Supplementary figures and tables

Influence of past climatic change on phylogeography and demographic history of narwhals, *Monodon monoceros*

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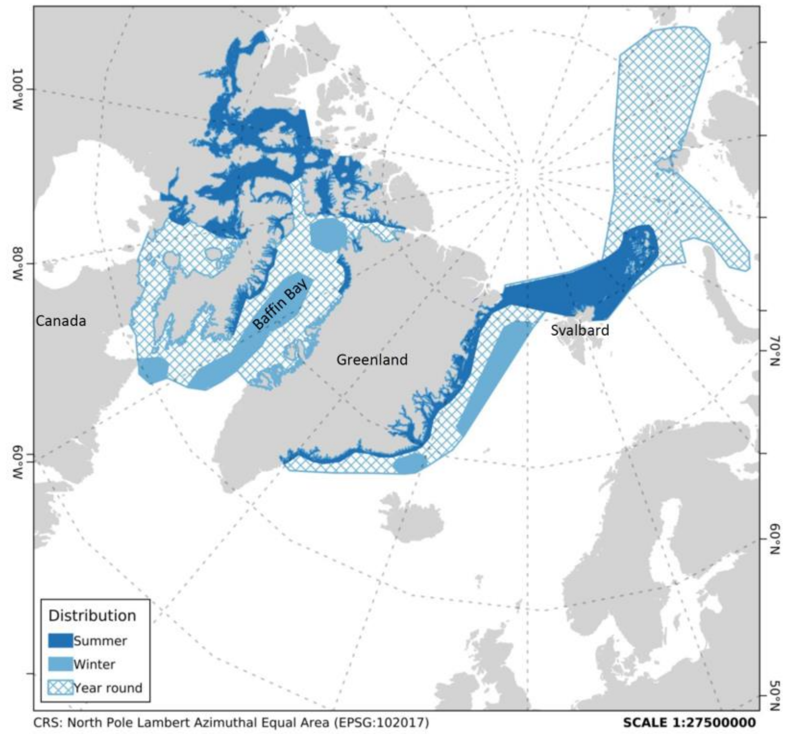

Figure S1. Distribution maps of narwhals for summer, winter and year-round. Adapted from maps recently compiled by a panel of narwhal experts at the NAMMCO meeting in 2018 [1]. Note that a recent study indicated that narwhals between North-East Greenland and Svalbard are present year-round [2].

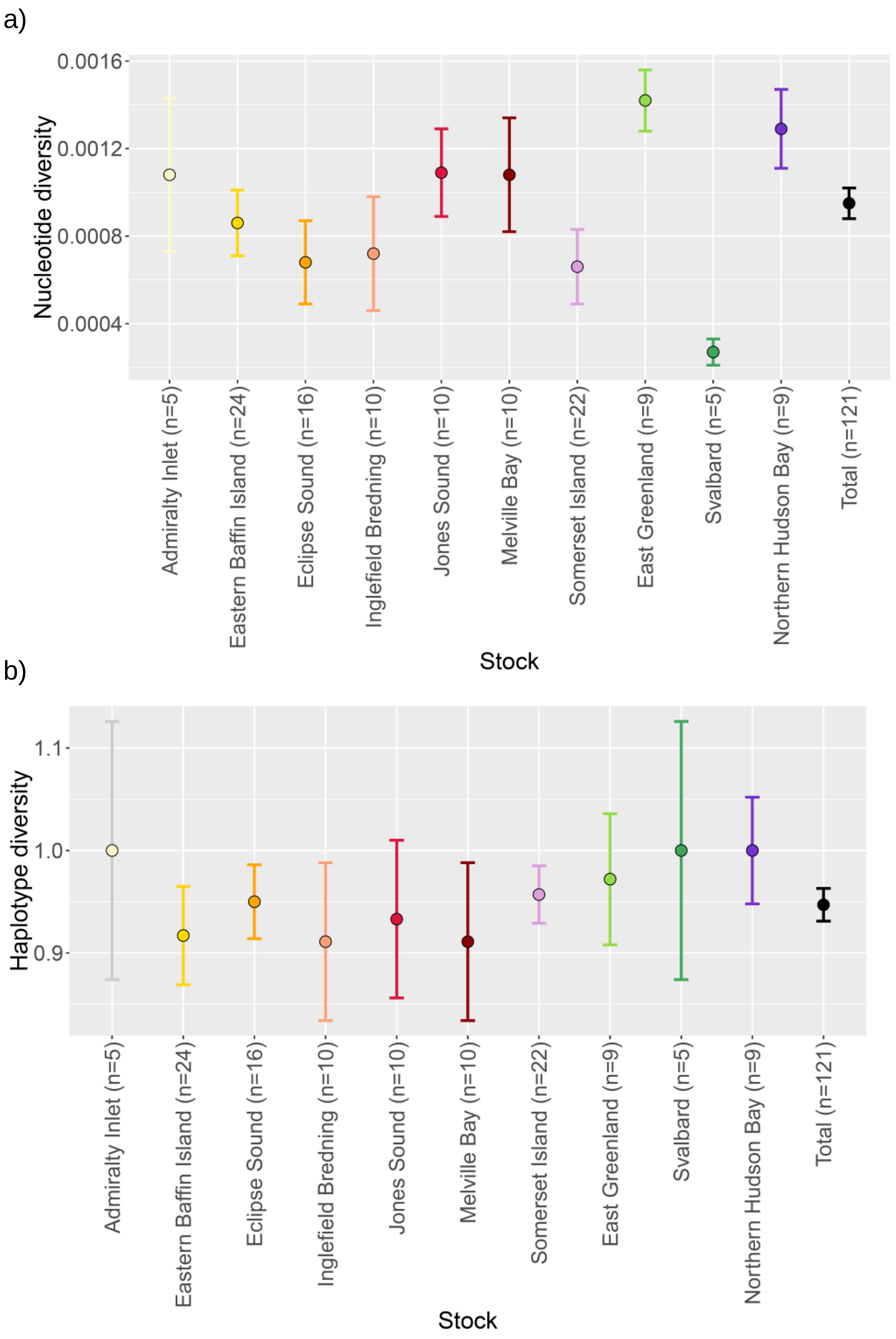

Figure S2. a) Nucleotide diversity and b) haplotype diversity for each narwhal summer stock (Smith Sound is excluded due to n=1) and for the whole dataset (n=121).

