

Table S1. Sequences of the primers used in this study.

Gene name	Primer direction	Primer sequence
For qRT-PCR analysis		
<i>CvNCED3</i>	Forward	GCTTCTGCTTCCACCTCTGG
	Reverse	GGTCCTCGGACTCGTTGAAG
<i>CvAREB1</i>	Forward	CTTTGGGGAATGGTTTGGTG
	Reverse	CGGCGACAGAGATGACATTG
<i>MGD1</i>	Forward	CTGGGGCTGCTGTTTCTTTG
	Reverse	AATGCGAGGAAGGAGATGGA
<i>MGD2</i>	Forward	ACTACGTGCCGGTGTACGTG
	Reverse	AGCGACACCGACATCACGA
<i>MGD3</i>	Forward	GTGTTCTGGGGCATCGATCT
	Reverse	AGGTGCTTCTGCTGCTGCTC
<i>DREB2A</i>	Forward	GACCTAAATGGCGACGATGT
	Reverse	TCGAGCTGAAACGGAGGTAT
<i>RD29A</i>	Forward	TGGATCTGAAGAACGAATCTGATATC
	Reverse	GGTCTTCCCTTCGCCAGAA
<i>NCED3</i>	Forward	CGAGCCGTGGCCTAAAGTCT
	Reverse	GCTCCGATGAATGTACCGTGAA
<i>GAPDH</i>	Forward	CTGCCCCAAGCAAAGATGCG
	Reverse	TTGGCAAGAGGAGCAAGGCA
For generation of transgenic plants		
<i>CvNCED3</i>	Forward	CACCATGGGGAGACCAACGGATTCTCAC
	Reverse	TCAGGCCTGGGCCTGGAGCT
<i>CvAREB1</i>	Forward	CACCATGGAATTTCCCGGCGGGA
	Reverse	TTACCAAGGACCTGTTAGTGT
<i>MGD1</i>	Forward	CACCATGGTTGTTGCCTGGGGCTGC
	Reverse	TCAAAGCGGCGCGGTGGCGGCGAACCA
<i>MGD2</i>	Forward	CACCATGGCTTCACGGGCCGCGGCG
	Reverse	TTAGGCATTGTTGTTGTTGCTCTTC
<i>MGD3</i>	Forward	CACCATGTCTGGCGGCGTCGGCCCGA
	Reverse	CTACGAATCCTTCTCCCTTCTTCCC

Table S2. Summary of raw and clean read statistics from *Chloris virgata* after Illumina sequencing.

Statistics	Number of sequences
Number of raw sequence reads	1,307,170,602
Number of raw sequence reads (trimmed)	1,281,678,077
Number of contigs	256,330 (N50-2,366 bp)
Number of super-contigs	46,628 (N50-2,723 bp)
Number of clusters	31,149 (N50-2,681 bp)
Number of contigs with predicted ORFs	25,469
Number of ORFs homologous to protein coding genes in <i>O. sativa</i>	22,683 (89%)
Number of ORFs homologous to protein coding genes in <i>A. thaliana</i>	21,501 (84%)

Table S3. The top 60 most significantly upregulated genes in *Chloris virgata* after 3 hr of dehydration. The *MGD1*, *MGD2*, and *MGD3* genes are highlighted in bold letters and underlined with three asterisks, and the selected genes as preliminary *MGD* candidate genes that transformed to *Arabidopsis* are highlighted in bold letters with one asterisk.

No	<i>Chloris virgata</i>	Log2 fold change	Adjusted p-value	<i>Arabidopsis thaliana</i>		<i>Oryza sativa</i>	
				Gene name	Gene code	Gene name	Gene code
1	ChlorisST26646	21.80	1.17E-05	Subtilase family protein	AT5G44530.1	Peptidase S8	Os01t0769200-01
2	ChlorisST44424	20.24	6.30E-05	Polynucleotidyl transferase	AT2G26970.1	Exonuclease domain containing protein	Os02t0465500-01
3	ChlorisST43350	19.91	1.39E-06	Unknown protein	None	Unknown protein	Os06t0329300-01
4	ChlorisST7790	19.67	2.11E-06	DNA primases	AT5G52800.3	Similar to DNA primase	Os07t0467900-01
5	ChlorisST41608	13.85	1.51E-17	RD29B	AT5G52300.1	Unknown protein	Os10t0505900-01
6	ChlorisST20239	12.25	1.24E-19	RAB18	AT5G66400.1	Similar to RAB16B	Os11t0454200-01
7	ChlorisST41155	11.63	1.72E-10	LEA like protein	AT1G72100.1	Similar to H0823A09.7	Os04t0434400-01
8	ChlorisST298	11.49	7.50E-37	Unknown protein	None	Similar to DHN1	Os11t0451700-00
9	ChlorisST21981	11.02	1.02E-14	Unknown protein	None	Similar to UFG2	Os03t0723400-01
10	ChlorisST1627	10.64	5.49E-29	RAB18	AT5G66400.1	Similar to RAB16B	Os11t0454200-01
11	ChlorisST2497	10.64	2.53E-29	RAB18	AT5G66400.1	Similar to RAB16B	Os11t0454200-01
12	ChlorisST25864	10.41	6.21E-10	SRP30	AT1G09140.1	Similar to SF2	Os05t0364600-01
13	ChlorisST22375	10.37	1.29E-41	LEA like protein	AT3G53040.1	LEA like protein	Os03t0322900-01
* 14	ChlorisST21980	10.24	2.56E-17	Unknown protein	AT5G66780.1	Similar to UFG2	Os03t0723400-01
*** 15	ChlorisST36889	10.13	1.13E-19	Unknown protein	AT5G52420.1	Unknown protein	Os10t0548100-01
16	ChlorisST35850	9.95	6.29E-11	HMT2	AT3G63250.1	Similar to Homocysteine S-methyltransferase 4	Os01t0772900-02
17	ChlorisST10941	9.92	2.27E-10	LEA like protein	AT3G53040.1	LEA like protein	Os03t0322900-01
18	ChlorisST445	9.81	3.78E-33	COR47	AT1G20440.1	Dehydrin like protein	Os11t0454200-01
*** 19	ChlorisST30368	9.73	3.00E-08	Unknown protein	AT5G45310.1	Unknown protein	Os01t0962100-01
20	ChlorisST9073	9.35	9.44E-33	LEA like protein	AT3G15670.1	LEA like protein	Os01t0705200-01
21	ChlorisST41397	9.25	1.45E-18	LEA14	AT1G01470.1	LEA14A	Os01t0225600-01
22	ChlorisST7108	9.22	1.32E-16	LEA like protein	AT1G52690.1	LEA like protein	Os05t0542500-02
23	ChlorisST17296	9.14	1.40E-07	EM1	AT3G51810.1	Similar to embryogenic abundant protein	Os05t0349800-01
24	ChlorisST1991	9.05	2.33E-28	Unknown protein	None	Similar to DHN1	Os11t0451700-00
* 25	ChlorisST11350	8.89	8.57E-14	Unknown protein	None	Unknown protein	None
26	ChlorisST34038	8.79	3.38E-06	DNA repair ATPase-related	AT2G24420.1	Similar to OSIGBa011313.10	Os04t0607150-00
* 27	ChlorisST41141	8.74	1.05E-07	Unknown protein	None	Unknown protein	None
28	ChlorisST8031	8.69	1.44E-07	ATOEP16-2 like protein	AT4G16160.2	Mitochondrial import inner membrane translocase	Os03t0305600-01
29	ChlorisST3820	8.60	9.56E-26	LEA76	AT3G15670.1	LEA like protein	Os05t0542500-02
30	ChlorisST18549	8.60	1.52E-12	transcription activator related	AT5G42290.1	Unknown protein	Os03t0133100-01
31	ChlorisST32738	8.56	0.00284	KJC1	AT1G74910.1	Similar to ADP-glucose pyrophosphorylase	Os03t0208900-01
32	ChlorisST33189	8.53	2.03E-06	bZIP62	AT1G19490.1	Similar to DNA-binding factor of bZIP	Os11t0154900-01
33	ChlorisST22299	8.48	2.14E-15	XERO1	AT3G50980.1	Dehydrin like protein	Os11t0454200-01
34	ChlorisST41118	8.39	0.00313	Unknown protein	AT1G16290.1	Unknown protein	Os02t0170900-02
35	ChlorisST32077	8.30	1.59E-06	Unknown protein	AT4G31830.1	Unknown protein	Os09t0127700-01
36	ChlorisST9860	8.26	5.73E-18	HB7	AT2G46680.1	HD-ZIP protein	Os02t0649300-01
37	ChlorisST19177	8.25	1.00E-08	Unknown protein	AT3G14880.1	Similar to tumor-related like protein	Os05t0560200-00
38	ChlorisST39682	8.16	2.10E-21	Unknown protein	None	Unknown protein	None
* 39	ChlorisST5845	8.11	3.35E-12	RAB28	AT3G22490.1	SMP domain containing protein	Os06t0341300-01
40	ChlorisST8032	8.10	1.87E-07	OEP16-2	AT4G16160.2	Similar to stress-inducible membrane pore protein	Os01t0303300-01
* 41	ChlorisST36430	8.06	8.12E-07	AWPM-19 family like protein	AT1G04560.1	AWPM-19 family like protein	Os07t0422100-01
42	ChlorisST739	8.05	4.42E-05	GSH1	AT4G23100.1	Glutamate-cysteine ligase	Os07t0462000-01
43	ChlorisST8017	8.00	4.45E-37	EIDL3	AT3G63060.1	Similar to ZGT factor	Os05t0494600-01
* 44	ChlorisST14249	7.92	9.24E-24	ABF4	AT3G19290.3	Similar to ABF4	Os02t0766700-01
45	ChlorisST28822	7.85	9.75E-18	NCED9	AT1G78390.1	Similar to NCED protein	Os03t0645900-01
46	ChlorisST6591	7.77	0.00172	NHX3	AT5G55470.1	Similar to Sodium/hydrogen exchanger	Os06t0318500-00
47	ChlorisST21571	7.70	1.22E-11	HAI3	AT2G29380.1	Similar to PP2C family protein	Os01t0656200-01
48	ChlorisST1019	7.66	8.64E-06	ALD1	AT2G13810.1	Similar to AGD2	Os03t0195100-01
49	ChlorisST10730	7.58	5.10E-29	Unknown protein	None	Unknown protein	Os03t0623100-01
*** 50	ChlorisST6804	7.55	1.93E-14	Unknown protein	AT5G07330.1	Unknown protein	Os11t0533400-01
51	ChlorisST41500	7.44	0.00277	Unknown protein	None	Unknown protein	None
52	ChlorisST42836	7.44	3.37E-06	Unknown protein	None	Unknown protein	Os11t0302800-01
53	ChlorisST23040	7.41	1.76E-05	Unknown protein	None	Unknown protein	Os03t0381500-01
54	ChlorisST4239	7.39	2.23E-19	EIDL3	AT3G63060.1	Similar to Circadian clock coupling factor ZGT	Os01t0802600-00
55	ChlorisST17995c	7.37	1.40E-24	Unknown protein	AT4G21920.1	Unknown protein	Os07t0516400-00
56	ChlorisST42610	7.34	5.11E-15	FTSH6	AT5G15250.2	Similar to FTSH homolog 2	Os06t0669400-02
57	ChlorisST23147	7.30	0.00912	MYB79	AT4G13480.1	MYB domain containing protein	Os03t0142600-00
58	ChlorisST6868	7.29	3.36E-08	Unknown protein	None	Unknown protein	None
59	ChlorisST42624	7.18	1.49E-05	LEA18	AT2G35300.1	LEA like protein	Os06t0110200-01
60	ChlorisST11390	7.17	0.00054	FPS2	AT4G17190.1	Farnesyl pyrophosphate synthase	Os04t0657100-01
129	ChlorisST40659	4.11	2.19E-16	9-cis-epoxycarotenoid dioxygenase	AT1G78390.1	9-cis-epoxycarotenoid dioxygenase	Os03t0645900-01
564	ChlorisST30712	2.20	4.69E-08	ABA-responsive element binding protein	AT3G56850.1	AREB1	Os06t0211200-02

