Figure S1. (A) Expression of *pLAS>>GFP-ER* (green), and (B) pattern of *AS1* promoter driven GUS expression in longitudinal sections through vegetative shoot apex of 25-day-old wild-type like plants showing cell type specific expression promoter activities. Bars = 50 µm

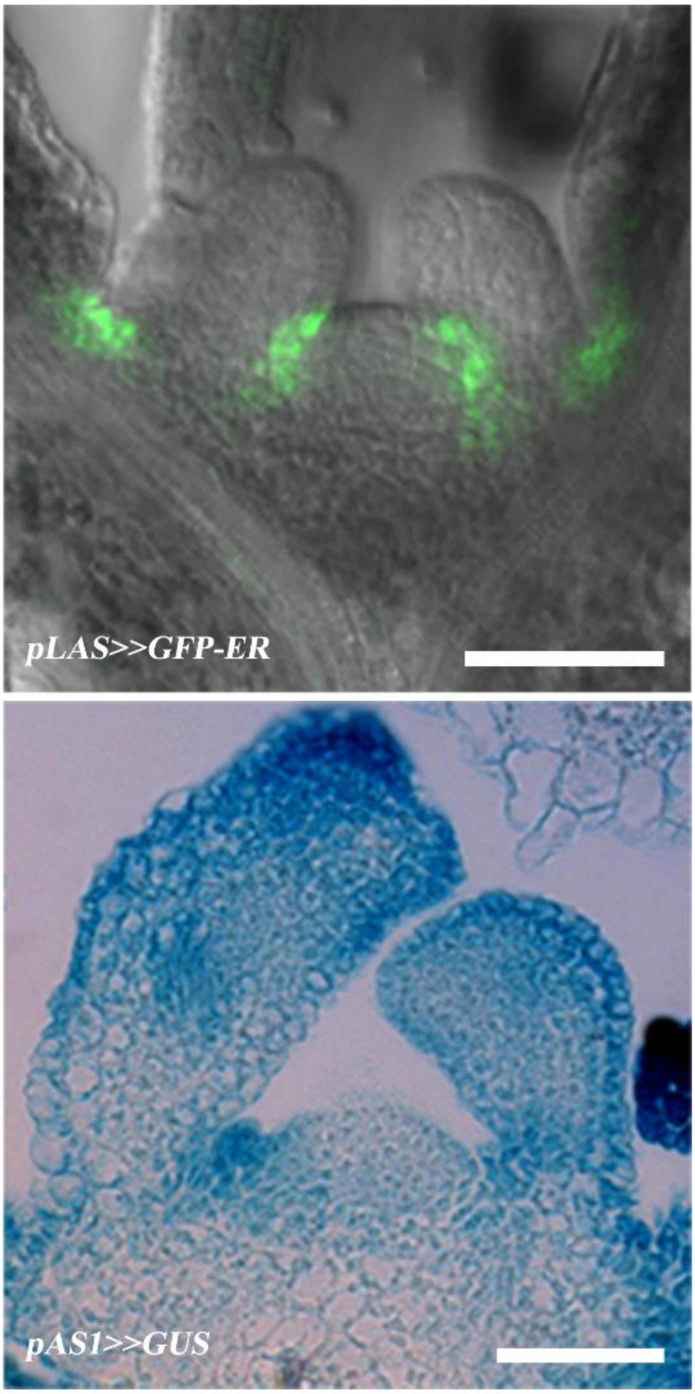


Figure S2. GO analysis identified significantly overrepresented (FDR adjusted $P < 0.01$) gene categories for the leaf cell-specific transcripts. Color bar: significance levels for categories by hypergeometric test with FDR correction.

