

Figure S1 Heatmap of differentially expressed genes. The log₂ value of the ratio between 'Kiyomi' and 'Shiranui' is presented. K1 and K2: 'Kiyomi' samples from first and second developmental stages, respectively; S1 and S2: 'Shiranui' samples from first and second developmental stages, respectively. The numbers in parentheses represent independent biological replicates.

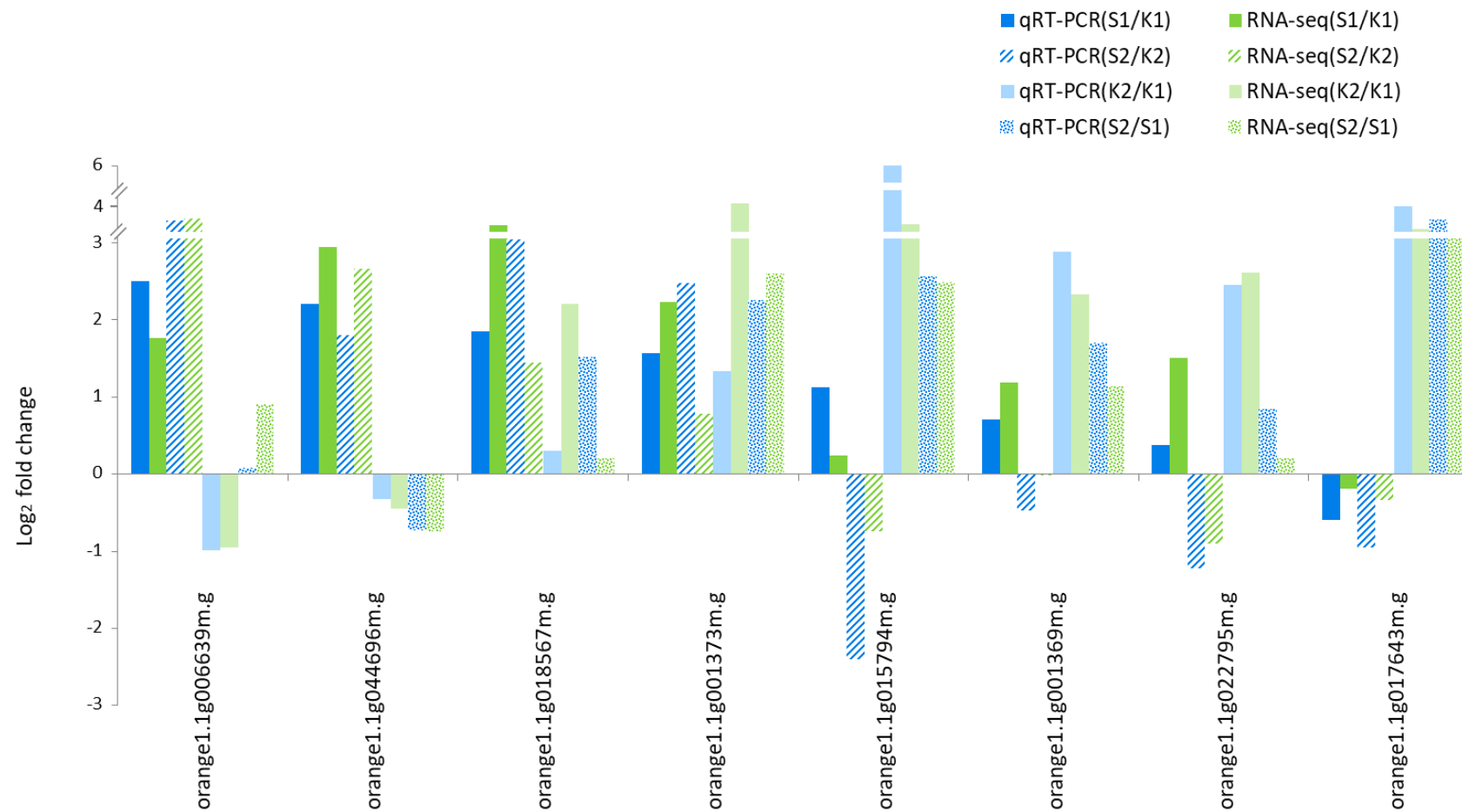


Figure S2 Verification of RNA-seq by qRT-PCT. S1/K1: Comparison of 'Shiranui' (first-stage) to 'Kiyomi' (first-stage); S2/K2: Comparison of 'Shiranui' (second-stage) to 'Kiyomi' (second-stage); K2/K1: Comparison of 'Kiyomi' (second-stage) to 'Kiyomi' (first-stage); S2/S1: Comparison of 'Shiranui' (second-stage) to 'Shiranui' (first-stage)

