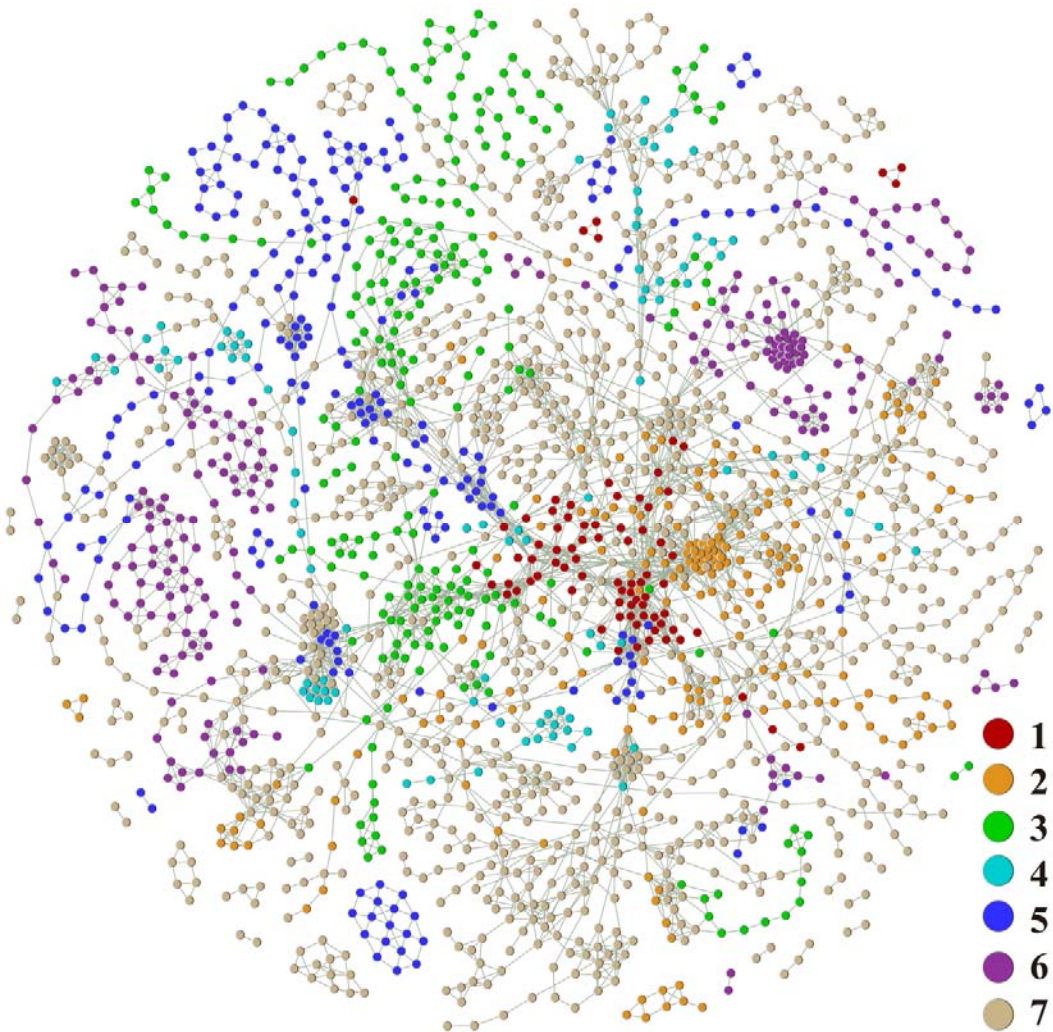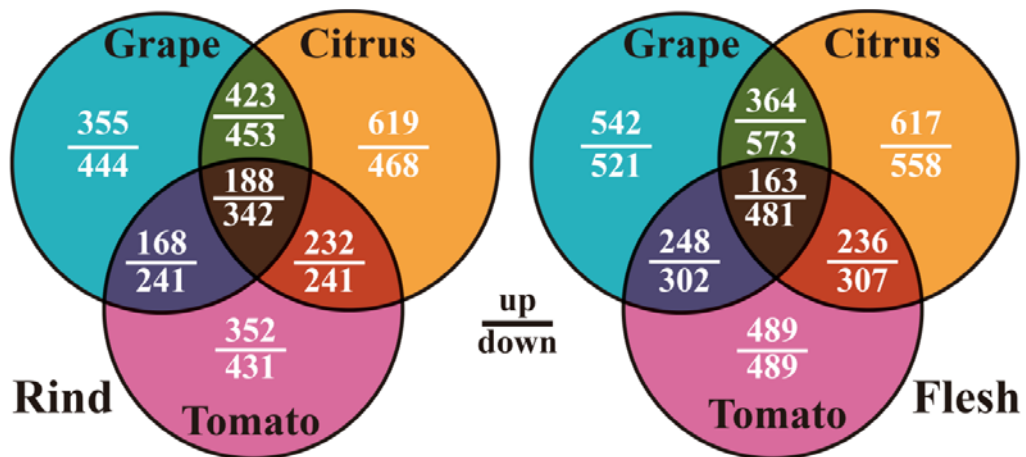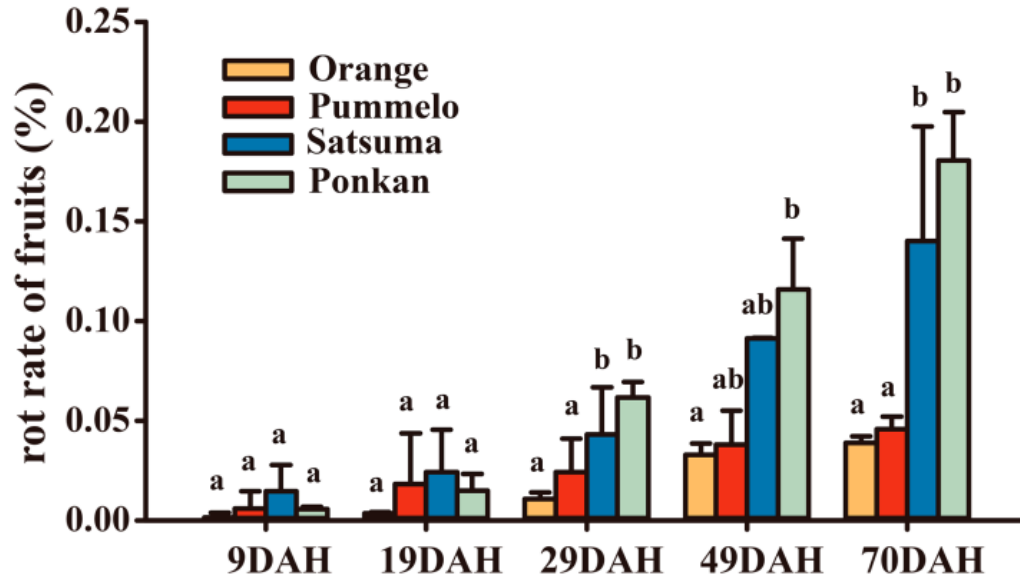**Supplemental Figure S1.** Principal component analysis (PCA) using conventional physiological quality data during 0-200 DAH.

