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**Table S3 – Table of all differentially expressed genes in *nac $\beta$ 1nac $\beta$ 2*.** The table consists of 13 columns as follows: Gene ID, fold change, fold change in log<sub>2</sub> scale, adjusted p-value, symbol of gene and brief description obtained from Araport database and GO terms for gene groups mentioned in the article. Genes are sorted according to their log<sub>2</sub>Fold Change.

**Table S4 – Table of all differentially expressed proteins in *nac $\beta$ 1nac $\beta$ 2*.** The table consists of 20 columns as follows: Protein group accession number, Gene ID, symbol, Brief Description obtained from v1.10.4, Araport11 Release 06/2016 database, logFC, FC, adjusted p-value, p-value and GO terms for protein groups mentioned in the article. Proteins are sorted according to log<sub>2</sub>Fold Change.

**Table S5 – Table of comparison of DE genes and proteins in *nac $\beta$ 1nac $\beta$ 2* proteome and transcriptome.** The table shows numbers of differentially expressed proteins/genes present in both analyses as well as total number of discovered upregulated/downregulated proteins and genes.

### Supplementary figure legends

**Figure S1 – Development of *nac $\beta$ 1nac $\beta$ 2* and Col-0 wt, and characterization of *nac $\beta$*  single mutant insertion lines.** A–C Comparison of the *nac $\beta$ 1nac $\beta$ 2* and Col-0 wt development under the same conditions. The first six rows of plants are represented by *nac $\beta$ 1nac $\beta$ 2* whereas the last three rows of plants are represented by Col-0 wt. A – 35 days after sowing. B – 41 days after sowing. C – 52 days after sowing. D – The scheme showing the position of the insert (indicated by grey triangle) in the T-DNA insertion line SALK\_043673 (in NAC $\beta$ 1). Arrows indicate the positions of primers used for genotyping. E – The scheme showing the position of the insert (indicated by grey triangle) in the T-DNA insertion line GK368-H02 (in NAC $\beta$ 2). Arrows indicate the positions of primers used for genotyping. F – Linear regressions of log<sub>2</sub>FPKM values obtained from RNA-seq data and cT values from RT-qPCR for NAC $\beta$ 1 (At1g73230), and NAC $\beta$ 2 (At1g17880) with correlation coefficient R<sup>2</sup>=0.9645 (NAC $\beta$ 1) or R<sup>2</sup>=0.6209 (NAC $\beta$ 2), respectively.

**Figure S2 – Flower and silique phenotype of the *nac $\beta$ 1nac $\beta$ 2* plants.** A – Column chart showing the distribution of various phenotype categories of *nac $\beta$ 1nac $\beta$ 2* flowers. Wild type flowers are highlighted in black. A total of 202 flowers was observed. C stands for petals, K for sepals, and A for anthers. The number of gynoecia was the same as in wt flowers. B – Box-and-whisker plot showing the median and quartiles revealing the silique length of the *nac $\beta$ 1nac $\beta$ 2*, and Col-0 wt. Both datasets were statistically compared by Student's t-test, p-value of which is given. C – Box-and-whisker plot showing the median and quartiles revealing the number of seeds per silique. Both datasets were statistically compared by Student's t-test, p-value of which is given. D – Column chart showing the proportion of viable green seeds in *nac $\beta$ 1nac $\beta$ 2* and Col-0 wt. Both datasets were statistically compared by Student's t-test, p-value of which is given.

**Figure S3 – Validation of RNAseq data with qRT-PCR.** Linear regression of log<sub>2</sub>FPKM values obtained from RNA-seq data and cT values from RT-qPCR for each genotype for twelve DE genes in *nac $\beta$ 1nac $\beta$ 2* (At1g17880, At1g73230, At2g20142, At5g64120, At2g43510, At3g12580, At5g52390, At3g12390, At3g49470, At5g13850, At4g10480, At1g33040) with correlation coefficient R<sup>2</sup> = 0.7842.

**Figure S4 – Germination of *nac $\beta$ 1nac $\beta$ 2* under salt and osmotic stress.** A – Germination rate of Col-0 wt compared to *nac $\beta$ 1nac $\beta$ 2* under salt stress caused by 50 mM, 100mM, 125 mM, and 150 mM NaCl. Error bars represent  $\pm$ 5%. The calculations of germinated seeds were performed 4, 6, 8, 11, and 13 days after seed sowing. B – Germination rate of Col-0 wt compared to *nac $\beta$ 1nac $\beta$ 2* under osmotic stress caused by 250 mM, 300mM, and 350 mM mannitol. Error bars represent  $\pm$ 5%. The calculations of germinated seeds were performed 4, 6, 8, 11, and 13 days after seed sowing. C – A representative plate of seedlings

13 days after sowing on 125 mM NaCl. D – A representative plate of seedlings 13 days after sowing on 150 mM NaCl. E – A representative plate of seedlings 13 days after sowing under control conditions without added stress agent.

