Supplemental Information S1:

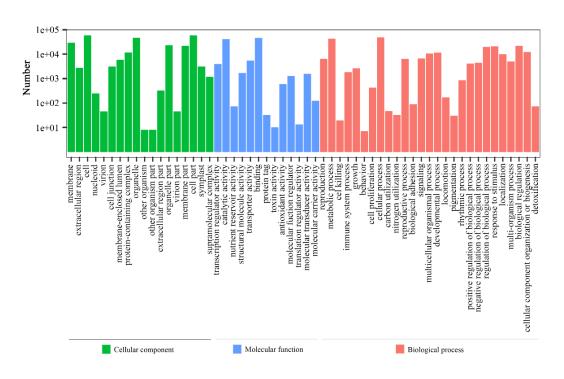
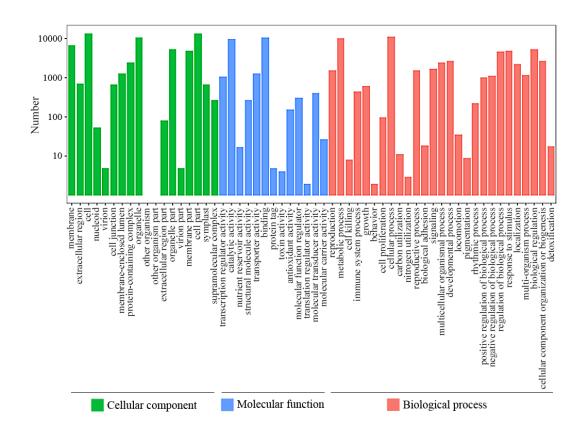


Figure S1 GO classification of the Luffa unigene library



FigureS2 GO classification of the DEGs identified in the unigene libraries between two *Luffa* cultivars.

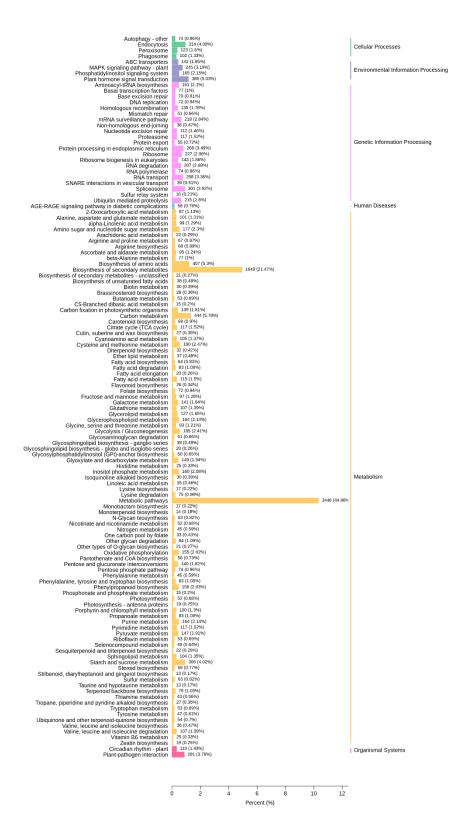


Figure S3 KEGG classification of the DEGs identified in the unigene libraries between two *Luffa* cultivars.

Table S3 Comparison of unigenes identified in transcriptome during browning of 'Fusi-3' fruits and transcriptome of two *Luffa* cultivars '2D-2' and '35D-7'.

'Fusi-3'		'2D-2' and '35D-3'				
Unigene ID	Expression trend	Unigene ID	Expression trend	Log2fold change	Annotation	
Unigene 0043875	up	Cluster-21832.13892	up	7.15	polyphenol oxidase	
Unigene0050171	up	none	none	none	polyphenol oxidase	
Unigene0015096	down	Cluster-21832.13892	up	7.15	polyphenol oxidase	
Unigene0044748	up	Cluster-21832.39888	-	-	phenylalanine ammonia-lyase	
Unigene0024978	up	Cluster-47379.0	up	2.16	phenylalanine ammonia-lyase	
Unigene0011770	up	Cluster-21832.19847	up	2.27	peroxidase	
Unigene 0036262	up	Cluster-21832.36955	up	2.72	catalase	
Unigene0033876	down	Cluster-21832.30636	up	2.21	catalase	
Unigene 0021782	up	Cluster-21832.29146	-	-	superoxide	
Unigene0008835	down	Cluster-45332.0	-	-	superoxide	
Unigene0015506	down	Cluster-21832.7745	up	9.46	superoxide	

'Fusi-3' represents the transcript analysis during the browning of 'Fusi-3' fruits. '2D-2' and '35D-7' represents the transcript analysis of browning-resistant *Luffa* cultivar '2D-2' and browning-prone *Luffa* cultivar '35D-7'. 'None' indicates no matching to the sequence. '-' indicates that no significant difference was found in gene expression. Green and red color represents the same and opposite expression trend, respectively.

Table S4 Information of WRKY transcription factors identified in the transcriptomes of Luffa '2D-2' and '35D-7'.

	Expression		Domain			
Unigene No.	log2FoldChange	og2FoldChange Regulated		Description	Accession No.	
Cluster-18244.0	12.4292	up	2		pfam03106	
Cluster-10926.1	10.0614	up 2			pfam03106	
Cluster-21832.2248	3.58428	up	1		smart00774	
Cluster-21832.38074	2.78687	up	1		smart00774	
Cluster-21832.39105	2.34574	up	2		pfam03106	
Cluster-21832.6008	2.27242	up	2		pfam03106,	
Cluster-21832.0008	2.27242				smart00774	
Cluster-21832.26783	2.06106	up	1		smart 00774	
Cluster-18244.1	1.99927	up	1	WDVV DNA binding domain	pfam03106	
Cluster-10926.2	1.79678	up	2	WRKY DNA-binding domain	pfam03106	
Cluster-21832.19413	-1.7055	down	2		pfam03106	
Cluster-21832.40922	-2.4811	down	2		pfam03106	
Cluster-21832.22382	-2.7626	down	2		pfam03106	
Cluster-21832.19423	-9.7218	down	2		pfam03106	
Cluster-21832.14119	-9.8482	down	2		pfam03106	
Cluster-21832.18531	-9.8809	down	2		pfam03106	
Cluster-21832.40775	-9.9233	down	2		pfam03106	
Cluster-18244.4	-12.376	down	2		pfam03106	