New Phytologist Supporting Information
Methods S1, Notes S1, Figs. S1 – S11, and Tables S1 – S13

Article title: Resolving the backbone of the Brassicaceae phylogeny for investigating trait diversity

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Methods S1 – Supplementary Materials and Methods

Plant Material. A total of 63 species with 65 accessions used in this study are listed in Table S1. Fresh flash-frozen, silica-gel dried, or herbarium material were used for DNA extraction using PowerPlant Pro DNA Isolation Kit (QIAgen Inc., Hilden, Germany). Three DNA samples were obtained from the Kew DNA collection (http://apps.kew.org/dnabank/introduction.html). DNA samples with visible impurities (green or brown tint, and/or flocculate) were additionally purified using QIAquick MinElute columns (QIAgen Inc., Hilden, Germany). For *Turritis glabra* L., total RNA was extracted from gibberellic acid (GA_3)–treated seedlings grown under short day conditions using RNeasy Mini Kit (Qiagen, Hilden, Germany). For comparative transcriptomics, eight species with contrasting leaf morphologies (simple leaves – *Aethionema arabicum*, *Arabis alpina*, *Arabidopsis thaliana*, *Boechera stricta*, and complex leaves – *Sisymbrium irio*, *Arabidopsis lyrata*, *Cardamine hirsuta*, *Capsella rubella*) were grown under short day conditions (8 h light (20C)/16 h dark (16C) cycle) in a growth chamber with humidity control. A triplicate of ~30 developing leaves (nodes 5 and 6) in an organogenetic stage (100 µm – 500 µm, depending on the species; one leaf per plant) were manually dissected between 10 am and 12 pm, and total RNA was extracted using RNeasy Plus Micro Kit (Qiagen, Hilden, Germany).

Library Preparation and Sequencing. Each DNA sample was sheared and selected to modal lengths of ~275 bp using a dual-step SPRI bead cleanup. Illumina sequencing libraries were prepared with the NEBNext Fast DNA Library Prep Kit (New England Biolabs, Ipswich, Massachusetts, USA), and amplified using KAPA HiFi HotStart ReadyMix (Kapa Biosystems, Wilmington, Massachusetts, USA) for 6 cycles using the manufacturer's recommended thermal profile and dual P7 and P5 indexing primers (see Kircher *et al*., 2012 for primer configurations). After SPRI bead purification, 500 ng of each library were enriched using the MYbaits-2 Target Enrichment system (MYcroarray, Ann Arbor, Michigan, USA) following manual version 3.0. Bead-bound libraries were additionally amplified for 12 cycles using universal P5/P7 primers, purified, and combined equimolarly to 1 ng/μL for sequencing. 2 x 75 paired end reads were generated on GAIIx (Illumina, San Diego, California, USA) in two separate runs at the Cologne Center for Genomics at the University of Cologne, and the raw reads have been deposited at the National Center for Biotechnology Information (NCBI) Sequence Read Archive (Bioproject PRJNA518905).

Transcriptome libraries were prepared after mRNA enrichment with NEBNext Poly(A) mRNA Magnetic Isolation Module (New England Biolabs, Ipswich, Massachusetts, USA) with NEBNext Ultra™ Directional RNA Library Prep Kit (New England Biolabs, Ipswich, Massachusetts, USA) for Illumina. Libraries were sequenced on HiSeq3000 (Illumina, San Diego, California, USA) as 2 x 150 paired end runs at the Genome Center of the Max Planck Institute for Plant Breeding Research, Cologne, Germany, and raw reads have been deposited at the NCBI Sequence Read Archive (Bioproject PRJNA518905).

Obtaining corresponding exons from sequenced genomes. To complement our *de novo* derived sequences, we included publicly available genome data from 16 Brassicaceae species and two outgroups (Table S2). Their genomes were queried with the exon sets for each of the three reference species using translated BLAT alignment (highest scoring hit was retained if the number of called positions divided by the size of the reference exons was greater than 40%). The target exons derived from each of the three references were oriented and consensus was called after alignment with MAFFT 6.851b (Katoh *et al*., 2002); non-overlapping fragments recovered from the different references were discarded. This resulted in 1748 shared exons (out of 1827 target Brassicaceae exons) with the immediate outgroup *Tarrenaya hassleriana* and 1101 shared exons with the more distantly related outgroup *Carica papaya*. Plastid-coding sequences were obtained from sequenced plastomes (Table S3) following the same protocol.

Notes S1

Tree description– Consistent with previous analyses (Beilstein *et al*., 2006; Huang *et al.*, 2015), *Aethionema* (Aethionemeae) is sister to the rest of Brassicaceae. Following *Aethionema*, the next branching event in the phylogeny separates representatives of the traditionally recognized Lineage III (clade E, Huang *et al.*, 2015) from the rest, with placement and composition universally supported across all nuclear datasets and analyses. Within Lineage III, the basal split included the sister taxa *Dontostemon integrifolius* (Dontostemoneae) and *Chorispora tenella* (Chorisporeae) and their sister clade was composed of a grade of *Hesperis matronalis* (Hesperideae), *Neotorularia torulosa* (Euclidieae), *Bunias orientalis* (Buniadeae), and *Matthiola incana* (Anchonieae) + the unassigned to a tribe *Veselskya griffithiana*. The placements of *Hesperis matronalis* and *Neotorularia torulosa* alternated in the plastid phylogeny (Fig. S9), as reported in Mandáková et al., 2017.

The next Brassicaceae clade, which we call Lineage IV (clade D, Huang *et al.*, 2015), is universally supported in all nuclear datasets and analyses, and consists of *Arabis alpina* (Arabideae) + *Pseudoturritis turrita* (Stevenieae), which are sisters to *Aurinia saxatilis* (Alysseae) + the unassigned to a tribe *Asperuginoides axillaris*. This clade includes the first (Arabideae) and the third (Alysseae) largest tribes in the family, harbors one-fifth of the family's species diversity, and has a center of diversity in the Mediterranean and the Irano-Turanian regions (Karl & Koch, 2013; Rešetnik *et al*., 2013).

The next clade consists of representatives of the traditionally recognized Lineage I (clade A excluding *Macropodium* in Huang *et al.*, 2015). Biscutelleae (Özüdoğru *et al.*, 2017), which included *Biscutella laevigata* sister to *Heldreichia bupleurifolia* and *Lunaria rediviva* sister to *Ricotia cretica*, were strongly supported and tentatively placed as sister to Lineage I in the maximum likelihood analyses after removing genes that contribute disproportionately to the phylogenetic signal. The earliest split in Lineage I includes (1) Cardamineae (*Cardamine hirsuta*, *Leavenworthia alabamica*, and the unassigned to a tribe *Andrzeiowskia cardamine*), followed by (2) Lepidieae (*Lepidium hirtum* and *Lepidium meyenii*), (3) a clade consisting of *Descurainia artemisioides* (Descurainieae) sister to *Yinshania acutangula* (Yinshanieae) + *Smelowskia calycina* (Smelowskieae), (4) a clade of *Erysimum cheiri* (Erysimeae) + *Malcolmia maritima* (Malcolmieae), (5) the *Arabidopsis* segregate of Camelineae, (6) *Physaria purpurea* (Physarieae), (7) a clade of *Murbeckiella* *pinnatifida* (Oreophytoneae) sister to *Turritis glabra* (Turritideae) + *Alyssopsis mollis* (Alyssopsideae), followed by (8) *Capsella rubella* and *Camelina sativa* (both Camelineae), (9) *Geococcus pusillus* (Microlepidieae) + the unassigned to a tribe *Hemilophia rockii* and *Dipoma iberideum*, and (10) *Boechera stricta* (Boechereae), *Halimolobos pubens* (Halimolobeae), and *Crucihimalaya himalaica* (Crucihimalayeae). The support for this branching order was robust among analyses, with the notable conflict for the relationship among the last three clades between coalescent and concatenation analyses. We confirm the polyphyly of Camelineae based on nuclear markers (Bailey *et al.*, 2006; Beilstein *et al.*, 2006), as well as the close relationship between *Malcolmia maritima* and *Erysimum cheiri* (Moazzeni *et al.*, 2014). In contrast to prior conflicting positions for Lepidieae (Kagale *et al.*, 2014; Huang *et al.*, 2015), our placement immediately after the divergence of Cardamineae is robust and universally supported in all nuclear analyses. *Lepidium* position only became unstable after removing data from our most exclusive dataset (not shown).

Another major clade of Brassicaceae includes relatives of the traditionally recognized Lineage II and some members of the 'expanded' Lineage II, which is sister to a clade consisting of *Megacarpaea* spp. (Megacarpaeeae) and *Lobularia maritima* (Anastaticeae) + *Cochlearia officinalis* (Cochlearieae) + *Iberis linifolia* (Iberideae). This resolution is supported in the maximum likelihood analyses after excluding genes that contribute disproportionally to the phylogenetic signal but unstable in the taxon-pruning experiments. The position of *Cochlearia officinalis* differs among the maximum likelihood analyses; however, it is resolved as a successive sister to *Kernera saxatilis* + *Petrocallis pyrenaica* preceding the *Conringia* clade in all ASTRAL-II analyses. The branching order of Lineage II includes a grade of (1) *Aphragmus bouffordii* (Aphragmeae), (2) *Kernera saxatilis* (Kernereae) + the unassigned to a tribe *Petrocallis pyrenaica*, (3) the *Conringia* clade, consisting of *Conringia orientalis* (Conringieae) + *Noccaea vesicaria* (Coluteocarpeae) + the unassigned to a tribe *Arabis ottonis-schulzii*, (4) *Calepina irregularis* (Calepineae), (5) a clade including *Eutrema salsugineum* (Eutremeae) sister to *Peltaria alliacea* + *Thlaspi arvense* (both Thlaspideae) and *Camelinopsis campylopoda*, (6) the unassigned to a tribe *Schrenkiella parvula*, (7) a clade consisting of *Bivonaea lutea* (Bivonaeeae) sister to the unassigned to a tribe taxa *Arabis josiae* + *Fourrea alpina*, (8) *Brassica* spp. (Brassiceae), (9) *Isatis tinctoria* (Isatideae) + the unassigned to a tribe

Conringia planisiliqua, (10) *Stanleya elata* (Thelypodieae) and the unassigned to a tribe *Raphanorhyncha crassa*, and (11) *Sisymbrium irio* (Sisymbrieae) sister to *Pseudofortuynia esfandiarii* and the unassigned to a tribe *Ochthodium aegyptiacum*. Many of these relationships are recovered in the plastid phylogeny, which also removes *Orychophragmus* spp., a taxon not sampled for nuclear markers, from other Brassiceae. Applying our phylogenomic approach at the infratribal level will help identify such divergent lineages in other tribes and is an obvious next step towards describing the global diversity of Brassicaceae.

Our results strongly support a novel clade, Lineage V, which includes 179 species in 21 genera primarily distributed in the Southern Hemisphere. The four exceptions are *Idahoa scapigera* (North America), *Asta shaffneri* and *Scoliaxon mexicanus* (Mexico), and *Subularia aquatica* (northern North American and northern Eurasia). This lineage includes two monophyletic sister groups, (1) the New Zealand *Notothlaspi australe* (Notothlaspideae) sister to the South African *Heliophila coronopifolia* (Heliophileae) + the unassigned to a tribe *Chamira circaeoides* and (2) the Mexican clade *Asta shaffneri* (Asteae) + *Scoliaxon mexicanus* (Scoliaxoneae) and sister to the South American CES clade (Salariato *et al*., 2016) *Bryopsis diapensioides* (Eudemeae) + (*Cremolobus peruvianus* (Cremolobeae) + *Schizopetalon walkeri* (Schizopetaleae)). The second lineage also includes the unassigned to a tribe *Subularia aquatica* and *Idahoa scapigera*, which are sometimes placed together as sisters to the rest in the maximum likelihood trees. Although the circumboreal distribution of *S. aquatica* appears exceptional in this clade, its sister species, *Subularia monticola*, is distributed in the highest elevation habitats of Africa, the Ethiopian highlands and Mount Kilimanjaro in Tanzania, and may represent the ancestral range of the genus. All species in Lineage V have exclusively simple trichomes or are glabrous (except Schizopetaleae and *Scoliaxon*, which feature dendritic trichomes). All have dehiscent fruits except four species of *Heliophila*, within which indehiscent fruits evolved three times. None has auriculate leaves except for two species of *Heliophila*, within which this feature evolved once. None of the species has leaves dissected into leaflets, though entire, dentate, and deeply pinnately (but not palmately) divided leaves are present. *Asta* and *Scoliaxon* in the Mexican clade share a unique feature not found in the other ca. 4000 species of Brassicaceae, the presence of large, ovate, white gland pairs at leaf and sometimes pedicel base. Because both genera form a strongly supported clade in all analyses, the tribe Scoliaxoneae should be united with the earlier-published Asteae.

Placing taxa unassigned to a tribe– Our sampling of Brassicaceae lineages allows confirming previously suggested relationships and associating unassigned to a tribe orphan taxa with related clades or tribes. The divergent positions of *Schrenkiella parvula*, *Subularia aquatica* (and likely *S. monticola*), and *Idahoa scapigera* justify the erection of new tribes, and the name Subularieae is available; new tribal names should be proposed for *Idahoa* and *Schrenkiella* (Table S9). New tribes can be proposed for *Dipoma iberideum* + *Hemilophia rockii* and *Arabis josiae* + *Fourrea alpina*, which are consistently recovered as sister taxa. *Petrocallis pyrenaica* can be included in Kernereae. In other cases, additional sampling of the closest relatives of unassigned to a tribe taxa may provide resolution. More exhaustively sampled *Sisymbrium* is needed to establish its boundaries with respect to *Pseudofortuynia esfandiarii* and *Ochthodium aegyptiacum* (Khosravi *et al*., 2009). Recent taxonomic work in the group proposed an expanded concept for *Sisymbrium* and synonymization of *Pseudofortuynia esfandiarii* with *Sisymbrium leucocladum* (German & Al-Shehbaz, 2018), raising interesting questions about the fruit evolution in this group. Broader sampling in Coluteocarpeae is similalry needed to confirm the sister position of *Arabis ottonis-schultzii*. Although *Chamira circaeoides* appears sister to *Heliophila cornopifolia* in our analyses and has been previously chosen as an outgroup in infratribal phylogenies of Heliophileae (Mandáková *et al*., 2012), broader sampling within *Heliophila*, an exceptionally diverse genus, is necessary to test whether *Chamira* could be nested within *Heliophila* or placed as a distinct genus in the same tribe.

To test whether some of the newly placed taxa fell outside of the variation of their sister tribes, we reconstructed the phylogenies of the respective tribes using broader taxon sampling (Fig. S11, Table S8). *Asperuginioides axillaris* falls outside of the molecular variation of the tribe Alysseae (Rešetnik *et al*., 2013) based on the plastid marker *ndhF* and additional taxon sampling in this part of the tree is necessary to determine its placement. *Vesselskya griffithiana* is placed as sister to Anchoneae with *rbcL*, although critical taxa (e.g., *Iskandera* spp.; Warwick *et al*., 2007) were not sampled. *Andrzeiowskia cardamine* belongs to Cardamineae and is sister to *Barbarea verna* (in the plastid phylogeny) or *Leavenworthia alabamica* (in the nuclear dataset). *Raphanorhyncha crassa*, which is only known from its type specimen (Al-Shehbaz, 2012), is placed within

Thelypodieae but its placement is not firmly resolved with the molecular marker *ndhF*. Based on the high degree of sequence polymorphism we observed, it is likely of hybrid origin. *Conringia planisiliqua* does not belong to Conringieae but is instead a member of Isatideae in the clade of *Isatis tinctoria*, a finding supported on morphological grounds (except fruit type). *Camelinopsis campylopoda* (now *Pseudocamelina campylopoda*) is firmly placed within Thlaspideae and most closely related to *Thalspi arvense* based on *ndhF*, a finding recently reported by Esmailbegi *et al.*, 2017; Esmailbegi *et al.*, 2018.

Supplementary References

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Supplementary Figure Legends

Figure S1. Phylogenetic reconstruction workflow.

Figure S2. Plastid coding sequences and sequenced plastid genomes obtained from skimming. **a**, Coverage among species. Complete plastid genomes were assembled for several species; maps for three of these (asterisks) are shown below. Note that *rps16* (yellow bar) has been lost in *Subularia aquatica*. **b**, Annotated plastid genome maps for *Arabis ottonis-schulzii, Pseudofortuynia esfandiarii* , and *Subularia aquatica* .

Figure S3. Density plots of metrics used to partition the exon set into 27 datasets after excluding the extreme outliers for each metric (grey shading in **a**, **c**, and **d**). **a**, Long-branch (*LB*) attraction score, *LB* upper quartile. Exons with *LB* score >60 were excluded, the rest were partitioned into three increasingly exclusive sets, L1, L2, and L3, with cutoffs 60, 45, and 37. **b**, Heat map of LB attraction score of exons across taxa. Species and exons with a higher score (shades of green) are prone to long-branch attraction. **c**, Exon-specific saturation score (*S*), saturation R^2. Exons with *S* score <0.6 were excluded, the rest were partitioned into three increasingly exclusive sets, S1, S2, and S3, with cutoffs 0.6, 0.7, and 0.85. **d**, Tree distances measured as 'matching splits' (*MS*). Exons with *MS* score>250 were excluded, the rest were partitioned into three increasingly exclusive sets, M1, M2, and M3, with cutoffs 250, 190, and 120. The inset depicts the tree space used to derive the tree distances.

Figure S4. Summary of the concatenation results represented by the tree space of the eight unique topologies (circles) from the maximum likelihood analysis, and the

topological differences among them. The summary tree on top is derived from the most inclusive dataset, *S1L1M1*, and color-coding marks the branches on the tree that are alternatively resolved with the other datasets. The tree space is divided into two areas (blue dotted line) based on the position of *Idahoa* and *Subularia* with respect to the Mexican (*Asta* + *Scoliaxon*) + CES (*Cremolobus* + *Schizopetalon* + *Brayopsis*) clade. It is further divided into two areas (orange dotted line) based on the position of the Biscutelleae + (*Lobularia* + *Iberis*) clade as sister to either *Megacarpaea* or Lineage I.

