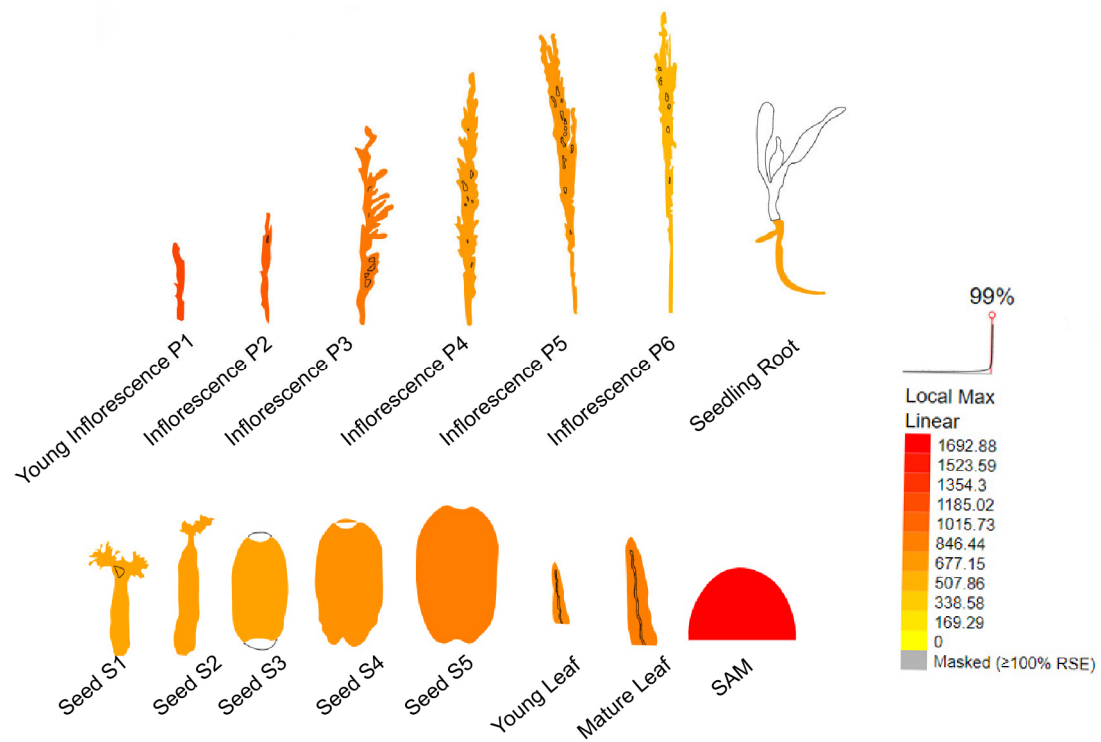


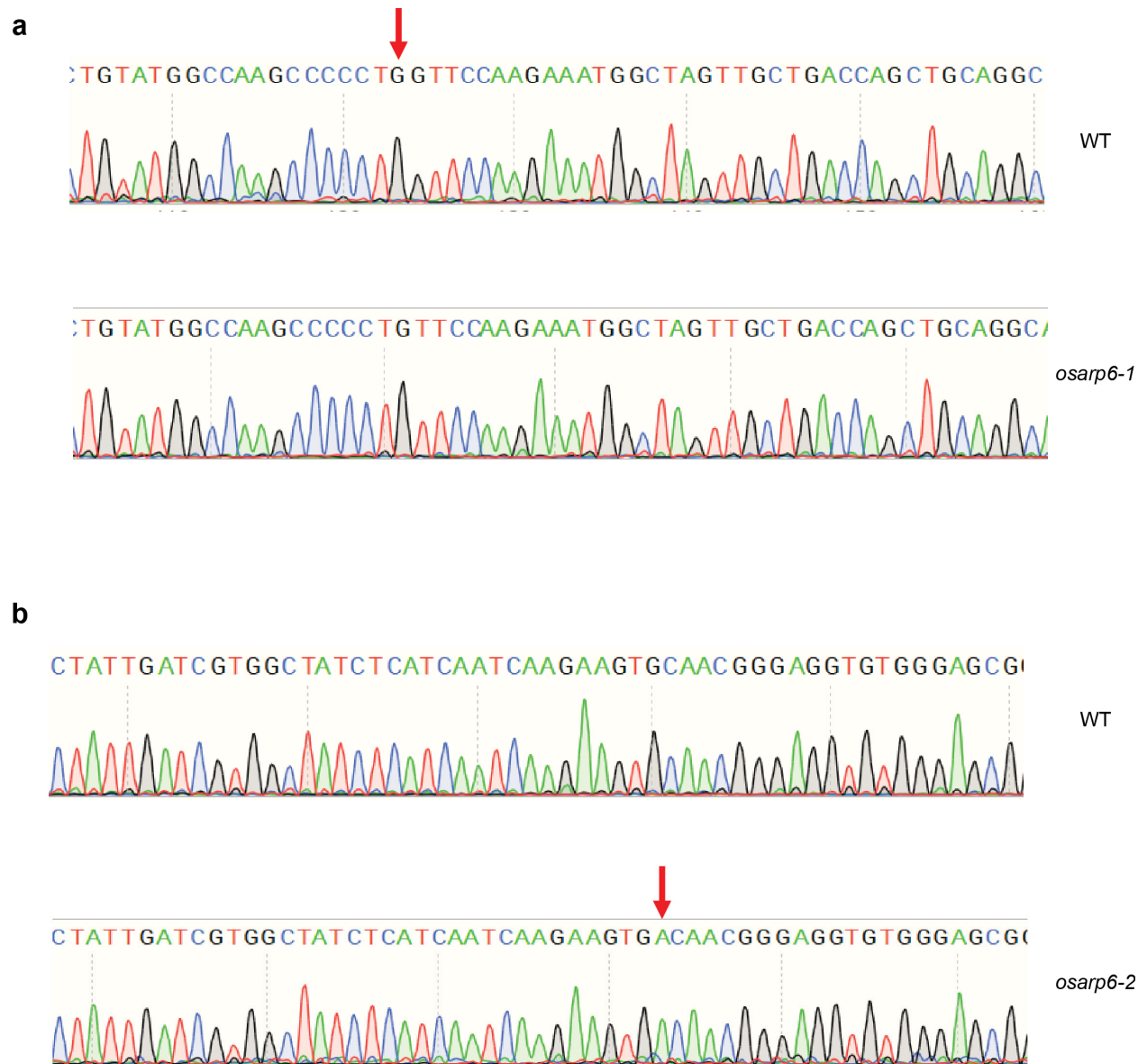
## Supplementary Materials

		(NBD_sugar-kinase_HSP70_actin domain)	
HsACTA1	1	MCDEDEITALVCDNGGGLKAGFAGDDAPRAVFPSIVGRPRHGGVMVGMGQKDSYVGDEAQSQRGILTLKYPIEHGILTNWDDMEKIWHHTFYNELRVAP	
OsACT1	1	MADAEDIQPLVCDNGIGTKAGFAGDDAPRAVFPSIVGRPRHGGVMVGMGQKDAYVGDEAQSQRGILTLKYPIEHGIVSNWDDMEKIWHHTFYNELRVAP	
AtACT1	1	MADGEDIQPLVCDNGIGTKAGFAGDDAPRAVFPSIVGRPRHGGVMVGMGQKDAYVGDEAQSQRGILTLKYPIEHGIVSNWDDMEKIWHHTFYNELRVAP	
ScACT1	1	--MDSEVAALVIDNGGGLKAGFAGDDAPRAVFPSIVGRPRHGGVMVGMGQKDSYVGDEAQSQRGILTLKYPIEHGIVTNWDDMEKIWHHTFYNELRVAP	
OsARP6	1	--MTGGSGVIVIDNGGGLKAGFGGDMNPFAVFNCGMAKPPGSKKWIVADQLQ--AQDVDDVIG---MTLRRPIIRGYIINQEVQREIWERVIRNLLQVDP	
AtARP6	1	-----MSNIVVIDNGGGLKAGQGGGRDPTTVIENCYKELSSKKFIHPSPLTTLSDIDLIS---AAVRRPIDRGYIINQDLQREIWSHUTSLHETAP	
ScARP6	1	----METPPVIVIDNGGGLKAGCPSTNKKPFRALNALANDFGTSYSNHIKN--KDISS-----ITFRREHQLQTLWELESCLWDYCLNPSEFDG	
		(NBD_sugar-kinase_HSP70_actin domain)	
HsACTA1	101	-----EEHPTLLTEAPLNPKANREKMTQIMFETFNVPANYYA--IQAVLSLY-----ASGRTT-----G	
OsACT1	101	-----EEHPTLLTEAPLNPKANREKMTQIMFETFNVPANYYA--IQAVLSLY-----ASGRTT-----G	
AtACT1	101	-----EEHPTLLTEAPLNPKANREKMTQIMFETFNVPANYYA--IQAVLSLY-----ASGRTT-----G	
