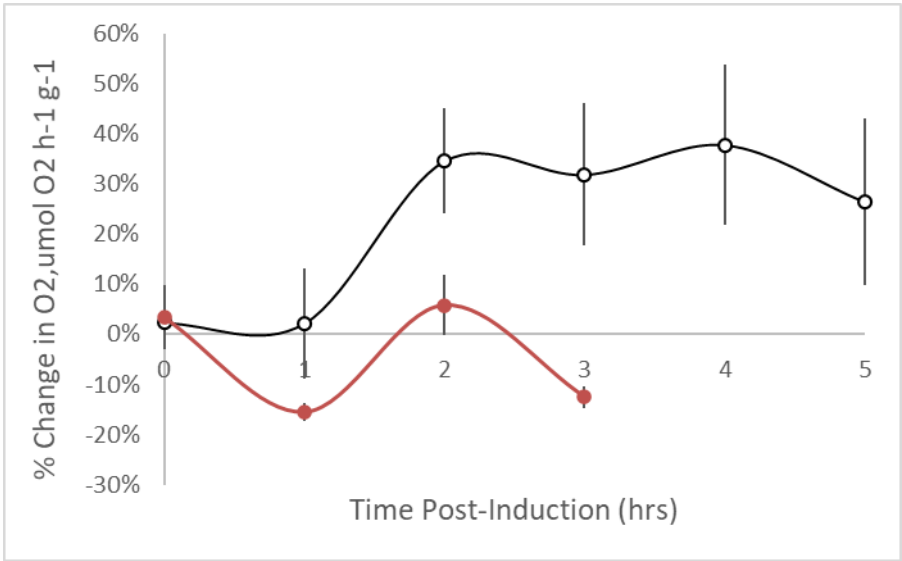
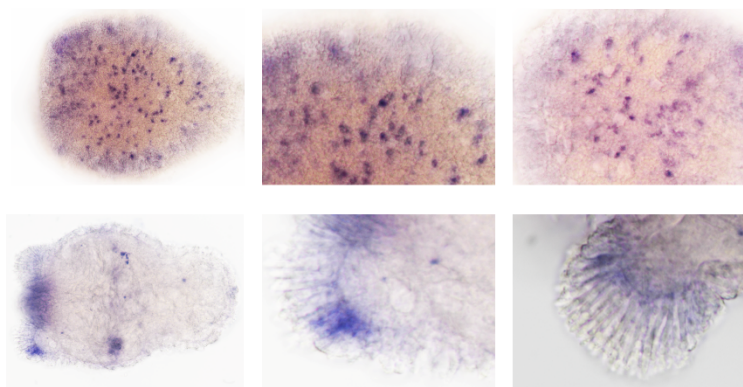


Figure S1. Change in oxygen consumption following the fishing line treatment (black) and in the untreated control (red).



S2A. NEP8-like is expressed in nematocytes in larvae and primary polyps and shares high sequence similarity with NEP8 toxin found in nematocysts. Signal peptide is shown in bold (identified by SignalP online tool, <http://www.cbs.dtu.dk/services/SignalP/>), ShKT domains are highlighted, and cystein residues forming the ShKT motives are in green.



Accession	Protein Name	Length
Nep8_Nve15921	MLRRPPLLVLVFTFVSTLYAKDLRGVSPDNESEAEVSPGDDEGPPEGNEDPVNWRTLTI	60
Nep8_like_Nve6865	MASLFWLLVACLVLAVDAKEIRRKLYRQ-----HESLRTIAETLERVHI	46
Nep8_Nve15921	DPEDDKDKGKDCESLADEGNLKKLNAYAVGNPWTIRFKKEN-GDSKKCKDLAGERHGN	119
Nep8_like_Nve6865	SPEDDKDYKSNCEFADEGSLKRFDYGFKEIPWSIRFKAKPEKYNTERTADLAGK-RQG	105
Nep8_Nve15921	GWKVGKGVRLRPDYMMQNNKLSLELGPETRFKYTDDEDVRPEWAQAGYCTSTNTDINLKG	179
Nep8_like_Nve6865	PWAQRSELRRLPEFMQQNKQSLDLGPENA--YTDDDVRLPYWGKEGYRTDAEINSR	163
Nep8_Nve15921	PHSIRKRYKQRAPASTPYPPYVEALHPYQYRVVLPSVTILQTTTA----APSTQPAETT-	233
Nep8_like_Nve6865	PYSIRKRYRSVSPAPQPYPIPTGLYPYQPTPVP-GVTVSQPKIVLQPYPAPYPYPYPVPS	222
Nep8_Nve15921	KAPPNTAAPTAA-----TPAPTAPAPAPTAPAPAPTAPAPAPATTPAPA	281
Nep8_like_Nve6865	PAPSPSPSPSPAPSPSPSPALSPSPAPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPS	282
Nep8_Nve15921	PVP---PAPAPAPAPAPAPP-APPVAPAPQTAPLAGSPPESTPEEQDD-----NSA-	328
Nep8_like_Nve6865	PSPEPSPSPAPSPAPEPSPAPSPASEPSPETTTAPKDPQTQAPVVVETQQPSTQLPAPTQ	342
Nep8_Nve15921	DESTEI---EAGEGGGELCDEKHSSQQ-----	352
Nep8_like_Nve6865	PTTEPIDSSGNPGESGNVWPQGQKPSAAPVTQPGSGEEEEVEEGVTTDAPVGSVPVE	402
Nep8_Nve15921	-----	352
Nep8_like_Nve6865	ATPGPAATNAPEATQAPEVVTQAPEATSAPEVTAAPTGQATPASNPIGTPPVVFDHRKSH	462
Nep8_Nve15921	-----	352
Nep8_like_Nve6865	RSRNAKNDAAHHNNNNHHNNHHNNHNNPHNNAPSTPPTAPPSAPVFSKKLPVSGLDKATN	522
Nep8_Nve15921	-----	352
Nep8_like_Nve6865	AAKAKRNKHGHRHIIE	539

