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ANALYSIS OF LNCRNAS AND CIRCRNAS IN *GLYCINE MAX* UNDER DROUGHT AND SALINE-ALKALINE STRESSES

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ABSTRACT

Long noncoding-RNAs (LncRNAs) and circular RNAs (circRNAs) are the major types of noncoding RNAs (ncRNAs) known to be involved during diverse biological processes in eukaryotes. However, less attention has been given to the identification, overall characteristics and expression analysis of LncRNAs and circRNAs under abiotic stresses in plants.. In our study, strand-specific RNA-seq data revealed the identification of a total 2,020 lncRNAs, including 1,979 known and 41 novel ones, and 830 circRNAs in soybean. Overall, 118 and 47 lncRNAs showed significant changes in expression levels under drought stress and saline-alkaline stress, respectively. In addition, soybean lncRNAs indicated diverse expression patterns suggesting a positive correlation with many biological processes including photosynthesis during stress responses by regulating gene expression in a *cis-/trans-*actingmanner. Our findings further indicated that transcriptional biosynthesis pathways and RNA transcriptional regulation were positively regulated during stress conditions. Furthermore, the back-splicing sites of circRNAs were also confirmed. Collectively, our study identified a group of stress-responsive lncRNAs and circRNAs in soybean, highlighting their potential contributions to abiotic stress responses, which pave the way for future functional studies.

Keywords: Strand-specific RNA sequencing; Stress response; lncRNA; circRNA; Expression pattern;

INTRODUCTION

Among the abiotic stresses that negatively affect the growth and development of crop plants, environmental factors are the most common inhibitors of yield(Bouain *et al*. 2019). *Glycine max* (soybean) is an economically important crop that is sensitive to abiotic stresses, particularly drought and saline-alkaline stresses(Kunert *et al*. 2016). This sensitivity means that there has been only limited success in breeding stress-resistant soybean cultivars. To overcome these limitations and increase the productivity of soybean, the molecular mechanisms of stress tolerance and their interaction with environmental factors should be better understood(Deinlein *et al*. 2014).

Noncoding RNAs are now recognized as crucial components of the stress response signaling networks that regulate plant defense systems. Long noncoding RNAs (lncRNAs) are defined as aheterogeneous group of noncoding RNAs whose transcripts are longer than 200 nucleotides (nt) (Kapranov *et al*. 2007). They do not contain any evolutionarily conserved open reading frames (Rivas *et al*. 2017). Previous studies have shown that they are expressed in a tissue- or stage-specific manner and their expression levels change in response to various environmental factors (Di *et al*. 2014; Liu *et al*. 2015; Qi *et al*. 2013; Rymarquis *et al*. 2008). The lncRNAs are functionally significant because they regulate RNA processing machinery in a *cis* or *trans* manner (Kung *et al*. 2013). Emerging evidence has indicated that some plant lncRNAs play multiple roles in the regulation of plant metabolism, development, stress responses, and other biological processes (Di *et al*. 2014; Shafiq *et al*. 2016; Wang *et al*. 2014). Numerous lncRNAs have been reported to participate in the responses to a wide variety of stresses in *Arabidopsis*,maize, medicago, and wheat (Liu *et al*. 2012; Wang *et al*. 2015b; Xin *et al*. 2011; Zhang *et al*. 2014). In addition, several stress-responsive lncRNAs such as COLDAIR, lncRNA16397, and Cdc28 have been functionally characterized in plants (Cui *et al*. 2016; Heo and Sung 2011; Nadal-Ribelles *et al*. 2014). However, we still have only a rudimentary understanding of the functions of most lncRNAs in response to stress.

Circular RNAs (circRNAs) are another categary of noncoding RNAs. They are circular in structure and are widespread in viroids or eukaryotes (Capel *et al*. 1993; Cocquerelle *et al*. 1993). CircRNAs can arise from exons or introns but are distinct structures with an independent manner of regulation (Memczak *et al*. 2013). Similar to lncRNAs, circRNAs show low expression levels and cell-type-specific patterns in eukaryotic cells (Salzman *et al*. 2013; Zuo *et al*. 2016). CircRNAs were suggested to be functionless when they have first identified in junk DNA some two decades ago (Nigro *et al*. 1991). However, recent studies have shown that circRNAs potentially play a role in enhancing the transcriptional activity of host genes (Hansen *et al*. 2013; Li *et al*. 2015; Memczak *et al*. 2013). Analyses of the expression patterns and regulatory functions of circRNAs have revealed that they are expressed in a range of eukaryotic organisms and have a regulatory pattern independent of, and different from, that of their cognate linear isoforms.

Stress-responsive lncRNAs and circRNAs have not been well studied in soybean. Little is known about how noncoding RNAs are expressed and responsible for gene expression regulation in soybean at the transcriptional or post-transcriptional levels during survival or acclimation responses. In this study, therefore, we conducted awhole-transcriptome analysis, identified comprehensive sets of soybeanlncRNAs and circRNAs, assessed the expression profiles of lncRNAs, and analyzed the regulatory mechanisms of lncRNAsunder drought and saline-alkaline stresses.

MATERIALS AND METHODS

Materials, stress treatments, and determination of physiological indexes: Seeds of the cultivated soybean variety "JY72" (a landrace cultivated in northeastern China) were placed in a sterile culture container in 1× Hoagland's solution (containing 4 mL/L Fe sequestrene, 6 mM K^+, and 4 mM Ca^{2+}). At the stage of four leaves, the plants were subjected to abiotic stress for 24 hours under continuous light (Liu *et al*. 2012). To impose the drought and saline-alkaline stresses, the seedlings were incubated in liquid Hoagland's medium containing 8% PEG and 110 mM NaCl + 50 mM $NaHCO_3$, respectively. Seedlings in liquid Hoagland's medium served as the control. The leaves were harvested from three groups per treatment, frozen with liquid nitrogen, and then stored at −80°C. Leaves were collected at 0 h, 6 h,12 h, and 24 h of the treatments to analyze superoxide dismutase (SOD) activity and malondialdehyde (MDA) content. A Tecan infinite M1000 Pro Microplate Reader(San Jose, CA, USA) was used to measure the absorbance of reaction solutions to determine SOD activity and calculate MDA content. The reaction solutions were prepared according to the instructions of a physiological assay kit (Nanjing Jiancheng Bioengineering Institute, Nanjing, China). All the processes were biologically and temporally repeated in three independent and parallel experiments.

Library construction for RNA-seq and sequencing procedures: mirVana™ miRNA Isolation Kit (Ambion, Foster City, CA, USA) was employed to isolate total RNAs. The TruSeq® Stranded RNA Sample Preparation reagent (Illumina, San Diego, CA, USA) was used to prepare Strand-specific libraries by following the manufacturer's instructions. We used Ribo-Zero rRNA removal beads to get rid of Ribosomal RNA from total RNA. After purification, total RNA was break up in to small pieces of fragments by using divalent cations at 95°C for 8 min. These RNA fragments were then synthesized into cDNA by using random primers. DNA Polymerase I was used to synthesis second-strand cDNA. Then, these cDNA fragments were precessed with end-repairment, including the addition of a single "A" base, and then ligated with adapters. Qubit® 2.0 Fluorometer (Life Technologies, Gaithersburg, MD,USA) was employed to quantify purified libraries and validated by Agilent 2100 bioanalyzer (Agilent Technologies, Palo Alto, CA, USA) to make sure the insert size and measure concentration . Clusters were generated by cBot with the library diluted to 10 pM and sequencing by Illumina HiSeq 2500 sequencer (Illumina, USA).

Bioinformatics analysis: Atfer filtering rRNAs, adapters and low-quality reads, and short-fragments, FASTQC tools (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/) were adopted to propress clean reads. We used TopHat v2.0.9 (Trapnell *et al*. 2009) to map the clean reads to the Glycine max v2.0 reference genome with two mismatches allowed. The transcriptomes of three libraries were assembled separately using Cufflinks and the whole genome sequence as a reference. by using Cuffcompare, when after comparing with the assembled transcript isoforms and the known protein coding transcripts, novel transcripts were gained. Putative lncRNAs were identified as novel transcripts, with the filters as followed: length more than 200 bp; exons more than 2; and ORF less than 300 bp (He *et al*. 2015; Wang *et al*. 2018; Wang *et al*. 2017); weak or non protein-coding ability (CPC score < 0 (Kong *et al*. 2007), CNCI score < 0 (Sun *et al*. 2013)), and no significant similarity with Pfam in a protein-coding database (Punta *et al*. 2012). We selected dynamicaly expressed lncRNAs used for predicting targets. The cis-acting target genes were considered as transcribed upstream or downstream of the lncRNAs within 10 kb distance. RNAplex software was emplpyed to predicted trans-acting targets.

We used CIRI version 1.2 (Gao *et al*. 2015) to characterize circRNAs. We used CIRI V1.2 to detect junction sites in sequence reads with PCC signals and PEM signals that reflected circRNA candidates by SAM alignment. Preliminary filtering was implemented using GT–AG splicing signals for the junction reads. After junction clustering, CIRI V1.2 was used to scan the SAM alignment again to detect junction-related reads and conduct further filtering to eliminate false-positive candidates.

qRT-PCR analyses: cDNA first strand was synthesized by using Reverse Transcript reagent (Takara, Dalian, China) with total RNA as template. All qRT-PCR reactions were operated on a Stratagene Mx3000P equipment (Agilent, USA) with a reaction volume of 25 µl consisting of 12.5 µl 2× SYBR premix Ex taq™

(Takara, Otsu, Japan), 2 µl cDNA and 10 µM specific primers. The soybean tubulin gene was employed as an internal control. $2^{-\Delta\Delta Ct}$ formula was used to calculate the relative gene expression.

Data analysis: Data was subjected to a one-way ANOVA or Student's t test to determine the statistical significance. SPSS was used for statistical analysis. Differences among groups were considered statistically significant at $P < 0.05$.

RESULTS

Identification of lncRNAs and circRNAs in soybean: The SOD activity and MDA content were significantlyincreased by 12 h of the drought and saline-alkaline treatments (Figure 1), confirming that the physiological status of these plants was seriously affected under these conditions. Therefore, plants at 12 hours of these stress treatments were used as the source of RNAs for library construction and sequencing (Table S1). A total of 119,631 transcripts were acquired from the three libraries (Control, drought stress (8% PEG-treated for 12 h), and saline-alkaline stress (110 mM NaCl + 50 mM $NaHCO_3$-treatedfor 12 h). The assembled transcripts showing alignment (P value $<1.0E^{-10}$, identity more than 90%, coverage more than 80%) to known soybean lncRNA transcripts significantly were identified as known lncRNAs (n=1,979, 47.81%) (NCBI Glycine_max_v2.0). The remaining transcripts were processed by size selection to identify novel lncRNAs. A total of 155 transcripts with length more than two hundreds nucleotides and with an ORF length of fewer than one hundred amino acids was extracted. After filtering based on exon number, 103 transcripts with two or more exons were selected. Finally, 41 novel lncRNAs were identified (Table S2). Of these, four were intronic lncRNAs, 28 were intergenic lncRNAs, and the remaining nine were antisense lncRNAs. We have supplied an annotation file of novel lncRNAs (Table S2) listing distinct lncRNAs that could be investigated by other researchers. A total of 2,020 lncRNAs were selected for further analysis. We compared the transcript length between lncRNAs and coding genes (Figure 2A). The transcript lengths of most lncRNAs were shorter than mRNAs, and fewer lncRNAs than mRNAs contained two or three exons (Figure 2B). Our analyses uncovered a set oflncRNAs expressed during the stress response in soybean. These results highlighted genes that may play functional roles in the stress response of soybean.

We also identified circRNAs from our dataset of mapping reads. We identified 830 non-redundant circRNAs, comprising 327, 452, and 353 candidate circRNAs that were recognized from junction reads in the datasets of Control, drought-, and saline–alkaline treated samples, respectively (Table S3). Most of the circRNAs were located in exonic and intergenic regions (Figure 2C). The mapping of junction reads showed that they were uniformly distributed among all the chromosomes (Figure 2D). . We detected circRNAs with different numbers of exons and from various intergenic regions. This may be attributed to their transcription sites in the genome or different regulatory functions.

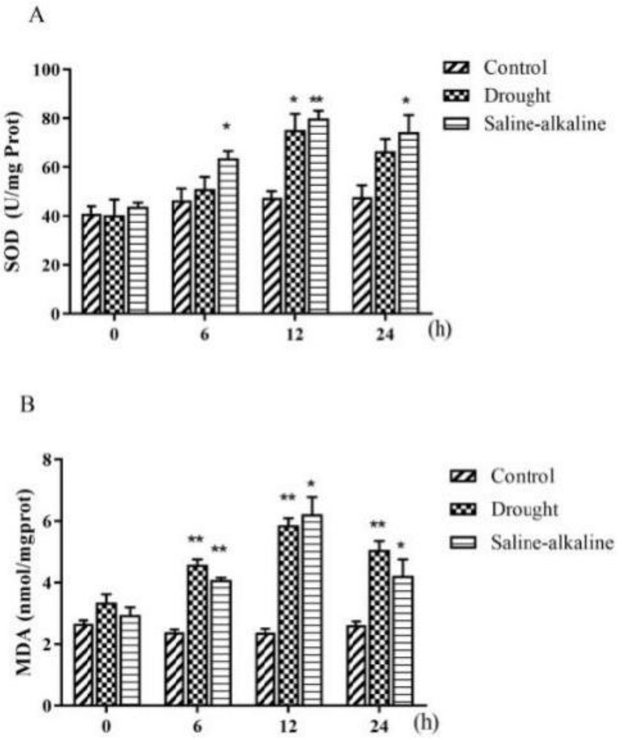

Figure 1.Superoxide dismutase activity and malondialdehyde content in soybean under drought and saline–alkaline stresses. $^{*}p < 0.05$, $^{**}p < 0.01$

Expression profiles of lncRNA: We determined the numbers of lncRNAs in the three libraries. In total, 1,765 (87.38%) of the lncRNAs were co-expressed among the control, drought, and saline-alkaline treatments.Interestingly, few lncRNAs were commonly expressed between control and the drought treatment, between control and the saline-alkaline treatment, or between the drought and saline-alkaline treatments. Only a few lncRNAs were explicitly expressed in the drought and saline-alkaline treatments (Figure 3A), implying that these lncRNAs were conserved regulators of plant development or the stress response.

