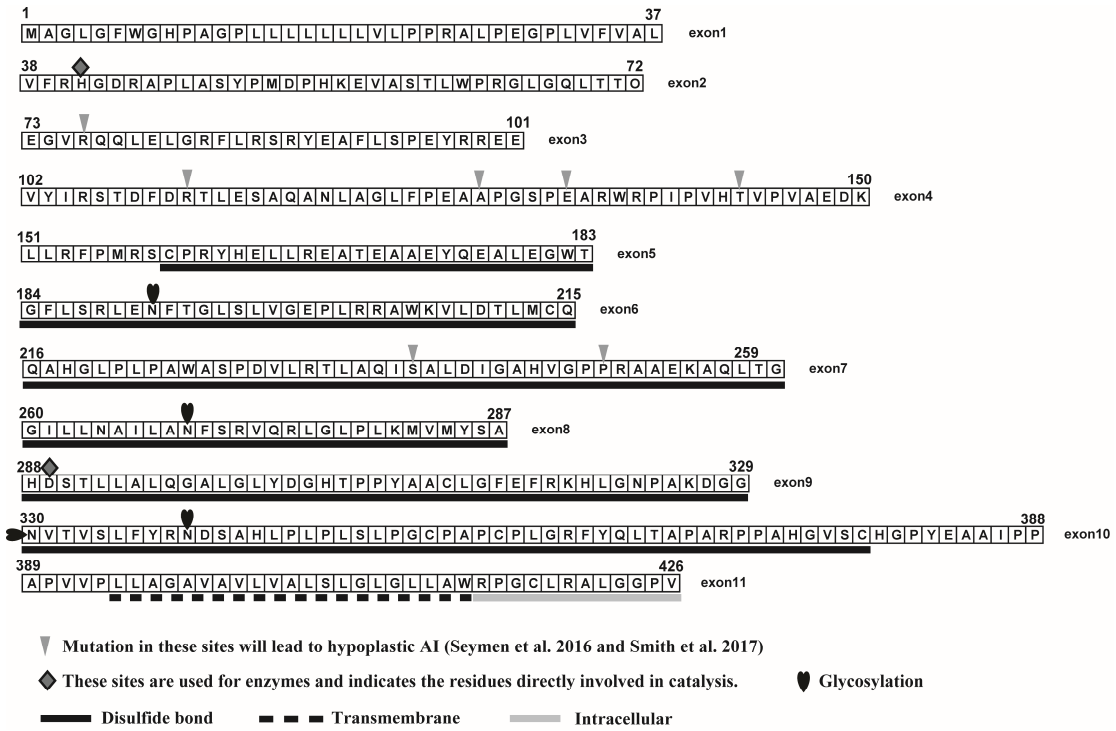


Appendix Figure 1 The tree topology of ACPT used to conduct the selective pressure analysis in PAML. The phylogeny is based on OrthoMaM (from: [http://orthomam2.mbb.univ-montp2.fr/OrthoMaM\\_v10b10/](http://orthomam2.mbb.univ-montp2.fr/OrthoMaM_v10b10/)) and some previous researches (Celine et al. 2019; Waddell et al. 2001; Sergey et al. 2007; Zhou et al. 2012; Gatesy et al. 2013; Kuntner et al. 2011)





Appendix Figure 3 The information of mutation sites in ACPT protein sequence about amelogenesis imperfecta.

Appendix Table 1 Mammalian species used in this study and the sources of sequences.

