

A rapid transcriptional activation is induced by the dormancy-breaking chemical hydrogen cyanamide in kiwifruit (*Actinidia deliciosa*) buds

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Supplementary Material

Supplementary Table S1 & Figures S1-S4

**Table S1:** List of PCR primers used, product size and unique identifier for each gene.

GenBank No.	Top blast hit	Forward primer sequence	Reverse primer sequence	Product size	Unique ID <sup>1</sup>
FG471021	ABC transporter	TGGTTGGGTCCTCATCTTCT	CAGAGGGGCTATGGTTTCTT	163	238017
FG473412	ABC transporter	TGCAGATGTTTTCCAAGCAG	TGATCACTGCATCGGATGTT	155	199232
FG440519	Actin	CCAAGGCCAACAGAGAGAAG	GACGGAGGATAGCATGAGGA	197	197478
FG466527	AdADH1	CATCCCTCCGTAGTCGAAA	TTCCTTCATGCTGATGATGC	148	194711
FG525579	AdADH2	TCGAGTACATGCTGAAAGGAGA	CACCAGCAAACACTGAAAAG	153	297810
FG458399	AdCatalase1	GGTGGTGTAAACCCTGGATG	AAAAGTCACGCCATGCAACT	143	319700
FG511122	AdCDKB1	TTCGGCAAAGAAAGCTATGG	TATCCTAATGGGACGCCAAA	134	299318
FG471388	5'-adenylylsulfate reductase	GGTGGCTTTTGTGAATGCTC	TGCACCTCTGTCCTTCTCTGT	143	195011
FG521122	AdGDBRPK1	GCAGCGGAGAAATCGTCTAC	AACAGAGTGGAAGGAAGCA	154	310648
FG475975	AdPDC	TGGACGACTAAGGTGCACTG	TAGCAGCAGCGAGAAGGATT	204	230204
FG473154	Brassinosteroid signalling	GAATGCTCGGGAGAAAAGGT	GGGCTCACCTCAATCACTGT	105	198972
FG474406	CBS domain-containing protein	TGAAGAAGAGGAAGCTGTTGG	AAACCAGCGTCGTCATGAAT	118	200316
FG471167	Cinnamyl-alcohol dehydrogenase	TAGTACCTCCCCTGGCAAGA	GGAGAGGGTGTGTGCTGAT	146	195091
FG478690	Curculin-like (mannose binding) lectin	TCAAGGTGTTGGATTGCGTA	GAAACCCTTCACCAGCATTC	190	241940
FG497462	DNAJ heat shock protein	CGCAACTTCATCGAGATTCA	ATTGTTTGTGCCGGTGATTT	203	304399
FG486662	Embryo-abundant protein	AATACAAATGCACCCCTCCA	AGGAGCCATTTGACTTGGTG	145	249883
FG479502	ERF/AP2 transcription factor	TCGTCCTCTGTGGTTGATTG	TCCGTCGACATGTCAAGATT	108	242757
FG459066	Expressed protein	TCCTGCTGCTACTGGTCTTG	GACTCTGATTGGGTGGTCGT	169	192836
FG475773	Expressed protein	GAAGAAGAAAGGCGGGTTTT	CGAACCCTTGTAGACATCACC	126	206599

