

Contrasting support for alternative models of genomic variation based on microhabitat preference: species-specific effects of climate change in alpine sedges

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SUPPORTING INFORMATION

Environmental niche modeling methodology

ENMs were generated from bioclimatic variables for the present and the LGM for each species with MAXENT v3.3.3e (Phillips *et al.* 2006) using the following parameters: regularization multiplier = 1, max number of background points = 10,000, replicates = 50, replicated run type = cross-validate. To avoid overfitting of the distribution models, the geographic extent of the environmental layers was reduced to an area approximately 20% larger than the known distribution of the species (Anderson & Raza 2010). To guard against the inherent difficulties involved in extrapolating distributions into novel climates (reviewed in Alvarado-Serrano & Knowles 2013), an iterative approach was used to generate ENMs for the LGM. Multivariate environmental similarity surfaces (MESS maps) were used to identify which of the 19 bioclimatic variables resulted in areas of low reliability predictions due to the variables being outside of the range present in the present-day environmental data (Elith *et al.* 2010). MAXENT was rerun excluding these out-of-range variables, and this process of analysis with MESS maps was repeated until no LGM variables were out-of-range compared to present-day bioclimatic variables. Because MESS maps do not indicate changes in the correlations among the environmental variables used for LGM reconstructions (Elith *et al.* 2010), we checked our LGM ENM using only the most informative variable (Bio5) to ensure we were not reporting errant distributional patterns. In addition, a present-day ENM was generated for the subset of variables that were not out-of-range and compared to a ENM constructed using all climatic variables with greater than 5% importance (determined by jackknifing) to assess their similarity.

Library construction and data processing

Anonymous genomic loci were developed from five Illumina 2500 sequencing runs using a restriction associated DNA sequencing (RADseq) approach (for details see Peterson *et al.* 2012). Briefly, DNA was doubly digested with *EcoRI* and *MseI* restriction enzymes, followed by the ligation of Illumina adaptor sequences and unique 10 base pair barcodes. Ligation products were pooled among samples and the fragments were amplified by 12 cycles of PCR. A Pippin Prep (Sage Science) was used to size select fragments between 400 and 500 base pairs. The library was sequenced at The Centre for Applied Genomics (Hospital for Sick Children, Toronto, Canada) to generate 50 base pair, single-end reads. Sequences were demultiplexed using `process_radtags.pl`, which is distributed as part of the Stacks pipeline (Catchen *et al.* 2013); only reads with Phred scores ≥ 32 , no adaptor contamination, and that had an unambiguous barcode and restriction cut site were retained. Potential chloroplast and mitochondrial sequences were filtered from the processed dataset using Bowtie 0.12.8 (Langmead *et al.* 2009) (see Massatti &

Knowles 2014). Reads showed consistently high sequence quality and remained untrimmed, except for the barcode and restriction enzyme cut site.

Single nucleotide polymorphisms (SNPs) were identified at each RADseq locus and genotypes were called using a multinomial-based likelihood model that accounts for sequencing error as implemented in Stacks v1.25 (Catchen *et al.* 2011; Hohenlohe *et al.* 2012; Catchen *et al.* 2013). A conservative upper bound of the error rate (ϵ) was set to 0.1 to avoid underestimating heterozygotes (Catchen *et al.* 2013). In the first step of the Stacks pipeline, loci and polymorphic nucleotide sites were identified in each individual using the USTACKS program, which groups reads with a minimum coverage depth (m) into a “stack”. The data were processed with $m = 3$; increasing the minimum depth helps to avoid erroneously calling convergent sequencing errors as stacks. Reads were filtered using a removal algorithm that eliminated highly repetitive stacks (i.e., stacks that exceed the expected number of reads for a single locus given the average depth of coverage, for example, when loci are members of multi-gene families) and a ‘deleveraging algorithm’ to resolve over-merged loci (i.e., non-homologous loci misidentified as a single locus). A catalog of consensus loci among individuals was constructed with the CSTACKS program from the USTACKS output files for each species, where loci were merged together across individuals if the distance between them (n) was ≤ 2 . This catalog was used to determine the allele(s) present in each individual at each homologous locus using the SSTACKS program. Our choice of parameters was determined with consideration of avoiding both over- and under-merging of homologous loci in the focal taxa, as well as with reference to other studies (e.g., Renaud *et al.* 2014). Similarity of the number of loci identified in the species for different parameter values used in USTACKS (m) and CSTACKS (n) suggests that the properties of the genomic libraries were similar (i.e., that the potential errors associated with over- or under-merged homologous loci did not differ substantially between the species). The close relatedness of the taxa and the short reads makes an $n \leq 2$ reasonable (also see Renaud *et al.* 2014), although we acknowledge this could be conservative if catalogs were assembled for taxa that were more distantly related, and/or for read lengths larger than 50 base pairs.

