**Table S2** Genomic information of species used in this study

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Common name | Latin name | Sequencing technology | Sequence coverage (×) | Scaffold N50 | NCBI Genomes version | RefSeq Assembly Accession | Genome resource | Assembly Completeness in BUSCO (%) |
| Bottlenose dolphin | *Tursiops truncatus* | Sanger, 454 FLX, Illumina HiSeq | 30 | 116,287 | Ttru\_1.4 | GCF\_001922835.1 | NCBI | 92.9 |
| Killer whale | *Orcinus orca* | Illumina HiSeq | 200 | 12,735,091 | Oorc\_1.1 | GCF\_000331955.2 | NCBI | 99.3 |
| Yangtze river dolphin | *Lipotes vexillifer* | Illumina HiSeq | 115 | 2,419,148 | Lipotes\_vexillifer\_v1 | GCF\_000442215.1 | NCBI | 98.8 |
| Yangtze finless porpoise | *Neophocaena asiaeorientalis* | Illumina HiSeq | 106 | 6,341,296 | Neophocaena\_asiaeorientalis\_v1 | GCF\_003031525.1 | NCBI | 99.1 |
| Sperm whale | *Physeter macrocephalus* | Illumina HiSeq | 75 | 427,290 | Physeter\_macrocephalus\_2.0.2 | GCF\_000472045.1 | NCBI | 99.5 |
| Minke whale | *Balaena acutorostrata* | Illumina HiSeq | 92 | 12,843,668 | BalAcu1.0 | GCF\_000493695.1 | NCBI | 99.1 |
| Bowhead whale | *Balaena mysticetus* | Illumina HiSeq | 154 | 877,000 | - | - | http://www.bowhead-whale.org | 74.6 |
| Cow | *Bos taurus* | Sanger, PacBio RS II | 19 | 6,806,220 | Btau\_5.0.1 | GCA\_000003205.6 | NCBI | 99.5 |
| Tibetan yak | *Bos mutus* | Illumina HiSeq, Illumina GA | 130 | 1,407,960 | BosGru\_v2.0 | GCF\_000298355.1 | NCBI | 98.1 |
| Sheep | *Ovis aries* | Illumina GAII, 454, PacBio RSII | 166 | 100,009,711 | Oar\_v4.0 | GCF\_000298735.2 | NCBI | 99.7 |
| Tibetan antelope | *Pantholops hodgsonii* | Illumina GA | 67 | 2,772,860 | PHO1.0 | GCF\_000400835.1 | NCBI | 98.6 |
| Dog | *Canis lupus familiaris* | Sanger | 7 | 45,876,610 | CanFam3.1 | GCF\_000002285.3 | NCBI | 99.2 |
| Weddell seal | *Leptonychotes weddellii* | Illumina HiSeq | 82 | 904,031 | LepWed1.0 | GCF\_000349705.1 | NCBI | 87.3 |
| Pacific walrus | *Odobenus rosmarus divergens* | Illumina HiSeq | 200 | 2,616,778 | Oros\_1.0 | GCF\_000321225.1 | NCBI | 99.6 |
| Horse | *Equus caballus* | Sanger | 6.8 | 46,749,900 | EquCab2.0 | GCF\_000002305.2 | NCBI | 99.7 |
| Microbat | *Myotis lucifugus* | Sanger | 7 | 4,293,315 | Myoluc2.0 | GCF\_000147115.1 | NCBI | 97.4 |
| Mouse | *Mus musculus* | Sanger | - | 52,589,046 | GRCm38.p4 | GCF\_000001635.24 | NCBI | 99.9 |
| Naked mole rat | *Heterocephalus glaber* | Illumina HiSeq | 90 | 20,532,749 | HetGla\_female\_1.0 | GCF\_000247695.1 | NCBI | 99.3 |
| African bush elephant | *Loxodonta africana* | Sanger, ABI | 7 | 46,401,353 | Loxafr3.0 | GCF\_000001905.1 | NCBI | 98.7 |
| Florida manatee | *Trichechus manatus latirostris* | Illumina HiSeq | 150 | 14,442,683 | TriManLat1.0 | GCF\_000243295.1 | NCBI | 98.1 |

