

Supplementary Figures and Tables for the following Manuscript

'The effect of depth on the composition and saturation of total fatty acids present within the tissues and skeletons of two reef-building corals'

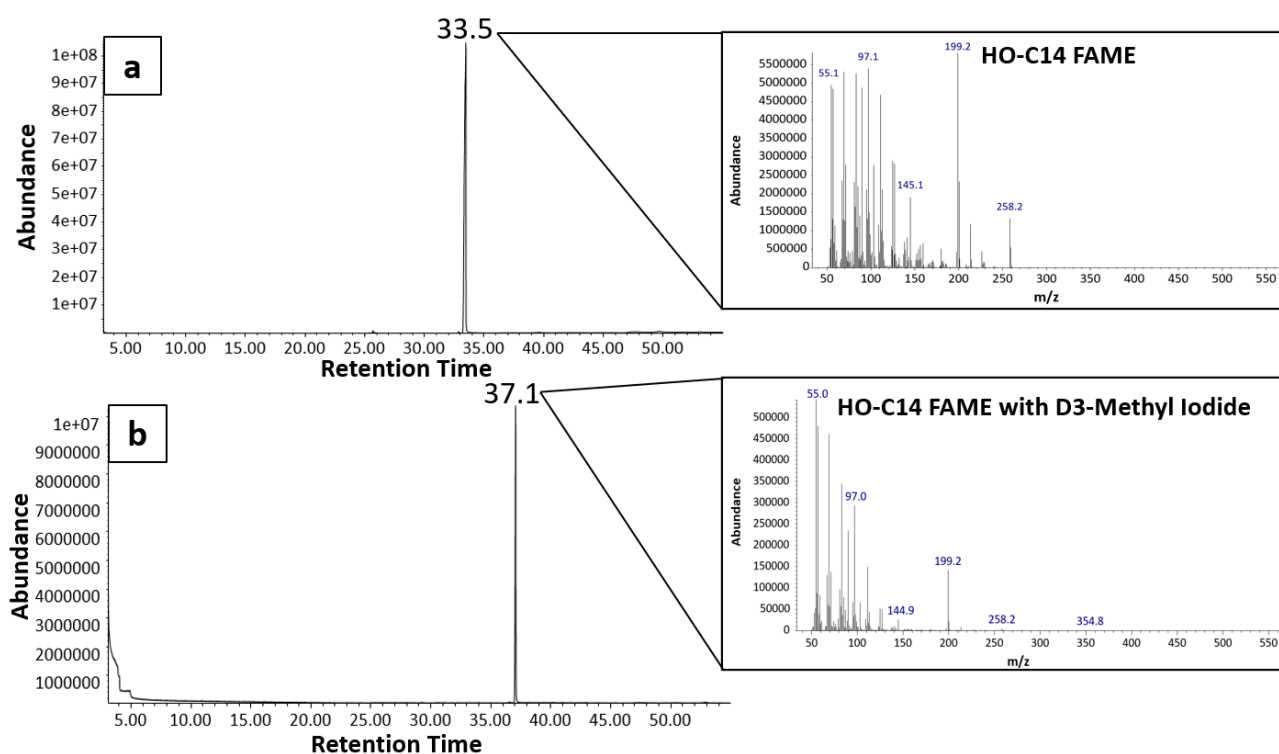
Authors: Nora S.H. von Xylander^{1,2}, Laetitia Hedouin³, Terry K. Smith¹, and Nicola Allison².

¹ Biomedical Sciences Research Complex, School of Biology, University of St Andrews, KY16 9ST, Fife, UK

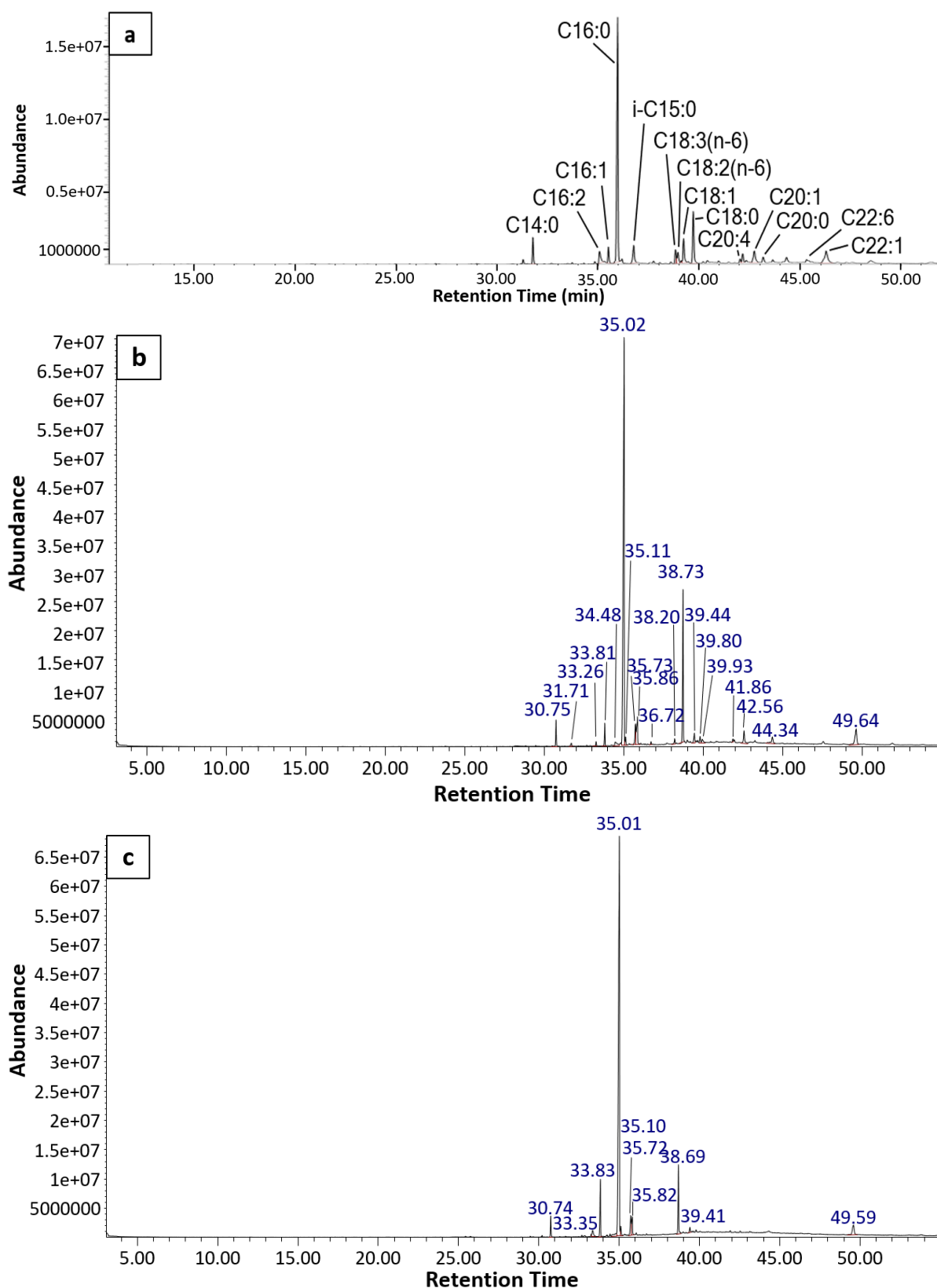
² School of Earth and Environmental Sciences, University of St. Andrews, St. Andrews, KY16 9AL, Fife, UK

