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<!-- Generated by BEAUTi v1.5.2
          -->
<!--       by Alexei J. Drummond and Andrew Rambaut
          -->
<!--       Department of Computer Science, University of Auckland
and        -->
<!--       Institute of Evolutionary Biology, University of
Edinburgh        -->
<!--       http://beast.bio.ed.ac.uk/
          -->
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                <sequence>
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AAAACTCCCAAACTAAATTACACAAACTCACTATCCCTTTCTCACACCGGTCCCATCCATACCTTT
CCGCTATCTCCCCCGCAACATCACCATCATAACATTACGCAAAAA
                </sequence>
                <sequence>
```

```
                        <taxon idref="2n31"/>

AAAACTCCCAAACTAAATTACACAGACCCACTATCCCTTTCTCGCACCAGTCCCATCCACACCTTT
TCACTAGCTCCCCCGCAACATTATCATCATAACATAATGCAAAAA
                </sequence>
                <sequence>
                        <taxon idref="2n38XY"/>

AAAACCCTTAAATAAAATTAGACAAACCCACCATCCCCTCCTCACATCAATCACGCCCGCACCCTT
TTACTAACCCTCACATAACATTCACACCACAGCATAATCCAAAAA
                </sequence>
                <sequence>
                        <taxon idref="2n38"/>

AAAACCCTTAAATAAAATTAGACAAACCCACCATCCCCTCCTCACATCAATCACGCCCGCACCCTT
TTACTAACCCTCACATAACATTCACACCACAGCATAACCAAAAAA
                </sequence>
        </alignment>


        <!-- The sequence alignment (each sequence refers to a
taxon above).         -->
        <!-- ntax=13 nchar=111
                  -->
        <alignment id="alignment6" dataType="nucleotide">
                <sequence>
                        <taxon idref="Medaka"/>

GTTATGTCCGCTTGGCAAAGCTCGACTATGAGAGTTTGGCATCGGATGTCACAACGAGGTTTTATA
TCCAGCGTTTGTTTTAGATAGGGACCCCGAAAGTGGTGTCTGCAT
                </sequence>
                <sequence>
                        <taxon idref="Carp"/>

GTTATGTCCGCTTAACATAGCTCGACTATGATAGTTTGACATCGGATGTCACAGCGAGGTTTTATA
TACAGCGCTTGTTCTAGATAAGGGCCCCGAAAGTGGTGCCTGCAT
                </sequence>
                <sequence>
                        <taxon idref="Tetraodon"/>

GTTATGTCCGCTTGGCACAGCTCGACTATGAGAGTTTGGCATCGGATGTCACACCGAGGTTTTATT
TTCAGCGCTTGTTCCAGATAAGGGCCCCGAGAGTGGTGCCTGCAT
                </sequence>
                <sequence>
                        <taxon idref="Salmon"/>

GTTATGTCTGCTCGACACAGCTCGACTATGATAGTTTGTCATCGGATGTCACAACGAGGTTTTATA
TACAGCGCTTGTTCTAGATAAGGGCCCCAAAAGTGGTGCCTGCAT
                </sequence>
                <sequence>
                        <taxon idref="Rainbow"/>

GTTATGTCCGCTTGACACAGCTCGACTATGATAGTTTGTCATCGGATGTCACAACGAGGTTTTATA
TACAGCGCTTGTTCTAGATAAGGGCTCCAAAAGTGGTGCCTGCAT
                </sequence>
                <sequence>
```

```
                        <taxon idref="Zebrafish"/>

GTTATGTCCGTTCAACATAGCTTGACTATGATAGTTTGGCATCGGATGTCACAACGAGGTTTTATC
TACAGCGCTTGTTCTAGATAAGGGCTTCGAAAGTGGTGCCTGCAT
                </sequence>
                <sequence>
                        <taxon idref="Stickleback"/>

GTTATGTCCGCTTAACACAGCTCGACTATGAGAGTTTGGCATCGGATGTCACACCGAGGTTTTATA
TACAGCGCTTGTTTTAGATAAGGGCCCTGAAAGTGGTGCCTGCAT
                </sequence>
                <sequence>
                        <taxon idref="Fugu"/>

GTTATGTCCGTTCAACAAAGCTCGACTATGATAGTTTGGCATCGGATGTCACACCGAGGTTTTATT
TTCAGCGCTTGTTCAAGATAGGGGCTCTGAGAGTGGTGCCTGCAT
                </sequence>
                <sequence>
                        <taxon idref="Japanese"/>

GTTATGTCCGCTCATCACAGTTCGACTATGATAGTTTGGCATCGGATGTTACATCGAGGTTTTATC
TCCAGCGCTTGTTCTAGATAAGGGCTCTGAAAGTGGTGCCTGCAT
                </sequence>
                <sequence>
                        <taxon idref="2n28"/>

GTTATGTCCCCTCAGCAAAGCTCGACTATGATAGTTTGGCATCGGATGTTACACCGAGGTTTTATA
TCCAGCGCTTGTTCTAGATAAGGGCTTCGAAAGTGGTGCCTGCAT
                </sequence>
                <sequence>
                        <taxon idref="2n31"/>

GTTATGTCCCCTCAGCAAAGCTCGACTATGATAGTTTGGCATCGGATGTTACACCGAGGTTTTATA
TCCAGCGCTTGTTCTAGATAAGGGCTTTGAAAGTGGTGCCTGCAT
                </sequence>
                <sequence>
                        <taxon idref="2n38XY"/>

GTTATGTCCCCTCAGCAGAGCTCGACTATGATAGTTTGGCATCGGATGTTACACCGAGGTTTTATA
TCCAGCGCTTGTTTTAGATAAGGGCTTTGAAAGTGGTGCCTGCAT
                </sequence>
                <sequence>
                        <taxon idref="2n38"/>

GTTATGTCCCCTCAGCAGAGCTCGACTATGATAGTTTGGCATCGGATGTTACACCGAGGTTTTATA
TCCAGCGCTTGTTTTAGATAAGGGCTTTGAAAGTGGTGCCTGCAT
                </sequence>
        </alignment>


        <!-- The sequence alignment (each sequence refers to a
taxon above).         -->
        <!-- ntax=13 nchar=173
                 -->
        <alignment id="alignment7" dataType="nucleotide">
                <sequence>
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```
                        <taxon idref="Medaka"/>

AACTGCTATCAGCGCGAAGATGATCTCCGTAGCGAAACGACCCAGCCCCCCGGGGGAATTTACTGG
GGAACTGATAAGTCTGCTGACCAACCCCAGAAAAGCTCACGTGCCCGTCCGGGCGTGTAAGCGTTA
TCACGCTGCCCCATCGA-CCCAATTGCATACGGGTGGTACA
                </sequence>
                <sequence>
                        <taxon idref="Carp"/>

AACTCCGACTTAGGCGAACATGATCTCCGTAGCGAAACGAACCAGCCCCCCGGGGAAATTCACGAG
GGAACTGAAAAGTAAGGTAAAGCTACAGAAATAGGTGCAAGCGCACTTACGGCCGTGCCAGCACTA
TCACGCTGCAACAGCAAGCCCCACTGATTATGGGTGGTACA
                </sequence>
                <sequence>
                        <taxon idref="Tetraodon"/>

AACTAAGTTCTGCCCGAAAAGAATCTCAGTAGCGAAACGAACCAGCCCCCCGGGGAAATTCACGAG
GGACCTGAAAAGTCAGCTGCCCAACCCCTATAACGCGCAAGCGCCCATCCGGCCGTGCAAGCGCTA
TCACGCTGCCCCCCCAA-CACCGACGGCTACAGGTGGCACA
                </sequence>
                <sequence>
                        <taxon idref="Salmon"/>

AACTGCAATCTATGCGAACATGATCTCCGTAGCGAAACGAACAAGCCTCCCGAGGAAATTTACGAG
GGAACTGAAAAGTCGGGTGACCCTCCCGAAAGACGCGCACGCGCGCTTTCGGCCGCGCAAGCACTA
TCACGCTGCAACGGCAAATTCCAGAGCCTACGGGTGGCACA
                </sequence>
                <sequence>
                        <taxon idref="Rainbow"/>

