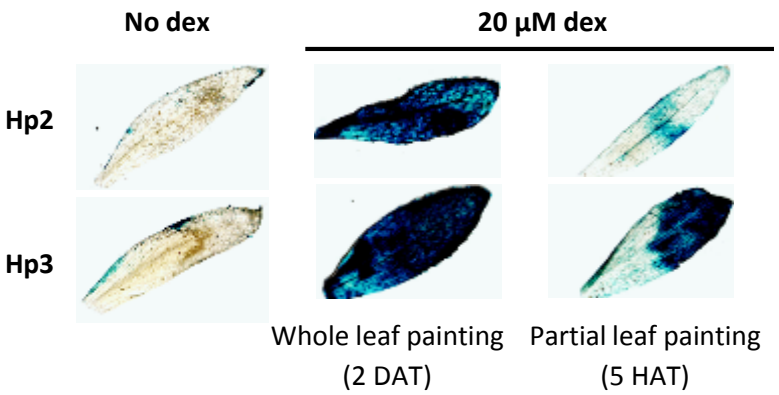
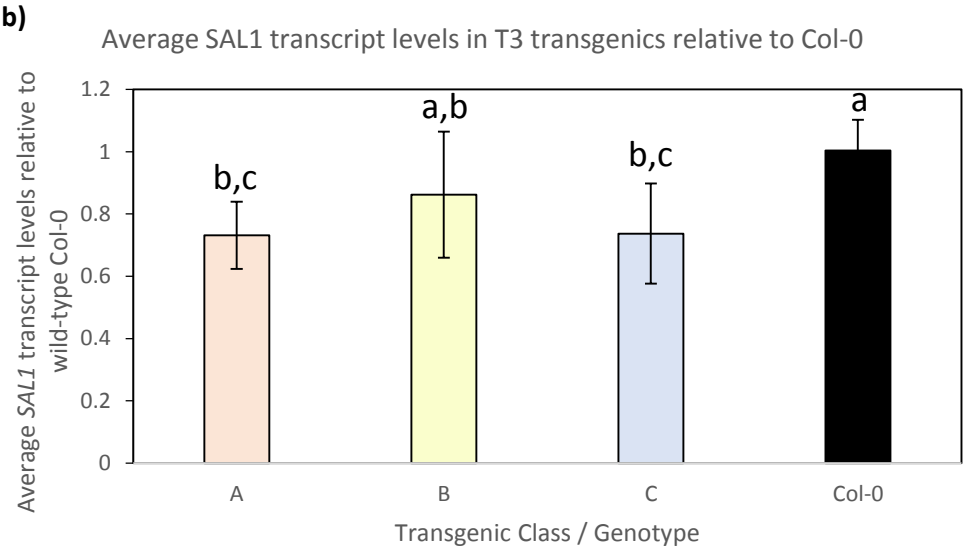
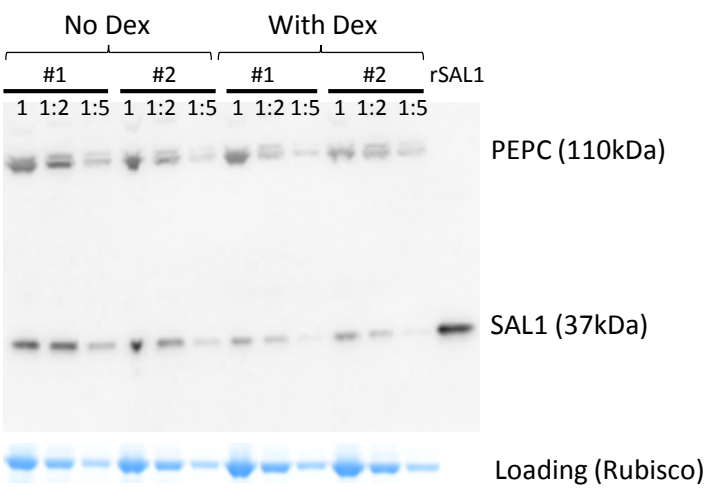
a)



b)



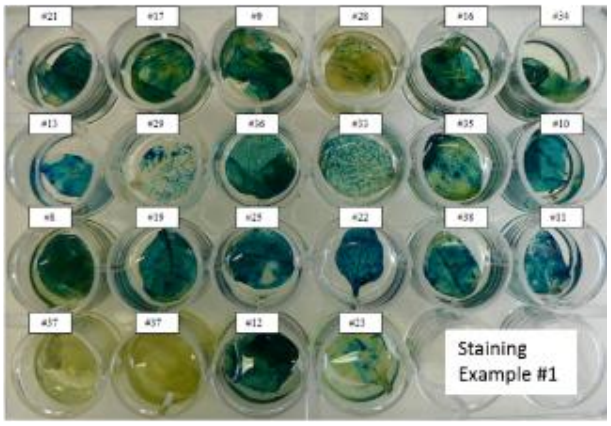
c)

