

Supplementary tables

Table S1. Sequencing data from Illumina short-read platform for DNA libraries.

DNA Libraries	Insert size	Raw reads	Base pairs	Coverage (\times)
Lib1	250 bp	101,870,358	15,280,553,700	61
Lib2	500 bp	122,533,262	18,379,989,300	74
Total		224,403,620	33,660,543,000	135

Table S2. Sequencing data from Illumina short-read platform for cDNA libraries.

cDNA libraries	Raw reads	Base pairs
Stem 1	40,210,176	6,031,526,400
Stem 2	40,205,606	6,030,840,900
Stem 3	41,150,940	6,172,641,000
Leaf 1	40,362,670	6,054,400,500
Leaf 2	41,263,088	6,189,463,200
Leaf 3	40,764,346	6,114,651,900
Root 1	41,456,368	6,218,455,200
Root 2	40,401,708	6,060,256,200
Root 3	40,273,416	6,041,012,400
Flower 1	41,339,918	6,200,987,700
Flower 2	41,257,872	6,188,680,800
Flower 3	41,490,398	6,223,559,700
Total	490,176,506	73,526,475,900

Table S3. Sequel sequencing data.

Libraries	Total subreads Bases	Total Subreads Number	Mean Subreads Length	Subreads N50 Length
1	442,857,329	70,596	6,273	9,799
2	431,416,109	48,054	8,978	12,573
3	5,687,024,287	1,004,749	5,660	9,139
4	4,670,937,546	887,852	5,260	8,823
5	4,236,671,187	592,902	7,146	9,879
6	6,709,010,250	871,675	7,697	10,539
7	5,350,553,189	933,711	5,730	9,161

Table S4. *C. tomentella* genome assembly and annotation.

FALCON-assembly	Genome Size (bp)	251,770,360
	Contigs	1,321
	Contig N50 (bp)	2,358,889
	Largest Contig (bp)	9,833,348
Redundans	Genome Size (bp)	248,888,647
	Contigs	1,022
	Contig N50 (bp)	2,521,020
	Largest Contig (bp)	9,833,348
	Completeness BUSCOs	97.7%
	complete single-copy BUSCOs	91.3%
	complete duplicated BUSCOs	6.4%
Annotation	No. of predicted coding genes	37,826
	Completeness BUSCOs	94.8%
	complete single-copy BUSCOs	89.9%
	complete duplicated BUSCOs	4.9%
	Average gene length (bp)	2,836
	Average CDS length (bp)	1,214
	Average exons per gene	4
	GC content of gene (%)	41.41
	Masked repeat sequence length (bp)	110,107,533
Percentage of repeat sequences in genome (%)	44.24%	

Table S5. Statistics of 8 pseudochromosome assembly of *C. tomentella* genome.

#Chr	Chr Length (bp)	N%	GC%
Chr1	40536129	0.106034	37.5104
Chr2	37299163	0.0368855	36.6152
Chr3	31783837	0.0570479	36.678
Chr4	29006148	0.149289	36.7006
Chr5	29005916	0.0289596	36.5334
Chr6	27659422	0.0579586	36.5756
Chr7	26708596	0.0326299	36.606
Chr8	26607089	0.0585145	36.5965
Others	330455	0	46.836

Table S6. Annotation of *C. tomentella* transposable elements (TEs).

Repeat Class	Elements number	Length (bp)	Percentage of sequence
RNA transposable elements	94,925	54,676,824	21.97%
non-LTR(Long terminal repeat)	13,295	6,466,568	2.60%
LINE	9383	5,950,033	2.39%
SINE	3912	516,535	0.21%
LTR(Long terminal repeat)	81,630	48,210,256	19.37%
Gypsy	22,370	15,056,200	6.05%
Copia	13,905	9,922,597	3.99%
Other	45,355	23,231,459	9.33%
DNA elements	30,293	12,072,982	4.85%
Unclassified TEs	134,756	33,987,290	13.66%
Small RNA	3289	3,574,491	1.44%
Satellites	1357	135,999	0.05%
Simple repeats	86,993	5,028,639	2.02%
Low complexity	12,999	631,308	0.25%
Total Repeats		110,107,533	44.24%

Table S7. Identification of simple sequence repeats in the *C. tomentella* genome.

