

## Supplementary information

### Telomere DNA length regulation is influenced by seasonal temperatures differences

#### in short-lived but not in long-lived reef-building corals

Alice Rouan<sup>1,3\*</sup>, Melanie Pousse<sup>1-3\*</sup>, Nadir Djerbi<sup>1-3\*</sup>, Barbara Porro<sup>1-3</sup>, Guillaume Bourdin<sup>4</sup>, Quentin Carradec<sup>5,6</sup>, Benjamin C Hume<sup>7</sup>, Julie Poulain<sup>5,6</sup>, Julie Lê-Hoang<sup>5,6</sup>, Eric Armstrong<sup>5,6</sup>, Sylvain Agostini<sup>8</sup>, Guillem Salazar<sup>9</sup>, Hans-Joachim Ruscheweyh<sup>9</sup>, Jean-Marc Aury<sup>5</sup>, David A. Paz-García<sup>10</sup>, Ryan McMinds<sup>1,11</sup>, Marie-Josèphe Giraud-Panis<sup>1-3</sup>, Romane Deshuraud<sup>1-3</sup>, Alexandre Ottaviani<sup>1-3</sup>, Lycia Die Morini<sup>1</sup>, Camille Leone<sup>1</sup>, Lia Wurzer<sup>1</sup>, Jessica Tran<sup>1</sup>, Didier Zoccola<sup>12,3</sup>, Alexis Pey<sup>1-3</sup>, Clémentine Moulin<sup>13</sup>, Emilie Boissin<sup>14</sup>, Guillaume Iwankow<sup>14</sup>, Sarah Romac<sup>14</sup>, Colomban de Vargas<sup>15,6</sup>, Bernard Banaigs<sup>14</sup>, Emmanuel Boss<sup>4</sup>, Chris Bowler<sup>16</sup>, Eric Douville<sup>17</sup>, Michel Flores<sup>18</sup>, Stéphanie Reynaud<sup>12,3</sup>, Olivier P. Thomas<sup>19</sup>, Romain Troublé<sup>13</sup>, Rebecca Vega Thurber<sup>20</sup>, Serge Planes<sup>14</sup>, Denis Allemand<sup>12,3</sup>, Stephane Pesant<sup>21</sup>, Pierre E. Galand<sup>22</sup>, Patrick Wincker<sup>5,6</sup>, Shinichi Sunagawa<sup>9</sup>, Eric Röttinger<sup>1-3</sup>, Paola Furla<sup>1-3</sup>, Christian R Voolstra<sup>7</sup>, Didier Forcioli<sup>1-3</sup>, Fabien Lombard<sup>23</sup> and Eric Gilson<sup>1-3,24</sup>

1 Université Côte d'Azur-CNRS- Inserm - Institute for Research on Cancer and Ageing, Nice (IRCAN), France.

2 Université Côte d'Azur, Institut Fédératif de Recherche - Ressources Marines (IFR MARRES)

3 Laboratoire International Associé Université Côte d'Azur - Centre Scientifique de Monaco (LIA ROPSE), France, Monaco.

4 School of Marine Sciences, University of Maine, Orono, Maine, United States of America

5 Génomique Métabolique, Genoscope, Institut François Jacob, CEA, CNRS, Univ Evry, Université Paris-Saclay, 91057, Evry, France.

6 Research Federation for the Study of Global Ocean Systems Ecology and Evolution, R2022/Tara Oceans GO-SEE, 75016, Paris, France.

7 Department of Biology, University of Konstanz, Konstanz, Germany

8 Shimoda Marine Research Center, University of Tsukuba, Shimoda, Japan.

9 Department of Biology, Institute of Microbiology and Swiss Institute of Bioinformatics, ETH Zurich, 8092 Zurich, Switzerland

10 CONAyT-Centro de Investigaciones Biológicas del Noroeste (CIBNOR), Laboratorio de Necton y Ecología de Arrecifes, La Paz, Baja California Sur 23096, México.

11 University of South Florida Center for Global Health and Infectious Diseases Research, Tampa, FL, United States

12 Centre Scientifique de Monaco, Principality of Monaco

13 Tara Ocean Foundation, 8 rue de Prague, 75012 Paris, France.

14 Laboratoire d'Excellence "CORAIL," PSL Research University: EPHE-UPVD-CNRS, USR 3278 CRIOBE, Université de Perpignan, Perpignan Cedex, France.

15 Sorbonne Université, CNRS, Station Biologique de Roscoff, AD2M, UMR 7144, ECOMAP, Roscoff, France.

16 Institut de Biologie de l'Ecole Normale Supérieure (IBENS), Ecole normale supérieure, CNRS, INSERM, Université PSL, 75005 Paris, France

17 Laboratoire des Sciences du Climat et de l'Environnement, LSCE/IPSL, CEA-CNRS-UVSQ, Université Paris-Saclay, F-91191 Gif-sur-Yvette, France

18 Weizmann Institute of Science, Department of Earth, and Planetary Sciences, 76100 Rehovot, Israel

19 School of Biological and Chemical Sciences, Ryan Institute, University of Galway, University Road H91TK33 Galway, Ireland

20 Oregon State University, Department of Microbiology, 220 Nash Hall, 97331 Corvallis OR USA

21 PANGEA, Data Publisher for Earth and Environment Science, Bremen, Germany,

22 Sorbonne Université, CNRS, Laboratoire d'Ecogéochimie des Environnements Benthiques, Observatoire Océanologique de Banyuls, Banyuls-sur-Mer, France

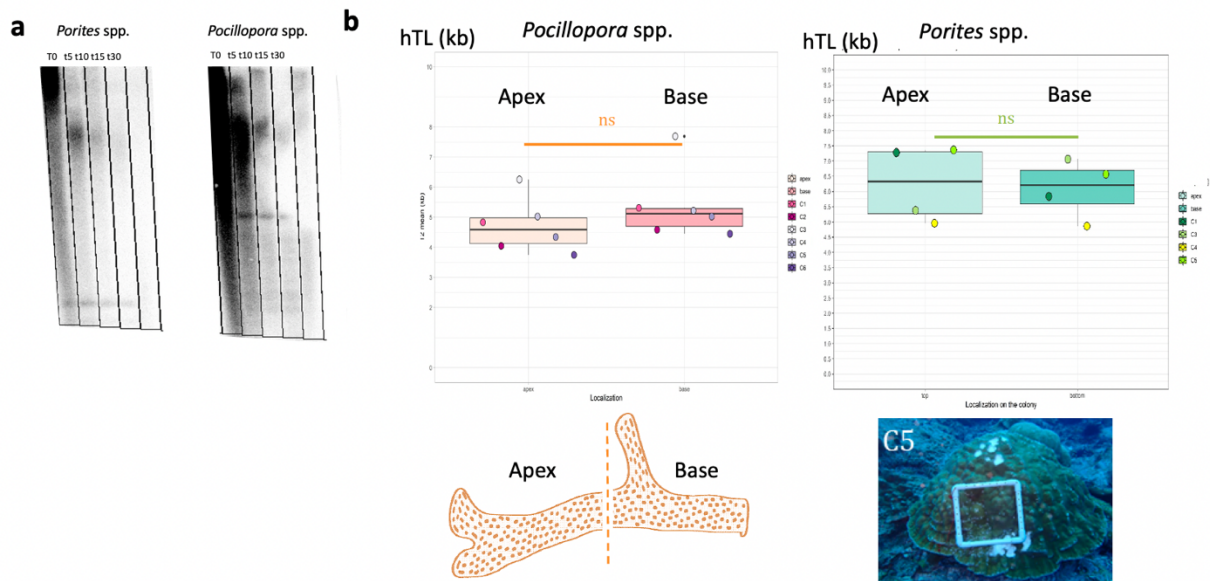
23 Sorbonne Université, Institut de la Mer de Villefranche sur mer, Laboratoire d'Océanographie de Villefranche, Villefranche-sur-Mer, France.

24 Department of Medical Genetics, CHU, Nice, France.

\* Contributed equally

✉ [Eric.Gilson@univ-cotedazur.fr](mailto:Eric.Gilson@univ-cotedazur.fr); [Alice.Rouan@outlook.fr](mailto:Alice.Rouan@outlook.fr)

**This pdf contains Supplementary Figure 1-13 and Supplementary Tables 1-6.**

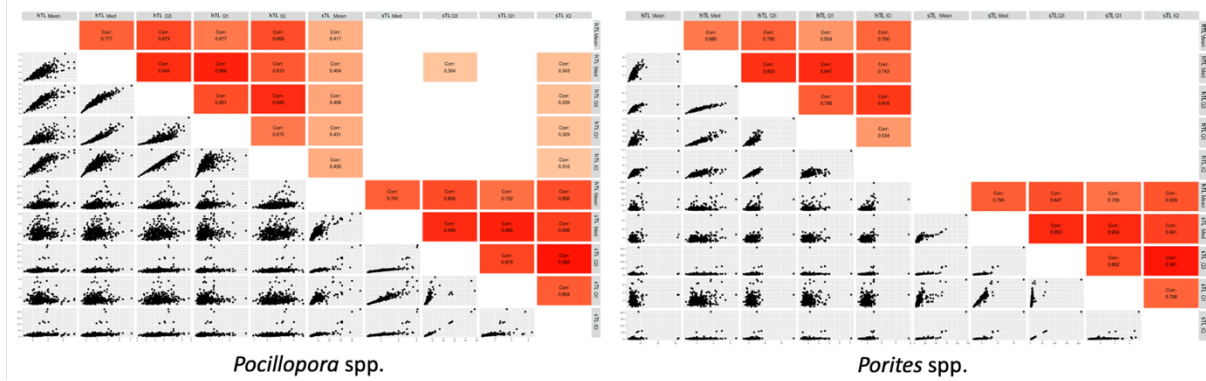


**Supplementary Figure 1: Controls of TL measurement in coral.**

**a)** Bal31 Telomere restriction fragment assay. For each lane 5µg of DNA was digested by the exonuclease Bal31 for (t0, 5, 10, 15 and 30 minutes). The reactions were then digested by *RsaI* and *HinfI* to perform the Southern blotting TRF analyses. Results show a decrease in the hTL smear with the increase of incubation time with Bal31 while the discrete band (Interstitial Telomeric Sequence) remains, showing that the smear signal is terminally located.

