

Supplementary Information Tables S1–S5

Table S1. The publicly available RNA-sequencing datasets used in this study

Species	Length of reads	NCBI Accession	Samples ID
<i>Arabidopsis thaliana</i>	101bp	PRJNA218215	SRR1004790, SRR1004791, SRR1004829, SRR1004830, SRR1004831, SRR1004832, SRR1004833, SRR1004834
	100bp	PRJNA213635	SRR944362, SRR944363, SRR944364, SRR944365, SRR944366, SRR944367, SRR944368, SRR944369, SRR944370, SRR944371
<i>Brachypodium distachyon</i>	50bp	PRJNA273411	SRR1772223, SRR1772224, SRR1772225, SRR1772226, SRR1772227, SRR1772228, SRR1772229, SRR1772230, SRR1772231, SRR1772232, SRR1772233, SRR1772234, SRR1772235, SRR1772236, SRR1772237, SRR1772238, SRR1850587, SRR1850670, SRR1850671, SRR1850716
<i>Glycine max</i>	50bp	PRJNA285677	SRR2048167, SRR2048168, SRR2048169, SRR2048170, SRR2048171, SRR2048172, SRR2048173, SRR2048174, SRR2048175, SRR2048176, SRR2048177, SRR2048178, SRR2048179, SRR2048180, SRR2048181, SRR2048182, SRR2048183, SRR2048184, SRR2048185, SRR2048186, SRR2048187, SRR2048188, SRR2048189, SRR2048190, SRR2048191, SRR2048192, SRR2048193, SRR2048194, SRR2048195, SRR2048196, SRR2048197, SRR2048198, SRR2048199, SRR2048200, SRR2048201, SRR2048202
<i>Hordeum vulgare</i>	101bp	PRJNA295482	SRR2379177, SRR2379209, SRR2379274, SRR2379393, SRR2379445, SRR2379446, SRR2379577, SRR2379602, SRR2379664, SRR2379887, SRR2379950, SRR2379972, SRR2380048, SRR2380049, SRR2380116
<i>Oryza sativa</i>	101bp	PRJNA215013	SRR1005257, SRR1005258, SRR1005259, SRR1005260, SRR1005261, SRR1005262, SRR1005302, SRR1005303, SRR1005304, SRR1005305, SRR1005306, SRR1005307, SRR1005320, SRR1005321, SRR1005322, SRR1005323, SRR1005324, SRR1005325, SRR1005365, SRR1005366, SRR1005367, SRR1005368, SRR1005369, SRR1005370
<i>Solanum lycopersicum</i>	100bp	PRJNA255271	SRR1514810, SRR1609960, SRR1609961, SRR2102073
<i>Zea mays</i>	100bp	PRJNA287309	SRR2070626, SRR2070627

Table S2. The reference genomes, transcriptomes and annotation files used in this study

Species	Species ID	Common Name	Release Version	Source
<i>Arabidopsis thaliana</i>	ath	Arabidopsis	TAIR10	http://www.arabidopsis.org/
<i>Brachypodium distachyon</i>	bdi	stiff brome	v1.0	ftp://ftp.ensemblgenomes.org/pub/current/plants/
<i>Glycine max</i>	gma	soybean	V1.0	ftp://ftp.ensemblgenomes.org/pub/current/plants/
<i>Hordeum vulgare</i>	hvu	barley	ASM32608v1	ftp://ftp.ensemblgenomes.org/pub/current/plants/
<i>Oryza sativa</i>	osa	rice	IRGSP-1.0	ftp://ftp.ensemblgenomes.org/pub/current/plants/
<i>Solanum lycopersicum</i>	sly	tomato	SL2.50	ftp://ftp.ensemblgenomes.org/pub/current/plants/
<i>Zea mays</i>	zma	maize	AGPv3	ftp://ftp.ensemblgenomes.org/pub/current/plants/

Table S3. Predicted circRNAs consistent with experimentally validated RNAs by comparison of back-spliced junction sites

