Figure S1. Phylogenetic tree of *Ludisia* sp. for the ITS DNA barcoding marker. In frame are highlighted the available *L. discolor* sequences in the database including the ITS sequences from this study. The percentage of replicate trees in which the associated taxa clustered together are shown next to the branches [12]. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using Neighbor-Joining method and Kimura 2-parameter model [13] and are in the units of the number of base substitutions per site. This analysis involved 45 nucleotide sequences. All ambiguous positions were removed for each sequence pair (pairwise deletion option).
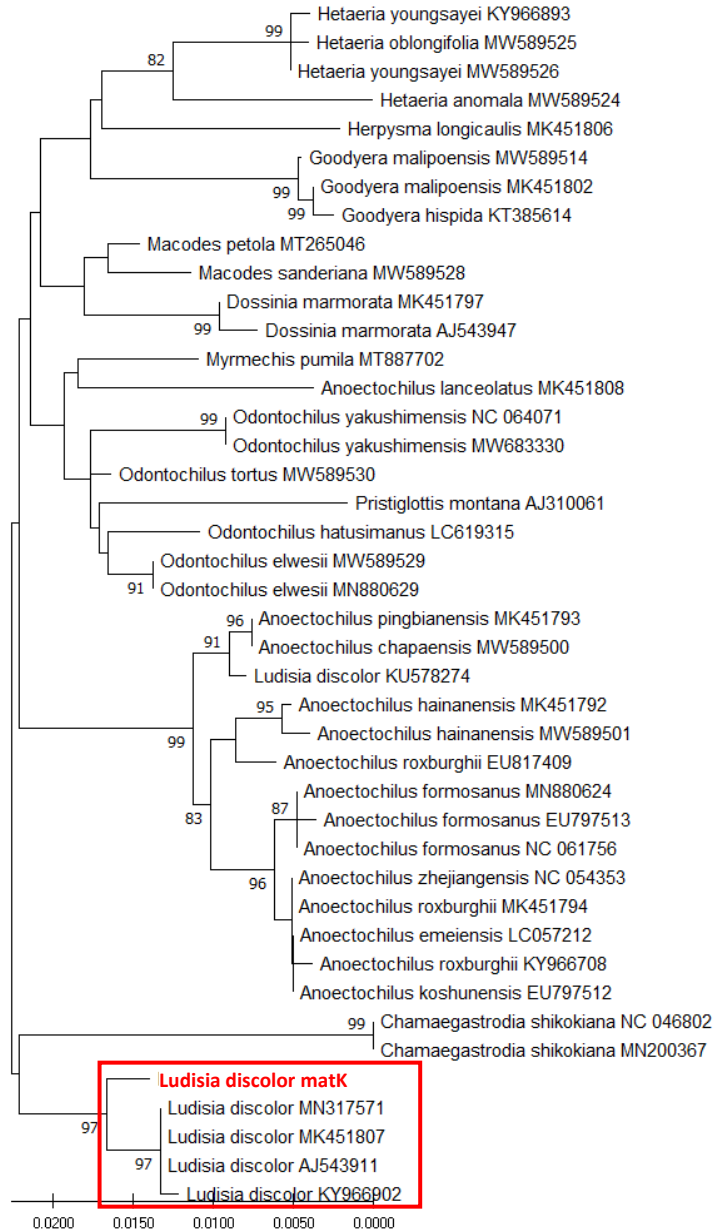
Figure S2. Phylogenetic tree of *Ludisia* sp. for the matK DNA barcoding marker. In frame are highlighted the available *L. discolor* sequences in the database including the matK sequences from this study. The percentage of replicate trees in which the associated taxa clustered together are shown next to the branches [12]. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using Neighbor-Joining method and Kimura 2-parameter model [13], and are in the units of the number of base substitutions per site. This analysis involved 42 nucleotide sequences for matK. All ambiguous positions were removed for each sequence pair (pairwise deletion option).
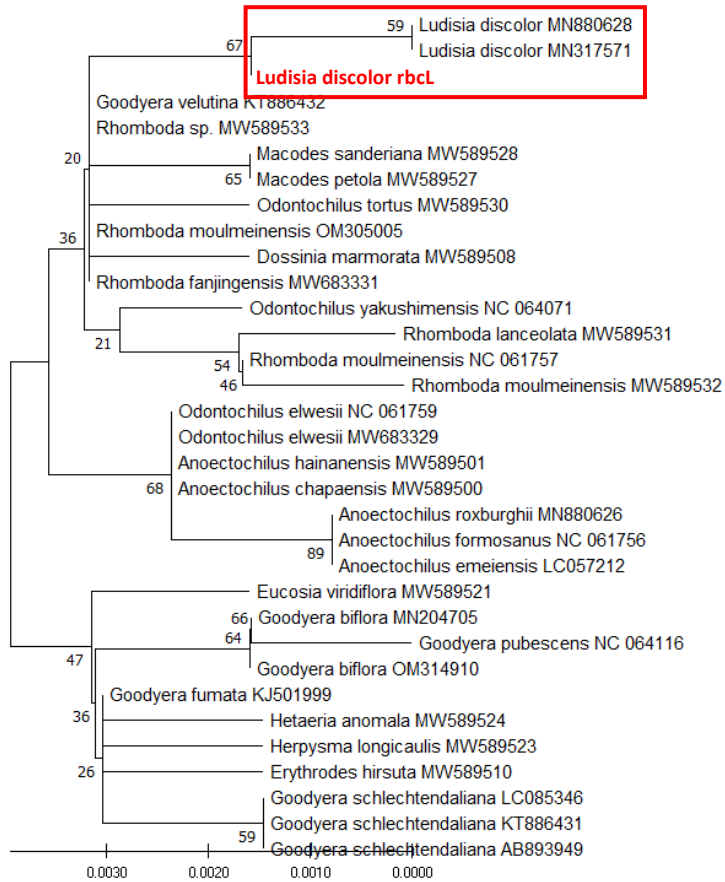
Figure S3. Phylogenetic tree of *Ludisia* sp. for the rbcL DNA barcoding marker. In frame are highlighted the available *L. discolor* sequences in the database including the rbcL sequences from this study. The percentage of replicate trees in which the associated taxa clustered together are shown next to the branches [12]. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using Neighbor-Joining method and Jukes-Cantor method [14] for rbcL and are in the units of the number of base substitutions per site. This analysis involved 33 nucleotide sequences. All ambiguous positions were removed for each sequence pair (pairwise deletion option).