Figure S5. Phylogenetic informativeness of the loci from the most inclusive datasets that produced unique topologies (*S1L1M1*, *S1L1M3*, *S1L2M2*, *S1L3M1*, *S1L3M3*, *S2L2M1*, *S3L1M1*, *S3L3M1*). Exons with phylogenetic informativeness >10 deemed strong contributors were excluded from the subsequent concatenation analyses.

Figure S6. Summary of the concatenation results after excluding exons with phylogenetic informativeness score >10. a, The summary tree in the upper left corner is derived from the most inclusive dataset, *S1L1M1R*, and color-coding marks the branches on the tree that are alternatively resolved with the other datasets. **b**, Tree distances derived from the maximum likelihood analyses before (blue) and after (yellow) exclusion of the strong contributors from the phylogenetic informativeness test mapped onto two parallel planes.

Figure S7. Pruning of taxa with unstable placement in different datasets and analyses. Relationships among *Aethionema*, Lineage III and Lineage IV did not vary among datasets and analyses and these are not represented. **a**, Excluding *Idahoa scapigera*. **b**, Excluding *Subularia aquatica*. **c**, Excluding *Cochlearia officinalis*. **d**, Excluding *Megacarpaea* spp. **e**, Excluding *Lobularia maritima*. **f**, Excluding *Iberis linifolia*.

Figure S8. Summary of the ASTRAL-II results represented by the tree space of the seven unique topologies (circles), and the differences among them. The summary tree on top is derived from the most inclusive dataset, *S1L1M1*, and color-coding marks the branches on the tree that are alternatively resolved with the other datasets.

Figure S9. Placing unassigned to a tribe species with expanded taxon sampling of associated sister tribes. a, *Asperuginoides axillaris*. **b**, *Raphanorhyncha crassa*. **c**, *Veselskya griffithiana*. **d**, *Camelinopsis campylopoda*. **e**, *Conringia planisiliqua*.

Figure S10. Plastid coding gene phylogeny (same tree depicted without and with branch transformation). Bootstrap support is 100 unless indicated otherwise.

Figure S11. Comparison between tree topologies derived from nuclear and plastid loci. Unmatched taxa between the two datasets are excluded, and multispecies genera (except *Arabis* spp. and *Conringia* spp.) are trimmed to a single species.

Supplementary Tables

Table S1. Taxon and voucher information for species with newly generated sequence data.

Table S2. Accession information for species with sequenced nuclear genomes included in this study.

Table S3. Accession information for species with sequenced plastid genomes.

Table S4. Sequencing reads and contig statistics for nuclear loci.

Table S5. Skimmed reads and whole plastome statistics.

Table S6. Concatenated dataset statistics.

Table S7. AU tests to evaluate the support of a given matrix for a given topology. Values of support are color coded, with highest support in blue and lowest support in red. Note that many of the unique topologies are indistinguishable based on the data.

Table S8. Accession information of marker genes used for the infratribal placement of unassigned to a tribe taxa.

Table S9. Summary of the phylogenetic placement of unassigned to a tribe taxa and taxonomic notes.

Table S10. Transcriptome assembly statistics.

Table S11. Genes that deviate from the background optimal expression value in the family in the core Brassicaceae.

Table S12. Genes that deviate from the background optimal expression value in the family along the branches leading to species with complex leaves.

Table S13. Genes and protein residues under positive selection in species with complex leaves.

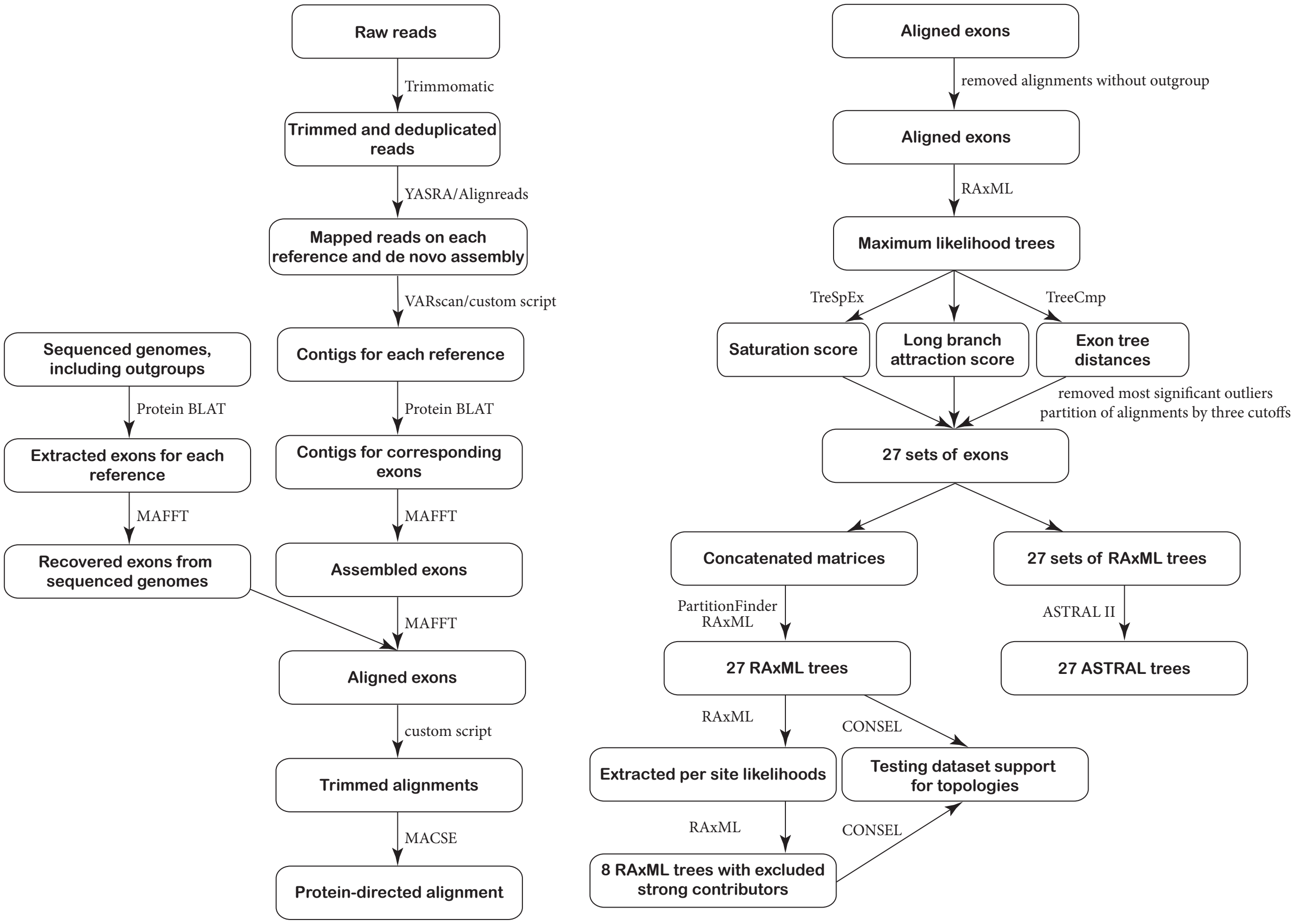
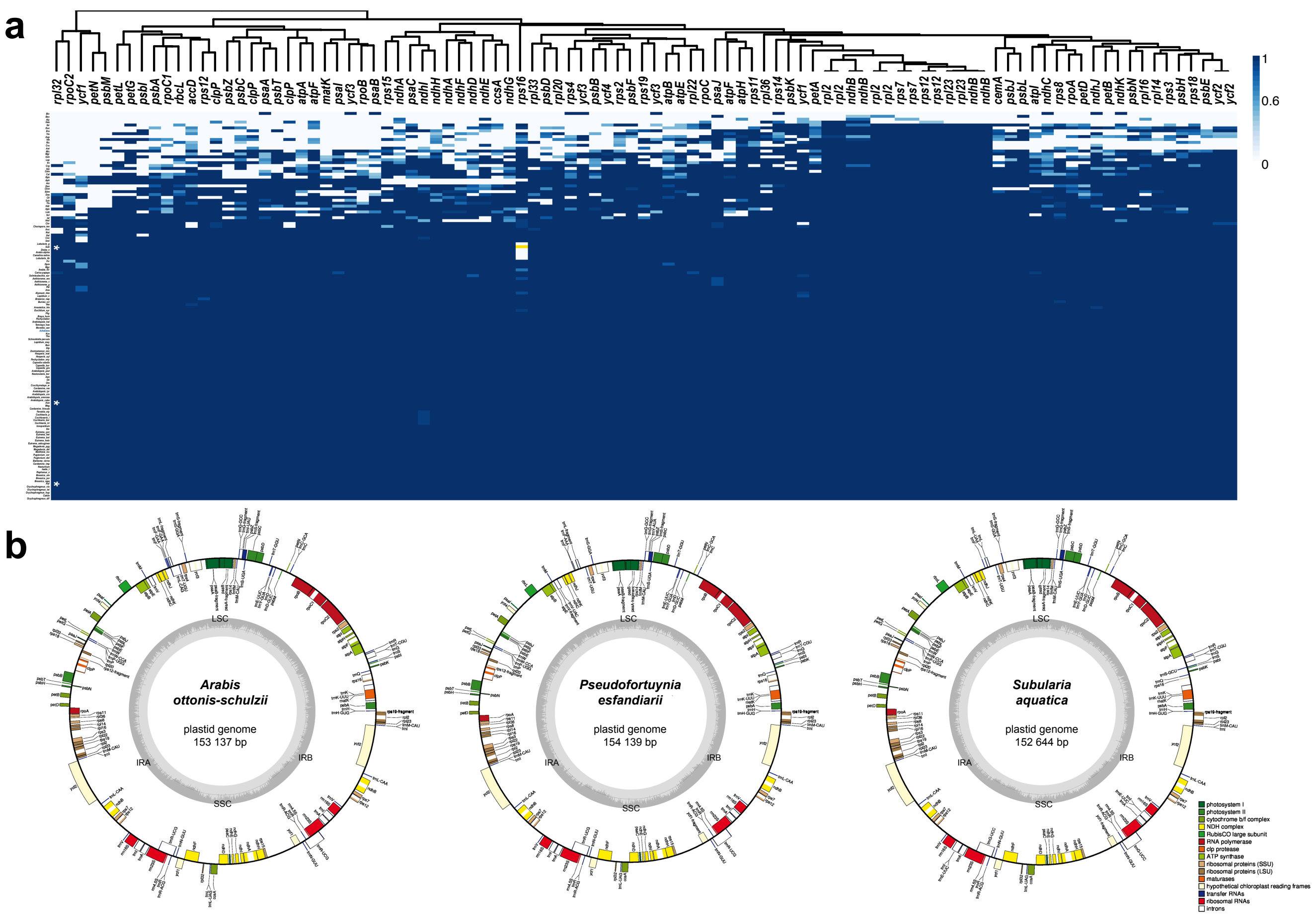


Figure S1. Phylogenetic reconstruction workflow.



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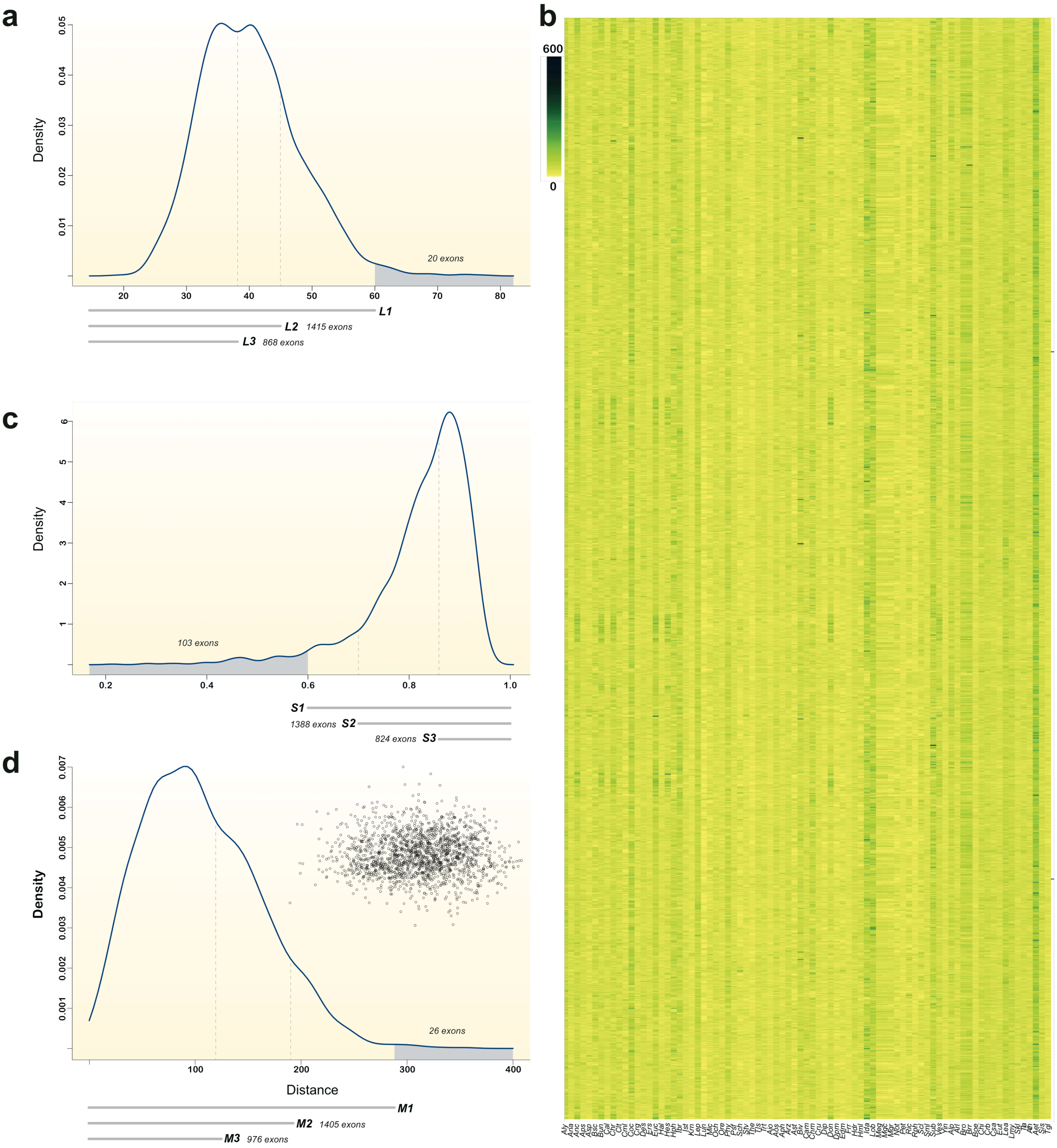a
Density
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L2 1415 exons
L3 868 exons
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600
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Aly
Ana
Anc
Aps
Asp
Bsc
Bun
Cal
Chr
Clt
Cml
Coc
Crg
Des
Ers
Euc
Hal
Hes
Hph
Ibr
Ist
Krn
Lep
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Ore
Phy
Psf
Sch
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Biv
Cam
Chm
Cru
Dip
Don
Dpm
Edm
Frr
Hdr
Hml
Ida
Lob
Meg
Mgc
Mgr
Not
Pet
Ric
Rph
Scl
Sml
Sub
Ves
Yin
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Bro
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Boe
Chi
Crb
Csa
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Lea
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c
Density
6
5
4
3
2
1
0.2
0.4
0.6
0.8
1.0
103 exons
S1
1388 exons S2
824 exons S3
d
Density
0.007
0.006
0.005
0.004
0.003
0.002
0.001
100
200
300
400
26 exons
Distance
M1
M2 1405 exons
M3 976 exons

Figure S3. Density plots of metrics used to partition the exon set into 27 datasets after excluding the extreme outliers for each metric (grey shading in **a**, **c**, and **d**). **a**, Long-branch (*LB*) attraction score, *LB* upper quartile. Exons with *LB* score >60 were excluded, the rest were partitioned into three increasingly exclusive sets, L1, L2, and L3, with cutoffs 60, 45, and 37. **b**, Heat map of LB attraction score of exons across taxa. Species and exons with a higher score (shades of green) are prone to long-branch attraction. **c**, Exon-specific saturation score (*S*), saturation R^2. Exons with *S* score <0.6 were excluded, the rest were partitioned into three increasingly exclusive sets, S1, S2, and S3, with cutoffs 0.6, 0.7, and 0.85. **d**, Tree distances measured as 'matching splits' (*MS*). Exons with *MS* score>250 were excluded, the rest were partitioned into three increasingly exclusive sets, M1, M2, and M3, with cutoffs 250, 190, and 120. The inset depicts the tree space used to derive the tree distances.