ScACT1	99	-----EEHPTLLTEAPLNPKSNREKMTQIMFETFNVPANYYA--IQAVLSLY-----SSGRTT-----G	
OsARP6	94	-----NNSSLLLEPQENPFALQHATDELVFEBELGFKSCVADAPSLVHLY-----EASRQPS--LFRAQCS	
AtARP6	93	-----SSSSLLLEAPLSIPSQVQRTDELVFEBELGFSSTYIAHPGSLVHLY-----EASRQPDSILSKTQCS	
ScARP6	89	FDLKEGKGGHVAESCSCTLPESLKHADQVIFEEHEFDSLEKSPVAVFPFFKTSYKGMRTISGKDEDIDIVRGNSDSTNSTSESCKNAQDSGSDYHFDQ	
		(NBD_sugar-kinase_HSP70_actin domain)	
HsACTA1	153	IVLDSGDGVTHNVPYIEGALPHAILRLDLAGRDLDYLMKILTERGYSFTTAAEREIVRDIKEKLCYVALDFENEMATAA---SSSSLEKSYELPDGQV	
OsACT1	153	IVLDSGDGVSHNVPYIEGALPHAILRLDLAGRDLDYLMKILTERGYSFTTAAEREIVRDIKEKLSYALDYDQEMETAK---TSSSVEKSYELPDGQV	
AtACT1	153	IVLDSGDGVSHNVPYIEGALPHAILRLDLAGRDLDYLMKILTERGYSFTTAAEREIVRDIKEKLCYALDYDQEMETAK---TSSSVEKNYELPDGQV	
ScACT1	151	IVLDSGDGVTHNVPYIEGSLPHAILRLDLAGRDLDYLMKILSERGYSFSTTAAEREIVRDIKEKLCYVALDFEQEMQTA---QSSSLEKSYELPDGQV	
OsARP6	154	IVLDGGSFSTHAPVPLQNETINAVRRMDLGGALTNYLKELISYR--SINVMDFTLLDDAKEKLCFVSLVPGDRLRLSSNDNPFRCSTYILPDGIT	
AtARP6	155	IVLDGGSFSTHAPVPLHNETINHAIKRDLGGAAFTNLYLKELISYR--SINVMDFTFLVDDAKEKLCFVSLDLLRLRLAR--NGNILLKSYVLLPDGVT	
ScARP6	189	IVLDGSGFNCTWILPMLKEIPYYKAMKRLDTGGREFLTGLKETLSFR--HNNMMDETILVNNIKQCLFVSPVSFLSFKTA---DKHALEYVLPEFQT	
		(NBD_sugar-kinase_HSP70_actin domain)	
HsACTA1	250	ITIG-----NFRFCPEVLFPQSFITGMEASAGIHETTYNSIMKCDIDRKLYLNNV	