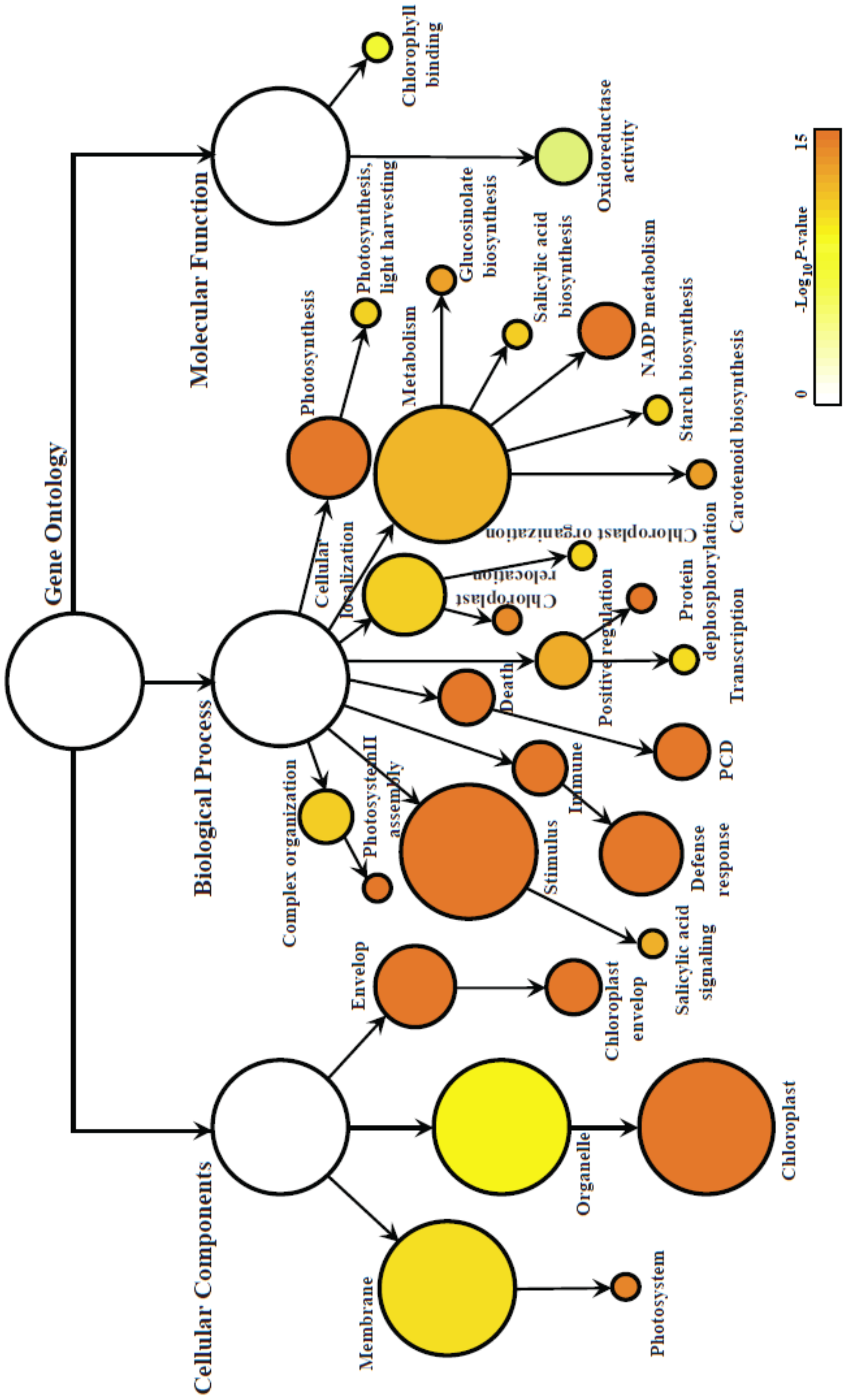


Figure S3. Reporter assay procedure and readout with a promoter fragment and 96 TF pools w/ and w/o AbA selection. Each TF pool used in the first round included four TFs, and each TF in positive pools was individually tested in the second-round screen.