Species	ACPT	Species	ACPT	Species	ACPT
<i>Acinonyx_jubatus</i>	XM_027037126.1	<i>Felis_catus</i>	ENSFCAG0000001872 7	<i>Oryctolagus_cuniculus</i>	XM_017340604.1
<i>Ailuropoda_melanoleuca</i>	ENSAMEG000000128 61	<i>Fukomys_damarensis</i>	ENSFDAG0000001487 4	<i>Otolemur_garnettii</i>	XM_003801446.2
<i>Aotus_nancymaae</i>	ENSANAG000000322 61	<i>Galeopterus_variegatus</i>	103608037	<i>Ovis_aries</i>	ENSOARG000000141 52
<i>Balaenoptera_acutorostrata</i>	XM_007179955.1	<i>Gorilla_gorilla</i>	—	<i>Pan_paniscus</i>	ENSPAG0000001092 7
<i>Balaena_mysticetus</i>	bmy_14018	<i>Heterocephalus_glaber</i>	ENSHGLG0000000494 9	<i>Pan_troglodytes</i>	ENSPTRG0000001135 2
<i>Bison_bison</i>	104995692	<i>Hipposideros_armiger</i>	109390983	<i>Panthera_pardus</i>	109252997
<i>Bos_taurus</i>	ENSBTAG0000001511 5	<i>Homo_sapiens</i>	ENSG00000142513	<i>Pantholops_hodgsonii</i>	XM_005955418.1
<i>Bos_indicus</i>	109571909	<i>Ictidomys_tridecemlineatus</i>	ENSSTOG00000010097	<i>Papio_anubis</i>	ENSPANG0000001066 5
<i>Bos_mutus</i>	102283597	<i>Jaculus_jaculus</i>	ENSJJAG00000014058	<i>Peromyscus_maniculatus</i>	ENSPEMG000000089 09
<i>Bubalus_bubalis</i>	102407119	<i>Lagenorhynchus_obliquidentis</i>	—	<i>Phascolarctos_cinereus</i>	110197749
<i>Callithrix_jacchus</i>	ENSCJAG0000001668 4	<i>Leptonychotes_weddellii</i>	102742150	<i>Phocoena_phocoena</i>	—
<i>Canis_familiaris</i>	ENSCAFG0000000292 0	<i>Lipotes_vexillifer</i>	XM_007463413.1	<i>Physeter_catodon</i>	102977978

<i>Cavia_aperea</i>	ENSCAPG0000000161 1	<i>Loxodonta_africana</i>	XM_003406840.2	<i>Ptilocolobus_tephrosceles</i>	111519955
<i>Cavia_porcellus</i>	ENSCPOG0000002680 6	<i>Macaca_fascicularis</i>	ENSMFAG0000000365 3	<i>Pongo_abelii</i>	ENSPPYG0000001029 4
<i>Camelus_bactrianus</i>	105062672	<i>Macaca_mulatta</i>	ENSMMUG000000035 83	<i>Procapra_capensis</i>	ENSPCAG0000000363 2
<i>Camelus_dromedarius</i>	105100227	<i>Macaca_nemestrina</i>	ENSMNEG0000003724 5	<i>Propithecus_coquereli</i>	ENSPCOG0000002491 1
<i>Camelus_ferus</i>	102516486	<i>Mandrillus_leucophaeus</i>	ENSMLEG0000001943 1	<i>Pteropus_alecto</i>	102898726
<i>Capra_hircus</i>	102191826	<i>Marmota_marmota</i>	107151208	<i>Pteropus_vampyrus</i>	ENSPVAG0000000343 2
<i>Castor_canadensis</i>	109683865	<i>Meriones_unguiculatus</i>	110541101	<i>Rattus_norvegicus</i>	ENSRNOG000000216 59
<i>Ceratotherium_simum</i>	101393590	<i>Mesocricetus_auratus</i>	ENSMAUG0000001689 5	<i>Rhinopithecus_bieti</i>	ENSRBIG0000002732 9
<i>Cebus_capucinus</i>	ENSCCAG0000003780 2	<i>Miniopterus_natalensis</i>	107531832	<i>Rhinopithecus_roxellana</i>	ENSRROG000000295 16
<i>Cercocebus_atys</i>	ENSCATG0000003216 6	<i>Microcebus_murinus</i>	ENSMICG0000000521	<i>Rhinolophus_sinicus</i>	109452514
<i>Chrysochloris_asiatica</i>	XM_006868138.1	<i>Microtus_ochrogaster</i>	ENSMOCG0000002266 8	<i>Rousettus_aegyptiacus</i>	107500452
<i>Chinchilla_lanigera</i>	ENSCLAG0000000602 3	<i>Mus_caroli</i>	XM_021167373.1	<i>Saimiri_boliviensis</i>	ENSSBOG0000002670 1
<i>Chlorocebus_sabaeus</i>	ENSCSAG0000000207 5	<i>Mus_musculus</i>	ENSMUSG0000001277 7	<i>Sorex_araneus</i>	XM_004619766.1