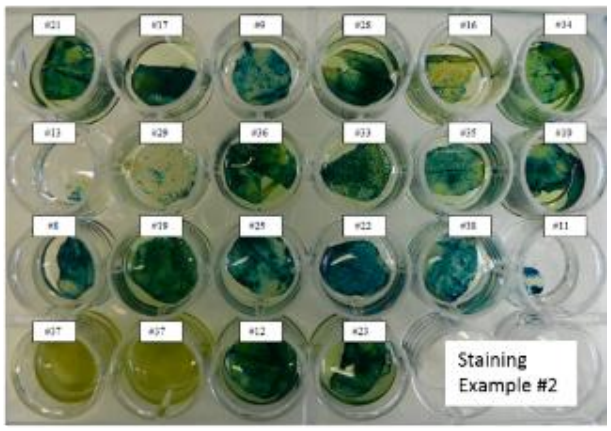


Supplementary Figure 1 – Preliminary testings of the dexamethasone-inducible system using a few selected pOpOff-*SAL1*hpRNAi lines in Arabidopsis. A) Leaves of T1 transformants were either painted with no dex or with 20 µM dex before GUS staining was checked 2 days after treatment (DAT) on whole leaf or 5 hours after treatment (HAT) on partial leaf painting. B) *SAL1* transcript quantification from leaf tissues of three-week-old T3 plants after one week of 20µM dex treatment via soil-drenching. n=3 and error bars indicate standard deviation. Significant differences (ANOVA, $p<0.05$) are denoted by a, b, c. C) Total protein was extracted from leaves of four-week-old T3 plants treated with or without dex via soil drenching every three days since germination (n=2), SAL1 and PEPC as loading control were probed. Dilution series of 1:1, 1:2 and 1:5 were loaded for each sample.

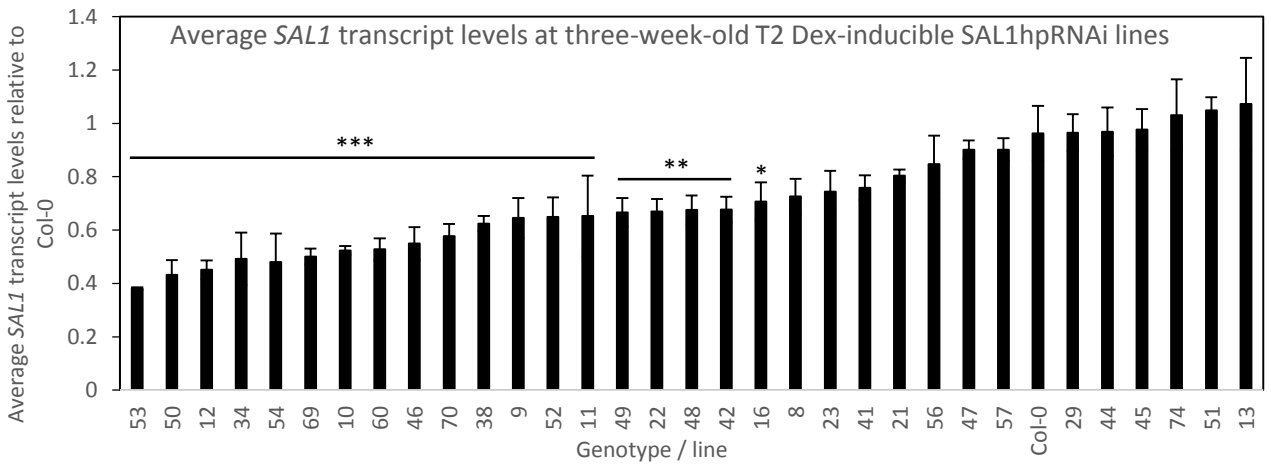
a)

Line #	GUS Staining Intensities (5 replicates)			Class
	Strong	Moderate	Weak	
8	5	0	0	A
12	5	0	0	A
17	5	0	0	A
19	5	0	0	A
21	5	0	0	A
36	5	0	0	A
10	4	1	0	B
11	4	1	0	B
22	4	1	0	B
38	4	1	0	B
9	3	1	1	C
13	3	1	1	C
16	3	1	1	C
23	3	1	1	C
25	3	2	0	C
33	3	1	1	C
28	2	0	3	D
34	2	3	0	D
35	2	3	0	D
29	0	2	3	E
37	0	0	0	False Positive

