

## Supplementary Data

### Polystyrene microplastics induce photosynthetic impairment in *Navicula sp.* at physiological and transcriptomic levels

Xi Li <sup>a,b</sup>, Zunyan Wang <sup>a,b</sup>, Yiyong Chen <sup>c\*</sup>, Qi Li <sup>a,b,\*</sup>

<sup>a</sup> College of Urban and Environmental Sciences, Northwest University, Xi'an, 710127, China.

<sup>b</sup> Shaanxi Key Laboratory of Earth Surface System and Environmental Carrying Capacity, Xi'an, 710127, China.

<sup>c</sup> Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing, China.

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Table S1. EC<sub>50</sub> of *Navicular sp.* under PS-NH<sub>2</sub> stress

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Fig. S1. Characterisations of NH<sub>2</sub>-PS and a TEM imaging of PS-NH<sub>2</sub>.

Fig. S2. Standard curve of *Navicula sp.*

Fig. S3. (A). Characterization of the transcriptome dataset. Principal component analysis (PCA) exhibits clear distinctions between Control and expression group. (B). Volcano map of DEGs in *Navicular sp.* ( $q\text{-value} \leq 0.05$ ). C: Control group; H: High concentration group; L: Low concentration group.

Fig. S4. KEGG pathway changes of *Navicular sp.* induced by PS-NH<sub>2</sub>. C: Control group; H: High concentration group; L: Low concentration group.

Fig. S5. Transcriptomic analysis of porphyrin and chlorophyll metabolic pathways in *Navicula sp.* after exposure to PS-NH<sub>2</sub>.

Fig. S6. Transcriptomic analysis of carbon fixation pathways in photosynthetic organisms after exposure of *Navicula sp.* to PS-NH<sub>2</sub>.

Fig. S7. Transcriptomic analysis of the Glycolytic/Glyco-isomeric pathway after exposure to PS-NH<sub>2</sub> in *Navicula sp.*

Fig. S8. Transcriptomic analysis of Endocytosis pathway in *Navicula sp.* exposed to PS-NH<sub>2</sub>.

## Supplementary tables

**Table S1.** Components of CSI medium

ID	Component	Dosage	Liquors concentration
1	$\text{Ca}(\text{NO}_3)_2 \cdot 4\text{H}_2\text{O}$	1 mL/L	15 g/100 mL dH <sub>2</sub> O
2	$\text{KNO}_3$	1 mL/L	10 g/100 mL dH <sub>2</sub> O
3	$\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$	1 mL/L	4 g/100 mL dH <sub>2</sub> O
4	$\beta\text{-Na}_2\text{glycerophosphate} \cdot 5\text{H}_2\text{O}$	1 mL/L	2.5 g/100 mL dH <sub>2</sub> O
5	Vitamin B <sub>12</sub>	0.1 ug/L	
6	Biotin	0.1 ug/L	
7	Thiamine HCl	10 ug/L	
8	HEPES	0.5 g/L	
9	$\text{Na}_2\text{SiO}_3 \cdot 9\text{H}_2\text{O}$	0.1 g/L	
10	Soil Extract	30 mL/L	
	$\text{Na}_2\text{EDTA}$		0.75 g/L dH <sub>2</sub> O
	$\text{MnCl}_2 \cdot 4\text{H}_2\text{O}$		0.041 g/L dH <sub>2</sub> O
11	$\text{ZnCl}_2 \cdot 7\text{H}_2\text{O}$	6 mL/L	0.005 g/L dH <sub>2</sub> O
(PIV)	$\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$		0.004 g/L dH <sub>2</sub> O
	$\text{FeCl}_3 \cdot 6\text{H}_2\text{O}$		0.097 g/L dH <sub>2</sub> O
	$\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$		0.002 g/L dH <sub>2</sub> O

Note 1: Soil extract: the ratio of soil and distilled water is 200:1 (g/L), sealed with a breathable plug, boiled in a water bath for 3 h, cooled and precipitated for 24 h, repeated three times, filtered to retain the supernatant, sterilized and stored in a refrigerator at 4 °C for later use.

