

Figure S2: Individual genotypes for all 72 outlier SNPs in the large LD cluster. Each row is a SNP, and each column is an individual. Contigs with outlier SNPs are roughly ordered by the strength of their membership in the LD cluster. Yellow = major allele homozygote; orange = heterozygote; red = minor allele homozygote.

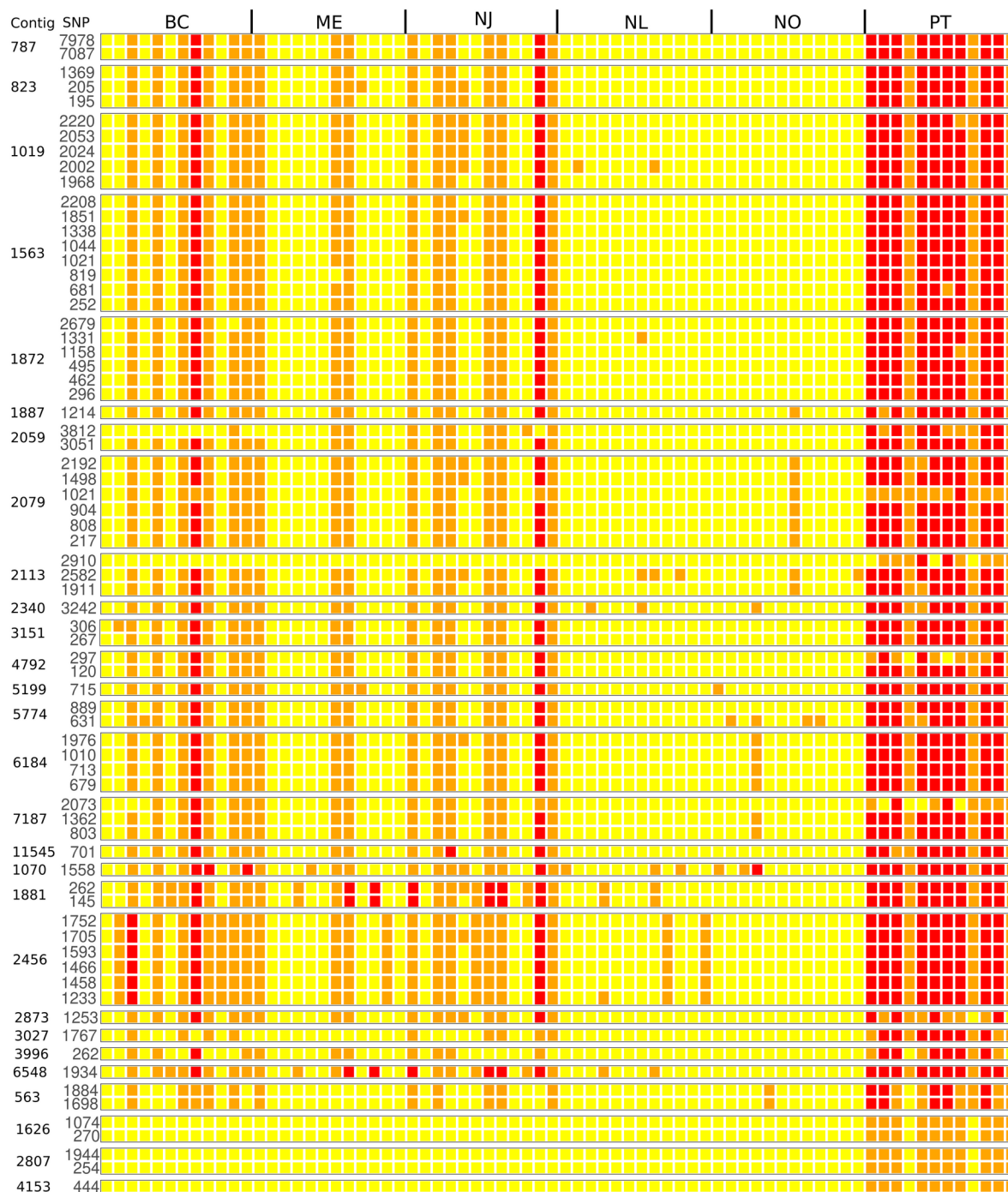
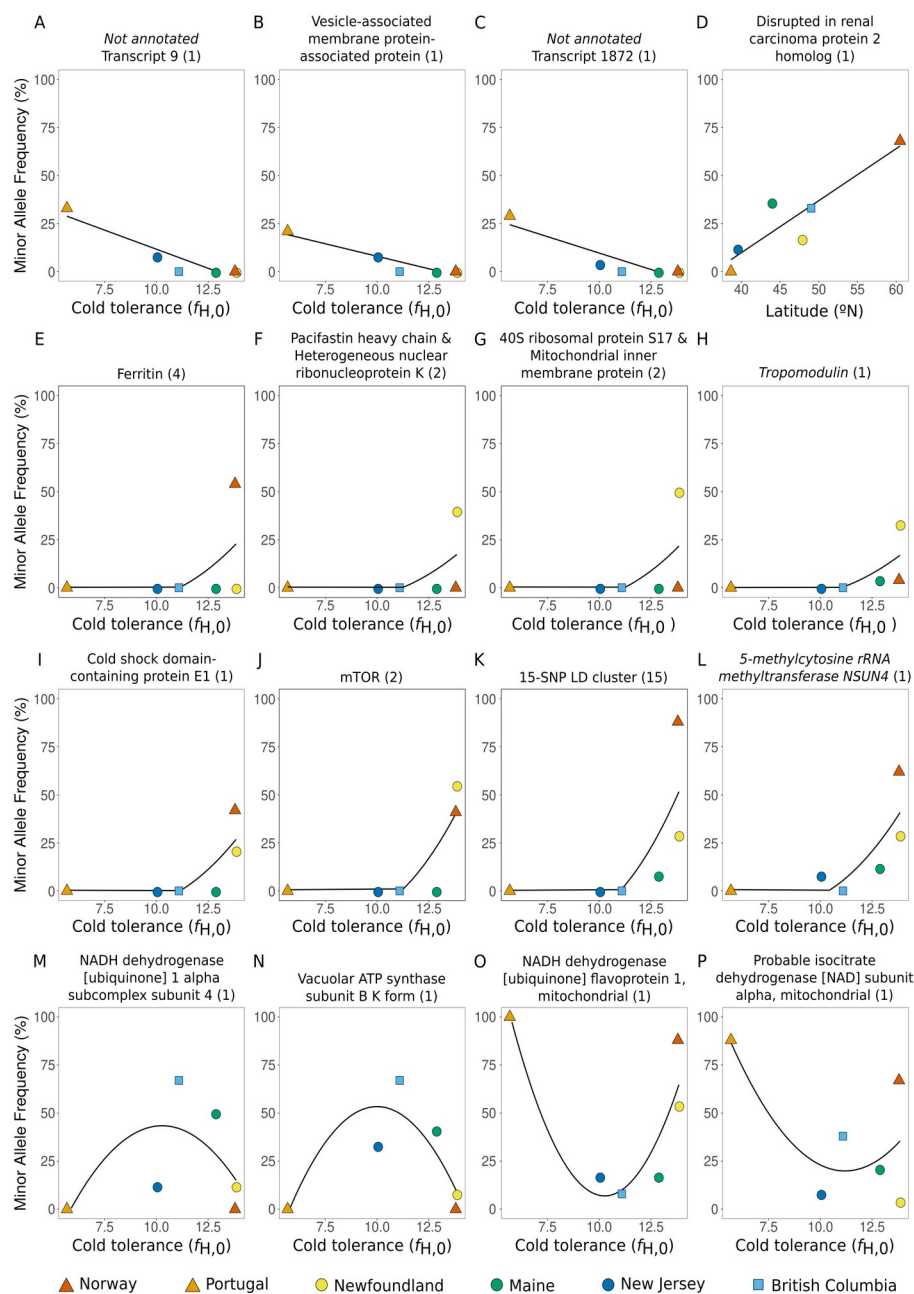