To identify drought and saline-alkaline stress-responsive lncRNAs, the normalized expression FPKM(fragments per kilobase of transcript, per million fragments sequenced) number of lncRNAs were compared among the three libraries. Among the 2,020 lncRNAs, 143 were identified as differentially expressed. Of them, 118 exhibited changes in transcript levels under drought stress and 47 did so under saline-alkaline stress(Figure 3B). In the drought treatment, 109 (71.19%) lncRNAs were significantly highly expressed and 9 (28.81%) lncRNAs were down-regulated, as compared with control. In the saline-alkalinetreatment, 25 (53.19%) lncRNAs were up expressed and 22 (46.81%) lncRNAs were down-regulated, as compared with control. In addition, 10 co-expressedlncRNAs were up-regulated under both stresses, and 3 co-expressedlncRNAs were down-regulated under both stresses.

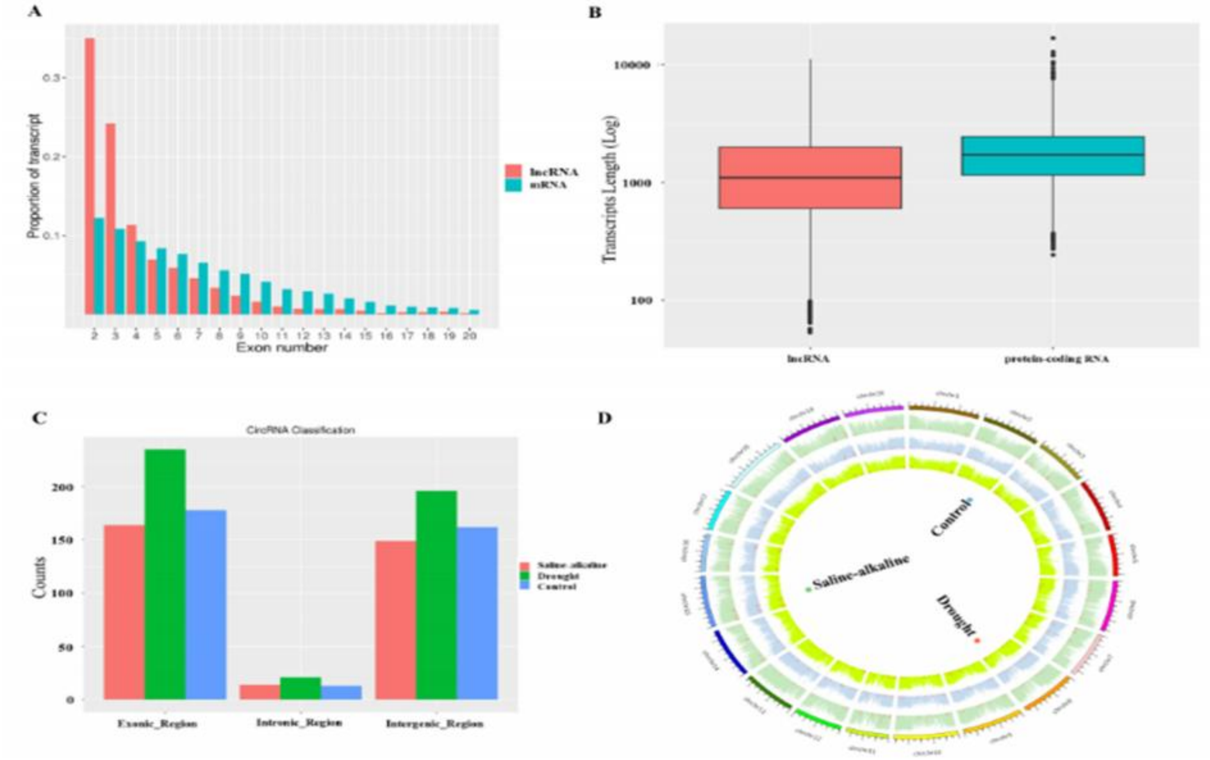

Figure 2. Identification of lncRNAs and circRNAs. a Number of exons in lncRNAs and coding RNAs. b Transcript levels of lncRNAs and coding RNAs. c Relative amount of each type of circRNAs. d Junction reads representing circRNAs (red) and mapping reads across treatment libraries mapped to genome.

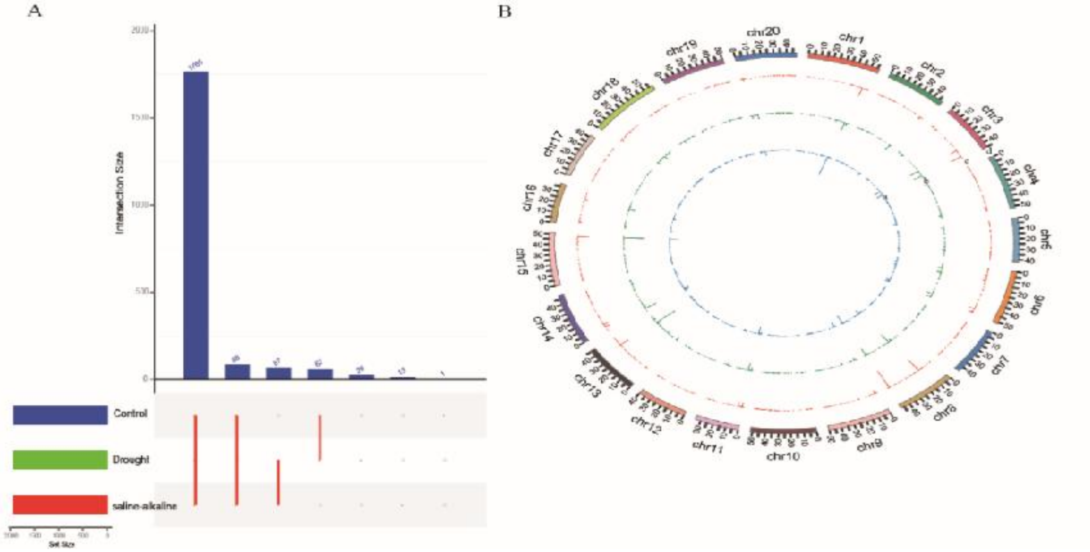

Figure 3. LncRNA expression profiles. a Categories of lncRNAs expressed under control, drought, and saline–alkaline conditions.b Relative abundance oflncRNA transcript levels under control (a, blue), drought (b, green), and saline-alkalineconditions (c, red).

Analyses of functional roles of potential targets of lncRNAs: The lncRNAs can take part in transcription process both in cis and in trans. Therefore, to predict the biological functions of genes affected by the differentially expressed lncRNAs underdrought and saline-alkalinestresses, we identified the mRNAs potentially regulated by the 143 differentially expressed lncRNAs incis or in trans.In this way, wepredicted 5,575 mRNA target genesof lncRNAs.

First, we analyzed the genes whose transcription could be regulated by lncRNAsin cis. We conducted Gene Ontology (GO) analyses of the target genes to assign functional categories. Comparing the drought treatment with control, the targets of the dynamically expressed lncRNAs were significantly enriched in the categories of nucleoplasm (p-value = 5.60e-04) and transcription from RNA polymerase II promoter (p-value = 1.31e-03).Comparing the saline-alkaline treatment with control, the targets of the 47 dynamically expressed lncRNAs were significantly enriched in the categories of transcription factor activity (p-value = 9.55e-03), and signal transduction (p-value = 1.36e-02)(Table S4).

We conducted the same analyses for the genes whose transcription could be regulated by lncRNAs in trans. The trans targets of the lncRNAs differentially expressed under drought were significantly enriched in biological processes, including ATPase activity (p-value =1.47e-03), r pyrophosphatase activity (p-value = 1.29e-03), and acting on acid anhydrides (p-value = 1.35e-03).In th saline-alkaline treatment, the trans targets of the differentiallyexpressedlncRNAs were significantly enriched in molecular functions, including hydrolyzing O-glycosyl compounds (p-value = 1.85e-04), acting on glycosyl bonds (p-value = 3.00e-04), and carbohydrate metabolic process (p-value = 2.47e-03). These results indicated that specific genes and pathways were regulated by differentially expressed lncRNAs during the plant stress response.

Together, these results showed that the lncRNAs whose expression levels changed upon exposure to drought and saline-alkaline stresses were functionally significant in pathways via their regulation of RNA processing ina cis- or trans-acting manner.

Expression validation of lncRNAs and targets: We selected 8 pairs of lncRNAs and the potential target mRNAsto validate their expression pattern under stresses by qRT-PCR. Excepted two pairs of lncRNA and potential targets (XR_001386720.1/LOC100792149 and XR_419416.2/LOC100815558), the others showed consistency with sequencing results (Figure 4).

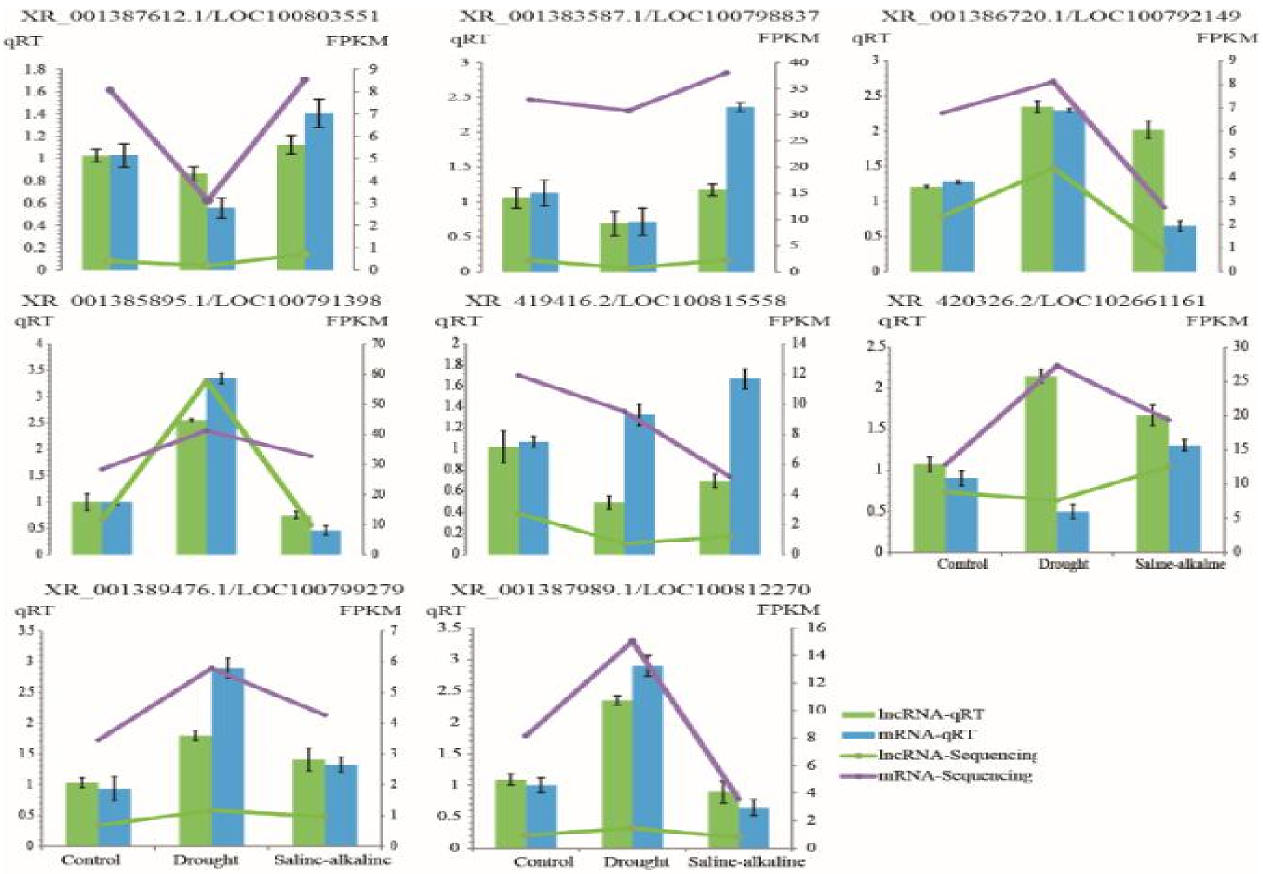

Figure 4.Expression validation of candidatelnRNAs and potential targets.

Characterization and validation of circRNAs: Soybean circRNAs generated from exonic, intergenic, and intronic regions were identified according to the transcriptomic data.Among the identified circRNAs, 123 were generated from exons of a single protein-coding gene and were classified as exoniccircRNAs, and 223 were generated from intergenic regions. There was a relatively low rate of circRNAs from the intron-flanking regions. Splicing junction sites are one of the most important factors delineating the origin of the circRNAs and in differentiating linear splicing from back-splicing. We found that seven of 12 circRNAs (four exoniccircRNAs, two intronic circRNA, and four intergenic circRNAs) had junction sites (Figure 6a and Figure S1). Primers were specifically designed for circRNA segment amplification (Figure 6b, c, d). The expression patterns of some circRNAs were verified by qRT-PCR (Figure 6e). Only circ_LOC100818869 was expressed at low levels under stress conditions. All the other circRNAs were expressed at high levels under stress conditions.