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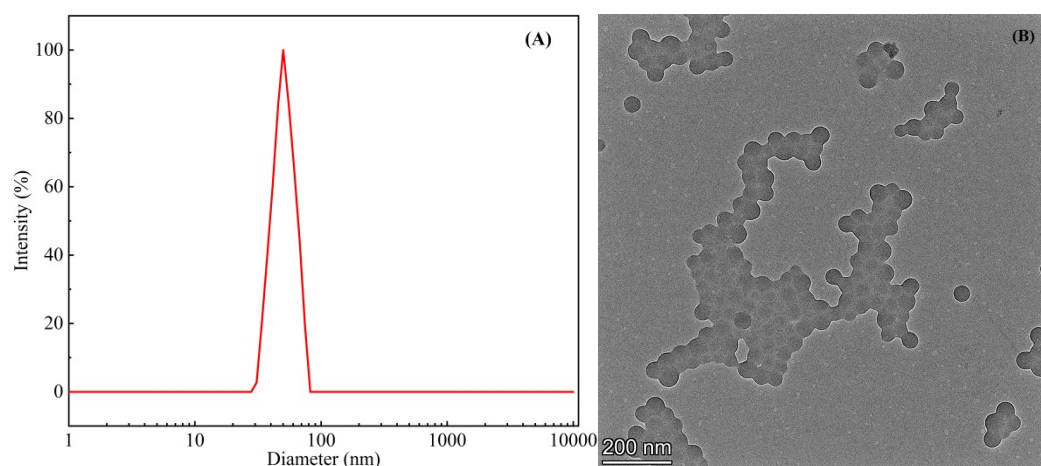
**Table S2.** EC<sub>50</sub> of *Navicular sp.* under PS-NH<sub>2</sub> stress

Exposed Time	Growth inhibition rates-EC <sub>50</sub>	R <sup>2</sup>
	(mg/L)	
24 h	4.158	0.972
48 h	4.691	0.993
96 h	5.479	0.994

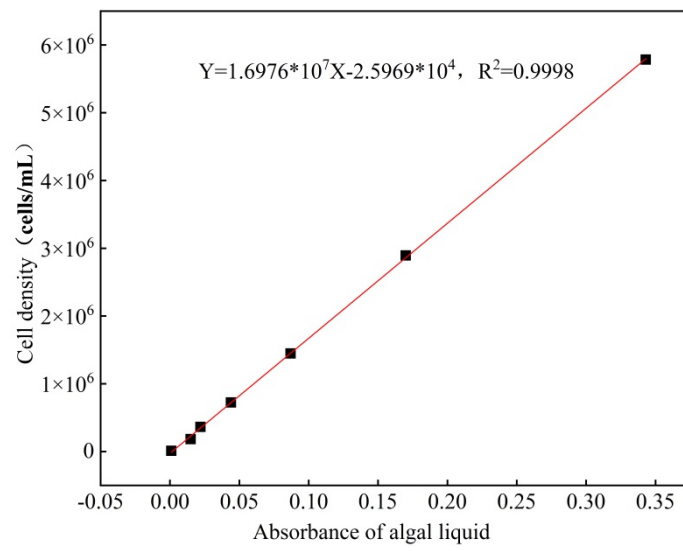
Table S3. KEGG pathways significantly enriched (p<0.05) in *Navicula sp.* exposed to PS-NH<sub>2</sub>.

Treatment	Pathways	Pathway category	Up-Genes	Down-Genes
Low concentration vs. Control	Ribosome biogenesis in eukaryotes	Translation	<i>SSUrRNA</i>	—
	Porphyrin and chlorophyll metabolism	Metabolism of cofactors and vitamins	—	<i>Por; chlP, bchP</i>
	Other glycan degradation	Glycan biosynthesis and metabolism	<i>E3.2.1.25, MANBA, manB</i>	—
	Endocytosis	Transport and catabolism	<i>VPS4; HSPA1s</i>	—
	Phenylpropanoid biosynthesis	Biosynthesis of other secondary metabolites	<i>katG</i>	—
	Glycolysis/Gluconeogenesis	Carbohydrate metabolism	<i>GAPDH, gapA; E4.1.1.49, pckA; ACSS1_2, acs</i>	—
	Carbon fixation in photosynthetic organisms	Energy metabolism	<i>GAPDH, gapA; E4.1.1.49, pckA</i>	—
	Homologous recombination	Replication and repair	<i>RAD51</i>	—
	Terpenoid backbone biosynthesis	Metabolism of terpenoids and polyketides	—	<i>chlP, bchP</i>
	Phenylalanine metabolism	Amino acid metabolism	<i>katG</i>	—
	Spliceosome	Transcription	<i>HSPA1s; PLRG1, PRL1, PRP46</i>	—
	Pyruvate metabolism	Carbohydrate metabolism	<i>E4.1.1.49, pckA; ACSS1_2, acs</i>	—
	Tryptophan metabolism	Amino acid metabolism	<i>katG</i>	—
	Porphyrin and chlorophyll metabolism	Metabolism of cofactors and vitamins	—	<i>por</i>
	Biosynthesis of secondary metabolites	Global and overview maps	—	<i>por</i>
High concentration vs. Control				

