

Supplementary information

Supplementary table S1: Proportions of the most frequent five topologies based on window sizes. NA - not in the five most frequent for that window size. Whitesided - Pacific white-sided dolphin, Pilotwhale - long-finned pilot whale, IndoBottlenose - Indo-Pacific bottlenose dolphin, Bottlenose - bottlenose dolphin, Killerwhale - killer whale, Beluga - beluga, Narwhal - narwhal, Harbour - harbour porpoise, Finless - finless porpoise, Baiji - Baiji (outgroup).

50 kb	100 kb	500 kb	1 Mb	Topology
0.24	0.32	0.64	0.79	(((((Whitesided,(Pilotwhale,(IndoBottlenose,Bottlenose))),Killerwhale)),((Beluga,Narwhal),(Harbour,Finless))),Baiji);
0.14	0.14	0.09	0.05	(((((Pilotwhale,(IndoBottlenose,Bottlenose)),(Whitesided,Killerwhale)),((Beluga,Narwhal),(Harbour,Finless))),Baiji);
0.13	0.14	0.14	0.10	(((((Pilotwhale,(Whitesided,(IndoBottlenose,Bottlenose))),Killerwhale)),((Beluga,Narwhal),(Harbour,Finless))),Baiji);
0.09	0.08	0.04	0.02	(((((Pilotwhale,Whitesided),(IndoBottlenose,Bottlenose)),Killerwhale)),((Beluga,Narwhal),(Harbour,Finless))),Baiji);
0.08	NA	NA	NA	(((((Killerwhale,(Pilotwhale,(IndoBottlenose,Bottlenose))),Whitesided)),((Beluga,Narwhal),(Harbour,Finless))),Baiji);
NA	0.07	0.03	0.02	((((Whitesided,((Pilotwhale,(IndoBottlenose,Bottlenose))),Killerwhale)),((Beluga,Narwhal),(Harbour,Finless))),Baiji);
0.69	0.76	0.94	0.98	Top 5 topologies combined

Supplementary table S2: Proportions of the most frequent five topologies based on GC content and a window size of 50 kb. NA - not in the five most frequent for that window size. Whitesided - Pacific white-sided dolphin, Pilotwhale - long-finned pilot whale, IndoBottlenose - Indo-Pacific bottlenose dolphin, Bottlenose - bottlenose dolphin, Killerwhale - killer whale, Beluga - beluga, Narwhal - narwhal, Harbour - harbour porpoise, Finless - finless porpoise, Baiji - Baiji (outgroup).

Low GC	Medium GC	High GC	Topology
2814	3395	4227	((((Killerwhale,(Whitesided,((IndoBottlenose,Bottlenose),Pilotwhale))),((Beluga,Narwhal),(Harbour,Finless))),Baiji);
2023	2107	2085	(((((Pilotwhale,(IndoBottlenose,Bottlenose)),(Whitesided,Killerwhale)),((Beluga,Narwhal),(Harbour,Finless))),Baiji);
1740	1898	1976	(((((Pilotwhale,(Whitesided,(IndoBottlenose,Bottlenose))),Killerwhale)),((Beluga,Narwhal),(Harbour,Finless))),Baiji);
1287	1289	1317	(((((Pilotwhale,Whitesided),(IndoBottlenose,Bottlenose)),Killerwhale)),((Beluga,Narwhal),(Harbour,Finless))),Baiji);
1152	NA	NA	(((((Whitesided,(IndoBottlenose,Bottlenose)),(Pilotwhale,Killerwhale)),((Beluga,Narwhal),(Harbour,Finless))),Baiji);
NA	1190	1149	((((Whitesided,((Pilotwhale,(IndoBottlenose,Bottlenose))),Killerwhale)),((Beluga,Narwhal),(Harbour,Finless))),Baiji);

Supplementary table S3: QuIBL results when using every twentieth tree from the 50 kb sliding window analysis - attached as spreadsheet.

Supplementary table S4: QuIBL results from trees constructed using 20 kb windows with a 1 Mb slide - attached as spreadsheet.

Supplementary table S5: D-statistics results for all triplet combinations phylogenetically concurrent with our results shown in Figure 1. Baiji was used as the outgroup/ancestral sequence. A non-significant result ($|Z| < 3$) is indicated in bold. Colours indicate the family of the given individual. Red = Delphinidae, yellow = Phocoenidae, blue = Monodontidae.

