

Table 1 Suppl. Chromosomal location, QTL name, marker with the greatest effect, peak position, confidence interval, LOD score, additive effect, and percentage variation accounted for QTLs for salt tolerance in three salinities with composite interval mapping (CIM) in barley RILs population developed from a cross of Igri×Arigashar (^B - logarithm of odds ratio, ^C - phenotypic variation explained by each QTL).

Trait	Salinity [mM]	Chromosome	QTL	Marker with the greatest effect	Peak [cM]	Confidence range	LOD ^B score	Additive effect	R ^{2C}
SL	0	L1	<i>QSlgL1a</i>	<i>XE36-M49</i>	0	0-6.2	3.3	0.8	0.08
	0	(2H)H2.2	<i>QSlgH2.2a</i>	<i>XHVM54</i>	38	35.8-41.2	2.7	-0.8	0.08
	250	4H	<i>QSlg4Hb1</i>	<i>XE35-M47</i>	84.6	84.5-86.9	2.6	0.25	0.06
	250	4H	<i>QSlg4Hb2</i>	<i>XE41-M61</i>	94.4	89.7-100.2	3.4	0.33	0.12
	350	6H	<i>QSlg6Hc1</i>	<i>XE35-M47</i>	6.7	6.6-9.3	2.8	0.12	0.07
	350	6H	<i>QSlg6Hc2</i>	<i>XHVWAXY4F</i>	20.3	17.6-22.9	4.5	0.14	0.12
CL	350	2H(H2.1)	<i>QSlgH2.1c</i>	<i>XE35-M47</i>	26	23.9-29.8	3	0.1	0.07
	0	-	-	-	-	-	-	-	-
	250	2H(H2.1)	<i>QClgH2.1b</i>	<i>XE37-M61</i>	0	0-6.8	3	0.44	0.1
	250	4H	<i>QClg4Hb</i>	<i>XE41-M61</i>	94.4	89.6-100.2	3.6	0.54	0.15
	350	6H	<i>QClg6Hc</i>	<i>XHVWAXY4F</i>	22.4	18.4-24.2	3.3	0.27	0.14
	350	6H	<i>QNrg6Ha</i>	<i>XE35-M47</i>	8.7	3.8-13.5	3.5	0.25	0.09
RN	250	2H(H2.1)	<i>QNrgH2.1b</i>	<i>XE36-M61</i>	44.2	43.5-45.1	2.7	-0.24	0.08
	350	-	-	-	-	-	-	-	-
	350	-	-	-	-	-	-	-	-
RL	0	L1	<i>QRlgL1a</i>	<i>XE36-M49</i>	0	0-1.6	2.7	0.77	0.06
	0	6H	<i>QRlg6Ha</i>	<i>XE35-M47</i>	6.7	6-7.7	2.6	0.72	0.06
	250,350	-	-	-	-	-	-	-	-
GP	0,250,350	-	-	-	-	-	-	-	-
RFM	0	6H	<i>QRwg6Ha</i>	<i>XE35-M47</i>	6.7	3-11.2	3.4	0.3	0.08
	250	-	-	-	-	-	-	-	-
	350	2H(H2.2)	<i>QRwgH2.2c</i>	<i>XEBMAC0415</i>	32	28.9-32.6	2.6	-0.07	0.09
SFM	0	-	-	-	-	-	-	-	-
	250	4H	<i>QSwg4Hb</i>	<i>XE41-M61</i>	94.4	91.3-97.4	2.8	0.17	0.11
	350	6H	<i>QSwg6Hc</i>	<i>XHVWAXY4F</i>	22.4	18.2-24.6	4.1	0.07	0.16
TFM	0	7H(H7.1)	<i>QTwgH7.1a</i>	<i>XE36-M48</i>	0	0-5.5	3.3	0.66	0.09
	0	6H	<i>QTwg6Ha</i>	<i>XE35-M47</i>	6.7	3.4-10.9	2.9	0.57	0.07
	250	-	-	-	-	-	-	-	-
	350	6H	<i>QTwg6Hc</i>	<i>XHVWAXY4F</i>	17.5	16.9-18.2	2.5	0.25	0.08
	350	2H(H2.2)	<i>QTwgH2.2c</i>	<i>XEBMAC0415</i>	29.2	24.9-34.5	3.2	-0.27	0.11
	350	4H	<i>QTwg4Hc</i>	<i>XE41-M61</i>	90.5	86.9-94	2.7	0.25	0.1
RDM	0,250,350	-	-	-	-	-	-	-	-
SDM	0	-	-	-	-	-	-	-	-
	250	3H	<i>QSdg3Hb</i>	<i>XE36-M50</i>	15.4	9.8-19.2	2.8	-0.01	0.06
	250	2H(H2.1)	<i>QSdgH2.1b</i>	<i>XE36-M48</i>	18.7	18.2-20	3.1	0.02	0.09
	350	6H	<i>QSdg6Hc</i>	<i>XHVWAXY4F</i>	20.4	18.5-23.8	3.3	0.01	0.09

