New Phytologist Supporting Information

Article title: The honeysuckle genome provides insight into the molecular mechanism of carotenoid metabolism underlying dynamic flower coloration

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Table S1. Primers used for qPCR analysis.

Gene	Primer
Actin-F3	CGACTACGAGCAAGAACTTGA
Actin-R3	CGAACCACCACTAAGCACAA
PSY1-F2	GAGAAGATGCCAGAAGAGGAAG
PSY1-R2	TGCCGATACAACAACAATGATG
PDS1-F3	ATTCACGGCGGAGGATGT
PDS1-R3	CACTCACCAATGCCAAATGC
PDS3-F1	ACTCTTGCCTGCCATTCTTG
PDS3-R1	TGAACCGTGCTTCTCCTGA
ZISO-1-F1	TTACTAGAGGTAGCGGCTGTT
ZISO-1-R1	CCAACCTTCTGTCTCCATTCC
ZISO-2-F3	GCAATACGATATGGCGAGGAT
ZISO-2-R3	CATAAGTGGGTGAGCAAGGTAT
ZDS1-F3	AGCAATGAAGGACATACGGAAT
ZDS1-R3	CTTAGTCGCAAACAACGAGAAA
ZDS2-F1	GCACACGCACAAGTATCCA
ZDS2-R1	TTTCTAATGGGACCGCTCAAAT
CRTISO1-F2	CACTTGAGGAGCCAATCTACC
CRTISO1-R2	ACACTCAGCATCTATGAAGGAC
CRTISO2-F1	TGGACTATGTTGTGGAGGACTA
CRTISO2-R1	TACTTGGCACATGGAATTGACT
LCYE-F2	AGGAGGTCATTCCAAGAACATG
LCYE-R2	GGCGAACAAGGCACATTCT
CYP97A3-F1	GTCCGCTCGTATTGCTTCC
CYP97A3-R1	ACCATAGGTGAGGTAGAGTTCA
CYP97C1-F2	ATAGACTTGCTGCTGGACCTA
CYP97C1-R2	TTCTTGTGAAGTGATGGAACCA
CYP97B3-F1	GATGACCTGATGACGATGCTTA
CYP97B3-R1	TGAGGATACAACCGCAGAGT
LCYB-F1	TTGGAGAAGAGGCGGACAA
LCYB-R1	GGAACAGGACACTTGGTAACA
CCD4-F1	CGACTAACGGCATTGGCTTA
CCD4-R1	TGAGGTACGGCGGAATAGG
BCH-F1	CTCCATTCTCACGCCCTCT
BCH-R1	CTTCCTCGCAATCTTCTCCTC
ZEP-F1	AGAGGACTTCCAGTGACAAGA
ZEP-R1	CGTATTCCATCAGCACCAACT
NSY-F1	CCTGATACAATGCGGCTCAT
NSY-R1	CCTCGTCTCGATTCTGTTCTC
NCED3-F2	GGAACCAGACACCGATGAAG
NCED3-R2	GCTTCCAGATTCACCTGTTCA

Table S2. Illumina short-read platform sequencing data.

DNA Libraries	Insert size	Raw reads	Base pairs	Coverage (×)
Lib1	250 bp	152,805,538	22,920,830,700	31
Lib2	500 bp	183,799,894	27,569,984,100	26
Total		336,605,432	50,490,814,800	57

cDNA libraries	Raw reads	Base pairs
Stem 1	42,081,900	6,312,285,000
Stem 2	51,523,748	7,728,562,200
Stem 3	48,658,368	7,298,755,200
Leaf 1	43,469,642	6,520,446,300
Leaf 2	45,951,270	6,892,690,500
Leaf 3	45,988,356	6,898,253,400
juvenile bud 1	45,443,312	6,816,496,800
juvenile bud 2	50,340,778	7,551,116,700
juvenile bud 3	45,631,772	6,844,765,800
third green 1	48,954,060	7,343,109,000
third green 2	47,367,982	7,105,197,300
third green 3	49,038,472	7,355,770,800
second white 1	54,644,630	8,196,694,500
second white 2	50,539,752	7,580,962,800
second white 3	42,594,592	6,389,188,800
silver flowering 1	50,400,598	7,560,089,700
silver flowering 2	41,648,340	6,247,251,000
silver flowering 3	41,494,904	6,224,235,600
gold flowering 1	42,125,280	6,318,792,000
gold flowering 2	39,627,268	5,944,090,200
gold flowering 3	48,516,140	7,277,421,000
tawny withering 1	43,238,934	6,485,840,100
tawny withering 2	46,640,496	6,996,074,400
tawny withering 3	47,658,704	7,148,805,600
Total	1,113,579,298	167,036,894,700

Table S3. ONT sequencing data.

