SUPPLEMENTARY DATA

Figure S1. *Myrcia s.l.* species from sect. *Aulomyrcia*: verticillate leaf arrangement in *Myrcia tetraphylla* (I); terminal inflorescence of *Myrcia amazonica* (II) and Staggemeier 799 (III); detail of free sepals on calyx of *Myrcia multiflora* mature fruit (IV); extended hypanthium in buds of *Myrcia racemosa* (V); free calyx lobes in fruits of *Myrcia racemosa* (VI), Staggemeier 792 (VII), and *Myrcia amazonica* (VIII); closed buds protected by bracteoles in *Marlierea neuweideana* (IX); irregularly splitting calyx lobes in mature fruits of *Marlierea neuweideana* (X); regularly splitting calyx lobes in immature fruit of *Marlierea sucrei* (XI); irregularly splitting calyx lobes in immature fruits of Staggemeier 764 (XII); inflorescence axes emerging from a single terminal whorl in *Marlierea tomentosa* during development (XIII); anthesis showing irregularly branched primary axes in *Marlierea tomentosa* (XIV); detail of closed bud and anthesis in *Marlierea tomentosa* (XV); old flowers showing irregular splitting of calyx in *Marlierea excoriata* (XVI).

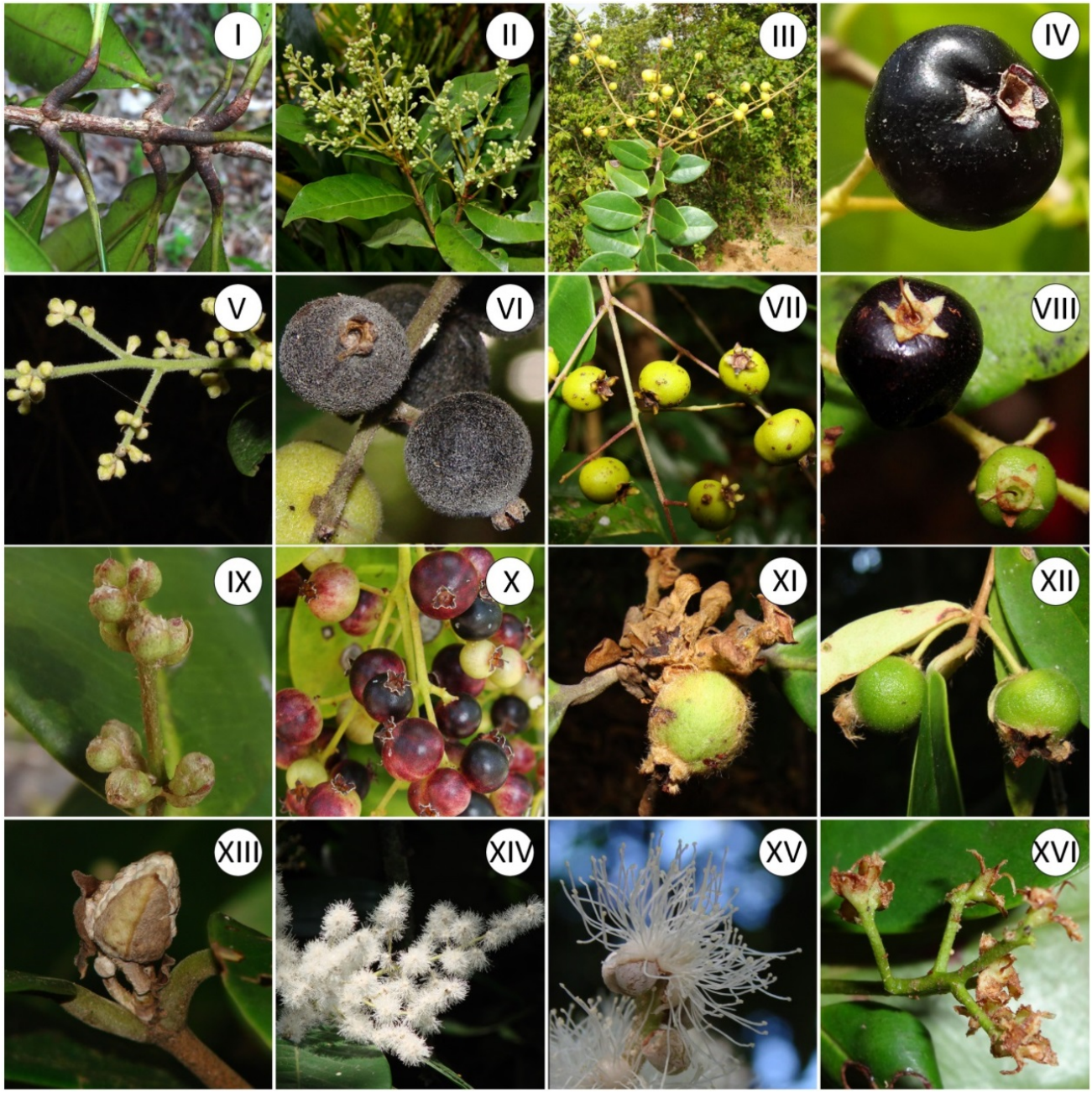

Figure S2. Phylogenetic hypothesis for *Myrcia* clade nine, consensus tree and branch lengths generated from maximum likelihood inference based on DNA combined dataset of nuclear and plastid regions (ITS, *psb*A-*trn*H, *trn*L-F, *trn*Q-rpS16, *ndh*F). Clades from Lucas *et al.* (2011) on bars and the colours of branches inside clade nine represent subclades (thinner vertical bars). Values near to branches are bootstrap percentages shown when above 50%.