H1	H2	H3	nABBA	nBABA	D-score	Z-score
Bottlenose	IndoBottlenose	Killer whale	597,251	554,780	0.037	23.26
Bottlenose	IndoBottlenose	Pilotwhale	748,948	691,844	0.040	24.13
Bottlenose	IndoBottlenose	Whitesided	721,498	665,420	0.040	25.20
Pilotwhale	Whitesided	Killer whale	2,224,888	2,119,068	0.024	11.77
Pilotwhale	Bottlenose	Killer whale	1,998,297	1,795,444	0.053	26.15
Pilotwhale	IndoBottlenose	Killer whale	2,004,478	1,757,429	0.066	31.95
Pilotwhale	Bottlenose	Whitesided	2,490,189	2,051,579	0.097	42.67
Pilotwhale	IndoBottlenose	Whitesided	2,508,755	2,007,966	0.111	48.64
Whitesided	Bottlenose	Killer whale	2,111,742	2,014,525	0.024	11.88
Whitesided	IndoBottlenose	Killer whale	2,117,925	1,975,800	0.035	17.25
Killer whale	Pilotwhale	Finless	928,942	840,273	0.050	51.99
Killer whale	Whitesided	Finless	924,323	829,525	0.054	56.12
Killer whale	Pilotwhale	Harbour porpoise	959,748	851,885	0.060	60.74
Killer whale	Whitesided	Harbour porpoise	956,686	840,318	0.065	65.46
Killer whale	Bottlenose	Finless	942,684	757,495	0.109	107.12
Killer whale	Bottlenose	Harbour porpoise	974,032	767,636	0.119	116.98
Killer whale	IndoBottlenose	Finless	943,526	728,185	0.129	120.99
Killer whale	IndoBottlenose	Harbour porpoise	974,967	739,024	0.138	130.60
Pilotwhale	Whitesided	Finless	861,276	855,083	0.004	4.41
Pilotwhale	Whitesided	Harbour porpoise	892,930	884,620	0.005	5.64
Pilotwhale	Bottlenose	Finless	828,193	724,397	0.067	73.75
Pilotwhale	Bottlenose	Harbour porpoise	857,823	749,827	0.067	76.38
Pilotwhale	IndoBottlenose	Finless	829,393	692,413	0.090	97.23
Pilotwhale	IndoBottlenose	Harbour porpoise	859,146	718,044	0.089	98.69

Whitesided	Bottlenose	Harbour porpoise	887,876	787,914	0.060	68.88
Whitesided	Bottlenose	Finless	857,483	760,224	0.060	69.75
Whitesided	IndoBottlenose	Harbour porpoise	888,872	755,955	0.081	92.25
Whitesided	IndoBottlenose	Finless	858,523	727,924	0.082	92.84
Bottlenose	IndoBottlenose	Narwhal	414,272	380,995	0.042	33.84
Bottlenose	IndoBottlenose	Beluga	434,366	396,566	0.045	37.67
Killer whale	Pilotwhale	Narwhal	955,756	837,598	0.066	61.58
Killer whale	Pilotwhale	Beluga	984,462	854,528	0.071	65.67
Killer whale	Whitesided	Narwhal	953,496	826,881	0.071	66.17
Killer whale	Whitesided	Beluga	982,162	844,661	0.075	67.95
Killer whale	Bottlenose	Narwhal	971,164	751,458	0.128	111.86
Killer whale	Bottlenose	Beluga	1,001,546	767,422	0.132	113.69
Killer whale	IndoBottlenose	Narwhal	974,507	722,249	0.149	126.51
Killer whale	IndoBottlenose	Beluga	1,007,582	736,424	0.155	128.87
Pilotwhale	Whitesided	Beluga	918,941	911,423	0.004	4.93
Pilotwhale	Whitesided	Narwhal	891,298	883,114	0.005	5.61
Pilotwhale	Bottlenose	Narwhal	859,652	743,735	0.072	78.60
Pilotwhale	Bottlenose	Beluga	887,196	766,562	0.073	81.55
Pilotwhale	IndoBottlenose	Narwhal	863,608	710,777	0.097	103.83
Pilotwhale	IndoBottlenose	Beluga	895,023	731,826	0.100	105.92
Whitesided	Bottlenose	Narwhal	888,390	780,573	0.065	74.77
Whitesided	Bottlenose	Beluga	917,400	804,237	0.066	76.44
Whitesided	IndoBottlenose	Narwhal	892,496	747,539	0.088	97.69
Whitesided	IndoBottlenose	Beluga	925,091	769,228	0.092	102.86
Finless	Harbour porpoise	Narwhal	452,411	450,657	0.002	1.59
Harbour porpoise	Finless	Beluga	570,767	552,830	0.016	13.47
Narwhal	Beluga	Harbour porpoise	532,605	502,660	0.029	25.72
Narwhal	Beluga	Finless	514,273	466,273	0.049	41.75
Finless	Narwhal	Killer whale	973,140	885,678	0.047	47.30
Finless	Narwhal	Bottlenose	1,077,206	966,370	0.054	55.93
Finless	Narwhal	IndoBottlenose	1,080,812	970,600	0.054	56.63
Finless	Narwhal	Pilotwhale	1,059,846	950,178	0.055	57.27
Finless	Beluga	Killer whale	989,901	875,364	0.061	57.51