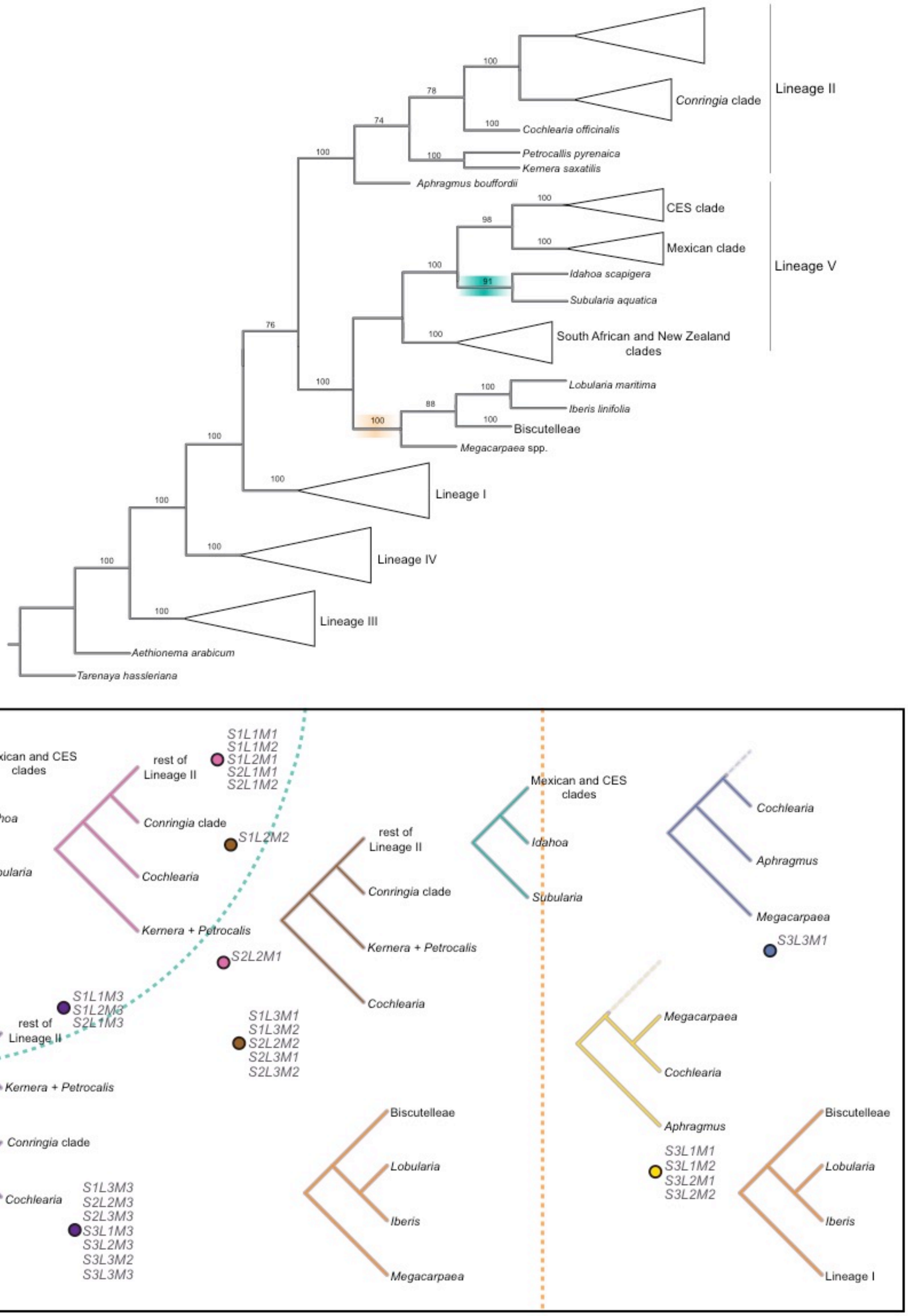

100
78
74
100
100
100
Cochlearia officinalis
Conringia clade
Lineage II
Petrocallis pyrenaica
Kernera saxatilis
Aphragmus bouffordii
100
CES clade
98
100
Mexican clade
Lineage V
100
91
Idahoa scapigera
Subularia aquatica
76
100
South African and New Zealand clades
100
100
Lobularia maritima
88
Iberis linifolia
100
100
Biscutelleae
Megacarpaea spp.
100
100
Lineage I
100
100
Lineage IV
100
100
Lineage III
Aethionema arabicum
Tarenaya hassleriana
Mexican and CES clades
Idahoa
Subularia
rest of Lineage II
Conringia clade
Cochlearia
Kernera + Petrocalis
S1L1M1
S1L1M2
S1L2M1
S2L1M1
S2L1M2
S1L2M2
S2L2M1
rest of Lineage II
Conringia clade
Kernera + Petrocalis
Cochlearia
S1L1M3
S1L2M3
S2L1M3
rest of Lineage II
Kernera + Petrocalis
Conringia clade
Cochlearia
S1L3M1
S1L3M2
S2L2M2
S2L3M1
S2L3M2
S1L3M3
S2L2M3
S2L3M3
S3L1M3
S3L2M3
S3L3M2
S3L3M3
Biscutelleae
Lobularia
Iberis
Megacarpaea
Mexican and CES clades
Idahoa
Subularia
Cochlearia
Aphragmus
Megacarpaea
S3L3M1
Megacarpaea
Cochlearia
Aphragmus
S3L1M1
S3L1M2
S3L2M1
S3L2M2
Biscutelleae
Lobularia
Iberis
Lineage I

Figure S4. Summary of the concatenation results represented by the tree space of the eight unique topologies (circles) from the maximum likelihood analysis, and the topological differences among them. The summary tree on top is derived from the most inclusive dataset, *S1L1M1*, and color-coding marks the branches on the tree that are alternatively resolved with the other datasets. The tree space is divided into two areas (blue dotted line) based on the position of *Idahoa* and *Subularia* with respect to the Mexican (*Asta* + *Scoliaxon*) + CES (*Cremolobus* + *Schizopetalon* + *Brayopsis*) clade. It is further divided into two areas (orange dotted line) based on the position of the Biscutelleae + (*Lobularia* + *Iberis*) clade as sister to either *Megacarpaea* or Lineage I.

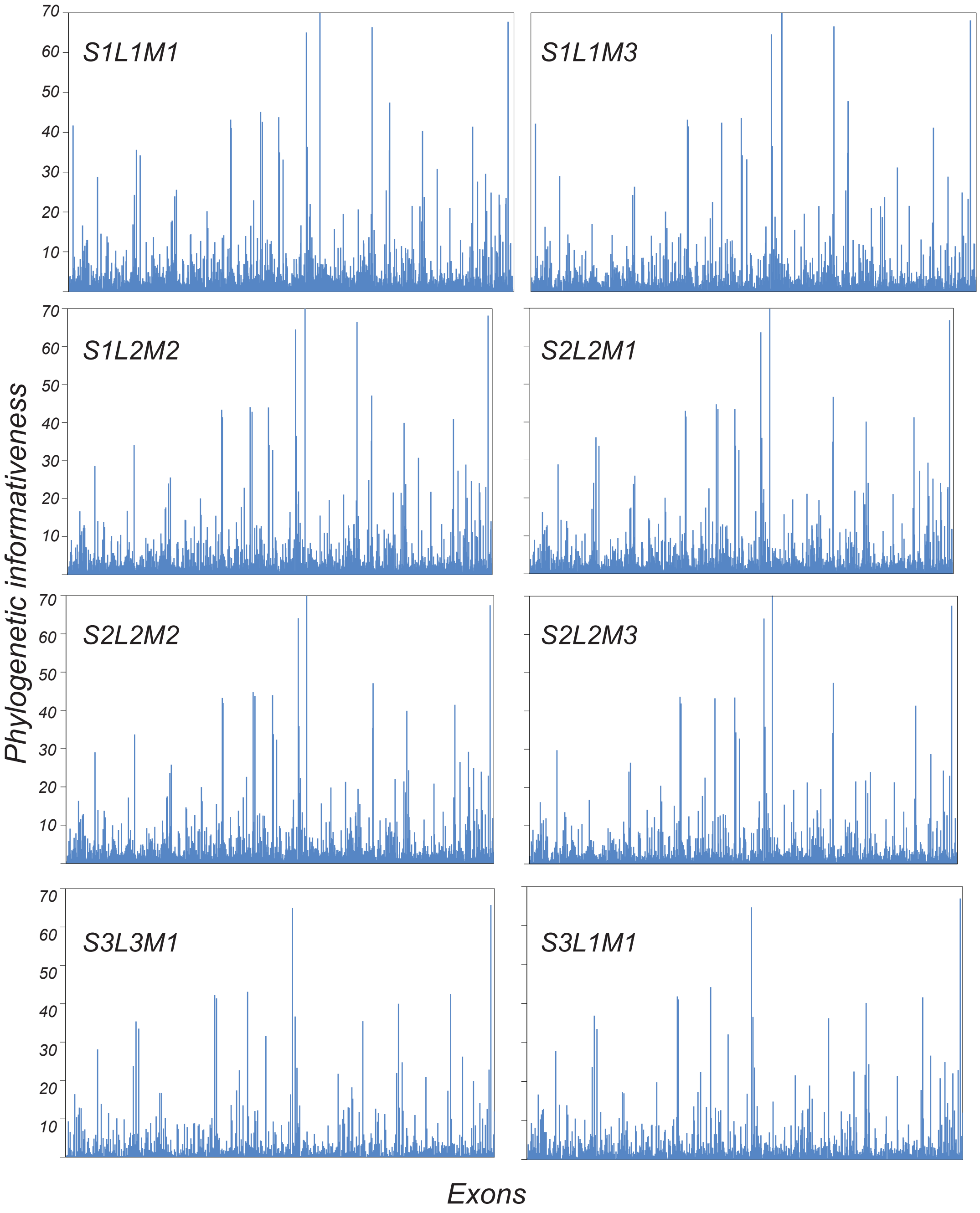


Figure S5. Phylogenetic informativeness of the loci from the most inclusive datasets that produced unique topologies (*S1L1M1*, *S1L1M3*, *S1L2M2*, *S1L3M1*, *S1L3M3*, *S2L2M1*, *S3L1M1*, *S3L3M1*). Exons with phylogenetic informativeness >10 deemed strong contributors were excluded from the subsequent concatenation analyses.

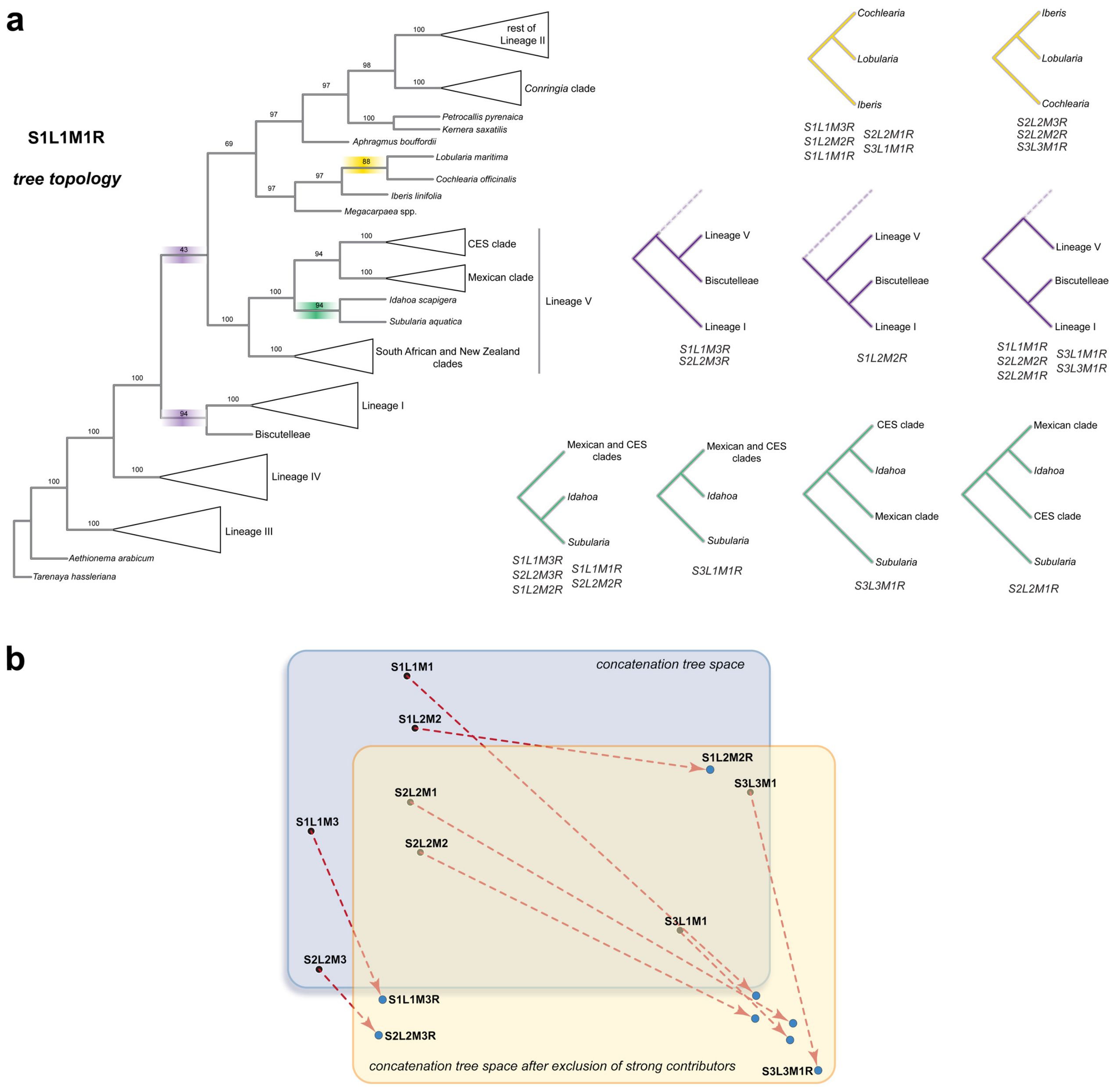


Figure S6. Summary of the concatenation results after excluding exons with phylogenetic informativeness score >10. a, The summary tree in the upper left corner is derived from the most inclusive dataset, *S1L1M1R*, and color-coding marks the branches on the tree that are alternatively resolved with the other datasets. **b**, Tree distances derived from the maximum likelihood analyses before (blue) and after (yellow) exclusion of the strong contributors from the phylogenetic informativeness test mapped onto two parallel planes.

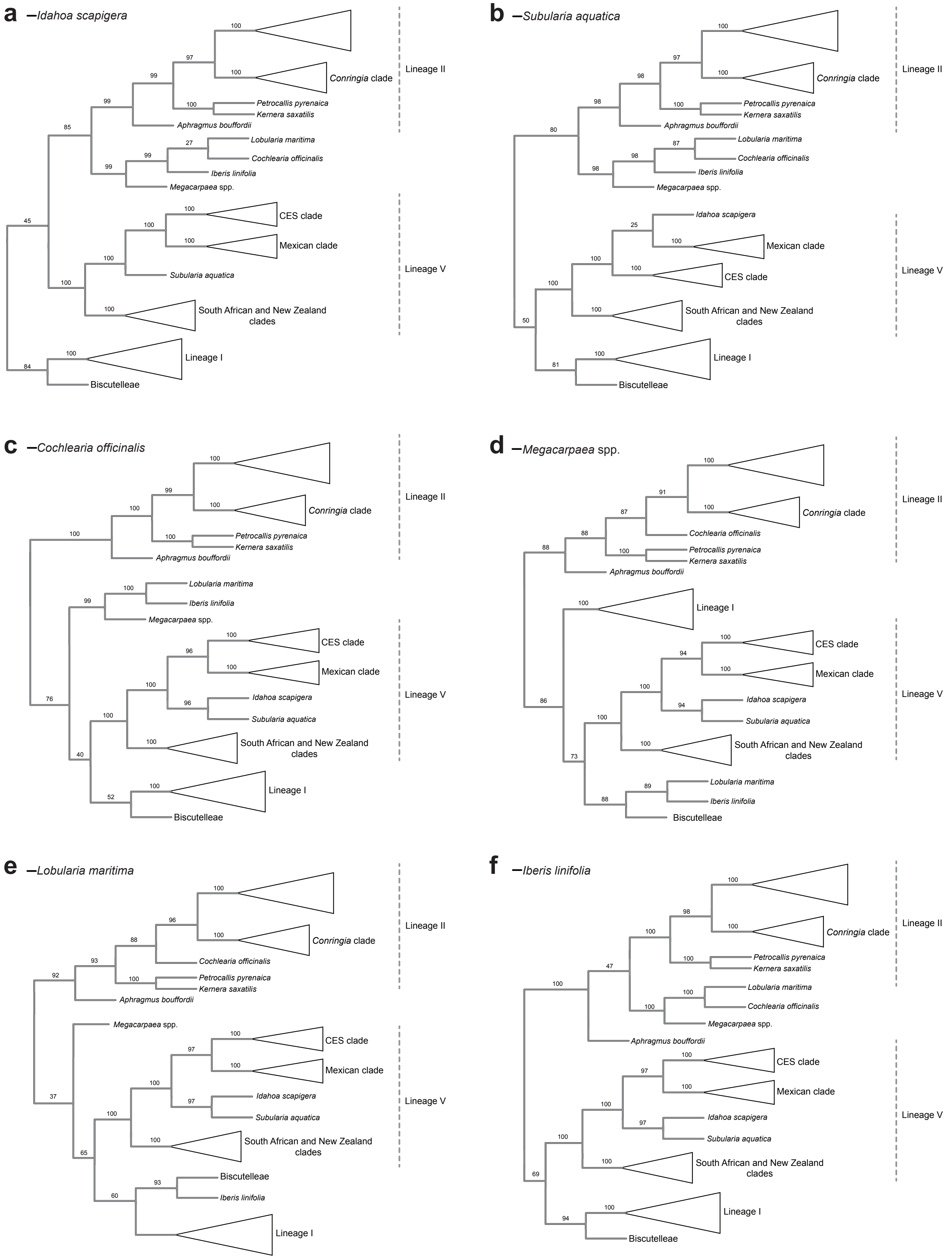
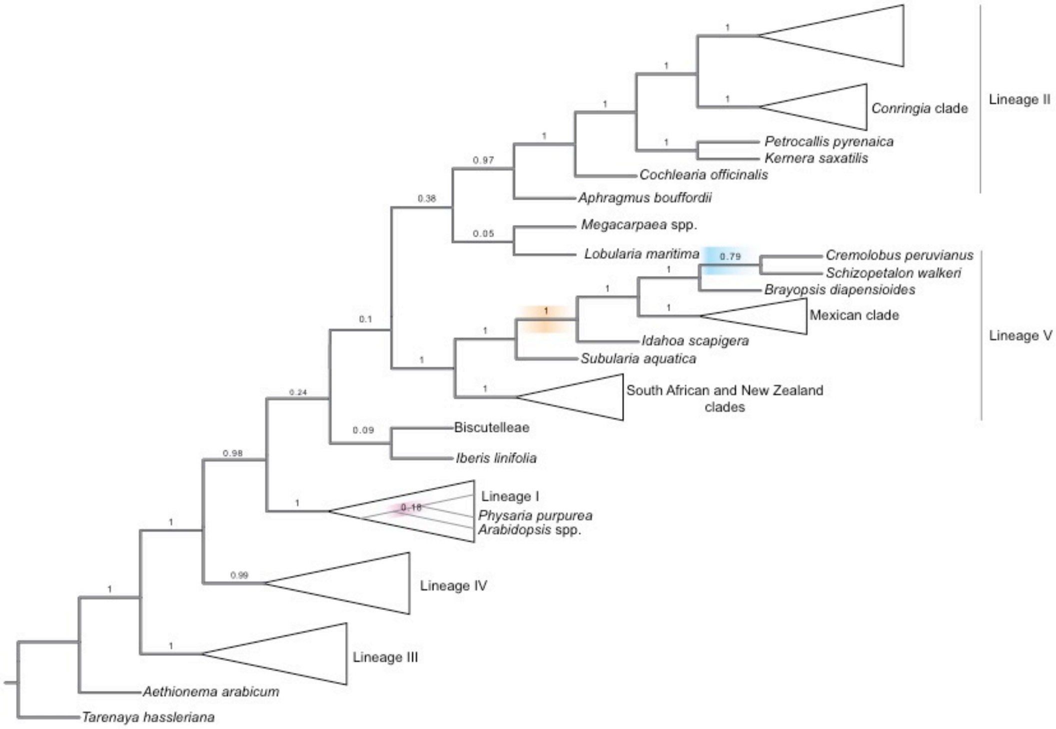

