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(54) Title: LONG NON-CODING RNAs FOR MODULATING PHOSPHATE USE EFFICIENCY IN PLANTS

(57) Abstract: Long non-coding RNAs in plants are provided, particularly non-polyadenylated long non-coding RNAs, which are differentially expressed under phosphate starvation conditions, such as long non-coding RNAs whose transcription is upregulated in plants during phosphate starvation. Modulation of the expression of such long non-coding RNAs can be used to alter phosphate use efficiency in plants.

Long non-coding RNAs for modulating phosphate use efficiency in plants

Field of the invention

[001] The present invention relates to the fields of the agriculture and molecular biology. More particularly, the invention is directed at methods for identification of long non-coding RNAs in plants, particularly non-polyadenylated long non-coding RNAs which are differentially expressed under phosphate starvation conditions, such as long non-coding RNAs whose transcription is upregulated in plants during phosphate starvation. Modulation of the expression of such long non-coding RNAs can be used to alter phosphate use efficiency in plants.

Background of the invention

[002] Recently, many novel lncRNAs have been found to fulfill essential roles in different species [8]. Because of their much lower expression level and evolutionary conservation than protein-coding mRNAs [9, 10], as well as uncertain functions for these transcripts, they were initially considered as transcriptional noise [11, 12]. But this hypothesis was soon challenged by the discovery that many lncRNAs were detected during specific developmental stages [13, 14]. Although most lncRNAs have not been well characterized due to difficulties of cloning, some have been extensively studied and are well known for us, such as Xist, an inactive X-specific lncRNA [15, 16], and COLDAIR, an intronic lncRNA [17].

[003] Plants possess an elaborate physiological system to respond to external stimuli and stress conditions [1]. Non-coding RNAs are the indispensable part of signal transduction networks during stress responses [2]. Sequencing of small RNA libraries from stressed A. thaliana seedlings has discovered 26 new miRNAs and 102 novel endogenous small RNAs, suggesting that they have roles in stress responses [3].

[004] In addition, nutrient homeostasis (e.g. phosphorus balance) is tightly regulated by many complex pathways, in which miRNAs are important members [4]. For example, Pi-

dependent miR-399 targets and cleaves PHO2 mRNA, which encodes the E2 conjugase that decreases the Pi content and weakens Pi remobilization [5]. While searching the Arabidopsis genome complementary to miR-399, biologists founding a new class of Pi starvation-associated long non-coding RNAs such as IPS1 (INDUCED BY PHOSPHATE STARVAYION1) and AT4, which act as target mimics to inhibit miRNA-399 activity [6, 7].

[005] Recent advances in next-generation sequencing technology known as cDNA sequencing or RNA-sequencing (RNA-seq) has been successfully applied in whole-transcriptome research [18]. Several well developed experimental protocols for strand-specific RNA-seq (such as SMART [19] and Bisulfite [20]) are powerful in identifying lots of nature antisense transcripts (NATs). Nearly 10,000 lncRNAs have been identified in human [21, 22]. Although most lncRNAs were suggested to be synthesized by RNA polymerase II and processed with polyadenylation [23], an increasing number of non-polyadenylated lncRNAs as well as those with short polyA tails have been discovered recently [24].

[006] Although some lncRNAs have been discovered to function in fundamental biological processes during Pi starvation, the role of others remains to be elucidated. Systematic identification of lncRNAs involved in Pi starvition in plants is warranted, especially identification of the less well known, non-polyadenylated ones.

[007] The prior art thus remains deficient in providing lncRNAs which can be used to modulate phosphate use efficiency in plants.

[008] These and other problems are solved as described hereinafter in the different embodiments, examples and claims.

Summary of the invention

[009] In one embodiment, the invention provides long non-coding RNA(lncRNA) molecules which are differentially expressed in a plant grown under phosphate starvation conditions when compared to a plant grown under normal conditions with adequate phosphate supply and which are unpolyadenylated such as lncRNA molecules comprising a nucleotide sequence having at least 80% percent identity with any one of SEQ ID No. 4; SEQ ID No. 5; SEQ ID No. 6; SEQ ID No. 15; SEQ ID No. 18; SEQ ID No. 26; SEQ ID No. 28; SEQ ID No. 32; SEQ ID No. 34; SEQ ID No. 36; SEQ ID No. 40; SEQ ID No. 42; SEQ ID No. 47; SEQ ID No. 52; SEQ ID No. 55; SEQ ID No. 57; SEQ ID No. 59; SEQ ID No. 60; SEQ ID No. 62; SEQ ID No. 64; SEQ ID No. 70; SEQ ID No. 72; SEQ ID No. 77; SEQ ID No. 79; SEQ ID No. 82; SEQ ID No. 83; SEQ ID No. 84; SEQ ID No. 86; SEQ ID No. 90; SEQ ID No. 91; SEQ ID No. 98; SEQ ID No. 99; SEQ ID No. 102; SEQ ID No. 107; SEQ ID No. 114; SEQ ID No. 115; SEQ ID No. 118; SEQ ID No. 119; SEQ ID No. 120; SEQ ID No. 121; SEQ ID No. 128; SEQ ID No. 132; SEQ ID No. 137; SEQ ID No. 139; SEQ ID No. 140; SEQ ID No. 145; SEQ ID No. 149; SEQ ID No. 151; SEQ ID No. 152; SEQ ID No. 158; SEQ ID No. 160; SEQ ID No. 162; SEQ ID No. 172; SEQ ID No. 174; SEQ ID No. 176; SEQ ID No. 178; SEQ ID No. 179; SEQ ID No. 180; SEQ ID No. 181; SEQ ID No. 183; SEQ ID No. 187; SEQ ID No. 194; SEQ ID No. 195; SEQ ID No. 200; SEQ ID No. 201; SEQ ID No. 204; SEQ ID No. 209 or SEQ ID No. 210 or a nucleotide sequence being identical with the mentioned sequences.

[010] In another embodiment, the invention provides single stranded DNA molecules which when transcribed yield RNA molecules comprising such lncRNA or the complement of such single stranded DNA molecules or double stranded DNA molecules.

[011] The expression of the lncRNA molecule may be upregulated as is the case for lncRNA molecules comprises a nucleotide sequence having at least 80% percent identity with any one of SEQ ID Nos. 34, 107, 139, 194 or 195.

[012] The lncRNA molecule may comprise at least two conserved hairpin loops, preferably further comprising two co-variance base pairings as is the case for lncRNA

molecules comprises a nucleotide sequence having at least 80% percent identity with SEQ ID No. 149.

[013] In yet another embodiment, the invention provides use of such lncRNA molecules or DNA molecules which when transcribed yield such lncRNA molecules, to modulate inorganic phosphate use efficiency in a plant.

[014] In still another embodiment, the invention provides the use of a lncRNA molecule which is differentially expressed in a plant grown under phosphate starvation conditions when compared to a plant grown under normal conditions with adequate phosphate supply, or a DNA molecule which when transcribed yields such lncRNA molecule, or the complement of the DNA molecule, to modulate inorganic phosphate use efficiency in a plant. This may also comprise lncRNA molecules which are polyadenylated such as lncRNA molecules comprising a nucleotide sequence having at least 80 % sequence identity to SEQ ID No. 216; SEQ ID No. 235; SEQ ID No. 240; SEQ ID No. 250; SEQ ID No. 266; SEQ ID No. 267; SEQ ID No. 278; SEQ ID No. 281; SEQ ID No. 283; SEQ ID No. 315; SEQ ID No. 320; SEQ ID No. 321; SEQ ID No. 325; SEQ ID No. 330; SEQ ID No. 361; SEQ ID No. 364; SEQ ID No. 368; SEQ ID No. 370; SEQ ID No. 378; SEQ ID No. 384; SEQ ID No. 388; SEQ ID No. 393; SEQ ID No. 396; SEQ ID No. 414; SEQ ID No. 420; SEQ ID No. 424; SEQ ID No. 429; SEQ ID No. 432; SEQ ID No. 433; SEQ ID No. 436; SEQ ID No. 437; SEQ ID No. 448; SEQ ID No. 459; SEQ ID No. 460; SEQ ID No. 461; SEQ ID No. 462; SEQ ID No. 463; SEQ ID No. 486; SEQ ID No. 504; SEQ ID No. 512; SEQ ID No. 533; SEQ ID No. 570; SEQ ID No. 571; SEQ ID No. 572; SEQ ID No. 600; SEQ ID No. 601; SEQ ID No. 617; SEQ ID No. 618; SEQ ID No. 649; SEQ ID No. 651; SEQ ID No. 652; SEQ ID No. 656; SEQ ID No. 660; SEQ ID No. 662; SEQ ID No. 707; SEQ ID No. 709; SEQ ID No. 712; SEQ ID No. 713; SEQ ID No. 715; SEQ ID No. 716; SEQ ID No. 725; SEQ ID No. 734; SEQ ID No. 783; SEQ ID No. 785; SEQ ID No. 786; SEQ ID No. 787; SEQ ID No. 788; SEQ ID No. 798; SEQ ID No. 817; SEQ ID No. 850; SEQ ID No. 857; SEQ ID No. 918; SEQ ID No. 921; SEQ ID No. 945; SEQ ID No. 946; SEQ ID No. 955; SEQ ID No. 957; SEQ ID No. 972; SEQ ID No. 985; SEQ ID No. 986; SEQ ID No. 990; SEQ ID No. 997; SEQ ID No. 998; SEQ ID No. 1020;

SEQ ID No. 1025; SEQ ID No. 1031; SEQ ID No. 1033; SEQ ID No. 1047; SEQ ID No. 1048; SEQ ID No. 1068 or SEQ ID No. 1080. The lncRNA molecule may also comprise a nucleotide sequence of any one of Tables 5 to 10.

[015] The invention further provides a method for modulating the phosphate use efficiency in a plant comprising the step of increasing or decreasing the transcription and/or concentration of an lncRNA molecule as herein described in a plant cell. The method may comprise a step of decreasing transcription and/or concentration of an lncRNA molecule which may be achieved by mutating the DNA region from which the lncRNA molecule is transcribed, or by expression of an inhibitory RNA molecule specifically recognizing the lncRNA molecule. The method may comprise a step of increasing transcription and/or concentration of an lncRNA molecule which may be achieved by mutating the DNA region from which the lncRNA molecule is transcribed, or by introducing a recombinant gene comprising:

a. a plant-expressible promoter
b. a DNA region which when transcribed encodes an RNA molecule comprising or consisting of said lncRNA molecule; and optionally
c. an appropriate transcription termination region, and/or polyadenylation region.

[016] The invention also provides modified plant cells comprising a modulated concentration or transcription of an lncRNA molecule as herein described, when compared to an unmodified plant cell and modified plant, or plant part, tissue or organ comprising a multitude of or consisting essentially of modified plant cells, as well as seeds of such plants comprising the mutation, genetic alteration or recombinant leading to or resulting in the modulated concentration or transcription of an lncRNA molecule as herein described.

[017] The invention also provides a method for isolating further lncRNA molecules involved in phosphate use efficiency in a plant comprising the step of identifying a nucleotide sequence having a degree of homology to the lncRNA molecules as herein

described and isolating or synthesizing such RNA molecule comprising or consisting of such nucleotide sequences.

Brief description of the drawings

[018] **Figure 1**: Flowchart of RNA sequencing and data processing suitable to identify non-polyadenylated long non-coding RNAs . Panel (A): Purification of non-polyA RNAs and total RNAs. Panel (B): Construction of strand-specific cDNA libraries and sequencing, sequencing at short and long read length are different at steps of size selection and Illumina sequencing. Panel (C): Sequencing data processing: trimming and assembling reads to transcripts.

[019] **Figure 2:** Comparison of total and non-polyA RNA-seq with short and long read length. Panel (A): Length distribution of clean-read assembled fragments from three sequencing data. Panel (B): Length distribution of novel lncRNAs from three sequencing data. Panel (C): Numbers of novel lncRNAs at different expressed values (RPKM) from non-polyA RNA-seq (short reads), gray bars. Overlap ratio with novel lncRNAs from total RNA-seq, black line. Panel (D): Genome location for identified novel lncRNAs from three methods. Panel (E) Validation of novel lncRNA candidates from non-polyA RNA-seq by RT-PCR. M: DNA ladder; ACT2: AT3G18780; Non-polyA and PolyA, candidates were amplified from two cDNA libraries: non-polyA RNAs and polyA RNAs; RT(-), negative control without reverse transcriptase; Left box, polyA RNA (control); Right box, non-polyA RNA.

[020] **Figure 3:** Identification of polyA and non-polyA lncRNAs associated with inorganic phosphate (Pi) starvation. Panel (A): Flowchart of polyA and non-polyA lncRNA prediction and characterization. Panel (B): Differential expression of polyA and non-polyA lncRNAs between plants grown under low Pi conditions and the control plants. Panel (C): Comparison of the proportion of differentially expressed polyA and non-polyA lncRNAs. !, !2 test p-value < 0.01; Gray box, differentially expressed polyA lncRNAs; Dotted box, differentially expressed polyA lncRNAs; gray plus dotted boxes, all identified polyA lncRNAs.

[021] **Figure 4:** Characterization of identified polyA and associated with Pi starvation. Panel (A): DNA conservation of novel lncRNAs in multiple plant species. Compared to coding genes and unexpressed intergenic control regions, lncRNAs show moderate DNA conservation. Panel (B) Comparison of DNA and protein conservation, RNA structure conservation and structure stability (free energy) of lncRNAs and coding genes. RNA structure conservation was normalized by their DNA conservation scores.Panel (C) GO enrichment of non-polyA lncRNA co-located (on cis-regulatory region) with coding genes. Pi-starvation associated GO terms are shown.

[022] **Figure 5:** Validation of novel non-polyA lncRNAs in Pi starvation. Panel (A) Up-regulated expression of novel non-polyA lncRNAs in low Pi samples. Relative expression of selected non-polyA lncRNAs from Table 4 were measured by real-time PCR. Panel (B) A non-polyA lncRNAs (lnc-34) supported by expression and epigenetics. H3K9ac and H2A.Z are raw reads from ChIP-seq data (GSE28398) and chAP-seq data (GSM954614), and inputs are background of them. Signals in non-polyA and polyA RNA-seq tracks are raw reads from four RNA-seq data. The signal is normalized by total mapped reads of each sample. Panel (C) An example of conserved secondary structure of the 5' end of a non-polyA lncRNA (lnc-149). Two conserved short hairpins are displayed in the top and left region, and one variable long hairpin onn the right. Covariance base-pairings are encircled with dark dots and conserved loops are indicted by darker boxes green (darkest means conserved in three genomes and lightest box in two genomes). The multiple alignments from lnc-146 as can be found in three plant genomes (A. thaliana SEQ ID No. 1328; A. lyrata SEQ ID No. 1329; and T. halophile SEQ ID No. 1330) are also provided to illustrate the conserved bases and loops in the primary sequences.

[023] **Figure 6:** Illustration of the Reads quality by FastQC. Raw reads quality is represented by uploading FastQ files of sequencing reads to the FastQC program (see Example 1/Methods).

[024] **Figure 7:** Novel non-polyA and polyA lncRNAs (both total and differentially expressed) were sub-typed as Transgenic elements, pseudogene, antisense, ambiguous and intergenic by aligning to TAIR10 genome (see Example 1/ Methods).

[025] **Figure 8:** GO enrichment of polyA lncRNAs co-located (on the cis-regulatory region) with coding genes.

Detailed description of different embodiments

[026] The current invention is based upon the identification of long non coding RNAs, including novel unpolyadenylated long non coding RNAs, which are differentially expressed upon growth of plants under conditions of inorganic phosphate starvation. The lncRNAs have been detected by processing raw sequencing data based upon an integrative computational model. Validation by RT-PCR indicates that the lncRNAs are bona fide transcripts rather than transcriptional noise.

[027] Accordingly, in a first embodiment the invention provides long non-coding RNA(lncRNA) molecules which are differentially expressed in a plant grown under phosphate starvation conditions when compared to a plant grown under normal conditions with adequate phosphate supply and which are unpolyadenylated.

[028] As used herein, "unpolyadenylated" or "non-polyadenylated" or "non-polyA" lncRNA molecules refers to lncRNA molecules which usually lack a polyA-tail. A lncRNA molecule may be classified as unpolyadenylated when, upon RNA sequencing according to methods described herein, particularly in Example 1, the maximum expression value (Reads per Kilobase per Million mapped reads or RPKM value) of each lncRNA determined separately in the polyA reads data and non-polyA reads data is four time greater in non-poly A data than in the polyA data.

[029] A lncRNA molecule is considered as "differentially expressed" upon Pi starvation compared to normally grown plants when read counts assigned to lncRNAs, e.g. using DEGseq package [30], normalized against the total mapped reads and analyzed using e.g. the MA-plot based method with random sampling with p-value of 0.05 have a fold-

change of 2 or more using RNA of the Pi-starved plants compared to normally grown plants.

[030] Table 4 lists long non-coding unpolyadenylated RNAs identified in *Arabidopsis thaliana* and indicates whether these molecules are differentially expressed under Pi starvation conditions.

[031] Thus, in another embodiment, the invention provides long non-coding RNA molecules comprising a nucleotide sequence which has at least 80% percent identity with any one of SEQ ID No. 4; SEQ ID No. 5; SEQ ID No. 6; SEQ ID No. 15; SEQ ID No. 18; SEQ ID No. 26; SEQ ID No. 28; SEQ ID No. 32; SEQ ID No. 34; SEQ ID No. 36; SEQ ID No. 40; SEQ ID No. 42; SEQ ID No. 47; SEQ ID No. 52; SEQ ID No. 55; SEQ ID No. 57; SEQ ID No. 59; SEQ ID No. 60; SEQ ID No. 62; SEQ ID No. 64; SEQ ID No. 70; SEQ ID No. 72; SEQ ID No. 77; SEQ ID No. 79; SEQ ID No. 82; SEQ ID No. 83; SEQ ID No. 84; SEQ ID No. 86; SEQ ID No. 90; SEQ ID No. 91; SEQ ID No. 98; SEQ ID No. 99; SEQ ID No. 102; SEQ ID No. 107; SEQ ID No. 114; SEQ ID No. 115; SEQ ID No. 118; SEQ ID No. 119; SEQ ID No. 120; SEQ ID No. 121; SEQ ID No. 128; SEQ ID No. 132; SEQ ID No. 137; SEQ ID No. 139; SEQ ID No. 140; SEQ ID No. 145; SEQ ID No. 149; SEQ ID No. 151; SEQ ID No. 152; SEQ ID No. 158; SEQ ID No. 160; SEQ ID No. 162; SEQ ID No. 172; SEQ ID No. 174; SEQ ID No. 176; SEQ ID No. 178; SEQ ID No. 179; SEQ ID No. 180; SEQ ID No. 181; SEQ ID No. 183; SEQ ID No. 187; SEQ ID No. 194; SEQ ID No. 195; SEQ ID No. 200; SEQ ID No. 201; SEQ ID No. 204; SEQ ID No. 209 or SEQ ID No. 210.

[032] The sequence identity may be larger than at least 80%, such as at least 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or be identical with any one of SEQ ID No. 4; SEQ ID No. 5; SEQ ID No. 6; SEQ ID No. 15; SEQ ID No. 18; SEQ ID No. 26; SEQ ID No. 28; SEQ ID No. 32; SEQ ID No. 34; SEQ ID No. 36; SEQ ID No. 40; SEQ ID No. 42; SEQ ID No. 47; SEQ ID No. 52; SEQ ID No. 55; SEQ ID No. 57; SEQ ID No. 59; SEQ ID No. 60; SEQ ID No. 62; SEQ ID No. 64; SEQ ID No. 70; SEQ ID No. 72; SEQ ID No. 77; SEQ ID No. 79; SEQ ID No. 82; SEQ ID No. 83; SEQ ID No. 84; SEQ ID No. 86; SEQ ID No. 90; SEQ ID No.

91; SEQ ID No. 98; SEQ ID No. 99; SEQ ID No. 102; SEQ ID No. 107; SEQ ID No. 114; SEQ ID No. 115; SEQ ID No. 118; SEQ ID No. 119; SEQ ID No. 120; SEQ ID No. 121; SEQ ID No. 128; SEQ ID No. 132; SEQ ID No. 137; SEQ ID No. 139; SEQ ID No. 140; SEQ ID No. 145; SEQ ID No. 149; SEQ ID No. 151; SEQ ID No. 152; SEQ ID No. 158; SEQ ID No. 160; SEQ ID No. 162; SEQ ID No. 172; SEQ ID No. 174; SEQ ID No. 176; SEQ ID No. 178; SEQ ID No. 179; SEQ ID No. 180; SEQ ID No. 181; SEQ ID No. 183; SEQ ID No. 187; SEQ ID No. 194; SEQ ID No. 195; SEQ ID No. 200; SEQ ID No. 201; SEQ ID No. 204; SEQ ID No. 209 or SEQ ID No. 210.

[033] The invention further provides DNA molecules which when transcribed yield an RNA molecule comprising said lncRNAs as herein described. Also provided by the invention are the complement of such DNA molecules. DNA molecules may be single-stranded or double stranded. Such DNA molecules may be referred herein as encoding the lncRNA molecules.

[034] Of particular interest are long non-coding RNA molecules (or the encoding DNA molecules) whose expression is upregulated during growth under inorganic phosphate starvation conditions such as lnc-34, lnc-107, lnc-139, lnc-194 or lnc-195. Thus in another embodiment, the invention provides lncRNA molecules comprising a nucleotide sequence which has at least 80% percent identity with any one of SEQ ID No. 34, SEQ ID No. 107, SEQ ID No. 139, SEQ ID No. 194 or SEQ ID No. 195, or having at least 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% sequence identity or be identical with any one of SEQ ID No. 34, SEQ ID No. 107, SEQ ID No. 139, SEQ ID No. 194 or SEQ ID No. 195.

[035] Other long non-coding RNA molecules of particular interest are those long-noncoding, unpolyadenylated RNA molecules, differentially expressed under Pi starvation conditions and which comprise a secondary structure, particularly which comprise at least two conserved hairpin loops, preferably further comprising two co-variance base pairings, such as lnc-149(SEQ ID No. 149).

[036] These non-polyA lncRNA molecules, or DNA molecules encoding such non-polyA lncRNA molecules, may be used to modulate inorganic phosphate use efficiency in a plant.

[037] It has also been determined that in addition to the unpolyadenylated lncRNA molecules, there are also polyadenylated lncRNA molecules which are differentially expressed under phosphate starvation conditions and these polyadenylated lncRNA may be used to similar effect to modulate inorganic phosphate use efficiency in a plant as the unpolyadenylated ones.

[038] A lncRNA molecule may be classified as polyadenylated (polyA) when, upon RNA sequencing according to methods described herein, particularly in Example 1, the maximum expression value (Reads per Kilobase per Million mapped reads or RPKM value) of each lncRNA determined separately in the polyA reads data and non-polyA reads data is four time greater in poly A data than in the non-polyA data, or is only identified in the polyA data.

[039] Table 4 also lists long non-coding polyadenylated RNAs identified in *Arabidopsis thaliana* and indicates whether these molecules are differentially expressed under Pi starvation conditions.

[040] Thus, the invention also relates to the use of a lncRNA molecule, whether polyadenylated or unpolyadenylated or "bimorphic", which is differentially expressed in a plant grown under phosphate starvation conditions when compared to a plant grown under normal conditions with adequate phosphate supply, or a DNA molecule which when transcribed yields such lncRNA molecule, or the complement of said DNA molecule, to modulate inorganic phosphate use efficiency in a plant.

[041] In particular the invention relates to the use of lncRNA molecule (or encoding DNA molecules) wherein a polyadenylated lncRNA molecule is used comprising a nucleotide sequence having at least 80% sequence identity, or at least 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% sequence identity or being identical with any one of SEQ ID No. 216; SEQ ID No.

235; SEQ ID No. 240; SEQ ID No. 250; SEQ ID No. 266; SEQ ID No. 267; SEQ ID No. 278; SEQ ID No. 281; SEQ ID No. 283; SEQ ID No. 315; SEQ ID No. 320; SEQ ID No. 321; SEQ ID No. 325; SEQ ID No. 330; SEQ ID No. 361; SEQ ID No. 364; SEQ ID No. 368; SEQ ID No. 370; SEQ ID No. 378; SEQ ID No. 384; SEQ ID No. 388; SEQ ID No. 393; SEQ ID No. 396; SEQ ID No. 414; SEQ ID No. 420; SEQ ID No. 424; SEQ ID No. 429; SEQ ID No. 432; SEQ ID No. 433; SEQ ID No. 436; SEQ ID No. 437; SEQ ID No. 448; SEQ ID No. 459; SEQ ID No. 460; SEQ ID No. 461; SEQ ID No. 462; SEQ ID No. 463; SEQ ID No. 486; SEQ ID No. 504; SEQ ID No. 512; SEQ ID No. 533; SEQ ID No. 570; SEQ ID No. 571; SEQ ID No. 572; SEQ ID No. 600; SEQ ID No. 601; SEQ ID No. 617; SEQ ID No. 618; SEQ ID No. 649; SEQ ID No. 651; SEQ ID No. 652; SEQ ID No. 656; SEQ ID No. 660; SEQ ID No. 662; SEQ ID No. 707; SEQ ID No. 709; SEQ ID No. 712; SEQ ID No. 713; SEQ ID No. 715; SEQ ID No. 716; SEQ ID No. 725; SEQ ID No. 734; SEQ ID No. 783; SEQ ID No. 785; SEQ ID No. 786; SEQ ID No. 787; SEQ ID No. 788; SEQ ID No. 798; SEQ ID No. 817; SEQ ID No. 850; SEQ ID No. 857; SEQ ID No. 918; SEQ ID No. 921; SEQ ID No. 945; SEQ ID No. 946; SEQ ID No. 955; SEQ ID No. 957; SEQ ID No. 972; SEQ ID No. 985; SEQ ID No. 986; SEQ ID No. 990; SEQ ID No. 997; SEQ ID No. 998; SEQ ID No. 1020; SEQ ID No. 1025; SEQ ID No. 1031; SEQ ID No. 1033; SEQ ID No. 1047; SEQ ID No. 1048; SEQ ID No. 1068 or SEQ ID No. 1080.

[042] Also of particular interest is the use of lncRNA molecules for phosphate use modulation in a plant, comprising a nucleotide sequence of any one of Tables 5 to 10, listing similar sequences found in other plant species, including rice, soybean, wheat, millet, sorghum or corn/maize.

[043] The invention thus provides a method of modulating the phosphate use efficiency in a plant comprising the step of increasing or decreasing the transcription and/or concentration of an lncRNA molecule as herein described, in a plant cell.

[044] Decrease of transcription and/or concentration of a lncRNA molecule as herein described can be achieved by mutation of the DNA region from which the lncRNA molecule is transcribed. Mutagenesis methods to achieve such mutations, including substitutions, small or large insertions or deletions, in plants are well known in the art.

[045] "Mutagenesis", as used herein, refers to the process in which plant cells (e.g., seed or tissues, such as pollen, etc.) are contacted one or more times to a mutagenic agent, such as a chemical substance (such as ethylmethylsulfonate (EMS), ethylnitrosourea (ENU), etc.) or ionizing radiation (neutrons (such as in fast neutron mutagenesis, etc.), gamma rays (such as that supplied by a Cobalt 60 source), X-rays, etc.), or a combination of the foregoing. While mutations created by irradiation are often large deletions or other gross lesions such as translocations or complex rearrangements, mutations created by chemical mutagens are often more discrete lesions such as point mutations. For example, EMS alkylates guanine bases, which results in base mispairing: an alkylated guanine will pair with a thymine base, resulting primarily in G/C to A/T transitions. Following mutagenesis, plants can be regenerated from the treated cells using known techniques. For instance, the resulting seeds may be planted in accordance with conventional growing procedures and following self-pollination seed is formed on the plants. Alternatively, doubled haploid plantlets may be extracted to immediately form homozygous plants. Additional seed which is formed as a result of such self-pollination in the present or a subsequent generation may be harvested and screened for the presence of mutant lncRNA encoding regions. Several techniques are known to screen for specific mutant sequences, e.g., DeleteageneTM (Delete-a-gene; Li et al., 2001, Plant J 27: 235-242) uses polymerase chain reaction (PCR) assays to screen for deletion mutants generated by fast neutron mutagenesis, TILLING (targeted induced local lesions in genomes; McCallum et al., 2000, Nat Biotechnol 18:455-457) identifies EMS-induced point mutations, etc.

[046] Decrease of transcription and/or concentration of lncRNA molecules as herein described can also be achieved using inhibitory RNA molecules specifically recognizing lncRNA molecules, introduced or expressed in the plant cells.

[047] In one embodiment, the lncRNA expression may be downregulated by introducing a chimeric DNA construct which yields a sense RNA molecule capable of down-regulating lncRNA expression by co-suppression. The transcribed DNA region will yield upon transcription a so-called sense RNA molecule capable of reducing the concentration of the lncRNA molecule in the target plant or plant cell in a transcriptional

or post-transcriptional manner. The transcribed DNA region (and resulting RNA molecule) comprises at least 20 consecutive nucleotides having at least 95% sequence identity to the nucleotide sequence of the lncRNA-encoding DNA region present in the plant cell or plant.

[048] In another embodiment, the lncRNA expression may be downregulated by introducing a chimeric DNA construct which yields an anti-sense RNA molecule capable of down-regulating lncRNA expression by co-suppression. The transcribed DNA region will yield upon transcription a so-called antisense RNA molecule capable of reducing the concentration of the lncRNA molecule in the target plant or plant cell in a transcriptional or post-transcriptional manner. The transcribed DNA region (and resulting RNA molecule) comprises at least 20 consecutive nucleotides having at least 95% sequence identity to the complement of the nucleotide sequence of the lncRNA molecule in the plant cell or plant.

[049] However, the minimum nucleotide sequence of the antisense or sense RNA region of about 20 nt of the lncRNA molecule may be comprised within a larger RNA molecule, varying in size from 20 nt to a length equal to the size of the target lncRNA molecule. The mentioned antisense or sense nucleotide regions may thus be about from about 21 nt to about 5000 nt long, such as 21 nt, 40 nt, 50 nt, 100 nt, 200 nt, 300 nt, 500 nt or 1000 nt in length. Moreover, it is not required for the purpose of the invention that the nucleotide sequence of the used inhibitory RNA molecule or the encoding region of the transgene, is completely identical or complementary to the lncRNA molecule, the expression of which is targeted to be reduced in the plant cell. The longer the sequence, the less stringent the requirement for the overall sequence identity is. Thus, the sense or antisense regions may have an overall sequence identity of about 40 % or 50 % or 60 % or 70 % or 80 % or 90 % or 100 % to the nucleotide sequence of the endogenous parp1 gene or the complement thereof. However, as mentioned, antisense or sense regions should comprise a nucleotide sequence of 20 consecutive nucleotides having about 95 to about 100 % sequence identity to the nucleotide sequence of the lncRNA molecule. The stretch of about 95 to about 100% sequence identity may be about 50, 75 or 100 nt.

[050] In yet another embodiment, lncRNA molecule transcription or concentration may be down-regulated by introducing a chimeric DNA construct which yields a double-stranded RNA molecule capable of down-regulating lncRNA expression. Upon transcription of the DNA region the RNA is able to form dsRNA molecule through conventional base paring between a sense and antisense region, whereby the sense and antisense region are nucleotide sequences as hereinbefore described. dsRNA-encoding parp1 expression-reducing chimeric genes according to the invention may further comprise an intron, such as a heterologous intron, located e.g. in the spacer sequence between the sense and antisense RNA regions in accordance with the disclosure of WO 99/53050 (incorporated herein by reference). To achieve the construction of such a transgene, use can be made of the vectors described in WO 02/059294 A1.

[051] In still another embodiment, lncRNA molecule transcription or concentration can be down-regulated by introducing a chimeric DNA construct which yields a pre-miRNA RNA molecule which is processed into a miRNA capable of guiding the cleavage of the lncRNA molecule. miRNAs are small endogenous RNAs that regulate gene expression in plants, but also in other eukaryotes. In plants, these about 21 nucleotide long RNAs are processed from the stem-loop regions of long endogenous pre-miRNAs by the cleavage activity of DICERLIKE1 (DCL1). Plant miRNAs are highly complementary to conserved target mRNAs, and guide the cleavage of their targets. miRNAs appear to be key components in regulating the gene expression of complex networks of pathways involved inter alia in development.

[052] As used herein, a “miRNA” is an RNA molecule of about 20 to 22 nucleotides in length which can be loaded into a RISC complex and direct the cleavage of a target RNA molecule, wherein the target RNA molecule comprises a nucleotide sequence essentially complementary to the nucleotide sequence of the miRNA molecule whereby one or more of the following mismatches may occur:

- A mismatch between the nucleotide at the 5’ end of said miRNA and the corresponding nucleotide sequence in the target RNA molecule;

- A mismatch between any one of the nucleotides in position 1 to position 9 of said miRNA and the corresponding nucleotide sequence in the target RNA molecule;

- Three mismatches between any one of the nucleotides in position 12 to position 21 of said miRNA and the corresponding nucleotide sequence in the target RNA molecule provided that there are no more than two consecutive mismatches.

No mismatch is allowed at positions 10 and 11 of the miRNA (all miRNA positions are indicated starting from the 5' end of the miRNA molecule).

[053] As used herein, a "pre-miRNA" molecule is an RNA molecule of about 100 to about 200 nucleotides, preferably about 100 to about 130 nucleotides which can adopt a secondary structure comprising a dsRNA stem and a single stranded RNA loop and further comprising the nucleotide sequence of the miRNA and its complement sequence of the miRNA* in the double-stranded RNA stem. Preferably, the miRNA and its complement are located about 10 to about 20 nucleotides from the free ends of the miRNA dsRNA stem. The length and sequence of the single stranded loop region are not critical and may vary considerably, e.g. between 30 and 50 nt in length. Preferably, the difference in free energy between unpaired and paired RNA structure is between -20 and -60 kcal/mole, particularly around -40 kcal/mole. The complementarity between the miRNA and the miRNA* do not need to be perfect and about 1 to 3 bulges of unpaired nucleotides can be tolerated. The secondary structure adopted by an RNA molecule can be predicted by computer algorithms conventional in the art such as mFold, UNAFold and RNAFold. The particular strand of the dsRNA stem from the pre-miRNA which is released by DCL activity and loaded onto the RISC complex is determined by the degree of complementarity at the 5' end, whereby the strand which at its 5' end is the least involved in hydrogen bounding between the nucleotides of the different strands of the cleaved dsRNA stem is loaded onto the RISC complex and will determine the sequence specificity of the target RNA molecule degradation. However, if empirically the miRNA molecule from a particular synthetic pre-miRNA molecule is not functional because the "wrong" strand is loaded on the RISC complex, it will be immediately evident that this problem can be solved by exchanging the position of the miRNA molecule and its complement on the respective strands of the dsRNA stem of the pre-miRNA molecule.

As is known in the art, binding between A and U involving two hydrogen bounds, or G and U involving two hydrogen bounds is less strong that between G and C involving three hydrogen bounds.

[054] miRNA molecules may be comprised within their naturally occurring pre-miRNA molecules but they can also be introduced into existing pre-miRNA molecule scaffolds by exchanging the nucleotide sequence of the miRNA molecule normally processed from such existing pre-miRNA molecule for the nucleotide sequence of another miRNA of interest. The scaffold of the pre-miRNA can also be completely synthetic. Likewise, synthetic miRNA molecules may be comprised within, and processed from, existing pre-miRNA molecule scaffolds or synthetic pre-miRNA scaffolds.

[055] Increase of transcription and/or concentration of a lncRNA molecule as herein described can be achieved by providing the plant cells with a recombinant gene, wherein the recombinant gene comprises a plant expressible promoter operably linked to a DNA region which when transcribed yields an RNA molecule comprising or consisting of that lncRNA molecule and optionally, an appropriate transcription termination region and/or polyadenylation region.

[056] For the purpose of the invention, the term "plant-operative promoter" or “plant-expressible promoter” means a promoter which is capable of driving transcription in a plant, plant tissue, plant organ, plant part, or plant cell. This includes any promoter of plant origin, but also any promoter of non-plant origin which is capable of directing transcription in a plant cell.

[057] Promoters that may be used in this respect are constitutive promoters, such as the promoter of the cauliflower mosaic virus (CaMV) 35S transcript (Hapster et al.,1988, Mol. Gen. Genet. 212: 182-190), the CaMV 19S promoter (U.S. Pat. No. 5,352,605; WO 84/02913; Benfey et al., 1989, EMBO J. 8:2195-2202), the subterranean clover virus promoter No 4 or No 7 (WO 96/06932), the Rubisco small subunit promoter (U.S. Pat. No. 4,962,028), the ubiquitin promoter (Holtorf et al., 1995, Plant Mol. Biol. 29:637-649), T-DNA gene promoters such as the octopine synthase (OCS) and nopaline synthase

(NOS) promoters from Agrobacterium, and further promoters of genes whose constitutive expression in plants is known to the person skilled in the art.

[058] Further promoters that may be used in this respect are tissue-specific or organ-specific promoters, preferably seed-specific promoters, such as the 2S albumin promoter (Joseffson et al., 1987, J. Biol. Chem. 262:12196-12201), the phaseolin promoter (U.S. Pat. No. 5,504,200; Bustos et al., 1989, Plant Cell 1.(9):839-53), the legumine promoter (Shirsat et al., 1989, Mol. Gen. Genet. 215(2):326-331), the "unknown seed protein" (USP) promoter (Baumlein et al., 1991, Mol. Gen. Genet. 225(3):459-67), the napin promoter (U.S. Pat. No. 5,608,152; Stalberg et al., 1996, Planta 199:515-519), the Arabidopsis oleosin promoter (WO 98/45461), the Brassica Bce4 promoter (WO 91/13980), and further promoters of genes whose seed-specific expression in plants is known to the person skilled in the art.

[059] Other promoters that can be used are tissue-specific or organ-specific promoters like organ primordia-specific promoters (An et al., 1996, Plant Cell 8: 15-30), stem-specific promoters (Keller et al., 1988, EMBO J. 7(12): 3625-3633), leaf-specific promoters (Hudspeth et al., 1989, Plant Mol. Biol. 12: 579-589), mesophyl-specific promoters (such as the light-inducible Rubisco promoters), root-specific promoters (Keller et al., 1989, Genes Dev. 3: 1639-1646), tuber-specific promoters (Keil et al., 1989, EMBO J. 8(5): 1323-1330), vascular tissue-specific promoters (Peleman et al., 1989, Gene 84: 359-369), stamen-selective promoters (WO 89/10396, WO 92/13956), dehiscence zone-specific promoters (WO 97/13865), and the like.

[060] In addition to promoters recognized by RNA polymerase I, also promoter recognized by RNA Polymerase I or RNA polymerase III promoters may be used including Type 3 Pol III promoters which can be found e.g. associated with the genes encoding 7SL RNA, U3 snRNA and U6 snRNA. Other nucleotide sequences for type 3 Pol III promoters can be found in nucleotide sequence databases under the entries for the *A. thaliana* gene AT7SL-1 for 7SL RNA (X72228), *A. thaliana* gene AT7SL-2 for 7SL RNA (X72229), *A. thaliana* gene AT7SL-3 for 7SL RNA (AJ290403), *Humulus lupulus* H17SL-1 gene (AJ236706), *Humulus lupulus* H17SL-2 gene (AJ236704), *Humulus*

lupulus H17SL-3 gene (AJ236705), *Humulus lupulus* H17SL-4 gene (AJ236703), *A. thaliana* U6-1 snRNA gene (X52527), *A. thaliana* U6-26 snRNA gene (X52528), *A. thaliana* U6-29 snRNA gene (X52529), *A. thaliana* U6-1 snRNA gene (X52527), *Zea mays* U3 snRNA gene (Z29641), *Solanum tuberosum* U6 snRNA gene (Z17301; X 60506; S83742), Tomato U6 smal nuclear RNA gene (X51447), *A. thaliana* U3C snRNA gene (X52630), A. thaliana U3B snRNA gene (X52629), *Oryza sativa* U3 snRNA promoter (X79685), Tomato U3 smal nuclear RNA gene (X14411), *Triticum aestivum* U3 snRNA gene (X63065), *Triticum aestivum* U6 snRNA gene (X63066).

[061] The recombinant DNA molecules as herein described optionally comprise a DNA region involved in transcription termination and/or polyadenylation. A variety of DNA region involved in transcription termination and/or polyadenylation functional in plants are known in the art and those skilled in the art will be aware of terminator and polyadenylation sequences that may be suitable in performing the methods herein described. The polyadenylation region may be derived from a natural gene, from a variety of other plant genes, from T-DNA genes or even from plant viral genomes. The 3' end sequence to be added may be derived from, for example, the nopaline synthase or octopine synthase genes, or alternatively from another plant gene, or from any other eukaryotic gene. Terminator regions for Pol III promoters include a so-called « oligo dT stretch » which is a stretch of consecutive T-residues that serve as a terminator for the RNA polymerase III activity. It should comprise at least 4 T-residues, but obviously may contain more T-residues.

[062] As used herein the term “providing a recombinant DNA molecule” may refer to introduction of an exogenous DNA molecule to a plant cell by transformation, optionally followed by regeneration of a plant from the transformed plant cell. The term may also refer to introduction of the recombinant DNA molecule by crossing of a transgenic plant comprising the recombinant DNA molecule with another plant and selecting progeny plants which have inherited the recombinant DNA molecule or transgene. Yet another alternative meaning of providing refers to introduction of the recombinant DNA molecule

by techniques such as protoplast fusion, optionally followed by regeneration of a plant from the fused protoplasts.

[063] It will be clear that the methods of transformation used are of minor relevance to the current invention. Transformation of plants is now a routine technique. Advantageously, any of several transformation methods may be used to introduce the nucleic acid/gene of interest into a suitable ancestor cell. Transformation methods include the use of liposomes, electroporation, chemicals that increase free DNA uptake, injection of the DNA directly into the plant, particle gun bombardment, transformation using viruses or pollen and microprojection. Methods may be selected from the calcium/polyethylene glycol method for protoplasts (Krens *et al.* (1982) Nature 296: 72-74 ; Negrutiu *et al.* (1987) Plant. Mol. Biol. 8: 363-373); electroporation of protoplasts (Shillito *et al.* (1985) Bio/Technol. 3: 1099-1102); microinjection into plant material (Crossway *et al.* (1986) Mol. Gen. Genet. 202: 179-185); DNA or RNA-coated particle bombardment (Klein *et al.* (1987) Nature 327: 70) infection with (non-integrative) viruses and the like. Transgenic rice plants can be produced via *Agrobacterium*-mediated transformation using any of the well-known methods for rice transformation, such as described in any of the following: European patent application EP 1198985 A1 ; Aldemita and Hodges (1996) Planta 199: 612-617 ; Chan *et al.* (1993) Plant. Mol. Biol. 22 (3): 491-506 ; Hiei *et al.* (1994) Plant J. 6 (2): 271-282), which disclosures are incorporated by reference herein as if fully set forth. In the case of corn transformation, a suitable method is as described in either Ishida *et al.* (1996) Nat. Biotechnol. 14(6): 745-50) or Frame *et al.* (2002) Plant Physiol. 129(1): 13-22), which disclosures are incorporated by reference herein as if fully set forth. In the case of canola, a suitable transformation method is that disclosed in De Block *et al.* (Plant Physiol. (1989) 91: 694-701), which disclosure is incorporated by reference herein as if fully set forth. Methods to transform cotton plants are also well known in the art. *Agrobacterium*-mediated transformation of cotton has been described e.g. in US patent 5,004,863 or in US patent 6,483,013 and cotton transformation by particle bombardment is reported e.g. in WO 92/15675. Other suitable cotton transformation methods are disclosed e.g. in

WO00071733 and US 5,159,135, which disclosures are incorporated by reference herein as if fully set forth.

[064] The recombinant DNA molecules according to the invention may be introduced into plants in a stable manner or in a transient manner using methods well known in the art. The chimeric genes may be introduced into plants, or may be generated inside the plant cell as described e.g. in EP 1339859.

[065] Other embodiments of the invention relate to the recombinant DNA molecules as herein described, as well as to plants, plant cells, plant tissues or seeds comprising the recombinant DNA molecules as herein described.

[066] It is also an object of the invention to provide plant cells and plants comprising a modulated, increased or decreased, concentration of an lncRNA molecule as herein described, when compared to an unmodified plant cell. Gametes, seeds, embryos, either zygotic or somatic, progeny or hybrids of plants which comprising such modulated lncRNA molecule concentration, which are produced by traditional breeding methods are also included within the scope of the present invention.

[067] The methods and means described herein are believed to be suitable for all plant cells and plants, both dicotyledonous and monocotyledonous plant cells and plants including but not limited to cotton, Brassica vegetables, oilseed rape, wheat, corn or maize, barley, sunflowers, sorghum, rice, oats, sugarcane, soybean, vegetables (including chicory, lettuce, tomato), tobacco, potato, sugarbeet, papaya, pineapple, mango, Arabidopsis thaliana, but also plants used in horticulture, floriculture or forestry.

[068] The invention also provides a method for isolating further lncRNA molecules involved in phosphate use efficiency, in a plant or plant cell, comprising the step of identifying a nucleotide sequence having a degree of homology to the lncRNA molecules herein described and isolating or synthesizing such RNA molecule comprising or consisting of such nucleotide sequence. The identification can occur via hybridization

under stringent conditions in plants using probes having the nucleotide sequence of the lncRNA molecules. Alternatively, sequence databases (of genomes or transcriptomes) can be searched using software such as BLASTN for sequences that share a defined degree of sequence identity with the sequences of the lncRNA molecules herein described.

[069] As used herein "sequence identity" of two related nucleotide or amino acid sequences, expressed as a percentage, refers to the number of positions in the two optimally aligned sequences which have identical residues (x100) divided by the number of positions compared. A gap, i.e., a position in an alignment where a residue is present in one sequence but not in the other is regarded as a position with non-identical residues. The alignment of the two sequences is performed by the Needleman and Wunsch algorithm (Needleman and Wunsch (1970) J. Mol Biol. 48: 443-453). The computer-assisted sequence alignment above, can be conveniently performed using standard software program such as GAP which is part of the Wisconsin Package Version 10.1 (Genetics Computer Group, Madision, Wisconsin, USA) using the default scoring matrix with a gap creation penalty of 50 and a gap extension penalty of 3. It is clear that when RNA sequences are to be essentially similar or have a certain degree of sequence identity with DNA sequences, thymine (T) in the DNA sequence is considered equal to uracil (U) in the RNA sequence.

[070] As used herein, the term “comprising” is to be interpreted as specifying the presence of the stated features, integers, steps or components as referred to, but does not preclude the presence or addition of one or more features, integers, steps or components, or groups thereof. Thus, e.g., a nucleic acid comprising a sequence of nucleotides, may comprise more nucleotides than the actually cited ones, i.e., be embedded in a larger nucleic acid. A chimeric gene as will be described further below which comprises a nucleic acid which is functionally or structurally defined may comprise additional nucleic acids etc. However, in context with the present disclosure, the term “comprising” also includes “consisting of”. In other words, the terminology relating to a nucleic acid “comprising” a certain nucleotide sequence, as used throughout the text, refers to a

nucleic acid or protein including or containing at least the described sequence, so that other nucleotide or amino acid sequences can be included at the 5' (or N-terminal) and/or 3' (or C-terminal) end, e.g. (the nucleotide sequence of) a selectable marker protein, (the nucleotide sequence of) a transit peptide, and/or a 5' leader sequence or a 3' trailer sequence.

[071] The following non-limiting Examples describe the identification of lncRNA molecules differentially expressed under inorganic phosphate starvation conditions as well as the use thereof for modulating phosphate use efficiency in plants.

[072] Unless stated otherwise in the Examples, all recombinant DNA techniques can be carried out according to standard protocols as described in Sambrook et al. (1989) Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor Laboratory Press, NY and in Volumes 1 and 2 of Ausubel et al. (1994) Current Protocols in Molecular Biology, Current Protocols, USA. Standard materials and methods for plant molecular work are described in Plant Molecular Biology Labfax (1993) by R.D.D. Croy, jointly published by BIOS Scientific Publications Ltd (UK) and Blackwell Scientific Publications, UK. Other references for standard molecular biology techniques include Sambrook and Russell (2001) Molecular Cloning: A Laboratory Manual, Third Edition, Cold Spring Harbor Laboratory Press, NY, Volumes I and II of Brown (1998) Molecular Biology LabFax, Second Edition, Academic Press (UK). Standard materials and methods for polymerase chain reactions can be found in Dieffenbach and Dveksler (1995) PCR Primer: A Laboratory Manual, Cold Spring Harbor Laboratory Press, and in McPherson at al. (2000) PCR - Basics: From Background to Bench, First Edition, Springer Verlag, Germany.

[073] Throughout the description and Examples, reference is made to the following sequences:

SEQ ID Nos. 1-211: nucleotide sequence of respectively NonpolyA_lnc 1 to NonpolyA_lnc 211 from *Arabidopsis thaliana.*

SEQ ID Nos. 212-1081 : nucleotide sequence of respectively PolyA_lnc 1 to PolyA_lnc 870 from *Arabidopsis thaliana.*

SEQ ID Nos. 1082-1096 : nucleotide sequence of orhologous lncRNA molecules from *Glycine max.*

SEQ ID Nos. 1097-1110 : nucleotide sequence of orhologous lncRNA molecules from *Oryza sativa.*

SEQ ID Nos. 1111-1121 : nucleotide sequence of orhologous lncRNA molecules from *Sorghum bicolor.*

SEQ ID Nos. 1122-1130 : nucleotide sequence of orhologous lncRNA molecules from *Setaria italica.*

SEQ ID Nos. 1131-1239 : nucleotide sequence of orhologous lncRNA molecules from *Triticum aestivum.*

SEQ ID Nos. 1240-1297 : nucleotide sequence of orhologous lncRNA molecules from *Zea mays.*

SEQ ID Nos. 1298-1327 : nucleotide sequence of RT-PCR primers listed in Table 3.

SEQ ID No. 1328 : nucleotide sequence of lnc-149 from *Arabidopsis thaliana.*

SEQ ID No. 1329 : nucleotide sequence of lnc-149 like from *Arabidopsis lyrata.*

SEQ ID No. 1330 : nucleotide sequence of lnc-149 from *Thellungiella halophile.*

[074] The sequence listing contained in the file named „BCS14-2001_ST25.txt“, which is 740 kilobytes (size as measured in Microsoft Windows®), contains 1330 sequences SEQ ID NO: 1 through SEQ ID NO: 1330, is filed herewith by electronic submission and is incorporated by reference herein.

Example 1: Materials and methods

[075] **Plant Materials and phosphate-starvation treatment.** Wild-type *Arabidopsis thaliana* seedlings were used in this study. Col-0 seeds were sterilized in household disinfectant and then washed in sterilized water five times. Then they were grown on full-strength MS medium supplemented with 1% sucrose and 1.2% agar under long day condition (24 °C, 16:8h light/dark, at light intensity of 100 μmol m-2 s-1). For Pi deficiency, 0.6 mM K2SO4 was used to substitute 1.2 mM KH_2PO_4 in P+ MS medium. Thirteen-day-old seedlings were collected and frozen in liquid nitrogen immediately and then store in -80 °C for following treatment.

[076] **Non-polyA RNA and total RNA (rRNA removed) purification.** Total RNA was extracted from thirteen-day-old seedlings using QIAGEN RNeasy Plant Mini Kit and then quantified by NanoDrop 1000 and 1% agarose gel electrophoresis. To enrich non-polyA RNA, we chose 10μg RNA to capture polyA RNA using Oligo dT_{30}-probe (Oligotex mRNA Mini Kit, QIAGEN) for four times. 5μl probes and 80μl binding buffer were used each time. After centrifuging, probes binding polyA RNAs were precipitated and the supernatant mainly consisted of non-polyA RNA and short-polyA RNA. Then ~8μg non-polyA RNA was collected and all used to remove rRNA (RiboMinus™ Plant Kit, Invitrogen) for two times. For total RNA collection, only rRNA-removing protocol was performed two times for 10ug RNA. Non-polyA RNAs and total RNAs were quantified using Agilent 2100 Bioanalyzer (allowing to see zonal distribution for total RNAs after rRNA removal) and then stored -80 °C.

[077] **Strand-specific cDNA library construction and high-throughput sequencing.** ~1μg RNA was used to construct a cDNA library. Sheared RNA was linked with different barcodes at its 3' and 5' end respectively and reverse transcript to cDNA to construct strand-specific cDNA library according to the SMART method [26]). For total RNA-seq and non-polyA RNA-seq (short reads), 320~420bp fragments were collected (containing 200~300bp cDNA fragments and 120bp barcodes) by gel recovery. After amplification, the cDNA library was sequenced by 36nt paired-end using Illumina HiSeq

2000. For non-polyA RNA-seq (long reads) in WT and Pi-starvation samples, 320~620 bp fragments containing 200~500 bp cDNA fragments and 120bp barcodes were purified,amplified and then sequenced by 100 nt single-end using Illumina HiSeq 2000. For each sample, ~20M raw reads were collected.