Finless	Narwhal	Whitesided	1,062,632	951,040	0.055	57.94
Finless	Beluga	Bottlenose	1,103,352	951,967	0.074	68.54
Finless	Beluga	Pilotwhale	1,084,679	936,511	0.073	68.84
Finless	Beluga	IndoBottlenose	1,109,158	955,589	0.074	69.72
Finless	Beluga	Whitesided	1,087,277	938,148	0.074	69.88
Harbour porpoise	Narwhal	Killer whale	1,004,793	891,909	0.060	59.43
Harbour porpoise	Beluga	Killer whale	1,028,676	885,849	0.075	69.85
Harbour porpoise	Narwhal	Pilotwhale	1,124,641	974,232	0.072	75.43
Harbour porpoise	Narwhal	Bottlenose	1,145,470	990,640	0.072	75.66
Harbour porpoise	Narwhal	Whitesided	1,127,578	976,951	0.072	75.84
Harbour porpoise	Narwhal	IndoBottlenose	1,153,263	994,022	0.074	78.93
Harbour porpoise	Beluga	Pilotwhale	1,163,136	965,266	0.093	88.73
Harbour porpoise	Beluga	Whitesided	1,165,862	968,086	0.093	89.42
Harbour porpoise	Beluga	Bottlenose	1,185,612	981,030	0.094	89.66
Harbour porpoise	Beluga	IndoBottlenose	1,197,547	984,311	0.098	93.10

Supplementary table S6: 100kb non-overlapping sliding window D-foil results for all quadruplet combinations [[H1,H2][H3,H4]] phylogenetically concurrent with our results shown in figure 1. Baiji was used as the outgroup/ancestral sequence. - attached as a spreadsheet

Supplementary table S7: Mapping statistics of each Delphinoidea species used in this study when specifying the reference genome as the baiji assembly.

Common name	Raw read pairs	Mapped reads	Coverage	Bp-mapped
Beluga	466,374,135	476,814,543	31.44	69,807,010,359
Bottlenose dolphin	578,690,171	732,418,659	47.61	105,524,983,813
Harbour porpoise	289,063,910	418,431,029	23.17	50,830,083,145
Indo-Pacific bottlenose dolphin	466,306,082	551,837,703	35.62	78,749,625,267
Indo-Pacific finless porpoise	523,612,238	557,766,873	24.96	54,450,935,944
Killer whale	1,467,089,287	1,047,260,000	39.53	88,692,400,000
Long-finned pilot whale	428,064,233	504,482,080	28.61	63,276,638,573
Narwhal	384,563,392	468,429,237	31.09	68,247,058,370
Pacific white-sided dolphin	453,348,710	499,704,592	28.83	63,800,396,300

Supplementary table S8: Mapping statistics of each Delphinoidea species used in this study when specifying the reference genome as a conspecific assembly.

Common name	Raw read pairs	Mapped reads	Coverage	Bp-mapped
Beluga	466,374,135	531,535,936	34.47	79,218,898,913
Bottlenose dolphin	578,690,171	779,210,277	54.03	114,530,169,747
Harbour porpoise	289,063,910	431,762,883	23.74	52,067,455,809
Indo-Pacific bottlenose dolphin	466,306,082	587,440,922	37.88	85,032,333,848
Indo-Pacific finless porpoise	523,612,238	620,580,505	27.33	61,286,732,910
Killer whale	1,467,089,287	1,213,221,913	44.93	100,903,316,971
Long-finned pilot whale	428,064,233	598,612,204	32.79	75,639,560,432
Narwhal	384,563,392	529,082,769	33.85	78,238,763,386
Pacific white-sided dolphin	453,348,710	592,814,373	33.02	76,299,243,217

Supplementary table S9: Genome-wide pairwise distance matrix of the nine Delphinoidea included in this study. Bottlenose = bottlenose dolphin, Finless = finless porpoise, Harbour = harbour porpoise, Indobottle = Indo-Pacific bottlenose dolphin, Killer = killer whale, Pilot = pilot whale, White = Pacific white-sided dolphin.

