

Figure S1. Size histograms for curated inversions (A), duplications (B) and deletions (C) under 1 Kb (left) and larger than 1 Kb (right).

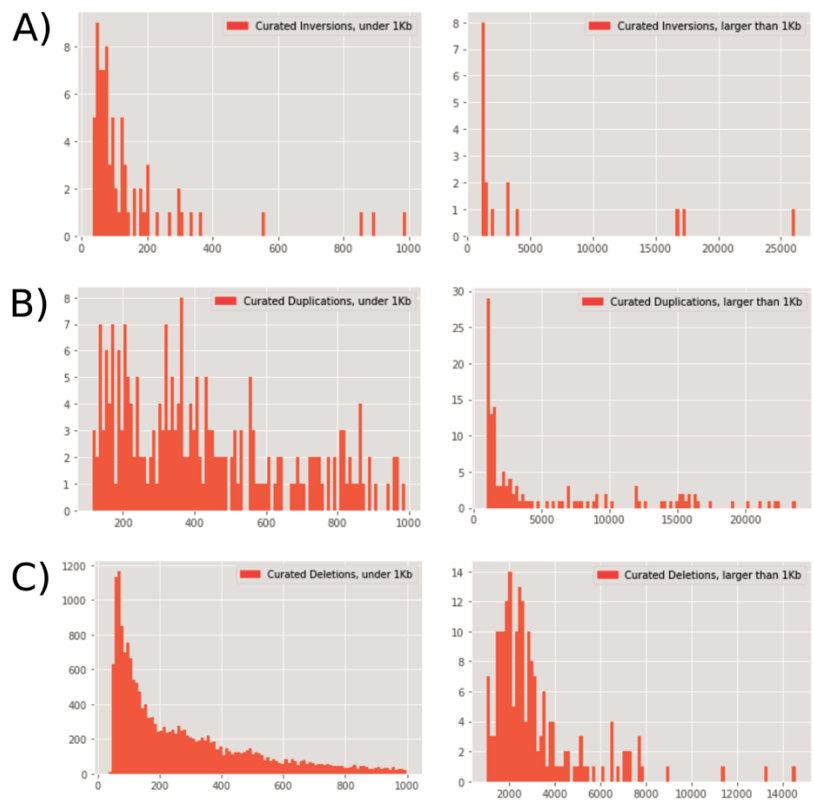


Figure S2. Heterozygosity across the *Lagopus muta* / *L. lagopus* complex superspecies.

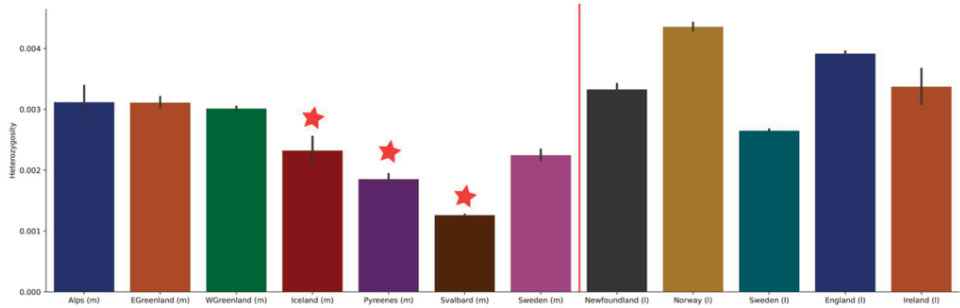


Figure S3. SMC++ (A: *L. muta* , C: *L. lagopus* complex) and Stairway Plot estimates (B: *L. muta*, D: *L. lagopus* complex).