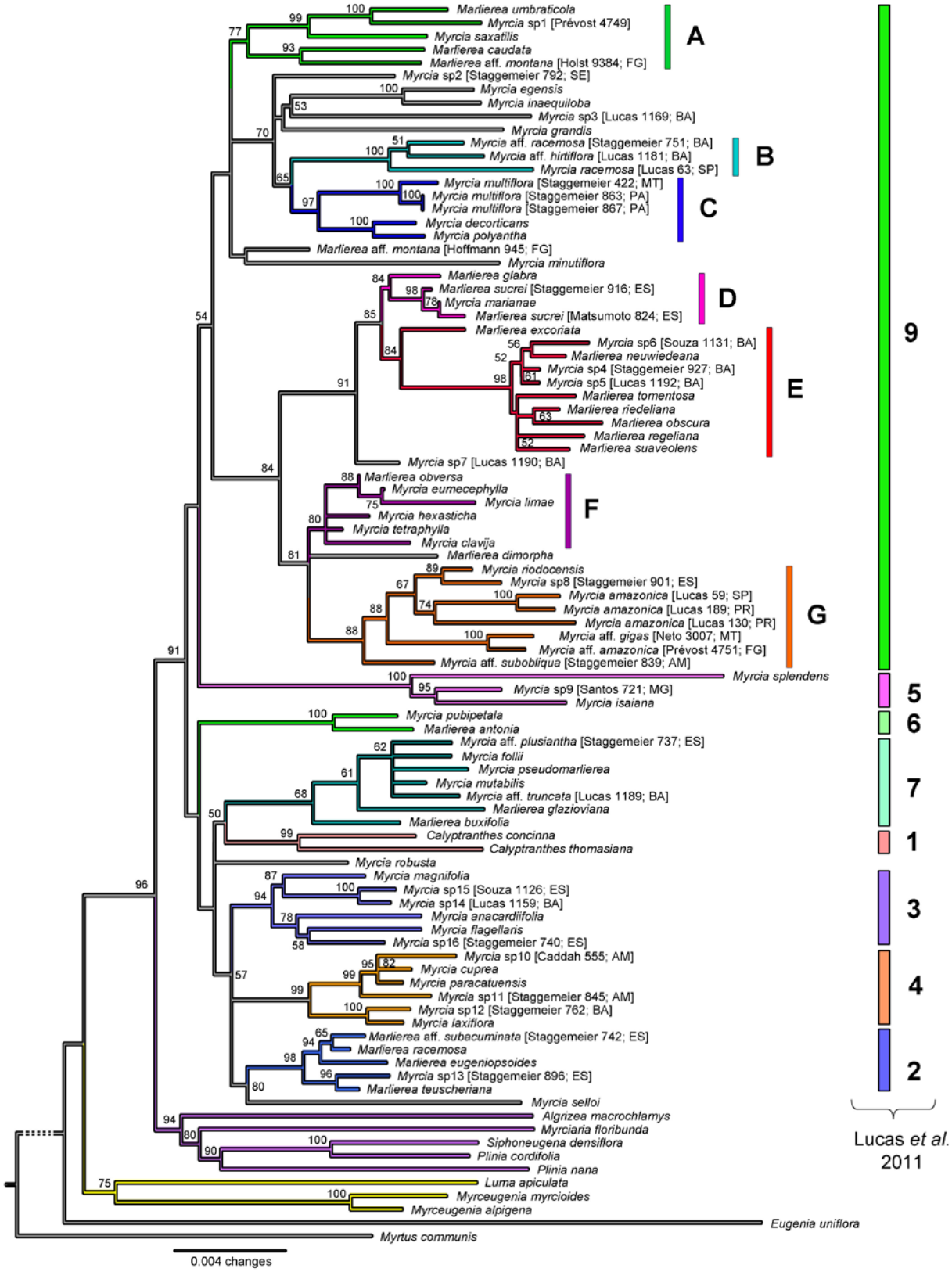

Table S1. Primers used for PCR

Molecular marker	Primer name	DNA sequence (5' - 3')	Reference
*trn*Q-5' rpS16 intergenic spacer			
	trnQ(UUG)	GCGTGGCCAAGYGGTAAGGC	Shaw *et al.* (2007)
	MYtrnQR	AGTTGATGTAAAGGAAGATTTAGACTC	Murillo-A. *et al.* (2012)
	MYrps16F	GCGTAAAAWGAGGAAATGCTTAATG	Murillo-A. *et al.* (2012)
	rpS16x1	GTTGCTTTYTACCACATCGTTT	Shaw *et al.* (2007)
ITS			
	AB101	ACGAATTCATGGTCCGGTGAAGTGTTCG	Sun *et al.* (1994)
	AB102	GAATTCCCCGGTTCGCTCGCCGTTAC	Sun *et al.* (1994)
	ITS-5	GGAAGTAAAAGTCGTAACAAGG	White *et al.* (1990)
	ITS-2	GCTGCGTTCTTCATCGATGC	White *et al.* (1990)
	ITS-3	GCATCGATGAAGAACGCAGC	White *et al.* (1990)
	ITS-4	TCCTCCGCTTATTGATATGC	White *et al.* (1990)
*psb*A (F) *trn*H (R)			
	psb A	CGAAGCTCCATCTACAAATGG	Hamilton (1999)
	trn H (GUG)	ACTGCCTTGATCCACTTGGC	Hamilton (1999)
	MYpsb A 1	TTTTGATTGCAAAATAAAGGAGCAA	this study
*trn*L-F			
trnL (UAA)	c B49317	CGAAATCGGTAGACGCTACG	Taberlet *et al.* (1991)
	d A49855	GGGGATAGAGGGACTTGAAC	Taberlet *et al.* (1991)
	e B49873	GGTTCAAGTCCCTCTATCCC	Taberlet *et al.* (1991)
trnF (GAA)	f A50272	ATTTGAACTGGTGACACGAG	Taberlet *et al.* (1991)
*ndh*F			
	1252f	GATGAAATTMTTAATGATAGTTGGT	Biffin *et al.* (2006)
	2063r	CATTTGGAATTCCATCAATTA	Biffin *et al.* (2006)

Biffin, E., Craven, L.A., Crisp, M.D., & Gadek, P.A. 2006. Molecular Systematics of Syzygium and Allied Genera (Myrtaceae): Evidence from the Chloroplast Genome. *Taxon* **55**: 79-94.

