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Identification of drought-inducible regulatory factors in *Lablab purpureus* by a comparative genomic approach

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Table S1. Measurements of drought indicators in roots of MEIDOU 2012 and NANHUI 23 seedlings.

Dehydration Time	Parameter	Measurements				Relative Change	
		M2012		N23		M2012	N23
		WW	WS	WW	WS	(WS-WW)/WW*100	
2d	MDA	10.72±1.07	13.04±1.63	9.18±2.15	15.77±4.97	21.64	71.79
	Free proline	56.62±7.25	70.72±8.8	37.49±1.95	40.16±9.93	24.90	7.12
	Root activity	51.22±4.46	50.29±6.21	55.24±5.41	50.84±3.97	-1.82	-7.97
4d	MDA	12.72±3.99	20.62±4.92	12.31±0.71	21.49±2.51	62.11	74.57
	Free proline	29.32±4.37	42.31±2.39	38.86±3.97	43.22±3.4	44.30	11.22
	Root activity	56.24±5.49	47.04±3.47	55.14±5.33	44.08±1.71	-16.36	-20.06
6d	MDA	14.27±2.93	21.7±5.54	14.15±3.83	30.76±3.44	52.07	117.39
	Free proline	35.09±1.35	66.21±4.17	100.66±1.69	123.26±2.56	88.69	22.45
	Root activity	54.66±4.8	42.74±3.36	52.84±0.84	38.64±1.59	-21.81	-26.87
8d	MDA	10.75±8.35	25.89±5.25	10.61±2.18	40.52±2.61	140.84	281.90
	Free proline	67.25±9.97	156.71±8.31	44.49±9.85	94.82±3.03	133.03	113.13
	Root activity	56.7±5.16	37.68±1.8	53.33±1.97	23.33±3.67	-33.54	-56.25
10d	MDA	15.66±1.21	31.43±7.8	13.05±0.25	43.65±3.29	100.70	234.48
	Free proline	20.75±6.07	70.44±1.54	28.79±0.93	67.83±2.51	239.47	135.60
	Root activity	51.57±5.49	33.5±2.69	51.62±7.39	15.6±4.49	-35.04	-69.78

* WS: water-stressed; WW: well-watered; M2012: MEIDOU 2012; N23: NANHUI 23.

Measurement units: MDA (mmol/g); Free proline (µg/g); Root activity µg/(g·h).

Table S2. KOG categorization of drought-induced *Lablab* root-related unigenes.

Num	KOG	Query	Subject	Keyword	TAIR root gene annotation
1	KOG0027	Contig365	Phvu1.010G085100.1	EF hand calcium-binding protein family	yes
2	KOG0048	M0802-200_M08022879_BAI1-880_M13-_H02	Medtr1g043080.1	myb domain protein 15	yes
3	KOG0055	Contig_259	Phvu1.003G122600.1	ATP binding cassette subfamily B4	yes
4	KOG0087	Contig_605	Glyma12g06280.2	RAB GTPase homolog A2B	yes
			Phvu1.011G061100.1	RAB GTPase homolog A2B	yes
			Medtr3g069510.1	RAB GTPase homolog A2B	yes
5	KOG0166	M0802-200_M08022308_BAI1-309_M13-_E03	Glyma10g29000.1	importin alpha isoform 1	yes
6	KOG0198	Contig77	Glyma19g42340.1	NPK1-related protein kinase 1	yes
			Phvu1.006G091500.1	NPK1-related protein kinase 1	yes
		M0802-200_M08022298_BAI1-299_M13-_C02	Medtr7g113490.1	NPK1-related protein kinase 1	yes
		M0802-200_M08022303_BAI1-304_M13-_H02	Medtr7g113490.1	NPK1-related protein kinase 1	yes
		M0813-201_M08132167_BAI1-1166_M13-_F09	Medtr7g113490.1	NPK1-related protein kinase 1	yes
		M0813-201_M08133444_BAI1-2443_M13-_C01	Medtr7g113490.1	NPK1-related protein kinase 1	yes
7	KOG0206	Contig_44_1	Glyma18g16990.2	aminophospholipid ATPase 3	yes
			Phvu1.003G072200.1	aminophospholipid ATPase 3	yes
			Medtr8g062150.1	aminophospholipid ATPase 3	yes
8	KOG0223	Contig346	Glyma01g41670.1	tonoplast intrinsic protein 2;3	yes
			Phvu1.002G057500.1	tonoplast intrinsic protein 2;3	yes
		M0813-201_M08132835_BAI1-1834_M13-_B09	Phvu1.002G057500.1	tonoplast intrinsic protein 2;3	yes
		M0802-200_M08022683_BAI1-684_M13-_D02	Medtr5g012810.1	tonoplast intrinsic protein 2;3	yes
		M0813-201_M08133217_BAI1-2216_M13-_H08	Medtr5g012810.1	tonoplast intrinsic protein 2;3	yes
9	KOG0232	Contig_538	Medtr8g076150.1	ATPase, F0/V0 complex, subunit C protein	yes
	KOG0246	M0813-201_M08132802_BAI1-1801_M13-_A05	Glyma07g37630.4	P-loop containing nucleoside triphosphate hydrolases superfamily protein	yes