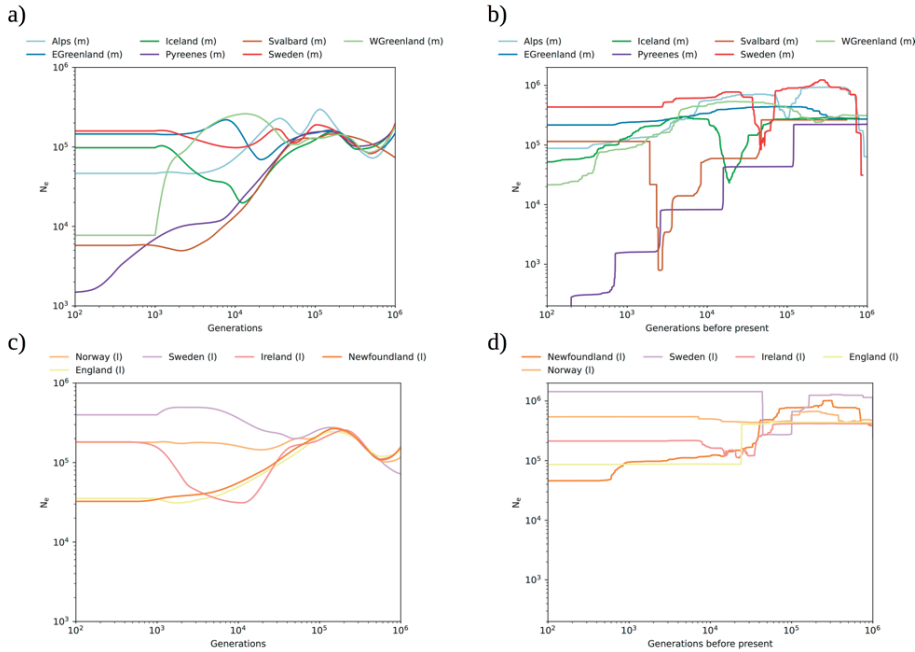


Figure S4. Genetic load in rock ptarmigan due to putatively deleterious duplications and inversions.

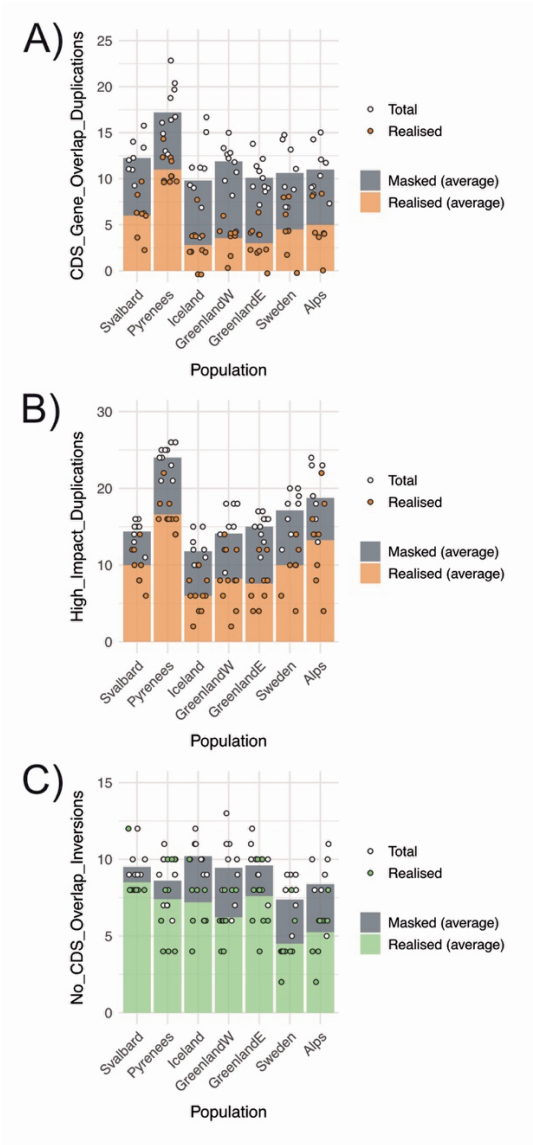


Figure S5. Repeat landscape for the Rock Ptarmigan (*Lagopus muta*).

