

Supplementary Information

Phylogenomics and pervasive genome-wide phylogenetic discordance among fin whales (*Balaenoptera physalus*)

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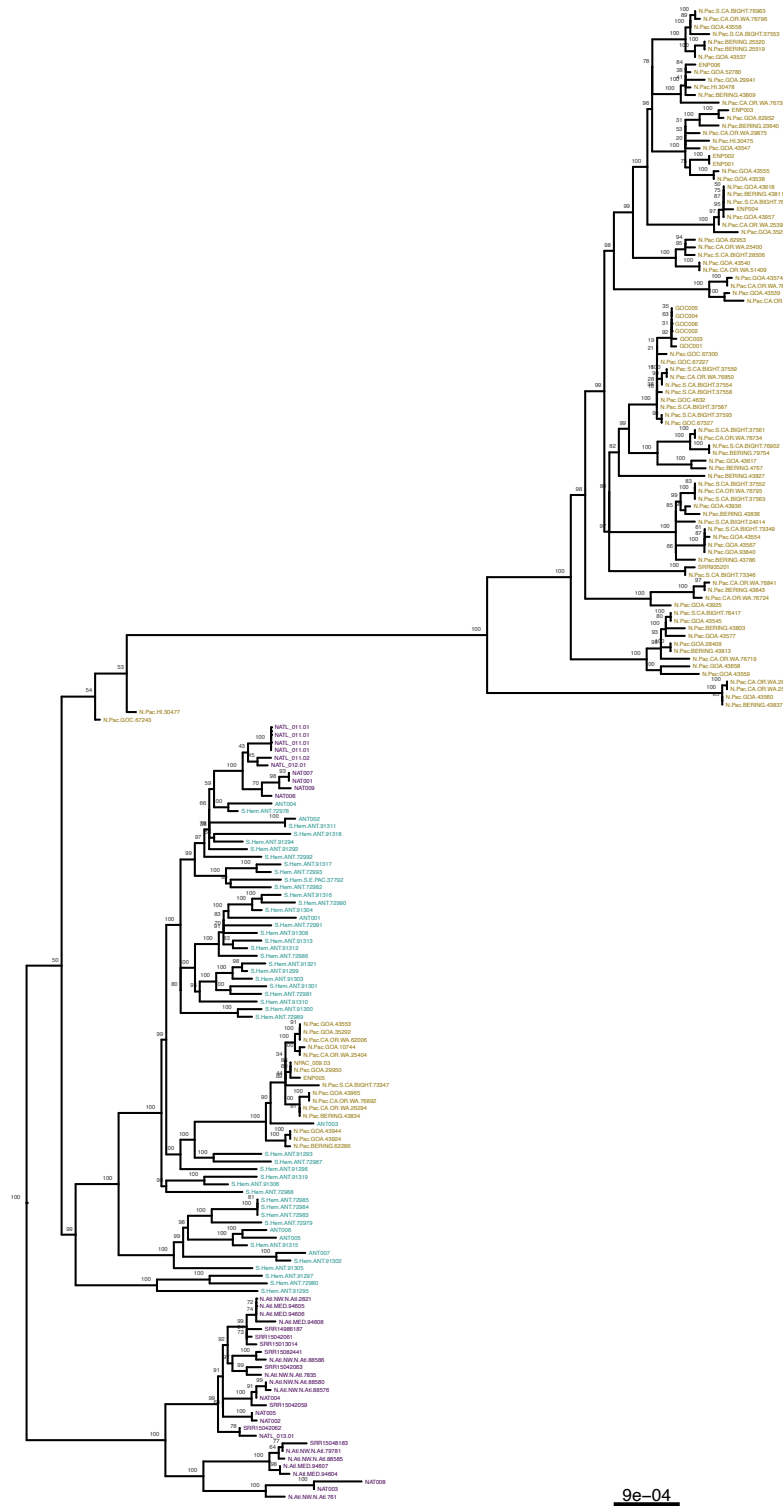
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Supplementary Figures



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Figure S1. Maximum likelihood phylogeny with tip labels using published and new whole mitochondrial genome data. Colours indicate sampling origin. North Atlantic (purple), Southern Ocean (blue), and North Pacific (brown). Bootstrap support is indicated with number and coloured circles.

