Supplementary Material

Table S1. Summary of three plastome sequences.

Taxon	Length (bp)				GC Content (%)			
	LSC	**SSC**	**IR**	**Total**	**LSC**	**SSC**	**IR**	**Total**
Lilium candidum	81,481	17,644	26,488	152,101	34.9	30.6	42.5	37.0
Lilium formosanum	82,101	17,524	26,514	152,653	34.9	30.8	42.4	37.0
Lilium leichtlinii var. *maximowiczii*	82,037	17,583	26,492	152,604	34.8	30.7	42.5	37.0

Table S2. List of estimated species trees according to different options.

Data Set	Type	Tool	Method	Modeltest	Tree Names
All_loci (189)	Partitioned	RAxML	Maximum-likelihood analysis	PartitionFinder 2	ALL_part_RAxML
		IQ-TREE	Maximum-likelihood analysis	ModelFinder	ALL_part_iqtree
		MrBayes	Bayesian inference	PartitionFinder 2	ALL_part_mrbayes
	Non-partitioned	RAxML	Maximum-likelihood analysis	Jmodeltest 2	ALL_nonpart_RAxML
		IQ-TREE	Maximum-likelihood analysis	Jmodeltest 2	ALL_nonpart_iqtree
		MrBayes	Bayesian inference	Jmodeltest 2	ALL_nonpart_mrbayes
CDSs (78)	Partitioned	RAxML	Maximum-likelihood analysis	PartitionFinder 2	CDSs_part_RAxML
		IQ-TREE	Maximum-likelihood analysis	ModelFinder	CDSs_part_iqtree
		MrBayes	Bayesian inference	PartitionFinder 2	CDSs_part_mrbayes
	Non-partitioned	RAxML	Maximum-likelihood analysis	Jmodeltest 2	CDSs_nonpart_RAxML
		IQ-TREE	Maximum-likelihood analysis	Jmodeltest 2	CDSs_nonpart_iqtree
		MrBayes	Bayesian inference	Jmodeltest 2	CDSs_nonpart_mrbayes
IGSs (90)	Partitioned	RAxML	Maximum-likelihood analysis	PartitionFinder 2	IGSs_part_RAxML
		IQ-TREE	Maximum-likelihood analysis	ModelFinder	IGSs_part_iqtree
		MrBayes	Bayesian inference	PartitionFinder 2	IGSs_part_mrbayes
	Non-partitioned	RAxML	Maximum-likelihood analysis	Jmodeltest 2	IGSs_nonpart_RAxML
		IQ-TREE	Maximum-likelihood analysis	Jmodeltest 2	IGSs_nonpart_iqtree
		MrBayes	Bayesian inference	Jmodeltest 2	IGSs_nonpart_mrbayes
Introns	Partitioned	RAxML	Maximum-likelihood analysis	PartitionFinder 2	INTRONs_part_RAxML

(21)		IQ-TREE	Maximum-likelihood analysis	ModelFinder	INTRONs_part_iqtree
		MrBayes	Bayesian inference	PartitionFinder 2	INTRONs_part_mrbayes
	Non-partitioned	RAxML	Maximum-likelihood analysis	Jmodeltest 2	INTRONs_nonpart_RAxML
		IQ-TREE	Maximum-likelihood analysis	Jmodeltest 2	INTRONs_nonpart_iqtree
		MrBayes	Bayesian inference	Jmodeltest 2	INTRONs_nonpart_mrbayes

Estimated Species Trees Using Gene Trees by ASTRAL

Data	Tree Names
189 gene trees from CDSs, IGSs, and introns	ASTRAL_ALL
78 gene trees from CDSs	ASTRAL_CDSs
90 gene trees from IGSs	ASTRAL_IGSs
21 gene trees from introns	ASTRAL_INTRONs

Table S3. 189 loci used for phylogenetic analyses in this paper.