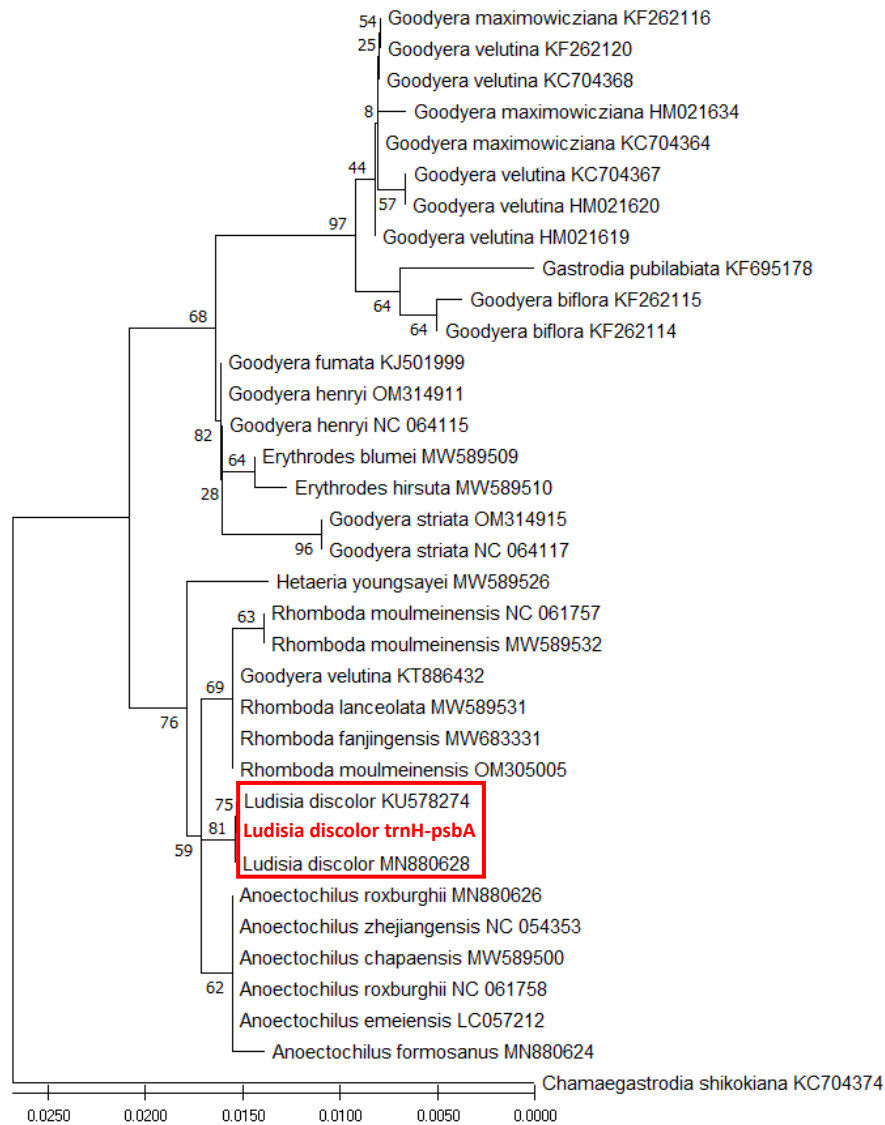
Figure S4. Phylogenetic tree of *Ludisia* sp. for the trnH-psbA DNA barcoding marker. In frame are highlighted the available *L. discolor* sequences in the database including the trnH-psbA sequences from this study. The percentage of replicate trees in which the associated taxa clustered together are shown next to the branches [12]. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using Neighbor-Joining method and Tamura 3-parameter model [15] and are in the units of the number of base substitutions per site. This analysis involved 35 nucleotide sequences. All ambiguous positions were removed for each sequence pair (pairwise deletion option).
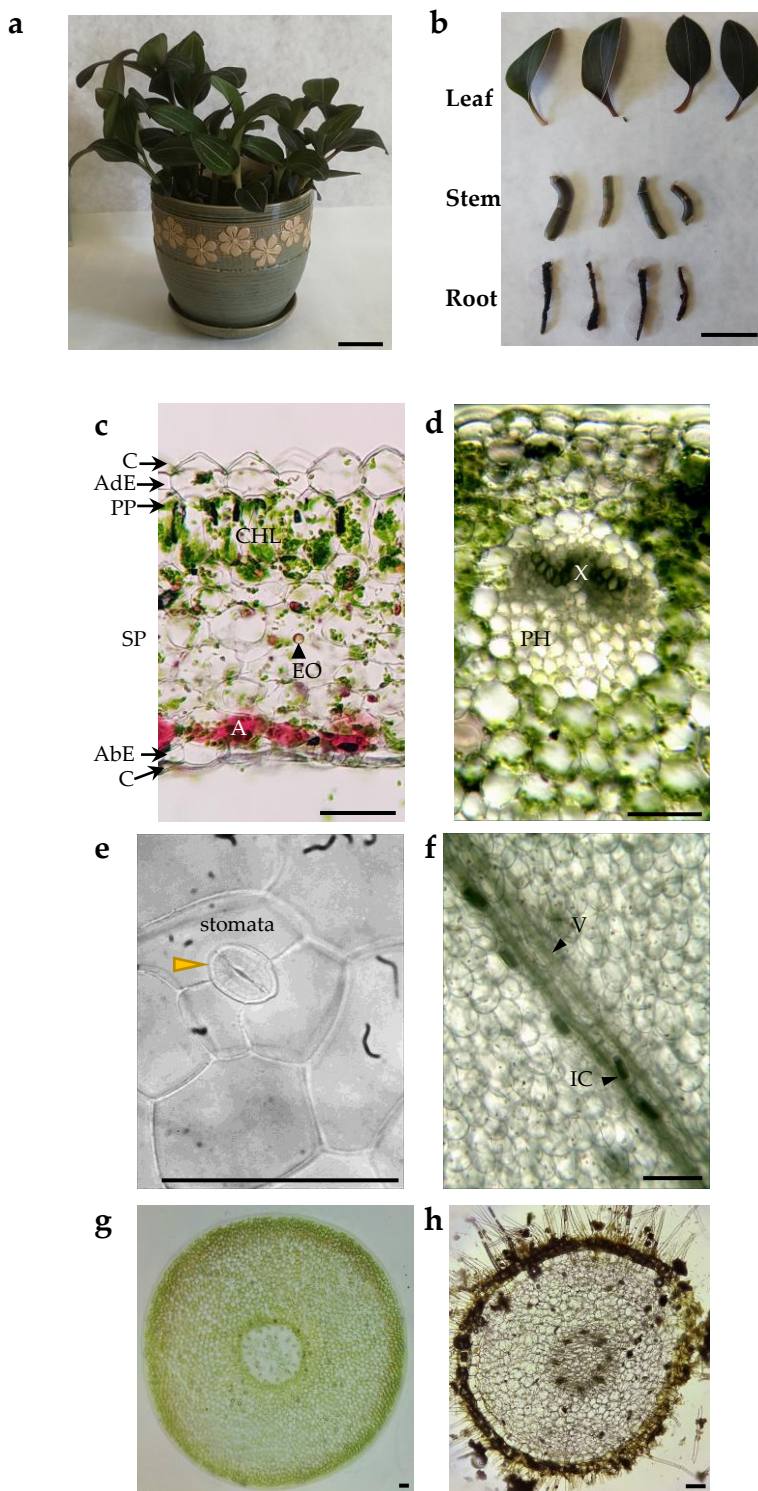