<i>Choloepus_hoffmanni</i>	—	<i>Mus_pahari</i>	XM_021222251.1	<i>Sus_scrofa</i>	ENSSSCG0000002473 6
<i>Colobus_angolensis</i>	ENSCANG0000002539 4	<i>Mustela_putorius</i>	ENSMPUG0000000161 0	<i>Trichechus_manatus</i>	101344314
<i>Condylura_cristata</i>	XM_004694037.1	<i>Myotis_brandtii</i>	102249381	<i>Tupaia_chinensis</i>	102500938
<i>Cricetulus_griseus</i>	ENSCGRG0000100368 7	<i>Myotis_davidii</i>	102769794	<i>Tursiops_truncatus</i>	ENSTTRG0000001104 7
<i>Dasypus_novemcinctus</i>	XM_023585546.1	<i>Myotis_lucifugus</i>	—	<i>Ursus_maritimus</i>	103657347
<i>Delphinapterus_leucas</i>	111180510	<i>Nannopalax_galili</i>	ENSNGAG0000002091 5	<i>Vicugna_pacos</i>	ENSVPAG0000000970 8
<i>Dipodomys_ordii</i>	ENSDORG0000001363 2	<i>Neomonachus_schauinslandi</i>	110572992	<i>Orycteropus_afer</i>	XM_007957636.1
<i>Echinops_telfairi</i>	XM_004710452.1	<i>Neophocaena_asiaeorientalis</i>	XM_024768516.1	<i>Equus_caballus</i>	XM_001917445.3
<i>Elephantulus_edwardii</i>	102863577	<i>Nomascus_leucogenys</i>	ENSNLEG0000000574 7	<i>Erinaceus_europaeus</i>	XM_007531289.1
<i>Enhydra_lutris</i>	111160580	<i>Notamacropus_eugenii</i>	ENSMEUG0000000852 4	<i>Eschrichtius_robustus</i>	Gonem-blast
<i>Eptesicus_fuscus</i>	103297603	<i>Ochotona_princeps</i>	ENSOPRG0000000735 1	<i>Odocoileus_virginianus</i>	110135451
<i>Equus_asinus</i>	106845328	<i>Octodon_degus</i>	ENSODEG0000001584 9	<i>Orcinus_orca</i>	101283727
<i>Equus_przewalskii</i>	103540878	<i>Odobenus_rosmarus</i>	101374821		

Appendix Table 2 The genome information of cetacean species used in this study.

Species	Version	Coverage	Genebank Assembly Accession	Assembly method	Sequencing technology
<i>Balaena mysticetus</i>	Database Statistics (v1.0)	~150x	Source: The Bowhead Whale Genome Resource ( <a href="http://www.bowhead-whale.org/">http://www.bowhead-whale.org/</a> )	ALLPATHS-LG	Illumina HiSeq
<i>Balaenoptera bonaerensis</i>	ASM97880v1	60x	GCA_000978805.1	PLATANUS v. 1.2.1	Illumina HiSeq2000
<i>Balaenoptera acutorostrata</i>	BalAcu1.0	92x	GCA_000493695.1	SOAPdenovo v. 16-Mar-2012	Illumina HiSeq 2000
<i>Eschrichtius robustus</i>	EscRob_v1_BIU U	40.5x	GCA_004363415.1	DISCOVAR de novo v. discovardenovo-52488	Illumina HiSeq
<i>Kogia breviceps</i>	KogBre_v1_BIU U	38.8x	GCA_004363705.1	DISCOVAR de novo v. discovardenovo-52488	Illumina HiSeq
<i>Megaptera novaeangliae</i>	megNov1	102.0x	GCA_004329385.1	Meraculous + HiRise v. Feb-2016	Illumina HiSeq

Appendix Table 3 The SRA information of 4 baleen whales species used in this study.

