

Supporting Information - Data S1

Individual exon-1 alignments, trees and RRTs

Data used for individual relative rate tests. Alignments of exon-1 Hox sequences were made using ClustalW2 and manually edited to remove gaps and maximize homology. Neighbor-Joining trees were generated (1,000 bootstrap replications) and Tajima RRTs were conducted using the aligned sequences. A graphical summary of these data is given in Fig. 5A and B in the main text.

HoxA1 alignment for relative rate tests.

```

Mm\A1      MNSFLEYPIILGGDSGTCSARAYPSDHGITTFQSCAVSANS SCGGDDRFLV
Hs\A1      MNSFLEYPIILSGDSGTCSARAYPSDHRIITTFQSCAVSANS SCGGDDRFLV
Lm\A1      MSSFLDYPIINGDTGTCCSRAYIPDHGITTFQSCAVTTNSCAGDDRFLV
Hf\A1      MNSFLDYSIINGETGTCCSRYSYHADQGITTYQSCAVSNNNCNADDRIYV
Dr\A1a     MSTFLDFSSISGSGGSCSVRAFHGHDHGLSTFQSCAVRLNSCSGDERFMS

Mm\A1      GRGVQISSPYQTSGNLGISYSHSSCGAQNFSA PYGPY
Hs\A1      GRGVQIGSPYQTSGNLGVSYSHSSCGSQNFSA PYSPYA
Lm\A1      GRGVHIGPPYQHNNLGIAYSHPSCGTQSFSTGYNHYS
Hf\A1      SRSVQIGAPYTHPNNLGIYSHPNCGAQSFNTGYSHYS
Dr\A1a     NISSQDVINYQSPGTLSTITYSHPSYGTQSFCTGYNHYA

Mm\A1      LNQEADVSGGYPPCAPAVYSGNLSTGYAGTVGSPQYIHHSYGQE
Hs\A1      LNQEADVSGGYPQCAPAVYSGNLSSGYAGAVGSPQYIHHSYGQE
Lm\A1      LNQDIEASGGYSQCAPAVYSGNLSSGFGGTMGPSQCIHHPYGSE
Hf\A1      LNQETDGNNGGYPQCAPAVYPGNIASSYGGMVGSGQYPHHPYGQE
Dr\A1a     LNQDVESVSVFPQCGPLVYSGNIISSGYSSNVHLHQYGSATYGSD

Mm\A1      QQTLALATYNNLSLPLHASHQEACRSPAETSSPAQTFDWMKVKRNP PKT
Hs\A1      HQSLALATYNNLSLPLHASHQEACRSPAETSSPAQTFDWMKVKRNP PKT
Lm\A1      QQNLSLAGCSNTLSPLLSGHQEDCRSPAEESSQAQTFDWMKVKRNP PKT
Hf\A1      QQGLALAAGCHSLSPVHGSHQEACCS PSETPPPAQTFDWMKVKRNP PKT
Dr\A1a     QANLTFVACSNPLSPLHVP HHDACCSPLDGVPTGQTFDWMKVKRNP PKT

```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxa1

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0.876	
Hf	Lm	DrA1a	0	**
Hf	Hs	DrA1a	0	**

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxa2 alignment for relative rate test

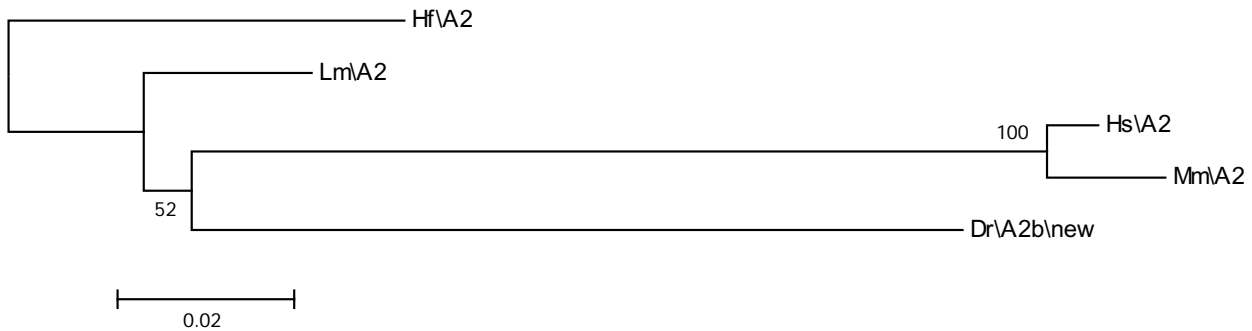
```

Hs \A2      MNYEFEREIGFINSQPSLAECLTSFPPVADTFQSSSIKTSTLSHSTLIPPPFEQTIPSLN
Mm \A2      MNYEFEREIGFINSQPSLAECLTSFPPVADTFQSSSIKTSTLSHSTLIPPPFEQTIPSLN
Lm \A2      MNYEFEREIGFINSQPSLAECLTSFPPVGDTFQSSSIKNSTLSHSTLIPPPFEQTIPSLN
Hf \A2      MNYEFEREIGFINSQPSLAECLTSFPPVGDTFQSSSIKNSTLSHSTVIIPPPFEQTIPSLN
Dr \A2b     MNYEFERETGFINSQPSLAECLTSFPPVGDADFQSSSIKSSTLSHSTLIPPPFEQTIPSLN
  
```

```

Hs \A2      PGSHPRHGPKPSAPAGSSPVPAGALPPEYPWMKEKKAAKKTCLSHK
Mm \A2      PGSHPRHGPKSSAPAGSSPVPAGALPPEYPWMKEKKAAKKTCLGHK
Lm \A2      PGSHPRHSPKQSPNGSSPLPAAALPPEYPWMKEKKTSKKNCFDQK
Hf \A2      PSSHPRQSPKQSPNGTSPPLPAATLPPEYPWMKEKKNKKNCLSQK
Dr \A2b     PGSHPRHSPKQNPNGSCPLPAASLPPEYPWMKEKKASKKNYFSPQ
  
```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxa2

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0.021	*
Hf	Lm	DrA2b	0.02	*
Hf	Hs	DrA2b	0.796	

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

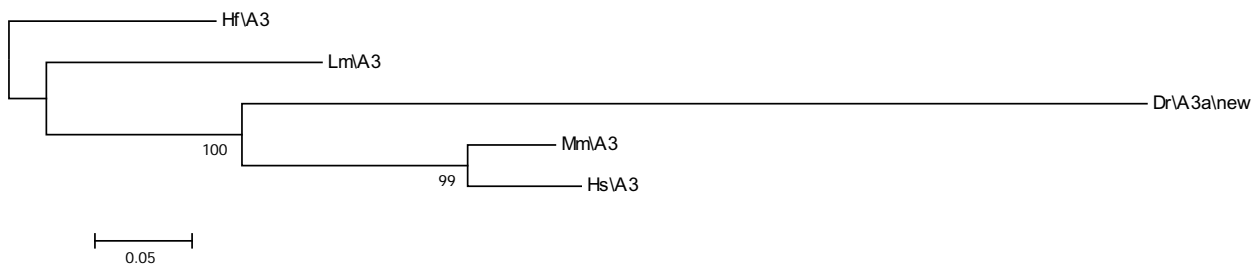
Hoxa3 alignment for relative rate test

```
Lm\A3      MQKATYYDSSAIYGGYPYQGANGFTYNASQQQYYHRPACSLQSPATV
Hf\A3      MQKATYYDSSAIFGGYTYQGANGFNYNASQQQYYHRPACSLQSPGTV
Mm\A3      MQKATYYDSSAIYGGYPYQAANGFAYNASQQPYHRPACSLQSPAAG
Hs\A3      MQKATYYDSSAIYGGYPYQAANGFAYNANQQPYHRPACSLQSPSAG
Dr\A3a     MQKATYCDGSAIYSGLPYQSANGLGYDASQQQYYHRPACSLQSPGSA
```

```
Lm\A3      PHHKHNDINESCMRTSNNQPPPPGISEP
Hf\A3      PHHKPNDINESCMRTSASQPSHHPVIAEP
Mm\A3      GHPKTHELSEACLRTLSTGPPSQPPGLGEP
Hs\A3      GHPKAHELSEACLRTLSTAPPSQPPSLGEP
Dr\A3a     GLHTSNEMSEVCQQINGTQATVTDTS DNP
```

```
Lm\A3      QPTNPVSPSQTSSNNSTPSNSNKNPGITSPPTIAKQIFPWMKESRQNSKQKNSSCSS
Hf\A3      PPPPSVSPQNTSSNSTQSSTSKNPTLTSATISKQIFPWMKESRQNAKQKTSSSSS
Mm\A3      PPPSSVSPQNSANSNPTPASTAKSPLLNSPTVGKQIFPWMKESRQNTKQKTSGSSS
Hs\A3      PPPSSASPPQNASNNPTPANAAKSPLLNSPTVAKQIFPWMKESRQNTKQKTSSSSS
Dr\A3a     TAPSGPSSPSSLNQPINIDSAAKNPVHVSPSTRKHIFPWMKESRQNTKQKSCSIIS
```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxa3