OsACT1	250	ITIG-----AERFRCPPEVLFPQSFITGMEAAGIHETTYNSIMKCDVDRKLYGNIV	
AtACT1	250	ITIG-----SERFRCPPEVLFPQSMIGMENAGIHETTYNSIMKCDVDRKLYGNIV	
ScACT1	248	ITIG-----NERFRAPEALFPQSVITGMEASAGIDQTTYSIMKCDVDRKLYGNIV	
OsARP6	252	YKKGFKVDLDEACRYSSLPANGESVRKSDSSDRSKFEDKKKPELSQNEFVLTNERFLVPEMLFHPIDLGMNQAGLARCIVRAIQACHPHQPVLSERIT	
AtARP6	251	HTKGYVKDPQAARKRFLSLSEKESVVVMD-----KVGERKKADMKNKNEIDLTNERFLVPELTFOPADLGMNQAGLARCIVRAINSCHSYQPVLYQSIL	
ScARP6	282	SFLGCVRNPRK-----ENVPLPEDAQIITITLDELFTTIPETTFHPPEISQITKEGIVBAILESLSMLPEIRPLVGNIV	
		(NBD_sugar-kinase_HSP70_actin domain)	
HsACTA1	301	MSGGTTMFPGIADRMKEITALAPSSMKIKVAPP-ERKYSVWIGGSILASLTFQOMWITKQYDEAGSPSIVHRKCF-----	
OsACT1	301	LSGGTTMFPGIADRMKEITALAPSSMKIKVAPP-ERKYSVWIGGSILASLTFQOMWIARAAYDESGPSIVHRKCF-----	
AtACT1	301	LSGGTTMFPGIADRMKEITALAPSSMKIKVAPP-ERKYSVWIGGSILASLTFQOMWIARAAYDESGPSIVHRKCF-----	
ScACT1	299	MSGGTTMFPGIADRMKEITALAPSSMKIKVAPP-ERKYSVWIGGSILASLTFQOMWISKQYDESGPSIVHRKCF-----	
OsARP6	352	ILGGTTIFRFRTEREKEIRELVPDDYQKILACE--IPILGAVRGGSLAHRPDESMCITKSEYHEMGSMRCRFRFHH-----	
AtARP6	344	ILGGTTIFPQIKERIEGELRELVPDHFVKITTQEE--IPILGVWRGGSLASSPDVESMCVTKAEYHEMGSARCRFRFHH-----	
ScARP6	355	CLGGNFNINFAQRLLAELQRLPTDWTCHVSVLEGICALFGVEVMSQFAKTDYRKARVTFEEYHEGPDWCTTHRGYQNWII	