AACTGCAATCTACGCGAGCATGATCTCCGTAGCGAAACGAACAAGCCCCCCGAGGAAATTTACGAG
GGAACTGAAAAGTCGGGTGACCCTCCCGAAAGATGCGCACGCGCGCTTCCGGCCGCGCAAGTACTA
TCACGCTGCAACGGCAAATTCCGAAGCCTACGGGTGGCACA
                </sequence>
                <sequence>
                        <taxon idref="Zebrafish"/>

AACTGCAATATACGCGAATATTATCTATGTAGTGAAATGAGCCAGCCCCCCGGGGAAATTCACGGG
GGAACTAAAAAGTATGCTGGAGACGCGAAAGAATGTGCAAGCGCACTTTCGGCCGTGCTAGCATTA
TCACGCAGTAACAACAAGCCACATCGAGTTCAGGTAGCACA
                </sequence>
                <sequence>
                        <taxon idref="Stickleback"/>

AACTATGACCTGTGCGAAAATGATCTCCGTAGCGAAACGAACCAGCCCCCCGGGGAAATTCACGAG
GGACCTGAAAAGTAAGCTGACCAACCCCAACAATGCGCAAGCGCCCTTCCGGCCGTGTAAGCAATA
TCACGCTGTCTCCGCTA-TACCGGCGCATACGGGTGGCACA
                </sequence>
                <sequence>
                        <taxon idref="Fugu"/>

AACTAAGTCTTGCCTGAAAAAAAACTCAGTAGCGAAACGAACCAGCCCCCCGAGGAAATTTACGGG
GGACCCGGAAAGTAAGCTGCCCGACCGCAAAAAAGTGTAAGCGCCCATCCGGACGCGCAAGCACGA
TCAAGCTTCCTCACCAA-CACTACCGACTACGGGTGGCACA
                </sequence>
                <sequence>
```

```
                        <taxon idref="Japanese"/>

AACTGATAACAATGCGAAAATGATCTCCGTAGCGAAACGAACCAGCCCCCGGGGAAATTCACGAG
GGCACTAAATAGTAAGCTGACCCTCCAAAAAAACGCGCAGGCGCACTTTCGGCCGCGCAAGCACTA
TCACGCAGCATCCTCGGGCCCAAACGGATGCGGGTGGTACA
                </sequence>
                <sequence>
                        <taxon idref="2n28"/>

AACTACAATCTACGCGAATATGATCTTCGTAGCGAAACGACCCAGCCCCCGGGGTAATTCACGAG
GGAACTGAAAAGTAAGGTAAAGCTCCCCAGCAACGCGCAAGCGCTCTTCCGGCCGCGTAAGCATTA
TCACGCTGCCACAGCAACCACCAACGCCTACAGGTGGCACA
                </sequence>
                <sequence>
                        <taxon idref="2n31"/>

AACTGCAATCTACGCGAATATGATCTTCGTAGCGAAACGACCCAGCCCCCGGGGTAATTCACGAG
GAAACTGAAAAGTAAGGTAAAGCTCCCCAGCAACGCGCAAGCGCCCTTCCGGCCGCGTAAGCACTA
TCACGCTGCCGCAGCAACCACCAACGCCTACAGGTGGCACA
                </sequence>
                <sequence>
                        <taxon idref="2n38XY"/>

AACTGCAATCTACGCGAATATGATCTCCGTAGCGAAACGACCCAGCCCCCGGGGTAATTCACGAG
GGAACTGAAAAGTAAGGTGAACTTCCCCAGTAACGCGCAAGCGCCCTTCCGGCCGCGAAAGCACTA
TCACGCTGCCACAGCAACCGCTAACGCCTACAGGTGGCACA
                </sequence>
                <sequence>
                        <taxon idref="2n38"/>

AACTGCAATCTACGCGAATATGATCTCCGTAGCGAAACGACCCAGCCCCCGGGGTAATTCACGAG
GGAACTGAAAAGTAAGGTGAACTTCCCCAGTAACGCGCAAGCGCCCTTCCGGCCGCGAAAGCACTA
TCACGCTGCCACAGCAACCGCTAACGCCTACAGGTGGCACA
                </sequence>
        </alignment>


        <!-- The sequence alignment (each sequence refers to a
taxon above).         -->
        <!-- ntax=13 nchar=173
                  -->
        <alignment id="alignment8" dataType="nucleotide">
                <sequence>
                        <taxon idref="Medaka"/>

TACATTCTTTTGTGTGCCTCTCGCAGTTCGTGTATACTCTTCTTCAAAACGCTACCCAATTTACCC
CCCTTTCGCCACGTCGAGATAATCACTCCTTTCTCTCTATGTCCTACGTCATTAGTATCCGTTTCC
GAATCCTCTTTATCCAT-CTTTCCTGTTCTTCGGGGGTAAC
                </sequence>
                <sequence>
                        <taxon idref="Carp"/>

TACAGGCCTTGGTGTGCCTCTCGCAGTTCGTGTATACTCTCCTTCAAAACGCTACCCAATTCACCC
CCTTTTCGCCACGTCGAGGTAATCACTCGCTTTCCTCTATGTCCTATGTCATTAGTATTCGTTTCC
GAATCCTCTTTACCACTACTTTCTTGTCCCTTGGGGGTAAC
                </sequence>
```

```
                <sequence>
                        <taxon idref="Tetraodon"/>

TGCATCCCTTTGTTTGCCTCCCGCAGTTCGTGTATACTCTTCTTCAAAACGCTACCCAATTCACCC
CCTTTTCGCCACGTCGAGATAATCACTCCCTTTTCTCTATGTCCTACGTCATTAGTATCCGTTTCC
GAATCCTCTTTATACA-ACCTTTTTGTTCCTTGGGGGTAAC
                </sequence>
                <sequence>
                        <taxon idref="Salmon"/>

TACATTCTTTCGTGTGCTTCTCGCAGTTCGTGTATACTCTTCTTCAACACGCTACCCAATTCACCC
CCTTTTCGCCACGTTGAGATAATCACTCCCCTTTCTCTATGTCCTATGTCATTAGTATCCGTTTCC
GAATCCTCTTTATCCCTACCTTTCTGTTCCTTGGGGGTAAC
                </sequence>
                <sequence>
                        <taxon idref="Rainbow"/>

TACATTCTTTCGTGTGCTTCTCGCAGTTCGTGTATACTCTTCTTCAAAACGCTACCCAATTCACCC
CCTTTTCGCCACGTTGAGATAATCACTCCCCTTTCTCTATGTCCTATGTCATTAGTATCCGTTTCC
GAATCCTCTTTATCCCTACCTTTCTGTTCCTTGGGGGTAAC
                </sequence>
                <sequence>
                        <taxon idref="Zebrafish"/>

TACATTTTTTCGTGTGCCTCTCGCAGTTCGTGTATACTCTTCTTCAAAACGCTACCCAATTTACCC
CCTTTTCGCCACGTCGAGATCGTCGCCCGCCTTTCTCTATGTCCTATGTCATTAGTATTCGTTTCC
GAATCCTCTTTACCACCACTTTCCTGTCCCTTGGGGGTAAC
                </sequence>
                <sequence>
                        <taxon idref="Stickleback"/>

TACTTTCCTTTGTGTGCCTCTCGCAGTTCGTGTATACTCTTCTTCAAAACGCTACCCAATTCACCG
CCTTTTCGCCACGTCGAGATAATCACTCTCTTCTCTCTATGTCCTACGTCATTAGTATCCGTTTCC
GAATCCTCTTTATACC-ACCTTTTTGTCCCTTGGGGGTAAC
                </sequence>
                <sequence>
                        <taxon idref="Fugu"/>

