

# **Comparative transcriptomic analysis reveals the involvement of auxin signaling in the heat tolerance of pakchoi under high-temperature stress**

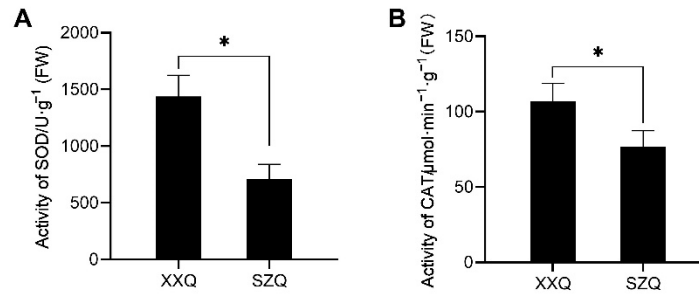
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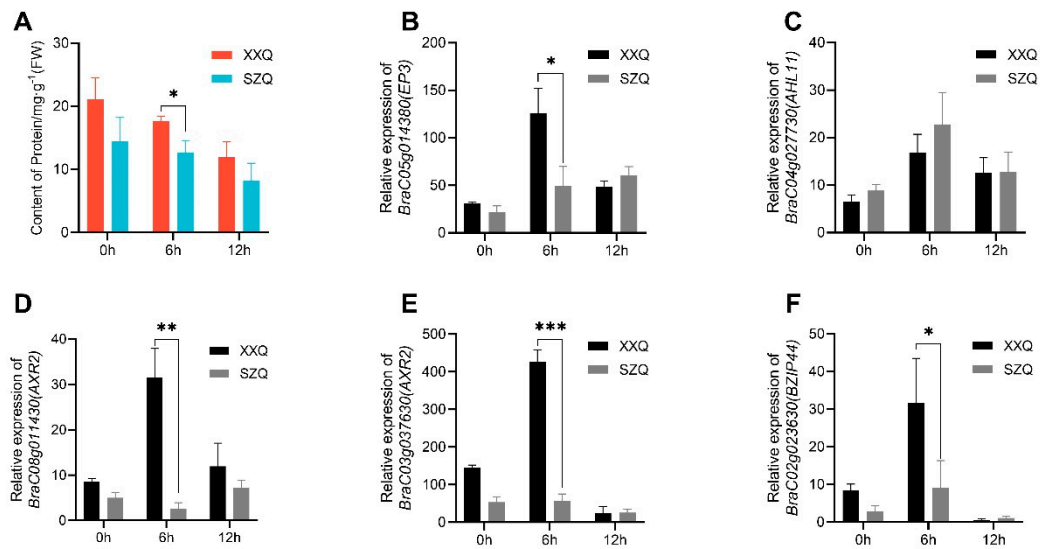
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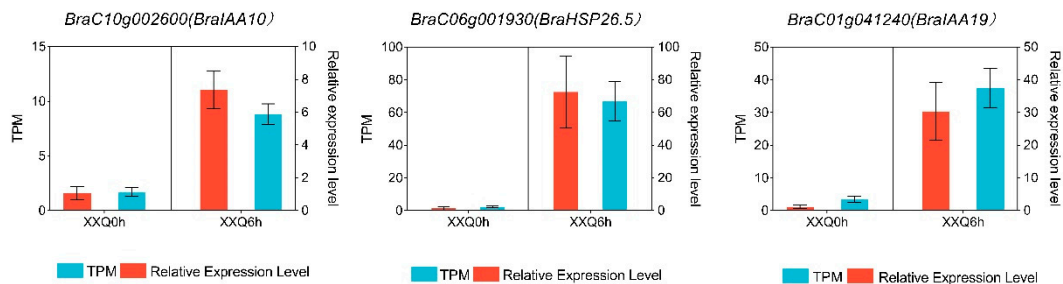
**Figure S1 SOD and CAT activities in SZQ and XXQ after high-temperature treatment**

Processing temperature: 42 °C. Processing time: 6h. Data are means ± SD (n = 3 biological replicates), \*P < 0.05 (*t*-test).



