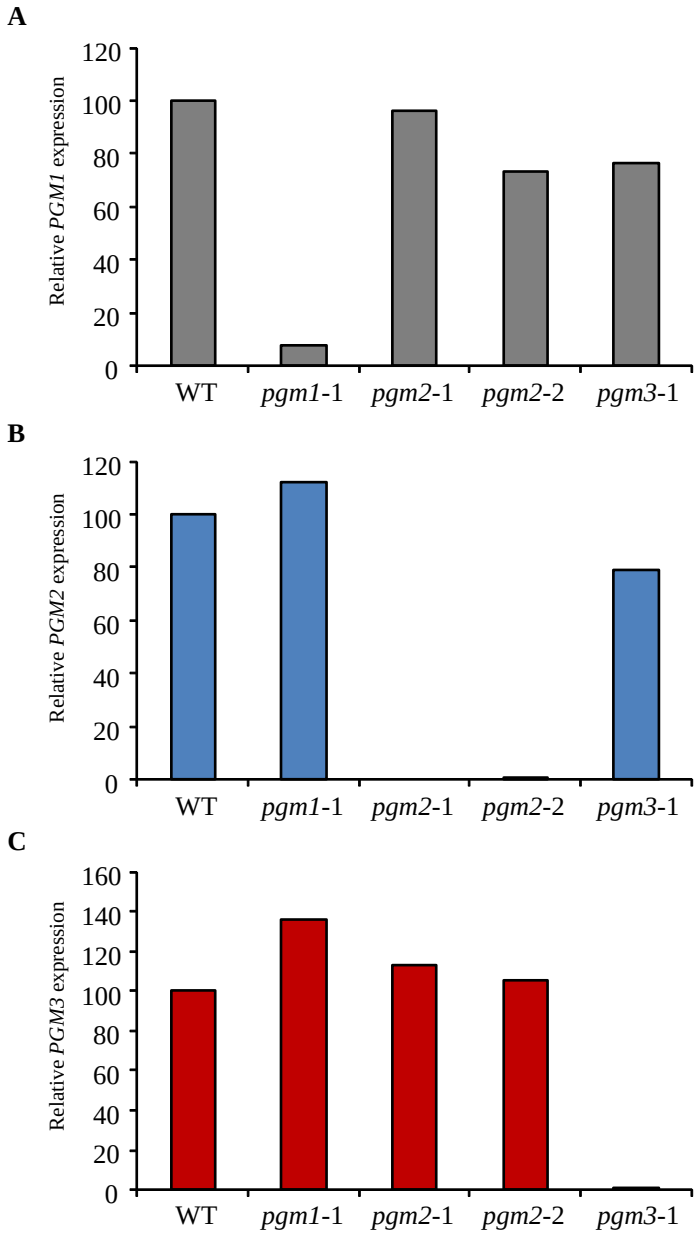
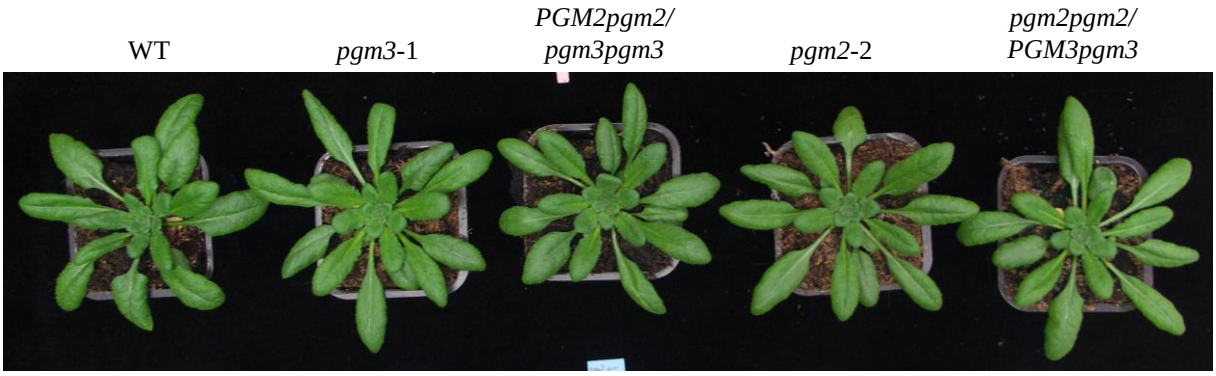
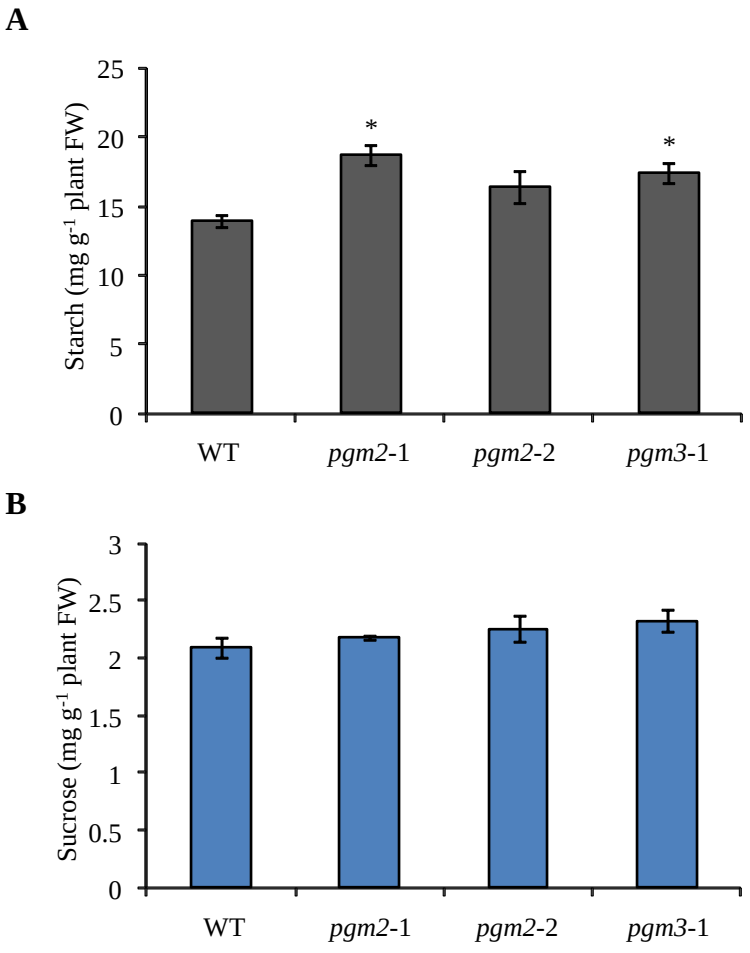


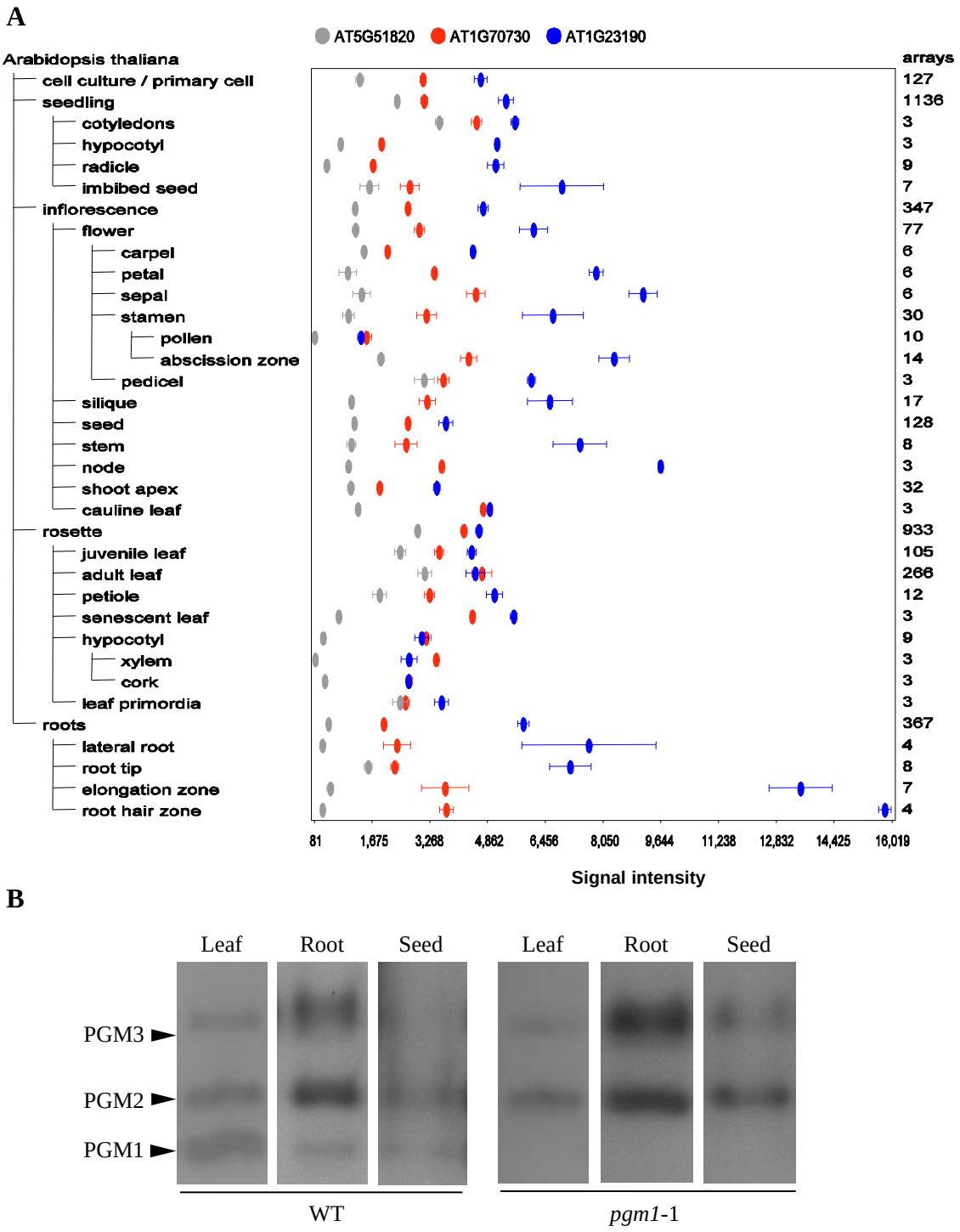
Supplementary Figure S1. Expression of the *PGM* genes in the wild type (WT) and *pgm* mutants. Expression analysis was done by quantitative RT-PCR in the wild type and in homozygous *pgm1*-1, *pgm2*-1, *pgm2*-2 and *pgm3*-1 single mutants. The data represent one experiment with three technical replicates from cDNA derived from three pooled mature plants. For each sample, *PGM* expression level was normalized to the expression of the house-keeping gene *PP2AA3*, and is presented as relative percentage of the wild type. A, *PGM1* (At5g51820). B, *PGM2* (At1g70730). C, *PGM3* (At1g23190).