Beluga	0.0000	0.0211	0.0151	0.0153	0.0211	0.0205	0.0056	0.0210	0.0209
Bottlenose	0.0211	0.0000	0.0230	0.0231	0.0040	0.0113	0.0210	0.0102	0.0107
Finless	0.0151	0.0230	0.0000	0.0056	0.0230	0.0224	0.0151	0.0229	0.0228
Harbour	0.0153	0.0231	0.0056	0.0000	0.0231	0.0225	0.0152	0.0231	0.0230
Indobottle	0.0211	0.0040	0.0230	0.0231	0.0000	0.0113	0.0210	0.0102	0.0107
Killer	0.0205	0.0113	0.0224	0.0225	0.0113	0.0000	0.0204	0.0113	0.0112
Narwhal	0.0056	0.0210	0.0151	0.0152	0.0210	0.0204	0.0000	0.0209	0.0208
Pilot	0.0210	0.0102	0.0229	0.0231	0.0102	0.0113	0.0209	0.0000	0.0109
White	0.0209	0.0107	0.0228	0.0230	0.0107	0.0112	0.0208	0.0109	0.0000

Supplementary table S10: Metrics used to calculate the mutation rate per year with the equation mutation rate = divergence time / 2x genetic distance. Mean divergences were taken from the full dataset 10-partition AR from McGowen et al 2020 (McGowen et al., 2020) and average genetic distances were calculated from the results shown in supplementary table S5.

Species	Closest relative	Divergence (Ma)	Distance	Mutation rate per year
Beluga	Narwhal	7.72	0.0056	3.63×10^{-10}
Killer whale	Delphinidae	10.16	0.0113	5.56×10^{-10}
Bottlenose dolphin	Indo-Pacific bottlenose dolphin	2.69	0.0040	7.51×10^{-10}
Harbour porpoise	Finless porpoise	5.36	0.0056	5.25×10^{-10}
Long-finned pilot whale	<i>Tursiops</i> spp.	7.46	0.0102	6.83×10^{-10}
Pacific white-sided dolphin	<i>Tursiops</i> + <i>Globicephala</i>	9.48	0.0108	5.69×10^{-10}

Supplementary table S11: Generation times, generational mutation rates and references for the generation times for each of the nine Delphinoidea species used in this study.