		M0813-201_M08132802_BAI1-1801_M13-_A05	Medtr4g119980.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein	yes
11	KOG0255	Contig_59	Glyma16g34220.2	organic cation/carnitine transporter1	yes
			Phvul.004G142000.1	organic cation/carnitine transporter1	yes
12	KOG0384	M0813-201_M08132523_BAI1-1522_M13-_B06	Glyma06g06720.1	chromatin remodeling factor CHD3 (PICKLE)	yes
			Phvul.009G088700.1	chromatin remodeling factor CHD3 (PICKLE)	yes
			Medtr3g106210.1	chromatin remodeling factor CHD3 (PICKLE)	yes
13	KOG0417	Contig81	Glyma06g33840.1	ubiquitin-conjugating enzyme 35	yes
		M0802-200_M08022590_BAI1-591_M13-_G02	Glyma13g34600.2	ubiquitin-conjugating enzyme 35	yes
		Contig81	Phvul.011G160100.2	ubiquitin-conjugating enzyme 35	yes
		M0802-200_M08022590_BAI1-591_M13-_G02	Phvul.005G066900.1	ubiquitin-conjugating enzyme 35	yes
14	KOG0446	Contig148	Glyma06g36650.1	Dynamamin related protein 5A	yes
			Phvul.011G158800.1	Dynamamin related protein 5A	yes
15	KOG0483	Contig_604_1	Glyma06g09100.1	homeobox gene 8	yes
			Phvul.009G110500.1	homeobox gene 8	yes
16	KOG0565	M0802-200_M08022165_BAI1-166_M13-_F09	Medtr4g098850.1	myo-inositol polyphosphate 5-phosphatase 2	yes
			Medtr4g098850.1	myo-inositol polyphosphate 5-phosphatase 2	yes
			Medtr4g098850.1	myo-inositol polyphosphate 5-phosphatase 2	yes
17	KOG0658	Contig_49	Glyma04g06760.1	Protein kinase superfamily protein	yes
18	KOG0660	Contig_238	Medtr7g078690.1	MAP kinase 4	yes
19	KOG0683	Contig_271_1	Glyma10g06820.1	glutamate-ammonia ligases;catalytics;glutamate-ammonia ligases	yes
			Phvul.007G152500.1	glutamate-ammonia ligases;catalytics;glutamate-ammonia ligases	yes
			Medtr3g035970.1	glutamate-ammonia ligases;catalytics;glutamate-ammonia ligases	yes
20	KOG0687	Contig_331_1	Glyma17g13640.1	26S proteasome, regulatory subunit Rpn7;Proteasome component (PCI) domain	yes
		M0813-201_M08132304_BAI1-1303_M13-_G02	Glyma17g13640.1	26S proteasome, regulatory subunit Rpn7;Proteasome component (PCI) domain	yes
		Contig_331_1	Phvul.003G208200.1	26S proteasome, regulatory subunit Rpn7;Proteasome component (PCI) domain	yes