Libraries	Total Reads Bases	Total Reads Number	Pass Reads Bases	Pass Reads Number	Pass Reads Mean Length	Pass Reads N50 Length	Pass Reads Medium Length	Pass Reads Max Length	Pass Reads Avg Score
1	5879,326,908	355,362	5,567,193,728	327,565	16,995	24,318	14,567	106,401	9.94
2	3,024,839,126	166,338	2,817,113,983	149,362	18,860	26,230	16,159	123,820	9.64
3	2,710,145,920	148,421	2,538,825,634	135,086	18,794	26,296	16,167	132,565	9.72
4	3,427,083,357	191,340	3,199,279,777	171,905	18,610	26,180	15,897	117,282	9.57
5	2,885,425,463	163,108	2,745,125,267	150,805	18,203	25,751	15,523	143,663	10.64
6	1,518,023,393	80,335	1,424,153,489	73,599	19,350	27,090	16,701	131,977	9.61
7	2,829,332,717	156,254	2,645,314,024	142,007	18,628	26,574	15,902	141,804	9.71
8	7,384,681,101	412,207	7,045,681,813	384,200	18,338	25,972	15,841	139,097	9.86
9	4,631,179,079	255,503	4,245,985,233	223,767	18,975	26,617	16,368	122,956	9.53
10	3,874,346,262	214,031	3,530,219,951	186,452	18,933	26,421	16,327	126,643	9.51
11	2,142,361,314	116,474	2,038,838,557	106,986	19,057	27,101	16,289	134,984	9.76
12	2,422,168,685	130,134	2,245,960,528	116,371	19,300	27,185	16,523	128,406	9.69
13	2,342,082,471	131,594	2,180,322,014	119,589	18,231	26,740	15,407	121,670	9.63
14	2,488,677,599	135,885	2,311,334,250	122,364	18,889	26,927	16,115	125,633	9.70
15	4,053,495,173	215,941	3,787,895,691	195,475	19,377	27,088	16,658	131,956	9.58

16	1,534,238,056	87,476	1,432,007,518	78,816	18,168	25,898	15,376	122,340	9.54
17	3,970,592,801	212,397	3,619,139,761	186,190	19,437	27,516	16,639	149,370	9.61
18	2,592,348,297	137,431	2,409,689,036	122,332	19,697	27,583	16,896	129,289	9.57
19	2,033,862,834	109,512	1,872,266,341	97,014	19,298	27,068	16,630	129,171	9.73
20	2,256,462,232	121,414	2,103,995,200	109,161	19,274	27,205	16,417	142,250	9.75
21	7,438,331,763	411,887	6,842,971,479	366,385	18,676	26,212	15,974	139,752	9.54
22	7,367,350,080	395,807	6,936,254,856	359,879	19,273	27,112	16,571	125,505	9.97

Table S4. *L. japonica* genome assembly statistics.

	CANU+ SMARTdenovo	CANU+ SMARTdenovo+ pilon 3×	CANU+ SMARTdenovo+ pilon 3× + Hi-C
Input Data	ONT	ONT+HiSeq	ONT+HiSeq+smHi-C
Genome Size (bp)	892,974,210	903,735,777	843,177,289
Contigs	919	919	-
Contig N50 (bp)	2,116,620	2,148,893	-
Largest Contig (bp)	19,355,532	19,544,413	-
Scaffolds	-	-	9
Scaffolds N50 (bp)	-	-	84,431,753
Largest Scaffold (bp)	-	-	125,163,164
N bases in scaffolds (%)	0	0	0.16%
Completeness BUSCOs	57.1%	94.7%	97.0%
complete single-copy BUSCOs	54.4%	90.5%	92.6%
complete duplicated BUSCOs	2.7%	4.2%	4.4%

Table S5. *L. japonica* genome annotation using sequence from different sequencing platforms.

Annotation	
No. of predicted coding genes	33,961
Average gene length (bp)	1 458
GC content (%)	43.5
Percentage of whole gene length in genome (%)	4.2
Masked repeat sequence length (bp)	526,123,083
Percentage of repeat sequences in genome (%)	58.21%
BUSCO assessment	C:90.9% [S:87.2%,D:3.7%], F:2.3%, M:6.8%

Table S6. Annotation of *L. japonica* transposable elements (TEs).

