

Supplementary materials

Table S1. Polyphenol content (mg/100gDW) in chlorogenic acid (A), neochlorogenic acid (B), rutin (C) and quercetin-3-glucuronide (D).

A

Genotype	Chlorogenic acid								
	2019			2020			Two years average		
	Mean	Sd	Significance	Mean	Sd	Significance	Mean	Sd	Significance
Canino	103,82	3,77	abc	103,02	3,83	a	103,42	3,43	a
Dama Rosa	525,47	54,31	f	727,48	22,50	f	626,48	116,73	d
Dama Taronja	95,05	5,44	ab	225,55	52,91	b	160,30	79,00	abc
GG9310	93,80	2,26	ab	276,97	20,84	bc	185,39	101,20	abc
GG979	276,77	6,35	de	432,58	70,34	de	354,67	96,33	c
Goldrich	270,33	5,87	d	339,74	9,26	cd	305,03	38,65	abc
GP9817	322,07	5,47	e	338,27	25,23	cd	330,17	18,58	bc
HG9821	148,30	1,14	c	405,31	23,07	d	276,81	141,53	abc
HG9850	77,85	3,13	a	199,56	10,33	ab	138,71	67,02	ab
HM964	236,15	5,93	d	422,72	10,24	d	329,43	102,46	bc
Mitger	147,31	4,06	c	524,40	26,66	e	335,86	207,24	bc
SEOP934	137,24	4,99	bc	203,33	21,56	b	170,29	38,81	abc

B

Neochlorogenic acid									
Genotype	2019			2020			Two years average		
	Mean	Sd	Significance	Mean	Sd	Significance	Mean	Sd	Significance
Canino	190,79	3,40	cd	167,15	4,92	ab	178,97	13,49	ab
Dama Rosa	418,98	40,09	f	533,02	18,74	d	476,00	68,45	d
Dama Taronja	205,53	7,25	cd	424,93	95,70	d	315,23	134,64	bcd
GG9310	380,90	2,50	f	459,17	33,65	d	420,03	47,88	cd
GG979	183,82	18,58	c	288,73	41,44	c	236,27	64,24	ab
Goldrich	190,45	4,22	cd	276,43	3,86	c	233,44	47,23	ab
GP9817	232,33	21,43	d	290,09	18,47	c	261,21	36,34	abc
HG9821	168,36	0,48	c	274,32	16,91	bc	221,34	59,02	ab
HG9850	71,19	2,30	a	156,55	5,29	a	113,87	46,90	a
HM964	286,94	7,09	e	214,70	4,89	abc	250,82	39,94	abc
Mitger	119,98	4,42	b	504,88	21,29	d	312,43	211,27	bcd
SEOP934	106,42	3,70	ab	235,29	27,66	abc	170,85	72,76	ab

C

Genotype	Rutin								
	2019			2020			Two years average		
	Mean	Sd	Significance	Mean	Sd	Significance	Mean	Sd	Significance
Canino	231,84	6,15	a	380,05	20,16	cde	305,95	82,26	abcd
Dama Rosa	696,75	115,40	f	262,81	19,49	bc	479,78	248,94	cd
Dama Taronja	344,06	14,34	bc	457,26	120,96	e	400,66	98,89	bcd
GG9310	510,34	2,52	de	259,25	24,30	bc	384,80	138,40	abcd
GG979	158,85	3,34	a	283,25	44,86	bc	221,05	73,84	ab
Goldrich	415,42	14,03	cd	249,89	14,45	abc	332,65	91,55	abcd
GP9817	575,79	1,57	e	271,24	22,95	bc	423,51	167,45	bcd
HG9821	186,99	1,90	a	125,81	10,89	a	156,40	34,23	a
HG9850	250,31	11,94	ab	317,01	23,57	cd	283,66	40,17	abcd
HM964	268,38	14,34	ab	163,78	8,28	ab	216,08	58,24	ab
Mitger	533,10	25,53	e	445,09	25,85	de	489,10	53,40	d
SEOP934	232,64	11,91	a	276,09	27,71	bc	254,36	30,50	abc