Table S4. The top 60 most significantly upregulated genes in *Chloris virgata* after 6 hr of dehydration. The *MGD1*, *MGD2*, and *MGD3* genes are highlighted in bold letters and underlined with three asterisks, and the selected genes as preliminary *MGD* candidate genes that transformed to *Arabidopsis* are highlighted in bold letters with one asterisk.

No	<i>Chloris virgata</i>	Log2 fold change	Adjusted p-value	<i>Arabidopsis thaliana</i>		<i>Oryza sativa</i>	
				Gene name	Gene code	Gene name	Gene code
1	ChlorisST7790	29.53	1.93E-14	DNA primases	AT5G52800.3	Similar to DNA primase	Os07t0467900-01
2	ChlorisST43350	29.40	2.20E-14	Unknown protein	None	Unknown protein	Os06t0329300-01
3	ChlorisST20256	24.02	5.01E-07	KOIN	AT5G58300.1	Protein kinase, core domain containing protein	Os03t0332900-01
4	ChlorisST30645	23.36	1.10E-06	TPS21	AT5G23960.1	Similar to Sesquiterpene cyclase	Os02t0458100-01
5	ChlorisST37000	23.23	1.29E-06	Nucleoside triphosphate hydrolases superfamily protein	AT1G16800.1	Similar to OSIGBa0076114.10 protein	Os04t0424200-00
6	ChlorisST18897	23.06	1.88E-09	AKS2	AT1G05805.1	Helix-loop-helix DNA-binding domain containing protein	Os01t0900800-01
7	ChlorisST44178	22.37	3.55E-06	Unknown protein	None	Unknown protein	Os03t0412900-00
8	ChlorisST298	15.97	4.71E-28	Unknown protein	None	Dehydrin like protein	Os11t0451700-00
9	ChlorisST41608	15.76	6.47E-23	RD29B	AT5G52300.1	Unknown protein	Os10t0505900-01
10	ChlorisST20239	14.61	4.78E-23	RAB18	AT5G66400.1	Dehydrin like protein	Os11t0454200-01
11	ChlorisST1991	13.96	8.78E-42	Unknown protein	None	Dehydrin like protein	Os11t0451700-00
12	ChlorisST1627	13.88	3.19E-34	RAB18	AT5G66400.1	Dehydrin like protein	Os11t0454200-01
13	ChlorisST23040	13.83	1.07E-09	Unknown protein	None	Unknown protein	Os03t0381500-01
14	ChlorisST41397	12.93	1.38E-25	LEA14	AT1G01470.1	LEA14	Os01t0225600-01
15	ChlorisST7108c	12.75	7.72E-29	LEA7	AT1G52690.1	LEA like protein	Os05t0542500-02
16	ChlorisST445c	12.73	2.77E-44	COR47	AT1G20440.1	Dehydrin like protein	Os11t0454200-01
17	ChlorisST2818	12.63	5.22E-09	Unknown protein	None	Similar to Helicase-like protein	Os04t0357300-01
18	ChlorisST43915	12.48	5.96E-17	PER1	AT1G48130.1	Cys-peroxiredoxin A	Os07t0638300-01
*** 19	<u>ChlorisST6804</u>	<u>12.41</u>	<u>1.86E-17</u>	<u>Unknown protein</u>	<u>AT5G07330.1</u>	<u>Unknown protein</u>	<u>Os11t0533400-01</u>
20	ChlorisST2497	12.35	2.11E-41	RAB18	AT5G66400.1	Dehydrin like protein	Os11t0454200-01
21	ChlorisST22375	12.28	7.16E-39	LEA like protein	AT3G53040.1	LEA like protein	Os03t0322900-01
22	ChlorisST22299	12.19	1.75E-24	XERO1	AT3G50980.1	Dehydrin like protein	Os11t0454200-01
23	ChlorisST41155	12.11	1.48E-11	LEA like protein	AT1G72100.1	Similar to H0823A09.7 protein	Os04t0434400-01
24	ChlorisST17995	12.11	1.74E-20	Unknown protein	AT4G21920.1	Unknown protein	Os07t0516400-00
25	ChlorisST4179	12.03	5.51E-15	Unknown protein	AT4G12680.1	Steroid nuclear receptor	Os06t0300500-01
26	ChlorisST7404	11.79	1.41E-14	CBS	AT1G15330.1	Similar to SNF4	Os02t0158900-01
27	ChlorisST3820	11.55	2.10E-45	LEA76	AT3G15670.1	LEA like protein	Os05t0542500-02
28	ChlorisST9073	11.45	9.05E-44	LEA76	AT3G15670.1	LEA 14	Os01t0705200-01
* 29	<u>ChlorisST21980</u>	<u>11.23</u>	<u>5.76E-22</u>	<u>Unknown protein</u>	<u>AT5G66780.1</u>	<u>Similar to UFG2</u>	<u>Os03t0723400-01</u>
30	ChlorisST39682	11.22	1.69E-16	Unknown protein	None	Unknown protein	None
31	ChlorisST22294	11.07	3.90E-24	ELIP1	AT3G22840.1	Similar to HV90	Os07t0178800-01
32	ChlorisST26902	10.95	9.94E-31	Remorin family protein	AT5G23750.1	Similar to Remorin family protein	Os02t0824500-01
*** 33	<u>ChlorisST30368</u>	<u>10.94</u>	<u>1.37E-10</u>	<u>Unknown protein</u>	<u>AT5G45310.1</u>	<u>Unknown protein</u>	<u>Os01t0962100-01</u>
34	ChlorisST32077	10.91	2.02E-11	Unknown protein	AT4G31830.1	Unknown protein	Os09t0127700-01
35	ChlorisST41609	10.82	6.57E-33	RD29B	AT5G52300.1	Unknown protein	Os10t0505900-01
36	ChlorisST21572	10.81	2.55E-07	ABI1	AT4G26080.1	Similar to PP2C	Os05t0572700-01
37	ChlorisST17350	10.73	2.03E-10	UGD3	AT5G15490.1	Similar to UDP-glucose 6-dehydrogenase	Os12t0443600-02
38	ChlorisST8583	10.52	5.66E-08	GBF3	AT2G46270.1	Similar to bZIP family protein	Os01t0658900-01
*** 39	<u>ChlorisST36889</u>	<u>10.51</u>	<u>1.62E-29</u>	<u>Unknown protein</u>	<u>AT5G52420.1</u>	<u>Unknown protein</u>	<u>Os10t0548100-01</u>
40	ChlorisST18549	10.49	5.10E-15	Transcription activator-related protein	AT5G42290.1	Unknown protein	Os03t0133100-01
41	ChlorisST5845	10.45	8.84E-19	RAB28	AT3G22490.1	SMP domain containing protein	Os06t0341300-01
42	ChlorisST41141	10.45	3.35E-11	Unknown protein	None	Unknown protein	None
43	ChlorisST10941	10.45	1.10E-11	LEA like protein	AT3G53040.1	LEA like protein	Os03t0322900-01
44	ChlorisST9005	10.44	7.94E-14	HSD1	AT5G50700.1	Short-chain dehydrogenase domain containing protein	Os04t0390700-01
45	ChlorisST17296	10.35	7.03E-10	EM1	AT3G51810.1	Similar to embryogenic abundant protein	Os05t0349800-01
46	ChlorisST46178	10.31	1.46E-10	PEG4	AT1G66630.1	Zinc finger containing protein	Os01t0123700-00
* 47	<u>ChlorisST18568</u>	<u>10.26</u>	<u>6.53E-07</u>	<u>XERO1</u>	<u>AT3G50980.1</u>	<u>Dehydrin like protein</u>	<u>Os11t0454200-01</u>
48	ChlorisST4239	10.20	1.59E-13	EDL3	AT3G63060.1	Similar to ZGT factor	Os01t0802600-00
49	ChlorisST8031	10.12	1.90E-10	OEP16-2	AT4G16160.2	Tim17/22 family protein	Os03t0305600-01
50	ChlorisST42624	10.10	3.48E-08	LEA18	AT2G35300.1	LEA like protein	Os06t0110200-01
51	ChlorisST19177	10.10	2.65E-11	Unknown protein	AT3G14880.1	Similar to tumor-related protein	Os05t0560200-00
52	ChlorisST35850	10.08	7.09E-14	HMT2	AT3G63250.1	Similar to Homocysteine S-methyltransferase 4	Os01t0772900-02
53	ChlorisST739	10.07	4.70E-08	GSH1	AT4G23100.1	Glutamate-cysteine ligase	Os07t0462000-01
54	ChlorisST9860	10.05	1.45E-25	HB7	AT2G46680.1	HD-ZIP protein	Os02t0649300-01
55	ChlorisST8032	10.05	6.04E-12	OEP16-2	AT4G16160.2	Similar to stress-inducible membrane pore protein	Os01t0303300-01
56	ChlorisST7311	10.02	8.83E-11	AOS	AT5G42650.1	Allene oxide synthase (CYP74A4)	Os02t0218800-01
57	ChlorisST16309	9.95	6.48E-08	HMT3	AT3G22740.1	Similar to HMT4	Os01t0772900-02
58	ChlorisST38202	9.91	0.0084147	Patched family protein	AT1G42470.1	Unknown protein	None
59	ChlorisST6592	9.89	0.005404	NHX3	AT5G55470.1	Similar to Sodium/hydrogen exchanger	Os06t0318500-00
60	ChlorisST3519	9.88	1.30E-10	Protein of unknown function (DUF300)	AT1G23070.1	DUF300 domain-containing protein	Os03t0406900-01
364	ChlorisST40659	4.41	3.81E-16	9-cis-epoxycarotenoid dioxygenase	AT1G78390.1	9-cis-epoxycarotenoid dioxygenase	Os03t0645900-01
736	ChlorisST30712	2.41	8.74E-10	ABA-responsive element binding protein	AT3G56850.1	AREB1	Os06t0211200-02