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0.02	*
Hf	Lm	DrA3a	0	**
Hf	Hs	DrA3a	0	**

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxa4 alignment for relative rate test

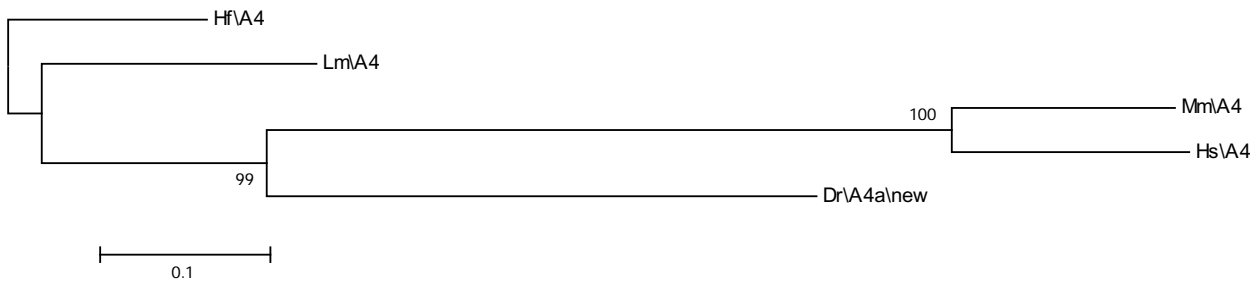
```

Lm\A4      MSSFLINSNYIEPKFPPCEEYSQNNRDPGFQQEALNQYSEPTYSYNNQTAGHEGIS
Hf\A4      MSSFLINSNYVEPKFPPCEEYSQNNRDPGFHHEALYPYPEPTYSFNNQGTGNQDMS
Dr\A4a     MSSYLINSNYIEPSFPPCEEYHQNGKDPGFPHHEASYPYQEYSYDYGNSNDLNDFS
Mm\A4      MSSFLINSNYIEPKFPPFEEFAPHGREPSYPGLYPAPAAACPYACRGAS PGRPEQS
Hs\A4      MSSFLINSNYIEPKFPPFEEYAQHSREPAYPALYPADHTAYPYGYRGAS PGRPPQP
    
```

```

Lm\A4      PRQSQECEAVPVTTDINKTPIGQNGKEPIVYPWMKKIHVCT
Hf\A4      PRQNQLCEVVPVATPALKNPTAQKGKEPIVYPWMKKIHVTT
Dr\A4a     PRLTTESECVGSDGNKDCALPGSQKSKEPVVYPWMKKVHVNT
Mm\A4      PGPTTPAVATGGSAPACQGPAGPKGKEPVVYPWMKKIHVSA
Hs\A4      AAPATPGVPAGGSAPACKSPLGLKGKEPVVYPWMKKIHVSA
    
```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxa4

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0	**
Hf	Lm	DrA4a	0.002	**
Hf	Hs	DrA4a	0.013	*

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxa5 alignment for relative rate test

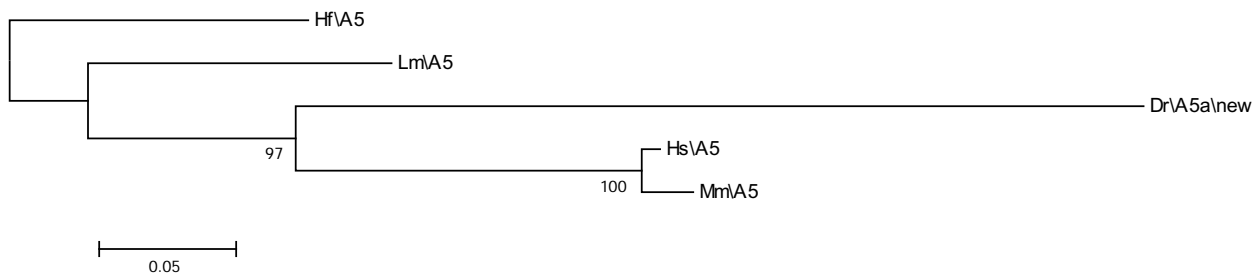
```

Lm\A5      MSSYFVNSFCGRYSNGPDYQLHNYGDHTSSEQYRDSASMHSSRYGYGYNGMDLSI
Hf\A5      MSSYFVNSFCGRYPNGPDYQLHNYGDHSSSEQYRDSATMHSSRYGYGYNGMDLSI
Hs\A5      MSSYFVNSFCGRYPNGPDYQLHNYGDHSSSEQFRDSASMHSGRYGYGYNGMDLSV
Mm\A5      MSSYFVNSFCGRYPNGPDYQLHNYGDHSSSEQFRDSASMHSGRYGYGYNGMDLSV
Dr\A5a     MSSYFVNSFCGRYPNGVDYPLHNYGDHNSSGQCRDSTGMHSGRYACGYNGMDLST

Lm\A5      GRSSSNHYDTSERTRRYSQPATSPPPDPLPCPAVATSSVNETHLAV
Hf\A5      SRPASNHFNASERSRRYNQPATSPSPDPLPCSAVVSPSAGDNHHGI
Hs\A5      GRSGSGHFGSGERARRYSQPATSPQPDPLPCSAVAPSPGSDSHHGG
Mm\A5      GRSGSGHFGSGERARRYSQPATSPPPDPLPCSAVAPSPGSDSHHGG
Dr\A5a     GHSSPGHFLSSERTQRYNQPVTEPSSDHLPCSSLANSVPVSESHRAL

Lm\A5      KNPIANTTSTNASSSTHIGREGVGTSSGAEDDTPASREQPSSQNPQIYPWMRKLHISH
Hf\A5      KNSIASTTSSNSSSSSHISRDLGVTSPGTEDDTPASSDPPSSQNPQIYPWMRKLHISH
Hs\A5      KNSLNSGASAAGSTHISREGVGTASGAEDDAPASSEQASAQSPQIYPWMRKLHISH
Mm\A5      KNSLNSGASAAGSTHISREGVGTASAAEEDAPASSEQAGAQSPQIYPWMRKLHISH
Dr\A5a     KISLSSTAGSAKSFQTVLSREGVSVSSSMEEEEKPPGSGQTASQNPQIYPWMRKLHISH
    
```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxa5

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0.04	*
Hf	Lm	DrA5a	0	**
Hf	Hs	DrA5a	0.004	**

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxa6 alignment for relative rate test

