

Figure S1 Mean minimum-maximum normalized values for all analyzed traits in parental lines and RILs. Error bars indicate 95% confidence interval. LL: leaf 4 final length, Lwe: leaf 4 final weight, LA: leaf 4 final area, Lwi: leaf 4 final width, LER: leaf 4 elongation rate, T_m : time to maximal LER, T_e : time to final leaf length, LED: leaf elongation duration, DZ size: leaf 4 division zone size, LN: leaf number 27 days after sowing, FW: fresh weight 27 days after sowing, DW: dry weight 27 days after sowing.



Figure S2 Some examples of RILs and the parental lines at seedling stage, 27 days after sowing. A. H99 (left) and B73 (right); B. From left to right: RIL100, RIL51, H99, RIL61, B73, RIL113, RIL89.

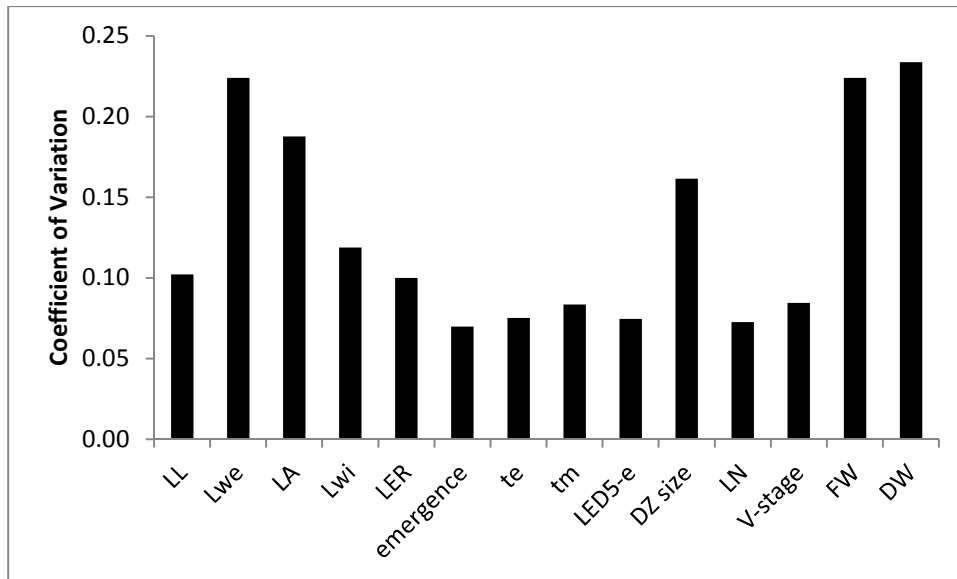


Figure S3 Coefficient of variation for the different traits measured.

LL: leaf 4 final length, Lwe: leaf 4 final weight, LA: leaf 4 final area, Lwi: leaf 4 final width, LER: leaf 4 elongation rate, T_m : time to maximal LER, T_e : time to final leaf length, LED_{5-e}: leaf elongation duration, DZS: leaf 4 division zone size, LN: leaf number, FW: fresh weight 27 days after sowing, DW: dry weight 27 days after sowing.

