

Table S1. The protein sequence information used for phylogenetic tree construction and proteins domain

Gene Name	Solgenomics accession ID	Gene accession No.	Protein ID
<i>SIMPK1</i>	Solyc12g019460.2	NM_001247082.2	NP_001234011.2
<i>SIMPK2</i>	Solyc08g014420.3	NM_001247426.1	NP_001234355.1
<i>SIMPK3</i>	Solyc06g005170.3	NM_001247431.2	NP_001234360.1
<i>SIMAPK4</i>	Solyc11g072630.2	HM367593.1	ADK38705.1
<i>SIMAPK5</i>	Solyc01g094960.3	HM036493.2	ADH43227.2
<i>SIMAPK6</i>	Solyc05g049970.3	JF791807.1	AEH42637.1
<i>SIMAPK7</i>	Solyc08g081490.2	JF791808.1	AEH42638.1
<i>SIMAPK8</i>	Solyc02g084870.3	HM189670.1	ADJ95343.1
<i>SIMAPK9</i>	Solyc04g080730.3	HM245320.1	ADK13095.1
<i>SIMAPK10</i>	Solyc10g007500.3	JF795445.1	AEH42667.1
<i>SIMAPK11</i> ,	Solyc07g062080.3	JF795446.1	AEH42668.1
<i>SIMAPK12</i>	Solyc07g056350.3	JF795447.1	AEH42669.1
<i>SIMAPK13</i>	Solyc01g080240.3	JF795448.1	AEH42670.1
<i>SIMAPK14</i>	Solyc04g007710.3	JF795449.1	AEH42671.1
<i>SIMAPK15</i>	Solyc05g008020.3	JF795451.1	AEH42673.1
<i>SIMAPK16</i>	Solyc12g040680.2	JF795450.1	AEH42672.1

Table S2. Primers used in the study

Genes	Primer sequences (5'-3')	
	Forward	Reverse
<i>SIMPK3</i>	CGGGATCCATGGTTGATGCTAATATGGGTG	GGCGCGAGCTCTTAAGCATATTCAGGATTCAACG
<i>NPTII</i>	TTCATGCTGGAGTTCTTCGC	GTCACCGACTTGAGCCATTG
<i>qSIMPK3</i>	CTCATCCCTACCTCGCAAAG	TCAGGATTCAACGCCAAAGC
<i>qSISOD</i>	ACTTGCTCCTGGACTTCACG	TCGGCATTGGCCACTATGTT
<i>qSIPOD</i>	GGAATGTGCCAACTGGTAGA	TGATGAGCAACGAGACTC
<i>qSICAT</i>	TGGAAGCCAACCTGTGGTGT	ACTGGGATCAACGGCAAGAG
<i>qSIAPX</i>	TGTGAGCGAGGAGTACCTCA	TGTGCTAGCTCCGCTTTGAA
<i>qSlActin</i>	TGGTCGGAATGGGACAGAAG	CTCAGTCAGGAGAACAGGGT

