

Supplementary Information

The location and translocation of *ndh* genes of chloroplast origin in the Orchidaceae family

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Table of Contents

Supplementary Table S1. Percentage of each <i>ndh</i> gene remaining within the transcriptomes of 16 orchid species.	Page 3
Supplementary Table S2. The orchid <i>ndh</i> sequence IDs in transcriptome databases.	Page 4
Supplementary Table S3. Plant cp <i>ndh</i> genes and their transfer to plant mt genomes.	Page 9
Supplementary Table S4. The accession numbers of the sequences that were identified in this report.	Page 10
Supplementary Table S5. Sequencing coverage of the seven assembled chloroplast genomes.	Page 12
Supplementary Table S6. Summary of the transcriptome, chloroplast and mitochondrial genome sequences of <i>Vanilla planifolia</i> (<i>ndh</i> -deleted), <i>Paphiopedilum armeniacum</i> (<i>ndh</i> -deleted), <i>Cypripedium formosanum</i> (<i>ndh</i> -complete), <i>Habenaria longidenticulata</i> , <i>Goodyera fumata</i> , <i>Erycina pusilla</i> (<i>ndh</i> -deleted) and <i>Masdevallia picturata</i> (<i>ndh</i> -complete).	Page 13
Supplemental Table S7. Mitochondrial-derived <i>ndh</i> transcripts.	Page 14
Supplementary Table S8. Summary of 68 cp-like mt gene fragments.	Page 15
Supplementary Table S9. Mitochondria and chloroplast genome accession numbers in identifying the <i>ndh</i> genes and cp-like DNA from the published plant mt genomes.	Page 17
Supplementary Table S10. Primer list for BAC clone screening.	Page 18
Supplemental Figure S1. Gene maps of orchid chloroplast genomes.	Page 19
Supplementary Figure S2. The cp <i>ndhJ-K-C</i> genes were transferred to the plant mt genome.	Page 22
Supplementary Figure S3. The cp <i>ndhF-D-E-G-I-A-H</i> region was transferred to the plant mt genome.	Page 23
Supplementary Figure S4. The cp <i>ndhB</i> gene fragment was transferred to the plant mt genome.	Page 24
Supplementary Figure S5. Flowchart of sequence annotation.	Page 25

Supplementary Table S1. Percentage of each *ndh* gene remaining within the transcriptomes of 16 orchid species.¹

<i>ndh</i> gene*	F	D	E	G	I	A	H	J	K	C	B
Apostasioideae											
<i>Apostasia shenzhenica</i>	-	96	-	-	80	40	-	64	86	100	34
<i>Neuwiedia malipoensis</i>	62	100	84	40	83	78	83	31	-	100	96
Vanilloideae											
<i>Vanilla shenzhenica</i>	-	-	-	-	-	-	-	-	35	-	8
<i>Galeola faberi</i>	-	-	-	-	-	16	-	-	-	40	6
<i>Vanilla planifolia</i>	-	-	-	-	-	-	-	25	15	44	8
Cypripedioideae											
<i>Cypripedium singchii</i>	7	94	100	94	83	8	74	98	98	100	65
<i>Paphiopedilum armeniacum</i>	-	30	-	-	-	6	80	100	100	100	62
Orchidoideae											
<i>Hemipilia forrestii</i>	58	71	64	46	100	76	78	-	4	-	44
<i>Habenaria delavayi</i>	50	84	100	100	100	88	58	-	89	100	96
<i>Drakaea elastica</i>	-	20	-	-	-	-	-	-	76	-	22
<i>Goodyera pubescens</i>	50	80	100	100	94	91	100	100	91	100	16
<i>Platanthera clavellata</i>	25	87	10	82	94	92	100	98	91	100	64
Epidendroideae											
<i>Masdevallia yuangensis</i>	67	79	82	72	68	44	88	100	100	100	100
<i>Phalaenopsis equestris</i>	10	30	-	24	20	-	-	96	26	58	74
<i>Cymbidium sinense</i>	79	100	42	84	100	90	100	100	94	91	94
<i>Erycina pusilla</i>	-	22	-	44	-	-	-	47	-	91	26

¹No. of aligned amino acids/no. of total amino acids. The sequence IDs are shown in Supplementary Table S2.

*The percentage amino acid identity is in comparison with the corresponding *ndh* gene that was translated from banana.

‘-’ indicates genes that were not found in the transcriptome of a species.

Supplementary Table S2. The orchid ndh sequence IDs in transcriptome databases.

Species	<i>ndh</i> transcripts			Material information	Reference
	ndhJ-K-C region	ndhF-D-E-G-I-A-H region	ndhB		
Apostasioideae					
<i>Apostasia shenzhenica</i>	>Unigene69269_Ap_fb >Unigene87795_Ap_fb >Unigene88477_Ap_fb >Unigene23503_Ap_fb >Unigene11539_Ap_fb >Unigene90084_Ap_fb >Unigene46738_Ap_fb >Unigene28081_Ap_fb >Unigene52144_Ap_fb	>Unigene41918_Ap_fb >Unigene53823_Ap_fb >Unigene72742_Ap_fb >Unigene73556_Ap_fb >Unigene76972_Ap_fb >Unigene79556_Ap_fb >Unigene81057_Ap_fb >Unigene85689_Ap_fb	>Unigene29767_Ap_fb >Unigene28875_Ap_fb >Unigene79060_Ap_fb >Unigene29163_Ap_fb >Unigene2188_Ap_fb >Unigene9034_Ap_fb >Unigene3335_Ap_fb	mature flower buds	Tsai et al. 2013
<i>Neuwiedia malipoensis</i>	>Unigene117027_Ne_fb >Unigene116386_Ne_fb >Unigene80802_Ne_fb >Unigene92339_Ne_fb	>Unigene116626_Ne_fb >Unigene120297_Ne_fb >Unigene129251_Ne_fb >Unigene13695_Ne_fb >Unigene139703_Ne_fb >Unigene140737_Ne_fb >Unigene143156_Ne_fb >Unigene146834_Ne_fb >Unigene148454_Ne_fb >Unigene154307_Ne_fb >Unigene157226_Ne_fb >Unigene48454_Ne_fb >Unigene65423_Ne_fb >Unigene65942_Ne_fb >Unigene66460_Ne_fb >Unigene72149_Ne_fb >Unigene73733_Ne_fb >Unigene80484_Ne_fb >Unigene84449_Ne_fb >Unigene85091_Ne_fb >Unigene86866_Ne_fb >Unigene94366_Ne_fb >Unigene96329_Ne_fb >Unigene99485_Ne_fb	>Unigene156751_Ne_fb >Unigene13393_Ne_fb >Unigene28019_Ne_fb >Unigene140983_Ne_fb >Unigene156912_Ne_fb >Unigene105627_Ne_fb >Unigene43751_Ne_fb >Unigene7472_Ne_fb	mature flower buds	Tsai et al. 2013

Species	<i>ndh</i> transcripts			Material information	Reference
	ndhJ-K-C region	ndhF-D-E-G-I-A-H region	ndhB		
<i>Cypripedioideae</i>					
<i>Cypripedium singchii</i>	>Unigene123012_Ch_fb >Unigene126895_Ch_fb >Unigene91373_Ch_fb >Unigene124112_Ch_fb >Unigene44022_Ch_fb >Unigene54875_Ch_fb >Unigene79119_Ch_fb >Unigene64311_Ch_fb	>Unigene108704_Ch_fb >Unigene86389_Ch_fb >Unigene38615_Ch_fb >Unigene132771_Ch_fb >Unigene117910_Ch_fb >Unigene110223_Ch_fb >Unigene133375_Ch_fb >Unigene117089_Ch_fb >Unigene15981_Ch_fb >Unigene120965_Ch_fb >Unigene76575_Ch_fb >Unigene117252_Ch_fb >Unigene36780_Ch_fb >Unigene50561_Ch_fb >Unigene35987_Ch_fb	>Unigene81774_Ch_fb >Unigene116499_Ch_fb >Unigene76103_Ch_fb >Unigene120814_Ch_fb >Unigene78391_Ch_fb >Unigene121760_Ch_fb	mature flower buds	Tsai et al. 2013
<i>Paphiopedilum armeniacum</i>	>Unigene17537_Pa_fb >Unigene19265_Pa_fb	>Unigene117683_Pa_fb >Unigene86259_Pa_fb >Unigene105103_Pa_fb >Unigene102973_Pa_fb >Unigene90098_Pa_fb	>Unigene105265_Pa_fb >Unigene66033_Pa_fb >Unigene102147_Pa_fb >Unigene19856_Pa_fb >Unigene102907_Pa_fb >Unigene42239_Pa_fb >Unigene57666_Pa_fb >Unigene36063_Pa_fb	mature flower buds	Tsai et al. 2013

Species	<i>ndh</i> transcripts			Material information	Reference
	ndhJ-K-C region	ndhF-D-E-G-I-A-H region	ndhB		
<i>Vanilloideae</i>					
<i>Vanilla planifolia</i>	>scaffold-THDM-2043406-Vanilla_planifolia >scaffold-THDM-2006247-Vanilla_planifolia		>scaffold-THDM-2032069-Vanilla_planifolia	No material information	Johnson et al. 2012
<i>Vanilla shenzhenica</i>	>Unigene147494_Va_fb >Unigene123_Va_fb >Unigene23174_Va_fb >Unigene81512_Va_fb		>Unigene54646_Va_fb	mature flower buds	Tsai et al. 2013
<i>Galeola faberi</i>	>Unigene71422_Ga_fb >Unigene107437_Ga_fb >Unigene20405_Ga_fb	>Unigene57147_Ga_fb >Unigene27278_Ga_fb >Unigene50721_Ga_fb		mature flower buds	Tsai et al. 2013