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Sun, Y., Skinner, D., Liang, G., & Hulbert, S. 1994. Phylogenetic analysis of Sorghum and related taxa using internal transcribed spacers of nuclear ribosomal DNA. *Theoretical and Applied Genetics* **89**: 26-32.

Taberlet, P., Gielly, L., Pautou, G., & Bouvet, J. 1991. Universal primers for amplification of three non-coding regions of chloroplast DNA. *Plant molecular biology* **17:** 1105-1109.

White, T.J., Bruns, T., Lee, S., & Taylor, J. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. *PCR protocols: a guide to methods and applications* **18**: 315-322.

Table S2. PCR conditions

Molecular Marker	Reaction	Conditions
ITS	AB101 - AB102	5 min at 94°C followed by 28 cycles of 1 min at 94°C, 1 min at 48°C, 1 min at 72°C and a last stage of 7 min 72°C
	AB101 - ITS 2 ITS 3 - AB102 ITS 2 - ITS 5 ITS 3 - ITS 4	4 min at 94°C followed by 30 cycles of 1 min at 94°C, 1 min at 49°C, 1.5 min at 72°C and a last stage of 4 min 72°C
*psb*A (F) *trn*H (R)	psb A - trn H	5 min at 94°C followed by 28 cycles of 1 min at 94°C, 1min at 48°C, 1 min at 72°C and a last stage of 7 min 72°C
*trn*L-F	c - f	5 min at 94°C followed by 32 cycles of 1 min at 94°C, 1min at 48°C, 1 min at 72°C and a last stage of 7 min 72°C
	c - d e - f	2 min at 94°C followed by 30 cycles of 1 min at 94°C, 1min at 50°C, 1 min at 72°C and a last stage of 4 min 72°C
*ndh*F	1252f-2063r	5 min at 80°C followed by 35 cycles of 1 min at 95°C, 1 min at 50°C, 5 min at 65°C and a last stage of 4 min 65°C
*trn*Q-5' rpS16	*trn*Q - rpS16	5 min at 80°C followed by 35 cycles of 1 min at 95°C, 1 min at 50°C, 5 min at 65°C and a last stage of 4 min 65°C