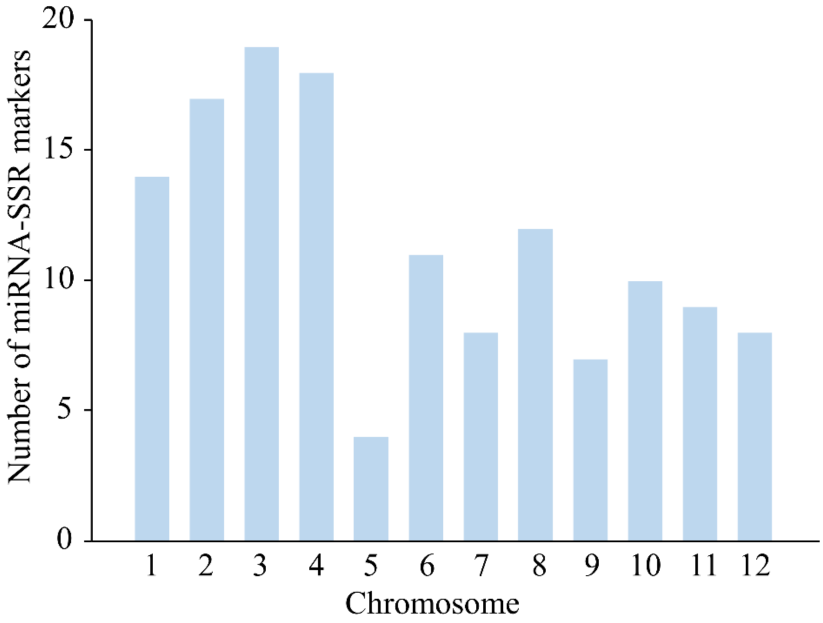

Fig. S1. Distribution of the salt stress-responsive miRNA-SSR markers across the 12 chromosomes.

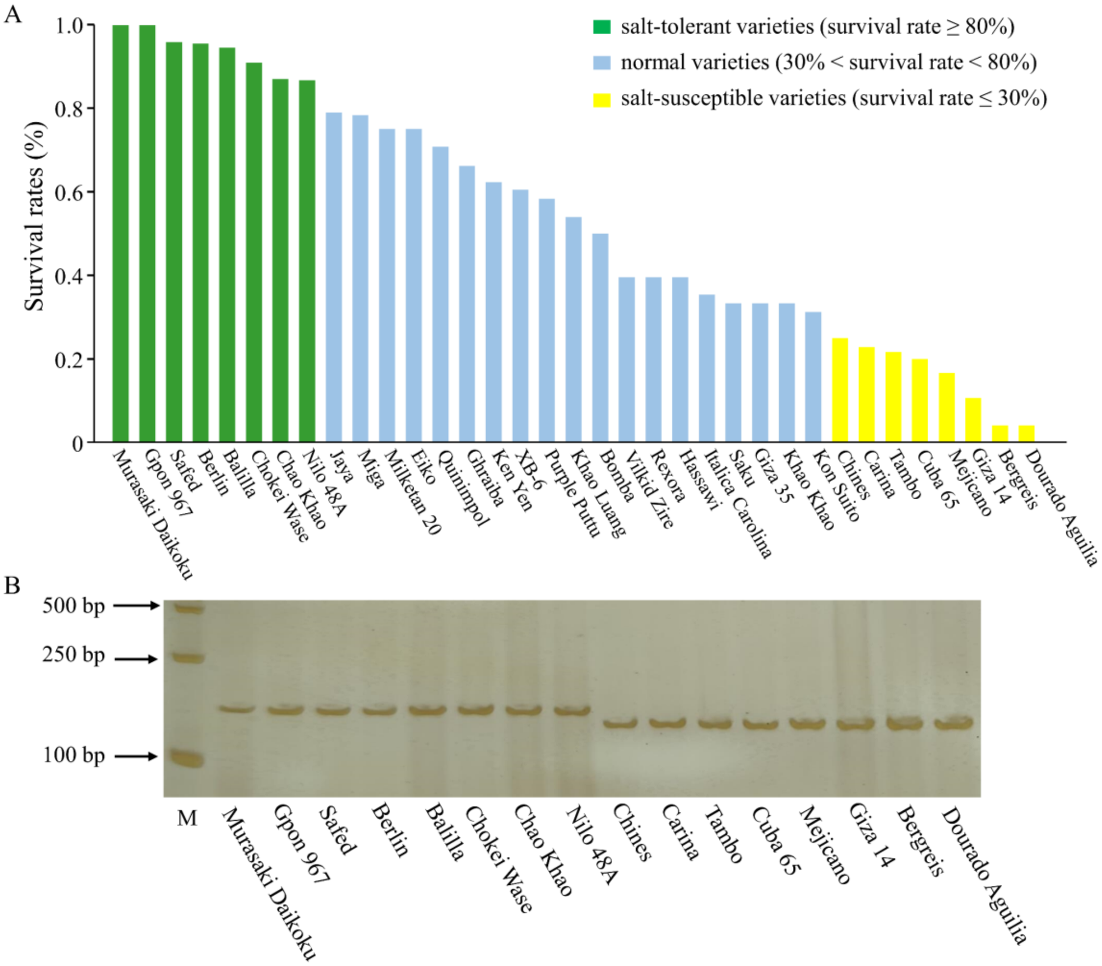

Fig. S2. The marker miR162a-SSR is a promising diagnostic tool for distinguishing salt stress-tolerant rice varieties from susceptible ones based on specific alleles. (a) Survival rates of the salt stress-treated rice plants after recovery. (b) Amplification profiles of the miR162a-SSR marker in salt stress-tolerant and susceptible rice varieties. M: DL 2000 marker.

