Supplementary Material for

Upstream regulator of genomic imprinting in rice endosperm is a small RNA-associated chromatin remodeler

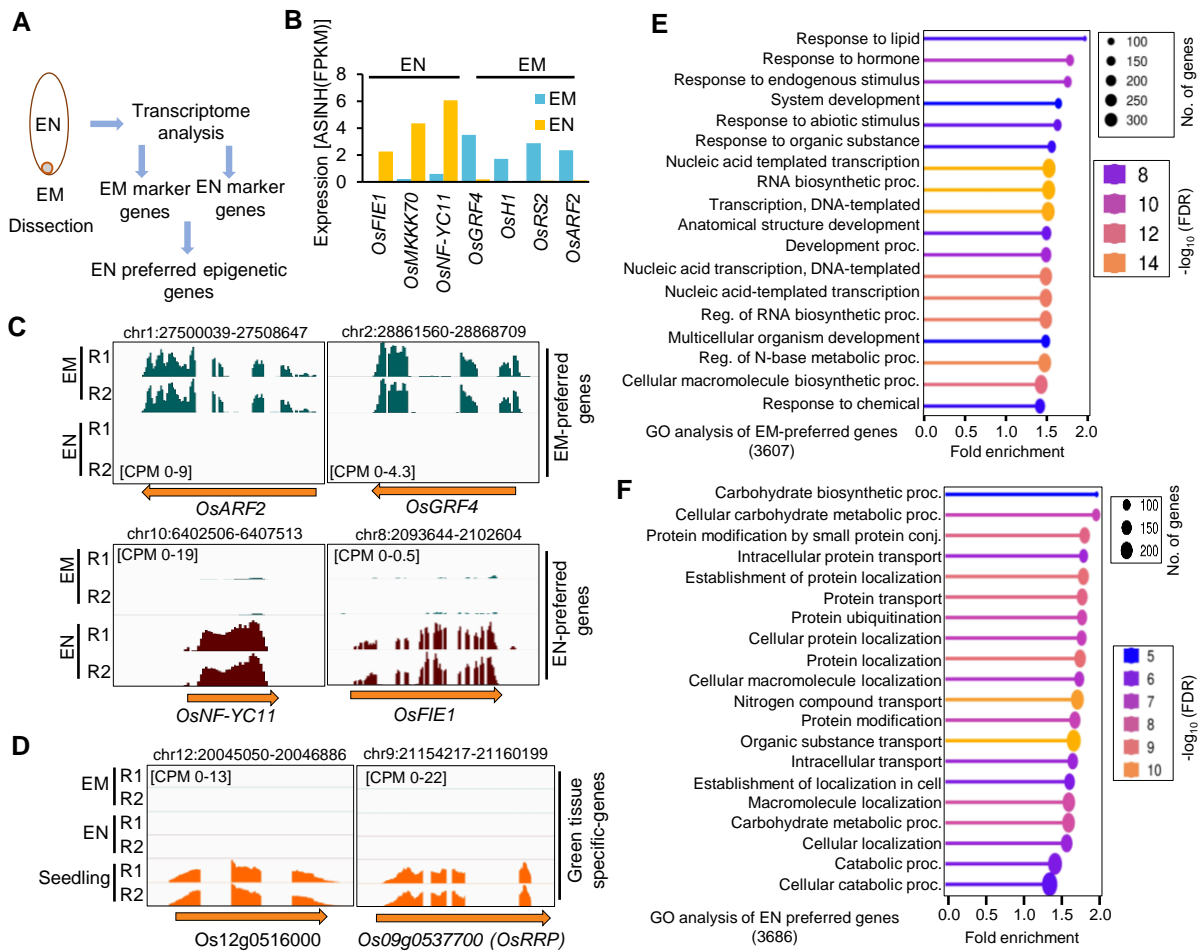**Avik Kumar Pal[1], Vivek Hari Sundar G[1], Amruta. B. Nambiar[1], and P.V. Shivaprasad[1*]**

