

**Combining QTL mapping and gene expression analysis to elucidate the genetic control of ‘crumbly’  
fruit in red raspberry (*Rubus idaeus*)**

Luca M. Scolari\*, Robert D. Hancock, Pete E. Hedley, Jenny Morris, Kay Smith and Julie Graham

The James Hutton Institute, Invergowrie, Dundee, DD25DA, Scotland, United Kingdom

\*corresponding author

**Table S1:** List of 120 microarray probes matching genes located within the three crumbly QTLs and significantly differentially expressed on a stage\*phenotype basis. The two QTLs, cr\_JHI\_1-15 and cr\_JHI\_3-15, previously identified by Graham et al. [1] are located on linkage group 1 and 3 respectively. The third crumbly QTL, cr\_JHI\_3-20, is identified during this work on linkage group 3. For each probe the gene ID of the matched *A. thaliana* gene and the scaffold of the *Rubus* (Glen Moy genome assembly) browser [9] to which the gene is located are reported. In the last column the *A. thaliana* name for each gene and where available a brief description of its function [10] are presented. In the fourth column (i.e. significant interaction effect), the stage/s to which the stage\*phenotype interaction is significant ( $p < 0.001$ ) are reported; the bold lowercase letters correspond to: **a** = only closed bud, **b** = open flower, **c** = green berry, **d** = closed bud and open flower, **e** = closed bud and green berry, **f** = open flower and green berry and **g** = closed bud, open flower and green berry.

Microarray probe	<i>A. thaliana</i> gene ID	QTL	scaffold	significant interaction effect	<sup>a</sup> Gene function
CUST_1115_P1426541283	AT4G20960.1	cr_JHI_1-15	5441	<b>c</b>	Pyrimidine Deaminase, an enzyme catalysing the second step in the riboflavin biosynthesis.
CUST_22099_P1426541283	AT5G52240.1	cr_JHI_1-15	260	<b>a</b>	Membrane Steroid Binding Protein 1, a protein with similarity to progesterone-binding proteins in animals.
CUST_25407_P1426541283	AT5G02790.1	cr_JHI_1-15	462	<b>a</b>	Glutathione S-transferase family protein.

CUST_25669_PI426541283	None	cr_JHI_1-15	3053	c	
CUST_27288_PI426541283	AT4G11740.1	cr_JHI_1-15	2164	c	SAY1, a novel protein with a small region of similarity to coil-coiled domain of yeast VSP27 protein.
CUST_30393_PI426541283	AT1G01770.1	cr_JHI_1-15	353	c	Propionyl-CoA carboxylase.
CUST_30947_PI426541283	AT1G03310.2	cr_JHI_1-15	318	e	Isoamylase 2, a protein with strong similarity to isoamylase but lacks critical residues known to be important for activity.
CUST_34519_PI426541283	AT2G38040.1	cr_JHI_1-15	353	c	CAC3, carboxyltransferase alpha subunit of acetyl-CoA carboxylase, involved in de novo fatty acid biosynthesis.
CUST_34561_PI426541283	None	cr_JHI_1-15	552	c	

CUST_37235_PI426541283	AT2G46000.1	cr_JHI_1-15	3053	<b>f</b>	LDL receptor wingless signalling/trafficking chaperone involved in protein folding.
CUST_41049_PI426541283	None	cr_JHI_1-15	3407	<b>b</b>	
CUST_41314_PI426541283	AT2G45990.1	cr_JHI_1-15	3053	<b>c</b>	ribosomal RNA small subunit methyltransferase G.
CUST_46143_PI426541283	None	cr_JHI_1-15	260	<b>c</b>	
CUST_51115_PI426541283	ATCG00020.1	cr_JHI_1-15	2451	<b>c</b>	PSBA, the chlorophyll binding protein D1, a part of the photosystem II reaction centre core.
CUST_5360_PI426541283	None	cr_JHI_1-15	462	<b>g</b>	

