Support information

A synchronized increase of stilbenes and flavonoids in metabolically engineered *Vitis vinifera* cv. Gamay Red cell culture

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Table S1. List of primers used for Gibson Assembly

Genes	**Primer Name**	**Sequence**
*AroG**	AroGFragment 1.FOR	ATCCAACGCGTTGGGAGCTCTCCCATATCGACCT GCAGGCATGCATATGTCG
	AroGFragment 1.REV	GTGTCGTGCTCCACCATGTTTCACTAGTAAGCTA GCTTGCATGCCT
FLS	FLSAcV5Fragment 2.FOR	GCAAGCTAGCTTACTAGTGAAACATGGTGGAGCA CGACAC
	FLSAcV5Fragment 2.REV	CATGCTCCCGGCCGCCATGGCCGCGGGATATCAC TAGTGCTAAGCTAGCTTGCATGCCTGCAGG

Table S2. List of primers used for quantitative real-time PCR. *STS (A): VvSTS10/15/17/19-21/26-31/35/37/41-42/45-48, STS (B): VvSTS 1-6, STS (C): VvSTS 8/10/21/42/46, STS (D): VvSTS 13/17-20/23-24/26-30/32*

Genes	Forward primer	Reverse primer
PAL	TTAAAATGGCTGGGATCGAG	CCTGCATCACTTCAGCAAAA
C4H	CGTTGTTCGTGAAGCTCAAA	GTCCTTGAAGAGCTGCAACC
4CL	AATGCTGAGCTCAAGGTCGT	CAATGTCACCGGTGTGTAGC
STS (A)	TCCGAAGATGCTTTGGACTC	GTGGTCGTTCAATCGAGACA
STS (B)	CCTTGTTTTGGATCGCTCAT	CACCTGTGGTGGTCCTTTCT
STS (C)	CAGCAGCCCAAACGTTTATT	CAGGGTGAGCAATCCAAAAT
STS (D)	ATCGAAGATCACCCACCTTG	AGAACTCGTGCTCCTGCATT
CHS1 / CHS2	CCAGGGTTGATTTCCAAGAA	CATGTTCCCATACTCGCTCA
CHS3	GTTTCAGCAGCCCAGACAAT	TGTGCAATCCAGAAAATGGA
CHI	GTCTCAAGTGCCGTCAGTCA	CCAGCCTCCTTGCAGAATAA
F3H	TGCTGGAGGTGTTGTCTGAG	AGGTTGAACGGTGATCCAAG
FLS	CGGATTCTTCTATGTGAAGG	CTTCATGCATATCAGGTGTG
F3'H	ATTTTCGCCATATCCGACAG	ATCAGCTCCACCACCATCTC
F3'5'H	AAGCGTGCTCACGAAGAAAT	TTCCCAGACATCAGGGTCTC
LAR	GGGTTGATAAACGAGCAGGA	CGAATTCAGACGGCAAAAAT
ANR	CTTGATGGGACAGGTCTGGT	GGCCATCAGAGTAGGGATGA
DFR	ACGATGAAAGCTGCTGGAGT	TCGGGGAAAGAGCAGTTATG
LDOX	CAAGCTTGCCAACAATGCTA	GTAGCTCTTCCATCCCACCA
UFGT	TGCAGGGCCTAACTCACTCT	GCAGTCGCCTTAGGTAGCAC
OMT	CTCCGCATAGCCGATATCAT	GAGAGTTTCTCCGCCATCTG
MYB14	TCTGAGGCCGGATATCAAAC	GGTTGTGCTTGAGCCTCTTC
MYB15	ACGCGCTGTCCTCTGATAAT	GCCGCCAGATCTAATGAAAA
MYBPA	TGCCAGAGAAGACACATTGC	GCCTACCTGCGATGAGAGAC
MYBA1/A2/A3	CTTTTCGGCTTCTGGAGAGA	CTGTGTTGCAGTTTCTTCTGTC
β-actin	GTAACATCTTCCACACCACG	GTCTACACCTAGTCGTTCGT
Ubiquitin	AACCTCCAATCCAGTCATCTAC	GTGGTATTATTGAGCCATCCTT

Table S3. Content of the quantified flavonoids and stilbenes (mg/g Dry Weight, mean ± SE, n = 8 for each line) in the control, *AroG and *AroG* + FLS* transformed cell lines.** Metabolites in bold are those with higher levels in the transgenic line in comparison to the control line, analyzed by one-way ANOVA, followed by Dunnett's post-hoc test. Abbreviations: glc, glucoside.