TACATCCCTTTGTTTGCCTCCCGCAGTTCGTGTATACTCTTCTTCAAAACGCTACCCAATTCACCC
CCCTTTCCCCACGTCGAGATAACCACTCCCTTCTCTCTATGTCCTACGTCATTAGTATCCGTTTCC
GAATCCTCTTTATACA-AACTTTTTCTTCTTTGGGGGTAAC
                </sequence>
                <sequence>
                        <taxon idref="Japanese"/>

TACATCTTTTCGTGTGCCTCTCGCAGTTCGTGTATACTCTTCTTCAAAACGCTACCCAATTCACCC
CCTTTTCCCCACGTCGAGATAATCACTTCCTCTTCTGTATGTCCTATGTCATTAGTATCCGTTTCC
GAATCCTCTTAATCCGTAACTTTTTGTTCCTTGGGGGTAAC
                </sequence>
                <sequence>
                        <taxon idref="2n28"/>

TACATTTTTTCGTGTGCCTCTCGCAGTTCGTGTATACTCTTCTTCAAAACGCTACCCAATTCACCC
CCCTTTCGCCACGTTGAGATACTCACTCTCTTCTCTCTATGTCCTATGTCATTAGTATCCGTTTCC
GAATCCTCTTTATCCTCACCTTCCTGTTCCTTGGGGGTAAC
                </sequence>
```

```
                <sequence>
                        <taxon idref="2n31"/>

TACATTTTTTCGTGTGCCTCTCGCAGTTCGTGTATACTCTTCTTCAAAACGCTACCCAATTCACCC
CCCTTTCGCCACGTTGAGATAATCACTCTCTTCTCTCTATGTCCTATGTCATTAGTATCCGTTTCC
GAATCCTCTTTATCCTCACCTTCCTGTTCCTTGGGGGTAAC
                </sequence>
                <sequence>
                        <taxon idref="2n38XY"/>

TACATTTTTTCGTGTGCCTCTCGCAGTTCGTGTATACTCTTCTTCAAAACGCTACCCAATTCACCC
CCCTTTCGCCACGTTGAGATAATCACTCTCTTCTCTCTATGTCCTATGTCATTAGTATCCGTTTCC
GAATCCTCTTTATCCTCACCTTCCTGTTCCTTGGGGGTAAC
                </sequence>
                <sequence>
                        <taxon idref="2n38"/>

TACATTTTTTCGTGTGCCTCTCGCAGTTCGTGTATACTCTTCTTCAAAACGCTACCCAATTCACCC
CCCTTTCGCCACGTTGAGATAATCACTCTCTTCTCTCTATGTCCTATGTCATTAGTATCCGTTTCC
GAATCCTCTTTATCCTCACCTTCCTGTTCCTTGGGGGTAAC
                </sequence>
        </alignment>


        <!-- The sequence alignment (each sequence refers to a
taxon above).         -->
        <!-- ntax=13 nchar=172
                  -->
        <alignment id="alignment9" dataType="nucleotide">
                <sequence>
                        <taxon idref="Medaka"/>

GCTCCTATATGCACCATAAATCTACGGAAAGCTAATACCCAATGCATTCCACAATTCATTATAACT
TTTCATCCATTTAGTTAATTGCCTCTTAAAGCCCCACAAAAACTTTTGTTAATAAGTAAACACATC
AAATACCCCCCGCTTA-CCATTCCACTCAAACCGGTCACC
                </sequence>
                <sequence>
                        <taxon idref="Carp"/>

GCATGCACAACCAGAACCACTTCTCACATAGCAATTGAACCCAGAATCCCTAAAATAATCACACCC
GAACACACAATCAAAAAACCTCGGCCCCCAATATCAATATATAAACCAAAGTAAAACGAAACCATC
AAACCAAGTTCAAAACCCAGAAAAAATACAATAAAGAATA
                </sequence>
                <sequence>
                        <taxon idref="Tetraodon"/>

GCTCTACCGATCACACAACCACCCCAATCAACAACCCCCTTCGACACCCAAAAGCACATCCAACCA
ACACACACACCAAGCAGAAGAAAACCTCCAATTTCGCAATAACAACTACAACCAAACAACACCCCA
AAGCACTCCCCATAAC-CAAGCCCAAGAAAACACAACACA
                </sequence>
                <sequence>
                        <taxon idref="Salmon"/>

GCCCATCCATTCACACACCCCCCCCACTAAACAACTTCTTCACAAAACCAAATATACATTAAAAAC
AAACCCCCTCCCAAAAAAACCGACCTAACCATAACTATATCAACTCCAAAACTAATACCAAACCAT
AAGCATCATATAACATCCTTACTGACTAAATAACAAACTA
```

```
                </sequence>
                <sequence>
                        <taxon idref="Rainbow"/>

GCCCACCCATTCAAACACCCTCCCCAATAAACAACTCACTCGCAGAACCCAACAAACGTTGAAACC
AAACTTCCCCCCAACGAAATCGAACAAATAAAAACCCCATAAACTCCAAAACTGATACTAAACGGC
AAACACTATATAACACCTTCATCACCTAAATGACATATTA
                </sequence>
                <sequence>
                        <taxon idref="Zebrafish"/>

GCTTCTATAACCATAACAATTTCACATACAAAAATTTAATCTAAAAACCAGAAACCAACCTTATTC
AAATACATAATCATAAAGTTATAACACCTAAAGTAGTCACTAAAATTAAAATTAAATGGAAATGAC
AAATCAAAATCAGCACTCTTTTAAAATTCTCTAGACATCA
                </sequence>
                <sequence>
                        <taxon idref="Stickleback"/>

GCCCTACCTCCTACACCCCACACCCGTCAAAAGGGTTTTTTACGAACCCTGAAAACCACCTCATAA
CTATTTCTACTAGGAAAAATAAACCTTAACACCAAACCACCTCAACTAAAATTAAACACAAATATA
AAAAATCTATACTTAA-CCCTCTAACCCCCTCACATCTCA
                </sequence>
                <sequence>
                        <taxon idref="Fugu"/>

GCTTTTCCTATCGGATATTATCCACAATAAGCAATCCATTCCAACAACCAAATACTAACCGTATCA
AACCCCATACCCAAACAAGAGATCCACAACATCTAACAATAACACCCACAAAAAAACTATATCGCA
AAACAACCTAAATATT-CAACACCCCCCCATCCAAGCATA
                </sequence>
                <sequence>
                        <taxon idref="Japanese"/>

GCATATCCAAACGAACCGCACTCACAACCAAAGATTAGTTTTTACACCCAATAAAAAACCTAACAA
AAAAATACAATAATAAAAACAAATCAACCATACTCAATAAAACAATTAAAACAACACACAAACGAA
AAAAACACATCACGAAAAGAAATAAAAATCCAAAACAGCA
                </sequence>
                <sequence>
                        <taxon idref="2n28"/>

GTATTTTCAAACCCCGCAATCCCCCAGCCAAATACCCAGTCAAACACCCCAAAGTACATTCAAACA
CATTATACACCCATAAAATTTCACCCCATCATCCAACAATACCAACCACCACTACTCATACTTAAC
AAACCCCCCGCACCATAACCAAACAACACCATAAAACACA
                </sequence>
                <sequence>
                        <taxon idref="2n31"/>

GTATCTTCAAACCCTGCAACCCCCCAGCCAAATACCCAGCCAAACACCCCAAAGTACATCTAAACA
CATTATACACCCATAAAATTTCACCCCATCACCCAACAATACCAACCATCACTACTCATACTTACC
GAACCCCCCGCACCATAAATAAGCACCGCCATAAAAAACA
                </sequence>
                <sequence>
                        <taxon idref="2n38XY"/>

GTACCTCTAGACCCAGTAACCCCCCGCTCAGGTATCCACCCGCACACCCAAGAATACACTTCAGCA
CATCATACACCCATGAAACTCCACCCTACCATCCTTCAATGCCCACCACTATCACTCACACCCAAT
AAACCACTCACATCATAGCCAACCTAAAACACCCAAAACA
```