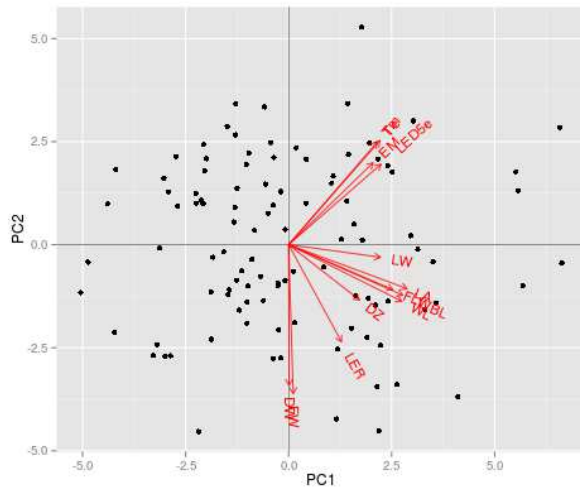
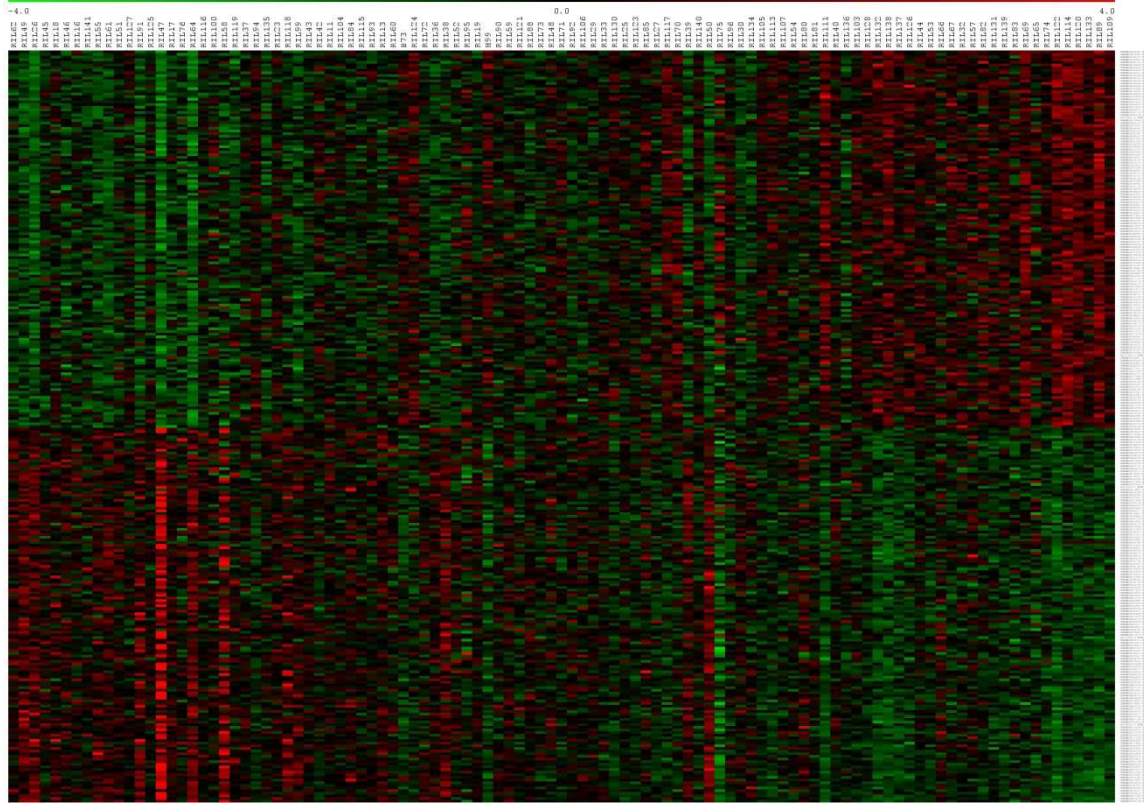
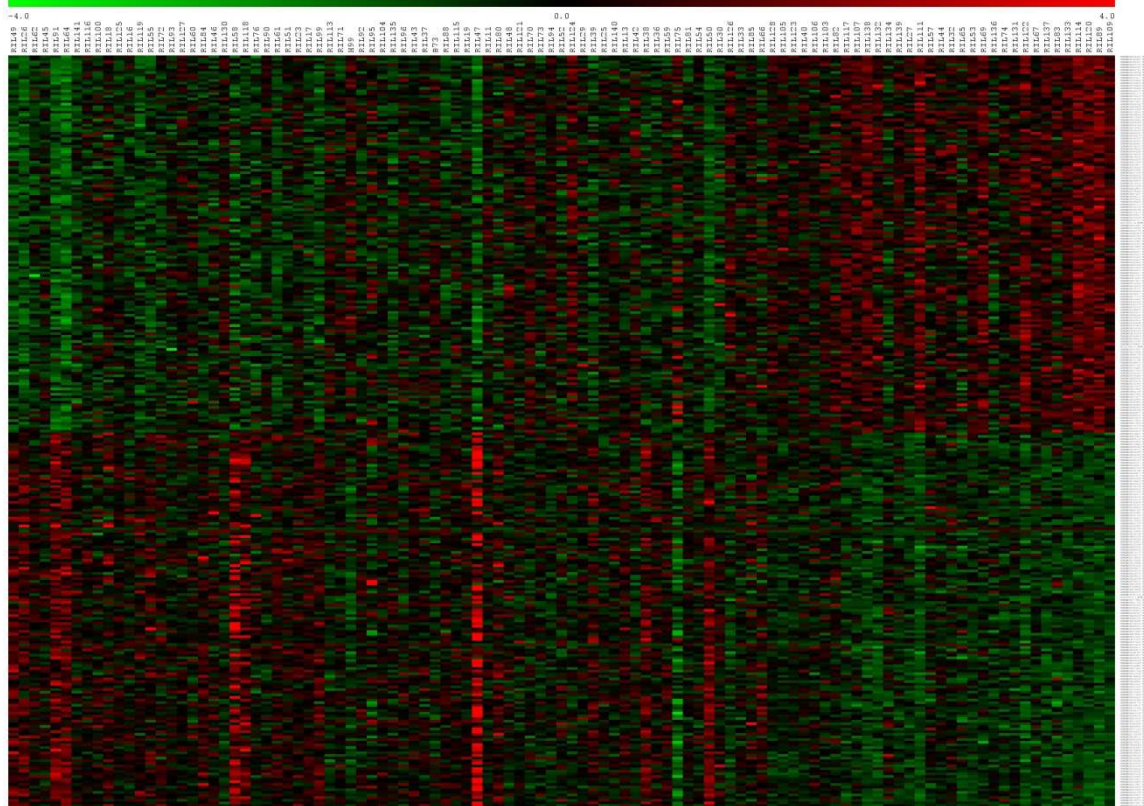


