

Figure S1. Mitochondrial genomes of the *Lingula anatina* collected from Buan, Korea (A) and Doson, Vietnam (B). Circular maps were drawn with the software Geneious v. 9.1.2. The arrows indicate the orientation of gene transcription. Abbreviations of gene names are: ATP6 and ATP8 for ATP synthase subunits 6 and 8; COX1–3 for Cytochrome oxidase subunits 1–3; CYTB for Cytochrome b, ND1–6 and ND4L for NADH dehydrogenase subunits 1–6 and 4l; and tRNA genes are indicated with their three-letter corresponding amino acids.

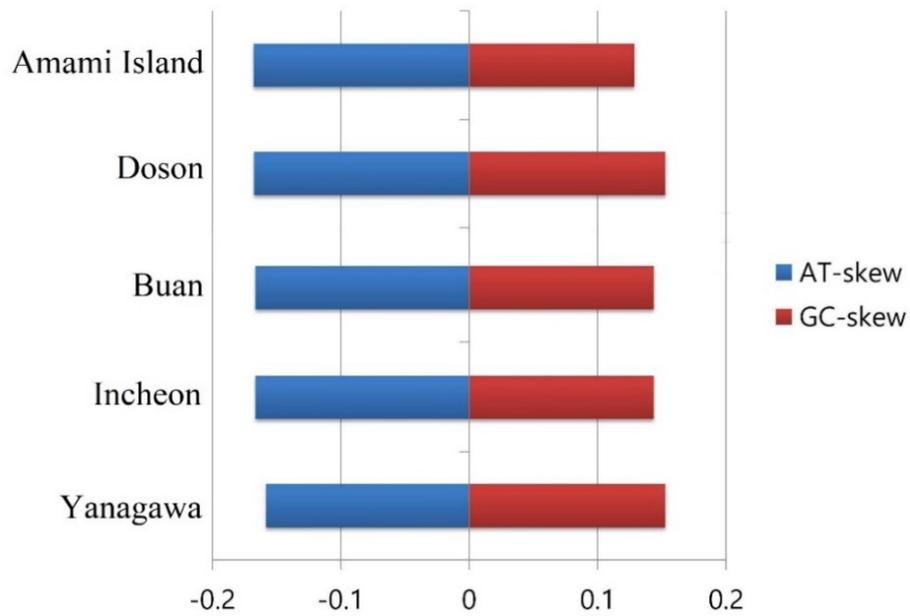


Figure S2. AT and GC skew values in the mitochondrial genome records of *Lingula anatina* specimens. The skewness was determined with a base composition of nucleotide sequences by using the formulae: AT skew = $[A - T]/[A + T]$; GC skew = $[G - C]/[G + C]$. The specimens are represented with localities: Buan, Korea (MW528457), Incheon, Korea (KX774482), Doson, Vietnam (MH371361), Yanagawa, Japan (AB178773) and Amami Island, Japan (KP881498).