Species	Accession	Library name	Sample	Size	Relative information
<i>Balaenoptera musculus</i>	SRX2901261	Bmu_8065(Bmus_1)	cell culture	45.3Gb	1 ILLUMINA (Illumina HiSeq 2000) run: 559.5M spots, 113G bases, 45.3Gb downloads
<i>Balaenoptera borealis</i>	SRX2901260	Bbo_E91(Bbor_1)	cell culture	20.9Gb	1 ILLUMINA (Illumina HiSeq 2500) run: 185.8M spots, 33.5G bases, 20.9Gb downloads
	SRX2901259	Bbo_D27(Bbor_2)	cell culture	20.5Gb	1 ILLUMINA (Illumina HiSeq 2500) run: 184.5M spots, 33.2G bases, 20.5Gb downloads
<i>Eubalaena glacialis</i>	SRX2901265	Egl_F68(Egla_1)	cell culture	20.7Gb	1 ILLUMINA (Illumina HiSeq 2500) run: 186M spots, 33.5G bases, 20.7Gb downloads
<i>Balaenoptera physalus</i>	SRX2901262	Bph_4966_PE300_1	cell culture	17.1Gb	1 ILLUMINA (Illumina HiSeq 2000) run: 205M spots, 41.4G bases, 17.1Gb downloads

Appendix Table 4 The information of exon/intron boundary in relative whales (obtained by BLAST by using python script *in silico*)

Species	Exon1	Intron1	Exon2	Intron2
<i>Balaena mysticetus</i>	.....	.....CTCCCCAG	GTGTTC.....ACCGGG	GTGAGAAG.....GTCCCCAG
<i>Balaenoptera bonaerensis</i>	.....	.....CTCCCCAG	GTGTTC.....GCCGGG	GTGAGAAG.....GTCCCCAG
<i>Balaenoptera acutorostrata</i>	.....	.....CTCCCCAG	GTGTTC.....ACCGGG	GTGAGAAG.....GTACCCAG
<i>Eubalaena japonica</i>	.....	.....CTCCCCAC	GTGTTC.....ACCGGG	GTGAGAAG.....GTCCCCAG
<i>Eschrichtius robustus</i>	.....	.....CTCCCCAG	GTGTTC.....ACCGGG	GTGAGAAG.....GTCCCCAG
<i>Megaptera novaeangliae</i>	.....	.....CTCCCCAG	GTGTTC.....GCCGGG	GTGAGAAG.....GTCCCCAG
<i>Kogia breviceps</i>				



Continued table

Exon3	Intron3	Exon4	Intron4	Exon5
GAAGGG.....GAGGAG	<b>GT</b> ACTGCC.....GCACCC <b>AG</b>	GTGTAC.....GACAAG	<b>GT</b> CAGGGG.....TCTTCC <b>AG</b>	CTGCTG.....TGGACG
GAAGGG.....GAGGAG	<b>GT</b> ACTGCC.....GCACCC <b>AG</b>	GTGTAC.....GACAAG	<b>GT</b> CAGGGG.....TCCTCC <b>AG</b>	CTGCTG.....TGGACG
GAAGGG.....GAGGAG	<b>GT</b> ACTGCC.....GCACCC <b>AG</b>	GTGTAC.....GACAAG	<b>GT</b> CAGGGG.....NNNNNNNN	NNNNNN.....TGGACG
GAAGGG.....GAGGAG	<b>GT</b> ACTGCC.....GCACCC <b>AG</b>	GTGTAC.....GACAAG	<b>GT</b> CAGGGG.....TCCTCC <b>AG</b>	CTGCTG.....TGGACG
GAAGGG.....GAGGAG	<b>GT</b> ACTGCC.....GCACCC <b>AG</b>	GTGTAC.....GACAAG	<b>GT</b> CAGGGG.....TCCTCC <b>AG</b>	CTGCTG.....TGGACG
GAAGGG.....GAGGAG	<b>GT</b> ACTGCC.....GCACCC <b>AG</b>	GTGTAC.....GACAAG	<b>GT</b> CAGGGG.....TCCTCC <b>AG</b>	CTGCTG.....TGGACG
	.....GCACCC <b>AG</b>	GTGTAC.....GACAAG	<b>GT</b> CAGGGG.....TCCTCC <b>AG</b>	CTGCTG.....TGGACG

