

Table S1. List of the top 200 expression correlated genes with *AtCIAP* (AT1G68110).

Num	Locus and Gene Ontology terms ^a	r-value	Annotation and Functional Description
1	AT1G05840 ^{PT, IPTI, PO, PE, EPLP, PLP, LM, FABO, PTP, MACP, IPTT, LO, PI, FAO, FACP, I-GV-MT, LT, VMT, LL, PTT, CLCP, PIPM, LIT, PP, VRTM}	0.81	Involved in proteolysis
2	AT1G58030 ^{PT, IPTI, PO, PE, EPLP, PLP, LM, FABO, PTP, MACP, IPTT, LO, PI, FAO, FACP, CLCP, PIPM, PP, VRTM}	0.73	Catalase-2, Cationic amino acid transporter 2, vacuolar
3	AT2G28910 ^{PT, IPTI, PE, EPLP, PLP, PTP, IPTT, PI, I-GV-MT, LT, VMT, LL, PTT, PIPM, LIT, PP, VRTM}	0.73	CAX-interacting protein 4
4	AT3G07560 ^{PT, IPTI, PO, EPLP, PLP, LM, FABO, PTP, MACP, IPTT, LO, PI, FAO, FACP, I-GV-MT, LT, VMT, LL, PTT, CLCP, PIPM, LIT}	0.72	Peroxisomal membrane protein 13
5	*AT1G26670 ^{PT, IPTI, EPLP, PLP, PLV, EPLV, PTP, PTV, IPTT, PI, I-GV-MT, LT, VMT, SB, SRA, LL, PTT, PIPM, LIT}	0.81	Vesicle transport V-SNARE family protein
6	*AT1G15880 ^{PT, I-GVMT, PLP, EPLP, PTP, PO, IPTI, IPTT, PI, LT, VMT, SB, SRA, LL, PTT, PIPM, LIT}	0.80	Golgi snare 11
7	AT5G66160 ^{PT, IPTI, PO, EPLP, PLP, PTP, IPTT, PI, I-GV-MT, LT, VMT, LL, PTT, PIPM, LIT}	0.73	Receptor homology region, transmembrane domain protein 1
8	AT1G64230 ^{PT, IPTI, PO, EPLP, PLP, LM, FABO, PTP, MACP, IPTT, LO, PI, FAO, FACP, VMT, PTT, CLCP, PIPM}	0.74	Ubiquitin-conjugating enzyme E2 28
9	AT1G05790 ^{PT, IPTI, PO, EPLP, PLP, LM, FABO, PTP, MACP, IPTT, LO, PI, FAO, FACP, ,PTT, CLCP, PIPM}	0.71	Lipase Class 3 family protein
10	AT3G19860 ^{PT, IPTI, EPLP, PLP, LM, FABO, PTP, MACP, IPTT, LO, PI, FAO, FACP, PTT, CLCP, PIPM}	0.77	Transcription factor bHLH121
11	AT1G16240 ^{PLV, EPLV, PTV, I-GV-MT, VMT, SB, SRA}	0.79	Syntaxin of plants 51
12	AT2G45980 ^{PLV, EPLV, PTV, VMT}	0.80	ATG8-interacting protein 1
13	AT5G06140 ^{PLV, EPLV, PTV, VMT}	0.78	Sorting nexin 1
14	*AT4G22750 ^{PLV, EPLV, PTV, VMT}	0.77	Probable protein S-acyltransferase 13
15	AT5G66030 ^{I-GV-MT, VMT}	0.74	Protein GRIP
16	*AT2G36900 ^{VMT, SB, SRA}	0.81	Membrin 11
17	*AT4G32150 ^{VMT, SB, SRA}	0.80	Vesicle-associated membrane protein 711
18	*AT4G17730 ^{VMT, SB, SRA}	0.78	Syntaxin of plants 23
19	AT2G28370 ^{VMT}	0.81	CASP-like protein 5A2

