

Supplementary Information Tables S1–S3.

Physical mapping of QTLs for root traits in a population of recombinant inbred lines of hexaploid wheat

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Table S1. Genetic map of root QTL with a LOD > 3.0. Shown are flanking marker positions in cM, LOD score, additive effect and percent variation contributed by the QTL.

QTL: name, trait and chromosome	Left marker	cM	Right marker	cM	LOD	Add*	% var'n
Root dry weight							
<i>Qrdw-2A</i>	wsnp_Ra_c66636_64922359	183.8	RAC875_c66695_1376	185.2	3.91	-0.013	7.0
<i>Qrdw-2B</i>	Excalibur_c30207_261	157.0	Excalibur_c34380_275	159.18	5.29	0.017	10.6
<i>Qrdw-4A</i>	Excalibur_c539_1253	138.9	wsnp_Ku_c1205_2398925	141.1	3.54	0.013	6.4
Root diameter							
<i>Qrd-4A</i>	BS00109722_51	104.2	wsnp_Ex_c1373_2628597	106.1	4.08	0.003	5.9
<i>Qrd-4B1</i>	RAC875_c56905_265	85.3	BS00063035_51	87.2	3.10	0.004	7.4
<i>Qrd-4B2</i>	IAAV9209	135.8	tplb0036n21_1765	137.3	6.82	-0.006	15.6
<i>Qrd-5A</i>	wsnp_Ex_c57094_58953404	24.8	RAC875_c30001_200	27.4	3.92	-0.003	4.9
<i>Qrd-5D</i>	RAC875_c51455_182	32.3	BS00021901_51	33.7	11.4 4	-0.005	13.8
<i>Qrd-6A</i>	Tdurum_contig30082_197	106.4	Excalibur_c49419_202	108.2	5.90	-0.004	7.6
<i>Qrd-7A</i>	IAAV1372	184.7	BS00073170_51	186.2	5.26	-0.004	7.5
Total nodal root number							
<i>Qnrn-2B</i>	RAC875_c102981_396	141.6	Kukri_c691_504	143.2	3.16	0.858	6.0
<i>Qnrn-4B</i>	Tdurum_contig33737_157	77.8	Tdurum_contig30537_228	79.6	4.28	-1.014	8.2
<i>Qnrn-6B</i>	JD_c8399_626	69.5	Tdurum_contig55201_928	81.7	3.69	-0.979	6.3
<i>Qnrn-7A1</i>	D_GDEEGVY01CQJ66_272	165.2	Tdurum_contig63598_188	167.2	3.13	-0.902	6.5
<i>Qnrn-7A2</i>	Excalibur_c12500_116	123.6	Tdurum_contig82510_574	126.9	6.28	-1.269	12.2
Nodal root number per stem							
<i>Qnrns-2B</i>	TA006140-0798	181.8	Ku_c66850_510	184.5	3.86	0.088	6.0
<i>Qnrns-4B</i>	Jagger_c1432_289	129.7	Tdurum_contig11735_1294	131.6	4.52	-0.096	7.2
<i>Qnrns-6D</i>	RFL_Contig6056_604	2.9	CAP7_c2537_344	4.6	3.48	0.080	5.1
<i>Qnrns-7A</i>	Excalibur_c12500_116	123.6	Tdurum_contig82510_574	126.9	13.1 4	-0.167	20.2
<i>Qnrns-7B</i>	BS00055861_51	133.9	RAC875_c79695_343	135.9	3.01	0.078	4.8
Root angle							
<i>Qra-4B</i>	Jagger_c1432_289	129.7	Tdurum_contig11735_1294	131.6	5.01	-0.026	24.1
Specific root length							
<i>Qsrl-4B1</i>	tplb0036n21_1765	137.3	Tdurum_contig64848_104	138.6	5.50	0.017	19.6
<i>Qsrl-6A</i>	CAP12_c2701_221	135.2	Tdurum_contig28847_322	138.1	4.62	0.012	9.5
Root to shoot ratio							
<i>Qrsr-3A</i>	IACX333	170.2	BS00050109_51	172.0	5.92	-0.008	15
Shoot dry weight							
<i>Qsdw-2A</i>	BobWhite_c16248_382	209.1	Kukri_c18104_1416	210.7	3.32	-0.04	5.5
<i>Qsdw-3B</i>	RAC875_c48556_278	183.6	RAC875_c28912_306	185.4	6.51	-0.059	11.2
<i>Qsdw-4A</i>	wsnp_Ex_c7011_12080274	94.0	IACX1427	95.4	3.11	0.035	5.9

*Positive alleles contributed by Spica and negative alleles contributed by Maringa.

