

**Table S1.** Summary of QTLs associated with waterlogging tolerance in maize, rice, wheat, and barley.

Species	Chr	QTL	Trait	LOD <sup>a</sup>	PVE (%) <sup>b</sup>	Population <sup>c</sup>	Population size	Population type	Reference
Maize	1	<i>R_GY</i>	Grain yield	6.4	5.0	<b>CAWL-46-3-1</b> ×CML311-2-1-3	211	RILs	166
Maize	1	<i>Qaer1.02-1.03</i>	Aerenchyma formation	4.1	10.8	B64 × <i>Zea nicaraguensis</i>	186	F <sub>2</sub>	112
Maize	1	<i>Qaer1.07</i>	Aerenchyma formation	5.3	11.7	B64 × <i>Zea nicaraguensis</i>	186	F <sub>2</sub>	112
Maize	1	<i>rl1</i>	Root length	2.74	5.1	HZ32 × <b>K12</b>	288	F <sub>2:3</sub>	43
Maize	1	<i>rdw1</i>	Root dry weight	2.89	4.4	HZ32 × <b>K12</b>	288	F <sub>2:3</sub>	43
Maize	2	<i>Qaer2.06</i>	Aerenchyma formation	4.1	9.1	B73 × <i>Zea luxurians</i>	195	F <sub>2</sub>	167
Maize	3	<i>R_GY</i>	Grain yield	6.1	4.2	<b>CAWL-46-3-1</b> ×CML311-2-1-3	211	RILs	166
Maize	3	<i>Qaer3.10</i>	Aerenchyma formation	1.8	6.3	<b>B73</b> × <i>Zea luxurians</i>	195	F <sub>2</sub>	167
Maize	3	<i>Qarf3.07-3.08</i>	Adventitious root formation	3.2	10.0	B64 × <b>Na4</b>	110	F <sub>2</sub>	115
Maize	3	<i>tdw3-3</i>	Total dry weight	2.64	12.2	HZ32 × <b>K12</b>	288	F <sub>2:3</sub>	43
Maize	3	<i>tdw3-4</i>	Total dry weight	2.77	12.8	HZ32 × <b>K12</b>	288	F <sub>2:3</sub>	43
Maize	3	<i>ph3</i>	Plant height	2.66	5.4	HZ32 × <b>K12</b>	288	F <sub>2:3</sub>	43
Maize	3	<i>sdw3-2</i>	Shoot dry weight	2.68	5.6	HZ32 × <b>K12</b>	288	F <sub>2:3</sub>	43
Maize	3	<i>rl3-1</i>	Root length	2.80	5.3	HZ32 × <b>K12</b>	288	F <sub>2:3</sub>	43
Maize	3	<i>rl3-2</i>	Root length	3.49	6.7	HZ32 × <b>K12</b>	288	F <sub>2:3</sub>	43
Maize	3	<i>rl3-3</i>	Root length	2.5	6.1	HZ32 × <b>K12</b>	288	F <sub>2:3</sub>	43
Maize	3	<i>rdw3</i>	Root dry weight	2.67	5.2	HZ32 × <b>K12</b>	288	F <sub>2:3</sub>	43
Maize	4	–	Leaf injury	11.9-25.5	29.0-49.0	<i>Zea.nicaraguensis</i> × Mi29	652	BC <sub>3</sub> F <sub>4</sub>	113
Maize	4	<i>Qarf4.07</i>	Adventitious root formation	4.1	9.0	B64 × <i>Zea mays ssp.</i> <i>Huehuetenangensis</i>	186	F <sub>2</sub>	56
Maize	4	<i>sdw4-3</i>	Shoot dry weight	2.60	5.1	HZ32 × <b>K12</b>	288	F <sub>2:3</sub>	43
Maize	5	<i>R_GY</i>	Grain yield	4.5	8.0	<b>CAWL-46-3-1</b> ×CML311-2-1-3	211	RILs	166