```
                </sequence>
                <sequence>
                        <taxon idref="2n38"/>

GTACCTCTAGACCCAGTAACCCCCCGCTCAGGTATCCACCCGCACACCCAAGAATACACTTCAGCA
CATCATACACCCATGAAACTCCACCCTACCATCCTTCAATGCCCACCACTATCACTCACACCCAAT
AAACCACTCACATCATAGCCAACCTAAAACACCCAAAACA
                </sequence>
        </alignment>


        <!-- The unique patterns from 1 to end
                -->
        <!-- npatterns=91
                -->
        <patterns id="ATPase.1st.patterns" from="1">
                <alignment idref="alignment1"/>
        </patterns>


        <!-- The unique patterns from 1 to end
                -->
        <!-- npatterns=87
                -->
        <patterns id="ATPase.2nd.patterns" from="1">
                <alignment idref="alignment2"/>
        </patterns>


        <!-- The unique patterns from 1 to end
                -->
        <!-- npatterns=188
                -->
        <patterns id="ATPase.3rd.patterns" from="1">
                <alignment idref="alignment3"/>
        </patterns>


        <!-- The unique patterns from 1 to end
                -->
        <!-- npatterns=18
                -->
        <patterns id="Cytb.1st.patterns" from="1">
                <alignment idref="alignment4"/>
        </patterns>


        <!-- The unique patterns from 1 to end
                -->
        <!-- npatterns=108
                -->
        <patterns id="Cytb.2nd.patterns" from="1">
                <alignment idref="alignment5"/>
        </patterns>
```

```
        <!-- The unique patterns from 1 to end
                  -->
        <!-- npatterns=29
                  -->
        <patterns id="Cytb.3rd.patterns" from="1">
                <alignment idref="alignment6"/>
        </patterns>


        <!-- The unique patterns from 1 to end
                  -->
        <!-- npatterns=95
                  -->
        <patterns id="ND2.1st.patterns" from="1">
                <alignment idref="alignment7"/>
        </patterns>


        <!-- The unique patterns from 1 to end
                  -->
        <!-- npatterns=51
                  -->
        <patterns id="ND2.2nd.patterns" from="1">
                <alignment idref="alignment8"/>
        </patterns>


        <!-- The unique patterns from 1 to end
                  -->
        <!-- npatterns=162
                  -->
        <patterns id="ND2.3rd.patterns" from="1">
                <alignment idref="alignment9"/>
        </patterns>

        <!-- A prior assumption that the population size has
remained constant       -->
        <!-- throughout the time spanned by the genealogy.
                  -->
        <constantSize id="constant" units="substitutions">
                <populationSize>
                        <parameter id="constant.popSize"
value="26.0" lower="0.0" upper="400.0"/>
                </populationSize>
        </constantSize>

        <!-- Generate a random starting tree under the coalescent
process            -->
        <!-- Has calibration
                  -->
        <coalescentTree id="startingTree">
                <constrainedTaxa>
                        <taxa idref="taxa"/>
                        <tmrca monophyletic="true">
                                <taxa idref="28_31"/>
                        </tmrca>
```

```
                        <tmrca monophyletic="true">
                                <taxa idref="38_38XY"/>
                        </tmrca>
                        <tmrca monophyletic="true">
                                <taxa idref="Clupeocephala"/>
                                <uniformDistributionModel>
                                        <lower>149.85</lower>
                                        <upper>165.2</upper>
                                </uniformDistributionModel>
                        </tmrca>
                        <tmrca monophyletic="true">
                                <taxa idref="Fugus"/>
                                <uniformDistributionModel>
                                        <lower>32.5</lower>
                                        <upper>56.0</upper>
                                </uniformDistributionModel>
                        </tmrca>
                        <tmrca monophyletic="false">
                                <taxa idref="Medaka_Fugus"/>
                                <uniformDistributionModel>
                                        <lower>96.9</lower>
                                        <upper>150.9</upper>
                                </uniformDistributionModel>
                        </tmrca>
                        <tmrca monophyletic="false">
                                <taxa idref="Eigenmannias"/>
                        </tmrca>
                </constrainedTaxa>
                <constantSize idref="constant"/>
        </coalescentTree>

        <!-- Generate a tree model
                  -->
        <treeModel id="treeModel">
                <coalescentTree idref="startingTree"/>
                <rootHeight>
                        <parameter id="treeModel.rootHeight"/>
                </rootHeight>
                <nodeHeights internalNodes="true">
                        <parameter
id="treeModel.internalNodeHeights"/>
                </nodeHeights>
                <nodeHeights internalNodes="true" rootNode="true">
                        <parameter
id="treeModel.allInternalNodeHeights"/>
                </nodeHeights>
        </treeModel>

        <!-- Generate a coalescent likelihood
                  -->
        <coalescentLikelihood id="coalescent">
                <model>
                        <constantSize idref="constant"/>
                </model>
                <populationTree>
                        <treeModel idref="treeModel"/>
```

```
                </populationTree>
        </coalescentLikelihood>

        <!-- The uncorrelated relaxed clock (Drummond, Ho,
Phillips & Rambaut, 2006) -->
        <discretizedBranchRates id="branchRates">
                <treeModel idref="treeModel"/>
                <distribution>
                        <logNormalDistributionModel
meanInRealSpace="true">
                                <mean>
                                        <parameter id="ucld.mean"
value="0.014" lower="0.0" upper="100.0"/>
                                </mean>
                                <stdev>
                                        <parameter id="ucld.stdev"
value="0.1" lower="0.0" upper="10.0"/>
                                </stdev>
                        </logNormalDistributionModel>
                </distribution>
                <rateCategories>
                        <parameter id="branchRates.categories"
dimension="24"/>
                </rateCategories>
        </discretizedBranchRates>

        <rateStatistic id="meanRate" name="meanRate" mode="mean"
internal="true" external="true">
                <treeModel idref="treeModel"/>
                <discretizedBranchRates idref="branchRates"/>
        </rateStatistic>

        <rateStatistic id="coefficientOfVariation"
name="coefficientOfVariation" mode="coefficientOfVariation"
internal="true" external="true">
                <treeModel idref="treeModel"/>
                <discretizedBranchRates idref="branchRates"/>
        </rateStatistic>

        <rateCovarianceStatistic id="covariance"
name="covariance">
                <treeModel idref="treeModel"/>
                <discretizedBranchRates idref="branchRates"/>
        </rateCovarianceStatistic>

        <!-- The HKY substitution model (Hasegawa, Kishino & Yano,
1985)             -->
        <HKYModel id="ATPase.1st.hky">
                <frequencies>
                        <frequencyModel dataType="nucleotide">
                                <frequencies>
                                        <parameter
id="ATPase.1st.frequencies" value="0.25 0.25 0.25 0.25"/>
                                </frequencies>
                        </frequencyModel>
                </frequencies>
```

```
                <kappa>
                        <parameter id="ATPase.1st.kappa" 
value="1.0" lower="1.0E-8" upper="100.0"/>
                </kappa>
        </HKYModel>

        <!-- The general time reversible (GTR) substitution model 
                  -->
        <gtrModel id="ATPase.2nd.gtr">
                <frequencies>
                        <frequencyModel dataType="nucleotide">
                                <frequencies>
                                        <parameter 
id="ATPase.2nd.frequencies" value="0.25 0.25 0.25 0.25"/>
                                </frequencies>
                        </frequencyModel>
                </frequencies>
                <rateAC>
                        <parameter id="ATPase.2nd.ac" value="1.0" 
lower="1.0E-8" upper="100.0"/>
                </rateAC>
                <rateAG>
                        <parameter id="ATPase.2nd.ag" value="1.0" 
lower="1.0E-8" upper="100.0"/>
                </rateAG>
                <rateAT>
                        <parameter id="ATPase.2nd.at" value="1.0" 
lower="1.0E-8" upper="100.0"/>
                </rateAT>
                <rateCG>
                        <parameter id="ATPase.2nd.cg" value="1.0" 
lower="1.0E-8" upper="100.0"/>
                </rateCG>
                <rateGT>
                        <parameter id="ATPase.2nd.gt" value="1.0" 
lower="1.0E-8" upper="100.0"/>
                </rateGT>
        </gtrModel>

