

Supplementary Tables:

Table S1. List of the primer sequences used for qRT-PCR analyses

Gene ID	Gene Name	Forward primer (5'-3')	Reverse primer (5'-3')
c131642.graph_c1	SS4	GTTTCCAATTGCCGCCATTG	ATCGATCCGAAGCAGGCTCA
c129481.graph_c0	SBE1	GGCAAGAGGCTATGCACCAA	CACGGAATCGACACAGCCTT
c119393.graph_c0	ISA1	AGTGGCCTCCCAGCAAGAAC	GGATTGCGAGTTTGGTGGTG
c135828.graph_c1	PWD	TGAGGAGTGGAAACGGAGGA	CGTTCCATGTCTCCCGTGAT
c130514.graph_c0	SUS1	CCACACGGTATAGCCCAGGA	CCATGCCGACTTCATCATCA
c129305.graph_c2	VIF1	TGCTCTACACCGGATCCACC	CGCATCCGACTTTGTCCACT
c118684.graph_c0	SUS1-like	TGAATGGCCACATCAGGTGG	CAGGCTGTACAAAGGCGCCT
c129337.graph_c0	TAR3	CCGACGCAGACAGTGGAAT	GGTAACGTAGCCCATCCGGT
c126329.graph_c0	PIN1B	GCAGTCGAGCTGCGAGAAGA	AAACCGGAGGCGCTAAATGA
c113758.graph_c0	IAA15	GTGCTGCGCGGTAACCTTTGT	TTGAGAACGCTGATCCCCAA
c130573.graph_c1	ARF15	AATGCACTCCACCCGGTTGT	CCTTCCCAGGAGCTTGTTC
c111520.graph_c0	PhyB	TTTCTGTCCAATGGTTGCA	GCTCGTCGGAGAGGTTTTTG
c130377.graph_c3	Dio A	GCCAACCTTGACGACTGCAT	AATACTCTCGCCAGCTCGG
c135265.graph_c3	Dio B	TTCACTGTTGCACGAGCAGC	GTGGCTATGGCATGGAGCAG
c129560.graph_c1	CESA7	GCAACACCATGATGGCCAAC	GGTGTACGTCGGAACCGGTT
c134554.graph_c3	CHI	GCCGCACTATGCATCTCCTG	CCTGTCGAGCATGCCTCTGT
c134934.graph_c0	EGase	GATGGCAAACCCCTCAATCGC	TAAGGCCTCCGATGTCCTCG
c124858.graph_c0	EXPA1_like	TGGCCATAGTGCAGTGTGGA	TCCAGACCCATTTTCCGTCA
c114615.graph_c0	NAC	AGTGCATTACCTCTGCCGGA	TACCTGGCAATTCCCAAGGA
c118218.graph_c0	C2H2	GACGTTTAGAGCGTTTGC	CCGTAGATGCAATCGCAACC
c116834.graph_c0	AP2	CAAAGGTGTCCGAGTGTGGC	GTTTGGCCTTCTTACCCCGA
c129895.graph_c0	C3H	CGGCCAGAGACAGTGCTGAT	GGCACCTTGAGGAAACACA
c125026.graph_c1	WRKY	TTGTAGAACGGACGGCTTGG	CACATACGAAGGCGAGCACC
c132918.graph_c1	bHLH	GATCCATTGCACCCCTCCTT	TCAGGTAATCCTCCGCACGA
	EF-1a-F	TCAGGCTGACTGTGCTGTCT	GTGGTGGCGTCCATCTTGTT

Table S2. Summary of RNA-seq reads in yam bulbil transcriptome

Sample	Replicates	No.base in dataset (after QC)	No.clean reads	Mapped Ratio (%)	≥Q30(%)
T01	1	16,655,479,736	56,017,015	73.59	94.27
	2	14,579,803,638	49,112,048	72.8	94.19
	3	19,681,813,798	66,142,499	72.18	93.99
T02	1	18,307,036,212	61,563,310	73.76	93.82
	2	17,066,897,702	57,421,095	73.57	93.8
	3	18,132,828,188	60,865,352	74.12	93.89
T03	1	18,176,433,892	61,253,397	71.76	93.5
	2	16,828,368,454	56,561,893	71.94	93.24
	3	15,525,725,344	52,251,678	72.85	93.59
T04	1	15,037,966,578	50,516,227	72.66	93.59
	2	18,097,731,650	61,231,289	72.38	93.88
	3	16,247,396,402	54,773,454	72.37	93.76

T1, T2, T3 and T4 mean the initiation, early, middle and mature stages of bulbil formation, respectively.

Table S3. Assembly statistics for yam bulbil transcriptome

item	Transcripts	Unigenes
No.of 200-300 bp reads	44,604 (22.38%)	400,88(40.92%)
No.of 300-500 bp reads	27,060(13.58%)	17308(17.67%)
No.of 500-1000 bp reads	41,173(20.66%)	18361(18.74%)
No.of 1000-2000 bp reads	44,579(22.37%)	12195(12.45%)
No. of >2000 bp reads	41,853(21.00%)	10003(10.21%)
Total Number	199,270	97,956
Total Length (bp)	250,797,988	79,527,036
N50 Length (bp)	2,173	1,579
Mean Length (bp)	1,258	812