Figure S4 PCA analysis of the phenotype data of the population. Shown is a biplot of the first two principal components of the phenotype data. Black dots correspond to the different samples, while the red arrows correspond to the different phenotypes. LL: leaf 4 final length, Lwe: leaf 4 final weight, LA: leaf 4 final area, Lwi: leaf 4 final width, LER: leaf 4 elongation rate, T_m: time to maximal LER, T_e: time to final leaf length, LED_{5-e}: leaf elongation duration, DZS: leaf 4 division zone size, FW: fresh weight 27 days after sowing, DW: dry weight 27 days after sowing.

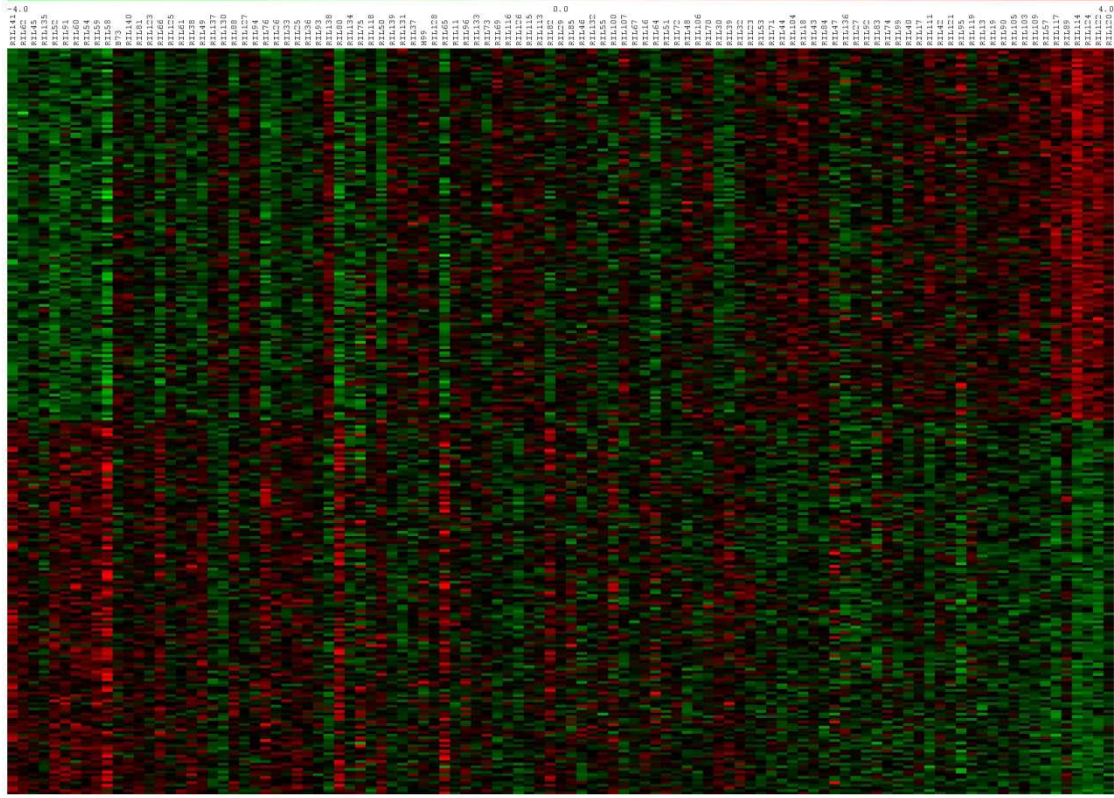
Leaf weight



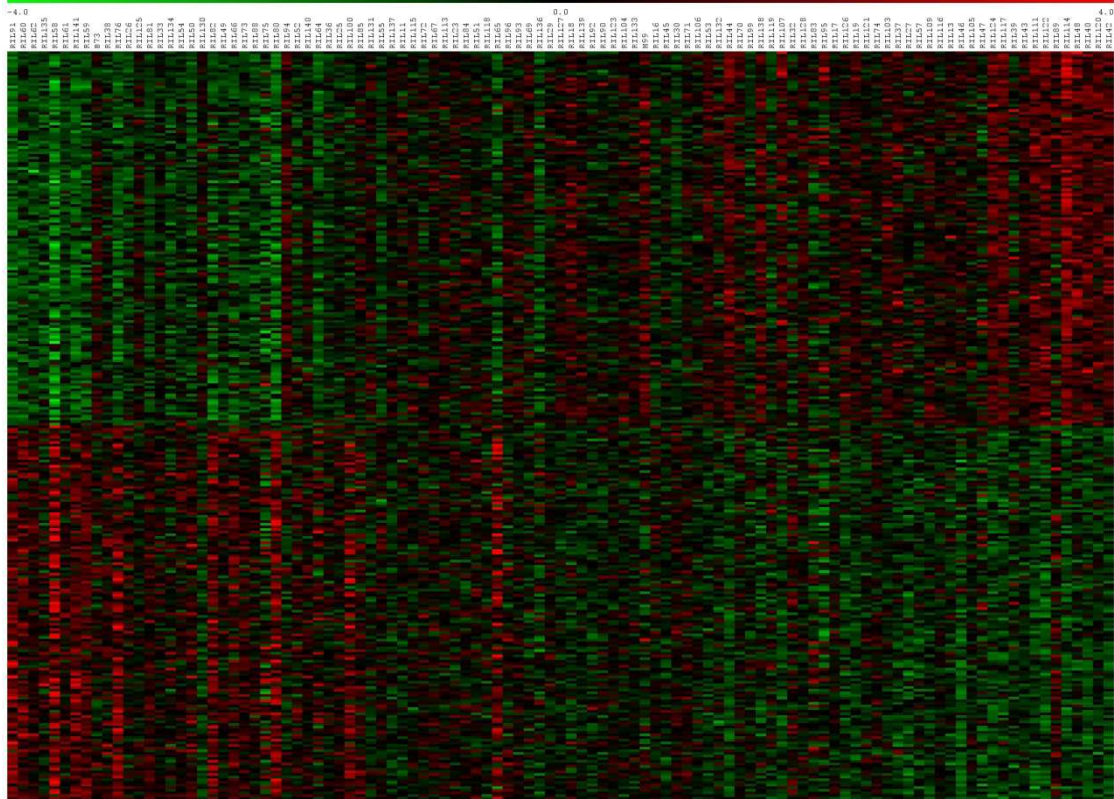
