

Supplemental Table S1. PCR primers used for Q-PCR amplification of lincRNA and functional genes

Primer	Forward primer sequence	Reverse primer sequence
T10.12768	5-TGTGCAGATAATTTCCAGCCAT-3	5-TTAACAGTAGCTGCGGCAAG-3
TraesCS1B01G243100	5-GCAAGCTTCCAAGGCCATTT-3	5-GGAAATTCGTGTCCCTCGGT-3
T16.1187	5-CCTCAGGATCATGCCTAGCG-3	5-GCAGACAGGCACCAATGTTC-3
TraesCS1B01G146800	5-TCTAGCGATCCCCAAACCTT-3	5-CTCGCCATGTGCTAGGTGAT-3
T10.65297	5-GCTCGTCGTGCACTACCTCT-3	5-AGATCCCAGGGGTGAAC TTG-3
TraesCS3D01G333100	5-AGACCGACTGGATCATGCAC-3	5-CTTGAGGGACCCCTTCTTGC-3
T13.19448	5-GGAGTGTGGCTCGATT CATCT-3	5-AACATCTCCTGAAGCGGCTG-3
TraesCS4D01G172200	5-ATATGGCGGAAATACGGGCA-3	5-GATCTGGGCTTGCTCTTGG-3
T4.45663	5-CATGACCCAGTCGGTGCG-3	5-CCGTGGGGAACAAGAAGACG-3
TraesCS5D01G279100	5-GACTGGAGTGGCGACTGAAA-3	5-TTGTGCGTCCACGATTCAGA-3
T16.26398	5-AGCACTCGCTTGATGGAGTT-3	5-CAAGCAAAGGCGGACAGAAC-3
TraesCS5B01G565100	5-CCTTCCCGGAGGATACATGC-3	5-TTCGCTTGTAAGCCATGC-3
T13.23192	5-AGGGCCTCGTCTACTACCTT-3	5-ACACGCGCACACCTTATCAA-3
TraesCS1B01G384100	5-CGCAAGTTCATGCTGCTTCA-3	5-CTTCCTTATCGGCACCCTCC-3
TraesCS1B01G384200	5-ACCGAGGAACCACAATCGTC-3	5-GAGTCTTGCCAGAGCATCG-3
T10.79431	5-CTCGTCACCTTCTACGGCTG-3	5-TTGGGCACGTACTCGTACAC-3
TraesCS1B01G394900	5-CTCGTCACCTTCTACGGCTG-3	5-TTGGGCACGTACTCGTACAC-3
T16.21355	5-ACACAAAGCAATCCACCAACA-3	5-CACATAAGGATCCATAGTCCGTCA-3
TraesCS1B01G416400	5-ACCAAACCAATCAATGGTGCC-3	5-TAGACGCTTTTGTCTGCCC-3
TraesCS1B01G416500	5-CAGGAGGAAGGCTACATGCC-3	5-CTCCTTGTTGGGTGTGCATGA-3
T16.13521	5-CATGACACAGGCCATGGGAG-3	5-GCAAGTAGCCAGTCCACCTCAC-3
TraesCS6A02G246400	5-TCAGTGGCAAGGT TAGACAATGG-3	5-GCGTTTTCTCATTTTCCAGCT-3
MiR1137	5-GGCGGGTAGTACAAAGTTGAGTCAT-3	
T13.17661	5-TATTGGTTTCTCTTCCATCACTTCC-3	5-GGATTTCTTGCTATTGGCGATT-3
TraesCS1B02G415800	5-GTGGCTGTTCTGTAGTTCTTCTGG-3	5-CTAGGTAGATT TGCCAAAGGAGATT-3
MiR399b	5-GTGCCAAAGGAGAATTGCCCTG-3	
T13.21716	5-CCTCGCCCTCTCGTTTGTCC-3	5-CGCGCCGGTGTCTACTACG-3
TraesCS2D02G400500	5-GAACAAGGAAGGTGTGCGAGTC-3	5-CTGCTCACTCATCTTCCTATCCG-3
MiR156d	5-GCGGCTCACTCCTCTTTCTGTGTCAG-3	
Actin	5-CTTGTATGCCAGCGGTGCGAAC-3	5-CTTGTAATCAAGGGCCACG-3

Supplemental Table S2. List of the identified adjacent functional genes nearby DE-lncRNAs regulated by fungi

