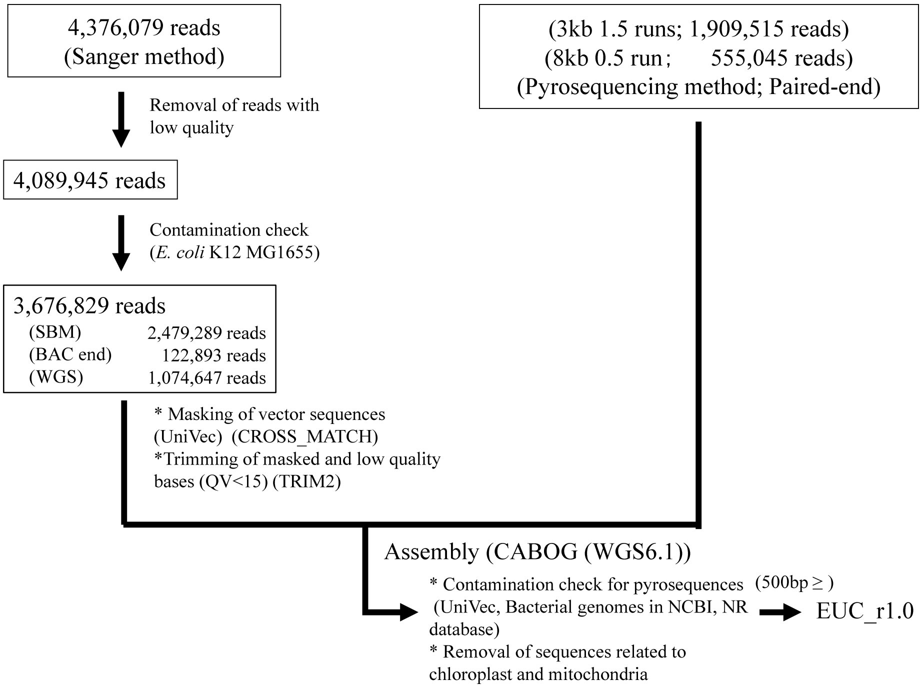

Supplemental Figure 1. Strategy and status of genome sequencing.

Supplemental Table 1. Motifs of simple-sequence repeats in the *E. camaldulensis* genomic sequences.

	Genome sequences			cDNA sequences		
SSR pattern	Count	Rate in same category	Freauency in 100 kb	Count	Rate in same category	Freauency in 100 kb
AG	40,019	81.9%	6.40	566	95.0%	4.43
AT	6,887	14.1%	1.10	12	2.0%	0.09
AC	1,870	3.8%	0.30	13	2.2%	0.10
GC	83	0.2%	0.01	5	0.8%	0.04
AAG	9,796	35.3%	1.57	146	14.6%	1.14
AAT	6,051	21.8%	0.97	11	1.1%	0.09
GGA	3,829	13.8%	0.61	197	19.7%	1.54
GGC	3,166	11.4%	0.51	372	37.3%	2.91
ATC	1,712	6.2%	0.27	36	3.6%	0.28
GGT	893	3.2%	0.14	76	7.6%	0.59
AGC	804	2.9%	0.13	77	7.7%	0.60
AAC	743	2.7%	0.12	24	2.4%	0.19
ACG	582	2.1%	0.09	57	5.7%	0.45
ACT	171	0.6%	0.03	2	0.2%	0.02
AAAT	7,074	47.3%	1.13	20	13.2%	0.16
AATT	1,629	10.9%	0.26	2	1.3%	0.02
AAAG	1,341	9.0%	0.21	15	9.9%	0.12
GGGA	1,298	8.7%	0.21	24	15.8%	0.19
ATAC	891	6.0%	0.14	4	2.6%	0.03
AAAC	399	2.7%	0.06	2	1.3%	0.02
AATC	354	2.4%	0.06	1	0.7%	0.01
GGAA	301	2.0%	0.05	18	11.8%	0.14
GAGC	242	1.6%	0.04	19	12.5%	0.15
AATG	182	1.2%	0.03	0	—	—
GACA	155	1.0%	0.02	4	2.6%	0.03
GTGC	132	0.9%	0.02	2	1.3%	0.02
GGAT	92	0.6%	0.01	2	1.3%	0.02
GATA	88	0.6%	0.01	1	0.7%	0.01
GCAT	78	0.5%	0.01	1	0.7%	0.01
GATC	77	0.5%	0.01	5	3.3%	0.04
GGGC	77	0.5%	0.01	6	3.9%	0.05
GGGT	76	0.5%	0.01	1	0.7%	0.01
GGTC	66	0.4%	0.01	5	3.3%	0.04
GGAC	62	0.4%	0.01	3	2.0%	0.02
AAGC	59	0.4%	0.01	3	2.0%	0.02
AACG	59	0.4%	0.01	3	2.0%	0.02
Other tetra-nucleotide	232	1.6%	0.04	11	7.2%	0.09
Total	91,570		14.64	1,746		13.65

Supplemental Table 2. Repetitive sequences in the *E. camaldulensis* genomic sequences.

	Copy number	Coverage (kb)	Fraction of genome (%)
Class I			
SINEs	9,704	1,433.0	0.22%
LINEs	3,571	3,190.4	0.49%
LTR: Ty1/copia	69,892	59,337.4	9.06%
LTR: Ty3/gypsy	82,191	51,959.2	7.93%
Other LTR	2,669	1,417.1	0.22%
TRIMs	6,273	2,130.2	0.33%
Total class I	174,300	119,467.5	18.24%
Class II			
Coding class II	9,539	3,509.3	0.54%
MITE	43,410	8,467.6	1.29%
Total class II	52,949	11,976.9	1.83%
Unclassified	140,066	35,752.4	24.24%

Supplemental Table 3. Gene classification according to the GO slim categories.

GO Term	*Eucalyptus camaldulensis* (total: 77,121)		*Popupus trichocarpa* (total: 27,665)		*Arabidopsis thaliana* (total: 35,386)		Category
	Count of gene products for which this is the most relevant slim term	Count of gene products inferred to be associated with slim term	Count of gene products for which this is the most relevant slim term	Count of gene products inferred to be associated with slim term	Count of gene products for which this is the most relevant slim term	Count of gene products inferred to be associated with slim term	
GO:0008150 biological_process (biological_process)	278	31,375	113	9,047	139	11,628	biological_process
GO:0009838 abscission (abscission)	0	0	0	0	0	0	biological_process
GO:0009653 anatomical structure morphogenesis (anatomical structure morphogenesis)	2	2	3	3	2	2	biological_process
GO:0007610 behavior (behavior)	0	0	0	0	0	0	biological_process
GO:0007267 cell-cell signaling (cell-cell signaling)	0	0	0	0	0	0	biological_process
GO:0016043 cellular component organization (cellular component organization)	831	831	315	315	423	423	biological_process
GO:0016049 cell growth (cell growth)	0	0	0	0	0	0	biological_process
GO:0009987 cellular process (cellular process)	4,773	22,577	2,659	5,887	3,417	7,611	biological_process
GO:0007154 cell communication (cell communication)	7	240	9	83	14	48	biological_process
GO:0007049 cell cycle (cell cycle)	33	33	62	62	82	82	biological_process
GO:0008219 cell death (cell death)	1,993	1,993	160	160	191	191	biological_process
GO:0030154 cell differentiation (cell differentiation)	0	0	1	1	0	0	biological_process
GO:0019725 cellular homeostasis (cellular homeostasis)	141	141	134	134	179	179	biological_process
GO:0006091 generation of precursor metabolites and energy (generation of precursor metabolites and energy)	275	275	103	103	145	145	biological_process
GO:0016301 kinase activity (kinase activity)	3,708	3,708	1,318	1,318	1,550	1,550	molecular_function
GO:0006139 nucleobase, nucleoside, nucleotide and nucleic acid metabolic process (nucleobase, nucleoside, nucleotide and nucleic acid metabolic process)	1,160	10,022	572	777	810	1,115	biological_process
GO:0006259 DNA metabolic process (DNA metabolic process)	8,864	8,864	208	208	309	309	biological_process
GO:0006350 transcription (?)	0	0	0	0	0	0	biological_process
GO:0003700 sequence-specific DNA binding transcription factor activity (sequence-specific DNA binding transcription factor activity)	764	764	594	594	781	781	molecular_function
GO:0015979 photosynthesis (photosynthesis)	164	164	68	68	78	78	biological_process
GO:0006464 protein modification process (protein modification process)	3,864	3,864	1,511	1,511	1,726	1,726	biological_process
GO:0006412 translation (translation)	803	803	510	510	699	699	biological_process
GO:0008135 translation factor activity, nucleic acid binding (translation factor activity, nucleic acid binding)	99	99	74	74	94	94	molecular_function
GO:0016265 death (death)	0	1,993	0	160	0	191	biological_process
GO:0009790 embryo development (embryo development)	2	2	2	2	3	3	biological_process
GO:0030234 enzyme regulator activity (enzyme regulator activity)	317	317	227	227	330	330	molecular_function
GO:0040007 growth (growth)	0	0	0	0	0	0	biological_process
GO:0008152 metabolic process (metabolic process)	5,436	24,281	2,325	6,728	3,025	8,687	biological_process
GO:0009058 biosynthetic process (biosynthetic process)	5,109	5,899	951	1,454	1,259	1,950	biological_process
GO:0005975 carbohydrate metabolic process (carbohydrate metabolic process)	1,720	1,720	728	728	918	918	biological_process
GO:0009056 catabolic process (catabolic process)	637	637	467	467	604	604	biological_process
GO:0003824 catalytic activity (catalytic activity)	7,233	19,802	2,731	6,444	3,571	8,256	molecular_function
GO:0016787 hydrolase activity (hydrolase activity)	4,192	4,808	1,828	2,006	2,315	2,584	molecular_function
GO:0003774 motor activity (motor activity)	147	147	77	77	107	107	molecular_function
GO:0004518 nuclease activity (nuclease activity)	476	476	110	110	174	174	molecular_function
GO:0016740 transferase activity (transferase activity)	4,603	8,310	795	2,112	1,045	2,594	molecular_function
GO:0006629 lipid metabolic process (lipid metabolic process)	731	731	467	467	571	571	biological_process

Supplemental Table 3. (Continued).

GO Term	*Eucalyptus camaldulensis* (total: 77,121)		*Popupus trichocarpa* (total: 27,665)		*Arabidopsis thaliana* (total: 35,386)		Category
	Count of gene products for which this is the most relevant slim term	Count of gene products inferred to be associated with slim term	Count of gene products for which this is the most relevant slim term	Count of gene products inferred to be associated with slim term	Count of gene products for which this is the most relevant slim term	Count of gene products inferred to be associated with slim term	
GO:0019538 protein metabolic process (protein metabolic process)	1,890	6,542	793	2,791	1,034	3,436	biological_process
GO:0019748 secondary metabolic process (secondary metabolic process)	83	83	59	59	52	52	biological_process
GO:0007275 multicellular organismal development (multicellular organismal development)	11	13	18	20	27	31	biological_process
GO:0009875 pollen-pistil interaction (pollen-pistil interaction)	233	233	74	74	34	34	biological_process
GO:0009856 pollination (pollination)	0	233	0	74	0	34	biological_process
GO:0009791 post-embryonic development (post-embryonic development)	0	0	0	0	1	1	biological_process
GO:0009908 flower development (flower development)	0	0	0	0	0	0	biological_process
GO:0040029 regulation of gene expression, epigenetic (regulation of gene expression, epigenetic)	20	20	9	9	20	20	biological_process
GO:0000003 reproduction (reproduction)	23	256	4	78	9	43	biological_process
GO:0009628 response to abiotic stimulus (response to abiotic stimulus)	47	47	61	61	65	65	biological_process
GO:0009607 response to biotic stimulus (response to biotic stimulus)	164	164	25	25	34	34	biological_process
GO:0009719 response to endogenous stimulus (response to endogenous stimulus)	14	14	27	27	35	35	biological_process
GO:0009605 response to external stimulus (response to external stimulus)	0	1	3	5	6	9	biological_process
GO:0009991 response to extracellular stimulus (response to extracellular stimulus)	1	1	2	2	3	3	biological_process
GO:0009606 tropism (tropism)	0	0	0	0	0	0	biological_process
GO:0006950 response to stress (response to stress)	2,979	2,979	455	455	718	718	biological_process
GO:0009835 ripening (ripening)	0	0	0	0	0	0	biological_process
GO:0007165 signal transduction (signal transduction)	1,488	1,488	321	321	627	627	biological_process
GO:0004871 signal transducer activity (signal transducer activity)	150	1,382	162	233	148	341	molecular_function
GO:0004872 receptor activity (receptor activity)	1,237	1,237	74	74	198	198	molecular_function
GO:0030528 transcription regulator activity (transcription regulator activity)	255	255	278	278	363	363	molecular_function
GO:0045182 translation regulator activity (translation regulator activity)	0	0	0	0	0	0	molecular_function
GO:0006810 transport (transport)	2,972	2,972	1,491	1,491	1,764	1,764	biological_process
GO:0005215 transporter activity (transporter activity)	1,457	1,457	768	768	894	894	molecular_function
GO:0005575 cellular_component (cellular_component)	46	9,692	41	4,817	41	6,308	cellular_component
GO:0005623 cell (cell)	40	9,385	50	4,671	55	6,154	cellular_component
GO:0005737 cytoplasm (cytoplasm)	585	1,637	418	1,123	596	1,542	cellular_component
GO:0005856 cytoskeleton (cytoskeleton)	114	114	82	82	105	105	cellular_component
GO:0005829 cytosol (cytosol)	55	55	26	26	25	25	cellular_component
GO:0005783 endoplasmic reticulum (endoplasmic reticulum)	145	145	99	99	147	147	cellular_component
GO:0005768 endosome (endosome)	0	0	0	0	0	0	cellular_component
GO:0030312 external encapsulating structure (external encapsulating structure)	52	252	35	128	19	120	cellular_component
GO:0005618 cell wall (cell wall)	200	200	93	93	101	101	cellular_component
GO:0005576 extracellular region (extracellular region)	306	314	168	171	164	172	cellular_component
GO:0005615 extracellular space (extracellular space)	5	5	1	1	4	4	cellular_component
GO:0005794 Golgi apparatus (Golgi apparatus)	71	71	46	46	58	58	cellular_component
GO:0005622 intracellular (intracellular)	2,163	4,641	1,101	2,852	1,404	3,876	cellular_component
GO:0016020 membrane (membrane)	5,026	5,031	2,038	2,045	2,589	2,596	cellular_component
GO:0005739 mitochondrion (mitochondrion)	129	129	144	144	160	160	cellular_component

Supplemental Table 3. (Continued).

GO Term	*Eucalyptus camaldulensis* (total: 77,121)		*Popupus trichocarpa* (total: 27,665)		*Arabidopsis thaliana* (total: 35,386)		Category
	Count of gene products for which this is the most relevant slim term	Count of gene products inferred to be associated with slim term	Count of gene products for which this is the most relevant slim term	Count of gene products inferred to be associated with slim term	Count of gene products for which this is the most relevant slim term	Count of gene products inferred to be associated with slim term	
GO:0005635 nuclear envelope (nuclear envelope)	35	35	16	16	24	24	cellular_component
GO:0005730 nucleolus (nucleolus)	4	4	6	6	16	16	cellular_component
GO:0005654 nucleoplasm (nucleoplasm)	45	45	43	43	71	71	cellular_component
GO:0005634 nucleus (nucleus)	1,517	1,591	873	922	1,243	1,328	cellular_component
GO:0005777 peroxisome (peroxisome)	14	14	16	16	28	28	cellular_component
GO:0005886 plasma membrane (plasma membrane)	21	21	29	29	40	40	cellular_component
GO:0009536 plastid (plastid)	129	129	41	41	60	60	cellular_component
GO:0005578 proteinaceous extracellular matrix (proteinaceous extracellular matrix)	3	3	2	2	4	4	cellular_component
GO:0005840 ribosome (ribosome)	523	523	358	358	488	488	cellular_component
GO:0009579 thylakoid (thylakoid)	170	170	59	59	80	80	cellular_component
GO:0005773 vacuole (vacuole)	11	11	2	2	4	4	cellular_component
GO:0005764 lysosome (lysosome)	0	0	0	0	0	0	cellular_component
GO:0003674 molecular_function (molecular_function)	1,437	43,262	562	14,447	637	18,473	molecular_function
GO:0005488 binding (binding)	10,237	34,107	4,453	10,786	5,275	13,509	molecular_function
GO:0030246 carbohydrate binding (carbohydrate binding)	438	438	199	199	152	152	molecular_function
GO:0003682 chromatin binding (chromatin binding)	460	460	2	2	5	5	molecular_function
GO:0008289 lipid binding (lipid binding)	121	121	82	82	97	97	molecular_function
GO:0003676 nucleic acid binding (nucleic acid binding)	3,792	14,193	853	2,801	1,015	3,529	molecular_function
GO:0003677 DNA binding (DNA binding)	7,638	7,638	1,693	1,693	2,127	2,127	molecular_function
GO:0003723 RNA binding (RNA binding)	3,608	3,685	348	404	484	552	molecular_function
GO:0000166 nucleotide binding (nucleotide binding)	8,388	8,388	2,887	2,887	3,485	3,485	molecular_function
GO:0019825 oxygen binding (oxygen binding)	8	8	4	4	3	3	molecular_function
GO:0005515 protein binding (protein binding)	6,057	6,067	3,558	3,564	4,665	4,672	molecular_function
GO:0005102 receptor binding (receptor binding)	10	10	6	6	7	7	molecular_function
GO:0005198 structural molecule activity (structural molecule activity)	608	608	438	438	578	578	molecular_function

Supplemental Table 4. Summary of gene assignments on KEGG pathways.

Map name	Map name	Map name	*E. camaldulensis*	*P. trichocarpa*	*A. thaliana*
1. Metabolism	1.1 Carbohydrate Metabolism	Glycolysis/Gluconeogenesis	26	29	28
		Citrate cycle (TCA cycle)	19	21	20
		Pentose phosphate pathway	17	18	16
		Pentose and glucuronate interconversions	14	13	13
		Fructose and mannose metabolism	17	19	19
		Galactose metabolism	13	15	13
		Ascorbate and aldarate metabolism	11	13	13
		Starch and sucrose metabolism	31	33	32
		Amino sugar and nucleotide sugar metabolism	36	39	38
		Pyruvate metabolism	25	28	29
		Glyoxylate and dicarboxylate metabolism	18	19	18
		Propanoate metabolism	17	18	20
		Butanoate metabolism	11	13	13
		C5-Branched dibasic acid metabolism	4	4	4
		Inositol phosphate metabolism	19	22	21
	1.2 Energy Metabolism	Oxidative phosphorylation	88	70	97
		Photosynthesis	41	32	55
		Photosynthesis-antenna proteins	8	12	12
		Carbon fixation in photosynthetic organisms	21	25	24
		Carbon fixation pathways in prokaryotes	12	13	14
		Methane metabolism	23	25	24
		Nitrogen metabolism	14	17	17
		Sulfur metabolism	10	11	10
	1.3 Lipid Metabolism	Fatty acid biosynthesis	13	14	15
		Fatty acid elongation in mitochondria	2	2	2
		Fatty acid metabolism	10	12	10
		Synthesis and degradation of ketone bodies	3	3	3
		Steroid biosynthesis	15	19	19
		Primary bile acid biosynthesis	2	2	1
		Secondary bile acid biosynthesis	0	0	0
		Steroid hormone biosynthesis	4	3	3
		Glycerolipid metabolism	27	26	24
		Glycerophospholipid metabolism	37	39	39
		Ether lipid metabolism	8	10	9
		Sphingolipid metabolism	12	16	16
		Arachidonic acid metabolism	8	9	7
		Linoleic acid metabolism	4	4	4
		alpha-Linolenic acid metabolism	13	13	13
		Biosynthesis of unsaturated fatty acids	1	1	2
	1.4 Nucleotide Metabolism	Purine metabolism	71	91	90
		Pyrimidine metabolism	59	75	73
	1.5 Amino Acid Metabolism	Alanine, aspartate and glutamate metabolism	21	25	25
		Glycine, serine and threonine metabolism	25	31	28
		Cysteine and methionine metabolism	31	33	32
		Valine, leucine and isoleucine degradation	20	20	20
		Valine, leucine and isoleucine biosynthesis	13	15	15
		Lysine biosynthesis	12	15	15
		Lysine degradation	11	13	11
		Arginine and proline metabolism	35	40	37
		Histidine metabolism	11	13	12
		Tyrosine metabolism	19	20	18
		Phenylalanine metabolism	18	17	17
		Tryptophan metabolism	10	15	19
		Phenylalanine, tyrosine and tryptophan biosynthesis	19	25	22
	1.6 Metabolism of Other Amino Acids	beta-Alanine metabolism	13	14	14
		Taurine and hypotaurine metabolism	3	3	3
		Phosphonate and phosphinate metabolism	2	3	3
		Selenoamino acid metabolism	10	10	9
		Cyanoamino acid metabolism	12	13	12
		D-Glutamine and D-glutamate metabolism	1	1	1
		D-Arginine and D-ornithine metabolism	1	1	1
		D-Alanine metabolism	0	0	0
		Glutathione metabolism	16	18	16
	1.7 Glycan Biosynthesis and Metabolism	*N*-Glycan biosynthesis	26	32	32
		Various types of *N*-glycan biosynthesis	7	8	8
		Mucin type *O*-Glycan biosynthesis	0	1	0
		Other types of *O*-glycan biosynthesis	0	0	0
		Glycosaminoglycan biosynthesis-chondroitin sulfate	0	2	0
		Glycosaminoglycan biosynthesis-heparan sulfate	2	2	2
		Glycosaminoglycan biosynthesis-keratan sulfate	0	0	0
		Glycosaminoglycan degradation	4	5	5
		Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	17	21	20
		Glycosphingolipid biosynthesis-lacto and neolacto series	0	0	0
		Glycosphingolipid biosynthesis-globo series	3	4	3
		Glycosphingolipid biosynthesis-ganglio series	1	3	2
		Lipopolysaccharide biosynthesis	7	8	8

Supplemental Table 4. (Coninued).