Group	Metabolite	Control line	*AroG** line	*AroG* + FLS* lines			
				2	5	22	27
Flavonols	Myricetin	0.12±0.01	**0.18±0.01**	**0.17±0.01**	**0.26±0.03**	**0.41±0.02**	**0.21±0.01**
	Quercetin-3-O-glc	0.06±0.01	0.09±0.01	0.06±0.01	0.08±0.01	**0.20±0.02**	**0.15±0.02**
Flavan-3-ols	Catechin	0.09±0.01	0.03±0.002	0.06±0.003	**0.20±0.01**	0.11±0.01	0.06±0.01
	Epicatechin	0.38±0.02	0.37±0.02	0.35±0.01	**0.63±0.05**	**0.66±0.02**	**0.51±0.03**
	Epigallocatechin	0.004±0.001	0.003±0.0003	0.001±0.0001	**0.021±0.002**	0.006±0.001	0.002±0.0002
	Procyanidin B1	0.02±0.002	0.01±0.0005	0.01±0.001	**0.04±0.005**	0.03±0.002	0.02±0.001
	Procyanidin B2	0.19±0.01	0.16±0.01	0.22±0.01	**0.30±0.02**	**0.38±0.02**	**0.31±0.02**
Anthocyanins	Cyanidin-3-O-glc	30.58±1.66	19.93±2.20	32.55±2.60	38.1±3.22	28.61±2.66	28.68±3.36
	Peonidin-3-O-glc	2.14±0.28	**3.18±0.24**	**3.51±0.44**	**3.63±0.24**	**3.78±0.34**	**3.36±0.34**
	Delphinidin-3-O-glc	0.10±0.01	0.09±0.01	0.01±0.0004	**0.17±0.02**	0.09±0.01	0.05±0.01
	Malvidin-3-O-glc	0.13±0.01	**0.55±0.06**	0.02±0.002	**0.49±0.04**	**0.73±0.07**	**0.25±0.02**
	Petuidin-3-O-glc	0.10±0.01	0.12±0.01	0.01±0.001	**0.21±0.01**	**0.18±0.02**	0.08±0.01
Stilbenes	*trans*-Piceid	0.20±0.01	**0.42±0.05**	0.28±0.03	**0.33±0.02**	**0.54±0.07**	**0.40±0.03**
	cis-Piceid	0.22±0.02	**0.40±0.04**	0.26±0.04	**0.38±0.03**	**0.42±0.05**	**0.33±0.02**
	Resveratrol	0.05±0.01	**0.36±0.06**	**0.15±0.02**	**0.25±0.04**	**0.29±0.05**	**0.16±0.02**
	ε-viniferin	0.01±0.002	**0.20±0.06**	**0.33±0.03**	**0.04±0.01**	**0.13±0.01**	**0.10±0.01**