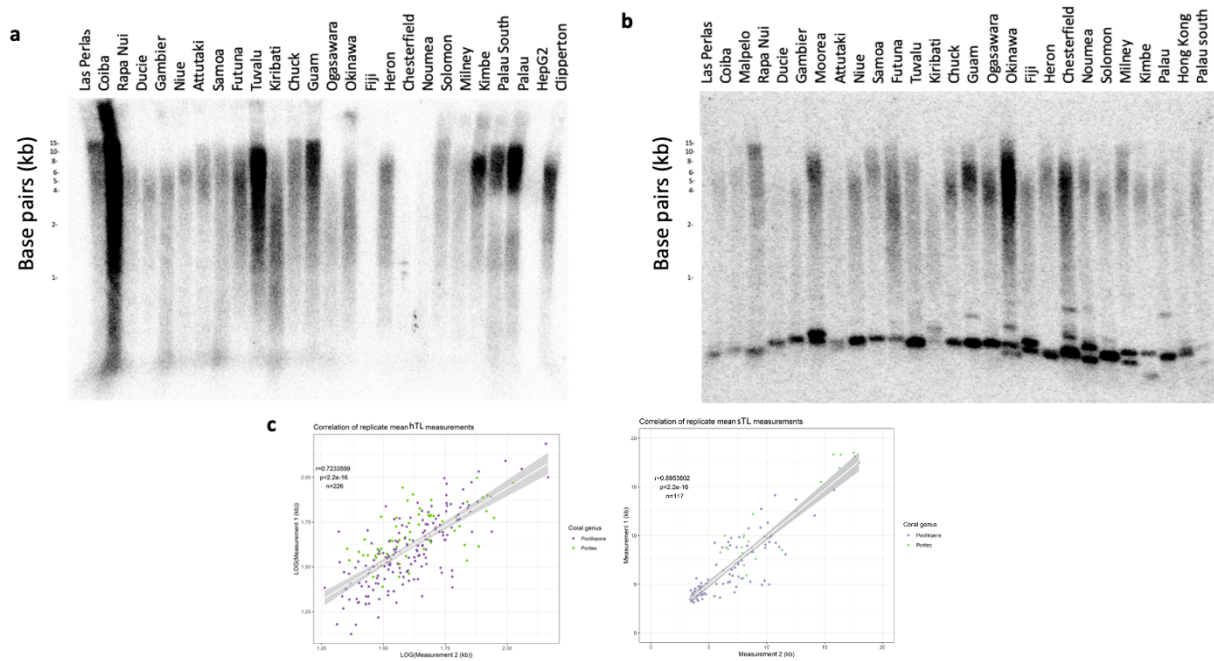
**b)** Boxplot of mean host TL measures (mean hTL) in 2 different localizations (apex or top of a branch/colony compared to base or edge of a branch/colony) of *Pocillopora* spp. and *Porites* spp. colonies. The colonies were sampled at the Clipperton island. The lower and upper bounds of the box represent the first (Q1) and the third (Q3) quartile, respectively. The entire box represents the interquartile range (IQ). The median is represented as a line across the box. Whiskers extending from Q1 and Q3 are defined as 1.5xIQ. The right box displays the colony part localized at the apex of a branch (*Pocillopora* spp.) or the top of the colony (*Porites* spp.). The right box displays the colony part localized at the base of a branch (*Pocillopora* spp.) or the edge of the colony (*Porites* spp.). Samples are colored by colony (6 colonies for *Pocillopora* spp. and 4 colonies *Porites* spp.) and displayed as dots. Apex and base groups were compared using the Wilcoxon nonparametric test (absence of normal distribution of data) (ns= not significant, pvalue=0.1797 and pvalue=0.4557 respectively). The scheme of the experimental design of branch sectioning is shown below the *Pocillopora* spp hTL results and a picture showing the apex and base sampling of a *Porites* spp colony is found below the *Porites* spp hTL results.

Source data are provided as a Source Data file.



### Supplementary Figure 2: Correlation among TL parameters

Correlation matrix between TL (hTL and sTL: mean, median, Q1: 1st quartile, Q3: 3rd quartile, IQ: interquartile distance) in *Pocillopora* and *Porites* samples with the distribution plots in the left half and significant correlation coefficient  $s$  ( $r_s > 0.3$ ,  $p < 0.05$ ) in the right half ( $n = 363$  samples).



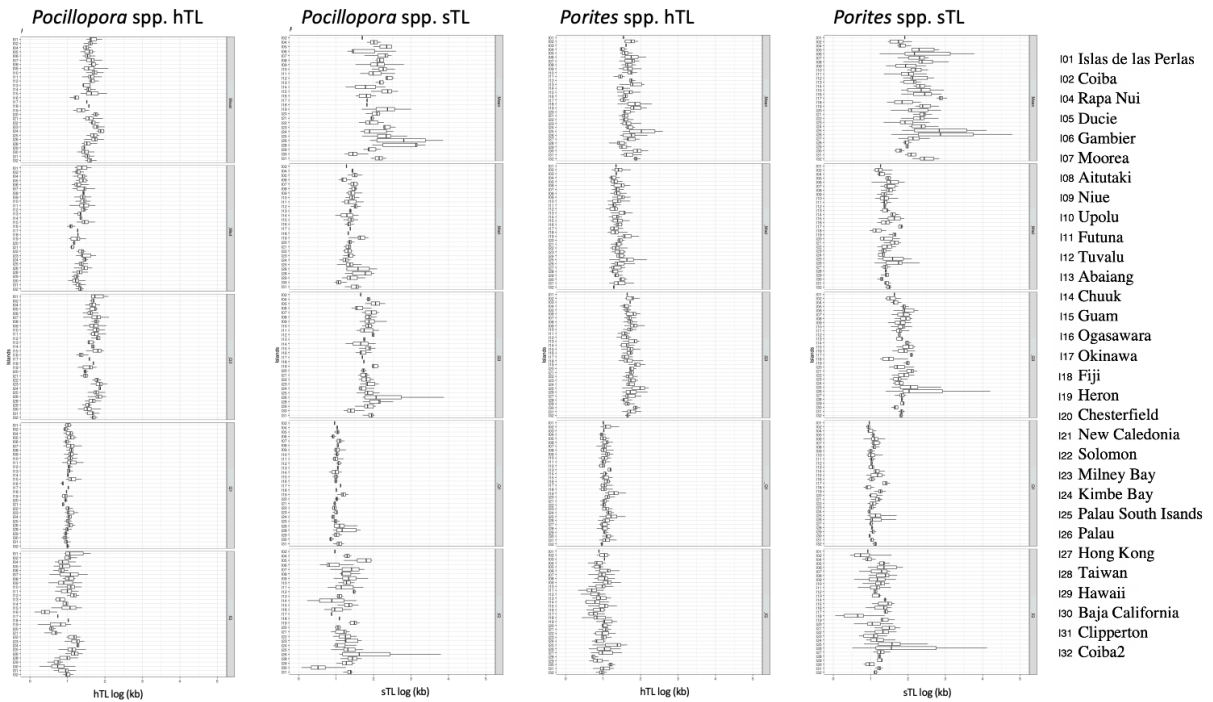
### Supplementary Figure 3: Southern control quality

**a-b)** Examples of Telomere Restriction Fragment (TRF) Southern blotting of *Pocillopora* spp. samples (left) and *Porites* spp. samples (right) hybridized with the radioactive labelled complementary probe to the host telomeric repeat sequence (hTL). The lane names are referring to the sampling island of the samples for *Pocillopora* spp. (blot #150120, samples names are displayed from left to right, M011C06, M021C10, M044C10, M053C10, M063C06, M091C04, M081C01, M102C06, M111C10, M122C01, M131C06, M142C01, M152C10, M163C10, M171C06, M183C07, M193C10, M202C10, M213C01, M223C10, M231C01, M241C01, M252C05, M261C01, HepG2 (human cells), M313C01) and *Porites* spp. (blot #080419, samples names are displayed from left to right, L012C16, L022C13, L031C04, L043C16, L051C16, L061C11, L071C16, L081C11, L093C16, L102C12, L113C11, L123C19, L141C16, L153C11, L163C16, L171C12, L182C16, L191C11, L201C15, L213C11, L222C11, L231C11, L243C11, L263C12, L272C11, L251C13)

**c)** Correlation analyses between technical replicates of TRF duplicated results for samples loaded at least twice in separate gels. The samples are displayed as dots and colored by genus (*Pocillopora* spp. in purple and *Porites* spp. in green) for mean hTL results on the left and mean sTL on the right. A smoothed linear regression curved is plot as a white line with a grey confidence interval. The hTL (left) data were log transformed, not the sTL (right), to perform a Pearson's correlation test between the technical duplicates ( $r=0.7233599$ ,  $pvalue<2.2e^{-16}$  and  $r=0.8953802$ ,  $pvalue<2.2e^{-16}$ , respectively),  $n$  indicates the number of samples.

Source data are provided as a Source Data file, including detailed information of all the blots used in the study to measure TL.

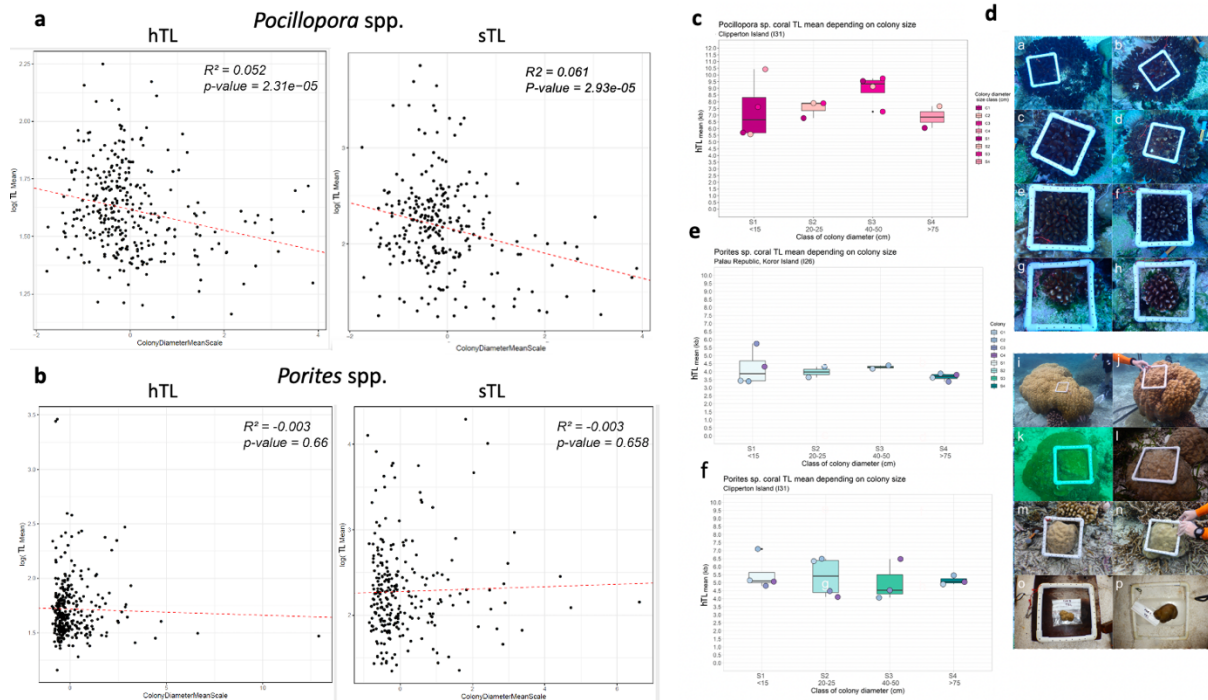




#### Supplementary Figure 4: Results of TL measurement

Boxplot of coral TLs analyzed in 32 islands of the Pacific Ocean. The various TL parameters analyzed by Southern blotting are shown (n = 444 samples (*Pocillopora* hTL), n = 363 samples (*Pocillopora* sTL), n = 409 samples (*Porites* hTL), n = 341 samples (*Porites* sTL)). The boxplots are defined as follows: the lower and upper bounds of the box represent the first (Q1) and the third (Q3) quartile, respectively. The entire box represents the interquartile range (IQ). The median is represented as a line across the box. Whiskers extending from Q1 and Q3 are defined as 1.5xIQ.