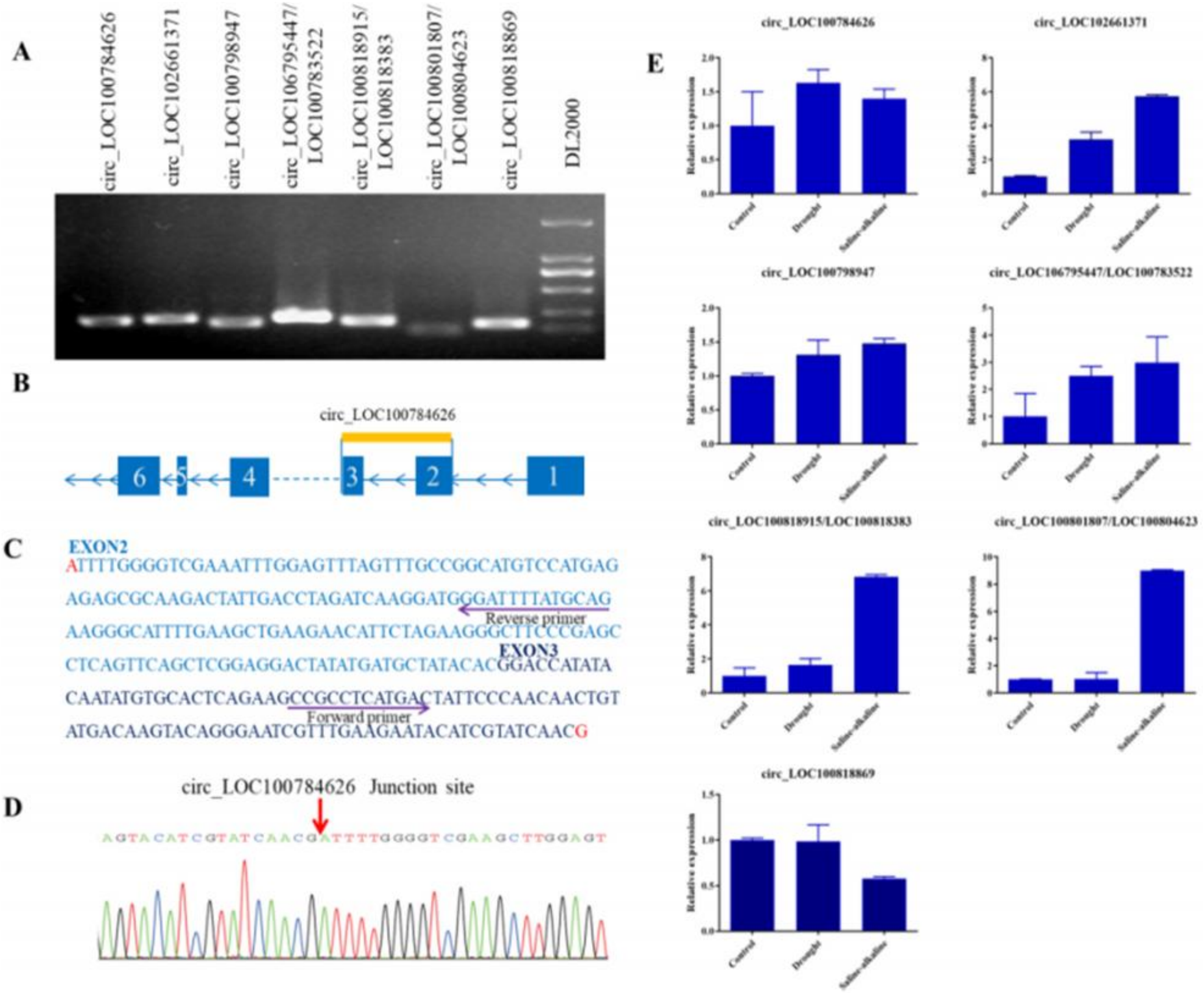

Figure 5. Characterization and validation of circRNAs. a PCR product amplified with lncRNA-specific primers from soybean cDNA. b Distribution of circ_LOC100784626 in cullin-1 exon. c Primers designed to amplify circ_LOC100784626. d Sequencing results showing junction sites in circ_LOC100784626. e Expression of circRNA validated by qRT-PCR. * $p < 0.05$, ** $p < 0.01$.

DISCUSSION

Noncoding RNAs such as lncRNAs have been detected out or identified by many different techniques, such as strand-specific microarrays, conventional expression arrays, next generation RNA sequencing, or real-time experiments (Herzog *et al*. 2014; Lu *et al*. 2012). Strand-specific next generation RNA sequencing permitred the recovery of antisense transcription activities and led to novel lncRNAs recognition. At present, plant biologists utilized this method to analyze transcriptomes and characterize a wide range of noncoding RNAs in many plant varieties (Cruz de Carvalho *et al*. 2016; Joshi *et al*. 2016; Wang *et al*. 2015a). Building on this work, we performed genome-wide identification of noncoding RNAs by analyzing strand-specific paired-end RNA sequencing data. A total of 2,020 lncRNAs and 830 circRNAs were identified from the strand-specific RNA sequencing data. We found far fewer lncRNAs than were found in another recent study (Li *et al*. 2014), possibly because we used more rigorous filtering criteria to identify lncRNAs.

The expression profiles of circRNAs were not considered in this study. After discarding low-mapping-quality reads and back-spliced junction sequences with homology to linear exon junctions, most of the identified circRNAs showed very low expression levels and high false-positive rates. Althoughnew methods such as CIRI-full have been proposed to evaluate transcript levels of circRNAs(Zheng *et al*. 2019), a comprehensive analysis of circRNA expression is still lacking.

We focused on the expression patterns and features of lncRNAs in this study. To understand the tolerance mechanisms of soybean, we first profiled the drought and saline-alkaline induced changes in the expression profiles of lncRNAs. We found 118 and 47 differentially expressed lncRNAs in response to dehydration or saline-alkaline conditions at the transcriptional level. According to recent studies, lncRNAs primarily regulate transcription in a *cis*- or *trans*- manner to positively or negatively control the expression of coding genes (Bumgarner *et al*. 2009; Guil and Esteller 2012). In our study, we found that lncRNAs targeted 5,575 mRNAs in a*cis*- or *trans*- manner, indicating that there arewidespread regulatory interactions between lncRNAs and coding RNAsin soybean. In the drought and saline-alkaline treatments, the regulation of cell signaling was affected by 6 and 8 differentially expressed lncRNAs, respectively. The putative targets of the dynamically expressed lncRNAs with *cis*-acting regulation included genes encoding auxin response factor 3 (ARF3), IAA, and ras-related protein (RABA1). These findings suggested that lncRNAs are pariticipated in regulating the expression of RNAs involved in signal transduction at the transcriptional level. This conclusion is consistent with the recent finding that lncRNAs function as regulators of cell signaling under stress (Saeedi Borujeni *et al*. 2018). Previous analyses have revealed that certain lncRNAs may improve plants' resistance to stress (Liu and Zhu 2014).Here, we identified differentially expressedlncRNAs under drought and saline–alkaline stresses.As an intergenic lncRNA, XR_001389476.1 regulates the expression of a gene encoding an F-box protein in a*cis*-acting manner in soybean. Drought caused a rapid change in the XR_001389476.1 expression level. Previous studies have shown that the F-box gene expression level increases underoxidative stress and affects the levels of signaling molecules such as reactive oxygen species (Kong *et al*. 2016). Further research is needed to elucidate the molecular mechanism of lncRNA in soybean.

CircRNAs are produced by head-to-tail back-splicing events and are participated in the RNA expression regulation at the translational level or the post-translational level (Darbani *et al*. 2016). CircRNAs was recently reported to be novel regulators of gene expression in plants (Zuo *et al*. 2016). Using strand-specific RNA-seq methods, we identified 830 circRNAs originating from diverse genomic regions under our stress conditions. Despite the low abundance of circRNAs, we validated the back-splicing sites to confirm the existence of circRNAs generated from exonic, intronic, and intergenic regions (Siegel *et al*. 2014). Taken together, our research indicated that circRNAs may have additional functions in plants and/or undiscovered functions in stress responses.

Conclusion: In summary, with the aid of strand-specific transcriptomic analysis, we identified 2,020 lncRNAs, including 1,979 known and 41 novel ones, in soybean. In addition, 830 circRNAs were identified. The results of GO functional enrichment analyses indicated that the dynamically expressed lncRNAs were paricipitated in the regulation of certain biological processes. Putative *trans*/*cis* targets of the dynamically expressed lncRNAs were predicted. Most circRNAs originated from exonic, intronic, and intergenic sequences of *G. max* and back-spliced junction sites of predicted circRNAs were validated through Sanger sequencing. These results increase our knowledge of the lncRNAs and circRNAs that are involved in soybean stress responses.

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Table S1: Sequencing read counts statistics.

	CK	Drought treated	Saline-alkaline treated
Raw reads	74,950,632	65,770,632	71,420,564
Clean reads	58,022,071	47,403,083	55,733,811
rRNA trimed reads	57,961,918	47,321,763	55,680,454
rRNA ratio	0.1%	0.2%	0.1%
Mapped reads	53,696,524	42,793,029	51,610,967
Mapped Unique reads	52,066,800	41,315,747	50,140,391
Mapped ratio	92.6%	90.4%	92.7%

Table S2: Identification of novel lncRNAs under drought and Saline-alkaline in soybean.

	lncRNA ID	class_code	lncRNA class	Cpc score	cnci_score	Pfam
1	TCONS_00012324	U	Intergenic LncRNA	-0.9221	-0.00783	no-significantly
2	TCONS_00023602	U	Intergenic LncRNA	-0.90843	-0.01005	no-significantly
3	TCONS_00025836	X	Antisense LncRNA	-0.93126	-0.01252	no-significantly
4	TCONS_00036595	U	Intergenic LncRNA	-1.26151	-0.09042	no-significantly
5	TCONS_00033253	U	Intergenic LncRNA	-1.22851	-0.00768	no-significantly
6	TCONS_00046989	X	Antisense LncRNA	-1.09754	-0.02199	no-significantly
7	TCONS_00046988	x	Antisense LncRNA	-1.06345	-0.00957	no-significantly
8	TCONS_00045400	x	Antisense LncRNA	-1.22812	-0.00239	no-significantly
9	TCONS_00052681	u	Intergenic LncRNA	-1.12832	-0.00969	no-significantly
10	TCONS_00057019	i	Intron LncRNA	-1.2064	-0.00518	no-significantly
11	TCONS_00059481	u	Intergenic LncRNA	-1.31747	-0.00761	no-significantly
12	TCONS_00057716	x	Antisense LncRNA	-0.98229	-0.01628	no-significantly
13	TCONS_00059767	u	Intergenic LncRNA	-1.29368	-0.00041	no-significantly
14	TCONS_00061791	x	Antisense LncRNA	-1.15556	-0.01043	no-significantly
15	TCONS_00004367	x	Antisense LncRNA	-1.24674	-0.00505	no-significantly
16	TCONS_00076768	u	Intergenic LncRNA	-0.23619	-0.00041	no-significantly
17	TCONS_00074610	u	Intergenic LncRNA	-0.90069	-0.07398	no-significantly
18	TCONS_00075173	u	Intergenic LncRNA	-1.0945	-0.0313	no-significantly
19	TCONS_00075171	u	Intergenic LncRNA	-1.21018	-0.00113	no-significantly
20	TCONS_00077280	u	Intergenic LncRNA	-1.1109	-0.00885	no-significantly
21	TCONS_00075496	u	Intergenic LncRNA	-1.28975	-0.02906	no-significantly
22	TCONS_00082373	i	Intron LncRNA	-0.80982	-0.01808	no-significantly
23	TCONS_00079757	i	Intron LncRNA	-0.67632	-0.01233	no-significantly
24	TCONS_00082403	u	Intergenic LncRNA	-1.01098	-0.00041	no-significantly
25	TCONS_00080978	i	Intron LncRNA	-1.30921	-0.00041	no-significantly
26	TCONS_00081627	u	Intergenic LncRNA	-1.2581	-0.00384	no-significantly
27	TCONS_00087583	u	Intergenic LncRNA	-1.12123	-0.00957	no-significantly
28	TCONS_00093860	u	Intergenic LncRNA	-1.02239	-0.0069	no-significantly
29	TCONS_00092205	x	Antisense LncRNA	-0.88372	-0.02035	no-significantly
30	TCONS_00092233	u	Intergenic LncRNA	-1.00057	-0.00656	no-significantly
31	TCONS_00093840	u	Intergenic LncRNA	-1.32728	-0.02142	no-significantly
32	TCONS_00101224	u	Intergenic LncRNA	-0.846	-0.01057	no-significantly
33	TCONS_00113917	u	Intergenic LncRNA	-0.25127	-0.00241	no-significantly
34	TCONS_00114666	x	Antisense LncRNA	-1.03661	-0.00041	no-significantly
35	TCONS_00114109	u	Intergenic LncRNA	-0.25629	-0.00187	no-significantly
36	TCONS_00114110	u	Intergenic LncRNA	-0.19471	-0.00452	no-significantly
37	TCONS_00114886	u	Intergenic LncRNA	-1.21534	-0.00696	no-significantly

38	TCONS_00113534	u	Intergenic LncRNA	-1.29174	-0.00221	no-significantly
39	TCONS_00117108	u	Intergenic LncRNA	-1.18054	-0.01071	no-significantly
40	TCONS_00120669	u	Intergenic LncRNA	-1.34841	-0.00848	no-significantly
41	TCONS_00119739	u	Intergenic LncRNA	-1.25763	-0.00946	no-significantly

Table S3: Identification of circRNA under Drought and Saline-alkaline in soybean.