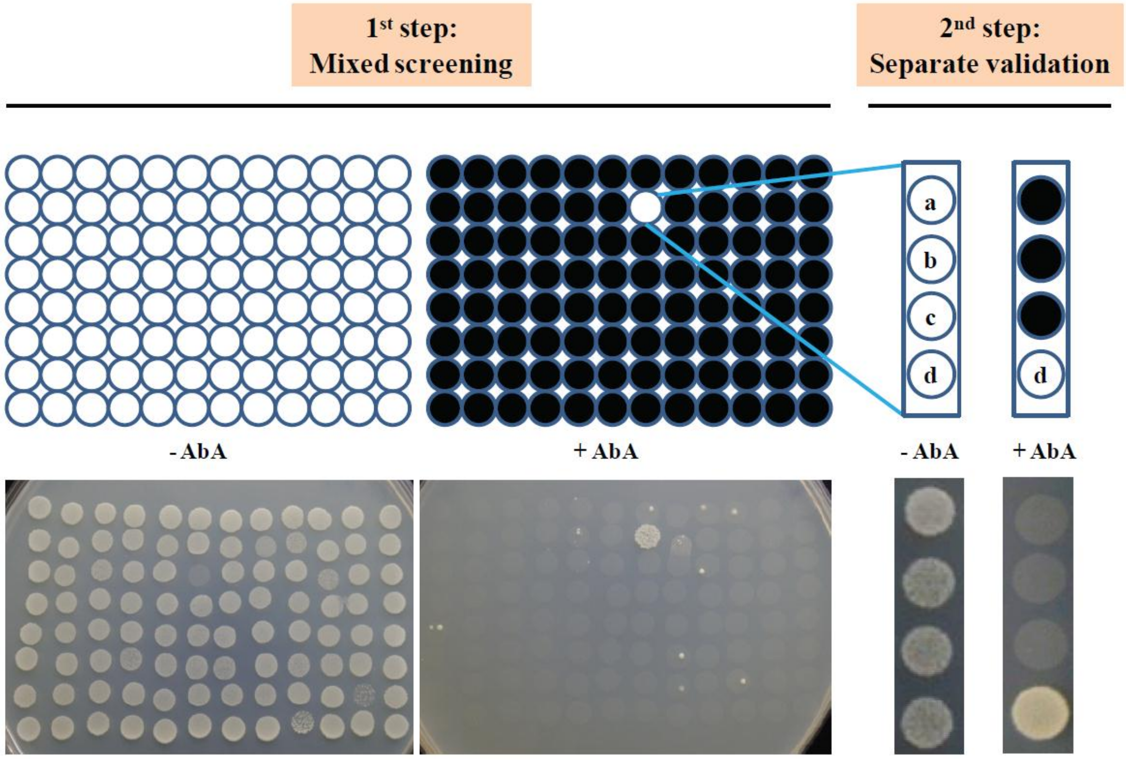
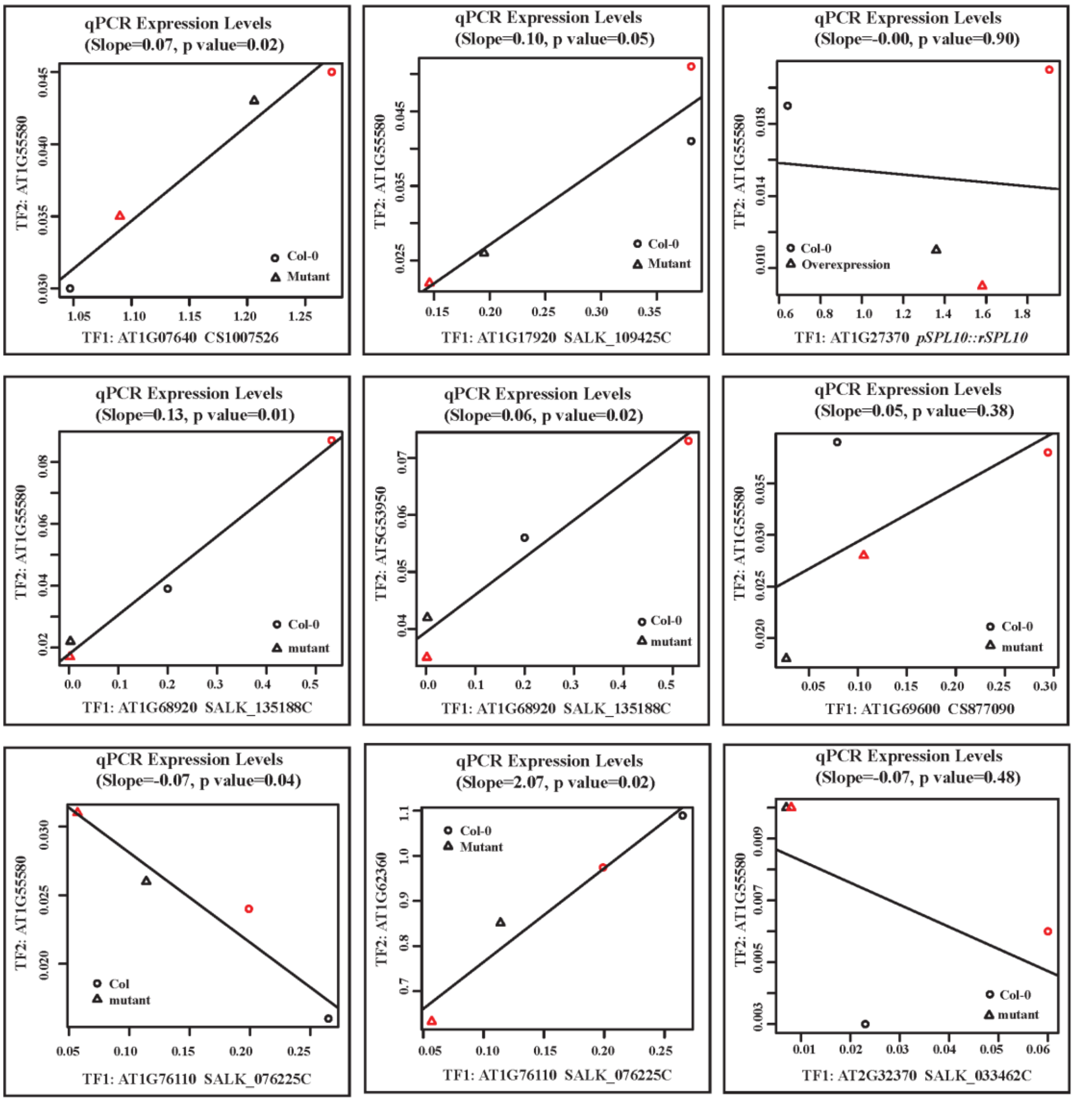
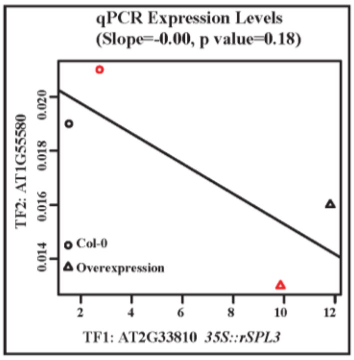
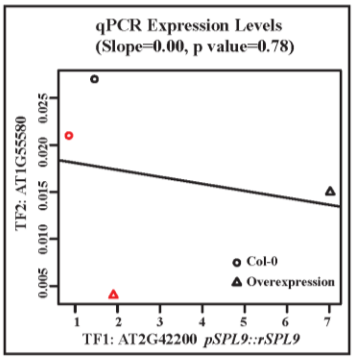
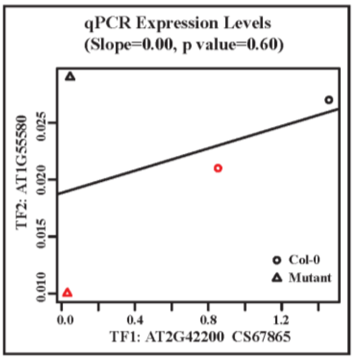


