7 Annexes

Table S1: ***Growing conditions of melon plants for libraries development.*** *Prior to stress exposure, seeds were sown and pre-germinated at 37 °C for 48 h, then germinated 24 h at 25 °C (16:8 photoperiod) and followed by a growth stage for 10 days at 28 °C/ 20 °C with 16 h light/8 h dark.*

Stress condition	Photoperiod (light/dark)	Temperature (light/dark)	Observations
C	16 h / 8 h	20 °C / 14 °C	Lower temperatures
D	16 h / 8 h	28 °C / 20 °C	No irrigation
SA	16 h / 8 h	28 °C / 20 °C	Irrigation solution with 200 mM LiCl
SD	8 h / 16 h	28 °C / 20 °C	Short day photoperiod
A	16 h / 8 h	28 °C / 20 °C	Agroinfiltration at 0.8 OD600, two cotyledons
HSVd	16 h / 8 h	28 °C / 20 °C	Two cotyledons infected with viroidal RNA
MON	16 h / 8 h	28 °C / 20 °C	50 mL solution with 1,000 CFU micellium from *M. cannonballus*
CONTROL	16 h / 8 h	28 °C / 20 °C	-

Time (dpi) / Stress condition	T1	T2	T3
CONTROL	CONTROL.1, CONTROL.2, CONTROL.3	CONTROL.1, CONTROL.2, CONTROL.3	CONTROL.2, CONTROL.3, CONTROL.4, CONTROL.5
A	A.1, A.2, A.3	A.1, A.2, A.3	A.2, A.3
C	C.1, C.2, C.3	C.1, C.2, C.3	C.1, C.2, C.3
D	D.1, D.2, D.3	D.1, D.2, D.3	D.1, D.2, D.3
HSVd	HSVd.1, HSVd.2, HSVd.3	HSVd.1, HSVd.2, HSVd.3	HSVd.1, HSVd.2, HSVd.3
MON	MON.1, MON.2, MON.3	MON.1, MON.2, MON.3	MON.1, MON.2, MON.3
SA	SA.1, SA.2, SA.3	SA.1, SA.2, SA.3	SA.1, SA.2, SA.3
SD	SD.1, SD.2, SD.3	SD.1, SD.2, SD.3	SD.1, SD.2, SD.3