FG512494	Expressed protein	TTGCACCATGGAGGTCAATA	GGGGACAATAGCATCAAACC	149	316318
FG470652	FAD-binding protein	ACTTTGCCTTCATGGTGGAC	GCACCGATTCAATATCTCTGG	122	240862
FG402777	F-box protein	TTGGAGGAACAAGGGTTTTG	TGCAACTTGTGACAGACATCA	125	158295
FG471302	Galactinol synthase	TTGTGCTGCTGGATCGAAG	TGAACAACACTTTAGCCTATGCTCT	242	194925
FG423204	Glutathione <i>S</i> -transferase	CTCAAGTTTCAAGCCCTTCG	TGAGATGGGAAGTTGTCCTTG	129	168251
FG523871	Glutathione <i>S</i> -transferase	TGCTGAAGCAGAAGTTTGGA	AGTGTCCACAGGGAACAACAC	100	313564
FG526647	Glycoside hydrolase	CGGGATGTGTGATTTTCCTC	GCATGGATGGCTTTGATACA	163	314813
FG526418	Glycosyltransferase	GAAGGATTTGGCCAAGGAAG	CACGAAAGACAAATCAAACCA	145	299752
FG460267	In2-1 protein	GTCAATTCAGTCTGGTAGACATTGC	CTGGGGCATTCAATTTCACTAC	230	243648
FG474947	LEA protein	GGTGGTGCCGGTTACAATTA	ACTCGGGGGTACCGAAAATA	186	202743
FG498083	Magnesium/proton exchanger	GTCGTGTTGTCTCCCTTAAA	CCCGCAGGGAATACAATACA	127	305021
FG470796	Myb transcription factor	ACAACCGACAATTTGTGGAA	CCACAATAATTAACTTTTCCTTCA	144	238243
FG510928	NF-X1-like zinc finger protein	CGGACTGGATGAACGAAGTC	TCCAGGTCCAGACAGAAAAA	201	299124
FG456774	Not determined by homology	GCCAATAATTTCTCCCACA	GAATTCCTAATTGAAGAGGCTCA	202	189927
FG508405	Ovule development protein	TGGTTGTACTGCGTCGGTTA	CACTTGGCCATTGTTATGGT	127	278316
FG477785	Protein kinase	TACACGACATAGCGGACGAA	CGATAAGGGAGTCGGTTCTT	162	232101
FG446808	SAM:carboxyl methyltransferase	CGGGCTTGAAGGAATTTTAA	GGATGAGACCAGACCACTTGA	179	107699
FG479735	Secretory protein	AAGTGGGTTTGTGGCAGAAC	ACACAGTTGTGCCATCGTCT	201	193221
FG491038	Wound-responsive protein	CCTCTTCGGTGATGGCTAAA	CTACAGCCCATATTGCAAGC	164	272022
FG511957	Zinc finger protein	GCTAACAGTTTTCCCCAGCA	CAAATTCAGCTCCGGTAGGA	134	314160

<sup>1</sup>The unique identifier is the number of the EST that is used for microarray oligonucleotide design.

**Fig. S1.** Expression profiles of genes selected that showed Profile 1 pattern of expression when analysed by qPCR over the extended time course (Day -1 to Day 42).

**Fig. S2.** Expression profiles of genes selected that showed Profile 2 pattern of expression when analysed by qPCR over the extended time course (Day -1 to Day 42).

**Fig. S3.** Expression profiles of genes selected that showed Profile 3 pattern of expression when analysed by qPCR over the extended time course (Day -1 to Day 42).

**Fig. S4.** Expression profiles of genes selected that did not fit into Profiles 1, 2 or 3 when analysed by qPCR over the extended time course (Day -1 to Day 42).