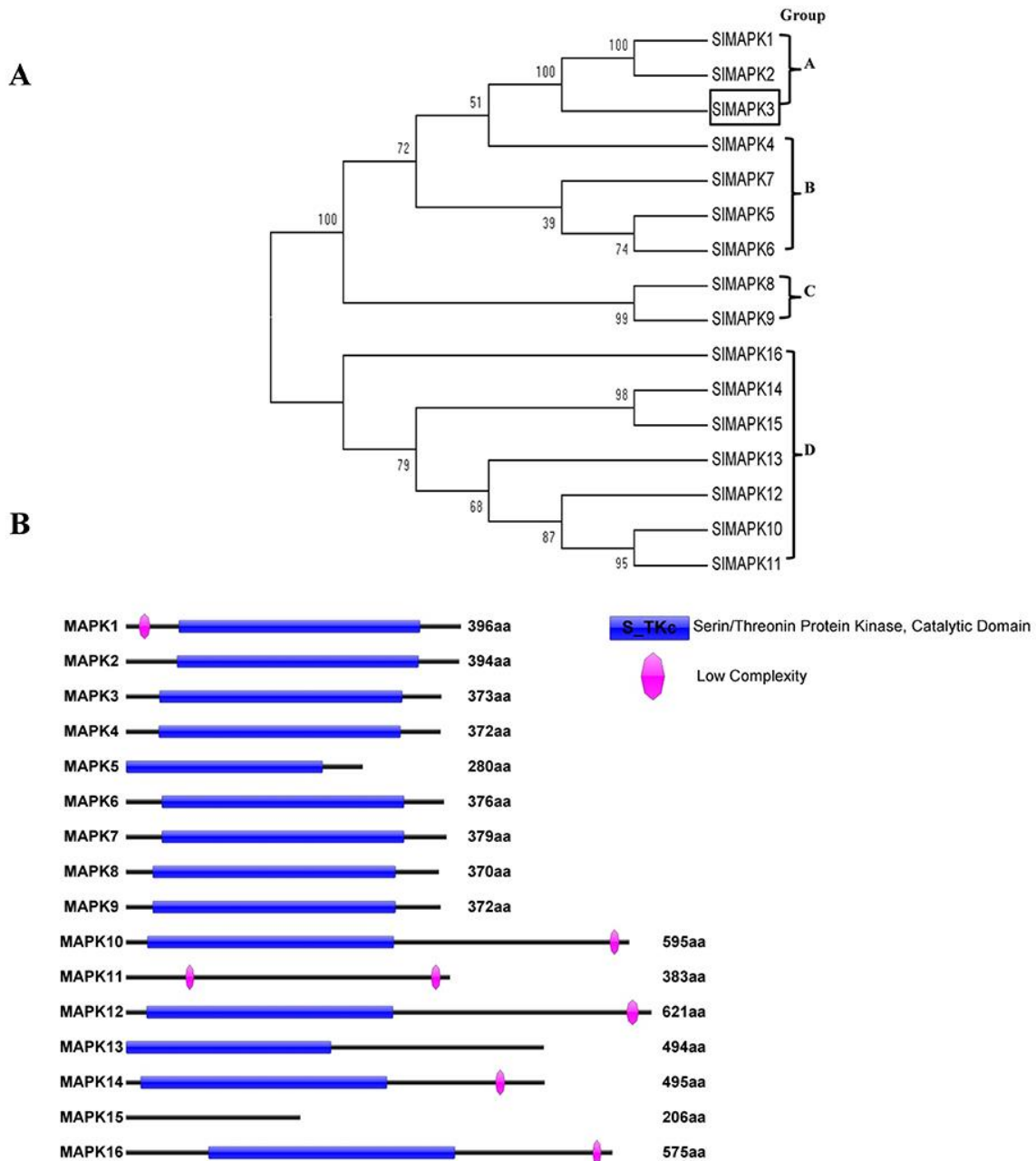


Figure S1. Phylogenetic and structural analysis based on the amino acid sequences of *Solanum lycopersicum* SIMAPKs. (A) Phylogenetic tree, the tree was generated using MEGA5 program by the neighbor-joining method. Bootstrap supports from 1000 replicates are indicated at each branch and (B) Domain position of SIMAPKs in tomato. Domains are indicated as boxes in different colors.