Table S5. The top 60 most significantly downregulated genes in *Chloris virgata* after 3 hr of dehydration.

No	<i>Chloris virgata</i>	Log2 fold change	Adjusted p-value	<i>Arabidopsis thaliana</i>		<i>Oryza sativa</i>	
				Gene name	Gene code	Gene name	Gene code
1	ChlorisST22479	-7.26	0.002311	NAP6	AT1G32500.1	SufBD family protein	Os01t0127300-01
2	ChlorisST38427	-7.08	0.024174	YBR159	AT1G67730.1	SDR domain containing protein	Os06t0298700-00
3	ChlorisST39674	-6.57	0.040870	toprim domain-containing protein	AT1G30680.1	Unknown protein	None
4	ChlorisST26451	-6.44	0.007404	TLD-domain containing nucleolar protein	AT2G05590.2	Unknown protein	Os07t0438700-01
5	ChlorisST7762	-6.18	0.042007	RK1	AT1G65790.1	S-Domain kinase-6	Os04t0631800-00
6	ChlorisST11193	-5.97	0.007772	Unknown protein	None	Sugar transporter	Os08t0535200-01
7	ChlorisST27437	-5.91	1.37E-07	Leucine-rich repeat protein kinase family protein	AT3G47570.1	Leucine-rich repeat containing protein	Os11t0568800-00
8	ChlorisST22249	-5.80	0.005759	PGIP1	AT5G06860.1	Similar to polygalacturonase inhibitor 1	Os03t0436600-00
9	ChlorisST11835	-5.61	0.049651	SAUR-like auxin-responsive protein	AT1G29420.1	SAUR family protein	Os09t0545300-01
10	ChlorisST32457	-5.03	4.89E-10	Unknown protein	None	Unknown protein	None
11	ChlorisST5286	-4.82	0.003278	SGR5	AT2G01940.3	C2H2 domain containing protein	Os08t0467100-02
12	ChlorisST38658	-4.54	7.01E-05	S-locus lectin protein kinase family protein	AT2G19130.1	S-Domain receptor like kinase-21	Os04t0103500-01
13	ChlorisST3492	-4.53	5.04E-07	dirigent-like protein	AT5G42510.1	Similar to H1005F08.21 protein	Os04t0666800-01
14	ChlorisST14943	-4.48	0.014467	Unknown protein	None	Unknown protein	None
15	ChlorisST5124	-4.29	0.016771	CRK10	AT4G23180.1	Unknown protein	Os07t0537600-01
16	ChlorisST11285	-4.16	0.000546	OCT2	AT1G79360.1	Major facilitator superfamily protein	Os07t0562400-01
17	ChlorisST9680	-4.15	0.000199	PYL5	AT5G05440.1	ABA receptor	Os03t0297600-01
18	ChlorisST43722	-4.11	0.011316	Protein of Unknown Function (DUF239)	AT5G50150.1	Protein of unknown function DUF239	Os06t0474500-02
19	ChlorisST21876	-3.91	0.001706	Nucleotide-diphospho-sugar transferases superfamily protein	AT2G19880.2	Similar to Ceramide glucosyltransferase	Os01t0906000-01
20	ChlorisST34388	-3.78	0.035243	CRK11	AT4G23190.1	Similar to KI domain interacting kinase 1	Os07t0541900-01
21	ChlorisST28555	-3.60	0.000184	Unknown protein	AT3G11600.1	Control of leaf rolling and bending	Os01t0863500-01
22	ChlorisST19558	-3.60	0.000600	PYL6	AT2G40330.1	Similar to AT-rich element binding factor 3	Os01t0827800-00
23	ChlorisST24909	-3.52	0.021228	RNA-binding family protein	AT1G22330.1	RNA recognition motif domain containing protein	Os06t0220600-01
24	ChlorisST15453	-3.44	0.049351	CID9	AT3G14450.1	Nucleotide-binding, alpha-beta plait domain containing protein	Os01t0209400-01
25	ChlorisST44523	-3.40	0.045591	PGM	AT5G51820.1	Plastidic phosphoglucomutase	Os10t0189100-01
26	ChlorisST15853	-3.37	6.51E-10	CRK25	AT4G05200.1	Similar to Receptor protein kinase	Os07t0542400-01
27	ChlorisST29260	-3.32	0.003972	sialyltransferase protein	AT1G08280.1	Glycosyl transferase	Os04t0506800-01
28	ChlorisST3935	-3.29	0.012758	KCO2	AT5G46370.1	Similar to outward rectifying potassium channel	Os01t0696100-00
29	ChlorisST29296	-3.28	0.012001	SAUR-like auxin-responsive protein	AT1G29450.1	Small auxin-up RNA (SAUR)	Os09t0546100-01
30	ChlorisST38389	-3.23	0.049947	Unknown protein	None	Similar to H0305E08.4 protein	Os04t0472700-00
31	ChlorisST12563	-3.12	0.019239	NDF4	AT3G16250.1	Beta-grasp fold, ferredoxin-type domain containing protein	Os07t0489800-01
32	ChlorisST27281	-3.07	0.028398	HTH	AT1G72970.1	Similar to HOTHEAD protein precursor	Os08t0401500-01
33	ChlorisST7238	-3.03	0.001127	Leucine-rich receptor-like protein kinase family protein	AT1G72180.1	Protein kinase, core domain containing protein	Os01t0878300-01
34	ChlorisST37766	-2.99	0.034279	NF-YC13	AT5G43250.1	Transcription factor subunit	Os01t0183400-01
35	ChlorisST23503	-2.97	0.022781	Protein phosphatase 2C family protein	AT1G03590.1	Similar to catalytic/ protein phosphatase type 2C	Os07t0566200-02
36	ChlorisST46377	-2.93	0.044248	CYP704B1	AT1G69500.1	Cytochrome P450 protein	Os03t0168600-01
37	ChlorisST38531	-2.92	0.033656	HRE2	AT2G47520.1	Similar to EREBP-5	Os09t0287000-01
38	ChlorisST44889	-2.87	0.031543	RPM1	AT3G07040.1	Rice blast resistance protein	Os08t0539700-01
39	ChlorisST12381	-2.85	0.037228	UGT74F1	AT2G43840.2	UDP:glucose salicylic acid glucosyltransferase	Os09t0518200-01
40	ChlorisST38899	-2.82	1.95E-06	SWEET10	AT5G50790.1	Sugar transporter	Os08t0535200-01
41	ChlorisST40221	-2.70	0.000133	Protein of unknown function (DUF1677)	AT4G14819.1	Protein of unknown function DUF1677	Os10t0422800-01
42	ChlorisST45408	-2.68	0.001568	Unknown protein	AT5G25840.1	Unknown protein	Os02t0229900-00
43	ChlorisST43947	-2.68	0.000208	UGT73B5	AT2G15480.1	Unknown protein	Os06t0187500-00
44	ChlorisST1671	-2.65	0.011680	ATRLI2	AT4G19210.1	Similar to 68 kDa protein	Os02t0282900-01
45	ChlorisST19085	-2.64	0.024577	Concanavalin A-like lectin protein kinase family protein	AT5G10530.1	Similar to protein kinase	Os07t0569550-00
46	ChlorisST9679	-2.64	0.044619	Eukaryotic aspartyl protease family protein	AT2G03200.1	Peptidase A1 domain containing protein	Os06t0209100-00
47	ChlorisST21126	-2.56	0.037025	CHY-type Zinc finger protein	AT5G22920.1	Similar to CHY zinc finger family protein	Os03t0145900-01
48	ChlorisST4329	-2.55	0.000983	AGP16	AT2G46330.1	Protein of unknown function DUF1070 family protein	Os01t0657000-01
49	ChlorisST22527	-2.54	8.10E-05	RING/U-box superfamily protein	AT1G20823.1	Zinc finger, RING/FYVE/PHD-type domain containing protein	Os09t0554200-01
50	ChlorisST20409	-2.53	1.66E-06	UGT85A2	AT1G22360.1	Glycosyltransferase	Os02t0755500-01
51	ChlorisST4005	-2.52	0.031959	Unknown protein	None	Unknown protein	None
52	ChlorisST33641	-2.48	7.07E-05	VQ motif-containing protein	AT3G58000.1	VQ domain containing protein	Os06t0618700-01
53	ChlorisST19810	-2.44	0.049820	Unknown protein	None	Unknown protein	Os02t0246900-01
54	ChlorisST24454	-2.42	0.018964	PDR11	AT1G66950.1	ATP-binding cassette (ABC) transporter	Os08t0544400-03
55	ChlorisST27381	-2.39	0.040829	ferric reductase transmembrane protein	AT2G30890.1	Cytochrome b561/ferric reductase transmembrane domain containing protein	Os05t0565100-01
56	ChlorisST39607	-2.39	0.002117	ARR9	AT3G57040.1	A-type response regulator	Os11t0143300-01
57	ChlorisST19025	-2.36	1.10E-06	Leucine-rich repeat protein kinase family protein	AT3G47570.1	Leucine-rich repeat (LRR) receptor kinase-like protein	Os11t0694850-01
58	ChlorisST24735	-2.34	0.039442	Acylhydrolase superfamily protein	AT5G45670.1	Lipase, GDSL domain containing protein	Os05t0518300-01
59	ChlorisST36871	-2.33	8.78E-11	ST91	AT1G23090.1	Ortholog of the sulfate transporter	Os04t0652400-01
60	ChlorisST31005	-2.33	0.001057	Chaperone DnaJ-domain superfamily protein	AT3G14200.1	Heat shock protein	Os01t0606900-01

