



Supplemental Figure S1: Correlations of the selected predictors for the growth related traits.

The graphics show the correlations between the selected predictors for each growth-related trait under the three different nutrient regimes (Control, K-, P-) and for the responses to the K- and Pregimes. Selected predictors are represented by full, black circles. Thin lines and bold lines represent significant correlations between the predictors (0,001 < Pvalue < 0,05 and Pvalue <0,001, respectively).





Supplemental Figure S1 (continued): Correlations of the selected predictors for the growth related traits.

The graphics show the correlations between the selected predictors for each growth-related trait under the three different nutrient regimes (control, K-, P-) and for the responses to the K- and Pregimes. Selected predictors are represented by full, black circles. Thin lines and bold lines represent significant correlations between the predictors (0,001 < Pvalue < 0,05 and Pvalue <0,001, respectively).



Supplemental Figure S2: QTL mapping for growth related traits (rosette weight, relative growth rate "RGR", root weight and root length), for chlorophyll (Chla, Chlb)-, protein-, hexose-, ionomic traits (for rosette "rs" and root "rt" tissue) and for leaf number at 22DAT (L22) and 32DAT (L32).

The five chromosomes of *A. thaliana* are represented on the left of each panel (top of chromosome 1 on the top and bottom of chromosome 5 at the bottom of each panel). The genetic position of the markers used to elaborate the genetic map are reported by horizontal bars on each chromosome.

The length of the QTL was determined according to an LOD -1 support interval. QTL with different  $R^2$  (% of explained variance) are reported in different width (see legend). More detailed characterization of these QTL are indicated in the supplemental table S1.

A: QTL detection for the traits quantified in the control hydroponic solution. The QTL model obtained for each trait was then tested for QTL x E significance (see Materials and Methods): Lilac and red QTL indicate that a significant different effect was detected between control and K- and between control and P- conditions, respectively. QTL reported in blue indicates that a significant different effect of this QTL was detected between control and both K- and P- conditions.

B: QTL detection for each trait quantified in the K- hydroponic solution. In lilac are the QTL with significant different effect between K- and control conditions.

C: QTL detection for each trait quantified in the P- hydroponic solution. In red are the QTL with significant different effect between P- and control conditions.

D: QTL detection for the response (see Materials and Methods) of each trait to K- (in lilac) and to P- (in red) conditions.

50% < R<sup>2</sup>

- = 25% <R<sup>2</sup>< 50%
- 10% <R<sup>2</sup>< 25%
- R<sup>2</sup> < 10%</p>





Supplemental Figure S3: Graphic presentation of the genotypes of Ler, RIL138 and the NILs

The graphic shows the physical map (of the five Arabidopsis chromosomes) with indicated marker positions of L*er*, RIL138 and the NIL1, NIL2 and NIL3. The different alleles at the marker positions are color coded: L*er* alleles are indicated in blue, Kas-2 alleles in orange and heterozygote alleles in green. Dark blue/orange colors represent tested marker positions and light blue/orange represent the assumed genotype at the respective marker positions according to flanking markers. The tested markers for chromosome 1 are: lkt1-1, NGA59, M1-10, CIW12, F6D8-94, F5I14, NGA692, M1-5; for chromosome 2 are: M2-5, M2-38, F15A24b, M2-17, T2N18, M2-33; for chromosome 3: NGA172, nt204, M3-20, M3-32, CF7M19, M3-21, F8J2, M3-18, NGA6; for chromosome 4: M4-39, NGA1111, M4-35, CIW7, M4-9, F8D20; for chromosome 5: lkt5-2, FLC, lkt5-5, M5-14, lkb5-1, M5-22, lkb5-2, SO191, lkb5-4, lkb5-6, NGA129, lkb5-15, lkb5-8, MUL3-1, F15L12, mbk5, K8A10.