Table S2. Genetic map of root QTL with a LOD < 3.0. Shown are flanking marker positions in cM, LOD score, additive effect and percent variation contributed by the QTL.

QTL: name, trait and chromosome	Left marker	cM	Right marker	cM	LOD	Add*	% var'n
Root dry weight							
<i>Qrdw-1A</i>	RAC875_c1599_342	260.9	BS00022824_51	266.1	2.722	-0.011	4.5
<i>Qrdw-1B</i>	Excalibur_rep_c107678_98	287.8	CAP7_c3847_204	290.1	1.654	-0.008	3.0
<i>Qrdw-4B</i>	TA004394-0527	126.2	BS00011085_51	128.2	1.613	0.009	3.0
<i>Qrdw-5A</i>	RAC875_rep_c76193_513	125.9	BS00088851_51	128.0	2.764	0.011	4.8
<i>Qrdw-5B</i>	BS00021993_51	0.0	Tdurum_contig28552_211	8.7	1.967	0.010	3.3
<i>Qrdw-6B</i>	Excalibur_c2328_1207	165.8	BobWhite_c42198_254	166.6	1.378	-0.008	2.6
<i>Qrdw-6D1</i>	wsnp_Ex_c14691_227631_71	27.4	BobWhite_c34996_280	28.3	2.198	0.009	3.6
<i>Qrdw-6D2</i>	CAP7_c2537_344	114.8	RFL_Contig6056_604	116.5	1.36	0.007	2.2
<i>Qrdw-7A</i>	RAC875_c35723_106	110.7	Tdurum_contig8615_370	112.6	2.144	-0.010	3.9
Root diameter							
<i>Qrd-3A</i>	wsnp_Ex_rep_c66685_650_03254	178.8	GENE-4795_75	180.2	2.70	-0.003	3.5
<i>Qrd-5B</i>	BS00068200_51	229.9	wsnp_Ra_c24619_3416810_4	234.7	2.93	0.003	3.7
<i>Qrd-7B</i>	RAC875_rep_c73965_114	116.8	Excalibur_c13444_235	118.8	2.00	-0.002	2.6
Total nodal root number							
<i>Qnrn-3B</i>	wsnp_JD_c10233_109365_35	212.6	BS00049639_51	214.6	2.514	-0.763	4.8
Nodal root number per stem							
<i>Qnrns-2A1</i>	RAC875_rep_c83950_222	16.9	Tdurum_contig66353_358	18.5	2.459	-0.067	3.6
<i>Qnrns-2A2</i>	Kukri_rep_c109732_72	215.8	Excalibur_c12980_2621	217.2	2.693	0.070	3.9
<i>Qnrns-3A</i>	BS00050109_51	112.6	IACX333	114.4	2.348	-0.066	3.6
Root angle							
<i>Qra-1A</i>	GENE-0235_245	104.4	D_contig04348_649	107.5	2.329	-0.017	10.9
<i>Qra-3A</i>	Kukri_rep_c106620_208	50.7	wsnp_CAP8_c6939_324253_0	51.6	2.558	-0.017	11.1
<i>Qra-5B</i>	RAC875_c31261_367	101.0	wsnp_Ku_c11138_1825246_1	101.6	2.248	-0.016	10.2
<i>Qra-6B</i>	CAP11_c816_470	46.7	Excalibur_c13206_108	50.5	2.292	-0.017	10.1
Specific root length							
<i>Qsrl-3B</i>	Kukri_c43588_354	62.9	Tdurum_contig45817_193	64.7	1.616	-0.007	3.2
<i>Qsrl-4A</i>	wsnp_Ex_c1373_2628597	195.4	BS00109722_51	197.3	1.803	-0.007	3.8
<i>Qsrl-4B2</i>	Excalibur_c56787_95	152.4	BS00063035_51	154.7	1.714	-0.009	6.5
<i>Qsrl-5D</i>	Kukri_c13045_302	203.0	BS00021901_51	204.8	2.255	0.008	4.4
<i>Qsrl-7A</i>	BobWhite_c5396_296	203.5	GENE-4508_109	205.5	2.628	0.009	5.7
Root to shoot ratio							
<i>Qrsr-2A</i>	BS00081195_51	104.4	BS00012320_51	109.4	1.886	-0.005	5.0
<i>Qrsr-3B</i>	RFL_Contig4667_3535	187.8	BS00022051_51	189.1	2.157	0.005	5.8
<i>Qrsr-3D</i>	Kukri_c908_584	183.2	BobWhite_c27145_731	184.3	2.197	0.005	5.4
<i>Qrsr-7B</i>	Kukri_c9405_379	128.4	Tdurum_contig74753_946	130.8	2.73	0.006	6.9
<i>Qrsr-7D</i>	D_GBQ4KXB02FR7XF_153	0.0	RAC875_c59686_292	1.3	2.824	0.005	6.5
Shoot dry weight							
<i>Qsdw-6D</i>	RFL_Contig6056_604	116.5	wsnp_BE445201D_Ta_1_1	119.4	1.87	0.029	2.9
Tiller number							
<i>Qtn-3A</i>	IACX333	114.4	BS00084158_51	117.3	2.896	0.338	6.9
<i>Qtn-4B</i>	wsnp_Ex_c6739_1164640_7	200.5	tp1b0024a16_411	203.1	1.915	-0.266	4.5
<i>Qtn-6A1</i>	Excalibur_c96749_512	22.0	Kukri_c40994_61	22.4	2.957	-0.331	6.8
<i>Qtn-6A2</i>	Excalibur_c49419_202	145.6	Tdurum_contig30082_197	147.4	1.941	0.267	4.5