Supplemental Figure S2. General map of CitrusCyc constructed based on Aracyc. Numbers represent: 1, TCA; 2, amino acid; 3, sugars; 4, secondary metabolites; 5, lipids; 6, hormones; 7, others;

Supplemental Figure S3. Venn diagrams of numbers of DEGs identified by comparing the transcription data of post- and pre-ripening samples of tomato, grape and citrus.

Supplemental Figure S4. Rot rate of four varieties during 70 DAH storage. Different letters (a and b) represent the statistical significances (p-value<0.05, analyzed by Student's T-test). Values represent the means of two bio-replicates and vertical bars represent standard deviations. It is demonstrated that Ponkan & Satsuma are more perishable than orange & pummelo.

Supplemental Table S1. Sample classification for identification of DEGs at the three levels.

Samples [2 repetition]	Time level	Tissue level	Varity level
Or.0DAH	g1-1	g1-1	g1-1
Or.10DAH	g1-2	g1-1	g1-1
Or.20DAH	g1-3	g1-1	g1-1
Or.30DAH	g1-4	g1-1	g1-1
Or.40DAH	g1-5	g1-1	g1-1
Or.50DAH	g1-6	g1-1	g1-1
Kr.0DAH	g2-1	g2-1	g1-2
Kr.10DAH	g2-2	g2-1	g1-2
Kr.20DAH	g2-3	g2-1	g1-2
Kr.30DAH	g2-4	g2-1	g1-2
Kr.40DAH	g2-5	g2-1	g1-2
Kr.50DAH	g2-6	g2-1	g1-2
Sr.0DAH	g3-1	g3-1	g1-3
Sr.10DAH	g3-2	g3-1	g1-3
Sr.20DAH	g3-3	g3-1	g1-3
Sr.30DAH	g3-4	g3-1	g1-3
Sr.40DAH	g3-5	g3-1	g1-3
Sr.50DAH	g3-6	g3-1	g1-3
Pr.0DAH	g4-1	g4-1	g1-4
Pr.10DAH	g4-2	g4-1	g1-4
Pr.20DAH	g4-3	g4-1	g1-4
Pr.30DAH	g4-4	g4-1	g1-4
Pr.40DAH	g4-5	g4-1	g1-4
Pr.50DAH	g4-6	g4-1	g1-4
Of.0DAH	g5-1	g1-2	g2-1
Of.10DAH	g5-2	g1-2	g2-1
Of.20DAH	g5-3	g1-2	g2-1
Of.30DAH	g5-4	g1-2	g2-1
Of.40DAH	g5-5	g1-2	g2-1
Of.50DAH	g5-6	g1-2	g2-1
Kf.0DAH	g6-1	g2-2	g2-2
Kf.10DAH	g6-2	g2-2	g2-2
Kf.20DAH	g6-3	g2-2	g2-2
Kf.30DAH	g6-4	g2-2	g2-2
Kf.40DAH	g6-5	g2-2	g2-2
Kf.50DAH	g6-6	g2-2	g2-2
Sf.0DAH	g7-1	g3-2	g2-3
Sf.10DAH	g7-2	g3-2	g2-3
Sf.20DAH	g7-3	g3-2	g2-3

Sf.30DAH	g7-4	g3-2	g2-3
Sf.40DAH	g7-5	g3-2	g2-3
Sf.50DAH	g7-6	g3-2	g2-3
Pf.0DAH	g8-1	g4-2	g2-4
Pf.10DAH	g8-2	g4-2	g2-4
Pf.20DAH	g8-3	g4-2	g2-4
Pf.30DAH	g8-4	g4-2	g2-4
Pf.40DAH	g8-5	g4-2	g2-4
Pf.50DAH	g8-6	g4-2	g2-4

Supplemental Table S2. Proportions of the first-level and second-level linkages to the total linkages in the correlation network between metabolites and RE-values (Network-MR).

Significant Correlation Reactions (%)	Rind 1st-level		Flesh 1st-level		Rind 2nd-level		Flesh 2nd-level	
	Pos.	Neg.	Pos.	Neg.	Pos.	Neg.	Pos.	Neg.
Glucose	0	0	**0.68**	0.18	0.03	0.1	**0.51**	0.19
Fructose	0	0	**0.67**	0	0.12	0	**0.39**	0.12
4-Ketoglucose	0	**0.33**	0.33	0	0	**0.67**	**0.33**	0
Galactose	0.13	0.19	0.06	**0.75**	0.17	**0.39**	0.17	0.2
Myo-Inositol	0	0.11	0	**0.33**	0.06	**0.31**	0.06	0.25
Sucrose	0	0	**0.43**	0	0	0.03	0.09	0.08
Glycerol	**0.5**	0	0	**0.5**	0.23	0.23	0	0
Citric acid	0	**0.33**	0	0	0.22	**0.33**	**0.33**	**0.35**
Aconitic acid	0	0	0	0	0	**0.33**	0.17	0
2-Butenedioic acid	0	0.14	**0.43**	0	0.07	0.05	0.27	0.09
Malic acid	**0.43**	0	0	0.14	**0.3**	**0.32**	0.04	0.27
Malonic acid	-	-	-	-	0.05	0	**0.62**	0.03
Butanedioic acid	**0.44**	**0.39**	**0.5**	0.17	**0.3**	0.19	0.14	0.11
Butanoic acid	0	0	0	0	-	-	-	-
Isocitric acid	0.2	**0.6**	0.2	0.2	**0.3**	**0.41**	0.16	0.14
Asparagine	0	0.2	0.2	**0.4**	0.23	0.08	0.23	0.23
Aspartic acid	0.14	0.07	0.14	0.07	0.11	0.15	0.03	0.02
Citrulline	**0.43**	0.14	0	0	0.13	0.19	0	0
Glycine	0	0.17	0.25	0.25	0.07	0.09	0.14	**0.31**
Alanine	0.06	0	0.13	0.19	0.04	0.07	**0.36**	0.12
Valine	0	0	1	0	0	0	**0.33**	0