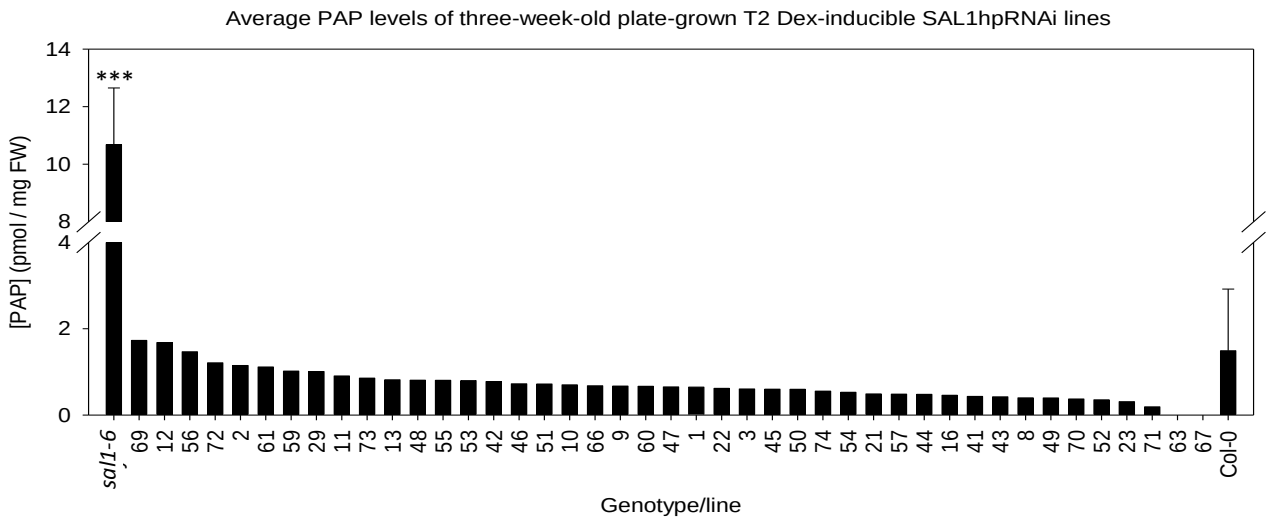




b)

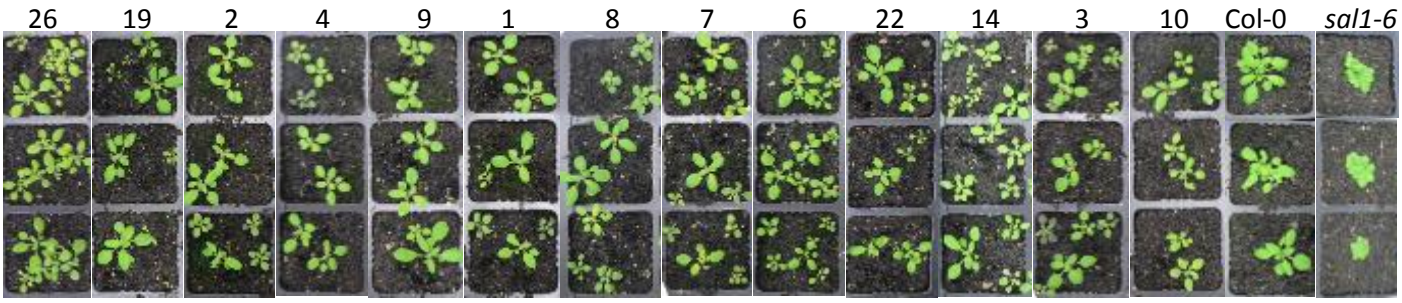


c)

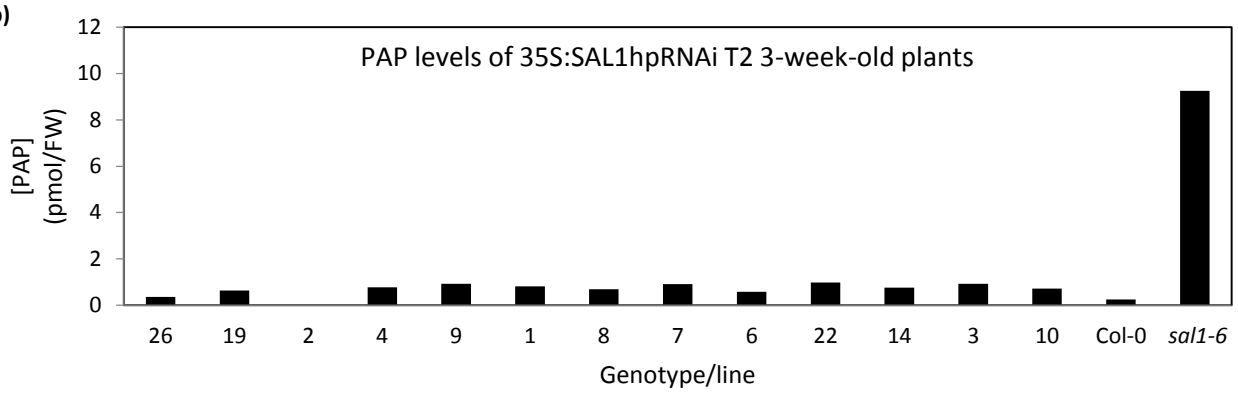


Supplementary Figure 2 – Screening transgenic lines to identify the potential of *SAL1* silencing efficiency of pOpOff system. A) Leaves of four-week-old T2 plants were harvested for GUS staining two days after painted with 20µM dex. Three-week-old seedlings germinated and grown on MS supplemented with 20µM dex were harvested for B) *SAL1* transcript quantification relative to the wild-type Col-0 control via qRT-PCR [n= 3 technical replicates, error bars = standard deviation, significant differences = ANOVA, post-hoc test relative to Col-0: *** denotes p<0.001, ** denotes p<0.01 and * denotes p<0.05] and C) PAP quantification using HPLC. At least 10 seedlings per transgenic line were pooled for each quantification [n=3 biological replicates for Col-0 and *sal1-6,* error bars = standard deviation]. Student T-Test relative to Col-0 control was performed; *** denotes p-value<0.001.

