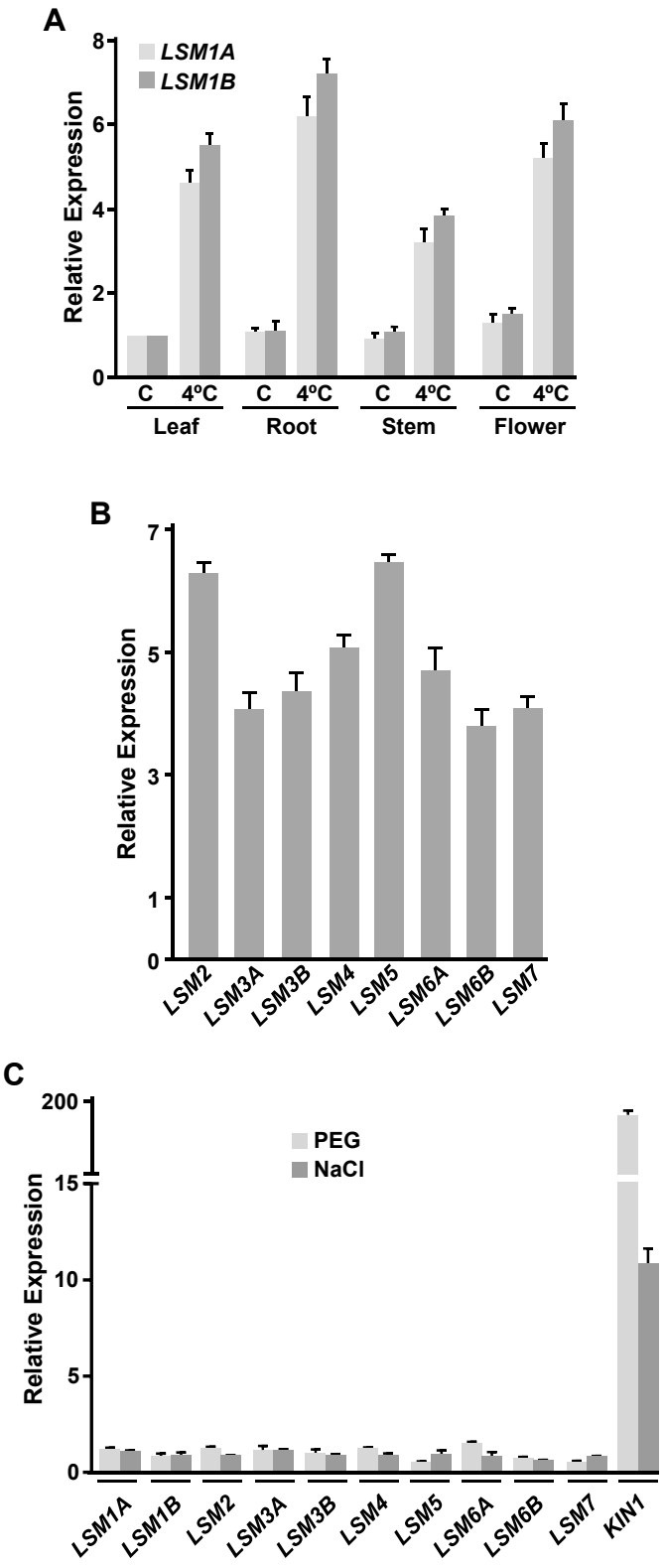
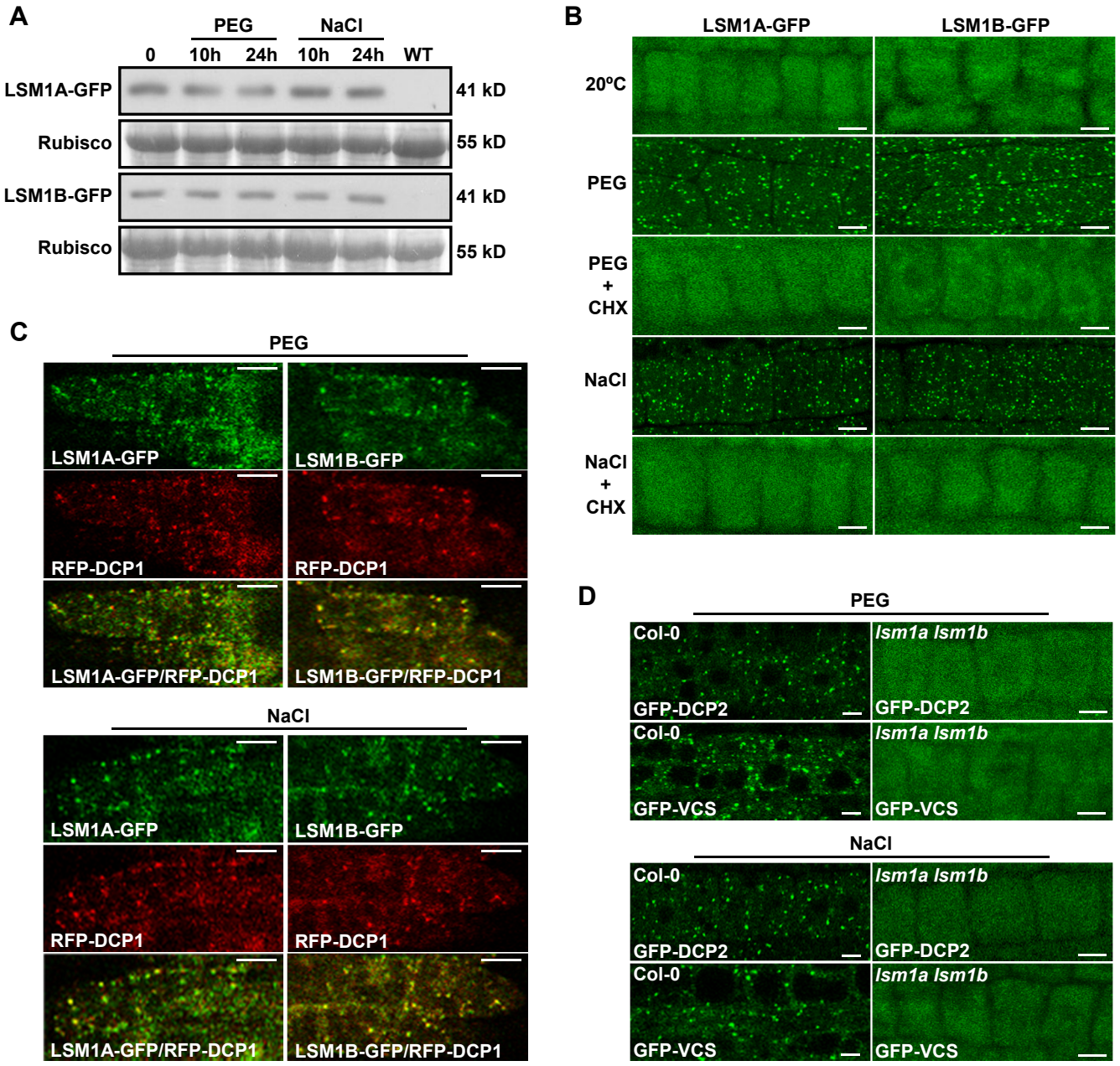
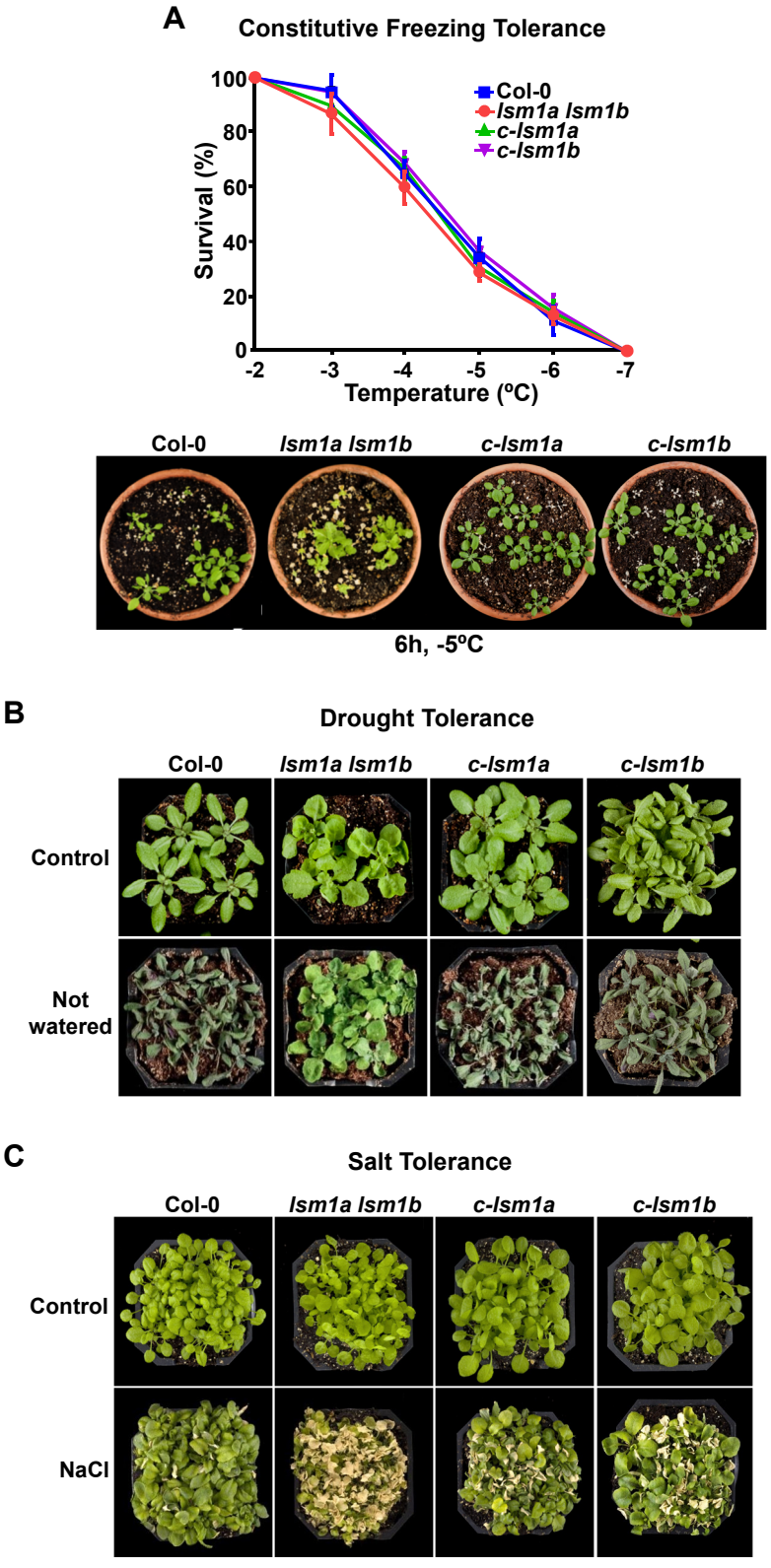


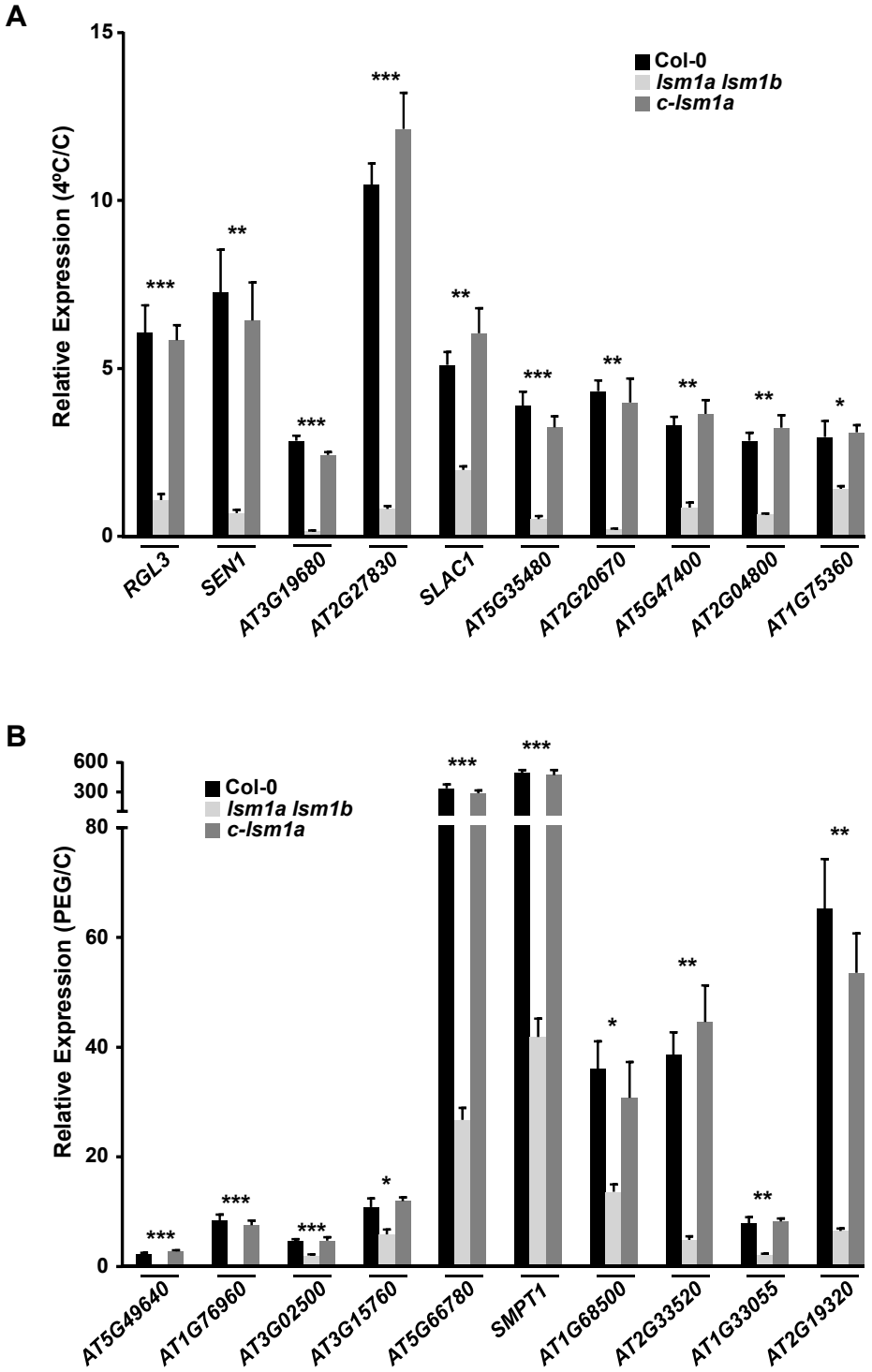
Supplemental Figure 1. Expression analysis of Arabidopsis *LSM1-7* genes in response to abiotic stresses. (**A**) Expression of *LSM1A* and *LSM1B* in different organs of 8-week-old Col-0 plants grown under control conditions (C) or exposed 24h to 4ºC. Levels are represented as relative to their values in control leaves. Error bars indicate the standard deviation of the mean ($n \geq 3$). In all organs, differences between cold and control samples were significant ($P \leq 0.0001$), as determined by ANOVA-test. (**B**) Expression of *LSM2-LSM7* in 2-week-old Col-0 plants exposed 24h to 4ºC. Levels are represented as relative to their corresponding values under control conditions. Error bars indicate the standard deviation of the mean ($n \geq 3$). For all genes, differences between cold-treated and control plants were significant ($P \leq 0.0001$), as determined by ANOVA-test. (**C**) Expression of *LSM1-LSM7* in 2-week-old Col-0 plants exposed to 55% PEG or 150mM NaCl for 10h. Levels are represented as relative to their corresponding values under control conditions. *KIN1* was used as a positive control for treatments. Error bars indicate the standard deviation of the mean ($n \geq 3$). In the case of *KIN1*, differences between stressed and control plants were significant ($P \leq 0.0001$), as determined by ANOVA-test. For *LSM* genes, no significant differences between stressed and control plants were observed in any case.