³ PSL Research University, EPHE-UPVD-CNRS, USR 3278 CRIOBE, BP 1013 Papetoi, 98729 Mo'orea, French Polynesia

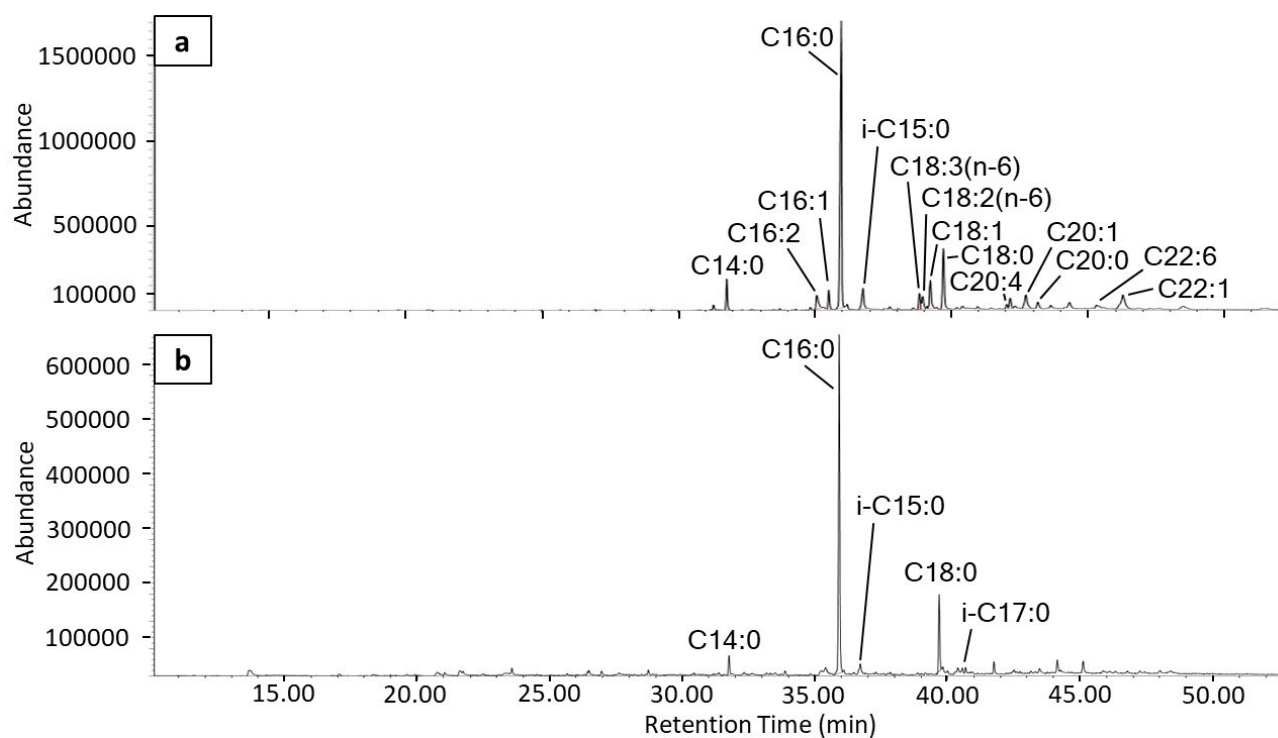
Corresponding author: Nora von Xylander (nshvx1@st-andrews.ac.uk)



