

Table S1. The inhibitory rates of copper on *Dunaliella salina*

Time (h)	Cu ($\mu\text{mol/L}$)			
	15	30	60	120
24	-10.8 ± 1.71	-5.73 ± 0.99	21.48 ± 2.63	31.30 ± 2.63
48	9.65 ± 0.63	28.34 ± 2.35	36.73 ± 3.68	47.40 ± 2.12
72	20.5 ± 1.92	44.53 ± 2.24	54.79 ± 2.37	62.64 ± 3.48
96	28.9 ± 3.40	50.39 ± 1.73	63.77 ± 4.19	78.05 ± 2.02

Table S5. KEGG pathway enrichment analysis of DEGs

Level 1	Level 2	Pathway	Pathway ID	No. of DEGs
Metabolism	Amino acid metabolism	Valine, leucine and isoleucine degradation	ko00280	11
Metabolism	Amino acid metabolism	Cysteine and methionine metabolism	ko00270	11
Metabolism	Amino acid metabolism	Lysine degradation	ko00310	6
Metabolism	Amino acid metabolism	Tryptophan metabolism	ko00380	4
Metabolism	Amino acid metabolism	Glycine, serine and threonine metabolism	ko00260	6
Metabolism	Amino acid metabolism	Arginine and proline metabolism	ko00330	5
Metabolism	Amino acid metabolism	Histidine metabolism	ko00340	2
Metabolism	Amino acid metabolism	Tyrosine metabolism	ko00350	2
Metabolism	Amino acid metabolism	Phenylalanine, tyrosine and tryptophan biosynthesis	ko00400	2
Metabolism	Amino acid metabolism	Lysine biosynthesis	ko00300	1
Metabolism	Amino acid metabolism	Alanine, aspartate and glutamate metabolism	ko00250	3
Metabolism	Amino acid metabolism	Arginine biosynthesis	ko00220	2
Metabolism	Carbohydrate metabolism	Pentose and glucuronate interconversions	ko00040	10
Metabolism	Carbohydrate metabolism	Ascorbate and aldarate metabolism	ko00053	8
Metabolism	Carbohydrate metabolism	Propanoate metabolism	ko00640	7
Metabolism	Carbohydrate metabolism	Galactose metabolism	ko00052	7
Metabolism	Carbohydrate metabolism	Glycolysis / gluconeogenesis	ko00010	14
Metabolism	Carbohydrate metabolism	Amino sugar and nucleotide sugar metabolism	ko00520	10
Metabolism	Carbohydrate metabolism	Starch and sucrose metabolism	ko00500	10
Metabolism	Carbohydrate metabolism	Pyruvate metabolism	ko00620	10
Metabolism	Carbohydrate metabolism	Glyoxylate and dicarboxylate metabolism	ko00630	8
Metabolism	Carbohydrate metabolism	Fructose and mannose metabolism	ko00051	5
Metabolism	Carbohydrate metabolism	Inositol phosphate metabolism	ko00562	3
Metabolism	Carbohydrate metabolism	Butanoate metabolism	ko00650	1
Metabolism	Carbohydrate metabolism	Citrate cycle (TCA cycle)	ko00020	3
Metabolism	Carbohydrate metabolism	Pentose phosphate pathway	ko00030	2
Metabolism	Energy metabolism	Photosynthesis	ko00195	19
Metabolism	Energy metabolism	Carbon fixation in photosynthetic organisms	ko00710	8
Metabolism	Energy metabolism	Photosynthesis - antenna proteins	ko00196	3
Metabolism	Energy metabolism	Oxidative phosphorylation	ko00190	10
Metabolism	Energy metabolism	Nitrogen metabolism	ko00910	2
Metabolism	Lipid metabolism	Fatty acid degradation	ko00071	8
Metabolism	Lipid metabolism	Alpha-linolenic acid metabolism	ko00592	6
Metabolism	Lipid metabolism	Biosynthesis of unsaturated fatty acids	ko01040	5
Metabolism	Lipid metabolism	Glycerolipid metabolism	ko00561	5
Metabolism	Lipid metabolism	Synthesis and degradation of ketone bodies	ko00072	1
Metabolism	Lipid metabolism	Sphingolipid metabolism	ko00600	3
Metabolism	lipid metabolism	Glycerophospholipid metabolism	ko00564	4
Metabolism	lipid metabolism	Fatty acid elongation	ko00062	1
Metabolism	Lipid metabolism	Steroid biosynthesis	ko00100	1
Metabolism	Lipid metabolism	Fatty acid biosynthesis	ko00061	2
Metabolism	Nucleotide metabolism	Pyrimidine metabolism	ko00240	18