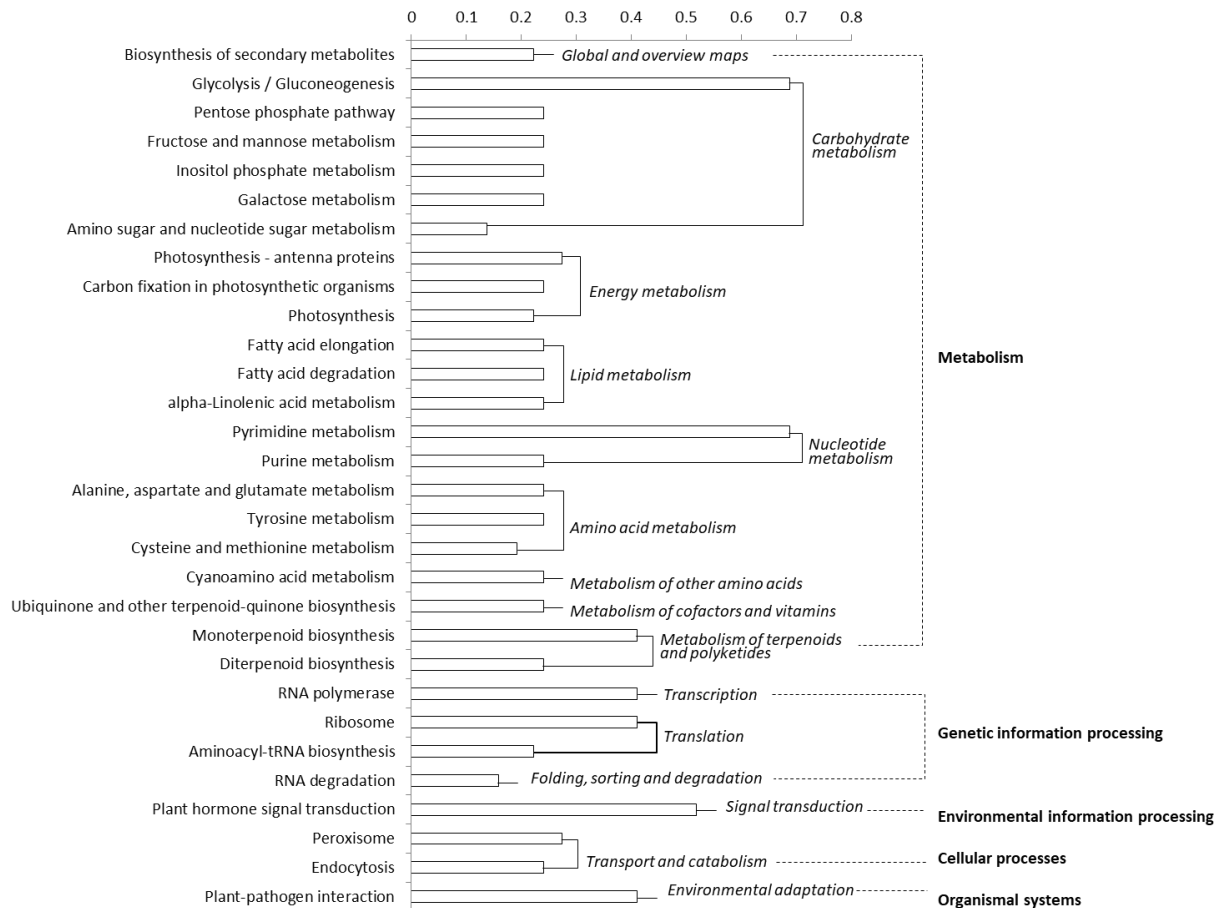


Figure S3 Top 30 significantly enriched pathways based on up-expressed genes in 'Kiyomi' compared with in 'Shiranui' at the first-stage. The pathways are grouped using solid lines according to <http://www.genome.jp/kegg/pathway.html> (group names are in italics). The groups are further classed into KEGG pathway maps using dotted lines (KEGG pathway map names are in bold). The pathway enrichment analysis was significant at FDR < 0.005. The x-axis represents the $-\log(\text{FDR value})$.

