

Supplementary Materials: Transcriptome Sequencing Analyses between the Cytoplasmic Male Sterile Line and Its Maintainer Line in Welsh Onion (*Allium fistulosum* L.)

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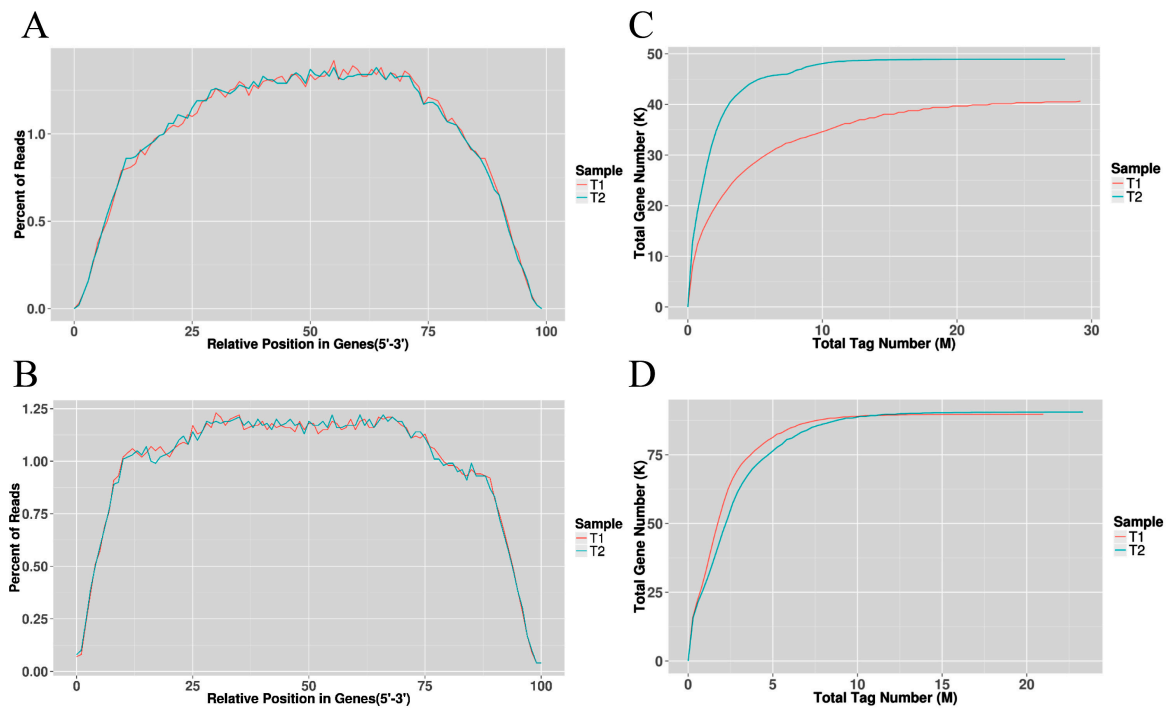


Figure S1. The sequencing quality testing of each sample: (A) Randomness test of cDNA fragments data from May 2013; (B) Randomness test of cDNA fragments data from May 2014; (C) Sequencing saturation analysis from May 2013; and (D) Sequencing saturation analysis from May 2014.