Figure S3: Relationship between minor allele frequency and temperature or physiology at outlier regions that were not top candidates for ongoing selection. A-D: Panels show the linear relationship between minor allele frequency and population-level cold tolerance or site latitude. E-P: Panels show the second-order polynomial relationship between minor allele frequency and population-level cold tolerance. Note that this polynomial relationship is used only to show approximate non-linear relationships between MAF and tolerance, and is not necessarily the best fit to the data. All panels: For each group of > 1 SNP, points and lines are shown for one representative SNP; all SNPs in these groups are in very strong LD ($R^2 > 0.9$) with each other.



Supplemental Tables

Table S1: Details on the contigs containing outlier SNPs in the 72-SNP linked group. Length is full contig length. Annotations in italics were unannotated or annotated with low confidence (e-value $> 1 \times 10^{-15}$). SNPs are characterized as being in the untranslated region (UTR; defined as outside the longest predicted ORF), or, if in the coding region, as synonymous or non-synonymous.

Transcript	Annotation	length	UTR	syn	non-syn
563	Aspartate aminotransferase	2884	-	2	-
787	Eukaryotic translation initiation factor 3, subunit E	10525	-	2	-
823	Uncharacterized peptidase C1-like protein	1436	-	-	3
1019	<i>5-methylcytosine rRNA methyltransferase NSUN4</i>	2551	5	-	-
1070	<i>Probable rRNA-processing protein EBP2 homolog</i>	2202	-	1	-
1563	Tyrosine-protein phosphatase non-receptor type 13	2357	-	8	-
1626	Sulfide:quinone oxidoreductase, mitochondrial precursor	1429	1	1	-
1872	<i>Not annotated</i>	2884	6	-	-
1881	<i>Fibrous sheath CABYR-binding protein</i>	445	-	-	2
1887	Ubiquitin associated protein 2-like protein	1884	-	-	1
2059	Hypoxia-inducible factor alpha	5602	-	1	1
2079	Lingerer, isoform H	2939	1	5	-
2113	Saposin, isoform 1	3400	-	2	1
2340	MICOS complex subunit Mic10	3972	1	-	-
2456	Tropomodulin-like isoform 1	1909	6	-	-
2807	Ribonuclease H1	2296	1	1	-
2873	pre-mRNA 3'-end-processing factor FIP1-like	1928	-	1	-
3027	Thrombospondin	4777	-	1	-
3151	<i>Not annotated</i>	466	-	-	2
3996	Cartilage oligomeric matrix protein-like	1046	-	1	-
4153	Sulfide:quinone oxidoreductase, mitochondrial	764	1	-	-
4792	39S ribosomal protein L46, mitochondrial	467	-	2	-

Transcript	Annotation	length	UTR	syn	non-syn
5199	<i>Not annotated</i>	1349	-	-	1
5774	NAD-dependent deacetylase sirtuin-5	1117	-	2	-
6184	Structural maintenance of chromosome protein 3	4240	-	4	-
6548	<i>Neurofilament heavy polypeptide</i>	2067	-	-	1
7187	Proliferation-associated protein 2G4	2575	1	2	-
11545	<i>Not annotated</i>	1208	1	-	-

Table S2: Details on outlier SNP regions. Correlation gives the r-value for a partial Mantel test for minor allele frequency with temperature (SST), cold tolerance (Cold), heat tolerance (Heat), or location latitude (Lat); neutral pairwise F_{ST} is used as a covariate to account for population structure. Stars denote significant: * < 0.05, ** < 0.01. Type of SNP gives the number of outlier SNPs in each substitution category based on predicted ORFS. UTR = untranslated region; syn = synonymous substitution; non-synon = non-synonymous substitution.

