

Transcriptome analysis reveals differential gene expression in tomato under high-temperature stress

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Electronic Supplementary Material (ESM)

The authors are fully responsible for both the content and the formal aspects of the electronic supplementary material. No editorial adjustments were made.

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Table S1. Primers used for quantitative RT-PCR in this study

Gene ID	Gene name	Primers (5'-3')
<i>Solyc03g078400</i>	<i>SlActin</i>	F: CTCTACATACTTGAGAGGTGCC R: AGACGAGGAGAAAACATCACAA
<i>Solyc01g102960.3</i>	<i>HSP22.7</i>	F: TTCCCACAAGAAGACCCA R: TTTCCAATCTGAACGAGC
<i>Solyc02g020940.3</i>	<i>GAPA</i>	F: GGCATTCTCTCCGTCTGT R: CATACCAAGCAATAACCT
<i>Solyc03g083770.1</i>	<i>PMEI11</i>	F: AATCTCTCTCCGTTAGCCTCG R: ATGTCAAATCTCTTCCCCTC
<i>Solyc03g123410.1</i>	<i>ABP19A</i>	F: GGATTTGTTTCATCAGCA R: GAAGTCCAGGATTAGAGC
<i>Solyc05g056050.3</i>	<i>CAB6A</i>	F: TAGCCATAGCCTTTGTAG R: CCTTGACTTTGAGTTCCT
<i>Solyc07g066150.1</i>	<i>PSAG</i>	F: ACTCTTCCCTCTTCCTCAA R: CGCTACATTTTCTCTCTGG
<i>Solyc10g078770.2</i>	<i>LE25</i>	F: CGGAGAGGATGACGACGA R: TGGCACCATAACCAGTAG
<i>Solyc07g063410.3</i>	<i>JA2L</i>	F: CGGTAGAAAAGTCGGAATCA R: CCAGTTTTTCGTTGTAGGTTT
<i>Solyc06g066370.4</i>	<i>WRKY24</i>	F: GAGCCCACAAAACAGAATG R: GACCTTTTCTGCTCCCTTA
<i>Solyc01g100460.3</i>	<i>bZIP53</i>	F: AAGTGAGCAGATTACAGGGT R: ACAATCCTGATGAAGCAATA
<i>Solyc04g071770.3</i>	<i>ERF110</i>	F: GGCAGCAGAGATAAGAGA R: TTGTGGTAATAACCGAAC
<i>Solyc03g005570.3</i>	<i>MYB15</i>	F: GTCAGCAATAGCAGCAAG R: TCTGGTGAGTTAGGAGCA
<i>Solyc08g062960.4</i>	<i>HSF30</i>	F: TTACTCCTCATCACACCA R: CAACCACTACTTCCTCTG
<i>Solyc02g092460.3</i>	<i>BT4</i>	F: GAAGAAAAAATGAAGGAG R: ATGACAAACAAGGCTAAG

Table S2. RNA quality assessment

No.	Sample	Concentration (ng/uL)	OD260/280	OD260/230	Contents (μg)
1	R-0-1	747	2.18	2.45	29.90
2	R-0-2	453	2.16	2.15	18.10
3	R-0-3	505	2.11	2.23	20.20
4	R-24-1	888	2.15	2.38	35.50
5	R-24-2	812	2.09	2.35	32.50
6	R-24-3	781	2.19	2.26	31.20
7	S-0-1	715	2.12	2.38	28.60
8	S-0-2	764	2.14	2.39	30.60
9	S-0-3	752	2.09	2.37	30.10
10	S-24-1	596	2.16	1.97	23.80
11	S-24-2	434	2.14	2.30	17.40
12	S-24-3	858	2.03	2.43	34.30

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Table S3. Compare ribosome statistics

Sample	Clean reads	Mapped reads	Unmapped reads
R-0-1	41 283 548	411 404 (1.00%)	40 872 144 (99.00%)
R-0-2	39 764 382	450 710 (1.13%)	39 313 672 (98.87%)
R-0-3	38 630 240	298 144 (0.77%)	38 332 096 (99.23%)
R-0 _{means}	39 892 723	386 752 (0.97%)	39 505 971 (99.03%)
R-24-1	35 917 834	734 462 (2.04%)	35 183 372 (97.96%)
R-24-2	39 622 846	709 618 (1.79%)	38 913 228 (98.21%)
R-24-3	41 519 418	1 026 006 (2.47%)	40 493 412 (97.53%)
R-24 _{means}	39 020 033	823 362 (2.10%)	38 196 671 (97.90%)
S-0-1	39 156 818	358 184 (0.91%)	38 798 634 (99.09%)
S-0-2	36 486 080	236 650 (0.65%)	36 249 430 (99.35%)
S-0-3	41 248 076	367 706 (0.89%)	40 880 370 (99.11%)
S-0 _{means}	38 963 658	320 847 (0.82%)	38 642 811 (99.18%)
S-24-1	38 818 190	834 016 (2.15%)	37 984 174 (97.85%)
S-24-2	38 629 388	1 052 446 (2.72%)	37 576 942 (97.28%)
S-24-3	37 251 742	675 606 (1.81%)	36 576 136 (98.19%)
S-24 _{means}	38 233 107	854 023 (2.23%)	37 379 084 (97.77%)

