

Supplementary Material

Physiological characterisation and fine mapping of a salt-tolerant mutant in rice (*Oryza sativa*)

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Table S1. Comparison of agronomic traits of the *rst1* mutant and Nipponbare (Nipp)

Data are presented as means \pm s.e.m. ($n = 10$). Statistically significant differences between the *rst1* mutant and Nipponbare are indicated: **, $P < 0.01$. PH, plant height; PP, number of panicles per plant; PL, panicle length; SP, number of spikelets per panicle; SF, spikelet fertility; GW, 1,000-grain weight; GY, grain yield per plant

	PH (cm)	PP	PL (cm)	SP	SF (%)	GW (g)	GY (g)
Nipp	88.4 \pm 0.9	16.0 \pm 0.7	19.5 \pm 0.4	84.6 \pm 1.5	85.2 \pm 2.3	23.3 \pm 0.1	23.0 \pm 1.2
<i>rst1</i>	89.5 \pm 0.8	15.8 \pm 0.7	21.2 \pm 0.5**	94.4 \pm 3.0**	85.6 \pm 1.9	24.7 \pm 0.2**	29.0 \pm 1.6**

Table S2. Insertion/deletion (InDel) markers used for mapping of the *rstI* locus

Marker	Primer sequence (5' - 3')	Chromosomal position
IM25659	Forward: AGGATGGAGATCCTGATTTT Reverse: ATATGTTAAACGGTCCGAAA	25659123-25659264
IM29308	Forward: AGAGAGAGAGACAGAGCGCA Reverse: CATTCTGGGAAGGAAACCC	29308454-29308573
IM29394	Forward: GGAGTACTGCATCGCCATT Reverse: GGCAGCAGTAGCACACAAT	29394177-29394288
IM29432	Forward: GGCAGAATCTCCCATTGTA Reverse: AACTTTGTGGATGCCATAGC	29432142-29432299
IM29505	Forward: GACAGGAAAGAATCAGGTCA Reverse: ATTAGAATGTGTCACGTCCC	29505467-29505597
IM29583	Forward: TTATATCGGAACAGCAGCTG Reverse: TTCACAGACGAATGGACGA	29583336-29583448
IM29702	Forward: AGCCCAGCTAGTACTATTTC Reverse: CACTGGAGTGAGTGTGACAG	29702745-29702874
IM29914	Forward: AACTTCACCCGATAGCTGTA Reverse: ACACAGATTGGAGTAATCGC	29914531-29914665
IM30014	Forward: CTGTTCCAGGAAAGGTAGCA Reverse: CGGTTCATGCCCTAGAGATA	30014916-30015030
IM30284	Forward: GTTGAGGATCCCAGTTGTAA Reverse: CACAAAAGGAAACTCCACT	30284907-30285082
IM30406	Forward: AGTAGTAGCAAAGAAGGGGC Reverse: GTGCATAGTGGGATCTGTG	30406882-30407024
IM30774	Forward: TCTCGAAGATGTTTCAGGTTT Reverse: CTGCAATATCTGCATCTTGA	30774725-30774893
IM30860	Forward: TCCTTCTTATCCAGAACACAAC Reverse: ATTTAACCTGCTGTCCTCTCA	30860165-30860307
IM31205	Forward: TTTCATCCATCCCTCTACTG Reverse: CCAAACACACCCAAATACTC	31205903-31206050

Table S3. Putative genes in the 270.4-kb region covering the *rst1* locus annotated in the Rice Annotation Project Database