a)



b)

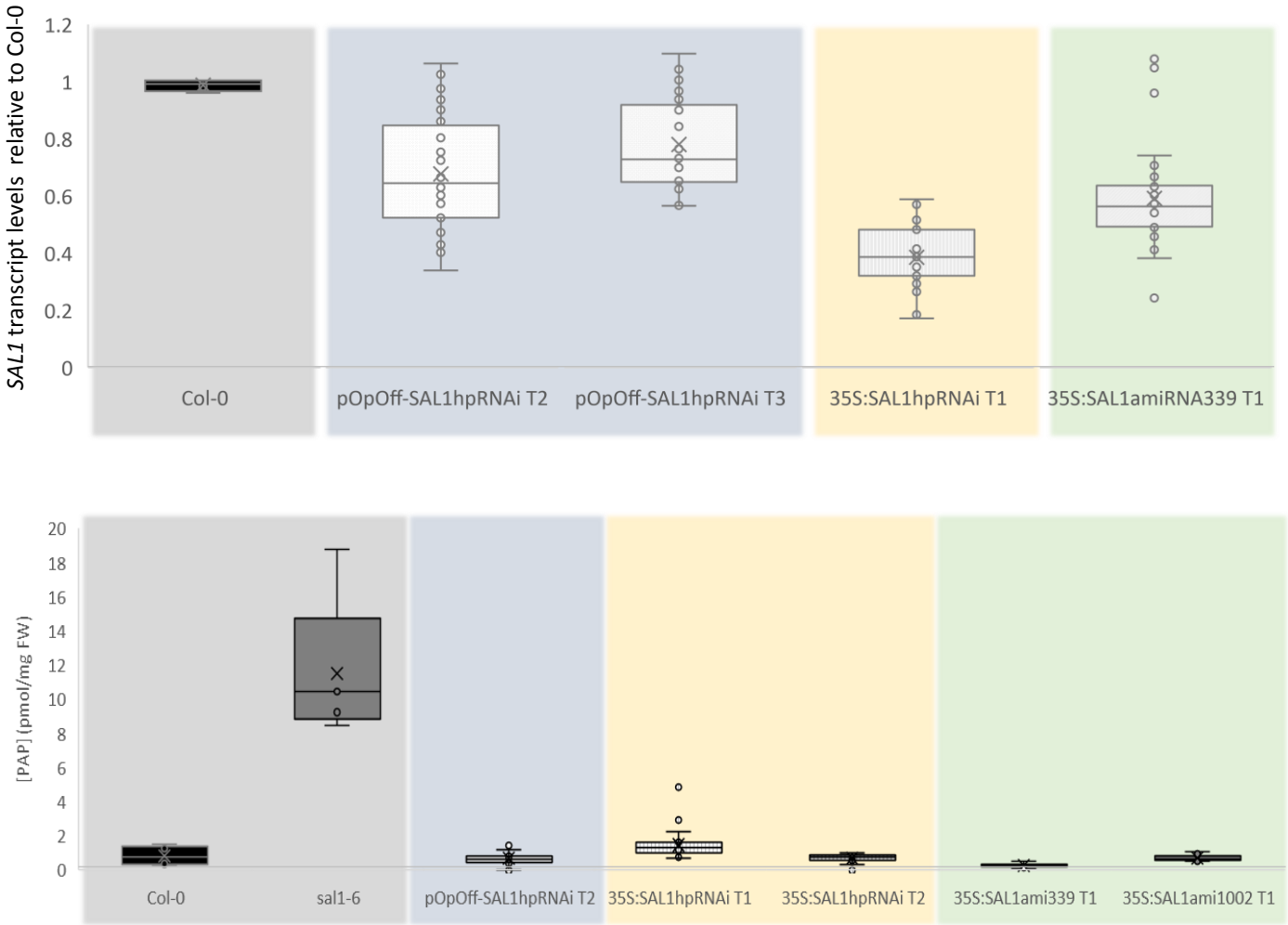


Supplementary Figure 3 – Characterization of T2 35S:*SAL1*hpRNAi lines. A) Representative photos of selected lines at 3.5 weeks old are shown. B) Selected 35S:*SAL1*hpRNAi lines, particularly those with "higher-than-Col-0" PAP accumulation at T1 generation, were re-tested for PAP levels at T2 generation, where five seedlings per line were pooled.

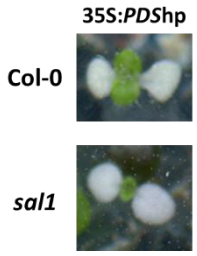
a)

b)

Supplementary Figure 4 – Representative images of T1 35S:*SAL1*amiRNA lines at four weeks old. A) 35S:*SAL1*ami339. B) 35S:*SAL1*ami1002. Each pot represents one independent transgenic line.