Continued table

Intron5	Exon6	Intron6	Exon7	Intron7
<b>GT</b> GAGCAG.....GCATCC <b>AG</b>	GATTTC.....TGCCAG	<b>GT</b> GGGTCC.....CTCCCC <b>AG</b>	CAAGCC.....CTGGGG	<b>GT</b> GAGGTG.....CCTGTC <b>AG</b>
<b>GT</b> GAGCAC.....GCGTCC <b>AG</b>	GACTTC.....TGCCAG	<b>GT</b> GGGTCC.....CTCCCC <b>AG</b>	CAAGCC.....CTGGGG	<b>GT</b> GAGGTG.....CCTGTC <b>AG</b>
<b>GT</b> GAGCAG.....GCGTCC <b>AG</b>	GACTTC.....TGCCAG	<b>GT</b> GGGTCC.....CTCCCC <b>AG</b>	CAAGCC.....CTGGGG	<b>GT</b> GAGGTG.....CCTGTC <b>AG</b>
<b>GT</b> GAGCAA.....GCATCC <b>AG</b>	GATTTC.....TGCCAG	<b>GT</b> GGGTCC.....CTCCCC <b>AG</b>	CAAGCC.....CTGGGG	<b>GT</b> GAGGTG.....CCTGTC <b>AG</b>
<b>GT</b> GATCAG.....GCGTCC <b>AG</b>	GACTTC.....TGCCAG	<b>GT</b> GGGTCC.....CTCCCC <b>AG</b>	CAAGCC.....CTGGGG	<b>GT</b> GAGGTG.....CCTGTC <b>AG</b>
<b>GT</b> GAGCAG.....GCGTCC <b>AG</b>	GACTTC.....TGCCAG	<b>GT</b> GGGTCC.....CTCCCC <b>AG</b>	CAAGCC.....CTGGGG	<b>GT</b> GAGGTG.....CCTGTC <b>AG</b>
<b>GT</b> GAGCGA.....GCATCC <b>AG</b>	GACTTC.....TGCCAG	<b>GT</b> GGCTCC.....CCCCTTC...	...TCTCCC.....CTGGGG	<b>GT</b> GAGGTG.....CCTGTC <b>AG</b>

Continued table

Exon8	Intron8	Exon9	Intron9	Exon10
GAATCC.....TCGGCT	<b>GT</b> GAGTCT.....GCCTGC <b>AG</b>	CACGAC.....CGCAGG	<b>GT</b> GAGGAG.....TCCTCC <b>AG</b>	GGATGT.....CCGCAG
GAATCC.....TCGGCT	<b>GT</b> GAGTCT.....GCCTGC <b>AG</b>	CGCGAC.....GACGCA	<b>GT</b> GTGAGG.....CCCTCC <b>AG</b>	GGATGT.....CCGCAG
GAATCC.....TCGGCT	<b>GT</b> GAGTCT.....GCCTGC <b>AG</b>	CGCGAC.....GACGCA	<b>GG</b> GTGGTA.....CCCTCC <b>AG</b>	GGATGT.....CCGCAG
GAATCT.....TCGGCT	<b>GT</b> GAGTCT.....GCCTGC <b>AA</b>	CACGAC.....CGCAGG	<b>GT</b> GAGGAG.....TCCTAC <b>AG</b>	GGATGT.....CCGCAG
GAATCC.....TCGGCT	<b>GT</b> GAGTCT.....GCCTGC <b>AG</b>	CGCGAC.....GACGCA	<b>GG</b> GTGAGG.....CCCTCC <b>AG</b>	GGATGT.....CCGCAG
GAATCC.....TCGGCT	<b>GT</b> GAGTCT.....GCCCGC <b>AG</b>	CGCGAC.....CGCAGG	<b>GT</b> GAGGAG.....CCTCCA <b>AG</b>	GATGTC.....CCGCAG
GAATCC.....TCGGCT	<b>GT</b> GAGTCT.....GCCCGC <b>AG</b>	CACGAC.....CACAGG	<b>GT</b> GAGGAG.....CCCTCC <b>AG</b>	GAATGT.....CCGCAG