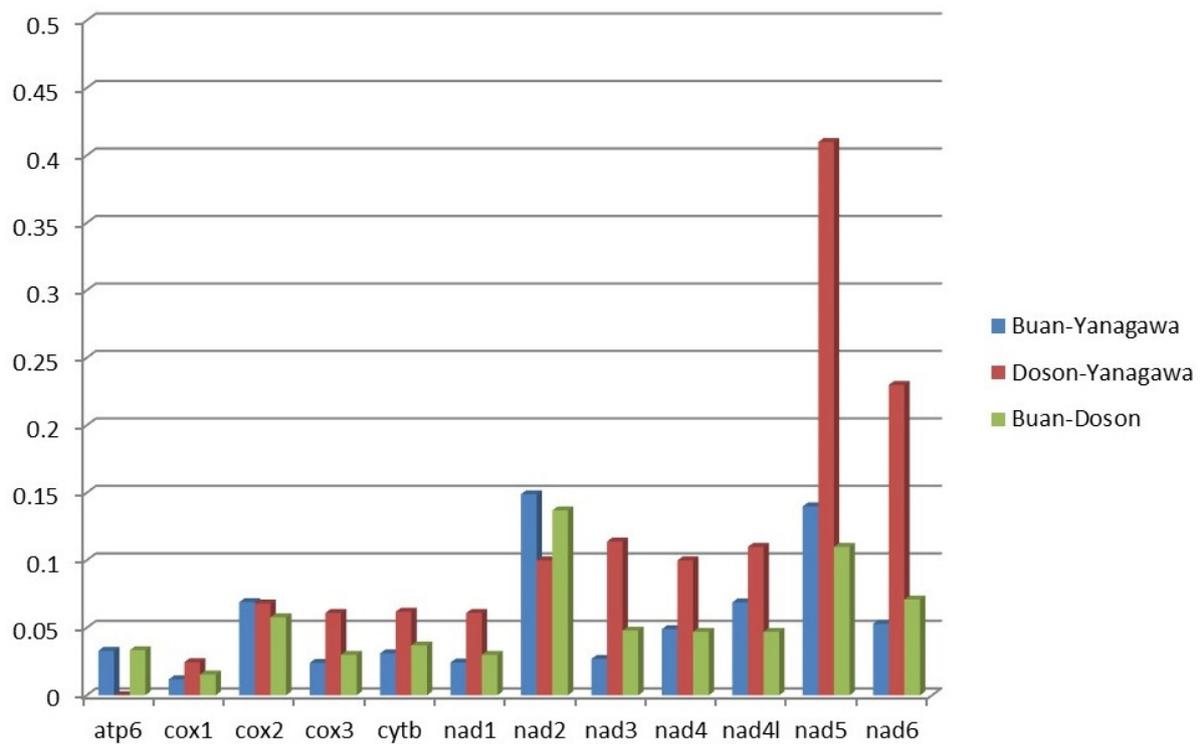
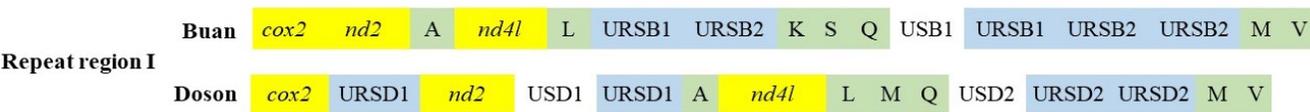


Figure S3. Calculations of nonsynonymous and synonymous Ka/Ks ratio of protein-coding genes of *Lingula anatina* specimens. For Ka/Ks calculation, protein-coding genes were compared between Buan, Korea (MW528457)-Yanagawa, Japan (AB178773), Doson, Vietnam (MH371361)-Yanagawa, Japan (AB178773), Buan, Korea (MW528457)-Doson, Vietnam (MH371361).

A



B

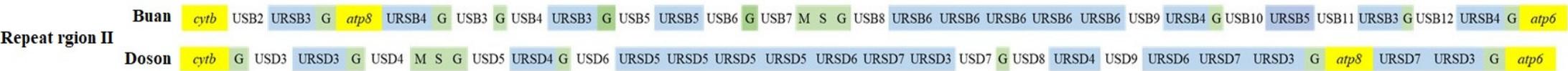


Figure S4. Structures of Repeat regions I and II of *Lingula anatina* mitogenomes from Buan and Doson. A: Repeat region I and B: Repeat Region II. Abbreviations are as follows: URSB1–6: unassigned repeated sequence 1–6 of the Buan mitogenome; URSD1–7: unassigned repeated sequence 1–7 of the Doson mitogenome; USB1–12, unassigned unique sequence 1–12 of the Buan mitogenome; USD1–9: unassigned unique sequence 1–9 of the Doson mitogenome.