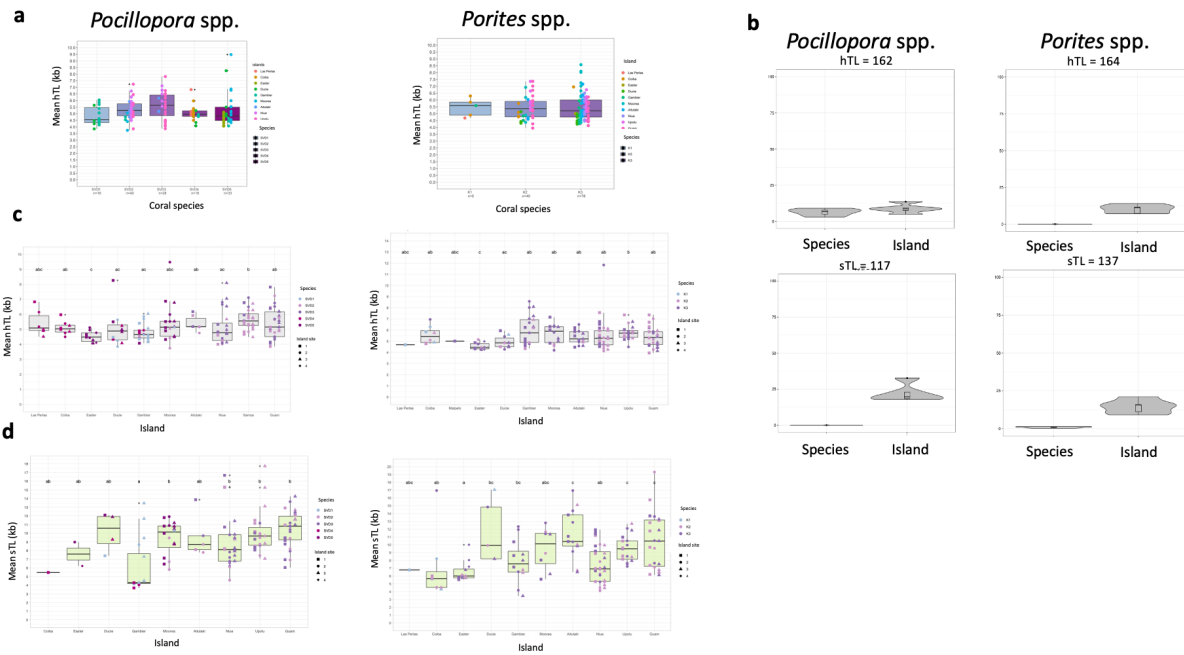
Source data are provided as a Source Data file.



### Supplementary Figure 5: TL and colony size

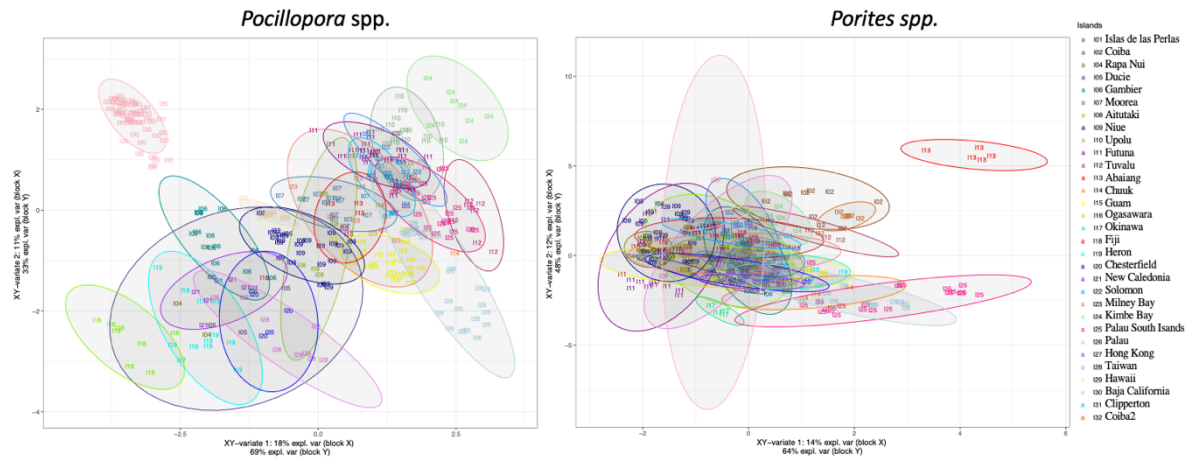
**a-b)** Log(TL) as a function of Colony diameter mean (scaled: centered and reduced) in *Pocillopora* (a) and *Porites* (b). The red dashed line is extracted from the linear model  $\log(\text{TL}) \sim \text{Colony diameter mean}$ . The p-value is obtained using a F-test on the linear model. **c)** Boxplot of mean hTL differences between *Pocillopora* of 4 different size classes from Clipperton Island (Colony diameter: S1 < 15 cm, cm 20 < S2 < 25 cm, cm 40 < S3 < 50 cm, S4 > 75 cm). **d)** Pictures of colonies of different sizes of *Pocillopora* spp. from Clipperton (a-h) and *Porites* spp. from Palau (i-p). Two colonies per size class are displayed ((a-b;i-j) = S4, (c-d;k-l) = S3, (e-f;m-n) = S2, (g-h;o-p) = S1). **e-f)** Boxplot of mean hTL differences between *Porites* samples of 4 different size classes from Palau and Clipperton (Colony diameter: S1 < 15 cm, cm 20 < S2 < 25 cm, cm 40 < S3 < 50 cm, S4 > 75 cm). For **c-e-f)** the lower and upper bounds of the box represent the first (Q1) and the third (Q3) quartile, respectively. The entire box represents the interquartile range (IQ). The median is represented as a line across the box. Whiskers extending from Q1 and Q3 are defined as  $1.5 \times \text{IQ}$ . Each individual sample is displayed as a dot on top of the box. TL was not significantly different between size group (Kruskal-Wallis test : (c)  $p = 0.4286$ , (e)  $p = 0.7748$ , (f)  $p = 0.4448$ ).

Source data are provided as a Source Data file.



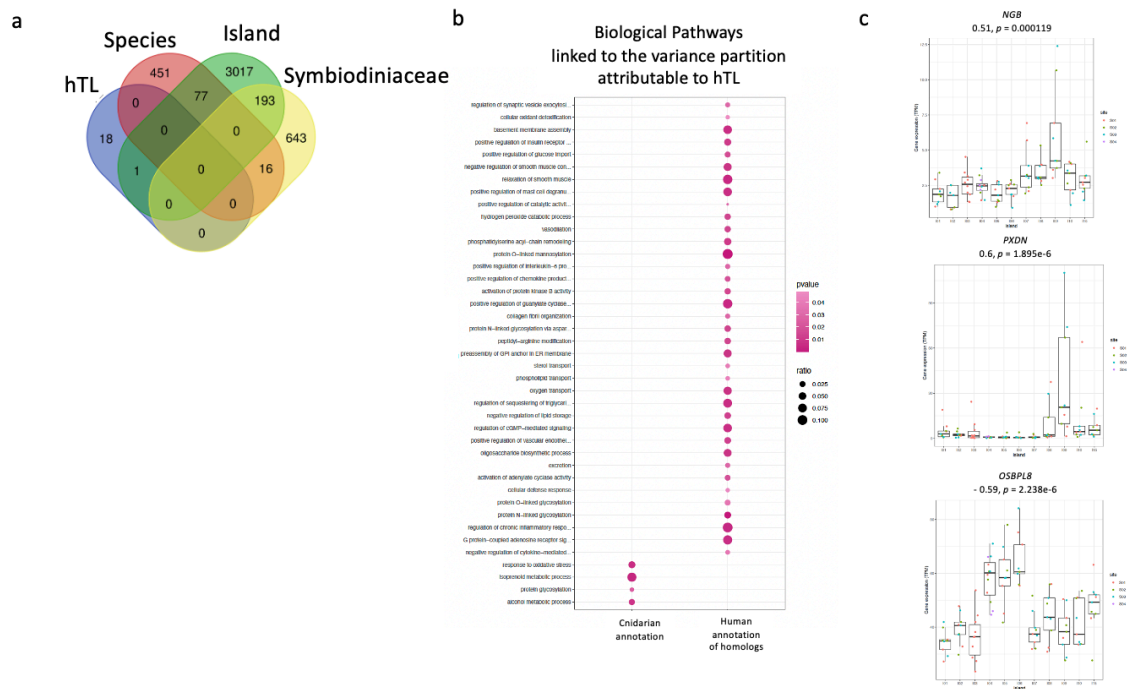
### Supplementary Figure 6: Species effect on TL variation

Box plot of mean hTL depending on genetic lineage for 11 islands across the Pacific Ocean. Individuals are colored by island. There are no significant differences neither for *Pocillopora* spp. (left) nor *Porites* spp. (right) (respectively  $0.082 < p < 0.476$  and  $p=0.93$ ). Genetic clusters are equivalent to species and n refers to the number of samples. **b**) Percentage of TL variation explained by the island of origin and host species for 11 islands across the Pacific Ocean. In this analysis, hTL/sTL mean, median, Q1, Q3 and IQ were used. n refers to the number of samples. **c-d**) Box plots of mean hTL and sTL depending on islands of origin for 11 islands for which the host species (genetic cluster) was determined. Individuals are colored by host species. Statistics in **a**, **c** and **d** are calculated using a pairwise wilcoxon test and are displayed as letters for **c** and **d**. Islands sharing at least one letter are not significantly different from each other. For all the boxplots, the lower and upper bounds of the box represent the first (Q1) and the third (Q3) quartile, respectively. The entire box represents the interquartile range (IQ). The median is represented as a line across the box. Whiskers extending from Q1 and Q3 are defined as  $1.5 \times IQ$ . Each individual sample is displayed as a dot on top of the box. Source data are provided as a Source Data file.



### Supplementary Figure 7: sPLS model between TL and environmental variables

Sample plot generated using the *plotIndiv* function corresponding to the sPLS model representing the relationship between hTL and environmental variables. Samples are labelled according to their island of origin.

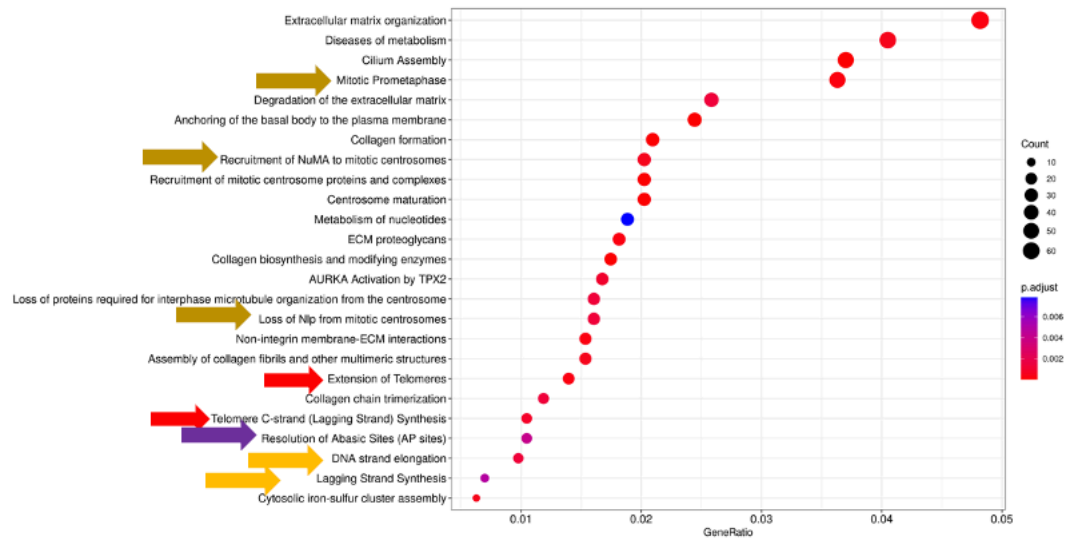


### Supplementary Figure 8: Characterization of the expression of hTL-correlated genes

a) Venn diagram of the hTL-correlated genes for which more than 25% of the variation in their expression is explained by one of four predictor variables: the island of origin, the host species (shown as “species”), the Symbiodiniaceae composition and hTL.

b) Functional enrichment analysis of the genes with expression variations explained by hTL. p-value of the Fisher’s exact test is given as a color gradient.