Species	<i>ndh</i> transcripts			Material information	Reference
	ndhJ-K-C region	ndhF-D-E-G-I-A-H region	ndhB		
Orchidoideae					
<i>Drakaea elastica</i>	>scaffold-XZME-2073613-Drakaea_elastica	>scaffold-XZME-2013708-Drakaea_elastica	>scaffold-XZME-2067623-Drakaea_elastica	leaves, flowers, and buds	Johnson et al. 2012
<i>Goodyera pubescens</i>	>scaffold-VTUS-2052198-Goodyera_pubescens	>scaffold-VTUS-2008714-Goodyera_pubescens	>scaffold-VTUS-2027247-Goodyera_pubescens	young leaves	Johnson et al. 2012
		>scaffold-VTUS-2049624-Goodyera_pubescens	>scaffold-VTUS-2017751-Goodyera_pubescens		
		>scaffold-VTUS-2050414-Goodyera_pubescens	>scaffold-VTUS-2024711-Goodyera_pubescens		
		>scaffold-VTUS-2044337-Goodyera_pubescens	>scaffold-VTUS-2026918-Goodyera_pubescens		
		>scaffold-VTUS-2008713-Goodyera_pubescens	>scaffold-VTUS-2040139-Goodyera_pubescens		
		>scaffold-VTUS-2043164-Goodyera_pubescens	>scaffold-VTUS-2010245-Goodyera_pubescens		
		>scaffold-VTUS-2037255-Goodyera_pubescens	>scaffold-VTUS-2008415-Goodyera_pubescens		
<i>Habenaria delavayi</i>	>Unigene11883_Ha_fb	>Unigene103331_Ha_fb	>Unigene100905_Ha_fb	mature flower buds	Tsai et al. 2013
	>Unigene2826_Ha_fb	>Unigene104496_Ha_fb	>Unigene11008_Ha_fb		
	>Unigene84798_Ha_fb	>Unigene105393_Ha_fb	>Unigene12605_Ha_fb		
		>Unigene109799_Ha_fb	>Unigene1993_Ha_fb		
		>Unigene29980_Ha_fb	>Unigene2468_Ha_fb		
		>Unigene30495_Ha_fb	>Unigene45846_Ha_fb		
		>Unigene38599_Ha_fb	>Unigene67111_Ha_fb		
		>Unigene40484_Ha_fb			
		>Unigene40484_Ha_fb			
		>Unigene50000_Ha_fb			
		>Unigene63124_Ha_fb			
		>Unigene83484_Ha_fb			
		>Unigene83500_Ha_fb			
		>Unigene8483_Ha_fb			
		>Unigene93473_Ha_fb			
		>Unigene97680_Ha_fb			
		>Unigene99504_Ha_fb			
<i>Hemipilia forrestii</i>	>Unigene107848_Hem	>Unigene100534_Hem	>Unigene104501_Hem	mature flower buds	Tsai et al. 2013
	>Unigene95563_Hem	>Unigene104197_Hem	>Unigene64030_Hem		
	>Unigene108373_Hem	>Unigene1054_Hem	>Unigene74470_Hem		
	>Unigene24273_Hem	>Unigene107907_Hem	>Unigene8168_Hem		
	>Unigene49469_Hem	>Unigene110892_Hem	>Unigene86982_Hem		
		>Unigene17478_Hem	>Unigene89656_Hem		
		>Unigene24809_Hem			
		>Unigene29088_Hem			
		>Unigene36004_Hem			
		>Unigene37397_Hem			
		>Unigene39152_Hem			
		>Unigene39228_Hem			
		>Unigene46424_Hem			
		>Unigene53948_Hem			
		>Unigene63135_Hem			
		>Unigene6863_Hem			
		>Unigene74818_Hem			
		>Unigene7947_Hem			
		>Unigene81760_Hem			
		>Unigene82799_Hem			
		>Unigene87191_Hem			

>Unigene91361_Hem

>Unigene99622_Hem

<i>Platanthera clavellata</i>	>scaffold-MTHW-2006569-Platanthera_clavellata	>scaffold-MTHW-2054067-Platanthera_clavellata	>scaffold-MTHW-2005097-Platanthera_clavellata	young leaves	Johnson et al. 2012
	>scaffold-MTHW-2012569-Platanthera_clavellata	>scaffold-MTHW-2005096-Platanthera_clavellata			
	>scaffold-MTHW-2012285-Platanthera_clavellata	>scaffold-MTHW-2033930-Platanthera_clavellata			
	>scaffold-MTHW-2002299-Platanthera_clavellata	>scaffold-MTHW-2030317-Platanthera_clavellata			
	>scaffold-MTHW-2002298-Platanthera_clavellata	>scaffold-MTHW-2002472-Platanthera_clavellata			
	>scaffold-MTHW-2044147-Platanthera_clavellata	>scaffold-MTHW-2049556-Platanthera_clavellata			
	>scaffold-MTHW-2010146-Platanthera_clavellata_r	>scaffold-MTHW-2011571-Platanthera_clavellata			
	>scaffold-MTHW-2039772-Platanthera_clavellata				
	>scaffold-MTHW-2048797-Platanthera_clavellata				
	>scaffold-MTHW-2039314-Platanthera_clavellata				
	>scaffold-MTHW-2038829-Platanthera_clavellata				
	>scaffold-MTHW-2021258-Platanthera_clavellata				

Species	<i>ndh</i> transcripts			Material information	Reference
	ndhJ-K-C region	ndhF-D-E-G-I-A-H region	ndhB		
Epidendroideae					
<i>Cymbidium sinense</i>	>Unigene91693_Cym_fb >Unigene58080_Cym_fb >Unigene91202_Cym_fb	>Unigene97292_Cym_fb >Unigene95349_Cym_fb >Unigene104107_Cym_fb >Unigene53349_Cym_fb >Unigene38535_Cym_fb >Unigene96064_Cym_fb >Unigene82889_Cym_fb >Unigene78331_Cym_fb >Unigene57645_Cym_fb >Unigene98811_Cym_fb >Unigene477_Cym_fb >Unigene108035_Cym_fb	>Unigene102171_Cym_fb >Unigene108654_Cym_fb	mature flower buds	Tsai et al. 2013
<i>Erycina pusilla</i>	>Unigene2294_All >Unigene18133_All >Unigene18740_All >Unigene53575_All	>Unigene48484_All >Unigene66487_All	>Unigene56611_All >Unigene63750_All	Root, leaves, flowers, fruits	Chou et al. 2013
<i>Masdevallia yuangensis</i>	>scaffold-JSAG-2016102-Masdevallia_yuangen	>scaffold-JSAG-2080352-Masdevallia_yuangensis >scaffold-JSAG-2015140-Masdevallia_yuangensis >scaffold-JSAG-2079074-Masdevallia_yuangensis >scaffold-JSAG-2078946-Masdevallia_yuangensis >scaffold-JSAG-2063713-Masdevallia_yuangensis >scaffold-JSAG-2073565-Masdevallia_yuangensis >scaffold-JSAG-2065747-Masdevallia_yuangensis >scaffold-JSAG-2014459-Masdevallia_yuangensis >scaffold-JSAG-2071180-Masdevallia_yuangensis >scaffold-JSAG-2071180-Masdevallia_yuangensis	>scaffold-JSAG-2017126-Masdevallia_yuangensis >scaffold-JSAG-2017125-Masdevallia_yuangensis	buds, leaves, roots	Johnson et al. 2012
<i>Phalaenopsis equestris</i>	>Unigene80637_Pe_fb >Unigene76415_Pe_fb	>Unigene70210_Pe_fb >Unigene55346_Pe_fb >Unigene82158_Pe_fb >Unigene7851_Pe_fb >Unigene91525_Pe_fb	>Unigene84064_Pe_fb >Unigene93337_Pe_fb >Unigene11847_Pe_fb	mature flower buds	Tsai et al. 2013

Supplementary Table S3. Plant cp *ndh* genes and their transfer to plant mt genomes.

