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

Accession	Species	Origin	Performance
LA1777	*S. habrochaites*	USA (TGRC)	chilling-tolerant; Heat-sensitive
LA2683	*S. lycopersicum*	USA (TGRC)	chilling-tolerant; Heat-sensitive
Pole red Siberian	*S. lycopersicum*	USA	moderately chilling and heat tolerant
LA3475	*S. lycopersicum*	USA (TGRC)	chilling-sensitive
Stupice	*S. lycopersicum*	USA	heat-tolerant

Table 2. Suppl. Primers in the experiment.

Primers	Sequence (5′to 3′)	Application
miR319a stem-loop RT	GTCGTATCCAGTGCGTGTCGTGGAGTCGGCAATTGCACTG GATACGACGGAGCTC	RT-PCR of miR319a
miR319b stem-loop RT	GTCGTATCCAGTGCGTGTCGTGGAGTCGGCAATTGCACTG GATACGACAGGGAGC	RT-PCR of miR319b
miR319c stem-loop RT	GTCGTATCCAGTGCGTGTCGTGGAGTCGGCAATTGCACTG GATACGACAAGGAGC	RT-PCR of miR319c
miR319d stem-loop RT	GTCGTATCCAGTGCGTGTCGTGGAGTCGGCAATTGCACTG GATACGACAGGAGCT	RT-PCR of miR319d
miR319aF	GGGCTTGGACTGAAGGGA	cloning and qPCR of miR319a
miR319bF	GCGTTGGACTGAAGGGAGC	cloning and qPCR of miR319b
miR319cF	GGTTGGACTGAAGGGAGC	cloning and qPCR of miR319c
miR319dF	GGGGTTGGACTGAAGGGAG	cloning and qPCR of miR319d
3’ universal primer	CAGTGCGTGTCGTGGAGT	
U6snRNA stem-loop RT	GTGCAGGGTCCGAGGTTTTGGACCATTTCTCGAT	RT-PCR of U6snRNA
U6snRNA-F	GGAACGATACAGAGAAGATTAGCA	reference gene of stem-loop qPCR
U6snRNA-R	GTGCAGGGTCCGAGGT	
sly-pre-aF	CTAGTACTCCACATTTCCTCTTTAA	cloning of MIR319a
sly-pre-aR	TTAACCCTAGCAAGTTAAACCA	
sly-319bpre1F	TGCATATCAAGTACTTATGAGTCCC	cloning of MIR319b
sly-319bpre2R	GTAAGGAGACTATGCCAAGC	
sly-319cpre3F	TTTGGTGATTACTAAGGCTGTTGAG	cloning of MIR319c
sly-319cpre1R	GGTAAAGACCAGGACGAACA	
sha-319-3-F	ATCTAAGTGCAACTTCATGTAGG	cloning of MIR319d
sha-319-3-R	AGCAATTAAACAACAGTATATGAAT	
5′RACE adaptor	GCUGAUGGCGAUGAAUGAACACUGCGUUUGCUGGCUUU GAUGAAA	universal primer of 5′RACE
Outer	GCTGATGGCGATGAATGAACACTG	
Inner1	CGCGGATCCGAACACTGCGTTTGCTGGCTTTGATG	
Inner2	TTGCTGGCTTTGATGAAA	
TCP3GSP1	AATGACGAGAATCAGAGGAAGCAGA	TCP3 specific primer of 5′RACE
TCP3GSP2	CAACATCACTTTCTGGCATCGGATT	
TCP3GSP3	GAATACATAGGAAACACAGCTTGAT	
TCP29GSP1	TCAACTTTCAACTATGGAGCTTCCC	TCP29 specific primer of 5′RACE
TCP29GSP2	GCATATATGGGTGCTTCCTTTGG	
TCP29GSP3	TGTCATATCCAGTTGTGGAACCAAG	
qTCP3F	AAATCAGTTTTTGTCTCAGAGGGGA	qPCR of TCP3
qTCP3R	CGATGCCAGAAAGTGATGTTGAATA	
qTCP29F	GACCAGTGTCTCCACCAATGTTTAG	qPCR of TCP29
qTCP29R	GGAACCAAGATATGATCCGTACCTC	
qTCP2F	CAGCAGCTATTCGGTCAAAATCAGT	qPCR of TCP2
qTCP2R	GCCAGGAATTGTTGATGGATACATT	
ActinF	GAAATAGCATAAGATGGCAGACG	reference gene of qPCR
ActinR	ATACCCACCATCACACCAGTAT	

Table 3. Suppl. MiR319 target prediction.