- Alvarado-Serrano DF, Knowles LL (2013) Ecological niche models in phylogeographic studies: applications, advances, and precautions. *Molecular Ecology Resources*, **14**, 233–248.
- Anderson RP, Raza A (2010) The effect of the extent of the study region on GIS models of species geographic distributions and estimates of niche evolution: preliminary tests with montane rodents (genus *Nephelomys*) in Venezuela. *Journal of Biogeography*, **37**, 1378–1393.
- Catchen J, Hohenlohe P, Bassham S, Amores A, Cresko WA (2013) Stacks: an analysis tool set for population genomics. *Molecular Ecology*, **22**, 3124–3140.
- Catchen JM, Amores A, Hohenlohe P, Cresko W, Postlethwait JH (2011) Stacks: Building and Genotyping Loci *De Novo* From Short-Read Sequences. *G3: Genes, Genomes, Genetics*, **1**, 171–182.
- Elith J, Kearney M, Phillips S (2010) The art of modeling range-shifting species. *Methods in Ecology and Evolution*, **1**, 330–342.
- Hohenlohe PA, Catchen J, Cresko WA (2012) Population genomic analysis of model and nonmodel organisms using sequenced RAD tags. *Methods in Molecular Biology*, **888**, 235–260.
- Langmead B, Trapnell C, Pop M, Salzberg SL (2009) Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. *Genome Biology*, **10**, R25.

- Massatti R, Knowles LL (2014) Microhabitat differences impact phylogeographic concordance of codistributed species: Genomic evidence in montane sedges (*Carex L.*) from the Rocky Mountains. *Evolution*, **68**, 2833-2846.
- Peterson BK, Weber JN, Kay EH, Fisher HS, Hoekstra HE (2012) Double digest RADseq: an inexpensive method for de novo SNP discovery and genotyping in model and non-model species. *PloS ONE*, **7**, e37135.
- Phillips SJ, Anderson RP, Schapire RE (2006) Maximum entropy modeling of species geographic distributions. *Ecological Modeling*, **190**, 231–259.
- Renaut S, Owens GL, Rieseberg LH (2014) Shared selective pressure and local genomic landscape lead to repeatable patterns of genomic divergence in sunflowers. *Molecular Ecology*, **23**, 311-324.

Table S1. Sampling localities for *Carex chalciolepis* and *C. nova*. Collections were made during the summer of 2011.

Population	Geographic region	Mountain Range	Geographic coordinates	Elevation (m)
Libby Flats	North	Medicine Bow	41.3499, -106.3202	2970 - 3550
Zirkel	North	Park	40.8184, -106.7015	3000 - 3430
Niwot	Central-North	Front	40.0694, -105.6216	3240 - 3630
Flat Tops	Central-North	Flat Tops	39.8649, -107.2383	3170 - 3570
Guanella	Central-North	Front	39.5941, -105.7117	3600 - 3900
Pikes	Central-South	Front	38.8621, -105.0668	3010 - 4200
Lamphier	Central-South	Sawatch	38.6772, -106.6069	3600 - 3900
Ouray	Central-South	Sawatch	38.4329, -106.2407	3400 - 3800
Lizard	South	San Juan	37.8256, -107.9391	3200 - 3700
Blanca	South	Sangre de Cristo	37.5991, -105.4782	3250 - 3800
Red Lakes	South	San Juan	37.1002, -106.4636	3430 - 3540

Table S2. Summary of genomic data collected for each individual for A) *Carex chalciolepis* and B) *C. nova*. Shown are the raw counts of reads from the Illumina runs ('Total') and the number of 'Retained' reads after processing for quality control (i.e., after excluding 'Low Quality' reads and 'No RadTag' reads). We also report the number of remaining reads after filtering out potential chloroplast and mitochondrial DNA ('Post-bowtie', see additional Methods above) and the number of reads retained by Stacks after filtering out potential paralogous loci and over-merged loci; this latter number (also represented by 'Total % retained') is the data which was used to identify homologous loci. Asterisks mark individuals excluded from analyses because they had too few reads.