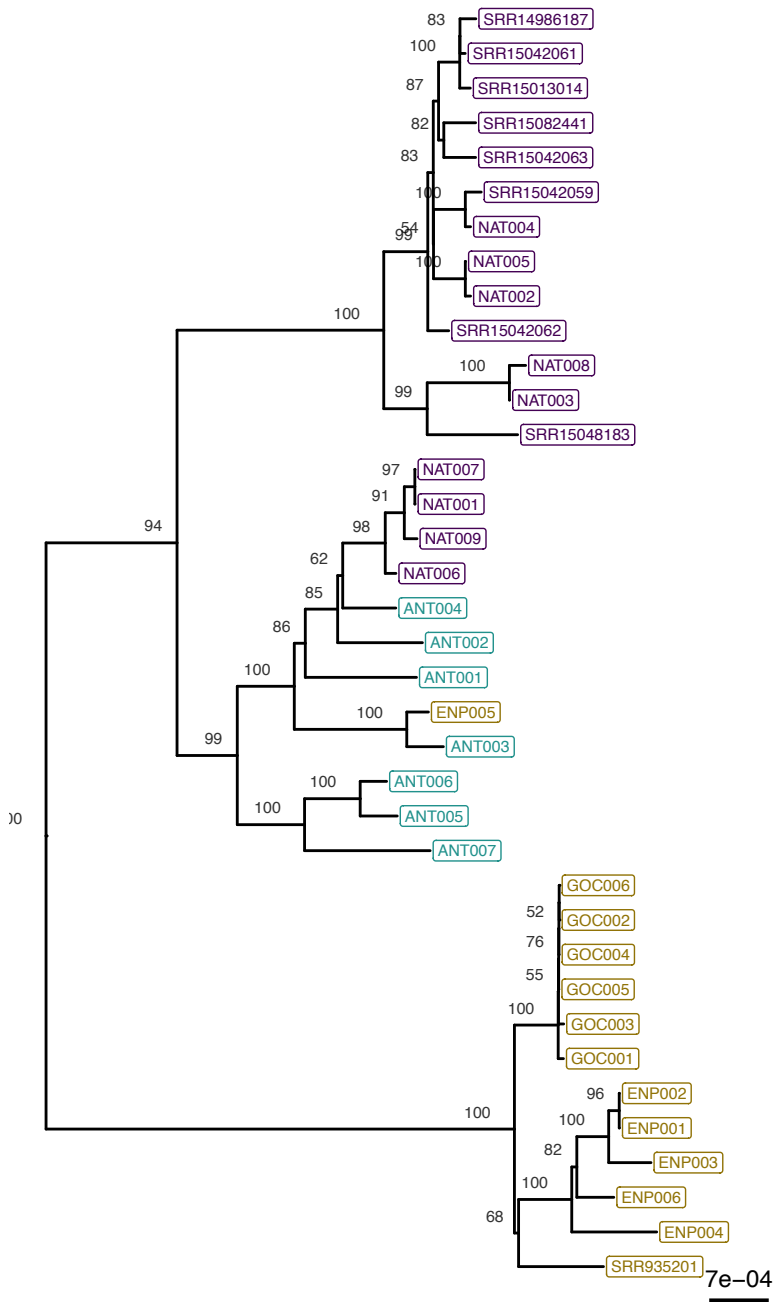


Figure S2. Maximum likelihood phylogeny with tip labels using only whole mitochondrial sequences with whole nuclear genomes. Colours indicate sampling origin. North Atlantic (purple), Southern Ocean (blue), and North Pacific (brown). Values indicate bootstrap support results.