Species	<i>ndh</i> genes										
	<i>F</i>	<i>D</i>	<i>E</i>	<i>G</i>	<i>I</i>	<i>A</i>	<i>H</i>	<i>J</i>	<i>K</i>	<i>C</i>	<i>B</i>
Chloroplast genome											
Vanilloideae											
<i>Vanilla planifolia</i>	-	-	-	-	-	-	-	-	-	-	16
Cypripedioideae											
<i>Paphiopedilum armeniacum</i>	-	78	-	-	-	-	-	100	100	100	100
<i>Paphiopedilum niveum</i>	-	78	-	-	-	-	-	100	100	100	100
<i>Cypripedium formosanum</i>	100	100	100	100	100	100	100	100	100	100	100
Orchidoideae											
<i>Habenaria longidenticulata</i>	100	100	100	100	100	100	100	100	100	100	100
<i>Goodyera fumata</i>	100	100	100	100	100	100	100	100	100	100	100
Epidendroideae											
<i>Erycina pusilla</i>	-	60	-	52	-	-	32	42	-	68	43
<i>Oncidium 'Gower Ramsey'</i>	-	65	99	100	48	40	15	43	13	100	99
<i>Phalaenopsis equestris</i>	-	50	-	24	18	-	-	98	27	60	79
<i>Cymbidium sinense*</i>	81	100	100	100	100	92	100	100	100	100	100
<i>Masdevallia picturata</i>	100	100	100	100	100	100	100	100	100	100	100
Mitochondrial genome											
Vanilloideae											
<i>Vanilla planifolia</i>	-	-	58	-	-	-	-	79	43	70	-
Cypripedioideae											
<i>Paphiopedilum armeniacum</i>	-	82	-	-	-	49	98	100	-	100	85
<i>Paphiopedilum niveum</i>	50	80	50	-	-	-	79	98	91	99	100
<i>Cypripedium formosanum</i>	-	-	-	-	-	-	-	-	-	63	-
Orchidoideae											
<i>Habenaria longidenticulata</i>	59	64	-	-	-	36	-	-	-	-	-
<i>Goodyera fumata</i>	-	35	100	-	99	44	8	96	-	80	7
Epidendroideae											
<i>Masdevallia picturata</i>	75	98	100	100	100	94	99	-	-	30	82
<i>Erycina pusilla</i>	41	78	100	98	28	91	100	48	-	96	50
<i>Oncidium 'Gower Ramsey'</i>	70	30	-	-	-	-	-	-	-	-	97
Others											
<i>Spirodela polyrhiza</i>	-	-	-	-	-	-	-	-	49	58	-
<i>Phoenix dactylifera</i>	-	-	-	-	100	44	-	100	96	-	-
<i>Bambusa oldhamii</i>	-	-	-	-	-	-	-	100	87	48	-
<i>Oryza rufipogon</i>	-	-	-	-	-	-	-	100	95	34	-
<i>Oryza sativa indica</i>	-	-	-	-	-	-	-	100	95	34	-
<i>Oryza sativa japonica</i>	-	-	-	-	-	-	-	100	95	34	-
<i>Triticum aestivum</i>	-	-	-	-	-	26	-	-	-	-	100
<i>Sorghum bicolor</i>	-	-	-	-	33	-	-	-	88	98	-
<i>Tripsacum dactyloides</i>	-	-	-	-	-	-	-	-	20	-	10
<i>Zea mays</i>	-	-	-	-	-	-	-	-	20	-	100
<i>Zea perennis</i>	-	-	-	-	-	-	-	-	20	-	100
<i>Amborella trichopoda</i>	87	97	98	99	100	49	100	99	99	100	100
<i>Vitis vinifera</i>	91	100	99	-	-	-	42	-	-	-	16
<i>Cucurbita pepo</i>	36	80	34	61	-	-	47	-	85	64	93
<i>Citrullus lanatus</i>	-	-	-	-	-	-	-	99	98	100	-
<i>Cucumis melo</i>	-	-	36	-	49	22	-	-	-	-	-
<i>Cucumis sativus</i>	-	91	59	85	11	-	-	58	-	-	100
<i>Beta macrocarpa</i>	-	-	-	-	-	-	-	-	83	-	-
<i>Silene vulgaris</i>	-	61	-	-	-	-	-	-	-	-	-
<i>Nicotiana tabacum</i>	-	-	-	-	-	-	12	-	-	-	85
<i>Carica papaya</i>	-	-	-	-	-	-	-	-	-	-	78
<i>Boea hygrometrica</i>	-	-	-	-	-	-	-	70	90	53	100

The light green rows of the table show the *ndh* genes in the orchid chloroplast genomes. The remainder of the table contains data from the available mitochondrial genomes. The numbers indicate the percentage of the nucleotide fragments that are similar to the *ndh* sequences.

The red numbers indicate that the *ndh* DNA is in frame and encodes the full-length *ndh* gene.

'-' indicates that there is no homolog in the mt genome.

Supplementary Table S4. The accession numbers of the sequences that were identified in this report.

Chloroplast genome Sequences

Subfamily	Name	Accession
Vanilloideae	<i>Vanilla planifolia</i>	KJ566306
Cyripedioideae	<i>Cypripedium formosanum</i>	KJ501998
	<i>Paphiopedilum armeniacum</i>	KJ566307
	<i>Paphiopedilum niveum</i>	KJ524105
Orchidoideae	<i>Goodyera fumata</i>	KJ501999
	<i>Habenaria longidenticulata</i>	KJ524104
Epidendroideae	<i>Masdevallia picturata</i>	KJ566305

Orchid *ndh* DNA sequences

Subfamily	Species	Name	Accession
Cyripedioideae	<i>Paphiopedilum niveum</i>	Paph_niveum_ndhB1	KJ501931
		Paph_niveum_ndhB2	KJ501932
		Paph_niveum_ndhB3	KJ501933
		Paph_niveum_ndhB4	KJ501989
		Paph_niveum_ndhB5	KJ501934
		Paph_niveum_ndhB6	KJ501935
		Paph_niveum_ndhB7	KJ501936
		Paph_niveum_ndhB8	KJ501937
		Paph_niveum_ndhE1	KJ501938
		Paph_niveum_ndhH	KJ501939
		Paph_niveum_ndhJKC2	KJ501941
		Paph_niveum_ndhJKC3	KJ501942
		Paph_niveum_ndhJ	KJ501943
		<i>Paphiopedilum armeniacum</i>	Paph_armeniaticum_ndhJC
Epidendroideae	<i>Masdevallia picturata</i>	Mas_ndhF	KJ501928
		Mas_ndhJK	KJ501929

Orchid mitochondria *ndh* DNA sequences

Subfamily	Species	Name	Accession
Vanilloideae	<i>Vanilla planifolia</i>	Vp-mt-ndhJ	KJ501948
		Vp-mt-ndhK	KJ501957
		Vp-mt-ndhC	KJ501923
		Vp-mt-ndhE	KJ501959
Cyripedioideae	<i>Cypripedium formosanum</i>	Cf-mt-ndhC	KJ501922
		Cf-mt-ndhH	KJ501956
		Pa-mt-ndhCD	KJ501961
		Pa-mt-ndhAH	KJ501962
		Pa-mt-ndhB	KJ501951
		Pn-mt-ndhJKC	KJ501944
		Pn-mt-ndhD	KJ501945
Orchidoideae	<i>Habenaria longidenticulata</i>	Ha-mt-ndhA	KJ501960
		Ha-mt-ndhD	KJ501926
		Ha-mt-ndhF	KJ501954
	<i>Goodyera fumata</i>	Go-mt-ndhH	KJ501955
		Go-mt-ndhAIE	KJ501963
		Go-mt-ndhD	KJ501927
		Go-mt-ndhB	KJ501921
Epidendroideae	<i>Erycina pusilla</i>	Ep-mt-ndhJC	KJ501950

Epidendroideae	<i>Erycina pusilla</i>	Ep-mt-ndhC	KJ501996
		Ep-mt-ndhDEGIAH	KJ501958
		Ep-mt-ndhDF	KJ501966
		Ep-mt-ndhD	KJ501975
		Ep-mt-ndhB	KJ501994
	<i>Goodyera fumata</i>	Go-mt-ndhJ	KJ501949
		Go-mt-ndhC	KJ501924
	<i>Masdevallia picturata</i>	Ma-mt-ndhC	KJ501930
		Ma-mt-ndhHAIGED	KJ501946
		Ma-mt-ndhB	KJ501947
	<i>Oncidium 'Gower Ramsey'</i>	Onc-mt-ndhF	KJ501953
		Onc-mt-ndhD	KJ501925
		Onc-mt-ndhB	KJ501920

Erycina pusilla mitochondria BAC clone sequences

Subfamily	Species	Name	Accession
Epidendroideae	<i>Erycina pusilla</i>	Ep-mt-cp1_002O08_c1	KJ501991
		Ep-mt-cp1_002O08_c2	KJ501964
		Ep-mt-ndhC 180K03_c1	KJ501978
		Ep-mt-ndhC 180K03_c2	KJ501996
		Ep-mt-ndhC 180K03_c3	KJ501997
		Ep-mt-cp2_163A04	KJ501976
		Ep-mt-ndhD162P19	KJ501975
		Ep-mt-cp3_123E16	KJ501973
		Ep-mt-cp4_092M20_c1	KJ501972
		Ep-mt-cp4_092M20_c2	KJ501979
		Ep-mt-ndhB 089F15_c1	KJ501993
		Ep-mt-ndhB 089F15_c2	KJ501994
		Ep-mt-ndhB 089F15_c3	KJ501995
		Ep-mt-cp5_041C10	KJ501971
		Ep-mt-cp5_037I23	KJ501970
		Ep-mt-ndhDEGIAH 037D12	KJ501969
		Ep-mt-cp6_034M07	KJ501992
		Ep-mt-cp7_024M14_c1	KJ501967
		Ep-mt-cp7_024M14_c2	KJ501968
		Ep-mt-ndhDF 015H07	KJ501966
Ep-mt-cp8_012N23	KJ501965		

Erycina pusilla mitochondria cDNA sequences

Subfamily	Species	Name	Accession
Epidendroideae	<i>Erycina pusilla</i>	C211673	KJ501980
		C92325	KJ501981
		C13581	KJ501982
		C115515	KJ501983
		C117162	KJ501984
		C16074	KJ501985
		C122767	KJ501986
		C74904	KJ501987
		C167460	KJ501988
		C92859	KJ501990
		Ec16074	KJ721582
		C18219	KJ721583

Supplementary Table S5. Sequencing coverage of the seven assembled chloroplast genomes.

Species	Total covered bases (bp)	Genome size (bp)	Coverage*
Vanilloideae			
<i>Vanilla planifolia</i>	127134011	150127	847
Cypripedioideae			
<i>Cypripedium formosanum</i>	34236744	180723	189
<i>Paphiopedilum armeniacum</i>	30040152	165008	182
<i>Paphiopedilum niveum</i>	82923695	161387	514
Orchidoideae			
<i>Goodyera fumata</i>	149360589	157868	946
<i>Habenaria longidenticulata</i>	126061558	156152	807
Epidendroideae			
<i>Masdevallia picturata</i>	158689021	158276	1003

*: The coverage was computed by BWA-aligning reads back to each chloroplast genome, summing the number of reads covered at each base using SAMtools, and dividing them by the genome size.