**Table S3** Amino acid sequence similarity (identity) between and within cytosolic GST subclass in seven cetaceans

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  |  |  |  |  |  |  |
| HPGDS |  |  |  |  |  |  |  |  |  |  |
| GSTA1 | 25.0% |  |  |  |  |  |  |  |  |  |
| GSTA2 | 21.4% | 56.0% |  |  |  |  |  |  |  |  |
| GSTM1 | 25.5% | 25.2% | 20.0% |  |  |  |  |  |  |  |
| GSTO1 | 17.2% | 19.1% | 17.2% | 15.7% |  |  |  |  |  |  |
| GSTO2 | 17.6% | 16.6% | 15.6% | 15.3% | 62.3% |  |  |  |  |  |
| GSTP1 | 24.5% | 30.7% | 27.2% | 31.1% | 15.7% | 20.8% |  |  |  |  |
| GSTP2 | 23.8% | 30.9% | 27.9% | 30.8% | 18.9% | 21.2% | 82.0% |  |  |  |
| GSTT1 | 15.4% | 21.1% | 17.8% | 18.6% | 16.6% | 18.9% | 21.5% | 22.3% |  |  |
| GSTZ1 | 19.9% | 21.3% | 21.3% | 15.6% | 21.2% | 21.0% | 21.1% | 21.0% | 25.5% |  |
|  | HPGDS | GSTA1 | GSTA2 | GSTM1 | GSTO1 | GSTO2 | GSTP1 | GSTP2 | GSTT1 | GSTZ1 |

Table S4 Positive selection detected in mammals by site models in PAML

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Gene | Model | lnLa | 2ΔlnL | *p* | Parameter | Positive selected sitesb |
| *GSTA1* | M8 | 4353.569 |  |  | ω =1.819 | 36-0.942, 37-0.870, 38-0.854, 45-0.871, 49-0.861, 96-0.952\*, 100-0.845, 103-0.988\*, 107-0.889, 112-0.972\*, 121-0.853, 166-0.844, 208-0.831, 212-0.975\*, 215-0.806, 222-0.805 |
|  | M8a | 4360.512 | 6.943 | 0.008 | ω =1 |  |
| *GSTM1* | M8 | 3852.094 |  |  | ω =2.141 | 107-0.987\*, 164-0.939, 204-0.917, 208-0.991\*\*, 210-0.929 |
|  | M8a | 3857.390 | 10.592 | 0.001 | ω =1 |  |
| *GSTO1* | M8 | 4455.405 |  |  | ω =1.942 | 69-0.949, 125-0.907, 127-0.963\*, 128-0.995\*\*, 133-0.958\*, 147-0.958\*, 211-0.930, 216-0.927, 217-0.831,219-0.866, 222-0.853, 223-0.841, 226-0.835, 227-0.884 |
|  | M8a | 4447.314 | 16.182 | <0.001 | ω =2.809 |  |
| *GSTO2* | M8 | 3316.001 |  |  | ω =5.410 | 14-0.989\*, 43-0.921, 141-0.945 |
|  | M8a | 3319.950 | 7.898 | 0.005 | ω =1 |  |
| *GSTP1* | M8 | 3617.554 |  |  | ω =4.046 | 12-0.837, 43-0.995\*\* |
|  | M8a | 3621.743 | 8.378 | 0.004 | ω =1 |  |
| *GSTP2* | M8 | 2700.044 |  |  | ω =3.412 | 11-0.826, 12 -0.998\*\*, 111-0.969\*, 118-0.948, 205-0.993\*\*, 210-0.999\*\* |
|  | M8a | 2712.339 | 24.590 | <0.001 | ω =1 |  |
| *GSTT2* | M8 | 3755.867 |  |  | ω =12.498 | 237-0.991\*\* |
|  | M8a | 3761.854 | 11.974 | <0.001 | ω =1 |  |
| *GSTZ1* | M8 | 3360.687 |  |  | ω =3.081 | 99-0.893, 137-0.947, 193-0.889 |
|  | M8a | 3349.357 | 11.330 | <0.001 | ω =1 |  |

Note: a lnL is the log-likelihood score.

b Codons with posterior probabilities (pp) >80% in the BEB analyses. \* pp >95%, \*\* pp >99%.