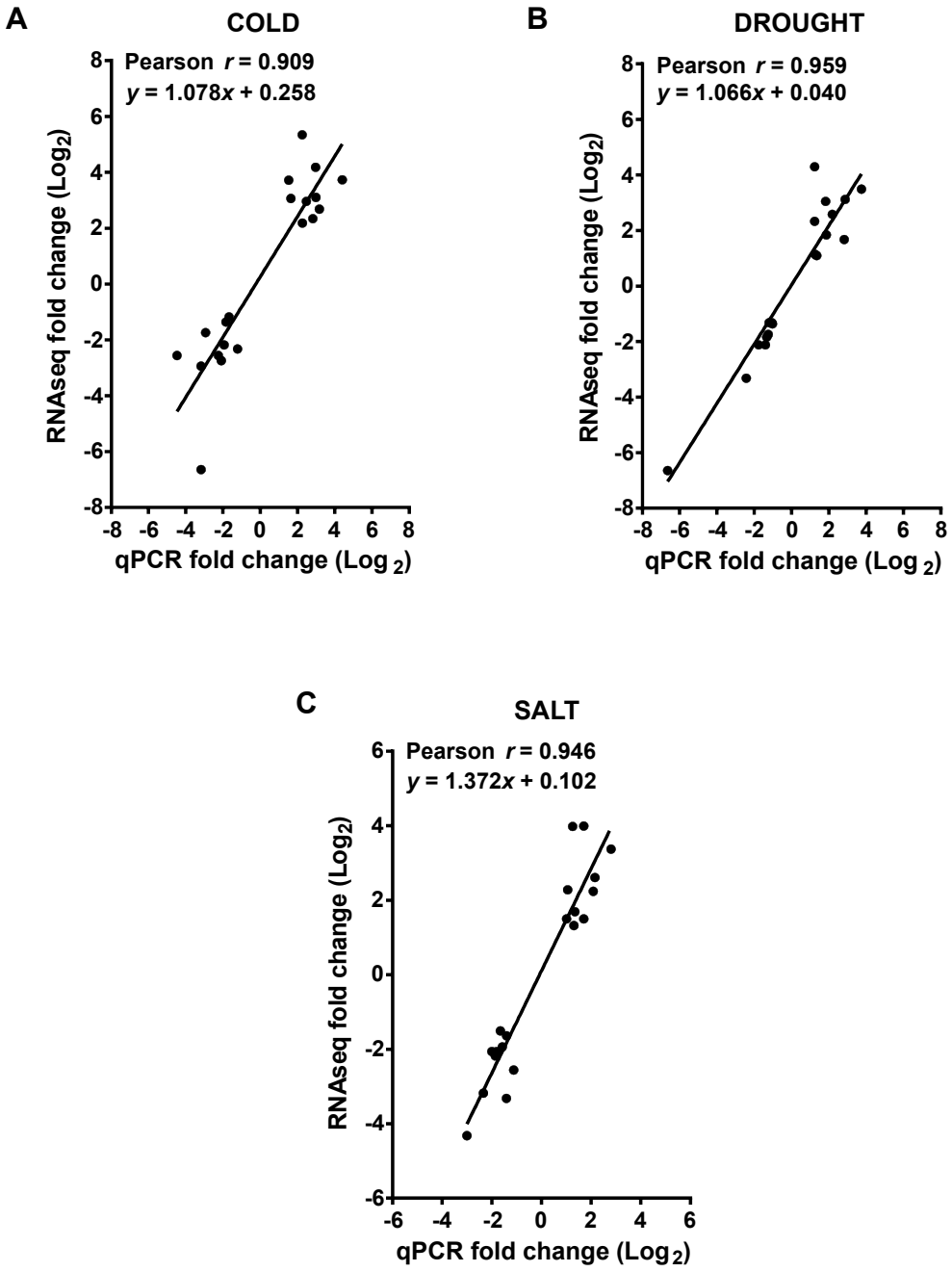
Supplemental Figure 2. Arabidopsis LSM1 proteins do not accumulate in response to drought and salinity but localize to P-bodies under these abiotic stresses. (**A**) Levels of LSM1A-GFP and LSM1B-GFP in 2-week-old transgenic Arabidopsis plants exposed for the indicated times to 55% PEG or 150mM NaCl. A lane with Col-0 plants was added as a negative control. Comassie staining of the large subunit of Rubisco was used as a loading control. (**B**) Subcellular localization of LSM1A-GFP and LSM1B-GFP in root tip cells from 6-day-old transgenic Arabidopsis seedlings grown under control conditions (20ºC) or exposed to 55% PEG for 10h, to 55% PEG with cycloheximide for 10h (PEG+CHX), to 150mM NaCl for 10h, and to 150mM NaCl with cycloheximide for 10h (NaCl+CHX). Bars = 20 μm. (**C**) Colocalization of LSM1A-GFP and LSM1B-GFP with RFP-DCP1 in root tip cells from 6-day-old transgenic Arabidopsis seedlings grown under control conditions and subsequently exposed to 55% PEG for 10h (top panel) or 150mM NaCl for 10h (bottom panel). Bars = 20 