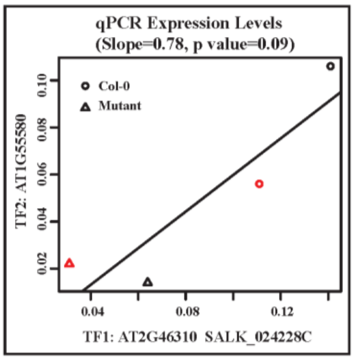
Figure S4. Weighted least square regression (WLSR) plots. WLSR was used to predict the potential of regulatory relationships between a target gene and its upstream TF. We used WLSR to fit a line that incorporates variance measurements across three technical replicates for each of the two biological replicates (six replicates in total). The slope of a line predicts the degree of activation or repression with a *P* value represents the confidence level for the regulation. See *Materials and Methods* for more details.

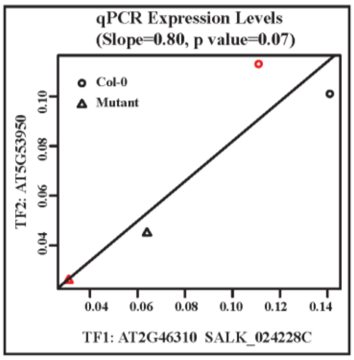


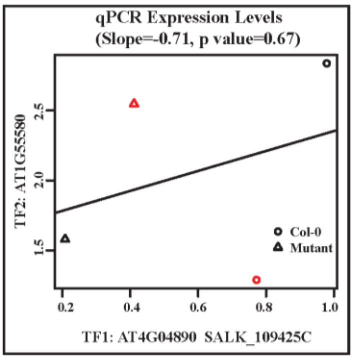

qPCR Expression Levels
(Slope=-0.00, p value=0.18)
TF2: AT1G55580
0.014
0.016
0.018
0.020
2
4
6
8
10
12
TF1: AT2G33810 *35S::rSPL3*
Col-0
Overexpression