Test	CONTROL V Chromo	one Marker Poston 200 Poston N	THE LOD THEY AMERICA	K. Chromesor	na Markai Postfor 0.00	Postlan Mig: LOD 7-Expl. Addition	L Church	monome Marker Position (20) Pos	man (Mag) LOD THEAST ADDRESS	Chronosome Marker Po	atton 2.00 Position (Mig) U.00	TELES ADDIVE	Construction Marker Position (199) Position (1994) LCD 11. Expl. Ad	10114
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No.11 Kie-19			1.00 0 0.00 0.04 0.0 1.02	4.46	040114 5.001 K7502 06,275	0.01     2.08     9.3     2.08       0.01     2.02     9     5.40       0.04     5.45     07.4     2.00	0.00 No	1 (MP-0) 9,46 2 (MP-0) 9,46	10 10 10 10 10000 10 10 10 10000	No-01. Ap-01.			4:05	
Card	5.01 Xe 0	4704 15,07 5.57 59(7)8 7784 4.48 4(50) 75,275 16,64	247 40 1017 406 00.7 1985 7.6 00.2 1985 7.6 00.2 1985	6.01 14 ST	·		3,843 No	2 PRIATUR 5144 5 NO104 05.00 5 NO4708 07.084 5 NO4708 07.084 5 NO4707 07.04	1-12     3.00     7.2     3.78(ps)       5.57     3.34     6.4     0.899888       4.68     3.63     7.5     8.24151       17.23     2.87     4.2     0.899598	, parts j	900	LUG LEVEN	40 CX	
21-19	0.030 1 4 5 5	Mill     Mill <th< td=""><td>1,01 7.3 -20,00 4,40 11.5 20,00 2,30 5,0 10,752 5,24 13,5 20,759</td><td>4.907 C</td><td>SMP3P     4.405       SMP3R     6.511       CPTW19     45.525       SA5     45.525       K1522     11.576</td><td>1.1     2.8     5.8     10,41       4.00     7.19     15.7     27,49       11,02     2.79     15.7     27,89       11,02     2.79     17.3     11,93       11,02     2.79     17.4     11,93       11,04     7.52     15.3     27,179</td><td>130</td><td>2     PeloA1128     47.614       5     SWP114     2.814       9     81.525     91.25       4     SMP124     41.129       5     SMP126     17.664       5     SMP144     15.144</td><td>11.7     12.89     8.5     19.4054       138     5.51     93.8     20.4966       15.99     7.82     93.8     20.4966       15.99     7.83     92.4     20.505       15.99     7.83     92.4     20.505       15.99     5.96     12.4     20.505       15.99     5.96     12.4     20.505       15.99     5.96     12.4     20.505       15.99     5.96     12.4     20.505       15.99     5.96     12.4     20.505       15.99     5.96     12.4     20.505       15.99     5.96     19.3     34.400</td><td>4o-Q1),</td><td></td><td></td><td>N: 07.</td><td></td></th<>	1,01 7.3 -20,00 4,40 11.5 20,00 2,30 5,0 10,752 5,24 13,5 20,759	4.907 C	SMP3P     4.405       SMP3R     6.511       CPTW19     45.525       SA5     45.525       K1522     11.576	1.1     2.8     5.8     10,41       4.00     7.19     15.7     27,49       11,02     2.79     15.7     27,89       11,02     2.79     17.3     11,93       11,02     2.79     17.4     11,93       11,04     7.52     15.3     27,179	130	2     PeloA1128     47.614       5     SWP114     2.814       9     81.525     91.25       4     SMP124     41.129       5     SMP126     17.664       5     SMP144     15.144	11.7     12.89     8.5     19.4054       138     5.51     93.8     20.4966       15.99     7.82     93.8     20.4966       15.99     7.83     92.4     20.505       15.99     7.83     92.4     20.505       15.99     5.96     12.4     20.505       15.99     5.96     12.4     20.505       15.99     5.96     12.4     20.505       15.99     5.96     12.4     20.505       15.99     5.96     12.4     20.505       15.99     5.96     12.4     20.505       15.99     5.96     19.3     34.400	4o-Q1),			N: 07.	
3.4		SMP2     17.88     0.08       SMP3     17.88     2.45       SMP3     17.98     2.45       SMP3     4.161     1.08       SMP3     2.451     1.08       SMP3     2.161     1.08       SMP3     2.161     1.08	60.32     90.7     60.92.0       10     90.4     507.82.0       51.0     2.5     90.94.4       51.0     2.5     90.94.4       51.0     1.0     90.24.7       60.0     1.1     102.97.9       60.0     1.1     10.92.9       4.17     6.6     -90.24.4	2.84	04210 M-01 M25 1 M4210 (M1	26.07 7.18 500 99.048 9.21 234 7.3 99.20 108 2.01 6.3 94.094	03,0	1 00110 21.08 1 00491 20.26 3 00491 7.01	D     D0     M     20,969       430     6     9,8     -07,9       4,00     4,05     20     06,659	1 5440 1 5490	10,000 0,000 0,000 00,275 0,04 2,07	TU LINES T CHINE	4.9X	
	5.440 <u>5</u>	MCA1130     55,518     16,44       58/597     40,309     11,25       56/562     11,029     22.5	10 5 550 40 0 8.03	-601	N.0. 1744	<u>- 20 10 10 108</u>	5.90	1 1015 1 438	AN TOT IN TORS.	1 10001	ANG 1 100 1 100	T 66 [04638	Ac (2),	