        <!-- The HKY substitution model (Hasegawa, Kishino & Yano, 
1985)             -->
        <HKYModel id="ATPase.3rd.hky">
                <frequencies>
                        <frequencyModel dataType="nucleotide">
                                <frequencies>
                                        <parameter 
id="ATPase.3rd.frequencies" value="0.25 0.25 0.25 0.25"/>
                                </frequencies>
                        </frequencyModel>
                </frequencies>
                <kappa>
                        <parameter id="ATPase.3rd.kappa" 
value="1.0" lower="1.0E-8" upper="100.0"/>
                </kappa>
        </HKYModel>
```

```
        <!-- The HKY substitution model (Hasegawa, Kishino & Yano,
1985)             -->
        <HKYModel id="Cytb.1st.hky">
                <frequencies>
                        <frequencyModel dataType="nucleotide">
                                <frequencies>
                                        <parameter
id="Cytb.1st.frequencies" value="0.25 0.25 0.25 0.25"/>
                                </frequencies>
                        </frequencyModel>
                </frequencies>
                <kappa>
                        <parameter id="Cytb.1st.kappa" value="1.0"
lower="1.0E-8" upper="100.0"/>
                </kappa>
        </HKYModel>

        <!-- The general time reversible (GTR) substitution model
                  -->
        <gtrModel id="Cytb.2nd.gtr">
                <frequencies>
                        <frequencyModel dataType="nucleotide">
                                <frequencies>
                                        <parameter
id="Cytb.2nd.frequencies" value="0.25 0.25 0.25 0.25"/>
                                </frequencies>
                        </frequencyModel>
                </frequencies>
                <rateAC>
                        <parameter id="Cytb.2nd.ac" value="1.0"
lower="1.0E-8" upper="100.0"/>
                </rateAC>
                <rateAG>
                        <parameter id="Cytb.2nd.ag" value="1.0"
lower="1.0E-8" upper="100.0"/>
                </rateAG>
                <rateAT>
                        <parameter id="Cytb.2nd.at" value="1.0"
lower="1.0E-8" upper="100.0"/>
                </rateAT>
                <rateCG>
                        <parameter id="Cytb.2nd.cg" value="1.0"
lower="1.0E-8" upper="100.0"/>
                </rateCG>
                <rateGT>
                        <parameter id="Cytb.2nd.gt" value="1.0"
lower="1.0E-8" upper="100.0"/>
                </rateGT>
        </gtrModel>

        <!-- The HKY substitution model (Hasegawa, Kishino & Yano,
1985)             -->
        <HKYModel id="Cytb.3rd.hky">
                <frequencies>
                        <frequencyModel dataType="nucleotide">
                                <frequencies>
```

```xml
                                        <parameter
id="Cytb.3rd.frequencies" value="0.25 0.25 0.25 0.25"/>
                                </frequencies>
                        </frequencyModel>
                </frequencies>
                <kappa>
                        <parameter id="Cytb.3rd.kappa" value="1.0"
lower="1.0E-8" upper="100.0"/>
                </kappa>
        </HKYModel>

        <!-- The general time reversible (GTR) substitution model
                  -->
        <gtrModel id="ND2.1st.gtr">
                <frequencies>
                        <frequencyModel dataType="nucleotide">
                                <frequencies>
                                        <parameter
id="ND2.1st.frequencies" value="0.25 0.25 0.25 0.25"/>
                                </frequencies>
                        </frequencyModel>
                </frequencies>
                <rateAC>
                        <parameter id="ND2.1st.ac" value="1.0"
lower="1.0E-8" upper="100.0"/>
                </rateAC>
                <rateAG>
                        <parameter id="ND2.1st.ag" value="1.0"
lower="1.0E-8" upper="100.0"/>
                </rateAG>
                <rateAT>
                        <parameter id="ND2.1st.at" value="1.0"
lower="1.0E-8" upper="100.0"/>
                </rateAT>
                <rateCG>
                        <parameter id="ND2.1st.cg" value="1.0"
lower="1.0E-8" upper="100.0"/>
                </rateCG>
                <rateGT>
                        <parameter id="ND2.1st.gt" value="1.0"
lower="1.0E-8" upper="100.0"/>
                </rateGT>
        </gtrModel>

        <!-- The general time reversible (GTR) substitution model
                  -->
        <gtrModel id="ND2.2nd.gtr">
                <frequencies>
                        <frequencyModel dataType="nucleotide">
                                <frequencies>
                                        <parameter
id="ND2.2nd.frequencies" value="0.25 0.25 0.25 0.25"/>
                                </frequencies>
                        </frequencyModel>
                </frequencies>
                <rateAC>
```

```
                        <parameter id="ND2.2nd.ac" value="1.0" 
lower="1.0E-8" upper="100.0"/>
                </rateAC>
                <rateAG>
                        <parameter id="ND2.2nd.ag" value="1.0" 
lower="1.0E-8" upper="100.0"/>
                </rateAG>
                <rateAT>
                        <parameter id="ND2.2nd.at" value="1.0" 
lower="1.0E-8" upper="100.0"/>
                </rateAT>
                <rateCG>
                        <parameter id="ND2.2nd.cg" value="1.0" 
lower="1.0E-8" upper="100.0"/>
                </rateCG>
                <rateGT>
                        <parameter id="ND2.2nd.gt" value="1.0" 
lower="1.0E-8" upper="100.0"/>
                </rateGT>
        </gtrModel>

        <!-- The HKY substitution model (Hasegawa, Kishino & Yano, 
1985)           -->
        <HKYModel id="ND2.3rd.hky">
                <frequencies>
                        <frequencyModel dataType="nucleotide">
                                <frequencies>
                                        <parameter 
id="ND2.3rd.frequencies" value="0.25 0.25 0.25 0.25"/>
                                </frequencies>
                        </frequencyModel>
                </frequencies>
                <kappa>
                        <parameter id="ND2.3rd.kappa" value="1.0" 
lower="1.0E-8" upper="100.0"/>
                </kappa>
        </HKYModel>

        <!-- site model
                  -->
        <siteModel id="ATPase.1st.siteModel">
                <substitutionModel>
                        <HKYModel idref="ATPase.1st.hky"/>
                </substitutionModel>
                <gammaShape gammaCategories="4">
                        <parameter id="ATPase.1st.alpha" 
value="0.5" lower="0.0" upper="100.0"/>
                </gammaShape>
        </siteModel>

        <!-- site model
                  -->
        <siteModel id="ATPase.2nd.siteModel">
                <substitutionModel>
                        <gtrModel idref="ATPase.2nd.gtr"/>
                </substitutionModel>
```

```
                <gammaShape gammaCategories="4">
                        <parameter id="ATPase.2nd.alpha" 
value="0.5" lower="0.0" upper="100.0"/>
                </gammaShape>
        </siteModel>

        <!-- site model 
                  -->
        <siteModel id="ATPase.3rd.siteModel">
                <substitutionModel>
                        <HKYModel idref="ATPase.3rd.hky"/>
                </substitutionModel>
                <gammaShape gammaCategories="4">
                        <parameter id="ATPase.3rd.alpha" 
value="0.5" lower="0.0" upper="100.0"/>
                </gammaShape>
                <proportionInvariant>
                        <parameter id="ATPase.3rd.pInv" 
value="0.5" lower="0.0" upper="1.0"/>
                </proportionInvariant>
        </siteModel>

        <!-- site model 
                  -->
        <siteModel id="Cytb.1st.siteModel">
                <substitutionModel>
                        <HKYModel idref="Cytb.1st.hky"/>
                </substitutionModel>
                <proportionInvariant>
                        <parameter id="Cytb.1st.pInv" value="0.5" 
lower="0.0" upper="1.0"/>
                </proportionInvariant>
        </siteModel>