[078] **Reads trimming, assembling and filtering.** The reads' sequencing quality was tested using FastQC v0.10.1 (www.bioinformatics.babraham.ac.uk/projects/fastqc/) (Figure 6). 5' terminal 2 and 8 nucleotides with bad quality were trimmed using FASTX-toolkit for short reads and long reads, respectively. rRNA was filtered out from these trimmed reads to get clean reads using Bowtie (v0.12.7) with one mismatch [27. The reads were mapped to the *Arabidopsis thaliana* reference genome (TAIR10) using TopHat (v2.0.5) with two mismatches. Mapped reads were assembled by Cufflinks (v2.0.1) and re-assembled by Cuffcompare (v2.0.1) following the protocol from [28]. Transcripts labeled CUFF are considered novel transcripts (without annotation). These transcripts were collected and then re-filtered out to remove those overlapping with coding genes and known ncRNAs. CPC tools [29] were used to calculate coding potential and those reads with CPC<0 (low coding potential) were retained. After length selection of transcripts longer than 200 nt transcripts, these were designated as novel lncRNA. Novel lncRNAs were re-located to transposable elements (TE) (>1 nt overlap with TE, no strand-specificity), pseudogene (>1 nt overlap with pseudogene, no strand-specificity), antisense (>50% overlap with mRNA, on opposite strand), intronic (100% overlap with intron, on the same strand), ambiguous (>1 nt overlap with known ncRNAs or coding genes) and intergenic region (the remainder).

[079] **RT-PCR validation of novel lncRNAs**. 9 novel lncRNAs candidates from non-polyA RNA-seq (long reads) were selected. PolyA and non-polyA RNAs were prepared as described above, and cDNAs were synthesized using the Superscript™ III First-Strand Synthesis System (Invitrogen) using Random hexamers as primers. qRT-PCR was performed with SYBR Premix Ex Taq (ABI StepOnePlus™system, TaKaRa), PCR reaction was performed for cDNAs and negative control using specific primers (Table 3).

[080] **Classification into polyA and non-polyA lncRNAs**. A published polyA RNA-seq database [25] and the 100 nt reads non-polyA RNA-seq generated in this study were used to classify polyA and non-polyA lncRNAs. The maximum expression value (Reads Per Kilobase per Million mapped reads, RPKM) of each lncRNA in polyA data and non-polyA data was determined separately. If a transcript's polyA RPKM was four times greater than its maximum non-polyA RPKM, or if the transcript was only identified in the polyA data, we defined the transcript as a polyA transcript, and vice versa. If a transcript could not be assigned to either the polyA class or or non-polyA class, the transcript was defined as a "biomorphic" transcript. For lncRNAs assembled from polyA RNA-seq, only the ones defined as polyA lncRNAs were retained. Using the same strategy a set of non-polyA lncRNAs was also defined.

[081] **Differential expression analysis** To find the differentially expressed lncRNAs responsive to Pi starvation, we first assigned reads count to lncRNAs with RNA-seq data using the DEGseq package [30].The raw read counts were normalized against the total mapped reads in each sample, and then used the MA-plot based method with random sampling model.was used The p-value of 0.05 and fold change of 2 were set as the cutoff. When comparing the ratios of differential expressed lncRNAs, we performed $\chi 2$ test with p-value < 0.01.

[082] **DNA conservation analysis.** A phylogenetic tree based on the plant species' divergent time was constructed (www.timetree.org) using MEGA5.0. DNA conservation scores between *Arabidopsis thaliana* and 16 other organisms were calculated using BLASTn followed by the calculation of the average DNA conservation score.

[083] **Calculation of sequence and structure features.** For convenient computational analysis, we split the entire *Arabidopsis thaliana* genome into 4,765,850 small bins (each with 100bp), two neighboring bins have 50 nt overlap [31], and calculated sequence and structure features (DNA sequence conservation, protein sequence conservation, RNA secondary structure stability and RNA structure conservation) for each genomic bin (every 100bp of genome). When measuring features for genomic elements (e.g. lncRNA),

we overlapped the genomic elements with bins and use the maximum or minimum (only RNA structure stability) bin scores for the comparison.

[084] DNA conservation scores were calculated across 31 plant species (genomes downloaded from PlantGDB) using BLASTn with default parameters. The maximum Bitscore was used as the feature score. Protein conservation scores were calculated using BLASTx in a similar manner. The coding potential of each bin was calculated using RNAcode with default parameters [32]. RNA secondary structure stability of each bin was calculated using RandFold [33], with 1000 times of dinucleotide randomshuffling, and the p-value was used as the feature score. The RNA structure conservation scores were denoted by SCI (structure conservation index) scores, which were calculated using RNAz based on multiple alignments between *Arabidopsis thaliana*, *Arabidopsis lyrata*, *Carica papaya*, *Thellungiella halophile* and *Citrus clementina* (downloaded from VISTA database).

[085] Dozens of RNA-seq and tiling array data [34-40], and a set of unexpressed intergenic regions was defined as negative control. The genomic regions with expression level lower than the mean expression level of all genomic element across all RNA-seq and array samples [31] were defined as unexpressed intergenic regions.

[086] **Gene Ontology Enrichment Analysis** . 1kb regions downstream or upstream the coding genes were defined as the potential cis-regulatory regions. Four gene sets were defined: two sets with polyA or non-polyA lncRNAs located on the cis-regulatory region; two sets with polyA or non-polyA lncRNAs located on the opposite strand (the antisense lncRNAs). The GOtoolbox (genome.crg.es/GOToolBox/) was used to find enriched Gene Ontology terms in these four gene sets using 0.01 as the p-value cutoff.

[087] **Identification of conserved local structures**. After calculating SCI (structure conservation index) scores of each bin (as described above), the maximum SCI score of the overlapping bins was assigned to all non-polyA lncRNA candidates. Those with high SCI value (>= 0.7) and multiple alignments across five plants (including *Arabidopsis thaliana*, *Arabidopsis lyrata*, *Thellungiella halophila*, *Carica papaya* and *Citrus*

clementina) were considered as highly conserved in both DNA sequence and RNA secondary structure. Based on the multiple genome alignments, the conserved RNA secondary structures were calculated using RNAalifold [41] and then visualized using VARNA [42].

Example 2: Development of a non-polyA RNA sequencing method to identify lncRNAs in the Arabidopsis thaliana genome

[088] High-throughput RNA sequencing technology could lead deeper insights into the transcriptome. Here we applied three kinds of RNA-sequencing methods to identify novel lncRNAs in *Arabidopsis*: (i) Sequencing of total RNAs (rRNA depleted) for short reads with 36nt in length; (ii) Sequencing of non-polyA RNAs separated from total RNAs by a general RNA-seq protocol for short reads with 36 nt in length; (iii) Sequencing of non-polyA RNAs for long reads with 100 nt in length (see Example 1). These three methods were compared by the length of assembled transcripts and the best one was selected for genome-wide lncRNAs identification.

[089] The identification of novel lncRNAs comprised three steps: (i) purifying specific RNA components; (ii) constructing strand-specific cDNA library and sequencing; (iii) high-throughput sequencing data processing to identify novel lncRNAs (Figure 1).

[090] As a the first step, we improved the polyA RNA and rRNA removing protocol by utilizing fewer oligo dT30-probes and rRNA-probes with more replicates. As a result, we found that only 13.04% and 18.72% of the non-polyA and total RNA-seq reads were mapped to TAIR10 rDNA region, respectively (Table 1). Previous studies revealed that polyadenylation regulates RNA stability and degradation. Polyadenylation of 18S rRNA also regulates its degradation in mitochondria [43]. So we assumed that the polyA RNA selection could also remove some rRNAs.

[091] High-throughput sequencing generated ~20 million reads for these three methods (Table 1). First, we trimmed nucleotides with low quality scores in raw sequencing reads

(Figure 6, see Example 1). After removing rRNA-matched reads, assembling transcripts, filtering annotated transcripts, selecting non-coding candidates and discarding short ones (see Example 1), we finally identified 97 novel lncRNAs in total RNA-seq with short readslength, 559 in non-polyA RNA-seq with short read length and 177 in non-polyA RNA-seq with long read length.

[092] Comparing the length distribution of the assembled transcript fragments, we found that 62.27% of the fragments are longer than 200 nt for long read RNA-seq library, while the percentages are only 43.14% and 16.33% for two short read RNA-seq libraries, respectively (Figure 2A). After filtering out transcript fragments with known genomic annotations and high coding potential (CPC>0) (see Example 1), the long read RNA-seq library and the short read total RNA-seq library still had the longest and shortest average read length, respectively (Figure 2B). Although the long read RNA-seq method results in a lower number of transcripts before and after lncRNA screening, it yields longer lncRNA candidates.

[093] Using the same RNA-seq protocol but with different RNAs , we identified 97 and 559 novel lncRNA candidates from total RNA-seq library and non-polyA RNA-seq library, respectively. For these, 64 out of 97 and 35 out of 559 are shared (with >50% nucleotides overlapped in at least one dataset). We examined these candidates using IGB [44] and found that several candidates from total RNA-seq library were pieces of longer transcripts from non-polyA RNA-seq library (data not shown). Non-polyA RNA-seq assay could enrich more reads derived from intergenic regions and with higher expression level. This has been proved by the percentage of overlapping candidates in two short-read RNA-seq. 95.5% of lncRNAs were expressed at low levels (RPKM 0~5) in non-polyA RNA-seq library, while 3.4% of them were rediscovered in total RNA-seq library. 1.25% of lncRNAs had the highest expression levels (RPKM 103~105) in non-polyA RNA-seq library, and 60% of them could also be detected in total RNA-seq library (Figure 2C). Because most lncRNAs are characterized by their extreme low expression level [9, 21], more robust experimental methods were needed to detect these low-expressed lncRNAs and non-polyA RNA-seq assay could be an ideal choice.

[094] Furthermore, we investigated the sources of these newly identified lncRNAs in three RNA-seq libraries. Constructing strand-specific cDNA library makes identification of novel lncRNA more sensitive, especially for those derived from antisense region. Locating these lncRNA candidates to TAIR10 genome, we found that the majority are derived from the antisense strand of coding genes and the second largest set are transcribed from intergenic regions (Figure 2D). Finally, 9 random-selected novel non-polyA lncRNA candidates were validated by RT-PCR. Because of non-polyA RNA remaining during polyA RNA selection, we also detected these lncRNAs in polyA samples, but at much lower levels (Figure 2E).

Example 3: Identification of non-polyA and polyA lncRNAs associated with Pi starvation

[095] LncRNAs IPS1 and At4 act as target mimics to inhibit the activity of miRNA-399, and are involved in response to Pi starvation in Arabidopsis [6]. However, a systematic understanding of the roles of lncRNAs in Pi starvation response is still lacking. We utilized non-polyA RNA-seq (long read) method (described above, see Examples 1 and 2) to identify lncRNAs which are differentially expressed in Arabidopsis seedling under normal and Pi-deficient condition. In addition, we also used published polyA RNA-seq data generated from Pi-stressed Arabidopsis for comparison (Table 2) [25].

[096] A computational framework was developed to detect and characterize lncRNAs specifically associated with Pi starvation in both polyA and non-polyA RNA-seq libraries (Figure 3A). We re-assembled the transcriptome, selected transcript fragments with low coding potential (CPC<0) and detected 870 and 210 lncRNAs after cross filtering in polyA and non-polyA RNA-seq libraries, respectively (see Example 1). 91 out of 870 (10.5%) and 68 out of 210 (32.2%) lncRNAs were differentially expressed under Pi-deficient and normal conditions (Figure 3B and 3C- See also Table 4). Most of the lncRNAs detected in polyA and non-polyA RNA-seq libraries, whether differentially expressed or not, were derived from intergenic regions (Figure 3C). Antisense lncRNAs, were more enriched in non-polyA RNA-seq library (Figure 7).

[097] Next, novel lncRNAs (both in polyA and non-polyA RNA-seq libraries) detected by their sequence and structural features were characterized including by Gene Ontology (GO) enrichment to identify lncRNA subgroups that are associated with Pi-starvation (Figure 3A). We found that novel lncRNAs in both polyA and non-polyA RNA-seq libraries are more conserved than unexpressed intergenic regions, but less conserved than coding genes (Figure 4A and 4B). Additionally, we compared RNA structural stability, RNA structure conservation and protein conservation between novel lncRNAs and coding genes. We observed that most novel lncRNAs have extreme low protein conservation, which supports that the detected novel lncRNAs are potentially non-protein coding. Overall, novel lncRNAs have an slightly lower RNA structure free energy than coding genes, which reflects higher RNA structural stability.

[098] We also found that only some novel lncRNAs had higher RNA structural conservation than coding genes, which might due to extreme high DNA sequence conservation of coding genes, even though we had normalized the structure conservation to DNA conservation scores (Figure 4B). These three features of lncRNAs described above are well consistent with previous reports [45, 46].

[099] The chromosomal locations of differentially expressed lncRNA candidates are listed in Table 4. Table 4 also includes a cross reference to the corresponding SEQ ID No. entry in the sequence listing. Also included are GO terms associated coding regions co-localized with the lncRNA as described below.

[0100] Non-polyA lncRNAs are mainly located in antisense and intergenic regions (Figure 1D), with limited clues to infer their potential cellular functions. Previous studies suggested that lncRNAs located around protein coding genes (no matter upstream, internal or downstream of the sense or antisense strand) can regulate the expression of their 'host' coding genes in Arabidopsis [17, 47]. Therefore we analyzed potential lncRNA functions based on genomic co-location with protein coding genes. 1 Kb regions were identified downstream and upstream the protein coding genes as the potential cis-regulatory regions. lncRNAs, differentially expressed under Pi starvation conditions,

which are located in the cis-regulatory regions could potentially regulate their 'host' protein coding genes.

[0101] Gene Ontology Enrichment Analysis was performed on non-polyA and polyA lncRNAs which were differentially expressed in control and low Pi samples to determine their putative cellular functions. Several GO biological processes (BP) terms are more enriched for non-polyA lncRNAs, such as gibberellin signaling transduction and root epidermal morphology (Figure 4C). Notably, GO BP terms for polyA lncRNAs exhibit strong preference for plant hormone signaling transduction and responses (Figure 8). Our findings are supported by previous studies that many plant hormones (e.g. gibberellins) are deeply involved in Pi starvation responses [48]. Therefore, part of the non-polyA lncRNAs in cis-regulatory regions might be involved in hormone signaling transduction during Pi starvation.

Example 4: Validation of novel non-poly lncRNAs responding to Pi starvation

[0102] Five intergenic non-polyA lncRNAs which were up-regulated under low Pi condition by the sequencing data were selected. The upregulated expression pattern of these intergenic non-polyA lncRNAs were validated by real-time PCR (Figure 5A).

[0103] The lnc-34 is transcribed from a region located upstream of a gene *AT1G74670*, which encodes a protein whose expression is responsive to gibberellins and sugar, two signals which function in Pi starvation responses [48, 49]. In non-polyA RNA sequencing data, differential expression for lnc-34 can be found between control and low Pi samples, while no similar phenomenon was found in polyA sequencing.

[0104] Apart from expression, we downloaded ChIP-seq data for H3K9ac (GSE28398) and chAP-seq data (GSM954614) for H2A.Z. The signals of H3K9ac were observed near lnc-34 and AT1G74670 and H2A.Z was showed of signal peaks at the 5' and 3' end of them (Figure 5B). Since H3K9ac is a general activator [50], while H2A.Z was reported to regulate the expression of several classes of Pi starvation responding genes (e.g. PHO1)

[51] and always shows a strong signal peak at 5' end and a smaller peak at 3' end of most genes [52], indicating lncRNA may function as a regulator in Pi starvation.

[0105] The conserved secondary structures of all novel non-polyA lncRNAs was also determined. Interestingly, a Pi starvation related lncRNA, lnc-149, was identified with a common local structure conserved in three plant genomes (Figure 5C, see Example 1).

[0106] The conserved structure is composed of two conserved short hairpins and one variable long hairpin located at the 5' end (3-70 nt) of lnc-149. Moreover, the three parts of the local structure are connected together by a multi-branch loop and an additional stem. The key points of the connection, one in the start region of the first conserved hairpin and the other in the start region of the variable hairpin, are constrained by base pairs with covariance (the bases change and the structures retain), implying the conserved structure is favored during evolution and may have a function in the stress response by low Pi conditions. Furthermore, the loop regions in the two conserved hairpins are also maintained in three or two genomes, demonstrating that the loops may have a function, for instance, to bind RNA-binding proteins.

Example 5: Identification of orthologues of lncRNA in other crop species.

[0107] Sequences with a high degree of similarity to several of the lncRNAs from Arabidopsis thaliana of Table 4 were identified in soybean (Table 5), rice (Table 6), sorghum (Table 7) Foxtail millet (Table 8) wheat (Table 9) and mais/corn (Table 10). The Tables indicate the identity of the lncRNA in Arabidopsis and the reference to the appropriate sequence entry for the sequence in Arabidopsis, and the reference to the sequence entry for the crop species as well as chromosome location and % sequence identity.

Example 6: Modulation of Pi-starvation related lncRNAs in plants

[0108] Recombinant genes are made comprising the following DNA regions

a) A plant expressible promoter such as a CaMV35S promoter

b) a DNA region which when transcribed yields an RNA comprising a nucleotide sequence of a lncRNA, preferably a non-polyA lncRNA upregulated under Pi starvation conditions, including a non-poly lncRNA selected from lnc-24, lnc-107, lnc-139, lnc-194, lnc-195 or lnc-149

[0109] The recombinant genes are introduced into plants, particularly Arabidopsis plants through transformation methods known in the art and transgenic plants are identified.

[0110] The behavior of the transgenic plants under Pi-starvation conditions is analyzed in comparison to transgenic plants under normal Pi conditions, as well as in comparison to wild-type non-transgenic plants under normal or Pi-starvation conditions.

[0111]

References

1. Hirayama, T. and K. Shinozaki, *Research on plant abiotic stress responses in the post-genome era: past, present and future.* The Plant journal : for cell and molecular biology, 2010. **61**(6): p. 1041-52.
2. Chen, W., et al., *Expression profile matrix of Arabidopsis transcription factor genes suggests their putative functions in response to environmental stresses.*The Plant cell, 2002. **14**(3): p. 559-74.
3. Sunkar, R. and J.K. Zhu, *Novel and stress-regulated microRNAs and other small RNAs from Arabidopsis.* The Plant cell, 2004. **16**(8): p. 2001-19.
4. Chiou, T.J., et al., *Regulation of phosphate homeostasis by MicroRNA in Arabidopsis.* The Plant cell, 2006. **18**(2): p. 412-21.
5. Bari, R., et al., *PHO2, microRNA399, and PHR1 define a phosphate-signaling pathway in plants.* Plant physiology, 2006. **141**(3): p. 988-99.
6. Franco-Zorrilla, J.M., et al., *Target mimicry provides a new mechanism for regulation of microRNA activity.* Nature genetics, 2007. **39**(8): p. 1033-7.
7. Shin, H., et al., *Loss of At4 function impacts phosphate distribution between the roots and the shoots during phosphate starvation.* The Plant journal : for cell and molecular biology, 2006. **45**(5): p. 712-26.
8. Rinn, J.L. and H.Y. Chang, *Genome regulation by long noncoding RNAs.* Annual review of biochemistry, 2012. **81**: p. 145-66.
9. Ravasi, T., et al., *Experimental validation of the regulated expression of large numbers of non-coding RNAs from the mouse genome.* Genome research, 2006. **16**(1): p. 11-9.
10. Ponjavic, J., C.P. Ponting, and G. Lunter, *Functionality or transcriptional noise? Evidence for selection within long noncoding RNAs.* Genome research, 2007.**17**(5): p. 556-65.
11. Struhl, K., *Transcriptional noise and the fidelity of initiation by RNA polymerase II.* Nature structural & molecular biology, 2007. **14**(2): p. 103-5.
12. Ebisuya, M., et al., *Ripples from neighbouring transcription.* Nature cell biology, 2008. **10**(9): p. 1106-13.

13. Dinger, M.E., et al., *Long noncoding RNAs in mouse embryonic stem cel pluripotency and differentiation.* Genome research, 2008. **18**(9): p. 1433-45.
14. Guttman, M., et al., *Ab initio reconstruction of cell type-specific transcriptomes in mouse reveals the conserved multi-exonic structure of lincRNAs.* Nature biotechnology, 2010. **28**(5): p. 503-10.
15. Borsani, G., et al., *Characterization of a murine gene expressed from the inactive X chromosome.* Nature, 1991. **351**(6324): p. 325-9.
16. Brown, C.J., et al., *The human XIST gene: analysis of a 17 kb inactive X-specific RNA that contains conserved repeats and is highly localized within the nucleus.* Cell, 1992. **71**(3): p. 527-42.
17. Heo, J.B. and S. Sung, *Vernalization-mediated epigenetic silencing by a long intronic noncoding RNA.* Science, 2011. **331**(6013): p. 76-9.
18. Marioni, J.C., et al., *RNA-seq: an assessment of technical reproducibility and comparison with gene expression arrays.* Genome research, 2008. **18**(9): p. 1509-17.
19. Zhu, Y.Y., et al., *Reverse transcriptase template switching: a SMART approach for full-length cDNA library construction.* BioTechniques, 2001. **30**(4): p. 892-7.
20. Schaefer, M., et al., *RNA cytosine methylation analysis by bisulfite sequencing.* Nucleic acids research, 2009. **37**(2): p. e12.
21. Cabili, M.N., et al., *Integrative annotation of human large intergenic noncoding RNAs reveals global properties and specific subclasses.* Genes & development, 2011. **25**(18): p. 1915-27.
22. Khalil, A.M., et al., *Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression.* Proceedings of the National Academy of Sciences of the United States of America, 2009. **106**(28): p. 11667-72.
23. Guttman, M., et al., *Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals.* Nature, 2009. **458**(7235): p. 223-7.
24. Yang, L., et al., *Genome wide characterization of non-polyadenylated RNAs* Genome biology, 2011. **12**(2): p. R16.

25. Lan, P., W. Li, and W. Schmidt, *Complementary proteome and transcriptome profiling in phosphate-deficient Arabidopsis roots reveals multiple levels of gene regulation.* Molecular & cellular proteomics : MCP, 2012. **11**(11): p. 1156-66.
26. Levin, J.Z., et al., *Comprehensive comparative analysis of strand-specific RNA sequencing methods.* Nature methods, 2010. **7**(9): p. 709-15.
27. Langmead, B., et al., *Ultrafast and memory-efficient alignment of short DNA sequences to the human genome.* Genome biology, 2009. **10**(3): p. R25.
28. Trapnell, C., et al., *Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks.* Nature protocols, 2012. **7**(3): p. 562-78.
29. Kong, L., et al., *CPC: assess the protein-coding potential of transcripts using sequence features and support vector machine.* Nucleic acids research, 2007. **35**(Web Server issue): p. W345-9.
30. Wang, L., et al., *DEGseq: an R package for identifying differentially expressed genes from RNA-seq data.* Bioinformatics, 2010. **26**(1): p. 136-8.
31. Lu, Z.J., et al., *Prediction and characterization of noncoding RNAs in C. elegans by integrating conservation, secondary structure, and high-throughput sequencing and array data.* Genome research, 2011. **21**(2): p. 276-85.
32. Washietl, S., et al., *RNAcode: robust discrimination of coding and noncoding regions in comparative sequence data.* RNA, 2011. **17**(4): p. 578-94.
33. Bonnet, E., et al., *Evidence that microRNA precursors, unlike other non-coding RNAs, have lower folding free energies than random sequences.* Bioinformatics, 2004. **20**(17): p. 2911-7.
34. Zeller, G., et al., *Stress-induced changes in the Arabidopsis thaliana transcriptome analyzed using whole-genome tiling arrays.* The Plant journal for cell and molecular biology, 2009. **58**(6): p. 1068-82.
35. Becker, C., et al., *Spontaneous epigenetic variation in the Arabidopsis thaliana methylome.* Nature, 2011. **480**(7376): p. 245-9.
36. Filichkin, S.A., et al., *Genome-wide mapping of alternative splicing in Arabidopsis thaliana.* Genome research, 2010. **20**(1): p. 45-58.

37. German, M.A., et al., *Global identification of microRNA-target RNA pairs by parallel analysis of RNA ends.* Nature biotechnology, 2008. **26**(8): p. 941-6.
38. Gregory, B.D., et al., *A link between RNA metabolism and silencing affecting Arabidopsis development.* Developmental cell, 2008. **14**(6): p. 854-66.
39. Laubinger, S., et al., *At-TAX: a whole genome tiling array resource for developmental expression analysis and transcript identification in Arabidopsis thaliana.* Genome biology, 2008. **9**(7): p. R112.
40. Lister, R., et al., *Highly integrated single-base resolution maps of the epigenome in Arabidopsis.* Cell, 2008. **133**(3): p. 523-36.
41. Bernhart, S.H., et al., *RNAalifold: improved consensus structure prediction for RNA alignments.* BMC bioinformatics, 2008. **9**: p. 474.
42. Darty, K., A. Denise, and Y. Ponty, *VARNA: Interactive drawing and editing of the RNA secondary structure.* Bioinformatics, 2009. **25**(15): p. 1974-5.
43. Perrin, R., et al., *AtmtPNPase is required for multiple aspects of the 18S rRNA metabolism in Arabidopsis thaliana mitochondria.* Nucleic acids research, 2004. **32**(17): p. 5174-82.
44. Nicol, J.W., et al., *The Integrated Genome Browser: free software for distribution and exploration of genome-scale datasets.* Bioinformatics, 2009. **25**(20): p. 2730-1.
45. Guttman, M. and J.L. Rinn, *Modular regulatory principles of large non-coding RNAs.* Nature, 2012. **482**(7385): p. 339-46.
46. Marques, A.C. and C.P. Ponting, *Catalogues of mammalian long noncoding RNAs: modest conservation and incompleteness.* Genome biology, 2009. **10**(11): p. R124.
47. Swiezewski, S., et al., *Cold-induced silencing by long antisense transcripts of an Arabidopsis Polycomb target.* Nature, 2009. **462**(7274): p. 799-802.
48. Devaiah, B.N., et al., *Phosphate starvation responses and gibberellic acid biosynthesis are regulated by the MYB62 transcription factor in Arabidopsis.* Molecular plant, 2009. **2**(1): p. 43-58.
49. Karthikeyan, A.S., et al., *Phosphate starvation responses are mediated by sugar signaling in Arabidopsis.* Planta, 2007. **225**(4): p. 907-18.

50. He, G., A.A. Elling, and X.W. Deng, *The epigenome and plant development.* Annual review of plant biology, 2011. **62**: p. 411-35.
51. Smith, A.P., et al., *Histone H2A.Z regulates the expression of several classes of phosphate starvation response genes but not as a transcriptional activator.*Plant physiology, 2010. **152**(1): p. 217-25.
52. Coleman-Derr, D. and D. Zilberman, *Deposition of histone variant H2A.Z within gene bodies regulates responsive genes.* PLoS genetics, 2012. **8**(10): p. e1002988.
53. Chiou, T.J. and S.I. Lin, *Signaling network in sensing phosphate availability in plants.* Annual review of plant biology, 2011. **62**: p. 185-206.
54. Jain, A., V.K. Nagarajan, and K.G. Raghothama, *Transcriptional regulation of phosphate acquisition by higher plants.* Cell Mol Life Sci, 2012. **69**(19): p.3207-24.
55. Wu, P., et al., *Phosphate starvation triggers distinct alterations of genome expression in Arabidopsis roots and leaves.* Plant physiology, 2003. **132**(3): p. 1260-71.
56. Jiang, C., et al., *Phosphate starvation root architecture and anthocyanin accumulation responses are modulated by the gibberellin-DELLA signaling pathway in Arabidopsis.* Plant physiology, 2007. **145**(4): p. 1460-70.
57. Chodroff, R.A., et al., *Long noncoding RNA genes: conservation of sequence and brain expression among diverse amniotes.* Genome biology, 2010. **11**(7): p. R72.

Table 1. Total and non-polyA RiboMinus RNA-seq data

Sample	Total RNA-seq (short reads)	Non-polyA RNA-seq (short reads)	Non-polyA RNA-seq (long reads)	Low Pi non-polyA RNA-seq (long reads)
Total reads	20,846,554	26,968,205	19,925,959	23,801,748
Total reads mapped	17,816,897	15,711,923	18,778,785	22,642,042
Total reads mapped ratio	85.47%	58.26%	94.24%	95.13%
Clean reads (rRNA free)	17,511,441	24,919,787	14,813,275	16,264,209
rRNA ratio	18.72%	13.04%	27.23%	33.29%
Clean reads mapped	11,035,904	11,637,842	13,666,101	15,104,503
Clean reads mapped ratio	63.00%	46.70%	92.26%	92.87%

Total RNA-seq (short reads) and non-polyA RNA-seq (short reads) were sequenced at 36nt single-end, non-polyA RNA-seq (long reads) for control and low Pi samples were sequenced at 100nt single-end. Reads were aligned to TAIR10 rRNA, and remaining were mapped to TAIR10 genome using Tophat with two mismatches.

Table 2. Downloaded Poly A RNA-seq data

Sample	PolyA RNA-seq	Low Pi polyA RNA-seq
ID	SRR420815	SRR420818
Total reads	22,403,178	23,489,371
Total reads mapped	13,037,229	13,432,208
Total reads mapped ratio	58.2%	57.2%

The data are downloaded from Ref [45]. Raw reads from polyA RNA-seq were mapped to TAIR10 genome using Tophat with two mismatches

Table 3. RT-PCR primers

Gene/lncRNA ID	Forward primer	SEQ ID No.	Reverse primer	SEQ ID No.	Source
Act2 (AT3G18780)	ATCACAGCACTTGCACCAAGC	1298	CCTTGGAGATCCACATCTGCTG	1313	Fig 2E
Control-1	ACATGAGCTTGTAACCCATG	1299	GGTTCAGATGAGATCGGACC	1314	
Control-2	ACGAGAGCTTGTAACCCAAG	1300	CACTGCTGAGAGCGGGAGGT	1315	
Control-3	GCTTTAACCACACTGAAAAG	1301	ATGTTGATAAGAGCTCGACA	1316	
Control-4	AACAACGGTGATGTGTGAAG	1302	CCACCATTTTCTTTCGTAGG	1317	
Control-5	GCAAGCAAATAAACAACTTC	1303	CATTCCATTCTGTGTAGTTC	1318	
Control-6	CCGAGCTAACCCCTGTCCAG	1304	CTGGCTTCTTATTCTCGTCT	1319	
Control-7	GTGCGTACTACTTCCCAACG	1305	TTCGCTCTTGTGGATGCTTC	1320	
Control-8	GGGACTTCCTTTTCAAGCTA	1306	GATTAGGGATCATCATCCGC	1321	
Control-9	TGTGATCCAAGTGGAGACAA	1307	CATAGTGGGCTCGGAAGGCA	1322	
lnc-139	GCTTTCATGGTGTAGCCAAA	1308	ACCGCAACCCGATCTTAAAAG	1323	Fig 5A
lnc-194	CTTTGAGAAGCTAGAAGAAG	1309	GGTTGCGGTTTAAGTTGTTA	1324	
lnc-195	CCAAAGACTCATACGGACTT	1310	ATACACATGACATCAAGTCA	1325	
lnc-107	AAGAAGGTTGGTTAGTGTTT	1311	TACTTAGGCTTACAAGATCG	1326	
lnc-34	TCCAGTGCAAGTGATTGGGA	1312	TGGCATAAATCCATGCCGAGA	1327	

Table 4: Long non-coding RNA from Arabidopsis thaliana

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
NonpolyA_lnc-1	Chr1	+	11861231	11861433	1	11861231,	11861433,	N	1	extracellular region
NonpolyA_lnc-2	Chr1	+	16188953	16189153	1	16188953,	16189153,	N	2	
NonpolyA_lnc-3	Chr1	+	16557097	16557323	1	16557097,	16557323,	N	3	
NonpolyA_lnc-4	Chr1	+	17233548	17233816	1	17233548,	17233816,	Y	4	protein binding,N-terminal protein myristoylation,sequence-specific DNA binding transcription factor activity,DNA binding,protein dimerization activity,nucleus,DNA binding,sequence-specific DNA binding transcription factor activity
NonpolyA_lnc-5	Chr1	+	18692611	18692838	1	18692611,	18692838,	Y	5	
NonpolyA_lnc-6	Chr1	+	22463302	22463699	1	22463302,	22463699,	Y	6	chloroplast,mitochondrion,glycine decarboxylation via glycine cleavage system,aminomethyltransferase activity,aminomethyltransferase activity,chloroplast,mitochondrion,glycine catabolic process,aminomethyltransferase activity,aminomethyltransferase activity,cytoplasm,glycine catabolic process,mitochondrion,cytoplasm,glycine catabolic process,cytoplasm,chloroplast
NonpolyA_lnc-7	Chr1	+	24190081	24190296	1	24190081,	24190296,	N	7	extracellular region,signal transduction
NonpolyA_lnc-8	Chr1	+	26168782	26169036	1	26168782,	26169036,	N	8	
NonpolyA_lnc-9	Chr1	+	4814939	4815156	1	4814939,	4815156,	N	9	
NonpolyA_lnc-10	Chr1	+	5571607	5571884	1	5571607,	5571884,	N	10	nucleus,molecular_function_unknown,chloroplast,vacuole,biological_process_unknown
NonpolyA_lnc-11	Chr1	+	5752698	5753060	1	5752698,	5753060,	N	11	cellular_component_unknown,nucleus,biological_process_unknown,poly(U) RNA binding
NonpolyA_lnc-12	Chr1	+	5973770	5973993	1	5973770,	5973993,	N	12	
NonpolyA_lnc-13	Chr1	+	7349419	7349649	1	7349419,	7349649,	N	13	
NonpolyA_lnc-14	Chr1	+	766711	766926	1	766711,	766926,	N	14	vegetative to reproductive phase transition of meristem,ovule development,positive regulation of transcription, DNA-dependent,GTP binding,rRNA processing,GTPase activity,ncRNA metabolic process,chloroplast membrane,chloroplast relocation,embryo development ending in seed dormancy,thiamine biosynthetic process,chloroplast,chloroplast,iron-sulfur cluster assembly,thiamine biosynthetic process,vegetative to reproductive phase transition of meristem,photosynthesis,transcription from plastid promoter,thiamine-phosphate diphosphorylase activity,thylakoid membrane organization,regulation of protein dephosphorylation,thylakoid membrane organization,photosystem II assembly,thiamine-phosphate diphosphorylase activity
NonpolyA_lnc-15	Chr1	+	8793474	8793820	1	8793474,	8793820,	Y	15	
NonpolyA_lnc-16	Chr1	-	10781346	10781597	1	10781346,	10781597,	N	16	molecular_function_unknown,vacuolar membrane,nucleus,nucleus,nucleus,biological_process_unknown
NonpolyA_lnc-17	Chr1	-	11556249	11556459	1	11556249,	11556459,	N	17	nucleus,biological_process_unknown,membrane,molecular_function_unknowr

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
NonpolyA_lnc-18	Chr1	-	11584500	11585079	3	11584500,11584656,11585054,	11584559,11584708,11585079,	Y	18	
NonpolyA_lnc-19	Chr1	-	13180843	13181047	1	13180843,	13181047,	N	19	
NonpolyA_lnc-20	Chr1	-	15746548	15746828	1	15746548,	15746828,	N	20	
NonpolyA_lnc-21	Chr1	-	16583107	16583307	1	16583107,	16583307,	N	21	
NonpolyA_lnc-22	Chr1	-	16608731	16608939	1	16608731,	16608939,	N	22	
NonpolyA_lnc-23	Chr1	-	17529760	17530043	1	17529760,	17530043,	N	23	
NonpolyA_lnc-24	Chr1	-	18088251	18088521	1	18088251,	18088521,	N	24	signal recognition particle, endoplasmic reticulum targeting,SRP-dependent cotranslational protein targeting to membrane,7S RNA binding,cytosol,signal recognition particle,production of ta-siRNAs involved in RNA interference,cytosol,SRP-dependent cotranslational protein targeting to membrane, signal sequence recognition,mRNA binding,nucleoside-triphosphatase activity,GTP binding,production of miRNAs involved in gene silencing by miRNA,7S RNA binding,cytoplasm,SRP-dependent cotranslational protein targeting to membrane,7S RNA binding,signal recognition particle,GTP binding,nucleotide binding,nucleotide binding,nucleoside-triphosphatase activity,GTP binding,defense response to virus,cytoplasm
NonpolyA_lnc-25	Chr1	-	18989069	18989274	1	18989069,	18989274,	N	25	nucleus,transferase activity, transferring hexosyl groups,cellular_component_unknown,transferase activity, transferring glycosyl groups,DNA repair,metabolic process,DNA recombination
NonpolyA_lnc-26	Chr1	-	20630309	20630549	1	20630309,	20630549,	Y	26	RNA splicing,production of miRNAs involved in gene silencing by miRNA,RNA processing,RNA binding,nucleus,identical protein binding,production of siRNA involved in RNA interference,post-translational protein modification,nuclear speck,plasma membrane,protein binding,protein binding,nucleolus,regulation of transcription, DNA-dependent,interchromatin granule,protein binding,mRNA splicing, via spliceosome,cell cycle process,nucleolus,plasma membrane,nucleus,identical protein binding,RNA binding,protein binding,nucleus,positive regulation of transcription, DNA-dependent,mRNA splicing, via spliceosome
NonpolyA_lnc-27	Chr1	-	20771994	20772194	1	20771994,	20772194,	N	27	nuclear-transcribed mRNA catabolic process,biological_process_unknown,cytoplasm
NonpolyA_lnc-28	Chr1	-	23762735	23762993	1	23762735,	23762993,	Y	28	nucleus,nucleus,cellular_component_unknown,biological_process_unknowr
NonpolyA_lnc-29	Chr1	-	24046304	24046510	1	24046304,	24046510,	N	29	nucleotide binding,oxidation-reduction process,oxidoreductase activity,oxidoreductase activity,nucleotide binding,zinc ion binding,oxidation-reduction process,cytoplasm,zinc ion binding,ethylene mediated signaling pathway,cytoplasm
NonpolyA_lnc-30	Chr1	-	24178209	24178487	1	24178209,	24178487,	N	30	protein insertion into membrane,integral to membrane,membrane

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
NonpolyA_lnc-31	Chr1	-	24242668	24242874	1	24242668,	24242874,	N	31	vacuolar membrane,endoplasmic reticulum,endoplasmic reticulum,molecular_function_unknown,vacuolar membrane,vacuolar membrane,biological_process_unknown
NonpolyA_lnc-32	Chr1	-	25279685	25279889	1	25279685,	25279889,	Y	32	molecular_function_unknown,cytoplasm,biological_process_unknown,cytoplasm;endoplasmic reticulum,mannosyl-oligosaccharide glucosidase activity,alpha-glucosidase activity,mannosyl-oligosaccharide glucosidase activity,endoplasmic reticulum,catalytic activity,oligosaccharide metabolic process,oligosaccharide metabolic process,catalytic activity,alpha-glucosidase activity,root epidermal cell differentiation,epidermal cell differentiation,endoplasmic reticulum
NonpolyA_lnc-33	Chr1	-	25996414	25996616	1	25996414,	25996616,	N	33	
NonpolyA_lnc-34	Chr1	-	28052395	28052650	1	28052395,	28052650,	Y	34	response to karrikin,response to fructose stimulus,response to gibberellin stimulus,seed dormancy process,response to glucose stimulus,gibberellic acid mediated signaling pathway,gibberellic acid mediated signaling pathway,extracellular region,response to sucrose stimulus,molecular_function_unknown
NonpolyA_lnc-35	Chr1	-	29329406	29329610	1	29329406,	29329610,	N	35	oligopeptide transport,sulfate transmembrane transporter activity,transmembrane transport,integral to membrane,response to nitrate,sulfate transmembrane transporter activity,selenate transport,membrane,secondary active sulfate transmembrane transporter activity,cellular response to sulfate starvation,plasma membrane,nitrate transport,integral to membrane,transporter activity,sulfate transport,secondary active sulfate transmembrane transporter activity,transporter activity,membrane,transport,transport,sulfate transport,sulfate transport,transmembrane transport,transition metal ion transport,sulfate transport
NonpolyA_lnc-36	Chr1	-	4663218	4663489	1	4663218,	4663489,	Y	36	extracellular region,mitochondrion
NonpolyA_lnc-37	Chr2	+	11890525	11890724	1	11890525,	11890724,	N	37	
NonpolyA_lnc-38	Chr2	+	13006915	13007129	1	13006915,	13007129,	N	38	
NonpolyA_lnc-39	Chr2	+	14567347	14567554	1	14567347,	14567554,	N	39	molecular_function_unknown,cellular_component_unknown,mitochondrion,mitochondrion biological_process_unknown

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
NonpolyA_lnc-40	Chr2	+	15445053	15445288	1	15445053,	15445288,	Y	40	water channel activity,vacuole,polyamine catabolic process,urea transport,plant-type vacuole membrane,glycolysis,cellular modified amino acid biosynthetic process,response to salt stress,vacuolar membrane,transporter activity,integral to membrane,response to salt stress,transport,urea transmembrane transporter activity,transmembrane transport,chloroplast envelope,water transport,water channel activity,response to cadmium ion,water transport,membrane,response to abscisic acid stimulus,phenylpropanoid metabolic process,membrane,cytoplasm,Golgi organization,central vacuole,water transport,response to cold,response to temperature stimulus,plant-type vacuole membrane,gibberellic acid mediated signaling pathway,response to desiccation,transport,calcium ion transport,plant-type vacuole membrane,protein storage vacuole,hydrogen peroxide transmembrane transport,hyperosmotic response
NonpolyA_lnc-41	Chr2	+	15982407	15982625	1	15982407,	15982625,	N	41	transferase activity,transferase activity, transferring glycosyl groups,Golgi stack,Golgi apparatus,galactosyltransferase activity
NonpolyA_lnc-42	Chr2	+	16610394	16610630	1	16610394,	16610630,	Y	42	membrane,membrane,biological_process_unknown,molecular_function_unknown
NonpolyA_lnc-43	Chr2	+	17224513	17224805	1	17224513,	17224805,	N	43	two-component response regulator activity,regulation of transcription, DNA-dependent,two-component response regulator activity,regulation of seed germination,protein binding,regulation of shoot development,two-component signal transduction system (phosphorelay),cytokinin mediated signaling pathway,two-component response regulator activity,cytokinin mediated signaling pathway,two-component signal transduction system (phosphorelay),regulation of transcription, DNA-dependent,nucleus,nucleus,regulation of anthocyanin metabolic process,circadian rhythm,cytokinin mediated signaling pathway,circadian rhythm
NonpolyA_lnc-44	Chr2	+	1944433	1944647	1	1944433,	1944647,	N	44	
NonpolyA_lnc-45	Chr2	+	2923653	2923973	1	2923653,	2923973,	N	45	
NonpolyA_lnc-46	Chr2	+	3297060	3297404	1	3297060,	3297404,	N	46	
NonpolyA_lnc-47	Chr2	+	3331063	3331491	1	3331063,	3331491,	Y	47	
NonpolyA_lnc-48	Chr2	+	3337485	3337811	1	3337485,	3337811,	N	48	oxidation-reduction process,mitochondrial electron transport, NADH to ubiquinone,NADH dehydrogenase (ubiquinone) activity,NADH dehydrogenase (ubiquinone) activity,membrane,ATP synthesis coupled electron transport,chloroplast
NonpolyA_lnc-49	Chr2	+	3377797	3379144	1	3377797,	3379144,	N	49	
NonpolyA_lnc-50	Chr2	+	3408478	3408698	1	3408478,	3408698,	N	50	cellular_component_unknown,molecular_function_unknown,biological_process_unknown,mitochondrion
NonpolyA_lnc-51	Chr2	+	3433945	3434435	1	3433945,	3434435,	N	51	molecular_function_unknown,biological_process_unknown,mitochondrion;mitochondrion,biological_process_unknown,molecular_function_unknown,cellular_component_unknown

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
NonpolyA_lnc-52	Chr2	+	3460853	3461193	1	3460853,	3461193,	Y	52	
NonpolyA_lnc-53	Chr2	+	3500742	3501306	1	3500742,	3501306,	N	53	chloroplast
NonpolyA_lnc-54	Chr2	+	3501367	3501643	1	3501367,	3501643,	N	54	hydrogen ion transmembrane transporter activity,proton-transporting ATP synthase complex, coupling factor F(o),mitochondrion,membrane,ATP synthesis coupled proton transport,proton transport,hydrogen ion transporting ATP synthase activity, rotational mechanism;chloroplast
NonpolyA_lnc-55	Chr2	+	6014066	6014575	1	6014066,	6014575,	Y	55	
NonpolyA_lnc-56	Chr2	+	6740949	6741192	1	6740949,	6741192,	N	56	
NonpolyA_lnc-57	Chr2	+	7520370	7520662	1	7520370,	7520662,	Y	57	abscisic acid mediated signaling pathway,protein autophosphorylation,ATP binding,response to auxin stimulus,defense response to fungus,endoplasmic reticulum unfolded protein response,cytosol,amino acid import,regulation of stomatal movement,ammonium transport,cell communication,signal transduction,systemic acquired resistance, salicylic acid mediated signaling pathway,protein serine/threonine kinase activity,response to jasmonic acid stimulus,kinase activity,plasma membrane,calmodulin-dependent protein kinase activity,protein kinase activity,N-terminal protein myristoylation,calcium ion binding,regulation of plant-type hypersensitive response,response to abscisic acid stimulus,response to ethylene stimulus,response to wounding,protein phosphorylation,negative regulation of programmed cell death,regulation of anion channel activity,anion transport,nucleus,protein serine/threonine kinase activity,MAPK cascade,regulation of anion channel activity,negative regulation of defense response,response to cold,jasmonic acid mediated signaling pathway,response to external stimulus,regulation of ion transport,nucleotide transport,abscisic acid mediated signaling pathway,transferase activity, transferring phosphorus-containing groups,cellular membrane fusion,protein binding,hyperosmotic salinity response,protein targeting to membrane,protein phosphorylation,intracellular signal transduction,response to water deprivation,basic amino acid transport,protein phosphorylation,membrane,ER to Golgi vesicle-mediated transport
NonpolyA_lnc-58	Chr2	+	8198338	8198539	1	8198338,	8198539,	N	58	regulation of circadian rhythm,ubiquitin-protein ligase activity,protein binding,lipid transport,signal transducer activity,regulation of circadian rhythm,protein binding,nucleus,circadian rhythm,ubiquitin-dependent protein catabolic process,circadian rhythm,signal transducer activity,regulation of transcription, DNA-dependent,long-day photoperiodism, flowering,signal transduction,regulation of transcription, DNA-dependent,Cajal body,cytosol,signal transduction,nucleus,protein binding,response to red or far red light;biological_process_unknown,molecular_function_unknown;cellular_component_unknown,molecular_function_unknown,biological_process_unknown,nucleus

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
NonpolyA_lnc-59	Chr2	+	8535600	8535804	1	8535600,	8535804,	Y	59	
NonpolyA_lnc-60	Chr2	-	10326688	10326889	1	10326688,	10326889,	Y	60	oxidoreductase activity,cytoplasm,oxidation-reduction process,oxidation-reduction process,cytoplasm,oxidoreductase activity,metabolic process,metabolic process,cysteine biosynthetic process,oxidoreductase activity,glyceraldehyde-3-phosphate dehydrogenase (NADP+) (non-phosphorylating) activity,oxidation-reduction process,metabolic process,metabolic process,cytoplasm,3-chloroallyl aldehyde dehydrogenase activity,oxidoreductase activity,oxidation-reduction process,cytoplasm,chloroplast relocation
NonpolyA_lnc-61	Chr2	-	1080817	1081027	1	1080817,	1081027,	N	61	cellular_component_unknown,ubiquitin-dependent protein catabolic process,ubiquitin-protein ligase activity,nucleus,ubiquitin-dependent protein catabolic process
NonpolyA_lnc-62	Chr2	-	14096976	14097211	1	14096976,	14097211,	Y	62	ATP binding,motor activity,mitochondrion localization,motor activity,myosin complex,peroxisome localization,motor activity,myosin complex,motor activity,actin filament based movement,Golgi apparatus,actin filament-based movement,Golgi localization;biological_process_unknown,molecular_function_unknown,mitochondrion
NonpolyA_lnc-63	Chr2	-	15003619	15003827	1	15003619,	15003827,	N	63	peroxisome,long-chain fatty acid metabolic process,defense response to insect,peroxisome,pollen development,defense response to insect,acyl-CoA oxidase activity,jasmonic acid biosynthetic process,acyl-CoA oxidase activity,fatty acid metabolic process,fatty acid beta-oxidation,fatty acid beta-oxidation,fatty acid biosynthetic process,oxidoreductase activity, acting on the CH-CH group of donors,flavin adenine dinucleotide binding,acyl-CoA dehydrogenase activity,metabolic process,oxidation-reduction process
NonpolyA_lnc-64	Chr2	-	15306349	15306570	1	15306349,	15306570,	Y	64	chromatin silencing by small RNA,zinc ion binding,regulation of telomere maintenance,meiosis,intracellular,meiotic chromosome segregation,nucleus,zinc ion binding,intracellular,sister chromatid cohesion,telomere maintenance in response to DNA damage,zinc ion binding,nucleus,intracellular,DNA recombination,response to gamma radiation,nucleus,biological_process_unknown;nucleus,biological_process_unknown,molecular_function_unknown
NonpolyA_lnc-65	Chr2	-	1553774	1554109	1	1553774,	1554109,	N	65	cellular_component_unknown,biological_process_unknown,molecular_function_unknown,chloroplast
NonpolyA_lnc-66	Chr2	-	16928195	16928474	1	16928195,	16928474,	N	66	biological_process_unknown,molecular_function_unknowr