Table S1. The rice materials used in this study

No.	Name	Origin
1	Dourado Aguilia	Costa Rica
2	Bergreis	Austria
3	Giza 14	Egypt
4	Mejicano	Peru
5	Cuba 65	Cuba
6	Tambo	Peru
7	Carina	Bulgaria
8	Chines	Portugal
9	Kon Suito	Mongolia
10	Khao Khao	Thailand
11	Saku	Mongolia
12	Giza 35	Egypt
13	Italica Carolina	Poland
14	Rexora	Mozambique
15	Hassawi	Saudi Arabia
16	Vilkid Zire	Azerbaijan
17	Bomba	Spain
18	Khao Luang	Laos
19	Purple Puttu	India
20	XB-6	Australia
21	Ken Yen	China
22	Ghraiba	Iraq
23	Quinimpol	Philippines
24	Milketan 20	Philippines
25	Eiko	France
26	Miga	Brazil
27	Jaya	India
28	Nilo 48A	El Salvador
29	Chao Khao	Laos
30	Chokei Wase	Japan
31	Balilla	Italy
32	Berlin	Costa Rica
33	Safed	India
34	Gpon 967	Guatemala
35	Murasaki Daikoku	Japan
36	Dongxiang wild rice 159 (Dongtangshang population)	China
37	Dongxiang wild rice 44 (Kanxialong population)	China
38	Dongxiang wild rice 80 (Zhangtang population)	China

Table S2. The detailed information of the miRNA-SSR markers developed from the salt stress-responsive miRNAs in Dongxiang wild rice

Markers’ name	Motif repeat	Primer-F (5’-3’)	Primer-R (5’-3’)	Chr.
miR6300_1ss18GC-SSR	(CA)3	ACCAAAGCAGAGATGAGAAA	TTACGGCTTTACCTGTGAGT	1
miR156a-p3-SSR	(TC)4	AGAGTGAGCACACGTGGTTG	TCAGGAATTACGAAGGGTGT	1
miR159a-p5-SSR	(GTG)4	CACAGCAACTCATCTGTCGAG	CGAATCTTCACAAGGGGTTC	1
miR167j-p3-SSR	(AT)4	TCGTGCTCACAAGACTACAA	TATATCTGCACCAGGACACC	1
miR169a-p3-SSR	(CTT)4	AGAAGGAAGGATCAGAGCAC	CCGGCTAGCTGCTTAATTTC	1
miR1846d-5p-SSR	(CGC)5	GATCTTACCGTCCATGTGTC	GGCCTACTCACTGGGAGAT	1
miR5083-p3_1ss20GA-SSR	(TA)3	CCAATATAACGAGTCCGGTA	AATGCAACAGTTGAAACCTC	1
miR5144-p5-SSR	(CCG)4	ATTGAAGGTCTCGGTCTTCT	TCAGATTCAGACTCTTGGTTG	1
miR5540-SSR	(GAC)3	AGCTTAGCTTAGCCGTGTG	GGCAGTAGTGAACCCATAAA	1
miR5802_1ss11CT-SSR	(TA)3	CGAGATCTTAGTCGGTTACG	AGGTTCAGGCCTTCTTATTC	1
PC-3p-118603_12-SSR	(CG)3	GAATCCGTGTGAGGGTTG	TTTTCCCTCTTTCTCTCCTC	1
PC-3p-6597_665-SSR	(TA)3	CTAGCACCCAAACAAAATCA	GATGACATAAGGGGTAGCAA	1
PC-3p-76359_30-SSR	(TA)4	CAAGCACATTCTCCCTACAT	CCCCCAACCTGAATATTACT	1
PC-5p-81638_26-SSR	(CT)3	GTTGGGACATTACTCACCAG	ATATGTGGTTTTCTGCAACG	1
miR444a_L-1R+1_1ss17GA-SSR	(TCA)3	TAGTGCTCCAGTAGCTTGGT	ATGGCCAGTCCATAATACAG	2
miR6300-p5_1ss6AG-SSR	(CGG)3	GAATTTTGGTCGGGTACATA	CTAATCTTTGTTGGCATTGG	2
miR162a-SSR	(CTCCC)3	CCAAATCCTACTCGTGTTGT	ATCTGGGGGATTTTATATGC	2
miR164d-p3-SSR	(ATGG)4	ATTAGAGTGGGGGCTTGA	CTTGTAGGACCTCGTTTCTG	2
miR166h-5p-SSR	(GT)5	GCTCGAGGTATCCACATCT	CAAACCCCTTAACCTAATCC	2
miR166k-3p-SSR	(GCT)3	CGCATCCTTCTCCTTTCTTG	GCCGGAGAGGAATTAAGATGT	2
miR167e-3p-SSR	(AGT)4	GAGGGACCATGTATGTATGC	TACACACAGGAAGGAGAAGG	2
osa-miR172d-5p_R+1-SSR	(AT)6	TCTGTTTGGCGTATGTGGTT	AATGGAGCTAGAGGGAGATCG	2