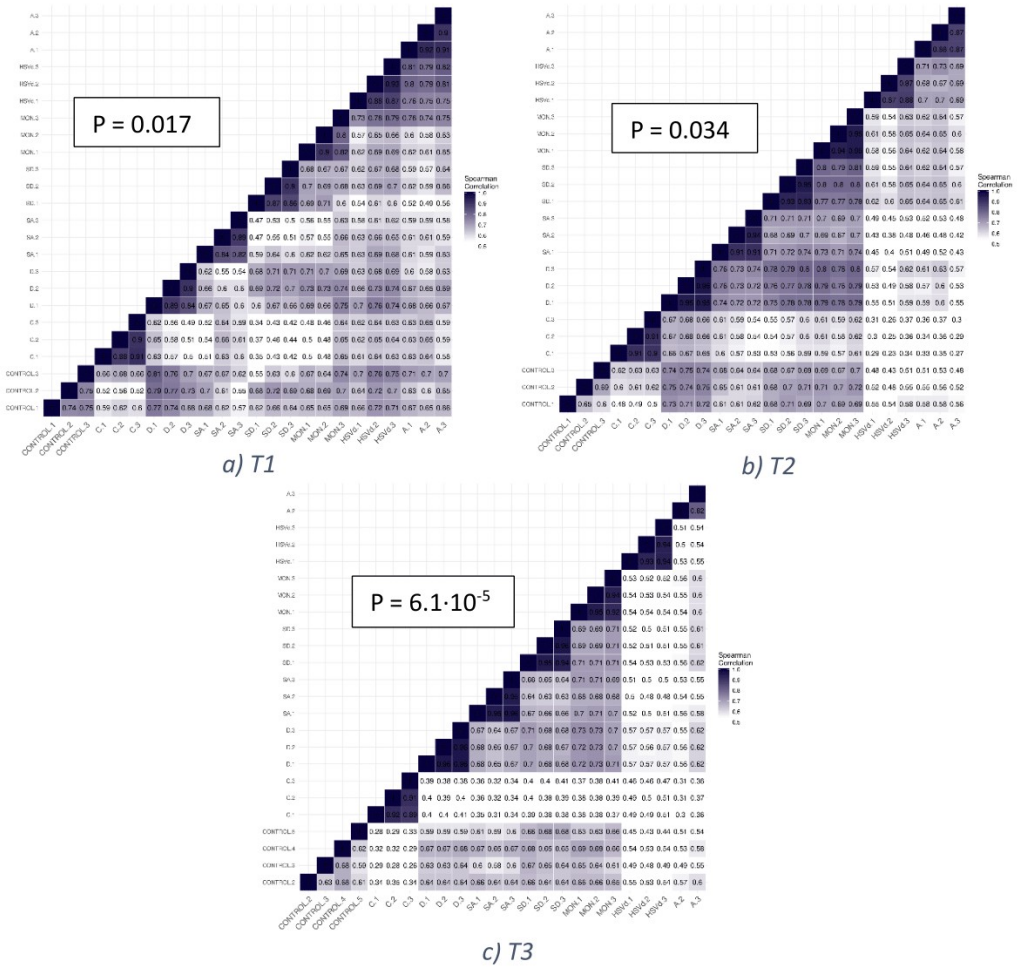

Figure S1: ***Replicates of samples from melon plants subjected to stress conditions and their corresponding statistical correlation between them.*** *Control plants and stress-treated plants are named in the upper table, whereas Spearman's correlation between all the replicates is depicted in image A (for T1), image B (for T2) and image C (for T3). High correlation is expected between replicates exposed to the same stress condition, i.e. the darker blue squares. P expresses the p-value of the null hypothesis, which is the probability of any of the samples to be statistically different.*

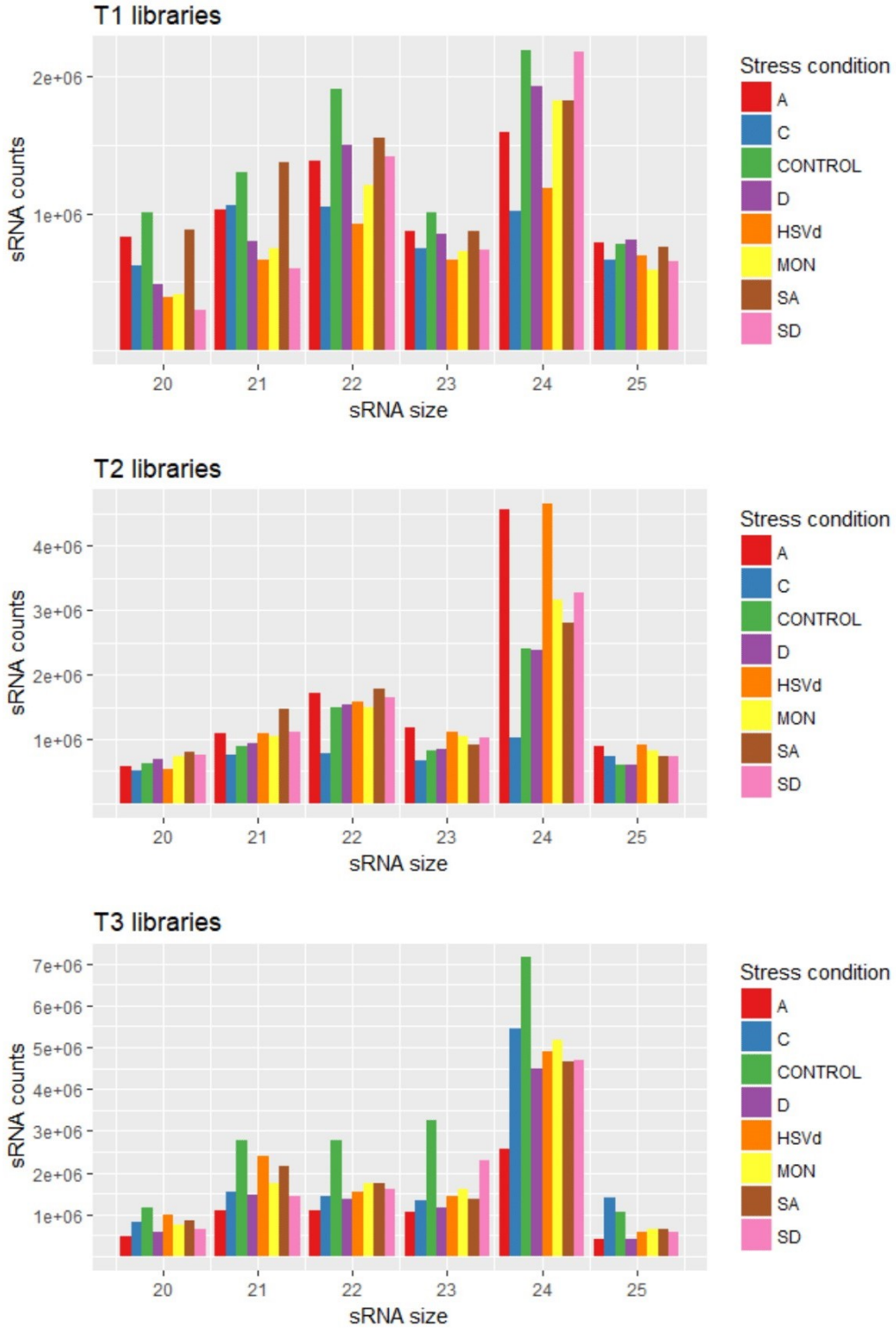

Figure S2: ***Accumulation profiles of unique sRNA counts identified in all the 96 constructed libraries, at the three different sampling times (T1, T2, T3), and classified by length for the control and exposed-to-stress samples.*** *These stress conditions are: A. tumefaciens (A), cold (C), drought (D), Hop Stunt Viroid (HSVd), M. cannonballus (MON), salinity (SA) and short day (SD). As shown in the picture, the number of sRNA counts increases, especially the 24-nt sRNAs, as the time passes since the initial application of the stress treatment.*