Metabolism	Nucleotide metabolism	Purine metabolism	ko00230	17	
Metabolism	Metabolism of other amino acids	Selenocompound metabolism	ko00450	7	
Metabolism	Metabolism of other amino acids	Cyanoamino acid metabolism	ko00460	2	
Metabolism	Metabolism of other amino acids	Beta-alanine metabolism	ko00410	3	
Metabolism	Metabolism of other amino acids	Taurine and hypotaurine metabolism	ko00430	1	
Metabolism	Metabolism of other amino acids	Glutathione metabolism	ko00480	5	
Metabolism	Metabolism of cofactors and vitamins	Nicotinate and nicotinamide metabolism	ko00760	4	
Metabolism	Metabolism of cofactors and vitamins	Porphyrin and chlorophyll metabolism	ko00860	7	
Metabolism	Metabolism of cofactors and vitamins	Riboflavin metabolism	ko00740	2	
Metabolism	Metabolism of cofactors and vitamins	Thiamine metabolism	ko00730	1	
Metabolism	Metabolism of cofactors and vitamins	Folate biosynthesis	ko00790	1	
Metabolism	Metabolism of cofactors and vitamins	Biotin metabolism	ko00780	1	
Metabolism	Metabolism of cofactors and vitamins	One carbon pool by folate	ko00670	1	
Metabolism	Metabolism of cofactors and vitamins	Pantothenate and coa biosynthesis	ko00770	1	
Metabolism	Metabolism of cofactors and vitamins	Ubiquinone and other terpenoid-quinone biosynthesis	ko00130	1	
Metabolism	Metabolism of terpenoids and polyketides	Limonene and pinene degradation	ko00903	2	
Metabolism	Metabolism of terpenoids and polyketides	Terpenoid backbone biosynthesis	ko00900	3	
Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis	ko00906	2	
Metabolism	Glycan biosynthesis and metabolism	Other glycan degradation	ko00511	9	
Metabolism	Gycan biosynthesis and metabolism	n-glycan biosynthesis	ko00510	1	
Metabolism	Biosynthesis of other secondary metabolites	Carbapenem biosynthesis	ko00332	1	
Metabolism	Biosynthesis of other secondary metabolites	Monobactam biosynthesis	ko00261	1	
Metabolism	Global and overview maps	Metabolic pathways	ko01100	141	
Metabolism	Global and overview maps	Degradation of aromatic compounds	ko01220	4	
Metabolism	Global and overview maps	Biosynthesis of secondary metabolites	ko01110	63	
Metabolism	Global and overview maps	Carbon metabolism	ko01200	20	
Metabolism	Gobal and overview maps	Biosynthesis of amino acids	ko01230	18	
Metabolism	Global and overview maps	Fatty acid metabolism	ko01212	7	
Metabolism	Global and overview maps	2-oxocarboxylic acid metabolism	ko01210	3	
Cellular processes	Transport and catabolism	Endocytosis	ko04144	10	
Cellular processes	Transport and catabolism	Peroxisome	ko04146	7	
Cellular processes	Transport and catabolism	Regulation of autophagy	ko04140	2	
Cellular processes	Transport and catabolism	Phagosome	ko04145	3	
Environmental processing	information	Signal transduction	Phosphatidylinositol signaling system	ko04070	6
Environmental processing	information	Signal transduction	Plant hormone signal transduction	ko04075	7
Environmental processing	information	Membrane transport	ABC transporters	ko02010	17
Genetic information processing	Folding, sorting and degradation	Protein processing in endoplasmic reticulum	ko04141	20	
Genetic information processing	Folding, sorting and degradation	Ubiquitin mediated proteolysis	ko04120	8	
Genetic information processing	Folding, sorting and degradation	Proteasome	ko03050	1	
Genetic information processing	Folding, sorting and degradation	RNA degradation	ko03018	4	
Genetic information processing	Replication and repair	DNA replication	ko03030	7	
Genetic information processing	Replication and repair	Base excision repair	ko03410	2	

Genetic information processing	Replication and repair	Mismatch repair	ko03430	2
Genetic information processing	Replication and repair	Homologous recombination	ko03440	1
Genetic information processing	Replication and repair	Nucleotide excision repair	ko03420	1
Genetic information processing	Transcription	RNA polymerase	ko03020	9
Genetic information processing	Transcription	Spliceosome	ko03040	13
Genetic information processing	Translation	Ribosome	ko03010	43
Genetic information processing	Translation	Aminoacyl-trna biosynthesis	ko00970	7
Genetic information processing	Translation	mRNA surveillance pathway	ko03015	3
Genetic information processing	Translation	Ribosome biogenesis in eukaryotes	ko03008	4
Genetic information processing	Translation	RNA transport	ko03013	3
Organismal systems	Environmental adaptation	Plant-pathogen interaction	ko04626	17

Table S6. DEGs related to photosynthesis, carbohydrate metabolism, copper transport and HSPs