D

Genotype	Quercetin-3-glucuronide								
	2019			2020			Two years average		
	Mean	Sd	Significance	Mean	Sd	Significance	Mean	Sd	Significance
Canino	13,18	0,64	a	19,30	1,18	ab	16,24	3,46	ab
Dama Rosa	84,01	12,43	g	42,18	3,78	c	63,09	24,34	c
Dama Taronja	55,08	1,33	f	63,44	17,45	d	59,26	11,98	c
GG9310	39,93	7,55	e	12,70	1,95	a	26,31	15,71	ab
GG979	10,66	0,38	a	14,17	2,70	a	12,41	2,58	a
Goldrich	17,82	1,33	ab	10,11	0,28	a	13,97	4,31	ab
GP9817	36,97	0,39	de	16,49	2,23	a	26,73	11,31	ab
HG9821	10,73	0,33	a	9,51	0,75	a	10,12	0,85	a
HG9850	23,42	1,65	abcd	22,51	1,86	ab	22,96	1,65	ab
HM964	31,36	1,66	bcde	24,23	1,40	ab	27,80	4,14	ab
Mitger	32,04	1,68	cde	34,77	3,34	bc	33,41	2,80	b
SEOP934	20,74	1,15	abc	23,33	3,89	ab	22,04	2,93	ab

Table S2. *Prunus persica* and *Prunus armeniaca* synteny and protein identity.

Gene name	<i>Prunus persica</i>			<i>Prunus armeniaca</i>		<i>Prunus persica</i> vs <i>Prunus armeniaca</i>		
	Sequence identifier	Gene location	LG	Obtained sequence	Position	Synteny block	Identity	E-value
<i>PpePAL1</i>	Prupe.2G211800.1	Pp02:24393791-24397929	2	PARG18722	LG5:20435326-20438772	appB272	710/719 (98.75%)	0
<i>PpePAL2</i>	Prupe.6G235400.1	Pp06:23639324-23642649	6	PARG02214	LG1:17635804-17638656	appB018	711/717 (99.16%)	0
<i>PpeDFR</i>	Prupe.1G376400.1	Pp01:34110835-34113473	1	PARG07267	LG2: 29288431-29290653	appB056	333/346 (96.24%)	0
<i>PpeFLS1</i>	Prupe.1G502700.1	Pp01:41577480-41579444	1	PARG08425	LG2:36614060-36616498	appB057	328/335 (97.91%)	0
<i>PpeFLS2</i>	Prupe.1G502800.1	Pp01:41580633-41583079	1	PARG08426	LG2:36622560-36624610	appB057	330/338 (97.63%)	0

Table S3. *Arabidopsis thaliana* and *Prunus armeniaca* protein identity.

<i>Arabidopsis thaliana</i>	<i>Prunus armeniaca</i>		<i>Arabidopsis thaliana</i> vs <i>Prunus persica</i>	
	Gene	ID	Identity with apricot	E-value
<i>AtPAL1</i>	<i>ParPAL2</i>	PARG02214m01	591/705 (83.83%)	0
<i>AtPAL2</i>	<i>ParPAL1</i>	PARG18722m01	576/692 (83.24%)	0
<i>AtPAL3</i>	<i>ParPAL1</i>	PARG18722m01	522/699 (74.68%)	0
<i>AtPAL4</i>	<i>ParPAL1</i>	PARG18722m01	579/709 (81.66%)	0
<i>AtDFR</i>	<i>ParDFR</i>	PARG07267m01	241/327 (73.7%)	$1.15 \cdot 10^{-161}$
<i>AtFLS1</i>	<i>ParFLS1</i>	PARG08425m01	200/333 (60.06%)	$3.35 \cdot 10^{-126}$
<i>AtFLS2</i>	<i>ParFLS2</i>	PARG08426m01	105/230 (45.65%)	$2.38 \cdot 10^{-50}$
<i>AtFLS3</i>	<i>ParFLS1</i>	PARG08425m01	158/294 (53.74%)	$3.23 \cdot 10^{-94}$

Table S4. p-distance for PAL (A), DFR (B) and FLS (C)proteins.