URFB1
MSCESLTSLSYSSPSFLISGSDGAVDTALVVGPLSLGPLAGIQWSSSPLDPPRPPPPFMGVGGGGPPLFGWKSPTLDTCFECLNSLPPRVGVKHSKQSIPMY
IWSSQIQDPDLGLWQASYTSHL

URFB2
MVIWLNKFKNKDLKPPYPQKFHFSLYSGKHPASILRGAPLDKSYIFHPGPP

URFB3
MKFLGVWGLKVLIFKFIKSNHHLSMFNLTkFKLNYMYLTGVPPLFTGGRGGKYTSYPEGPPVSWTPDVYLYMEKNEIFGGMGA

URFB4
MVIWLNKFKNKDLKPPYPQKFHFSLYSGKHPASILRGAPLDKSYIFHPGPP

URFB5
MPTIGPCLFWFFSSFIVFGLVYLFFMSFIQGQSCCKNWPVKLNFSRMGTNFRKSVSK

URFB6
MKNFNRAVVMKMMIGSFFFFFFSLMTKGYFMPYMMSWFILWFIKPMVDPVVYNKLRIFISGLCLVTLVLSWFFIPIDYIFDDNLKRFMKSLMGWMKLSSA
SELSNLGEHCLGELDASKFKK

URFB7
MEDFGWNFMRKVLHSSFFLFIFGWMTGGYLLHFMLGGTLVFKPLVDQEVYEKLRIFIYGMCVVISFVYWFFIPIDFIFDEYMKCFLDLSLMDEIKLINSEMP
NFDEPCSCSPCFSEAKK

URFB8
MKKIDFNFIVKVVNLNLLVFGLMINWTNGLFLPMYMGGFILYFVKPMVDLETYYKIMIFIMCMCFAVTMIYWLFVPVEFVFFPEIKCSRPEPSYSLNSVYHAI
KSIIYIK

URFB9
MWRSTHEFLKKVVSYCTVFSVFTLMLPPSMPIVFSVVILKFIQPLIDDPKTFNKIQIFVVCMCIVTYILFIFIPLEFPVE

URFB10
MPEAGAVMPAAELLQPEPIVVEGGPLPEAGAVMPAAELLQPEPIVVEGGPLPEAGAVMPAAELLQPEPIVVEGGPLPEAGAVMPAAELLQPEPIVVEGGPLPE
AGAVMPAAELLQPEPIVVEGGPLPEAGA

URFB11
MPEFDKFIIVSVLSNLIVFGLLVHMSNGLFLPVFLGGFILYFVKPLVSLEVYYSLMIFIMMGFMVFILNWLFFPSNFDVYVKFPVCYQERKYYLYSIYKEIES
FIYS

URFB12
MFMLSFQCVIKNENTIYTQFMKKLSLSFILNKS YKTLNPVKIEDILAMIGPCLFWFFSSFIVFGLVYLFFMSFIQGQSCCKNWPVKLDFSRMGTNFRKSVSK

URFB13
MSNRQQDYIFALCYFIFSLFYMWFIIEFTYGIMALMEWFSTADSSLVQYGCLQGDKIIPTVVCEGFPLAKEDLPMSGYEQFLPLIEPECLKIKKPLPEIPVIVA

AFAK
URFB14
MSMDYFAKAATMTGISGSGFLILSHSGSIKGNCSYPLMGSSSLAKGGNPSHTTVGMILSPWHPYWTKLLSAVLNHSINAMIPYVNSMMNHM
URFB15
MGVFSVMKLSLQLCVKDFPLWLKKTFLWVGMSNFCLWLSLNVLSLSSPFLKFLLLLRLQNNLWT

URFD1
MKTLDNYKHKSNNLPLAFDYYWDKQVKFAGKSVTLRVWKARTDSSEQESSTLKASLWVIVLMVGKFMKLVGVFLLLIWFGFFLGKNEKAYKSFSLSLKK
YEYCFSIQKYADKVPKWLFFTAFYSVSVIAITCHVVIEYNFKTGTLRIESEGMHRFKKNE