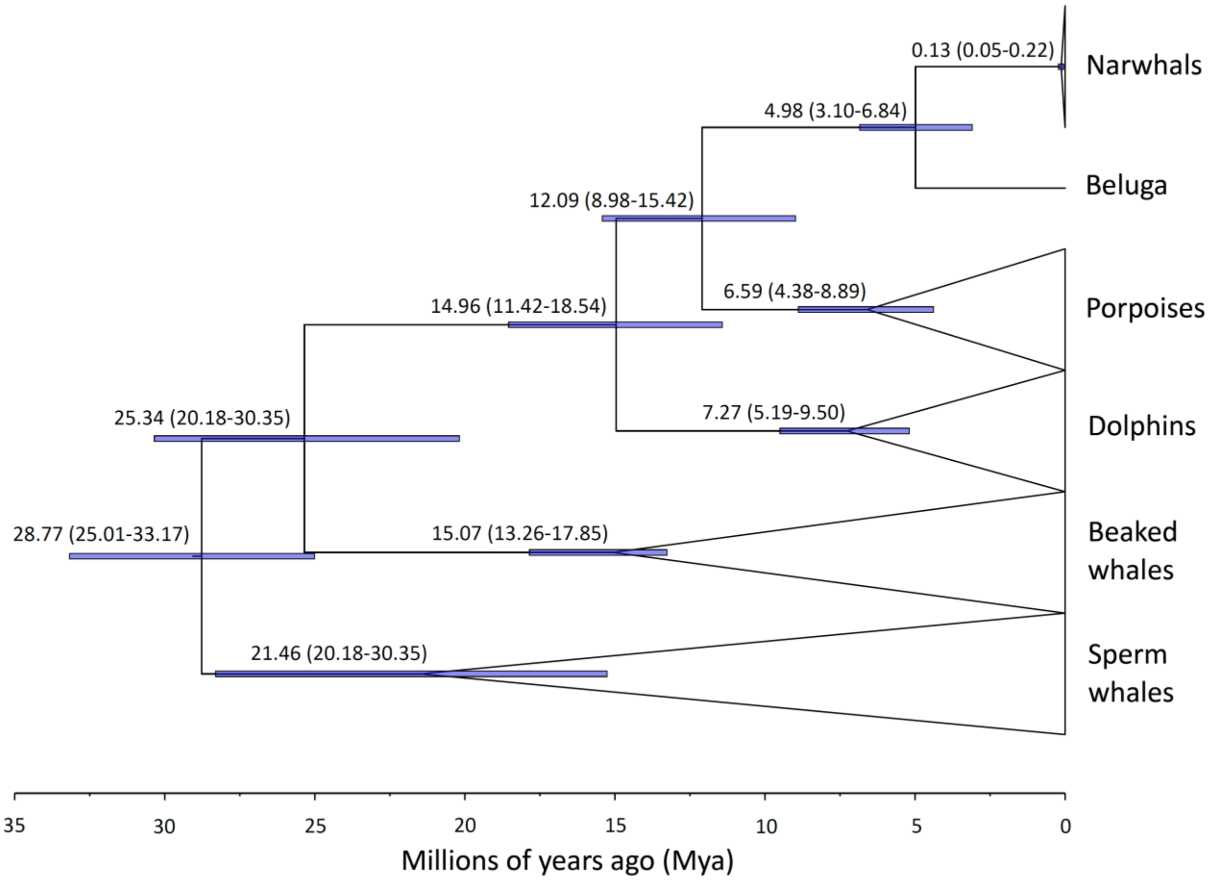

Figure S3. Fossil-calibrated phylogeny of 15 toothed whales inferred using a calibrated Yule prior model using the tRNAs, rRNAs, first and second codon positions of the protein coding regions. Only nodes with a posterior probability >0.9 are shown, and nodes for species within each family, apart from the Monodontidae, were collapsed. Numbers represent mean TMRCA and 95% HPD. The 95% HPD of divergence time estimates are also represented by horizontal blue bars. The four narwhal sequences included were from the most divergent clades in the haplotype network.

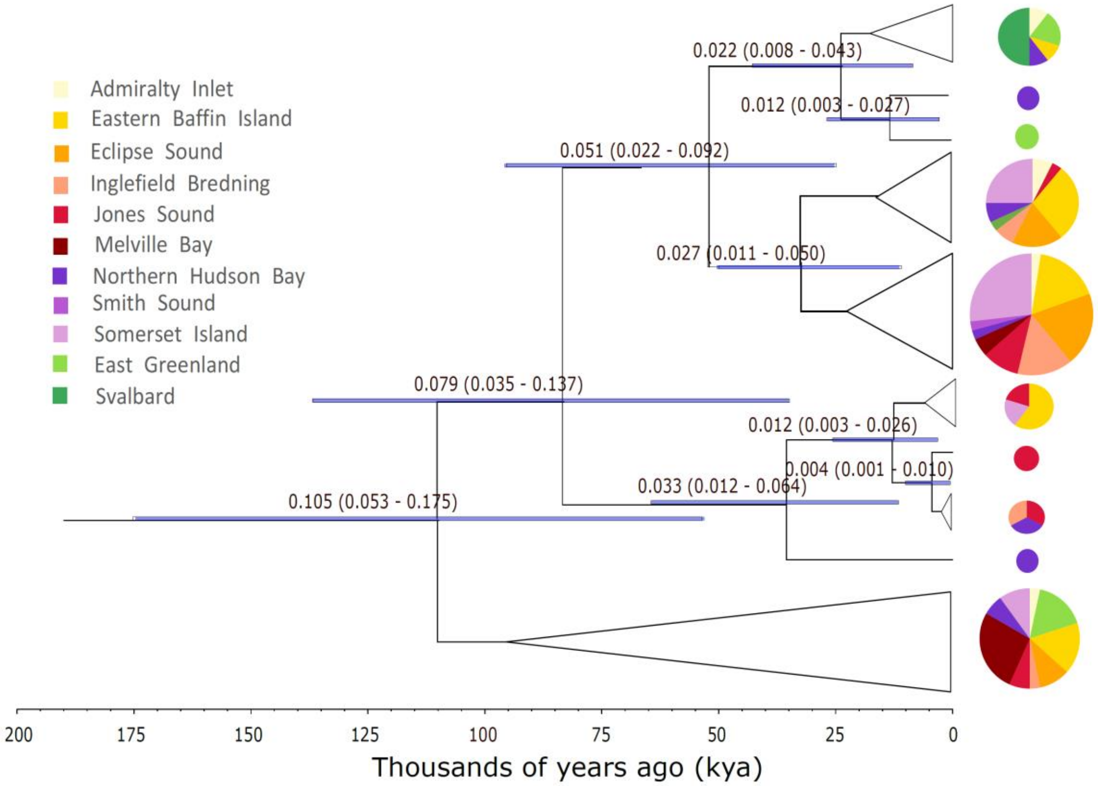

Figure S4.Time-calibrated phylogeny of 64 haplotypes found among the 121 narwhal mitogenome sequences inferred with a coalescent constant population size model using the tRNAs, rRNAs, first, second and third codon positions of the protein coding regions and the control region. Nodes which lack support (posterior values < 0.9) are collapsed. Numbers represent the mean TMRCA and 95% HPD. The 95% HPD of divergence time estimates are also represented by horizontal blue bars. Pie chart colours and size indicate which stocks are represented in each clade, and relative number of individuals, respectively.

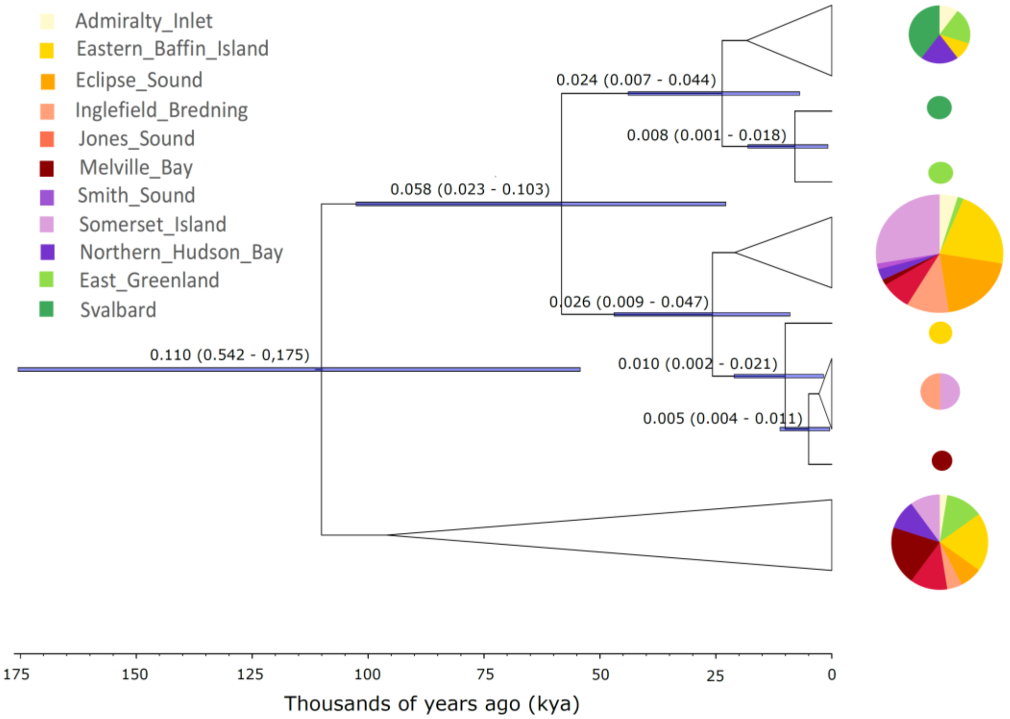

Figure S5. Time-calibrated phylogeny of 43 haplotypes found among the 121 narwhal third codon positions only of the mitogenome sequences inferred with a coalescent constant population size model. Nodes which lack support (posterior values < 0.9) are collapsed. Numbers represent the mean TMRCA and 95% HPD in TMRCA. The 95% HPD of divergence time estimates are also represented by horizontal blue bars. Pie chart colours and size indicate which stocks are represented in each clade, and relative number of individuals, respectively.