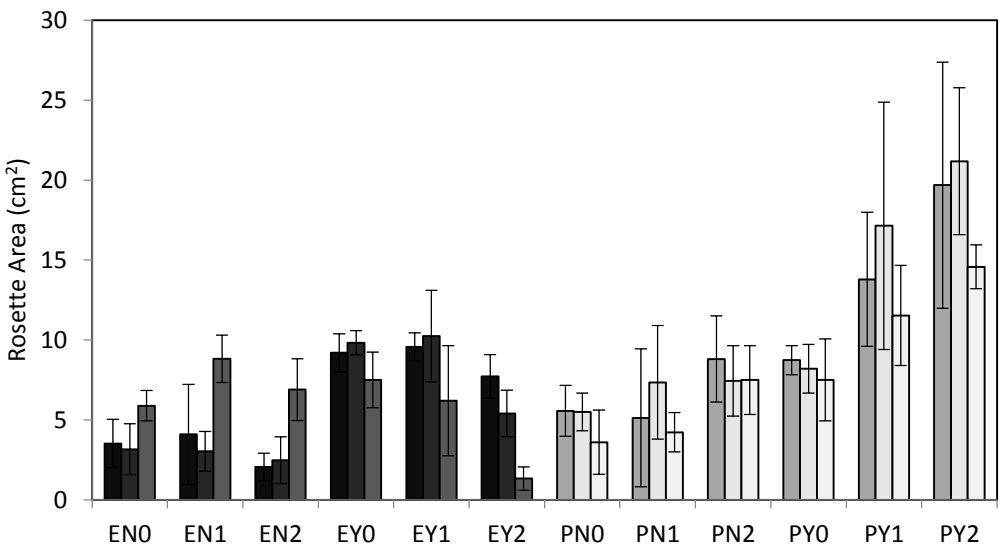


Supplementary Figure 5 – Summary findings of *SAL1* silencing strategies using: dex-inducible *SAL1*hpRNAi (blue), strong constitutive hpRNAi (yellow) and amiRNA (green). A) Boxplot of SAL1 transcript levels relative to wild-type Col-0. B) Boxplot of PAP levels.

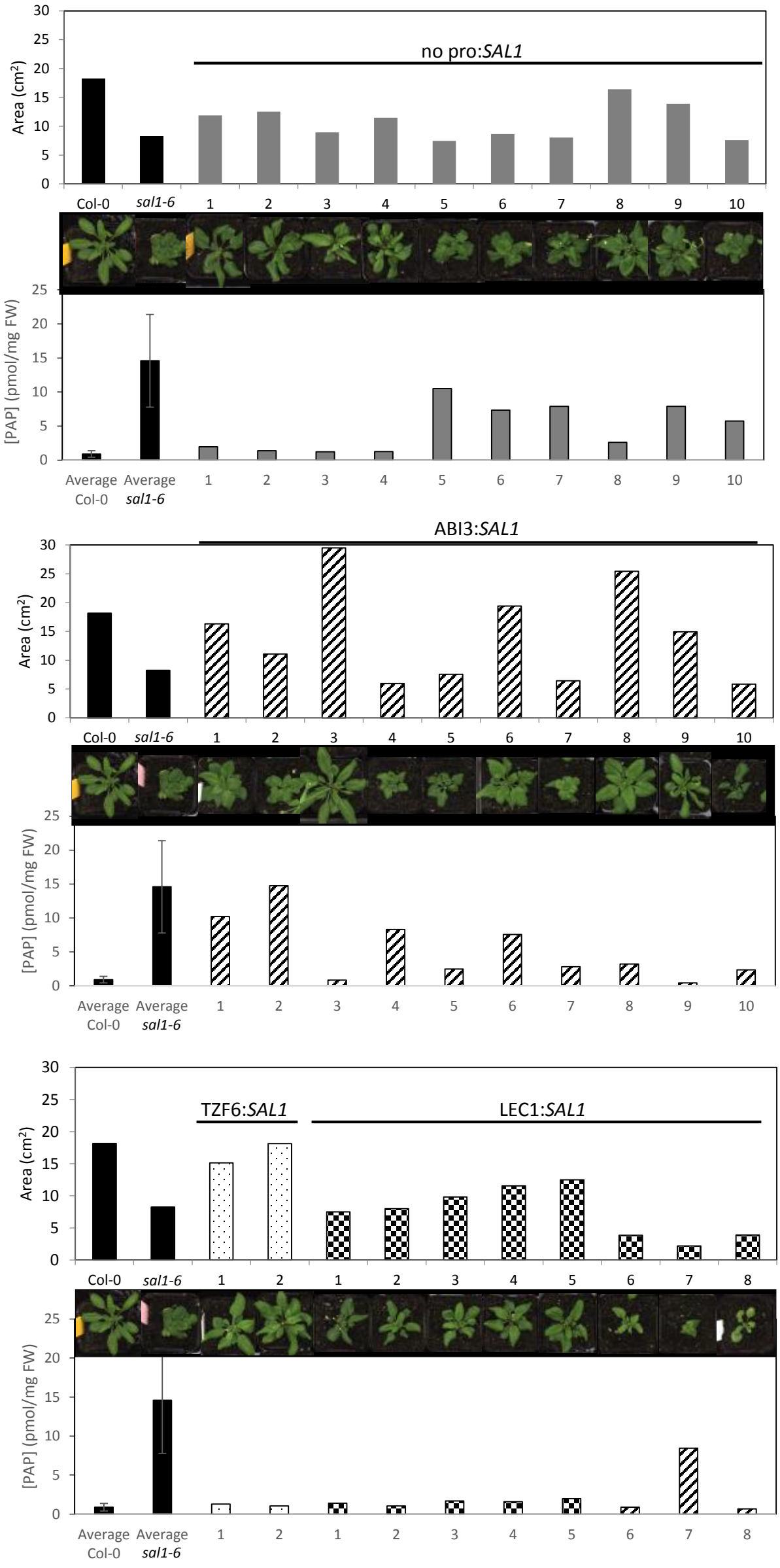


Supplementary Figure 6 – Silencing of *PDS* in Col-0 and *sal1* transformed with 35S:*PDS*hpRNAi.

