

**Manuscript title :**

Genome-wide identification and characterization of genes involved in carotenoid metabolism in three stages of grapevine fruit development

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**Supplementary tables:**

**Table S1** The gene expression patterns of carotenoid metabolic pathway genes in three stages of grapevine fruit development.

**Table S2** The gene expression patterns of chlorophyll synthesis and degradation pathway genes in three stages of grapevine fruit development.

**Table S3** The primers sequences of carotenoid biosynthesis genes for qRT-PCR.

**Supplementary figures:**

**Fig. S1** Summary diagram of carotenoid metabolism pathways in grapevine (MVA, MEP, carotenoid biosynthetic and catabolic pathways). MVA pathway: *ACAT*, acetyl-CoA acetyltransferase; *HMGS*, 3-hydroxy-3-methylglutaryl-CoA synthase; *HMGR*, 3-hydroxy-3-methylglutaryl-CoA reductase; *MVK*, mevalonate kinase; *pMVK*, phosphomevalonate kinase; *MDC*, mevalonate diphosphate decarboxylase; *FPS*, farnesyl diphosphate synthase; MEP pathway: *DXS*, 1-deoxy-D-xylulose-5-phosphate synthase; *DXR*, 1-deoxy-D-xylulose-5-phosphate reductoisomerase; *MCT*, 4-diphosphocytidyl-2-C-methyl-D-erythritol synthase; *CMK*, 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase; *MDS*, 2-C-methyl-D-erythritol 2,4-cyclodiphosphate

synthase; *HDS*, 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase; *HDR*, 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate reductase; *IDI*, isopentenyl diphosphate isomerase; carotenoid biosynthetic pathway: *GGPPS*, geranylgeranyldiphosphate synthase; *PSY*, phytoene synthase; *PDS*, phytoene desaturase; *Z-ISO*,  $\zeta$ -carotene isomerase; *ZDS*,  $\zeta$ -carotene desaturase; *CRTISO*, carotene isomerase; *LCYE*, lycopene  $\epsilon$ -cyclase; *LCYB*, lycopene  $\beta$ -cyclase; *CHYB*,  $\beta$ -carotene hydroxylase; *CYP97C*, cytochrome P450-type monooxygenase 97C; *CYP97A*, cytochrome P450-type monooxygenase 97A (LUTEIN DEFICIENT 5); *ZEP*, zeaxanthin epoxidase; *VDE*, violaxanthin de-epoxidase; *NXS*, neoxanthin synthase; Carotenoid catabolic, *NCED*, 9-cis-epoxycarotenoid dioxygenase; *CCS*, capsanthin-capsorubin synthase; *CCD*, carotenoid cleavage dioxygenase. The asterisks identify enzymes encoded by several gene isoforms.

**Fig. S2** Summary diagram of chlorophyll metabolic pathways in grapevine. Genes encode the following enzymes. Chlorophyll synthesis: *GLTX*, glutamyl-tRNA synthetase; *HEMA*, glutamyl-tRNA reductase; *GSA*, glutamate-1-semialdehyde 2,1-aminomutase; *ALAD*, Delta-aminolevulinic acid dehydratase; *PBGD*, porphobilinogen deaminase; *UROS*, uroporphyrinogen-III synthase; *UROD*, uroporphyrinogen decarboxylase; *CPOX*, coproporphyrinogen III oxidase; *PPOX*, protoporphyrinogen oxidase; *CHLH/G/I*, magnesium-chelatase H/D/I subunit; *CHLM*, magnesium protoporphyrin IX methyltransferase; *CRDI*, magnesium-protoporphyrin IX monomethylester [oxidative] cyclase; *PORA/PORC*, protochlorophyllide reductase A/C; *DVR*, divinyl chlorophyllide a 8-vinyl-reductase; *CHLG*, chlorophyll synthase; Chlorophyll cycle: *CAO*, chlorophyllide a oxygenase; *NYCI*, chlorophyll b reductase; *NOL*, chlorophyll b reductase-like; *HCAR*, 7-hydroxymethyl chlorophyll a reductase; Chlorophyll degradation: *CLH2*, chlorophyllase 2; *PPH*, pheophytinase; *PaO*,

pheophorbide a oxygenase; *RCCR*, red chlorophyll catabolite reductase. *MCS*, metal-chelating substance. In the diagram, the enzymes with down-regulated gene expression level are indicated in black, the enzymes with up-regulated gene expression level in red, while the enzymes with no change in blue. The asterisks identify enzymes encoded by several gene isoforms.