Repeat Class	Elements number	Length (bp)	Percentage of sequence
RNA transposable elements	**154,966**	**262,416,892**	**29.03%**
non-LTR(Long terminal repeat)	54,997	22,622,030	2.50%
LINE	42,518	21,052,604	2.33 %
SINE	12,479	1,569,426	0.17 %
LTR(Long terminal repeat)	254,934	239,794,862	26.53 %
Gypsy	133,600	124,472,322	13.77%
Copia	86,958	81,164,557	8.98%
Other	34,376	34,157,983	3.78%
DNA elements	**211,061**	**69,291,452**	**7.67 %**
Unclassified TEs	**672,515**	**178,395,949**	**19.74 %**
Small RNA	9,308	1,713,470	0.19 %
Satellites	2,463	1,707,950	0.19 %
Simple repeats	267,908	12,634,132	1.40 %
Low complexity	40,422	1,967,278	0.22 %
Total Repeats		**526,123,083**	**58.21 %**

Table S7. Identification of simple sequence repeats in the *L. japonica* genome.

Types	Unit size	Cut-off	Number of SSR
Monomer	1	10	169,840
Dimer	2	6	144,713
Trimer	3	5	31,248
Tetramer	4	5	4,580
Pentamer	5	5	1,100
Hexamer	6	5	566
Total			352,047

Table S8. Annotation of *L. japonica* noncoding RNAs.

ncRNA type	#Loci	Average length (bp)	Total length (bp)
miRNA	33	140	4,636
tRNA	104	74	7,667
rRNA(5S)	67	113	7,590
rRNA(18s)	28	1,781	49,860
rRNA(28s)	43	6,118	263,076
snoRNA	224	104	23,319

Table S9. Annotation of *L. japonica* rRNAs.

Chromosome	Start	End	Length		Type
chr1	34474202	34474306	104	+	8s_rRNA
chr1	122516099	122516207	108	+	8s_rRNA
chr2	64162129	64162242	113	+	8s_rRNA
chr2	86342440	86342553	113	+	8s_rRNA
chr2	92526438	92526554	116	+	8s_rRNA
chr2	122585188	122585292	104	-	8s_rRNA
chr3	11874047	11874161	114	-	8s_rRNA
chr3	23972697	23972811	114	-	8s_rRNA
chr3	23973008	23973122	114	-	8s_rRNA
chr3	23973323	23973428	105	-	8s_rRNA
chr3	23973929	23974051	122	-	8s_rRNA
chr3	23974235	23974354	119	-	8s_rRNA
chr3	23974398	23974513	115	-	8s_rRNA
chr3	23974557	23974670	113	-	8s_rRNA
chr3	23974835	23974949	114	-	8s_rRNA
chr3	23975080	23975214	134	-	8s_rRNA
chr3	30795452	30795563	111	+	8s_rRNA
chr3	38063103	38063215	112	-	8s_rRNA
chr3	48734666	48734793	127	+	8s_rRNA
chr3	89438304	89438403	99	+	8s_rRNA
chr4	7303357	7303471	114	+	8s_rRNA
chr6	27186749	27186856	107	+	8s_rRNA
chr8	1588027	1588139	112	-	8s_rRNA
chr8	51729395	51729503	108	-	8s_rRNA
chr8	52022298	52022410	112	-	8s_rRNA
chr8	52023205	52023319	114	-	8s_rRNA
chr8	52023500	52023616	116	-	8s_rRNA
chr8	52023776	52023886	110	-	8s_rRNA
chr8	52024034	52024148	114	-	8s_rRNA
chr8	52024483	52024593	110	-	8s_rRNA
chr8	52025378	52025493	115	-	8s_rRNA
chr8	52025662	52025774	112	-	8s_rRNA
chr8	52025850	52025995	145	-	8s_rRNA
chr8	52026669	52026780	111	-	8s_rRNA
chr8	52026946	52027060	114	-	8s_rRNA
chr8	52027493	52027607	114	-	8s_rRNA
chr8	52027775	52027889	114	-	8s_rRNA
chr8	52028266	52028380	114	-	8s_rRNA
chr8	52028518	52028632	114	-	8s_rRNA
chr8	52028782	52028895	113	-	8s_rRNA