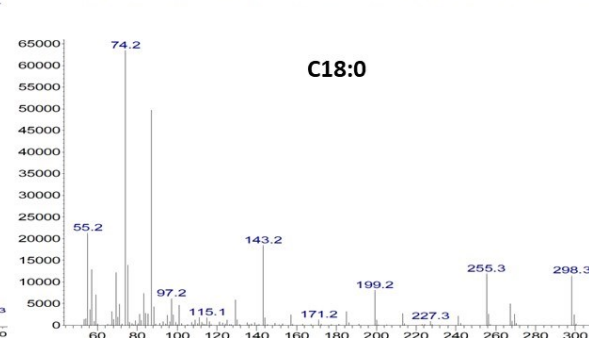
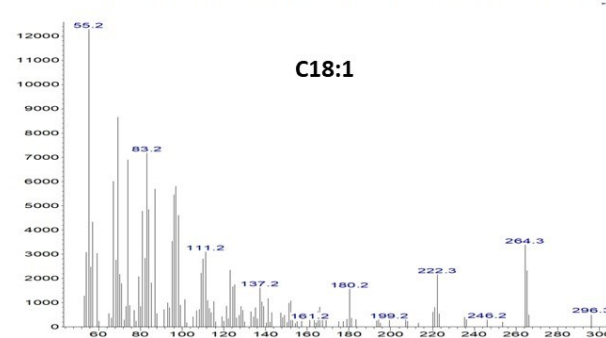
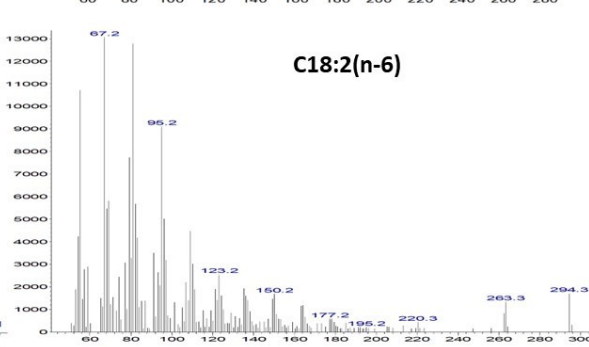
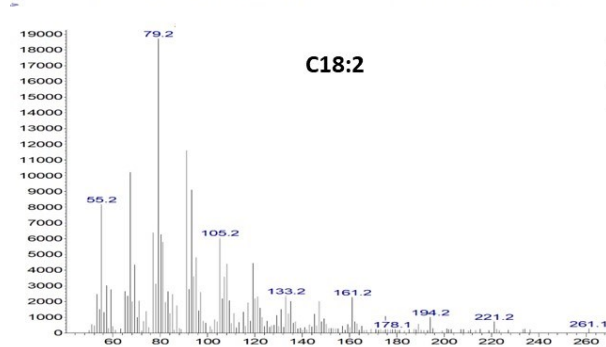
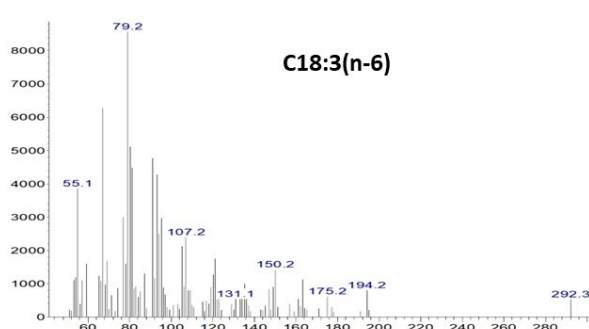
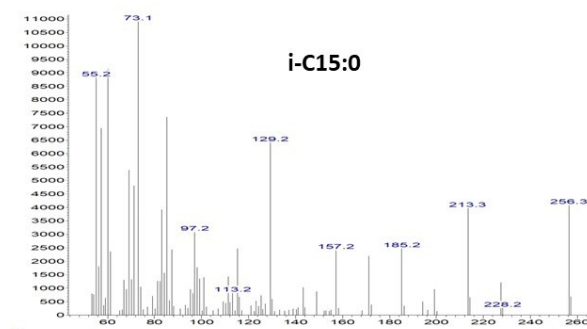
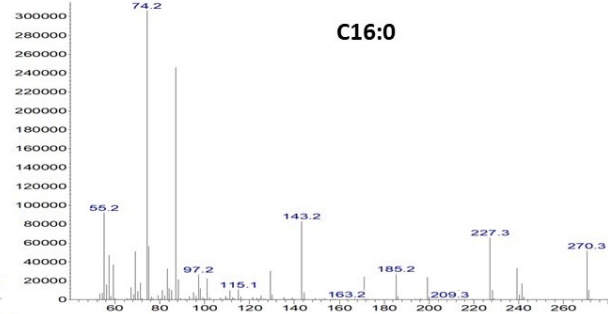
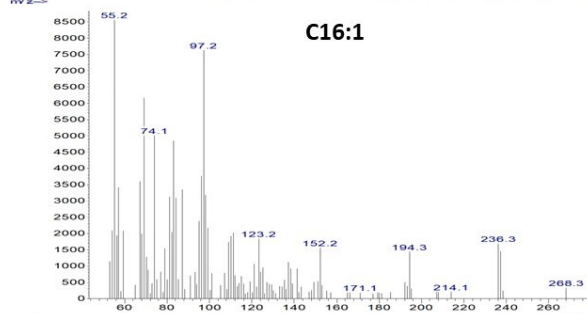
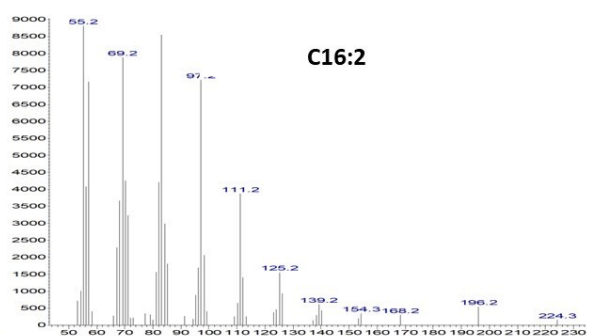
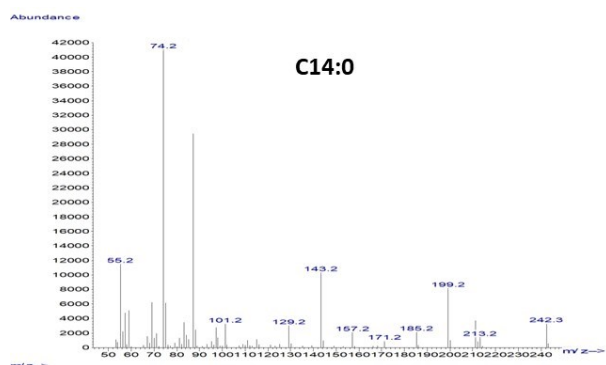
Supplementary figure 1. GC-MS chromatogram of a) Hydroxyl-C14:0 FAME and b) Hydroxyl-C14:0 FAME with D3-Methyl iodide. Inserts: showing the mass spectra of each peak.