miR2106_R+1-SSR	(ATT)3	ATTCGATCTGAATGTCCTTG	CTACCAGACGAGCATAACATC	2
miR2122-p3_2ss8CT20TG-SSR	(CGA)6	TTTCGTCAGCACCATCTT	ATGAGCATGAGGAGGAGAG	2
miR2865-p3_2ss16AC19AT-SSR	(AGT)3	GGAAAATTACTGCTGCTTGA	GACTCGACGACATATCAGGT	2
miR396a-3p_R+1-SSR	(CTT)3	CATGCATGCACTGTTGTGAG	TTGGGGAAATACTGTGTTGG	2
miR827-SSR	(GT)4	CTCCGCCTTAAGAAGAAGCA	CACGCATAAACACGGAATTG	2
miR9777_1ss7CT-SSR	(CGC)6	GGCCCATCACTAATTAAACA	AACATCAATCAGACCAGCAG	2
PC-3p-24288_182-SSR	(TG)4	GCTGTGTTTAGTTCCACACC	CACATTTGATGCTCCATACA	2
PC-5p-57749_50-SSR	(AATAGA)3	GTTTCACTCCTGTAAGAAACTCTTG	GTGCGATATGTTGGGAATAG	2
PC-5p-63767_42-SSR	(AT)3	TGCAGTACTCCCTCTGTCC	ATGATCTGAGGACAAGCAAC	2
miR169c-p3_2ss12GC17TG-SSR	(GA)4	AGGAAGTTGGTGAACTGATG	TCATAGGGTCTTTCTGTCCA	3
miR5368-p3_1ss17CA-SSR	(GA)4	CGAAATTCCTTGTCGGGTAA	CCAATCCCAGGGAACAGTAA	3
miR6300_R+5-SSR	(TGT)3	TGTCTGGACTGAAGGCTCTA	ACAAAGCACAGCTCTCAAGT	3
mtr-miR166a_L+1R-1_1ss21CT-SSR	(TCAT)3	GACATAAAGCTGCTCAAAGC	AGACAACATTCCCCTCAACT	3
miR164e-SSR	(AT)3	CGATTACATCCTATTCTGGTTG	TCCATGTAGCGAGTTGTTGC	3
miR166i-5p-SSR	(TA)5	GCGTTAGCTTTGCCTTTTGT	CAAACTGCATTCCAAACACC	3
miR166j-5p-SSR	(CTCC)3	GGTAGGCAGGTAGGCAGATG	CGAAGCACGAAAAGCAAGTA	3
miR167b-p3-SSR	(CCT)7	ATGGCCGCGATAAACTAC	ATTCGATCGACATTGACACT	3
miR169r-3p-SSR	(CCA)3	ACACCAACAATGAGGTAAGC	GTTTTCAGCCGAAGTGTAAC	3
miR171e-5p-SSR	(CGA)3	CGTGCCAATATCTTAGTGCT	CAAGAACTCCATAGCCCATA	3
miR171f-p5-SSR	(GATC)4	CAGATGACAGATGACAAACG	CGTAAGGGAAGAAGAAGTAGG	3
miR171i-5p-SSR	(CT)4	TAATCCCCAAACATCGCTTT	CATCAAACCAAAGCAGCAAA	3
miR390-5p-SSR	(GA)7	CTCCCCCATACCTCAAGAAA	CAGTGGTGCCTCTTGCTCTA	3
miR435-SSR	(TC)3	CCCTAAGAAAGGGAAATGTT	AAGATGAGGGACATGTTTTG	3
miR821a-p5_1ss3AC-SSR	(TA)3	GGTGACGGGCTTTAGTTAAT	CAAATGACCATCATCTGTGA	3
miR6478_1ss21GA-SSR	(TC)3	CTGGGTCCATGTGTTGTTA	TCGAAAATGATGGTGGTC	3
miR6478_R+4_1ss21GA-SSR	(CT)4	TGATGATGATGTGGCTCTCTCT	GCCATTGGATTAAAAGGGTTC	3

PC-5p-24732_177-SSR	(TA)4	GCAAAAATACCACTGCACA	TTTTCCTCCCACATATAGCA	3
PC-5p-54266_56-SSR	(TA)4	TTTTCCTCCCACATATAGCA	GCAAAAATACCACTGCACA	3
miR169f-p3-SSR	(TTGG)3	CCATTTTAGGGATGTGATGA	AATAGGAACAGGCGAACAG	4
miR169h-p5_2ss8CT18TC-SSR	(AT)3	TGTTACCCTCACCTTTCAAC	ATGAAAATATGGCCTGCTC	4
miR1423-5p_L-2R+2-SSR	(AGG)3	ACACAACGATTTGGAAGAAG	CCAGTATCAAGCAGAAAGGA	4
miR162b-SSR	(TC)5	ATTGCTGTTTCTGTTGCTCT	CGATTCCTGCGTTGTATATT	4
miR169g-p3-SSR	(AT)3	TGTTACCCTCACCTTTCAAC	ATGAAAATATGGCCTGCTC	4
miR171c-5p-SSR	(TCT)9	GGCTCCTCCTCCTATATGTC	ATGCAGAAGCAGAAGTGAAG	4
miR1849-p3_2ss18TA23CT-SSR	(AT)4	GAACAGTTGCCCTGATGTGA	TTGTTCAGCTCCAGTGATGG	4
miR2877-SSR	(GA)3	CCACTTTTCATCCACAAAGA	AGCAAGGTTAGCAGACAAGA	4
miR399j_R-1-SSR	(CT)4	TCTACCTGCTTTGTTCCCTA	TAGCCTTAAGCTGAGTCCAG	4
miR444b.1-SSR	(TCA)3	CAATCAGGTGCTGGAAGTAT	CAAGAAAATCATCGGTATGG	4
miR5150-3p_L-1R+1-SSR	(TCC)3	CTTCGATTAGCTTCAGCAAG	TGTTGAGTTGGCTAAATTGG	4
miR5542-p3_1ss17AG-SSR	(ATG)3	CGTCCAATCGAGCTTAACTA	CTCATCCTAATCGCTGAGAC	4
miR10521-p5_1ss4AG-SSR	(TA)4	GCTGTCACGTTAGGCTTGTG	ACGTGGGGAGTACTCTCGTT	4
miR9774-p5_1ss22AT-SSR	(CTT)3	AACCACTGAAAACGAATCTG	ACCTAAAGCAGTGAACCAAA	4
PC-3p-100468_17-SSR	(TG)3	CCACCCTTATCTCAGTGGTA	AGGATACATACCCATGACACTT	4
PC-3p-129422_10-SSR	(TC)4	TCGGGGGTGATTCATACTTC	AGCGTATGCAGATGGTTCAA	4
PC-5p-60444_47-SSR	(TAA)3	GGTGCAACTTTCATGTGATT	GATTCGTTGTCCTACGATGT	4
PC-5p-86609_24-SSR	(TC)6	TACATTGCCTCGTTTTTCTC	ATTCAGTTGATTCCTGATCG	4
miR6300_R+4-SSR	(TA)3	CCTGGCCTAGTTTAGTGTTG	CGACCATAGCATTTGTACCT	5
miR164f-p3-SSR	(CTT)5	CTCACTCACTCGGTCACTCG	TGGCTGTCTCGTTTCATCAC	5
miR1850.1-SSR	(TG)4	GCGTGAACTGATCTTGCTGT	GTTGGGAATTTGGAGGAAGA	5
PC-3p-31535_128-SSR	(CA)5	TGCAACGGATGGAGTATCTAA	CGTGCTACGAGTATTCAAAAG	5
miR8175_L-1-SSR	(AG)3	ATTTCACCCGAGAGTATTCC	GCTTGTGTGTCACTCTACCC	6
miR6300_R+1-SSR	(AC)3	CAGCTGAAGACCAGCATAAG	AGTATGTGGTATGCCAGGAG	6