---

---

CUST_10102_P1426541283	AT1G05280.1	cr_JHI_3-15	4	e	ERV-F (C)1 provirus ancestral Env polypotein, putative (DUF604).
CUST_10197_P1426541283	AT2G32540.1	cr_JHI_3-15	4	d	Cellulose Synthase-like B4.
CUST_11545_P1426541283	AT2G04570.1	cr_JHI_3-15	52	f	OSP1, GDSL-motif esterase/acyltransferase/lipase.
CUST_12005_P1426541283	AT5G42570.1	cr_JHI_3-15	4	f	B-cell receptor-associated 31-like protein.
CUST_12159_P1426541283	AT2G19130.1	cr_JHI_3-15	858	c	S-locus lectin protein kinase family protein.
CUST_12989_P1426541283	AT5G15180.1	cr_JHI_3-15	4	c	PRX56, Peroxidase superfamily protein.

CUST_13398_PI426541283	AT2G04240.1	cr_JHI_3-15	826	d	XERICO, a small protein with an N-terminal trans-membrane domain and a RING-H2 zinc finger motif located at the C-terminus involved in ABA metabolism.
CUST_13557_PI426541283	AT1G26320.1	cr_JHI_3-15	4	e	Zinc-binding dehydrogenase family protein.
CUST_13601_PI426541283	AT5G35840.1	cr_JHI_3-15	76	e	PHYTOCHROME C, the apoprotein of phytochrome;one of a family of photoreceptors that modulate plant growth and development.
CUST_14918_PI426541283	AT5G38690.1	cr_JHI_3-15	43	e	DDR1, Zinc-finger domain of monoamine-oxidase A repressor R1 protein.
CUST_17056_PI426541283	AT5G14180.1	cr_JHI_3-15	52	g	MPL1, Myzus persicae-induced lipase 1.
CUST_17098_PI426541283	AT4G15240.1	cr_JHI_3-15	4	f	Glycosyltransferase (DUF604).

CUST_17219_PI426541283	AT3G21610.1	cr_JHI_3-15	4	<b>c</b>	Acid phosphatase/vanadium-dependent haloperoxidase-related protein.
CUST_17686_PI426541283	none	cr_JHI_3-15	52	<b>b</b>	
CUST_18985_PI426541283	none	cr_JHI_3-15	43	<b>c</b>	
CUST_19076_PI426541283	AT3G21670.1	cr_JHI_3-15	4	<b>a</b>	NRT1/ PTR FAMILY 6.4, Major facilitator superfamily protein.
CUST_1913_PI426541283	AT4G13500.1	cr_JHI_3-15	76	<b>c</b>	Transmembrane protein.
CUST_19139_PI426541283	AT4G05120.1	cr_JHI_3-15	65	<b>f</b>	Equilibrative Nucleoside Transporter (ENT3).

CUST_19325_P1426541283	AT5G38510.1	cr_JHI_3-15	43	<b>b</b>	Rhomboid-related intramembrane serine protease family protein.
CUST_20489_P1426541283	AT1G11910.1	cr_JHI_3-15	4	<b>e</b>	Aspartic Proteinase 1 (APA 1).
CUST_20853_P1426541283	AT5G38530.1	cr_JHI_3-15	43	<b>b</b>	Tryptophan synthase beta subunit type 2 that catalyses a condensation reaction between serine and indole to generate tryptophan.
CUST_21037_P1426541283	AT5G42570.1	cr_JHI_3-15	4	<b>b</b>	B-cell receptor-associated 31-like protein.
CUST_21963_P1426541283	AT3G29760.1	cr_JHI_3-15	509	<b>c</b>	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein.
CUST_2371_P1426541283	AT5G08080.3	cr_JHI_3-15	4	<b>b</b>	Syntaxin of Plants 132 (SYP132).



CUST_23715_PI426541283	none	cr_JHI_3-15	43	<b>c</b>	
CUST_24407_PI426541283	AT5G12210.1	cr_JHI_3-15	734	<b>b</b>	RAB geranylgeranyl transferase beta subunit 1.
CUST_24998_PI426541283	AT3G21710.2	cr_JHI_3-15	4	<b>a</b>	Vascular-related unknown protein 1 (VUP1), a transmembrane protein.
CUST_26242_PI426541283	AT4G14103.2	cr_JHI_3-15	734	<b>c</b>	F-box/RNI-like superfamily protein.
CUST_26372_PI426541283	AT4G03260.1	cr_JHI_3-15	858	<b>b</b>	Microtubule Associated Stress Protein 1 (MASP1).
CUST_2738_PI426541283	AT5G15870.1	cr_JHI_3-15	43	<b>b</b>	Glycosyl hydrolase family 81 protein.