LncRNA ID	start	end	gene ID	gene ID	gene ID	type
T10.42929	365493280	365494086	TraesCS1A01G203600	-	TraesCS1A01G203700	i
T10.71817	365508001	365508486	TraesCS1A01G203700	-	TraesCS1A01G203800	i
T10.72915	426270941	426272137	TraesCS1A01G238900	-	TraesCS1A01G239000	i
T10.79431	549711921	549712334		TraesCS1A01G374700		in
T13.26624	566688953	566689218	TraesCS1A01G403800	-	TraesCS1A01G403900	i
T16.32365	99019224	99019529				i
T16.538	566689202	566689416	TraesCS1A01G403800	-	TraesCS1A01G403900	i
T16.6110	316260175	316264040	TraesCS1A01G176500	-	TraesCS1A01G176600	i
T16.83333	34166173	34167056		TraesCS1A01G052200		in
T16.89858	461357093	461357500		TraesCS1A01G265800		u
T19.38037	114544760	114545415	-	TraesCS1A01G112500	-	in
T19.51424	16388823	16389423	-	TraesCS1A01G033500	-	in
T4.10971	292014696	292015079	TraesCS1A01G162500	-	TraesCS1A01G162600	i
T4.17456	457945904	457946310	TraesCS1A01G262500	-	TraesCS1A01G262600	i
T4.31722	298565430	298566465	-	TraesCS1A01G165700	-	in
T4.9130	361058780	361059226	TraesCS1A01G200400	-	TraesCS1A01G200500	i
T10.12768	431455644	431456002	TraesCS1B01G243100		TraesCS1B01G243200	i
T10.79431	626687757	626688170		TraesCS1B01G394900		in
T13.23192	616651220	616652165	TraesCS1B01G384100		TraesCS1B01G384200	i
T13.23369	503874785	503875642		TraesCS1B01G289100		in
T13.24210	505069710	505070418		TraesCS1B01G289600		in
T13.26624	657506840	657507105		TraesCS1B01G433300		in
T13.51457	637369280	637370142		TraesCS1B01G410300		in
T16.1187	207139786	207140379	TraesCS1B01G146700		TraesCS1B01G146800	i
T16.13852	123340257	123343863	TraesCS1B01G110200		TraesCS1B01G110300	i
T16.16515	359499444	359500832	TraesCS1B01G200700		TraesCS1B01G200800	i
T16.21355	641286324	641286654	TraesCS1B01G416400		TraesCS1B01G416500	i
T16.32365	132938865	132939173		TraesCS1B01G113500		u
T16.3724	314571476	314571953		TraesCS1B01G174600		in
T16.538	657507089	657507303		TraesCS1B01G433300		in
T16.7005	637370555	637370944		TraesCS1B01G410300		u
T16.83333	54880186	54881077		TraesCS1B01G069300		in
T16.89858	484366323	484366757		TraesCS1B01G276800		u
T19.42425	283123319	283125402	TraesCS1B01G163000		TraesCS1B01G163100	i
T4.17456	480327328	480327728		TraesCS1B01G273100		u
T7.4304	484376735	484376944		TraesCS1B01G276900		u
T10.79431	457073878	457074291		TraesCS1D01G381800		in
T13.13743	443719827	443720639	TraesCS1D01G360600		TraesCS1D01G360700	i
T13.24210	377804285	377804992		TraesCS1D01G279700		in
T13.26624	473034324	473034589		TraesCS1D01G411600		in
T16.13108	63544353	63544806		TraesCS1D01G081200		u
T16.32365	80448920	80449212		TraesCS1D01G094700		u
T16.3724	219485377	219485881		TraesCS1D01G155900		in