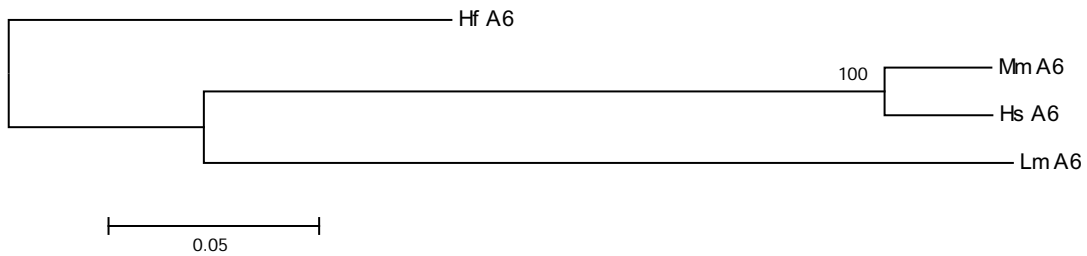
```

Hf_A6  MSSYFVNPTFPVSLPSGQDSFLGQIPLYTTGYDALRHFPSYGAATLQ
Lm_A6  MSSYFVNSTFPSPNPSSQDSFLGQIPLYTAGYDALRHFQSYGATTLQ
Mm_A6  MSSYFVNPTFPGSLPSGQDSFLGQLPLYPAGYDALRPFPSYGASSLP
Hs_A6  MSSYFVNPTFPGSLPSGQDSFLGQLPLYQAGYDALRPFPSYGASSLP

Hf_A6  DKSYSPPCYQQSNSVIACNRASYDYGASCFYPEKDLASVSPSSGK
Lm_A6  DKTYSSSCFYQQSNSVFACNRTPYECGASCLYPEKDTDVSSPSSSK
Mm_A6  DKTYTSPCFYQQSNSVLACNRASYEYGASCFYSDKDLSGASPSNNK
Hs_A6  DKTYTSPCFYQQSNSVLACNRASYEYGASCFYSDKDLSGASPSGK

Hf_A6  HRAQDDFFSSDQHYKPDCAQNKILSEEGNDRKYSTPIYPWMQRMNSSS
Lm_A6  QRAHGDYLFHDQQHKSECVQNKILNEEVNDRRYTTPIFPWMQRMNSCT
Mm_A6  QRGPGDYLFHEQQYKPDGVQGKALHEEGTDRKYTSPVYPWMQRMNSCA
Hs_A6  QRGPGDYLFHEQQYKPDGSGQKALHDEGADRKYTSPVYPWMQRMNSCA
  
```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxa6

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>
Hf	Hs	Lm	0.866

Hf – *Heterodontus francisci*, Hs – *Homo sapiens*, Lm – *Latimeria menadoensis*, Mm – *Mus musculus*

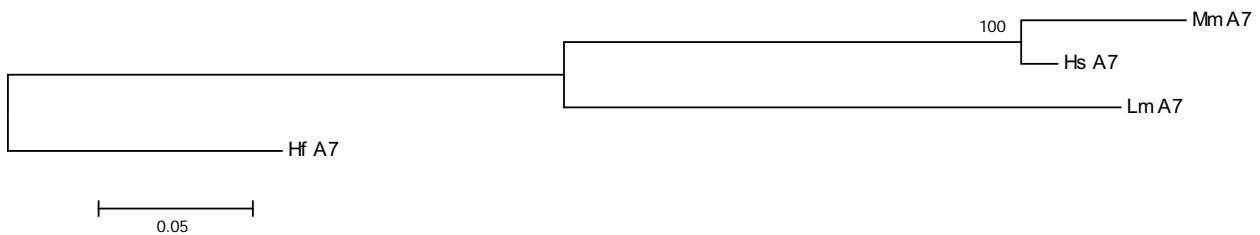
Hoxa7 alignment for relative rate test

```
Hf_A7  MSSSYVNALFPKYTAGTSVFNASATSCAFATNSQRSSYGAGAS
Lm_A7  MSSSYVNTFFSKYTTGASLFQNAEPNSCSFATNSQRSSYGPGAG
Mm_A7  MSSSYVNALFSKYTAGASLFQNAEPTSCSFAPNSQRSGYGAPAPA
Hs_A7  MSSSYVNALFSKYTAGASLFQNAEPTSCSFAPNSQRSGYGAGAG
```

```
Hf_A7  AFPAPMAGLYNVNSAIYHGPNYNTGYNLNSDSYNLRCAL
Lm_A7  AFPPSLPGLYNMTSTLYQNPFTSGYNIGSDAYNLHCSSF
Mm_A7  AFASTVPGLYNVNSPLYQSPFASGYGLGADAYNLPCASY
Hs_A7  AFASTVPGLYNVNSPLYQSPFASGYGLGADAYNLPCASY
```

```
Hf_A7  DQIPVLCSDLKQGEKLDQTNVHPQAESNFRIYPWMRNAGPDR
Lm_A7  DQIPVLCNDLTKSNEKSNESSLHPQDENNFRIYPWMRSSGPK
Mm_A7  DQIPGLCSDLAKGADKADEGLHGPAEASFRIYPWMRSSGPK
Hs_A7  DQIPGLCSDLAKGADKTDEGALHGAAEANFRIYPWMRSSGPK
```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxa7

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>
Hf	Hs	Lm	0.67

Hf – *Heterodontus francisci*, Hs – *Homo sapiens*, Lm – *Latimeria menadoensis*, Mm – *Mus musculus*

Hoxa9 alignment for relative rate test

```

Hs\A9      MATTGALGYVDSRYAPGTLGQPPRQLAEHPDFSPCSFQSKATVFGASWNPVGRYMRSW
Mm\A9      MATTGALGYVDSRYAPGTLGQPPRQLAEHPDFSPCSFQSKAAVFGASWNPVGRYMRSW
Lm\A9      MSTSGTISYFVDSRYNSGALTQPPRQLPDPDFPCSFQSKASVFTTSWNPVSRYMRSW
Hf\A9      MSTSGTISYYVDSRYASGSLAQASRQLTEHPDFSPCNFQSKATVFTSWSVPVGRYMRSW
Dr\A9b\new MSTLGTLSYYADSRFSSGPVVQQQSRLLLEYSEQEPYTFQAKSSIFGASWSPVGASVRPW
Dr\A9a\new MSTSGALTYVDSRFSSGLGLIQHRPPADLSDLGPCCTFPAKQPVYGTSWGHI GDYVQSW
    
```

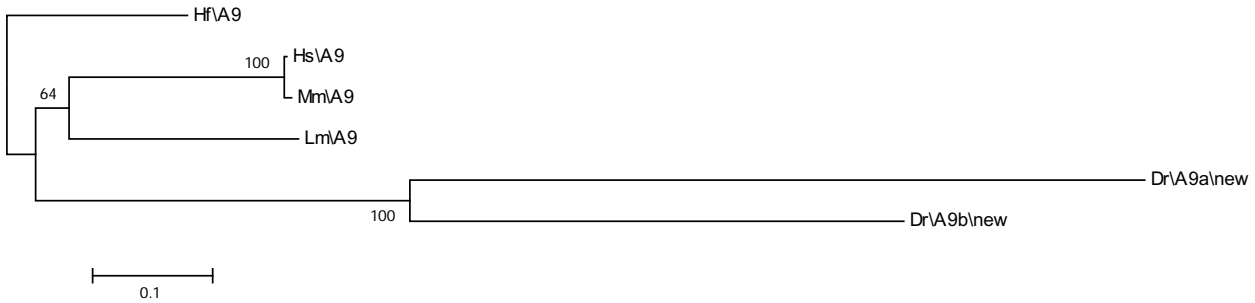
```

Hs\A9      LEPTPALSFAGLPSSRPYGIKPEPLSARTHHTLSLTDYACGSPPVEGAFSE
Mm\A9      LEPTPALSFAGLPSSRPYGIKPEPLSARTHHTLSLTDYACGSPPVEGAFSE
Lm\A9      LESMPSLSFAGLPSSRHYGIKPEPLIARAHTLTFSDYGCGSSPVDGILPE
Hf\A9      LDPMPTLSFPGLPSSRHYGIKPEPVASRTHHTLALSEYTCGTSPAEVSFSE
Dr\A9b\new LEPLPALPFTGLSTDTHQDIKLEPLVGSHTHTLLVAETDNNTTQTDAVNSG
Dr\A9a\new LLDSAGLPQTEPPTVNHNHAKSDTNETNPHTIILQPVFTNGGCSTEAESSR
    
```

```

Hs\A9      NNAENESGGDKPPIDP
Mm\A9      NNAENESGGDKPPIDP
Lm\A9      NNGESESIGDKPQIDP
Hf\A9      NNGETESNADKLHMDP
Dr\A9b\new SHDEKI PAETKLDLDP
Dr\A9a\new TAEKSGDIEGKPGADP
    
```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxa9

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0.645	
Hf	Lm	DrA9a	0	**
Hf	Lm	DrA9b	0	**
Hf	Hs	DrA9a	0	**
Hf	Hs	DrA9b	0	**

