

Transcriptional transitions in Alphonso mango (*Mangifera indica* L.) during fruit development and ripening explain distinct aroma and shelf life characteristics

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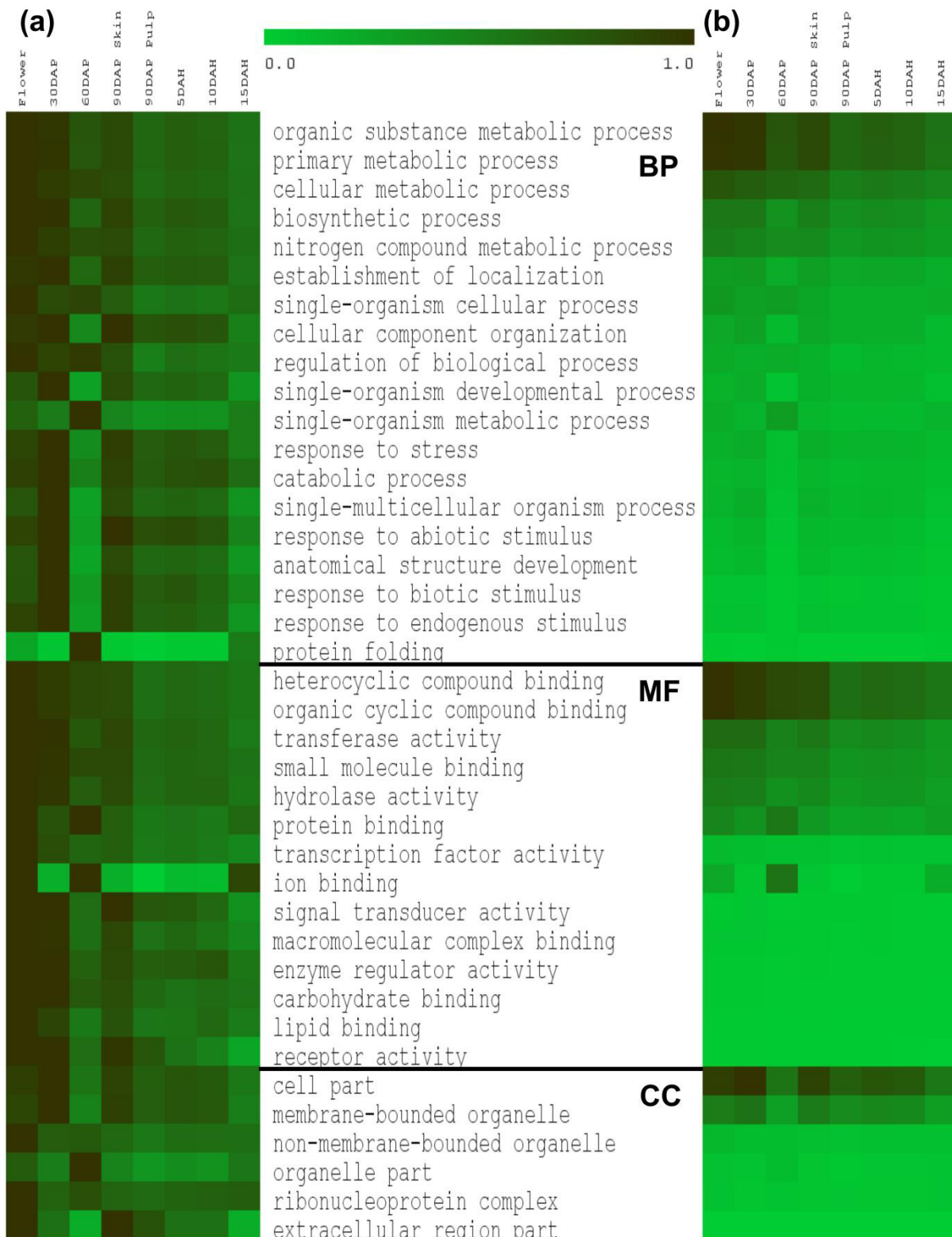
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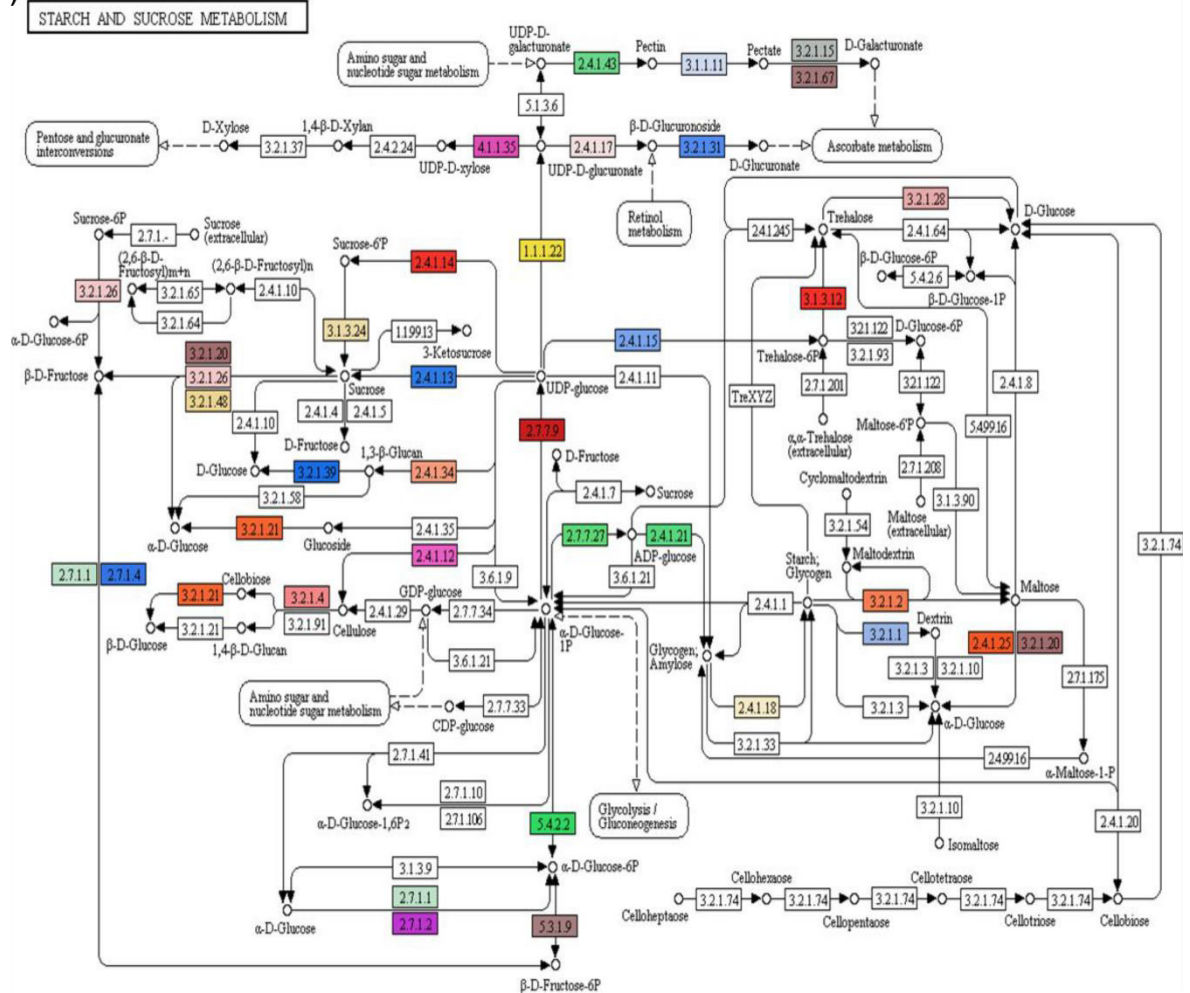
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Supplementary Figure SF1: Heatmap representing expression profiles of various gene ontologies from biological process (BP), molecular function (MF) and cellular components (CC) in different tissues, (a) Stage wise normalization and (b) global normalization for each GO category presented.