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Supplementary References

Supplementary Figure 1. Transcriptome analysis of endosperm and embryo tissues.
(A) Schematic showing tissue collection for transcriptome analysis. (B) Barplots showing expression of embryo (EM) and endosperm (EN)-specific marker genes in transcriptome analysis. (C) IGV screenshots showing expression of known EM- and EN-specific marker genes in transcriptome. (D) IGV screenshots showing expression of non-seed expressing genes in transcriptome. (E) GO analysis of EM-preferred genes. proc.-process. (F) GO analysis of EN-preferred genes. Source data are provided as a Source Data file.
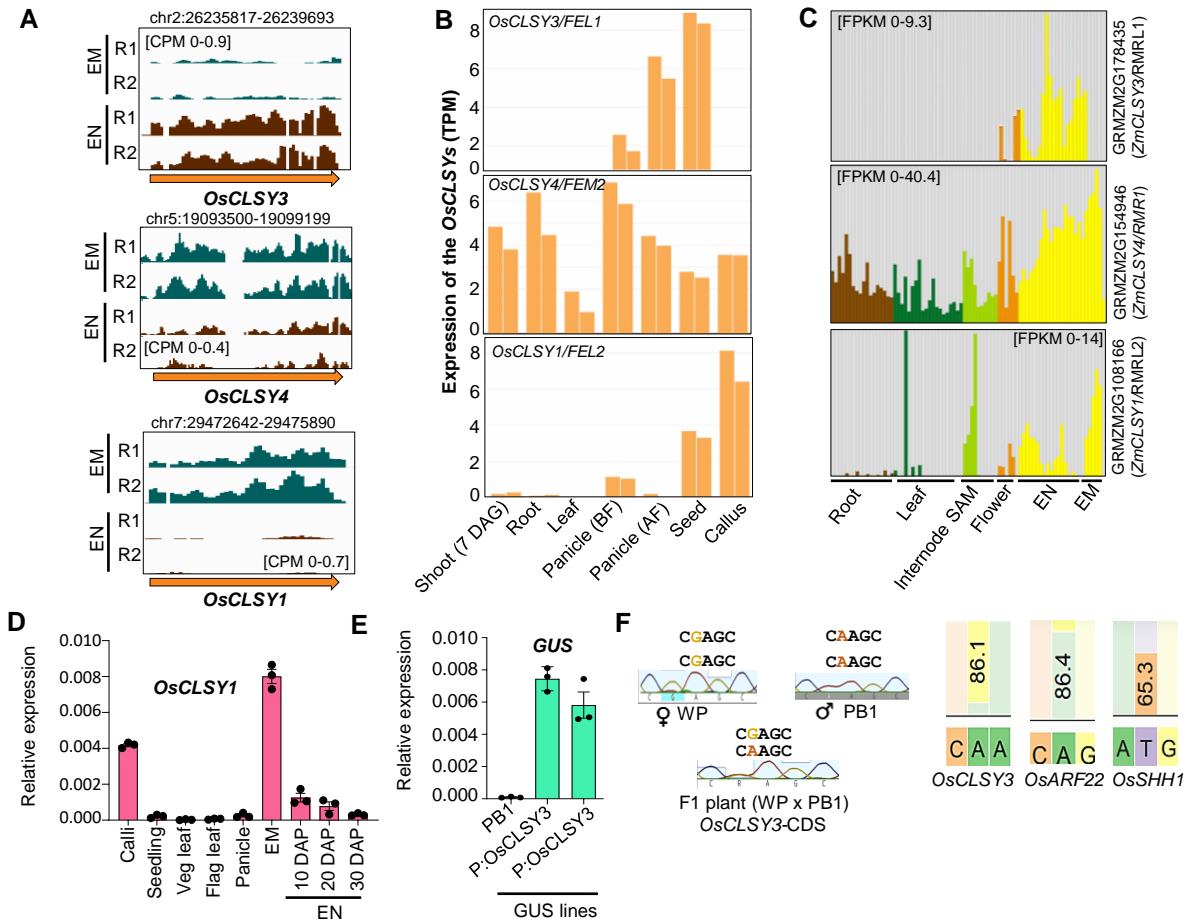
Supplementary Figure 2. *OsCLSY3* is an endosperm-preferred gene among monocots.
(A) IGV screenshots showing expression of *OsCLSYs* in EN and EM. (B) Barplots representing expression of *OsCLSYs* across different tissues (The Rice Annotation Project-https://rapdb.dna.affrc.go.jp/). (C) Barplots representing expression of maize *CLSYs* across different tissues (MaizeDB-https://www.maizegdb.org/). (D) Barplot showing expression of *OsCLSY1* across tissues. *OsActin* served as control. Data represent means ± standard error (SE). n=3. Experiment repeated at least twice with independent samples and consistent results were obtained. (E) Barplot showing expression of GUS in the EN of P:OsCLSY3:GUS transgenic lines. *OsGAPDH* served as control. Data represent means ± SE of 2 independent biological replicates with 3 technical replicates each. (F) Scheme depicting validation of WP and PB1 cross and the SNPs identified in CDS of *OsCLSY3*. Stacked barplots showing observed transcript contribution of three genes in WWP EN (mismatches were calculated in crispresso2). Source data are provided as a Source Data file.
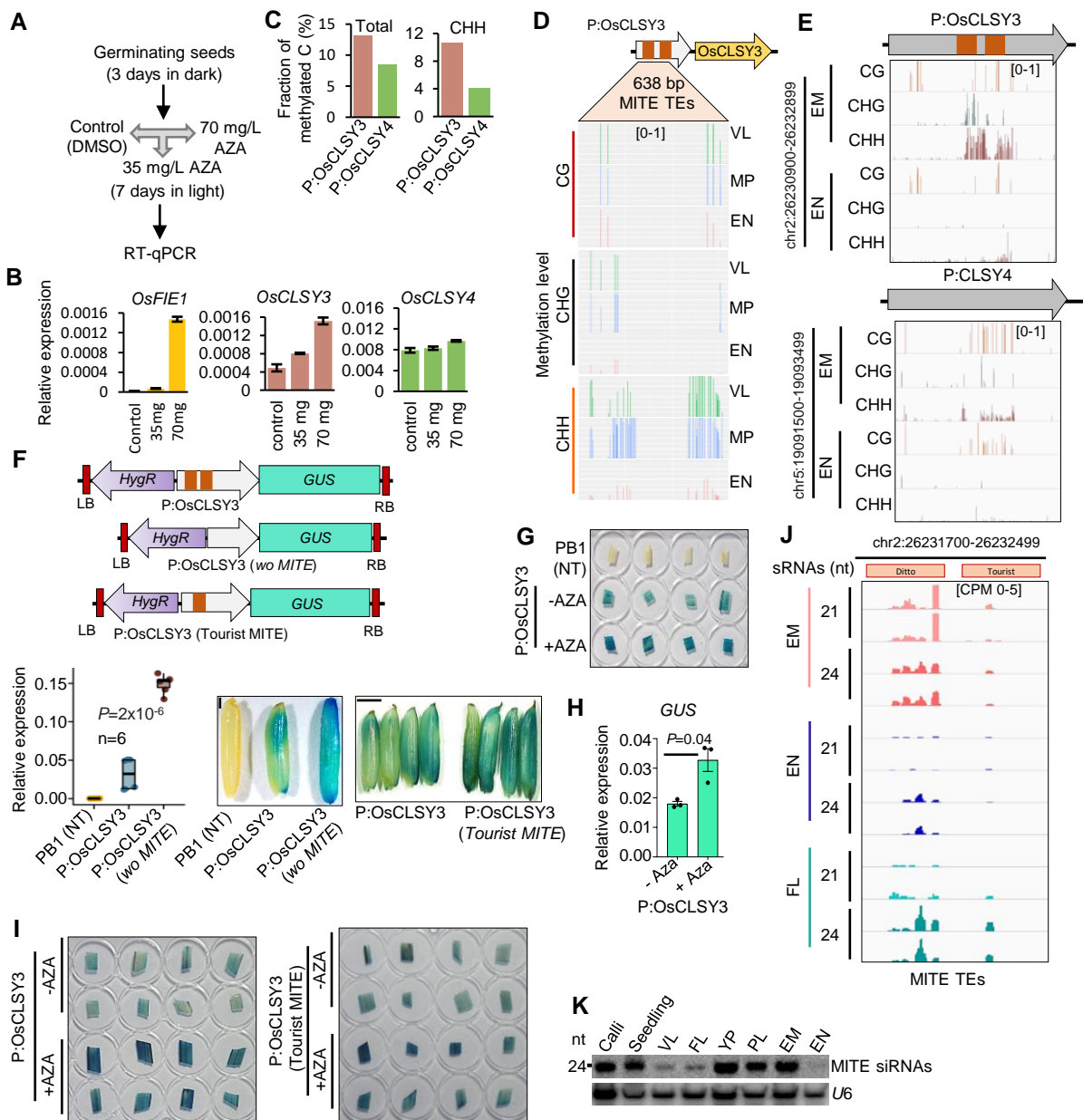
Supplementary Figure 3. DNA methylation at MITE TEs controls expression of *OsCLSY3*.
(A) Scheme used for AZA treatment. (B) RT-qPCR showing relative expression of *OsCLSY*s and *OsFIE1,* normalised to *OsActin*. Data represents mean ± SE. Experiment repeated at least twice with independent samples and consistent results were obtained. (C) Barplots showing total (left) and only CHH (right) DNA methylation status of 2 kb promoters of *OsCLSY*s in leaf (GSE130168). (D) Analysis of DNA methylation level of MITE TEs by targeted BS-PCR sequencing across tissues. (E) IGV screenshots showing DNA methylation status of 2kb promoters of *OsCLSY*s in EM and EN (GSE130122). MITE TEs are shown in brown boxes. (F) Linear maps of GUS reporter constructs with 1.1 kb native *OsCLSY3* promoter or 600 bp deletion of MITE TEs in its promoter (*wo MITE*), P:OsCLSY3 (single MITE):GUS. NT-non-transgenic. Boxplots showing relative expression of *GUS* in transgenic panicles. Boxes show median values and interquartile range. Whiskers show minimum and maximum values, data points were represented as round dots. Comparisons were made with paired two-tailed Student's *t*-tests (*P*<0.05 was considered significant). Mature seeds showing levels of GUS (SB-1 mm) (N-5). Same P:OsCLSY3 seed was also used in Fig.1H. (G) Image showing GUS expression in 10 d-old AZA treated seedlings (n=5). (H) Barplot showing *GUS* level upon AZA treatment. Experiments repeated twice. Comparisons were made with paired two-tailed Student's *t*-tests (*P*<0.05 was considered significant). (I) Images showing GUS expression in 10 d-old AZA treated seedlings in transgenic lines. (J) IGV screenshots showing MITE derived 21 nt and 24 nt sRNAs across different tissues. (K) Northern blot showing MITE derived sRNA levels across tissues. *U*6 served as loading control (PL-palea-lemma). Source data are provided as a Source Data file.
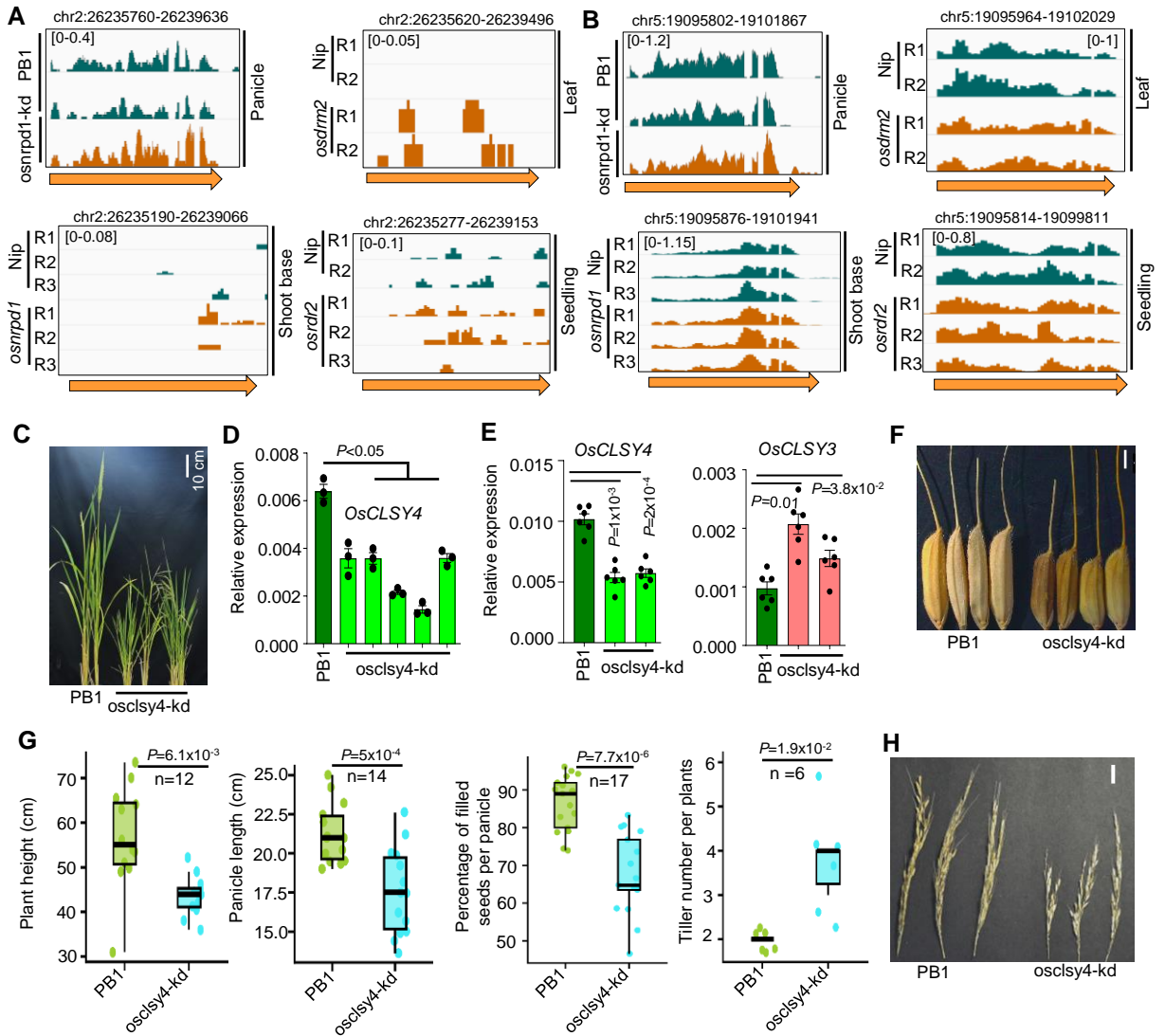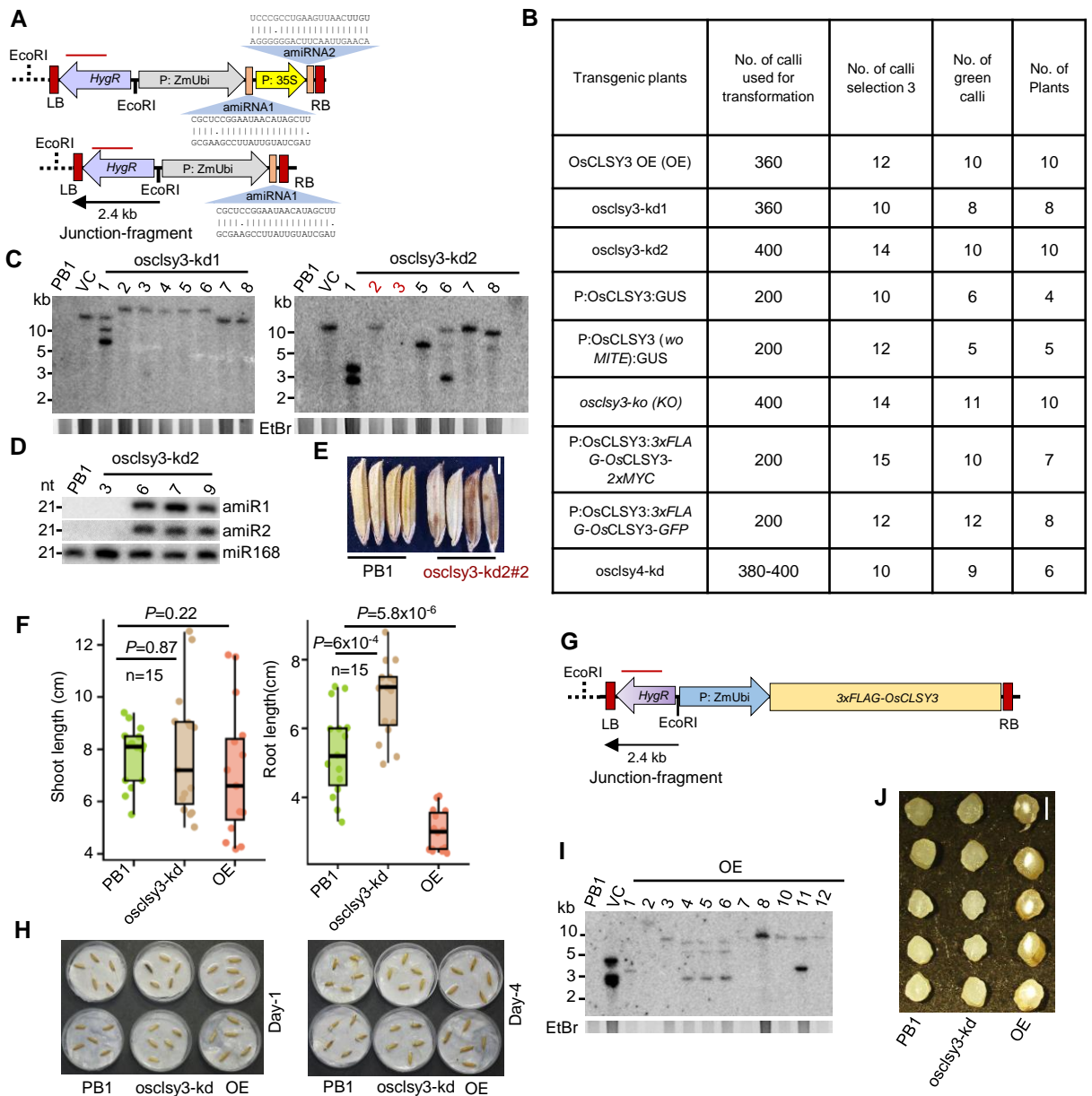
Supplementary Figure 4. Expression of OsCLSY3 in different RdDM pathway mutants.
(A) and (B) IGV screenshots showing expression of *OsCLSY3* and *OsCLSY4* in different RdDM pathway mutants, respectively (GSE180457, GSE138705, GSE130165, GSE131319, Nip-*japonica* cultivar Nipponbare). (C) Image showing phenotype 90 d-old of osclsy4-kd plants. (D) Bar plot showing expression of *OsCLSY4* in osclsy4-kd lines (60 d-old leaf). Data represents mean ± SE of 5 independent transgenic lines with 3 technical replicates each. Comparisons were made with paired two-tailed Student's *t*-tests (*P*<0.05 considered significant). (E) Bar plot showing expression of *OsCLSY4* (left) and expression of *OsCLSY3* (right) in 5 d-old osclsy4-kd seedings. (*OsActin* was used as internal control. Data represents mean ± SE of 2 biological replicates with 6 technical replicates each. Comparisons were made with paired two-tailed Student's *t*-tests (*P*<0.05 was considered significant). (F) Image showing seed size of osclsy4-kd. Scale bar (SB)-1 mm. (G) Box plots showing plant height, panicle length, grain filling percentage, triller numbers of osclsy4-kd plants. Boxes show median values and interquartile range. Whiskers show minimum and maximum values, data points were represented as round dots. Comparisons were made with paired two-tailed Student's *t*-tests (*P*<0.05 was considered significant). (H) Image showing panicles of osclsy4-kd plants (SB-2 cm). Source data are provided as a Source Data file.
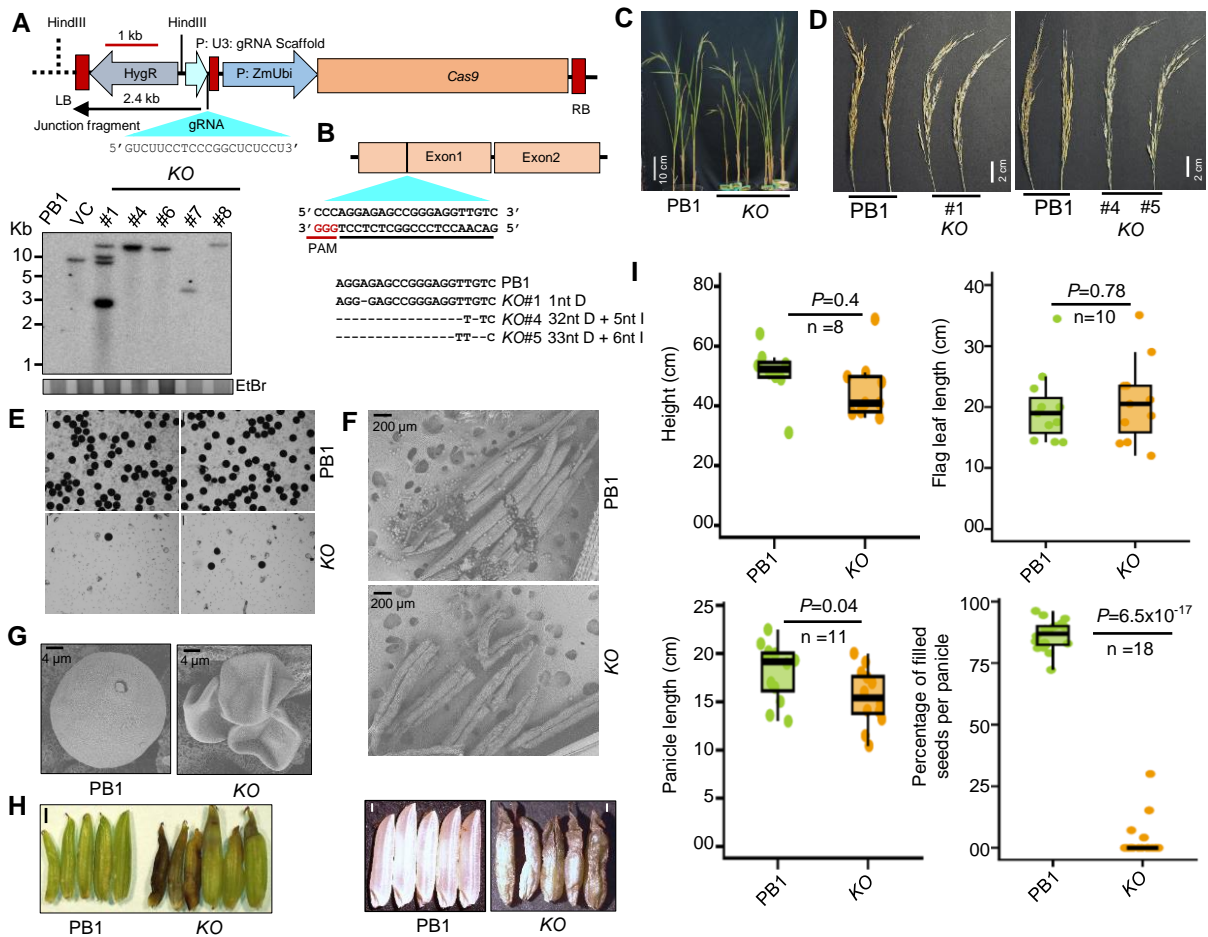
Supplementary Figure 5. *KO* transgenic plants show reproductive abnormalities.
(A) Vector map of *KO* construct and DNA blots showing the T-DNA junction corresponding to digestion of DNA with mentioned restriction sites. Minimum lengths of junction fragments sizes are mentioned in the map. Probe region is shown in red line. VC- empty vector transformed line. (B) Schematic showing editing in guide RNA targeted region of *OsCLSY3* gene in *KO* lines (D-deletion, I-insertion). (C) Image showing *KO* plants with equally grown PB1 plants. (D) Panicle morphology of *KO* lines. (E) Pollen viability assay of *KO* pollen (*KO#4* and *KO#5* used for the assay, Scale bar (SB)-50µm). (F) Anther and pollen morphology of *KO* under the electron microscope (*KO#4*). (G) Detailed pollen morphology of *KO* under the electron microscope. (H) Images showing EN morphology in *KO (KO#1)* seeds. SB-1mm. (I) Box plots representing various agronomic phenotypes measured in PB1 and KO plants. Boxes show median values and interquartile range. Whiskers show minimum and maximum values, data points were represented as round dots. Comparisons were made with paired two-tailed Student's *t*-tests (*P*<0.05 considered significant). Source data are provided as a Source Data file.