Figure S5. Anatomical overview of vegetative organs of *L. discolor* grown in soil. (a) Pot-grown plant; (b) Morphology of the vegetative organs studied; (c) Leaf cross section; C – cuticle; AdE – adaxial epidermis; PP – palisade parenchyma; SP – spongy parenchyma; AbE – abaxial epidermis. Marked are CHL – chloroplasts; A – anthocyanins; EO – essential oil drop. (d) Leaf cross section at vascular bundle; PH – phloem; X – xylem. (e) Abaxial epidermis – arrow indicates anisocytic type of stomata. (f) Idioblast cells (IC) and vasculature (V). (g) Stem cross section. (h) Root cross section. Scale bar 10 μm.
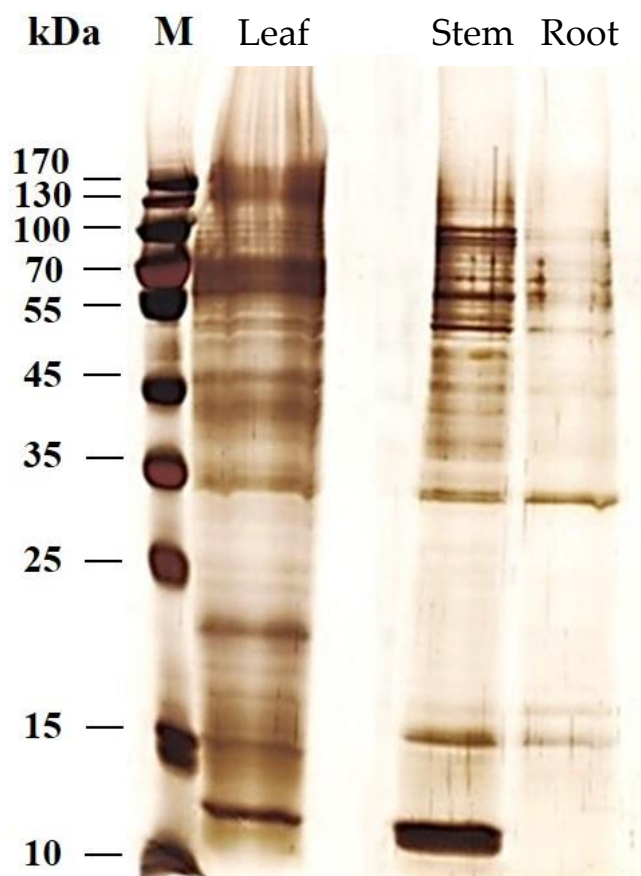
Figure S6. SDS PAGE protein profiles of *L. discolor* leaf, stem and root. Equal amount of extract was loaded on to each line.
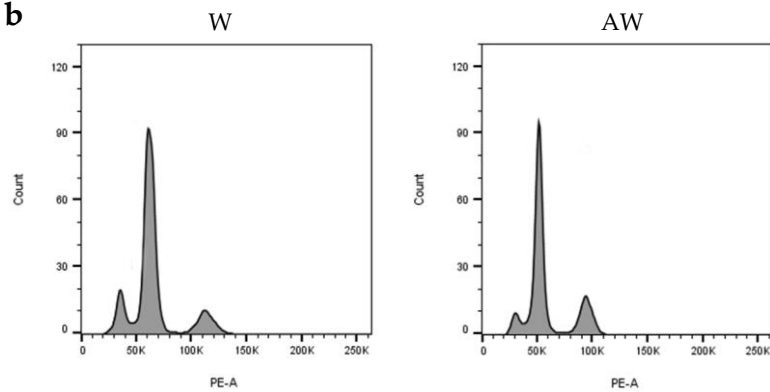
Figure S7. Flowcytometric analysis of W and AW leaves of *L. discolor* grown in soil. (a) Leaf samples for analysis. The cut leaf region taken for analysis is shown. (b) Flowcytometric data. W – water; AW – aquaponics water.