Maize	5	-	Root and shoot fresh and dry weight	3.02-6.10	6.32-12.01	<b>HZ32</b> × <b>K12</b>	180	BC <sub>2</sub> F <sub>2</sub>	116
Maize	5	<i>Qaer5.05-5.06</i>	Aerenchyma formation	2.6	4.2	B73 × <i>Zea luxurians</i>	195	F <sub>2</sub>	167
Maize	5	<i>Qaer5.09</i>	Aerenchyma formation	4.6	10.9	<b>B64</b> × <i>Zea nicaraguensis</i>	186	F <sub>2</sub>	112
Maize	6	<i>sdw6-1</i>	Shoot dry weight	2.96	5.4	<b>HZ32</b> × <b>K12</b>	288	F <sub>2:3</sub>	43
Maize	6	<i>Subtol6</i>	Mean leaf senescence score	-	22.0	<b>Mo18W</b> × <b>B73</b>	166	RILs	114
Maize	7	<i>rl7-3</i>	Root length	2.68	4.0	HZ32 × <b>K12</b>	288	F <sub>2:3</sub>	43
Maize	7	<i>rl7-5</i>	Root length	2.79	5.5	<b>HZ32</b> × <b>K12</b>	288	F <sub>2:3</sub>	43
Maize	7	<i>R_GY</i>	Grain yield	11.6	6.1	<b>CAWL-46-3-1</b> × <b>CML311-2-1-3</b>	211	RILs	166
Maize	7	<i>Qarf7.04-7.05</i>	Adventitious root formation	5.1	21.0	B64 × <b>Na4</b>	110	F <sub>2</sub>	115
Maize	8	<i>Qaer8.06-7</i>	Aerenchyma formation	4.5	11.6	<b>B64</b> × <i>Zea nicaraguensis</i>	186	F <sub>2</sub>	112

Maize	8	Qarf8.05	Adventitious root formation	4.9	5.0	B64 × Na4	110	F <sub>2</sub>	115
Maize	8	Qarf8.03	Adventitious root formation	4.0	10.0	B64 × <i>Zea mays ssp. Huehuetenangensis</i>	186	F <sub>2</sub>	56
Maize	8	Qarf8.05	Adventitious root formation	7.0	25.0	B64 × <i>Zea mays ssp. Huehuetenangensis</i>	186	F <sub>2</sub>	56
Maize	9	Qaer9.07-9.08	Aerenchyma formation	1.5	4.5	B73 × <i>Zea luxurians</i>	195	F <sub>2</sub>	167
Maize	9	sdw9-4	Shoot dry weight	7.03	20.8	HZ32 × K12	288	F <sub>2:3</sub>	43
Maize	9	tdw9-2	Total dry weight	5.92	31.7	HZ32 × K12	288	F <sub>2:3</sub>	43
Maize	9	tdw9-3	Total dry weight	5.91	30.7	HZ32 × K12	288	F <sub>2:3</sub>	43
Maize	10	R_GY	Grain yield	5.4	3.6	CAWL-46-3-1 × CML311-2-1-3	211	RILs	166
Maize	10	Qaer10.04	Aerenchyma formation	1.8	3.7	B73 × <i>Zea luxurians</i>	195	F <sub>2</sub>	167
Maize	10	ph10-1	Plant height	3.06	7.1	HZ32 × K12	288	F <sub>2:3</sub>	43
Maize	10	ph10-2	Plant height	3.23	5.2	HZ32 × K12	288	F <sub>2:3</sub>	43
Maize	10	rl10	Root length	2.77	5.6	HZ32 × K12	288	F <sub>2:3</sub>	43
Rice	1	qTIL1 <sup>C9285</sup>	Total internode elongation length	4.43	22.0	C9285 × T65	94	F <sub>2</sub>	118
Rice	1	qTIL1 <sup>T65</sup>	Total internode elongation length	3.86	20.0	W0120 × T65	94	F <sub>2</sub>	118
Rice	3	qLEI3 <sup>C9285</sup>	Lowest elongated internode	3.14	14.0	C9285 × T65	94	F <sub>2</sub>	118