Species	Experimentally identified circRNAs	Chr	Start	End	circRNA	Reference
<i>Oryza sativa</i>	Chr1_22121499_22122046	Chr1	22121499	22122046	OSA_circ00869	PMID: 27739910
<i>Oryza sativa</i>	Chr11_13707993_13708205	Chr11	13707993	13708205	OSA_circ08079	PMID: 27739910
<i>Oryza sativa</i>	Chr10_20890579_20890904	Chr10	20890579	20890904	OSA_circ07792	PMID: 27739910
<i>Oryza sativa</i>	Chr10_23115090_23115651	Chr10	23115090	23115651	OSA_circ07893	PMID: 27739911
<i>Oryza sativa</i>	Chr11_21179446_21180854	Chr11	21179446	21180854	OSA_circ08151	PMID: 27739912
<i>Oryza sativa</i>	Chr12_3795288_3795604	Chr12	3795288	3795604	OSA_circ08363	PMID: 27739913
<i>Oryza sativa</i>	Chr3_11550444_11551137	Chr3	11550444	11551137	OSA_circ03522	PMID: 27739914
<i>Oryza sativa</i>	Chr4_29982442_29982821	Chr4	29982442	29982821	OSA_circ04545	PMID: 27739915
<i>Oryza sativa</i>	Chr5_17342446_17342852	Chr5	17342446	17342852	OSA_circ05013	PMID: 27739916
<i>Oryza sativa</i>	Chr5_28580407_28580547	Chr5	28580407	28580547	OSA_circ05293	PMID: 27739917
<i>Oryza sativa</i>	Chr5_29522019_29522678	Chr5	29522019	29522678	OSA_circ05328	PMID: 27739918
<i>Oryza sativa</i>	Chr5_3617186_3617467	Chr5	3617186	3617467	OSA_circ04874	PMID: 27739919
<i>Oryza sativa</i>	Chr7_11593140_11593419	Chr7	11593140	11593419	OSA_circ06066	PMID: 27739920
<i>Oryza sativa</i>	Chr7_28426089_28426740	Chr7	28426089	28426740	OSA_circ06338	PMID: 27739921
<i>Oryza sativa</i>	Chr8_19735841_19736366	Chr8	19735841	19736366		PMID: 27739922
<i>Oryza sativa</i>	Chr3_267627_268062	Chr3	267627	268062	OSA_circ09450	PMID: 27739923
<i>Oryza sativa</i>	Chr4_35476588_35477345	Chr4	35476588	35477345	OSA_circ04754	PMID: 27739924
<i>Oryza sativa</i>	Os_ciR133	Chr3	11550444	11551137	OSA_circ03522	PMID: 26204923
<i>Oryza sativa</i>	Os_ciR182	Chr5	29522019	29522678	OSA_circ05328	PMID: 26204923
<i>Oryza sativa</i>	Os_ciR190	Chr5	3617186	3617467	OSA_circ04874	PMID: 26204923
<i>Oryza sativa</i>	Os_ciR158	Chr1	21424261	21426198	OSA_circ00838	PMID: 26204923
<i>Oryza sativa</i>	Os_ciR308	Chr11	21179446	21180854	OSA_circ08150	PMID: 26204923
<i>Oryza sativa</i>	Os_ciR455	Chr5	28580407	28580547	OSA_circ05293	PMID: 26204923
<i>Oryza sativa</i>	Os_ciR207	Chr3	27106436	27107773	OSA_circ09523	PMID: 26204923
<i>Oryza sativa</i>	Os_ciR239	Chr3	30220074	30221928	OSA_circ11640	PMID: 26204923
<i>Oryza sativa</i>	Os_ciR198	Chr7	28426089	28426740	OSA_circ06338	PMID: 26204923
<i>Oryza sativa</i>	Os_ciR300	Chr5	17342446	17342852	OSA_circ05013	PMID: 26204923
<i>Hordeum vulgare</i>	Cax2_circular RNA	Chr4	356281355	356282249	HVU_circ03367	PMID: 27375638