a
Idahoa scapigera
100
97
100
Conringia clade
99
100
Petrocallis pyrenaica
Kernera saxatilis
99
Aphragmus bouffordii
85
27
Lobularia maritima
99
Cochlearia officinalis
99
Iberis linifolia
Megacarpaea spp.
45
100
CES clade
100
100
Mexican clade
100
Subularia aquatica
100
100
South African and New Zealand clades
100
Lineage I
84
Biscutelleae
Lineage II
Lineage V
b
Subularia aquatica
100
97
100
Conringia clade
98
100
Petrocallis pyrenaica
Kernera saxatilis
98
Aphragmus bouffordii
80
87
Lobularia maritima
98
Cochlearia officinalis
98
Iberis linifolia
Megacarpaea spp.
Idahoa scapigera
25
100
Mexican clade
100
100
CES clade
100
100
South African and New Zealand clades
50
100
Lineage I
81
Biscutelleae
Lineage II
Lineage V
c
Cochlearia officinalis
100
99
100
Conringia clade
100
100
Petrocallis pyrenaica
Kernera saxatilis
100
Aphragmus bouffordii
100
Lobularia maritima
99
Iberis linifolia
Megacarpaea spp.
100
CES clade
96
100
Mexican clade
100
96
Idahoa scapigera
Subularia aquatica
100
100
South African and New Zealand clades
76
40
100
Lineage I
52
Biscutelleae
Lineage II
Lineage V
d
Megacarpaea spp.
100
91
100
Conringia clade
87
Cochlearia officinalis
88
100
Petrocallis pyrenaica
Kernera saxatilis
88
Aphragmus bouffordii
100
Lineage I
100
CES clade
94
100
Mexican clade
100
94
Idahoa scapigera
Subularia aquatica
100
100
South African and New Zealand clades
86
73
89
Lobularia maritima
88
Iberis linifolia
Biscutelleae
Lineage II
Lineage V
e
Lobularia maritima
100
96
100
Conringia clade
88
Cochlearia officinalis
93
100
Petrocallis pyrenaica
Kernera saxatilis
92
Aphragmus bouffordii
Megacarpaea spp.
100
CES clade
97
100
Mexican clade
100
97
Idahoa scapigera
Subularia aquatica
100
100
South African and New Zealand clades
37
65
93
Biscutelleae
60
Iberis linifolia
Lineage I
Lineage II
Lineage V
f
Iberis linifolia
100
98
100
Conringia clade
100
100
Petrocallis pyrenaica
Kernera saxatilis
47
100
100
Lobularia maritima
100
Cochlearia officinalis
Megacarpaea spp.
Aphragmus bouffordii
100
CES clade
97
100
Mexican clade
100
97
Idahoa scapigera
Subularia aquatica
100
100
South African and New Zealand clades
69
100
Lineage I
94
Biscutelleae
Lineage II
Lineage V

Figure S7. Pruning of taxa with unstable placement in different datasets and analyses. Relationships among *Aethionema*, Lineage III and Lineage IV did not vary among datasets and analyses and these are not represented. **a**, Excluding *Idahoa scapigera*. **b**, Excluding *Subularia aquatica*. **c**, Excluding *Cochlearia officinalis*. **d**, Excluding *Megacarpaea* spp. **e**, Excluding *Lobularia maritima*. **f**, Excluding *Iberis linifolia*.


1
1
1
Conringia clade
Lineage II
1
1
Petrocallis pyrenaica
Kernera saxatilis
0.97
Cochlearia officinalis
Aphragmus bouffordii
0.38
Megacarpaea spp.
0.05
Lobularia maritima
0.79
Cremolobus peruvianus
Schizopetalon walkeri
1
Brayopsis diapensioides
1
1
Mexican clade
1
Lineage V
0.1
1
Idahoa scapigera
Subularia aquatica
1
1
South African and New Zealand clades
0.24
0.09
Biscutelleae
Iberis linifolia
0.98
Lineage I
1
0.18
Physaria purpurea
Arabidopsis spp.
1
0.99
Lineage IV
1
1
Lineage III
Aethionema arabicum
Tarenaya hassleriana

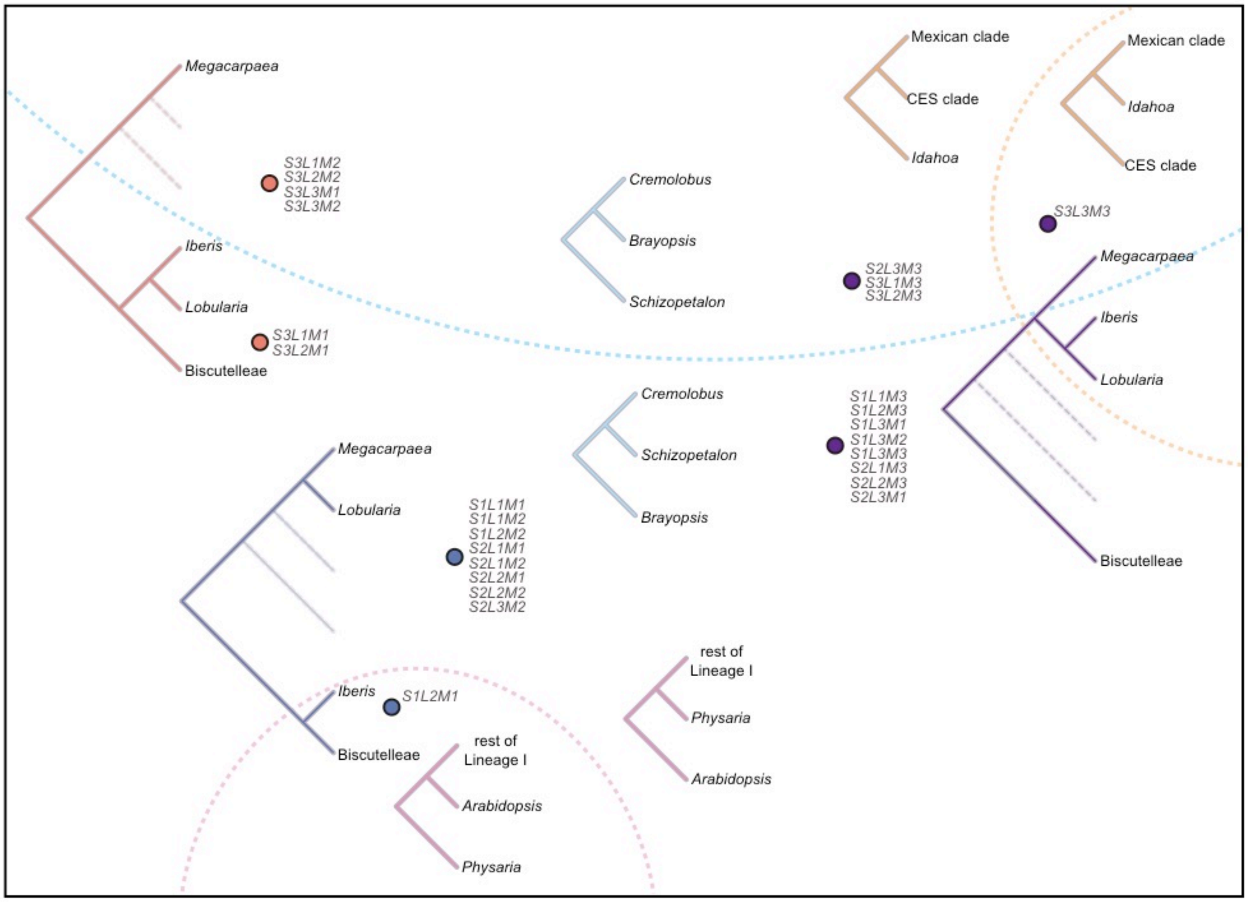

Megacarpaea
S3L1M2
S3L2M2
S3L3M1
S3L3M2
Iberis
Lobularia
S3L1M1
S3L2M1
Biscutelleae
Mexican clade
CES clade
Idahoa
Mexican clade
Idahoa
CES clade
Cremolobus
Brayopsis
Schizopetalon
S3L3M3
S2L3M3
S3L1M3
S3L2M3
Megacarpaea
Iberis
Lobularia
Cremolobus
Schizopetalon
Brayopsis
S1L1M3
S1L2M3
S1L3M1
S1L3M2
S1L3M3
S2L1M3
S2L2M3
S2L3M1
Biscutelleae
Megacarpaea
Lobularia
S1L1M1
S1L1M2
S1L2M2
S2L1M1
S2L1M2
S2L2M1
S2L2M2
S2L3M2
Iberis
S1L2M1
Biscutelleae
rest of Lineage I
Arabidopsis
Physaria
rest of Lineage I
Physaria
Arabidopsis

Figure S8. Summary of the ASTRAL-II results represented by the tree space of the seven unique topologies (circles), and the differences among them. The summary tree on top is derived from the most inclusive dataset, *S1L1M1*, and color-coding marks the branches on the tree that are alternatively resolved with the other datasets.

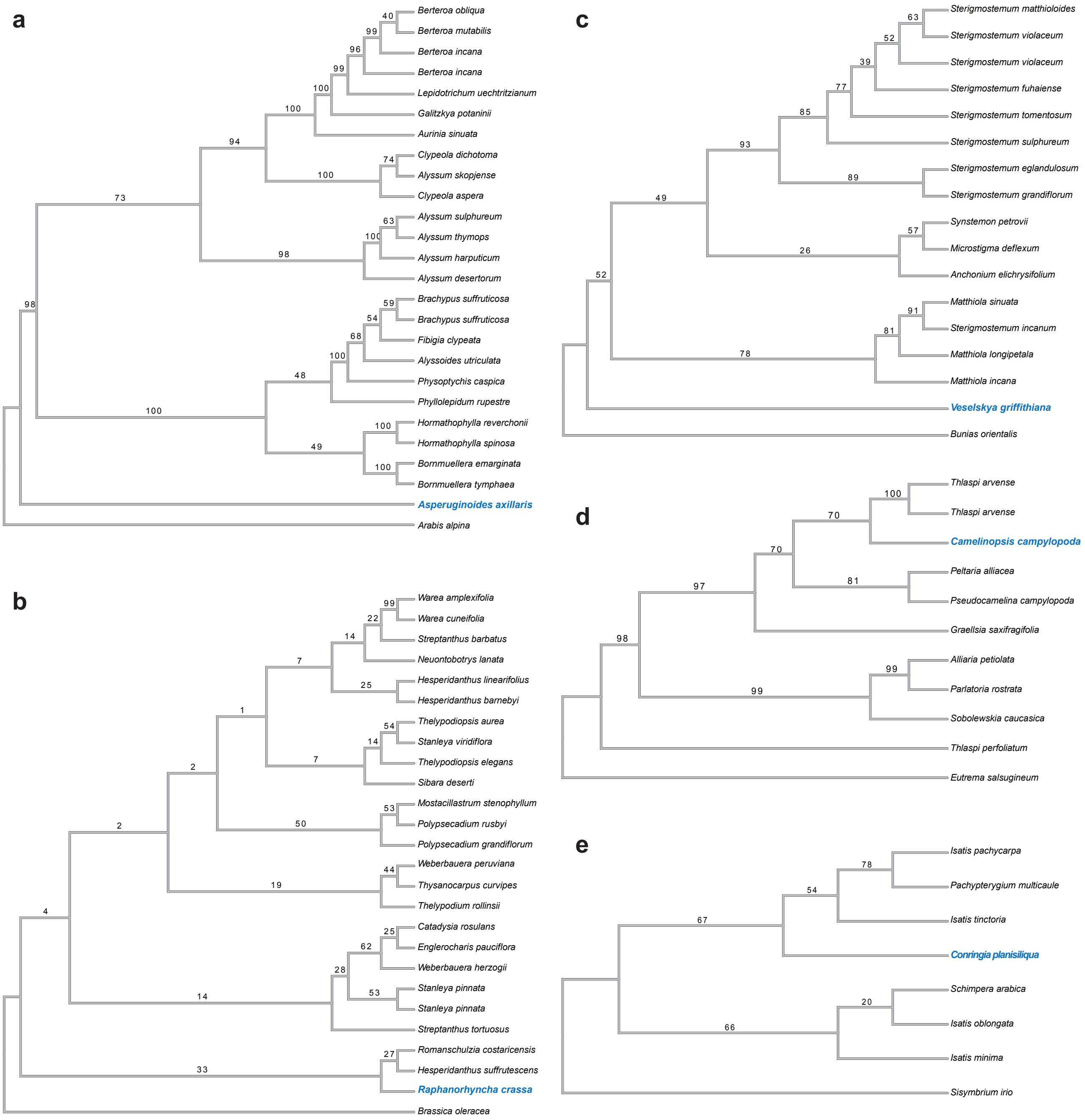


Figure S9. Placing unassigned to a tribe species with expanded taxon sampling of associated sister tribes. a, *Asperuginoides axillaris*. **b**, *Raphanorhyncha crassa*. **c**, *Veselskya griffithiana*. **d**, *Camelinopsis campylopoda*. **e**, *Conringia planisiliqua*.


Brassica rapa
Brassica juncea
Brassica oleracea
Brassica napus
Raphanus sativus
Cakile arabica
Brassiceae
Bivonaea lutea
Bivonaeeae
Orychophragmus hupehensis
Orychophragmus taibaiensis
Orychophragmus violaceus
Orychophragmus diffusus
Brassiceae
Raphanorhyncha crassa
unplaced
Stanleya elata
Thelypodieae
Pseudofortuynia esfandiarii
Ochthodium aegyptiacum
unplaced
Isatis tinctoria
Isatis tinctoria
Conringia planisiliqua
Isatideae
Arabis josiae
Fourraea alpina
Schrenkiella parvula
unplaced
Calepina irregularis
Calepineae
Eutrema salsugineum
Eutrema halophilum
Eutrema botschantzevii
Eutrema heterophyllum
Eutremeae
Eutrema yunnanense
Peltaria alliacea
Thlaspideae
Camelinopsis campylopoda
unplaced
Draba nemorosa
Arabis hirsuta
Arabis alpina
Arabideae
Pseudoturritis turrita
Stevenieae
Lobularia maritima
Lobularia maritima
Lobularia libyca
Anastatica hierochuntica
Morettia canescens
Farsetia stylosa
Anastaticeae
Iberis linifolia
Iberideae
Megacarpaea delavayi
Megacarpaea delavayi
Megacarpaea delavayi
Megacarpaea polyandra
Pugionium cornutum
Pugionium dolabratum
Megacarpaeeae
Cochlearia officinalis
Cochlearia pyrenaica
Cochlearia islandica
Cochlearia borzaeana
Cochlearia tridactylites
Ionopsidium acaule
Cochlearieae
Asta schaffneri
Asteae
Scoliaxon mexicanus
Scoliaxoneae
Idahoa scapigera
Subularia aquatica
unplaced
Brayopsis diapensioides
Eudemeae
Schizopetalon walkeri
Schizopetaleae
Petrocallis pyrenaica
unplaced
Kernera saxatilis
Kernereae
Noccaea vesicaria
Coluteocarpeae
Arabis ottonis-schulzii
unplaced
Conringia orientalis
Conringieae
Aphragmus bouffordii
Aphragmeae
Heliophila coronopifolia
Heliophileae
Chamira circaeoides
unplaced
Notothlaspi australe
Notothlaspideae
Aurinia saxatilis
Alyssum desertorum
Alysseae
Biscutella laevigata
Megadenia pygmaea
Heldreichia bupleurifolia
Ricotia cretica
Biscutelleae
Asperuginoides axillaris
unplaced
Matthiola incana
Matthiola incana
Anchonieae
Veselskya griffithiana
unplaced
Bunias orientalis
Bunias orientalis
Buniadeae
Hesperis matronalis
Hesperis matronalis
Hesperis sylvestris
Hesperideae
Euclidium syriacum
Neotorularia korolkowii
Solms-laubachia eurycarpa
Neotorularia torulosa
Braya humilis
Euclidieae
Chorispora tenella
Chorispora tenella
Chorisporeae
Dontostemon micranthus
Dontostemon integrifolius
Dontostemoneae
Arabidopsis halleri
Arabidopsis arenosa
Arabidopsis lyrata
Arabidopsis pedemontana
Arabidopsis cebennensis
Arabidopsis croatica
Arabidopsis thaliana
Capsella rubella
Capsella grandiflora
Capsella bursa-pastoris
Camelina sativa
Camelineae
Murbeckiella pinnatifida
Oreophytoneae
Erysimum cheiri
Erysimeae
Malcolmia maritima
Malcolmieae
Olimarabidopsis pumila
Alyssopsis mollis
Alyssopsideae
Hemilophia rockii
unplaced
Crucihimalaya wallichii
Crucihimalaya himalaica
Crucihimalayeae
Dipoma iberideum
Dipoma iberideum
unplaced
Pachycladon enysii
Pachycladon cheesmanii
Geococcus pusillus
Microlepidieae
Halimolobos pubens
Halimolobeae
Physaria purpurea
Physarieae
Cardamine hirsuta
Cardamine impatiens
Cardamine resedifolia
Nasturtium officinale
Cardamineae
Andrzeiowskia cardamine
unplaced
Barbarea verna
Cardamineae
Lepidium meyenii
Lepidium virginicum
Lepidium hirtum
Lepidieae
Smelowskia calycina
Smelowskieae
Yinshania acutangula
Yinshanieae
Descurainia artemisioides
Descurainieae
Aethionema cordifolium
Aethionema arabicum
Aethionema grandiflorum
Aethionemeae
Tarenaya hassleriana
Carica papaya
outgroups
84
86
51
74
90
96
89
75
98
93
84
93
47
67
77
96
96
72
94
99
39
99
91
23
50
28
22
55
61
37
43
59
96
43
36
68
38
60
97
51
29
99
98
99
99
99
93
93
97
62
97
93
97
85
97
97
97
98
67
98
97
97
0.04 substitions per site
0.02 substitions per site