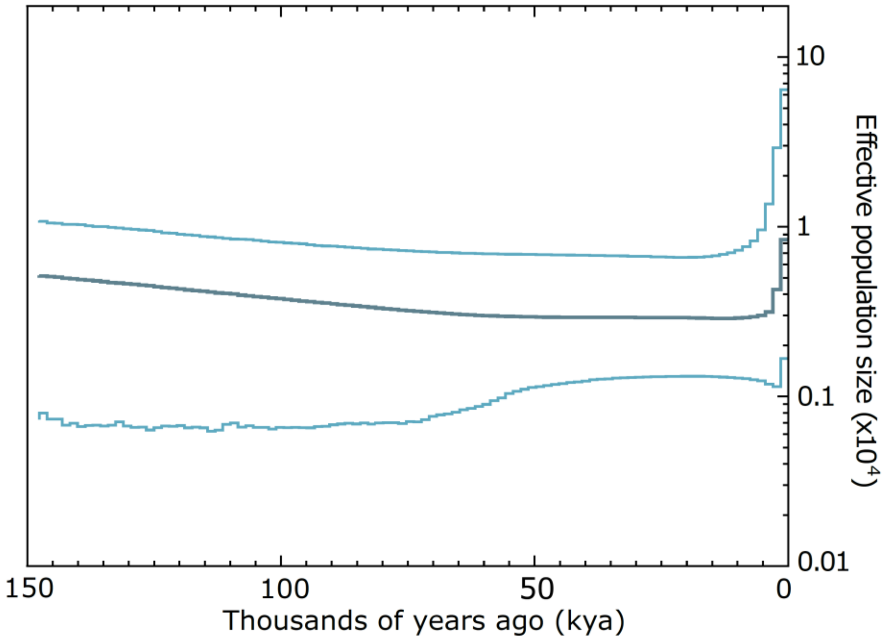

Figure S6. Bayesian skyline plot of narwhal median (turquoise line) female effective population size (*Nef*) and 95% CI (lighter turquoise lines) through time with only the third codon positions of the mitogenomes.

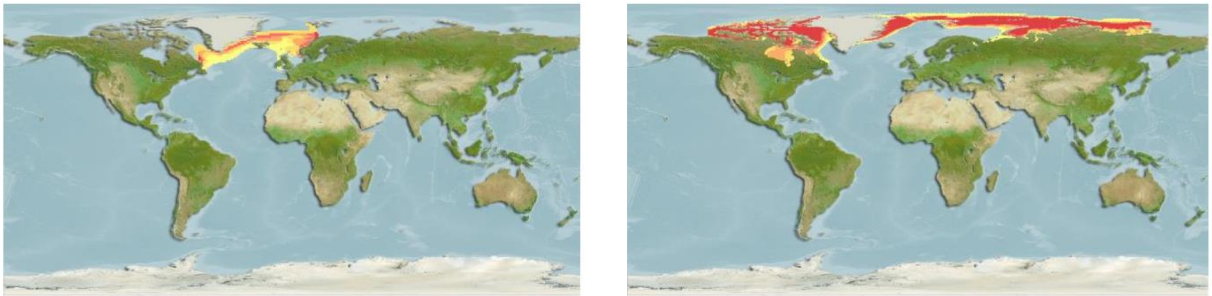

Figure S7. Extent of sea ice and suitable habitat for the narwhal in the summer estimated using Aquamaps during the Last Glacial Maximum (LGM, 20 kya, left) and at present (right). Sea surface temperature, depth and sea ice concentration are included as parameters. The colour scale indicates habitat suitability (0-1) with a score of 1 in red.

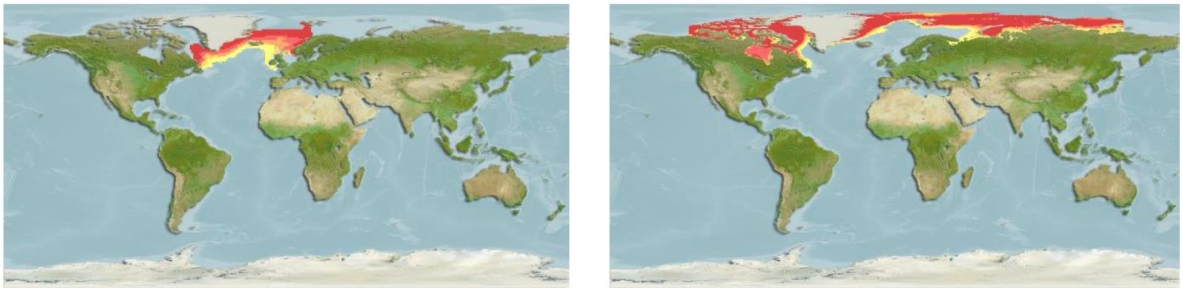

Figure S8. Extent of sea ice and suitable habitat for narwhals year-round estimated using Aquamaps during the Last Glacial Maximum (LGM, 20 kya, left) and at present (right). Sea surface temperature, depth and sea ice concentration are included as parameters. The colour scale indicates habitat suitability (0-1) with a score of 1 in red.

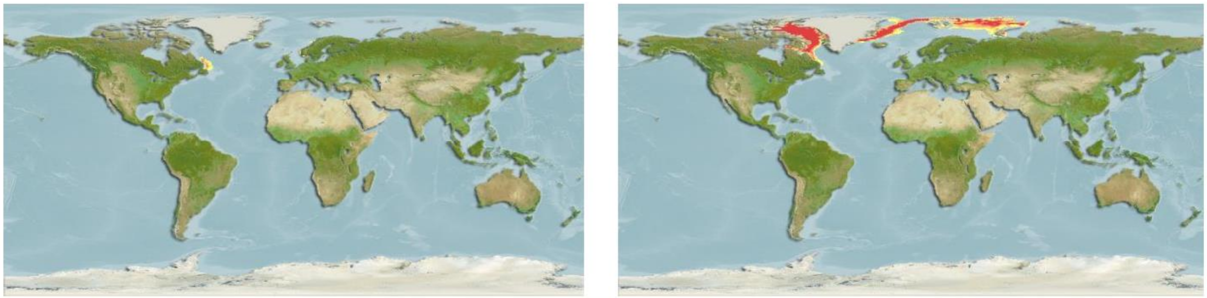

Figure S9. Extent of sea ice and suitable habitat for the narwhal in the winter estimated using Aquamaps during the Last Glacial Maximum (LGM, 20 kya, left) and at present (right). Sea surface temperature, depth, sea ice concentration and salinity are included as parameters. The colour scale indicates habitat suitability (0-1) with a score of 1 in red.

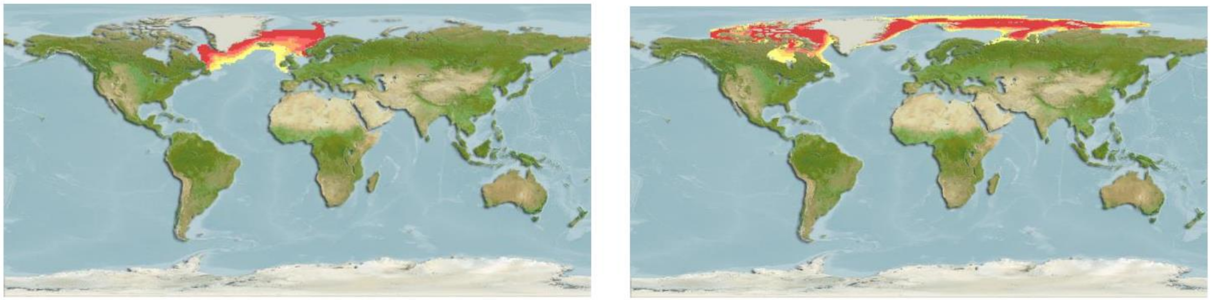

Figure S10. Extent of sea ice and suitable habitat for the narwhal in the summer estimated using Aquamaps during the Last Glacial Maximum (LGM, 20 kya, left) and at present (right).

Sea surface temperature, depth, sea ice concentration and salinity are included as parameters. The colour scale indicates habitat suitability (0-1) with a score of 1 in red.