Ra-1	1 3 3 5 5 5	WGA1281     ML09     0.1       SW2142     4.041     1.08       SW2144     0.202     5.57       X1002     71.579     10.46       ML09     90.202     5.57       X1002     71.579     10.46       ML09     90.202     50.77       SW224     44.002     56.00	4.9, 12 0.09 2.00 17 020 4.9 057 020 2.04 0.0 057 020 2.04 0.0 057 020 1.02 7.3 0.09 2.04 0.0 0.00	-274	John Col M. Mar	1 200 1 20 1 20 1 200 1	0,00 %	1 204713 20.00 5 204504 27.00	26.0 1.22 43 4.286 23.0 1.0 46 4.25.994	1 Mir 0 5 SAPTIA 5 SAPTIA 6 OK	80.004 22.55 3.04 1.041 108 3.50 87.39 235.50 5	0.8 4.094422 0.5 8.0463679 1.5 8.0463679	4-0X	
Mp-rs	4,941 1 2 3	SWP5     LOIS     C/I       E305-54     63,471     158       MGA108     63,471     158       MGA108     63,471     157       SWP5     25,666     8,17       SWP5     25,666     8,17	1.00 4.1 1.009 1.00 3.1 0.340 01.05 10.2 -2.001 4.64 5.9 0.001	4.94 2 3 5	V.914 V.914 V.914 V.914 V.914 V.919 V.1914 V.191 V.1914 V.191	34,37     2,29     4,3     9,577       11,7     51,54     21     -1,459       5,57     6,09     (2,7     -1,09       4,48     4,25     6,1     -6,99       38,17     4,25     6,1     -6,99	1.60	1 (2447-02) (31,445 2 (44,11)(3) (2,445 3 (44,12)(5) (2,445 5 (44,12)(5) (2,445 5 (44,12)(5) (2,445 5 (44,12)(5) (44,12)(5) 5 (44,12)(5) (44,12)(5)	1.1 11.11 9.3 2.084 1.7 8/42 4/3 4.294 1.5 8/4 4/3 4.1 18092 1/21 2.94 2 0.094 1.2 194 2 0.094	2 89600A 3 940	40.810 10.02 5.45 45.60 19.8 4.18	14.1 (4.04007 11.8 (4.07485)	1 2007-07 01.00 3.1 2.0 0.1 0.0 2 2007/34 04.602 11.22 20 01.9 1.2 5 25.0 11.0 1.0 1.0 1.0 1.0 1.0 1.0	27.15 (17%)
Mart		100000 1000 1000 100000 1000 1000 100000 0000 0000	(8.56) (3.5) (4.69) (8.56) (2.7) (3.7,80) (2.96) (3.7) (4.05)	6,82 1	00200 00.00 9495 00.00 8.902 00.59	11.87     15.98     A01     11.984       01.92     2.98     5.94     5.103       01.94     2.93     5.94     5.103       01.94     2.75     5.93     5.227	4801	2 30654x 1 4040 1	102 116 1 16 1 10 10 10 10 10 10 10 10 10 10 10 10 1	2 (MCCA 5 (MCCA 5 (MC23) 1 (MC23)	8082 102 736 1231 439 222 5.04 112 230	21.3 3.046 4.02942 4.02942	1.0X	
64-11 64-1	0.600 %0-0 0.607	ineast i reat i rest v	1281 9 1 930	6.40 No.011	Metra 12.80	0.8 10 07 696	0.401 Au 3.745	9 - 991. 2 - 346641138 [ - 40,818 - [	10 101 N 1998	No 01. No 01.			40.0%. Nr GN,	
cu	0.014 3	04223 50.00 1143 198274 40.20 1122 198274 1 100	( <u>5.5</u> ) <u>565</u> <u>6094</u> <u>5.44</u> <u>6.7</u> <u>6.588</u> <u>5.4</u> <u>7</u> <u>6.588</u>	6.04	19495 9,30 19495 9,30 19495 20,30	- 25.00 + 350 + 85.0 + 35.00 - 5.07 - 450 - 55.2 - 0.307 - 8.17 - 3502 - 9.2 - 0.307 - 9.17 - 3502 - 9.2 - 0.301	0.07	1     104/271     101.44       1     104/271     31.85       1     1700-14     51.950       2     104/21     41.61       2     104/21     41.91       2     104/21     41.92       3     14.2     41.97       4     544     5       5     104/20     11.01	100     200     35     400000       110     400     927     400000       112     322     72     9,044000       112     324     63     4,04000       112     324     63     4,04000       112     324     63     4,0000       112     328     72     4,0000       112     328     72     4,0000       112     328     63     4,0000       112     328     64     52,000       112     328     64     52,000       112     328     64     52,000       112     328     64     52,000       112     328     64     52,000       112     328     64     52,000       112     328     64     52,000       112     329     64     52,000       115     229     64     52,000	Ar 01.				
0.e	0.829 1 2 3 3 4	MMP101     MO300     11.44       1000101     MO300     11.42       10001014     MO301     11.02       10001014     MO301     1.08       FML     Get MO1     1.08       FML     Get MO1     1.08       FML     Get MO1     1.08	8/05     90.8     -1.3/25       5.75     11     -0.301       5.61     91.3     -0.401       4.02     7.5     6.800       4.08     7.6     0.119	0.05	SMP15     25,8       SMP15     34,207       SMP107     1,508       F48     0       SMP107     15,201	5.87     4.89     440     -1.897       4.17     5.88     123     -1.898       21.00     2.84     5.3     4.216       5.17     4.88     13.3     -1.298       5.17     4.88     13.3     -1.298       23.46     2.64     5.3     4.216	0.930	JHE17     MEP2       1     199725     19,892       3     199726     19,892       3     199726     19,892       4     194     9       5     199728     31,402	com     1.100     7.3     9.403.04       1.101     4.02     9.5     -1.500.04       4.02     9.5     -1.500.04     -1.000.04       4.02     9.2     -1.000.04     -1.000.02       9.8     5.7     -1.4     -1.000.02       9.2     -1.000.04     -1.74     -1.000.02       9.2     -1.000.04     -1.74     -1.000.02       9.2     -1.000.04     -1.74     -1.000.02       9.2     -1.000.04     -1.74     -1.000.02       9.2     -1.000.04     -1.74     -1.000.02	Ac-01.			4:0%	
1	1	1000 44.30 44.30 160.17 96.00 26.96	247 44 4.620 4.98 1.4 1.980		NP 0 1 96.90	1 20.96 4.49 10.3 4.992		5 JM5-17 5 H(H2	208 [408] H3 [ 00419					