Grow lights

"Flood and drain" type Grow beds

Grow lights

Sedimentaion filter

Bio-filter

"Flood and drain" type Grow beds

Fish rearing tank

Sump tank with pumps

AWS

L. discolor

Figure S8. Aquaponic water system (AWS). The AWS has vertical aquaponics set-up, using a Media Bed system based on the model of "Info-graphic of an Aquaponic system made by Els Engel". Adapted from [37]. Zoomed view of *L. discolor* in AWS.
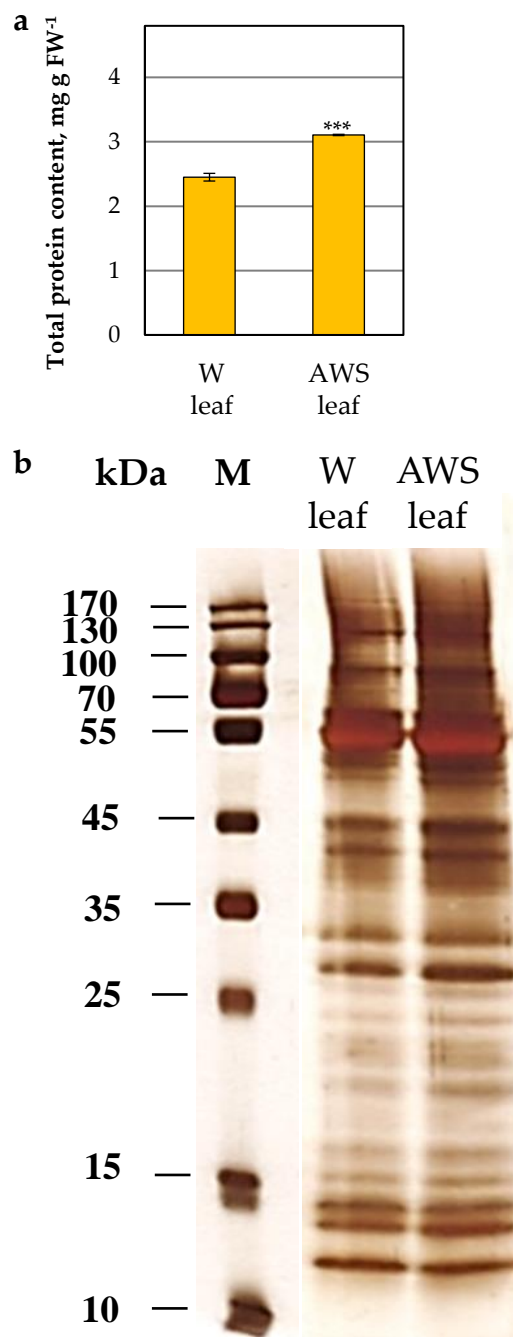
Figure S9. Protein content in *L. discolor* leaves grown in AWS in comparison with soil-grown control. (a) Total protein. (b) SDS-PAGE protein profile. Equal amount of extract was loaded on to each line. Protein ladder (M) indicates the approximate band sizes.