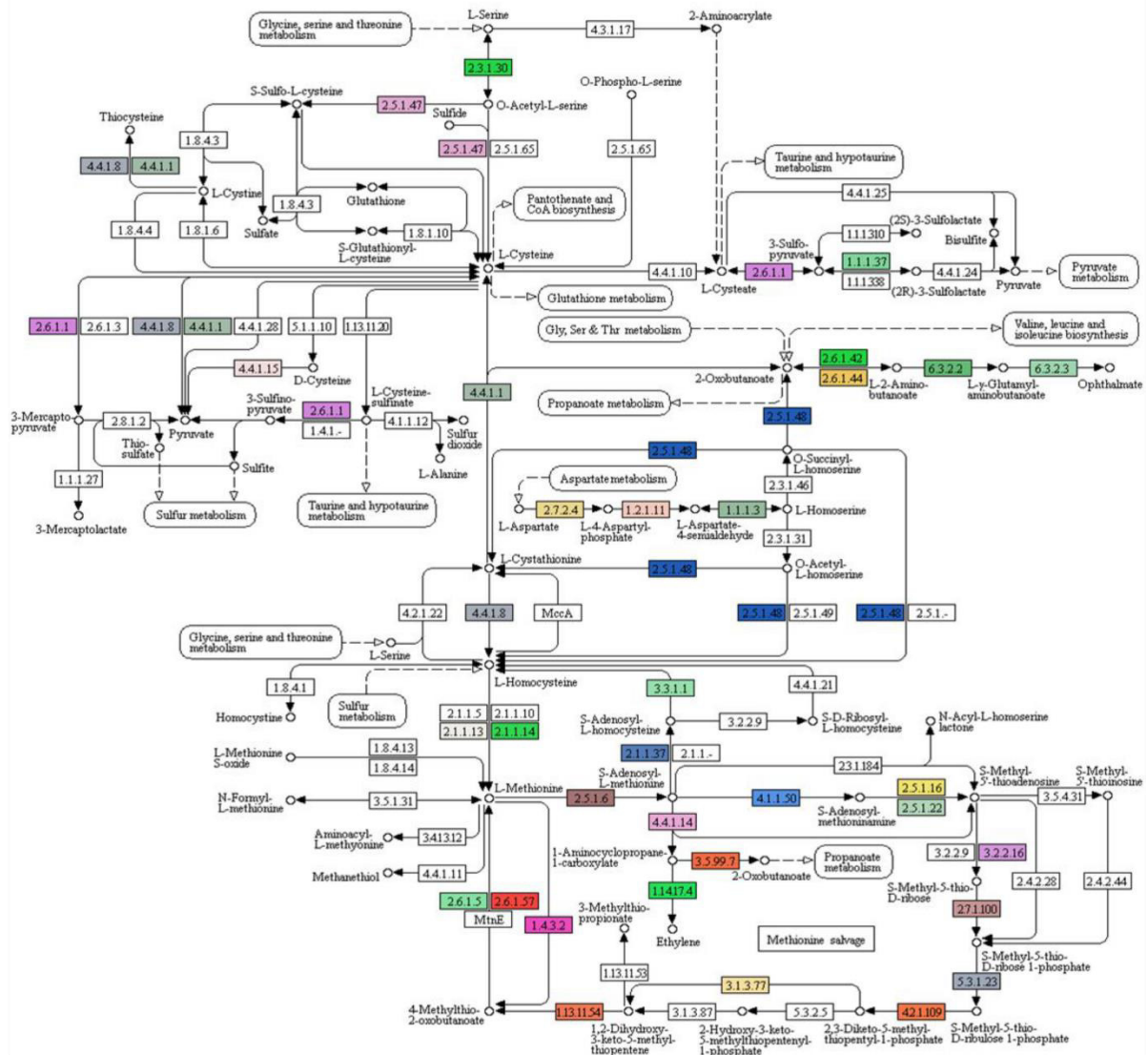
Supplementary Figure SF2: Important pathways, such as (a) starch and sucrose metabolism, (b) cysteine and methionine metabolism and ethylene biosynthesis, (c) phenylpropanoid biosynthesis and (d) flavonoid biosynthesis, which are functional in Alphonso mango. Data sourced from the KEGG pathway database (Kanehisa laboratories).