S2B. NveSkT1 is expressed in pharyngeal gland cells in planulae and primary polyps. Signal peptide is in bold (identified by SignalP online tool, <http://www.cbs.dtu.dk/services/SignalP/>), peptidoglycan binding domain is in blue, metallopeptidase is in grey, and ShKT domain is underlined with cysteins in green (domains were identified by Interpro, <https://www.ebi.ac.uk/interpro/>). The ShKT domain of NveSkT1 shares noticeable sequence similarity with potassium channel blocker ShK from the sea anemone *Stichodactyla helianthus*.



>NveSkT1

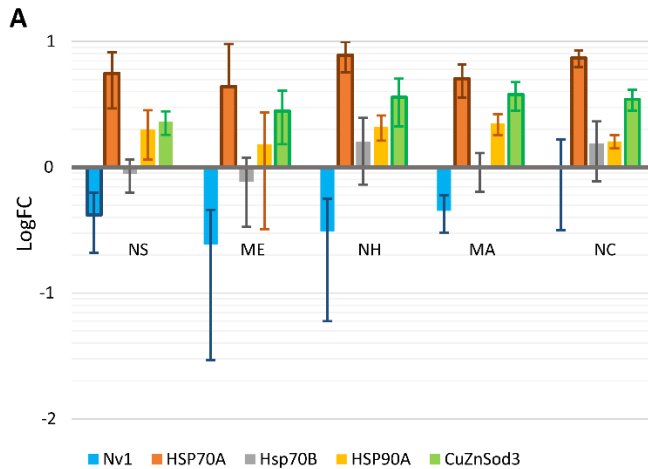
MKTLVFAGLLCLIAFAVSEDDDDQTM**ALKYLNQFHYISPARSGNHNVKTALEKFQSFAGLPVTGEIDAATIA**
QMKMPCRCMPDVEDDGLRIRRYKL**LGSKWNKKHLTYHISHGQDLSSSVQDRVFAKALDYWARVSGLTFSRTM**
 DGENADLKISFGPKSHGGTHDPEGTCSPFDGPGGVLAHAFFPRNGRAHFDEDEDFDGTYYEGTNLLWVAT
 HEFGHSLGLHHS DVRDAVMYPYYTGYKPGFDLKADDIAGIRAHYGDENSGGSQ**P**VDNNQS**P**DWTIY**C**TN
 NEYVIAN**CRKS****CGSC**

ShK_Stichodactyla	RS C IDTIPKSR C TAFQ C KHSMKYRLSF C RKTC CGTC	35
NveSkT1-ShKt_domain	- P VDNNQS C PDWTIY C -TNNEYVIAN CRKS CGSC	33
	: . . . :: * . :* :: ***:**:*	

Figure S3. Gene expression dynamics under UV light stress.

NS – Nova Scotia, ME – Maine, NH – New Hampshire, MA – Massachusetts, NC - North Carolina

S3A) Gene expression dynamics under UV light stress among the populations from the North to the South. If the change in expression of a gene is greater than 2.4 times and $p < 0.05$ (Student's t-test), the corresponding data point is outlined in bold.



S3B and S3C) Expression of toxins in Massachusetts (B) and North Carolina (C) following UV light stress. Gene expression is represented as Log_{10} of normalized fluorescence units measured by nCounter technology. P-values calculated by Student's t-test are shown for each gene. If the change in expression of a gene is greater than 2.4 times and $p < 0.05$, the corresponding p-value is shown in red. MA-ctr-Av – average values for control samples in MA; MA-UV-Av – average values for samples exposed to the UV light in MA; NC-ctr-Av – average values for control samples in NC; NC-UV-Av – average values for samples exposed to the UV light in NC.

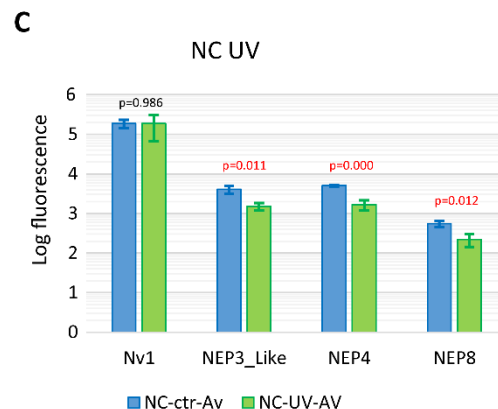
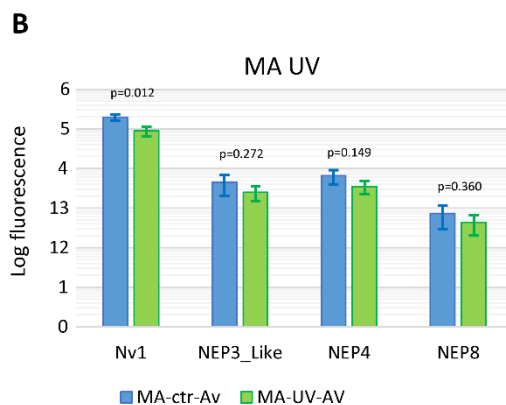


Figure S4. PCA analysis was conducted using the built in Trinity toolkit script PtR.

