Table 1. Suppl. Sources of the *Solanum* genotypes used in the experiment. TGRC - Tomato Genetics Resource Center, USA.

<table>
<thead>
<tr>
<th>Accession</th>
<th>Species</th>
<th>Origin</th>
<th>Performance</th>
</tr>
</thead>
<tbody>
<tr>
<td>LA1777</td>
<td><em>S. habrochaites</em></td>
<td>USA (TGRC)</td>
<td>chilling-tolerant; Heat-sensitive</td>
</tr>
<tr>
<td>LA2683</td>
<td><em>S. lycopersicum</em></td>
<td>USA (TGRC)</td>
<td>chilling-tolerant; Heat-sensitive</td>
</tr>
<tr>
<td>Pole red Siberian</td>
<td><em>S. lycopersicum</em></td>
<td>USA</td>
<td>moderately chilling and heat tolerant</td>
</tr>
<tr>
<td>LA3475</td>
<td><em>S. lycopersicum</em></td>
<td>USA (TGRC)</td>
<td>chilling-sensitive</td>
</tr>
<tr>
<td>Stupice</td>
<td><em>S. lycopersicum</em></td>
<td>USA</td>
<td></td>
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</table>

Table 2. Suppl. Primers in the experiment.

<table>
<thead>
<tr>
<th>Primers</th>
<th>Sequence (5´ to 3´)</th>
<th>Application</th>
</tr>
</thead>
<tbody>
<tr>
<td>miR319a stem-loop RT</td>
<td>GTCGTATGCCAGTCGATGGAGTCGGCAATTGCACTG RT-PCR of miR319a</td>
<td></td>
</tr>
<tr>
<td>miR319b stem-loop RT</td>
<td>GTCGTATGCCAGTCGATGGAGTCGGCAATTGCACTG RT-PCR of miR319b</td>
<td></td>
</tr>
<tr>
<td>miR319c stem-loop RT</td>
<td>GTCGTATGCCAGTCGATGGAGTCGGCAATTGCACTG RT-PCR of miR319c</td>
<td></td>
</tr>
<tr>
<td>miR319d stem-loop RT</td>
<td>GTCGTATGCCAGTCGATGGAGTCGGCAATTGCACTG RT-PCR of miR319d</td>
<td></td>
</tr>
<tr>
<td>miR319aF</td>
<td>GGGCTTGGAGCTGAAGGGGA</td>
<td>cloning and qPCR of miR319a</td>
</tr>
<tr>
<td>miR319bF</td>
<td>GCGTTGGAGCTGAAGGGGAG</td>
<td>cloning and qPCR of miR319b</td>
</tr>
<tr>
<td>miR319cF</td>
<td>GGTGGAGCTGAAGGGAG</td>
<td>cloning and qPCR of miR319c</td>
</tr>
<tr>
<td>miR319dF</td>
<td>GGAGTTGGAGCTGAAGGGGAG</td>
<td>cloning and qPCR of miR319d</td>
</tr>
<tr>
<td>3´ universal primer</td>
<td>CAGTGCGTGAGGTGGAG</td>
<td>RT-PCR of U6snRNA</td>
</tr>
<tr>
<td>U6snRNA-F</td>
<td>GGAGGCAGTACGAGAGATTAGGA</td>
<td>reference gene of stem-loop qPCR</td>
</tr>
<tr>
<td>U6snRNA-R</td>
<td>GGAGGCAGTACGAGAGATTAGGA</td>
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</tr>
<tr>
<td>sly-pre-aF</td>
<td>CTAGTACTCACATATCTCTTCTAAA</td>
<td>cloning of MIR319a</td>
</tr>
<tr>
<td>sly-pre-aR</td>
<td>TTAACCTAGCAATGTTAAACC</td>
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</tr>
<tr>
<td>sly-319bpre1F</td>
<td>TGCAATATACAGTAAGTAGTATAGG</td>
<td>cloning of MIR319b</td>
</tr>
<tr>
<td>sly-319bpre2R</td>
<td>GTAAGGGAGCATATGCAAAGG</td>
<td>cloning of MIR319c</td>
</tr>
<tr>
<td>sly-319cpre3F</td>
<td>TTGTGTAGATCTAAGGAAGGTCGAGG</td>
<td>cloning of MIR319c</td>
</tr>
<tr>
<td>sly-319cpre1R</td>
<td>GGTAAAGACGAGCAAGGG</td>
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<tr>
<td>sha-319-3-F</td>
<td>ATCTAAGTGGCAACTTTGAGG</td>
<td>cloning of MIR319d</td>
</tr>
<tr>
<td>5´ RACE adaptor</td>
<td>GCUGAUGGGCGAGUAUGAACACUCGGUUUGCUUGCUUU</td>
<td>universal primer of 5´RACE</td>
</tr>
<tr>
<td>Outer</td>
<td>GCTGATGGGCGAGTAAGTAAAGC</td>
<td></td>
</tr>
<tr>
<td>Inner1</td>
<td>CGCGGATCCGACACTCGTGCTGGCTGGGTGGAT</td>
<td></td>
</tr>
<tr>
<td>Inner2</td>
<td>TTGTGCTGGCTGGTGGTGA</td>
<td></td>
</tr>
<tr>
<td>TCP3GSP1</td>
<td>AATGAGCAGAAGAATCAGAGGAGAGA</td>
<td>TCP3 specific primer of 5´RACE</td>
</tr>
<tr>
<td>TCP3GSP2</td>
<td>CAAATCAGCTTCTCTCATCGAGT</td>
<td>TCP29 specific primer of 5´RACE</td>
</tr>
<tr>
<td>TCP3GSP3</td>