Network-MR was constructed by Jaccard distance. Jaccard distance had two values positive value (Pos.) and negative value (Neg.) The threshold was set to |Jaccard distance value| >= 0.4. First-level and second-level linkages in the network was counted (%). The letter "-" presents miss values. Proportion values >=0.3 was in bold.

Supplemental Table S3. Ratio of array covered genes from different information resources of citrus genes.

Sequences resources	NO. of genes in Array	Total genes	Array coverage ratio
CDSs in genome of clementine mandarin (Wu et al., 2014)	19018	33929	0.56
CDSs in genome of sweet orange (Wu et al., 2014)	24007	46174	0.52
CDSs in genome of sweet orange (Xu et al., 2013)	22776	44275	0.51
Genes in genome of sweet orange (Xu et al., 2014)	15083	29655	0.51
Genes expressed in fruit of sweet orange [deteced by RNAseq](Xu et al., 2013)	11380	14543	0.78
ESTs of *Poncirus trifoliata* [NCBI]	18427	61874	0.30
ESTs of *Citrus paradisi* x *Citrus trifoliata* [NCBI]	5181	8039	0.64
ESTs of *Citrus paradisi* [NCBI]	5076	7954	0.64

To investigate citrus microarray coverage, CDSs sequences from 3 citrus genomes (Clementine mandarin (Wu et al., 2014), sweet oranges (Xu et al., 2013; Wu et al., 2014) were downloaded. We also investigated the microarray coverage for the genes expressed in the fruit of sweet orange (as supported by RNAseq evidence (Xu et al., 2014)). In addition, ESTs sequences from other citrus varieties were also downloaded from NCBI, including *Poncirus trifoliata* which was chosen as the negative control, and *Citrus paradisi*, a closely related species of pummelo (adequate information of pummelo sequences is still not available yet). BLAST (E value<=1e-5) was used to find the sequence similarities of the probesets to the genes.

Supplemental Table S4. Numbers of DEGs at early stage (0-10 DAH) by comparing samples of loose- and tight-skin citrus.

loose-skin / tight-skin	All GEG	flesh-up	flesh-down	rind-up	rind-down
cell wall.modification	37	11	5	10	6
fermentation.ADH	3	2	0	0	0
fermentation.LDH	1	1	0	1	0
fermentation.PDC	3	1	0	1	0
gluconeogenese/ glyoxylate cycle.PEPCK	2	1	0	1	0
glycolysis.cytosolic branch.phosphoglucomutase (PGM)	3	1	0	1	0
glycolysis.cytosolic branch.pyruvate kinase (PK)	5	1	0	2	0
glycolysis.plastid branch.pyruvate kinase (PK)	6	2	1	1	0
hormone metabolism.ethylene.induced-regulated-responsive-activated	18	1	0	1	2
hormone metabolism.ethylene.signal transduction	37	7	7	8	6
hormone metabolism.ethylene.synthesis-degradation	8	0	1	2	1
hormone metabolism.ethylene.synthesis-degradation.1-aminocyclopropane-1-carb oxylate synthase	4	1	0	2	1
major CHO metabolism	39	10	3	8	6
minor CHO metabolism	79	22	5	20	9
mitochondrial electron transport / ATP synthesis.alternative oxidase	2	1	0	1	0
mitochondrial electron transport / ATP synthesis.cytochrome c	6	0	0	1	0
mitochondrial electron transport / ATP synthesis.F1-ATPase	12	0	0	1	0
mitochondrial electron transport / ATP synthesis.NADH-DH.type II.external	3	0	0	1	0
mitochondrial electron transport / ATP synthesis.NADH-DH.type II.internal matrix	2	2	0	1	0
mitochondrial electron transport / ATP synthesis.uncoupling protein	3	1	0	1	0
redox.ascorbate and glutathione.ascorbate	15	2	1	4	1
redox.ascorbate and glutathione.ascorbate.GME	1	1	0	1	0
redox.ascorbate and glutathione.glutathione	12	5	0	4	0
redox.dismutases and catalases	14	4	0	5	1
redox.glutaredoxins	17	3	0	2	3
redox.heme	3	1	0	1	0
redox.peroxiredoxin.BAS1	1	1	0	1	0
RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	43	13	3	16	0
RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene	13	8	2	6	1