**Table S5** Identification of the domain location of each positively selected sites.

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene** | **Positively selected sitesa** | **Residue annotation from InterProScan** | **Functional Information** |
| ***GSTA1*** | 36 | 36 | C-terminal domain interface |
|  | 49 | 49 | GSH binding site |
|  | 96 | 96 | C-terminal dimer interface (polypeptide binding site) |
|  | 100 | 100 | C-terminal dimer interface (polypeptide binding site) |
|  | 103 | 103 | C-terminal dimer interface (polypeptide binding site) |
|  | 208 | 208 | substrate binding pocket |
|  | 215 | 215 | substrate binding pocket |
|  | 222 | 222 | substrate binding pocket |
| ***GSTM1*** | 107 | 107 | substrate binding pocket |
| ***GSTO1*** | 23 | 29 | C-terminal domain interface |
|  | 47 | 44 | C-terminal domain interface |
|  | 69 | 71 | GSH binding site |
|  | 125 | 125 | substrate binding pocket |
|  | 127 | 128 | substrate binding pocket |
|  | 128 | 128 | substrate binding pocket |
|  | 216 | 215 | N-terminal domain interface |
|  | 226 | 225 | N-terminal domain interface |
|  | 227 | 229 | N-terminal domain interface |
| ***GSTO2*** | 43 | 43 | C-terminal domain interface |
| ***GSTP1*** | 12 | 12 | C-terminal domain interface |
|  | 40 | 39 | GSH binding site |
| ***GSTP2*** | 11 | 11 | C-terminal domain interface |
|  | 12 | 12 | C-terminal domain interface |
|  | 76 | 75 | dimer interface |
| ***GSTT2*** | 25 | 23 | C-terminal domain interface |
| ***GSTZ1*** | 71 | 71 | putative dimer interface |
|  | 125 | 123 | dimer interface |
|  | 137 | 135 | dimer interface |

Note: a Positive selected sites are located or close to the residue annotation from InterProScan.

