

Table S1 Root traits associated QTLs in direct-seeded rice (DSR) conditions

Trait	Donor	Population	QTLs	Chromosome	Flanking marker	References
Root length	-	HKR47 × MAS26	<i>qRL_{8.1}</i>	8	RM8243	[1]
	-	HKR47 × MAS26	<i>qRL_{9.1}</i>	9	RM524-RM257 (13.2-66.1 cM)	
	IR94225-B-82-B,	MASARB25 × PB1460	<i>qRL_{8.2}</i>	8	RM547-RM331 (58.1-65.0 cM),	[1,2]
	IR94226-B-177-B	HKR47 × MAS26			RM310-RM547 (57.0-58.1 cM)	
Root hair length	IR94225-B-82-B,	-	<i>qRHL_{1.1}</i>	1	-	[3]
Root hair density	IR94226-B-177-B					
	IR94225-B-82-B,	-	<i>qRHD_{1.1}</i>	1	-	[3]
	IR94226-B-177-B		<i>qRHD_{5.1}</i>	5		
Nodal root number	IR94225-B-82-B,	-	<i>qNR_{5.1}</i>	5	-	[3]
	IR94226-B-177-B		<i>qNR_{4.1}</i>	4		
Root volume	-	-	<i>qRV_{2.1}</i>	2	RM485-RM7033 (0.0-7.9 cM)	[4,5]
Root thickness	-	HKR47 × MAS26	<i>qRT_{1.1}</i>	1	RM488-RM237 (101.4-112.9 cM)	[4-6]
Fresh root weight	-	MASARB25 × PB1460	<i>qFRW_{2.1}</i>	2	RM485-RM7033 (0.0-7.9 cM)	[4,5]
Anaerobic germination	IR93312-30- 101-20-13-66-6	Donor:Khao Hlan On, Recipient: IR64	<i>qAG_{9.1}</i>	9	RM8303-RM5526	[7]
Early uniform emergence	IR91648-B- 32-B	Donor: Moroberekan Receipient: Swarna	<i>qAG_{9.2}</i>	9		
			<i>qEUE_{11.1}</i>	11	id1100085-id11001535	[8]
			<i>qEMM1.1</i>	1		[8]
Early vigor	IR94226-B- 177-B	Aus276 × MTU1010	<i>qEVV_{9.1}</i> (Donor: Aus276)	9	Flanking markers: id5000759-id5001182, ud9000737-id9002704,id1005271-id1006691; peak markers: id5001182, ud9000737, id1005271	[3]
Drought tolerance	IR74371-46- 1-1	IR74371-46-1-1/2*Sabitri	<i>qDTY_{12.1}</i>	12	<i>qDTY_{12.1}</i> RM28166-RM28199	[4,5,9,10]
			<i>qDTY_{2.3}</i>	2	<i>qDTY_{2.3}</i> RM3212-RM250	
			<i>qDTY_{3.2}</i>	3	<i>qDTY_{3.2}</i> RM22-RM545	

	IR6322-34- 223	Donors: N22, Apo N22/Swarna, Apo/2*Swarna Ldg Rm8213	$qDTY_{3.1}$	3	$qDTY_{3.1}$; RM416	[6,8,10–12]
			$qDTY_{1.1}$	1	$qDTY_{1.1}$; RM11943-RM12091	
			$qDTY_{2.1}$	2	$qDTY$; RM324	
Lodging resistance	IR91648-B- 289-B	Donor: Swarna	$qLDG_{3.1}$	3	id3000090-id300057	[8]
Lodging resistance	IR91648-B- 289-B	Donor Moroberekan	$qLDG_{4.1}$	4	id4004461-id4009390	[8]

Table S2 Chromosome wise QTLs/genes related to root developmental traits in rice along with their locus ID and encoded protein

