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Supplementary Fig. 1 KEGG pathway mapping of amino sugar and nucleotide sugar metabolism AMINO SUGAR AND NUCLEOTIDE SUGAR METABOLISM 2.7.1.221 MurNAc (Peptidoglycan biosyr ►O MurNAc-1P 3.1 3.105 D-Gln & D-Glu metab ► MurNAc-6P 2.7.1.192 1.3.1.98 5.1.3.8 UDP-GlcNAc-enopyruvate GlcNAc (extracellular) 5.1.3.9 2.5.1.7 2.7.7.43 UDP-GlcNAc 3.5.1.2 3.5.1.41 Chitosan biosynthesis 2.4.1.16 ►O Chitin 1.6.2.2 1.1418.2 1.14.18.2 Dyt b5 (ox) D-Glucosaminide 32.1.132 DO 32.1.165 UDP-ManNAc

5.1.3.14 → ○ 11.1.336 → ○ UDP-ManNAc A D-GlcN-1P UDP-GlcNAc3NAcA 23.1.201 ►O 5.1.3.23 ►O Lipopolysaccharid biosynthesis UDP-3-k 111335 → 2.6.1.98 ▶○ UDP-3-amino-GlcNAcA UDP-ManNAc3NAcA 5.1.3.-2.6.1.16 UDP-GalNAc

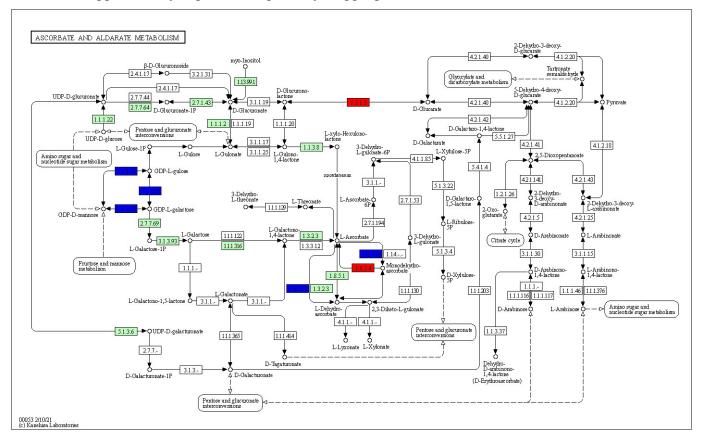
5.1.3.7 O 1.1.1.- OUDP-GalNAcA Fru-6P Glycolysis / glucone ogenesis Pec

| VDP-4-keto| G-deoxy-AliNAc AliNAc-QN | AlixiNAc | AlixiNA UDP-4-keto-6-deoxy-AltNAc | America | Amer L-Ara-1P Pentose and glucuronate Pentose and glucuronate 5.3.1.9 AXS GlcA UDP-GlcA Undecaprenyl phosphate-o-L-Ara4FN 1.1.1.22 Glycolysis/ gluconeogen Ascorbate and aldarate metabolism Acarbose and validam win biosynthesis 5.4.2.2 Glc-1F UDP-G1 2.7.1.2 2.7.1.63 5.4.2.5 3.13.1.1 -►O UDP-SQ 5.1.3.2 5.1.3.6 Polyketide sugar unit biosynthesis Galactose metabolism 2.7.1.6 5.4.99.9 **►O** UDP-Galf N-Glycan biosynthesis 1.1.1.-GalA UDP-GalA Pentose and glucuronate interconversions 2.7.1.44 2.4.1.43 GDP-L-Gul Ascorbate and alderate metabolism Man (extracellular) o-D-Rha 1.1.1.187 2.7.7.13 1.1.1.281 O GDP-6-deoxy-D-Tal GDP-D-Per → O 23.1.227 → O GDP-N-acetyl-D-Per AxE ►O AxF ►O CDP-ascarylose 2.7.1.2 2.7.1.63 Glc-6P CDP-4-ke to-3,6-dideoxy-D-Glc epime CDP suga 111341 → O CDP-abequose 11.1.342 **O** 5.1.3.10 **O** CDP-Tyw 4.2.1.45 **O** 1.17.1.1 CDP-4-ke to-6-deoxy-D-Glc CDP-4-ke to-3,6-deoxy-D-Glc