Map name	Map name	Map name	*E. camaldulensis*	*P. trichocarpa*	*A. thaliana*
	1.7 Glycan Biosynthesis and Metabolism	Peptidoglycan biosynthesis	2	4	3
		Other glycan degradation	0	0	0
	1.8 Metabolism of Cofactors and Vitamins	Thiamine metabolism	7	9	8
		Riboflavin metabolism	8	8	8
		Vitamin B6 metabolism	7	8	8
		Nicotinate and nicotinamide metabolism	9	12	11
		Pantothenate and CoA biosynthesis	14	17	17
		Biotin metabolism	4	5	5
		Lipoic acid metabolism	3	3	3
		Folate biosynthesis	9	9	9
		One carbon pool by folate	13	13	14
		Retinol metabolism	7	11	7
		Porphyrin and chlorophyll metabolism	28	31	32
		Ubiquinone and other terpenoid-quinone biosynthesis	17	18	18
	1.9 Metabolism of Terpenoids and Polyketides	Terpenoid backbone biosynthesis	20	22	21
		Monoterpenoid biosynthesis	2	2	2
		Sesquiterpenoid biosynthesis	1	1	1
		Diterpenoid biosynthesis	9	9	9
		Carotenoid biosynthesis	15	16	16
		Brassinosteroid biosynthesis	7	7	8
		Insect hormone biosynthesis	0	0	0
		Zeatin biosynthesis	6	6	5
		Limonene and pinene degradation	5	6	6
		Geraniol degradation	2	2	2
		Type I polyketide structures	0	0	0
		Biosynthesis of 12-, 14- and 16-membered macrolides	0	0	0
		Biosynthesis of ansamycins	1	1	1
		Biosynthesis of type II polyketide backbone	0	0	0
		Biosynthesis of type II polyketide products	0	0	0
		Tetracycline biosynthesis	3	3	4
		Polyketide sugar unit biosynthesis	2	3	3
		Nonribosomal peptide structures	0	0	0
		Biosynthesis of siderophore group nonribosomal peptides	1	2	2
		Biosynthesis of vancomycin group antibiotics	1	1	1
	1.10 Biosynthesis of Other Secondary Metabolites	Phenylpropanoid biosynthesis	20	20	20
		Stilbenoid, diarylheptanoid and gingerol biosynthesis	5	5	5
		Flavonoid biosynthesis	15	15	13
		Flavone and flavonol biosynthesis	4	4	4
		Anthocyanin biosynthesis	2	2	1
		Isoflavonoid biosynthesis	0	0	0
		Indole alkaloid biosynthesis	2	2	2
		Isoquinoline alkaloid biosynthesis	7	6	5
		Tropane, piperidine and pyridine alkaloid biosynthesis	7	9	7
		Acridone alkaloid biosynthesis	0	0	0
		Caffeine metabolism	0	2	2
		Betalain biosynthesis	1	0	0
		Glucosinolate biosynthesis	0	0	0
		Benzoxazinoid biosynthesis	2	4	1
		Penicillin and cephalosporin biosynthesis	2	3	2
		beta-Lactam resistance	0	0	0
		Streptomycin biosynthesis	7	7	7
		Butirosin and neomycin biosynthesis	1	1	1
		Clavulanic acid biosynthesis	0	0	0
		Puromycin biosynthesis	0	0	0
		Novobiocin biosynthesis	4	5	4
	1.11 Xenobiotics Biodegradation and Metabolism	Benzoate degradation	5	7	6
		Aminobenzoate degradation	10	12	11
		Fluorobenzoate degradation	1	2	1
		Chloroalkane and chloroalkene degradation	7	8	6
		Chlorocyclohexane and chlorobenzene degradation	4	6	4
		Toluene degradation	1	3	1
		Xylene degradation	0	0	0
		Nitrotoluene degradation	0	0	0
		Ethylbenzene degradation	2	1	2
		Styrene degradation	3	5	5
		Atrazine degradation	1	1	1
		Caprolactam degradation	2	2	2
		DDT degradation	1	1	1
		Bisphenol degradation	5	6	5
		Dioxin degradation	1	1	1
		Naphthalene degradation	6	8	6
		Polycyclic aromatic hydrocarbon degradation	5	6	5
		Metabolism of xenobiotics by cytochrome P450	3	4	4
		Drug metabolism-cytochrome P450	4	5	4
		Drug metabolism-other enzymes	9	13	13

Supplemental Table 5. Cytochrome P450 genes in the genomes of *E. camaldulensis* and *A. thaliana*.

CYP subfamily	*E. camaludlensis*	*A. thaliana*
CYP51G	2	2
CYP71A	31	17
CYP71B	70	38
CYP72A	67	9
CYP72C	3	1
CYP73A	1	1
CYP74A	11	1
CYP74B	1	1
CYP75B	33	1
CYP76C	53	8
CYP76F	1	0
CYP76G	21	1
CYP76H	1	0
CYP77A	4	6
CYP77B	3	1
CYP78A	12	6
CYP79A	3	3
CYP79B	22	3
CYP79C	0	5
CYP79F	0	2
CYP81D	66	10
CYP81F	6	4
CYP81G	1	1
CYP81H	5	1
CYP81K	0	2
CYP82C	87	3
CYP82F	3	1
CYP82G	5	1
CYP83A	0	1
CYP83B	0	1
CYP84A	9	2
CYP85A	4	2
CYP86A	6	5
CYP86B	1	2
CYP86C	3	4
CYP87A	18	2
CYP87D	1	0
CYP88A	24	2
CYP89A	29	7
CYP90A	6	1
CYP90B	7	1
CYP90C	6	1
CYP90D	1	1
CYP93D	6	1
CYP94B	20	3
CYP94C	4	1
CYP94D	14	3
CYP96A	16	15
CYP97A	1	1
CYP97B	1	1
CYP97C	6	1
CYP98A	13	3
CYP701A	8	1
CYP702A	0	8
CYP703A	1	1
CYP704A	39	2
CYP704B	2	1
CYP705A	0	33
CYP706A	52	7
CYP707A	11	4
CYP708A	0	4
CYP709B	3	3
CYP710A	1	4
CYP711A	3	1
CYP712A	9	2
CYP714A	22	2
CYP715A	14	1
CYP716A	66	2
CYP716D	3	0
CYP718A	18	1
CYP720A	3	1
CYP721A	11	1
CYP722A	5	1
CYP724A	4	1
CP728	7	1
CYP734A	22	1
CYP735A	9	2
Total	1,021	275

Supplemental Table 6. List of primers for amplification of the SSR markers.

Marker name	Polymorphic in 6 species	SSR pattern		Estimated product size	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)
		Motif	Size (total bp)			
Gnome-SSR						
EcGAS2001	+	AAG	30	161	TGGCATTGTAGTGGTGCATT	TGCTTGTGGAGCTATCGTTG
EcGAS2002	+	AG	30	278	TCTGCAGCTTTGTTTGCACT	AGTCCCTGCAACGACTCAAC
EcGAS2003	+	AAAG	28	250	TGTCGTATGGGCGTTTGTAA	TAGCTCCATCGTCACGTCAG
EcGAS2004	+	AG	28	127	TCTAACTGCCCGGTTTTGAG	AGTGAACCCACTGGTCTTGG
EcGAS2005	+	AAG	27	206	TGTTGTCCTGCAGCATTCTC	AATGCAGATCTTCCAATGCC
EcGAS2006	+	AAT	27	172	ATTGACATTACCGCGTTTCC	CCTCTCGAGACCTGAAGCTG
EcGAS2007	+	AG	26	94	GAGAAGAAGCAGAAATGGCG	TTTGATACACGGTCGGAGTG
EcGAS2008	+	AT	26	192	TAGCAATGCTGTGTTTGGGA	GATATCGCACGCTAAGGCTC
EcGAS2009	+	AAAC	24	266	GTTGCGTTGAGCTAGGGTTG	CGGTCACTGCAAATATGACG
EcGAS2010	+	AAAG	24	144	GACGTCAGAGAGGGTGTGGT	TTAAATCCAAGGGCATTTCG
EcGAS2011	+	AC	24	250	AGCATTCGGTAAGCAAAATG	GGTGAAAGCCAAAAGACACC
EcGAS2012	+	ACG	24	222	TAGCGTGACTACGAGGAGCA	CAGAGGAAGCAGGTCTCCAG
EcGAS2013	+	AC	22	242	GAATTGGCACCTTCTTGAGG	GTCAAGCTTACCACCGCTTC
EcGAS2014	+	AG	22	181	CCCAAGGAGCTTGTTCTCAG	ATGATAGGCGCAAATGATCC
EcGAS2015	−	AT	22	238	ATAAAGGACATTGGGCCGTT	CCTAGCGACTGTTCGGTGA
EcGAS2016	+	AG	22	287	GGCACACCTTGGTCAATAGG	CTGGAATCGGGACAAGAATC
EcGAS2017	+	AAT	30	225	TATGCAACAAGCTGGCAAAG	AATCGATTGCAAAGGGATTG
EcGAS2018	+	GGA	30	245	CAAGGGACTAGCAGCCTACG	TTCTCTTTACGCCGCTTGAT
EcGAS2019	+	AAAT	28	287	TTTGGCCAAGGTGGTAATGT	TTACATTTGGCCCTTCCATC
EcGAS2020	+	AT	28	209	TAGTGAGAATGCAGGGGGAC	GCGGATTAAGTTGCCCTTTT
EcGAS2021	−	AAG	27	181	AGAACTGGCAGATGACGACC	GCTCTCGGGAACAGATTGAG
EcGAS2022	+	AAT	27	182	CAGTCAACTAGCCGCATCAA	ATAAGGCTTGCATTGGGATG
EcGAS2023	+	AG	26	130	TGGTCTAAAAGGCAATTCGG	CGTGCAGACAAAAATGGATG
EcGAS2024	+	AT	26	294	AATACGCGACGAAGAAAGGA	CGTCAACAATTCCTGATGGA
EcGAS2025	+	AAG	24	282	GGTCCCCCATATTTGACCTC	TTTCGACCCTTGTTGGTAGG
EcGAS2026	+	AAG	24	226	TGGTGACTTAGAGCCATTCG	CGCCGAAGATTTTCTAGCAC
EcGAS2027	+	AATG	24	297	CGGTGGAATCCAGTTAAAGG	CTTCTGCAGGCATTTGTACG
EcGAS2028	−	AG	24	282	TGAGTGTCAAGCTCCACGTC	TTCCTCCAACATTCTCCGAC
EcGAS2029	+	AC	22	278	CAATAATGCGTGCATAACCA	TGGGGGAATAACGACTTTTC
EcGAS2030	+	AG	22	299	CCTTATGGTGGGTGGATGAG	TCGCGTGCTGTTTTGTTTAG
EcGAS2031	+	AG	22	192	GGAACGTTTCTTTCTCGACG	GTGGACATACCAATCATGCG
EcGAS2032	+	AT	22	93	ACGAAGTTGGTCCTTGATGG	GCCCACTTTCGTGGAAATTA
EcGAS2033	+	AAC	21	187	TCTGGGTTCTTGGGTGTTTC	GCGCAAAATCAAGATCAACA
EcGAS2034	+	AAC	21	268	TTTCTGAGGTGAGCTTCGGT	ATGAAGGCTTCCATTGTTGC
EcGAS2035	+	AAG	21	128	CCTCACTTCTCAGCGATTCC	CGTAGCTCTTGGGGTGAGAG
EcGAS2036	+	AAT	21	177	AGCGTGGGAAAATAAACACG	AACATGGTTACCACCCAAGG
EcGAS2037	+	AAAG	20	251	CCTTCTTGGGTTGCAGAGAG	TGCCAGTATCAGGGAGGATT
EcGAS2038	+	AAAT	20	250	TGGACTAACAAAGGGTTCGG	AAATGCTCTCCCAAATGCAC
EcGAS2039	+	AATT	20	291	CCAGATTCCGAAACCAAGAA	GATCGAACTAGATCGGCCAG
EcGAS2040	+	AG	20	146	AACACGCCCAACATCTCTTC	TCCTCTACCATTTGCCCATC
EcGAS2041	+	AG	20	203	CTCGTCCGACATACTCAGCA	ATCTGCTCCCACCGTCATAG
EcGAS2042	+	AT	20	277	GCGTATCCCGATCTGTGACT	ACGTCTCCATCCAACCAATC
EcGAS2043	+	AT	20	259	CGTCTCGCATGCAAAGATTA	AAGTTAAGGGAAGGATGGCG
EcGAS2044	+	AAG	18	211	ACATCCGCAATAGTTCTCGC	TTTCTGAATGCAGTTCGTGC
EcGAS2045	+	AAT	18	165	GCTACCAAAAGCTCCACGTC	ATGACCCTTTGTTGCTTTGG
EcGAS2046	+	GGA	18	266	AGTTGTTGGCAATCCGAAAC	CAACTTAGTGGCTGCTCACG
EcGAS2047	−	AAAT	16	97	TATGTCTGGCTTCGTTGCAG	TTGAAAAACCCAGGAGATGG
EcGAS2048	+	AATC	16	134	TCGGTGTTTCCTGCACATAA	TCCGCAATTTTATTTCTCGG
EcGAS2049	+	AAG	21	290	CCGAGCTCTAATTGCTTTGG	CTCAATGAGAAGCACGGACA
EcGAS2050	+	AAG	21	231	ATCGGGTTGTTTGACATCCT	TGACATCCCCATAGCATGAA
EcGAS2051	+	AAT	21	279	TATTTTGGCAACATGACCCA	AGCTGCTAAGCAAACGGAAA
EcGAS2052	+	AGC	21	179	CACATGCCTTTTTCCAACCT	CCTGCAGATGGCTCTACTCC
EcGAS2053	+	AAAG	20	242	TGATTCATGGACACCGTTTG	AGGGGGAAGACGTGCTTAAT
EcGAS2054	+	AAAT	20	273	CTGATGAAAAGGCATGCAAC	TATATTTGGCTTTGGGCAGC
EcGAS2055	+	AC	20	214	TGGGGCCATCTAGAACTTTG	GACACTGCATTATCCGGTCA
EcGAS2056	−	AG	20	241	GGATGGAGATCAGCACGAAT	TCCTACTCTAGCGTGGGTGG
EcGAS2057	+	AG	20	284	AATGTGCCATCCCAATCAAT	CGTCCCATGAGAAAAGGAAG
EcGAS2058	+	AT	20	281	GGAGCAGAGCCACATCAAAT	AAGGACGGCTTACACACACG
EcGAS2059	+	AAG	18	270	GTTTCCACTCATGCACATCG	AATTTACCCCGTAACCGTCC
EcGAS2060	+	AAT	18	181	AACACGGTAGAAACCCACCA	CGAGGGTTGCATTTGCTTAT
EcGAS2061	+	ATC	18	214	CTTGGGAATCAGAGGGATCA	TCTCCTCTTTTCCACGCACT
EcGAS2062	+	GGA	18	233	ATATGCTTGAACCCTCACCG	CTTAGCCGGAGACTCATTGC

Supplemental Table 6. (Continued).

Marker name	Polymorphic in 6 species	SSR pattern		Estimated product size	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)
		Motif	Size (total bp)			
EcGAS2063	+	AAAT	16	262	ATCAGAGAGACGGCATGCTT	TTGTATGTTGACACCTGCCC
EcGAS2064	+	AGC	15	131	AACTTGTCGTTCCCTTGCAC	CAAAGGCGACAACGTAGGAT
EcGAS2065	+	AAT	57	174	CGGAAATTGCTAATACCGACG	AGCCCTCTCTCCAAAACCAT
EcGAS2066	+	GGC	48	296	CCTACGGGAACAACCTCAAG	TATGGTCCGAAAAATGGAGC
EcGAS2067	+	GGA	45	226	GAAAGACACCAAGCACAGCA	GCAGGTCAAGCAAGAAGGC
EcGAS2068	−	GGC	45	293	CTCTCTTCCTTGAAGGGGCT	AAAAACCCTAATTTCCCCCA
EcGAS2069	+	GGC	45	276	ATGGATCACACGGATCACAA	GGGACGTTCCGATTTCTGTA
EcGAS2070	+	AAAT	44	251	TGCCGAGGGGATAAACTATG	TTTTGGTGCATGCTTTGGTA
EcGAS2071	+	AAG	42	281	AGGGATCGACCCAGAAAACT	GATCGCTTCTCGACTTGGTC
EcGAS2072	+	GGA	42	136	CGGCATTAGCACTAGCACAA	GGTTTTTATCCGATCGACCA
EcGAS2073	+	AAAG	40	272	CCTTTCGACATGCAGAGGTT	TCGATTGAACACCTCGTCAG
EcGAS2074	+	AAAT	40	257	AAGCACCACTGAACTCAGCA	CCTTCGCATGTTAGGTGGTT
EcGAS2075	+	AAG	39	243	AACACCAACAATCTCGAGGG	CATGTGCATCACACTTGCTG
EcGAS2076	+	GGC	39	251	AATACGACGCGGTTGAAAAC	ATCGAACGGGATCTTGATTG
EcGAS2077	+	GGGA	38	212	CGCCTGGTCTTCCATAAGAG	GACCTCCCTTTTATGGGCTC
EcGAS2078	+	AAAT	36	239	AGAAGGCTGTTCATTGTGCC	CCCATCAGTTGCTGTTGAGA
EcGAS2079	+	AAC	36	293	GACGAAGGAGAAACATCGGA	CCCGATCTTGGTGATCTCAT
EcGAS2080	+	GGGA	36	232	TGGAAGATGAGGGAAGATGG	TCGTTGCCACAGCTACTGAC
EcGAS2081	+	AAT	42	299	ACCACATGCATGGATCAAAA	CCCATTTCATGTGCCTCTCT
EcGAS2082	+	AAAT	40	221	CGAACAAAGTGAGGTGAGCA	CAGTTGGTTCAACCCAAACC
EcGAS2083	+	GGGA	40	275	CATGAAAGTCGAAAAGGGGA	GAGGAAATAGGGGCTGAAGG
EcGAS2084	+	AAAT	40	300	TGGTGACTTTGCACTTGGAG	TCTCTTCCAACACGCTCTGA
EcGAS2085	+	AAAT	40	264	CCCTCACTTTCTCCTCCTCC	GAGGCTAGAGTTGGCCTGTG
EcGAS2086	+	AAT	39	277	CCAGCTGTAGGGTCTCGAAG	AACCGAACGCAGAAGACATC
EcGAS2087	+	AAT	39	211	TGGCCATTTTGTCCTATTCC	TCAATTGCAAGGGACAATGA
EcGAS2088	+	AAG	37	283	AATGGCAATCGCGGTAGTAG	AGAAAACGAATAAGGCCCGT
EcGAS2089	+	GGC	36	290	AAAACACGCCGAGCTCTATG	ACGAGGACAACAAAGCGAAG
EcGAS2090	+	AAAT	36	272	CCGGTTGGCATTGATAATTT	TGAGCGTACCATTCATTGGA
EcGAS2091	+	AAAT	36	269	CCACATTCTCAAAATGCAGC	ACAACACAACCATCCCCAAT
EcGAS2092	+	AAG	36	234	AGGTAAATTCCACACGACCG	AATACGGGGTACAGATGCGA
EcGAS2093	+	AGC	36	208	TTCAAGCGGGAAAGAAGAGA	CCGCTTAGAAAAAGGTGCAG
EcGAS2094	−	ATC	36	220	TTGGAGAAGGATTTGAACCG	TACACTTGACCGGACACACG
EcGAS2095	+	GGGA	36	235	TGGCCATCTATAAAAGCCCTAA	GTAAGTTTCGCGGGAACAGA
EcGAS2096	+	AAG	36	254	ACCCAGTTAGCACCACGTTC	CCATTCCAAGGTACCTCATCA
EcGAS2097	+	AAT	30	291	GGAAACGTAGGAGAGGGACC	ATTGCTTTCCTCTAACGGCA
EcGAS2098	+	AAT	30	270	ACCCCATTAGGGGAAAGTTG	TGGCCTCTCTAGCTCATCGT
EcGAS2099	+	AAT	30	171	ATTCATAACTGCCCCTGCAC	ACTGCGTTAGTTTTCGCGTT
EcGAS2100	+	AAT	30	289	TCCAGGACTGACCGGTAAAA	TCTGCGATGAAGTTGTGGAG
EcGAS2101	−	AC	30	160	TATTTGTCAAACACGGGCAA	GTTGAATCACGTCCGTGTGA
EcGAS2102	+	AC	30	211	CGGAGGCATCAAGGATCTTA	CAAACATACAGCGCTCTCCA
EcGAS2103	+	ACG	30	296	GCTTTTCCCCTTCTTATCCG	AGACCGAACCTGTAAAGCGA
EcGAS2104	−	ACG	30	220	GCAAAAGTGAGATTTTCGCC	TACTCGCAATAATGCGTTGG
EcGAS2105	+	AG	30	249	TTACTGCTCAGCACATTGCC	ACAGAAGGCTTGCAGAGGTT
EcGAS2106	+	AG	30	225	GCCTTACAGGAGTGTAGCCG	AACCATTTTCCACGCACTTC
EcGAS2107	+	AG	30	282	CCAAGTCAACAGTCTTCGCA	CTGCAAAGGGAGCTGAAAAG
EcGAS2108	+	AG	30	171	TCTTGATCATGTTCCGCAAG	TTGTTCTCAAAATGGCGATG
EcGAS2109	+	AGC	30	210	CACGACAAGAAGACGACGAA	GTTTCGGTCGAGATTTTGGA
EcGAS2110	+	AGC	30	233	TGACATAAGGAGGAGGGACG	GAGGGACCTTCCCTTTTACG
EcGAS2111	+	AT	30	207	TCCAGTTCACGGTCTCCTCT	CCCTTAAGGTCAGGACGACA
EcGAS2112	+	AT	30	292	CAATGAGATCATGGAACCCC	TTAAATCAGCGTCTGTTGCG
EcGAS2113	+	AAAC	28	125	CTCTGAGTGCCGTTTTCCTC	ACTTGCTAGCTCCCAAAGCA
EcGAS2114	+	AAAC	28	221	CTATTGGGAATCATGGCACC	TGGAAGATGAGGGTGAAAGG
EcGAS2115	+	AAAG	28	241	TCCAGCTCGTCTTCGTTCTT	GGAGAGACATACCCACCAGC
EcGAS2116	+	AAAG	28	282	TTTTTGGCCATCAGAAGAGG	GCAAAACAAATGCACCGTTA
EcGAS2117	+	AAAT	28	287	ATGACCCACAACTGGGAGAG	ACGACAAGTGGAGTTGGGAC
EcGAS2118	+	AAAT	28	299	TTACCAATTCCCCTTCATGC	GGATGTGAAACACATGCTGG
EcGAS2119	+	AC	28	225	GATCTCATGGTGCGAGGATT	GATGGGGAACTGATCCTTGA
EcGAS2120	+	AC	28	299	AAATCACGCAAGATGAAGCA	TGGAGCCAACTGCTCTTGTA
EcGAS2121	+	AG	28	186	GCAGGGCTCAGGTAGTTCAG	CGGTTGATTCTTCGTTCCAT
EcGAS2122	+	AG	28	227	ATAACATCATGGAGGAGCGG	TGAACGGTCCAGACATTACG
EcGAS2123	+	AG	28	277	GCAAGTTTGCCATTGATCCT	ATCTCATGAAACCAAACGGC
EcGAS2124	+	AT	28	295	CTCTTTCGGTGCAAACATCA	GATTTAAAAGCACCACCCCA
EcGAS2125	+	GACG	28	256	TTCCGGTGAGAAAATCGTTC	AAAATTCAGATCAATCGCCG

