

Supplementary Tables

Supplementary Table S1 Primer sequences for RT-qPCR

Gene ID	Sense primer sequence (5'-3')	Anti-sense primer sequence (5'-3')
Isoform0032817	TTGTCACCTTCACCACTCC	CCTCATCCCAACCATCTTC
Isoform0014291	GAGCCATCCATCAACAGG	TTCACATACGATACTCCCCAT
Isoform0032534	AGACAAGAACGCCAACACA	TTGAAATCTCAGCAACCGA
Isoform0019056	TTATGCCTCTGCCGATGAT	CCTGTGTTGGTGTTCCTGTCT
Isoform0030613	TTCGGAGTGAGAGTGGTTG	ACAGCATCATCGGCAGAG
Isoform0022813	TTCGTCAAGACAAGAACACC	TGAAATCTCAGCAACCGTAT
Isoform0016654	TGTTTCGCTCTTCGCTATTT	GACAACACTGGCAAACCTG
Isoform0023526	CAAGTTCGCTCTTCGCTAT	CAACACTGGCAAACCTGG
Isoform0023929	TGTTTCGCTCTTCGCTATTT	GACAACACTGGCAAACCTG
<i>ACT7</i>	AACCCCAAGGCTAACAGG	TGGCATACAGAGACAGGACA

Supplementary Table S2 Information of raw reads in *C. album* from SMRT data

total base(bp)	20302433620
subreads number	9196552
average length	2207
N50	2897

Supplementary Table S3 Categorize information of transcripts in *C. album* from SMRT data

Classify	Numbers
Number of consensus reads	433875
Number of five prime reads	411428

Number of three prime reads	409230
Number of poly-A reads	400999
Number of filtered short reads	246
Number of non-full-length reads	53494
Number of full-length reads	380135
Number of full-length non-chimeric reads	378289
Number of full-length non-chimeric bases	1010171676
Mean full-length non-chimeric read length	2670

Supplementary Table S4 Function annotation of isoforms in *C. album* from SMRT data

Database	Numbers	Percent (%)
Total Isoform	135439	100.00
Nr	131160	96.84
Swissport	111664	82.45
KOG	95019	70.16
GO	70942	52.38
KEGG	59342	43.81
annotation gene	131258	96.91
without annotation gene number	4181	3.09

Supplementary Table S5 Statistics of data filtering from RNA-Seq data

Sample	Before Filter				After Filter				Reads Len	GC(%)	adapter(%)	low quality(%)
	Reads Num	Before Filter Data(bp)	Q20(%)	Q30(%)	Reads Num(%)	After Filter Data(bp)	Q20(%)	Q30(%)				
DAF2 0-1	41190 164	6178524600	6056456449	5820060086	41136360	6152183942	6035088663	5801095798	150	44.6	13552	79752
			(98.02%)	(94.2%)	(99.87%)		(98.1%)	(94.29%)		3	(0.03%)	(0.1%)
DAF2 0-2	47608 214	7141232100	7006211531	6732569904	47558602	7109529827	6979731262	6708829769	150	44.7	12754	73012
			(98.11%)	(94.28%)	(99.9%)		(98.17%)	(94.36%)		2	(0.03%)	(0.08%)
DAF2 0-3	42035 418	6305312700	6165398974	5904081022	41972498	6276363895	6142076738	5883489599	150	44.4	16386	92276
			(97.78%)	(93.64%)	(99.85%)		(97.86%)	(93.74%)		2	(0.04%)	(0.11%)
DAF4 0-1	38087 886	5713182900	5590009924	5357500221	38031584	5685757635	5568062300	5338149321	150	44.5	13130	85584
			(97.84%)	(93.77%)	(99.85%)		(97.93%)	(93.89%)		3	(0.03%)	(0.11%)
DAF4 0-2	36259 860	5438979000	5321379843	5099687454	36204780	5411632526	5299491105	5080403949	150	44.5	12898	83700
			(97.84%)	(93.76%)	(99.85%)		(97.93%)	(93.88%)		4	(0.04%)	(0.12%)
DAF4 0-3	47704 276	7155641400	7001495622	6709453893	47636404	7120689394	6973190491	6684388091	150	44.4	16204	102404
			(97.85%)	(93.76%)	(99.86%)		(97.93%)	(93.87%)		3	(0.03%)	(0.11%)

