1 **Phylogenetic approaches reveal biodiversity threats under climate change**

2 Carlos E. González-Orozco[1,2*], Laura J. Pollock[3,4,5], Andrew H. Thornhill[6,7,8], Brent D.

3 Mishler[6], Nunzio Knerr[7], Shawn W. Laffan[8], Joseph T. Miller[7,9], Dan F. Rosauer[11], Daniel P.

4 Faith[12], David A. Nipperess[13], Heini Kujala[5], Simon Linke[14], Nathalie Butt[15], Carsten

5 Külheim[11], Michael D. Crisp[11], Bernd Gruber[1].

6

7 [1]Institute for Applied Ecology and Collaborative Research Network for Murray-Darling

8 Basin Futures, University of Canberra, ACT 2601, Australia. [2]Corporación Colombiana de

9 Investigación Agropecuaria, Corpoica, km 17 Vía Puerto López, Meta, Colombia. *e-mail:

10 cegonzalez@corpoica.org.co. [3]Univ. Grenoble Alpes, Laboratoire d'Écologie Alpine

11 (LECA), F-38000 Grenoble, France. [4]CNRS, Laboratoire d'Écologie Alpine (LECA), F-

12 38000 Grenoble, France. [5]National Environmental Research Program, School of Biosciences,

13 The University of Melbourne, Melbourne, Victoria 3010, Australia.[6]University and Jepson

14 Herbaria, and Dept. of Integrative Biology, University of California, Berkeley, CA 94720-

15 2465, USA. [7]National Research Collections Australia, CSIRO National Facilities and

16 Collections, GPO Box 1600, Canberra, ACT 2601, Australia.[8]Australian Tropical Herbarium,

17 James Cook University, Cairns QLD 4870, Australia. [9]Division of Environmental Biology,

18 National Science Foundation, Arlington, Virginia 22230 USA. [10] Centre for Ecosystem

19 Science, School of Biological, Earth and Environmental Sciences, University of New South

20 Wales, Sydney 2052, Australia.[11]Research School of Biology, Australian National

21 University, Acton, ACT, 2601, Australia.[12] The Australian Museum Research Institute, The

22 Australian Museum, Sydney, NSW 2010, Australia.[13]Department of Biological Sciences,

23 Macquarie University, NSW 2109, Australia. [14]Australian Rivers Institute, Griffith

24 University, Nathan, Qld, 4111, Australia. [15]ARC Centre of Excellence for Environmental

25 Decisions and School of Biological Sciences, The University of Queensland, St. Lucia, 4072.

Predicting the consequences of climate change for biodiversity is critical to conservation efforts[1,2,3]. Extensive range losses have been predicted for thousands of individual species[4], but less is known about how climate change might impact whole clades[1] and landscape-scale patterns of biodiversity[5]. Here, we show that climate change scenarios imply significant changes in phylogenetic diversity and phylogenetic endemism at a continental scale in Australia using the hyper-diverse clade of eucalypts. We predict that within the next 60 years the vast majority of species distributions (91%) across Australia will shrink in size (on average by 51%) and shift south based on projected suitable climatic space. Geographic areas currently with high phylogenetic diversity and endemism are predicted to change substantially in future climate scenarios. Approximately 90% of the current areas with concentrations of paleo-endemism[6] (i.e. places with old evolutionary diversity) are predicted to disappear or shift their location. These findings show that climate change threatens whole clades of the phylogenetic tree, and can be used to forecast areas of biodiversity losses and continental scale impacts of climate change.

By combining species distribution models (SDMs) with measures of evolutionary diversity, we can predict how climate change might impact the tree of life in the future[1,7,8]. Preserving the tree of life is increasingly recognised as an important consideration for conservation in Australia; globally, this evolutionary heritage provides a storehouse of unanticipated benefits for future generations, and locally it helps ensure resilient ecosystems and ongoing delivery of their services[9,10,11,12]. The most commonly used metric to quantify the diversity represented by the tree of life is phylogenetic diversity (PD), which represents the shared evolutionary history of species present in a region and is measured as the sum of branch lengths in the phylogenetic tree linking the species present[10]. PD does not include information on rarity of lineages, which is another important concern for conservation

51 priorities. Phylogenetic endemism (PE) addresses this problem by incorporating the degree of

52 spatial restriction of phylogenetic branches found in an area, relative to all other areas[13]. This

53 useful property means that PE can be used to identify areas that host relatively unique

54 diversity, such as range-restricted "long branch" lineages (i.e., *paleoendemics* - species or

55 clades with no living close relatives such as the reptile Tuatara, *Sphenodon*, or the fish

56 Coelacanth, *Latimeria*).

57   In addition to preserving past evolutionary heritage, protecting areas that hold rapidly

58 diversifying, range-restricted lineages (i.e., *neoendemics*) is a priority, because those lineages

59 hold the key to future evolutionary potential. Previous studies have considered how climate

60 change will impact the evolutionary heritage represented by PD[1,7,8]. PD is expected to be

61 correlated with species richness. Therefore we applied a spatial randomization to evaluate

62 departures of PD and PE from expectations[6]. Consequently, our PD-based metrics are

63 decoupled from their corresponding species-based metrics. Here we present the first analysis

64 describing how both the past and future of evolution might be impacted by climate change

65 using model predictions and newly-developed phylogenetic metrics that take into account

66 relative branch lengths.

67   We explored our approach for a key taxonomic group, Australian eucalypts (genera

68 *Eucalyptus, Corymbia,* and *Angophora*). Australian eucalypts are an appropriate biological

69 model because they are a hyper-diverse group (> 800 species) that dominate forest canopies

70 and ecosystems across much of the continent. Eucalypts are mostly endemic to Australia and

71 have a broad biogeographical diversity[14]. They are of global interest due to their widespread

72 use in forestry[15]. They form a monophyletic lineage within the Myrtaceae family [16,17,18,19],

73 including the few eucalypt species that occur outside of Australia. Here we examine the

74 expected shift in the geographic ranges of 657 species of eucalypt across Australia,

75 comparing present ranges to those under forecast climate change scenarios for the years 2025,

76   2045, 2065 and 2085. We used SDMs to predict changes in geographic ranges and the

77   direction in which ranges are likely to shift under future climate scenarios. SDMs have

78   limitations when predicting responses to climate change[20] in species (e.g., climatic

79   adaptability) and communities (e.g., species interactions). We accounted for some of the

80   well-known weaknesses of SDMs by explicitly considering spatial bias and over-fitting, and

81   comparing models with and without dispersal. The dispersal and non-dispersal scenarios

82   produced very similar patterns, so we report only the results from the dispersal scenario.

