

**Table S1. MeCA related gene in transcriptome sequencing and their primers for qRT-PCR**

Primer Name		sequence (5' - 3')	PCR product size (bp)	RNA-seq gene ID	log2FC	KEGG blast
E1	Forwards	CACCGTCTTCGTCGAATGGA	168	Cluster-1420.27977	4.163989	K00505 tyrosinase [EC:1.14.18.1]   (RefSeq) Di-copper centre-containing (A)
	Reverse	GCACAGCTGATAGGCACTGA				
E2	Forwards	TTGTTCTCGATTGGCTGCCT	122	Cluster-2800.0	3.278433	K18386 FAD dependent monooxygenase [EC:1.14.13.-]   (RefSeq) FAD binding domain protein (A)
	Reverse	ACTCGCCGAGGCTGAATATG				
E3	Forwards	AAAAGCCGGCAGCTTGATTG	169	Cluster-1420.24841	2.518436	K00505 tyrosinase [EC:1.14.18.1]   (GenBank) tyrosinase 2 (A)
	Reverse	GGTTTGACCAGAGCGAGTGA				
E4	Forwards	GGTCCTGAAAATGGCCTGGA	168	Cluster-1420.10766	1.594481	K01904 4-coumarate--CoA ligase [EC:6.2.1.12]   (RefSeq) 4-coumarate:coenzyme A ligase (A)
	Reverse	GGTTGTGATCAAACGCTCCG				
Tk-tef1	Forwards	TACAAGGGCTGGGAGAAGGA	196	-	-	-
	Reverse	TACCGGGCTTGAGGATACCA				

**Table S2. Comparison of DNA sequencing of T-51 and 51-13**

<b>T-51 (reference genome)</b>	<b>51-13 (Resequencing)</b>			
<b>Total sequence length (nt)</b>	<b>Total_reads</b>	<b>Mapped_reads</b>	<b>Mapping_rate</b>	<b>Avg.Depth(X)</b>
38274022	13289446	13098381	98.56%	37.01

**Table S3. SNP and indel analysis of 51-13**

<b>SNP</b>		<b>Indel</b>	
<b>Type</b>	<b>Number</b>	<b>Type</b>	<b>Number</b>
Exonic	20	exonic	4
Synonymous	7	frameshift_deletion	1
Nonsynonymous	13	frameshift_insertion	2
Intronic	7	nonframeshift_deletion	1
Intergenic	214	intronic	5
Upstream	11	intergenic	33
Downstream	11	upstream	13
upstream;downstream	1	downstream	22
		upstream;downstream	4
<b>Total</b>	<b>264</b>	<b>Total</b>	<b>81</b>