Data Set	Locus	Length	Data Set	Locus	Length	Data Set	Locus	Length
CDS[a]	*accD*	1584	CDS	*psaJ*	141	CDS	*rps4*	612
	atpA	1524		*psbA*	1062		*rps7*	468
	atpB	1503		*psbB*	1527		*rps8*	429
	atpE	408		*psbC*	1422		*rps11*	423
	atpF	570		*psbD*	1062		*rps12*	372
	atpH	246		*psbE*	252		*rps14*	303
	atpI	744		*psbF*	120		*rps15*	273
	ccsA	972		*psbH*	222		*rps16*	252
	cemA	702		*psbI*	111		*rps18*	306
	clpP	621		*psbJ*	123		*rps19*	279
	matK	1557		*psbK*	192		*ycf1*	5631
	ndhA	1095		*psbL*	117		*ycf2*	6798
	ndhB	1533		*psbM*	105		*ycf3*	513
	ndhC	363		*psbN*	132		*ycf4*	555
	ndhD	1510		*psbT*	102	IGS[b]	*accD-psaI*	1061
	ndhE	308		*psbZ*	189		*atpB-rbcL*	876
	ndhF	2308		*rbcL*	1443		*atpF-atpH*	582
	ndhG	547		*rpl2*	825		*atpH-atpI*	1098
	ndhH	1182		*rpl14*	369		*atpI-rps2*	301
	ndhI	543		*rpl16*	408		*ccsA-ndhD*	194
	ndhJ	477		*rpl20*	361		*cemA-petA*	261
	ndhK	791		*rpl22*	412		*clpP-psbB*	522
	petA	963		*rpl23*	282		*ndhB-rps7*	314
	petB	654		*rpl32*	195		*ndhC-trnV*	1121
	petD	504		*rpl33*	204		*ndhD-psaC*	143
	petG	114		*rpl36*	114		*ndhE-ndhG*	235
	petL	96		*rpoA*	1088		*ndhF-rpl32*	791
	petN	90		*rpoB*	3207		*ndhG-ndhI*	409
	psaA	2253		*rpoC1*	2079		*ndhH-rps15*	137
	psaB	2205		*rpoC2*	4227		*ndhJ-ndhK*	187
	psaC	246		*rps2*	711		*petA-psbJ*	921