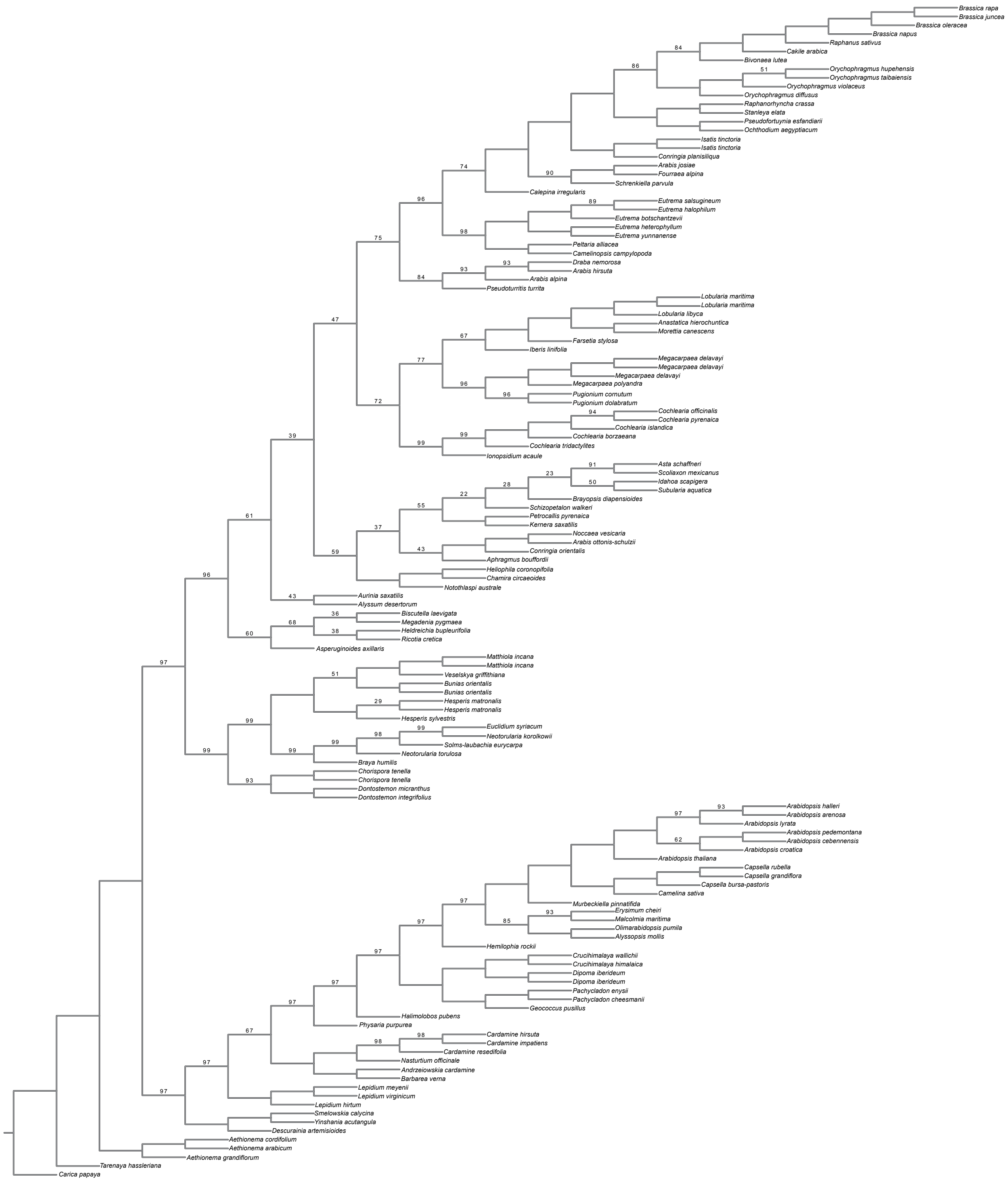


Figure S10. Plastid coding gene phylogeny (same tree depicted without and with branch transformation). Bootstrap support is 100 unless indicated otherwise.

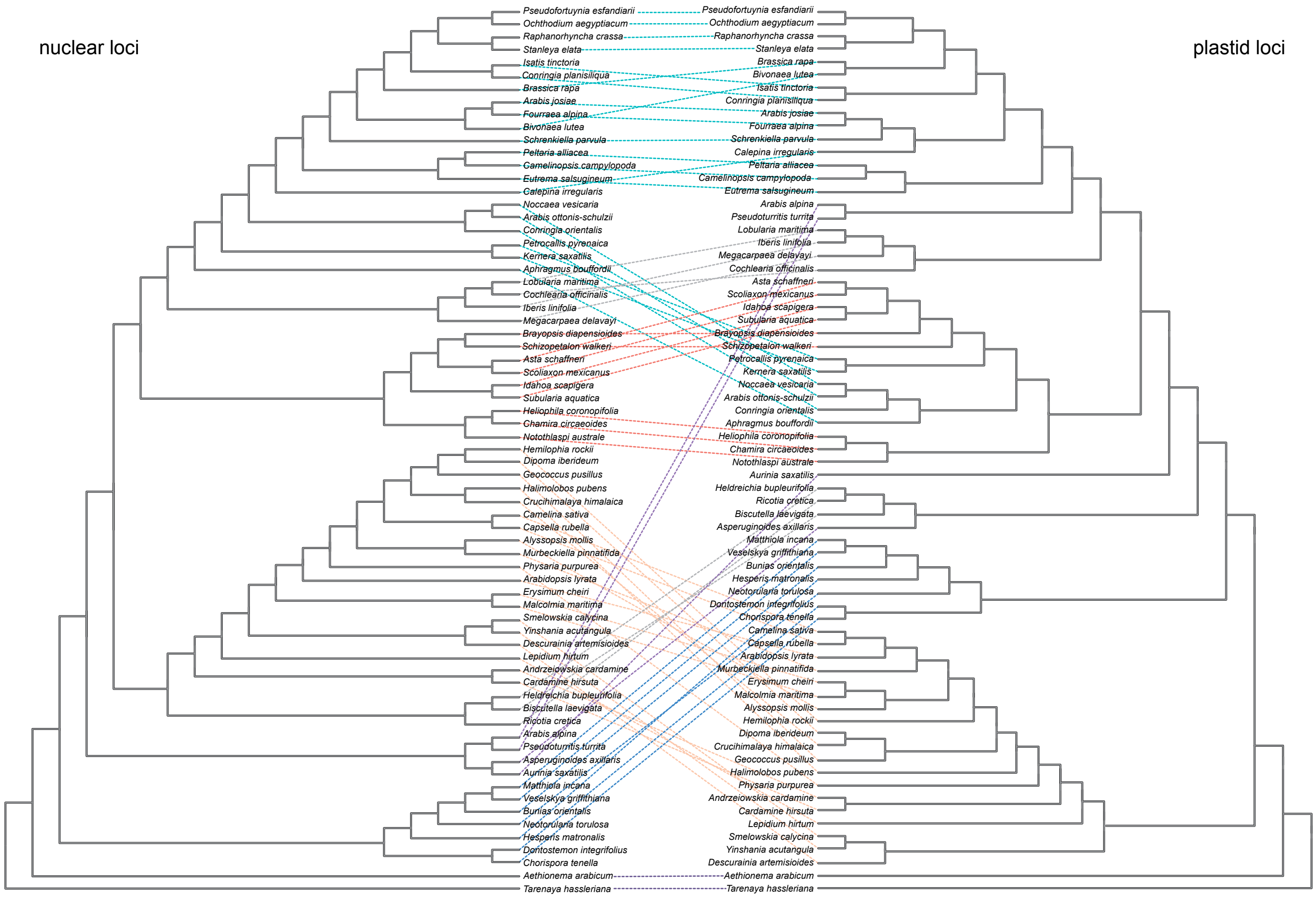


Figure S11. Comparison between tree topologies derived from nuclear and plastid loci. Unmatched taxa between the two datasets are excluded, and multispecies genera (except *Arabis* spp. and *Conringia* spp.) are trimmed to a single species.

Table S1. Taxon and voucher information for species with newly generated sequence data

Name	***Tribe***	***Figure code***	***Voucher information***
Alyssopsis mollis (Jacq.) O.E.Schulz	Alyssopsideae	Aps	B-2011-0216*, HEID
Andrzeiowskia cardamine Rchb.	unplaced	Arz	Gangale and Uzunov 11-2-17, B
Aphragmus bouffordii Al-Shehbaz	Aphragmeae	Aph	Boufford et al. 31446, A
Arabis josiae Jahand. & Maire	unplaced	Ajo	Nikolov 3829, BONN
Arabis ottonis-schulzii Bornm. & Gauba	unplaced	Aos	Nikolov 3830, BONN
Asperuginoides axillaris (Boiss. & Hohen.) Rauschert	unplaced	Asp	Freizi 36120, FUMH
Asta schaffneri (S.Watson) O.E.Schulz var. *pringlei* (O.E.Schulz) Rollins	Asteae	Ast	Hinton et al. 20193, GH
Aurinia saxatilis (L.) Desv.	Alysseae	Aly	xx-0-BONN-29279*, BONN
Biscutella laevigata L.	Biscutelleae	Bsc	FR-0-BONN-36028*, BONN
Bivonaea lutea DC.	Bivonaeeae	Biv	F. Wirtgen**, B100517564, B
Brayopsis diapensioides Gilg & Muschl.	Eudemeae	Edm	Fuentes et al. 12659, MOBOT
Bunias orientalis L.	Buniadeae	Bun	xx-0-BONN-3323*, BONN
Calepina irregularis (Asso) Thell.	Calepineae	Cal	xx-0-BONN-23168*, BONN
Camelinopsis campylopoda (Bornm. & Gauba) A.G. Mill. (syn. Pseudocamelina camplylopoda)	Thlaspideae	Cam	Sorkh-e Hesar 12438, TUH
Chamira circaeoides (L. f.) Zahlbr.	unplaced	Chm	Helme 3533, K
Chorispora tenella (Pallas) DC.	Chorisporeae	Chr	B-2006-0629*, HEID
Cochlearia officinalis L.	Cochlearieae	Coc	xx-0-BONN-19077*, BONN
Conringia orientalis (L.) C.Presl	Conringieae	Crg	xx-0-BONN-21509*, BONN
Conringia planisiliqua Fischer & C.A. Meyer	unplaced	Trt	B-2006-0697*, HEID; Nikolov 3818, BONN
Cremolobus peruvianus (Lam.) DC.	Cremolobeae	Cml	Woytkowski 8243, GH
Crucihimalaya himalaica (Edgeworth) Al-Shehbaz, O'Kane & Price	Crucihimalayeae	Cru	Al-Shehbaz 9354, GH
Descurainia artemisioides Svent.	Descurainieae	Des	Nikolov 3814, BONN
Dipoma iberideum Franch.	unplaced	Dpm	Borosova et al. 10CS2304, K
Dipoma iberideum Franch.	unplaced	Dip	Rock 25136, GH
Dontostemon integrifolius (L.) C.A. Mey	Dontostemoneae	Don	Nikolov 3822, BONN
Erysimum cheiri (L.) Crantz	Erysimeae	Ers	xx-0-STGAL-1993/647*, BONN
Fourraea alpina (L.) Greuter & Burdet.	unplaced	Frr	Nikolov 3815
Geococcus pusillus J.Drumm. ex Harv.	Microlepidieae	Mic	B-2001-0352*, HEID
Halimolobos pubens (A.Gray) Al-Shehbaz & C.D.Bailey	Halimolobeae	Hal	Nikolov 3824, BONN
Heldreichia bupleurifolia Boiss.	Biscutelleae	Hdr	Döring et al. 6693, B
Heliophila coronopifolia L.	Heliophileae	Hph	Nikolov 3821, BONN
Hemilophia rockii O.E. Schulz	unplaced	Hml	Boufford et al. 33431, A
Hesperis matronalis L.	Hesperideae	Hes	DE-0-BONN-34419*, BONN
Iberis linifolia L. subsp. *boppardensis* (Jord.) Korneck	Iberideae	Ibr	DE-0-BONN-5874*, BONN
Idahoa scapigera (Hook.) A. Nels. & J.F. Macbr.	unplaced	Ida	Baum 364, A
Isatis tinctoria L.	Isatideae	Ist	GE-0-BONN-35893*, BONN
Kernera saxatilis (L.) Sweet	Kernereae	Krn	Nikolov 3825, BONN
Lepidium hirtum (L.) Sm.	Lepidieae	Lep	B-2014-0057*, HEID
Lobularia maritima (L.) Desv.	Anastaticeae	Lob	FR-0-BONN-32257*, BONN
Lunaria rediviva L.	Biscutelleae	Lun	xx-0-BONN-9709*, BONN

Malcolmia maritima (L.) W.T.Aiton	Malcolmieae	Ana	Nikolov 3817, BONN
Matthiola incana (L.) W.T.Aiton	Anchonieae	Anc	xx-0-BONN-28336*, BONN
Megacarpaea delavayi Franch.	Megacarpaeeae	Mgc	Sino-American Botanical Exp. 1031, B
Megacarpaea delavayi Franch.	Megacarpaeeae	Meg	Borosova et al. 10CS2307, K
Megacarpaea polyandra Benth.	Megacarpaeeae	Mgr	Chase 565, K
Murbeckiella pinnatifida (Lam.) Rothm.	Oreophytoneae	Ore	B-2011-0222*, HEID
Neotorularia torulosa (Desf.) Hedge & J. Léonard	Euclidieae	Euc	Nikolov 3828, BONN
Noccaea vesicaria (L.) Al-Shehbaz	Coluteocarpeae	Clt	GE-0-BONN-35746*, BONN
Notothlaspi australe Hook.f.	Notothlaspideae	Not	Heenan 2015, BONN
Ochthodium aegyptiacum (L.) DC.	unplaced	Och	Nikolov 3823, BONN
Peltaria alliacea Jacq.	Thlaspideae	Tls	xx-0-BONN-3341*, BONN
Petrocallis pyrenaica (L.) W.T. Aiton.	unplaced	Pet	Nikolov 3820, BONN
Physaria purpurea (A.Gray) O'Kane & Al-Shehbaz	Physarieae	Phy	Nikolov 3826, BONN
Pseudofortuynia esfandiarii Hedge.	Sisymbrieae	Psf	Nikolov 3827, BONN
Pseudoturritis turrita (L.) Al-Shehbaz	Stevenieae	Stv	DE-0-BONN-14285*, BONN
Raphanorhyncha crassa Roll.	unplaced	Rph	Johnson et al. 10536, GH
Ricotia cretica Boiss. & Heldr.	Biscutelleae	Ric	Kamari and Turland 1322, B
Schizopetalon walkeri Sims.	Schizopetaleae	Sch	Nikolov 3819, BONN
Scoliaxon mexicanus (S.Watson) Payson	Scoliaxoneae	Scl	Henrickson 13702a, GH
Smelowskia calycina (Stephan ex Willd.) C.A.Mey.	Smelowskieae	Sml	B-2011-0226*, HEID
Stanleya elata M.E.Jones	Thelypodieae	The	Nikolov 3816, BONN
Subularia aquatica L.	unplaced	Sub	Štěpánek, B
Turritis glabra L.	Turritideae	Tgl	xx-0-BONN-15131*, BONN
Veselskya griffithiana (Boiss.) Opiz.	unplaced	Ves	Rechinger 33377, B
Yinshania acutangula (O.E.Schulz) Y.H.Zhang subsp. *acutangula*	Yinshanieae	Yin	Boufford et al. 36219, A

*cultivated specimen, collector name N/A

**collector and collection year unknown (acquired by B in 1936)

Table S2. Accession information for species with sequenced nuclear genomes

Name	***Tribe***	***Figure code***	***Genome assembly***
Aethionema arabicum (L.) Andrz. ex DC.	Aethionemeae	Aet	GCA_000411095.1
Arabidopsis lyrata (L.) O'Kane & Al-Shehbaz	Camelineae	Arl	GCA_000004255.1
Arabidopsis thaliana (L.) Heynh.	Camelineae	Ath	GCA_000001735.1
Arabis alpina L.	Arabideae	Alp	GCA_000733195.1
Boechera stricta (Graham) Al-Shehbaz	Boechereae	Boe	GCA_002079875.1
Brassica oleracea L.	Brassiceae	Bro	GCF_000695525.1
Brassica rapa L.	Brassiceae	Brr	GCF_000309985.1
Camelina sativa (L.) Crantz	Camelineae	Csa	GCA_000633955.1
Capsella rubella Reut.	Camelineae	Crb	GCF_000375325.1
Cardamine hirsuta L.	Cardamineae	Chi	chi_v1
Eutrema salsugineum (Pall.) Al-Shehbaz & S.I. Warwick	Eutremeae	Eut	GCA_000478725.1
Leavenworthia alabamica Rollins	Cardamineae	Lea	GCA_000411055.1
Lepidium meyenii Walp.	Lepidieae	Lmy	
Carica papaya L.	outgroup	Car	GCA_001310045.1
Schrenkiella parvula (Schrenk) D.A. German & Al-Shehbaz	unplaced	Skl	GCA_000218505.1
Sisymbrium irio L.	Sisymbrieae	Sis	GCA_000411075.1
Tarenaya hassleriana (Chodat) Iltis	outgroup	Tar	GCF_000463585.1
Thlaspi arvense L.	Thlaspideae	Tla	GCA_000956625.1