A	<i>AtPAL1</i>	<i>AtPAL2</i>	<i>AtPAL3</i>	<i>AtPAL4</i>	<i>PpePAL1</i>	<i>PpePAL2</i>	<i>ParPAL1</i>	<i>ParPAL2</i>	<i>VvPAL1</i>	<i>MdPAL1</i>	<i>MdPAL2</i>	<i>FvPAL1</i>
<i>AtPAL1</i>												
<i>AtPAL2</i>	0.09 ± 0.01											
<i>AtPAL3</i>	0.26 ± 0.02	0.26 ± 0.02										
<i>AtPAL4</i>	0.19 ± 0.01	0.19 ± 0.01	0.16 ± 0.01									
<i>PpePAL1</i>	0.19 ± 0.01	0.19 ± 0.01	0.24 ± 0.02	0.17 ± 0.01								
<i>PpePAL2</i>	0.18 ± 0.01	0.19 ± 0.01	0.26 ± 0.02	0.20 ± 0.02	0.16 ± 0.01							
<i>ParPAL1</i>	0.19 ± 0.01	0.19 ± 0.01	0.24 ± 0.02	0.18 ± 0.01	0.01 ± 0.00	0.16 ± 0.01						
<i>ParPAL2</i>	0.18 ± 0.01	0.19 ± 0.01	0.26 ± 0.02	0.20 ± 0.02	0.16 ± 0.01	0.01 ± 0.00	0.16 ± 0.01					
<i>VvPAL1</i>	0.23 ± 0.02	0.21 ± 0.02	0.26 ± 0.02	0.19 ± 0.02	0.17 ± 0.02	0.18 ± 0.02	0.17 ± 0.02	0.18 ± 0.02				
<i>MdPAL1</i>	0.20 ± 0.01	0.19 ± 0.01	0.26 ± 0.02	0.19 ± 0.01	0.08 ± 0.01	0.16 ± 0.01	0.09 ± 0.01	0.16 ± 0.01	0.18 ± 0.02			
<i>MdPAL2</i>	0.18 ± 0.01	0.19 ± 0.01	0.26 ± 0.02	0.19 ± 0.01	0.15 ± 0.01	0.07 ± 0.01	0.16 ± 0.01	0.07 ± 0.01	0.18 ± 0.02	0.16 ± 0.01		
<i>FvPAL1</i>	0.22 ± 0.02	0.22 ± 0.02	0.26 ± 0.02	0.20 ± 0.01	0.16 ± 0.01	0.19 ± 0.01	0.16 ± 0.01	0.19 ± 0.01	0.21 ± 0.02	0.15 ± 0.01	0.19 ± 0.01	
<i>FvPAL2</i>	0.20 ± 0.01	0.21 ± 0.01	0.27 ± 0.02	0.20 ± 0.02	0.17 ± 0.01	0.11 ± 0.01	0.17 ± 0.01	0.11 ± 0.01	0.19 ± 0.02	0.17 ± 0.01	0.10 ± 0.01	0.19 ± 0.01

B	<i>AtDFR</i>	<i>PpeDFR</i>	<i>ParDFR</i>	<i>VvDFR</i>	<i>FvDFR</i>
<i>AtDFR</i>					
<i>PpeDFR</i>	0.31 ± 0.02				
<i>ParDFR</i>	0.30 ± 0.02	0.04 ± 0.01			
<i>VvDFR</i>	0.42 ± 0.04	0.39 ± 0.04	0.39 ± 0.04		
<i>FvDFR</i>	0.29 ± 0.02	0.17 ± 0.02	0.17 ± 0.02	0.41 ± 0.04	
<i>MdDFR</i>	0.36 ± 0.05	0.24 ± 0.04	0.24 ± 0.04	0.60 ± 0.05	0.31 ± 0.05

C	<i>ATFLS1</i>	<i>AtFLS2</i>	<i>AtFLS3</i>	<i>AtFLS3</i>	<i>PpeFLS1</i>	<i>PpeFLS2</i>	<i>ParFLS1</i>	<i>ParFLS2</i>	<i>VvFLS1</i>	<i>MdFLS1</i>
<i>AtFLS1</i>										
<i>AtFLS2</i>	0.39 ± 0.03									
<i>AtFLS3</i>	0.30 ± 0.03	0.40 ± 0.03								
<i>PpeFLS1</i>	0.42 ± 0.03	0.57 ± 0.03	0.48 ± 0.03							
<i>PpeFLS2</i>	0.42 ± 0.03	0.57 ± 0.03	0.48 ± 0.03	0.22 ± 0.02						
<i>ParFLS1</i>	0.43 ± 0.03	0.57 ± 0.03	0.48 ± 0.03	0.02 ± 0.01	0.22 ± 0.02					
<i>ParFLS2</i>	0.42 ± 0.03	0.57 ± 0.03	0.49 ± 0.03	0.22 ± 0.02	0.02 ± 0.01	0.23 ± 0.02				
<i>VvFLS1</i>	0.37 ± 0.03	0.56 ± 0.04	0.50 ± 0.03	0.29 ± 0.03	0.28 ± 0.03	0.30 ± 0.03	0.28 ± 0.03			
<i>FvFLS1</i>	0.43 ± 0.03	0.57 ± 0.03	0.49 ± 0.03	0.22 ± 0.02	0.20 ± 0.02	0.22 ± 0.02	0.20 ± 0.02	0.28 ± 0.03		
<i>MdFLS1</i>	0.44 ± 0.04	0.58 ± 0.04	0.50 ± 0.04	0.23 ± 0.03	0.33 ± 0.04	0.23 ± 0.03	0.33 ± 0.04	0.35 ± 0.05	0.27 ± 0.04	
<i>MdFLS2</i>	0.60 ± 0.03	0.70 ± 0.03	0.65 ± 0.03	0.52 ± 0.03	0.45 ± 0.03	0.52 ± 0.03	0.46 ± 0.03	0.66 ± 0.04	0.52 ± 0.03	0.32 ± 0.04