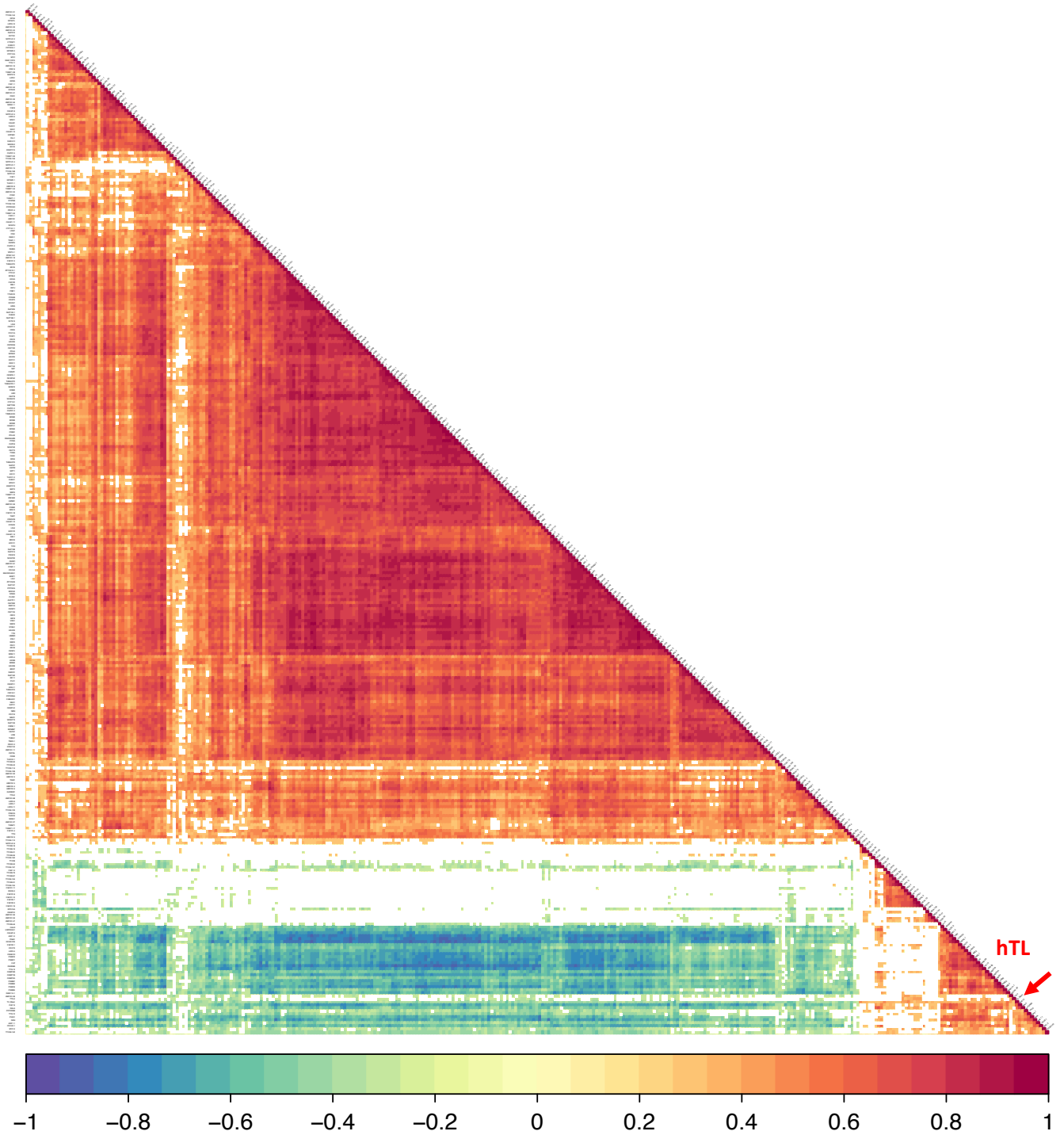
c) Expression by island of three genes correlated to hTL and involved in redox functions ( $n = 103$  samples). Correlation values from Spearman correlation and adjusted p-value using Benjamini–Hochberg method are given. The boxplots are defined as follows: the lower and upper bounds of the box represent the first (Q1) and the third (Q3) quartile, respectively. The entire box represents the interquartile range (IQ). The median is represented as a line across the box. Whiskers extending from Q1 and Q3 are defined as  $1.5 \times IQ$ . Source data are provided as a Source Data file.



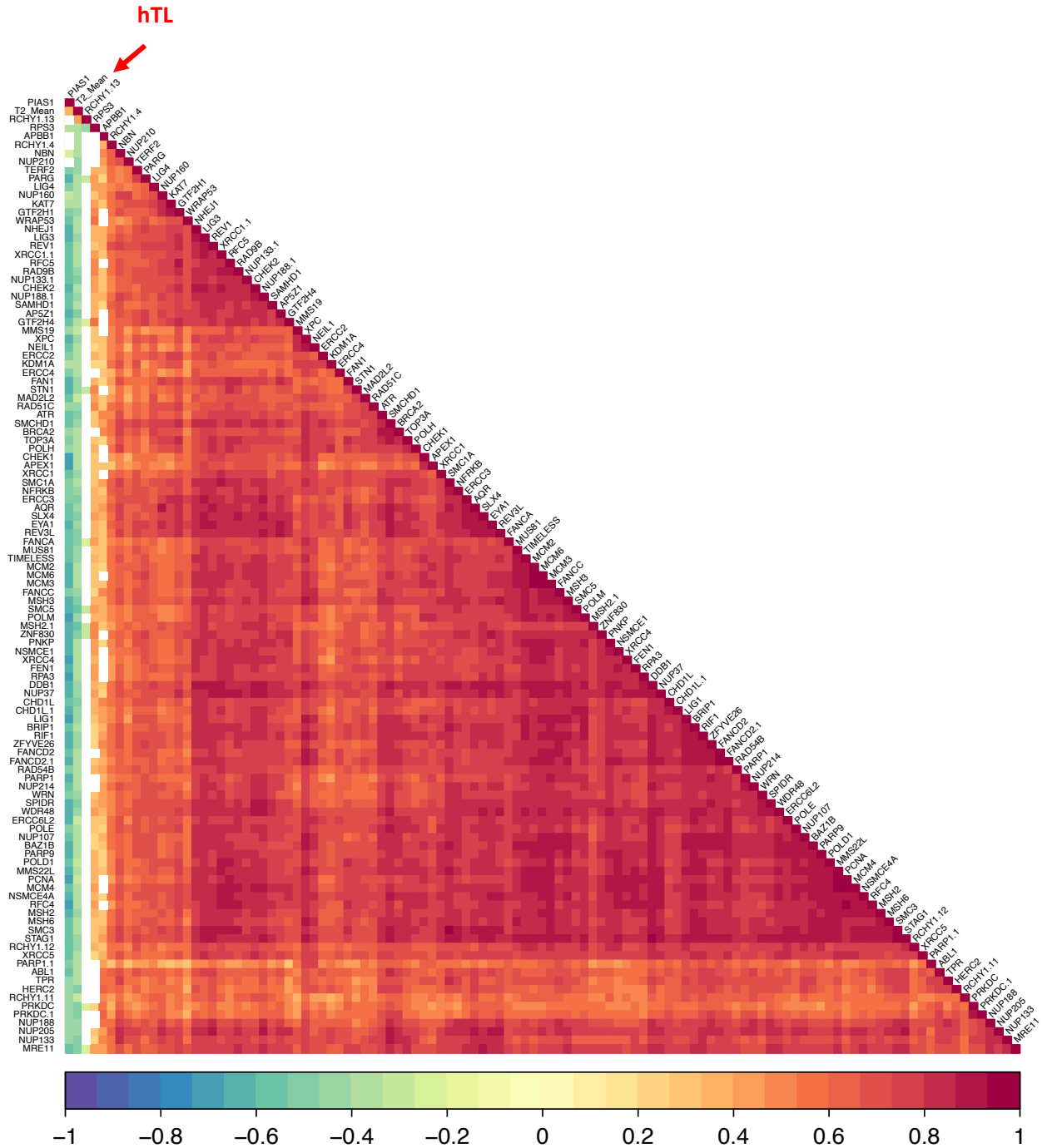
### Supplementary Figure 9: Reactome analysis of the expression of hTL-correlated genes

Significant pathways (adjusted p-value < 0.05, hypergeometric test, FDR adjustment) from Reactome analysis of the human homologs of the hTL-correlated genes for which at least 25% of their expression variance is explained by the island of origin (see **Fig. 4a**). Terms and pathways related to telomeres, DNA repair, DNA replication and cell cycle are represented by colored arrows.