Rice	8	qTIL8 <sup>T65</sup>	Total internode elongation length	3.36	17.0	W0120 × T65	94	F <sub>2</sub>	118
Rice	9	Sub1	Green leaf recovery	36.0	69.0	IR40931-26 × PI543851	169	F <sub>2</sub>	120
Rice	12	qTIL12 <sup>C9285</sup>	Total internode elongation length	6.19	27.0	C9285 × T65	94	F <sub>2</sub>	118
Rice	12	qTIL12 <sup>W0120</sup>	Total internode elongation length	5.89	36.0	W0120 × T65	94	F <sub>2</sub>	118
Rice	12	qNEI12 <sup>C9285</sup>	Number of elongated internodes	6.25	27.0	C9285 × T65	94	F <sub>2</sub>	118
Rice	12	qNEI12 <sup>W0120</sup>	Number of elongated internodes	4.47	27.0	W0120 × T65	94	F <sub>2</sub>	118
Rice	12	qLEI12 <sup>C9285</sup>	Lowest elongated internode	7.75	36.0	C9285 × T65	94	F <sub>2</sub>	118
Rice	12	qLEI12 <sup>W0120</sup>	Lowest elongated internode	5.63	26.9	W0120 × T65	94	F <sub>2</sub>	118
Wheat	1BL	QRfbio.ua-1B-WGH	Root fresh biomass	6.6	22.0	USG3209 × Jaypee	130	RILs	122
Wheat	1BL	QRdbio.ua-1B-WGH	Root dry biomass	3.7	18.0	USG3209 × Jaypee	130	RILs	122
Wheat	1BL	QSfbio.ua-1B-WGH	Shoot fresh biomass	6.7	27.0	USG3209 × Jaypee	130	RILs	122
Wheat	1BL	QSpadpost.ua-1B-WF	Chlorophyll content	4.8	32.0	USG3209 × Jaypee	130	RILs	122
Wheat	2B	—	Root/shoot dry weight	3.00-8.29	9.5-23.3	W7984 × Opata 85	112	RILs	124
Wheat	6B	—	Survival rate	3.45	10.3	W7984 × Opata 85	112	RILs	124

Wheat	6D	<i>QRlength.ua-6D-WGH</i>	Root length	3.8	8.0	USG3209 × Jaypee	130	RILs	122
Wheat	6D	<i>QSdbio.us-6D-WGH</i>	Shoot dry biomass	3.6	6.0	USG3209 × Jaypee	130	RILs	122
Wheat	6D	<i>QSpadpost.ua-6D-WF</i>	Chlorophyll content	3.2	6.0	USG3209 × Jaypee	130	RILs	122
Wheat	7A	<i>GRI-7A</i>	Germination rate index	2.93-7.64	11.4-23.9	W7984 × Opata 85	112	RILs	124
Wheat	7B	–	Plant height index Survival rate	2.97-4.27 4.66	8.7-12.1 13.6	W7984 × Opata 85	112	RILs	124
Barley	1H	<i>yfy2.2-2</i>	Leaf yellowing	2.77	5.0	Yerong × Franklin	177	DH lines	126
Barley	1H	<i>tfy1.1-3</i>	Leaf yellowing	2.75	7.1	TX9425 × Franklin	177	DH lines	126
Barley	2H	<i>KWw1.1</i> <i>KWw1.2</i>	Kernel weight	4.48 7.34	6.82 16.59	Yerong × Franklin	156	DH lines	125
Barley	2H	<i>KWw2.1</i> <i>KWw2.2</i>	Kernel weight	9.10 3.94	27.35 6.78	Yerong × Franklin	156	DH lines	125
Barley	2H	<i>SLw2.1</i> <i>SLw2.2</i>	Spike length	11.16 8.74	17.44 13.05	Yerong × Franklin	156	DH lines	125