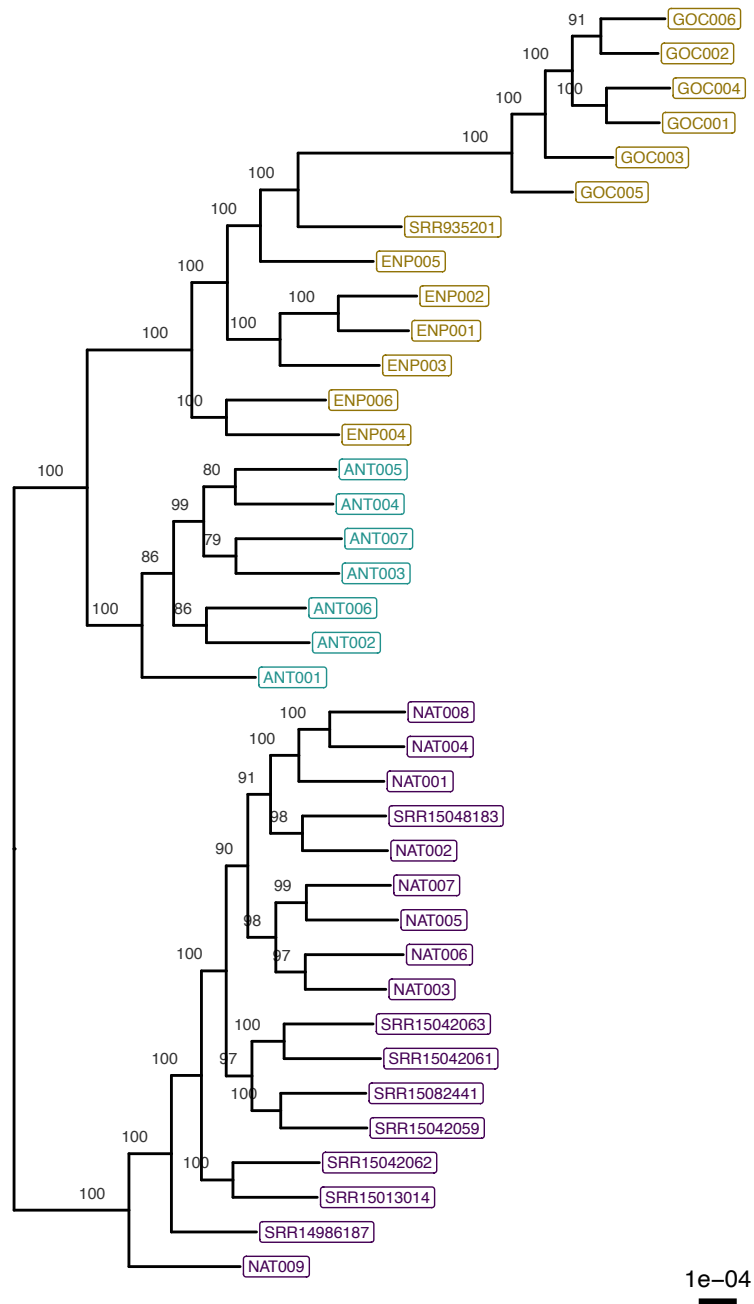


Figure S3. Concatenated autosomal genome maximum likelihood phylogeny with tip labels. Colours indicate sampling origin. North Atlantic (purple), Southern Ocean (blue), and North Pacific (brown). Values indicate bootstrap support results.