**Table S6** Results from Clade model C (CmC) test for divergent partitioned by habitats.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Gene | Model and Partitiona | npb | -ln*L*c | Parameters | | Null | | LRT | df | *p* |
| ω0/ω1 | ω2/ωd |
| *GSTA1* | M2a\_rel | 45 | 4358.113 | 0.117/1 | 2.390 |  |  |  |  |  |
|  | CmC: Ceta | 46 | 4360.012 | 0.040/1 | 0.276 |  | M2a\_rel | 3.798 |  | 0.050 |
|  |  |  |  |  | Ceta: 0.371 |  |  |  |  |  |
|  | CmC: Pinn | 46 | 4341.526 | 0.088/1 | 0.091 |  | M2a\_rel | 33.174 |  | <0.001 |
|  |  |  |  |  | Pinn: 5.682 |  |  |  |  |  |
|  | CmC: Sire | 46 | 4360.126 | 0.046/1 | 0.302 |  | M2a\_rel | 4.026 |  | 0.044 |
|  |  |  |  |  | Sire: 0.322 |  |  |  |  |  |
|  | CmC: Mari | 46 | 4349.410 | 0.022/1 | 0.151 |  | M2a\_rel | 17.406 | 1 | <0.001 |
|  |  |  |  |  | Mari: 0.667 |  |  |  |  |  |
|  | CmC: Ceta/Pinn+Sire | 47 | 4347.092 | 0.075/1 | 0.070 |  | M2a\_rel | 22.042 | 2 | <0.001 |
|  |  |  |  |  | Ceta/Pinn: 1.416 |  | Mari | 4.636 | 1 | 0.031 |
|  |  |  |  |  | Sire: 0.0001 |  |  |  |  |  |
|  | CmC: Ceta+Pinn+Sire | 48 | 4339.168 | 0.093/1 | 0.039 |  | M2a\_rel | 37.89 | 3 | <0.001 |
|  |  |  |  |  | Ceta: 0.472 |  | Mari | 20.484 | 2 | <0.001 |
|  |  |  |  |  | Pinn: 7.115 |  | Ceta/Pinn+Sire | 15.848 | 1 | <0.001 |
|  |  |  |  |  | Sire: 0.0001 |  |  |  |  |  |
| *GSTA4* | M2a\_rel | 43 | 2756.675 | 0.021/1 | 0.359 |  |  |  |  |  |
|  | CmC: Ceta | 44 | 2752.474 | 0.024/1 | 0.402 |  | M2a\_rel | 8.402 | 1 | 0.004 |
|  |  |  |  |  | Ceta: 0.039 |  |  |  |  |  |
|  | CmC: Pinn | 44 | 2753.047 | 0.001/1 | 0.032 |  | M2a\_rel | 7.256 | 1 | 0.007 |
|  |  |  |  |  | Pinn: 0.000 |  |  |  |  |  |
|  | CmC: Mari | 44 | 2748.316 | 0.020/1 | 0. 434 |  | M2a\_rel | 16.718 | 1 | <0.001 |
|  |  |  |  |  | Mari: 0.035 |  |  |  |  |  |
|  | CmC: Ceta/Pinn+Sire | 45 | 2748.076 | 0.019/1 | 0.425 |  | M2a\_rel | 17.198 | 2 | <0.001 |
|  |  |  |  |  | Ceta/Pinn: 0.026 |  | Mari | 0.24 | 1 | 0.624 |
|  |  |  |  |  | Sire: 0.103 |  |  |  |  |  |
|  | CmC: Ceta+Pinn+Sire | 46 | 2747.692 | 0.014/1 | 0.411 |  | M2a\_rel | 17.966 | 3 | <0.001 |
|  |  |  |  |  | Ceta: 0.044 |  | Mari | 1.248 | 2 | 0.535 |
|  |  |  |  |  | Pinn: 0.0001 |  | Ceta/Pinn+Sire | 0.768 | 1 | 0.381 |
|  |  |  |  |  | Sire: 0.106 |  |  |  |  |  |
| *GSTM1* | M2a\_rel | 37 | 3856.569 | 0.069/1 | 0.407 |  |  |  |  |  |
|  | CmC: Ceta | 38 | 3853.307 | 0.063/1 | 0.340 |  | M2a\_rel | 6.524 | 1 | 0.011 |