## Supplemental Table S1: List of all detected QTL

QTL for rosette weight, relative growth rate (RGR), root weight, root length and total chlorophyll- (Chl a,b), protein and hexose-content in the rosette, as well as ion-content in the rosette (-rs) and the root (-rt) and leaf number at 22DAT and 32DAT (L22, L32) are reported. QTL were detected for each trait in each nutritional regime (control, K- and P-) and for the response to reduced potassium (K response) and reduced phosphate (P response) conditions. The heritability ( $h^2$ ), position of the closest marker with the highest LOD-score (in cM and Mbp), LOD-score, explained variance (% Expl.;  $R^2$ ) and additive effect (Additive; 2a) is given (if the additive effect is positive, the L*er* allele increases the trait value).

marker name	chromosome	phys pos (Mbp)	forward seq	reverse seq	enzyme for CAPS	annealing temperature
lkt1-1	1	4,9	CAAATCATCCATATGGCAAAGC	CTAGAGCCTCCCACCATGAC	-	60°C
lkt5-2	5	2,19	CAAGAAGGCCGAGAATGAATAG	GTATGAGCCACTATGTCCTTGTC	-	60°C
lkt5-5	5	5,62	GAAAAGGCAAGGGAAAG	GCTGCCGTCACCAAAG	-	55°C
lkb5-1	5	10,1	GAAGAGAGATTTGTGTGGTG	GTTTGTCAAGGTATTTGGATG	-	55°C
lkb5-2	5	14,8	GGAACGGTATTGAGAATGAAC	CGTGGCAAAATAATGGAGAG	-	55°C
lkb5-4	5	17,6	CTGAGCATGTGTTAGTCCTG	CAAACACCACAACAATTCAC	-	55°C
lkb5-6	5	18,6	GAGGGTCTTTTATTATTCGC	CTTACCGACACAACCAGC	-	50°C
lkb5-8	5	22,4	CTCAATCTCGATCCTACACC	CTCTCTCTTCTTGCTTATACTG	-	55°C
lkb5-15	5	21,3	CTCGTTTTCCCGCCATTTC	GCTCCACCGATCAAAATCTC	Hinf I	55°C

Supplemental Table S2: Primers designed for genotyping of the near isogenic lines. The primers were designed to be used as SSLP marker or CAPS marker to genotype the NILs presented in Figure 2. The table lists the position of the polymorphism (in Mbp), the primer sequence, the restriction enzyme (for the CAPS marker) and the annealing temperature of the primer pairs.