A

EcoRI

UCCCGCCUGAAGUUAACUUGU
|||||.||||||||||||||||
AGGGGGACUUCAAUUGAACA
amiRNA2

LB — HygR — P: ZmUbi — P: 35S — RB
EcoRI

amiRNA1
CGCUCCGGAAUAACAUAGCUU
|||||.||||||||||||||||
GCGAAGCCUUAUUGUAUCGAU

EcoRI

LB — HygR — P: ZmUbi — RB
EcoRI
← 2.4 kb
Junction-fragment

amiRNA1
CGCUCCGGAAUAACAUAGCUU
|||||.||||||||||||||||
GCGAAGCCUUAUUGUAUCGAU

B

Transgenic plants	No. of calli used for transformation	No. of calli selection 3	No. of green calli	No. of Plants
OsCLSY3 OE (OE)	360	12	10	10
osclsy3-kd1	360	10	8	8
osclsy3-kd2	400	14	10	10
P:OsCLSY3:GUS	200	10	6	4
P:OsCLSY3 (wo MITE):GUS	200	12	5	5
osclsy3-ko (KO)	400	14	11	10
P:OsCLSY3:3xFLAG-OsCLSY3-2xMYC	200	15	10	7
P:OsCLSY3:3xFLAG-OsCLSY3-GFP	200	12	12	8
osclsy4-kd	380-400	10	9	6

C

osclsy3-kd1: PB1 VC 1 2 3 4 5 6 7 8
kb — 10 — 5 — 3 — 2
EtBr

osclsy3-kd2: PB1 VC 1 2 3 5 6 7 8
kb — 10 — 5 — 3 — 2
EtBr

D

osclsy3-kd2
nt: PB1 3 6 7 9
21- amiR1
21- amiR2
21- miR168

E

PB1   osclsy3-kd2#2

F

Shoot length (cm)
P=0.22
P=0.87
n=15
PB1 osclsy3-kd OE

Root length(cm)
P=5.8x10⁻⁶
P=6x10⁻⁴
n=15
PB1 osclsy3-kd OE

G

EcoRI

LB — HygR — P: ZmUbi — 3xFLAG-OsCLSY3 — RB
EcoRI
← 2.4 kb
Junction-fragment

H

Day-1   Day-4
PB1 osclsy3-kd OE   PB1 osclsy3-kd OE

I

OE
kb: PB1 VC 1 2 3 4 5 6 7 8 10 11 12
10 — 5 — 3 — 2
EtBr

J

PB1 osclsy3-kd OE

Supplementary Figure 6. Validation of *OsCLSY3* transgenic lines.
(A) Vector maps of amiRNA constructs to target *OsCLSY3*. (B) Table showing approximate number of calli used and transgenic plants obtained in this study. (C) DNA blots showing the T-DNA junction corresponding to digestion of DNA with mentioned restriction sites. Minimum lengths of junction fragments sizes are mentioned in the map. Probe region is shown in red line. The line osclsy3-kd #2 (brown) had proper T-DNA insertion. (D) Northern blots showing amiR expression in osclsy3-kd plants. The osclsy3-kd2 #3 (marked in brown), did not express amiRs. (E) Image of osclsy3-kd2 #2 seeds. SB-2mm. (F) Box plots showing the shoot and root lengths of 12 d-old osclsy3-kd and OE seedlings. Boxes show median values and interquartile range. Whiskers show minimum and maximum values, data points were represented as round dots. Comparisons were made with paired two-tailed Student's *t*-tests (*P*<0.05 was considered significant). (G) Vector map of OE construct. (H) Images showing seed germination in rice CLSY3 mis-expression lines. (I) Southern blots confirming OE transgenic lines. T-DNA junction fragment length upon digestion with EcoRI is shown in G. VC-vector control. (J) Cross sections of dry osclsy3-kd and OE EN (SB-1 mm). Source data are provided as a Source Data file.
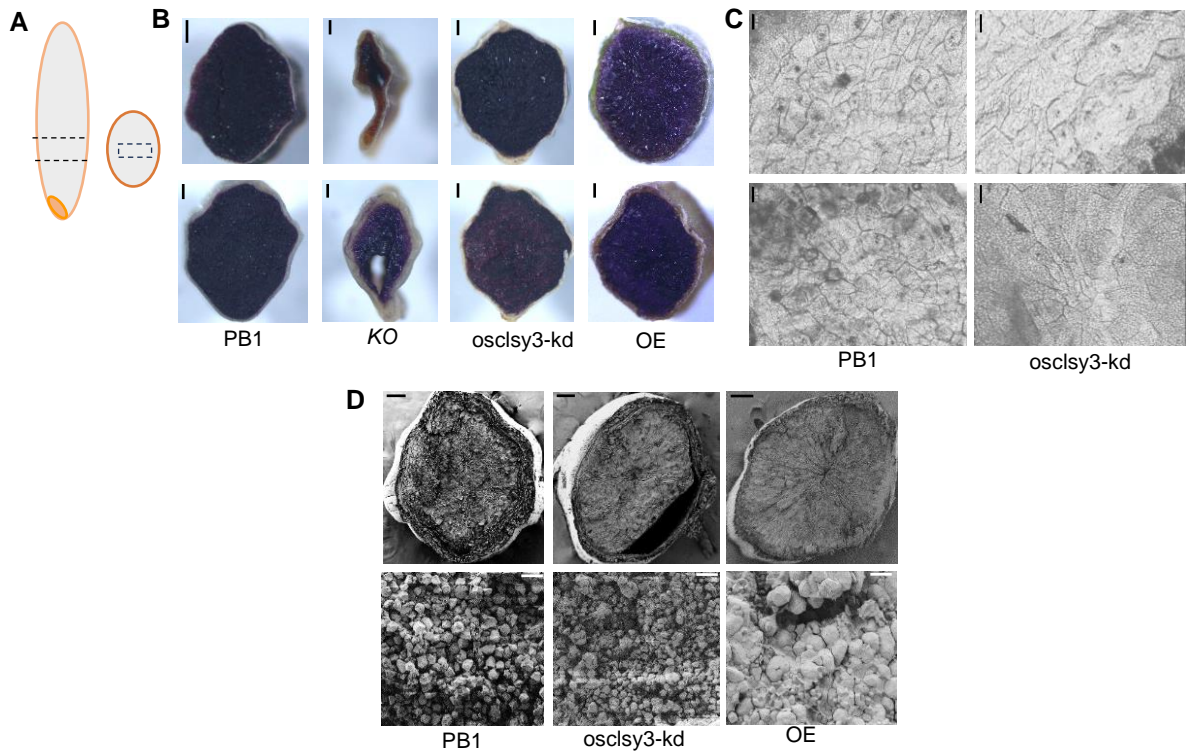
**Supplementary Figure 7. Endosperm morphology of *OsCLSY3* transgenic lines.**
(A) Schematic showing sections used for imaging EN (dotted lines indicate sections used for imaging). (B) Images showing manually dissected EN (SB-1 mm) (15 DAP). (C) Images showing 50 µm cross-section of EN (10 DAP). (D) Morphology of EN cross section under SEM (15 DAP). SB-200 µm (top) and 10 µm (bottom). Source data are provided as a Source Data file.
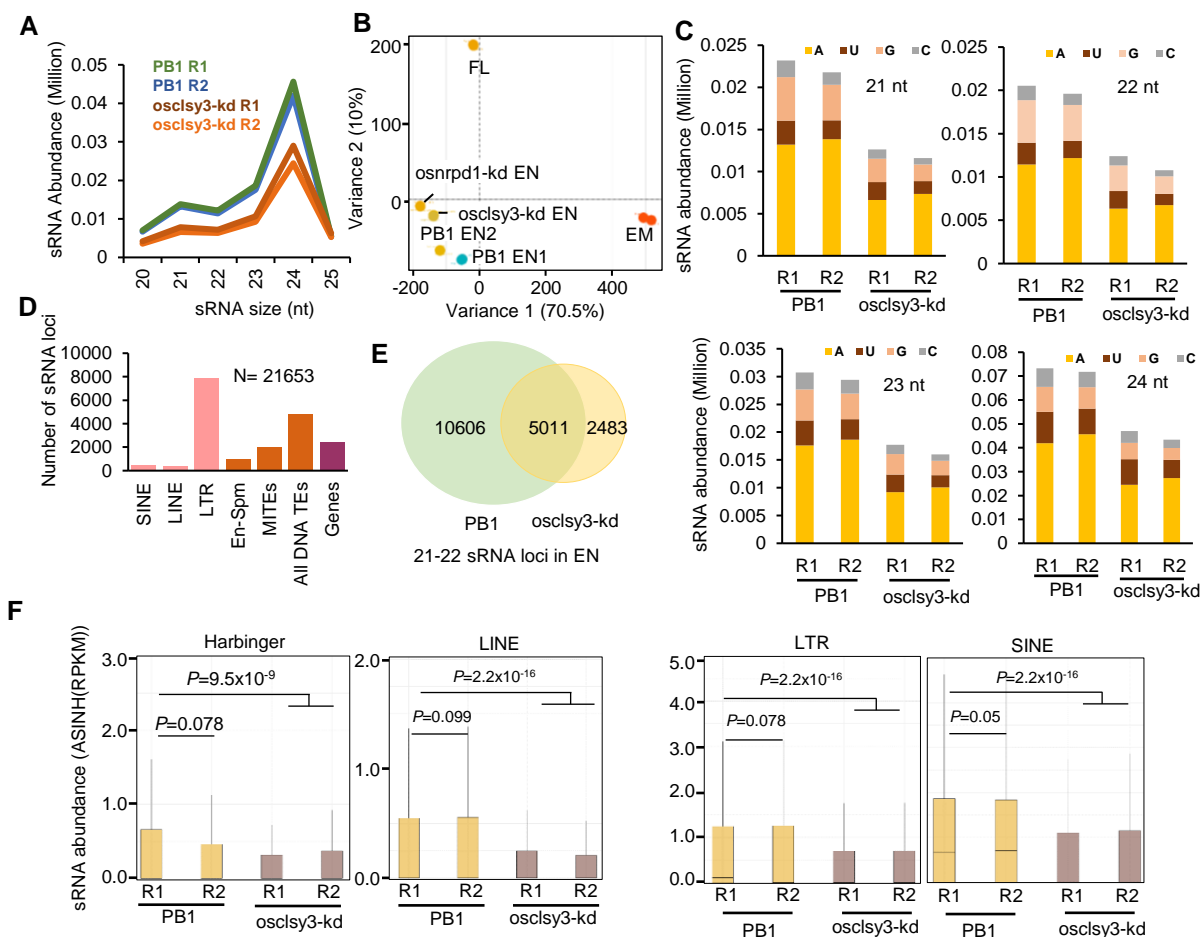
Supplementary Figure 8. Endosperm sRNAs are globally reduced in osclsy3-kd.
(A) Plot showing mapped sRNA abundance (20-25 nt) in EN. (B) PCA plot comparing the mapped sRNAs (23-24 nt) across different tissues and genotypes. osnrpd1-kd EN (16-20 DAP) dataset is GSE180456. (PB1 EN2-GSE180456). (C) Stacked barplot showing abundance of first 5' nucleotide of mapped sRNAs in PB1 and osclsy3-kd EN. (D) Barplot showing number of different TEs and genes overlapped with CLSY3-dependent sRNA loci. (E) Venn diagram showing status of 21-22 nt sRNAs in osclsy3-kd EN. (F) Boxplots representing normalised sRNA reads across different class I TEs and class II TEs in PB1 and osclsy3-kd EN. Boxes show median values and interquartile range. Whiskers show minimum and maximum values, excluding outliers. Comparisons were made with two-sided Wilcoxon test (*P*<0.01 was considered significant). Source data are provided as a Source Data file.
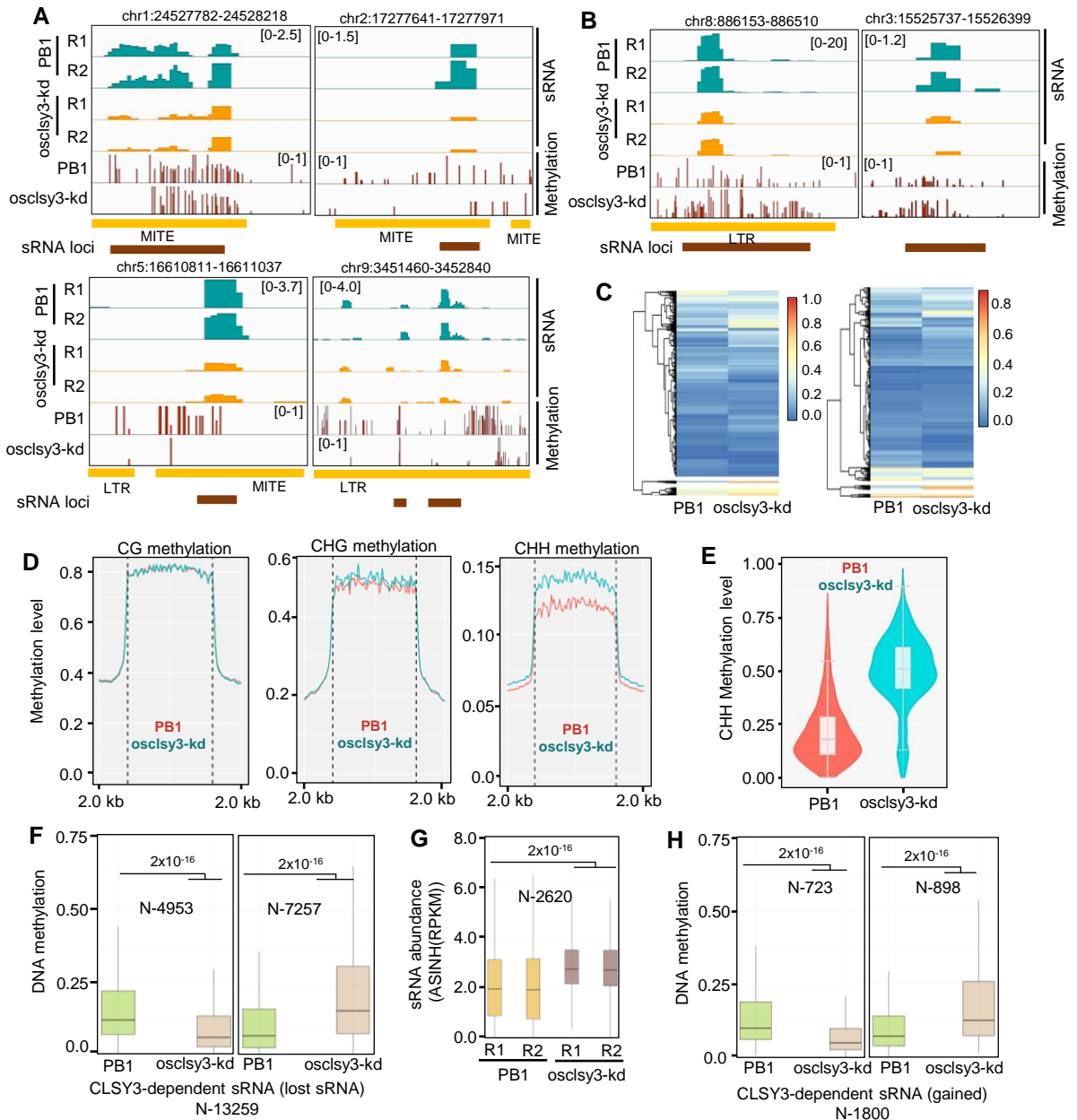
Supplementary Figure 9. Whole genome DNA methylation analysis in osclsy3-kd endosperm.
(A) IGV screenshots showing sRNA (sRNA-seq) and CHH methylation (methylome) across selected loci in PB1 and osclsy3-kd EN. (B) IGV screenshots showing sRNA and CHH methylation status of hypermethylated loci in PB1 and osclsy3-kd EN. (C) Heatmap showing DNA methylation status of CLSY3-dependent sRNA loci (lost sRNA-left, gain-right) in CHH context. (D) Metaplots showing DNA methylation in CLSY3-dependent sRNA loci (lost sRNA) in CG, CHG and CHH contexts in PB1 and osclsy3-kd EN. (E) Violin plot showing DNA methylation across CLSY3-dependent sRNA loci (lost sRNA) in CHH context. (F) Box plots showing methylation status of CLSY3-dependent sRNA (lost sRNA) loci in CHH context. (G) Box plot showing sRNA status of 2620 CLSY3-dependent gained sRNA loci. (H) Box plots showing methylation status of CLSY3-dependent sRNA (gained sRNA) loci in CHH context. In (F), (G) and (H), boxes show median values and interquartile range. Whiskers show minimum and maximum values, excluding outliers. Comparisons were made with two-sided Wilcoxon test *(P*<0.01 was considered significant). Source data are provided as a Source Data file.