**Fig. S3** qRT-PCR validation of differentially expressed transcripts from RNA-seq.

**Fig. S4** Phylogenetic relationship of plant DXSs. The rooted Neighbor-Joining tree was constructed using the MEGA program (version 7.0) with default parameters. DXSs included are *Vitis vinifera* *VvDXS1* (VIT\_05s0020g02130.t01), *VvDXS2* (VIT\_11s0052g01730.t01), *VvDXS3* (VIT\_04s0008g04970.t01), *VvDXS4* (VIT\_11s0052g01780.t01), *VvDXS5* (VIT\_00s0218g00110.t0), *VvDXS6* (VIT\_11s0052g01240.t01); *Arabidopsis thaliana* *AtDXS1* (At4g15560), *AtDXS2* (At3g21500), *AtDXS3* (At5g11380); *Oryza sativa* *OsDXS1* (NP\_001055524), *OsDXS2* (NP\_001059086), *OsDXS3* (BAA83576); *Populus trichocarpa* *PtDXS1* (XP\_002312717), *PtDXS2A* (XP\_002303416), *PtDXS2B* (XP\_002331678), *PtDXS3* (XP\_002308644); *Salvia miltiorrhiza* *SmDXS1* (EU670744), *SmDXS2* (FJ643618), *SmDXS3* (JN831116), *SmDXS4* (JN831117), *SmDXS5* (JN831118).

**Fig. S5** Phylogenetic relationships of PSYs from Grapevine and various other plants. PSYs included are *Vitis vinifera* *VvPSY1* (VIT\_04s0079g00680.t01), *VvPSY2* (VIT\_12s0028g00960.t01), *VvPSY3* (VIT\_06s0004g00820.t01); *Arabidopsis thaliana* *AtPSY* (AT5G17230); *Solanum lycopersicum* *SlPSY1* (Solyc03g031860), *SlPSY2* (Solyc02g081330), *SlPSY3* (Solyc01g005940); *Oryza sativa* *OsPSY1* (AAS18307), *OsPSY2* (AAK07735), *OsPSY3* (DQ356431); *Zea mays* *ZmPSY1* (P49085), *ZmPSY2* (AAQ91837), *ZmPSY3* (DQ356430).