T16.538	473034573	473034787		TraesCS1D01G411600	in
T16.64464	7348702	7349723		TraesCS1D01G015900	in
T16.67303	322394686	322395435	TraesCS1D01G234200	TraesCS1D01G234300	i
T16.89858	361907905	361908277		TraesCS1D01G266000	u
T19.2493	104155	105425	TraesCS1D01G000300	TraesCS1D01G000400	i
T4.16520	364836045	364836674	TraesCS1D01G269300	TraesCS1D01G269400	i
T4.17456	356860393	356860803		TraesCS1D01G262500	u
T4.31722	249136868	249137893		TraesCS1D01G175000	in
T7.4304	361914907	361915130		TraesCS1D01G266100	in
T10.50565	602479115	602479747		TraesCS2A01G358100	in
T10.67324	729296885	729297184		TraesCS2A01G500400	in
T10.69481	62369737	62371288		TraesCS2A01G111000	in
T10.71740	460905193	460906023		TraesCS2A01G278000	in
T10.72188	30125872	30126341		TraesCS2A01G067300	in
T10.74750	448571241	448572037		TraesCS2A01G274100	in
T10.75971	30048457	30048961		TraesCS2A01G066800	in
T13.29133	268994552	268995254		TraesCS2A01G231000	in
T13.40810	551530311	551531318		TraesCS2A01G322300	in
T13.46035	624460537	624460792		TraesCS2A01G381100	u
T13.48890	105523008	105523303		TraesCS2A01G158600	u
T16.10620	583159783	583161218	TraesCS2A01G345100	TraesCS2A01G345200	i
T16.16253	59724640	59725797	TraesCS2A01G107300	TraesCS2A01G107400	i
T16.4584	671339831	671340612			i
T16.5516	414499697	414500456		TraesCS2A01G262500	in
T16.6511	689630237	689630654		TraesCS2A01G438200	p
T16.68377	716708130	716708882	TraesCS2A01G477700	TraesCS2A01G477800	i
T16.8598	682011760	682014906	TraesCS2A01G428600	TraesCS2A01G428700	i
T16.87060	105531924	105532259		TraesCS2A01G158700	u
T16.89589	166630189	166630494		TraesCS2A01G196700	u
T19.34110	547266321	547266684	TraesCS2A01G319600	TraesCS2A01G319700	i
T19.56093	593310485	593310756		TraesCS2A01G352600	u
T19.61316	735560797	735561173		TraesCS2A01G510200	in
T4.17514	78345493	78345850		TraesCS2A01G130600	u
T4.26251	51583892	51584222		TraesCS2A01G098100	u
T4.36308	15757314	15757723		TraesCS2A01G036900	u
T7.10731	748542176	748542455		TraesCS2A01G531500	in
T1.12879	510059680	510061857		TraesCS2B01G357100	p
T10.50565	540705854	540706476		TraesCS2B01G377500	in
T10.67324	722633618	722633908		TraesCS2B01G528300	in
T10.71740	412405394	412406213		TraesCS2B01G295400	in
T10.72188	44360418	44360889		TraesCS2B01G079500	p
T10.74750	108905698	108906745	TraesCS2B01G142000	TraesCS2B01G142100	i
T10.74750	405648407	405649203		TraesCS2B01G291800	in
T10.75971	44286307	44286807		TraesCS2B01G079200	in
T10.81367	109139515	109140687	TraesCS2B01G142200	TraesCS2B01G142300	i
T13.40810	513589721	513590747		TraesCS2B01G360500	in

T13.46035	565212256	565212515		TraesCS2B01G398400		u
T16.10620	517700918	517702353	TraesCS2B01G363400		TraesCS2B01G363500	i
T16.21059	198424322	198425098	TraesCS2B01G213700		TraesCS2B01G213800	i
T16.4584	622702202	622702986		TraesCS2B01G433400		in
T16.7920	632395984	632396417	TraesCS2B01G440200		TraesCS2B01G440300	i
T16.89589	214315030	214315312		TraesCS2B01G224300		u
T16.94408	680074917	680075223		TraesCS2B01G482300		u
T19.18549	746101349	746101791		TraesCS2B01G550200		p
T19.49300	214283177	214283452		TraesCS2B01G224000		u
T4.17514	121354555	121354911		TraesCS2B01G152900		p
T4.21651	447817437	447817914	TraesCS2B01G312300		TraesCS2B01G312400	i
T4.26251	77170642	77170974		TraesCS2B01G113800		u
T7.25929	250069475	250069839		TraesCS2B01G246000		p
T7.26350	565078675	565078983		TraesCS2B01G398200		u
T7.27596	564878008	564878632	TraesCS2B01G397800	TraesCS2B01G397900	TraesCS2B01G398000	i
T7.621	798713436	798713920	TraesCS2B01G626400		TraesCS2B01G626500	i
T7.62448	528472283	528473057	TraesCS2B01G370500		TraesCS2B01G370600	i
T10.50565	459311870	459312510		TraesCS2D01G356900		in
T10.63803	480323325	480323721		TraesCS2D01G376100		p
T10.67324	595165219	595165577		TraesCS2D01G500600		in
T10.72188	27901150	27901621		TraesCS2D01G065600		in
T10.74750	72171151	72172204		TraesCS2D01G123300		in
T10.75971	27860313	27860817		TraesCS2D01G065200		in
T13.14484	15967174	15967548		TraesCS2D01G044100		u
T13.21477	459313288	459313729	TraesCS2D01G356900		TraesCS2D01G357000	i
T13.29133	223912433	223913132		TraesCS2D01G235600		in
T13.40810	435147270	435148268		TraesCS2D01G340800		in
T13.46035	481990642	481990896	TraesCS2D01G377400		TraesCS2D01G377500	i
T16.10620	439957572	439959006	TraesCS2D01G343600		TraesCS2D01G343700	i
T16.16253	59727886	59729058		TraesCS2D01G107600		u
T16.4584	526375315	526376095		TraesCS2D01G411600		in
T16.5516	318078518	318079232		TraesCS2D01G261500		in
T16.87060	109737735	109738076		TraesCS2D01G165500		u
T16.89589	156709561	156709866		TraesCS2D01G204700		u
T16.94408	567057671	567057940		TraesCS2D01G460800		u
T19.44012	493193756	493194447	TraesCS2D01G387800		TraesCS2D01G387900	i
T19.56093	449698511	449698808		TraesCS2D01G351600		p
T4.26251	49877689	49878020		TraesCS2D01G097500		u
T1.26311	113713641	113713917		TraesCS3A01G136100		in
T10.67718	687527450	687527688		TraesCS3A01G447500		in
T10.68603	673922818	673923227		TraesCS3A01G432600		p
T10.71969	687526451	687526828		TraesCS3A01G447500		in
T13.15115	223705918	223706903		TraesCS3A01G187400		p
T13.18884	687527201	687527467		TraesCS3A01G447500		in
T13.49502	662931137	662931497		TraesCS3A01G421400		p
T16.10482	208227551	208228628	TraesCS3A01G180200		TraesCS3A01G180300	i