<b>CUST_27619_PI426541283</b>	AT4G28240.1	cr_JHI_3-15	65	<b>c</b>	WIP 1, member of the wound-induced polypeptide (WIP) family.
<b>CUST_2769_PI426541283</b>	AT3G21760.1	cr_JHI_3-15	10689	<b>c</b>	HYR1, a UDP glycosyltransferase (UGT).
<b>CUST_28007_PI426541283</b>	AT3G29770.1	cr_JHI_3-15	509	<b>c</b>	Methyl Esterase 11, an enzyme protein predicted to act as a carboxylesterase.
<b>CUST_28343_PI426541283</b>	AT5G38600.1	cr_JHI_3-15	43	<b>c</b>	Proline-rich spliceosome-associated (PSP) family protein / zinc knuckle (CCHC-type) family protein.
<b>CUST_28997_PI426541283</b>	AT2G32640.1	cr_JHI_3-15	4	<b>c</b>	Lycopene beta cyclase that catalyses the addition of beta-ionone end groups to the end of lycopene molecules.
<b>CUST_29286_PI426541283</b>	AT2G32250.1	cr_JHI_3-15	835	<b>b</b>	FAR1-related sequence 2 (FARS2).

CUST_29379_PI426541283	AT5G54970.1	cr_JHI_3-15	4	<b>f</b>	Hypothetical protein.
CUST_30238_PI426541283	none	cr_JHI_3-15	858	<b>c</b>	
CUST_31018_PI426541283	AT2G04790.2	cr_JHI_3-15	294	<b>e</b>	PTB domain engulfment adapter.
CUST_31157_PI426541283	none	cr_JHI_3-15	65	<b>b</b>	
CUST_33454_PI426541283	AT1G05180.1	cr_JHI_3-15	4	<b>e</b>	Auxin Resistant 1.
CUST_33675_PI426541283	AT5G38470.1	cr_JHI_3-15	182	<b>g</b>	Radiation sensitive23D (RAD23) proteins play an essential role in the cell cycle, morphology, and fertility of plants through their delivery of UPS (ubiquitin/26S proteasome system) substrates to the 26S proteasome.

CUST_33751_PI426541283	AT5G36930.2	cr_JHI_3-15	76	<b>d</b>	Disease resistance protein (TIR-NBS-LRR class) family.
CUST_34549_PI426541283	AT4G01575.1	cr_JHI_3-15	294	<b>b</b>	KPI-2 a putative Kazal-type serine proteinase inhibitor that is highly expressed in seeds, mature roots and flowers.
CUST_34605_PI426541283	AT5G16970.1	cr_JHI_3-15	4	<b>c</b>	AER, a 2-alkenal reductase that plays a key role in the detoxification of reactive carbonyls.
CUST_34852_PI426541283	AT1G03560.1	cr_JHI_3-15	263	<b>c</b>	Pentatricopeptide repeat (PPR-like) superfamily protein.
CUST_35039_PI426541283	AT3G21630.1	cr_JHI_3-15	76	<b>b</b>	Chitin Elicitor Receptor Kinase 1, Involved in the perception and transduction of the chitin oligosaccharide elicitor.
CUST_35767_PI426541283	AT2G32970.2	cr_JHI_3-15	52	<b>b</b>	G1/S-specific cyclin-E protein.