83   Our study's novel findings regarding effects of climate change on phylogenetic

84   diversity are grounded in our descriptions of impacts at the species level that corroborate

85   previous findings. Eucalypt species are known to be threatened by climate change in

86   Australia with previous results suggesting 53% of all *Eucalyptus* species predicted to be

87   outside of their current climate conditions by 2070 under a 3˚C warming scenario[21]. More

88   recent SDM modelling for eucalypts suggests species ranges across the continent will

89   contract and shift in both lateral and poleward directions, and the central desert areas will be

90   particularly affected[22]. Our models predicted that by 2085, the current geographic range of

91   91% of the 657 eucalypt species will shrink by an average of 51%, with 2.4% of species

92   predicted to become extinct because their climate space will disappear entirely. Relatively

93   few species (9%) are predicted to expand their geographic range (Fig. 1; see also SI_2 for

94   range size, % change, type of shift, shift magnitude and shift direction; and SI_4 for maps for

95   each of the 657 species).

96   To understand how these losses in species will manifest as changes in evolutionary

97   diversity across the landscape, we calculated present and future PD[10] and PE[13] for all grid

98   cells (~25km × 25km). These analyses predict that on average 2% of PD (decline in PD grid

99   cells) will be lost across Australia by 2085 (Extended Data Fig. 1). Losses will occur in

100   places recognised as national[14] and global biodiversity hotspots[23]. Additionally, we found that

101   the rate of turnover of PD increases over time, with a higher proportion of major changes

102   occurring in southern Australia (Extended Data Fig. 9). Specifically, Mediterranean,

103   temperate, and grassland ecosystems will face the greatest proportional change in clades

104   present over time. This trend is accompanied by an increasing homogenization over the

105   landscape. The average rate of phylogenetic turnover between all pairs of cells within a given

106   year will decrease from 0.58 in the present to 0.50 in 2085 (Extended Data Table 1),

107   suggesting an increase in average spatial homogeneity of phylogenetic composition (or

108   phylogenetic homogenization) in the future. This spatial homogenization of PD has been

109   documented previously for diverse groups in Europe[1], and is suggested by past and current

110   climate-driven plant extinctions for Thoreau's woods in the US and some temperate tree

111   floras in Europe[24,25]. Here, for the first time, we show the potential effects of climate-change

112   leading to PD loss in the future for a significant biological group of the southern hemisphere.

113   In contrast, PE is predicted to increase spatially in some of the areas of key diversity

114   hotspots. In general, species endemism and PE are measures of rarity, and therefore,

115   endemism tends to increase in the areas that hold the remaining portions of species ranges.

116   The increase in PE is a result of lineages becoming more range-restricted. For example, in

117   southwestern Western Australia, an internationally recognized biodiversity hotspot, species

118   are predicted to retract toward the coast causing some coastal cells to have high PE in the

119   future (Extended Data Fig. 1e). Predicting the location of high PE areas in the future is

120   important from a conservation standpoint because these locations are likely to be the sites of

121   concentrations of rare elements of diversity in the future, and, therefore, will be strategic

122   areas for preventing further PD losses.

123   Two derived metrics, relative phylogenetic diversity (RPD) and relative phylogenetic

124   endemism (RPE)[6], can be used to better understand anticipated impacts on unusually long or

125   short branches. These metrics reveal information about the underlying evolutionary processes

126 that we seek to understand and conserve[6] and also because they store old and highly unique

127 lineages that, once lost, will significantly reduce the breadth of biodiversity. Sites with many

128 very long branches are important repositories of unique evolutionary history and trait

129 diversity[26]; sites with many short branches might indicate places with the potential for

130 generating evolutionary adaptation and speciation in the future.

131   The RPD and RPE metrics reveal these patterns through an assessment that asks

132 whether the contribution of unusually long or short branches to PD or PE in a grid cell is

133 greater or less than expected by chance. RPD (or RPE) is the ratio of PD (or PE) measured

134 using the set of species in that grid cell on the observed tree of the 657 eucalypt species to

135 that measured on a comparison tree with the same topology but with all branches adjusted to

136 be of equal (average) length[6], with significant large or small ratios determined by a spatial

137 randomization test (see Methods for details of randomization test)[27]. We find both areas of

138 significantly high and significantly low RPD are predicted to decline in size (~10%) by 2085

139 (Extended Data Fig. 2), indicating that unusually long- and short-branch lineages will

140 disappear within sites.

141   Endemism can result either from younger lineages that have yet to expand their range

142 or from older lineages that are relicts of a previously broader distribution. RPE allows the

143 identification of centres of paleo-endemism (range-restricted long branches), centres of neo-

144 endemism (range-restricted short branches), or both (centres of mixed endemism, termed

145 "super endemism"), through a recently-developed method called CANAPE (Categorical

146 Analysis of Neo- And Paleo-Endemism; see methods)[6]. We find that the current areas of

147 paleo-, neo-, and super-endemism are predicted to significantly shrink (~50%) in size by

148 2085 (Fig. 2; Extended Data Fig. 3a-e). This suggests that current areas of significant

149 phylogenetic endemism may decline as lineages either go extinct or move to different

150 locations (Figs. 2 and 3) with climate change.