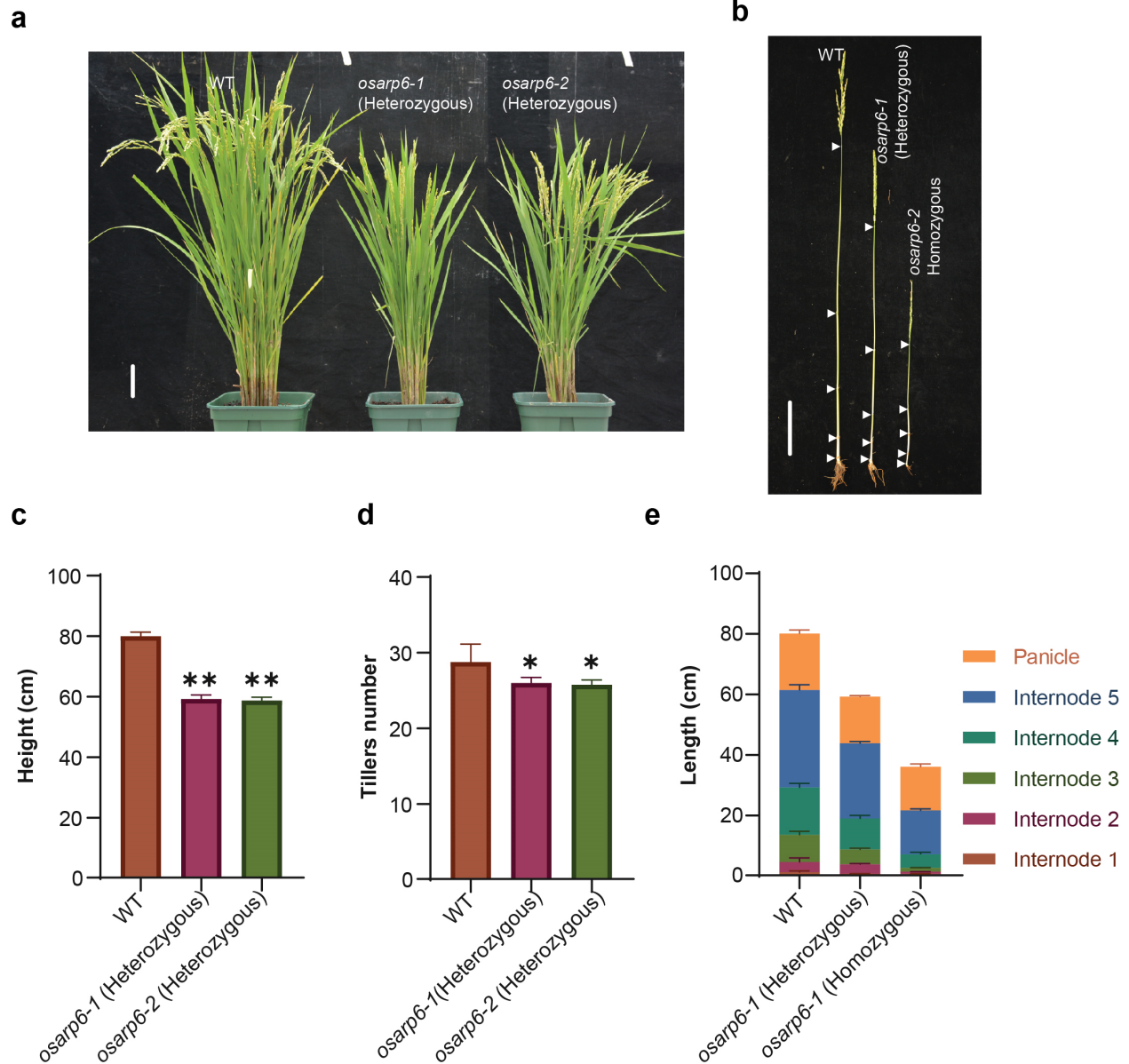
**Figure S1.** Alignment of ARP6 proteins from rice, *Arabidopsis* and yeast with conventional actins. Conventional actins from human, rice, *Arabidopsis* and yeast were used as reference. The Nucleotide-Binding Domain of the sugar ki-nase/HSP70/Actin super family (NBD\_sugar-kinase\_HSP70\_actin) is shown with red line. The conserved amino acid residues involved in nucleotide binding are shown in red boxes. The sequences were aligned with MultAlin and visualized with BoxShade version 3.21.