(a)

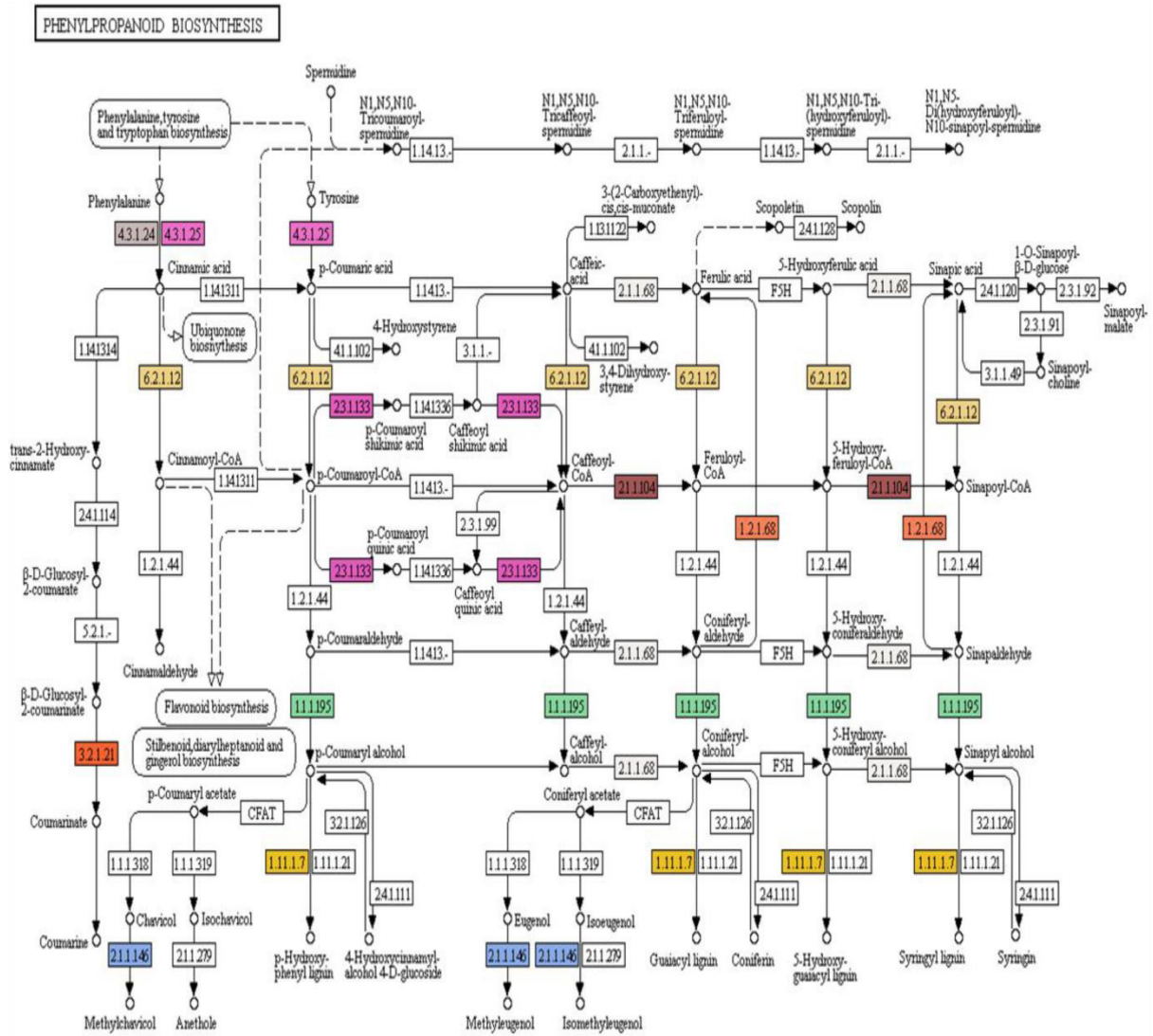


(b)

CYSTEINE AND METHIONINE METABOLISM



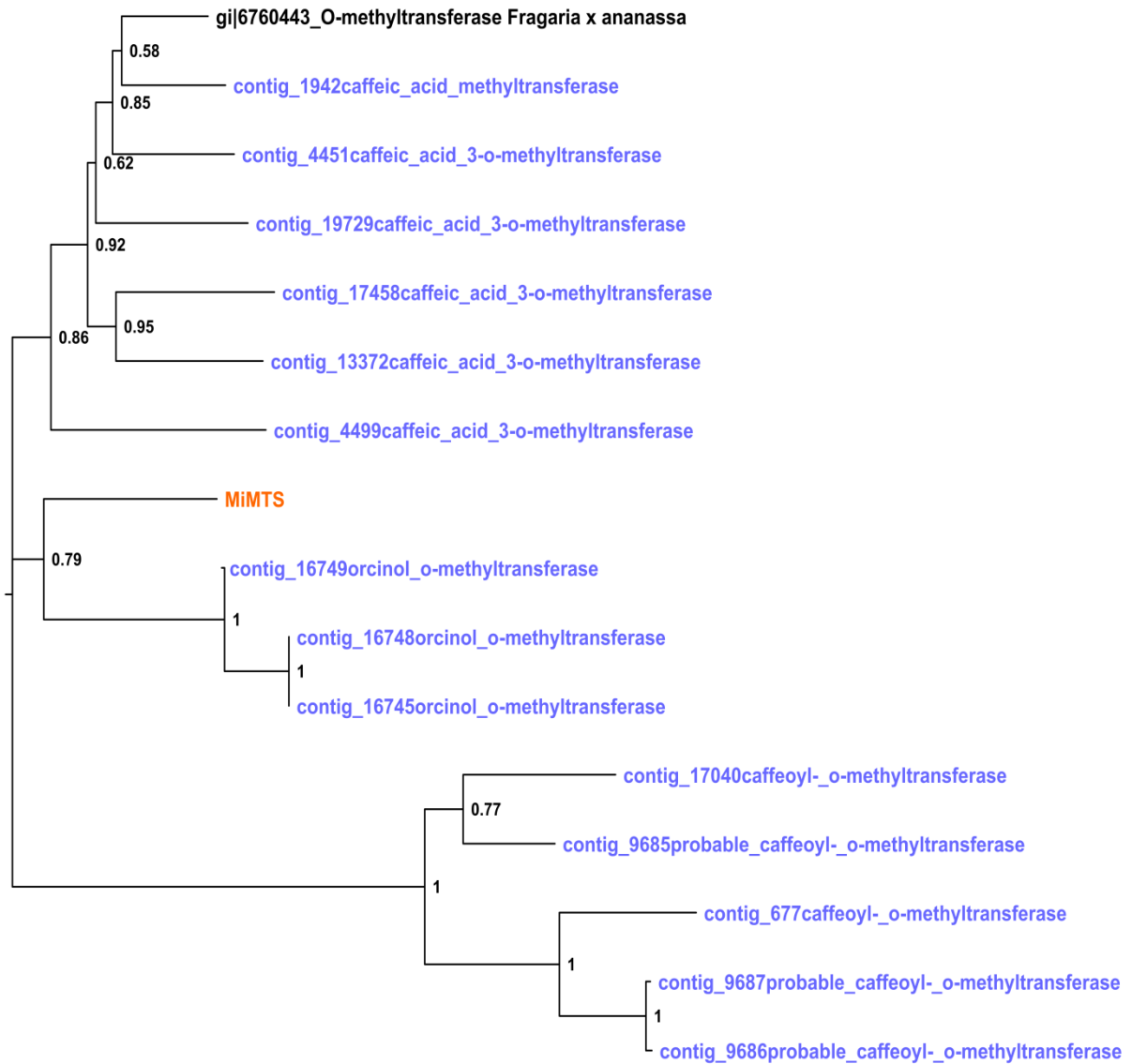
(c)



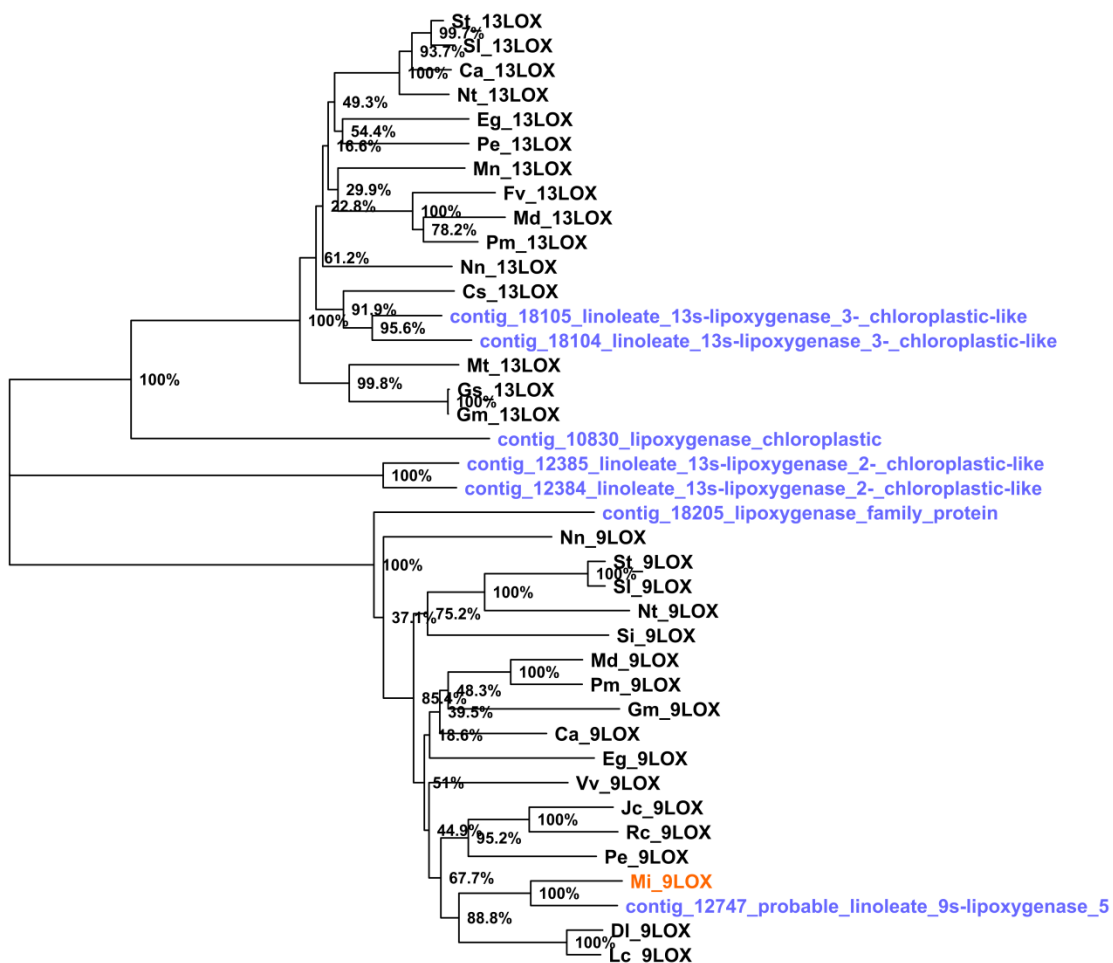
Supplementary Figure SF3: Phylogenetic analysis by neighbor-joining of proteins encoded by Enone oxidoreductase (gi|387135418) involved in the biosynthesis of furaneol from *Mangifera indica* (orange color) and other contigs representing quinone oxidoreductases from the present study (blue color) and other characterized oxidoreductases (black color) from *Nicotiana tabacum_2*-alkenal_reductase_(gi|75206691), *Fragaria vesca*_Enone_oxidoreductase (gi|613785129), *Solanum lycopersicum_2*-methylene-furan-3-one_reductase (gi|823630988), *Fragaria* × *Ananassa*_ Enone_Oxidoreductase (gi|480312155) and *Fragaria* × *Ananassa*_ quinone_oxidoreductase (gi|29468088)



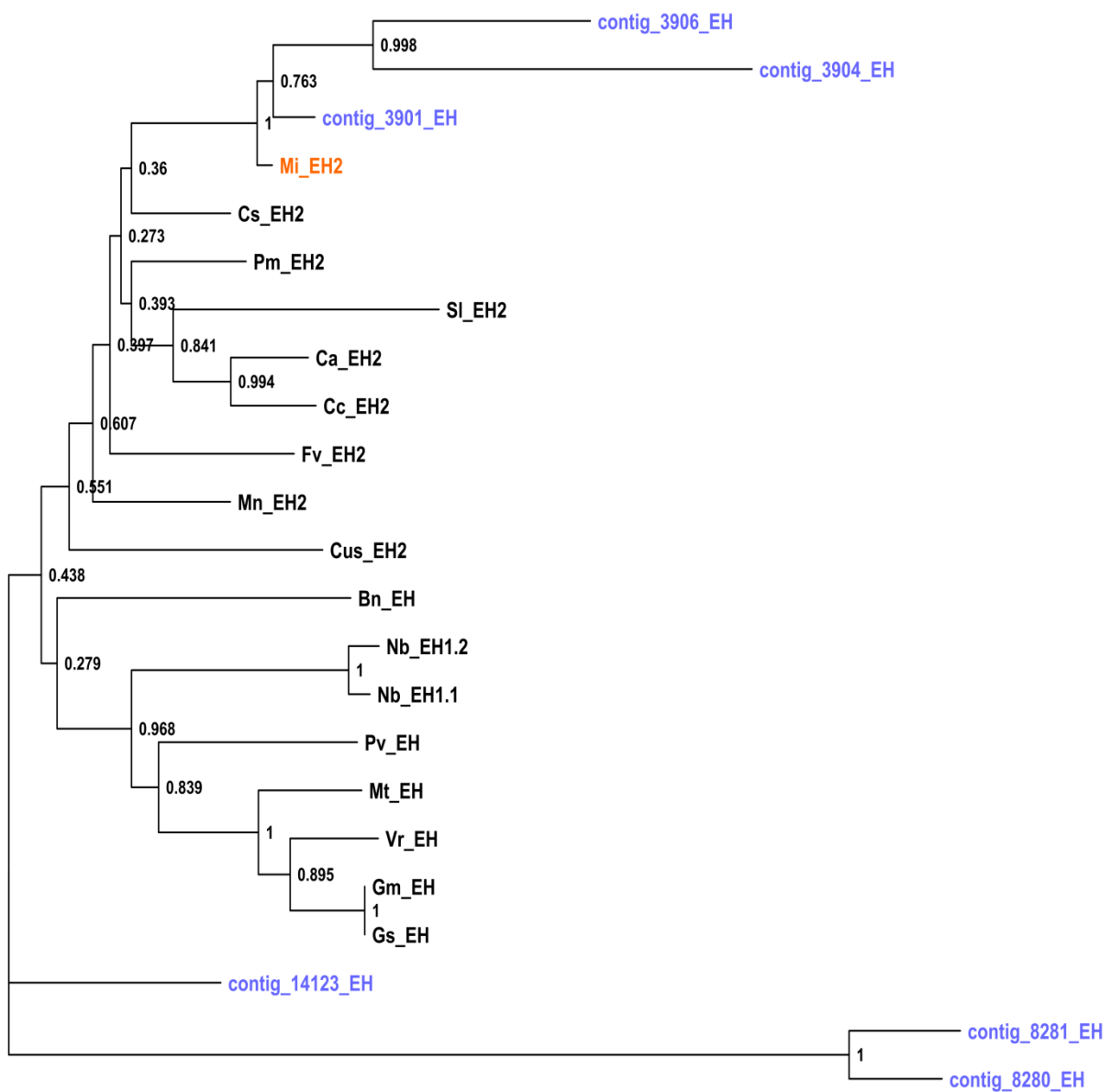