Barley	2H	<i>GSw1.1</i> <i>GSw2.1</i>	Grains per spike	11.53 5.63	35.35 55.34	Yerong × Franklin	156	DH lines	125
Barley	2H	<i>GSw1.2</i> <i>GSw2.2</i>	Grains per spike	6.29 4.76	12.18 8.22	Yerong × Franklin	156	DH lines	125
Barley	2H	<i>GYw1.1</i>	Grain yield	2.85	4.74	Yerong × Franklin	156	DH lines	125
Barley	2H	<i>tfy1.1-1</i>	Leaf chlorosis	9.21	23.3	TX9425 × Franklin	92	DH lines	126
Barley	2H	<i>tfsur-1</i>	Survival rate	3.29	19.0	TX9425 × Franklin	92	DH lines	126
Barley	2H	<i>tfsur-2</i>	Survival rate	2.75	13.2	TX9425 × Franklin	92	DH lines	126
Barley	2H	<i>yfsur-1</i>	Plant survival	3.15	7.1	Yerong × Franklin	177	DH lines	126
Barley	2H	<i>QWL.YeFr.2H.1</i> <i>QWL.YeFr.2H.2</i>	Survival rate	4.62 10.21	8.4 17.2	Yerong × Franklin	177	DH lines	104
Barley	2H	–	Yellow leaf percentage	2.95-10.21	4.0-17.2	Yerong × Franklin	177	DH lines	104
Barley	2H	<i>QWI.YyFr.2H</i>	Plant healthiness	18.68	30.1	YYXT × Franklin	172	DH lines	127
Barley	3H	<i>SLw2.3</i>	Spike length	7.74	14.37	Yerong × Franklin	156	DH lines	125
Barley	3H	<i>tfy1.2-1</i> <i>tfy2.1-1</i>	Leaf chlorosis	7.31 9.28	36.0 34.1	TX9425 × Franklin	92	DH lines	126
Barley	3H	<i>tfy1.1-2</i>	Leaf chlorosis	7.31	36.0	TX9425 × Franklin	92	DH lines	126
Barley	3H	<i>yfy2.1-2</i> <i>yfy2.2-1</i>	Leaf yellowing	6.41 4.5	11.9 9.5	Yerong × Franklin	177	DH lines	126
Barley	3H	<i>QWI.YyFr.3H</i>	Plant healthiness	10.94	15.7	YYXT × Franklin	172	DH lines	127
Barley	3H	<i>QWL.YeFr.3H</i>	Survival rate	4.83	6.8	Yerong × Franklin	177	DH lines	104

Barley	4H	-	Yellow leaf percentage	3.78-16.51	6.7-26.7	Yerong × Franklin	177	DH lines	104
Barley	4H	<i>QWL.YeFr.4H</i>	Survival rate	14.48	23.9	Yerong × Franklin	177	DH lines	104
Barley	4H	QTL-AER	Aerenchyma formation	51.4	76.8	TAM407227 × Franklin	163	DH lines	108
Barley	4H	<i>QTL-WL-4H</i>	Waterlogging tolerance	19.2	34.6	TAM407227 × Franklin	163	DH lines	108
Barley	4H	-	Root porosity	6.4	25.6	Yerong × Franklin	177	DH lines	111
			Aerenchyma formation	9.4	44				
Barley	4H	<i>yfy2.1-3</i> <i>yfy2.2-3</i>	Leaf yellowing	9.25 10.37	18.5 22.4	Yerong × Franklin	177	DH lines	126
Barley	4H	-	Root porosity	12.1-13.5	35.7-39.0	YYXT × Franklin	126	DH lines	110
Barley	4H	<i>tfmas</i>	Biomass reduction	2.75	16.3	TX9425 × Franklin	92	DH lines	126