		M0813-201_M08132304_BAI1-1303_M13-_G02	Phvul.003G208200.1	26S proteasome, regulatory subunit Rpn7;Proteasome component (PCI) domain	yes
		Contig_331_1	Medtr4g104080.1	26S proteasome, regulatory subunit Rpn7;Proteasome component (PCI) domain	yes
		M0813-201_M08132304_BAI1-1303_M13-_G02	Medtr4g104080.1	26S proteasome, regulatory subunit Rpn7;Proteasome component (PCI) domain	yes
21	KOG0713	M0813-201_M08132986_BAI1-1985_M13-_A04	Glyma10g41860.1	Chaperone DnaJ-domain superfamily protein	yes
			Phvul.007G029600.1	Chaperone DnaJ-domain superfamily protein	yes
			Medtr1g110310.1	Chaperone DnaJ-domain superfamily protein	yes
22	KOG0725	Contig236	Glyma17g01300.1	indole-3-butyric acid response 1	yes
		Contig236	Phvul.003G082700.1	indole-3-butyric acid response 1	yes
		M0802-200_M08022387_BAI1-388_M13-_D01	Medtr4g132850.1	indole-3-butyric acid response 1	yes
		M0813-201_M08132094_BAI1-1093_M13-_E12	Medtr4g132850.1	indole-3-butyric acid response 1	yes
23	KOG0749	M0813-201_M08132699_BAI1-1698_M13-_B04	Phvul.002G329900.2	endoplasmic reticulum-adenine nucleotide transporter 1	yes
24	KOG0841	Contig_319	Glyma13g36690.1	general regulatory factor 9	yes
25	KOG0903	Contig_424	Glyma04g39150.2	phosphatidylinositol 4-OH kinase beta 1	yes
			Glyma04g39150.2	phosphatidylinositol 4-OH kinase beta 1	yes
			Phvul.009G149800.1	phosphatidylinositol 4-OH kinase beta 1	yes
			Phvul.009G149800.1	phosphatidylinositol 4-OH kinase beta 1	yes
26	KOG1036	M0802-200_M08022199_BAI1-200_M13-_H01	Glyma20g26960.1	Transducin/WD40 repeat-like superfamily protein (BUB3)	yes
			Phvul.007G044700.1	Transducin/WD40 repeat-like superfamily protein (BUB3)	yes
27	KOG1169	Contig_398_1	Phvul.003G149800.1	diacylglycerol kinase 7	yes
28	KOG1187	Contig221	Glyma02g05020.2	protein kinase family protein	yes
		Contig325	Glyma05g33700.1	receptor-like kinase 1	yes
		Contig_280	Glyma13g32280.2	S-locus lectin protein kinase family protein	yes
		M0813-201_M08133233_BAI1-2232_M13-_H10	Glyma17g16780.1	Leucine-rich receptor-like protein kinase family protein	yes
		M0813-201_M08133241_BAI1-2240_M13-_H11	Glyma04g09370.2	Leucine-rich repeat transmembrane protein kinase family protein	yes
		Contig325	Phvul.002G331400.1	receptor-like kinase 1	yes

		M0813-201_M08133241_BAI1-2240_M13-_H11	Phvul.009G114400.1	Leucine-rich repeat transmembrane protein kinase family protein	yes
		M0813-201_M08133233_BAI1-2232_M13-_H10	Phvul.003G231400.1	Leucine-rich receptor-like protein kinase family protein	yes
		M0802-200_M08022673_BAI1-674_M13-_B01	Medtr8g107470.1	receptor-like kinase 1	yes
		M0813-201_M08133584_BAI1-2583_M13-_G03	Medtr8g107470.1	receptor-like kinase 1	yes
		M0813-201_M08133233_BAI1-2232_M13-_H10	Medtr5g014700.1	Leucine-rich receptor-like protein kinase family protein	yes
		Contig_419_1	Medtr8g074920.1	protein kinase family protein	yes
		M0813-201_M08133245_BAI1-2244_M13-_D12	Medtr8g074920.1	protein kinase family protein	yes
29	KOG1192	M0802-200_M08022261_BAI1-262_M13-_F09	Glyma01g02670.1	UDP-glucosyl transferase 85A3	yes
		M0813-201_M08132822_BAI1-1821_M13-_E07	Glyma14g35160.1	UDP-glucosyl transferase 85A2	yes
		M0813-201_M08132822_BAI1-1821_M13-_E07	Phvul.008G174700.1	UDP-glucosyl transferase 85A2	yes
30	KOG1252	M0813-201_M08132407_BAI1-1406_M13-_F03	Glyma19g43150.1	O-acetylserine (thiol) lyase (OAS-TL) isoform A1	yes
			Phvul.006G099100.1	O-acetylserine (thiol) lyase (OAS-TL) isoform A1	yes
			Medtr1g081610.1	O-acetylserine (thiol) lyase (OAS-TL) isoform A1	yes
31	KOG1254	M0802-200_M08022205_BAI1-206_M13-_F02	Glyma02g04120.1	ATP-citrate lyase A-1	yes
		M0802-200_M08022427_BAI1-428_M13-_D06	Glyma02g04120.1	ATP-citrate lyase A-1	yes
		Contig_515	Phvul.002G064600.1	ATP-citrate lyase A-1	yes
		M0802-200_M08022205_BAI1-206_M13-_F02	Phvul.002G064600.1	ATP-citrate lyase A-1	yes
		M0802-200_M08022427_BAI1-428_M13-_D06	Phvul.002G064600.1	ATP-citrate lyase A-1	yes
		M0802-200_M08022427_BAI1-428_M13-_D06	Medtr5g033920.1	ATP-citrate lyase A-1	yes
32	KOG1291	M0813-201_M08132880_BAI1-1879_M13-_G02	Glyma07g02680.2	natural resistance-associated macrophage protein 1	yes
33	KOG1370	Contig_571	Glyma05g28480.1	S-adenosyl-L-homocysteine hydrolase	yes
			Phvul.003G051200.1	S-adenosyl-L-homocysteine hydrolase	yes
			Medtr8g083090.1	S-adenosyl-L-homocysteine hydrolase	yes
34	KOG1375	Contig_205	Glyma10g37960.1	tubulin beta 8	yes
		Contig_260	Glyma06g02650.1	tubulin beta-1 chain	yes