circRNA_id	locus	circRNA_type	gene_id	Gene_symbol
circRNA1	chr18:1884830|1885872(+)	Exon	100788781	LOC100788781
circRNA2	NW_014573484.1:15615|24814(-)	Intron	100499660	LOC100499660
circRNA3	chr19:49657767|49661626(+)	Exon	100775991	LOC100775991
circRNA4	chr3:28532292|28532473(+)	exon	100809668	LOC100809668
circRNA5	chr20:46722693|46727982(-)	exon	100790062	LOC100790062
circRNA6	chr8:47160960|47164126(-)	exon	100799467	LOC100799467
circRNA7	chr2:47568773|47583823(-)	intergenic region	n/a	-
circRNA8	chr17:24450022|24466703(+)	exon	100775929	LOC100775929
circRNA9	chr15:15637548|15656589(+)	intergenic region	n/a	-
circRNA10	chr20:46116509|46120220(-)	exon	100817872	LOC100817872
circRNA11	chr1:56815648|56816260(-)	exon	100780905	LOC100780905
circRNA12	chr12:40193|43348(+)	exon	100799920	LOC100799920
circRNA13	chr9:5772046|5774924(+)	exon	100820121	LOC100820121
circRNA14	chr20:2508603|2551745(-)	intergenic region	n/a	-
circRNA15	chrPltd:335|5514(-)	intergenic region	n/a	-
circRNA16	chrPltd:5368|6725(-)	exon	3989271	rbcL
circRNA17	chr7:7658602|7672377(-)	intergenic region	n/a	-
circRNA18	chr2:11494849|11616531(-)	intergenic region	n/a	-
circRNA19	chr12:32880|43348(+)	exon	100799920	LOC100799920
circRNA20	chr11:8391413|8392550(-)	exon	100813590	LOC100813590
circRNA21	chr14:1314546|1335196(-)	intergenic region	n/a	-
circRNA22	chr17:36354902|36355447(-)	exon	547792	LOC547792
circRNA23	chr3:9655011|9783089(-)	intergenic region	n/a	-
circRNA24	chr2:15872048|15873057(+)	exon	100800938	LOC100800938
circRNA25	chr3:6122686|6276422(-)	intergenic region	n/a	-
circRNA26	chr10:1959804|1970140(-)	intergenic region	n/a	-
circRNA27	chr18:39078403|39079643(+)	exon	102660444	LOC102660444
circRNA28	chr2:46960851|46961461(+)	exon	100789468	LOC100789468
circRNA29	chr17:40831152|40871234(-)	intergenic region	n/a	-
circRNA30	chr18:49836569|49849800(+)	intergenic region	n/a	-
circRNA31	chr8:44683812|44705494(+)	intergenic region	n/a	-
circRNA32	chr18:57506054|57507716(-)	exon	100811073	LOC100811073
circRNA33	chr3:27913096|27915318(-)	exon	100813936	LOC100813936
circRNA34	chr5:40299361|40304875(+)	exon	100791130	LOC100791130
circRNA35	chr11:27859973|27860542(-)	exon	100798309	LOC100798309
circRNA36	chr15:7218238|7222390(+)	intergenic region	n/a	-
circRNA37	chr13:30568820|30569013(-)	exon	100777805	LOC100777805
circRNA38	chr8:40889591|40891415(-)	exon	100787473	LOC100787473
circRNA39	chr12:16512230|16736082(+)	intergenic region	n/a	-
circRNA40	chr13:36343547|36345126(+)	exon	100816142	LOC100816142
circRNA41	chr14:12305639|12321322(-)	exon	100500679	LOC100500679
circRNA42	chr10:30293099|30293740(+)	exon	100798991	LOC100798991
circRNA43	chr2:32745356|32746444(+)	exon	100794561	LOC100794561
circRNA44	chr12:5573114|5573957(-)	exon	100805061	LOC100805061
circRNA45	chr10:43763701|43765098(+)	exon	100803596	LOC100803596
circRNA46	chr18:9120644|9144957(+)	intergenic region	n/a	-
circRNA47	chr2:14648729|14667584(+)	intergenic region	n/a	-
circRNA48	chr19:778328|778923(+)	exon	100781868	LOC100781868

circRNA49	chr12:39177164|39206976(-)	intergenic region	n/a	-
circRNA50	chr13:14415558|14436083(+)	intergenic region	n/a	-
circRNA51	chr15:1655878|1689424(+)	intergenic region	n/a	-
circRNA52	NW_014573484.1:15243|33868(-)	intergenic region	n/a	-
circRNA53	chr4:2706439|2714687(+)	intergenic region	n/a	-
circRNA54	chr20:1005647|1021407(+)	intergenic region	n/a	-
circRNA55	chr12:1286106|1292115(+)	intergenic region	n/a	-
circRNA56	chrPltd:6292|6408(-)	exon	3989271	rbcL
circRNA57	chr8:42660284|42660951(-)	exon	100782497	LOC100782497
circRNA58	chr18:50313127|50313492(+)	exon	100796148	LOC100796148
circRNA59	chr5:35568183|35578395(-)	intergenic region	n/a	-
circRNA60	chr20:16899360|16922585(-)	exon	102665764	LOC102665764
circRNA61	chr9:48932795|48934044(-)	exon	100811378	LOC100811378
circRNA62	chr9:24716008|24737521(+)	intergenic region	n/a	-
circRNA63	chr16:33084437|33251415(-)	intergenic region	n/a	-
circRNA64	chr13:29047135|29060169(-)	exon	100814539	LOC100814539
circRNA65	chr4:13572434|13573325(+)	exon	100789878	LOC100789878
circRNA66	chr13:14430407|14448409(+)	intergenic region	n/a	-
circRNA67	chr13:36343727|36345126(+)	exon	100816142	LOC100816142
circRNA68	chrPltd:1211|6911(-)	intergenic region	n/a	-
circRNA69	chr8:6307674|6310633(+)	exon	100807979	LOC100807979
circRNA70	chr19:38082939|38083918(+)	exon	100782594	LOC100782594
circRNA71	chr5:32741577|32742040(+)	exon	100802419	LOC100802419
circRNA72	chr18:9300525|9301248(+)	exon	106797140	LOC106797140
circRNA73	chr3:5477689|5523589(+)	intergenic region	n/a	-
circRNA74	chr3:235414|236481(-)	exon	100779711	LOC100779711
circRNA75	chr12:39171698|39201930(-)	intergenic region	n/a	-
circRNA76	chr12:35935071|35948579(-)	intron	100807714	LOC100807714
circRNA77	chrPltd:877|979(-)	exon	3989259	psbA
circRNA78	chr19:37245872|37251761(-)	exon	100785430	LOC100785430
circRNA79	chr13:30370619|30439972(-)	intergenic region	n/a	-
circRNA80	chr12:791508|805053(+)	intergenic region	n/a	-
circRNA81	chr1:3493520|3504862(+)	intergenic region	n/a	-
circRNA82	chr14:1457027|1471866(+)	intergenic region	n/a	-
circRNA83	chr7:5652654|5726099(-)	intron	100780862	LOC100780862
circRNA84	chr20:47534333|47534877(+)	exon	100811473	LOC100811473
circRNA85	chr7:15811552|15811976(-)	exon	100795391	LOC100795391
circRNA86	chr8:45413699|45428606(-)	intergenic region	n/a	-
circRNA87	chr10:30309271|30310511(+)	exon	100798991	LOC100798991
circRNA88	chr16:387312|388102(-)	exon	100804966	LOC100804966
circRNA89	chr7:6617619|6640644(+)	intergenic region	n/a	-
circRNA90	chrPltd:5383|6900(-)	intergenic region	n/a	-
circRNA91	chr8:44900765|44917039(-)	intergenic region	n/a	-
circRNA92	chr10:19655305|19665468(+)	intergenic region	n/a	-
circRNA93	NW_014573526.1:2705|17929(-)	intergenic region	n/a	-
circRNA94	chr12:16511175|16733760(+)	intergenic region	n/a	-
circRNA95	chr19:7190007|7253858(+)	intergenic region	n/a	-
circRNA96	chrPltd:132706|132974(-)	intergenic region	n/a	-
circRNA97	chr10:13923926|13925267(-)	exon	100814107	LOC100814107
circRNA98	chr2:14380600|14381817(+)	exon	547616	MAPK2
circRNA99	chr12:26068628|26068918(-)	exon	100796730	LOC100796730
circRNA100	chr16:20371089|20371938(-)	exon	100792777	LOC100792777
circRNA101	chr15:12786696|12787221(+)	exon	100784626	LOC100784626
circRNA102	chr6:44787569|44831144(-)	intergenic region	n/a	-
circRNA103	chr20:40308573|40316905(+)	intergenic region	n/a	-
circRNA104	chr19:5539449|5646201(+)	intergenic region	n/a	-

circRNA105	chr13:2011919|2012373(-)	exon	100783198	LOC100783198
circRNA106	chrPltd:292|532(-)	intergenic region	n/a	-
circRNA107	chr6:10377283|10378900(+)	exon	100815774	LOC100815774
circRNA108	chr7:35234977|35235530(+)	exon	100798214	LOC100798214
circRNA109	chrPltd:542|1151(-)	exon	3989259	psbA
circRNA110	chr3:44106649|44107117(-)	exon	100790207	LOC100790207
circRNA111	chr9:18439107|18505640(-)	intergenic region	n/a	-
circRNA112	chr15:23326207|23327192(-)	exon	100798669	LOC100798669
circRNA113	chr11:10552718|10554646(-)	exon	100797436	LOC100797436
circRNA114	chr1:40769039|40810598(+)	intergenic region	n/a	-
circRNA115	chr6:22933744|22935605(-)	exon	100783185	LOC100783185
circRNA116	chr9:191797|195693(-)	exon	100787334	LOC100787334
circRNA117	chr11:794904|795841(-)	exon	100776523	LOC100776523
circRNA118	chr4:41849024|42290025(+)	intergenic region	n/a	-
circRNA119	chr8:14980418|14982102(+)	exon	100795772	LOC100795772
circRNA120	chr20:40309646|40317081(+)	intergenic region	n/a	-
circRNA121	chr10:31033852|31120951(-)	intergenic region	n/a	-
circRNA122	chr18:2172273|2181785(-)	intergenic region	n/a	-
circRNA123	chr5:31230154|31230868(+)	exon	100810940	LOC100810940
circRNA124	chr1:55927718|56185545(+)	intergenic region	n/a	-
circRNA125	chr17:3261202|3263694(+)	exon	100782540	LOC100782540
circRNA126	chr13:37975092|37985968(-)	intergenic region	n/a	-
circRNA127	chr9:64393|81608(+)	intergenic region	n/a	-
circRNA128	chr9:10053318|10055815(-)	exon	100777704	LOC100777704
circRNA129	chr4:3174493|3189631(-)	intergenic region	n/a	-
circRNA130	chr13:14428824|14448409(+)	intergenic region	n/a	-
circRNA131	chr7:17921799|17935529(-)	intergenic region	n/a	-
circRNA132	chr15:9813151|9818094(+)	intergenic region	n/a	-
circRNA133	chr7:5657042|5757743(-)	intron	100780862	LOC100780862
circRNA134	chr5:41257574|41258431(+)	exon	100819489	LOC100819489
circRNA135	chr19:37738765|37740055(-)	exon	100794420	LOC100794420
circRNA136	chrPltd:1334|6331(-)	intergenic region	n/a	-
circRNA137	chr3:28917416|28918382(+)	exon	100786632	LOC100786632
circRNA138	chr11:5927662|5935738(+)	intergenic region	n/a	-
circRNA139	chr16:31135686|31161545(-)	intergenic region	n/a	-
circRNA140	chr12:39171381|39201509(-)	intergenic region	n/a	-
circRNA141	chr19:39072981|39073308(+)	exon	100809299	LOC100809299
circRNA142	chr9:27017380|27026534(-)	intergenic region	n/a	-
circRNA143	chr18:47705623|47726024(-)	intergenic region	n/a	-
circRNA144	chr9:33972255|33996509(+)	intergenic region	n/a	-
circRNA145	chrPltd:9507|9631(+)	intergenic region	n/a	-
circRNA146	chr20:37772851|37802721(-)	intergenic region	n/a	-
circRNA147	chr16:31516460|31524228(-)	intergenic region	n/a	-
circRNA148	chr19:45711045|45731347(+)	intergenic region	n/a	-
circRNA149	chr3:4545901|4597563(+)	intergenic region	n/a	-
circRNA150	chr13:10973964|10974580(+)	exon	100786712	LOC100786712
circRNA151	chr16:31124428|31159320(-)	intergenic region	n/a	-
circRNA152	chr4:3176618|3194504(-)	intergenic region	n/a	-
circRNA153	chr4:19122731|19124097(-)	exon	100781333	LOC100781333
circRNA154	chr13:30370619|30439929(-)	intergenic region	n/a	-
circRNA155	chrPltd:626|132481(-)	intergenic region	n/a	-
circRNA156	chr3:40132578|40132842(-)	exon	100812152	LOC100812152
circRNA157	chr8:20205875|20206460(-)	exon	100819005	LOC100819005
circRNA158	chr20:19887772|19902316(-)	intergenic region	n/a	-
circRNA159	chr10:20673681|20682531(-)	exon	100798812	LOC100798812
circRNA160	chr3:1326887|1339399(+)	intergenic region	n/a	-

