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Supplementary Data

Salt- or alkaline-stress-induced transgenerational alteration in DNA methylation in rice (*Oryza sativa*)

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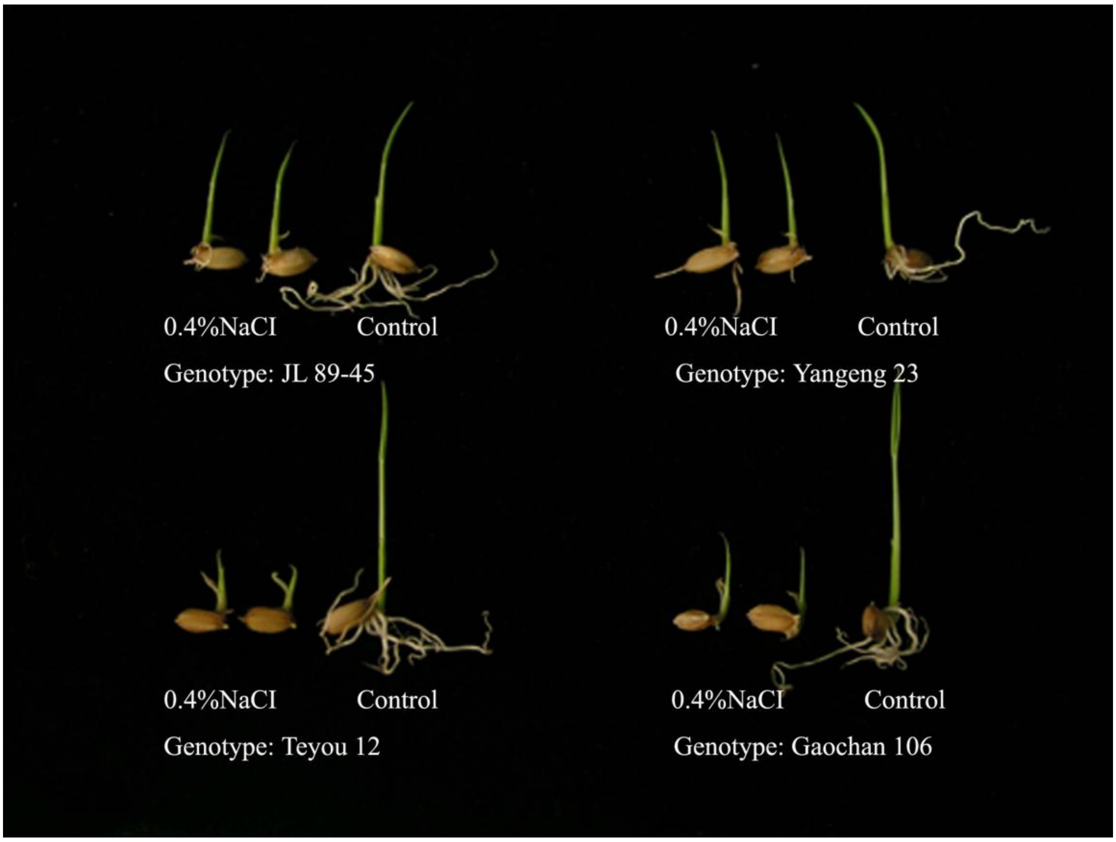

Supplementary Fig. 1 Four rice (*Oryza sativa* L.) ssp. *japonica* genotypes, including two salt-tolerant (JL 89-45 and Yangeng 23) and two salt-sensitive (Teyou 12 and Gaochan 106) were germinated and grown in the petri dishes including 0.4% NaCl for 7 days. Control plants were germinated and grown in distilled water for 7days. Treatment solutions (including distilled water) were changed daily.