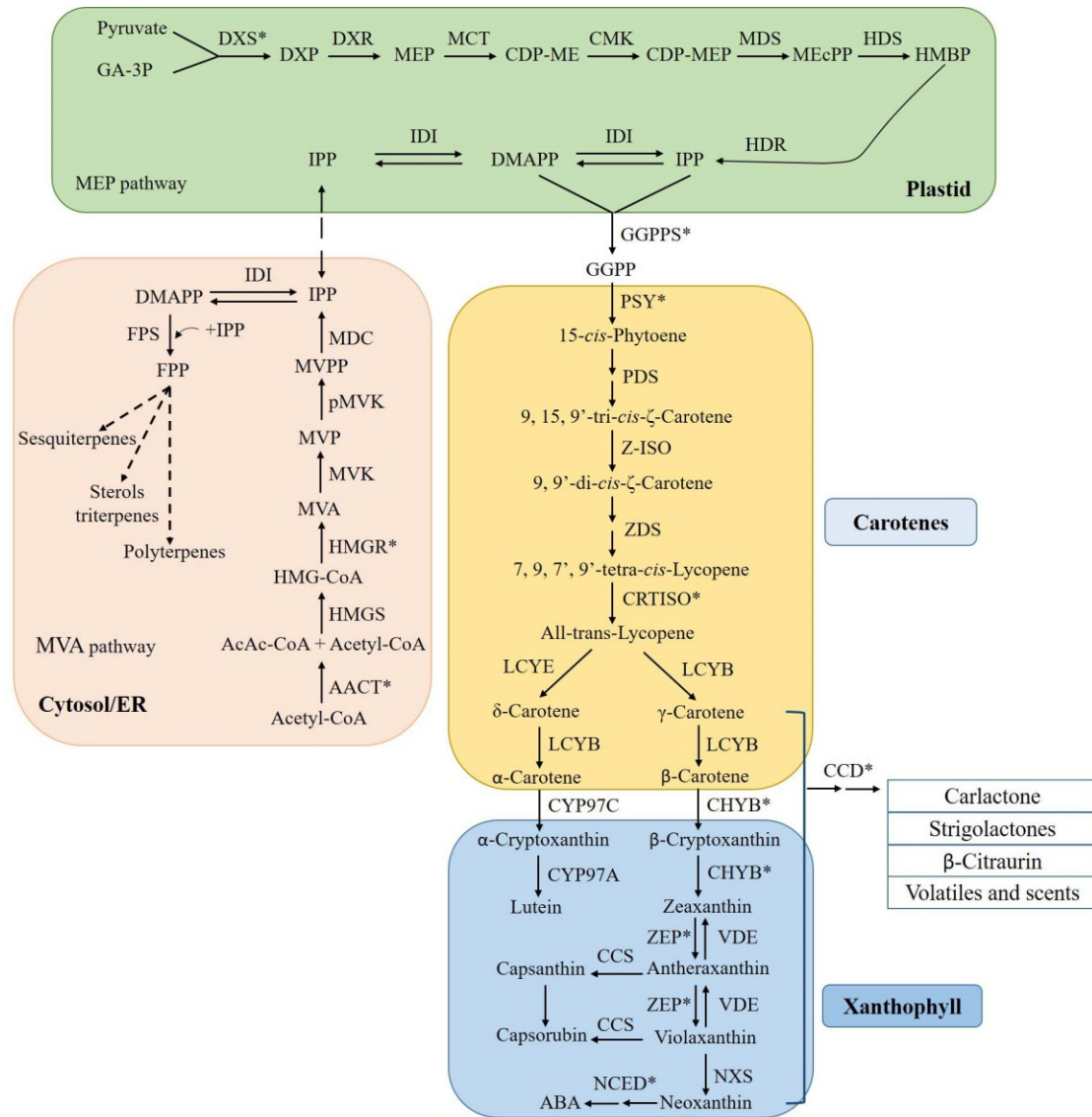
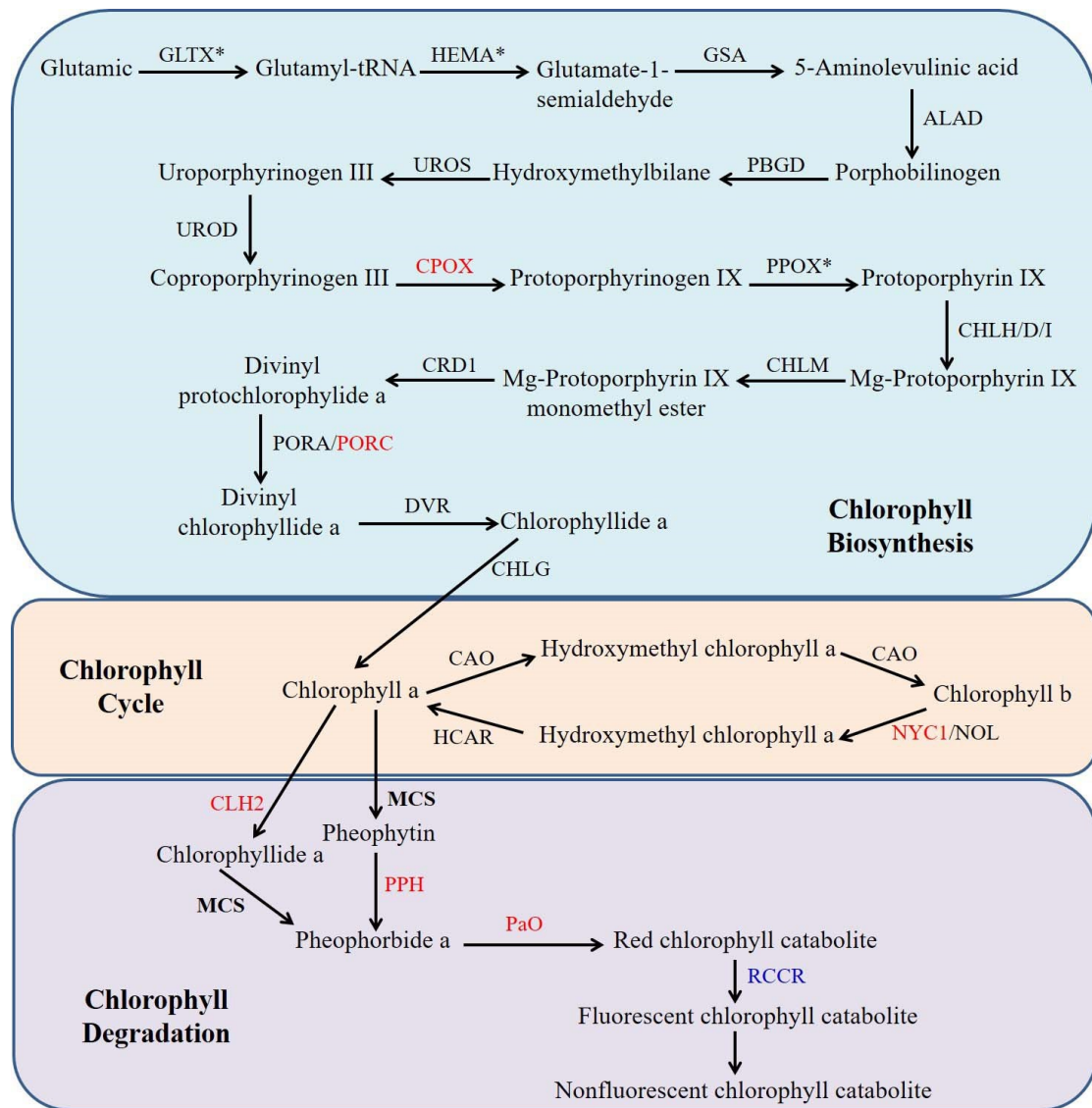
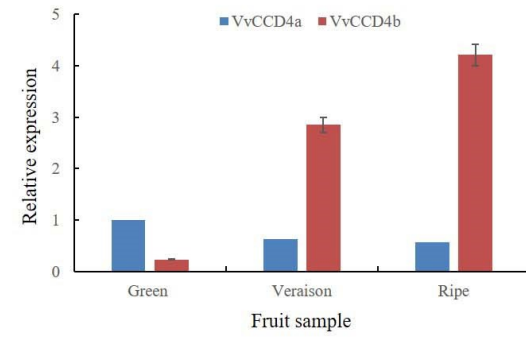
