

## Supplementary Data

**MANUSCRIPT TITLE:** Reconstruction of long-chain polyunsaturated acids synthesis pathways in marine microalga *Porphyridium cruentum* using lipidomics and transcriptomics

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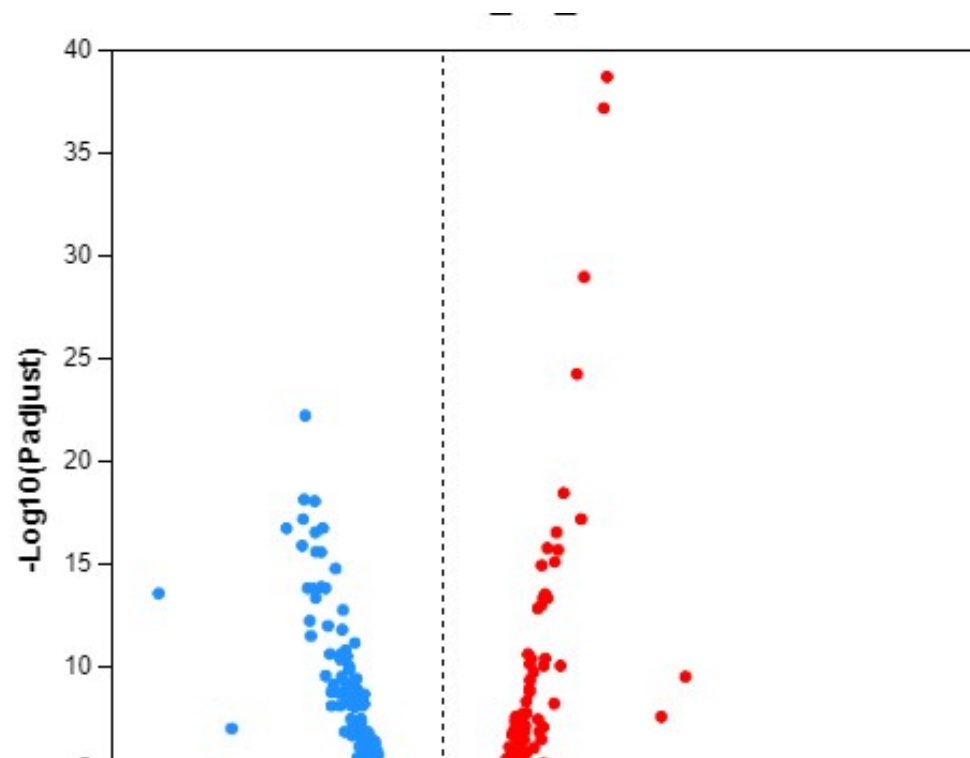
**Table S1.** Summary of output statistics by Illumina sequencing

Sample	Raw reads	Clean reads	Error rate(%)	Q30(%)	GC content	Total reads	Total mapped	Total mapped(%)
N-limitation	49327784	48762135	0.026	93.35	58.58	48762135	44972016	92.20
N-repletion	47751462	47199666	0.026	93.52	57.77	47199666	44103622	93.44

**Table S2** The annotation statistics of unigenes in *Porphyridium cruentum* CCALA 415

	GO	KEGG	COG	NR	Swiss-Prot	Pfam	Total
Unigenes	6364	3879	6136	6989	5439	7082	9898

\*NR: Non-redundant protein sequence database; NT: Nucleotide Sequence Database; KEGG: Kyoto Encyclopedia of Genes and Genomes; COG: clusters of orthologous groups; GO: Gene ontology



**Figure S1.** Statistics of differentially expressed genes in *Porphyridium cruentum* CCALA 415 under N-limited and N-replete conditions