<td>GAATTACAGGAAACACAGCAGT</td>
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</tr>
<tr>
<td>TCP29GSP1</td>
<td>TCAACCTTCGACTAGGAGGAGG</td>
<td>TCP29 specific primer of 5´RACE</td>
</tr>
<tr>
<td>TCP29GSP2</td>
<td>GCTATATGGGACTGACTGACTG</td>
<td></td>
</tr>
<tr>
<td>TCP29GSP3</td>
<td>GCTATATGGGACTGACTGACTG</td>
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</tr>
<tr>
<td>qTCP3F</td>
<td>AAATCGATTTTTTCTCTCTAGGAGG</td>
<td>qPCR of TCP3</td>
</tr>
<tr>
<td>qTCP3R</td>
<td>CGATGCGAAAGAATTAGTGTTGA</td>
<td>qPCR of TCP3</td>
</tr>
<tr>
<td>qTCP29F</td>
<td>GACCAGTGTCTCCGACAAGTTTAG</td>
<td>qPCR of TCP2</td>
</tr>
<tr>
<td>qTCP29R</td>
<td>GCCACCGATAATGATGACGAGG</td>
<td>qPCR of TCP2</td>
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<tr>
<td>ActinF</td>
<td>GAAATAGTCATAAGTGGGCAGAG</td>
<td>reference gene of qPCR</td>
</tr>
<tr>
<td>ActinR</td>
<td>ATACCCACCATCACACAGT</td>
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</tr>
<tr>
<td>Target mRNA</td>
<td>Target function annotation</td>
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<tr>
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<td>---------------------------------------------------</td>
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<tr>
<td>Solyc08g048390.1.1</td>
<td>transcription factor CYCLOIDEA (Fragment)</td>
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<tr>
<td>Solyc08g048370.2.1</td>
<td>TCP family transcription factor 29</td>
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<td>Solyc02g077250.2.1</td>
<td>TCP domain protein 10</td>
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<tr>
<td>Solyc02g079010.2.1</td>
<td>protein of unknown function (DUF761)</td>
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<tr>
<td>Solyc01g009070.2.1</td>
<td>MYB transcription factor</td>
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<tr>
<td>Solyc05g012840.1.1</td>
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<td>Solyc06g073640.2.1</td>
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<td>TCP family transcription factor 4</td>
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</table>
Fig. 1. Suppl. Sequence analysis of miR319d stem-loop RT-PCR products (A) and secondary structure of sha-MIR319a (B), sha-MIR319b (C), sha-MIR319c (D), sha-MIR319d (E), and sly-MIR319d (F). The MiRNA secondary structures are colored by positional entropy.
Fig. 2. Suppl. 5′ fragments of TCP3 (A) and TCP29 (B) cleaved by miR319.

Fig. 3. Suppl. Temporal expression patterns of miR319 and target genes in 1 h (A-D) and 8 h (E-H) of different tomato genotypes under heat stress. The left y-axis corresponds to miR319 expression, and the right y-axis corresponds to target genes expression. Reference genes for miRNAs and target genes were U6snRNA and Actin, respectively. Means ± SEs, n = 3.
Fig. 4. Suppl. Functional interaction of TCP3 (A) and TCP29 (B).

Fig. 5. Suppl. The possible regulatory network of tomato response to chilling or heat stress. Under chilling stress, miR319 is up-regulated. Under heat stress miR319a, b, and d are up-regulated and miR319c is down-regulated. The altered miR319 expression leading to the expression changes of its target TCPs and possibly TCPs indirectly affect ROS signaling, Ca$^{2+}$ signaling and anthocyanin synthesis by interaction with CIPK6, GAMYB-like, and ANT2, which results in the enhanced chilling or heat tolerance of tomato plants.