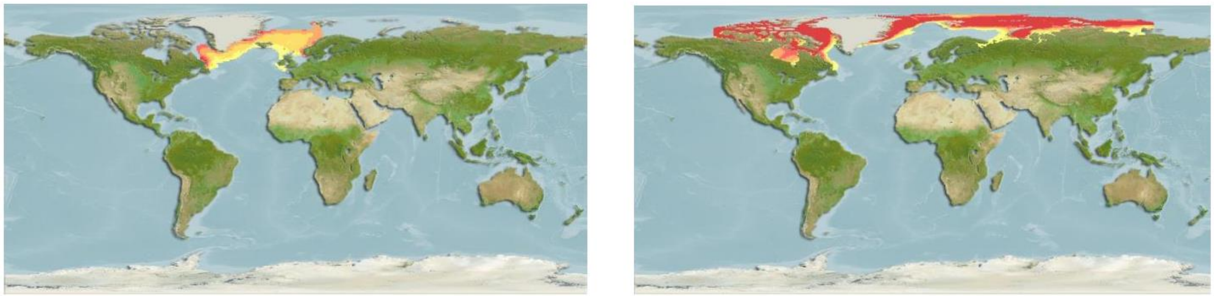

Figure S11. Extent of sea ice and suitable habitat for the narwhal in the summer estimated using Aquamaps during the Last Glacial Maximum (LGM, 20 kya, left) and at present (right). Sea surface temperature, depth, sea ice concentration and salinity are included as parameters. The colour scale indicates habitat suitability (0-1) with a score of 1 in red.

Table S1. Narwhal samples included in this study. Sample_CGG_ID in the sample ID refer to the Centre for GeoGenetics database sample ID at the University of Copenhagen while sample_ID refers to the sample ID provided by the source institution.

sample_CGG_ID	**sample_ID**	**stock**	**locality**	**date**	**haplotypes**	**Genbank Acc**
CGG_1_012748	M.sv.4/SV08	Svalbard	Svalbard	August-2014	Mmon_52	MT251277
CGG_1_017165	*MM98-1*	Svalbard	svalbard	August-1998	Mmon_1	MT251226
CGG_1_017166	*MM98-2*	Svalbard	svalbard	August-1998	Mmon_2	MT251227
CGG_1_017167	*MM98-3*	Svalbard	svalbard	August-1998	Mmon_3	MT251228
CGG_1_017173	*829*	Eclipse Sound	Tremblay Sound	15-August-1999	Mmon_17	MT251242
CGG_1_017186	*964*	East Greenland	Hjørnedal	01-August-2012	Mmon_53	MT251278
CGG_1_017187	*965*	East Greenland	Hjørnedal	01-August-2012	Mmon_54	MT251279
CGG_1_017188	*968*	East Greenland	Hjørnedal	01-August-2012	Mmon_55	MT251280

CGG_1_017190	*987*	East Greenland	Hjørnedal	19-August-2012	Mmon_6	MT251231
CGG_1_017191	*988*	East Greenland	Hjørnedal	19-August-2012	Mmon_8	MT251233
CGG_1_017192	*989*	East Greenland	Hjørnedal	19-August-2012	Mmon_16	MT251241
CGG_1_017193	*990*	East Greenland	Hjørnedal	19-August-2012	Mmon_4	MT251229
CGG_1_017194	*992*	East Greenland	Hjørnedal	17-August-2012	Mmon_5	MT251230
CGG_1_017195	*994*	East Greenland	Hjørnedal	17-August-2012	Mmon_6	MT251231
CGG_1_017198	*1000*	Smith Sound	Smith Sound	14-August-2013	Mmon_56	MT251281
CGG_1_017208	*AB87-105*	Admiralty Inlet	Arctic Bay	16-July-1987	Mmon_44	MT251269
CGG_1_017209	*AB87-108*	Admiralty Inlet	Arctic Bay	17-July-1987	Mmon_5	MT251230
CGG_1_017212	*AB04-007*	Admiralty Inlet	Arctic Bay	2004	Mmon_4	MT251229
CGG_1_017213	*AB09-001*	Admiralty Inlet	Arctic Bay	15-August-2009	Mmon_4	MT251229
CGG_1_017214	*AB09-006*	Admiralty Inlet	Arctic Bay	18-August-2009	Mmon_57	MT251282
CGG_1_017217	*BI95-288*	Eastern Baffin Island	Broughton Island	02-August-1995	Mmon_4	MT251229
CGG_1_017220	*BI95-328*	Eastern Baffin Island	Broughton Island	30-July-1995	Mmon_4	MT251229
CGG_1_017221	*BI04-1085*	Eastern Baffin Island	Broughton Island	10-August-2004	Mmon_4	MT251229
CGG_1_017222	*BI04-1086*	Eastern Baffin Island	Broughton Island	10-July-2004	Mmon_7	MT251232
CGG_1_017223	*BI07-1119*	Eastern Baffin Island	Broughton Island	2007	Mmon_8	MT251233
CGG_1_017224	*BI07-1126*	Eastern Baffin Island	Broughton Island	2007	Mmon_4	MT251229
CGG_1_017225	*BI08-1118*	Eastern Baffin Island	Broughton Island	2007	Mmon_9	MT251234
CGG_1_017226	*CR94-203*	Eastern Baffin Island	Clyde River	31-July-1994	Mmon_10	MT251235

CGG_1_017227	*CR94-206*	Eastern Baffin Island	Clyde River	01-July-1994	Mmon_11	MT251236
CGG_1_017228	*CR95-361*	Eastern Baffin Island	Clyde River	06-August-1995	Mmon_12	MT251237
CGG_1_017229	*CR04-1010*	Eastern Baffin Island	Clyde River	2004	Mmon_13	MT251238
CGG_1_017230	*CR04-1012*	Eastern Baffin Island	Clyde River	2004	Mmon_4	MT251229
CGG_1_017231	*CR04-1014*	Eastern Baffin Island	Clyde River	2004	Mmon_4	MT251229
CGG_1_017232	*CR04-1017*	Eastern Baffin Island	Clyde River	2004	Mmon_14	MT251239
CGG_1_017233	*CR05-1032*	Eastern Baffin Island	Clyde River	2005	Mmon_15	MT251240
CGG_1_017234	*CR05-1048*	Eastern Baffin Island	Clyde River	2005	Mmon_16	MT251241
CGG_1_017235	*CB00-7929*	Somerset Island	Creswell Bay	24-August-2000	Mmon_17	MT251242
CGG_1_017237	*CB01-20692*	Somerset Island	Creswell Bay	09-August-2001	Mmon_4	MT251229
CGG_1_017238	*CB01-3960*	Somerset Island	Creswell Bay	09-August-2001	Mmon_18	MT251243
CGG_1_017239	*CB01-7927*	Somerset Island	Creswell Bay	07-August-2001	Mmon_19	MT251244
CGG_1_017240	*CB01-7928*	Somerset Island	Creswell Bay	08-August-2001	Mmon_5	MT251230
CGG_1_017242	*GF99-1010*	Jones Sound	Grise Fiord	16-August-1999	Mmon_58	MT251283
CGG_1_017243	*GF99-1015*	Jones Sound	Grise Fiord	16-August-1999	Mmon_23	MT251248
CGG_1_017244	*GF99-1017*	Jones Sound	Grise Fiord	16-August-1999	Mmon_20	MT251245
CGG_1_017245	*GF99-1022*	Jones Sound	Grise Fiord	16-August-1999	Mmon_21	MT251246
CGG_1_017246	*GF03-1095*	Jones Sound	Grise Fiord	09-August-2003	Mmon_22	MT251247
CGG_1_017247	*GF03-1107*	Jones Sound	Grise Fiord	10-August-2003	Mmon_5	MT251230
CGG_1_017248	*GF07-1124*	Jones Sound	Grise Fiord	27-July-2007	Mmon_4	MT251229
CGG_1_017249	*GF07-1129*	Jones Sound	Grise Fiord	31-July-2007	Mmon_23	MT251248