CUST_35866_P1426541283	AT4G28210.1	cr_JHI_3-15	65	<b>f</b>	Embryo defective 1923.
CUST_36166_P1426541283	AT3G04090.1	cr_JHI_3-15	4	<b>g</b>	Small and basic intrinsic protein 1A, a family of plant aquaporins located on endoplasmic reticulum (ER).
CUST_3643_P1426541283	AT5G15950.1	cr_JHI_3-15	43	<b>b</b>	SAMDC2, adenosylmethionine decarboxylase family protein.
CUST_36601_P1426541283	none	cr_JHI_3-15	4	<b>d</b>	
CUST_37835_P1426541283	AT1G30330.2	cr_JHI_3-15	664	<b>b</b>	Auxin Response Factor 6 (ARF6).
CUST_38020_P1426541283	AT4G15417.1	cr_JHI_3-15	4	<b>d</b>	RTL1, a RNase II-like 1 protein.

CUST_38488_PI426541283	none	cr_JHI_3-15	52	<b>g</b>	
CUST_38657_PI426541283	AT2G46410.1	cr_JHI_3-15	4	<b>c</b>	CAPRICE, Nuclear-localized R3-type MYB transcription factor.
CUST_39870_PI426541283	none	cr_JHI_3-15	43	<b>f</b>	
CUST_39944_PI426541283	AT3G22060.1	cr_JHI_3-15	4	<b>a</b>	Protein with Pfam profile: PF01657 Domain of unknown function.
CUST_43180_PI426541283	AT1G05200.1	cr_JHI_3-15	4	<b>c</b>	Glutamate receptor 3.4, a putative glutamate receptor GLR3 with dual localization in plastid and plasma membrane.
CUST_44276_PI426541283	AT1G05030.1	cr_JHI_3-15	4	<b>a</b>	Major facilitator superfamily protein.

<b>CUST_44285_PI426541283</b>	AT4G10270.1	cr_JHI_3-15	65	<b>a</b>	WIP4, Member of the wound-induced polypeptide (WIP) family.
<b>CUST_45148_PI426541283</b>	AT1G61900.1	cr_JHI_3-15	4	<b>c</b>	Hypothetical protein.
<b>CUST_45239_PI426541283</b>	AT1G22900.1	cr_JHI_3-15	4	<b>a</b>	Disease resistance-responsive (dirigent-like protein) family protein.
<b>CUST_45845_PI426541283</b>	AT4G28230.1	cr_JHI_3-15	65	<b>c</b>	Hypothetical protein.
<b>CUST_45962_PI426541283</b>	AT1G06570.1	cr_JHI_3-15	676	<b>f</b>	Phytoene desaturation 1 (PDS 1), enzyme involved in the biosynthesis of both plastoquinone and tocopherols in plants.
<b>CUST_46865_PI426541283</b>	AT2G04270.5	cr_JHI_3-15	826	<b>b</b>	RNASE E, a ribonuclease located in the chloroplast and is involved in its development.

CUST_47338_P1426541283	AT3G30841.1	cr_JHI_3-15	43	<b>a</b>	Cofactor-independent phosphoglycerate mutase.
CUST_47982_P1426541283	none	cr_JHI_3-15	76	<b>a</b>	
CUST_51233_P1426541283	AT3G15850.1	cr_JHI_3-15	52	<b>c</b>	Fatty Acid Desaturase B (JB67), a chloroplastic enzyme responsible for the synthesis of 16:1 fatty acids from galactolipids and sulpholipids.
CUST_51593_P1426541283	AT2G05810.1	cr_JHI_3-15	52	<b>a</b>	ARM repeat superfamily protein.
CUST_51688_P1426541283	AT2G20890.1	cr_JHI_3-15	65	<b>e</b>	Thylakoid Formation1, a chloroplast-localized Thylakoid formation1 gene product involved in vesicle-mediated formation of thylakoid membranes.
CUST_52187_P1426541283	AT5G48150.1	cr_JHI_3-15	162	<b>f</b>	Phytochrome A signal transduction 1.



