

Table S1. Transcriptome data statistics of different treatment groups

Sample	Raw_reads	Clean_reads	Error_rate	Q20	Q30	GC_pct
WS_CK_1	21874743	21324562	0.03	97.32	92.7	45.9
WS_CK_2	21645713	20604190	0.03	97.28	92.46	45.03
WS_CK_3	21374492	20748685	0.03	97.24	92.34	44.78
WS_5_1	23325380	23069280	0.03	97.3	92.69	45.02
WS_5_2	21948662	21534312	0.03	97.72	93.39	44.16
WS_5_3	21039785	20612134	0.03	97.59	93.09	44.22
WS_10_1	23412414	23126040	0.03	97.42	92.92	45.57
WS_10_2	23189662	22557210	0.03	97.29	92.43	44.77
WS_10_3	23862838	23280532	0.03	97.35	92.56	44.94
WS_20_1	22179600	21892648	0.03	97.5	93.11	45.68
WS_20_2	25327581	24719744	0.03	97.08	91.98	45.06
WS_20_3	23503783	22723337	0.03	97.71	93.37	45.03
WS_40_1	23108706	22881848	0.03	97.63	93.38	46
WS_40_2	23501155	22976668	0.03	97.71	93.36	45.13
WS_40_3	24948672	24172623	0.03	97.68	93.29	45.22

Table S2. Annotated information of 60 differentially expressed genes screened from two modules

Module	Gene Cluster	Gene name	Gene Description
blue	Cluster-81632.49952	TTL3	inactive TPR repeat-containing thioredoxin TTL3-like
blue	Cluster-81632.35098	NTRC	NADPH-dependent thioredoxin reductase 3-like
blue	Cluster-81632.32620	MOT2	molybdate transporter 2, transcript variant X1
blue	Cluster-81632.38228	TDX	TPR repeat-containing thioredoxin TDX
blue	Cluster-81632.49237	APRL5	5'-adenylylsulfate reductase-like 5
blue	Cluster-81632.33364	APS1	ATP sulfurylase 1
blue	Cluster-81632.37541	AAED1	thioredoxin-like protein AAED1
blue	Cluster-81632.39167	SULTR3;3	probable sulfate transporter 3.3
blue	Cluster-81632.26232	RWK1	Eukaryotic glutathione synthase
blue	Cluster-81632.36048	GSTF8	glutathione S-transferase F8, chloroplastic-like
blue	Cluster-81632.45303	PIP5K9	phosphatidylinositol 4-phosphate 5-kinase 9
blue	Cluster-81632.31474	STR2	thiosulfate/3-mercaptopropruvate sulfurtransferase 1, mitochondrial
blue	Cluster-81632.21924	TRXM2	Thioredoxin M2, chloroplastic
blue	Cluster-81632.40195	DIT2-1	dicarboxylate transporter 2.1, chloroplastic-like
blue	Cluster-81632.32717	ISS1	aspartate aminotransferase-like
blue	Cluster-81632.45384	GLX2-1	hydroxyacylglutathione hydrolase 1, mitochondrial-like
blue	Cluster-81632.31680	NTRC	NADPH-dependent thioredoxin reductase 3
blue	Cluster-81632.43978	At1g43560	thioredoxin Y2, chloroplastic
blue	Cluster-81632.15847	GSTL3	Glutathione S-transferase L3
blue	Cluster-81632.37348	GSTF9	Glutathione S-transferase F9
blue	Cluster-81632.36334	GSTU16	Glutathione S-transferase U16
blue	Cluster-81632.20905	At2g37240	thioredoxin-like protein AAED1, chloroplastic
blue	Cluster-81632.41462	SBP1	selenium-binding protein 1-like
blue	Cluster-81632.56902	SULTR4;1	sulfate transporter 4.1, chloroplastic
blue	Cluster-81632.31607	GSTT2	Glutathione S-transferase T2
blue	Cluster-81632.40972	PHO1-H8	Brassica napus phosphate transporter PHO1 homolog 8-like
blue	Cluster-81632.49268	TXNRD2	Thioredoxin reductase SEP1
blue	Cluster-81632.37650	NTRC	NADPH-dependent thioredoxin reductase 3-like
blue	Cluster-81632.42766	WDR26	WD repeat-containing protein 26-like
blue	Cluster-81632.38192	GSTF9	Glutathione S-transferase F9
blue	Cluster-81632.49952	TTL3	inactive TPR repeat-containing thioredoxin TTL3-like
turquoise	Cluster-81632.28496	yqjG	glutathionyl-hydroquinone reductase YqjG-like
turquoise	Cluster-81632.37456	APR2	5'-adenylylsulfate reductase 2
turquoise	Cluster-81632.33037	NIFS1	Cysteine desulfurase NFS1
turquoise	Cluster-81632.30832	flad1	3'-phosphoadenosine 5'-phosphosulfate sulfotransferase
turquoise	Cluster-81632.25707	GSTU5	Glutathione S-transferase U5
turquoise	Cluster-81632.8037	GSTU4	Glutathione S-transferase U4
turquoise	Cluster-81632.36631	GSTZ1	Glutathione S-transferase Z1
turquoise	Cluster-81632.13618	MGST3	Microsomal glutathione S-transferase 3
turquoise	Cluster-81632.44615	GSTF3	Glutathione S-transferase F3
turquoise	Cluster-81632.38210	GPX6	probable phospholipid hydroperoxide glutathione