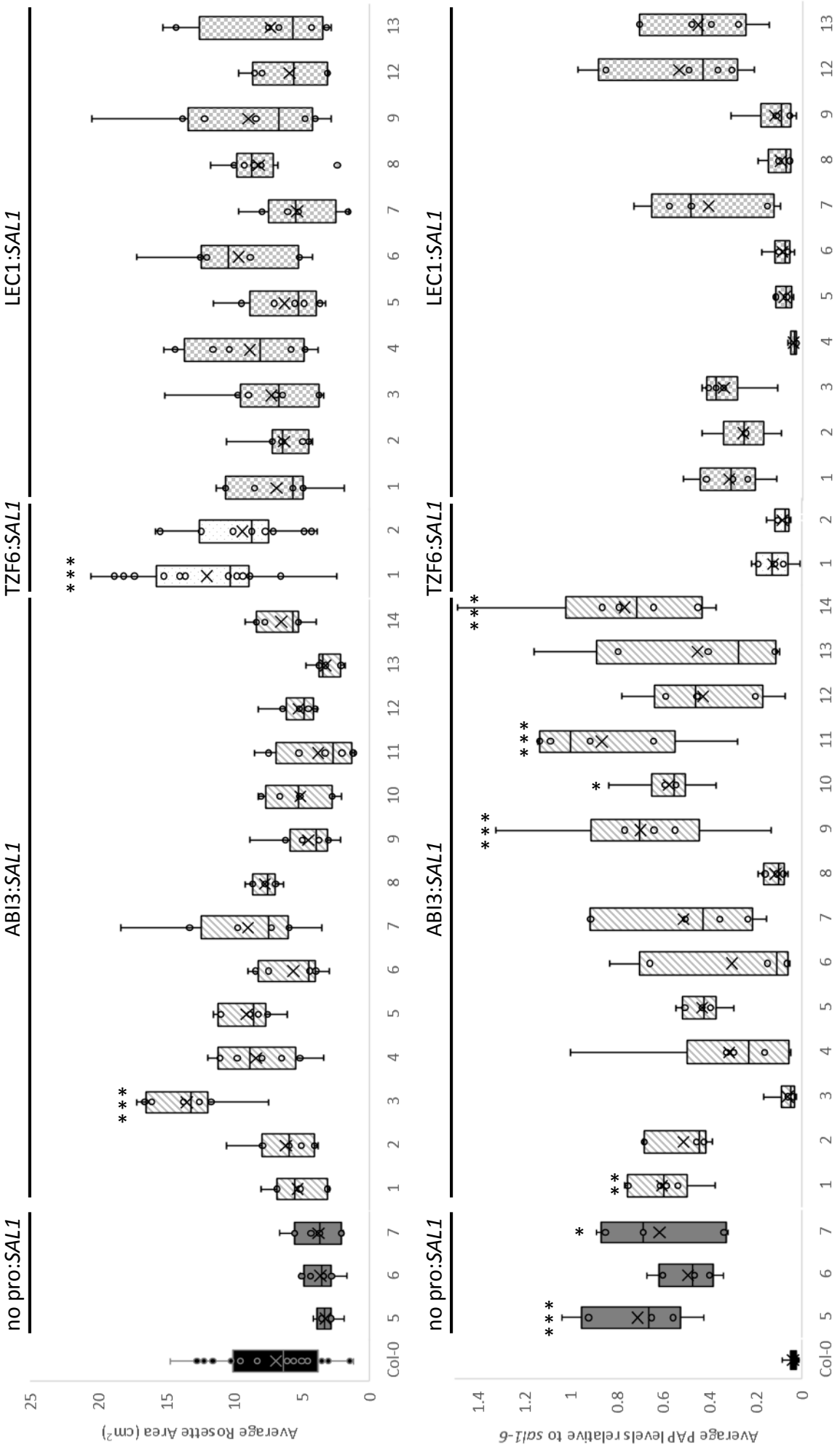
Vector	Empty Vector						pOpON*SAL1*					
Dex treatment on germination	No			Yes			No			Yes		
Dex treatment duration on soil (weeks)	0	1	2	0	1	2	0	1	2	0	1	2
Abbreviation	EN0	EN1	EN2	EY0	EY1	EY2	PN0	PN1	PN2	PY0	PY1	PY2