Table S5. Similarity (1-p-distance) among protein sequences of PAL (A), DFR (B), FLS (C).

A	<i>AtPAL1</i>	<i>AtPAL2</i>	<i>AtPAL3</i>	<i>AtPAL4</i>	<i>PpePAL1</i>	<i>PpePAL2</i>	<i>ParPAL1</i>	<i>ParPAL2</i>	<i>VvPAL1</i>	<i>MdPAL1</i>	<i>MdPAL2</i>	<i>FvPAL1</i>
<i>AtPAL1</i>												
<i>AtPAL2</i>	0.91 ± 0.01											
<i>AtPAL3</i>	0.74 ± 0.02	0.74 ± 0.02										
<i>AtPAL4</i>	0.81 ± 0.01	0.81 ± 0.01	0.84 ± 0.01									
<i>PpePAL1</i>	0.81 ± 0.01	0.81 ± 0.01	0.76 ± 0.02	0.83 ± 0.01								
<i>PpePAL2</i>	0.82 ± 0.01	0.81 ± 0.01	0.74 ± 0.02	0.80 ± 0.02	0.84 ± 0.01							
<i>ParPAL1</i>	0.81 ± 0.01	0.81 ± 0.01	0.76 ± 0.02	0.82 ± 0.01	0.99 ± 0.00	0.84 ± 0.01						
<i>ParPAL2</i>	0.82 ± 0.01	0.81 ± 0.01	0.74 ± 0.02	0.80 ± 0.02	0.84 ± 0.01	0.99 ± 0.00	0.84 ± 0.01					
<i>VvPAL1</i>	0.77 ± 0.02	0.79 ± 0.02	0.74 ± 0.02	0.81 ± 0.02	0.83 ± 0.02	0.82 ± 0.02	0.83 ± 0.02	0.82 ± 0.02				
<i>MdPAL1</i>	0.80 ± 0.01	0.81 ± 0.01	0.74 ± 0.02	0.81 ± 0.01	0.92 ± 0.01	0.84 ± 0.01	0.91 ± 0.01	0.84 ± 0.01	0.82 ± 0.02			
<i>MdPAL2</i>	0.82 ± 0.01	0.81 ± 0.01	0.74 ± 0.02	0.81 ± 0.01	0.85 ± 0.01	0.93 ± 0.01	0.84 ± 0.01	0.93 ± 0.01	0.82 ± 0.02	0.84 ± 0.01		
<i>FvPAL1</i>	0.78 ± 0.02	0.78 ± 0.02	0.74 ± 0.02	0.80 ± 0.01	0.84 ± 0.01	0.81 ± 0.01	0.84 ± 0.01	0.81 ± 0.01	0.79 ± 0.02	0.85 ± 0.01	0.81 ± 0.01	
<i>FvPAL2</i>	0.80 ± 0.01	0.79 ± 0.01	0.73 ± 0.02	0.80 ± 0.02	0.83 ± 0.01	0.89 ± 0.01	0.83 ± 0.01	0.89 ± 0.01	0.81 ± 0.02	0.83 ± 0.01	0.90 ± 0.01	0.81 ± 0.01

B	<i>AtDFR</i>	<i>PpeDFR</i>	<i>ParDFR</i>	<i>VvDFR</i>	<i>FvDFR</i>
<i>AtDFR</i>					
<i>PpeDFR</i>	0.69 ± 0.02				
<i>ParDFR</i>	0.70 ± 0.02	0.96 ± 0.01			
<i>VvDFR</i>	0.58 ± 0.04	0.61 ± 0.04	0.61 ± 0.04		
<i>FvDFR</i>	0.71 ± 0.02	0.83 ± 0.02	0.83 ± 0.02	0.59 ± 0.04	
<i>MdDFR</i>	0.64 ± 0.05	0.76 ± 0.04	0.76 ± 0.04	0.40 ± 0.05	0.69 ± 0.05