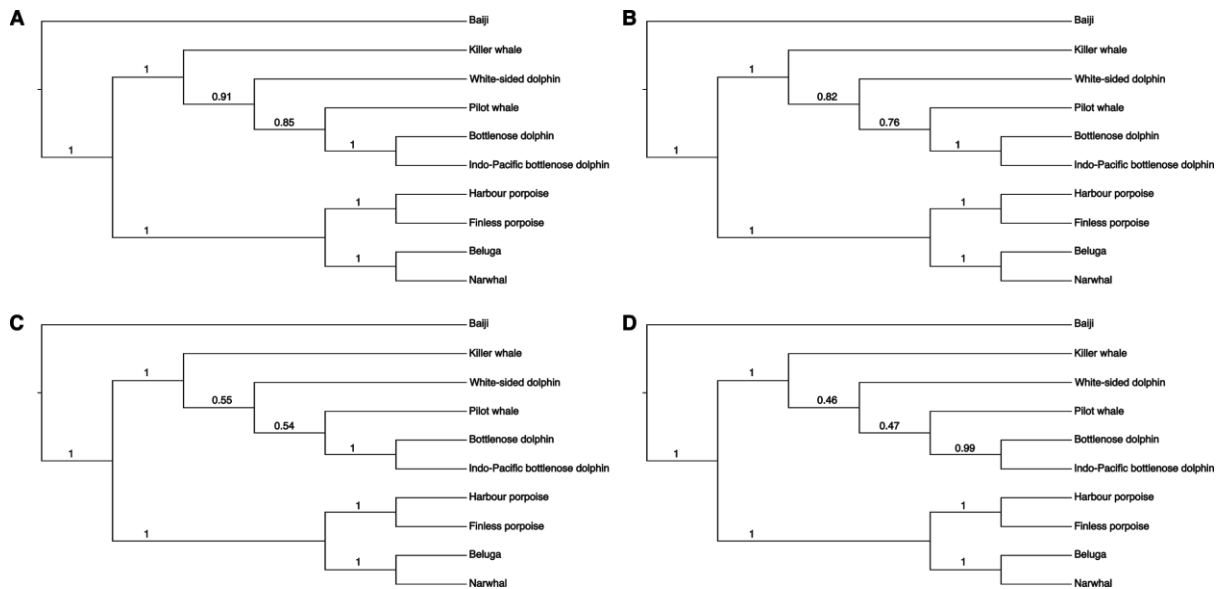
Common name	Generation time	Generational mutation rate	Generation time reference	Bp-mapped
Beluga	32	1.16×10^{-8}	(Garde et al., 2015)	79,218,898,913
Bottlenose dolphin	21	1.58×10^{-8}	(Taylor et al., 2007)	114,530,169,747
Harbour porpoise	10	5.25×10^{-9}	(Birkun and Frantzis, 2008)	52,067,455,809
Indo-Pacific bottlenose dolphin	21	1.58×10^{-8}	(Taylor et al., 2007)	85,032,333,848
Indo-Pacific finless porpoise	8	4.20×10^{-9}	(Zhou et al., 2018)	61,286,732,910
Killer whale	26	1.43×10^{-8}	(Foote et al., 2016)	100,903,316,971
Long-finned pilot whale	24	1.64×10^{-8}	(Taylor et al., 2007)	75,639,560,432
Narwhal	30	1.09×10^{-8}	(Garde et al., 2015)	78,238,763,386
Pacific white-sided dolphin	21	1.21×10^{-8}	(Taylor et al., 2007)	76,299,243,217

Supplementary table S12: The pre-divergence N_e , divergence time intervals, and the increments specified for each of the species pair used for the simulations to compare against the hPSMC results.

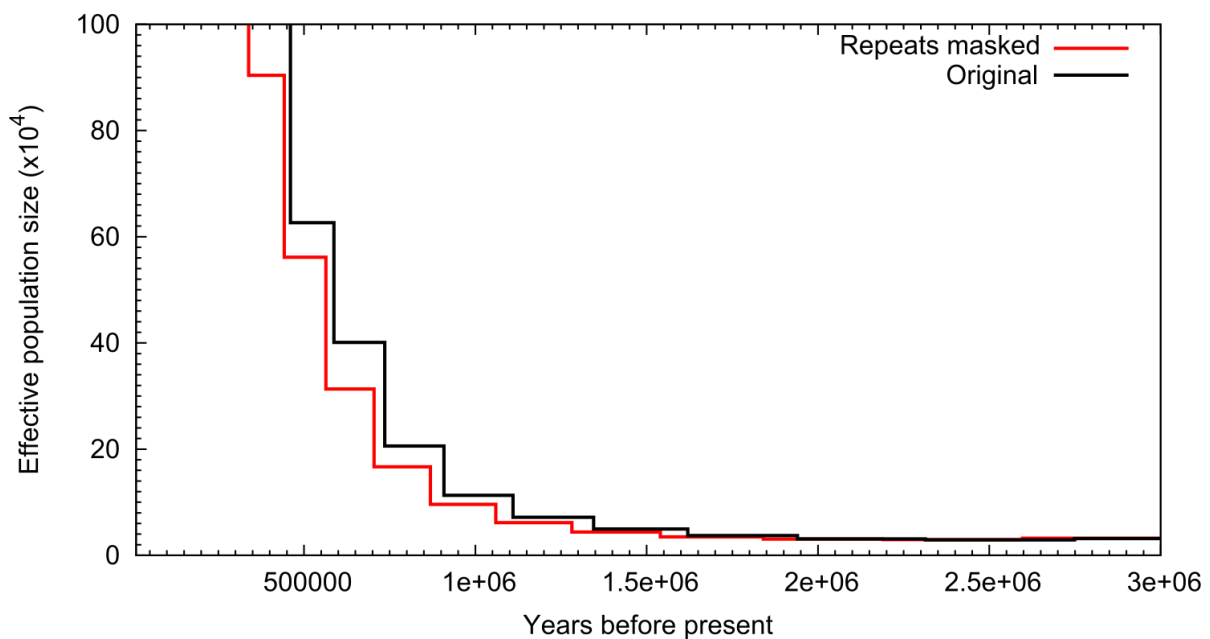
Species pair	Pre-divergence N_e	Range (Ma)	Increments (years)
Beluga whale + Narwhal	30,000	1-2	100,000
Beluga whale + Finless porpoise	60,000	3-7	200,000
Beluga whale + Harbour porpoise	60,000	3-7	200,000
Narwhal + Finless porpoise	60,000	3-7	200,000
Narwhal + Harbour porpoise	60,000	3-7	200,000
Beluga whale + Bottlenose dolphin	105,000	3.9-8.5	200,000
Beluga whale + Indo-Pacific bottlenose dolphin	105,000	3.9-8.5	200,000
Narwhal + Bottlenose dolphin	105,000	3.9-8.5	200,000
Narwhal + Indo-Pacific bottlenose dolphin	105,000	3.9-8.5	200,000
Narwhal + Killer whale	105,000	3.9-8.5	200,000
Narwhal + Long-finned pilot whale	105,000	3.9-8.5	200,000
Narwhal + Pacific white-sided dolphin	105,000	3.9-8.5	200,000
Beluga whale + Killer whale	105,000	3.9-8.5	200,000
Beluga whale + Long-finned pilot whale	105,000	3.9-8.5	200,000
Beluga whale + Pacific white-sided dolphin	105,000	3.9-8.5	200,000
Harbour porpoise + Bottlenose dolphin	105,000	3.9-8.5	200,000
Harbour porpoise + Indo-Pacific bottlenose dolphin	105,000	3.9-8.5	200,000
Finless porpoise + Bottlenose dolphin	105,000	3.9-8.5	200,000
Finless porpoise + Indo-Pacific bottlenose dolphin	105,000	3.9-8.5	200,000
Finless porpoise + Killer whale	105,000	3.9-8.5	200,000
Finless porpoise + Long-finned pilot whale	105,000	3.9-8.5	200,000
Finless porpoise + Pacific white-sided dolphin	105,000	3.9-8.5	200,000
Harbour porpoise + Killer whale	105,000	3.9-8.5	200,000

