

1 Short title: Genetic and phenotypic spatial patterns in California oaks

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3 **Association of genetic and phenotypic variability with geography and climate in three**  
4 **southern California oaks (Fagaceae)<sup>1</sup>**

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21 <sup>1</sup>Manuscript received \_\_\_\_\_; revision accepted \_\_\_\_\_.

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23 The authors thank the members of the Sork lab who have helped with field sampling over the  
24 years. PFG received post-doctoral support from a UCLA research award to VLS. During this  
25 work JO was supported by José Castillejo and Severo Ochoa (EBD) (SEV-2012-0262) research  
26 fellowships. This work received UCLA research support to VLS.

27

28 **ABSTRACT**

29 *Premise of the study:* Geography and climate shape the distribution of organisms, their  
30 genotypes, and their phenotypes. To understand historical and future evolutionary and ecological  
31 responses to climate, we compared the association of geography and climate of three oak species  
32 (*Quercus engelmannii*, *Quercus berberidifolia*, and *Quercus cornelius-mulleri*) in an  
33 environmentally heterogeneous region of southern California at three organizational levels:  
34 regional species distributions, genetic variation, and phenotypic variation.

35 *Methods:* We identified climatic variables influencing regional distribution patterns using species  
36 distribution models (SDMs), and then tested whether those individual variables are important in  
37 shaping genetic (microsatellite) and phenotypic (leaf morphology) variation. We estimated the  
38 relative contributions of geography and climate using multivariate redundancy analyses (RDA)  
39 with variance partitioning.

40 *Key results:* The SDM of each species was influenced by climate differently. Our analysis of  
41 genetic variation using RDA identified small but significant associations between genetic  
42 variation with climate and geography in *Q. engelmannii* and *Q. cornelius-mulleri*, but not in *Q.*  
43 *berberidifolia*, and climate explained more of the variation. Our analysis of phenotypic variation  
44 in *Q. engelmannii* indicated that climate had more impact than geography, but not in *Q.*  
45 *berberidifolia*. Throughout our analyses, we did not find a consistent impact due to the same  
46 climate variable.

47 *Conclusions:* Our comparative analysis illustrates that climate influences tree response at all  
48 organizational levels, but the important climate factors vary depending on the level and on the  
49 species. Because of these species-specific and level-specific responses, today's sympatric  
50 species are unlike to have similar distributions in the future.

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52 Key words: California; climate; genetic variation; geography; isolation by distance; isolation by  
53 environment; microsatellite markers; morphology; *Quercus*; species distribution modeling

54 Climate impacts plant species on multiple levels of biological organization and scale—  
55 geographic distribution, genetic composition, and phenotype. At the broadest scales,  
56 physiological tolerances to climatic conditions define global patterns of species distribution (e.g.,  
57 Woodward, 1987). Climate also affects historical demographic events, such as population  
58 expansion and contraction, and migration (Awise, 2000), which in turn influence the fine scale  
59 structure of species distributions. In a similar manner, the genetic composition of a population  
60 can be shaped by both climate and evolutionary history (Awise, 2000). For example, Gugger,  
61 Ikegami, and Sork (2013) found evidence that current and historical climate at the last glacial  
62 maximum (~20,000 years ago) was associated with the genetic composition of valley oak,  
63 *Quercus lobata*, more ~~that~~ its geographic location. They propose that climate could have  
64 influenced gene flow through local expansion-contraction dynamics and flowering phenology  
65 and/or reinforced local adaptation by selecting against immigrants from populations with  
66 different climates. In fact, in a recent survey, over 70% of the studies indicated that the  
67 environment was important in ~~the movement of genes~~ (Sexton, Hangartner, and Hoffmann,  
68 2014). Finally, climate and history can both shape phenotypic variation within a species  
69 (Stebbins, 1950). Populations found in the same climate may share phenotypes because of local  
70 adaptation or phenotypic plasticity or because of their common ancestry (West-Eberhard, 1989a;  
71 Marais, Hernandez, and Juenger, 2013). At all three levels, the movement of individuals and  
72 genes determines the range of species, their genetic composition, and their phenotypes.

73 The geographic distribution of a species reflects the complex interplay of evolutionary  
74 and ecological processes influenced by limiting environmental conditions as well as dispersal  
75 and extinction dynamics (Brown, Stevens, and Kaufman, 1996; Gaston, 2003). The strength and  
76 type of environmental influences on species distribution varies with scale, often hierarchically,

77 with abiotic factors such as climate dominating at coarse scales and biotic interactions at fine  
78 scales (Woodward and Williams, 1987; Pearson and Dawson, 2003; Guisan and Thuiller, 2005;  
79 Soberon, 2007). Species distribution modeling (SDM), which relates species occurrence data  
80 with environmental information, allows the prediction of species geographic distributions  
81 (Guisan and Thuiller, 2005; Elith and Leathwick, 2009; Franklin, 2009) and can be used to test  
82 hypotheses about the important climatic factors influencing various ecological and evolutionary  
83 processes on the landscape. However, it is critical that the scale of modeling and data match the  
84 scale of processes under investigation, as the nature and shape of species–environment  
85 relationships are scale dependent (Guisan and Thuiller, 2005). Furthermore, because populations  
86 within a species can also vary in their response to climate (Rehfeldt et al., 2002), species with  
87 broad ranges that cross many climatic regions may exhibit different relationships with climate  
88 when modeled at regional versus species-wide scales (e.g. Sork et al., 2010). Thus, it may be  
89 more appropriate to focus on regional patterns of species distribution when examining climatic  
90 influences across multiple biological processes, especially in areas of high environmental  
91 heterogeneity.

92         Recently SDM has been applied to landscape genetics (referred to as Ecological Niche  
93 Modeling, ENM) to investigate the association of genetic variation with environmental gradients  
94 and make inference about the role of gene flow and selection (Kozak and Wiens, 2006;  
95 Freedman et al., 2010; Sork et al., 2010; Ortego et al., 2012; Poelchau and Hamrick, 2012).  
96 These studies often use model predictions, referred to as habitat or climatic suitability, as a single  
97 integrated measure of multiple complex environmental factors, which is then assessed in terms of  
98 its influence on genetic patterns. At a regional level, genetic patterns are determined either  
99 through restricted gene flow, creating isolation by distance (IBD) (Wright, 1943; Slatkin, 1993)

100 or isolation by environment (IBE) whereby gene flow is higher among similar environments due  
101 to selective forces or ecological barriers restricting movement (Andrew et al., 2012; Shafer and  
102 Wolf, 2013; Sexton, Hangartner, and Hoffmann, 2014; Wang and Bradburd, 2014). For example,  
103 climate can influence mating patterns when phenological differences among populations lead to  
104 assortative mating, as has been shown in some tree species (Soularue and Kremer, 2014).  
105 Alternatively, immigrants not adapted to local climatic conditions may be selected against,  
106 resulting in a positive relationship between adaptive divergence and genetic differentiation, a  
107 pattern also known as isolation by adaptation (IBA) (Nosil, Egan, and Funk, 2008 and citations  
108 therein; Andrew et al., 2012).

109         Geographic patterns of phenotypic variation also reflect the influence of the environment  
110 (Stebbins, 1950). Many traits will have diverged across sites in response to environmental  
111 gradients, creating locally adaptive genetic differences driven by selective forces (e.g., Clausen,  
112 Keck, and Hiesey, 1947; Endler, 1986; Savolainen, Pyhajarvi, and Knurr, 2007). For example,  
113 Ramírez-Valiente et al. (2009) show differentiation in ecophysiological traits related to drought  
114 stress (specific leaf area, leaf size, and nitrogen leaf content) among populations of cork oak  
115 (*Quercus suber*) along a climatic gradient. Such traits are likely to have ~~genes underlying those~~  
116 ~~traits~~, but they may also reflect phenotypic plasticity (Bradshaw, 1965; West-Eberhard, 1989b;  
117 Scheiner, 1993; Nicotra et al., 2010). Therefore, while an association of phenotype with  
118 environmental gradients provides initial evidence that traits may be under selection (Endler,  
119 1986; Linhart and Grant, 1996), additional evidence is needed to identify an underlying genetic  
120 basis (Anderson, Willis, and Mitchell-Olds, 2011).

121         The overall goal of this study is to analyze the association of climate in three levels of  
122 biological organization—the species distribution, its genetic composition, and its phenotypic

123 variation for one tree oak, *Quercus engelmannii* Greene, and two scrub oaks, *Q. berberidifolia*  
124 Liebm. and *Q. cornelius-mulleri* Nixon & K. P. Steele (Fagaceae). First, we use SDM to identify  
125 the climatic variables important in shaping regional distribution patterns for each of the three  
126 species. Second, we assess the relative impacts of climate and geography on genetic and  
127 phenotypic variation using redundancy and partial redundancy models (Legendre and Fortin,  
128 2010; Legendre and Legendre, 2012). Third, we investigate whether the climate variables  
129 important in defining regional patterns of species distribution also shape landscape-level patterns  
130 of genetic and phenotypic variation. Given that these three species co-occur in an  
131 environmentally heterogeneous region of southern California, each has an opportunity to be  
132 shaped by strong environmental differences at relatively fine spatial scales. Previous work has  
133 shown that environmental heterogeneity promoted genetic differentiation in *Q. engelmannii*  
134 (Engelmann oak) (Ortego et al., 2012) and that climate plays a role in the persistence of hybrids  
135 between *Q. engelmannii* and co-occurring scrub oaks (Ortego et al., 2014). Here we add  
136 morphological data to our analyses and utilize different statistical approaches to investigate how  
137 much climate, independent of geography, shapes genetic and phenotypic differences between  
138 these species. We discuss similarities and differences in the roles of climate and geography  
139 among species, lending insight into the response of these currently co-occurring species to future  
140 climates.

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## MATERIALS AND METHODS

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144

145

***Study species and field sampling***—We focus our study on three oak species in southern California (USA). *Quercus engelmannii* (Engelmann oak) is a rare oak species found in southern



146 California and northwestern Baja California (Mexico) and has one of the smallest ranges of any  
147 California oak species (Scott, 1991; Roberts, 1995). These large, single stemmed trees grow to  
148 5–25 m and have leaves that are oblong to ovate, abaxially pubescent, and pale blue-green in  
149 color (Baldwin, Goldman, and Vorobik, 2012). Additionally, *Q. engelmannii* is drought-tolerant,  
150 occurring in dry, open oak woodlands and mostly interior cismontane foothills below 1300 m  
151 (Scott, 1991; Roberts, 1995). This oak hybridizes with sympatric species in the scrub oak  
152 complex, including the two other study species (J Ortego and VL Sork, unpublished data).  
153 *Quercus berberidifolia* (California scrub oak) and *Q. cornelius-mulleri* (Muller’s oak) are multi-  
154 stemmed with spiny or very pubescent leaves with fewer spines (Roberts, 1995). The abaxial leaf  
155 surface of *Q. cornelius-mulleri* has particularly dense stellate trichomes. *Quercus berberidifolia*  
156 is widespread in southern California, tending to occur in more mesic habitats compared to *Q.*  
157 *cornelius-mulleri*, which is restricted to dry washes and slopes, typically on granitic soils, in the  
158 interior desert margins and juniper-piñon woodlands of southern California and northern Baja  
159 California (Nixon, 2002). Both scrub oak species are considered drought-tolerant (Pavlik et al.,  
160 1991).

161 Oaks were sampled across southern California where the ranges of all three species  
162 partially overlap from southern Los Angeles County to the international border with Mexico.  
163 During 2008–2011, we sampled leaf tissues from 343 total adult trees, 2–15 trees across 31  
164 localities (Table 1, Fig. 1) as described in Ortego et al. (2012) and Ortego et al. (2014). Spatial  
165 coordinates of each individual tree were recorded using a Global Positioning System (GPS) unit.  
166 Leaf samples for genetic analyses were stored frozen (–20 °C) and samples for morphological  
167 measurements were dried. We selected 291 individual trees genetically assigned to one of the

168 three study species (see below) for subsequent analysis, 174 of which were also measured for  
169 morphological leaf traits.

170

171 ***Species distribution modeling***—We used SDM to identify the climatic factors  
172 influencing regional patterns of oak species distribution and predict the geographic distribution  
173 of climatically suitable habitat. Occurrence data were obtained from oak sampling sites and  
174 digitized herbarium records collected since 1900 downloaded from the Consortium of California  
175 Herbaria on January 18, 2015 (CCH; <http://ucjeps.berkeley.edu/consortium/>). For *Q.*  
176 *berberidifolia*, which is broadly distributed throughout the state, we only modeled the southern  
177 portion of the species range that partially overlaps with *Q. engelmannii* and *Q. cornelius-mulleri*.  
178 To ensure high quality of herbarium record data, we excluded records of planted or cultivated  
179 individuals and any records having  $\geq 2.5$  km error or uncertainty associated with the geo-  
180 referenced location. We also excluded obvious species misidentifications. Occurrences were then  
181 thinned to one record per grid cell of the climatic data. The final numbers of occurrence records  
182 used for modeling were 367 for *Q. engelmannii*, 497 for *Q. berberidifolia*, and 238 for *Q.*  
183 *cornelius-mulleri*.

184 We obtained 30-year averages of contemporary (1951–1980) climate data from the  
185 California Basin Characterization Model (BCM; Flint and Flint, 2012; Flint et al., 2013), which  
186 applies a regional water-balance model to simulate hydrologic responses to climate at high (270  
187 m) resolution. We calculated 19 bioclimatic variables (Nix, 1986) from the monthly BCM  
188 temperature and precipitation data, which are downscaled from the parameter–elevation  
189 regressions on independent slopes model (PRISM; Daly, Neilson, and Phillips, 1994). We  
190 selected a subset of variables to use in SDMs that: (1) are important drivers of western US plant

191 distributions (Stephenson, 1998; Rehfeldt et al., 2006), (2) maximize model performance, and (3)  
192 minimize correlations between variables (Pearson's  $r < 0.8$ ). These eight climatic variables were:  
193 minimum winter temperature (Tmin), calculated as the average minimum temperature over the  
194 coldest months (December-February); summer maximum temperature (Tmax), calculated as the  
195 average maximum temperature over the hottest months (June-August); temperature seasonality  
196 (Bio4); precipitation seasonality (Bio15); summer precipitation (precipitation of the warmest  
197 quarter; Bio18); winter precipitation (precipitation of the coldest quarter; Bio19); climatic water  
198 deficit (CWD); and actual evapotranspiration (AET). Climatic water deficit is the evaporative  
199 demand exceeding soil moisture, or the difference between potential and actual  
200 evapotranspiration, and can be interpreted as a measure of drought stress (Stephenson, 1998;  
201 Flint et al., 2013). Because the BCM climate data does not include Mexico, we were unable to  
202 include the southernmost distributional limit of the three species in northwestern Baja California.

203 We modeled the contemporary species-climate relationship for each oak species using  
204 MaxEnt (Phillips, Anderson, and Schapire, 2006), a maximum-entropy modeling method tailored  
205 for presence-only species data that is robust to irregularly sampled data, such as herbarium  
206 records (Elith et al., 2006; Loiselle et al., 2008; Phillips et al., 2009). Models were run using  
207 linear, quadratic, and product features in MaxEnt. We used a targeted background consisting of  
208 CCH herbarium records for all California plant taxa to control for the effects of sampling bias  
209 from occurrence records and to improve model performance (Phillips et al., 2009; Kramer-  
210 Schadt et al., 2013). To limit our models to the environmental conditions likely sampled by the  
211 species and thus most relevant in driving distributional patterns (VanDerWal et al., 2009; Barbet-  
212 Massin et al., 2012), we used a 100 km buffer around species occurrences as the spatial domain.  
213 We evaluated overall model performance using the area under the receiver operator curve (AUC)

214 statistic (Fielding and Bell, 1997; but see Lobo, Jimenez-Valverde, and Real, 2008) averaged  
215 over five-fold cross-validation replicates. Predicted climatic habitat suitability maps were  
216 produced for each species using MaxEnt's logistic output, which provide an estimate of  
217 probability of presence ranging from 0 (low suitability) and 1 (high suitability) in geographic  
218 space. We identified important climatic variables using MaxEnt's metrics of variable  
219 contribution and permutation importance. Because these metrics are sensitive to correlations  
220 among variables, we also used MaxEnt's jackknife tests of variable importance which calculate  
221 the (1) predictive power measured as the model gain of individual variables when used in  
222 isolation and (2) the unique contribution of individual variables measured as the drop in model  
223 gain when a variable is excluded from the model.

224

225         **Genotyping**—To confirm the species classification of our 343 samples with putative field  
226 identifications, applying laboratory methods commonly used in our lab (Sork et al., 2002; Grivet  
227 et al., 2008), we used nine polymorphic microsatellite markers developed for other *Quercus*  
228 species: QpZAG7, MSQ4, QpZAG9, QpZAG36, QpZAG110, QrZAG20, QM69-2M1,  
229 QpZAG1/5, and QrZAG1 (Steinkellner et al., 1997; Kampfer et al., 1998).

