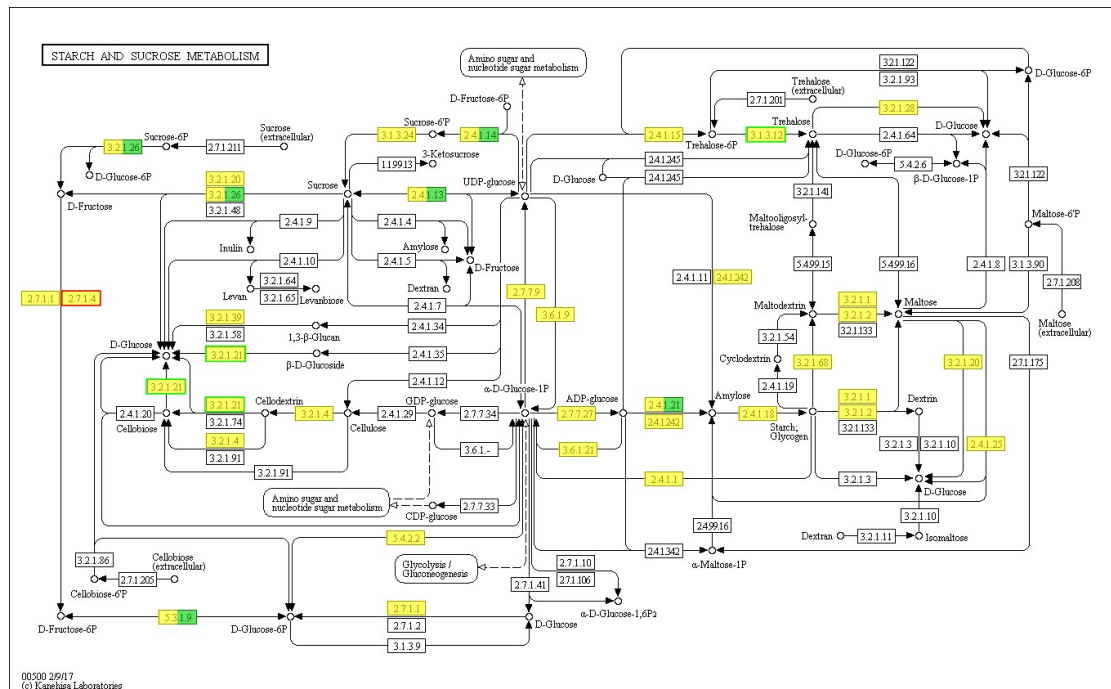


Supplemental datas



Supplement Figure S1. Schematic of starch and sucrose metabolism affected by high temperature in Zhu 1S. The red and green *squares* indicate starch and sucrose metabolism that were up-regulated or down-regulated by high temperature, respectively. The protein processing in starch and sucrose metabolism was prepared using the KEGG web service (www.genome.jp/kegg/).

Table S1. List of PCR Primers

Name	Primer sequences	Purposes
Os01g0816100F	CGAGGTCGACCTCTACAAGCTC	Q-PCR analysis of <i>Os01g0816100</i>
Os01g0816100R	GTCGCCTTCCAGTACCCTCT	
Os01g0826400F	GTCGTCCTTCTTCAACAGCCC	Q-PCR analysis of <i>Os01g0826400</i>
Os01g0826400R	CTCGTCCTTGCCGCCTTGAT	
Os02g0181300F	GTGCTCGTCGAGGAGGACTTCT	Q-PCR analysis of <i>Os02g0181300</i>
Os02g0181300R	ACCATGTCGCTGAACTGGCTCT	
Os02g0641300F	ACCAGAAGCTCCGCGACTAC	Q-PCR analysis of <i>Os02g0641300</i>
Os02g0641300R	TCATCACCGTCTCCTCCTCC	
Os03g0180900F	GGGGCAGCAGTTCACGATCT	Q-PCR analysis of <i>Os03g0180900</i>
Os03g0180900R	CTTCAGCGACGCCTTCCTC	
Os03g0182800F	AGAGTTTGGCCGTGTCATGTGT	Q-PCR analysis of <i>Os03g0182800</i>
Os03g0182800R	CGCCCCTGTACTTGCTCTTCTT	
Os03g0741100F	TCAGCCAGAGCTACGCCGA	Q-PCR analysis of <i>Os03g0741100</i>
Os03g0741100R	GATCTGGGCCTTCAGCTCCTC	
Os04g0470600F	TGGACGCCCGAGGAGGACAA	Q-PCR analysis of <i>Os04g0470600</i>
Os04g0470600R	AACTCGCCGTGCTTGAGGTCG	
Os05g0343400F	GCGACTTCTCCTTCCACACCA	Q-PCR analysis of <i>Os05g0343400</i>
Os05g0343400R	GCTCCCCCTTCACCTGCTTCT	
Os06g0649000F	AGGACTGCAAGCCCAAGGTCT	Q-PCR analysis of <i>Os06g0649000</i>
Os06g0649000R	CGCTGCACCTTCTTCTTACC	
Os06g0728700F	GTGCCTTGTGAACCAACAGTGATAG	Q-PCR analysis of <i>Os06g0728700</i>
Os06g0728700R	AACTGTCCTCCCAAATAGCTTCAA	
Os07g0615200F	GGGAGGCGGAGAGGAAGAA	Q-PCR analysis of <i>Os07g0615200</i>
Os07g0615200R	AACACGAGCACCTTCCCACCAT	
Os08g0157600F	ATAACCACCGTAGATTTAGGAGCAG	Q-PCR analysis of <i>Os08g0157600</i>
Os08g0157600R	TTCATCTTCTTCCTCCTTGCTAATC	
OsActin1F	CAATGTGCCAGCTATGTATGTCGCC	Q-PCR analysis of <i>OsActin</i>
OsActin1R	TTCCCGTTCAGCAGTGGTAGTGAAG	

