

Table S1. Correlation (below diagonal) and P -values (above diagonal) among independent variables used in general linear models to test the role of past niche suitability and stability on present genetic diversity

	N_{LIG}	N_{LGM}	N_P	S_{LIG}	S_{LGM}
N_{LIG}	-	3×10^{-7}	7×10^{-9}	0.004	0.138
N_{LGM}	0.53	-	0.008	0.005	2×10^{-9}
N_P	0.59	0.29	-	0.538	0.121
S_{LIG}	0.32	-0.31	0.07	-	3×10^{-6}
S_{LGM}	-0.17	-0.61	0.17	0.49	-

Table S2. Mean log likelihood ($\ln P(K)$), its standard deviation (SD), and ΔK calculated from 10 replicates for each of 1 – 10 clusters (K) using a Bayesian clustering analysis implemented in STRUCTURE

K	$\ln P(K)$	SD	ΔK
1	-6384.2	0.2	-
2	-6066.6	1.1	269.9
3	-6044.3	8.4	1.8
4	-6036.6	8.7	4.9
5	-5986.5	9.5	8.5
6	-6016.3	23.0	23.2
7	-6579.7	296.3	1.9
8	-6582.7	169.9	0.1
9	-6562.5	131.2	1.9
10	-6790.2	205.2	-

Table S3. Analyses of molecular variance based on Φ -statistics for nuclear microsatellite (nSSR) sample sites within STRUCTURE clusters, chloroplast microsatellite (cpSSR) sites, and cpSSR BAPS clusters

Source	Degrees of freedom	Sum of squares	Mean squares	Variance	Percent of variation	Φ -statistic	<i>P</i>
nSSR sites/clusters							
Among clusters	1	127.92	127.92	0.97	17%	$\Phi_{RT} = 0.17$	0.010
Among sites within clusters	60	410.13	6.84	0.61	10%	$\Phi_{PR} = 0.13$	0.010
Within sites	205	867.24	4.23	4.23	73%	$\Phi_{PT} = 0.27$	0.010
Total	266	1405.28		5.80	100%		
cpSSR sites							
Among sites	63	690.90	10.97	3.53	88%	$\Phi_{PT} = 0.88$	0.010
Within sites	126	60.17	0.48	0.48	12%		
Total	189	751.06		4.01	100%		
cpSSR BAPS clusters							
Among clusters	24	288.82	12.03	1.58	92%	$\Phi_{PT} = 0.92$	0.010
Within sites	165	22.86	0.14	0.14	8%		
Total	189	311.68		1.72	100%		

Table S4. Percent contribution and permutation importance of each variable used to construct valley oak (*Quercus lobata*) ecological niche models in MAXENT

Variable	Definition	Percent contribution	Permutation importance
bio_18	Precipitation of warmest quarter	48.4	68.8
bio_15	Precipitation seasonality	27.4	0.8
bio_19	Precipitation of coldest quarter	17.6	6.3
bio_5	Maximum temperature	2.4	2.1
bio_6	Minimum temperature	1.9	17.4
bio_4	Temperature seasonality	1.2	0.5
bio_1	Annual mean temperature	0.6	1.1
bio_12	Annual precipitation	0.4	2.9

Table S5. Nuclear microsatellite (nSSR) allelic richness and heterozygosity, niche suitabilities, and niche stabilities by site for samples used in genetic analyses (additional sites were used to construct niche models)