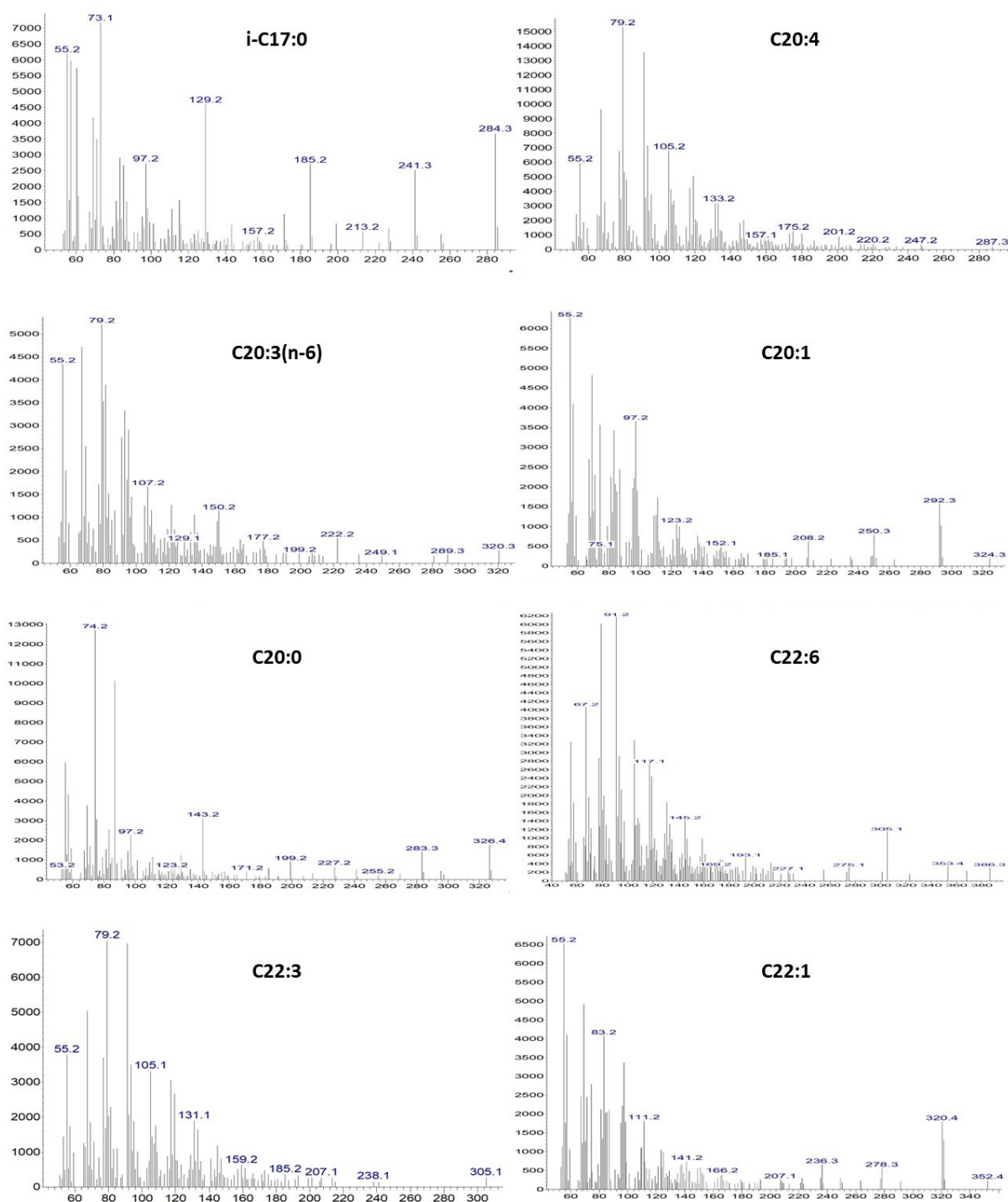


Supplementary figure 2. Representative tissue GC-MS chromatogram of a) non-methylated FAME samples collected at 5 m; versus methylated FAME samples obtained at either b) 5 m or c) 25 m.