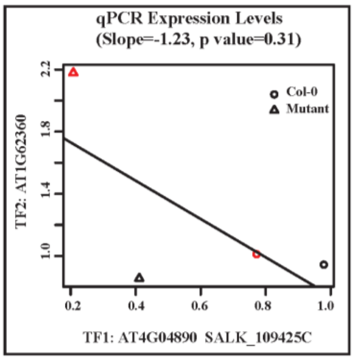

qPCR Expression Levels
(Slope=0.00, p value=0.78)
TF2: AT1G55580
0.005
0.010
0.015
0.020
0.025
1
2
3
4
5
6
7
TF1: AT2G42200 *pSPL9::rSPL9*
Col-0
Overexpression

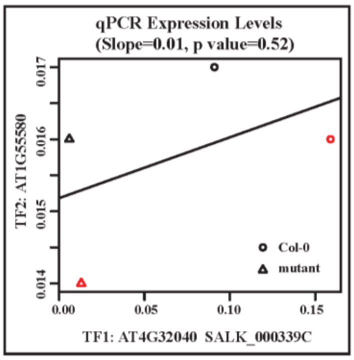

qPCR Expression Levels
(Slope=0.00, p value=0.60)
TF2: AT1G55580
0.010
0.015
0.020
0.025
0.0
0.4
0.8
1.2
TF1: AT2G42200 CS67865
Col-0
Mutant

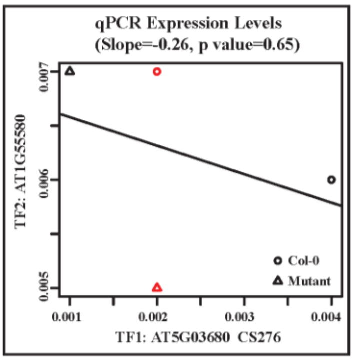

qPCR Expression Levels
(Slope=0.78, p value=0.09)
TF2: AT1G55580
0.02
0.04
0.06
0.08
0.10
0.04
0.08
0.12
TF1: AT2G46310 SALK_024228C
Col-0
Mutant


qPCR Expression Levels
(Slope=0.80, p value=0.07)
TF2: AT5G53950
0.04
0.06
0.08
0.10
0.04
0.06
0.08
0.10
0.12
0.14
TF1: AT2G46310 SALK_024228C
Col-0
Mutant


qPCR Expression Levels
(Slope=-0.71, p value=0.67)
TF2: AT1G55580
1.5
2.0
2.5
0.2
0.4
0.6
0.8
1.0
TF1: AT4G04890 SALK_109425C
Col-0
Mutant


qPCR Expression Levels
(Slope=-1.23, p value=0.31)
TF2: AT1G62360
1.0
1.4
1.8
2.2
0.2
0.4
0.6
0.8
1.0
TF1: AT4G04890 SALK_109425C
Col-0
Mutant


qPCR Expression Levels
(Slope=0.01, p value=0.52)
TF2: AT1G55580
0.014
0.015
0.016
0.017
0.00
0.05
0.10
0.15
TF1: AT4G32040 SALK_000339C
Col-0
mutant


qPCR Expression Levels
(Slope=-0.26, p value=0.65)
TF2: AT1G55580
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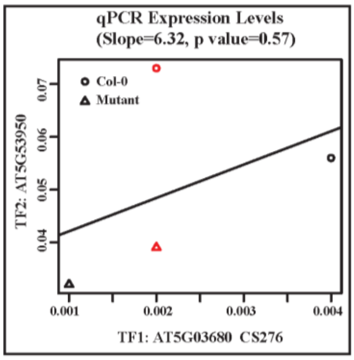
0.006
0.007
0.001
0.002
0.003
0.004
TF1: AT5G03680 CS276
Col-0
Mutant


qPCR Expression Levels
(Slope=6.32, p value=0.57)
Col-0
Mutant
TF2: AT5G53950
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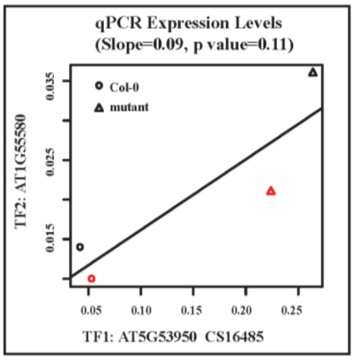
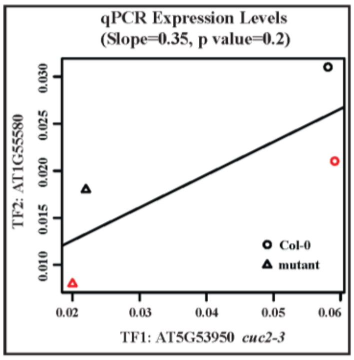
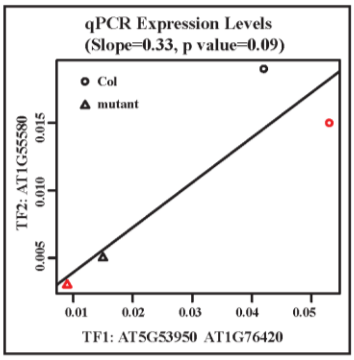
0.05
0.06
0.07
0.001
0.002
0.003
0.004
TF1: AT5G03680 CS276