A) *Carex chalciolepis*

Individual	Total	No RadTag	Low Quality	Retained	Post-bowtie	# retained by stacks	Total % retained
Libby Flats 1	2269864	6142	10146	2240426	2048756	1985763	0.87
Libby Flats 2	2573898	3335	10804	2541563	2379309	2320139	0.90
Libby Flats 3	1504829	980	7860	1485750	1375851	1319219	0.88
Libby Flats 4	1755431	2211	7437	1732805	1612477	1554853	0.89
Libby Flats 5	970330	1102	4127	958742	900554	855331	0.88
Libby Flats 6	742915	818	3583	734324	681104	633809	0.85
Libby Flats 7	835137	1030	3431	825805	759477	712137	0.85
Libby Flats 8	437541	344	2044	432501	400529	365003	0.83
Libby Flats 9	1341269	3005	6190	1324363	1201995	1157381	0.86
Libby Flats 10	1665439	2337	6625	1645436	1527170	1473164	0.88
Zirkel 1	1063134	1777	4531	1047625	992120	942644	0.89
Zirkel 2	1346474	2608	6102	1328265	1219778	1166800	0.87
Zirkel 3	576525	1267	2762	568487	525998	491704	0.85
Zirkel 4	607590	706	3442	599091	547372	513109	0.84
Zirkel 5	872180	798	5114	861119	793244	749972	0.86
Zirkel 6	647245	3598	3081	635940	594267	552664	0.85
Zirkel 7	2139688	2319	9483	2114055	1970048	1907541	0.89
Zirkel 8	2944771	3545	12273	2907035	2710240	2645211	0.90
Zirkel 9	1818223	2204	7449	1796689	1664415	1604871	0.88
Zirkel 10	1155351	1025	5252	1142082	1025115	976428	0.85
Niwot 1	1550383	1115	7668	1532100	1423214	1365514	0.88
Niwot 2	790991	1313	3446	781804	713742	665585	0.84
Niwot 3	405252	1647	2353	398680	364674	331555	0.82
Niwot 4	715457	2334	3606	704831	647777	601083	0.84
Niwot 5	1745519	3812	7043	1724517	1567758	1509504	0.86
Niwot 6	801720	1477	3199	791859	732237	681640	0.85
Niwot 7	913065	2052	3840	901643	832593	778875	0.85
Niwot 8	1563337	2572	9074	1543008	1407370	1345624	0.86
Niwot 9*	1357108	2323	5841	1339197	1238262	1163446	0.86
Niwot 10	1993594	3599	8279	1973450	1796709	1741820	0.87

Table S2. Continued

A) *Carex chalciolepis* (continued)

Individual	Total	No RadTag	Low Quality	Retained	Post-bowtie	# retained by stacks	Total % retained
Flat Tops 1	1281735	2146	9117	1264583	1170587	1124335	0.88
Flat Tops 2	949146	1502	8949	932787	878658	843867	0.89
Flat Tops 3	1222176	766	10798	1205174	1101017	1057760	0.87
Flat Tops 4*	1159794	4026	7675	1142138	1057284	999909	0.86
Flat Tops 5	1639642	5258	9267	1617543	1507478	1456427	0.89
Flat Tops 6	1509101	3735	7108	1492288	1371029	1324377	0.88
Flat Tops 7	1665466	2654	9352	1645704	1535509	1483874	0.89
Flat Tops 8*	1274850	3290	8434	1257126	1143598	1096990	0.86
Flat Tops 9	1860772	11046	10889	1831375	1684843	1635382	0.88
Flat Tops 10	1912967	4609	9293	1890250	1763882	1713542	0.90
Guanella 1	1458271	3534	7190	1434169	1308310	1261141	0.86
Guanella 2	2971729	5286	16340	2926574	2584773	2541363	0.86
Guanella 3	1492005	2609	7948	1469964	1323578	1273845	0.85
Guanella 4	3127383	8849	14782	3080278	2759085	2719368	0.87
Guanella 5	2715139	6064	14184	2672038	2462410	2420913	0.89
Guanella 6	1537937	6191	5841	1515598	1378722	1323276	0.86
Guanella 7	1669606	3243	6980	1648436	1518827	1472562	0.88
Guanella 8	4211731	15359	19153	4148991	3755221	3705054	0.88
Guanella 9	1469160	4198	6315	1449804	1335305	1280162	0.87
Guanella 10*	3111472	7269	14339	3074200	2825746	2764526	0.89
Pikes 1	1619770	2917	13632	1595195	1510606	1462900	0.90
Pikes 2	1222818	2240	6408	1208780	1117193	1079582	0.88
Pikes 3	1638230	2437	8842	1619832	1480713	1435332	0.88
Pikes 4	1775795	3662	13461	1751523	1615896	1568548	0.88
Pikes 5	1833297	3720	11525	1809224	1693295	1648734	0.90
Pikes 6	1268042	1322	8963	1251667	1180047	1130373	0.89
Pikes 7	1862884	5477	13155	1834941	1723379	1666946	0.89
Pikes 8	1807463	3582	9117	1786450	1687921	1638245	0.91
Pikes 9*	1569717	2645	10025	1550728	1442070	1390945	0.89
Pikes 10	1588975	3551	11303	1565188	1486937	1445114	0.91

Table S2. Continued

A) *Carex chalciolepis* (continued)