Supplementary Figure SF4: Phylogenetic analysis by neighbor-joining of proteins encoded by *O*-methyltransferase (KP993176) involved in the biosynthesis of mesifuran from *Mangifera indica* (orange color) along with the characterized *O*-methyltransferase (black color) from *Fragaria x ananassa* (AAF28353) and other contigs representing *O*-methyltransferase from the present study (blue color).



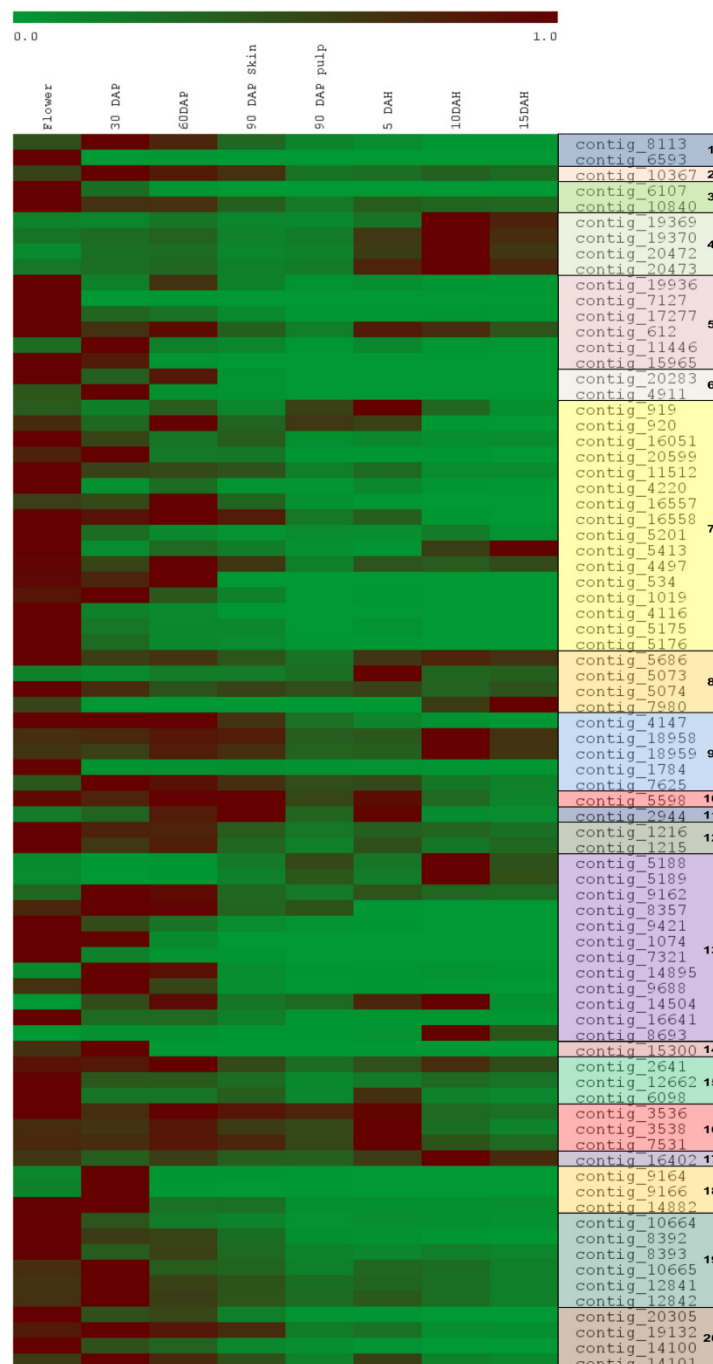
Supplementary Figure SF5: Phylogenetic analysis by neighbor-joining of proteins encoded by *9-lipoxygenase* (KX090178) involved in the biosynthesis of aroma volatiles from *Mangifera indica* (orange color) and other contigs representing *lipoxygenases* from present study (blue color) along with the other plant *9* and *13* *lipoxygenases* (black color) from *Vitis vinifera_9LOX* (XP_010659859), *Malus domestica_9LOX* (NP_001281030), *Prunus mume_9LOX* (XP_008246456), *Glycine max_9LOX* (XP_003521704), *Solanum tuberosum_9LOX* (NP_001274916), *Nicotiana tabacum_9LOX* (XP_016433823), *Dimocarpus longan_9LOX* (ANF89411), *Corylus