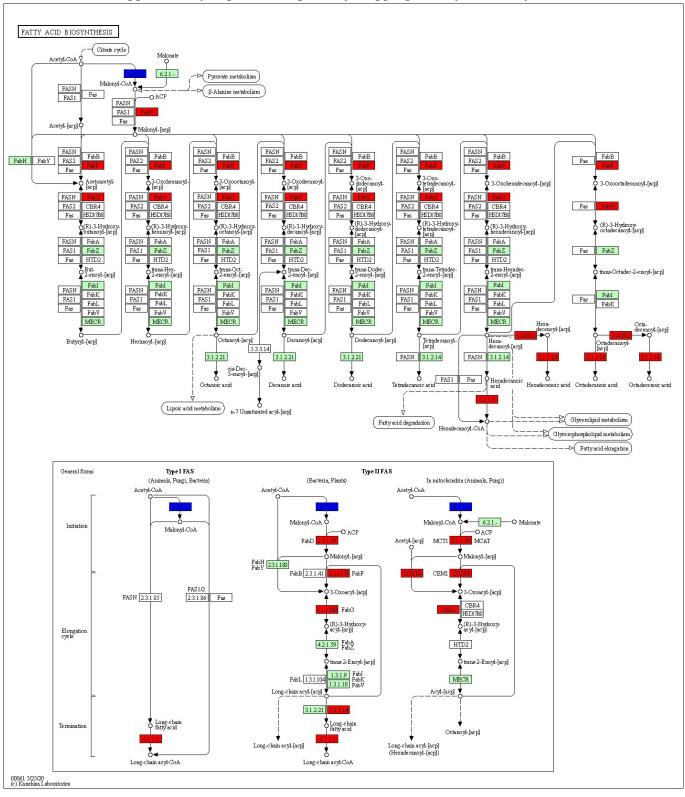
Box means gene or enzyme, and circle means chemical compound. Red represents up-regulation, while blue represents down-regulation. Green means particular gene or enzyme in this species.

—⊳(Starch and sucrose metabolism)

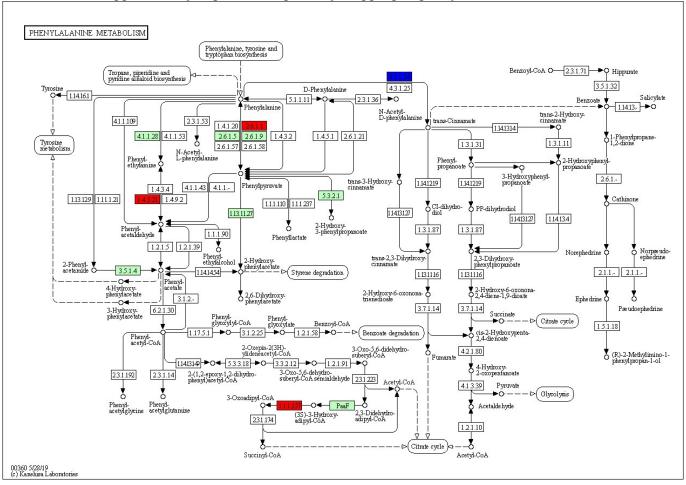
Supplementary Fig.2 KEGG pathway mapping of ascorbate and aldarate metabolism



