Table 3 Functional enrichment analysis of *LDOX* genes

GO Enrichment		Term description	False discovery rate (FDR)
	Biology Process	Flavonoid biosynthetic process	2.38E-27
		Flavonoid metabolic process	8.09E-27
		Phenylpropanoid metabolic process	4.83E-17
		Secondary metabolic process	5.29E-14
		Organic substance biosynthetic process	5.56E-11
		Organic substance metabolic process	1.03E-09
		Response to karrikin	3.61E-09
		Phenylpropanoid biosynthetic process	8.93E-08
		Regulation of flavonoid biosynthetic process	1.33E-07
		Response to abiotic stimulus	2.11E-07
	Cell component	Extrinsic component of endoplasmic reticulum membrane	0.00038
		Endoplasmic reticulum	0.00041
		Vacuolar membrane	0.0322
		Endoplasmic reticulum membrane	0.0322
		Plant-type vacuole membrane	0.0322
		Intracellular part	0.0322
		Endoplasmic reticulum subcompartment	0.0322
		Cytoplasm	0.0372
		Organelle membrane	0.0413
	Molecular Function	Catalytic activity	3.93E-09
		4-coumarate-CoA ligase activity	2.75E-07
		Oxidoreductase activity	2.75E-07
		Cofactor binding	2.75E-07
		Coenzyme binding	2.75E-07
		2-oxoglutarate-dependent dioxygenase activity	6.08E-07
KEGG Enrichment	Enrichment of LDOX related pathways	Flavonoid biosynthesis	4.23E-30
		Biosynthesis of secondary metabolites	1.76E-24
		Metabolic pathways	5.30E-18
		Phenylpropanoid biosynthesis	1.11E-12
		Phenylalanine metabolism	4.73E-10
		Ubiquinone and other terpenoid-quinone biosynthesis	3.07E-08
		Flavone and flavonol biosynthesis	1.19E-05
		Stilbenoid, diarylheptanoid and gingerol biosynthesis	2.50E-05