CGG_1_017250	*GF07-1131*	Jones Sound	Grise Fiord	28-July-2007	Mmon_23	MT251248
CGG_1_017251	*GF07-1137*	Jones Sound	Grise Fiord	27-July-2007	Mmon_5	MT251230
CGG_1_017252	*IG95-441*	Somerset Island	Igloolik	03-August-1995	Mmon_24	MT251249
CGG_1_017253	*IG95-462*	Somerset Island	Igloolik	04-August-1995	Mmon_4	MT251229
CGG_1_017254	*IG95-465*	Somerset Island	Igloolik	04-August-1995	Mmon_24	MT251249
CGG_1_017255	*IG95-480*	Somerset Island	Igloolik	05-August-1995	Mmon_24	MT251249
CGG_1_017256	*IG95-481*	Somerset Island	Igloolik	04-August-1995	Mmon_7	MT251232
CGG_1_017257	*IG06-1222*	Somerset Island	Igloolik	2006	Mmon_4	MT251229
CGG_1_017258	*IG06-1231*	Somerset Island	Igloolik	2006	Mmon_4	MT251229
CGG_1_017259	*IG06-1238*	Somerset Island	Igloolik	2006	Mmon_24	MT251249
CGG_1_017260	*IG06-1242*	Somerset Island	Igloolik	2006	Mmon_25	MT251250
CGG_1_017261	*PG96-524*	Eastern Baffin Island	Pangnirtung	27-July-1996	Mmon_34	MT251259
CGG_1_017262	*PG95-548*	Eastern Baffin Island	Pangnirtung	27-July-1996	Mmon_4	MT251229
CGG_1_017263	*PG93-170*	Eastern Baffin Island	Pangnirtung	27-July-1996	Mmon_26	MT251251
CGG_1_017264	*PG96-151*	Eastern Baffin Island	Pangnirtung	25-August-1996	Mmon_27	MT251252
CGG_1_017265	*PG04-1032*	Eastern Baffin Island	Pangnirtung	07-July-2004	Mmon_26	MT251251
CGG_1_017266	*PG04-1179*	Eastern Baffin Island	Pangnirtung	07-July-2004	Mmon_21	MT251246
CGG_1_017267	*PG04-1183*	Eastern Baffin Island	Pangnirtung	07-July-2004	Mmon_21	MT251246
CGG_1_017268	*PI82-19*	Eclipse Sound	Pond Inlet	08-August-1982	Mmon_28	MT251253
CGG_1_017272	*PI10-1323*	Eclipse Sound	Pond Inlet	22-August-2010	Mmon_4	MT251229
CGG_1_017273	*PI11-001*	Eclipse Sound	Pond Inlet	18-August-2011	Mmon_29	MT251254
CGG_1_017274	*PI11-003*	Eclipse Sound	Pond Inlet	19-August-2011	Mmon_9	MT251234

CGG_1_017275	*PI11-006*	Eclipse Sound	Pond Inlet	16-August-2011	Mmon_4	MT251229
CGG_1_017276	*PI12-001*	Eclipse Sound	Pond Inlet	13-August-2012	Mmon_29	MT251254
CGG_1_017277	*PI12-003*	Eclipse Sound	Pond Inlet	14-August-2012	Mmon_30	MT251255
CGG_1_017280	*RB95-146*	Northern Hudson Bay	Repulse Bay	17-August-1995	Mmon_31	MT251256
CGG_1_017282	*RB00-1092*	Northern Hudson Bay	Repulse Bay	21-July-2000	Mmon_32	MT251257
CGG_1_017283	*RB00-1094*	Northern Hudson Bay	Repulse Bay	24-July-2000	Mmon_33	MT251258
CGG_1_017284	*RB00-1100*	Northern Hudson Bay	Repulse Bay	07-July-2000	Mmon_34	MT251259
CGG_1_017285	*RB01-1142*	Northern Hudson Bay	Repulse Bay	27-July-2001	Mmon_35	MT251260
CGG_1_017286	*RB06-1231*	Northern Hudson Bay	Repulse Bay	15-July-2006	Mmon_36	MT251261
CGG_1_017287	*RB06-1251*	Northern Hudson Bay	Repulse Bay	15-July-2006	Mmon_4	MT251229
CGG_1_017288	*RB07-001*	Northern Hudson Bay	Repulse Bay	2007	Mmon_37	MT251262
CGG_1_017289	*RB07-002A*	Northern Hudson Bay	Repulse Bay	2007	Mmon_38	MT251263
CGG_1_017295	*RE02-1094*	Somerset Island	Resolute Bay	14-August-2002	Mmon_4	MT251229
CGG_1_017296	*RE02-1106*	Somerset Island	Resolute Bay	14-August-2002	Mmon_39	MT251264
CGG_1_017297	*RE06-1158*	Somerset Island	Resolute Bay	01-09-2006	Mmon_40	MT251265
CGG_1_017298	*RE02-1100*	Somerset Island	Resolute Bay	14-August-2002	Mmon_41	MT251266
CGG_1_017302	*SB96-398*	Somerset Island	Taloyoak	20-August-1996	Mmon_4	MT251229
CGG_1_017303	*SB09-1050*	Somerset Island	Taloyoak	29-August-2009	Mmon_42	MT251267
CGG_1_017304	*SB09-1053*	Somerset Island	Taloyoak	29-August-2009	Mmon_59	MT251284
CGG_1_017305	*SB09-1060*	Somerset Island	Taloyoak	29-August-2009	Mmon_5	MT251230

CGG_1_017528	*363*	Eastern Baffin Island	Broughton Island	19-June-1905	Mmon_4	MT251229
CGG_1_017529	*574*	Eclipse Sound	Tremblay Sound	21-August-1997	Mmon_43	MT251268
CGG_1_017530	*579*	Eclipse Sound	Tremblay Sound	19-August-1997	Mmon_43	MT251268
CGG_1_017531	*590*	Eclipse Sound	Tremblay Sound	21-August-1997	Mmon_4	MT251229
CGG_1_017532	*591*	Eclipse Sound	Tremblay Sound	24-August-1997	Mmon_44	MT251269
CGG_1_017533	*640*	Eclipse Sound	Tremblay Sound	24-August-1997	Mmon_17	MT251242
CGG_1_017534	*829*	Eclipse Sound	Tremblay Sound	15-August-1999	Mmon_4	MT251229
CGG_1_017536	*831*	Eclipse Sound	Tremblay Sound	16-August-1999	Mmon_24	MT251249
CGG_1_017537	*832*	Eclipse Sound	Tremblay Sound	15-August-1999	Mmon_4	MT251229
CGG_1_017542	*841*	Melville Bay	Melville Bugten	10-September-2006	Mmon_45	MT251270
CGG_1_017543	*842*	Melville Bay	Melville Bugten	11-September-2006	Mmon_46	MT251271
CGG_1_017544	*843*	Melville Bay	Melville Bugten	11-September-2006	Mmon_47	MT251272
CGG_1_017545	*844*	Melville Bay	Melville Bugten	11-September-2006	Mmon_47	MT251272
CGG_1_017546	*845*	Melville Bay	Melville Bugten	11-September-2006	Mmon_48	MT251273
CGG_1_017547	*846*	Melville Bay	Melville Bugten	11-September-2006	Mmon_46	MT251271

CGG_1_017548	*847*	Melville Bay	Melville Bugten	11-September-2006	Mmon_46	MT251271
CGG_1_017549	*869*	Melville Bay	Melville Bugten	26-September-2007	Mmon_60	MT251285
CGG_1_017550	*870*	Melville Bay	Melville Bugten	03-September-2007	Mmon_61	MT251286
CGG_1_017551	*871*	Melville Bay	Melville Bugten	04-September-2007	Mmon_49	MT251274
CGG_1_017565	*1679*	Inglefield Bredning	Qaanaaq	August-1993	Mmon_62	MT251287
CGG_1_017566	*1680*	Inglefield Bredning	Qaanaaq	August-1993	Mmon_50	MT251275
CGG_1_017567	*1681*	Inglefield Bredning	Qaanaaq	August-1993	Mmon_17	MT251242
CGG_1_017568	*1682*	Inglefield Bredning	Qaanaaq	August-1993	Mmon_63	MT251288
CGG_1_017569	*1683*	Inglefield Bredning	Qaanaaq	August-1993	Mmon_4	MT251229
CGG_1_017570	*1684*	Inglefield Bredning	Qaanaaq	August-1993	Mmon_22	MT251247
CGG_1_017571	*1685*	Inglefield Bredning	Qaanaaq	August-1993	Mmon_51	MT251276
CGG_1_017572	*1686*	Inglefield Bredning	Qaanaaq	August-1993	Mmon_17	MT251242
CGG_1_017573	*1687*	Inglefield Bredning	Qaanaaq	August-1993	Mmon_17	MT251242
CGG_1_017574	*1688*	Inglefield Bredning	Qaanaaq	August-1993	Mmon_4	MT251229
CGG_1_017631	*MM2012/01*	Svalbard	Svalbard	23-August-2012	Mmon_64	MT251289

Table S2. Accession numbers of the mitochondrial genome sequences of the 15 species of odontocetes analyzed in the fossil calibrated phylogenetic tree.