avellana_9LOX* (CAD10740), *Litchi chinensis_9LOX* (AEQ30071), *Populus euphratica_9LOX* (XP_011023610), *Eucalyptus grandis_9LOX* (XP_010025195), *Jatropha curcas_9LOX* (XP_012089053), *Ricinus communis_9LOX* (XP_002512386), *Solanum lycopersicum_9LOX* (XP_004244890), *Sesamum indicum_9LOX* (XP_011087404), *Nelumbo nucifera_9LOX* (XP_010256003), *Malus domestica_13LOX* (NP_001280985), *Prunus mume_13LOX* (XP_008228181), *Medicago truncatula_13LOX* (XP_003627308), *Solanum tuberosum_13LOX* (NP_001275115), *Glycine soja_13LOX* (KHN39622), *Fragaria vesca_13LOX* (XP_004303702), *Morus notabilis_13LOX* (XP_010086794), *Eucalyptus grandis_13LOX* (XP_010033729), *Populus euphratica_13LOX* (XP_011035732), *Nelumbo nucifera_13LOX* (XP_010273845), *Capsicum annuum_13LOX* (NP_001311748), *Nicotiana tabacum_13LOX* (XP_016495606), *Citrus sinensis_13LOX* (XP_006465905), *Solanum lycopersicum_13LOX* (AAB65767) and *Glycine max_13LOX* (XP_014624448).



