

## SUPPLEMENTAL MATERIAL

### Title

Heterologous expression analyzes of rice *OsCAS* in Arabidopsis and in yeast provide evidences for its roles in cyanide detoxification rather than in cysteine synthesis *in vivo*.

### Authors' full names

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### *Institute addresses*

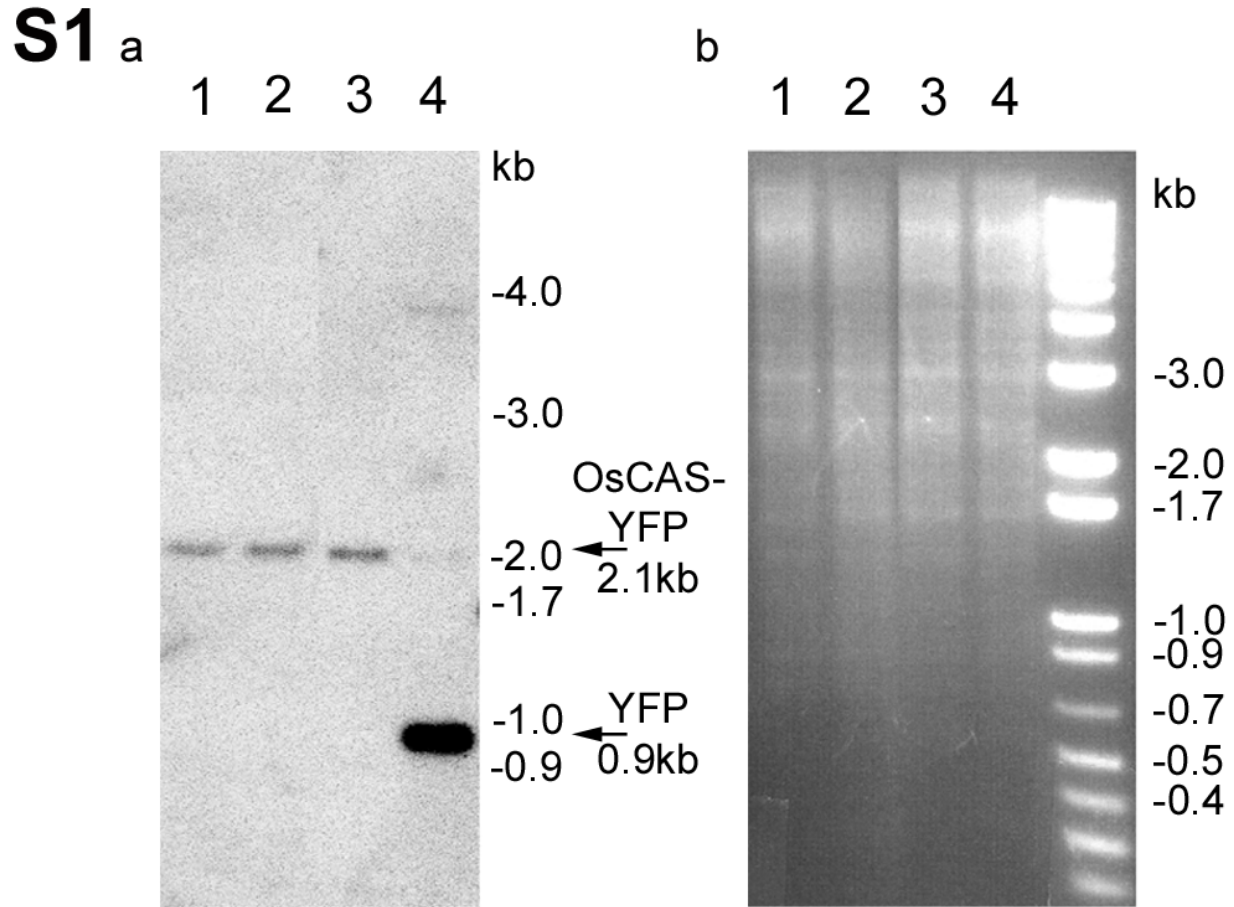
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**Figure S1** Integrations of OsCAS-YFP and YFP encoding sequences in Arabidopsis genome were analyzed by Southern blotting. Eight micrograms of genomic DNA from OsCAS-YFP lines including line 1, 4 and 5 (lane 1 to 3) and YFP transgenic line (lane 4) digested with *EcoRV* and *SacI* and probed with a  $^{32}\text{P}$ -labelled YFP fragment (A). Digested genomic DNAs from these lines were separated in 0.8% agarose gel (B).