**Figure S2.** Expression pattern of OsARP6 obtained from ePlant Rice ([http://bar.utoronto.ca/eplant\\_rice/](http://bar.utoronto.ca/eplant_rice/)). Expression profile showed that OsARP6 was highly expressed mainly in somatic apical meristem (SAM), young panicle, young leaf and mature leaf. The expression in root, mature panicle and early stages of seed development was low.



**Figure S3.** Sequence comparisons of wild type, and knockout *osarp6* mutants. (a) Sequence comparisons of wild type with *osarp6-1*. The deletion is marked with red arrow in wild type. (b) Sequence comparisons of wild type with *osarp6-2*. The insertion is marked with red arrow in *osarp6-2*.



**Figure S4.** Phenotypes of heterozygous *osarp6* plants. (a) Representative image of 120-day-old wild type and *osarp6* (heterozygous) plants. Scale bar = 10 cm. (b) Culms of wild type and *osarp6-1* (heterozygous) and *osarp6* homozygous plants at mature stage. All leaves were removed to clearly show the elongated stems. White arrowheads indicate the nodes. Scale bar=10 cm. (c) Quantification of height of wild type and *osarp6-1* (heterozygous) plants. Error bars indicate SD (n=10). Asterisks indicate  $P < 0.01$  (\*\*) as determined by Student's *t* test analysis. (d) Quantification of tillers number from wild type and *osarp6-1* (heterozygous) plants. Error bars indicate SD (n=10). Asterisks indicate  $P < 0.05$  (\*) as determined by Student's *t* test analysis. (e) Internodes and panicle lengths of wild type, *osarp6-1* (heterozygous) and *osarp6-1* (homozygous) plants at the mature stage. Error bars indicate SD (n=12).

