

Figure S1. Targeted gene deletion of *ChTHR1* in *C. higginsianum*. (A) Strategic map of gene disruption vector construction and sites for restriction enzymes at the *ChTHR1* genomic region. A bold line below the disruption construct represents the sequence used as a probe in Southern blot analysis. (B) Southern blot analysis of the WT and *Chthr1Δ* mutants. Genomic DNA was digested with *Bsu36I* and *EcoRI*, and subsequently separated in 0.8% agarose gel. Blot was hybridized with the probe amplified from genomic DNA of the WT.

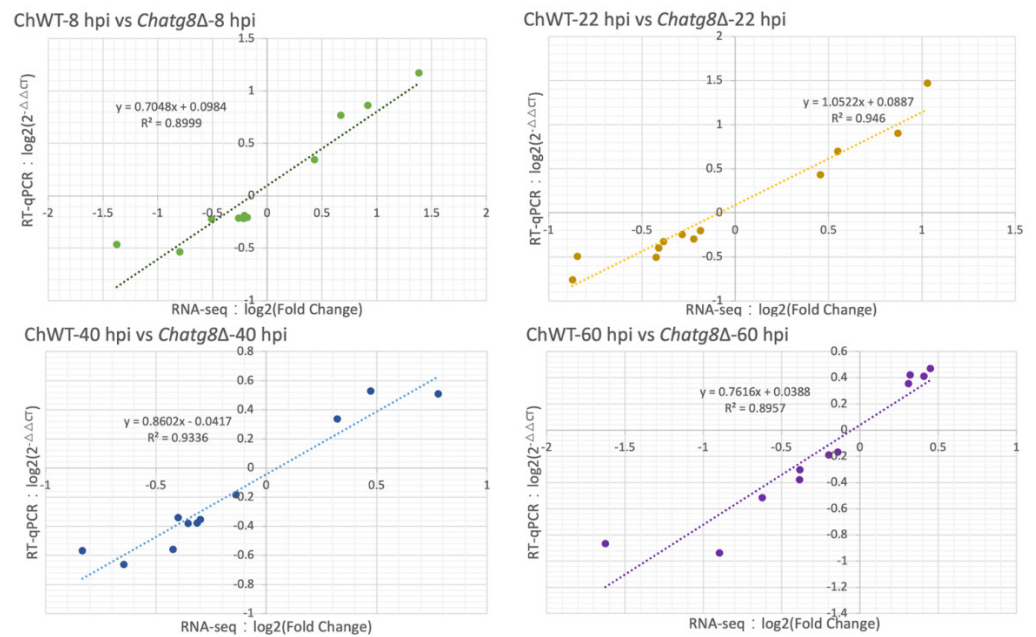


Figure S2. Correlations of the fold changes of six DEGs each from *C. higginsianum* and *A. thaliana* determined by RNA-seq and RT-qPCR analysis.

Table S1. Summary of RNA-Seq data and sequence assembly. *C. higginsianum* (Reference Genes: 14651; Sequenced Reference Genes: 13677, 93.35%; Sequenced Novel Genes: 1378; Sequenced Total_Genes: 15055, 93.92%) and *A. thaliana* (Reference Genes: 27416; Sequenced Reference Genes: 23670, 86.34%; Sequenced Novel Genes: 286; Sequenced Total_Genes: 23956, 86.48%).