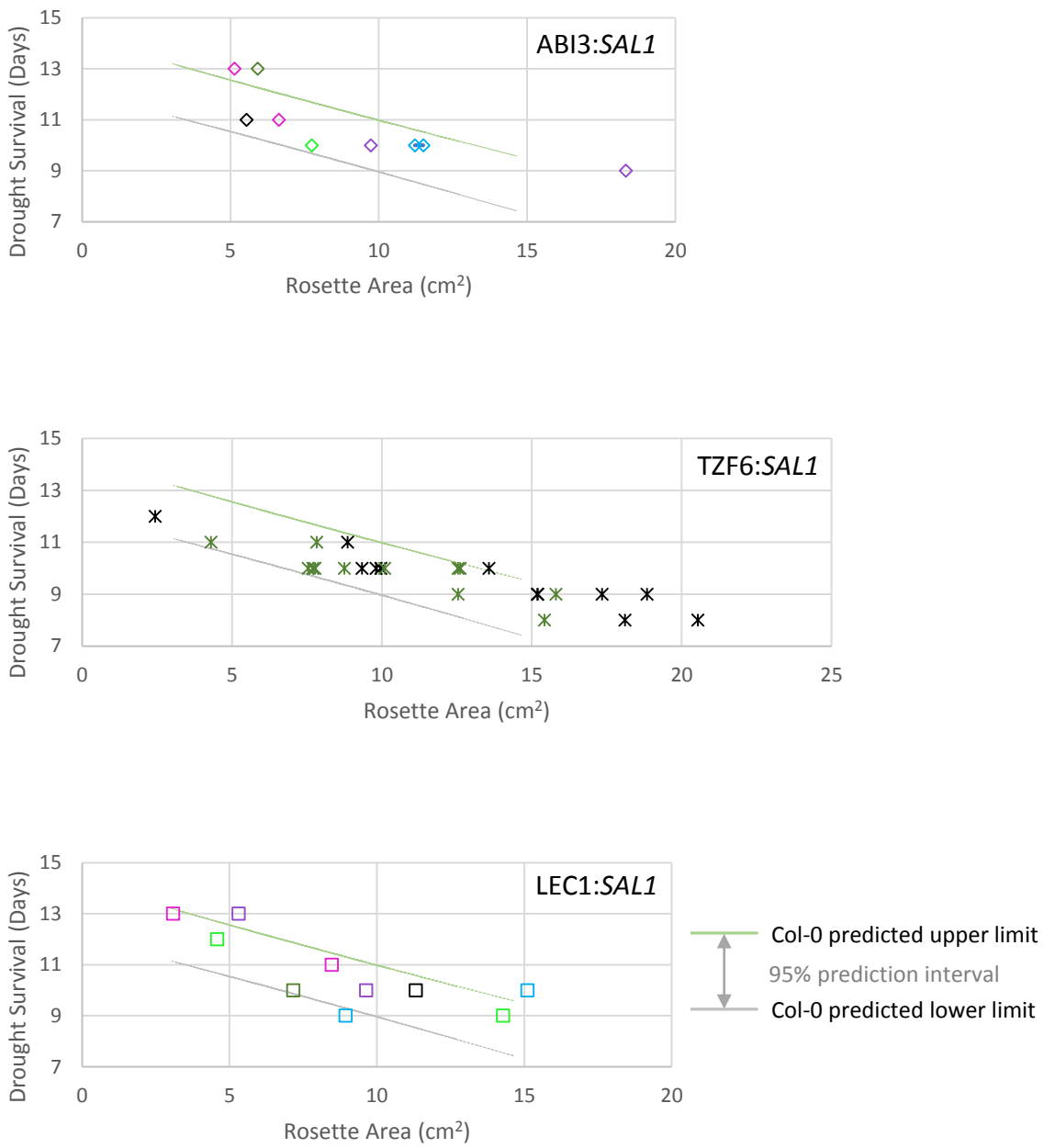
Supplementary Figure 7 – Average rosette area of three independent transgenic lines of empty vector control and pOpON-*SAL1* at the end of the different dex treatment regimes. Average rosette area of 3 to 4 plants per line at 38 days old was quantified using LemnaTec Scanalyzer and the error bars represent standard deviation. The abbreviated label on the x-axis is defined in the table above the bar graph.



Supplementary Figure 8 – Rosette area, plant images and PAP quantification of individual T1 early developmental stage specific complementation of *sal1* transgenics together with Col-0 and *sal1*-6.