20	AT1G13450 ^{VM}	0.78	Trihelix trancription factor GT-1
21	AT1G49240 ^{VM}	0.77	Actin-8
22	AT4G24520 ^{VM}	0.75	NADPH-cytochrome P450 reductase 1
23	AT1G53400 ^{VM}	0.75	Uncharacterized protein
24	AT3G24315 ^{VM}	0.72	AtSec20 family protein
25	AT5G39590 ^{VM}	0.71	TLD-domain containing nucleolar protein
26	AT5G46410 ^{VM}	0.71	SCP1-like small phosphatase 4
27	AT1G26580 ^{mRNACP, RNACP, PTT, N-TMCP}	0.77	Cpn60-beta4
28	AT5G12230 ^{mRNACP, RNACP, N-TMCP}	0.76	Mediator of RNA polymerase II transcription subunit 19A
29	AT5G19330 ^{mRNACP, RNACP, N-TMCP}	0.73	ARIA ARM REPEAT PROTEIN INTERACTING WITH ABF2
30	AT3G10030 ^{mRNACP, RNACP, PF, N-TMCP, PP, VRTM}	0.75	Aspartate/glutamate/uridylylate kinase family protein
31	AT2G45620 ^{mRNACP, RNACP, PF, N-TMCP, PP, VRTM}	0.72	UTP:RNA uridylyltransferase 1
32	AT5G04910 ^{PF, LM, FABO, MCP, LO,FAO, FACP, CLCP, PP, VRTM}	0.76	Peptidylprolyl isomerase
33	AT5G42820 ^{PF, LL, PP, VRTM}	0.72	Splicing factor U2AF small subunit B
34	AT5G14080 ^{PF, PP, VRTM}	0.79	Pentatricopeptide repeat-containing protein
35	*AT3G11100 ^{PF, PP, VRTM}	0.78	Trihelix transcription factor ASIL1
36	AT5G20520 ^{PF, PP, VRTM}	0.77	WAV2 alpha/beta-Hydrolases superfamily protein
37	AT4G38800 ^{PF, PP, VRTM}	0.76	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 1
38	AT3G14750 ^{PF, PP, VRTM}	0.76	Protein FLX-like 1
39	AT2G26430 ^{PF, PP, VRTM}	0.76	Cyclin-L11
40	AT3G01770 ^{PF, PP, VRTM}	0.76	Transcription factor GTE11
41	AT1G12910 ^{PF, PP, VRTM}	0.75	WD repeat-containing protein LWD1

42	AT3G47610 ^{PF, PP, VRTM}	0.75	Transcription regulator/zinc ion binding protein
43	AT2G43430 ^{PF, PP, VRTM}	0.73	Hydroxyacylglutathione hydrolase 1, mitochondrial
44	AT1G76460 ^{PF, PP, VRTM}	0.72	RNA-binding (RRM/RBD/RNP motifs) family protein
45	AT1G15920 ^{VRTM}	0.74	Probable CCR4-associated factor 1 homolog 2
46	AT2G33810 ^{RB, VRTM}	0.72	Squamosa promoter-binding-like protein 3
47	AT3G17100 ^{RB}	0.76	Transcription factor bHLH147
48	AT4G00720 ^{RB}	0.74	Shaggy-related protein kinase theta
49	AT1G06390 ^{RB}	0.74	Shaggy-related protein kinase iota
50	AT1G17120 ^{RB}	0.74	Cationic amino acid transporter 8, vacuolar
51	AT2G34690 ^{LT, LL, Ap}	0.74	Accelerated cell death 11
52	AT1G29970 ^{Ap}	0.86	60S ribosomal protein L18a-like protein
53	*AT5G17290 ^{Ap}	0.83	ATG5 Autophagy protein
54	AT1G28960 ^{Ap}	0.76	Nudix hydrolase 15, mitochondrial
55	AT5G64880 ^{Ap}	0.75	Transmembrane protein
56	*AT4G20380 ^{Ap}	0.74	Protein LSD1
57	*AT2G07180	0.85	Probable serine/threonine-protein kinase PBL17
58	*AT4G26400	0.85	RING/U-box superfamily protein
59	AT5G53360	0.84	TRAF-like superfamily protein
60	*AT2G42780	0.83	Transcription elongation factor B polypeptide
61	*AT5G32440	0.83	Ubiquitin system component Cue protein
62	*AT3G07870	0.83	F-Box PROTEIN92