qPCR Expression Levels
(Slope=0.09, p value=0.11)
Col-0
mutant
TF2: AT1G55580
0.015
0.025
0.035
0.05
0.10
0.15
0.20
0.25
TF1: AT5G53950 CS16485


qPCR Expression Levels
(Slope=0.35, p value=0.2)
Col-0
mutant
TF2: AT1G55580
0.010
0.015
0.020
0.025
0.030
0.02
0.03
0.04
0.05
0.06
TF1: AT5G53950 cuc2-3


qPCR Expression Levels
(Slope=0.33, p value=0.09)
Col
mutant
TF2: AT1G55580
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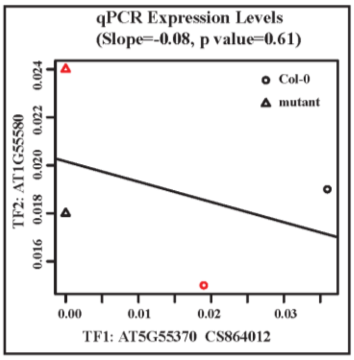
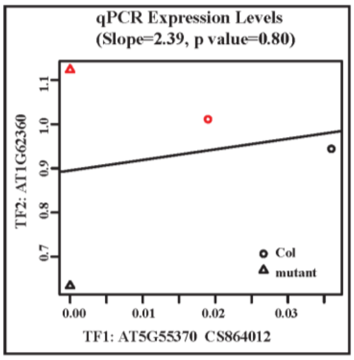
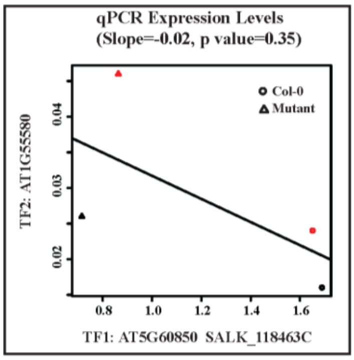
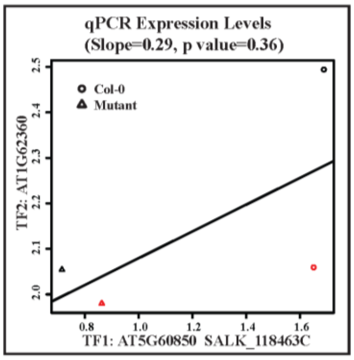
0.010
0.015
0.01
0.02
0.03
0.04
0.05
TF1: AT5G53950 AT1G76420


qPCR Expression Levels
(Slope=-0.08, p value=0.61)
Col-0
mutant
TF2: AT1G55580
0.016
0.018
0.020
0.022
0.024
0.00
0.01
0.02
0.03
TF1: AT5G55370 CS864012


qPCR Expression Levels
(Slope=2.39, p value=0.80)
Col
mutant
TF2: AT1G62360
0.7
0.8
0.9
1.0
1.1
0.00
0.01
0.02
0.03
TF1: AT5G55370 CS864012


qPCR Expression Levels
(Slope=-0.02, p value=0.35)
Col-0
Mutant
TF2: AT1G55580
0.02
0.03
0.04
0.8
1.0
1.2
1.4
1.6
TF1: AT5G60850 SALK_118463C


qPCR Expression Levels
(Slope=0.29, p value=0.36)
Col-0
Mutant
TF2: AT1G62360
2.0
2.1
2.2
2.3
2.4
2.5
0.8
1.0
1.2
1.4
1.6
TF1: AT5G60850 SALK_118463C

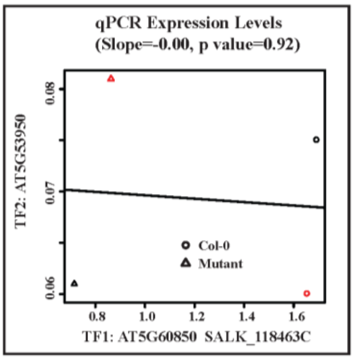

qPCR Expression Levels
(Slope=-0.00, p value=0.92)
Col-0
Mutant
TF2: AT5G53950
0.06
0.07
0.08
0.8
1.0
1.2
1.4
1.6
TF1: AT5G60850 SALK_118463C

Figure S5. Interactions between TFs and their targets indicated by WLSR analysis. Regulatory interaction strength is shown by arrow and edge width. The opacity represents the interaction *P* value, in which darker arrow or edge opacity indicates a more-significant interaction.