Green highlight denotes gene with significantly faster rate of evolution
 Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxa10 alignment for relative rate test

```

Hs\A10      MSCSESPAANSFLVDSLISGRYYAHGGVYLPPAADLPYGLQSCGLFPTL
Mm\A10      MSCSESPAANSFLVDSLISGRYYAHGGVYLPPASDLPYGLQSCGLFPAL
Hf\A10      MSCSDSPSANSFLVDSLISGRYYPNSSVYLPPASELSYGTQNCGLFPSL
Lm\A10      MSCSDSSAANPFLVDSLIVSGRYFPNSSVYLPQASDLPYGLQNCGLFPVL
Dr\A10b\new MSCSDSPSGNSFLVDSLIIHGRYYQNSGVYLQPTSEYSYGLSNCGYFSGL

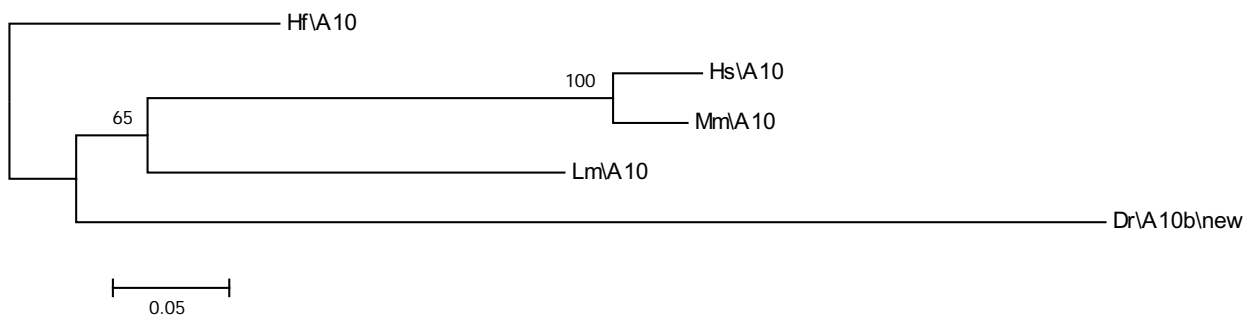
Hs\A10      QATSCSFAQNIKEESSYCLYDADKCPKVSAAAEL
Mm\A10      QATSCSFAQNIKEESSYCLYDADKCPKGSAAADL
Hf\A10      QVATCSFPQNIKEENAYCLYDSEKCPKSAAATDL
Lm\A10      QVTSCSFAQNIKEENAYCLYESEKCPKGTATTDL
Dr\A10b\new QITPRFSPTIKEENSYCLYESEKCPKETITEDI

Hs\A10      AFPRPPPDGCSGVPVPGYFRLSQAYGTAKQLGAPFPAQP
Mm\A10      AFPRPPPDGCSGVPVPGYFRLSQAYGTAKQLASPFPAQP
Hf\A10      SFPRLTSESCGVPVPGYFRLSQAYPTSKQVGAPFVPQS
Lm\A10      SYPRLSTEVC SVIPVPGYFRLSQAYGISKQVGAQFTPPP
Dr\A10b\new SYSRLTPNSCGCVVPGYFRLSQCTTTSKQTI PHVVAQR

Hs\A10      PGRFDLPLASGSADAARKEAHASSPAPSESSKASPEKDSL
Mm\A10      PGRFDPPPLASGSTEAAGKEAHASSPAPSENSKASPEKDSL
Hf\A10      QIRFGTPSASTPTELGRKEAAAASSPVPSESNKNSPEKETK
Lm\A10      QVRFDMSSLSSASTETVMKEAHASSPAPSESSKTS PDKEAI
Dr\A10b\new STRFDSSLSAIAAEASRDELRGSSPEPPDSPEKAVTVTKA

```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxa10

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0.21	
Hf	Lm	DrA10b	0.001	**
Hf	Hs	DrA10b	0.024	*

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxa11 alignment for relative rate test

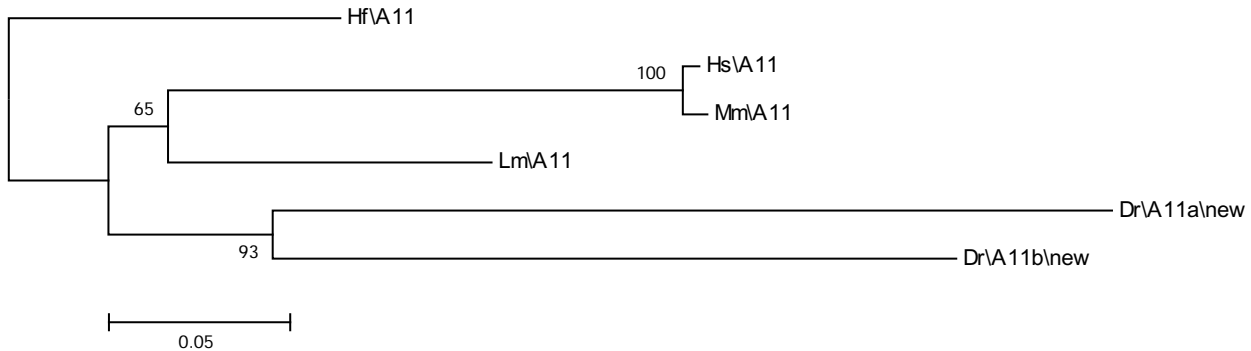
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Hs\A11      MDFDERGPCSSNMYLPSCITYVSGPDFSSLPFLPQTPSSSRPMTYSYSSNLPQVQPVREVTFR
Mm\A11      MDFDERGPCSSNMYLPSCITYVSGPDFSSLPFLPQTPSSSRPMTYSYSSNLPQVQPVREVTFR
Lm\A11      MDFDERVSCSSNMYLPSCITYVSGPDFSSLPFLPQTPSSSRPMTYSYSSNLPQVQPVREVTFR
Hf\A11      MDFDERVSCGSNLYLPSCITYVSGPDFSSLPFLPQTPASRPMTYSYSSNIPQVQPVREVTFR
Dr\A11b\new MDFDERVPVGSNMYLPGCTYYVSGTDFSSLPFLPQTPSSCPMTYSYSSSLPQVQSVREVSFR
Dr\A11a\new MDFDERVSVGSNMYLPSCITYVPGADFSTLPSFLSQSPSTRPVTYSYASNLPQVQHREVTFR

Hs\A11      EYAIEPATKWHPRGNLAHCYSAEELVHRDCLGDVLAKESSANVYTPAVSSNFYSTVGRNGVL
Mm\A11      EYAIEPATKWHPRGNLAHCYSAEELVHRDCLGDVLAKESSANVYTPAVSSNFYSTVGRNGVL
Lm\A11      DYAITDTSNKWHPRSNLPHCYSTEEILHRDCLGEIFGKGNANVYGSSTSSNFYNTVGRNGVL
Hf\A11      DYAITDPSNKWHHRGNLPHCYSAEELMHRECLGEMLMKNSASVYSSNASSSFYNPVGRNGVL
Dr\A11b\new DYAITDSSKWHSRGNLPHCYATEDMVHRECLGDMLSKNNSVLYNSSHTSNVYGSVGRNGVL
Dr\A11a\new DYAITDPSTKWPHRGLAHCYSEDSVHRECLGEMFPKNNASAYTSTNTSNFYGNVGRNGVL

Hs\A11      PQAFDQFFETAYGTPENASSDYDKSAEKG PATSSSDSSSP ESSSGHTEDKAGGS
Mm\A11      PQAFDQFFETAYGTPENASSDYDKNAEKG PATSSSDGSSPESSSGHTEDKAGGS
Lm\A11      PQAFDQFFETAYGT TENHSSDYDKNSDKI PATSRSETSSPESSSGNNEEKSSSS
Hf\A11      PQGFDQFFETAYGSSENQQSEYEKSPDKVPATSSSETSSPESSSGNNEEKGSNS
Dr\A11b\new PQAFDQFFETAYGNVENQPT EHDRATSKAPAESGSDSSSPEPSSGNNEEDKFSGS
Dr\A11a\new PQAFDQFFDTAYGGSDSVDNDYDKMHSSKQAPAPEQQSSPESSSGNNEEKTSGA
    