Fig. S1

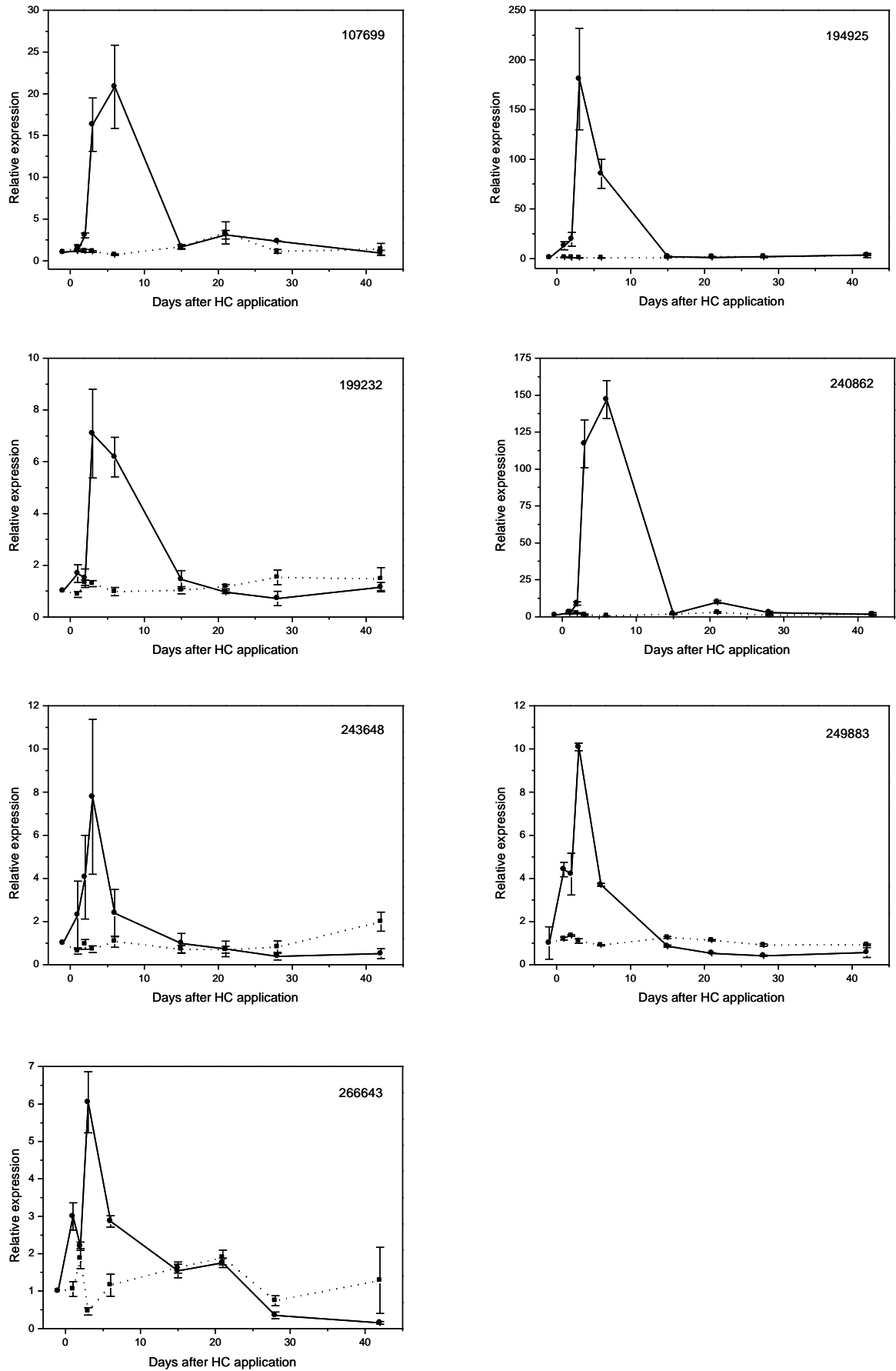
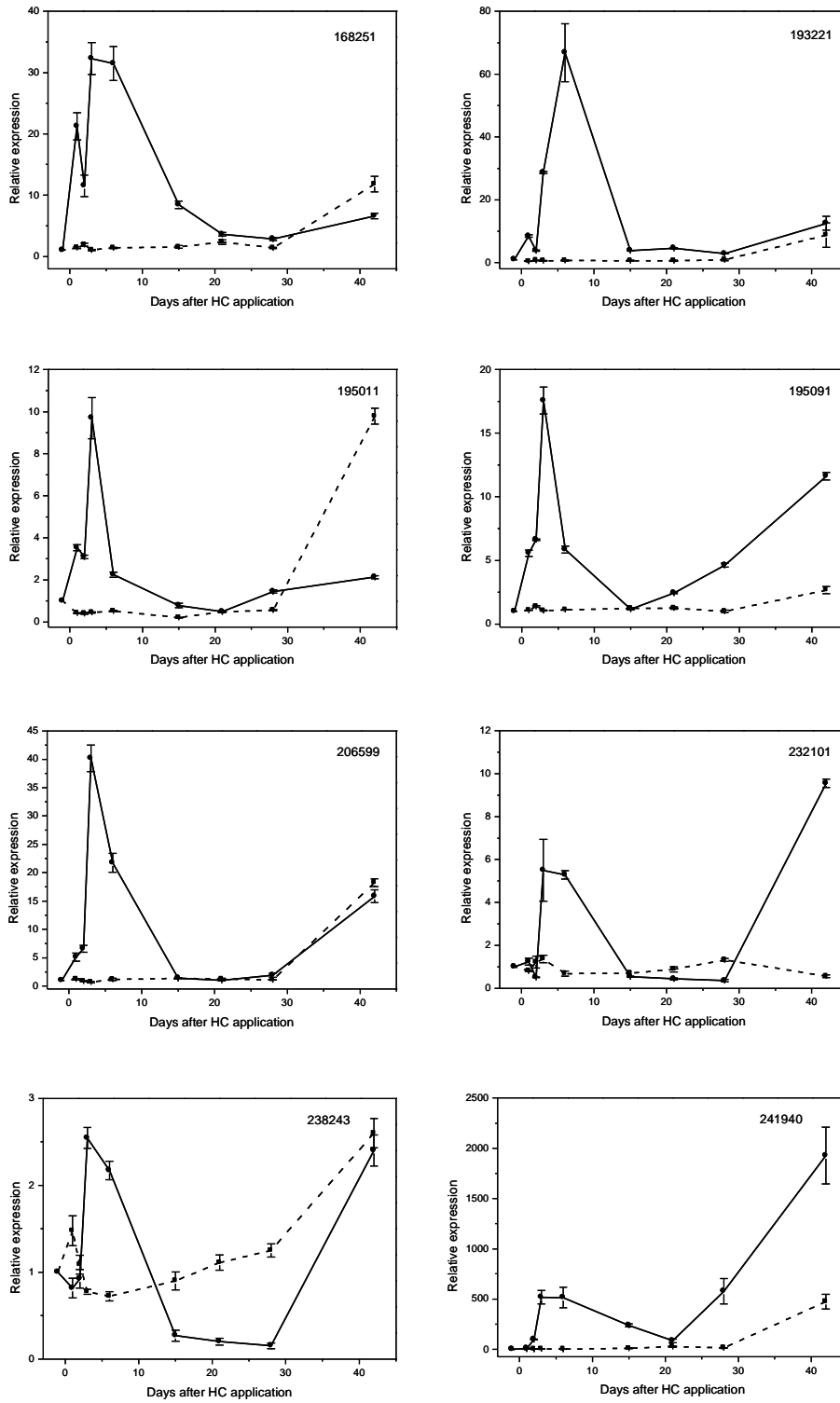