Leaf area



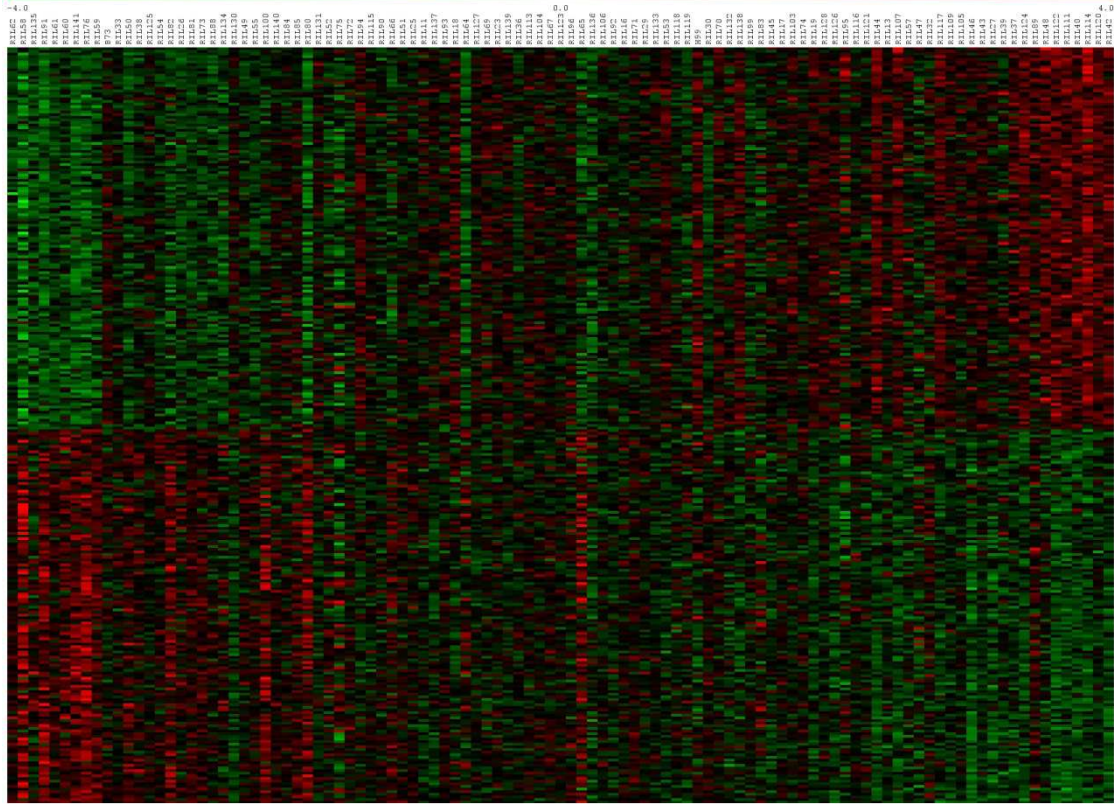
emergence



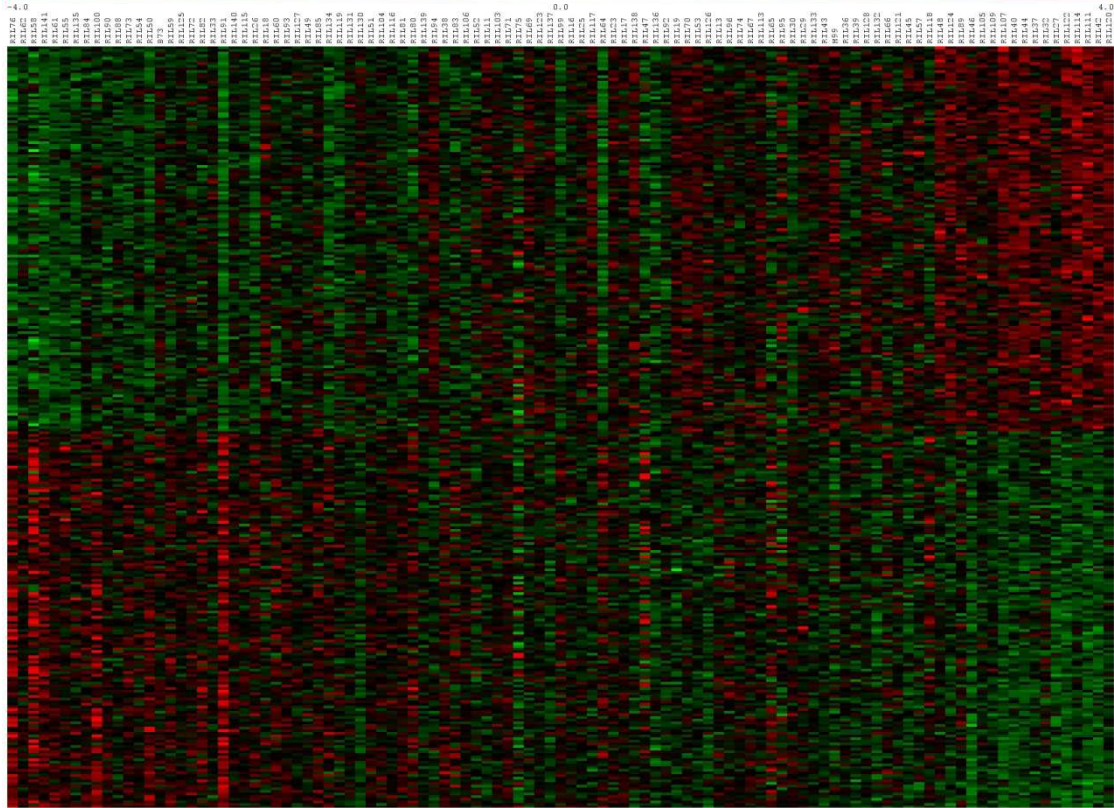
T_m



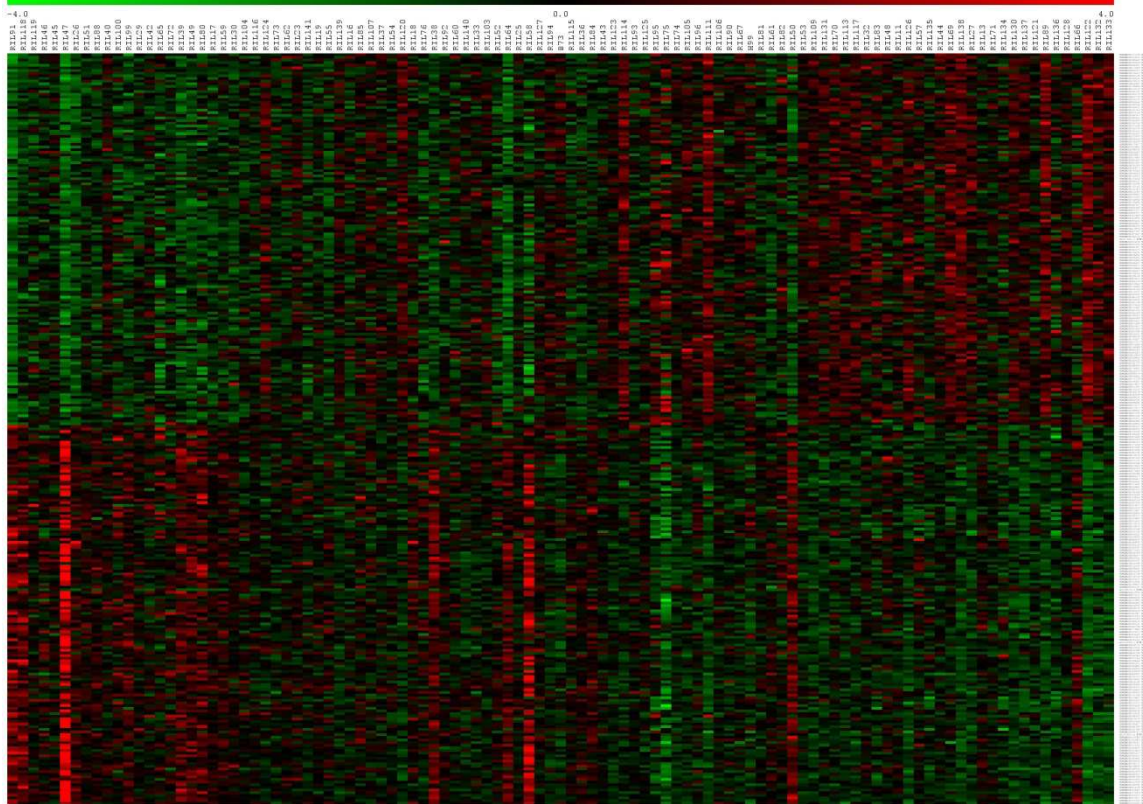
T_e



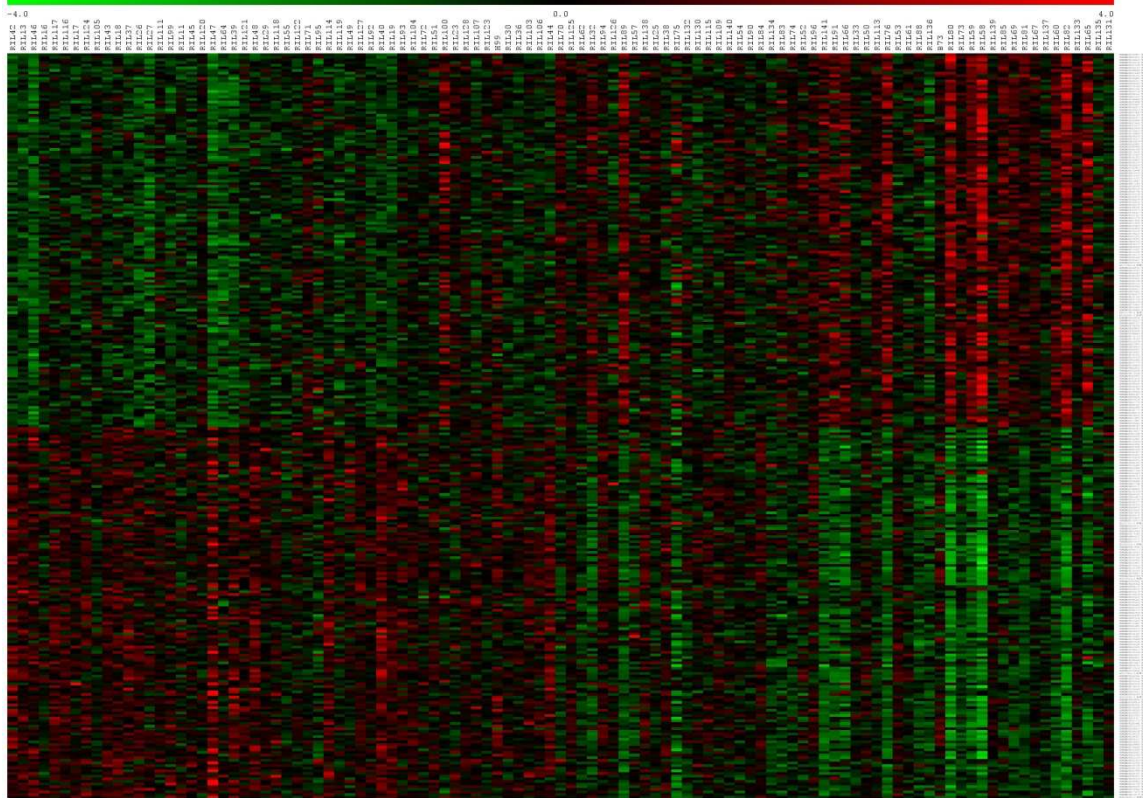
LED_{5-e}



Division zone size



Fresh weight



Dry weight

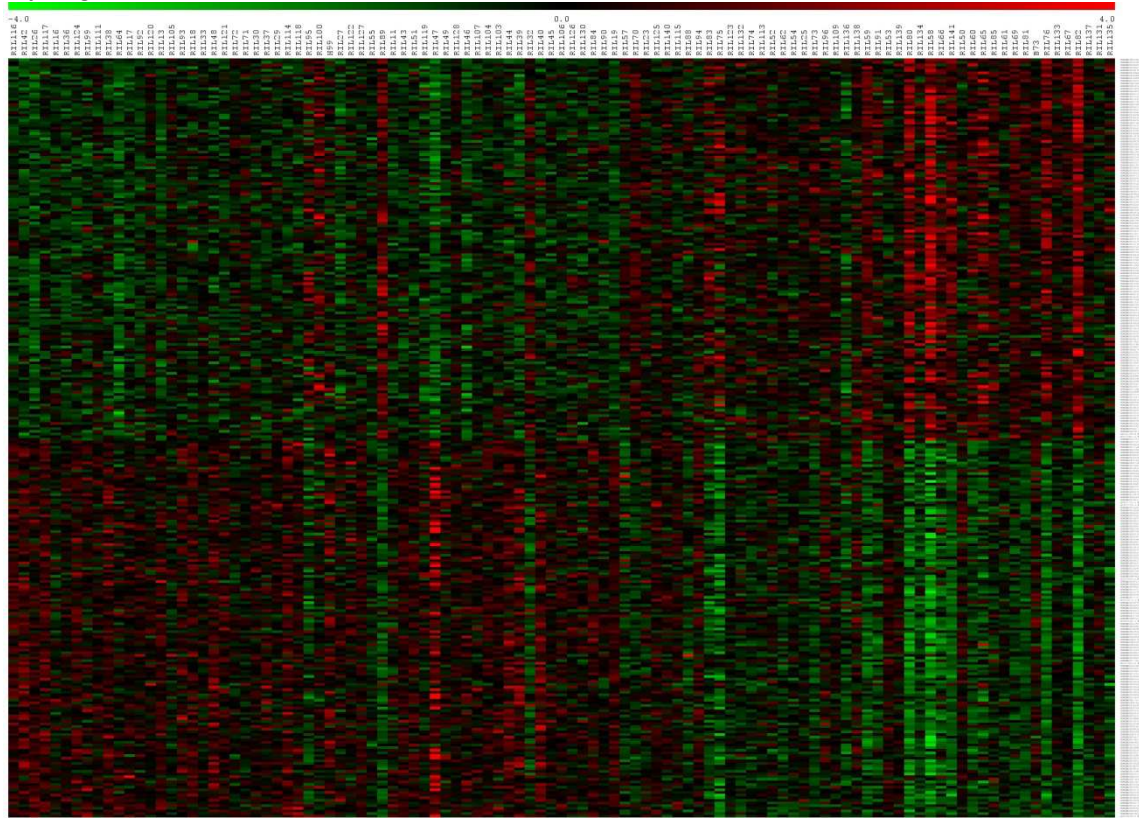


Figure S5 Expression patterns of the top one percent genes (anti-)correlated with the different traits. Columns represent the 103 RILs and parental lines B73 and H99 organized from small (left) to large (right) for the specific trait. Genes, shown in the rows, above the line are correlating genes, below the line anti-correlating genes. Green: low expression, red: high expression.

