

# Supplementary Material

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**Supplementary Table S1.** Expression levels of the genes related to biomineralization from the transcriptome data

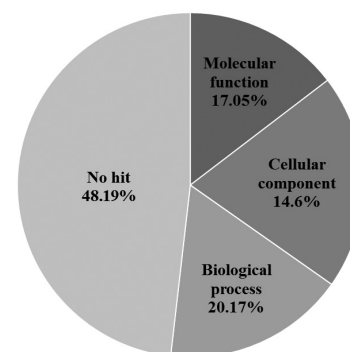
Gene name	JGI protein ID	Full name	Normalized FPKM	
			371	2090
CAX3	416800	Cation/H <sup>+</sup> exchanger 3	4.03546496	4.41494259
ECA2	522053	ER-type Ca <sup>2+</sup> ATPase 2	1.83182601	1.57045475
AEL1	198643	Anion exchanger like 1	3.17617623	3.77948769
γ-EhCA2	432493	Gamma carbonic anhydrase	2.01238146	1.9816862
ATPvc/c'	359783	Subunit c of the V <sub>o</sub> sector of a Vacuolar H <sup>+</sup> -ATPase	1.40320328	2.12901068
GPA	431830	Glutamic acid, proline and alanine rich Ca <sup>2+</sup> binding protein	5.1876001	5.79731775

Genes speculated to be related to the biomineralization process (Mackinder et al. 2011) were shown.

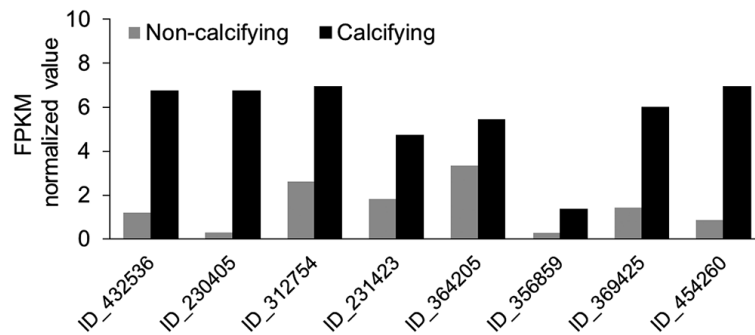
	Sample	Total bases	Read count	GC (%)
Raw data	CCMP 371	6,882,278,572	68,141,372	55.32
	CCMP 2090	8,175,017,568	80,940,768	52.97

Sample	Merge
	ALL transcript contigs
Total trinity 'genes'	51,065
Total trinity transcripts	89,048
GC (%)	67.76
N50	1,166
Maximum contig length	36,131
Minimum contig length	201
Median contig length	627
Average contig length	846.99
Total assembled bases	75,422,929

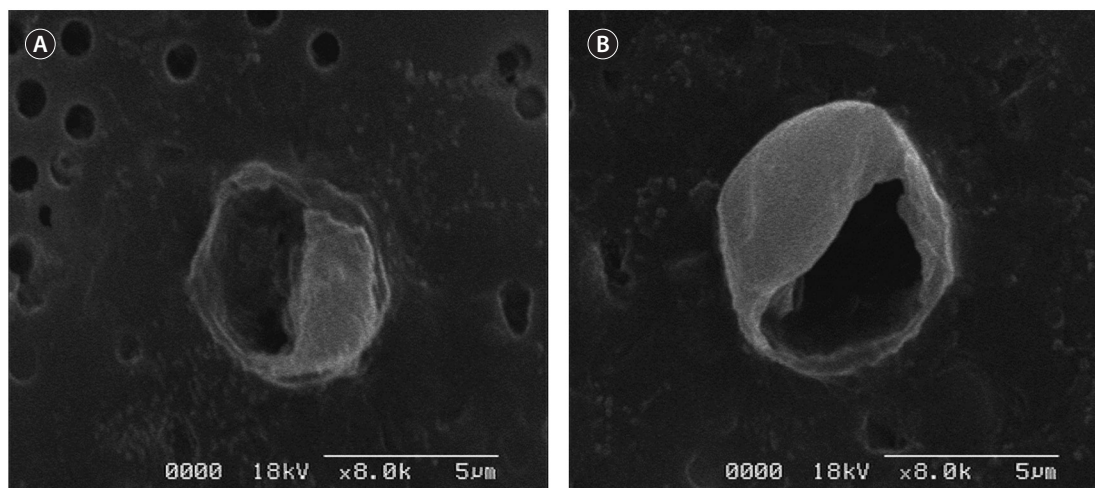
**Gene ontology (GO) analysis**



**Supplementary Fig. S1.** Transcriptome statistics of CCMP 371 and CCMP 2090.



**Supplementary Fig. S2.** Normalized fragments per kilobase of transcript per million mapped reads values of candidate genes based on transcriptomic analysis for genes differentially expressed in CCMP 2090 (gray) and CCMP 371 (black).



**Supplementary Fig. S3.** Scanning electron microscope images of CCMP 2090 grown at different calcium concentrations: 0.1 mM (A) and 10 mM (B) calcium. Scale bars represent: A & B, 5 μm.

## REFERENCE

Mackinder, L., Wheeler, G., Schroeder, D., von Dassow, P., Riebesell, U. & Brownlee, C. 2011. Expression of biomineralization-related ion transport genes in *Emiliania huxleyi*. *Environ. Microbiol.* 13:3250-3265.