Site #	Latitude	Longitude	Niche suitabilities			Niche stabilities		nSSR diversity	
			N_{LIG}	N_{LGM}	N_{Pres}	$S_{LIG-LGM}$	$S_{LGM-Pres}$	A_r	H_e
1	34.81650	-118.88120	0.136	0.101	0.480	0.036	0.379	3.83	0.620
2	36.05960	-119.03430	0.128	0.287	0.374	0.160	0.087	3.83	0.648
3	36.09730	-118.86430	0.241	0.247	0.647	0.006	0.400	4.00	0.657
4	36.09870	-118.86670	0.241	0.247	0.647	0.006	0.400	3.50	0.620
5	36.48600	-119.12120	0.337	0.570	0.321	0.233	0.249	2.33	0.426
8	36.72520	-119.45910	0.250	0.319	0.237	0.069	0.082	3.67	0.667
9	37.15660	-119.73780	0.490	0.698	0.479	0.208	0.219	2.67	0.481
10	37.46190	-119.88000	0.392	0.396	0.505	0.003	0.109	3.00	0.519
11	37.97930	-120.38840	0.498	0.449	0.574	0.049	0.124	3.17	0.528
13	38.71400	-120.81170	0.242	0.206	0.478	0.036	0.271	2.67	0.519
14	38.99560	-121.10850	0.555	0.432	0.614	0.124	0.182	4.00	0.694
16	39.49730	-121.72940	0.545	0.551	0.388	0.005	0.162	2.83	0.491
17	39.71140	-122.00420	0.248	0.493	0.383	0.245	0.110	3.33	0.574
20	40.57150	-122.37780	0.429	0.090	0.468	0.339	0.378	3.17	0.593
25	39.38420	-123.34350	0.458	0.059	0.537	0.399	0.478	3.00	0.528
26	39.04240	-122.74910	0.270	0.383	0.542	0.112	0.159		
27	39.10600	-122.31040	0.217	0.353	0.521	0.136	0.168	3.33	0.602
28	38.74760	-122.61840	0.583	0.492	0.711	0.091	0.219	3.17	0.556
29	38.48290	-122.44310	0.767	0.668	0.651	0.099	0.017		
30	38.23920	-122.26750	0.619	0.708	0.673	0.089	0.035		
31	37.86470	-122.03450	0.664	0.597	0.498	0.067	0.099	3.50	0.648
32	37.60160	-121.87310	0.540	0.611	0.511	0.071	0.100		
33	37.15560	-121.69040	0.546	0.685	0.591	0.139	0.094		
34	35.86520	-120.81690	0.121	0.242	0.175	0.121	0.067		
35	35.52820	-120.70370	0.564	0.415	0.632	0.149	0.217		
36	34.72320	-120.21620	0.621	0.412	0.461	0.210	0.050		
37	38.53510	-121.74940	0.459	0.588	0.433	0.130	0.156		
40	38.38560	-122.46340	0.725	0.565	0.669	0.160	0.104		
41	40.08540	-122.17350	0.402	0.418	0.218	0.015	0.200	3.00	0.565
42	39.90950	-122.08972	0.431	0.461	0.319	0.030	0.142	2.67	0.472
43	39.78218	-122.29360	0.508	0.471	0.343	0.038	0.128	2.50	0.542
45	34.87422	-118.89391	0.150	0.101	0.595	0.049	0.494		
46	34.40974	-118.57401	0.250	0.607	0.322	0.357	0.285	3.17	0.556
47	34.18697	-118.89005	0.491	0.468	0.659	0.023	0.191		
48	34.69370	-120.04140	0.549	0.456	0.649	0.093	0.193		
49	34.75480	-118.70950	0.131	0.181	0.340	0.050	0.159	3.83	0.639
50	34.83080	-118.87630	0.113	0.168	0.482	0.056	0.313		
51	34.91730	-118.71690	0.050	0.123	0.464	0.074	0.341	2.50	0.463

