

Supplemental Table S3: List of oligos and probes used in this study

Oligo Name	Oligo ID	Oligo sequence (5' – 3')	Purpose	Reference
PollV_miR-s I	330	agcaggagattcagttga	amiR:NRPD1 construct	This study
PollV_miR-a II	331	tgatgtccaagagtaaacactatactgctgctacagcc	amiR:NRPD1 construct	This study
PollV_miR*s III	332	ctatgtcgaagtgaaacactatattctgctgctaggctg	amiR:NRPD1 construct	This study
PollV_miR*a IV	333	aatatagtgttacctcgcacatagagaggcaaaagtga	amiR:NRPD1 construct	This study
OsNRPD1b_CDS_Fwd	1859	atggaggagccaagtctgaggtgaaaatgcctgaagc	OsNRPD1b complementation construct	This study
OsNRPD1b_CDS_Rev	1860	ctacaactgatgtggccgaattgctctattagatagatcttc	OsNRPD1b complementation construct	This study
OsNRPD1b_miRRES_F	2665	cgggttactttgtccaggagtaaacctcaccgtaac	OsNRPD1b complementation construct	This study
OsNRPD1b_miRRES_R	2666	gttacggtgaagttactcctggcaaaagtaaccg	OsNRPD1b complementation construct	This study
OsNRPD1b_Prom_F	2191	gagagtaaccaacacagaacagggtggccttg	OsNRPD1b complementation construct	This study
OsNRPD1_Prom_R	2185	cctgaacaataaacacgactagaaaacattaacatacatac aagtacc	OsNRPD1b complementation construct	This study
qPCR_NRPD1a&b_F	1769	ttgcaagtattgctcaaaggatgg	RT-qPCR and RT-PCR	This study
qPCR_NRPD1a&b_R	1770	ccaccagcaactctcgataattg	RT-PCR	This study
qPCR_NRPD1b_R	3623	cccaccagcaactctgcg	RT-qPCR	This study
qPCR_NRPD1a_R	3622	cttgacttatgtgccaccccg	RT-qPCR	This study
Tos17_TP_RT_F	2061	caccaggtgtggaagctccac	RT-qPCR and RT-PCR	(Nosaka et al. 2012)
Tos17_TP_RT_F	2062	taccactgagctgaagcgtgc	RT-qPCR and RT-PCR	(Nosaka et al. 2012)
HygR_F	415	aaagcctgaactcaccgc	RT-PCR and Southern probe	This study
HygR_R	416	ggttccactactcggcga	RT-PCR and Southern probe	This study
BlpR_F	340	tcaaatctcggtagcggcag	RT-PCR	This study
BlpR_R	341	atgagcccagaacgacgc	RT-PCR	This study

OsActin1_F	1786	gctatgtacgtcgccatccagg	RT-qPCR and RT-PCR	This study
OsActin1_R	1787	tgagatcacgcccagcaagg	RT-qPCR and RT-PCR	This study
rRNA S7A and S7B (Region marked as 1)	3478 and 3479	tgtttggtcagggtcacgacaatgatcct and gcggtctgtttggtcagggtcacg	mRNA northern	(Hang et al. 2018)
rRNA p23 (Region marked as 2)	3476	gctgctcatagcctacgcagccac	mRNA northern	(Hang et al. 2018)
rRNA p42 (Region marked as 3)	3480	gcctcgcgcgcgagcgcctcggcgggcaggggtga	mRNA northern	(Hang et al. 2018)
rRNA p22 (Region marked as 4)	3477	ctgtcgtcttccgagagcatct	mRNA northern	(Hang et al. 2018)
rRNA p4 (Region marked as 5)	3481	cggtggatttaactcgtggtatc	mRNA northern	(Hang et al. 2018)
SB_probe_Ubi_P_F	2282	ctgcagtcagcgtgacccggctg	Southern probe	This study
SB_probe_Ubi_P_R	2283	ctgcagaagtaacaccaaacaacag	Southern probe	This study
SB_probe_LINE-1_F	2344	tctctggacgagcctgttccaa	Southern probe	(Cui et al. 2013)
SB_probe_LINE-1_R	2345	ggctaagtcgtcagttgaatgc	Southern probe	(Cui et al. 2013)
Linear_UBCE2_F	2943	cctcggagacacctttgaagg	ECC DNA analyses	This study
Linear_UBCE2_R	2944	gtacgcagagaaggcaatgcag	ECC DNA analyses	This study
Linear_Tos17_F	2229	gctacccttcttgactat	ECC DNA analyses	This study
Linear_Tos17_R	2230	ctgaaatcggagcactgaca	ECC DNA analyses	This study
Circular_Tos17_F	2955	aactcgagagcatcatcggttaca	ECC DNA analyses	(Lanciano et al. 2017)
Circular_Tos17_R	2966	cattagctgtatgaacggtggcac	ECC DNA analyses	(Lanciano et al. 2017)
Circular_PopRice_F	2953	acaactcgtctcctaactgtcct	ECC DNA analyses	(Lanciano et al. 2017)
Circular_PopRice_R	2954	gcagctataaatatgtatccaatcct	ECC DNA analyses	(Lanciano et al. 2017)
Linear_PopRice_F	2951	gttatttctcgtcgtcgtcgac	ECC DNA analyses	(Lanciano et al. 2017)
Linear_PopRice_R	2952	gtgccgagaagatcctccatc	ECC DNA analyses	(Lanciano et al. 2017)
miRNA168	32	gtgccgagaagatcctccatc	sRNA northern	This study
U6_probes	13 and 14	ggccatgctaactctctgtatcggt and ccaattttatcggatgtccccgaaggac	sRNA northern	This study