<i>Hordeum vulgare</i>	Ctr1 like_circular RNA	Chr3	351423944	351425007	HVU_circ03016	PMID: 27375639
<i>Hordeum vulgare</i>	MicroRNA1126_circular RNA	Chr2	467982888	467983386	HVU_circ02772	PMID: 27375640
<i>Hordeum vulgare</i>	Aux1_circular RNA	Chr3	486789367	486789848	HVU_circ00990	PMID: 27375641
<i>Hordeum vulgare</i>	AbcI3_circular RNA	Morex_contig1661226	956	1173		PMID: 27375642
<i>Hordeum vulgare</i>	18S rRNA_circular RNA1	Chr1	429515268	429515439	HVU_circ02592	PMID: 27375643
<i>Hordeum vulgare</i>	18S rRNA_circular RNA2	Chr1	429515283	429515435	HVU_circ02596	PMID: 27375644
<i>Hordeum vulgare</i>	18S rRNA_circular RNA3	Chr1	429515253	429515394	HVU_circ02588	PMID: 27375645
<i>Hordeum vulgare</i>	18S rRNA_circular RNA4	Chr1	429515283	429515394	HVU_circ02595	PMID: 27375646
<i>Hordeum vulgare</i>	18S rRNA_circular RNA5	Chr1	429515275	429515370	HVU_circ02104	PMID: 27375647
<i>Hordeum vulgare</i>	18S rRNA_circular RNA6	Chr1	429515253	429515403	HVU_circ02589	PMID: 27375648
<i>Hordeum vulgare</i>	18S rRNA_circular RNA7	Chr1	429513196	429513343		PMID: 27375649
<i>Hordeum vulgare</i>	Internal transcribed spacer 2 of 18S,5.8S,26S rRNA_circular RNA1	Chr1	429512475	429512569	HVU_circ02578	PMID: 27375650
<i>Hordeum vulgare</i>	Internal transcribed spacer 2 of 18S,5.8S,26S rRNA_circular RNA2	Chr1	177434203	177434347		PMID: 27375651
<i>Hordeum vulgare</i>	Nad9_circular RNA	Morex_contig_70567	2809	3204		PMID: 27375652
<i>Hordeum vulgare</i>	Mit. Apocytochrome b_circular RNA	Morex_contig_42365	12844	13477		PMID: 27375653
<i>Hordeum vulgare</i>	Cox1_circular RNA1	Chr1	23865393	238657407		PMID: 27375654
<i>Hordeum vulgare</i>	Cox1_circular RNA2	Chr1	23865228	23865597	HVU_circ02390	PMID: 27375655
<i>Hordeum vulgare</i>	Cox1_circular RNA3	Chr1	23865348	23865740	HVU_circ00286	PMID: 27375656
<i>Hordeum vulgare</i>	Cox1_circular RNA4	Chr1	23864364	23866057	HVU_circ00336	PMID: 27375657
<i>Hordeum vulgare</i>	Cox1_circular RNA5	Chr1	23864474	23866037	HVU_circ00155	PMID: 27375658
<i>Hordeum vulgare</i>	Cox1_circular RNA6	Chr1	23864318	23866037	HVU_circ00037	PMID: 27375659
<i>Hordeum vulgare</i>	Cystathionine beta lyase_circular RNA	Chr7	53946083	53946582	HVU_circ01734	PMID: 27375660
<i>Hordeum vulgare</i>	BZip11_circular RNA	Chr6	52088926	52089401	HVU_circ03830	PMID: 27375661
<i>Hordeum vulgare</i>	ADP ribosylation factor 1_circular RNA	Chr1	389129363	389130325	HVU_circ02532	PMID: 27375662
<i>Hordeum vulgare</i>	Sec23/Sec24 transport protein_circular RNA	Chr2	482080734	482081397	HVU_circ00698	PMID: 27375663
<i>Hordeum vulgare</i>	Fumarase 2_circular RNA	Chr4	243159573	243159671		PMID: 27375664
<i>Hordeum vulgare</i>	Inositol transporter 2_circular RNA	Chr2	483514445	483514888	HVU_circ00699	PMID: 27375665

<i>Hordeum vulgare</i>	Formin like protein 20_circular RNA1	Chr4	491530198	491530553		PMID: 27375666
<i>Hordeum vulgare</i>	Formin like protein 20_circular RNA1	Chr4	491530332	491530553		PMID: 27375667
<i>Hordeum vulgare</i>	Alpha mannosidase 1_circular RNA	Chr2	566491430	566492027	HVU_circ00798	PMID: 27375668
<i>Hordeum vulgare</i>	Chromosome segregation protein_circular RNA	Chr5	361207403	361207861		PMID: 27375669
<i>Hordeum vulgare</i>	Laccase 12_circular RNA	Chr3	499962355	499962651	HVU_circ03115	PMID: 27375670
<i>Hordeum vulgare</i>	ARID/BRIGHT DNA binding protein_circular RNA	Chr2	532048153	532048410	HVU_circ02138	PMID: 27375671
<i>Hordeum vulgare</i>	Ubiquitin conjugating enzyme 11_circular RNA	Chr3	473869516	473869731	HVU_circ03099	PMID: 27375672
<i>Hordeum vulgare</i>	Probable microtubule stabilizing protein_circular RNA	Chr4	330511991	330512323		PMID: 27375673
<i>Hordeum vulgare</i>	RNA binding (RRM/RBD/RNP motifs) protein_circular RNA	Chr4	252670767	252671078	HVU_circ01152	PMID: 27375674
<i>Hordeum vulgare</i>	RNA binding (RRM/RBD/RNP motifs) protein_circular RNA	Chr6	308455217	308455370	HVU_circ01625	PMID: 27375675
<i>Hordeum vulgare</i>	RNA binding (RRM/RBD/RNP motifs) protein_circular RNA	Chr6	260427394	260427518	HVU_circ01604	PMID: 27375676
<i>Hordeum vulgare</i>	Ribosomal protein L30/L7_circular RNA	Chr5	524054971	524055497	HVU_circ01625	PMID: 27375677
<i>Hordeum vulgare</i>	Transducin/WD40 repeat like protein_circular RNA	Chr5	484562574	484563329	HVU_circ01416	PMID: 27375678
<i>Hordeum vulgare</i>	Abscisic acid responsive (TB2/DP1, HVA22) protein_circular RNA	Chr6	20988426	20990992	HVU_circ01496	PMID: 27375679
<i>Hordeum vulgare</i>	Far upstream element binding protein 2_circular RNA	Chr6	245908278	245908734	HVU_circ03867	PMID: 27375680
<i>Hordeum vulgare</i>	Sec independent protein translocase_circular RNA	Morex_contig_106453	2137	3175		PMID: 27375681
<i>Hordeum vulgare</i>	Ubiquitin specific protease 17_circular RNA	Chr7	307483097	307485269	HVU_circ04178	PMID: 27375682