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
NonpolyA_lnc-67	Chr2	-	1718079	1718321	1	1718079,	1718321,	N	67	sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,positive regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,sequence-specific DNA binding transcription factor activity,zinc ion binding,sequence-specific DNA binding transcription factor activity,salicylic acid mediated signaling pathway,sequence-specific DNA binding,sequence-specific DNA binding transcription factor activity,regulation of transcription, DNA-dependent,nucleus,regulation of transcription, DNA-dependent,nucleus,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding
NonpolyA_lnc-68	Chr2	-	18888936	18889169	1	18888936,	18889169,	N	68	molecular_function_unknown,plasmodesma,nucleus,response to gibberellin stimulus
NonpolyA_lnc-69	Chr2	-	18934043	18934280	1	18934043,	18934280,	N	69	acid-amino acid ligase activity,ubiquitin-protein ligase activity,postreplication repair,ubiquitin-protein ligase activity,ubiquitin-dependent protein catabolic process,ubiquitin-dependent protein catabolic process,ubiquitin-protein ligase activity,nucleus,ubiquitin-dependent protein catabolic process
NonpolyA_lnc-70	Chr2	-	2079821	2080063	1	2079821,	2080063,	Y	70	
NonpolyA_lnc-71	Chr2	-	2184895	2185245	1	2184895,	2185245,	N	71	transmembrane transport,membrane,cytoplasm,transport,transporter activity,transmembrane transporter activity,membrane,plasmodesma,transmembrane transporter activity
NonpolyA_lnc-72	Chr2	-	2517302	2517591	1	2517302,	2517591,	Y	72	
NonpolyA_lnc-73	Chr2	-	3279707	3280739	1	3279707,	3280739,	N	73	
NonpolyA_lnc-74	Chr2	-	3283590	3283867	1	3283590,	3283867,	N	74	mitochondrion,biological_process_unknown,cellular_component_unknown,molecular_function_unknown
NonpolyA_lnc-75	Chr2	-	3376361	3377129	1	3376361,	3377129,	N	75	
NonpolyA_lnc-76	Chr2	-	3377424	3378312	1	3377424,	3378312,	N	76	
NonpolyA_lnc-77	Chr2	-	3434008	3434401	1	3434008,	3434401,	Y	77	molecular_function_unknown,biological_process_unknown,mitochondrion;mitochondrion,biological_process_unknown,molecular_function_unknown,cellular_component_unknown
NonpolyA_lnc-78	Chr2	-	3463168	3463407	1	3463168,	3463407,	N	78	
NonpolyA_lnc-79	Chr2	-	3464405	3464693	1	3464405,	3464693,	Y	79	
NonpolyA_lnc-80	Chr2	-	3482285	3482581	1	3482285,	3482581,	N	80	cellular_component_unknown,mitochondrion,molecular_function_unknown,biological_process_unknown
NonpolyA_lnc-81	Chr2	-	3482361	3482727	1	3482361,	3482727,	N	81	cellular_component_unknown,mitochondrion,molecular_function_unknown,biological_process_unknown
NonpolyA_lnc-82	Chr2	-	3486046	3486345	1	3486046,	3486345,	Y	82	chloroplast,biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown
NonpolyA_lnc-83	Chr2	-	3488489	3488724	1	3488489,	3488724,	Y	83	chloroplast,biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
NonpolyA_lnc-84	Chr2	-	3490533	3491376	1	3490533,	3491376,	Y	84	cellular_component_unknown,biological_process_unknown,molecular_function_unknown
NonpolyA_lnc-85	Chr2	-	3500724	3501104	1	3500724,	3501104,	N	85	chloroplast
NonpolyA_lnc-86	Chr2	-	3607053	3607318	1	3607053,	3607318,	Y	86	
NonpolyA_lnc-87	Chr2	-	3621519	3622085	1	3621519,	3622085,	N	87	cellular_component_unknown,biological_process_unknown,molecular_function_unknown
NonpolyA_lnc-88	Chr2	-	7877837	7878125	1	7877837,	7878125,	N	88	cellular_component_unknown,molecular_function_unknown,nucleus,biological_process_unknown
NonpolyA_lnc-89	Chr3	+	10168101	10168401	1	10168101,	10168401,	N	89	
NonpolyA_lnc-90	Chr3	+	10497353	10497733	1	10497353,	10497733,	Y	90	molecular_function_unknown,biological_process_unknown,cellular_component_unknown
NonpolyA_lnc-91	Chr3	+	10497487	10497808	1	10497487,	10497808,	Y	91	molecular_function_unknown,biological_process_unknown,cellular_component_unknown
NonpolyA_lnc-92	Chr3	+	11349363	11349573	1	11349363,	11349573,	N	92	
NonpolyA_lnc-93	Chr3	+	11663950	11664160	1	11663950,	11664160,	N	93	
NonpolyA_lnc-94	Chr3	+	13588786	13589007	1	13588786,	13589007,	N	94	
NonpolyA_lnc-95	Chr3	+	15905247	15905452	1	15905247,	15905452,	N	95	cortical microtubule organization,microtubule-based process,trichome morphogenesis,cortical microtubule,cell wall organization,cell adhesion,root hair cell differentiation,actin nucleation,protein kinase activity,epidermal cell differentiation,kinase activity,nucleus
NonpolyA_lnc-96	Chr3	+	16070632	16070865	1	16070632,	16070865,	N	96	mitochondrion,molecular_function_unknown,biological_process_unknown;cellular_component_unknown,biological_process_unknown,molecular_function_unknown
NonpolyA_lnc-97	Chr3	+	17097863	17098131	1	17097863,	17098131,	N	97	
NonpolyA_lnc-98	Chr3	+	17188402	17188623	1	17188402,	17188623,	Y	98	UDP-glycosyltransferase activity,metabolic process,plasmodesma,transferase activity, transferring hexosyl groups,transferase activity, transferring glycosyl groups;fatty acid catabolic process,UDP-glycosyltransferase activity,quercetin 3-O-glucosyltransferase activity,quercetin 7-O-glucosyltransferase activity,transferase activity, transferring hexosyl groups,fatty acid beta-oxidation,cellular_component_unknown,metabolic process,transferase activity, transferring glycosyl groups
NonpolyA_lnc-99	Chr3	+	19615781	19616070	1	19615781,	19616070,	Y	99	leaf development,regulation of transcription, DNA-dependent,hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides,nucleus,nucleus,protein targeting to mitochondrion,ATP binding
NonpolyA_lnc-100	Chr3	+	19749510	19749741	1	19749510,	19749741,	N	100	nucleus,nucleus,nucleus,molecular_function_unknown,biological_process_unknown,nucleus nucleus,cellular_component_unknown,nucleus
NonpolyA_lnc-101	Chr3	+	2628449	2628656	1	2628449,	2628656,	N	101	
NonpolyA_lnc-102	Chr3	+	4724638	4724875	1	4724638,	4724875,	Y	102	
NonpolyA_lnc-103	Chr3	+	5646491	5646705	1	5646491,	5646705,	N	103	molecular_function_unknown,cytoplasm,vacuole,biological_process_unknowr
NonpolyA_lnc-104	Chr3	+	8108675	8108951	1	8108675,	8108951,	N	104	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
NonpolyA_lnc-105	Chr3	-	11897896	11898140	1	11897896,	11898140,	N	105	
NonpolyA_lnc-106	Chr3	-	12953465	12953674	1	12953465,	12953674,	N	106	
NonpolyA_lnc-107	Chr3	-	13589291	13589594	1	13589291,	13589594,	Y	107	
NonpolyA_lnc-108	Chr3	-	17177119	17177342	1	17177119,	17177342,	N	108	
NonpolyA_lnc-109	Chr3	-	17815582	17815835	1	17815582,	17815835,	N	109	chromosome segregation,synapsis,DNA metabolic process,regulation of chromosome organization,meiosis,chromatin organization,reciprocal meiotic recombination,plasmodesma,tissue development,DNA recombination,protein serine/threonine kinase activity,regulation of chromosome organization,multicellular organism reproduction,meiotic chromosome segregation,meiotic DNA double-strand break formation,nucleus,response to gamma radiation,organ morphogenesis,trichome morphogenesis,meiosis,reproduction,telomere maintenance in response to DNA damage,post-translational protein modification,phosphotransferase activity, alcohol group as acceptor,chloroplast,regulation of transcription, DNA-dependent,response to ionizing radiation,regulation of telomere maintenance,sister chromatid cohesion,transferase activity, transferring phosphorus-containing groups,response to gamma radiation,double-strand break repair via homologous recombination,response to ionizing radiation,1-phosphatidylinositol-3-phosphate 5-kinase activity,multicellular organism reproduction,DNA repair,telomere maintenance in response to DNA damage,positive regulation of transcription DNA-dependent,positive regulation of organelle organization,regulation of telomere maintenance
NonpolyA_lnc-110	Chr3	-	18301845	18302102	1	18301845,	18302102,	N	110	carbohydrate metabolic process,carbohydrate metabolic process,vacuolar membrane,catalytic activity,pentose-phosphate shunt,chloroplast,6-phosphogluconolactonase activity
NonpolyA_lnc-111	Chr3	-	18943979	18944186	1	18943979,	18944186,	N	111	heme binding,response to oxidative stress,oxidation-reduction process,peroxidase activity,peroxidase activity,extracellular region
NonpolyA_lnc-112	Chr3	-	19903012	19903216	1	19903012,	19903216,	N	112	iron-sulfur cluster assembly,embryo development ending in seed dormancy,ovule development,vegetative to reproductive phase transition of meristem,mitochondrion,embryo development ending in seed dormancy,chloroplast,thylakoid membrane organization;ARF GTPase activator activity,cellulose biosynthetic process,ARF GTPase activator activity,DNA binding,zinc ion binding,cytosol,nucleus,zinc ion binding,regulation of ARF GTPase activity,nucleus,regulation of ARF GTPase activity,Golgi vesicle transport
NonpolyA_lnc-113	Chr3	-	2084420	2084632	1	2084420,	2084632,	N	113	biological_process_unknown,response to gamma radiation,DNA recombination,molecular_function_unknown,telomere maintenance in response to DNA damage,nucleus,cellular_component_unknown,regulation of telomere maintenance,nucleus,meiosis
NonpolyA_lnc-114	Chr3	-	22347040	22347258	1	22347040,	22347258,	Y	114	cellular_component_unknown,biological_process_unknown,plasma membrane

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
NonpolyA_lnc-115	Chr3	-	23181953	23182189	1	23181953,	23182189,	Y	115	root hair cell differentiation,cell wall,root development,anatomical structure morphogenesis,developmental growth,plasmodesma,lateral root development,trichoblast differentiation,cellular response to calcium ion starvation,cellular response to ethylene stimulus,cellular developmental process,root hair elongation,cellular response to auxin stimulus,trichoblast differentiation
NonpolyA_lnc-116	Chr3	-	4680257	4680465	1	4680257,	4680465,	N	116	nucleus,nuclear envelope,nucleus,transport,nuclear pore,nuclear pore,transport,transport,nucleus,nuclear pore,protein binding
NonpolyA_lnc-117	Chr3	-	5550243	5550459	1	5550243,	5550459,	N	117	DNA binding,response to gibberellin stimulus,sequence-specific DNA binding transcription factor activity,response to jasmonic acid stimulus,response to ethylene stimulus,DNA binding,response to cadmium ion,zinc ion binding,nucleic acid binding,regulation of transcription, DNA-dependent,sequence-specific DNA binding transcription factor activity,response to auxin stimulus,response to salt stress,nucleus
NonpolyA_lnc-118	Chr3	-	581076	581347	1	581076,	581347,	Y	118	chloroplast,membrane,chloroplast,membrane
NonpolyA_lnc-119	Chr3	-	6062437	6062654	1	6062437,	6062654,	Y	119	catalytic activity,carboxy-lyase activity,glutamate metabolic process,pyridoxal phosphate binding,carboxy-lyase activity,carboxylic acid metabolic process,glutamate decarboxylase activity,cellular amino acid metabolic process
NonpolyA_lnc-120	Chr3	-	655331	655687	1	655331,	655687,	Y	120	endoplasmic reticulum
NonpolyA_lnc-121	Chr3	-	9397980	9398234	1	9397980,	9398234,	Y	121	N-terminal protein amino acid modification,chloroplast,metalloexopeptidase activity,aminopeptidase activity,cellular process,proteolysis,mitochondrion,metalloexopeptidase activity,proteolysis
NonpolyA_lnc-122	Chr4	+	1110229	1110454	1	1110229,	1110454,	N	122	plasmodesma,plasma membrane,membrane,response to cadmium ion,glutathione transferase activity,cytoplasm,intracellular membrane-bounded organelle,defense response to bacterium,glutathione binding,cytosol,response to salt stress,chloroplast,response to cold,defense response to fungus,glutathione transferase activity,quercitrin binding,chloroplast stroma,chloroplast stroma,apoplast,chloroplast stroma,response to cadmium ion,chloroplast,vacuole,plasma membrane,toxin catabolic process,response to zinc ion,camalexin binding
NonpolyA_lnc-123	Chr4	+	1116553	1116788	1	1116553,	1116788,	N	123	nucleus,protein-disulfide reductase activity,zinc ion binding,protein-disulfide reductase activity,biological_process_unknown,oxidation-reduction process,cellular_component_unknown,nucleus,oxidation-reduction process

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
NonpolyA_lnc-124	Chr4	+	1122710	1122918	1	1122710,	1122918,	N	124	nucleus,nucleus,regulation of defense response,cellular_component_unknown,nucleus,molecular_function_unknown,nucleus,heat acclimation;sequence-specific DNA binding,positive regulation of flower development,protein binding,nucleus,vegetative to reproductive phase transition of meristem,protein binding,regulation of transcription, DNA-dependent,sequence-specific DNA binding transcription factor activity,nucleus,regulation of transcription, DNA-dependent,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,nucleus,sequence-specific DNA binding,sequence-specific DNA binding transcription factor activity,nucleus
NonpolyA_lnc-125	Chr4	+	14022168	14022383	1	14022168,	14022383,	N	125	biological_process_unknown,cellular_component_unknown,molecular_function_unknown
NonpolyA_lnc-126	Chr4	+	1472730	1472995	1	1472730,	1472995,	N	126	vegetative to reproductive phase transition of meristem,nucleus,cytoplasm,leaf development,molecular_function_unknown
NonpolyA_lnc-127	Chr4	+	1476287	1476581	1	1476287,	1476581,	N	127	cellular_component_unknown,nucleotide-excision repair,nucleus,molecular_function_unknown,nucleus
NonpolyA_lnc-128	Chr4	+	15074597	15074830	1	15074597,	15074830,	Y	128	cellular_component_unknown,molecular_function_unknown,biological_process_unknown,mitochondrion
NonpolyA_lnc-129	Chr4	+	15393140	15393356	1	15393140,	15393356,	N	129	signal transducer activity,late endosome,flower development,basipetal auxin transport,positive regulation of flower development,cotyledon development,phyllome development,response to light stimulus,plasma membrane,signal transducer activity,cotyledon development,inflorescence development,response to light stimulus,plasma membrane,apical protein localization
NonpolyA_lnc-130	Chr4	+	17642102	17642303	1	17642102,	17642303,	N	130	
NonpolyA_lnc-131	Chr4	+	1851496	1851772	1	1851496,	1851772,	N	131	
NonpolyA_lnc-132	Chr4	+	200799	201176	1	200799,	201176,	Y	132	
NonpolyA_lnc-133	Chr4	+	2194942	2195198	1	2194942,	2195198,	N	133	
NonpolyA_lnc-134	Chr4	+	2196887	2197097	1	2196887,	2197097,	N	134	
NonpolyA_lnc-135	Chr4	+	2196968	2197188	1	2196968,	2197188,	N	135	
NonpolyA_lnc-136	Chr4	+	2251646	2251864	1	2251646,	2251864,	N	136	
NonpolyA_lnc-137	Chr4	+	3760214	3760454	1	3760214,	3760454,	Y	137	
NonpolyA_lnc-138	Chr4	+	3950523	3950743	1	3950523,	3950743,	N	138	
NonpolyA_lnc-139	Chr4	+	3950843	3951218	1	3950843,	3951218,	Y	139	
NonpolyA_lnc-140	Chr4	+	3954249	3955004	1	3954249,	3955004,	Y	140	
NonpolyA_lnc-141	Chr4	+	4693322	4693531	1	4693322,	4693531,	N	141	
NonpolyA_lnc-142	Chr4	+	5994401	5994669	1	5994401,	5994669,	N	142	regulation of transcription, DNA-dependent,DNA binding,nucleus,response to salicylic acid stimulus,response to gibberellin stimulus,sequence-specific DNA binding transcription factor activity,DNA binding,DNA binding,response to jasmonic acid stimulus

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
NonpolyA_lnc-143	Chr4	+	630839	631073	1	630839,	631073,	N	143	
NonpolyA_lnc-144	Chr4	+	6662088	6662334	1	6662088,	6662334,	N	144	
NonpolyA_lnc-145	Chr4	+	7634763	7634989	1	7634763,	7634989,	Y	145	extracellular region
NonpolyA_lnc-146	Chr4	+	8460983	8461206	1	8460983,	8461206,	N	146	
NonpolyA_lnc-147	Chr4	-	1318886	1319186	1	1318886,	1319186,	N	147	signal recognition particle, endoplasmic reticulum targeting,molecular_function_unknown,nucleus
NonpolyA_lnc-148	Chr4	-	14396734	14396946	1	14396734,	14396946,	N	148	
NonpolyA_lnc-149	Chr4	-	15413767	15414071	1	15413767,	15414071,	Y	149	
NonpolyA_lnc-150	Chr4	-	2671080	2671301	1	2671080,	2671301,	N	150	peptidyl-cysteine S-nitrosylation,calcium ion binding,chloroplast thylakoid membrane,chloroplast,chloroplast thylakoid lumen,chloroplast,photosynthesis,thylakoid,extrinsic to membrane,photosystem II,thylakoid lumen,chloroplast thylakoid membrane,oxygen evolving complex,thylakoid,chloroplast photosystem II,divalent metal ion transport,chloroplast thylakoid,chloroplast stroma,chloroplast,chloroplast thylakoid lumen,apoplast,chloroplast thylakoid membrane,thylakoid,oxygen evolving complex,cellular cation homeostasis,photosynthesis,photorespiration
NonpolyA_lnc-151	Chr4	-	3453930	3454163	1	3453930,	3454163,	Y	151	
NonpolyA_lnc-152	Chr4	-	5059714	5060024	1	5059714,	5060024,	Y	152	
NonpolyA_lnc-153	Chr4	-	5083611	5083866	1	5083611,	5083866,	N	153	
NonpolyA_lnc-154	Chr4	-	5200800	5201003	1	5200800,	5201003,	N	154	
NonpolyA_lnc-155	Chr4	-	5337071	5337287	1	5337071,	5337287,	N	155	
NonpolyA_lnc-156	Chr4	-	7390281	7390513	1	7390281,	7390513,	N	156	
NonpolyA_lnc-157	Chr4	-	7561785	7561998	1	7561785,	7561998,	N	157	
NonpolyA_lnc-158	Chr4	-	7881419	7881678	1	7881419,	7881678,	Y	158	
NonpolyA_lnc-159	Chr4	-	7890989	7891477	1	7890989,	7891477,	N	159	cellular_component_unknown,molecular_function_unknown,biological_process_unknown,mitochondrion
NonpolyA_lnc-160	Chr4	-	7891883	7892107	1	7891883,	7892107,	Y	160	cellular_component_unknown,molecular_function_unknown,biological_process_unknown,mitochondrion
NonpolyA_lnc-161	Chr5	+	10793563	10793770	1	10793563,	10793770,	N	161	
NonpolyA_lnc-162	Chr5	+	11703878	11704167	1	11703878,	11704167,	Y	162	
NonpolyA_lnc-163	Chr5	+	11945816	11946026	1	11945816,	11946026,	N	163	
NonpolyA_lnc-164	Chr5	+	12744204	12744437	1	12744204,	12744437,	N	164	
NonpolyA_lnc-165	Chr5	+	13031010	13031251	1	13031010,	13031251,	N	165	
NonpolyA_lnc-166	Chr5	+	13299777	13300090	1	13299777,	13300090,	N	166	
NonpolyA_lnc-167	Chr5	+	15540953	15541202	1	15540953,	15541202,	N	167	nucleus,molecular_function_unknown,cellular_component_unknown,biological_process_unknown

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
NonpolyA_lnc-168	Chr5	+	18367555	18367772	1	18367555,	18367772,	N	168	chloroplast;iron ion binding,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen,heme binding,response to water deprivation,oxidation-reduction process,oxidation-reduction process,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen,(+)-abscisic acid 8'-hydroxylase activity,abscisic acid catabolic process,response to red or far red light,electron carrier activity,iron ion binding,response to chitin,oxygen binding,extracellular region,electron carrier activity,heme binding
NonpolyA_lnc-169	Chr5	+	18425549	18425748	1	18425549,	18425748,	N	169	biological_process_unknown,plasma membrane,molecular_function_unknown,plasma membrane;plasma membrane,biological_process_unknown,tryptophan catabolic process,plasma membrane,nitrate transport,response to nitrate,molecular_function_unknown,indoleacetic acid biosynthetic process
NonpolyA_lnc-170	Chr5	+	18804263	18804558	1	18804263,	18804558,	N	170	sequence-specific DNA binding transcription factor activity,response to abscisic acid stimulus,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding,nucleus,defense response to fungus,nucleus,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,cellular response to hydrogen peroxide,regulation of transcription, DNA-dependent,sequence-specific DNA binding transcription factor activity,defense response to bacterium,regulation of transcription, DNA-dependent
NonpolyA_lnc-171	Chr5	+	19538715	19538924	1	19538715,	19538924,	N	171	biological_process_unknown,molecular_function_unknowr
NonpolyA_lnc-172	Chr5	+	20203237	20203519	1	20203237,	20203519,	Y	172	membrane,nucleus,iron ion binding,response to light stimulus,integral to membrane,oxidoreductase activity,membrane,ferric-chelate reductase activity,plasma membrane,flavin adenine dinucleotide binding,electron carrier activity,oxidation-reduction process,oxidoreductase activity
NonpolyA_lnc-173	Chr5	+	21057308	21057533	1	21057308,	21057533,	N	173	unidimensional cell growth,oxidation-reduction process,response to gibberellin stimulus,response to red or far red light,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors,flower development,cytoplasm,gibberellin 20-oxidase activity,iron ion binding,oxidoreductase activity,response to karrikin,response to gibberellin stimulus,gibberellin biosynthetic process
NonpolyA_lnc-174	Chr5	+	23384414	23384696	1	23384414,	23384696,	Y	174	cytoplasm,response to karrikin,ATP binding
NonpolyA_lnc-175	Chr5	+	23604830	23605073	1	23604830,	23605073,	N	175	extracellular region,peroxidase activity,oxidation-reduction process,heme binding,response to oxidative stress,peroxidase activity
NonpolyA_lnc-176	Chr5	+	24413868	24414262	1	24413868,	24414262,	Y	176	extracellular region,ubiquitin-protein ligase activity,plasma membrane,cytokinin metabolic process,zinc ion binding,zinc ion binding,N-terminal protein myristoylation

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
NonpolyA_lnc-177	Chr5	+	3014933	3015175	1	3014933,	3015175,	N	177	membrane,metal ion transmembrane transporter activity,nucleus,metal ion transport;hydrolase activity, hydrolyzing O-glycosyl compounds,arabinan catabolic process,extracellular region,alpha-N-arabinofuranosidase activity
NonpolyA_lnc-178	Chr5	+	3172981	3173198	1	3172981,	3173198,	Y	178	extracellular region,molecular_function_unknown,biological_process_unknown,extracellular space;sequence-specific DNA binding transcription factor activity,nucleus,sequence-specific DNA binding transcription factor activity,protein dimerization activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,regulation of transcription, DNA-dependent,nucleus,protein complex,nucleus,regulation of transcription, DNA-dependent,nucleus,carpel development,sequence-specific DNA binding transcription factor activity,regulation of transcription, DNA-dependent,DNA binding,vernalization response,nucleus,vernalization response,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,regulation of transcription, DNA-dependent,DNA binding,protein dimerization activity,protein dimerization activity,nucleus,regulation of circadian rhythm,nucleus,nucleus,DNA binding,protein dimerization activity,DNA binding,response to temperature stimulus,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,anthocyanin accumulation in tissues in response to UV light,negative regulation of flower development
NonpolyA_lnc-179	Chr5	+	5448887	5449119	1	5448887,	5449119,	Y	179	nucleus,cellular_component_unknown,biological_process_unknown,nucleus,molecular_function_unknown
NonpolyA_lnc-180	Chr5	+	5449246	5449477	1	5449246,	5449477,	Y	180	nucleus,cellular_component_unknown,biological_process_unknown,nucleus,molecular_function_unknown
NonpolyA_lnc-181	Chr5	+	6055892	6056145	1	6055892,	6056145,	Y	181	transport,transport,endoplasmic reticulum,transporter activity,transporter activity,response to arsenic-containing substance,water channel activity,water channel activity,membrane,membrane
NonpolyA_lnc-182	Chr5	+	6482831	6483037	1	6482831,	6483037,	N	182	
NonpolyA_lnc-183	Chr5	+	76854	77072	1	76854,	77072,	Y	183	regulation of transcription, DNA-dependent,DNA binding,sequence-specific DNA binding transcription factor activity,DNA binding,sequence-specific DNA binding transcription factor activity,nucleus
NonpolyA_lnc-184	Chr5	+	869456	869724	1	869456,	869724,	N	184	nucleus,nucleotide binding,nucleic acid binding,biological_process_unknown,nucleus
NonpolyA_lnc-185	Chr5	+	9902687	9903121	1	9902687,	9903121,	N	185	molecular_function_unknown,biological_process_unknown,cellular_component_unknown;molecular_function_unknown,nucleus,cellular_component_unknown,biological_process_unknown

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
NonpolyA_lnc-186	Chr5	+	9902894	9903426	1	9902894,	9903426,	N	186	molecular_function_unknown,biological_process_unknown,cellular_component_unknown;molecular_function_unknown,nucleus,cellular_component_unknown,biological_process_unknown
NonpolyA_lnc-187	Chr5	-	10425877	10426104	1	10425877,	10426104,	Y	187	
NonpolyA_lnc-188	Chr5	-	10667184	10667405	1	10667184,	10667405,	N	188	
NonpolyA_lnc-189	Chr5	-	10823973	10824182	1	10823973,	10824182,	N	189	mitochondrion,cellular_component_unknown,molecular_function_unknown,biological_process_unknown;chloroplast,cellular_component_unknown,biological_process_unknown,molecular_function_unknown
NonpolyA_lnc-190	Chr5	-	11726632	11727010	1	11726632,	11727010,	N	190	
NonpolyA_lnc-191	Chr5	-	11727773	11728010	1	11727773,	11728010,	N	191	
NonpolyA_lnc-192	Chr5	-	11728299	11728767	1	11728299,	11728767,	N	192	
NonpolyA_lnc-193	Chr5	-	11731433	11731680	1	11731433,	11731680,	N	193	
NonpolyA_lnc-194	Chr5	-	11731986	11732645	1	11731986,	11732645,	Y	194	
NonpolyA_lnc-195	Chr5	-	11734757	11734968	1	11734757,	11734968,	Y	195	
NonpolyA_lnc-196	Chr5	-	13371183	13371390	1	13371183,	13371390,	N	196	
NonpolyA_lnc-197	Chr5	-	13794664	13794887	1	13794664,	13794887,	N	197	
NonpolyA_lnc-198	Chr5	-	16156701	16156997	1	16156701,	16156997,	N	198	
NonpolyA_lnc-199	Chr5	-	18899946	18900153	1	18899946,	18900153,	N	199	protein targeting to chloroplast,embryo development ending in seed dormancy,chloroplast,stomatal complex morphogenesis,chloroplast,biological_process_unknown,aromatic amino acid family biosynthetic process,iron-sulfur cluster assembly
NonpolyA_lnc-200	Chr5	-	207051	207253	1	207051,	207253,	Y	200	nucleus,zinc ion binding,zinc ion binding,chlorophyll catabolic proces
NonpolyA_lnc-201	Chr5	-	21104807	21105054	1	21104807,	21105054,	Y	201	DNA-directed RNA polymerase activity,transcription, DNA-dependent,DNA binding,DNA-directed RNA polymerase II, core complex,RNA splicing, via endonucleolytic cleavage and ligation,DNA-directed RNA polymerase activity,transcription from RNA polymerase II promoter,DNA binding,RNA polymerase complex,DNA-directed RNA polymerase IV complex,transcription, DNA-dependent,DNA-directed RNA polymerase V complex,nucleus
NonpolyA_lnc-202	Chr5	-	21625024	21625250	1	21625024,	21625250,	N	202	
NonpolyA_lnc-203	Chr5	-	23269170	23269400	1	23269170,	23269400,	N	203	sequence-specific DNA binding transcription factor activity,nucleus,response to auxin stimulus,regulation of transcription, DNA-dependent,protein dimerization activity,nucleus

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
NonpolyA_lnc-204	Chr5	-	23997664	23997952	1	23997664,	23997952,	Y	204	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors,oxidoreductase activity,cytoplasm,oxidation-reduction process,cellular_component_unknown,biological_process_unknown,oxidoreductase activity,oxidoreductase activity,cytoplasm,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors,nitrate transport,response to nitrate,oxidation-reduction process;ethylene mediated signaling pathway,nucleus,respiratory burst involved in defense response,response to chitin,protein autoubiquitination,ubiquitin-protein ligase activity,zinc ion binding,ethylene biosynthetic process,response to chitin,endoplasmic reticulum unfolded protein response,zinc ion binding,response to abscisic acid stimulus,response to water deprivation,intracellular signal transduction
NonpolyA_lnc-205	Chr5	-	4628937	4629168	1	4628937,	4629168,	N	205	mitochondrion,biological_process_unknown,cellular_component_unknown,molecular_function_unknown
NonpolyA_lnc-206	Chr5	-	5042152	5042363	1	5042152,	5042363,	N	206	
NonpolyA_lnc-207	Chr5	-	6513157	6513384	1	6513157,	6513384,	N	207	plasma membrane,negative regulation of seed germination,response to abscisic acid stimulus,nucleus,nucleus,response to salt stress,nuclear-transcribed mRNA catabolic process,protein binding,plasma membrane,plasma membrane,protein binding,response to abscisic acid stimulus,cytoplasm
NonpolyA_lnc-208	Chr5	-	6850883	6851092	1	6850883,	6851092,	N	208	plasmodesma,transferase activity, transferring glycosyl groups,biosynthetic process,cytosol,sucrose-phosphate synthase activity,sucrose metabolic process,sucrose-phosphate synthase activity,plasma membrane,plasma membrane,nucleus;structural constituent of ribosome,structural constituent of ribosome,nucleolus,ribosome biogenesis,ribosome,plasma membrane,cytoplasm,cytosolic ribosome,structural constituent of ribosome,RNA methylation,translational elongation,maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA),intracellular,plasmodesma,cytosolic small ribosomal subunit,translation,translation,structural constituent of ribosome,cytosolic ribosome,cytosol,ribosome,membrane,cytosolic ribosome,chloroplast,chloroplast,cell wall,translation,cytosolic small ribosomal subunit
NonpolyA_lnc-209	Chr5	-	7493661	7493875	1	7493661,	7493875,	Y	209	cellular_component_unknown,plasma membrane,biological_process_unknowr
NonpolyA_lnc-210	Chr5	-	9577500	9577733	1	9577500,	9577733,	Y	210	
NonpolyA_lnc-211	Chr5	-	9636998	9637227	1	9636998,	9637227,	N	211	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-1	Chr1	+	11616594	11617128	1	11616594,	11617128,	N	212	abscisic acid mediated signaling pathway,cell communication,cell death,cellular membrane fusion,cytoplasm,defense response to bacterium, incompatible interaction,defense response to fungus,embryo development,endoplasmic reticulum unfolded protein response,ethylene mediated signaling pathway,ethylene mediated signaling pathway,glycolysis,Golgi organization,Golgi vesicle transport,hyperosmotic response,jasmonic acid mediated signaling pathway,jasmonic acid mediated signaling pathway,lateral root morphogenesis,MAPK cascade,NAD+ ADP-ribosyltransferase activity,NAD+ ADP-ribosyltransferase activity,NAD+ ADP-ribosyltransferase activity,negative regulation of defense response,negative regulation of programmed cell death,nitric oxide biosynthetic process,nucleus,nucleus,nucleus,nucleus,programmed cell death,protein binding,protein binding,protein binding,protein binding,protein glycosylation,protein targeting to membrane,protein targeting to vacuole,regulation of plant-type hypersensitive response,regulation of reactive oxygen species metabolic process,response to abscisic acid stimulus,response to auxin stimulus,response to cadmium ion,response to carbohydrate stimulus,response to cold,response to ethylene stimulus,response to external stimulus,response to osmotic stress,response to oxidative stress,response to ozone,response to salicylic acid stimulus,response to salt stress,response to salt stress,response to superoxide,response to superoxide,response to temperature stimulus,response to water deprivation,salicylic acid mediated signaling pathway,systemic acquired resistance, salicylic acid mediated signaling pathway,vesicle-mediated transport,water transport

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-2	Chr1	+	11616839	11617263	1	11616839,	11617263,	N	213	abscisic acid mediated signaling pathway,cell communication,cell death,cellular membrane fusion,cytoplasm,defense response to bacterium, incompatible interaction,defense response to fungus,embryo development,endoplasmic reticulum unfolded protein response,ethylene mediated signaling pathway,ethylene mediated signaling pathway,glycolysis,Golgi organization,Golgi vesicle transport,hyperosmotic response,jasmonic acid mediated signaling pathway,jasmonic acid mediated signaling pathway,lateral root morphogenesis,MAPK cascade,NAD+ ADP-ribosyltransferase activity,NAD+ ADP-ribosyltransferase activity,NAD+ ADP-ribosyltransferase activity,negative regulation of defense response,negative regulation of programmed cell death,nitric oxide biosynthetic process,nucleus,nucleus,nucleus,nucleus,programmed cell death,protein binding,protein binding,protein binding,protein binding,protein glycosylation,protein targeting to membrane,protein targeting to vacuole,regulation of plant-type hypersensitive response,regulation of reactive oxygen species metabolic process,response to abscisic acid stimulus,response to auxin stimulus,response to cadmium ion,response to carbohydrate stimulus,response to cold,response to ethylene stimulus,response to external stimulus,response to osmotic stress,response to oxidative stress,response to ozone,response to salicylic acid stimulus,response to salt stress,response to salt stress,response to superoxide,response to superoxide,response to temperature stimulus,response to water deprivation,salicylic acid mediated signaling pathway,systemic acquired resistance, salicylic acid mediated signaling pathway,vesicle-mediated transport,water transport
PolyA_lnc-3	Chr1	+	12087007	12087236	1	12087007,	12087236,	N	214	chloroplast,heme biosynthetic process,translational termination,translational termination,translation release factor activity,translation release factor activity;1-phosphatidylinositol binding,clathrin binding,clathrin coat,clathrin coat assembly,phospholipid binding
PolyA_lnc-4	Chr1	+	12514201	12516759	2	12514201,12514491,	12514235,12516759,	N	215	
PolyA_lnc-5	Chr1	+	12930955	12931230	1	12930955,	12931230,	Y	216	
PolyA_lnc-6	Chr1	+	12931743	12932724	1	12931743,	12932724,	N	217	
PolyA_lnc-7	Chr1	+	13871335	13872422	2	13871335,13871460,	13871376,13872422,	N	218	
PolyA_lnc-8	Chr1	+	20436219	20437123	2	20436219,20436751,	20436659,20437123,	N	219	biological_process_unknown,molecular_function_unknown,nucleus,protein targeting to mitochondrion;extracellular region
PolyA_lnc-9	Chr1	+	20436219	20437123	3	20436219,20436751,20437109,	20436659,20436880,20437123,	N	220	biological_process_unknown,molecular_function_unknown,nucleus,protein targeting to mitochondrion;extracellular region
PolyA_lnc-10	Chr1	+	22085565	22086345	1	22085565,	22086345,	N	221	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-11	Chr1	+	22555720	22556334	1	22555720,	22556334,	N	222	
PolyA_lnc-12	Chr1	+	22555720	22556334	2	22555720,22556177,	22555986,22556334,	N	223	
PolyA_lnc-13	Chr1	+	2443843	2445321	3	2443843,2444642,2444932,	2444103,2444774,2445321,	N	224	
PolyA_lnc-14	Chr1	+	2443867	2444916	3	2443867,2444642,2444872,	2444103,2444774,2444916,	N	225	
PolyA_lnc-15	Chr1	+	24969891	24970139	1	24969891,	24970139,	N	226	ATP binding,cellular_component_unknown,kinase activity,plasma membrane,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,protein tyrosine kinase activity,transferase activity, transferring phosphorus-containing groups
PolyA_lnc-16	Chr1	+	25119388	25119959	3	25119388,25119578,25119700,	25119482,25119616,25119959,	N	227	
PolyA_lnc-17	Chr1	+	25119394	25119986	2	25119394,25119578,	25119482,25119986,	N	228	
PolyA_lnc-18	Chr1	+	258839	259202	1	258839,	259202,	N	229	cellular_component_unknown,nucleus,Rho guanyl-nucleotide exchange factor activity,Rho guanyl-nucleotide exchange factor activity
PolyA_lnc-19	Chr1	+	25975364	25975608	2	25975364,25975503,	25975403,25975608,	N	230	
PolyA_lnc-20	Chr1	+	27627840	27628319	1	27627840,	27628319,	N	231	biological_process_unknown,chloroplast,chloroplast,molecular_function_unknown;cytoplasm,hydrolase activity,hyperosmotic salinity response,response to abscisic acid stimulus,response to cold,response to water deprivation
PolyA_lnc-21	Chr1	+	28784803	28785011	1	28784803,	28785011,	N	232	
PolyA_lnc-22	Chr1	+	28784967	28785206	2	28784967,28785134,	28785046,28785206,	N	233	
PolyA_lnc-23	Chr1	+	29754607	29755170	2	29754607,29754988,	29754662,29755170,	N	234	biological_process_unknown,cellular_component_unknown,molecular_function_unknown
PolyA_lnc-24	Chr1	+	3223831	3224378	1	3223831,	3224378,	Y	235	carbohydrate binding,carbohydrate metabolic process,catalytic activity,cellular_component_unknown,extracellular region,lyase activity
PolyA_lnc-25	Chr1	+	3991432	3991676	1	3991432,	3991676,	N	236	carbohydrate metabolic process,carbohydrate metabolic process,catalytic activity,catalytic activity,cation binding,cation binding,extracellular region,hydrolase activity, hydrolyzing O-glycosyl compounds,hydrolase activity, hydrolyzing O-glycosyl compounds,hydrolase activity, hydrolyzing O-glycosyl compounds,plasma membrane

WO 2015/117265 PCT/CN2014/071873

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-26	Chr1	+	4449507	4449723	1	4449507,	4449723,	N	237	abscisic acid biosynthetic process,biological_process_unknown,mitochondrion,terpenoid biosynthetic process,vacuolar membrane;biological_process_unknown,embryo development ending in seed dormancy,embryo sac egg cell differentiation,extracellular region,lipid storage,meristem structural organization,mitotic recombination,molecular_function_unknown,nucleus,photomorphogenesis,positive regulation of cellular process,protein ubiquitination,regulation of flower development,response to freezing,response to xenobiotic stimulus,seed dormancy process,seed germination,sugar mediated signaling pathway,vegetative to reproductive phase transition of meristem
PolyA_lnc-27	Chr1	+	4478102	4478762	2	4478102,4478696,	4478304,4478762,	N	238	electron carrier activity,electron carrier activity,heme binding,heme binding,iron ion binding,iron ion binding,oxidation-reduction process,oxidation-reduction process,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen,oxygen binding,pollen exine formation
PolyA_lnc-28	Chr1	+	6054738	6055141	2	6054738,6055084,	6054853,6055141,	N	239	ADP binding,cytoplasm,defense response,defense response,innate immune response,intracellular,negative regulation of defense response,salicylic acid biosynthetic process,salicylic acid mediated signaling pathway,signal transduction,systemic acquired resistance
PolyA_lnc-29	Chr1	+	6318139	6318801	1	6318139,	6318801,	Y	240	cell wall biogenesis,hydrolase activity
PolyA_lnc-30	Chr1	+	8076042	8076523	2	8076042,8076442,	8076121,8076523,	N	241	biological_process_unknown,cellular_component_unknown,mitochondrion,mitochondrion
PolyA_lnc-31	Chr1	+	8297622	8298659	2	8297622,8297884,	8297811,8298659,	N	242	determination of bilateral symmetry,DNA binding,DNA binding,DNA binding,fatty acid catabolic process,meristem initiation,meristem maintenance,meristem maintenance,nucleus,nucleus,nucleus,nucleus,organ development,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,sequence-specific DNA binding,sequence-specific DNA binding,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity
PolyA_lnc-32	Chr1	+	9189087	9189350	1	9189087,	9189350,	N	243	intracellular,nucleic acid binding,nucleus,regulation of transcription, DNA-dependent,sequence-specific DNA binding transcription factor activity,zinc ion binding,zinc ion binding
PolyA_lnc-33	Chr1	+	9831362	9832782	2	9831362,9832580,	9831467,9832782,	N	244	biological_process_unknown,chloroplast,chloroplast,molecular_function_unknown
PolyA_lnc-34	Chr1	-	10300231	10300951	1	10300231,	10300951,	N	245	biological_process_unknown,mitochondrion,molecular_function_unknowr
PolyA_lnc-35	Chr1	-	10328161	10329036	2	10328161,10328884,	10328285,10329036,	N	246	biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-36	Chr1	-	12194499	12194868	2	12194499,12194685,	12194599,12194868,	N	247	biological_process_unknown,molecular_function_unknown
PolyA_lnc-37	Chr1	-	12194962	12195591	2	12194962,12195565,	12195478,12195591,	N	248	biological_process_unknown,molecular_function_unknown
PolyA_lnc-38	Chr1	-	12194962	12195594	2	12194962,12195565,	12195466,12195594,	N	249	biological_process_unknown,molecular_function_unknown
PolyA_lnc-39	Chr1	-	12271087	12271679	2	12271087,12271646,	12271472,12271679,	Y	250	
PolyA_lnc-40	Chr1	-	12384761	12385228	2	12384761,12385195,	12384886,12385228,	N	251	
PolyA_lnc-41	Chr1	-	12923634	12923937	2	12923634,12923829,	12923746,12923937,	N	252	
PolyA_lnc-42	Chr1	-	1480039	1480839	2	1480039,1480754,	1480566,1480839,	N	253	biological_process_unknown,cellular_component_unknown,molecular_function_unknown
PolyA_lnc-43	Chr1	-	16153839	16154257	2	16153839,16154207,	16154133,16154257,	N	254	biological_process_unknown,biological_process_unknown,cellular_component_unknown,cellular_component_unknown,mitochondrion,mitochondrion,molecular_function_unknown,molecular_function_unknown
PolyA_lnc-44	Chr1	-	18074507	18075082	2	18074507,18074771,	18074571,18075082,	N	255	heterotrimeric G-protein complex,nucleus,protein phosphatase type 2A complex,protein phosphatase type 2A regulator activity,signal transducer activity,signal transduction,signal transduction
PolyA_lnc-45	Chr1	-	18080533	18081101	1	18080533,	18081101,	N	256	biological_process_unknown
PolyA_lnc-46	Chr1	-	1942756	1943357	1	1942756,	1943357,	N	257	
PolyA_lnc-47	Chr1	-	2055891	2056423	2	2055891,2056233,	2056148,2056423,	N	258	ATP binding,ATP binding,kinase activity,plasma membrane,plasma membrane,plasma membrane,plasma membrane,plasmodesma,protein kinase activity,protein kinase activity,protein kinase binding,protein phosphorylation,protein phosphorylation,protein tyrosine kinase activity,protein tyrosine kinase activity,transferase activity, transferring phosphorus-containing groups,transferase activity, transferring phosphorus-containing groups;mitochondrion
PolyA_lnc-48	Chr1	-	21616442	21617230	2	21616442,21617204,	21616795,21617230,	N	259	
PolyA_lnc-49	Chr1	-	21998363	21999596	1	21998363,	21999596,	N	260	ADP binding,cellular_component_unknown,defense response,defense response
PolyA_lnc-50	Chr1	-	22378782	22379831	3	22378782,22379047,22379444,	22378968,22379255,22379831,	N	261	
PolyA_lnc-51	Chr1	-	22693131	22693444	1	22693131,	22693444,	N	262	ATP binding,carbohydrate binding,carbohydrate binding,kinase activity,plasma membrane,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,protein tyrosine kinase activity,recognition of pollen,transferase activity, transferring phosphorus-containing groups

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-52	Chr1	-	22693131	22693736	2	22693131,22693482,	22693336,22693736,	N	263	ATP binding,carbohydrate binding,carbohydrate binding,kinase activity,plasma membrane,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,protein tyrosine kinase activity,recognition of pollen,transferase activity, transferring phosphorus-containing groups
PolyA_lnc-53	Chr1	-	22767492	22768328	2	22767492,22767968,	22767805,22768328,	N	264	biological_process_unknown,chloroplast,molecular_function_unknown
PolyA_lnc-54	Chr1	-	22767552	22768580	3	22767552,22767968,22768367,	22767805,22768085,22768580,	N	265	
PolyA_lnc-55	Chr1	-	23963610	23964339	2	23963610,23964154,	23963837,23964339,	Y	266	nucleus,sequence-specific DNA binding transcription factor activity
PolyA_lnc-56	Chr1	-	23963612	23964377	2	23963612,23964154,	23963852,23964377,	Y	267	nucleus,sequence-specific DNA binding transcription factor activity
PolyA_lnc-57	Chr1	-	24911994	24913005	1	24911994,	24913005,	N	268	antiporter activity,antiporter activity,drug transmembrane transport,drug transmembrane transporter activity,membrane,membrane,oligopeptide transport,plasma membrane,transmembrane transport,transporter activity
PolyA_lnc-58	Chr1	-	24911994	24913005	2	24911994,24912880,	24912543,24913005,	N	269	antiporter activity,antiporter activity,drug transmembrane transport,drug transmembrane transporter activity,membrane,membrane,oligopeptide transport,plasma membrane,transmembrane transport,transporter activity
PolyA_lnc-59	Chr1	-	2617431	2617731	1	2617431,	2617731,	N	270	biological_process_unknown,molecular_function_unknowr
PolyA_lnc-60	Chr1	-	28936248	28937277	2	28936248,28936828,	28936705,28937277,	N	271	
PolyA_lnc-61	Chr1	-	28936248	28937277	2	28936248,28936828,	28936726,28937277,	N	272	
PolyA_lnc-62	Chr1	-	29208757	29210196	3	29208757,29209864,29210029,	29208971,29209938,29210196,	N	273	biological_process_unknown,phosphatidylinositol biosynthetic process;ATP binding,cell-cell signaling,chromatin silencing,chromatin silencing by small RNA,cytokinesis by cell plate formation,DNA methylation,floral organ formation,gene silencing by RNA,histone H3-K9 methylation,histone modification,kinase activity,methylation-dependent chromatin silencing,microtubule cytoskeleton organization,nucleus,production of miRNAs involved in gene silencing by miRNA,production of ta-siRNAs involved in RNA interference,protein autophosphorylation,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,protein serine/threonine kinase activity,regulation of flower development,transferase activity, transferring phosphorus-containing groups,virus induced gene silencing
PolyA_lnc-63	Chr1	-	3352331	3352860	2	3352331,3352615,	3352363,3352860,	N	274	biological_process_unknown,mitochondrion,mitochondrion,molecular_function_unknown
PolyA_lnc-64	Chr1	-	913179	913722	3	913179,913350,913653,	913236,913531,913722,	N	275	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-65	Chr1	-	9726694	9727689	3	9726694,9727376,9727579,	9727027,9727488,9727689,	N	276	anaphase,biological_process_unknown,microtubule,microtubule cytoskeleton organization,molecular_function_unknown,phragmoplast,spindle
PolyA_lnc-66	Chr1	.	10127934	10128158	1	10127934,	10128158,	N	277	calcium ion binding;biological_process_unknown,cytoso
PolyA_lnc-67	Chr1	.	10228579	10228847	1	10228579,	10228847,	Y	278	
PolyA_lnc-68	Chr1	.	10229392	10229613	1	10229392,	10229613,	N	279	biological_process_unknown,chloroplast,molecular_function_unknowr
PolyA_lnc-69	Chr1	.	10283448	10283814	1	10283448,	10283814,	N	280	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus;biological_process_unknown,molecular_function_unknown,plasma membrane
PolyA_lnc-70	Chr1	.	11374317	11374635	1	11374317,	11374635,	Y	281	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus;ATPase activity,ATPase activity, coupled to transmembrane movement of substances,ATP binding,membrane,nucleoside-triphosphatase activity,nucleotide binding
lyA_lnc-71	Chr1	.	11378375	11378640	1	11378375,	11378640,	N	282	ATPase activity,ATPase activity, coupled to transmembrane movement of substances,ATP binding,membrane,nucleoside-triphosphatase activity,nucleotide binding;extracellular region
PolyA_lnc-72	Chr1	.	11453756	11455525	1	11453756,	11455525,	Y	283	
PolyA_lnc-73	Chr1	.	11472001	11472777	1	11472001,	11472777,	N	284	nucleus,plasma membrane
PolyA_lnc-74	Chr1	.	11473164	11473432	1	11473164,	11473432,	N	285	
PolyA_lnc-75	Chr1	.	11474341	11474636	1	11474341,	11474636,	N	286	
PolyA_lnc-76	Chr1	.	11475060	11475415	1	11475060,	11475415,	N	287	
PolyA_lnc-77	Chr1	.	11523631	11523833	1	11523631,	11523833,	N	288	
PolyA_lnc-78	Chr1	.	11685230	11685451	1	11685230,	11685451,	N	289	cellular biosynthetic process,chloroplast,magnesium ion binding,nucleoside metabolic process,nucleotide biosynthetic process,nucleotide biosynthetic process,ribonucleoside monophosphate biosynthetic process,ribose phosphate diphosphokinase activity,ribose phosphate diphosphokinase activity
PolyA_lnc-79	Chr1	.	11777702	11778033	1	11777702,	11778033,	N	290	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus,nucleus
PolyA_lnc-80	Chr1	.	11781477	11781795	1	11781477,	11781795,	N	291	
PolyA_lnc-81	Chr1	.	12055905	12056140	1	12055905,	12056140,	N	292	
PolyA_lnc-82	Chr1	.	12194754	12195248	1	12194754,	12195248,	N	293	biological_process_unknown,molecular_function_unknowr
PolyA_lnc-83	Chr1	.	12196629	12196897	1	12196629,	12196897,	N	294	
PolyA_lnc-84	Chr1	.	12196744	12196973	1	12196744,	12196973,	N	295	
PolyA_lnc-85	Chr1	.	12309755	12309992	1	12309755,	12309992,	N	296	
PolyA_lnc-86	Chr1	.	12380967	12381397	1	12380967,	12381397,	N	297	
PolyA_lnc-87	Chr1	.	12382746	12383014	1	12382746,	12383014,	N	298	
PolyA_lnc-88	Chr1	.	12382857	12383131	1	12382857,	12383131,	N	299	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-89	Chr1	.	12600170	12600627	1	12600170,	12600627,	N	300	cyclin-dependent protein kinase regulator activity,regulation of cell cycle
PolyA_lnc-90	Chr1	.	12923021	12923373	1	12923021,	12923373,	N	301	
PolyA_lnc-91	Chr1	.	12938917	12939252	1	12938917,	12939252,	N	302	
PolyA_lnc-92	Chr1	.	12995939	12996190	1	12995939,	12996190,	N	303	
PolyA_lnc-93	Chr1	.	13219603	13219820	1	13219603,	13219820,	N	304	
PolyA_lnc-94	Chr1	.	13281205	13282031	1	13281205,	13282031,	N	305	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus
PolyA_lnc-95	Chr1	.	1362382	1362639	1	1362382,	1362639,	N	306	cytoplasm,cytoplasm,intracellular,intracellular,RAB GTPase activator activity,RAB GTPase activator activity,regulation of Rab GTPase activity,regulation of Rab GTPase activity;biological_process_unknown,cellular_component_unknown,chloroplast,molecular_function_unknown
PolyA_lnc-96	Chr1	.	1418552	1418788	1	1418552,	1418788,	N	307	biological_process_unknown,mitochondrion,molecular_function_unknown;biological_process_unknown,circadian rhythm,nucleic acid binding,nucleic acid binding,nucleic acid binding,nucleus,nucleus,zinc ion binding,zinc ion binding
PolyA_lnc-97	Chr1	.	15926232	15926471	1	15926232,	15926471,	N	308	hedgehog receptor activity,hedgehog receptor activity,integral to membrane,membrane,membrane,plasma membrane,plasmodesma
PolyA_lnc-98	Chr1	.	15944294	15944521	1	15944294,	15944521,	N	309	
PolyA_lnc-99	Chr1	.	16131722	16131963	1	16131722,	16131963,	N	310	
PolyA_lnc-100	Chr1	.	16154630	16154865	1	16154630,	16154865,	N	311	biological_process_unknown,biological_process_unknown,cellular_component_unknown,cellular_component_unknown,mitochondrion,mitochondrion,molecular_function_unknown,molecular_function_unknown;biological_process_unknown,cellular_component_unknown,chloroplast,chloroplast,molecular_function_unknown,root hair cell differentiation
PolyA_lnc-101	Chr1	.	16416571	16416783	1	16416571,	16416783,	N	312	mitochondrion,nucleus,phosphoprotein phosphatase activity
PolyA_lnc-102	Chr1	.	16417415	16417796	1	16417415,	16417796,	N	313	
PolyA_lnc-103	Chr1	.	1728964	1730039	1	1728964,	1730039,	N	314	biological_process_unknown,chloroplast,molecular_function_unknown;cellular_component_unknown,molecular_function_unknown,plasma membrane,plasma membrane,vesicle-mediated transport,vesicle-mediated transport,vesicle-mediated transport
PolyA_lnc-104	Chr1	.	17292412	17292991	1	17292412,	17292991,	Y	315	
PolyA_lnc-105	Chr1	.	17295541	17296304	1	17295541,	17296304,	N	316	
PolyA_lnc-106	Chr1	.	17464514	17464899	1	17464514,	17464899,	N	317	biological_process_unknown,exocyst,plasma membrane,plasma membrane
PolyA_lnc-107	Chr1	.	17464691	17465010	1	17464691,	17465010,	N	318	biological_process_unknown,exocyst,plasma membrane,plasma membrane
PolyA_lnc-108	Chr1	.	17477535	17478545	1	17477535,	17478545,	N	319	
PolyA_lnc-109	Chr1	.	17498995	17499498	1	17498995,	17499498,	Y	320	
PolyA_lnc-110	Chr1	.	17573616	17574173	1	17573616,	17574173,	Y	321	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-111	Chr1	.	17895815	17896388	1	17895815,	17896388,	N	322	1-aminocyclopropane-1-carboxylate deaminase activity,catalytic activity,chloroplast,chloroplast,cobalt ion binding,cytosol,D-cysteine catabolic process,D-cysteine desulfhydrase activity,D-cysteine desulfhydrase activity,ethylene biosynthetic process,gluconeogenesis,glucosinolate biosynthetic process,glycolysis,hydrogen peroxide catabolic process,isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway,mitochondrion,regulation of protein localization,response to cadmium ion,response to cadmium ion,response to salt stress
PolyA_lnc-112	Chr1	.	18207628	18207862	1	18207628,	18207862,	N	323	zinc ion binding,zinc ion binding
PolyA_lnc-113	Chr1	.	18486508	18486776	1	18486508,	18486776,	N	324	biological_process_unknown,cellular_component_unknown,chloroplast,molecular_function_unknown;biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown
PolyA_lnc-114	Chr1	.	18486855	18487090	1	18486855,	18487090,	Y	325	biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown
PolyA_lnc-115	Chr1	.	18491621	18492045	1	18491621,	18492045,	N	326	biological_process_unknown,chloroplast,molecular_function_unknowr
PolyA_lnc-116	Chr1	.	1866633	1866999	1	1866633,	1866999,	N	327	mitochondrial mRNA modification,mitochondrion,molecular_function_unknown;chloroplast,nucleus,sequence-specific DNA binding transcription factor activity
PolyA_lnc-117	Chr1	.	18884604	18884853	1	18884604,	18884853,	N	328	cell redox homeostasis
PolyA_lnc-118	Chr1	.	20000389	20000780	1	20000389,	20000780,	N	329	chloroplast,plasma membrane,vacuole;biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown
PolyA_lnc-119	Chr1	.	20006497	20006992	1	20006497,	20006992,	Y	330	
PolyA_lnc-120	Chr1	.	20007884	20008195	1	20007884,	20008195,	N	331	biological_process_unknown,molecular_function_unknowr
PolyA_lnc-121	Chr1	.	20010631	20010834	1	20010631,	20010834,	N	332	cellular response to hypoxia,molecular_function_unknowr
PolyA_lnc-122	Chr1	.	20093441	20093844	1	20093441,	20093844,	N	333	
PolyA_lnc-123	Chr1	.	20367096	20367329	1	20367096,	20367329,	N	334	
PolyA_lnc-124	Chr1	.	20592761	20593012	1	20592761,	20593012,	N	335	ATP binding,kinase activity,nucleus,plasma membrane,protein kinase activity,protein phosphorylation,protein tyrosine kinase activity,transferase activity, transferring phosphorus-containing groups
PolyA_lnc-125	Chr1	.	20910540	20910774	1	20910540,	20910774,	N	336	biological_process_unknown,intracellular,nucleus,zinc ion binding
PolyA_lnc-126	Chr1	.	20910652	20910853	1	20910652,	20910853,	N	337	
PolyA_lnc-127	Chr1	.	21052298	21052620	1	21052298,	21052620,	N	338	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-128	Chr1	.	2107495	2107753	1	2107495,	2107753,	N	339	DNA binding,nucleus,nucleus,protein dimerization activity,protein dimerization activity,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,sequence-specific DNA binding,sequence-specific DNA binding,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity;chloroplast,integral to membrane,membrane,membrane,peptidase activity,proteolysis,proteolysis,serine-type peptidase activity
PolyA_lnc-129	Chr1	.	21309260	21309592	1	21309260,	21309592,	N	340	biological_process_unknown,cellular_component_unknown,methionine biosynthetic process,mitochondrion,mitochondrion,mitochondrion,molecular_function_unknown,phosphatidylinositol biosynthetic process,RNA splicing, via endonucleolytic cleavage and ligation
PolyA_lnc-130	Chr1	.	21376360	21376797	1	21376360,	21376797,	N	341	cell wall,cell wall,copper ion binding,copper ion binding,cytosol,cytosol,eukaryotic translation elongation factor 1 complex,eukaryotic translation elongation factor 1 complex,membrane,membrane,plasma membrane,plasma membrane,plasmodesma,response to cadmium ion,response to cadmium ion,response to zinc ion,translational elongation,translational elongation,translation elongation factor activity,translation elongation factor activity,translation elongation factor activity,translation elongation factor activity,vacuole,vacuole
PolyA_lnc-131	Chr1	.	21523044	21523322	1	21523044,	21523322,	N	342	pollen tube growth;mitochondrion
PolyA_lnc-132	Chr1	.	21614516	21614796	1	21614516,	21614796,	N	343	biological_process_unknown,cytoplasm,molecular_function_unknown,plasmodesma
PolyA_lnc-133	Chr1	.	21998292	21999353	1	21998292,	21999353,	N	344	ADP binding,cellular_component_unknown,defense response,defense response
PolyA_lnc-134	Chr1	.	22076696	22077110	1	22076696,	22077110,	N	345	
PolyA_lnc-135	Chr1	.	22086545	22086761	1	22086545,	22086761,	N	346	
PolyA_lnc-136	Chr1	.	22087914	22088114	1	22087914,	22088114,	N	347	
PolyA_lnc-137	Chr1	.	22206232	22206453	1	22206232,	22206453,	N	348	
PolyA_lnc-138	Chr1	.	22298858	22299169	1	22298858,	22299169,	N	349	cellular_component_unknown,cytoplasm,GTPase activity,GTP binding,GTP binding
PolyA_lnc-139	Chr1	.	22556386	22556585	1	22556386,	22556585,	N	350	
PolyA_lnc-140	Chr1	.	22557225	22557424	1	22557225,	22557424,	N	351	ADP binding,cellular_component_unknown,defense response,defense response,N-terminal protein myristoylation