miR1870-p5-SSR	(AT)3	CGTTAGAAAAGTCAACGGTGT	TGCCCACTAGGTCTAATTCA	6
miR399d-SSR	(TA)5	TAGTAGGCAGCTCTCCTCTG	GGTGAATTCAATCGCTACAT	6
miR444f-SSR	(AT)3	TACGTACCATGTCCATTCCT	AGGAGAATGAAGATCCCAAA	6
miR5072_L-4-SSR	(TC)3	TTCTTTTTCGGTCACCCTGT	CACGGCAAGAAAATTTGGAT	6
miR6476a-p3_2ss6AG18AC-SSR	(TC)3	TGTGAAGCCATATAGGCAAT	TTTGGTAAACAGACCAAAGC	6
miR10520-p3_1ss6TC-SSR	(CGC)4	TTGTGACGTGCTTACACAAT	GAAGCCATTGGTTTGGTC	6
miR9779-p3_2ss14TC18GC-SSR	(TG)3	CTATCCTTCCGCATGTTAAG	ATCAAAATGGACGGTGAGTA	6
PC-3p-38283_97-SSR	(TA)3	CTACTTCCTCGTCCTCTGTG	ATTCAAGCCAACACTCATTC	6
PC-5p-16439_287-SSR	(TCC)3	GTTCCCTCTCAATAGGTTCC	AAATCCCGGTCTCTTATTGT	6
miR5054-SSR	(TTG)3	GTCACTTGCGGATGGACT	ATGCGACAGAACATGACAC	7
miR164a-p3-SSR	(TCA)3	TTTCTCAGCAGGGTGAGTGT	AACTTCCAACCCACACAAGG	7
miR167d-3p-SSR	(TA)5	CAATGGGACCACCACATTAG	TGGCTCCAAATTACTCTGACC	7
miR171g-p3-SSR	(AT)4	GTTGACCCAGAGTATGTTGTATAAG	GAAACACGTCGAACTGACTG	7
miR820a_R+1-SSR	(AT)4	CGCAATTGCAGTATGAAAG	ACGGCACTTAGTTTTGACC	7
miR821b-p3-SSR	(TTCAAA)3	CCATCACTTTGTCGTATGAAGA	ATCACTGAACGACTTCAACTG	7
miR10516_L+3R+3-SSR	(AT)4	GACCTAAGTCCCTCCTAGACA	CTGCAGAGGATCTTAATCCA	7
PC-5p-72419_34-SSR	(CT)3	TCATATTCCGAAATCTGTCC	CTGCTTCCATGTCCATATCT	7
miR8175_L+1_1ss3AT-SSR	(AC)3	CGTGGAATTTCTTGACAGAC	TGGTAGTATCGGTGAAAACC	8
miR160c-3p-SSR	(AT)4	TTGAGGGAGGTTCGTAAAGC	CCCAAAAGAATAGTCCAAATCC	8
miR160f-3p-SSR	(ACG)3	GGTAGGAGATGGGATTAACG	AGCAAAGCGTCTTGAATAAG	8
miR166m-SSR	(TTCT)4	GTCTTGCCTTGCAGCTATT	CTTGAACCAGACAACAAACC	8
miR169h-p3-SSR	(AT)4	AGGTCGAGCGATCTTGTGTT	CTAGCTAGCTGCCCCTCTCA	8
miR169l-p3-SSR	(TA)4	GAGGCCCTACATAGACACAA	CATGTAAGGCTGCTTCTCTC	8
miR169m-p3-SSR	(TA)5	CAAGGATGACTTGCCTGTAT	CGATCGAGCTCAGATTAAGA	8
miR171b-SSR	(TA)26	GATGTTTCTTTCATGCAGGT	ATTCCATGCTTGCTAAACAG	8
miR2874-SSR	(TG)4	GTCTCCGCAATATACTCAGC	ACGACACGCTTAACACAGTT	8