Types	Unit size	Cut-off	Number of SSR
Monomer	1	10	86,722
Dimer	2	6	26,479
Trimer	3	5	19,784
Tetramer	4	5	2028
Pentamer	5	5	564
Hexamer	6	5	753
Total			136,330

Table S8. The numbers of BIA biosynthetic genes in studied species from Ranunculales and Proteales.

	<i>Corydalis tomentella</i>	<i>Macleaya cordata</i>	<i>Papaver somniferum</i>	<i>Aquilegia coerulea</i>	<i>Nelumbo nucifera</i>
TAT	2	4	11	3	3
TYDC	4	14	39	3	21
TYR	7	11	41	14	8
NCS	9	12	58	13	4
OMT	20	15	66	43	21
NMT	21	12	22	11	1
CMT	19	17	51	31	30
CYP80B-NMCH	2	1	2	6	2
BBE	1	1	1	2	0
BBEL	34	42	43	17	16
CYP719A-CHS	2	1	8	7	0
CYP719A-STs	2	2	3	0	0
CYP82N-P6H	7	6	2	0	0
CYP82N-MSH	2	1	2	0	0
CYP82X	0	0	5	0	0
CYP82Y	0	0	6	0	0

TYDC: Tyrosine decarboxylase, TYR: tyramine 3-hydroxylase, TAT tyrosine aminotransferase, NCS: norcoclaurine synthase, NMCH: *N*-methylcoclaurine 3'-hydroxylase, CHS: cheilanthifoline synthase, STS: stylophine synthase, MSH: methylstylophine hydroxylase, P6H: protopine 6-hydroxylase, OMT: *O*-methyltransferase, CMT: *C*-methyltransferase, NMT: *N*-methyltransferase, BBE: berberine bridge enzyme, BBEL: berberine bridge enzyme-like.

Table S9. Gene expression (FPKM values) analysis of BIA biosynthetic genes in *C. tomentella*.

		Root	Flower	Stem	Leaf
CtTAT1	contig25A5T216.1	206.32	160.87	145.31	144.29
CtTAT2	contig100R5T19.1	0.14	11.18	0.82	5.64
CtTYDC1	contig17R19T24.1	718.99	212.41	172.60	163.05
CtTYDC2	contig71R6T11.1	858.08	115.62	211.53	133.05
CtTYDC3	contig13R20T7.1	13.21	6.11	7.39	9.14
CtTYDC4	contig32R6T19.1	0.40	83.87	1.85	15.68
CtTYR1	contig14R18T29.1	131.58	171.70	103.85	99.66
CtTYR2	contig2R6T10.1	0.08	0.16	0.27	0.20
CtTYR3	contig25A14T108.1	1.37	425.55	19.22	20.64
CtTYR4	contig2R6T12.1	0.00	0.00	2.26	0.34
CtTYR5	contig25A14T109.1	869.01	80.76	45.23	12.03
CtTYR6	contig25A14T118.1	0.04	0.46	0.02	0.00
CtTYR7	contig21A25T167.1	186.42	40.65	68.47	75.39
CtNCS1	contig63A1T161.1	135.40	104.45	184.32	180.79
CtNCS2	contig63A2T159.1	28.37	28.31	4.98	2.31
CtNCS3	contig63A2T160.1	67.63	91.18	75.06	26.12
CtNCS4	contig63A2T161.1	1067.05	5.30	17.11	3.50
CtNCS5	contig63A2T164.1	1.25	3.54	16.69	89.43
CtNCS6	contig63R2T14.1	1.80	3.64	5.29	13.74
CtNCS7	contig63R2T16.1	0.00	0.07	0.00	0.00
CtNCS8	contig9A1T121.1	0.00	7.64	20.65	135.94
CtNCS9	contig9R1T18.1	0.34	0.13	0.00	0.00
Ct4'OMT	contig7A15T244.1	197.64	265.79	239.96	97.53
Ct6OMT	contig8A30T137.1	83.06	123.45	107.41	47.22
Ct9OMT	contig31A21T126.1	1160.85	229.51	563.71	394.27
CtOMT1	contig1R33T23.1	0.04	0.00	0.00	0.00
CtOMT2	contig1R33T24.1	34.09	1.47	10.43	3.17
CtOMT3	contig1R33T25.1	4.06	0.04	1.60	0.45
CtOMT4	contig1R33T27.1	6.73	48.27	48.78	38.14
CtOMT5	contig7R8T20.1	14.20	46.58	115.69	82.07
CtOMT6	contig7R17T13.1	0.13	12.60	0.08	0.15
CtOMT7	contig8A29T84.1	2.93	5.19	5.72	2.53
CtOMT8	contig8R29T24.1	7.64	7.49	9.06	4.56
CtOMT9	contig11A19T248.1	32.42	42.28	43.49	44.43
CtOMT10	contig23A13T106.1	0.00	0.09	0.07	0.04
CtOMT11	contig44A5T120.1	0.00	0.00	0.00	0.04
CtOMT12	contig44R6T22.1	160.81	159.26	261.78	157.15
CtOMT13	contig45A9T133.1	0.48	348.41	0.27	0.41
CtOMT14	contig45A9T134.1	4.44	2.30	5.93	1.27
CtOMT15	contig45A9T135.1	27.51	75.19	137.21	49.61
CtOMT16	contig45A9T137.1	0.00	0.47	0.22	0.13
CtOMT17	contig45A9T138.1	421.84	256.17	247.80	350.46