Pathway	Gene name	Gene description	Number of DEGs	Up/Down	Log2(FC)	
Photosynthesis	PsbA	Photosystem II P680 protein D1	1	up	2.52	
	PsbB	Photosystem II cp47 chlorophyll apoprotein	1	up	3.37	
	PsbC	Photosystem II cp43 chlorophyll apoprotein	1	up	3.84	
	PsbD	Photosystem II P680 protein D2	1	up	1.09	
	PsbE	Photosystem II cytochrome b559 subunit alpha	1	up	2.93	
	PsbM	Photosystem II PsbM protein	1	up	4.44	
	PsbH	Photosystem II protein H	1	up	3.65	
	PsbO	PSII oxygen-evolving enhancer protein 1	1	up	2.38	
	PsbP	PSII oxygen-evolving enhancer protein 2	2	up	1.81	
	PsbQ	PSII oxygen-evolving enhancer protein 3	1	up	1.37	
	PsbZ	Photosystem II PsbZ protein	2	up	5.47	
	PsaA	Photosystem I P700 chlorophyll a apoprotein a1	1	up	1.14	
	PsaC	Photosystem I subunit vii	1	up	3.04	
	PsaE	Photosystem I subunit iv	1	up	1.14	
	lhca1	Light-harvesting complex I chlorophyll a/b protein 1	1	down	-1.37	
	lhca3	Light-harvesting complex I chlorophyll a/b protein 3	1	up	1.05	
	lhcb2	Light-harvesting complex II chlorophyll a/b protein 2	1	down	-1.05	
	lhcb4	Light-harvesting complex II chlorophyll a/b protein 4	1	up	1.08	
	PetA	Apocytochrome f	1	up	1.43	
	PetB	Pytochrome b6	1	up	2.05	
	PetC	Pytochrome b6-f complex iron-sulfur subunit	2	up	2.03	
	PetH	Ferredoxin-NADP+ reductase	1	down	-5.53	
	ATPF1A	F-type H+-transporting ATPase alpha subunit	1	up	4.55	
	ATPF1B	F-type H+-transporting ATPase beta subunit	1	up	3.00	
	ATPF0C	F-type H+-transporting ATPase c subunit	1	up	3.25	
	Carbohydrate metabolism	RbcL	Ribulose biphosphate carboxylase large chain	1	up	2.71
		Tkta	Transketolase	1	up	5.10
		Pgm	Phosphoglucomutase	1	up	2.49
		Mdh1	Malate dehydrogenase	3	up	2.56
		Idh	Isocitrate dehydrogenase	1	up	2.12
		Cs	Citrate synthase	1	down	-4.47
		Sdhc/Frdc	Succinate dehydrogenase / Fumarate reductase, Cytochrome b subunit	1	down	-4.29
Glycolysis	Aldo	Fructose-bisphosphate aldolase	2	up	5.17	
	Gapdh	Glyceraldehyde-3-phosphate dehydrogenase	1	up	2.93	
	Adh	Alcohol dehydrogenase (NADP+)	2	up	1.88	
	Pgk	Phosphoglycerate kinase	1	up	1.70	
	Tpi	Triose phosphate isomerase	1	up	5.11	
	Pdc	Pyruvate decarboxylase	1	up	1.77	

	Pyk	Pyruvate kinase	1	down	-5.57
	Gpi	Glucose-6-phosphate isomerase	1	down	-1.35
Ion transport	CopA	Heavy metal transporting ATPase	3	up	4.78
	CopB	heavy metal transporting ATPase	3	up	1.78
	CutC	Copper homeostasis protein	1	down	-1.29
	Vps4	Vacuolar protein-sorting-associated protein 4	1	up	1.17
	Vps36	Vacuolar protein-sorting-associated protein 36	1	up	1.26
	Mrs2	Magnesium transporter	1	down	-1.80
	Zip	Zinc transporter	3	up	6.03
	ABCB1	ATP-binding cassette, subfamily b, member 1	1	up	1.69
	ABCC1	ATP-binding cassette, subfamily c, member 1	1	up	1.34
	ABCC10	ATP-binding cassette, subfamily c, member 2	1	up	1.22
	ABCA1	ATP-binding cassette, subfamily a, member 1	1	down	-1.25
	ABCB8	ATP-binding cassette, subfamily b, member 8	1	down	-1.19
Response to stress	Hsp20	Heat shock protein HSP20	3	up	3.00
	DnaK	Molecular chaperone DnaK	3	up	2.85
	DnaJC13	Molecular chaperone DnaJ homolog subfamily c member 13	1	up	2.75
	Hsp33	Heat shock protein 33	1	up	1.34
	GroEL	Heat shock protein 60 kDa	4	down	-6.25
	Hsp70	Heat shock protein 70	1	down	-1.04
	DnaJC11	DnaJ heat shock protein family (hsp40) member c11	1	down	-4.38
	DnaJC7	DnaJ homolog subfamily C member 7	1	down	-2.08
	Sod1	Cu/Zn superoxide dismutase	3	up	1.33
	Cat	Catalase	2	up	1.75