63	AT5G51400	0.82	GENE1000 PLAC8 family
64	AT2G46900	0.82	Transcription factor-like protein
65	*AT5G64920	0.82	CIP8 E3 ubiquitination
66	AT4G08330	0.82	Hypothetical protein
67	*AT4G03030	0.82	OR23 F-box/Kelch repeat family
68	AT5G16110	0.82	Hypothetical protein
69	AT2G18280	0.81	Tubby-like protein 2
70	AT1G15400	0.81	Hypothetical protein
71	AT1G15350	0.81	DUF4050 family protein
72	*AT1G06700	0.81	PTI1-like tyrosine-protein kinase 1
73	AT1G33250	0.81	Beta-1,3-n-acetylglucosaminyltransferase radical fringe protein
74	*AT4G27880	0.81	SINAT4 E3 ubiquitin-dependent protein catabolic process
75	AT5G23670	0.81	Long chain base
76	*AT5G16480	0.80	Plant/Fungal atypical dual-specificity phosphatase
77	*AT5G46150	0.80	Putative ALA-interacting subunit 2
78	AT5G56750	0.80	N-MYC down-regulated-like 1
79	AT2G47700	0.80	RFI2 RING/U-box super family
80	*AT2G39100	0.79	Putative RING zinc finger protein
81	AT2G46490	0.79	Uncharacterized protein
82	AT3G58670	0.79	Plant cysteine oxidase 5
83	AT4G15780	0.79	Vesicle-associated membrane protein 724
84	*AT3G61160	0.79	Shaggy-related protein kinase beta

85	AT1G33050	0.79	Protein DETOXIFICATION
86	AT1G78895	0.79	Reticulon-like protein B22
87	AT1G49170	0.79	Uncharacterized protein
88	AT3G02700	0.79	UNE6
89	AT1G56090	0.79	Aspartate aminotransferase
90	AT1G13570	0.79	F-box/FBD/LRR-repeat protein
91	AT1G12790	0.79	Protein PARTING DANCERS
92	AT5G67380	0.78	Casein kinase II subunit alpha-1
93	AT2G26210	0.78	Ankyrin repeat family protein
94	AT3G60300	0.78	RWD domain-containing protein
95	AT3G55770	0.78	LIM domain-containing protein WLIM2b
96	AT1G43700	0.78	VIP1i Transcription factor
97	*AT3G10770	0.78	Single-stranded nucleic acid binding R3H protein
98	*AT2G29400	0.78	Serine/threonine-protein phosphatase PP1 isozyme 1
99	AT4G12570	0.78	E3 ubiquitin-protein ligase UPL5
100	AT1G47270	0.78	Tubby-like F-box protein 6
101	AT1G73380	0.78	Uncharacterized protein
102	AT1G12810	0.77	Uncharacterized protein
103	AT5G03470	0.77	B'ALPHA Serine/threonine protein phosphatase 2A
104	AT5G23380	0.77	Hexosyltransferase
105	AT5G05750	0.77	DNAJ heat shock N-terminal domain-containing protein

106	AT3G02340	0.77	Uncharacterized protein
107	AT2G46260	0.77	BTB/POZ domain-containing protein
108	AT2G15570	0.76	GAT1 Thioredoxin M3, chloroplastic
109	AT2G15240	0.76	Uncharacterized protein
110	AT3G03020	0.76	WOX11
111	AT2G37478	0.76	CPuORF52 conserved PEPTIDE upstream reading frame
112	AT2G31350	0.76	Hydroxyacylglutathione hydrolase 2, mitochondrial
113	AT5G01800	0.76	Saposin B domain-containing protein
114	AT5G40190	0.76	RING-type E3 ubiquitin transferase
115	AT5G58575	0.76	SAGA-associated factor 11
116	AT4G27750	0.76	ISI1 binding protein
117	AT5G12390	0.76	Mitochondrial fission 1 protein B
118	AT5G14390	0.76	Alpha/beta-hydrolases superfamily protein
119	AT2G41710	0.76	AP2-like ethylene-responsive transcription factor
120	AT3G11530	0.75	Vacuolar protein sorting 55 family protein
121	AT3G05250	0.75	RING/U-box superfamily protein
122	AT1G51550	0.75	F-box/Kelch-repeat protein
123	AT5G37055	0.75	SWC6 SWR1 complex subunit 6
124	AT2G42890	0.75	Protein MEI2-like 2
125	AT5G45360	0.75	F-box protein SKIP31
126	AT5G45080	0.75	HGO Protein PHLOEM PROTEIN 2-LIKE A6
127	AT1G19680	0.75	Uncharacterized protein