chr8	52028991	52029104	113	-	8s_rRNA
chr8	52029284	52029398	114	-	8s_rRNA
chr8	52030084	52030198	114	-	8s_rRNA
chr8	52030376	52030490	114	-	8s_rRNA
chr8	52030679	52030791	112	-	8s_rRNA
chr8	52031237	52031351	114	-	8s_rRNA
chr8	52031512	52031626	114	-	8s_rRNA
chr8	52031808	52031922	114	-	8s_rRNA
chr8	52032093	52032206	113	-	8s_rRNA
chr8	52032366	52032480	114	-	8s_rRNA
chr8	52032656	52032770	114	-	8s_rRNA
chr8	52032949	52033063	114	-	8s_rRNA
chr8	52549827	52549935	108	-	8s_rRNA
chr8	52857307	52857415	108	-	8s_rRNA
chr9	4310114	4310225	111	+	8s_rRNA
utg361	1688433	1688547	114	+	8s_rRNA
utg891	386047	386159	112	-	8s_rRNA
utg891	386344	386458	114	-	8s_rRNA
utg891	386956	387067	111	-	8s_rRNA
utg891	387260	387373	113	-	8s_rRNA
utg891	387545	387655	110	-	8s_rRNA
utg891	387830	387944	114	-	8s_rRNA
utg891	388415	388529	114	-	8s_rRNA
utg891	389000	389114	114	-	8s_rRNA
utg891	389600	389704	104	-	8s_rRNA
utg891	389881	389995	114	-	8s_rRNA
utg891	390186	390297	111	-	8s_rRNA
chr2	85550137	85551933	1796	+	18s_rRNA
chr2	85560285	85563175	2890	+	18s_rRNA
chr2	88033564	88035660	2096	+	18s_rRNA
chr2	122585463	122587377	1914	-	18s_rRNA
chr2	122615151	122617063	1912	+	18s_rRNA
chr2	123845191	123846676	1485	+	18s_rRNA
chr2	123988057	123989534	1477	-	18s_rRNA
chr6	11504747	11506502	1755	-	18s_rRNA
chr6	11973995	11975757	1762	-	18s_rRNA
chr9	8265	10025	1760	+	18s_rRNA
chr9	36195	37963	1768	+	18s_rRNA
utg1953	8878	10622	1744	-	18s_rRNA
utg1953	17124	18846	1722	-	18s_rRNA
utg1953	24979	26715	1736	-	18s_rRNA
utg1953	33057	34802	1745	-	18s_rRNA
utg1953	41004	42758	1754	-	18s_rRNA
utg1953	49132	50868	1736	-	18s_rRNA

utg1953	56969	58733	1764	-	18s_rRNA
utg1953	65174	66910	1736	-	18s_rRNA
utg1953	85537	87046	1509	-	18s_rRNA
utg41	6258158	6259965	1807	-	18s_rRNA
utg41	6268341	6270099	1758	-	18s_rRNA
utg470	22806	24613	1807	+	18s_rRNA
utg5009	29708	31187	1479	+	18s_rRNA
utg8921	13213	14938	1725	+	18s_rRNA
utg8921	22056	23808	1752	+	18s_rRNA
utg8921	39904	41624	1720	+	18s_rRNA
utg8921	63122	64873	1751	+	18s_rRNA
chr2	85552158	85560213	8055	+	28s_rRNA
chr2	85780408	85785391	4983	+	28s_rRNA
chr2	88027984	88033600	5616	+	28s_rRNA
chr2	88047225	88052588	5363	+	28s_rRNA
chr2	113287754	113291928	4174	+	28s_rRNA
chr2	123849111	123855522	6411	+	28s_rRNA
chr2	123982156	123985633	3477	-	28s_rRNA
chr9	870	7522	6652	+	28s_rRNA
chr9	10237	17118	6881	+	28s_rRNA
chr9	19806	26447	6641	+	28s_rRNA
chr9	29159	36059	6900	+	28s_rRNA
chr9	38169	45217	7048	+	28s_rRNA
utg1953	2290	8669	6379	-	28s_rRNA
utg1953	11546	16914	5368	-	28s_rRNA
utg1953	19768	24768	5000	-	28s_rRNA
utg1953	26683	32836	6153	-	28s_rRNA
utg1953	34769	40780	6011	-	28s_rRNA
utg1953	43678	48914	5236	-	28s_rRNA
utg1953	51796	56750	4954	-	28s_rRNA
utg1953	58701	64964	6263	-	28s_rRNA
utg1953	67845	75163	7318	-	28s_rRNA
utg1953	87013	93863	6850	-	28s_rRNA
utg1953	97006	102284	5278	-	28s_rRNA
utg225	278818	285831	7013	-	28s_rRNA
utg41	6252104	6257923	5819	-	28s_rRNA
utg41	6261105	6268112	7007	-	28s_rRNA
utg41	6271111	6278195	7084	-	28s_rRNA
utg427	300266	307163	6897	+	28s_rRNA
utg470	9440	15311	5871	+	28s_rRNA
utg470	24848	30180	5332	+	28s_rRNA
utg50	227329	231299	3970	+	28s_rRNA
utg50	2718098	2721775	3677	+	28s_rRNA
utg5009	33618	37108	3490	+	28s_rRNA