Supplemental Table 6. (Continued).

Marker name	Polymorphic in 6 species	SSR pattern		Estimated product size	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)
		Motif	Size (total bp)			
EcGAS2126	+	GC	28	272	TGAGACATTTGCTCCAATCG	ATGCACAAGGAGCTTGCTTT
EcGAS2127	+	GGAT	28	283	GCTAAGACTCCCCAGCCTCT	TCAGGCATTGCATTACTTCG
EcGAS2128	+	GGGA	28	197	GCTTTGTTGTGTTTGACCGA	TGCAAGAAGCAACAACCAAC
EcGAS2129	+	AAC	27	291	GAGGAAAATATGACGCCGAT	TGCCAGAGTTCCCAAACATT
EcGAS2130	+	AAC	27	277	CTCCACCAGAAACCTTTGGA	AACACAAGGCTCAAGCAGGT
EcGAS2131	+	AAG	27	285	CCATTTGTTGGAAACCATCC	CTACAGGTGATTGTGCCGTG
EcGAS2132	+	AAG	27	172	GCAGACACTTGTGGAGGTCA	ATCACTCATTGCTCGACACG
EcGAS2133	+	AAT	27	234	AAAGAAGAGGAGCGGCATTT	AGTCCAAACCCATCAACTCG
EcGAS2134	+	AAT	27	103	AATTTTCCATGCACTCAGGC	CCTAGCCCAAATTGGTTTGA
EcGAS2135	+	ACG	27	229	CGCCGTTCTGAAGTTAGGAG	TTTGTGGTCCCTAAACGAGG
EcGAS2136	+	ACG	27	272	CGTAGCAGCTGAAGATCACG	CTCGTCTCCAAACAGGCTTC
EcGAS2137	+	AGC	27	193	TATGCCTACCCCTGGTCAAG	ACCCTTCGTACAATCGCATC
EcGAS2138	+	AGC	27	276	AGGGAACCGAAAATATGCCT	GTCCCTGGAGAGGTCGTGT
EcGAS2139	+	ATC	27	135	ACACGTGATAAAGGAACCCG	GGATGACTAGACCAAGCCCA
EcGAS2140	+	ATC	27	240	GCATTGTTCTTCCGGTGTTT	GCAGAAGCAGTCTCCAAACC
EcGAS2141	+	GGA	27	248	CATACCGGAGGTGAAAGCAT	ACATCAGAATGCCCAGAAGG
EcGAS2142	+	GGA	27	137	TCCTCCTCGTTGAATAACGG	GGAAAAGCTCGTGGGAGAG
EcGAS2143	+	GGC	27	297	TCTCGTGGGATGACTCCTTC	GACAAGCTCCAAGCACACAA
EcGAS2144	+	GGC	27	272	AACTGGGAACTTCCGAATCC	CGATCGTGTAGGACAGAGGC
EcGAS2145	+	AC	26	200	GACGTTGGGTTTGAAAGAGC	GCAAAACCTTCACCAAGGAA
EcGAS2146	+	AC	26	299	CGTGCAATCTCCTCATATCG	CGCTCCACATGGTAAAGAGC
EcGAS2147	+	AG	26	239	ACTTGAAGGGGCGTAGGTTC	CCACCTAATCCAATCCGAAA
EcGAS2148	+	AG	26	285	TTTGCTGGAACAGTCAGGTG	GATGCTTGATCAATCCCACA
EcGAS2149	+	AC	26	189	TCCAGTGAAGTGGAAAAGCA	ATCCCTGATATGCCAGCAAG
EcGAS2150	+	AC	26	213	ACCCAACTCCATCTCCCTCT	TGTCGGATCTGATGAAGCTG
EcGAS2151	+	AG	26	282	ACACACTCAAGGGGCAAGAG	ACAATATGCTGAACGGAGGG
EcGAS2152	+	AG	26	299	CATTCACCATTGCGTGATCT	TGGCTCTAGCCCAACAAAAT
EcGAS2153	+	AG	26	281	TTTCTCATGAGTTCGTCCCC	CACTTGGGTGTGCAGAGAGA
EcGAS2154	+	AG	26	127	TGCCAAATTCCCGTAGAATC	TTGTTGGCTCCGAAAAGACT
EcGAS2155	+	AG	26	285	TACCTACCGACTGAGGACGG	ACATTGGAACCTTGGAGACG
EcGAS2156	+	AG	26	144	TGTGGCGAACAAGAAAATGA	AGACGACCTGGTGGTTTGTC
EcGAS2157	+	AT	26	273	GCGTTCCCCAGATTTACTCA	ATTTAGGACGGGGTTTCAGG
EcGAS2158	+	AT	26	187	TAGGGGTAGGCCCTTCTAGC	TGTTTTGGTGCTGACATGGT
EcGAS2159	+	AT	26	219	TTCGTTACGCCGAGTCAAAT	GACACGTCAGCGCTTTGTAA
EcGAS2160	+	AT	26	237	CGAACATTTTATGTGGCACG	TTCATCAATGGCTGATGGAG
EcGAS2161	+	AAAC	24	272	TCATTTTACCACCGTCCCTC	GTTTGTTGTTGCAAGGGGTT
EcGAS2162	+	AAAC	24	266	TGTGGGGCTGAGGAGTTAGT	ACCCCAGTCACCACCACATA
EcGAS2163	+	AAAG	24	204	TGTTAACGTTGCATTGGAGG	TGGCCTTGTTTGTCACGTAG
EcGAS2164	+	AAAG	24	206	ATGAGCTTCTGTCGTGCTGA	TGAAGAACCATGGAAGGAGG
EcGAS2165	+	AAAT	24	232	GTGCCAAATCCTAAAAGGCA	CCAAAAAGTGCTTACCAGGC
EcGAS2166	+	AAAT	24	184	TGATGACGGAGACACCACAT	TGATTTGGGAGCTCTTTGCT
EcGAS2167	+	AAC	24	138	CAACAGAGGCATTCAAAGCA	TTTTGATGGCAGTTACGGTG
EcGAS2168	+	AAC	24	248	GGTGTCGCCAATCTGATTTT	GGCACTGGAGAGTTGTGTGA
EcGAS2169	+	AACG	24	144	CAACTTCAGGCGAGTTCCTC	AAGCGAAACGAGCTTTACCA
EcGAS2170	+	AACG	24	189	GGACCCCAGGAATTATGCTT	ATCGTACCGGGGATCCTAAC
EcGAS2171	+	AAG	24	153	TCACGCTCTTGGTCAATCTG	GGAGAGCTCGAGAAGAGCAA
EcGAS2172	+	AAG	24	275	TGCACGTAACCATAATTGCC	ACAATCTTCCTTCACCCCCT
EcGAS2173	+	AAT	24	248	TCTCTTGCGATGTCACGTTC	GTTGTTATTATGGCCGGTGG
EcGAS2174	+	AAT	24	244	ATGTCCTCAACAATTCCCCA	ATAGTCGCATGCCATCATCA
EcGAS2175	+	AATC	24	224	CTTTACCCATTGTCGCCTGT	TGAGGCACAAGAAACTGCTG
EcGAS2176	+	AATC	24	262	TTGTGACACCGAATGTGGTT	ATTCAATCATTGCTCGCACA
EcGAS2177	+	AATG	24	237	AACGGAAGTGTTACCAAGCG	AGTCACCACAACACATCGACA
EcGAS2178	+	AATG	24	252	CAAAGGTTGCATTTGCTTCA	GTTTGAAACTTTGGGTGCGT
EcGAS2179	+	AATT	24	135	GTCATCGGCGATCTCAATCT	ACCGTGGTGAATCCCATTTA
EcGAS2180	+	AATT	24	224	ATGGACATACATGCCCAATG	AGCAAGCTGACCATCGAAGT
EcGAS2181	+	AC	24	224	AACTAAAGAGAGGGAGGCGG	AACAAAGATGGCAGGCAGAG
EcGAS2182	+	AC	24	146	ATGCAACTGGTCATGCAAAA	GTTTGCTCTTCCTTCGCAAC
EcGAS2183	+	ACG	24	249	GAAGCAATGAAGCACGATGA	CGAGGGAGTCGAGAAAAGG
EcGAS2184	+	ACG	24	250	CATTGACAGGCAAAGCTCAA	GTGTTCTCGCCTTCGATCTC
EcGAS2185	+	ACG	24	292	GAAGATCAAGACAAAGGCGG	GCATTATCTCCCCGTTGCTA
EcGAS2186	+	ACT	24	224	CAACAGGAAAAGGGTCCAGA	TGTGGCATTCAATGATCCTC
EcGAS2187	+	AG	24	262	GCTCAGGTGGTCCATGTTTT	ACTCCCCACTCACACACTCC
EcGAS2188	+	AG	24	256	ATCTTGGGAGTTTCACACCG	TAAAGGCTTGACATTTCGGG

Supplemental Table 6. (Continued).

Marker name	Polymorphic in 6 species	SSR pattern		Estimated product size	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)
		Motif	Size (total bp)			
EcGAS2189	+	AGC	24	160	TGAAATGCAGGTTGTTGGAA	ACCCCACTCTTCCACATCAG
EcGAS2190	+	AGC	24	286	GCATGCACTCCAATTCACAC	AAAATCAGAGACACCCACCG
EcGAS2191	+	AGGC	24	238	CATATTGGGAACATGGGGAG	TTGGAATGGAATGGAATGGT
EcGAS2192	+	AGGC	24	209	CAGTCGGAACCGACAAAAAT	TGTTGAGCTCGTTTGAGGTG
EcGAS2193	−	AC	22	256	AACACAAATCTCACCTCCCG	TGTTTTGGTTTCTCTTGGCTC
EcGAS2194	−	AC	22	238	TCTTCGAGGCATTCTTTCGT	TTTGGAAAGCTCAAACACCC
EcGAS2195	−	AG	22	273	GCTTCTGCTGAGTGGGTTTC	GGAGGACAGGCAGTTCAGAG
EcGAS2196	−	AG	22	214	ATTCTGGTTCCACGCTCATC	ATTCAAGGACATGGCACCTC
EcGAS2197	+	AG	22	297	GAGGCACAAAGGTTCCAAAA	GTCGAGTCGCCAAATGAGAT
EcGAS2198	+	AG	22	228	CAGAGTCCTCTGCCACACAA	CACAGCAGAAAAGGCTAGGG
EcGAS2199	+	AT	22	124	CCATCGACATGTAGACACCG	GGCCTCCTAGTGCTGTTGAG
EcGAS2200	+	AT	22	241	AATGTTGGGATCAAATGGGA	AAATTGCCGGCACACTCTAC
EcGAS2201	+	AAG	21	153	TTGAAAATGGGAAGGCAAAG	CGTAATTGACCGGAGGCTAA
EcGAS2202	−	AAG	21	104	CGACAAAGTTGGATGTCCCT	CCACTTCCGTTTCGTGATTC
EcGAS2203	+	AAT	21	175	AGAGTCCAAGCCAACACGTC	CGAGAAAGGGAGGAGAAGGT
EcGAS2204	+	AAT	21	273	AAGATTACACTTGCGCAGCC	ATGGCCGTTATCAATCGAAG
EcGAS2205	+	AGC	21	200	CGATGTCCATGACTTCCTCC	CAACATAGGTGCAATGACGG
EcGAS2206	+	AGC	21	275	CAAAAACGGAGAATCCGAAA	AGAATTGCTCGGTTTTGGC
EcGAS2207	+	ATC	21	269	ACGAGTTTCCAGATGGGATG	CCGGAGAGAATAGATGCCAA
EcGAS2208	+	ATC	21	142	AGGACTCCGGTCCTGATTTT	CGTTTTAGGCACTCCTCTGC
EcGAS2209	+	AG	20	272	TATGAGGCCCCAGAACTGAC	GGAGCAAAAGCAGGAGTCTG
EcGAS2210	+	AG	20	288	ACCATGAGAGTGTTCCAGGG	CCCTTCTCGTGTCTCTACGC
EcGAS2211	−	AT	20	275	CACGTAGACTGCCACGTCAT	TTCTTTCGCAACACAAGCAC
EcGAS2212	+	AT	20	290	TGTCCTCTCACCCTCTTTGC	GCGAATGGAAAAGACTGCAT
EcGAS2213	+	GATC	20	269	ATAACCGAACCCCTCGAATC	GTAACTGCCCTAATTGCCCA
EcGAS2214	+	GC	20	253	ATATGGTTGGGTGTCGGTGT	TCTTATTGCCGCGTTTCTTT
EcGAS2215	+	GGAT	20	277	AGGAAATGGTCTGCCCTTCT	TCATCTGTCTTTGTGCCTCG
EcGAS2216	+	GGGA	20	208	GTCGAATGAAGATGCCGATT	GAGGGTTGCTCGTGCTAGTC
EcGAS2217	−	AAG	18	299	TCCCCTCGATTCACCAATAC	TTAGATCTGTGCGCGATTTG
EcGAS2218	+	AAG	18	177	GTCTTCAAGCTCCTGGTTCG	ACCGAATAGTGGGCTGTCAC
EcGAS2219	−	AAT	18	273	ACTTTTGAAATCCGTGGCAA	TAGTGAGTCTGCAAAGGCCC
EcGAS2220	+	AAT	18	142	GCCTCCAACGACATGAGAGT	CATAAAGGTGCGAGGAAAGC
EcGAS2221	+	ACG	18	146	GTTGTGCTTGCTTCAGGTCA	GACCGGAGAAAAGAAAAGGG
EcGAS2222	+	ACT	18	228	AATGCCAGATAACGGACCTG	TACTTGCTTCACATCAGCCG
EcGAS2223	+	AGC	18	174	CGGCATGTACACATGGTCTC	GTCCGCATCAATAGGAGGAA
EcGAS2224	+	AGC	18	278	TTCACCTGGTAGCTCACGAA	AGCAAGAAGCTGGACCAGAG
EcGAS2225	−	AAC	36	251	CATTTGACGCTCATCACCAC	AATTGCTAGGGAGGAACCGT
EcGAS2226	+	AAG	36	285	CAGAACACCAGATCTGCGAA	GAAGAAGGGGGAGAATCCAC
EcGAS2227	+	ACG	36	271	TAAATCCTCAAACCCATCGC	AATTCGATGGGAGTGTCGTC
EcGAS2228	−	ATC	36	297	GACGATGGTAGTTTTTGGGG	TGTTGGCATCTCCTGTTTCA
EcGAS2229	+	AAC	33	299	TAGCCAAGTCACATCGCAAG	ACCCGGTTTCAGTCGATATG
EcGAS2230	+	AAG	33	252	CAGGAGGTAAGGGAAGGAGG	TGTCTCCCTCACCATCATCA
EcGAS2231	−	AAT	33	175	ATAGAGCAATCCGGATGAGG	CTCGCTCTGGAGAATTCCTG
EcGAS2232	+	ACG	33	291	AATTTACGCAGATGAAGGCG	TTGGAGGGGTGTTTTAGTCG
EcGAS2233	+	ACT	33	255	CTAGCCAAGTGTCTGAGGGG	AACCTCCCGTTTATTCCCAT
EcGAS2234	+	AG	33	289	TATTACTGGCTTTCCCCGTG	CGCAACTCCGATCCTTTTAG
EcGAS2235	+	GGA	33	202	GTCGAGCTAAATTGACGGGA	ACGAAAGGCAAATTGCAAAC
EcGAS2236	+	GGC	33	261	GCAGAATGGCTACTTCTCCG	TGATGATGTTCCACGTAGGC
EcGAS2237	+	AG	32	167	TTGTACCTAACGCTGCGAGA	AACCAACTTTCCCTTCGCTT
EcGAS2238	+	AG	32	201	AGATGATGCCAAGAAATGCC	CACGAGTCCCACACATATCG
EcGAS2239	+	AAAG	32	269	GGGAATGGTTGCCATACATC	AGGAGGAAGAGAGAGGGCTG
EcGAS2240	+	AAAT	32	296	CTGCCAATTCAAAACCCACT	ATGTCCTCACCCGTGACACT
EcGAS2241	+	AAC	30	299	GGATCTCGGAGTCCATTTGA	CTTGAGCAGCTTCATTGCTG
EcGAS2242	+	AAG	30	180	AAGAAGCTGCAACGGAAAAA	GAAACGCAGAAAGATGAGCC
EcGAS2243	+	AAG	30	275	TGGAGTGTGGGGAAGATGAT	AGGCCTCGTTTAGTTCAGCA
EcGAS2244	+	AAG	30	275	TCCTCATCTGAACATGCTGC	GCATAAGCTCCTCATGCACA
EcGAS2245	+	AAT	30	259	AGGTCCCTTGGCTATTCGAT	CCCCAAAGACTACGAAACCA
EcGAS2246	+	ACG	30	270	CCGCCATCATCTTCTTCATT	GAGATTCGGGTAGCTGAGGA
EcGAS2247	+	AG	30	259	ATGCGAGCAGAACTTCGATT	GCAAAACACACGTGCTCCTA
EcGAS2248	+	AG	30	212	AGTAAAATTCATGCCGCGAG	ACTGGCTTTATCACCATCGG
EcGAS2249	+	AGC	30	274	GATAGGAGGCGGAGGAGAAG	AATAGCCAACGCCACTCATC
EcGAS2250	+	AGC	30	298	GGCACAGGGAGAGGATAACA	CCCTGTGTGATAATTTGGGG
EcGAS2251	+	AT	30	123	CCTTGCATTTAGGGGTGTGT	TCGCACATGAGATTCACTCC

Supplemental Table 6. (Continued).