Gene ID	Description	Gene Start (bp)	Gene End (bp)
Os06g0685200	hypothetical conserved gene	29432641	29434911
Os06g0685300	predicted protein	29435361	29441079
Os06g0685400	conserved hypothetical protein	29443196	29443975
Os06g0685550	IAA15-auxin-responsive Aux/IAA family member	29455330	29455906
Os06g0685700	auxin response factor 16	29463494	29467207
Os06g0686400	plant lipid transfer protein/seed storage domain containing protein	29494449	29497312
Os06g0686500	peptidase M3A and M3B, thimet/oligopeptidase F domain containing protein	29497995	29505006
Os06g0686600	conserved hypothetical protein	29506135	29506906
Os06g0686700	hypothetical conserved gene	29516440	29518589
Os06g0686900	conserved hypothetical protein	29519550	29520211
Os06g0687000	hypothetical conserved gene	29521142	29524599
Os06g0687100	predicted protein	29528072	29529596
Os06g0687200	zinc finger, RING-type domain containing protein	29529795	29531125
Os06g0687400	auxin-independent growth promoter-like protein	29535267	29539370
Os06g0687450	dehydration-responsive protein-related	29540552	29544821
Os06g0687500	RNA-binding region RNP-1 domain containing protein	29547226	29551824
Os06g0687600	protein of unknown function DUF579	29556479	29557931
Os06g0687700	T-complex protein 1	29559067	29561966
Os06g0687800	pincher (EH-domain containing 4)	29565946	29570952
Os06g0687900	UDP-glucuronyltransferase-I	29573440	29575396
Os06g0688100	hypothetical conserved gene	29576603	29583419
Os06g0688200	blight-associated protein p12	29584336	29585351
Os06g0688500	MYC protein	29603889	29604134
Os06g0688800	hypothetical conserved gene	29610632	29611974
Os06g0689600	hypothetical conserved gene	29629551	29634406
Os06g0689700	hypothetical conserved gene	29635923	29636357
Os06g0690100	conserved hypothetical protein	29645496	29647139
Os06g0690200	serine/threonine protein kinase-related domain containing protein	29647376	29651433
Os06g0690600	conserved hypothetical protein	29664766	29665333

Os06g0690700	potential cadmium/zinc-transporting ATPase HMA1	29666038	29674547
Os06g0690900	pentatricopeptide repeat domain containing protein	29678753	29681728
Os06g0691000	DNA repair protein, Rev1 family protein	29683783	29693146
Os06g0691100	pathogenesis-related transcriptional factor and ERF domain containing protein	29695259	29696237
Os06g0691200	thaumatin-like protein precursor	29702833	29703962

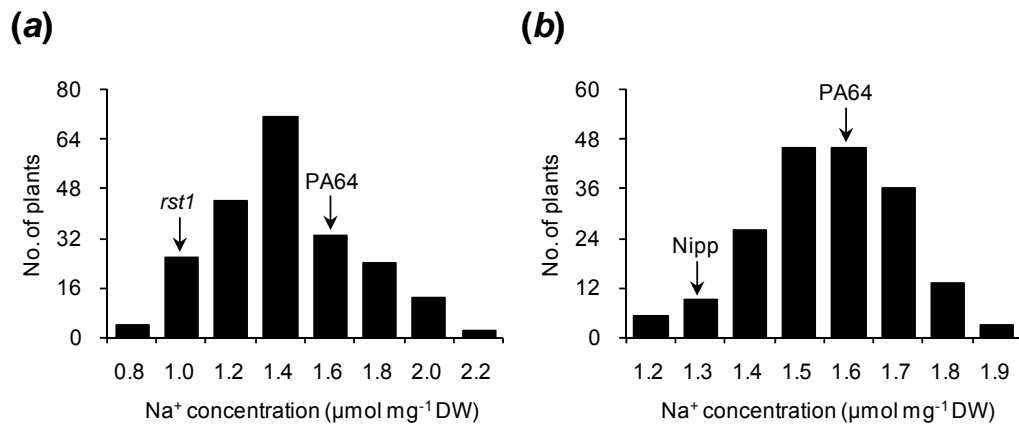


Fig. S1. Frequency distribution of shoot Na⁺ concentration in F₂ populations of *rst1*/PA64 and Nipponbare/PA64. (a) *rst1*/PA64 F₂ population ($n = 217$). (b) Nipponbare/PA64 F₂ population ($n = 184$). PA64, Peiai 64; Nipp, Nipponbare.