URFD2
MASNSNHRNPMCECCKEPLSHLISMLLNTKTMLMFLSNKSKSFVCLLIFTKKTSTSN

URFD3
MSSHTKDFLLFLSNMSIVLVFKSMLMSCLSGFSLQHSMGFRWLLLLAMSWLNMILKLELFVSSLKDLCTVLSSMSSL

URFD4
MLCFKCFTPTRGGSELHLKQVSNVGDHFKSGGPPAPYPHKGRGGAGGV

URFD5
MSCEALTSYSSPSSLISGSDGAVDTALVVGPLSLGPLAGIQWSSSPLDPPRPPPPFMGVGGGGPPAFWVEISYIGYLL

URFD6
MMIWLKSFKNKDHKPPYPQKFHFSLYSGKHPASILRGAPLTKSYIFHPGPP

URFD7
MEDFGWNFMRKVIIHGLFLFLFGWMSGGFFLHFMLGGLTLVFKPLVDEDTYNKLRILYGMCMVIGFMYWFFIPIDFIFDEYMKCFIDSLMDGIKLINSEV
PSLDEPCSCGPCFPEPKK

URFD8
MPKLGFEFYLVVWYCFMLSGATYPLPVLFPVVFVLSLNFQPLVSDVFGKMQVFSMAMCFTTIFIFGFLPIEFIDD

URFD9
MKSLTRVVVMKMVVGSGFFFFFFSFMTKGYFMPYMMSWFILWFIKPLVDPVVYSKLRIFISGLCLVTLVLYWFFIPIDYIFDDDLKRFIKSLMKWIKSSSGSEL
SNLGEHCLGELDDSKINK

URFD10
MSNWRFSMLMVLISFTFLSFIWVVDVTETLNLVVELVKEYTTNHHRSTSILPEVEFGATAGELTSPKFLQPEAIVVEGGPLSEVEAVLPEAEFLQPEAIVVE
GGPLSEVEAVLPEAEFPQPEAIVVEGGPLSEVEAVLPEAEFPQPEAIVVEGGPLSEVEA

URFD11
MEFWCRLGFSSISYLSLSTHAKAANLMNYSRHRSEKWKSLPLMNNFQMPLFFHPLLLVFTMKVRKSAPTREKFNFTGQFFLQDWPWMKHKKKMNT
LSQKQWMS

URFD12

MSKFDLNFIIKVVLNLLVFGLIIDYTNGFLFLPMYMGGLILYFVKPMVDLETTYKIMIFIMCMCFVVTMIYWLFVPAEFVFFPEIKCSRPEPSYTLNSVFHAIKS
IYYIK

URFD13

MSPKWLQELIFAVSYLIFSLFYTWLVMECTCGIMMLFEWFNSADTSCLAQCGALQGDEVVPSAVCEGSPSLIKENTPMPENGEFLPCPEPECFKVKERIPV
LAAAFQAQ

URFD14

MLSMQIYCAKAAASTGISGMRSLLKHSKSGQKNSPFSGMGVFSLIKEGDPSTAEGTTSSPWSAPHWAKQLVSALLNHSNNIMIPQVHSMTSHV

URFD15

MKLFLQLCVKDLLLWLKKMLLYLSMESSCLVLSLSVSSLSSAFLKFLFLLRLLHSKSVYSTFLVKFFSCWNCLPTPLWQN

URFD16

MVEFDLKFIVSVLSNLIVFGLLDMSNGLFLPVFLGGFVLCFIKPLVSLEVYYSLIFIMMSFMVFILNWLFFPSNFDVYVSFPVCYQEPKYLYSICKEIKSFI
YA

URFD17

MFMLGSQCVIKNQNTIYTQFAKKLSLSFMLNKFYKTLSLVKIEDIWPTIGSYKWKKNWKVCCLSAELVIFYFFSLMPTIGPCLFWFFSSFIVFGLVYLFFLCFI
QGQSCCKNWPVKLNFSRVGTDERTFMVKTNNKGWKNNGI

Figure S5. Amino acid sequences encoded by unassigned open reading frames in non-coding regions of the Buan mitogenome (URFB1-URFB15) and Doson mitogenome (URFD1-URFD17).