Individual	Total	No RadTag	Low Quality	Retained	Post-bowtie	# retained by stacks	Total % retained
Lamphier 1	1636336	2996	9463	1609267	1445797	1400435	0.86
Lamphier 2	1841268	4584	13063	1807495	1663778	1617433	0.88
Lamphier 3	2873259	5229	16737	2823532	2561462	2518649	0.88
Lamphier 4	3004800	3924	14867	2961664	2589076	2545177	0.85
Lamphier 5	1905873	5031	10807	1875059	1660991	1611309	0.85
Lamphier 6	2545975	2975	9972	2519010	2292639	2238556	0.88
Lamphier 7	394867	6493	1749	383721	354203	328423	0.83
Lamphier 8	1687309	1819	10905	1663247	1501340	1445282	0.86
Lamphier 9	1035984	2084	4542	1023101	940008	887141	0.86
Lamphier 10	1411129	1982	6511	1393838	1284176	1229416	0.87
Ouray 1	3506390	9107	19502	2310542	2138571	2094172	0.60
Ouray 2	1500608	2701	13081	1471015	1354440	1306657	0.87
Ouray 3	2834687	11417	14591	2787490	2427877	2385520	0.84
Ouray 4*	1118144	2585	7568	1098638	1006616	941060	0.84
Ouray 5*	2389863	7812	14712	2345401	2176674	2123558	0.89
Ouray 6	2045589	4848	10946	2018812	1826892	1775259	0.87
Ouray 7	2027806	7582	9901	1998708	1841996	1785629	0.88
Ouray 8	1994387	3058	7691	1972088	1806177	1750776	0.88
Ouray 9*	1677496	3152	6086	1660990	1485781	1418445	0.85
Ouray 10	1023713	1078	5628	1010293	918117	865384	0.85
Lizard 1	1675863	1920	7351	1654055	1471929	1417190	0.85
Lizard 2	2148107	3077	11186	2119317	1896099	1842942	0.86
Lizard 3	3131109	5919	20730	3075716	2836319	2790949	0.89
Lizard 4	2207051	2811	11723	2176388	1955333	1908209	0.86
Lizard 5	2994538	3486	15385	2953216	2568118	2524555	0.84
Lizard 6	1177007	1173	4976	1164175	1063852	1003116	0.85
Lizard 7	1508159	2379	6375	1488943	1342463	1284054	0.85
Lizard 8	1472946	1284	6976	1454974	1318444	1265080	0.86
Lizard 9	1417728	4366	6103	1399090	1258805	1203953	0.85
Lizard 10	1330078	1613	5665	1313702	1209197	1152877	0.87

Table S2. Continued

A) *Carex chalciolepis* (continued)

Individual	Total	No RadTag	Low Quality	Retained	Post-bowtie	# retained by stacks	Total % retained
Blanca 1	1562719	4225	10372	1532369	1386816	1329958	0.85
Blanca 2	1753655	5743	10744	1723013	1576806	1525892	0.87
Blanca 3	2234245	25494	11511	2177979	2012159	1830924	0.82
Blanca 4	1979090	7448	11922	1944761	1797427	1755035	0.89
Blanca 5	835078	2307	4543	819391	740622	690421	0.83
Blanca 6	2116307	5558	12194	2078169	1886437	1842756	0.87
Blanca 7	1007990	5456	5325	986646	889344	844002	0.84
Blanca 8	1502721	3533	7672	1478947	1344292	1291318	0.86
Blanca 9	2577594	4851	15463	2533168	2275093	2232178	0.87
Blanca 10	1938477	5664	12638	1903194	1715201	1668293	0.86
Red Lakes 1	927162	861	5189	915076	841728	791382	0.85
Red Lakes 2	1040497	1014	5199	1027506	927637	878116	0.84
Red Lakes 3	949432	2037	4225	936043	865723	814952	0.86
Red Lakes 4	1585695	2465	7265	1566591	1436470	1380761	0.87
Red Lakes 5	666296	850	2604	658327	603939	562694	0.84
Red Lakes 6*	376839	398	1624	372826	332856	306750	0.81
Red Lakes 7	732250	947	2566	724151	663214	617900	0.84
Red Lakes 8	1780382	2317	7837	1759078	1613762	1558417	0.88
Red Lakes 9	1293224	3017	8868	1272830	1155884	1110401	0.86
Red Lakes 10	1421735	2741	6072	1403902	1306778	1253594	0.88

Table S2. Continued

B) *Carex nova*

Individual	Total	No RadTag	Low Quality	Retained	Post- bowtie	# retained by stacks	Total % retained
Libby Flats 1	2839544	8949	15530	2784008	2533428	2500386	0.88
Libby Flats 2	1424530	4104	7377	1398837	1294738	1251058	0.88
Libby Flats 3	2786782	8502	18805	2731054	2534674	2495825	0.90
Libby Flats 4	1140254	2343	6497	1118951	1046745	991595	0.87
Libby Flats 5	1594281	2699	10072	1565307	1467794	1423378	0.89
Libby Flats 6	1539315	3731	8628	1515512	1362497	1318823	0.86
Libby Flats 7	1331829	2004	6243	1312948	1180772	1140793	0.86
Libby Flats 8	1965130	3114	11005	1937037	1731268	1693540	0.86
Libby Flats 9	2713249	7620	14792	2672865	2392125	2352075	0.87
Zirkel 1	1073382	1911	8342	1051600	978356	919552	0.86
Zirkel 2	1289822	1206	9941	1267232	1157776	1104180	0.86
Zirkel 3	1552260	7397	9337	1521159	1418164	1372391	0.88
Zirkel 4	1668094	3858	9057	1640267	1521502	1476176	0.88
Zirkel 5	3281087	9389	16949	3225692	3003577	2962763	0.90
Zirkel 6	2498606	5670	13717	2457125	2279927	2215288	0.89
Zirkel 7	1904644	4513	11585	1869362	1766131	1724315	0.91
Zirkel 8	1101950	10667	6303	1073662	978695	932277	0.85
Zirkel 9	2064636	6312	10224	2030063	1897568	1856236	0.90
Zirkel 10	2287641	6399	15951	2244013	2098058	2055577	0.90
Niwot 1	2030466	3500	14676	1995845	1829983	1785708	0.88
Niwot 2	2001624	7733	12220	1962323	1829839	1788093	0.89
Niwot 3	2710605	6361	13526	2666675	2505161	2464430	0.91
Niwot 4	1291454	2088	5799	1271894	1184785	1139019	0.88
Niwot 5	1291026	2446	6703	1268767	1183554	1137097	0.88
Niwot 6	1190172	2026	9293	1166854	1107520	1056340	0.89
Niwot 7	2343084	4146	12808	2302162	2147806	2107614	0.90
Niwot 8	1809134	3966	9589	1779032	1666026	1622921	0.90
Niwot 9	2620391	6479	14318	2579303	2387382	2345214	0.89
Niwot 10	620585	772	3307	611239	572858	517588	0.83