Species scientific name	**Species common name**	**Accession number (NCBI)**
Berardius bairdii	Baird's beaked whale	NC005274
Cephalorhynchus heavisidii	Heaviside's dolphin	NC020696
Delphinus capensis	Long-beaked common dolphin	NC012061
Globicephala melas	Long-finned pilot whale	HM060334
Hyperoodon ampullatus	Northern bottlenose whale	NC005273
Kogia breviceps	Pygmy sperm whale	NC005272
Mesoplodon densirostris	Blainville's beaked whale	KF032860
Mesoplodon grayi	Gray's beaked whale	KF981442
Delphinapterus leucas	Beluga whale	MT251225
Neophocaena asiaeorientalis	Narrow-ridged finless porpoise	KP170488
Neophocaena phocaenoides	Indo-Pacific finless porpoise	NC 021461
Orcinus orca	Killer whale	GU187155
Phocoena phocoena	Harbour porpoise	NC 005280
Physeter macrocephalus	Sperm whale	NC 002503
Monodon monoceros	Narwhal	MT251227
Monodon monoceros	Narwhal	MT251230
Monodon monoceros	Narwhal	MT251249
Monodon monoceros	Narwhal	MT251262

Table S3a. Partitioning scheme and substitution models used for the fossil-calibrated phylogeny of 15 species of toothed whales, identified by Partition Finder 2.1.1 using AIC [3]. Partitions 14, 17, 20, 22, 23, 26, 27, 29 and 30 only included third codon position of protein coding regions or the control region and were excluded due to substitution saturation or poor alignment. +I: Estimate the proportion of invariable sites. +X: Estimate the base frequencies using maximum likelihoods. +G: Estimate the shape of the gamma distribution describing the evolutionary rate of sites.

Partition	Model	Length	Subsets
1	TRN+G+X	207	tRNA_Cys, tRNA_Glu, tRNA_Ala
2	GTR+G+X	284	tRNA_Arg, tRNA_Lys, tRNA_His, tRNA_Phe
3	TRN+I+G+X	213	tRNA_Asn, tRNA_Ser_1, tRNA_Leu_2
4	TRN+G+X	137	tRNA_Asp, tRNA_Ile
5	HKY+G+X	143	tRNA_Gln, tRNA_Tyr
6	GTR+I+G+X	1673	tRNA_Gly, rRNA_16S
7	GTR+I+G+X	775	tRNA_Leu_1, CDS_CYTB_1, CDS_ND1_1
8	TRNEF+I+G	588	CDS_COX1_1, tRNA_Met
9	HKY+I+X	245	CDS_ND6_2, tRNA_Pro
10	GTR+G+X	385	tRNA_Val, tRNA_Thr, CDS_ND3_1, tRNA_Ser_2, tRNA_Trp
11	TRN+I+G+X	982	rRNA_12S
12	GTR+G+X	835	CDS_ND5_1, CDS_ATP6_1
13	GTR+I+G+X	1049	CDS_ND5_2, CDS_ND3_2, CDS_ND4L_2, CDS_ATP6_2
14	TRN+I+G+X	671	CDS_ATP8_3, CDS_ND3_3, CDS_ATP6_3, CDS_COX3_3
15	GTR+G+X	482	CDS_ND2_1, CDS_ATP8_2, CDS_ATP8_1
16	HKY+I+X	518	CDS_COX1_2
17	GTR+I+G+X	518	CDS_COX1_3
18	TRN+G+X	490	CDS_COX3_1, CDS_COX2_1
19	TRN+I+G+X	228	CDS_COX2_2
20	TRN+I+G+X	228	CDS_COX2_3
21	GTR+I+G+X	1420	CDS_COX3_2, CDS_ND4_2, CDS_CYTB_2, CDS_ND1_2
22	TRN+I+G+X	380	CDS_CYTB_3
23	GTR+I+G+X	667	CDS_ND1_3, CDS_ND2_3
24	TRN+G+X	348	CDS_ND2_2
25	TRN+G+X	558	CDS_ND4_1, CDS_ND4L_1
26	TRN+I+G+X	459	CDS_ND4_3
27	TRN+I+G+X	707	CDS_ND4L_3, CDS_ND5_3
28	TRN+G+X	176	CDS_ND6_1
29	HKY+G+X	176	CDS_ND6_3
30	HKY+G+X	972	Ctrl-Reg_D-loop

Table S3b. Partitioning scheme and substitution models used in the construction of the narwhal time-calibrated phylogeny, identified by Partition Finder 2.1.1 [3]. +I: Estimate the proportion of invariable sites. +X: Estimate the base frequencies using maximum likelihoods. +G: Estimate the shape of the gamma distribution describing the evolutionary rate of sites.

Partition	Model	Length	Subset
1	TRN+X	3802	CDS_ALL_1st
2	HKY+X	3802	CDS_ALL_2st
3	TRN+G+X	3802	CDS_ALL_3st
4	HKY+X	917	Ctrl-Reg_D-loop
5	HKY+X	2553	rRNA_ALL
6	HKY+X	1516	tRNA_ALL

Table S4. P-values of the test of significant differences in diversity indices between narwhal stocks (nucleotide diversity below diagonal and haplotype diversity above diagonal) calculated from the proportion of simulated values from the bootstraps (n=1000) that were equal to or greater than the observed value. Differences were considered significant if they were <0.05 and are indicated by blue shading and bold font.

P-values (Pi)\(Hap)		1	2	3	4	5	6	7	8	9	10
Admiralty Inlet	1	--	0.98	0.381	0.933	0.876	0.876	0.869	0.186	0.985	0.486
Eastern Baffin Island	2	0.98	--	0.196	0.996	0.726	0.741	0.759	0.123	0.782	0.137
East Greenland	3	0.265	0.088	--	0.21	0.331	0.35	0.353	0.744	0.224	0.776
Eclipse Sound	4	0.527	0.323	**0.025**	--	0.708	0.748	0.753	0.143	0.761	0.149
Inglefield Bredning	5	0.575	0.463	**0.047**	0.976	--	1	1	0.223	0.891	0.274
Jones Sound	6	0.686	0.548	0.367	0.179	0.26	--	1	0.222	0.916	0.31
Melville Bay	7	0.681	0.539	0.369	0.172	0.25	0.986	--	0.229	0.911	0.304
Northern Hudson Bay	8	0.358	0.182	0.789	**0.047**	0.079	0.502	0.513	--	0.151	1

Somerset Island	9	0.485	0.228	**0.009**	0.925	0.912	0.117	0.117	**0.026**	--	0.17
Svalbard	10	0.249	0.154	**0.018**	0.416	0.439	0.097	0.089	**0.035**	0.455	--

Table S5. Pairwise mitochondrial F_{ST} (above diagonal) and Φ_{ST} (below diagonal) between narwhal stocks in the High Arctic. The colour gradient ranging from light yellow to red indicates the strength of the F_{ST} values in bins of 0.1; significant values ($p<0.05$) are indicated in bold font.