utg8921	6291	13246	6955	+	28s_rRNA
utg8921	15154	22089	6935	+	28s_rRNA
utg8921	24003	31024	7021	+	28s_rRNA
utg8921	32917	39937	7020	+	28s_rRNA
utg8921	41826	48744	6918	+	28s_rRNA
utg8921	56156	63155	6999	+	28s_rRNA
utg8921	65087	72079	6992	+	28s_rRNA
utg8921	73971	80960	6989	+	28s_rRNA
utg8921	82855	89905	7050	+	28s_rRNA
utg8921	91803	98829	7026	+	28s_rRNA

Table S10. Location of MIR2911 in genome.

	Chromosomes	Position
MIR2911	Chr6	11980227
MIR2911	Chr4	87400607
MIR2911	Chr2	48586293

Table S12. K_S distributions of orthologous and paralogous genes among *L. japonica*, *C. nankingense*, *L. sativa*, and *C. canephora*.

Species	Species	K_S peak 1	Density	Divergence time for speciation (MYA)	Synonymous substitutions per site per MYA
Chrysanthemum	Chrysanthemum	0.117409	1.275659	0	
Chrysanthemum	Honeysuckle	1.3971671	0.7090722	87.345029	0.007997977
Coffee	Coffee	2.2072892	0.4131199	0	
Honeysuckle	Coffee	1.2797581	0.9856402	97.963607	0.006531804
Honeysuckle	Honeysuckle	0.7866403	1.050899	0	
Honeysuckle	Lettuce	1.4793534	0.6471449	87.345029	0.008468447
Lettuce	Lettuce	1.0214583	1.141869	0	
Mean					0.007666076

Table S13. Mining and expression analysis of *L. japonica* carotenogenesis genes.

Gene[1]	Gene[2]	Accession[3]	Identity	Gene_ID	Location	JB	GB	WB	SF	GF	TWF[4]
LjPSY1	*AtPSY*	AT5G17230	83.768	Lj4C251T7	chr4:25122945-25126671	12.87	13.15	15.17	20.60	2005.33	2494.88
LjPSY2	*AtPSY*	AT5G17230	84.615	Lj8C97G11	chr8:9759952-9763473	8.80	16.01	10.82	1.44	1.38	0.69
LjPSY3	*AtPSY*	AT5G17230	73.394	Lj2C511G6	chr2:51118195-51130069	33.01	24.63	25.37	20.39	127.88	188.97
LjPSY4	*AtPSY*	AT5G17230	71.538	Lj2C707G6	chr2:70784483-70787590	0.00	0.00	0.00	0.00	0.00	0.00
LjPSY5	*AtPSY*	AT5G17230	66.409	Lj2A718G15	chr2:71825303-71827477	0.00	0.00	0.00	0.00	0.00	0.00
LjPDS1	*AtPDS1*	AT1G06570	70.115	Lj8C8T1	chr8:795491-797804	83.00	62.78	93.70	993.95	1124.88	1873.35
LjPDS2	*AtPDS2*	AT3G11945	73.968	Lj2C359T6	chr2:35966798-35973274	8.57	6.44	7.55	8.51	10.47	7.66
LjPDS3	*AtPDS3*	AT4G14210	80	Lj9A539T91	chr9:53967053-53972482	70.57	100.68	142.18	858.63	1760.72	1795.51
LjZ-ISO1	*AtZ-ISO*	AT1G10830	82.456	Lj3A376T54	chr3:37623104-37624999	10.45	12.09	26.51	205.27	235.74	210.68
LjZ-ISO2	*AtZ-ISO*	AT1G10830	81.215	Lj3A357T51	chr3:35727716-35728899	5.98	10.33	18.87	228.38	256.93	235.46
LjZDS1	*AtZDS*	AT3G04870	83.21	Lj9A669T11	chr9:66972168-66982409	26.45	54.95	89.01	110.33	265.16	321.76
LjZDS2	*AtZDS*	AT3G04870	83.21	Lj9A666T47	chr9:66615468-66624762	19.08	33.36	54.13	58.96	176.89	195.75
LjCRTISO1	*AtCRTISO1*	AT1G06820	78.12	Lj1A1059G39	chr1:105932098-105947433	10.84	15.17	15.79	2.69	4.59	3.00
LjCRTISO2	*AtCRTISO2*	AT1G57770	78.395	Lj5C267G12	chr5:26749800-26758240	6.58	4.79	6.41	6.02	11.12	7.67
LjLCYB	*AtLCYB*	AT3G10230	57.461	Lj1P256T46	chr1:25684897-25686385	39.38	104.41	138.20	909.30	1287.31	845.44
LjLCYE	*AtLCYE*	AT5G57030	62.075	Lj4A290G39	chr4:29044891-29057495	15.10	3.08	1.72	0.46	2.12	4.92