230         To conduct our multivariate analyses, we transformed single locus genotypes into allelic  
231 variables by assigning a score of 0, 0.5, or 1, depending on whether the individual possessed  
232 homozygous or heterozygous alleles at that locus (Westfall and Conkle, 1992). The number of  
233 single variables created at each locus is the number of alleles minus one, which yielded 248  
234 allelic variables. We then used principal component analysis implemented in PROC PRINCOM  
235 in SAS (SAS Institute 1989) to reduce the 248 variables into a smaller set of 50 orthogonal axes.  
236 With these data, we reassigned the field species identifications of all individuals based on

237 assignments of canonical discriminant analysis (CDA) implemented in PROC DISCRIM, which  
238 also estimated the percentage of each individual's genotype that was assignable to one of the  
239 three species. We assigned an individual to a single species if its genetic assignment was at least  
240 90% associated with that species. This classification, which resulted in 157 *Q. engelmannii*, 91  
241 *Q. berberidifolia*, and 43 *Q. cornelius-mulleri* individuals, did not differ notably from the results  
242 based on STRUCTURE (Ortego et al., 2014), except that we divided the scrub oaks into separate  
243 species as justified by our CDA, and excluded hybrids from analyses. These multi-locus  
244 genotypes were used in subsequent statistical analyses (as described below).

245

246 ***Morphological Traits***—We analyzed phenotypic variation in leaf morphology of 174  
247 individuals assigned to a single species (109 *Q. engelmannii*, 53 *Q. berberidifolia*, and 12 *Q.*  
248 *cornelius-mulleri*). Leaf measurements included: lamina width, lamina length, petiole length,  
249 lamina thickness, number of veins, number of leaf lobes, leaf spines, abaxial leaf trichome  
250 density, and adaxial leaf pubescence density. Lamina width was measured as the widest part of  
251 the leaf for entire leaves or the width from the largest lobe to the main vein for leaves with lobed  
252 or toothed margins. Lamina length was measured from the bottom of the leaf (excluding the  
253 petiole) to the end of the blade. Petiole length was measured from the bud to the base of the leaf.  
254 Lamina thickness was measured in a portion of the leaf without veins using a micrometer.  
255 Number of veins was measured abaxially and only included the first veins expanding from the  
256 main vein. Number of leaf lobes was a summation of curved or rounded projections occurring  
257 along the leaf margin. We recorded the presence or absence of teeth surrounding the leaf (leaf  
258 spines). We used an index of trichome density, which was quantified under a dissecting scope,  
259 using a scale from 1 (few trichomes) to 6 (high trichome density), following other studies in oaks

260 (Kissling, 1977; Kremer et al., 2002). We calculated an additional variable, petiole ratio (petiole  
261 length/ (petiole length + lamina length)) to normalize for differences in leaf size across  
262 individuals. We averaged measurements across three mature leaves collected per individual tree.  
263 For statistical analyses (see below) we log<sub>10</sub>-transformed the variables lamina width, lamina  
264 length, lamina thickness, and petiole ratio to correct for skew.

265  
266 ***Statistical Analyses***—We measured the similarity between predictions of climatic habitat  
267 suitability between pairs of oaks species using two estimates of niche overlap, Schoener’s *D*  
268 (Schoener, 1968) and Warren’s *I* statistic (Warren, Glor, and Turelli, 2008). Both measures range  
269 from 0 (completely discordant SDMs) to 1 (identical SDMs) and were calculated from MaxEnt’s  
270 raw suitability scores. We then used the niche identity test statistic (Warren, Glor, and Turelli,  
271 2008) with 100 pseudoreplicates to determine if the SDMs of species pairs were more different  
272 than expected if they were drawn from the same underlying distribution (i.e., the pooled sample  
273 of occurrence points from both species). A rejection of the null hypothesis indicates species  
274 models are climatically distinct and is suggestive of distinct climatic niches. Niche overlap  
275 calculations and identity tests were implemented in R with the ‘niche.equivalency.test’ function  
276 in the *phyloclim* package (Heibl, 2011).

277 To test the genetic and morphological differences among species, we conducted two  
278 separate canonical discriminant analyses (Proc CANDISC, SAS v9). First, we examined the  
279 genetic differences using the 291 multilocus genotypes assigned to a given species. Then, we  
280 tested whether the three species differed morphologically based on eight leaf traits: lamina width,  
281 lamina length, petiole ratio, and lamina thickness, number of leaf veins, number of leaf lobes,  
282 adaxial leaf pubescence, and abaxial leaf trichome density measured for 174 individuals.

283 To examine genetic structure within each species, we first conducted AMOVA and  
284 calculated pairwise  $F_{ST}$  among sites in GenAlEx 6.5 (Peakall and Smouse, 2012) using the nine  
285 microsatellite markers. A few sample sites had one or two samples and were grouped following  
286 Ortego et al. (2014), or otherwise discarded from these analyses. We then tested for isolation by  
287 distance using Mantel tests of geographic distance, calculated assuming the WGS84 spherical  
288 model of the Earth, versus pair-wise genetic distance of subpopulations estimated by  $F_{ST}$ . We  
289 tested for isolation by environment for each species individually using partial Mantel tests of  
290 genetic distance with environmental distance controlling for geographic distance. Environmental  
291 distance was calculated as Euclidean distance among pairs of sample sites based on the centered  
292 and scaled climate variables used in the SDM modeling. Each test was performed ~~in~~ in R 3.1.2  
293 (R Core Development Team) based on 1000 permutations, except for *Q. cornelius-mulleri*,  
294 which was based on 120 permutations due to small sample size.

295 We further investigated the effects of climate and geography on neutral genetic structure  
296 for each species using a series of full and partial redundancy analyses (RDA) with variance  
297 partitioning. Redundancy analysis, a form of constrained ordination, is the canonical extension of  
298 multiple linear regression to multivariate response data in which the canonical axes built from  
299 linear combinations of response data are also constrained to be linear combinations of the  
300 explanatory variables (Legendre and Legendre, 2012). Redundancy analysis has proven more  
301 powerful in detecting complex species-environment relationships and spatial structures in  
302 multivariate genetic data than Mantel tests or regression on distance matrices when response and  
303 explanatory variables are not limited to distance measures (Legendre and Fortin, 2010; Guillot  
304 and Rousset, 2013). We used the 248 allelic variables created from the nine microsatellite loci as  
305 the response matrix (Smouse and Williams, 1982) for RDA models of genetic structure. We

306 divided explanatory variables into two matrices (1) climatic, consisting of the same eight  
307 variables identified in SDMs, and (2) geographic, consisting of the five variables of first- and  
308 second-order orthogonal polynomials calculated from the centered latitude and longitude of the  
309 oak sampling localities using the ‘poly’ function in the R package *stats*. To reduce geographic  
310 and climatic matrices to their most relevant and significant components, we applied a stepwise  
311 forward model selection process with the Blanchet, Legendre, and Borcard (2008) double  
312 stopping criterion to individual models of geographic and climatic explanatory matrices for each  
313 species (Borcard, Gillet, and Legendre, 2011).

314 To disentangle the effects of geography and climate on genetic structure, we ran three  
315 different RDAs for individual species: (1) a full model including both climatic and geographic  
316 explanatory variables identified in the forward selection procedure (climate + geography), (2) a  
317 partial model of climatic variables controlling for geographic effects (climate | geography), and  
318 (3) a partial model of geographic variables controlling for climatic effects (geography | climate).  
319 We then used variance partitioning to calculate the proportions of variation in genetic structure  
320 that are explained by the independent contributions of climate and geography (Borcard,  
321 Legendre, and Drapeau, 1992; Peres-Neto et al., 2006). The pure climatic contribution was  
322 calculated as the proportion of explained variance in the full RDA (climate + geography) and  
323 also explained by the partial (climate | geography) RDA. The pure geographic contribution was  
324 calculated as the proportion of explained variance in the full RDA, also explained by the partial  
325 (geography | climate) RDA. Finally, we calculated the geographic component of climatic  
326 influence, or joint contribution of climate and geography (climate  $\cap$  geography), as the  
327 remaining explained variance in the full RDA not contributed to either pure climatic or  
328 geographic effects. For each model, we determined the overall model significance and marginal



329 significance of individual explanatory variables using permutation tests with a minimum of 1000  
330 permutations. We calculated the adjusted coefficient of multiple determination ( $R^2_{adj}$ ) for full  
331 models and the individual geographic and climatic components of variance (Peres-Neto et al.,  
332 2006). Mantel tests, RDA, and tests for the significance of explanatory variables were  
333 implemented in R using the *vegan* package (Oksanen et al., 2015). Stepwise forward selection  
334 with the Blanchet et al. (2008) double stopping criterion was implemented in R with the  
335 ‘forwardsel’ function in the *packfor* package (Dray, Blanchet, and Legendre, 2013).

336 We repeated full and partial RDAs on morphological data for *Q. engelmannii* and *Q.*  
337 *berberidifolia*, but excluded *Q. cornelius-mulleri* due to a small sample size of individuals with  
338 morphological measurements. As in the CDA, we  $\log_{10}$ -transformed variables of lamina width,  
339 lamina length, petiole ratio, and lamina thickness to correct for skew and excluded the variable  
340 for leaf spines due to correlation with other morphological variables and issues with non-  
341 normality. All morphological variables were centered and standardized prior to RDA.

342

## 343 RESULTS

344

345 ***Species distribution models***—Predicted climatic habitat suitability maps were consistent  
346 with the known distributions of each oak in southern California. High AUC scores for all three  
347 species;  $0.890 \pm 0.0098$  (mean  $\pm$  standard deviation) for *Q. engelmannii*,  $0.791 \pm 0.0176$  for *Q.*  
348 *berberidifolia*, and  $0.931 \pm 0.0101$  for *Q. cornelius-mulleri*; indicated overall high model  
349 performance. Although species have high geographic overlap (Fig. 1), the results from pairwise  
350 **Niche Identity Tests** indicate that the habitat suitability of each species is climatically distinct ( $D$ :  
351  $P < 0.001$ ;  $I$ :  $P < 0.001$  for all pairwise species tests), suggesting distinct climatic niches.

352 Overlap in climatic suitability was high between *Q. engelmannii* and *Q. berberidifolia* ( $D =$   
353  $0.612$ ;  $I = 0.864$ ), and low between *Q. berberidifolia* and *Q. cornelius-mulleri* ( $D = 0.180$ ;  $I =$   
354  $0.409$ ) and *Q. engelmannii* and *Q. cornelius-mulleri* ( $D = 0.138$ ;  $I = 0.327$ ). The contribution of  
355 individual climatic variables to SDMs varied across species (Table 2). Jackknife tests identified  
356 temperature seasonality (Bio 4) as highly important in determining *Q. engelmannii* and *Q.*  
357 *berberidifolia* habitat suitability, having both the greatest predictive power when used in  
358 isolation, and the greatest unique information not present in the other climatic variables. Climatic  
359 water deficit and AET also had high contributions to habitat suitability models for both species.  
360 In contrast, summer precipitation (Bio 18) was the single most important variable for *Q.*  
361 *cornelius-mulleri*, having greatest predictive power when used in isolation, and the greatest  
362 information not present in the other climatic variables.

363  
364 ***Genetic and morphological differences among oak species***—Canonical discriminant  
365 analysis revealed that the three species differed based on multilocus genotypes for both canonical  
366 axes (Table 3, Fig. 2A). This result is expected because we pre-screened these genotypes to be  
367 90% assignable to one of three species, although we obtained the same result using field  
368 identifications and not omitting hybrid individuals. Using the genetically based species  
369 assignments, we found that the multivariate leaf morphology differed significantly among the  
370 three species for both canonical axes (Table 3). For morphology, there was much greater  
371 variation within the species compared to variation in genotype, with some individuals falling  
372 within the distribution of a different species (Fig. 2B). The first CDA axis distinguished between  
373 *Q. engelmannii* and *Q. cornelius-mulleri* and was most highly correlated with abaxial leaf

374 trichome density and lamina length. The second CDA axis separated *Q. cornelius-mulleri* from  
375 the other two oaks and was most highly correlated with adaxial leaf pubescence.

376

377 ***Genetic structure and tests of isolation by distance***—Overall, each species had low  
378 values of population differentiation ( $F_{ST} = 0.03$  for *Q. engelmannii*;  $F_{ST} = 0.02$  for *Q.*  
379 *berberidifolia*; and  $F_{ST} = 0.05$  for *Q. cornelius-mulleri*). We found evidence for isolation by  
380 distance and isolation by environment in only one species, *Q. cornelius-mulleri*, which exhibited  
381 significant correlation between genetic distance ( $F_{ST}$ ) and geographic distance (Mantel test;  $r =$   
382  $0.54$ ,  $P = 0.05$ ), and between environmental distance defined by climate variables and genetic  
383 distance controlling for geographic distance (partial Mantel test:  $r = 0.76$ ,  $P = 0.04$ ). We did not  
384 find significant correlations in the other two species ( $-0.17 < r < 0.09$ ;  $P > 0.26$ ).

385

386 ***Effect of geography and climate on genetic structure***—Full RDA models of combined  
387 geographic and climatic variables explained a small but significant portion of variation in allelic  
388 frequencies for *Q. engelmannii* (RDA;  $R^2_{adj} = 2.8\%$ ,  $P = 0.001$ ) and *Q. cornelius-mulleri* (RDA;  
389  $R^2_{adj} = 7.4\%$ ,  $P = 0.001$ ), but not for *Q. berberidifolia* (RDA;  $R^2_{adj} = 0.6\%$ ,  $P = 0.064$ ) (Table  
390 4A). In the first two species, we found significant unique associations between genetic variation  
391 and climate (climate | spatial) and geography (spatial | climate) (partial RDA; all  $P < 0.01$ ). For  
392 *Q. engelmannii*, five climatic variables were significantly associated with genetic variation,  
393 temperature seasonality, precipitation seasonality, winter precipitation, AET, and CWD, with  
394 both precipitation seasonality and AET retaining significance after controlling for geography  
395 (Table 4B). For *Q. cornelius-mulleri* precipitation seasonality, winter precipitation, AET, and  
396 summer maximum temperature were significantly associated with genetic variation, with all but

397 AET retaining significance after controlling for geography. Additionally, climate had a greater  
398 unique contribution to genetic variation compared to geography (53.6% versus 33.2% for *Q.*  
399 *engelmannii* and 48.3% versus 35.4% for *Q. cornelius-mulleri*). We found a similar trend of  
400 greater contribution of climate to genetic variation compared to geography in *Q. berberidifolia*,  
401 though the individual unique contributions were not statistically significant ( $P > 0.20$ ).  
402 Precipitation seasonality significantly associated with genetic variation in *Q. berberidifolia*, but  
403 not after controlling for geography. The proportion of genetic variation explained by climate that  
404 was also spatially structured (spatial  $\cap$  climate) was similar across all three oaks (12–16%)  
405 (Table 4A).

406

407 ***Effects of geography and climate on morphological traits***—Full RDA models of  
408 combined geographic and climatic variables explained a significant portion of variation in leaf  
409 morphology for both *Q. engelmannii* (RDA;  $R^2_{adj} = 0.127$ ,  $P = 0.001$ ) and *Q. berberidifolia*  
410 (RDA;  $R^2_{adj} = 0.058$ ,  $P = 0.005$ ) and explained a higher portion of morphological variation  
411 compared to genetic variation (Table 5A). Partial RDAs identified unique, significant  
412 associations between climate and morphological variation in both species after controlling for  
413 geographic effects (climate | spatial) (*Q. engelmannii*:  $R^2_{adj} = 0.014$ ,  $P = 0.04$ ; *Q. berberidifolia*:  
414  $R^2_{adj} = 0.026$ ,  $P = 0.028$ ). Precipitation seasonality and summer precipitation were significantly  
415 associated with morphological variation in *Q. engelmannii*, but only summer precipitation  
416 remained significant after controlling for geography (Table 5B). In *Q. engelmannii*, geography  
417 (51.3%) had a greater unique contribution relative to climate (19.0%). Additionally, a large  
418 (29.7%) proportion of the morphological variation in *Q. engelmannii* explained by climate was  
419 also spatially structured (spatial  $\cap$  climate). In contrast, climate had a greater contribution

420 (45.9%) to morphological variation compared to geography (37.8%) in *Q. berberidifolia*,  
421 however, the unique contribution of geography, was not significant (Table 5A,  $P = 0.068$ ) after  
422 controlling for climate. Only one climatic variable, maximum summer temperature significantly  
423 contributed to morphological variation (Table 5B).

425 ***Contribution of individual climate variables to habitat suitability, genetic structure,***

426 ***and morphology***—We found all three oak species differed in the contribution of individual

427 climatic variables to habitat suitability, genetic structure, and leaf morphology (Table 6).