ΦST\FST		1	2	3	4	5	6	7	8	9	10
Admiralty Inlet	1		-0.033	-0.007	-0.038	0.015	0.015	0.094	0.001	-0.034	0.05
Eastern Baffin Island	2	-0.048		0.027	0.002	0.035	**0.060**	**0.100**	0.018	0.010	0.065
East Greenland	3	-0.009	**0.131**		0.037	0.037	0.026	**0.059**	0.002	0.025	0.015
Eclipse Sound	4	-0.083	0.018	**0.173**		-0.001	**0.070**	**0.100**	0.023	-0.001	0.063
Inglefield Bredning	5	-0.072	-0.019	**0.168**	-0.041		0.061	**0.089**	0.023	0.026	0.050
Jones Sound	6	-0.042	0.015	0.068	0.067	0.026		**0.089**	0.034	0.049	0.050
Melville Bay	7	**0.315**	**0.413**	**0.186**	**0.435**	**0.439**	**0.305**		0.045	**0.092**	0.050
Northern Hudson Bay	8	-0.085	-0.027	0.019	0.054	0.008	-0.043	**0.303**		0.022	0
Somerset Island	9	-0.068	0.018	**0.212**	-0.034	-0.041	0.073	**0.481**	0.067		0.057
Svalbard	10	**0.317**	**0.331**	**0.252**	**0.454**	**0.451**	**0.372**	**0.599**	**0.204**	**0.448**	

Table S6.The mean and Effective Sample Size (ESS) values for the different parameters in the two combined runs of the toothed whale phylogeny. The models were run with tRNAs, rRNAs, first and second codon positions of the protein coding regions using a calibrated Yule prior model and relaxed log normal clock with an estimated rate.

Statistic	**Mean**	**ESS**
posterior	-43964.08	3669
likelihood	-43707.25	3665
prior	-256.83	2677
treeLikelihood.Subset1	-691.691	5036
treeLikelihood.Subset10	-1694.719	4310

treeLikelihood.Subset11	-3774.62	7743
treeLikelihood.Subset12	-3943.278	6166
treeLikelihood.Subset13	-3008.306	4809
treeLikelihood.Subset15	-2271.965	4837
treeLikelihood.Subset16	-920.577	3744
treeLikelihood.Subset18	-1784.83	5563
treeLikelihood.Subset19	-470.004	4150
treeLikelihood.Subset2	-1395.139	4150
treeLikelihood.Subset21	-3127.104	4091
treeLikelihood.Subset22	-3297.297	5478
treeLikelihood.Subset24	-888.324	4407
treeLikelihood.Subset25	-2450.3	4723
treeLikelihood.Subset28	-720.021	3356
treeLikelihood.Subset3	-734.661	5882
treeLikelihood.Subset4	-441.184	2955
treeLikelihood.Subset5	-508.207	5172
treeLikelihood.Subset6	-5972.501	5913
treeLikelihood.Subset7	-3046.176	4448
treeLikelihood.Subset8	-1758.111	7502
treeLikelihood.Subset9	-808.237	5061
TreeHeight	28.756	8793
ucldMean	4.03E-03	3397
ucldStdev	0.262	3771
rate.mean	3.84E-03	5855
rate.variance	1.16E-06	2907
rate.coefficientOfVariation	0.257	3707
CalibratedYuleModel	-83.422	5978
birthRateY	0.147	10589
kappa1.1	30.046	3090
kappa1.11	9.72	4183
kappa1.18	14.098	2766
kappa1.19	24.516	2140
kappa1.22	44.534	2049
kappa1.24	1.995	2543
kappa1.25	18.303	3792
kappa1.28	8.29	4006
kappa1.3	12.147	4326
kappa1.4	69.837	1596
kappa1.8	14.255	2592
kappa2.1	5.975	2674
kappa2.11	24.488	3866
kappa2.18	47.363	2634
kappa2.19	8.967	2476
kappa2.22	38.587	2064
kappa2.24	12.563	4291

kappa2.25	47.69	3023
kappa2.28	40.528	1707
kappa2.3	6.781	3743
kappa2.4	47.538	1548
kappa2.8	40.15	2625
mutationRate.1	0.634	6309
mutationRate.10	0.959	3733
mutationRate.11	0.978	3094
mutationRate.12	1.016	3314
mutationRate.13	0.599	3736
mutationRate.15	1.009	4527
mutationRate.16	8.17E-02	4381
mutationRate.18	1.072	3003
mutationRate.19	0.165	6055
mutationRate.2	1.071	5337
mutationRate.21	0.289	3192
mutationRate.22	7.258	1163
mutationRate.24	0.394	5811
mutationRate.25	1.712	2649
mutationRate.28	1.028	5313
mutationRate.3	0.71	5462
mutationRate.4	0.703	6210
mutationRate.5	0.769	6185
mutationRate.6	0.918	2203
mutationRate.7	1.222	2523
mutationRate.8	0.64	4678
mutationRate.9	0.508	6670
gammaShape.1	0.398	4208
gammaShape.11	0.209	7370
gammaShape.13	4.07E-02	3721
gammaShape.18	0.103	2914
gammaShape.19	0.103	1665
gammaShape.21	3.51E-02	3722
gammaShape.22	4.299	3225
gammaShape.24	7.59E-02	3382
gammaShape.25	0.147	6551
gammaShape.28	0.408	4091
gammaShape.3	0.12	3431
gammaShape.4	6.81E-02	3061
gammaShape.5	0.145	2681
gammaShape.6	0.141	5943
gammaShape.7	0.159	6254
gammaShape.8	5.10E-02	3375
freqParameter.11	0.265	3210
freqParameter.12	0.144	3889

freqParameter.13	0.243	3041
freqParameter.14	0.348	3220
freqParameter.101	0.311	2478
freqParameter.102	0.236	2657
freqParameter.103	0.177	2726
freqParameter.104	0.276	2274
freqParameter.111	0.357	3040
freqParameter.112	0.241	3121
freqParameter.113	0.184	2723
freqParameter.114	0.218	3147
freqParameter.121	0.344	2321
freqParameter.122	0.239	2696
freqParameter.123	0.181	2679
freqParameter.124	0.236	2398
freqParameter.131	0.203	3316
freqParameter.132	0.283	3370
freqParameter.133	9.33E-02	2950
freqParameter.134	0.421	2809
freqParameter.151	0.367	2813
freqParameter.152	0.26	2939
freqParameter.153	0.126	2683
freqParameter.154	0.247	2483
freqParameter.161	0.181	3670
freqParameter.162	0.263	3187
freqParameter.163	0.148	3211
freqParameter.164	0.407	3092
freqParameter.181	0.268	3244
freqParameter.182	0.301	2962
freqParameter.183	0.222	2867
freqParameter.184	0.208	2751
freqParameter.191	0.263	3551
freqParameter.192	0.247	3395
freqParameter.193	0.117	3403
freqParameter.194	0.373	2984
freqParameter.181	0.268	3244
freqParameter.182	0.301	2962
freqParameter.183	0.222	2867
freqParameter.184	0.208	2751
freqParameter.191	0.263	3551
freqParameter.192	0.247	3395
freqParameter.193	0.117	3403
freqParameter.194	0.373	2984
freqParameter.21	0.359	2670
freqParameter.22	0.191	2838
freqParameter.23	0.164	2523

freqParameter.24	0.286	2719
freqParameter.211	0.189	3617
freqParameter.212	0.268	3706
freqParameter.213	0.128	3045
freqParameter.214	0.415	3291
freqParameter.221	0.408	1100
freqParameter.222	0.39	1236
freqParameter.223	3.82E-02	1257
freqParameter.224	0.163	1382
freqParameter.241	0.17	3830
freqParameter.242	0.323	2957
freqParameter.243	8.14E-02	3997
freqParameter.244	0.426	2858
freqParameter.251	0.344	2330
freqParameter.252	0.319	2699
freqParameter.253	0.148	3107
freqParameter.254	0.189	2362
freqParameter.281	0.228	3312
freqParameter.282	4.76E-02	1344
freqParameter.283	0.433	2604
freqParameter.284	0.291	2877
freqParameter.31	0.322	3204
freqParameter.32	0.158	2763
freqParameter.33	0.225	3652
freqParameter.34	0.295	3052
freqParameter.41	0.393	2701
freqParameter.42	0.157	3673
freqParameter.43	0.137	3058
freqParameter.44	0.313	2783
freqParameter.51	0.309	3515
freqParameter.52	0.138	3913
freqParameter.53	0.261	3512
freqParameter.54	0.292	3591
freqParameter.61	0.365	2544
freqParameter.62	0.219	2572
freqParameter.63	0.168	2336
freqParameter.64	0.247	2606
freqParameter.71	0.299	2600
freqParameter.72	0.304	2306
freqParameter.73	0.195	2732
freqParameter.74	0.202	2602
freqParameter.91	0.169	4056
freqParameter.92	0.153	3998
freqParameter.93	0.264	3543
freqParameter.94	0.414	2966