LjBCH	*AtBCH1*	AT4G25700	69.204	Lj1A1004T81	chr1:100480495-100483995	83.77	113.36	164.31	1060.97	1154.84	2266.04
	AtBCH2	AT5G52570	68.942	Lj1A1004T81							
LjZEP	*AtZEP*	AT5G67030	71.54	Lj4C149T12	chr4:14948117-14953170	48.42	58.99	135.48	365.60	305.18	112.32
LjNSY	*AtNSY*	AT1G67080	69.73	Lj2A442G45	chr2:44202073-44203474	313.58	584.76	854.88	888.26	315.72	70.57
LjCYP97A3	*AtCYP97A3*	AT1G31800	77.076	Lj2C52G4	chr2:5199239-5206023	26.50	28.14	27.77	16.74	50.42	55.26
LjCYP97C1	*AtCYP97C1*	AT3G53130	74.725	Lj3A994T59	chr3:99482420-99489205	21.88	24.45	26.25	39.11	52.68	57.70
LjCYP97B3	*AtCYP97B3*	AT4G15110	78.237	Lj1A1044G23	chr1:104379355-104390723	14.19	11.52	9.48	11.00	11.34	4.75
LjNCED3	*AtNCED3*	AT3G14440	81.276	Lj1P809T13	chr1:80909801-80911337	69.68	51.52	77.73	573.36	235.59	1220.64

Gene[1], *L. japonica* gene

Gene[2], *A. thaliana* gene

Accession[3], Arabidopsis gene Accession

TWF[4], Juvenile bud, JB. Green bud, GB. White bud, WB. Silver flower, SF. Golden flower, GF. Tawny withering flower, TWF.

Table S14. Mining and expression analysis of *L. japonica* CCD genes.

Gene	Gene_ID	Location	JB	GB	WB	SF	GF	TWF[1]
LjCCD1a	Lj9C633G15	chr9:63351139-63364265	0.04	0.06	0.04	0.00	0.00	0.06
LjCCD1b	Lj7C571T11	chr7:57170156-57180723	43.52	67.96	89.40	41.14	44.36	17.84
LjCCD1L	Lj7C703T4	chr7:70304945-70312220	0.06	0.00	0.00	0.71	0.00	0.11
LjCCD4	Lj7A208T26	chr7:20793476-20797709	125.49	58.97	44.43	10.06	1.78	3.19
LjCCD7	Lj7C540G12	chr7:54038462-54051909	1.04	1.88	1.02	1.29	0.74	0.52
LjCCD8a	Lj8A581T28	chr8:58181148-58184306	0.16	0.32	0.08	0.00	0.00	0.00
LjCCD8b	Lj7A701T19	chr7:70094945-70098505	0.00	0.00	0.00	0.00	0.00	0.00

TWF[1], Juvenile bud, JB. Green bud, GB. White bud, WB. Silver flower, SF. Golden flower, GF. Tawny withering flower, TWF.

Table S15. Primers used for cloning *LjCCD4*.

Gene	Primer
LjCCD4-F	ATGGATGCCCTCTCCTCTTCTT
LjCCD4-R	CCGCCGTTACAATTTATTGAGG