

Additional file 2

**Table S1:** Enriched GO terms of DEGs between the black and the white sesame

GO	GO Title	Category	5DPA	8DPA	11DPA	14DPA	17DPA	20DPA	23DPA	26DPA	30DPA	Total
<b>GO:0016491</b>	oxidoreductase activity	MF	Y*	Y	Y	Y	Y	Y		Y	Y	8
<b>GO:0055114</b>	oxidation-reduction process	BP	Y	Y	Y	Y	Y	Y		Y		7
<b>GO:0003824</b>	catalytic activity	MF		Y	Y	Y	Y	Y	Y			6
<b>GO:0005506</b>	iron ion binding	MF		Y	Y	Y	Y	Y		Y		6
<b>GO:0004497</b>	monooxygenase activity	MF		Y	Y	Y	Y			Y		5
<b>GO:0009055</b>	electron carrier activity	MF		Y	Y	Y	Y			Y		5
<b>GO:0020037</b>	heme binding	MF		Y	Y	Y	Y			Y		5
<b>GO:0008152</b>	metabolic process	BP			Y	Y		Y			Y	4
<b>GO:0009607</b>	response to biotic stimulus	BP			Y	Y				Y		3
<b>GO:0004097</b>	catechol oxidase activity	MF			Y	Y						2
<b>GO:0005507</b>	copper ion binding	MF		Y		Y						2
<b>GO:0005618</b>	cell wall	CC			Y	Y						2
<b>GO:0006629</b>	lipid metabolic process	BP			Y	Y						2
<b>GO:0008171</b>	O-methyltransferase activity	MF		Y		Y						2
<b>GO:0016757</b>	transferase activity, transferring glycosyl groups	MF		Y	Y							2
<b>GO:0016758</b>	transferase activity, transferring hexosyl groups	MF		Y	Y							2
<b>GO:0016998</b>	cell wall macromolecule catabolic process	BP			Y	Y						2
<b>GO:0048544</b>	recognition of pollen	BP			Y	Y						2
<b>GO:0050662</b>	coenzyme binding	MF		Y		Y						2
<b>GO:0071554</b>	cell wall organization or biogenesis	BP			Y	Y						2
<b>GO:0000003</b>	reproduction	BP			Y							1

<b>GO:0003723</b>	RNA binding	MF		Y	1
<b>GO:0003735</b>	structural constituent of ribosome	MF		Y	1
<b>GO:0004553</b>	hydrolase activity, hydrolyzing O-glycosyl compounds	MF	Y		1
<b>GO:0004672</b>	protein kinase activity	MF		Y	1
<b>GO:0004674</b>	protein serine/threonine kinase activity	MF		Y	1
<b>GO:0004842</b>	ubiquitin-protein ligase activity	MF		Y	1
<b>GO:0005198</b>	structural molecule activity	MF		Y	1
<b>GO:0005215</b>	transporter activity	MF		Y	1
<b>GO:0005529</b>	sugar binding	MF	Y		1
<b>GO:0005576</b>	extracellular region	CC	Y		1
<b>GO:0005622</b>	intracellular	CC		Y	1
<b>GO:0005737</b>	cytoplasm	CC		Y	1
<b>GO:0005840</b>	ribosome	CC		Y	1
<b>GO:0005975</b>	carbohydrate metabolic process	BP	Y		1
<b>GO:0005976</b>	polysaccharide metabolic process	BP		Y	1
<b>GO:0006221</b>	pyrimidine nucleotide biosynthetic process	BP		Y	1
<b>GO:0006412</b>	translation	BP		Y	1
<b>GO:0006468</b>	protein phosphorylation	BP		Y	1
<b>GO:0006631</b>	fatty acid metabolic process	BP		Y	1
<b>GO:0006855</b>	drug transmembrane transport	BP		Y	1
<b>GO:0006857</b>	oligopeptide transport	BP		Y	1
<b>GO:0006869</b>	lipid transport	BP	Y		1
<b>GO:0008061</b>	chitin binding	MF		Y	1
<b>GO:0008194</b>	UDP-glycosyltransferase activity	MF		Y	1
<b>GO:0008289</b>	lipid binding	MF	Y		1
<b>GO:0009058</b>	biosynthetic process	BP		Y	1
<b>GO:0009059</b>	macromolecule biosynthetic process	BP		Y	1

<b>GO:0009415</b>	response to water	BP	Y	1
<b>GO:0009521</b>	photosystem	CC	Y	1
<b>GO:0009523</b>	photosystem II	CC	Y	1
<b>GO:0009538</b>	photosystem I reaction center	CC	Y	1
<b>GO:0009690</b>	cytokinin metabolic process	BP	Y	1
<b>GO:0010467</b>	gene expression	BP	Y	1
<b>GO:0012511</b>	monolayer-surrounded lipid storage body	CC	Y	1
<b>GO:0016301</b>	kinase activity	MF	Y	1
<b>GO:0016310</b>	phosphorylation	BP	Y	1
<b>GO:0016567</b>	protein ubiquitination	BP	Y	1
<b>GO:0016620</b>	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	MF	Y	1
<b>GO:0016740</b>	transferase activity	MF	Y	1
<b>GO:0016773</b>	phosphotransferase activity, alcohol group as acceptor	MF	Y	1
<b>GO:0016798</b>	hydrolase activity, acting on glycosyl bonds	MF	Y	1
<b>GO:0016841</b>	ammonia-lyase activity	MF	Y	1
<b>GO:0016903</b>	oxidoreductase activity, acting on the aldehyde or oxo group of donors	MF	Y	1
<b>GO:0019139</b>	cytokinin dehydrogenase activity	MF	Y	1
<b>GO:0030246</b>	carbohydrate binding	MF	Y	1
<b>GO:0030312</b>	external encapsulating structure	CC	Y	1
<b>GO:0030529</b>	ribonucleoprotein complex	CC	Y	1
<b>GO:0032501</b>	multicellular organismal process	BP	Y	1
<b>GO:0032991</b>	macromolecular complex	CC	Y	1
<b>GO:0033897</b>	ribonuclease T2 activity	MF	Y	1