Table S1. Oligonucleotide primers used for amplification of DNA barcode regions.

Barcode Region	Primers	Primer Sequences 5′-3′	PCR Conditions	Reference
ITS	AB101	ACGAATTCATGGTCCGGTGAAGTGTTCG	94°C 5 min 94°C 30 s 58°C 1 min	[38]
	AB102	GAAACGGTCTCTCCAACGCAT	72°C 1 min, 35x 72°C 5 min	
rbcL	rbcLa-F	ATGTCACCACAAACAGAGACTAAAGC	94°C 4 min 94°C 30 s 55°C 30 s	[39]
	rbcLajf634R	GAAACGGTCTCTCCAACGCAT	72°C 1 min, 35x 72°C 10 min	[40]
matK	matK-KIM1R-f	ACCCAGTCCATCTGGAAATCTTGGTTC	94°C 4 min 94°C 30 s 51°C 60 s	[41]
	matK-KIM3F-r	CGTACAGTACTTTTGTGTTTACGAG	72°C 60 s, 40x 72°C 4 min	
trnH-psbA	psbA-trnH	CGCGCATGGTGGATTCACAATCC	94°C 4 min 94°C 30 s 55°C 30 s	[42]
	psbA-3F	GTTATGCATGAACGTAATGCTC	72°C 1 min, 35x 72°C 7 min	[43]

Table S2. Sequences information for DNA barcoding of *L. discolor*.