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-141	Chr1	.	22604152	22604482	1	22604152,	22604482,	N	352	biological_process_unknown,cellular_component_unknown,chloroplast,molecular_function_unknown;cellular membrane fusion,cellular membrane fusion,intracellular protein transport,intracellular protein transport,membrane,plasma membrane,plasma membrane,pollen tube growth,SNAP receptor activity,SNAP receptor activity,transport vesicle,vesicle-mediated transport
PolyA_lnc-142	Chr1	.	22611275	22611531	1	22611275,	22611531,	N	353	
PolyA_lnc-143	Chr1	.	22689226	22689575	1	22689226,	22689575,	N	354	ATP binding,carbohydrate binding,carbohydrate binding,kinase activity,plasma membrane,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,recognition of pollen,transferase activity, transferring phosphorus-containing groups;ATP binding,carbohydrate binding,carbohydrate binding,kinase activity,plasma membrane,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,protein tyrosine kinase activity,recognition of pollen,transferase activity, transferring phosphorus-containing groups
PolyA_lnc-144	Chr1	.	22842812	22843019	1	22842812,	22843019,	N	355	
PolyA_lnc-145	Chr1	.	23034536	23035524	1	23034536,	23035524,	N	356	nucleus,regulation of transcription, DNA-dependent,sequence-specific DNA binding transcription factor activity,zinc ion binding
PolyA_lnc-146	Chr1	.	23089824	23090079	1	23089824,	23090079,	N	357	ATP binding,kinase activity,kinase activity,nucleus,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,protein serine/threonine/tyrosine kinase activity,protein tyrosine kinase activity,regulation of stomatal movement,transferase activity, transferring phosphorus-containing groups
PolyA_lnc-147	Chr1	.	23089901	23090190	1	23089901,	23090190,	N	358	ATP binding,kinase activity,kinase activity,nucleus,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,protein serine/threonine/tyrosine kinase activity,protein tyrosine kinase activity,regulation of stomatal movement,transferase activity, transferring phosphorus-containing groups
PolyA_lnc-148	Chr1	.	23280566	23281262	1	23280566,	23281262,	N	359	
PolyA_lnc-149	Chr1	.	23281239	23281461	1	23281239,	23281461,	N	360	
PolyA_lnc-150	Chr1	.	23344304	23344883	1	23344304,	23344883,	Y	361	apoplast,cytosol,dTDP-4-dehydrorhamnose 3,5-epimerase activity,dTDP-4-dehydrorhamnose reductase activity,dTDP-4-dehydrorhamnose reductase activity,dTDP-rhamnose biosynthetic process,extracellular polysaccharide biosynthetic process,nucleotide binding,plasma membrane,plasmodesma,UDP-4-keto-6-deoxy-glucose-3,5-epimerase activity,UDP-4-keto-rhamnose-4-keto-reductase activity,UDP-rhamnose biosynthetic process
PolyA_lnc-151	Chr1	.	23459214	23459701	1	23459214,	23459701,	N	362	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus;apoplast,mitochondrion,receptor binding,signal transduction

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-152	Chr1	.	23701073	23701317	1	23701073,	23701317,	N	363	biological_process_unknown,cellular_component_unknown,molecular_function_unknown;ADP binding,ADP binding,chloroplast,defense response,defense response,intracellular,intracellular,signal transduction,signal transduction
PolyA_lnc-153	Chr1	.	2407522	2408135	1	2407522,	2408135,	Y	364	cell wall,cell wall,chloroplast,chloroplast,cytosol,cytosol,cytosolic ribosome,cytosolic ribosome,cytosolic ribosome,cytosolic ribosome,cytosolic ribosome,cytosolic small ribosomal subunit,intracellular,intracellular,membrane,membrane,plasma membrane,plasma membrane,plasmodesma,ribosome,ribosome,structural constituent of ribosome,structural constituent of ribosome,structural constituent of ribosome,translation,translation,translation,vacuolar membrane,vacuolar membrane
PolyA_lnc-154	Chr1	.	24542371	24542650	1	24542371,	24542650,	N	365	apoplast,chloroplast,chloroplast stroma,copper ion binding,cytosol,cytosol,defense response to bacterium,gluconeogenesis,glycolysis,Golgi organization,hyperosmotic response,isocitrate dehydrogenase (NADP+) activity,isocitrate dehydrogenase (NADP+) activity,isocitrate dehydrogenase (NADP+) activity,isocitrate metabolic process,isocitrate metabolic process,magnesium ion binding,metabolic process,NAD binding,NADP metabolic process,oxidation-reduction process,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor,photorespiration,plasma membrane,plasmodesma,proteasome core complex assembly,regulation of transport,response to cadmium ion,response to cadmium ion,response to misfolded protein,response to osmotic stress,response to salt stress,response to salt stress,response to temperature stimulus,response to zinc ion,ubiquitin-dependent protein catabolic process,water transport
PolyA_lnc-155	Chr1	.	25306100	25306332	1	25306100,	25306332,	N	366	ATP binding,carbohydrate binding,carbohydrate binding,kinase activity,plasma membrane,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,protein tyrosine kinase activity,transferase activity, transferring phosphorus-containing groups
PolyA_lnc-156	Chr1	.	25424528	25424857	1	25424528,	25424857,	N	367	
PolyA_lnc-157	Chr1	.	25424914	25425182	1	25424914,	25425182,	Y	368	
PolyA_lnc-158	Chr1	.	25893186	25893480	1	25893186,	25893480,	N	369	biological_process_unknown,extracellular region,molecular_function_unknown,pollen exine formation;cellular response to iron ion starvation,DNA binding,iron ion transport,nitrate transport,nucleus,protein dimerization activity,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,response to nitrate,sequence-specific DNA binding,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-159	Chr1	.	26637325	26637773	1	26637325,	26637773,	Y	370	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus;acid-amino acid ligase activity,intracellular,intracellular,mitochondrion,mitochondrion,zinc ion binding,zinc ion binding
PolyA_lnc-160	Chr1	.	26642874	26643122	1	26642874,	26643122,	N	371	acid-amino acid ligase activity,intracellular,intracellular,mitochondrion,mitochondrion,zinc ion binding,zinc ion binding;acid-amino acid ligase activity,acid-amino acid ligase activity,nucleus,nucleus,photoperiodism, flowering,postreplication repair,postreplication repair,protein binding,protein binding,UBC13-MMS2 complex,ubiquitin-dependent protein catabolic process,ubiquitin-protein ligase activity,ubiquitin-protein ligase activity
PolyA_lnc-161	Chr1	.	26794439	26794716	1	26794439,	26794716,	N	372	anthocyanin-containing compound biosynthetic process,anthocyanin-containing compound biosynthetic process,DNA binding,DNA binding,nucleus,proanthocyanidin biosynthetic process,regulation of transcription, DNA-dependent,response to abscisic acid stimulus,response to cadmium ion,response to ethylene stimulus,response to gibberellin stimulus,response to high light intensity,response to jasmonic acid stimulus,response to salicylic acid stimulus,response to salt stress,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity
PolyA_lnc-162	Chr1	.	27483989	27484230	1	27483989,	27484230,	N	373	biological_process_unknown,plasma membrane;abscisic acid mediated signaling pathway,ATP binding,ATP binding,defense response by callose deposition,guanylate cyclase activity,immune response,innate immune response,intracellular signal transduction,kinase activity,peptide receptor activity,plasma membrane,plasma membrane,plasma membrane,plasmodesma,protein binding,protein binding,protein kinase activity,protein phosphorylation,protein phosphorylation,protein serine/threonine kinase activity,protein serine/threonine kinase activity,response to ethylene stimulus,response to jasmonic acid stimulus,response to wounding,transferase activity, transferring phosphorus-containing groups,transmembrane receptor protein tyrosine kinase signaling pathway

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-163	Chr1	.	28046451	28046779	1	28046451,	28046779,	N	374	brassinosteroid biosynthetic process,cytokinin mediated signaling pathway,DNA binding,DNA binding,multicellular organismal development,negative regulation of DNA binding,negative regulation of transcription, DNA-dependent,nucleus,photomorphogenesis,regulation of meristem development,response to abscisic acid stimulus,response to auxin stimulus,response to auxin stimulus,response to brassinosteroid stimulus,response to brassinosteroid stimulus,response to cyclopentenone,response to cytokinin stimulus,response to gibberellin stimulus,sequence-specific DNA binding transcription factor activity
PolyA_lnc-164	Chr1	.	28085971	28086484	1	28085971,	28086484,	N	375	chloroplast
PolyA_lnc-165	Chr1	.	28115346	28115614	1	28115346,	28115614,	N	376	biological_process_unknown,Golgi apparatus,molecular_function_unknown;DNA binding,DNA binding,DNA binding,nucleus,nucleus,positive regulation of flavonoid biosynthetic process,protein targeting to membrane,regulation of plant-type hypersensitive response,regulation of transcription, DNA-dependent,response to abscisic acid stimulus,response to auxin stimulus,response to cadmium ion,response to ethylene stimulus,response to gibberellin stimulus,response to jasmonic acid stimulus,response to salicylic acid stimulus,response to salt stress,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity
PolyA_lnc-166	Chr1	.	28199423	28199878	1	28199423,	28199878,	N	377	endoplasmic reticulum,root hair cell development;electron carrier activity,heme binding,iron ion binding,oxidation-reduction process,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen,oxygen binding
PolyA_lnc-167	Chr1	.	28420302	28420789	1	28420302,	28420789,	Y	378	
PolyA_lnc-168	Chr1	.	2864566	2864810	1	2864566,	2864810,	N	379	
PolyA_lnc-169	Chr1	.	28787946	28788323	1	28787946,	28788323,	N	380	biological_process_unknown,calmodulin binding,cellular_component_unknown,mitochondrion
PolyA_lnc-170	Chr1	.	28837180	28837439	1	28837180,	28837439,	N	381	cytoplasm,GTPase activity,GTP binding,plasma membrane,translation factor activity, nucleic acid binding;cellular_component_unknown,cytoplasm,GTPase activity,GTP binding
PolyA_lnc-171	Chr1	.	28884692	28884965	1	28884692,	28884965,	N	382	nucleus,nucleus,phosphoric diester hydrolase activity,positive regulation of transcription, DNA-dependent,post-translational protein modification,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity
PolyA_lnc-172	Chr1	.	29208305	29208651	1	29208305,	29208651,	N	383	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-173	Chr1	.	29344694	29345177	1	29344694,	29345177,	Y	384	biological_process_unknown,cellular_component_unknown,molecular_function_unknown;acetate fermentation,aerobic glycerol catabolic process,cysteine biosynthetic process,extracellular region,extracellular region,gluconeogenesis,glucose catabolic process to butanediol,glucose catabolic process to D-lactate and ethanol,glucose catabolic process to lactate and acetate,glyceraldehyde-3-phosphate catabolic process,glycolysis,molecular_function_unknown,serine-isocitrate lyase pathway
PolyA_lnc-174	Chr1	.	29427960	29428227	1	29427960,	29428227,	N	385	cellular_component_unknown,cytoplasm,protein domain specific binding,protein phosphorylated amino acid binding
PolyA_lnc-175	Chr1	.	29527363	29527613	1	29527363,	29527613,	N	386	
PolyA_lnc-176	Chr1	.	29527810	29528109	1	29527810,	29528109,	N	387	electron carrier activity,heme binding,iron ion binding,oxidation-reduction process,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen,oxygen binding
PolyA_lnc-177	Chr1	.	29630919	29631220	1	29630919,	29631220,	Y	388	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus,nucleus;biological_process_unknown,cytokinin biosynthetic process,molecular_function_unknown,nucleus
lyA_lnc-178	Chr1	.	29631316	29631694	1	29631316,	29631694,	N	389	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus,nucleus;biological_process_unknown,cytokinin biosynthetic process,molecular_function_unknown,nucleus
PolyA_lnc-179	Chr1	.	29741089	29741323	1	29741089,	29741323,	N	390	ATP binding,ATP binding,cytokinin biosynthetic process,DNA binding,DNA binding,DNA binding,DNA-dependent ATPase activity,DNA-dependent ATPase activity,DNA-dependent ATPase activity,DNA recombination,DNA repair,nucleoside-triphosphatase activity,nucleoside triphosphatase activity,nucleotide binding,nucleotide binding,reciprocal meiotic recombination,response to DNA damage stimulus,single-stranded DNA binding,single-stranded DNA binding,SOS response;biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus
PolyA_lnc-180	Chr1	.	29840950	29841231	1	29840950,	29841231,	N	391	
PolyA_lnc-181	Chr1	.	29841476	29842122	1	29841476,	29842122,	N	392	
PolyA_lnc-182	Chr1	.	30115520	30115781	1	30115520,	30115781,	Y	393	cellular_component_unknown,molecular_function_unknown,nucleus
PolyA_lnc-183	Chr1	.	30394689	30394954	1	30394689,	30394954,	N	394	ATP binding,kinase activity,plasma membrane,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,transferase activity, transferring phosphorus-containing groups;biological_process_unknown,mitochondrion

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-184	Chr1	.	310068	310288	1	310068,	310288,	N	395	catalytic activity,catalytic activity,cellular_component_unknown,DNA binding,DNA binding,DNA repair,DNA repair,DNA repair,nuclease activity,nuclease activity,nuclease activity,nucleus,nucleus;apoplast,cell wall,extracellular matrix,extracellular region,identical protein binding,negative regulation of catalytic activity,proteolysis,proteolysis,serine-type endopeptidase activity,serine-type endopeptidase activity
PolyA_lnc-185	Chr1	.	3108003	3108377	1	3108003,	3108377,	Y	396	chloroplast,cytoplasm,cytosolic large ribosomal subunit,cytosolic ribosome,cytosolic ribosome,intracellular,nucleolus,ribosome,ribosome,structural constituent of ribosome,structural constituent of ribosome,translation,translation;ATP binding,epidermal cell fate specification,kinase activity,N-terminal protein myristoylation,nucleus,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,protein tyrosine kinase activity,transferase activity, transferring phosphorus-containing groups
PolyA_lnc-186	Chr1	.	3296916	3297220	1	3296916,	3297220,	N	397	biological_process_unknown,extracellular region,membrane,molecular_function_unknown;cellular_component_unknown,nucleus,protein prenylation,protein prenyltransferase activity
PolyA_lnc-187	Chr1	.	3441461	3441662	1	3441461,	3441662,	N	398	circadian rhythm,circadian rhythm,cytokinin mediated signaling pathway,cytokinin mediated signaling pathway,cytokinin mediated signaling pathway,cytoplasm,cytoplasm,embryo development ending in seed dormancy,nucleus,nucleus,nucleus,positive regulation of flavonoid biosynthetic process,protein autophosphorylation,protein binding,protein binding,protein binding,protein binding,protein serine/threonine kinase activity,protein targeting to membrane,red or far-red light signaling pathway,regulation of circadian rhythm,regulation of plant-type hypersensitive response,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,response to cytokinin stimulus,response to cytokinin stimulus,response to red light,response to stress,two-component response regulator activity,two-component response regulator activity,two-component response regulator activity,two-component response regulator activity,two-component signal transduction system (phosphorelay)
PolyA_lnc-188	Chr1	.	3937144	3937429	1	3937144,	3937429,	N	399	
PolyA_lnc-189	Chr1	.	4061416	4062087	1	4061416,	4062087,	N	400	biological_process_unknown,molecular_function_unknowr
PolyA_lnc-190	Chr1	.	4481564	4481843	1	4481564,	4481843,	N	401	electron carrier activity,heme binding,iron ion binding,oxidation-reduction process,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen,oxygen binding

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-191	Chr1	.	471067	471566	1	471067,	471566,	N	402	mitochondrion,molecular_function_unknown,siroheme biosynthetic process;amino acid transport,carbohydrate metabolic process,cell wall macromolecule catabolic process,chitinase activity,chitinase activity,defense response to fungus,extracellular region,nitrate transport,respiratory burst involved in defense response,response to chitin,response to nitrate
PolyA_lnc-192	Chr1	.	4842461	4842863	1	4842461,	4842863,	N	403	biological_process_unknown,cellular_component_unknown,molecular_function_unknown;cellular_component_unknown,nucleic acid binding,nucleus,nucleus,nucleus,response to abscisic acid stimulus,RNA binding,RNA binding,RNA binding
PolyA_lnc-193	Chr1	.	5192073	5192620	1	5192073,	5192620,	N	404	positive regulation of abscisic acid mediated signaling pathway,protein binding,protein binding,protein ubiquitination,regulation of response to osmotic stress,response to salt stress,ubiquitin-protein ligase activity,ubiquitin-protein ligase activity,zinc ion binding,zinc ion binding
PolyA_lnc-194	Chr1	.	5895830	5896046	1	5895830,	5896046,	N	405	ATP binding,extracellular region,protein kinase activity,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,protein tyrosine kinase activity,response to molecule of bacterial origin,signal transduction,stamen development,stomatal complex morphogenesis,transferase activity, transferring phosphorus-containing groups;cellular_component_unknown,mitochondrion,molecular_function_unknown,regulation of cell proliferation;plasma membrane,protein kinase activity,signal transduction
PolyA_lnc-195	Chr1	.	6271722	6272146	1	6271722,	6272146,	N	406	
PolyA_lnc-196	Chr1	.	641470	642063	1	641470,	642063,	N	407	ATP binding,ATP binding,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,cytoplasm,cytosol,thiamine diphosphate biosynthetic process,thiamine diphosphate biosynthetic process,thiamine diphosphate biosynthetic process,thiamine diphosphate biosynthetic process,thiamine diphosphokinase activity,thiamine diphosphokinase activity,thiamine diphosphokinase activity,thiamine diphosphokinase activity,thiamine diphosphokinase activity,thiamine diphosphokinase activity,thiamine metabolic process,thiamine metabolic process,thiamine metabolic process,thiamine metabolic process,thiamine metabolic process,thiamine metabolic process

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-197	Chr1	.	6460016	6460225	1	6460016,	6460225,	N	408	biological_process_unknown,chloroplast,molecular_function_unknown;cellular cation homeostasis,chlorophyll biosynthetic process,chloroplast,chloroplast,chloroplast,chloroplast,chloroplast,chloroplast thylakoid membrane,chloroplast thylakoid membrane,divalent metal ion transport,maltose metabolic process,molecular_function_unknown,NAD(P)H dehydrogenase complex (plastoquinone),pentose-phosphate shunt,photorespiration,photosynthesis,photosynthesis, light reaction,photosynthetic electron transport in photosystem I,rRNA processing,starch biosynthetic process
PolyA_lnc-198	Chr1	.	6460104	6460351	1	6460104,	6460351,	N	409	biological_process_unknown,chloroplast,molecular_function_unknown;cellular cation homeostasis,chlorophyll biosynthetic process,chloroplast,chloroplast,chloroplast,chloroplast,chloroplast,chloroplast thylakoid membrane,chloroplast thylakoid membrane,divalent metal ion transport,maltose metabolic process,molecular_function_unknown,NAD(P)H dehydrogenase complex (plastoquinone),pentose-phosphate shunt,photorespiration,photosynthesis,photosynthesis, light reaction,photosynthetic electron transport in photosystem I,rRNA processing,starch biosynthetic process
PolyA_lnc-199	Chr1	.	6499737	6500138	1	6499737,	6500138,	N	410	biological_process_unknown,calmodulin binding,vacuole,vacuole
PolyA_lnc-200	Chr1	.	6718600	6718907	1	6718600,	6718907,	N	411	
PolyA_lnc-201	Chr1	.	6771976	6772482	1	6771976,	6772482,	N	412	apoplast,apoplast,chloroplast,chloroplast,chloroplast stroma,copper ion binding,cytoplasm,cytoplasm,cytosol,cytosol,glutathione dehydrogenase (ascorbate) activity,glutathione dehydrogenase (ascorbate) activity,mitochondrion,peroxisome,plasma membrane,plasma membrane,protein glutathionylation,regulation of symbiosis, encompassing mutualism through parasitism,response to jasmonic acid stimulus,response to ozone,response to symbiotic fungus,response to zinc ion,vacuole

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-202	Chr1	.	6941877	6942120	1	6941877,	6942120,	N	413	apoplast,apoplast,apoplast,chloroplast,chloroplast,chloroplast,chloroplast,chloroplast,chloroplast,chloroplast,chloroplast stroma,chloroplast stroma,chloroplast stroma,chloroplast stroma,chloroplast thylakoid,chloroplast thylakoid membrane,chloroplast thylakoid membrane,chloroplast thylakoid membrane,chloroplast thylakoid membrane,defense response, incompatible interaction,defense response to bacterium,defense response to bacterium,defense response to bacterium,defense response to bacterium,defense response to fungus,defense response to fungus, incompatible interaction,detection of biotic stimulus,ferredoxin-NADP+ reductase activity,ferredoxin-NADP+ reductase activity,ferredoxin-NADP+ reductase activity,flavin adenine dinucleotide binding,flavin adenine dinucleotide binding,flavin adenine dinucleotide binding,glucosinolate biosynthetic process,jasmonic acid mediated signaling pathway,MAPK cascade,NADP binding,NADP binding,NADP binding,NADPH dehydrogenase activity,negative regulation of defense response,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity,pentose-phosphate shunt,photorespiration,photosynthesis,photosynthesis, light reaction,photosynthetic electron transport in photosystem I,photosystem II assembly,plastid organization,poly(U) RNA binding,protein targeting to membrane,regulation of hydrogen peroxide metabolic process,regulation of multi-organism process,regulation of plant-type hypersensitive response,regulation of response to biotic stimulus,response to chitin,response to cold,rRNA processing,salicylic acid biosynthetic process,stomatal complex morphogenesis,systemic acquired resistance, salicylic acid mediated signaling pathway,thylakoid,thylakoid,thylakoid
PolyA_lnc-203	Chr1	.	7461534	7461898	1	7461534,	7461898,	Y	414	biological_process_unknown,cellular_component_unknown,nucleic acid binding,nucleic acid binding,nucleotide binding,nucleotide binding,nucleus,nucleus
PolyA_lnc-204	Chr1	.	7462080	7462299	1	7462080,	7462299,	N	415	biological_process_unknown,cellular_component_unknown,nucleic acid binding,nucleic acid binding,nucleotide binding,nucleotide binding,nucleus,nucleus
PolyA_lnc-205	Chr1	.	7765916	7766238	1	7765916,	7766238,	N	416	
PolyA_lnc-206	Chr1	.	82212	82426	1	82212,	82426,	N	417	electron carrier activity,heme binding,iron ion binding,oxidation-reduction process,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen,oxygen binding
PolyA_lnc-207	Chr1	.	889804	890020	1	889804,	890020,	N	418	biological_process_unknown,mitochondrion

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-208	Chr1	.	8910205	8910607	1	8910205,	8910607,	N	419	biological_process_unknown,jasmonic acid mediated signaling pathway,molecular_function_unknown,negative regulation of defense response,nucleus,nucleus,protein targeting to membrane,regulation of plant-type hypersensitive response,response to chitin,response to insect,salicylic acid mediated signaling pathway,systemic acquired resistance, salicylic acid mediated signaling pathway
PolyA_lnc-209	Chr1	.	9031713	9031982	1	9031713,	9031982,	Y	420	carboxylesterase activity,chloroplast,endoplasmic reticulum membrane,Golgi membrane,hydrolase activity,metabolic process,metabolic process
PolyA_lnc-210	Chr1	.	9069655	9069862	1	9069655,	9069862,	N	421	
PolyA_lnc-211	Chr1	.	9070786	9071025	1	9070786,	9071025,	N	422	chloroplast,metabolic process,N-acetyltransferase activity,N-acetyltransferase activity,photosynthesis, light reaction
PolyA_lnc-212	Chr1	.	9335309	9335551	1	9335309,	9335551,	N	423	
PolyA_lnc-213	Chr2	+	10494730	10495179	1	10494730,	10495179,	Y	424	cellular_component_unknown,DNA binding,DNA binding,DNA binding,nucleus,nucleus,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,sequence-specific DNA binding transcription factor activity
PolyA_lnc-214	Chr2	+	12366531	12366741	1	12366531,	12366741,	N	425	defense response to bacterium,DNA-dependent transcription, elongation,intracellular,kinesin binding,kinesin complex,nucleus,protein ubiquitination,response to chitin,ribosome,rRNA binding,structural constituent of ribosome,translation,ubiquitin ligase complex,ubiquitin-protein ligase activity,ubiquitin-protein ligase activity
PolyA_lnc-215	Chr2	+	13105864	13106117	1	13105864,	13106117,	N	426	biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown
PolyA_lnc-216	Chr2	+	14248493	14249333	3	14248493,14248747,14249223,	14248574,14248797,14249333,	N	427	calmodulin binding,cell death,cell death,defense response,integral to membrane,plant-type cell wall modification,plasma membrane,pollen tube growth;biological_process_unknown,cellular_component_unknown
PolyA_lnc-217	Chr2	+	14248493	14249421	4	14248493,14248747,14249223,14249385,	14248574,14248797,14249297,14249421,	N	428	calmodulin binding,cell death,cell death,defense response,integral to membrane,plant-type cell wall modification,plasma membrane,pollen tube growth;biological_process_unknown,cellular_component_unknown
PolyA_lnc-218	Chr2	+	15402978	15403566	1	15402978,	15403566,	Y	429	
PolyA_lnc-219	Chr2	+	19200859	19202819	2	19200859,19201943,	19201612,19202819,	N	430	
PolyA_lnc-220	Chr2	+	19235431	19237330	2	19235431,19237292,	19235659,19237330,	N	431	
PolyA_lnc-221	Chr2	+	2214381	2214722	1	2214381,	2214722,	Y	432	cellular_component_unknown
PolyA_lnc-222	Chr2	+	2360420	2360706	1	2360420,	2360706,	Y	433	
PolyA_lnc-223	Chr2	+	4485494	4486208	2	4485494,4486160,	4485570,4486208,	N	434	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-224	Chr2	+	4486187	4487577	2	4486187,4486366,	4486252,4487577,	N	435	
PolyA_lnc-225	Chr2	+	4871323	4871813	2	4871323,4871652,	4871501,4871813,	Y	436	
PolyA_lnc-226	Chr2	+	4871658	4871915	1	4871658,	4871915,	Y	437	
PolyA_lnc-227	Chr2	+	565050	566158	2	565050,565540,	565157,566158,	N	438	
PolyA_lnc-228	Chr2	+	5864099	5864801	2	5864099,5864256,	5864175,5864801,	N	439	
PolyA_lnc-229	Chr2	+	635056	636638	2	635056,635455,	635225,636638,	N	440	
PolyA_lnc-230	Chr2	+	635452	636638	2	635452,635877,	635629,636638,	N	441	
PolyA_lnc-231	Chr2	+	7632579	7633026	1	7632579,	7633026,	N	442	biological_process_unknown,molecular_function_unknowr
PolyA_lnc-232	Chr2	+	7632579	7633703	2	7632579,7633401,	7633010,7633703,	N	443	biological_process_unknown,molecular_function_unknown;biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus,nucleus
PolyA_lnc-233	Chr2	+	8352653	8355923	2	8352653,8353851,	8353770,8355923,	N	444	
PolyA_lnc-234	Chr2	+	8352653	8355923	5	8352653,8353640,8354065,8354712,8355230,	8353352,8353954,8354324,8354846,8355923,	N	445	
PolyA_lnc-235	Chr2	+	8352685	8355924	3	8352685,8354695,8355230,	8354324,8354846,8355924,	N	446	
PolyA_lnc-236	Chr2	+	8352685	8355924	4	8352685,8353640,8353851,8354720,	8353352,8353770,8354324,8355924,	N	447	
PolyA_lnc-237	Chr2	+	9024703	9024954	2	9024703,9024887,	9024781,9024954,	Y	448	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus
PolyA_lnc-238	Chr2	+	9213462	9214282	2	9213462,9214035,	9213798,9214282,	N	449	cytoplasm,heat shock protein binding,protein folding,protein folding,unfolded protein binding
PolyA_lnc-239	Chr2	+	9213969	9214282	1	9213969,	9214282,	N	450	cytoplasm,heat shock protein binding,protein folding,protein folding,unfolded protein binding
PolyA_lnc-240	Chr2	+	976343	976673	1	976343,	976673,	N	451	cellular response to phosphate starvation,endosome,Golgi apparatus,integral to membrane,integral to membrane,phosphate ion transport,plasma membrane,trans-Golgi network

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-241	Chr2	-	10673968	10674376	2	10673968,10674346,	10674245,10674376,	N	452	
PolyA_lnc-242	Chr2	-	14487370	14488113	2	14487370,14487837,	14487533,14488113,	N	453	mitochondrion
PolyA_lnc-243	Chr2	-	15401524	15403566	2	15401524,15403190,	15401582,15403566,	N	454	biological_process_unknown,molecular_function_unknown
PolyA_lnc-244	Chr2	-	16211883	16212155	1	16211883,	16212155,	N	455	biological_process_unknown,chloroplast,molecular_function_unknowr
PolyA_lnc-245	Chr2	-	16277001	16279354	8	16277001,16277428,16277725,16277898,16278049,16278718,16278883,16279035,	16277348,16277504,16277833,16277965,16278240,16278784,16278958,16279354,	N	456	
PolyA_lnc-246	Chr2	-	16971171	16971790	2	16971171,16971667,	16971507,16971790,	N	457	circadian rhythm,cytokinin mediated signaling pathway,cytokinin mediated signaling pathway,cytoplasm,nucleus,nucleus,protein binding,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,response to cytokinin stimulus,two-component response regulator activity,two-component response regulator activity,two-component response regulator activity,two-component response regulator activity,two-component response regulator activity,two-component signal transduction system (phosphorelay),two-component signal transduction system (phosphorelay)
PolyA_lnc-247	Chr2	-	16983156	16983841	2	16983156,16983495,	16983327,16983841,	N	458	mitochondrion
PolyA_lnc-248	Chr2	-	17312118	17312925	2	17312118,17312808,	17312412,17312925,	Y	459	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-249	Chr2	-	17312374	17314059	4	17312374,17312808,17313296,17313656,	17312412,17312868,17313411,17314059,	Y	460	catalytic activity,catalytic activity,cell wall macromolecule metabolic process,cell wall macromolecule metabolic process,cytokinin catabolic process,cytokinin catabolic process,cytokinin catabolic process,cytokinin catabolic process,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin metabolic process,cytokinin metabolic process,extracellular region,extracellular region,flavin adenine dinucleotide binding,flavin adenine dinucleotide binding,meristem development,meristem development,N-terminal protein myristoylation,N-terminal protein myristoylation,oxidation-reduction process,oxidation-reduction process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on CH-OH group of donors,oxidoreductase activity, acting on CH-OH group of donors,UDP-N-acetylmuramate dehydrogenase activity,UDP-N-acetylmuramate dehydrogenase activity,vacuole,vacuole,xylem development,xylem development
PolyA_lnc-250	Chr2	-	17312655	17314059	4	17312655,17312808,17313296,17313656,	17312681,17312868,17313411,17314059,	Y	461	catalytic activity,catalytic activity,cell wall macromolecule metabolic process,cell wall macromolecule metabolic process,cytokinin catabolic process,cytokinin catabolic process,cytokinin catabolic process,cytokinin catabolic process,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin metabolic process,cytokinin metabolic process,extracellular region,extracellular region,flavin adenine dinucleotide binding,flavin adenine dinucleotide binding,meristem development,meristem development,N-terminal protein myristoylation,N-terminal protein myristoylation,oxidation-reduction process,oxidation-reduction process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on CH-OH group of donors,oxidoreductase activity, acting on CH-OH group of donors,UDP-N-acetylmuramate dehydrogenase activity,UDP-N-acetylmuramate dehydrogenase activity,vacuole,vacuole,xylem development,xylem development

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-251	Chr2	-	17313659	17317301	2	17313659,17317134,	17314310,17317301,	Y	462	catalytic activity,catalytic activity,cell wall macromolecule metabolic process,cell wall macromolecule metabolic process,cytokinin catabolic process,cytokinin catabolic process,cytokinin catabolic process,cytokinin catabolic process,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin metabolic process,cytokinin metabolic process,extracellular region,extracellular region,flavin adenine dinucleotide binding,flavin adenine dinucleotide binding,meristem development,meristem development,N-terminal protein myristoylation,N-terminal protein myristoylation,oxidation-reduction process,oxidation-reduction process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on CH-OH group of donors,oxidoreductase activity, acting on CH-OH group of donors,UDP-N-acetylmuramate dehydrogenase activity,UDP-N-acetylmuramate dehydrogenase activity,vacuole,vacuole,xylem development,xylem development
PolyA_lnc-252	Chr2	-	17313659	17317301	3	17313659,17314249,17317134,	17313845,17314310,17317301,	Y	463	catalytic activity,catalytic activity,cell wall macromolecule metabolic process,cell wall macromolecule metabolic process,cytokinin catabolic process,cytokinin catabolic process,cytokinin catabolic process,cytokinin catabolic process,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin metabolic process,cytokinin metabolic process,extracellular region,extracellular region,flavin adenine dinucleotide binding,flavin adenine dinucleotide binding,meristem development,meristem development,N-terminal protein myristoylation,N-terminal protein myristoylation,oxidation-reduction process,oxidation-reduction process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on CH-OH group of donors,oxidoreductase activity, acting on CH-OH group of donors,UDP-N-acetylmuramate dehydrogenase activity,UDP-N-acetylmuramate dehydrogenase activity,vacuole,vacuole,xylem development,xylem development
PolyA_lnc-253	Chr2	-	18154541	18155664	2	18154541,18155604,	18155519,18155664,	N	464	
PolyA_lnc-254	Chr2	-	18797743	18799150	2	18797743,18799049,	18798462,18799150,	N	465	cofactor binding,cytoplasm,metabolic process,metabolic process,NAD binding,NAD binding,nucleotide binding,nucleotide binding,oxidation-reduction process,oxidation-reduction process,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;fatty acid catabolic process,nucleolus,nucleus,nucleus,protein binding,protein binding,protein binding,response to abscisic acid stimulus,response to salt stress

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-255	Chr2	-	2978940	2979162	2	2978940,2979075,	2978990,2979162,	N	466	cell proliferation,chromatin silencing by small RNA,cytokinesis,cytoplasm,DNA replication initiation,gene silencing,histone H3-K9 methylation,histone lysine methylation,intracellular protein transport,membrane coat,methylation-dependent chromatin silencing,microtubule-based process,regulation of cell cycle,regulation of DNA replication,regulation of flower development,vesicle-mediated transport
PolyA_lnc-256	Chr2	-	8932591	8933185	2	8932591,8933150,	8933074,8933185,	N	467	
PolyA_lnc-257	Chr2	-	9257436	9257752	2	9257436,9257661,	9257465,9257752,	N	468	
PolyA_lnc-258	Chr2	-	9257542	9261034	3	9257542,9258159,9261003,	9257859,9258220,9261034,	N	469	DNA binding,DNA binding,embryo development ending in seed dormancy,gravitropism,nucleus,regulation of transcription, DNA-dependent,response to red light,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity
PolyA_lnc-259	Chr2	.	10017054	10017309	1	10017054,	10017309,	N	470	catalytic activity,plasma membrane,pyridoxal phosphate binding
lyA_lnc-260	Chr2	.	10340288	10340563	1	10340288,	10340563,	N	471	biological_process_unknown,methionine biosynthetic process,molecular_function_unknown,RNA splicing, via endonucleolytic cleavage and ligation;biological_process_unknown,calmodulin binding,calmodulin binding,nucleus
PolyA_lnc-261	Chr2	.	10390689	10390933	1	10390689,	10390933,	N	472	cell redox homeostasis,cellular_component_unknown,nucleus,selenium binding
PolyA_lnc-262	Chr2	.	10425320	10425661	1	10425320,	10425661,	N	473	cellular_component_unknown,cytoplasm,flavonoid biosynthetic process,myo-inositol hexakisphosphate biosynthetic process,protein binding,protein binding,protein binding,red, far-red light phototransduction,red or far-red light signaling pathway,response to sucrose stimulus,response to UV-B
PolyA_lnc-263	Chr2	.	10435584	10435855	1	10435584,	10435855,	N	474	
PolyA_lnc-264	Chr2	.	10675978	10676232	1	10675978,	10676232,	N	475	
PolyA_lnc-265	Chr2	.	10741689	10742182	1	10741689,	10742182,	N	476	ATP binding,ATP binding,kinase activity,plasma membrane,plasma membrane,protein kinase activity,protein kinase activity,protein phosphorylation,protein phosphorylation,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein tyrosine kinase activity,protein tyrosine kinase activity,transferase activity, transferring phosphorus-containing groups,transferase activity, transferring phosphorus-containing groups
PolyA_lnc-266	Chr2	.	10950487	10950696	1	10950487,	10950696,	N	477	
PolyA_lnc-267	Chr2	.	11094285	11094510	1	11094285,	11094510,	N	478	abscisic acid mediated signaling pathway,abscisic acid mediated signaling pathway,cellular_component_unknown,fatty acid catabolic process,nucleus,protein binding,protein binding,protein binding,protein homodimerization activity,receptor activity
PolyA_lnc-268	Chr2	.	11163228	11163975	1	11163228,	11163975,	N	479	
PolyA_lnc-269	Chr2	.	11217214	11217418	1	11217214,	11217418,	N	480	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-270	Chr2	.	11278217	11278420	1	11278217,	11278420,	N	481	chloroplast,chloroplast,membrane,membrane,membrane,plasma membrane,plasma membrane,plasmodesma,transmembrane transport,transmembrane transport,transmembrane transporter activity,transmembrane transporter activity,transport,transport,transporter activity,transporter activity;mitochondrion
PolyA_lnc-271	Chr2	.	11278488	11278719	1	11278488,	11278719,	N	482	chloroplast,chloroplast,membrane,membrane,membrane,plasma membrane,plasma membrane,plasmodesma,transmembrane transport,transmembrane transport,transmembrane transporter activity,transmembrane transporter activity,transport,transport,transporter activity,transporter activity;mitochondrion
PolyA_lnc-272	Chr2	.	11278562	11278782	1	11278562,	11278782,	N	483	chloroplast,chloroplast,membrane,membrane,membrane,plasma membrane,plasma membrane,plasmodesma,transmembrane transport,transmembrane transport,transmembrane transporter activity,transmembrane transporter activity,transport,transport,transporter activity,transporter activity;mitochondrion
PolyA_lnc-273	Chr2	.	11424187	11424582	1	11424187,	11424582,	N	484	biological_process_unknown,membrane;biological_process_unknown,mitochondrion
lyA_lnc-274	Chr2	.	11424705	11425268	1	11424705,	11425268,	N	485	biological_process_unknown,membrane;biological_process_unknown,mitochondrion
PolyA_lnc-275	Chr2	.	11671492	11671803	1	11671492,	11671803,	Y	486	biological_process_unknown,molecular_function_unknown,nucleus,plasmodesma;biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus
PolyA_lnc-276	Chr2	.	11688327	11688640	1	11688327,	11688640,	N	487	biological_process_unknown,membrane,molecular_function_unknown,molecular_function_unknown
PolyA_lnc-277	Chr2	.	11688595	11689207	1	11688595,	11689207,	N	488	biological_process_unknown,membrane,molecular_function_unknown,molecular_function_unknown
PolyA_lnc-278	Chr2	.	11751250	11751524	1	11751250,	11751524,	N	489	anchored to plasma membrane,anchored to plasma membrane,anchored to plasma membrane,carbohydrate metabolic process,carbohydrate metabolic process,carbohydrate metabolic process,catalytic activity,catalytic activity,catalytic activity,cation binding,cation binding,cation binding,cytoplasm,extracellular region,extracellular region,extracellular region,hydrolase activity, hydrolyzing O-glycosyl compounds,hydrolase activity, hydrolyzing O glycosyl compounds,hydrolase activity, hydrolyzing O-glycosyl compounds,hydrolase activity, hydrolyzing O-glycosyl compounds,jasmonic acid mediated signaling pathway,nucleus,protein targeting to membrane,regulation of plant-type hypersensitive response,salicylic acid mediated signaling pathway
PolyA_lnc-279	Chr2	.	11812726	11813065	1	11812726,	11813065,	N	490	cytoplasm,cytoplasm,GTPase activity,GTPase activity,GTP binding,GTP binding,translation factor activity, nucleic acid binding
PolyA_lnc-280	Chr2	.	11937744	11938017	1	11937744,	11938017,	N	491	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-281	Chr2	.	12319280	12319610	1	12319280,	12319610,	N	492	DNA binding,DNA binding,nucleus,protein dimerization activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity
PolyA_lnc-282	Chr2	.	12331028	12331239	1	12331028,	12331239,	N	493	
PolyA_lnc-283	Chr2	.	12349195	12349416	1	12349195,	12349416,	N	494	
PolyA_lnc-284	Chr2	.	12517427	12517650	1	12517427,	12517650,	N	495	
PolyA_lnc-285	Chr2	.	12796524	12796801	1	12796524,	12796801,	N	496	flavin adenine dinucleotide binding,intrinsic to mitochondrial inner membrane,mitochondrion,mitochondrion,mitochondrion,mitochondrion,NADH dehydrogenase activity,oxidation-reduction process,oxidoreductase activity,peroxisome;biological_process_unknown,mitochondrion,molecular_function_unknown
PolyA_lnc-286	Chr2	.	13278911	13279316	1	13278911,	13279316,	N	497	biological_process_unknown,determination of bilateral symmetry,floral whorl development,flower morphogenesis,meristem initiation,molecular_function_unknown,nucleus,pattern specification process,polarity specification of adaxial/abaxial axis,regulation of meristem growth
PolyA_lnc-287	Chr2	.	13502338	13502645	1	13502338,	13502645,	N	498	
PolyA_lnc-288	Chr2	.	13502615	13504069	1	13502615,	13504069,	N	499	
PolyA_lnc-289	Chr2	.	13503826	13504433	1	13503826,	13504433,	N	500	
PolyA_lnc-290	Chr2	.	13504150	13504729	1	13504150,	13504729,	N	501	
PolyA_lnc-291	Chr2	.	13504524	13505384	1	13504524,	13505384,	N	502	
PolyA_lnc-292	Chr2	.	13570257	13570570	1	13570257,	13570570,	N	503	actin filament-based movement,actin filament-based movement,ATP binding,cell wall macromolecule metabolic process,Golgi localization,mitochondrion localization,motor activity,motor activity,myosin complex,peroxisome localization,protein binding,response to nematode,unconventional myosin complex,xylem development;cation transport,chloroplast,integral to membrane,lithium ion transport,pollen tube guidance,sodium:hydrogen antiporter activity,sodium ion transmembrane transport,sodium ion transport,solute:hydrogen antiporter activity,transmembrane transport
PolyA_lnc-293	Chr2	.	1365203	1365516	1	1365203,	1365516,	Y	504	antiporter activity,drug transmembrane transport,drug transmembrane transporter activity,membrane,membrane,plasma membrane,transmembrane transport,transporter activity
PolyA_lnc-294	Chr2	.	13717735	13717934	1	13717735,	13717934,	N	505	
PolyA_lnc-295	Chr2	.	13823700	13823923	1	13823700,	13823923,	N	506	cellular_component_unknown,multicellular organismal development,nucleus;biological_process_unknown,extracellular region,molecular_function_unknown
PolyA_lnc-296	Chr2	.	1393433	1393741	1	1393433,	1393741,	N	507	
PolyA_lnc-297	Chr2	.	14286986	14287296	1	14286986,	14287296,	N	508	
PolyA_lnc-298	Chr2	.	14310562	14310782	1	14310562,	14310782,	N	509	cellular_component_unknown,nucleus,nucleus

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-299	Chr2	.	14454354	14454603	1	14454354,	14454603,	N	510	chloroplast,embryo development ending in seed dormancy,molecular_function_unknown,nucleus,pollen development;mitochondrion;biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus,nucleus
PolyA_lnc-300	Chr2	.	14736141	14737006	1	14736141,	14737006,	N	511	cell wall,defense response,defense response to fungus,defense response to fungus,signal transduction
PolyA_lnc-301	Chr2	.	14907198	14907571	1	14907198,	14907571,	Y	512	cellular_component_unknown
PolyA_lnc-302	Chr2	.	14954876	14955116	1	14954876,	14955116,	N	513	biological_process_unknown,molecular_function_unknown,molecular_function_unknown
PolyA_lnc-303	Chr2	.	15069205	15069517	1	15069205,	15069517,	N	514	ATP binding,calmodulin-dependent protein kinase activity,kinase activity,N-terminal protein myristoylation,nucleus,protein kinase activity,protein phosphorylation,protein phosphorylation,protein serine/threonine kinase activity,transferase activity, transferring phosphorus-containing groups;biological_process_unknown,molecular_function_unknown,nucleus,nucleus
PolyA_lnc-304	Chr2	.	16028733	16029460	1	16028733,	16029460,	N	515	
PolyA_lnc-305	Chr2	.	1604530	1604942	1	1604530,	1604942,	N	516	
PolyA_lnc-306	Chr2	.	16101657	16101867	1	16101657,	16101867,	N	517	
PolyA_lnc-307	Chr2	.	16168474	16168698	1	16168474,	16168698,	N	518	catalytic activity,catalytic activity,catalytic activity,catalytic activity,catalytic activity,cytoplasm,cytoplasm,cytoplasm,folic acid-containing compound biosynthetic process,folic acid-containing compound biosynthetic process,folic acid-containing compound biosynthetic process,folic acid-containing compound biosynthetic process,folic acid-containing compound biosynthetic process,methylenetetrahydrofolate dehydrogenase (NADP+) activity,methylenetetrahydrofolate dehydrogenase (NADP+) activity,methylenetetrahydrofolate dehydrogenase (NADP+) activity,methylenetetrahydrofolate dehydrogenase (NADP+) activity,mitochondrion,nucleotide binding,nucleotide binding,nucleotide binding,nucleotide binding,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process;biosynthetic process,biosynthetic process,catalytic activity,ethanolamine-phosphate cytidylyltransferase activity,ethanolamine-phosphate cytidylyltransferase activity,integral to mitochondrial outer membrane,mitochondrion,mitochondrion,nucleotidyltransferase activity,nucleus,phosphatidylethanolamine biosynthetic process
PolyA_lnc-308	Chr2	.	16339879	16340240	1	16339879,	16340240,	N	519	
PolyA_lnc-309	Chr2	.	16566757	16566977	1	16566757,	16566977,	N	520	zinc ion binding,zinc ion binding
PolyA_lnc-310	Chr2	.	16645596	16645848	1	16645596,	16645848,	N	521	biological_process_unknown,cellular_component_unknown,molecular_function_unknown
PolyA_lnc-311	Chr2	.	16982403	16982741	1	16982403,	16982741,	N	522	mitochondrion