Table S6. The top 60 most significantly downregulated genes in *Chloris virgata* after 6 hr of dehydration.

No	<i>Chloris virgata</i>	Log2 fold change	Adjusted p-value	<i>Arabidopsis thaliana</i>		<i>Oryza sativa</i>	
				Gene name	Gene code	Gene name	Gene code
1	ChlorisST31612	-9.76	1.01E-11	SUVH1	AT5G04940.1	Similar to YDG/SRA domain containing protein	Os12t0128450-00
2	ChlorisST12570	-9.13	3.87E-05	Trypsin family protein with PDZ domain	AT5G27660.1	PDZ/DHR/GLGF domain containing protein	Os09t0436700-01
3	ChlorisST25177	-8.73	8.09E-10	Unknown protein	None	Unknown protein	Os08t0299300-01
4	ChlorisST24328	-8.45	8.12E-08	PLP2	AT2G26560.1	Similar to Patatin-like protein 1	Os11t0614400-01
5	ChlorisST19792	-8.19	0.002121	SWAP domain-containing protein	AT4G31200.2	Similar to SWAP domain-containing protein.	Os06t0682700-00
6	ChlorisST25682	-8.17	5.62E-07	Unknown protein	None	Unknown protein	Os07t0530700-01
7	ChlorisST17644	-8.03	0.001790	mRNA capping enzyme family protein	AT3G20650.1	mRNA capping enzyme	Os08t0180000-02
8	ChlorisST43495	-7.91	0.00945	hydrolases	AT1G77030.1	DEAD-like helicase	Os08t0416100-01
9	ChlorisST14837	-7.90	8.36E-06	Core-2/1-branching beta-1,6-N-acetylglucosaminyltransferase family protein	AT4G31350.1	Similar to OSIGBa0113I13.9 protein	Os08t0225400-01
10	ChlorisST5936	-7.86	0.034789	alpha/beta-Hydrolases superfamily protein	AT5G67050.1	Lipase	Os04t0657500-01
11	ChlorisST38785	-7.82	0.006420	Protein of unknown function (DUF247)	AT3G50120.1	Protein of unknown function DUF247	Os08t0120900-01
12	ChlorisST32157	-7.82	9.73E-05	lipid-transfer protein	AT2G45180.1	Root-specific RCc3 protein	Os02t0662000-01
13	ChlorisST18866	-7.82	0.006789	Unknown protein	AT2G38570.1	PRC-barrel-like domain containing protein	Os03t0334100-01
14	ChlorisST22479	-7.74	0.000515	NAP6	AT1G32500.1	SufBD family protein	Os01t0127300-01
15	ChlorisST15208	-7.73	0.001673	PGM	AT5G51820.1	Plastidic phosphoglucomutase	Os10t0189100-01
16	ChlorisST38393	-7.71	3.90E-05	CYP72A9	AT3G14630.1	Cytochrome P450	Os01t0628700-01
17	ChlorisST17161	-7.66	0.010431	Integrase-type DNA-binding superfamily protein	AT4G18450.1	Ethylene response factor	Os03t0860100-01
18	ChlorisST32706	-7.49	0.000583	Unknown protein	AT3G52240.1	Similar to H0811D08.6 protein	Os01t0857600-01
19	ChlorisST20856	-7.48	0.005779	VDAC1	AT3G01280.1	Similar to VDAC3.1	Os03t0137500-03
20	ChlorisST15726	-7.46	2.98E-06	Leucine-rich receptor-like protein kinase family protein	AT1G72300.1	Leucine-rich repeat receptor-like kinase	Os02t0153400-01
21	ChlorisST40103	-7.43	0.006728	Nucleotide-diphospho-sugar transferase family protein	AT1G70630.1	Reticulon domain containing protein	Os05t0513700-00
22	ChlorisST26034	-7.40	0.001184	Aluminium activated malate transporter family protein	AT2G27240.1	Similar to Aluminum-activated malate transporter	Os04t0417000-01
23	ChlorisST8290	-7.32	0.001921	leucine-rich repeat transmembrane protein	AT5G10290.1	Similar to BRI1-associated receptor kinase 1	Os11t0607200-02
24	ChlorisST20160	-7.15	0.000839	UBP27	AT4G39370.3	Peptidase C19	Os04t0429200-01
25	ChlorisST24418	-7.09	1.95E-09	Pentatricopeptide repeat superfamily protein	AT2G15630.1	Pentatricopeptide repeat domain containing protein	Os04t0477200-01
26	ChlorisST25031	-7.08	0.040657	FtsJ-like methyltransferase family protein	AT5G13830.1	Ribosomal RNA methyltransferase J domain containing protein	Os03t0822300-01
27	ChlorisST24906	-7.05	0.014206	NF-YC6	AT5G50480.1	Histone-fold domain containing protein	Os01t0580400-01
28	ChlorisST44494	-7.03	0.011096	Unknown protein	None	Unknown protein	None
29	ChlorisST22467	-6.97	0.012361	PAC	AT2G48120.1	Similar to PAC	Os05t0393400-03
30	ChlorisST26329	-6.88	0.010934	alpha/beta-Hydrolases superfamily protein	AT4G18550.1	Lipase	Os05t0574100-01
31	ChlorisST43503	-6.82	0.000257	UXS2	AT3G62830.1	UDP-glucuronic acid decarboxylase	Os07t0674100-02
32	ChlorisST18739	-6.82	0.000276	BCS1	AT3G50930.1	ATPase, AAA-type containing protein	Os03t0584400-01
33	ChlorisST38427	-6.72	0.021330	YBR159	AT1G67730.1	SDR domain containing protein	Os06t0298700-00
34	ChlorisST23891	-6.55	3.25E-07	Unknown protein	None	Unknown protein	Os01t0510200-01
35	ChlorisST39594	-6.55	0.009840	GSTF13	AT3G62760.1	Glutathione S-transferase	Os01t0372400-01
36	ChlorisST37401	-6.53	0.033307	Unknown protein	None	Unknown protein	None
37	ChlorisST24544	-6.52	0.000138	PEBP	AT1G65480.1	Similar to ZCN24	Os09t0513500-00
38	ChlorisST41351	-6.45	0.011263	Unknown protein	None	Leucine Rich Repeat family protein	Os04t0115650-01
39	ChlorisST30099	-6.45	0.025594	Glutamyl cyclase	AT4G25720.1	Similar to glutamine cyclotransferase	Os06t0103700-02
40	ChlorisST45470	-6.39	0.017658	Protein of unknown function (DUF821)	AT5G23850.1	Protein of unknown function DUF821	Os06t0152700-01
41	ChlorisST18456	-6.34	0.019896	CRK26	AT4G38830.1	Serine/threonine protein kinase-related domain containing protein	Os12t0608500-01
42	ChlorisST25235	-6.34	0.019337	ATH6	AT3G47780.1	Similar to ABC transporter family	Os08t0398350-00
43	ChlorisST18650	-6.28	0.000779	Major facilitator superfamily protein	AT5G14940.1	TGF-beta receptor	Os06t0239500-01
44	ChlorisST18923	-6.26	0.021656	Unknown protein	None	Unknown protein	None
45	ChlorisST40758	-6.23	0.024307	TPR-like superfamily protein	AT3G47840.1	Unknown protein	Os05t0581300-00
46	ChlorisST41405	-6.13	0.038179	RLP45	AT3G53240.1	Leucine-rich repeat domain containing protein	Os01t0601700-01
47	ChlorisST6104	-6.12	0.013582	RNA-directed DNA polymerase-related family protein	AT4G10613.1	Unknown protein	Os01t0685100-02
48	ChlorisST2356	-6.11	0.047516	RPS2	AT4G26090.1	Disease resistance protein domain containing protein	Os01t0788500-01
49	ChlorisST35261	-6.07	0.047635	ACT-like protein tyrosine kinase family protein	AT2G17700.1	Similar to serine/threonine-protein kinase CTR1	Os08t0103000-01
50	ChlorisST23316	-6.07	0.008459	SIGF	AT2G36990.1	Similar to Sigma factor SIG6	Os08t0242800-02
51	ChlorisST38658	-6.06	3.27E-07	S-locus lectin protein kinase family protein	AT2G19130.1	S-Domain receptor like kinase-21	Os04t0103500-01
52	ChlorisST17747	-6.04	0.004438	WRKY34	AT4G26440.1	Unknown protein	Os03t0657400-00
53	ChlorisST30211	-6.02	0.007378	CYP87A2	AT1G12740.2	Cytochrome P450 87A3	Os04t0570000-01
54	ChlorisST15928	-6.01	0.017214	Calmodulin-binding protein	AT5G57580.1	Calmodulin binding protein-like family protein	Os01t0134700-01
55	ChlorisST35986	-5.97	0.019187	Unknown protein	None	Unknown protein	None
56	ChlorisST38989	-5.92	0.033655	Transmembrane amino acid transporter family protein	AT3G28960.1	Amino acid transporter	Os06t0228500-01
57	ChlorisST28397	-5.83	0.000367	Unknown protein	AT2G02148.1	Unknown protein	None
58	ChlorisST44610	-5.76	0.019040	Pathogenesis-related thaumatin superfamily protein	AT4G36010.1	Similar to thaumatin-like protein 1	Os03t0244200-01
59	ChlorisST39506	-5.71	0.004926	Unknown protein	None	Unknown protein	Os02t0248100-00
60	ChlorisST40404	-5.66	0.041157	CPK13	AT3G51850.1	Calcium-dependent protein kinase 29	Os12t0230200-02