Harbour porpoise + Long-finned pilot whale	105,000	3.9-8.5	200,000
Harbour porpoise + Pacific white-sided dolphin	105,000	3.9-8.5	200,000
Harbour porpoise + Finless porpoise	40,000	0.3-1.4	100,000
Indo-Pacific Bottlenose dolphin + Bottlenose dolphin	20,000	0.2-1.2	100,000
Indo-Pacific bottlenose dolphin + Killer whale	50,000	0.9-2.1 & 3.4-7	200,000
Indo-Pacific bottlenose dolphin + Long-finned pilot whale	50,000	0.9-2.1 & 3.4-7	200,000
Indo-Pacific bottlenose dolphin + Pacific white-sided dolphin	50,000	0.9-2.1 & 3.4-7	200,000
Bottlenose dolphin + Killer whale	50,000	0.9-2.1 & 3.4-7	200,000
Bottlenose dolphin + Long-finned pilot whale	50,000	0.9-2.1 & 3.4-7	200,000
Bottlenose dolphin + Pacific white-sided dolphin	50,000	0.9-2.1 & 3.4-7	200,000
Long-finned pilot whale + Killer whale	60,000	0.9-2.1 & 3.4-7	200,000
Pacific white-sided dolphin + Killer whale	50,000	0.9-2.1 & 3.4-7	200,000
Pacific white-sided dolphin + Long-finned pilot whale	50,000	0.9-2.1 & 3.4-7	200,000