52	34.94160	-118.63210	0.074	0.096	0.430	0.022	0.334	3.50	0.574
54	34.85850	-118.69690	0.102	0.169	0.275	0.067	0.106		
55	35.05200	-118.73400	0.159	0.284	0.232	0.126	0.052	3.92	0.710
56	40.33570	-121.91520	0.122	0.042	0.175	0.080	0.133	3.19	0.623
59	38.26460	-121.43950	0.357	0.580	0.292	0.222	0.288	3.04	0.573
60	38.26140	-122.39870	0.691	0.764	0.690	0.074	0.075	3.15	0.589
61	38.45193	-122.63369	0.760	0.561	0.721	0.199	0.160	4.01	0.708
62	38.43770	-122.50350	0.708	0.732	0.684	0.024	0.048	3.69	0.693
63	38.83200	-123.01020	0.728	0.583	0.560	0.145	0.023	3.68	0.663
64	39.07940	-123.21600	0.432	0.090	0.502	0.342	0.412	2.33	0.490
65	39.38780	-123.34550	0.458	0.059	0.537	0.399	0.478	2.67	0.523
67	39.64390	-123.53090	0.515	0.042	0.273	0.473	0.230	2.80	0.567
68	39.04350	-122.77590	0.275	0.397	0.525	0.121	0.128	3.50	0.653
70	38.77960	-122.27790	0.568	0.475	0.611	0.092	0.136	3.79	0.690
71	38.48790	-122.14850	0.654	0.654	0.549	0.000	0.105	3.85	0.673
72	37.88620	-122.19630	0.596	0.610	0.469	0.015	0.141	3.72	0.640
73	37.89970	-122.20980	0.596	0.610	0.469	0.015	0.141	3.44	0.641
76	37.84420	-121.94950	0.608	0.637	0.573	0.029	0.064	3.29	0.557
77	37.60410	-121.87350	0.540	0.611	0.511	0.071	0.100	2.57	0.473
79	37.16540	-121.71530	0.546	0.685	0.591	0.139	0.094	3.19	0.630
80	37.06330	-121.19750	0.307	0.374	0.282	0.067	0.092	4.05	0.703
81	36.75940	-121.50410	0.590	0.605	0.617	0.015	0.012	3.36	0.594
83	36.49660	-121.14250	0.234	0.320	0.409	0.086	0.089	3.50	0.593
84	36.10170	-121.14510	0.401	0.339	0.509	0.062	0.169	3.74	0.681
85	36.06090	-121.31050	0.714	0.293	0.626	0.421	0.333	3.73	0.707
86	36.38680	-121.55100	0.795	0.234	0.688	0.560	0.454	3.49	0.646
88	36.23630	-121.47810	0.801	0.300	0.658	0.501	0.359	3.18	0.630
89	35.79200	-120.92390	0.270	0.305	0.449	0.035	0.144	3.27	0.587
90	35.66890	-120.93110	0.676	0.328	0.664	0.348	0.335	3.21	0.583
91	34.73410	-120.28030	0.531	0.226	0.239	0.306	0.013	3.77	0.663
92	36.42130	-121.61260	0.658	0.532	0.507	0.126	0.025	2.83	0.500
93	35.97650	-121.33780	0.719	0.324	0.598	0.394	0.274	2.74	0.484
94	35.93580	-121.12110	0.343	0.288	0.503	0.055	0.215	3.58	0.633
97	37.35770	-121.74720	0.416	0.633	0.491	0.217	0.142	3.55	0.653
98	37.32460	-121.66790	0.587	0.721	0.531	0.135	0.191	3.59	0.700
100	37.33670	-121.65490	0.587	0.721	0.531	0.135	0.191		
101	38.26670	-120.50310	0.250	0.103	0.428	0.146	0.324		0.680
102	38.04960	-120.63076	0.451	0.333	0.495	0.118	0.162	3.67	0.593
112	34.45439	-119.23015	0.464	0.538	0.619	0.074	0.081	2.88	0.556
113	34.99289	-119.80299	0.491	0.279	0.436	0.212	0.157	3.83	0.736
114	34.99281	-119.88918	0.624	0.056	0.575	0.568	0.519	3.80	0.728
115	34.99833	-120.20089	0.642	0.443	0.608	0.198	0.165	3.10	0.599
116	34.09750	-118.72000	0.484	0.409	0.605	0.075	0.195	3.53	0.671