Continued table

Intron10	Exon11
<b>GT</b> GACGGC.....CCCCC <b>AG</b>	CCACCG.....CCCGTGTGA
.....	CCACCG.....CCCCTGTGA
<b>GT</b> GACGGC.....CCCCG <b>AG</b>	CCACCG.....CCCCTGTGA
<b>GT</b> GACGGC.....CCCCC <b>AG</b>	CCACCG.....CCCGTGTGA
<b>GT</b> GACGGC.....CCCTG <b>AG</b>	CCACCG.....GCCCTGTGA
<b>GT</b> GACGGC.....	CCACCG.....GCCTGG
<b>GT</b> GACGGC.....	

NOTE: The red GT/AG is the normal boundary of intro/exon. The blue color represents the splice mutation.

Appendix Table 5 Likelihood and  $\omega$  values estimated under two ratio branch model on *ACPT* gene among toothless and enamel-less branches.

Models and some relative branches	$\omega$	-ln L	np	Models comparison	2 $\Delta$ (ln L)	P-value
<b>The terminal branch of <i>Balaenoptera physalus</i></b>						
A. All branches have one $\omega$	0.118	23204.622	208			
B. All branches have one $\omega = 1$	1	25437.563	207	A vs B	4465.882	0
C. The terminal branch of <i>Balaenoptera physalus</i> with pseudogenized <i>ACPT</i> has $\omega_2$ , others have $\omega_1$	$\omega_1=0.116$ $\omega_2=1.883$	23190.070	209	A vs C	29.104	<0.01
D. The terminal branch of <i>Balaenoptera physalus</i> with pseudogenized <i>ACPT</i> has $\omega_2 = 1$ , others have $\omega_1$	$\omega_1=0.116$ $\omega_2=1$	23190.624	208	D vs C	1.108	0.293
<b>The terminal branch of <i>Megaptera novaeangliae</i></b>						
A. All branches have one $\omega$	0.117	23161.978	208			
B. All branches have one $\omega = 1$	1	25405.725	207	A vs B	4487.494	0
C. The terminal branch of <i>Megaptera novaeangliae</i> with pseudogenized <i>ACPT</i> has $\omega_2$ , others have $\omega_1$	$\omega_1=0.116$ $\omega_2=0.641$	23156.277	209	A vs C	11.402	<0.01
D. The terminal branch of <i>Megaptera novaeangliae</i> with pseudogenized <i>ACPT</i> has $\omega_2 = 1$ , others have $\omega_1$	$\omega_1=0.116$ $\omega_2=1$	23156.626	208	D vs C	0.698	0.403
<b>The terminal branch of <i>Balaena mysticetus</i></b>						
A. All branches have one $\omega$	0.117	23149.887	208			
B. All branches have one $\omega = 1$	1	25394.078	207	A vs B	4488.382	0
C. The terminal branch of <i>Balaena mysticetus</i> with pseudogenized	$\omega_1=0.116$ $\omega_2=0.551$	23146.023	209	A vs C	7.728	<0.01