Marker name	Polymorphic in 6 species	SSR pattern		Estimated product size	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)
		Motif	Size (total bp)			
EcGAS2252	+	ATC	30	162	GTTGCCTAGGAGGCATGTGT	TCACAAGGATCATGAAGCCA
EcGAS2253	+	GGA	30	152	TAGGAGCAGCAGCAGCAGTA	ACCAGTTCCCAGTGTTGAGC
EcGAS2254	+	GGA	30	153	CAACAACATTCGAGAGGGGT	CTTCTGCAAGATCCTTTGGC
EcGAS2255	+	GGC	30	188	AGCACGGTATGAAATCCACC	CCTCTCCTTCTACTCCGCCT
EcGAS2256	−	GGC	30	271	TCTCTCTTCTAAACCCCCGC	AACCCATTTCTAACGCATCG
EcGAS2257	+	AAAC	28	177	GCTGAAGAGGAGAAAAACGG	TCAGCTCGTCCTCAGTCATC
EcGAS2258	+	AAAG	28	265	TCCAAATTGACCCATTTCACT	GTTGAGCCTTGCTGGATTTC
EcGAS2259	+	AAAG	28	243	TCGCTATTCTGCCTTCCATT	CATCATTGTTGGCCCTTTTC
EcGAS2260	+	AAAT	28	219	TGGAAAATATCGCTCGAACC	TTCAAAATTCGGAATCGAGG
EcGAS2261	+	AC	28	139	CGACCAACTGCTTTTCCTTC	CCATGGGGAAATTTGTTTTG
EcGAS2262	+	AC	28	249	ATCAAACCACCCGCATACAT	CACCACTTCAGGACAAACCC
EcGAS2263	+	AG	28	262	TCCTTCTTCCCCCTTCTCTC	GACCCGTGAAGAAGATCGAG
EcGAS2264	+	AG	28	185	ACATGATTTGGTAGACGGGC	TAATGGGGAGACTGATTCGG
EcGAS2265	+	AG	28	140	AGCGAAGACAAGAAGGGACA	TTCAAAGTTGCAGACAACGG
EcGAS2266	+	AG	28	139	TATGTTGATGCAGCCGTGTT	ATTCTAGGAAATGTGCACGC
EcGAS2267	+	AT	28	272	CGTTGCTCGCCTAGAGAACT	AACGTCTCCCCGAAGAAAGT
EcGAS2268	+	AT	28	223	GAGTTGGCAAGGTGATCCAT	CAGGGGAGCAAACTTTCAAC
EcGAS2269	+	AG	28	270	AAGCACATGCCCAGTCTTCT	GAGACCAGTGCCCATAGCTC
EcGAS2270	+	AG	28	279	CGGCTCAGTTCCTTTCTTTG	AAGATCCCAACAACGACGAC
EcGAS2271	+	AT	28	288	ATGATGCACAATTTCCCCAT	GGCTCGTTCAATTTCTGAGC
EcGAS2272	+	AT	28	231	CCATACAAGTAATGCCGCAA	TGCCGAATTGGGAAACTAAG
EcGAS2273	+	AAC	27	230	TCGACCAAGATTGGCATACA	GCATGGATCCTCCCAATTTA
EcGAS2274	+	AAG	27	166	CTCTCGAGCATAAGCCTTGG	CGAAGAGAGAGAGGGAGGGT
EcGAS2275	+	AAG	27	259	TTCTCAAGGCGTTCGAAGTT	TTTGTGCAGCGACTATCGAC
EcGAS2276	+	AAG	27	241	CTTCATTCCAGGGTCTCCAA	GACAAAAAGCAAGCGACTCC
EcGAS2277	+	AAT	27	183	AATCCCACCAGCAGATCAAC	GAAGCAATCCGAAGCAAGTC
EcGAS2278	+	AAT	27	159	ATGCACGTGGCATTTCTACA	ATGTGGACTTCATCTTCGGC
EcGAS2279	+	ACT	27	286	TGGAACTGCTTCTGCTGCTA	GCCACCAGGCCTTTATTCTA
EcGAS2280	+	AGC	27	271	CCCACGGGGAATAAATAGGA	CTCCCTTGATGTCCAAGCAT
EcGAS2281	+	ATC	27	236	CTTAATGGGTTCGGTTCCAA	TGGGAGCTGGCCTACTTATG
EcGAS2282	+	ATC	27	287	GCGGTTTCCCACACTCTAAA	GTGATGAAGTGGGTGGTGTG
EcGAS2283	+	GGA	27	231	AGGTGATGAAACCGAGAACG	GACAAGAAAACGAAACCCCA
EcGAS2284	+	GGA	27	292	GCTTCAGCAGTAGGCAAAGG	ACCTCCCTCATCGACCTCTT
EcGAS2285	+	GGC	27	121	GATACGAAGCGGGAGAGTTG	GAACGAGCCCGAATGATGT
EcGAS2286	+	GGC	27	244	GCCATAATTGGGAAAGGGTT	GTCCCTCCATTTCACGTCAT
EcGAS2287	+	GGT	27	251	CGTTTTGCAGGTTTTTGTGA	CAGCAGTTCTGCACTTGAGC
EcGAS2288	+	GGT	27	231	AAGTTTGGTGGGAACACTGC	GGAATCACCCATGGATAAGG
EcGAS2289	+	AC	26	298	TGGTTCTAAAACCCTCCACG	AGCGATAGGCGACAAAAGAA
EcGAS2290	+	AC	26	217	TATTCCTGGGTCAGGGACAG	GTGTCGTCATCAAAACCGTG
EcGAS2291	+	AG	26	285	CCTGCTCTAACTGCCAGTCC	CTTCTTGACTCTTCTGGCCG
EcGAS2292	+	AG	26	270	CTAGGACTCACAGGGACCGA	TTAACCCCCTACAGACGTGC
EcGAS2293	+	AG	26	289	TGCCGTCAGTTTCTGTTTCA	TCTTGAAATTTTTCCCGTGG
EcGAS2294	+	AG	26	276	GGACAGGGTTGCAGAGGTAG	GGGGAAATACGATTTTTCGG
EcGAS2295	+	AG	26	136	GCTGGTCGCAAATAAATCGT	CACGACCACAAACCAATCAG
EcGAS2296	+	AG	26	151	GCGAGCAACAAAAACCTCTC	GTGCACTGACAAAATGCAGG
EcGAS2297	+	AG	26	215	CAGGGCTGAAGAGAAGATCG	ATGCATGCTTTGTCTTGCTG
EcGAS2298	+	AG	26	287	ATGCGACGATCCATACTTCC	TGCTCCATCGATCCATAACA
EcGAS2299	+	AG	26	253	ATTGCATGCGTAGTGAAACG	GGTCGATCCCCTCCATAAAT
EcGAS2300	+	AG	26	177	CAAGGAAGTTTCCGCAAGAG	CATCGCCTGATTTCATTCCT
EcGAS2301	+	AT	26	298	GGATGCCGTGAGAACTCTTC	GGAGCTCAGGATCTGTCCAA
EcGAS2302	+	AT	26	270	CTAGGCTGCAAAGGCTCATC	CTTGGGTGGCCTTATTTTGA
EcGAS2303	+	AT	26	184	CCTCGGCCCTTACATCATTA	AGCAATCAAGTCTACGCGCT
EcGAS2304	−	AT	26	294	TGCGGATGTTCTGACTCTTG	AATGCGTTGGATGGAGAAAC
EcGAS2305	+	AAAC	24	247	TCCCAAAGTAGATCCACCCA	GGGTGCGCTAGTTGTAGAGG
EcGAS2306	+	AAAC	24	245	TGGTTTGATATCCCCTCCAA	CAGAAAGAAAGGCGAGATGG
EcGAS2307	+	AAAG	24	94	GCAATCATTCAGGTCCAGGT	AAATTCATTGGGCGACAAAG
EcGAS2308	+	AAAG	24	216	TGGCAAAGGGATGAAGAAAG	CTCCCCTTATTGATTGGTGC
EcGAS2309	+	AAAT	24	281	GGCCTAAGCATTTATTGGCA	GGCATTATAAACCGACGCTC
EcGAS2310	+	AAAT	24	297	TATGTTCATCCGGCTCCTTC	AGGCATAACCAGATTGTCGC
EcGAS2311	+	AAAT	24	193	CTGTTGTTTGGGTGCTCCTT	TGGGAAATGCTGTGGTCATA
EcGAS2312	+	AAAT	24	228	TAATGGAACATCGGCTGACA	ATGATGTAGAGCCGCGAAGT
EcGAS2313	+	AAC	24	201	TCCAGTGATTCCACTCCCTC	TGAACGGTGTCCAAAACTCA
EcGAS2314	+	AAC	24	293	TGTACGCATCAAAAGCCTGA	CTACGCACGATATGAAGCCA

Supplemental Table 6. (Continued).

Marker name	Polymorphic in 6 species	SSR pattern		Estimated product size	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)
		Motif	Size (total bp)			
EcGAS2315	+	AAG	24	164	CTACCAGCTGTACGGGGTTC	ATCACGCCTGTAAATCTCGG
EcGAS2316	+	AAG	24	227	CACTGCACACCGTAAAATCG	CCATTTCCCGAAACATGACT
EcGAS2317	−	AC	24	234	TGAATTCCAAAATGGTGTGC	TCACGGTTAATTTCCCAAGC
EcGAS2318	+	AG	24	299	TAAGCTGGGGATGATTTTGC	TCATCAATCAAGAGCTGGGA
EcGAS2319	+	AG	24	232	CCTCCTCATGGTGGACTTGT	GAGAGCAGTCAAAACCCTCG
EcGAS2320	+	AG	24	279	TGGTGAAGACTGCTCATTGG	CTCCCCAGAAAGATTCGATG
EcGAS2321	+	AAC	30	293	TGCTCCTGCATTCTTTTTCC	TATCCTGAAAAGCCACGAGC
EcGAS2322	+	AAG	30	203	CCTTTCCTCCATGCACTCAT	GCAAGTTCGGCCTTACCATA
EcGAS2323	+	AAG	30	280	ATTGCTCTTCGGAGCAAGAA	GCATTTAAGTTTTTGCGGGA
EcGAS2324	+	AAT	30	197	ATCACAAGAAAGAGGCGGAA	AACACGACGCCCAAAAGTAG
EcGAS2325	+	AAG	30	240	TTTCTTATCTTTTGCCCCCA	TCCCACAATTCCTTCACTCA
EcGAS2326	−	AAT	30	260	CGCGTTAATCGATTTGGTTT	TTTCCAATGTTGGTCAGTTCC
EcGAS2327	+	GGA	30	252	GTCGAGTGCGGTGGATACTT	TTGCTACGTGGACCTCAACA
EcGAS2328	+	ATC	30	298	GAACGATCATGCCTCTGGTT	TCGATGTGGGATAACTCCAA
EcGAS2329	+	GGA	30	298	TGAGCACGTTACTGGCTTTG	TTTTCATGCTGCAACTCCAC
EcGAS2330	+	GGA	30	288	TTTGATGGGCTGAAACCTTC	GGAGGGAGGAGAGAAGGAGA
EcGAS2331	+	GGC	30	152	AAAACCCCCGAAAAACAATC	TTCGGTATTACCCTTGTCGC
EcGAS2332	+	GGT	30	260	CTCAATTTGGTGATTGGGGT	GGGTTTGAAAGAGGGAAAGG
EcGAS2333	+	GGT	30	129	ACGATGGCCATTCAAAATGT	CCGCATCTGTCTTATCCGTT
EcGAS2334	−	AAT	30	273	GCTGCCTTCTTCCTCTTCCT	ACCAAAATCGGAGCAAAATG
EcGAS2335	+	AG	30	279	CAATAAACCCTATCGCCGAA	CATGGGAAAAGGACAGGAGA
EcGAS2336	+	AG	30	159	TGGTGTGAGATCGATGTGGT	AGCCCGACTCTTCCTCTTTC
EcGAS2337	+	AAAG	28	196	AGGGAGTGAGAGATGCGAAA	TGTACGACCCTTCGGAGAAT
EcGAS2338	+	AAAT	28	295	GACGCAAATTAGGATGGAGC	TTTTTGTGAAAATGATCGCTTA
EcGAS2339	+	AAAT	28	261	AGCACTTAGGCTCAGGTCCA	TAGATGAGGGATGGGCTCAC
EcGAS2340	+	AAAT	28	180	AGCAAGCGTTCCAGACAAGT	CAGGAGAAGAGGGTTTATCCG
EcGAS2341	+	AAAT	28	296	AGGGCTGACCCAGTAAATCA	CGCCAACAATTTTCATCAAC
EcGAS2342	−	AAAT	28	264	GCATGAAATGCAAGGAATGA	TGGCTAGCAGCTGGCTAAAT
EcGAS2343	+	AATT	28	226	TCGGATCACATAAGGGGAAA	TCAAGCTAAAATTCGAAGACCA
EcGAS2344	+	AG	28	166	CTTTCCCCTCTCTCCAGCTT	TATCGGGCCTATTCTGATGC
EcGAS2345	+	AT	28	258	AATGGCGTTTCAATGCTTTC	CCTATTGCCTGCTTGGAAGA
EcGAS2346	+	GGGA	28	107	GCCCCAATCAAAAGTCAAAA	CGTGACGAAGAGGAAGGAAC
EcGAS2347	+	AAAG	28	231	AGTAAAGAAGACCCGAGCCC	ATGCCTTTGCTTTGCTGAGT
EcGAS2348	+	AAAG	28	266	TAAGAGCGACGCCTCAAACT	ACATTTACTCCTCTCCGCGA
EcGAS2349	+	AAAT	28	277	ACTCCCCATGATCAAATCCA	CGGCGACAAAGGTTATGAGT
EcGAS2350	+	AAAT	28	91	AAACCCGGCCATATTTAACC	ACATGTGGCACGAGCATATC
EcGAS2351	−	AG	28	203	CGCCCCAAGAGTAAAGAGTG	TCCACGAAACAAATGGAACA
EcGAS2352	+	AG	28	265	CTTCAACGGCATTGGTAAGC	TTGGAAATCACCAACCTCAA
EcGAS2353	+	AAG	27	286	ACAGAGGCGTAGGGGAAGAT	GGAAAGCGTGGTACAAGTGTT
EcGAS2354	+	AAG	27	246	TCTATGCGTGTGTTGCCAAT	ATCTTTCGACGACAACTCCG
EcGAS2355	+	AAG	27	165	GCCAAAATTGAAGGAGACCA	ACGTTCGGCCCTCTTTTACT
EcGAS2356	−	AAT	27	90	TTTACAATAAGGAGGGCGCA	TGAAGCATCATGAGCGGTTA
EcGAS2357	+	AAT	27	294	GGTGCTACCCAAAAGGATCA	TGAGCCACCAAAAACAAAAA
EcGAS2358	+	AAT	27	287	TAGCAACCAATGACGATGGA	AGGCCCTTTTTGGTAACTGG
EcGAS2359	+	AAT	27	190	GCACTCCTTAGCTGCCATTC	TGAACGACATTACTGCCCAA
EcGAS2360	+	AGC	27	164	CAGTGAAGGCCAAAAGAAGC	CTGCGGTCTCTTTCTCTCTCA
EcGAS2361	+	ATC	27	182	AAGGGGAATGAGGAGGAGAA	CCTCCAACGGTCAAAAGAAA
EcGAS2362	+	ATC	27	295	CTCCTCCTTGGAATGGTTCA	GCTCCATGTTCTCCACGATT
EcGAS2363	+	GGA	27	227	GCCTAGTAAGGTCTGGCGTG	TTACAGGGCATCTTCGCTTT
EcGAS2364	+	GGA	27	202	GATTGTAGCTGCGGAAGAGG	TGCTAAGTCCCATCGGAAAC
EcGAS2365	+	GGT	27	143	CTGGCTAGGCAGTGACGATT	GTTCCATAGCCATCACCACC
EcGAS2366	+	AAG	27	128	TTCAAGTCCACCGTCCTTTC	CCCTGAAGTGATTCGACGAT
EcGAS2367	+	AAT	27	273	CCCGTTTGTTTTGAAAATCG	AAACGCAAGCTTACAAGGGA
EcGAS2368	+	ACT	27	225	ATGAGGACTAACAGAGGCCG	CACGAGAATTTCATCAGCCA
EcGAS2369	+	AG	26	272	CAAGTGCAATTGCCAAGGTA	CCAGTCTGGTGAAAGGGTTC
EcGAS2370	+	AG	26	294	CGAACTTTCTACAGCCCAGC	ACCTTCAGTCCACCAGCATC
EcGAS2371	+	AG	26	151	CAGCGTACGTCAAAGGACAA	GGAGGAGGGGTAGAAGTTGG
EcGAS2372	+	AT	26	157	CCTAACGATGGTGAGGCAAT	TGTGGTGATGATGTGGCTAAA
EcGAS2373	+	AT	26	169	CTAGCCACGAACCATCCATT	CTTCGACTCGTGCAAGACAA
EcGAS2374	+	AT	26	251	CAGCCACGAAGGTTTAAGGT	CCCGCAATCGATAACAATCT
EcGAS2375	+	AG	26	287	TACCCCTAAGGTCTCGCTTG	GGGAAGAAGGAAGGAGAAGC
EcGAS2376	+	AG	26	211	TGCCGTGAGATCATACCAAA	TGCGCCCTATTATTGTCCTC
EcGAS2377	+	AG	26	207	CCTTCGCATGAAACCCTAGA	TCGCTCAGGCTCTCTTTTTC

Supplemental Table 6. (Continued).