A

HygR — 3xFLAG-OsCLSY3-GFP

HygR — 3xFLAG-OsCLSY3-2Xmyc

LB   P: OsCLSY3   RB

B

8864

1420   1425   1410   1092

Rep1   Rep2   Rep1   Rep2

OsCLSY3-GFP   OsCLSY3-2Xmyc

7958

C

Number of ChIP-seq peaks

400
300
200
100
0

En-spm, Harbinger, hAT, Helitron, Tc1/mariner, MuDR, TC Mariner-Pogo, MITEs, hAT-AC, Non-LTRs, LINE, SINE, Retroelements, Copia, rRNA, Genes, miRNAs, Promoters, Terminators

Type II TEs   Type I TEs   Other

D

Motif3   Sites-1623   E-Value-3.1Xe⁻¹⁷¹

Motif4   Sites-1648   E-Value-7.4xe⁻¹⁷¹
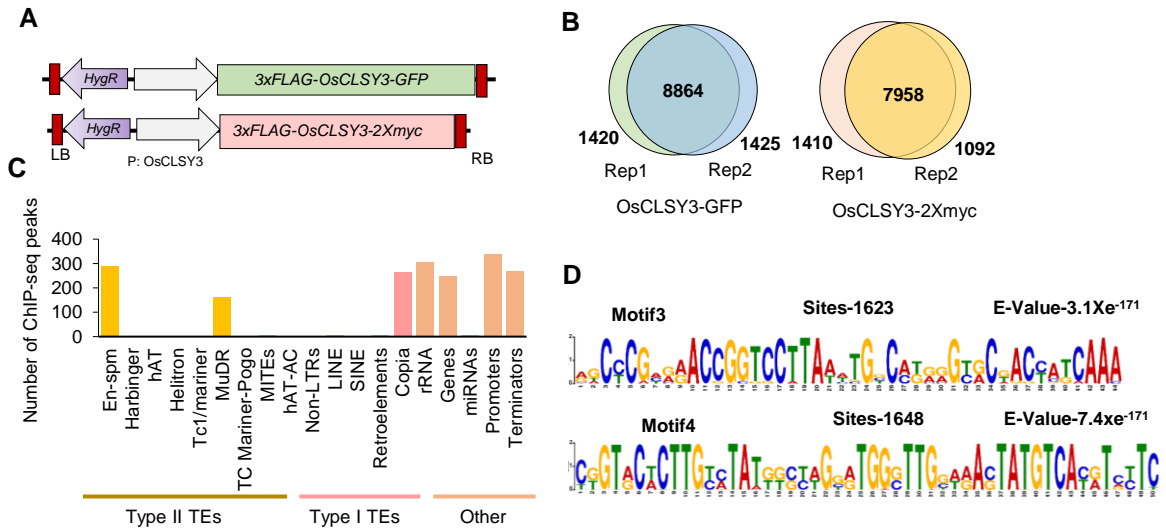
Supplementary Figure 10. OsCLSY3-ChIP analysis.