```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxa11

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0.072	
Hf	Lm	DrA11a	0.001	**
Hf	Lm	DrA11b	0.001	**
Hf	Hs	DrA11a	0.069	
Hf	Hs	DrA11b	0.114	

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf - Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxa13 alignment for relative rate test

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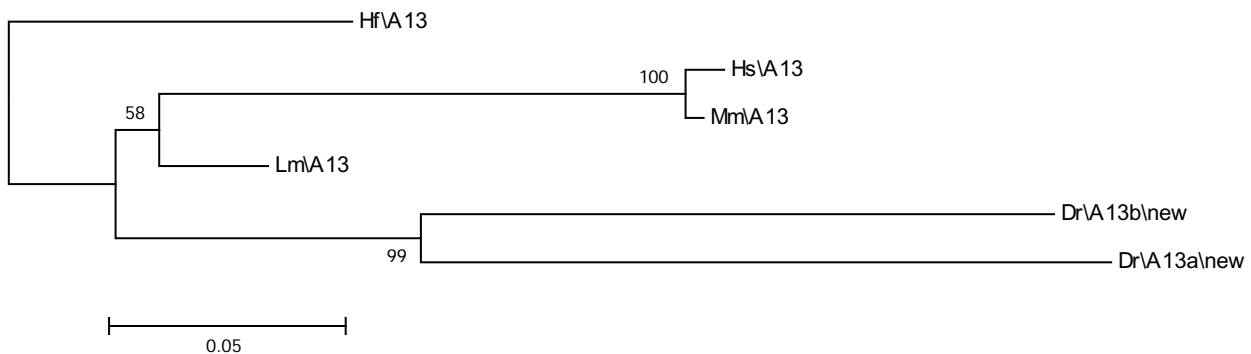
Hs\A13      MTASVLLHPRWIEPVMFLYDNGDELNKNMEGCRNLMAHAPAPLAPKQCSPCSAAAQ
Mm\A13      MTASVLLHPRWIEPVMFLYDNGDELNKNMEGCRNLMAHAPAPLAPKQCSPCSAAAQ
Lm\A13      MTASVLLHPRWIDPVMFLYDNGDEVNKNMEGCRNLMAHAPASLAPKQCSPCSAAQS
Hf\A13      MTASVILHPRWIDTVMFVYDNSDEINKNMDGCRNLMAHAPASLAPKQCSPCPAAQT
Dr\A13b\new MTASLLLHSRWIDPVMFLYDNGDDMSKNMEGCRNLI AHPSTLAPKQCSPCS AVQN
Dr\A13a\new MTTSLLLRPRWIDPVMFLYDNGDDT SKNMEGCRNLM SHPASLAPKQCSPCS AVQG

Hs\A13      SSSAALPYGYFGSGYYPCCKSQAQKYMDTAAEEFSSRAKEFAFYQGYAGPYQPMPGYLDMP
Mm\A13      SSSAALPYGYFGSGYYPCCKSQAQKYMDTAAEEFSSRAKEFAFYQGYAGPYQPVPGYLDMP
Lm\A13      SSSASLPYGYFGSSYYPCCKSQAQKYMDTSGEEFTSRAKEFAFYQGYAGPYQPVPSYLDVP
Hf\A13      SSSAALPYGYFGSSYYPCCKSQAQKYMDTSGEEFTSRAKEFAFYQGYAGPYQPMPSYLDVP
Dr\A13b\new TPSASLPYGYFGGSYYPCCKSCTQKYMDTSGEEFSSRAKEFAFYQGYSGPYQPVPSYLDVP
Dr\A13a\new SASASISYGYFGGGYYPCKTCAQKYMDTSGEDYTSRAKEFALYSSYASPYQPVPSYLDVP

Hs\A13      VVPGLGGPGESRHEPLLPMEYQPWALPNGWNGQMYCPKEQAQPPHLWKSTLP
Mm\A13      VVPGLGGPGESRHEPLLPMEYQPWALPNGWNGQMYCPKEQTQPPHLWKSTLP
Lm\A13      VVPTIGGPGEP RHEPLLPMEYQPWAITNGWNGQVYCSKEQAQPNHLWKSTLP
Hf\A13      VVPTISAPGEP RHD TLLPMEYQPWAITNGWNGQVCCSKEQPQATHLWKSSLP
Dr\A13b\new VVPALSAPSEPRHESLLPVEYQPWAITNGWSSPVYCPKDQTQSSTLWKSSIQ
Dr\A13a\new VVQAISGPSEPRHESLLPMEYQPWAIITGWNGQVYCTKEQQQTGNVWKSSIP

```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxa13

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0.003	**
Hf	Lm	DrA13a	0	**
Hf	Lm	DrA13b	0	**
Hf	Hs	DrA13a	0.086	
Hf	Hs	DrA13b	0.105	

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxb1 alignment for relative rate test

```

Hs\B1      MNSFLEYPLCNRGPSAYSFPPSSAQAVDYASEGRYGGGLSSPSTLGVPFPSSASGYAPAACS
Mm\B1      MSSFLEYPLCNRGPSAYSFPPCSAPAVDYAGESRYGGGLPSSSSSLGVSFSPASGYAPAACN
Lm\B1      MNSFLEYAICNRGTSAYSFPPCSGTTNDYNGDGRFLGGSAPVSNMGIPYASTGSGYTPQTCN
Hf\B1      MNSFLEYAICNRGTSAYAFAPCAGNVDCNGDGRFLGGSAHNSSLGNPYASSGNNYTTQTCN
Dr\B1a\gb  MNSFLEYTICNRGTNAYPGPFHTGHASDYNADGRLYGGSNQPPTGMGLTYGGTGTSYGTQACA
Dr\B1b\new MNSYLDYTIYNRGSNTYEYLPACASTNYIPEGRPVGNTFTSFHLNVDMGKTGSNFCKQTRP
    
```

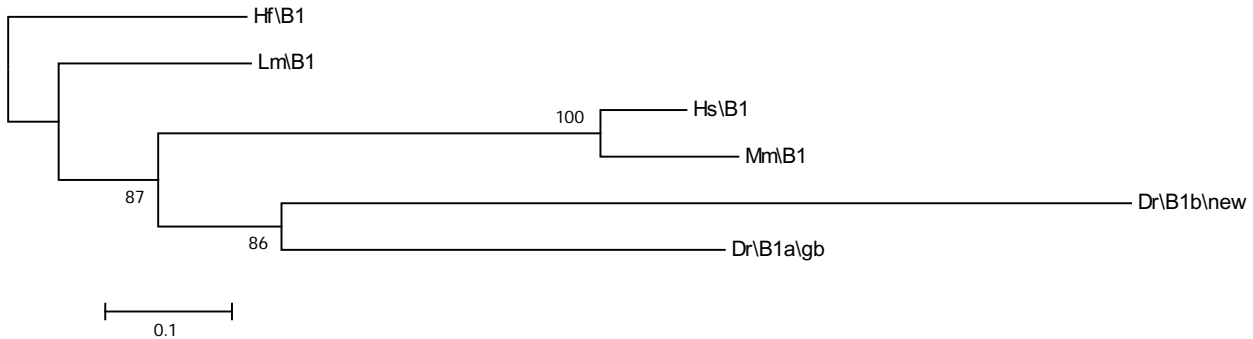
```

Hs\B1      PSYGQYYPLGQEGDGGYFHPSSYGAQLGGGGAGPGPYGNEQTASFAPAYD
Mm\B1      PSYGQYYSVGQEGDGSYFHPSSYGAQLGGGGVSGPGPYGTEQTATFASAYD
Lm\B1      PGYGHQYYFGQEPDGMFYQSSGYSNSIGSGVSGPGQYYPHEHQGFLQGTYN
Hf\B1      PGYNHHYFFNQESDGAYFQTSCTGNIASGVSGPGQYYGQEQGLAYGIYN
Dr\B1a\gb  NSDYHQYFINPEQDGMYYHSSGFSTSNASGAVPAAPYQGDHQRAYSQGTQYD
Dr\B1b\new PHSDHQHVLTLQADDHMLQSPGFSVVMGGSVSASHYYGEPEP-HGYGSFK
    
```

```

Hs\B1      LLESENTPTARTFDWMKVKNPPKT
Mm\B1      LLESTLTPTRTFDWMKVKNPPKT
Lm\B1      ASSPQTSTGQTFEWMKVKNPPKT
Hf\B1      LSPSSSSSGQTFDWMKVKNPPKT
Dr\B1a\gb  LSASQPPPGKTFDWMKVKNPPKT
Dr\B1b\new YQVSNIKQAPTFDWMKVKNPPKT
    
```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – HoxB1