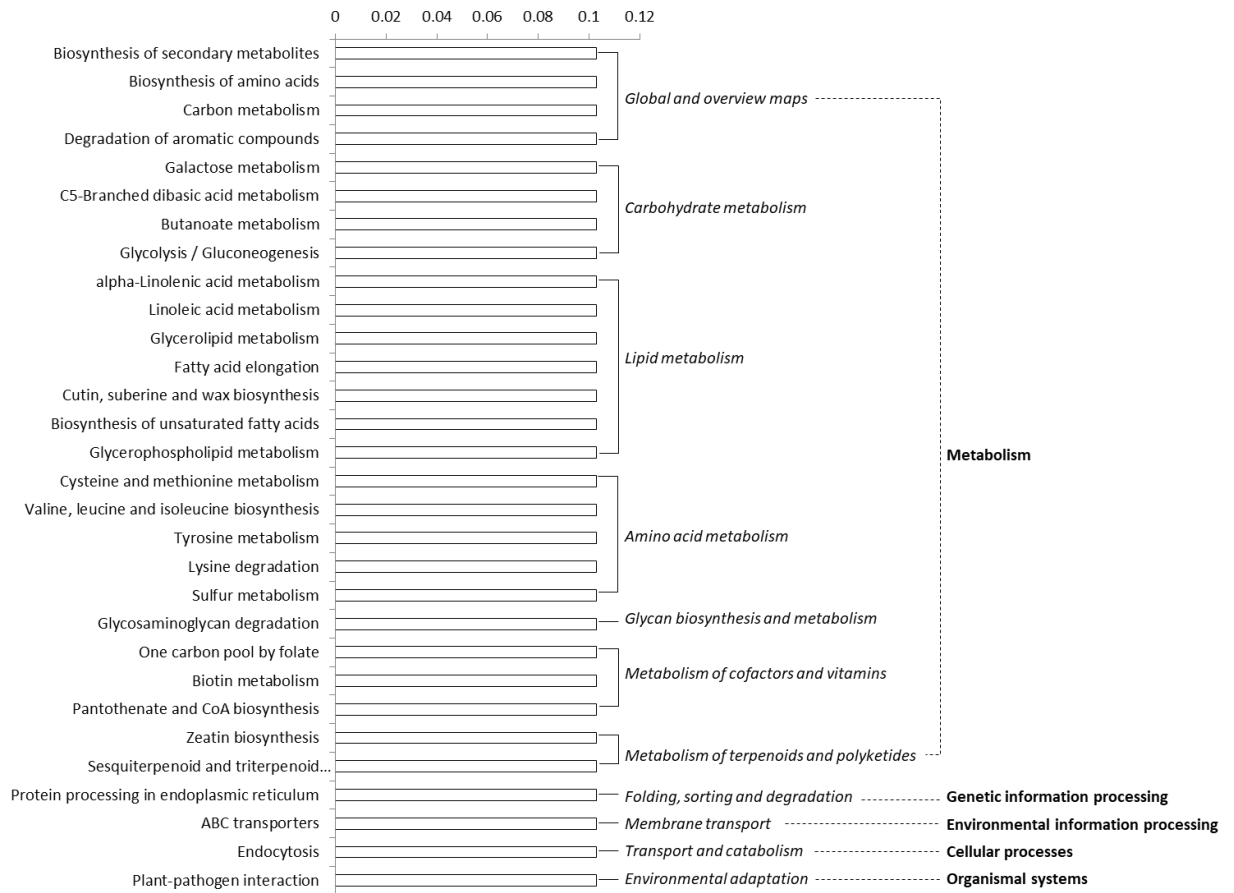


Figure S4 Top 30 significantly enriched pathways based on up-expressed genes in 'Shiranui' compared with in 'Kiyomi' at the first-stage. The pathways are grouped using solid lines according to <http://www.genome.jp/kegg/pathway.html> (group names are in italics). The groups are further classed into KEGG pathway maps using dotted lines (KEGG pathway map names are in bold). The pathway enrichment analysis was significant at FDR < 0.005. The x-axis represents the $-\log(\text{FDR value})$.

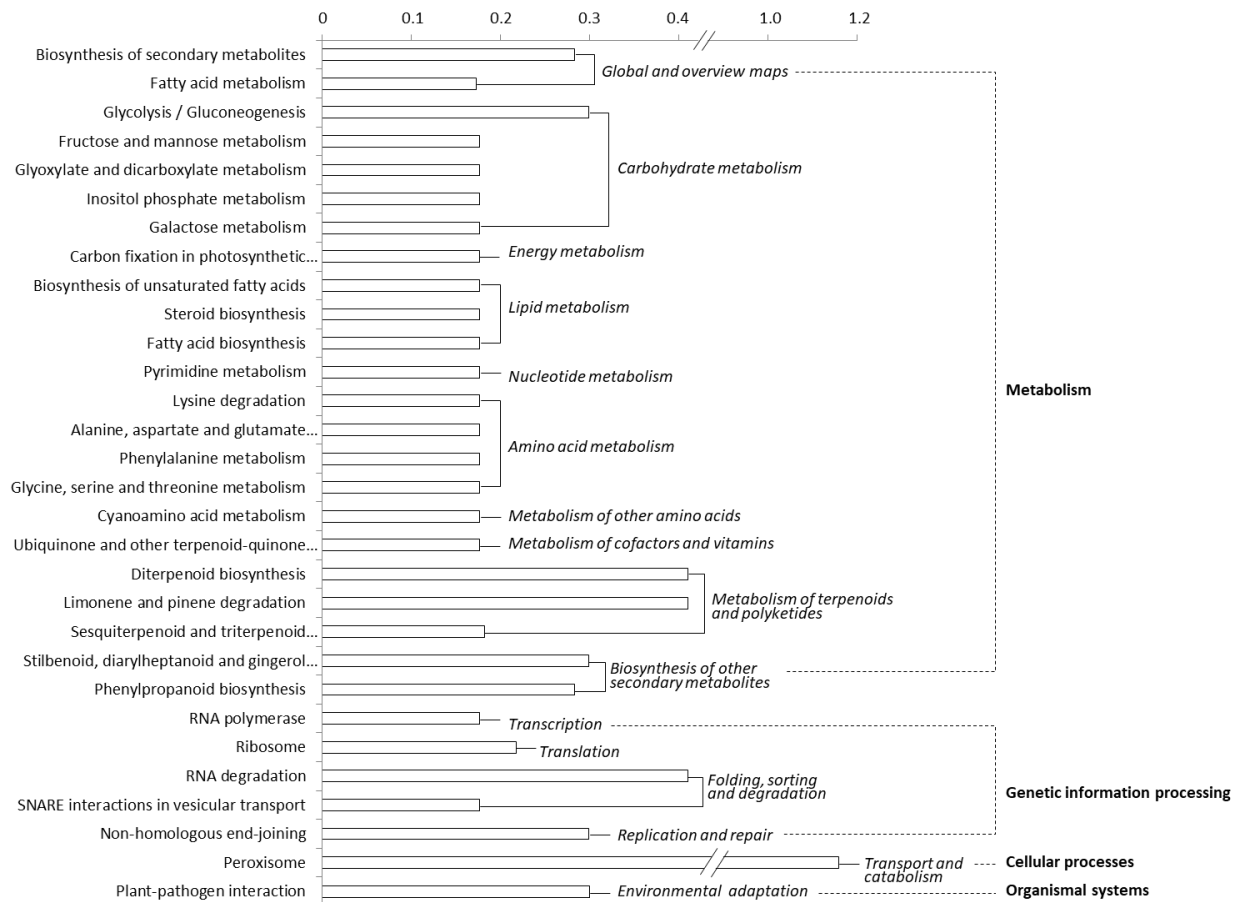


Figure S5 Top 30 significantly enriched pathways based on up-expressed genes in 'Kiyomi' compared with in 'Shiranui' at the second-stage. The pathways are grouped using solid lines according to <http://www.genome.jp/kegg/pathway.html> (group names are in italics). The groups are further classed into KEGG pathway maps using dotted lines (KEGG pathway map names are in bold). The pathway enrichment analysis was significant at FDR < 0.005. The x-axis represents the $-\log(\text{FDR value})$.