Table 2 Suppl. Chromosomal location, QTL name, marker with the greatest effect, peak position, confidence range, LOD score, additive effect, and percentage variation accounted for QTLs for STI with composite interval mapping (CIM) in barley RILs population developed from a cross of Igri×Arigashar (^B - logarithm of odds ratio, ^C - phenotypic variation explained by each QTL).

Trait	Salinity [mM]	Chromosome name	QTL name	Marker with the greatest effect	Peak [cM]	Confidence range	LOD ^B score	Additive effect	R ^{2C}
SL	250	L1	<i>QSlgL1a</i>	<i>XE36-M62</i>	24.1	23.9-26.2	2.9	0.02	0.07
	250	5H	<i>QSlg5Ha</i>	<i>XGMS061</i>	22.3	15.3-24.2	3.1	-0.02	0.11
	250	4H	<i>QSlg4Ha1</i>	<i>XE41-M59</i>	86.6	84-87.3	2.9	0.02	0.07
	250	4H	<i>QSlg4Ha2</i>	<i>XE41-M61</i>	94.4	88.7-99.4	3.3	0.02	0.12
	350	6H	<i>QSlg6Hb</i>	<i>XHVWAXY4F</i>	22.4	18-25	4.5	0.01	0.17
	350	2H(H2.1)	<i>QSlgH2.1b</i>	<i>XE35-M47</i>	26.2	23.9-30.4	3.4	0.01	0.09
CL	250	2H(H2.1)	<i>QClgH2.1a1</i>	<i>XE41-M61</i>	22.1	20.9-22.3	2.9	0.06	0.07
	250	2H(H2.1)	<i>QClgH2.1a2</i>	<i>XE36-M49</i>	42.3	41.9-43.4	2.8	-0.06	0.08
	350	6H	<i>QClg6Hb</i>	<i>XHVWAXY4F</i>	22.4	19.1-24.7	3.6	0.04	0.15
	350	2H(H2.1)	<i>QClgH2.1b</i>	<i>XE35-M47</i>	26.2	23.9-30	3.3	0.03	0.09
RN	250	2H(H2.1)	<i>QNrgH2.1a</i>	<i>XE36-M49</i>	42.3	41.7-44.1	3.1	-0/05	0.08
	350	-	-	-	-	-	-	-	-
RL	250,350	-	-	-	-	-	-	-	-
GP	250	2H(H2.1)	<i>QGgH2.1a</i>	<i>XE36-M49</i>	42.3	42.1-43.3	2.8	-0.05	0.07
	350	-	-	-	-	-	-	-	-
RFM	250	2H(H2.1)	<i>QRwgH2.1a</i>	<i>XE36-M49</i>	42.3	42.1-43	2.7	-0.05	0.07
	350	-	-	-	-	-	-	-	-
SFM	250	-	-	-	-	-	-	-	-
	350	6H	<i>QSwg6Hb</i>	<i>XHVWAXY4F</i>	22.4	19.3-23.6	3.2	0.02	0.13
	350	2H(H2.1)	<i>QSwgH2.1b</i>	<i>XE35-M47</i>	27.1	26.8-29.5	2.7	0.01	0.07
TFM	250	2H(H2.1)	<i>QTwgH2.1a</i>	<i>XE36-M49</i>	42.3	40.9-45.8	2.5	-0.03	0.07
	350	2H(H2.1)	<i>QTwgH2.1b</i>	<i>XE35-M47</i>	78.9	74.6-80.2	2.5	0.03	0.11
	350	2H(H2.2)	<i>QTwgH2.2a</i>	<i>XEBMAC0415</i>	32	26.5-31.1	2.5	-0.02	0.09
RDM	250,350	-	-	-	-	-	-	-	-
SDM	250,350	-	-	-	-	-	-	-	-