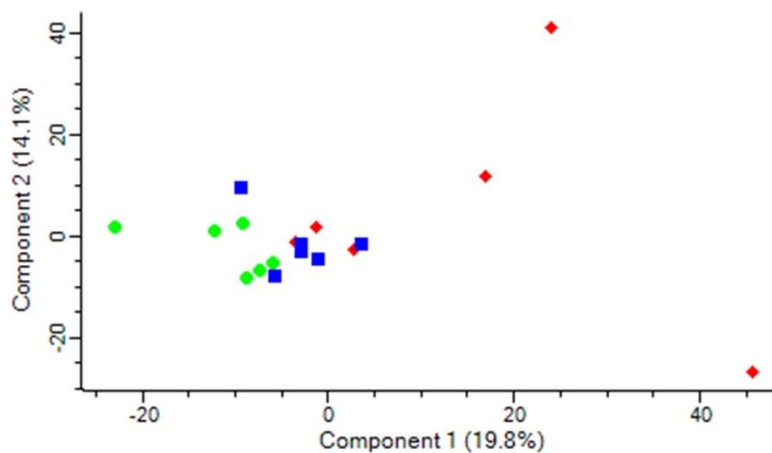


**Fig. S1.** Temperature fluctuations in treatment tanks during the experiments. Reported values were measured daily at 3-hours intervals using temperature loggers.



**Fig. S2.** Principal Component Analysis (PCA) plot of significantly abundant proteins in *Amphimedon navalis* at 26 °C (filled circles), 28 °C (filled squares) and 30 °C (filled diamonds). PCA was constructed using all detected proteins. Each point represents a biological sponge replicate (n = 6 per treatment).

**Table S1.** Results of time \* temperature *post hoc* pairwise comparisons test (with the sequential Sidak correction applied) from general linear mixed models for percentage change in buoyant weight, holobiont oxygen consumption and pumping rates of *Amphimedon navalis* in response to elevated temperature. Significant p-values are reported in bold. (n = 9 *per* treatment *per* time point)

Time (Weeks)	Temp	Contrast Estimate	Std. Error	t	df	P	CI (lower)	CI (upper)	
<b>Buoyant weight</b>									
<b>0</b>	28°C	26°C	-	-	-	-	-	-	
	30°C	26°C	-	-	-	-	-	-	
	30°C	28°C	-	-	-	-	-	-	
<b>1</b>	28°C	26°C	-0.007	0.002	-2.830	60	<b>0.013</b>	-0.013	-0.001
	30°C	26°C	-0.009	0.002	-3.620	60	<b>0.002</b>	-0.015	-0.003
	30°C	28°C	-0.002	0.002	-0.790	60	0.433	-0.007	0.003
<b>2</b>	28°C	26°C	-0.012	0.002	-4.783	60	<b>&lt;0.001</b>	-0.017	-0.006
	30°C	26°C	-0.018	0.002	-7.280	60	<b>&lt;0.001</b>	-0.024	-0.012
	30°C	28°C	-0.006	0.002	-2.497	60	<b>0.015</b>	-0.011	-0.001
<b>3</b>	28°C	26°C	-0.016	0.002	-6.537	60	<b>&lt;0.001</b>	-0.022	-0.010
	30°C	26°C	-0.026	0.002	-10.396	60	<b>&lt;0.001</b>	-0.032	-0.020
	30°C	28°C	-0.010	0.002	-3.859	60	<b>&lt;0.001</b>	-0.014	-0.005
<b>4</b>	28°C	26°C	-0.020	0.002	-8.209	60	<b>&lt;0.001</b>	-0.026	-0.015
	30°C	26°C	-0.034	0.002	-13.751	60	<b>&lt;0.001</b>	-0.040	-0.028
	30°C	28°C	-0.014	0.002	-5.542	60	<b>&lt;0.001</b>	-0.019	-0.009
<b>Holobiont oxygen consumption rate</b>									
<b>0</b>	28°C	26°C	-0.001	0.003	-0.247	27	0.993	-0.009	0.007
	30°C	26°C	-0.001	0.003	-0.003	27	0.998	-0.007	0.006
	30°C	28°C	0.001	0.003	0.245	27	0.993	-0.007	0.009
<b>1</b>	28°C	26°C	0.003	0.003	1.066	27	0.504	-0.004	0.011
	30°C	26°C	0.005	0.003	1.687	27	0.279	-0.003	0.013
	30°C	28°C	0.002	0.003	0.621	27	0.540	-0.005	0.008
<b>2</b>	28°C	26°C	0.005	0.003	1.539	27	0.135	-0.002	-0.004
	30°C	26°C	0.012	0.003	3.670	27	<b>0.003</b>	0.004	0.020
	30°C	28°C	0.007	0.003	2.131	27	0.083	-0.001	0.014
<b>3</b>	28°C	26°C	0.007	0.003	2.224	27	<b>0.035</b>	0.001	0.014
	30°C	26°C	0.016	0.003	5.159	27	<b>&lt;0.001</b>	0.008	0.024
	30°C	28°C	0.009	0.003	2.935	27	<b>0.014</b>	0.002	0.017
<b>4</b>	28°C	26°C	0.009	0.003	2.690	27	<b>0.012</b>	0.002	0.015
	30°C	26°C	0.020	0.003	6.224	27	<b>&lt;0.001</b>	0.012	0.028
	30°C	28°C	0.011	0.003	3.534	27	<b>0.003</b>	0.004	0.019