Table S4. Summary of reads mapping to the reference genome

Sample	Total reads	Unmapped reads	Unique mapped reads	Multiple mapped reads	Total mapped reads
R-0-1	40 872 144	1 445 204 (3.54%)	37 988 430 (92.94%)	1 438 510 (3.52%)	39 426 940 (96.46%)
R-0-2	39 313 672	1 345 399 (3.42%)	36 485 509 (92.81%)	1 482 764 (3.77%)	37 968 273 (96.58%)
R-0-3	38 332 096	1 234 563 (3.22%)	35 754 065 (93.27%)	1 343 468 (3.50%)	37 097 533 (96.78%)
R-0 _{means}	39 505 971	1 341 722 (3.39%)	36 742 668 (93.01%)	1 421 581 (3.60%)	38 164 249 (96.61%)
R-24-1	35 183 372	1 388 793 (3.95%)	32 400 805 (92.09%)	1 393 774 (3.96%)	33 794 579 (96.05%)
R-24-2	38 913 228	1 497 938 (3.85%)	36 039 278 (92.61%)	1 376 012 (3.54%)	37 415 290 (96.15%)
R-24-3	40 493 412	1 397 209 (3.45%)	37 277 869 (92.06%)	1 818 334 (4.49%)	39 096 203 (96.55%)
R-24 _{means}	38 196 671	1 427 980 (3.75%)	35 239 317 (92.25%)	1 529 373 (4.00%)	36 768 691 (96.25%)
S-0-1	38 798 634	1 326 398 (3.42%)	36 072 938 (92.97%)	1 399 298 (3.61%)	37 472 236 (96.58%)
S-0-2	36 249 430	1 125 672 (3.11%)	33 632 848 (92.78%)	1 490 910 (4.11%)	35 123 758 (96.89%)
S-0-3	40 880 370	1 114 976 (2.73%)	38 250 794 (93.57%)	1 514 600 (3.70%)	39 765 394 (97.27%)
S-0 _{means}	38 642 811	1 189 015 (3.09%)	35 985 527 (93.11%)	1 468 269 (3.81%)	37 453 796 (96.91%)
S-24-1	37 984 174	1 630 684 (4.29%)	35 368 959 (93.11%)	984 531 (2.59%)	36 353 490 (95.71%)
S-24-2	37 576 942	1 393 167 (3.71%)	35 114 038 (93.45%)	1 069 737 (2.85%)	36 183 775 (96.29%)
S-24-3	36 576 136	938 511 (2.57%)	34 683 713 (94.83%)	953 912 (2.61%)	35 637 625 (97.43%)
S-24 _{means}	37 379 084	1 320 787 (3.52%)	35 055 570 (93.80%)	1 002 727 (2.68%)	36 058 297 (96.48%)

Table S9. AP2-EREBP transcription factor genes identified as differentially expressed