psaI	105	*rps3*	657	*petB-petD*	216

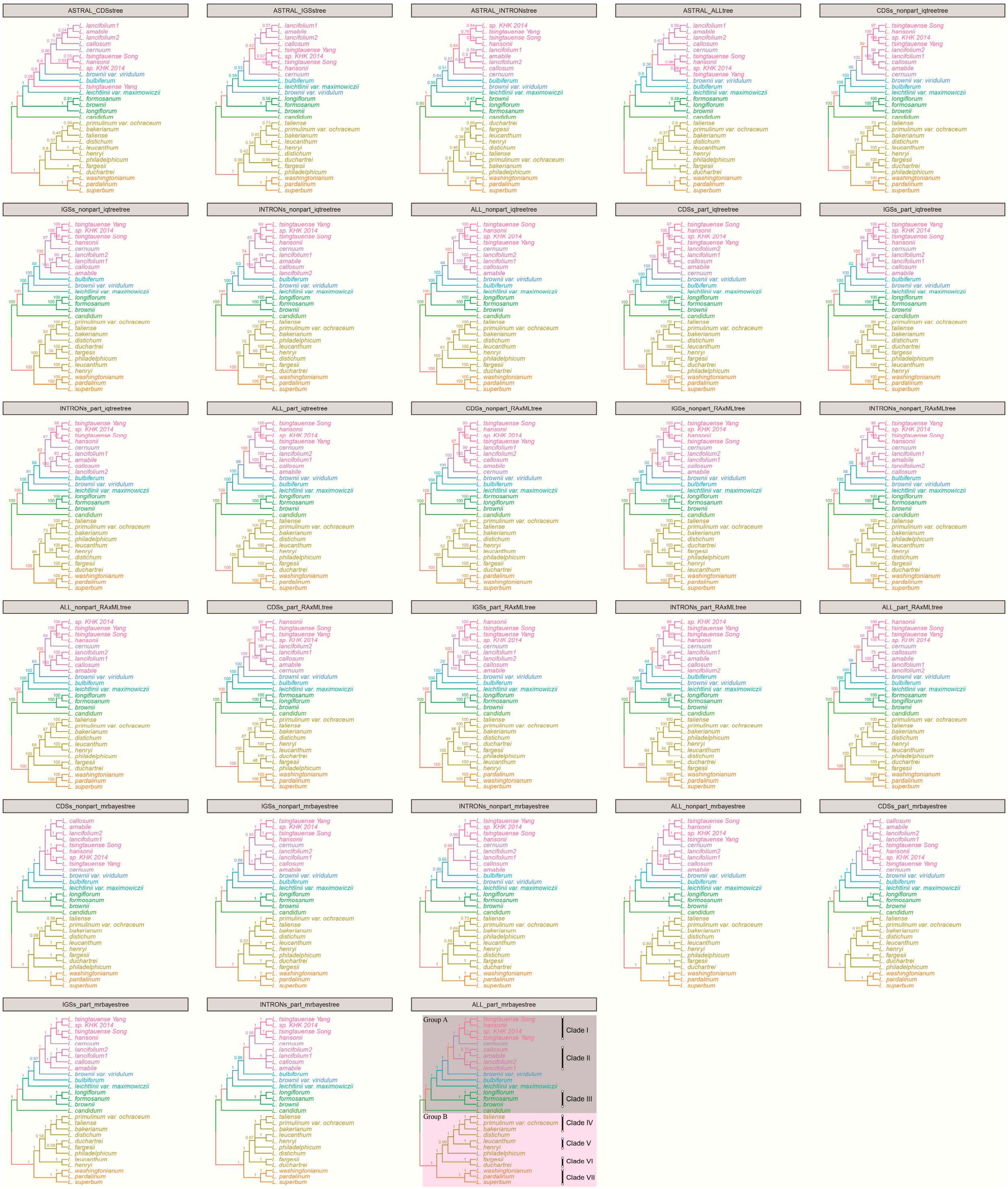
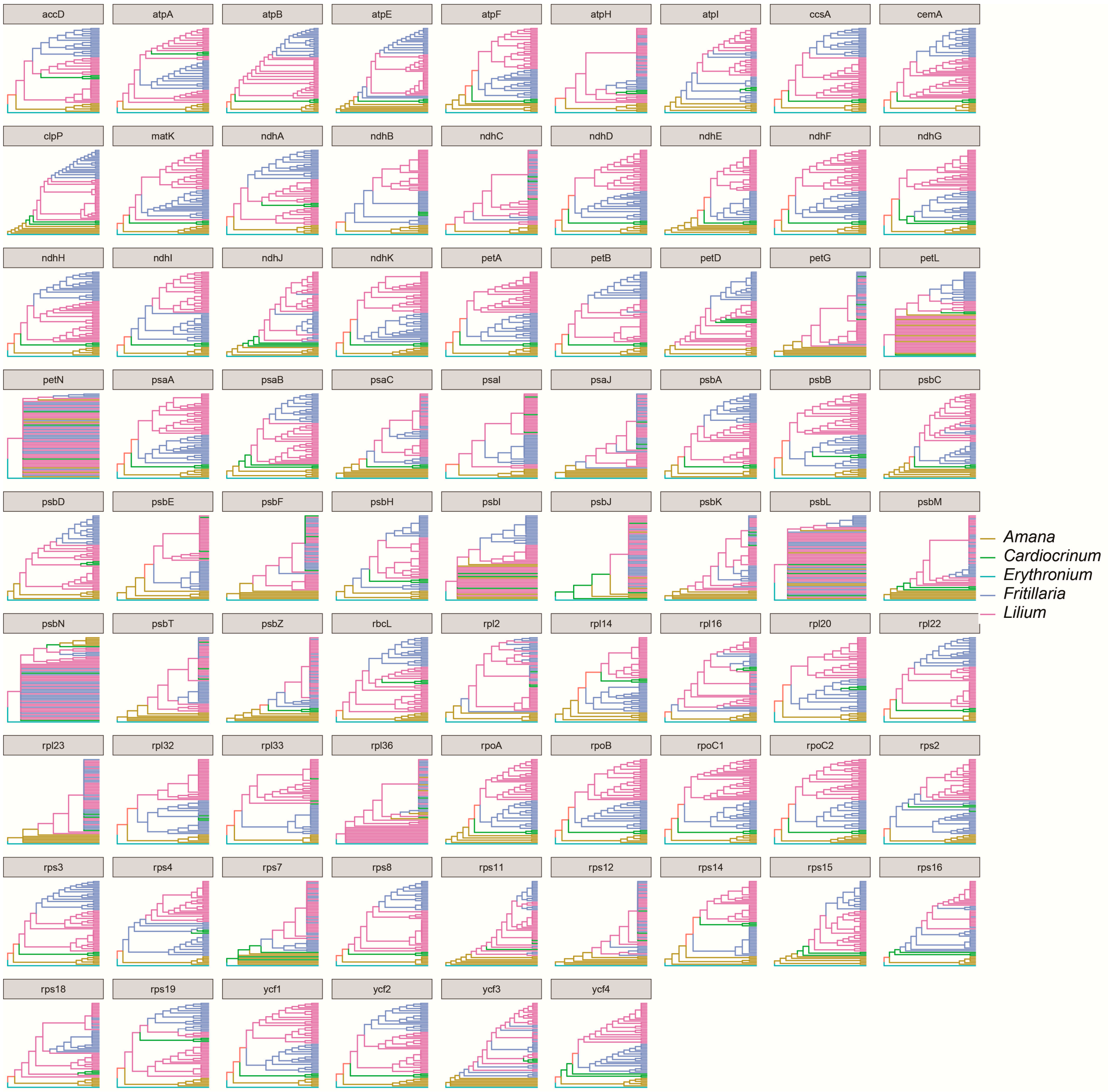