μm. (**D**) Subcellular localization of GFP-DCP2 and GFP-VCS in root tip cells from 6-day-old wild-type (WT) and *lsm1a lsm1b* Arabidopsis seedlings grown under control conditions and subsequently exposed to 55% PEG for 10h (top panel) or 150mM NaCl for 10h (bottom panel). Bars = 20 μm.



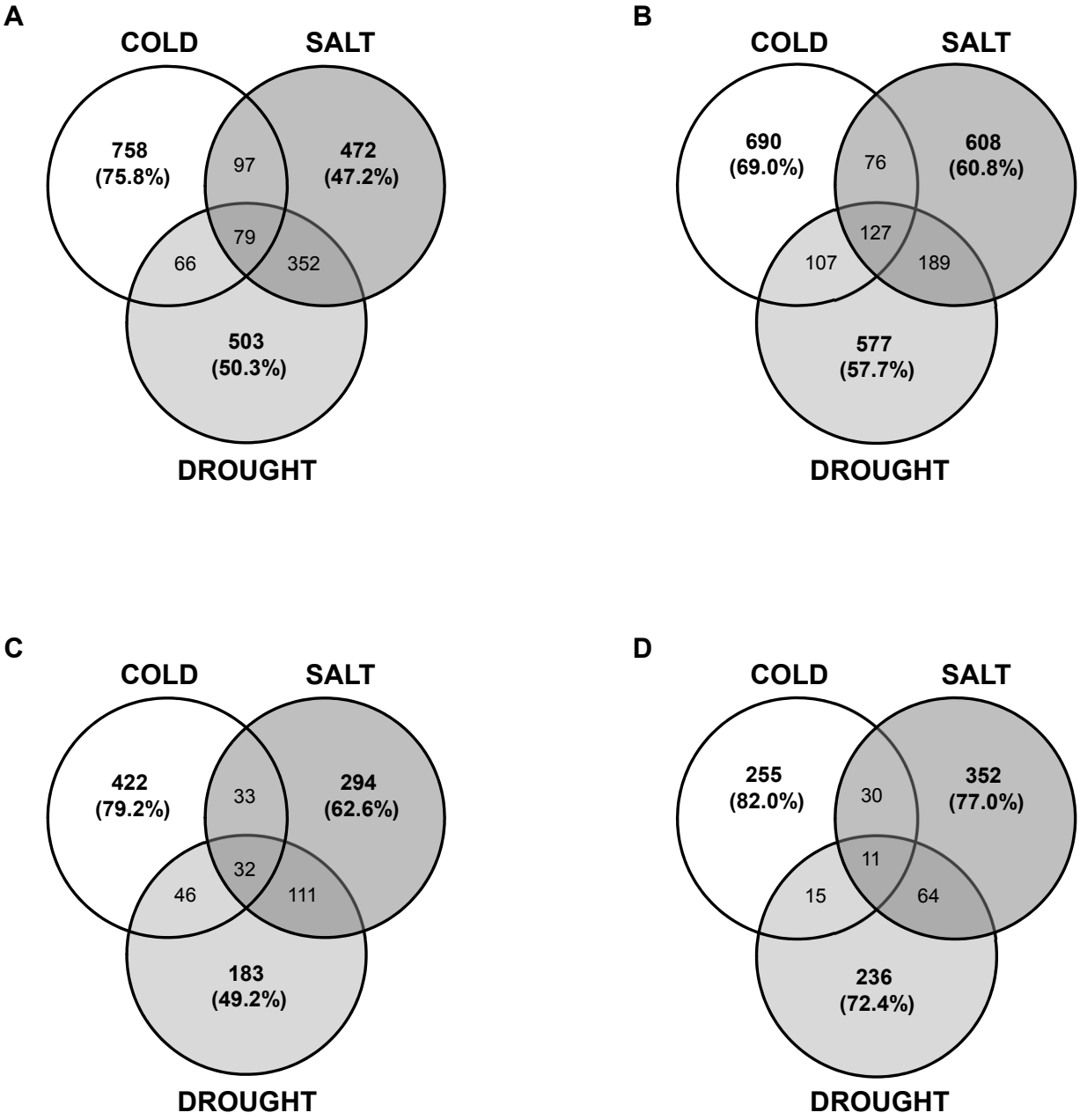
Supplemental Figure 3. Constitutive freezing tolerance and tolerance to drought and salinity of *lsm1a lsm1b* plants grown on soil. (**A**) Constitutive freezing tolerance of 2-week-old Col-0, *lsm1a lsm1b*, *c-lsm1a* and *c-lsm1b* plants. Error bars indicate the standard deviation of the mean ($n \geq 3$). No significant differences between *lsm1a lsm1b* and the other plants were found in any case, as determined by ANOVA-test (top). Representative plants 7d after being exposed to -5ºC for 6h (bottom). (**B**) Drought tolerance of 2-week-old Col-0, *lsm1a lsm1b*, *c-lsm1a* and *c-lsm1b* plants. Plants grown under control conditions (Control) were deprived of water for 10 days (Not watered). (**C**) Salt tolerance of 2-week-old Col-0, *lsm1a lsm1b, c-lsm1a* and *c-lsm1b* plants. Plants grown under control conditions (Control) were watered with 250mM NaCl during10 days (NaCl).