T16.67438	674271154	674272464		TraesCS3A01G432900	in
T16.92879	623058201	623058899		TraesCS3A01G372500	in
T19.47487	153076942	153077529		TraesCS3A01G156800	in
T7.36158	537508810	537509254		TraesCS3A01G303200	u
T7.55773	108888847	108889339	TraesCS3A01G132100	TraesCS3A01G132200	i
T1.13377	737672046	737672571	TraesCS3B01G491200	TraesCS3B01G491300	i
T1.26311	146553731	146554007		TraesCS3B01G154000	in
T10.67718	730234449	730234691		TraesCS3B01G483500	in
T10.68603	713391331	713391732		TraesCS3B01G468500	p
T10.71969	730233456	730233833		TraesCS3B01G483500	in
T13.17661	159568814	159569883		TraesCS3B01G162300	in
T13.18884	730234206	730234466		TraesCS3B01G483500	in
T16.78117	99699391	99700457		TraesCS3B01G125300	in
T16.92879	640071918	640072655	TraesCS3B01G384000	TraesCS3B01G384100	i
T19.47487	194326317	194326872		TraesCS3B01G183300	in
T19.63822	71911452	71911887	TraesCS3B01G106300	TraesCS3B01G106400	i
T4.30836	146187526	146188248		TraesCS3B01G153900	in
T7.36158	539559885	539560300		TraesCS3B01G333100	in
T1.26311	95564527	95564803		TraesCS3D01G136900	in
T1.48244	26790623	26790885	TraesCS3D01G061600	TraesCS3D01G061700	i
T10.61947	419682168	419682616	TraesCS3D01G305800	TraesCS3D01G305900	i
T10.65297	445037895	445038202		TraesCS3D01G333100	in
T10.67718	550652992	550653233		TraesCS3D01G440200	in
T10.68603	538515121	538515520		TraesCS3D01G425900	p
T10.71969	550651991	550652368		TraesCS3D01G440200	in
T13.18281	276434578	276435245	TraesCS3D01G209000	TraesCS3D01G209100	i
T13.18884	550652741	550653009		TraesCS3D01G440200	in
T13.26060	57155246	57156785		TraesCS3D01G104500	in
T13.82017	585084548	585084928		TraesCS3D01G491400	p
T16.31058	48820058	48820682		TraesCS3D01G096300	in
T16.84582	39301170	39302025		TraesCS3D01G078700	in
T16.90046	577250939	577251243		TraesCS3D01G476600	u
T16.92879	479626137	479626828	TraesCS3D01G365300	TraesCS3D01G365400	i
T19.40646	49872403	49873046	TraesCS3D01G097900	TraesCS3D01G098000	i
T19.47487	136041146	136041733		TraesCS3D01G164700	i
T4.30836	95250806	95251527	TraesCS3D01G136600		i
T7.36158	412784489	412784925		TraesCS3D01G298600	p
T7.43633	577240216	577240631		TraesCS3D01G476500	u
T10.13072	278953126	278953897	TraesCS4A01G148300	TraesCS4A01G148400	i
T10.77159	63012762	63013094		TraesCS4A01G065700	in
T13.20318	215223675	215223930	TraesCS4A01G140200	TraesCS4A01G140300	i
T13.25967	570467566	570468644		TraesCS4A01G257700	in
T13.42245	111293320	111293831		TraesCS4A01G099300	in
T16.22835	312728491	312729260	TraesCS4A01G156500	TraesCS4A01G156600	i
T16.63733	629943296	629943971	TraesCS4A01G356700	TraesCS4A01G356800	i
T16.65568	517345915	517347693	TraesCS4A01G217600	TraesCS4A01G217700	i