ASTRAL_CDSstree
ASTRAL_IGSstree
ASTRAL_INTRONstree
ASTRAL_ALLtree
CDSs_nonpart_iqtreetree
IGSs_nonpart_iqtreetree
INTRONs_nonpart_iqtreetree
ALL_nonpart_iqtreetree
CDSs_part_iqtreetree
IGSs_part_iqtreetree
INTRONs_part_iqtreetree
ALL_part_iqtreetree
CDSs_nonpart_RAxMLtree
IGSs_nonpart_RAxMLtree
INTRONs_nonpart_RAxMLtree
ALL_nonpart_RAxMLtree
CDSs_part_RAxMLtree
IGSs_part_RAxMLtree
INTRONs_part_RAxMLtree
ALL_part_RAxMLtree
CDSs_nonpart_mrbayestree
IGSs_nonpart_mrbayestree
INTRONs_nonpart_mrbayestree
ALL_nonpart_mrbayestree
CDSs_part_mrbayestree
IGSs_part_mrbayestree
INTRONs_part_mrbayestree
ALL_part_mrbayestree
Group A
Clade I
Clade II
Clade III
Group B
Clade IV
Clade V
Clade VI
Clade VII

Figure S1. A clade of *Lilium* species extracted from 28 species trees.


accD
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atpB
atpE
atpF
atpH
atpI
ccsA
cemA
clpP
matK
ndhA
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ndhD
ndhE
ndhF
ndhG
ndhH
ndhI
ndhJ
ndhK
petA
petB
petD
petG
petL
petN
psaA
psaB
psaC
psaI
psaJ
psbA
psbB
psbC
psbD
psbE
psbF
psbH
psbI
psbJ
psbK
psbL
psbM
psbN
psbT
psbZ
rbcL
rpl2
rpl14
rpl16
rpl20
rpl22
rpl23
rpl32
rpl33
rpl36
rpoA
rpoB
rpoC1
rpoC2
rps2
rps3
rps4
rps7
rps8
rps11
rps12
rps14
rps15
rps16
rps18
rps19
ycf1
ycf2
ycf3
ycf4
Amana
Cardiocrinum
Erythronium
Fritillaria
Lilium

Figure S2. Gene trees constructed using 78 coding regions. Coloured line refers to each genus.