128	AT3G01850	0.75	Ribulose-phosphate 3-epimerase
129	AT5G20030	0.75	NUDX19
130	AT2G20740	0.75	TOM2AH3 Tetraspanin-19
131	AT3G12630	0.75	A20 and AN1 domain-containing stress-associated protein 5
132	AT5G43930	0.74	Transducin family protein/WD-40 repeat family protein
133	AT5G04880	0.74	Laccase
134	AT2G44850	0.74	Uncharacterized protein
135	AT1G69220	0.74	Protein kinase superfamily protein
136	AT5G20120	0.74	Uncharacterized protein
137	AT5G05100	0.74	Single-stranded nucleic acid binding SH4 protein
138	AT1G14290	0.74	Sphinganine C4-monooxygenase 2
139	AT4G32760	0.74	TOM1-like protein 9
140	AT2G21950	0.74	F-box/Kelch-repeat protein SKIP6
141	AT3G22290	0.74	Endoplasmic reticulum vesicle transporter protein
142	AT1G14740	0.74	Protein OBERON3
143	AT1G20880	0.74	V-type proton ATPase proteolipid subunit
144	AT4G31080	0.74	Integral membrane metal-binding family protein
145	AT2G18670	0.74	RING-H2 finger protein ATL56
146	AT3G09030	0.74	BTB/POZ domain-containing protein
147	AT1G27290	0.74	Transmembrane protein
148	AT4G24370	0.74	SUPPRESSOR OF K ⁺ TRANSPORT GROWTH DEFECT 1

149	AT4G00560	0.74	NAD(P)-binding Rossmann-fold superfamily protein
150	*AT3G09320	0.74	Probable protein S-acyltransferase 16
151	AT5G41560	0.73	DET1 complexing ubiquitin ligase
152	AT3G12570	0.73	FYD-FYD
153	AT5G23590	0.73	Uncharacterized protein
154	AT1G26665	0.73	Mediator of RNA polymerase II transcription subunit 10b
155	AT5G21170	0.73	SNF1-related protein kinase regulatory subunit beta-1
156	AT1G70360	0.73	F-box protein
157	AT5G47180	0.73	Vesicle-associated protein 21
158	AT3G04880	0.73	DNA-damage-repair/toleration protein 102
159	AT2G17440	0.73	Plant intracellular Ras-group-related LRR protein 5
160	At3g10770	0.73	Sequence-specific DNA binding transcription factor
161	AT3G62290	0.73	ADP-ribosylation factor A1E
162	AT5G38895	0.73	RING/U-box superfamily protein
163	AT5G05710	0.73	CASP-like protein
164	AT5G14240	0.73	Carbonic anhydrase
165	AT3G11770	0.73	Polynucleotidyl transferase, ribonuclease H-like family protein
166	AT5G63190	0.72	MA3 domain-containing protein
167	AT1G70150	0.72	Zinc ion binding protein
168	AT4G12690	0.72	DUF868 family protein
169	AT5G23130	0.72	Peptidoglycan-binding LysM domain-containing protein
170	AT5G47520	0.72	Ras-related protein RABA5a

171	AT1G34300	0.72	G-type lectin S-receptor-like serine/threonine-protein kinase
172	AT3G09880	0.72	B'BETA serine/threonine protein phosphatase 2A
173	AT3G18295	0.72	DUF1639 family protein, putative
174	AT3G07274	0.72	Pseudogene
175	AT4G36780	0.72	BES1/BZR1 homolog protein 2
176	AT1G28410	0.72	Myosin heavy chain-like protein
177	AT1G36070	0.72	Transducin/WD40 repeat-like superfamily protein
178	AT1G05090	0.72	Dentin Sialophosphoprotein-like protein
179	AT5G06560	0.72	Myosin-binding protein 7
180	AT2G21240	0.72	Protein BASIC PENTACYSTEINE 4
181	AT1G22890	0.72	Transmembrane protein
182	AT5G59380	0.72	Methyl-CpG-binding domain-containing protein 6
183	AT5G19950	0.72	Tudor domain protein (DUF1767)
184	AT3G13550	0.72	Constitutive photomorphogenesis protein 10
185	AT5G65960	0.72	GTP binding protein
186	AT4G32160	0.72	PX domain-containing protein EREL1
187	AT3G04350	0.72	Zeta-carotene desaturase
188	AT1G43130	0.71	Protein-LIKE COV 2
189	AT2G44900	0.71	FBX5 protein ARABIDILLO 1
190	AT5G22360	0.71	Vesicle-associated membrane protein 714
191	AT1G34150	0.71	tRNA pseudouridine synthase