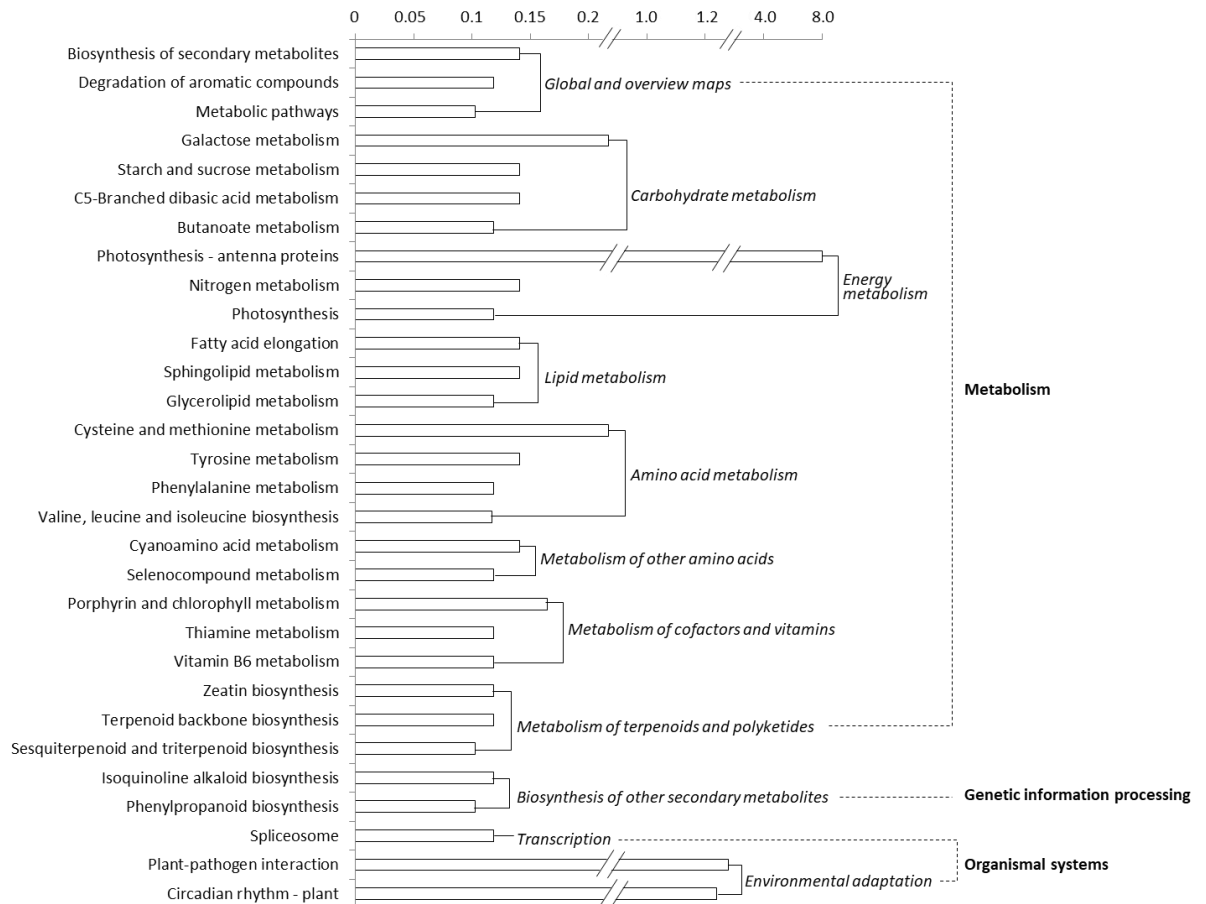


Figure S6 Top 30 significantly enriched pathways based on up-expressed genes in 'Shiranui' compared with in 'Kiyomi' at the second-stage. The pathways are grouped using solid lines according to <http://www.genome.jp/kegg/pathway.html> (group names are in italics). The groups are further classed into KEGG pathway maps using dotted lines (KEGG pathway map names are in bold). The pathway enrichment analysis was significant at $\text{FDR} < 0.005$. The x -axis represents the $-\log(\text{FDR value})$.

Table S1 Primers used in quantitative qRT-PCR experiments

Contigs	InterPro description	Primers (5'-3')
orange1.1g006639m.g	cellulose synthase-like B3	Former: GTGGATCCTTACTTGGGGCT Reverse: GCAGGAAAGTGGAGTTGGTG
orange1.1g044696m.g	6-phosphogluconate dehydrogenase family protein	Former: CCCTTTACAGCATCCCTCCA Reverse: ATCAGATTGTGGTGGGAGCA
orange1.1g018567m.g	galacturonosyltransferase-like 2	Former: TGAAGAAGGTTGTTTGCCTCTT Reverse: CATTCACTCCGTCCTACAACAC
orange1.1g001373m.g	cellulose synthase A9	Former: AGTGGACGGGATGAAGAAG Reverse: AATGTGGTGCGGTCTTTTC
orange1.1g015794m.g	Plant invertase/pectin methylesterase inhibitor superfamily	Former: GGGCTTATTTGAGAACGTGGA Reverse: TTCACTACTGTTTTGCCGATCC
orange1.1g001369m.g	cellulose synthase 6	Former: TTGTGTACCCTTGGACCTCC Reverse: TCCCAGTGAGAAGGCAGAAG
orange1.1g022795m.g	cellulose synthase-like D6	Former: CGCTTGATTATCCGCCAGAG Reverse: TGCAAACCTCCAAGCTTCCC
orange1.1g017643m.g	galacturonosyltransferase-like 7	Former: TTAGATCCTCACACCTCGACAG Reverse: GGAATACGGAGGCTTTTCGAAA

InterPro descriptions are based on the *Arabidopsis thaliana* database.