Table S2. Continued

B) *Carex nova* (continued)

Individual	Total	No RadTag	Low Quality	Retained	Post-bowtie	# retained by stacks	Total % retained
Flat Tops 1	810170	949	5067	798597	756411	697079	0.86
Flat Tops 2	1023357	7056	8562	1000654	938142	893188	0.87
Flat Tops 3	1164665	3420	7727	1146008	1058107	1019706	0.88
Flat Tops 4	526658	1044	2463	519550	480866	454152	0.86
Flat Tops 5	1102549	1543	9717	1085986	1012971		0.00
Flat Tops 6	1321773	3391	5767	1303501	1193859	1153086	0.87
Flat Tops 7	507149	786	3326	499780	460283	430725	0.85
Flat Tops 8	343938	421	2591	338730	317708	265775	0.77
Flat Tops 9	567203	1942	2997	557796	530467	470203	0.83
Flat Tops 10	549947	1210	2316	542903	499604	443961	0.81
Guanella 1	1211961	7079	5487	1189739	1072559	1024498	0.85
Guanella 2	1231002	2506	5772	1214365	1120575	1066358	0.87
Guanella 3	3584067	11845	14019	3536390	3182524	3128547	0.87
Guanella 4	3201045	3856	14415	3162440	2838739	2780679	0.87
Guanella 5	2491327	4947	10452	2460699	2200591	2140934	0.86
Guanella 6	1544413	5246	8453	1517411	1406985	1364925	0.88
Guanella 7	819044	2015	4184	806862	745568	698961	0.85
Guanella 8	857027	2261	4801	843634	770759	709405	0.83
Guanella 9	2948088	7397	18044	2897628	2654812	2608655	0.88
Guanella 10	1807001	6426	12091	1772102	1644002	1600492	0.89
Pikes 1	1602846	5186	8286	1579714	1454106	1406076	0.88
Pikes 2	414410	2696	3090	405745	391030	334458	0.81
Pikes 3	1008799	3460	7084	990296	945571	901448	0.89
Pikes 4	884506	7799	4566	865769	824611	779829	0.88
Pikes 5	1564878	3466	11058	1538011	1492117	1444438	0.92
Pikes 6	710198	2505	4052	698471	666069	628063	0.88
Pikes 7	1151385	2118	7379	1133267	1072035	1030474	0.89
Pikes 8	984305	4585	5024	966830	912318	874828	0.89
Pikes 9	898930	1622	5300	886068	838042	795041	0.88
Pikes 10	1158679	2038	8509	1138853	1078539	1039516	0.90

Table S2. Continued

B) *Carex nova* (continued)