*Positive alleles contributed by Spica and negative alleles contributed by Maringa.

Table S3. List of wheat root genes and the wheat homologs of genes associated with root development and architecture cloned from other monocotyledons. Gene names used the same nomenclature as original references and are preceded with *Ta* to indicate *Triticum aestivum*, followed by designation of the particular homeolog (-*A*, -*B* or -*D*). Gene names and physical locations are provided for the IWGSC v1.0 genome. A brief description of the trait, reference, and species from which the genes were cloned are also provided.

Gene name	Trait	Species	Reference	IWGSC v 1.0 gene name	Physical location
<i>TaMOR-A*</i>	Root architecture	Wheat	[36]	<i>TraesCS4A02G415400</i>	chr4A: 685380302-685381598
<i>TaMOR-B</i>				<i>TraesCS4B02G316200</i>	chr4B: 605691920-605693239
<i>TaMOR-D</i>				<i>TraesCS4D02G312800</i>	chr4D: 478997945-478999338
<i>TaANDRO-A</i>	Deeper rooting	Wheat	[37]	<i>TraesCS5A02G213300</i>	chr5A: 428994186-428997632
<i>TaBNDRO-B</i>				<i>TraesCS5B02G210500</i>	chr5B: 381041995-381044714
<i>TaDNDRO-D</i>				<i>TraesCS5D02G218700</i>	chr5D: 327631371-327634216
<i>TaARF4-A</i>	Root and shoot traits- auxin response factors	Wheat	[38]	<i>TraesCS3A02G442000</i>	chr3A: 684040773-684045606
<i>TaARF4-B</i>				<i>TraesCS3B02G475800</i>	chr3B: 724737433-724742425
<i>TaARF4-D</i>				<i>TraesCS3D02G434700</i>	chr3D: 547298032-547302973
<i>TaSERK-A</i>	Root and shoot traits	Wheat	[39]	<i>TraesCS2A02G343100</i>	chr2A: 580017609-580023752
<i>TaSERK-B</i>				<i>TraesCS2B02G340700</i>	chr2B: 486190984-486197028
<i>TaSERK-D</i>				<i>TraesCS2D02G321400</i>	chr2D: 412833158-412839366
<i>TaBRI1-A</i>	Interacts with <i>TaSERK</i>	Wheat	[40]	<i>TraesCS3A02G245000</i>	chr3A: 458678631-458682691
<i>TaBRI1-B</i>				<i>TraesCS3B02G275000</i>	chr3B: 443803664-443807278
<i>TaBRI1-D</i>				<i>TraesCS3D02G246500</i>	chr3D: 344337925-344342369
<i>TaVP1-A</i>	Vacuolar-PPase	Wheat	[41]	<i>TraesCS7A02G141300</i>	chr7A: 92888389-92893250
<i>TaVP1-B</i>				<i>TraesCS7B02G042600</i>	chr7B: 42027289-42032517
<i>TaVP1-D</i>				<i>TraesCS7D02G142600</i>	chr7D: 90848363-90854069
<i>TaVRN-A1</i>	Root system architecture	Wheat	[18]	<i>TraesCS5A02G391700</i>	chr5A: 587411454-587423416
<i>TaVRN-B1</i>				<i>TraesCS5B02G396600</i>	chr5B: 573802883-573816070
<i>TaVRN-D1</i>				<i>TraesCS5D02G401500</i>	chr5D: 467176609-467184508
<i>TaPSTOL</i>	Root biomass	Wheat	[42]	Not annotated	chr5A: 41374604-41378275
Other species					
<i>TaCRL5-A</i>	Crown roots	Rice <i>CRL5</i>	[17]	<i>TraesCS2A02G267600</i>	chr2A: 428908059-428911931
<i>TaCRL5-B</i>				<i>TraesCS2B02G268100</i>	chr2B: 361422652-361426297
<i>TaCRL5-D</i>				<i>TraesCS2D02G256600</i>	chr2D: 311715447-311719061
<i>TaEXP10-A</i>	Root cell elongation	Rice <i>OsEXP10</i>	[19]	<i>TraesCS2A02G393700</i>	chr2A: 643439927-643444151
<i>TaEXP10-B</i>				<i>TraesCS2B02G411700</i>	chr2B: 585891499-585895732
<i>TaEXP10-D</i>				<i>TraesCS2D02G391600</i>	chr2D: 498768162-498772341
<i>TaSNAC1-A</i>	Root size	Rice <i>SNAC1</i>	[43]	<i>TraesCS5A02G468300</i>	chr5A: 645726140-645727775
<i>TaSNAC1-B</i>				<i>TraesCS5B02G480900</i>	chr5B: 653432387-653434033
<i>TaSNAC1-D</i>				<i>TraesCS5D02G481200</i>	chr5D: 519277079-519278774
<i>TaSOR1-A</i>	Root ethylene responses	Rice <i>SOR1</i>	[44]	<i>TraesCS2A02G045100</i>	chr2A: 17738033-17741923
<i>TaSOR1-B</i>				<i>TraesCS2B02G057300</i>	chr2B: 27895909-27899621
<i>TaSOR1-D</i>				<i>TraesCS2D02G043700</i>	chr2D: 15730614-15734542
<i>TaRUM1-A</i>	Root initiation	Maize <i>RUM1</i>	[45]	<i>TraesCS3A02G270000</i>	chr3A: 496704577-496707472
<i>TaRUM1-B</i>				<i>TraesCS3B02G303900</i>	chr3B: 487906086-487911438
<i>TaRUM1-D</i>				<i>TraesCS3D02G269700</i>	chr3D: 374205888-374211351
<i>TaPIN1-A</i>	Root emergence and tillering	Rice <i>OsPIN1</i>	[46]	<i>TraesCS4A02G188100</i>	chr4A: 466938697-466941682
<i>TaPIN1-B</i>				<i>TraesCS4B02G130100</i>	chr4B: 170926810-170929710
<i>TaPIN1-D</i>				<i>TraesCS4D02G125300</i>	chr4D: 109469533-109472292