Table S2 Top 30 significantly enriched pathways based on up-regulated genes

Based on up-expressed genes in	Enriched pathways	$-\log(\text{FDR})$	Groups within KEGG pathway maps	KEGG pathway maps
K1 (K1 vs. K2)	Fatty acid metabolism	0.4705	Global and overview maps	Metabolism
	Inositol phosphate metabolism	0.1286	Carbohydrate metabolism	Metabolism
	Galactose metabolism	0.1286	Carbohydrate metabolism	Metabolism
	Glycolysis / Gluconeogenesis	0.1230	Carbohydrate metabolism	Metabolism
	Photosynthesis - antenna proteins	0.2982	Energy metabolism	Metabolism
	Nitrogen metabolism	0.1732	Energy metabolism	Metabolism
	Biosynthesis of unsaturated fatty acids	0.6036	Lipid metabolism	Metabolism
	Ether lipid metabolism	0.5475	Lipid metabolism	Metabolism
	Fatty acid biosynthesis	0.5475	Lipid metabolism	Metabolism
	Arachidonic acid metabolism	0.3654	Lipid metabolism	Metabolism
	Cutin, suberine and wax biosynthesis	0.1914	Lipid metabolism	Metabolism
	Cysteine and methionine metabolism	0.4705	Amino acid metabolism	Metabolism
	Valine, leucine and isoleucine biosynthesis	0.2934	Amino acid metabolism	Metabolism
	Tyrosine metabolism	0.5475	Amino acid metabolism	Metabolism
	Phenylalanine metabolism	0.1914	Amino acid metabolism	Metabolism
	Arginine and proline metabolism	0.1914	Amino acid metabolism	Metabolism
	Glutathione metabolism	0.5475	Metabolism of other amino acids	Metabolism
	Glycosphingolipid biosynthesis - ganglio series	0.1914	Glycan biosynthesis and metabolism	Metabolism
	Glycosaminoglycan degradation	0.1230	Glycan biosynthesis and metabolism	Metabolism
	Pantothenate and CoA biosynthesis	0.1914	Metabolism of cofactors and vitamins	Metabolism

	Thiamine metabolism	0.1286	Metabolism of cofactors and vitamins	Metabolism
	Ubiquinone and other terpenoid-quinone biosynthesis	0.1286	Metabolism of cofactors and vitamins	Metabolism
	Vitamin B6 metabolism	0.1230	Metabolism of cofactors and vitamins	Metabolism
	Tropane, piperidine and pyridine alkaloid biosynthesis	0.7342	Biosynthesis of other secondary metabolites	Metabolism
	Isoquinoline alkaloid biosynthesis	0.5475	Biosynthesis of other secondary metabolites	Metabolism
	Protein processing in endoplasmic reticulum	3.2613	Folding, sorting and degradation	Genetic information processing
	Plant hormone signal transduction	0.2982	Signal transduction	Environmental information processing
	Endocytosis	0.2497	Transport and catabolism	Cellular processes
	Circadian rhythm - plant	2.5470	Environmental adaptation	Organismal systems
	Plant-pathogen interaction	0.1978	Environmental adaptation	Organismal systems
K2 (K1 vs. K2)	Biosynthesis of secondary metabolites	0.8153	Global and overview maps	Metabolism
	Fatty acid metabolism	0.4995	Global and overview maps	Metabolism
	Metabolic pathways	0.4995	Global and overview maps	Metabolism
	Inositol phosphate metabolism	0.0634	Carbohydrate metabolism	Metabolism
	Starch and sucrose metabolism	0.0634	Carbohydrate metabolism	Metabolism
	Amino sugar and nucleotide sugar metabolism	0.0634	Carbohydrate metabolism	Metabolism
	Ascorbate and aldarate metabolism	0.0634	Carbohydrate metabolism	Metabolism
	Pentose and glucuronate interconversions	0.0634	Carbohydrate metabolism	Metabolism
	Photosynthesis	0.4989	Energy metabolism	Metabolism
	Fatty acid elongation	1.7468	Lipid metabolism	Metabolism
	Cutin, suberine and wax biosynthesis	0.6167	Lipid metabolism	Metabolism
	Fatty acid biosynthesis	0.4350	Lipid metabolism	Metabolism
	Sphingolipid metabolism	0.0634	Lipid metabolism	Metabolism
	Biosynthesis of unsaturated fatty acids	0.0634	Lipid metabolism	Metabolism
	Steroid biosynthesis	0.0634	Lipid metabolism	Metabolism
	Linoleic acid metabolism	0.0634	Lipid metabolism	Metabolism