Table S3. Accession information for species with sequenced plastid genomes

Name	***Tribe***	***Accession number***
Aethionema arabicum (L.) Andrz. ex DC.	Aethionemeae	KX886357
Aethionema coridifolium DC.	Aethionemeae	NC_009265.1
Aethionema grandiflorum Boiss. & Hohen.	Aethionemeae	NC_009266.1
Alyssum desertorum Stapf	Alysseae	NC_034299.1
Anastatica hierochuntica L.	Anastaticeae	KY912021.1
Arabidopsis arenosa (L.) Lawalrée	Camelineae	NC_029334.1
Arabidopsis cebennensis (DC.) O'Kane & Al-Shehbaz	Camelineae	NC_029335.1
Arabidopsis croatica (Schott) O'Kane & Al-Shehbaz	Camelineae	NC_030347.1
Arabidopsis halleri (L.) O'Kane & Al-Shehbaz	Camelineae	KX886356
Arabidopsis lyrata (L.) O'Kane & Al-Shehbaz	Camelineae	KX886355
Arabidopsis pedemontana (Boiss.) O'Kane & Al-Shehbaz	Camelineae	LN877384
Arabidopsis thaliana (L.) Heynh.	Camelineae	NC_000932.1
Arabis alpina L.	Arabideae	NC_023367.1
Arabis hirsuta (L.) Scop.	Arabideae	AP009369
Barbarea verna (Mill.) Asch.	Cardamineae	NC_009269.1
Brassica juncea (L.) Czern.	Brassiceae	KT581449
Brassica napus L.	Brassiceae	GQ861354
Brassica oleracea L.	Brassiceae	KR233156
Brassica rapa subsp. *pekinensis* Kitam.	Brassiceae	NC_015139.1
Braya humilis (C.A. Mey.) B.L. Rob.	Euclidieae	KY912032.1
Bunias orientalis L.	Buniadeae	KY912022.1
Cakile arabica Velen. & Bornm.	Brassiceae	NC_030775.1
Camelina sativa (L.) Crantz	Camelineae	NC_029337.1
Capsella bursa-pastoris (L.) Medik.	Camelineae	AP009371
Capsella grandiflora Boiss.	Camelineae	NC028517
Capsella rubella Reut.	Camelineae	NC_027693.1
Cardamine hirsuta L.	Cardamineae	chi_v1
Cardamine impatiens L.	Cardamineae	KJ136821
Cardamine resedifolia L.	Cardamineae	KJ136822
Carica papaya L.	outgroup	NC_010323.1
Chorispora tenella (Pall.) DC.	Chorisporeae	KY912028.1
Cochlearia borzaeana Pobed.	Cochlearieae	LN866844
Cochlearia islandica Pobed.	Cochlearieae	NC_029254.1
Cochlearia pyrenaica DC.	Cochlearieae	NC_029331.1
Cochlearia tridactylites Banks ex DC.	Cochlearieae	LN866847
Crucihimalaya wallichii (Hook. f. & Thomson) Al-Shehbaz, O'Kane & R.A. Price	Crucihimalayeae	NC_009271.1
Draba nemorosa L.	Arabideae	NC_009272.1
Dontostemon micranthus C.A. Mey.	Dontostemoneae	KY912023.1

Euclidium syriacum (L.) W.T. Aiton	Euclidieae	KY912024.1
Eutrema botschantzevii (D.A. German) Al-Shehbaz & S.I. Warwick	Eutremeae	KT962847
Eutrema halophilum (C.A. Mey.) Al-Shehbaz & S.I. Warwick	Eutremeae	NC_029378.1
Eutrema heterophyllum (W.W. Sm.) H. Hara	Eutremeae	KT270358
Eutrema salsugineum (Pall.) Al-Shehbaz & S.I. Warwick	Eutremeae	NC_028170.1
Eutrema yunnanense Franch.	Eutremeae	KT270357
Farsetia stylosa R. Br.	Anastaticeae	KY912025.1
Hesperis matronalis L.	Hesperideae	KY912026.1
Hesperis sylvestris Crantz	Hesperideae	KY912027.1
Ionopsidium acaule (Desf.) DC. ex Rchb.	Cochlearieae	NC_029333.1
Isatis tinctoria L.	Isatideae	NC_028415.1
Lepidium meyenii Walp.	Lepidieae	KX886353
Lepidium virginicum L.	Lepidieae	NC_009273.1
Lobularia libyca Webb & Berthel.	Anastaticeae	KY912029.1
Lobularia maritima (L.) Desv.	Anastaticeae	NC_009274.1
Matthiola incana (L.) W.T. Aiton	Anchonieae	KY912030.1
Megacarpaea delavayi Franch.	Megacarpaeeae	KX886349
Megadenia pygmaea Maxim.	Biscutelleae	KX371593
Morettia canescens Boiss.	Anastaticeae	KY912031.1
Nasturtium officinale W.T. Aiton	Cardamineae	NC_009275.1
Neotorularia korolkowii (Regel & Schmalh.) Hedge & J. Léonard	Euclidieae	KX886350
Olimarabidopsis pumila (Stephan) Al-Shehbaz, O'Kane & R.A. Price	Alyssopsideae	NC_009267.1
Orychophragmus diffusus Z.M. Tan & J.M. Xu	Brassiceae	NC_033498.1
Orychophragmus hupehensis (Pamp.) Z.M. Tan & X.L. Zhang	Brassiceae	NC_033500.1
Orychophragmus taibaiensis Z.M. Tan & B.X. Zhao	Brassiceae	NC_033499.1
Orychophragmus violaceus (L.) O.E. Schulz	Brassiceae	KX364399.1
Pachycladon cheesmanii Heenan & A.D.Mitch.	Microlepidieae	NC_021102.1
Pachycladon enysii (Cheeseman) Heenan & A.D.Mitch.	Microlepidieae	JX205495
Pugionium cornutum (L.) Gaertn.	Megacarpaeeae	KT844941
Pugionium dolabratum Maxim.	Megacarpaeeae	KT844940
Raphanus sativus L.	Brassiceae	NC_024469.1
Schrenkiella parvula (Schrenk) D.A. German & Al-Shehbaz	unplaced	NC_028726.1
Solms-laubachia eurycarpa (Maxim.) Botsch.	Euclidieae	KX886348
Tarenaya hassleriana (Chodat) Iltis	outgroup	KX886354.1

Table S4. Reads and contig statistics

Species	Initial reads	Trimmed reads	Deduplicated reads	*Arabidopsis* reference					*Aethionema* reference					*Sisymbrium* reference					Exons called
				Mapped reads	Contigs called	Contigs mapped	Positions called	Average coverage	Mapped reads	Contigs called	Contigs mapped	Positions called	Average coverage	Mapped reads	Contigs called	Contigs mapped	Positions called	Average coverage	
Ajo	21088980	20186973	7236479	1891793	2042	2023	1083822	124	1258004	3446	3265	941018	95	2001543	1937	1907	1099196	129	1827
Aly	7299616	7036025	4415819	1254300	2320	2232	1100259	104	816748	3331	3032	904721	82	1222755	2389	2283	1085227	103	1818
Ana	10655622	10279538	5928709	1839951	1893	1875	1180126	140	1161567	3006	2832	1010716	104	1706579	1989	1962	1155236	133	1827
Anc	8331770	7954100	5014105	1203472	2407	2305	1102574	100	832515	3317	3032	933537	81	1184682	2379	2284	1094053	99	1824
Aos	14443682	13866406	6173326	1524028	2136	2113	1071993	103	983006	3560	3334	900424	79	1549808	2096	2067	1077888	104	1827
Aph	27476918	26717159	9837212	1800303	2114	2097	1080586	119	1239315	3431	3252	943148	94	1794264	2140	2113	1080448	119	1826
Aps	10244638	9826460	5774737	1792444	1904	1899	1183882	137	1113256	3185	2985	1002864	100	1637668	2101	2065	1153692	128	1825
Arz	27245170	26479549	9925925	1767448	2037	2019	1086891	117	1131965	3549	3320	922742	88	1649043	2263	2214	1066861	111	1827
Asp	11604350	11183056	6879718	1885942	2059	2032	1134945	144	1297128	3148	2944	1008385	112	1860940	2111	2086	1131798	143	1827
Ast	22827346	22181923	8255994	1721665	2117	2089	1054222	114	1196654	3304	3110	931526	90	1701810	2127	2096	1049114	113	1822
Biv	24089978	23456084	2778699	203019	4118	3438	663874	19	130344	4412	3364	470228	17	224283	3892	3294	707115	19	1730
Bsc	9095296	8657698	6069868	1380331	2165	2109	1125202	109	925892	3207	2964	964155	86	1331769	2228	2173	1113970	106	1825
Bun	9627858	9252002	6705928	1103160	2303	2209	1111904	92	774915	3267	2963	948775	75	1084075	2350	2252	1105860	91	1823
Cal	11260696	10776155	5630398	1850394	2017	1985	1157675	143	1201405	3119	2910	989935	109	1907213	2002	1967	1166319	146	1826
Cam	22775172	22081638	6300269	1250434	2277	2234	1051793	84	801267	3660	3419	874431	65	1305118	2137	2101	1063475	87	1827
Chm	3068382	2971687	864985	286419	2637	2447	884373	23	203279	3503	3088	698273	20	279810	2699	2512	871658	23	1812
Chr	8702986	8356420	5554750	1316326	2169	2084	1113521	108	906290	3173	2912	946973	88	1296917	2164	2086	1109753	107	1824
Clt	8153628	7775634	5028631	1518686	2116	2086	1148628	120	969980	3312	3067	966928	91	1552980	2079	2042	1154761	121	1824
Cml	9270092	8821576	5876127	1257534	2091	2049	1122970	101	845775	3199	2970	962551	79	1246721	2086	2043	1117382	100	1826
Coc	11058294	10609462	7290312	1330638	2493	2339	1062263	111	848633	3419	3048	865035	87	1355098	2483	2347	1070912	112	1814
Crg	13994564	13468921	6503383	2062271	2029	2011	1173621	156	1377648	3144	2961	1023276	120	2092620	1981	1967	1175943	158	1827
Cru	22285532	21662204	7148442	1856950	1925	1918	1096952	122	1153525	3522	3340	924265	90	1681256	2266	2215	1068974	113	1827
Des	13865706	13276141	7144241	2135733	1917	1903	1178807	160	1336920	2985	2813	1014691	117	1991967	1959	1928	1158182	152	1827
Dip	21074238	20582565	6267172	1450491	1931	1920	1055628	95	924610	3432	3225	904428	71	1329803	2214	2178	1036324	89	1826
Don	22663108	22060167	10759260	1477916	2453	2379	1030529	102	1030574	3563	3305	892372	82	1455770	2518	2431	1025193	101	1825
Dpm	29627694	28969045	11134866	2069635	1911	1903	1069129	133	1320999	3378	3178	932769	99	1895321	2174	2148	1052792	125	1826
Edm	28324008	27291944	11639799	2040671	2118	2096	1052808	132	1375331	3475	3299	929694	102	2019272	2137	2111	1049883	131	1823
Ers	11130202	10722802	5913035	1862451	1920	1916	1182704	141	1175085	3147	2967	1015881	104	1729933	2061	2039	1159305	134	1827
Euc	8260374	7937133	4706539	1368147	2310	2239	1104463	113	931286	3288	3017	938790	90	1341920	2377	2266	1095646	111	1825
Frr	24129880	23383135	8047309	1826792	2112	2097	1085140	120	1205628	3578	3364	934140	92	1934503	1940	1927	1100428	125	1827
Hal	10782772	10395564	5340814	1888353	1906	1898	1186826	143	1178971	3118	2943	1010544	105	1738064	2069	2036	1160162	135	1827
Hdr	40420378	38345390	8259028	1847060	2145	2123	1072104	117	1212201	3587	3356	918394	90	1800576	2196	2167	1063494	115	1825
Hes	11543578	11057974	7504020	1296500	2214	2117	1114708	105	926774	3130	2868	971897	86	1276515	2269	2134	1108059	104	1823
Hml	46211756	44779475	11154122	2278628	1961	1939	1066695	145	1403384	3508	3263	909941	106	2035043	2325	2263	1040825	133	1820
Hph	13841056	13344045	7402019	1730349	2132	2060	1101726	136	1177614	3101	2860	949295	107	1701015	2125	2047	1096591	134	1824
Ibr	9517236	9148343	5686491	1382578	2227	2146	1105422	112	952928	3195	2930	944957	90	1343124	2270	2167	1093169	110	1821
Ida	26546786	25719931	5708715	723270	3010	2832	913203	54	506482	3871	3447	752332	45	703741	3131	2923	901049	53	1809
Ist	10731682	10267273	6798089	1819965	2087	2070	1161469	139	1181267	3261	3062	998169	106	1965420	1906	1895	1180819	148	1827
Krn	15878788	15241186	7275546	2273222	1982	1969	1178903	169	1542696	3049	2893	1041619	130	2296602	1983	1965	1181639	171	1827
Lep	10984084	10604616	5366464	1652499	2126	2042	1137596	132	1027973	3365	3057	938239	99	1500026	2309	2187	1100786	123	1812
Lob	22063064	21430221	9803717	1385031	2912	2770	983182	98	881449	3961	3559	793629	77	1376781	2915	2767	977162	98	1820
Lun	9974422	9582612	6452912	1656659	1968	1945	1143472	127	1154172	3004	2804	1028199	99	1652591	1926	1903	1140348	127	1827
Meg	30140858	28788167	11719016	767115	2245	2173	1007164	52	515863	3596	3312	841153	42	762102	2277	2206	1003845	52	1826
Mgc	19682190	19258960	9264817	1578842	2211	2179	1052854	106	1067926	3526	3309	912556	83	1569028	2206	2173	1050817	106	1825
Mgr	19032210	18559264	8111057	1621367	2172	2139	1054012	109	1101384	3473	3267	918076	85	1611596	2194	2158	1052640	108	1824

Mic	10357532	9891495	6137622	1867095	1908	1893	1155775	140	1145254	3153	2942	987618	102	1708765	2057	2033	1130697	132	1826
Not	27323496	26694964	9405503	1898037	2152	2119	1055521	126	1318405	3334	3163	928834	100	1873134	2202	2161	1052545	125	1817
Och	11585916	11170541	6225147	1795346	2094	2067	1159841	139	1145402	3328	3090	989664	104	1980367	1879	1865	1190111	149	1827
Ore	17103922	16410951	7411560	2404777	1901	1892	1190904	177	1497333	3137	2959	1026273	128	2207032	2103	2066	1165798	166	1824
Pet	30536488	29687163	9624017	2047407	2054	2041	1090575	133	1394726	3419	3220	956652	104	2065990	2028	2009	1092905	134	1827
Phy	15078646	14505604	11620874	1454884	2028	1978	1133130	115	892111	3221	2934	938728	85	1278086	2296	2189	1088993	105	1823
Psf	13159552	12707278	9448740	1515034	2038	2018	1160902	119	982985	3247	3027	993508	90	1649188	1857	1852	1187411	126	1826
Ric	27650286	26862269	7690382	1768835	2159	2123	1049782	116	1227475	3382	3206	929711	92	1732666	2241	2199	1043481	115	1827
Rph	37265244	36071593	14330040	2253336	2052	2030	1055533	145	1501622	3350	3160	942447	109	2442472	1875	1856	1068613	154	1827
Sch	8217830	7910301	5194347	1499933	2041	1993	1131982	118	1037514	3063	2849	992353	93	1487467	2020	1976	1126848	117	1819
Scl	21889346	21339856	8946367	1573955	2226	2181	1045297	106	1112560	3420	3201	919752	85	1552107	2283	2228	1040545	105	1822
Sml	24259666	22952366	10719799	1912307	1957	1948	1090851	123	1207591	3561	3365	932786	91	1784883	2183	2156	1072725	117	1823
Stv	9684514	9281572	5394934	1703160	1993	1974	1174003	131	1182923	3063	2900	1036245	103	1690466	2009	1992	1170980	131	1827
Sub	24228390	23583054	10038613	1394430	2689	2540	971816	100	905903	3806	3460	803384	78	1352415	2813	2660	958921	98	1815
Tgl	N/A	N/A	N/A	895903	1906	1814	1154105	95	574107	2952	2523	956714	74	841295	2175	1999	1129243	92	1781
The	11357328	10888548	8386347	1693010	2002	1982	1128794	130	1126429	3077	2882	1001507	99	1817078	1886	1854	1143942	137	1827
Tls	11616146	11145218	6135238	1860097	2113	2082	1161930	143	1189931	3330	3103	985666	108	1928674	2026	2003	1169640	147	1827
Trt	12394428	11966371	5975655	1879218	2086	2062	1165522	145	1203468	3251	3045	993659	109	2028961	1927	1903	1188849	153	1827
Ves	27649518	26872285	6274275	764037	2369	2256	1003110	52	528129	3554	3216	845236	43	749735	2388	2267	994395	52	1827
Yin	24328992	23671627	6661675	1745645	1946	1938	1091344	114	1135833	3501	3307	937555	87	1641831	2145	2115	1075556	109	1827

