

Supplementary Table S2. Putative candidate genes in the QTL regions showing probable functions and references

Characters	QTL name	Chr.	Position (bp)	Number of locus	Candidate gene	Possible function	Reference
SES	<i>qSES1</i>	1	38723347-38724165	16	<i>LOC_Os01g66670</i>	expressed protein (drought-induced proteins, anther and pollen wall remodelling/metabolism proteins contribute to the tolerance of rice to salt stress)	Ke <i>et al.</i> (2009) Sarhadi <i>et al.</i> (2012)
Survival rate (%)	<i>qSUR11</i>	11	5357710-5359379	15	<i>LOC_Os11g09990</i>	mTERF family protein, expressed (coordinate mitochondrial transcription, growth, development and stress response)	Roberti <i>et. al.</i> (2010) Zhao <i>et al.</i> (2014)
Shoot length	<i>qSL1</i>	1	39794226-39799341	18	<i>LOC_Os01g68490</i>	tetratricopeptide-like helical, putative, expressed (abscisic acid responses and osmotic stress tolerance, enable plants to cope up with adverse environmental conditions)	Schapiro <i>et al.</i> (2008) Sharma <i>et al.</i> (2016)
	<i>qSL8</i>	8	5613578-5616235	20	<i>LOC_Os08g09715</i>	F-box domain containing protein, expressed (F-box protein-encoding genes during floral transition as well as panicle and seed development, play a variety of roles in developmental processes including plant hormonal signal transduction, floral development, secondary metabolism, senescence, circadian rhythms, and responses to both biotic and abiotic stresses)	Jain <i>et al.</i> (2007) Zhang <i>et al.</i> (2019)

Characters	QTL name	Chr.	Position (bp)	Number of locus	Candidate gene	Possible function	Reference
Shoot dry weight	<i>qSDW1</i>	1	31473897-31477599	17	<i>LOC_Os01g54700</i>	retrotransposon protein, putative, Ty1-copia subclass, expressed (tuning gene expression during plant development salinity, played a major role in shaping genome structure).	Wang <i>et al.</i> (1999)
	<i>qSDW10</i>	10	17499639-17503204	12	<i>LOC_Os10g33310</i>	cyclin-dependent kinase inhibitor, putative, expressed (control cell growth, controlling cell cycle progression)	De <i>et al.</i> (2017) Vieira <i>et al.</i> (2017)
Root length	<i>qRL1</i>	1	10713139-10714271	16	<i>LOC_Os01g18950</i>	peroxidase precursor, putative, expressed (increases protection against oxidative stress, highly tolerant to different stresses allowing survival when water supply is a limiting factor).	Prabhu <i>et al.</i> (1997) Wang <i>et al.</i> (2011) Martínez <i>et al.</i> (2021)
SPAD value	<i>qSPAD7</i>	7	23314482-23319154	20	<i>LOC_Os07g38860</i>	OsGH3.10 - Probable indole-3-acetic acid-amidosynthetase, expressed	Ding <i>et al.</i> (2008)
Na ⁺ conc.	<i>qNa2</i>	2	34274401-34276956	17	<i>LOC_Os02g56010</i>	anthocyanidin 3-O-glucosyltransferase, putative, expressed	Fukuchi-Mizutani <i>et al.</i> (2003)
	<i>qNa10</i>	10	17547961-17548260	11	<i>LOC_Os10g33360</i>	expressed protein (drought-induced proteins, anther and pollen wall remodelling/metabolism proteins contribute to the tolerance of rice to salt stress)	Ke <i>et al.</i> (2009) Sarhadi <i>et al.</i> (2012)
K ⁺ conc.	<i>qK1</i>	1	39922192-39923794	16	<i>LOC_Os01g68730</i>	RNA-binding protein FUS, putative, expressed (involved in cellular stress)	Tischbein <i>et al.</i> (2019)

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Na-K ratio	<i>qNaK12</i>	12	10048848-10053017	19	<i>LOC_Os12g17530</i>	response, responses against pathogen infection). expressed protein (drought-induced proteins, anther and pollen wall remodelling/metabolism proteins contribute to the tolerance of rice to salt stress)	Woloshen <i>et al.</i> (2011) Ke <i>et al.</i> (2009) Sarhadi <i>et al.</i> (2012)