Table S1 Information for the Primer used in this study.

Gene Name	Gene ID	Primer sequence (5'→3')
POD1	VaccDscaff2-processed-gene-374.3	F: AAATTCGCGGCAAAAGGACT R: TGTGAAGAAGGACGTGTCGA
POD2	VaccDscaff34-snap-gene-283.23	F: GCTTCCAGTCTCAGTTCCCT R: GGTGACGTCGAGAGGAGAAA
TPP	VaccDscaff20-snap-gene-26.33	F: TGCACAAGTATCCCTCAGCA R: TCCATCCCATGACTACCAGC
TLP	VaccDscaff43-snap-gene-245.31	F: GCTGAATATGCGCTGAACCA R: ACGGGTTGTTACATCCACCT
FAD	VaccDscaff11-snap-gene-249.30	F: TTGGGCCATTAGAGGAGGTG R: TGCATCAATGGGAGGAGTGT
LTP	VaccDscaff22-snap-gene-75.28	F: CTTCAACACAAGCAGTCCCC R: CTTGGATGCAGTCTTGAGGC
WRKY	VaccDscaff6-augustus-gene-310.35	F: GATCAAGCCCTCCTCCTCTC R: GCTCCCTCACTTTCCTCCTT
ASR	VaccDscaff15-augustus-gene-376.34	F: AGAAAGACCCAGAGCATGCT R: AGAGGTGGTGGTGCTTCTTT
DREB1D	VaccDscaff33-snap-gene-267.37	F: TACTCGACGCTGACTCATCC R: CGTCGGAGGGAGATTCTTGT

Supplemental Table S2 The quality indicators of transcriptome sequencing data

Sample	Read Sum	Base Sum	GC (%)	Q20 (%)	Q30 (%)	Mapped Reads
CK-WW-1	28549842	8538263712	45.84	98.38	95.16	51674156 (90.50%)
CK-WW-2	22780725	6814516416	45.79	98.3	94.94	41420757 (90.91%)
CK-WW-3	25929818	7760535444	45.67	98.16	94.46	46995505 (90.62%)
CK-DS-1	26594189	7958144192	45.82	98.38	95.16	46816502 (88.02%)
CK-DS-2	20887029	6249853306	45.84	98.2	94.63	36677289 (87.80%)
CK-DS-3	21076960	6294267870	45.69	98.53	95.61	37311598 (88.51%)
PI-WW-1	29132120	8716470946	45.8	98.22	94.64	53088429 (91.12%)
PI-WW-2	29291282	8761916396	45.85	98.26	94.8	53320173 (91.02%)
PI-WW-3	26770996	8008436584	46.03	98.13	94.49	48618186 (90.80%)
PI-DS-1	21458148	6424147982	46.14	98.53	95.56	38670069 (90.11%)
PI-DS-2	23317101	6978661152	45.92	97.82	93.56	41858439 (89.76%)
PI-DS-3	25851549	7733423848	46.01	98.4	95.15	46414126 (89.77%)