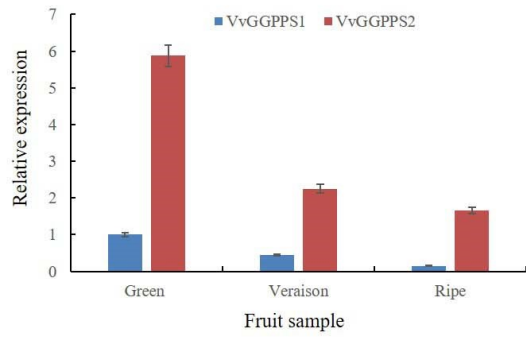
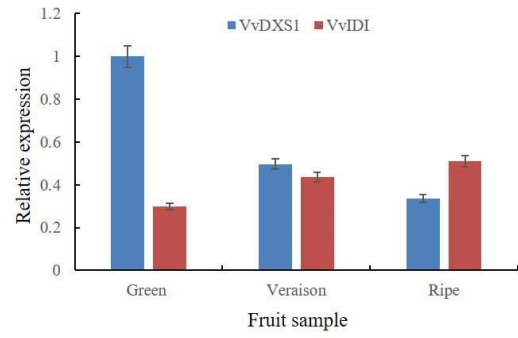
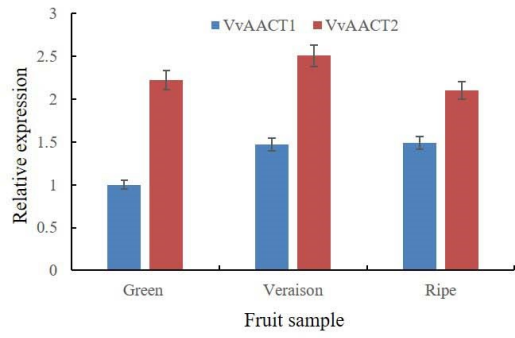