Sample	Raw Reads	Clean Reads (%)	Raw (bp)	Data	Clean (bp)	Data	Q20 (%)	Q30 (%)	<i>C. higginsianum</i>				<i>A. thaliana</i>		
									Sequenced Reference Genes	Sequenced Novel Genes	Sequenced Genes	Total	Sequenced Reference Genes	Sequenced Novel Genes	Sequenced Genes
ChWT-8 hpi-1	95715576	95607716 (99.89%)	14357336400	14121532219	13769677256 (97.51%)	13104671951 (92.80%)	10211 (69.69%)	619 (44.92%)	10830 (67.57%)	20717 (75.57%)	275 (96.15%)	20992 (75.78%)			
ChWT-8 hpi-2	90214224	90112506 (99.89%)	13532133600	13432281220	13095002760 (97.49%)	12455288188 (92.73%)	9179 (62.65%)	432 (31.35%)	9611 (59.96%)	20518 (74.84%)	270 (94.41%)	20788 (75.04%)			
ChWT-8 hpi-3	63256348	63181086 (99.88%)	9488452200	9421649854	9142452445 (97.04%)	8651933548 (91.83%)	9124 (62.28%)	406 (29.46%)	9530 (59.45%)	20433 (74.53%)	270 (94.41%)	20703 (74.73%)			
<i>Chatg8Δ</i> -8 hpi-1	79490366	79389750 (99.87%)	11923554900	11848474748	11546266278 (97.45%)	10979434460 (92.67%)	9305 (63.51%)	432 (31.35%)	9737 (60.75%)	20507 (74.80%)	271 (94.76%)	20778 (75.01%)			
<i>Chatg8Δ</i> -8 hpi-2	79566370	79472186 (99.88%)	11934955500	11855442126	11552373824 (97.44%)	10983778041 (92.65%)	9273 (63.29%)	432 (31.35%)	9705 (60.55%)	20462 (74.64%)	269 (94.06%)	20731 (74.84%)			
<i>Chatg8Δ</i> -8 hpi-3	82019434	81924600 (99.88%)	12302915100	12187079104	11889821109 (97.56%)	11326041763 (92.93%)	9647 (65.85%)	498 (36.14%)	10145 (63.29%)	20653 (75.33%)	269 (94.06%)	20922 (75.53%)			
ChWT-22 hpi-1	97034188	96938994 (99.90%)	14555128200	14417167196	14029929722 (97.31%)	13313926982 (92.35%)	9345 (63.78%)	454 (32.95%)	9799 (61.13%)	20952 (76.42%)	275 (96.15%)	21227 (76.63%)			
ChWT-22 hpi-2	88555308	88464200 (99.90%)	13283296200	13169889069	12822481654 (97.36%)	12177168183 (92.46%)	8453 (57.70%)	346 (25.11%)	8799 (54.89%)	20672 (75.40%)	270 (94.41%)	20942 (75.60%)			
ChWT-22 hpi-3	72358928	72305502 (99.93%)	10853839200	10710036206	10471893924 (97.78%)	10004697432 (93.41%)	9673 (66.02%)	494 (35.85%)	10167 (63.43%)	20684 (75.44%)	277 (96.85%)	20961 (75.67%)			
<i>Chatg8Δ</i> -22 hpi-1	77768214	77680294 (99.89%)	11665232100	11537014741	11234077127 (97.37%)	10670559433 (92.49%)	9732 (66.43%)	535 (38.82%)	10267 (64.05%)	20738 (75.64%)	271 (94.76%)	21009 (75.84%)			
<i>Chatg8Δ</i> -22 hpi-2	81762346	81674452 (99.89%)	12264351900	12166769470	11854587811 (97.43%)	11268327124 (92.62%)	9516 (64.95%)	539 (39.11%)	10055 (62.73%)	20568 (75.02%)	273 (95.45%)	20841 (75.23%)			
<i>Chatg8Δ</i> -22 hpi-3	78869142	78784002 (99.89%)	11830371300	11745636651	11443187620 (97.43%)	10876602946 (92.60%)	9439 (64.43%)	492 (35.70%)	9931 (61.96%)	20516 (74.83%)	270 (94.41%)	20786 (75.03%)			