Supplementary Table 1 ISSR primers sequence

Primer name	Primer sequence
5	VHV(GT)$_7$
6	DBD(GA)$_7$
7	(CT)$_8$RG
9	(CT)$_8$RC
15	CCC(GT)$_6$
16	GSG(GT)$_6$
17	CSC(GA)$_6$
18	GCW(GA)$_6$G
20	CCAG(TGG)$_3$TG
21	GCGA(CA)$_6$
22	SSWN(GACA)$_3$
31	(AG)$_8$T
32	(AG)$_8$C
33	(GA)$_8$T
34	(GA)$_8$C
36	(AG)$_8$YT
37	(AG)$_8$YC
w1	(AG)$_8$G
w3	(AC)$_8$C
w6	(GA)8YC
w7	GGGT(GGGGT)2G
w11	(TC)8A
w12	(TC)8C
w16	(GA)8YT
w18	(CA)$_8$RC
w19	(CA)8RG
w20	(GT)8YA
w23	(AC)8YT
w24	(AC)8YA
w25	(AC)8YG
w27	(TG)8RA
w28	(ATG)6
w29	(GACA)4
w30	(GGAGA)3

R----A/G; Y----C/T; M----A/C; K----G/T; S----G/C; W----A/T; H----A/T/C; B----G/T/C; V----G/A/C; D----G/A/T; N----A/G/C/T

Supplementary Table 2 Database information of sequence-specific primers used for Southern blotting probe amplification (from genomic DNA).

probe	Genbank Accession	Sequence primers Forward (5’-3’)	Sequence primers Reverse (5’-3’)	Blastx
P1	AC111016.2	TCAGGTCGGGACTCAAAAACA	GCAAAAGCCACAGATGGAGTTA	gb|AAS89034.1| delta-1-pyrroline-5-carboxylate synthetase [Oryza sativa Japonica Group]
P2	AK066495.1	CGGACATCTGACAACGCTAA	CTGAGAGCGCAAAGGATCTTATA	dbj|BAF15584.1| Os04g0584600 [Oryza sativa Japonica Group] GENE ID: 4336783 Os04g0584600 hypothetical protein（Similar to Calcium dependent protein kinase）
P3	AY328087.1	GGTGCACTGCTTCTTCATTG	TCGAGTTGTCCTCGTCCTCT	AY328087.1 putative Na+/H+ antiporter [Oryza sativa Japonica Group].
P4	AP004790.3	GCCGGCAACAGATAACCATA	TGTTCTTTTTGCTGCTGCTG	ref|NP_001173001.1 Os02g0530100 GENE ID: 9272622 Os02g0530100 Heavy metal transport/detoxification protein domain containing protein~contains InterPro domain
P5	AL663000.4	GTGTGGGTTCCAATTCATCCTC	TGGAGCATCCTCCTCCTCAT	ref|NP_001053485. | Os04g0549600 [Oryza sativa Japonica Group] GENE ID: 4336584 Os04g0549600 Heat shock protein DnaJ family protein~contains InterPro domain
P10	AP004139.3	GCGAACAGGTACTCGGAGAGG	ACATGTGAGTCCCTGGCATTCC	ref|NP_001047672.1 Os02g0666200 GENE ID: 4330248 Os02g0666200 Aquaporin contains InterPro domain
P11	AP004026.3	GTGTAGACGAGGACGAAGGTGC	GGGAAGGAGGAGGATGTGAGG	dbj|BAA81820.1| water channel protein RWC3 [Oryza sativa]
P14	AC151537.1	GGCAACGCGGTATTTAAGAG	AAGAAGGGCTGCCATCAATA	gb|EEE59078.1| hypothetical protein OsJ_10890 [Oryza sativa Japonica Group]
P15	AC097627.1	GCTTTGGCCAATCTCTCAAC	TGGCAGGCATTTCCTAGTCT	SNF2P
P16	AP006048.3	SSWN(GACA)3	SSWN(GACA)3	dbj|CI687429.1| CI687429 Oryza sativa (japonica) cultivar-group) young ear Oryza sativa Japonica Group cDNA clone J07B5083D20T3 5', mRNA sequence.
P17	AP003683.3.	(AC)8YA	(AC)8YA	ref|XP_001739457.1| tuberin [Entamoeba dispar SAW760] gb|EDR24158.1| tuberin, putative [Entamoeba dispar SAW760]

Supplementary Table 3 [a]Putative function and identity of methylation alteration locis detected by methylation-sensitive ISSR in different genotype.