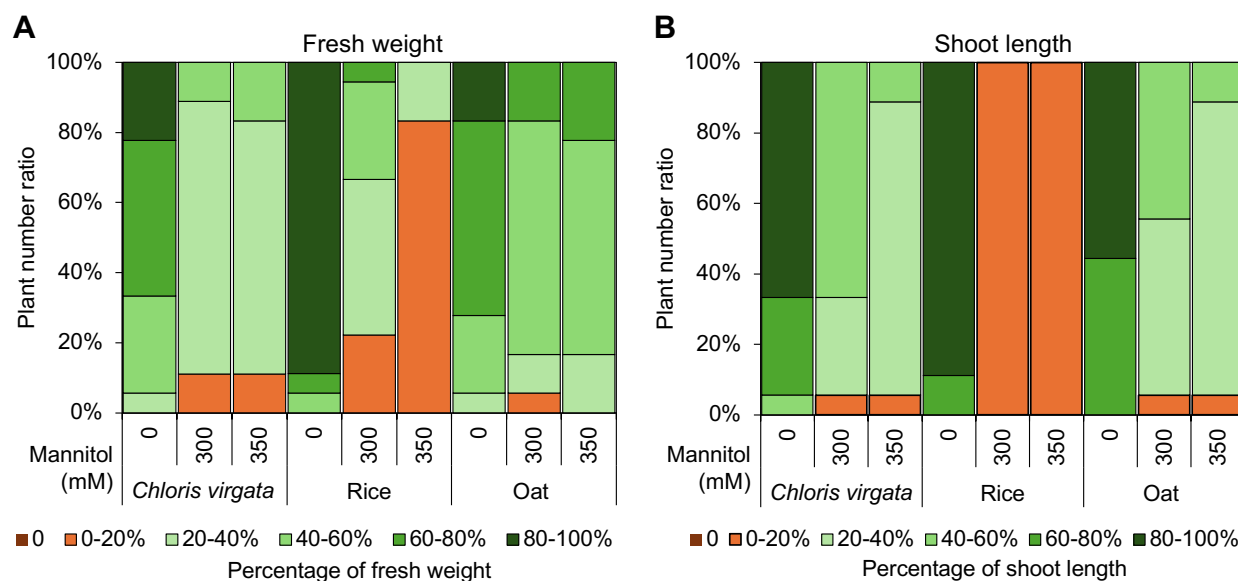


Fig. S1. Osmotic stress sensitivity of *Chloris virgata*. (A, B) Plant fresh weight (A) and shoot length (B) of *Chloris virgata*, rice, and oat under mannitol treatment. Seven-day-old seedlings grown on $\frac{1}{2}$ MS medium were transplanted to $\frac{1}{2}$ MS medium supplemented with or without various concentrations of mannitol. The fresh weight and shoot length were measured after 3 weeks of treatment with mannitol. The three highest values were converted to 100% in each treatment. n=18.

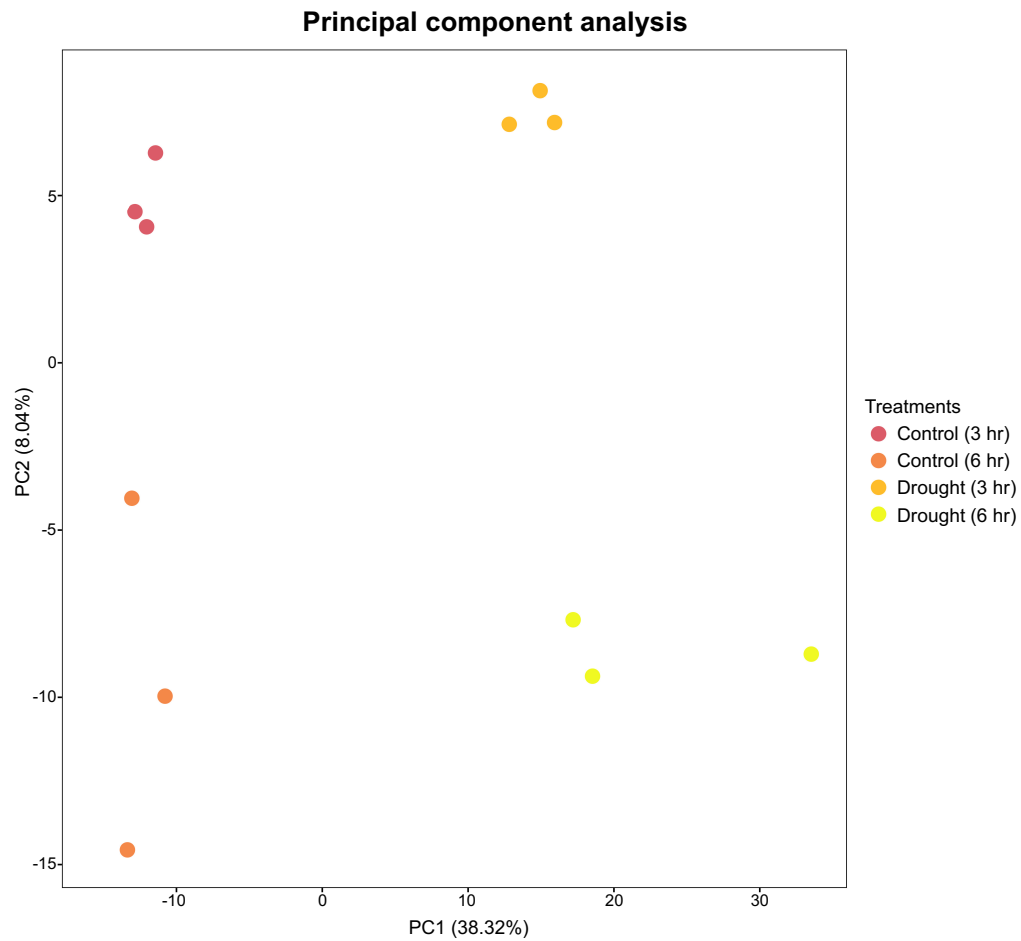


Fig. S2. Principal Component Analysis (PCA) of gene expression profiles based on transcripts per million (TPM) counts (log₁₀-transformed). The plot shows the distribution of plant samples along the first two components, PC1 (38.32% variance explained) and PC2 (8.04% variance explained). The treatment series includes control samples at 3 hr and 6 hr, and drought samples at 3 hr and 6 hr.