rateAC.10	7.58E-02	5284
rateAC.12	9.56E-02	5082
rateAC.13	0.165	6195
rateAC.15	0.117	5027
rateAC.2	0.18	4683
rateAC.21	8.41E-02	4917
rateAC.6	0.103	4537
rateAC.7	3.01E-02	3835
rateAG.10	0.362	2801
rateAG.12	0.483	2777
rateAG.13	1.759	4527
rateAG.15	0.777	2955
rateAG.2	0.756	2477
rateAG.21	0.799	5279
rateAG.6	0.36	2991
rateAG.7	0.492	2876
rateAT.10	2.75E-02	4123
rateAT.12	7.13E-02	5732
rateAT.13	9.05E-02	6251
rateAT.15	0.118	6100
rateAT.2	0.112	4506
rateAT.21	8.77E-02	5914
rateAT.6	7.34E-02	5061
rateAT.7	5.05E-02	4984
rateCG.10	3.02E-02	4009
rateCG.12	1.80E-02	4408
rateCG.13	0.235	5324
rateCG.15	4.67E-02	3692
rateCG.2	7.24E-02	3595
rateCG.21	0.171	5305
rateCG.6	1.86E-02	3705
rateCG.7	9.20E-03	3601
rateGT.10	2.25E-02	3470
rateGT.12	3.37E-02	5058
rateGT.13	5.17E-02	3488
rateGT.15	7.08E-02	4308
rateGT.2	3.64E-02	3538
rateGT.21	3.27E-02	2779
rateGT.6	2.81E-02	5086
rateGT.7	2.97E-02	4194
proportionInvariant.11	0.00E+00	-
proportionInvariant.13	0.00E+00	-
proportionInvariant.16	0.00E+00	-
proportionInvariant.19	0.00E+00	-
proportionInvariant.21	0.00E+00	-

proportionInvariant.22	0.00E+00	-
proportionInvariant.3	0.00E+00	-
proportionInvariant.6	0.00E+00	-
proportionInvariant.7	0.00E+00	-
proportionInvariant.8	0.00E+00	-
proportionInvariant.9	0.00E+00	-
kappa.16	4.167	4595
kappa.5	55.386	3360
kappa.9	11.866	5599
logP(mrca(F.kelloggi_root))	-3.127	11349
mrca.age(F.kelloggi_root)	28.756	8793
logP(mrca(K.Pernix_Delphinidae+Ziphiidae))	-3.197	3871
mrca.age(K.Pernix_Delphinidae+Ziphiidae)	25.354	4174
logP(mrca(S.Stocktoni_Monodontoidae))	-3.039	2533
mrca.age(S.Stocktoni_Monodontoidae)	12.109	2695
logP(mrca(A.Microglenoideus_Crown_Ziphiidae))	-1.593	8280
mrca.age(A.Microglenoideus_Crown_Ziphiidae)	15.068	8162

Table S7. The mean and Effective Sample Size (ESS) values for the different parameters in the two combined runs of the narwhal phylogeny. The models were run with the full partitioned mitochondrial genome, using a coalescent constant population model and a strict clock.

Statistic	**Mean**	**ESS**
posterior	-23060.075	15857
likelihood	-23049.402	7378
prior	-10.673	18223
treeLikelihood.Subset1	-5410.325	9683
treeLikelihood.Subset2	-5005.363	6926
treeLikelihood.Subset3	-5454.521	2059

treeLikelihood.Subset4	-1480.404	1139
treeLikelihood.Subset5	-3561.676	10099
treeLikelihood.Subset6	-2137.112	5446
TreeHeight	0.11	37851
kappa1.1	21.859	3120
kappa1.3	57.234	2608
kappa2.1	7.042	3224
kappa2.3	29.808	2566
mutationRate.1	0.479	10796
mutationRate.2	0.231	9880
mutationRate.3	2.547	6992
mutationRate.4	2.273	14506
mutationRate.5	0.423	13666
mutationRate.6	0.555	16010
kappa.2	20.383	2466
kappa.4	28.592	4177
kappa.5	9.215	3726
kappa.6	25.232	2049
gammaShape.3	0.299	2356

clockRate	9.95E-03	31802
popSize	0.247	24908
CoalescentConstant	28.713	25919
logP(mrca(tree_age_prioir))	1.896	52508
mrca.age(tree_age_prioir)	0.11	37851
freqParameter.11	0.323	4477
freqParameter.12	0.255	4276
freqParameter.13	0.199	5121
freqParameter.14	0.223	4739
freqParameter.21	0.196	5344
freqParameter.22	0.267	4409
freqParameter.23	0.12	5628
freqParameter.24	0.417	4509
freqParameter.31	0.417	4493
freqParameter.32	0.335	4768
freqParameter.33	4.68E-02	4804
freqParameter.34	0.201	5551
freqParameter.41	0.299	4860
freqParameter.42	0.248	5434

freqParameter.43	0.14	5929
freqParameter.44	0.313	5098
freqParameter.51	0.368	4669
freqParameter.52	0.218	4966
freqParameter.53	0.175	5126
freqParameter.54	0.238	5234
freqParameter.61	0.325	5043
freqParameter.62	0.18	4922
freqParameter.63	0.192	5400
freqParameter.64	0.303	5221

Table S8. The mean and Effective Sample Size (ESS) values for the different parameters two combined runs of the coalescent Bayesian skyline analysis. The models were run with the full partitioned mitochondrial genome, using a strict clock.

Statistic	**Mean**	**ESS**
posterior	-23058.5	9464
likelihood	-23130	3412
prior	71.426	9471
treeLikelihood.Subset1	-5424.87	6573

treeLikelihood.Subset2	-5007.34	5860
treeLikelihood.Subset3	-5493.42	734
treeLikelihood.Subset4	-1486.61	368
treeLikelihood.Subset5	-3563.89	7975
treeLikelihood.Subset6	-2153.83	526
TreeHeight	9.16E-02	15574
kappa1.1	20.964	2347
kappa1.3	59.88	2092
kappa2.1	8.588	2340
kappa2.3	29.564	2024
mutationRate.1	0.492	11496
mutationRate.2	0.227	11950
mutationRate.3	2.543	7798
mutationRate.4	2.211	14099
mutationRate.5	0.415	13804
mutationRate.6	0.595	17656
kappa.2	20.121	2146
kappa.4	28.076	3718
kappa.5	9.06	3652

kappa.6	13.71	2978
gammaShape.3	0.345	2184
clockRate	1.10E-02	12632
BayesianSkyline	107.04	9524
bPopSizes.1	0.409	8974
bPopSizes.2	0.271	9436
bPopSizes.3	0.199	6367
bPopSizes.4	0.129	5438
bPopSizes.5	8.12E-02	16505
bGroupSizes.1	24.918	3873
bGroupSizes.2	24.577	8170
bGroupSizes.3	23.413	10956
bGroupSizes.4	24.147	8166
bGroupSizes.5	22.945	4543
logP(mrca(tree_prior))	2.041	24262
mrca.age(tree_prior)	9.16E-02	15574
freqParameter.11	0.323	3977
freqParameter.12	0.255	4404
freqParameter.13	0.199	3924

freqParameter.14	0.223	4316
freqParameter.21	0.196	4241
freqParameter.22	0.267	4099
freqParameter.23	0.12	4086
freqParameter.24	0.417	3635
freqParameter.31	0.417	3621
freqParameter.32	0.335	3795
freqParameter.33	4.68E-02	3468
freqParameter.34	0.201	4201
freqParameter.41	0.299	4130
freqParameter.42	0.248	4126
freqParameter.64	0.14	4659
freqParameter.44	0.313	4011
freqParameter.51	0.368	3922
freqParameter.52	0.218	4585
freqParameter.53	0.175	4273
freqParameter.54	0.238	4489
freqParameter.61	0.324	4223
freqParameter.62	0.18	4764

freqParameter.63	0.192	4608
freqParameter.64	0.304	4579

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