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-312	Chr2	.	16982850	16983109	1	16982850,	16983109,	N	523	mitochondrion
PolyA_lnc-313	Chr2	.	16983497	16983966	1	16983497,	16983966,	N	524	
PolyA_lnc-314	Chr2	.	16983907	16984236	1	16983907,	16984236,	N	525	
PolyA_lnc-315	Chr2	.	16984028	16984331	1	16984028,	16984331,	N	526	
PolyA_lnc-316	Chr2	.	16984319	16984618	1	16984319,	16984618,	N	527	
PolyA_lnc-317	Chr2	.	16984436	16984813	1	16984436,	16984813,	N	528	
PolyA_lnc-318	Chr2	.	16984691	16986061	1	16984691,	16986061,	N	529	
PolyA_lnc-319	Chr2	.	17317222	17317435	1	17317222,	17317435,	N	530	catalytic activity,catalytic activity,cell wall macromolecule metabolic process,cell wall macromolecule metabolic process,cytokinin catabolic process,cytokinin catabolic process,cytokinin catabolic process,cytokinin catabolic process,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin dehydrogenase activity,cytokinin metabolic process,cytokinin metabolic process,extracellular region,extracellular region,flavin adenine dinucleotide binding,flavin adenine dinucleotide binding,meristem development,meristem development,N-terminal protein myristoylation,N-terminal protein myristoylation,oxidation-reduction process,oxidation-reduction process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on CH-OH group of donors,oxidoreductase activity, acting on CH-OH group of donors,UDP-N-acetylmuramate dehydrogenase activity,UDP-N-acetylmuramate dehydrogenase activity,vacuole,vacuole,xylem development,xylem development;heat shock protein binding,heat shock protein binding,nucleus,nucleus,protein folding
PolyA_lnc-320	Chr2	.	1780888	1781779	1	1780888,	1781779,	N	531	
PolyA_lnc-321	Chr2	.	1788219	1788527	1	1788219,	1788527,	N	532	
PolyA_lnc-322	Chr2	.	18092457	18092805	1	18092457,	18092805,	Y	533	amino acid transport,apoplast,carbohydrate metabolic process,cell wall macromolecule catabolic process,chitinase activity,chitinase activity,chitin binding,extracellular region,proline transport,respiratory burst involved in defense response,response to chitin
PolyA_lnc-323	Chr2	.	18300713	18300918	1	18300713,	18300918,	N	534	ATP binding,ATP binding,cell cycle process,cullin deneddylation,cytoplasm,cytoplasm,cytoplasm,embryo sac egg cell differentiation,G2 phase of mitotic cell cycle,histone methylation,photomorphogenesis,positive regulation of cellular process,positive regulation of transcription, DNA-dependent,post-translational protein modification,protein deubiquitination,protein ubiquitination,regulation of plant-type cell wall organization or biogenesis,regulation of transcription, DNA-dependent,response to reactive oxygen species,response to xenobiotic stimulus,RNA processing,tRNA binding,tRNA processing,tRNA processing,tRNA thio-modification;biological_process_unknown,cellular_component_unknown,molecular_function_unknown

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-324	Chr2	.	18797629	18798041	1	18797629,	18798041,	N	535	cofactor binding,cytoplasm,metabolic process,metabolic process,NAD binding,NAD binding,nucleotide binding,nucleotide binding,oxidation-reduction process,oxidation-reduction process,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
PolyA_lnc-325	Chr2	.	18832264	18832605	1	18832264,	18832605,	N	536	cytoplasm,cytosol,cytosolic ribosome,cytosolic ribosome,cytosolic small ribosomal subunit,intracellular,nucleolus,plasma membrane,plasmodesma,ribosome,ribosome,ribosome biogenesis,RNA methylation,structural constituent of ribosome,structural constituent of ribosome,translation,translation;biological_process_unknown,glucuronoxylan metabolic process,xylan biosynthetic process
PolyA_lnc-326	Chr2	.	19162224	19162582	1	19162224,	19162582,	N	537	
PolyA_lnc-327	Chr2	.	19163573	19164071	1	19163573,	19164071,	N	538	
PolyA_lnc-328	Chr2	.	19177153	19177356	1	19177153,	19177356,	N	539	
PolyA_lnc-329	Chr2	.	19682474	19683022	1	19682474,	19683022,	N	540	amyloplast,carotenoid biosynthetic process,cellular response to light stimulus,chloroplast,chloroplast,chloroplast,chloroplast mRNA processing,chloroplast organization,chromoplast,etioplast,leaf morphogenesis,molecular_function_unknown,molecular_function_unknown,proplastid;cytoplasm,mitochondrion
PolyA_lnc-330	Chr2	.	19683895	19684132	1	19683895,	19684132,	N	541	anchored to membrane,anchored to membrane,cellular response to iron ion starvation,iron ion transport,lipid binding,lipid binding,lipid transport,lipid transport,nitrate transport,plasma membrane,response to nitrate,transition metal ion transport
PolyA_lnc-331	Chr2	.	230045	230276	1	230045,	230276,	N	542	apoplast,extracellular region,receptor binding,signal transduction;biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown
PolyA_lnc-332	Chr2	.	2930836	2931497	1	2930836,	2931497,	N	543	carotenoid biosynthetic process,catalytic activity,chlorophyll biosynthetic process,cycloartenol synthase activity,intramolecular transferase activity,isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway,pentacyclic triterpenoid biosynthetic process,pentacyclic triterpenoid biosynthetic process,pentacyclic triterpenoid biosynthetic process,phosphatidylglycerol biosynthetic process,pollen development,sterol biosynthetic process,thylakoid membrane organization,unsaturated fatty acid biosynthetic process,vacuole,vacuole
PolyA_lnc-333	Chr2	.	415693	415954	1	415693,	415954,	N	544	mitochondrion,regulation of cell cycle;anaphase,anaphase,microtubule binding,microtubule cytoskeleton organization,microtubule nucleation,mitochondrion,nucleus,phragmoplast,plastid,preprophase band
PolyA_lnc-334	Chr2	.	4416047	4416400	1	4416047,	4416400,	N	545	
PolyA_lnc-335	Chr2	.	4757320	4757854	1	4757320,	4757854,	N	546	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-336	Chr2	.	5080266	5080573	1	5080266,	5080573,	N	547	
PolyA_lnc-337	Chr2	.	5080563	5080819	1	5080563,	5080819,	N	548	
PolyA_lnc-338	Chr2	.	5081290	5082025	1	5081290,	5082025,	N	549	
PolyA_lnc-339	Chr2	.	5081982	5082371	1	5081982,	5082371,	N	550	
PolyA_lnc-340	Chr2	.	5082292	5082955	1	5082292,	5082955,	N	551	
PolyA_lnc-341	Chr2	.	5083009	5083448	1	5083009,	5083448,	N	552	
PolyA_lnc-342	Chr2	.	5913972	5914382	1	5913972,	5914382,	N	553	ATP binding,ATP binding,DNA binding,DNA binding,DNA-dependent ATPase activity,DNA replication,DNA replication initiation,nucleoside-triphosphatase activity,nucleotide binding,nucleus;fatty acid biosynthetic process,membrane,methyltransferase activity,S-adenosylmethionine-dependent methyltransferase activity
PolyA_lnc-343	Chr2	.	6503754	6504020	1	6503754,	6504020,	N	554	chloroplast
PolyA_lnc-344	Chr2	.	7269213	7269438	1	7269213,	7269438,	N	555	
PolyA_lnc-345	Chr2	.	7269864	7270369	1	7269864,	7270369,	N	556	acid-amino acid ligase activity,cellular_component_unknown,cytoplasm,DNA endoreduplication,proteasomal ubiquitin-dependent protein catabolic process,proteasome assembly,regulation of unidimensional cell growth,response to misfolded protein,ubiquitin-dependent protein catabolic process,ubiquitin-protein ligase activity,ubiquitin-protein ligase activity;ATP binding,kinase activity,plasma membrane,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,transferase activity, transferring phosphorus-containing groups
PolyA_lnc-346	Chr2	.	7417183	7417476	1	7417183,	7417476,	N	557	cytoplasm,intracellular,signal transduction
PolyA_lnc-347	Chr2	.	8535740	8536091	1	8535740,	8536091,	N	558	
PolyA_lnc-348	Chr2	.	8536214	8536438	1	8536214,	8536438,	N	559	
PolyA_lnc-349	Chr2	.	8625077	8625567	1	8625077,	8625567,	N	560	biological_process_unknown,determination of bilateral symmetry,extracellular region,extracellular region,meristem initiation,molecular_function_unknown,polarity specification of adaxial/abaxial axis,regulation of meristem growth
PolyA_lnc-350	Chr2	.	8625971	8626192	1	8625971,	8626192,	N	561	
PolyA_lnc-351	Chr2	.	8626108	8626346	1	8626108,	8626346,	N	562	
PolyA_lnc-352	Chr2	.	881726	882271	1	881726,	882271,	N	563	biological_process_unknown,molecular_function_unknown;aspartic-type endopeptidase activity,aspartic-type endopeptidase activity,cellular_component_unknown,cytoplasm,cytoplasm,proteolysis,proteolysis
PolyA_lnc-353	Chr2	.	882234	882522	1	882234,	882522,	N	564	biological_process_unknown,molecular_function_unknown;aspartic-type endopeptidase activity,aspartic-type endopeptidase activity,cellular_component_unknown,cytoplasm,cytoplasm,proteolysis,proteolysis
PolyA_lnc-354	Chr2	.	8869495	8869817	1	8869495,	8869817,	N	565	biological_process_unknown,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,nucleus,nucleus

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-355	Chr2	.	8869568	8870032	1	8869568,	8870032,	N	566	biological_process_unknown,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,nucleus,nucleus
PolyA_lnc-356	Chr2	.	8869923	8870315	1	8869923,	8870315,	N	567	biological_process_unknown,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,nucleus,nucleus
PolyA_lnc-357	Chr2	.	8870099	8870421	1	8870099,	8870421,	N	568	biological_process_unknown,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,nucleus,nucleus
PolyA_lnc-358	Chr2	.	8981427	8981638	1	8981427,	8981638,	N	569	4 iron, 4 sulfur cluster binding,aromatic amino acid family biosynthetic process,aromatic amino acid family metabolic process,catalytic activity,cell differentiation,cellular amino acid biosynthetic process,chlorophyll biosynthetic process,chloroplast,coenzyme biosynthetic process,cysteine biosynthetic process,glycine catabolic process,glycine catabolic process,iron-sulfur cluster binding,isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway,jasmonic acid biosynthetic process,leaf morphogenesis,lipoate biosynthetic process,lipoate biosynthetic process,lipoate metabolic process,lipoate synthase activity,lipoate synthase activity,lipoate synthase activity,mitochondrial matrix,mitochondrion,nucleotide metabolic process,oxidoreduction coenzyme metabolic process,positive regulation of transcription, DNA-dependent,secondary metabolic process,sulfur amino acid metabolic process,sulfur compound biosynthetic process,unsaturated fatty acid biosynthetic process,vitamin metabolic process;biological_process_unknown,molecular_function_unknown,plasma membrane,regulation of anthocyanin biosynthetic process
PolyA_lnc-359	Chr2	.	9079983	9080379	1	9079983,	9080379,	Y	570	ER retention sequence binding,integral to membrane,integral to membrane,protein retention in ER lumen,protein transport,receptor activity
PolyA_lnc-360	Chr2	.	9256887	9257130	1	9256887,	9257130,	Y	571	
PolyA_lnc-361	Chr2	.	9257034	9257324	1	9257034,	9257324,	Y	572	
PolyA_lnc-362	Chr2	.	9809423	9809647	1	9809423,	9809647,	N	573	biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown,terpenoid biosynthetic process
PolyA_lnc-363	Chr2	.	9936609	9936808	1	9936609,	9936808,	N	574	
PolyA_lnc-364	Chr3	+	10075559	10076145	1	10075559,	10076145,	N	575	chloroplast,membrane,membrane,mitochondrial respiratory chain complex I,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion,plant-type cell wall,plasma membrane,response to stress,RNA methylation,vacuolar membrane,vacuolar membrane,vacuole,vacuole
PolyA_lnc-365	Chr3	+	10609989	10610924	2	10609989,10610734,	10610146,10610924,	N	576	
PolyA_lnc-366	Chr3	+	12360802	12363497	2	12360802,12363434,	12361016,12363497,	N	577	
PolyA_lnc-367	Chr3	+	12360833	12361150	1	12360833,	12361150,	N	578	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-368	Chr3	+	15699780	15700208	1	15699780,	15700208,	N	579	cytoplasm,integral to membrane,lipid metabolic process,oxidoreductase activity, acting on the CH-CH group of donors
PolyA_lnc-369	Chr3	+	15701524	15701837	1	15701524,	15701837,	N	580	cytoplasm,integral to membrane,lipid metabolic process,oxidoreductase activity, acting on the CH-CH group of donors;biological_process_unknown,molecular_function_unknown,nucleus,vacuole
PolyA_lnc-370	Chr3	+	16277543	16277854	1	16277543,	16277854,	N	581	
PolyA_lnc-371	Chr3	+	16277543	16278433	2	16277543,16278196,	16277686,16278433,	N	582	
PolyA_lnc-372	Chr3	+	16278188	16278502	1	16278188,	16278502,	N	583	
PolyA_lnc-373	Chr3	+	16301616	16301893	1	16301616,	16301893,	N	584	
PolyA_lnc-374	Chr3	+	16310606	16311860	4	16310606,16310936,16311085,16311721,	16310663,16311003,16311208,16311860,	N	585	
PolyA_lnc-375	Chr3	+	16314869	16315122	2	16314869,16315045,	16314956,16315122,	N	586	biological_process_unknown,mitochondrion,molecular_function_unknown
PolyA_lnc-376	Chr3	+	16315050	16315317	2	16315050,16315229,	16315122,16315317,	N	587	biological_process_unknown,mitochondrion,molecular_function_unknown
PolyA_lnc-377	Chr3	+	17446054	17446516	2	17446054,17446169,	17446080,17446516,	N	588	chloroplast,chloroplast,metabolic process,metabolic process,nucleotide binding,nucleotide binding,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity
PolyA_lnc-378	Chr3	+	17899938	17900559	3	17899938,17900318,17900510,	17900069,17900379,17900559,	N	589	cysteine-type peptidase activity,cysteine-type peptidase activity,extracellular region,proteolysis,proteolysis
PolyA_lnc-379	Chr3	+	17900906	17901548	1	17900906,	17901548,	N	590	biological_process_unknown,biological_process_unknown,cellular_component_unknown,cellular_component_unknown,molecular_function_unknown,molecular_function_unknown
PolyA_lnc-380	Chr3	+	17901525	17901962	1	17901525,	17901962,	N	591	biological_process_unknown,biological_process_unknown,cellular_component_unknown,cellular_component_unknown,molecular_function_unknown,molecular_function_unknown
PolyA_lnc-381	Chr3	+	17901762	17902027	1	17901762,	17902027,	N	592	biological_process_unknown,biological_process_unknown,cellular_component_unknown,cellular_component_unknown,molecular_function_unknown,molecular_function_unknown
PolyA_lnc-382	Chr3	+	17902020	17902401	2	17902020,17902315,	17902237,17902401,	N	593	biological_process_unknown,biological_process_unknown,cellular_component_unknown,cellular_component_unknown,molecular_function_unknown,molecular_function_unknown

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-383	Chr3	+	17902431	17902840	1	17902431,	17902840,	N	594	biological_process_unknown,biological_process_unknown,cellular_component_unknown,cellular_component_unknown,molecular_function_unknown,molecular_function_unknown;biological_process_unknown,cellular_component_unknown,molecular_function_unknown
PolyA_lnc-384	Chr3	+	17904345	17905028	1	17904345,	17905028,	N	595	biological_process_unknown,cellular_component_unknown,molecular_function_unknown;cysteine-type peptidase activity,cysteine-type peptidase activity,extracellular region,proteolysis,proteolysis
PolyA_lnc-385	Chr3	+	19357866	19358236	2	19357866,19358017,	19357907,19358236,	N	596	
PolyA_lnc-386	Chr3	+	1958900	1963916	1	1958900,	1963916,	N	597	
PolyA_lnc-387	Chr3	+	22535153	22535586	1	22535153,	22535586,	N	598	
PolyA_lnc-388	Chr3	+	231158	231483	1	231158,	231483,	N	599	DNA binding,multicellular organismal development,nucleus,regulation of transcription, DNA-dependent,sequence-specific DNA binding transcription factor activity;ATPase activity,ATP binding,cell cycle process,cullin deneddylation,embryo development ending in seed dormancy,G2 phase of mitotic cell cycle,histone methylation,mRNA splicing, via spliceosome,nucleoside-triphosphatase activity,nucleotide binding,photomorphogenesis,plasma membrane,positive regulation of transcription, DNA-dependent,post-translational protein modification,production of miRNAs involved in gene silencing by miRNA,production of siRNA involved in RNA interference,protein deubiquitination,protein ubiquitination,regulation of transcription, DNA-dependent,RNA processing
PolyA_lnc-389	Chr3	+	23122502	23122968	2	23122502,23122765,	23122554,23122968,	Y	600	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus;biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus
PolyA_lnc-390	Chr3	+	23122780	23123129	1	23122780,	23123129,	Y	601	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus;biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus
PolyA_lnc-391	Chr3	+	3473437	3473658	1	3473437,	3473658,	N	602	defense response,kinase activity,signal transductior
PolyA_lnc-392	Chr3	+	421849	422502	3	421849,422147,422344,	421962,422221,422502,	N	603	
PolyA_lnc-393	Chr3	+	422332	422688	1	422332,	422688,	N	604	
PolyA_lnc-394	Chr3	+	4283723	4288839	2	4283723,4288193,	4283777,4288839,	N	605	
PolyA_lnc-395	Chr3	+	4283742	4288839	3	4283742,4287422,4288193,	4283777,4287518,4288839,	N	606	
PolyA_lnc-396	Chr3	+	4292772	4293974	1	4292772,	4293974,	N	607	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-397	Chr3	+	4293218	4294872	2	4293218,4294219,	4294076,4294872,	N	608	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus
PolyA_lnc-398	Chr3	+	4294052	4294872	1	4294052,	4294872,	N	609	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus
PolyA_lnc-399	Chr3	+	4372673	4373071	2	4372673,4372941,	4372697,4373071,	N	610	biological_process_unknown,molecular_function_unknown
PolyA_lnc-400	Chr3	+	652162	652459	1	652162,	652459,	N	611	biological_process_unknown,DNA-dependent DNA replication,nucleic acid binding,nucleic acid binding,nucleus,nucleus
PolyA_lnc-401	Chr3	+	872193	873510	2	872193,872906,	872347,873510,	N	612	abscisic acid mediated signaling pathway,cellular response to phosphate starvation,cellular response to water deprivation,cytoskeleton,galactolipid biosynthetic process,hyperosmotic salinity response,mitochondrion,molecular_function_unknown,phagocytosis,response to cyclopentenone,response to water deprivation,response to wounding,toxin catabolic process;antiporter activity,antiporter activity,drug transmembrane transport,drug transmembrane transporter activity,membrane,membrane,plasma membrane,transmembrane transport,transporter activity
PolyA_lnc-402	Chr3	+	9024864	9025080	1	9024864,	9025080,	N	613	biological_process_unknown,molecular_function_unknown,nucleus;ATP binding,cellular process involved in reproduction,cytoplasm,pollen tube development,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,transferase activity, transferring phosphorus-containing groups
PolyA_lnc-403	Chr3	+	9244324	9250768	8	9244324,9244994,9245148,9245340,9246222,9246906,9247104,924781 2,	9244663,9245061,9245234,9246124,9246821,9246984,9247709,9250768,	N	614	
PolyA_lnc-404	Chr3	-	10400110	10401739	3	10400110,10400766,10401204,	10400402,10401057,10401739,	N	615	
PolyA_lnc-405	Chr3	-	10400132	10401712	4	10400132,10400766,10400992,10401204,	10400402,10400894,10401057,10401712,	N	616	
PolyA_lnc-406	Chr3	-	10488160	10488389	1	10488160,	10488389,	Y	617	
PolyA_lnc-407	Chr3	-	10488299	10488512	2	10488299,10488399,	10488316,10488512,	Y	618	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-408	Chr3	-	1100454	1101463	2	1100454,1101438,	1100915,1101463,	N	619	mitochondrion;apoplast,biological_process_unknown,extracellular region,manganese ion binding,nutrient reservoir activity
PolyA_lnc-409	Chr3	-	11758490	11761094	6	11758490,11759782,11759928,11760259,11760461,11760649,	11759029,11759861,11760184,11760334,11760502,11761094,	N	620	
PolyA_lnc-410	Chr3	-	11758490	11761102	7	11758490,11759782,11759928,11760135,11760259,11760461,11760649,	11759029,11759842,11760065,11760184,11760334,11760502,11761102,	N	621	
PolyA_lnc-411	Chr3	-	12360802	12361484	1	12360802,	12361484,	N	622	
PolyA_lnc-412	Chr3	-	12559385	12560050	2	12559385,12559814,	12559692,12560050,	N	623	
PolyA_lnc-413	Chr3	-	13064625	13066311	3	13064625,13066065,13066622,	13064817,13066156,13066311,	N	624	
PolyA_lnc-414	Chr3	-	13064718	13066202	2	13064718,13066065,	13064817,13066202,	N	625	
PolyA_lnc-415	Chr3	-	1382512	1383041	2	1382512,1382906,	1382548,1383041,	N	626	cellular_component_unknown,cytoplasm,heat shock protein binding,protein folding,protein folding,unfolded protein binding;biological_process_unknown,cellular_component_unknown,cytoplasm,molecular_function_unknown
PolyA_lnc-416	Chr3	-	15079970	15080684	1	15079970,	15080684,	N	627	
PolyA_lnc-417	Chr3	-	15080153	15080684	2	15080153,15080399,	15080204,15080684,	N	628	
PolyA_lnc-418	Chr3	-	1534569	1535140	2	1534569,1534985,	1534707,1535140,	N	629	aminopeptidase activity,cellular process,chloroplast,chloroplast,chloroplast stroma,chloroplast stroma,chloroplast stroma,hydrolase activity,proteolysis;defense response,kinase activity,plasma membrane,signal transduction
PolyA_lnc-419	Chr3	-	16997646	16997996	2	16997646,16997788,	16997688,16997996,	N	630	biological_process_unknown,extracellular region,molecular_function_unknown
PolyA_lnc-420	Chr3	-	17065443	17066571	2	17065443,17066317,	17066067,17066571,	N	631	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-421	Chr3	-	17065443	17066571	3	17065443,17065995,17066388,	17065892,17066067,17066571,	N	632	
PolyA_lnc-422	Chr3	-	17065447	17066571	3	17065447,17065995,17066317,	17065892,17066067,17066571,	N	633	
PolyA_lnc-423	Chr3	-	17168177	17168428	2	17168177,17168398,	17168320,17168428,	N	634	
PolyA_lnc-424	Chr3	-	17175525	17176305	2	17175525,17176114,	17175562,17176305,	N	635	
PolyA_lnc-425	Chr3	-	17254314	17255212	1	17254314,	17255212,	N	636	cell wall,extracellular region,identical protein binding,metabolic process,negative regulation of catalytic activity,proteolysis,proteolysis,serine-type endopeptidase activity,serine-type endopeptidase activity
PolyA_lnc-426	Chr3	-	17254314	17255212	2	17254314,17254719,	17254542,17255212,	N	637	cell wall,extracellular region,identical protein binding,metabolic process,negative regulation of catalytic activity,proteolysis,proteolysis,serine-type endopeptidase activity,serine-type endopeptidase activity
PolyA_lnc-427	Chr3	-	22174478	22175286	2	22174478,22175213,	22174655,22175286,	N	638	N-terminal protein myristoylation,nucleic acid binding,nucleus,vacuolar membrane
PolyA_lnc-428	Chr3	-	22174706	22175286	1	22174706,	22175286,	N	639	N-terminal protein myristoylation,nucleic acid binding,nucleus,vacuolar membrane
PolyA_lnc-429	Chr3	-	2705313	2705670	2	2705313,2705642,	2705555,2705670,	N	640	
PolyA_lnc-430	Chr3	-	575321	575714	2	575321,575642,	575549,575714,	N	641	molecular_function_unknown;anaphase,chromatin organization,chromatin silencing by small RNA,chromosome segregation,cullin deneddylation,cytokinesis by cell plate formation,DNA metabolic process,DNA recombination,double-strand break repair,double-strand break repair via homologous recombination,embryo sac egg cell differentiation,G2 phase of mitotic cell cycle,histone methylation,male meiosis,meiosis,meiotic chromosome segregation,meiotic DNA double-strand break formation,mitosis,mitotic recombination,molecular_function_unknown,multicellular organism reproduction,nucleus,petal formation,photomorphogenesis,positive regulation of organelle organization,positive regulation of transcription, DNA-dependent,post-translational protein modification,protein deubiquitination,protein ubiquitination,reciprocal meiotic recombination,reciprocal meiotic recombination,regulation of cell cycle process,regulation of chromosome organization,regulation of telomere maintenance,regulation of transcription, DNA-dependent,reproduction,response to gamma radiation,sepal formation,sister chromatid cohesion,somatic cell DNA recombination,synapsis,synapsis,telomere maintenance in response to DNA damage,trichome morphogenesis

WO 2015/117265 PCT/CN2014/071873

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-431	Chr3	-	575473	575872	3	575473,575642,575838,	575549,575763,575872,	N	642	molecular_function_unknown;anaphase,chromatin organization,chromatin silencing by small RNA,chromosome segregation,cullin deneddylation,cytokinesis by cell plate formation,DNA metabolic process,DNA recombination,double-strand break repair,double-strand break repair via homologous recombination,embryo sac egg cell differentiation,G2 phase of mitotic cell cycle,histone methylation,male meiosis,meiosis,meiotic chromosome segregation,meiotic DNA double-strand break formation,mitosis,mitotic recombination,molecular_function_unknown,multicellular organism reproduction,nucleus,petal formation,photomorphogenesis,positive regulation of organelle organization,positive regulation of transcription, DNA-dependent,post-translational protein modification,protein deubiquitination,protein ubiquitination,reciprocal meiotic recombination,reciprocal meiotic recombination,regulation of cell cycle process,regulation of chromosome organization,regulation of telomere maintenance,regulation of transcription, DNA-dependent,reproduction,response to gamma radiation,sepal formation,sister chromatid cohesion,somatic cell DNA recombination,synapsis,synapsis,telomere maintenance in response to DNA damage,trichome morphogenesis
PolyA_lnc-432	Chr3	-	7305892	7306341	1	7305892,	7306341,	N	643	ATP binding,kinase activity,plasma membrane,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,protein tyrosine kinase activity,transferase activity, transferring phosphorus-containing groups
PolyA_lnc-433	Chr3	-	9556009	9556585	2	9556009,9556391,	9556218,9556585,	N	644	carbohydrate metabolic process,catalytic activity,cation binding,hydrolase activity, hydrolyzing O-glycosyl compounds,hydrolase activity, hydrolyzing O-glycosyl compounds
PolyA_lnc-434	Chr3	-	9556009	9556585	2	9556009,9556391,	9556306,9556585,	N	645	carbohydrate metabolic process,catalytic activity,cation binding,hydrolase activity, hydrolyzing O-glycosyl compounds,hydrolase activity, hydrolyzing O-glycosyl compounds
PolyA_lnc-435	Chr3	.	10172318	10172724	1	10172318,	10172724,	N	646	intracellular signal transduction,intracellular signal transduction,molecular_function_unknown,nucleus,nucleus,oxidation-reduction process,oxidation-reduction process,protein-disulfide reductase activity,protein-disulfide reductase activity
PolyA_lnc-436	Chr3	.	10181802	10182020	1	10181802,	10182020,	N	647	intracellular signal transduction,nucleus,oxidation-reduction process,protein-disulfide reductase activity,zinc ion binding

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-437	Chr3	.	10354819	10355307	1	10354819,	10355307,	N	648	
PolyA_lnc-438	Chr3	.	10469543	10469926	1	10469543,	10469926,	Y	649	biological_process_unknown,chloroplast,chloroplast,membrane,membrane;calmodulin binding,catalytic activity,catalytic activity,intracellular,intracellular,phosphatidylinositol biosynthetic process,RNA metabolic process,RNA metabolic process
PolyA_lnc-439	Chr3	.	10484475	10484716	1	10484475,	10484716,	N	650	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus
PolyA_lnc-440	Chr3	.	10601408	10601783	1	10601408,	10601783,	Y	651	
PolyA_lnc-441	Chr3	.	10753942	10754194	1	10753942,	10754194,	Y	652	
PolyA_lnc-442	Chr3	.	10758599	10759199	1	10758599,	10759199,	N	653	
PolyA_lnc-443	Chr3	.	10934666	10934910	1	10934666,	10934910,	N	654	
PolyA_lnc-444	Chr3	.	10963025	10963429	1	10963025,	10963429,	N	655	
PolyA_lnc-445	Chr3	.	11100307	11100599	1	11100307,	11100599,	Y	656	
PolyA_lnc-446	Chr3	.	11138073	11138423	1	11138073,	11138423,	N	657	biological_process_unknown,molecular_function_unknown,nucleus
PolyA_lnc-447	Chr3	.	11138282	11138521	1	11138282,	11138521,	N	658	biological_process_unknown,molecular_function_unknown,nucleus
PolyA_lnc-448	Chr3	.	11138517	11139128	1	11138517,	11139128,	N	659	biological_process_unknown,molecular_function_unknown,nucleus
PolyA_lnc-449	Chr3	.	11154236	11154715	1	11154236,	11154715,	Y	660	biological_process_unknown,chloroplast,chloroplast,embryo development ending in seed dormancy,iron-sulfur cluster assembly,isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway,maltose metabolic process,molecular_function_unknown,phosphatidylglycerol biosynthetic process,positive regulation of catalytic activity,starch biosynthetic process,stomatal complex morphogenesis,thylakoid membrane organization
PolyA_lnc-450	Chr3	.	11509430	11510487	1	11509430,	11510487,	N	661	
PolyA_lnc-451	Chr3	.	11585795	11586304	1	11585795,	11586304,	Y	662	
PolyA_lnc-452	Chr3	.	11647327	11647720	1	11647327,	11647720,	N	663	
PolyA_lnc-453	Chr3	.	14308624	14308853	1	14308624,	14308853,	N	664	biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown;biological_process_unknown,molecular_function_unknown
PolyA_lnc-454	Chr3	.	15270124	15270429	1	15270124,	15270429,	N	665	
PolyA_lnc-455	Chr3	.	15677008	15677360	1	15677008,	15677360,	N	666	
PolyA_lnc-456	Chr3	.	15725	16131	1	15725,	16131,	N	667	chloroplast,circadian rhythm,molecular_function_unknown,myo-inositol hexakisphosphate biosynthetic process
PolyA_lnc-457	Chr3	.	15971646	15972642	1	15971646,	15972642,	N	668	biological_process_unknown,molecular_function_unknown;cellular_component_unknown,DNA binding,multicellular organismal development,nucleus,regulation of transcription, DNA-dependent,sequence-specific DNA binding transcription factor activity
PolyA_lnc-458	Chr3	.	16050450	16050665	1	16050450,	16050665,	N	669	
PolyA_lnc-459	Chr3	.	16236109	16236324	1	16236109,	16236324,	N	670	biological_process_unknown,molecular_function_unknown,plasma membrane
PolyA_lnc-460	Chr3	.	16278665	16278912	1	16278665,	16278912,	N	671	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-461	Chr3	.	16301208	16301435	1	16301208,	16301435,	N	672	biological_process_unknown,cellular_component_unknown,extracellular region,molecular_function_unknown
PolyA_lnc-462	Chr3	.	16498020	16498485	1	16498020,	16498485,	N	673	extracellular region,plasmodesma
PolyA_lnc-463	Chr3	.	16499283	16499491	1	16499283,	16499491,	N	674	
PolyA_lnc-464	Chr3	.	16659794	16660104	1	16659794,	16660104,	N	675	ATP binding,kinase activity,mitochondrion,plasma membrane,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,transferase activity, transferring phosphorus-containing groups;ATP binding,kinase activity,plasma membrane,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,protein tyrosine kinase activity,transferase activity, transferring phosphorus-containing groups
PolyA_lnc-465	Chr3	.	16954016	16954269	1	16954016,	16954269,	N	676	cellular_component_unknown,metabolic process,nucleotide binding,oxidoreductase activity,oxidoreductase activity,response to cadmium ion;galactose transmembrane transporter activity,transmembrane transport
PolyA_lnc-466	Chr3	.	17166996	17167259	1	17166996,	17167259,	N	677	cellular_component_unknown,molecular_function_unknown,nucleus,shoot development
PolyA_lnc-467	Chr3	.	17167255	17167720	1	17167255,	17167720,	N	678	
PolyA_lnc-468	Chr3	.	17177701	17177922	1	17177701,	17177922,	N	679	cytoplasm,ethylene biosynthetic process,ethylene mediated signaling pathway,intracellular signal transduction,nucleus,protein autoubiquitination,respiratory burst involved in defense response,response to abscisic acid stimulus,response to chitin,response to chitin,response to mechanical stimulus,response to water deprivation,response to wounding,ubiquitin-protein ligase activity,zinc ion binding,zinc ion binding
PolyA_lnc-469	Chr3	.	17345045	17345421	1	17345045,	17345421,	N	680	ATP binding,ATP binding,chloroplast,kinase activity,plasma membrane,protein kinase activity,protein phosphorylation,protein phosphorylation,protein serine/threonine kinase activity,protein serine/threonine kinase activity,transferase activity, transferring phosphorus-containing groups,transmembrane receptor protein tyrosine kinase signaling pathway;biological_process_unknown,mitochondrion,molecular_function_unknown
PolyA_lnc-470	Chr3	.	1736325	1736553	1	1736325,	1736553,	N	681	beta-fructofuranosidase activity,catalytic activity;biological_process_unknown,cellular_component_unknown,cytoplasm,cytoplasm,molecular_function_unknown
PolyA_lnc-471	Chr3	.	1747188	1747405	1	1747188,	1747405,	N	682	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-472	Chr3	.	17512132	17512397	1	17512132,	17512397,	N	683	biological_process_unknown,extracellular region,molecular_function_unknown;apoplast,carbohydrate metabolic process,catalytic activity,cellular carbohydrate metabolic process,chloroplast,chloroplast,chloroplast,chloroplast,chloroplast,chloroplast envelope,chloroplast stroma,chloroplast stroma,L-malate dehydrogenase activity,L-malate dehydrogenase activity,malate dehydrogenase activity,malate dehydrogenase activity,malate metabolic process,membrane,mitochondrion,nucleotide binding,oxidation-reduction process,oxidoreductase activity,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor,plastid,response to cold,stromule,vacuolar membrane
PolyA_lnc-473	Chr3	.	18314000	18314326	1	18314000,	18314326,	N	684	biological_process_unknown,calmodulin binding,cellular_component_unknown,nucleus;biological_process_unknown,cellular_component_unknown,nucleic acid binding,nucleic acid binding,nucleotide binding,nucleotide binding,nucleus,nucleus,RNA binding
PolyA_lnc-474	Chr3	.	18515643	18516104	1	18515643,	18516104,	N	685	biological_process_unknown,cellular_component_unknown,nitrate transport,nucleus,response to nitrate
PolyA_lnc-475	Chr3	.	18639624	18639833	1	18639624,	18639833,	N	686	cellular_component_unknown,cytoplasm,transferase activity,transferase activity, transferring acyl groups other than amino-acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups
PolyA_lnc-476	Chr3	.	1893074	1893294	1	1893074,	1893294,	N	687	cellular_component_unknown,nucleus,response to red or far red light,zinc ion binding;actin filament-based movement,carbohydrate biosynthetic process,Golgi apparatus,pollen tube,polygalacturonate 4-alpha-galacturonosyltransferase activity,transferase activity, transferring glycosyl groups,transferase activity, transferring glycosyl groups,transferase activity, transferring hexosyl groups
PolyA_lnc-477	Chr3	.	18972642	18972842	1	18972642,	18972842,	N	688	Golgi apparatus,methyltransferase activity;DNA binding,nucleus,nucleus,positive regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,response to light stimulus,sequence-specific DNA binding,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,zinc ion binding

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-478	Chr3	.	19152454	19153413	1	19152454,	19153413,	N	689	ATP binding,ATP binding,photoperiodism, flowering,plasma membrane,plasma membrane,protein binding,protein histidine kinase binding,protein kinase activity,protein kinase activity,protein kinase activity,protein phosphorylation,protein phosphorylation,protein phosphorylation,protein serine/threonine kinase activity,protein serine/threonine kinase activity,transferase activity, transferring phosphorus-containing groups,transferase activity, transferring phosphorus-containing groups;mitochondrion;biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown;biological_process_unknown,molecular_function_unknown,nucleus
PolyA_lnc-479	Chr3	.	1923937	1924179	1	1923937,	1924179,	N	690	cytoplasm,cytoplasm,cytoplasm,heat shock protein binding,heat shock protein binding,heat shock protein binding,protein folding,protein folding,protein folding,protein folding,protein glycosylation,unfolded protein binding,unfolded protein binding,unfolded protein binding;3-dehydroquinate dehydratase activity,3-dehydroquinate dehydratase activity,amino acid transport,catalytic activity,chloroplast,chloroplast,chloroplast stroma,chloroplast stroma,embryo development ending in seed dormancy,embryo development ending in seed dormancy,NADP binding,nucleotide binding,oxidation-reduction process,shikimate 3-dehydrogenase (NADP+) activity,shikimate 3-dehydrogenase (NADP+) activity,shikimate metabolic process
PolyA_lnc-480	Chr3	.	1964972	1965761	1	1964972,	1965761,	N	691	
PolyA_lnc-481	Chr3	.	19892631	19892847	1	19892631,	19892847,	N	692	mitochondrion;amino acid import,biological_process_unknown,ER to Golgi vesicle-mediated transport,molecular_function_unknown,nucleus,nucleus;DNA binding,nucleus,nucleus,regulation of transcription, DNA-dependent,zinc ion binding
PolyA_lnc-482	Chr3	.	19964149	19964578	1	19964149,	19964578,	N	693	cellular response to light stimulus,cellular response to light stimulus,cellular response to light stimulus,chloroplast,chloroplast,chloroplast,chloroplast,DNA binding,DNA-dependent transcription, initiation,DNA-dependent transcription, initiation,DNA-directed RNA polymerase activity,DNA-directed RNA polymerase activity,DNA-directed RNA polymerase activity,photosynthesis, dark reaction,plastid sigma factor activity,regulation of RNA biosynthetic process,regulation of transcription, DNA-dependent,sequence-specific DNA binding transcription factor activity,sigma factor activity
PolyA_lnc-483	Chr3	.	2069433	2070338	1	2069433,	2070338,	N	694	ATP binding,cytoplasm,protein autophosphorylation,protein kinase activity,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,regulation of proton transport,regulation of transcription, DNA-dependent,signal transducer activity,signal transducer activity,signal transduction,signal transduction,transferase activity, transferring phosphorus-containing groups,two-component sensor activity,two-component signal transduction system (phosphorelay)

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-484	Chr3	.	20941190	20941414	1	20941190,	20941414,	N	695	adenylylsulfatase activity,catalytic activity,peroxisome,peroxisome,plasma membrane,protein kinase C binding,purine ribonucleotide metabolic process,sulfur compound metabolic process,zinc ion binding
PolyA_lnc-485	Chr3	.	21103369	21103688	1	21103369,	21103688,	N	696	alkaloid biosynthetic process,biosynthetic process,chloroplast,endoplasmic reticulum,endoplasmic reticulum,plant-type cell wall,plasma membrane,plasmodesma,strictosidine synthase activity,strictosidine synthase activity
PolyA_lnc-486	Chr3	.	21127820	21128020	1	21127820,	21128020,	N	697	DNA binding,DNA binding,DNA-directed RNA polymerase activity,DNA-directed RNA polymerase activity,DNA-directed RNA polymerase V complex,nucleus,nucleus,transcription, DNA-dependent,transcription, DNA-dependent;chloroplast,chloroplast,mitochondrion,mitochondrion organization,peroxisome,peroxisome,peroxisome fission,protein binding
PolyA_lnc-487	Chr3	.	21727762	21728156	1	21727762,	21728156,	N	698	cellular carbohydrate metabolic process,citrate (SI)-synthase activity,citrate (SI)-synthase activity,citrate (SI)-synthase activity,cytoplasm,fatty acid beta-oxidation,fatty acid beta-oxidation,methylglyoxal catabolic process to D-lactate,peroxisome,plasmodesma,proteasomal ubiquitin-dependent protein catabolic process,proteasome core complex assembly,response to misfolded protein,toxin catabolic process,transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer,tricarboxylic acid cycle,tricarboxylic acid cycle;ATP binding,kinase activity,plasma membrane,plasma membrane,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,protein serine/threonine/tyrosine kinase activity,protein tyrosine kinase activity,regulation of signal transduction,transferase activity, transferring phosphorus-containing groups
PolyA_lnc-488	Chr3	.	22031166	22031414	1	22031166,	22031414,	N	699	biological_process_unknown,mitochondrion,mitochondrion,molecular_function_unknown
PolyA_lnc-489	Chr3	.	22174346	22174663	1	22174346,	22174663,	N	700	
PolyA_lnc-490	Chr3	.	22520896	22521100	1	22520896,	22521100,	N	701	
PolyA_lnc-491	Chr3	.	22711969	22712175	1	22711969,	22712175,	N	702	biological_process_unknown,molecular_function_unknown,nucleus,plasma membrane
PolyA_lnc-492	Chr3	.	2704588	2704850	1	2704588,	2704850,	N	703	biological_process_unknown,molecular_function_unknown,nucleus
PolyA_lnc-493	Chr3	.	2760464	2760688	1	2760464,	2760688,	N	704	biological_process_unknown,carbohydrate binding,plasma membrane;biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown
PolyA_lnc-494	Chr3	.	2854770	2854975	1	2854770,	2854975,	N	705	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-495	Chr3	.	3627812	3628300	1	3627812,	3628300,	N	706	anaphase,cell cycle,chromatin silencing,cyclin-dependent protein kinase regulator activity,cytokinesis by cell plate formation,DNA endoreduplication,histone H3-K9 methylation,histone lysine methylation,M phase of mitotic cell cycle,nuclear division,nucleus,nucleus,protein binding,protein kinase binding,regulation of cell cycle,regulation of cell cycle,regulation of cyclin-dependent protein kinase activity,regulation of DNA replication,regulation of flower development,regulation of G2/M transition of mitotic cell cycle,response to cyclopentenone,spindle assembly,stomatal lineage progression;phosphatidylinositol biosynthetic process,transport,transporter activity,vacuole,vacuole
PolyA_lnc-496	Chr3	.	4370632	4371355	1	4370632,	4371355,	Y	707	biological_process_unknown,molecular_function_unknowr
PolyA_lnc-497	Chr3	.	4709854	4710104	1	4709854,	4710104,	N	708	anaphase,biological_process_unknown,cell proliferation,cellular_component_unknown,cytokinesis by cell plate formation,gene silencing,histone lysine methylation,molecular_function_unknown,nucleus,regulation of DNA replication,regulation of flower development,regulation of G2/M transition of mitotic cell cycle
PolyA_lnc-498	Chr3	.	4856598	4856903	1	4856598,	4856903,	Y	709	ADP binding,defense response,defense response,nucleus
lyA_lnc-499	Chr3	.	4872926	4873346	1	4872926,	4873346,	N	710	
PolyA_lnc-500	Chr3	.	4873875	4874180	1	4873875,	4874180,	N	711	
PolyA_lnc-501	Chr3	.	4886659	4887002	1	4886659,	4887002,	Y	712	chloroplast,etioplast,farnesyltranstransferase activity,farnesyltranstransferase activity,isoprenoid biosynthetic process,isoprenoid biosynthetic process,isoprenoid biosynthetic process
PolyA_lnc-502	Chr3	.	4886803	4887349	1	4886803,	4887349,	Y	713	chloroplast,etioplast,farnesyltranstransferase activity,farnesyltranstransferase activity,isoprenoid biosynthetic process,isoprenoid biosynthetic process,isoprenoid biosynthetic process
PolyA_lnc-503	Chr3	.	508521	508722	1	508521,	508722,	N	714	cytoplasm,intracellular,intracellular,nucleus,RAB GTPase activator activity,RAB GTPase activator activity,regulation of Rab GTPase activity,regulation of Rab GTPase activity;adenosylmethionine decarboxylase activity,adenosylmethionine decarboxylase activity,adenosylmethionine decarboxylase activity,adenosylmethionine decarboxylase activity,cellular membrane fusion,cellular modified amino acid biosynthetic process,coumarin biosynthetic process,endosomal transport,gene silencing,phenylpropanoid metabolic process,polyamine biosynthetic process,polyamine catabolic process,protein binding,protein targeting to vacuole,response to wounding,spermidine biosynthetic process,spermidine biosynthetic process,spermidine biosynthetic process,spermine biosynthetic process,spermine biosynthetic process,spermine biosynthetic process,vesicle-mediated transport,viral genome replication

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-504	Chr3	.	5122821	5123148	1	5122821,	5123148,	Y	715	DNA binding,DNA binding,induced systemic resistance, jasmonic acid mediated signaling pathway,intracellular signal transduction,negative regulation of ethylene mediated signaling pathway,negative regulation of transcription, DNA-dependent,negative regulation of transcription, DNA-dependent,nuclear body,nucleus,nucleus,nucleus,protein binding,protein binding,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,respiratory burst involved in defense response,response to abscisic acid stimulus,response to chitin,response to chitin,response to ethylene stimulus,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity
PolyA_lnc-505	Chr3	.	5123206	5123456	1	5123206,	5123456,	Y	716	DNA binding,DNA binding,induced systemic resistance, jasmonic acid mediated signaling pathway,intracellular signal transduction,negative regulation of ethylene mediated signaling pathway,negative regulation of transcription, DNA-dependent,negative regulation of transcription, DNA-dependent,nuclear body,nucleus,nucleus,nucleus,protein binding,protein binding,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,respiratory burst involved in defense response,response to abscisic acid stimulus,response to chitin,response to chitin,response to ethylene stimulus,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity
PolyA_lnc-506	Chr3	.	5436392	5436816	1	5436392,	5436816,	N	717	biological_process_unknown,mitochondrion
PolyA_lnc-507	Chr3	.	5438942	5439192	1	5438942,	5439192,	N	718	intracellular signal transduction,lipid metabolic process,meiotic chromosome segregation,meiotic DNA double-strand break formation,nucleus,phospholipase C activity,reciprocal meiotic recombination,regulation of chromosome organization,sister chromatid cohesion,vernalization response;ATP binding,carbohydrate binding,carbohydrate binding,kinase activity,plasma membrane,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,protein tyrosine kinase activity,transferase activity, transferring phosphorus-containing groups
PolyA_lnc-508	Chr3	.	5439248	5439525	1	5439248,	5439525,	N	719	intracellular signal transduction,lipid metabolic process,meiotic chromosome segregation,meiotic DNA double-strand break formation,nucleus,phospholipase C activity,reciprocal meiotic recombination,regulation of chromosome organization,sister chromatid cohesion,vernalization response;ATP binding,carbohydrate binding,carbohydrate binding,kinase activity,plasma membrane,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,protein tyrosine kinase activity,transferase activity, transferring phosphorus-containing groups

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-509	Chr3	.	5539445	5539720	1	5539445,	5539720,	N	720	ATPase activity,ATPase activity,ATPase activity, coupled to transmembrane movement of substances,ATP binding,ATP binding,coumarin biosynthetic process,drug transmembrane transport,nucleoside-triphosphatase activity,nucleoside-triphosphatase activity,nucleotide binding,nucleotide binding,organic hydroxy compound transport,p-coumaryl alcohol transport,plasma membrane,plasma membrane,positive regulation of flavonoid biosynthetic process,protein targeting to membrane,regulation of lignin biosynthetic process,regulation of plant-type hypersensitive response,response to wounding
PolyA_lnc-510	Chr3	.	5546920	5547162	1	5546920,	5547162,	N	721	ATPase activity,ATPase activity,ATPase activity, coupled to transmembrane movement of substances,ATP binding,ATP binding,coumarin biosynthetic process,drug transmembrane transport,nucleoside-triphosphatase activity,nucleoside-triphosphatase activity,nucleotide binding,nucleotide binding,organic hydroxy compound transport,p-coumaryl alcohol transport,plasma membrane,plasma membrane,positive regulation of flavonoid biosynthetic process,protein targeting to membrane,regulation of lignin biosynthetic process,regulation of plant-type hypersensitive response,response to wounding;DNA binding,DNA binding,nucleic acid binding,nucleus,regulation of transcription, DNA-dependent,response to auxin stimulus,response to cadmium ion,response to ethylene stimulus,response to gibberellin stimulus,response to jasmonic acid stimulus,response to salt stress,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,zinc ion binding
PolyA_lnc-511	Chr3	.	5570687	5571198	1	5570687,	5571198,	N	722	
PolyA_lnc-512	Chr3	.	5609076	5609368	1	5609076,	5609368,	N	723	
PolyA_lnc-513	Chr3	.	5768056	5768287	1	5768056,	5768287,	N	724	biological_process_unknown,cellular_component_unknown,cytoplasm,molecular_function_unknown;mitochondrial ATP synthesis coupled electron transport,mitochondrion,mitochondrion,response to abscisic acid stimulus,response to oxidative stress,response to salt stress
PolyA_lnc-514	Chr3	.	5808723	5809023	1	5808723,	5809023,	Y	725	biological_process_unknown,cellular_component_unknown,DNA-dependent DNA replication,embryo sac egg cell differentiation,nucleus;cell differentiation,chloroplast,chloroplast,chloroplast envelope,chloroplast relocation,leaf morphogenesis,ncRNA metabolic process,nucleus,photosystem II assembly,plastid organization,plastid organization,positive regulation of transcription, DNA-dependent,regulation of protein dephosphorylation,regulation of translation,regulation of translation,RNA processing,RNA processing,RNA processing,rRNA processing,thylakoid membrane organization,transcription from plastid promoter,vacuolar membrane

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-515	Chr3	.	5894947	5895656	1	5894947,	5895656,	N	726	catalytic activity,protein dephosphorylation,protein serine/threonine phosphatase activity,protein serine/threonine phosphatase activity,protein serine/threonine phosphatase complex
PolyA_lnc-516	Chr3	.	5903007	5903261	1	5903007,	5903261,	N	727	biological_process_unknown,cellular_component_unknown,cytoplasm,molecular_function_unknown;biological_process_unknown,cellular_component_unknown,cytoplasm,meiotic chromosome segregation,meiotic DNA double-strand break formation,molecular_function_unknown,reciprocal meiotic recombination,regulation of chromosome organization,sister chromatid cohesion
PolyA_lnc-517	Chr3	.	6126404	6126816	1	6126404,	6126816,	N	728	cell redox homeostasis,cell redox homeostasis,cellular_component_unknown,cytoplasm,cytoplasm,heat acclimation,Hsp70 protein binding,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,protein binding,protein folding,protein oligomerization;biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus
PolyA_lnc-518	Chr3	.	6178805	6179128	1	6178805,	6179128,	N	729	abscisic acid mediated signaling pathway,ATP binding,ATP binding,cytosol,MAP kinase activity,MAP kinase activity,MAP kinase activity,mitochondrion,nucleus,nucleus,nucleus,protein kinase activity,protein kinase activity,protein phosphorylation,protein phosphorylation,protein tyrosine kinase activity,signal transduction,transferase activity, transferring phosphorus-containing groups,transferase activity, transferring phosphorus-containing groups
PolyA_lnc-519	Chr3	.	6525689	6525899	1	6525689,	6525899,	N	730	ethylene biosynthetic process,nucleus,nucleus,zinc ion binding,zinc ion binding,zinc ion binding
PolyA_lnc-520	Chr3	.	7026119	7026524	1	7026119,	7026524,	N	731	electron carrier activity,electron carrier activity,heme binding,heme binding,iron ion binding,iron ion binding,mitochondrion,mitochondrion,oxidation-reduction process,oxidation-reduction process,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen,oxygen binding;brassinosteroid biosynthetic process,electron carrier activity,electron carrier activity,heme binding,heme binding,iron ion binding,iron ion binding,oxidation-reduction process,oxidation-reduction process,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen,oxygen binding
PolyA_lnc-521	Chr3	.	720138	720873	1	720138,	720873,	N	732	
PolyA_lnc-522	Chr3	.	7387494	7387718	1	7387494,	7387718,	N	733	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-523	Chr3	.	7493017	7493318	1	7493017,	7493318,	Y	734	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus;cytoplasm,RNA binding,RNA methyltransferase activity,RNA methyltransferase activity,RNA processing
PolyA_lnc-524	Chr3	.	7544026	7544407	1	7544026,	7544407,	N	735	cellular_component_unknown,cytoplasm,metabolic process,oxidation-reduction process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;biological_process_unknown,DNA binding,glucuronoxylan metabolic process,gravitropism,nucleus,protein binding,xylan biosynthetic process
PolyA_lnc-525	Chr3	.	7798220	7798905	1	7798220,	7798905,	N	736	
PolyA_lnc-526	Chr3	.	8404907	8405111	1	8404907,	8405111,	N	737	cellular_component_unknown,embryo development ending in seed dormancy,megagametogenesis,mitochondrion,molecular_function_unknown
PolyA_lnc-527	Chr3	.	9109425	9109643	1	9109425,	9109643,	N	738	chloroplast,signal transduction;defense response,kinase activity,response to endoplasmic reticulum stress,signal transduction,systemic acquired resistance
PolyA_lnc-528	Chr3	.	9120444	9120685	1	9120444,	9120685,	N	739	
PolyA_lnc-529	Chr3	.	9306863	9307141	1	9306863,	9307141,	N	740	biological_process_unknown,calcium ion binding,calcium ion binding,Golgi apparatus,response to chitin
PolyA_lnc-530	Chr4	+	13620248	13621171	3	13620248,13620376,13621130,	13620303,13620502,13621171,	N	741	ADP binding,cellular_component_unknown,defense response,defense response,mitochondrion,nucleoside-triphosphatase activity,nucleotide binding
PolyA_lnc-531	Chr4	+	14884061	14884699	2	14884061,14884533,	14884111,14884699,	N	742	carbohydrate metabolic process,catalytic activity,catalytic activity,cellular metabolic process,coenzyme binding,endosome,Golgi apparatus,Golgi apparatus,Golgi apparatus,nucleotide binding,nucleotide-sugar metabolic process,racemase and epimerase activity, acting on carbohydrates and derivatives,trans-Golgi network,UDP-glucuronate 4-epimerase activity
PolyA_lnc-532	Chr4	+	14979448	14980112	2	14979448,14979679,	14979580,14980112,	N	743	biological_process_unknown,molecular_function_unknown,nucleus
PolyA_lnc-533	Chr4	+	16289842	16290352	2	16289842,16290307,	16290191,16290352,	N	744	embryo development ending in seed dormancy,mitochondrion
PolyA_lnc-534	Chr4	+	17543553	17543834	1	17543553,	17543834,	N	745	ATPase activity,ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism,ATP binding,ATP biosynthetic process,cadmium-transporting ATPase activity,calcium ion transport,calcium-transporting ATPase activity,catalytic activity,cation transport,cellular copper ion homeostasis,chloroplast,chloroplast envelope,chloroplast envelope,chloroplast envelope,chloroplast envelope,copper-exporting ATPase activity,hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides,integral to membrane,membrane,metabolic process,metal ion binding,metal ion transmembrane transporter activity,metal ion transport,nucleotide binding,plasma membrane,plastid,response to light intensity,response to toxin,zinc ion homeostasis,zinc transporting ATPase activity