*ACPT* has  $\omega_2$ , others have  $\omega_1$

D. The terminal branch of *Balaena mysticetus* with pseudogenized *ACPT* has  $\omega_2 = 1$ , others have  $\omega_1$

$\omega_1=0.116$   $\omega_2=1$  23146.532 208 D vs C 0.509 0.476

**The terminal branch of *Eschrichtius robustus***

A. All branches have one  $\omega$

0.117 23181.416 208

B. All branches have one  $\omega = 1$

1 25415.085 207 A vs B 4467.338 0

C. The terminal branch of *Eschrichtius robustus* with pseudogenized *ACPT* has  $\omega_2$ , others have  $\omega_1$

$\omega_1=0.116$   $\omega_2=2.688$  23167.178 209 A vs C 14.238 <0.01

D. The terminal branch of *Eschrichtius robustus* with pseudogenized *ACPT* has  $\omega_2 = 1$ , others have  $\omega_1$

$\omega_1=0.116$   $\omega_2=1$  23168.159 208 D vs C 1.962 0.161

**The terminal branch of *Balaenoptera musculus***

A. All branches have one  $\omega$

0.117 23199.599 208

B. All branches have one  $\omega = 1$

1 25435.255 207 A vs B 4471.312 0

C. The terminal branch of *Balaenoptera musculus* with pseudogenized *ACPT* has  $\omega_2$ , others have  $\omega_1$

$\omega_1=0.116$   $\omega_2=1.395$  23187.344 209 A vs C 24.510 <0.01

D. The terminal branch of *Balaenoptera musculus* with pseudogenized *ACPT* has  $\omega_2 = 1$ , others have  $\omega_1$

$\omega_1=0.116$   $\omega_2=1$  23188.136 208 D vs C 1.584 0.208

**The terminal branch of *Eubalaena glacialis***

A. All branches have one  $\omega$

0.117 23163.917 208

B. All branches have one  $\omega = 1$

1 25407.391 207 A vs B 4486.948 0

C. The terminal branch of *Eubalaena glacialis* with pseudogenized

$\omega_1=0.116$   $\omega_2=0.503$  23159.695 209 A vs C 8.444 <0.01

*ACPT* has  $\omega_2$ , others have  $\omega_1$

D. The terminal branch of <i>Eubalaena glacialis</i> with pseudogenized <i>ACPT</i> has $\omega_2 = 1$ , others have $\omega_1$	$\omega_1=0.116$	$\omega_2=1$	23160.587	208	D vs C	1.784	0.182
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**The terminal branch of *Balaenoptera bonaerensis***

A. All branches have one $\omega$	0.117		23200.981	208			
B. All branches have one $\omega = 1$	1		25437.712	207	A vs B	4473.462	0
C. The terminal branch of <i>Balaenoptera bonaerensis</i> with pseudogenized <i>ACPT</i> has $\omega_2$ , others have $\omega_1$	$\omega_1=0.116$	$\omega_2=1.045$	23190.135	209	A vs C	21.692	<0.01
D. The terminal branch of <i>Balaenoptera bonaerensis</i> with pseudogenized <i>ACPT</i> has $\omega_2 = 1$ , others have $\omega_1$	$\omega_1=0.116$	$\omega_2=1$	23190.138	208	D vs C	0.006	0.938

**The terminal branch of *Balaenoptera acutorostrata***

A. All branches have one $\omega$	0.117		23178.238	208			
B. All branches have one $\omega = 1$	1		25420.510	207	A vs B	4484.544	0
C. The terminal branch of <i>Balaenoptera acutorostrata</i> with pseudogenized <i>ACPT</i> has $\omega_2$ , others have $\omega_1$	$\omega_1=0.116$	$\omega_2=0.613$	23172.147	209	A vs C	12.182	<0.01
D. The terminal branch of <i>Balaenoptera acutorostrata</i> with pseudogenized <i>ACPT</i> has $\omega_2 = 1$ , others have $\omega_1$	$\omega_1=0.116$	$\omega_2=1$	23172.621	208	D vs C	0.948	0.330