	Fatty acid degradation	0.0634	Lipid metabolism	Metabolism
	Phenylalanine, tyrosine and tryptophan biosynthesis	0.3555	Amino acid metabolism	Metabolism
	Phenylalanine metabolism	0.0634	Amino acid metabolism	Metabolism
	beta-Alanine metabolism	0.0634	Metabolism of other amino acids	Metabolism
	Glycosaminoglycan degradation	0.3555	Glycan biosynthesis and metabolism	Metabolism
	Biotin metabolism	0.0634	Metabolism of cofactors and vitamins	Metabolism
	Porphyrin and chlorophyll metabolism	0.0634	Metabolism of cofactors and vitamins	Metabolism
	Sesquiterpenoid and triterpenoid biosynthesis	0.4995	Metabolism of terpenoids and polyketides	Metabolism
	Brassinosteroid biosynthesis	0.3555	Metabolism of terpenoids and polyketides	Metabolism
	Limonene and pinene degradation	0.0634	Metabolism of terpenoids and polyketides	Metabolism
	Phenylpropanoid biosynthesis	1.7468	Biosynthesis of other secondary metabolites	Metabolism
	Flavonoid biosynthesis	0.0634	Biosynthesis of other secondary metabolites	Metabolism
	Ribosome biogenesis in eukaryotes	0.0634	Translation	Genetic information processing
	ABC transporters	0.0634	Membrane transport	Environmental information processing
S1 (S1 vs. S2)	Fatty acid metabolism	0.2452	Global and overview maps	Metabolism
	Metabolic pathways	0.0787	Global and overview maps	Metabolism
	Biosynthesis of secondary metabolites	0.0787	Global and overview maps	Metabolism
	Butanoate metabolism	0.0787	Carbohydrate metabolism	Metabolism
	Glyoxylate and dicarboxylate metabolism	0.2452	Carbohydrate metabolism	Metabolism
	Inositol phosphate metabolism	0.1191	Carbohydrate metabolism	Metabolism
	Pentose and glucuronate interconversions	0.0787	Carbohydrate metabolism	Metabolism
	Starch and sucrose metabolism	0.0787	Carbohydrate metabolism	Metabolism
	Ether lipid metabolism	0.8660	Lipid metabolism	Metabolism
	Fatty acid biosynthesis	0.3085	Lipid metabolism	Metabolism
	Biosynthesis of unsaturated fatty acids	0.2452	Lipid metabolism	Metabolism
	Cutin, suberine and wax biosynthesis	0.1694	Lipid metabolism	Metabolism

	Glycerophospholipid metabolism	0.1694	Lipid metabolism	Metabolism
	Cysteine and methionine metabolism	0.2452	Amino acid metabolism	Metabolism
	Valine, leucine and isoleucine biosynthesis	0.0787	Amino acid metabolism	Metabolism
	Phenylalanine, tyrosine and tryptophan biosynthesis	0.2452	Amino acid metabolism	Metabolism
	Tyrosine metabolism	0.2452	Amino acid metabolism	Metabolism
	Phenylalanine metabolism	0.1847	Amino acid metabolism	Metabolism
	Glycosaminoglycan degradation	0.0787	Glycan biosynthesis and metabolism	Metabolism
	Ubiquinone and other terpenoid-quinone biosynthesis	0.2452	Metabolism of cofactors and vitamins	Metabolism
	Porphyrin and chlorophyll metabolism	0.2452	Metabolism of cofactors and vitamins	Metabolism
	Nicotinate and nicotinamide metabolism	0.0787	Metabolism of cofactors and vitamins	Metabolism
	Zeatin biosynthesis	0.0787	Metabolism of terpenoids and polyketides	Metabolism
	Tropane, piperidine and pyridine alkaloid biosynthesis	0.8660	Biosynthesis of other secondary metabolites	Metabolism
	Isoquinoline alkaloid biosynthesis	0.2452	Biosynthesis of other secondary metabolites	Metabolism
	Protein processing in endoplasmic reticulum	4.1924	Folding, sorting and degradation	Genetic information processing
	ABC transporters	0.1847	Membrane transport	Environmental information processing
	Plant hormone signal transduction	0.0787	Signal transduction	Environmental information processing
	Endocytosis	0.2452	Transport and catabolism	Cellular processes
	Peroxisome	0.1684	Transport and catabolism	Cellular processes
S1 (S1 vs. S2)	Fatty acid metabolism	0.3312	Global and overview maps	Metabolism
	Metabolic pathways	0.2067	Global and overview maps	Metabolism
	Biosynthesis of secondary metabolites	0.1584	Global and overview maps	Metabolism
	Galactose metabolism	0.2021	Carbohydrate metabolism	Metabolism
	Ascorbate and aldarate metabolism	0.2021	Carbohydrate metabolism	Metabolism
	Pentose and glucuronate interconversions	0.1584	Carbohydrate metabolism	Metabolism
	Starch and sucrose metabolism	0.1508	Carbohydrate metabolism	Metabolism
	Amino sugar and nucleotide sugar metabolism	0.0808	Carbohydrate metabolism	Metabolism

Pentose phosphate pathway	0.0618	Carbohydrate metabolism	Metabolism
Photosynthesis - antenna proteins	6.1531	Energy metabolism	Metabolism
Photosynthesis	3.3883	Energy metabolism	Metabolism
Nitrogen metabolism	0.1508	Energy metabolism	Metabolism
Fatty acid elongation	3.3883	Lipid metabolism	Metabolism
Cutin, suberine and wax biosynthesis	0.9580	Lipid metabolism	Metabolism
Fatty acid biosynthesis	0.2021	Lipid metabolism	Metabolism
Biosynthesis of unsaturated fatty acids	0.1508	Lipid metabolism	Metabolism
Valine, leucine and isoleucine biosynthesis	0.0618	Amino acid metabolism	Metabolism
Phenylalanine metabolism	0.1584	Amino acid metabolism	Metabolism
Phenylalanine, tyrosine and tryptophan biosynthesis	0.0618	Amino acid metabolism	Metabolism
Arginine and proline metabolism	0.0618	Amino acid metabolism	Metabolism
Cyanoamino acid metabolism	0.1508	Metabolism of other amino acids	Metabolism
beta-Alanine metabolism	0.0618	Metabolism of other amino acids	Metabolism
Porphyrin and chlorophyll metabolism	0.2021	Metabolism of cofactors and vitamins	Metabolism
Limonene and pinene degradation	0.1508	Metabolism of terpenoids and polyketides	Metabolism
Brassinosteroid biosynthesis	0.0618	Metabolism of terpenoids and polyketides	Metabolism
Phenylpropanoid biosynthesis	0.9580	Biosynthesis of other secondary metabolites	Metabolism
Isoquinoline alkaloid biosynthesis	0.0808	Biosynthesis of other secondary metabolites	Metabolism
Stilbenoid, diarylheptanoid and gingerol biosynthesis	0.0618	Biosynthesis of other secondary metabolites	Metabolism
Flavonoid biosynthesis	0.0618	Biosynthesis of other secondary metabolites	Metabolism
Plant hormone signal transduction	0.2067	Signal transduction	Environmental information processing