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-535	Chr4	+	2181466	2181818	2	2181466,2181631,	2181531,2181818,	N	746	
PolyA_lnc-536	Chr4	+	4309155	4311891	3	4309155,4310945,4311245,	4310775,4311170,4311891,	N	747	
PolyA_lnc-537	Chr4	+	4309155	4311897	3	4309155,4310945,4311250,	4310775,4311170,4311897,	N	748	
PolyA_lnc-538	Chr4	+	4309155	4311897	3	4309155,4310945,4311645,	4310775,4311397,4311897,	N	749	
PolyA_lnc-539	Chr4	+	5425626	5425971	2	5425626,5425880,	5425774,5425971,	N	750	
PolyA_lnc-540	Chr4	+	5426203	5426441	2	5426203,5426333,	5426236,5426441,	N	751	
ılyA_lnc-541	Chr4	+	6666575	6667266	4	6666575,6666840,6667007,6667235,	6666700,6666933,6667142,6667266,	N	752	
PolyA_lnc-542	Chr4	+	6667197	6669497	5	6667197,6667566,6667728,6668039,6668307,	6667284,6667616,6667953,6668083,6669497,	N	753	
PolyA_lnc-543	Chr4	+	6667723	6667949	1	6667723,	6667949,	N	754	
PolyA_lnc-544	Chr4	+	7280398	7280757	1	7280398,	7280757,	N	755	
PolyA_lnc-545	Chr4	+	761552	762615	2	761552,762350,	761840,762615,	N	756	
PolyA_lnc-546	Chr4	+	7902779	7902985	1	7902779,	7902985,	N	757	chloroplast,chloroplast,chloroplast,chloroplast envelope,chloroplast inner membrane,membrane,membrane
PolyA_lnc-547	Chr4	+	837675	838324	1	837675,	838324,	N	758	intracellular signal transduction,nucleus,oxidation-reduction process,protein-disulfide reductase activity,zinc ion binding
PolyA_lnc-548	Chr4	+	837726	838469	2	837726,838095,	837926,838469,	N	759	intracellular signal transduction,nucleus,oxidation-reduction process,protein-disulfide reductase activity,zinc ion binding
PolyA_lnc-549	Chr4	+	8671382	8671935	2	8671382,8671602,	8671526,8671935,	N	760	ATPase activity,ATP binding,drug transmembrane transport,membrane,nucleoside-triphosphatase activity,nucleotide binding,nucleus

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-550	Chr4	+	9225526	9225764	2	9225526,9225626,	9225549,9225764,	N	761	auxin biosynthetic process,cotyledon development,inflorescence development,mitochondrion,oxidation-reduction process,oxidoreductase activity,primary amine oxidase activity;chloroplast,cytoplasm,flavonoid biosynthetic process,oxidation-reduction process,oxidation-reduction process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors,peroxisome
PolyA_lnc-551	Chr4	-	10992371	10992809	2	10992371,10992773,	10992665,10992809,	N	762	apoplast,chloroplast,chloroplast,chloroplast,chloroplast envelope,chloroplast envelope,chloroplast stroma,chloroplast stroma,chloroplast stroma,chloroplast thylakoid,chloroplast thylakoid membrane,chloroplast thylakoid membrane,cuticle development,GTPase activity,GTP binding,intracellular,membrane,nucleoid,nucleolus,nucleus,peptidyl-cysteine S-nitrosylation,plastid,protein binding,translational elongation,translation elongation factor activity,translation elongation factor activity,very long-chain fatty acid metabolic process
PolyA_lnc-552	Chr4	-	11244990	11245860	2	11244990,11245785,	11245627,11245860,	N	763	carbohydrate binding,carbohydrate binding,galactosyltransferase activity,galactosyltransferase activity,Golgi apparatus,Golgi apparatus,membrane,membrane,protein glycosylation,protein glycosylation,transferase activity, transferring glycosyl groups,transferase activity, transferring hexosyl groups
PolyA_lnc-553	Chr4	-	13980939	13981516	1	13980939,	13981516,	N	764	molecular_function_unknown,response to gibberellin stimulus
PolyA_lnc-554	Chr4	-	14917155	14917474	1	14917155,	14917474,	N	765	
PolyA_lnc-555	Chr4	-	14917155	14917681	2	14917155,14917520,	14917376,14917681,	N	766	
PolyA_lnc-556	Chr4	-	15118051	15118526	2	15118051,15118335,	15118264,15118526,	N	767	DNA binding,DNA binding,nucleus,nucleus,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity;biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown
PolyA_lnc-557	Chr4	-	1527332	1527790	2	1527332,1527766,	1527662,1527790,	N	768	biological_process_unknown,biological_process_unknown,cellular_component_unknown,cellular_component_unknown,mitochondrion,mitochondrion,molecular_function_unknown,molecular_function_unknown

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-558	Chr4	-	17026557	17027093	2	17026557,17026990,	17026598,17027093,	N	769	actin filament organization,cytoplasm,GTP binding,GTP binding,intracellular,nucleus,small GTPase mediated signal transduction
PolyA_lnc-559	Chr4	-	17027245	17027790	2	17027245,17027627,	17027452,17027790,	N	770	cellular_component_unknown,heme binding,L-ascorbate peroxidase activity,oxidation-reduction process,peroxidase activity,peroxidase activity,response to oxidative stress
PolyA_lnc-560	Chr4	-	1874895	1876258	2	1874895,1875909,	1875551,1876258,	N	771	
PolyA_lnc-561	Chr4	-	1875497	1876836	3	1875497,1875909,1876342,	1875551,1876195,1876836,	N	772	
PolyA_lnc-562	Chr4	-	1875883	1876733	3	1875883,1876130,1876342,	1876037,1876195,1876733,	N	773	biological_process_unknown,cellular_component_unknown,molecular_function_unknown
PolyA_lnc-563	Chr4	-	2757839	2758487	2	2757839,2758057,	2757870,2758487,	N	774	cytoplasm,cytoplasm,molecular_function_unknown,polar nucleus fusion,protein folding,response to endoplasmic reticulum stress,response to heat,response to high light intensity,response to hydrogen peroxide
PolyA_lnc-564	Chr4	-	5770139	5770966	2	5770139,5770929,	5770846,5770966,	N	775	
PolyA_lnc-565	Chr4	-	7376661	7382689	3	7376661,7382175,7382427,	7376704,7382298,7382689,	N	776	adenine phosphoribosyltransferase activity,adenine phosphoribosyltransferase activity,adenine salvage,adenine salvage,cytoplasm,cytoplasm,cytoplasm,nucleoside metabolic process,nucleoside metabolic process
PolyA_lnc-566	Chr4	-	7382260	7382626	2	7382260,7382427,	7382287,7382626,	N	777	
PolyA_lnc-567	Chr4	-	765073	765406	1	765073,	765406,	N	778	chloroplast,endoplasmic reticulum,Golgi apparatus,rhamnogalacturonan II biosynthetic process,UDP-xylosyltransferase activity
PolyA_lnc-568	Chr4	.	10210695	10210899	1	10210695,	10210899,	N	779	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus;apoplast,apoplast,cell-cell signaling involved in cell fate commitment,extracellular region,receptor binding,receptor serine/threonine kinase binding,signal transduction
PolyA_lnc-569	Chr4	.	10211660	10211864	1	10211660,	10211864,	N	780	apoplast,apoplast,cell-cell signaling involved in cell fate commitment,extracellular region,receptor binding,receptor serine/threonine kinase binding,signal transduction
PolyA_lnc-570	Chr4	.	10251924	10252165	1	10251924,	10252165,	N	781	biological_process_unknown,cytokinin biosynthetic process,glucuronoxylan metabolic process,molecular_function_unknown,nucleus,xylan biosynthetic process
PolyA_lnc-571	Chr4	.	10252281	10252482	1	10252281,	10252482,	N	782	biological_process_unknown,cytokinin biosynthetic process,glucuronoxylan metabolic process,molecular_function_unknown,nucleus,xylan biosynthetic process
PolyA_lnc-572	Chr4	.	10252672	10252995	1	10252672,	10252995,	Y	783	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-573	Chr4	.	10268497	10268769	1	10268497,	10268769,	N	784	
PolyA_lnc-574	Chr4	.	10811345	10811694	1	10811345,	10811694,	Y	785	biological_process_unknown,cellular_component_unknown,cytoplasm,molecular_function_unknown
PolyA_lnc-575	Chr4	.	10944969	10945477	1	10944969,	10945477,	Y	786	
PolyA_lnc-576	Chr4	.	10945445	10945925	1	10945445,	10945925,	Y	787	
PolyA_lnc-577	Chr4	.	10945613	10946107	1	10945613,	10946107,	Y	788	
PolyA_lnc-578	Chr4	.	11110485	11110771	1	11110485,	11110771,	N	789	
PolyA_lnc-579	Chr4	.	11568327	11568607	1	11568327,	11568607,	N	790	biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown
PolyA_lnc-580	Chr4	.	12487431	12487717	1	12487431,	12487717,	N	791	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus;biological_process_unknown,molecular_function_unknown;alpha,alpha-trehalase activity,alpha,alpha-trehalase activity,catalytic activity,plasma membrane,plasma membrane,trehalase activity,trehalose catabolic process,trehalose metabolic process
PolyA_lnc-581	Chr4	.	13318741	13319293	1	13318741,	13319293,	N	792	
PolyA_lnc-582	Chr4	.	13332951	13333191	1	13332951,	13333191,	N	793	aromatic amino acid family biosynthetic process,chloroplast,chloroplast,chloroplast,iron-sulfur cluster assembly,mitochondrion,positive regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,RNA binding,RNA binding,stomatal complex morphogenesis,transcription from plastid promoter
PolyA_lnc-583	Chr4	.	13633131	13633398	1	13633131,	13633398,	N	794	ADP binding,defense response,defense response,nucleus
PolyA_lnc-584	Chr4	.	1445647	1445874	1	1445647,	1445874,	N	795	cellular_component_unknown,mitochondrion,N-terminal protein myristoylation,nucleic acid binding;biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown
PolyA_lnc-585	Chr4	.	14724759	14725004	1	14724759,	14725004,	N	796	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism,ATP binding,ATP biosynthetic process,cadmium-transporting ATPase activity,cadmium-transporting ATPase activity,catalytic activity,cation transport,hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides,integral to membrane,membrane,metabolic process,metal ion binding,metal ion transmembrane transporter activity,metal ion transport,nucleotide binding,plasma membrane,zinc ion homeostasis
PolyA_lnc-586	Chr4	.	14885116	14885341	1	14885116,	14885341,	N	797	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-587	Chr4	.	15045386	15045627	1	15045386,	15045627,	Y	798	aminopeptidase activity,aminopeptidase activity,chloroplast,chloroplast,chloroplast stroma,cytoplasm,intracellular,manganese ion binding,metalloexopeptidase activity,protein metabolic process,proteolysis,proteolysis;aminopeptidase activity,aminopeptidase activity,aminopeptidase activity,chloroplast,chloroplast,chloroplast stroma,cytoplasm,cytosol,intracellular,leaf senescence,manganese ion binding,metalloexopeptidase activity,protein metabolic process,proteolysis,proteolysis,vacuole
PolyA_lnc-588	Chr4	.	15216745	15217493	1	15216745,	15217493,	N	799	cellular_component_unknown,membrane,membrane,mitochondrion,mitochondrion,transferase activity, transferring glycosyl groups;biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown
PolyA_lnc-589	Chr4	.	15219940	15220971	1	15219940,	15220971,	N	800	biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown;biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown;cell redox homeostasis,nucleus,selenium binding
PolyA_lnc-590	Chr4	.	15220241	15221172	1	15220241,	15221172,	N	801	biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown;biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown;cell redox homeostasis,nucleus,selenium binding
PolyA_lnc-591	Chr4	.	15239484	15239903	1	15239484,	15239903,	N	802	damaged DNA binding,DNA-directed DNA polymerase activity,DNA repair,embryo development,embryo sac development,nucleus,sister chromatid cohesion
PolyA_lnc-592	Chr4	.	15239962	15240703	1	15239962,	15240703,	N	803	damaged DNA binding,DNA-directed DNA polymerase activity,DNA repair,embryo development,embryo sac development,nucleus,sister chromatid cohesion
PolyA_lnc-593	Chr4	.	15240298	15240820	1	15240298,	15240820,	N	804	damaged DNA binding,DNA-directed DNA polymerase activity,DNA repair,embryo development,embryo sac development,nucleus,sister chromatid cohesion
PolyA_lnc-594	Chr4	.	15240905	15241412	1	15240905,	15241412,	N	805	
PolyA_lnc-595	Chr4	.	15242515	15242725	1	15242515,	15242725,	N	806	biological_process_unknown,fatty acid beta-oxidation,molecular_function_unknown,nucleus,nucleus,photoperiodism, flowering,protein import into peroxisome matrix
PolyA_lnc-596	Chr4	.	1528687	1529133	1	1528687,	1529133,	N	807	biological_process_unknown,biological_process_unknown,cellular_component_unknown,cellular_component_unknown,mitochondrion,mitochondrion,molecular_function_unknown,molecular_function_unknown;defense response to bacterium,defense response to fungus,detection of biotic stimulus,detection of external stimulus,MAPK cascade,negative regulation of defense response,regulation of hydrogen peroxide metabolic process,regulation of innate immune response,response to molecule of bacterial origin,salicylic acid biosynthetic process,systemic acquired resistance,systemic acquired resistance, salicylic acid mediated signaling pathway

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-597	Chr4	.	15993596	15993809	1	15993596,	15993809,	N	808	cellular_component_unknown,nucleus,ubiquitin-dependent protein catabolic process,ubiquitin-dependent protein catabolic process,ubiquitin-protein ligase activity
PolyA_lnc-598	Chr4	.	16426017	16426236	1	16426017,	16426236,	N	809	cellular_component_unknown,molecular_function_unknown,N-terminal protein myristoylation;biological_process_unknown,cellular_component_unknown,DNA binding,nucleus
PolyA_lnc-599	Chr4	.	16826669	16826999	1	16826669,	16826999,	N	810	ARF guanyl-nucleotide exchange factor activity,ARF guanyl-nucleotide exchange factor activity,cytoplasm,guanyl-nucleotide exchange factor activity,intracellular,regulation of ARF protein signal transduction,regulation of catalytic activity,transition metal ion transport,vesicle-mediated transport
PolyA_lnc-600	Chr4	.	16828362	16828566	1	16828362,	16828566,	N	811	negative regulation of gibberellic acid mediated signaling pathway,nucleus,sequence-specific DNA binding transcription factor activity
PolyA_lnc-601	Chr4	.	16831661	16831917	1	16831661,	16831917,	N	812	
lyA_lnc-602	Chr4	.	16891481	16891843	1	16891481,	16891843,	N	813	calmodulin binding,negative regulation of transcription, DNA-dependent,nuclear-transcribed mRNA catabolic process,nucleus,nucleus,nucleus,nucleus,positive regulation of cell proliferation,protein binding,protein N-linked glycosylation,regulation of defense response,regulation of transcription, DNA-dependent,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity;mitochondrion
PolyA_lnc-603	Chr4	.	17393678	17394124	1	17393678,	17394124,	N	814	cell redox homeostasis,chloroplast,chloroplast,chloroplast,molecular_function_unknown
PolyA_lnc-604	Chr4	.	17394200	17394477	1	17394200,	17394477,	N	815	
PolyA_lnc-605	Chr4	.	17394371	17394606	1	17394371,	17394606,	N	816	
PolyA_lnc-606	Chr4	.	1770424	1771162	1	1770424,	1771162,	Y	817	biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown,nucleus
PolyA_lnc-607	Chr4	.	17706553	17706820	1	17706553,	17706820,	N	818	biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown
PolyA_lnc-608	Chr4	.	1774661	1774903	1	1774661,	1774903,	N	819	biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown,nucleus
PolyA_lnc-609	Chr4	.	17820023	17820266	1	17820023,	17820266,	N	820	
PolyA_lnc-610	Chr4	.	17971601	17971806	1	17971601,	17971806,	N	821	catalytic activity,cytosol,metabolic process,nucleus;antiporter activity,chloroplast,drug transmembrane transport,drug transmembrane transporter activity,membrane,plasma membrane,transmembrane transport
PolyA_lnc-611	Chr4	.	18201583	18201795	1	18201583,	18201795,	N	822	
PolyA_lnc-612	Chr4	.	18202004	18202293	1	18202004,	18202293,	N	823	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus
PolyA_lnc-613	Chr4	.	1875561	1875769	1	1875561,	1875769,	N	824	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-614	Chr4	.	1934179	1934539	1	1934179,	1934539,	N	825	chloroplast,chloroplast,chloroplast,chloroplast,chloroplast stroma,chloroplast thylakoid,chloroplast thylakoid membrane,chloroplast thylakoid membrane,chloroplast thylakoid membrane,nucleus,photoinhibition,plastoglobule,plastoglobule,plastoglobule,protein binding,response to abscisic acid stimulus,response to cold,stromule,structural molecule activity,structural molecule activity,thylakoid,thylakoid,thylakoid,thylakoid lumen
PolyA_lnc-615	Chr4	.	2447729	2448043	1	2447729,	2448043,	N	826	
PolyA_lnc-616	Chr4	.	2447880	2448262	1	2447880,	2448262,	N	827	chloroplast,chloroplast,cysteine biosynthetic process,cytosol,oxidation-reduction process,oxidation-reduction process,peptide-methionine (S)-S-oxide reductase activity,peptide-methionine (S)-S-oxide reductase activity
PolyA_lnc-617	Chr4	.	2716446	2717381	1	2716446,	2717381,	N	828	
PolyA_lnc-618	Chr4	.	4825033	4825328	1	4825033,	4825328,	N	829	cytoplasm,cytoplasm,heat shock protein binding,heat shock protein binding,protein folding,response to high light intensity,response to hydrogen peroxide
PolyA_lnc-619	Chr4	.	4971424	4971623	1	4971424,	4971623,	N	830	
PolyA_lnc-620	Chr4	.	4971549	4971861	1	4971549,	4971861,	N	831	
PolyA_lnc-621	Chr4	.	5156068	5156391	1	5156068,	5156391,	N	832	
lyA_lnc-622	Chr4	.	5156416	5156748	1	5156416,	5156748,	N	833	
PolyA_lnc-623	Chr4	.	5317545	5317787	1	5317545,	5317787,	N	834	
PolyA_lnc-624	Chr4	.	5371940	5372512	1	5371940,	5372512,	N	835	ADP binding,cytoplasm,defense response,defense response,intracellular,nucleoside-triphosphatase activity,nucleotide binding,signal transduction
PolyA_lnc-625	Chr4	.	5424974	5425181	1	5424974,	5425181,	N	836	
PolyA_lnc-626	Chr4	.	5425022	5425246	1	5425022,	5425246,	N	837	
PolyA_lnc-627	Chr4	.	6430348	6430604	1	6430348,	6430604,	N	838	arsenite transmembrane transporter activity,arsenite transport,borate transmembrane transporter activity,borate transport,borate transport,borate uptake transmembrane transporter activity,cellular response to boron-containing substance levels,cellular response to iron ion starvation,iron ion transport,lateral plasma membrane,membrane,membrane,nitrate transport,plasma membrane,response to arsenic-containing substance,response to arsenic-containing substance,response to boron-containing substance,response to boron-containing substance,response to nitrate,transition metal ion transport,transport,transport,transporter activity,water channel activity,water channel activity

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-628	Chr4	.	6430603	6430870	1	6430603,	6430870,	N	839	arsenite transmembrane transporter activity,arsenite transport,borate transmembrane transporter activity,borate transport,borate transport,borate uptake transmembrane transporter activity,cellular response to boron-containing substance levels,cellular response to iron ion starvation,iron ion transport,lateral plasma membrane,membrane,membrane,nitrate transport,plasma membrane,response to arsenic-containing substance,response to arsenic-containing substance,response to boron-containing substance,response to boron-containing substance,response to nitrate,transition metal ion transport,transport,transport,transporter activity,water channel activity,water channel activity
PolyA_lnc-629	Chr4	.	6644966	6645518	1	6644966,	6645518,	N	840	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus;biological_process_unknown,molecular_function_unknown,nucleus
PolyA_lnc-630	Chr4	.	6669973	6670219	1	6669973,	6670219,	N	841	
PolyA_lnc-631	Chr4	.	688334	688573	1	688334,	688573,	N	842	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus,nucleus,nucleus
PolyA_lnc-632	Chr4	.	6993290	6993559	1	6993290,	6993559,	N	843	
PolyA_lnc-633	Chr4	.	70173	70377	1	70173,	70377,	N	844	extracellular region,extracellular region,lipid binding,lipid transport,lipid transport,lipid transport,N-terminal protein myristoylation;biological_process_unknown,endoplasmic reticulum,N-terminal protein myristoylation,structural molecule activity,structural molecule activity
PolyA_lnc-634	Chr4	.	7243189	7243429	1	7243189,	7243429,	N	845	intracellular signal transduction,membrane,membrane,molecular_function_unknown
PolyA_lnc-635	Chr4	.	7661529	7661749	1	7661529,	7661749,	N	846	ATP binding,chloroplast,kinase activity,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,transferase activity, transferring phosphorus-containing groups;apoplast,axillary shoot meristem initiation,mitochondrion,molecular_function_unknown,phloem or xylem histogenesis,procambium histogenesis,receptor serine/threonine kinase binding,xylem development
PolyA_lnc-636	Chr4	.	7661900	7662142	1	7661900,	7662142,	N	847	ATP binding,chloroplast,kinase activity,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,transferase activity, transferring phosphorus-containing groups;apoplast,axillary shoot meristem initiation,mitochondrion,molecular_function_unknown,phloem or xylem histogenesis,procambium histogenesis,receptor serine/threonine kinase binding,xylem development
PolyA_lnc-637	Chr4	.	7809229	7809825	1	7809229,	7809825,	N	848	biological_process_unknown,calcium ion binding,calcium ion binding,cellular_component_unknown
PolyA_lnc-638	Chr4	.	7811676	7811897	1	7811676,	7811897,	N	849	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-639	Chr4	.	7945778	7946031	1	7945778,	7946031,	Y	850	cellular response to iron ion starvation,coumarin biosynthetic process,cytoplasm,iron ion transport,lignan biosynthetic process,nitrate transport,nucleotide binding,pinoresinol reductase activity,pinoresinol reductase activity,plasmodesma,positive regulation of flavonoid biosynthetic process,response to nitrate,response to wounding
PolyA_lnc-640	Chr4	.	8076221	8076518	1	8076221,	8076518,	N	851	biological_process_unknown,cellular_component_unknown,nucleus,zinc ion binding;DNA binding,nuclear-transcribed mRNA catabolic process,nucleus,nucleus,regulation of transcription, DNA-dependent,sequence-specific DNA binding,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity
PolyA_lnc-641	Chr4	.	8346011	8346424	1	8346011,	8346424,	N	852	DNA binding,intracellular,nucleus,nucleus,regulation of transcription, DNA-dependent,sequence-specific DNA binding,sequence-specific DNA binding transcription factor activity
PolyA_lnc-642	Chr4	.	8717893	8718186	1	8717893,	8718186,	N	853	cellular_component_unknown,metabolic process,transferase activity, transferring glycosyl groups,transferase activity, transferring hexosyl groups;cellular_component_unknown,metabolic process,quercetin 3-O-glucosyltransferase activity,transferase activity, transferring glycosyl groups,transferase activity, transferring hexosyl groups,UDP-glycosyltransferase activity
PolyA_lnc-643	Chr4	.	876174	876476	1	876174,	876476,	N	854	
PolyA_lnc-644	Chr4	.	8859826	8860041	1	8859826,	8860041,	N	855	calcium ion binding,calcium ion binding,calcium ion binding,chloroplast,chloroplast,chloroplast,chloroplast,chloroplast,chloroplast,chloroplast,chloroplast photosystem II,chloroplast stroma,chloroplast thylakoid lumen,chloroplast thylakoid lumen,chloroplast thylakoid membrane,chloroplast thylakoid membrane,extrinsic to membrane,extrinsic to membrane,extrinsic to membrane,membrane,membrane,membrane,oxygen evolving complex,oxygen evolving complex,oxygen evolving complex,oxygen evolving complex,photosynthesis,photosynthesis,photosynthesis,photosystem II,photosystem II,photosystem II,thylakoid,thylakoid,thylakoid,thylakoid,thylakoid,thylakoid,thylakoid,thylakoid lumen
PolyA_lnc-645	Chr4	.	9300718	9300928	1	9300718,	9300928,	N	856	cell wall,cysteine-type endopeptidase inhibitor activity,cytosol,enzyme regulator activity,extracellular region,plasmodesma,vacuole
PolyA_lnc-646	Chr4	.	9482537	9482852	1	9482537,	9482852,	Y	857	biological_process_unknown,cellular_component_unknown,molecular_function_unknown;mitochondrion
PolyA_lnc-647	Chr4	.	9483592	9483835	1	9483592,	9483835,	N	858	
PolyA_lnc-648	Chr4	.	9532500	9532784	1	9532500,	9532784,	N	859	ADP binding,cytoplasm,defense response,defense response,intracellular,mitochondrion,nucleoside-triphosphatase activity,nucleotide binding,signal transduction

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-649	Chr5	+	1269106	1271340	2	1269106,1271169,	1269153,1271340,	N	860	biosynthetic process,biosynthetic process,endosome,Golgi apparatus,Golgi apparatus,nucleus,nucleus,transferase activity, transferring glycosyl groups,trans-Golgi network
PolyA_lnc-650	Chr5	+	1270998	1271301	2	1270998,1271169,	1271026,1271301,	N	861	biosynthetic process,biosynthetic process,endosome,Golgi apparatus,Golgi apparatus,nucleus,nucleus,transferase activity, transferring glycosyl groups,trans-Golgi network
PolyA_lnc-651	Chr5	+	13098842	13099654	2	13098842,13099571,	13098869,13099654,	N	862	
PolyA_lnc-652	Chr5	+	13099618	13099853	1	13099618,	13099853,	N	863	
PolyA_lnc-653	Chr5	+	1340815	1341543	1	1340815,	1341543,	N	864	biological_process_unknown,biological_process_unknown,molecular_function_unknown,molecular_function_unknown,nucleus,nucleus
PolyA_lnc-654	Chr5	+	13666762	13667308	1	13666762,	13667308,	N	865	biological_process_unknown,cellular_component_unknown,glucose catabolic process;ADP binding,defense response,defense response,plasma membrane
PolyA_lnc-655	Chr5	+	13908432	13910231	2	13908432,13909050,	13908530,13910231,	N	866	
PolyA_lnc-656	Chr5	+	13908681	13910761	1	13908681,	13910761,	N	867	
PolyA_lnc-657	Chr5	+	15089701	15092749	2	15089701,15092724,	15089915,15092749,	N	868	
PolyA_lnc-658	Chr5	+	15089764	15090042	1	15089764,	15090042,	N	869	intracellular,multicellular organismal development,multicellular organismal development,nucleus,nucleus,nucleus,protein ubiquitination,ubiquitin-dependent protein catabolic process,ubiquitin-dependent protein catabolic process,ubiquitin-protein ligase activity,zinc ion binding
PolyA_lnc-659	Chr5	+	15516133	15516471	1	15516133,	15516471,	N	870	
PolyA_lnc-660	Chr5	+	15516369	15516806	1	15516369,	15516806,	N	871	
PolyA_lnc-661	Chr5	+	15516531	15517087	1	15516531,	15517087,	N	872	
PolyA_lnc-662	Chr5	+	15516860	15517203	1	15516860,	15517203,	N	873	
PolyA_lnc-663	Chr5	+	15517253	15518213	4	15517253,15517700,15517963,15518190,	15517562,15517832,15518007,15518213,	N	874	
PolyA_lnc-664	Chr5	+	15519776	15520554	4	15519776,15519961,15520147,15520392,	15519889,15520059,15520270,15520554,	N	875	
PolyA_lnc-665	Chr5	+	15520206	15520622	3	15520206,15520392,15520595,	15520270,15520503,15520622,	N	876	
PolyA_lnc-666	Chr5	+	15520759	15521364	2	15520759,15520910,	15520815,15521364,	N	877	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-667	Chr5	+	15520943	15521684	1	15520943,	15521684,	N	878	asparaginyl-tRNA synthase (glutamine-hydrolyzing) activity,chloroplast,N-terminal protein myristoylation,tRNA aminoacylation for protein translation
PolyA_lnc-668	Chr5	+	16714406	16714679	1	16714406,	16714679,	N	879	
PolyA_lnc-669	Chr5	+	16714480	16716598	5	16714480,16714775,16715223,16715527,16715845,	16714689,16714842,16715294,16715749,16716598,	N	880	
PolyA_lnc-670	Chr5	+	16715235	16715705	2	16715235,16715623,	16715294,16715705,	N	881	
PolyA_lnc-671	Chr5	+	17045375	17045772	1	17045375,	17045772,	N	882	
PolyA_lnc-672	Chr5	+	17045375	17046996	2	17045375,17046810,	17045659,17046996,	N	883	
PolyA_lnc-673	Chr5	+	17046756	17046996	1	17046756,	17046996,	N	884	
PolyA_lnc-674	Chr5	+	17958358	17958767	1	17958358,	17958767,	N	885	
PolyA_lnc-675	Chr5	+	17958359	17959751	2	17958359,17959315,	17958518,17959751,	N	886	
PolyA_lnc-676	Chr5	+	17959079	17959746	1	17959079,	17959746,	N	887	
PolyA_lnc-677	Chr5	+	19889946	19890729	2	19889946,19890163,	19889985,19890729,	N	888	catalytic activity,catalytic activity,chloroplast,chloroplast,cuticle development,cuticle development,fatty acid biosynthetic process,fatty acid biosynthetic process,lipid biosynthetic process,membrane,membrane,metabolic process,metabolic process,response to cold,transferase activity, transferring acyl groups,transferase activity, transferring acyl groups other than amino-acyl groups,transferase activity, transferring acyl groups other than amino-acyl groups,very long-chain fatty acid metabolic process,very long-chain fatty acid metabolic process
PolyA_lnc-678	Chr5	+	20540464	20541132	2	20540464,20540838,	20540742,20541132,	N	889	
PolyA_lnc-679	Chr5	+	22478242	22479618	2	22478242,22479469,	22478493,22479618,	N	890	chloroplast,embryo development,embryo sac development,identical protein binding,integral to plasma membrane,plasma membrane,pollen development
PolyA_lnc-680	Chr5	+	22956285	22957267	2	22956285,22956971,	22956748,22957267,	N	891	
PolyA_lnc-681	Chr5	+	23856968	23857425	2	23856968,23857121,	23857018,23857425,	N	892	
PolyA_lnc-682	Chr5	+	25980256	25980817	2	25980256,25980598,	25980401,25980817,	N	893	
PolyA_lnc-683	Chr5	+	26066923	26067963	2	26066923,26067911,	26067127,26067963,	N	894	DNA binding,DNA binding,nucleus,regulation of transcription, DNA-dependent,sequence-specific DNA binding transcription factor activity
PolyA_lnc-684	Chr5	+	26829720	26834854	2	26829720,26834729,	26829798,26834854,	N	895	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-685	Chr5	+	288369	288711	1	288369,	288711,	N	896	
PolyA_lnc-686	Chr5	+	4791118	4791947	1	4791118,	4791947,	N	897	
PolyA_lnc-687	Chr5	+	7614166	7615165	2	7614166,7614385,	7614300,7615165,	N	898	
PolyA_lnc-688	Chr5	+	8447387	8447780	2	8447387,8447505,	8447415,8447780,	N	899	
PolyA_lnc-689	Chr5	-	10367509	10368317	2	10367509,10367939,	10367868,10368317,	N	900	
PolyA_lnc-690	Chr5	-	10395413	10395925	2	10395413,10395875,	10395692,10395925,	N	901	
PolyA_lnc-691	Chr5	-	1341868	1343470	3	1341868,1342314,1343267,	1342046,1342938,1343470,	N	902	biological_process_unknown,biological_process_unknown,molecular_function_unknown,molecular_function_unknown,nucleus,nucleus
PolyA_lnc-692	Chr5	-	1420712	1422582	2	1420712,1421184,	1421093,1422582,	N	903	
PolyA_lnc-693	Chr5	-	1420712	1422582	2	1420712,1421597,	1421397,1422582,	N	904	
PolyA_lnc-694	Chr5	-	14550325	14550822	1	14550325,	14550822,	N	905	
PolyA_lnc-695	Chr5	-	14550325	14550822	2	14550325,14550699,	14550564,14550822,	N	906	
PolyA_lnc-696	Chr5	-	15562063	15562734	2	15562063,15562606,	15562514,15562734,	N	907	
PolyA_lnc-697	Chr5	-	1562024	1562949	2	1562024,1562569,	1562460,1562949,	N	908	electron carrier activity,glucosinolate biosynthetic process,glucosinolate biosynthetic process,heme binding,indoleacetic acid biosynthetic process,iron ion binding,oxidation-reduction process,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen,oxygen binding,tryptophan catabolic process;anthocyanin-containing compound biosynthetic process,cellular_component_unknown,cellular modified amino acid biosynthetic process,cellular modified amino acid biosynthetic process,chalcone isomerase activity,chalcone isomerase activity,chloroplast,chloroplast,flavonoid biosynthetic process,flavonoid biosynthetic process,flavonoid biosynthetic process,intramolecular lyase activity,intramolecular lyase activity,response to karrikin,response to sucrose stimulus,response to UV-B
PolyA_lnc-698	Chr5	-	15813616	15814180	2	15813616,15814042,	15813690,15814180,	N	909	
PolyA_lnc-699	Chr5	-	17328291	17329343	1	17328291,	17329343,	N	910	biological_process_unknown

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-700	Chr5	-	18238171	18238835	2	18238171,18238734,	18238606,18238835,	N	911	
PolyA_lnc-701	Chr5	-	18238171	18238835	2	18238171,18238734,	18238613,18238835,	N	912	
PolyA_lnc-702	Chr5	-	18238171	18238835	2	18238171,18238734,	18238644,18238835,	N	913	
PolyA_lnc-703	Chr5	-	1891938	1892178	1	1891938,	1892178,	N	914	cellular_component_unknown,DNA binding,DNA binding,fatty acid catabolic process,leaf development,leaf shaping,meristem maintenance,negative regulation of transcription, DNA-dependent,nucleus,nucleus,regulation of transcription, DNA-dependent,sequence-specific DNA binding transcription factor activity
PolyA_lnc-704	Chr5	-	19987695	19988115	2	19987695,19987885,	19987795,19988115,	N	915	
PolyA_lnc-705	Chr5	-	19989531	19989927	2	19989531,19989758,	19989682,19989927,	N	916	
PolyA_lnc-706	Chr5	-	19990788	19991448	2	19990788,19991149,	19990840,19991448,	N	917	cytoplasm,cytoplasm,intracellular protein transport,nucleus,protein import into nucleus,protein transporter activity,protein transporter activity,toxin catabolic process
PolyA_lnc-707	Chr5	-	20191734	20192329	2	20191734,20192202,	20191970,20192329,	Y	918	autophagy,cytosol,extracellular region,metabolic process,transferase activity, transferring glycosyl groups,transferase activity, transferring hexosyl groups;biological_process_unknown,nucleus
PolyA_lnc-708	Chr5	-	22578786	22579699	2	22578786,22579235,	22579137,22579699,	N	919	intracellular signal transduction,nucleus,oxidation-reduction process,protein-disulfide reductase activity,purine nucleobase transport,zinc ion binding;biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown,vernalization response
PolyA_lnc-709	Chr5	-	22578786	22579699	2	22578786,22579235,	22579155,22579699,	N	920	intracellular signal transduction,nucleus,oxidation-reduction process,protein-disulfide reductase activity,purine nucleobase transport,zinc ion binding;biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown,vernalization response
PolyA_lnc-710	Chr5	-	25490173	25490474	1	25490173,	25490474,	Y	921	catalytic activity,cytoplasm,cytosol,glycolysis,glycolysis,magnesium ion binding,plasma membrane,potassium ion binding,pyruvate kinase activity,pyruvate kinase activity,response to cadmium ion
PolyA_lnc-711	Chr5	-	25861550	25861781	2	25861550,25861680,	25861587,25861781,	N	922	
PolyA_lnc-712	Chr5	-	26146469	26147723	2	26146469,26147578,	26147142,26147723,	N	923	
PolyA_lnc-713	Chr5	-	26146531	26147151	1	26146531,	26147151,	N	924	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-714	Chr5	-	26147359	26147710	1	26147359,	26147710,	N	925	brassinosteroid mediated signaling pathway,cell wall,cell wall,chloroplast,chloroplast,cytoplasm,cytoplasm,cytoplasm,cytoplasm,nucleus,nucleus,nucleus,plant-type cell wall,plasma membrane,protein domain specific binding,protein domain specific binding,protein domain specific binding,protein phosphorylated amino acid binding,toxin catabolic process
PolyA_lnc-715	Chr5	-	26218206	26218459	1	26218206,	26218459,	N	926	ATP binding,kinase activity,plasma membrane,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,response to ethylene stimulus,transferase activity, transferring phosphorus-containing groups;biological_process_unknown,molecular_function_unknown;biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown
PolyA_lnc-716	Chr5	-	2744107	2744521	2	2744107,2744483,	2744402,2744521,	N	927	biological_process_unknown,molecular_function_unknown,nucleus,nucleus
PolyA_lnc-717	Chr5	-	30209	30825	2	30209,30759,	30402,30825,	N	928	
PolyA_lnc-718	Chr5	-	3471426	3472010	2	3471426,3471954,	3471504,3472010,	N	929	DNA binding,DNA binding,nucleosome,nucleosome assembly,nucleus
PolyA_lnc-719	Chr5	-	3592668	3593228	2	3592668,3593122,	3592746,3593228,	N	930	ADP binding,defense response,defense response,intracellular,signal transduction;calcium-mediated signaling,chromosome organization,DNA binding,DNA binding,DNA binding,double-stranded DNA binding,gibberellic acid mediated signaling pathway,maintenance of meristem identity,mRNA export from nucleus,nucleus,nucleus,nucleus,nucleus,nucleus,nucleus,photomorphogenesis,photomorphogenesis,positive regulation of anthocyanin metabolic process,positive regulation of cell proliferation,positive regulation of circadian rhythm,positive regulation of flavonoid biosynthetic process,positive regulation of transcription, DNA-dependent,post-translational protein modification,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein dimerization activity,red or far-red light signaling pathway,regulation of flower development,regulation of photomorphogenesis,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,response to abscisic acid stimulus,response to far red light,response to karrikin,response to red light,response to UV-B,response to UV-B,response to UV-B,sequence-specific DNA binding,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-720	Chr5	-	4545865	4547934	3	4545865,4546304,4546925,	4546027,4546448,4547934,	N	931	biological_process_unknown,biological_process_unknown,cellular_component_unknown,cellular_component_unknown,molecular_function_unknown,molecular_function_unknown,nucleus,nucleus
PolyA_lnc-721	Chr5	-	4546309	4547141	2	4546309,4546925,	4546387,4547141,	N	932	biological_process_unknown,biological_process_unknown,cellular_component_unknown,cellular_component_unknown,molecular_function_unknown,molecular_function_unknown,nucleus,nucleus
PolyA_lnc-722	Chr5	-	5041357	5042449	3	5041357,5042205,5042352,	5041410,5042259,5042449,	N	933	
PolyA_lnc-723	Chr5	-	5041734	5042449	2	5041734,5042352,	5042259,5042449,	N	934	acetyl-CoA carboxylase activity,acetyl-CoA carboxylase complex,biotin binding,chloroplast,chloroplast,chloroplast envelope,chloroplast stroma,fatty acid biosynthetic process,fatty acid biosynthetic process
PolyA_lnc-724	Chr5	-	5041873	5042448	2	5041873,5042339,	5042259,5042448,	N	935	
PolyA_lnc-725	Chr5	-	7856657	7857093	1	7856657,	7857093,	N	936	biological_process_unknown,cytoplasm
PolyA_lnc-726	Chr5	-	8553996	8554246	1	8553996,	8554246,	N	937	biological_process_unknown
PolyA_lnc-727	Chr5	-	8858200	8858957	1	8858200,	8858957,	N	938	
PolyA_lnc-728	Chr5	-	8858200	8859132	3	8858200,8858852,8859077,	8858772,8858976,8859132,	N	939	
PolyA_lnc-729	Chr5	-	8957947	8959571	3	8957947,8959205,8959358,	8958983,8959249,8959571,	N	940	
PolyA_lnc-730	Chr5	-	8959394	8960058	3	8959394,8959679,8960008,	8959566,8959728,8960058,	N	941	
PolyA_lnc-731	Chr5	-	8960190	8960766	3	8960190,8960358,8960589,	8960288,8960451,8960766,	N	942	
PolyA_lnc-732	Chr5	-	8960211	8960644	3	8960211,8960358,8960589,	8960285,8960451,8960644,	N	943	
PolyA_lnc-733	Chr5	-	9206946	9207147	1	9206946,	9207147,	N	944	biological_process_unknown,molecular_function_unknown,nucleus,nucleus
PolyA_lnc-734	Chr5	.	10018902	10019278	1	10018902,	10019278,	Y	945	
PolyA_lnc-735	Chr5	.	10019358	10019771	1	10019358,	10019771,	Y	946	
PolyA_lnc-736	Chr5	.	1270719	1270926	1	1270719,	1270926,	N	947	biosynthetic process,biosynthetic process,endosome,Golgi apparatus,Golgi apparatus,nucleus,nucleus,transferase activity, transferring glycosyl groups,trans-Golgi network
PolyA_lnc-737	Chr5	.	13098337	13098584	1	13098337,	13098584,	N	948	
PolyA_lnc-738	Chr5	.	13100639	13100872	1	13100639,	13100872,	N	949	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-739	Chr5	.	13100710	13100934	1	13100710,	13100934,	N	950	
PolyA_lnc-740	Chr5	.	13102712	13103107	1	13102712,	13103107,	N	951	
PolyA_lnc-741	Chr5	.	13312346	13312569	1	13312346,	13312569,	N	952	biological_process_unknown,cellular_component_unknown,chloroplast,molecular_function_unknown
PolyA_lnc-742	Chr5	.	13612756	13613013	1	13612756,	13613013,	N	953	
PolyA_lnc-743	Chr5	.	13626200	13626789	1	13626200,	13626789,	N	954	
PolyA_lnc-744	Chr5	.	13985065	13985871	1	13985065,	13985871,	Y	955	
PolyA_lnc-745	Chr5	.	13987776	13988166	1	13987776,	13988166,	N	956	
PolyA_lnc-746	Chr5	.	13988216	13988501	1	13988216,	13988501,	Y	957	
lyA_lnc-747	Chr5	.	1450188	1450454	1	1450188,	1450454,	N	958	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism,ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism,ATP binding,catalytic activity,cation transport,hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances,magnesium ion binding,metabolic process,metal ion binding,nucleotide binding,phospholipid-translocating ATPase activity,phospholipid transport,plasma membrane,plasma membrane,plasma membrane,plasma membrane,positive regulation of flavonoid biosynthetic process,protein binding,protein targeting to membrane,regulation of plant-type hypersensitive response
PolyA_lnc-748	Chr5	.	14822212	14822430	1	14822212,	14822430,	N	959	
PolyA_lnc-749	Chr5	.	14889242	14889477	1	14889242,	14889477,	N	960	ethylene biosynthetic process,intracellular signal transduction,nucleus,protein ubiquitination,respiratory burst involved in defense response,response to chitin,response to chitin,ubiquitin-protein ligase activity;cyclic nucleotide binding,ion channel activity,ion transport,membrane,nucleus,nucleus,outward rectifier potassium channel activity,outward rectifier potassium channel activity,potassium ion transport,protein binding,response to abscisic acid stimulus,response to cold,response to jasmonic acid stimulus,response to water deprivation,transmembrane transport,voltage-gated potassium channel activity
PolyA_lnc-750	Chr5	.	14998447	14998746	1	14998447,	14998746,	N	961	cellular_component_unknown,cytoplasm,heat shock protein binding,protein folding,protein folding,unfolded protein binding;actin cytoskeleton,calcium ion binding,calcium ion binding,calcium ion binding,calcium ion binding,Golgi apparatus,innate immune response,long-day photoperiodism, flowering,plasma membrane,regulation of flower development,regulation of nitric oxide metabolic process,response to abscisic acid stimulus,response to abscisic acid stimulus,response to absence of light,response to auxin stimulus,response to calcium ion,response to chitin,response to cold,response to heat,response to heat,response to hydrogen peroxide,response to mechanical stimulus,response to mechanical stimulus,response to mechanical stimulus,response to metal ion,response to wounding
PolyA_lnc-751	Chr5	.	15027787	15028153	1	15027787,	15028153,	N	962	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-752	Chr5	.	15189124	15189360	1	15189124,	15189360,	N	963	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus;biological_process_unknown,molecular_function_unknown;cytoplasm,ubiquitin-protein ligase activity,zinc ion binding,zinc ion binding
PolyA_lnc-753	Chr5	.	15327015	15327576	1	15327015,	15327576,	N	964	
PolyA_lnc-754	Chr5	.	15327481	15327734	1	15327481,	15327734,	N	965	
PolyA_lnc-755	Chr5	.	15414814	15415066	1	15414814,	15415066,	N	966	cellular_component_unknown,DNA binding,nucleus,regulation of transcription, DNA-dependent
PolyA_lnc-756	Chr5	.	15631689	15632008	1	15631689,	15632008,	N	967	
PolyA_lnc-757	Chr5	.	15632123	15632335	1	15632123,	15632335,	N	968	
PolyA_lnc-758	Chr5	.	15725866	15726087	1	15725866,	15726087,	N	969	molecular_function_unknown,nucleus;extracellular region,extracellular region,plant-type cell wall loosening,plant-type cell wall loosening,plant-type cell wall modification involved in multidimensional cell growth,plant-type cell wall organization,unidimensional cell growth,unidimensional cell growth
PolyA_lnc-759	Chr5	.	15750559	15750783	1	15750559,	15750783,	N	970	cytokinin mediated signaling pathway,cytokinin mediated signaling pathway,cytoplasm,cytoplasm,cytoplasm,histidine phosphotransfer kinase activity,histidine phosphotransfer kinase activity,histidine phosphotransfer kinase activity,histidine phosphotransfer kinase activity,nucleus,nucleus,nucleus,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein histidine kinase binding,protein histidine kinase binding,protein histidine kinase binding,regulation of anthocyanin metabolic process,regulation of cytokinin mediated signaling pathway,regulation of seed germination,regulation of shoot development,signal transducer activity,two-component signal transduction system (phosphorelay),two-component signal transduction system (phosphorelay);biological_process_unknown,mitochondrion,molecular_function_unknown
PolyA_lnc-760	Chr5	.	15803488	15803693	1	15803488,	15803693,	N	971	biological_process_unknown,molecular_function_unknowr
PolyA_lnc-761	Chr5	.	1600840	1601244	1	1600840,	1601244,	Y	972	ADP binding,cellular response to iron ion starvation,defense response,defense response,iron ion transport,nitrate transport,N-terminal protein myristoylation,nucleus,response to nitrate;DNA binding,heat acclimation,heat acclimation,nucleus,nucleus,nucleus,nucleus,nucleus,nucleus,protein binding,protein binding,protein binding,protein folding,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,response to chitin,response to heat,response to high light intensity,response to hydrogen peroxide,response to hydrogen peroxide,response to UV-B,response to UV-B,response to water deprivation,response to water deprivation,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-762	Chr5	.	16081820	16082053	1	16081820,	16082053,	N	973	membrane,membrane,molecular_function_unknown;membrane,membrane,membrane,molecular_function_unknown
PolyA_lnc-763	Chr5	.	1619707	1619940	1	1619707,	1619940,	N	974	cytoplasm,cytoplasm,hydrolase activity, acting on glycosyl bonds,mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase activity,mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase activity,N-glycan processing,protein deglycosylation,vacuole;cullin deneddylation,cytoplasm,cytosol,eukaryotic translation initiation factor 2 complex,G2 phase of mitotic cell cycle,photomorphogenesis,pyrimidine ribonucleotide biosynthetic process,RNA binding,RNA binding,translation initiation factor activity,translation initiation factor activity
PolyA_lnc-764	Chr5	.	16316995	16317257	1	16316995,	16317257,	N	975	cell division,cell growth,lateral root development,membrane,mitochondrial respiratory chain complex I,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion organization,nucleolus,plasma membrane,protein targeting to mitochondrion,response to auxin stimulus,response to endoplasmic reticulum stress,response to ethylene stimulus,response to nitric oxide,response to salt stress,response to salt stress,response to stress,RNA methylation,vacuolar membrane,vacuole
PolyA_lnc-765	Chr5	.	16399620	16399824	1	16399620,	16399824,	N	976	ADP binding,defense response,defense response,intracellular,nucleoside-triphosphatase activity,nucleotide binding,signal transduction
PolyA_lnc-766	Chr5	.	16717315	16717632	1	16717315,	16717632,	N	977	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus;intracellular,intracellular,nucleus,RNA processing,RNA processing
PolyA_lnc-767	Chr5	.	16774092	16774404	1	16774092,	16774404,	N	978	
PolyA_lnc-768	Chr5	.	16774713	16775034	1	16774713,	16775034,	N	979	
PolyA_lnc-769	Chr5	.	16774964	16775503	1	16774964,	16775503,	N	980	
PolyA_lnc-770	Chr5	.	16813593	16813820	1	16813593,	16813820,	N	981	actin nucleation,biological_process_unknown,cellular_component_unknown,chloroplast,molecular_function_unknown,trichome morphogenesis;peptidase activity,proteasome regulatory particle,proteasome regulatory particle,proteolysis,proteolysis

