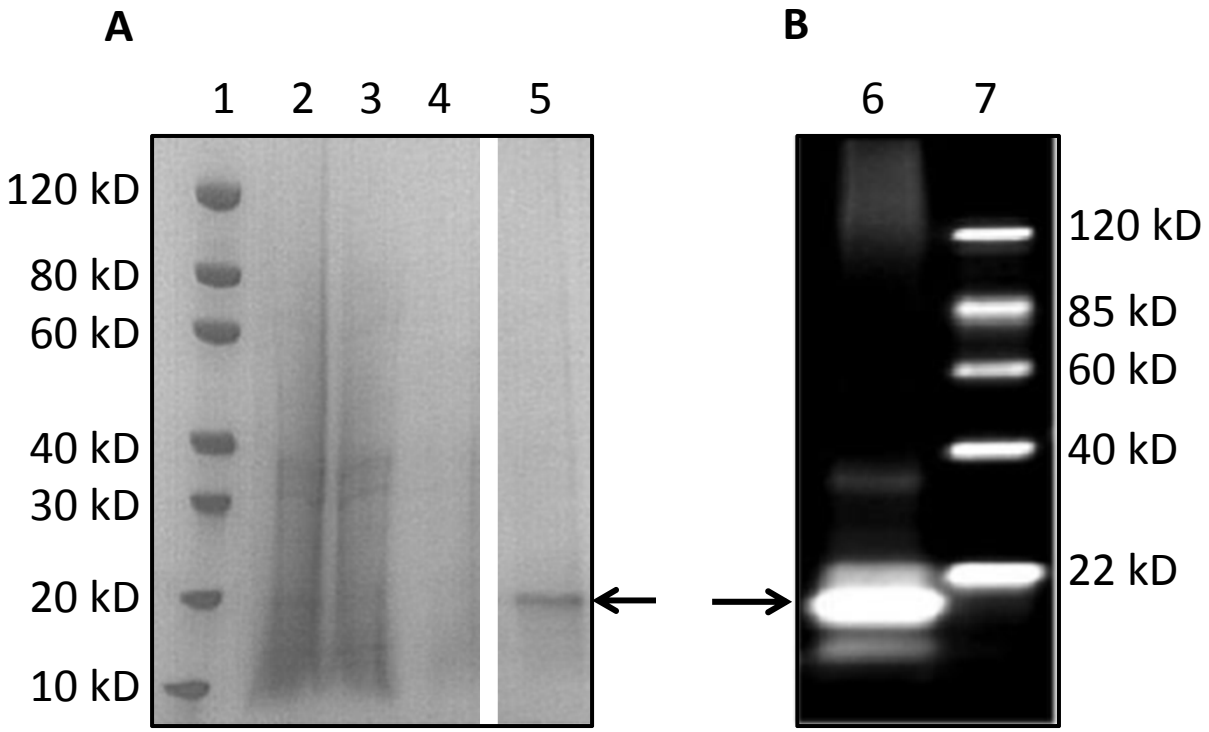

Figure S2. SDS-page (A) and Western Blot (B) analysis of the recombinant CvML3912 protein (rCvML3912). The SDS-PAGE was run on 4%~20% gradient gel, followed by Coomassie Blue staining. Lane 1: Protein marker (M00516, GenScript), Lane 2: Load, Lane 3: Flow through, Lane 4: Final wash, Lane 5: Elution with urea buffer and 300 mM imidazole, Lane 6: Western blot using anti-His antibody (A00186, GenScript), Lane 7: Protein marker (MM0908, GenScript). Arrows indicate rCvML3912.