<i>Hordeum vulgare</i>	Probable KH domain containing splicing factor_circular RNA	Chr7	457516955	457517152	HVU_circ04202	PMID: 27375683
<i>Hordeum vulgare</i>	Ribosomal protein L6_circular RNA	Chr6	245896672	245897042	HVU_circ01588	PMID: 27375684
<i>Hordeum vulgare</i>	Glycyl tRNA synthetase 2_circular RNA2	Chr6	268555508	268556210	HVU_circ01610	PMID: 27375685
<i>Hordeum vulgare</i>	Glycyl tRNA synthetase 2_circular RNA2	Chr6	268555508	268556362	HVU_circ01611	PMID: 27375686
<i>Hordeum vulgare</i>	Kinesin related protein 11 like_circular RNA	Chr1	128008822	128014221	HVU_circ00397	PMID: 27375687
<i>Hordeum vulgare</i>	SAD1/UNC 84 domain protein 2_circular RNA	Chr1	60689841	60690191	HVU_circ00356	PMID: 27375688
<i>Hordeum vulgare</i>	Probable beta-1-4-glucosyltransferase_circular RNA	Chr4	71095325	71097097	HVU_circ01081	PMID: 27375689
<i>Hordeum vulgare</i>	Unknown_circular RNA	Chr7	4237959	4238849		PMID: 27375690
<i>Hordeum vulgare</i>	Unknown_circular RNA	Chr2	476367671	476368169	HVU_circ02134	PMID: 27375691
<i>Hordeum vulgare</i>	Probable long non coding RNA_circular RNA	Chr2	605441109	605441443	HVU_circ02152	PMID: 27375692
<i>Hordeum vulgare</i>	Unknown_circular RNA	Chr3	100501939	100502294	HVU_circ02165	PMID: 27375693
<i>Hordeum vulgare</i>	Probable long non coding RNA_circular RNA	Chr4	247058951	247059280	HVU_circ03322	PMID: 27375694
<i>Hordeum vulgare</i>	Probable aminopeptidase_circular RNA	Chr5	286201637	286202872	HVU_circ03589	PMID: 27375695
<i>Hordeum vulgare</i>	Unknown_circular RNA	Chr5	6888869	6889034	HVU_circ03486	PMID: 27375696
<i>Hordeum vulgare</i>	Probable long non coding RNA_circular RNA	Chr5	53926495	53926935		PMID: 27375697
<i>Hordeum vulgare</i>	Probable long non coding RNA_circular RNA	Chr1	363958561	363959513	HVU_circ02523	PMID: 27375697

Table S4. Gene ontology (GO) enrichment analysis for the genes in the miR156a-related network