C	<i>ATFLS1</i>	<i>AtFLS2</i>	<i>AtFLS3</i>	<i>AtFLS3</i>	<i>PpeFLS1</i>	<i>PpeFLS2</i>	<i>ParFLS1</i>	<i>ParFLS2</i>	<i>VvFLS1</i>	<i>MdFLS1</i>
<i>AtFLS1</i>										
<i>AtFLS2</i>	0.61 ± 0.03									
<i>AtFLS3</i>	0.70 ± 0.03	0.60 ± 0.03								
<i>PpeFLS1</i>	0.58 ± 0.03	0.43 ± 0.03	0.52 ± 0.03							
<i>PpeFLS2</i>	0.58 ± 0.03	0.43 ± 0.03	0.52 ± 0.03	0.78 ± 0.02						
<i>ParFLS1</i>	0.57 ± 0.03	0.43 ± 0.03	0.52 ± 0.03	0.98 ± 0.01	0.78 ± 0.02					
<i>ParFLS2</i>	0.58 ± 0.03	0.43 ± 0.03	0.51 ± 0.03	0.78 ± 0.02	0.98 ± 0.01	0.77 ± 0.02				
<i>VvFLS1</i>	0.63 ± 0.03	0.44 ± 0.04	0.50 ± 0.03	0.71 ± 0.03	0.72 ± 0.03	0.70 ± 0.03	0.72 ± 0.03			
<i>FvFLS1</i>	0.57 ± 0.03	0.43 ± 0.03	0.51 ± 0.03	0.78 ± 0.02	0.80 ± 0.02	0.78 ± 0.02	0.80 ± 0.02	0.72 ± 0.03		
<i>MdFLS1</i>	0.56 ± 0.04	0.42 ± 0.04	0.50 ± 0.04	0.77 ± 0.03	0.67 ± 0.04	0.77 ± 0.03	0.67 ± 0.04	0.65 ± 0.05	0.73 ± 0.04	
<i>MdFLS2</i>	0.40 ± 0.03	0.30 ± 0.03	0.35 ± 0.03	0.48 ± 0.03	0.55 ± 0.03	0.48 ± 0.03	0.54 ± 0.03	0.34 ± 0.04	0.48 ± 0.03	0.68 ± 0.04

Table S6: Genetic expression of studied genotypes. Different letter means significant differences among genotypes.

2019															
Genotype	<i>ParDFR</i>			<i>ParFLS1</i>			<i>ParFLS2</i>			<i>ParPAL1</i>			<i>ParPAL2</i>		
	Mean	Sd	Sig.	Mean	Sd	Sig.	Mean	Sd	Sig.	Mean	Sd	Sig.	Mean	Sd	Sig.
Canino	0.75	0.15	bc	0.97	0.48	a	2.34	0.39	ab	1.18	0.06	ab	1.77	0.29	bc
Dama Rosa	0.38	0.04	ab	0.61	0.32	a	2.19	0.58	ab	1.13	0.17	ab	0.56	0.02	ab
Dama Taronja	2.52	0.25	d	0.51	0.35	a	0.42	0.14	ab	1.95	0.14	b	1.78	0.33	bc
GG9310	0.50	0.30	ab	0.84	0.50	a	5.05	2.17	c	1.00	0.52	ab	0.46	0.20	a
GG979	0.12	0.03	a	3.73	2.56	a	0.84	0.10	ab	1.68	0.59	b	0.29	0.10	a
Goldrich	0.51	0.05	ab	1.07	0.41	a	0.24	0.08	a	1.94	0.60	b	0.86	0.30	ab
GP9817	0.38	0.07	ab	1.21	1.22	a	1.25	0.04	ab	1.17	0.20	ab	0.63	0.10	ab
HG9821	0.93	0.02	bc	0.41	0.25	a	2.59	0.76	b	1.13	0.32	ab	1.06	0.10	abc
HG9850	2.27	0.13	d	0.34	0.24	a	0.76	0.06	ab	1.01	0.21	ab	2.29	0.70	cd
HM964	1.10	0.15	c	0.76	0.30	a	1.44	0.09	ab	2.02	0.29	b	1.06	0.37	abc
Mitger	2.27	0.36	d	0.57	0.01	a	0.81	0.19	ab	1.65	0.54	b	3.44	0.97	d
SEOP934	0.83	0.18	bc	1.69	1.63	a	1.02	0.28	ab	0.30	0.02	a	0.78	0.05	ab