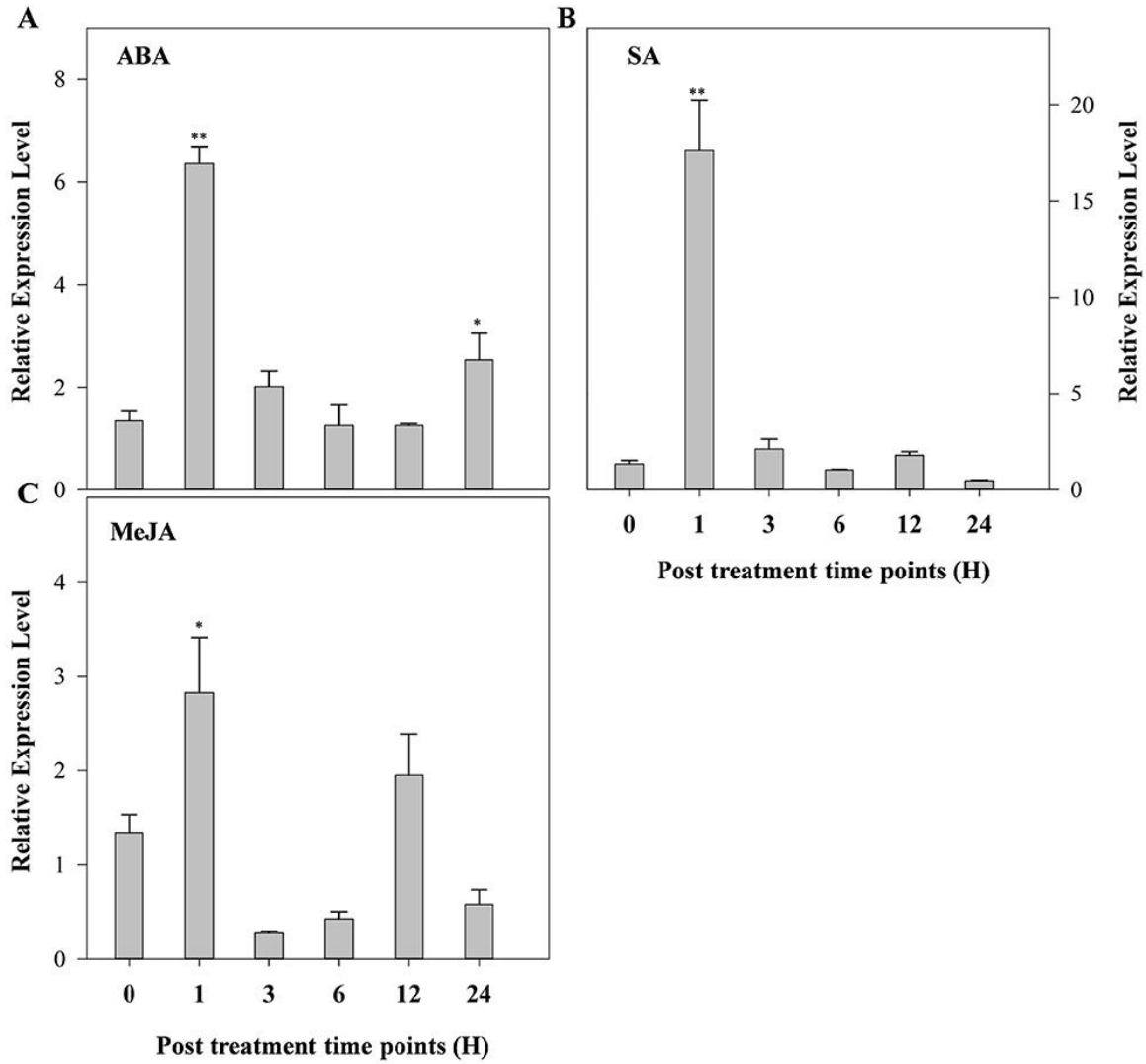


Figure S2. Expression patterns of *SIMAPK3* after different hormonal treatments. Expression patterns of *SIMAPK3* gene under different exogenous hormones. (A) ABA -100 μ M, (B) SA -100 μ M and (C) MeJA -100 μ M for 0, 1, 3, 6, 12, and 24h. Zero (0) represents seedlings without any treatment. The tomato actin gene was used as the internal control for normalization. Data represent mean \pm SE of three biological replicates.

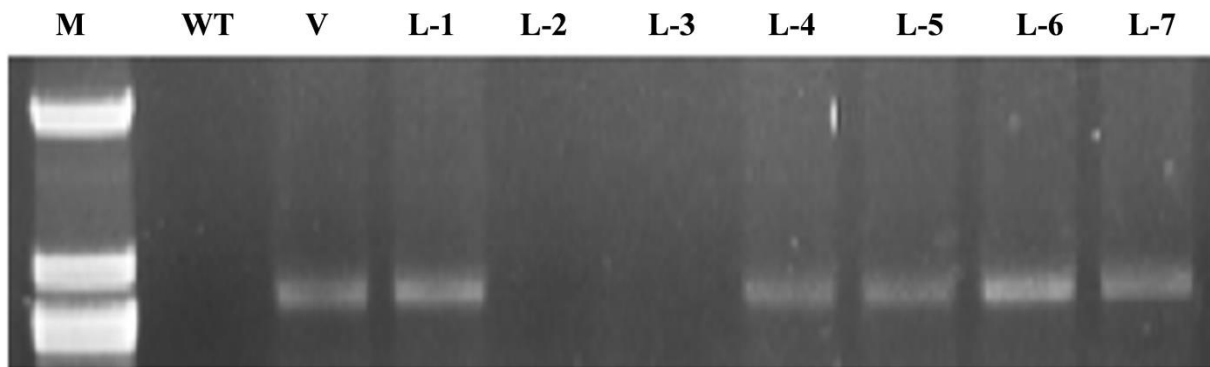


Figure S3. Confirmation of transgenic plants. PCR detection of NPTII fragments in T₀ transgenic plants. M: DNA marker, WT: Wild-type plants, V: pVBG2307-MPK3 vector and L1~7: 7 lines of T₀ transgenic plants.