428 Variables most important in defining climatic suitability were not necessarily significantly

429 associated with genetic structure or leaf morphology. For example, summer precipitation

430 (Bio18), which was the single most important variable contributing to habitat suitability in *Q.*

431 *cornelius-mulleri*, was not significantly associated with genetic variation in the species.

432 Precipitation seasonality (Bio15) was significantly associated with genetic variation in all three

433 species but had low contribution to species distribution models.

434 For *Q. engelmannii*, variables related to water balance (AET, CWD) and temperature

435 seasonality had important contributions to both habitat suitability and genetic variation, whereas

436 precipitation seasonality and summer precipitation (Bio18) had the greatest contributions to leaf

437 morphology. For *Q. berberidifolia*, the contribution of individual climate variables to habitat

438 suitability was similar to that of *Q. engelmannii*—temperature seasonality and water balance

439 variables (AET, CWD). Climatic influences on genetic variation, however, were weak and lost

440 entirely after controlling for geographic effects. The species also differed in climatic associations

441 with morphology with summer maximum temperature having a strong contribution to variation

442 in leaf morphology. *Quercus cornelius-mulleri* was most distinct in its ~~habitat suitability~~, with

443 particularly a high contribution of summer precipitation, and to a lesser extent winter minimum  
444 and summer maximum temperatures. Summer maximum temperature also contributed to genetic  
445 variation in the species, along with precipitation seasonality, winter precipitation, and AET.  
446 Thus, the climatic factors influencing habitat suitability and regional distribution patterns  
447 differed from those influencing genetic and morphological variation in all three oaks, indicating  
448 species-specific responses to different climatic factors.

449

450

## DISCUSSION

451

452 Climate shaped regional patterns of geographic distribution, neutral genetic variation, and  
453 morphological variation of the three southern California oak species in different ways. Species  
454 differed notably in the specific climatic variables influencing regional patterns of distribution,  
455 despite a high degree of geographic overlap. Our use of SDMs identified individual climate  
456 variables that shaped habitat suitability, and we utilized the climate variables directly to assess  
457 the association of climate with species' distributions. As we examined the importance of climate  
458 variables to genetic and morphological spatial patterns, controlling for geography, we found that  
459 climate has an independent role in shaping patterns of geographic variation in genetic and  
460 phenotypic variation and that different climate variables were important at each level of  
461 biological organization.

462

463 *Species Distribution Models*—SDM revealed species-specific differences in the climatic  
464 factors influencing regional patterns of distribution of the three oak species in southern  
465 California. Not surprisingly, the two species with the greatest geographic overlap also had the

466 greatest similarity in the importance of individual climatic variables to habitat suitability (e.g.,  
467 shared importance of temperature seasonality, CWD, and AET for both *Q. engelmannii* and *Q.*  
468 *berberidifolia*). In contrast, summer precipitation was most important in defining habitat  
469 suitability for *Q. cornelius-mulleri*, which has the most interior distribution of all three oaks,  
470 occurring in dry washes and slopes in desert margins and juniper-piñon woodlands of inland  
471 southern California. We found the use of individual climatic variables identified by SDMs was  
472 much more informative in identifying important climatic associations with genetic and  
473 morphological variation than a single, integrated measure like that of habitat suitability. Indeed,  
474 partial ~~mantel~~ tests and constrained ordinations where habitat suitability scores were substituted  
475 for individual climatic variables failed to explain significant variation in either genetic structure  
476 or leaf morphology (results not shown). These findings suggest careful consideration is  
477 necessary before applying SDMs and single habitat suitability metrics to landscape genetic  
478 studies.

479

480 ***Genetic structure--geography versus climate***—Despite the fact that southern California  
481 is a topographically and climatically complex region (Vandergast et al., 2008), we found only  
482 subtle genetic structure across populations within each species (all three species have  $F_{ST} <$   
483 0.05). These values are lower than those observed in other California oak studies. For example,  
484 *Quercus lobata* (valley oak) had higher levels of genetic differentiation using microsatellite  
485 markers ( $F_{ST} = 0.12$ ) (Grivet et al., 2008), possibly due to a species-wide rather than regional  
486 focus for sampling. However, higher levels of genetic structure ( $F_{ST} = 0.16$ ) in *Q. lobata* were  
487 also found using randomly sampled single nucleotide polymorphisms (SNPs) of three  
488 populations sampled on a similar geographic scale to this study, though those populations were

489 separated by mountain ranges (Platt et al., 2015). The pattern of low genetic differentiation in  
490 southern California oaks found in our current study could reflect long-distance pollen flow or  
491 recent expansions from a common ancestral population in the region. Nonetheless, the genetic  
492 structure we find is significant among localities for each of the species, suggesting climate could  
493 have an influence on the distribution of genotypes.

494         Constrained ordinations of combined geographic and climatic variables explained only a  
495 small portion of the total genetic variation (2.8%, 0.6%, and 7.41% for *Q. engelmannii*, *Q.*  
496 *berberidifolia*, and *Q. cornelius-mulleri*, respectively). These low adjusted  $R^2$  values are not  
497 surprising given the number of other unmeasured factors, such as additional genotypes,  
498 localities, environmental variables and stochastic effects, not included in our analyses. More  
499 importantly, most genetic variation is likely within sites/samples as is commonly observed in  $F_{ST}$   
500 /AMOVA-type analyses. For example, the low values of  $F_{ST}$  that we report in this study reflects  
501 that about 5% of variation is among sites, which is what we are partitioning in the RDA. For  
502 example, for *Q. berberidifolia*, the most widely and continuously distributed of the three species,  
503  $F_{ST} = 2\%$  and in the RDA, the association between genetic variation and climate and geography  
504 was not significant. It is possible that *Q. berberidifolia* may maintain large effective population  
505 sizes and/or high gene flow among populations, which could homogenize genetic differences  
506 among populations and create large genetic variation within populations. Consequently, for this  
507 species, we cannot assess the partial associations of climate or geography on genetic variation in  
508 microsatellite loci. Because our interests lie in the explainable variation, the explained  
509 constrained variance is of greater interested. For the other two species with significant  
510 associations between genetic variation and climate/geography (*Q. engelmannii* and *Q. cornelius-*  
511 *mulleri*), we found a greater unique contribution of climate alone (54% and 61%, respectively).



512 This finding suggests that isolation by environment (climate) is influencing the distribution of  
513 genetic variation and is similar to what we reported for *Q. engelmannii* previously (Ortego et al.,  
514 2012), using causal modeling (Cushman et al., 2006) to analyze the potential influence of  
515 climatic factors. In studies examining *Q. lobata*, climate also played a strong role in multivariate  
516 genetic gradients (Sork et al., 2010; Gugger, Ikegami, and Sork, 2013). One possible explanation  
517 for the impact of climate in this heterogeneous southern California region is that gene flow from  
518 neighboring dissimilar habitats may be disfavored (Sexton et al., 2014; Wang and Bradburd,  
519 2014), creating mosaics of genetic variation that correlates with climate variables.

520         The life histories and habitat distributions of *Quercus engelmannii* and *Q. cornelius-*  
521 *mulleri* differ sharply—*Q. engelmannii* is a tree that grows in higher elevations or more mesic  
522 slopes while *Q. cornelius-mulleri* is a desert shrub. Interestingly, they shared three climate  
523 variables that were significantly associated with multivariate genetic variation: precipitation  
524 seasonality, winter precipitation, and actual evapotranspiration. Despite these similarities, there  
525 were some differences in climatic relationships: for *Q. engelmannii*, climatic water deficit and  
526 temperature seasonality are important, and for *Q. cornelius-mulleri*, maximum temperature was  
527 important. Taken collectively, our results suggest that certain climatic factors shape genetic  
528 patterns more than spatial factors even in the presence of presumed high gene flow. Variation in  
529 the importance of specific climate variables among species suggests different aspects of  
530 environmental heterogeneity may influence gene flow and demography differently in each  
531 species.

532

533         ***Leaf morphology--geography versus climate***—We anticipated that leaf morphology  
534 would be correlated with climate, as several leaf traits in oaks improve drought response

535 (Abrams, 1990). Moreover, given that some leaf traits respond with phenotypic plasticity to the  
536 environment, morphological variation could have both genetic and non-genetic associations with  
537 climate that could be even stronger than those found for genetic variation. Indeed, the overall  
538 percent of variation explained by the two full RDA models of morphology was greater than was  
539 explained for the genetic RDA models for both *Q. engelmannii* and *Q. berberidifolia*. In *Q.*  
540 *engelmannii*, geography had a greater unique contribution to leaf morphology relative to climate.  
541 Additionally, the proportion of variance explained by climate that was spatially structured was  
542 relatively large. These strong geographic effects may be due to the fact that *Q. engelmannii* has  
543 spatially separated subpopulations that are sufficiently distinguishable to be detected as  
544 subgroups with Bayesian clustering analyses (Ortego et al., 2012). In contrast, climate had a  
545 greater unique contribution to morphological variation in *Q. berberidifolia* relative to geography.

546       Even though we find for both species that climate is significantly correlated with  
547 morphology, the association is not strong, which may be due to multiple factors—weak selection,  
548 low plasticity, extensive gene flow, and/or low intraspecific variability for the measured traits. It  
549 is also possible that we see a weak association with climate variables because we are not  
550 measuring climate at the appropriate spatial scale. Although relatively fine scale with respect to  
551 regional distribution patterns, the 270 m climate data downscaled by BCM may not capture topo-  
552 and micro-climatic variability influences local patterns of both morphological and genetic  
553 variation. Nonetheless, given that phenotypes in natural populations often show larger  
554 differences than those measured in common gardens because they include both genetic and  
555 environmental effects, our results indicate these traits may not be very genetically differentiated  
556 across this heterogeneous region, which is consistent with the low genetic structure we found  
557 using microsatellite markers.

558

559           ***Impacts of climate on species' response***—Each species varied in its relationship with  
560 individual climatic variables with respect to habitat suitability, genetic variation, and  
561 morphological variation (see Table 6). In general, the critical climate variables at all three levels  
562 of biological organization differed among species, with one exception--precipitation seasonality,  
563 which was important in explaining associations between genetic variation and climate for all  
564 three species. This finding could indicate a potential common selective pressure for the three  
565 species in southern California, where the precipitation regime is highly variable, both within and  
566 between years. Otherwise, the three species showed very species' specific patterns.

567           Given concerns about the impact of rapid climate change, it is useful to assess the extent  
568 to which certain climate variables will have an impact at multiple levels of biological process.  
569 For example, Loarie et al. (2008) predict shifts in suitable habitat for California's endemic flora  
570 that could result in multiple extinctions. Our comparative analysis here indicates that we will be  
571 unable to make predictions based on habitat suitability and regional distribution patterns about  
572 whether the critical climate variables for habitat suitability will be the same ones affecting  
573 genetic structure or phenotypic patterns. In *Q. berberidifolia*, only one of the variables,  
574 maximum summer temperature, played a role in three of the models (habitat suitability, genetic  
575 variation, morphology), and for the other species, the role of climate differed across models.  
576 Thus, we advise some caution when applying regional SDMs to make inferences about landscape  
577 genetic patterns of populations or about evolutionary and ecological responses of organisms.  
578 Because a species distribution modeling approach applies a single predictive relationship  
579 throughout the range of a species or focal region, it is unlikely to take into account local  
580 adaptation, IBE and variable responses among populations within a species range (Rehfeldt et

581 al., 2002; Rehfeldt et al., 2006). We assume that the climatic variables included in our species  
582 distribution models are limiting factors for our species (e.g., that temperature or water  
583 availability are eco-physiological limiting factors for the species) (Guisan and Thuiller, 2005),  
584 and that the spatial resolution of our environmental data is relevant to the mechanisms shaping  
585 both geographic distribution and genetic and phenotypic responses. Another limitation of any  
586 climate study is that it may overlook other important environmental factors influencing  
587 ecological and evolutionary processes, such as soil composition and biotic interactions. This  
588 problem is relevant to climate change studies because climate can affect species interactions, soil  
589 biochemistry, and many other environmental factors affected by climate. Thus, the climate  
590 variables important in predicting a species distribution do not necessarily indicate high selective  
591 pressure on individuals and therefore may not be as important in shaping migration, historical  
592 demography, or natural selection.

593

594 ***Conclusions***—Species-specific responses to different environmental factors illustrate that  
595 the drivers of genetic and phenotypic differentiation can strongly differ even among related  
596 species distributed in similar landscapes. Our findings highlight the importance of integrating  
597 genetic, phenotypic, and climatic data across multiple species and spatial scales to better  
598 understand the factors that shape demographic trajectories of populations and their responses to  
599 climate (Wiens, 1989). Our results showing differences in how environment shapes  
600 contemporary distributions, genetic variation, and phenotypic variation in these species imply  
601 that different patterns of local adaptation and therefore different local to regional responses to  
602 projected climate change are likely. As a result, even currently overlapping species with similar  
603 dispersal capabilities will not necessarily share distributions in the future. To better understand

604 the interactions of species with their climate, forthcoming research should attempt to measure  
605 climate at the same spatial scale and degree of sensitivity for the SDMs as the individual  
606 genotypic and phenotypic samples.. Due to the emergence of next generation sequencing, it now  
607 feasible to examine both neutral genetic variation that distinguishes the impacts of historical  
608 demographic processes and climate-associated selection on spatially divergent patterns of genetic  
609 variation (Sork et al., 2013). Moreover, models exist that will allow spatial modeling that  
610 combines genomic data and SDM approaches that will generate predictions about the geographic  
611 distribution of genetic data in response to climate change (Fitzpatrick and Keller, 2015). The  
612 incorporation of genetic and phenotypic responses to species distribution models will provide  
613 better predictions of the distribution of species, their genetic response to change, and the future  
614 composition of communities.

615

## 616 **LITERATURE CITED**

617

618 ABRAMS, M. D. 1990. Adaptations and responses to drought in *Quercus* species of North  
619 America. *Tree Physiology* 7: 227-238.

620 ANDERSON, J. T., J. H. WILLIS, AND T. MITCHELL-OLDS. 2011. Evolutionary genetics of plant  
621 adaptation. *Trends in Genetics* 27: 258-266.

622 ANDREW, R. L., K. L. OSTEVIK, D. P. EBERT, AND L. H. RIESEBERG. 2012. Adaptation with gene  
623 flow across the landscape in a dune sunflower. *Molecular Ecology* 21: 2078–2091.

624 AVISE, J. C. 2000. Phylogeography : the history and formation of species. Harvard University  
625 Press, Cambridge, Mass.

- 626 BALDWIN, B. G., D. H. GOLDMAN, AND L. A. VOROBİK. 2012. The Jepson Manual: Vascular  
627 Plants of California. 2nd ed. University of California Press, Berkeley.
- 628 BARBET-MASSIN, M., F. JIGUET, C. H. ALBERT, AND W. THUILLER. 2012. Selecting pseudo-  
629 absences for species distribution models: how, where and how many? *Methods in*  
630 *Ecology and Evolution* 3: 327-338.
- 631 BLANCHET, F. G., P. LEGENDRE, AND D. BORCARD. 2008. Forward selection of explanatory  
632 variables. *Ecology* 89: 2623-2632.
- 633 BORCARD, D., P. LEGENDRE, AND P. DRAPEAU. 1992. Partialling out the spatial component of  
634 ecological variation. *Ecology* 73: 1045-1055.
- 635 BORCARD, D., F. GILLET, AND P. LEGENDRE. 2011. Numerical ecology with R, xi, 306 p.  
636 Springer,, New York.
- 637 BRADSHAW, A. D. 1965. Evolutionary significance of phenotypic plasticity in plants. *Advances*  
638 *in Genetics* 13: 115-155.
- 639 BROWN, J. H., G. C. STEVENS, AND D. M. KAUFMAN. 1996. The geographic range: Size, shape,  
640 boundaries, and internal structure. *Annual Review of Ecology and Systematics* 27: 597-  
641 623.
- 642 CLAUSEN, J., D. D. KECK, AND W. M. HIESEY. 1947. Heredity of geographically and  
643 ecologically isolated races. *American Naturalist* 81: 114-133.
- 644 CUSHMAN, S. A., K. S. MCKELVEY, J. HAYDEN, AND M. K. SCHWARTZ. 2006. Gene flow in  
645 complex landscapes: testing multiple hypotheses with causal modeling. *American*  
646 *Naturalist* 168,: 486–499.

647 DALY, C., R. P. NEILSON, AND D. L. PHILLIPS. 1994. A statistical topographic model for  
648 mapping climatological precipitation over mountainous terrain. *Journal of Applied*  
649 *Meteorology* 33: 140-158.

