

## SUPPLEMENTARY MATERIAL

**Table S1.** Exon-primed intron-crossing (EPIC) oligonucleotides designed from GenBank accessions for amplification of plant nuclear introns (note that orientation of reverse primer is presented in 3' to 5' direction).(a) “Ros $W_{xy}$ ” primers for amplification of granule-bound starch synthase ( $W_{xy}$ ) intron

Family	Species (GenBank accession)	Upstream alignment	Downstream alignment	bp
Rosaceae	<i>Adenostoma fasciculatum</i> (AF500389)	CTGGTGGACTCGGTGATGTTCTTGG	GGTATGGGGGAAAACATCGAA	545
	<i>Cercocarpus betuloides</i> (DQ904400)	.....	.....T.....T..C..	544
	<i>Chaenomeles speciosa</i> (DQ874902)	.....	.....C.....G...C..	593
	<i>Chamaebatiaria millefolium</i> (DQ904403)	.....	.....G.....C..	525
	<i>Coluria geoides</i> (AJ534183)	.....	...T....A.....A..	?
	<i>Dryas octopetala</i> (AM116868)	.....	.....T.....G...C..	529
	<i>Eriobotrya japonica</i> (DQ874901)	.....	.....A.....G...C..	589
	<i>Fallugia paradoxa</i> (AM116869)	.....	.....AT.....G...C..	520
	<i>Filipendula vulgaris</i> (AM116870)	.....	.....T.....G...C..	523
	<i>Geum urbanum</i> (AJ534193)	.....	...T....A.....A..	?
	<i>Peraphyllum ramosissimum</i> (DQ874903)	.....	.....C.....G...C..	592
	<i>Prunus virginiana</i> (AF500453)	.....	...T.....C.....C..	515
	<i>Purshia tridentate</i> (DQ904405)	.....	.....T.....G...C..	496
	<i>Rhaphiolepis indica</i> (AF500461)	.....	.....C.....G...C..	592
	<i>Rhodotypos scandens</i> (DQ904406)	.....	.....G.....C..	563
	<i>Sorbaria sorbifolia</i> (DQ904407)	.....	.....T.....G...C..	552
	<i>Sorbus americana</i> (AF500465)	.....	.....C.....G...C..	574
	<i>Spiraea trilobata</i> (DQ904408)	A.....	.....T..G...A...C..	584
	<i>Stranvaesia davidiana</i> (AF500472)	.....	.....C.....G...C..	588
	<i>Tormalis clusii</i> (AF500474)	.....	...G.....C..	683
Moraceae	<i>Ficus robusta</i> (DQ367648)	.....	...T.....GT..C..	?
<b>Primer sequences</b>		F: 5'- ctggtggactcggatgatggttcttgg -3'	R: 3'- ccawacccnttttgacgtaggtt -5'	

**Table S1** *continued*

**(b)** “Ros*Lfy*” primers for amplification of floral meristem identity protein (*Lfy*) intron

Family	Species (GenBank accession)	Upstream alignment	Downstream alignment	bp
Rosaceae	<i>Aronia</i> sp. (EF127080)	TACCTCTTCCATCTCTACGAGCA	AGGTGACAAACCAAGTGTITAGGT	588
	<i>Crataegus opaca</i> (EF127059)	.....	.....	320
	<i>Eriobotrya japonica</i> (AY551183)	.....	.....G.....	1023
	<i>Fragaria nubicola</i> (AF487165)	.....	.....T...G.G.....A.	438
	<i>Malus angustifolia</i> (EF127079)	.....	.....	588
	<i>Mespilus canescens</i> (EF127076)	.....	.....	324
Brassicaceae	<i>Arabidopsis thaliana</i> (NM_125579)	.....	.....G.....A..C....	?
	<i>Brassica oleracea</i> (DQ078783)	.....	.....G.....R..C....	?
	<i>Camelina sativa</i> (DQ083760)	.....	.....G.....R..C....	?
Goodeniaceae	<i>Scaevola gaudichaudiana</i> (AY894436)	.....	.....G.....C....	1771
<b>Primer sequences</b>		F: 5'- tacctcttccatctctacgagca -3'	R: 3'- tccactgyttggttcacaaagcca -5'	