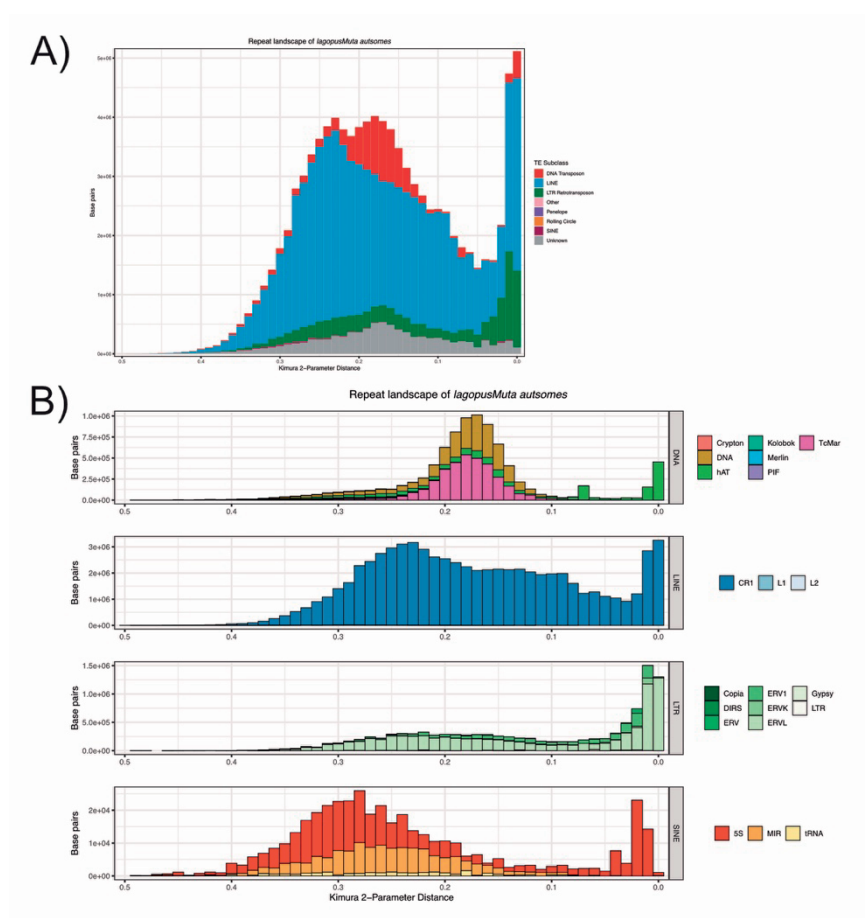


Table S1. Sampling and re-sequencing information.

Species	Population	Individual	Depth of coverage	% mapped reads
<i>L. muta</i>	Alps	Al1	37.21	98.8
		Al2	37.58	99.3
		Al3	35.06	99.1
		Al4	43.76	99.5
		Al5	42.61	98.3
		Al6	38.78	99.1
		Al7	44.81	98.3
		Al8	47.13	99.0
	East Greenland	Gr10	35.00	99.3
		Gr1	35.00	99.2
		Gr2	40.77	98.9
		Gr3	30.00	98.9
		Gr4	34.54	98.9
		Gr5	45.53	99.2
		Gr6	31.64	98.4
		Gr7	27.30	99.3
		Gr8	35.00	98.4
		Gr9	40.27	97.3
	West Greenland	JHGO281	35.00	99.3
		JHGO283	35.00	99.1
		JHGO293	41.72	99.4
		Muta1	28.78	99.0
		Muta2	29.28	99.0
		Muta3	29.46	98.7
		Muta4	32.59	99.0
		Muta5	30.75	99.2
		Muta6	29.55	99.0
	Iceland	Ice10	43.16	97.5
		Ice1	35.00	98.1
		Ice2	35.00	97.5
		Ice3	35.00	98.1
		Ice4	34.53	98.3
		Ice5	35.00	98.6
		Ice6	35.00	98.1
		Ice7	42.40	98.0
		Ice8	35.00	97.7
		Ice9	38.42	98.1

	Sweden	Jam35	39.42	98.5
		JHGO938	35.00	98.7
		JHGO939	36.90	98.9
		JHGO940	34.44	98.5
		JHGO941	43.11	98.6
		JHGO942	34.92	98.3
		P25065_110_S10	20.13	99.2
		P25065_111_S11	20.00	98.9
	Pyrenees	Py10	42.91	98.3
		Py1	45.36	99.0
		Py2	48.55	98.8
		Py3	42.07	99.3
		Py4	48.85	98.7
		Py5	30.80	99.4
		Py6	35.00	99.3
		Py7	43.76	99.1
		Py8	35.00	99.5
	Svalbard	Py9	35.00	99.1
		Sva115	42.77	99.2
Sva126		43.92	99.2	
Sva129		32.13	99.2	
Sva188		50.13	99.2	
Sva294		35.00	99.2	
Sva296		25.64	99.2	
Sva299		40.17	99.2	
	SvaG194	38.99	99.2	
<i>L. lagopus</i>	Ireland	Ire_Scot1	26.21	98.6
		Ire_Scot2	27.87	98.8
		Ire_Scot3	27.28	98.9
		Ire_Scot5	29.21	98.9
		Ire_Scot6	26.13	99.1
		Ire_Scot9	25.95	98.0
	Norway	Lago10	28.15	99.0
		Lago11	33.67	98.9
		Lago12	30.40	98.9
		Lago13	26.72	98.9
		Lago14	31.85	98.9
		Lago15	31.24	98.5
		Lago7	33.24	99.0
		Lago8	31.90	98.8
		Lago9	29.70	99.0