T19.31149	626168480	626168877		TraesCS4A01G349500		u
T19.36312	710173573	710174163	TraesCS4A01G441800		TraesCS4A01G441900	i
T19.39526	60345042	60345487		TraesCS4A01G063600		u
T19.47131	558414573	558416304		TraesCS4A01G247300		in
T19.66363	625164578	625164981		TraesCS4A01G346100		p
T4.2342	60670891	60671261		TraesCS4A01G063800		u
T4.28944	125029766	125030253		TraesCS4A01G107700		u
T4.9309	504789792	504790712		TraesCS4A01G211100		in
T7.54351	216436753	216437197		TraesCS4A01G140700		p
T10.65362	548185215	548185467		TraesCS4B01G271900		in
T10.69095	582825841	582826356		TraesCS4B01G297300		in
T10.7014	673203631	673205039	TraesCS4B01G399000		TraesCS4B01G399100	i
T10.77159	503564971	503565303		TraesCS4B01G243100		in
T13.20318	362149576	362149828		TraesCS4B01G166800		u
T13.20374	499848047	499848671		TraesCS4B01G240800		in
T13.25967	46618847	46619871		TraesCS4B01G056800		in
T13.42245	437073011	437073508		TraesCS4B01G205000		in
T16.1111	536118599	536119466		TraesCS4B01G265100		in
T16.11885	439320127	439320420		TraesCS4B01G206700		p
T16.13521	650683897	650684597		TraesCS4B01G360800		in
T16.82271	499901459	499901778		TraesCS4B01G240900		u
T4.2342	499901460	499901826		TraesCS4B01G240900		u
T4.28944	423774882	423775339		TraesCS4B01G196800		in
T7.56285	374658974	374659291	TraesCS4B01G171100		TraesCS4B01G171200	i
T7.59997	78817807	78818223		TraesCS4B01G081200		p
T10.77159	405323544	405323876		TraesCS4D01G242700		in
T13.19448	299348879	299349379	TraesCS4D01G172100		TraesCS4D01G172200	i
T13.20318	294352079	294352334		TraesCS4D01G169400		u
T13.25967	32234329	32235379			TraesCS4D01G057200	i
T13.40522	435230791	435231191			TraesCS4D01G265400	i
T13.42245	353521581	353522092		TraesCS4D01G205900		in
T16.11885	355858318	355858606	TraesCS4D01G208300		TraesCS4D01G208400	i
T16.89122	11866008	11866469		TraesCS4D01G026800		in
T4.28944	341694781	341695240		TraesCS4D01G197100		p
T4.36197	280179201	280180674		TraesCS4D01G166200	TraesCS4D01G166200	in
T7.52205	16798697	16799035		TraesCS4D01G039100		u
T1.37489	631329487	631330277		TraesCS5A01G449000		in
T1.39963	593089391	593089930		TraesCS5A01G399800		in
T1.41418	553421460	553421925		TraesCS5A01G350600		u
T10.59108	3284959	3285626		TraesCS5A01G004900		in
T10.61842	511904202	511904892		TraesCS5A01G302400		in
T10.64534	3285867	3286948	TraesCS5A01G004900		TraesCS5A01G005000	i
T10.70983	546263475	546264127		TraesCS5A01G338400		u
T10.72364	565533965	565534868	TraesCS5A01G365500		TraesCS5A01G365600	i
T13.22353	126274365	126275578		TraesCS5A01G091500		in
T13.30088	365701388	365702233	TraesCS5A01G172600		TraesCS5A01G172700	i