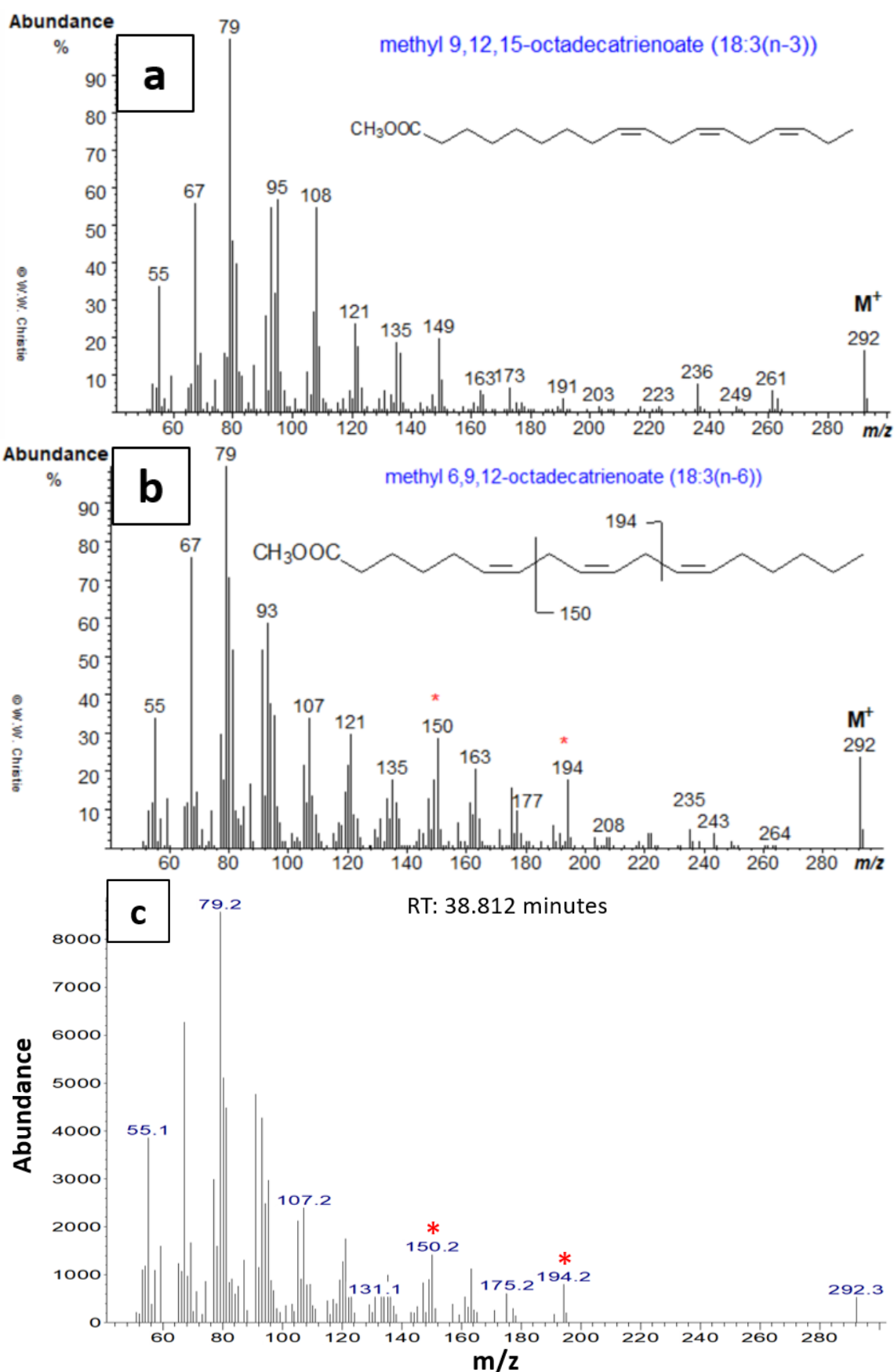


Supplementary figure 3. Representative GC-MS chromatogram showing the composition of fatty acids (FAs) identified within the a) tissues and b) skeletons, of either *A. retusa* or *P. meandrina* coral species.





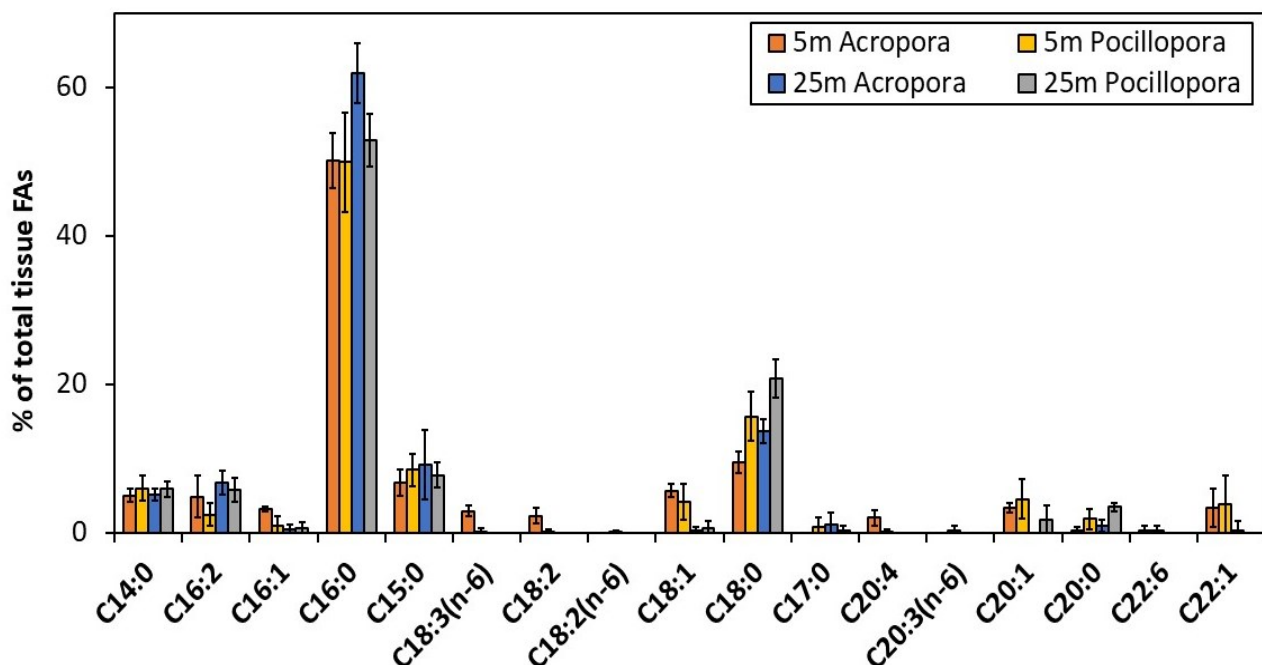
Supplementary figure 4. Mass Spectra of all fatty acid methyl esters (FAME) identified within the tissues and/or skeletal extracts of *A. retusa* and/or *P. meandrina* coral species. This serves as a molecular ‘fingerprint’ of the compound allowing for the identification of the individual FAs by comparing the individual spectra to the LipidMaps FAME database.