The pathways are grouped according to KEGG pathway maps (<http://www.genome.jp/kegg/pathway.html>). The pathway-enrichment analysis was significant with FDR < 0.005. K1: 'Kiyomi' at first stage; K2: 'Kiyomi' at second stage; S1: 'Shiranui' at first stage; S2: 'Shiranui' at second stage.

Table S3 The genes involved in pectin metabolism

Gene	Gene expression levels					Contigs ID
	K1	S1	K2	S2	Average	
GAUT (α -1,4-D-galacturonosyltransferase)						
GAUT8	8.948	13.160	23.602	23.337	17.261	orange1.1g008561m.g
GAUT9	6.666	14.830	15.204	24.885	15.396	orange1.1g034721m.g
GAUT4	10.790	7.408	24.553	18.060	15.203	orange1.1g005035m.g
GAUT15	7.433	7.528	8.930	11.478	8.842	orange1.1g009468m.g
GAUT1	1.591	2.392	6.531	5.739	4.063	orange1.1g005683m.g
GAUT7	2.405	3.621	4.466	4.620	3.778	orange1.1g006506m.g
GATL (GAUT-like)						
GATL3	4.082	7.028	21.453	33.278	16.460	orange1.1g042515m.g
GATL10	5.113	6.207	7.445	38.788	14.388	orange1.1g023261m.g
GATL9	5.600	7.454	14.934	26.867	13.714	orange1.1g047424m.g
GATL7	1.356	1.189	13.853	10.995	6.848	orange1.1g017643m.g
PME (Pectin methylesterase)						
PME31	360.666	265.745	249.429	229.491	276.333	orange1.1g021162m.g
PME3	56.331	134.925	179.135	229.123	149.878	orange1.1g008261m.g
PME1	93.437	104.005	69.602	82.923	87.491	orange1.1g007830m.g
PME61	6.760	11.931	100.757	89.896	52.336	orange1.1g017225m.g
PME40	4.841	5.739	53.799	32.092	24.117	orange1.1g015794m.g
PME12	2.809	2.343	37.975	42.902	21.507	orange1.1g044734m.g
PME18	14.888	7.804	17.930	18.825	14.862	orange1.1g008722m.g
PME32	4.846	15.279	18.484	14.359	13.242	orange1.1g010718m.g
PME21	0.045	36.388	0.049	10.456	11.734	orange1.1g039111m.g
PME51	2.498	3.416	13.995	10.313	7.555	orange1.1g009085m.g
PME54	0.046	1.343	7.468	19.630	7.122	orange1.1g009418m.g
PMEI (PME inhibitor)						
	163.747	565.485	608.092	1411.688	687.253	orange1.1g029436m.g
	934.878	808.492	95.787	215.350	513.627	orange1.1g038081m.g
	16.625	41.428	67.400	120.620	61.518	orange1.1g027094m.g
	71.714	103.412	33.365	23.903	58.098	orange1.1g031799m.g
	89.300	35.788	49.355	40.896	53.835	orange1.1g037982m.g
	26.002	23.973	48.052	49.829	36.964	orange1.1g026791m.g
	13.600	7.628	18.318	6.540	11.522	orange1.1g029211m.g
	0.719	2.564	19.448	6.856	7.397	orange1.1g028183m.g
	5.601	0.288	12.779	3.746	5.603	orange1.1g040679m.g
PAE (pectin acetylesterase)						
PAE8	144.567	105.868	102.675	78.796	107.976	orange1.1g013734m.g
PAE2	21.930	20.612	21.044	20.727	21.078	orange1.1g026496m.g

PAE6	6.394	13.686	21.871	19.165	15.279	orange1.1g014548m.g
Pectate lyase /Pectin lyase						
	161.484	240.564	441.108	450.867	323.505	orange1.1g015702m.g
	426.901	460.503	199.835	115.311	300.637	orange1.1g015569m.g
	136.012	351.736	110.389	125.756	180.973	orange1.1g010437m.g
	181.484	137.324	128.988	111.794	139.897	orange1.1g013402m.g
	0.492	0.467	156.139	95.815	63.228	orange1.1g012057m.g
	47.112	61.330	34.023	44.671	46.784	orange1.1g038762m.g
	15.615	18.191	50.206	55.748	34.940	orange1.1g011204m.g
	1.277	2.246	46.330	42.612	23.116	orange1.1g009075m.g
	39.103	35.315	3.151	7.273	21.211	orange1.1g039631m.g
	12.561	14.578	16.818	17.674	15.408	orange1.1g020121m.g
	9.502	17.828	15.139	17.566	15.008	orange1.1g021449m.g
	2.875	2.739	13.482	13.031	8.031	orange1.1g009748m.g

Genes with expression levels greater than 10, except for *GAUT1* and *GAUT7*, are shown. The average expression levels are from the two citrus cultivars at two developmental stages. The genes/contigs are listed in the order of the average expression levels. K1: 'Kiyomi' at first stage; K2: 'Kiyomi' at second stage; S1: 'Shiranui' at first stage; S2: 'Shiranui' at second stage.

