

Additional file 5 - Cowpea drought responsive genes annotated in SSHdb (after sequencing of selected clones)

Forward library

Group number	Representative clone ID	BLAST2GO annotations		SSHscreen annotations				SSHdb annotations					
		Sequence description	GO-terms	logFC (ER3)*	adj.P.Val	B	invER2	Vector free sequence (bp)	BLAST priority (X/N)	BLAST AccNr	BLAST Hit Def	BLAST Eval	RedPartner
1	25C06-F	glutathione s-transferase	P: defense response to bacterium F: glutathione transferase activity C: vacuole F: copper ion binding C: plasma membrane C: chloroplast stroma C: apoplast F: glutathione binding	2.92	4.E-08	17.5	-2.92	705	X	AAM34480	glutathione S-transferase [<i>Phaseolus acutifolius</i>] [GST]	7.E-104	19
2	46D11-F	protein	C: extracellular region	2.10	1.E-05	10.0	-4.04	543	X	AAD33696	PR1a precursor [<i>Glycine max</i>] [PR1]	5.E-64	16
3	33D04-F	thaumatin-like protein	C: extracellular region P: defense response	2.08	5.E-05	8.1	-4.91	780	X	DQ269446	thaumatin-like [<i>G. max</i>] [THAU]	2.E-66	5
4	26H07-F	wound-induced protein win2	P: defense response to bacterium F: chitinase activity P: chitin catabolic process F: protein binding P: defense response to fungus F: chitin binding P: cell wall macromolecule catabolic process P: response to salt stress	1.69	1.E-06	14.0	-2.9	524	X	P09762	wound-induced protein 2 [<i>Solanum tuberosum</i>]	3.E-63	2
5	07F09-F	late embryogenesis abundant protein	P: response to stress	1.15	5.E-07	14.9	0.05	473	X	AAB38782	late embryogenesis abundant 5 [<i>G.max</i>] [LEA]	1.E-27	0
6	46E07-F	19-like protein	C: cytoplasmic membrane-bounded vesicle	1.10	2.E-04	6.4	-0.81	538	X	AAU14999	MtN19-like protein [<i>Pisum sativum</i>]	7.E-73	0
7	29F12-F	kunitz-type protease inhibitor kpi-f4	F: endopeptidase inhibitor activity	1.06	1.E-04	7.0	-3.47	404	X	BAA82840	miraculin [<i>Youngia japonica</i>] [MIR]	2.E-10	3
8	26B01-F	protein	F: FAD binding F: oxidoreductase activity	0.82	7.E-04	5.1	-2.92	360	X	BAB33033	CPRD2 [<i>Vigna unguiculata</i>]	2.E-60	0
9	26B07-F	ammonium transporter	C: membrane P: ammonium transport	0.50	9.E-04	4.9	-3.45	516	X	NP_193087	ammonium transmembrane transporter [<i>Arabidopsis thaliana</i>]	1.E-63	0
10	29D02-F	universal stress protein family	C: cytosol P: response to stress C: plastid	0.30	3.E-02	1.1	-1.96	359	X	NP_563888	universal stress protein (USP) [<i>A.thaliana</i>]	1.E-14	0
11	30B02-F	---	---	0.25	3.E-02	0.9	-2.64	487	X	NP_564894	zinc finger (MYND type) family protein / F-box [<i>A.thaliana</i>]	9.E-10	0
12	14B10-F	calmodulin-binding protein	F: calmodulin binding	0.22	1.E-01	-0.5	-1.75	276	X	AAN65367	calmodulin-binding protein 60-A [<i>Phaseolus vulgaris</i>]	3.E-11	0
13	46G04-F	protein	C: cytoplasmic membrane-bounded vesicle F: protein binding C: membrane	0.17	1.E-01	-0.7	-1.12	161	N	AK285943	cDNA, clone: GMFL01-19-A06 [<i>G. max</i>]	1.E-48	0
14	31A10-F	---	---	-0.09	3.E-01	-1.4	1.84	356	N	AF479110	26S ribosomal RNA [<i>Medicago sativa</i>]	5.E-176	0