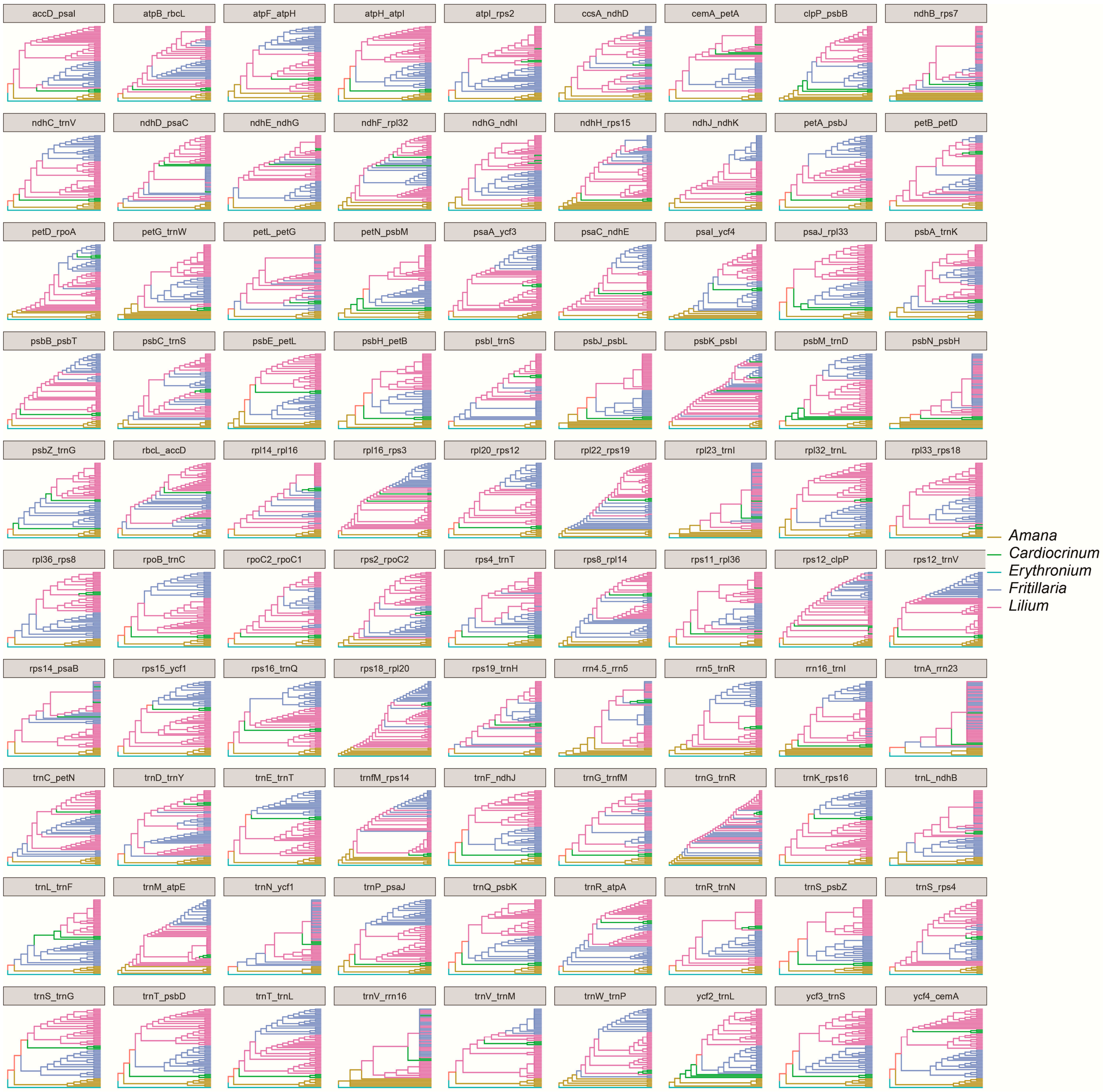
accD_psaI
atpB_rbcL
atpF_atpH
atpH_atpI
atpI_rps2
ccsA_ndhD
cemA_petA
clpP_psbB
ndhB_rps7
ndhC_trnV
ndhD_psaC
ndhE_ndhG
ndhF_rpl32
ndhG_ndhI
ndhH_rps15
ndhJ_ndhK
petA_psbJ
petB_petD
petD_rpoA
petG_trnW
petL_petG
petN_psbM
psaA_ycf3
psaC_ndhE
psaI_ycf4
psaJ_rpl33
psbA_trnK
psbB_psbT
psbC_trnS
psbE_petL
psbH_petB
psbI_trnS
psbJ_psbL
psbK_psbI
psbM_trnD
psbN_psbH
psbZ_trnG
rbcL_accD
rpl14_rpl16
rpl16_rps3
rpl20_rps12
rpl22_rps19
rpl23_trnI
rpl32_trnL
rpl33_rps18
rpl36_rps8
rpoB_trnC
rpoC2_rpoC1
rps2_rpoC2
rps4_trnT
rps8_rpl14
rps11_rpl36
rps12_clpP
rps12_trnV
rps14_psaB
rps15_ycf1
rps16_trnQ
rps18_rpl20
rps19_trnH
rrn4.5_rrn5
rrn5_trnR
rrn16_trnI
trnA_rrn23
trnC_petN
trnD_trnY
trnE_trnT
trnfM_rps14
trnF_ndhJ
trnG_trnfM
trnG_trnR
trnK_rps16
trnL_ndhB
trnL_trnF
trnM_atpE
trnN_ycf1
trnP_psaJ
trnQ_psbK
trnR_atpA
trnR_trnN
trnS_psbZ
trnS_rps4
trnS_trnG
trnT_psbD
trnT_trnL
trnV_rrn16
trnV_trnM
trnW_trnP
ycf2_trnL
ycf3_trnS
ycf4_cemA
Amana
Cardiocrinum
Erythronium
Fritillaria
Lilium

Figure S3. Gene trees constructed using 90 intergenic spacers. Coloured line refers to each genus.