Contig	Fig.	Annotation	Correlation				Type of SNP		
			SST	Cold	Heat	Lat	UTR	syn	non-syn
SNPs associated with temperature or thermal tolerance with BayPass covariate models:									
	4A	72-SNP linkage disequilibrium cluster	0.82**	0.96**	0.21	-0.06	details in Table 3		
	S3K	15-SNP linkage disequilibrium cluster ^{1,‡}	-0.18	-0.11	0.41	0.63	11	3	1
9	S3A	Not annotated [†]	0.83*	0.89*	0.25	0.09	1	-	-
325	S3B	Vesicle-associated membrane protein-associated protein [†]	0.83*	0.89*	0.25	0.09	-	1	-
551	4B	Ryanodine receptor	0.79*	0.91**	0.35	0.24	1	2	1
1580	S3H	Tropomodulin ^{†,‡}	0.30	0.10	0.23	-0.14	1	-	-
1582	4D	Muscle M-line assembly protein unc-89	0.80*	0.77*	0.13	0.08	-	2	-
1872	S3C	Not annotated ^{*,†}	0.83*	0.89*	0.25	0.09	1	-	-
3029	S3I	Cold shock domain-containing protein E1	only variable in NO & NL				1	-	-
3259	S3J	mTOR	only variable in NO & NL				2	-	-
5987	4F	Probable complex I intermediate-associated protein 30, mitochondrial	0.38	0.46*	0.54*	0.37	-	1	-
14335	S3D	Disrupted in renal carcinoma protein 2 homolog	0.07	0.05	0.09	0.73*	-	1	-
Additional SNPs identified as outliers with BayPass core model:									
	S3E	4-SNP Ferritin linkage disequilibrium cluster ²	only variable in NO				1	-	3
	S3F	2-SNP linkage disequilibrium cluster ³	only variable in NL				2	-	-
	S3G	2-SNP linkage disequilibrium cluster ⁴	only variable in NL				-	2	-
466	4C	Muscle M-line assembly protein unc-89	0.69	0.79*	0.34	0.15	-	1	-

Contig	Fig.	Annotation	Correlation				Type of SNP		
			SST	Cold	Heat	Lat	UTR	syn	non-syn
475	S3O	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	0.58*	0.58*	-0.04	-0.55	-	-	1
505	S3M	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	-0.37	-0.35	-0.28	-0.26	1	-	-
732	S3P	Probable isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	0.47	0.32	-0.22	-0.07	-	1	-
1019	S3L	<i>5-methylcytosine rRNA methyltransferase NSUN4^{*,‡}</i>	-0.19	-0.12	0.36	0.60	1	-	-
2059	4E	Hypoxia-inducible factor alpha [*]	0.89**	0.68	0.09	-0.02	1	-	-
2214	S3N	Vacuolar ATP synthase subunit B K form	-0.36	-0.29	-0.17	-0.37	1	-	-

*SNP is in a contig represented in the 72-SNP LD cluster, but is not part of that LD cluster.

†Minor allele rare - present at <35% in its most common location.

‡Minor allele rare (<15%) in invasive range outside of NL.

¹Contains contigs 3546 (*Ubiquitin-conjugating enzyme E2 H*: 1 SNP), 4494 (*Not annotated*: 1 SNP), 4794 (*Not annotated*: 10 SNPs), and 6625 (*T-complex protein 11-like protein 1*: 3 SNPs).

²Contains contigs 175 (*Ferritin 2*: 3 SNPs) and 856 (*Ferritin 1*: 1 SNP).

³Contains contigs 323 (*Pacifastin heavy chain*: 1 SNP) and 1392 (*Heterogeneous nuclear ribonucleoprotein K*: 1 SNP).

⁴Contains contigs 531 (*40S ribosomal protein S17*: 1 SNP) and 3075 (*Mitochondrial inner membrane protein*: 1 SNP).