151   Areas of paleo-endemism are particularly impacted; $\geq$ 90% of the current areas with

152 significantly high paleo-endemism will disappear or shift to new places by 2085 (Fig. 2

153 ellipses). Most of the large loss of paleo-endemism is due to shrinking geographic range of

154 lineages (Extended Data Fig. 4). This large loss of paleo-endemism is a loss in the number of

155 grid cells falling into that category. Shrinking ranges can increase the paleo-endemism of a

156 cell that retains those long branches, but overall decreases of paleo-endemism areas reflects

157 the loss of those branches from areas. For example, between the present and 2085, 64.6% of

158 species' geographic ranges within current paleo-endemism areas will shrink (Extended Data

159 Fig. 4), thus impacting their contribution to overall PE of these areas. There are currently 73

160 grid cells with significant eucalypt paleo-endemism in Australia, containing 240 species. By

161 2085, 52 of these species are predicted to go extinct or migrate elsewhere (Fig. 3).

162 Consequently, most of these grid cells will cease to be areas of paleo-endemism by 2085.

163 Declines of paleo-endemic areas tended to be even larger in the no-dispersal scenario, which

164 otherwise gave similar results to the dispersal scenario reported in the text (Extended Data

165 Fig. 3 f-j). These results show that areas of paleo-endemism are not necessarily places of

166 long-term stability, but instead may be highly threatened and mobile.

167   We also found that, in a few cases, new areas of paleo-endemism (Fig. 2, squares) are

168 predicted to form. The main reason that paleo-endemic sites appear is because current

169 widespread long-branch lineages become more range-restricted under climate change. These

170 predicted new centres of paleo-endemism will be important for future conservation because

171 they represent predicted areas that have the potential to harbour rare long branches.

172   Lineages are also predicted to disappear from places where new concentrations of

173 paleo-endemism will form (see the square in central Australia and the larger rectangle in the

174 far top-left in Fig. 2b). These sites currently contain 70 and 57 species and we predict that

175 23.3% and 7% of those species, respectively, will be locally extinct by 2085 (Fig. 2;

176 Extended Data Fig. 5c, d).

177   Overall, the extinction of whole lineages is likely to occur as a result of severe

178 reductions of climatic space (Extended Data Fig. 5a-d; and species list in SI_1, Tables 1-4).

179 The effect on the phylogeny was not evenly distributed as has been previously reported in

180 some cases[24], and we identified potential extinction of five species of *Eucalyptus* in

181 Southwest Australia and three of *Corymbia* in southeast Queensland. This could be

182 considered as an early sign of phylogenetic extirpation[25] or extinction of lineages of eucalypts

183 (Fig. 3).

184   Few studies have addressed the impact of climate change on PD[28] and ours is the first

185 to take the additional step of showing how climate change might affect PE including centres

186 of paleo- (old) and neo- (young) -endemism across a continental-scale landscape. Our

187 approach can be considered as an early warning system for forecasting biodiversity loss

188 across the landscape, critically expressed as loss of evolutionary heritage and evolutionary

189 potential. Here we show that the contraction of lineage ranges expected with climate change

190 is likely to reduce diversity at most locations, homogenise the landscape, and particularly

191 impact rare long- and short-branch lineages, which might cause significant losses to the tree

192 of life and reduce genetic adaptive potential of eucalypts under climate change[29,30]. Faced

193 with substantial losses to biodiversity with climate change, our approach allows the

194 identification of areas that are key to preventing further biodiversity loss.

195   Specifically, we found major shifts in eucalypts' modelled distributions which, if

196 realized, would lead to a shrinkage of current areas of high phylogenetic endemism for the

197 species group along all the southwest, southeast, and southern coastal regions of Australia.

198 We find that Tasmania, due to its lower latitude and more temperate climate, might become a

199 very important refugium, while Victoria is more prone to losing areas of neo-endemism.

200 Current hotspots of paleo-endemism in southeast Queensland, northern coastal NSW, and

201 central Australia are also predicted to be impacted severely. Conversely, new concentrations

202 of paleo-endemism are predicted to occur in the Kimberley and northern coastal region

203 demonstrating the potential of our methods to identify key areas that might be important

204 refugia in the future.

205

206 **References**

207 1. Thuiller, W. *et al.* Consequences of climate change on the tree of life in Europe. *Nature*

208 **470,** 531–534 (2011).

209 2. Araujo, M.B., Thuiller, W. & Pearson, R.G. Climate warming and the decline of

210 amphibians and reptiles in Europe. *Journal of Biogeography* **33,** 1712–1728 (2006).

211 3. Purvis, A. & Hector, A. Getting the measure of biodiversity. *Nature* **405,** 212–219

212 (2000).

213 4. Hof, C., Araujo, M.B., Jetz, W. & Rahbek, C. Additive threats from pathogens, climate

214 and land-use change for global amphibian diversity. *Nature* **480,** 22–29 (2011).

215 5. Warren, R. *et al.* Quantifying the benefit of early climate change mitigation in avoiding

216 biodiversity loss. *Nature Climate Change* **3,** 678-682 (2013).

217 6. Mishler, B.D. *et al.* Phylogenetic measures of biodiversity and neo- and paleo-endemism

218 in Australian *Acacia*. *Nature Communications* **5**, 4473 (2014).

219 7. Faith, D.P. & Richards, Z.T. Climate change impacts on the tree of life: changes in

220 Phylogenetic Diversity illustrated for Acropoda corals. *Biology* **1**, 906–932 (2012).

221 8. Loyola, R.D. *et al.* Clade-specific consequences of climate change to amphibians in

222 Atlantic Forest protected areas. *Ecography* **37**, 65–72 (2014).

223 9. Faith, D.P. & Pollock, L.J. (2014) Phylogenetic diversity and the sustainable use of

224   biodiversity. pp 35-52. In: Applied ecology and human dimensions in biological

225   conservation (ed. L.M Verdade et al.) Springer.

226   10. Faith, D.P. Conservation evaluation and phylogenetic diversity. *Biological Conservation*

227   **61**, 1-10 (1992).