Barley	4H	<i>QWL.YyFr.4H</i>	Plant healthiness	5.25	7.0	YYXT × Franklin	172	DH lines	127
Barley	5H	<i>yfy1.1-2</i>	Leaf yellowing	3.94	7.6	Yerong × Franklin	177	DH lines	126
Barley	5H	<i>yfsur-2</i>	Leaf yellowing	5.05	13.1	Yerong × Franklin	177	DH lines	126
Barley	6H	<i>PHw2.1</i>	Plant height	5.52	9.74	Yerong × Franklin	156	DH lines	125
Barley	6H	-	Root porosity	3.7	10.2	Yerong × Franklin	177	DH lines	111
Barley	6H	<i>QWL.YyFr.6H</i>	Plant healthiness	4.72	6.2	YYXT × Franklin	172	DH lines	127
Barley	6H	-	Yellow leaf percentage	3.72-7.56	6.7-11.4	Yerong × Franklin	177	DH lines	104
Barley	6H	QTL-WL-6H	Waterlogging tolerance	4.4	6.3	TAM407227 × Franklin	163	DH lines	108
Barley	7H	QTL-WL-7H	Waterlogging tolerance	3.7	5.3	TAM407227 × Franklin	163	DH lines	108
Barley	7H	<i>yfy2.1-1</i>	Leaf yellowing	3.72	6.7	Yerong × Franklin	177	DH lines	126
Barley	7H	GYw1.2	Grain yield	7.45	30.43	Yerong × Franklin	156	DH lines	125
Barley	7H	<i>SPw1.1</i>	Spike per plant	3.31	8.13	Yerong × Franklin	156	DH lines	125
Barley	7H	<i>GSw1.3</i>	Grains per spike	7.35	9.06	Yerong × Franklin	156	DH lines	125

**Table S2.** The detailed information of syntenic candidate genes in barley, wheat, rice, and maize.

Gene	Annotation	Barley	Wheat A genome	Wheat B genome	Wheat D genome	Rice	Maize
<i>HRE2</i> ( <i>At2g47520</i> )	Ethylene-responsive transcription	ERF1 (HORVU.MOREX.r3.1HG0060770.1)	ERF1 (TraesCS1A02G231200.1)	ERF1 (TraesCS1B02G243200.1)	ERF1 (TraesCS1D02G230900.1)	ERF1 (Os05t0361700-01)	ERF1 (Zm00001d037941_P001)
<i>ZmEREB180</i>	Ethylene-responsive transcription	ERF2 (HORVU.MOREX.r3.4HG0405650)	ERF2 (TraesCS4A02G005600.1)	ERF2 (TraesCS4B02G299400.1)	ERF2 (TraesCS4D02G298400.1)	ERF2 (Os03t0183000)	ERF2 (Zm00001d027925_P001)
<i>SNORKEL1</i>	Ethylene-responsive transcription	ERF3 (HORVU.MOREX.r3.5HG0481240)	ERF3 (TraesCS5A02G215900.1)	ERF3 (TraesCS5B02G214400.1)	ERF3 (TraesCS5D02G223700.1)	ERF3 (Os09t0434500-01)	ERF3 (Zm00001d020595_P001)
<i>GRMZM2G053503</i>	Ethylene-responsive transcription	ERF4 (HORVU.MOREX.r3.5HG0497970.1)	ERF4 (TraesCS5A02G314600.1)	ERF4 (TraesCS5B02G315500.1)	ERF4 (TraesCS5D02G320800.1)	ERF4 (Os01t0313300-01)	ERF4 (Zm00001d009103_P001)
<i>Sub1A</i>	Ethylene-responsive transcription	N	ERF5 (TraesCS5A02G174700.1)	N	N	ERF5.1 (Os09t0287000)	N