(A) Linear maps of OsCLSY3 epitope tagged constructs driven by OsCLSY3 native promoter. (B) Venn diagrams showing overlap between replicates of ChIP-seq peaks in two different OsCLSY3 tagged lines. (C) Enrichment of OsCLSY3 ChIP-seq peaks across different genomic features. (D) Less conserved OsCLSY3-bound sequence-specific motifs. Source data are provided as a Source Data file.
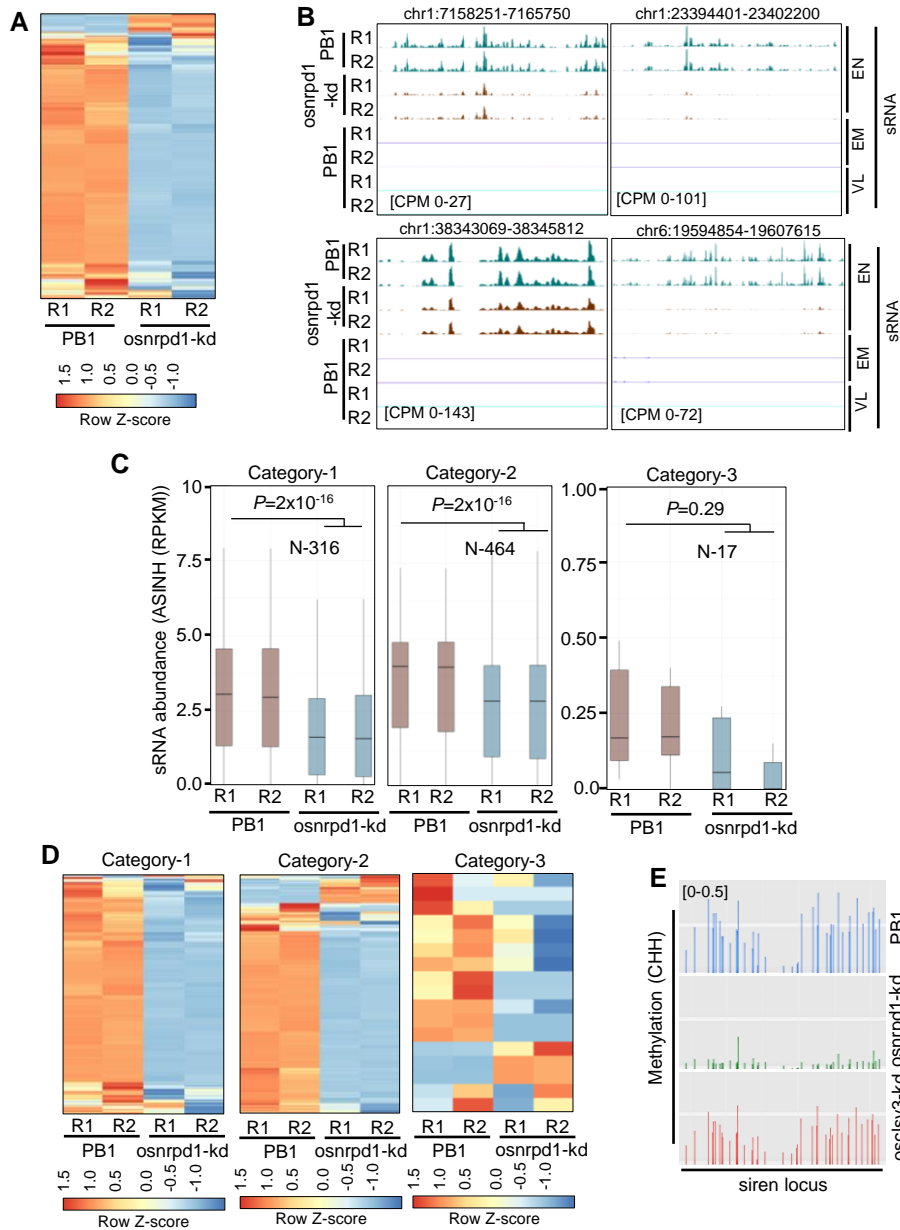
Supplementary Figure 11. RdDM pathway regulates expression of siren loci in rice.
(A) Heatmap showing expression of siren sRNAs (23-24 nt) in osnrpd1-kd EN. Row Z-score was plotted (N-797 loci). (B) IGV screenshot representing sRNA levels (23-24 nt) in some selected siren loci in osnrpd1-kd EN. (C) Boxplots showing expression of siren loci in osnrpd1-kd EN (category wise). Boxes show median values and interquartile range. Whiskers show minimum and maximum values excluding outliers. Comparisons were made with two-sided Wilcoxon test (*P*<0.01 was considered significant). (D) Heatmaps showing expression of siren loci in osnrpd1-kd EN (category wise). (E) BS-PCR showing DNA methylation status of selected siren locus in osclsy3-kd and osnrpd1-kd EN. Source data are provided as a Source Data file.
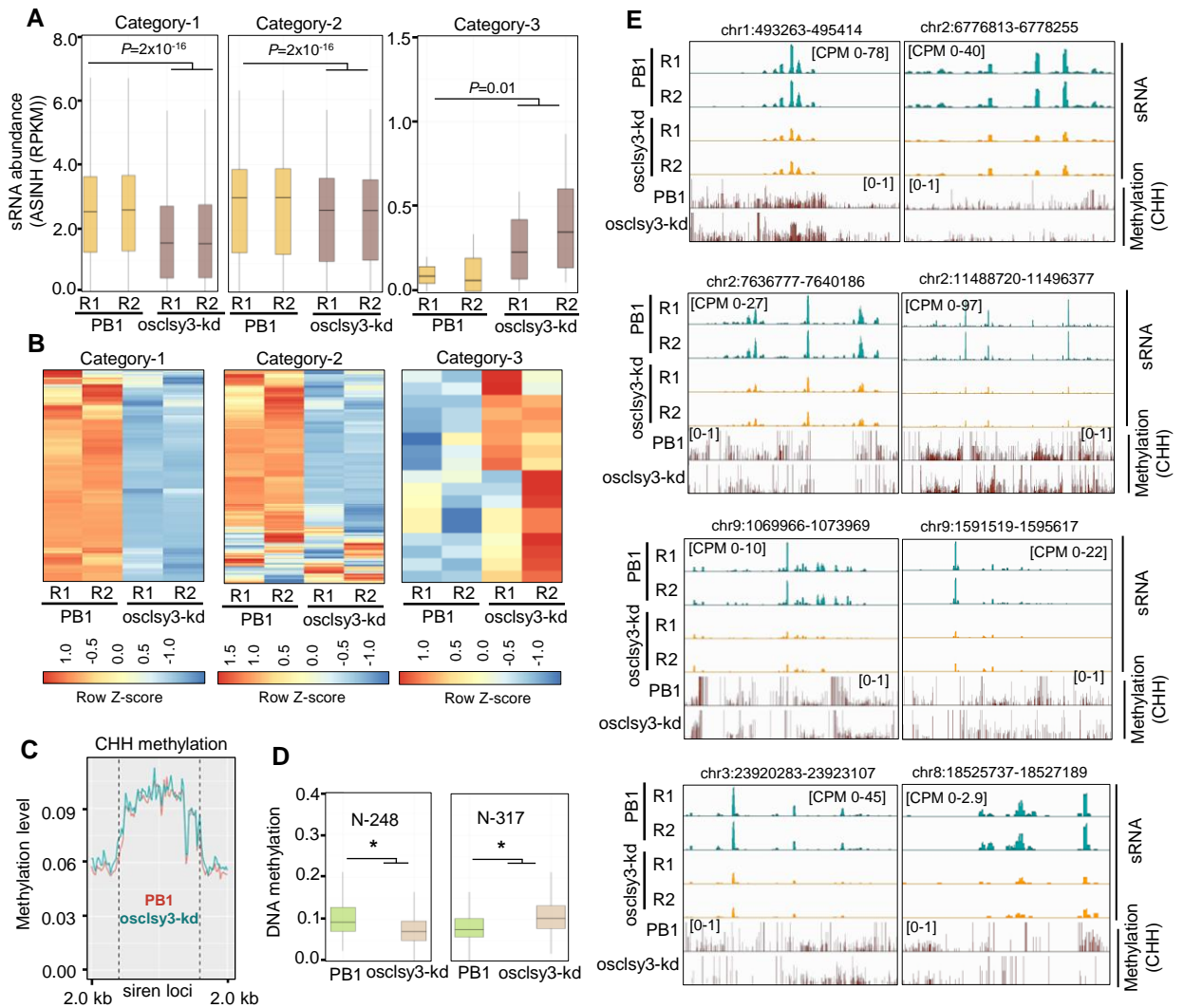
Supplementary Figure 12. The OsCLSY3 regulates expression of siren RNAs in rice.
(A) Boxplots showing expression of siren RNAs (23-24 nt) in osclsy3-kd EN. Row Z-score was plotted. (B) Heatmap showing expression of siren RNAs in 3 categories. (C) Metaplot showing DNA methylation status of all siren loci in rice (CHH context). (D) Boxplots showing hypomethylated (left) and hypermethylated (right) siren loci in osclsy3-kd EN (CHH context). Boxes show median values and interquartile range. Whiskers show minimum and maximum values excluding outliers. Comparisons were made with two-sided Wilcoxon test (*P*<0.01 considered significant). (E) IGV screenshots showing sRNA expression and DNA methylation status of a few siren loci in osclsy3-kd EN. Source data are provided as a Source Data file.
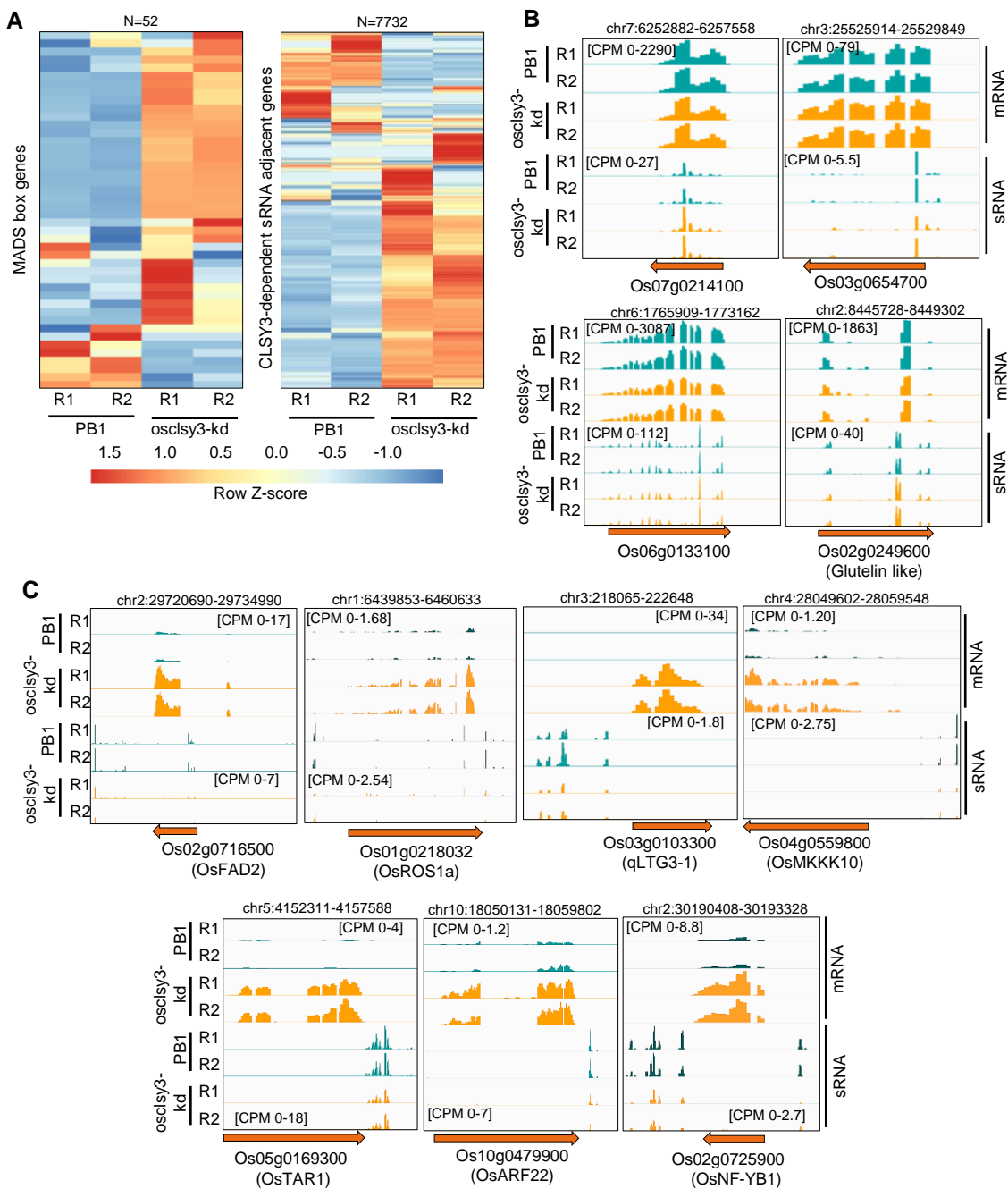
Supplementary Figure 13. OsCLSY3-dependent sRNAs regulate protein coding genes.
(A) Heatmap showing MADS box and CLSY3-dependent sRNA adjacent genes in osclsy3-kd
EN. Row Z-score was plotted. (B) IGV screenshots showing four control genes in which sRNA
and mRNA levels unaltered in osclsy3-kd EN. (C) IGV screenshots showing expression of few
selected seed development and yield related genes in osclsy3-kd EN. Source data are
provided as a Source Data file.
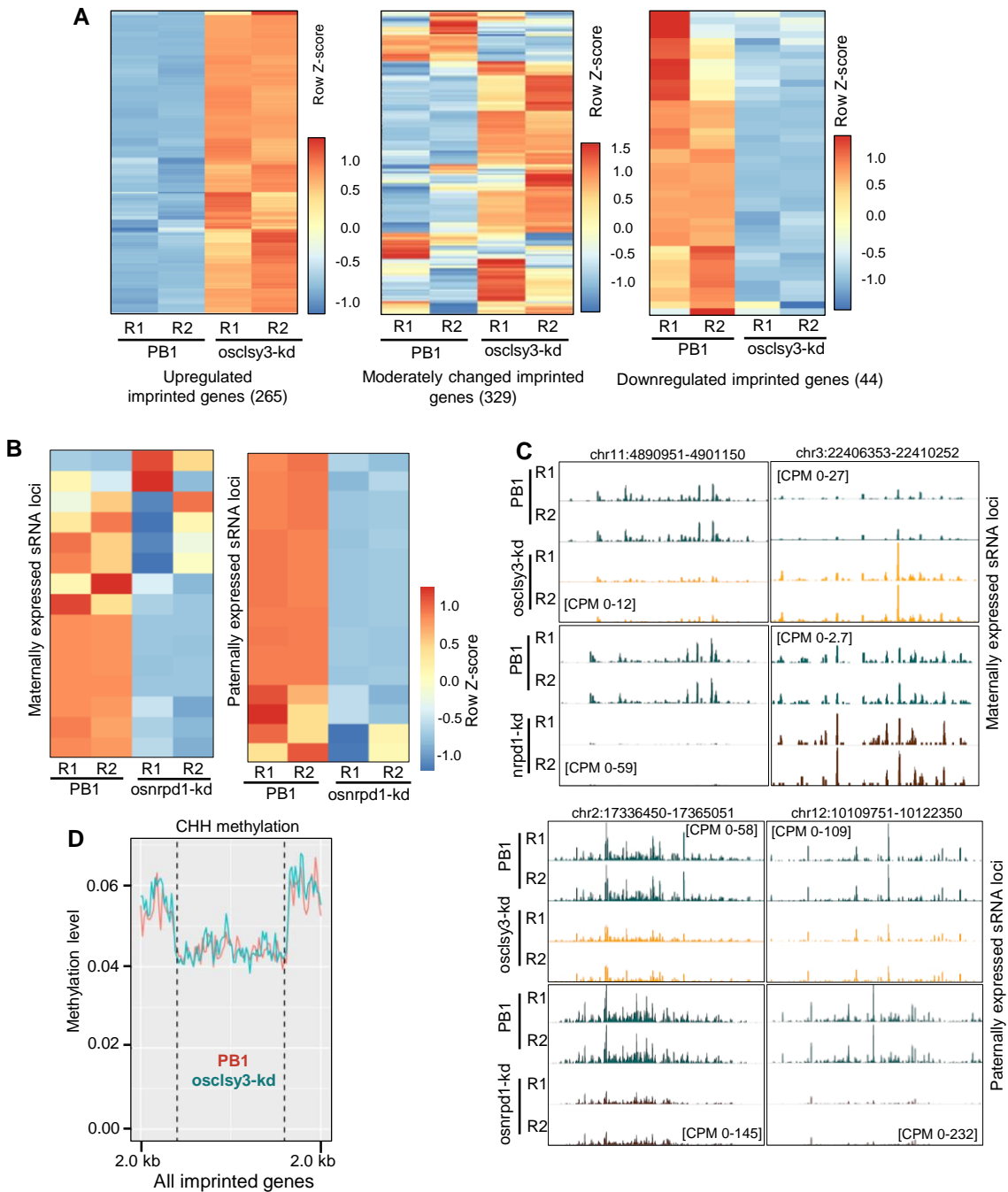
Supplementary Figure 14. Imprinted genes and imprinted sRNAs are regulated by OsCLSY3.
(A) Heatmap showing expression of imprinted genes osclsy3-kd EN. Row Z-score was plotted. (B) Heatmap showing expression of imprinted sRNAs loci in osnrpd1-kd EN. Row Z-score was plotted. (C) IGV screenshots representing expression of imprinted sRNAs (23-24 nt) in osnrpd1-kd and osclsy3-kd EN. (D) Metaplot showing DNA methylation of all imprinted genes in osclsy3-kd EN in CHH context. Source data are provided as a Source Data file.
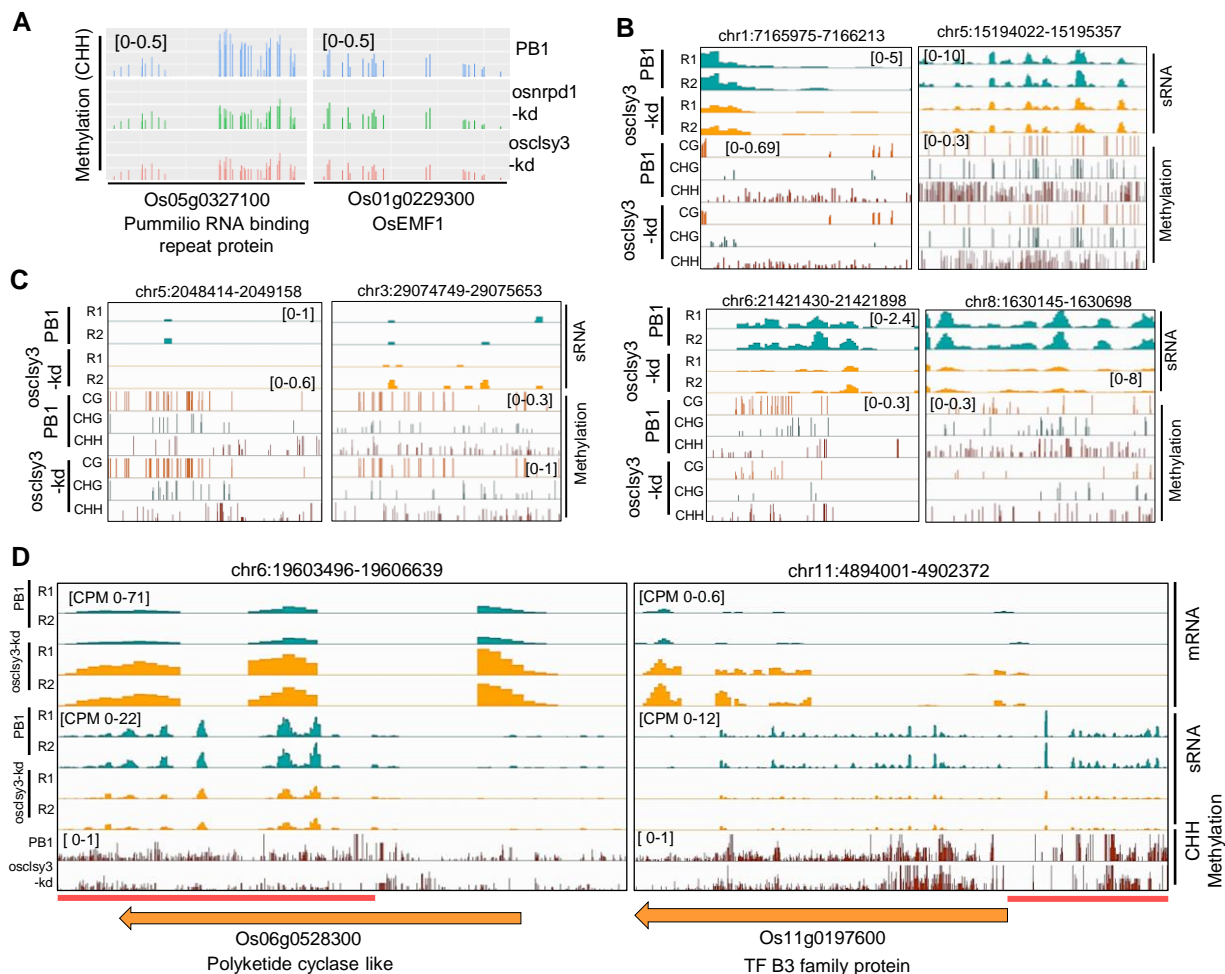
Supplementary Figure 15. DNA methylation level in selected imprinted genes adjacent to imprinted sRNA loci.
(A) BS-PCR showing DNA methylation status of two imprinted genes. (B) IGV screenshots showing sRNA and DNA methylation status of selected regions of imprinted sRNA loci used in chop-PCR analysis. (C) IGV screenshots showing DNA methylation of *OsActin* and a control locus. (D) IGV screenshots showing DNA methylation, sRNA and mRNA expression of two selected imprinted genes. Red lines indicate hypomethylated regions. Source data are provided as a Source Data file.
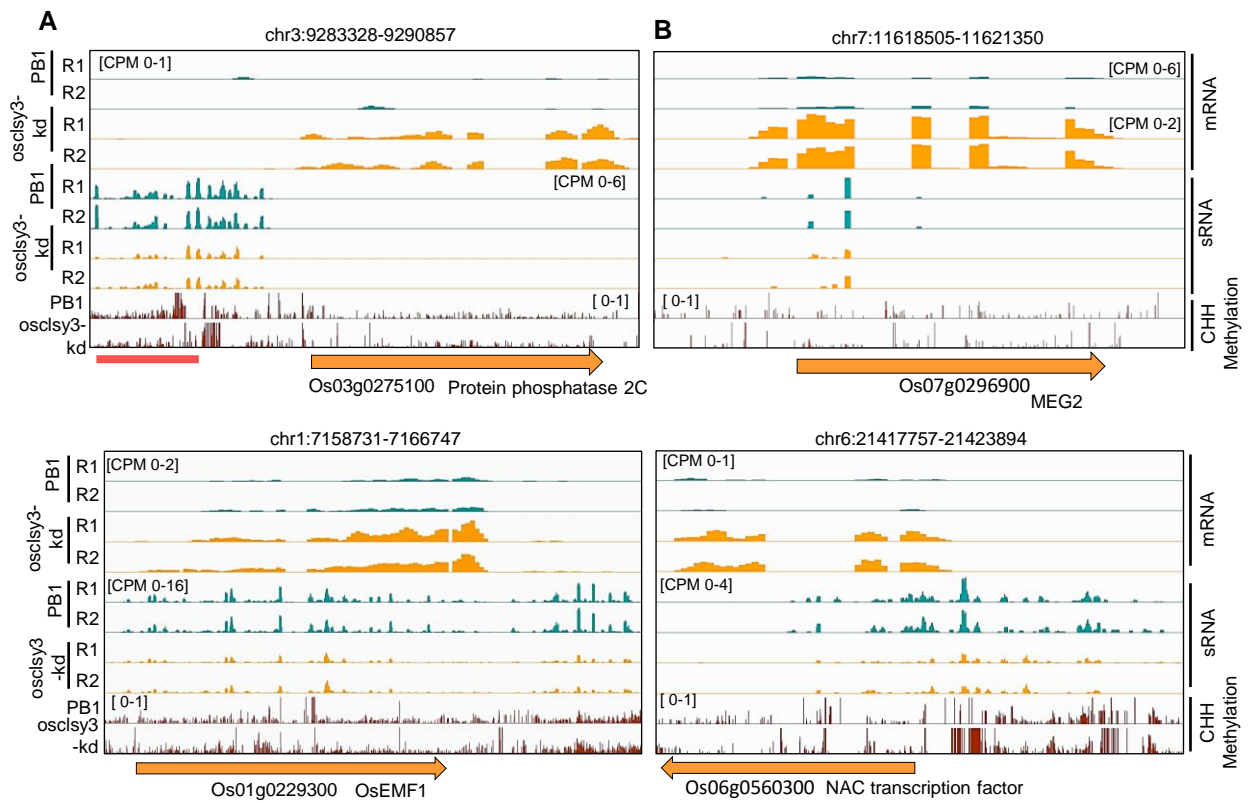
Supplementary Figure 16. DNA methylation levels across selected imprinted genes in osclsy3-kd endosperm.
(A) IGV screenshots showing RNA, sRNA and DNA methylation status of an imprinted gene Os03g0275100 (red line - hypomethylated region). (B) IGV screenshots showing mRNA, sRNA and DNA methylation status of imprinted genes in which DNA methylation is either not changed or redistributed. Source data are provided as a Source Data file.