Barcode Region	Sequence 5′-3′ of *L. discolor*, sequence length (bp)
ITS ~889 bp	CATGGTCCGGTGAAGTGTTCGGATCGCTGTGACGTAGGTGGTTCGCTGCCCGCGACTCTGCGAGA AGTCCATTGAACCTTATCATTTAGAGGAAGGAGAAGTCGTAACAAGGTTTCCGTAGGTGAACCTG CGGAAGGATCATTGTCGAGACCCTAAAGAGGATTGGATGACTTTGGATAACACGTGAACAATTG ACGACGATTGTCGTCTATAAGCACCATCCATCTATTGTCATTTCTTGATCGAAGTTACAATGAAAA GATGGAAGGAAAACAACTCGGGCGCAGTTATGTGCCAAGGAAGTATGCTGCATAGGCATCGATG GCTATTCGGCAAAGCCTGGCGTGCTTTGCGGAGTGCTGTTGTTGCTTCTTAAGTATTGTATGACTCT CGGCAATGGATATCTTGGCTCTTGCATCGATGAAGAGCGCAGCGAAATGCGATACGTGGTGTGAA TTGCAGAATCCCGTGAACCATCAAATCTTTGAACGCAAGTTGCGCCCGAGGCCATTTGGCTAAGG GCACGTCCGCCTGGGCGTCAAGCATTACATCGCTTCATTCGACACCGATTGCCCAATTTTGTGCGG TGGTGCCGATTCGAATGCGGAGAGTGGCCCTTCGCGCGTACTTGTGCGACGGGTTGAAGAACAGT TTGCTTTCCTCTGGCCATGTTTTGATAAAGGGGTGGTGTATGCTGCCATTTGGCCCACGCTATCATC TCATTGTCTTGAGGAAAATATCTGTACACATTCCTGGCTGTTCACCCGATATTGTCGTAGGTGGCG CCCTGAAATGCGACCCCAGGTTGGGCGGGATGACCCGCTGAGTTTAAGCATATCAATAAGCGGA GGAGAAGAAACTTACAAGGATTCCCTTAGTAACGGCGAGC
rbcL 635 bp	AAACAGAGACTAAAGCAAGCGTTGGATTTAAAGCTGGTGTTAAAGATTACAAGTTGACTTATTAT ACTCCTGACTACGAAACCAAAAGTACTGATATCTTGGCAGCATTCCGAGTAACTCCTCAACCGGG AGTTCCGCCTGAAGAAGCGGGCGCTGCGGTAGCAGCCGAATCTTCTACTGGTACATGGACAACTG TGTGGACTGATGGACTTACCAGTCTTGATCGTTACAAAGGACGATGCTACCACATTGAGCCCGTT GTTGGGGAGGAAAATCAATATATTGCTTATGTAGCTTATCCTTTAGACCTTTTTGAAGAAGGTTCT GTTACTAACATGTTTACTTCCATTGTGGGTAATGTTTTTGGTTTCAAAGCCCTGCGAGCTCTACGTC TGGAAGATCTGCGAATTCCCCCTTCTTATTCCAAAACTTTCCAAGGCCCGCCTCATGGCATCCAAG TTGAAAGAGATAAATTGAACAAGTATGGTCGTCCCCTATTGGGATGTACTATTAAACCAAAATTG GGATTATCCGCAAAAAACTACGGTCGAGCGGTTTATGAATGTTTACGGGGTGGACTTGATTTTACT AAGGATGATGAAAACGTGAACTCACAACCATTTATGCGTTGGAGG
matK 825 bp	TGGAATCTTGGTTCAAATGCTTCAATGCTGGATCAAAGATGTTCCTTCTTTGCATTTGTTGCGATTT ATTTTCCACGAATATTATAATTTGAAGAGTATCATTACTTCAAAGAAATCCATTCACGTTTTTTCAA AAAAAAAGAAAAGATTTTTTTGGCTCCTACATAATTTTTATGTATATGAATGCGAATATCTTTTTCT TTTTCTTCGTAAAAAGTCTTCTTATTTACGATCAACATCTTTTGGAGTCTTTATTGAGCGAACACTTT TTCATGTAAAAAATGGAATCTATTTTAGTAGTGTATTTTAATTCTTTTCAGAGGATTCTCTGGTTCCTC AAAGATCCTTTCATACATTATGTTCGATATCAAGGAAAAGTAATTCTGGCTTCAAAGGGAACTCTT ATTCTGATGAAGAAATGGAATTTTCATGTTGTGAATTTTTGGCAATTTTATTTTCACTTTTGGTCTCA ACCTTATAGGATCCATATAAAGCAATTACCCAACTATTCCTTCTCTTTTCTGGGGTATTTTTTAAGT GTACAAAAAAAAACTTTGGTAGTAAGAAATCAAATGCTAGAGAATTCCTTTCTAATAAATACTCT GACTAAGAAATTAGATACCATAGCCCCAGTTATTTCTCTTATTGGATCATTGTCGAAAGCTCAATT TTGTACTATATCGGGTCATCCTATTAGTAAACCAATTTGGACCGATTTATCGGATTCTGATATTATT GATCGATTTTGTCGAAAATGTAGAAATCTTTGTCGTTATCACAGCGGATCCTCAAAAAAAAAAGT TTTGTATCGTATAAAATATATACT
trnH-psbA 723 bp	AAAAARGTAAAAAAAAAAAAAAAAAAAAAGGAGTAATCGGCCGTGACACGTTCACTAAAAAA AAATCCTTTTGTAGCTAATCATTTATCGGTAAAAATTGAAAAACTCAACATGAGGGAGGAGAAA GAAATAATAGTGACTTGGTCTAGGGCATCTACCATTATACCCACAATGATTGGCCATACAATCGC TATTCATAATGGAAAGGAACATTTACCTATTTATATAACAGATCGTATGGTCGGTCACAAATTGG GAGAATTCGCACCTACTCTCACTTTCGTGAGACATGCGAGAAATGATAATAAATCTCGTCGTTAG TCGTTCTACTAAGTATTCATGTGAAAAGTCTTATCTTAATAGTATTTCAACTTAAGAGTCTTTATCT TATAGTAAGAGTATAGGTATAGTCTTTTATAGTATACTAATATACTAAGACTTAGATTTTTCTTACT TATCTTATACTATACTTCACCTAGGCACTTATCATTCATTGGCGGGGGAGAACTTTCTTTTATGATA AAGAACGAAAATTCGGAGAAATCGGATAAAGAAGCAAAGTGTTAGCTCAACATATACATATGT CTGTTTTCAAAGCACGAAGAGTAATAGCAATCCCCAATATCCAACATATTGGATATTGGGGATTG CTACCTTAAAGAATTCATCTACATAGAAAATAAATAAATACAAAGTATTATCCATTTGTAGATG GAGCTCC