Supplemental material

Genetic dissection of fruit quality traits in the octoploid cultivated strawberry highlights the role of homoeo-QTLs in their control

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Online Resource 2: Significant QTLs detected for 'Capitola' and for 'CF1116' for all the traits based on CIM analysis with LOD>LOD threshold (2.86 for the female map and 2.90 for the male map). Potential homoeo-QTLs are in boxes and QTL detected in male and female linkage maps are underlined in grey.

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	Trait ^{a}	Unique QTLs ^{b}	Year ^{c}	Marker ^{d}	LG ^{e}	LOD ^{f}	Mean Effect ^{g}	$R^{2\ h}$
Development								
(41, 28)	FD^{3}	FD_IIb_m13	1&3	gttg135-ggat205	IIb-m	3.10-4.12	-1.53	0.06-0.08
		FD_IIIa_m12	1&2	EMFv016/EMFv004	IIIa-m	3.51-4.51	1.61	0.06-0.09
		FD_IIIc1_m3	3	UDF004	IIIc1-m	4.11	1.53	0.08
		FD_IVa_m2	2	EMFvi136	IVa-m	3.47	-2.19	0.07
	FL^{3}	FL_IIa_f3	3	gaac370	IIa-f	2.91	1.66	0.06
		FL_IIc_m123	1&2&3	tgta420-tgtc201	IIc-m	3.61-4.21	-3.05	0.07-0.10
		FL_IIIa_m1	1	BFACT036	IIIa-m	3.38	-2.87	0.06
		FL_IIId_m1	1	BFACT026	IIId-m	3.64	-3.05	0.07
		FL_IVd_f1	1	gtgx440	IVd2-f	4.53	-3.84	0.11
		FL_Vb_f3	3	tcaa166	Vb-f	3.33	1.91	0.08
		FL_VIb_m1	1	tgaa195	VIb-m	3.05	2.84	0.06
	FD/FL^{3}	FD/FL_IIIa_m123 / f23	1&2&3 /2&3	gata165-BFACT048 / UDF001-gtat374	IIIa-m / f	3.58-8.06 / 4.14-4.20	-0.14 / -0.1	0.07-0.14 / 0.09-0.11
		FD/FL_IIId_m12	1&2	EMFv004-tgac108	IIId-m	3.09-3.97	-0.09	0.05-0.07
		FD/FL_Va_m12	1&2	UDF003-gatc168	Va-m	3.99-4.39	0.09	0.06-0.07
		FD/FL_Vb_m2	2	UDF009	Vb-m	3.60	-0.08	0.06
		FD/FL_VIa_m12	1&2	gata170-ccta102	VIa-m	3.81-3.03	-0.08	0.05-0.06
	DW^{2}	DW_IIIa_f2	2	tcaa312	IIIa-f	3.67	-0.90	0.12
		DW_VIa_m1	1	tgtt320	VIa-m	3.61	1.31	0.12
		DW_VIIb_m1	1	EMFvi175	VIIb-m	3.14	-0.27	0.11
	FW^{3}	FW_Ia_f1	1	tcaa370	Ia-f	3.61	2.28	0.08
		FW_IIb_m13	1&3	gttg135-BAFACT028	IIb-m	4.23-5.37	-1.94	0.08-0.10
		FW_IIIc1_m3	3	UDF004	IIIc1-m	3.78	1.30	0.07
	RD^{3}	RD_IIb_m3	3	tgac460	IIb-m	5.10	-2.75	0.11
		RD_IIId_f1	1	gtaa268	IIId-f	4.99	4.99	0.14
		RD_IVc_m1	1	gaac250	IVc-m	3.56	4.69	0.12
		RD_Vc_m2	2	caaa336	Vc-m	4.09	4.79	0.13
		RD_VIb_m3	3	tcac235	VIb-m	3.15	2.09	0.06
		RD_VIIa_m12	1&2	gatt560	VIIa-m	3.25-3.77	-4.06	0.08-0.11
Firmness								
(8, 7)	FIRM^{3}	FIRM_IIb_m3	3	gttg135	IIb-m	3.91	-3.10	0.07
		FIRM_IIIa_m1	1	gaaa370	IIIa-m	4.00	2.56	0.08
		FIRM_IIIb_m2	2	cctc288	IIIb-m	3.00	-4.90	0.10
		FIRM_IIIa_f2	2	UDF001	IIIa-f	3.11	3.72	0.06
		FIRM_IIIc_f2	2	tcag435	IIIc-f	4.64	-4.90	0.10
		FIRM_IVa_f1	1	EMFvi175	IVa-f	3.48	2.69	0.09
		FIRM_Vc_m3 / f3	3	tgtt140 / gtta320	Vc-m / f	3.82 / 5.29	3.36 / -3.73	0.09 / 0.11
Colour								
(29, 19)	a^{3}	a_Ia_f2	2	tcac248	Ia-f	3.03	2.11	0.07
		a_IIa_f123	1&2&3	BFACT037-Fvi11	IIa-f	3.65-4.03	-1.94	0.08-0.09
		a_IVd_m1	1	tgac408	IVd-m	4.05	-3.58	0.13
		a_Vb_m3	3	tgat148	Vb-m	2.99	1.39	0.06
		a_VIa_m3 / f1	3 / 1	tcaa168 / Fvi020	VIa-m / f	4.88 / 3.19	1.79 / -1.64	0.07-0.10
		a_VIb_f2	2	EMFv010	VIb-f	3.20	2.13	0.07
	b^{3}	b_Ia_m3	3	caaa179	Ia-m	4.37	0.09	0.08
		b_IIIa_f3	3	gtat256**	IIIa-f	5.02	-0.11	0.12
		b_VIa_m3 / f1	3 / 1	tcaa168 / ccta303	VIa-m / f	3.53 / 3.25	0.08 / -1.84	0.06-0.07
		b_VIb_f2	2	EMFv010	VIb-f	3.26	2.02	0.08
	L^{3}	L_IIa_f3	3	BFACT037	IIa-f	2.90	-0.03	0.05
		L_IIIa_m2 / f23	2 / 2&3	gata165 / gtat256	IIIa-m / f	2.92 / 3.01-4.17	-1.27 / -0.70	0.06 / 0.08-0.11