amiR_PollV_probe	1697	atgtccaagagtaaacactata	sRNA northern	This study
miRNA444	245	aagcttgaggcagcaactgca	sRNA northern	This study
miRNA156	3094	gtgctcactctctgtgtaa	sRNA northern	This study
MITE siRNA	3430	ggccccacctgcatacacact	sRNA northern	This study
Tos17 siRNA	2091	ggcctcataccaaccgatat	sRNA northern	This study
miRNA815	3345	cccaatctcctaaccctt	sRNA northern	(Zhang et al. 2016)
miRNA397	511	ggttcatcaacgctgactcaa	sRNA northern	(Swetha et al. 2018)
miRNA820	3343	cctggccatccacgaggccga	sRNA northern	(Nosaka et al. 2012)
CACTA siRNA	2086	acgtcaatacaatctcgccgct	sRNA northern	This study
OsPollV suppressed locus1	3318	gctgacagaagagaagtgagc	sRNA northern	This study
OsPollV suppressed locus2	3319	tatagtgtactctggact	sRNA northern	This study
miRNA845	3344	ccgacaattggtatcagagca	sRNA northern	This study
Simplehat	3676	tgggtaccattttgacacccta	sRNA northern	(Mosher et al. 2009)
AtRep2	3677	gcgggacgggttggcaggacgtactaat	sRNA northern	(Mosher et al. 2009)
miR158	3620	tgcttctacatttggga	sRNA northern	This study
AtPollV suppressed locus 1	3736	attgtctaccgcatcattcatt	sRNA northern	This study

- Cui X, Jin P, Cui X, Gu L, Lu Z, Xue Y, Wei L, Qi J, Song X, Luo M, et al. 2013. Control of transposon activity by a histone H3K4 demethylase in rice. *Proc Natl Acad Sci U S A* **110**: 1953–1958.
- Hang R, Wang Z, Deng X, Liu C, Yan B, Yang C, Song X, Mo B, Cao X. 2018. Ribosomal RNA biogenesis and its response to chilling stress in *Oryza sativa*. *Plant Physiol* **177**: 381–397.
- Lanciano S, Carpentier M-C, Llauro C, Jobet E, Robakowska-Hyzorek D, Lasserre E, Ghesquière A, Panaud O, Mirouze M. 2017. Sequencing the extrachromosomal circular mobilome reveals retrotransposon activity in plants. *PLoS Genet* **13**: e1006630.
- Mosher RA, Melnyk CW, Kelly KA, Dunn RM, Studholme DJ, Baulcombe DC. 2009. Uniparental expression of PolIV-dependent siRNAs in developing endosperm of *Arabidopsis*. *Nature* **460**: 283–286.
- Nosaka M, Itoh J-I, Nagato Y, Ono A, Ishiwata A, Sato Y. 2012. Role of transposon-derived small RNAs in the interplay between genomes and parasitic DNA in rice. *PLoS Genet* **8**: e1002953.
- Swetha C, Basu D, Pachamuthu K, Tirumalai V, Nair A, Prasad M, Shivaprasad PV. 2018. Major domestication-related phenotypes in Indica rice are due to loss of miRNA-mediated laccase silencing. *Plant Cell* **30**: 2649–2662.
- Zhang H, Tao Z, Hong H, Chen Z, Wu C, Li X, Xiao J, Wang S. 2016. Transposon-derived small RNA is responsible for modified function of WRKY45 locus. *Nat Plants* **2**: 16016.