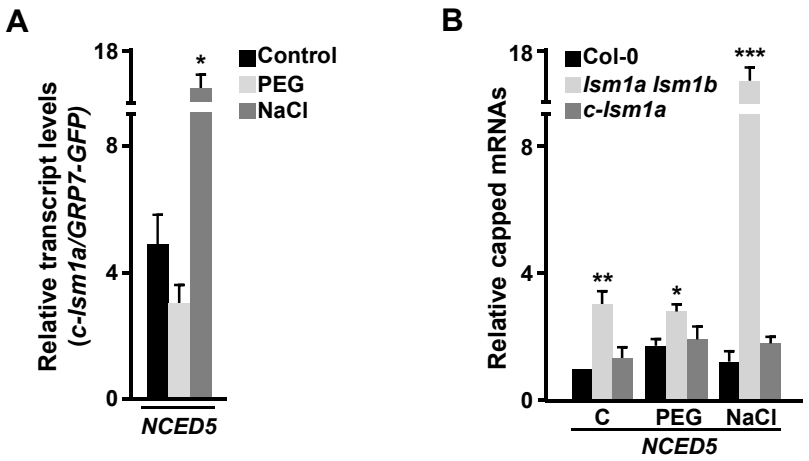
Supplemental Figure 4. Expression levels of genes down-regulated in *lsm1a lsm1b* plants in response to cold and drought. (**A**) Expression of different cold-inducible genes down-regulated in *lsm1a lsm1b*. Levels, determined by qPCR, in 2-week-old Col-0, *lsm1a lsm1b* and *c-lsm1a* plants exposed 24h to 4ºC are represented as relative to their corresponding values in control plants (C). (**B**) Expression of different drought-inducible genes down-regulated in *lsm1a lsm1b*. Levels, determined by qPCR, in 2-week-old Col-0, *lsm1a lsm1b* and *c-lsm1a* plants exposed 10h to 55% PEG are represented as relative to their corresponding values in control plants (C). Differences between *lsm1a lsm1b* and Col-0 or *c-lsm1a* plants were always significant (*$P \leq 0.01$, **$P \leq 0.001$, ***$P \leq 0.0001$), as determined by ANOVA-test. No significant differences between Col-0 and *c-lsm1a* plants were observed in any case.