Table S4 The genes involved in cellulose metabolism

Gene	Gene expression levels					Contigs ID
	K1	S1	K2	S2	Average	
CESA (cellulose synthase)						
CESA9	4.011	18.808	66.307	114.029	50.788	orange1.1g001373m.g
CESA3	11.205	21.171	49.690	49.374	32.860	orange1.1g001413m.g
CESA1	9.561	28.445	37.000	42.463	29.367	orange1.1g001399m.g
CESA6	3.057	6.938	15.380	15.247	10.155	orange1.1g001369m.g
CESA8	0.017	0.171	0.396	0.237	0.205	orange1.1g002020m.g
CESA7	0.006	0.005	0.405	0.298	0.178	orange1.1g039060m.g
CESA4	0.012	0.032	0.242	0.182	0.117	orange1.1g001574m.g
SUS (sucrose synthase)						
SUS3	120.941	168.212	74.538	113.362	119.263	orange1.1g003492m.g
SUS4	40.360	52.039	91.822	88.906	68.281	orange1.1g003661m.g
SUS6	1.794	1.366	1.995	1.536	1.673	orange1.1g002909m.g
SUS2	0.000	0.060	0.077	0.112	0.062	orange1.1g003726m.g
CEL (cellulase)						
CEL1	0.695	1.123	7.052	10.352	4.805	orange1.1g012581m.g
CEL3	0.765	2.988	0.765	1.676	1.548	orange1.1g015354m.g
CEL2	0.040	0.030	0.012	0.017	0.025	orange1.1g010632m.g

The average expression levels are from the two citrus cultivars at two developmental stages.

The genes/contigs are listed in the order of the average expression levels. K1: 'Kiyomi' at first stage; K2: 'Kiyomi' at second stage; S1: 'Shiranui' at first stage; S2: 'Shiranui' at second stage.

Table S5 The genes involved in hemicellulose (xyloglucans and xylan) metabolism

Gene	Gene expression levels					Contigs ID
	K1	S1	K2	S2	Average	
CSLC (cellulose synthase-like C)						
CSLC4	1.433	1.256	4.256	3.291	2.559	orange1.1g006104m.g
CSLC5	2.879	1.442	5.915	2.906	3.285	orange1.1g005507m.g
CSLC12	1.973	11.843	16.548	46.068	19.108	orange1.1g005700m.g
XXT (xyloglucan xylosyltransferase)						
XXT1	14.899	17.675	20.451	21.754	18.695	orange1.1g012077m.g
XXT2	14.211	17.591	46.982	52.042	32.706	orange1.1g047753m.g
XXT3	7.564	7.522	8.641	10.988	8.679	orange1.1g012705m.g
MUR						
MUR2	3.027	2.781	10.670	8.840	6.329	orange1.1g039620m.g
MUR3	3.142	4.516	9.263	23.693	10.153	orange1.1g007197m.g
XLT (xyloglucan galactosyltransferase)						
XLT2	16.916	18.515	85.522	80.970	50.481	orange1.1g011220m.g
AXY (acetyltransferase)						
AXY4	0.879	0.463	2.476	1.837	1.414	orange1.1g013153m.g
AXY4L (AXY4 Like)	0.585	0.583	2.345	1.548	1.265	orange1.1g014612m.g
BGAL (Beta galactosidase)						
BGAL10	2.612	3.191	3.203	3.362	3.092	orange1.1g004525m.g
XYL (xylosidase)						
XYL1	4.737	4.792	27.915	19.161	14.151	orange1.1g002256m.g
IRX (irregular xylem phenotype)						
IRX7	60.792	61.008	55.310	71.390	62.125	orange1.1g039568m.g
IRX8/GAUT12	7.746	5.306	6.650	4.645	6.086	orange1.1g007529m.g
IRX9-L (IRX9-Like)	6.963	10.757	15.223	15.339	12.070	orange1.1g016070m.g
IRX10	1.679	2.085	2.069	1.972	1.951	orange1.1g038885m.g
IRX10-L (IRX10-Like)	6.330	9.254	7.262	9.126	7.993	orange1.1g048016m.g
IRX14-L (IRX14-Like)	10.713	16.027	14.428	13.478	13.661	orange1.1g010452m.g
IRX15-L (IRX15-Like)	0.000	0.350	0.074	0.190	0.153	orange1.1g021017m.g

The average expression levels are from the two citrus cultivars at two developmental stages.

The genes/contigs are listed in the order of the gene names. *MUR2*, also known as *FUT1*,

encodes a fucosyl transferase. *MUR3* encodes a xyloglucan galactosyltransferase specific for

transferring the galactosyl residue to the third xylosyl residue (Madson *et al.*, 2003*). K1: 'Kiyomi' at first stage; K2: 'Kiyomi' at second stage; S1: 'Shiranui' at first stage; S2: 'Shiranui' at second stage.

*Madson M, Dunand C, Li X, Verma R, Vanzin GF, Caplan J, Shoue DA, Carpita NC, Reiter WD. The MUR3 gene of Arabidopsis encodes a xyloglucan galactosyltransferase that is evolutionarily related to animal exostosins. *Plant Cell*. 2003;15:1662–1670.