Supplementary Table S6. Summary of the transcriptome, chloroplast and mitochondrial genome sequences of *Vanilla planifolia* (*ndh* deleted), *Paphiopedilum armeniacum* (*ndh* deleted), *Cypripedium formosanum* (*ndh* complete), *Habenaria longidenticulata*, *Goodyera fumata*, *Erycina pusilla* (*ndh* deleted) and *Masdevallia picturata* (*ndh* complete).

<i>ndh</i> gene	F	D	E	G	I	A	H	J	K	C	B
Vanilloideae											
<i>Vanilla planifolia</i> cDNA	-	-	-	-	-	-	-	25	15	44	8
<i>Vanilla planifolia</i> cp	-	-	-	-	-	-	-	-	-	-	19
<i>Vanilla planifolia</i> mt	-	-	59	-	-	-	-	81	46	69	99
Cypripedioideae											
<i>Paphiopedilum armeniacum</i> cDNA	-	30	-	-	-	6	80	100	100	100	62
<i>Paphiopedilum armeniacum</i> cp	-	78	-	-	-	-	-	100	100	100	100
<i>Paphiopedilum armeniacum</i> mt	55	78	60	-	-	60	98	-	-	78	85
<i>Cypripedium singchii</i> cDNA	7	94	100	94	83	8	74	98	98	100	65
<i>Cypripedium formosanum</i> cp	100	100	100	100	100	100	100	100	100	100	100
<i>Cypripedium formosanum</i> mt	6	-	-	-	-	-	-	-	-	58	-
Orchidoideae											
<i>Habenaria delavayi</i>	50	84	100	100	100	88	58	16	89	100	96
<i>Habenaria longidenticulata</i> cp	100	100	100	100	100	100	100	100	100	100	100
<i>Habenaria longidenticulata</i> mt	64	62	86	-	-	39	-	-	-	-	-
<i>Goodyera pubescens</i> cDNA	50	80	100	100	94	91	100	100	91	100	16
<i>Goodyera fumata</i> cp	100	100	100	100	100	100	100	100	100	100	100
<i>Goodyera fumata</i> mt	-	36	100	-	99	54	8	82	51	77	6
Epidendroideae											
<i>Masdevallia yuangensis</i> cDNA	67	79	82	72	68	44	88	100	100	100	100
<i>Masdevallia picturata</i> cp	100	100	100	100	100	100	100	100	100	100	100
<i>Masdevallia picturata</i> mt	-	99	100	100	98	93	99			30	84
<i>Erycina pusilla</i> cDNA	-	22	-	44	-	-	-	44	-	91	26
<i>Erycina pusilla</i> cp	-	60	-	52	-	-	32	42	-	68	43
<i>Erycina pusilla</i> mt	66	81	83	99	27	91	93	44		91	52

The numbers indicate the percentage of the nucleotide fragments that are similar to the *ndh* sequences. Red numbers indicate that the *ndh* DNA is in frame and encodes the full-length *ndh* gene.

Supplemental Table S7. Mitochondrial-derived *ndh* transcripts.

<i>ndh</i>	Species	Transcript ID	Reference
<i>C</i>	<i>Vanilla planifolia</i>	scaffold-THDM-2006247	Johnson et al. 2012
<i>K</i>	<i>Vanilla shenzhenica</i>	Unigene123_Va_fb	Tsai et al. 2013
<i>C</i>	<i>Phalaenopsis equestris</i>	Unigene17537_Pa	Tsai et al. 2013
<i>C</i>	<i>Erycina pusilla</i>	Unigene18133	Chou et al. 2013
<i>J</i>	<i>Erycina pusilla</i>	Unigene18740	Chou et al. 2013
<i>D</i>	<i>Erycina pusilla</i>	Unigene48484	Chou et al. 2013
<i>B</i>	<i>Vanilla planifolia</i>	scaffold-THDM-2032069	Johnson et al. 2012

Supplementary Table S8. Summary of 68 cp-like mt gene fragments.

Gene name	BAC clone ID	Position start	Position end	Coverage	RNA	Protein	Note
<i>rps12</i>	KJ501975	9650	9767	26/123	KJ501980		
	KJ501994	44996	44766	76/123	-		
<i>psbA</i>	KJ501968	17868	16944	334/353	-		
<i>matK</i>	-			0/518	-		
<i>rps16</i>	KJ501964	4875	5934	87/92	KJ501981		
	KJ501973	25866	24807	87/92	KJ501981		
<i>psbK</i>	KJ501970	15664	15483	61/61	-		
<i>psbI</i>	KJ501970	15247	15140	36/36	?	+	= cp
<i>atpA</i>	-			0/509	-		
<i>atpF</i>	-			0/184			
<i>atpH</i>	KJ501970	10590	10781	64/81	-		
<i>atpI</i>	KJ501970	9127	9867	247/247	-		*
<i>rps2</i>	KJ501970	43441	44148	236/236	-	+	
		8463	8828	118/236	-		
<i>rpoC2</i>	KJ501991	48917	49056	47/1385	-		
	KJ501970	39717	43208	1238/1385	-		
		6979	8396	504/1385	-		
<i>rpoC1</i>	KJ501991	46157	48720	680/680	-		indel
<i>rpoB</i>	KJ501991	43024	46127	1070/1070	-		indel
<i>petN</i>	KJ501991	40985	40899	29/29	-	+	
<i>psbM</i>	KJ501991	40363	40464	34/34	-	-	*
<i>psbD</i>	KJ501966	55970	56409	167/353	-		
	KJ501970	22390	22817	163/353	-		
	KJ501969	18498	18982	179/353	-		
	KJ501978	20972	21456	179/353	-		
<i>psbC</i>	KJ501969	19130	20279	407/407	-		indel
	KJ501978	21604	22753	407/407	-		indel
<i>psbZ</i>	KJ501969	20731	20907	62/62	-		*
	KJ501978	23205	23381	62/62	-		*
<i>rps14</i>	KJ501969	21840	21562	96/100	KJ501982		*
	KJ501978	24314	24036	96/100	KJ501982		*
<i>psaB</i>	KJ501969	23734	21916	606/734	-		
	KJ501978	26208	24390	606/734	-		
<i>psaA</i>	KJ501969	25073	23784	430/750	--		
	KJ501978	27547	26258	430/750	--		
<i>ycf3</i>	-			0/168			
<i>rps4</i>	-			0/201			
<i>atpE</i>	KJ501972	13239	13637	133/133	-	+	
	KJ501971	17639	17241	133/133	-	+	
	KJ501991	13373	13771	133/133	-	+	
	KJ501994	69656	69258	133/133	-	+	
<i>atpB</i>	KJ501972	11781	13222	489/497	--		indel
	KJ501971	19097	17656	489/497	-		indel
	KJ501991	11915	13356	489/497	-		indel
	KJ501994	71114	69673	489/497	-		indel
<i>rbcL</i>	KJ501972	11037	9646	464/480	KJ501983		indel
	KJ501971	19841	21232	464/480	KJ501983		indel
	KJ501991	11171	9780	464/480	KJ501983		indel
	KJ501994	71858	73249	464/480	KJ501983		indel
<i>accD</i>	KJ501972	8962	7563	488/488	KJ501984		indel
	KJ501971	21916	23315	488/488	KJ501984		indel
	KJ501991	9096	7697	488/488	KJ501984		indel
	KJ501994	73933	75332	488/488	KJ501984		indel
<i>psaI</i>	-			0/36	-		
<i>ycf4</i>	KJ501972	6510	5959	184/184	-		*
	KJ501971	24368	24919	184/184	-		*
	KJ501991	6644	6093	184/184	-		*