**The terminal branch of *Balaenoptera borealis***

A. All branches have one $\omega$	0.118		23231.146	208			
B. All branches have one $\omega = 1$	1		25466.547	207	A vs B	4470.802	0
C. The terminal branch of <i>Balaenoptera borealis</i> with	$\omega_1=0.116$	$\omega_2=0.902$	23219.198	209	A vs C	23.896	<0.01

pseudogenized *ACPT* has  $\omega_2$ , others have  $\omega_1$

D. The terminal branch of *Balaenoptera borealis* with pseudogenized *ACPT* has  $\omega_2 = 1$ , others have  $\omega_1$   $\omega_1=0.116$   $\omega_2=1$  23219.224 208 D vs C 0.052 0.820

### The stem group of Mysticeti

A. All branches have one  $\omega$  0.121 23747.298 224

B. All branches have one  $\omega = 1$  1 25976.514 223 A vs B 4458.432 0

C. The ancestral branch of stem mysticeti with *ACPT* has  $\omega_2$ , others have  $\omega_1$   $\omega_1=0.120$   $\omega_2=1.436$  23741.059 225 A vs C 12.478 <0.01

D. The ancestral branch of stem mysticeti with *ACPT* has  $\omega_2 = 1$ , others have  $\omega_1$   $\omega_1=0.116$   $\omega_2=1$  23741.164 224 D vs C 0.210 0.647

### The crown group of Mysticeti

A. All branches have one  $\omega$  0.121 23747.298 224

B. All branches have one  $\omega = 1$  1 25976.514 223 A vs B 4458.432 0

C. The clade of crown mysticeti with *ACPT* has  $\omega_2$ , others have  $\omega_1$   $\omega_1=0.116$   $\omega_2=0.522$  23720.907 225 A vs C 52.782 <0.01

D. The clade of crown mysticeti with *ACPT* has  $\omega_2 = 1$ , others have  $\omega_1$   $\omega_1=$   $\omega_2=1$  23725.565 224 D vs C 9.316 <0.01

### The terminal branch of *Kogia breviceps*

A. All branches have one  $\omega$  0.117 23212.116 208

B. All branches have one  $\omega = 1$  1 25455.901 207 A vs B 4487.570 0

C. The clade of *Kogia breviceps* with *ACPT* has  $\omega_2$ , others have  $\omega_1$   $\omega_1=0.116$   $\omega_2=0.581$  23203.192 209 A vs C 17.848 <0.01

D. The clade of <i>Kogia breviceps</i> with <i>ACPT</i> has $\omega_2 = 1$ , others have $\omega_1$	$\omega_1=0.116$	$\omega_2=1$	23204.052	208	D vs C	1.720	0.190
<b>The terminal branch of <i>Dasypus novemcinctus</i></b>							
A. All branches have one $\omega$	0.117		23387.077	208			
B. All branches have one $\omega = 1$	1		25653.621	207	A vs B	4533.088	0
C. The terminal branch of <i>Dasypus novemcinctus</i> with pseudogenized <i>ACPT</i> has $\omega_2$ , others have $\omega_1$	$\omega_1=0.116$	$\omega_2=0.206$	23384.542	209	A vs C	5.070	0.024
D. The terminal branch of <i>Dasypus novemcinctus</i> with pseudogenized <i>ACPT</i> has $\omega_2 = 1$ , others have $\omega_1$	$\omega_1=0.116$	$\omega_2=1$	23403.931	208	D vs C	38.778	<0.01
<b>The terminal branch of <i>Orycteropus afer</i></b>							
A. All branches have one $\omega$	0.119		23456.631	208			
B. All branches have one $\omega = 1$	1		25695.648	207	A vs B	4478.034	0
C. The terminal branch of <i>Orycteropus afer</i> with pseudogenized <i>ACPT</i> has $\omega_2$ , others have $\omega_1$	$\omega_1=0.116$	$\omega_2=0.414$	23441.822	209	A vs C	29.618	<0.01
D. The terminal branch of <i>Orycteropus afer</i> with pseudogenized <i>ACPT</i> has $\omega_2 = 1$ , others have $\omega_1$	$\omega_1=0.116$	$\omega_2=1$	23448.875	208	D vs C	14.106	<0.01

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