Time (Weeks)	Temp		Contrast Estimate	Std. Error	t	df	P	CI (lower)	CI (upper)
<i>Pumping rate</i>									
<b>0</b>	28°C	26°C	0.008	0.003	2.801	38	<b>0.024</b>	0.001	0.015
	30°C	26°C	0.006	0.003	2.032	38	0.096	-0.001	0.013
	30°C	28°C	-0.002	0.003	-0.769	38	0.447	-0.008	0.004
<b>1</b>	28°C	26°C	0.009	0.003	3.273	38	<b>0.005</b>	0.003	0.016
	30°C	26°C	0.013	0.003	4.404	38	<b>&lt;0.001</b>	0.005	0.020
	30°C	28°C	0.003	0.003	1.131	38	0.265	-0.003	0.009
<b>2</b>	28°C	26°C	0.010	0.003	3.338	38	<b>0.004</b>	0.003	0.016
	30°C	26°C	0.018	0.003	6.431	38	<b>&lt;0.001</b>	0.011	0.026
	30°C	28°C	0.009	0.003	3.094	38	<b>0.004</b>	0.003	0.015
<b>3</b>	28°C	26°C	0.020	0.003	6.999	38	<b>&lt;0.001</b>	0.013	0.027
	30°C	26°C	0.033	0.003	11.401	38	<b>&lt;0.001</b>	0.026	0.040
	30°C	28°C	0.013	0.003	4.402	38	<b>&lt;0.001</b>	0.007	0.018
<b>4</b>	28°C	26°C	0.022	0.003	7.743	38	<b>&lt;0.001</b>	0.016	0.029
	30°C	26°C	0.040	0.003	13.980	38	<b>&lt;0.001</b>	0.003	0.047
	30°C	28°C	0.018	0.003	6.237	38	<b>&lt;0.001</b>	0.012	0.024

**Table S2.** Results of pairwise comparisons between temperature treatments for differentially abundant proteins from *Amphimedon navalis* from Miss test using an FDR threshold of 0.1 and log-ratio (fold-change) of  $\pm 0.25$ . Significant p-values are reported in bold.