650 DRAY, S., F. G. BLANCHET, AND P. LEGENDRE. 2013. packfor: Forward Selection with  
651 permutation (Canoco p.46), version 0.0-8/r109. website: [http://R-Forge.R-](http://R-Forge.R-project.org/projects/sedar/)  
652 [project.org/projects/sedar/](http://R-Forge.R-project.org/projects/sedar/).

653 ELITH, J., AND J. R. LEATHWICK. 2009. Species distribution models: ecological explanation and  
654 prediction across space and time. *Annual Review of Ecology, Evolution, and Systematics*  
655 40: 677-697.

656 ELITH, J., C. H. GRAHAM, R. P. ANDERSON, M. DUDIK, S. FERRIER, A. GUISAN, R. J. HIJMANS, et  
657 al. 2006. Novel methods improve prediction of species' distributions from occurrence  
658 data. *Ecography* 29: 129-151.

659 ENDLER, J. A. 1986. Natural selection in the wild, vol. 21. Princeton University Press, Princeton,  
660 N.J.

661 FIELDING, A. H., AND J. F. BELL. 1997. A review of methods for the assessment of prediction  
662 errors in conservation presence/absence models. *Environmental Conservation* 24: 38-49.

663 FITZPATRICK, M. C., AND S. R. KELLER. 2015. Ecological genomics meets community-level  
664 modelling of biodiversity: mapping the genomic landscape of current and future  
665 environmental adaptation. *Ecology Letters* 18: 1-16.

666 FLINT, L. E., AND A. L. FLINT. 2012. Downscaling future climate scenarios to fine scales for  
667 hydrologic and ecological modeling and analysis. *Ecological Processes* 1.

668 FLINT, L. E., A. L. FLINT, J. H. THORNE, AND R. BOYNTON. 2013. Fine-scale hydrologic  
669 modeling for regional landscape applications: the California Basin Characterization  
670 Model development and performance. *Ecological Processes* 2.

671 FRANKLIN, J. 2009. Mapping species distributions: spatial inference and prediction. . Cambridge  
672 University Press, New York.

673 FREEDMAN, A. H., H. A. THOMASSEN, W. BUERMANN, AND T. B. SMITH. 2010. Genomic signals  
674 of diversification along ecological gradients in a tropical lizard. *Molecular Ecology* 19:  
675 3773-3788.

676 GASTON, K. J. 2003. The structure and dynamics of geographic ranges. . Oxford University  
677 Press, Oxford, UK.

678 GRIVET, D., V. L. SORK, R. D. WESTFALL, AND F. W. DAVIS. 2008. Conserving the evolutionary  
679 potential of California valley oak (*Quercus lobata* Née): a multivariate genetic approach  
680 to conservation planning. *Molecular Ecology* 17: 139-156.

681 GUGGER, P. F., M. IKEGAMI, AND V. L. SORK. 2013. Influence of late Quaternary climate  
682 change on present patterns of genetic variation in valley oak, *Quercus lobata* Née.  
683 *Molecular Ecology* 22: 3598-3612.

684 GUILLOT, G., AND F. ROUSSET. 2013. Dismantling the Mantel tests. *Methods in Ecology and*  
685 *Evolution* 4: 336-344.

686 GUISAN, A., AND W. THUILLER. 2005. Predicting species distribution: offering more than  
687 simple habitat models. *Ecology Letters* 8: 993-1009.

688 HEIBL, C. 2011. phyloclim: Integrating Phylogenetics and Climatic Niche Modeling, version  
689 0.8.1. website: <http://CRAN.R-project.org/package=phyloclim>.



690 KAMPFER, S., C. LEXER, J. GLOSSL, AND H. STEINKELLNER. 1998. Characterization of (GA)n  
691 microsatellite loci from *Quercus robur*. *Hereditas* 129: 183-186.

692 KISSLING, P. 1977. Les poils des quatre espèces de chênes du Jura (*Quercus pubescens*, *Q.*  
693 *petraea*, *Q. robur* et *Q. cerris*). *Berichte der Schweizerischen botanischen Gesellschaft*  
694 87: 1-18.

695 KOZAK, K. H., AND J. WIENS. 2006. Does niche conservatism promote speciation? A case study  
696 in North American salamanders. *Evolution* 60: 2604-2621.

697 KRAMER-SCHADT, S., J. NIEDBALLA, J. D. PILGRIM, B. SCHRODER, J. LINDENBORN, V.  
698 REINFELDER, M. STILLFRIED, et al. 2013. The importance of correcting for sampling bias  
699 in MaxEnt species distribution models. *Diversity and Distributions* 19: 1366-1379.

700 KREMER, A., J. L. DUPOUEY, J. D. DEANS, J. COTTRELL, U. CSAIKL, R. FINKELDEY, S. ESPINELG,  
701 et al. 2002. Leaf morphological differentiation between *Quercus robur* and *Quercus*  
702 *petraea* is stable across western European mixed oak stands. *Annals of Forest Science* 59:  
703 777-787.

704 LEGENDRE, P., AND M.-J. FORTIN. 2010. Comparison of the Mantel test and alternative  
705 approaches for detecting complex multivariate relationships in the spatial analysis of  
706 genetic data. *Molecular Ecology Resources* 10: 831-844.

707 LEGENDRE, P., AND L. LEGENDRE. 2012. Numerical ecology. 3rd English ed., vol. 24. Elsevier,  
708 Amsterdam ; Boston ; London.

709 LINHART, Y. B., AND M. C. GRANT. 1996. Evolutionary significance of local genetic  
710 differentiation in plants. *Annual Review of Ecology and Systematics* 27: 237-277.

711 LOARIE, S. R., B. E. CARTER, K. HAYHOE, S. MCMAHON, R. MOE, C. A. KNIGHT, AND D. D.  
712 ACKERLY. 2008. Climate Change and the Future of California's Endemic Flora. *Plos One*  
713 3: Article No.: e2502.

714 LOBO, J. M., A. JIMENEZ-VALVERDE, AND R. REAL. 2008. AUC: a misleading measure of the  
715 performance of predictive distribution models. *Global Ecology and Biogeography* 17:  
716 145-151.

717 LOISELLE, B. A., P. M. JORGENSEN, T. CONSIGLIO, I. JIMENEZ, J. G. BLAKE, L. G. LOHMANN, AND  
718 O. M. MONTIEL. 2008. Predicting species distributions from herbarium collections: does  
719 climate bias in collection sampling influence model outcomes? *Journal of Biogeography*  
720 35: 105-116.

721 MARAIS, D. L. D., K. M. HERNANDEZ, AND T. E. JUENGER. 2013. Genotype-by-environment  
722 interaction and plasticity: Exploring genomic responses of plants to the abiotic  
723 environment. *Annual Review of Ecology, Evolution, and Systematics* 44: 5-29.

724 NICOTRA, A. B., O. K. ATKIN, S. P. BONSER, A. M. DAVIDSON, E. J. FINNEGAN, U. MATHESIUS, P.  
725 POOT, et al. 2010. Plant phenotypic plasticity in a changing climate. *Trends in Plant*  
726 *Science* 15: 684-692.

727 NIX, H. 1986. A biogeographic analysis of Australian elapid snakes. In R. Longmore [ed.], Atlas  
728 of Elapid Snakes of Australia, 4-15. Australian Government Publishing Service,  
729 Canberra.

730 NIXON, K. C. 2002. The oak (*Quercus*) biodiversity of California and adjacent regions. Pacific  
731 Southwest Research Station, Forest Service, US Department of Agriculture, Albany, CA,  
732 USA.

733 NOSIL, P., S. P. EGAN, AND D. J. FUNK. 2008. Heterogeneous genomic differentiation between  
734 walking-stick ecotypes: 'isolation by adpatation' and multiple roles for divergent  
735 selection. *Evolution* 62: 316-336.

736 OKSANEN, J., F. G. BLANCHET, R. KINDT, P. LEGENDRE, P. R. MINCHIN, R. B. O'HARA, G. L.  
737 SIMPSON, et al. 2015. vegan: Community Ecology Package, version 2.2-1. website:  
738 <http://CRAN.R-project.org/package=vegan>.

739 ORTEGO, J., E. C. RIORDAN, P. F. GUGGER, AND V. L. SORK. 2012. Influence of environmental  
740 heterogeneity on genetic diversity and structure in an endemic southern Californian oak.  
741 *Molecular Ecology* 21: 3210-3223.

742 ORTEGO, J., P. F. GUGGER, E. C. RIORDAN, AND V. L. SORK. 2014. Influence of climatic niche  
743 suitability and geographical overlap on hybridization patterns among southern  
744 Californian oaks. *Journal of Biogeography* 41: 1895-1908.

745 PAVLIK, B. M., P. C. MUICK, S. G. JOHNSON, AND M. POPPER. 1991. Oaks of California.  
746 Cachuma Press, Los Olivos, California, USA.

747 PEAKALL, R., AND P. E. SMOUSE. 2012. GenAIEx 6.5: genetic analysis in Excel. Population  
748 genetic software for teaching and research-an update. *Bioinformatics* 28: 2537-2539.

749 PEARSON, R. G., AND T. P. DAWSON. 2003. Predicting the impacts of climate change on the  
750 distribution of species: are bioclimate envelope models useful? *Global Ecology and*  
751 *Biogeography* 12: 361-371.

752 PERES-NETO, P. R., P. LEGENDRE, S. DRAY, AND D. BORCARD. 2006. Variation partitioning of  
753 species data matrices: estimation and comparison of fractions. *Ecology* 87: 2614-2625.

754 PHILLIPS, S. J., R. P. ANDERSON, AND R. E. SCHAPIRE. 2006. Maximum entropy modeling of  
755 species geographic distributions. *Ecological Modelling* 190: 231-259.

756 PHILLIPS, S. J., M. DUDIK, J. ELITH, C. H. GRAHAM, A. LEHMANN, J. LEATHWICK, AND S.  
757 FERRIER. 2009. Sample selection bias and presence-only distribution models:  
758 implications for background and pseudo-absence data. *Ecological Applications* 19: 181-  
759 197.

760 PLATT, A., P. F. GUGGER, M. PELLEGRINI, AND V. L. SORK. 2015. Genome-wide signature of  
761 local adaptation linked to variable CpG methylation in oak populations. *Molecular*  
762 *Ecology* 24: 3823-2824.

763 POELCHAU, M. F., AND J. L. HAMRICK. 2012. Differential effects of landscape-level  
764 environmental features on genetic structure in three codistributed tree species in Central  
765 America. *Molecular Ecology* 21: 4970-4982.

766 RAMÍREZ-VALIENTE, J. A., Z. LORENZO, A. SOTO, F. VALLADARES, L. GIL, AND I. ARANDA.  
767 2009. Elucidating the role of genetic drift and natural selection in cork oak differentiation  
768 regarding drought tolerance. *Molecular Ecology* 18: 3803-3815.

769 REHFELDT, G. E., N. L. CROOKSTON, M. V. WARWELL, AND J. S. EVANS. 2006. Empirical  
770 analyses of plant-climate relationships for the western United States. . *International*  
771 *Journal of Plant Sciences* 187: 1123–1150.

772 REHFELDT, G. E., N. M. TCHEBAKOVA, Y. I. PARFENOVA, W. R. WYKOFF, N. A. KUZMINA, AND  
773 L. I. MILYUTIN. 2002. Intraspecific responses to climate in *Pinus sylvestris*. *Global*  
774 *Change Biology* 8: 912-929.

775 ROBERTS, F. M. 1995. The Oaks of the Southern California Floristic Province. F. M. Roberts  
776 Publications, Encinitas, CA USA.

777 SAVOLAINEN, O., T. PYHAJARVI, AND T. KNURR. 2007. Gene flow and local adaptation in trees.  
778 *Annual Review of Ecology Evolution and Systematics* 38: 595-619.

779 SCHEINER, S. M. 1993. Genetics and evolution of phenotypic plasticity. *Annual Review of*  
780 *Ecology and Systematics* 24: 35-68.

781 SCHOENER, T. W. 1968. The *Anolis* lizards of Bimini: resource partitioning in a complex fauna.  
782 *Ecology* 49: 704-726.

783 SCOTT, T. A. 1991. The distribution of Engelmann Oak (*Quercus engelmannii*) in California.  
784 USDA Forest Service General Technical Report PSW-126:351-359.

785 SEXTON, J. P., S. B. HANGARTNER, AND A. A. HOFFMANN. 2014. Genetic isolation by  
786 environment or distance: which pattern of gene flow is most common? *Evolution* 68: 1-  
787 15.

788 SHAFER, A. B. A., AND J. B. W. WOLF. 2013. Widespread evidence for incipient ecological  
789 speciation: a meta-analysis of isolation-by-ecology. *Ecology Letters* 16: 940-950.

790 SLATKIN, M. 1993. Isolation by distance in equilibrium and nonequilibrium populations.  
791 *Evolution* 47: 264-279.

792 SMOUSE, P. E., AND R. C. WILLIAMS. 1982. Multivariate analysis of HLA-disease associations.  
793 *Biometrics* 38: 757-768.

794 SOBERON, J. 2007. Grinnellian and Eltonian niches and geographic distributions of species.  
795 *Ecology Letters* 10: 1115-1123.

796 SORK, V. L., S. N. AITKEN, R. J. DYER, A. J. ECKERT, P. LEGENDRE, AND D. B. NEALE. 2013.  
797 Putting the landscape into the genomics of trees: approaches for understanding local  
798 adaptation and population responses to changing climate. *Tree Genetics and Genomics* 9:  
799 901-911.

800 SORK, V. L., F. W. DAVIS, P. E. SMOUSE, V. J. APSIT, R. J. DYER, J. F. FERNANDEZ-M, AND B.  
801 KUHN. 2002. Pollen movement in declining populations of California Valley oak,  
802 *Quercus lobata*: Where have all the fathers gone? *Molecular Ecology* 11: 1657-1668.

803 SORK, V. L., F. W. DAVIS, R. WESTFALL, A. FLINT, M. IKEGAMI, H. F. WANG, AND D. GRIVET.  
804 2010. Gene movement and genetic association with regional climate gradients in  
805 California valley oak (*Quercus lobata* Née) in the face of climate change. *Molecular*  
806 *Ecology* 19: 3806-3823.

807 SOULARUE, J. P., AND A. KREMER. 2014. Evolutionary responses of tree phenology to the  
808 combined effects of assortative mating, gene flow and divergent selection. *Heredity* 113:  
809 485-494.

810 STEBBINS, G. L. 1950. Variations and Evolution in Plants. Columbia University Press, New  
811 York.

812 STEINKELLNER, H., C. LEXER, E. TURETSCHKE, AND J. GLOSSL. 1997. Conservation of (GA)n  
813 microsatellite loci between *Quercus* species. *Molecular Ecology* 6: 1189-1194.

814 STEPHENSON, N. L. 1998. Actual evapotranspiration and deficit: biologically meaningful  
815 correlates of vegetation distribution across spatial scales. *Journal of Biogeography* 25:  
816 855-870.

817 VANDERGAST, A. G., A. J. BOHONAK, S. A. HATHAWAY, J. BOYS, AND R. N. FISHER. 2008. Are  
818 hotspots of evolutionary potential adequately protected in southern California? *Biological*  
819 *Conservation* 141: 1648-1664.

820 VANDERWAL, J., L. P. SHOO, C. GRAHAM, AND S. E. WILLIAMS. 2009. Selecting pseudo-  
821 absence data for presence-only distribution modeling: How far should you stray from  
822 what you know? *Ecological Modelling* 220: 589-594.

- 823 WANG, I. J., AND G. S. BRADBURD. 2014. Isolation by environment. *Molecular Ecology* 23:  
824 5649-5662.
- 825 WARREN, D. L., R. E. GLOR, AND M. TURELLI. 2008. Environmental niche equivalency versus  
826 conservatism: quantitative approaches to niche evolution. *Evolution* 62: 2868-2883.
- 827 WEST-EBERHARD, M. J. 1989a. Phenotypic plasticity and the origins of diversity. *Annual Review*  
828 *of Ecology and Systematics*: 249-278.
- 829 WEST-EBERHARD, M. J. 1989b. Phenotypic plasticity and the origin of diversity. *Annual Review*  
830 *of Ecology and Systematics* 20: 249-278.
- 831 WESTFALL, R. D., AND M. T. CONKLE. 1992. Allozyme markers in breeding zone designation.  
832 *New Forests* 6: 279-309.
- 833 WIENS, J. A. 1989. Spatial scaling in ecology. *Functional ecology*: 385-397.
- 834 WOODWARD, F. I. 1987. Climate and plant distribution. Cambridge University Press, Cambridge  
835 Cambridgeshire ; New York.
- 836 WOODWARD, F. I., AND B. G. WILLIAMS. 1987. Climate and plant-distribution at global and  
837 local scales. *Vegetatio* 69: 189-197.
- 838 WRIGHT, S. 1943. Isolation by distance. *Genetics* 28: 114-138.
- 839

840 **TABLES**

841

842 **Table 1.** Geographic location of oak sampling sites in southern California. The number of  
 843 genetically defined *Quercus engelmannii* (N<sub>ENG</sub>), *Quercus berberidifolia* (N<sub>BER</sub>), and *Quercus*  
 844 *cornelius-mulleri* (N<sub>CMU</sub>) are indicated for each locality.