192	AT4G31250	0.71	Probable LRR receptor-like serine/threonine-protein kinase
193	AT1G60140	0.71	Trehalose phosphate synthase 10
194	AT4G39910	0.71	Ubiquitin carboxyl-terminal hydrolase 3
195	AT1G09280	0.71	Rhodanese-like domain-containing protein 6
196	AT4G11240	0.71	Serine/threonine-protein phosphatase PP1 isozyme 6
197	AT4G38260	0.71	Transport/Golgi organization-like protein
198	AT1G67710	0.71	ARR11 Two-component response regulator
199	AT4G24990	0.71	Membrane-anchored ubiquitin-fold protein 3
200	AT2G31810	0.71	Acetolactate synthase small subunit 2, chloroplastic

PT: Peroxisomal transport ($P = 3.05e^{-08}$), IPTI: Intracellular protein transmembrane import ($P = 2.93e^{-07}$), PO: Peroxisome organization ($P = 3.05e^{-08}$), PF: Photoperiodic flowering ($P = 1.85e^{-15}$), EPLP: Establishment of protein localization to peroxisome ($P = 3.05e^{-08}$), PLP: Protein localization to peroxisome ($P = 3.05e^{-08}$), LM: Lipid modification ($P = 3.22e^{-02}$), FABO: Fatty acid beta-oxidation ($P = 3.79e^{-03}$), PTP: Protein targeting to peroxisome ($P = 3.05e^{-08}$), MACP: Monocarboxylic acid catabolic process ($P = 1.88e^{-02}$), IPTT: Intracellular protein transmembrane transport ($P = 3.82e^{-07}$), LO: Lipid oxidation ($P = 4.68e^{-03}$), PI: Protein import ($P = 2.76e^{-04}$), FAO: Fatty acid oxidation ($P = 4.00e^{-03}$), FACP: Fatty acid catabolic process ($P = 1.55e^{-02}$), I-GV-MT: Intra-Golgi vesicle-mediated transport ($P = 2.52e^{-07}$), LT: Lipid transport ($P = 1.02e^{-03}$), VMT: Vesicle mediated transport ($P = 8.4e^{-03}$), LL: Lipid localization ($P = 2.76e^{-03}$), PTT: Protein transmembrane transport ($P = 3.82e^{-07}$), CLCP: Cellular lipid catabolic process ($P = 2.92e^{-02}$), PIPM: Protein import into peroxisome matrix ($P = 3.05e^{-08}$), LIT: Lithium ion transport ($P = 5.38e^{-06}$), PP: Photoperiodism ($P = 2.79e^{-15}$), VRTM: Vegetative to reproductive phase transition of meristem ($P = 8.71e^{-11}$), PLV: Protein localization to vacuole ($P = 3.32e^{-02}$), EPLV: Establishment of protein localization to vacuole ($P = 3.32e^{-02}$), PTV: Protein targeting to vacuole ($P = 3.32e^{-02}$), SB: Snare binding ($P = 2.03e^{-06}$), SRA: SNAP receptor activity ($P = 1.84e^{-06}$), mRNACP: mRNA catabolic process ($P = 2.32e^{-02}$), RNACP: RNA catabolic process ($P = 3.29e^{-02}$), N-TMCP: Nuclear-transcribed mRNA catabolic process ($P = 2.22e^{-02}$), RB: Response to brassinosteroid ($P = 2.04e^{-02}$), Ap: Autophagy ($P = 1.21e^{-03}$). *25 expression-correlated genes selected for stimulus-specific microarray analysis.