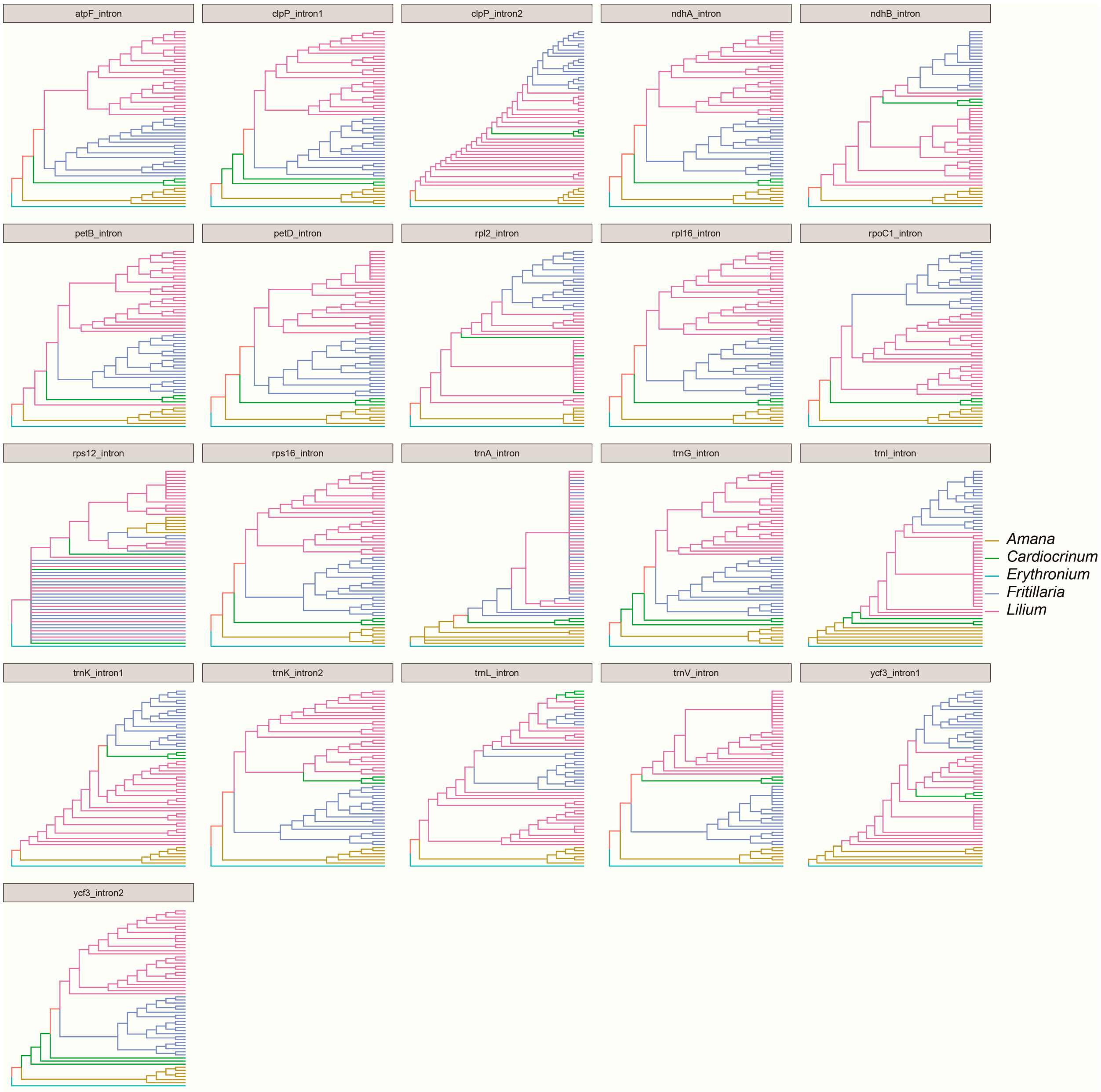
atpF_intron
clpP_intron1
clpP_intron2
ndhA_intron
ndhB_intron
petB_intron
petD_intron
rpl2_intron
rpl16_intron
rpoC1_intron
rps12_intron
rps16_intron
trnA_intron
trnG_intron
trnI_intron
trnK_intron1
trnK_intron2
trnL_intron
trnV_intron
ycf3_intron1
ycf3_intron2
Amana
Cardiocrinum
Erythronium
Fritillaria
Lilium