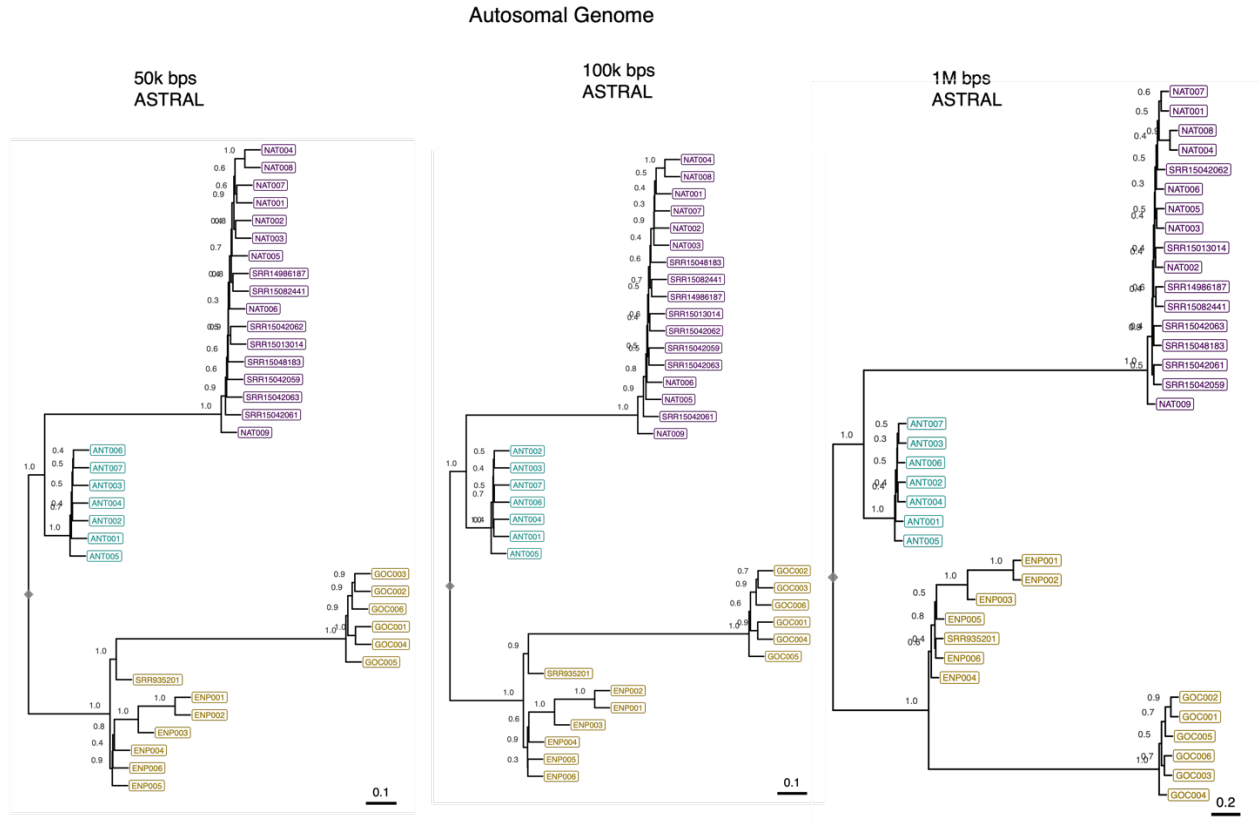


Figure S4. Multi-coalescent ASTRAL autosomal genome consensus phylogenies for the windows-based analyses. Different window sizes converged to the same consensus phylogeny with similar support values. North Atlantic (purple), Southern Ocean (blue), and North Pacific (brown). Values indicate ASTRAL posterior support results.

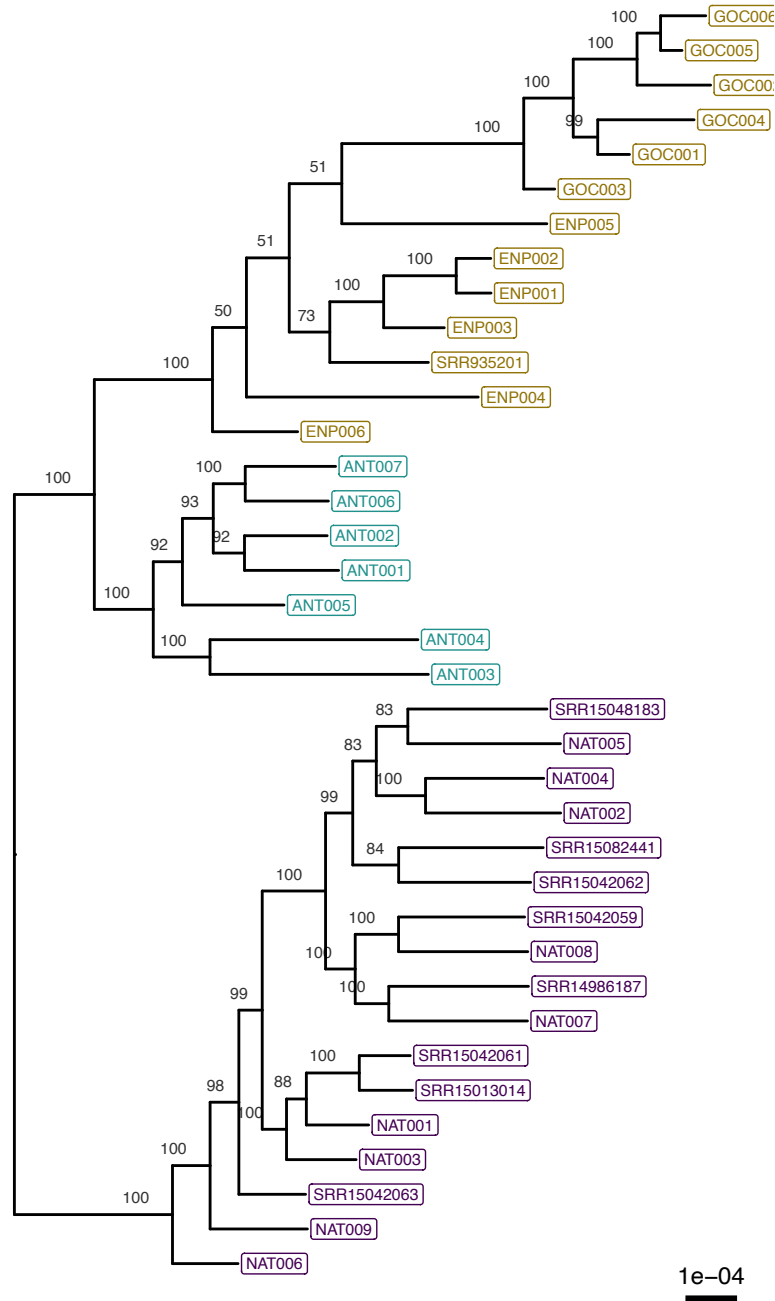


Figure S5. X chromosome concatenated maximum likelihood phylogeny with tip labels. Colours indicate sampling origin. North Atlantic (purple), Southern Ocean (blue), and North Pacific (brown). Values indicate bootstrap support results.