Fig. S2



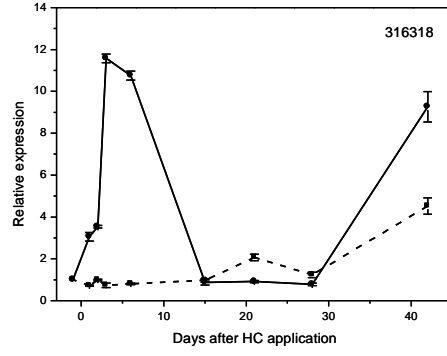
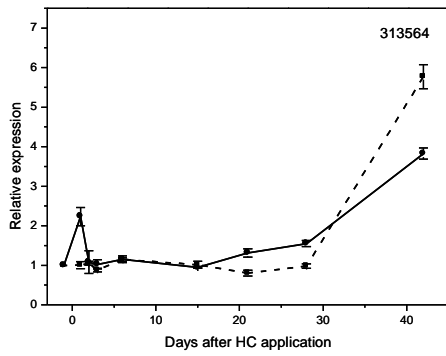
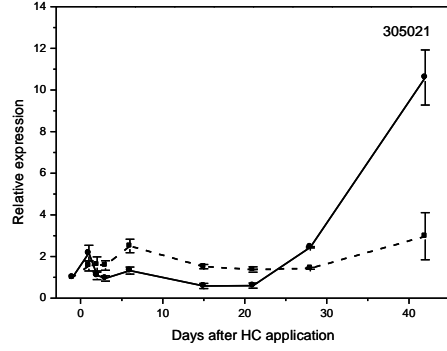
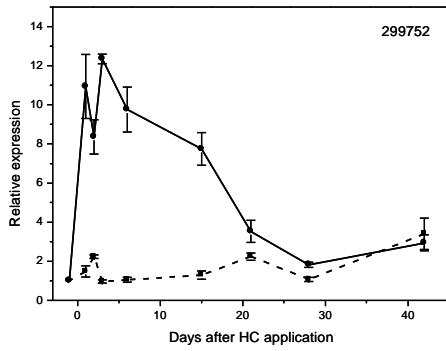
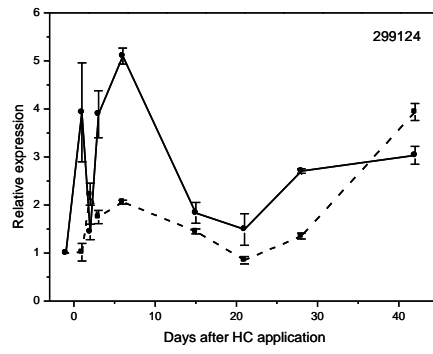
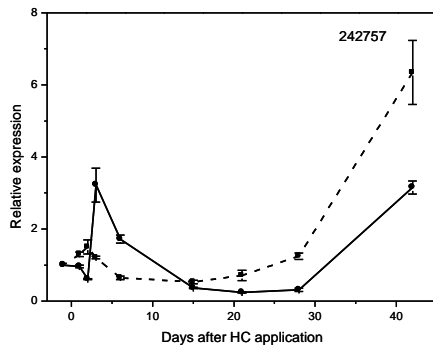