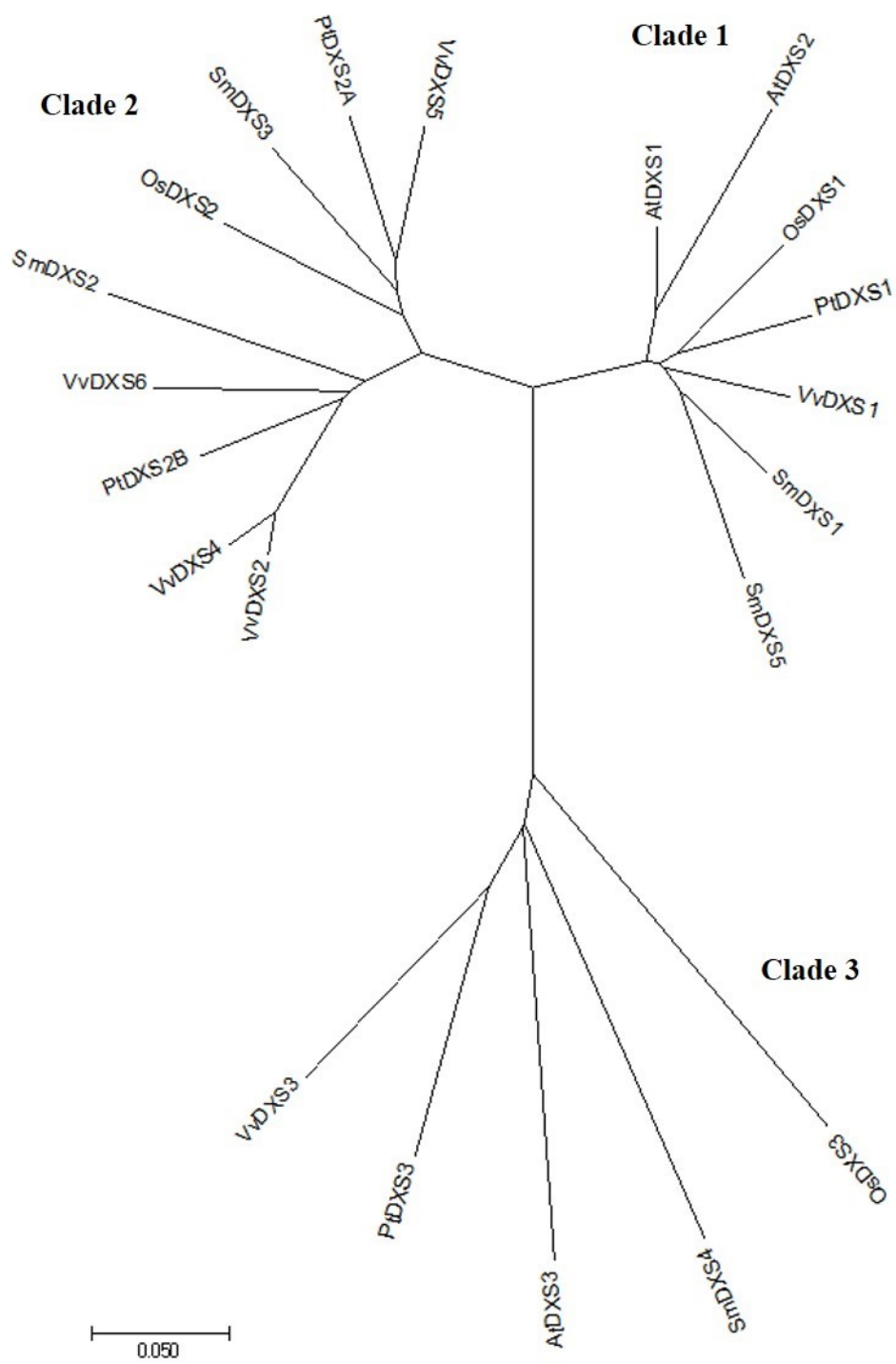
Fig. S1



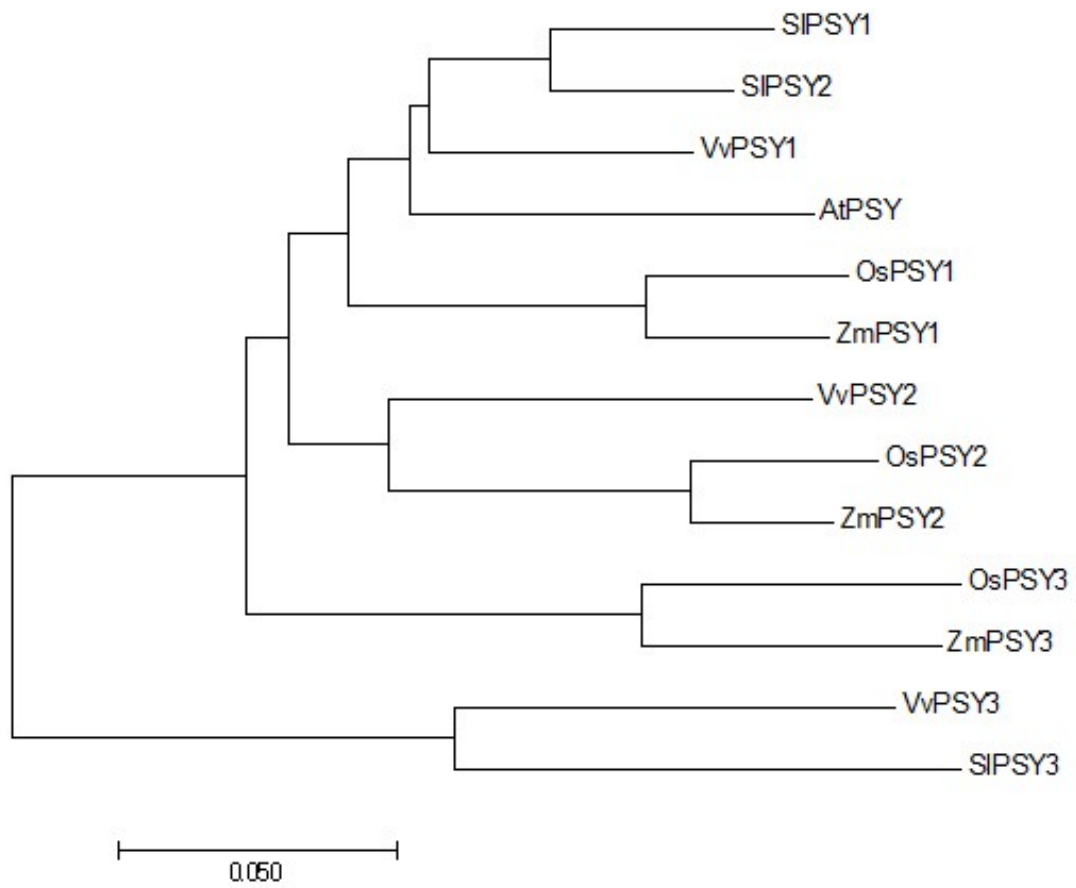
**Fig. S2**



**Fig. S3**



**Fig. 4**



**Fig. S5**