circRNA161	chr16:14844159|14848870(+)	intergenic region	n/a	-
circRNA162	chr11:27859973|27860888(-)	exon	100798309	LOC100798309
circRNA163	chr8:8369331|8516096(-)	intergenic region	n/a	-
circRNA164	chrPltd:1334|5484(-)	intergenic region	n/a	-
circRNA165	chr20:44394506|44395149(+)	exon	100802781	LOC100802781
circRNA166	chr6:50840970|50844495(-)	exon	100776945	LOC100776945
circRNA167	chr8:30760157|30768879(-)	exon	100820096	LOC100820096
circRNA168	chr14:29788489|30062860(-)	intergenic region	n/a	-
circRNA169	chr20:1005654|1021407(+)	intergenic region	n/a	-
circRNA170	chr19:37242977|37251761(-)	exon	100785430	LOC100785430
circRNA171	chr20:34004446|34029487(+)	intergenic region	n/a	-
circRNA172	chr9:64104|81299(+)	intergenic region	n/a	-
circRNA173	chr7:17922785|17935680(-)	intergenic region	n/a	-
circRNA174	chr3:14468483|14468812(+)	exon	102668539	LOC102668539
circRNA175	chr11:7552065|7559088(-)	intergenic region	n/a	-
circRNA176	chrPltd:5461|5622(-)	exon	3989271	rbcL
circRNA177	chr1:40786535|40827205(+)	intergenic region	n/a	-
circRNA178	chr20:2506759|2549623(-)	intergenic region	n/a	-
circRNA179	chrPltd:133206|133620(-)	intron	3989373	trnI-UAG
circRNA180	chr6:4483790|4494067(-)	intron	100785124	LOC100785124
circRNA181	chr12:32096391|32100150(+)	exon	100800447	LOC100800447
circRNA182	chr14:40928724|40956103(-)	intergenic region	n/a	-
circRNA183	chr18:46934714|46936264(-)	exon	100305446	LOC100305446
circRNA184	chr3:1328507|1341190(+)	intergenic region	n/a	-
circRNA185	chr3:28917416|28918379(+)	exon	100786632	LOC100786632
circRNA186	chr3:32868274|32911501(+)	intergenic region	n/a	-
circRNA187	NW_014574060.1:521|3875(+)	intergenic region	n/a	-
circRNA188	chr4:13791756|13793984(-)	exon	100794972	LOC100794972
circRNA189	chr16:4913081|4926458(+)	intergenic region	n/a	-
circRNA190	chr2:47565637|47580782(-)	intergenic region	n/a	-
circRNA191	chr2:46152749|46154820(+)	exon	100820132	LOC100820132
circRNA192	chr8:44911922|44917185(-)	intergenic region	n/a	-
circRNA193	chr5:36906191|36906573(-)	exon	100801361	LOC100801361
circRNA194	chr7:15549263|15553072(+)	exon	100803526	LOC100803526
circRNA195	chr15:47836263|47843921(-)	intergenic region	n/a	-
circRNA196	chr15:3669200|3670897(-)	exon	100815107	LOC100815107
circRNA197	chr16:2978592|3003970(+)	intergenic region	n/a	-
circRNA198	chr20:47237921|47239194(-)	exon	100803121	LOC100803121
circRNA199	chrPltd:430|998(-)	exon	3989259	psbA
circRNA200	chr2:11466195|11523591(-)	intergenic region	n/a	-
circRNA201	chr10:863419|864940(-)	exon	100820160	LOC100820160
circRNA202	chr18:9735298|9750657(+)	intergenic region	n/a	-
circRNA203	chr11:30285324|30314856(-)	intergenic region	n/a	-
circRNA204	chr17:32909354|32910593(-)	exon	100788741	LOC100788741
circRNA205	NW_014573410.1:47527|56640(+)	intergenic region	n/a	-
circRNA206	chr4:102297|103240(+)	exon	100819848	LOC100819848
circRNA207	chr11:10376551|10397935(-)	intergenic region	n/a	-
circRNA208	chr7:2201472|2213268(+)	intergenic region	n/a	-
circRNA209	chr12:4359910|4387150(-)	intergenic region	n/a	-
circRNA210	chr4:7315218|7324979(+)	intergenic region	n/a	-
circRNA211	chr2:11468224|11557778(-)	intergenic region	n/a	-
circRNA212	chr6:14547681|14549278(+)	exon	100807766	LOC100807766
circRNA213	chrPltd:5246|5927(-)	intergenic region	n/a	-
circRNA214	chr1:52131183|52131984(+)	exon	100792600	LOC100792600
circRNA215	chr15:9813383|9819778(+)	intergenic region	n/a	-
circRNA216	chr16:2971678|2992343(+)	intergenic region	n/a	-

circRNA217	chr2:21066335|21066881(-)	exon	100785390	LOC100785390
circRNA218	chr2:32249856|32251696(+)	exon	100788765	LOC100788765
circRNA219	chr10:22028105|22029156(-)	exon	100793515	LOC100793515
circRNA220	chr12:36484497|36489389(+)	exon	100819307	LOC100819307
circRNA221	chr12:39176011|39206326(-)	intergenic region	n/a	-
circRNA222	chr20:34004505|34029487(+)	intergenic region	n/a	-
circRNA223	chr9:31173293|31173778(-)	exon	100816030	LOC100816030
circRNA224	chr1:53842717|53844884(+)	exon	100807112	LOC100807112
circRNA225	chr13:13639664|13681722(-)	intergenic region	n/a	-
circRNA226	chr8:15951432|16038560(-)	intergenic region	n/a	-
circRNA227	chr20:385688|391272(+)	exon	100789712	LOC100789712
circRNA228	chr1:3461288|3492739(+)	intergenic region	n/a	-
circRNA229	chr7:5583072|5614007(-)	exon	100808315	LOC100808315
circRNA230	chrPltd:1179|5347(-)	intergenic region	n/a	-
circRNA231	chr15:12790117|12790338(+)	intron	100784626	LOC100784626
circRNA232	NW_014573484.1:28490|37523(-)	intergenic region	n/a	-
circRNA233	chrPltd:633|5964(-)	intergenic region	n/a	-
circRNA234	chr7:5656878|5731898(-)	intron	100780862	LOC100780862
circRNA235	chr17:18178233|18186666(+)	exon	100800186	ZEP
circRNA236	chr3:23066214|23066760(+)	exon	100780970	LOC100780970
circRNA237	chrPltd:9840|10263(+)	intron	3989275	trnV-UAC
circRNA238	chr2:11526908|11556538(-)	intergenic region	n/a	-
circRNA239	chr10:45606873|45608241(-)	exon	100812684	LOC100812684
circRNA240	chr1:40785159|40810914(+)	intergenic region	n/a	-
circRNA241	chr14:21814581|21829377(-)	exon	100779257	LOC100779257
circRNA242	NW_014573413.1:165611|166172(+)	exon	100811292	LOC100811292
circRNA243	chr10:51526197|51526934(-)	exon	100798296	LOC100798296
circRNA244	chr9:49712857|49713414(-)	exon	102664796	LOC102664796
circRNA245	chr9:2391817|2392758(+)	exon	778173	LOC778173
circRNA246	chr15:5590004|5600707(+)	intergenic region	n/a	-
circRNA247	chr14:16760177|16762546(-)	exon	100798031	LOC100798031
circRNA248	chr17:8194399|8197820(-)	exon	100780025	LOC100780025
circRNA249	chr19:777173|777327(+)	exon	100781868	LOC100781868
circRNA250	chr13:9580102|9580490(+)	intergenic region	n/a	-
circRNA251	chr11:33098778|33099370(+)	exon	100813586	LOC100813586
circRNA252	chr4:9878470|9886594(+)	intergenic region	n/a	-
circRNA253	chr19:49181759|49191822(-)	intergenic region	n/a	-
circRNA254	chr8:818630|818893(-)	exon	100816702	LOC100816702
circRNA255	chr18:49532142|49539485(+)	intergenic region	n/a	-
circRNA256	chr2:11526158|11588303(-)	intergenic region	n/a	-
circRNA257	chr15:13671345|13671512(-)	intergenic region	n/a	-
circRNA258	chr20:47873733|47874480(-)	exon	100779579	LOC100779579
circRNA259	chr10:7879254|7881864(+)	exon	100793363	LOC100793363
circRNA260	chr8:13601186|13612458(+)	intergenic region	n/a	-
circRNA261	chr1:5506067|5508778(+)	exon	100807287	LOC100807287
circRNA262	chr18:9300508|9301248(+)	exon	106797140	LOC106797140
circRNA263	chr16:35732103|35740925(+)	exon	100810667	LOC100810667
circRNA264	chr1:53935062|53936075(+)	exon	100790851	LOC100790851
circRNA265	chrPltd:5419|5598(-)	exon	3989271	rbcL
circRNA266	chr7:1333801|1345817(-)	intergenic region	n/a	-
circRNA267	chr4:19464519|19465559(+)	exon	100782956	LOC100782956
circRNA268	chr6:7553758|7554264(-)	exon	100796777	LOC100796777
circRNA269	chrPltd:572|5598(-)	intergenic region	n/a	-
circRNA270	chrPltd:1211|5927(-)	intergenic region	n/a	-
circRNA271	chr15:35365065|35367804(-)	exon	100797874	LOC100797874
circRNA272	chr10:22028105|22029151(-)	exon	100793515	LOC100793515

circRNA273	chr6:10308428|10308900(+)	exon	100814187	LOC100814187
circRNA274	chrPltd:992|5418(-)	intergenic region	n/a	-
circRNA275	chr14:8964282|8986373(-)	intergenic region	n/a	-
circRNA276	chr3:27913096|27921314(-)	exon	100813936	LOC100813936
circRNA277	chr10:3959982|3961351(+)	exon	100794242	LOC100794242
circRNA278	chr2:6424549|6436781(-)	intergenic region	n/a	-
circRNA279	chr15:3178780|3183716(+)	intergenic region	n/a	-
circRNA280	chr3:34288577|34293474(+)	exon	548016	LOC548016
circRNA281	chr7:1337588|1349472(-)	intergenic region	n/a	-
circRNA282	chr3:4570759|4894600(+)	intergenic region	n/a	-
circRNA283	chrPltd:1334|6030(-)	intergenic region	n/a	-
circRNA284	NW_014573403.1:3476693|3480114(+)	exon	100786845	LOC100786845
circRNA285	chr6:47141085|47141651(+)	exon	100786541	LOC100786541
circRNA286	chrPltd:6798|32218(-)	intergenic region	n/a	-
circRNA287	chr13:28041005|28047156(+)	intron	102661733	LOC102661733
circRNA288	chr19:48928138|48968214(-)	intergenic region	n/a	-
circRNA289	chr12:4360128|4387377(-)	intergenic region	n/a	-
circRNA290	chr4:23760483|23761143(+)	exon	100812174	LOC100812174
circRNA291	chr17:40827810|40869109(+)	intergenic region	n/a	-
circRNA292	chr13:10447778|10470877(-)	intergenic region	n/a	-
circRNA293	chr20:37122805|37131872(+)	intergenic region	n/a	-
circRNA294	chr16:34412557|34682363(-)	intergenic region	n/a	-
circRNA295	chr8:11501656|11507851(+)	intergenic region	n/a	-
circRNA296	chr13:30007848|30023925(+)	intergenic region	n/a	-
circRNA297	chr8:30765388|30766580(-)	exon	100820096	LOC100820096
circRNA298	chr5:3981095|4011431(+)	intergenic region	n/a	-
circRNA299	chr6:45102685|45254175(+)	intergenic region	n/a	-
circRNA300	chr16:923887|931704(+)	intergenic region	n/a	-
circRNA301	chr6:11318309|11325740(-)	intergenic region	n/a	-
circRNA302	chr19:36659723|36664203(+)	exon	100793739	LOC100793739
circRNA303	chr1:46803408|46803829(-)	intron	106794272	LOC106794272
circRNA304	chrPltd:5776|6042(-)	exon	3989271	rbcL
circRNA305	chr4:137984|138510(-)	exon	100788288	LOC100788288
circRNA306	chr8:37078609|37092568(+)	intergenic region	n/a	-
circRNA307	chr12:39185836|39186051(+)	intergenic region	n/a	-
circRNA308	chrPltd:282|5526(-)	intergenic region	n/a	-
circRNA309	chr1:56072739|56076395(-)	exon	100799306	LOC100799306
circRNA310	chr8:7420347|7440559(-)	intergenic region	n/a	-
circRNA311	chr20:46162027|46163376(+)	exon	100818409	LOC100818409
circRNA312	chr7:5818456|5888529(+)	intergenic region	n/a	-
circRNA313	chr6:10302651|10308900(+)	exon	100814187	LOC100814187
circRNA314	chr3:28917416|28918014(+)	exon	100786632	LOC100786632
circRNA315	chrPltd:377|5347(-)	intergenic region	n/a	-
circRNA316	chr6:40400733|40400774(-)	exon	100799589	LOC100799589
circRNA317	chr4:8324414|8325968(-)	exon	100800444	LOC100800444
circRNA318	NW_014573484.1:24753|33868(-)	intergenic region	n/a	-
circRNA319	chr16:18633081|18640675(-)	exon	100804783	LOC100804783
circRNA320	chr11:2399523|2408669(-)	intergenic region	n/a	-
circRNA321	chr8:8532001|8535752(+)	intergenic region	n/a	-
circRNA322	chr12:3933041|3939585(+)	intergenic region	n/a	-
circRNA323	chr14:1314153|1334576(-)	intergenic region	n/a	-
circRNA324	chr13:10446662|10468981(-)	intergenic region	n/a	-
circRNA325	chr3:1158932|1210925(-)	intergenic region	n/a	-
circRNA326	chr3:42262802|42267433(+)	exon	100789841	LOC100789841
circRNA327	chr2:11464189|11584195(-)	intergenic region	n/a	-
circRNA328	chr10:45843564|45857438(+)	intergenic region	n/a	-