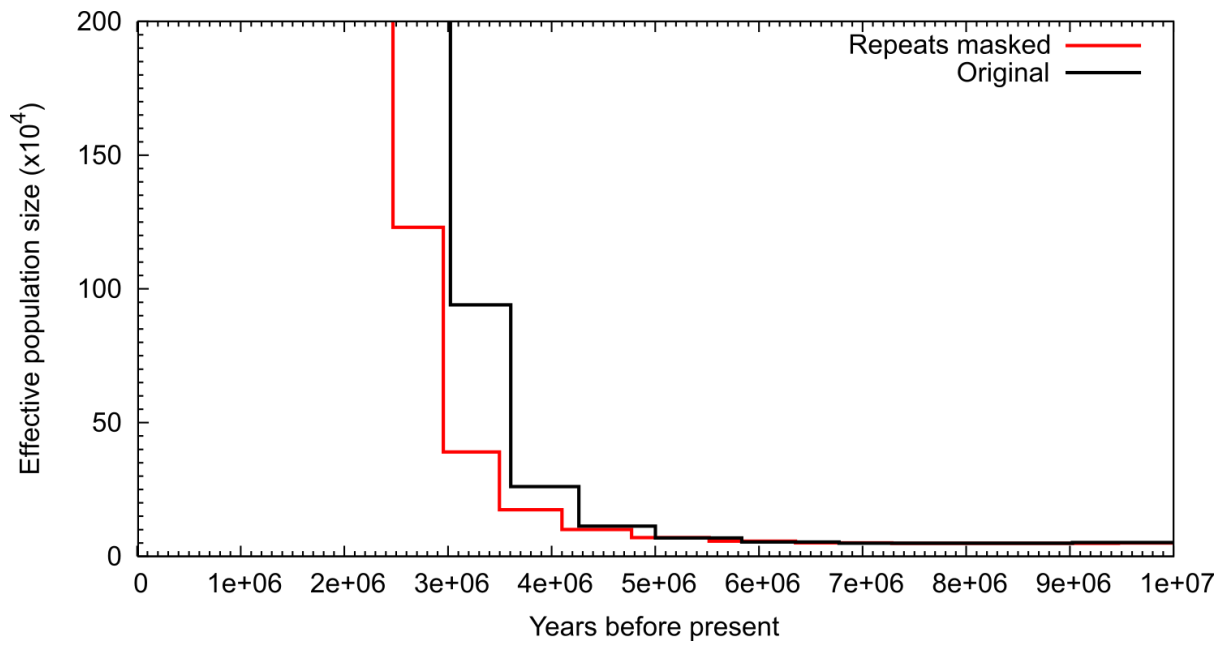
Supplementary figures



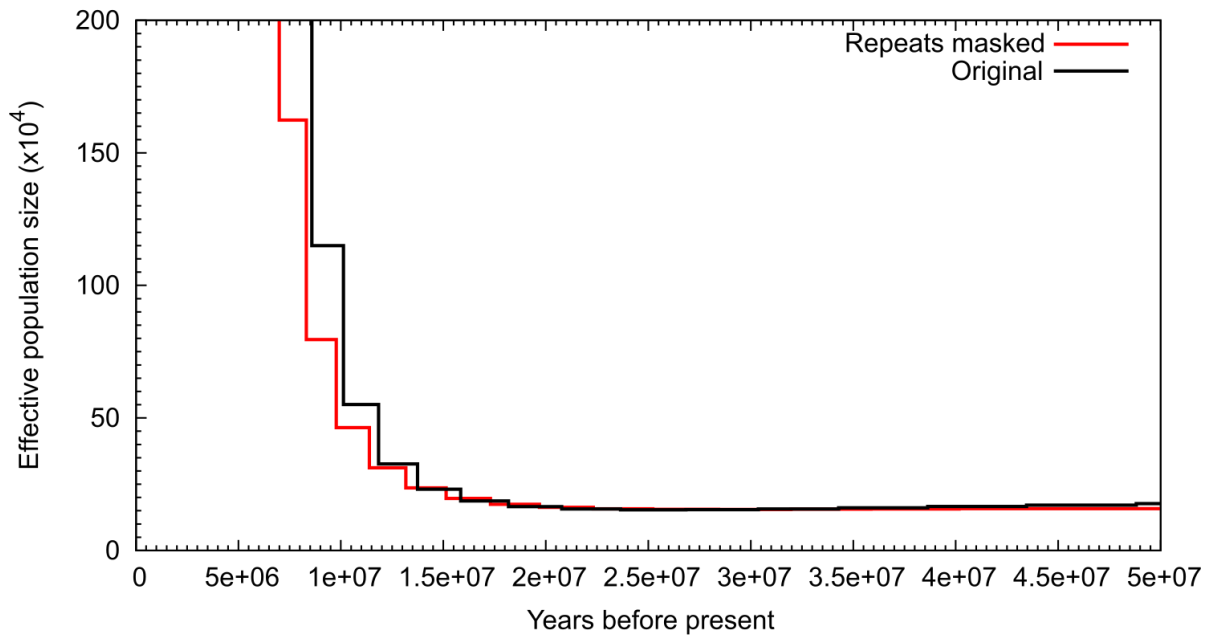
Supplementary figure S1: Consensus trees of independent Maximum-Likelihood trees constructed from non-overlapping sliding windows of (A) 1 Mb, (B) 500 kb, (C) 100 kb, or (D) 50 kb in length. Branch numbers represent the number of independent trees supporting each node.



