**Supplementary file**

# Transient regulation of three clustered tomato class-I small heat-shock chaperone genes by ethylene is mediated by SlMADS-RIN transcription factor

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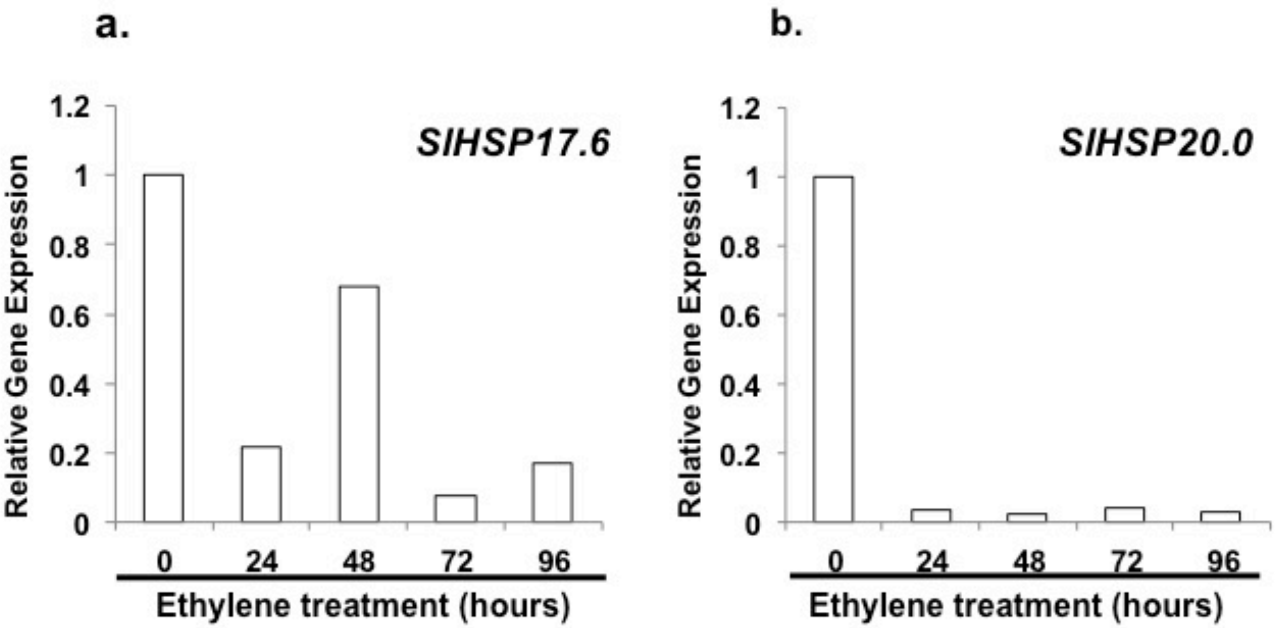
**Supplementary Figure S1**.

**Quantitative RT-PCR expression analysis of class-I *SlHSP (17.6, 20.0 and 20.1)* genes in ethylene-treated leaves of wild type tomato (***Solanum lycoersicum* cv. **Ailsa Craig).** Fully expanded leaves were harvested from mature Ailsa Craig plants and treated with 25 ppm ethylene for 0, 24, 48, 72 and 96 hours. RNA isolation and cDNA preparation methodologies were the same as described in the Materials and Methods section. For Q-PCR, a 10-fold diluted cDNA was used for transcript quantification using gene specific primers.



## Supplementary Table S1.
## List of genes and their primer sequences used for quantitative real–time PCR analyses

| Abbreviated Name | Gene Bank ID | SGN Gene ID | Forward Primer (5′-3′) | Reverse Primer (5′-3′) |
|---|---|---|---|---|
| *Actin* | BT012695 | Solyc04g011500.2.1 | TGGTCGTACCACCGGTATTGTG | AATGGCATGTGGAAGGGCATAC |
| *SlHSP17.6* | AY150039 | Solyc06g076560.1.1 | AGGTCAAGTCCATTGAGATTTCTG | ACAGAGCAACTTCAAACCTTCAAC |
| *SlHSP20.0* | AJ225048 | Solyc06g076570.1.1 | AAGATTTAGACTTCCGGAGAATGC | GCCCATACAAGGATACAATAAATTCACAT |
| *SlHSP20.1* | AJ225046 | Solyc06g076540.1.1 | CTGTTCCAAAGGAAGAAGTGAAGA | AGAAACAGCGACAACTCAAACACT |
| *ACS6* | NM_001247235.2 | Solyc08g008100.2.1 | GGGAGTTGAAGTTGCAACAAA | CCTTGCCTGGACCATAGGAGA |
| *NR* | NM_001246965 | Solyc09g075440.2.1 | AGAATATTGCTTTGGATGTAGC | GAGAGCACAGAGCAATAACTGCA |
| *TAG11* | NM_001247265.2 | Solyc11g028020.1.1 | CATGATGCCATCTGGTGGGG | CCTTTTGTGATCAGGAGACAATGGA |
| *TAG1* | NM_001308296.2 | Solyc02g071730.2.1 | GTGCCTCCACCTCAGCAATT | GGGGTTGGTCTTGTCTAGGGT |
| *RIN* | NM_001247047.1 | Solyc05g056620.1.1 | TCGAGAAAGAACCAACTCATGCA | GTTTGCTGGTGCCATTCACC |
| *PG* | NM_001247092 | Solyc10g080210.1.1 | GTGGTCCAGGTCATGGTATAAGTATTGG | GATCCTAACTCCATTTTCGGCACC |
| *SR3L* | XM_010316362.1 | Solyc12g099340.1.1 | TCCGGAGTAATGACAGTGAGCA | GATTCGGGAGTTGGATCGTCTA |