Individual	Total	No RadTag	Low Quality	Retained	Post- bowtie	# retained by stacks	Total % retained
Lamphier 1	1207998	2612	8513	1205269	1112923	1055301	0.87
Lamphier 2	584168	830	4448	583221	544214	506544	0.87
Lamphier 3	598713	593	1433	598003	559209	518713	0.87
Lamphier 4	1058901	1699	5229	1057085	978864	925553	0.87
Lamphier 5	1340400	2932	5540	1337351	1248669	1190282	0.89
Lamphier 6	1768369	2249	16084	1734711	1580734	1536471	0.87
Lamphier 7	1378070	2089	7599	1355526	1256279	1202878	0.87
Lamphier 8	1497783	1915	9865	1471572	1403911	1361772	0.91
Lamphier 9	2603490	4631	12481	2564801	2408237	2367964	0.91
Lamphier 10	3394716	7405	18013	3387194	3148673	3108451	0.92
Ouray 1	925230	2458	4293	912831	809603	761216	0.82
Ouray 2	3932347	9885	21090	3875347	3581075	3531749	0.90
Ouray 3	1736257	8139	7764	1541492	1395841	1339145	0.77
Ouray 4	1977064	7707	12509	1943969	1731037	1671777	0.85
Ouray 5	1802514	10704	7747	1770767	1641652	1588909	0.88
Ouray 6	1395209	1631	7004	1374300	1265140	1221092	0.88
Ouray 7	1568824	2354	7592	1543603	1416011	1369568	0.87
Ouray 8	1116198	1387	7429	1096480	1038920	989745	0.89
Ouray 9	1670200	1868	12303	1638869	1541219	1498637	0.90
Ouray 10	1084383	803	7744	1065857	995310	939625	0.87
Lizard 1	1536985	2310	5476	1517004	1378427	1321729	0.86
Lizard 2	2487989	5924	9890	2458239	2180260	2125758	0.85
Lizard 3	2715118	3354	9835	2687524	2406839	2343368	0.86
Lizard 4	1331422	2163	5861	1314424	1173924	1121514	0.84
Lizard 5	682648	772	3637	673691	602966	563331	0.83
Lizard 6	1562742	1120	10000	1534944	1387372	1340917	0.86
Lizard 7	2137479	2462	12451	2102749	1912627	1867963	0.87
Lizard 8	1937613	3616	10180	1906210	1726094	1681383	0.87
Lizard 9	1583255	1612	11994	1553392	1427103	1379960	0.87
Lizard 10	1505177	1037	9793	1479450	1389034	1346518	0.89

Table S2. Continued

B) *Carex nova* (continued)

Individual	Total	No RadTag	Low Quality	Retained	Post-bowtie	# retained by stacks	Total % retained
Blanca 1	927985	1007	3217	923761	881899	832796	0.90
Blanca 2	1305721	1703	4760	1299258	1183868	1126511	0.86
Blanca 3	935678	2365	2537	930776	885593	836250	0.89
Blanca 4	968218	5351	6616	956251	901180	851092	0.88
Blanca 5	1103123	2611	2190	1098322	1055760	998406	0.91
Blanca 6	1472012	14483	5556	1451973	1328549	1271697	0.86
Blanca 7	1098224	3993	7485	1086746	998237	954405	0.87
Blanca 8	1755689	2960	8116	1744613	1628886	1570506	0.89
Blanca 9	970736	2027	5045	963664	899690	850013	0.88
Blanca 10	1878365	7078	7326	1863961	1737225	1669506	0.89
Red Lakes 1	1391009	1480	7197	1370117	1225492	1183143	0.85
Red Lakes 2	2616139	4289	15347	2572327	2334633	2283918	0.87
Red Lakes 3	1635262	2222	7779	1610001	1487183	1446554	0.88
Red Lakes 4	1123129	1115	6570	1104941	1020171	967227	0.86
Red Lakes 5	1551242	2554	6827	1528216	1399386	1349936	0.87
Red Lakes 6	1673811	2329	9655	1648000	1499799	1448806	0.87
Red Lakes 7	1318874	5296	13129	1284025	1200077	1153884	0.87
Red Lakes 8	2318899	3787	12724	2281156	2108525	2062472	0.89
Red Lakes 9	1548360	14584	6888	1512846	1407475	1362440	0.88
Red Lakes 10	2481807	20173	12870	2424165	2292654	2247581	0.91

Table S3. The number of reads distributed across populations and those removed during processing of data (average per population and ± 1 SD are shown) of A) *Carex chalciolepis* and B) *C. nova*. The raw number of reads ('Total') was filtered to exclude low quality reads ('Low Quality') and those without barcodes and a restriction cutsite ('No RadTag'). The demultiplexed reads were filtered to exclude haploid data ('Post-bowtie') and exclude potential paralogs and over-merged loci (implemented in Stacks). Lastly, the total number of reads used in construction of the final datasets after removing loci with missing data is shown (see Methods for more processing details).

A) *Carex chalciolepis*

Population	Total	Low Quality	No RadTag	Post-bowtie	Final Dataset
Libby Flats	1409665 (648596)	6225 (2781)	2130 (1639)	1288722 (594364)	1237680 (587291)
Zirkel	1317118 (732607)	5949 (2874)	1985 (1005)	1204260 (676465)	1155094 (666738)
Niwtot	1183643 (497878)	5435 (2311)	2224 (868)	1072434 (448979)	1018465 (442073)
Flat Tops	1447565 (302467)	9088 (1126)	3903 (2721)	1321389 (279198)	1273646 (276458)
Guanella	2376443 (926967)	11307 (4671)	6260 (3544)	2125198 (820562)	2076221 (821515)
Pikes	1618699 (211976)	10643 (2261)	3155 (1065)	1493806 (197116)	1446672 (194732)
Lamphier	1833680 (768785)	9862 (4360)	3712 (1512)	1629347 (671004)	1582182 (668465)
Ouray	2011868 (721359)	10971 (4245)	5334 (3244)	1698314 (474795)	1644646 (479188)
Lizard	1906259 (658434)	9647 (4856)	2803 (1415)	1692056 (575632)	1639293 (580534)
Blanca	1750788 (512394)	10238 (3237)	7028 (6296)	1562420 (458337)	1501078 (448923)
Red Lakes	1077351 (416764)	5145 (2298)	1665 (897)	974799 (379863)	927497 (372987)