<i>TaWOX11-A</i>	Crown root development	Rice <i>WOX11</i>	[47]	<i>TraesCS2A02G100700</i>	chr2A: 53782606-53785288
<i>TaWOX11-B</i>				<i>TraesCS2B02G117900</i>	chr2B: 81755546-81758516
<i>TaWOX11-D</i>				<i>TraesCS2D02G100200</i>	chr2D: 52227203-52229885
<i>TaGNA1-A</i>	Root cell shape	Rice <i>OsGNA1</i>	[48]	<i>TraesCS5A02G264900</i>	chr5A: 476850991-476855275
<i>TaGNA1-B</i>				<i>TraesCS5B02G264500</i>	chr5B: 448600463-448601077
<i>TaGNA1-D</i>				<i>TraesCS5D02G272900</i>	chr5D: 375745767-375748324
<i>TaSPR1-A</i>	Short postembryonic root	Rice <i>OsSPR1</i>	[49]	<i>TraesCS3A02G397500</i>	chr3A: 644803705-644811301
<i>TaSPR1-B</i>				<i>TraesCS3B02G429400</i>	chr3B: 668069692-668076933
<i>TaSPR1-D</i>				<i>TraesCS3D02G391300</i>	chr3D: 506172242-506178602
<i>TaCOW1-A</i>	Root to shoot ratio	Rice <i>OsCOW1</i>	[50]	<i>TraesCS4A02G027500</i>	chr4A: 19447812-19450783
<i>TaCOW1-B</i>				<i>TraesCS4B02G278300</i>	chr4B: 560663067-560665760
<i>TaCOW1-D</i>				<i>TraesCS4D02G276600</i>	chr4D: 447910002-447913028
<i>TaWAK1-A1</i>	Root growth	Barley <i>HvWAK1</i>	[51]	<i>TraesCS4A02G499928</i>	chr4A: 744536044-744539773
<i>TaWAK1-A2</i>				<i>TraesCS7A02G000100</i>	chr7A: 238043-241215
<i>TaHDAC1-A</i>	Lateral root formation	Rice <i>OsHDAC1</i>	[52]	<i>TraesCS7A02G365600</i>	chr7A: 539543850-539554190
<i>TaHDAC1-B</i>				<i>TraesCS7B02G261800</i>	chr7B: 482237779-482248552
<i>TaHDAC1-D</i>				<i>TraesCS7D02G356800</i>	chr7D: 459923113-459936250
<i>TaGSK2-A</i>	Lateral root formation	Rice <i>OsGSK2</i>	[52]	<i>TraesCS3A02G136500</i>	chr3A: 114041077-114045106
<i>TaGSK2-D</i>				<i>TraesCS3D02G137200</i>	chr3D: 95945752-95950119
<i>TaBZR1-A</i>	Lateral root formation	Rice <i>OsBZR1</i>	[52]	<i>TraesCS2A02G187800</i>	chr2A: 150123158-150124982
<i>TaBZR1-B</i>				<i>TraesCS2B02G219300</i>	chr2B: 209436541-209438293
<i>TaBZR1-D</i>				<i>TraesCS2D02G199900</i>	chr2D: 151325675-151327278
<i>TaCRD1-A</i>	Crown root development	Rice <i>CRD1</i>	[53]	<i>TraesCS3A02G199400</i>	chr3A: 325281188-325311105
<i>TaCRD1-B</i>				<i>TraesCS3B02G229100</i>	chr3B: 335836563-335873333
<i>TaCRD1-D</i>				<i>TraesCS3D02G205700</i>	chr3D: 264696256-264720565