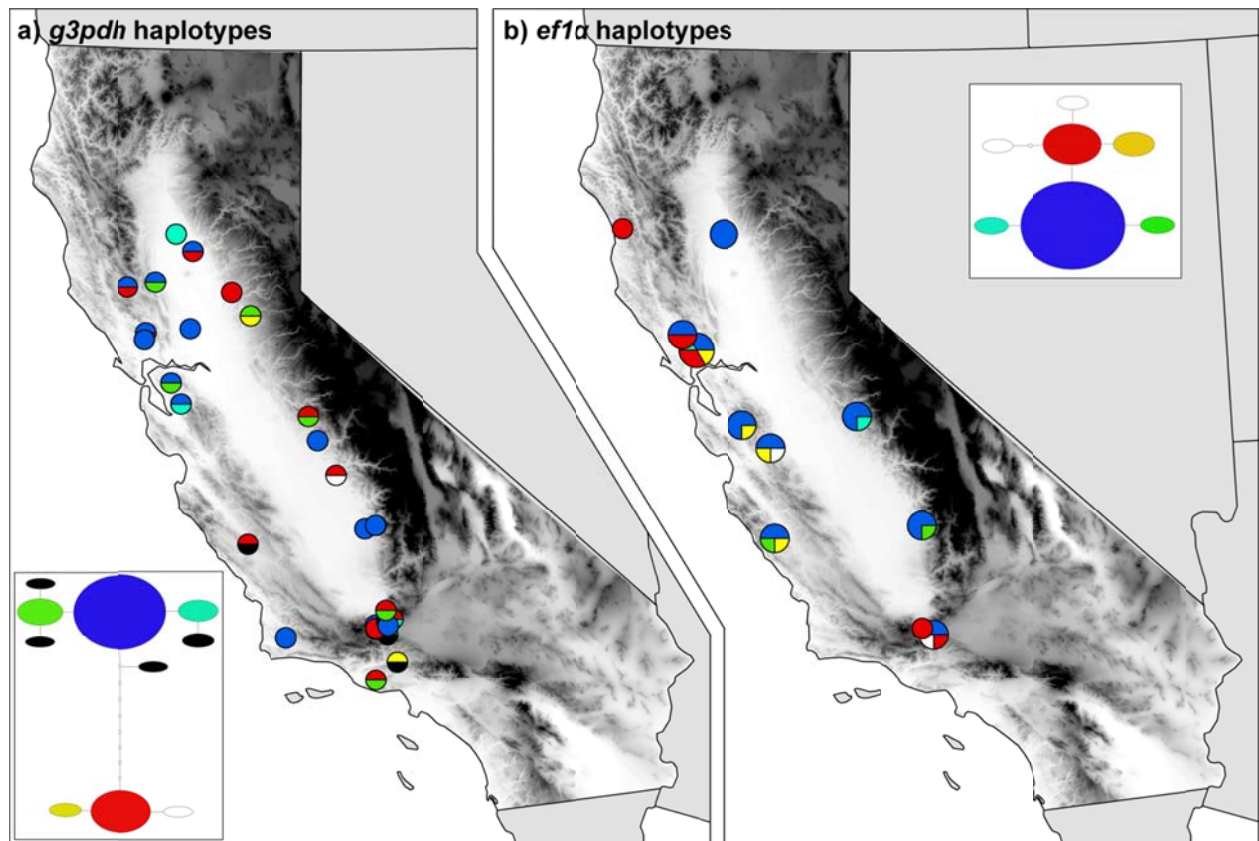


Figure S1. Maps of genetic variation in valley oak showing haplotype distributions for (a) *glyceraldehyde 3-phosphate dehydrogenase* (*g3pdh*) and (b) *elongation factor 1- α* (*ef1 α*). Sample sites are colored according to the inset parsimony network.

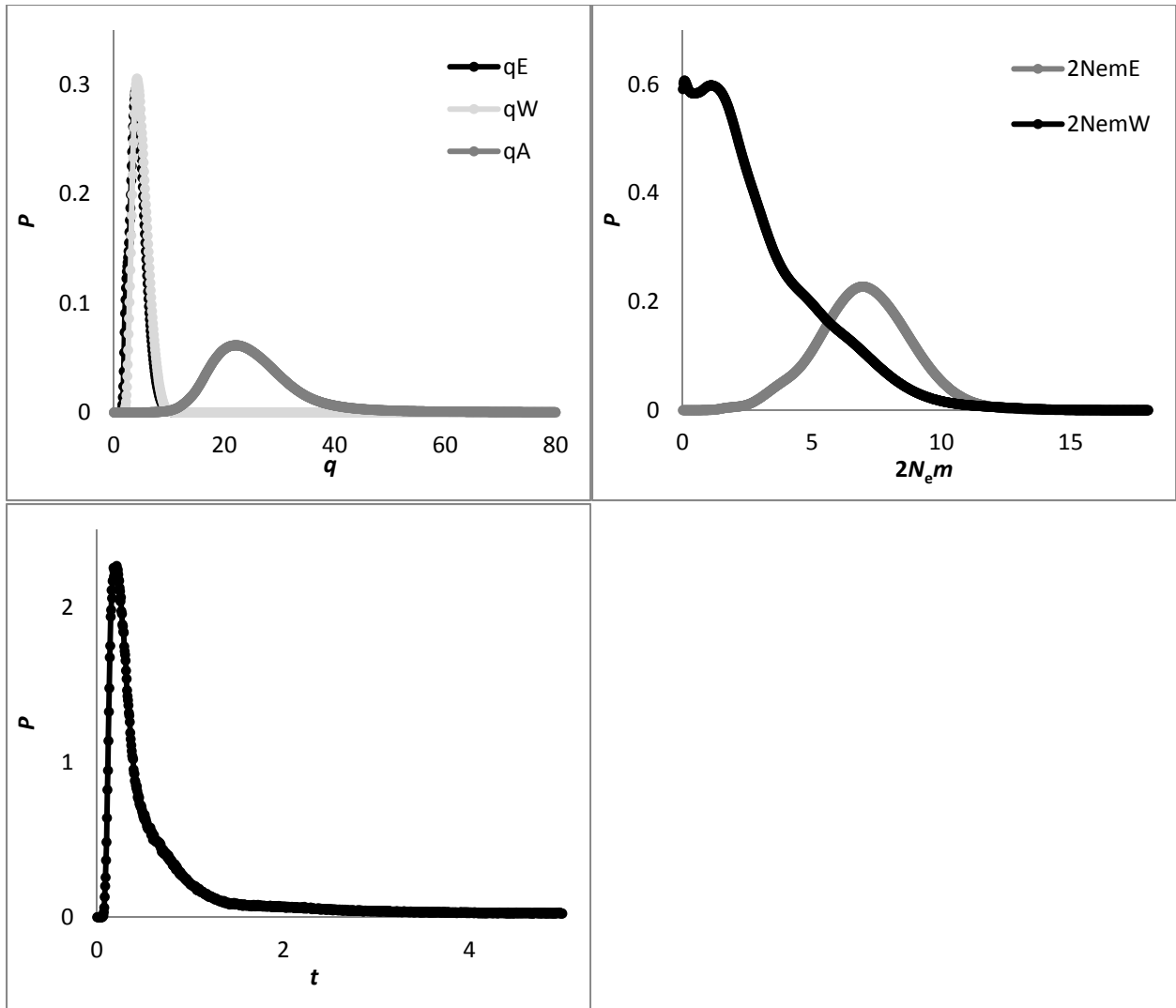
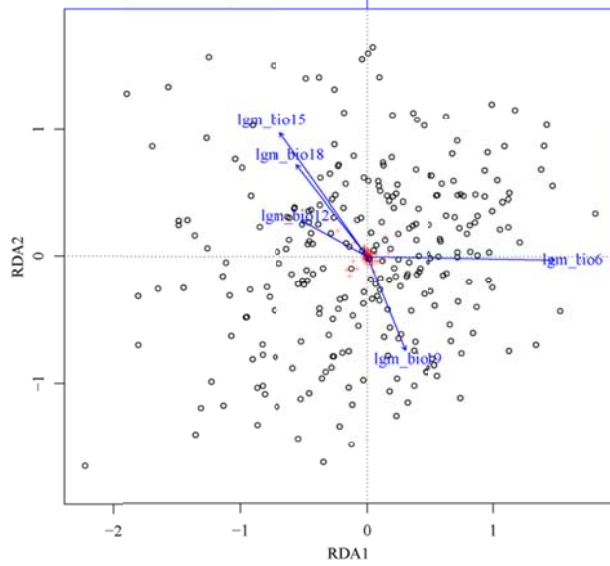