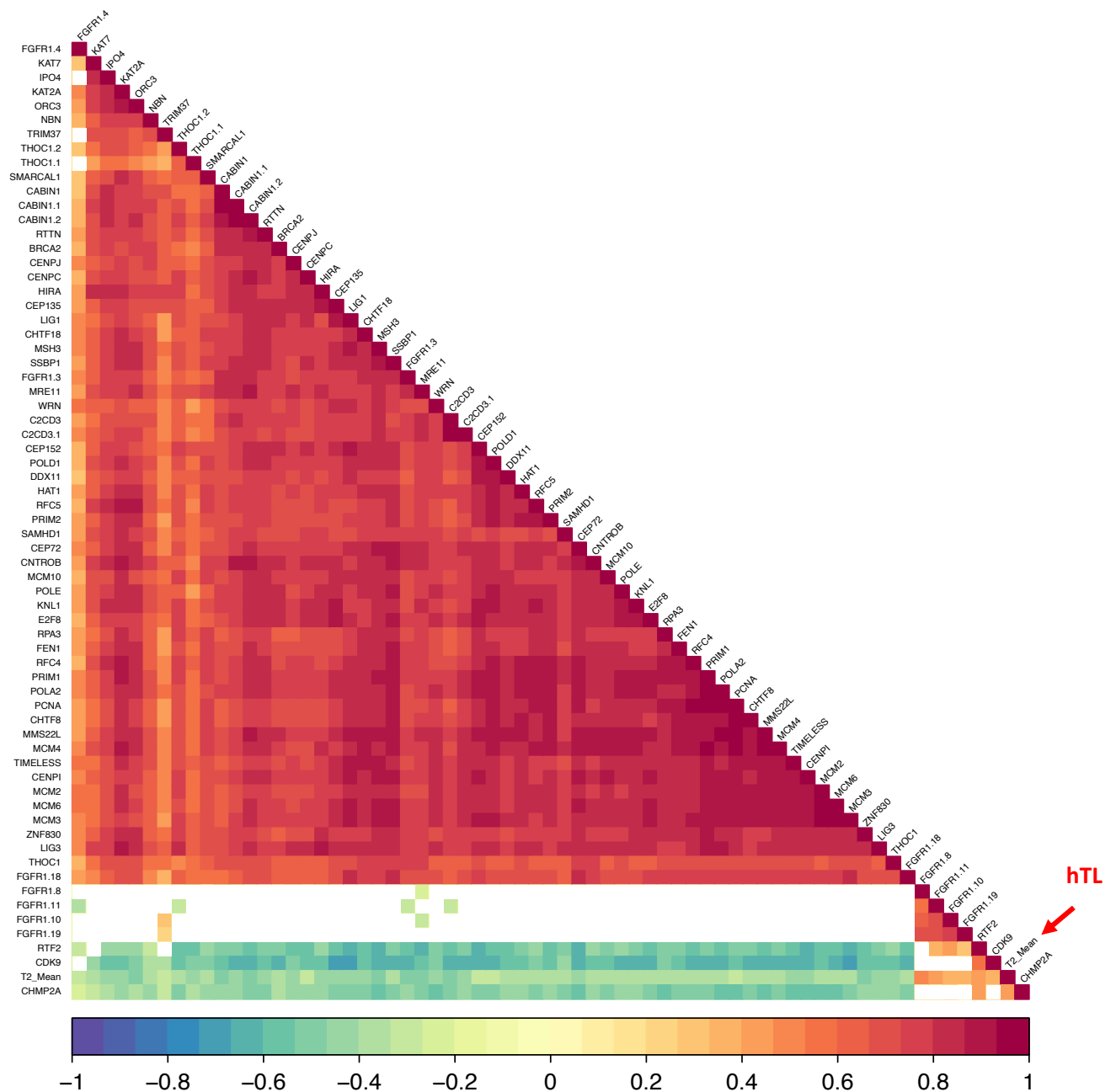




**Cell cycle genes whose expression variance  
is explained by islands and correlated with hTL**



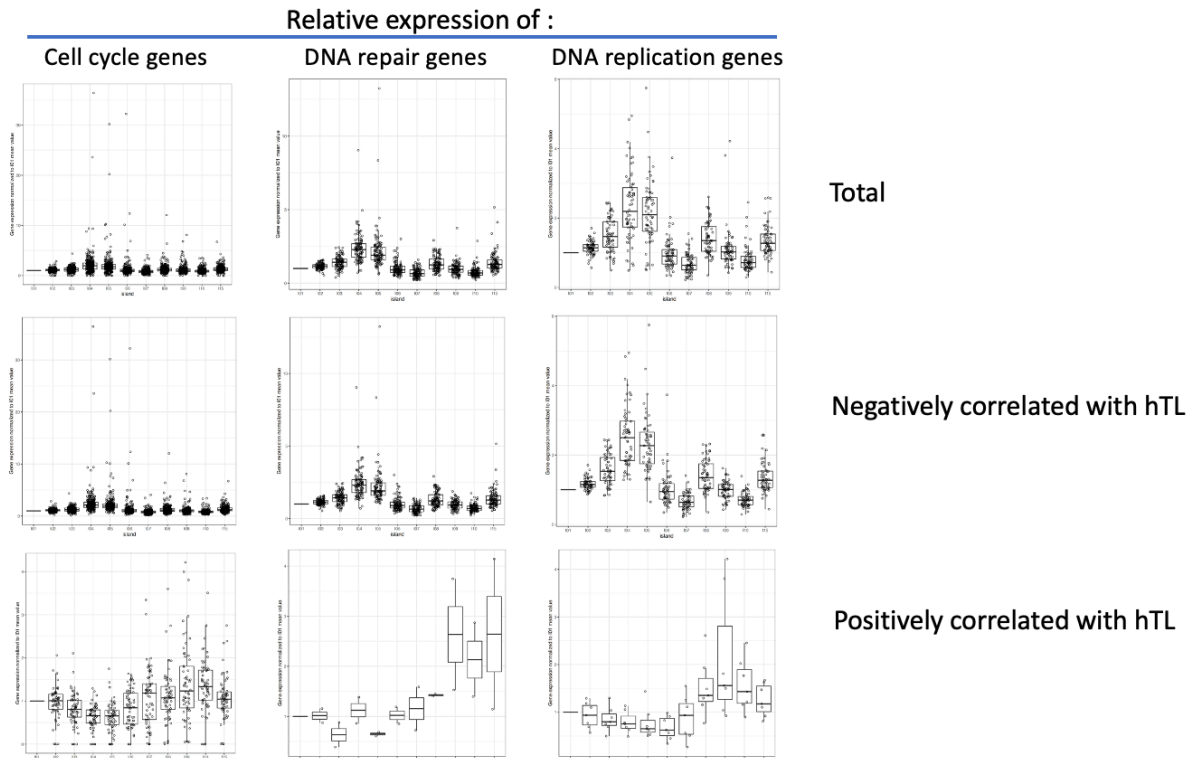
**DNA repair genes** whose expression variance is explained by islands and correlated with hTL



**DNA replication genes whose expression variance**  
is explained by islands and correlated with T2L

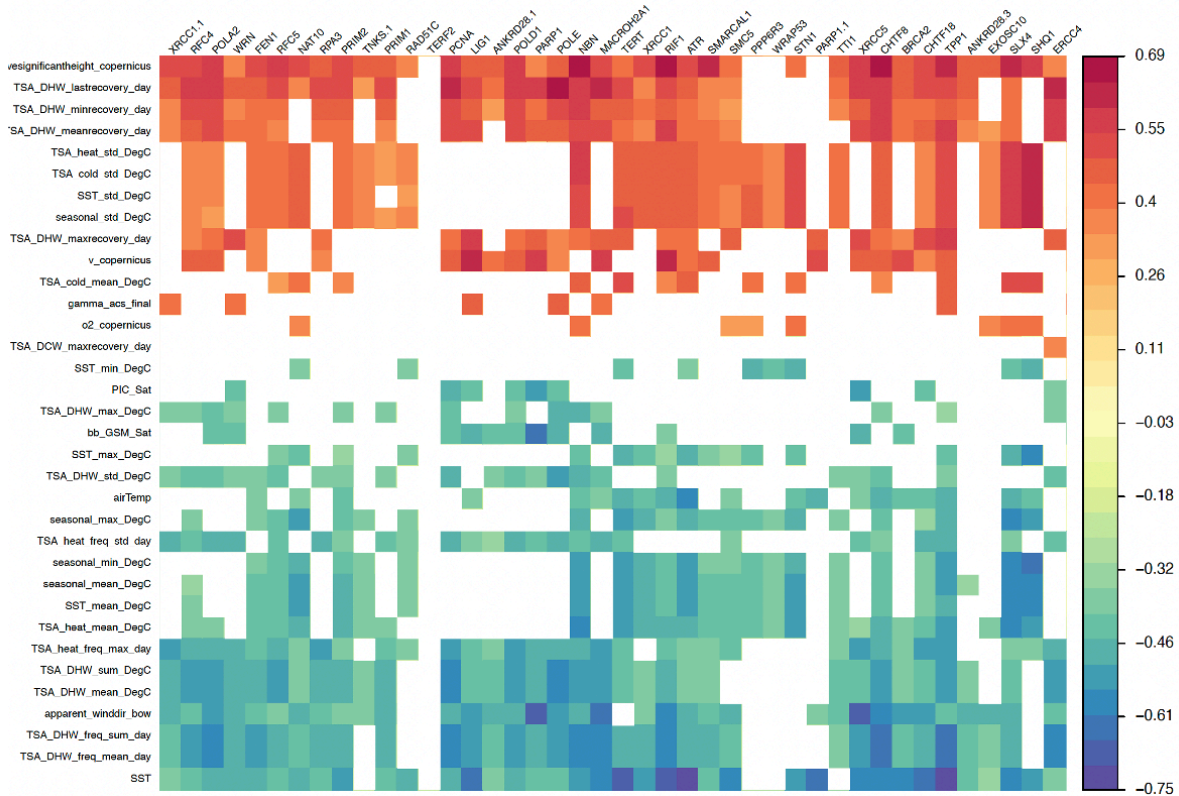
### Supplementary Figure 10: Correlation among hTL-correlated genes

Correlograms obtained with Spearman correlation of hTL and genes involved in cell cycle, DNA repair, and DNA replication from the variance partition attributable to island (**Figure 4a-c**). The genes shown here are significantly ( $r > 0.3$ ,  $p < 0.05$ ) correlated with hTL. When the genes are significantly correlated between each other ( $p < 0.05$ ) they are shown according to the color scale of the correlation coefficient. Blank cells indicate genes that are not significantly correlated ( $p > 0.05$ ).  $p$ -values were adjusted by the Benjamini–Hochberg method.



**Supplementary Figure 11: Expression of hTL-correlated genes between islands**

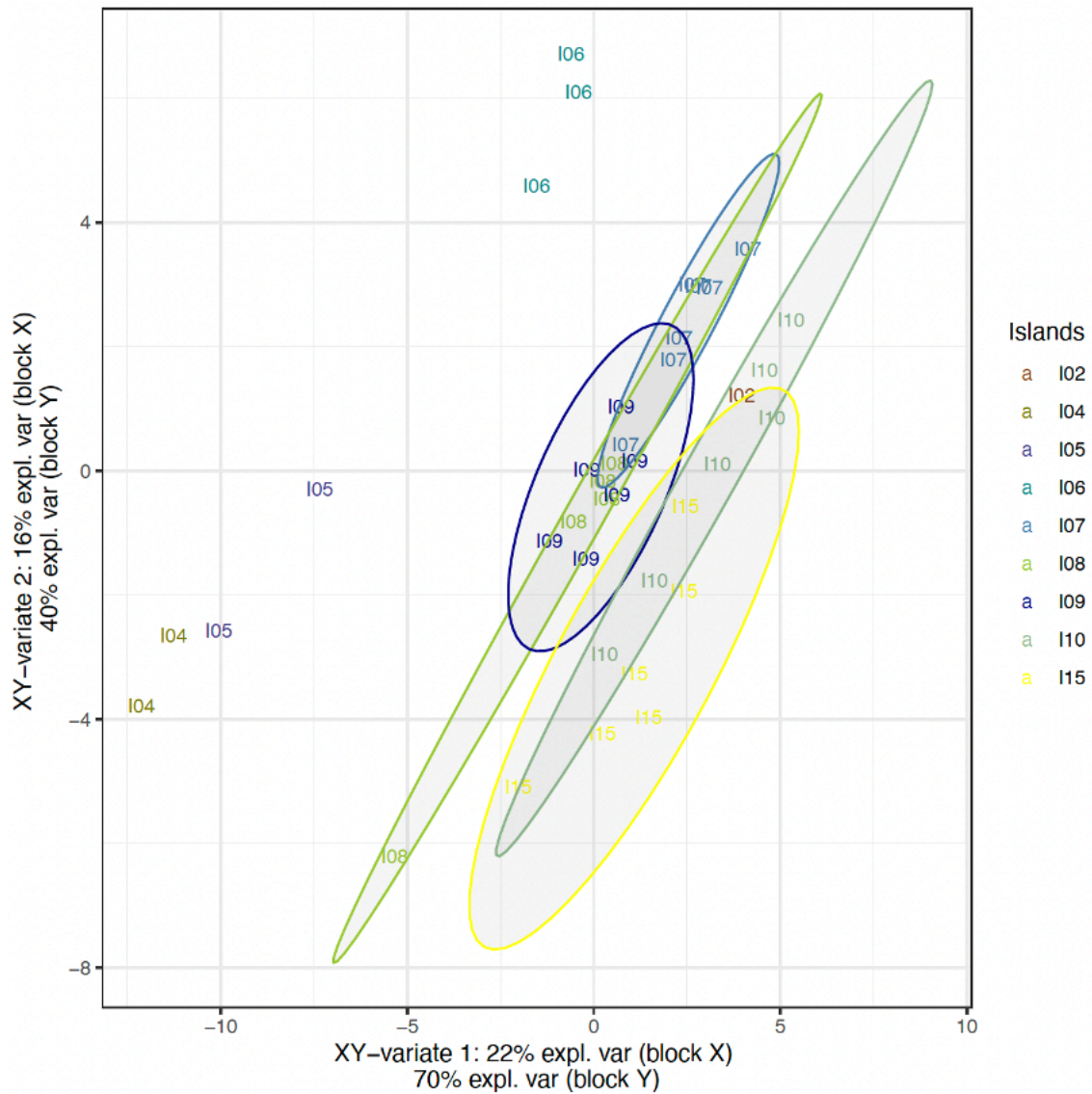
Gene expression by island for the genes correlated with hTL in the different terms/pathways (Supplementary Fig. 9). The expression of each gene is normalized to the mean expression value of I01 (Las Perlas). The results for total, negatively correlated and positively correlated genes are shown separately. (n = 103 samples). The boxplots are defined as follows: the lower and upper bounds of the box represent the first (Q1) and the third (Q3) quartile, respectively. The entire box represents the interquartile range (IQ). The median is represented as a line across the box. Whiskers extending from Q1 and Q3 are defined as 1.5xIQ. Source data are provided as a Source Data file.