Supplementary Table 1: Details of high-throughput genomics data generated in this study

Sl. No	Dataset type	Genotype	Replicate	Source tissue	GSM Number	GSE Number	Total number of mapped reads obtained	Sequencing mode
1	Small RNA-seq	WT (PB1)	Rep1	20 days Endosperm	GSM7181918	GSE229958	39570183	Single end 50bp
2	Small RNA-seq	WT (PB1)	Rep2	20 days Endosperm	GSM7181919	GSE229958	29825291	Single end 50bp
3	Small RNA-seq	osclsy3-kd	Rep1	20 days Endosperm	GSM7181916	GSE229958	41731266	Single end 50bp
4	Small RNA-seq	osclsy3-kd	Rep2	20 days Endosperm	GSM7181917	GSE229958	26694590	Single end 50bp
5	Small RNA-seq	WT (PB1)	Rep1	25 days Embryo	GSM7181920	GSE229958	34720489	Single end 50bp
6	Small RNA-seq	WT (PB1)	Rep2	25 days Embryo	GSM7181921	GSE229958	29840669	Single end 50bp
5	RNA-seq	WT (PB1)	Rep1	20 days Endosperm	GSM7181930	GSE229959	12941016	Paired end 100bp
6	RNA-seq	WT (PB1)	Rep2	20 days Endosperm	GSM7181931	GSE229959	14608494	Paired end 100bp
7	RNA-seq	osclsy3-kd	Rep1	20 days Endosperm	GSM7181928	GSE229959	13857932	Paired end 100bp
8	RNA-seq	osclsy3-kd	Rep2	20 days Endosperm	GSM7181929	GSE229959	13461363	Paired end 100bp
9	RNA-seq	Embryo	Rep1	25 days Embryo	GSM7181922	GSE229959	44252442	Paired end 100bp
10	RNA-seq	Embryo	Rep2	25 days Embryo	GSM7181923	GSE229959	32808865	Paired end 100bp
11	RNA-seq	Endosperm	Rep1	25 days Endosperm	GSM7181924	GSE229959	35622255	Paired end 100bp
12	RNA-seq	Endosperm	Rep2	25 days Endosperm	GSM7181925	GSE229959	30799873	Paired end 100bp
13	RNA-seq	Endosperm	Rep1	15 days Endosperm	GSM7181926	GSE229959	37858782	Paired end 100bp
14	RNA-seq	Endosperm	Rep2	15 days Endosperm	GSM7181927	GSE229959	33080996	Paired end 100bp
15	Targeted bisulfite	WT Leaf (PB1)	NA	60 days Leaf	GSM7181933	GSE229960	1031542	Paired end 100bp
16	Targeted bisulfite	WT Panicle (PB1)	NA	Mature panicle (12-15 cm)	GSM7181934	GSE229960	1074742	Paired end 100bp
17	Targeted bisulfite	WT (PB1) Endosperm	NA	20 days Endosperm	GSM7181932	GSE229960	1166935	Paired end 100bp
18	Targeted bisulfite	Untreated DNA	NA	Untreated Leaf DNA	GSM7181935	GSE229960	925634	Paired end 100bp
19	Targeted bisulfite	WT (PB1) Endosperm (TEs)	NA	20 days Endosperm	GSM7181936	GSE229960	991160	Paired end 100bp
20	Targeted bisulfite	osclsy3-kd Endosperm (TEs)	NA	20 days Endosperm	GSM7181937	GSE229960	961552	Paired end 100bp
21	Bisulfite-Seq	WT (PB1) Endosperm	NA	20 days Endosperm	GSM8121738	GSE260651	18706477	Paired end 150 bp
22	Bisulfite-Seq	osclsy3-kd Endosperm	NA	20 days Endosperm	GSM8121739	GSE260651	15268917	Paired end 150 bp
23	Targeted bisulfite	osclsy4-kd Leaf	NA	60 days Leaf	GSM8121725	GSE260648	779686	Paired end 100bp
24	Targeted bisulfite	osclsy3-kd EN (Genes,siren)	NA	20 days Endosperm	GSM8121722	GSE260648	948357	Paired end 100bp
25	Targeted bisulfite	WT EN (PB1) (Genes,siren)	NA	20 days Endosperm	GSM8121724	GSE260648	692822	Paired end 100bp

26	Targeted bisulfite	osnrpd1-kd EN (Genes,siren)	NA	20 days Endosperm	GSM8121723	GSE260648	787135	Paired end 100bp
27	ChIP-seq	OsCLSY3-GFP	Rep1	Panicle before anthesis	GSM8121726	GSE260649	6139543	Paired end 100bp
28	ChIP-seq	OsCLSY3-GFP	Rep2	Panicle before anthesis	GSM8121727	GSE260649	6247648	Paired end 100bp
29	ChIP-seq	OsCLSY3-2XMYC	Rep1	Panicle before anthesis	GSM8121728	GSE260649	3837279	Paired end 100bp
30	ChIP-seq	OsCLSY3-2XMYC	Rep2	Panicle before anthesis	GSM8121729	GSE260649	3542186	Paired end 100bp
31	ChIP-seq	INPUT	Rep1	Panicle before anthesis	GSM8121730	GSE260649	22074726	Paired end 100bp
32	ChIP-seq	INPUT	Rep2	Panicle before anthesis	GSM8121731	GSE260649	19555683	Paired end 100bp
33	Imprinting study	OsARF22 and OsSHH1	NA	10 days Endosperm	GSM8121720	GSE260647	951812	Paired end 100bp
34	Imprinting study	OsCLSY3	NA	10 days Endosperm	GSM8121721	GSE260647	54474	Paired end 300bp

Supplementary Table 2: Sequences of DRD1 family proteins

> LOC_Os02g43460/Os02g0650800/OsCLSY3/CHR740/FEL1

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VSGNLMDEIDKYRSKAAKYGKKKKKKIEMEEMESDLGWNGPIGNVVHKRNGPHSRIRSVSRETGVS
EEPQIYKKRTLSAGAYNKLIDSYMSRIDSTIAAKDKATNVVEQWQGLKNPASFSIEAEERLSEEEEDDG
ETSENEILWREMELCLASSYILDDHEVRVDNEAFHKATCDCEHDYELNEEIGMCCRLCGHVGTEIKHV
SAPFARHKKWTTETKQINEDDINTTIVNQDGVESHTFTIPVASSDMPSAEESDNVWSLIPQLKRKLHLH
QKKAFEFLWKNLAGSVVPAMMDPSSDKIGGCVVSHTPGAGKTFLIIAFLASYLKIFPGKRPLVLAPKTT
LYTWYKEFIKWEIPVPVHLLHGRRTYCMSKEKTIQFEGIPKPSQDVMHVLDCLDKIQKWHAQPSVLVM
GYTSFLTLMREDSKFAHRKYMAKVLRESPGLLVLDEGHNPRSTKSRLRKALMKVDTDLRILLSGTLFQ
NNFCEYFNTLCLARPKFVHEVLVELDKKFQTNQAEQKAPHLLENRARKFFLDIIAKKIDTKVGDERLQG
LNMLRNMTSGFIDNYEGSGSGSGDVLPGLQIYTLLMNSTDVQHKSLTKLQNIMSTYHGYPLELELLITL
AAIHPWLVKTTTCCAKFFNPQELLEIEKLKHDAKKGSKVMFVLNLVFRVVKREKILIFCHNIAPIRLFLEL
FENVFRWKRGRELLTLTGDLELFERGRVIDKFEEPGGQSRVLLASITACAEGISLTAASRVIMLDSEW
NPSKTKQAIARAFRPGQQKVVYVYQLLSRGTLEEDKYRRTTWKEWVSSMIFSEEFVEDPSQWQAEKI
EDDVLREIVEEDKVKSFHMIMKNEKASTGG

>DRD1(AT2G16390)

MGFVYIVMTGYYKNVHKRKQNQVDDGPEAKRVKSSAKVIDYSNPFAVSNMLEALDSGKFGSVSKEL
EEIADMRMDLVKRSIWLYPSLAYTVFEAEKTMDNQQVVEGVINLDDDDDDDTDVEKKALCVVPSSSEI
VLLDSDDEDNERQRPMYQFQSTLVQHQKNQGDVTPLIPQCSFEEVDLGRGKEMPSAIKAIVEGQTSR
GKVLPIENGVVNEKGVYVGVEEDDSDNESEAADEDLGNIWNEMALSIECSKDVARETSHKEKADVVE
DCEHSFILKDDMGYVCRVCGVIEKSILEIIDVQFTKAKRNTRTYASETRTKRFGESDNELKFSEEGLMI
GGLAAHPTHAAEMKPHQIEGFQFLCSNLVADDPGGCIMAHAPGSGKTFMIISFMQSFLAKYPQAKPL
VVLPKGILPTWKKEFVRWQVEDIPLLDFYSAKAENRAQQLSILKQWMEKKSILFLGYQQFSTIVCDDTT
DSLSCQEILLKVPSILILDEGHTPRNEDTNLLQSLAQVQTPRKVVLSGTLYQNHVKEVFNILNLVRPKFL
KLDTSKSAVKRILAYTPCDVRGRLTGSNSDMASMFNETVEHTLQKSEDFTVKIKVIQDLREMTKKVLH
YYKGDFLDELPGLADFTVVLNLSPKQLNEVKKLRREKRKFKVSAVGSAIYLHPKLKVFSDKSDDVSDT
TMDEMVEKLDLNEGVKAKFFLNLINLCDSAGEKLLVFSQYLIPLKFLERLAALAKGWKLGKEVFVLTGN
TSSEQREWSMETFNSSPDAKIFFGSIKACGEGISLVGASRILILDVPLNPSVTRQAIGRAFRPGQKKMV
HAYRLIAGSSPEEEDHNTCFKKEVISKMWFEWNEYCGYQNFEVETIDVDEAGDTFLESPALREDIRVL
YKR

>GRMZM2G178435(RML1/CHR167/ZmCLSY3)