Newfoundland	NL1001	33.23	99.1
	NL1003	43.18	99.2
	NL1007	27.41	99.1
	NL1010	49.09	99.1
	NL1011	42.66	99.1
	NL1013	33.48	99.2
Sweden	P25065_104_S4	28.94	99.2
	P25065_105_S5	20.05	99.0
	P25065_106_S6	15.96	99.0
	P25065_107_S7	18.72	99.4
	P25065_108_S8	18.55	99.4
	P25065_109_S9	22.58	99.1
England	Scot1	28.74	98.6
	Scot2	29.00	98.6
	Scot3	33.29	99.0
	Scot4	28.53	98.4
	Scot5	32.03	98.6
	Scot6	28.83	98.9
	Scot7	29.45	98.6
	Scot8	29.70	98.9
	Scot9	31.09	98.6

Table S2. Effective population size estimates.

Population	Onesamp	min_lower		max_upper_ CI_onesamp	theta	smcpp	lower_CI_ smcpp		upper_CI_ smcpp	lower CI		upper CI
		onesamp	CI_onesamp				stairway	stairway				
Alps	290	117	500	281120	74575	66087	85564	307182	297273	317774		
E Greenland	215	89	516	240043	128298	118519	139835	353847	351286	356446		
W Greenland	240	123	457	221659	86311	62013	141919	310437	298844	322966		
Iceland	286	97	648	133243	46221	40722	53438	54439	53455	55459		
Pyrenees	181	57	460	97979	17123	14175	21619	1211	1139	1293		
Svalbard	237	113	533	68155	10981	9067	13920	1495	1463	1528		
Sweden (Iago)	195	99	459	366633	317722	293181	346746	580202	539833	627098		
Sweden (muta)	194	84	510	252940	125662	120214	131628	222592	216123	229459		
Ireland (Iago)	203	74	548	250662	57532	50181	67406	155750	154288	157240		
Scot	243	99	511	257346	50941	45525	57819	103784	102621	104974		
Newfoundland	198	88	326	293452	58398	52088	66447	125552	123817	127336		
Norway (Iago)	225	131	538	346887	172471	168228	176934	456196	455012	457387		

Table S3. Linear regression statistics for diversity ratio comparisons (fig. 1).