**Table S1.** Quantification of cell length and cell number in 5<sup>th</sup> internodes of wild type and *osarp6* mutants

	Fifth internode length (cm)	Cell length (μm)	Cell number in a row /cm*	Estimated total cell number in a row in 5 <sup>th</sup> internode
WT	32.2 ±1.8	46.1±7.9	218.9±7.5	7.05x10 <sup>3</sup> ±13.5
<i>osarp6-1</i>	14.7 ±0.6	46.9±8.1	212.7±4.6	3.13 x10 <sup>3</sup> ±2.76
<i>osarp6-2</i>	14.5 ±0.5	45.7±8.6	221.3±8.8	3.21 x10 <sup>3</sup> ±4.4
Ratios	WT/ <i>osarp6-1</i>	2.19	0.98	1.03
	WT/ <i>osarp6-1</i>	2.22	1.01	0.99

\*For quantification of cell number, three sections of 1 cm lengths were obtained from top, middle and bottom portions of the 5<sup>th</sup> internodes and the cell number in row was counted. The average data of the 9 sections for each genotype is shown.

**Table S2.** Primers used in this study**Cas9 targets***osarp6-1-sense*

GGCAAGCCATTTCTTGAACCAGG

*osarp6-1-antisense*

AAACCCTGGTTCCAAGAAATGGCT

*osarp6-2-sense*

GGCATCATCAATCAAGAAGTGCAA

*osarp6-2-antisense*

AAACTTGCACTTCTTGATTGATGA

**Genotyping primers***osarp6-1 and osarp6-2*

Forward primer (5'-AGGATAGGCAAGAATAGGAGGAA-3')

Reverse primer (5'-TGAAAGAGAAGCCACAGTCAACA-3')

**Primers used for BiFC***OsARP6*

Forward primer (5'-GGACTAGTATGACGGGTGGATCAGGTGTTG-3')

Reverse primer (5'-CGGGGTACCGTGAAAGAATCTACGACGGCAC-3')

*OsPIE1*

Forward primer (5'-GGACTAGTATGGAATTTTCATCAAGCCT-3')

Reverse primer (5'-CGGGGTACCTCCGATGTCTGTGAAATCTGTA-3')

**Primers used for yeast two hybrid assay (Y2H)***OsARP6*

Forward primer (5'-CCGGAATTCATGACGGGTGGATCAGGTGTTGTGG-3')

Reverse primer (5'-CCGGAATTCTCAGTGAAAGAATCTACGACGGCAC-3')

*OsPIE1*

Forward primer (5'-GGGTTTCATATGATGGAATTTTCATCAAGCCT-3')

Reverse primer (5'-ACGCGTCGACTCATCCGATGTCTGTGAAATCTGTA-3')

**qPCR primers**

*OsARP6*

Forward primer (5'-ACTTCGTCCTCTTGTGCCTG-3')  
Reverse primer (5'-GTGCGCCAAAAGAGATCCAC-3')  
Forward primer (5'-GGTGGATCAGGTGTTGTGGT-3')  
Reverse primer (5'-GGCCATACAGTTGGGGACAA-3')  
Forward primer (5'-GGTGTGGGAGCGGGTTATAC-3')  
Reverse primer (5'-TCACCAGGGACATCAAGGGA-3')

*OsCDKA;1*

Forward primer (5'-ATCACGGCAACATCGTCAGG-3')  
Reverse primer (5'-AGTAAGCAACGCCGCGGAGTA-3')

*OsCDKA;2*

Forward primer (5'-ACCACCGCATAGTCAAATCGTT-3')  
Reverse primer (5'-ACCACAATGTCACCACCTCGTGA-3')

*OsR2*

Forward primer (5'-TCTGCACCTCCACTTCGCTCA-3')  
Reverse primer (5'-TAGGTGGTGGCCTTGAAGCT-3')

*OsCYCA3;2*

Forward primer (5'-GACATTCCTCAGGCGGTTCA-3')  
Reverse primer (5'-CGGAGACAGCCGTAGTCAAG-3')