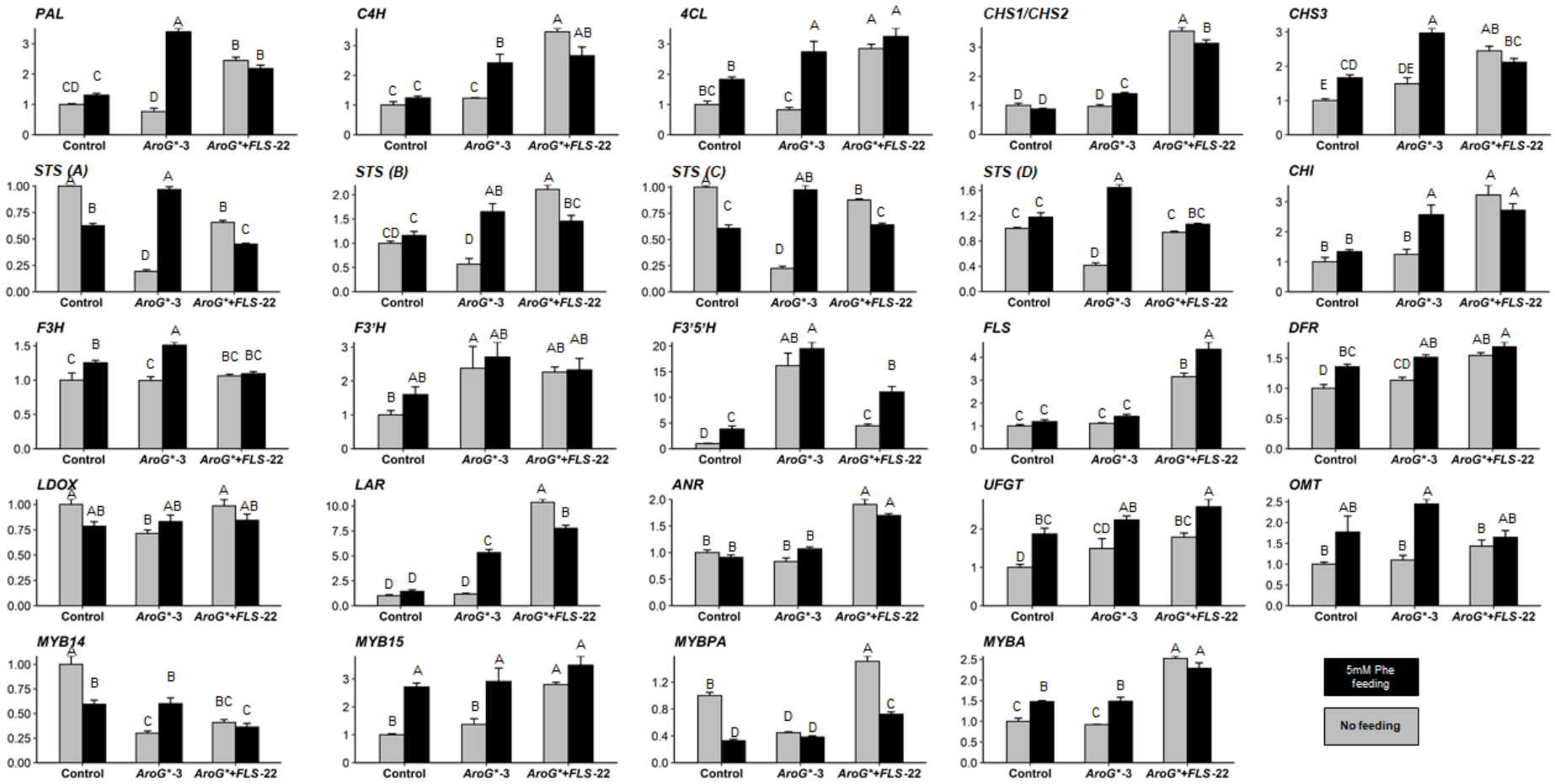

Figure S1. Effect of transformation with *AroG and *FLS*, and exogenous feeding of Phe on the gene expression levels.** Gene expression

levels (mean ± SE, n=6) are presented as fold change normalized to control samples (non-treated control). Statistical significance was analyzed by two-way ANOVA, followed by Tukey-HSD post-hoc test ($P < 0.05$). *STS (A)*: *VvSTS10/15/17/19-21/26-31/35/37/41-42/45-48*, *STS (B)*: *VvSTS 1-6*, *STS (C)*: *VvSTS 8/10/21/42/46*, *STS (D)*: *VvSTS 13/17-20/23-24/26-30/32.* Abbreviations: PAL, phenylalanine ammonia-lyase; C4H, cinnamate 4-hydroxylase; 4CL, 4-coumaroyl:CoA ligase; CHS, chalcone synthase; CHI, chalcone isomerase; F3H, flavanone 3-hydroxylase; F3′H and F3′5′H, flavonoid 3′ and 3′ 5′ hydroxylase; FLS, flavonol synthase; DFR, dihydroflavonol 4-reductase; LDOX, leucoanthocyanidin dioxygenase; LAR**,** leucoanthocyanidin reductase; ANR, anthocyanidin reductase; UFGT, uridine diphosphate-glucose:flavonoid 3-O-glucosyltransferase; OMT, O-methyltransferases; STS, Stilbene synthase.

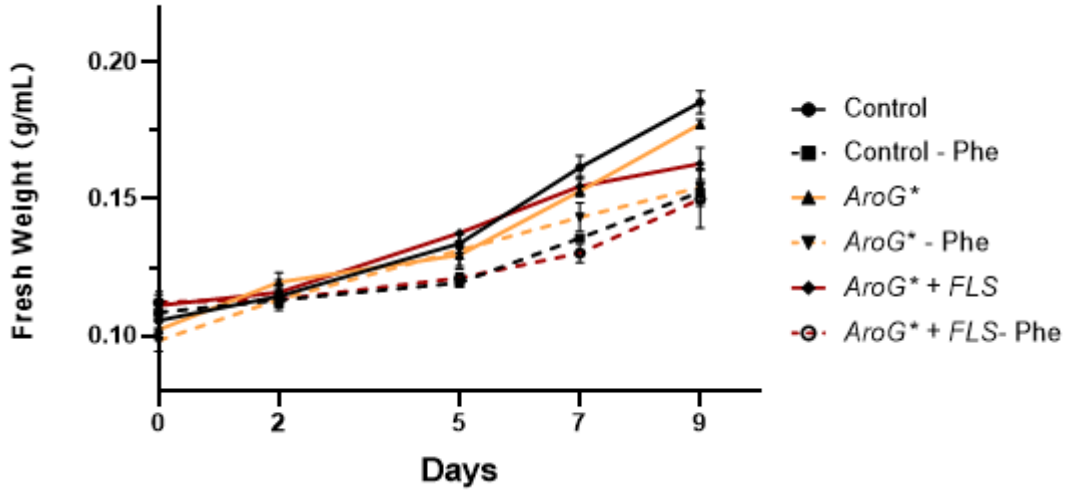

Figure S2. Growth curves of the control, *AroG and *AroG** + *FLS* lines before and after Phe feeding.** The curves were determined by the increase in fresh weight from the day of re-culturing (day 0) until the beginning of cell death.