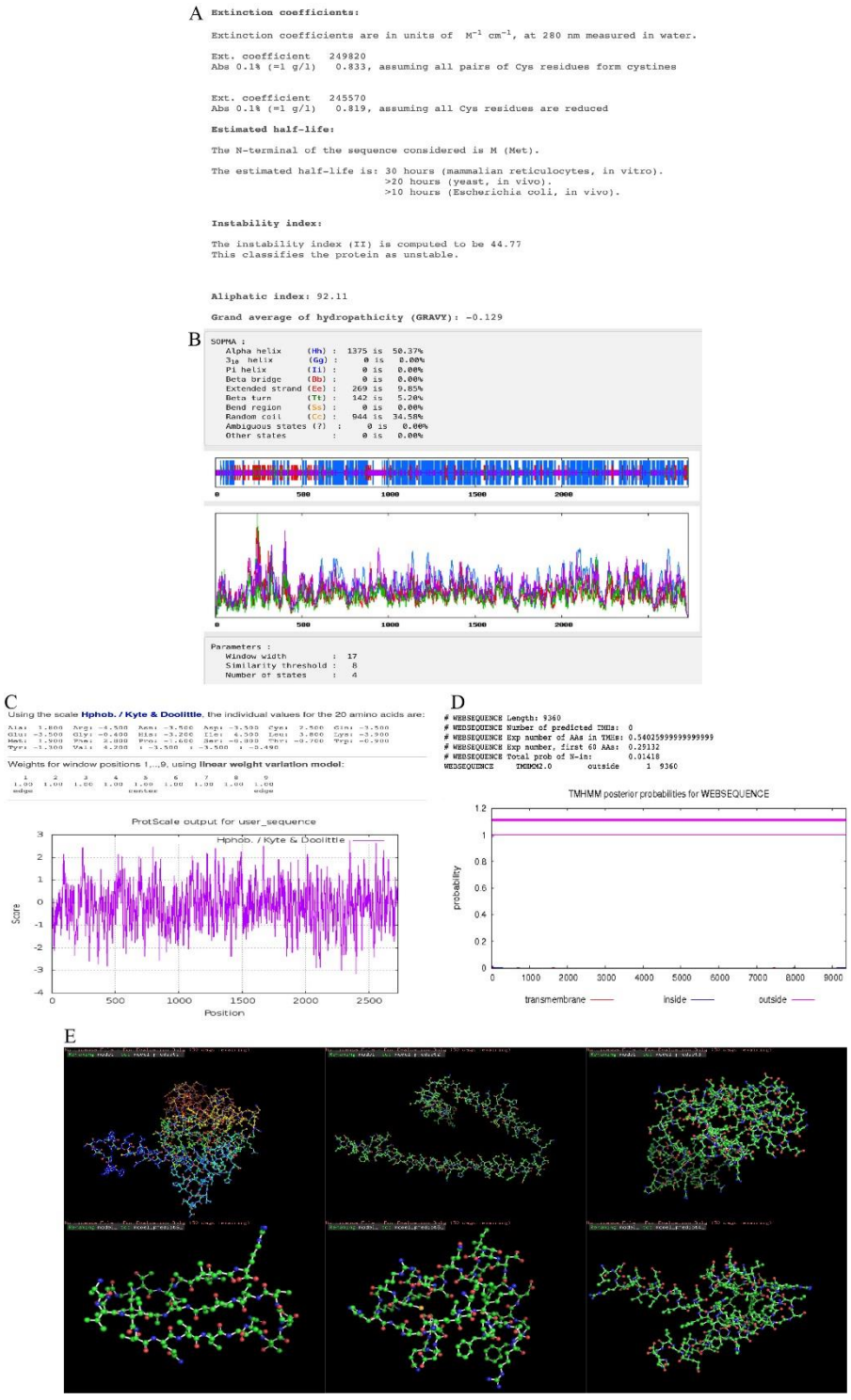
Supplementary Material

Supplementary Table 1 | Primers used in this experiment.