	KJ501994	76385	76936	184/184	-		*
<i>cemA</i>	KJ501972	2160	1483	229/229	KJ721582		*
	KJ501971	28718	29395	229/229	KJ721582		*
	KJ501991	2294	1617	229/229	KJ721582		*
	KJ501994	80735	81412	229/229	KJ721582		*
<i>petA</i>	-			0/320	-		
<i>psbJ</i>	-			0/40	-		
<i>psbL</i>	KJ501976	24797	24887	33/38	KJ501986		
<i>psbF</i>	KJ501976	24655	24771	39/39	KJ501986		*
<i>psbE</i>	KJ501976	24421	24636	78/83	-		
<i>petL</i>	KJ501973	20048	20140	31/31	KJ501987		*
<i>petG</i>	KJ501973	20325	20435	37/37	KJ501987		*
<i>psaJ</i>	KJ501975	12331	12212	44/44	KJ501988	+	
<i>rpl33</i>	KJ501975	11746	11549	66/66	-		*
<i>rps18</i>	KJ501975	11362	11051	104/104	KJ501980		*
<i>rpl20</i>	KJ501975	10408	10717	103/120	KJ501980		indel
<i>rps12</i>	KJ501994	44996	44766	77/123	-		
	KJ501975	9650	9767	38/123	KJ501980		
<i>clpP</i>	KJ501975	7537	9533	202/202	KJ501980		indel
<i>psbB</i>	KJ501975	6964	5509	508/508	-		indel
<i>psbT</i>	KJ501975	5170	5066	35/35	-		*
<i>psbN</i>	KJ501975	4915	5043	43/43	-		*
<i>psbH</i>	KJ501975	4803	4585	73/73	-	+	
<i>petB</i>	KJ501975	3684	3071	214/217	-		
<i>petD</i>	KJ501968	18529	18096	148/163	-		
<i>rpoA</i>	KJ501976	23700	22817	315/339	KJ501986		
<i>rps11</i>	KJ501976	24099	23777	136/138	KJ501986		
<i>rpl36</i>	KJ501976	24351	24241	35/35	KJ501986	+	
<i>infA</i>	KJ501973	2763	2912	49/77	-		
		24316	24414	32/77	KJ501981		
	KJ501964	6425	6327	32/77	KJ501981		
<i>rps8</i>	KJ501964	7376	7007	131/131	KJ501981		indel
	KJ501973	2287	2637	122/131	KJ501981		
		24149	24196	16/131	-		
<i>rpl14</i>	KJ501973	1744	2109	122/122	KJ501981		
	KJ501964	7919	7554	122/122	KJ501981		
<i>rpl16</i>	KJ501973	1219	1611	132/136	KJ501981		
	KJ501964	8444	8052	132/136	KJ501981		
<i>rps3</i>	KJ501973	46223	46399	59/219	KJ501990		
		23730	24102	137/219	KJ501990		
	KJ501964	10641	10075	219/219	KJ501990		indel
<i>rpl22</i>	KJ501973	11059	10697	121/121	KJ501990	+	
	KJ501964	45805	46167	121/121	KJ501990	+	
<i>rps19</i>	KJ501973	45343	45618	91/92	KJ501990		
	KJ501964	11521	11246	91/92	KJ501990		
<i>rpl2</i>	KJ501973	44668	45099	143/272	KJ501990		
	KJ501964	12196	11765	143/272	KJ501990		
<i>rpl23</i>	KJ501968	9239	9469	77/93	KJ721583		
<i>ycf2</i>	KJ501994	34804	41254	2225/2225	-		indel
<i>rps7</i>	KJ501994	44150	43707	154/155	-		
<i>rpl32</i>	KJ501978	10929	10774	52/56	-		
	KJ501969	8455	8300	52/56	-		
<i>ccsA</i>	KJ501975	12929	13805	326/326	KJ501988		indel
<i>psaC</i>	KJ501978	9344	9586	81/81	-	+	
	KJ501969	6870	7112	81/81	-	+	
<i>rps15</i>	KJ501978	3922	4191	90/90	-	-	*
	KJ501969	1448	1717	90/90	-	-	*

Supplementary Table S9. Mitochondria and chloroplast genome accession numbers in identifying the *ndh* genes and cp-like DNA from the published plant mt genomes.

Species	mt DNA accession	cp DNA accession
<i>Amborella trichopoda</i>	KF754803.1	NC_005086.1
<i>Anomodon rugelii</i>	NC_016121.1	-
<i>Arabidopsis thaliana</i>	NC_001284.2	NC_000932.1
<i>Bambusa oldhamii</i>	EU365401.1	FJ970915.1
<i>Beta macrocarpa</i>	NC_015994.1	EF534108.1 (<i>Beta vulgaris</i>)*
<i>Beta vulgaris</i>	BA000024.1	EF534108.1
<i>Boea hygrometrica</i>	NC_016741.1	NC_016468.1
<i>Brassica carinata</i>	NC_016120.1	NC_016734.1 (<i>Brassica napus</i>)
<i>Brassica juncea</i>	NC_016123.1	NC_016734.1 (<i>Brassica napus</i>)
<i>Brassica napus</i>	NC_008285.1	NC_016734.1
<i>Brassica oleracea</i>	NC_016118.1	NC_016734.1 (<i>Brassica napus</i>)
<i>Carica papaya</i>	NC_012116.1	EU431223.1
<i>Chlorokybus atmophyticus</i>	NC_009630.1	DQ422812.2
<i>Citrullus lanatus</i>	NC_014043.1	DQ865976.1 (<i>Cucumis sativus</i>)
<i>Cucumis melo</i>	JF412792.1	DQ865976.1 (<i>Cucumis sativus</i>)
<i>Cucumis sativus</i>	HQ860792.1	DQ865976.1
<i>Cucurbita pepo</i>	NC_014050.1	DQ865976.1 (<i>Cucumis sativus</i>)
<i>Cycas taitungensis</i>	NC_010303.1	NC_009618.1
<i>Cymbidium sinense</i> *		NC_021430.1
<i>Cypripedium formosanum</i>		KJ501998
<i>Daucus carota</i>	NC_017855.1	NC_008325.1
<i>Erycina pusilla</i>		NC_018114.1
<i>Goodyera fumata</i>		KJ501999
<i>Habenaria longidenticulata</i>		KJ524104
<i>Lotus japonicus</i>	NC_016743.2	NC_002694.1
<i>Marchantia polymorpha</i>	NC_001660.1	NC_001319.1
<i>Masdevallia picturata</i>		KJ566305
<i>Megaceros aenigmaticus</i>	NC_012651.1	-
<i>Millettia pinnata</i>	NC_016742.1	NC_016708.2
<i>Nicotiana tabacum</i>	NC_006581.1	Z00044.2
<i>Oncidium 'Gower Ramsey'</i>		NC_014056.1
<i>Oryza rufipogon</i>	NC_013816.1	AY522330.1 (<i>Oryza sativa</i> subsp. <i>japonica</i>)
<i>Oryza sativa</i> subsp. <i>indica</i>	NC_007886.1	AY522330.1 (<i>Oryza sativa</i> subsp. <i>japonica</i>)
<i>Oryza sativa</i> subsp. <i>japonica</i>	NC_011033.1	AY522330.1
<i>Paphiopedilum armeniacum</i>		KJ566307
<i>Paphiopedilum niveum</i>		KJ524105
<i>Phaeoceros laevis</i>	NC_013765.1	-
<i>Phoenix dactylifera</i>	JN375330.1	GU811709.2
<i>Physcomitrella patens</i>	NC_007945.1	NC_005087.1
<i>Pleurozia purpurea</i>	NC_013444.1	-
<i>Ricinus communis</i>	NC_015141.1	NC_016736.1
<i>Silene latifolia</i>	NC_014487.1	NC_016730.1
<i>Silene vulgaris</i>	JF750427.1	NC_016727.1
<i>Sorghum bicolor</i>	NC_008360.1	EF115542.1
<i>Spirodela polyrhiza</i>	NC_017840.1	NC_015891.1
<i>Tripsacum dactyloides</i>	NC_008362.1	EF115542.1 (<i>Sorghum bicolor</i>)
<i>Triticum aestivum</i>	NC_007579.1	AB042240.3
<i>Vanilla planifolia</i>		KJ566306
<i>Vigna radiate</i>	NC_015121.1	NC_013843.1
<i>Vitis vinifera</i>	NC_012119.1	DQ424856.1
<i>Zea luxurians</i>	NC_008333.1	AY928077.1 (<i>Zea mays</i>)
<i>Zea mays</i>	NC_007982.1	AY928077.1
<i>Zea perennis</i>	NC_008331.1	AY928077.1 (<i>Zea mays</i>)

- Unavailable

* indicates there is no mt genome available. The mt genome of the species in parenthesis is used for further analysis

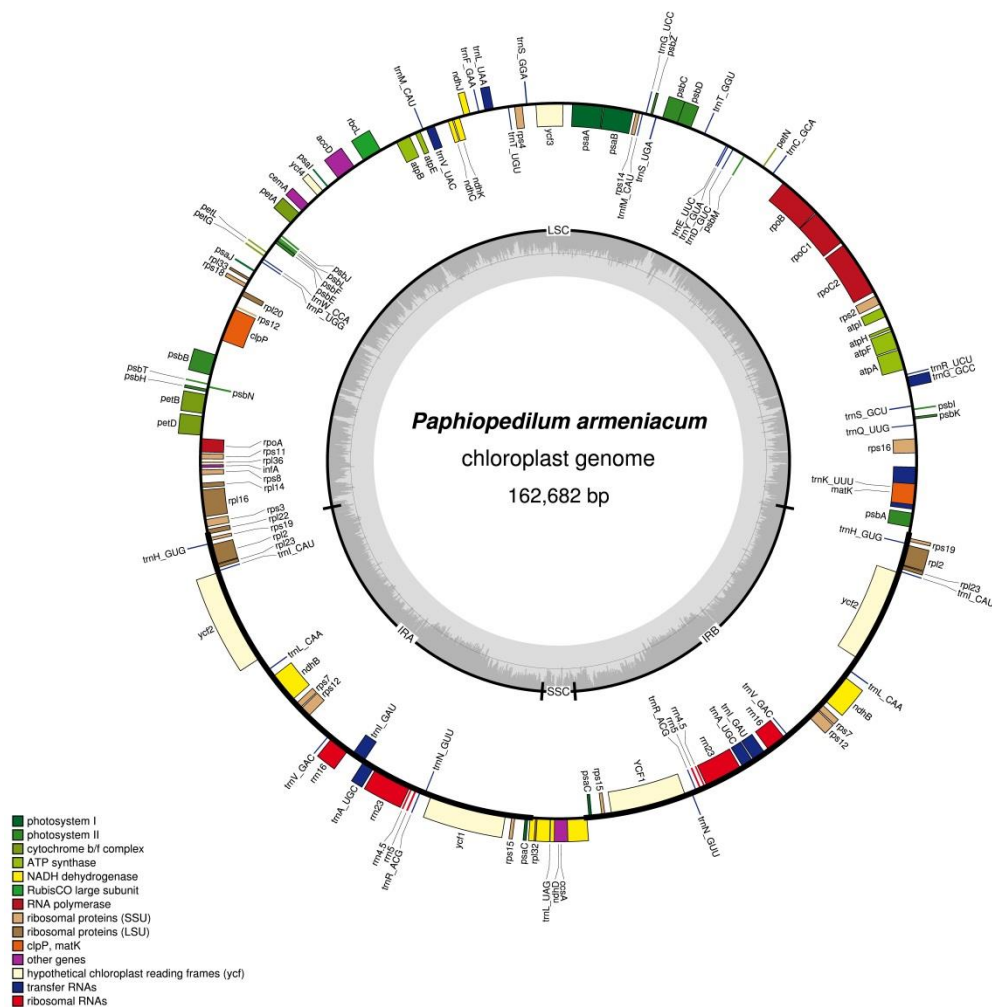
Supplementary Table S10. Primer list for BAC clone screening.