B) *Carex nova*

Population	Total	Low Quality	No RadTag	Post-bowtie	Final Dataset
Libby Flats	1926102 (639294)	10994 (4194)	4785 (2616)	1727116 (566969)	1685275 (571077)
Zirkel	1872212 (655942)	11141 (3238)	5732 (2853)	1709975 (606864)	1661876 (608927)
Niwot	1790854 (645816)	10224 (3731)	3952 (2152)	1641491 (589545)	1596402 (593673)
Flat Tops	791741 (321133)	5053 (2631)	2176 (1898)	724842 (290576)	647542 (290579)
Guanella	1969498 (961299)	9772 (4538)	5358 (2858)	1763711 (849065)	1712345 (847969)
Pikes	1037894 (341618)	6435 (2325)	3548 (1780)	967444 (316093)	923417 (316767)
Lamphier	1543261 (826571)	8921 (5006)	2696 (1899)	1424171 (764452)	1377393 (766317)
Ouray	1720823 (806145)	9548 (4491)	4694 (3714)	1541581 (735238)	1491146 (735221)
Lizard	1748043 (560715)	8912 (2763)	2437 (1471)	1558465 (492788)	1509244 (488461)
Blanca	1241575 (332677)	5285 (2015)	4358 (3791)	1150089 (300909)	1096118 (295411)
Red Lakes	1765853 (491296)	9899 (3136)	5783 (6052)	1597540 (448828)	1550596 (448903)