Marker name	Polymorphic in 6 species	SSR pattern		Estimated product size	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)
		Motif	Size (total bp)			
EcGAS2378	+	AG	26	186	TGGAAAGTGAGGGAAAATGG	TGAGTCTCCAAAGGCTTCGT
EcGAS2379	+	AT	26	164	TGCACATAAGCGTTGGTTGT	TTGCCTTGTAGGCCAAAGAT
EcGAS2380	+	AT	26	217	CTCGGCGTGAGAGAATAGGT	ACTTCATCCCTTTTGGCCTT
EcGAS2381	+	AT	26	237	GAATCCTATGCCGGTCAAGA	TTGCGATTGAAACATGGGTA
EcGAS2382	+	AT	26	252	TGCAAACACGCTTTTGACTC	ATTGCAATTCACAGCACAGC
EcGAS2383	+	AT	26	267	AACGGAAGCGTAAGTCGAAA	TTCGATACTCCGTCAACACG
EcGAS2384	+	AG	26	274	TCCATGATGGTCACGTTTTG	TCAATGTTGCCAAGACTCCA
EcGAS2385	+	AT	24	153	CTTAGCAAATGGCCACGAAT	TGCAATTCTTTTCAAAGCCC
EcGAS2386	+	AT	24	241	TGCAGAAATGATTAGCACGC	CCGGAGGTTGTGCATATTTC
EcGAS2387	+	AT	24	272	GCCCTGAACTGGCAGAAATA	TTTTCGGAGAGGATCGCTTA
EcGAS2388	+	AT	24	124	ATTCGGCAAGGCCTAGAGTT	TATGAGAATTCCGCAGACCC
EcGAS2389	+	AT	24	300	GGTCCATTTCGCTGGTCTTA	CCATTATTGTCACACCCCAA
EcGAS2390	+	GGA	24	185	AATCTCCCAACAAATGCGTC	AAATTTCAACGAGTCCCACC
EcGAS2391	+	GGA	24	269	GAGGGAGGAGGAGAAGGAGA	GGCGATGGAAACAGAGTGAT
EcGAS2392	+	GGGA	24	200	AACAACCCAGCACTGTTTCC	TCTTCTTGGTGGCCACTTTC
EcGAS2393	+	AG	24	270	GACAGATTTTGACGCGGTTT	CGTAATGCAAGGCAAGTTGA
EcGAS2394	+	AG	24	210	TTACATGGCATGATCAGCGT	GGAGGTTGCAAGACACCAAT
EcGAS2395	+	AG	24	231	GCAATACAAGTCCGAGAGCC	TTCCCATAATTTCCTCACGC
EcGAS2396	+	AG	24	236	GTCTTGGCTGGCGTACTCTT	TCTTTTATCTTTCCCCCGCT
EcGAS2397	+	AAT	24	134	ATTTGTTTGTGTTGGAGCCC	GTGATTTACCTCCAGCTGCC
EcGAS2398	+	AATC	24	178	AAGGGAGAAAGAGGGTCCAA	AGTCCAACTAATGCGGTTGC
EcGAS2399	−	AATG	24	298	TGGACAATTTTCCCCATGAT	GGACTTTTGCCCAATTTTCA
EcGAS2400	−	AATT	24	299	TGCTCTATCGGCCAAGGATA	CCCATTACGGGCTTCAATTA
EcGAS2401	+	AAAG	24	188	TAGAGGTGGAAGATGGACCG	ACATGAGGACTTGGGTTTCG
EcGAS2402	+	AAAG	24	218	ATCCCCTTCTTTGGTTCTGC	TTTTTCATTCGAGTCGGTCC
EcGAS2403	+	AAAT	24	231	GGTCATCATCTCGCTGGATT	AAGGAGGGAATTACGGATGG
EcGAS2404	+	AAAT	24	242	GTCAATCCTTGACCGATGCT	TGAGCAGGTAGTGTTGCTCG
EcGAS2405	+	AAAT	24	202	GTCTTAGGTGAGCCATTCGG	TCAATGACTCGTTGCCATGT
EcGAS2406	+	AAAT	24	180	TAATGGAAGTCCGGTCAAGC	AAGAGCCGCTTCTTTAGATGG
EcGAS2407	+	AAAT	24	140	TTTTGGTTTTGGGTCCAGTC	AGTGGATCTTAATGCCAAACG
EcGAS2408	+	AAAT	24	294	TAAGGAAGAGCAATCCCGAA	GGGATGACTGCACACAAAAG
EcGAS2409	+	AAC	24	299	TAAGGGAAGTGGAGGCAATG	ATCCGATCCAACTGAAGTGC
EcGAS2410	+	AAG	24	278	GGAAAACTTTGGTGTCGCAT	TTCTTTTGCATTGACATCGG
EcGAS2411	+	AAG	24	191	CCGGTCGACATTGACCTACT	TCTTTCCTTTTCCCTCCACC
EcGAS2412	+	AAAT	24	150	GCAGTGTACCCTCTCTCCGT	GATTTCTCCGATGGGTTGTG
EcGAS2413	+	AAAT	24	158	TTCAAGGCAACAAAGCAAGA	AAAGATCGCCCAGGCTAAAT
EcGAS2414	+	AAG	24	230	AGTCCACATGCGACAACAAA	ACGAGTGGTGGACGGTAGAA
EcGAS2415	+	AAT	24	263	TAACACGCGCTAGAATGCTT	CCCATTTTGGAATTTTCCCT
EcGAS2416	+	AAT	24	205	AGAAAGCATAGGTTGATGCAAT	TGGGGGTTTCAATCTTTGAG
EcGAS2417	+	AG	22	211	TCCATCCATGTCCCTTCTCT	ACGACCGAATTCAAAGGAGA
EcGAS2418	+	AG	22	192	GAAAAGCCCAAAAAGGAACC	GCACAGAGAGAAAAGGTCGG
EcGAS2419	+	AG	22	295	ACAATCACCATGTCACTCGC	TCGAAGTGGAAGAGGAAGGA
EcGAS2420	+	AG	22	293	TCGCGACTCCAAGTTACTCC	GCAATCCCAAGCCAATCATA
EcGAS2421	+	AC	22	187	TGAGAACTTCGCAATGTGGA	GACATGTCACTTTCAGGCCA
EcGAS2422	+	AG	22	228	CCTTTATGCCGTGTGTGATG	TGAACTGAAGAATCCCCTGG
EcGAS2423	+	AT	22	181	GAAGTGGTGTAGCGGGTGAT	TCGTCAACCCATTCGTGTTA
EcGAS2424	−	AT	22	298	ACGAATTTGGTGATGCCTTC	GGATTTGTTGCTTCTTCTCCTC
EcGAS2425	+	AT	22	261	AATTTGGCAGGGCGTATCTT	GGGTTGCTTCACCATCATTC
EcGAS2426	+	AT	22	253	TCTTCCGACTCTTATTTCCCA	CATGTTAACCCGTCATTTCTCA
EcGAS2427	+	AAG	21	267	TAAGGAGGAAAGGGTTTCGG	AATTGAGGGACAACGTGAGG
EcGAS2428	+	AAG	21	273	CCCAGCCTGAGGTCACTATT	GCCATTTGTCCCCAAGATAG
EcGAS2429	+	AAG	21	217	AAGGTTGCGCGATAAATCTG	GAACCCCATTTCCCAAGAGT
EcGAS2430	+	AAT	21	252	CAAGACAATGGAACGAGCCT	AGCTCTGTAGGATTTGCCCA
EcGAS2431	+	AGC	21	222	AGGCTTGAACCCAAACCTCT	CCGGAATAAAAGCAACAGGA
EcGAS2432	+	AGC	21	149	AGGATGCTCAACATGAAGGG	GAGCAAGTCTACGAGGACCG
EcGAS2433	+	AAAT	20	280	GCGACGCTCAAATAAACACA	TACGGCTTGTAAAATGTGCG
EcGAS2434	+	AAAT	20	145	CTCTTGCTAGTTGCCAAGCC	CGCCACTGATGTTAATGTGG
EcGAS2435	+	AG	20	267	GTGGAACGGTAAGAGGACGA	TCTTCTTTGCCATGTGCTTG
EcGAS2436	+	AG	20	286	TCCTTCGTGTTTAACCCTCG	CGTTTGATGGAGGTGTTGTG
EcGAS2437	+	AT	20	294	GGGAATTTTGCCGTGACTTA	GAGTTCAGTTCACCGCCATT
EcGAS2438	−	AT	20	293	AGGCAAATCTCCTACCCGTT	CAAATCTTGAAACATGCACGA
EcGAS2439	+	GGGA	20	221	CCGTTTCGGAAAAGATACGA	GGGATGATGGGACTGAGAGA
EcGAS2440	+	AAAT	20	237	CTAAGCTGTTGCGACCCTTC	GCAAAAGATTGGGTTGAGGA

Supplemental Table 6. (Continued).

Marker name	Polymorphic in 6 species	SSR pattern		Estimated product size	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)
		Motif	Size (total bp)			
EcGAS2441	+	AGC	18	161	CCAATTCCAACTGGATCGTC	GATTCACTCCCTTGTTGGGA
EcGAS2442	+	GGC	18	163	ATCGACGATTACCGCCAGT	GATCAACGGTGATGGTTGG
EcGAS2443	+	AAT	18	254	GAGAGTGAGGCTTGGAGGTG	CATCGGTCCAATTCTTGGTT
EcGAS2444	+	AAT	18	244	CTGGAAGTCAAGCTTTTCGG	TCTCGAGATCCCCACTTCTC
EcGAS2445	+	AAAT	16	266	AATGAGCGGTGAAAGAAGGA	CGTTCCTTTGATGGAAAACG
EcGAS2446	+	AAAT	16	134	TGGGTACCTGAATTTGTGGA	AATTGGCCAAATTTGTGAGC
EcGAS2447	+	AATT	16	282	CAACGCCCGGTAATTCTCTA	TGGTTTGGAACTTTTCCAGG
EcGAS2448	+	GGGA	16	291	GTGATGTGATGAGCCACACC	ATCAAGGTCGATGAGAACGG
EcGAS2449	+	AAG	33	214	TATCATGCAAAATCGGCAAA	TCCTAAAGTCGGCCAAAGAA
EcGAS2450	+	AAG	33	266	TATATGCATCACAATGGGCG	AAATAAAAATTGGCACGCGA
EcGAS2451	+	AAT	33	280	CTAGAGCGGACATAAAGCGG	CCCGTCTCTCCCTCTCTCTT
EcGAS2452	+	GGC	33	204	CGGAGATATGATCGGGAAAA	TTTGCCCTTTTGACTTGACC
EcGAS2453	+	AAAG	32	210	CCTTTTCCGTTTGCTTGTGT	TGAATTGACGGTGCTAGGTG
EcGAS2454	+	GGGA	32	205	AATGTGACGTTGGATCACACA	GTAAGAAGCGGCAGTGAAGG
EcGAS2455	+	AAG	30	256	CCCTTGTCTAGCTGGTCGTT	TTCTTTTGTTTCGGGGAATG
EcGAS2456	+	AAG	30	239	CAATCACTGGCTAGGACGGT	TGTTATGGCACCTCGACAAG
EcGAS2457	+	AAG	30	229	GATCAGATCAGACCAGACCCA	GCATGCAAGTCACGCTTTAG
EcGAS2458	+	AAG	30	171	ATTTGGAGTACATGCCCAGC	AAATGCAAAGCAATTCCACC
EcGAS2459	+	AAT	30	231	TGAACATGCACGGAGTCAAT	ATATTTTGGACTTGCGTGGC
EcGAS2460	+	AAT	30	160	AATGCGCGGGAATTATTGTA	ATGGCTGCATCAAATGTCAA
EcGAS2461	+	AG	30	204	ATACCCTCACTTGATTGCCG	GTCGTGCAACGTTATCCCTT
EcGAS2462	+	AT	30	274	GAGGAGTGAAAAAGCTCCCC	AGATCGCTCAAGAGAGACGG
EcGAS2463	+	ATC	30	105	GAAAGTAAATGGTCCCGCAA	AGAACTTTTGCTCTTGGCGA
EcGAS2464	+	GGT	30	279	CCGTTCTGGTGTTCCAATCT	GTGGCATCAAGTAGGCTCGT
EcGAS2465	+	AAAG	28	161	AAGCCCTTCTCTTTTGGAGC	TTGTTTCTCGTGCAAAATGC
EcGAS2466	+	AAAG	28	93	GAAACCTGCAAAGTGAGCCT	CCACAAATTTTGACAACGGA
EcGAS2467	+	AAAT	28	293	GAAAGCTCCTCACGACCGTA	CCGGATAGATTGAATTGGCA
EcGAS2468	+	AAAT	28	92	CCGAATCATGTAAGGCCAAG	ACAAGCTGAAAAAGCCCAGA
EcGAS2469	+	AAAT	28	289	TAGGTTGGAAGTTGCTGACG	CGTCCACAAGCAAAGTCTGA
EcGAS2470	+	AAAT	28	111	TATTTTGCTTCCCGTCCTTG	CTGTTCATGCGCTGTCAAGT
EcGAS2471	+	AG	28	188	TCTCCAATCTCCCTTTGCAT	GACCCCATAGCAGCAAGAAA
EcGAS2472	+	AG	28	298	TATGGATGACAAAAGGGGGA	GCAATGCTCCACGGATCTA
EcGAS2473	+	AG	28	237	CCCAATGTTCAAAGCCCTTA	CAATTGAATCCCCGAAAATG
EcGAS2474	+	AG	28	139	TCGAAATGACCTCCCTATCG	TGATGCTTTCTTCTTCCCCA
EcGAS2475	+	AT	28	188	TTGGTTTTGGGCATTCTAGG	TCAAACCATTCACAAGTTCCA
EcGAS2476	+	AT	28	199	AGGGAACAATGAATCTGCAA	TGGAGAGAATGATAAAACGGG
EcGAS2477	+	GGGA	28	206	AACTTTGAGAGCACGGAATGA	CCATATTTGATGGCCGAGTT
EcGAS2478	+	GGGA	28	177	TTTCTGCGGATTGAACTTGA	AACTTTTTAGTGGGACCGAGC
EcGAS2479	+	AAAT	28	166	TGATGGGGTCATGAGAGTGA	AAAGGGACGGCAATTTCTCT
EcGAS2480	+	AG	28	295	ACTTTCGTACGGAGAAGCCA	AATCGAAGGGTAACGGCTTT
EcGAS2481	−	AAC	27	145	TCTCTGTGCTTTGATTGGGA	ATTAAAGGGCATGTGCGTGT
EcGAS2482	+	AAG	27	251	CGTGTGATGGAAGTATCCGA	GTGGCAATTTTGGAGGAAAA
EcGAS2483	+	AAG	27	243	TGCTCATTGCTCAGTCCAAG	GGAAGGAGGAGGAGGATGTC
EcGAS2484	+	AAG	27	273	TGGGCCTCATTTGATATGGT	GGCTCAAATAGGGCAGATCA
EcGAS2485	+	GGC	27	253	TTCCGGTATACTGTGCCACC	ACCGTCACCACCGATCAC
EcGAS2486	+	GGC	27	253	CGATCGTCCCTGAGAAGAAG	ATCTTCTCCAGCAACCCCTT
EcGAS2487	+	GGT	27	291	GGTCAAAGGAAGTGGCTTCA	TTGTGGTGGACAAAGGACAA
EcGAS2488	+	AAG	27	233	TGATTTCTCATGGCCAAGTTC	CGATCACAAAAAGACCAGGA
EcGAS2489	+	AAG	27	238	GTCATCAGCCCTCGTCTAGC	CTTGGACGAGTTTCTGGACA
EcGAS2490	+	AAG	27	154	AGGGGAGTCCCAGAAAGAAA	ACCCCACCAAATCAAATCAG
EcGAS2491	+	AAT	27	164	TAGCCAATGCCTAGTGACCC	TGAGTCCATCCAGCCAATTT
EcGAS2492	+	AAT	27	227	GGAAAGGAACCCACAACGTA	CTCTTGTATCGGAGAAGCGG
EcGAS2493	+	AGC	27	210	CGTCAGACAGGTGACGAGAA	CTGTCACCCCGGTAAAACTC
EcGAS2494	+	ATC	27	216	GCACTCAAGGATCTGGAAGC	ATGCCTTGCATGTGATCTGA
EcGAS2495	+	GGA	27	298	GCCATGAAAAACAATTGAAGC	CCAATAGAATGCCTGCATGA
EcGAS2496	+	GGA	27	185	ATCCCAGAAGGAAGGAAGGA	ATGTCACTCCTCCGGCTCTA
EcGAS2497	+	AC	26	254	GTGTGCAGTCCCTCGTTTCT	TCCTTCTGACCAAATATCCAAA
EcGAS2498	+	AT	26	293	GCAAAAGGGTAACAAACCCA	TGGTAATGTGCAAAGCACAAA
EcGAS2499	−	AT	26	223	CCTGCTGATAGGAGGCAACT	TTATTTTGGTGAGGCTTGAATTA
EcGAS2500	+	AAAG	24	219	GACCCTTGTCTTTATGGGGG	AAACGCAGGTAACCAAGGTG
EcGAS2501	+	AAAG	24	203	CCAAACACCTTTTCCCCTTT	GAGAGAGTCGGTTCCGTGAG
EcGAS2502	+	AAAT	24	244	CGACCAACTGAAGAAGGAGG	GGTTTCGTTTGATTCGTGAAA
EcGAS2503	−	AAAT	24	298	CATCCACTCTGCACTCTCTCC	TCAATGGGACGTTTGAAAGA

Supplemental Table 6. (Continued).

Marker name	Polymorphic in 6 species	SSR pattern		Estimated product size	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)
		Motif	Size (total bp)			
EcGAS2504	+	AAAT	24	260	CCACAGCTTGGAACTCCTTT	CACGCAGGAGCTATGGATAA
EcGAS2505	+	AAAT	24	257	CGAAGAAGACGACATGCAAA	ATGATTAGCGGCTGAAATGG
EcGAS2506	+	AAAT	24	264	CGAGAAGATCCCAGAAAGGA	TGGTCGTGACCAACCATTATT
EcGAS2507	+	AAAT	24	263	TATTGCCGTGCTTGGTTGTA	TGGGGATAAACACTGAGTTCTTG
EcGAS2508	+	AAT	24	270	GCCATAAAGGCTTGTCCAAT	AACCGGCTCGAATTCTTTTT
EcGAS2509	+	AAT	24	294	GACCCTTGCCGGAAATACTA	AAAAACTCAGCCCTCAGCC
EcGAS2510	+	AAT	24	285	TCTCGACGATGCAATTTGTT	TTGCATTAAATTTGGAGGGC
EcGAS2511	+	AAT	24	280	TTCCAATCATGGGTCGAAAT	CATATCGTGGCAAAGAAGCA
EcGAS2512	+	AATT	24	274	GTTCCGCGTAAACATCCATC	GGAGGAGTGACTCGTTGAGC
EST-SSR						
EcES0001	+	GGA	24	95	CCATGTCCATGGCCTTATCT	GAGTGCAGGAGCTATGGAGG
EcES0002	+	AGC	15	90	CTCCATGCTCTACCCTCAGC	AGGATGTTGAATCCTGTGCC
EcES0003	+	AG	32	93	CATTCTAACCTTCCTCGCCA	GAGTCGGATTGACTCTTCGG
EcES0004	+	AG	30	93	TGCTAATGATAGCAAGGTGTCTTC	CTTCAACCATGTGCAGGTGT
EcES0005	+	AG	30	96	CAAATCCTCCGTCGCTGTAT	GCGAAGCCAATTGAGAAAAG
EcES0006	+	ATC	30	96	TTCAAGAGGATCCGCAAGTT	TCATCACCACAGATTCACCG
EcES0007	+	GGA	21	101	TCACTCTCTCTCTCCGTCGC	TACACCTTCTTCGCGAGCTT
EcES0008	+	AGC	18	98	CTTTCTGACCATGGGCTTTC	TCCAACTGTTAGGCCATCCT
EcES0009	+	AG	24	100	AGAGCTCGCTTCAGTCCAAC	AAACAGAGAAGGGTTCACGC
EcES0010	+	AAG	21	101	GAGAGGCATCTTGTCTTGCC	TCACAAGTCACTGCCAAAGC
EcES0011	+	AAT	15	101	AAAACCCCAGCAAGAATGTG	GTTTGAGCAACGCAGATTGA
EcES0012	+	GGC	27	110	TCTTCTTCGTCTCTCCTCCG	TCGAACTCTCTCTGGTTGCC
EcES0013	+	AG	30	91	TAACTTTTGAGACAGCCGCA	CCGCCATAACTTTTCTTTCG
EcES0014	+	AG	24	105	TGTCGTCTTCTTCGTCGTTG	CAAAAGCTGTGTGCACTCGT
EcES0015	+	AT	24	112	ATCACTACGCCATCGCTTCT	CAGAGTGTCTCTGCTCCACG
EcES0016	+	AG	32	107	CGAGAAAATTGACATCCTCTCTG	CTCAGATCTCGCCTCTCCAC
EcES0017	+	GGC	27	102	GACCTCGCTCAAAGCTCAAT	CGCTCTCGGAGAAGAAGATG
EcES0018	+	AAAG	20	112	GGGGGTGAAATTTGGAGTAA	AAGTCAAACACCGTCGAACC
EcES0019	+	AAAT	16	112	TCCGTCGTGTTAGTGGTTCC	GCCACATAGCCCAAGAAAAA
EcES0020	+	AAG	15	112	CGGCTGATTACAGAGCCATT	CTGATAGATCCACAGATCCGC
EcES0021	+	AAG	18	114	CTAAAATGGCCAGGAACCAG	TCGCGCATTCTAATCTGTTG
EcES0022	+	GGA	15	113	CTTGCCCATGTTGTCGTATG	GAGACCGAAATCCCATCAAA
EcES0023	+	AG	22	112	TTTCCACCACATCAGAGCAC	GGATTTGGAAAGAGCAGCAG
EcES0024	+	AAG	18	116	TCGTCTCCCTCGAAGAGCTA	CTAACGAAGGACGCGCTAAG
EcES0025	+	GGA	40	118	GAATATGAAGGAAATGGCTTGC	TCTTCTCGCAAGCAAGTGAA
EcES0026	+	AAAT	24	118	TAAGCTGTAAGCTGGCAGGG	GATCCCGAAACGAGTGACC
EcES0027	+	AGC	27	125	GAGAAAAAGAAAGGGCCTCC	AATCCGGGACATCATGAGAA
EcES0028	+	AG	24	120	TGTATGTGTGAGGCGAGAGC	TGGCCATACCAAATCTCCTC
EcES0029	+	GGA	27	120	AGATCCACCACCAGCAGAAG	TCCGCTTCGAGTAGGTCACT
EcES0030	+	AAG	21	124	CGGAAGCACCTGAAAAGAAG	AGGGAGTGAGGAGCAAGTGA
EcES0031	+	AG	20	126	CGAAAATCAAAAGAGACGCC	GGGATTGGGAAAACCCTAGA
EcES0032	+	AG	20	119	AAAAAGGACCAAGAAAGGGG	TGACCATTAGAAGTCCCCGA
EcES0033	+	ACT	15	127	TTGGGACTTGTGGGTTATGG	CCTTTGGGATATGATGGTGG
EcES0034	+	GGA	30	125	ACCATGAGAAACTTGGTCGC	AACCTCTTGCATGGTTGGTC
EcES0035	+	GGA	15	129	GTGATCCAAGATGCCCAGTT	CTTGTGCCCAAACTTCATCC
EcES0036	+	AG	20	114	TTCTTCGATATTTCCTCTCGC	AAGCCGGGACACAGTTATTG
EcES0037	+	AG	18	130	TTCCATTTGCAATTTCGTGA	AATCCCCACATTAGACAGCG
EcES0038	+	GGT	15	130	TCGGAGGATTACTTTGTCCG	CAGAAACACCCCTCGACCTA
EcES0039	+	AG	34	139	CCTCATCCATGGAGGTTCTC	CTGCCTTCAATTCGCTTCTC
EcES0040	+	AG	32	133	CCTCCCATTTGATGTCAACC	AGGCCGCAGGTACTACTGAA
EcES0041	+	AGC	24	123	GAAGTGCAGACATTGGCAGA	CGAACATCAAACCGACACAC
EcES0042	+	GGT	30	113	CCTTCACTCCGACTCTCCAC	TATTGGATCGGAAGGACGAG
EcES0043	+	AGC	18	132	CGTGTTTCTGACTACCCCGT	AAGCCCAGTCCTGCTTGTAA
EcES0044	+	AG	32	129	TCTGCAACATGCACAACAAA	CCCCAACTCAAGCACTGAAT
EcES0045	+	GGT	21	132	CAGCGAAACGAAGTCCAAAT	AATTGCATGTTACGGTGCAG
EcES0046	+	GGC	30	139	CGTCTCTCAAGTCGGCTCTC	CGAGGGAGAGAGAAGGAGGT
EcES0047	+	AAG	15	136	TAACCGCTTGCAGTTCCTCT	TTTACAATTGCTTGGGCCTT
EcES0048	+	AG	24	117	CATCTCCGAGTCGTCTCCTC	GGCTTCTTGTCTTCCTCGTG
EcES0049	+	AAG	27	126	CTGGGAAGAGGACGAAGATG	TAAATGACGCGGATTTCTCC
EcES0050	+	AG	22	138	TCTTCCCCCTTACCTCACCT	TTCCATGATTGAAGCCATGA
EcES0051	+	GGC	33	149	CGGTTGCTCTCCTGAAAAAG	GAGGCGTACGAGTTCCAATC
EcES0052	+	AG	26	144	TCGACAGCACATCGTTTCTC	TGACCTCTTCTTCCTCGTCG

Supplemental Table 6. (Continued).