miR821c-p5_1ss3AC-SSR	(TA)3	GGTGTCGGGCTTTAGTTAAT	CGTGACGTGCACTAACTTG	8
miR6478_R+2_1ss21GA-SSR	(TA)4	TTTGTATTTCTAGGCGCAAG	TGGTCATTGGGTACTGATTT	8
miR3630-p3_2ss19AT20CT-SSR	(TTG)4	ACACACGCATCTCTCTTTTT	GATCTGATGTCCCTGTCTTG	8
miR166l-p5-SSR	(TCC)3	TACGAAGATGGCCAAAAACC	TGCTGCAAATGGGACTTTTA	9
miR169j-p3-SSR	(CT)4	TGATCGGGACATTCTCGTTA	CTGTTCGTCTTCGTCCACAG	9
miR1846e-p5_1ss15AG-SSR	(CCA)3	TCGGGATGTAGAGACTGAGA	GTAGTAACGAGGGCGGTAG	9
miR1878-SSR	(AGC)3	ATGTAATAGGGTCCCTCCAC	GTCCAGATTAAGTCTGCAGTG	9
miR6251-SSR	(TC)3	AATGTTCCACCTCACAAAAG	ATTGAGGGCTCAGACAATC	9
miR6478_2ss20TC21GA-SSR	(TA)5	GCTTCGATTATGACTTTGCTG	AAACTACAGTCCTCCGCTCT	9
PC-5p-88433_23-SSR	(TG)3	TAGCTAGCGAGCAAATGAAT	GTTTGCTGCATGGTTGAT	9
miR166c_R-2_2ss17CT19CT-SSR	(AG)4	GCACTCCTTGACACAATTGC	TGCTGCAATGCTTTTCCACA	10
miR166a-3p-SSR	(TTC)3	GCATGTGTAAGGCTGTGGAA	ATCTCAGGCCAGACGACATT	10
miR166a-5p-SSR	(TC)4	TTGGTGTAATGATGGCTTGC	AGCAGGGAAAAGAACACCTG	10
miR171d-5p-SSR	(TTC)7	AAGGAATCACGTAGCAGAGA	GACCAAGCTCTGAAGAACAA	10
miR1862c-p5-SSR	(AAT)3	GTAGTAAGATTGTACCCCGAAA	AGCCCAACACTCACTCTTTA	10
miR1876-SSR	(CT)3	TGGCACTTCCTAGTCCTGTA	TCCATCCCAAGGTGTAACTA	10
miR5504_R-3-SSR	(TA)3	GGCTGGCATTACTTATCTGA	ACCTCTACATCCAACAATGC	10
miR5526-p3_2ss16TG17AG-SSR	(TTTC)3	TCAGGTATGAGCTCTACGTTATC	GTTGCCATGCCAGTATATTT	10
PC-3p-71127_35-SSR	(AT)3	CTTCTGCAGTTCTGCTCTGT	GCCACTAACCAAGGTGATCT	10
PC-5p-93370_20-SSR	(CT)7	ACATGTCAATGTCAGTGTGG	CCTCTCCGCTAGTCTACTCC	10
miR5054_1ss10TA-SSR	(CTG)3	CTCATGGGTGTTTTCTCTGT	CTGTGCCAGTACGCTATACA	11
miR169n-SSR	(GA)8	ACTTCCTTTCTGGCTTATCC	CCATGGCAGATAGATAGACG	11
miR3979-3p-SSR	(AT)5	TTGGAGTGCAGTCAAGAAAT	ATTTTACCTGCGGACTTGTA	11
miR5159-SSR	(GT)3	ACGGGTACCCACAGAGTAAT	TCTATCAGTGGCATACACACA	11
miR810a-p3_1ss17CT-SSR	(TA)4	ACAGAGGATGGCTCGTGAGT	CTGTGGTCGTCATCGTAAGC	11
miR810a-p5_1ss17CT-SSR	(TA)4	CTGGAAGAGCAGTACTCCAA	GCTCGCATGCTTAAATAACT	11

miR812r-p3-SSR	(CAGC)3	CCCTCATCGTCGTGTTACCT	CGAGCTGAGCTAATGATGGA	11
PC-5p-84508_25-SSR	(AT)4	GATTCCATGCGAAATTTGTG	TTGGACACGAAAATCCAGAG	11
PC-5p-92202_21-SSR	(TTG)4	GCACGGATTGTTCCTACTC	TGTCATTGGTGTTGTGCTAA	11
miR8175_L-2_1ss20AT-SSR	(AT)3	CCTGAAATGCTTGTTGGTAT	CCCCTGCTTAGACTATGGTT	12
miR11343-p3-SSR	(CAG)3	TGTACAGAGGGGAGAACTGA	AAGGTTCAACATGGAGAGG	12
miR1430-p3-SSR	(AT)3	CTGGCTAAGCTAGGATTTTGT	CAGCTAGTGTGCACCAAGTA	12
miR1441-p5_2ss19TC24TC-SSR	(TA)3	CTCATGAACCAGCTCAGAAT	ACAGTGCTAGAACACCCAAC	12
miR167h-3p-SSR	(TGA)5	AATTATTCGCCCATCTCTCT	CTGATCGATTGATCCGTAAT	12
miR5510-p3-SSR	(TG)3	TCTTTCTGAACTCCCAAATG	AACATTCTCCCACTTGATTG	12
miR6254-SSR	(AT)3	GAACGAGTTAGTGCTTCACC	ACAATTGCTGCCATCTTTAG	12
PC-5p-68044_38-SSR	(CA)4	ACGGGGAATCATCTAGTTTT	TCGATAGTGTGGTTTTGTGA	12

Table S3. Distribution and description of genes in the pre-miRNAs and their flanking regions

miRNAs	Chr.	Position	Gene distribution in the pre-miRNAs and their flanking regions	Gene description
miR166c_R-2_2ss17CT19CT	10	14483242-14483336	-	-
miR8175_L+1_1ss3AT	8	12033214-12033362	*LOC_Os08g20070*	expressed protein
miR8175_L-1	6	15949233-15949280	*LOC_Os06g28080*	retrotransposon protein, putative, unclassified
miR8175_L-2_1ss20AT	12	4279471-4279562	*LOC_Os12g08420*	retrotransposon protein, putative, unclassified, expressed
miR169f-p3	4	30712390-30712562	*Os04g0607250*	Non-protein coding transcript
miR169h-p5_2ss8CT18TC	4	19420064-19420202	*Os04g0394766* *Os04g0394733*	Non-protein coding transcript
miR444a_L-1R+1_1ss17GA	2	30461212-30461265	*Os02g0731200* *Os02g0731300*	*OsMADS57*, MADS-box transcription factor; Non-protein coding transcript
miR5054	7	4637518-4637623	*LOC_Os07g08920*	retrotransposon protein, putative, unclassified, expressed
miR5054_1ss10TA	1	31151105-31151141	*LOC_Os11g44770*	retrotransposon protein, putative, unclassified, expressed
miR169c-p3_2ss12GC17TG	4	9100508-9100638	-	-
miR5368-p3_1ss17CA	3	31813892-31814060	-	-
miR6300_1ss18GC	1	30735144-30735285	*Os01g0736750*	Non-protein coding transcript. (*Os01t0736750-00*)
miR6300_R+1	6	702340-702432	*LOC_Os06g02240* *Os06g0112550*	*PIBP2*, RNA recognition motif containing protein; Non-protein coding transcript. (*Os06t0112550-00*)
miR6300_R+4	5	24723725-24723876	*Os05g0502150*	Non-protein coding transcript. (*Os05t0502150-00*)
miR6300_R+5	3	22380289-22380344	*Os03g0599700* *Os03g0599600*	Non-protein coding transcript. (*Os03t0599700-00*); Regulator of omosome condensation, RCC1 domain containing protein. (*Os03t0599600-01*)