228   11. Faith, D.P. *et al.* Evosystem Services: an evolutionary perspective on the links between

229   biodiversity and human-well-being. *Current Opinion in Environmental Sustainability* **2**,

230   66-74 (2010).

231   12. Cadotte, M.W. *et al.* Phylogenetic diversity metrics for ecological communities:

232   integrating species richness, abundance and evolutionary history. *Ecology Letters* **13**,

233   96–105 (2010).

234   13. Rosauer, D., Laffan, S.W., Crisp, M.D., Donnellan, S.C. & Cook, L.G. Phylogenetic

235   endemism: a new approach for identifying geographical concentrations of evolutionary

236   history. *Molecular Ecology* **18**, 4061–4072 (2009).

237   14. González-Orozco, C.E., Thornhill, A.H., Knerr, N., Laffan, S. & Miller, J.T.

238   Biogeographical regions and phytogeography of the eucalypts. *Diversity & Distributions*

239   **20**, 46–58 (2014).

240   15. Wilson P.G. (2011) Myrtaceae. The Families and Genera of Vascular Plants. Volume X.

241   Flowering Plants Eudicots: Sapindales, Cucurbitales, Myrtaceae (ed. by K. Kubitzki), pp.

242   212–271. Springer-Verlag, Heidelberg.

243   16. Thornhill, A.H., Ho S.Y.W., Külheim C. & Crisp M.D. Interpreting the modern

244   distribution of Myrtaceae using a dated molecular phylogeny. *Molecular Phylogenetics*

245   *and Evolution* **93**, 29–43 (2015).

246   17. Thornhill, A.H., Popple L.W., Carter R.J., Ho S.Y.W. & Crisp M.D. Are pollen fossils

247   useful for calibrating relaxed molecular clock dating of phylogenies? A comparative

248   study using Myrtaceae. *Molecular Phylogenetics and Evolution* **63**, 15–27 (2012).

249   18. Crisp, M.D., Burrows G.E., Cook L.G., Thornhill A.H. & Bowman D.M.J.S. Flammable

250   biomes dominated by eucalypts originated at the Cretaceous-Palaeogene boundary.

251   *Nature Communications* **2**, 1–8 (2011).

252   19. Bayly M.J., *et al.* Chloroplast genome analysis of Australian eucalypts-*Eucalyptus*,

253   *Corymbia*, *Angophora*, *Allosyncarpia* and *Stockwellia* (Myrtaceae). *Molecular*

254   *Phylogenetics and Evolution* **69**, 704–16 (2013).

255   20. Booth, T.H. *et al.* Native forest and climate change: Lessons from eucalypts. *Forest*

256   *Ecology and Management* **347,** 18-29 (2015).

257   21. Hughes, L., Cawsey, E.M. & Westoby, M. Climatic range sizes of *Eucalyptus* species in

258   relation to future climate change. *Global Ecology and Biogeography Letters* **5**, 23–29

259   (1996).

260   22. Butt, N., Pollock, L.J. & McAlpine, C.A. Eucalypts face increasing climate stress.

261   *Ecology and Evolution* **3**, 5011–5022 (2013).

262   23. Myers, N., Mittermeier, R.A., Mittermeier, C.G., da Fonseca, G.A.B. & Kent, J.

263   Biodiversity hotspots for conservation priorities. *Nature* **403,** 853-858 (2000).

264   24. Eiserhardt, W.L., Borchsenius, F., Plum, C.M., Ordoñez, A. & Svening, J-C. Climate-

265   driven extinctions shape the phylogenetic structure of temperate tree floras. *Ecology*

266   *Letters* **18**, 263-272 (2015).

267   25. Willis, C.G. *et al.* Phylogenetic patterns of species loss in Thoreau's woods are driven by

268   climate change. *Proc. Natl Acad. Sci. USA* **105**, 17029–17033 (2008).

269   26. Forest, F *et al.* Preserving the evolutionary potential of floras in biodiversity hotspots.

270   *Nature* **445**, 757-760 (2007).

271   27. Thornhill, A. H *et al.* Continental-scale spatial phylogenetics of Australian angiosperms

272   provides insights into ecology, evolution and conservation. *Journal of Biogeography.*

273   doi/10.1111/jbi.12797 (2016).

274   28. Zhang, J., Nielsen, S.E., Stolar, J., Chen, Y & Thuiller, W. Gains and losses of plant

275   species and phylogenetic diversity for a northern high-latitude region. *Diversity &*

276   *Distributions* 1-14 (2015).

277   29. Cardinale, B.J. *et al.* Biodiversity loss and its impact on humanity. *Nature* **486**, 59-67

278   (2012).

279   30. Hoffmann, A.A. & Sgro, C.M. Climate change and evolutionary adaptation. *Nature* **470,**

280   479–485 (2011).

281

282   **Supplementary Information** is available in the online version of the paper

283

284   **Corresponding authors**

285   Correspondence to: Carlos E. Gonzalez-Orozco (cegonzalez@corpoica.org.co) or Bernd
286   Gruber (bernd.gruber@canberra.edu.au)

287

Author contributions

296

297 All authors contributed to project conception. C.G-O, L.J.P, A.H.T, N.K, B.G and S.W.L.

298 conducted analyses. A.H.T, M.D, C.K and J.T.M developed the phylogeny. A.H.T, N.K,

299 C.G-O, L.J.P and N.B compiled and corrected species spatial data records. C.G-O wrote the

300 manuscript draft and all authors contributed to interpretation of the results and writing of the

301 final paper.

302

303

304

305

306

307

308

309

Methods

311

Spatial Data and Species Distribution Modelling

313   We modelled present and future distributions of current and four future time points

314   (2025, 2045, 2065 and 2085) for all 766 eucalypt species (~163,000 occurrence records)

315   found in Australia (only 16 are endemic to another country) at a 5-km pixel resolution using a

316   dispersal and a no-dispersal scenario. Data (presence-only) were extracted from Australia's

317   Virtual Herbarium database [AVH] accessed in October 2011 (http://avh.chah.org.au/).

318   Species names were rectified using the current species list found in Euclid Version 3.0[31] and

319   experts were consulted in particular cases when naming history was difficult to reconstruct.