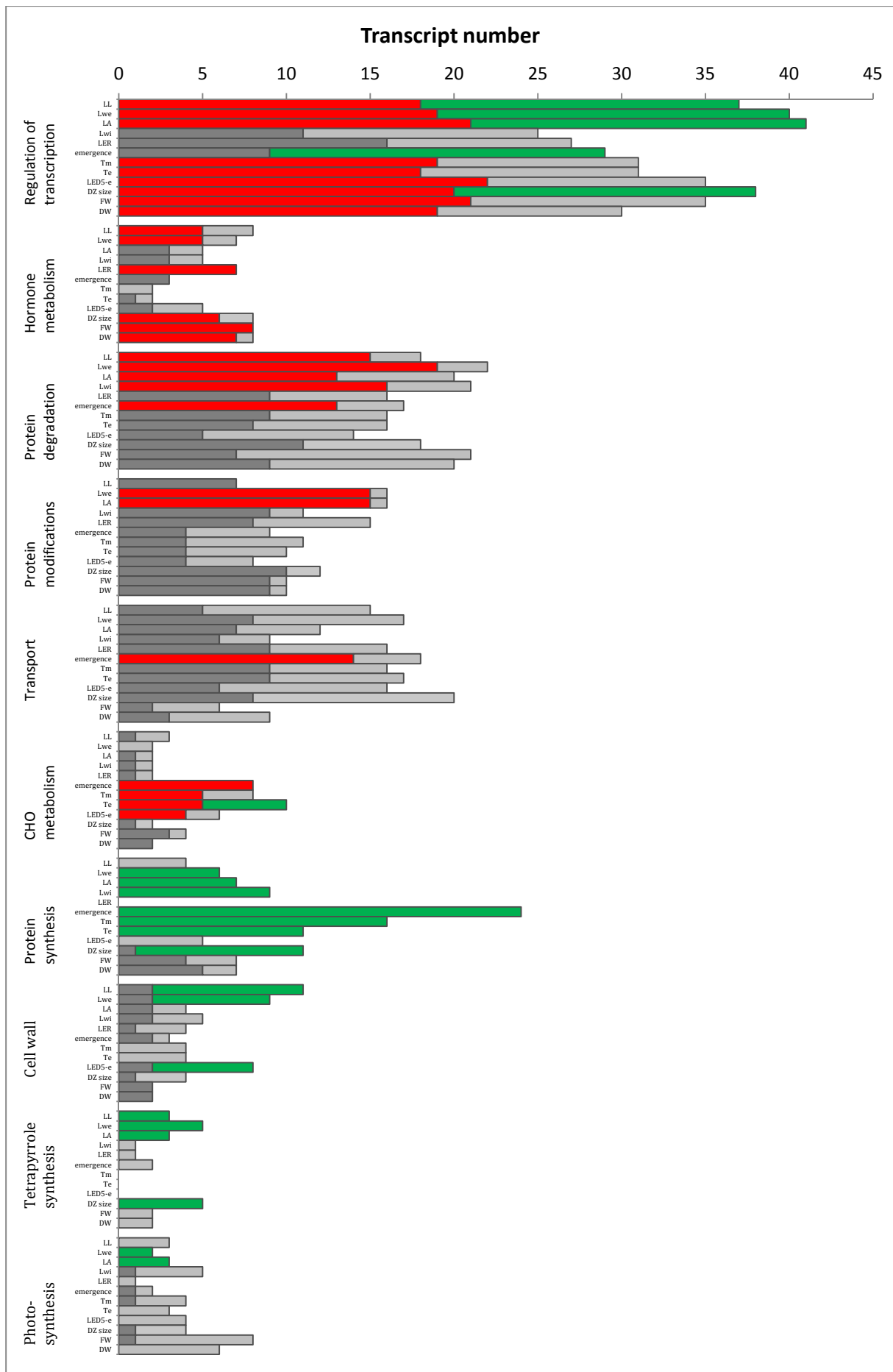


Figure S6 Overrepresented MapMan categories of top one percent genes (anti-)correlated with phenotypic traits. Positive correlation in dark grey bars, negative correlation in light grey bars. Red (positive correlation) and green bars (negative correlation) indicate enrichment for the functional category using Fisher's exact test ($P < 0.05$). LL: leaf 4 final length, Lwe: leaf 4 final weight, LA: leaf 4 final area, Lwi: leaf 4 final width, LER: leaf 4 elongation rate, T_m : time to maximal LER, T_e : time to