Family					
RNA.regulation of transcription.Aux/IAA family	16	5	1	5	2
RNA.regulation of transcription.WRKY domain transcription factor family	31	11	5	12	3
signalling.calcium	141	27	12	24	11
signalling.in sugar and nutrient physiology	21	4	3	6	2
stress.abiotic.drought/salt	40	10	4	11	3
stress.abiotic.touch/wounding	13	5	1	7	2
stress.biotic.respiratory burst	5	1	0	3	0
TCA / org. transformation.carbonic anhydrases	5	1	0	1	2
TCA / org. transformation.other organic acid transformaitons.cyt MDH	3	1	0	0	0
TCA / org. transformation.other organic acid transformaitons.malic	5	0	0	1	0
TCA / org. transformation.TCA.aconitase	3	1	0	0	0
TCA / org. transformation.TCA.IDH	5	1	0	1	0
TCA / org. transformation.TCA.malate DH	2	1	0	0	0
TCA / org. transformation.TCA.succinyl-CoA ligase	4	1	0	1	0
transport.phosphate	14	2	1	3	1
transporter.sugars	35	11	5	14	4

Supplemental Table S5. Quantitative real-time PCR verification of selective probesets in orange rind and flesh.

Tissue	cit	cor	Forward primer	Reverse primer
Rind	ACTIN		CCAAGCAGCATGAAGATCAA	ATCTGCTGGAAGGTGCTGAG
Rind	Cit.39752.1.S1_at	0.691	CTGGTTGTGGTGCATGCTTT	TTCCTCTGCCGCTACACAGA
Rind	Cit.11241.1.S1_s_at	0.645	TGGAAGGATGGAACGAACA	CGGTCAGAGGGTGAAAGC
Rind	Cit.15919.1.S1_at	0.727	TCGGAAACTTCCTGAACAGC	CCAACCCTTCTCCCCATT
Rind	Cit.11731.1.S1_s_at	0.741	GTTCGGCATCTTCTTGTTCTT	CTTCAATCGGCACATTCTTT
Rind	Cit.21919.1.S1_s_at	0.788	AATGCTCGTGACCTTGATACTT	GGTTGCTTTGCCCCTTAG
Rind	Cit.18023.1.S1_at	0.779	CGACGTTGTTGGTCTCCTC	CCACTTTGGTATCTTCTTTTGC
Rind	Cit.35761.1.S1_at	0.797	CTGGCTATTGTGCGTGCTTAGT	TTGTAAGGAATGGCCCAGAAA
Rind	Cit.37918.1.S1_at	0.875	CGTGGCGCTTTCATTGC	ACCACCAGGCTAAGATTCCAAA
Rind	Cit.20698.1.S1_at	0.623	GCTGGTGCTGGAGGTGCTTA	GCCATTCATCTTCAGCAATCG
Rind	Cit.2071.1.S1_s_at	0.723	AAAAGCGCATTGGCATCAC	ACCCTTCTTCTCCGGTTCGT
Rind	Cit.29959.1.S1_at	0.617	GCATGCCTGAAAAGGATTCG	CAACCACAGCCTCGTCTGAA
Rind	Cit.39208.1.S1_s_at	0.872	TCTGCTGCTGCATGACGAA	GAGGTAGAATGAGCAGAAGAAAGATTC
Rind	Cit.21825.1.S1_s_at	0.765	CGACCACCGTGGAATCAGA	CTCAGGGTCATAAGATGGCAATC
Rind	Cit.4697.1.S1_at	0.978	TGGGAAAGCACCAAGGTTGT	CTCACTCCCGTGCGGAAT
Rind	Cit.326.1.S1_at	0.649	CTCTGTCACTGGAACTGGCATC	CCTTCTCCTTGTTGTAAATCACC
Flesh	ACTIN		CCAAGCAGCATGAAGATCAA	ATCTGCTGGAAGGTGCTGAG
Flesh	Cit.29933.1.S1_at	0.618	ACGGATGAAATGGGAAACC	ACCAACCCCTACTGTCTGCT
Flesh	Cit.5117.1.S1_at	0.79	AGCCACGGTTATGGTTTCA	CAATAATCACTCACGCTTCCTA
Flesh	Cit.10350.1.S1_s_at	0.895	AGGAGCAACGAGTCCAGTAAA	TTCATATCCAGGGCACAGC
Flesh	Cit.18884.1.S1_at	0.574	ATTAAATAACGATGTGGAACTCAG	AAACTCACCAAATGTCCTCTACTA
Flesh	Cit.40270.1.S1_s_at	0.771	GCTACTGTGCGTGACCTAAATA	CAACAGCGGAGTCAAAAGAT
Flesh	Cit.19396.1.S1_s_at	0.602	CGGACCACGATGCACGAC	GCACTTGGCACAGCACTTTT