T13.33891	48737582	48738658	TraesCS5A01G053400	TraesCS5A01G053500	i
T13.86345	650554527	650554909	TraesCS5A01G475300		in
T16.15844	510163581	510165424	TraesCS5A01G300900	TraesCS5A01G301000	i
T16.6266	423253576	423254292	TraesCS5A01G210100		in
T19.46503	306879691	306880534	TraesCS5A01G135700		in
T19.49358	523615525	523616107	TraesCS5A01G312000		p
T7.15783	32881583	32881998	TraesCS5A01G035500	TraesCS5A01G035600	i
T1.37489	626337310	626338112	TraesCS5B01G453800		in
T1.39963	580514597	580515136	TraesCS5B01G404600		in
T10.43083	650045881	650046237	TraesCS5B01G478100		in
T10.61842	487220964	487221661	TraesCS5B01G302500		in
T13.22353	129717765	129718976	TraesCS5B01G098000		in
T13.33010	41094825	41095657	TraesCS5B01G036800		in
T13.38179	691797025	691797340	TraesCS5B01G535800		p
T13.42814	204613382	204614459	TraesCS5B01G117000		in
T13.49097	700224979	700225370	TraesCS5B01G547000		u
T13.86345	658776107	658776441	TraesCS5B01G488300		in
T16.26398	710231891	710233057	TraesCS5B01G565100		in
T16.29097	323704369	323705251	TraesCS5B01G177300		in
T16.6266	377544673	377545384	TraesCS5B01G208100		in
T16.68333	484822509	484823220	TraesCS5B01G300100	TraesCS5B01G300200	i
T16.69540	91108972	91109503	TraesCS5B01G076100		u
T16.92969	25267361	25267726	TraesCS5B01G026400		p
T19.46503	251904371	251905210	TraesCS5B01G134500	TraesCS5B01G134600	i
T4.63565	216650854	216651120	TraesCS5B01G121400		in
T7.1464	410597566	410597852	TraesCS5B01G232600		p
T1.37489	502595554	502596359	TraesCS5D01G455500		in
T1.39963	473116856	473117396	TraesCS5D01G409500	TraesCS5D01G409600	in
T10.10058	524259916	524260403	TraesCS5D01G488900		in
T10.61842	406331833	406332579	TraesCS5D01G309000		in
T10.63275	510564974	510565595	TraesCS5D01G469500	TraesCS5D01G469600	i
T10.64534	6385125	6386204	TraesCS5D01G011800		in
T10.70609	28669697	28670421	TraesCS5D01G031300		in
T10.70689	445963438	445963918	TraesCS5D01G371800	TraesCS5D01G371900	i
T13.21716	76963820	76964529	TraesCS5D01G077000	TraesCS5D01G077100	i
T13.22353	117267252	117268512	TraesCS5D01G103600		in
T13.29048	152316919	152317926	TraesCS5D01G117800	TraesCS5D01G117900	i
T13.48939	531510459	531510831	TraesCS5D01G505700		in
T13.83915	324746326	324746831	TraesCS5D01G215600	TraesCS5D01G215700	i
T13.86345	522511919	522512301	TraesCS5D01G487600		in
T16.14974	517417430	517419218	TraesCS5D01G478800	TraesCS5D01G478900	i
T16.2284	46980988	46981368	TraesCS5D01G049200		u
T16.26398	556550564	556551751	TraesCS5D01G549600		in
T16.34184	423969606	423970532	TraesCS5D01G334200	TraesCS5D01G334300	i
T16.6266	325094765	325095466	TraesCS5D01G216300		in
T16.85315	428826923	428827697	TraesCS5D01G340400		in

T19.15126	175945099	175945610	TraesCS5D01G122000	TraesCS5D01G122100	i
T19.42350	92463964	92464404		TraesCS5D01G087400	p
T19.44304	23298258	23299031		TraesCS5D01G026000	in
T19.46503	228247598	228248437	TraesCS5D01G142200	TraesCS5D01G142300	i
T4.45663	381036427	381036898		TraesCS5D01G279100	in
T10.43307	610642897	610643295		TraesCS6A01G403200	u
T10.52330	79951268	79951996		TraesCS6A01G110800	in
T10.70585	456752186	456752507		TraesCS6A01G245100	in
T13.39161	55891909	55892308		TraesCS6A01G087700	p
T16.29292	99203113	99203716		TraesCS6A01G125800	in
T16.88703	482085429	482086047		TraesCS6A01G259300	p
T16.94232	574608987	574610550	TraesCS6A01G342000	TraesCS6A01G342100	i
T19.53578	588230950	588232333		TraesCS6A01G358100	in
T4.22567	378187391	378187870	TraesCS6A01G209100	TraesCS6A01G209200	i
T4.47960	53113919	53114668	TraesCS6A01G085700	TraesCS6A01G085800	i
T7.13344	582096054	582096399		TraesCS6A01G350300	u
T10.37616	643424590	643425082	TraesCS6B01G369800	TraesCS6B01G369900	i
T10.52330	136118551	136119300		TraesCS6B01G139000	in
T10.70585	504584139	504584460		TraesCS6B01G279200	in
T10.74527	245976412	245977123		TraesCS6B01G201600	in
T10.74990	338015260	338015868		TraesCS6B01G224100	u
T13.34604	412954525	412957905	TraesCS6B01G237600	TraesCS6B01G237700	i
T16.32266	712125644	712126904	TraesCS6B01G454500	TraesCS6B01G454600	i
T16.71332	307071843	307072935	TraesCS6B01G219100	TraesCS6B01G219200	i
T16.88703	516486482	516487105		TraesCS6B01G286600	p
T19.25423	233089949	233090543	TraesCS6B01G196800	TraesCS6B01G196900	i
T19.44037	539625932	539626853		TraesCS6B01G301300	in
T4.22567	414344127	414344612		TraesCS6B01G238200	u
T1.21563	56277221	56277626	TraesCS6D01G090300	TraesCS6D01G090400	i
T10.52330	62503293	62503998		TraesCS6D01G099400	in
T10.60580	426114896	426115317		TraesCS6D01G317700	p
T10.70585	318954745	318955066		TraesCS6D01G227500	in
T13.51403	32062287	32063118		TraesCS6D01G065600	in
T16.34261	138806544	138807275	TraesCS6D01G160300	TraesCS6D01G160400	i
T16.66043	368370698	368371073		TraesCS6D01G260900	p
T16.88703	342026691	342027315		TraesCS6D01G240400	p
T19.44037	358225888	358226808		TraesCS6D01G254000	in
T19.51118	86141902	86142549		TraesCS6D01G121100	p
T19.54493	307417112	307417613	TraesCS6D01G217700	TraesCS6D01G217800	i
T4.22567	266783533	266784040		TraesCS6D01G192700	u
T1.10042	151376416	151377037	TraesCS7A01G192400	TraesCS7A01G192500	i
T10.74444	679230672	679230913		TraesCS7A01G489000	in
T10.78030	516996689	516997212		TraesCS7A01G353300	p
T10.78590	436787087	436788281		TraesCS7A01G308600	in
T13.14637	95223963	95224752	TraesCS7A01G144300	TraesCS7A01G144400	i
T13.36817	621320325	621320827	TraesCS7A01G428100	TraesCS7A01G428200	i