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GVGDRSGSTKKARGAPGKTRRGGGTRRERSTSAAPANLVGGSATVGSRIRLRSRQQGRVQCATYS
ARVSSEDTGEDEKHMQEQTRVEDVEFMEVDDDYDDVNVAGNVIDQESEQDEALEGRSSQDSHGYS
EDKEGKDSAALSDNEEDVGGKELLEEEEGADQEESHIIYDGEGEQEEDASEEETQELDETGEAQPF
NPSNTMAGSTMRSGGDGKQVFRRRVFEGIYLPENPHRTVGKGIQGRTRSQRKCKDKKLLKRGTFSK
PYNIDIPDSTSDSEEEIEPPAPQQGLLSSSEEDNMTFGKRKRRAAINKRWDKRLSASSDEEDYGAS
AMDAKERPFRRLKKGLSNLQAAKEGCRNYEGSNPGHARYSGPNGGNLENMSSAQDDISFKRNVHM
IRIKKRGRAAKAVYDELLDSLFSGWENHIGNPVHAEAGNSLPLVFSFGDEDAEENTENDKYQEQEDL
WMECGIAFQSMNIGSNGCEEDGKEIPPVKVTSCNIGQHEFIIDEQIGVRCKHCHVVDLEIRDVLPTLGK
CSAERGSAINPEFDRMLKEMLNVFEQNDVLVSNGHELPCNFGDHKAGSVWNLIPGVKETMFPHQQD
AFEFMWTKLAGGTTIEQLKHTIKSDAGGGCVISHAPGTGKTRLAITFVQSYLEVFPHCSPVIIAPRGML
ATWEKEFRKWKATGEARVLDERKLANHEGMDGDKVRKLLLEKPNLLVLDEGHTPRNKKSLIWKVLK
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PIVHIHSGRFLQKSLPGLRESVVILNPLLYQKEVIASMEKTVAMGLDAEYKISLASIHPSLLASAKLSMKE
ESILDKPKLESLRSNPSGGVKTRFVLEIVRLCEALNERVLVFSQYLEPLSLIMEQLKERFSWAEGEEILL
MSGKVLVKKRQTMMEVFNNMKSKAKVMLASTKACCEGITLVGASRVVLLDVVWNPSVGRQAIGRAY

RIGQRKIVYTYNLIAEGTTEKRKYDRQAKKEHMSKLLFSNELERGGCNLPPELTFNDRVLEELTARED
LKNLFV

>GRMZM2G154946(RMR1/ZmCLSY4)

MDRATPRVCGRRGVSQAAVEAAPSSSRARRRDKAPAVVMDLGDDDCGGGGARKTVGGAAGRCE
GSTKAPLPLLPPMMVPAGAVALRTRSRRRAMLAAAVVEEAPTKKKKKEGAIPDAAEAPRGHGSKAAA
TSMATSSHKRRAGTSRSTSRDKRRARSGRASEPARVGRARKRKRNELEAPARRERVKAPCVSESD
DNSGRGDDASHDGDAEPRVGVAIGTDLVNGDHPAAKEVVEGAGDEDTGDGGNSGLASTADVFAEE
MAPFEDDYDDEMLEEQLVGDVIRAYSNGRNFDSDGVDWEAEDEMEFNDDADNSDFMDDADDSDF
MDDAYEGGNSKPIQNHAKLEIQDWVNQKVVLSGGRCEARGEGDLEEELDVGKEADEEDVEPKSEAA
PGSDKRVLQLEILGSDEEIKVLENMSSAPSRKASVQSKLPTIPSCVAWRTRSSWGVNQDRLSYDTYF
EELSDEPKEDDDDTEVELDEVEDDNNDDDSSDAYDKDDEEKEEEEEEAERRKLNNRICTSDEDMINI
TVPTSRYDMFKKKNSSRYDIEWVEDEDASVDMLQPVSFKKDSSWKPVAVGNDTFTEQQKRSRFTW
ELERRKKLKLEMKTNPLHERDLDSDPNSSGSDQIRKYGFKSDGSHKVDRKKKHTSPKSGKKPSSAIIL
KRQSLLKLLVDKMSGDKSLASFPFDQNPQLQFIFKEMHPLVFSFGDEDLVAADRPEQDVGLDMLWA
DFDFALESENIGTYYDDECQEGNQLDFSLAPVTPCSRGKHEFVIDDQIGIRCKYCSLVNLEIKFMFPSL
VSVFAEKSAWPNDKGVKNTLMFHDLYEQGVNDTEQSQDIHQYGTVWNLIPGVISTMYEHQREAFEF
MWTNLVGDIRLDEIKHGAKPDVVGGCVICHAPGTGKTRLAIVFIQTYMKVFPDCRPVIIAPRGMLFAW
DEEFKKWNVDVPFHILNTTDYTGKEDREICKLIKKEHRTEKLTRLVKLLSWNKGHGILGISYGLYTKLTS
EKPGCTEENKVRSILLDNPGLLVLDEGHTPRNERSVMWKTLGNVKTEKRIILSGTPFQNNFLELYNILC
LVRPRFGEMFLTKSRVGRRHYVSKKQKDKFSDKYEKGVWASLTSNVTDDNAEKVRSILKPFVHIHNG
NILRTLPGLRESVIILKPLPLQKSIIKKVENIGSGNNFEHEYVISLASTHPSLVTAINMSEEEASLIDKPML
AKVRSNPYEGVKTRFVIEVVRLSEALREKVLIFSQFIQPLELIKEHLRKFFKWREGKEILQMDGKILPRY
RQASIEAFNNPNNDSRVLLASTRACCEGISLTGASRIVLLDVVWNPAVGRQAISRAFRIGQKKFVYTY
NLITYGTGEGDKYDRQAEKDHLSKLVFSTEDEFNNVRNMLSKAEMEHCSKFISEDKVLEEMTSHDQL
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>GRMZM2G108166 (CHR166/RMRL2)

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NSAVDCFHHNRSKLLSARFSLEVAYLIVLSSLRRMEFNIKMVDGNIIYQIIKGDQARDSIDSMSIPPGFG
KNMDIISFKPRGEALRPITRTVPVTQVEEGNLTEDGCIAVKGESDSAQDVEILYAHVDIRRSKRMKTQP
DRFTSYDARNFNRTYNKKEADGPSTKYEDSESGLSCDSSEQRESSDEEALENPRSMAAEHKYPVKR
NQCSLPVKEKQISMEIKKNTTDQGCSDSYIPHTPAKNTERPRFRLKPFASSRSLDGNSEPAFCQKRG
RKRKKHMCQIEYKRMIDQCIGNIQCEVERDSDFKFGDQILDGCVRAYQEVDFTWPSSADSQEEKDEL
DELWKEMDYALATVAILEQKQMTDSEVVHESNTDLGKGGEHCHHDCMLDEQLGLTCRLCNVVCIEA
KDIFPPMFTGKDHERPERNHFGQDGHVLDLSFFEICAPEFSKIKESGNVWASITDLEPKLLAHQRKAF
EFIWKNLAGSLQLEEMDGSTSRGGCVVAHTPGAGKTLLLISFLVSYLKVHPRSRPLVLTPKAAIHTWR
TEFQKWGILLPLHVLHHSNRTSKLMGGLSSKLQAVLKSFHQPSWKTMRIMHCLDKLCKWHEEPSILL
MTYSSFLSLTKEDSKLRHQAFITKVLMNNPGLLILDEGHNPRSNKSKLRKLLMKVKTEFRILLSGTVFQ
NNFEEYFNTLSLARPRFVNDVMTTLVTESEKRTRSRTGKHQEALARHVFVERVGHKIESSSKHDRMD
GISLLNELTQGFIDSFEGTKLNILPGIRVYTLFMKPTDVQEEVLAKLLMPLSGNARYPLEYELLITIASIHP
WLINTTKCASTYFTPAEVASVDKYKRNFAAGCKAKFVIDLLHKSSFRGERVLVFCHNVAPIAFLVTLIEI
VFGWRLGQEVLVLQGDQELHVRSDVMDKFNSDRRGKRKVLIASTTACAEGISLTGASRLVMLDSEW
NHSKTRQAIARAFRPGQERMVFVYLLVASGTWEEDKYNSNRRKAWIAKMVFFGRHFDDPLQNRVTE
IDDEVLKELADEDETNTFHMIVKQD

>GRMZM2G393742(RML3)

MSQSPGGREGIYYSRQRKPSERNGSVFTPIAAMYPSGHALPDANRNHSLVFGGTSKDWDNIRQFIA
SLERASENSSAIASKTGGGKSTNHSVEPAEQKGKGDIIVLDSDDEDGDGNSPEHNKLASEMNKELGT
SVLASNIAERMATNGSQTFETVHAYGGSKNTQIVPYGQGSALVNQFPLQTSWQPSIQFERVVLTKRP
EEQRMQDLVAATIAEKRAETQMFLSLPTERKRRTDHSLLMLDSFVPKQRRRKGDTGLAPADLSLDL
HQTATSQEPDIAIEEEEKRKNDGDGLEDYWKDFALAVESTKLDDVDEAAANEKEDNGKMEDIDCNHD
IRIHEDLGHVCRVCGMIVRRADSIIDYQWKKASRRRMNGYGGNSKDADEIDCGTVKLSEDFIVADIAIH
PRHAQAMKPHQVEGFNFLVKNLIGDKPGGCILAHAPGSGKTFLLISFIQSFMARYPSARPLVVLPKGIL

VIWKKEIQRWQVQDIPVYDFYSVKAEKRVEQLQILKSWEDKMGILFLGYKQFSTIVTDDGGSKVTAAC
RDRLLKVPNLLILDEGHTPRNKETDVLESLSRVETPRKVVLSGTLFQNHVEEVFNILNLVRPKFLRMES
SRPIARRIMSQVEIFGRSSKGLADGAFTEAVEGTLLNDENFKRKVHVIRGLRELTRDVLHYYKGAILDE
LPGLVDFSVFLKLTPKQKDIVHKLEMHDRFKRSAVGSALYIHPCLSGLSEVNAENRAHTLRDDSVDSL
MDSINVRDGVKANFFMNILSLANSAGEKVLAFSQYILPMTFFERLLVKKKGWHVGREIFMISGDTSQE
DREAAVDRFNSSADAKVLFGSIRACGEGISIVGASRVVILDVHLNPSVTRQAIGRAFRPGQQKKVFVY
RLVAADSDEVKVHETAFKKEVIQKLWFEWSEQCTTENFKLGQVDIDDSGDELLDTRAIRQDIKALYRR

>AtSHH1 (AT1G15215)

MAASDDSSHYFTEFTLSEIVDMENLYKELGDQSLHKDFCQTVASTFSCSVNRNGKSSITWKQVQIWF
QEKLKHQSQPKSKTLPSPPLQIHDLSNPSSYASNASNATFVGNSTFVQTRKGKASDLADLAFEAKSA
RDYAWYDVSSFLTYRVLRTGELEVRVRFSGFDNRHDEWVNVKTSVRERSIPVEPSECGRVNVGDLL
LCFQEREDQALYCDGHVLNIKRGIHDHARCNCVFLVRYELDNTEVRRLISAFLLGVGTIDEVLC

Supplementary Table 3: Details of high-throughput genomics data obtained from publicly available datasets

Sl.No	Dataset type	Genotype	Source tissue	SRA number	GSE number	Reference
1	RNAseq	WT (PB1)	pre-emerged panicle	SRX11493038	GSE180457	[1]
2	RNAseq	WT (PB1)	pre-emerged panicle	SRX11493039	GSE180457	[1]
3	RNAseq	osnrpd1-kd	pre-emerged panicle	SRX11493040	GSE180457	[1]
4	RNAseq	osnrpd1-kd	pre-emerged panicle	SRX11493041	GSE180457	[1]
5	RNAseq	WT (PB1)	Anther	SRX11493042	GSE180457	[1]
6	RNAseq	WT (PB1)	Anther	SRX11493043	GSE180457	[1]
7	RNAseq	osnrpd1-kd	Anther	SRX11493044	GSE180457	[1]
8	RNAseq	osnrpd1-kd	Anther	SRX11493037	GSE180457	[1]
9	RNAseq	WT_T1_r1	Leaf	SRX6976682	GSE138705	[2]
10	RNAseq	WT_T1_r2	Leaf	SRX6976683	GSE138705	[2]
11	RNAseq	osdrm2_T1_r1	Leaf	SRX6976688	GSE138705	[2]
12	RNAseq	osdrm2_T1_r2	Leaf	SRX6976689	GSE138705	[2]
13	RNAseq	Nip_se_rep1	Seedling	SRX5724238	GSE130168	[3]
14	RNAseq	Nip_se_rep2	Seedling	SRX5724239	GSE130168	[3]
15	RNAseq	osrdr2-6_se_rep1	Seedling	SRX5724240	GSE130168	[3]
16	RNAseq	osrdr2-6_se_rep2	Seedling	SRX5724241	GSE130168	[3]
17	RNAseq	osrdr2-6_se_rep3	Seedling	SRX5724242	GSE130168	[3]
18	RNAseq	WT_base_rep1	Shoot base of seedling	SRX5846194	GSE131319	[4]
19	RNAseq	WT_base_rep2	Shoot base of seedling	SRX5846195	GSE131319	[4]
20	RNAseq	WT_base_rep3	Shoot base of seedling	SRX5846196	GSE131319	[4]
21	RNAseq	osnrpd1ab_base_rep1	Shoot base of seedling	SRX5846203	GSE131319	[4]
22	RNAseq	osnrpd1ab_base_rep2	Shoot base of seedling	SRX5846204	GSE131319	[4]
23	RNAseq	osnrpd1ab_base_rep3	Shoot base of seedling	SRX5846205	GSE131319	[4]
24	sRNA-seq	WT (PB1)	Endosperm (16-20 days after anthesis)	SRX11504321	GSE180457	[1]
25	sRNA-seq	WT (PB1)	Endosperm (16-20 days after anthesis)	SRX11504322	GSE180457	[1]
26	sRNA-seq	osnrpd1-kd	Endosperm (16-20 days after anthesis)	SRX11504323	GSE180457	[1]
27	sRNA-seq	osnrpd1-kd	Endosperm (16-20 days after anthesis)	SRX11504324	GSE180457	[1]
28	sRNA-seq	WT (PB1)	pre-emerged panicle	SRX11504325	GSE180457	[1]
29	sRNA-seq	WT (PB1)	pre-emerged panicle	SRX11504326	GSE180457	[1]