*OsCYCB1;4*

Forward primer (5'-AGCTCATGCCAGAGACCCTA-3')  
Reverse primer (5'-GAAGTCGTTACCTCTGGGG-3')

*OsCYC-B2;2*

Forward primer (5'-GGAGGAGTGAGGGTTTGAGC-3')  
Reverse primer (5'-GCGAGCCAAGAATCGGTCTA-3')

**Primers for ChIP-qPCR**

*OsACTIN1*

Forward primer (5'- TCGACGTGGATATTAGGAA-3')  
Reverse primer (5'- AAGGCAGTGATCTCCTTGCT-3')

*OsCDKA;1*

Region 1  
Forward primer (5'-CTGAGATCAGGATAGCTCTAGCAC-3')  
Reverse primer (5'-TTCCGCTTGTGTGGTTTAGTAG-3')  
Region 2  
Forward primer (5'-AAGGCCGAGTCAAAGAGAGTC-3')  
Reverse primer (5'-GAGGAGAGGTGGGCAAAAGC-3')  
Region 3  
Forward primer (5'-GCGGCGTTGCTTACTGTC-3')  
Reverse primer (5'-ACCTCGTGAGTAAACGTGCG-3')

*OsCDKA<sub>2</sub>*

Region 1

Forward primer (5'-GTACAAAGGTTCTCACGGGC-3')

Reverse primer (5'-CGTAATGCCTCCACACGAACAC-3')

Region 2

Forward primer (5'-ATATGAGGAGAGAGCGACAATGC-3')

Reverse primer (5'-TGGGAGTGGATGGGTTGTGG-3')

Region 3

Forward primer (5'-CGTTCCTCTACCAGATTCTCCGG-3')

Reverse primer (5'-AAGTCCGCGAGCTTCAATGAG-3')

*OsCYCB1<sub>4</sub>*

Region 1

Forward primer (5'-CCATACCTACACCCAACGGC-3')

Reverse primer (5'-CGTTGCCTTTTTTACGTGGAGC-3')

Region 2

Forward primer (5'-CTAGCTCGCTATATCTCGCCCC-3')

Reverse primer (5'-CCTCCTCCTCTTGCCCAATC-3')

Region 3

Forward primer (5'-ATTACATCGACACCCAGGTGGA-3')

Reverse primer (5'-CATCGAGAGGTACCGGTCTGA-3')

*CYC-B2<sub>2</sub>*

Region 1

Forward primer (5'-GTGCGGGTAGCCGTTAAGG-3')

Reverse primer (5'-GGTAGGAAGGCGTAATTTGGCC-3')

Region 2

Forward primer (5'-CCTTTGTCTCCCCTCTCCTCC-3')

Reverse primer (5'-CCACCTCTCTCCCCCTCTC-3')

Region 3

Forward primer (5'-ACATTGAGGAGGCAGCACC-3')

Reverse primer (5'-CCTCACTCCTCCTGTAGAAGCTG-3')

*OsCYCA3<sub>2</sub>*

Region 1

Forward primer (5'-AATTCCATGGAATTCCCAATGCC-3')

Reverse primer (5'-CATGACTCGGCGCCAAAAC-3')

Region 2

Forward primer (5'-GCCCCGCGATCCCCAGATTC-3')

Reverse primer (5'-CGCGCCTACGAGATGAATCG-3')

Region 3

Forward primer (5'-GAGATTAGCCCTCCTCATGTGG-3')

Reverse primer (5'-GATTGCCCATCTCGAACTCGAG-3')

*OsR2*

Region 1

Forward primer (5'-CCTGGTTTTTCTGAAGGAGGTCC-3')

Reverse primer (5'-TCCCGACCGTTCGAGTTCG-3')

Region 2

Forward primer (5'-AAGCGCACACAAGGACCTC-3')

Reverse primer (5'-GAGGCGAGAGAGGGTGACG-3')

Region 3

Forward primer (5'-AGGTCTTTGCACGATGGTACC-3')

Reverse primer (5'-CTGGAGAAACGGTCGCCTAAG-3')