miR6300-p5_1ss6AG	2	3623224-3623302	*Os02g0167400* *Os02g0167300*	Non-protein coding transcript. (*Os02t0167400-00*); Tubulin beta-3 chain (Beta-3 tubulin). (*Os02t0167300-01*); Similar to tubulin beta-5 chain. (*Os02t0167300-02*);
miR166a_L+1R-1_1ss21CT	3	3487786-3487914	*Os03g0164901*	Hypothetical gene. (*Os03t0164901-00*)
miR11343-p3	12	16169048-16169184	*Os12g0460400*	Hypothetical conserved gene. (*Os12t0460400-00*)
miR1423-5p_L-2R+2	4	19715117-19715252	*Os04g0399000*	Similar to ribosomal protein S27. (*Os04t0399000-00*)
miR1430-p3	12	6825011-6825152	-	-
miR1441-p5_2ss19TC24TC	12	19485741-19485920	-	-
miR156a-p3	1	22524147-22524246	-	-
miR159a-p5	1	17681923-17682194	*Os01g0507000*	Non-protein coding transcript. (*Os01t0507000-01*), Conserved hypothetical protein. (*Os01t0507000-02*)
miR160c-3p	8	1707568-1707666	*Os08g0130250*	Non-protein coding transcript. (*Os08t0130250-01*)
miR160f-3p	8	24396882-24396981	*Os08g0494200*	Conserved hypothetical protein. (*Os08t0494200-01*)
miR162a	2	23605799-23605969	*Os02g0602900*	Conserved hypothetical protein. (*Os02t0602900-01)*
miR162b	4	24405899-24406032	*Os04g0488650*	Primary microRNA of miR162b; Target gene(s): *OsTRE1* (*Os10g0521000*), Resistance to drought stress (*Os04t0488650-01*)
miR164a-p3	7	28523341-28523496	-	-
miR164d-p3	2	33143567-33143660	-	-
miR164e	3	10542157-10542288	-	-
miR164f-p3	5	23343908-23344117	-	-
miR166a-3p	10	14483290-14483396	-	-
miR166a-5p	10	19987135-19987279	*Os10g0517050*	Hypothetical conserved gene. (*Os10t0517050-01*);
miR166h-5p	2	32435174-32435292	*Os02g0769250*	Non-protein coding transcript. (*Os02t0769250-00*);
miR166i-5p	3	25294953-25295097	*Os03g0651201*	Hypothetical protein. (*Os03t0651201-01*)
miR166j-5p	3	30392782-30392881	*LOC_Os03g52990*	hypothetical protein
miR166k-3p	2	32435003-32435129	-	-

miR166l-p5	9	16951817-16951933	*LOC_Os09g27870*	hypothetical protein
miR166m	8	23045356-23045555	-	-
miR167b-p3	3	30546928-30547090	-	-
miR167d-3p	7	4166295-4166404	-	-
miR167e-3p	2	3742241-3742513	*LOC_Os02g07300*	hypothetical protein;
			Os02g0169275	Non-protein coding transcript. (*Os02t0169275-00*)
miR167h-3p	12	25480618-25480737	*Os12g0604000*	Non-protein coding transcript. (*Os12t0604000-02*)
miR167j-p3	1	32686068-32686227	*Os01g0773350*	Non-protein coding transcript. (*Os01t0773350-01*)
miR169a-p3	1	8729104-8729276	*Os01g0259966*	Non-protein coding transcript. (*Os01t0259966-00*)
miR169g-p3	4	19420077-19420202	*Os04g0394766*	Non-protein coding transcript. (*Os04t0394766-00*);
			Os04g0394733	Non-protein coding transcript. (*Os04t0394733-00*)
miR169h-p3	8	26807349-26807470	*Os08g0536350*	Non-protein coding transcript. (*Os08t0536350-01*)
miR169j-p3	9	19788861-19788985	*Os09g0509800*	Non-protein coding transcript. (*Os09t0509800-00*)
miR169l-p3	8	26817488-26817595	*Os08g0536366*	Non-protein coding transcript. (*Os08t0536366-00*);
			Os08g0536383	Non-protein coding transcript. (*Os08t0536383-00*)
miR169m-p3	8	26813897-26814034	*Os08g0536358*	Non-protein coding transcript. (*Os08t0536358-00*)
miR169n	11	6081528-6081700	-	-
miR169r-3p	3	35782416-35782544	-	-
miR171b	8	5369153-5369252	-	-
miR171c-5p	4	31713472-31713570	*Os04g0623901*	Primary microRNA of osa-miR171c
miR171d-5p	10	21237313-21237447	-	
miR171e-5p	3	1970487-1970605	*Os03g0135550*	Hypothetical gene. (*Os03t0135550-01*);
			Os03g0135600	ankyrin repeat domain containing protein, expressed
miR171f-p5	3	30027774-30027900	*Os03g0733200*	Non-protein coding transcript. (*Os03t0733200-00*);
			LOC_Os03g52284	expressed protein
miR171g-p3	7	15636744-15636832	*Os07g0452950*	Hypothetical conserved gene. (*Os07t0452950-01*)