Target mRNA	Target function annotation
Solyc08g048390.1.1	transcription factor CYCLOIDEA (Fragment)
Solyc08g048370.2.1	TCP family transcription factor 29
Solyc02g077250.2.1	TCP domain protein 10
Solyc02g079010.2.1	protein of unknown function (DUF761)
Solyc01g009070.2.1	MYB transcription factor
Solyc05g012840.1.1	TCP family transcription factor 4
Solyc06g073640.2.1	MYB domain protein 65
Solyc07g053410.2.1	TCP family transcription factor 4
Solyc07g062680.1.1	TCP family transcription factor 2
Solyc10g008780.1.1	TCP domain protein 10
Solyc12g014140.1.1	TCP family transcription factor 3

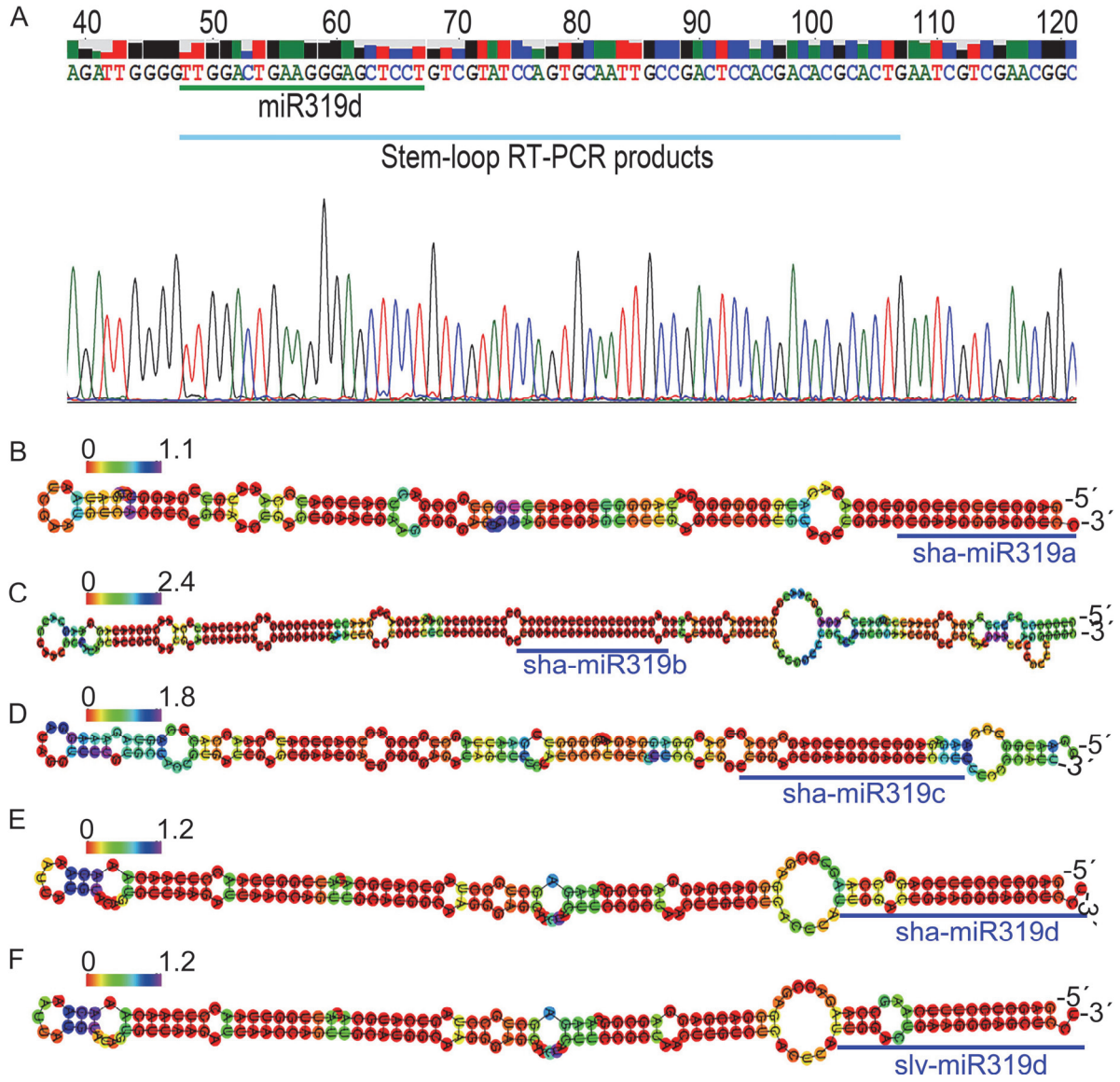