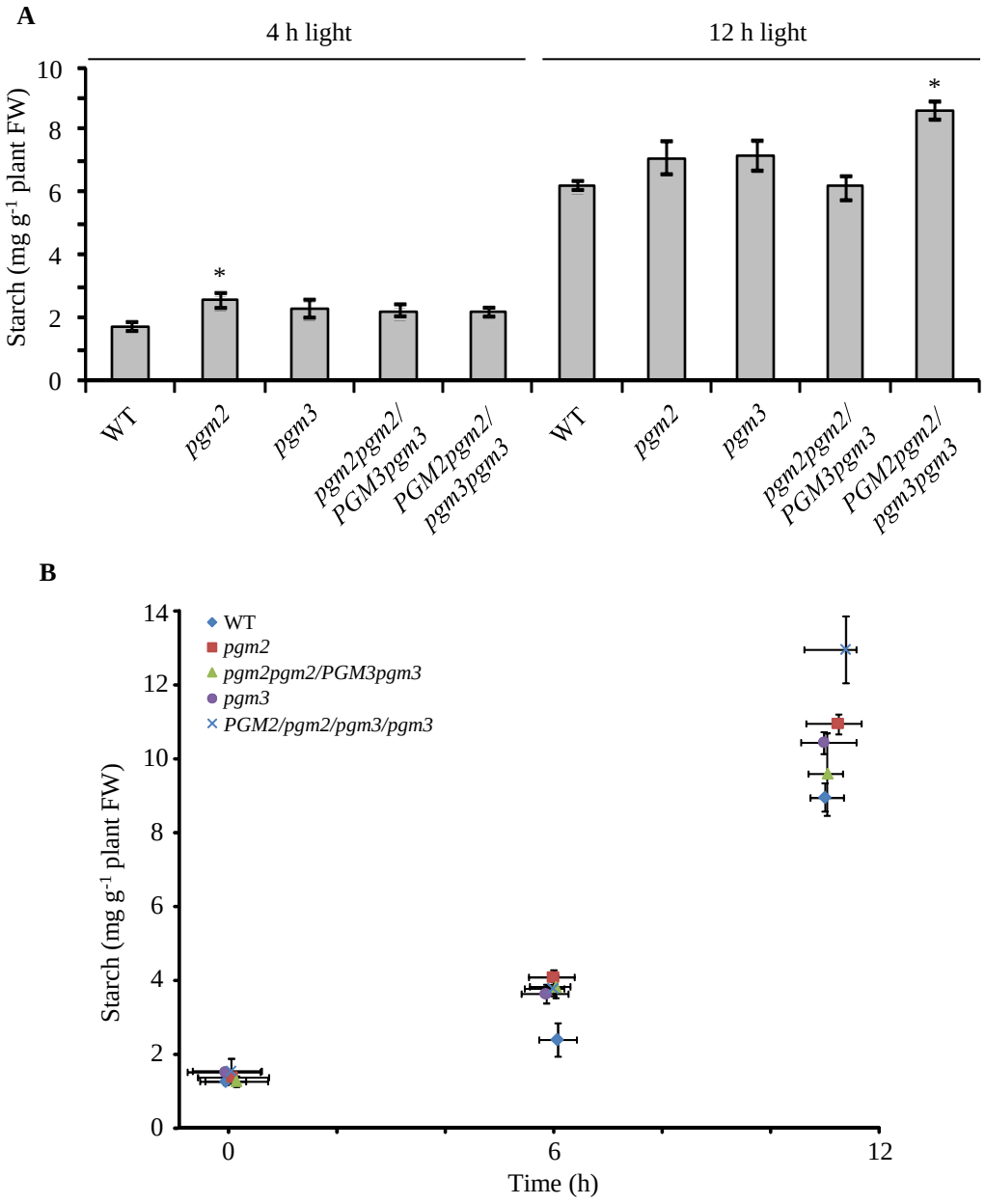
Supplementary Figure S2. Growth phenotype of the wild type (WT), the homozygous single mutants *pgm2* and *pgm3*, and plants carrying a single functional *PGM* allele, *PGM2pgm2/pgm3pgm3* and *pgm2pgm2/PGM3pgm3*. Plant were grown in 12-h light / 12-h dark regime. Rosette weights and sizes were similar. Representative plants are shown.