320   Latitudinal biases were corrected by spatial geo-rectifications. Points outside the known

321   natural range were removed for each species based on range maps and expert opinion, and

322   pre-1950 records were removed to limit spatial uncertainty[32].

323   We used the Representative Cost Pathway (RCP) 6.0 scenario for the Hadley global

324   climate model (hadcm3, http://wallaceinitiative.org/). We focused on this moderate climate

325   scenario because of its fit with the Australian strategy on emission reductions, and because

326   the literature suggests that eucalypts will be significantly affected under a 3˚C warming by

327   2070[21]. Strictly our predictions are therefore only valid for this scenario, but as it is an

328   intermediate scenario our predicted responses are most likely also of the intermediate type. In

329   case there is a reason in the future to suggest a different scenario to be more likely our

330   approach can be easily adapted to such a scenario. We used a simplified set of predictor

331   variables that we believe to be physiologically relevant (maximum temperature and dry

332   season rainfall) with strong predictive power[22], spatial variables (latitude and longitude) and

333   one edaphic variable (median % clay content derived from the 1:2 M Atlas of Australian

334   Soils[33,34]). Spatial predictors were included in the models because they help constrain the

335   modelled distributions to a more realistic spatial extent based on an initial trial of 20 species

336   with good distribution data.

337   The AVH dataset is heavily influenced by road-based sampling, which was accounted

338   for by including distance-to-roads as a predictor in each model, then setting distance-to-roads

339   to zero for prediction (for present and future scenarios). Models were fitted using MaxEnt[35]

340   in the R package 'dismo' with a random background sample of 20,000 records (the same

341   sample for each species), randomly distributed across Australia and uniform for all species.

342   We used only 'hinge features' because they tend to increase model performance without

343   increasing model complexity[36]. Hinge features provide smoother response curves, which may

344   more closely approximate the species' fundamental niche[37]. Model fit was evaluated with

345   Area Under the ROC Curve from a 5-fold cross-validation for each species (see AUC values

346   in SI_3). A Maxent logistic threshold (maximum training sensitivity plus specificity) for each

347   species was applied to convert habitat suitability into presences and absences for present and

348   future scenarios.

349   In the no-dispersal scenario, we used the same set of modelling parameters described

350   above, but prevented colonization. The present distributions are identical in the dispersal and

351   no-dispersal scenario. In each subsequent time period, species are not allowed to disperse to

352   cells not occupied in the previous time step.

353   **Molecular data**

354   DNA data for the study was gathered by using existing and newly generated nuclear (ITS and

355   ETS) and chloroplast sequences (*matK* and *psba-trnH*) that were successfully amplified for

356   711 eucalypt species (See Table in SI_5 for GenBank accessions). Leaves for DNA

357   extraction were sourced from numerous field trips, botanical gardens, arboreta, and herbaria

358   from multiple locations around Australia. In total 2560 gene sequences were used in the

359   study, 237 were mined from GenBank, and 2323 were newly generated for this project. These

360   sequences represented the 711 eucalypt species and 21 taxa from other Myrtaceae tribes

361   which were used to root the phylogeny (Extended Data Fig. 6). Individual locus alignments

362   were constructed using Muscle[38] and adjusted manually in Se-Al[39].

363   The phylogenetic analysis was performed on the concatenated alignment using

364   maximum likelihood in the CIPRES Portal (www.phylo.org), utilising the RAxML HPC

365   BlackBox tool with a partition model set for each locus, with bootstrapping set to

366   automatically halt, which occurred after 550 replicates. The ML tree with bootstrap values is

367   shown in Extended Data Fig. 7. Extended Data figure 8 is a bi-plot of branch length vs,

368   bootstrap score, and shows that low bootstrap scores were restricted to very short branches.

369   The uncertainty in these short branches did not affect the analyses presented here, since the

370   better supported long branches contribute most of the PD.

Species range shift analyses

372   The mean centre of distributional area using the Maxent habitat suitability maps under

373   present and future scenarios was estimated for the 657 species with matching phylogenetic

374   data and SDMs following established methods[40]. This analysis showed the magnitude and

375   direction of change of the mean centre of the climate space for each species between the

376   present and 2085. Species were grouped according to their distribution change from the

377   present, namely into "expanding" or "shrinking" if the predicted suitable climate space of a

378   species increased or decreased between the present and 2085, respectively. Species whose

379   suitable climate space was predicted to become extinct by 2085 were classified as

380   "extinct". The 'dispersal' scenario assumes all species can disperse across the landscape.

381   However, the use of spatial variables in the models indirectly accounts for some dispersal

382   limitation, effectively limiting the potential of species to disperse to distant sites. We believe

383   this spatial dispersal limitation is realistic given the biology of eucalypts, with most species

384   having relatively heavy seeds without specialized dispersal mechanisms that simply drop to

385   the ground when shed. Given the tree height, seed weights, and average wind speeds, most

386   eucalypt species would not be expected to disperse beyond a single grid cell during the time

387   period in this study without a rare long-distance dispersal event[41].

388   **Spatial phylogenetic analyses of modelled distributions**

389   The SDM suitability values were aggregated at ~25km × 25km to a total of 12,813 grid cells

390   and used to calculate Species Richness (SR), Weighted Endemism (WE), Phylogenetic

391   Diversity (PD)[10], Phylogenetic Endemism (PE)[13], Relative Phylogenetic Diversity (RPD) and

392   Relative Phylogenetic Endemism (RPE) in the Biodiverse software[42] for 657 species. SR and

393   WE results reported in Extended Data Fig. 1 were calculated on the basis of all 766 species

394   because they did not require a phylogenetic tree. All phylogenetic metrics were calculated on

395   the basis of the 657 species that are in the phylogeny. A spatial randomization based on 999

396   trials was applied to these metrics[6]. The purpose of the randomization is to identify whether

397   the observed values were significantly different from a random selection of the same number

398   of terminal taxa from the tree.