Figure S2. Posterior distributions for per-locus mutation rate-scaled parameter estimates from the IMA2 run with the highest effective sample size ($ESS > 50$): effective population sizes of eastern genetic cluster (q_E), western genetic cluster (q_W), and ancestor (q_A); population migration rate from west to east ($2N_e m_E$) and east to west ($2N_e m_W$); and divergence time (t). Replicate runs produced similar patterns.

a) nSSR pRDA biplot



b) cpSSR pRDA biplot

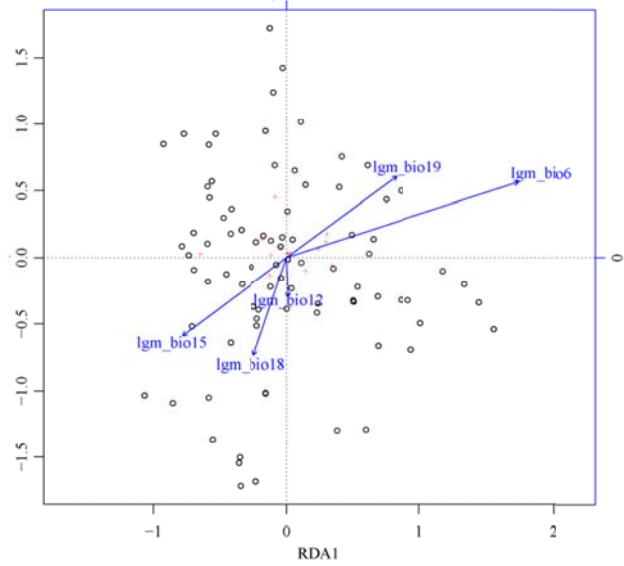


Figure S3. Biplots from partial redundancy analyses (pRDA) of (a) nuclear microsatellite (nSSR) and (b) chloroplast microsatellite (cpSSR) variation on Last Glacial Maximum (~21 ka) climate after controlling for present climate and geographic position. Minimum temperature during the Last Glacial Maximum (lgm_bio6) has the highest loading on the first RDA axes for both molecular markers.