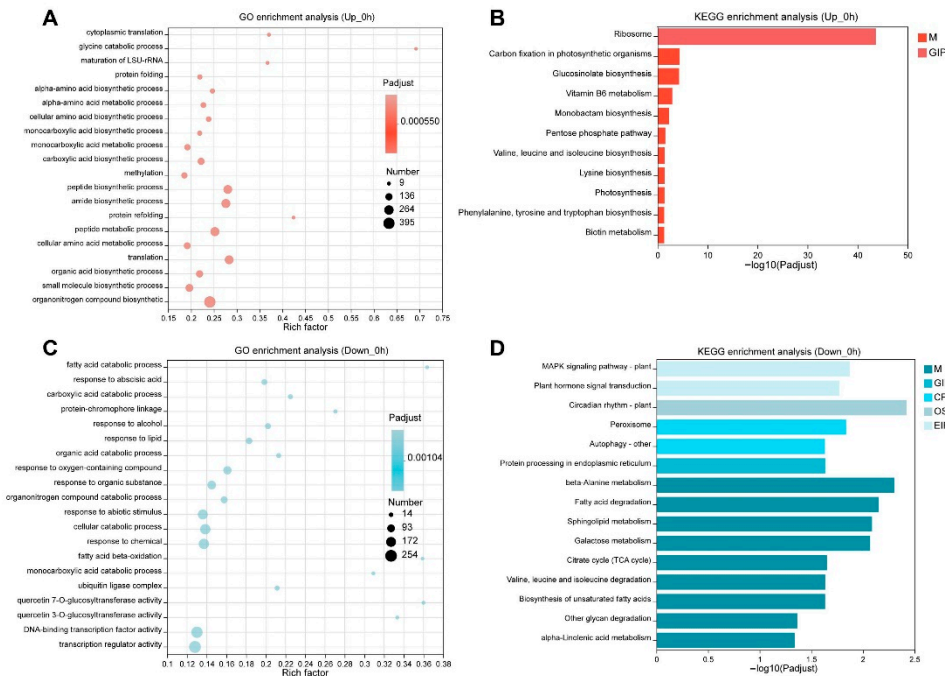
**Figure S2 Protein content and expression level of nitrogen metabolism-related genes in XXQ and SZQ during high-temperature treatment.**

(A) Protein content in XXQ and SZQ during high temperature treatment. (B-F) Expression level of nitrogen metabolism-related genes in XXQ and SZQ during high temperature treatment. High temperature treatment: 42 °C; Data are means ± SD (*n* = 3 biological replicates), \*P < 0.05, \*\*P < 0.01, \*\*\*P < 0.001 (*t*-test).



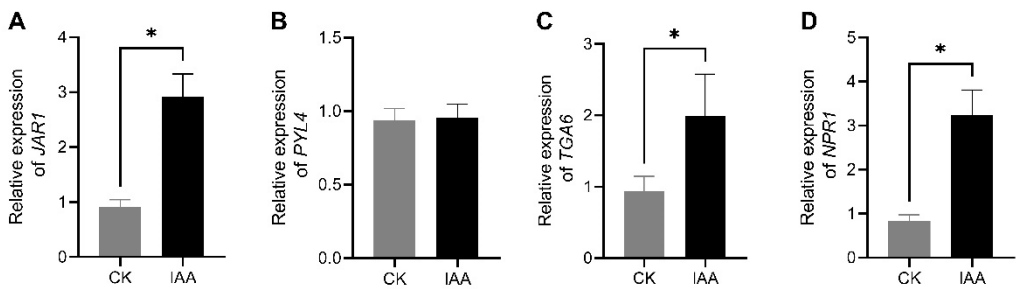
**Figure S3. Comparison of gene expression patterns between RNA-seq and qRT-PCR results.**

Data are means  $\pm$  SD ( $n = 3$  biological replicates). Primers were listed in Table S2.



**Figure S4. Analysis of the transcriptional differences between XXQ and SZQ under normal conditions**

(A-B) GO and KEGG analysis of the upregulated differentially expressed genes between XXQ and SZQ; (C-D) GO and KEGG analysis of the downregulated differentially expressed genes between XXQ and SZQ; Data are means  $\pm$  SD ( $n = 3$  biological replicates).



**Figure S5 Phytohormone-related gene expression pattern in response to IAA under high-temperature treatment**

High temperature treatment: 42 °C for 2 day; IAA concentration: 250  $\mu$ M/L. Data are means  $\pm$  SD ( $n = 3$  biological replicates), \*P < 0.05 ( $t$ -test).