Figure S4. Gene trees were constructed using 21 introns. Coloured line refers to each genus.

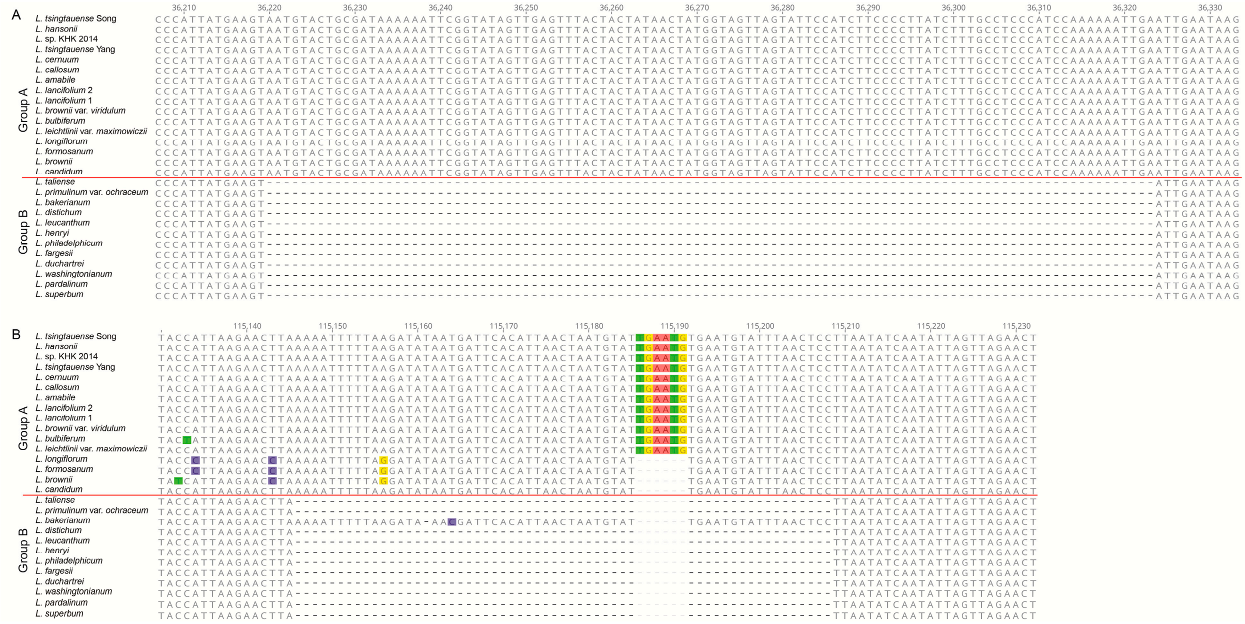
A
36,210
36,220
36,230
36,240
36,250
36,260
36,270
36,280
36,290
36,300
36,310
36,320
36,330
Group A
Group B
L. tsingtauense Song
L. hansonii
L. sp. KHK 2014
L. tsingtauense Yang
L. cernuum
L. callosum
L. amabile
L. lancifolium 2
L. lancifolium 1
L. brownii var. viridulum
L. bulbiferum
L. leichtlinii var. maximowiczii
L. longiflorum
L. formosanum
L. brownii
L. candidum
L. taliense
L. primulinum var. ochraceum
L. bakerianum
L. distichum
L. leucanthum
L. henryi
L. philadelphicum
L. fargesii
L. duchartrei
L. washingtonianum
L. pardalinum
L. superbum
B
115,140
115,150
115,160
115,170
115,180
115,190
115,200
115,210
115,220
115,230

Figure S5. Large indertions/deletions occurring at least five species with longer than 50 bp. Red line distinguishes between two groups.