		Contig_260	Phvul.009G017300.1	tubulin beta-1 chain	yes
		Contig_269	Phvul.009G017300.1	tubulin beta-1 chain	yes
		Contig_205	Phvul.007G070800.1	tubulin beta 8	yes
		Contig_205	Medtr7g089120.1	beta-6 tubulin	yes
		Contig_260	Medtr3g113970.1	tubulin beta-1 chain	yes
35	KOG1395	Contig_257_1	Glyma18g12090.1	tryptophan synthase beta-subunit 2	yes
			Phvul.006G040500.1	tryptophan synthase beta-subunit 2	yes
			Medtr3g051120.1	tryptophan synthase beta-subunit 2	yes
36	KOG1474	Contig_17_1	Glyma15g06570.1	global transcription factor group E4	yes
37	KOG1506	M0802-200_M08022676_BAI1-677_M13-_E01	Phvul.001G216700.1	S-adenosylmethionine synthetase 1	yes
38	KOG1530	Contig222	Glyma12g02040.1	Rhodanese/Cell cycle control phosphatase superfamily protein	yes
			Phvul.011G020400.1	Rhodanese/Cell cycle control phosphatase superfamily protein	yes
		M0802-200_M08022457_BAI1-458_M13-_B10	Medtr2g017630.1	Rhodanese/Cell cycle control phosphatase superfamily protein	yes
		M0813-201_M08133240_BAI1-2239_M13-_G11	Medtr2g017630.1	Rhodanese/Cell cycle control phosphatase superfamily protein	yes
39	KOG1619	Contig145	Glyma10g38070.1	Cytochrome b561/ferric reductase transmembrane protein family	yes
			Phvul.007G069600.1	Cytochrome b561/ferric reductase transmembrane protein family	yes
40	KOG1643	Contig245	Glyma03g34300.1	triosephosphate isomerase	yes
			Phvul.001G181000.1	triosephosphate isomerase	yes
41	KOG1646	Contig_255_1	Glyma13g31130.1	Ribosomal protein S6e	yes
			Phvul.006G184300.1	Ribosomal protein S6e	yes
			Medtr2g014030.1	Ribosomal protein S6e	yes
42	KOG1684	M0813-201_M08132538_BAI1-1537_M13-_A08	Glyma08g42070.1	ATP-dependent caseinolytic (Clp) protease/crotonase family protein	yes
43	KOG1724	Contig_47_1	Glyma02g05120.1	S phase kinase-associated protein 1	yes
			Phvul.003G265900.1	S phase kinase-associated protein 1	yes
44	KOG1778	M0813-201_M08132541_BAI1-1540_M13-_D08	Glyma08g24290.1	histone acetyltransferase of the CBP family 12	yes

