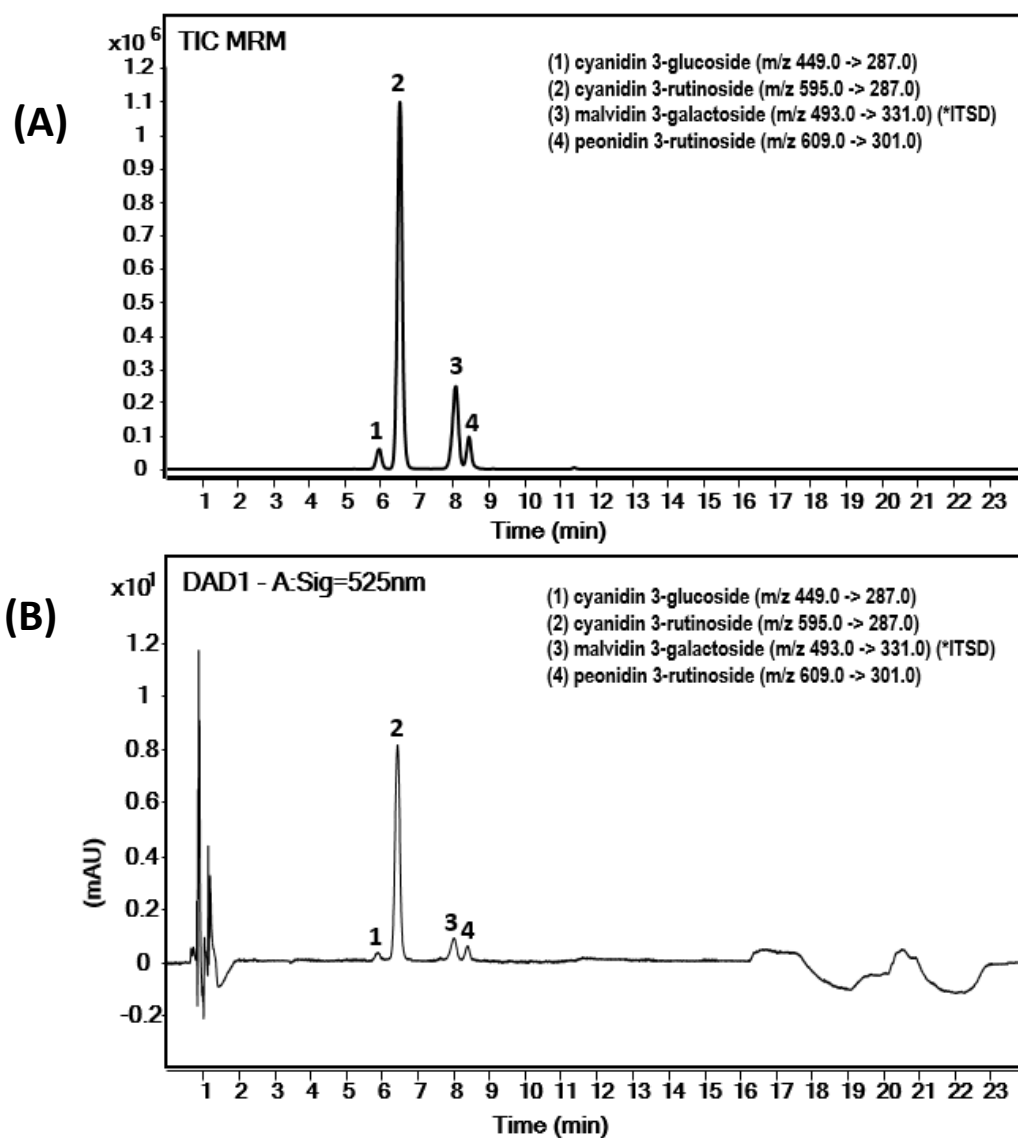
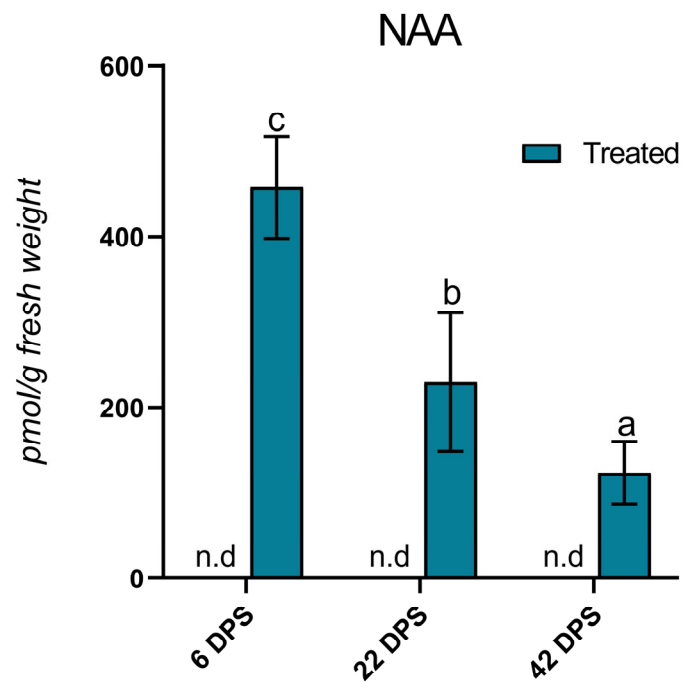


## Supplementary Material



**Figure S1.** (A) LC-MS/MS MRM and (B) UV chromatograms of detectable anthocyanins found within the Sweet Georgia cherry variety and the anthocyanin used as an internal standard (malvidin 3-galactoside). TIC MRM: total ion chromatogram multiple reaction monitoring, DAD: diode array detector, mAU: milli-absorbance unit.



