

**Table S1.** Number of genes important for resistance to oxidative stress in SH4 and related cyanobacterial strains. Taxa: 1, candidatus *S. spongiarum* SH4; 2, *Synechococcus* sp. RCC307; 3, *Synechococcus* sp. RS9917; 4, *Synechococcus* sp. WH 5701; 5, *Synechococcus* sp. CC9311; 6, *P. marinus* CCMP137; 7, *Cyanobium* sp. PCC 7001; 8, *C. gracile* PCC 6307.

<b>Function</b>	<b>1</b>	<b>2</b>	<b>3</b>	<b>4</b>	<b>5</b>	<b>6</b>	<b>7</b>	<b>8</b>
Glutathione reductase (EC 1.8.1.7)	2	1	1	1	1	1	1	1
Glutathione peroxidase (EC 1.11.1.9)	0	1	1	1	1	1	1	1
Glutathione synthetase (EC 6.3.2.3)	1	1	1	1	1	1	1	1
Gamma-glutamyltranspeptidase (EC 2.3.2.2);	0	1	0	1	0	1	1	1
Methylhydantoinses A, B (EC 3.5.2.14)	0	1	0	1	1	0	1	1
Rubredoxin	1	3	2	2	2	4	1	1
Non-specific DNA-binding protein Dps;	0	1	1	1	1	0	1	1
Metallothionein	0	0	0	1	1	0	0	1
Alkyl hydroperoxide reductase subunit C-like protein	1	4	4	4	3	2	4	3
Peroxide stress regulator	1	1	1	1	1	0	1	1
Transcriptional regulator, Crp/Fnr family	0	1	2	2	1	1	2	3
Zinc uptake regulation protein ZUR	0	1	1	1	1	1	1	1
Ferric uptake regulation protein FUR	1	1	1	1	1	1	1	1
Superoxide dismutase [Fe] (EC 1.15.1.1)	0	1	1	1	0	0	1	1
Superoxide dismutase [Cu-Zn] (EC 1.15.1.1)	0	1	0	0	1	0	0	0
Rubrerythrin	1	1	0	0	0	0	0	0
Glutaredoxins	2	4	6	6	5	5	7	6
Glutathione S-transferase, omega (EC 2.5.1.18)	1	1	1	2	1	1	2	2
Glutathione S-transferase, unnamed subgroup	0	0	0	1	0	0	1	0
Glutathione S-transferase (EC 2.5.1.18)	0	1	1	1	2	0	0	0
Microsomal glutathione S-transferase	0	0	0	1	0	0	1	1
Glutathione S-transferase family protein	1	2	2	1	2	2	1	3
Phytochelatin synthase (EC 2.3.2.15)	0	0	0	1	0	0	0	1
In total	12	28	26	32	26	21	29	31