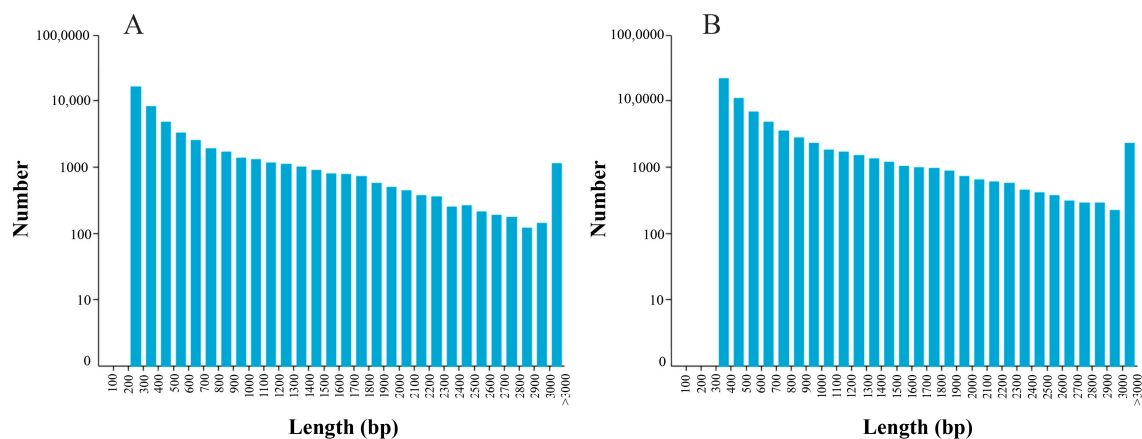


Figure S2. ORF (open reading frame) length distribution: (A) ORF length distribution data in May 2013; and (B) ORF length distribution data in May 2014.

Table S1. Length distribution of assembled contigs, transcripts, and unigenes.

Nucleotide Length (bp)	Contigs		Transcripts		Unigenes	
	May 2013/May 2014		May 2013/May 2014		May 2013/May 2014	
200–300	2,473,748 (98.20%)/3,814,290 (97.60%)		21,140 (21.74%)/57,966 (18.80%)		16,261 (31.20%)/0 (0%)	
300–500	17,693 (0.70%)/43,811 (1.12%)		20,653 (21.24%)/57,631 (18.69%)		12,799 (24.55%)/32,039 (45.54%)	
500–1000	14,321 (0.57%)/28,689 (0.73%)		24,109 (24.80%)/68,847 (22.33%)		10,660 (20.45%)/20,006 (28.43%)	
1000–2000	9866 (0.39%)/15,289 (0.39%)		21,790 (22.41%)/73,238 (23.75%)		8779 (16.84%)/11,948 (16.98%)	
2000+	3541 (0.14%)/6132 (0.16%)		9538 (9.81%)/50,671 (16.43%)		3627 (6.96%)/6367 (9.05%)	
Total number	2,519,169/3,908,211		97,230/308,353		52,126/70,360	
Total length	150,905,138/287,324,074		89,214,332/346,171,877		39,390,976/61,896,802	
N50 length	70/101		1419/1813		1247/1267	
Mean length	59.90/73.51		917.56/1122.648		755.69/879.7158	

Table S2. Functional annotation of unigenes.

Annotation	Annotated Number		DEGSs Number	
	May 2013	May 2014	May 2013	May 2014
Nr Annotation	26,110	27,653	1057	1834
Swissprot Annotation	17,501	17,149	779	1296
COG Annotation	8326	8201	312	529
GO Annotation	20,599	17,541	819	1201
KEGG Annotation	5907	5423	184	284
All Annotated	26,262	29,491	-	-

Table S3. Primers used to perform qPCR of CMS-related gene biosynthesis and gene regulation.

Unigene ID	Primer Sequence (5' to 3')
c116086	Forward: GGGTATCGTTGTGCTCCTGA
	Reverse: CCCCATTTTCCATCTCTGAA
c175619	Forward: TGCCATCATTTGTCTTTCCA
	Reverse: GTGCTTTCAGGCTCTTCCAG
c159049	Forward: ACTTCGCTCGCCTTCTGTC
	Reverse: CGCCTCCTGCTTTCATAGAG
c160965	Forward: CCGCTGCCAATACCAATAGT
	Reverse: CTTCGCTTACACCGCTCAAT
c113452	Forward: AGGTCTCTAAGGCAGGCAAA
	Reverse: GGA CTGAGGTGGCGAAATAC
c50467	Forward: TCAAGCCGTCCAGTTTAGGA
	Reverse: CCTCACCATCATCACCATCA
Actin	Forward: ACACGGCCTGGATAGCAACAT
	Reverse: AGAGCAGTATCCCAAGCATT