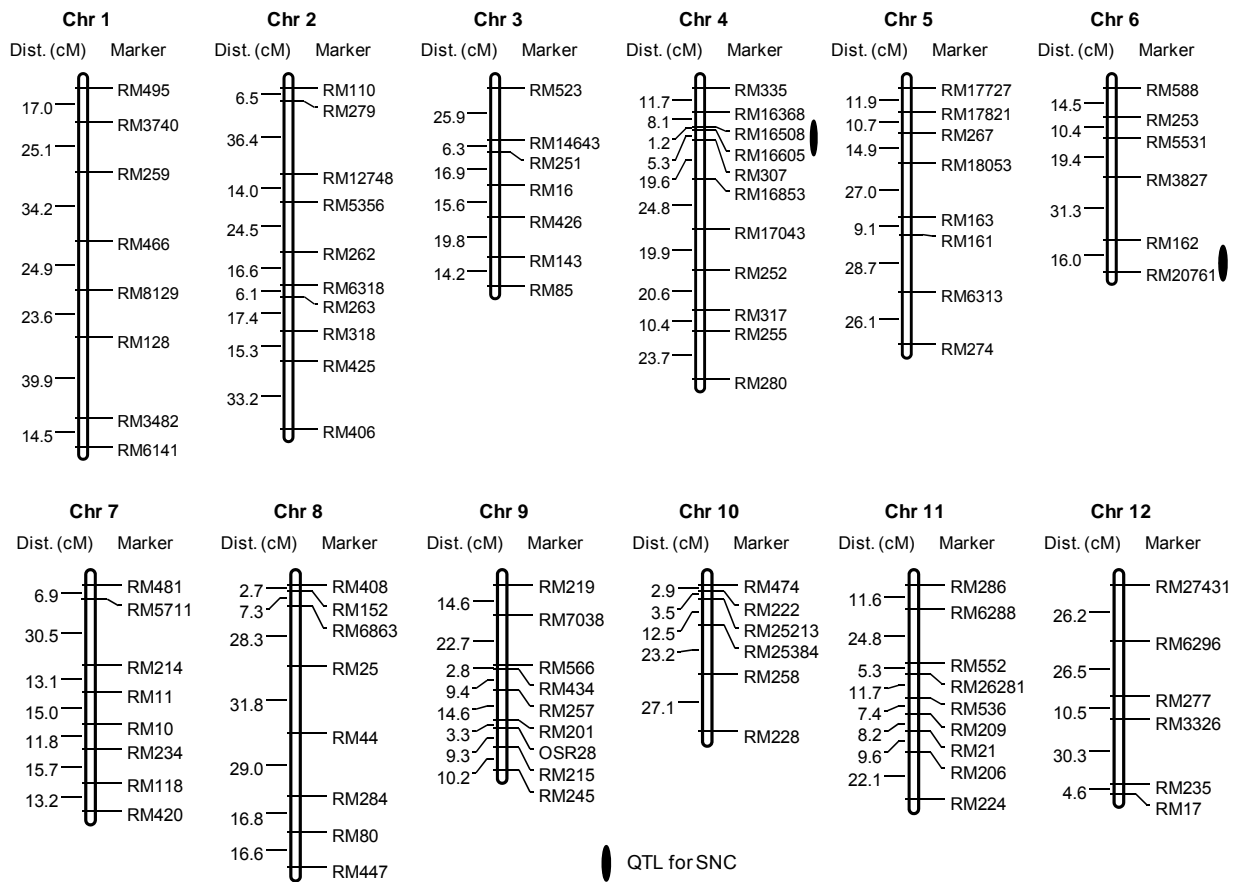


Fig. S2. Genetic linkage map and locations of QTLs for shoot Na^+ concentration (SNC) identified in the F_2 population of *rst1/Peiai 64* using composite interval mapping. Dist, distance.