**(c)** “Ros*Adh*” primers for amplification of alcohol dehydrogenase (*Adh*) intron

Family	Species (GenBank accession)	Upstream alignment	Downstream alignment	bp
Brassicaceae	<i>Arabidopsis lyrata</i> (AJ251284)	TTCGGCCATGAAGCTGGAGGGT	GACAAAGTTTGATTGTTAGT	425
	<i>Capsella rubella</i> (DQ343321)	.....A.....	.....C..T.....C....	412
	<i>Neslia paniculata</i> (DQ343325)	.....	.....C..T..C..C....	422
	<i>Transberingia bursifolia</i> (DQ343327)	.....	.....T..C..C....	418
Betulaceae	<i>Betula pendula</i> (AJ549107)	C.T.....G..A.....	.....T..CC.C....	443
	<i>Corylus avellana</i> (AJ535656)	..T.....G..A.....	.....T..C.C....	448
Fabaceae	<i>Pisum sativum</i> (X06281)	..T..T.....	.....T..C.C..C	481
Rosaceae	<i>Fragaria x ananassa</i> (X15588)	.AT.....A.....	.....CC.C..C	457
Salicaceae	<i>Populus tremula</i> (AJ842887)	.A...T.....	.....T..C....C	445
<b>Primer sequences</b>		F: 5'- ttygghcatgargcwgagggt -3'	R: 3'- ctgtttcagacatagcagtca -5'	

**Table S1** continued

**(d)** “Ros*Pi*” primers for amplification of pistillata (*Pi*) intron

Family	Species (GenBank accession)	Upstream alignment	Downstream alignment	bp
Brassicaceae	<i>Arabidopsis thaliana</i> (AF055190)	TGGAGCCACAAAACATGGAAG	CATACAGAGGCTTTTATACCA	396
	<i>Boechera stricta</i> (AF307605)	.....	.....G..G.....	417
	<i>Capsella rubella</i> (DQ343500)	..A.....	.....G..G.....	441
	<i>Cusickiella douglasii</i> (AF307607)	.....	.....G..G.....	421
	<i>Halimolobos jaegeri</i> (AF055191)	...A.....	.....G..G.....	411
	<i>Halimolobos berlandieri</i> (AF307608)	..A.....	.....G..G.....	441
	<i>Lepidium hyssopifolium</i> (AY114249)	.....	..C..T...AG..A.....	381
	<i>Lepidium virginicum</i> (AY114285)	.....	..C.....T.A..A.....	399
	<i>Mancoa bracteata</i> (AF307604)	...A.....	.....G..G.....	424
	<i>Neslia paniculata</i> (DQ343501)	.A..A.....	.....GC.G.....	424
	<i>Sphaerocardamum stellatum</i> (AF307583)	.C..A.....	.....G..G.....	413
<b>Primer sequences</b>		F: 5'- tggarccacaaaacatggaag -3'	R: 3'- gtatgtctccsaahatatggt -5'	