|  |  |  |  |  | Ceta: 1.071 |  |  |  |  |  |
|  | CmC: Pinn | 38 | 3849.571 | 0.062/1 | 0.256 |  | M2a\_rel | 13.996 | 1 | <0.001 |
|  |  |  |  |  | Pinn: 1.028 |  |  |  |  |  |
|  | CmC: Mari | 38 | 3847.817 | 0.058/1 | 0.181 |  | M2a\_rel | 15.704 | 1 | <0.001 |
|  |  |  |  |  | Mari: 0.824 |  |  |  |  |  |
|  | CmC: Ceta/Pinn+Sire | 39 | 3847.717 | 0.058/1 | 0.188 |  | M2a\_rel | 17.704 | 2 | <0.001 |
|  |  |  |  |  | Ceta/Pinn: 0.895 |  | Mari | 0.2 | 1 | 0.655 |
|  |  |  |  |  | Sire: 0.691 |  |  |  |  |  |
|  | CmC: Ceta+Pinn+Sire | 40 | 3847.459 | 0.060/1 | 0.181 |  | M2a\_rel | 18.22 | 3 | <0.001 |
|  |  |  |  |  | Ceta: 0.755 |  | Mari | 0.716 | 2 | 0.699 |
|  |  |  |  |  | Pinn: 1.143 |  | Ceta/Pinn+Sire | 0.516 | 1 | 0.773 |
|  |  |  |  |  | Sire: 0.718 |  |  |  |  |  |
| *GSTM3* | M2a\_rel | 41 | 2774.645 | 0.025/1 | 0.407 |  |  |  |  |  |
|  | CmC: Ceta | 42 | 2772.569 | 0.043/1 | 0.235 |  | M2a\_rel | 4.152 | 1 | 0.042 |
|  |  |  |  |  | Ceta: 0.661 |  |  |  |  |  |
|  | CmC: Pinn | 42 | 2761.181 | 0.000/1 | 0.132 |  | M2a\_rel | 26.928 | 1 | <0.001 |
|  |  |  |  |  | Pinn: 0.824 |  |  |  |  |  |
|  | CmC: Mari | 42 | 2758.621 | 0.000/1 | 0.104 |  | M2a\_rel | 32.048 | 1 | <0.001 |
|  |  |  |  |  | Mari: 0.566 |  |  |  |  |  |
|  | CmC: Ceta+Pinn+Sire | 43 | 2757.128 | 0.000/1 | 0.106 |  | M2a\_rel | 35.034 | 2 | <0.001 |
|  |  |  |  |  | Ceta: 0.368 |  | Mari | 2.986 | 1 | 0.083 |
|  |  |  |  |  | Pinn: 0.804 |  |  |  |  |  |
|  |  |  |  |  | Sire: - |  |  |  |  |  |
| *GSTT1* | M2a\_rel | 33 | 3410.240 | 0.026/1 | 0.268 |  |  |  |  |  |
|  | CmC: Ceta | 34 | 3406.695 | 0.022/1 | 0.248 |  | M2a\_rel | 7.090 | 1 | 0.008 |
|  |  |  |  |  | Ceta: 4.118 |  |  |  |  |  |
|  | CmC: Pinn | 34 | 3408.060 | 0.014/1 | 0.232 |  | M2a\_rel | 4.360 | 1 | 0.037 |
|  |  |  |  |  | Pinn: 0.597 |  |  |  |  |  |
|  | CmC: Mari | 34 | 3404.419 | 0.015/1 | 0.221 |  | M2a\_rel | 11.642 | 1 | <0.001 |
|  |  |  |  |  | Mari: 0.727 |  |  |  |  |  |
|  | CmC: Ceta/Pinn+Sire | 35 | 3404.414 | 0.015/1 | 0.221 |  | M2a\_rel | 11.652 | 2 | 0.002 |
|  |  |  |  |  | Ceta/Pinn: 0.740 |  | Mari | 0.010 | 1 | 0.920 |
|  |  |  |  |  | Sire: 0.687 |  |  |  |  |  |
|  | CmC: Ceta+Pinn+Sire | 36 | 3402.884 | 0.014/1 | 0.214 |  | M2a\_rel | 14.712 | 3 | <0.001 |
|  |  |  |  |  | Ceta: 4.122 |  | Mari | 3.07 | 2 | 0.080 |
|  |  |  |  |  | Pinn: 0.533 |  | Ceta/Pinn+Sire | 3.06 | 1 | 0.080 |
|  |  |  |  |  | Sire: 0.724 |  |  |  |  |  |