**Supplementary Table S2.**
**CArG box motifs found in the promoter of small heat shock protein genes (*sHSPs*)**

| Gene Name | SGN Database Gene Locus | CArG Motif Positions in (-)3Kb Promoter Region | CArG Motif Sequence | PLACE Motif Nomenclature | Motif Type |
|---|---|---|---|---|---|
| *SlHSP17.6* | Solyc06g076560.1.1 | (-)2221 | CAAAAAAAAG | CARGCW$_8$GAT | Atypical [C(A/T)$_8$G] |
| | | (-)2306 | CTTATTTATG | CARGCW$_8$GAT | Atypical [C(A/T)$_8$G] |
| | | (-)2345 | CAATATTTAG | CARGCW8GAT | Atypical [C(A/T)$_8$G] |
| | | (-)2686 | CTATAATAAG | CARGCW$_8$GAT | Atypical [C(A/T)$_8$G] |
| *SlHSP20.0* | Solyc06g076570.1.1 | (-)303 | CTAAATTTTG | CARGCW$_8$GAT | Atypical [C(A/T)$_8$G] |
| | | (-)917 | CTTAATTATG | CARGCW$_8$GAT | Atypical [C(A/T)$_8$G] |
| | | (-)1047 | CATTATTTTG | CARGCW$_8$GAT | Atypical [C(A/T)$_8$G] |
| | | (-)2014 | CATATATATG | CARGCW$_8$GAT | Atypical [C(A/T)$_8$G] |
| *SlHSP20.1* | Solyc06g076540.1.1 | (-)901 | CATATAAATG | CARGCW$_8$GAT | Atypical [C(A/T)$_8$G] |
| | | (-)994 | CAAAATTTTG | CARGCW$_8$GAT | Atypical [C(A/T)$_8$G] |
| | | (-)1323 | CATATTTTTG | CARGCW$_8$GAT | Atypical [C(A/T)$_8$G] |
| | | (-)1341 | CCATTTAAGG | CARGAT CONSENSUS | Possible [C(C/T)(A/T)$_6$(A/G)G] |
| | | (-)1933 | CCAAAAAAGG | CARGAT CONSENSUS | Possible [C(C/T)(A/T)$_6$(A/G)G] |

## Supplementary Table S3.
## Primers pairs specific to the CArG-box/CArG-box-like sites present in the three *sHSP* promoters used in CHIP enrichment assay

| Gene | Position name | Locations (-)3Kb upstream to ATG | Position includes | Forward Primer (5′-3′) | Reverse Primer (5′-3′) |
|---|---|---|---|---|---|
| ***SlHSP17.6*** | **P1** | **(-)2221** | **P1** | **AAGGAGAAAATTAAGGGGGGAA** | **AAATAGAATATATTGTGGAATGAAT** |
|  | **P2** | **(-)2306** | **P2 & P3** | **TATTTTAGCATTTAAGAGGACTCA** | **CCTTAATTTTCTCCTTTTTGTTAT** |
|  | **P3** | **(-)2345** |  |  |  |
| ***SlHSP20.0*** | **P1** | **(-)303** | **P1** | **TTAATTGTTCGGTCTGTTGTTCTT** | **CCACGTCACAGATCATACAAGT** |
|  | **P2** | **(-)917** | **P2** | **CAAGTTATCTTTGAGTTAATTCATTA** | **AACCCAAACTACTTCTACTGC** |
|  | **P3** | **(-)1047** | **P3** | **TGCTATTATTATGTTCCCCATG** | **TTGTTTTAGCGGTACCTAAAATT** |
|  | **P4** | **(-)2014** | **P4** | **CAGCAAGGGCTAAACATGAAAA** | **CACACCATCATCCATGAAGAATT** |
| ***SlHSP*20.1** | **P1** | **(-) 901** | **P1** | **GGTTGATTTATGGGTCGGATTA** | **CTTATGGACGTTAGTTGCCATGTT** |
|  | **P2** | **(-) 994** | **P2** | **GAATATTTGACATTAATTTTATAC** | **TAATCCGACCCATAAATCAACC** |
|  | **P3** | **(-) 1323** | **P3 & P4** | **CAATGAAGTTGAAAGAGGAATTC** | **CAACAAATCCCAAAAATGAGT** |
|  | **P4** | **(-)1341** |  |  |  |
|  | **P5** | **(-)1933** | **P5** | **GGCTCTGTTATTACTGGACAAGTG** | **TGGCTAACAATCTTATGCTTCCT** |