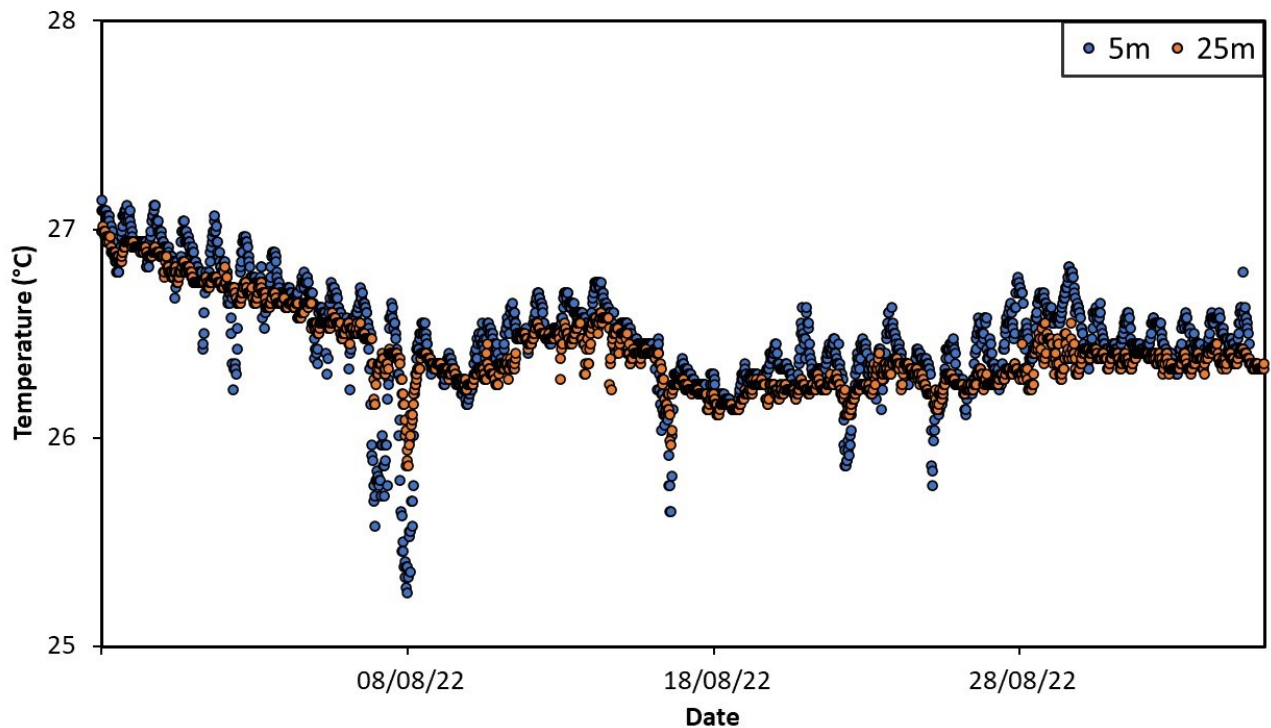
Supplementary figure 5. Comparison of the mass spectra from the LipidMaps database of a) C18:3(n-3) and b) C18:3(n-6) FAMES to the mass spectrum obtained from our samples which we identified as c) C18:3(n-6) FAME.

Supplementary table 1. Percentage (%) contributions of each FA to total FA (n = 10, mean $\pm$ SD) within the tissues of both coral species at both depths.

FA	<i>A. retusa</i> – 5 m	<i>A. retusa</i> – 25 m	<i>P. meandrina</i> - 5 m	<i>P. meandrina</i> - 25 m
C14:0	5.1 $\pm$ 0.8	5.2 $\pm$ 0.7	6.0 $\pm$ 1.7	5.9 $\pm$ 1.1
C16:2	4.9 $\pm$ 2.8	6.8 $\pm$ 1.5	2.5 $\pm$ 1.5	5.8 $\pm$ 1.7
C16:1	3.3 $\pm$ 0.4	0.4 $\pm$ 0.7	1.0 $\pm$ 1.3	0.6 $\pm$ 0.9
C16:0	50.2 $\pm$ 3.7	61.9 $\pm$ 4.1	49.9 $\pm$ 6.7	52.9 $\pm$ 3.6
i-C15:0	6.7 $\pm$ 1.8	9.2 $\pm$ 4.6	8.5 $\pm$ 2.2	7.8 $\pm$ 1.8
C18:3(n-6)	3.0 $\pm$ 0.7	-	0.2 $\pm$ 0.4	-
C18:2	2.3 $\pm$ 1.1	-	0.1 $\pm$ 0.4	-
C18:2(n-6)	-	-	0.1 $\pm$ 0.3	-
C18:1	5.7 $\pm$ 0.9	0.3 $\pm$ 0.5	4.2 $\pm$ 2.5	0.6 $\pm$ 1.0
C18:0	9.5 $\pm$ 1.4	13.7 $\pm$ 1.7	15.7 $\pm$ 3.3	20.8 $\pm$ 2.6
i-C17:0	-	1.2 $\pm$ 1.5	0.9 $\pm$ 1.2	0.4 $\pm$ 0.6
C20:4	2.0 $\pm$ 1.0	-	0.2 $\pm$ 0.4	-
C20:3(n-6)	-	-	0.4 $\pm$ 0.6	-
C20:1	3.4 $\pm$ 0.6	-	4.6 $\pm$ 2.6	1.7 $\pm$ 2.0
C20:0	0.3 $\pm$ 0.5	1.0 $\pm$ 0.9	1.9 $\pm$ 1.4	3.5 $\pm$ 0.6
C22:6	0.3 $\pm$ 0.7	-	0.3 $\pm$ 0.7	-
C22:1	3.4 $\pm$ 2.5	0.4 $\pm$ 1.2	3.9 $\pm$ 3.9	-



