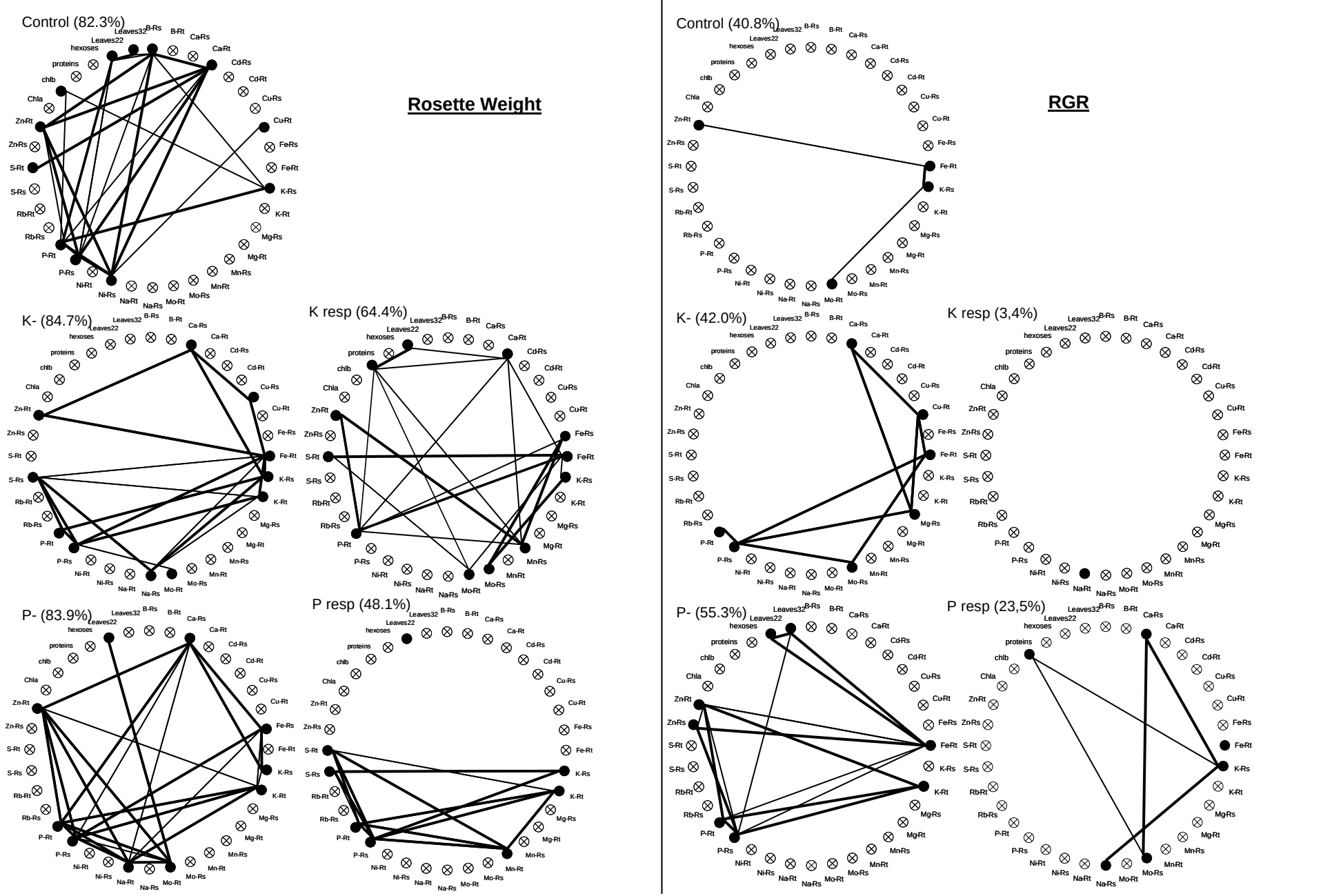
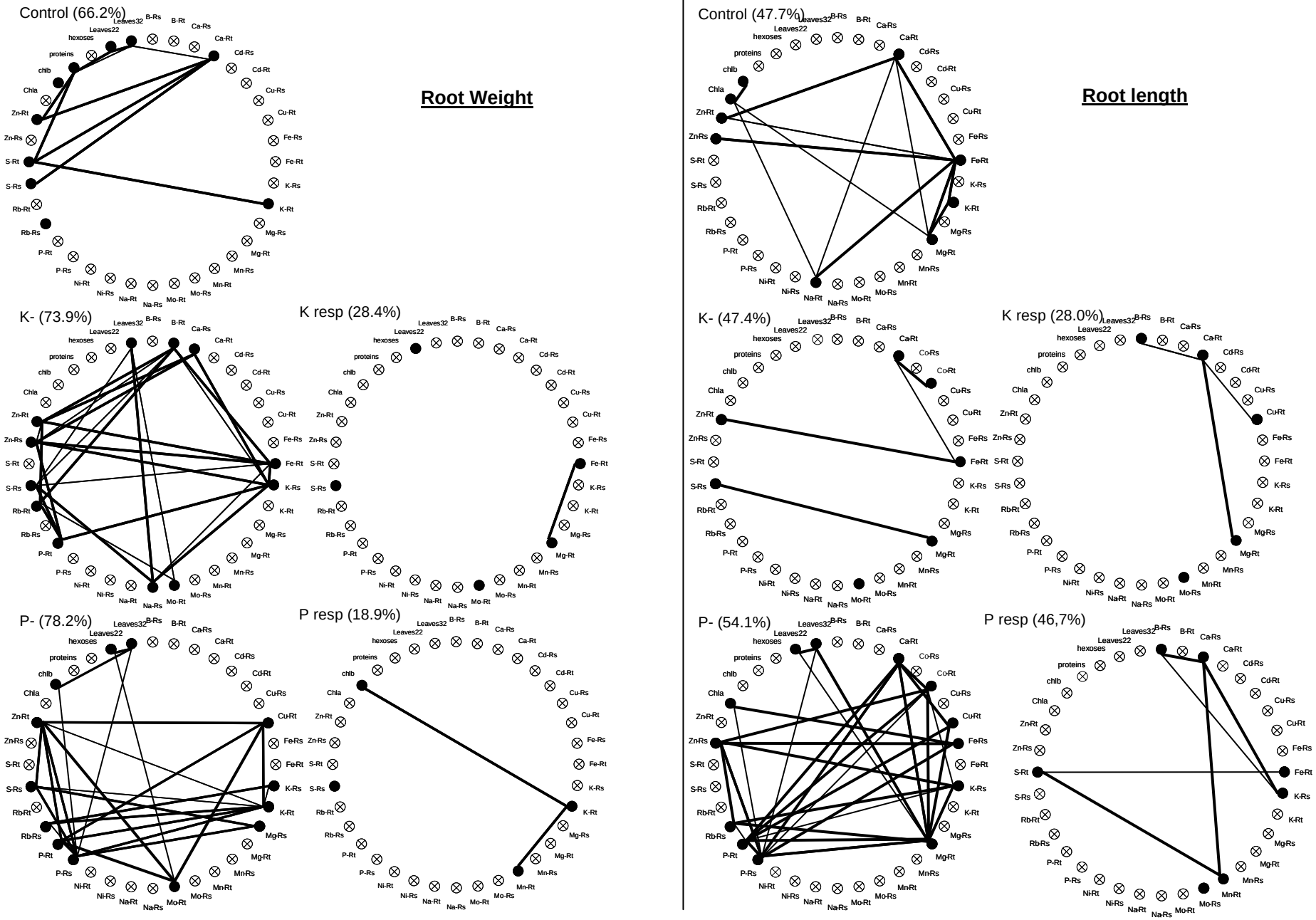
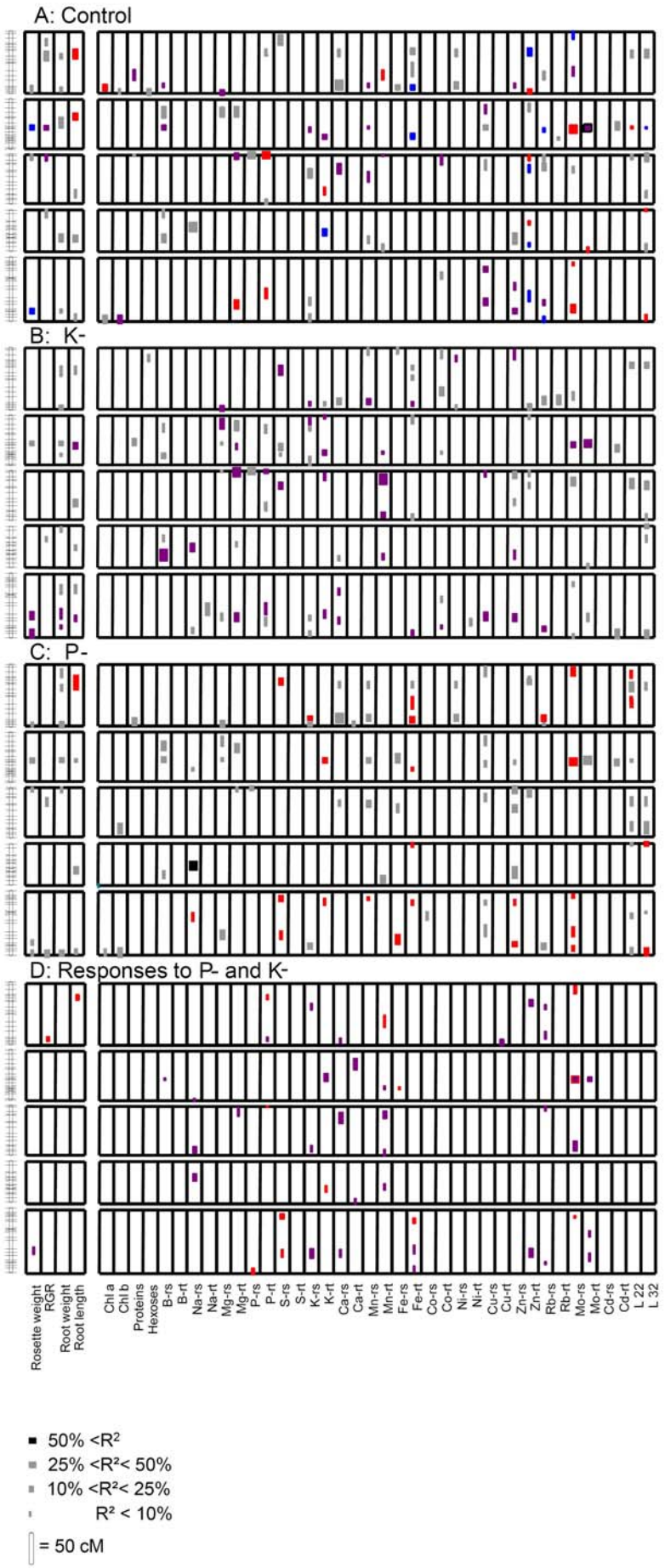


Supplemental Figure S1: Correlations of the selected predictors for the growth related traits.
The graphics show the correlations between the selected predictors for each growth-related trait under the three different nutrient regimes (Control, K-, P-) and for the responses to the K- and P-regimes. Selected 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).