**Table S1. Statistical sequence alignment between our sequencing results and the**

**reference genome (A represents Xinxiaqing, B represents Suzhouqing).**

Sample	Total reads	Total mapped	Multiple mapped	Uniquely mapped	Q20(%)	Q30(%)	GC content(%)
ckA0h_1	43,166,518	38,578,277(89.37%)	1,972,634(4.57%)	36,605,643(84.8%)	97.2	92.15	47.76
ckA0h_2	44,667,918	39,980,488(89.51%)	1,814,735(4.06%)	38,165,753(85.44%)	96.89	91.41	47.68
ckA0h_3	45,865,888	41,092,449(89.59%)	1,859,699(4.05%)	39,232,750(85.54%)	97.12	91.94	47.59
ckA6h_1	44,412,506	39,532,186(89.01%)	1,725,570(3.89%)	37,806,616(85.13%)	97.01	91.67	47.8
ckA6h_2	46,003,470	41,009,301(89.14%)	1,813,918(3.94%)	39,195,383(85.2%)	97.16	92	47.72
ckA6h_3	47,968,026	42,661,423(88.94%)	2,039,864(4.25%)	40,621,559(84.68%)	97.13	92	47.73
ckB0h_1	40,970,678	36,637,889(89.42%)	2,086,284(5.09%)	34,551,605(84.33%)	97.05	91.78	47.6
ckB0h_2	43,443,440	34,631,741(79.72%)	7,046,762(16.22%)	27,584,979(63.5%)	97.49	92.81	49.7
ckB0h_3	42,352,646	37,294,956(88.06%)	3,086,551(7.29%)	34,208,405(80.77%)	97.4	92.55	48.13
ckB6h_1	44,991,172	40,677,646(90.41%)	1,820,950(4.05%)	38,856,696(86.37%)	97.12	91.9	47.84
ckB6h_2	42,811,384	38,702,137(90.4%)	17,440,23(4.07%)	36,958,114(86.33%)	97.19	92.03	47.72
ckB6h_3	42,649,434	37,978,812(89.05%)	1,592,481(3.73%)	36,386,331(85.31%)	96.19	89.98	47.32

**Table S2. Primer sequences were used in the present study.**

Gene ID	Gene name	Forward sequence	Reverse sequence
<i>BraC02g018670</i>	<i>HSFA8</i>	GGTTACCGACACGAAGATGC	TGGTGGCTGCTGGTATGTTA
<i>BraC08g015400</i>	<i>HSP20</i>	ATCCGTTGGTCTCAGTCTCC	TCACAGTCAACACACCGTCT
<i>BraC05g048410</i>	<i>HSFA1E</i>	TGGGAATTTGCAAACGAGGG	CTCTTGGGTGAGGACGTTCT
<i>BraC02g029130</i>	<i>HIP1</i>	GGAGGAGGAGAGGGAGAAGA	TCTCTGCCTCTCTCAACAGC
<i>BraC09g060570</i>	<i>HSFA7B</i>	TGATGTCTTTCCTGAGGCGT	TCGTCGAGTTCCTTCTCCAC
<i>BraC06g001930</i>	<i>HSP26.5</i>	AAGCTGAGGTACGAGGTTCC	CACACCGTTCTTGAGTTCCG
<i>BraC10g002600</i>	<i>IAA10</i>	TGAAGCCTTGCGCAAAACAT	CAGTCTTTTCACGCACCCAA
<i>BraC01g041240</i>	<i>IAA19</i>	CGGAGCTGAGACTTGGACTION	CACCACCTGAGTTTTCACCG
<i>BraC05g001840</i>	<i>JAR1</i>	GCCGTCCAAAGTTTGTTCCT	TCTCATCCCGGCTTTGAAGT
<i>BraC01g011050</i>	<i>NPR1</i>	GCGGAGATCACATTCTGAAGG	CGCAAGTGGAACCTCAACA
<i>BraC04g029110</i>	<i>PYL4</i>	TTCAAGAAATCTCCGCCCT	GACATGCCTCTCGTCGTCTA
<i>BraC05g041370</i>	<i>TGA6</i>	GTTCCGCTCATCCGAACTTC	TGGCCATCTGACCCATGTAG