X chromosome

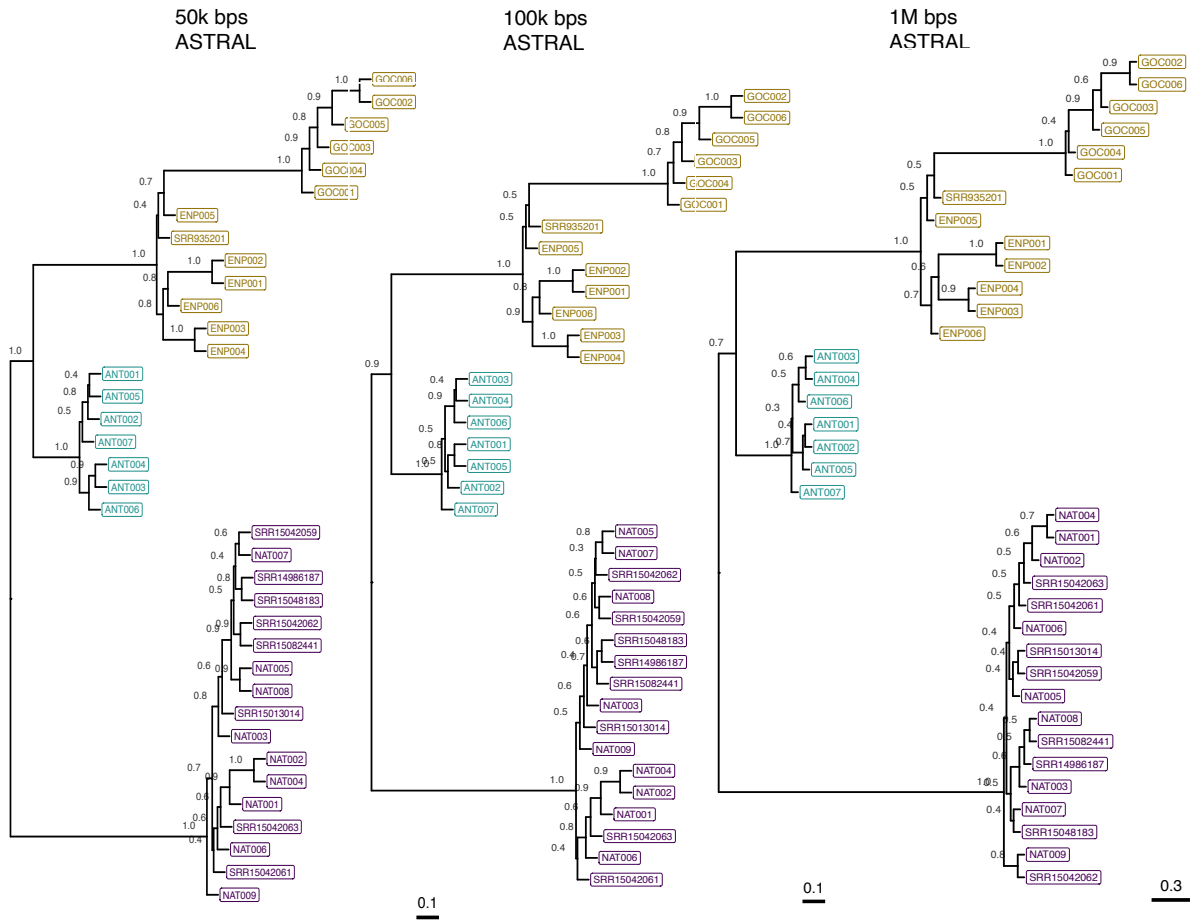


Figure S6. X chromosome multi-coalescent ASTRAL consensus phylogenies for the windows-based analyses. Different window sizes displayed a similar consensus phylogeny with equivalent support values. North Atlantic (purple), Southern Ocean (blue), and North Pacific (brown). Values indicate ASTRAL posterior support results.