Uniprot Accession number	Protein annotation	Proteins in cluster	26°C vs 28°C	26°C vs 30°C	28°C vs 30°C
<b>Oxidation-reduction process (Oxidative stress)</b>					
A0A1X7V4C4	Aldedh domain-containing protein	2	<b>1.22E-05</b>	<b>5.24E-06</b>	0.980313
IIGFQ7	Ferritin	2	<b>3.53E-06</b>	<b>5.24E-06</b>	1
A0A1X7SUN1	VOC domain-containing protein	2	0.831446	<b>0.054828</b>	1
A0A1X7VNW3	Catalase (Heme cofactor)	2	0.311372	<b>0.001572</b>	<b>0.090423</b>
A0A1X7VQL2	Uncharacterized (Thioredoxin-like superfamily)	1	1	<b>0.012566</b>	<b>0.090423</b>
A0A1X7UNX4	Uncharacterized (Glutathione S-transferase superfamily)	1	1	0.192653	<b>0.050264</b>
A0A1X7T3Q9	E1_dh domain-containing protein	2	1	<b>0.000314</b>	<b>0.003458</b>
A0A1X7VJL6	Peroxiredoxin	1	0.83146	<b>0.049142</b>	1
A0A1X7U633	Cytochrome c domain-containing protein	2	0.795518	<b>0.000314</b>	<b>0.035267</b>
A0A1X7V4Y0	Proton-translocating NAD(P) (+) transhydrogenase	1	<b>0.071665</b>	<b>0.063899</b>	0.683634
<b>Protein transport</b>					
A0A1X7U4A4	Protein kinase domain-containing protein	1	<b>0.023796</b>	<b>0.047885</b>	1
A0A1X7UVI1	Protein kinase domain-containing protein	1	0.559622	<b>0.042849</b>	0.683634
A0A1X7VH72	Uncharacterized (inositol phosphokinase family)	1	<b>0.066834</b>	<b>0.012566</b>	1
A0A1X7V114	Vacuolar protein sorting-associated protein 11 homolog	1	0.63163	<b>0.001937</b>	0.115427
A0A1X7UHM1	Ras-related protein Rab-14	1	1	<b>0.055495</b>	0.40943
A0A1X7VLI5	Protein kinase domain-containing protein	1	1	<b>0.005623</b>	<b>0.03029</b>
A0A1X7VL10	ATP synthase subunit beta	1	<b>0.023366</b>	0.207581	1
A0A1X7VVN1	Uncharacterized (ABC transporter-like family)	1	<b>0.066834</b>	<b>0.001133</b>	<b>0.079628</b>
A0A1X7VJC1	Uncharacterized (DUOXA family)	1	<b>0.024449</b>	0.222406	0.683634
A0A1X7VXP7	Uncharacterized (SNF7 family)	1	<b>0.015008</b>	<b>0.003536</b>	0.61806
<b>Cytoskeletal organization</b>					
A0A1X7UKK7	Costars domain-containing protein	1	<b>0.066834</b>	<b>0.001937</b>	0.61806
A0A1X7VU79	Fascin	1	<b>0.066834</b>	0.2606	0.40943
A0A1X7UPB4	Tubulin alpha chain	1	<b>0.066834</b>	<b>0.000171</b>	0.393734
A0A1X7UIF6	F-actin-capping protein subunit beta	1	1	0.680671	<b>0.079628</b>
A0A1X7V1D4	Tubulin alpha chain	1	<b>0.024449</b>	<b>5.24E-06</b>	<b>0.005016</b>
A0A1X7U6V8	Septin-type G domain-containing protein	2	<b>0.047777</b>	1	<b>0.005016</b>
A0A1X7VTE3	Uncharacterized (small GTPase family)	1	0.232523	<b>0.005506</b>	0.269237
A0A1X7UXJ8	Uncharacterized (alpha-actinin family)	1	<b>0.023366</b>	<b>0.008162</b>	1
A0A1X7V9U2	Uncharacterized (WASH complex, subunit strumpellin)	1	1	<b>0.033781</b>	<b>0.090423</b>
A0A1X7U0F7	PDZ domain-containing protein	1	1	<b>0.092884</b>	<b>0.954823</b>
<b>Signal transduction</b>					
A0A1X7VAN2	Calmodulin	3	<b>0.004717</b>	<b>6.59E-07</b>	<b>0.090423</b>
A0A1X7UI48	Histidine-tRNA ligase	1	<b>0.024449</b>	<b>5.24E-06</b>	0.182332
A0A1X7VIG0	ADP-ribosylation factor 6 (Arf family)	1	0.318505	<b>0.054828</b>	0.683634
<b>Protein translation</b>					
A0A1X7VB92	Aspartate-tRNA ligase, cytoplasmic	1	<b>0.047777</b>	<b>0.009516</b>	0.303402
A0A1X7V8E5	Uncharacterized (Universal ribosomal protein S8 family)	1	1	<b>0.000838</b>	0.244596
A0A1X7V0I1	Ubiquitin - 60S ribosomal protein L40	6	<b>0.023366</b>	<b>0.008763</b>	0.090423
<b>Protein catabolism</b>					
A0A1X7VN30	Proteasome subunit beta	2	<b>0.061227</b>	<b>0.001937</b>	<b>0.090423</b>
A0A1X7VGM8	Palmitoyl-protein hydrolase 1	1	<b>0.089645</b>	0.680671	1
A0A1X7VV07	Sulfatase domain-containing protein (Ca <sup>2+</sup> Cofactor)	1	<b>0.003762</b>	<b>5.24E-06</b>	<b>0.090423</b>

\*Table continues next page

Uniprot Accession number	Protein annotation	Proteins in cluster	26°C vs 28°C	26°C vs 30°C	28°C vs 30°C
<b>Metabolic process</b>					
A0A1X7VEB3	Adenosylhomocysteinase (NAD <sup>+</sup> cofactor)	1	<b>0.089645</b>	<b>0.000314</b>	<b>0.016798</b>
<b>Others</b>					
A0A1X7SVR6	Uncharacterized	4	<b>3.53E-06</b>	<b>5.24E-06</b>	0.40943
A0A1X7VMX7	Septin-type G domain containing protein	1	0.831446	<b>0.001133</b>	0.576949
A0A1X7SMT9	Uncharacterized	1	<b>0.066834</b>	<b>0.012566</b>	1
A0A1X7VLW9	Transket_pyr domain-containing protein (Co <sup>2+</sup> and Mg <sup>2+</sup> cofactor)	1	1	<b>0.055495</b>	0.40943
A0A1X7V015	DUF3504 domain-containing protein	1	1	<b>0.040336</b>	0.269237
A0A1X7SJZ1	Uncharacterized	3	1	<b>0.054828</b>	0.683634
A0A1X7SYB4	Uncharacterized	1	0.398718	<b>0.054828</b>	<b>0.153691</b>
A0A1X7U869	Store-operated calcium entry-associated regulatory factor	1	1	<b>0.054143</b>	0.393734
A0A1X7VNC8	Uncharacterized (RNA helicase family)	1	1	<b>0.042849</b>	0.116539
A0A1X7T7Q1	Uncharacterized	2	0.24654	<b>0.049142</b>	0.393734

**Table S3.** Protein cluster report including identification probabilities, sequence coverage, and numbers of unique peptides and spectra.

[Click here to download Table S3](#)