845

Locality	Code	Latitude	Longitude	N <sub>ENG</sub>	N <sub>BER</sub>	N <sub>CMU</sub>
Glendora	GLE	34.177483	-118.095	2	0	0
Pasadena	PAS	34.134079	-118.0989	16	0	0
Yucaipa	YUC	34.038817	-117.0217	0	2	1
Joshua Tree National Park	JOS	34.01738	-116.1674	0	0	4
Beaumont	BEA	33.909783	-116.9832	0	0	5
Hemet	HEM	33.628262	-117.0129	18	3	0
Avocado Mesa	AVO	33.513735	-117.3089	10	5	1
Pauba Ranch	PAU	33.508552	-117.0882	8	26	0
De Luz	LUZ	33.423553	-117.3214	5	9	0
Pala Reservation	PAL	33.390607	-117.0393	8	5	1
Harold's	HAR	33.302025	-116.893	5	1	0
Oak Knoll	OAK	33.29821	-116.9221	10	0	0
Lake Henshaw	HEN	33.276442	-116.855	5	0	0
Warner Springs	WAR	33.27523	-116.6241	2	7	0
Ranchita	RAN	33.211081	-116.4855	0	0	18
Daley Ranch	DAL	33.16599	-117.047	2	0	0
Santa Ysabel	YSA	33.10279	-116.6694	8	6	0
Julian	JUL	33.07477	-116.5491	12	3	0



Locality	Code	Latitude	Longitude	N <sub>ENG</sub>	N <sub>BER</sub>	N <sub>CMU</sub>
Lake Hodges	HOD	33.0747	-117.1181	3	0	0
Ramona	RAM	33.029917	-116.8231	7	0	0
Louis A. Stelzer County Park	LOU	32.881655	-116.9012	2	1	1
Laguna Mountain	LAG	32.849683	-116.4852	0	5	0
Japatul	JAP	32.82338	-116.6275	1	2	0
Alpine	ALP	32.81409	-116.7724	7	0	0
Cleveland National Forest	CLE	32.776504	-116.4948	5	5	0
McCain Valley Road	CAI	32.77026	-116.2586	0	0	6
Lawson Valley Road	LAW	32.74461	-116.8057	9	6	0
Jamul	JAM	32.730587	-116.8757	3	0	0
North Tecate/Dulzura	DUL	32.631651	-116.7615	8	0	0
Jacumba	JAC	32.622233	-116.2183	0	0	6
Potrero	POT	32.597267	-116.5549	1	5	0

846 **Table 2.** Importance of climatic variables in species distribution models in three southern California oak species. *Italic font indicates*  
 847 *the variable with the greatest predictive power and bold font indicates the variable with the greatest unique contribution, determined*  
 848 *from jackknife tests of variable importance in MaxEnt (see methods for further details).*

Climate Variable	<i>Q. engelmannii</i>		<i>Q. berberidifolia</i>		<i>Q. cornelius-mulleri</i>	
	Percent	Permutation	Percent	Permutation	Percent	Permutation
	Contribution	Importance	Contribution	Importance	Contribution	Importance
T <sub>seas</sub> (Bio4)	<b><i>14.5</i></b>	<b><i>40.8</i></b>	<b><i>8.2</i></b>	<b><i>17.8</i></b>	1.5	0.9
PPT <sub>seas</sub> (Bio15)	4.1	7.2	10.3	8.5	7.7	11.2
Summer PPT	3.7	15.4	2.2	9.7	<b><i>32</i></b>	<b><i>52.1</i></b>
Winter PPT (Bio19)	7.8	13.5	9.6	8.6	8	18.5
AET	30.1	1.3	28.4	7.7	0.9	2.8
CWD	24.3	2.7	26.3	18.9	10.2	0.3
Winter Tmin	2	2	4.5	17.6	20.6	5.8
Summer Tmax	13.5	17.1	10.6	11.2	19.2	8.3

849 **Table 3.** Summary of three canonical discriminant function analyses (Proc CANDISC, SAS V9) testing the genetic (A) and  
 850 morphological (B) differences among *Q. engelmannii*, *Q. berberidifolia*, and *Q. cornelius-mulleri*. The genetic differences are based  
 851 on nine microsatellite loci and the morphological differences are based on leaf traits described in text.

	Canonical correlation	Adjusted Canonical correlation	Squared Canonical Correlation	Eigen-value	Approximate F Value	Numerator Degrees of Freedom	Denominator Degrees of Freedom	Pr > F
<b>A. Genetic</b>								
1	0.9488	0.9316	0.9003	9.03	14.26	200	418	<.0001
2	0.9144	0.8871	0.8362	5.11	10.83	99	210	<.0001
<b>B. Morphological</b>								
1	0.8759	0.8701	0.7672	3.30	31.76	16	328	<.0001
2	0.5822	0.5649	0.3390	0.51	12.09	7	165	<.0001

852

853

**Table 4. (A)** Results of redundancy analyses (RDAs) on microsatellite genetic variation for *Q. engelmannii* ( $Q_{ENG}$ ), *Q. berberidifolia* ( $Q_{BER}$ ), and *Q. cornelius-mulleri* ( $Q_{CMU}$ ). Partitioning of variance into pure climatic (Climate | Spatial) and pure spatial (Spatial | Climate), and joint (Spatial  $\cap$  Climatic) components are shown. Proportion constrained corresponds to the partitioned variance relative to the constrained variance of the full RDA model (Spatial + Climate). **(B)** Significance of individual climatic variables in simple RDAs of genetic variation and climate. Bold face indicates variables that are still significantly associated with genetic variation after controlling for geography in partial RDAs.

**A. Summary of RDA results for genetic variation.**

Species	Microsatellite genetic variation	Partitioned Variance	Proportion Constrained	$R^2_{adj}$	$P$ -Value
$Q_{ENG}$	Total Variance	3.912			
	Full Model: Spatial + Climate (constrained variance)	0.303	1	0.028	0.001
	Pure Climate: (CWD+Bio19+AET+ Bio4+Bio15)   Spatial	0.162	0.536	0.011	0.001
	Pure Spatial: (XY+Y+Y <sup>2</sup> )   Climate	0.097	0.322	0.006	0.004
	Spatial $\cap$ Climate	0.043	0.142	0.011	NA
$Q_{BER}$	Total Variance	3.919			
	Full Model: Spatial + Climate (constrained variance)	0.154	1	0.006	0.064
	Pure Climate: (Tmax+Bio15)   Spatial	0.095	0.614	0.002	0.220
	Pure Spatial: (X <sup>2</sup> )   Climate	0.041	0.267	-0.001	0.607
	Spatial $\cap$ Climate	0.018	0.119	0.005	NA

Species	Microsatellite genetic variation	Partitioned Variance	Proportion Constrained	R <sup>2</sup> <sub>adj</sub>	P-Value
Q <sub>CMU</sub>	Total Variance	4.183			
	Full Model: Spatial + Climate (constrained variance)	0.954	1	0.074	0.001
	Pure Climate: (Tmax+Bio19+AET+Bio15)   Spatial	0.461	0.483	0.024	0.001
	Pure Spatial: (XY+Y+Y <sup>2</sup> )   Climate	0.338	0.354	0.016	0.031
	Spatial ∩ Climate	0.156	0.163	0.034	NA

### B. Significance of individual climatic variables.

Species	Climate Variable	Total Variance	Percent Constrained	F	P-value
Q <sub>ENG</sub>	T <sub>seas</sub> (Bio4)	0.98	18.7	1.565	0.010
	<b>PPT<sub>seas</sub> (Bio15)</b>	<b>0.95</b>	<b>18.0</b>	<b>1.513</b>	<b>0.017</b>
	Winter PPT (Bio19)	1.16	22.1	1.851	0.001
	<b>AET</b>	<b>1.06</b>	<b>20.2</b>	<b>1.694</b>	<b>0.002</b>
	CWD	1.21	23.1	1.936	0.001
Q <sub>BER</sub>	PPT <sub>seas</sub> (Bio15)	1.72	59.7	1.555	0.006
	Summer Tmax	1.25	43.5	1.134	0.235
Q <sub>CMU</sub>	<b>PPT<sub>seas</sub> (Bio15)</b>	<b>3.13</b>	<b>21.2</b>	<b>1.395</b>	<b>0.035</b>
	<b>Winter PPT (Bio19)</b>	<b>3.59</b>	<b>24.3</b>	<b>1.600</b>	<b>0.001</b>
	AET	3.59	24.4	1.601	0.005
	<b>Summer Tmax</b>	<b>3.61</b>	<b>24.5</b>	<b>1.610</b>	<b>0.004</b>

**Table 5. (A)** Results of redundancy analyses (RDAs) on morphological leaf trait variation for *Q. engelmannii* ( $Q_{ENG}$ ) and *Q. berberidifolia* ( $Q_{BER}$ ). Partitioning of variance into components and significance of levels are the same as Table 4. **(B)** Significance of individual climatic variables in simple RDAs of morphology and climate. Bold face indicates variables that are still significantly associated with morphological variation after controlling for geography in partial RDAs.

<b>A. Summary of RDA results for leaf trait variation.</b>					
Species	Morphological leaf variation	Partitioned Variance	Proportion Constrained	$R^2_{adj}$	$P$ -value
$Q_{ENG}$	Total Variance	8.000			
	Full Model: Spatial + Climate	1.271	1	0.127	0.001
	Pure Climate: (Bio15+Bio18)   Spatial	0.241	0.190	0.014	0.040
	Pure Spatial: (XY+Y)   Climate	0.652	0.513	0.067	0.001
	Spatial $\cap$ Climate	0.378	0.297	0.046	NA
$Q_{BER}$	Total Variance	8.000			
	Full Model: Spatial + Climate	0.752	1	0.058	0.005
	Pure Climate: (Tmax)   Spatial	0.345	0.459	0.026	0.028
	Pure Spatial: (X)   Climate	0.284	0.378	0.018	0.068
	Spatial $\cap$ Climate	0.123	0.163	0.014	NA
<b>B. Significance of individual climatic variables.</b>					
	Climate Variable	Total Variance	Percent Constrained	$F$	$P$ -value
$Q_{ENG}$	PPT <sub>seas</sub> (Bio15)	4.55	58.8	5.231	0.001
	<b>Summer PPT (Bio18)</b>	<b>1.98</b>	<b>25.6</b>	<b>2.276</b>	<b>0.048</b>
$Q_{BER}$	<b>Summer Tmax</b>	<b>5.85</b>	<b>100</b>	<b>3.166</b>	<b>0.003</b>

**Table 6.** Importance of climatic variables in oak habitat suitability, genetic, and morphological trait models. Species are abbreviated as follows: *Q. engelmannii* (Q<sub>ENG</sub>), *Q. berberidifolia* (Q<sub>BER</sub>), and *Q. cornelius-mulleri* (Q<sub>CMU</sub>). XX=Variables with high values for habitat suitability or that retain significance in genetic variation and leaf morphology, after controlling for geography. X=variables with moderate values. Low and non-significant values are blank. Data is summarized from Tables 2, 4B, and 5B. (Q<sub>CMU</sub> has no test for leaf morphology.)

Species	Climate Variable	Habitat Suitability		Genetic Variation	Leaf Morphology
		Percent Contribution	Permutation Importance		
Q <sub>ENG</sub>	T <sub>seas</sub> (Bio4)	X	XX	X	
	PPT <sub>seas</sub> (Bio15)			XX	X
	Summer PPT (Bio18)		X		XX
	Winter PPT (Bio19)		X	X	
	AET	XX		XX	
	CWD	X		X	
	Winter Tmin				
	Summer Tmax	X	X		
Q <sub>BER</sub>	T <sub>seas</sub> (Bio4)		X		
	PPT <sub>seas</sub> (Bio15)	X		X	
	Summer PPT (Bio18)				
	Winter PPT (Bio19)				
	AET	X			

Species	Climate Variable	Habitat Suitability		Genetic Variation	Leaf Morphology
		Percent Contribution	Permutation Importance		
	CWD	X	X		
	Winter Tmin		X		
	Summer Tmax	X	X	X	XX
Q <sub>CMU</sub>	T <sub>seas</sub> (Bio4)				
	PPT <sub>seas</sub> (Bio15)		X	XX	
	Summer PPT (Bio18)	XX	XX		
	Winter PPT (Bio19)		X	XX	
	AET		X	X	
	CWD	X			
	Winter Tmin	X			
	Summer Tmax	X		XX	



1 **Appendices**

2

3 **Appendix 1.** Climatic variables at oak sampling localities. Climate variables were extracted  
4 using sampling site latitude and longitude from 30-year averages of recent historical (1951–  
5 1980) climate data from the California Basin Characterization Model (BCM; Flint and Flint,  
6 2012; Flint et al., 2013).

7

8 **Figures**

9

10 **Fig. 1.** Localities (A-C) of sampling sites (red) and herbarium records (black), and modeled  
11 habitat suitability maps (D-F) for *Q. engelmannii* (A, D) *Q. berberidifolia* (B, E), and *Q.*  
12 *cornelius-mulleri* (F, C).

13

14 **Fig. 2.** Genetic (A) and morphological (B) differentiation of oaks species. Axes correspond to  
15 the first and second canonical discriminant functions. Species are represented by colors as  
16 follows: *Q. engelmannii* (blue), *Q. berberidifolia* (red), and *Q. cornelius-mulleri* (yellow).

17

18

Figure 1

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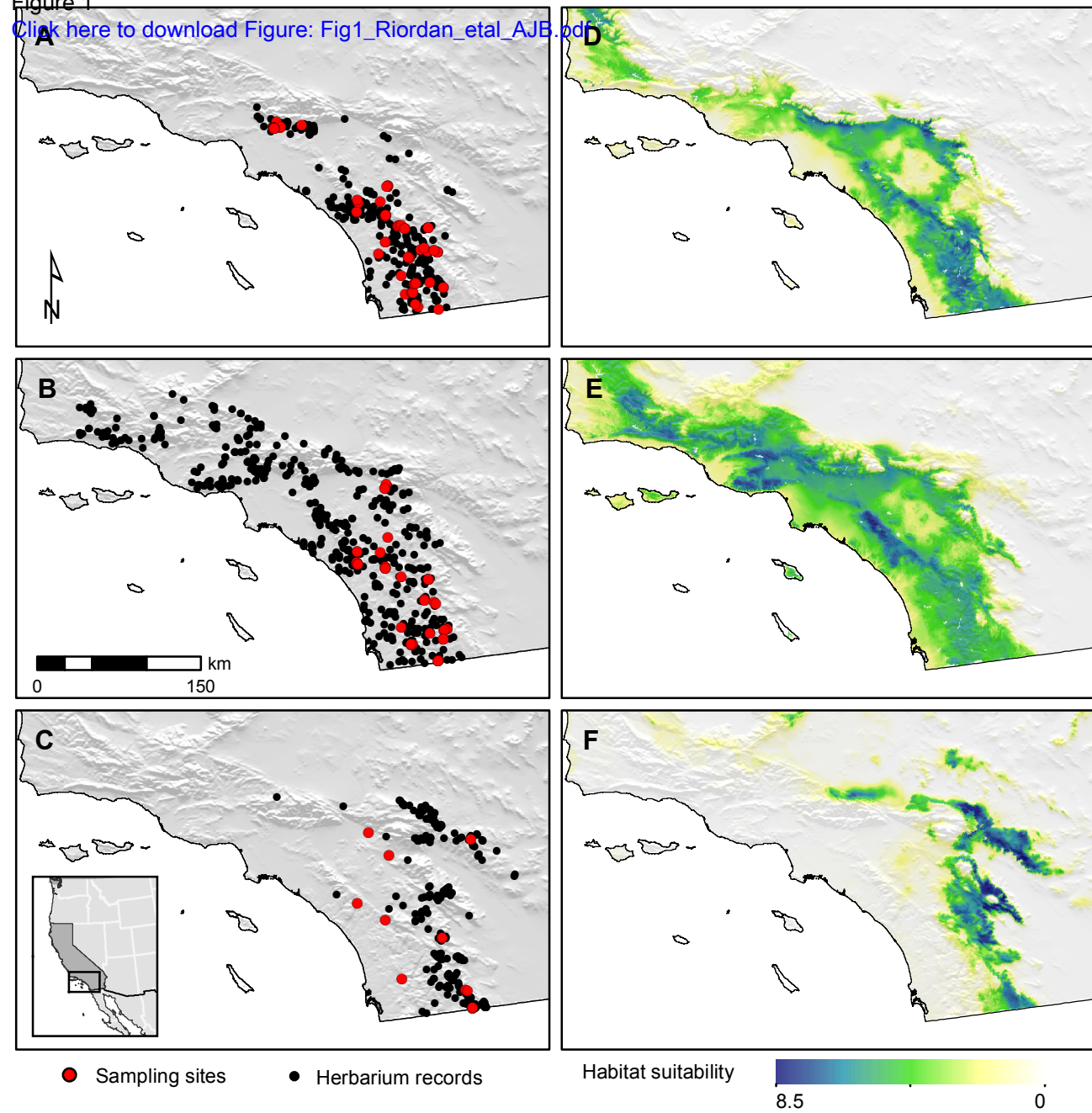
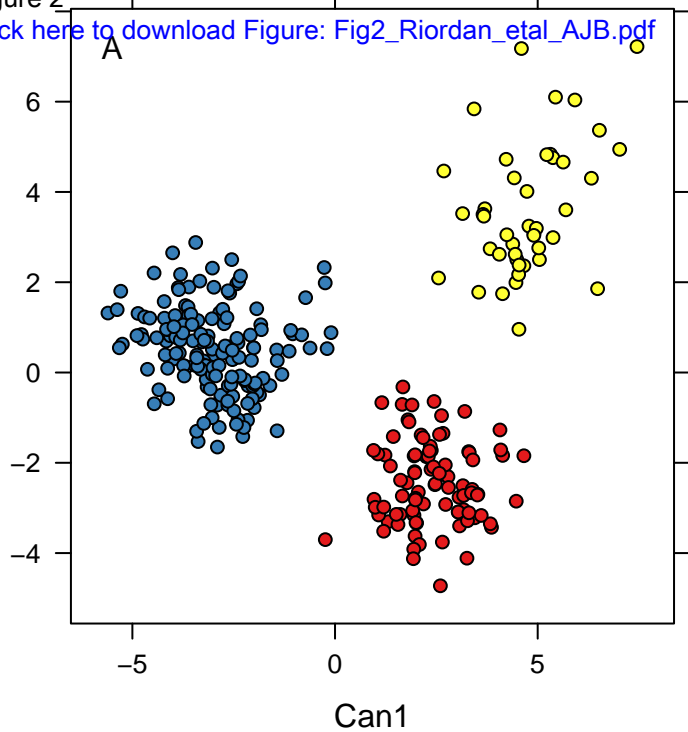