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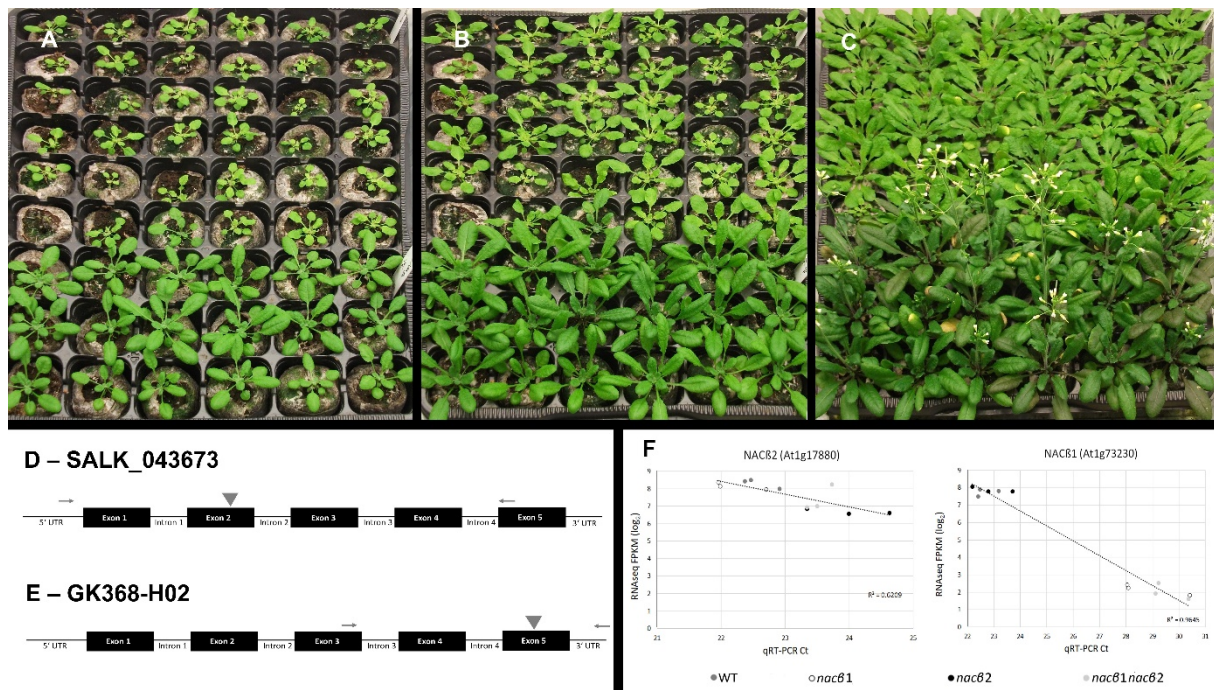
Tables S1–S4 are available as \*.xls files.

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The table shows numbers of differentially expressed proteins/genes present in both analyses as well as total number of discovered upregulated/downregulated proteins and genes.