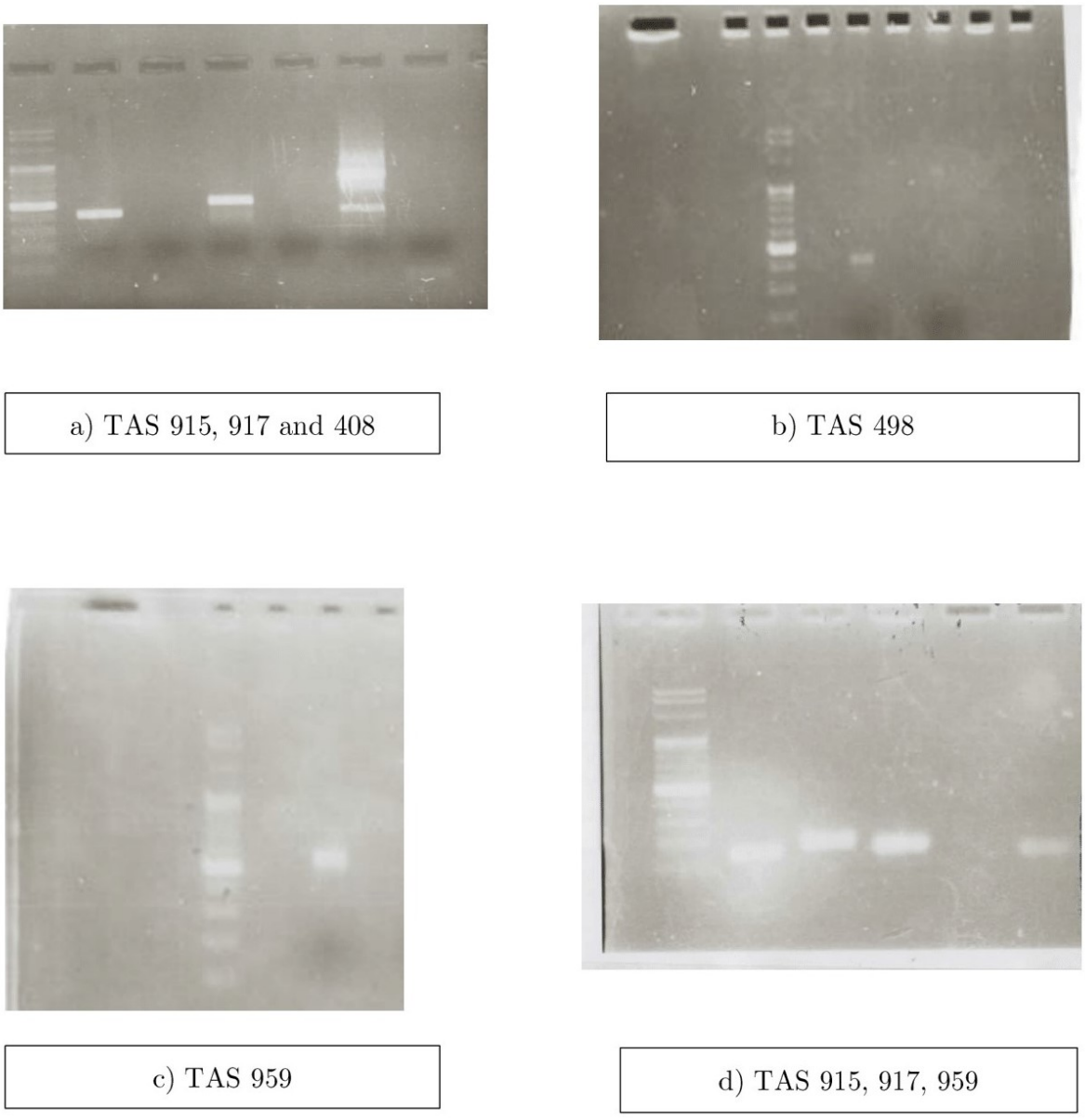

Figure S3: ***Agarose gel electrophoresis showing genomic amplification of TAS genes.*** *Concretely: in gel A, lane 1 corresponds to the marker of 1 kb, lane 2 to TAS 915, lane 4 to TAS 917, lane 6 to TAS 408, and lanes 3, 5 and 7 to negative controls of respective TAS 915, 917 and 408. For gel B, lane 3 depicts the mass ladder, lane 4 the negative control and lane 5 the amplified TAS 498. Same pattern is observed for gel C, but concerning lanes 2, 3 and 4. On the other hand, subfigure D depicts results of RT-PCR from RNA extraction. Here, ladder marker is in lane 1, amplified TAS 915 with two sets of primers correspond to lanes 2 and 3, amplified TAS 917 was placed in lane 4, and lane 5 shows no amplification of TAS 959. Lane 6 is considered to contain the positive control, a gene coding for auxin response factor 3 (ARF3), which is proven to be expressed. For A, B, C and D, the brightest band of molecular mass marker is 600-bp long, increasing or decreasing 100 bp each band on.*