T13.49993	719580088	719580484		TraesCS7A01G543100	p
T13.51285	81785328	81785678		TraesCS7A01G127400	u
T16.22544	474296034	474296275		TraesCS7A01G326400	in
T16.34607	191266090	191267072	TraesCS7A01G221900	TraesCS7A01G222000	i
T16.4332	632588313	632589027		TraesCS7A01G438600	in
T19.3424	3984169	3984989		TraesCS7A01G009100	in
T1.29171	708954967	708955342		TraesCS7B01G444600	u
T10.70962	611741554	611741766		TraesCS7B01G354000	in
T10.78590	381835642	381836804		TraesCS7B01G208700	in
T13.26008	478469112	478470159	TraesCS7B01G257500	TraesCS7B01G257600	i
T13.49912	465551989	465552380	TraesCS7B01G252500	TraesCS7B01G252600	i
T16.22544	427302646	427302893		TraesCS7B01G227000	in
T19.12077	553106441	553107385	TraesCS7B01G309000	TraesCS7B01G309100	i
T19.25513	364048336	364048716	TraesCS7B01G200500	TraesCS7B01G200600	i
T19.55749	744019439	744020450	TraesCS7B01G491000	TraesCS7B01G491100	i
T10.38424	78768941	78769358		TraesCS7D01G125900	in
T10.48402	511628242	511628942	TraesCS7D01G396900	TraesCS7D01G397000	i
T10.67416	113959136	113959675	TraesCS7D01G164700	TraesCS7D01G164800	i
T10.78590	386756271	386757476		TraesCS7D01G305300	in
T10.79603	111114829	111115340		TraesCS7D01G161200	u
T13.30347	254151091	254154186	TraesCS7D01G269300	TraesCS7D01G269400	i
T13.49085	198621480	198621758		TraesCS7D01G235700	p
T13.83254	596674952	596675900		TraesCS7D01G486200	u
T16.17652	117265770	117267087	TraesCS7D01G166500	TraesCS7D01G166600	i
T16.22544	412885465	412885712		TraesCS7D01G323100	in
T16.23889	117262727	117264407	TraesCS7D01G166500	TraesCS7D01G166600	i
T16.59590	16242682	16243036	TraesCS7D01G030900	TraesCS7D01G031000	i
T16.83398	298377642	298378263	TraesCS7D01G284000	TraesCS7D01G284100	i
T19.43209	635388451	635390074		TraesCS7D01G552200	p
T4.19936	384027350	384028014	TraesCS7D01G303400	TraesCS7D01G303500	i
T7.40941	618883627	618884327	TraesCS7D01G521800	TraesCS7D01G521900	i
T16.40226	314617752	314618013		TraesCSU01G212400	p
T4.2208	87231725	87232061		TraesCSU01G098500	p
T4.40145	98088507	98088972		TraesCSU01G113900	u
T4.9944	263127382	263127906		TraesCSU01G175000	in
T7.35185	41802368	41802853	TraesCSU01G052200	TraesCSU01G052300	i

Note: The location of lncRNA were given according to the reference genome. The types of lncRNA were given in the symbols i, in, p, and u representing long intergenic ncRNAs, long intron ncRNAs, promoter lncRNAs and untranslation region lncRNA.