*ER3 for forward library calculated as $\log_2(\text{drought stressed/control})$

Reverse library

		BLAST2GO annotations		SSHscreen annotations				SSHdb annotations					
Group number	Representative clone ID	Sequence description	GO-terms	logFC (ER3)*	adj.P.Val	B	invER2	Vector free sequence (bp)	BLAST priority (X/N)	BLAST AccNr	BLAST Hit Def	BLAST Eval	RedPartner
15	16C12-R	light-harvesting complex ii protein lhcb1	P: photosynthesis, light harvesting C: photosystem II F: magnesium ion binding P: protein-chromophore linkage F: chlorophyll binding C: integral to membrane C: chloroplast C: photosystem I	1.99	5.E-06	11.6	-1.13	653	X	AAA50172	photosystem II chlorophyll a/b-binding (type I) [<i>G.max</i>] [CHL]	3.E-120	10
16	16B08-R	plastidic aldolase	P: glycolysis F: fructose-bisphosphate aldolase activity C: chloroplast C: mitochondrion	1.53	2.E-05	10.47	-1.24	570	X	Q01516	Fructose-bisphosphate aldolase 1, chloroplastic [<i>P.sativum</i>]	4.E-92	2
17	38A07-R	chlorophyll a b binding protein	C: membrane C: thylakoid F: protein binding P: photosynthesis, light harvesting C: chloroplast	1.32	2.E-05	10.29	-2.35	432	X	NP_181539	LHCB4.3(light harvesting complex PSII)[<i>A.thaliana</i>] [LHC]	2.E-43	4
18	17C04-R	---	---	1.17	3.E-03	5.3	-2.75	439	X	ACA23202	Kunitz trypsin inhibitor p20-1 [<i>G. max</i>]	9.E-14	1
19	37F06-R	ribulose - bisphosphate carboxylase	P: reductive pentose-phosphate cycle F: ribulose-bisphosphate carboxylase activity F: monooxygenase activity P: photorespiration P: oxidation reduction C: chloroplast C: mitochondrion	0.94	4.E-04	7.73	-0.9	369	X	AAG24882	ribulose-1,5-bisphosphate carboxylase rbcS1 [<i>G.max</i>]	1.E-23	0
20	36G04-R	---	---	0.76	1.E-04	8.95	-2.94	669	X	AAQ74628	lipid transfer protein II [<i>Vigna radiata</i>] [LTP]	1.E-30	3
21	38A10-R	lipid transfer protein precursor	P: defense response to fungus P: lipid transport P: defense response to Gram-positive bacterium F: lipid binding F: transporter activity	0.75	5.E-03	4.39	-2.08	422	X	ABF06565	non-specific lipid transfer-like protein [<i>Prosopis juliflora</i>]	2.E-16	0
22	21F04-R	type iii chlorophyll a b-binding protein	P: photosynthesis, light harvesting C: photosystem II F: magnesium ion binding P: protein-chromophore linkage F: chlorophyll binding C: integral to membrane C: photosystem I C: chloroplast thylakoid membrane C: mitochondrion	0.46	2.E-02	2.44	-1.67	492	X	1609235A	chlorophyll a/b binding protein 8 [<i>Solanum lycopersicum</i>]	1.E-61	1
23	42G12-R	---	---	0.43	2.E-01	-0.05	-3.2	505			No significant similarity		0
24	16F09-R	---	---	0.30	3.E-03	5.15	-0.48	521	N	EU196765	23S chloroplast rRNA [<i>P. vulgaris</i>]	0.00E+00	1
25	35F12-R	lipid transfer protein	F: lipid binding P: lipid transport	0.29	1.E-01	0.49	-2.78	523	X	Q43019	lipid-transfer protein 3 [<i>Prunus dulcis</i>]	2.00E-31	0