CtCNMT	contig18A6T184.1	211.23	148.63	131.94	88.70
CtNMT1	contig18A7T145.1	0.38	3.70	1.79	19.67
CtNMT2	contig18R7T13.1	47.90	6.47	1.75	1.10
CtNMT3	contig18A7T148.1	2.35	3.95	3.11	4.66
CtNMT4	contig18A7T149.1	1.49	2.99	2.15	3.60
CtNMT5	contig18A7T150.1	296.01	59.52	77.37	27.55
CtNMT6	contig18A7T152.1	61.78	208.72	41.82	48.47
CtNMT7	contig18A7T153.1	22.89	12.59	35.81	26.57
CtNMT8	contig18A8T95.1	25.68	30.76	27.38	41.03
CtNMT9	contig2A2T155.1	0.38	0.87	1.72	0.70
CtNMT10	contig2P3T152.1	0.00	0.00	0.00	0.00
CtNMT11	contig2A3T220.1	0.00	0.00	0.00	0.00
CtNMT12	contig35A10T121.1	1505.88	420.89	842.14	324.38
CtNMT13	contig39R2T12.1	0.00	0.00	0.00	0.00
CtNMT14	contig39A2T141.1	0.33	203.91	3.00	20.19
CtNMT15	contig39A2T142.1	0.00	6.50	0.00	0.00
CtNMT16	contig39R2T17.1	0.00	0.00	0.00	0.00
CtNMT17	contig39R2T18.1	0.00	0.00	0.00	0.00
CtNMT18	contig39R4T12.1	16.71	0.14	0.95	0.00
CtNMT19	contig39A4T208.1	124.70	20.42	8.93	0.99
CtNMT20	contig82A7T170.1	45.93	17.08	47.78	50.95
CtCMT1	contig14A4T182.1	12.28	6.79	10.74	13.25
CtCMT2	contig22A18T123.1	1.02	0.11	0.00	0.00
CtCMT3	contig29A23T171.1	0.00	7.89	0.00	0.18
CtCMT4	contig2A5T189.1	20.58	21.32	3.95	4.27
CtCMT5	contig2R5T20.1	0.15	36.72	3.42	70.23
CtCMT6	contig2R5T21.1	0.00	1.01	0.57	1.25
CtCMT7	contig2R5T23.1	0.00	10.08	0.70	11.82
CtCMT8	contig2R5T26.1	0.00	0.00	0.00	0.00
CtCMT9	contig2R5T27.1	0.65	84.67	11.94	562.58
CtCMT10	contig2R66T23.1	84.35	88.95	113.26	102.69
CtCMT11	contig34A11T163.1	2.39	37.60	2.24	1.35
CtCMT12	contig40R5T16.1	11.36	9.34	11.42	18.07
CtCMT13	contig4A35T127.1	83.65	52.95	75.70	73.44
CtCMT14	contig4A62T167.1	0.08	2.91	1.25	3.26
CtCMT15	contig59A13T111.1	0.00	0.06	0.69	0.74
CtCMT16	contig59R13T11.1	3.99	1.55	4.71	0.27
CtCMT17	contig63A11T216.1	26.09	58.70	38.12	85.99
CtCMT18	contig7R1T29.1	2.79	3.72	22.01	10.61
CtCMT19	contig97A2T69.1	5.80	0.62	3.17	1.12
CtBBE	contig139R1T30.1	77.93	62.32	44.35	29.87
CtBBEL1	contig18A1T129.1	0.17	10.65	0.87	0.09
CtBBEL2	contig3R9T21.1	13.76	90.69	12.59	19.96
CtBBEL3	contig44R9T10.1	2.29	1.85	63.36	379.32