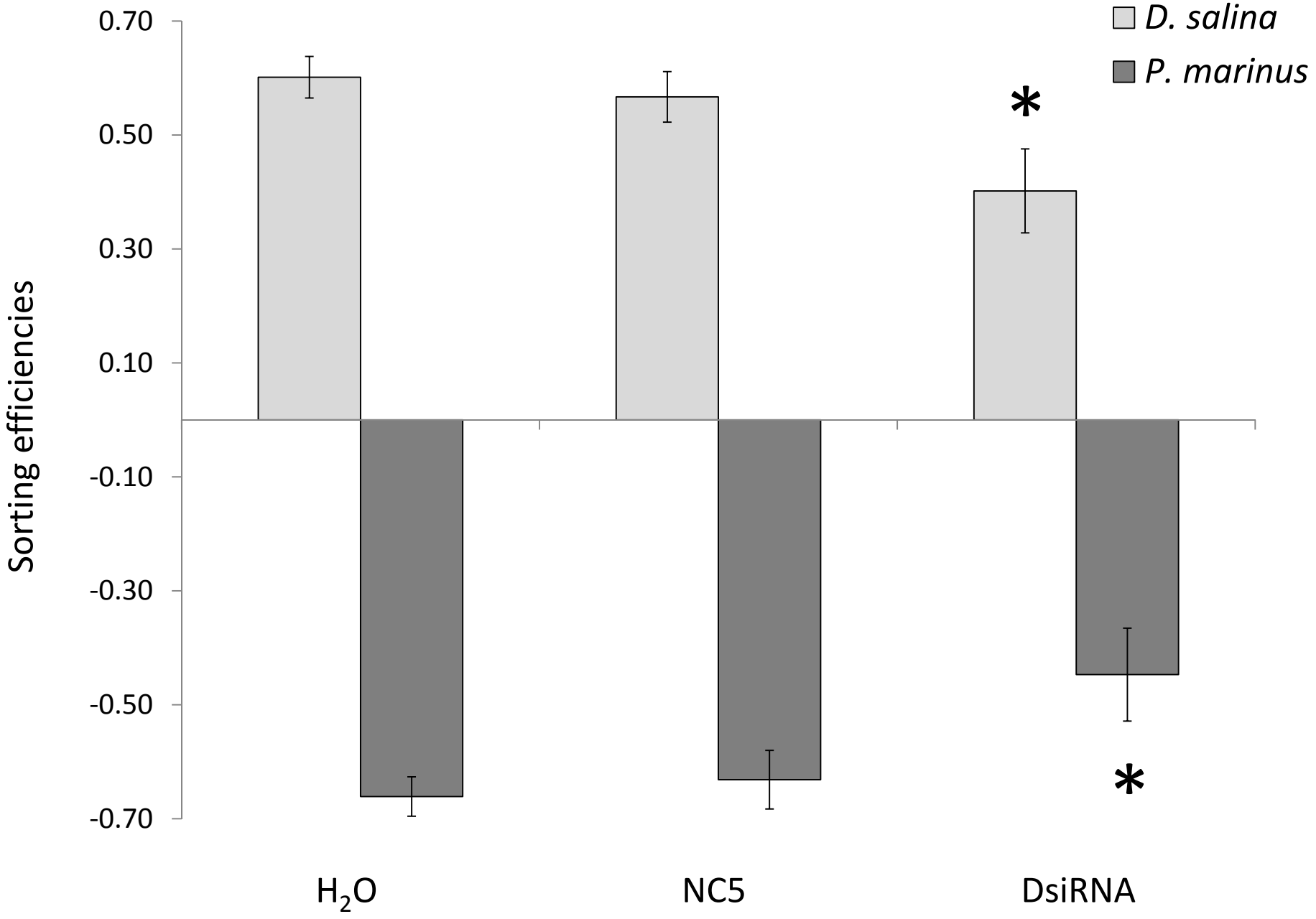

Figure S3.

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Figure S3. Sorting efficiencies (SE, mean ± SEM) of *C. virginica* injected (34 days post-injection, experiment 2) with either seawater (H2O), NC5 or DsiRNAs and fed a diet made with equal proportions of the *D. salina* and *P. marinus*. SE are significantly different from 0 for all treatments (one sample *t*-test, n =12, $p<0.001$). Asterisks indicate a significant change in SE (G-test, n=12, $p<0.001$) among silenced oysters (DsiRNAs) as compared to oysters from the two other treatments. No difference was observed between the two controls (H2O and NC5).

Table S1. LC-MS/MS detection of specific peptides from the two proteins CvML3912 and CvML3914. Position (starting and ending) of each peptide on the corresponding protein sequences, number of spectral count and Log(e) values (subscript) are indicated.