	Probe	Size (bp)	Genbank Acc. (BlastN)	Chr.	Genbank Acc. (Blastx)	Alignment	Genbank Acc. (BlastN EST)	Alignment Query coverage
1	902X	409	dbj|AP004997.2|	2	none		dbj|CI112614.1|	UniGene info CI112614 Oryza sativa (japonica cultivar-group) Panicles two weeks after flowering Oryza sativa Japonica Group cDNA clone Expect = 4e-58
2	1501	631	emb|AL732646.5| emb|AL731786.3|	12	none		dbj|CI491552.1|	CI491552 Oryza sativa (japonica cultivar-group) 3rd week immature panicle Oryza sativa Japonica Group cDNA clone Expect = 3e-37
3	1801	625	dbj|AP005170.3| dbj|AP004785.2|	6	non		dbj|CI295268.1|	UniGene info CI295268 Oryza sativa (japonica cultivar-group) etiolated shoot Expect = 4e-29
4	2002	453	emb|BX000494.2|	12	ref|NP_001065933.1|	UniGene infoGene info Os12g0105600 [Oryza sativa] Expect = 3e-16	gb|CF324977.1|	UniGene info JMT1--01-P17.g1 Oryza sativa Japonica Group cDNA clone JMT1--01-P17, mRNA sequence. Expect = 1e-46
5	2003	628	dbj|AP005692.3| dbj|AP005728.2|	9	dbj|BAD26116.1|	hypothetical protein [Oryza sativa] Expect(2) = 6e-33	dbj|CI325969.1|	UniGene info CI325969 Oryza sativa (japonica cultivar-group) shoot Oryza sativa Expect = 4e-60
6	2207	405	dbj|AP006048.3|	6	none		dbj|CI687429.1|	UniGene info CI687429 Oryza sativa (japonica cultivar-group) young ear Oryza Expect = 2e-100
7	W301	621	dbj|AP004745.2|	6	none		gb|CV942823.1|	PMrpct_6368 mating of 88069 (A1) and 618 (A2) Phytophthora infestans cDNA, mRNA sequence. Expect = 4e-10
8	W601	619	dbj|AP004376.3|	8	none		gb|CA764434.2|	AF53-Rpf_03_I23_T7_086.ab1 IRRI Drought Stress Panicle Library Oryza sativa Indica Group cDNA clone C0000983 5' similar to unknown, mRNA sequence. Expect = 1e-2 7
9	W140	547	gb|AC0	3	none		dbj|CI619683.	UniGene info CI619683

	2		93018.4|				1|	Oryza sativa (japonica cultivar-group) callus Oryza sativa Japonica Group cDNA clone Expect = 8e-157
10	W1801	620	gb|DQ448817.1|		gb|EEC72739.1|	hypothetical protein OsI_06360 [Oryza sativa] Expect = 6e-07	dbj|CI572682.1|	UniGene info CI572682 Oryza sativa (japonica cultivar-group) shoot Expect = 0.0
11	W2301	619	gb|AC134048.3|	11	none		gb|EB273648.1|	CNSN02-F-021333-501 Normalized CNS library (juvenile 2) Aplysia californica cDNA clone CNSN02-F-021333 5', mRNA sequence.
12	W2402	630	dbj|AP003683.3|	1	gb|AAF91388.1|AF263243_1	SocE [Myxococcus xanthus] Expect = 1e-18	gb|DV777948.1|	UniGene info Hw_Fat_37_050805_H07 Bos taurus CF-24-HW fat cDNA library Bos taurus cDNA, mRNA sequence.
13	W2905	405	dbj|AP006048.3|	6	none		dbj|BJ744024.1|	BJ744024 MF015DA cDNA Oryzias latipes cDNA clone MF015DA022n04 3', mRNA sequence.
14	W3002	629	dbj|AP005487.3|	8	none		gb|CB214097.1|	Expect = 1e-10
15	W3003	587	dbj|AP004063.3|	2	none		dbj|CI736623.1|	UniGene info CI736623 Oryza sativa (japonica cultivar-group) after pollination Expect = 4e-28
16	W3004	627	emb|AL731622.1|	4	none		dbj|CI092120.1|	UniGene info CI092120 Oryza sativa (japonica cultivar-group) Cd treated callus Expect = 5e-40
17	W2903	629	gb|AC125411.1|	3	ref|NP_001048656.1|	UniGene infoGene info Os03g0101700 [Oryza sativa] Expect = 3e-12	dbj|CI441030.1|	UniGene info CI441030 Oryza sativa (japonica cultivar-group) 14 days after transferring callus Expect = 1e-143
18	902S	545	gb|AF488413.1|	6	ref|NP_001056697.1|	UniGene infoGene info Os06g0131700 [Oryza sativa] Expect = 2e-25	dbj|CI642507.1|	UniGene info CI642507 Oryza sativa (japonica cultivar-group) leaf of seedling 10mM H2O2 (10min), 24hr after treatment Expect = 3e-175
19	903q	630	emb|AL844880.3|	12	none		dbj|CI158290.1|	UniGene info CI158290 Oryza sativa (japonica cultivar-group) Panicles