			peroxidase 6
turquoise	Cluster-81632.38203	GPX6	probable phospholipid hydroperoxide glutathione peroxidase 6
turquoise	Cluster-81632.36062	SBP2	Selenium-binding protein 2
turquoise	Cluster-81632.3700	MGST3	Microsomal glutathione S-transferase 3
turquoise	Cluster-81632.35892	STR16	Thiosulfate sulfurtransferase 16
turquoise	Cluster-81632.38978	APS1	ATP sulfurylase 1
turquoise	Cluster-81632.22952	GPX2	probable glutathione peroxidase 2
turquoise	Cluster-81632.28993	APR3	5'-adenylylsulfate reductase 3
turquoise	Cluster-81632.28990	APR3	5'-adenylylsulfate reductase 3
turquoise	Cluster-81632.24050	APR3	5'-adenylylsulfate reductase 3
turquoise	Cluster-81632.44949	LGUL	LGUL mRNA for putative lactoylglutathione lyase
turquoise	Cluster-81632.29854	GSTL2	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase 2
turquoise	Cluster-81632.38724	At3g24170	glutathione reductase, cytosolic-like
turquoise	Cluster-81632.53780	APR1	5'-adenylylsulfate reductase 1, chloroplastic
turquoise	Cluster-81632.34125	GSTU26	Glutathione S-transferase U26
turquoise	Cluster-81632.38515	NFS2	cysteine desulfurase 1, chloroplastic-like
turquoise	Cluster-81632.38510	DHAR2	glutathione S-transferase DHAR1, mitochondrial
turquoise	Cluster-81632.40069	DHAR1	glutathione S-transferase DHAR1, mitochondrial-like
turquoise	Cluster-81632.27420	APR1	5'-adenylylsulfate reductase 1, chloroplastic
turquoise	Cluster-81632.38725	GR1	glutathione reductase, cytosolic
turquoise	Cluster-81632.28933	APR3	5'-adenylylsulfate reductase 3, chloroplastic

Figure S1. Changes in water content of mustard treated with different concentrations of sodium selenite.