		c102634_g1_i1_3912		c102634_g1_i2_3914	
PEPTIDES	**Position**	**Assay1**	**Assay2**	**Assay1**	**Assay2**
MKTQIIILLAVLTAVLATCPADWQSYGD	1-28		1 (-1.9)		
TCPADWQSYGDK	18-29	2 (-5.7)	2 (-4.1)		
TCPADWNHYR	18-27			7(-3.5)	
DKCFFLSR	28-35			2 (-2.8)	
LCEVIGSQYGR	46-66			2 (-6.9)	4 (-6.3)
LCEMIGSQYR	46-65	6 (-5.6)	14 (-6.6)		
RVASLATIDDAGTQK	66-70	3 (-4.7)			
VASLATIDDAGTQNHIANLIK	67-77			21 (-14.7)	14 (-11.3)
VASLATIDDAGTQK	67-70	2 (-13.2)	2 (-11.0)		
TIDDAGTQNHIANLIK	62-70			2 (-5.0)	2 (-6.5)
VFTYTNWGPQQPNNR	105-119	7 (-5.5)	4 (-8.5)		
DGAENCAVLNYLPDEGFDMK	120-139			4 (-13.3)	6 (-4.2)
GGDENCAVLR	120-129	2 (-3.8)	3 (-2.7)		

Table S2. FITC lectins used to characterize microalgae cell surface carbohydrates. Origin and carbohydrate specificity (provided by the manufacturer EYLabs) of each lectin are given.

Name	Origin	Carbohydrate specificity
ConA	*Canavalia ensiformis*	α-D-Mannose, α-D-Glucose, branched mannose
PEA	*Pisum sativum*	Methyl-D-Mannopyranoside, D-Mannose
PNA	*Arachis hypogaea*	Terminal β-Galactose
PWM	*Phytolacca americana*	Oligomers of β(1,4)-linked N-Acetylglucosamine
SBA	*Glycine maxima*	α and β- N-Acetylgalactosamine, α and β- Galactose
UEA	*Ulex europaeus*	α-L-Fucose
WGA	*Triticum vulgaris*	Chitobiose, N-Acetyl-glucosamine

Table S3. Primers and DsiRNA used in this study. NC5 represents the negative control DsiRNA and was used in both experiments.

Name	Sequence (5’-3’)
qRT-PCR primers	
18S-F	CGCCGGCGACGTATCTTTCAA
18S-R	CTGATTCCCCGTTACCCGTTA
CvML3912-F	GTTCCTGGCAAATTTTATGCGAA
CvML3912-R	AATGAAAGCCGCAGAATCGG
CvML3914-F	CCACATAGCAAACCTCATTAAAC
CvML3914-R	AATCTGAAGCACATGGGTC

Name	Sequence (5’-3’)	Exp1	Exp2
DsiRNA			
DsiRNA-1_Sense	rCrArGrCrArGrArUrCrArArGrUrArUrUrCrCrArCrArUrGCA	✓	
DsiRNA-1_AntiSense	rUrGrCrArUrGrUrGrGrArArUrArCrUrUrGrArUrCrUrGrCrUrGrArG	✓	
DsiRNA-2_Sense	rCrUrGrArCrArGrCrArGrUrUrCrUrUrGrCrArArCrArUrGCC		✓
DsiRNA-2_AntiSense	rGrGrCrArUrGrUrUrGrCrArArGrArArCrUrGrCrUrGrUrCrArGrGrA		✓
DsiRNA-3_Sense	rGrUrGrArGrArUrGrArUrUrGrGrUrUrCrArCrArArUrArCCG	✓	✓
DsiRNA-3_AntiSense	rCrGrGrUrArUrUrGrUrGrArArCrCrArArUrCrArUrCrUrCrArCrArG	✓	✓
DsiRNA-4_Sense	rCrCrArUrGrUrGrCrUrUrCrArGrArUrUrUrCrArArUrUrATA		✓
DsiRNA-4_AntiSense	rUrArUrArArUrUrGrArArArUrCrUrGrArArGrCrArCrArUrGrGrGrU		✓
DsiRNA-5_Sense	rGrCrCrArCrCrGrArCrArUrCrGrUrCrCrArUrGrArArGrATA		✓
DsiRNA-5_AntiSense	rUrArUrCrUrUrCrArUrGrGrArCrGrArUrGrUrCrGrGrUrGrGrCrUrC		✓
DsiRNA-6_Sense	rGrUrGrCrCrGrUrGrCrUrUrArArUrUrArCrUrUrArCrCrAGA		✓
DsiRNA-6_AntiSense	rUrCrUrGrGrUrArArGrUrArArUrUrArArGrCrArCrGrGrCrArCrArG		✓
NC5_Sense	rCrArUrArUrUrGrCrGrCrGrUrArUrArGrUrCrGrCrGrUrUrArG	C	C
NC5_AntiSense	rUrGrGrUrArUrArArCrGrCrGrCrArUrArUrCrArGrCrGrCrArArUrC	C	C