Root Phenotype	Gene	Chromosome	Locus ID		Encoded protein	References
			RAP	MSU		
Crown root	<i>OsRAA1</i>	1	Os01g0257300	LOC_Os01g15340	GTP-binding protein	[13]
	<i>OsYUC1</i>	1	Os01g0645400	LOC_Os01g45760	Flavin monooxygenase	[14]
	<i>OsPIN3t (OsPIN10a)</i>	1	Os01g0643300	LOC_Os01g45550	Auxin efflux carrier	[15]
	<i>OsmiR393a</i>	1	-	-	MicroRNA	[16]
	<i>FIB/OsTAA1</i>	1	Os01g0169800	LOC_Os01g07500	Aminotransferase	[17]
	<i>ERF3</i>	1	Os01g0797600	LOC_Os01g58420	AP2/ERF transcription factor	[18]
	<i>REH1/ OsPIN1b</i>	2	Os02g0743400	LOC_Os02g50960	Auxin efflux carrier	[19]
	<i>OsRR2</i>	2	Os02g0557800	LOC_Os02g35180	Type-A response regulator	[20]
	<i>OsCAND1</i>	2	Os02g0167700	LOC_Os02g07120	SCF ^{TIR1} ubiquitin ligase	[21]
	<i>CRL1/ARL1</i>	3	Os03g0149100	LOC_Os03g05510	LOB/ASL transcription factor	[22,23]
	<i>OsCOW1 (OsYUC8)</i>	3	Os03g0162000	LOC_Os03g06654	Flavin monooxygenase	[24]
	<i>CRL4/ OsGNOM1</i>	3	Os03g0666100	LOC_Os03g46330	Arf-GEF	[25,26]
	<i>OsRR1</i>	4	Os04g0442300	LOC_Os04g36070	Type-A response regulator	[27]
	<i>OsmiR393b</i>	4	-	-	MicroRNA	[16]
	<i>OsMT2b</i>	5	Os05g0111300	LOC_Os05g02070	Metallothionein	[28]
	<i>OsPIN2</i>	6	Os06g0660200	LOC_Os06g44970	Auxin efflux carrier	[29]
	<i>WOX11</i>	7	Os07g0684900	LOC_Os07g48560	WUS-related homeobox protein	[20]
	<i>CRL5</i>	7	Os07g0124700	LOC_Os07g03250	AP2/ERF transcription factor	[27]
	<i>CRL6</i>	7	Os07g0497100	LOC_Os07g31450	CHD family protein	[30]
	<i>OsIAA3 (OsIAA31)</i>	12	Os12g0601400	LOC_Os12g40900	Aux/IAA protein	[31]
	<i>OsPID</i>	12	Os12g0614600	LOC_Os12g42020	Serine/threonine kinase	[32]
Lateral root	<i>OsAUX1</i>	1	Os01g0856500	LOC_Os01g63770	Auxin influx carrier	[33]
	<i>LRL2/ OsCYP2</i>	2	Os02g0121300	LOC_Os02g02890	Cyclophilin	[34]
	<i>OsIAA11</i>	3	Os03g0633500	LOC_Os03g43400	Aux/IAA protein	[35]
	<i>OsIAA13</i>	3	Os03g0742900	LOC_Os03g53150	Aux/IAA protein	[36]
	<i>OsHO1</i>	6	Os06g0603000	LOC_Os06g40080	Heme oxygenase	[29]
	<i>OsORC3</i>	10	Os10g0402200	LOC_Os10g26280	Origin recognition complex protein	[37]