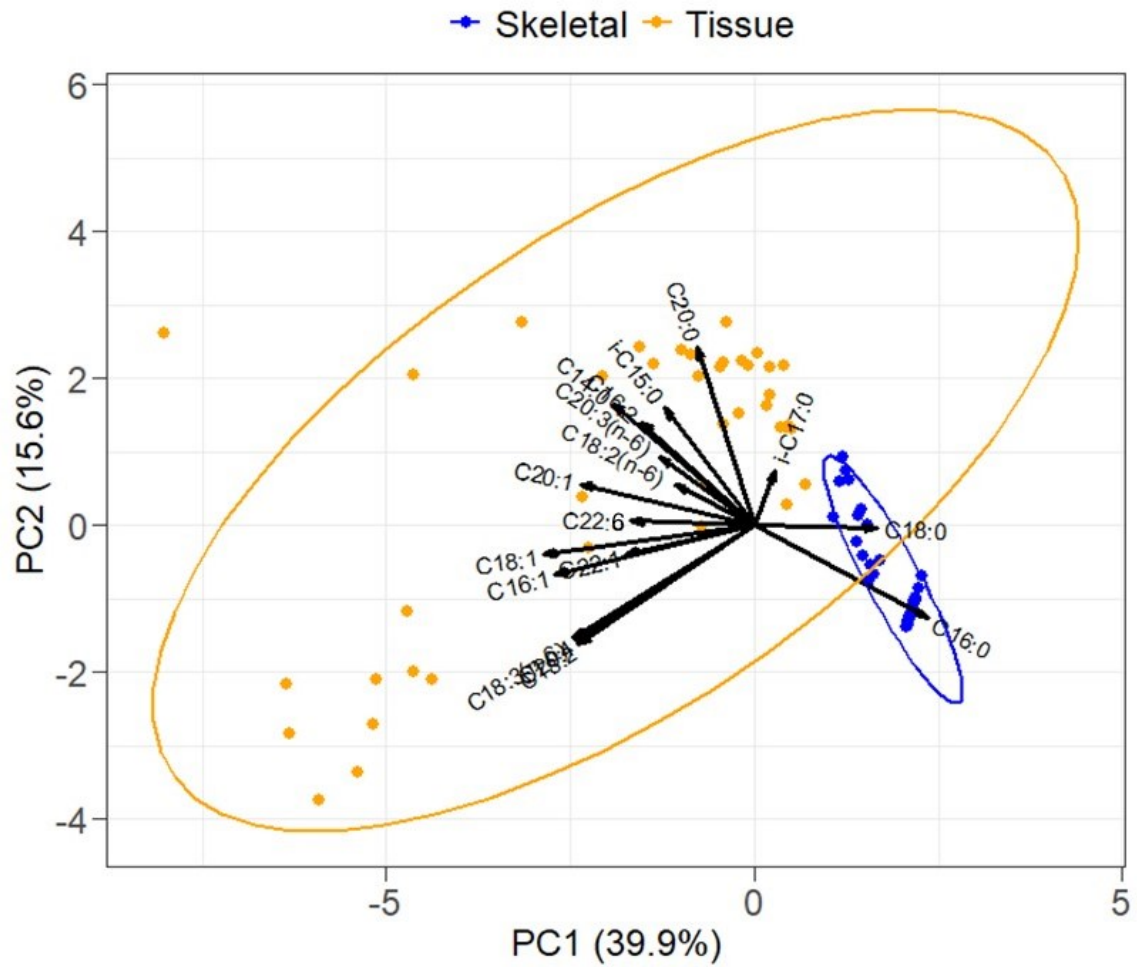
Supplementary figure 6. % Tissue FAs comparison between *A. retusa* and *P. meandrina*.



Supplementary figure 7. Graph showing the recorded seawater temperature at both 5 m and 25 m throughout the duration of the study in Moorea, French Polynesia.

Supplementary table 2. % Skeletal FAs (mean $\pm$ SD) found within *A. retusa* and *P. meandrina* at both 5 m and 25 m depth.

FA	5 m <i>Acropora</i>	25 m <i>Acropora</i>	5 m <i>Pocillopora</i>	25 m <i>Pocillopora</i>
C14:0	2.1 $\pm$ 2.8	1.1 $\pm$ 2.3	Not detected	Not detected
C16:0	75.5 $\pm$ 7.6	71.7 $\pm$ 12.2	71.6 $\pm$ 11.0	76.4 $\pm$ 6.1
i-C15:0	4.7 $\pm$ 6.4	6.5 $\pm$ 7.1	Not detected	Not detected
C18:0	15.4 $\pm$ 2.7	17.1 $\pm$ 3.4	28.4 $\pm$ 11.0	23.6 $\pm$ 6.1
i-C17:0	2.3 $\pm$ 3.2	3.7 $\pm$ 4.9	Not detected	Not detected



Supplementary figure 8. Principal Component Analysis (PCA) biplots of the total FA lipids compositions detected clustered according to source (tissue vs. skeletal). The 95% C.I. ellipsoid clusters represent in yellow = all tissue samples and dark blue = skeletal samples. The black arrows on each biplot show the correlation of each of the FA lipids with PC1 and PC2.