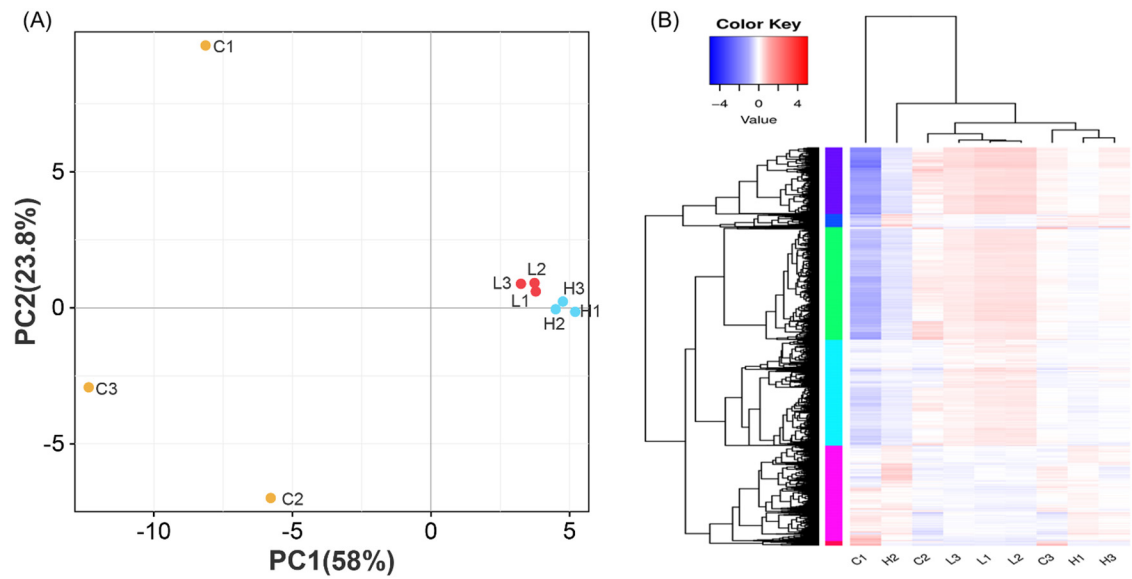
## Supplementary figures



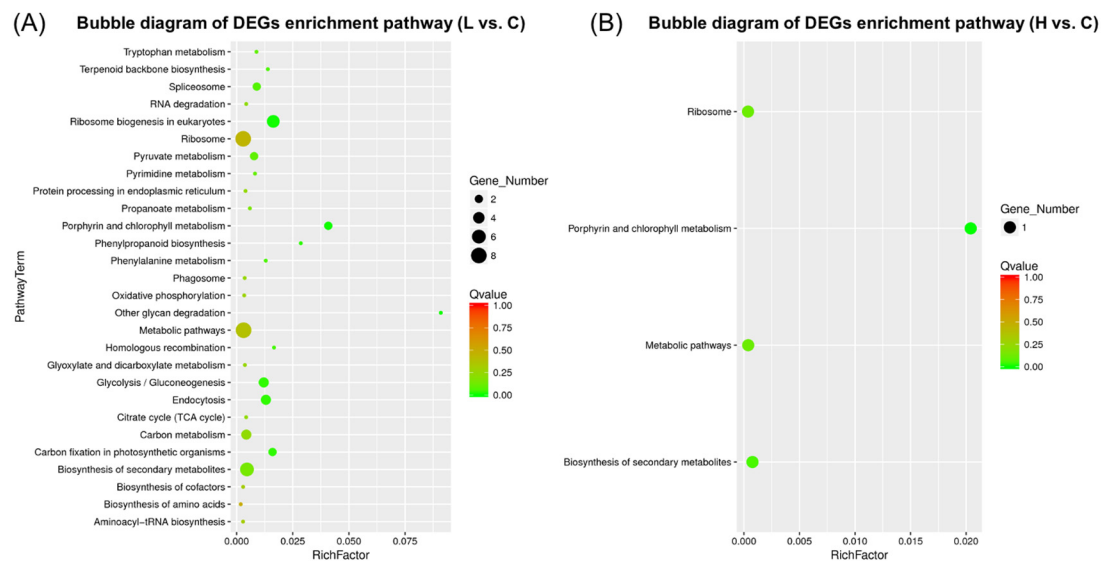
**Fig. S1.** Characterisations of  $\text{NH}_2\text{-PS}$  and a TEM imaging of  $\text{PS-NH}_2$ . (A) Particle size distribution characterization of  $\text{PS-MPs}$ . (B) The transmission electron microscopy (TEM) characterization.