        <!-- site model 
                  -->
        <siteModel id="Cytb.2nd.siteModel">
                <substitutionModel>
                        <gtrModel idref="Cytb.2nd.gtr"/>
                </substitutionModel>
                <gammaShape gammaCategories="4">
                        <parameter id="Cytb.2nd.alpha" value="0.5" 
lower="0.0" upper="100.0"/>
                </gammaShape>
                <proportionInvariant>
                        <parameter id="Cytb.2nd.pInv" value="0.5" 
lower="0.0" upper="1.0"/>
                </proportionInvariant>
        </siteModel>

        <!-- site model 
                  -->
        <siteModel id="Cytb.3rd.siteModel">
                <substitutionModel>
                        <HKYModel idref="Cytb.3rd.hky"/>
                </substitutionModel>
```

```
                <gammaShape gammaCategories="4">
                        <parameter id="Cytb.3rd.alpha" value="0.5"
lower="0.0" upper="100.0"/>
                </gammaShape>
        </siteModel>

        <!-- site model
                  -->
        <siteModel id="ND2.1st.siteModel">
                <substitutionModel>
                        <gtrModel idref="ND2.1st.gtr"/>
                </substitutionModel>
                <gammaShape gammaCategories="4">
                        <parameter id="ND2.1st.alpha" value="0.5"
lower="0.0" upper="100.0"/>
                </gammaShape>
        </siteModel>

        <!-- site model
                  -->
        <siteModel id="ND2.2nd.siteModel">
                <substitutionModel>
                        <gtrModel idref="ND2.2nd.gtr"/>
                </substitutionModel>
                <proportionInvariant>
                        <parameter id="ND2.2nd.pInv" value="0.5"
lower="0.0" upper="1.0"/>
                </proportionInvariant>
        </siteModel>

        <!-- site model
                  -->
        <siteModel id="ND2.3rd.siteModel">
                <substitutionModel>
                        <HKYModel idref="ND2.3rd.hky"/>
                </substitutionModel>
                <gammaShape gammaCategories="4">
                        <parameter id="ND2.3rd.alpha" value="0.5"
lower="0.0" upper="100.0"/>
                </gammaShape>
                <proportionInvariant>
                        <parameter id="ND2.3rd.pInv" value="0.5"
lower="0.0" upper="1.0"/>
                </proportionInvariant>
        </siteModel>

        <treeLikelihood id="ATPase.1st.ATPase.1st.treeLikelihood"
useAmbiguities="false">
                <patterns idref="ATPase.1st.patterns"/>
                <treeModel idref="treeModel"/>
                <siteModel idref="ATPase.1st.siteModel"/>
                <discretizedBranchRates idref="branchRates"/>
        </treeLikelihood>

        <treeLikelihood id="ATPase.2nd.ATPase.2nd.treeLikelihood"
useAmbiguities="false">
```

```
                <patterns idref="ATPase.2nd.patterns"/>
                <treeModel idref="treeModel"/>
                <siteModel idref="ATPase.2nd.siteModel"/>
                <discretizedBranchRates idref="branchRates"/>
        </treeLikelihood>

        <treeLikelihood id="ATPase.3rd.ATPase.3rd.treeLikelihood"
useAmbiguities="false">
                <patterns idref="ATPase.3rd.patterns"/>
                <treeModel idref="treeModel"/>
                <siteModel idref="ATPase.3rd.siteModel"/>
                <discretizedBranchRates idref="branchRates"/>
        </treeLikelihood>

        <treeLikelihood id="Cytb.1st.Cytb.1st.treeLikelihood"
useAmbiguities="false">
                <patterns idref="Cytb.1st.patterns"/>
                <treeModel idref="treeModel"/>
                <siteModel idref="Cytb.1st.siteModel"/>
                <discretizedBranchRates idref="branchRates"/>
        </treeLikelihood>

        <treeLikelihood id="Cytb.2nd.Cytb.2nd.treeLikelihood"
useAmbiguities="false">
                <patterns idref="Cytb.2nd.patterns"/>
                <treeModel idref="treeModel"/>
                <siteModel idref="Cytb.2nd.siteModel"/>
                <discretizedBranchRates idref="branchRates"/>
        </treeLikelihood>

        <treeLikelihood id="Cytb.3rd.Cytb.3rd.treeLikelihood"
useAmbiguities="false">
                <patterns idref="Cytb.3rd.patterns"/>
                <treeModel idref="treeModel"/>
                <siteModel idref="Cytb.3rd.siteModel"/>
                <discretizedBranchRates idref="branchRates"/>
        </treeLikelihood>

        <treeLikelihood id="ND2.1st.ND2.1st.treeLikelihood"
useAmbiguities="false">
                <patterns idref="ND2.1st.patterns"/>
                <treeModel idref="treeModel"/>
                <siteModel idref="ND2.1st.siteModel"/>
                <discretizedBranchRates idref="branchRates"/>
        </treeLikelihood>

        <treeLikelihood id="ND2.2nd.ND2.2nd.treeLikelihood"
useAmbiguities="false">
                <patterns idref="ND2.2nd.patterns"/>
                <treeModel idref="treeModel"/>
                <siteModel idref="ND2.2nd.siteModel"/>
                <discretizedBranchRates idref="branchRates"/>
        </treeLikelihood>

        <treeLikelihood id="ND2.3rd.ND2.3rd.treeLikelihood"
useAmbiguities="false">
```

```
                <patterns idref="ND2.3rd.patterns"/>
                <treeModel idref="treeModel"/>
                <siteModel idref="ND2.3rd.siteModel"/>
                <discretizedBranchRates idref="branchRates"/>
        </treeLikelihood>


        <tmrcaStatistic id="tmrca(28_31)">
                <mrca>
                        <taxa idref="28_31"/>
                </mrca>
                <treeModel idref="treeModel"/>
        </tmrcaStatistic>
        <monophylyStatistic id="monophyly(28_31)">
                <mrca>
                        <taxa idref="28_31"/>
                </mrca>
                <treeModel idref="treeModel"/>
        </monophylyStatistic>
        <tmrcaStatistic id="tmrca(38_38XY)">
                <mrca>
                        <taxa idref="38_38XY"/>
                </mrca>
                <treeModel idref="treeModel"/>
        </tmrcaStatistic>
        <monophylyStatistic id="monophyly(38_38XY)">
                <mrca>
                        <taxa idref="38_38XY"/>
                </mrca>
                <treeModel idref="treeModel"/>
        </monophylyStatistic>
        <tmrcaStatistic id="tmrca(Clupeocephala)">
                <mrca>
                        <taxa idref="Clupeocephala"/>
                </mrca>
                <treeModel idref="treeModel"/>
        </tmrcaStatistic>
        <monophylyStatistic id="monophyly(Clupeocephala)">
                <mrca>
                        <taxa idref="Clupeocephala"/>
                </mrca>
                <treeModel idref="treeModel"/>
        </monophylyStatistic>
        <tmrcaStatistic id="tmrca(Fugus)">
                <mrca>
                        <taxa idref="Fugus"/>
                </mrca>
                <treeModel idref="treeModel"/>
        </tmrcaStatistic>
        <monophylyStatistic id="monophyly(Fugus)">
                <mrca>
                        <taxa idref="Fugus"/>
                </mrca>
                <treeModel idref="treeModel"/>
        </monophylyStatistic>
        <tmrcaStatistic id="tmrca(Medaka_Fugus)">
```