Supplemental Table S3. List of the detailed relative expression values used to infer the correlation

Background	gene	0hpi	6hpi	12hpi	24hpi	36hpi	48hpi	72hpi	120hpi	168hpi	240hpi	r-value
N9134R	T16.1187	1	1.067	1.869	1.690	0.562	0.359	1.421	0.283	4.901	0.344	
N9134R	C2H2	1	1.291	2.352	2.386	1.492	0.752	0.766	1.166	6.858	1.472	0.940
N9134S	T16.1187	1	0.751	1.659	0.304	0.433	1.058	0.609	2.006	0.525	0.084	
N9134S	C2H2	1	1.434	0.318	0.255	8.988	0.151	0.124	3.537	1.244	1.173	-0.048
N9134R	T10.65297	1	2.816	7.725	7.208	2.898	0.772	3.067	7.293	13.363	1.426	
N9134R	NAC68L	1	2.530	9.663	5.541	2.479	1.343	6.453	5.648	21.830	0.682	0.922
N9134S	T10.65297	1	3.856	5.582	1.040	8.788	1.383	1.922	23.745	3.946	1.300	
N9134S	NAC68L	1	14.251	5.414	1.424	8.143	1.563	1.514	4.130	4.382	0.818	0.213
N9134R	T4.45663	1	0.127	0.753	1.014	2.865	0.250	0.410	0.465	5.764	4.664	
N9134R	NAC17	1	0.531	1.065	0.410	1.055	0.580	0.562	1.140	6.019	0.201	0.653
N9134S	T4.45663	1	0.555	0.574	0.442	4.037	0.114	0.138	1.934	1.148	0.921	
N9134S	NAC17	1	1.995	1.330	1.356	1.414	1.832	1.990	1.869	2.459	0.426	-0.087
N9134R	T10.12768	1	1.351	1.307	2.275	1.306	0.720	0.711	0.570	0.688	2.092	
N9134R	WRKY55L	1	2.189	0.563	3.481	2.625	1.914	1.290	0.589	1.276	4.948	0.810
N9134S	T10.12768	1	2.197	2.212	5.849	2.287	0.589	0.248	2.061	1.125	0.951	
N9134S	WRKY55L	1	0.921	1.584	2.599	1.532	0.658	0.527	3.822	0.228	3.723	0.361
N9134R	T13.19448	1	1.364	0.727	0.689	0.987	0.849	0.574	0.293	0.311	1.624	
N9134R	WRKY64/70	1	0.088	1.082	1.686	6.577	2.199	1.869	0.322	1.401	8.080	0.555
N9134S	T13.19448	1	1.672	2.327	4.349	2.487	0.721	0.135	1.112	1.478	1.676	
N9134S	WRKY64/70	1	0.063	0.227	0.089	0.215	0.016	0.015	0.283	0.037	0.556	-0.113
N9134R	T10.79431	1	1.468	1.105	6.803	4.788	2.923	4.009	2.358	9.000	55.426	
N9134R	RLK	1	1.262	1.668	4.467	4.049	2.313	2.844	1.284	4.557	33.925	0.998
N9134S	T10.79431	1	1.495	0.936	4.752	1.916	0.716	1.254	9.637	15.382	20.027	
N9134S	RLK	1	1.014	1.304	2.319	2.183	0.570	0.837	13.793	2.028	16.173	0.753
N9134R	T16.26398	1	1.649	2.131	0.833	1.093	0.464	1.675	2.215	14.101	0.887	
N9134R	MAPK	1	0.204	0.443	0.331	1.511	0.128	0.308	0.159	7.842	0.224	0.968
N9134S	T16.26398	1	0.867	0.398	0.299	1.239	0.502	0.731	0.613	3.263	0.105	
N9134S	MAPK	1	0.262	0.271	0.305	1.146	0.453	0.329	0.987	1.331	0.329	0.739
N9134R	T16.21355	1	0.286	0.773	0.364	0.891	0.414	0.527	0.488	3.158	0.748	
N9134R	Ferredoxin3	1	4.481	2.909	1.464	1.336	1.104	1.775	5.824	13.256	0.628	0.810
N9134R	SF8a	1	5.593	0.374	0.473	0.128	1.460	1.210	2.290	0.098	1.301	-0.426
N9134S	T16.21355	1	0.692	0.382	0.335	1.482	0.547	0.613	2.429	1.141	0.930	
N9134S	Ferredoxin3	1	1.280	1.550	1.150	8.165	0.531	0.188	8.498	4.730	1.110	0.869
N9134S	SF8a	1	3.200	1.389	4.805	3.181	1.475	0.821	1.123	1.313	2.069	-0.265
N9134R	T3.23192	1	0.333	0.966	1.238	2.713	0.360	0.607	1.231	11.466	3.072	
N9134R	DNAJ10	1	1.405	2.355	2.330	0.606	0.784	2.615	2.161	5.311	0.265	0.708
N9134R	Unnamed	1	0.359	2.169	1.998	0.400	0.656	0.908	0.731	0.665	0.968	-0.193
N9134S	T3.23192	1	0.887	1.024	1.295	4.269	0.882	0.373	3.381	5.253	5.469	
N9134S	DNAJ10	1	3.102	4.203	0.313	0.610	1.239	1.333	11.231	1.314	0.106	-0.003
N9134S	Unnamed	1	27.111	10.320	2.855	107.319	0.298	0.761	111.887	94.930	44.875	0.788

Note: Value for significance at $P = 0.05$ and 8 df is 0.549.