Supplement Table 1. Computer performance of HybPhyloMaker for 6 pairs of FASTQ input files containing 1.3-1.9 million raw reads each and targeting 4,926 exons (1,164 loci); samples from the plant genus *Oxalis*[11]. Scripts were run on a computer equipped with Intel Xeon E7-4860 CPU using 4 cores at 2.27 GHz and running CentOS 7.3.1611.

SCRIPT	RUN TIME [HH:MM:SS]	SIZE OF GENERATED FILES [MB]	PEAK RAM [GB]
0a - data preparation	0:00:03	963	0.01
0b - pseudoreference generation	0:00:01	3	0.01
1 - raw read processing	0:29:05	1 888	2.66
2 - read mapping & consensus calling	1:09:15	702	1.91
3 - exons to probe match	0:00:05	24	0.05
4 - exon alignment & loci concatenation	0:10:13	43	0.03*
4b - reading frame correction, exon alignment & loci concatenation	0:21:27	101	0.02*
5 - missing data calculation[a]	0:03:52	15	0.25
6a - RAxML gene trees[b]	1:39:33	85	0.01*
6a2 - RAxML gene tree properties & summary	0:00:46	30	0.17*
6b - FastTree gene trees[c]	0:02:25	9	0.17*
7 - gene tree combination	0:00:01	1	<0.01
8a - ASTRAL[d]	0:00:20	13	2.08*
8b - ASTRID[d]	0:00:05	< 1	0.04*
8c - MRL[b]	0:00:03	< 1	0.04*
8e - FastTree (concatenation)[c]	0:02:43	< 1	4.32*
8f - ExaML (concatenation), incl. PartitionFinder[e]	5:45:25	127	9.37*
9 – update	0:00:12	3	0.17
10 - gene tree collapsing & subselect	0:00:05	1	0.17
TOTAL	8:06:06	4 008	

[a]missing data filter: 70% of missing data per sample per gene allowed, 75% presence of samples per gene, [b]100 rapid bootstrap replicates, [c]without bootstrapping, [d]100 multilocus bootstrap replicates, [e]100 bootstrap replicates, *increases with number of samples.

Supplement Table 2. Comparison of three different read mapping software (Bowtie 2.2.4 with very-sensitive-local settings, BWA 0.7.15 with default settings using 'bwa mem', and Geneious 6.1.5 with medium sensitivity). Raw 2×150 bp Illumina reads from six samples from the plant genus *Oxalis*[11] were pre-processed (adapter-trimmed, quality-filtered, and de-duplicated) using HybPhyloMaker1. Both paired-end and orphaned reads were mapped to a "pseudoreference" consisting of 4,926 exon sequences separated by 400 Ns each. Number and percentage of mapped reads (for all three mappers) and percentage of reads mapped relatively to Geneious are presented.

						BOWTIE 2			BWA			GENEIOUS
NAME AND CODE	NR. OF RAW READS	NR. OF PAIRED READS	NR. OF FORWARD UNPAIRED READS	NR. OF REVERSE UNPAIRED READS	NR. OF MAPPED READS	% OF MAPPED READS	% OF MAPPED READS RELATIVE TO GENEIOUS	NR. OF MAPPED READS	% OF MAPPED READS	% OF MAPPED READS RELATIVE TO GENEIOUS	NR. OF MAPPED READS	% OF MAPPED READS
Oxalis blastorrhiza J557	1,303,985	1,231,666	55,107	17,212	193,596	14.9%	80.9%	223,885	17.1%	93.4%	239,171	18.3%
Oxalis creaseyii J11-961	1,167,004	1,119,048	32,483	15,473	243,657	20.9%	80.9%	281,520	24.0%	93.1%	301,336	25.8%
Oxalis gracilis J558	1,051,773	1,006,128	32,432	13,213	304,092	28.9%	81.6%	347,434	32.9%	92.8%	372,499	35.4%
Oxalis helicoides J319	1,489,410	1,432,492	38,972	17,946	263,261	17.7%	77.4%	304,272	20.4%	89.1%	340,109	22.8%
Oxalis inconspicua J595	1,231,224	1,169,552	43,894	17,778	211,367	17.2%	79.3%	242,862	19.7%	90.9%	266,399	21.6%
Oxalis polyphylla J11-44	1,425,204	1,348,436	61,618	15,150	160,534	11.3%	67.6%	186,046	13.0%	78.2%	237,300	16.7%