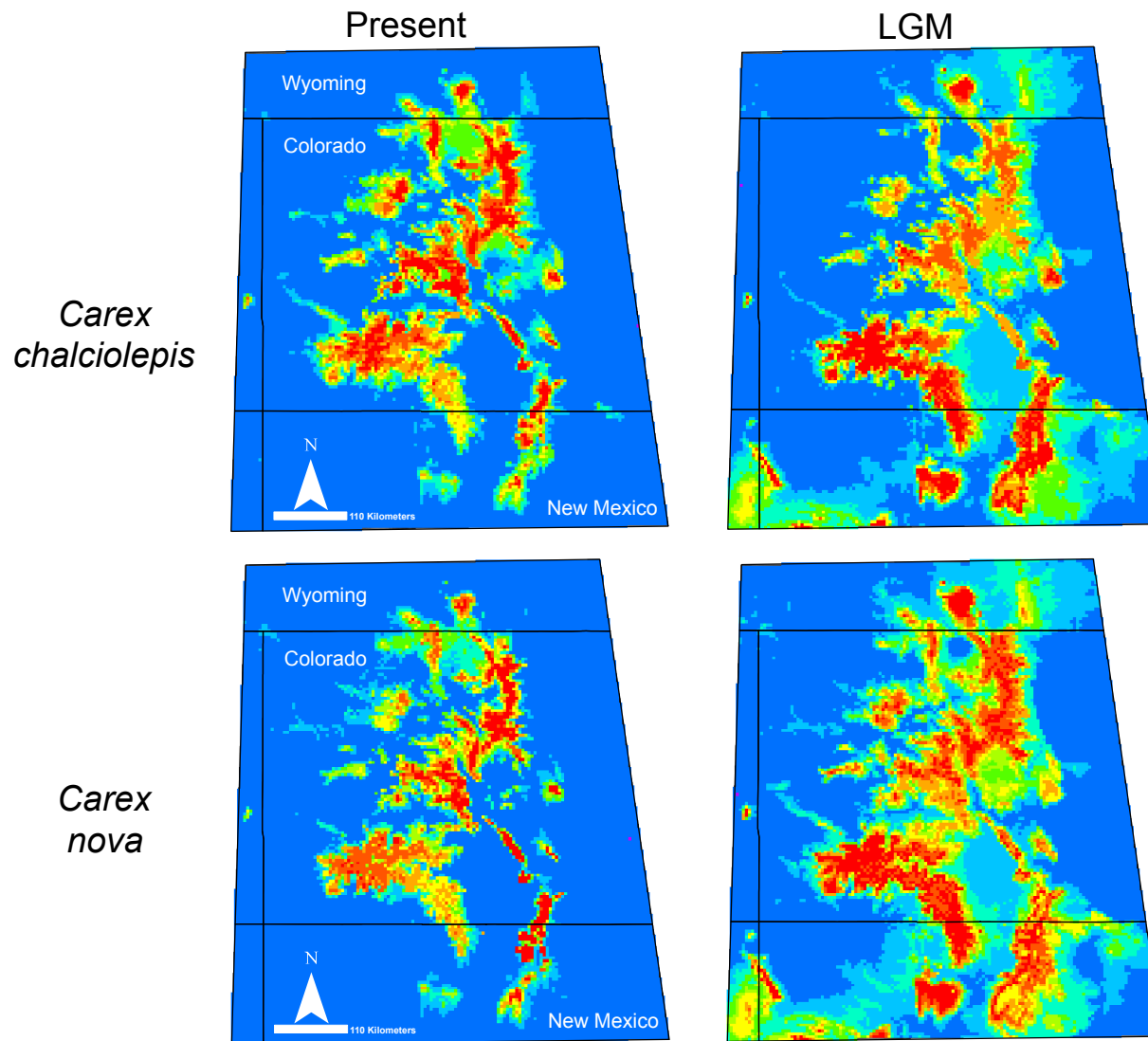


Figure S1. Present (left) and LGM (right) ENMs for *Carex chalciolepis* and *C. nova* estimated with MAXENT. Due to their similarity for each time period, an average ENM between the species for each period was used to inform the demographic modeling of the iDDC approach (see Methods). Warmer colors indicate higher estimated habitat suitability.

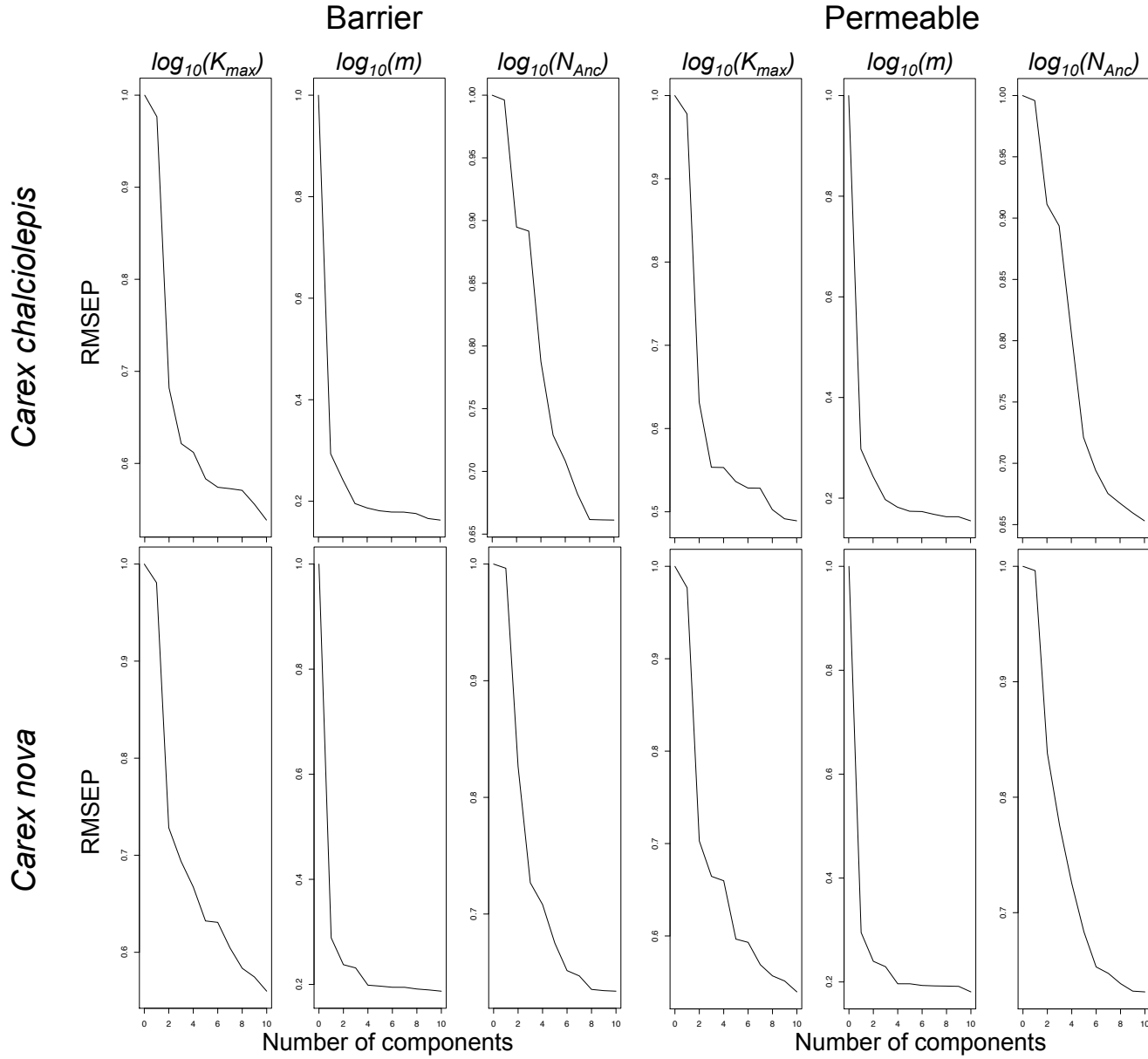


Figure S2. Root Mean Square Error (RMSE) of parameter estimates against the number of PLSs used to test the competing models: the glaciated regions as barriers (3 left columns) versus permeable glaciated regions (3 right columns) for *C. chalciolepis* (top) and *C. nova* (bottom).