399   RPE is applied in a two-step test called categorical analysis of neo- and paleo-

400   endemism (CANAPE) using the same spatial randomization[6]. The first step of CANAPE

401   determines whether a location is a center of high phylogenetic endemism by applying a one-

402   tailed test (for large values) to both the numerator and denominator of RPE (i.e., PE measured

403   on the observed tree in the numerator and PE measured on a comparison tree where all

404   branches are of equal (average) length in the denominator). Then, for grid cells passing this

405   test, the second step applies a two-tailed test to the RPE ratio to identify cells dominated by

406   unusually short range-restricted branches (centres of neo-endemism), unusually long range-

407 restricted branches (centres of paleo-endemism), or both (centres of mixed endemism, termed

408 "super endemism" if both the numerator and denominator of RPE are highly significant)[6].

409 **Phylogenetic turnover analyses of modelled distributions**

410 Two spatial turnover analyses using the Phylo Sørenson index[43] were conducted in

411 Biodiverse[42] for 657 species to cross validate the observed patterns of the modelled PD

412 distribution results: (1) a mean pair-wise rate of turnover between all pairs of cells within

413 each time period, summarised using the mean and standard deviation for each year; and (2)

414 the rate of phylogenetic turnover from the present to each modelled time period for each cell.

415   **References**

416 31. Euclid v3.0- Eucalypts of Australia (2002). https://www.anbg.gov.au/cpbr/cd-
417   keys/euclid3/euclidsample/html/index.htm.

418 32. Kujala, H., Moilanen, A., Araújo, M.B. & Cabeza, M. Conservation planning with
419   uncertain climate change projections. *Plos One* **8**, e53315 (2013).

420 33. Williams, K. J. *et al.* Harnessing continent-wide biodiversity datasets for prioritising
421   national conservation investment. CSIRO Ecosystem Sciences, Canberra (A report
422   prepared for the Department of Sustainability, Environment, Water, Population and
423   Communities, Australian Government, Canberra) (2010).

424 34. McKenzie, N. J., Jacquier, D. W., Ashton, L. J & Cresswell, H. P. Estimation of soil
425   properties using the Atlas of Australian soils. CSIRO, Canberra (2000).

426 35. Elith, J. *et al*. A statistical explanation of Maxent for ecologists. *Diversity and*
427   *Distributions* **17,** 43-57 (2011).

428 36. Pollock, L.J. *et al.* Phylogenetic diversity meets conservation policy: small areas are key
429   to preserving eucalypt lineages. *Philosophical Transactions of the Royal Society B:*
430   *Biological Sciences* **370**, 1662 (2015).

431   37. Phillips, S.J & Dudik, M. Modeling of species distributions with Maxent: new extensions

432   and a comprehensive evaluation. *Ecography* **31**, 161-175 (2008).

433   38. Edgar, R.C. MUSCLE: multiple sequence alignment with high accuracy and high

434   throughput. *Nucleic Acids Research* **32**, 1792–1797 (2004).

435   39. Rambaut, A. (2002) Sequence Alignment Editor (Se-Al) v2.0.

436   40. VanDerWal, J. *et al.* Focus on poleward shifts in species' distribution underestimates the

437   fingerprint of climate change. *Nature Climate Change* **3**, 239–243 (2013).

438   41. Cremer. Distance of seed dispersal in eucalypts estimated from seed weights. *Australian*

439   *Forest Research* **7**, *225-228* (1977).

440   42. Laffan, S.W., Lubarsky, E. & Rosauer, D.F. Biodiverse, a tool for the spatial analysis of

441   biological and related diversity. *Ecography* **33**, 634–647 (2010).

442   43. Ferrier, S., Manion, G., Elith, J. & Richardson, K. Using generalized dissimilarity

443   modelling to analyse and predict patterns of beta diversity in regional biodiversity

444   assessment. *Diversity and Distributions* **13**, 252–264 (2007).

445

446
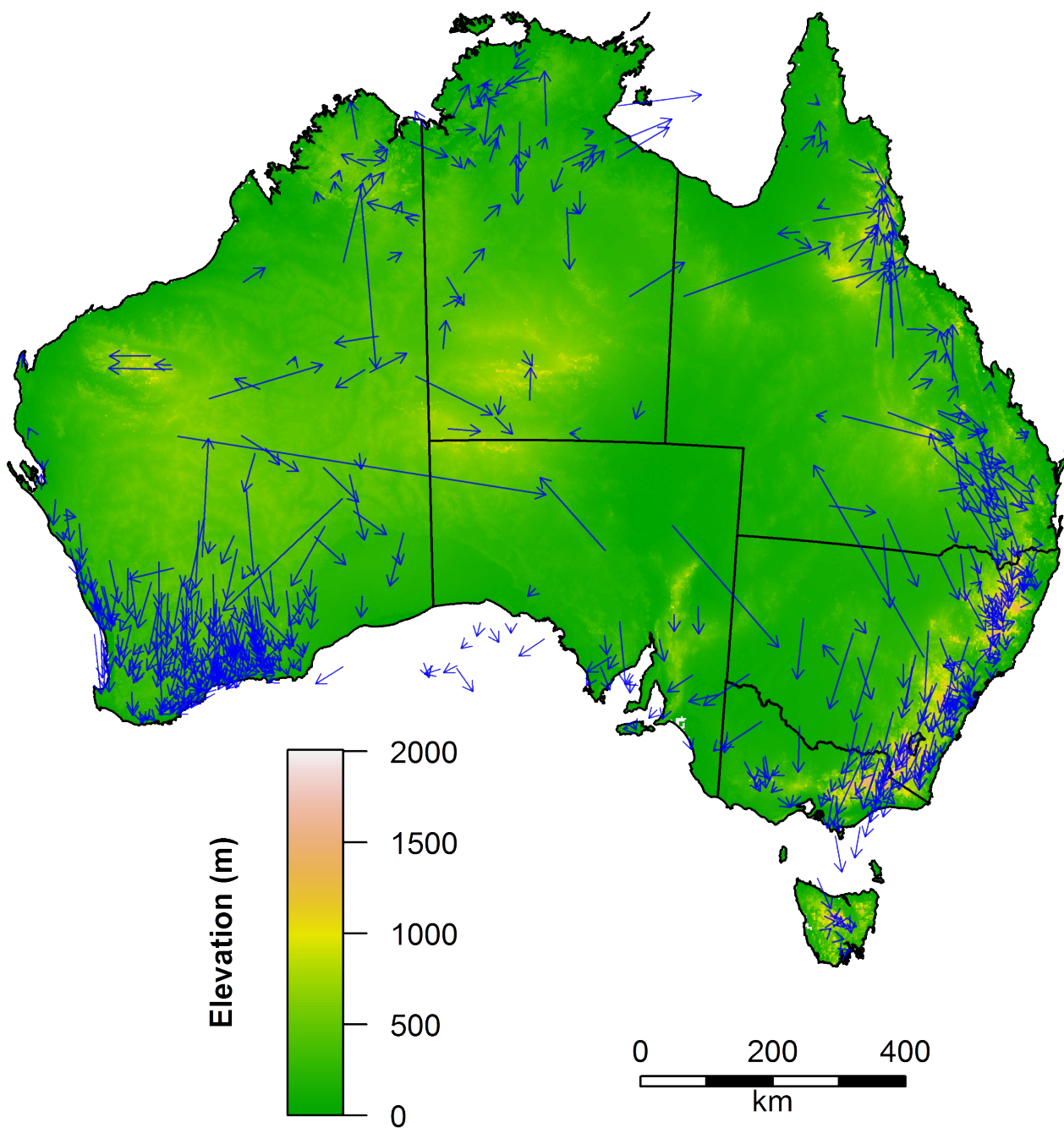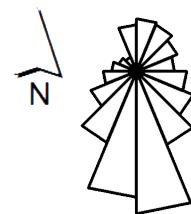
447
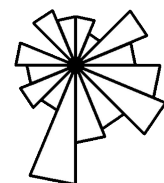
448