26	15F11-R	---	---	0.19	2.E-01	0.09	2.99	620	N	AF479110	26S ribosomal RNA [<i>M. sativa</i>]	5.E-176	1
27	24B10-R	pg1 protein	C: chloroplast	0.18	3.E-01	-0.4	-2.82	569	N	EU196765	16S chloroplast rRNA [<i>P. vulgaris</i>]	0.E+00	5
28	36A11-R	carbonic anhydrase	F: zinc ion binding C: chloroplast stroma F: carbonate dehydratase activity P: carbon utilization	0.04	8.E-01	-1.5	-2.39	611	X	AAD27876	carbonic anhydrase [<i>V. radiata</i>]	1.E-100	0
29	43B08-R	---	---	-0.05	7.E-01	-1.4	-0.69	144			No significant similarity		0
30	36A10-R	---	---	-0.09	4.E-01	-1.1	-4.31	766	X	AAG13810	RNA-binding protein Virp1a [<i>S. lycopersicum</i>]	7.E-49	1
31	18C04-R	signal recognition particle 54 kda subunit	F: mRNA binding P: SRP-dependent cotranslational protein targeting to membrane, signal sequence recognition F: GTP binding F: protein binding C: signal recognition particle, endoplasmic reticulum targeting F: nucleoside-triphosphatase activity F: 7S RNA binding	-0.10	3.E-01	-0.5	-2.02	305	X	P49972	Signal recognition particle SRP54 [<i>S. lycopersicum</i>]	5.E-23	0
32	38E10-R	protein	F: protein binding	-0.10	3.E-01	-0.6	-2.53	254	X	NP_190638	leucine-rich repeat family protein [<i>A. thaliana</i>]	2.E-26	0
33	16B07-R	aldo keto reductase	P: oxidation reduction F: oxidoreductase activity C: plastid	-0.11	2.E-01	-0.1	-3.65	723	X	NP_565656	aldo/keto reductase family protein [<i>A. thaliana</i>]	1.E-109	0
34	21H08-R	---	---	-0.13	5.E-01	-1.1	-2.48	746	X	NP_568178	proline-rich family protein [<i>A. thaliana</i>]	2.E-23	0
35	43E12-R	prolyl endopeptidase	P: proteolysis F: serine-type endopeptidase activity	-0.13	3.E-01	-0.6	-0.28	147	X	AAL86330	prolyl endopeptidase [<i>A. thaliana</i>]	1.E-13	0
36	21D09-R	at1g06530-like protein	C: plastid	-0.14	1.E-01	0.3	-3.77	437	X	ABH03547	ubiquitin-interacting factor 7 [<i>A. thaliana</i>]	2.E-14	0
37	24G10-R	unknown [Glycine max]	P: biosynthetic process F: transferase activity	-0.16	1.E-01	0.6	-1.97	323	X	Q9SSU8	Phytoene synthase, chloroplastic [<i>Daucus carota</i>]	3.E-02	0
38	43G10-R	cell elongation protein	F: FAD binding F: oxidoreductase activity F: metalloproteinase activity F: zinc ion binding	-0.16	7.E-02	1.0	-0.36	115	X	AAK15493	brassinosteroid biosynthetic protein LKB [<i>P. sativum</i>]	3.E-13	0
39	37B02-R	---	---	-0.34	2.E-02	2.7	-0.82	541	N	EU196765	23S chloroplast rRNA [<i>P. vulgaris</i>]	0.E+00	0
40	38A04-R	---	---	-0.40	9.E-04	6.8	-0.16	695	N	AF479105	26S ribosomal RNA [<i>Juglans nigra</i>] [26S]	0.E+00	5

[#]ER3 for reverse library calculated as $\log_2(\text{control/drought stressed})$

Each redundant partner *Group* (column 1) is represented by a *Representative clone ID* (column 2). By default SSHdb selects the clone that is the longest sequence from the group. Columns 3-4 give the Blast2GO consensus annotation and GO terms. Columns 5-8 give the regulation (*ER3*), statistical support for the *ER3* value (*adj.P.Val* and *B*) and abundance (*invER2*) for each group calculated by SSHscreen. Columns 9-11 are annotations added by SSHdb for each group: *Length* is the length of the representative clone sequence after vector and adaptor fragments are removed, *Priority* indicates whether the BLASTN or BLASTX hit was selected (this can be manually curated), *BLAST* Accession number (*AccNr*), Hit Definition (*HitDef*) and E-value (*Eval*) are for the selected BLAST hit (from the top 10 hits) from either BLASTX/BLASTN results, *RedPartners* are the number of redundant partner clones in that group (grouped by SSHdb after performing local BLAST searches with a E-value cut off of $1E^{-10}$)