Y chromosome

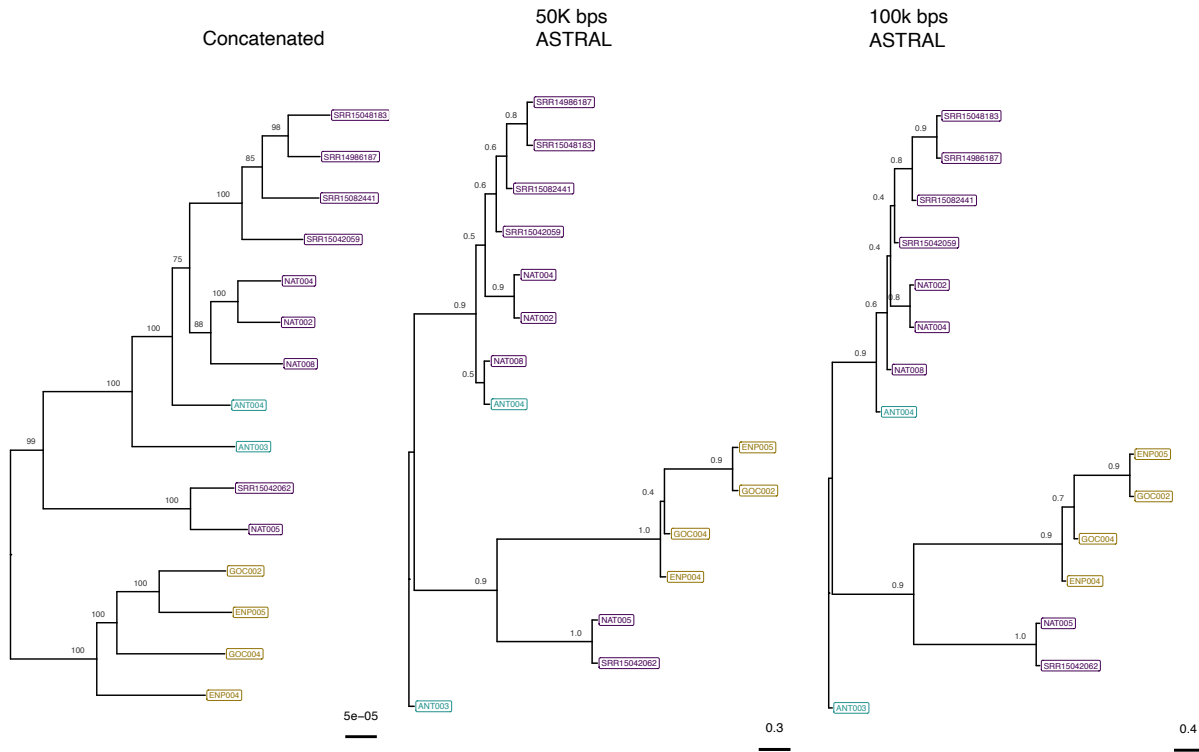


Figure S7. Y chromosome concatenated maximum likelihood phylogeny and ASTRAL consensus phylogenies for windows-based analyses. Different window sizes displayed a similar consensus phylogeny with similar support. North Atlantic (purple), Southern Ocean (blue), and North Pacific (brown). Values indicate bootstrap support results for the concatenated phylogeny and ASTRAL posterior support values for the consensus phylogenies,

Supplementary Tables

Table S1. Sampling, sequencing, and alignment information for fin whale samples used in this study.

Sample	Origin	Species/Subspecies	Ocean	Location	Sex	Number of Raw Reads	% Reads Aligned	% Duplicates	Mean Genome Depth	Mapping rate	Mean Autosomal Depth
ANT001	<i>This study</i>	<i>B. physalus pathaconica</i> or <i>B. p. quoyi</i>	Southern Ocean	Western Antarctic Peninsula	female	304820830	98.55	9.82	7.012866	98.1064	10.9738
ANT002	<i>This study</i>	<i>B. physalus pathaconica</i> or <i>B. p. quoyi</i>	Southern Ocean	Western Antarctic Peninsula	female	327897212	98.33	7.41	7.574109	98.1441	12.0005
ANT003	<i>This study</i>	<i>B. physalus pathaconica</i> or <i>B. p. quoyi</i>	Southern Ocean	Western Antarctic Peninsula	male	317439522	98.43	7.95	7.414822	98.1388	11.9685
ANT004	<i>This study</i>	<i>B. physalus pathaconica</i> or <i>B. p. quoyi</i>	Southern Ocean	Western Antarctic Peninsula	male	378702354	98.18	10.51	8.116773	98.2342	13.7446
ANT005	<i>This study</i>	<i>B. physalus pathaconica</i> or <i>B. p. quoyi</i>	Southern Ocean	Western Antarctic Peninsula	female	326149530	98.35	9.22	7.337591	98.157	11.8704
ANT006	<i>This study</i>	<i>B. physalus pathaconica</i> or <i>B. p. quoyi</i>	Southern Ocean	Western Antarctic Peninsula	female	366820128	98.41	10.93	7.850812	98.2124	12.9872
ANT007	<i>This study</i>	<i>B. physalus pathaconica</i> or <i>B. p. quoyi</i>	Southern Ocean	Western Antarctic Peninsula	female	308218122	98.4	17.79	7.144842	98.1107	11.3605
NAT001	<i>This study</i>	<i>B. physalus physalus</i>	North Atlantic	eastern North American sea border	female	445317238	98.42	15.31	8.443355	98.0471	16.2024
NAT002	<i>This study</i>	<i>B. physalus physalus</i>	North Atlantic	eastern North American sea border	male	391421130	98.55	12.59	7.923763	98.1167	14.9304