**Figure S2.** LC-MS/MS analysis of 1-naphthaleneacetic acid (NAA) concentration in sweet cherry (*Prunus avium* L.) fruit at three timepoints after the pre-ripening application of 100 mg/L NAA. All data represent means  $\pm$  s. e. ( $n = 3$ ), letters represent significant statistical differences of the mean values of NAA-treated samples from the mean values of control samples. n.d = not detected.

**Table S1.** Anthocyanin compounds, transitions, fragmentor and collision energy voltages used in LC-MS/MS analysis.

Compound	GasTemp (°C)	GasFlow (L/min)	Nebu- lizer (psi)	Sheath Gas Heater (°C)	Sheath Gas Flow (L/min)	Capillary (V)	Charging (V)	Precursor Ion MS [M-H] +	Product Ion MS/MS	Frag- mentor (V)	Colli- sion En- ergy (eV)
Peonidin 3- rutinoside	230	20	40	300	12	3000	500	609.0	301.0	166	22
Cyanidin 3- rutinoside	230	20	40	300	12	3000	500	595.5	287.0	166	22
Malvidin 3- galactoside	230	20	40	300	12	3000	500	493.0	331.0	166	22
Cyanidin 3- glucoside	230	20	40	300	12	3000	500	449.0	287.0	166	22

**Table S2.** LC-MS/MS run parameters, transitions, fragmentor and collision energy voltages of hormone compounds detectable in Sweet Georgia cherry.

Com- pound	Gas- Temp (°C)	GasFlo w (L/min)	Nebu- lizer (psi)	Sheath Gas Heater (°C)	Sheath Gas Flow (L/min)	Capil- lary (V)	Charging (V)	Precursor Ion MS [M-H] -	Product Ion MS/MS	Fragmen- tor (v)	Collision Energy (eV)
ABA	300	8	35	350	11	2000	1200	263.1	219.1	86	12
ABA-GE	300	8	35	350	11	2000	1200	425.2	263.0	100	4
DPA	300	8	35	350	11	2000	1200	281.1	237.0	100	8
PA	300	8	35	350	11	2000	1200	279.1	205.1	106	12
ACC	300	8	55	350	11	3500	500	102.1	61.1	58	4
IAA	300	8	55	350	11	3500	500	176.1	144	68	4
IAA-Asp	300	8	55	350	11	3500	500	291.1	176.2	78	8

**Table S3.** Gene-specific qPCR primers, with PCR product sizes in base pairs and optimal acquisition temperatures for the genes analysed.

Gene	Forward Primer (5'-3')	Reverse Primer (5'-3')	Amplicon bp	Acquisition Temperature °C
<i>CHS1</i>	CAGGAGATGGACTGGATTGG	CGAAC- GAAACAGATGCATAAAA	148	77
<i>CHS3</i>	ATGTCGAGTGCTTGTGTGCTG	TACACCATGATGCATCTGGAAG	285	78
<i>LDOX</i>	CGAG- TATGCTAAGGAACTGAGG	TGAGGGCAAACCTGGGTAGTAG	156	78
<i>UFGT</i>	TGTTGAGGATGGGGTTTTTAC	AG- TACAGCTCGGTTATTCTTATGC	243	80
<i>DFR</i>	CTTGAGGACATGTTCGTAGG	AAAGAACCCAACAGACAC- TAATCC	189	81
<i>PAL</i>	ACAGCTATCTGCGAGGGAAA	CACAGTCTACCAGCAATGCAA	165	79
<i>bHLH3</i>	AGAGTGACGGGTGTTGGAG	CCCTCAGCTCAGCTACGAAG	144	80
<i>GST</i>	TGTGAATGCTTGGTGGAAG	TCTCAGTTCTTTCTTCCACATGA	124	78
<i>EIN4</i>	GGAGGAACATGTGTGGGAGA	TGTGCTCATTAGAGAGCCTGAA	153	79
<i>ETR2</i>	ATGTTTGACAGAGTGGCATCA	CCGCACAAGAGAGAAAAAGG	198	80
<i>ACO</i>	CTATGCTGGCGTCAAGTTCC	AAAGACTTTGGCCACACACA	171	78
<i>ACS</i>	CCAGGTTGGTTTAGGGTGTG	TGGGTAGGATCACAA- TAGGAAGA	154	80
<i>PIN6</i>	GTGAGGATGGTGTGGGAGTC	GACACCGTTTGTCCCCTTC	165	79
<i>SAUR50</i>	TTCTTGACTCGCCCTGAGTT	TCAGCCATTTTCTCCCAAAG	212	81
<i>NCED1</i>	TTCAACTACCCTCCAGAG- TTCC	GGGGGCGTATCAGATAGCTT	158	78
<i>MYB10.1-1</i>	ATCGTAATAAGAC- CTCAACCCCA	CTCGACCGTTTGAATATGGTCC	160	78
<i>ACTB</i>	AACTATGTTCCCCGGTATTGC	TGACATGACACGAAAATCCAA	282	80
<i>CYP</i>	CGGATCTCAGTTCTTCGTCTG	CCTAATCAGACCCCAGCCTAC	300	83
<i>TUBA1A</i>	TGCTCTGGAGAAGGATTACGA	AGCAGCAGCAAATAAAACCAA	247	78
<i>EFA</i>	CTGGTGCTAAGATCAC- CAAGG	GCCTAACAATGACGACCAAAA	185	78