Flesh	Cit.8763.1.S1_s_at	0.764	CCATCCCATTCAAGTCCAA	TCAAGAACCACAAACACCGA
Flesh	Cit.1625.1.S1_s_at	0.929	CTGGATGCTTGTTGGTGATG	TCCAATAGCCTCTGAACCTTT
Flesh	Cit.39752.1.S1_at	0.727	CTGCTGGTGTTCCTTCCC	TGGTTCCTCTGCCGCTAC
Flesh	Cit.4893.1.S1_s_at	0.567	CTTCTGGAAATGGACCGC	TTCTAACCTTGTTCAGGGTATCA
Flesh	Cit.11731.1.S1_s_at	0.927	GCTCCCCGAGACAAAGAA	AAACCATCGTCAACCATAAAAT
Flesh	Cit.6756.1.S1_at	0.94	TTCCGACTTGAAGCCTGTT	AAGGAAGGTCTTGATGTAAACG
Flesh	Cit.13424.1.S1_at	0.667	CAGGGAATGAGTTAGCCAAGC	GCCCACCACTGTCCATCTGT
Flesh	Cit.1200.1.S1_s_at	0.888	CCCGTGTTCAAGACCGAC	GCGTCATCCTTAGGGTAACTG
Flesh	Cit.580.1.S1_x_at	0.752	CCACTTATCACCTCTACCACCCT	TGCCGTCAAGTCCCATCC

Supplemental Table S6. Database resources for the investigation of homologous gene copies.

Species	URL
apple	http://www.rosaceae.org/species/malus/malus_x_domestica/genome_v1.0p
tomato	ftp://ftp.solgenomics.net/tomato_genome/annotation/ITAG2.4_release/
banana	http://banana-genome.cirad.fr/content/download-dh-pahang
papaya	ftp://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Cpapaya/assembly/Cpapaya_113.fa.gz
peach	ftp://ftp.bioinfo.wsu.edu/species/Prunus_persica/Prunus_persica-genome.v1.0/genes/
citrus clementina	http://genome.jgi.doe.gov/pages/dynamicOrganismDownload.jsf?organism=PhytozomeV9
citrus sinensis [JGI]	http://genome.jgi.doe.gov/pages/dynamicOrganismDownload.jsf?organism=PhytozomeV9
citrus sinensis [HZAU]	http://citrus.hzau.edu.cn/orange/
cherry	ftp://ftp.bioinfo.wsu.edu/species/Pyrus_communis/Pcommunis-draft_genome.v1.0/genes/
strawberry [hybrid]	http://www.rosaceae.org/species/fragaria/fragaria_vesca/genome_v1.0
strawberry [abinitio]	http://www.rosaceae.org/species/fragaria/fragaria_vesca/genome_v1.0
watermelon	ftp://www.icugi.org/pub/genome/watermelon/97103/v1/
cucumber[1]	ftp://www.icugi.org/pub/genome/cucumber/Chinese_long/v1/
cucumber[2]	ftp://www.icugi.org/pub/genome/cucumber/Chinese_long/v2/
cucumber[3]	ftp://www.icugi.org/pub/genome/cucumber/PI183967/
cucumber[4]	ftp://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Csativus/annotation/Csativus_122_protein.fa.gz
grape [1]	https://urgi.versailles.inra.fr/Species/Vitis/Annotations
grape [2]	ftp://ftp.jgi-psf.org/pub/compgen/phytozome/v9.0/Vvinifera/assembly/Vvinifera_145.fa.gz

