

Table S1: List of upregulated candidate DAPs of apples in response to storage days and treatment.

Protein ID	Protein name	Fold Change (Base vs Control Day 3)	Fold Change (Base vs Control Day 6)	Fold Change (Base vs Control Day 10)	Fold Change (Base vs AEW Day 3)	Fold Change (Base vs AEW Day 6)	Fold Change (Base vs AEW Day 10)	Fold Change (Base vs ALEW Day 3)	Fold Change (Base vs ALEW Day 6)	Fold Change (Base vs ALEW Day 10)
Defense response										
Q4VPI0	Major allergen Mal d 1.03F	Not detected	0.00	13.18	Not detected	0.00	1.05	Not detected	0.00	0.53
Q941P6	Mal d 1.0109	0.00	5.32	19.97	0.00	2.68	1.13	0.00	4.00	1.17
A0A498HBZ1	BZIP domain-containing protein	0.01	8.88	13.54	0.01	7.55	1.10	5.60	8.44	0.82
J9PZB2	Dehydrin 9	1.91	0.00	21.28	0.20	8.66	1.34	3.62	0.00	1.11
A0A498HFI4	BRO1 domain-containing protein	1.36	52.85	46.45	2.68	72.65	1.64	4.00	51.53	0.13
A0A498HRC7	Syntaxin 6 N-terminal domain- containing protein	0.00	5.48	0.33	0.00	5.23	-0.54	0.00	5.28	0.29
A0A498JZC0	Uncharacterized/Cytochrome P450	0.04	6.64	19.84	1.36	4.57	0.91	2.68	4.95	1.08
ATP binding										
A0A498IFG8	Diadenosine tetraphosphate synthetase	0.68	0.00	63.41	2.34	0.00	1.55	1.34	0.00	0.13
A0A498K274	Uncharacterized protein	0.00	0.04	21.25	0.00	0.04	1.37	0.00	2.68	1.00
A0A498JWP0	Peptidase M16C associated domain- containing protein	2.14	46.24	0.16	2.67	40.96	-0.51	0.54	38.32	-0.05
A0A498HWF0	Uncharacterized protein	0.97	0.00	11.23	1.56	0.00	1.08	1.41	0.00	-0.71
Fatty acid biosynthesis										
A0A498KTG5	Oxoglutarate dehydrogenase (succinyl- transferring) (EC 1.2.4.2)	6.65	2.68	0.02	10.63	1.36	-1.68	7.32	1.36	0.16
A0A498KUG9	PKS ER domain-containing protein	0.96	0.00	0.01	1.46	0.00	-1.85	1.54	0.00	-0.34
Glycolysis / Gluconeogenesis										
Q45TX6	1,4-alpha-glucan branching enzyme Uncharacterized/ UDP-	1.79	7.99	10.20	0.01	11.09	1.21	2.67	11.09	0.43
A0A498J662	glycosyltransferases domain-containing protein	0.00	1.35	0.68	0.00	5.33	0.67	0.00	10.63	1.14
A0A1Z1GDX9	Glycosyltransferase (EC 2.4.1.-)	1.33	103.01	0.25	2.08	117.53	-0.90	1.38	0.00	0.04
Amino acid metabolism										
A0A498HW02	Methylenetetrahydrofolate reductase	1.23	0.04	0.01	1.40	0.04	-0.46	1.37	0.04	0.00
Isoprenoid biosynthesis										
A0A498K4Z1	HMG-CoA synthase (EC 2.3.3.10)	0.89	25.89	27.88	1.34	22.57	1.54	1.12	29.87	0.86
Proton transport										
A9X9A3	H(+)-exporting diphosphatase (EC 7.1.3.1)	0.00	31.20	4.44	0.00	33.85	0.35	0.00	41.15	0.93
Q9M6R1	High molecular weight heat shock protein	0.00	0.46	0.00	1.57	1.34	0.00	1.32	0.90	-0.87

Energy										
A0A223A9T0	Photosystem I P700 chlorophyll a apoprotein A2 (EC 1.97.1.12) (PsaB)	0.63	0.00	4.15	1.19	0.00	0.63	1.16	0.00	-0.13
Protein synthesis										
A0A498HT82	40S ribosomal protein S3	No detection	19.84	No detected	No detected	47.56	No detection	No detected	17.20	No detected
Transport and cell structure										
A0A498INY5	Tubulin alpha chain	0.89	25.71	10.43	0.00	28.81	1.05	1.78	27.03	0.76
A0A498HCI5	Uncharacterized protein	1.21	32.52	1.35	1.70	32.52	0.13	1.58	39.82	-0.17