Marker name	Polymorphic in 6 species	SSR pattern		Estimated product size	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)
		Motif	Size (total bp)			
EcES0053	+	AG	22	141	GTCTCGACTTCGACTCCGTC	ATTCATTCGCCGATCAACC
EcES0054	+	AG	34	130	TGCTTCTTGAAATCTGGGCT	GTGGTGGCTCATCAGGTTTT
EcES0055	+	AG	30	144	CGAGGGACCACCTCTTTTA	CAAGGAAACCGAGAAAGCAG
EcES0056	+	AG	28	119	TTGGATAGTGTCAGATGGTCG	GACTCCGATGCAACCAAAAT
EcES0057	+	AG	32	147	GCACCAACAAACAATTCATCA	AAGCACCAGTCGCATTCTCT
EcES0058	+	AAG	21	145	TATAAGAGTGCATGCGGCTG	TAACGGCAATAAAACCAGGC
EcES0059	+	AGC	27	147	ATGCCTCAATTTTCTGCTCG	GTCTAAAAAGCTTGGGTGCG
EcES0060	+	AG	22	127	CCTTCTCTACACTACACAGCAACA	CGAAGCAAATGGGTTTTTGT
EcES0061	+	AC	18	148	CGGTAGAACAGCGTCGTCTT	GGGGGCAACACCCTAATAAT
EcES0062	+	GGT	24	152	CGTACGGTGAAGATTTGACG	GCGGCGAGACAAGTAAGAAG
EcES0063	+	AG	52	151	TCGTCAAGCTCTTGCCCTAT	AATGGACCCAAGGAAGAACC
EcES0064	+	AG	32	170	CGCTTACTCCATAGCCAAGC	GGAAGCAAACAAGAGCCAAG
EcES0065	+	AAG	27	152	TGAGGGAAGTGAAGGAGTGC	TCCATGGAGAAGTTGAAGCC
EcES0066	+	AAAG	20	152	TTTGGTAGAAGAGGGGGTCA	TCATCTCACATGAAGTCGTTCC
EcES0067	+	AG	18	159	TTCGTTTTCTCTTCTTCCCAA	TGAGGGGACGGAAAGTTATG
EcES0068	+	AAT	45	178	GAAGCTCCAGACGTTCGTTC	GTGTTTTGATGGCGGAAGAT
EcES0069	+	AG	38	165	AAATAATCCCACCCCACCTC	ATTCCACGAAACTGAAACCG
EcES0070	+	ACT	18	158	TCAACAATCCTTTCATCCCC	ATCGATCTCCATCGCTGTCT
EcES0071	+	AAAG	24	163	AAATTTCTCCCCTCCGAAAA	GGAGAGAAAATCACAGCCCA
EcES0072	+	ATC	27	163	ACTTGGTGAAGGGCAAAGTG	TCAACAGCAACGGAGACATC
EcES0073	+	GATC	20	158	GCACCAAAATTTGCAGGAAT	GTTGATCTTCAGCACCAGCA
EcES0074	+	ATC	18	164	ACCATCAAACATTCCGCTCT	GTCAGAAAACTCTCTCGCCG
EcES0075	+	AAG	39	156	AACGGCATATGACTTCTAAGTTGA	CAGAACACACCTCCAGGACA
EcES0076	+	AGC	27	165	ACCCAGTACTTTCCCTGGCT	AGGGGAAGGCTGTGATTCTT
EcES0077	+	AAG	33	160	AGCTACACGACCAATGACCC	GCTCAGTGTGCTCGTCACTC
EcES0078	+	AGC	15	166	ACGCAATTGGTCTGAGGAAG	GGAAGCTTTCGAGCAGAATG
EcES0079	+	AGC	18	167	AAGTGAGAGTCCAGGAGGCA	ACACCGAGATGGGTCTCAAC
EcES0080	+	AAG	30	169	CACCCCCGATTCTCTTGTAA	AAAGAAAAGCGAAAGCACCA
EcES0081	+	ATC	21	171	GGGAAACGTTTTACCAGATCC	TCGAAGGAGAGACTTGTGGG
EcES0082	+	ATC	27	171	CAAGCAACCAGATCAAAGCA	TCCAGATCCTAGGCATCACC
EcES0083	+	AAG	21	185	GCAGGTGAGTCCACATTCAG	AGCTGTGTGGACAAGGGAAG
EcES0084	+	AAAG	16	172	CGCCTGAAGTTTCTCTTTGG	TTGGAAGGGATGCTTGTTTC
EcES0085	+	AG	30	179	CAGCCAAATATCACCTCCCA	TGTCTGCAACTCGACTGTCC
EcES0086	+	GGT	18	178	CCTCTTTTGATTTGGCAAAGG	GGTTCAAAACCCTCCCATTT
EcES0087	+	AG	34	179	CAGAAGAACCAGAAATTCCAGTG	GGAGAGAGATGGGGGAGTTC
EcES0088	+	GGA	27	179	TCTCGAGATGCAAGTAAATAAGGA	CGCCATTTCTAGCTCTGGTC
EcES0089	+	AG	22	179	ACGATTCGTCAGAAGCTGGT	TTCCCTAGTAAGGGGGCACT
EcES0090	+	AG	18	179	TTTCTGGCTGCATCAGTTTG	CAAAGCATGCTATTTTCGCA
EcES0091	+	AAG	30	178	TACTCCGTCCTCCTGTTGCT	TTCCACTGTGGGAATCCAAT
EcES0092	+	AAG	21	181	AATCGTTCGGCTTCCTCAG	TGAGTCTTGGCCATGTGGTA
EcES0093	+	GGA	18	184	CCGAAAACCTTCGAAAATGA	GTCATTGTGCGTCTTGATGG
EcES0094	+	GGA	21	179	CTCCTGGAACTGAGCCAAAG	TGCTTTCTTGCCATCAACAG
EcES0095	+	GGC	27	182	CCCCCTCTCTCTCTTATCGG	GAGATCCTGATCGGAGACCA
EcES0096	+	GGA	15	182	CACCGGATTAATGTCGAACC	TGATGGAGATGAAAATGCCA
EcES0097	+	AG	38	186	TATCGAACGTCGCCTCTCTT	ACTCCTTGAGGGTCTCCCAC
EcES0098	+	AAG	36	179	GCAAAAGTCCATAGCTTCGC	AGCGTCAACGCAATCTTCTT
EcES0099	+	GGGA	28	185	TCTATCTCCCATCCGTTTGC	GGACTACACTGGTTTCCCGA
EcES0100	+	AAG	24	176	CCTCTCTTCCGCTTCTCCAC	GGACTCGTGCAATGAGGTTT
EcES0101	+	AG	32	181	AGAGCCCCAAGGGCATTC	TCTGCACTCTCCCGAAGTCT
EcES0102	+	ATC	24	201	TCTCCAGGACATTTCGATCC	GGATGAGGTAGACGCACCAT
EcES0103	+	AG	20	168	CCATCCTACTATGCTCGGTAGTTT	GACAGTATTCACGCCCAGGT
EcES0104	+	AG	24	191	GCGAGTCTTTCCCACAGTTT	TTGGATGATTGGATGGAAGG
EcES0105	+	AG	48	199	GGGGACGAAGATGGTAATGA	ACAAACCAGCCAAAGGAGTG
EcES0106	+	AGC	24	189	TCTGCAACAATAACAAGCGG	AGAAACTGAACCCATGTGGC
EcES0107	+	AGC	28	190	AAGAGCTGAGAAGGCTGCTG	ACTGGCTTGACTAGCCCTTG
EcES0108	+	AGC	36	210	CCCACCGTTAGATTTTTCTTCTT	ACGGTGGTGTTCACAGCATA
EcES0109	+	AG	22	178	CACAAACAAAGGTACTCATGCC	AAGGAGGAGCATGAGGGATT
EcES0110	+	GGA	21	194	GGGGCATTTGGGTAAATTCT	CCGCAGATATCATCGGTCTT
EcES0111	+	AG	38	163	GGACTAGACATGCTGTGGCA	TCCCAACCTCCTAACAACCA
EcES0112	+	AAAT	20	195	AAAAGGAAAGAAAAAGAAAACGG	CCACCGTGACTTCCTTTGAC
EcES0113	+	AGC	21	262	TTCATCCTCCCCATCTTACG	CGATTTCTCCAGGTGTAGCC
EcES0114	+	GGC	18	197	CTGAAAGTAGGGTGGCAAGG	TGAACCTGATGAAGACGCTG
EcES0115	+	GGA	18	198	CAGAGCTTCCTTGAAAACGG	GCGCTTTGGTTTAGCATCTC

Supplemental Table 6. (Continued).

Marker name	Polymorphic in 6 species	SSR pattern		Estimated product size	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)
		Motif	Size (total bp)			
EcES0116	+	AG	30	203	CAGAACGCCTTTACATGCAC	GAGCTCTCCCTTGTGCTTTG
EcES0117	+	GATC	16	180	GCAATGTTGCGGAGATTTTT	CAGGAAAGAAAGAAGCCACG
EcES0118	+	AAAG	16	199	ATATTGTTCTGGGTCGGTCG	ATCAGACCAGACGCTTTCGT
EcES0119	+	AAAG	24	200	GTCAAGGAATGTCTTGCGGT	AACAAATCAAACTCCCGTGC
EcES0120	+	AG	24	191	GCGTGCTTGCGTGTCTCT	CAGCGATCAAAATCCGAAAT
EcES0121	+	GGA	27	209	CCTTCCTCGACGACCAATTA	CACCTTCTCCTTGTCCTCGT
EcES0122	+	AAG	21	209	GTTGGTGACTGACTGAGCGA	TTCTTGAGAGGAGGAGCGAG
EcES0123	+	ACG	24	226	ACAGAAGCAGCTCAAGCCAT	CGTCTTCGTCATCTTCCTCC
EcES0124	+	GGC	30	215	CTCTCCTTCCTCTTGCCCTC	AAGAAGAGCGTGTTGGCGTA
EcES0125	+	GGC	18	216	GCAATGTTCCTGGGACTGAT	ACGCTTCTCACAAATCCACC
EcES0126	+	GGA	27	200	GGCCAGGAGCATGAAGAGT	TCACCCTTTAGCATGGGAAG
EcES0127	+	AG	18	224	CCTTGGTCGGATCATTCAGT	TGTGGTGGCCAAGAGATGTA
EcES0128	+	AT	22	167	TGATCAAGGAAAGTCGGGTC	TCGATGAATAGGAAAATTATACATGG
EcES0129	+	AG	30	220	CATGGAGGGGATGCATTTTA	ATGGCTCCAACAATCTCAGG
EcES0130	+	AAG	24	223	CTGACCAGGATGGGACAACT	AAAAGGCAGCCAACTTGCTA
EcES0131	+	AGC	27	237	AGGCGTGTAATCTTTCGTGG	ACCGATTCTGGCGTATTTTG
EcES0132	+	AG	36	214	ACCTTGTACCTCGCCCTTTT	CTCCAGAGGACCTTCACAGC
EcES0133	+	GGC	21	233	TTCTATTCACCCTCCATCCG	GATGATGAGGGTCTTCGCAT
EcES0134	+	AG	22	216	TGACGGAATAAAAGACCCCA	ATTACAGGCCCAAAGGGAAC
EcES0135	+	AGC	24	233	CGTCAGCATGGAAGGAGATT	TCCGTCGGGCTCTTTACATA
EcES0136	+	AGC	15	230	CGATCGATCAGAAGATGAAGG	ATCTTCGAAGTTGGGGTCCT
EcES0137	+	GGT	21	231	TGAGAAGGGAATGACGGGTA	CTCTCAGGGTCCTTGTCAGC
EcES0138	+	GGA	21	224	TTTCTCGTACCCATCGAACC	GATCCTCCTCCTCGAAATCC
EcES0139	+	GGA	27	236	CCTTCCCTGAGCCCTAATTC	CGAATCGCATAGCCCATATT
EcES0140	+	GGA	15	236	CTTCGCTTATACCCAGCAGC	CCCGAACTGAACGGAATAAA
EcES0141	+	AG	36	249	GTTCTCTCTCCACACGCCTC	TTCAGAGATTCCTGGTTGGC
EcES0142	+	AG	18	238	TGTGTCCTACCACACCCTCA	AGGAGCCATCTTCCCAGTTT
EcES0143	+	AAG	24	242	TCCTGCATCTGGTTTTGTCA	TACGGCTGCGTAACACACTC
EcES0144	+	GGC	21	238	TTGGTGGGAGGTTGAAGAAG	GAAGATCGAGAAGGCGAGAA
EcES0145	+	AAAG	37	241	ACAAAATTTGGGTGTTGGGA	AAAAAGGGAGATTCGCAGGT
EcES0146	+	AAAT	20	242	AATCGGGTTTTCTCCCATTC	TTGGTGTTGGCAAATAATCG
EcES0147	+	GGGA	20	244	ATAGCGCTTCAGTGGCAGTT	GAGCAAATGAGTGCAGGGAT
EcES0148	+	AAG	24	246	CTCGAGTACCTTGAGGAGCG	CTTGTTCACCAGGGACCACT
EcES0149	+	AG	22	257	CAAATGTAAATAGCGATTGATTGT	GAATCAACTTGGGCAAGCAT
EcES0150	+	AAG	33	253	TGTCTCCCTCACCATCATCA	CAGGAGGTAAGGGAAGGAGG
EcES0151	+	AGC	33	261	ACACAACCTCAAATGCCTCC	GATGTTGGCTAGTCCGGTGT
EcES0152	+	AGC	27	253	CAAGTATGGCGGGATTCAGT	GGGTCAAAGTTGGAGTGACC
EcES0153	+	AG	28	252	ATCTTCACCCAAACACCACC	GCTTCAGCGCATTGTGTAAA
EcES0154	+	GGA	27	261	CTGAAGCCCCTCCTCTTCTT	AGGCGACATTTTTGTTCCTG
EcES0155	−	AAGC	16	257	ACCGATATCGAAACAACCCA	CCGGAACTTGCTTCCAATAA
EcES0156	+	AG	32	269	TCCGGATCTAACACCCTTTG	CACGATTGGCTCACCTGAAT
EcES0157	+	GGC	27	260	GTTTGACCTCTGTTCGAGGC	AGCAAGAAGAGAGCAGCGAC
EcES0158	+	AAG	27	254	ACTTGGCAGCTCATTGCTTT	TTGATTCCTTGATTGCCTCC
EcES0159	+	GGC	27	258	TTCCGGAAAATCTCACTGCT	GAGGATCGGAAGGGAAAAAG
EcES0160	+	AGC	24	156	CTCCAAGTGCACAGCCTACA	GAAATCTCGGTCGAGTCGTG
EcES0161	+	GGGA	24	260	TCTCTCTCTCGCTCTCACGC	GCAGCACCCTCATGTAGTGA
EcES0162	+	AAAG	20	297	CCTGGCCTGGATTCACATAC	ACCCAACTCAGAATTGTCGC
EcES0163	+	AAG	21	262	CCATCTTCGATTTTGCCATT	CGAGAATGATCTCTTTACAAAAGG
EcES0164	+	GGGA	20	266	CCGTGACTGGCTCTTCTTTC	GCGTCTTCCGACATTGATTT
EcES0165	+	AAG	18	270	ATGTCGTGTCGAGGGAAGTC	CCTCGGCCTCCTTTATTTTC
EcES0166	+	ACG	24	270	ATATCAAGTGGTTGCCCCAG	CCACTTCCCGGTCTCTGTTA
EcES0167	+	AG	22	268	GCCGAGAGTGGTGAAAGAAG	AAAGAGAAGGGGGATGGTGT
EcES0168	+	AG	26	255	TCTCTCACAAGCAGGGGACT	AGCAGAGCATCTGTGAGCAA
EcES0169	+	GGC	27	262	GCTCAATGGCTTCTCCTCAC	CTGTTCCGCTTCCGGTAGTA
EcES0170	+	AAG	21	277	AGCTCCAAAAAGGGGGAATA	TTTTGTTAAGGGTGCCTTGG
EcES0171	+	GGA	15	277	AGTTGGAATTCGAGGCCTTT	TTCACCTTCGACTCGCTCTT
EcES0172	+	GGA	45	279	CACCGCCTTCTCTCTCCTCT	ACGAACACCTTCTTCCCCTT
EcES0173	+	AG	20	276	CCTGTGAACCCTTTCGTGTT	GGATACGGCGAGCTCAATTA
EcES0174	+	GGA	21	282	TCTCACCAGGAAGAGGGAGA	ATATCCCCCTCCACAGGAAC
EcES0175	+	AAG	18	282	GAAGAATGCAGCTGGAAAGC	TGAGGGACCCTTTCATCTTG
EcES0176	+	AG	20	280	CTTGCCATGGACACTTGAGA	AAGAGAAGCCATGAGGGGAT
EcES0177	+	GAGC	28	284	ACGAGAAGAGGACGACGAAG	CCTTGATGTCCAGGAGGAAC
EcES0178	+	AG	32	277	GACGTGCTGGGGTTAGAGAG	TGATCAGAACCCCAAAAAGC

Supplemental Table 6. (Continued).