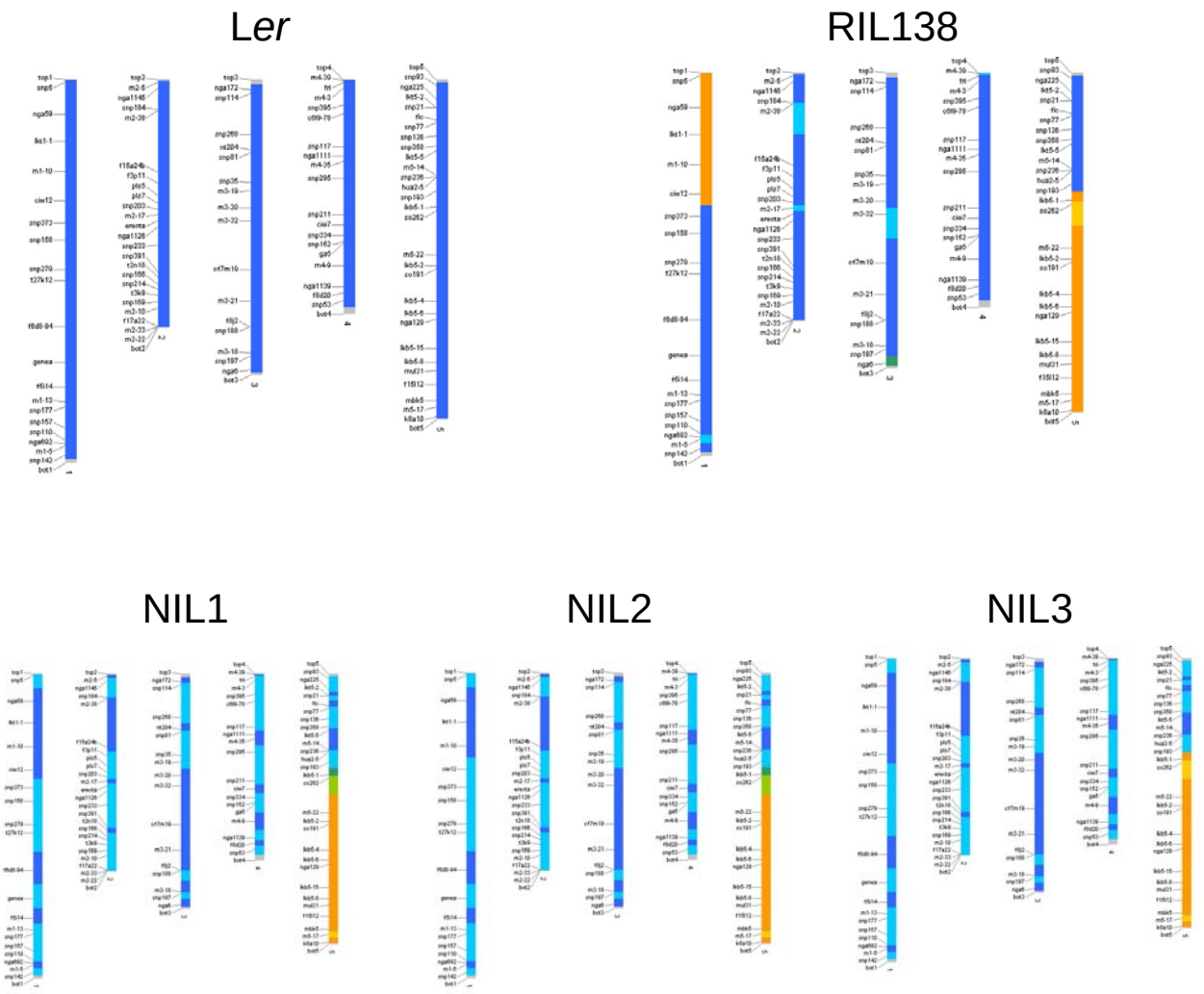


Supplemental Figure S1 (continued): Correlations of the selected predictors for the growth related traits.
The graphics show the correlations between the selected predictors for each growth-related trait under the three different nutrient regimes (control, K-, P-) and for the responses to the K- and P-regimes. 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).