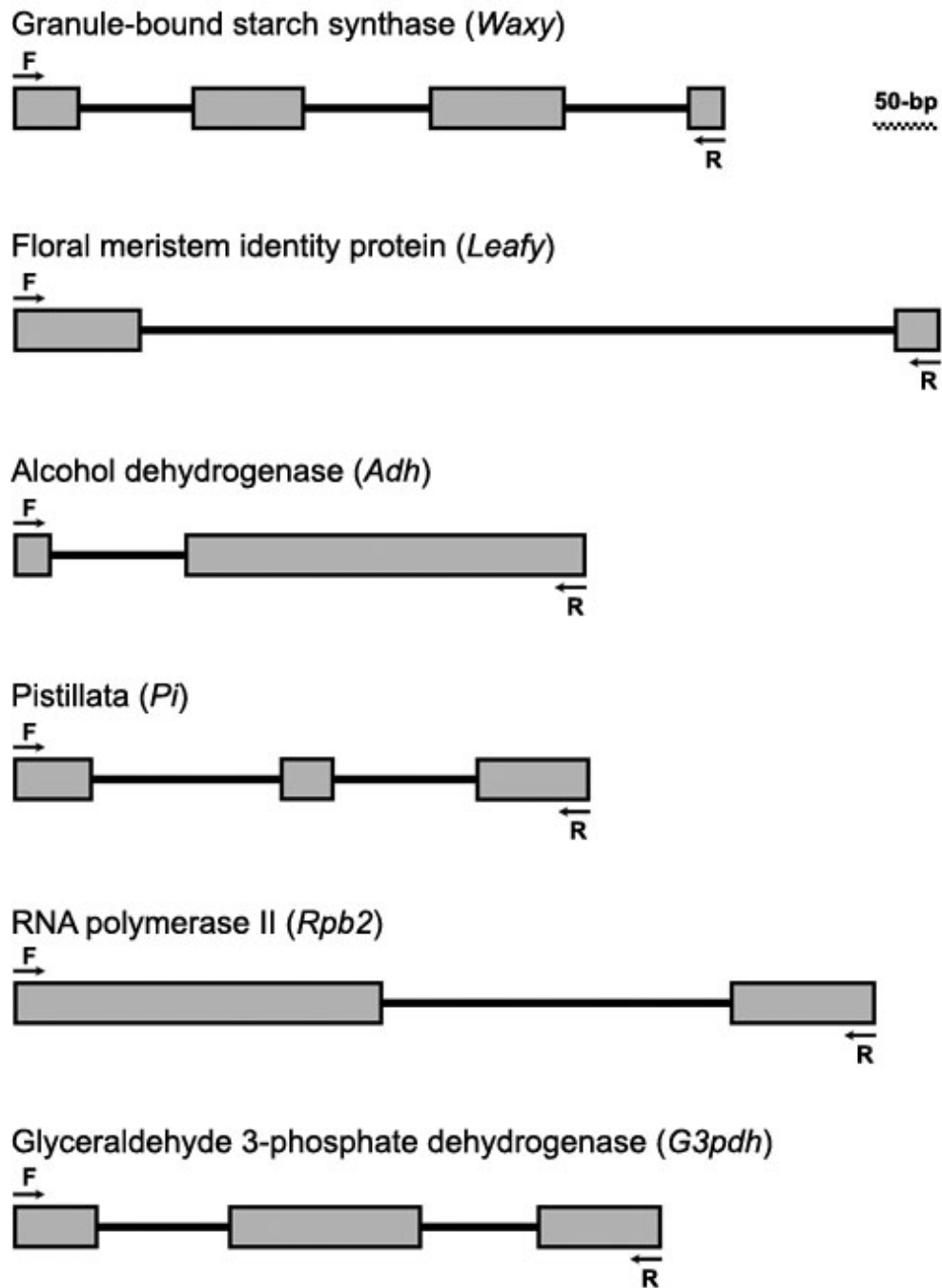
**(e)** “Ros*Rpb2*” primers for amplification of RNA polymerase II (*Rpb2*) intron

Family	Species (GenBank accession)	Upstream alignment	Downstream alignment	bp
Araliaceae	<i>Hedera helix</i> (AJ563601)	CAAATGCTGATGGGCTGAGATTGT	CTTACAGCTATGATATTCCTTGGC	725
Aquifoliaceae	<i>Ilex x meserveae</i> (AJ557240)	.....	.....T.....C.....	398
Cornaceae	<i>Cornus kousa</i> (AJ556175)	.....C.....T.R.....	.....G...	1238
	<i>Davidia involucrata</i> (AJ557003)	.....C.....	.....T.....NNNNNN	875
Convolvulaceae	<i>Evolvulus</i> sp. (AJ565861)	.....C.....T.A....C..	.....C.....C..A	398
Phrymaceae	<i>Mimulus guttatus</i> (AJ558242)	.....A....G.....		?
Stilbaceae	<i>Retzia capensis</i> (AJ133215)	.G..Y.....TT.A.....	.....	398
<b>Primer sequences</b>		F: 5'- caaatgctgatgggctgagatttgt -3'	R: 3'- gaatgtcgatactataaggaaccg -5'	