**Supplementary Figure 12: Correlation between gene expression and environmental variables**

Correlation matrix obtained with Spearman correlation between telomere gene expression and environmental variables in *Pocillopora* spp. ( $r_s > 0.3$ ,  $p < 0.05$ ) (related to **Figure 5**).  $p$ -values were adjusted by the Benjamini–Hochberg method.





**Supplementary Figure 13: sPLS model of gene expression and environmental variables**  
 Sample plot generated using the *plotIndiv* function corresponding to the sPLS model representing the relationship between gene expression and environmental variables (related to Fig. 5). Samples are labelled according to their island of origin.

Pocillopora hTL													
r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual	nobs	error.rate	frml
0.08021973	0.077538138	0.178735877	29.91514696	8.71482E-08	1	105.506231	-205.0120462	-193.4814129	10.95765426	343	345	0.03516845	log(hTL_Mean) ~ ColonyDiameterMean
0.081163371	0.075790057	0.178905151	15.10490115	5.17308E-07	2	105.6830921	-203.3661841	-187.9920064	10.94641214	342	345	0.035201757	log(hTL_Mean) ~ poly(ColonyDiameterMean, 2)
0.072889158	0.070186211	0.179446717	26.96655017	3.55605E-07	1	104.1366652	-202.2733304	-190.7426971	11.04988565	343	345	0.033038317	log(hTL_Mean) ~ log(ColonyDiameterMean)
0.069382148	0.066968976	0.180881406	25.57234057	6.95255E-07	1	-474.7639061	955.5278122	967.0584455	316.695254	343	345	0.189050063	hTL_Mean ~ ColonyDiameterMean
0.070154353	0.064716559	0.180186564	12.90149036	3.96513E-06	2	-474.6207101	957.2412023	972.615536	316.4267437	342	345	0.1852627	hTL_Mean ~ poly(ColonyDiameterMean, 2)
0.062693965	0.05961294	0.184328066	22.9423795	2.48827E-06	1	-475.959199	957.998398	969.5290312	318.9556161	343	345	0.189743235	hTL_Mean ~ log(ColonyDiameterMean)
Pocillopora sTL													
r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual	nobs	error.rate	frml
0.096339772	0.093189121	0.467604059	30.49063585	7.53464E-08	1	-188.732299	383.4647979	394.4536794	62.53491703	286	288	0.049048977	log(sTL_Mean) ~ ColonyDiameterMean
0.096478113	0.090137609	0.468387842	15.21615727	5.26334E-07	2	-188.7103524	385.4207049	400.0725468	62.52534361	285	288	0.049131191	log(sTL_Mean) ~ poly(ColonyDiameterMean, 2)
0.079578651	0.076360395	0.471920703	24.72725601	1.14052E-06	1	-191.3788479	388.7578958	399.7465772	63.69481683	286	288	0.049501768	log(sTL_Mean) ~ poly(ColonyDiameterMean)
0.05144387	0.048127341	5.768561821	15.51091865	0.000103123	1	-912.2487062	1830.497412	1841.486294	9510.425278	286	288	0.604879172	sTL_Mean ~ ColonyDiameterMean
0.05144993	0.044793199	5.776652311	7.729248707	0.000538397	2	-912.2478374	1832.495675	1847.147517	9510.367899	285	288	0.605937606	sTL_Mean ~ poly(ColonyDiameterMean, 2)
0.042026741	0.038677184	5.795116231	12.54695553	0.000463229	1	-913.6712629	1833.342566	1844.331447	9604.944428	286	288	0.607874365	sTL_Mean ~ log(ColonyDiameterMean)
Porites hTL													
r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual	nobs	error.rate	frml
0.001333042	-0.001837329	0.273785377	0.420488828	0.511717508	1	-38.06249038	82.12498975	83.49168607	23.59810949	315	317	0.04663208	log(hTL_Mean) ~ ColonyDiameterMean
0.000823237	-0.002249345	0.273785177	0.29116757	0.589889855	1	-38.12752662	82.25500724	83.53171257	23.60779391	315	317	0.046672779	log(hTL_Mean) ~ log(ColonyDiameterMean)
0.00371468	-0.002631086	0.273813784	0.585379334	0.557501137	2	-37.8840454	83.3680908	86.4006979	23.54183231	314	317	0.04668169	log(hTL_Mean) ~ poly(ColonyDiameterMean, 2)
0.002642093	-0.000524123	2.588364947	0.834464046	0.361883519	1	-750.2757101	1506.55142	1517.828126	2110.384426	315	317	0.441282568	hTL_Mean ~ log(ColonyDiameterMean)
0.001304451	-0.001866011	2.590100104	0.411438735	0.521706601	1	-750.4881457	1506.976291	1518.252997	2113.214844	315	317	0.44157839	hTL_Mean ~ ColonyDiameterMean
0.001520221	-0.004839523	2.593940931	0.239038015	0.787528099	2	-750.4538978	1508.907796	1523.943403	2112.75828	314	317	0.442233201	hTL_Mean ~ poly(ColonyDiameterMean, 2)
Porites sTL													
r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual	nobs	error.rate	frml
0.001835688	-0.001974099	0.52342528	0.48183476	0.488207434	1	-202.7013898	411.4027795	422.1396288	71.7859393	262	264	0.045762928	log(sTL_Mean) ~ ColonyDiameterMean
0.00079896	-0.003015086	0.523714421	0.209416056	0.647604739	1	-202.8384581	411.6769161	422.4047635	71.8053203	262	264	0.045786594	log(sTL_Mean) ~ log(ColonyDiameterMean)
0.00222553	-0.00491942	0.52421135	0.356283066	0.700628386	2	-202.5840562	413.1681124	427.4719088	71.72215784	261	264	0.045830139	log(sTL_Mean) ~ poly(ColonyDiameterMean, 2)
0.004252114	0.0045155	9.054554982	1.11881127	0.291148819	1	-955.2587029	1916.517406	1927.245253	21480.06107	262	264	0.791611085	sTL_Mean ~ log(ColonyDiameterMean)
0.00155384	-0.002257023	9.066814683	0.407739688	0.523676759	1	-955.6159122	1917.231824	1927.959672	21538.26766	262	264	0.792882912	sTL_Mean ~ ColonyDiameterMean
0.006598002	-0.001014274	9.061191739	0.866758103	0.421518186	2	-954.9473565	1917.894713	1932.198609	21429.45609	261	264	0.792191316	sTL_Mean ~ poly(ColonyDiameterMean, 2)

### Supplementary Table 1 Regression model for the 32 islands

Regression models between TL and colony diameter mean for the 32 islands. r.squared: multiple R<sup>2</sup>; adj.r.squared: adjusted R<sup>2</sup>; sigma: Residual Standard Error (RSE); statistic: F-test value; p.value: p-value of the F-test; df: degree of freedom of the overall F-test; logLik: log-likelihood of the model; AIC: Akaike's Information Criterion; BIC: Bayesian Information Criterion; df.residual: Residual degrees of freedom; error.rate: RSE divided by the mean of TL; frml: formula of the model

Pocillopora		
Variable	R2_conditior	R2_marginal
hTL_Mean	0.385564468	0.00148136575877723
hTL_Med	0.348170197	0.0180681054639989
hTL_Q3	0.435161114	0.00944006944738771
hTL_Q1	0.297177488	0.0201407626550593
hTL_IQ	0.456166650	0.0044539748181321
sTL_Mean	0.453202394	0.000307014721826544
sTL_Med	0.380238778	1.0723315191928e-07
sTL_Q3	0.268080119	0.00328138754819394
sTL_Q1	0.381634366	0.000340510802483626
sTL_IQ	0.259583308	0.00353045040265365
Porites		
Variable	R2_conditior	R2_marginal
hTL_Mean	0.158962699	0.00711728202982334
hTL_Med	0.200836769	0.000403365007582494
hTL_Q3	0.189367375	0.002667874999667
hTL_Q1	0.152205307	0.001892524897665
hTL_IQ	0.184209367	0.00212670109477538
sTL_Mean	0.234392958	0.00162385206679871
sTL_Med	0.240415948	0.00177927789304019
sTL_Q3	0.087560389	0.00202833862581076
sTL_Q1	0.217739106	0.00774035538845887
sTL_IQ	0.084065245	0.00365071106071572

**Supplementary Table 2: R2 values of variance partition**

Marginal and conditional R2 related to the variance partition analysis in **Fig. 2**. The marginal R2 considers only the variance of the fixed effects, while the conditional R2 considers both the fixed and random effects (i.e., the total model).