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0	**
Hf	Lm	DrB1a	0	**
Hf	Lm	DrB1b	0	**
Hf	Hs	DrB1a	0.873	
Hf	Hs	DrB1b	0.01	**

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxb2 alignment for relative rate test

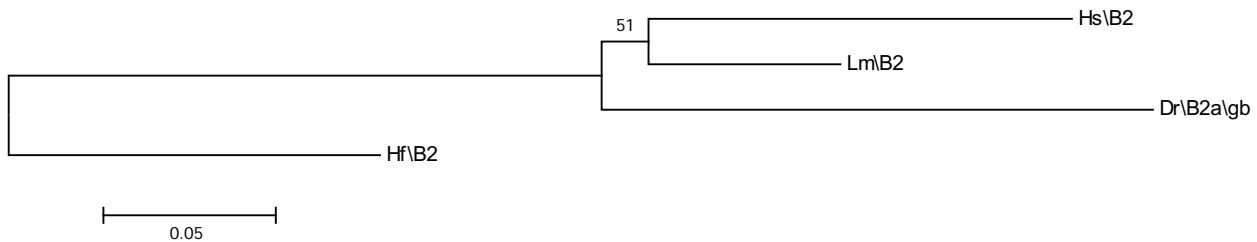
```

Dr\B2a\gb      MNFEFEREIGFINSQPSLAECLTSFPAVLESFQTSSIKDSTAIPPPFEHTIPS
Hs\B2          MNFEFEREIGFINSQPSLAECLTSFPAVLETFQTSSIKESTLIPPPFEQTFPS
Lm\B2          MNFEFEREIGFINSQPSLAECLTSFPAVLETFQTSSIKESTLIPPPFEQTFPS
Hf\B2          MNFELEEREIGFINSQPSLAECLTSFPAVADTFQSSSIKNSTLIPPPFEQTFPS
  
```

```

Dr\B2a\gb      LSPCTGNQARPRSQKRAHEFPWMKEKKSSKAAAASPSQASSGYTTAGLESPT
Hs\B2          LQPGASTLQRPRSQKRAPEFPWMKEKKSAKQSATSPSPAASAVPASGVGSPA
Lm\B2          LNPCSSSQPRPRSQKRAAEFPWMKEKKSSKASSSSSSPASSSVSGSGVGSPT
Hf\B2          LNP-SSNQPPSREKRAAEFPWMKEKKSSKNEAPLSLSAPVLGSSQAESP
  
```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxb2

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0.034	*
Hf	Lm	DrB2a	0.035	*
Hf	Hs	DrB2a	0.763	

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxb3 alignment for relative rate test

```

Dr\B3a      MQKTTYDNSTLFGGYSYQGANGFGYDAPAPAFQNSAHLEGDYQRSACSLQSLGTS
Lm\B3      MQKTTYDNSTLFGGYSFQGTNGFGYDTPQQPFQASPHIENDYHRSACSLQSLGNN
Hf\B3      MQKTTYDNCTLFGGTYTQGANGFSEVAQEPYPPSSHVENDYQRSACSLQPAGTS
Hs\B3      MQKATYYDNAALFGGYSYPGSENGFGFDVPQPPFQAATHLEGDYQRSACSLQSLGNA
Mm\B3      MQKATYYDNAALFGGYSYPGSENGFGYDGPQPPFQAATHLEGDYQRSACSLQSLGNA
  
```

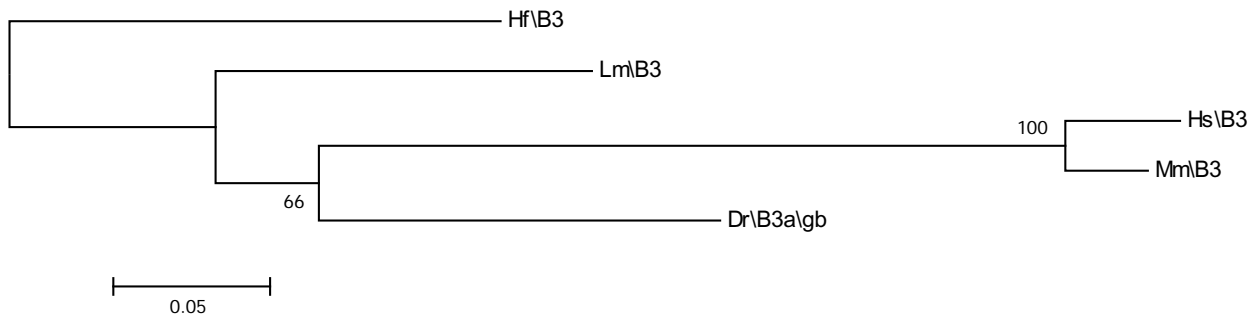
```

Dr\B3a      APHAKTKELNGSCMRPSLPEHHPPPQVSPQNTVNV
Lm\B3      APHAKSKDLNGSCMRASLPEHHQPPVSPQNTTNS
Hf\B3      VPHPKSKDINGSCMRSNLPEHRQPPVSPQNSSNS
Hs\B3      APHAKSKELNGSCMRPGLAETLSAPPGPSPPSAPTS
Mm\B3      APHAKSKELNGSCMRPGLAELPAPPGPSPPSAPTS
  
```

```

Dr\B3a      SKSSSKSSSMATPTLTKQIFPWMKESRQNTKQKNSSPSA
Lm\B3      SKTATSKSNLSSASITKQIFPWMKESRQNSKQKNSSPST
Hf\B3      SKTLSKSSHTSTPSTLTKQIFPWMKESRQNSKQKNNSPST
Hs\B3      SKSGPPKCGPGTSTLTKQIFPWMKESRQTSKLNNSPGT
Mm\B3      SKSCPPKCGSGSSTLTKQIFPWMKESRQTSKLNNSPST
  
```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxb3

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0.002	**
Hf	Lm	DrB3a	0.683	
Hf	Hs	DrB3a	0.013	*

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

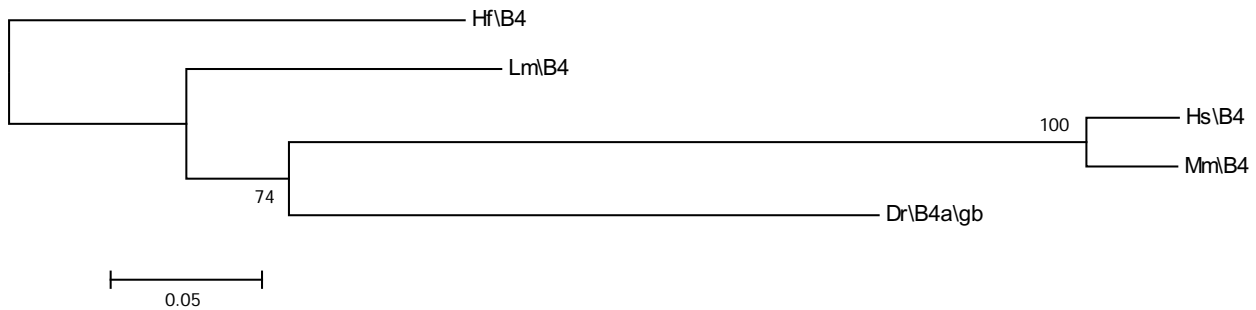
Hoxb4 alignment for relative rate test

```
Lm\B4      MSSFLINSNYVDPKFPPCEEYSQNDYLPSHSPEYYSSQRETTFQHEATYQRSAC
Hf\B4      MSSFLINSNYVDPKFPPCEEYSQNNYLPSHSPEYFTRAREPGFQHEAMYPR SAY
Dr\B4a     MSSYLINSNYVDPKFPPCEEYSQSDYLPSHSPDYSAQRDPSFQHESIYHRSGC
Hs\B4      MSSFLINSNYVDPKFPPCEEYSQSDYLPSHSPGYAGQRESSFQPEAGFGRAAC
Mm\B4      MSSFLINSNYVDPKFPPCEEYSQSDYLPSHSPGYAGQRESGFQPEAAFGRAPC
```

```
Lm\B4      NEQPFSSCSPRGPVHLQTGLPEQIHHCESVTPSP
Hf\B4      SEQPYSSCAPRGHVQSQTGLAKHGHQCVSVTPSP
Dr\B4a     ADPPYSSCSPRGHVLP T TALPEP SHHCDSVTPSP
Hs\B4      TVQRYAACSPRAPAPPAGLPEPGQRCEAVSSSP
Mm\B4      TVQRYAACSPRAPVQPTAGLPEPGQRSEAVSSSP
```

```
Lm\B4      PCSQNSMNQSISSSKEPIVYPWMKKVHVNT
Hf\B4      PCSQNF SNQNTPCSKEPVVYPWMKKLHINA
Dr\B4a     PCGQTPTSQNTSTVKDPVVYPWMKKVHVNI
Hs\B4      PCAQNPLHPSPSHSKEPVVYPWMRKVHVST
Mm\B4      PCAQNPLHPSPSHSKEPVVYPWMRKVHVST
```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxb4

