Supplementary Figure 1: photo of rosettes at 37 DAS and 44 DAS

Photo of representative rosettes at 37 DAS (A) and 44 DAS (B).

Α

В



6 cm



Supplementary Figure 2: rosette biomass, leaf microscopy, and expression of cell proliferation genes

A) Rosette fresh weight (FW) biomass relative to Col-0 at each timepoint. Points represent the mean of 5 rosettes, and error bars show the SEM. T-test results can be found in Table S1. (B) Histological cross-sections of mature leaves at 35 DAS. Samples were stained with 0.05% of Toluidine blue in water. Scale = 50 μ m. (C) Number of cells (N) normalized to cross-section area (mm²). Bar height corresponds to mean of 6-9 leaves, and error bars represent the standard error of the mean (SEM). (D) Comparison of leaf epithelial cells of mature leaves at 30 and 37 DAS. Scale = 37 μ m. (E) The distributions of epithelial cell area for 40 cells per genotype are depicted by boxplot. The boxes contain cell areas between the 25th and 75th percentiles, whiskers correspond to the 10th and 90th percentile. (C, E) Statistical significance was assessed using t-tests, and p-values were adjusted by Benjamini-Yekutieli method. Compact Letter Display (CLD) identifies lines that are statistically different (adjusted $p \le 0.05$) from each other. (F) Heatmap representation of gene expression differences determined by RNA-seq. Genes shown are annotated to various cell proliferation genes (Vercruysse et al., 2021). Heatmap color corresponds to log2 of the fold change (log2FC) relative to Col-0 at each timepoint determined from 3 biological replicates. Wald test results for genes shown can be found in Table S1.





В

Α









С

F



Supplementary Figure 3: Differentially expressed gene count

The number of differentially expressed genes (DEG) at each timepoint in each contrast is shown. All DEG have an adjusted p-value < 0.05. The total number of genes tested for differential expression by Wald test at each timepoint is indicated in parentheses.



Supplementary Figure 4: sulfur metabolism and ROS/redox related gene expression

The concentration of major sulfur-containing compounds (A-D) in rosette tissue normalized to FW is shown. Bar height corresponds to mean of 3 biological replicates, dots correspond to the concentration determined in individual samples, and error bars represent the standard error of the mean (SEM). Statistical significance was assessed using t-tests within each timepoint. T-test results can be found in Table S1. P-values were adjusted by Benjamini-Yekutieli method. Compact Letter Display (CLD) identifies lines that are statistically different (adjusted $p \le 0.05$) from each other at each timepoint. Heatmap representation of expression differences determined by RNA-seq of sulfur metabolism related genes (E) and genes annotated to (cellular) response to ROS (GO:0000302, GO:0034614), response to redox state (GO:0051775), and antioxidant activity (GO:0016209) (F). Heatmap color corresponds to log2 of the fold change (log2FC) relative to Col-0 at each timepoint determined from 3 biological replicates. Wald test results for genes shown can be found in Table S1.



Supplementary Figure 4



Supplementary Figure 4

F

30DAS	6 3	B7DA	S	4	4DA	S		
							AT5G52310 COR78 AT5G01600 ATFER1 AT5G37670 HSP15.7 AT2G40300 ATFER3 AT4G34890 ATXDH1 AT3G56090 ATFER3 AT4G34890 ATXDH1 AT3G08640 RER3 AT1G60740 PRXIID AT4G23140 CRK6 AT4G17490 ATERF6 AT3G01420 ALPHA-DOX1 AT1G19020 SDA1 AT4G02380 SAG21 AT4G18880 AT-HSFA4A AT1G07890 APX1 AT3G50310 MAPKKK20 AT3G04120 GAPC AT4G08390 SAPX AT5G58070 ATTIL AT1G65980 TPX1 AT2G01980 SOS1 AT4G00860 ATOZI1 AT4G00860 ATOZI1 AT1G08830 CSD1 AT2G37240 ThrSP2 AT5G18100 CSD3 AT3G06050 PRXIIF AT5G24400 EMB2024 AT4G32320 APX6 AT1G66950 PDR11 AT4G35000 APX3 AT5G65840 ThrSP3 AT3G66550 SVR3 AT1G18150 ATMPK8 AT5G565830 NADP-MDH AT5G51020 CRL AT2G37860 LCD1 AT1G65970 TPX2 AT5G13650 SVR3 AT1G18150 ATMPK8 AT5G58330 NADP-MDH AT5G51020 CRL AT2G37860 LCD1 AT1G64860 SIGA AT3G52960 PRXIIE AT4G23150 CRK7 AT3G56400 WRKY70 AT2G40750 WRKY54 AT2G28190 CSD2 AT1G21350 ThrSP AT4G35970 APX5 AT1G77490 TAPX AT4G35970 APX5 AT1G77490 TAPX AT4G09010 APX4 AT3G11630 2CPA AT5G06290 2-Cys Prx B AT3G26060 ATPRX Q	log2FC 4 2 0 -2 -4
<i>slim1-cr</i> v Col-0 35S::SLIM1 #17 v Col-0	35S::SLIM1 #25 v Col-0 slim1-cr v Col-0	35S::SLIM1 #17 v Col-0	35S::SLIM1 #25 v Col-0	slim1-cr v Col-0	35S::SLIM1 #17 v Col-0	35S::SLIM1 #25 v Col-0		