ChWT-40 hpi-1	75795496	75713222 (99.89%)	11369324400	11285769073	10981729143 (97.31%)	10424212710 (92.37%)	9692 (66.15%)	525 (38.10%)	10217 (63.74%)	20938 (76.37%)	271 (94.76%)	21209 (76.56%)
ChWT-40 hpi-2	73596550	73527540 (99.91%)	11039482500	10968636339	10696685533 (97.52%)	10186300040 (92.87%)	9818 (67.01%)	535 (38.82%)	10353 (64.59%)	21017 (76.66%)	273 (95.45%)	21290 (76.85%)
ChWT-40 hpi-3	59280912	59221372 (99.90%)	8892136800	8790719466	8567481013 (97.46%)	8151187861 (92.72%)	9160 (62.52%)	461 (33.45%)	9621 (60.02%)	20565 (75.01%)	269 (94.06%)	20834 (75.21%)
<i>Chatg8Δ</i> -40 hpi-1	76507870	76427090 (99.89%)	11476180500	11405522247	11110025056 (97.41%)	10558964946 (92.58%)	9106 (62.15%)	440 (31.93%)	9546 (59.55%)	20429 (74.51%)	274 (95.80%)	20703 (74.73%)
<i>Chatg8Δ</i> -40 hpi-2	77155780	77072802 (99.89%)	11573367000	11491538600	11195665317 (97.43%)	10640739123 (92.60%)	8788 (59.98%)	447 (32.44%)	9235 (57.61%)	20567 (75.02%)	267 (93.36%)	20834 (75.21%)
<i>Chatg8Δ</i> -40 hpi-3	83400778	83315682 (99.90%)	12510116700	12421517638	12128893059 (97.64%)	11568620128 (93.13%)	8937 (61.00%)	461 (33.45%)	9398 (58.63%)	20655 (75.34%)	273 (95.45%)	20928 (75.55%)
ChWT-60 hpi-1	78276806	78175806 (99.87%)	11741520900	11615432099	11313230463 (97.40%)	10760244358 (92.64%)	12051 (82.25%)	1020 (74.02%)	13071 (81.55%)	20996 (76.58%)	266 (93.01%)	21262 (76.75%)
ChWT-60 hpi-2	80758858	80675568 (99.90%)	12113828700	12018443675	11720063668 (97.52%)	11159313402 (92.85%)	11089 (75.69%)	766 (55.59%)	11855 (73.96%)	20993 (76.57%)	272 (95.10%)	21265 (76.76%)
ChWT-60 hpi-3	95345372	95232228 (99.88%)	14301805800	14173946131	13781325348 (97.23%)	13069065237 (92.20%)	11352 (77.48%)	847 (61.47%)	12199 (76.11%)	20947 (76.40%)	271 (94.76%)	21218 (76.59%)
<i>Chatg8Δ</i> -60 hpi-1	71040494	70952912 (99.88%)	10656074100	10563745393	10265260915 (97.17%)	9723366735 (92.04%)	8164 (55.72%)	388 (28.16%)	8552 (53.35%)	20528 (74.88%)	268 (93.71%)	20796 (75.07%)
<i>Chatg8Δ</i> -60 hpi-2	73369986	73282734 (99.88%)	11005497900	10922707207	10654317783 (97.54%)	10148614576 (92.91%)	7558 (51.59%)	337 (24.46%)	7895 (49.25%)	20439 (74.55%)	267 (93.36%)	20706 (74.75%)
<i>Chatg8Δ</i> -60 hpi-3	71288290	71206044 (99.88%)	10693243500	10615886799	10349987494 (97.50%)	9846294440 (92.75%)	7419 (50.64%)	321 (23.29%)	7740 (48.29%)	20439 (74.55%)	270 (94.41%)	20709 (74.76%)

Note: Q20/30 (%): Percentage of bases whose clean data mass value is greater than or equal to 20/30

Table S2. 21 candidate genes of plant hormone signal transduction in Figure 6.

Plant hormone		Gene ID	Description	
Auxin	ARF	AT1G19850	Auxin-responsive factor AUX/IAA-related	
		GH3	AT4G37390	Auxin-responsive GH3 family protein
			AT1G28130	Auxin-responsive GH3 family protein
			AT5G54510	Auxin-responsive GH3 family protein
			AT2G23170	Auxin-responsive GH3 family protein
			AT4G27260	Auxin-responsive GH3 family protein
			AT5G13320	Auxin-responsive GH3 family protein
	SAUR	AT4G22620	SAUR-like auxin-responsive protein family	
		AT5G50760	SAUR-like auxin-responsive protein family	
		AT2G45210	SAUR-like auxin-responsive protein family	
SA	TGA	AT1G08320	bZIP transcription factor family protein	
	PR-1	AT4G33720	CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein)	
		AT2G14610	Pathogenesis-related gene 1	
Cytokinin	AHP	AT3G21510	Histidine-containing phosphotransmitter 1	
ABA	PP2C	AT5G59220	Highly ABA-induced PP2C gene 1	
ETH	ERF1/2	AT3G23240	Ethylene response factor 1	
		AT5G47220	Ethylene responsive element binding factor 2	
BR	TCH4	AT5G57560	Xyloglucan endotransglucosylase/hydrolase family protein	
JA	JAZ	AT1G17380	Jasmonate-zim-domain protein 5	
		AT1G19180	Jasmonate-zim-domain protein 1	
		AT5G13220	Jasmonate-zim-domain protein 10	

Table S3. Primer sequences used in the present study.