CUST_52902_PI426541283	AT1G05120.1	cr_JHI_3-15	4	<b>b</b>	Helicase protein with RING/U-box domain-containing protein.
CUST_5304_PI426541283	AT5G38640.1	cr_JHI_3-15	43	<b>b</b>	NagB/RpiA/CoA transferase-like superfamily protein.
CUST_5432_PI426541283	AT3G22220.1	cr_JHI_3-15	2858	<b>3</b>	hAT transposon superfamily.
CUST_54460_PI426541283	AT1G62360.1	cr_JHI_3-15	4	<b>e</b>	Shoot Meristemless (STM), class I knotted-like homeodomain protein that is required for shoot apical meristem (SAM) formation during embryogenesis and for SAM function throughout the lifetime of the plant.
CUST_6848_PI426541283	AT4G26840.1	cr_JHI_3-15	52	<b>d</b>	SUMO 1, a small ubiquitin-like modifier (SUMO). polypeptide that becomes covalently attached to various intracellular protein targets, much like ubiquitination, leading to post-translational modification of those targets.
CUST_8109_PI426541283	AT1G68590.1	cr_JHI_3-15	182	<b>e</b>	PSRP3/1, a ribosomal protein PSRP-3/Ycf65.

---

---

CUST_10154_PI426541283	AT3G63440.1	cr_JHI_3_20	1500	e	Cytokinin oxidase/dehydrogenase 6, the enzyme catalyses the degradation of cytokinins.
CUST_1076_PI426541283	AT3G14460.1	cr_JHI_3_20	419	g	LRRAC1, a leucine rich repeat protein that also contains an adenylate cyclase catalytic core motif.
CUST_1418_PI426541283	AT5G43822.1	cr_JHI_3_20	419	c	OPENER, an essential protein of unknown function.
CUST_27324_PI426541283	AT3G63440.1	cr_JHI_3_20	1500	e	Cytokinin oxidase/dehydrogenase 6, the enzyme catalyses the degradation of cytokinins.
CUST_16284_PI426541283	AT2G41700.1	cr_JHI_3_20	79	e	ATP-binding cassette A1.
CUST_17728_PI426541283	none	cr_JHI_3_20	6951	b	

CUST_19120_P1426541283	none	cr_JHI_3_20	567	<b>f</b>	
CUST_2016_P1426541283	AT5G06750.1	cr_JHI_3_20	3486	<b>c</b>	Arabidopsis PP2C CLADE D 8, a phosphatase 2C family protein.
CUST_20312_P1426541283	AT3G55600.1	cr_JHI_3_20	874	<b>e</b>	Membrane fusion protein Use1.
CUST_21749_P1426541283	none	cr_JHI_3_20	1541	<b>a</b>	
CUST_26373_P1426541283	AT2G21540.1	cr_JHI_3_20	499	<b>b</b>	SEC14-like 3 protein.
CUST_26573_P1426541283	none	cr_JHI_3_20	1541	<b>a</b>	

CUST_27462_PI426541283	none	cr_JHI_3_20	2505	<b>g</b>	
CUST_28494_PI426541283	AT2G41900.1	cr_JHI_3_20	419	<b>a</b>	Tandem zinc finger protein 7 (TZF7).
CUST_30381_PI426541283	AT3G16250.1	cr_JHI_3_20	377	<b>e</b>	NDF4, a novel subunit of the chloroplast NAD(P)H dehydrogenase complex, involved in cyclic electron flow around photosystem I to produce ATP.
CUST_30711_PI426541283	AT1G68030.1	cr_JHI_3_20	10179	<b>c</b>	RING/FYVE/PHD zinc finger superfamily protein.
CUST_33239_PI426541283	AT5G06860.1	cr_JHI_3_20	4005	<b>e</b>	PGIP1, a polygalacturonase inhibiting protein involved in defense response.
CUST_38171_PI426541283	AT3G57540.1	cr_JHI_3_20	419	<b>a</b>	REM4.1, a remorin family protein.

CUST_40106_P1426541283	AT1G03780.3	cr_JHI_3_20	1094	<b>e</b>	Targeting protein for XKLP2, has three domains involved in nuclear targeting, one in nuclear export and two in microtubule binding. Involved in mitotic spindle assembly during late prophase and early prometaphase.
CUST_42366_P1426541283	AT3G29240.1	cr_JHI_3_20	874	<b>c</b>	PPR containing protein (DUF179).
CUST_42627_P1426541283	none	cr_JHI_3_20	3006	<b>g</b>	
CUST_4327_P1426541283	AT5G17000.1	cr_JHI_3_20	10179	<b>f</b>	Zinc-binding dehydrogenase family protein.
CUST_43612_P1426541283	none	cr_JHI_3_20	2505	<b>b</b>	
CUST_44619_P1426541283	AT3G12110.1	cr_JHI_3_20	3486	<b>e</b>	ACTIN-11, an actin that is expressed predominantly during reproductive development.