**Table S1** Results of the protein identities for immuno- purified proteins by database searching

Mass, <i>m/z</i> submitted	Monoproton ated masses, MH <sup>+</sup> matched	Delta ppm	Modifi- cation	Residue matched	Prosposed peptide sequence	Sequence coverage (%)	MOWSE score
<b>Protein band 1</b>						28	2.86e+05
Beta-cyanoalanine synthase (40154 Da; pI 8.4)							
(Accession No. AY720933)							
1186.6991	1186.6683	26		296-306	(K) VLEVKGEDAVK (M)		
1215.7026	1215.6810	33		58-68	(K) IRDSASQLIGR (T)		
1327.7301	1327.6898	30		355-365	(R) YLSSALFEELR (A)		
1474.7654	1474.7212	30		100-112	(K) DRPAISMLED A EK (K)		
1481.9455	1481.9055	27		341-354	(K) GKLIVTVLPSLGER (Y)		
1490.7468	1490.7161	21	Met-ox	100-112	(K) DRPAISMLED A EK (K)		
1560.8586	1560.8420	11	Met-ox	169-183	(K) LVLTDPTKGMGGTVR (K)		
1602.8591	1602.8161	27		100-113	(K) DRPALSML EDA EKK (G)		
1618.8295	1618.8110	11	Met-ox	100-113	(K) DRPALSML EDA EKK (G)		
1677.9906	1677.9580	19		85-99	(R) IAAKLEFQPSFSVK (D)		
1872.9688	1872.9417	14		143-158	(K) GYELILTMP SYSLER (R)		
<b>Protein band 2</b>						43	3.73e+08
Large subunit of ribulose-1,5-bisphosphate carboxylase/ oxygenase; (52956 Da; pI 5.9)							
(Accession No. BAA84393)							

1021.6002	1021.5318	67		33-41	(K) DTDLAAFR (V)
1154.6407	1154.5642	66		304-312	(R) QKNHGMHFR (V)
1187.7456	1187.6649	68		286-295	(R) DNGLLLHIHR (A)
1228.7384	1228.6537	69		436-446	(R) DLAVEGNEIIR (E)
1240.8140	1240.7377	61		129-139	(K) ALAALRLEDLR (I)
1249.7701	1249.6792	73		340-350	(R) ESTLGFVDLLR (D)
1407.7597	1407.6684	65		22-32	(K) LTYYTPEYETK (D)
1447.8646	1447.7658	68		320-334	(R) LSGGDHIHAGTVVVGK (L)
1465.8621	1465.7522	73		147-159	(K) TFQGPPHGIQVER (D)
1516.9731	1516.8674	70		165-177	(K) YGRPLLGCTIKPK (L)
1546.8291	1546.7728	36		216-227	(R) DRFLFCAEAIYK (S)
1820.0867	1819.9554	72		335-350	(K) LEGDRESTLGFVDLLR (D)
1867.0361	1866.9125	66		464-479	(K) EITFNFPTIDKLDGQE (-)
1965.0705	1964.9322	70		237-253	(K) GHYLNATAGTCEEMIKR (A)
2170.1389	2169.9875	70		195-213	(R) GGLDFTKDDENVNSQPFMR (W)
2186.1170	2185.9824	62	Met-ox	195-213	(R) GGLDFTKDDENVNSQPFMR (W)
2410.3256	2410.1818	60		22-41	(K) LTYYTPEYETKDTDILAAFR (V)
3052.6474	3052.4661	59		259-285	(R) ELGVPIVMHDYLTGGFTANTSLSHYCR (D)

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**Protein band 3**

31

19089

Green fluorescent protein. RSGFP4 variant; (29253 Da; pI 6.1)

(Accession No. AAA79304.1)

1282.6946	1282.5738	94	Met-ox	86-96	(K) SAMPEGYVQER (T)
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1503.7958	1503.6603	90		27-41	(K) FSVSGEGEGDATYGK (L)
1542.9446	1542.7916	99		127-140	(K) GIDFKEDGNILGHK (L)
1941.0797	1940.8965	94		81-96	(R) H D F F K S A M P E G Y V Q E R (T)
1974.0768	1973.9067	86		141-156	(K) L E Y N Y N S H N V Y M A D K (Q)
1990.0665	1989.9017	83	Met-ox	141-156	(K) L E Y N Y N S H N V Y M A D K (Q)
2408.2491	2408.2511	-0.82		53-73	(K) L P V P W P T L V T T M G Y G V L C F S R (Y)
2437.4166	2437.2615	64		4-26	(K) G E E L F T G V V P I L V E L D G D V N G H K (F)
2664.4841	2664.3885	36	AcetN	1-26	(-) G K G E E T G V V P I L V E L D G D V N G H K (F)

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