final leaf length, LED: leaf elongation duration, DZ size: leaf 4 division zone size, FW: fresh weight 27 days after sowing, DW: dry weight 27 days after sowing.

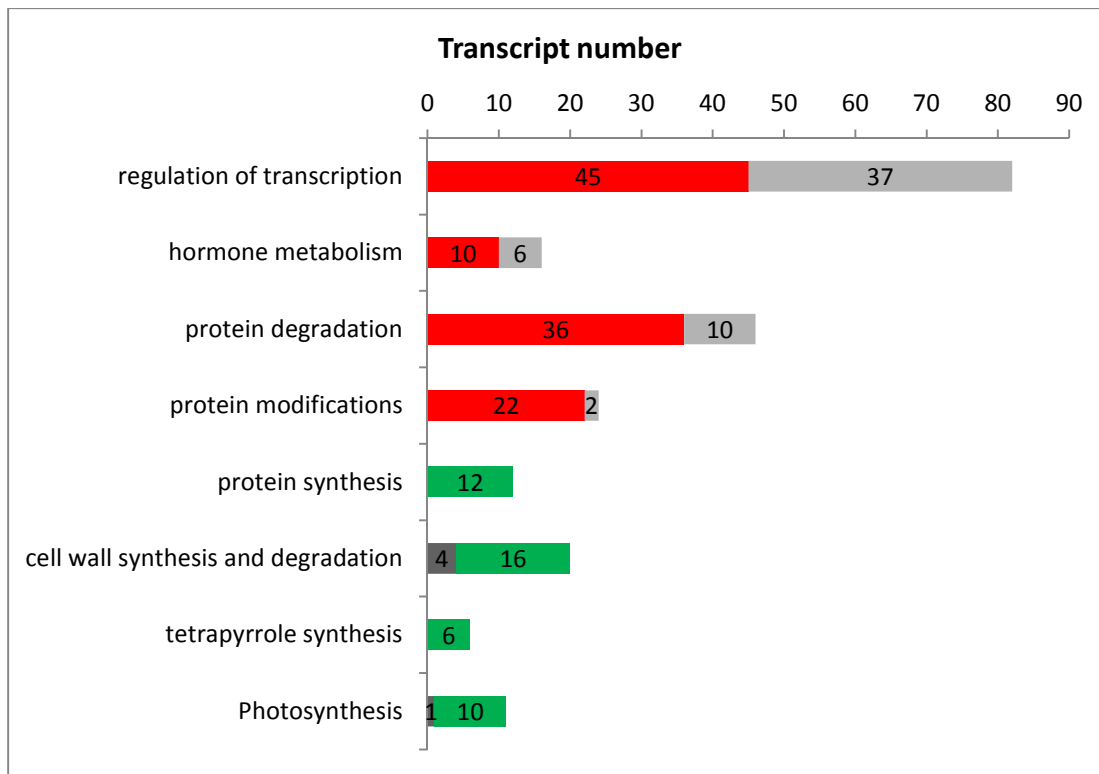


Figure S7 Overrepresented MapMan categories of top one percent genes (anti-)correlated with final leaf size traits. Positive correlation in dark grey bars, negative correlation in light grey bars. Red (positive correlation) and green bars (negative correlation) indicate enrichment for the functional category using Fisher's exact test ($P < 0.05$).