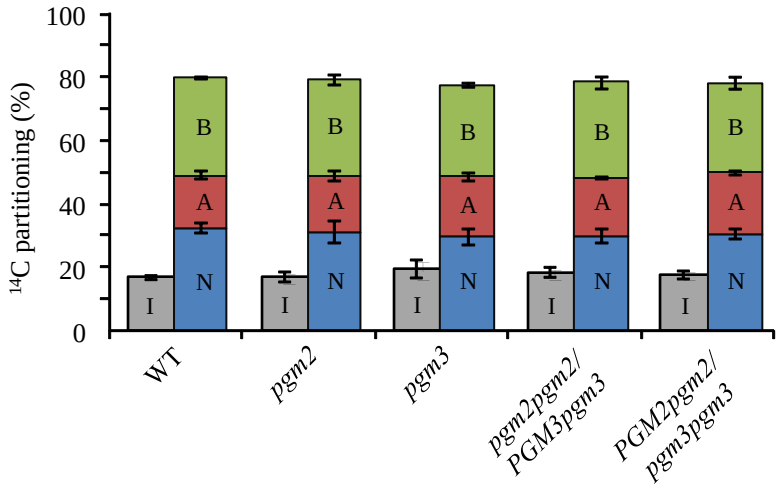
Supplementary Figure S3. Starch and sucrose content in wild-type (WT) and homozygous single mutant plants, *pgm2* and *pgm3*. A, Starch content of three-weeks old rosettes harvested at the end of their12-h photoperiod. Values are the means of four biological replicates ± SE. FW, fresh weight. Asterisks indicate values that differ significantly from the wild type (Student's T-test; $p \leq 0.05$). B, Sucrose content from the same plants as used for starch measurements in A. Further starch and sugar data are in Figure 7 and Supplementary Figure S5.



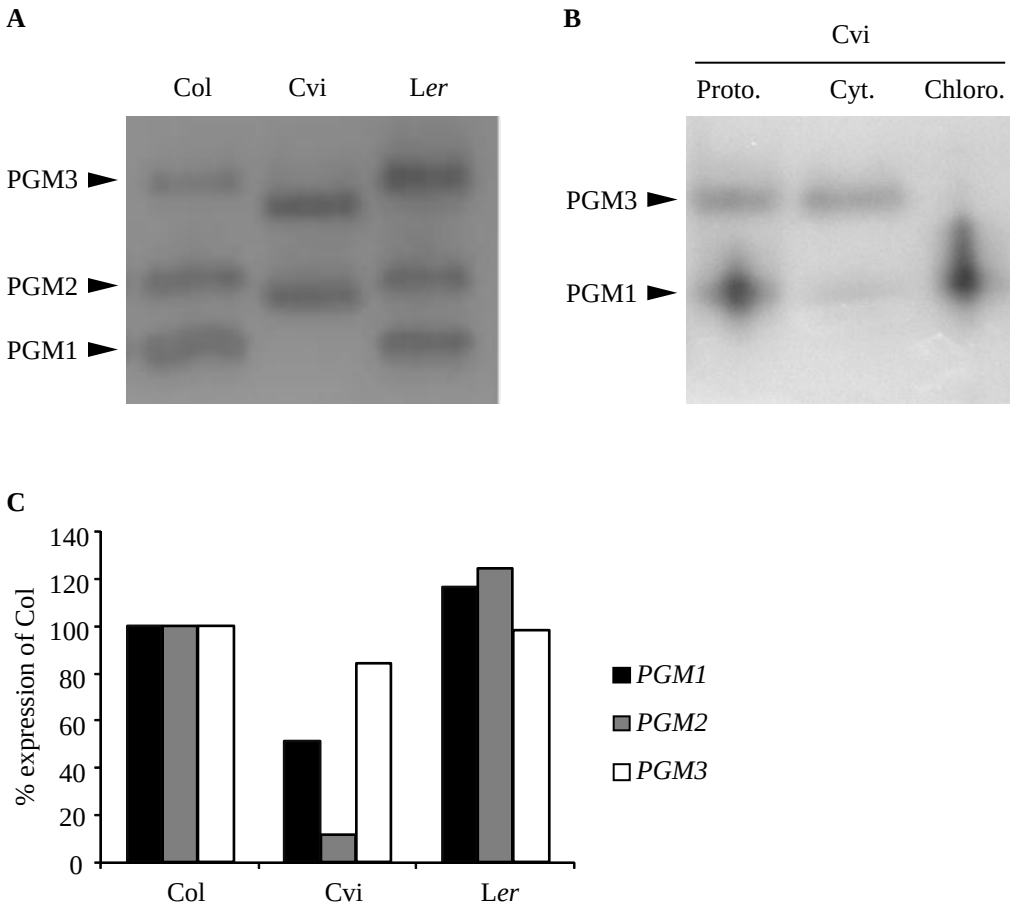
Supplementary Figure S4. Expression and activity of PGMs in different tissues. A, Expression data from published microarray experiments for Columbia wild-type plants. Meta-profile analyses were performed using Genevestigator (Hruz et al., 2008) for At5g51820 (*PGM1*; grey), At1g70730 (*PGM2*; red) and At1g23190 (*PGM3*; blue). The number of microarrays included in the data set is shown on the right. B, PGM enzyme activity in leaf, root and seed from the wild type (WT) and mutants lacking PGM1 (*pgm1*-1). All PGMs are present in all three tissues.



Supplementary Figure S5. Effect of reduced cPGM activity on starch content in the leaf at different time points throughout the light period and in plants of different ages. Wild-type plants (WT), homozygous single mutant plants (*pgm2* and *pgm3*) and plants with one functional allele (*PGM2pgm2/pgm3pgm3* and *pgm2pgm2/PGM3pgm3*) were analyzed. Whole rosettes grown in a 12-h photoperiod were harvested at the time points indicated and starch contents were determined. FW, fresh weight. A, Starch content in six-week old plants. Values are the means of four biological replicates ± SE. B, Starch content of ten-day old plants. Values are the means of between five and 50 biological replicates ± SE. Error bars in x-axis direction indicate the range of harvest time for the biological replicates.