Marker name	Polymorphic in 6 species	SSR pattern		Estimated product size	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)
		Motif	Size (total bp)			
EcES0179	+	AAG	24	285	ACTTTGAATAATGCCGCTGG	ATTCCCATCAGACTGCAACC
EcES0180	+	AAG	18	286	TACCCGAATGCTCTTCATCC	TGACCATCTCTTCTGCATCG
EcES0181	+	GGA	24	286	GAGCTTGATAGCCAACCTCG	CATCCACGAGAATGATTCCA
EcES0182	+	AG	24	291	GGCTTCATACCAGGAAGCAA	TCCATCATCCACTAGGCACA
EcES0183	+	GGC	18	288	GTCCCTCCTCTTCTCCTGCT	AACTCCTCGTCTGACTCCCA
EcES0184	+	AAG	15	286	AAGCTTCCCATCAAAAGCAA	AAGACTTCATTAGCCAGGCTGT
EcES0185	+	GGA	18	293	AGCCAAAGCTCTTACCCCTC	GAACTGGTAGATGGTGGCGT
EcES0186	+	GGC	24	291	GTCGTCGACCTTCTTCTCCC	GAATTGTACGTCCCGGAGTG
EcES0187	+	ATC	21	291	CTCTGCAAGGGAAAGTCTGC	CAGTCCTCCCTCCCATTACA
EcES0188	+	ACG	21	294	ACAGCAACAGCAACGTCAAC	TGAGATGTGATCAGCTTCGG
EcES0189	+	AAC	24	295	CATCATCGCTCCCTTCTAGC	CAGCTCCCACTGTTGCTGTA
EcES0190	+	AAG	21	274	GTGTCCTCCTACTTCACGGC	CCAAACCTCAGATGTCCTCC
EcES0191	+	AG	30	283	TAAAAGCAGCACCCATCACA	CGGAGATAAGCAAGCTGTCC
EcES0192	+	GGA	18	299	GTCTTCACCAACAACGGCTC	CTCACCACGTTCTTGTCCCT
EcES0193	+	AG	18	300	CAAAAGAATGAACAAGCGCA	TTTGTGAGGCCAAATTGTGA
EcES0194	+	AG	28	292	GATTGCAGCGAAAGTTGTCA	AACCATTTTCCACTGAAGCG
EcES0195	+	ACG	27	296	ATCTGTCGCCCAAATTTCAC	AATTCGATGGGAGTGTCGTC
EcES0196	+	AAG	27	155	AGGTTGTCCAAGCGAGAGAA	ATTCACCAACACCCTCCTCA
EcES0197	+	AATC	16	254	CGGCCACATTTCCTGTTACT	GCAAGAGTAGCCAAGTTCGG
EcES0198	+	AAG	18	199	TTTCTCTGTAAAGCCCCCAG	TCGTCGTTGATGATCTGGAA
EcES0199	+	GGC	24	269	TGTTTCTTGCTCCTCCTGCT	CGGACGCAGTACAATGAGAA
EcES0200	+	GGC	24	241	CCAGTCAACTCGGTCCTCTT	AAGGGGAAGATAACGAACCG
EcES0201	+	GGA	18	235	GAGCCATGTGTTTGACGAGA	AAGGAATTCCATGGCTTGTG
EcES0202	+	AG	34	283	CCAGCTCTATGGGAGGATGA	TCTCGGAAAGAATGCTTCAAA
EcES0203	+	AG	26	296	TTTGGAGTTTTTGGGCAATC	TTCGTGTAGTCCCAGTTCCC
EcES0204	+	AG	24	297	GATTCCGCCATAAAAGACGA	TGCTTCGTCAAATTCAGCAC
EcES0205	+	AAG	18	266	CGTCGAGAAATTTCGAGGAA	TCAGCTTGCGAGAACTCAGA
EcES0206	+	AAG	18	291	TCAGTTTCCTTGCTCCACCT	GGCAACACCCAAATATGACC
EcES0207	+	AG	42	294	TGCAGAAAAATCACCAAAACC	AGTCCCCTGCTTGTGAGAGA
EcES0208	+	AT	24	203	TTAAGCGAAGGACATGAGGG	CATCGACGAACTCTGCTTACA
EcES0209	+	AG	22	275	ATTCAGTCTCCCTCTCCCGT	CCAAAACCACTCTCCCGTTA
EcES0210	+	GGA	24	198	AAATCGCAACCTTCGACCTA	CGGAGAATCCATGAGACGAT
EcES0211	+	AG	32	255	CTTGCTCCTCCACCTGAAAC	CCGCCACGAGTACCATATCT
EcES0212	+	AGC	18	298	GAGCACCCACAGAGGAAATC	TTCATGACCCGAATAGGAGC
EcES0213	+	AAG	45	196	GAGGGAAGGTCAAGTTGCAG	GAAGGAGGAGGACCGGAAT
EcES0214	+	GGC	42	212	GGTGGGAGGTAAAGCAGACA	GAAGGACAGCATAGCAAGCC
EcES0215	+	AG	40	186	TCTAGGGATTTCGGTGATCG	TCACAGTGAAAATTGAATTGCAG
EcES0216	+	AG	40	139	AGTTTCCATTGCCTGTCCAC	TTATCGCATGGGACCATTTT
EcES0217	+	AAG	39	226	GAAGGACCAAATGGGTCAGA	ACAGGAGATGGCATGATGTG
EcES0218	+	AAG	39	168	GTTCGCCAGAACAAAACGAC	GAGAGGGAAACAACTGTCGC
EcES0219	−	AAG	39	240	CGATGATGAAGGAGAGGAGG	CAGTTAGCCAGGCTTTCCAG
EcES0220	+	AAG	39	239	TCATCTCTCTCTCTCTCTCTCTCTCA	TTTGAGCTCCAAAAGGAGGA
EcES0221	+	AG	38	221	AGGACACCTATCTCCCTCCC	GCTCTCTGACTTGTCCCAGG
EcES0222	+	AAAG	36	254	GCTCTCTCCTTTTACTTTTTCTGG	ATTTGGGTGAAAAATGCAGC
EcES0223	−	AGC	36	283	CTCTCCAAAAGCCAAGATCG	CTCCCTCGATCTTTTCACCA
EcES0224	+	AG	36	186	CTGCGTGCACAAGTTCAAGT	TGTGTTCTCGTGTCATTCCAA
EcES0225	+	GGA	36	173	GAGAGCTCCCTTCTGGGTCT	CTGATCGAATCACGCAGAGA
EcES0226	+	AG	36	285	GATGGAGCGGTGTACAAGGT	CAGGAGAGCTACTATGGCGG
EcES0227	+	AG	34	162	GATCGATCGCAGAGCAAAAG	AATACACTTGCCCGCAGTTC
EcES0228	−	AG	34	273	TTGAGACGGGAAGAGAGGTG	ACTTGCAGGGTGTAGTCGCT
EcES0229	+	AAG	34	233	GAAGGAGATGCGGAGAAGTG	ACACGTCAAGAACGAGGAGC
EcES0230	+	AG	34	247	ATGAAACGAAAACGAAACGC	TGTTTCACTCTTACGTGCCG
EcES0231	+	GGC	33	221	AGCTACTGCTGCTCGCTCTT	GTACTTCTCGGACGGCATGT
EcES0232	+	GGC	33	251	ATTTGCAGATGGAGTCCCCT	GCAGACACTTCTTTTTCCGC
EcES0233	+	GGA	33	216	CTCTCTAGCGTCTCCGTCGT	TCCCCAACAGAGAGATGGAC
EcES0234	+	GGC	33	103	CGTACGAATCGGAGAGAAGG	GTCCCTCCATTTCACGTCAT
EcES0235	+	AG	32	282	TTGTAACCCCAGTTGCAATAA	TTGATTCCCTTCTGGAGTGG
EcES0236	+	AG	32	157	GATGCTCGAGGTGGATGAAT	CTGCTTCTGTGCTTCTCGTG
EcES0237	+	GGGA	32	223	GCAGCCACGTTTCTCTCTCT	ATGCGTGCGGATCCTTATAG
EcES0238	+	AG	32	98	CTTTTATTCGTAAAAGGCGACTA	GTCTTTTGGGAGGGAGAAGG
EcES0239	+	AG	32	235	CTGATCGCTAGGTAGCAGCC	AACAGGATCTTGGCCTCCTT
EcES0240	+	AG	32	223	TCGAAGTGCTGTCTGCTCAC	CGAGCTGAACTTCCTTGGTC
EcES0241	+	AG	30	91	GTCTTCTCGTCTCGTCCTCC	GTCGCCTTCAGCCCTATCAG

Supplemental Table 6. (Continued).

Marker name	Polymorphic in 6 species	SSR pattern		Estimated product size	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)
		Motif	Size (total bp)			
EcES0242	+	AG	30	127	AACTGGGTAGCGAAAAGGGT	CCCTTGATCATCCAGCAGAT
EcES0243	+	GGA	30	299	CTCGCCTTTTTCCCTTCTCT	TCGGTTCTGCTTTGATGTTG
EcES0244	−	AGC	30	163	GGAAAATCTGCGGGAAAATC	CCACTTGCGATCGGTTCTAT
EcES0245	+	GGA	30	281	CCGCACTTCTTCACCACTTC	GGAGCAATCACGCCTCTTAC
EcES0246	+	AG	30	121	CTCGCATCTCCTCCACAATC	TCGTCCTTTGTGATGCTTTG
EcES0247	−	AG	30	300	TTTTGCCTTGCAGTTGTTTG	ATGTAGGCCGAAGACACAGC
EcES0248	+	GGT	30	285	TGCTGTCCAACAAGATCGAG	GAAAACGACCTCTCTCGCAG
EcES0249	+	AAG	30	95	GCTCTCTCTCTCTCTCGCTCC	TCGAGGAGAGCTTGCAGAAT
EcES0250	+	AG	30	193	TGATCAGGATCCAGAAAGCC	TCCAGACCGAGTACAGGACC
EcES0251	−	AG	28	229	CAGTTCTCGATCTTCCTCCG	ACTTCCGTTTTATCCCCACC
EcES0252	−	AG	28	271	GCACTGTCTGAAGCTTTCCC	ACTCAGCAAAAGCACCGAAT
EcES0253	+	GGA	27	260	TCTCTTCCCAGTCGACGC	GAGGGAAGGCGAGAACTCTT
EcES0254	+	GGT	27	225	TTGAGGAGGGAAAAACATGG	GTTGCACCTGCAAACACATC
EcES0255	+	AAG	27	249	TGCTTTCCTTTGAATTTTCCC	CGAGGAAGATCTTGAGGACG
EcES0256	−	GGA	27	261	CTTTGCTGTCGTCTCCCTTC	GTCGCATCGTTCCATTACCT
EcES0257	+	AG	26	249	TGCCAGTACTCCAGAAAGGC	GCCATCTCAGCCTACAGCTC
EcES0258	+	AG	26	238	CTGAAGCACGTCTCTTTCCC	GAGAACCTTCAGCTTGGACG
EcES0259	+	AT	26	273	CCTTGAAAGCATGTTGCTGA	CCTACGAAAGCTCGAACACC
EcES0260	+	AG	26	139	CCGTCGCAGACATTCTCTCT	AAAGAGTAGGCCACCGGAGT
EcES0261	+	AG	26	160	TTTCTCCCATCCCTTTTCCT	ATAACCCATCTCCCAAAGGG
EcES0262	+	AG	26	274	CTCTGCCAATTCTCTGGGAG	ACACCGAAGTTGGAGTGGAC
EcES0263	+	AG	26	230	ACCCCCATTTCGGAATTTCT	ACATTGAGGCCATCCTTGAG
EcES0264	+	AG	26	259	GAGGGGTTGGTGAGAGAACA	GGTCGAGTTGTCGGTGAAGT
EcES0265	+	AG	26	213	TCGTGCACTTGTCATCCCT	TAATTGGTCGTCGAGGAAGG
EcES0266	+	AG	26	234	TCTTCTGCGGAACTGGAAGT	CTGTGCAGAGTGATCGGAAA
EcES0267	+	AG	26	248	CGTTAAACCCTTCGAATCCA	GCGATTCTTGATTTCCCAAA
EcES0268	+	AG	26	173	GTACCCGAGCTTCTCACCAA	TTCTTTTTGCCTTGTGGTCC
EcES0269	+	AG	24	200	TTGCTTGTTGCCTGACAGAG	CAGAGACACGGAGAGGAAGG
EcES0270	+	AAG	24	209	GCCATTTCTAGGGTTTTGGA	AACGAATCAATTGGTCTGCC
EcES0271	−	GGC	24	278	AACCACCATCGTCTCAGTCC	TCTCTGCGGTTCTGGAAGTT
EcES0272	+	AG	24	296	CTTCATCCTCCTCCTCCTCC	CTCAAAAAGGCGAAAATCCA
EcES0273	+	AAAT	24	111	CAAAAGATTGCGTGCTGCTA	CACTTGACCAGTGAACCACG
EcES0274	+	GGC	24	289	CAGTCTCGCTAGTTGAGCCG	AGCGAAAGACACCATCCACT
EcES0275	−	GGA	24	171	TCGCGATCCTTTTCTTCATT	CGTCCGAAAATCTCAAGAGC
EcES0276	+	ACG	24	221	AAAGAATACCGTGTGCTCGC	AATGGGAGTCGATGAAGCTG
EcES0277	+	AAG	24	251	CAAAACCGTAGACCGGACAT	ACACAAGGTCCTTCCACAGC
EcES0278	+	AT	24	109	GATTGCAAGTTGTGGTCGTG	AATTCCACCAGCACTGATGAC
EcES0279	+	AGC	24	252	CCCGACTGCAAAATCTATGG	GCTCTCGTTTGGAAAACTGC
EcES0280	+	GGC	24	298	ATCTAGGGGCTCTCTCCAGC	CGGGGATCAGAGCAAGATAA
EcES0281	+	ATC	24	243	GTCCCGGAGAGACAGAGATG	GCATCACGTTGTGAAATTGG
EcES0282	−	AGC	24	223	CAGCCGATCGAGAGAAAAAC	TTCTCAGCCCTCTCGACAAT
EcES0283	+	AG	24	297	GCATTACAACACTGCATCGG	GATTCTTCTTGCGGCCAATA
EcES0284	+	AAG	24	186	GATTTGGGGATTTGGGTTTT	CATCGTTGAGCCTCTTCTCC
EcES0285	+	AG	24	204	CTTCTTTTTCGAGAACCCCC	GCCCGTGCTTCTGAATGTAT
EcES0286	+	AAG	24	270	GTCGATGTCCAGTCCAAGGT	CATAAGCAGCAAAGACGTGC
EcES0287	+	GAGC	24	220	TCCCTTCACCCTAACACGAG	GCTTGCACTGGGAAGATTGT
EcES0288	+	AGC	24	213	GTGAATTCTTCTCCGCTTCG	CATTCGGGGTTCCATAGAGA
EcES0289	+	AG	24	256	GTGAAGTTTGCATTGCTGGA	AGCATCATGCAGGATCATTG
EcES0290	+	GATC	24	201	ACTCCTCCTCTCTTCCTCGC	TTGTCAAGCGTTCAGCTCAC
EcES0291	+	AG	24	295	GCGTTTCATCGAGAAAGAGG	CCATGTCCTCGCAACAACTA
EcES0292	−	AG	24	298	GGGACACACACACACACACA	TTTGTGAACCCCCATTCATT
EcES0293	+	GGA	24	300	CATTTGCCTGTCCCTCTCTC	GGCTCCGTAATGTCCTCAAA
EcES0294	+	AG	22	209	CTCTTCGTGCTCTCTTCGCT	GTCCACCCGAGTCAAGATGT
EcES0295	+	AG	22	175	AGCAATGCCAGAAGCAGAAT	TCATCCAGAGCAAAATCGAA
EcES0296	+	AG	22	92	ACTCGGTACTCAGCATGACG	CATTCTGACAACAGAGGGGG
EcES0297	+	AG	22	262	TTCTCTAGCACCAACGCTGA	ATCGCCTAGCTTCTCCTTCC
EcES0298	+	AG	22	159	CACAAGCACGAGCACAAAAT	AGATGGTGCCACAGAACCTC
EcES0299	+	AG	22	148	GATTGAATCTTCCTGTCGGC	ACAGGACTGGAGGGAAGGAT
EcES0300	+	GC	22	106	CCTCCCCTCTCCTCTCTTTC	TCGATTACGCGCTACAACTG
EcES0301	+	GGC	21	215	TCCTCTTCGTTCTCGTCGTT	CGGAGATCTAAAAGACCGCA
EcES0302	+	AAG	21	170	CTGTCGAGTCCAAAAGCCTC	AGCGATTGTTTCCACGATCT
EcES0303	+	AGC	21	267	GGGAAGGTGGACAAGCTGTA	GCCAAGAGCAAGAGTATCCG
EcES0304	−	AAG	21	292	CAAGCAAACACACCATCACC	ACGGTGATGAGGCATAGTCC

Supplemental Table 6. (Continued).

Marker name	Polymorphic in 6 species	SSR pattern		Estimated product size	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)
		Motif	Size (total bp)			
EcES0305	−	AGC	21	288	GCTCGAGAAGCGATTTCTGT	TCAAGCCCTTTGGATTGTTC
EcES0306	+	AAT	21	243	CGCTTGATACAAGTGCCAAA	ATTGATTGACTGGGAAACGC
EcES0307	+	AAG	21	279	ACATGAAAGGTCTGGATGGC	TCAATGCCCTCTTCGATACC
EcES0308	+	AAT	21	249	CAGTTTGAGGCGGATAAAGC	GGTTACAAAATTTGCATTCTGG
EcES0309	+	AAG	21	241	GTAGATCTGCTTCGCCTGCT	ACGACGTTGCTCTGGATCTC
EcES0310	+	GGC	21	181	ACCAAAAACCACCGACTCAC	ACTCGAGCGAGTTCAGGAAA
EcES0311	+	AGC	21	115	TGGCATCACTGAGAACTTGC	TGAGCTCAAACTTCCCGAGT
EcES0312	+	AGC	21	170	GGAACAGCTCTTCTTCCACG	ATTACTGCTGGACCACCTGC
EcES0313	−	ATC	21	273	TCCTCTTTCCTTTCTTCCCC	GACAGCACACAGGAAACCCT
EcES0314	+	AAG	21	245	AAATCGCCCATAGCCTACCT	GCACACCAAAGACCGTATCA
EcES0315	+	GGAC	20	185	AAAAGCGAAAATCCCCACTT	GTCGGATTTCAAGACGGGTA
EcES0316	+	AAAG	20	257	AGCCACATCAAACAGTGACG	TGCGAGAGGTGAAGAAGGTT
EcES0317	+	AG	20	200	CATCGCTGAACTGAAGGTGA	CCACCCCAGCTGATCTAAAA
EcES0318	+	AG	20	276	AGGAAAGAGAAGGAGTGGGG	GTGAAGGGCTTGAGGAACTG
EcES0319	+	AAAT	20	194	AAAAAGCTTGTAGGATTGGCA	GCCCAAAAAGTTCCAACAAA
EcES0320	+	GGA	18	297	TATCGGAGAAATTGGCTTGG	TCAAACTCGAACTCAACCCC
EcES0321	+	AGC	18	243	GCTCATACCAGAAGCCAACC	GCACCACCGACTTACCACTT
EcES0322	+	AAAT	16	261	CCCAATGCATGATGAGACTG	GCCTTGACCAAGCTGTCTTC
EcES0323	+	AG	46	280	AGCACCCAAAAACCTGACAT	GGCAAGATCAAGAGAACCCA
EcES0324	+	AG	44	181	ACGTCAATTTGCAGAGGGAG	TCTGCCGACAGATATCGAGG
EcES0325	+	AG	38	237	ACCGCAGGCAGAGTAGAGAA	ATGCCTTGCAAAGGCTTAAT
EcES0326	−	AG	36	278	TTCTTCCTCTCCTTCCTCTGC	GCTCTAGGCACATGCTTTCC
EcES0327	+	GGGA	36	276	ACCCTTTCTTCCCCTCAAAT	GGACTTGGACTCGAGGTTGA
EcES0328	−	AG	34	252	CTTCAACCTCCATCCCAAGA	ACGAGAGATTGGTGAATGCC
EcES0329	−	AG	34	264	GCACTTCACACCTCCCAAAT	CATGATCAATGGAGGAGGCT
EcES0330	−	AG	34	176	TTAAACTGGGGACAACCTCG	ATGGCTCTCCCATGTCTTTG
EcES0331	+	GGA	33	185	ACACGAGCAAGACCCATTTC	CCACTCCACCTCGTACACCT
EcES0332	+	AAG	33	221	CGAGAAGGAGACGAAGATCG	TGACAAGCAATTTGAAACGC
EcES0333	+	AG	32	138	ATCTCGAAGCGAATGGATTG	TGCCAACCTCAAAATGAAAA
EcES0334	+	AG	32	147	AATTGCAACAGATCAACCCC	GATAGGAATGAATTGGGCGA
EcES0335	+	AG	30	202	AGATCGCAAAAGCTCGTGAT	AGAAAAGGAAAAGACGGGGA
EcES0336	+	AAC	30	244	AGACCCCATGTGATGAAAGC	ATCAGACGACAGCAGCAATG
EcES0337	+	GGA	30	207	CCCTCCACGATCTTCCATAA	ACTGAGTGACTGCACAACGC
EcES0338	+	AG	30	234	GCCGCAGCATTTACATATCA	GGCATCTGTCCTCAAACGAT
EcES0339	+	AG	30	178	CCAAGGCAAACAAGCAAGTG	TGTCCATGGTGATTGCTCTC
EcES0340	+	AAAG	28	289	TGATAGGGGAAGTTTCACGG	CAGGAGAAACCAGAAAATTGAAA
EcES0341	−	GGA	27	295	GAAGATGAAGATGGCGCTG	TTCCGATGGGAACTTTTCAG
EcES0342	+	GGC	27	169	CGATCGCAAGAGGAAGAGAC	CTTGATGAGGATGTGCGAAG
EcES0343	+	AAG	27	207	TCACCCTTTTGGTTTCGTTC	TAAAGAGGGTGCGTAGCGAT
EcES0344	+	AAG	27	286	AAGCACCGCATGCTAAAGAT	CCCATGTCCAAGAAGTGGAT
EcES0345	+	GGA	27	250	CCTCTCTCTCTCTCTCGCCA	GTAGATGCCTTCCTCCACCA
EcES0346	+	GGA	27	203	CTTCCTCCTCTTCCGCTTC	GCATTCTCGATGGTCCAGTT
EcES0347	+	AGC	27	179	CTATGGCGGTTATGCTGGAT	GCTCGCAATAGGCAAGAAAG
EcES0348	+	AG	26	213	TTTCTTCAGTGGCCATCTCC	ATGACCCAAACGAAATCTGC
EcES0349	+	AG	26	190	AAAAACGGCGGAGCTAAAAT	GTTGTCGAAGTCGTCGTCCT
EcES0350	−	AG	26	231	TCTCTCTCACTTCCGTCTCC	AAATCTGGACCACTGCATCC
EcES0351	+	ACG	24	214	CGATCCATTTCGCCACTTAC	GATTTCCGACGAAGAGATGC
EcES0352	+	GGGA	24	290	GCTATAAGACCCGATCGCTG	TTGATTCTTCTCAGGGTGGG
EcES0353	+	ACG	24	298	GCAGAGATGGCTGATGGAAT	GCACTGGAAGGAGATGTGGT
EcES0354	+	AAG	24	297	AGAGGGAAGAAAGTCGGCTC	CGTTTCAGTGACAGTCGCAT
EcES0355	+	AG	24	177	ATCCGATTCTCCTCCTGCTT	CCGCTCCATAGTGTTTGGTT
EcES0356	+	AGC	24	92	ACCTCGTTCTCATGGAGCTG	AAAAGAAAAGCCGAGAAGGC
EcES0357	+	GAGC	24	232	TCTCTCTCTCTCTCCCTTTCTCC	GACCTGAGAGCATCTCCTCG
EcES0358	+	GGA	24	126	TGAGAAACTTGGTCGCACAC	GGACAAACCTCTTGCATGGT
EcES0359	+	GGC	24	287	GACTCCTCGAGACTCGCAAC	CCGGCGATATCGTAGAGAGA
EcES0360	+	AG	24	202	TTTGAGGCAGTGTGCGTAAG	AGAGGGAGAGACGGAGGAAG
EcES0361	+	AAG	24	290	GAAGCAGAAGCAGAGCACAA	ACAGTCTCGGGCCCTTCTAT
EcES0362	+	AG	24	169	CTCTCGATCTCCCACGGAT	GAGAAACCAATGGCGGTTTA
EcES0363	+	AGC	24	292	GAAATTGGAGGCTCTGCTTG	AGCAGCCTTCTTAGCTGCTG
EcES0364	+	AGC	24	268	CACTGCTACTGCTTCTCCCC	TATTCGACTGCGCAACAAAG
EcES0365	+	ATC	24	295	AGAGAAGAGGCGCACTGAAG	AACCACAGAATTCAGCAGGG
EcES0366	+	GGA	24	280	TCTCTCCGTTCGCAAACAAT	AATCCATGCTCGACAGATCC
EcES0367	+	AAAG	24	105	TTGTGACCCAGGAACTAGGG	CACAGCAAGACAAGATATATGCAC

Supplemental Table 6. (Continued).