TF family	Gene ID	Description
AP2-EREBP	<i>Solyc01g090340.3</i>	ethylene-responsive transcription factor 1
AP2-EREBP	<i>Solyc01g090560.4</i>	ethylene-responsive transcription factor <i>ERF038-like</i>
AP2-EREBP	<i>Solyc01g095500.3</i>	pathogenesis-related genes transcriptional activator <i>PTI6</i>
AP2-EREBP	<i>Solyc01g108240.3</i>	ethylene-responsive transcription factor <i>ERF109</i>
AP2-EREBP	<i>Solyc02g077370.1</i>	pathogenesis-related genes transcriptional activator <i>PTI5</i>
AP2-EREBP	<i>Solyc02g092050.3</i>	AP2-like ethylene-responsive transcription factor <i>ANT</i> isoform X2
AP2-EREBP	<i>Solyc03g006320.1</i>	ethylene-responsive transcription factor 4-like
AP2-EREBP	<i>Solyc03g007460.3</i>	ethylene-responsive transcription factor <i>CRF4-like</i>
AP2-EREBP	<i>Solyc03g026280.3</i>	CBF1 protein
AP2-EREBP	<i>Solyc03g093560.1</i>	ethylene response factor 5
AP2-EREBP	<i>Solyc03g114440.1</i>	ethylene-responsive transcription factor <i>ERF071-like</i>
AP2-EREBP	<i>Solyc03g118190.4</i>	ethylene-responsive transcription factor <i>ERF114</i>
AP2-EREBP	<i>Solyc03g119580.1</i>	ethylene-responsive transcription factor <i>ERF118</i>
AP2-EREBP	<i>Solyc03g119800.3</i>	ethylene-responsive transcription factor <i>ERF043-like</i>
AP2-EREBP	<i>Solyc03g124110.2</i>	dehydration-responsive element-binding protein 1A
AP2-EREBP	<i>Solyc04g071770.3</i>	ethylene-responsive transcription factor <i>ABR1-like</i>
AP2-EREBP	<i>Solyc04g072900.1</i>	dehydration-responsive element binding protein 3
AP2-EREBP	<i>Solyc04g077490.3</i>	AP2-like ethylene-responsive transcription factor <i>ANT-like</i>
AP2-EREBP	<i>Solyc05g050830.3</i>	ethylene-responsive transcription factor <i>ERF038-like</i>
AP2-EREBP	<i>Solyc05g051200.1</i>	ethylene-responsive transcription factor 1
AP2-EREBP	<i>Solyc05g052040.1</i>	ethylene-responsive transcription factor 5
AP2-EREBP	<i>Solyc05g052050.1</i>	DNA-binding protein <i>Pti4</i>
AP2-EREBP	<i>Solyc05g052410.3</i>	ethylene-responsive transcription factor 1
AP2-EREBP	<i>Solyc06g050520.3</i>	dehydration responsive element binding protein
AP2-EREBP	<i>Solyc06g065820.3</i>	ethylene response factor 3-like
AP2-EREBP	<i>Solyc06g066390.3</i>	AP2-like ethylene-responsive transcription factor <i>At1g16060</i>
AP2-EREBP	<i>Solyc06g068360.3</i>	ethylene-responsive transcription factor <i>ERF003-like</i>
AP2-EREBP	<i>Solyc06g068570.4</i>	AP2-like ethylene-responsive transcription factor <i>At1g16060</i> isoform X3
AP2-EREBP	<i>Solyc06g075510.4</i>	AP2 transcription factor <i>SLAP2e</i>
AP2-EREBP	<i>Solyc06g082590.1</i>	pathogenesis-related genes transcriptional activator <i>PTI6</i>
AP2-EREBP	<i>Solyc07g054220.1</i>	ethylene-responsive transcription factor <i>ERF054</i>
AP2-EREBP	<i>Solyc08g007820.1</i>	dehydration-responsive element-binding protein 1E-like
AP2-EREBP	<i>Solyc08g078170.1</i>	ethylene-responsive transcription factor 1A-like
AP2-EREBP	<i>Solyc08g078180.1</i>	ethylene-responsive transcription factor 2
AP2-EREBP	<i>Solyc08g078190.2</i>	ethylene-responsive transcription factor
AP2-EREBP	<i>Solyc09g075420.3</i>	ethylene response factor 2
AP2-EREBP	<i>Solyc10g006130.1</i>	ethylene-responsive transcription factor 3-like
AP2-EREBP	<i>Solyc10g009110.1</i>	ethylene response factor 3
AP2-EREBP	<i>Solyc10g050970.1</i>	ethylene-responsive transcription factor <i>ERF109-like</i>
AP2-EREBP	<i>Solyc10g076370.3</i>	dehydration-responsive element-binding protein 2A-like
AP2-EREBP	<i>Solyc12g009240.1</i>	ethylene-responsive transcription factor <i>ERF017</i>
AP2-EREBP	<i>Solyc12g044390.3</i>	dehydration-responsive element-binding protein 3
AP2-EREBP	<i>Solyc12g056590.2</i>	ethylene-responsive transcription factor 2a isoform 2

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Table S10. MYB transcription factor genes identified as differentially expressed