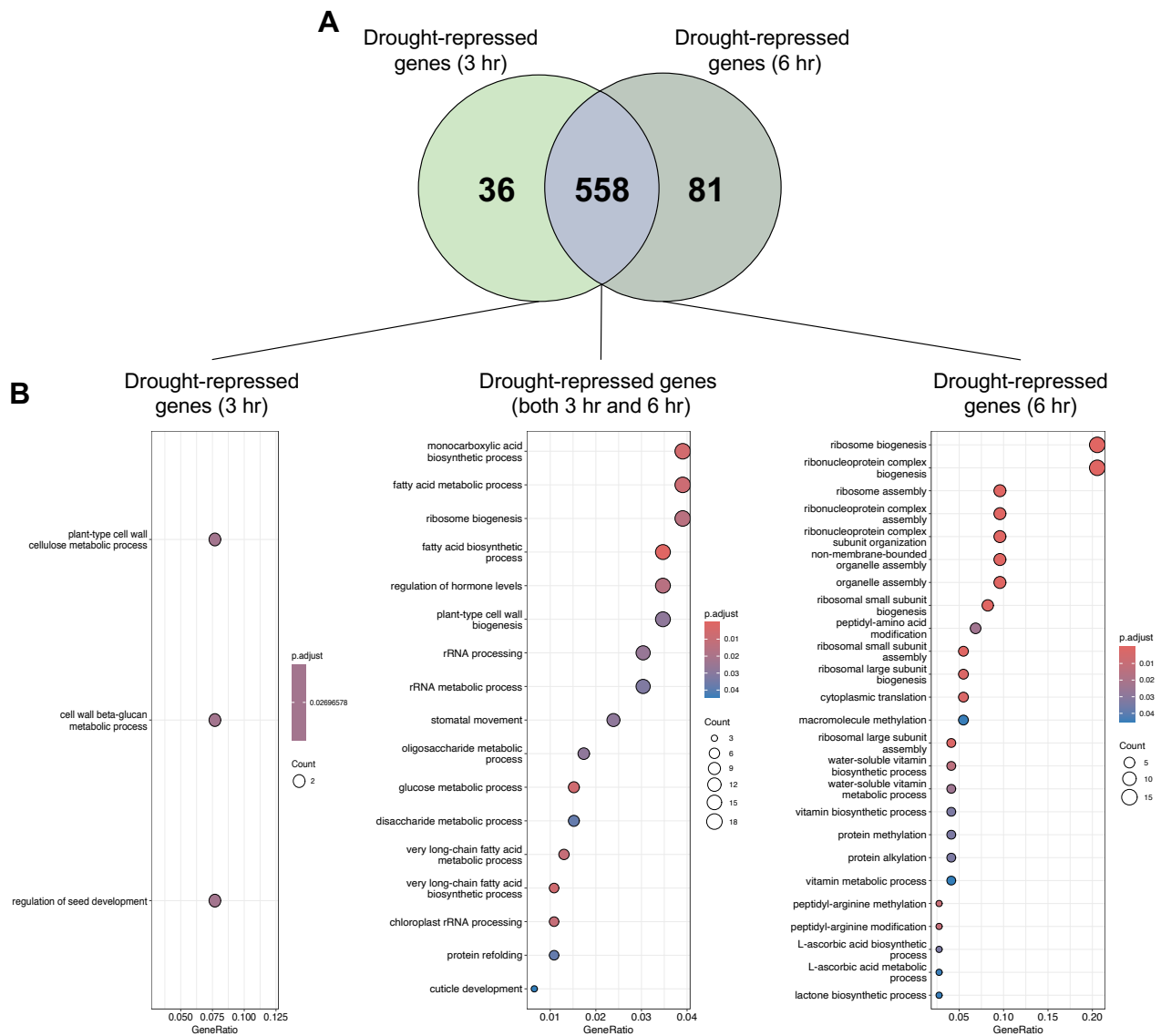


Fig. S3. Gene Ontology (GO) analysis of downregulated genes in *Chloris virgata*. (A) Venn diagram showing the downregulated genes ($p < 0.05$, fold change < -1.5) in *Chloris virgata* after dehydration for 3 hr and 6 hr. (B) Enrichment of GO annotations in biological process categories for genes downregulated after treatment with both 3 hr and 6 hr of dehydration. The y-axis indicates the pathway name, and the x-axis indicates the gene ratio. The p-adjusted value is represented by the colour of each dot, and the number of DEGs is represented by the size of each dot.

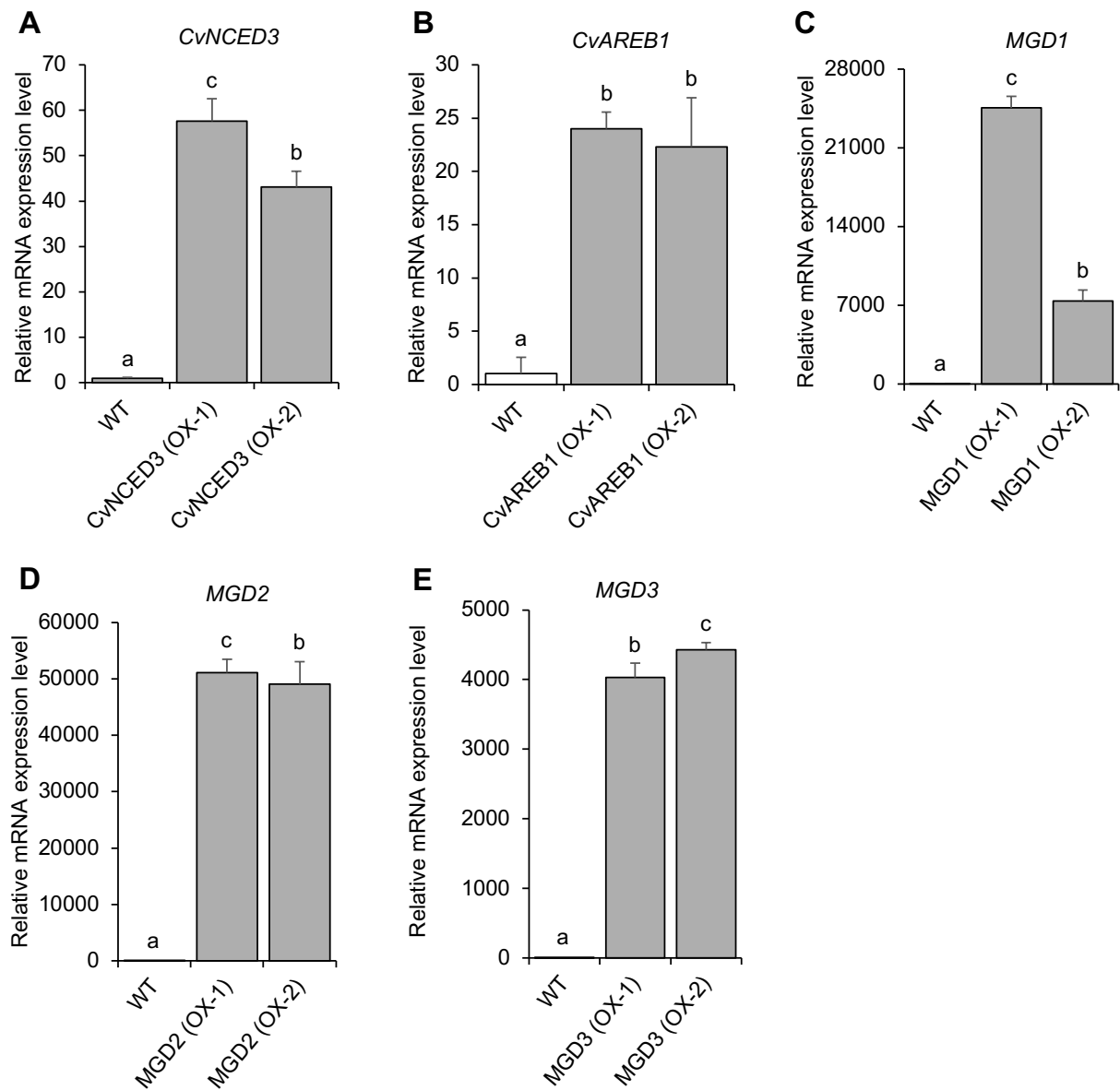


Fig. S4. Expression analysis of transgenes in transgenic *Arabidopsis* overexpression lines. (A-E) Transgene expression levels in *CvNCED3*-OX (A), *CvAREB1*-OX (B), *MGD1*-OX (C), *MGD2*-OX (D), and *MGD3*-OX (E) compared with those in WT. The error bars represent the means $\pm$ SDs from four replicated samples. The different letters above the bars indicate that the means are significantly different (One-way ANOVA with post-hoc Tukey HSD test ($P < 0.05$)).