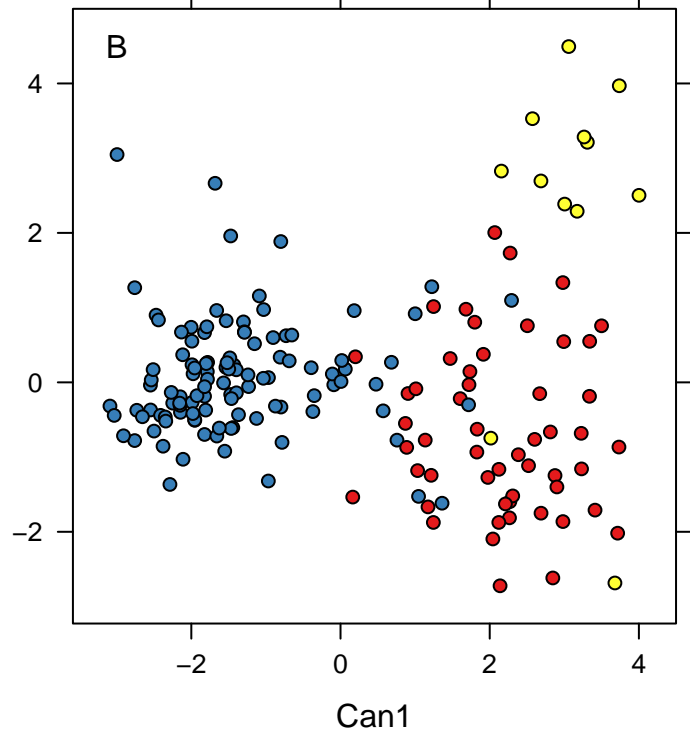
Figure 2

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Can2



Can2



Tree ID	Scientific Name	Locality Name	Latitude	Longitude	Elevation (meters)	Morphology data (0=missing)
1--3	<i>Quercus berberidifolia</i>	De Luz	33.431967	-117.322733	114	1
1--4	<i>Quercus berberidifolia</i>	De Luz	33.432100	-117.322700	114	1
1--6	<i>Quercus berberidifolia</i>	De Luz	33.417783	-117.311983	139	1
1--9	<i>Quercus berberidifolia</i>	De Luz	33.417200	-117.312800	139	1
1--11	<i>Quercus berberidifolia</i>	De Luz	33.416300	-117.318383	96	1
1--12	<i>Quercus berberidifolia</i>	De Luz	33.415850	-117.318167	96	1
1--15	<i>Quercus engelmannii</i>	De Luz	33.421050	-117.320267	112	1
1--16	<i>Quercus engelmannii</i>	De Luz	33.421250	-117.320467	112	1
1--17	<i>Quercus berberidifolia</i>	De Luz	33.422383	-117.321333	106	1
1--18	<i>Quercus berberidifolia</i>	De Luz	33.422833	-117.321583	106	1
1--19	<i>Quercus engelmannii</i>	De Luz	33.424533	-117.322233	93	1
1--20	<i>Quercus engelmannii</i>	De Luz	33.424517	-117.322183	93	0
1--22	<i>Quercus engelmannii</i>	De Luz	33.426417	-117.321750	104	1
1--25	<i>Quercus berberidifolia</i>	De Luz	33.426617	-117.321583	104	1
2--2	<i>Quercus berberidifolia</i>	Pala Reservation	33.375217	-117.044967	249	1
2--4	<i>Quercus engelmannii</i>	Pala Reservation	33.379617	-117.044800	273	1
2--5	<i>Quercus engelmannii</i>	Pala Reservation	33.394683	-117.036100	495	1
2--6	<i>Quercus engelmannii</i>	Pala Reservation	33.394283	-117.036533	495	0
2--7	<i>Quercus engelmannii</i>	Pala Reservation	33.392783	-117.037817	495	1
2--9	<i>Quercus engelmannii</i>	Pala Reservation	33.391950	-117.038467	475	1
2--10	<i>Quercus berberidifolia</i>	Pala Reservation	33.391550	-117.040217	475	1
2--11	<i>Quercus engelmannii</i>	Pala Reservation	33.391533	-117.040783	475	1
2--12	<i>Quercus engelmannii</i>	Pala Reservation	33.391400	-117.041033	475	1
2--13	<i>Quercus engelmannii</i>	Pala Reservation	33.389400	-117.040250	410	1
2--15	<i>Quercus berberidifolia</i>	Pala Reservation	33.377067	-117.045600	263	1
2--16	<i>Quercus berberidifolia</i>	Pala Reservation	33.376833	-117.045667	263	1
2--17	<i>Quercus cornelius-mulleri</i>	Pala Reservation	33.375833	-117.045300	263	1
2--18	<i>Quercus berberidifolia</i>	Pala Reservation	33.375633	-117.045167	263	1
3--1	<i>Quercus engelmannii</i>	Harolds	33.302200	-116.910467	774	0
3--3	<i>Quercus engelmannii</i>	Harolds	33.301967	-116.886200	1168	0
3--4	<i>Quercus engelmannii</i>	Harolds	33.301967	-116.886200	1168	1
3--5	<i>Quercus engelmannii</i>	Harolds	33.301950	-116.887517	1168	0
3--6	<i>Quercus engelmannii</i>	Harolds	33.301983	-116.887650	1168	0
3--7	<i>Quercus berberidifolia</i>	Harolds	33.302800	-116.885817	1168	1
4--1	<i>Quercus engelmannii</i>	Lake Henshaw	33.276817	-116.853300	719	1
4--2	<i>Quercus engelmannii</i>	Lake Henshaw	33.276150	-116.853967	719	1
4--3	<i>Quercus engelmannii</i>	Lake Henshaw	33.275767	-116.853617	719	1
4--4	<i>Quercus engelmannii</i>	Lake Henshaw	33.277417	-116.858433	721	1
4--5	<i>Quercus engelmannii</i>	Lake Henshaw	33.277033	-116.859267	721	1
5--2	<i>Quercus berberidifolia</i>	Warner Springs	33.275067	-116.622900	1074	1
5--4	<i>Quercus berberidifolia</i>	Warner Springs	33.275033	-116.622400	1099	0
5--6	<i>Quercus berberidifolia</i>	Warner Springs	33.275050	-116.621817	1099	0
5--8	<i>Quercus berberidifolia</i>	Warner Springs	33.275230	-116.624060	1074	1
5--9	<i>Quercus berberidifolia</i>	Warner Springs	33.275360	-116.624340	1074	1
5--10	<i>Quercus berberidifolia</i>	Warner Springs	33.275360	-116.624340	1074	0
5--11	<i>Quercus engelmannii</i>	Warner Springs	33.275510	-116.624410	1074	1
5--12	<i>Quercus engelmannii</i>	Warner Springs	33.273670	-116.620640	1099	1
5--13	<i>Quercus berberidifolia</i>	Warner Springs	33.272250	-116.619720	1107	1
6--1	<i>Quercus engelmannii</i>	Lake Hodges	33.074400	-117.118100	91	1
6--2	<i>Quercus engelmannii</i>	Lake Hodges	33.074750	-117.118017	91	1
6--3	<i>Quercus engelmannii</i>	Lake Hodges	33.074950	-117.118100	91	1
7--1	<i>Quercus engelmannii</i>	Ramona	33.027867	-116.820017	501	1
7--2	<i>Quercus engelmannii</i>	Ramona	33.028700	-116.819733	525	1
7--3	<i>Quercus engelmannii</i>	Ramona	33.026583	-116.820833	501	1
7--4	<i>Quercus engelmannii</i>	Ramona	33.026000	-116.820783	501	1

7--5	<i>Quercus engelmannii</i>	Ramona	33.026317	-116.820733	501	1
7--7	<i>Quercus engelmannii</i>	Ramona	33.037450	-116.829817	529	1
7--8	<i>Quercus engelmannii</i>	Ramona	33.036500	-116.829433	529	1
8--1	<i>Quercus engelmannii</i>	Santa Ysabel	33.093333	-116.702067	889	1
8--2	<i>Quercus engelmannii</i>	Santa Ysabel	33.110217	-116.670150	928	1
8--3	<i>Quercus engelmannii</i>	Santa Ysabel	33.109300	-116.669300	963	1
8--4	<i>Quercus engelmannii</i>	Santa Ysabel	33.109367	-116.669133	963	1
8--6	<i>Quercus engelmannii</i>	Santa Ysabel	33.108833	-116.668983	931	1
8--7	<i>Quercus berberidifolia</i>	Santa Ysabel	33.109133	-116.668933	963	1
8--8	<i>Quercus engelmannii</i>	Santa Ysabel	33.108783	-116.669000	931	1
8--9	<i>Quercus engelmannii</i>	Santa Ysabel	33.108633	-116.668900	931	1
8--10	<i>Quercus berberidifolia</i>	Santa Ysabel	33.108550	-116.668850	931	1
8--11	<i>Quercus berberidifolia</i>	Santa Ysabel	33.108033	-116.668617	931	1
8--12	<i>Quercus berberidifolia</i>	Santa Ysabel	33.107667	-116.668467	931	1
8--13	<i>Quercus berberidifolia</i>	Santa Ysabel	33.107317	-116.668300	931	1
8--15	<i>Quercus berberidifolia</i>	Santa Ysabel	33.098300	-116.664983	962	1
8--17	<i>Quercus engelmannii</i>	Santa Ysabel	33.079850	-116.637083	1142	1
9--1	<i>Quercus berberidifolia</i>	Julian	33.080450	-116.572150	960	1
9--2	<i>Quercus engelmannii</i>	Julian	33.080400	-116.572550	960	1
9--3	<i>Quercus engelmannii</i>	Julian	33.080883	-116.572767	960	1
9--4	<i>Quercus engelmannii</i>	Julian	33.081133	-116.572233	960	1
9--5	<i>Quercus engelmannii</i>	Julian	33.081817	-116.572067	979	1
9--6	<i>Quercus berberidifolia</i>	Julian	33.080333	-116.571983	960	1
9--12	<i>Quercus berberidifolia</i>	Julian	33.072583	-116.558467	873	1
9--16	<i>Quercus engelmannii</i>	Julian	33.071250	-116.542650	922	1
9--17	<i>Quercus engelmannii</i>	Julian	33.071617	-116.541900	922	1
9--18	<i>Quercus engelmannii</i>	Julian	33.071700	-116.541667	922	1
9--19	<i>Quercus engelmannii</i>	Julian	33.072233	-116.540717	835	1
9--20	<i>Quercus engelmannii</i>	Julian	33.072500	-116.539983	835	1
9--21	<i>Quercus engelmannii</i>	Julian	33.073000	-116.539050	835	1
9--22	<i>Quercus engelmannii</i>	Julian	33.073250	-116.538767	835	1
9--23	<i>Quercus engelmannii</i>	Julian	33.073817	-116.538300	797	1
11--1	<i>Quercus berberidifolia</i>	Laguna Mountain	32.853817	-116.454283	1745	1
11--4	<i>Quercus berberidifolia</i>	Laguna Mountain	32.857467	-116.457467	1683	1
11--6	<i>Quercus berberidifolia</i>	Laguna Mountain	32.849683	-116.485150	1509	1
11--9	<i>Quercus berberidifolia</i>	Laguna Mountain	32.849517	-116.485567	1509	1
11--11	<i>Quercus berberidifolia</i>	Laguna Mountain	32.849450	-116.485967	1509	1
12--1	<i>Quercus engelmannii</i>	Forest Cleveland National	32.776250	-116.494517	1041	1
12--2	<i>Quercus engelmannii</i>	Forest Cleveland National	32.776350	-116.494683	1041	1
12--3	<i>Quercus engelmannii</i>	Forest Cleveland National	32.776500	-116.494767	1041	1
12--4	<i>Quercus berberidifolia</i>	Forest Cleveland National	32.776650	-116.494850	1041	1
12--5	<i>Quercus berberidifolia</i>	Forest Cleveland National	32.776733	-116.494933	1041	1
12--6	<i>Quercus engelmannii</i>	Forest Cleveland National	32.776917	-116.495167	1041	1
12--7	<i>Quercus berberidifolia</i>	Forest Cleveland National	32.777033	-116.495250	1044	1
12--8	<i>Quercus engelmannii</i>	Forest Cleveland National	32.776117	-116.494483	1041	1
12--9	<i>Quercus berberidifolia</i>	Forest Cleveland National	32.776250	-116.494317	1041	1
12--11	<i>Quercus berberidifolia</i>	Forest	32.776317	-116.494150	1041	1
13--2	<i>Quercus cornelius-mulleri</i>	Jacumba	32.622833	-116.218883	938	1
13--4	<i>Quercus cornelius-mulleri</i>	Jacumba	32.622633	-116.218600	938	1