		Biological Process	
GO Term	Description	Genes	P-value
GO:0000103	sulfate assimilation	[AT2G17640]	1.88E-02
GO:0000302	response to reactive oxygen species	[AT2G37860]	3.24E-02
GO:0006355	regulation of transcription, DNA-templated	[AT2G42200] [AT1G27360] [AT1G53160] [AT3G57920] [AT1G69170] [AT5G50570] [AT3G15270] [AT5G43270]	5.36E-04
GO:0006535	cysteine biosynthetic process from serine	[AT2G17640]	1.88E-02
GO:0009267	cellular response to starvation	[AT3G62420]	8.83E-03
GO:0009648	photoperiodism	[AT2G37860]	7.57E-03
GO:0009827	plant-type cell wall modification	[AT2G33810] [AT3G57920]	2.00E-02
GO:0009860	pollen tube growth	[AT2G33810] [AT3G57920]	3.79E-02
GO:0009886	post-embryonic animal morphogenesis	[AT2G33810]	7.57E-03
GO:0009911	positive regulation of flower development	[AT2G33810]	4.70E-02
GO:0010038	response to metal ion	[AT1G03980]	1.01E-02
GO:0010228	vegetative to reproductive phase transition of meristem	[AT2G42200] [AT2G33810] [AT3G57920]	5.79E-03
GO:0010229	inflorescence development	[AT2G33810]	2.38E-02
GO:0010321	regulation of vegetative phase change	[AT1G53160] [AT2G33810] [AT3G15270]	6.50E-08
GO:0010358	leaf shaping	[AT1G27370]	1.01E-02
GO:0046938	phytochelatin biosynthetic process	[AT1G03980]	3.79E-03
GO:0048366	leaf development	[AT2G42200] [AT2G37860]	7.84E-03
GO:0048507	meristem development	[AT2G33810]	3.49E-02
GO:0048510	regulation of timing of transition from vegetative to reproductive phase	[AT1G27360] [AT1G27370] [AT5G43270]	9.02E-06
GO:0048653	anther development	[AT2G42200] [AT3G57920] [AT5G50570] [AT5G50670] [AT5G43270]	1.76E-08
GO:2000025	regulation of leaf formation	[AT2G42200]	3.79E-03
GO:2000693	positive regulation of seed maturation	[AT3G62420]	5.06E-03

Molecular Function			
GO Term	Description	Genes	P-value
GO:0003700	transcription factor activity, sequence-specific DNA binding	[AT2G42200] [AT1G27360] [AT1G53160] [AT2G33810] [AT3G57920] [AT1G69170] [AT5G50570] [AT3G15270] [AT1G27370] [AT3G62420] [AT5G43270]	4.85E-06
GO:0009001	serine O-acetyltransferase activity	[AT2G17640]	7.57E-03
GO:0016756	glutathione gamma-glutamylcysteinyltransferase activity	[AT1G03980]	7.57E-03

Cellular Component			
GO Term	Description	Genes	P-value
GO:0005634	nucleus	[AT2G42200] [AT2G36810] [AT1G27360] [AT1G26890] [AT1G05910] [AT1G53160] [AT5G25560] [AT4G35170] [AT2G33810] [AT2G21840] [AT3G57920] [AT1G69170] [AT5G50570] [AT3G15270] [AT1G22000] [AT1G27370] [AT3G62420] [AT5G50670] [AT4G24270] [AT5G43270]	2.10E-03

Table S5. The expression levels of circRNAs in the miR156a-related network

Tools	Name	Treatment										
		E2LLA	E2HL30 A	E2HL30 B	E2HL2 HA	E2HL2 Hb	TNR1L LA	TNR1H L30A	TNR1H L2HA			
Finder	ATH_circ03766	0	0	0	0	0	0	0	0.0525	0		
Finder	ATH_circ03768	0	0	0	0	0	0	0	0.0525	0		
Finder	ATH_circ05254	0	0	0	0.0334	0	0	0	0	0		
UROBORUS	ATH_circ09695	0	0	0	0	0	0	0	0	0.0147		
UROBORUS	ATH_circ09697	0	0.0298	0	0	0	0	0	0	0		
UROBORUS	ATH_circ09698	0.0143	0	0	0.0167	0	0	0	0	0		
UROBORUS	ATH_circ09699	0.0428	0.1192	0.1124	0.3177	0.2040	0.0759	0.0787	0.1761			
UROBORUS	ATH_circ09700	0	0	0	0.0167	0	0	0	0	0.0147		
UROBORUS	ATH_circ09701	0.0143	0	0	0	0.0170	0.0190	0.0262	0			
		No treatment		4 CEL		37 CEL		200mM NaCl		300mM mannitol		
UROBORUS	ATH_circ09695	0	0	0	0	0	0	0	0	0	0.0388	0
UROBORUS	ATH_circ09696	0.0511	0	0	0	0	0	0	0	0	0	0
UROBORUS	ATH_circ09697	0	0	0	0	0.0261	0	0	0	0	0	0

E2LLA: E2 Low Light bioreplicate A**E2HL30A:** E2 High-Light 30 minutes bioreplicate A**E2HL30B:** E2 High-Light 30 minutes bioreplicate B**E2HL2HA:** E2 High-Light 120 minutes bioreplicate A**E2HL2HB:** E2 High-Light 120 minutes bioreplicate B**TNR1LLA:** tnr-1 Low Light bioreplicate A**TNR1HL30A:** tnr-1 High-Light 30 minutes bioreplicate A**TNR1HL30B:** tnr-1 High-Light 120 minutes bioreplicate A