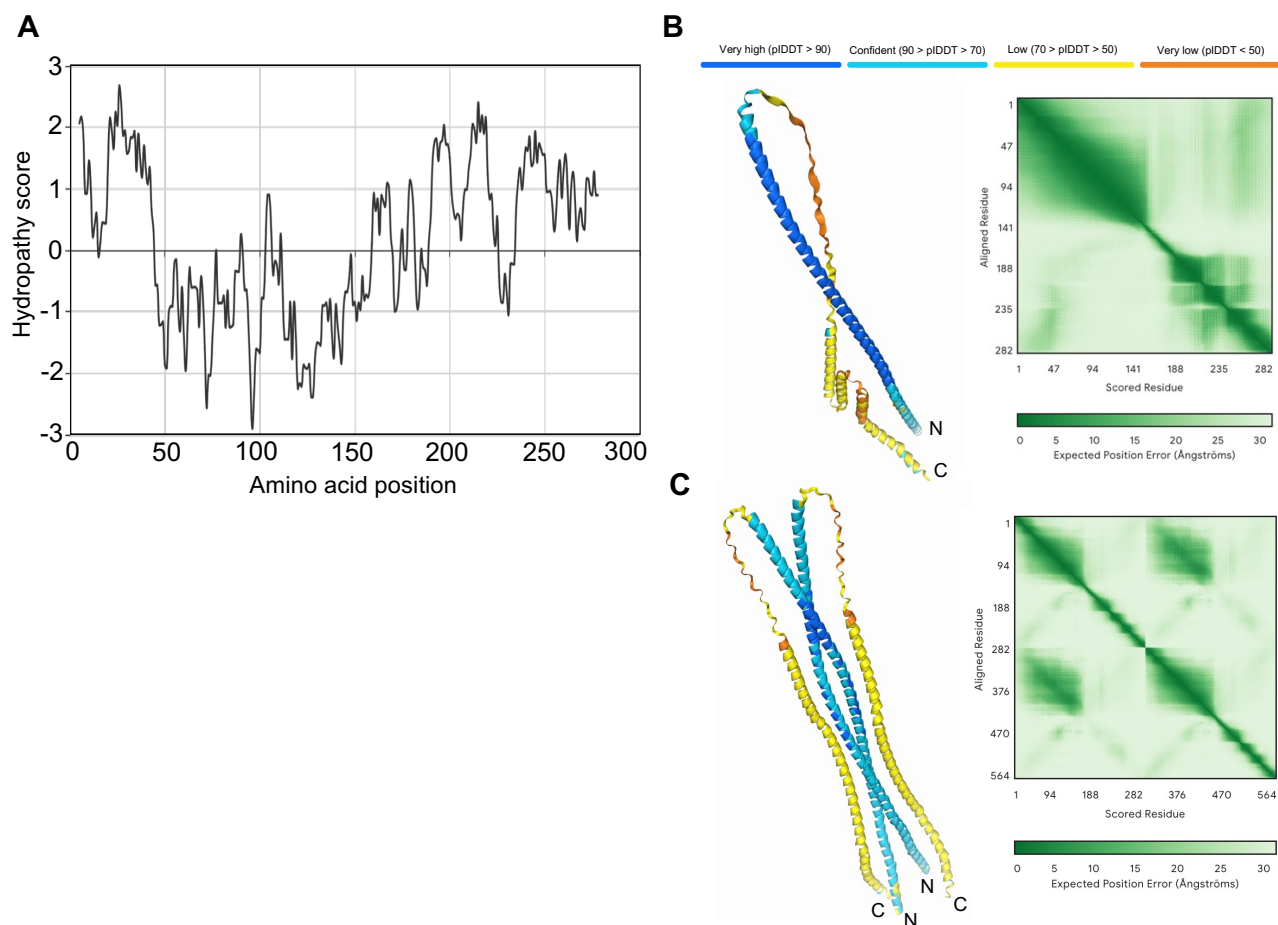


Fig. S5. Structure prediction of MGD1. (A) Hydropathy plot of MGD1. The plot was generated using the NovoPro server (42) with the Kyte & Doolittle scale (43). (B, C) The structural models and predicted alignment errors of the MGD1 monomer (B) and dimer (C), were generated using the AlphaFold3 server (35). The N- and C-termini are indicated by the letters N and C, respectively.

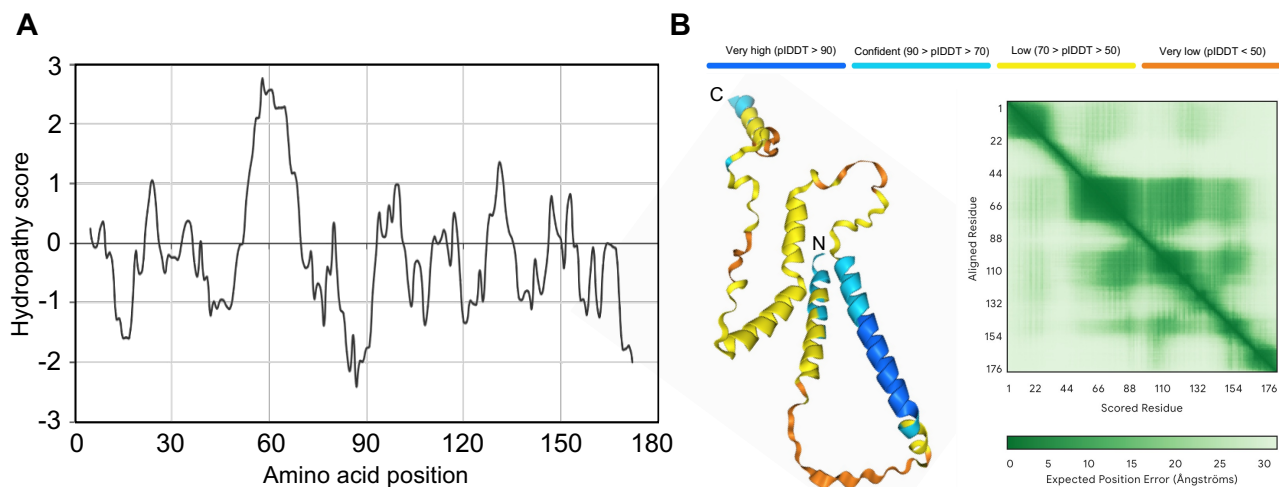


Fig. S6. Structure prediction of MGD2. (A) Hydropathy plot of MGD2. The plot was generated using the NovoPro server with the Kyte & Doolittle scale. (B) The structural models and predicted alignment errors of MGD2 were generated using the AlphaFold3 server. The N- and C-termini are indicated by the letters N and C, respectively.

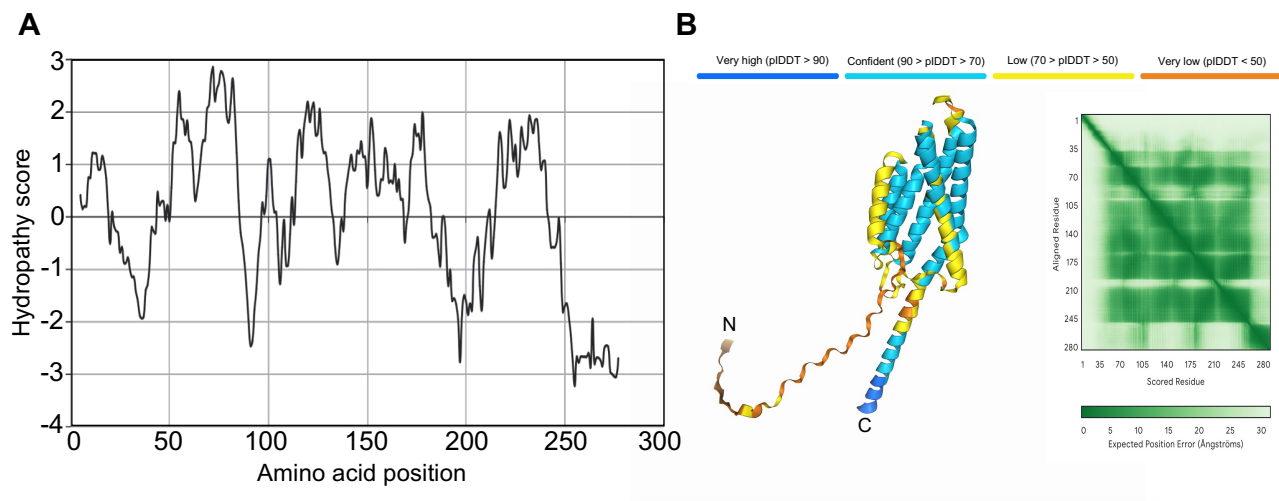


Fig. S7. Structure prediction of MGD3. (A) Hydropathy plot of MGD3. The plot was generated using the NovoPro server with the Kyte & Doolittle scale. (B) The structural models and predicted alignment errors of MGD3 were generated using the AlphaFold3 server. The N- and C-termini are indicated by the letters N and C, respectively.