<i>TaEGT1-A</i>	Root angle	Barley <i>EGT1</i>	[54]	<i>TraesCS6A02G272800</i>	chr6A: 499397353-499400701
<i>TaEGT1-B</i>				<i>TraesCS6B02G300200</i>	chr6B: 538363931-538367345
<i>TaEGT1-D</i>				<i>TraesCS6D02G252800</i>	chr6D: 357002985-357006388
<i>TaEGT2-A</i>	Root angle	Barley <i>EGT2</i>	[20]	<i>TraesCS5A02G102000</i>	chr5A: 151732800-151736140
<i>TaEGT2-B</i>				<i>TraesCS5B02G164200</i>	chr5B: 143293893-143296491
<i>TaEGT2-D</i>				<i>TraesCS5D02G171500</i>	chr5D: 131504758-131508027
<i>TaLAA11-A</i>	Lateral root growth	Rice <i>OsLAA11</i>	[55]	<i>TraesCS5A02G378300</i>	chr5A: 575657011-575659289
<i>TaLAA11-B</i>				<i>TraesCS5B02G381900</i>	chr5B: 559990916-559992903
<i>TaLAA11-D</i>				<i>TraesCS5D02G388300</i>	chr5D: 457775681-457777965
<i>TaLAA13-A</i>	Lateral root growth	Rice <i>OsLAA13**</i>	[56]	<i>TraesCS5A02G382600</i>	chr5A: 580464947-580467685
<i>TaLAA13-B</i>				<i>TraesCS5B02G386800</i>	chr5B: 565928821-565931697
<i>TaLAA13-D</i>				<i>TraesCS5D02G392000</i>	chr5D: 460393490-460396369
<i>TaLAA9-A</i>	Gravitropic response	Rice <i>OsLAA9</i>	[57]	<i>TraesCS6A02G373300</i>	chr6A: 596739621-596740759
<i>TaLAA9-B</i>				<i>TraesCS6B02G411000</i>	chr6B: 685017015-685018041
<i>TaLAA9-D</i>				<i>TraesCS6D02G357500</i>	chr6D: 451082161-451083072
<i>TaLAA15a-A***</i>	Gravitropic response	Rice <i>OsLAA15</i>	[16]	<i>TraesCS7A02G371500</i>	chr7A: 545472957-545474340
<i>TaLAA15a-B***</i>				<i>TraesCS7B02G256100</i>	chr7B: 474642958-474643848
<i>TaLAA15a-D***</i>				<i>TraesCS7D02G351400</i>	chr7D: 452153857-452154744
<i>TaLAA3-A</i>	Gravitropic response	Rice <i>OsLAA3</i>	[58]	<i>TraesCS5A02G058700</i>	chr5A: 57562924-57564218
<i>TaLAA3-B</i>				<i>TraesCS5B02G058800</i>	chr5B: 64418744-64420036
<i>TaLAA3-D</i>				<i>TraesCS5D02G069200</i>	chr5D: 66667985-66669320
<i>TaPIN2-A</i>	Root angle	Rice <i>OsPIN2</i>	[59]	<i>TraesCS7A02G492400</i>	chr7A: 681011336-681015619
<i>TaPIN2-B</i>				<i>TraesCS7B02G398100</i>	chr7B: 664106649-664110679
<i>TaPIN2-D</i>				<i>TraesCS7D02G478800</i>	chr7D: 589512605-589516322
<i>TaCYP2-A</i>	Lateral root development	Rice <i>OsCYP2</i>	[60]	<i>TraesCS6A02G068900</i>	chr6A: 37407147-37408119