circRNA329	chr4:36385564|36390772(+)	exon	100802776	LOC100802776
circRNA330	chr4:7317376|7327424(+)	intergenic region	n/a	-
circRNA331	chr6:1103449|1109238(-)	intron	100810431	LOC100810431
circRNA332	chr8:3719682|3720386(+)	intergenic region	n/a	-
circRNA333	chr10:48018585|48019731(-)	exon	100527205	LOC100527205
circRNA334	chr6:11227827|11233143(-)	intergenic region	n/a	-
circRNA335	chr7:49936|51389(+)	exon	100809207	LOC100809207
circRNA336	chr3:39375739|39377161(-)	exon	100813574	LOC100813574
circRNA337	chr6:4486683|4496806(-)	intron	100785124	LOC100785124
circRNA338	chrPltd:1334|6179(-)	intergenic region	n/a	-
circRNA339	chrPltd:1049|5769(-)	intergenic region	n/a	-
circRNA340	chr8:7188226|7188902(+)	exon	100792580	LOC100792580
circRNA341	chr1:40785846|40826530(+)	intergenic region	n/a	-
circRNA342	chr20:1006131|1021407(+)	intergenic region	n/a	-
circRNA343	chr15:915450|936881(+)	intergenic region	n/a	-
circRNA344	chr8:16365101|16376243(-)	intergenic region	n/a	-
circRNA345	chr8:75121|76650(-)	exon	102666240	LOC102666240
circRNA346	chr8:47796962|47797769(-)	exon	100819381	LOC100819381
circRNA347	chr6:49814463|49828200(+)	intergenic region	n/a	-
circRNA348	chr4:36567203|36567727(-)	exon	100806823	LOC100806823
circRNA349	chr10:51486078|51486491(-)	exon	100796688	LOC100796688
circRNA350	chr3:28917416|28917704(+)	exon	100786632	LOC100786632
circRNA351	chr20:12826184|12829486(-)	exon	100810922	LOC100810922
circRNA352	chr14:8966193|8988940(-)	intergenic region	n/a	-
circRNA353	chr8:42021557|42025348(+)	exon	100797527	LOC100797527
circRNA354	chr18:56252463|56269397(-)	intergenic region	n/a	-
circRNA355	chr3:44497299|44500474(-)	intergenic region	n/a	-
circRNA356	chr18:53367914|53372053(-)	intergenic region	n/a	-
circRNA357	chr1:40771890|40773726(-)	intron	100798947	LOC100798947
circRNA358	chr6:14637715|14640541(+)	exon	100809371	LOC100809371
circRNA359	chr11:571108|574697(+)	exon	100811424	LOC100811424
circRNA360	chr15:46896807|46974363(-)	intergenic region	n/a	-
circRNA361	chr15:47836267|47843921(-)	intergenic region	n/a	-
circRNA362	chr2:11464363|11552345(-)	intergenic region	n/a	-
circRNA363	chr2:4502992|4513141(-)	intergenic region	n/a	-
circRNA364	chr19:35364051|35365400(+)	exon	100819645	LOC100819645
circRNA365	chr11:813724|815308(+)	exon	100787912	LOC100787912
circRNA366	chr17:35897816|36081885(-)	intergenic region	n/a	-
circRNA367	chrPltd:6079|6579(-)	exon	3989271	rbcL
circRNA368	chrPltd:102870|103328(+)	intron	3989347	trnA-UGC
circRNA369	chr6:45102182|45254042(+)	intergenic region	n/a	-
circRNA370	chr5:35142714|35143144(+)	exon	100810237	LOC100810237
circRNA371	chr16:4790284|4799283(+)	intergenic region	n/a	-
circRNA372	chr11:2577854|2579263(-)	exon	100779024	LOC100779024
circRNA373	NW_014573484.1:34721|63753(-)	intergenic region	n/a	-
circRNA374	chr1:14066764|14067633(-)	exon	100797182	LOC100797182
circRNA375	chr12:30691510|30693925(+)	exon	100782437	LOC100782437
circRNA376	chr8:18737081|18738917(-)	exon	100792410	LOC100792410
circRNA377	chr14:8138504|8177289(-)	intergenic region	n/a	-
circRNA378	chr2:48058096|48059921(+)	exon	100781655	LOC100781655
circRNA379	chr6:4487693|4497730(-)	intron	100785124	LOC100785124
circRNA380	chr10:39936497|39937548(+)	exon	100794911	LOC100794911
circRNA381	chr8:33257202|33258020(+)	exon	100786931	LOC100786931
circRNA382	chr12:4470195|4490394(+)	intergenic region	n/a	-
circRNA383	chr1:51532362|51538884(-)	intergenic region	n/a	-
circRNA384	chr6:23193531|23197354(-)	exon	100789027	LOC100789027

circRNA385	chr20:2814577|2815634(+)	exon	100814882	LOC100814882
circRNA386	chr8:37880531|37882399(+)	exon	100796816	LOC100796816
circRNA387	chrPltd:1181|6611(-)	intergenic region	n/a	-
circRNA388	chr12:1287231|1293233(+)	intergenic region	n/a	-
circRNA389	chr18:55772619|55773937(-)	exon	100793178	LOC100793178
circRNA390	chr10:30293099|30310511(+)	exon	100798991	LOC100798991
circRNA391	chr17:3800722|3802514(+)	exon	100801645	LOC100801645
circRNA392	chr3:41848632|41849015(+)	exon	100784188	LOC100784188
circRNA393	chr6:2636196|2643514(+)	intergenic region	n/a	-
circRNA394	chr7:17920647|17933805(-)	intergenic region	n/a	-
circRNA395	chrPltd:58664|58709(+)	intergenic region	n/a	-
circRNA396	chr14:2860491|2876806(+)	intergenic region	n/a	-
circRNA397	chrPltd:6617|62647(-)	intergenic region	n/a	-
circRNA398	chr6:18324693|18398819(-)	intergenic region	n/a	-
circRNA399	chr20:384307|387477(+)	exon	100789712	LOC100789712
circRNA400	chr11:10012736|10013350(-)	exon	100789855	LOC100789855
circRNA401	chr3:18838854|18840058(-)	exon	100808588	LOC100808588
circRNA402	chr12:1215614|1220684(-)	intergenic region	n/a	-
circRNA403	chr3:10814925|10816669(-)	exon	100784706	LOC100784706
circRNA404	chr1:16836073|16837051(+)	exon	100796646	LOC100796646
circRNA405	chr18:50041099|50043084(+)	exon	100807514	LOC100807514
circRNA406	chr19:834176|839119(+)	intergenic region	n/a	-
circRNA407	chr8:43752918|43761102(-)	intergenic region	n/a	-
circRNA408	chr20:37121678|37130681(+)	intergenic region	n/a	-
circRNA409	chr8:14047911|14048116(+)	exon	100777674	LOC100777674
circRNA410	chr9:43216289|43217581(+)	exon	100800190	LOC100800190
circRNA411	chr18:57756398|57756679(-)	exon	100818553	LOC100818553
circRNA412	chr3:2832111|2896774(+)	intergenic region	n/a	-
circRNA413	chr20:47802450|47802973(-)	exon	100306581	LOC100306581
circRNA414	chr15:33417004|33427556(+)	exon	100812785	LOC100812785
circRNA415	chr2:1938628|1939750(-)	exon	100812482	LOC100812482
circRNA416	chr11:6225224|6228417(+)	exon	100819979	LOC100819979
circRNA417	chr9:5778704|5782165(+)	exon	100820121	LOC100820121
circRNA418	chr4:2553357|2555253(-)	exon	100796383	LOC100796383
circRNA419	chr20:46343586|46346482(+)	exon	100777257	LOC100777257
circRNA420	chr9:3677492|3684587(-)	intergenic region	n/a	-
circRNA421	chr3:38374249|38375242(+)	exon	100795648	LOC100795648
circRNA422	chr1:1094199|1136368(-)	intergenic region	n/a	-
circRNA423	chr5:35568721|35578613(-)	intergenic region	n/a	-
circRNA424	chr12:32986247|32987034(-)	exon	100819481	LOC100819481
circRNA425	chr11:574273|574697(+)	exon	100811424	LOC100811424
circRNA426	chr8:44901395|44911975(-)	intergenic region	n/a	-
circRNA427	NW_014573484.1:34349|63189(-)	intergenic region	n/a	-
circRNA428	chr3:9574537|9786039(-)	intergenic region	n/a	-
circRNA429	chrPltd:1334|6819(-)	intergenic region	n/a	-
circRNA430	chr16:924014|932357(+)	intergenic region	n/a	-
circRNA431	chr15:45648205|45649041(-)	exon	100800878	LOC100800878
circRNA432	chr1:40768871|40865437(+)	intergenic region	n/a	-
circRNA433	chr2:38755328|38755758(+)	exon	100780041	LOC100780041
circRNA434	chr17:8728097|8729452(-)	exon	100802507	LOC100802507
circRNA435	chr1:55134092|55137396(-)	exon	100780539	LOC100780539
circRNA436	chr16:33923291|33926590(-)	intergenic region	n/a	-
circRNA437	chr8:46678777|46681744(-)	intergenic region	n/a	-
circRNA438	chr17:4494181|4495631(-)	exon	102665860	LOC102665860
circRNA439	chr17:24453911|24469413(+)	exon	100775929	LOC100775929
circRNA440	chr8:8532014|8535752(+)	intergenic region	n/a	-

circRNA441	chr16:20941272|20941776(+)	exon	100818307	LOC100818307
circRNA442	chr10:2371824|2372135(+)	exon	100808741	LOC100808741
circRNA443	chrPltd:542|6911(-)	intergenic region	n/a	-
circRNA444	chr19:7190036|7254196(+)	intergenic region	n/a	-
circRNA445	chr1:14666006|14667229(+)	exon	100790337	LOC100790337
circRNA446	chr20:14775471|14777079(-)	exon	100813099	LOC100813099
circRNA447	chr8:3719672|3720386(+)	intergenic region	n/a	-
circRNA448	chr17:8386898|8387265(+)	intergenic region	n/a	-
circRNA449	chr8:41285540|41286106(+)	exon	100788193	LOC100788193
circRNA450	chr9:30315905|30320737(-)	intergenic region	n/a	-
circRNA451	chr10:20673681|20675114(-)	exon	100798812	LOC100798812
circRNA452	chr20:2814582|2815634(+)	exon	100814882	LOC100814882
circRNA453	chrPltd:917|6111(-)	intergenic region	n/a	-
circRNA454	chr18:3487168|3490245(+)	exon	100813040	LOC100813040
circRNA455	chr2:11523527|11585788(-)	intergenic region	n/a	-
circRNA456	chr19:45710381|45730939(+)	intergenic region	n/a	-
circRNA457	chr16:35007029|35078566(+)	intergenic region	n/a	-
circRNA458	chr19:7331679|7333066(-)	exon	102668567	LOC102668567
circRNA459	chr18:9120644|9145234(+)	intergenic region	n/a	-
circRNA460	chr9:45043768|45064896(-)	intergenic region	n/a	-
circRNA461	chr6:47133711|47146242(+)	intergenic region	n/a	-
circRNA462	chr1:40765144|40863424(+)	intergenic region	n/a	-
circRNA463	chr17:27563226|27564727(-)	exon	100802522	LOC100802522
circRNA464	chr18:53641714|53679942(+)	intergenic region	n/a	-
circRNA465	chrPltd:1164|6911(-)	intergenic region	n/a	-
circRNA466	chr10:49533428|49537563(+)	exon	100812875	LOC100812875
circRNA467	chr4:8651533|8653804(+)	exon	100801328	LOC100801328
circRNA468	chr1:40765144|40806696(+)	intergenic region	n/a	-
circRNA469	chr13:6820332|6841031(+)	exon	100781560	LOC100781560
circRNA470	chr16:4791276|4800308(+)	intergenic region	n/a	-
circRNA471	chr14:4501144|4513332(+)	intergenic region	n/a	-
circRNA472	chr17:15105982|15124542(-)	intergenic region	n/a	-
circRNA473	chrPltd:9820|10336(+)	intergenic region	n/a	-
circRNA474	chr13:30369914|30439244(-)	intergenic region	n/a	-
circRNA475	chr8:15967756|16006670(+)	intergenic region	n/a	-
circRNA476	chr20:34006730|34030841(+)	intergenic region	n/a	-
circRNA477	chr7:5598591|5642775(-)	exon	100780862	LOC100780862
circRNA478	chr13:14433658|14450955(+)	intergenic region	n/a	-
circRNA479	chrPltd:542|5567(-)	intergenic region	n/a	-
circRNA480	chrPltd:6007|6723(-)	exon	3989271	rbcL
circRNA481	NW_014573484.1:16062|64105(-)	intergenic region	n/a	-
circRNA482	chr2:42885381|42885672(+)	intron	100791567	LOC100791567
circRNA483	chr7:6618814|6642147(+)	intergenic region	n/a	-
circRNA484	chr20:2506759|2550951(-)	intergenic region	n/a	-
circRNA485	chr16:2984274|3010428(+)	intergenic region	n/a	-
circRNA486	chr6:49818526|49828200(+)	intergenic region	n/a	-
circRNA487	chr7:1332233|1344285(-)	intergenic region	n/a	-
circRNA488	chrPltd:959|6423(-)	intergenic region	n/a	-
circRNA489	chr11:841379|842960(+)	exon	100799181	LOC100799181
circRNA490	chrPltd:1046|6150(-)	intergenic region	n/a	-
circRNA491	chr9:41106857|41109855(+)	exon	100782181	LOC100782181
circRNA492	chr17:35521047|35522019(+)	exon	102668239	LOC102668239
circRNA493	chr7:1338146|1349989(-)	intergenic region	n/a	-
circRNA494	chr10:5027202|5028970(+)	exon	100817671	LOC100817671
circRNA495	chr8:42087512|42088359(-)	intron	102664025	LOC102664025
circRNA496	chr6:29627338|29630373(+)	exon	100792534	LOC100792534