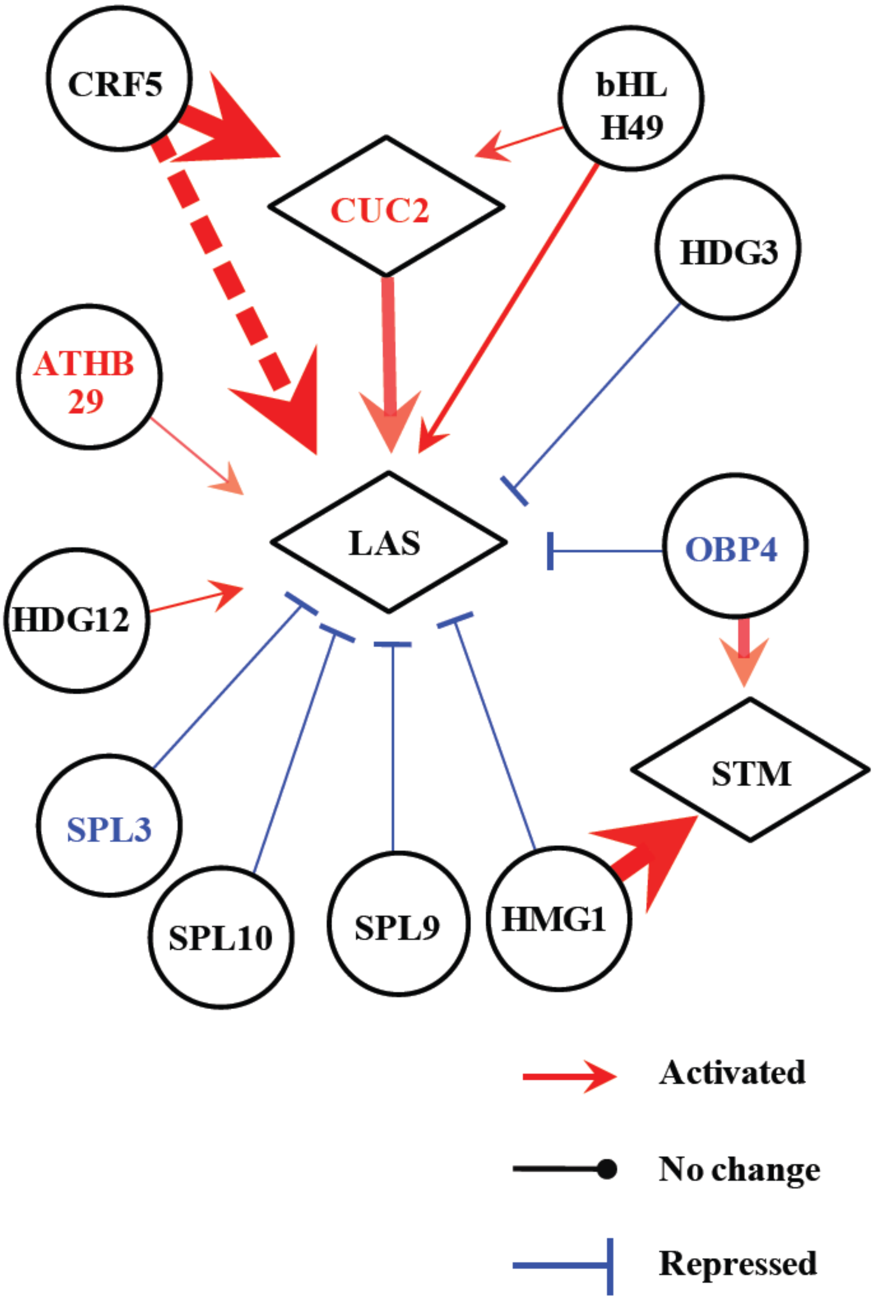
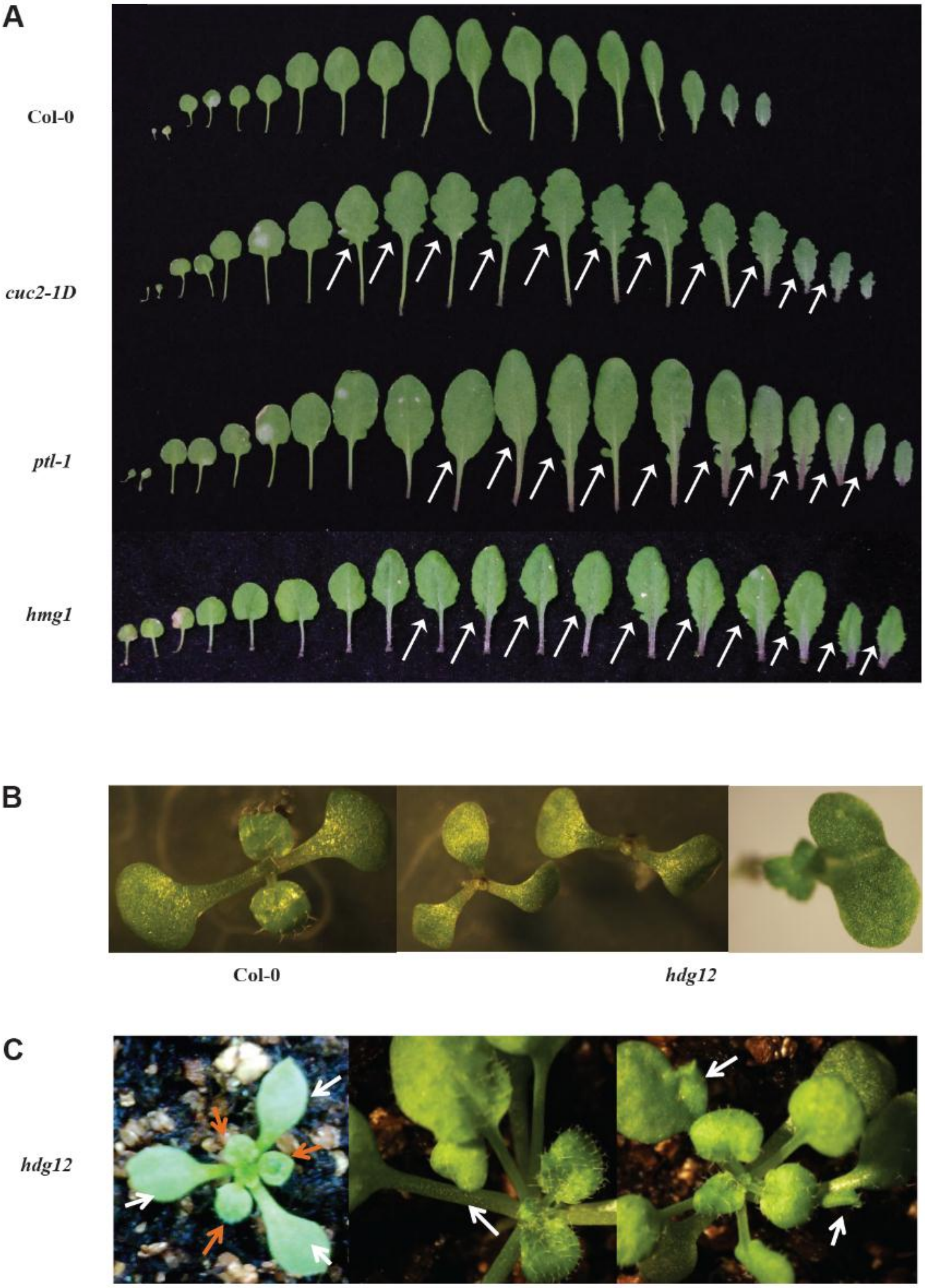


Figure S6. Phenotypic characterization of new mutants affecting leaf margin development and cotyledon formation. (**A**) Leaf series of Col-0, *cuc2-1D*, *ptl-1* and *hmg1*. Leaves with enhanced margin serration are highlighted by arrows. (**B**) Cotyledon morphology of Col-0 and *hdg12*. Tricots and fused cotyledons in the *hdg12* mutant are shown. (**C**) Disordered leaf phyllotaxy and fusion phenotypes of *hdg12*.(**D**) Phenotype statistics of *hdg12*.



D

	Three cotyledons	Fused cotyledons	Delayed development
Col-0	**0/120 (0%)**	**0/120 (0%)**	**0/120 (0%)**
hdg12	**13/248(5.2%)**	**13/248 (2.20%)**	**248/248 (100%)**