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-771	Chr5	.	16828530	16828782	1	16828530,	16828782,	N	982	chloroplast,endosome,Golgi apparatus,Golgi apparatus,integral to membrane,trans-Golgi network;anchored to membrane,anchored to membrane,anchored to plasma membrane,anchored to plasma membrane,carbohydrate metabolic process,carbohydrate metabolic process,catalytic activity,catalytic activity,cation binding,cation binding,cell communication,cell wall,cell wall,endoplasmic reticulum,extracellular region,glucan endo-1,3-beta-D-glucosidase activity,hydrolase activity, hydrolyzing O-glycosyl compounds,hydrolase activity, hydrolyzing O-glycosyl compounds,hydrolase activity, hydrolyzing O-glycosyl compounds,plant-type cell wall,plasma membrane,plasma membrane,plasma membrane,plasmodesma,plasmodesma,plasmodesma,regulation of protein localization
PolyA_lnc-772	Chr5	.	1685898	1686103	1	1685898,	1686103,	N	983	biological_process_unknown,membrane,molecular_function_unknown;biological_process_unknown,cellular_component_unknown,extracellular region,molecular_function_unknown
PolyA_lnc-773	Chr5	.	16878112	16878331	1	16878112,	16878331,	N	984	
PolyA_lnc-774	Chr5	.	16887634	16888056	1	16887634,	16888056,	Y	985	biological_process_unknown,extracellular region,membrane,molecular_function_unknown,molecular_function_unknown;cell wall,extracellular region,proteolysis,proteolysis,serine-type carboxypeptidase activity,serine-type carboxypeptidase activity
PolyA_lnc-775	Chr5	.	17045929	17046249	1	17045929,	17046249,	Y	986	
PolyA_lnc-776	Chr5	.	17326507	17327098	1	17326507,	17327098,	N	987	biological_process_unknown,chlorophyll catabolic process,mitochondrion,molecular_function_unknown
PolyA_lnc-777	Chr5	.	17986028	17986294	1	17986028,	17986294,	N	988	biological_process_unknown,molecular_function_unknowr
PolyA_lnc-778	Chr5	.	18277214	18277493	1	18277214,	18277493,	N	989	flavin adenine dinucleotide binding,monooxygenase activity,NADP binding,N,N-dimethylaniline monooxygenase activity,oxidation-reduction process;cyclin-dependent protein kinase activity,flower development,gravitropism,leaf development,nucleus,nucleus,positive regulation of cell proliferation,protein glycosylation,protein kinase binding,protein kinase binding,regulation of cell cycle,regulation of cyclin-dependent protein kinase activity,regulation of cyclin-dependent protein kinase activity,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,regulation of viral reproduction,response to virus,RNA splicing, via endonucleolytic cleavage and ligation,transcription from RNA polymerase II promoter,trichome morphogenesis
PolyA_lnc-779	Chr5	.	18416255	18416468	1	18416255,	18416468,	Y	990	extracellular region,molecular_function_unknown,transmembrane transport;biological_process_unknown,cellular_component_unknown
PolyA_lnc-780	Chr5	.	1934048	1934424	1	1934048,	1934424,	N	991	biological_process_unknown,cellular_component_unknown,molecular_function_unknown

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-781	Chr5	.	194432	194794	1	194432,	194794,	N	992	intracellular signal transduction,nucleus,oxidation-reduction process,protein-disulfide reductase activity,zinc ion binding;calcium:cation antiporter activity,calcium:cation antiporter activity,calcium:hydrogen antiporter activity,calcium:hydrogen antiporter activity,calcium ion transport,calcium ion transport,cation:cation antiporter activity,cation:cation antiporter activity,cation:cation antiporter activity,cation transmembrane transporter activity,cation transport,cellular response to iron ion starvation,cellular zinc ion homeostasis,integral to membrane,iron ion transport,nitrate transport,plant-type vacuole membrane,response to auxin stimulus,response to nematode,response to nitrate,root development,transition metal ion transport,transmembrane transport,vacuolar membrane
PolyA_lnc-782	Chr5	.	19540331	19540613	1	19540331,	19540613,	N	993	biological_process_unknown,molecular_function_unknown;cytoplasm,cytosol,fatty acid beta oxidation,glucosinolate catabolic process,molecular_function_unknown,nitrile biosynthetic process,proteasomal ubiquitin-dependent protein catabolic process,proteasome core complex assembly,response to misfolded protein,toxin catabolic process
PolyA_lnc-783	Chr5	.	19730362	19730701	1	19730362,	19730701,	N	994	cytoplasm,cytosol,intracellular,nucleic acid binding,nucleocytoplasmic transport,nucleotide binding,RNA binding,transport;nucleus,nucleus,nucleus,response to chitin,zinc ion binding,zinc ion binding,zinc ion binding,zinc ion binding
PolyA_lnc-784	Chr5	.	19807937	19808154	1	19807937,	19808154,	N	995	cellular response to sulfur starvation,nucleus,regulation of sulfur utilizatior
PolyA_lnc-785	Chr5	.	19975234	19975501	1	19975234,	19975501,	N	996	anchored to membrane,anchored to membrane,anchored to membrane,cell tip growth,developmental growth,lateral root development,plasma membrane,root epidermal cell differentiation,root hair cell differentiation,root hair cell differentiation,root hair elongation,trichoblast differentiation
PolyA_lnc-786	Chr5	.	19988612	19989094	1	19988612,	19989094,	Y	997	
PolyA_lnc-787	Chr5	.	20046366	20046634	1	20046366,	20046634,	Y	998	biological_process_unknown,CUL4-RING ubiquitin ligase complex,CUL4-RING ubiquitin ligase complex,nucleotide binding,nucleus
PolyA_lnc-788	Chr5	.	20156004	20156458	1	20156004,	20156458,	N	999	carbohydrate metabolic process,carbohydrate metabolic process,cytosol,cytosol,cytosol,phosphotransferase activity, alcohol group as acceptor,phosphotransferase activity, alcohol group as acceptor,xylulokinase activity,xylulokinase activity,xylulose metabolic process
PolyA_lnc-789	Chr5	.	20191604	20191820	1	20191604,	20191820,	N	1000	autophagy,cytosol,extracellular region,metabolic process,transferase activity, transferring glycosyl groups,transferase activity, transferring hexosyl groups;biological_process_unknown,nucleus
PolyA_lnc-790	Chr5	.	21024258	21024470	1	21024258,	21024470,	N	1001	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-791	Chr5	.	21025948	21026154	1	21025948,	21026154,	N	1002	catalytic activity,embryo development ending in seed dormancy,fatty acid catabolic process,lipid storage,meristem structural organization,nucleus,photomorphogenesis,protein dephosphorylation,protein serine/threonine phosphatase activity,protein serine/threonine phosphatase activity,protein serine/threonine phosphatase complex,protein ubiquitination,regulation of flower development,response to abscisic acid stimulus,response to abscisic acid stimulus,response to freezing,seed development,seed dormancy process,seed germination,seed germination,sugar mediated signaling pathway,terpenoid biosynthetic process,vegetative to reproductive phase transition of meristem
PolyA_lnc-792	Chr5	.	21144520	21144795	1	21144520,	21144795,	N	1003	
PolyA_lnc-793	Chr5	.	21394564	21395016	1	21394564,	21395016,	N	1004	biological_process_unknown,molecular_function_unknown,plasma membrane;cellular_component_unknown,DNA primase activity,DNA primase activity,DNA replication,DNA replication,nucleus,nucleus,nucleus
PolyA_lnc-794	Chr5	.	21692630	21692990	1	21692630,	21692990,	N	1005	ATP binding,ATP binding,chloroplast,chloroplast,kinase activity,protein kinase activity,protein kinase activity,protein phosphorylation,protein phosphorylation,structural molecule activity,structural molecule activity,transferase activity, transferring phosphorus-containing groups,transferase activity, transferring phosphorus-containing groups;biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown
PolyA_lnc-795	Chr5	.	22253147	22253529	1	22253147,	22253529,	N	1006	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus
PolyA_lnc-796	Chr5	.	22578843	22580198	1	22578843,	22580198,	N	1007	intracellular signal transduction,nucleus,oxidation-reduction process,protein-disulfide reductase activity,purine nucleobase transport,zinc ion binding;biological_process_unknown,cellular_component_unknown,mitochondrion,molecular_function_unknown,vernalization response
PolyA_lnc-797	Chr5	.	22828462	22829027	1	22828462,	22829027,	N	1008	calmodulin binding,calmodulin binding,cellulose biosynthetic process,chloroplast,defense response to bacterium,endoplasmic reticulum,Golgi vesicle transport,methionine biosynthetic process,RNA splicing, via endonucleolytic cleavage and ligation
PolyA_lnc-798	Chr5	.	23408542	23408753	1	23408542,	23408753,	N	1009	
PolyA_lnc-799	Chr5	.	24246222	24246845	1	24246222,	24246845,	N	1010	extracellular region,extracellular region,plasma membrane,regulation of cell proliferation
PolyA_lnc-800	Chr5	.	24247246	24247537	1	24247246,	24247537,	N	1011	
PolyA_lnc-801	Chr5	.	24247564	24247836	1	24247564,	24247836,	N	1012	
PolyA_lnc-802	Chr5	.	24304930	24305135	1	24304930,	24305135,	N	1013	
PolyA_lnc-803	Chr5	.	24305334	24305774	1	24305334,	24305774,	N	1014	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-804	Chr5	.	24961491	24961815	1	24961491,	24961815,	N	1015	cation transmembrane transporter activity,cation transmembrane transporter activity,cation transport,cation transport,cell fate specification,cellular response to iron ion starvation,integral to membrane,iron ion transport,membrane,metal ion transmembrane transporter activity,metal ion transmembrane transporter activity,metal ion transport,plasma membrane,purine nucleobase transport,transmembrane transport,water transport,zinc ion transmembrane transport,zinc ion transmembrane transporter activity
PolyA_lnc-805	Chr5	.	25581864	25582213	1	25581864,	25582213,	N	1016	chromatin silencing,chromosome,chromosome segregation,DNA binding,DNA binding,DNA-dependent DNA replication,DNA methylation,DNA repair,DNA replication initiation,DNA topoisomerase activity,DNA topoisomerase activity,DNA topoisomerase type I activity,DNA topological change,DNA topological change,DNA unwinding involved in replication,gene silencing by RNA,histone H3-K9 methylation,meiosis,mitosis,nucleic acid binding,nucleus,petal formation,regulation of cell cycle,regulation of DNA replication,resolution of meiotic recombination intermediates,sepal formation,zinc ion binding;ATP binding,ATP binding,plasma membrane,plasma membrane,protein kinase activity,protein phosphorylation,protein phosphorylation,protein serine/threonine kinase activity,protein serine/threonine kinase activity,response to molecule of bacterial origin,signal transduction,stamen development,stomatal complex morphogenesis,transferase activity, transferring phosphorus-containing groups,transmembrane receptor protein tyrosine kinase signaling pathway
PolyA_lnc-806	Chr5	.	25859264	25859783	1	25859264,	25859783,	N	1017	
PolyA_lnc-807	Chr5	.	25890428	25890632	1	25890428,	25890632,	N	1018	defense response to fungus,DNA binding,DNA binding,negative regulation of abscisic acid mediated signaling pathway,nucleus,nucleus,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,response to abscisic acid stimulus,response to glucose stimulus,response to osmotic stress,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity
PolyA_lnc-808	Chr5	.	25923744	25924142	1	25923744,	25924142,	N	1019	biological_process_unknown,molecular_function_unknown,myo-inositol hexakisphosphate biosynthetic process,nucleus,plasma membrane
PolyA_lnc-809	Chr5	.	26053570	26054152	1	26053570,	26054152,	Y	1020	biological_process_unknown,cellular_component_unknown,molecular_function_unknown
PolyA_lnc-810	Chr5	.	26064072	26064370	1	26064072,	26064370,	N	1021	
PolyA_lnc-811	Chr5	.	26228885	26229096	1	26228885,	26229096,	N	1022	DNA binding,DNA mediated transformation,DNA mediated transformation,nucleus
PolyA_lnc-812	Chr5	.	26275972	26276290	1	26275972,	26276290,	N	1023	
PolyA_lnc-813	Chr5	.	26290047	26290283	1	26290047,	26290283,	N	1024	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-814	Chr5	.	26336723	26337092	1	26336723,	26337092,	Y	1025	endosome,Golgi apparatus,Golgi apparatus,Golgi apparatus,Golgi membrane,homogalacturonan metabolic process,molecular_function_unknown,pectin metabolic process,trans-Golgi network
PolyA_lnc-815	Chr5	.	26379626	26380039	1	26379626,	26380039,	N	1026	3-hydroxyisobutyryl-CoA hydrolase activity,3-hydroxyisobutyryl-CoA hydrolase activity,catalytic activity,catalytic activity,catalytic activity,fatty acid beta-oxidation,metabolic process,metabolic process,metabolic process,response to auxin stimulus,response to cold,valine catabolic process,valine catabolic process;biological_process_unknown,cellulose biosynthetic process,Golgi vesicle transport,molecular_function_unknown,nucleus,protein glycosylation
PolyA_lnc-816	Chr5	.	26465401	26465612	1	26465401,	26465612,	N	1027	CUL4-RING ubiquitin ligase complex,CUL4-RING ubiquitin ligase complex,cytoplasm,cytoplasm,cytoplasm,nucleotide binding,photoperiodism, flowering
PolyA_lnc-817	Chr5	.	26581010	26581511	1	26581010,	26581511,	N	1028	
PolyA_lnc-818	Chr5	.	26607212	26607515	1	26607212,	26607515,	N	1029	
PolyA_lnc-819	Chr5	.	26613054	26613259	1	26613054,	26613259,	N	1030	
PolyA_lnc-820	Chr5	.	26683321	26683788	1	26683321,	26683788,	Y	1031	
PolyA_lnc-821	Chr5	.	26686170	26686563	1	26686170,	26686563,	N	1032	
lyA_lnc-822	Chr5	.	2672090	2672411	1	2672090,	2672411,	Y	1033	mitochondrion;biological_process_unknown,mitochondrior
PolyA_lnc-823	Chr5	.	2727355	2727600	1	2727355,	2727600,	N	1034	biological_process_unknown,molecular_function_unknown,nucleus,plasma membrane;biological_process_unknown,chromosome segregation,glucuronoxylan metabolic process,meiotic chromosome segregation,meiotic DNA double-strand break formation,molecular_function_unknown,multicellular organism reproduction,nucleus,nucleus,nucleus,organ morphogenesis,positive regulation of organelle organization,protein desumoylation,protein glycosylation,reciprocal meiotic recombination,regulation of chromosome organization,regulation of telomere maintenance,response to gamma radiation,sister chromatid cohesion,synapsis,telomere maintenance in response to DNA damage,tissue development,xylan biosynthetic process
PolyA_lnc-824	Chr5	.	288056	288356	1	288056,	288356,	N	1035	
PolyA_lnc-825	Chr5	.	288846	289185	1	288846,	289185,	N	1036	biological_process_unknown,cellular cation homeostasis,cellular response to nitrogen starvation,chloroplast,chloroplast,divalent metal ion transport,indoleacetic acid biosynthetic process,molecular_function_unknown,tryptophan catabolic process
PolyA_lnc-826	Chr5	.	288967	289386	1	288967,	289386,	N	1037	biological_process_unknown,cellular cation homeostasis,cellular response to nitrogen starvation,chloroplast,chloroplast,divalent metal ion transport,indoleacetic acid biosynthetic process,molecular_function_unknown,tryptophan catabolic process

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-827	Chr5	.	3120013	3120240	1	3120013,	3120240,	N	1038	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus;mitochondrion
PolyA_lnc-828	Chr5	.	3227292	3227493	1	3227292,	3227493,	N	1039	
PolyA_lnc-829	Chr5	.	3250349	3250602	1	3250349,	3250602,	N	1040	
PolyA_lnc-830	Chr5	.	3250655	3251446	1	3250655,	3251446,	N	1041	
PolyA_lnc-831	Chr5	.	3251522	3251887	1	3251522,	3251887,	N	1042	biological_process_unknown,cellular_component_unknown,molecular_function_unknown
PolyA_lnc-832	Chr5	.	3327122	3327337	1	3327122,	3327337,	N	1043	ATP binding,kinase activity,plasma membrane,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,transferase activity, transferring phosphorus-containing groups;apoplast,chloroplast,cytosol,cytosol,metalloendopeptidase activity,metalloendopeptidase activity,methylglyoxal catabolic process to D-lactate,proteolysis,proteolysis,response to cadmium ion
lyA_lnc-833	Chr5	.	3327279	3327563	1	3327279,	3327563,	N	1044	ATP binding,kinase activity,plasma membrane,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,transferase activity, transferring phosphorus-containing groups;apoplast,chloroplast,cytosol,cytosol,metalloendopeptidase activity,metalloendopeptidase activity,methylglyoxal catabolic process to D-lactate,proteolysis,proteolysis,response to cadmium ion

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-834	Chr5	.	3592371	3592746	1	3592371,	3592746,	N	1045	ADP binding,defense response,defense response,intracellular,signal transduction;calcium-mediated signaling,chromosome organization,DNA binding,DNA binding,DNA binding,double-stranded DNA binding,gibberellic acid mediated signaling pathway,maintenance of meristem identity,mRNA export from nucleus,nucleus,nucleus,nucleus,nucleus,nucleus,nucleus,photomorphogenesis,photomorphogenesis,positive regulation of anthocyanin metabolic process,positive regulation of cell proliferation,positive regulation of circadian rhythm,positive regulation of flavonoid biosynthetic process,positive regulation of transcription, DNA-dependent,post-translational protein modification,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein dimerization activity,red or far-red light signaling pathway,regulation of flower development,regulation of photomorphogenesis,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,response to abscisic acid stimulus,response to far red light,response to karrikin,response to red light,response to UV-B,response to UV-B,response to UV-B,sequence-specific DNA binding,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity
PolyA_lnc-835	Chr5	.	400629	400830	1	400629,	400830,	N	1046	endoplasmic reticulum,ER to Golgi vesicle-mediated transport,intra-Golgi vesicle-mediated transport,lipid transport,lithium ion transport,molecular_function_unknown,nucleus,nucleus,protein import into peroxisome matrix,vesicle-mediated transport
PolyA_lnc-836	Chr5	.	4213004	4213211	1	4213004,	4213211,	Y	1047	
PolyA_lnc-837	Chr5	.	4213196	4213470	1	4213196,	4213470,	Y	1048	
PolyA_lnc-838	Chr5	.	4214204	4214432	1	4214204,	4214432,	N	1049	chloroplast
PolyA_lnc-839	Chr5	.	440935	441230	1	440935,	441230,	N	1050	biological_process_unknown,cellular_component_unknown,nucleus,protein binding
PolyA_lnc-840	Chr5	.	4545738	4546026	1	4545738,	4546026,	N	1051	biological_process_unknown,chloroplast,mitochondrion,photoperiodism, flowering
PolyA_lnc-841	Chr5	.	4581986	4582204	1	4581986,	4582204,	N	1052	ATP binding,ATP binding,mitochondrion,plasma membrane,protein kinase activity,protein kinase activity,protein phosphorylation,protein phosphorylation,protein serine/threonine kinase activity,transferase activity, transferring phosphorus-containing groups,transmembrane receptor protein tyrosine kinase signaling pathway
PolyA_lnc-842	Chr5	.	4735407	4735804	1	4735407,	4735804,	N	1053	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus,response to arsenic-containing substance

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-843	Chr5	.	4801054	4801265	1	4801054,	4801265,	N	1054	endoplasmic reticulum membrane,GPI anchor biosynthetic process,GPI anchor biosynthetic process,GPI anchor metabolic process,intrinsic to endoplasmic reticulum membrane,intrinsic to endoplasmic reticulum membrane,mannosyltransferase activity,nucleus,nucleus,transferase activity, transferring glycosyl groups,transferase activity, transferring glycosyl groups,transferase activity, transferring glycosyl groups
PolyA_lnc-844	Chr5	.	500135	500479	1	500135,	500479,	N	1055	biological_process_unknown,intracellular,nucleus,oxidation-reduction process,protein disulfide reductase activity,zinc ion binding
PolyA_lnc-845	Chr5	.	5040921	5041146	1	5040921,	5041146,	N	1056	
PolyA_lnc-846	Chr5	.	5041450	5041804	1	5041450,	5041804,	N	1057	acetyl-CoA carboxylase activity,acetyl-CoA carboxylase complex,biotin binding,chloroplast,chloroplast,chloroplast envelope,chloroplast stroma,fatty acid biosynthetic process,fatty acid biosynthetic process
lyA_lnc-847	Chr5	.	5094674	5095108	1	5094674,	5095108,	N	1058	cell junction,cellulose biosynthetic process,cell wall,cell wall,cell wall organization,cytosolic ribosome,glycogenin glucosyltransferase activity,membrane,nucleus,response to cadmium ion,response to salt stress,transferase activity, transferring hexosyl groups,UDP-arabinopyranose mutase activity,UDP-L-arabinose metabolic process;biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus
PolyA_lnc-848	Chr5	.	5170283	5170501	1	5170283,	5170501,	N	1059	calcium-mediated signaling,DNA binding,nucleus,protein dimerization activity,regulation of transcription, DNA-dependent,regulation of transcription, DNA-dependent,response to mechanical stimulus,sequence-specific DNA binding,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity;circadian rhythm,DNA repair,far-red light signaling pathway,intracellular,intracellular,negative regulation of photomorphogenesis,nucleus,nucleus,nucleus,nucleus,protein binding,protein binding,protein binding,regulation of flower development,reproductive structure development,response to far red light,sequence-specific DNA binding transcription factor activity,zinc ion binding,zinc ion binding,zinc ion binding
PolyA_lnc-849	Chr5	.	5980743	5981002	1	5980743,	5981002,	N	1060	biological_process_unknown,cellular_component_unknown,molecular_function_unknown;carbohydrate metabolic process,chloroplast,cytosol,glucose 1-phosphate metabolic process,intramolecular transferase activity, phosphotransferases,mitochondrion,phosphoacetylglucosamine mutase activity,phosphoacetylglucosamine mutase activity,phosphoglucomutase activity,photoreactive repair,plasmodesma,response to UV,UDP-N-acetylglucosamine biosynthetic process

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-850	Chr5	.	6084540	6084874	1	6084540,	6084874,	N	1061	biological_process_unknown,cellular_component_unknown,chloroplast,molecular_function_unknown;ADP binding,cytoplasm,defense response,defense response,defense response,intracellular,nucleoside-triphosphatase activity,nucleotide binding,signal transduction
PolyA_lnc-851	Chr5	.	6210736	6210963	1	6210736,	6210963,	N	1062	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,molecular_function_unknown,nucleus
PolyA_lnc-852	Chr5	.	6211044	6211261	1	6211044,	6211261,	N	1063	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,molecular_function_unknown,nucleus
lyA_lnc-853	Chr5	.	6223212	6223597	1	6223212,	6223597,	N	1064	3,8-divinyl protochlorophyllide a 8-vinyl reductase activity,aromatic amino acid family biosynthetic process,carotenoid biosynthetic process,cell differentiation,chlorophyll biosynthetic process,chlorophyll biosynthetic process,chlorophyll biosynthetic process,chloroplast,chloroplast,chloroplast envelope,chloroplast envelope,chloroplast thylakoid,cysteine biosynthetic process,isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway,leaf morphogenesis,membrane,mitochondrion,nucleotide binding,pentose-phosphate shunt,positive regulation of transcription, DNA-dependent,rRNA processing,unsaturated fatty acid biosynthetic process;biological_process_unknown,cellular_component_unknown,molecular_function_unknown
PolyA_lnc-854	Chr5	.	6663650	6664281	1	6663650,	6664281,	N	1065	
PolyA_lnc-855	Chr5	.	7083508	7083823	1	7083508,	7083823,	N	1066	biological_process_unknown,positive regulation of flavonoid biosynthetic process,protein targeting to membrane,regulation of plant-type hypersensitive response,zinc ion binding,zinc ion binding
PolyA_lnc-856	Chr5	.	714067	714512	1	714067,	714512,	N	1067	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus
PolyA_lnc-857	Chr5	.	714528	714858	1	714528,	714858,	Y	1068	biological_process_unknown,cellular_component_unknown,molecular_function_unknown,nucleus
PolyA_lnc-858	Chr5	.	7602160	7602361	1	7602160,	7602361,	N	1069	biological_process_unknown,chloroplast envelope,chloroplast envelope,chloroplast inner membrane,mitochondrion,molecular_function_unknown,plastid,plastid

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-859	Chr5	.	7739277	7739581	1	7739277,	7739581,	N	1070	cellular response to calcium ion,cellular response to calcium ion,chlorophyll metabolic process,chloroplast,chloroplast,chloroplast,chloroplast,chloroplast thylakoid,chloroplast thylakoid membrane,chloroplast thylakoid membrane,chloroplast thylakoid membrane,cysteine biosynthetic process,de-etiolation,isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway,maltose metabolic process,mitochondrion,oxylipin biosynthetic process,pentose-phosphate shunt,photosynthesis,photosynthesis, light reaction,photosynthetic electron transport in photosystem I,photosystem II assembly,plastid organization,positive regulation of catalytic activity,regulation of lipid metabolic process,regulation of stomatal closure,response to blue light,response to far red light,response to light stimulus,response to red light,rRNA processing,starch biosynthetic process,thylakoid,thylakoid,unsaturated fatty acid biosynthetic process
PolyA_lnc-860	Chr5	.	7852767	7853095	1	7852767,	7853095,	N	1071	chloroplast,chloroplast,chloroplast,chloroplast,metal ion binding,nucleoid,oxidation-reduction process,plastid nucleoid,removal of superoxide radicals,superoxide dismutase activity,superoxide dismutase activity,superoxide metabolic process,thylakoid;carboxyl-O-methyltransferase activity,C-terminal protein methylation,C-terminal protein methylation,C-terminal protein methylation,C-terminal protein methylation,endoplasmic reticulum,flower development,integral to membrane,negative regulation of abscisic acid mediated signaling pathway,protein C-terminal S-isoprenylcysteine carboxyl O-methyltransferase activity,protein C-terminal S-isoprenylcysteine carboxyl O-methyltransferase activity,protein C-terminal S-isoprenylcysteine carboxyl O-methyltransferase activity,protein C-terminal S-isoprenylcysteine carboxyl O-methyltransferase activity,protein C-terminal S-isoprenylcysteine carboxyl O-methyltransferase activity,protein C-terminal S-isoprenylcysteine carboxyl O-methyltransferase activity,shoot development
PolyA_lnc-861	Chr5	.	7891167	7891395	1	7891167,	7891395,	N	1072	DNA binding,DNA-dependent DNA replication,nucleus,nucleus,nucleus,sequence-specific DNA binding transcription factor activity
PolyA_lnc-862	Chr5	.	8084196	8084506	1	8084196,	8084506,	N	1073	
PolyA_lnc-863	Chr5	.	8084631	8085047	1	8084631,	8085047,	N	1074	
PolyA_lnc-864	Chr5	.	8141596	8141847	1	8141596,	8141847,	N	1075	ATP binding,cellular_component_unknown,kinase activity,plasma membrane,protein kinase activity,protein phosphorylation,protein serine/threonine kinase activity,protein tyrosine kinase activity,transferase activity, transferring phosphorus-containing groups
PolyA_lnc-865	Chr5	.	8527907	8528113	1	8527907,	8528113,	N	1076	
PolyA_lnc-866	Chr5	.	8528076	8528436	1	8528076,	8528436,	N	1077	
PolyA_lnc-867	Chr5	.	8955861	8957190	1	8955861,	8957190,	N	1078	
PolyA_lnc-868	Chr5	.	8960749	8961082	1	8960749,	8961082,	N	1079	

lncRNA ID	Chr	strand	Tr_start	Tr_end	Exon num	Exon_start	Exon_end	Differential expression	SEQ ID NO	Potential functions
PolyA_lnc-869	Chr5	.	9041430	9041844	1	9041430,	9041844,	Y	1080	defense response,defense response to fungus,kinase activity,plasma membrane,response to chitin,response to molecule of bacterial origin,signal transduction,signal transduction,stamen development,stomatal complex morphogenesis
PolyA_lnc-870	Chr5	.	9534446	9534983	1	9534446,	9534983,	N	1081	cellular calcium ion homeostasis,cellular cation homeostasis,extracellular-glutamate-gated ion channel activity,extracellular region,intracellular ligand-gated ion channel activity,ionotropic glutamate receptor activity,membrane,protein binding,response to light stimulus,transport,transporter activity

Table 5. Orthologs in *Glycine max*

A. thaliana		*Glycine max*	
lncRNA ID	**SEQ ID No**	**SEQ ID NO**	**chromosome; qstart; qend; sstart; send; identity; evalue; bitscore;**
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1082	scaffold_886;1-325;1281-960;87.46;4e-99;364;
NonpolyA_lnc-65	SEQ ID No 65	SEQ ID No 1083	Gm18;166-399;518162-518398;76.86;2e-26;124;
NonpolyA_lnc-126	SEQ ID No 126	SEQ ID No 1084	Gm15;168-240;39860771-39860699;89.04;6e-17;91.6;
NonpolyA_lnc-126	SEQ ID No 126	SEQ ID No 1085	Gm10;172-206;6625165-6625199;97.14;2e-07;60.2;
NonpolyA_lnc-127	SEQ ID No 127	SEQ ID No 1086	Gm15;169-241;39860771-39860699;90.41;1e-18;97.1;
NonpolyA_lnc-127	SEQ ID No 127	SEQ ID No 1087	Gm10;179-245;6625171-6625237;82.86;7e-07;58.4;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1088	Gm02;144-242;48228044-48228141;78.85;2e-07;60.2;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1089	Gm02;179-213;49075946-49075911;94.44;9e-06;54.7;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1090	Gm14;186-213;2854311-2854338;100.00;3e-05;52.8
PolyA_lnc-65	PolyA_lnc-65	SEQ ID No 1091	Gm18;166-399;518162-518398;76.86;2e-26;124;
PolyA_lnc-65	PolyA_lnc-65	SEQ ID No 1092	Gm11;207-399;38352977-38353169;77.66;5e-23;113;
olyA_lnc-65	PolyA_lnc-65	SEQ ID No 1093	Gm02;366-398;9411572-9411604;100.00;2e-07;62.1;
PolyA_lnc-65	PolyA_lnc-65	SEQ ID No 1094	Gm20;366-394;161421-161449;100.00;3e-05;54.7;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1095	Gm08;391-418;4650912-4650939;100.00;6e-05;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1096	Gm06;391-418;9453599-9453572;100.00;6e-05;52.8;

Table 6. Orthologs in *Oryza sativa*

Arabidopsis thaliana		*Oryza sativa*	
lncRNA ID	**SEQ ID No**	**SEQ ID No**	**chromosome; qstart; qend; sstart; send; identity; evalue; bitscore;**
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1097	Chr1;1-280;33536311-33536028;87.93;2e-88;327
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1098	Chr12;1-63;13388837-13388775;98.41;2e-23;111;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1099	Chr3;1-55;28877554-28877608;98.18;6e-19;97.1;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1100	Chr10;38-73;7967796-7967831;100.00;5e-10;67.6;
NonpolyA_lnc-126	SEQ ID No 126	SEQ ID No 1101	Chr10;161-235;19040600-19040527;85.33;7e-13;76.8;
NonpolyA_lnc-126	SEQ ID No 126	SEQ ID No 1102	Chr10;161-235;19154047-19154120;85.33;7e-13;76.8;
NonpolyA_lnc-126	SEQ ID No 126	SEQ ID No 1103	Chr6;179-235;26220170-26220114;89.47;9e-12;73.1;
NonpolyA_lnc-127	SEQ ID No 127	SEQ ID No 1104	Chr6;155-236;26220194-26220114;83.33;1e-11;73.1;
NonpolyA_lnc-127	SEQ ID No 127	SEQ ID No 1105	Chr10;162-236;19040600-19040527;84.00;3e-11;71.3;
NonpolyA_lnc-127	SEQ ID No 127	SEQ ID No 1106	Chr10;162-236;19154047-19154120;84.00;3e-11;71.3;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1107	Chr3;140-247;29382509-29382616;80.70;2e-13;78.7;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1108	Chr3;186-242;4701397-4701453;87.93;5e-10;67.6;
onpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1109	Chr1;186-242;23323767-23323823;87.93;5e-10;67.6;
PolyA_lnc-435	SEQ ID NO 646	SEQ ID No 1110	Chr1;173-244;39669061-39669132;83.78;6e-10;67.6

Table 7. Orthologs in *Sorghum bicolor*

Arabidopsis thaliana		*Sorghum bicolor*	
lncRNA ID	**SEQ ID No**	**SEQ ID No**	**chromosome; qstart; qend; sstart; send; identity; evalue; bitscore;**
NonpolyA_lnc-126	SEQ ID No 126	SEQ ID No 1111	chromosome_1;179-240;67690391-67690330;85.94;3e-09;65.8;
NonpolyA_lnc-127	SEQ ID No 127	SEQ ID No 1112	chromosome_1;180-241;67690391-67690330;87.30;7e-11;71.3;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1113	chromosome_10;186-247;54381680-54381619;87.30;7e-11;71.3;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1114	chromosome_10;183-236;2606458-2606404;87.50;4e-08;62.1;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1115	chromosome_10;183-236;3059507-3059561;85.71;2e-06;56.5;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1116	chromosome_2;183-213;63632604-63632635;96.88;3e-05;52.8;
PolyA_lnc-412	SEQ ID NO 623	SEQ ID No 1117	chromosome_3;308-349;62844387-62844345;90.70;5e-06;56.5;
PolyA_lnc-435	SEQ ID NO 646	SEQ ID No 1118	chromosome_4;173-250;19246707-19246785;82.72;1e-09;67.6;
PolyA_lnc-435	SEQ ID NO 646	SEQ ID No 1119	chromosome_3;173-244;70741759-70741830;82.43;6e-08;62.1;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1120	chromosome_8;391-418;4867746-4867719;100.00;4e-05;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1121	chromosome_1;391-418;11254895-11254922;100.00;4e-05;52.8;

Table 8. Orthologs in *Setaria italica*

Arabidopsis thaliana		*Setaria italica*	
lncRNA ID	**SEQ ID No**	**SEQ ID No**	**chromosome; qstart; qend; sstart; send; identity; evalue; bitscore;**
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1122	scaffold_12;1-280;235180-234897;87.93;2e-88;327;
NonpolyA_lnc-126	SEQ ID No 126	SEQ ID No 1123	scaffold_9;179-240;54276563-54276502;87.30;3e-11;71.3;
NonpolyA_lnc-127	SEQ ID No 127	SEQ ID No 1124	scaffold_9;180-241;54276563-54276502;88.71;8e-13;76.8;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1125	scaffold_9;168-247;14435814-14435892;86.25;1e-15;86.1;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1126	scaffold_9;168-247;14454505-14454427;86.25;1e-15;86.1;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1127	scaffold_3;168-247;4385370-4385448;86.25;1e-15;86.1;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1128	scaffold_4;186-247;32037730-32037791;87.30;4e-11;71.3;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1129	scaffold_4;183-236;2049280-2049225;85.96;3e-07;58.4;
PolyA_lnc-435	SEQ ID NO 646	SEQ ID No 1130	scaffold_5;213-244;44423128-44423159;100.00;1e-07;60.2;

Table 9. Orthologs in *Triticum aestivum*

Arabidopsis thaliana		*Triticum aestivum*	
lncRNA ID	**SEQ ID No**	**SEQ ID No**	**chromosome; qstart; qend; sstart; send; identity; evalue; bitscore;**
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1131	IWGSC_CSS_2AL_scaff_6436162;1-326;9280-9607;90.80;5e-119;433;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1132	IWGSC_CSS_1DL_scaff_2243306;1-280;11875-12158;87.59;1e-85;322;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1133	IWGSC_CSS_1DL_scaff_2289211;1-280;1569-1286;87.59;1e-85;322;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1134	IWGSC_CSS_1DL_scaff_2289212;1-280;284-567;87.59;1e-85;322;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1135	IWGSC_CSS_3AL_scaff_4354759;1-280;4211-3928;87.59;1e-85;322;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1136	IWGSC_CSS_5AS_scaff_1550288;1-280;10149-9866;87.24;5e-84;316;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1137	IWGSC_CSS_5AS_scaff_1547701;1-280;508-791;87.24;5e-84;316;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1138	IWGSC_CSS_5AS_scaff_1547700;1-280;508-791;87.24;5e-84;316;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1139	IWGSC_CSS_6DL_scaff_3237060;1-280;9116-8833;86.90;2e-82;311;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1140	IWGSC_CSS_6DS_scaff_2081400;1-287;2399-2688;86.58;2e-82;311;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1141	IWGSC_CSS_6DS_scaff_2081400;1-287;1607-1896;85.86;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1142	IWGSC_CSS_2AS_scaff_5207814;1-280;27556-27834;86.55;5e-79;300;
lonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1143	IWGSC_CSS_2AS_scaff_5227991;1-280;25058-25336;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1144	IWGSC_CSS_2AS_scaff_5195196;1-280;26969-26691;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1145	IWGSC_CSS_5BS_scaff_2294722;1-280;22589-22311;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1146	IWGSC_CSS_2AL_scaff_6438663;1-280;17890-18173;86.25;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1147	IWGSC_CSS_1BL_scaff_3878281;1-280;8733-9011;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1148	IWGSC_CSS_1BS_scaff_3429085;1-280;843-565;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1149	IWGSC_CSS_2AS_scaff_5194735;1-280;1883-2161;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1150	IWGSC_CSS_2AS_scaff_5305319;1-280;12169-11891;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1151	IWGSC_CSS_3AS_scaff_3337215;1-280;9110-8832;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1152	IWGSC_CSS_6BL_scaff_4333267;1-280;9113-8835;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1153	IWGSC_CSS_5DL_scaff_4608711;1-280;5581-5303;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1154	IWGSC_CSS_4AL_scaff_4AL_7170381;1-280;6269-6547;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1155	IWGSC_CSS_6AL_scaff_5830891;1-280;2804-2526;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1156	IWGSC_CSS_5AL_scaff_2811448;1-280;2166-2444;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1157	IWGSC_CSS_5BL_scaff_10917779;1-280;4610-4888;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1158	IWGSC_CSS_6AS_scaff_4348773;1-280;1291-1569;86.55;5e-79;300;

Arabidopsis thaliana		*Triticum aestivum*	
lncRNA ID	**SEQ ID No**	**SEQ ID No**	**chromosome; qstart; qend; sstart; send; identity; evalue; bitscore;**
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1159	IWGSC_CSS_3DL_scaff_6939560;1-280;406-684;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1160	IWGSC_CSS_5DS_scaff_1474536;1-280;1122-844;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1161	IWGSC_CSS_4BL_scaff_6982286;1-280;2276-1998;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1162	IWGSC_CSS_2DL_scaff_9823338;1-280;2186-1908;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1163	IWGSC_CSS_4DL_scaff_4DL_14467542;1-280;768-1046;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1164	IWGSC_CSS_1BS_scaff_3429084;1-280;843-565;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1165	IWGSC_CSS_2DL_scaff_9827981;1-280;2625-2347;86.55;5e-79;300;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1166	IWGSC_CSS_1AL_scaff_3878661;1-280;3509-3231;86.21;2e-77;294;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1167	IWGSC_CSS_3AL_scaff_4250688;26-259;1486-1722;83.40;3e-51;207;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1168	IWGSC_CSS_6DL_scaff_3268384;14-184;5458-5290;88.51;4e-50;204;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1169	IWGSC_CSS_1AS_scaff_3303174;1-83;6708-6790;98.80;2e-33;148;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1170	IWGSC_CSS_2DL_scaff_9847553;1-70;1519-1588;94.37;3e-21;108;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1171	IWGSC_CSS_3B_scaff_10549569;1-35;3574-3540;97.14;1e-06;60.2;
lonpolyA_lnc-49	SEQ ID No 49	SEQ ID No 1172	IWGSC_CSS_2AL_scaff_6413459;865-960;864-773;91.67;3e-27;130;
NonpolyA_lnc-82	SEQ ID No 82	SEQ ID No 1173	IWGSC_CSS_2AL_scaff_6336469;24-169;24116-24265;94.67;6e-58;230;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1174	IWGSC_CSS_4AL_scaff_4AL_7177208;186-247;9069-9130;90.32;2e-13;82.4;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1175	IWGSC_CSS_7DL_scaff_3340407;186-247;14133-14072;88.71;9e-12;76.8;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1176	IWGSC_CSS_4AL_scaff_4AL_7169960;186-247;10832-10893;88.71;9e-12;76.8;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1177	IWGSC_CSS_4AL_scaff_4AL_7169960;186-247;13652-13713;88.71;9e-12;76.8;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1178	IWGSC_CSS_4AL_scaff_4AL_7169960;186-247;15664-15725;88.71;9e-12;76.8;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1179	IWGSC_CSS_4AL_scaff_4AL_7169960;186-242;7357-7413;87.72;5e-09;67.6;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1180	IWGSC_CSS_4AL_scaff_4AL_7116879;186-247;2457-2518;88.71;9e-12;76.8;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1181	IWGSC_CSS_4AL_scaff_4AL_7173214;186-247;2997-2936;88.71;9e-12;76.8;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1182	IWGSC_CSS_4AL_scaff_4AL_7073411;186-247;1300-1361;88.71;9e-12;76.8;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1183	IWGSC_CSS_7DS_scaff_3965048;186-247;1034-973;88.71;9e-12;76.8;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1184	IWGSC_CSS_4AL_scaff_4AL_7066578;186-247;2415-2354;87.30;4e-10;71.3;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1185	IWGSC_CSS_4AL_scaff_4AL_7066578;186-247;4928-4867;87.30;4e-10;71.3;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1186	IWGSC_CSS_4AL_scaff_4AL_7088686;186-247;11372-11433;85.48;2e-08;65.8;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1187	IWGSC_CSS_4AL_scaff_4AL_7171683;186-247;644-583;85.48;2e-08;65.8;

Arabidopsis thaliana		*Triticum aestivum*	
lncRNA ID	**SEQ ID No**	**SEQ ID No**	**chromosome; qstart; qend; sstart; send; identity; evalue; bitscore;**
NonpolyA_lnc-177	SEQ ID No 177	SEQ ID No 1188	IWGSC_CSS_5BL_scaff_10858767;178-206;4618-4646;100.00;3e-05;54.7;
PolyA_lnc-435	SEQ ID NO 646	SEQ ID No 1189	IWGSC_CSS_3DL_scaff_6953034;173-244;1478-1407;83.78;7e-09;67.6;
PolyA_lnc-435	SEQ ID NO 646	SEQ ID No 1190	IWGSC_CSS_3AL_scaff_4452177;197-244;1306-1259;89.58;3e-07;62.1;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1191	IWGSC_CSS_4AS_scaff_5935152;391-423;3964-3996;100.00;4e-07;62.1;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1192	IWGSC_CSS_5BS_scaff_2296561;391-423;85-53;100.00;4e-07;62.1;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1193	IWGSC_CSS_2AS_scaff_5193107;391-419;603-575;100.00;7e-05;54.7;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1194	IWGSC_CSS_7DS_scaff_3912759;391-419;4807-4779;100.00;7e-05;54.7;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1195	IWGSC_CSS_2AL_scaff_6429709;391-419;6296-6268;100.00;7e-05;54.7;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1196	IWGSC_CSS_2AL_scaff_6429709;391-418;5814-5787;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1197	IWGSC_CSS_2DS_scaff_5350599;391-419;2671-2699;100.00;7e-05;54.7;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1198	IWGSC_CSS_5DL_scaff_4503468;391-418;4977-5004;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1199	IWGSC_CSS_5DL_scaff_4503468;391-418;9823-9850;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1200	IWGSC_CSS_4AS_scaff_6014835;391-418;7805-7778;100.00;3e-04;52.8;
olyA_lnc-451	SEQ ID NO 662	SEQ ID No 1201	IWGSC_CSS_4AL_scaff_4AL_7092989;391-418;6829-6802;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1202	IWGSC_CSS_4AL_scaff_4AL_7092989;391-418;9253-9226;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1203	IWGSC_CSS_5DS_scaff_2748235;391-418;4913-4940;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1204	IWGSC_CSS_5BL_scaff_10798163;391-418;16619-16646;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1205	IWGSC_CSS_5BL_scaff_10798163;391-418;16795-16822;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1206	IWGSC_CSS_5BL_scaff_10798163;391-418;17539-17566;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1207	IWGSC_CSS_5BL_scaff_10798163;391-418;18153-18180;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1208	IWGSC_CSS_2AL_scaff_6437397;391-418;2451-2424;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1209	IWGSC_CSS_4BS_scaff_4889343;391-418;20118-20145;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1210	IWGSC_CSS_5DL_scaff_4543496;391-418;5967-5940;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1211	IWGSC_CSS_4DS_scaff_2306721;391-418;10360-10387;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1212	IWGSC_CSS_4DS_scaff_2306721;391-418;11732-11759;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1213	IWGSC_CSS_4DS_scaff_2306721;391-418;12356-12383;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1214	IWGSC_CSS_5AL_scaff_2756579;391-418;6242-6215;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1215	IWGSC_CSS_4BS_scaff_4950863;391-418;102-129;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1216	IWGSC_CSS_2BL_scaff_8023843;391-418;5751-5724;100.00;3e-04;52.8;

Arabidopsis thaliana		*Triticum aestivum*	
lncRNA ID	**SEQ ID No**	**SEQ ID No**	**chromosome; qstart; qend; sstart; send; identity; evalue; bitscore;**
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1217	IWGSC_CSS_5AL_scaff_2794385;391-418;6034-6061;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1218	IWGSC_CSS_5BS_scaff_2296520;391-418;5936-5909;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1219	IWGSC_CSS_4AL_scaff_4AL_7087304;391-418;1132-1159;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1220	IWGSC_CSS_7BS_scaff_3098840;391-418;448-475;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1221	IWGSC_CSS_5DL_scaff_4511932;391-418;8665-8638;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1222	IWGSC_CSS_7AS_scaff_4248846;391-418;4961-4934;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1223	IWGSC_CSS_7AS_scaff_4248846;391-418;5011-4984;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1224	IWGSC_CSS_7AS_scaff_4248846;391-418;5061-5034;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1225	IWGSC_CSS_2BL_scaff_7972185;391-418;7536-7563;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1226	IWGSC_CSS_3B_scaff_10665334;391-418;636-609;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1227	IWGSC_CSS_4BS_scaff_4911970;391-418;5640-5667;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1228	IWGSC_CSS_5BL_scaff_10922260;391-418;2449-2422;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1229	IWGSC_CSS_5BL_scaff_10791023;391-418;4967-4994;100.00;3e-04;52.8;
olyA_lnc-451	SEQ ID NO 662	SEQ ID No 1230	IWGSC_CSS_2DL_scaff_9886524;391-418;6282-6255;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1231	IWGSC_CSS_5AL_scaff_2708813;391-418;3651-3678;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1232	IWGSC_CSS_3AS_scaff_3442110;391-418;2214-2241;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1233	IWGSC_CSS_4AL_scaff_4AL_7086800;391-418;168-141;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1234	IWGSC_CSS_4AL_scaff_4AL_7086800;391-418;1155-1128;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1235	IWGSC_CSS_2DL_scaff_9885893;391-418;366-339;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1236	IWGSC_CSS_2BS_scaff_5241586;391-418;2106-2133;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1237	IWGSC_CSS_5BL_scaff_10881918;391-418;28-1;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1238	IWGSC_CSS_1AS_scaff_3303186;396-423;2474-2447;100.00;3e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1239	IWGSC_CSS_1AS_scaff_3303185;396-423;2474-2447;100.00;3e-04;52.8;

Table 10. Orthologs in *Zea mays*

Arabidopsis thaliana		*Zea mays*	
lncRNA ID	**SEQ ID No**	**SEQ ID No**	**chromosome; qstart; qend; sstart; send; identity; evalue; bitscore;**
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1240	ChrMt;1-280;58035-57752;87.93;1e-87;327;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1241	ChrMt;1-280;114985-115268;87.93;1e-87;327;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1242	Chr9;1-280;6951662-6951945;87.93;1e-87;327;
NonpolyA_lnc-48	SEQ ID No 48	SEQ ID No 1243	Chr9;1-280;68055713-68055997;86.25;2e-79;300;
NonpolyA_lnc-126	SEQ ID No 126	SEQ ID No 1244	Chr8;137-235;167831320-167831417;80.20;2e-10;71.3;
NonpolyA_lnc-126	SEQ ID No 126	SEQ ID No 1245	Chr8;172-235;167806071-167806134;86.15;6e-10;69.4;
NonpolyA_lnc-126	SEQ ID No 126	SEQ ID No 1246	Chr8;172-235;167951586-167951649;86.15;6e-10;69.4;
NonpolyA_lnc-126	SEQ ID No 126	SEQ ID No 1247	Chr8;176-235;167899457-167899516;86.89;2e-09;67.6;
NonpolyA_lnc-126	SEQ ID No 126	SEQ ID No 1248	Chr8;176-235;167970289-167970348;86.89;2e-09;67.6;
NonpolyA_lnc-126	SEQ ID No 126	SEQ ID No 1249	Chr8;172-235;167787858-167787921;84.62;3e-08;63.9;
NonpolyA_lnc-126	SEQ ID No 126	SEQ ID No 1250	Chr8;172-235;167864582-167864645;84.85;3e-08;63.9;
NonpolyA_lnc-126	SEQ ID No 126	SEQ ID No 1251	Chr8;176-235;167880446-167880505;85.48;1e-07;62.1;
NonpolyA_lnc-126	SEQ ID No 126	SEQ ID No 1252	Chr1;168-235;226179247-226179314;84.06;8e-09;65.8;
NonpolyA_lnc-127	SEQ ID No 127	SEQ ID No 1253	Chr8;173-236;167806071-167806134;87.69;1e-11;75.0;
NonpolyA_lnc-127	SEQ ID No 127	SEQ ID No 1254	Chr8;173-236;167831354-167831417;87.69;1e-11;75.0;
NonpolyA_lnc-127	SEQ ID No 127	SEQ ID No 1255	Chr8;173-236;167951586-167951649;87.69;1e-11;75.0;
NonpolyA_lnc-127	SEQ ID No 127	SEQ ID No 1256	Chr8;175-236;167899455-167899516;87.30;2e-10;71.3;
NonpolyA_lnc-127	SEQ ID No 127	SEQ ID No 1257	Chr8;173-236;167787858-167787921;86.15;7e-10;69.4;
NonpolyA_lnc-127	SEQ ID No 127	SEQ ID No 1258	Chr8;173-236;167864582-167864645;86.36;7e-10;69.4;
NonpolyA_lnc-127	SEQ ID No 127	SEQ ID No 1259	Chr8;176-236;167970288-167970348;87.10;7e-10;69.4;
NonpolyA_lnc-127	SEQ ID No 127	SEQ ID No 1260	Chr8;174-236;167880443-167880505;86.15;2e-09;67.6;
NonpolyA_lnc-127	SEQ ID No 127	SEQ ID No 1261	Chr1;169-236;226179247-226179314;85.51;2e-10;71.3;
NonpolyA_lnc-127	SEQ ID No 127	SEQ ID No 1262	Chr7;173-236;163665468-163665405;86.15;7e-10;69.4;
NonpolyA_lnc-127	SEQ ID No 127	SEQ ID No 1263	Chr7;173-236;163753613-163753550;86.15;7e-10;69.4;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1264	Chr9;183-247;20588971-20588906;85.29;9e-09;65.8;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1265	Chr9;186-236;20459259-20459309;88.46;1e-07;62.1;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1266	Chr9;183-213;20461154-20461185;96.88;7e-05;52.8;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1267	Chr1;183-247;217831454-217831519;85.29;9e-09;65.8;

Arabidopsis thaliana		*Zea mays*	
lncRNA ID	**SEQ ID No**	**SEQ ID No**	**chromosome; qstart; qend; sstart; send; identity; evalue; bitscore;**
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1268	Chr10;185-242;4090263-4090206;86.44;3e-08;63.9;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1269	Chr10;185-242;4170911-4170854;86.44;3e-08;63.9;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1270	Chr10;185-242;4172779-4172722;86.44;3e-08;63.9;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1271	Chr10;185-242;4177042-4176985;86.44;3e-08;63.9;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1272	Chr10;185-242;4178911-4178854;86.44;3e-08;63.9;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1273	Chr10;185-242;4180776-4180719;86.44;3e-08;63.9;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1274	Chr10;185-242;4183897-4183840;86.44;3e-08;63.9;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1275	Chr10;185-242;4185768-4185711;86.44;3e-08;63.9;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1276	Chr10;185-242;4199325-4199382;86.44;3e-08;63.9;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1277	Chr10;185-242;4201193-4201250;86.44;3e-08;63.9;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1278	Chr10;185-242;106706976-106706919;86.44;3e-08;63.9;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1279	Chr10;185-242;4089153-4089096;84.75;2e-06;58.4;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1280	Chr10;185-242;4093239-4093182;84.75;2e-06;58.4;
lonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1281	Chr10;185-242;4187637-4187580;85.00;2e-06;58.4;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1282	Chr10;185-224;4194923-4194962;92.50;2e-06;58.4;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1283	Chr10;185-242;4197454-4197511;85.00;2e-06;58.4;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1284	Chr10;185-242;106597654-106597597;84.75;2e-06;58.4;
NonpolyA_lnc-147	SEQ ID No 147	SEQ ID No 1285	Chr10;185-224;106686842-106686803;92.50;2e-06;58.4;
PolyA_lnc-386	SEQ ID NO 597	SEQ ID No 1286	Chr8;2295-2322;160842283-160842256;100.00;0.001;52.8;
PolyA_lnc-435	SEQ ID NO 646	SEQ ID No 1287	Chr5;173-250;131459437-131459515;83.95;7e-11;73.1;
PolyA_lnc-435	SEQ ID NO 646	SEQ ID No 1288	Chr4;173-244;97536526-97536597;83.78;3e-09;67.6;
PolyA_lnc-435	SEQ ID NO 646	SEQ ID No 1289	Chr8;213-244;46220656-46220625;100.00;6e-07;60.2;
PolyA_lnc-435	SEQ ID NO 646	SEQ ID No 1290	Chr7;213-244;26709167-26709136;100.00;6e-07;60.2;
PolyA_lnc-435	SEQ ID NO 646	SEQ ID No 1291	Chr6;213-244;16191137-16191106;100.00;6e-07;60.2;
PolyA_lnc-435	SEQ ID NO 646	SEQ ID No 1292	Chr6;213-244;64638749-64638718;100.00;6e-07;60.2;
PolyA_lnc-435	SEQ ID NO 646	SEQ ID No 1293	Chr3;213-244;163997262-163997231;100.00;6e-07;60.2;
PolyA_lnc-435	SEQ ID NO 646	SEQ ID No 1294	Chr10;213-244;60861853-60861822;100.00;6e-07;60.2;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1295	Chr3;391-418;141620220-141620247;100.00;1e-04;52.8;
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1296	Chr3;391-418;141646614-141646641;100.00;1e-04;52.8;

Arabidopsis thaliana		*Zea mays*	
lncRNA ID	**SEQ ID No**	**SEQ ID No**	**chromosome; qstart; qend; sstart; send; identity; evalue; bitscore;**
PolyA_lnc-451	SEQ ID NO 662	SEQ ID No 1297	Chr1;391-418;110316506-110316533;100.00;1e-04;52.8;

CLAIMS

WE CLAIM

1. A long non-coding RNA(lncRNA) molecule which is differentially expressed in a plant grown under phosphate starvation conditions when compared to a plant grown under normal conditions with adequate phosphate supply and which is unpolyadenylated or a DNA molecule which when transcribed yields an RNA molecule comprising said lncRNA or the complement of said DNA molecule.