<i>Sub1B</i>	Ethylene-responsive transcription	N	ERF5 (TraesCS5A02G174700.1)	N	N	ERF5.1 (Os09t0287000-01)	ERF5.1 (Zm00001d052087_P001)
<i>Sub1C</i>	Ethylene-responsive transcription	N	ERF5 (TraesCS5A02G174700.1)	N	N	ERF5.2 (Os09t0286600)	ERF5.2 (Zm00001d032095_P001)
<i>SNORKEL2</i>	Ethylene-responsive transcription	N	ERF6 (TraesCS7A02G120100.1)	ERF6 (TraesCS7B02G018400.1)	ERF6 (TraesCS7D02G118000.1)	ERF6 (Os12t0603300-01)	ERF6.1 (Zm00001d036251_P001), ERF6.2 (Zm00001d045262_P001)
<i>HRE1</i> ( <i>At1g72360</i> )	Ethylene-responsive transcription	ERF7 (HORVU.MOREX.r3.7HG0661060.1)	ERF7 (TraesCS7A02G158000.1)	ERF7 (TraesCS7B02G062200.2)	ERF7 (TraesCS7D02G158500.2)	ERF7 (Os06t0194000-02)	ERF7 (Zm00001d045044_P001)
<i>RAP2.2</i> ( <i>At3g14230</i> )	Ethylene-responsive transcription	ERF7 (HORVU.MOREX.r3.7HG0661060.1)	ERF7 (TraesCS7A02G158000.1)	ERF7 (TraesCS7B02G062200.1)	ERF7 (TraesCS7D02G158500.1)	ERF7 (Os06t0194000-01)	ERF7 (Zm00001d045044_P001)
<i>RAP2.12</i> ( <i>At1g53910</i> )	Ethylene-responsive transcription	ERF7 (HORVU.MOREX.r3.7HG0661060.1)	ERF7 (TraesCS7A02G158000.1)	ERF7 (TraesCS7B02G062200.1)	ERF7 (TraesCS7D02G158500.1)	ERF7 (Os06t0194000-01)	ERF7 (Zm00001d045044_P001)
<i>WRK45</i>	WRKY transcription	WRKY1 (HORVU.MOREX.r3.2HG0096750.1)	WRKY1 (TraesCS2A02G011000.1)	WRKY1 (TraesCS2B02G010500.1)	WRKY1 (TraesCS2D02G011700.1)	WRKY2 (Os11t0409000-01)	WRKY1 (Zm00001d007329_P001)
<i>WRK40</i>	WRKY transcription	WRKY2 (HORVU.MOREX.r3.6HG0568570.1)	WRKY2 (TraesCS6A02G146900.1)	WRKY2 (TraesCS6B02G175100.2)	WRKY2 (TraesCS6D02G136200.1)	WRKY1 (Os02t0181300-01)	WRKY2 (Zm00001d015515_P001)
<i>GRMZM2G416632</i>	Glutathione S-transferase	GST1 (HORVU.MOREX.r3.5HG0487860.1)	GST1 (TraesCS5A02G247500.2)	GST1 (TraesCS5B02G244700.1)	GST1 (TraesCS5D02G254000.1)	GST1 (Os09t0467200-01)	GST1 (Zm00001d020780_P001; <span style="color: red;">GST23</span> )
<i>GRMZM2G300965</i>	Respiratory burst oxidase, putative	RBOH1 (HORVU.MOREX.r3.5HG0444960.1)	RBOH1 (TraesCS5A02G093600.1)	RBOH1 (TraesCS5B02G099700.1)	RBOH1 (TraesCS5D02G105900.1)	RBOH1 (Os12t0541300-01)	RBOH1 (Zm00001d023859_P001)
<i>GRMZM2G055704</i>	Heavy metal transport/detoxification superfamily protein	HMS1 (HORVU.MOREX.r3.4HG0410950.1)	HMS1 (TraesCS5A02G492100.1)	HMS1 (TraesCS4B02G319800.1)	N	HMS1 (Os03t0126700-01)	HMS1 (Zm00001d027454_P001)