Fig. 1. Suppl. Sequence analysis of miR319d stem-loop RT-PCR products (*A*) and secondary structure of sha-MIR319a (*B*), sha-MIR319b (*C*), sha-MIR319c (*D*), sha-MIR319d (*E*), and sly-MIR319d (*F*). The MiRNA secondary structures are colored by positional entropy.

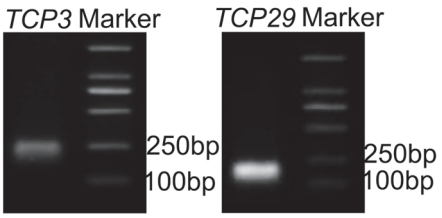

Fig. 2. Suppl. 5′ fragments of *TCP3* (*A*) and *TCP29* (*B*) cleaved by miR319.

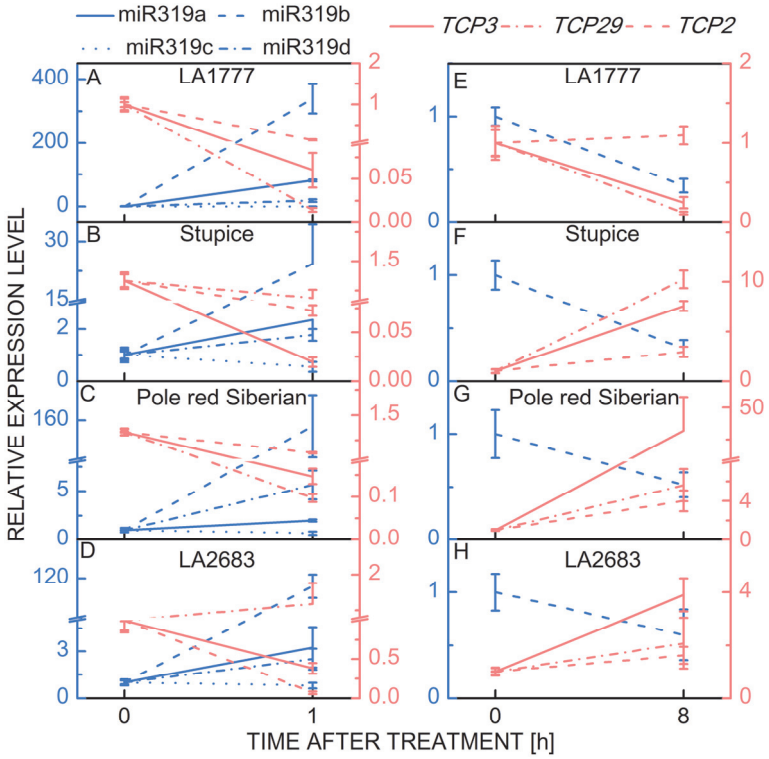

Fig. 3. Suppl. Temporal expression patterns of miR319 and target genes in 1 h (*A-D*) and 8 h (*E-H*) of different tomato genotypes under heat stress. The *left y-axis* corresponds to miR319 expression, and the *right y-axis* corresponds to target genes expression. Reference genes for miRNAs and target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