449

450

451

452

453

Figures legends

455   **Figure 1 │Variation in the predicted distribution of the suitable climate space of 657**

456   **Australian eucalypt species from 2014 to 2085. a,** Shift in the predicted species

457   distribution where arrows present the magnitude and direction of change in distribution at the

458   centroid of the climatic space. **b,** plots showing the general direction of the distributional

459   change for species that have shrinking distributions, expanding distributions or go extinct at

460   the last time point.

461   **Figure 2 │Areas of phylogenetic endemism using Categorical Analysis of Neo- And**

462   **Paleo-Endemism (CANAPE) for 657 species of eucalypts in Australia for projected**

463   **climate change scenarios at 2014 and 2085. a,** CANAPE map for 2014, and **b,** 2085.

464   Ellipses indicate places where current areas of paleo-endemism disappear; rectangles indicate

465   places where new areas of paleo-endemism appear; triangles indicate where current areas of

466   paleo or neo-endemism weaken. Beige areas do not depart significantly from random
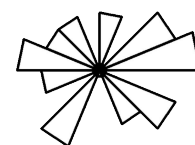
467   expectation.

468   **Figure 3 │Effects of projected climate change scenarios, between 2014 and 2085, on**

469   **species of eucalypts found in current areas of paleo-endemism across Australia.**

470   **Highlighted branches in the phylogenetic tree are present in the 73 grid cells that had**

471   **significant paleo-endemism in Australia in 2014 (blue grid cells in ellipses Fig 2a).**

472   Branches predicted to be lost from the 73 grid cells by 2085 are shown in blue, branches

473   predicted to immigrate by 2085 are shown in green, and branches common to both periods

474   are shown in red. Clades marked with an asterisk refer to places in the phylogeny

475   corresponding to paleo-endemism where individual branches were removed from the

476   phylogeny consistently over time.