```
                <mrca>
                        <taxa idref="Medaka_Fugus"/>
                </mrca>
                <treeModel idref="treeModel"/>
        </tmrcaStatistic>
        <tmrcaStatistic id="tmrca(Eigenmannias)">
                <mrca>
                        <taxa idref="Eigenmannias"/>
                </mrca>
                <treeModel idref="treeModel"/>
        </tmrcaStatistic>
        <!-- Define operators
                  -->
        <operators id="operators">
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ATPase.1st.kappa"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ATPase.1st.alpha"/>
                </scaleOperator>
                <deltaExchange delta="0.01" weight="1">
                        <parameter
idref="ATPase.1st.frequencies"/>
                </deltaExchange>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ATPase.2nd.ac"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ATPase.2nd.ag"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ATPase.2nd.at"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ATPase.2nd.cg"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ATPase.2nd.gt"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ATPase.2nd.alpha"/>
                </scaleOperator>
                <deltaExchange delta="0.01" weight="1">
                        <parameter
idref="ATPase.2nd.frequencies"/>
                </deltaExchange>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ATPase.3rd.kappa"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ATPase.3rd.alpha"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ATPase.3rd.pInv"/>
                </scaleOperator>
                <deltaExchange delta="0.01" weight="1">
```

```
                        <parameter 
idref="ATPase.3rd.frequencies"/>
                </deltaExchange>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="Cytb.1st.kappa"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="Cytb.1st.pInv"/>
                </scaleOperator>
                <deltaExchange delta="0.01" weight="1">
                        <parameter idref="Cytb.1st.frequencies"/>
                </deltaExchange>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="Cytb.2nd.ac"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="Cytb.2nd.ag"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="Cytb.2nd.at"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="Cytb.2nd.cg"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="Cytb.2nd.gt"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="Cytb.2nd.alpha"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="Cytb.2nd.pInv"/>
                </scaleOperator>
                <deltaExchange delta="0.01" weight="1">
                        <parameter idref="Cytb.2nd.frequencies"/>
                </deltaExchange>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="Cytb.3rd.kappa"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="Cytb.3rd.alpha"/>
                </scaleOperator>
                <deltaExchange delta="0.01" weight="1">
                        <parameter idref="Cytb.3rd.frequencies"/>
                </deltaExchange>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ND2.1st.ac"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ND2.1st.ag"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ND2.1st.at"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ND2.1st.cg"/>
```

```
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ND2.1st.gt"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ND2.1st.alpha"/>
                </scaleOperator>
                <deltaExchange delta="0.01" weight="1">
                        <parameter idref="ND2.1st.frequencies"/>
                </deltaExchange>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ND2.2nd.ac"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ND2.2nd.ag"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ND2.2nd.at"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ND2.2nd.cg"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ND2.2nd.gt"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ND2.2nd.pInv"/>
                </scaleOperator>
                <deltaExchange delta="0.01" weight="1">
                        <parameter idref="ND2.2nd.frequencies"/>
                </deltaExchange>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ND2.3rd.kappa"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ND2.3rd.alpha"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="1">
                        <parameter idref="ND2.3rd.pInv"/>
                </scaleOperator>
                <deltaExchange delta="0.01" weight="1">
                        <parameter idref="ND2.3rd.frequencies"/>
                </deltaExchange>
                <scaleOperator scaleFactor="0.75" weight="3">
                        <parameter idref="ucld.mean"/>
                </scaleOperator>
                <scaleOperator scaleFactor="0.75" weight="3">
                        <parameter idref="ucld.stdev"/>
                </scaleOperator>
                <subtreeSlide size="2.6" gaussian="true"
weight="15">
                        <treeModel idref="treeModel"/>
                </subtreeSlide>
                <narrowExchange weight="15">
                        <treeModel idref="treeModel"/>
                </narrowExchange>
```

```
                <wideExchange weight="3">
                        <treeModel idref="treeModel"/>
                </wideExchange>
                <wilsonBalding weight="3">
                        <treeModel idref="treeModel"/>
                </wilsonBalding>
                <scaleOperator scaleFactor="0.75" weight="3">
                        <parameter idref="treeModel.rootHeight"/>
                </scaleOperator>
                <uniformOperator weight="30">
                        <parameter
idref="treeModel.internalNodeHeights"/>
                </uniformOperator>
                <scaleOperator scaleFactor="0.75" weight="3">
                        <parameter idref="constant.popSize"/>
                </scaleOperator>
                <upDownOperator scaleFactor="0.75" weight="3">
                        <up>
                                <parameter idref="ucld.mean"/>
                        </up>
                        <down>
                                <parameter
idref="treeModel.allInternalNodeHeights"/>
                        </down>
                </upDownOperator>
                <swapOperator size="1" weight="10"
autoOptimize="false">
                        <parameter
idref="branchRates.categories"/>
                </swapOperator>
                <randomWalkIntegerOperator windowSize="1"
weight="10">
                        <parameter
idref="branchRates.categories"/>
                </randomWalkIntegerOperator>
                <uniformIntegerOperator weight="10">
                        <parameter
idref="branchRates.categories"/>
                </uniformIntegerOperator>
        </operators>

        <!-- Define MCMC
                     -->
        <mcmc id="mcmc" chainLength="40000000"
autoOptimize="true">
                <posterior id="posterior">
                        <prior id="prior">
                                <booleanLikelihood>
                                        <monophylyStatistic
idref="monophyly(Fugus)"/>
                                        <monophylyStatistic
idref="monophyly(28_31)"/>
                                        <monophylyStatistic
idref="monophyly(38_38XY)"/>
                                        <monophylyStatistic
idref="monophyly(Clupeocephala)"/>
```

```
                                </booleanLikelihood>
                                <uniformPrior lower="149.85"
upper="165.2">
                                        <statistic
idref="tmrca(Clupeocephala)"/>
                                </uniformPrior>
                                <uniformPrior lower="32.5"
upper="56.0">
                                        <statistic
idref="tmrca(Fugus)"/>
                                </uniformPrior>
                                <uniformPrior lower="96.9"
upper="150.9">
                                        <statistic
idref="tmrca(Medaka_Fugus)"/>
                                </uniformPrior>
                                <oneOnXPrior>
                                        <parameter
idref="ATPase.1st.kappa"/>
                                </oneOnXPrior>
                                <oneOnXPrior>
                                        <parameter
idref="ATPase.2nd.ac"/>
                                </oneOnXPrior>
                                <oneOnXPrior>
                                        <parameter
idref="ATPase.2nd.ag"/>
                                </oneOnXPrior>
                                <oneOnXPrior>
                                        <parameter
idref="ATPase.2nd.at"/>
                                </oneOnXPrior>
                                <oneOnXPrior>
                                        <parameter
idref="ATPase.2nd.cg"/>
                                </oneOnXPrior>
                                <oneOnXPrior>
                                        <parameter
idref="ATPase.2nd.gt"/>
                                </oneOnXPrior>
                                <oneOnXPrior>
                                        <parameter
idref="ATPase.3rd.kappa"/>
                                </oneOnXPrior>
                                <oneOnXPrior>
                                        <parameter
idref="Cytb.1st.kappa"/>
                                </oneOnXPrior>
                                <oneOnXPrior>
                                        <parameter
idref="Cytb.2nd.ac"/>
                                </oneOnXPrior>
                                <oneOnXPrior>
                                        <parameter
idref="Cytb.2nd.ag"/>
                                </oneOnXPrior>
```

```
				<oneOnXPrior>
					<parameter
idref="Cytb.2nd.at"/>
				</oneOnXPrior>
				<oneOnXPrior>
					<parameter
idref="Cytb.2nd.cg"/>
				</oneOnXPrior>
				<oneOnXPrior>
					<parameter
idref="Cytb.2nd.gt"/>
				</oneOnXPrior>
				<oneOnXPrior>
					<parameter
idref="Cytb.3rd.kappa"/>
				</oneOnXPrior>
				<oneOnXPrior>
					<parameter
idref="ND2.1st.ac"/>
				</oneOnXPrior>
				<oneOnXPrior>
					<parameter
idref="ND2.1st.ag"/>
				</oneOnXPrior>
				<oneOnXPrior>
					<parameter
idref="ND2.1st.at"/>
				</oneOnXPrior>
				<oneOnXPrior>
					<parameter
idref="ND2.1st.cg"/>
				</oneOnXPrior>
				<oneOnXPrior>
					<parameter
idref="ND2.1st.gt"/>
				</oneOnXPrior>
				<oneOnXPrior>
					<parameter
idref="ND2.2nd.ac"/>
				</oneOnXPrior>
				<oneOnXPrior>
					<parameter
idref="ND2.2nd.ag"/>
				</oneOnXPrior>
				<oneOnXPrior>
					<parameter
idref="ND2.2nd.at"/>
				</oneOnXPrior>
				<oneOnXPrior>
					<parameter
idref="ND2.2nd.cg"/>
				</oneOnXPrior>
				<oneOnXPrior>
					<parameter
idref="ND2.2nd.gt"/>
				</oneOnXPrior>
```