TF family	Gene ID	Description
MYB	<i>Solyc01g057910.3</i>	transcription factor <i>MYB108-like</i>
MYB	<i>Solyc01g102340.3</i>	transcription factor <i>MYB35</i>
MYB	<i>Solyc02g079280.3</i>	transcription factor <i>MYB80</i>
MYB	<i>Solyc02g088190.4</i>	myb-related protein 306
MYB	<i>Solyc02g090400.4</i>	myb family transcription factor <i>EFM-like</i>
MYB	<i>Solyc03g005570.3</i>	myb-related protein Myb4
MYB	<i>Solyc03g093890.3</i>	R2R3MYB transcription factor 52
MYB	<i>Solyc03g119370.2</i>	transcription factor <i>MYB108-like</i>
MYB	<i>Solyc04g005710.3</i>	transcription factor <i>RAX3-like</i>
MYB	<i>Solyc05g007870.3</i>	R2R3MYB transcription factor 117
MYB	<i>Solyc05g009230.3</i>	transcription factor <i>MYB108</i>
MYB	<i>Solyc05g053330.3</i>	transcription factor <i>MYB108-like</i>
MYB	<i>Solyc06g005310.3</i>	transcription factor <i>MYB48-like</i>
MYB	<i>Solyc06g005330.3</i>	transcription factor <i>MYB48-like</i>
MYB	<i>Solyc06g069850.3</i>	myb-related protein 306-like
MYB	<i>Solyc06g083900.3</i>	myb-related protein Myb4-like
MYB	<i>Solyc07g054840.4</i>	protein ODORANT1-like
MYB	<i>Solyc08g065910.1</i>	transcription factor <i>MYB36-like</i>
MYB	<i>Solyc08g066190.2</i>	cyclin-D-binding Myb-like transcription factor 1
MYB	<i>Solyc08g068320.3</i>	myb-related protein 3R-1-like
MYB	<i>Solyc09g011780.3</i>	myb-related protein 315
MYB	<i>Solyc09g090130.3</i>	myb-related protein Myb4-like
MYB	<i>Solyc10g005460.3</i>	transcription factor <i>MYB3-like</i>
MYB	<i>Solyc10g044680.2</i>	transcription factor <i>MYB86-like</i>
MYB	<i>Solyc10g083900.2</i>	transcription factor <i>MYB48</i>
MYB	<i>Solyc11g071300.2</i>	myb-related protein 3R-1-like
MYB	<i>Solyc11g072060.3</i>	transcription factor <i>MYB36-like</i> isoform X1
MYB	<i>Solyc11g073120.2</i>	transcription factor <i>MYB48</i>
MYB	<i>Solyc12g049350.2</i>	transcription factor <i>MYB12-like</i> isoform X2

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Table S11. WRKY transcription factor genes identified as differentially expressed

TF family	Gene ID	Description
WRKY	<i>Solyc01g079260.4</i>	probable WRKY transcription factor 23
WRKY	<i>Solyc01g095100.4</i>	WRKY transcription factor 22
WRKY	<i>Solyc01g095630.3</i>	WRKY transcription factor
WRKY	<i>Solyc01g104550.3</i>	probable WRKY transcription factor 9
WRKY	<i>Solyc02g032950.3</i>	WRKY transcription factor 6
WRKY	<i>Solyc02g072190.4</i>	probable WRKY transcription factor 65 isoform X2
WRKY	<i>Solyc02g080890.3</i>	probable WRKY transcription factor 31 isoform X1
WRKY	<i>Solyc02g093050.3</i>	WRKY transcription factor IId-4
WRKY	<i>Solyc03g007380.2</i>	probable WRKY transcription factor 41
WRKY	<i>Solyc03g113120.4</i>	transcription factor <i>WRKY72</i>
WRKY	<i>Solyc03g116890.3</i>	probable WRKY transcription factor 40
WRKY	<i>Solyc04g078550.3</i>	probable WRKY transcription factor 7
WRKY	<i>Solyc05g012500.3</i>	probable WRKY transcription factor 57
WRKY	<i>Solyc05g015850.4</i>	probable WRKY transcription factor 75
WRKY	<i>Solyc05g055750.3</i>	probable WRKY transcription factor 26
WRKY	<i>Solyc06g066370.4</i>	WRKY transcription factor 33A
WRKY	<i>Solyc06g068460.3</i>	WRKY transcription factor 1
WRKY	<i>Solyc07g005650.4</i>	probable WRKY transcription factor 32
WRKY	<i>Solyc07g051840.4</i>	probable WRKY transcription factor 31
WRKY	<i>Solyc08g006320.4</i>	WRKY transcription factor IId-1
WRKY	<i>Solyc08g008280.3</i>	probable WRKY transcription factor 53
WRKY	<i>Solyc08g067340.4</i>	probable WRKY transcription factor 40
WRKY	<i>Solyc08g067360.3</i>	probable WRKY transcription factor 40
WRKY	<i>Solyc08g081610.4</i>	probable WRKY transcription factor 29
WRKY	<i>Solyc08g082110.4</i>	probable WRKY transcription factor 53
WRKY	<i>Solyc09g014990.4</i>	probable WRKY transcription factor 26
WRKY	<i>Solyc10g011910.4</i>	WRKY transcription factor 22-like
WRKY	<i>Solyc10g084380.1</i>	WRKY transcription factor 44
WRKY	<i>Solyc12g096350.2</i>	probable WRKY transcription factor 17

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Table S12. NAC transcription factor genes identified as differentially expressed