<b>CUST_46278_PI426541283</b>	AT4G34670.1	cr_JHI_3_20	874	<b>b</b>	Ribosomal protein S3Ae.
<b>CUST_46771_PI426541283</b>	AT4G19860.1	cr_JHI_3_20	73	<b>c</b>	Cytosolic calcium-independent phospholipase A.
<b>CUST_561_PI426541283</b>	AT1G53050.1	cr_JHI_3_20	4488	<b>e</b>	Protein kinase superfamily protein.

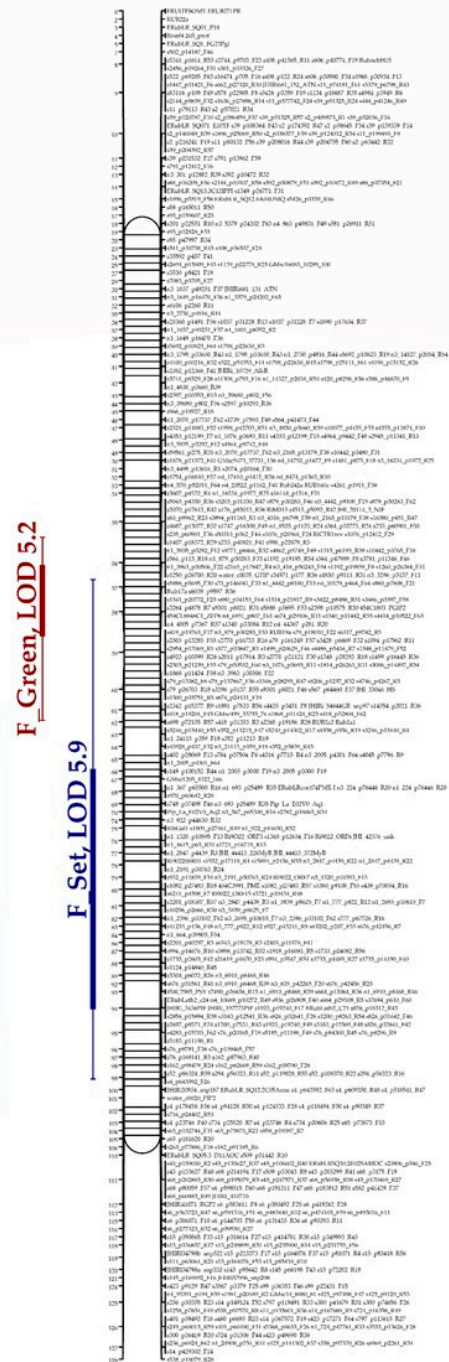
---

<sup>a</sup>source The Arabidopsis Information Resource TAIR [10]

## linkage group 1



## linkage group 3



**Figure S1.** Genotype by Sequencing (GbS) linkage maps for linkage groups 1 and 3 of the Glen Moy x Latham mapping population [4]. Bars and whiskers (to the left of the chromosome) show one- and two-LOD support intervals for QTL locations. The linkage group 1 shows a crumbly fruit QTL in black colour (cr\_JHI\_1-15 with LOD 6.1 and with 1-12 cM and 0-15 cM of one and two LOD supporting intervals). The linkage group 3 shows two crumbly fruit QTLs, one in red (cr\_JHI\_3-20 with LOD 6.3 and with 52-60 cM and 50-64 of one and two LOD supporting intervals) and one in green (cr\_JHI\_3-15 with LOD 6.0 and 106-112 cM and 93-118 of one and two LOD supporting intervals) colour, and three fruit ripening QTLs (i.e. fruit set, green fruit), in blue, purple red and pink respectively.