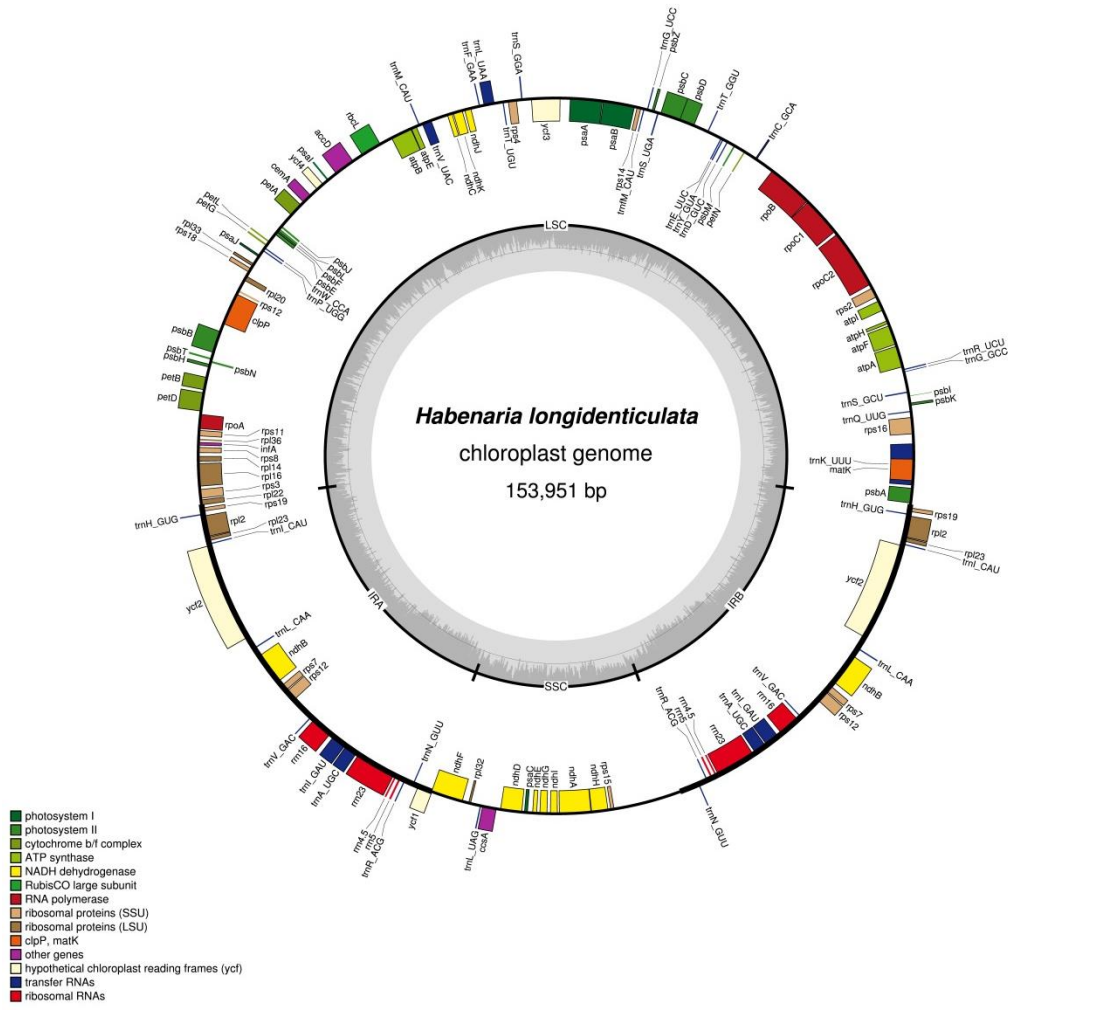
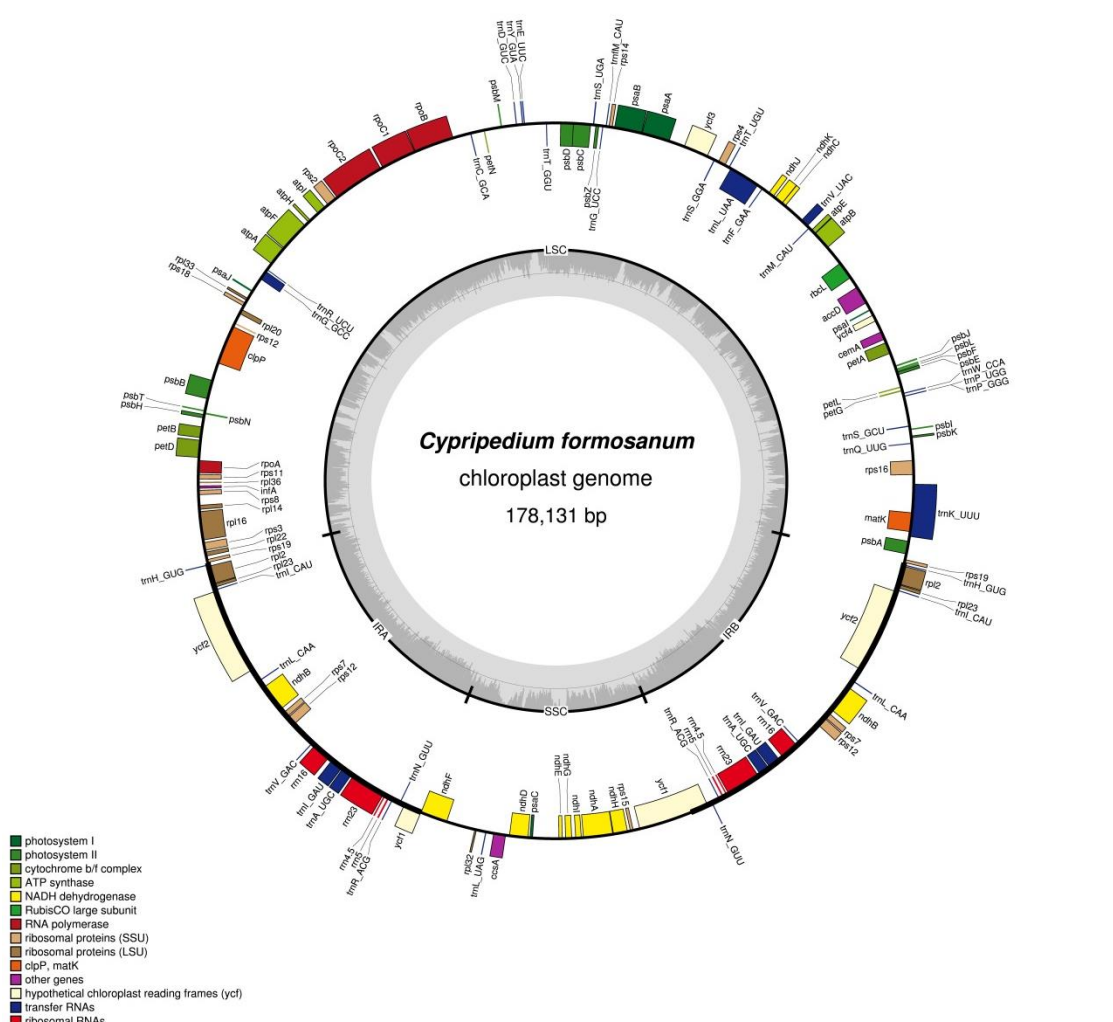
For BAC clone screening			
Sequence ID	Forward	Reverse	Clone
Ep-mt-circle1-175J16	TGGGGCATTAGTGAAAGGAT	AAGCCTGCCAGCAAGCATT	175J16
Ep-mt-circle2_162I22	TCGCTATTTGATTTTCATCCT	GCACGAAAAAGTAACCAGAC	162I22
Ep-mt- <i>ndhJC</i> _002O08	TGCGCGGTACAAAGTTCA	CCAGGCGAATTGTTAGGC	002O08
Ep-mt-cp1_002O08	GCCATGCAACCGGATAAG	TAGCTCCGGGTCCAGAAA	002O08
Ep-mt- <i>ndhC</i> _180K03	TATATATGCCGGATGCTCTT	TTATTCGGAGAGTCACCTTG	180K03
Ep-mt-cp2_163A04	TCGAGCTACCGCCCTATG	TTGGCCGTAGAAGGATCG	163A04
Ep-mt- <i>ndhD</i> _162P19	TGATCCATTGCTAACATCAA	TTTGTGTTGTCTTTCTGGTCC	162P19
Ep-mt-cp3_123E16	TTTGCACTTTCATTCCTTTT	GTCGGAGGAGGTTATTTCTT	123E16
Ep-mt-cp4_092M20	AGCAAGCTAACCTCTCGCTTT	TAAGTACCATTGCAGCGCCTA	092M20
Ep-mt- <i>ndhB</i> _089F15	CAGACCTTTCCTCTTTTG TG	GAAACGAAGTGGATAACAGC	089F15
Ep-mt-cp5_041C10	AGAAACGCGAGGGAATCA	TGGGGTGAGTTTGATTCAAGT	041C10
Ep-mt-cp5_037I23	TAGTGGGAGGTCGCGAAG	TCCCCACCCAAGTATT	037I23
Ep-mt- <i>ndhDH</i> _037D12	AAGTGACGCACTCTTTCATT	GAGGCACCATTGTGACTAT	037D12
Ep-mt-cp6_034M07	GGAGGGAGAAGCGGAGTC	CAGGGAGGTTCCGGGAAGT	034M07
Ep-mt-cp7_024M14	TGAAAATGCTCCTTTCTCAT	GACATCGCTAGTCATCCATT	024M14
Ep-mt- <i>ndhDF</i> _015H07	AGAAACTGCAGTCGTTAAGC	TTTGCTCTGATTAGGAGGAG	015H17
Ep-mt-cp8_012N23	GGAGAGCAGCTTCTTGAGTA	GTACTGAACGGATTGGAATG	012N23