TF family	Gene ID	Description
NAC	<i>Solyc01g104900.3</i>	NAC domain-containing protein 104
NAC	<i>Solyc02g061910.1</i>	NAC domain-containing protein 101-like
NAC	<i>Solyc02g081270.4</i>	NAC domain-containing protein 86 isoform X1
NAC	<i>Solyc02g088180.3</i>	NAC2-domain containing protein
NAC	<i>Solyc03g097650.3</i>	NAC domain-containing protein 83
NAC	<i>Solyc03g115850.3</i>	NAC domain-containing protein
NAC	<i>Solyc04g005610.3</i>	NAC transcription factor 29
NAC	<i>Solyc04g009440.3</i>	NAC domain protein
NAC	<i>Solyc04g078670.3</i>	NAC domain-containing protein 19-like
NAC	<i>Solyc04g079940.3</i>	NAC domain-containing protein 19-like
NAC	<i>Solyc05g007770.3</i>	NAC transcription factor family protein
NAC	<i>Solyc06g060230.3</i>	Nam-like protein 1
NAC	<i>Solyc06g069710.3</i>	NAC domain-containing protein 100-like
NAC	<i>Solyc06g074170.3</i>	NAC domain-containing protein 40-like
NAC	<i>Solyc07g063410.3</i>	JA2-like
NAC	<i>Solyc07g063420.3</i>	NAC domain transcription factor
NAC	<i>Solyc07g066330.3</i>	NAC domain-containing protein 21/22 isoform X1
NAC	<i>Solyc10g083450.3</i>	NAC transcription factor 29-like
NAC	<i>Solyc11g008010.2</i>	NAM-like protein
NAC	<i>Solyc11g017470.2</i>	NAC domain-containing protein 2-like
NAC	<i>Solyc12g013620.2</i>	jasmonic acid 2

Table S13. BHLH transcription factor genes identified as differentially expressed

TF family	Gene ID	Description
bHLH	<i>Solyc01g086870.3</i>	transcription factor <i>bHLH130-like</i>
bHLH	<i>Solyc01g096370.4</i>	transcription factor <i>MYC2-like</i> isoform X2
bHLH	<i>Solyc01g098720.3</i>	transcription factor <i>bHLH96-like</i> isoform X2
bHLH	<i>Solyc01g102300.3</i>	transcription factor <i>PIF3</i>
bHLH	<i>Solyc01g109700.3</i>	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
bHLH	<i>Solyc02g078130.3</i>	transcription factor <i>bHLH55-like</i>
bHLH	<i>Solyc02g087860.3</i>	transcription factor style2.1
bHLH	<i>Solyc02g093280.2</i>	transcription factor SPATULA isoform X1
bHLH	<i>Solyc03g097820.2</i>	basic helix-loop-helix
bHLH	<i>Solyc03g118310.4</i>	transcription factor <i>ICE1-like</i>
bHLH	<i>Solyc03g119390.4</i>	transcription factor <i>BEE 3</i>
bHLH	<i>Solyc03g121240.1</i>	transcription factor <i>bHLH87</i>
bHLH	<i>Solyc04g007430.2</i>	transcription factor <i>PIF5-like</i> isoform X4
bHLH	<i>Solyc04g078790.3</i>	transcription factor <i>HEC2-like</i>
bHLH	<i>Solyc05g007210.2</i>	transcription factor <i>PRE6-like</i>
bHLH	<i>Solyc06g008030.3</i>	transcription factor <i>PIF1</i> isoform X1
bHLH	<i>Solyc08g062780.2</i>	transcription factor ABORTED MICROSPORES isoform X1
bHLH	<i>Solyc08g076820.3</i>	Hop-interacting protein THI018
bHLH	<i>Solyc09g097870.4</i>	transcription factor <i>bHLH62</i>
bHLH	<i>Solyc12g010170.2</i>	transcription factor <i>bHLH66-like</i>

Table S14. BHLH transcription factor genes identified as differentially expressed

TF family	Gene ID	Description
bZIP	<i>Solyc01g100460.3</i>	anaerobic basic leucine zipper protein
bZIP	<i>Solyc01g108080.4</i>	ABSCISIC ACID-INSENSITIVE 5-like protein 7
bZIP	<i>Solyc02g085610.4</i>	G-box binding protein isoform X1
bZIP	<i>Solyc02g092090.3</i>	bZIP transcription factor 2 [<i>Solanum lycopersicum</i>]
bZIP	<i>Solyc04g071510.3</i>	G-box-binding factor 4 isoform X1
bZIP	<i>Solyc04g081190.3</i>	transcription factor <i>VSF-1</i>
bZIP	<i>Solyc05g050220.3</i>	transcriptional activator TAF-1-like isoform X1
bZIP	<i>Solyc06g009640.2</i>	bZIP transcription factor 53-like
bZIP	<i>Solyc07g062710.4</i>	basic leucine zipper 61-like
bZIP	<i>Solyc08g061130.3</i>	transcription factor <i>HY5</i>
bZIP	<i>Solyc10g055550.3</i>	basic leucine zipper 23-like
bZIP	<i>Solyc10g078670.3</i>	transcription factor <i>TGA2-like</i>
bZIP	<i>Solyc10g080770.3</i>	TGACG-sequence-specific DNA-binding protein TGA-2.1
bZIP	<i>Solyc12g010800.2</i>	basic leucine zipper 34-like