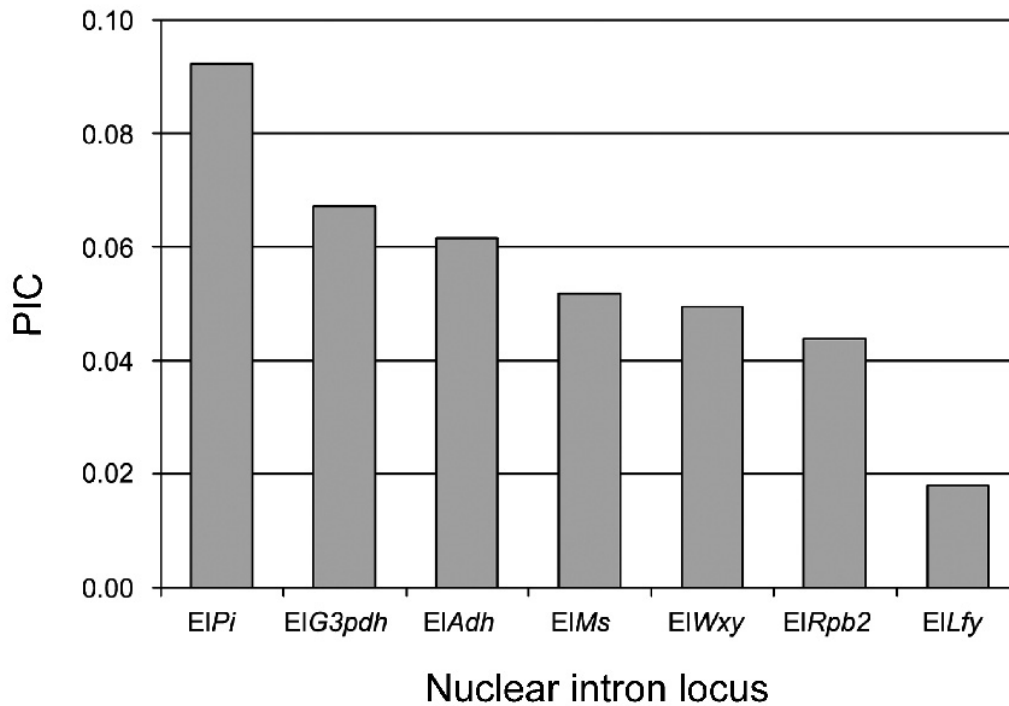
**Table S1** *continued*

(f) “Ros*G3pdh*” primers for amplification of glyceraldehyde 3-phosphate dehydrogenase (*G3pdh*) intron

Family	Species (GenBank accession)	Upstream alignment	Downstream alignment	bp
Moraceae	<i>Ficus adelpha</i> (DQ367615)	ACTGGAGAGGTGGAAGAGC	CGTTGGTGACAGCAGGTAA	466
	<i>Ficus bullenei</i> (AY967991)	.....	.....	467
	<i>Ficus costaricana</i> (AY967952)	.....	.....	466
	<i>Ficus bernaysii</i> (DQ367618)	.....	.....	466
	<i>Ficus robusta</i> (DQ367628)	.....	.....	466
Euphorbiaceae	<i>Manihot esculenta</i> (AF136149)	.....C.....	.....T.....	555
	<i>Manihot esculenta</i> (AF136146)	.....	.....A..T.....	555
	<i>Manihot pruinosa</i> (AF136132)	.....	.....T.....	555
<b>Primer sequences</b>		F: 5'- actggagaggyggaagagc -3'	R: 3'- gcaaccactrtcgtccatt -5'	



**Figure S1.** Maps of nuclear gene regions targeted by EPIC primers generated in this study. Primers are represented by arrows (F, forward; R, reverse), and grey boxes designate putative exons. Approximate lengths of each intron (black lines) were determined by averaging across accessions included in the alignment (see Table S1).



**Figure S2.** Comparison of phylogenetic signal carried by seven nuclear introns based on joint analysis of sequences from four *Euphorbia* species. Potentially informative characters (PIC) calculated as number of substitutions plus number of indels divided by total number of base pairs (where contiguous alignment gaps were treated as a single-event fifth character state). Locus abbreviations follow the main text.