<i>CvNCED3</i>	1	MGRPTDSSLPPPSHRPKPTPIPPNPTPMQGLA--PPTSSL SIHRHRSPATSVRFAPR---	55
<i>OsNCED3</i>	1	MAITIT-----TPGYAHIQRQHRC--STTAG-----RRGASNSVRFSARAVS	40
<i>AtNCED3</i>	1	MASFTI-----ATAAVSGRWLGHNHTOPPLSS-SQSSDL SYCSSLPMASRVT-	45
<i>CvNCED3</i>	56	-----AALSSAPADAP-PFQLRAPLNKSPKP----ATGAPRPVAPASAPRKPAAAEPAK	105
<i>OsNCED3</i>	41	SVPHAAAASSAPAFLPVPF---VPGADAPSPSGKSAIGVPK-----APRK----GEEGK	87
<i>AtNCED3</i>	46	-----RKLNVSSALHT-PPALHFPKQSSNSP----ATVV-----KPKAKESNTK	84
<i>CvNCED3</i>	106	ELNFFQRAAAALDAFEEGFVANVLERPHGLPRITADPAVQIAGNFAPVGEHPPAHALPVA	165
<i>OsNCED3</i>	88	RLNFFQRAAAALDAFEEGFVANVLERPHGLPSTADPAVQIAGNFAPVGETPPARALPVS	147
<i>AtNCED3</i>	85	QNLFFQRAAAALDAFEGLVLSH--EKLHPLPKTADPSVQIAGNFAPVNEQPVRRNLPPVV	142
<i>CvNCED3</i>	166	GRIPPPFINGVYARNGANPCFDPVAGHHFDGDGMVHALRIRNGAAESYACRFTETARLQQ	225
<i>OsNCED3</i>	148	GRIPPPFINGVYARNGANPHFDPVAGHHFDGDGMVHAVRIRNGAAESYACRFTETARLRQ	207
<i>AtNCED3</i>	143	GKLPDSTIKGVYVRNGANPLHEPVTGHHFFDGDGMVHAVKFEHCSA-SYACRFTQTNRVQ	201
<i>CvNCED3</i>	226	ERALGRPVFPKAIAGELHGHSGVARLALFYARAACGLVDPSRGTGVANAGLIVFYNGRLLAM	285
<i>OsNCED3</i>	208	ERAMGRPMFPKAIAGELHGHSGVARLALFYARAACGLLDPSHGTGVANAGLIIFYNGRLLAM	267
<i>AtNCED3</i>	202	ERQLGRPVFPKAIAGELHGHGTGLARLMLFYARAAAGLVDPAHGTGVANAGLIVFYNGRLLAM	261
<i>CvNCED3</i>	286	SEDDLPHYVRVTAAGDLETVGRYDFDQGLEHAMIAHPKLDPOSSELHALSYDVIRKPYLR	345
<i>OsNCED3</i>	268	SEDDLPHYQVRVTADGDLETVGRYDFDQGLEGCAMIAHPKLDPATGELHALSYDVIRKPYLK	327
<i>AtNCED3</i>	262	SEDDLPHYQVQITPNGDLKTVGRFDFDQGLESTMIAHPKVDPESELFALSYDVVSKPYLK	321
<i>CvNCED3</i>	346	YFYFRPDGTKSDDVEIPLDQPTMTHDFAITENFVVVPDQVVFKLPEMLRGGSPVVLDEKE	405
<i>OsNCED3</i>	328	YFYFAPDGTKSADVEIPLDQPTMTHDFAITENYVVVPDQVVFKLQEMLRGGSPVVLDEKE	387
<i>AtNCED3</i>	322	YFRFSPDGTKSPDVEIQLDQPTMTHDFAITENFVVVPDQVVFKLPEMLRGGSPVVDKKN	381
<i>CvNCED3</i>	406	KTSRFGVLPKHAADASEMLWVDVDCFCFHLWNAWEE--SDEITVIGSCMTPADSIFNES	463
<i>OsNCED3</i>	388	KTSRFGVLPKHAADASEMWVDVDCFCFHLWNAWEEADTDEVVIGSCMTPADSIFNES	447
<i>AtNCED3</i>	382	KVARFGILDKYAEDSSNIKWIDAPDCFCFHLWNAWEEPETDEVVIGSCMTPADSIFNES	441
<i>CvNCED3</i>	464	EDRLLESVLTEIRLNTRTGASTRRVLA PAD-QVNLEVGMVNRNLLGRKTRHAYLAVAEPW	522
<i>OsNCED3</i>	448	DDRLESVLTEIRLNTRTGESTRRAILPPSS-QVNLEVGMVNRNLLGRKTRYAYLAVAEPW	506
<i>AtNCED3</i>	442	DENLKSVLSEIRLNLTGESTRRPIISNEDQQVNLEAGMVNRNLLGRKTKFAYLAVAEPW	501
<i>CvNCED3</i>	523	PKVSGFAKVDLTGTGELTKFDYGEGRFGGEPCEFVPMDPAYATPRGEDDGYVLAFVHDERAG	582
<i>OsNCED3</i>	507	PKVSGFAKVDLATGTGELTKFEYGEGRFGGEPCEFVPMDAAAATPRGEDDGYILSFVHDERAG	566
<i>AtNCED3</i>	502	PKVSGFAKVDLTTGGEVKKHLYGDNRYGGEPLFLPGEGE-----EDEGYILCFVHDEKTV	556
<i>CvNCED3</i>	583	TSELLVNVNADMRL EATVOLPSRVPGFHGTFITASELQAQA-	624
<i>OsNCED3</i>	567	TSELLVNVNADMRL EATVOLPSRVPGFHGTFITGDELTTQA-	608
<i>AtNCED3</i>	557	KSELQIVNAVSLLEVATVKLPSRVPGFHGTFIGADDLAKQVV	599

Fig. S8. Amino acid sequence alignment of *CvNCED3* (ChlorisST40659) with *AtNCED3* (accession AEE75526.1) and *OsNCED3* (accession NP_001405315.1). Identical amino acids are indicated in black and grey. The red line represents the RPE65 domain. The green line indicates possible AC motifs.

<i>CvAREB1</i>	1	M-----EFPGSGSGWRQQQLEEHLPMTPLPLARQGSVYSLTFDEFQSAALGGPNKD	52
<i>OsAREB1</i>	1	M-----DFPGSG---RQQQ----LPPMTPLPLARQGSVYSLTFDEFQSTLGGVGKD	45
<i>AtAREB1</i>	1	MDGSMNLGNPPGDDGGGG-----GLTRQGSIVYSLTFDEFQSSVG---KD	42
<i>CvAREB1</i>	53	FGSMNMDELLRSIWTAEESHAVGAAN-----AAAAAQAAARAAAIQRQGSLLPRTL	105
<i>OsAREB1</i>	46	FGSMNMDELLRSIWTAEESHAVGAATTTATTASVAAAEHAAVGAPPVQRQGSLLPRTL	105
<i>AtAREB1</i>	43	FGSMNMDELLKNIWSAEETQAM--AS-----GVVPVLGGGQEGQLQRQGSLLPRTL	93
<i>CvAREB1</i>	106	SQKTLDEVVRDIMYF-----GGPSAAPVAAAPTPTQROP TLGEITLEEFVLRAGVVRE	159
<i>OsAREB1</i>	106	SQKTVDEVVRDMMCFG----GGGASTAPAAAEPPPAHRQQT LGEITLEEFVLRAGVVRE	161
<i>AtAREB1</i>	94	SQKTVQVWKDLSKVGSSGVGGSNLSQVAAQASQSQSQRQT LGEVTLEEFVLRAGVVRE	153
<i>CvAREB1</i>	160	D-----MNAGPSAP-PVQATAPP-----	176
<i>OsAREB1</i>	162	D-----MSVPPVPAPTPTAAV-----	179
<i>AtAREB1</i>	154	EAQVAARAQIAENNKGGYFGNDANTGFSVEFQQPSPRVVAAGVMGNLGAETANS LQVQGS	213
<i>CvAREB1</i>	177	-----PPPPPTSQPM-----FPQGNVFAPLPPLTLGNGLV-----T---	211
<i>OsAREB1</i>	180	-----PPPPPPQQQT PML-----FGQSNVFPPMVPPLSLGNGLV-----SGAV	217
<i>AtAREB1</i>	214	SLPLNVNGARTTYQSSQQQOPI MPKQPGFGYGTQMGQLNSPGIRGGGLVGLGDQSLTNNV	273
<i>CvAREB1</i>	212	--GGGGAAS-----SLSPVRPVT SNGFGKMEAGDLSMSSLSPSPVPYVFNGGLRGRK	261
<i>OsAREB1</i>	218	GHGGGGAAS-----LVSPVRPVSSNGFGKMEGGDLSMSSLSPSPVPYVFKGGLRGRK	267
<i>AtAREB1</i>	274	GFVQGASAAIPGALGVGAVSPVTPLSSEGI GK-SNGDS--SSLSPS--PYMFNGGVRGRK	328
<i>CvAREB1</i>	262	PSAMEKVVERRQRRMIKNRESAARSRORKQAYMMELEAEVAKLKE LNEELQKKQVEMLEK	321
<i>OsAREB1</i>	268	APGI EKVVERRQRRMIKNRESAARSRORKQAYMMELEAEVAKLKE LNEELQKKQDEMLEK	327
<i>AtAREB1</i>	329	SGTVEKVVERRQRRMIKNRESAARSRA RKQAYTVLEAEVAKLKE ENDELQKKQARIMEM	388
<i>CvAREB1</i>	322	QKNEVLE-RMTRQVGPTAKRICLRRTLTPGW	351
<i>OsAREB1</i>	328	QKNEVLE-RMSRQVGPTAKRICLRRTLTPGW	357
<i>AtAREB1</i>	389	QKNQETEMRNLLQGPKKK---LRRTESGPW	416

Fig. S9. Amino acid sequence alignment of *CvAREB1* (ChlorisST30712) with *AtAREB1* (accession BAB12404.1) and *OsAREB1* (accession NP_001403850.1). Identical amino acids are indicated in black and grey. The red line represents the bZIP domain. The yellow highlighted regions indicate the deleted sequence of the *AtAREB1*ΔQT constitutively active form.