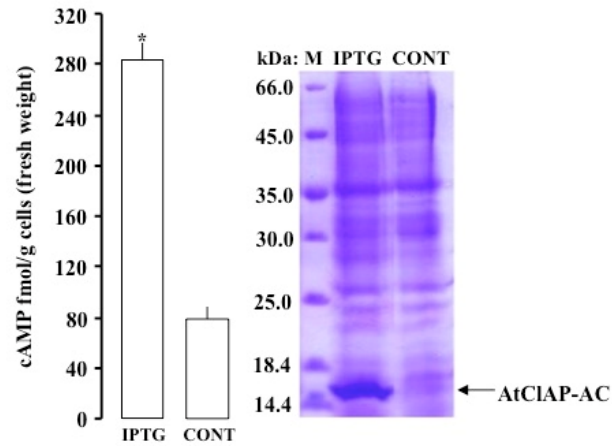


Figure S1. Cyclic AMP generated by the induced (IPTG) and un-induced (CONT) *E. coli* EXPRESS BL21 (DE3) pLysS DUOs cells harbouring the AtCIAP-AC gene fragment. The cAMP was measured by enzyme immunoassay following the acetylation protocol described in the supplier's manual (Sigma-Aldrich Corporation, code: CA201). Inset: SDS-PAGE of protein fractions from the induced (IPTG) and un-induced (CONT) cell cultures. Data are mean values ($n = 3$) and error bars show SE of the mean. Asterisk indicates significant difference ($p < 0.05$) determined by ANOVA and *post hoc* Student–Newman–Keuls multiple range tests.

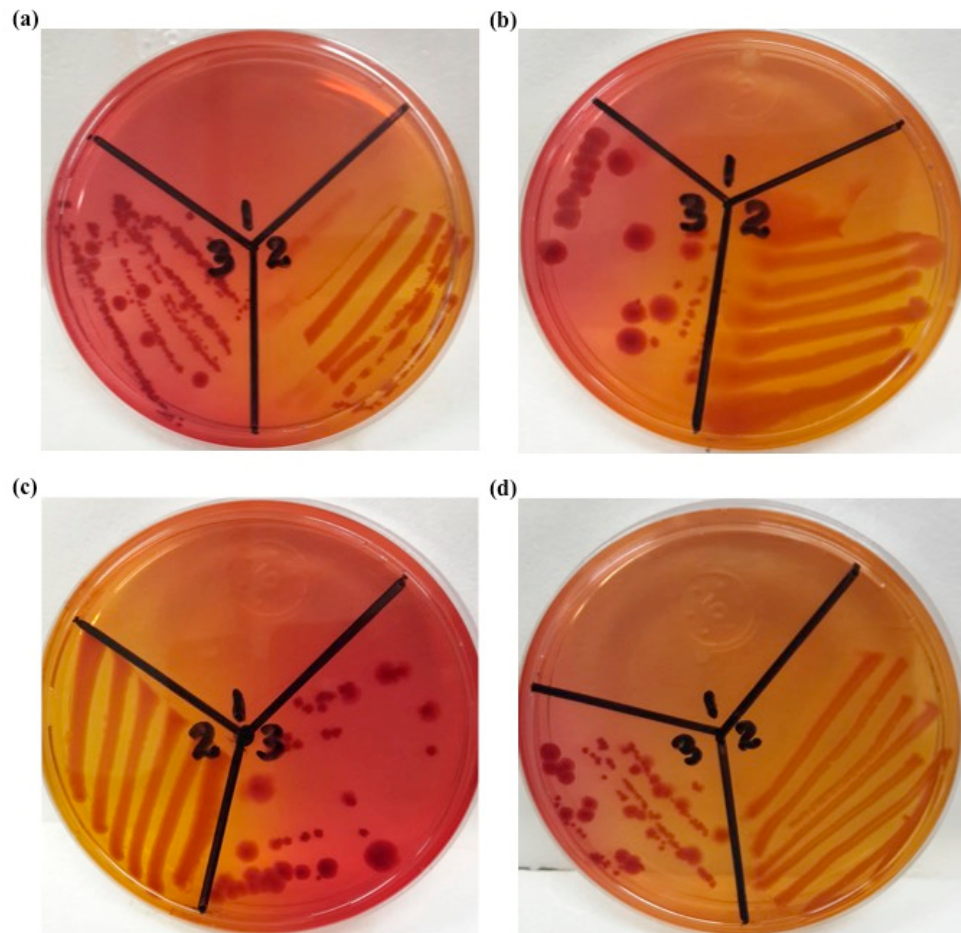


Figure S2. (a–d) Crystal violet containing MacConkey agar plates supplemented with 15 µg/L kanamycin and 0.1 mM IPTG, and uniformly inoculated with (1) no cells, (2) *cyaA* mutant cells and (3) *cyaA* mutant cells transformed with the pTrcHis2-TOPO:AtCIAP-AC fusion construct. The plates were incubated at 37°C for 40 h to develop the displayed colony growth patterns.