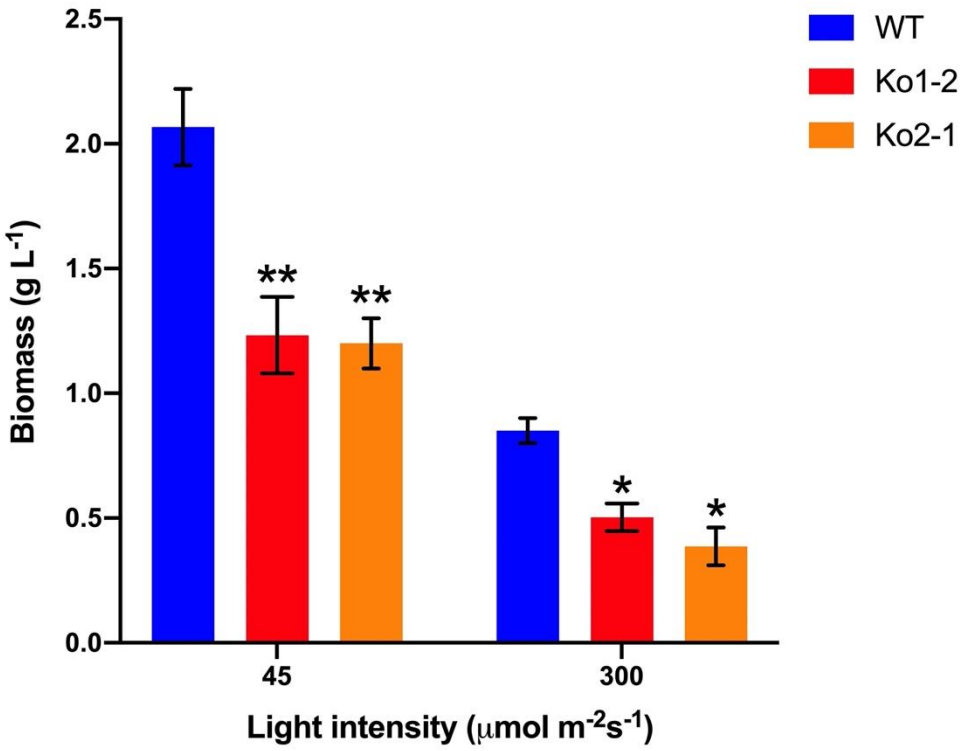
Primer name	Primer sequence 5′—3′	Annotation
Fragments of *P. tricornutum NXS*		
F1-F	CACGGCGATATGAACGAGGA	amplify the fragment of *NXS* (F1) from *P. tricornutum*
F1-R	CAATCCGTTTCGATGGCGAC	amplify the fragment of *NXS* (F1) from *P. tricornutum*
F2-F	GTGCGTGAGGTTCTGAGTGA	amplify the fragment of *NXS* (F2) from *P. tricornutum*
F2-R	GACAATCCGTTTCGATGGCG	amplify the fragment of *NXS* (F2) from *P. tricornutum*
F3-F	AGACAAGCCTGGTTACGTGG	amplify the fragment of *NXS* (F3) from *P. tricornutum*
F3-R	GAAGCTCATGCATTCGGCTG	amplify the fragment of *NXS* (F3) from *P. tricornutum*
The cDNA fragments amplified from the total cDNA of *P. tricornutum*.		
NXS1-F	TAAAGAGGAATGTTCCGGGC	amplify the cDNA fragment of *NXS* (Part1) from *P. tricornutum*
NXS1-R	AGCAATCTGACAGTAAATGAC	amplify the cDNA fragment of *NXS* (Part1) from *P. tricornutum*
NXS2-F	CACGAGATGCGGCTACTCTACGG	amplify the cDNA fragment of *NXS* (Part2) from *P. tricornutum*
NXS2-R	AATACGGGCACACCAATC	amplify the cDNA fragment of *NXS* (Part2) from *P. tricornutum*
NXS3-F	GATTGGTGTGCCTCGTATT	amplify the cDNA fragment of *NXS* (Part3) from *P. tricornutum*
NXS3-R	AGCAATCTGACAGTAAATGAC	amplify the cDNA fragment of *NXS* (Part3) from *P. tricornutum*
qRT PCR		
qNXS-F	GGGTTTACACGAGATGCGGC	detect *NXS* using qRT-PCR in *P. tricornutum*
qNXS-R	GACGGCCCTTTGCCTTGGTC	detect *NXS* using qRT-PCR in *P. tricornutum*
Actin-F	TACGCTTCTGGTCGCAC	detect*β-actin* using qRT-PCR in *P. tricornutum*
Actin-R	GCAACATCGCTCCTCAC	detect*β-actin* using qRT-PCR in *P. tricornutum*
RNAi vector		
NXS400 insert1-F	tgtctgccgtttcgagaattcGGATTGGATCCCCGACTCG	amplify the long fragment of *NXS* from *P. tricornutum* for RNAi
NXS400 insert1-R	tagacattcctgCGACGAGTCGCACCGACG	amplify the long fragment of *NXS* from *P. tricornutum* for RNAi
NXS400 insert2-F	actcgtcgCAGGAATGTCTACCTGCATTGCA	amplify the short fragment of *NXS* from *P. tricornutum* for RNAi
NXS400 insert2-R	ttagtcgatgatatcgaattcGGATTGGATCCCCACTCG	amplify the short fragment of *NXS* from *P. tricornutum* for RNAi
gRNA designed to target the exon region of *NXS*		
sgRNA1-F	TAGGAAGTGACGGTAGCGATCCG	to form double-strand gRNA 1
sgRNA1-R	AAACCGGATCGCTACCGTCACTT	to form double-strand gRNA 1
sgRNA2-F	TAGGTCGGCTCTCGAATCTCCCGT	to form double-strand gRNA 2
sgRNA2-R	AAACACGGGAGATTCGAGAGCCGA	to form double-strand gRNA 2

Supplementary Figure 1



Supplementary Figure 1 | (A) The tability coefficient of predection *P. tricornutum* NXS by SOPMA; (B) Prediction of protein secondary structure; (C) Hydrophobic amino acid prediction; (D) Transmembrane domain prediction by TMHMM; (E) The prediction three-dimensional structure of diatom NXS by pyMOL.

Supplementary Figure 2



Supplementary Figure 2 | Biomass of the *P. tricornutum NXS* knockout strains and WT under different light intensities. Data are shown as means ± standard error (n=3). The asterisk indicates statistical significance (* $p < 0.05$; ** $p < 0.01$).