		L_IVd_m2	2	tggx104	IVd-m	3.42	1.38	0.07
		L_VIa_m13	1&3	tgta383-gatt255	VIa-m	3.36-3.78	0.76	0.07
	ANTH^{2}	ANTH_Ia_f2	2	ccaa280	Ia-f	3.22	-0.12	0.06
		ANTH_IIa_f23	2&3	BFACT0026gtgx115	IIa-f	3.03-3.78	0.11	0.06-0.07
		ANTH_IIIa_f3	3	tcta277	IIIa-f	3.56	-0.11	0.08
		ANTH_VIa_m23 / f3	2 / 3	gata170 / caag162	VIa-m / f	8.16-9.80 / 4.09	-1.55	0.15-0.17 / 0.08
		ANTH_VIb_f2	2	ccaa278	VIb-f	3.84	-0.13	0.07
Sugar related traits (15, 12)	SSC^{3}	SSC_IIIa_m2 / f2	2	EMFv004 / gtat256	IIIa-m / f	3.52 / 2.91	1.01 / -0.68	0.09
		SSC_Va_f3	3	tcaa355	Va-f	3.84	0.57	0.08
		SSC_VIa_m2 / f3	2	EMFv006 / ccta303	VIa-m / f	2.90 / 4.10	0.52 / -0.59	0.06 / 0.08
	FRU^{2}	FRU_IVb_m1	1	BFCAT008*	IVb-m	3.04	2.01	0.06
		FRU_Vc_f1	1	BFACT005	Vc-f	3.32	2.18	0.07
	GLU^{2}	GLU_Ib_f1	1	tgaa114	Ib-f	3.13	2.19	0.05
		GLU_IIIa_f2	2	UDF001*	IIIa-f	2.98	-1.96	0.08
		GLU_IIIc_f1	1	UDF016	IIIc-f	4.47	2.56	0.07
		GLU_IVa_f1	1	gtag267	IVa-f	4.06	2.44	0.07
		GLU_VIa_f1	1	gctg280	VIa-f	3.71	-2.80	0.09
	SUCR^{2}	SUCR_VIa_m1	1	EMFv006	VIa-m	4.66	5.54	0.09
		SUCR_VIIa_f12	1&2	caat163-BFACT044	VIIa-f	3.93-5.32	4.86	0.08-0.13
Acid related traits (22, 21)	pH^{3}	pH_Ia_m3	3	caaa179	Ia-m	5.90	0.08	0.11
		pH_IIIb_m2	2	EMFv004	IIIb-m	3.14	0.07	0.08
		pH_IIIc_f2	2	UDF016	IIIc-f	5.32	0.08	0.10
		pH_IVc_f1	1	tcac210*	IVc-f	2.87	-0.08	0.07
		pH_Vb_f3	3	tgaa460*	Vb-f	6.38	0.08	0.13
		pH_VIa_f3	3	gtgx540	VIa-f	4.97	-0.07	0.09
	TA^{3}	TA_Ia_m3	3	tgaa197	Ia-m	4.51	-9.04	0.09
		TA_IIc_m1	1	tgtg270	IIc-m	3.43	-8.35	0.07
		TA_IIId_m2	2	caaa263	IIId-m	3.36	8.23	0.07
		TA_IVa_f2	2	tggx136	IVa-f	3.32	-10.87	0.07
		TA_Vb_m2 / f3	2 / 3	gaaa310 / cttg195	Vb-m / f	3.73 / 5.80	0.82	0.07 / 0.12
	CIT^{2}	CIT_Ia_f1	1	gtgx575	Ia-f	4.81	-0.79	0.10
		CIT_IIc_m2	2	tcaa435	IIc-m	3.15	-0.09	0.06
		CIT_IIIa_f1	1	ggat355	IIIa-f	3.47	-0.67	0.07
		CIT_Vb_f2	2	gaat430	Vb-f	3.23	-0.59	0.09
		CIT_VIa_f1	1	gtgx540	VIa-f	3.48	0.62	0.06
		CIT_VIIb_f1	1	caaa154	VIIb-f	4.14	0.71	0.08
	MAL^{2}	MAL_Vd_f2	2	gtat550	Vd-f	2.93	0.15	0.07
		MAL_VIa_m1	1	catc138	VIa-m	5.93	-0.33	0.11
		MAL_VIb_m1	1	caag140	VIb-m	3.51	-0.30	0.09
		MAL_VIId_m1	1	EMFv021	VIId-m	3.94	-0.27	0.07