Table S5. Skimmed read and whole plastome statistics

Species	Mapped reads	Recovered genes	Plastome length, bp	LSC length, bp	IR length, bp	SSC length, bp	LSC average coverage	IR average coverage	SSC average coverage
Ajo	67834	77							
Aly	7734	9							
Ana	73735	97							
Anc	41302	95							
***Aos** **	254651	97	153138	82310	26354	18119	71	186	70
Aph	384416	84							
***Aps** **	66260	97	154839	83969	26497	17875	29	64	30
Arz	635876	85							
Asp	17750	52							
Ast	54810	36							
Biv	201720	10							
Bsc	7771	6							
***Bun** **	178742	97	153877	83598	26246	17786	82	167	93
Cal	28199	85							
Cam	81437	78							
Chm	81595	86							
Chr	639418	94							
Clt	30161	89							
Coc	348163	96							
Crg	20405	72							
Cru	44184	29							
Des	27616	85							
***Dip** **	362478	97	153804	82865	26502	17934	108	239	110
Don	76302	82							
Dpm	116263	97							
Edm	91717	82							
Ers	25159	46							
Euc	18935	54							
Frr	131664	97							
Hal	46096	96							
Hdr	98839	92							
Hes	18074	16							
Hml	178494	93							
Hph	29413	88							
Ibr	17583	43							
Ida	54263	55							
Ist	31213	93							
***Krn** **	61373	97	154832	84079	26426	17900	26	60	27
Lep	23612	69							
Lob	75841	90							
Meg	251510	97							
Mgc	198169	97							
Mgr	58369	71							
Mic	22618	68							
Not	96214	96							
Och	23607	72							

***Ore* ***	80037	97	154918	84344	26460	17653	31	86	31
Pet	154123	97							
Phy	613614	97							
***Psf* ***	1342274	97	154140	84032	26236	17635	635	1268	684
Ric	52321	37							
Rph	80327	86							
Sch	34029	88							
Scl	97717	88							
Sml	602344	96							
Stv	51868	97							
***Sub* ***	205509	96	152645	82178	26347	17772	65	124	73
***The* ***	801408	97	153669	83498	26258	17654	386	756	396
Tls	31247	92							
Trt	21847	75							
Ves	153925	97							
Yin	52177	49							

* species with complete plastomes

LSC, large single copy region
IR, inverted regions
SSC, small single copy region

Table S6. Dataset statistics

Dataset	Number of exons	Total sites, bp	Variable sites, bp	Variable sites, %	Missing data, %	Number of partitions
S1L1M1	1540	739071	463726	62.74%	2.57%	114
S1L1M2	1405	698340	434653	62.24%	2.60%	73
S1L1M3	976	540603	343343	63.51%	2.77%	63
S1L2M1	1415	691641	434639	62.84%	2.60%	90
S1L2M2	1300	655620	414212	63.18%	2.62%	97
S1L2M3	916	510426	326616	63.99%	2.79%	62
S1L3M1	868	478356	307797	64.34%	2.65%	47
S1L3M2	816	460569	297533	64.60%	2.67%	50
S1L3M3	588	366363	241174	65.83%	2.86%	46
S2L1M1	1388	672252	415974	61.88%	2.49%	79
S2L1M2	1260	633354	390995	61.73%	2.51%	49
S2L1M3	873	486444	307730	63.26%	2.68%	59
S2L2M1	1274	632925	390145	61.64%	2.52%	49
S2L2M2	1166	598737	374078	62.48%	2.54%	59
S2L2M3	822	463935	294973	63.58%	2.71%	56
S2L3M1	777	442203	283718	64.16%	2.58%	43
S2L3M2	726	424614	274830	64.72%	2.59%	47
S2L3M3	526	337437	221305	65.58%	2.77%	45
S3L1M1	824	412113	249405	60.52%	1.97%	43
S3L1M2	744	387561	234330	60.46%	1.96%	43
S3L1M3	508	293640	180128	61.34%	2.06%	39
S3L2M1	751	391251	238922	61.07%	1.99%	45
S3L2M2	686	370416	225825	60.97%	1.98%	44
S3L2M3	478	284811	176300	61.90%	2.07%	38
S3L3M1	469	289896	182959	63.11%	2.01%	39
S3L3M2	439	277785	174174	62.70%	1.99%	34
S3L3M3	319	220428	140436	63.71%	2.08%	36
S1L1M1R	1421	551271	335897	60.93%	2.48%	58
S1L1M3R	885	391167	245249	62.70%	2.68%	52
S1L2M2R	1191	483141	297630	61.60%	2.53%	48
S2L2M1R	1170	464361	283666	61.09%	2.42%	50
S2L2M2R	1068	436908	267883	61.31%	2.45%	44
S2L2M3R	744	331263	209055	63.11%	2.61%	55
S3L1M1R	750	288645	172071	59.61%	1.91%	39
S3L3M1R	407	186840	117218	62.74%	2.01%	33

Table S7. Approximate unbiased (AU) test for evaluating the support of a given dataset matrix for unique topologies.

matrix / ***topology***	***S1L1M1***	***S1L1M3***	***S1L2M2***	***S1L3M1***	***S1L3M3***	***S2L2M1***	***S3L1M1***	***S3L3M1***
S1L1M1	0.885	0.165	0.337	0.052	0.015	0.065	3.00E-06	2.00E-04
S1L1M3	0.272	0.864	0.154	0.006	0.017	0.009	1.00E-70	1.00E-09
S1L2M2	0.543	0.418	0.642	0.449	0.268	0.352	3.00E-08	9.00E-06
S1L3M1	0.002	0.001	0.002	0.693	0.188	0.597	0.002	0.042
S1L3M3	0.001	0.007	0.002	0.115	0.931	0.143	4.00E-13	2.00E-41
S2L2M1	0.158	0.08	0.121	0.569	0.324	0.813	0.016	0.044
S3L1M1	0.051	0.021	0.052	0.196	0.043	0.118	0.845	0.343
S3L3M1	0.001	6.00E-05	4.00E-04	0.423	0.187	0.113	0.558	0.642

matrix / ***topology***	***S1L1M1R***	***S1L1M3R***	***S1L2M2R***	***S2L2M1R***	***S2L2M2R***	***S2L2M3R***	***S3L1M1R***	***S3L3M1R***
S1L1M1	0.754	0.168	0.614	0.119	0.252	0.063	0.001	0.004
S1L1M3	0.095	0.815	0.367	0.004	0.053	0.247	2.00E-41	0.001
S1L2M2	0.522	0.193	0.724	0.244	0.531	0.17	0.067	0.02
S2L2M1	0.497	0.07	0.066	0.723	0.553	0.051	0.223	0.02
S2L2M2	0.509	0.151	0.077	0.501	0.775	0.129	0.268	0.013
S2L2M3	0.189	0.53	0.079	0.089	0.232	0.755	0.059	1.00E-04
S3L1M1	0.114	0.001	9.00E-05	0.499	0.677	0.007	0.524	0.197
S3L3M1	0.042	0.024	2.00E-05	0.371	0.14	0.051	0.09	0.835

Table S8. Leaf stability indices.

Taxon	Concatenated trees			ASTRAL trees		
	lsDif	*lsEnt*	*lsMax*	*lsDif*	*lsEnt*	*lsMax*
Aet	0.960575	0.954088	0.970431	0.991716	0.993077	0.993787
Alp	0.960575	0.954088	0.970431	0.991716	0.993077	0.993787
Ajo	0.966576	0.962266	0.974932	0.98816	0.99012	0.99112
Aly	0.960575	0.954088	0.970431	0.991716	0.993077	0.993787
Arl	0.972451	0.968075	0.979339	0.991039	0.991759	0.993279
Ana	0.972451	0.968075	0.979339	0.991716	0.993077	0.993787
Anc	0.960575	0.954088	0.970431	0.991716	0.993077	0.993787
Aos	0.943152	0.94352	0.957364	0.98816	0.99012	0.99112
Aph	0.957506	0.949003	0.96813	0.98816	0.99012	0.99112
Aps	0.972451	0.968075	0.979339	0.99162	0.992891	0.993715
Arz	0.972451	0.968075	0.979339	0.991716	0.993077	0.993787
Asp	0.960575	0.954088	0.970431	0.991716	0.993077	0.993787
Ast	0.94677	0.938001	0.960078	0.977302	0.980881	0.982977
Ath	0.972451	0.968075	0.979339	0.991039	0.991759	0.993279
Biv	0.966576	0.962266	0.974932	0.98816	0.99012	0.99112
Bro	0.966576	0.962266	0.974932	0.98816	0.99012	0.99112
Brr	0.966576	0.962266	0.974932	0.98816	0.99012	0.99112
Bsc	0.882394	0.862021	0.911795	0.971259	0.976076	0.978445
Boe	0.972451	0.968075	0.979339	0.99162	0.992891	0.993715
Bun	0.960575	0.954088	0.970431	0.991716	0.993077	0.993787
Cal	0.966576	0.962266	0.974932	0.98816	0.99012	0.99112
Cam	0.966576	0.962266	0.974932	0.98816	0.99012	0.99112
Chi	0.972451	0.968075	0.979339	0.991716	0.993077	0.993787
Chm	0.947317	0.938476	0.960488	0.977495	0.981256	0.983121
Chr	0.960575	0.954088	0.970431	0.991716	0.993077	0.993787
Clt	0.943152	0.94352	0.957364	0.98816	0.99012	0.99112
Cml	0.94677	0.938001	0.960078	0.976826	0.980504	0.98262
Coc	0.916828	0.913296	0.937621	0.98816	0.99012	0.99112
Crg	0.943152	0.94352	0.957364	0.98816	0.99012	0.99112
Cru	0.972451	0.968075	0.979339	0.99162	0.992891	0.993715
Crb	0.972451	0.968075	0.979339	0.99162	0.992891	0.993715
Csa	0.972451	0.968075	0.979339	0.99162	0.992891	0.993715
Des	0.972451	0.968075	0.979339	0.991716	0.993077	0.993787
Dip	0.972451	0.968075	0.979339	0.99162	0.992891	0.993715
Don	0.960575	0.954088	0.970431	0.991716	0.993077	0.993787
Dpm	0.972451	0.968075	0.979339	0.99162	0.992891	0.993715
Edm	0.94677	0.938001	0.960078	0.976826	0.980504	0.98262
Ers	0.972451	0.968075	0.979339	0.991716	0.993077	0.993787
Eut	0.966576	0.962266	0.974932	0.98816	0.99012	0.99112

Euc	0.960575	0.954088	0.970431	0.991716	0.993077	0.993787
Frr	0.966576	0.962266	0.974932	0.98816	0.99012	0.99112
Hal	0.972451	0.968075	0.979339	0.99162	0.992891	0.993715
Hdr	0.882394	0.862021	0.911795	0.971259	0.976076	0.978445
Hes	0.960575	0.954088	0.970431	0.991716	0.993077	0.993787
Hml	0.972451	0.968075	0.979339	0.99162	0.992891	0.993715
Hph	0.947317	0.938476	0.960488	0.977495	0.981256	0.983121
Ibr	0.882394	0.862021	0.911795	0.760208	0.82856	0.820156
Ida	0.944426	0.935964	0.95832	0.977104	0.980496	0.982828
Ist	0.966576	0.962266	0.974932	0.98816	0.99012	0.99112
Krn	0.937003	0.937075	0.952752	0.98816	0.99012	0.99112
Lea	0.972451	0.968075	0.979339	0.991716	0.993077	0.993787
Lep	0.972451	0.968075	0.979339	0.991716	0.993077	0.993787
Lmy	0.972451	0.968075	0.979339	0.991716	0.993077	0.993787
Lob	0.882394	0.862021	0.911795	0.871871	0.864523	0.903904
Lun	0.882394	0.862021	0.911795	0.971259	0.976076	0.978445
Meg	0.89856	0.880125	0.92392	0.970111	0.975121	0.977583
Mgc	0.89856	0.880125	0.92392	0.970111	0.975121	0.977583
Mgr	0.89856	0.880125	0.92392	0.970111	0.975121	0.977583
Mic	0.972451	0.968075	0.979339	0.99162	0.992891	0.993715
Not	0.947317	0.938476	0.960488	0.977495	0.981256	0.983121
Och	0.966576	0.962266	0.974932	0.98816	0.99012	0.99112
Ore	0.972451	0.968075	0.979339	0.99162	0.992891	0.993715
Pet	0.937003	0.937075	0.952752	0.98816	0.99012	0.99112
Phy	0.972451	0.968075	0.979339	0.990341	0.9904	0.992755
Psf	0.966576	0.962266	0.974932	0.98816	0.99012	0.99112
Ric	0.882394	0.862021	0.911795	0.971259	0.976076	0.978445
Rph	0.966576	0.962266	0.974932	0.98816	0.99012	0.99112
Sch	0.94677	0.938001	0.960078	0.976826	0.980504	0.98262
Scl	0.94677	0.938001	0.960078	0.977302	0.980881	0.982977
Sis	0.966576	0.962266	0.974932	0.98816	0.99012	0.99112
Sml	0.972451	0.968075	0.979339	0.991716	0.993077	0.993787
Skl	0.966576	0.962266	0.974932	0.98816	0.99012	0.99112
Stv	0.960575	0.954088	0.970431	0.991716	0.993077	0.993787
Sub	0.944426	0.935964	0.95832	0.977495	0.981256	0.983121
Tla	0.966576	0.962266	0.974932	0.98816	0.99012	0.99112
Tgl	0.972451	0.968075	0.979339	0.99162	0.992891	0.993715
Tar	0.960575	0.954088	0.970431	0.991716	0.993077	0.993787
The	0.966576	0.962266	0.974932	0.98816	0.99012	0.99112
Tls	0.966576	0.962266	0.974932	0.98816	0.99012	0.99112
Trt	0.966576	0.962266	0.974932	0.98816	0.99012	0.99112
Ves	0.960575	0.954088	0.970431	0.991716	0.993077	0.993787
Yin	0.972451	0.968075	0.979339	0.991716	0.993077	0.993787

Table S9. Accession information of marker genes used for infratribal placement

Alysseae phylogeny	***ndhF***
Alyssoides utriculata	KF022860.1
Alyssum desertorum	KY498535.1
Alyssum harputicum	KF022881.1
Alyssum skopjense	KF022923.1
Alyssum sulphureum	KF022927.1
Alyssum thymops	KF022929.1
Arabis alpina (outgroup: Arabideae)	DQ288731.1
Asperuginoides axillaris	this study
Aurinia sinuata	KF022952.1
Berteroa incana	LC090120.2
Berteroa incana	AY330097.1
Berteroa mutabilis	KF022956.1
Berteroa obliqua	KF022957.1
Bornmuellera emarginata, as *Leptoplax emarginata*	KF022989.1
Bornmuellera tymphaea	KF022963.1
Brachypus suffruticosus, as *Fibigia suffruticosa*	KF022978.1
Clypeola aspera	EU907360.1
Clypeola dichotoma	KF022968.1
Fibigia clypeata	KF022972.1
Fibigia suffruticosa	EU907361.1
Galitzkya potaninii	KF022983.1
Hormathophylla reverchonii	KP276171.1
Hormathophylla spinosa	KP276173.1
Lepidotrichum uechtritzianum	KF022988.1
Phyllolepidum rupestre	KF022993.1
Physoptychis caspica	KF022994.1

Anchonieae phylogeny	***rbcL***
Anchonium elichrysifolium	FN594834.1
Bunias orientalis (outgroup: Buniadeae)	KM360682.1
Matthiola incana	HM850161.1
Matthiola longipetala	KX282876.1
Matthiola sinuata	JN892935.1
Microstigma deflexum	KX527519.1
Sterigmostemum eglandulosum	KX434805.1
Sterigmostemum grandiflorum	KX434804.1
Sterigmostemum incanum	KX434806.1
Sterigmostemum fuhaiense	KX434802.1
Sterigmostemum matthioloides	JN847817.1
Sterigmostemum tomentosum	KX434800.1
Sterigmostemum sulphureum	KX434803.1
Sterigmostemum violaceum	JN847818.1
Sterigmostemum violaceum	KX434801.1
Synstemon petrovii	KX527518.1
Veselskya griffithiana	this study

Isatideae phylogeny	***rbcL***
Conringia planisiliqua	this study
Isatis minima	KJ765843.1
Isatis oblongata	KJ765844.1
Isatis pachycarpa	FN594830.1
Isatis tinctoria	JN847841.1
Pachypterygium multicaule	JN847842.1
Schimpera arabica	KX283017.1
Sisymbrium irio (outgroup: Sisymbrieae)	AY167982.1

Thelypodieae phylogeny	***ndhF***
Brassica oleracea (outgroup: Brassiceae)	DQ288742.1
Catadysia rosulans	EU718526.1
Englerocharis pauciflora	EU718543.1
Hesperidanthus barnebyi	EU718550.1
Hesperidanthus linearifolius	EU718553.1
Hesperidanthus suffrutescens	EU718554.1
Mostacillastrum stenophyllum	EU718558.1
Neuontobotrys lanata	EU718559.1
Polypsecadium grandiflorum	EU718560.1
Polypsecadium rusbyi	EU718562.1
Raphanorhyncha crassa	this study
Romanschulzia costaricensis	EU718564.1
Sibara deserti	EU718568.1
Stanleya pinnata	EU718574.1
Stanleya pinnata	EU718575.1
Stanleya viridiflora	EU718577.1
Streptanthus barbatus	EU718581.1
Streptanthus tortuosus	EU718598.1
Thelypodiopsis aurea	EU718600.1
Thelypodiopsis elegans	EU718602.1
Thelypodium rollinsii	EU718608.1
Thysanocarpus curvipes	EU718613.1
Warea amplexifolia	EU718614.1
Warea cuneifolia	EU718615.1
Weberbauera herzogii	EU718616.1
Weberbauera peruviana	EU718618.1

Thlaspideae phylogeny	***ndhF***
Alliaria petiolata	DQ288727.1
Camelinopsis campylopoda	this study
Eutrema salsugineum (outgroup: Eutremeae)	KR584659.1
Graellsia saxifragifolia	DQ288772.1
Parlatoria rostrata	DQ288809.1
Peltaria alliacea	KF023033.1
Pseudocamelina campylopoda	DQ288817.1
Sobolewskia caucasica	KF023034.1
Thlaspi arvense	LC090145.2
Thlaspi arvense	DQ288839.1
Thlaspi perfoliatum	KF023022.1