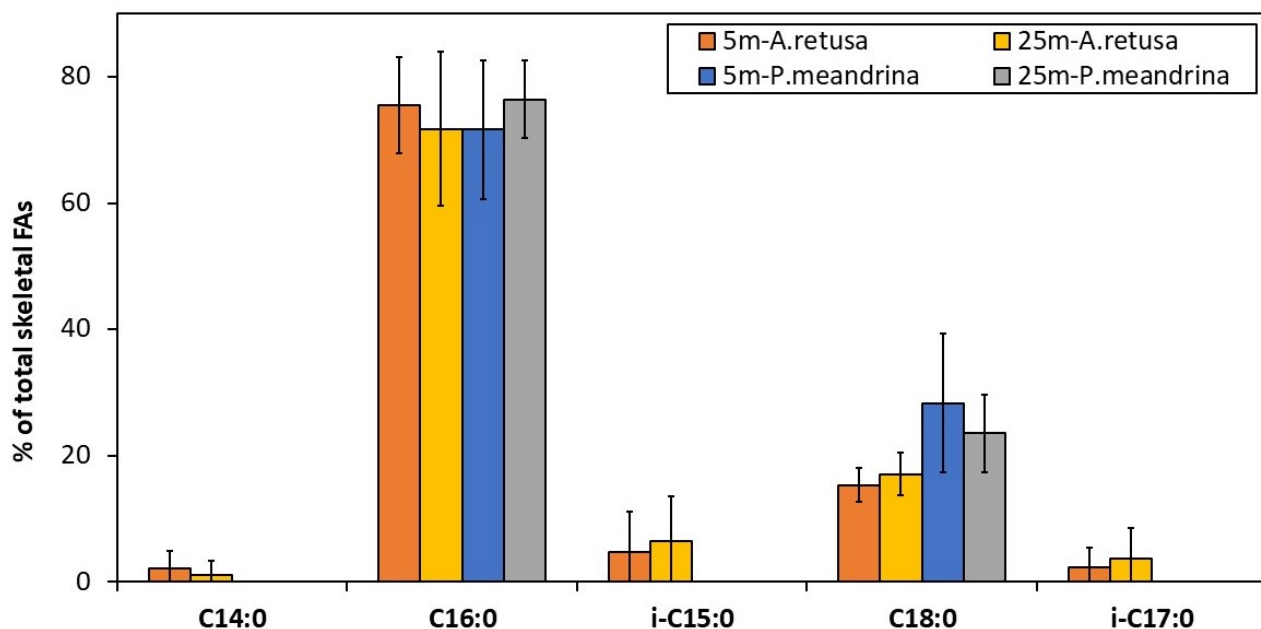
Supplementary table 3. Summary of t-test results comparing skeletal % contributions of each FA to total FA between a) depths for each species and b) species for each depth. P-values are shown in parentheses and are considered significant if $p \leq 0.0046$. n.s. = not significant and n.d.= not detected.

a) 5 m vs. 25 m depth

FA	<i>A. retusa</i>	<i>P. meandrina</i>
C14:0	n.s. (0.36)	n.d.
C16:0	n.s. (0.42)	n.s. (0.24)
i-C15:0	n.s. (0.57)	n.d.
C18:0	n.s. (0.24)	n.s. (0.24)
i-C17:0	n.s. (0.46)	n.d.

b) *A. retusa* vs. *P. meandrina*

FA	5m	25m
C14:0	n.d. in <i>P. meandrina</i>	n.d. in <i>P. meandrina</i>
C16:0	n.s. (0.38)	n.s. (0.29)
i-C15:0	n.d. in <i>P. meandrina</i>	n.d. in <i>P. meandrina</i>
C18:0	<i>A. retusa</i> < <i>P. meandrina</i> (2.0×10^{-3})	n.s. (8.9×10^{-3})
i-C17:0	n.d. in <i>P. meandrina</i>	n.d. in <i>P. meandrina</i>



Supplementary figure 9. % FAs to total FAs detected within the skeletons of both *A. retusa* and *P. meandrina* at both depths (5m and 25m).

Supplementary table 4. Summary of t-test results comparing the % contributions of each FA to total FA between the tissue and skeleton of both coral species at a) 5m and b) 25 m depth. p values are shown in parentheses and are considered significant if $p \leq 0.0046$. n.s. = not significant and n.d.= not detected.

a) 5 m depth		
FA	<i>A. retusa</i>	<i>P. meandrina</i>
C14:0	n.s. (0.0049)	Not detected in skeleton
C16:0	Tissue < Skeleton (2.1×10^{-8})	Tissue < Skeleton (4.5×10^{-5})
i-C15:0	n.s. (0.35)	Not detected in skeleton
C18:0	Tissue < Skeleton (9.4×10^{-6})	Tissue < Skeleton (0.0026)
i-C17:0	not detected in tissue	Not detected in skeleton
b) 25 m depth		
FA	<i>A. retusa</i>	<i>P. meandrina</i>
C14:0	Tissue > Skeleton (3.3×10^{-5})	Not detected in skeleton
C16:0	n.s. (0.026)	Tissue < Skeleton (4.3×10^{-9})
i-C15:0	n.s. (0.32)	Not detected in skeleton
C18:0	n.s. (0.012)	n.s. (0.20)
i-C17:0	n.s. (0.13)	Not detected in skeleton

Supplementary table 5. Summary table of the skeletal lipid contents of both *Acropora retusa* and *Pocillopora meandrina* coral collected at different depths (5 m vs. 25 m).

Coral Species	Depth	Sample	Skeletal lipids (mg)	% skeletal lipids of total skeletal mass (% wt)
<i>A. retusa</i>	5 m	Colony 1	0.80	0.03
		Colony 2	0.70	0.04
		Colony 3	0.90	0.04
		Colony 4	31.40	1.70
		Colony 5	0.60	0.04
		Colony 6	2.20	0.06
		Colony 7	0.50	0.02
		Colony 8	1.10	0.08
		Colony 9	10.20	0.23
		Colony 10	14.80	0.67
<i>P. meandrina</i>	25 m	Colony 1	46.40	1.50
		Colony 2	26.70	0.74