<i>TaCYP2-B</i>				<i>TraesCS6B02G093100</i>	chr6B: 68922518-68923420
<i>TaCYP2-D</i>				<i>TraesCS6D02G066700</i>	chr6D: 32693962-32694930
<i>TaRSA3.2-A</i>	Root angle	Maize <i>ZmRSA3.2</i>	[61]	<i>TraesCS3A02G397900</i>	chr3A: 645129450-645133585
<i>TaRSA3.2-B</i>				<i>TraesCS3B02G429900</i>	chr3B: 669424620-669428960
<i>TaRSA3.2-D</i>				<i>TraesCS3D02G391800</i>	chr3D: 507026845-507030741
<i>TaCBLI-A</i>	Root angle	Maize <i>CBLI</i>	[62]	<i>TraesCS5A02G377900</i>	chr5A: 575594327-575595945
<i>TaCBLI-B</i>				<i>TraesCS5B02G381500</i>	chr5B: 559763470-559765063
<i>TaCBLI-D</i>				<i>TraesCS5D02G387900</i>	chr5D: 457663678-457665461
<i>TaBIGE-A</i>	Seminal root number	Maize <i>BIGE</i>	[63]	<i>TraesCS4A02G350200</i>	chr4A: 626439275-626443664
<i>TaBIGE-B</i>				<i>TraesCS5B02G522900</i>	chr5B: 684227667-684231381
<i>TaBIGE-D</i>				<i>TraesCS5D02G521600</i>	chr5D: 542589766-542592882

* The *TaMOR* genes of wheat are homologous to the *CRL1* and *RTCS* genes originally identified in rice and maize [64].

** The recently cloned gene *ZmRSA3.1* from maize that controls root angle is a homologue of *OsIAA13* [61].

*** A *TaIAA15* gene was previously described as controlling shoot architecture [65]. To differentiate the wheat homologs of *OsIAA15* from *TaIAA15* we included the suffix “a” after 15 in the gene name.

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