

1 **Supplementary information**

2 **Supple. Table S1. The overview of PAS-Seq sequencing statistics.** CK, control condition; HT,
3 heat stress; LT, cold stress. UniqTag, unique tags of un-redundant reads. DUP, duplication level
4 calculated as the ratio of duplicated reads.

5 **Supple. Table S2. The statistics of reads mapping to the reference genome.** CK, control
6 condition; HT, heat stress; LT, cold stress. Input, the clean reads. End_A indicates the percentage
7 and number of reads after trimming the As at the end of reads, and the reads are further trimmed at
8 the start of reads (Start_A). End uniq mapped, the number and mapping rate of End_A reads to the
9 reference genome. Start uniq mapped, the number and mapping rate of Start_A reads to the reference
10 genome. Final PAS-reads, the reads after trimming of As for downstream analysis.

11 **Supple. Table S3. Distribution of number and percentages of polyA-site cluster (PAC).** CK,
12 control condition; HT, heat stress; LT, cold stress. For combined analysis, the PACs were filtered
13 with TPM ≥ 5 . For individual sample, the PACs were using threshold of TPM ≥ 3 .

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15 **Supple. Dataset 1.** The 50 bp upstream and downstream sequences of PACs detected under control,
16 cold and heat conditions.

17 **Supple. Dataset 2.** Identification of shifted PACs under heat stress.

18 **Supple. Dataset 3.** Identification of shifted PACs under cold stress.

19 **Supple. Dataset 4.** The 50 bp upstream and downstream sequences of PACs of shifted genes under
20 heat stress.

21 **Supple. Dataset 5.** The 50 bp upstream and downstream sequences of PACs of shifted genes under
22 cold stress.

23 **Supple. Dataset 6.** The enriched GO terms under heat and cold stresses.

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27 **Supple. Table S1. The overview of PAS-Seq sequencing statistics.** CK, control condition; HT,
28 heat stress; LT, cold stress. UniqTag, unique tags of un-redundant reads. DUP, duplication level
29 calculated as the ratio of duplicated reads.
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sampl e	raw	clean	clean_p er	uniqTag	raw_ba se	clean_ base	base_p er	Q20	Q30	GC	DUP
CK	3844213 4	2443912 7	63.57%	1458970 3 (59.7%)	5.77G	3.07G	53.31 %	89.98 %	80.31 %	32 %	78.30 %
HT	3668974 2	2338695 7	63.74%	1302608 5 (55.7%)	5.50G	3.07G	55.85 %	90.12 %	80.46 %	31 %	82.26 %
LT	4298341 2	2706941 2	62.98%	1598335 5 (59.05%)	6.45G	3.49G	54.13 %	89.83 %	79.89 %	33 %	78.77 %

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Supple. Table S2. The statistics of reads mapping to the reference genome. CK, control condition; HT, heat stress; LT, cold stress. Input, the clean reads. End_A indicates the percentage and number of reads after trimming the As at the end of reads, and the reads are further trimmed at the start of reads (Start_A). End uniq mapped, the number and mapping rate of End_A reads to the reference genome. Start uniq mapped, the number and mapping rate of Start_A reads to the reference genome. Final PAS-reads, the reads after trimming of As for downstream analysis.

Sample	Input	End_A	Start_A	End uniq mapped	Start uniq mapped	total merged uniq mapped	Final PAS-reads
CK	24439127	9945011 (40.69%)	436622 (1.79%)	5325224 (53.55%)	183495 (42.03%)	5484086 (55.14%)	4902037 (49.29%)
HT	23386957	8935917 (38.21%)	390980 (1.67%)	4370962 (48.91%)	148518 (37.99%)	4500543 (50.36%)	3909828 (43.75%)
LT	27069412	10187140 (37.63%)	427362 (1.58%)	5261676 (51.65%)	177236 (41.47%)	5415587 (53.16%)	4824585 (47.36%)

Supple. Table S3. Distribution of number and percentages of polyA-site cluster (PAC). CK, control condition; HT, heat stress; LT, cold stress. For combined analysis, the PACs were filtered with TPM ≥ 5 . For individual sample, the PACs were using threshold of TPM ≥ 3 .

Sample	tts_down_1000	5'UTR	3'UTR	CDS	Introns	Intergenic	Antisense
CK	4445 (11.18%)	243 (0.61%)	27568 (69.36%)	1011 (2.54%)	2033 (5.11%)	3606 (9.07%)	842 (2.12%)
HT	4314 (11.49%)	260 (0.69%)	24176 (64.38%)	978 (2.60%)	2643 (7.04%)	3640 (9.69%)	1543 (4.11%)
LT	4614 (11.69%)	207 (0.52%)	27212 (68.92%)	901 (2.28%)	2065 (5.23%)	3593 (9.10%)	889 (2.25%)
Combined analysis	3180 (12.68%)	304 (1.21%)	15631 (62.34%)	860 (3.43%)	1754 (7.00%)	1813 (7.23%)	1533 (6.11%)