13--6	<i>Quercus cornelius-mulleri</i>	Jacumba	32.622233	-116.218267	938	1
13--8	<i>Quercus cornelius-mulleri</i>	Jacumba	32.621900	-116.217817	938	1
13--9	<i>Quercus cornelius-mulleri</i>	Jacumba	32.621717	-116.217817	938	1
13--10	<i>Quercus cornelius-mulleri</i>	Jacumba	32.621700	-116.217967	938	1
14--1	<i>Quercus engelmannii</i>	Potrero	32.598100	-116.551133	761	1
14--2	<i>Quercus berberidifolia</i>	Potrero	32.599717	-116.552817	757	1
14--3	<i>Quercus berberidifolia</i>	Potrero	32.597217	-116.554550	731	1
14--4	<i>Quercus berberidifolia</i>	Potrero	32.597267	-116.554867	731	1
14--5	<i>Quercus berberidifolia</i>	Potrero	32.597267	-116.557017	741	1
14--6	<i>Quercus berberidifolia</i>	Potrero	32.597283	-116.557200	741	1
15--1	<i>Quercus engelmannii</i>	Jamul	32.730700	-116.874340	254	1
15--2	<i>Quercus engelmannii</i>	Jamul	32.730530	-116.876400	275	1
15--3	<i>Quercus engelmannii</i>	Jamul	32.730530	-116.876400	275	1
16--1	<i>Quercus engelmannii</i>	Lawson Valley Road	32.743030	-116.810740	581	1
16--2	<i>Quercus engelmannii</i>	Lawson Valley Road	32.743030	-116.810740	581	1
16--3	<i>Quercus engelmannii</i>	Lawson Valley Road	32.743030	-116.810740	581	1
16--4	<i>Quercus engelmannii</i>	Lawson Valley Road	32.743030	-116.810740	581	1
16--7	<i>Quercus engelmannii</i>	Lawson Valley Road	32.746880	-116.797650	609	1
16--8	<i>Quercus engelmannii</i>	Lawson Valley Road	32.746720	-116.798620	609	1
16--11	<i>Quercus berberidifolia</i>	Lawson Valley Road	32.746820	-116.799220	609	1
16--12	<i>Quercus engelmannii</i>	Lawson Valley Road	32.746820	-116.799220	609	1
16--13	<i>Quercus berberidifolia</i>	Lawson Valley Road	32.746820	-116.799220	609	1
16--14	<i>Quercus engelmannii</i>	Lawson Valley Road	32.746450	-116.799800	609	1
16--15	<i>Quercus berberidifolia</i>	Lawson Valley Road	32.746420	-116.800550	595	1
16--17	<i>Quercus engelmannii</i>	Lawson Valley Road	32.745610	-116.802520	595	1
16--21	<i>Quercus berberidifolia</i>	Lawson Valley Road	32.738880	-116.813790	551	1
16--23	<i>Quercus berberidifolia</i>	Lawson Valley Road	32.739920	-116.812410	551	1
16--25	<i>Quercus berberidifolia</i>	Lawson Valley Road	32.739640	-116.811690	563	1
17--1	<i>Quercus engelmannii</i>	Alpine	32.811980	-116.778210	537	1
17--2	<i>Quercus engelmannii</i>	Alpine	32.811740	-116.778340	537	1
17--3	<i>Quercus engelmannii</i>	Alpine	32.811650	-116.778400	537	1
17--5	<i>Quercus engelmannii</i>	Alpine	32.813440	-116.772100	577	1
17--6	<i>Quercus engelmannii</i>	Alpine	32.815660	-116.771870	557	1
17--8	<i>Quercus engelmannii</i>	Alpine	32.816330	-116.764050	581	1
17--9	<i>Quercus engelmannii</i>	Alpine	32.816200	-116.764600	581	1
18--1	<i>Quercus cornelius-mulleri</i>	Louis A. Stelzer County Park	32.881980	-116.900320	264	1
18--4	<i>Quercus berberidifolia</i>	Louis A. Stelzer County Park	32.881760	-116.900860	264	1
18--5	<i>Quercus engelmannii</i>	Louis A. Stelzer County Park	32.881800	-116.901170	264	1
18--7	<i>Quercus engelmannii</i>	Louis A. Stelzer County Park	32.881510	-116.901280	206	1
20--2	<i>Quercus cornelius-mulleri</i>	Beumont	33.909933	-116.982617	784	1

20--3	<i>Quercus cornelius-mulleri</i>	Beumont	33.909783	-116.982733	779	1
20--5	<i>Quercus cornelius-mulleri</i>	Beumont	33.909467	-116.983250	779	0
20--8	<i>Quercus cornelius-mulleri</i>	Beumont	33.910000	-116.983200	784	1
20--11	<i>Quercus cornelius-mulleri</i>	Beumont	33.910900	-116.983467	784	1
21--1	<i>Quercus engelmannii</i>	Hemet	33.631817	-117.005217	659	1
21--2	<i>Quercus engelmannii</i>	Hemet	33.631600	-117.005767	659	1
21--3	<i>Quercus engelmannii</i>	Hemet	33.631433	-117.005917	659	1
21--4	<i>Quercus engelmannii</i>	Hemet	33.631467	-117.006033	659	0
21--5	<i>Quercus engelmannii</i>	Hemet	33.631283	-117.006250	641	1
21--6	<i>Quercus engelmannii</i>	Hemet	33.631000	-117.006867	641	1
21--7	<i>Quercus engelmannii</i>	Hemet	33.631167	-117.006483	641	1
21--8	<i>Quercus engelmannii</i>	Hemet	33.631033	-117.006050	659	1
21--9	<i>Quercus berberidifolia</i>	Hemet	33.630983	-117.005850	659	1
21--12	<i>Quercus berberidifolia</i>	Hemet	33.630850	-117.005750	659	1
21--20	<i>Quercus engelmannii</i>	Hemet	33.631183	-117.005300	659	1
21--21	<i>Quercus berberidifolia</i>	Hemet	33.631100	-117.005100	659	1
21--22	<i>Quercus engelmannii</i>	Hemet	33.630967	-117.004950	659	1
21--24	<i>Quercus engelmannii</i>	Hemet	33.625867	-117.018733	587	1
21--25	<i>Quercus engelmannii</i>	Hemet	33.625683	-117.018833	590	1
21--26	<i>Quercus engelmannii</i>	Hemet	33.625600	-117.018817	590	1
21--27	<i>Quercus engelmannii</i>	Hemet	33.625583	-117.018850	590	1
21--28	<i>Quercus engelmannii</i>	Hemet	33.625550	-117.018783	590	1
21--29	<i>Quercus engelmannii</i>	Hemet	33.625433	-117.018867	590	1
21--30	<i>Quercus engelmannii</i>	Hemet	33.625267	-117.018817	590	1
21--32	<i>Quercus engelmannii</i>	Hemet	33.625183	-117.018733	590	1
22--1	<i>Quercus engelmannii</i>	Avocado Mesa	33.504630	-117.302040	591	0
22--2	<i>Quercus engelmannii</i>	Avocado Mesa	33.504360	-117.302090	591	0
22--3	<i>Quercus engelmannii</i>	Avocado Mesa	33.503700	-117.302760	599	0
22--4	<i>Quercus engelmannii</i>	Avocado Mesa	33.503860	-117.301230	616	0
23--1	<i>Quercus berberidifolia</i>	Avocado Mesa	33.522460	-117.314670	687	0
23--2	<i>Quercus berberidifolia</i>	Avocado Mesa	33.521990	-117.315170	687	0
23--6	<i>Quercus cornelius-mulleri</i>	Avocado Mesa	33.522310	-117.315300	687	0
23--7	<i>Quercus berberidifolia</i>	Avocado Mesa	33.522320	-117.315320	687	0
23--9	<i>Quercus berberidifolia</i>	Avocado Mesa	33.523170	-117.315670	656	0
23--10	<i>Quercus engelmannii</i>	Avocado Mesa	33.523180	-117.315750	656	0
23--11	<i>Quercus engelmannii</i>	Avocado Mesa	33.523270	-117.315710	656	0
23--12	<i>Quercus berberidifolia</i>	Avocado Mesa	33.522750	-117.315720	656	0
23--13	<i>Quercus engelmannii</i>	Avocado Mesa	33.522990	-117.315800	656	0
23--14	<i>Quercus engelmannii</i>	Avocado Mesa	33.523330	-117.315850	656	0
23--15	<i>Quercus engelmannii</i>	Avocado Mesa	33.523410	-117.315790	656	0
23--16	<i>Quercus engelmannii</i>	Avocado Mesa	33.523740	-117.315790	679	0
24--1	<i>Quercus engelmannii</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--2	<i>Quercus engelmannii</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--3	<i>Quercus engelmannii</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--5	<i>Quercus engelmannii</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--6	<i>Quercus engelmannii</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--7	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--8	<i>Quercus engelmannii</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--9	<i>Quercus engelmannii</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--10	<i>Quercus engelmannii</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--11	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--12	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--13	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--14	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--15	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--17	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--18	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--19	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--20	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0

24--21	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--22	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--23	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--24	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--25	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--27	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
24--016A	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
25--1	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
25--2	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
25--3	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
25--4	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
25--6	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
25--7	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
25--9	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
25--11	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
25--12	<i>Quercus berberidifolia</i>	Pauba Ranch	33.508552	-117.088208	384	0
26--1	<i>Quercus engelmannii</i>	North Tecate/Dulzura	32.623390	-116.749540	472	0
26--2	<i>Quercus engelmannii</i>	North Tecate/Dulzura	32.623440	-116.749420	472	0
26--3	<i>Quercus engelmannii</i>	North Tecate/Dulzura	32.623480	-116.748600	472	0
26--4	<i>Quercus engelmannii</i>	North Tecate/Dulzura	32.623480	-116.748600	472	0
26--5	<i>Quercus engelmannii</i>	North Tecate/Dulzura	32.623480	-116.748600	472	0
26--6	<i>Quercus engelmannii</i>	North Tecate/Dulzura	32.642430	-116.777770	333	0
26--7	<i>Quercus engelmannii</i>	North Tecate/Dulzura	32.642560	-116.777810	333	0
26--8	<i>Quercus engelmannii</i>	North Tecate/Dulzura	32.642780	-116.778920	330	0
27--2	<i>Quercus engelmannii</i>	Oak Knoll	33.298210	-116.922127	696	0
27--3	<i>Quercus engelmannii</i>	Oak Knoll	33.298210	-116.922127	696	0
27--4	<i>Quercus engelmannii</i>	Oak Knoll	33.298210	-116.922127	696	0
27--6	<i>Quercus engelmannii</i>	Oak Knoll	33.298210	-116.922127	696	0
27--7	<i>Quercus engelmannii</i>	Oak Knoll	33.298210	-116.922127	696	0
27--8	<i>Quercus engelmannii</i>	Oak Knoll	33.298210	-116.922127	696	0
27--9	<i>Quercus engelmannii</i>	Oak Knoll	33.298210	-116.922127	696	0
27--10	<i>Quercus engelmannii</i>	Oak Knoll	33.298210	-116.922127	696	0
27--11	<i>Quercus engelmannii</i>	Oak Knoll	33.298210	-116.922127	696	0
27--12	<i>Quercus engelmannii</i>	Oak Knoll	33.298210	-116.922127	696	0
28--1	<i>Quercus cornelius-mulleri</i>	Ranchita	33.211081	-116.485548	1233	0
28--2	<i>Quercus cornelius-mulleri</i>	Ranchita	33.211081	-116.485548	1233	0
28--3	<i>Quercus cornelius-mulleri</i>	Ranchita	33.211081	-116.485548	1233	0
28--4	<i>Quercus cornelius-mulleri</i>	Ranchita	33.211081	-116.485548	1233	0
28--5	<i>Quercus cornelius-mulleri</i>	Ranchita	33.211081	-116.485548	1233	0
28--6	<i>Quercus cornelius-mulleri</i>	Ranchita	33.211081	-116.485548	1233	0
28--7	<i>Quercus cornelius-mulleri</i>	Ranchita	33.211081	-116.485548	1233	0
28--8	<i>Quercus cornelius-mulleri</i>	Ranchita	33.211081	-116.485548	1233	0
28--9	<i>Quercus cornelius-mulleri</i>	Ranchita	33.211081	-116.485548	1233	0
28--10	<i>Quercus cornelius-mulleri</i>	Ranchita	33.211081	-116.485548	1233	0
28--11	<i>Quercus cornelius-mulleri</i>	Ranchita	33.211081	-116.485548	1233	0
28--12	<i>Quercus cornelius-mulleri</i>	Ranchita	33.211081	-116.485548	1233	0
28--13	<i>Quercus cornelius-mulleri</i>	Ranchita	33.211081	-116.485548	1233	0
28--14	<i>Quercus cornelius-mulleri</i>	Ranchita	33.211081	-116.485548	1233	0
28--15	<i>Quercus cornelius-mulleri</i>	Ranchita	33.211081	-116.485548	1233	0
28--16	<i>Quercus cornelius-mulleri</i>	Ranchita	33.211081	-116.485548	1233	0
28--17	<i>Quercus cornelius-mulleri</i>	Ranchita	33.211081	-116.485548	1233	0



28--18	<i>Quercus cornelius-mulleri</i>	Ranchita	33.211081	-116.485548	1233	0
29--1	<i>Quercus cornelius-mulleri</i>	Mc Cain Valley Road	32.774040	-116.281570	1222	0
29--2	<i>Quercus cornelius-mulleri</i>	Mc Cain Valley Road	32.774220	-116.281050	1222	0
29--3	<i>Quercus cornelius-mulleri</i>	Mc Cain Valley Road	32.774210	-116.280960	1222	0
29--4	<i>Quercus cornelius-mulleri</i>	Mc Cain Valley Road	32.774390	-116.280720	1187	0
29--5	<i>Quercus cornelius-mulleri</i>	Mc Cain Valley Road	32.774430	-116.280620	1187	0
31--1	<i>Quercus cornelius-mulleri</i>	Mc Cain Valley Road	32.770260	-116.258620	1061	0
32--3	<i>Quercus berberidifolia</i>	Japatul	32.823380	-116.627470	1022	0
32--4	<i>Quercus berberidifolia</i>	Japatul	32.823380	-116.627470	1022	0
32--5	<i>Quercus engelmannii</i>	Japatul	32.823380	-116.627470	1022	0
34--2	<i>Quercus cornelius-mulleri</i>	Joshua Tree National Park	34.017380	-116.167374	1314	0
34--3	<i>Quercus cornelius-mulleri</i>	Joshua Tree National Park	34.017380	-116.167374	1314	0
34--6	<i>Quercus cornelius-mulleri</i>	Joshua Tree National Park	34.017380	-116.167374	1314	0
34--7	<i>Quercus cornelius-mulleri</i>	Joshua Tree National Park	34.017380	-116.167374	1314	0
41--1	<i>Quercus cornelius-mulleri</i>	Yucaipa	34.102467	-117.182283	391	0
42--10	<i>Quercus berberidifolia</i>	Yucaipa	34.069250	-117.005850	1106	0
43--2	<i>Quercus berberidifolia</i>	Yucaipa	34.038817	-117.021700	928	0
45--7	<i>Quercus engelmannii</i>	Glendora	34.185567	-118.095283	396	0
45--13	<i>Quercus engelmannii</i>	Glendora	34.153133	-117.846033	319	0
50--2	<i>Quercus engelmannii</i>	Daley Ranch	33.165724	-117.044648	375	0
50--4	<i>Quercus engelmannii</i>	Daley Ranch	33.166256	-117.049365	376	0
51--6	<i>Quercus engelmannii</i>	Pasadena	34.147693	-118.052012	181	1
51--7	<i>Quercus engelmannii</i>	Pasadena	34.139128	-118.057162	170	1
51--12	<i>Quercus engelmannii</i>	Pasadena	34.139128	-118.057162	170	1
51--13	<i>Quercus engelmannii</i>	Pasadena	34.139128	-118.057162	170	1
51--14	<i>Quercus engelmannii</i>	Pasadena	34.139128	-118.057162	170	1
51--16	<i>Quercus engelmannii</i>	Pasadena	34.139128	-118.057162	170	1
51--18	<i>Quercus engelmannii</i>	Pasadena	34.139128	-118.057162	170	1
51--19	<i>Quercus engelmannii</i>	Pasadena	34.139128	-118.057162	170	1
52--1	<i>Quercus engelmannii</i>	Pasadena	34.134150	-118.118803	223	1
52--2	<i>Quercus engelmannii</i>	Pasadena	34.129225	-118.120617	213	1
52--3	<i>Quercus engelmannii</i>	Pasadena	34.131655	-118.121470	221	1
52--5	<i>Quercus engelmannii</i>	Pasadena	34.130833	-118.120256	212	1
52--7	<i>Quercus engelmannii</i>	Pasadena	34.132678	-118.117842	219	1
52--8	<i>Quercus engelmannii</i>	Pasadena	34.130789	-118.119753	212	1
52--10	<i>Quercus engelmannii</i>	Pasadena	34.137130	-118.125649	230	1
52--11	<i>Quercus engelmannii</i>	Pasadena	34.137084	-118.122379	229	1