CtBBEL4	contig45A12T109.1	0.10	0.00	0.00	0.03
CtBBEL5	contig5A28T166.1	0.01	0.19	0.05	0.16
CtBBEL6	contig63R8T29.1	2.00	49.14	2.01	1.47
CtBBEL7	contig7R0T3.1	0.31	0.09	0.00	0.00
*CtBBEL8	contig7R5T1.1	6.56	70.54	29.50	20.47
*CtBBEL9	contig7R5T2.1	0.00	0.00	0.00	0.03
*CtBBEL10	contig7R5T3.1	10.09	48.98	1.86	1.25
*CtBBEL11	contig7R5T15.1	0.00	0.18	0.00	0.00
*CtBBEL12	contig7R5T16.1	0.25	149.87	4.21	115.50
*CtBBEL13	contig7R5T17.1	0.00	0.00	0.00	0.00
*CtBBEL14	contig7R5T5.1	0.03	0.97	0.10	0.04
*CtBBEL15	contig7R5T19.1	0.00	0.00	0.00	0.00
*CtBBEL16	contig7R5T21.1	0.00	0.00	0.00	0.00
*CtBBEL17	contig7R5T6.1	0.00	0.20	0.00	0.00
*CtBBEL18	contig7R5T7.1	0.00	0.00	0.00	0.00
*CtBBEL19	contig7R5T23.1	0.00	4.19	0.07	0.18
*CtBBEL20	contig7R5T8.1	0.29	19.76	0.45	0.38
*CtBBEL21	contig7R5T11.1	2.35	25.08	4.53	3.24
*CtBBEL22	contig7R6T12.1	0.88	93.66	5.69	1.84
*CtBBEL23	contig7R5T12.1	0.04	0.08	0.00	0.00
*CtBBEL24	contig7R5T13.1	0.00	0.39	0.00	0.00
*CtBBEL25	contig7R5T14.1	0.00	0.00	0.00	0.00
*CtBBEL26	contig7R6T13.1	0.32	0.30	0.47	0.57
*CtBBEL27	contig7R6T14.1	0.37	0.35	0.38	0.56
*CtBBEL28	contig7A6T217.1	0.29	0.15	0.25	0.38
*CtBBEL29	contig7R6T35.1	141.96	54.62	13.75	3.52
*CtBBEL30	contig7R6T36.1	99.31	21.16	4.81	2.47
*CtBBEL31	contig7R6T37.1	1310.60	603.26	207.37	86.17
*CtBBEL32	contig7A6T215.1	46.18	16.00	1.59	2.16
CtBBEL33	contig84A3T136.1	0.00	0.00	0.00	0.00
CtBBEL34	contig8A24T157.1	0.04	0.00	0.14	0.04
CtCYP719A2	contig71R6T19.1	900.89	363.89	558.50	359.71
CtCYP719A14-2	contig71R6T6.1	0.19	0.13	0.07	0.10
CtCYP719A14	contig44R5T13.1	1594.85	1308.75	1242.58	817.01
CtCYP719A2-2	contig44R5T17.1	12.09	8.51	5.38	0.82
CtCYP82N1	contig26A22T120.1	9.15	11.05	9.38	32.46
CtCYP82N2	contig102R1T8.1	5.19	7.83	11.00	2.26
CtCYP82N3	contig4R46T24.1	3.67	181.26	15.90	102.67
CtCYP82N4	contig102R2T31.1	78.27	69.40	23.00	37.65
CtCYP82N5	contig17R7T10.1	3.75	1.15	1.32	4.25
CtCYP82N6	contig17R7T16.1	0.07	0.29	0.04	0.59
CtCYP82N7	contig17R7T9.1	887.32	398.27	262.79	162.73
CtCYP82N8	contig8R23T18.1	1507.32	560.02	652.02	486.11
CtCYP82N9	contig8R23T17.1	12.73	4.09	7.03	0.52

CtNMCH1	contig8A32T95.1	40.89	48.30	65.30	34.47
CtNMCH2	contig8A32T94.1	0.00	0.00	0.00	0.00

*showed the clustered BBEL genes.