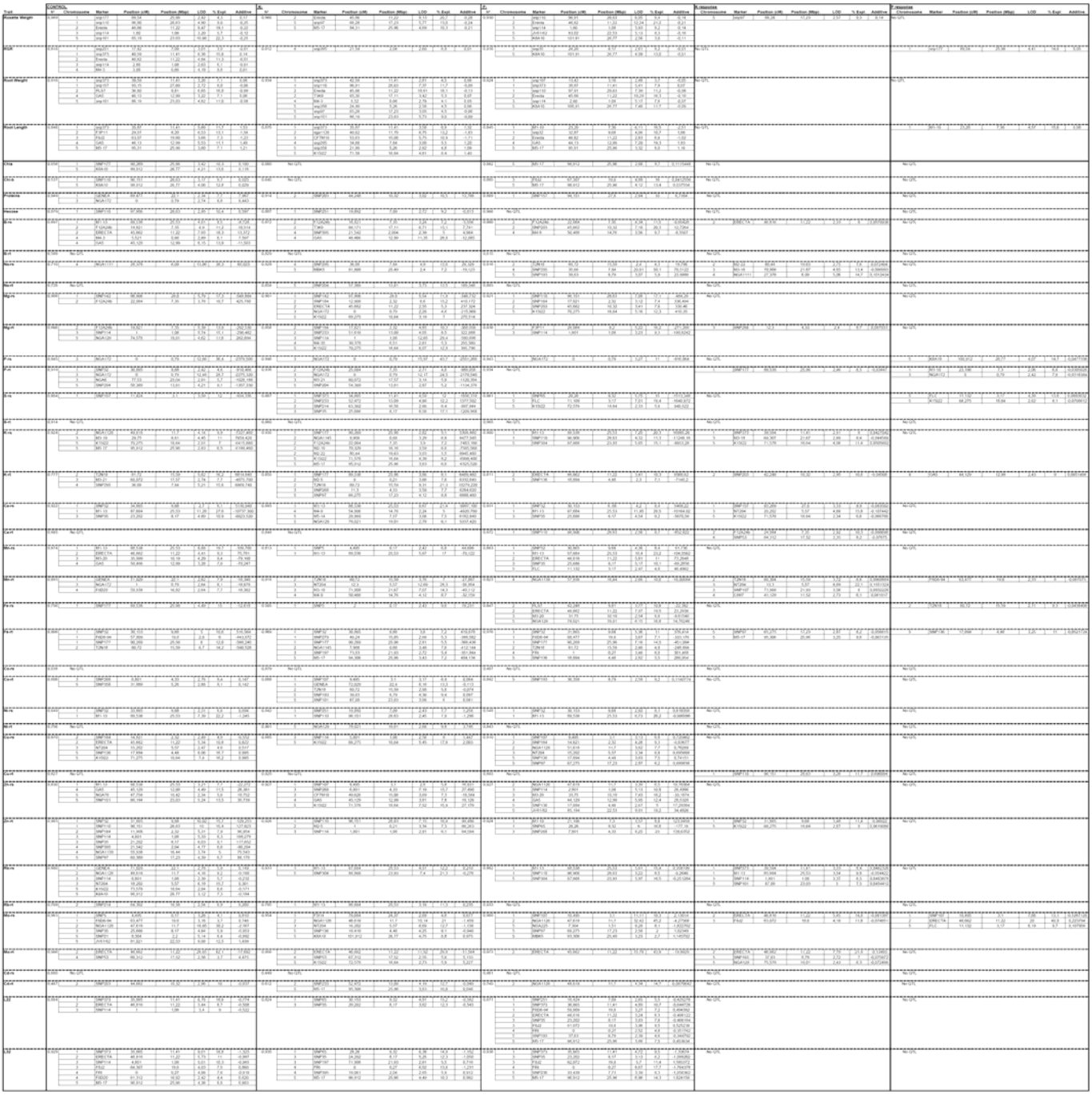
Supplemental Figure S2: QTL mapping for growth related traits (rosette weight, relative growth rate "RGR", root weight and root length), for chlorophyll (Chla, Chlb)-, protein-, hexose-, ionomic traits (for rosette "rs" and root "rt" tissue) and for leaf number at 22DAT (L22) and 32DAT (L32).

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.



Supplemental Figure S3: Graphic presentation of the genotypes of L*er*, 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.



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.