Table S10. Tribal associations of unplaced taxa

Unplaced taxon	Recommended tribal assignments
Andrzeiowskia cardamine Rchb.	Cardamineae
Arabis josiae Jahand. & Maire	new genus and tribe including *Fourraea alpina,* sister to Bivonaeeae
Arabis ottonis-schulzii Bornm. & Gauba	new genus and tribe sister to Coluteocarpeae
Asperuginoides axillaris (Boiss. & Hohen.) Rauschert	sister to Alysseae, better sampling needed
Camelinopsis campylopoda (Bornm. & Gauba) A.G. Mill.*	Thlaspideae
Chamira circaeoides (L. f.) Zahlbr.	sister to Heliophileae, better sampling needed
Conringia planisiliqua Fisch. & C.A. Mey.	new genus in Isatideae
Dipoma iberideum Franch.	new tribe with *Hemilophia,* sister to Microlepidieae
Fourraea alpina (L.) Greuter & Burdet.	new tribe with *Arabis josiae,* sister to Bivonaeeae
Heldreichia bupleurifolia Boiss.	Biscutelleae**
Hemilophia rockii O.E. Schulz	new tribe with *Dipoma iberideum,* sister to Microlepidieae
Idahoa scapigera (Hook.) A. Nels. & J.F. Macbr.	near *Subularia aquatic*a in the Mexican + South American (CES) clade, currently unresolved
Lunaria rediviva L.	Biscutelleae**
Ochthodium aegyptiacum (L.) DC.	Sisymbrieae
Petrocallis pyrenaica (L.) W.T. Aiton.	Kernereae
Pseudofortuynia esfandiarii Hedge.***	Sisymbrieae
Raphanorhyncha crassa Roll.	Thelypodieae
Ricotia cretica Boiss. & Heldr.	Biscutelleae**
Schrenkiella parvula (Schrenk) D.A. German & Al-Shehbaz	new monospecific tribe
Subularia aquatica L.	near *Idahoa scapigera* in the Mexican + South American (CES) clade, currently unresolved
Veselskya griffithiana (Boiss.) Opiz.	Anchonieae

* *Pseudocamelina campylopoda* (Bornm. & Gauba) Hadač & Chtrek, Esmailbegi *et al.*, 2018

** confirms placement by Özüdoğru *et al.*, 2015, 2017

*** *Sisymbrium leucocladum* (Boiss.) D.A. German & Al-Shehbaz

Table S11. Transcriptome assembly statistics

Species	Number of genes	All contigs				Only longest isoforms				Orthologous groups
		N50	Median	Average	Total length	N50	Median	Average	Total length	
Aethionema arabicum	66554	1672	601	1004.62	112438062	1390	426.5	795.35	52933457	35685
Arabidopsis lyrata	65605	1577	491	903.94	92706157	1397	355	738.29	48435496	29468
Arabidopsis thaliana	23003	2072	1204	1476.42	61020502	2021	1172	1403.13	32276268	16891
Arabis alpina	83281	1471	501	877.85	130812662	1205	347	682.73	56858816	34144
Boechera stricta	53468	1717	684	1062.73	110844442	1592	434	864.45	46220627	27368
Capsella rubella	66075	1685	564	985.39	103507838	1417	403	778.21	51419898	33615
Cardamine hirsuta	25273	2061	1178	1462.35	69214395	2012	1100	1361.6	34411777	17610
Sisymbrium irio	62074	1677	520	953.64	97873933	1520	353	768.17	47683330	26080

Table S12. Gene expression change in the core Brassicaceae

Locus	Gene Symbol	Full Name
AT1G03150		Acyl-CoA N-acyltransferases (NAT) superfamily protein
AT1G03750	*CHR9*	CHROMATIN REMODELING 9, SWITCH 2
AT1G08600	*ATRX*	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT1G09910		Rhamnogalacturonate lyase family protein
AT1G10130	*ECA3, ATECA3*	endoplasmic reticulum-type calcium-transporting ATPase 3
AT1G12450		SNARE associated Golgi protein family
AT1G26160		Metal-dependent phosphohydrolase
AT1G60000		RNA-binding (RRM/RBD/RNP motifs) family protein
AT1G62830	*LDL1, SWP1*	LSD1-like 1
AT1G64260		MuDR family transposase
AT1G65900		unknown protein
AT1G67280		Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily protein
AT1G77260		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT1G79120		Ubiquitin carboxyl-terminal hydrolase family protein
AT2G25010		Aminotransferase-like, plant mobile domain family protein
AT2G26280	*CID7*	CTC-interacting domain 7
AT2G32040		Major facilitator superfamily protein
AT2G33860	*ETT, ARF3*	Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related
AT2G42610	*LSH10*	LIGHT SENSITIVE HYPOCOTYLS 10 (DUF640)
AT2G47250		RNA helicase family protein
AT3G03950	*ECT1*	evolutionarily conserved C-terminal region 1
AT3G04610	*FLK*	RNA-binding KH domain-containing protein
AT3G07130	*ATPAP15, PAP15*	purple acid phosphatase 15
AT3G11230		Yippee family putative zinc-binding protein
AT3G12150		alpha/beta hydrolase family protein
AT3G14270	*FAB1B*	phosphatidylinositol-4-phosphate 5-kinase family protein
AT3G15000	*MORF8*	MULTIPLE ORGANELLAR RNA EDITING FACTOR 8
AT3G19910		RING/U-box superfamily protein
AT3G23150	*ETR2*	Signal transduction histidine kinase, hybrid-type, ethylene sensor
AT3G51480	*ATGLR3.6, GLR3.6*	glutamate receptor 3.6
AT3G53540		afadin
AT3G58030		RING/U-box superfamily protein
AT3G62600	*ATERDJ3B, ERDJ3B*	DNAJ heat shock family protein
AT3G66654		Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein
AT4G03270	*CYCD6;1*	Cyclin D6;1

AT4G04885	*PCFS4*	PCF11P-similar protein 4
AT4G12130		Glycine cleavage T-protein family
AT4G25030		Serine/Threonine-kinase
AT4G30000		Dihydropterin pyrophosphokinase / Dihydropteroate synthase
AT4G31430	*KAKU4*	(JAPANESE FOR NUCLEUS) 4
AT4G32620		Enhancer of polycomb-like transcription factor protein
AT4G34310		alpha/beta-Hydrolases superfamily protein
AT4G35870		early-responsive to dehydration stress protein (ERD4)
AT4G39530		Tetratricopeptide repeat (TPR)-like superfamily protein
AT5G04410	*NAC2, anac078*	NAC domain containing protein 2
AT5G04430	*BTR1, BTR1L*	binding to TOMV RNA 1L (long form)
AT5G04530	*KCS19*	3-ketoacyl-CoA synthase 19
AT5G11390	*WIT1*	WPP domain-interacting protein 1
AT5G12120		Ubiquitin-associated/translation elongation factor EF1B protein
AT5G12130	*PDE149, ATTERC*	integral membrane TerC family protein
AT5G15340		Pentatricopeptide repeat (PPR) superfamily protein
AT5G17900		microfibrillar-associated protein-related
AT5G21140	*emb1379*	embryo defective 1379
AT5G42450		Pentatricopeptide repeat (PPR) superfamily protein
AT5G46840		RNA-binding (RRM/RBD/RNP motifs) family protein
AT5G49530		SIN-like family protein *
AT5G53080		Tetratricopeptide repeat (TPR)-like superfamily protein
AT5G56730		Insulinase (Peptidase family M16) protein
AT5G56930	*emb1789*	CCCH-type zinc finger family protein
AT5G57870	*eIFiso4G1*	MIF4G domain-containing protein / MA3 domain-containing protein
AT5G59710	*VIP2, AtVIP2*	VIRE2 interacting protein 2
AT5G62710		Leucine-rich repeat protein kinase family protein
AT5G63940		Protein kinase protein with adenine nucleotide alpha hydrolases-like domain
AT5G64830		programmed cell death 2 C-terminal domain-containing protein

Table S13. Gene expression change leading to complex-leaved Brassicaceae

Locus	Gene Symbol	Full Name
AT1G05370		Sec14p-like phosphatidylinositol transfer family protein
AT1G09010		glycoside hydrolase family 2 protein
AT1G17930		Aminotransferase-like, plant mobile domain family protein
AT1G19485		Transducin/WD40 repeat-like superfamily protein
AT1G20510	*OPCL1*	OPC-8:0 CoA ligase1
AT1G26500		Pentatricopeptide repeat (PPR) superfamily protein
AT1G76990	*ACR3*	ACT domain repeat 3
AT1G77250		RING/FYVE/PHD-type zinc finger family protein
AT1G77930		Chaperone DnaJ-domain superfamily protein
AT2G01450	*ATMPK17, MPK17*	MAP kinase 17
AT2G14680	*MEE13*	myosin heavy chain-related
AT2G26570	*WEB1*	WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT-like protein (DUF827)
AT2G41520	*TPR15*	Heat shock protein DnaJ with tetratricopeptide repeat
AT2G42880	*ATMPK20, MPK20*	MAP kinase 20
AT3G01810		EEIG1/EHBP1 protein amino-terminal domain protein
AT3G05510		Phospholipid/glycerol acyltransferase family protein
AT3G11945	*PDS2, ATHST, HST*	homogentisate prenyltransferase
AT3G19720	*ARC5, DRP5B*	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT3G43540		initiation factor 4F subunit (DUF1350)
AT3G53320	*GPT2*	GROWING PLUS-END TRACKING PROTEIN 2
AT3G61360		Tetratricopeptide repeat (TPR)-like superfamily protein
AT4G01730		DHHC-type zinc finger family protein
AT4G18060	*SH3P3*	SH3 domain-containing protein
AT4G24530		O-fucosyltransferase family protein
AT4G29490		Metallopeptidase M24 family protein
AT4G38350	*ATNPC1-2*	Patched family protein
AT5G45030		Trypsin family protein
AT5G49530		SIN-like family protein
AT5G51740		Peptidase family M48 family protein

Table S14. Genes and protein residues under positive selection in complex-leaved species

Locus	Gene Symbol	Full Name	sites under selection (P > 95%)	sites under selection (P > 99%)
AT1G05790		lipase class 3 family protein		
AT1G08030	*TPST*	tyrosylprotein sulfotransferase	21M 28T	
AT1G08210		Eukaryotic aspartyl protease family protein	503F	
AT1G08600	*ATRX*	P-loop containing nucleoside triphosphate hydrolases superfamily protein	1V 6E 9S 56S 57S 129S 149S 169K 189S 202S 211S 225S 236L 280P 284N 301R 311S 379S 386T 396S	
AT1G13120	*ATGLE1, GLE1*	nucleoporin GLE1-like protein		
AT1G18750	*AGL65*	AGAMOUS-like 65	360-	325-
AT1G19010		unknown protein		
AT1G19485		Transducin/WD40 repeat-like superfamily protein	5- 6- 8- 13- 23- 28-	10-
AT1G20720		RAD3-like DNA-binding helicase protein	410M	
AT1G22310	*MBD8, ATMBD8*	methyl-CPG-binding domain 8	263V	112R
AT1G23360	*MENG*	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	1N 23L	22R
AT1G26330		DNA binding	19L	
AT1G27980	*DPL1, ATDPL1*	dihydrosphingosine phosphate lyase		
AT1G34355	*ATPS1, PS1*	forkhead-associated (FHA) domain-containing protein		
AT1G34360		translation initiation factor 3 (IF-3) family protein	53D	
AT1G59760		R helicase, ATP-dependent, SK12/DOB1 protein		
AT1G61667		serine protease (DUF538)		
AT1G67420		Zn-dependent exopeptidases superfamily protein	2- 4- 31E	18- 25A 30F
AT1G68890		magnesium ion binding; thiamin pyrophosphate binding; hydro-lyases; 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclo		
AT1G70570		anthranilate phosphoribosyltransferase, putative		
AT1G72416		Chaperone DJ-domain superfamily protein	138V	
AT1G72500		inter alpha-trypsin inhibitor, heavy chain-like protein		
AT1G73730	*EIL3, SLIM1, ATSLIM, AtEIL3*	ETHYLENE-INSENSITIVE3-like 3	569G	6P
AT1G73990	*SPPA, SPPA1*	sigl peptide peptidase	2N	
AT1G74700	*NUZ, TRZ1*	tRNAse Z1	2V	
AT1G75100	*JAC1*	J-domain protein required for chloroplast accumulation response 1	267S	
AT1G75150		DNA ligase-like protein	2E 197T	
AT1G79440	*ALDH5F1, SSADH1, SSADH*	aldehyde dehydrogese 5F1	11D 14S 17R	12L 15P 16R
AT1G79890		RAD3-like DNA-binding helicase protein	10S 117K	
AT2G04340		cytoplasmic dynein 2 light intermediate chain	155D 156V 162A 163R 167S	
AT2G13600		Pentatricopeptide repeat (PPR) superfamily protein		
AT2G19600	*ATKEA4, KEA4*	K+ efflux antiporter 4	14- 21-	15-
AT2G21370	*XK-1, XK1*	xylulose kise-1	8A 9S 10E	
AT2G24640	*UBP19*	ubiquitin-specific protease 19	147G 569D 625L 631D 633E 637A	558G 565V 596D 624P 636D
AT2G27760	*ATIPT2, IPPT, IPT2*	tRNA isopentenyltransferase 2		
AT2G27800		Tetratricopeptide repeat (TPR)-like superfamily protein		3-
AT2G27900		Protein of unknown function DUF2451		
AT2G30530	*MADA4*	zinc finger CCCH domain protein	29-	
AT2G32810	*BGAL9*	beta galactosidase 9	892L 894F	
AT2G32950	*COP1, DET340, FUS1, EMB168*	Transducin/WD40 repeat-like superfamily protein	3T	
AT2G33490		hydroxyproline-rich glycoprotein family protein		
AT2G35130		Tetratricopeptide repeat (TPR)-like superfamily protein	2I 4S 6C	8L
AT2G36960	*TKI1*	TSL-kise interacting protein 1		
AT2G38330		MATE efflux family protein		
AT2G39340		SAC3/GANP/Nin1/mts3/eIF-3 p25 family	115H	
AT2G43210		Ubiquitin-like superfamily protein		
AT2G45460		SMAD/FHA domain-containing protein		

AT2G45670		calcineurin B subunit-related		
AT3G03630	*CS26*	cysteine synthase 26	10A 12D	
AT3G06980		DEA(D/H)-box R helicase family protein		
AT3G07740	*ADA2A*	homolog of yeast ADA2 2A	4S 11D	
AT3G15130		Tetratricopeptide repeat (TPR)-like superfamily protein		
AT3G15290		3-hydroxyacyl-CoA dehydrogese family protein	306Q	
AT3G16565		alanine-tRNA ligases		168V
AT3G18215		Protein of unknown function, DUF599		
AT3G25600		Calcium-binding EF-hand family protein	15Q	
AT3G45890	*RUS1*	Protein of unknown function, DUF647	95G	
AT3G49320		Metal-dependent protein hydrolase		4E
AT3G53920	*SIGC, SIG3*	Rpolymerase sigma-subunit C		
AT3G55080		SET domain-containing protein	89T	
AT3G59090		tobamovirus multiplication protein		397H
AT3G59680		Serine/Threonine-kinase	8F 15L 16S	27I 29F 30M 35T 36S 38A
AT3G59780		Rhodanese/Cell cycle control phosphatase superfamily protein	89R 109T	
AT3G61540		alpha/beta-Hydrolases superfamily protein	53G	
AT4G00980		zinc knuckle (CCHC-type) family protein		
AT4G03110	*AtRBP-DR1, RBP-DR1*	R-binding protein-defense related 1	407A 409Q 413N 414M 417G 421G 428Q 436G 443- 446S	399F 401S 402Y 403D 404S 410N 420L 430K 439-
AT4G03960		Phosphotyrosine protein phosphatases superfamily protein	6F 204Y	
AT4G11970		YTH family protein	408R	
AT4G16510		YbaK/aminoacyl-tRNA synthetase-associated domain	14K 23A	18I
AT4G16765		2-oxoglutarate (2OG) and Fe(II)-dependent oxygese superfamily protein	7F	5S 6K 10E
AT4G18600	*WAVE5, ATSCAR-LIKE, SCARL*	SCAR family protein		
AT4G19020	*CMT2*	chromomethylase 2	788S	
AT4G24060		Dof-type zinc finger DNA-binding family protein	5G	
AT4G26660		kinesin-like protein	13- 16L 25L 89H 137L	
AT4G27510		2-isopropylmalate synthase		
AT4G27640		ARM repeat superfamily protein		
AT4G32190		Myosin heavy chain-related protein		
AT4G34530	*CIB1*	cryptochrome-interacting basic-helix-loop-helix 1	14L 15N	2F 7F 16P
AT4G35250		D(P)-binding Rossmann-fold superfamily protein	4K 7A 10V 11V	
AT4G39410	*WRKY13, ATWRKY13*	WRKY DNA-binding protein 13	2Q	
AT5G01030		Protein of unknown function (DUF3527)		
AT5G01950		Leucine-rich repeat protein kise family protein		
AT5G06610		lipase (DUF620)	10E 372T	
AT5G08470	*PEX1*	peroxisome 1		
AT5G11040	*TRS120, AtTRS120*	TRS120		
AT5G11640		Thioredoxin superfamily protein	11F	
AT5G13410		FKBP-like peptidyl-prolyl cis-trans isomerase family protein		
AT5G14970		seed maturation-like protein	10-	8-
AT5G15410	*DND1, ATCNGC2*	Cyclic nucleotide-regulated ion channel family protein		
AT5G16715	*EMB2247*	ATP binding; valine-tRNA ligases; aminoacyl-tRNA ligases		
AT5G23050	*AAE17*	acyl-activating enzyme 17		
AT5G35930		AMP-dependent synthetase and ligase family protein	113S	
AT5G36740		Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein	609K	
AT5G45710	*AT-HSFA4C, RHA1, HSFA4C*	winged-helix DNA-binding transcription factor family protein		207N
AT5G46390		Peptidase S41 family protein		
AT5G47860		Gut esterase (DUF1350)	29K	
AT5G48030	*GFA2*	gametophytic factor 2		
AT5G51690	*ACS12*	1-amino-cyclopropane-1-carboxylate synthase 12		6S 7T
AT5G55760	*SRT1*	sirtuin 1	15P	
AT5G62770		membrane-associated kise regulator, putative (DUF1645)	239E	
AT5G63990		Inositol monophosphatase family protein	11R	