								mixture of one, two weeks after flowering Expect = 1e-09
20	2101	629	dbj|AP005105.3|	7	ref|YP_572476.1|	DNA-directed RNA polymerase subunit beta' GENE ID: 4025879 Csal_0415 | Expect = 1e-36	none	None
21	2102	555	dbj|AP000615.1|	3	gb|EAY88383.1|	hypothetical protein OsI_09845 [Oryza sativa Indica Group] Expect = 7e-23	dbj|CI662158.1|	UniGene info CI662158 Oryza sativa (japonica cultivar-group) germinating seeds Expect = 8e-138
22	3102	610	dbj|AP003227.3|	1	dbj|BAD81672.1|	hypothetical protein [Oryza sativa Japonica Group] Length=207 Expect = 4e-15	dbj|CI585447.1|	UniGene info CI585447 Oryza sativa (japonica cultivar-group) flower Expect = 0.0
23	3103	621	dbj|AP003227.3|	1	dbj|BAD81672.1|	hypothetical protein [Oryza sativa] Expect = 4e-15	dbj|CI585447.1|	UniGene info CI585447 Oryza sativa (japonica cultivar-group) flower Expect = 0.0
24	3401	503	dbj|AP003448.3|	1	gb|EAY77382.1|	hypothetical protein OsI_05369 [Oryza sativa] Expect = 8e-45	dbj|AU223128.1|	UniGene info AU223128 Rice shoot Oryza sativa Japonica Group cDNA clone S3905, mRNA sequence. Expect = 0.0
25	3601	624	dbj|AP004778.3|	2	gb|EAZ24280.1|	hypothetical protein OsJ_08031 [Oryza sativa] Expect = 0.005	dbj|CI288345.1|	UniGene info CI288345 Oryza sativa (japonica cultivar-group) etiolated shoot Length=280 Expect = 1e-104
26	W101a	617	gb|AC108758.2|	9	gb|EEC84792.1|	hypothetical protein OsI_31849 [Oryza sativa] Expect = 1e-04	dbj|CI620107.1|	UniGene info CI620107 Oryza sativa (japonica cultivar-group) callus Oryza sativa Japonica Group cDNA clone Expect = 1e-160
27	W101c	318	dbj|AP003455.2|	1	none		dbj|CI434402.1|	UniGene info CI434402 Oryza sativa (japonica cultivar-group) 4 days after transferring callus Expect = 4e-44
28	W1202	624	gb|AC151537.1|	3	gb|EEE59078.1|	hypothetical protein OsJ_10890	gb|CB674782.1|	UniGene info OSJNEe10A07.f OSJNEe Oryza sativa Japonica

						[Oryza sativa] Expect(2) = 5e-37		Group cDNA clone OSJNEe10A07 5', mRNA sequence. Expect = 1e-66

[a] Based on search at NCBI.