Supplemental Table S7. List of collected samples of tomato and grape from GEO database.

species	GEO_number	post-ripening	pre-ripening
grape	GSE11406	Red_soft	Green_soft
grape	GSE11406	Red_soft	Green_hard
grape	GSE11406	Pink_soft	Green_soft
grape	GSE11406	Pink_soft	Green_hard
grape	GSE20511	**Withering_III**	Pre-veraison
grape	GSE20511	**Withering_III**	Veraison
grape	GSE20511	**Withering_III**	Pre-ripening
grape	GSE20511	**Withering_II**	Pre-veraison
grape	GSE20511	**Withering_II**	Veraison
grape	GSE20511	**Withering_II**	Pre-ripening
grape	GSE20511	**Withering_I**	Pre-veraison
grape	GSE20511	**Withering_I**	Veraison
grape	GSE20511	**Withering_I**	Pre-ripening
grape	GSE20511	Ripening	Pre-veraison
grape	GSE20511	Ripening	Veraison
grape	GSE20511	Ripening	Pre-ripening
grape	GSE28779	ripe	green
grape	GSE28779	ripe	medium_green
grape	GSE28779	ripe	veraison
grape	GSE34634	**HARvest**	GREen
grape	GSE34634	**HARvest**	VERasion
grape	GSE35172	RipE	VeraisoN
grape	GSE41206	flesh_R2	flesh_P
grape	GSE41206	flesh_R2	flesh_V1
grape	GSE41206	flesh_R2	flesh_V2
grape	GSE41206	flesh_R1	flesh_P
grape	GSE41206	flesh_R1	flesh_V1
grape	GSE41206	flesh_R1	flesh_V2
grape	GSE41206	skin_R2	skin_P
grape	GSE41206	skin_R2	skin_V1
grape	GSE41206	skin_R2	skin_V2
grape	GSE41206	skin_R1	skin_P
grape	GSE41206	skin_R1	skin_V1
grape	GSE41206	skin_R1	skin_V2
grape	GSE49569	mature_Pulp	PV_Pulp

grape	GSE49569	mature_Pulp	midverasion_Pulp
grape	GSE49569	mature_Skin	PV_Skin
grape	GSE49569	mature_Skin	midverasion_Skin
Tomato	GSE22300	breaker +3 days fruit	1-3mm fruit
Tomato	GSE22300	breaker +3 days fruit	5-7mm fruit
Tomato	GSE22300	breaker +3 days fruit	11-14mm fruit
Tomato	GSE22300	breaker +3 days fruit	mature green fruit
Tomato	GSE22300	breaker +3 days fruit	breaker stage fruit
Tomato	GSE22300	breaker +5 days fruit	1-3mm fruit
Tomato	GSE22300	breaker +5 days fruit	5-7mm fruit
Tomato	GSE22300	breaker +5 days fruit	11-14mm fruit
Tomato	GSE22300	breaker +5 days fruit	mature green fruit
Tomato	GSE22300	breaker +5 days fruit	breaker stage fruit
Tomato	GSE22300	breaker +7 days fruit	1-3mm fruit
Tomato	GSE22300	breaker +7 days fruit	5-7mm fruit
Tomato	GSE22300	breaker +7 days fruit	11-14mm fruit
Tomato	GSE22300	breaker +7 days fruit	mature green fruit
Tomato	GSE22300	breaker +7 days fruit	breaker stage fruit
Tomato	GSE28564	normal_pink_coloring	normal_mature_green
Tomato	GSE42783	AC_RR	AC_MG
Tomato	GSE42783	AC_RR	AC_T

A total of 247 array samples collected in 10 independent experiments on the terminal stage in fruit

life history of the two model fruits from GEO database. Samples from fruits after harvest are in bold.