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0	**
Hf	Lm	DrB4a	0.05	*
Hf	Hs	DrB4a	0.068	

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

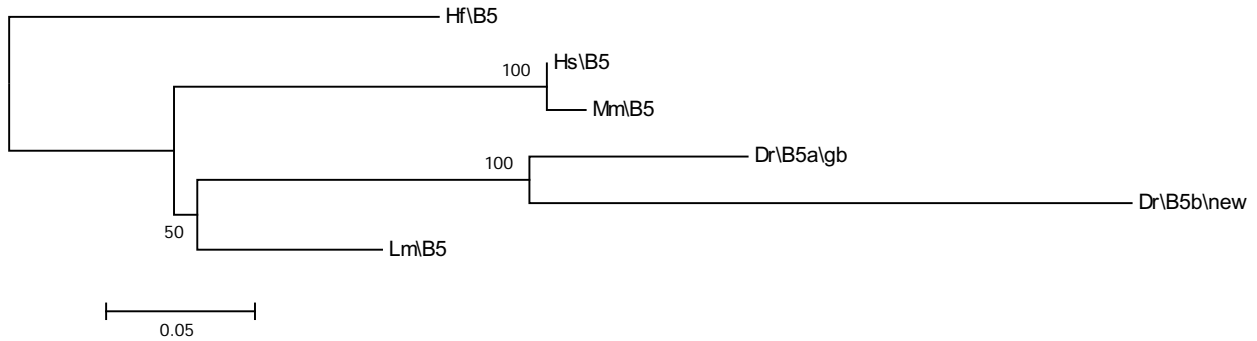
Hoxb5 alignment for relative rate test

```
Dr\B5a      MSSYFVNSFSGRYPNGPDYQLLNYGTSSAMNASYRDSGTMHSGSYGYNYNGMDLSVNR
Dr\B5b      MSSYFLNSFSGRYPNGSDYQLLNYGTNGAMNASYRDSSTMHSGSFGYNYNGIDL SVNR
Hs\B5       MSSYFVNSFSGRYPNGPDYQLLNYGSGSSLSGSYRDPAAMHTGSYGYNYNGMDLSVNR
Mm\B5       MSSYFVNSFSGRYPNGPDYQLLNYGSGSSLSGSYRDPAAMHTGSYGYNYNGMDLSVNR
Lm\B5       MSSYFVNSFSGRYPNGPDYQLLNYGTSSSMNGSYRDSSTMHSSSYGYNYNGMDLSINR
Hf\B5       MSSYFVNSFSGRYQNGPDYQLLNYGTSSSENGPYRDSGTMHSGTYGYNYNGMDLSITR
```

```
Dr\B5a      TSTGHFGAVGDNSRVFQSPAPETRFRQC SLASPEPLPCSNSESLGPKPS
Dr\B5b      PNNGHFGAVGDNSRAFQNPSEQETRYRQC SLSSPDPLSCATSDTLELKPS
Hs\B5       SASSHFGAVGESSRAFPAQAQEPFRFRQC SLSSPELPCSTNGD SHGAKPS
Mm\B5       SASSHFGAVGESSRAFPAQAQEPFRFRQC SLSSPELPCSTNGD SHGAKPS
Lm\B5       SASSHFGAVGENSRGFPSAQENRFRFRQC SLSSPELPCSNSESLGAKPS
Hf\B5       SASSHFGVNEKRSRYP-PATETRFRQC TLSSPEPLPCSGKDSHG VVKPS
```

```
Dr\B5a      DQSTTHFTEIDEASASSETEEASHKQETTATSTTSAQAPQIFPWMRKLHISH
Dr\B5b      DQSTTHFADTDETNVSSETEEGAQKQESVATSTTTPQTPQIFPWMRKLHISH
Hs\B5       DQATANFTEIDEASASSEPEEAASRAQPEPMATSTAQTPQIFPWMRKLHISH
Mm\B5       DQATANFTEIDEASASSEPEEAASRAQPEPMATSTAQTPQIFPWMRKLHISH
Lm\B5       EQATTNFTELDETSASSETEEGAPRAQTEPTATSTTQTPQIFPWMRKLHISH
Hf\B5       DPTTSNFTEMDEAGASSDAEEGTPRAQQEPTQATTPQQPQIFPWMRKLHIGH
```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxb5

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0.134	
Hf	Lm	DrB5a	0.019	*
Hf	Lm	DrB5b	0	**
Hf	Hs	DrB5a	0.273	
Hf	Hs	DrB5b	0.002	**

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxb6 alignment for relative rate test

```

Hs\B6      MSSYFVNSTFPVTLASGQESFLGQLPLYSSGYADPLRHYPAPYGGPGGQDKGFATSYY
Mm\B6      MSSYFVNSTFPVTLASGQESFLGQLPLYSSGYADPLRHYPAPYGGPGGQDKGFAASY
Hf\B6      MSSYFVNSTFPVTLASGQESFLGQIPLYSSGY-DPLRHYPATYGATSMQDKSYSSYY
Lm\B6      MSSYFVNSTFPVTLPGGQESFLGQIPLYSSGYADPLRHYPGTYGATTVQDKGYSSYY
Dr\B6a\gb  MSSYFVNSTFPVTLPGGQESFLGQIPLYSSGYTDPLRHYPAAYGSSVQEKAYPSSFY
Dr\B6b\new MSSYFVNSTFPVSLPGGQESFLGQIPLYSSGYTDSL RHYPATFGATNVQDKVYTSSYY
    
```

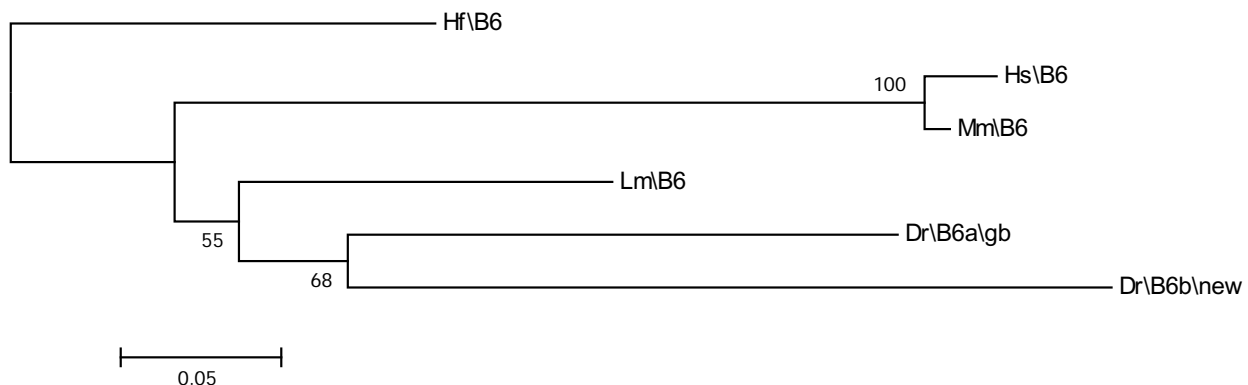
```

Hs\B6      PPAGGGYGRAAPCDYGAPAFYREKESACALSGADEQPPFHPEPRKSDCA
Mm\B6      PPAGGGYGRAAPCDYGAPAFYREKDAACALSGADEPPPFHPEPRKSDCA
Hf\B6      QQANGAYGCRTPCDYGSFSFYREKDPSCGASSLEDPTHFNSEQRKFECA
Lm\B6      QQANGAYSRTAACDFGTAGFYREKDPSCAISTLEDYSQFNQDQRKLDCC
Dr\B6a\gb  QQANGAYSRRAGPCDYATASFYREKDPACALASEEHSFVLSQDHRKTDCT
Dr\B6b\new QQAGGVFGRTSACDYSTPNIYRSADRSCAIGSLEDLSLVLTQDQCKTDCT
    
```

```

Hs\B6      QDKSVFGETEEKCSTPVYPWMQRMNSCN
Mm\B6      QDKSVFGETEEKCSTPVYPWMQRMNSCN
Hf\B6      QNRILYGEVDDKSSLPVYPWMQRMNSSS
Lm\B6      QNKSVFGESEEEKCSTPVYPWMQRMNSCT
Dr\B6a\gb  TGKSIYPEADEKPSAPVYPWMQRMNSCN
Dr\B6b\new QGTERYFSTEDKPCTPVYPWMQRMNSCN
    
```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxb6