circRNA497	chr1:11290327|11291065(+)	exon	100785017	LOC100785017
circRNA498	chr3:2879639|2950454(+)	intergenic region	n/a	-
circRNA499	chr2:24765266|24765892(-)	exon	100807496	LOC100807496
circRNA500	NW_014573484.1:18217|25651(-)	intron	100499660	LOC100499660
circRNA501	chrPltd:1164|5496(-)	intergenic region	n/a	-
circRNA502	chr18:44967265|44971082(+)	exon	100775230	LOC100775230
circRNA503	chr14:28564345|28566845(+)	exon	100779093	LOC100779093
circRNA504	chr18:47025919|47057559(+)	intergenic region	n/a	-
circRNA505	chrPltd:537|919(-)	exon	3989259	psbA
circRNA506	chr16:31124428|31159292(-)	intergenic region	n/a	-
circRNA507	chr11:12533077|12534023(-)	exon	100800977	LOC100800977
circRNA508	chr2:11470224|11618890(-)	intergenic region	n/a	-
circRNA509	chr4:6449418|6452039(+)	exon	100790916	LOC100790916
circRNA510	chr10:51439654|51441948(+)	exon	100795105	LOC100795105
circRNA511	chr7:5616468|5737802(-)	intron	100780862	LOC100780862
circRNA512	chr10:30293099|30314447(+)	exon	100798991	LOC100798991
circRNA513	chr18:12237604|12587876(+)	intergenic region	n/a	-
circRNA514	chr4:45441851|45442249(-)	exon	100794615	LOC100794615
circRNA515	NW_014573484.1:27849|35247(-)	intergenic region	n/a	-
circRNA516	chrPltd:13750|14143(-)	intron	3989280	trnL-UAA
circRNA517	chr6:39232956|39234731(+)	exon	100806517	LOC100806517
circRNA518	chr1:40786124|40883182(+)	intergenic region	n/a	-
circRNA519	chr1:3456828|3487889(+)	intergenic region	n/a	-
circRNA520	chr9:37589871|37594714(-)	intergenic region	n/a	-
circRNA521	chr3:2832111|2879746(+)	intergenic region	n/a	-
circRNA522	chr2:1807162|1808637(-)	exon	100808200	LOC100808200
circRNA523	chr2:11527971|11618890(-)	intergenic region	n/a	-
circRNA524	chr8:16365515|16377618(-)	intergenic region	n/a	-
circRNA525	chr20:45575598|45576203(-)	intergenic region	n/a	-
circRNA526	chr13:42278004|42279321(-)	exon	100803144	LOC100803144
circRNA527	chr11:8483683|8497403(-)	intergenic region	n/a	-
circRNA528	chr10:45052893|45053786(-)	exon	100815875	LOC100815875
circRNA529	chr13:14936060|14948575(-)	intergenic region	n/a	-
circRNA530	chr20:24827235|24830481(+)	exon	100815591	LOC100815591
circRNA531	chr15:11462686|11478125(-)	intergenic region	n/a	-
circRNA532	chrPltd:671|5398(-)	intergenic region	n/a	-
circRNA533	chrPltd:1049|5721(-)	intergenic region	n/a	-
circRNA534	chr15:919396|942380(+)	intergenic region	n/a	-
circRNA535	chr18:51497586|51620823(+)	intergenic region	n/a	-
circRNA536	chr2:11590205|11618890(-)	intergenic region	n/a	-
circRNA537	chrPltd:731|6721(-)	intergenic region	n/a	-
circRNA538	chr9:43219537|43223182(+)	exon	100800190	LOC100800190
circRNA539	chr16:26320094|26321368(-)	exon	100775901	LOC100775901
circRNA540	chr14:21796188|21797950(-)	exon	100779257	LOC100779257
circRNA541	chr9:45043492|45064608(-)	intergenic region	n/a	-
circRNA542	chr3:9528007|9786039(-)	intergenic region	n/a	-
circRNA543	chr6:704808|709514(+)	exon	100785855	LOC100785855
circRNA544	chr11:12539404|12540944(-)	exon	100800977	LOC100800977
circRNA545	chrPltd:6617|13742(-)	intergenic region	n/a	-
circRNA546	chr16:35881396|35886401(+)	intergenic region	n/a	-
circRNA547	chr4:44929057|44931900(+)	exon	100788458	LOC100788458
circRNA548	chr3:465865|484729(-)	intron	100788960	LOC100788960
circRNA549	chr8:3341690|3341916(-)	exon	100814574	LOC100814574
circRNA550	chr19:34074859|34076290(-)	exon	100806108	LOC100806108
circRNA551	chr20:2503798|2548226(-)	intergenic region	n/a	-
circRNA552	chr19:38372706|38378483(-)	intergenic region	n/a	-

circRNA553	chr1:53591944|53601538(-)	exon	100796650	LOC100796650
circRNA554	chr2:42885773|42886064(+)	intron	100791567	LOC100791567
circRNA555	chr8:45415924|45430992(-)	intergenic region	n/a	-
circRNA556	chr6:45214792|45238902(+)	intergenic region	n/a	-
circRNA557	chr12:39184138|39184692(+)	intergenic region	n/a	-
circRNA558	chr5:3977468|4003127(+)	intergenic region	n/a	-
circRNA559	chrPltd:1334|5452(-)	intergenic region	n/a	-
circRNA560	chr10:1958039|1968140(-)	intergenic region	n/a	-
circRNA561	chr1:3461948|3504862(+)	intergenic region	n/a	-
circRNA562	chr19:38966003|38966542(-)	exon	100814485	LOC100814485
circRNA563	chr7:4931363|4934848(-)	exon	100808136	LOC100808136
circRNA564	chr9:187830|195693(-)	exon	100787334	LOC100787334
circRNA565	chr3:9489221|9786039(-)	intergenic region	n/a	-
circRNA566	chr8:42671873|42675652(-)	exon	100782497	LOC100782497
circRNA567	chr9:28752908|28756519(-)	exon	100791541	LOC100791541
circRNA568	chr4:1272169|1272550(-)	exon	100500173	LOC100500173
circRNA569	chr4:49076905|49081918(+)	exon	100801705	LOC100801705
circRNA570	chr9:30316147|30321342(-)	intergenic region	n/a	-
circRNA571	chr15:21056604|21057039(-)	exon	100807099	LOC100807099
circRNA572	chr14:34295690|34296306(+)	exon	100810450	LOC100810450
circRNA573	chr17:23824263|23833586(-)	exon	100818869	LOC100818869
circRNA574	chr18:51251234|51269583(+)	intergenic region	n/a	-
circRNA575	chr12:26068859|26068918(-)	exon	100796730	LOC100796730
circRNA576	chr3:39353007|39362821(+)	intergenic region	n/a	-
circRNA577	chr5:4118913|4132521(-)	intergenic region	n/a	-
circRNA578	chr11:8927977|8931149(-)	intergenic region	n/a	-
circRNA579	chr2:11494849|11587639(-)	intergenic region	n/a	-
circRNA580	chr10:15340377|15341056(-)	exon	100796678	LOC100796678
circRNA581	chr20:385741|391272(+)	exon	100789712	LOC100789712
circRNA582	chr20:32240050|32241606(+)	exon	100784393	LOC100784393
circRNA583	chr1:51378408|51379239(-)	exon	100808533	LOC100808533
circRNA584	chr2:24200228|24203368(-)	exon	100804313	LOC100804313
circRNA585	chr20:129203|131337(-)	exon	100781736	LOC100781736
circRNA586	chr19:37044897|37080087(+)	intergenic region	n/a	-
circRNA587	chrPltd:1049|5347(-)	intergenic region	n/a	-
circRNA588	chr8:23358371|23361893(+)	exon	100800879	LOC100800879
circRNA589	chrPltd:5246|6900(-)	intergenic region	n/a	-
circRNA590	chr14:1313759|1334359(-)	intergenic region	n/a	-
circRNA591	chrPltd:1181|6603(-)	intergenic region	n/a	-
circRNA592	chr15:4322950|4324170(+)	exon	100776255	LOC100776255
circRNA593	chr5:27718317|27718897(+)	exon	100819679	LOC100819679
circRNA594	chr13:14936060|14948150(-)	intergenic region	n/a	-
circRNA595	chr19:44906123|44918231(+)	intergenic region	n/a	-
circRNA596	chr7:42473036|42473578(+)	intergenic region	n/a	-
circRNA597	chr12:31887941|31888453(+)	exon	100801333	LOC100801333
circRNA598	chr18:17167950|17168533(+)	exon	102661320	LOC102661320
circRNA599	chr14:4760468|4761097(+)	exon	100795722	LOC100795722
circRNA600	chr18:47058227|47089306(+)	intergenic region	n/a	-
circRNA601	chr2:30936356|30936846(-)	exon	100804634	LOC100804634
circRNA602	chr14:1389083|1394515(+)	exon	100785869	LOC100785869
circRNA603	chr5:4117012|4132020(-)	intergenic region	n/a	-
circRNA604	chr7:1862042|1944358(-)	intergenic region	n/a	-
circRNA605	chr1:3461321|3504695(+)	intergenic region	n/a	-
circRNA606	chr16:33437015|33492350(+)	intergenic region	n/a	-
circRNA607	chr19:39072996|39073308(+)	exon	100809299	LOC100809299
circRNA608	chr11:18326812|18439336(-)	intergenic region	n/a	-

circRNA609	chr5:4116687|4131112(-)	intergenic region	n/a	-
circRNA610	chr15:20902156|20908672(-)	exon	100804432	LOC100804432
circRNA611	chr9:45042379|45063446(-)	intergenic region	n/a	-
circRNA612	chrMT:42344|42620(+)	intergenic region	n/a	-
circRNA613	chr9:45042640|45063769(-)	intergenic region	n/a	-
circRNA614	chr1:3493493|3504862(+)	intergenic region	n/a	-
circRNA615	chrPltd:102420|103021(+)	intergenic region	n/a	-
circRNA616	chr9:41496971|41497611(+)	exon	100775562	LOC100775562
circRNA617	chr20:372302|385614(+)	exon	100789712	LOC100789712
circRNA618	chr2:11525980|11616531(-)	intergenic region	n/a	-
circRNA619	chr14:28661848|28668769(+)	exon	100807603	LOC100807603
circRNA620	chr18:53635793|53672379(+)	intergenic region	n/a	-
circRNA621	chr18:53880118|53883466(-)	exon	100818890	LOC100818890
circRNA622	chr16:36808057|36812010(+)	exon	100800352	LOC100800352
circRNA623	chr18:41246638|41296638(-)	intergenic region	n/a	-
circRNA624	chr9:46987019|46987225(+)	exon	100776652	LOC100776652
circRNA625	chr12:39172032|39202220(-)	intergenic region	n/a	-
circRNA626	chr11:33084644|33104103(+)	intergenic region	n/a	-
circRNA627	chr17:23824263|23825603(-)	exon	100818869	LOC100818869
circRNA628	chr1:18850487|18852875(+)	exon	100799827	LOC100799827
circRNA629	chr7:5879136|5883809(+)	exon	100783381	LOC100783381
circRNA630	chr16:4790967|4799454(+)	intergenic region	n/a	-
circRNA631	chrPltd:10079|10213(+)	intron	3989275	trnV-UAC
circRNA632	chr16:32565209|32582792(+)	intergenic region	n/a	-
circRNA633	chrPltd:992|1349(-)	exon	3989259	psbA
circRNA634	chr20:34671296|34671744(-)	exon	100787418	LOC100787418
circRNA635	chr9:49013639|49014125(-)	intergenic region	n/a	-
circRNA636	chr2:12773477|12798698(+)	intergenic region	n/a	-
circRNA637	chr4:45004008|45006078(+)	exon	100788458	LOC100788458
circRNA638	chr1:49275216|49277073(+)	exon	100782701	LOC100782701
circRNA639	chr20:47359638|47359992(-)	intron	100804890	LOC100804890
circRNA640	chr15:1655721|1689193(+)	intergenic region	n/a	-
circRNA641	chr9:5181613|5181889(-)	exon	100809968	LOC100809968
circRNA642	chr6:4486042|4494546(-)	intron	100785124	LOC100785124
circRNA643	chr17:37182620|37200573(-)	intergenic region	n/a	-
circRNA644	chr11:30287670|30317704(-)	intergenic region	n/a	-
circRNA645	chr11:10052071|10063439(-)	intergenic region	n/a	-
circRNA646	chr14:8138838|8177736(-)	intergenic region	n/a	-
circRNA647	chr3:2880809|2899803(+)	intergenic region	n/a	-
circRNA648	chr9:65301|82486(+)	intergenic region	n/a	-
circRNA649	chr12:18579993|18959633(-)	intergenic region	n/a	-
circRNA650	chr17:15106671|15125224(-)	intergenic region	n/a	-
circRNA651	chr19:37222664|37225402(-)	exon	100785430	LOC100785430
circRNA652	chrPltd:18994|19115(+)	exon	3989266	psaA
circRNA653	NW_014573484.1:15243|24253(-)	intron	100499660	LOC100499660
circRNA654	chr19:48927123|48967266(-)	intergenic region	n/a	-
circRNA655	chr8:37880518|37882399(+)	intron	100796816	LOC100796816
circRNA656	chr6:42502018|42700635(+)	intergenic region	n/a	-
circRNA657	chr3:5475546|5946000(+)	intergenic region	n/a	-
circRNA658	chr12:5347411|5349201(+)	exon	100787759	LOC100787759
circRNA659	chr12:791788|805322(+)	intergenic region	n/a	-
circRNA660	chr11:16525588|16660259(+)	intergenic region	n/a	-
circRNA661	chr3:2833514|2898802(+)	intergenic region	n/a	-
circRNA662	chr6:45215558|45239558(+)	intergenic region	n/a	-
circRNA663	chrPltd:1334|52726(-)	intergenic region	n/a	-
circRNA664	chr3:2886488|2954409(+)	intergenic region	n/a	-