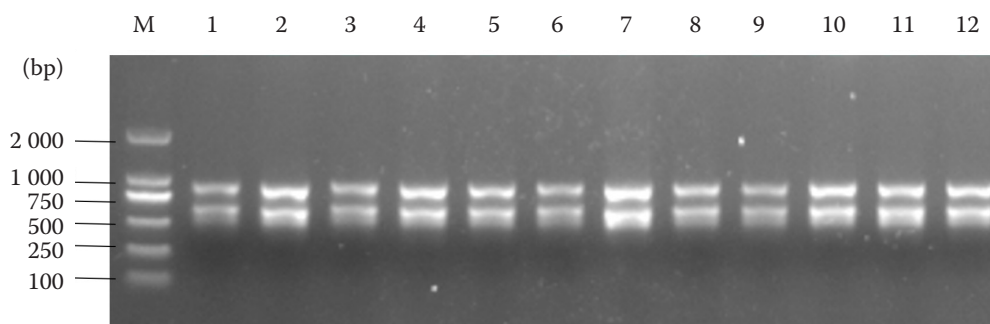


Figure S1. Agarose gel electrophoresis picture

M – Mark DL 2000; 1 – R-0-1; 2 – R-0-2; 3 – R-0-3; 4 – R-24-1; 5 – R-24-2; 6 – R-24-3; 7 – S-0-1; 8 – S-0-2; 9 – S-0-3; 10 – S-24-1; 11 – S-24-2; 12 – S-24-3

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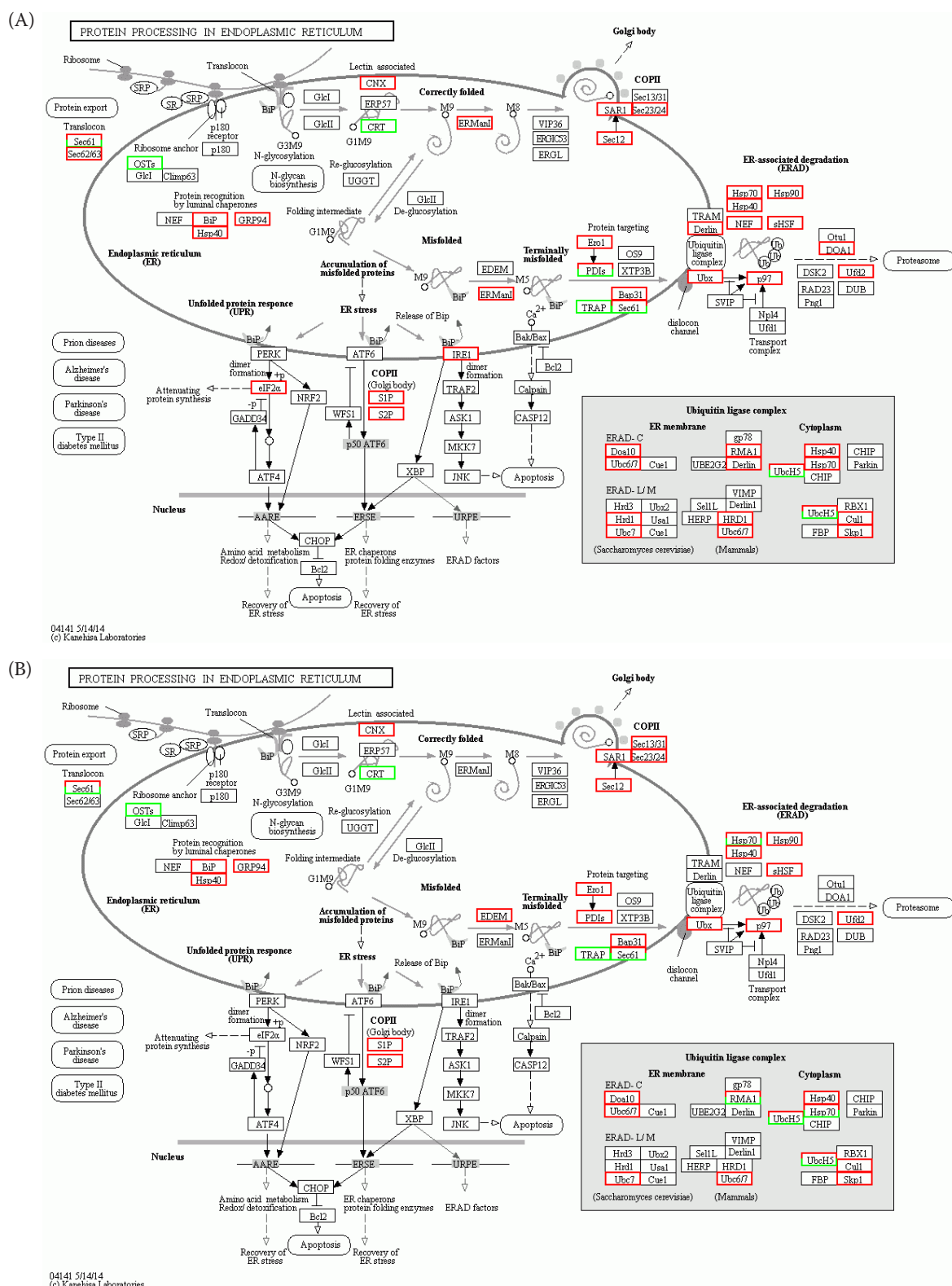