DAF7	44821	6723175200	6581504297	6309973771	44758266	6679993070	6545258130	6277457787	150	44.5	14632	95704
0-1	168		(97.89%)	(93.85%)	(99.86%)		(97.98%)	(93.97%)		3	(0.03%)	(0.11%)
DAF7	44268	6640224300	6512456312	6261073942	44214850	6607327855	6485340692	6236844811	150	44.6	11228	83344
0-2	162		(98.08%)	(94.29%)	(99.88%)		(98.15%)	(94.39%)		2	(0.03%)	(0.09%)
DAF7	48120	7218143100	7058216271	6748544516	48062684	7184081669	7030267347	6723743733	150	44.6	14044	87780
0-3	954		(97.78%)	(93.49%)	(99.88%)		(97.86%)	(93.59%)		6	(0.03%)	(0.09%)
DAF1	49247	7387190700	7251250470	6975102525	49191836	7357479776	7226688119	6953091971	150	44.7	10800	89896
10-1	938		(98.16%)	(94.42%)	(99.89%)		(98.22%)	(94.5%)			(0.02%)	(0.09%)
DAF1	46554	6983138100	6826902751	6532669763	46490692	6951637966	6801162969	6509802010	150	44.7	12864	100556
10-2	254		(97.76%)	(93.55%)	(99.86%)		(97.84%)	(93.64%)			(0.03%)	(0.11%)
DAF1	37513	5627088300	5499579544	5258646219	37465892	5600357827	5477434930	5238865646	150	44.8	9468	76380
10-3	922		(97.73%)	(93.45%)	(99.87%)		(97.81%)	(93.55%)			(0.03%)	(0.1%)
Total	52341	7851183240			522724448	7813703538						1050388
	2216	0				2						

Supplementary Table S6 Results of clean reads mapped to the *C. album* full-length transcripts

Sample	All Reads Num	Unmapped Reads	Unique Mapped Reads	Multiple Mapped Reads	Mapping Ratio (%)
DAF20-1	41135964	2338563	3152748	35644653	94.32
DAF20-2	47558052	2604354	3519318	41434380	94.52
DAF20-3	41972212	2478539	3200107	36293566	94.09
DAF40-1	38030952	2071373	2775892	33183687	94.55
DAF40-2	36204382	1958453	2638971	31606958	94.59
DAF40-3	47635946	2640426	3481202	41514318	94.46
DAF70-1	44757910	3143112	3295979	38318819	92.98
DAF70-2	44214324	2201403	3173152	38839769	95.02
DAF70-3	48062288	2300809	3419593	42341886	95.21
DAF110-1	49191184	2280946	3421627	43488611	95.36
DAF110-2	46490286	2136570	3178577	41175139	95.4
DAF110-3	37465484	1703588	2566175	33195721	95.45

Supplementary Table S7 The number of genes expressed in each sample in *C. album* from RNA-Seq data

Sample	Genes Num	Ratio
All Reference Genes	135439	
All Samples Genes	113803	84.03%
DAF20-1	90717	66.98%
DAF20-2	91630	67.65%
DAF20-3	91455	67.52%
DAF40-1	91243	67.37%
DAF40-2	90959	67.16%
DAF40-3	92817	68.53%

DAF70-1	92049	67.96%
DAF70-2	91964	67.90%
DAF70-3	92079	67.99%
DAF110-1	90909	67.12%
DAF110-2	90421	66.76%
DAF110-3	88481	65.33%