# Pocillopora hTL

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual	emr.rate	fmi	log(TL_Mean)	logTL	logTL_Mean
0.50992234	0.42794573	0.14666739	6.22033918	6.28624233	47	200.0697101	-304.134021	-122.9609279	5.441232123	275	0.627371958	log(TL_Mean)	-	0.50992234	0.42794573
0.50922458	0.42585806	0.14020219	6.06585281	1.58521E-22	48	200.069728	-302.1394571	-117.1864314	5.441231193	274	0.627421859	log(TL_Mean)	-	0.50922458	0.42585806
0.48572792	0.41042376	0.142801788	6.45021658	1.69342E-22	42	192.311262	-296.8226525	-116.3165936	5.708925213	280	0.627787998	log(TL_Mean)	-	0.48572792	0.41042376
0.48746988	0.40823452	0.14748567	6.21482685	4.33351E-22	43	192.311262	-296.8226525	-116.3165936	5.708925213	279	0.627832328	log(TL_Mean)	-	0.48746988	0.40823452
0.42390307	0.31711835	0.14748567	7.53205915	6.37685E-22	30	175.1642397	-288.3284795	-117.1373815	6.351543377	292	0.628699533	log(TL_Mean)	-	0.42390307	0.31711835
0.42801329	0.36904564	0.14772795	7.25843543	1.74523E-21	31	175.1642397	-288.3284795	-117.1373815	6.351543377	291	0.628746855	log(TL_Mean)	-	0.42801329	0.36904564
0.44155413	0.37529678	0.14698266	6.97420027	4.59153E-21	35	179.0406294	-286.09152	-116.200310744	6.200310744	287	0.629680137	log(TL_Mean)	-	0.44155413	0.37529678
0.44130649	0.37326211	0.14723267	6.46233427	1.18953E-20	36	179.0406294	-286.09152	-116.200310744	6.200310744	286	0.629680137	log(TL_Mean)	-	0.44130649	0.37326211
0.22718751	0.225971379	0.163822183	5.93281206	1.04597E-12	20	136.3807187	-230.6143733	-151.3518549	8.085210067	302	0.631834846	log(TL_Mean)	-	0.22718751	0.225971379
0.26458012	0.226891818	0.16415819	6.05860829	1.48739E-12	19	134.7233764	-229.4467528	-153.9557219	8.165211752	303	0.631943788	log(TL_Mean)	-	0.26458012	0.226891818
0.224901736	0.189555236	0.161420987	5.27427209	3.21229E-11	15	128.261125	-220.562295	-160.134003	8.60275826	307	0.632079642	log(TL_Mean)	-	0.224901736	0.189555236
0.20922748	0.175853801	0.168836365	6.268143104	1.76117E-10	14	123.0406294	-216.805388	-159.4622656	8.779761149	308	0.6328541	log(TL_Mean)	-	0.20922748	0.175853801
0.092971735	0.078629544	0.187517507	4.91343808	2.77014E-05	8	101.9804105	-185.9680209	-151.9289229	10.00670913	314	0.634737967	log(TL_Mean)	-	0.092971735	0.078629544
0.05452907	0.051574474	0.181118933	18.45587327	2.30989E-05	2	94.27348682	-182.8489736	-171.223319	10.49737128	320	0.63524299	log(TL_Mean)	-	0.05452907	0.051574474
0.06345496	0.046023653	0.18164776	3.180550005	0.00189304	7	95.86043923	-175.738785	-145.5424661	10.39382763	315	0.635347285	log(TL_Mean)	-	0.06345496	0.046023653
0.08454932	0.0629815	0.178947587	5.205380271	1.34589E-08	47	355.893316	808.8768631	988.1571373	171.5170622	275	0.53677719	log(TL_Mean)	-	0.08454932	0.0629815
0.465330181	0.373851051	0.791123286	5.077828068	3.05399E-18	48	-355.463935	808.8768631	988.1571373	171.5170622	274	0.53677719	log(TL_Mean)	-	0.465330181	0.373851051
0.440387896	0.35844496	0.800798992	5.37436735	3.85519E-18	42	-362.604909	811.729816	974.0353182	179.8571855	280	0.55828189	log(TL_Mean)	-	0.440387896	0.35844496
0.40420659	0.3561622	0.802262148	5.22792259	8.32566E-18	43	-362.604909	811.729816	974.0353182	179.8571855	279	0.55828189	log(TL_Mean)	-	0.40420659	0.3561622
0.39734608	0.317473319	0.825971658	6.148864979	1.98992E-17	30	-379.5880396	821.1769792	938.1877122	199.2102027	292	0.56072691	log(TL_Mean)	-	0.39734608	0.317473319
0.37931376	0.315389043	0.827231858	5.929314673	4.78414E-17	31	-379.5880396	821.1769792	938.1877122	199.2102027	291	0.56072691	log(TL_Mean)	-	0.37931376	0.315389043
0.39246012	0.32102028	0.823816631	5.463973054	1.1705E-16	35	-375.966092	823.921859	959.8100396	194.7793924	287	0.56037611	log(TL_Mean)	-	0.39246012	0.32102028
0.39315123	0.318886265	0.825116047	5.293919318	2.68944E-16	36	-375.9139232	825.8232624	965.4816896	194.7315163	286	0.56056046	log(TL_Mean)	-	0.39315123	0.318886265
0.242320396	0.200935053	0.893708678	5.248345009	6.05248E-11	20	-410.3662731	862.7785462	942.044287	241.2119905	302	0.173980001	log(TL_Mean)	-	0.242320396	0.200935053
0.242718003	0.197739004	0.827231858	5.929314673	6.35337E-11	19	-410.3662731	862.7785462	942.044287	241.2119905	303	0.173980001	log(TL_Mean)	-	0.242718003	0.197739004
0.203572769	0.165120835	0.91351826	5.574165137	1.62447E-09	15	-420.972363	872.1842702	932.5775449	256.1962613	307	0.17762764	log(TL_Mean)	-	0.203572769	0.165120835
0.188130102	0.15382826	0.91966584	5.94009069	5.7918E-09	14	-422.7272673	875.5447527	932.5775449	260.4968132	308	0.179957239	log(TL_Mean)	-	0.188130102	0.15382826
0.090272021	0.06948056	0.893708678	5.248345009	8.81117E-08	20	-410.3662731	862.7785462	942.044287	241.2119905	302	0.18742725	log(TL_Mean)	-	0.090272021	0.06948056
0.047241889	0.044445082	0.97371828	18.9504669	8.153E-05	2	-448.5053473	903.016847	914.3343453	305.644291	320	0.190176453	log(TL_Mean)	-	0.047241889	0.044445082
0.062240631	0.044378547	0.97345852	3.484511289	0.002379025	7	-448.5053473	903.016847	914.3343453	305.644291	315	0.190183074	log(TL_Mean)	-	0.062240631	0.044378547

# Pocillopora sTL

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual	emr.rate	fmi	log(TL_Mean)	logTL	logTL_Mean
0.81288833	0.54514728	0.315272162	4.143765818	6.70035E-28	49	48.71828634	179.4365272	326.3599213	22.46418239	226	0.616585361	log(TL_Mean)	-	0.81288833	0.54514728
0.613431961	0.544708754	0.31642881	4.91765361	1.44485E-28	41	-48.25868082	180.5136718	331.0204628	22.38637225	225	0.631680641	log(TL_Mean)	-	0.613431961	0.544708754
0.57338016	0.52491861	0.322186861	1.117458919	9.94728E-28	61	-31.36593993	180.7318799	284.6532728	24.70528744	238	0.632393933	log(TL_Mean)	-	0.57338016	0.52491861
0.573058547	0.525403801	0.322025741	1.148003375	1.96989E-28	59	-30.67370992	181.3474198	288.8523091	24.70528744	237	0.632344427	log(TL_Mean)	-	0.573058547	0.525403801
0.61912689	0.54532429	0.315204566	8.392350084	8.81472E-24	44	-46.28298392	182.5656778	343.8230117	22.05658991	222	0.631658173	log(TL_Mean)	-	0.61912689	0.54532429
0.62059638	0.545005103	0.316308906	8.215753308	1.73351E-27	45	-46.28298392	182.5656778	343.8230117	22.05658991	221	0.631658173	log(TL_Mean)	-	0.62059638	0.545005103
0.578328632	0.519832928	0.323998177	10.24714334	7.11035E-29	32	-60.8072335	187.2074487	305.4628249	24.56410756	234	0.632541376	log(TL_Mean)	-	0.578328632	0.519832928
0.57833369	0.520142072	0.323998177	10.24714334	1.23235E-28	33	-60.8072335	187.2074487	305.4628249	24.56410756	233	0.632541376	log(TL_Mean)	-	0.57833369	0.520142072
0.384533019	0.338861174	0.379886071	8.573406574	8.7956E-19	110	-111.115719	260.2231438	331.89307	35.4203851	247	0.638152776	log(TL_Mean)	-	0.384533019	0.338861174
0.86737127	0.339408998	0.379946351	8.186101773	1.76537E-17	20	-109.6286272	261.253645	336.5070769	35.51237052	246	0.638160638	log(TL_Mean)	-	0.86737127	0.339408998
0.52933333	0.291925945	0.38363616	8.60302803	1.51933E-15	15	-121.550005	275.070017	332.405958	38.83869808	251	0.639608327	log(TL_Mean)	-	0.52933333	0.291925945
0.523286789	0.287389151	0.384023065	8.60302803	1.87024E-14	16	-121.550005	275.070017	332.405958	38.83869808	252	0.639608327	log(TL_Mean)	-	0.523286789	0.287389151
0.515656079	0.128639898	0.48370126	6.588848749	3.58585E-05	8	-152.7919133	335.835266	355.835266	49.12807288	258	0.643827668	log(TL_Mean)	-	0.515656079	0.128639898
0.129643408	0.10948077	0.441141197	6.429893165	2.47966E-06	7	-156.198857	328.3979174	357.056879	50.40283902	259	0.64430886	log(TL_Mean)	-	0.129643408	0.10948077
0.05411786	0.050012778	0.452002678	1.280372178	1.93235E-05	2	-162.603921	379.079584	348.4554847	60.44557298	248	0.645529958	log(TL_Mean)	-	0.05411786	0.050012778
0.553309808	0.502627487	0.194111127	10.01880588	2.52828E-28	74	-160.0496636	156.172673	160.0496636	41.89150938	232	0.642137439	log(TL_Mean)	-	0.553309808	0.502627487
0.553419688	0.500695648	0.203734913	10.4822796	4.98811E-28	72	-160.0496636	156.172673	160.0496636	41.89150938	231	0.642221054	log(TL_Mean)	-	0.553419688	0.500695648
0.553696366	0.499462283	0.221364858	9.428269973	1.05063E-26	32	-743.4724934	1552.944987	1671.203085	41.89150938	234	0.642390824	log(TL_Mean)	-	0.553696366	0.499462283
0.555510661	0.494464918	0.229278878	9.090971799	3.16032E-26	33	-743.4724934	1552.944987	1671.203085	41.89150938	233	0.642482068	log(TL_Mean)	-	0.555510661	0.494464918
0.579983608	0.502815801	0.196447957	8.781783265	5.15813E-25	40	-737.1571005	1556.31420	1703.23755	39.76486156	226	0.642192489	log(TL_Mean)	-	0.579983608	0.502815801
0.578010489	0.500634578	0.203839179	7.61437624	4.56926E-24	41	-737.1571005	1556.31420	1703.23755	39.76486156	225	0.642222066	log(TL_Mean)	-	0.578010489	0.500634578
0.579993206	0.498460488	0.212225778	1.280372178	1.23235E-24	44	-741.788504	1561.788504	1723.046984	41.89150938	222	0.642082723	log(TL_Mean)	-	0.579993206	0.498460488
0.580024489	0.496400455	0.21258018	6.938844608	3.29691E-23	45	-735.8847731	1563.788574	1728.609584	39.38165261	221	0.642003064	log(TL_Mean)	-	0.580024489	0.496400455
0.285105274	0.211550193	0.282309997	4.950142321	1.58849E-09	19	-101.3018969	160.603982	1732.273888	899.919329	247	0.635038905	log(TL_Mean)	-	0.285105274	0.2115

Pocillopora		
Variable	R2_conditior	R2_marginal
hTL_Mean	0.116721607	0
hTL_Med	0.154398860	0
hTL_Q3	0.164377142	0
hTL_Q1	0.140371332	0
hTL_IQ	0.186773575	0
sTL_Mean	0.196642379	0
sTL_Med	0.178153814	0
sTL_Q3	0.228716366	0
sTL_Q1	0.184217637	0
sTL_IQ	0.326476388	0
Porites		
Variable	R2_conditior	R2_marginal
hTL_Mean	0.069784033	0
hTL_Med	0.115918231	0
hTL_Q3	0.140117746	0
hTL_Q1	0.073030285	0
hTL_IQ	0.111594215	0
sTL_Mean	0.158229362	0
sTL_Med	0.225056949	0
sTL_Q3	0.121876166	0
sTL_Q1	0.172565639	0
sTL_IQ	0.096695425	0

**Supplementary Table 4: R2 of variance partition analysis**

Marginal and conditional R2 related to the variance partition analysis in **Supplementary Fig. 6b**. The marginal R2 considers only the variance of the fixed effects, while the conditional R2 considers both the fixed and random effects (i.e., the total model). Since the island and the host species are random effects, the marginal R2 is null.