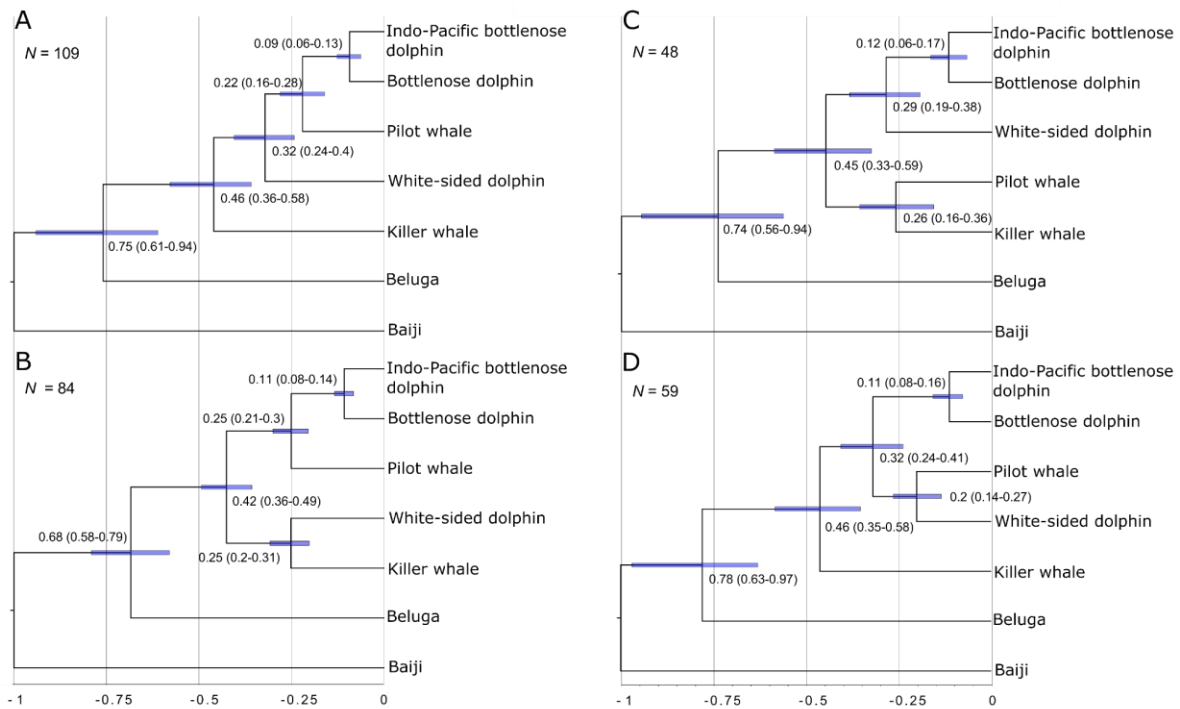
Supplementary figure S2: Comparison of hPSMC results using a pseudodiploid sequence from the bottlenose and Indo-Pacific bottlenose dolphins (shallow divergence) with either repeat regions masked or not.



Supplementary figure S3: Comparison of hPSMC results using a pseudodiploid sequence from the beluga and narwhal (medium divergence) with either repeat regions masked or not.



Supplementary figure S4: Comparison of hPSMC results using a pseudodiploid sequence from the bottlenose dolphin and beluga (deep divergence) with either repeat regions masked or not.



Supplementary figure S5: Relative divergence times of alternative topologies assumed to arise due to incomplete lineage sorting (ILS) or gene flow. N represents the number of independent loci supporting said topology. A) Consensus species topology. B) ILS/gene flow between the killer whale and Pacific white-sided dolphin. C) ILS/gene flow between killer whale and long-finned pilot whale. D) ILS/gene flow between Pacific white-sided dolphin and the long-finned pilot whale. Blue bars and numbers in parentheses show 95% credibility intervals.

Supplementary results

Additional plots of the hPSMC empirical and simulated data can be found under the following link: https://sid.erda.dk/cgi-sid/lis.py?share_id=ewvczfS2hH on the University of Copenhagen's electronic research data archive (ERDA). Bold lines show the hPSMC empirical data, faded lines show the simulated data, and the black lines show the simulated data that most closely match the empirical data without overlapping it between 1.5x and 10x the pre-divergence N_e .

Supplementary references

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