Supplementary Figure SF6: Phylogenetic analysis by neighbor-joining of proteins encoded by *epoxide hydrolase 2* (KX090179) involved in the biosynthesis of aroma volatile lactones from *Mangifera indica* (orange color) and other contigs representing *epoxide hydrolases* from the present study (blue color) along with the other plant *epoxide hydrolases* (black color) from *Nicotiana benthamiana_EH1.2* (ACE82566), *Nicotiana benthamiana_EH1.1* (ACE82565), *Phaseolus vulgaris_EH* (AKJ75509), *Glycine max_EH* (CAA55294), *Medicago truncatula_EH* (XP_003626202), *Glycine soja_EH* (KHN43314), *Vigna radiata_EH* (AIJ27456), *Brassica napus_EH* (NP_001302895), *Citrus sinensis_EH2* (XP_006489040), *Prunus mume_EH2* (XP_016647751), *Cicer arietinum_EH2* (XP_004508197), *Fragaria vesca_EH2* (XP_004290776), *Cajanus cajan_EH2* (KYP58120), *Cucumis sativus_EH2* (XP_004134492), *Solanum lycopersicum_EH2* (XP_004252913) and *Morus notabilis_EH2* (XP_010105136).



Supplementary Figure SF8: Heatmap representing differential expression of various contigs coding for 20 different inhibitors. Description for group 1-20 as follows, 1: alpha-amylase inhibitor, 2: androgen induced inhibitor of proliferation pds5, 3: apoptosis inhibitor, 4: bax inhibitor, 5: bifunctional inhibitor of lipid-transfer protein seed storage, 6: cell wall and vascular inhibitor of beta-fructosidase, 7: kinase inhibitor, 8: cysteine proteinase inhibitor, 9: trypsin inhibitor, 10: guanosine nucleotide diphosphate dissociation inhibitor, 11: macrophage migration inhibitory factor, 12: nf-kappa-b inhibitor, 13: pectinesterase inhibitor, 14: polygalacturonase inhibiting protein, 15: phosphoprotein phosphatase inhibitors, 16: plasminogen activator inhibitor 1 rna-binding, 17: proteasome inhibitor, 18: protein reversion to ethylene sensitivity, 19: protein transport inhibitor and 20: rho gdp-dissociation inhibitor.



Supplementary Figure SF9: Terpene biosynthesis pathway from Alphonso mango