Root hair number	<i>OsWOX3A/ OsNS (NAL2)</i>	11	Os11g0102100	LOC_Os11g01130	WUS-related homeobox protein	[38]
	<i>OsWOX3A/ OsNS (NAL3)</i>	12	Os12g0101600	LOC_Os12g01120	WUS-related homeobox protein	[38]
	<i>SOR1</i>	4	Os04g0101800	LOC_Os04g01160	E3 ubiquitin ligase	[39]
	<i>OsFHI</i>	1	Os01g0897700	LOC_Os01g67240	Multidomain protein	[40]
	<i>SRH2</i>	3	Os03g0300000	LOC_Os03g18820	Xyloglucan 6-xylosyltransferase	[41]
	<i>OsRHL1</i>	6	Os06g0184000	LOC_Os06g08500	bHLH transcription factor	[42]
	<i>OsEXPA17</i>	6	Os06g0108600	LOC_Os06g01920	Expansin	[43]
	<i>RTH1/ OsAPY1</i>	7	Os07g0682800	LOC_Os07g48430	ATP diphosphohydrolase	[44]
	<i>OsSDNP1</i>	10	Os10g0122600	LOC_Os10g03400	Phosphatidylinositol transfer protein	[45]
	<i>OsEXPA30</i>	10	Os10g0535900	LOC_Os10g39110	Expansin	[43]
Root meristem formation	<i>RTH2/ OsCSLD1</i>	10	Os10g0578200	LOC_Os10g42750	Cellulose synthase-like protein	[46,47])
	<i>QHB</i>	1	Os01g0854500	LOC_Os01g63510	WUSCHEL-type homeobox protein	[48]
	<i>DOCS1</i>	2	Os02g0236100	LOC_Os02g14120	LRR-RLK	[49]
	<i>OsIAA23</i>	6	Os06g0597000	LOC_Os06g39590	Aux/IAA protein	[50]
	<i>OsSHR1</i>	7	Os07g0586900	LOC_Os07g39820	GRAS transcription factor	[48,51]
Root length	<i>OsSCR1</i>	11	Os11g0124300	LOC_Os11g03110	GRAS transcription factor	[51,52]
	<i>OsSPR1</i>	1	Os01g0898300	LOC_Os01g67290	Armadillo-like repeat domain protein	[53]
	<i>OsEXPA8</i>	1	Os01g0248900	LOC_Os01g14650	Expansin	[54]
	<i>OsMOGS</i>	1	Os01g0921200	LOC_Os01g69210	Mannosyl-oligosaccharide glucosidase	[55]
	<i>OsCK11</i>	2	Os02g0622100	LOC_Os02g40860	Putative casein kinase I	[45]
	<i>OsCYT-INV1</i>	2	Os02g0550600	LOC_Os02g34560	Alkaline/neutral invertase	[56]
	<i>OsARF12</i>	4	Os04g0671900	LOC_Os04g57610	Auxin response factor	[57]
	<i>RT/OsGLU3</i>	4	Os04g0497200	LOC_Os04g41970	Endo-1,4- β -D-glucanase	[58,59]
	<i>OsRPK1</i>	5	Os05g0486100	LOC_Os05g40770	LRR-RLK	[60]
	<i>OsDGL1</i>	7	Os07g0209000	LOC_Os07g10830	Dolichyl-diphosphooligosaccharide-protein glycosyltransferase	[61]

Nutrient uptake related genes	<i>OsGNA1</i>	9	Os09g0488000	LOC_Os09g31310	Glucosamine-6-P acetyltransferase	[62]
	<i>DRO1</i>	9	Os09g0439800	LOC_Os09g26840		[63]
	<i>PSTOL1</i>	12	Os12g0448900	LOC_Os12g26290	receptor-like cytoplasmic kinase	
	<i>OsPT1</i>	3	Os03g0150600	LOC_Os03g05620	inorganic phosphate transporter	[64]
	<i>OsPT8</i>	10	Os10g0444700	LOC_Os10g30790	inorganic phosphate transporter	[53]
	<i>OsNAR2.2</i>	4	Os04g0480200	LOC_Os04g40410	high affinity nitrate transporter	[65]
	<i>OsEXP3</i>	5	Os05g0276500	LOC_Os05g19570	Alpha-expansin-3	[66]
	<i>OsZIP4</i>	8	Os08g0207500	LOC_Os08g10630	Zrt-Irt-like protein	[67]
	<i>TOND1</i>	12	Os12g0630100	LOC_Os12g43440	4,metal cation transporter thaumatin	[68]

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