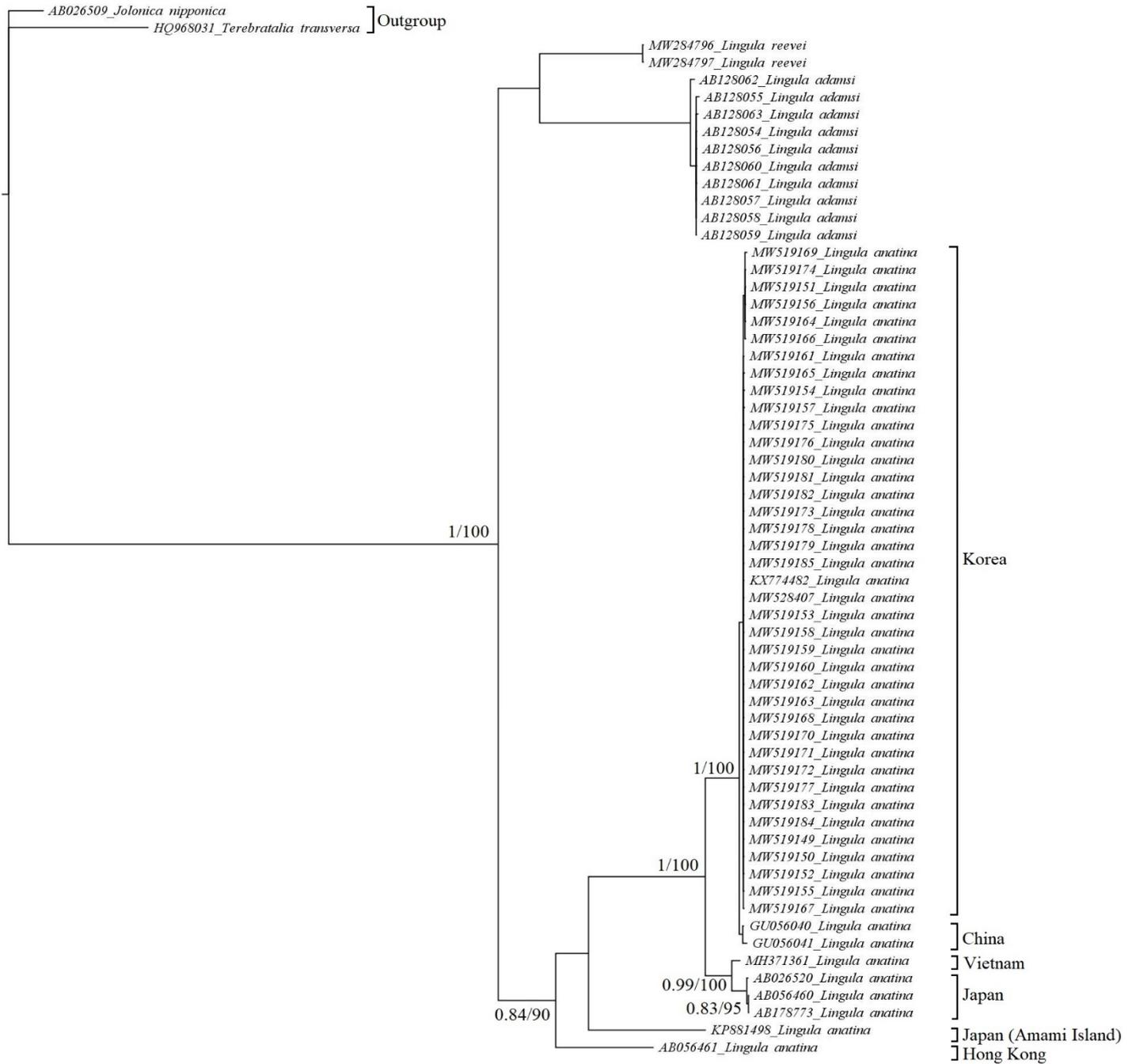


Figure S6. Phylogenetic relationships of *Lingula* species based on partial sequences of the mitochondrial *cox1* gene. Bootstrap support value (left) > 70 and posterior probability value (right) > 0.7 (left) are shown at nodes.