circRNA665	chr16:3423143|3424288(+)	exon	100819741	LOC100819741
circRNA666	chr9:42911177|42911692(-)	exon	100790691	LOC100790691
circRNA667	chr2:5914840|5917782(+)	exon	100776137	LOC100776137
circRNA668	chr11:11730051|11731824(+)	exon	100798497	LOC100798497
circRNA669	chr3:27920667|27921314(-)	exon	100813936	LOC100813936
circRNA670	chr11:5595343|5596154(-)	exon	100795117	LOC100795117
circRNA671	chr4:52054899|52056237(+)	exon	100775631	LOC100775631
circRNA672	chr14:9303047|9389492(-)	intergenic region	n/a	-
circRNA673	chr20:46232035|46233159(-)	exon	100816122	LOC100816122
circRNA674	chr13:36343547|36350053(+)	exon	100816142	LOC100816142
circRNA675	chrMT:47104|47375(+)	intergenic region	n/a	-
circRNA676	chr6:15350288|15350698(-)	exon	100778359	LOC100778359
circRNA677	NW_014573484.1:19046|28545(-)	intron	100499660	LOC100499660
circRNA678	NW_014573484.1:116|19533(-)	intergenic region	n/a	-
circRNA679	chr5:91365|93631(-)	exon	100798000	LOC100798000
circRNA680	chr2:11589139|11617353(-)	intergenic region	n/a	-
circRNA681	chrPltd:9820|10340(+)	intergenic region	n/a	-
circRNA682	chr2:13814031|13817247(+)	exon	100797559	LOC100797559
circRNA683	chrPltd:1334|6423(-)	intergenic region	n/a	-
circRNA684	chr4:41688385|41689222(+)	exon	100798329	LOC100798329
circRNA685	chr11:463972|464617(+)	exon	100808747	LOC100808747
circRNA686	chr15:46456111|46462169(+)	intergenic region	n/a	-
circRNA687	chr5:15714461|15715073(+)	exon	100787957	LOC100787957
circRNA688	chr6:11892438|11893851(-)	exon	100791330	LOC100791330
circRNA689	chr7:5307300|5313427(+)	intergenic region	n/a	-
circRNA690	chr7:10472719|10484541(-)	intergenic region	n/a	-
circRNA691	chr20:34018305|34034475(+)	intergenic region	n/a	-
circRNA692	chr20:25333849|25336387(+)	exon	100337655	LOC100337655
circRNA693	chr6:6457880|6461165(+)	intergenic region	n/a	-
circRNA694	chr20:45829100|45830084(+)	intergenic region	n/a	-
circRNA695	chr4:48019423|48020758(+)	exon	100810372	LOC100810372
circRNA696	chr19:1879350|1893556(+)	intergenic region	n/a	-
circRNA697	chr7:19647953|19648541(+)	exon	100807255	LOC100807255
circRNA698	chr8:44684764|44705621(+)	intergenic region	n/a	-
circRNA699	chr15:915233|936673(+)	intergenic region	n/a	-
circRNA700	chr13:22495827|22497063(+)	exon	100788136	LOC100788136
circRNA701	chr1:40763642|40803484(+)	intergenic region	n/a	-
circRNA702	chr8:44292005|44296495(+)	intergenic region	n/a	-
circRNA703	chr17:12179480|12181447(-)	exon	100780029	LOC100780029
circRNA704	chr5:682855|683335(+)	exon	100500448	LOC100500448
circRNA705	chr13:15500721|15501426(+)	exon	100792021	LOC100792021
circRNA706	chrPltd:1334|6190(-)	intergenic region	n/a	-
circRNA707	chr15:4750651|4752561(+)	exon	100793450	LOC100793450
circRNA708	chr1:40764103|40805360(+)	intergenic region	n/a	-
circRNA709	chr20:27308877|27395942(-)	intergenic region	n/a	-
circRNA710	chr1:40766818|40864749(+)	intergenic region	n/a	-
circRNA711	chr15:15637009|15654719(+)	intergenic region	n/a	-
circRNA712	chr15:11466928|11481396(-)	intergenic region	n/a	-
circRNA713	chr4:7316309|7326365(+)	intergenic region	n/a	-
circRNA714	chrPltd:1049|6642(-)	intergenic region	n/a	-
circRNA715	chr8:16370065|16382792(-)	intergenic region	n/a	-
circRNA716	chrPltd:1049|6582(-)	intergenic region	n/a	-
circRNA717	chrPltd:6376|6801(-)	intergenic region	n/a	-
circRNA718	chr3:39759591|39760220(+)	exon	100799358	LOC100799358
circRNA719	chr2:11527161|11618108(-)	intergenic region	n/a	-
circRNA720	chr17:39769754|39770767(+)	exon	100814610	LOC100814610

circRNA721	chr11:405214|413342(+)	intergenic region	n/a	-
circRNA722	chr12:14916220|14953212(-)	intergenic region	n/a	-
circRNA723	chr7:5883734|5883809(+)	exon	100783381	LOC100783381
circRNA724	chr1:40769208|40870116(+)	intergenic region	n/a	-
circRNA725	chr19:7331679|7333071(-)	exon	102668567	LOC102668567
circRNA726	chr12:16512715|16737230(+)	intergenic region	n/a	-
circRNA727	chr6:22933744|22939330(-)	exon	100783185	LOC100783185
circRNA728	chr9:45275349|45279479(-)	exon	100809429	LOC100809429
circRNA729	chrPltd:1046|6022(-)	intergenic region	n/a	-
circRNA730	chr13:42278598|42280386(-)	exon	100803144	LOC100803144
circRNA731	chrPltd:965|5831(-)	intergenic region	n/a	-
circRNA732	chr7:6616976|6639868(+)	intergenic region	n/a	-
circRNA733	chr17:34578204|34579654(-)	exon	100816565	LOC100816565
circRNA734	chr7:15549263|15551752(+)	exon	100803526	LOC100803526
circRNA735	chr7:5883746|5883809(+)	exon	100783381	LOC100783381
circRNA736	chr5:17918842|17919263(+)	exon	100791478	LOC100791478
circRNA737	chr1:40826151|40870281(+)	intergenic region	n/a	-
circRNA738	chr2:24200228|24211971(-)	exon	100804313	LOC100804313
circRNA739	chr11:10342035|10342821(-)	exon	100790051	LOC100790051
circRNA740	chr18:7034744|7036702(-)	exon	100809649	LOC100809649
circRNA741	chr20:35683676|35684970(+)	exon	100777969	LOC100777969
circRNA742	chrPltd:1334|5979(-)	intergenic region	n/a	-
circRNA743	chr11:15566414|15575817(-)	intergenic region	n/a	-
circRNA744	chr13:14412571|14430796(+)	intergenic region	n/a	-
circRNA745	chr17:32901153|32910593(-)	exon	100788741	LOC100788741
circRNA746	chr11:28468445|28514562(+)	intergenic region	n/a	-
circRNA747	chr20:36115002|36143608(-)	intergenic region	n/a	-
circRNA748	chr9:4010101|4010606(-)	exon	100779134	LOC100779134
circRNA749	chr3:45174287|45175859(+)	exon	100816236	LOC100816236
circRNA750	chr14:13655490|13724529(-)	intergenic region	n/a	-
circRNA751	chr12:35934159|35947677(-)	intron	100807714	LOC100807714
circRNA752	chr3:5026677|5051006(+)	intergenic region	n/a	-
circRNA753	chr12:3366413|3368360(+)	exon	100783343	LOC100783343
circRNA754	chr3:2889318|2956200(+)	intergenic region	n/a	-
circRNA755	chr16:2984739|3010585(+)	intergenic region	n/a	-
circRNA756	chr12:37054496|37056330(-)	exon	100804362	LOC100804362
circRNA757	chr7:5616308|5737485(-)	intron	100780862	LOC100780862
circRNA758	chr11:406172|414451(+)	intergenic region	n/a	-
circRNA759	chr6:44787166|44830669(-)	intergenic region	n/a	-
circRNA760	chr17:27301206|27304033(-)	exon	106796783	LOC106796783
circRNA761	chr13:4159199|4165789(-)	intergenic region	n/a	-
circRNA762	chr15:1649919|1683496(+)	intergenic region	n/a	-
circRNA763	chr9:48491035|48491617(+)	exon	100800714	LOC100800714
circRNA764	chr12:2142564|2144715(-)	exon	100306616	LOC100306616
circRNA765	chr17:35870205|36081663(-)	intergenic region	n/a	-
circRNA766	chr7:5568052|5642775(-)	intergenic region	n/a	-
circRNA767	chr15:15637208|15656311(+)	intergenic region	n/a	-
circRNA768	chr16:31136928|31164051(-)	intergenic region	n/a	-
circRNA769	NW_014573403.1:447609|452435(-)	intergenic region	n/a	-
circRNA770	chr12:39171046|39201052(-)	intergenic region	n/a	-
circRNA771	chr8:34225120|34225496(+)	exon	100780532	LOC100780532
circRNA772	chr17:30723779|30726287(-)	exon	100788049	LOC100788049
circRNA773	chr8:11323834|11328246(-)	exon	100803721	LOC100803721
circRNA774	chr4:52380522|52380592(+)	exon	100786150	LOC100786150
circRNA775	chr6:4019007|4020713(-)	exon	100788141	LOC100788141
circRNA776	chr18:43345766|43346768(+)	exon	100792819	LOC100792819

circRNA777	chr8:44020129|44038088(+)	intergenic region	n/a	-
circRNA778	chr15:12789840|12790338(+)	intron	100784626	LOC100784626
circRNA779	chr8:12661447|12667988(-)	exon	100788022	LOC100788022
circRNA780	chr1:65205|66320(-)	exon	102661143	LOC102661143
circRNA781	chr15:10846721|10847648(+)	exon	100780698	LOC100780698
circRNA782	chr1:1092992|1135833(-)	intergenic region	n/a	-
circRNA783	chr8:33250697|33253207(+)	exon	100786931	LOC100786931
circRNA784	chrPltd:5419|5742(-)	exon	3989271	rbcL
circRNA785	chr1:53934829|53936075(+)	exon	100790851	LOC100790851
circRNA786	chr3:29505798|29510259(+)	exon	100500111	LOC100500111
circRNA787	chr4:44234918|44248694(-)	intergenic region	n/a	-
circRNA788	chr7:16581545|16586973(+)	intergenic region	n/a	-
circRNA789	chr4:20611036|20612674(-)	exon	100807902	LOC100807902
circRNA790	chr9:10445089|10448959(+)	exon	100780371	LOC100780371
circRNA791	chr16:31516054|31523831(-)	intergenic region	n/a	-
circRNA792	chr13:18691319|18691999(-)	exon	100777822	LOC100777822
circRNA793	chr12:39175298|39205563(-)	intergenic region	n/a	-
circRNA794	chr3:11451080|11454212(-)	exon	100819282	LOC100819282
circRNA795	chr7:41734490|41736319(-)	exon	100789933	LOC100789933
circRNA796	chr13:28350331|28351147(-)	intron	100819150	LOC100819150
circRNA797	chr13:30627515|30632709(+)	exon	100813299	LOC100813299
circRNA798	chr7:43007302|43007672(-)	exon	100301901	DXS1
circRNA799	chr10:42469222|42471814(+)	exon	100810184	LOC100810184
circRNA800	chr8:15991994|15996000(+)	exon	100776818	LOC100776818
circRNA801	chr18:24821791|24846120(-)	exon	100818895	LOC100818895
circRNA802	chr16:36345772|36387941(+)	intergenic region	n/a	-
circRNA803	chr20:35485340|35486636(-)	exon	100818587	LOC100818587
circRNA804	chrPltd:1049|1428(-)	intergenic region	n/a	-
circRNA805	chr11:15567014|15576696(-)	intergenic region	n/a	-
circRNA806	chr7:5337328|5344129(-)	intergenic region	n/a	-
circRNA807	chr6:47133484|47144602(+)	intergenic region	n/a	-
circRNA808	chr3:23079358|23080745(+)	exon	100780970	LOC100780970
circRNA809	chr16:7174054|7174914(+)	exon	100799113	LOC100799113
circRNA810	chr1:64055|64199(-)	exon	102661143	LOC102661143
circRNA811	chr15:49961001|49961874(+)	exon	100811882	LOC100811882
circRNA812	chr2:11463971|11545580(-)	intergenic region	n/a	-
circRNA813	chr10:46239930|46246023(-)	intergenic region	n/a	-
circRNA814	chr12:26067884|26068699(-)	exon	100796730	LOC100796730
circRNA815	chr18:51534325|51601919(+)	intergenic region	n/a	-
circRNA816	chr15:916064|938793(+)	intergenic region	n/a	-
circRNA817	chr9:24718305|24739833(+)	intergenic region	n/a	-
circRNA818	chr20:34666212|34666927(+)	exon	102669236	LOC102669236
circRNA819	chr8:11667794|11668295(+)	exon	100811720	LOC100811720
circRNA820	chr8:12191899|12192399(-)	intron	100780527	LOC100780527
circRNA821	chr7:15549263|15553458(+)	exon	100803526	LOC100803526
circRNA822	chr3:27908660|27921314(-)	exon	100813936	LOC100813936
circRNA823	chr8:20585673|20586101(+)	exon	100783218	LOC100783218
circRNA824	chr12:39176507|39206477(-)	intergenic region	n/a	-
circRNA825	chr12:4469844|4490071(+)	intergenic region	n/a	-
circRNA826	chr3:44856675|44860262(+)	exon	100814483	LOC100814483
circRNA827	chr1:27707|28264(-)	intergenic region	n/a	-
circRNA828	chr2:45645550|45645620(-)	exon	100783265	LOC100783265
circRNA829	chr13:18691319|18691996(-)	exon	100777822	LOC100777822
circRNA830	chr10:50445129|50445829(-)	exon	100794236	LOC100794236

Table S4: Significant GO enrichment analysis of differently expressed lncRNA targets.

		GO terms	Type	Q-value	lncRNAs Number
Cis-actiing manner	Drought	nucleoplasm	cellular_component	5.60E-04	4
		transcription from RNA polymerase II promoter	biological_process	1.31E-03	4
		RNA binding	molecular_function	7.76E-03	6
		RNA processing	biological_process	2.68E-02	4
		structural constituent of ribosome	molecular_function	2.99E-02	4
	Saline-alkaline	transcription factor activity	molecular_function	9.55E-03	4
		signal transduction	biological_process	1.36E-02	4
		phosphate-containing compound metabolic process	biological_process	1.66E-02	4
		transcription, DNA-templated	biological_process	4.05E-03	7
		cellular response to stimulus	biological_process	1.33E-02	5
Trans-acting manner	Drought	ATPase activity	molecular_function	1.47E-03	4
		pyrophosphatase activity	molecular_function	1.29E-03	5
		acting on acid anhydrides	molecular_function	1.35E-03	5
		phosphate-containing compound metabolic process	biological_process	1.49E-03	5
		hydrolase activity, acting on acid anhydrides	molecular_function	5.98E-03	5
	Saline-alkaline	hydrolyzing O-glycosyl compounds	molecular_function	1.85E-04	4
		acting on glycosyl bonds	molecular_function	3.00E-04	4
		carbohydrate metabolic process	biological_process	2.47E-03	5
		cellular protein modification process	biological_process	8.46E-03	4
		regulation of transcription, DNA-templated	biological_process	1.17E-02	4