2. The lncRNA molecule according to claim 1 which comprises a nucleotide sequence having at least 80% identity with any one of SEQ ID No. 4; SEQ ID No. 5; SEQ ID No. 6; SEQ ID No. 15; SEQ ID No. 18; SEQ ID No. 26; SEQ ID No. 28; SEQ ID No. 32; SEQ ID No. 34; SEQ ID No. 36; SEQ ID No. 40; SEQ ID No. 42; SEQ ID No. 47; SEQ ID No. 52; SEQ ID No. 55; SEQ ID No. 57; SEQ ID No. 59; SEQ ID No. 60; SEQ ID No. 62; SEQ ID No. 64; SEQ ID No. 70; SEQ ID No. 72; SEQ ID No. 77; SEQ ID No. 79; SEQ ID No. 82; SEQ ID No. 83; SEQ ID No. 84; SEQ ID No. 86; SEQ ID No. 90; SEQ ID No. 91; SEQ ID No. 98; SEQ ID No. 99; SEQ ID No. 102; SEQ ID No. 107; SEQ ID No. 114; SEQ ID No. 115; SEQ ID No. 118; SEQ ID No. 119; SEQ ID No. 120; SEQ ID No. 121; SEQ ID No. 128; SEQ ID No. 132; SEQ ID No. 137; SEQ ID No. 139; SEQ ID No. 140; SEQ ID No. 145; SEQ ID No. 149; SEQ ID No. 151; SEQ ID No. 152; SEQ ID No. 158; SEQ ID No. 160; SEQ ID No. 162; SEQ ID No. 172; SEQ ID No. 174; SEQ ID No. 176; SEQ ID No. 178; SEQ ID No. 179; SEQ ID No. 180; SEQ ID No. 181; SEQ ID No. 183; SEQ ID No. 187; SEQ ID No. 194; SEQ ID No. 195; SEQ ID No. 200; SEQ ID No. 201; SEQ ID No. 204; SEQ ID No. 209 or SEQ ID No. 210 or a DNA molecule which when transcribed yields an RNA molecule comprising said lncRNA.

3. The lncRNA molecule according to claim 1 having a nucleotide sequence comprising any one of SEQ ID No. 4; SEQ ID No. 5; SEQ ID No. 6; SEQ ID No.

15; SEQ ID No. 18; SEQ ID No. 26; SEQ ID No. 28; SEQ ID No. 32; SEQ ID No. 34; SEQ ID No. 36; SEQ ID No. 40; SEQ ID No. 42; SEQ ID No. 47; SEQ ID No. 52; SEQ ID No. 55; SEQ ID No. 57; SEQ ID No. 59; SEQ ID No. 60; SEQ ID No. 62; SEQ ID No. 64; SEQ ID No. 70; SEQ ID No. 72; SEQ ID No. 77; SEQ ID No. 79; SEQ ID No. 82; SEQ ID No. 83; SEQ ID No. 84; SEQ ID No. 86; SEQ ID No. 90; SEQ ID No. 91; SEQ ID No. 98; SEQ ID No. 99; SEQ ID No. 102; SEQ ID No. 107; SEQ ID No. 114; SEQ ID No. 115; SEQ ID No. 118; SEQ ID No. 119; SEQ ID No. 120; SEQ ID No. 121; SEQ ID No. 128; SEQ ID No. 132; SEQ ID No. 137; SEQ ID No. 139; SEQ ID No. 140; SEQ ID No. 145; SEQ ID No. 149; SEQ ID No. 151; SEQ ID No. 152; SEQ ID No. 158; SEQ ID No. 160; SEQ ID No. 162; SEQ ID No. 172; SEQ ID No. 174; SEQ ID No. 176; SEQ ID No. 178; SEQ ID No. 179; SEQ ID No. 180; SEQ ID No. 181; SEQ ID No. 183; SEQ ID No. 187; SEQ ID No. 194; SEQ ID No. 195; SEQ ID No. 200; SEQ ID No. 201; SEQ ID No. 204; SEQ ID No. 209 or SEQ ID No. 210 or a DNA molecule which when transcribed yields an RNA molecule comprising said lncRNA.

4. The lncRNA molecule according to claim 1, wherein said differential expression is upregulation, or a DNA molecule which when transcribed yields an RNA molecule comprising said lncRNA or comprises the complement of said nucleotide sequence.

5. The lncRNA molecule according to claim 4, wherein said lncRNA molecule comprises a nucleotide sequence having at least 80% identity with any one of SEQ ID Nos. 34, 107, 139, 194 or 195 or a DNA molecule which when transcribed yields an RNA molecule comprising said lncRNA.

6. The lncRNA molecule according to claim 4, having a nucleotide sequence comprising any one of SEQ ID Nos. 34, 107, 139, 194 or 195 or a DNA molecule which when transcribed yields an RNA molecule comprising said lncRNA.

7. The lncRNA molecule according to claim 1, wherein said lncRNA molecule comprises at least two conserved hairpin loops, preferably further comprising two co-variance base pairings or a DNA molecule which when transcribed yields an RNA molecule comprising said lncRNA.

8. The lncRNA molecule according to claim 7, wherein said lncRNA molecule comprises a nucleotide sequence having at least 80% sequence identity with SEQ ID No. 149 or a DNA molecule which when transcribed yields an RNA molecule comprising said lncRNA.

9. The lncRNA molecule according to claim 8, having a nucleotide sequence comprising SEQ ID No. 149 or a DNA molecule which when transcribed yields an RNA molecule comprising said lncRNA.

10. Use of a lncRNA molecule according to any one of claims 1 to 3, or a DNA molecule which when transcribed yields such lncRNA molecule, to modulate inorganic phosphate use efficiency in a plant.

11. Use of a lncRNA molecule which is differentially expressed in a plant grown under phosphate starvation conditions when compared to a plant grown under normal conditions with adequate phosphate supply, or a DNA molecule which when transcribed yields such lncRNA molecule, or the complement of said DNA molecule, to modulate inorganic phosphate use efficiency in a plant.

12. The use according to claim 11, wherein said lncRNA molecule comprises a nucleotide sequence having at least 80 % sequence identity to SEQ ID No. 216; SEQ ID No. 235; SEQ ID No. 240; SEQ ID No. 250; SEQ ID No. 266; SEQ ID No. 267; SEQ ID No. 278; SEQ ID No. 281; SEQ ID No. 283; SEQ ID No. 315; SEQ ID No. 320; SEQ ID No. 321; SEQ ID No. 325; SEQ ID No. 330; SEQ ID No. 361; SEQ ID No. 364; SEQ ID No. 368; SEQ ID No. 370; SEQ ID No. 378; SEQ ID No. 384; SEQ ID No. 388; SEQ ID No. 393; SEQ ID No. 396; SEQ ID

No. 414; SEQ ID No. 420; SEQ ID No. 424; SEQ ID No. 429; SEQ ID No. 432; SEQ ID No. 433; SEQ ID No. 436; SEQ ID No. 437; SEQ ID No. 448; SEQ ID No. 459; SEQ ID No. 460; SEQ ID No. 461; SEQ ID No. 462; SEQ ID No. 463; SEQ ID No. 486; SEQ ID No. 504; SEQ ID No. 512; SEQ ID No. 533; SEQ ID No. 570; SEQ ID No. 571; SEQ ID No. 572; SEQ ID No. 600; SEQ ID No. 601; SEQ ID No. 617; SEQ ID No. 618; SEQ ID No. 649; SEQ ID No. 651; SEQ ID No. 652; SEQ ID No. 656; SEQ ID No. 660; SEQ ID No. 662; SEQ ID No. 707; SEQ ID No. 709; SEQ ID No. 712; SEQ ID No. 713; SEQ ID No. 715; SEQ ID No. 716; SEQ ID No. 725; SEQ ID No. 734; SEQ ID No. 783; SEQ ID No. 785; SEQ ID No. 786; SEQ ID No. 787; SEQ ID No. 788; SEQ ID No. 798; SEQ ID No. 817; SEQ ID No. 850; SEQ ID No. 857; SEQ ID No. 918; SEQ ID No. 921; SEQ ID No. 945; SEQ ID No. 946; SEQ ID No. 955; SEQ ID No. 957; SEQ ID No. 972; SEQ ID No. 985; SEQ ID No. 986; SEQ ID No. 990; SEQ ID No. 997; SEQ ID No. 998; SEQ ID No. 1020; SEQ ID No. 1025; SEQ ID No. 1031; SEQ ID No. 1033; SEQ ID No. 1047; SEQ ID No. 1048; SEQ ID No. 1068 or SEQ ID No. 1080.

13. The use according to claim 5, wherein said lncRNA molecule comprises a nucleotide sequence of SEQ ID No. 216; SEQ ID No. 235; SEQ ID No. 240; SEQ ID No. 250; SEQ ID No. 266; SEQ ID No. 267; SEQ ID No. 278; SEQ ID No. 281; SEQ ID No. 283; SEQ ID No. 315; SEQ ID No. 320; SEQ ID No. 321; SEQ ID No. 325; SEQ ID No. 330; SEQ ID No. 361; SEQ ID No. 364; SEQ ID No. 368; SEQ ID No. 370; SEQ ID No. 378; SEQ ID No. 384; SEQ ID No. 388; SEQ ID No. 393; SEQ ID No. 396; SEQ ID No. 414; SEQ ID No. 420; SEQ ID No. 424; SEQ ID No. 429; SEQ ID No. 432; SEQ ID No. 433; SEQ ID No. 436; SEQ ID No. 437; SEQ ID No. 448; SEQ ID No. 459; SEQ ID No. 460; SEQ ID No. 461; SEQ ID No. 462; SEQ ID No. 463; SEQ ID No. 486; SEQ ID No. 504; SEQ ID No. 512; SEQ ID No. 533; SEQ ID No. 570; SEQ ID No. 571; SEQ ID No. 572; SEQ ID No. 600; SEQ ID No. 601; SEQ ID No. 617; SEQ ID No. 618; SEQ ID No. 649; SEQ ID No. 651; SEQ ID No. 652; SEQ ID No. 656; SEQ ID No. 660; SEQ ID No. 662; SEQ ID No. 707; SEQ ID No. 709; SEQ ID No. 712; SEQ

ID No. 713; SEQ ID No. 715; SEQ ID No. 716; SEQ ID No. 725; SEQ ID No. 734; SEQ ID No. 783; SEQ ID No. 785; SEQ ID No. 786; SEQ ID No. 787; SEQ ID No. 788; SEQ ID No. 798; SEQ ID No. 817; SEQ ID No. 850; SEQ ID No. 857; SEQ ID No. 918; SEQ ID No. 921; SEQ ID No. 945; SEQ ID No. 946; SEQ ID No. 955; SEQ ID No. 957; SEQ ID No. 972; SEQ ID No. 985; SEQ ID No. 986; SEQ ID No. 990; SEQ ID No. 997; SEQ ID No. 998; SEQ ID No. 1020; SEQ ID No. 1025; SEQ ID No. 1031; SEQ ID No. 1033; SEQ ID No. 1047; SEQ ID No. 1048; SEQ ID No. 1068 or SEQ ID No. 1080.

14. The use according to claim 5, wherein said lncRNA molecule comprises a nucleotide sequence of any one of Tables 5 to 10.

15. A method for modulating the phosphate use efficiency in a plant comprising the step of increasing or decreasing the transcription and/or concentration of an lncRNA molecule according to any one of claims 1 to 14 in a plant cell.

16. The method according to claim 15, comprising the step of increasing the transcription and/or concentration of an lncRNA molecule according to any one of claims 1 to 14 in a plant cell.

17. The method according to claim 16, wherein said phosphate use efficiency is increased.

18. The method according to claim 15, comprising the step of decreasing the transcription and/or concentration of an lncRNA molecule according to any one of claims 1 to 14 in a plant cell.

19. The method according to claim 16, wherein said phosphate use efficiency is increased.

20. The method according to claim 18, wherein said decrease in transcription or concentration is achieved by mutating the DNA region from which said lncRNA molecule is transcribed.

21. The method according to claim 18, wherein said decrease in transcription or concentration is achieved by expression of an inhibitory RNA molecule specifically recognizing said lncRNA molecule.

22. The method according to claim 16, wherein said increase in transcription or concentration is achieved by mutating the DNA region from which said lncRNA molecule is transcribed.

23. The method according to claim 16, comprising introducing a recombinant gene comprising:
    a. a plant-expressible promoter
    b. a DNA region which when transcribed encodes an RNA molecule comprising or consisting of said lncRNA molecule; and optionally
    c. an appropriate transcription termination region, and/or polyadenylation region.

24. A modified plant cell comprising a modulated concentration or transcription of an lncRNA molecule according to any one of claims 1 to 14 when compared to an unmodified plant cell.

25. A modified plant, or plant part, tissue or organ comprising a multitude of or consisting essentially of modified plant cells according to claim 24.

26. A seed of the modified plant according to claim 25.

27. A method for isolating further lncRNA molecules involved in phosphate use efficiency in a plant comprising the step of identifying a nucleotide sequence

having a degree of homology to the lncRNA molecules of any one of claims 1 to 14 and isolating or synthesizing such RNA molecule comprising or consisting of such nucleotide sequence.

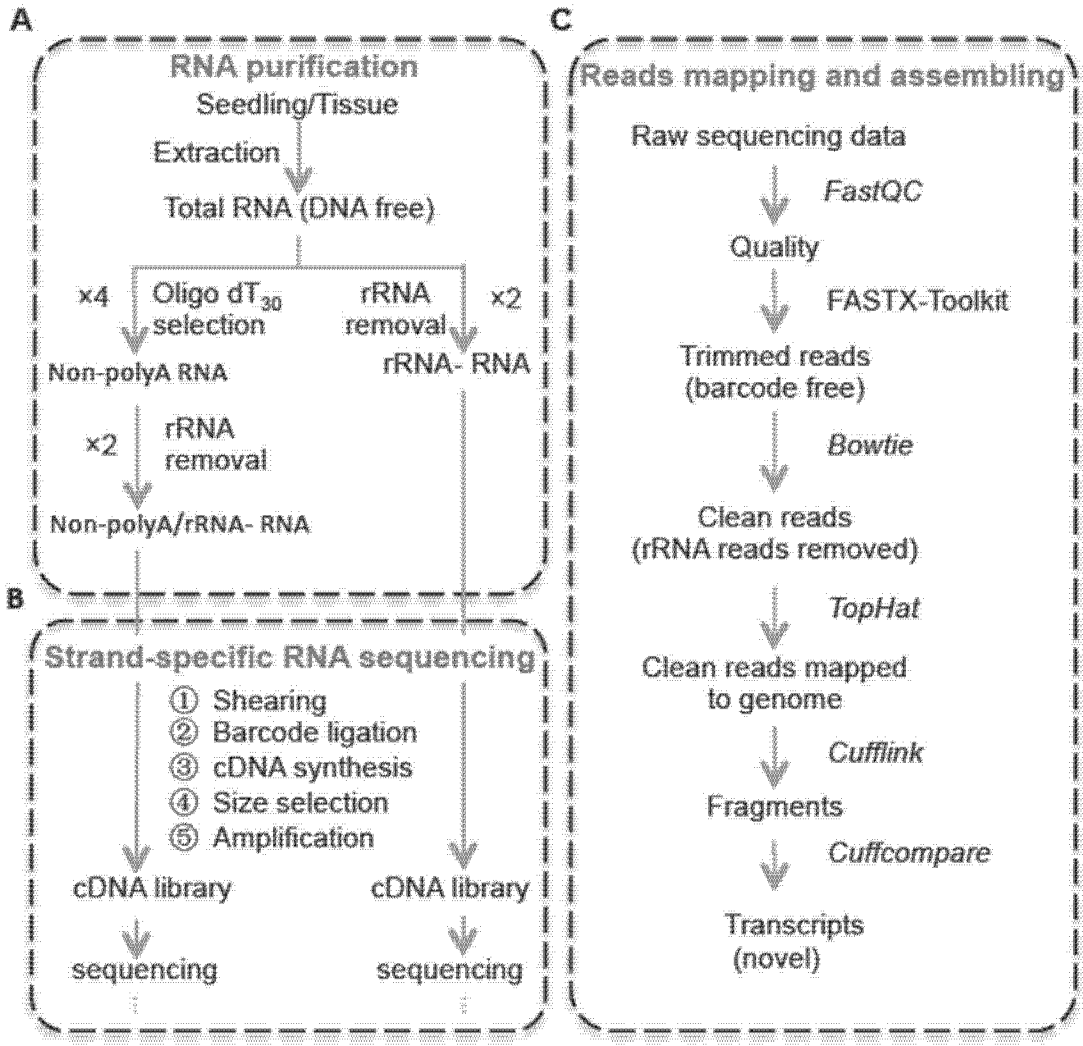

A
RNA purification
Seedling/Tissue
Extraction
Total RNA (DNA free)
×4
Oligo dT30 selection
rRNA removal
×2
Non-polyA RNA
rRNA- RNA
×2
rRNA removal
Non-polyA/rRNA- RNA
B
Strand-specific RNA sequencing
① Shearing
② Barcode ligation
③ cDNA synthesis
④ Size selection
⑤ Amplification
cDNA library
cDNA library
sequencing
sequencing
C
Reads mapping and assembling
Raw sequencing data
FastQC
Quality
FASTX-Toolkit
Trimmed reads (barcode free)
Bowtie
Clean reads (rRNA reads removed)
TopHat
Clean reads mapped to genome
Cufflink
Fragments
Cuffcompare
Transcripts (novel)

Figure 1

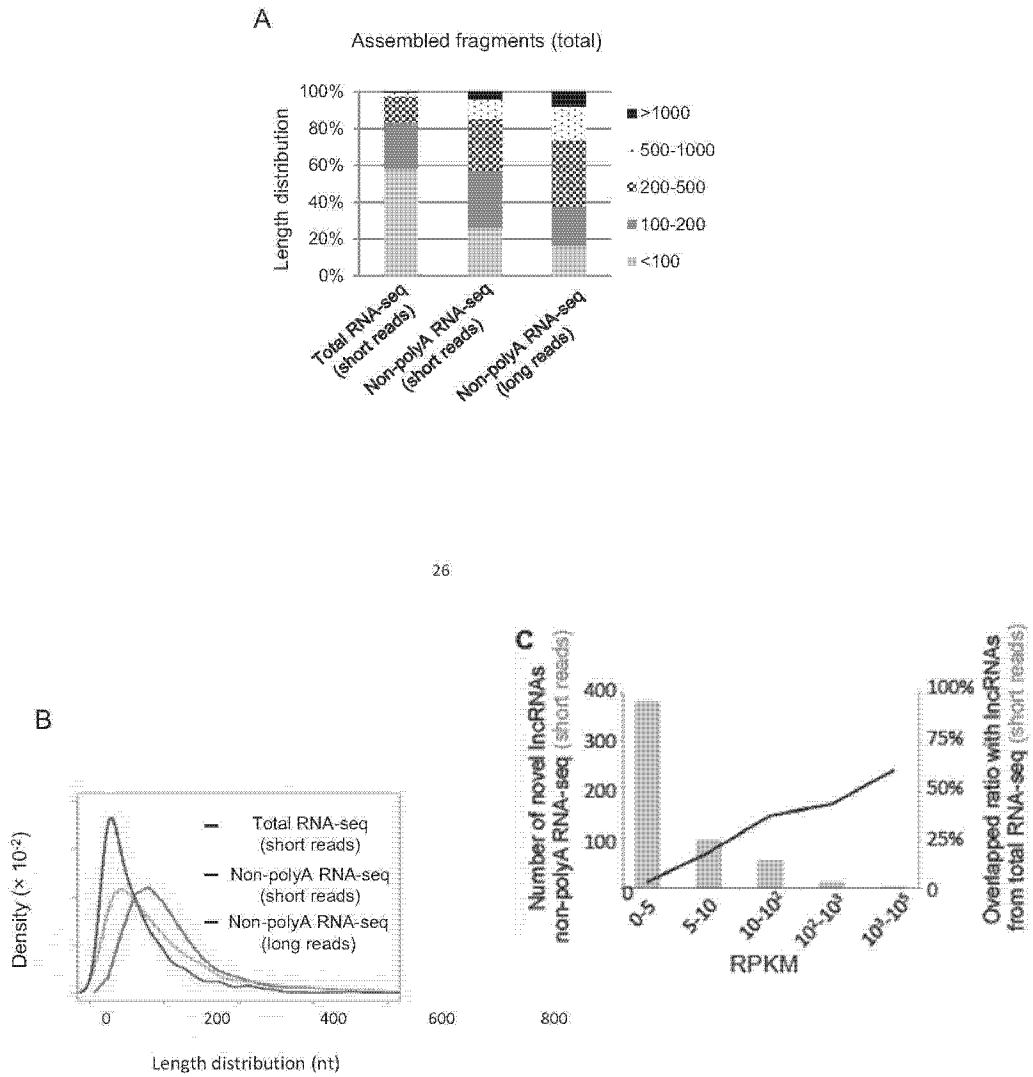
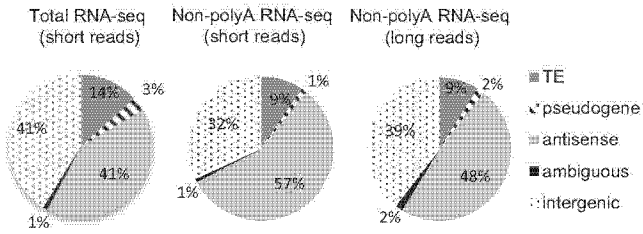

A
Assembled fragments (total)
Length distribution
100%
80%
60%
40%
20%
0%
>1000
500-1000
200-500
100-200
<100
Total RNA-seq (short reads)
Non-polyA RNA-seq (short reads)
Non-polyA RNA-seq (long reads)
B
Density (× 10⁻²)
Total RNA-seq (short reads)
Non-polyA RNA-seq (short reads)
Non-polyA RNA-seq (long reads)
0
200
400
600
800
Length distribution (nt)
C
Number of novel lncRNAs non-polyA RNA-seq (short reads)
400
300
200
100
0
100%
75%
50%
25%
0
Overlapped ratio with lncRNAs from total RNA-seq (short reads)
0-5
5-10
10-10²
10²-10³
10³-10⁵
RPKM

Figure 2

D



E

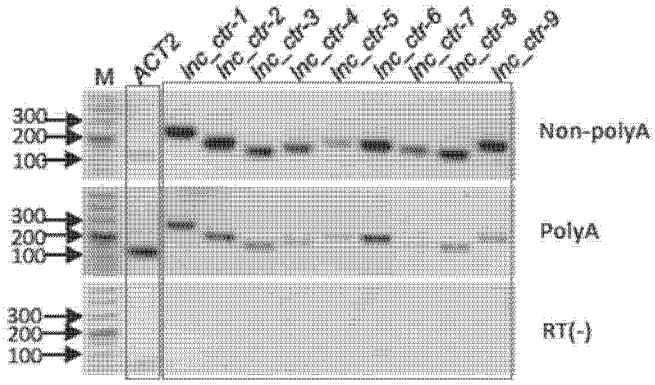
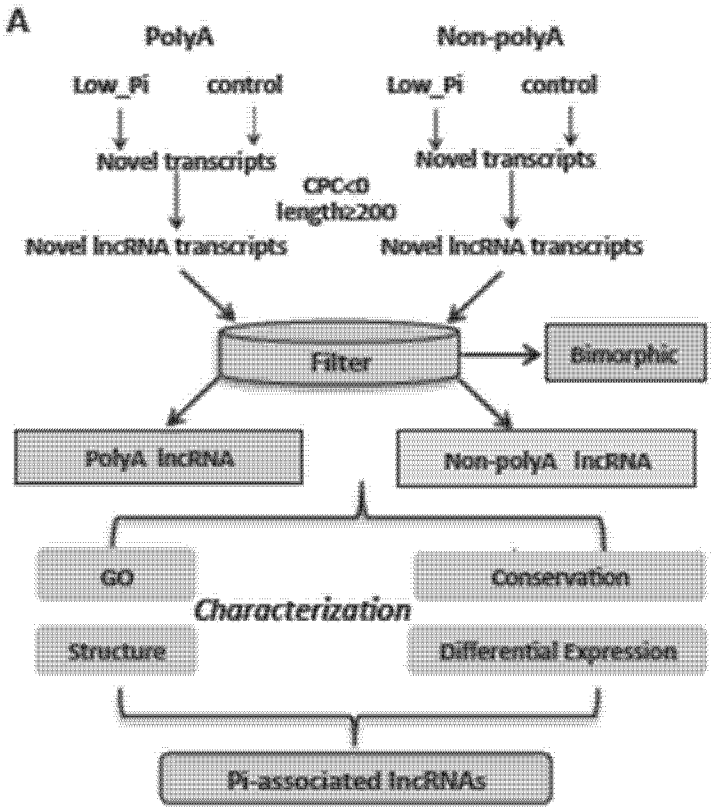


Figure 2 cont'd


A
PolyA
Non-polyA
Low_Pi
control
Low_Pi
control
Novel transcripts
Novel transcripts
CPC<0
length≥200
Novel lncRNA transcripts
Novel lncRNA transcripts
Filter
Bimorphic
PolyA lncRNA
Non-polyA lncRNA
GO
Conservation
Characterization
Structure
Differential Expression
Pi-associated lncRNAs

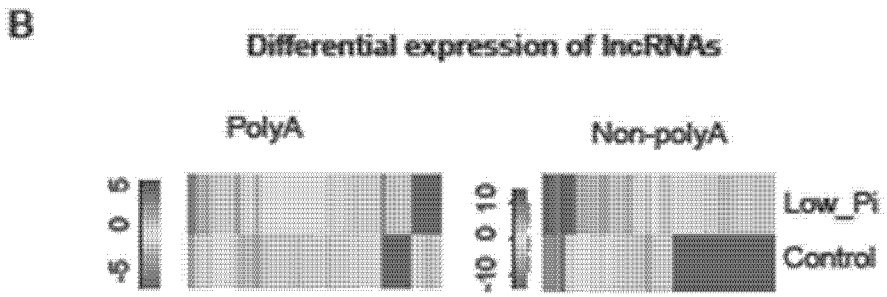

B
Differential expression of lncRNAs
PolyA
Non-polyA
5
0
-5
10
0
-10
Low_Pi
Control

Figure 3

C

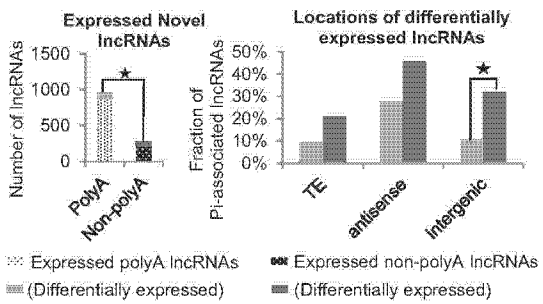


Figure 3 cont'd

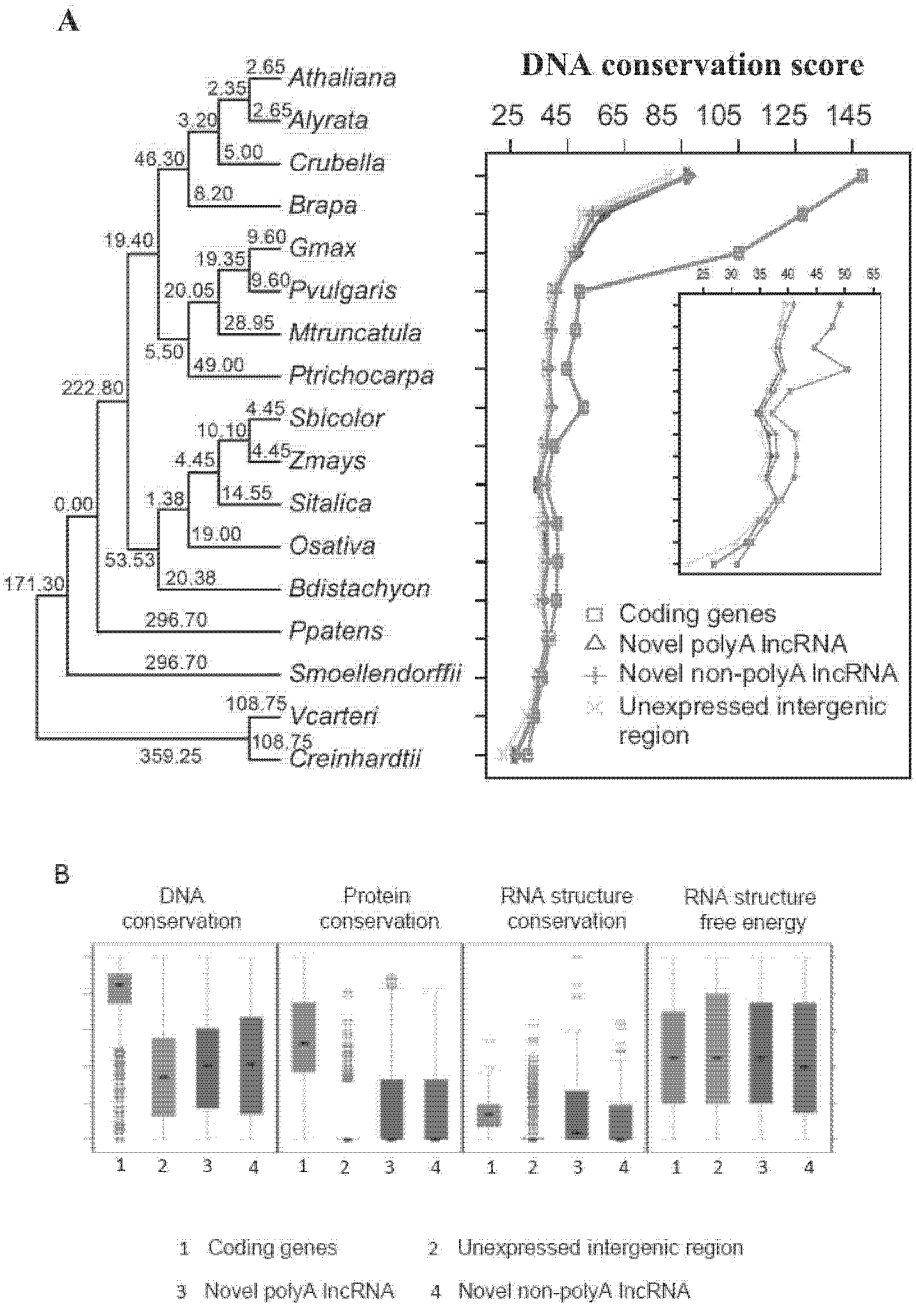

A
DNA conservation score
25 45 65 85 105 125 145
25 30 35 40 45 50 55
2.65 Athaliana
2.35
2.65 Alyrata
3.20
5.00 Crubella
46.30
8.20 Brapa
19.40
9.60 Gmax
19.35
9.60 Pvulgaris
20.05
28.95 Mtruncatula
5.50
49.00 Ptrichocarpa
222.80
4.45 Sbicolor
10.10
4.45 Zmays
4.45
14.55 Sitalica
0.00
1.38
19.00 Osativa
53.53
20.38 Bdistachyon
171.30
296.70 Ppatens
296.70 Smoellendorffii
108.75 Vcarteri
108.75
359.25 Creinhardtii
Coding genes
Novel polyA lncRNA
Novel non-polyA lncRNA
Unexpressed intergenic region
B
DNA conservation
Protein conservation
RNA structure conservation
RNA structure free energy
1 2 3 4 1 2 3 4 1 2 3 4 1 2 3 4
1 Coding genes
2 Unexpressed intergenic region
3 Novel polyA lncRNA
4 Novel non-polyA lncRNA

Figure 4

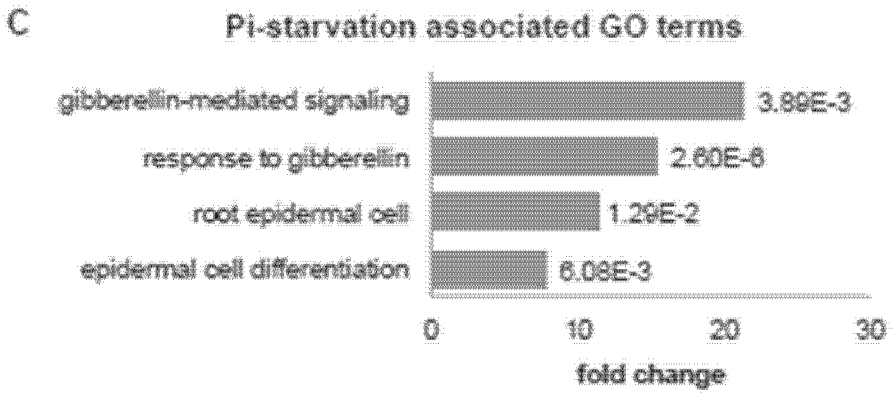


Figure 4 cont'd

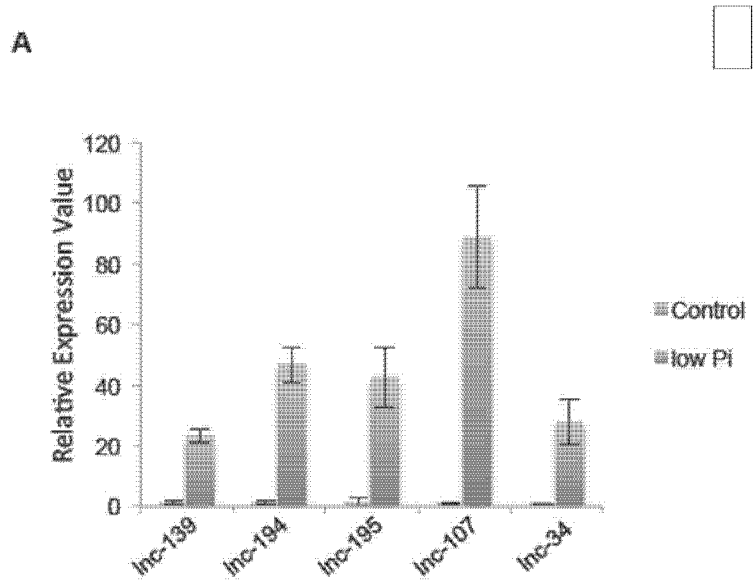


Figure 5

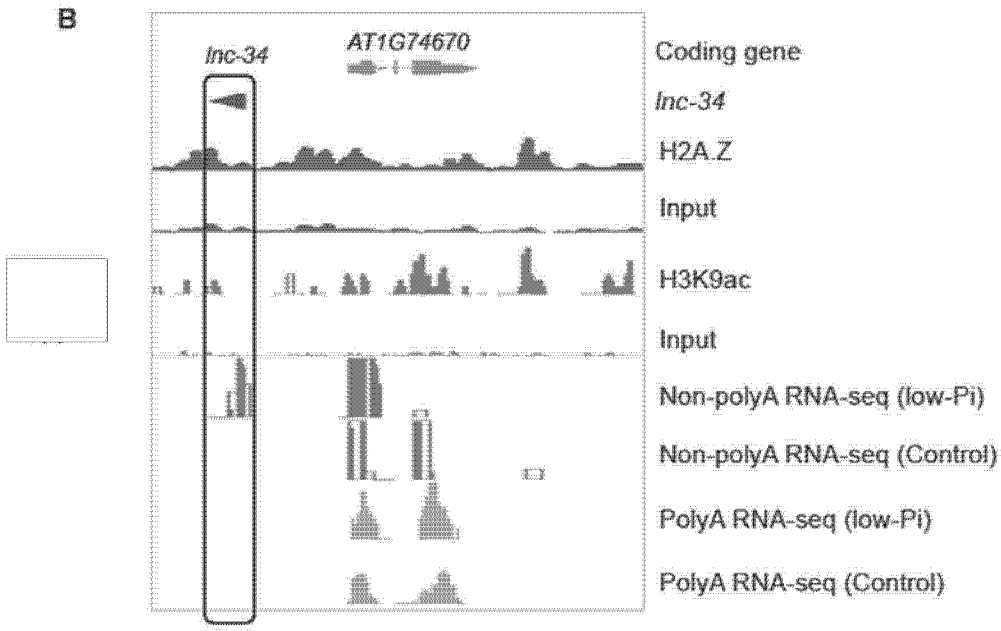


Figure 5 cont'd

Figure 5 cont'd

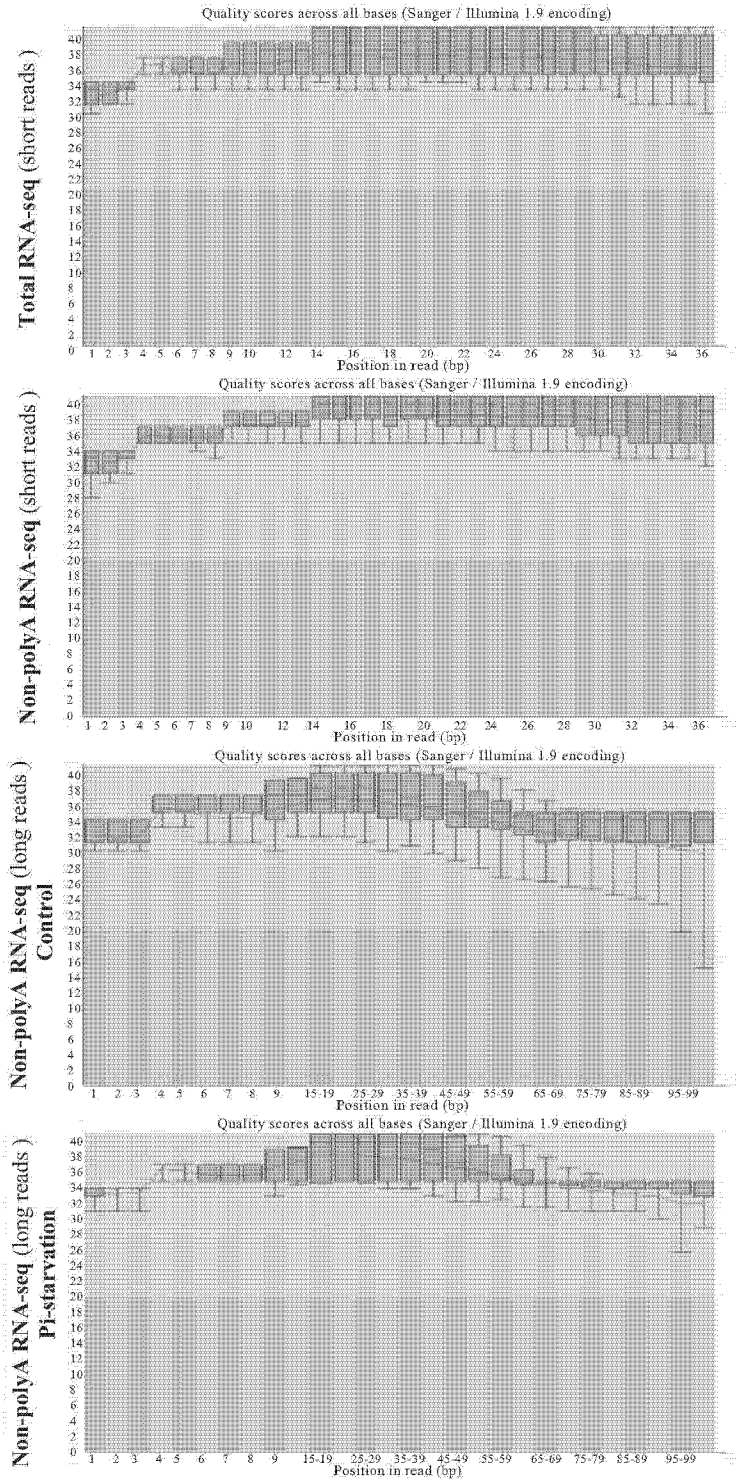

Total RNA-seq (short reads)
Quality scores across all bases (Sanger / Illumina 1.9 encoding)
Position in read (bp)
Non-polyA RNA-seq (short reads)
Quality scores across all bases (Sanger / Illumina 1.9 encoding)
Position in read (bp)
Non-polyA RNA-seq (long reads)
Control
Quality scores across all bases (Sanger / Illumina 1.9 encoding)
Position in read (bp)
Non-polyA RNA-seq (long reads)
Pi-starvation
Quality scores across all bases (Sanger / Illumina 1.9 encoding)
Position in read (bp)

Figure 6

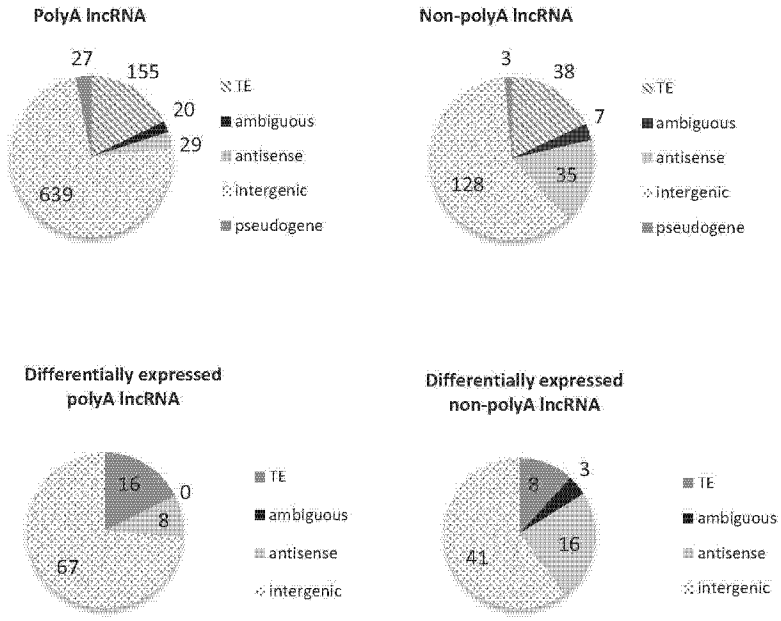

PolyA lncRNA
27
155
20
29
639
TE
ambiguous
antisense
intergenic
pseudogene
Non-polyA lncRNA
3
38
7
35
128
TE
ambiguous
antisense
intergenic
pseudogene
Differentially expressed polyA lncRNA
16
0
8
67
TE
ambiguous
antisense
intergenic
Differentially expressed non-polyA lncRNA
8
3
16
41
TE
ambiguous
antisense
intergenic

Figure 7

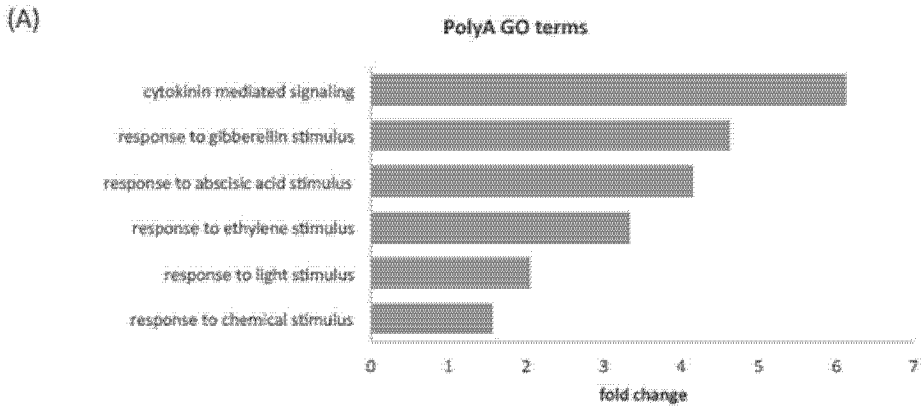

(A)
PolyA GO terms
cytokinin mediated signaling
response to gibberellin stimulus
response to abscisic acid stimulus
response to ethylene stimulus
response to light stimulus
response to chemical stimulus
0
1
2
3
4
5
6
7
fold change

Figure 8

INTERNATIONAL SEARCH REPORT

International application No.
PCT/CN2014/071873

A. CLASSIFICATION OF SUBJECT MATTER

C12N 15/11(2006.01)i; C12N 15/82(2006.01)i

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Data base:DWPI;SIPOABS;CATXT;USTXT;EPTXT;CNABS;WOTXT;KRTXT;JPTXT;CNKI;ISI WEB OF KNOWLEDGE; PUBMED;EMBL;GENBANK;DDBJ Search terms:lncrna, polyadenylation, ployA, non-coding rna, plant, phosphate, starvation, stress, sequence search on SEQ ID NO:4

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 2013090620 A1 (GENOMEDX BIOSCIENCES INC) 20 June 2013 (2013-06-20) see the whole document	1-4, 7, 10, 15-27(all partially)
X	Besma Ben Amor et al. "Novel long non-protein coding RNAs involved in Arabidopsis differentiation and stress responses" *Genome Res.*, Vol. vol.19, No. no.1, 31 January 2009 (2009-01-31), pages 57-69, see "Methods", and page 59, right column, page 61, left column, paragraph 2 to page 62, left column, paragraph 1	1-4, 7, 10, 15-27(all partially)
A	Andrzej T Wierzbicki. "The role of long non-coding RNA in transcriptional gene silencing" *Current Opinion in Plant Biology*, Vol. vol.15, No. no.5, 06 September 2012 (2012-09-06), ISSN: ISSN:1369-5266, pages 517-522, see page 517, right column, paragraph 7	1-4, 7, 10, 15-27(all partially)
A	SHU Yong-jun et al. "Computational identification and functional analysis of long non-coding RNA in Triticum aestivum" *Chinese Journal of Bioinformatics*, Vol. vol.11, No. no.2, 30 June 2013 (2013-06-30), ISSN: ISSN:1672-5565, pages 153-157, see the whole document	1-4, 7, 10, 15-27(all partially)

☑ Further documents are listed in the continuation of Box C. ☑ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
27 October 2014	**18 November 2014**
Name and mailing address of the ISA/CN **STATE INTELLECTUAL PROPERTY OFFICE OF THE P.R.CHINA(ISA/CN)** **6,Xitucheng Rd., Jimen Bridge, Haidian District, Beijing 100088 China** Facsimile No. **(86-10)62019451**	Authorized officer **PAN,Junyu** Telephone No. **(86-10)62089155**

INTERNATIONAL SEARCH REPORT

International application No.
PCT/CN2014/071873

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	Jeremy E. Wilusz et al. "A triple helix stabilizes the 3' ends of long noncoding RNAs that lack poly(A) tails" *Genes Dev.*, Vol. vol.26, No. no.21, 01 November 2012 (2012-11-01), ISSN: ISSN:0890-9369, pages 2392-2407, see the whole document	1-4, 7, 10, 15-27(all partially)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/CN2014/071873

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☑ Claims Nos.: **14** (**partly**)
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

[1] The nucleotide sequence of PolyA_lnc-65 in table 5 in claim 14 does not describe in the description, so the person skilled in the art would not know the sequence of PolyA_lnc-65 in table 5 of claim 14.

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

[1] Claims 1-27 can be divided into following groups:

[2] Groups 1-61: part of claims 1-4, 7, 10, 15-27 related to SEQ ID NOs: 4-6, 15, 18, 26, 28, 32, 36, 40, 42, 47, 52, 55, 57, 59, 60, 62, 64, 70, 72, 77, 79, 83-84, 86, 90, 91, 98, 99, 102, 114, 115, 118-121, 128, 132, 137, 140, 145, 151, 152, 158, 160, 162, 172, 174, 176, 178-181, 183, 187, 200, 201, 204, 209, 210, respectively.

[3] Groups 62-66: part of claims 1-7, 10, 15-27 related to long non-coding RNA(lncRNA) molecules having sequences as defined in SEQ ID NOs: 34, 107, 139, 194, 195, respectively.

[4] Groups 67: part of claims 1-4, 7-10, 15-27 related to long non-coding RNA(lncRNA) molecules having sequences as defined in SEQ ID NOs: 149.

[5] Groups 68: part of claims 1-4, 7, 10-11, 14-27 related to long non-coding RNA (lncRNA) molecules having sequences as defined in SEQ ID NOs: 82.

[6] Groups 69-158: part of claims 11-13, 15-27 related to long non-coding RNA (lncRNA) molecules having sequences as defined in SEQ ID NOs: 216, 235, 240, 250, 266, 267, 278, 281, 283, 315, 320, 321, 325, 330, 361, 364, 368, 370, 378, 384, 388, 393, 396, 414, 420, 424, 429, 432, 433, 436, 437, 448, 459-463, 486, 504, 512, 533, 570-572, 600, 601, 617, 618, 649, 651, 652, 656, 660, 707, 709, 712, 713, 715, 716, 725, 734, 783, 785-788, 798, 817, 850, 857, 918, 921, 945, 946, 955, 957, 972, 985, 986, 990, 997, 998, 1020, 1025, 1031, 1033, 1047, 1048, 1068, 1080, respectively.

[7] Groups 159: part of claims 11-27 related to long non-coding RNA (lncRNA) molecules having sequences as defined in SEQ ID NOs: 662.

[8] Groups 160-385: part of claims 11, 14-27 related to long non-coding RNA (lncRNA) molecules having sequences as defined in SEQ ID NOs: 48, 49, 65, 126, 127, 147, 177, 597, 623, 646, 1082-1297, respectively.

[9] The same or corresponding technical feature among Groups 1-385 is the unpolyadenylated long non-coding RNA (lncRNA) molecule. For a person skilled in the art, the unpolyadenylated long non-coding RNA (lncRNA) molecule is known in the prior art, such as Jeremy E. Wilusz et al., "A triple helix stabilizes the 3' ends of long noncoding RNAs that lack poly(A) tails", Genes Dev., Vol.26, No.21, pp.2392-2407, 01.11.2012, which discloses an unpolyadenylated long non-coding RNA (lncRNA) molecule (see the abstract, page 2402, left column, paragraph 2). Therefore, the 385 inventions related to long non-coding RNA(lncRNA) molecules do not share a same or corresponding special technical feature that makes a contribution over the prior art. Above all, unity of invention is lacking and thus does not meet the requirements of Rule 13.1, 13.2.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/CN2014/071873

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☑ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: **1-4, 7, 10, 15-27(all partially) related to SEQ ID NO：4**

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT
Information on patent family members

International application No.
PCT/CN2014/071873

Patent document cited in search report	Publication date (day/month/year)	Patent family member(s)	Publication date (day/month/year)
WO 2013090620 A1	20 June 2013	CA 2858581 A1	20 June 2013
		AU 2012352153 A1	26 June 2014