30	sRNA-seq	osnrpd1-kd	pre-emerged panicle	SRX11504327	GSE180457	[1]
31	sRNA-seq	osnrpd1-kd	pre-emerged panicle	SRX11504328	GSE180457	[1]
32	sRNA-seq	WT (Nipponbare)	Seedlings	SRX5724235	GSE130168	[3]
33	sRNA-seq	WT (Nipponbare)	Seedlings	SRX5724236	GSE130168	[3]
34	sRNA-seq	rdr2-6	Seedlings	SRX5724237	GSE130168	[3]
35	sRNA-seq	WT (Nipponbare)	Panicle	SRX5724233	GSE130168	[3]
36	sRNA-seq	osrdr2-6	Panicle	SRX5724234	GSE130168	[3]
37	sRNA-seq	osnrpd1	Seedlings	SRX9211921	GSE158709	[5]
38	sRNA-seq	osnrpe1	Seedlings	SRX9211922	GSE158709	[5]
39	sRNA-seq	osnrpe1	Seedlings	SRX9211920	GSE158709	[5]
40	sRNA-seq	WT rep1 (Hwayoung)	Leaf	SRX11930857	PRJNA758109	[6]
41	sRNA-seq	WT rep2 (Hwayoung)	Leaf	SRX11930858	PRJNA758109	[6]
42	sRNA-seq	WT rep3 (Hwayoung)	Leaf	SRX11930859	PRJNA758109	[6]
43	sRNA-seq	nrp(d/e)2 Rep1	Leaf	SRX11930854	PRJNA758109	[6]
44	sRNA-seq	nrp(d/e)2 Rep1	Leaf	SRX11930855	PRJNA758109	[6]
45	sRNA-seq	nrp(d/e)2 Rep1	Leaf	SRX11930856	PRJNA758109	[6]
46	Bisulfite-Seq	WT (IR64)	Endosperm	SRR8937051	GSE130122	[7]
47	Bisulfite-Seq	WT (IR64)	Embryo	SRR8937043	GSE130122	[7]
48	Bisulfite-Seq	WT (Nipponbare)	70-days leaf	SRX6976659	GSE138705	[2]
49	Bisulfite-Seq	oscmt2/cmt3a	70-days leaf	SRX6976664	GSE138705	[2]
50	Bisulfite-Seq	osdrm2	70-days leaf	SRX6976666	GSE138705	[2]
51	Bisulfite-Seq	osdrm2	70-days leaf	SRX6976667	GSE138705	[2]
52	Bisulfite-Seq	osdrm1a/drm1b	70-days leaf	SRX6976671	GSE138705	[2]
53	Bisulfite-Seq	osdrm2/drm3	70-days leaf	SRX6976672	GSE138705	[2]
54	Bisulfite-Seq	oscmt2/cmt3a/cmt3b/drm2/drm3	70-days leaf	SRX6976677	GSE138705	[2]
55	Bisulfite-Seq	oscmt2/cmt3a/cmt3b/drm2/drm3	70-days leaf	SRX6976678	GSE138705	[2]
56	Bisulfite-Seq	BS-seq_Nip_se_rep1	Seedlings	SRX5724238	GSE130168	[3]
57	Bisulfite-Seq	BS-seq_Nip_se_rep2	Seedlings	SRX5724239	GSE130168	[3]
58	Bisulfite-Seq	BS-seq_osrdr2-6_se	Seedlings	SRX5724232	GSE130168	[3]

59	OsAGO1 a-IP	WT (Nipponbare)	Seedling	SRX014804	GSE18251	[8]
60	OsAGO1 b-IP	WT (Nipponbare)	Seedling	SRX014805	GSE18251	[8]
61	OsAGO1 c-IP	WT (Nipponbare)	Seedling	SRX014806	GSE18251	[8]
62	OsAGO4 a-IP	WT (Nipponbare)	Seedling	SRX017394	GSE20748	[8]
63	OsAGO4 b-IP	WT (Nipponbare)	Seedling	SRX017395	GSE20748	[8]

Supplementary Table 4: List of oligos and probes used in this study

Oligo Name	Oligo ID	Oligo sequence (5'-3')	Purpose	Reference
AP_OsCLSY3_F3	2571	CCATCTCCAACGCGGAGCAGAGTAGAACACC	Amplification of OsCLSY3 from genome	This study
AP_OsCLSY3_R1	2472	CTGTTAGTGAGAATGGAGAATCTTCAC	Amplification of OsCLSY3 from genome	This study
AP_CLSY3_EX3_RT_F2	3709	GGTGTGAGCTATACGCTTTTCAGG	RT-qPCR and RTPCR of OsCLSY3	This study
AP_CLSY3_EX3_RT_R2	3710	GCGAAGTGTCTTGCAAACTTTGGTC	RT-qPCR and RTPCR of OsCLSY3	This study
AP_CLSY3_Prom_F3	2817	GGCCAGCTAGTACTTTCAGAGGATCTTCATCG	Amplification from genome of OsCLSY3 promoter	This study
AP_CLSY3_prom_R2	2818	GTCGATGATCTCTAGCGAGGGGCTACGTGCAC	Amplification from genome of OsCLSY3 promoter	This study
pRGEB32_Seq_F	1435	CCGGCTCGTATGTTGTGTGG	Amplification of OsCLSY3 gRNA	This study
AP_OsCLSY3_gRNA2_R	2602	TATAGGTCTCAAAACAGGAGAGCCGGGAGGTTGTCTGCCACGGATCATCTGCACAACTC	Amplification of OsCLSY3 gRNA	This study
Hyg_F	415	AAAGCCTGAACTCACCGC	RT-PCR and Southern probe	This study
Hyg_R	416	GGTTTCCACTATCGGCGA	RT-PCR and Southern probe	This study
STN_OsRAC1_F	2563	GCTATGTACGTCGCCATCCAGG	RT-qPCR	This study
STN_OsRAC1_R	2564	TGAGATCACGCCCAGCAAGG	RT-qPCR	This study
STN_OsGAPDH_qPCR_F	3873	GGGTATTCTGGGTTACGTTGAGGAG	RT-qPCR	This study
STN_OsGAPDH_qPCR_R	3874	ACGGATCAGGTCAACAACGCGAGAG	RT-qPCR	This study
AP_CLSY4_RT_F	3419	GTGGTGGATCCAGTGAATGAAGAGTTGG	RT-qPCR	This study
AP_CLSY4_RT_R	3420	CCCAAAATTATCACCGTCGTCATCAGC	RT-qPCR	This study
AP_FIE1_qpcr_F	3602	AAAAAGATGTGGCACCGAAT	RT-qPCR	[9]
AP_FIE1_qpcr_R	3603	GGTTCACCTTCACCAGCAGT	RT-qPCR	[9]
qPCR_NRPD1a&b _F	1769	TTGCAAGTATTGCTCAAAGGATGG	RT-qPCR	[1]
qPCR_NRPD1a&b _R	1770	CCACCAGCAACTTCTGCGATAATTG	RT-qPCR	[1]
VHS_GUS_qRT_PCR_Fwd	1863	CCCTTACGCTGAAGAGATGC	RT-qPCR	This study

VHS_GUS_qRT_PCR_rev	1864	TTCGTTGGCAATACTCCACA	RT-qPCR	This study
AP_CHOP_PCR_1A_F	4820	CATCCACTGTCCAGATGAAGTCAG	RT-CHOP_PCR	This study
AP_CHOP_PCR_1A_R	4821	ACTTCGATAATGGTAAAACGCCTCC	RT-CHOP_PCR	This study
AP_CHOP_PCR_3B_F	4826	AACCATTTCCATCCCATCCCAACTCG	RT-CHOP_PCR	This study
AP_CHOP_PCR_3B_R	4827	CTAGCGATTCTACTATATTTTAAAGACACATATTC	RT-CHOP_PCR	This study
AP_CHOP_PCR_6A_F	4836	CCTCCGACATGTACTTGCGGTGCTCC	RT-CHOP_PCR	This study
AP_CHOP_PCR_6A_R	4837	TCTCCCTCCCCATGTGAGTGATCCTGC	RT-CHOP_PCR	This study
AP_CHOP_PCR_2B_F	4824	CTGCAGAAAGGCACCAACCTCAGAG	RT-CHOP_PCR	This study
AP_CHOP_PCR_2B_R	4825	AGGACAACTTTGTTCTCCATTATGATC	RT-CHOP_PCR	This study
AP_CHOP_PCR_5A_F	4834	GTCGACATGGAAAGGAGCTTGAGATACCC	RT-CHOP_PCR	This study
AP_CHOP_PCR_5A_R	4835	CGACTCTTGTGTTCCCTTACACATCATAGC	RT-CHOP_PCR	This study
AP_CHOP_PCR_8A_F	4842	CAATGGTGAGAAGATGCATTTGATGATGC	RT-CHOP_PCR	This study
AP_CHOP_PCR_8A_R	4843	CCACGGCATCCATTCTCTCAGATGG	RT-CHOP_PCR	This study
5A_F_VHS_OsChOP	3997	AAATGTACTTACCCTCACGAGCAT	RT-CHOP_PCR	[6]
5A_R_VHS_OsChOP	3998	AATTTTACTACACTTGCGAGCCAA	RT-CHOP_PCR	[6]
SGH_OsActin_RT_F	2929	ATGAAGTGCGACGTGGATATTAG	RT-qPCR	This study
SGH_OsActin_RT_R	2930	GGGCGACCACCTTGATCTTC	RT-qPCR	This study
AP_BS_Os01g0229300_F1	4991	ATTTTTTGTGTTTTGGAGTTGTATT	Bisulfite-PCR	This study
AP_BS_Os01g0229300_R1	4992	AACCATACTTTATATATATTACCCACACTT	Bisulfite-PCR	This study
AP_BS_Os05g0327100_F1	4997	TAATTTTTGTTTTAGTTTATGAATT	Bisulfite-PCR	This study
AP_BS_Os05g0327100_R1	4998	CCTATAATACATCCTCAAATATCTTAC	Bisulfite-PCR	This study
AP_BS_Os05g0327100_F2	4999	GAGGTAGGTTATTAATATGTTTTTTTTT	Bisulfite-PCR	This study
AP_BS_Os05g0327100_R2	5000	AATATCTCAAACTCCTTTCCATATC	Bisulfite-PCR	This study
AP_siren2_BS_F2	5025	TTTAGTTGATTTAATGGTTAATATG	Bisulfite-PCR	This study
AP_siren2_BS_R2	5026	AAAAAACACTTTCATCTAAAATATC	Bisulfite-PCR	This study
AP_siren2_BS_F4	5029	GGAGATATTTATTTGTTATGGGGAT	Bisulfite-PCR	This study
AP_siren2_BS_R4	5030	AAAATCAAAAATTACCCTATTTACTCTACT	Bisulfite-PCR	This study
AP_ARF22_CRS_F1	5071	GCACCAGCCCATGACAATATCTCTTGTTTG	Imprinting study	This study
AP_ARF22_CRS_R1	5073	TGCTCAGTAAATATAGCCTTTCCAAACAGC	Imprinting study	This study
AP_SHH1_CRS_F2	5076	GACCTTGTCCTCTGTTTCAAGGAGAGC	Imprinting study	This study
AP_SHH1_CRS_R2	5078	CCATCATGGTCGTATTCGACAAGGAAGACAC	Imprinting study	This study
AP_CLSY3_CRS_F1	5079	GAGAAATGTAAAGATTGCTCAGAGGAGGAAGC	Imprinting study	This study
AP_CLSY3_CRS_R1	5081	CAGGAACAGGCTCATATTGGTTGCTCTC	Imprinting study	This study
AP_WP/PB1_F	3934	TCCACAATGCGTCAGAAACAATG	Imprinting study	This study
AP_WP/PB1_R	3937	CAGTTCATCTTCATCCTGTAACTTGTC	Imprinting study	This study
miRNA168	32	GTCGCCGAGAAGATCCTCCATC	sRNA northern	This study
U6_probes	13 and 14	GGCCATGCTAATCTTCTCTGTATCGTT AND CCAATTTTATCGGATGTCCCCGAAGGGAC	sRNA northern	This study
amiR_PolIV probe	1697	ATGTCCAAGAGTAACACTATA	sRNA northern	[1]
MITE siRNA	3430	GGTCCCACCTGTCATACACACACT	sRNA northern	This study
AP_CLSY3_amiR1_probe	3877	GCGAGGCCTTATTGTATCGAA	sRNA northern	This study
AP_CLSY3_amiR2_probe	3878	AGGGCGGACTTCAATTGAACA	sRNA northern	This study

AP_CLSY4_amiR1_probe	3880	GAGAGGTCATTCGTGCTTACA	sRNA northern	This study
AP_siren_probe2	4751	CCCGTGTGCAGGTTCTAGTTCCGG	sRNA northern	This study
AP_siren_probe3	4752	CCGTGTGCAGGTTCTAGTTCCGG	sRNA northern	This study

Supplementary References:

1. Hari Sundar G, V. *et al.* Plant polymerase IV sensitizes chromatin through histone modifications to preclude spread of silencing into protein-coding domains. *Genome Res.* (2023) doi:10.1101/gr.277353.122.

2. Hu, D. *et al.* Multiplex CRISPR-Cas9 editing of DNA methyltransferases in rice uncovers a class of non-CG methylation specific for GC-rich regions. *Plant Cell* **33**, 2950–2964 (2021).

3. Wang, L. *et al.* Reinforcement of CHH methylation through RNA-directed DNA methylation ensures sexual reproduction in rice. *Plant Physiol.* **188**, 1189–1209 (2022).

4. Xu, L. *et al.* Regulation of rice tillering by RNA-directed DNA methylation at miniature inverted-repeat transposable elements. *Mol. Plant* **13**, 851–863 (2020).

5. Zheng, K. *et al.* The effect of RNA polymerase V on 24-nt siRNA accumulation depends on DNA methylation contexts and histone modifications in rice. *Proc. Natl. Acad. Sci. U. S. A.* **118**, e2100709118 (2021).

6. Chakraborty, T., Trujillo, J. T., Kendall, T. & Mosher, R. A. A null allele of the pol IV second subunit impacts stature and reproductive development in Oryza sativa. *Plant J.* **111**, 748–755 (2022).

7. Rodrigues, J. A. *et al.* Divergence among rice cultivars reveals roles for transposition and epimutation in ongoing evolution of genomic imprinting. *Proc. Natl. Acad. Sci. U. S. A.* **118**, e2104445118 (2021).

8. Wu, L. *et al.* Rice MicroRNA effector complexes and targets. *Plant Cell* **21**, 3421–3435 (2009).

9. Chen, C. *et al.* Characterization of imprinted genes in rice reveals conservation of regulation and imprinting with other plant species. *Plant Physiology* **177**, 1754–1771 (2018).