**Fig. S2.** Standard curve of *Navicula sp.*



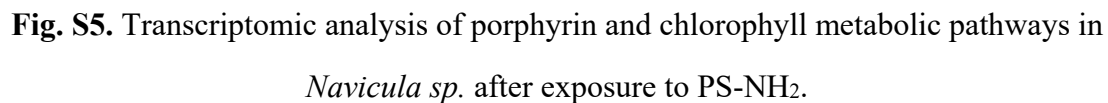
**Fig. S3.** (A). Characterization of the transcriptome dataset. Principal component analysis (PCA) exhibits clear distinctions between Control and expression group. (B). Volcano map of DEGs in *Navicular sp.* ( $q\text{-value} \leq 0.05$ ). C: Control group; H: High concentration group; L: Low concentration group.

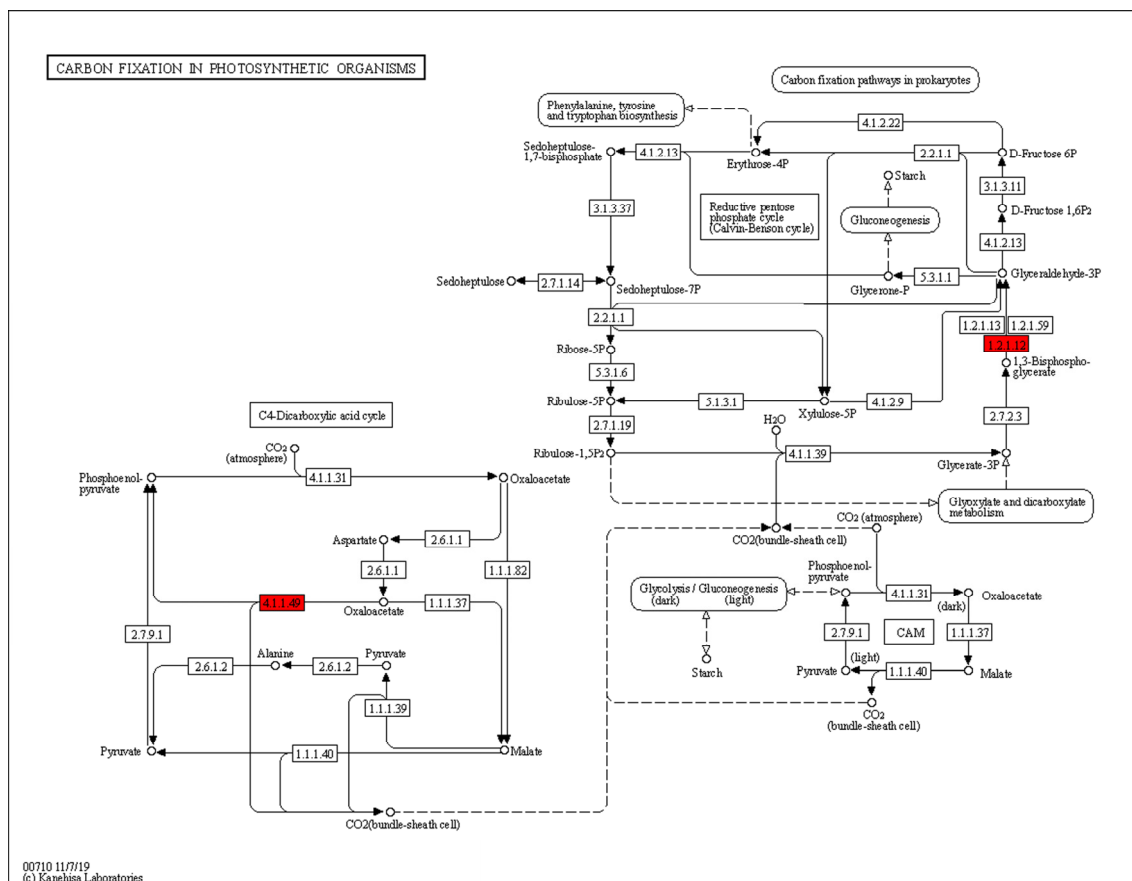


**Fig. S4.** KEGG pathway changes of *Navicular sp.* induced by PS-NH<sub>2</sub>. (A) Low concentration.

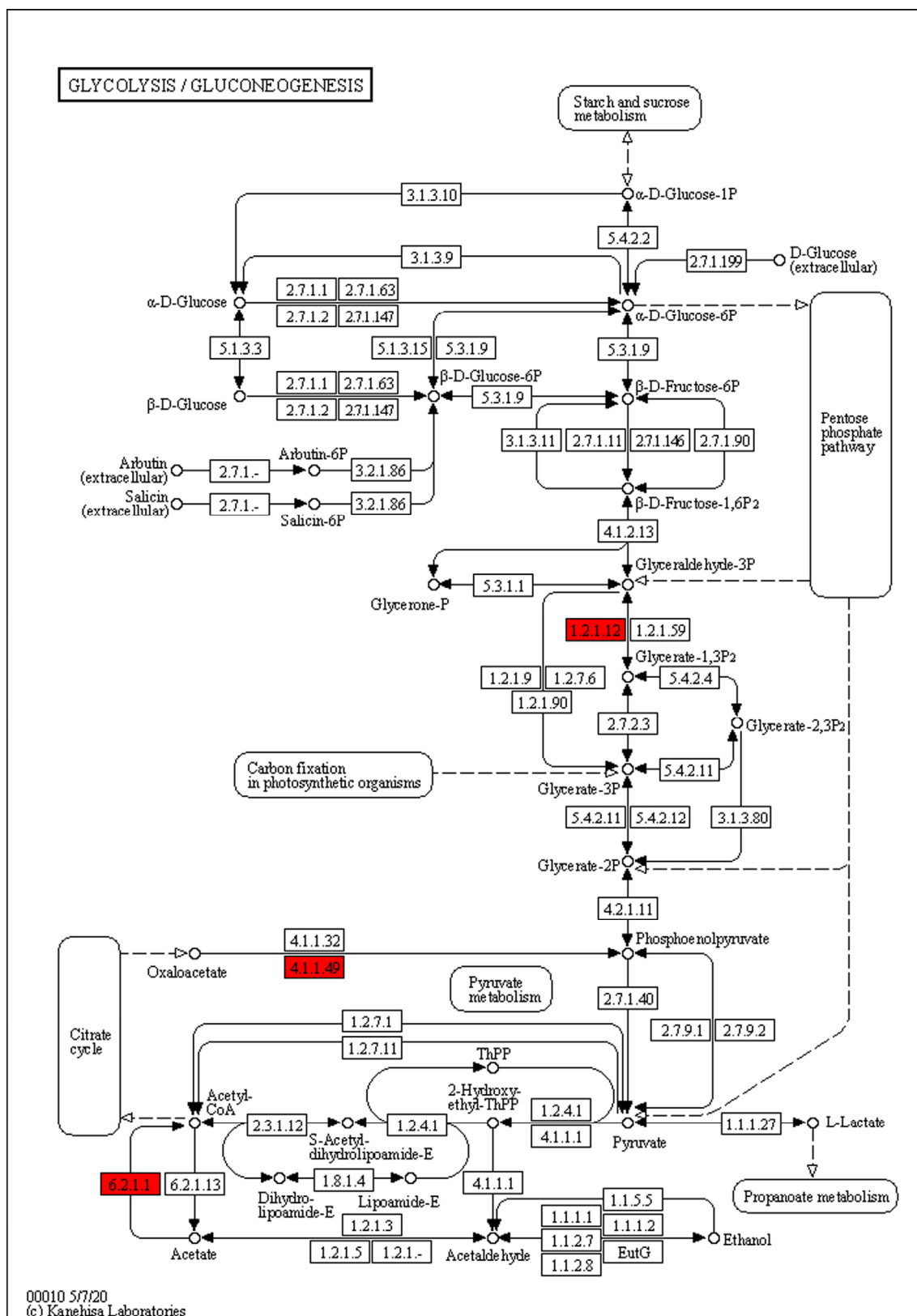
(B) High concentration. C: Control group; H: High concentration group; L: Low concentration group.