a

Elevation (m)
2000
1500
1000
500
0

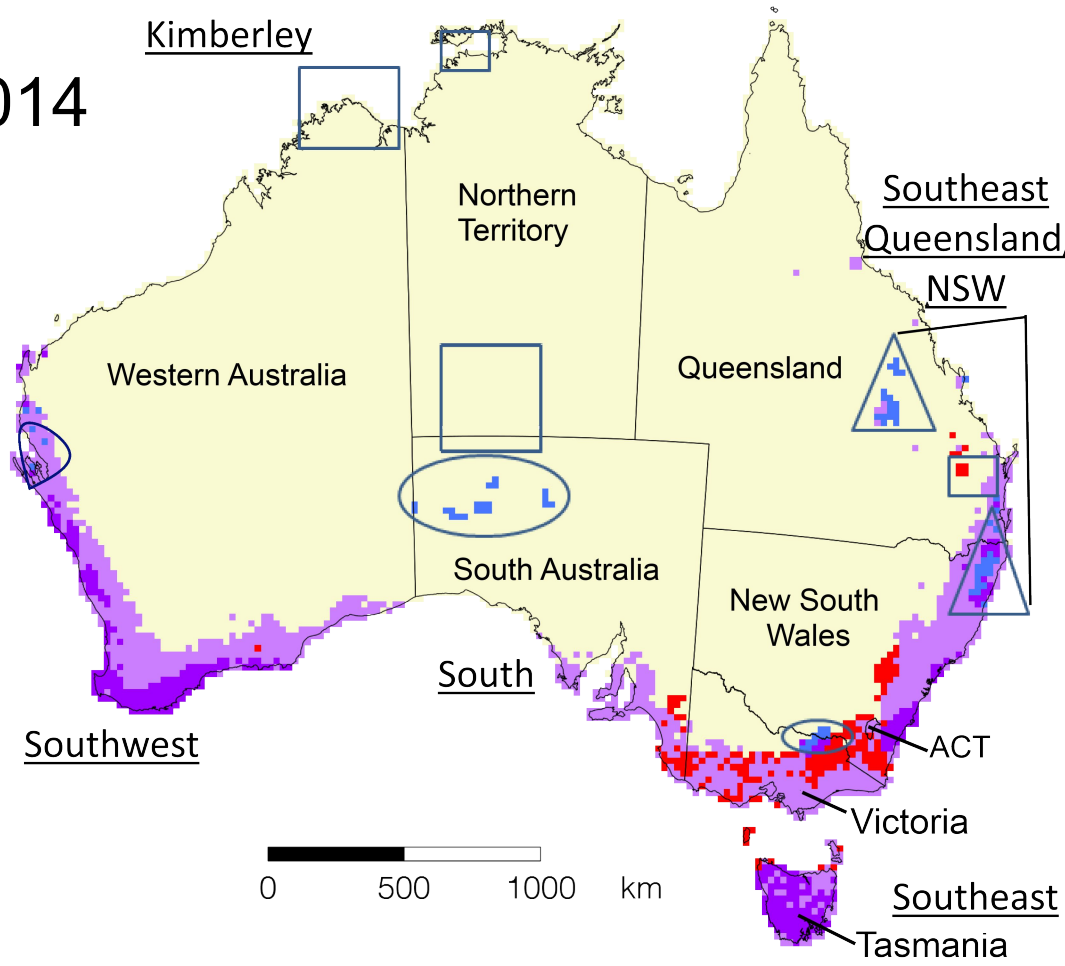0   200   400
km

b

N

shrinking
N=580

expanding
N=61

extinct
N=16

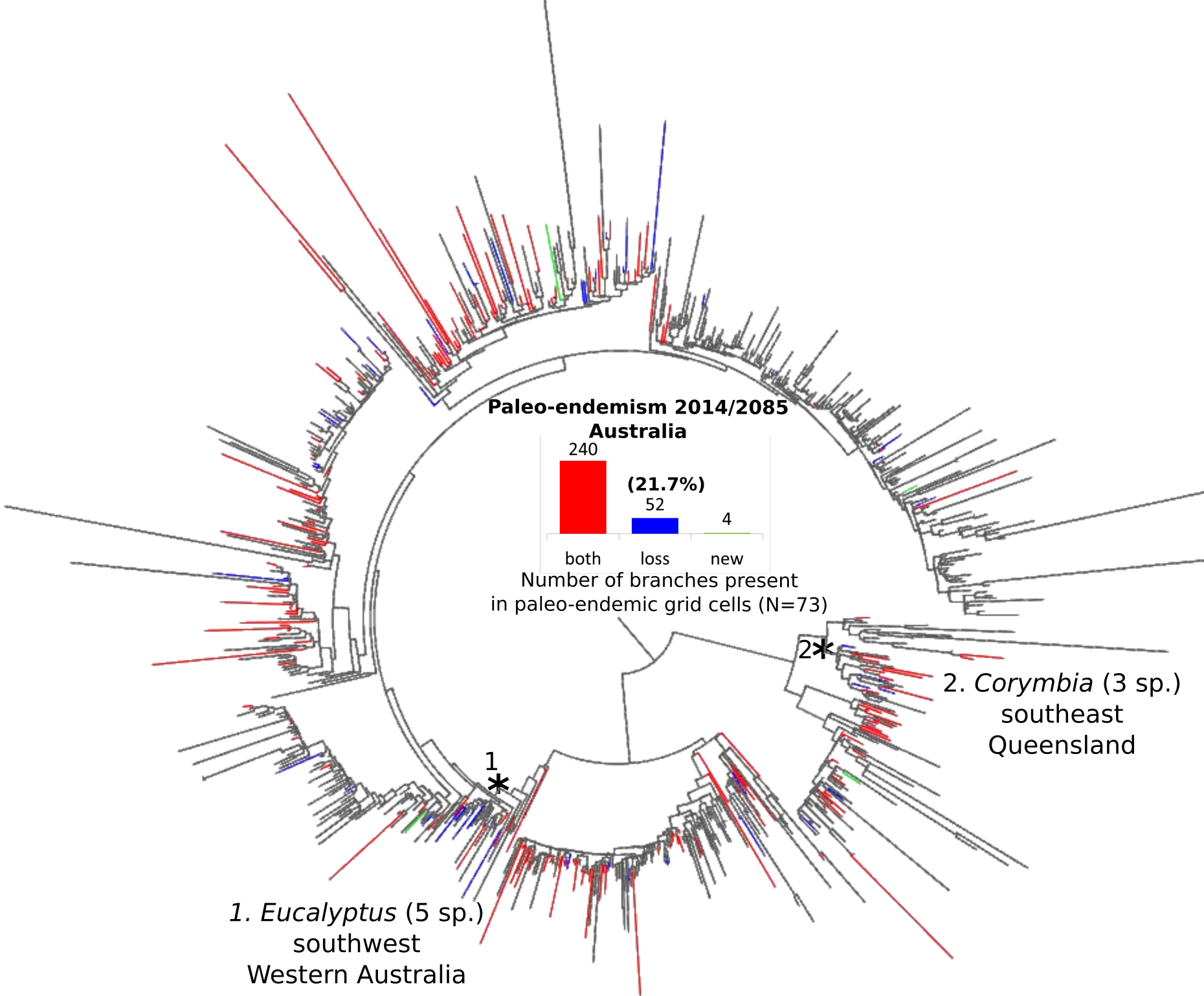# Categorical Analysis of Neo- And Paleo- Endemism

a

2014

Kimberley

Northern Territory

Southeast Queensland/ NSW

Western Australia

Queensland

South Australia

New South Wales

South

Southwest

ACT

Victoria

Southeast

Tasmania

0   500   1000   km

b

2085

0   500   1000   km

Neo   Paleo   Mixed   Super

Not significant

Paleo-endemism 2014/2085 Australia

(21.7%)

240 both
52 loss
4 new

Number of branches present in paleo-endemic grid cells (N=73)

1. *Eucalyptus* (5 sp.) southwest Western Australia

2. *Corymbia* (3 sp.) southeast Queensland

0.03