Table S2. Preprocessing results of sequencing data quality

Sample	Raw reads	Clean reads	Clean bases	Valid bases (%)	Q30 (%)
Zhu1s-L1	45023554	44293650	6448062425	98.24	94.84
Zhu1s-L2	50405498	49703734	7251224961	98.32	94.95
Zhu1s-H1	49168698	48175496	6873422873	98.22	94.81
Zhu1s-H2	49223546	48268758	6900912964	98.08	94.44

Table S3. Differentially expressed genes involved in transcription factor in Zhu 1S under high temperature

Identifer	Fold-change (Zhu 1S-L/Zhu 1S-H)	P-value	Annotation
Os07g0139000	123.78	1.00E-02	Basic helix-loop-helix transcription factor bHLH
Os03g0180900	31.05	2.00E-03	TIFY family transcription factor OsTIFY11c
Os07g0684800	26.44	2.00E-04	NAC domain-containing protein 87
Os05g0163900	17.76	1.00E-03	Transcription factor bHLH107
Os03g0182800	13.31	1.00E-03	EREBP transcription factor OsEBP89
Os01g0246700	12.88	1.00E-03	WRKY transcription factor OsWRKY1
Os03g0745000	10.67	2.00E-03	Heat shock transcription factor OsHsfA2a
Os12g0123700	9	3.00E-04	NAC transcription factor OsNAC131
Os01g0826400	7.95	5.00E-03	WRKY transcription factor OsWRKY24
Os11g0126900	6.9	2.00E-06	NAC transcription factor OsNAC10
Os05g0343400	5	3.00E-02	WRKY transcription factor OsWRKY53
Os06g0649000	4.19	3.00E-03	WRKY transcription factor OsWRKY28
Os01g0868000	4	5.00E-01	EREBP transcription factor OsEREBP2
Os05g0322900	3.69	3.00E-03	WRKY transcription factor OsWRKY45
Os01g0159800	3.5	2.00E-04	Basic helix-loop-helix transcription factor bHLH107
Os02g0181300	3.46	4.00E-02	WRKY transcription factor OsWRKY71
Os01g0954500	3.3	2.00E-03	Lateral root primordium 1 OsLRP1
Os03g0741100	3.15	1.00E-03	Basic helix-loop-helix transcription factor OsbHLH148
Os02g0724000	3.06	2.00E-03	Constans-like gene DTH2
Os01g0816100	2.89	1.00E-03	NAC domain transcription factor OsNAC4
Os07g0674800	2.81	2.00E-03	Ethylene-responsive transcription factor RAP2-3
Os07g0615200	2.71	1.00E-02	TIFY family transcription factor OsTIFY10b
Os01g0693400	2.56	1.00E-03	AP2/ERF and B3 domain-containing protein
Os06g0298200	2.48	3.00E-03	CCT domain-containing protein OsCCT22
Os06g0728700	-3.69	1.00E-03	MYB transcription factor OsEPR1
Os04g0470600	-11.72	3.00E-02	MYB transcription factor OsMYB80
Os08g0157600	-12.96	2.00E-03	Circadian clock associated1 OsCCA1