2020															
Genotype	<i>ParDFR</i>			<i>ParFLS1</i>			<i>ParFLS2</i>			<i>ParPAL1</i>			<i>ParPAL2</i>		
	Mean	Sd	Sig.	Mean	Sd	Sig.	Mean	Sd	Sig.	Mean	Sd	Sig.	Mean	Sd	Sig.
Canino	0.57	0.16	a	4.09	3.10	b	0.54	0.08	ab	3.74	1.42	b	1.95	0.58	bc
Dama Rosa	0.44	0.14	a	2.91	0.81	ab	1.21	0.37	bc	1.10	0.14	a	0.90	0.37	abc
Dama Taronja	0.27	0.05	a	0.54	0.32	a	0.13	0.02	a	0.41	0.04	a	0.81	0.10	abc
GG9310	0.17	0.03	a	2.20	1.79	ab	1.18	0.34	bc	0.70	0.22	a	0.17	0.01	ab
GG979	0.14	0.03	a	0.41	0.20	a	0.57	0.17	ab	1.64	0.44	a	0.49	0.12	abc
Goldrich	0.97	0.33	ab	0.30	0.13	a	0.04	0.02	a	3.58	1.14	b	2.00	0.86	c
GP9817	0.16	0.05	a	0.41	0.29	a	0.97	0.03	bc	0.32	0.01	a	0.16	0.04	a
HG9821	2.05	0.53	bc	2.54	1.39	ab	1.14	0.29	bc	1.33	0.32	a	0.74	0.17	abc
HG9850	2.66	0.97	c	1.95	1.46	ab	0.64	0.07	abc	1.01	0.36	a	4.55	1.48	d
HM964	0.61	0.11	a	1.98	0.70	ab	1.38	0.30	c	0.38	0.03	a	0.37	0.06	abc
Mitger	5.14	0.14	d	0.59	0.31	a	3.34	0.53	d	0.59	0.14	a	4.68	0.57	d
SEOP934	1.11	0.13	ab	1.19	0.56	a	2.61	0.09	d	0.48	0.05	a	1.15	0.24	abc

Table S7: Linear regression model in caffeate-derivates.

NEOCHLORGENIC ACID					
2019					
Parameter	Estimation	Sd	T	P-value	R2
CONSTANT	185.653	42.8202	4.33564	0.0002	0.6191
<i>ParDFR</i>	-81.7058	33.5748	-2.43355	0.0216	
<i>ParFLS2</i>	34.5919	10.6549	3.24656	0.003	
<i>ParPAL1</i>	106.167	33.3428	3.1841	0.0035	
<i>ParPAL2</i>	-108.959	36.882	-2.95426	0.0063	
<i>ParPAL1Par / FLS2</i>	-49.3894	19.9979	-2.46973	0.0199	
<i>ParPAL2 / ParFLS2</i>	92.9533	37.829	2.4572	0.0205	
2020					
Parameter	Estimation	Sd	T	P-value	R2
CONSTANT	275.686	32.8475	8.39292	0	0.0784
<i>ParFLS2</i>	37.5785	22.0911	1.70107	0.0981	
2019-2020					
Parameter	Estimation	Sd	T	P-value	R2
CONSTANT	294.892	21.027	14.0244	0	0.063
<i>ParPAL2 / ParFLS1</i>	-18.5607	8.70188	-2.13296	0.0366	

CHLOROGENIC ACID					
2019					
Parameter	Estimation	Sd	T	P-value	R2
CONSTANT	290.902	29.6794	9.80146	0	0.293
<i>ParDFR</i>	-84.0371	22.3848	-3.75421	0.0007	
2020					
Parameter	Estimation	Sd	T	P-value	R2
CONSTANT	386.407	39.5198	9.77757	0	0.04616
<i>ParPAL1</i>	-28.6776	22.355	-1.28283	0.2082	
2019-2020					
Parameter	Estimation	Sd	T	P-value	R2
CONSTANT	318.278	27.1345	11.7296	0	0.0816
<i>ParPAL2 / ParFLS1</i>	-27.4045	11.2294	-2.44043	0.0173	