Marker name	Polymorphic in 6 species	SSR pattern		Estimated product size	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)
		Motif	Size (total bp)			
EcES0368	+	GGA	24	289	CGAAGCAAAAGAGGAGCAAG	GGGGCCAAAGTTACCAAGAT
EcES0369	+	GGA	24	249	AGATCCTCTGGACAGTGCCT	TATGTAGCTCAGCGTGTCGG
EcES0370	+	GGGA	24	233	CATGGCATCCATCACTTCAG	GGGTGGGTAGACCTAACGGT
EcES0371	+	GGC	24	169	TATTCTTCGAATGCTTCCGC	AAACAAGGTCGACGCAGACT
EcES0372	+	AAC	24	288	CTCCTGAAGTTGATGGGCTC	AGGCAAAAACTCTGCCTCAA
EcES0373	+	GGA	24	179	GAAGTGCTCTTTCGTCAGCC	TGGCTGCTCTATCTCCACCT
EcES0374	+	AG	22	158	ATCACCAGCAGCGAGCTATT	CCCTTCATGAACGACATCCT
EcES0375	−	AG	22	222	TTTCGGATAGAGGAGACTTTTTG	AAACCCATCCCTTACATCCC
EcES0376	+	AG	22	293	ACACGAGCGTTCACAAACTC	TACCTCTCCGCTTCCTCAGA
EcES0377	+	AG	22	294	ACATCAAGATCTTTACATCAATGG	CAACGATGGAAAAGCAGTCA
EcES0378	+	AG	22	247	CGGAAACGGAAGTACCGTAA	AGCTTCAGAACCGATTGCAT
EcES0379	+	AG	22	221	TGGGACGAAACCTGAGAAAC	CCTCGAACTGATCGGAGAAG
EcES0380	+	AGC	21	178	GTCAAACGCCAGTGACAGAG	GTGGTATTGTCCCATCCTGG
EcES0381	+	ATC	21	214	CCCCACTTCCTTCTTCACAA	CAGCAAGTGAGAGCTGAACG
EcES0382	+	GGA	21	218	GAATCTCTTCGCCTTGTTCG	GTGTGCCGAGGAGAAGAAAG
EcES0383	+	GGC	21	280	ACTTGCTCCTCATCTCTCCG	TCAATATCCCGAGCTCAACC
EcES0384	+	GGC	21	116	GCTACGAGGAGATGGTGGAG	GCCGATCACGTTCTTGTAGG
EcES0385	+	AAG	21	153	GAGGATAGAAAATCCGTTTTATGG	GGTGCAATTCCAAATGTGAAG
EcES0386	+	AGC	21	267	ATTCCTCTTAGCCTGCGTGA	AAGGAGAGATTGCGGCAGTA
EcES0387	+	AAT	21	158	TCTTATGGAAAATGTGCCCC	ATGACGACGGTTCAACTTCC
EcES0388	+	ACG	21	179	CTCCCCGTTTCATTTTCTCA	GGAATTCATGCCTTGCAAAT
EcES0389	+	AAT	21	276	CAAAGAAGAACCAGCTTGGG	GAATCACGGGGAACTCTTCA
EcES0390	+	GGA	21	184	AAGTGTCAGTGTCGCACGTC	TAAGAGGCGAAAAGGACGAA
EcES0391	+	GGT	21	288	TTGCCAGCAACAAACTAACG	TGTTCATCTTCCGAATGCAG
EcES0392	+	AAG	21	168	GTCAGCACATTGGAGCAAGA	ATCACCAGCAATCTCCCTTG
EcES0393	+	GGA	21	217	CTCCAGTCCTGCTTCCTCTG	TGGACGACTCCGATTTTCTC
EcES0394	+	AAG	21	179	AGAGACTCTGCATCGGAGGA	TTTGCCTTTTCCAGCTCTGT
EcES0395	+	GGA	21	90	GAAAGCAAGGAAGAGGAGGC	ATGCCCTCTTCATCCACAGT
EcES0396	+	AAG	21	261	GATCTCCAGAGCTTTCCTTGG	TTCACCGTTGAGGTAGGGAG
EcES0397	−	GGC	21	249	ATCATCAGCAGCAAAAACCG	TGCAAAAGAGGAAGGCTGTT
EcES0398	+	AAG	21	281	GAGTATAATGCGGCGGTGTT	ACTTTCTTTGTAGCCCCCGT
EcES0399	−	AG	20	130	ATGGCCTCCCACCTTCTC	CGGAATGAATGCACAGTGTC
EcES0400	−	AAAG	20	283	ATGCCCAAGCTTTTTATCCA	GAAGAGGAGCAAGCACAACC
EcES0401	+	AAAC	20	175	AAAATCGGCCTCCAAAGATT	ATGTCTCCCTCCACTTGTCG
EcES0402	+	AG	20	288	TCCTCACACGGTTTCTCTCTC	CGAGATCTGAGTCCTAGCGG
EcES0403	+	AAAT	20	135	TTGCTGATTGATTGCGTCTC	CCATCGTTTGAGAAAATACGG
EcES0404	+	AG	20	121	CCCTTCTCTCTCCTCCCTCT	CGAAGCATCCTGACACAGAA
EcES0405	+	AG	20	223	ATGAAGGTCAGTGGACCAGG	ACATTTGAAGAAACCGTGGC
EcES0406	+	AG	20	279	ATCTCCTCTCCGAGCACAAG	TTTGGATTTCAAGACGGAGG
EcES0407	+	GGGA	20	247	TTTGCTCTGTTTCCTTGCCT	CCATCAGATCCGCTTTCATT
EcES0408	+	AG	20	114	TCTCTCTCCGTCTCTCCCAA	CGTCAGCTTATGTCCGTTGA
EcES0409	−	AG	20	238	CACCTTTCGTCTCCATTAGAAG	ATTTGCCAACACCAGAGTCC
EcES0410	+	AAAT	20	150	CAAATGATGCCTCTCTGCAA	CCTTGGGAACTGAGCCATAA
EcES0411	−	GGA	18	177	TTAACCGCCATTTTCACCTG	AGACAGACAACCTTCCCCCT
EcES0412	+	ACG	18	280	GGGAGAGCAGCAAGTACCAG	AGAGACAGGGTTGGTCGCTA
EcES0413	−	AAG	18	292	TTTCTTCAATCCCACGGAAG	ATGCTATTTCAGCCTGCGTT
EcES0414	+	AAG	18	135	GCGGCGTCAACACATAGTTT	CACGAGGAAGCTCTTCACAA
EcES0415	+	AAG	18	251	TGTTGTTCAGGACCTTGCAG	CCTTATCACTGCCTTCCCAA
EcES0416	−	GGA	18	268	ATTTCACCGTCGTCATCTCC	CCAATTGTTGACATGTTCCG
EcES0417	−	AG	18	290	TCCCCTCTCTCTCTAAAAGCAA	AAAAGTGATGCATAGCGCCT
EcES0418	−	AGC	18	258	CAGCGGCTTACTTCTGGTTC	TCATAGCCCCTCTTCTTCCA
EcES0419	+	AAG	18	133	TTGAAAAGTCCAGCCAAACC	ATCCATGCTTCTGTCGATCC
EcES0420	+	AAG	18	266	CTCACCAGTTTGGGATCCTT	ACAGAAGGCTGAGACCCAGA
EcES0421	+	GGA	18	268	GAGCAAGATCCTGGTCAACG	AGTGGTGTCGAGCTTCGATT
EcES0422	+	AG	18	279	CAAGCTCAACAGACCGGAAT	AGCTACTCAGTGGTGGCGAT
EcES0423	−	ACG	18	248	TTCCGCAGAAGAGGAAGAGA	TTTGCTGCTCGATCTCCTTT
EcES0424	+	AGC	18	195	TGACATACACACGCCGTCTC	ACCTGGCTCCCTTGAAGAAT
EcES0425	−	AGC	18	289	GCGACGCTCTTTCTCTCACT	TTTGTCATTGGGGTCTCCAT
EcES0426	+	AAC	18	240	CCAACTCCAATCCTTTTACCC	ATGACCCTCCATGGATTCAC
EcES0427	+	AGC	18	137	TGTGGGTGTTGCTTCTTCAG	GTGCTCGATCAAGAACCGAT
EcES0428	+	AG	18	98	CTTCGTATCGCCGTACCTTC	TTCTTCCATCAAGTCAACAGACA
EcES0429	+	ATC	18	219	CAAGGGAGGAGGCACAATTA	GATGAAACGAGGAGTCGCAT
EcES0430	+	AG	18	282	CCAGCTCACACCCACTTACA	GTCACCGGAACTAACGGAAA

Supplemental Table 6. (Continued).

Marker name	Polymorphic in 6 species	SSR pattern		Estimated product size	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)
		Motif	Size (total bp)			
EcES0431	+	AAG	18	264	TGCCAAAGGCTGAAACTACA	GTTGAGGACTTTCTGCCAGC
EcES0432	+	AG	18	211	CACAGCACTGCCGATCTAAA	GACTCCAACGACACAGCGTA
EcES0433	+	AAG	18	284	CTTAAAAATAGTTGGCGGCG	GTTGCAGGAAGATGGGAAAA
EcES0434	+	AAG	18	238	CAGGTCACTCAGGAGCTGTG	CAATGGCTAACAAAGCAGCA
EcES0435	+	GGT	18	297	TTTTAGCTGCGCGTTATGTG	TGGAACATCAACCAAAACCA
EcES0436	+	AG	18	136	GAGCTGTTTCTGTGGCTTCC	TAGGCCTACACACAGGAGGG
EcES0437	−	GGC	18	232	AGCGAAAAGATGGGCTTTTT	AGATGGAGGAGGCCAGAAAT
EcES0438	+	GGC	18	298	GCGAATTGGCTGATCTTCTC	CAAATTCGCTAGCAAGCTCC
EcES0439	−	AGC	18	172	GGAGAAGCTTCGAGCAGAGA	GTAGCCTTCCAGACCAGCAG
EcES0440	−	AG	18	178	GCAAACCCTAATCCTCAAAAT	CCCACTGATGGCATTAGCTT
EcES0441	−	GGA	18	294	CTCTTGAAGCAGACGAAGCA	TCGATCGTCTCTGCATGTTC
EcES0442	+	AAG	18	295	TCTTTTTGGTGCTCCTTTCG	GCAAACGTCCGGATGATACT
EcES0443	+	GGA	18	288	AAGACGATGCCGAAGAGAAA	ATTAGGGGGTGGGAGAGAGA
EcES0444	+	ATC	18	292	GAAGAAGCCAAAGGAGCAGA	ATTCAAACGAACCGTCTTGG
EcES0445	+	ATC	18	253	CGAAGAAGCACCTTCGAGTC	TCATCGGACCACAAAACAGA
EcES0446	+	GGA	18	163	CTCTCGCTCCTCTCTCCTCC	CAGTAGAAGCGGAAGTGGCT
EcES0447	+	GGA	18	119	TTTTTGTCTTCCGTTTTGGG	AACCACAAACCAGACAAGCC
EcES0448	+	AG	18	296	CGATCAACCGCTTCTTCTTC	CAGTGGGGGACAGAGACAAT
EcES0449	+	GGA	18	243	AGTGAGGCGAGGAGTGAGAA	CAACTGCCTCTGCAATTCAA
EcES0450	+	AAAT	16	259	TACAACGAATCGGGGAAGTC	CCCCCAACCTATAACGAACA
EcES0451	+	AAGC	16	109	AGGGGCAAAAGAAAAAGGAA	GGTCCAAATCCTCTCCACAA
EcES0452	−	AAGC	16	184	TTCCCATCTCCATCTCCATC	AGCTCTCATAGCCAGTCCCA
EcES0453	−	GGA	15	204	GGTTTGAGCTTCCAAACTGC	GCTTCTTTTGTGAAGCCAGG
EcES0454	+	AAG	15	300	TAACAGTGGCGGTGAAACAG	CAATGGCGTTTCCTTTGATT
EcES0455	+	AGC	15	255	TATCATGTGCCACTCTTCGC	GACCAAAATTATGCCCCCTT
EcES0456	+	AAG	15	203	TGGGTTTGTGGAAGGTTTTT	TGCAATCTTCAAATGCCAAA
EcES0457	−	AAG	15	279	TTGTTACTCTGGGGATTGCC	CCAATGCCTAGTGCGAGTCT
EcES0458	−	AAG	15	168	GAATGGGGCTGAACTTTTGA	GCACGTTCGATCTCTGTTGA
EcES0459	−	GGT	15	234	TGAGGTCGCCTTCTTGAGAT	ATATTAATGGTGCCGCTTCG
EcES0460	−	GGA	15	300	ACCGCGTCTTATCTGAAACC	GTGGCCATAGCCTTGATCTC
EcES0461	+	AAC	15	277	TTATTTGGATCCGGGAAGTG	GGCTAGCGAGAGAGATGGTG
EcES0462	+	GGA	15	154	ACGTCATTTCATCTGTGCCA	CGCTTCAAATGCTGATCCTT
EcES0463	+	GGA	15	213	CAAAAGCTCGCTCAATTTCC	TAGGGAGACGTGATGTGCAA
EcES0464	+	AAG	15	138	TTCTATCTCCGCATCAGCCT	CTGGGTCCCATGTTTTTCTC
EcES0465	+	ACG	15	233	AAACACCCAGAAGCGAACAC	GGGAAGGGGAAGATGAAGAA
EcES0466	−	AAG	15	96	TACTGCTGAAGCTGTGCAGG	GCCTCCATAGCTCGTTTCTG
EcES0467	+	ACG	15	91	ATTCAATCCGAAGTCAACCG	ATCCGGTGAACCCGATCTA
EcES0468	+	AAG	15	248	GTGTGTACTTTGGCCAGCCT	CATCAAACTCCGATTCGGTC
EcES0469	+	ATC	15	212	GACTGTGAACTGTTTTTGTGGC	CATCCGAAGAAAGCGATGAT
EcES0470	−	ATC	15	262	GGAATTGGAGATGGCACAGT	CCTTTTCCAATTTCCAAGCA
EcES0471	+	GGT	15	268	ATGGTGAAGCCAACAAGGAC	GCCATTCAGCAGCAATAACA
EcES0472	+	AAT	15	212	GAGCTTCCCAAATCACTGGA	CAATCCAAGCCTTGCAAAAT
EcES0473	+	GGA	15	131	AGCTGGTTATGGTCCTGCAC	CCTTCATAGCAAGCTCAGCC
EcES0474	+	ACG	15	115	GAGGAAAGTCGATCCTCGC	GTCTGCAACTCCTCAAAGCC
EcES0475	+	AAG	15	256	GGAAACGGTTCCTCAACAAA	TCAAAGTCCCAACGATCTCC
EcES0476	+	GGA	15	167	CTCATACACAACGACGGGAA	AATACCAGCTTCTTCGGCAG
EcES0477	+	GGC	15	221	CTGACGAGCGAGGACATCTT	GGCTTGGTGAAGATCTGGAG
EcES0478	+	AAG	15	295	CCATGATTTTCGCCAACTCT	CTCCTCCCTTTCCTGATTCC
EcES0479	−	GGA	60	251	AAGCTCGCTTTCAACCAGAC	CACCTGCACTTGAACCCC
EcES0480	+	AAG	57	211	ATGGCGATTTCTCGTTGTCT	AGCCACATTGCACCACTACA
EcES0481	+	AAG	57	205	CATGCGCCTGTAAAAGTCAA	AAGACGTTTCATGGTCGAGG
EcES0482	+	ATC	45	298	AGCTGGGAAAGAGAGAAGGG	AGCGACCGAAATTTGCTAGA
EcES0483	+	ACG	42	272	CACGAGTTCAGTTTTCAGCG	GATTTCCGACGAAGAGATGC
EcES0484	−	GGC	42	238	GATCGAGATCTAACGCTGCC	TCGCAGTATGCCACAGGTAA
EcES0485	+	ACG	42	228	CCCTTCCCTGACCTACTTCC	GCACAACAAGCAGCAGAGAG
EcES0486	+	AAG	42	266	CCCGTCTTCCCTTGAAAACT	AAATCAACGCAACTCGCTCT
EcES0487	−	AG	40	234	CTCCTCCTCCTCCACACAAA	TTGCATGACAGTTGGGTGTT
EcES0488	−	AGC	39	237	GGTCGCTCCTCGTCTCAG	TTGCCAAATCCAATAGCTCC
EcES0489	+	AG	38	196	GAGGAGAATCGTTTGGTGGA	AGGAGGAGGAAGCCATTGAT
EcES0490	+	AAG	36	121	CCTTCATCAGTCTTTCTGCG	GTTGCATATGAACACCACGC
EcES0491	−	ACG	36	179	CGTGCTCTTCCTCTTCTGCT	TCGAGTTGTAGTTCCCCAGG
EcES0492	+	GGC	36	109	CGAAAAGCTGTTTGCTGTTG	ATTTGAATTCACTGAGGGCG
EcES0493	+	AAG	36	202	CATCTAACTTCCGAACCCCA	ACGGCACGTTTTATTGTTCC

Supplemental Table 6. (Continued).

Marker name	Polymorphic in 6 species	SSR pattern		Estimated product size	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)
		Motif	Size (total bp)			
EcES0494	+	AG	36	105	AATCGTTTGCTTCGCTTCAC	GCACGATCCTCATGGTTTCT
EcES0495	+	GGA	36	128	ATGCGGTGTCGAAACTCTG	GAACCCTAGGAGGAGATCGG
EcES0496	+	AG	34	278	TGATGCAAGCTTTATGGCTG	AGAACGAGTTCGTGCTCCAT
EcES0497	+	AG	34	168	AATCACAGCCACTGCAACTG	GCAGGACTCTCTGCCTATCG
EcES0498	+	AG	34	255	CATGTGCAGGTGCTGTCTTT	TGAGAGTTTCGGCCAGAGTT
EcES0499	+	AG	34	99	GAGGCCTGAAGCTTCTGAAT	CGAGGAAGACTGAGACCGAG
EcES0500	+	AAG	33	277	GAAAGAGCTTCGAGTGAGCG	AATGAAATTCTCGTCCGTGC

Supplemental Table 7. Number of microsatellite markers that detected null alleles.

	Genome	EST
E. dunnii	66 (14.7)	45 (10.3)
E. globuless	47 (10.5)	45 (10.3)
E. garandis	52 (11.6)	44 (10.1)
E. nitens	53 (11.8)	49 (11.4)
E. urophylla	46 (10.2)	49 (11.4)
E. camaldulensis	68 (15.1)	53 (12.4)

Parenthesis show the percentage to the total number of amplified markers with any DNA of the six species