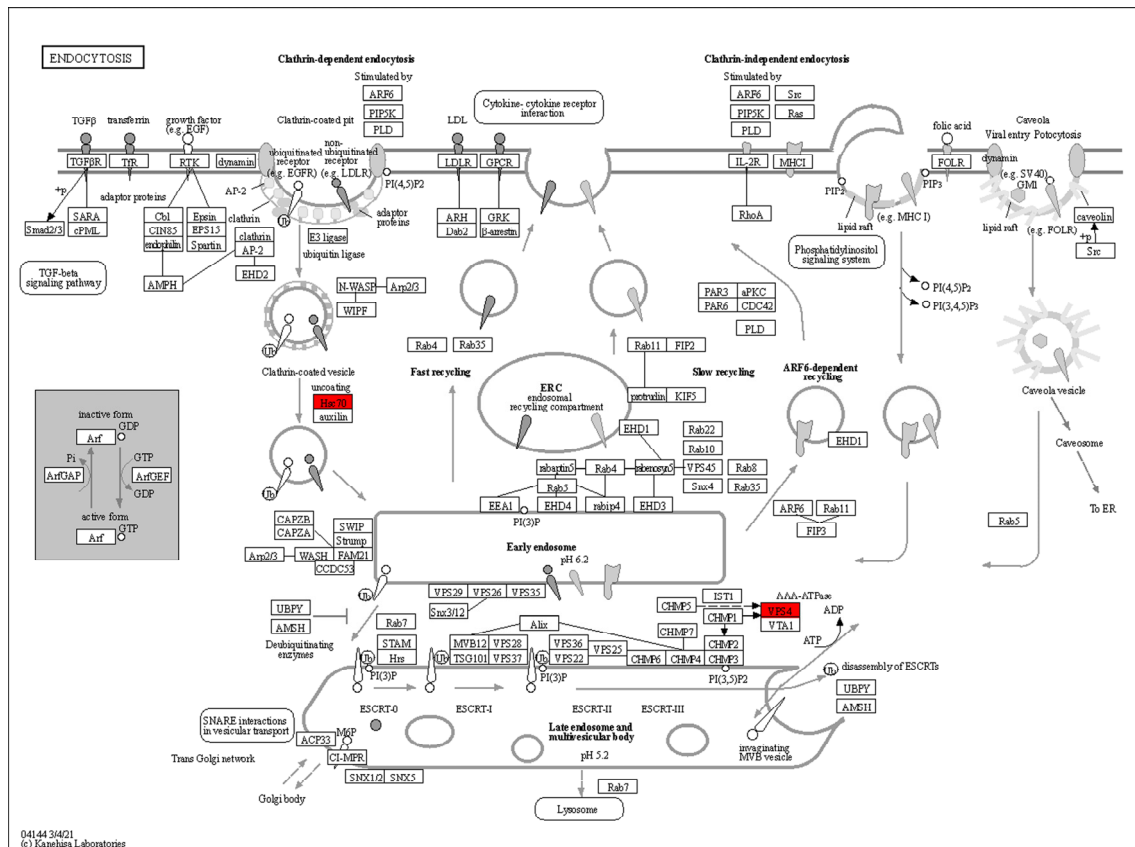




**Fig. S6.** Transcriptomic analysis of carbon fixation pathways in photosynthetic organisms after exposure of *Navicula sp.* to PS-NH<sub>2</sub>.



**Fig. S7.** Transcriptomic analysis of the Glycolytic/Glyco-isomeric pathway after exposure to PS-NH<sub>2</sub> in *Navicula sp.*



**Fig. S8.** Transcriptomic analysis of Endocytosis pathway in *Navicula sp.* exposed to PS-NH<sub>2</sub>.