CHLOROGENIC AND NEOCHLOROGENIC TOTAL CONTENT					
2019					
Parameter	Estimation	Sd	T	P-value	R2
CONSTANT	525.668	80.5319	6.52744	0	0.5339
<i>ParDFR</i>	-241.336	72.6906	-3.32005	0.0024	
<i>ParPAL1</i>	233.953	71.6001	3.26749	0.0028	
<i>ParPAL2</i>	-204.74	79.8529	-2.56397	0.0158	
<i>ParPAL1 / ParFLS2</i>	-112.661	43.0388	-2.61765	0.0139	
<i>ParPAL2 / ParFLS2</i>	190.943	81.5529	2.34134	0.0263	
2020					
Parameter	Estimation	Sd	T	P-value	R2
CONSTANT	746.592	62.4755	11.9501	0	0.0810975
<i>ParPAL1</i>	-61.218	35.3404	-1.73224	0.0923	
2019-2020					
Parameter	Estimation	Sd	T	P-value	R2
CONSTANT	613.17	43.8595	13.9803	0	0.0873
<i>ParPAL2/ParFLS1</i>	-45.9653	18.1509	-2.53239	0.0137	

Table S8: Linear regression model in flavonols.

RUTIN					
2019					
Parameter	Estimation	Sd	T	P-value	R2
CONSTANT	562.793	90.0062	6.25283	0	0.366
<i>ParDFR</i>	-294.562	78.952	-3.7309	0.0009	
<i>ParPAL1</i>	251.179	86.265	2.91171	0.007	
<i>ParPAL2</i>	-251.405	86.1836	-2.91709	0.0069	
<i>ParPAL1 / ParPAL2</i>	-58.0325	26.0671	-2.22627	0.0342	
<i>ParPAL1 / ParFLS2</i>	-151.616	44.6125	-3.39851	0.0021	
<i>ParPAL2 / ParFLS2</i>	304.215	84.1984	3.61308	0.0012	
2020					
Parameter	Estimation	Sd	T	P-value	R2
CONSTANT	211.629	21.3124	9.92987	0	0.515868
<i>ParFLS1 / ParFLS2</i>	9.19147	2.2127	4.15396	0.0003	
<i>ParPAL2</i>	38.4111	8.62697	4.45244	0.0001	
<i>ParPAL1 / ParFLS2</i>	-2.59935	0.720061	-3.6099	0.0011	
2019-2020					
Parameter	Estimation	Sd	T	P-value	R2
CONSTANT	356.984	23.5464	15.1609	0	0.0425
<i>ParFLS1</i>	-19.4258	11.2636	-1.72466	0.0892	

QUERCETIN_3-GLUCURONIDE					
2019					
Parameter	Estimation	Sd	T	P-value	R2
CONSTANT	48.7709	8.15762	5.97857	0	0.1815
<i>ParPAL2</i>	-23.0258	8.99826	-2.55892	0.0156	
<i>ParPAL1 / ParFLS2</i>	-8.35646	3.44867	-2.42309	0.0214	
<i>ParPAL2 / ParFLS2</i>	17.4134	6.84919	2.5424	0.0162	
2020					
Parameter	Estimation	Sd	T	P-value	R2
CONSTANT	28.3714	2.98273	9.51191	0	0.5852
<i>ParFLS1 / ParFLS2</i>	1.40385	0.294044	4.7743	0	
<i>ParPAL1 / ParPAL2</i>	-4.4801	1.31522	-3.40636	0.0019	
<i>ParPAL1 / ParFLS2</i>	-0.448444	0.0963081	-4.65634	0.0001	
2019-2020					
Parameter	Estimation	Sd	T	P-value	R2
CONSTANT	32.7225	3.31507	9.87083	0	0.04786
<i>ParPAL1 / ParPAL2</i>	-2.83612	1.52274	-1.8625	0.0668	