Supplementary Figure S6. Photosynthetic partitioning of ^{14}C into major metabolite pools in different cPGM mutants. Wild-type plants (WT), homozygous single mutant plants (*pgm2* and *pgm3*) and plants with one functional allele (*PGM2pgm2/pgm3pgm3* and *pgm2pgm2/PGM3pgm3*) were analyzed. Six hours into their 12-h photoperiod, single leaves of five-week old plants were exposed to a 5-min pulse of $^{14}CO_2$ followed by a 5-min chase in air. Samples were quenched in hot 80% ethanol and extracts separated into soluble and insoluble fractions. The insoluble fraction (I) contained mostly starch. The soluble fraction was further fractionated into neutral (N, blue), acidic (A, red) and basic (G, green) compounds by ion-exchange chromatography.



Supplementary Figure S7. Loss of function of the *PGM2* gene in the Arabidopsis Cvi ecotype. A, PGM activity resolved by native PAGE in three *Arabidopsis* ecotypes (Col: Columbia, Cvi: Cape Verde Islands; Ler: Landsberg *erecta*). B, Protein localization of the PGMs in Cvi. Separation of isolated protoplasts (Prot) into an enriched cytosolic (Cyt) and a chloroplast (Chloro) fraction showed that the fastest migrating band in Cvi is PGM1 and only one cytosolic PGM band remains. C, Expression analysis by quantitative RT-PCR of *PGM1*, *PGM2* and *PGM3* in the Col, Cvi and L*er* ecotypes. For each sample, *PGM* expression level was normalized to the expression of the house-keeping gene *PP2AA3*, and is presented as relative percentage of the wild type. These data substantiate publicly available microarray data suggesting that PGM2 expression is below the limit of detection in Cvi (Lempe et al., 2005).