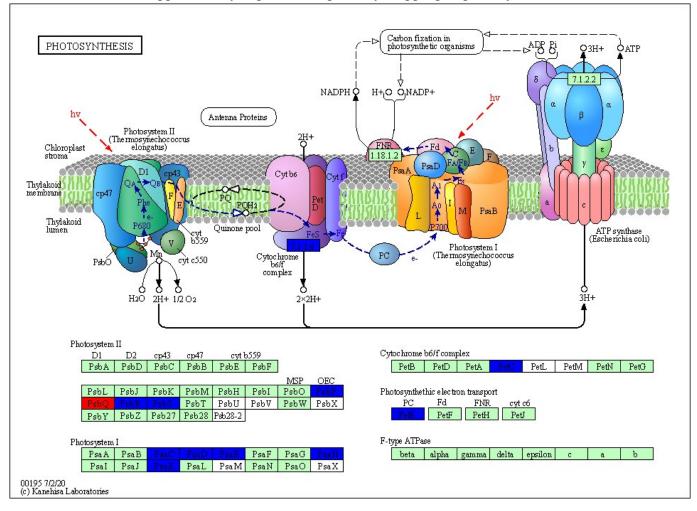
Supplementary Fig.3 KEGG pathway mapping of fatty acid biosynthesis



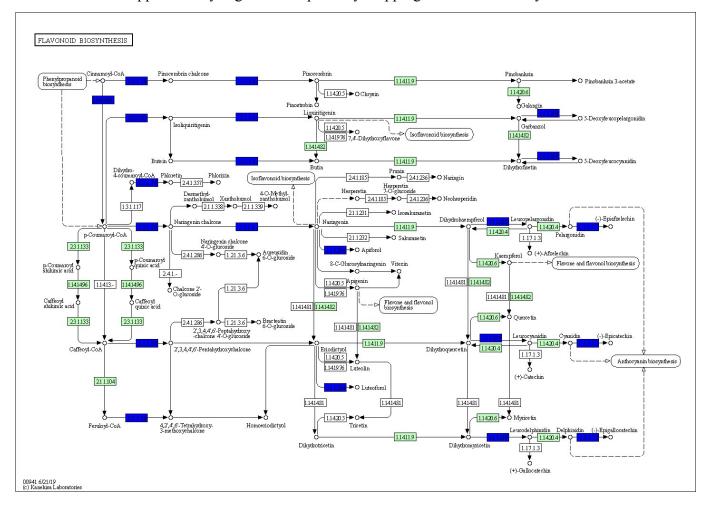
Supplementary Fig.4 KEGG pathway mapping of phenylalanine metabolism



Supplementary Fig.5 KEGG pathway mapping of photosynthesis



Supplementary Fig.6 KEGG pathway mapping of flavonoid biosynthesis.



Supplementary Table 1 The top three enriched GO terms for DEPs in jujubes

Gene Ontology term		P-value adjusted	count
76 DAF vs 55 DAF			
	single-organism metabolic process	5.45E-22	135
Biological process	catabolic process	7.02E-12	62
	response to chemical	1.8E-09	69
	cell periphery	8.37E-20	74
Cellular component	plasma membrane	1.56E-10	49
	apoplast	7.91E-10	20
	oxidoreductase activity	1.63E-06	48
Molecular function	hydrolase activity	3.7E-06	77
	lyase activity	0.00641	14
96 DAF vs 76 DAF			
	single-organism metabolic process	1.35E-26	164
Biological process	response to abiotic stimulus	3.25E-15	67
	response to chemical	2.01E-14	90
	cell periphery	1.77E-19	85
Cellular component	intracellular part	1.12E-18	212
	intracellular	2.62E-16	214
	oxidoreductase activity	7.23E-09	60
Molecular function	carbohydrate transporter activity	3.91E-04	7
	protein binding	4.18E-04	57
116 DAF vs 96 DAF			
	response to abiotic stimulus	1.9E-30	118
Biological process Cellular component	response to chemical	1.92E-25	149
	single-organism metabolic process	1.92E-25	228
	intracellular part	6E-40	357
	intracellular	1.87E-39	366
	intracellular organelle part	1.09E-32	188
	protein binding	1.8E-16	120
Molecular function	oxidoreductase activity	8.16E-06	74
	peroxidase activity	1.42E-06	14