<b>GO:0034645</b>	cellular macromolecule biosynthetic process	BP		Y	1
<b>GO:0042026</b>	protein refolding	BP		Y	1
<b>GO:0043169</b>	cation binding	MF	Y		1
<b>GO:0043229</b>	intracellular organelle	CC		Y	1
<b>GO:0043232</b>	intracellular non-membrane-bounded organelle	CC		Y	1
<b>GO:0044036</b>	cell wall macromolecule metabolic process	BP	Y		1
<b>GO:0044237</b>	cellular metabolic process	BP		Y	1
<b>GO:0044238</b>	primary metabolic process	BP		Y	1
<b>GO:0044249</b>	cellular biosynthetic process	BP		Y	1
<b>GO:0044267</b>	cellular protein metabolic process	BP		Y	1
<b>GO:0044424</b>	intracellular part	CC		Y	1
<b>GO:0044444</b>	cytoplasmic part	CC		Y	1
<b>GO:0045735</b>	nutrient reservoir activity	MF	Y		1
<b>GO:0046872</b>	metal ion binding	MF		Y	1
<b>GO:0046906</b>	tetrapyrrole binding	MF		Y	1
<b>GO:0046914</b>	transition metal ion binding	MF		Y	1
<b>GO:0048037</b>	cofactor binding	MF		Y	1
<b>GO:0050660</b>	flavin adenine dinucleotide binding	MF	Y		1
<b>GO:0052689</b>	carboxylic ester hydrolase activity	MF	Y		1
<b>GO:0071702</b>	organic substance transport	BP	Y		1
<b>GO:0072528</b>	pyrimidine-containing compound biosynthetic process	BP		Y	1

Y\*: Yes

**Table S2:** Enriched KEGG pathways of DEGs between the black and the white sesame

MapID	MapTitle	5DPA	8DPA	11DPA	14DPA	17DPA	20DPA	23DPA	26DPA	30DPA	Total
map00941	Flavonoid biosynthesis		Y	Y	Y	Y	Y	Y	Y		7
map01110	Biosynthesis of secondary metabolites	Y	Y	Y	Y	Y	Y		Y		7
map01100	Metabolic pathways	Y	Y	Y	Y	Y			Y		6
map00363	Bisphenol degradation		Y	Y	Y	Y			Y		5
map00624	Polycyclic aromatic hydrocarbon degradation		Y	Y	Y	Y			Y		5
map00627	Aminobenzoate degradation		Y	Y	Y	Y			Y		5
map00903	Limonene and pinene degradation		Y	Y	Y	Y			Y		5
map00944	Flavone and flavonol biosynthesis		Y	Y	Y	Y			Y		5
map00945	Stilbenoid, diarylheptanoid and gingerol biosynthesis		Y	Y	Y	Y			Y		5
map04976	Bile secretion			Y	Y			Y	Y		4
map00904	Diterpenoid biosynthesis			Y		Y			Y		3
map00906	Carotenoid biosynthesis			Y	Y		Y				3
map00940	Phenylpropanoid biosynthesis			Y	Y	Y					3
map01120	Microbial metabolism in diverse environments				Y	Y			Y		3
map02010	ABC transporters				Y			Y	Y		3
map00196	Photosynthesis - antenna proteins	Y						Y			2
map00360	Phenylalanine metabolism			Y	Y						2
map00592	alpha-Linolenic acid metabolism	Y		Y							2
map00010	Glycolysis / Gluconeogenesis	Y									1
map00040	Pentose and glucuronate interconversions			Y							1
map00053	Ascorbate and aldarate metabolism				Y						1

<b>map00270</b>	Cysteine and methionine metabolism	Y	1
<b>map00950</b>	Isoquinoline alkaloid biosynthesis	Y	1
<b>map01040</b>	Biosynthesis of unsaturated fatty acids	Y	1
<b>map03010</b>	Ribosome	Y	1
<b>map04075</b>	Plant hormone signal transduction	Y	1
<b>map04210</b>	Apoptosis	Y	1
<b>map04620</b>	Toll-like receptor signaling pathway	Y	1
<b>map04626</b>	Plant-pathogen interaction	Y	1
<b>map04722</b>	Neurotrophin signaling pathway	Y	1
<b>map04740</b>	Olfactory transduction	Y	1
<b>map04916</b>	Melanogenesis	Y	1
<b>map04970</b>	Salivary secretion	Y	1
<b>map04971</b>	Gastric acid secretion	Y	1
<b>map04974</b>	Protein digestion and absorption	Y	1
<b>map05140</b>	Leishmaniasis	Y	1
<b>map05145</b>	Toxoplasmosis	Y	1

Y\*: Yes