Note:

a Partitions for diet, habitat and living habitats are explained in figure S1

b np: number of parameters

c ln L: In likehood

d Mari: Marine mammals; Ceta: Cetaceans; Pinn: Pinnipeds; Sire: Sirenians; Ceta/Pinni: Cetaceans/Pinnipeds

**Table S7** Likelihood ratio tests of various models on the selective pressures on pseudogenes in the cytosolic GST subclass in cetacean lineages

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Genes** | **Models** | **ω** | **-lnL** | | **np** | **Models compared** | **2Δ(lnL)** | **p-value** |
| *GSTAP* | All branches have one ω (A) | ω = 0.262 | 1614.650 | | 27 |  |  |  |
| All branches have one ω = 1 (B) | ω = 1 | 1640.199 | | 26 | B vs. A | 51.098 | <0.001 |
| Cetacean branches with pseudogenes have ω2,  Cetacean branches with intact genes have ω1 (C) | ω1 = 0.022  ω2 = 0.331 | 1607.909 | | 28 | A vs. C | 13.482 | 0.001 |
| Cetacean branches with pseudogenes have ω2 = 1, Cetacean branches with intact genes have ω1 (D) | ω1 = 0.023  ω2 = 1 | 1622.859 | | 27 | D vs. C | 29.900 | <0.001 |
| Each branch has its own ω (E) | Variable ω | 1598.614 | | 51 | C vs. E | 18.590 | 0.725 |
| *GSTMP1* | All branches have one ω (A) | ω = 0.645 | | 2731.702 | 27 |  |  |  |
| All branches have one ω = 1 (B) | ω = 1 | | 2737.880 | 26 | B vs. A | 12.356 | <0.001 |
| Cetacean branches with pseudogenes have ω2,  Cetacean branches with intact genes have ω1 (C) | ω1 = 0.511  ω2 = 0.667 | | 2731.410 | 28 | A vs. C | 0.584 | 0.445 |
| Cetacean branches with pseudogenes have ω2 = 1, Cetacean branches with intact genes have ω1 (D) | ω1 = 0.524  ω2 = 1 | | 2736.020 | 27 | D vs. C | 9.220 | 0.002 |
| Each branch has its own ω (E) | Variable ω | | 2711.784 | 51 | C vs. E | 39.252 | 0.019 |
| *GSTMP2* | All branches have one ω (A) | ω = 1.116 | | 1929.245 | 27 |  |  |  |
| All branches have one ω = 1 (B) | ω = 1 | | 1929.438 | 26 | B vs. A | 0.386 | 0.534 |
| Cetacean branches with pseudogenes have ω2,  Cetacean branches with intact genes have ω1 (C) | ω1 = 0.635  ω2 = 1.355 | | 1927.385 | 28 | A vs. C | 3.720 | 0.054 |
| Cetacean branches with pseudogenes have ω2 = 1, Cetacean branches with intact genes have ω1 (D) | ω1 = 0.627  ω2 = 1 | | 1928.479 | 27 | D vs. C | 2.188 | 0.139 |
| Each branch has its own ω (E) | Variable ω | | 1908.534 | 51 | C vs. E | 37.702 | 0.027 |
| *GSTMP3* | All branches have one ω (A) | ω = 0.724 | | 1615.475 | 25 |  |  |  |
| All branches have one ω = 1 (B) | ω = 1 | | 1616.706 | 24 | B vs. A | 2.462 | 0.117 |
| Cetacean branches with pseudogenes have ω2,  Cetacean branches with intact genes have ω1 (C) | ω1 = 0.502  ω2 = 0.868 | | 1614.572 | 26 | A vs. C | 1.806 | 0.179 |
| Cetacean branches with pseudogenes have ω2 = 1, Cetacean branches with intact genes have ω1 (D) | ω1 = 0.507  ω2 = 1 | | 1614.734 | 25 | D vs. C | 0.324 | 0.569 |
| Each branch has its own ω (E) | Variable ω | | 1605.964 | 47 | C vs. E | 17.216 | 0.751 |
| *GSTMP4* | All branches have one ω (A) | ω = 0.348 | | 2113.165 | 21 |  |  |  |
| All branches have one ω = 1 (B) | ω = 1 | | 2137.373 | 20 | B vs. A | 48.416 | <0.001 |
| Cetacean branches with pseudogenes have ω2,  Cetacean branches with intact genes have ω1 (C) | ω1 = 0.411  ω2 = 0.335 | | 2113.009 | 22 | A vs. C | 0.312 | 0.576 |
| Cetacean branches with pseudogenes have ω2 = 1, Cetacean branches with intact genes have ω1 (D) | ω1 = 0.446  ω2 = 1 | | 2134.604 | 21 | D vs. C | 43.190 | <0.001 |
| Each branch has its own ω (E) | Variable ω | | 2097.915 | 39 | C vs. E | 30.188 | 0.036 |
| *GSTPP* | All branches have one ω (A) | ω = 0.331 | | 2676.809 | 28 |  |  |  |
| All branches have one ω = 1 (B) | ω = 1 | | 2718.359 | 27 | B vs. A | 83.100 | <0.001 |
| Cetacean branches with pseudogenes have ω2,  Cetacean branches with intact genes have ω1 (C) | ω1 = 0.222  ω2 = 0.431 | | 2673.058 | 29 | A vs. C | 7.502 | 0.006 |
| Cetacean branches with pseudogenes have ω2 = 1, Cetacean branches with intact genes have ω1 (D) | ω1 = 0.216  ω2 = 1 | | 2686.023 | 28 | D vs. C | 25.930 | <0.001 |
| Each branch has its own ω (E) | Variable ω | | 2651.512 | 53 | C vs. E | 43.092 | 0.014 |
| *GSTTP* | All branches have one ω (A) | ω = 0.252 | | 1995.490 | 26 |  |  |  |
| All branches have one ω = 1 (B) | ω = 1 | | 2034.266 | 25 | B vs. A | 77.552 | <0.001 |
| Cetacean branches with pseudogenes have ω2,  Cetacean branches with intact genes have ω1 (C) | ω1 = 0.094  ω2 = 0.852 | | 1981.855 | 27 | A vs. C | 27.270 | <0.001 |
| Cetacean branches with pseudogenes have ω2 = 1, Cetacean branches with intact genes have ω1 (D) | ω1 = 0.095  ω2 = 1 | | 1981.961 | 26 | D vs. C | 0.212 | 0.645 |
| Each branch has its own ω (E) | Variable ω | | 1974.393 | 49 | C vs. E | 14.924 | 0.897 |