NAT003	<i>This study</i>	<i>B. physalus physalus</i>	North Atlantic	eastern North American sea border	female	423207376	98.51	14.99	8.43042	98.0305	15.4489
NAT004	<i>This study</i>	<i>B. physalus physalus</i>	North Atlantic	eastern North American sea border	male	463612558	98.56	15.27	8.376384	98.2257	17.1651
NAT005	<i>This study</i>	<i>B. physalus physalus</i>	North Atlantic	eastern North American sea border	male	349684036	98.51	12.88	7.899698	97.2774	13.1057
NAT006	<i>This study</i>	<i>B. physalus physalus</i>	North Atlantic	eastern North American sea border	female	194053259	98.75	23.69	9.221873	97.7672	11.68
NAT007	<i>This study</i>	<i>B. physalus physalus</i>	North Atlantic	eastern North American sea border	female	221265807	98.67	8.53	11.160656	97.9063	13.76
NAT008	<i>This study</i>	<i>B. physalus physalus</i>	North Atlantic	eastern North American sea border	male	444423012	98.54	14.25	8.062452	98.2556	16.6124
NAT009	<i>This study</i>	<i>B. physalus physalus</i>	North Atlantic	Iceland	female	186952047	99.07	28.44	7.118317	97.8244	11.1176
ENP001	<i>This study</i>	<i>B. physalus velifera</i>	North Pacific	North Pacific	female	320235236	98.5	9.63	7.233823	98.1029	11.6001
ENP002	<i>This study</i>	<i>B. physalus velifera</i>	North Pacific	North Pacific	female	315992044	98.44	9.45	7.051071	98.1412	11.4724
ENP003	<i>This study</i>	<i>B. physalus velifera</i>	North Pacific	North Pacific	female	321578960	98.42	9.45	7.21088	98.1369	11.6719
ENP004	<i>This study</i>	<i>B. physalus velifera</i>	North Pacific	North Pacific	male	331918644	98.26	10.67	7.467253	98.1653	12.2389
ENP005	<i>This study</i>	<i>B. physalus velifera</i>	North Pacific	North Pacific	male	307955476	98.43	12.15	7.20787	98.1014	11.3969
ENP006	<i>This study</i>	<i>B. physalus velifera</i>	North Pacific	North Pacific	female	372343430	98.37	10.76	7.815663	98.2244	13.1685

GOC001	<i>This study</i>	<i>B. physalus velifera</i>	North Pacific	Gulf of California	female	418000350	98.44	13.23	8.136104	98.2187	15.3565
GOC002	<i>This study</i>	<i>B. physalus velifera</i>	North Pacific	Gulf of California	male	387290480	98.58	12.91	7.909096	98.1848	14.6326
GOC003	<i>This study</i>	<i>B. physalus velifera</i>	North Pacific	Gulf of California	female	443442860	98.62	14.48	8.314592	98.2716	16.1577
GOC004	<i>This study</i>	<i>B. physalus velifera</i>	North Pacific	Gulf of California	male	341795768	98.52	11.9	7.416384	98.168	13.0286
GOC005	<i>This study</i>	<i>B. physalus velifera</i>	North Pacific	Gulf of California	female	389612504	98.56	12.13	7.84734	98.2173	14.5803
GOC006	<i>This study</i>	<i>B. physalus velifera</i>	North Pacific	Gulf of California	female	352647834	98.58	13.65	7.421539	98.1607	12.9628
SRR1498 6187	<i>(Wolf et al., 2022)</i>	<i>B. physalus physalus</i>	North Atlantic	Iceland	male	230446491	98.03	22.72	10.892353	98.0431	14.0717
SRR1501 3014	<i>(Wolf et al., 2022)</i>	<i>B. physalus physalus</i>	North Atlantic	Iceland	female	203304828	98.28	20.72	9.552075	97.9934	12.192
SRR1504 2059	<i>(Wolf et al., 2022)</i>	<i>B. physalus physalus</i>	North Atlantic	Iceland	male	195360322	98.04	19.18	9.245023	97.9738	11.9643
SRR1504 2061	<i>(Wolf et al., 2022)</i>	<i>B. physalus physalus</i>	North Atlantic	Iceland	female	186283152	98.4	20.14	8.795315	97.9301	11.2643
SRR1504 2062	<i>(Wolf et al., 2022)</i>	<i>B. physalus physalus</i>	North Atlantic	Iceland	male	211546602	98.13	20.47	9.978597	97.9955	12.9412
SRR1504 2063	<i>(Wolf et al., 2022)</i>	<i>B. physalus physalus</i>	North Atlantic	Iceland	female	206010219	98.36	21.61	9.73968	97.9881	12.3997
SRR1504 8183	<i>(Wolf et al., 2022)</i>	<i>B. physalus physalus</i>	North Atlantic	Iceland	male	226863947	98.2	21.38	10.724377	98.0474	13.9123
SRR1508 2441	<i>(Wolf et al., 2022)</i>	<i>B. physalus physalus</i>	North Atlantic	Iceland	male	227755671	98.14	21.04	10.741208	98.0335	13.9342
SRR9352 01	<i>(Yim et al., 2014)</i>	<i>B. physalus physalus</i>	North Pacific	-	female	481695932	98.57	22.68	11.378417	98.0018	14.8213