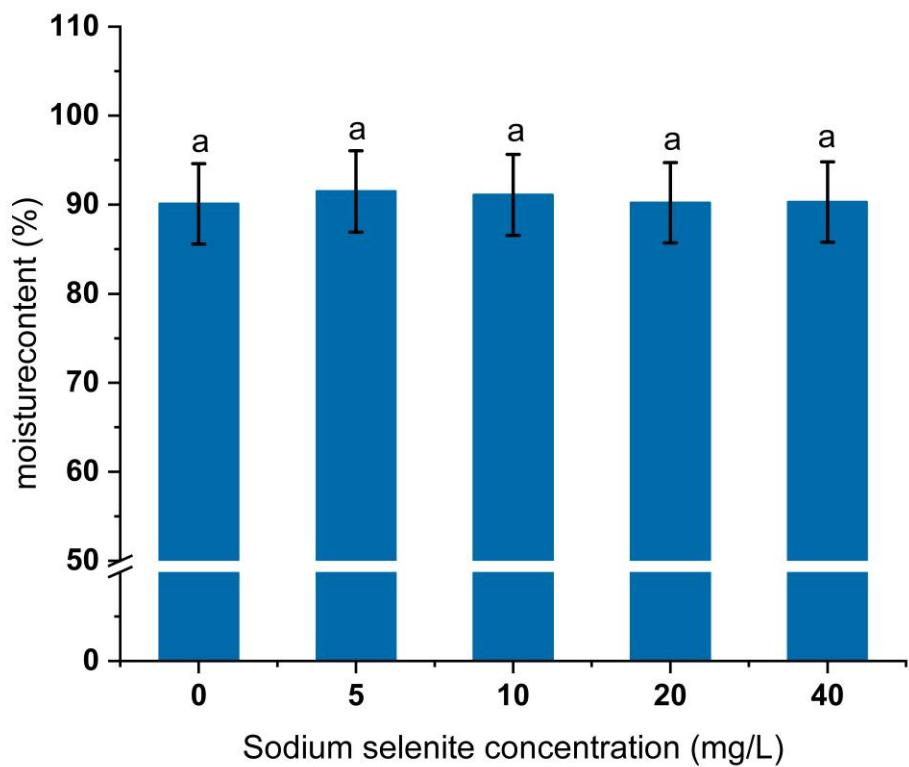


Figure S2. Heat map of correlation of gene expression level in test samples.

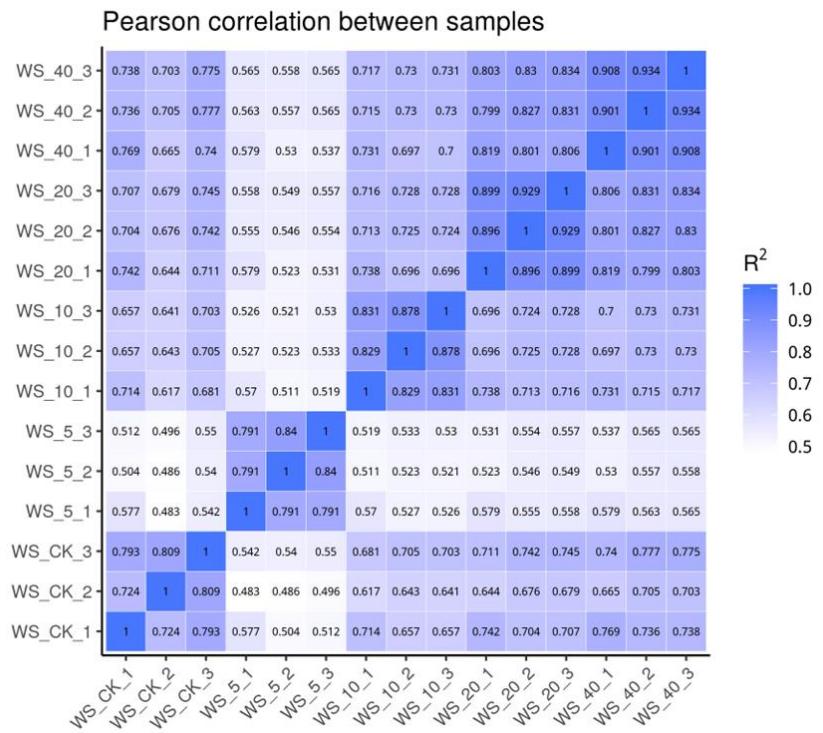


Figure S3. Statistics of differentially expressed genes in samples treated with different concentrations of Na_2SeO_3 .