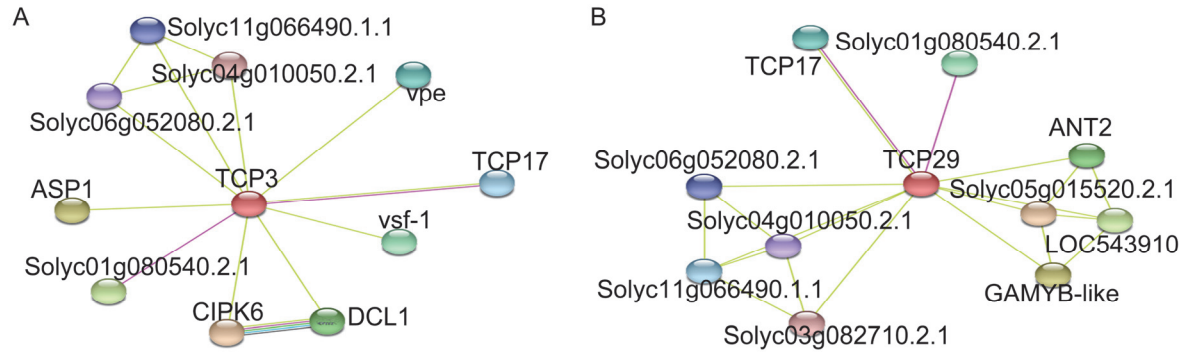

Fig. 4. Suppl. Functional interaction of TCP3 (*A*) and TCP29 (*B*).

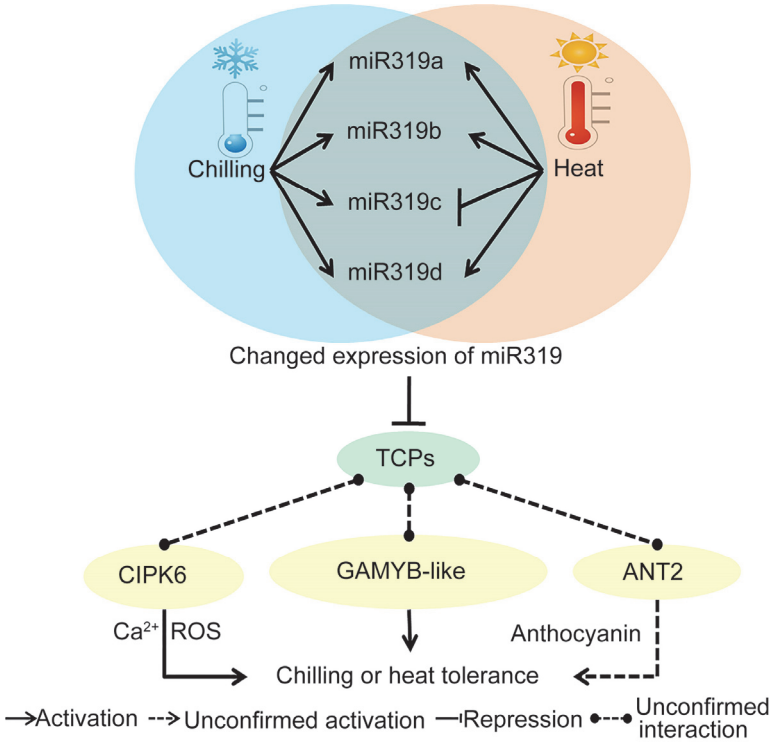

Fig. 5. Suppl. The possible regulatory network of tomato response to chilling or heat stress. Under chilling stress, miR319 is up-regulated. Under heat stress miR319a, b, and d are up-regulated and miR319c is down-regulated. The altered miR319 expression leading to the expression changes of its target *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.