[a], Traits are the following: Development: FD fruit diameter, FL fruit length, FD/FL ratio, DW dry weight, FW fruit weigth, RD ripening date of the fruit. Texture: FIRM fruit firmness. Colour: skin colour parameters a, b and L, ANTH total anthocyanin. Sugar related traits: SSC soluble-solids content, FRU fructose, GLU glucose, SUCR sucrose. Acid related traits : pH, TA titratable acidity, CIT citrate, MAL malate. The numbers indicated in brackets under the traits are the total number QTLs detected and the total number of unique QTL per trait. The number nearby each trait corresponds to the number of years of measurements (2 or 3).

[b], name of the QTL, which includes the names of the trait, the linkage group, the parental map on which the QTL was detected (male (m) or female (f)) and the year of observation. When QTL were observed several years, the number of year is separated by &. When the QTL was observed on male and female on the same linkage group, the number of year is separated by /.

[c], year of observation of the QTL.

[d], The most-closely associated marker locus is indicated. When more than two QTLs (several years of observation) were observed, the interval is given. Distorted markers are noted with asterisks at the end of their name (*0.01 ≥ P ≥ 0.001 and **P < 0.001).

[e], Name of the linkage group according to Rousseau-Gueutin et al. (2008). The Roman number indicates the homoeologous group number. The letter, a, b c, or d, indicates one the four homoeologous linkage group and the final letter, m or f, indicates if the linkage group belongs to the male or the female linkage maps.

[f], LOD is the log-likelihood at that position. When more than two QTLs were observed the range is given.

[g], Mean effect (or range of the mean effect when at least two QTLs were merged) on a trait mean value of the presence of one allele at a marker by comparison with the presence of the second allele. + and - indicates the direction of the additive effect. A positive effect means a higher value for 'Capitola' allele on the female map or a higher value for 'CF1116' on the male map.

[h], R^2 is the percentage of phenotypic variation explained by the QTL. When more than two QTLs were observed the range is given.