miR171i-5p	3	21191603-21191722	*LOC_Os03g38170*	expressed protein
miR172d-5p_R+1	2	35143537-35143666	-	-
miR1846d-5p	1	39637065-39637180	-	-
miR1846e-p5_1ss15AG	9	13211437-13211505	*Os09g0386800* *Os09g0387150*	*OsFBX327*-F-box domain containing protein, expressed;
miR1849-p3_2ss18TA23CT	4	22224813-22224902	*Os04g0445800*	LSM domain containing protein, expressed
miR1850.1	5	26275207-26275339	*Os05g0528701*	Non-protein coding transcript. (*Os05t0528701-01*)
miR1862c-p5	10	16093884-16093972	*Os10g0445500*	nicotiana lesion-inducing like, putative, expressed
miR1870-p5	6	21164755-21164963	*Os06g0555400*	40S ribosomal protein S24, putative, expressed
miR1876	10	4833365-4833521	*Os10g0170200*	S10/S20 domain containing ribosomal protein, putative, expressed
miR1878	9	16555509-16555608	*LOC_Os09g27230* *Os09g0444550*	brevis radix, putative, expressed; Hypothetical protein. (*Os09t0444550-00*)
miR2106_R+1	2	23768609-23768694	*Os02g0606600*	expressed protein
miR2122-p3_2ss8CT20TG	2	8715222-8715433	*Os02g0254600*	Conserved hypothetical protein. (*Os02t0254600-01*)
miR2865-p3_2ss16AC19AT	2	35319360-35319467	-	-
miR2874	8	15598028-15598128	*Os08g0344600*	Similar to triose phosphate/phosphate translocator, non-green plastid, chloroplast precursor (CTPT). (*Os08t0344600-01*) Similar to phosphoenolpyruvate/phosphate translocator. (*Os08t0344600-02*)
miR2877	4	28585208-28585568	*Os04g0568800*	Similar to OSIGBa0139P06.4 protein. (*Os04t0568800-01*)
miR390-5p	3	34275140-34275230	*Os03g0817300*	Primary microRNA of OsmiR390; Target gene(s): *OsTAS3a* (*Oryza sativa* Trans-Acting Short RNA precursor 3a siRNA, *Os02g0610950*), OsSRK (*Os02g0194400*), promotion of lateral root growth, negative regulator of Cd tolerance
miR396a-3p_R+1	2	34280384-34280537	-	-

miR3979-3p	2	34280384-34280537	-	-
miR399d	6	1561789-1562074	-	-
miR399j_R-1	4	28873121-28873226	*LOC_Os04g48400* *Os04g0573100*	HOTHEAD precursor, putative, expressed; Putative glucose-methanol-choline (GMC) oxidoreductase, Cutin biosynthesis, anther development, Pollen fertility (*Os04t0573100-01*)
miR435	3	18209450-18209581	-	-
miR444b.1	4	23046686-23046794	*Os04g0461300* *Os04g0461400*	*OsMADS61*, Similar to MIKC-type MADS-box transcription factor WM30; Conserved hypothetical protein.
miR444f	6	8940380-8940416	*Os06g0268600*	Non-protein coding transcript. (*Os06t0268600-01*)
miR5072_L-4	6	17458695-17458770	-	-
miR5083-p3_1ss20GA	1	41010573-41010952	*Os01g0934901* *Os01g0935000*	Non-protein coding transcript. (*Os01t0934901-00*); Zinc finger, C2H2-type domain containing protein. (*Os01t0935000-01*)
miR5144-p5	1	25326388-25326810	*Os01g0632550*	expressed protein
miR5150-3p_L-1R+1	4	18470790-18470868	*Os04g0378200* *Os04g0378066*	Sterile alpha motif SAM domain containing protein. (*Os04t0378200-01*); Hypothetical gene. (*Os04t0378066-00*)
miR5159	11	11920712-11920787	*Os11g0310800*	DEAD-like helicase, N-terminal domain containing protein. (*Os11t0310800-01*)
miR5504_R-3	10	17228165-17228262	*Os10g0466700*	Similar to 60S ribosomal protein L17. (*Os10t0466700-01*)
miR5510-p3	12	19127914-19128038	*Os12g0502100*	Similar to SKIP interacting protein 15. (*Os12t0502100-01*)
miR5526-p3_2ss16TG17AG	10	1584735-1584987	-	-
miR5540	1	35552728-35553070	-	-
miR5542-p3_1ss17AG	4	32797606-32797757	*LOC_Os04g55170*	LTPL126 - Protease inhibitor/seed storage/LTP family protein precursor, expressed

miR5802_1ss11CT	1	13088727-13088790	-	-
miR6251	9	15792337-15792550	*Os09g0431600*	Cystathionine beta-synthase, core domain containing protein. (*Os09t0431600-00*)
miR6254	12	1970862-1971199	-	-
miR810a-p3_1ss17CT	11	959561-959591	*Os11g0121500*	protein kinase, putative, expressed
miR810a-p5_1ss17CT	11	969694-969774	*Os11g0122150*	Similar to serine/threonine-protein kinase NAK. (*Os11t0122150-00*)
miR812r-p3	11	18809746-18809963	-	-
miR820a_R+1	7	13120534-13120734	*LOC_Os07g23270*	transposon protein, putative, CACTA, En/Spm sub-class, expressed
miR821a-p5_1ss3AC	3	22974225-22974498	-	-
miR821b-p3	7	16417225-16417511	-	-
miR821c-p5_1ss3AC	8	19925129-19925394	-	-
miR827	2	23901168-23901284	*Os02g0609000*	Hypothetical protein. (*Os02t0609000-01*)
miR6476a-p3_2ss6AG18AC	6	923823-923889	*Os06g0116600*	Proteinase inhibitor, propeptide domain containing protein. (*Os06t0116600-01*)
miR6478_1ss21GA	2	31853021-31853053	*Os03g0190301* *Os03g0190400*	Non-protein coding transcript. (*Os03t0190301-00*); Hypothetical gene. (*Os03t0190400-01*)
miR6478_2ss20TC21GA	9	12145700-12145793	*Os09g0368101*	Non-protein coding transcript. (*Os09t0368101-00*)
miR6478_R+2_1ss21GA	8	5862001-5862070	-	-
miR6478_R+4_1ss21GA	3	23552628-23552722	*Os03g0621201*	Non-protein coding transcript. (*Os03t0621201-00*)
miR10516_L+3R+3	7	24923079-24923199	-	-
miR10520-p3_1ss6TC	6	28255980-28256030	*Os06g0678950* *LOC_Os06g46540*	-; cell division cycle protein 23, putative, expressed
miR10521-p5_1ss4AG	4	20109329-20109479	*Os04g0405300*	Similar to stem secoisolariciresinol dehydrogenase (Fragment). (*Os04t0405300-01*)
miR9774-p5_1ss22AT	4	9137261-9137329	*LOC_Os04g16770* *LOC_Os04g16772*	photosynthetic reaction center protein, putative, expressed; chloroplast 30S ribosomal protein S19, putative