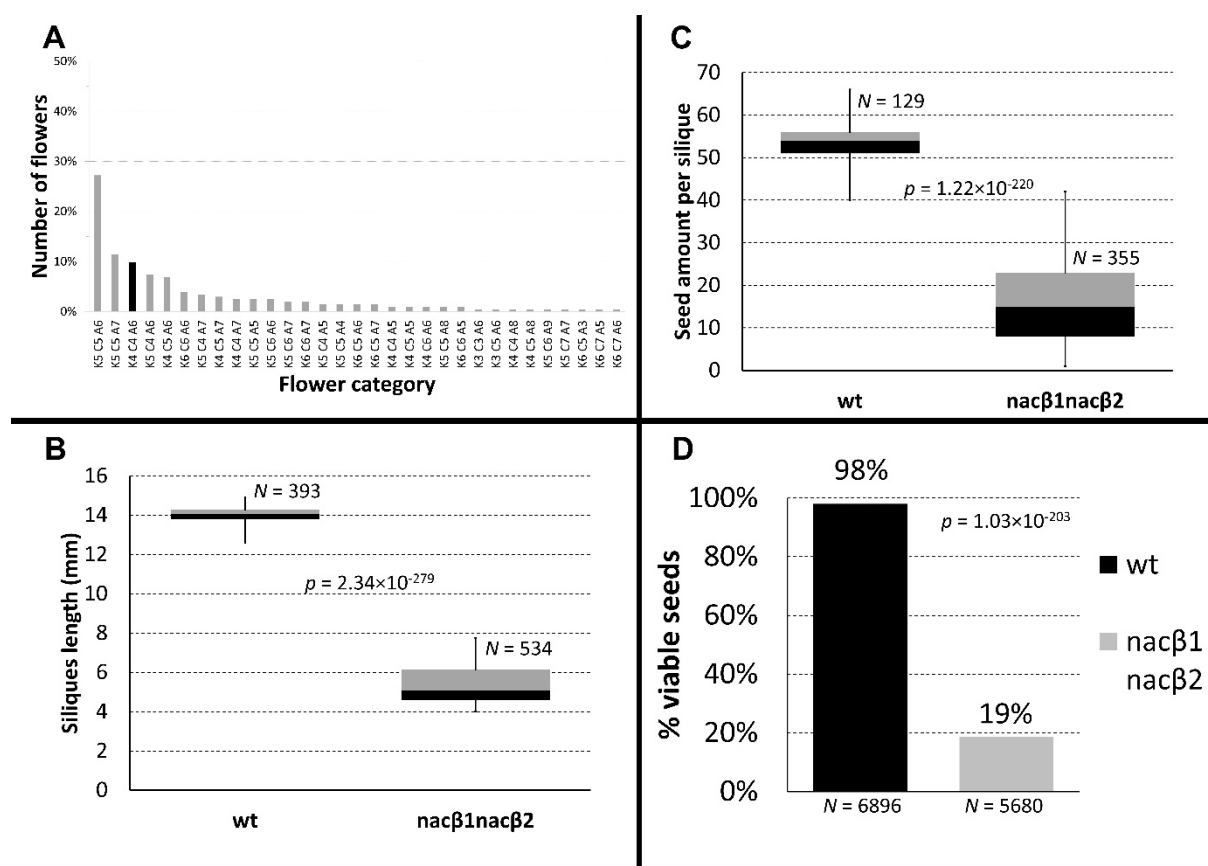
		transcriptome		total
		up-regulated	down-reguated	
proteome	up-regulated	15	1	170
	down-regulated	0	98	290
total		363	1602	

### Supplementary figure legends

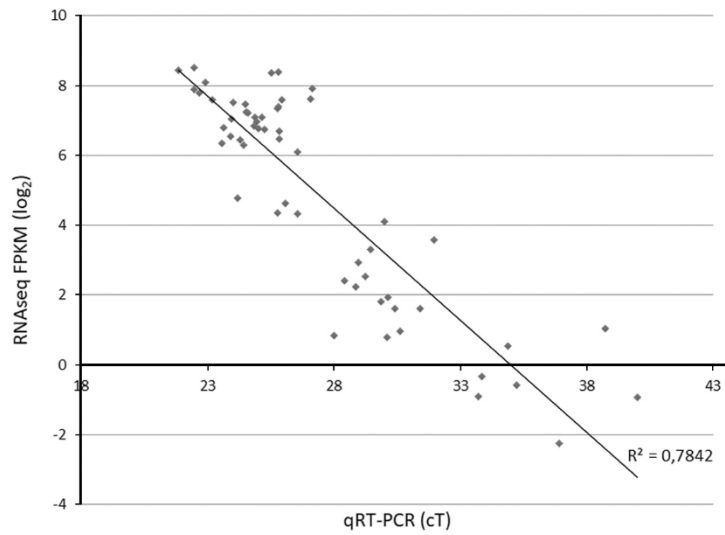
**Figure S1 – Development of *nacβ1nacβ2* and Col-0 wt, and characterization of *nacβ* single mutant insertion lines.** A–C Comparison of the *nacβ1nacβ2* and Col-0 wt development under the same conditions. The first six rows of plants are represented by *nacβ1nacβ2* whereas the last three rows of plants are represented by Col-0 wt. A – 35 days after sowing. B – 41 days after sowing. C – 52 days after sowing. D – The scheme showing the position of the insert (indicated by grey triangle) in the T-DNA insertion line SALK\_043673 (in *NACβ1*). Arrows indicate the positions of primers used for genotyping. E – The scheme showing the position of the insert (indicated by grey triangle) in the T-DNA insertion line GK368-H02 (in *NACβ2*). Arrows indicate the positions of primers used for genotyping. F – Linear regressions of log<sub>2</sub>FPKM values obtained from RNA-seq data and cT values from RT-qPCR for *NACβ1* (At1g73230), and *NACβ2* (At1g17880) with correlation coefficient  $R^2=0.9645$  (*NACβ1*) or  $R^2=0.6209$  (*NACβ2*), respectively.



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