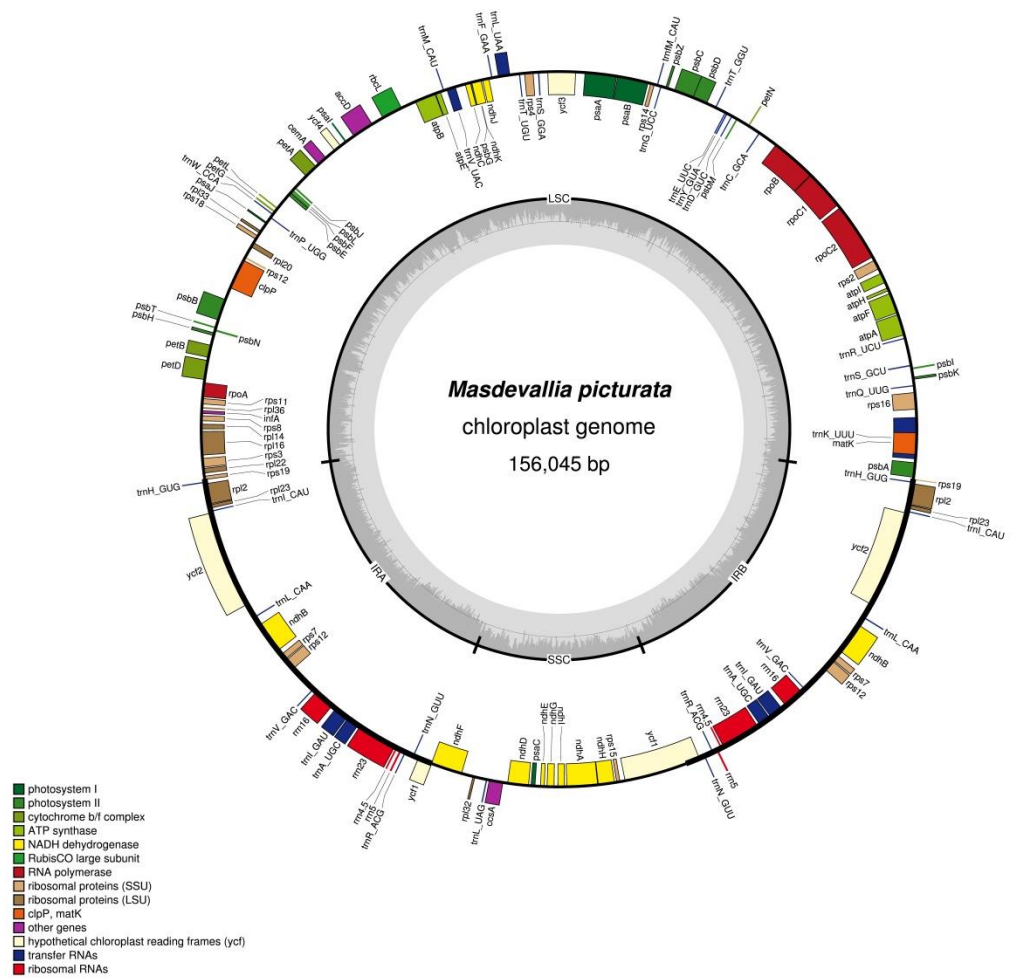
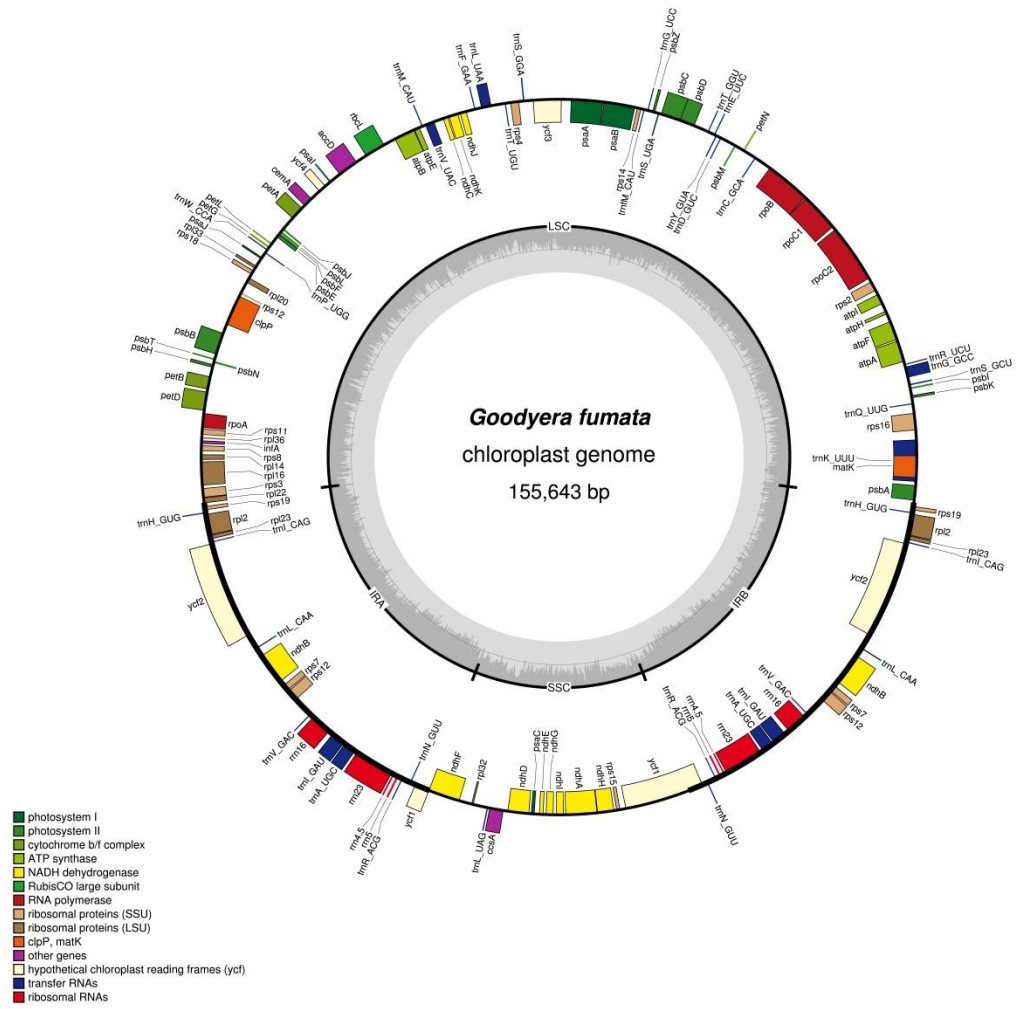
For circle form demonstration			
Sequence ID	Forward	Reverse	Clone
Ep-mt-cp8_012N23	GAGGCAGGTGAGAGTCTTGG	ACGCAAAGAGAGGTCGTGAT	012N23
Ep-mt- <i>ndhDH</i> _037D12	TCCAGCTTTGAGGAAGCAAT	TCAGCCCATGAGTCAGTGTC	037D12
Ep-mt-cp3_123E16	CGGTCACAAATTGGGAGAAT	CATCCTTCCCTTTTTCCACA	123E16
Ep-mt-circle2_162I22	TCACTGATGGATTTCGGTCAA	AGTCACTCTCGACGGGAGAA	162I22
Ep-mt-cp2_163A04	AGCCTTAGTGCACCAACCAC	TTAGGGCGAAACTGCCTATG	163A04
Ep-mt-circle1-175J16	GGACCGTCAACTCCAAGTGT	TGGATAGGAAGAGGCATTGG	175J16

Supplemental Figure S1. Gene maps of orchid chloroplast genomes.