3	Gene name	Primer	Amplicon Length (bp)	Amplification efficiency (%)	Primer <i>T_m</i> (°C)
RT-qPCR	<i>ChACT-qFor</i>	<i>GTCCTACGAGCTTCCCG</i>	201	90.27	51.9
	<i>ChACT-qRev</i>	<i>ATGGTGGTACCACCAGAC</i>			50.3
RT-qPCR	<i>TUB2-qFor</i>	<i>ATCCGTGAAGAGTACCCAGAT</i>	144	104.87	52.4
	<i>TUB2-qRev</i>	<i>AAGAACCATGCACTCATCAGC</i>			52.4
RT-qPCR	<i>CH63R_01708-qFor</i>	<i>GTCAAAGTCACTACGGCTGC</i>	115	95.33	53.8
	<i>CH63R_01708-qRev</i>	<i>GCTCCTCGACGATTCCCATA</i>			53.8
RT-qPCR	<i>CH63R_03174-qFor</i>	<i>CTACCCTGCCAGCATCTTTG</i>	268	93.72	53.8
	<i>CH63R_03174-qRev</i>	<i>GATGACCTTGACCTTGGACG</i>			53.8
RT-qPCR	<i>CH63R_01918-qFor</i>	<i>CAGCAGAATCTCCCAGGCTA</i>	193	99.48	53.8
	<i>CH63R_01918-qRev</i>	<i>GACAAGGCTTCGGCAACAC</i>			53.8
RT-qPCR	<i>CH63R_09049-qFor</i>	<i>GTCTCCAAGTCTCTTCCC</i>	194	94.84	55.9
	<i>CH63R_09049-qRev</i>	<i>AGTAGTCGCTGTTGAGGATGT</i>			52.4
RT-qPCR	<i>CH63R_03670-qFor</i>	<i>TCACCGTTACCGTATCCACC</i>	132	98.9	53.8
	<i>CH63R_03670-qRev</i>	<i>TCTTGTAGCAGTCCAGACCG</i>			53.8
RT-qPCR	<i>CH63R_06437-qFor</i>	<i>AGAGACCGACACGCTGATTA</i>	135	101.23	51.8
	<i>CH63R_06437-qRev</i>	<i>CGGGCTTCCAACATTGTGAT</i>			51.8
RT-qPCR	<i>AT3G60120.1-qFor</i>	<i>AGGTGTAAGAGGTGGTTCGG</i>	217	107.88	53.8
	<i>AT3G60120.1-qRev</i>	<i>GGCTTGTTGGATGCTTTGGA</i>			51.8
RT-qPCR	<i>AT5G50760.1-qFor</i>	<i>GCTTTGGCGGATATGAAGTCT</i>	90	98.62	52.4
	<i>AT5G50760.1-qRev</i>	<i>GCAAATCGGGGAATTCGTGA</i>			51.8
RT-qPCR	<i>AT5G59220.1-qFor</i>	<i>CGAGCTAGTCCGTGAAGAGT</i>	93	96.63	53.8
	<i>AT5G59220.1-qRev</i>	<i>AACGCAACAACCTCCATGTC</i>			51.8
RT-qPCR	<i>AT1G64780.1-qFor</i>	<i>CGCAGGTCAGGAGTTGTTT</i>	146	102.39	53.8
	<i>AT1G64780.1-qRev</i>	<i>TACCAAGCACGACAAGGGAT</i>			51.8
RT-qPCR	<i>AT5G58310.1-qFor</i>	<i>GCTGGCTAATTCAGTGAAGG</i>	153	91.9	53.8
	<i>AT5G58310.1-qRev</i>	<i>TGATCGTTGGGAAGTTGGGA</i>			53.8
RT-qPCR	<i>AT4G35090.1-qFor</i>	<i>ACAACCTCCTCATGACCGTT</i>	92	98.82	51.8
	<i>AT4G35090.1-qRev</i>	<i>CCGTTCCCTGTCGAAATTGG</i>			53.8
PCR	<i>THR1upF</i>	<i>ACGACGGCCAGTGCCAA- GCTTCCGCAAAACACGAGGATTTC</i>	1542		60.5
	<i>THR1upR</i>	<i>GACCTGCAGGCATGCAA- GCTTCTGAAA- GATTGTGGGGGGG</i>			61.5
PCR	<i>THR1dsF</i>	<i>CCGGGTACCGAGCTCGAATTCAC- CACATTCAACCACCTAACTGTAGT</i>	1542		60.6
	<i>THR1dsR</i>	<i>TATGGAGAACTCGA- GAATTCGCGACAAGCAGAAAC- GTGTGG</i>			63.9
PCR	<i>THR1probeF</i>	<i>CGCGTCGGCGGATG</i>	700		58.0
	<i>THR1probeR</i>	<i>CCCGGATGCCCCGTG</i>			56.2