Bio4	Bio15	Bio18	Bio19	AET	CWD	Tmn	Tmx
380.1364	97.3892	10.1223	198.8824	266.9767	1095.6433	5.6746	27.1754
380.1364	97.3892	10.1223	198.8824	266.9767	1095.6433	5.6746	27.1754
370.2700	98.4751	10.3097	227.8383	271.5767	1097.4301	6.5644	27.1258
369.2776	97.5917	10.2504	223.1429	268.8400	1091.0967	6.2719	26.9641
370.0009	97.5239	10.2224	220.4200	339.5033	1017.2700	6.3659	27.0147
370.0009	97.5239	10.2224	220.4200	339.5033	1017.2700	6.3659	27.0147
373.9874	97.5115	10.2564	206.5997	333.7500	1030.5634	6.2270	27.1378
373.9874	97.5115	10.2564	206.5997	333.7500	1030.5634	6.2270	27.1378
373.9874	97.5115	10.2564	206.5997	333.7500	1030.5634	6.2270	27.1378
374.0985	97.4593	10.2830	214.7017	333.2400	1033.0000	6.2141	27.2172
374.0985	97.4593	10.2830	214.7017	333.2400	1033.0000	6.2141	27.2172
374.0985	97.4593	10.2830	214.7017	333.2400	1033.0000	6.2141	27.2172
378.2494	97.3497	10.1684	202.8957	333.2467	1028.6033	5.9076	27.2664
378.2494	97.3497	10.1684	202.8957	333.2467	1028.6033	5.9076	27.2664
438.8159	92.1400	13.1310	220.2800	371.5300	1008.7067	5.2637	30.1226
439.5643	92.3695	13.2423	221.7277	334.6100	1040.4733	5.3694	30.2230
477.3221	92.7517	15.8276	261.3906	411.2567	978.3800	5.8033	30.8449
467.0341	92.9702	15.0943	257.8180	324.9567	1067.7600	5.7570	30.9136
470.2392	92.7860	15.2823	258.0377	406.7367	979.9167	5.6803	30.8587
470.2392	92.7860	15.2823	258.0377	406.7367	979.9167	5.6803	30.8587
459.1645	93.0333	14.6077	254.6253	375.2333	1017.2367	5.6799	30.9626
459.1645	93.0333	14.6077	254.6253	375.2333	1017.2367	5.6799	30.9626
459.1645	93.0333	14.6077	254.6253	375.2333	1017.2367	5.6799	30.9626
458.8594	93.0007	14.5886	254.4893	304.9567	1081.5634	5.6598	30.9502
434.2958	92.0631	12.8876	217.1597	332.0667	1046.1899	5.2913	30.0104
434.2958	92.0631	12.8876	217.1597	332.0667	1046.1899	5.2913	30.0104
438.8159	92.1400	13.1310	220.2800	371.5300	1008.7067	5.2637	30.1226
438.8159	92.1400	13.1310	220.2800	371.5300	1008.7067	5.2637	30.1226
576.2894	91.0272	22.7684	277.1040	373.1167	983.2700	3.0804	32.5149
629.1365	85.5563	34.2197	309.8180	472.1333	886.1467	2.1594	31.0288
629.1365	85.5563	34.2197	309.8180	472.1333	886.1467	2.1594	31.0288
629.1365	85.5563	34.2197	309.8180	472.1333	886.1467	2.1594	31.0288
629.1365	85.5563	34.2197	309.8180	472.1333	886.1467	2.1594	31.0288
628.5595	85.1225	35.3570	312.2357	374.7100	984.4933	2.1316	30.9558
591.1665	87.9083	29.1979	293.1047	441.9267	901.0100	1.5434	33.3664
591.0498	88.2075	28.6613	291.4730	437.1867	897.1600	1.5357	33.5461
591.0498	88.2075	28.6613	291.4730	437.1867	897.1600	1.5357	33.5461
590.6892	88.3595	28.3473	290.0426	336.3200	1008.8133	1.6612	33.3259
590.6892	88.3595	28.3473	290.0426	336.3200	1008.8133	1.6612	33.3259
595.0372	72.5893	55.0823	221.0423	293.9633	944.3300	-0.6444	31.6790
595.0372	72.5893	55.0823	221.0423	293.9633	944.3300	-0.6444	31.6790
595.0372	72.5893	55.0823	221.0423	293.9633	944.3300	-0.6444	31.6790
595.7227	72.3635	55.0151	218.7166	291.0067	940.1100	-0.8712	31.8237
595.7227	72.3635	55.0151	218.7166	291.0067	940.1100	-0.8712	31.8237
595.7227	72.3635	55.0151	218.7166	291.0067	940.1100	-0.8712	31.8237
595.7227	72.3635	55.0151	218.7166	291.0067	940.1100	-0.8712	31.8237
595.1228	72.4333	55.6597	223.3609	296.9967	943.4967	-0.6829	31.5688
595.3404	72.3422	56.1543	226.0340	300.6600	944.5967	-0.5432	31.4323
424.1799	89.2308	10.8634	182.0436	290.5133	1072.4733	5.4009	28.9638
424.1799	89.2308	10.8634	182.0436	290.5133	1072.4733	5.4009	28.9638
424.1799	89.2308	10.8634	182.0436	290.5133	1072.4733	5.4009	28.9638
486.7906	86.5695	14.4440	208.8703	309.8333	1047.7333	3.2761	31.8762
486.7906	86.5695	14.4440	208.8703	309.8333	1047.7333	3.2761	31.8762
484.0013	86.7524	14.1674	207.8947	343.1233	1012.3867	3.1508	32.0899
484.0013	86.7524	14.1674	207.8947	343.1233	1012.3867	3.1508	32.0899

484.0013	86.7524	14.1674	207.8947	343.1233	1012.3867	3.1508	32.0899
484.6028	86.4464	14.6947	208.2640	311.5967	1031.0900	3.2532	31.8492
486.7600	86.3605	14.8267	209.3064	314.6900	1035.2933	3.3448	31.7353
578.5043	83.1494	30.3453	279.1177	334.8667	967.8067	2.1519	31.6718
576.0093	82.4472	32.8696	294.9427	399.7233	859.7233	1.5962	31.3068
576.0093	82.4472	32.8696	294.9427	399.7233	859.7233	1.5962	31.3068
576.0093	82.4472	32.8696	294.9427	399.7233	859.7233	1.5962	31.3068
576.0093	82.4472	32.8696	294.9427	399.7233	859.7233	1.5962	31.3068
576.0093	82.4472	32.8696	294.9427	399.7233	859.7233	1.5962	31.3068
576.0093	82.4472	32.8696	294.9427	399.7233	859.7233	1.5962	31.3068
576.0093	82.4472	32.8696	294.9427	399.7233	859.7233	1.5962	31.3068
576.0093	82.4472	32.8696	294.9427	399.7233	859.7233	1.5962	31.3068
576.0093	82.4472	32.8696	294.9427	399.7233	859.7233	1.5962	31.3068
574.8914	82.6703	32.4713	290.9890	404.4267	868.5867	1.6461	31.5582
574.8914	82.6703	32.4713	290.9890	404.4267	868.5867	1.6461	31.5582
580.4568	81.9983	33.7061	298.7904	360.3067	910.8267	1.6970	31.1319
589.7266	79.2732	38.4704	331.9111	508.8900	757.4333	1.7506	29.6564
569.9323	81.8352	41.6803	335.2399	362.6367	890.4633	1.1870	31.7301
569.9323	81.8352	41.6803	335.2399	362.6367	890.4633	1.1870	31.7301
579.5109	81.4345	42.4523	332.5860	373.6500	907.7633	1.6139	31.6443
579.5109	81.4345	42.4523	332.5860	373.6500	907.7633	1.6139	31.6443
579.5109	81.4345	42.4523	332.5860	373.6500	907.7633	1.6139	31.6443
569.9323	81.8352	41.6803	335.2399	362.6367	890.4633	1.1870	31.7301
582.6415	80.2860	37.4563	274.5073	332.5967	945.8233	1.0448	32.9506
600.2476	79.0623	35.7639	246.3356	315.6967	991.2300	0.8502	33.1650
610.8379	77.6105	34.0413	216.9031	371.1867	922.8167	0.5490	33.7404
610.8379	77.6105	34.0413	216.9031	371.1867	922.8167	0.5490	33.7404
610.8379	77.6105	34.0413	216.9031	371.1867	922.8167	0.5490	33.7404
621.8040	75.7177	32.7863	192.6657	282.9533	1035.0333	0.6176	34.3213
618.9254	75.6537	33.1863	193.4190	343.4700	968.2400	0.6704	34.2583
618.9254	75.6537	33.1863	193.4190	343.4700	968.2400	0.6704	34.2583
618.9254	75.6537	33.1863	193.4190	343.4700	968.2400	0.6704	34.2583
612.3323	77.8606	51.5206	367.9579	378.3333	689.9600	-1.9514	27.5531
613.6111	78.5271	49.8343	371.2664	408.1967	668.3600	-1.7757	27.6808
607.0230	81.3031	39.6603	359.1536	338.8867	808.3267	-0.9068	28.0386
607.0230	81.3031	39.6603	359.1536	338.8867	808.3267	-0.9068	28.0386
607.0169	81.3256	39.2463	357.4363	330.9467	817.4100	-0.8869	28.0281
555.0564	79.3772	30.1353	230.8517	306.1100	937.0567	0.2806	31.6334
554.6608	79.4054	30.2267	231.1196	302.6867	941.5067	0.3666	31.5946
554.6608	79.4054	30.2267	231.1196	302.6867	941.5067	0.3666	31.5946
554.6608	79.4054	30.2267	231.1196	302.6867	941.5067	0.3666	31.5946
554.6608	79.4054	30.2267	231.1196	302.6867	941.5067	0.3666	31.5946
554.6608	79.4054	30.2267	231.1196	302.6867	941.5067	0.3666	31.5946
554.6608	79.4054	30.2267	231.1196	302.6867	941.5067	0.3666	31.5946
555.0564	79.3772	30.1353	230.8517	306.1100	937.0567	0.2806	31.6334
555.0564	79.3772	30.1353	230.8517	306.1100	937.0567	0.2806	31.6334
555.0564	79.3772	30.1353	230.8517	306.1100	937.0567	0.2806	31.6334
553.6221	75.3658	33.2117	163.1417	263.9033	1026.1567	0.9832	31.4209
555.3928	75.3475	33.1590	162.8717	263.6100	1026.7700	0.9557	31.4562

555.3928	75.3475	33.1590	162.8717	263.6100	1026.7700	0.9557	31.4562
555.3928	75.3475	33.1590	162.8717	263.6100	1026.7700	0.9557	31.4562
555.3928	75.3475	33.1590	162.8717	263.6100	1026.7700	0.9557	31.4562
555.3928	75.3475	33.1590	162.8717	263.6100	1026.7700	0.9557	31.4562
549.1346	81.7484	24.8850	192.7637	286.5600	1046.0267	1.5194	32.0478
549.7033	81.8236	24.8687	193.3321	286.6967	1042.0367	1.6104	31.9716
547.4017	82.0205	24.6663	193.5746	288.1733	1047.4667	1.5930	31.9602
547.4017	82.0205	24.6663	193.5746	288.1733	1047.4667	1.5930	31.9602
547.4017	82.0205	24.6663	193.5746	288.1733	1047.4667	1.5930	31.9602
547.5016	82.0355	24.4060	194.1287	290.9000	1056.6567	1.5941	31.9649
435.7986	86.6003	11.9040	179.1353	300.6567	1019.9367	4.7250	29.7848
435.7986	86.6003	11.9040	179.1353	300.6567	1019.9367	4.7250	29.7848
435.7986	86.6003	11.9040	179.1353	300.6567	1019.9367	4.7250	29.7848
486.7124	85.3683	16.5353	218.3247	312.0533	1010.4200	4.2133	31.1232
486.7124	85.3683	16.5353	218.3247	312.0533	1010.4200	4.2133	31.1232
486.7124	85.3683	16.5353	218.3247	312.0533	1010.4200	4.2133	31.1232
486.7124	85.3683	16.5353	218.3247	312.0533	1010.4200	4.2133	31.1232
496.0538	85.2838	17.0480	221.5853	315.4300	999.9600	3.8827	31.1367
500.4679	85.2451	17.1100	221.8370	313.8700	1005.5467	3.7170	31.0994
500.4679	85.2451	17.1100	221.8370	313.8700	1005.5467	3.7170	31.0994
500.4679	85.2451	17.1100	221.8370	313.8700	1005.5467	3.7170	31.0994
500.4679	85.2451	17.1100	221.8370	313.8700	1005.5467	3.7170	31.0994
500.4679	85.2451	17.1100	221.8370	313.8700	1005.5467	3.7170	31.0994
500.4679	85.2451	17.1100	221.8370	313.8700	1005.5467	3.7170	31.0994
500.4679	85.2451	17.1100	221.8370	313.8700	1005.5467	3.7170	31.0994
500.4679	85.2451	17.1100	221.8370	313.8700	1005.5467	3.7170	31.0994
491.8141	85.1956	16.9910	219.9160	315.8967	1002.9933	3.9869	31.0233
481.8214	85.5794	16.1957	218.4880	368.2833	947.0667	4.2812	31.2217
489.6395	85.3523	16.7690	220.0287	311.1233	1000.8067	4.0246	31.0702
489.6395	85.3523	16.7690	220.0287	311.1233	1000.8067	4.0246	31.0702
488.7370	84.0830	16.6531	206.4296	392.9833	969.0733	4.6167	31.5930
488.7370	84.0830	16.6531	206.4296	392.9833	969.0733	4.6167	31.5930
490.6395	83.9263	16.8110	206.4753	369.7200	997.7100	4.8198	31.5370
491.9266	83.9593	17.0303	207.5510	351.6300	1011.1933	4.7639	31.5282
491.9266	83.9593	17.0303	207.5510	351.6300	1011.1933	4.7639	31.5282
492.8613	84.0850	17.2221	210.3427	366.4400	992.2433	4.5687	31.5124
492.8613	84.0850	17.2221	210.3427	366.4400	992.2433	4.5687	31.5124
455.8214	87.3179	13.9237	193.2837	309.8200	1058.9667	4.6767	31.0046
455.8214	87.3179	13.9237	193.2837	309.8200	1058.9667	4.6767	31.0046
455.8214	87.3179	13.9237	193.2837	309.8200	1058.9667	4.6767	31.0046
455.8214	87.3179	13.9237	193.2837	309.8200	1058.9667	4.6767	31.0046
589.3147	84.6608	22.8960	222.6654	322.8533	1111.7800	3.8684	33.6287





662.6185	66.9198	48.8130	160.1556	302.0800	1077.4000	2.2377	31.4097
627.3567	74.4334	38.4769	194.9559	297.8800	1055.0601	2.0179	30.3397
627.3567	74.4334	38.4769	194.9559	297.8800	1055.0601	2.0179	30.3397
627.3567	74.4334	38.4769	194.9559	297.8800	1055.0601	2.0179	30.3397
627.3567	74.4334	38.4769	194.9559	297.8800	1055.0601	2.0179	30.3397
627.3567	74.4334	38.4769	194.9559	297.8800	1055.0601	2.0179	30.3397
623.1758	73.7847	35.4147	166.7344	274.5900	1109.7900	2.7034	32.1259
575.9579	85.1717	23.0976	303.4927	475.1933	826.0367	1.8777	31.8282
575.9579	85.1717	23.0976	303.4927	475.1933	826.0367	1.8777	31.8282
575.9579	85.1717	23.0976	303.4927	475.1933	826.0367	1.8777	31.8282
705.4928	69.5020	53.9587	115.0303	192.0000	1097.8033	-0.2228	32.1726
705.4928	69.5020	53.9587	115.0303	192.0000	1097.8033	-0.2228	32.1726
705.4928	69.5020	53.9587	115.0303	192.0000	1097.8033	-0.2228	32.1726
705.4928	69.5020	53.9587	115.0303	192.0000	1097.8033	-0.2228	32.1726
538.7769	86.5944	16.3506	179.4683	311.4133	1144.5200	4.3690	33.3533
587.3458	77.0261	38.9309	278.8337	473.6233	910.0833	2.7858	30.2922
589.2693	81.1778	29.4617	261.1390	352.3933	1035.2500	3.4763	31.7341
449.9070	96.4526	15.5174	334.4863	403.1400	1018.5733	6.6146	30.1487
447.3210	96.1826	16.2613	323.3467	383.4367	1062.7867	5.8034	30.5354
432.1971	92.6876	11.6744	219.9007	305.7767	1064.3000	4.3389	29.8892
430.6538	92.4782	11.7403	219.0403	305.9767	1065.4067	4.3653	29.8372
430.9745	97.9927	12.0467	270.3863	338.0067	1097.3733	6.2701	30.8770
430.5948	98.5373	11.6650	260.9733	329.3333	1100.6899	6.1744	30.8812
430.5948	98.5373	11.6650	260.9733	329.3333	1100.6899	6.1744	30.8812
430.5948	98.5373	11.6650	260.9733	329.3333	1100.6899	6.1744	30.8812
430.5948	98.5373	11.6650	260.9733	329.3333	1100.6899	6.1744	30.8812
430.5948	98.5373	11.6650	260.9733	329.3333	1100.6899	6.1744	30.8812
430.5948	98.5373	11.6650	260.9733	329.3333	1100.6899	6.1744	30.8812
430.5948	98.5373	11.6650	260.9733	329.3333	1100.6899	6.1744	30.8812
424.2923	100.0189	11.7950	279.1964	337.6567	1084.6533	6.0121	30.3599
423.1475	100.3171	11.6763	276.7510	335.9633	1088.8433	5.9866	30.3800
424.1457	100.0716	11.7693	278.6053	337.4300	1086.2032	6.0043	30.3660
424.1457	100.0716	11.7693	278.6053	337.4300	1086.2032	6.0043	30.3660
424.9162	100.0536	11.8170	277.8597	337.0300	1085.9667	5.9673	30.3781
424.1457	100.0716	11.7693	278.6053	337.4300	1086.2032	6.0043	30.3660
423.4190	100.0772	11.8169	279.7927	337.8367	1084.6467	6.0554	30.3339
423.7306	100.0175	11.7910	279.7327	337.6800	1083.7032	6.0277	30.3367