MNG01	<i>This study</i>	<i>Megaptera novaeangliae</i>	Outgroup	-	male	336620542	98.44	7.59	7.776657	98.221	14.3702
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Table S2. Whole mitochondrial genome alignment metrics for samples generated in this study.

Sample	Number of reads aligned mitochondria	Mitochondrial genome coverage	% of mitochondrial genome coverage	Mitochondrial genome mean depth
ANT001	76035	16321	99.5001	447.827
ANT002	130568	16336	99.5915	767.685
ANT003	123988	16331	99.5611	728.375
ANT004	110662	16336	99.5915	651.624
ANT005	103426	16338	99.6037	609.247
ANT006	97792	16332	99.5672	576.236
ANT007	112277	16321	99.5001	659.662
NAT001	130575	16278	99.2379	769.203
NAT002	108344	16331	99.5611	638.907
NAT003	133614	16331	99.5611	787.748
NAT004	160751	16332	99.5672	946.986
NAT005	130882	16331	99.5611	770.88
NAT006	92966	16280	99.2501	822.635
NAT007	22997	16327	99.5367	203.593
NAT008	185102	16369	99.7927	1091.29
NAT009	103288	16321	99.5001	914.048
ENP001	177864	16347	99.6586	1047.37
ENP002	129434	16338	99.6037	762.186
ENP003	119138	16338	99.6037	701.301
ENP004	89506	16338	99.6037	528.49

ENP005	88215	16322	99.5062	519.918
ENP006	124212	16338	99.6037	731.793
GOC001	114693	16338	99.6037	673.95
GOC002	174185	16338	99.6037	1025.54
GOC003	179020	16338	99.6037	1054.74
GOC004	143075	16338	99.6037	841.75
GOC005	142710	16339	99.6098	839.423
GOC006	141715	16339	99.6098	833.227
SRR14986187	216076	16331	99.5611	1920.08
SRR15013014	244870	16331	99.5611	2185.13
SRR15042059	147936	16332	99.5672	1318.45
SRR15042061	204390	16331	99.5611	1823.66
SRR15042062	96951	16331	99.5611	858.432
SRR15042063	131275	16331	99.5611	1165.11
SRR15048183	96012	16322	99.5062	846.255
SRR15082441	237075	16331	99.5611	2106.27
SRR935201	100194	16342	99.6281	585.27
MNG01	136174	16327	99.5367	806.001

References

- Wolf, M., de Jong, M., Halldórsson, S. D., Árnason, Ú., & Janke, A. (2022). Genomic Impact of Whaling in North Atlantic Fin Whales. *Molecular Biology and Evolution*, 39(5), msac094. <https://doi.org/10.1093/molbev/msac094>
- Yim, H.-S., Cho, Y. S., Guang, X., Kang, S. G., Jeong, J.-Y., Cha, S.-S., Oh, H.-M., Lee, J.-H., Yang, E. C., Kwon, K. K., Kim, Y. J., Kim, T. W., Kim, W., Jeon, J. H., Kim, S.-J., Choi, D. H., Jho, S., Kim, H.-M., Ko, J., ... Lee, J.-H. (2014). Minke whale genome and aquatic adaptation in cetaceans. *Nature Genetics*, 46(1), 88–92. <https://doi.org/10.1038/ng.2835>