	data	species	slope	intercept	r_value	r_squared	p_value	std_err
0fold/4fold		muta	-1.14E-07	0.645704916	-0.77593	0.60208	0.04029	4.13E-08
		lago	-8.26E-08	0.618008544	-0.95380	0.90974	0.01184	1.50E-08
		both	-1.77E-07	0.652971727	-0.86676	0.75127	0.00026	3.22E-08
0fold_derived/4fold_derived		muta	-1.03E-07	1.0554622	-0.69151	0.47818	0.08526	4.81E-08
		lago	-4.59E-09	0.955724478	-0.04112	0.00169	0.94766	6.44E-08
		both	-3.49E-07	1.083834864	-0.74092	0.54896	0.00584	9.99E-08
0fold/20Kb		muta	-8.21E-09	0.081414679	-0.36054	0.12999	0.42692	9.50E-09
		lago	-9.30E-09	0.070755681	-0.54843	0.30078	0.33850	8.18E-09
		both	-4.87E-08	0.08632324	-0.70915	0.50289	0.00981	1.53E-08
0fold_derived/20Kb_derived		muta	-1.08E-08	0.171911139	-0.21915	0.04803	0.63683	2.15E-08
		lago	-1.78E-09	0.142727927	-0.03935	0.00155	0.94991	2.60E-08
		both	-1.07E-07	0.183411521	-0.67281	0.45268	0.01650	3.72E-08
gene_overlap/20Kb		muta	5.36E-07	3.870791489	0.84694	0.71730	0.01618	1.50E-07
		lago	-6.72E-08	3.805382655	-0.13498	0.01822	0.82866	2.85E-07
		both	-4.46E-07	3.997378113	-0.39539	0.15634	0.20331	3.28E-07
gene_overlap_derived/20Kb_derived		muta	5.06E-07	4.069701843	0.76445	0.58438	0.04535	1.91E-07
		lago	-3.25E-08	3.972916115	-0.06255	0.00391	0.92042	3.00E-07
		both	-5.12E-07	4.199751675	-0.42132	0.17751	0.17255	3.49E-07
Deletion/20Kb		muta	-3.83E-09	0.003889707	-0.87763	0.77024	0.00941	9.36E-10
		lago	-3.83E-09	0.00419836	-0.61393	0.37691	0.27066	2.84E-09
		both	-2.69E-09	0.00375217	-0.72688	0.52835	0.00740	8.05E-10

Duplication/20Kb	muta	-5.13E-10	0.000244874	-0.89246	0.79648	0.00687	1.16E-10
	lago	-1.80E-10	0.000141128	-0.82605	0.68237	0.08478	7.07E-11
	both	-4.84E-10	2.37E-04	-0.91706	0.84101	0.00003	6.66E-11
Inversion/20Kb	muta	-2.39E-11	2.22E-05	-0.60602	0.36726	0.14919	1.40E-11
	lago	-2.94E-11	2.52E-05	-0.58350	0.34048	0.30169	2.37E-11
	both	-1.97E-11	2.18E-05	-0.60357	0.36429	0.03771	8.24E-12
TE_deletion/20Kb	muta	-1.59E-09	0.001592674	-0.83867	0.70337	0.01837	4.62E-10
	lago	-8.33E-10	0.001295248	-0.55573	0.30883	0.33075	7.20E-10
	both	-1.75E-09	0.001602134	-0.88549	0.78409	0.00013	2.91E-10
TE_duplication/20Kb	muta	-2.86E-10	0.000143025	-0.89633	0.80341	0.00628	6.33E-11
	lago	-8.22E-11	7.65E-05	-0.79466	0.63148	0.10819	3.63E-11
	both	-2.80E-10	1.40E-04	-0.91624	0.83950	0.00003	3.87E-11
Deletion/4fold	muta	-3.18E-08	0.030779948	-0.87511	0.76582	0.00989	7.87E-09
	lago	-3.36E-08	0.036714931	-0.60110	0.36133	0.28363	2.58E-08
	both	-1.22E-08	0.02843574	-0.37894	0.14359	0.22446	9.45E-09
Duplication/4fold	muta	-4.06E-09	0.001923964	-0.91600	0.83906	0.00375	7.96E-10
	lago	-1.58E-09	0.001235978	-0.79542	0.63269	0.10761	6.95E-10
	both	-3.54E-09	1.83E-03	-0.92333	0.85253	0.00002	4.65E-10
Inversion/4fold	muta	-1.97E-10	0.000175467	-0.63951	0.40897	0.12196	1.06E-10
	lago	-2.57E-10	0.000220013	-0.57935	0.33565	0.30599	2.09E-10
	both	-1.07E-10	0.000165455	-0.41820	0.17489	0.17609	7.37E-11
TE_deletion/4fold	muta	-1.32E-08	0.012616134	-0.80937	0.65508	0.02742	4.30E-09
	lago	-7.32E-09	0.011320628	-0.54708	0.29930	0.33994	6.47E-09
	both	-1.07E-08	0.012232323	-0.80664	0.65066	0.00152	2.48E-09

TE_duplication/4fold	muta	-2.27E-09	0.001124236	-0.92133	0.84885	0.00319	4.28E-10
	lago	-7.24E-10	0.000670156	-0.75788	0.57438	0.13770	3.60E-10
	both	-2.04E-09	1.08E-03	-0.92613	0.85772	0.00002	2.62E-10