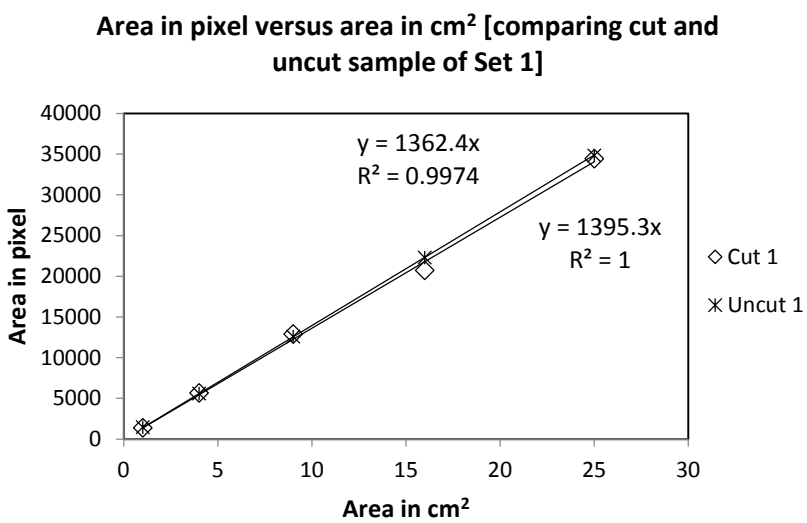


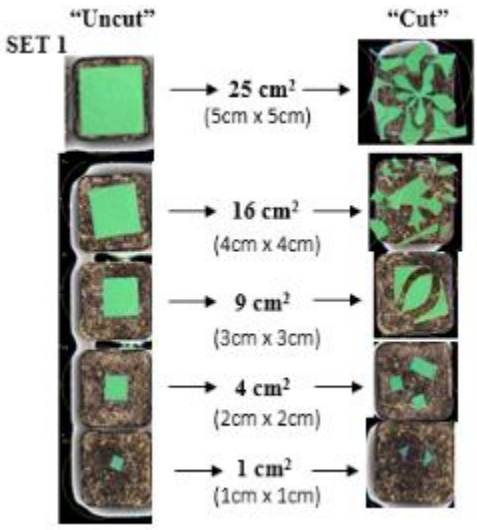
Supplementary Figure 9 – Rosette area and PAP levels of T2 early developmental stage specific complementation of *sal1* transgenics in comparison to Col-0 and no pro:*SAL1* controls. N≥5.

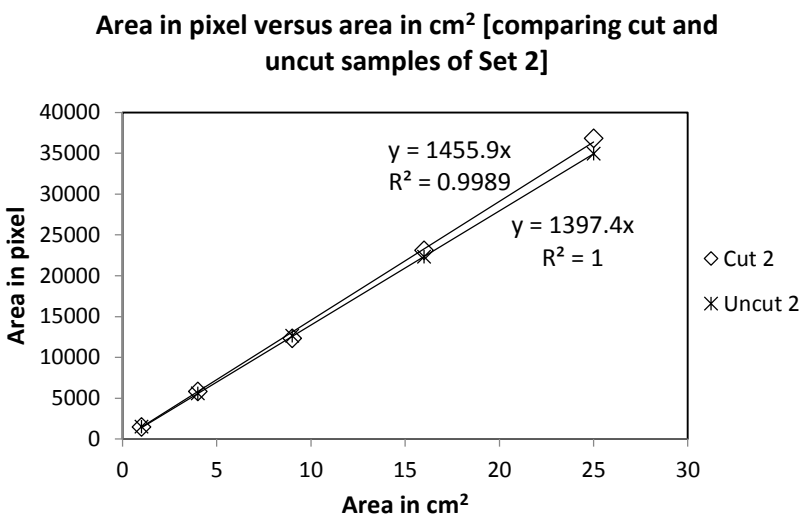


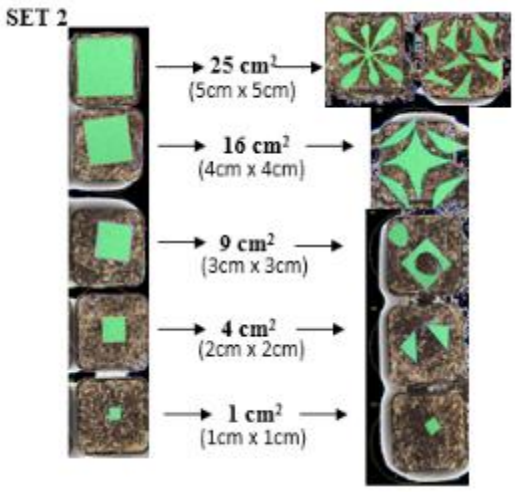
Supplementary Figure 10 – Days of survival during drought and their corresponding rosette area of T2 individuals of ABI3:*SAL1,* TZF6:*SAL1* and LEC1:*SAL1* plotted in comparison to the predicted upper and lower limits of Col-0 control. Different colours denote different independent lines.

Supplementary Figure 11 - *SAL1* genomic sequence. Exons are highlighted in yellow. Region (excluding introns) indicated in black bracket is targeted by *SAL1*hpRNAi; blue box is targeted by 5'-targetting *SAL1*amiRNA; red box is targeted by 3'-targetting *SAL1*amiRNA; green bracket denotes region amplified during qRT-PCR for *SAL1* transcript quantification.









$$\text{Average conversion coefficient} = \frac{1362+1395+1455+1397}{4} = 1402.25$$

Supplementary Figure 12 – Calibration curve for the conversion of rosette area in pixel format from LemnaTec Scanlyzer software to area in cm². Green colour cards were cut into duplicated squares of specific dimensions (1cm X 1cm, 2cm X 2cm, up to 5cm X 5cm) and their images were captured and analysed using the Scanalyzer. These corresponding squares of known area were then cut into a series of interconnected pieces resembling an Arabidopsis rosette, or into disconnected pieces before images of them are captured and analysed again. This is to ensure the capacity of the image analysis to accurately detect and measure rosette area of Arabidopsis plants of varying size and rosette morphology.