		M0813-201_M08132541_BAI1-1540_M13-_D08	Phvul.010G165900.1	histone acetyltransferase of the CBP family 12	yes
45	KOG1909	Contig_66	Glyma20g28130.3	RAN GTPase activating protein 2	yes
			Phvul.007G054100.1	RAN GTPase activating protein 2	yes
			Medtr1g105040.1	RAN GTPase activating protein 2	yes
46	KOG2344	M0802-200_M08022701_BAI1-702_M13-_F04	Glyma07g04600.2	exocyst subunit exo70 family protein D1	yes
		M0813-201_M08132397_BAI1-1396_M13-_D02	Glyma10g23810.1	exocyst subunit exo70 family protein A1	yes
		M0802-200_M08022701_BAI1-702_M13-_F04	Phvul.010G127600.1	exocyst subunit exo70 family protein D1	yes
		M0813-201_M08132397_BAI1-1396_M13-_D02	Phvul.007G234500.1	exocyst subunit exo70 family protein A1	yes
		M0813-201_M08132397_BAI1-1396_M13-_D02	Medtr1g090620.1	exocyst subunit exo70 family protein A1	yes
47	KOG2533	Contig242	Phvul.011G083500.1	nitrate transporter 2:1	yes
		M0802-200_M08022074_BAI-75_M13+_C10	Phvul.011G083500.1	nitrate transporter 2:1	yes
		M0802-200_M08022900_BAI1-901_M13-_E05	Phvul.011G083500.1	nitrate transporter 2:1	yes
		M0813-201_M08133175_BAI1-2174_M13-_F03	Phvul.011G083500.1	nitrate transporter 2:1	yes
		M0813-201_M08133497_BAI1-2496_M13-_H07	Phvul.011G083500.1	nitrate transporter 2:1	yes
		M0802-200_M08022380_BAI1-381_M13-_E12	Medtr2g085510.1	nitrate transporter 2:1	yes
		M0802-200_M08022900_BAI1-901_M13-_E05	Medtr2g085510.1	nitrate transporter 2:1	yes
		M0813-201_M08133175_BAI1-2174_M13-_F03	Medtr2g085510.1	nitrate transporter 2:1	yes
		M0813-201_M08133432_BAI1-2431_M13-_G11	Medtr2g085510.1	nitrate transporter 2:1	yes
		M0813-201_M08133497_BAI1-2496_M13-_H07	AC233663_23.1	nitrate transporter 2:1	yes
48	KOG2615	M0813-201_M08132221_BAI1-1220_M13-_D04	Glyma13g25620.1	zinc induced facilitator-like 1	yes
			Phvul.011G189900.1	zinc induced facilitator-like 1	yes
49	KOG2628	Contig_498_1	Glyma16g34480.2	Isoprenylcysteine carboxyl methyltransferase (ICMT) family	yes
		Contig_498_1	Phvul.004G144800.1	Isoprenylcysteine carboxyl methyltransferase (ICMT) family	yes
50	KOG2662	M0813-201_M08133501_BAI1-2500_M13-_D08	Glyma15g00510.1	magnesium transporter 2	yes
			Phvul.005G183100.1	magnesium transporter 2	yes

		M0813-201_M08133501_BAI1-2500_M13-_D08	AC233655_24.1	magnesium transporter 2	yes
51	KOG2666	M0813-201_M08132886_BAI1-1885_M13-_E03	Glyma13g06050.1	UDP-glucose 6-dehydrogenase family protein	yes
			Phvul.004G034500.1	UDP-glucose 6-dehydrogenase family protein	yes
			Medtr7g012950.1	UDP-glucose 6-dehydrogenase family protein	yes
52	KOG2868	Contig_157_1	Glyma19g38280.1	decapping 1	yes
			Phvul.001G192600.1	decapping 1	yes
53	KOG3151	M0802-200_M08022576_BAI1-577_M13-_A01	Glyma08g08690.1	regulatory particle non-ATPase 12A	yes
			Phvul.002G197600.1	regulatory particle non-ATPase 12A	yes
			Medtr1g016750.1	regulatory particle non-ATPase 12A	yes
54	KOG3205	Contig_152	Glyma19g34980.1	Immunoglobulin E-set superfamily protein	yes
			Phvul.001G163100.1	Immunoglobulin E-set superfamily protein	yes
55	KOG3786	M0813-201_M08132153_BAI1-1152_M13-_H07	Glyma11g01020.1	PLANT HOMOLOGOUS TO PARAFIBROMIN	yes
			Phvul.002G042300.1	PLANT HOMOLOGOUS TO PARAFIBROMIN	yes
56	KOG4172	M0813-201_M08133439_BAI1-2438_M13-_F12	Glyma05g24230.6	RING domain ligase2	yes
			Phvul.004G061800.2	RING domain ligase1	yes
			Medtr6g021730.1	RING domain ligase2	yes
57	KOG4536	Contig_262	Glyma05g00490.2	Protein of unknown function, transmembrane-40	yes
		Contig_374	Glyma20g37380.1	Protein of unknown function, transmembrane-40	yes
		M0813-201_M08132554_BAI1-1553_M13-_A10	Glyma05g00490.2	Protein of unknown function, transmembrane-40	yes
		Contig_262	Phvul.003G185400.1	Protein of unknown function, transmembrane-40	yes
		Contig_374	Phvul.007G184000.1	Protein of unknown function, transmembrane-40	yes
		M0813-201_M08132554_BAI1-1553_M13-_A10	Phvul.003G185400.1	Protein of unknown function, transmembrane-40	yes
58	KOG4642	Contig_321_1	Phvul.008G222100.1	plant U-box 13	yes
59	KOG4742	M0802-200_M08022572_BAI1-573_M13-_E12	Glyma11g13270.2	homolog of carrot EP3-3 chitinase	yes
			Phvul.011G051500.1	homolog of carrot EP3-3 chitinase	yes