Supplemental Figure 5. Correlation between RNAseq and qPCR results. Comparison of $\log_2$ fold change of 20 differentially expressed genes between Col-0 and *lsm1a lsm1b* plants under cold (**A**), drought (**B**) or salinity (**C**) obtained by RNAseq (y axis) and qPCR (x axis). A linear regression line and the calculated values of Pearson correlation coefficients (Pearson *r*) are shown in each panel.



Supplemental Figure 6. Venn diagrams of de-regulated transcripts in *lsm1a lsm1b* plants under cold, drought and salt stresses. (**A, B**) Venn diagrams showing the top 1000 genes with increased (**A**) or decreased (**B**) expression in *lsm1a lsm1b* plants in response to low temperature, drought or high salt. (**C, D**) Venn diagrams showing the number of genes with increased (**C**) or decreased (**D**) expression in *lsm1a lsm1b* plants in response to low temperature, drought or salinity that have been described to be induced by cold, drought or high salt, respectively. In all cases, transcripts specifically de-regulated in response to a single stress are in bold and the percentages they represent relative to the total number of de-regulated genes in each case (specific and nonspecific) are indicated.



Supplemental Figure 7. The Arabidopsis LSM1-7 complex differentially interacts with and promotes the decapping of *NCED5* transcripts in response to drought and high salt. (**A**) RIP assays on 2-week-old *c-lsm1a* plants grown under control conditions (Control), exposed 10h to 55% PEG, or 10h to 150mM NaCl, using an anti-GFP antibody. RIP assays on Arabidopsis containing a $GRP7_{PRO}$-*GRP7-GFP* fusion grown under control and stressed conditions were also carried out as interaction specificity controls. Co-immunoprecipitated RNA samples corresponding to *NCED5* genes were quantified by qPCR. Transcript levels in *c-lsm1a* plants were corrected with respect to their corresponding input values and represented relative to the levels obtained from RIP control assays. Error bars indicate the standard deviation of the mean ($n \geq 3$). Asterisks (*) indicate significant differences ($^*P \leq 0.01$) in transcript levels between RIP assays from stressed and control plants, as determined by ANOVA-test. (**B**) Capped transcripts in 2-week-old Col-0, *lsm1a lsm1b* and *c-lsm1a* plants grown under control conditions (C), exposed 10h to 55% PEG, or 10h to 150mM NaCl. The levels of capped transcripts corresponding to *NCED5* genes were corrected with respect to the levels of their corresponding total transcripts and represented relative to control Col-0 plants. Error bars indicate the standard deviation of the mean ($n \geq 3$). Asterisks (*) indicate significant differences ($^*P \leq 0.01$, $^{**}P \leq 0.001$, $^{***}P \leq 0.0001$) between *lsm1a lsm1b* and Col-0 or *c-lsm1a* plants, as determined by ANOVA-test. No significant differences between Col-0 and *c-lsm1a* plants were observed in any case.