Fig. S3

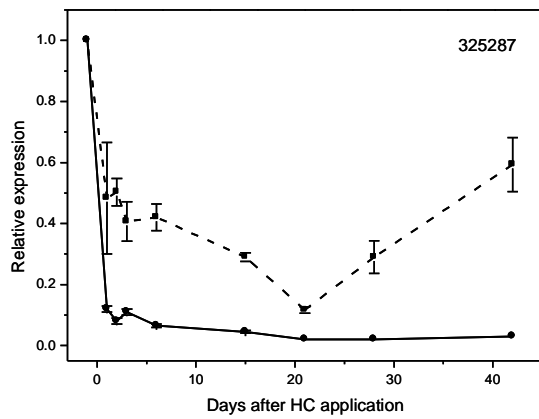
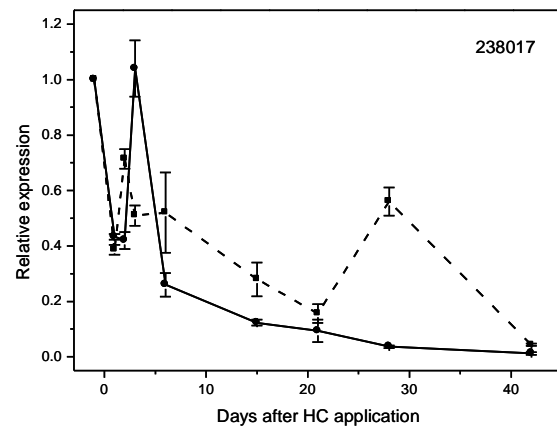
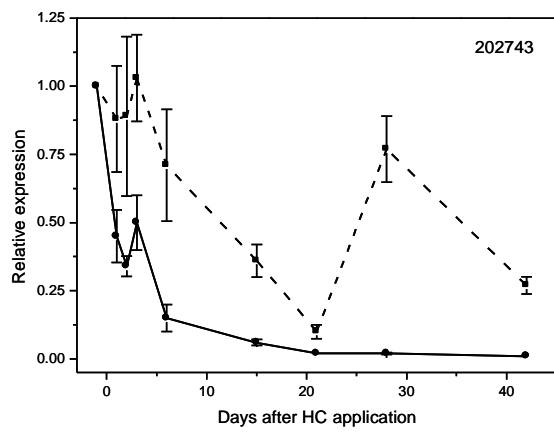
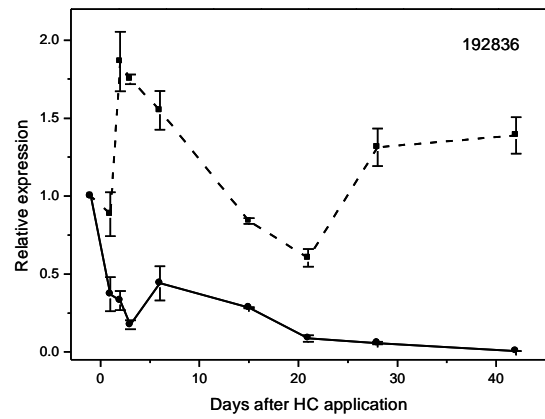
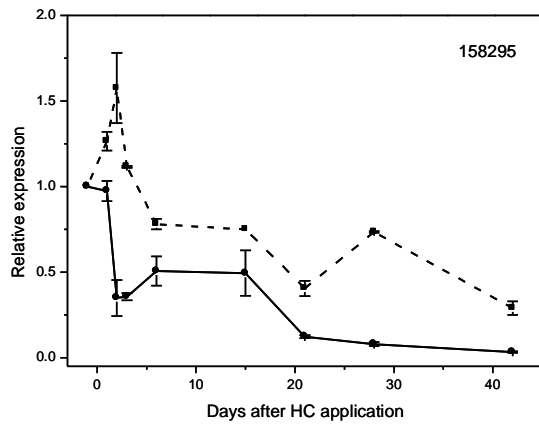




Fig. S4