```
                <oneOnXPrior>
                    <parameter
idref="ND2.3rd.kappa"/>
                </oneOnXPrior>
                <oneOnXPrior>
                    <parameter
idref="constant.popSize"/>
                </oneOnXPrior>
                <coalescentLikelihood
idref="coalescent"/>

            </prior>
            <likelihood id="likelihood">
                <treeLikelihood
idref="ATPase.1st.ATPase.1st.treeLikelihood"/>
                <treeLikelihood
idref="ATPase.2nd.ATPase.2nd.treeLikelihood"/>
                <treeLikelihood
idref="ATPase.3rd.ATPase.3rd.treeLikelihood"/>
                <treeLikelihood
idref="Cytb.1st.Cytb.1st.treeLikelihood"/>
                <treeLikelihood
idref="Cytb.2nd.Cytb.2nd.treeLikelihood"/>
                <treeLikelihood
idref="Cytb.3rd.Cytb.3rd.treeLikelihood"/>
                <treeLikelihood
idref="ND2.1st.ND2.1st.treeLikelihood"/>
                <treeLikelihood
idref="ND2.2nd.ND2.2nd.treeLikelihood"/>
                <treeLikelihood
idref="ND2.3rd.ND2.3rd.treeLikelihood"/>
            </likelihood>
        </posterior>
        <operators idref="operators"/>
        <!-- write log to screen
              -->
        <log id="screenLog" logEvery="1000">
            <column label="Posterior" dp="4"
width="12">
                <posterior idref="posterior"/>
            </column>
            <column label="Prior" dp="4" width="12">
                <prior idref="prior"/>
            </column>
            <column label="Likelihood" dp="4"
width="12">
                <likelihood idref="likelihood"/>
            </column>
            <column label="rootHeight" sf="6"
width="12">
                <parameter
idref="treeModel.rootHeight"/>
            </column>
            <column label="ucld.mean" sf="6"
width="12">
                <parameter idref="ucld.mean"/>
```

```
                        </column>
                </log>
                <!-- write log to file
                          -->
                <log id="fileLog" logEvery="1000"
fileName="Codon.NoEigen.4x.log">
                        <posterior idref="posterior"/>
                        <prior idref="prior"/>
                        <likelihood idref="likelihood"/>
                        <parameter idref="treeModel.rootHeight"/>
                        <tmrcaStatistic idref="tmrca(28_31)"/>
                        <tmrcaStatistic idref="tmrca(38_38XY)"/>
                        <tmrcaStatistic
idref="tmrca(Clupeocephala)"/>
                        <tmrcaStatistic idref="tmrca(Fugus)"/>
                        <tmrcaStatistic
idref="tmrca(Medaka_Fugus)"/>
                        <tmrcaStatistic
idref="tmrca(Eigenmannias)"/>
                        <parameter idref="constant.popSize"/>
                        <parameter idref="ATPase.1st.kappa"/>
                        <parameter
idref="ATPase.1st.frequencies"/>
                        <parameter idref="ATPase.1st.alpha"/>
                        <parameter idref="ATPase.2nd.ac"/>
                        <parameter idref="ATPase.2nd.ag"/>
                        <parameter idref="ATPase.2nd.at"/>
                        <parameter idref="ATPase.2nd.cg"/>
                        <parameter idref="ATPase.2nd.gt"/>
                        <parameter
idref="ATPase.2nd.frequencies"/>
                        <parameter idref="ATPase.2nd.alpha"/>
                        <parameter idref="ATPase.3rd.kappa"/>
                        <parameter
idref="ATPase.3rd.frequencies"/>
                        <parameter idref="ATPase.3rd.alpha"/>
                        <parameter idref="ATPase.3rd.pInv"/>
                        <parameter idref="Cytb.1st.kappa"/>
                        <parameter idref="Cytb.1st.frequencies"/>
                        <parameter idref="Cytb.1st.pInv"/>
                        <parameter idref="Cytb.2nd.ac"/>
                        <parameter idref="Cytb.2nd.ag"/>
                        <parameter idref="Cytb.2nd.at"/>
                        <parameter idref="Cytb.2nd.cg"/>
                        <parameter idref="Cytb.2nd.gt"/>
                        <parameter idref="Cytb.2nd.frequencies"/>
                        <parameter idref="Cytb.2nd.alpha"/>
                        <parameter idref="Cytb.2nd.pInv"/>
                        <parameter idref="Cytb.3rd.kappa"/>
                        <parameter idref="Cytb.3rd.frequencies"/>
                        <parameter idref="Cytb.3rd.alpha"/>
                        <parameter idref="ND2.1st.ac"/>
                        <parameter idref="ND2.1st.ag"/>
                        <parameter idref="ND2.1st.at"/>
                        <parameter idref="ND2.1st.cg"/>
                        <parameter idref="ND2.1st.gt"/>
```

```
                        <parameter idref="ND2.1st.frequencies"/>
                        <parameter idref="ND2.1st.alpha"/>
                        <parameter idref="ND2.2nd.ac"/>
                        <parameter idref="ND2.2nd.ag"/>
                        <parameter idref="ND2.2nd.at"/>
                        <parameter idref="ND2.2nd.cg"/>
                        <parameter idref="ND2.2nd.gt"/>
                        <parameter idref="ND2.2nd.frequencies"/>
                        <parameter idref="ND2.2nd.pInv"/>
                        <parameter idref="ND2.3rd.kappa"/>
                        <parameter idref="ND2.3rd.frequencies"/>
                        <parameter idref="ND2.3rd.alpha"/>
                        <parameter idref="ND2.3rd.pInv"/>
                        <parameter idref="ucld.mean"/>
                        <parameter idref="ucld.stdev"/>
                        <rateStatistic idref="meanRate"/>
                        <rateStatistic
idref="coefficientOfVariation"/>
                        <rateCovarianceStatistic
idref="covariance"/>
                        <treeLikelihood
idref="ATPase.1st.ATPase.1st.treeLikelihood"/>
                        <treeLikelihood
idref="ATPase.2nd.ATPase.2nd.treeLikelihood"/>
                        <treeLikelihood
idref="ATPase.3rd.ATPase.3rd.treeLikelihood"/>
                        <treeLikelihood
idref="Cytb.1st.Cytb.1st.treeLikelihood"/>
                        <treeLikelihood
idref="Cytb.2nd.Cytb.2nd.treeLikelihood"/>
                        <treeLikelihood
idref="Cytb.3rd.Cytb.3rd.treeLikelihood"/>
                        <treeLikelihood
idref="ND2.1st.ND2.1st.treeLikelihood"/>
                        <treeLikelihood
idref="ND2.2nd.ND2.2nd.treeLikelihood"/>
                        <treeLikelihood
idref="ND2.3rd.ND2.3rd.treeLikelihood"/>
                        <coalescentLikelihood idref="coalescent"/>

                </log>
                <!-- write tree log to file
                          -->
                <logTree id="treeFileLog" logEvery="1000"
nexusFormat="true" fileName="Codon.NoEigen.trees"
sortTranslationTable="true">
                        <treeModel idref="treeModel"/>
                        <discretizedBranchRates
idref="branchRates"/>
                        <posterior idref="posterior"/>
                </logTree>
        </mcmc>

        <report>
                <property name="timer">
                        <mcmc idref="mcmc"/>
```

```
                </property>
        </report>

</beast>
```