ROUTIN+QUERCETIN-3-GLUCURONIDE					
2019					
Parameter	Estimation	Sd	T	P-value	R2
CONSTANT	615.21	98.5015	6.24569	0	
<i>ParDFR</i>	-313.956	86.4039	-3.63358	0.0011	
<i>ParPAL1</i>	282.717	94.4072	2.99465	0.0057	
<i>ParPAL2</i>	-293.832	94.3181	-3.11533	0.0042	0.368
<i>ParPAL1 / ParPAL2</i>	-64.1542	28.5275	-2.24885	0.0326	
<i>ParPAL1 / ParFLS2</i>	-172.127	48.8232	-3.52552	0.0015	
<i>ParPAL2 / FLS2</i>	341.894	92.1456	3.71037	0.0009	
2020					
Parameter	Estimation	Sd	T	P-value	R2
CONSTANT	227.956	23.062	9.88451	0	
<i>ParFLS1 / Par FLS2</i>	10.8076	2.39435	4.51382	0.0001	0.536877
<i>ParPAL2</i>	41.3101	9.33517	4.42521	0.0001	
<i>ParPAL1 / ParFLS2</i>	-3.12702	0.779172	-4.01326	0.0004	
2019-2020					
Parameter	Estimation	Sd	T	P-value	R2
CONSTANT	387.332	25.922	14.9423	0	0.0417
<i>ParFLS1</i>	-21.1966	12.3999	-1.70941	0.092	

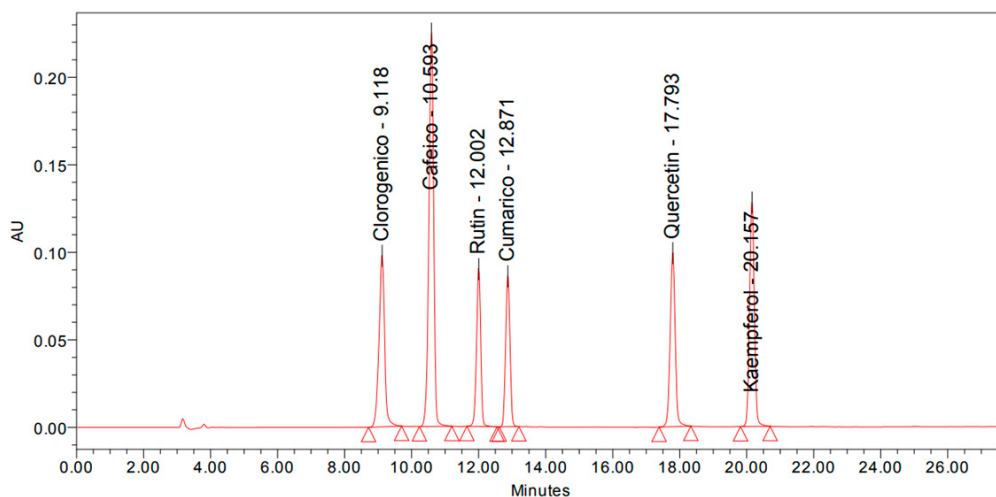


Figure S1. Standard chromatogram and retention times for chlorogenic acid (Clorogenico), caffeic acid (Cafeico), rutin, coumaric (Cumarico), quercetin and kaempferol.

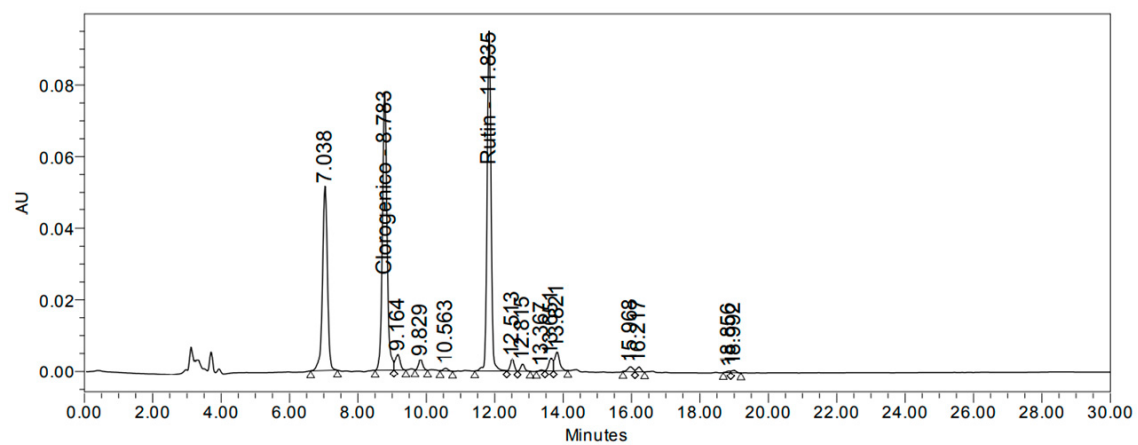


Figure S2. 'Canino' chromatogram from one biological replicate sample.