Figure S2. Protein processing in endoplasmic reticulum pathway: in the R-0 vs. R-24 comparison (A), in the S-0 vs. S-24 comparison (B)

R-0 – Hm 2-2 plants treated at 40 °C for 0 h; R-24 – Hm 2-2 plants treated at 40 °C for 24 h; S-0 – BY 1-2 plants treated at 40 °C for 0 h; S-24 – BY 1-2 plants treated at 40 °C for 24 h; red borders indicate up-regulated genes, green borders indicate down-regulated genes and black borders indicate non-changed genes

(A)

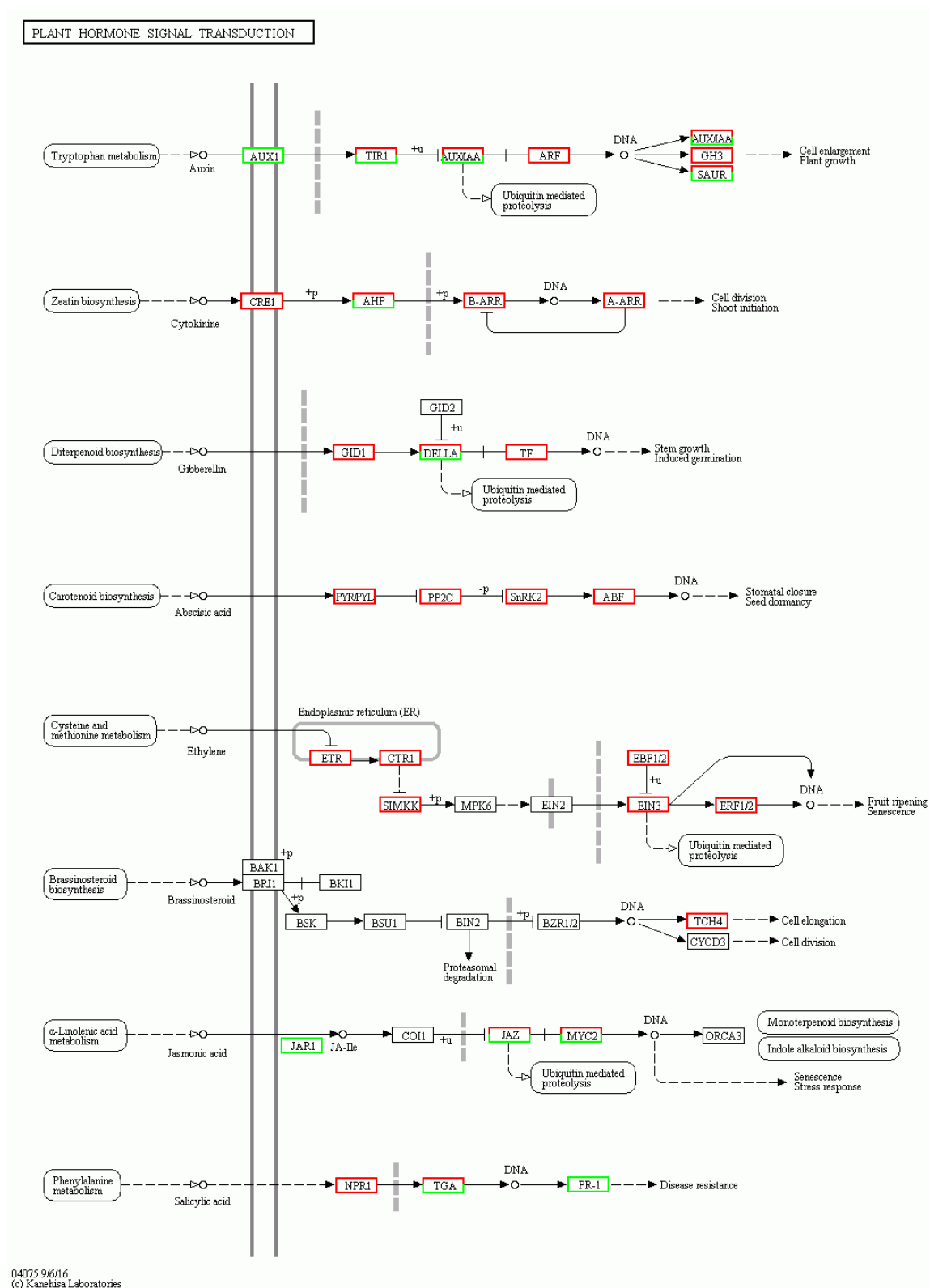
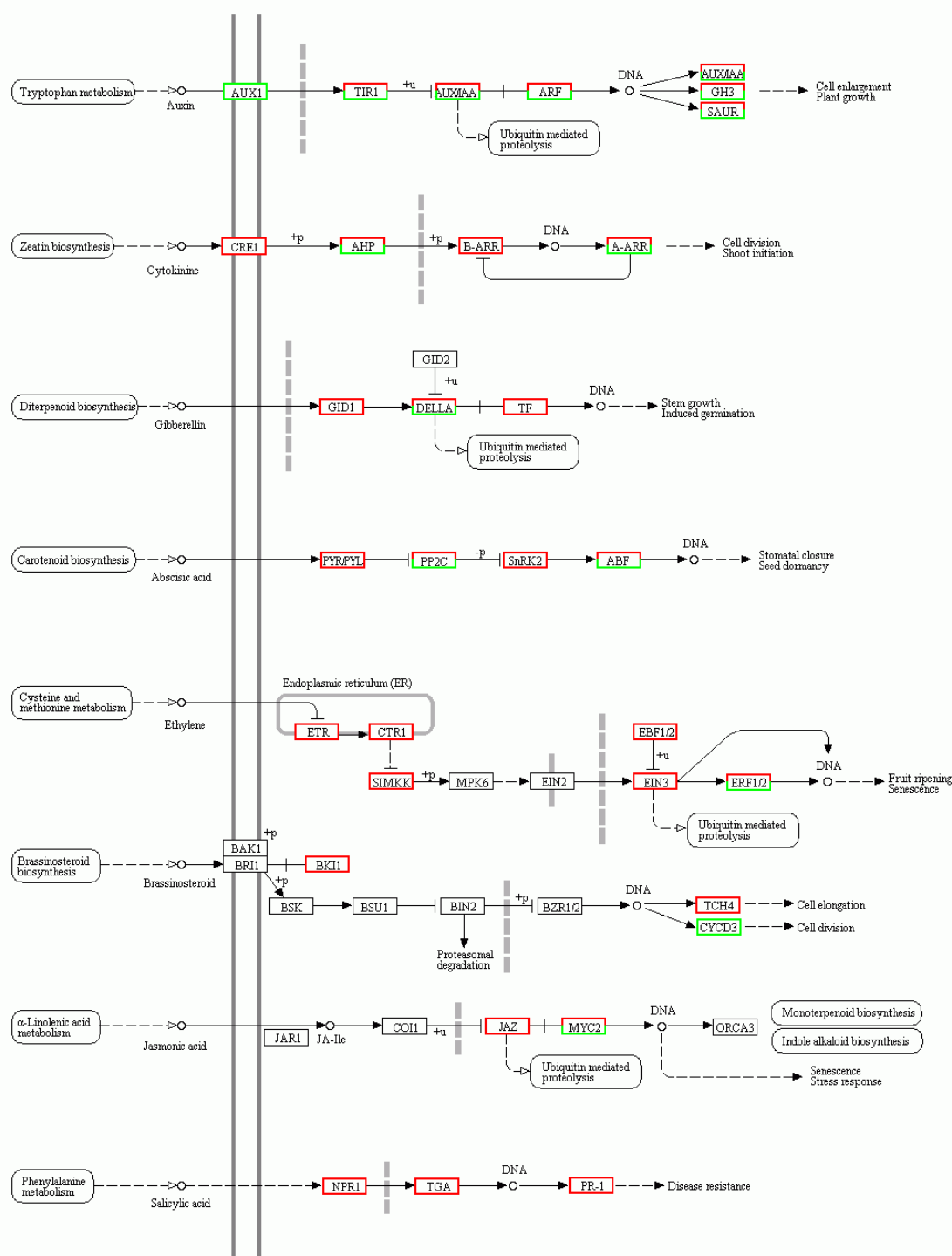


Figure S3 continues on the next page

<https://doi.org/10.17221/45/2025-CJGPB>

(B)

PLANT HORMONE SIGNAL TRANSDUCTION



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Figure S3. Plant hormone signal transduction pathway: in the R-0 vs. R-24 comparison (A), in the S-0 vs. S-24 comparison (B)

R-0 – Hm 2-2 plants treated at 40 °C for 0 h; R-24 – Hm 2-2 plants treated at 40 °C for 24 h; S-0 – BY 1-2 plants treated at 40 °C for 0 h; S-24 – BY 1-2 plants treated at 40 °C for 24 h; red borders indicate up-regulated genes, green borders indicate down-regulated genes and black borders indicate non-changed genes