Table S4. Student's t-test for diversity ratio contrasts between *L. muta* and *L. lagopus* complex

Diversity ratio	T	dof	alternative	p-val	CI95%	cohen-d	BF10	power
piN/intergenic_SNP	14.533016	8.937715	two-sided	1.60E-07	[0.01, 0.01]	7.563981	1.28E+05	1
piNon_neutral(DEL)/intergenic_SNP	1.389022	9.997457	two-sided	0.194988	[-0.0, 0.0]	0.760359	0.84	0.217467
piNon_neutral(DUP)/intergenic_SNP	3.348533	6.905991	two-sided	0.012523	[0.0, 0.0]	1.665669	6.41	0.727318
piNon_neutral(INV)/intergenic_SNP	0.876768	9.799207	two-sided	0.401595	[-0.0, 0.0]	0.492775	0.599	0.118943

Table S5. Estimates of historical effective population size (N_e), approximate census size (N_c) and N_e/N_c ratios for the Rock Ptarmigan (*Lagopus muta*).

Population	N_e		N_c		N_e (W. theta)/ Min N_c		N_e (W. theta)/ Max N_c		N_e (SMC++)/ Min N_c		N_e (SMC++)/ Max N_c	
	(W. theta)	(SMC++)	Min N_c	Max N_c	Min N_c	Max N_c	Min N_c	Max N_c	Min N_c	Max N_c	Min N_c	Max N_c
Svalbard	68155	10981	5000	25000	13.631	2.726			2.196		0.439	
Pyrenees	97979	17123	5000	12000	19.596	8.165			3.425		1.427	
Iceland	133243	46221	51300	122100	2.597	1.091			0.901		0.379	
Sweden	252940	125662	80000	160000	3.162	1.581			1.571		0.785	
Alps	281120	74575	50000	100000	5.622	2.811			1.492		0.746	

Sources:

- Svalbard (<https://npolar.no/en/species/svalbard-rock-ptarmigan/>)
- Pyrenees (<https://birdsoftheworld.org/bow/species/rocpal1/cur/demography>)
- Iceland: (Johnson and Nielsen, 2024)
- Sweden: <https://jagareforbundet.se/vilt/vilt-vetande2/artpresentation/faglar/fjallripa/>
- Alps: <https://birdsoftheworld.org/bow/species/rocpal1/cur/demography>

Table S6. Average counts for realised and masked load, weighted by "Low" impact SNPs.

	Population	Realised	Masked
High Impact SNPs	Svalbard	0.00409	0.00462
	Pyrenees	0.00362	0.00456
	Iceland	0.00322	0.00400
	W Greenland	0.00366	0.00385
	E Greenland	0.00350	0.00387
	Sweden	0.00384	0.00492
	Alps	0.00355	0.00405
High Impact Deletions	Svalbard	0.00068	0.00061
	Pyrenees	0.00067	0.00085
	Iceland	0.00086	0.00064
	W Greenland	0.00045	0.00062
	E Greenland	0.00042	0.00060
	Sweden	0.00063	0.00058
	Alps	0.00045	0.00058
High Impact Duplications	Svalbard	0.00021	0.00037
	Pyrenees	0.00026	0.00044
	Iceland	0.00033	0.00029

W Greenland	0.00028	0.00021
E Greenland	0.00025	0.00026
Sweden	0.00025	0.00030
Alps	0.00032	0.00019

Table S7. Realised to masked load ratios in the rock ptarmigan (*L. muta*).

	slope	intercept	r_value	r_squared	p_value	std_err
SNP_HIGH	-2.50E-11	2.65536449	-0.6172923	0.3810498	7.11E-08	4.09E-12
DEL_HIGH	-3.44E-11	3.29333079	-0.5816877	0.33836063	5.74E-07	6.16E-12
DUP_HIGH	1.76E-13	2.09455794	0.00257393	6.6251E-06	0.98402673	8.78E-12
SNP_MODERATE	-2.71E-11	2.91392234	-0.63524	0.40352985	2.24E-08	4.22E-12
DEL_NO_CDS	-3.41E-11	3.35578664	-0.8309722	0.69051474	3.54E-17	2.93E-12
DUP_NO_CDS	-2.37E-13	1.40746865	-0.0087125	7.5908E-05	0.94596877	3.48E-12