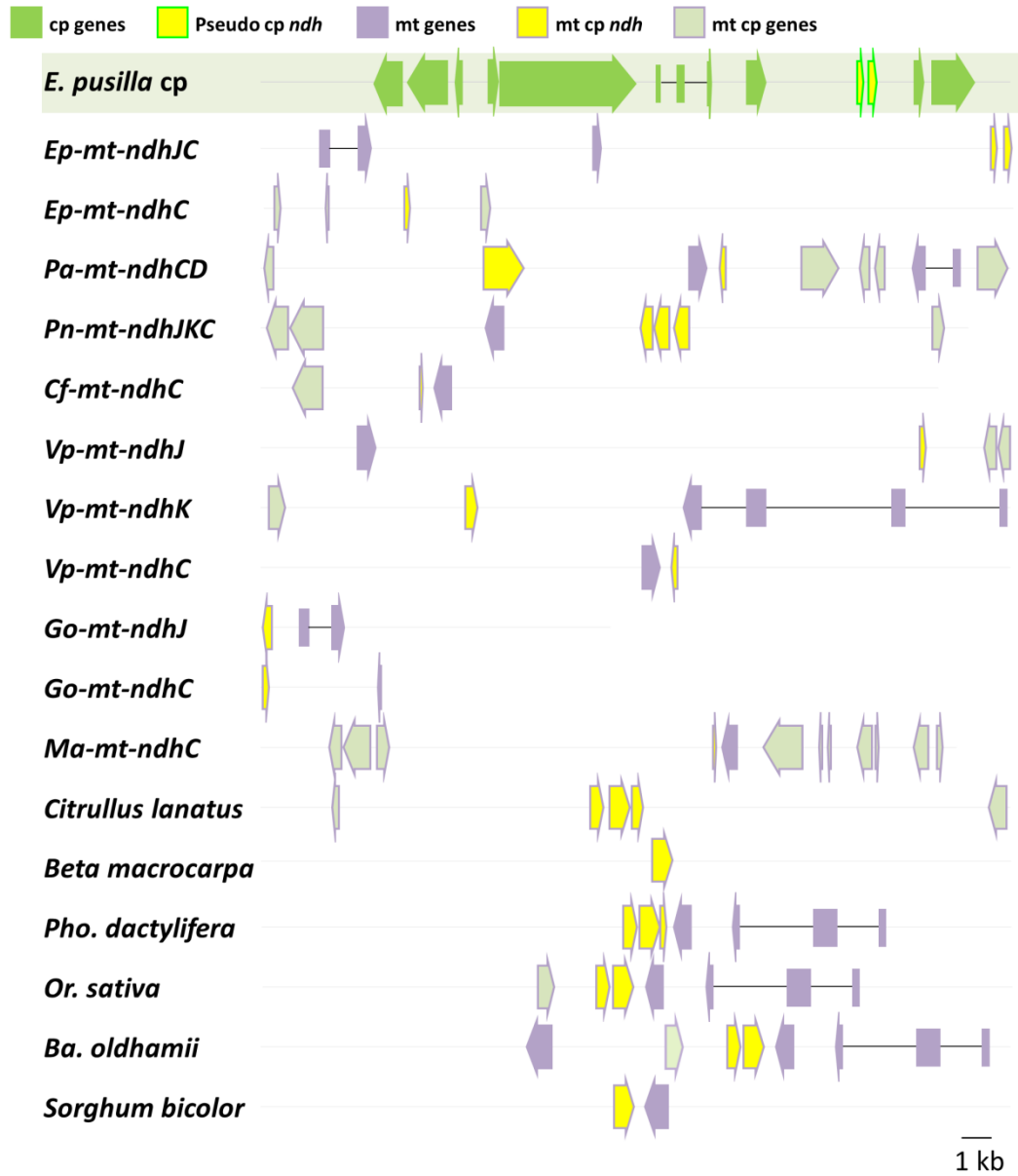
Genes on the outside of the map are transcribed clockwise whereas genes on the inside of the map are transcribed counterclockwise. Colors indicate genes with different functional groups. *Paphiopedilum niveum* and *Paphiopedilum armeniacum* have the same genome structure



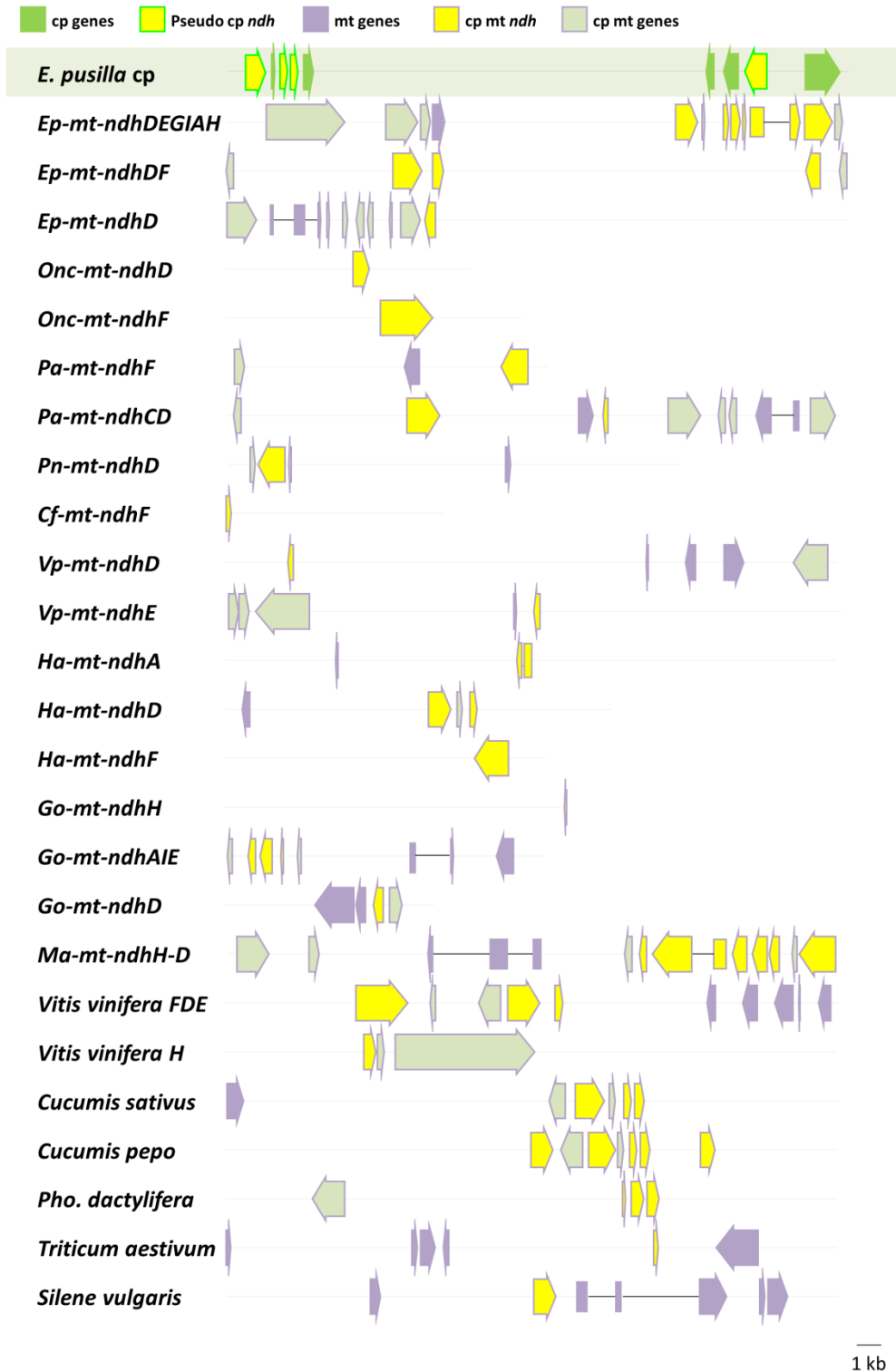




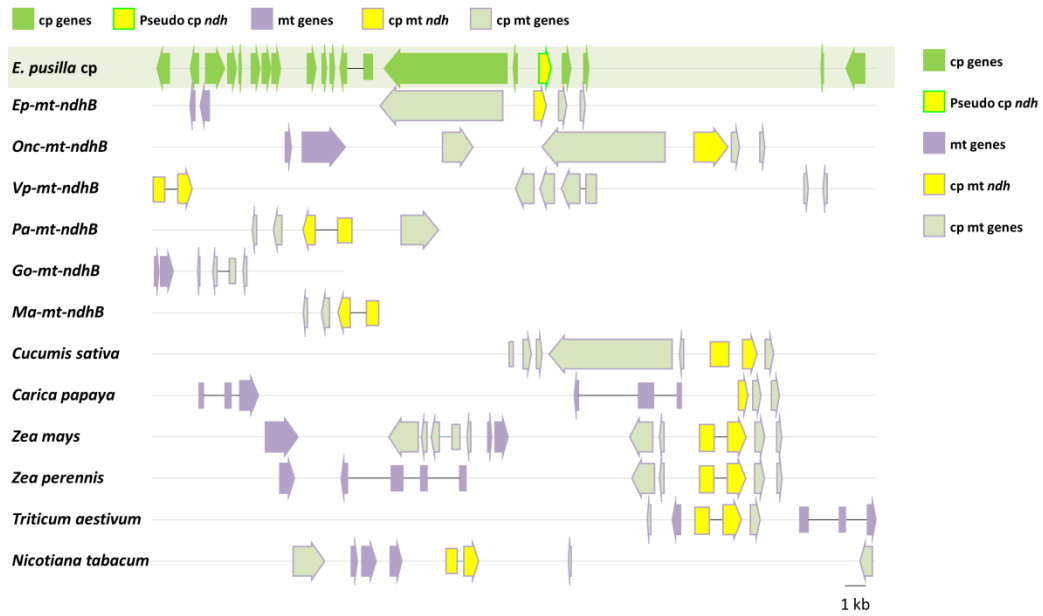
Supplementary Figure S2. The cp *ndhJ-K-C* genes were transferred to the plant mt genome. The boxes indicate the putative coding regions of the genes. The arrowheads indicate the direction of the genes. The accession no. of the sequences are listed in Supplementary Table S4.



Supplementary Figure S3. The cp *ndhF-D-E-G-I-A-H* region was transferred to the plant mt genome. The boxes indicate the putative coding regions of the genes. The arrowheads indicate the direction of the genes. The accession no. of the sequences are listed in Supplementary Table S4.



Supplementary Figure S4. The cp *ndhB* gene fragment was transferred to the plant mt genome. The boxes indicate the putative coding regions of the genes. The arrowheads indicate the direction of the genes. The accession no. of the sequences are listed in Supplementary Table S4.



Supplementary Figure S5. Flow chart of sequence annotation.