Pocillopora hTL												
r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual	error.rate	frml
0.202067663	0.13197903	0.158884393	2.893030063	0.000969446	14	75,46477246	-120,9295449	-74,61559989	3,736149036	148	0,030391336	log(hTL_Mean) ~ island+genetic_clusters
0.140855452	0.08998505	0.182632334	2,789907844	0,004984471	10	69,47778666	-116,9555733	-82,99201363	4,022762341	152	0,031117805	log(sTL_Mean) ~ island
0.048999584	0.02477027	0.168410667	2,022326864	0,093888148	5	61,25002398	-110,500048	-91,97446995	4,452857982	157	0,032213518	log(hTL_Mean) ~ genetic_clusters
0.186960057	0.11554439	0.895032951	2,617913614	0,0026232	14	-204,58198484	439,1639696	485,4779146	118,5604296	148	0,171201506	hTL_Mean ~ island+genetic_clusters
0.123802299	0.07192217	0.91683926	2,386314484	0,014838497	10	-210,6417173	443,2834347	477,2469944	127,7703226	152	0,175372607	hTL_Mean ~ island
0.050992184	0.02681364	0.93885805	2,108984969	0,082205165	5	-217,1075652	446,2151305	464,7407085	138,3877573	157	0,179583969	hTL_Mean ~ genetic_clusters
Pocillopora sTL												
r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual	error.rate	frml
0.42082145	0.35399316	0.27223361	6,297055076	2,93173E-08	13	-6,897418546	41,7948371	80,46527216	7,707558409	104	0,029625902	log(sTL_Mean) ~ island+genetic_clusters
0.363789458	0.31666275	0.279988846	7,719390594	3,8483E-08	9	-12,39166501	44,78333003	72,40506938	8,466525415	108	0,030469868	log(sTL_Mean) ~ island
0.193020434	0.16419974	0.309652389	6,697285016	7,18655E-05	5	-26,30113962	64,60227925	81,17532286	10,73907543	112	0,03698012	log(sTL_Mean) ~ genetic_clusters
0.254461129	0.19923603	2,562716831	4,60770776	7,3698E-05	9	-271,438261	562,8765221	590,4982614	709,2918959	108	0,27888407	sTL_Mean ~ island
0.296376284	0.21518893	2,53706105	3,650522866	0,000140044	13	-268,0532431	564,1064861	602,7769212	669,4145922	104	0,276096409	sTL_Mean ~ island+genetic_clusters
0.133314859	0.10236182	2,713307512	4,30700363	0,002804756	5	-280,246517	572,493034	589,0660776	824,5482171	112	0,295276481	sTL_Mean ~ genetic_clusters
Porites hTL												
r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual	error.rate	frml
0.142073195	0.08599955	0.166593368	2,533899203	0,00747818	11	-66,90791282	-109,8158256	-72,61742851	4,246262588	153	0,030325808	log(T2_Mean) ~ island
0.14635611	0.07237364	0.16783056	1,978253888	0,026132454	14	67,31829582	-104,6365916	-58,13859523	4,225064531	150	0,03055102	log(T2_Mean) ~ island+genetic_clusters
0.002596979	-0.01610433	0.175652224	0.13886619	0,936634757	4	54,55574977	-99,11149955	-83,61216741	4,936592618	160	0,031974836	log(T2_Mean) ~ genetic_clusters
0.12241199	0.0650533	1,029939819	2,134148863	0,02493011	11	-231,8508431	487,7016861	524,9000833	162,2987329	153	0,187484999	T2_Mean ~ island
0.127986001	0.05241537	1,036877443	1,693561328	0,067540845	14	-231,3280195	492,656039	539,1540354	161,2672248	150	0,188747889	T2_Mean ~ island+genetic_clusters
0.002286532	-0.0164206	1,073878507	0,12222783	0,946890342	4	-242,3705315	494,741063	510,2403951	184,5144076	160	0,195483374	T2_Mean ~ genetic_clusters
Porites sTL												
r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual	error.rate	frml
0.245278708	0.19179452	0.39062856	4,58600431	2,98463E-05	10	-60,42295518	142,8459104	174,9657006	19,37901533	127	0,040116012	log(sTL_Mean) ~ island
0.259077024	0.1873748	0.391695192	3,613235561	0,000121033	13	-59,15900294	146,3180059	187,1977388	19,0247153	124	0,040225551	log(sTL_Mean) ~ island+genetic_clusters
0.054117079	0.03278137	0.42732008	2,536456098	0,059457359	4	-75,88821851	161,776437	176,3763416	24,28748177	133	0,043885311	log(sTL_Mean) ~ genetic_clusters
0.217285814	0.16181788	5,024730036	3,917322978	0,000203343	10	-410,3716278	842,7432556	874,8630458	3206,484815	127	0,516019947	sTL_Mean ~ island
0.223816321	0.14870177	5,063891619	2,97966668	0,001099035	13	-409,7977066	847,5954131	888,4751461	3179,731793	124	0,520041687	sTL_Mean ~ island+genetic_clusters
0.037532043	0.01582224	5,444779675	1,72880621	0,164137788	4	-424,5328499	859,0656998	873,6656044	3942,86822	133	0,559157388	sTL_Mean ~ genetic_clusters
Commonality analysis												
Variable	Coefficient	Total %										
Pocillopora hTL: log(hTL_Mean) ~ island + genetic_clusters (R2 adj = 0.13)												
Unique to island	0.1531	75,75										
Unique to genetic_clusters	0.0612	30,29										
Common to island, and genetic_clusters	-0.0122	-6,04										
Total	0.2021	100										
Pocillopora sTL: log(sTL_Mean) ~ island + genetic_clusters (R2 adj = 0.35)												
Unique to island	0.2278	54,13										
Unique to genetic_clusters	0.057	13,55										
Common to island, and genetic_clusters	0.136	32,31										
Total	0.4208	100										
Porites hTL: log(hTL_Mean) ~ island (R2 adj = 0.09)												
Porites sTL: log(sTL_Mean) ~ island (R2 adj = 0.19)												

## Supplementary Table 5

Regression models between TL, island of sampling and genetic lineages for the 11 islands. r.squared: multiple R<sup>2</sup>; adj.r.squared: adjusted R<sup>2</sup>; sigma: Residual Standard Error (RSE); statistic: F-test value; p.value: p-value of the F-test; df: degree of freedom of the overall F-test; logLik: log-likelihood of the model; AIC: Akaike's Information Criterion; BIC: Bayesian Information Criterion; df.residual: Residual degrees of freedom; error.rate: RSE divided by the mean of TL; frml: formula of the model. The last sheet describes the commonality analysis (see Table 1 for details).

Variable	Type of environmental data
lat	Historical
lon	Historical
SST_min_DegC	Historical
SST_max_DegC	Historical
SST_mean_DegC	Historical
SST_std_DegC	Historical
seasonal_min_DegC	Historical
seasonal_max_DegC	Historical
seasonal_mean_DegC	Historical
seasonal_std_DegC	Historical
SST_anomaly_min_DegC	Historical
SST_anomaly_max_DegC	Historical
SST_anomaly_mean_DegC	Historical
SST_anomaly_std_DegC	Historical
SST_anomaly_freq_max_day	Historical
SST_anomaly_freq_mean_day	Historical
SST_anomaly_freq_std_day	Historical
TSA_heat_max_DegC	Historical
TSA_heat_mean_DegC	Historical
TSA_heat_std_DegC	Historical
TSA_heat_freq_max_day	Historical
TSA_heat_freq_sum_day	Historical
TSA_heat_freq_mean_day	Historical
TSA_heat_freq_std_day	Historical
TSA_DHW_max_DegC	Historical
TSA_DHW_sum_DegC	Historical
TSA_DHW_mean_DegC	Historical
TSA_DHW_std_DegC	Historical
TSA_DHW_freq_max_day	Historical
TSA_DHW_freq_sum_day	Historical
TSA_DHW_freq_mean_day	Historical
TSA_DHW_freq_std_day	Historical
TSA_DHW_minlength_day	Historical
TSA_DHW_maxlength_day	Historical
TSA_DHW_meanlength_day	Historical
TSA_DHW_stdlength_day	Historical
TSA_DHW_lastmax_DegC	Historical
TSA_DHW_lastsum_DegC	Historical
TSA_DHW_lastduration_day	Historical
TSA_DHW_minrecovery_day	Historical
TSA_DHW_maxrecovery_day	Historical
TSA_DHW_meanrecovery_day	Historical
TSA_DHW_lastrecovery_day	Historical
TSA_cold_min_DegC	Historical
TSA_cold_mean_DegC	Historical
TSA_cold_std_DegC	Historical
TSA_cold_freq_max_day	Historical
TSA_cold_freq_sum_day	Historical
TSA_cold_freq_mean_day	Historical
TSA_cold_freq_std_day	Historical
TSA_DCW_min_DegC	Historical
TSA_DCW_sum_DegC	Historical

TSA_DCW_mean_DegC	Historical
TSA_DCW_std_DegC	Historical
TSA_DCW_freq_max_DegC	Historical
TSA_DCW_freq_sum_day	Historical
TSA_DCW_freq_mean_day	Historical
TSA_DCW_freq_std_day	Historical
TSA_DCW_minlenght_day	Historical
TSA_DCW_maxlenght_day	Historical
TSA_DCW_meanlenght_day	Historical
TSA_DCW_stdlenght_day	Historical
TSA_DCW_lastmin_DegC	Historical
TSA_DCW_lastsum_DegC	Historical
TSA_DCW_lasdduration_day	Historical
TSA_DCW_minrecovery_day	Historical
TSA_DCW_maxrecovery_day	Historical
TSA_DCW_meanrecovery_day	Historical
TSA_DCW_lastrecovery_day	Historical
Moon_light_lux	Contextual
barometer_hp	Contextual
airTemp	Contextual
dewPoint	Contextual
Course_Over_Ground	Contextual
Speed_over_Ground	Contextual
apparent_windspeed_bow	Contextual
apparent_winddir_bow	Contextual
true_wind_speed	Contextual
true_wind_dir	Contextual
gamma_acs_final	Contextual
fCDOM_ppb	Contextual
PAR	Contextual
ssh_copernicus	Contextual
u_copernicus	Contextual
v_copernicus	Contextual
current_speed_copernicus	Contextual
MLD_copernicus	Contextual
wavesignificantheight_copernicus	Contextual
windspeed_copernicus	Contextual
eastward_wind_copernicus	Contextual
orthward_wind_copernicus	Contextual
o2_copernicus	Contextual
nppv_copernicus	Contextual
phyc_copernicus	Contextual
spco2_copernicus	Contextual
mergedPOC	Contextual
SST	Contextual
SSS	Contextual
chl	Contextual
daily_min_zenith	Contextual
Aerosols_conc	Contextual
PAR_Sat	Contextual
PIC_Sat	Contextual
bb_GSM_Sat	Contextual
KD490_Sat	Contextual

NO2__mole_L_	Contextual
Proc_mL	Contextual
Syn_mL	Contextual
Pico_mL	Contextual
Nano_mL	Contextual
OrgNano_mL	Contextual
TotalEuks_mL	Contextual
CorrectedBact_mL	Contextual
corrected_AT	Contextual
corrected_CT	Contextual
NO3	Contextual
PO4	Contextual
SiOH	Contextual
pH	Contextual
MoonLength	Contextual
SunLength	Contextual

**Supplementary Table 6: List of the historical and contextual environmental data used for the sPLS analysis.**