miR9777_1ss7CT	2	1797874-1798087	*Os02g0134100*	Hypothetical gene. (*Os02t0134100-01*)
miR9779-p3_2ss14TC18GC	6	28265421-28265484	*Os06g0679200*	Non-protein coding transcript. (*Os06t0679200-01*)
miR3630-p3_2ss19AT20CT	8	21041998-21042099	-	-
PC-3p-100468_17	4	16876132-16876223	*LOC_Os04g28490*	expressed protein
PC-3p-118603_12	1	15442195-15442316	-	-
PC-3p-129422_10	4	26222580-26222724	-	-
PC-3p-24288_182	2	24573952-24574116	*Os02g0618301* *Os02g0618250*	Non-protein coding transcript. (*Os02t0618301-00*); Similar to H/ACA ribonucleoprotein complex subunit 3-like protein. (*Os02t0618250-01*)
PC-3p-31535_128	5	14210357-14210560	-	-
PC-3p-38283_97	6	21165713-21165855	*Os06g0555400*	Similar to 40S ribosomal protein S19-like. (*Os06t0555400-01*)
PC-3p-6597_665	1	30151239-30151387	-	-
PC-3p-71127_35	10	10158620-10158802	-	-
PC-3p-76359_30	1	841112-841300	*Os01g0115533* *Os01g0115500*	Non-protein coding transcript. (*Os01t0115533-00*); Similar to receptor-like kinase. (*Os01t0115500-00*)
PC-5p-16439_287	6	124596-124763	*LOC_Os06g01140*	expressed protein
PC-5p-24732_177	3	4784972-4785111	-	-
PC-5p-54266_56	3	4784901-4785040	-	-
PC-5p-57749_50	2	14279604-14279662	-	-
PC-5p-60444_47	4	34047090-34047243	*Os04g0666900*	kinesin motor domain containing protein; Similar to H1005F08.22 protein. (*Os04t0666900-01*); Similar to H1005F08.22 protein. (*Os04t0666900-02*);
PC-5p-63767_42	2	12385000-12385156	*Os02g0313500*	Conserved hypothetical protein. (*Os02t0313500-01*)
PC-5p-68044_38	12	18944454-18944636	-	-
PC-5p-72419_34	7	25780747-25780881	*LOC_Os07g43030*	calmodulin-binding transcription activator, putative, expressed

PC-5p-81638_26	1	30381-30593	*Os01g0100800*	Protein of unknown function DUF1664 family protein. (*Os01t0100800-01*)
PC-5p-84508_25	11	1094779-1094938	-	-
PC-5p-86609_24	4	34071183-34071325	*Os04g0667400*	Melatonin 2-hydroxylase, control of the melatonin level in plants (*Os04t0667400-01*)
PC-5p-88433_23	9	7554819-7554934	*LOC_Os09g13110*	retrotransposon protein, putative, unclassified, expressed
PC-5p-92202_21	11	20197287-20197388	-	-
PC-5p-93370_20	10	19674988-19675083	-	-
gma-miR4995-p5_1ss18GC	3	31812320-31812369	-	-
gma-miR6300_R+6_2	3	17204613-17204770	*Os03g0415050*	Non-protein coding transcript. (*Os03t0415050-00*)
osa-miR1860-p5	1	934420-934567	*Os01g0116900* *Os01g0116600*	Protein kinase, catalytic domain domain containing protein. (*Os01t0116900-00*); *SPL33*, Eukaryotic translation elongation factor 1 alpha (eEF1A)-like protein, negative regulation of cell death, defense response
osa-miR3982-3p_L+1R-1	2	34280384-34280537	*Os11g0130100*	Conserved hypothetical protein. (*Os11t0130100-01*)
osa-miR812k-p5	2	18844569-18844724	*Os01g0875300*	Similar to universal stress protein family protein. (*Os01t0875300-00*)
vvi-miR3638-p5_2ss17GT18CT	2	4667515-4667649	*Os02g0183900*	Similar to isoleucine-tRNA ligase-like protein. (*Os02t0183900-00*)
PC-5p-75382_31	4	12835119-12835290	-	-

Note: The genes that have been reported to be related to stress tolerance are underlined.

Table S4. Amplification results of the polymorphic miRNA-SSR markers analyzed in this study

SSR marker	Major allele frequency	Number of alleles	Gene diversity	PIC[*] value
miR162a-SSR	0.34	6	0.74	0.70
miR166h-5p-SSR	0.55	3	0.58	0.50
miR167b-p3-SSR	0.32	4	0.73	0.68
miR169n-SSR	0.37	4	0.70	0.65
miR1862c-p5-SSR	0.76	4	0.40	0.37
miR2106_R+1-SSR	0.43	4	0.63	0.55
miR2865-p3_2ss16AC19AT-SSR	0.86	3	0.24	0.23
miR390-5p-SSR	0.82	3	0.31	0.27
miR5054_1ss10TA-SSR	0.50	4	0.59	0.50
PC-3p-100468_17-SSR	0.68	3	0.49	0.43
PC-3p-31535_128-SSR	0.45	7	0.72	0.69
PC-3p-71127_35-SSR	0.50	3	0.55	0.44
PC-3p-76359_30-SSR	0.73	4	0.43	0.39
Mean value	0.56	4	0.55	0.49

[*] PIC: polymorphism information content