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0.041	*
Hf	Lm	DrB6a	0.102	
Hf	Lm	DrB6b	0.012	*
Hf	Hs	DrB6a	0.577	
Hf	Hs	DrB6b	0.739	

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxb7 alignment for relative rate test

```

Hs\B7      MSSLYYANALFSKYPASSSVFATGAFPEQTSCAFASNPQRPGYGAGSASFAAS
Mm\B7      MSSLYYANALFSKYPAASSVFAPGAFPEQTSCAFASNPQRPGYGAGPAPFSAS
Lm\B7      MSSLYYANALFSKYQAASSVFPSTGAFPEQTSCAFASNSQVRSYGGSGSASFAAS
Hf\B7      MSSLYYANALFSKYTAGTSVFPTGVFSEPTSCAFASNSQVRSYGGSGSASYAAT
Dr\B7a     MSSLYYANALFSKYQVASSAFSTGVFPEQTSCAFSCSSQRAGYGSASSSSSVS
    
```

```

Hs\B7      MQGLYPGGGMAGQSAAVYAAGYGLEPSSFNMHCAPFEQNLSPGDSAKAAGA
Mm\B7      VQGLYSGGGAMAGQSAAVYAAGYGLEPSSFNMHCAPFEQNLSPGDAKAGGA
Lm\B7      MPGLYNSGSSMHPQTPSMYSASYGLEASSFNMHCSPFEQNLSPGDLSKQNC
Hf\B7      VPGLYSTANSLHHQTPMTYSPYGLNANSFNMHCSSFDHNSAGESCKQSCS
Dr\B7a     LPSMYTNGTSLSSHTQGMYPYAYELGAVSLNMHSSLFDHNLPAAGDLCKASSG
    
```

```

Hs\B7      KEQRDSDLAAENFRIYPWMRST
Mm\B7      KEQRDSDLAAENFRIYPWMRST
Lm\B7      KEQRDSEQQNENFRIYPWMRST
Hf\B7      KEQKETDPQSENFRIYPWMKSS
Dr\B7a     KEQRGYHQNNENLRIYPWMRST
    
```

NJ tree rooted to horn shark



Tajima relative rate test – Hoxb7

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0.003	**
Hf	Lm	DrB7a	0.001	**
Hf	Hs	DrB7a	0.398	

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxb8 alignment for relative rate test

```

Hs\B8      MSSYFVNSLFSKYKTGESLRPNYYDCGFAQDLGGRPTVVYGPSSGGSFQHPSQIQEFYH
Mm\B8      MSSYFVNSLFSKYKTGESLRPNYYDCGFAQDLGGRPTVVYGPSSGGSFQHPSQIQEFYH
Lm\B8      MSSYFVNSLFSKYKTGDSLRPNYYDCGFAQDLGGRPTVVYGPSTGGTFQHPTQIQEFYH
Hf\B8      MSSYFVNSLFSKYKGGETLRPNYYDCGFTQDLGGRPTVVYGPSTGGTFQHPSQIQDFYH
Dr\B8a     MSSYFVNSLFTKYKSGDTLRPNYYECGFAQDLGTRPTVVYGPSTGGTFQHAPQIQEFYH
Dr\B8b     MSSYFVNSLFTKFKGGDSLRSNYYDCPYTPDLGGRPSVLYGHNTGSAFQHAAQFPDFYH
    
```

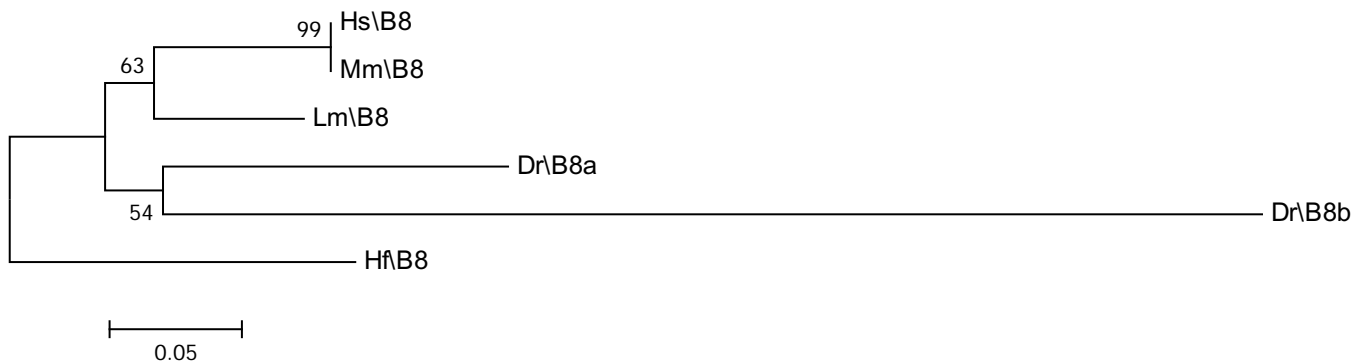
```

Hs\B8      GPSSLSTAPYQQNPCAVACHGDPGNFYGYDPLQRQSLFGAQDPDLVQYADCKLAAA
Mm\B8      GPSSLSTAPYQQNPCAVACHGDPGNFYGYDPLQRQSLFGAQDPDLVQYADCKLAAA
Lm\B8      GTSSLSTSPYQQNPCAVTCHGDPGNFYGYDPLQRQTLFTAQDSDLVQFTDCKLASN
Hf\B8      GAATLSTSAAYQQNPCAVTCHGDAGSFYGYDALQRQPIFAAQEAELIQYPDCKSTAN
Dr\B8a     GASTLSAAPYQQSPCAVTCHGEPGNFYGYDALQRQTLFGAQDADLVQYSDCKLATG
Dr\B8b     GTSSFPHASYQQTPCAVAYPGDAGNILGQDGLQKQSFAGAPDSDFTQFGDCNLKVS
    
```

```

Hs\B8      GLGEEAEGSEPSPTQLFPWMRPQ
Mm\B8      GLGEEAEGSEPSPTQLFPWMRPQ
Lm\B8      GVGEEAENSEPSPTQLFPWMRPQ
Hf\B8      SLGEEAENSESSPTQLFPWMRPQ
Dr\B8a     GIGDETDNTEPSPTQLFPWMRPQ
Dr\B8b     GIRDDLESAEPTAQLFPWMRPQ
    
```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxb8

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0.564	
Hf	Lm	DrB8a	0.275	
Hf	Lm	DrB8b	0	**
Hf	Hs	DrB8a	0.162	
Hf	Hs	DrB8b	0	**

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxb9 alignment for relative rate test

```

Hs\B9      MSISGTLSSYYVDSIISHESEDAPPAKFPSGQYASSRQPGHAEHLEFPSCSFQPKAPVFG
Mm\B9      MSISGTLSSYYVDSIISHESEDAPPAKFPSGQYANPRQPGHAEHLDFPSCSFQPKAPVFG
Lm\B9      MSISGALSNNYYVDSIISHESEEEASSAKFSSGQYVSSRQPGHSEHLEFPSCSFQPKPPVFS
Dr\B9a     MSISGTLNYYVDSIISHEGEDPNASRFNSNVQYSSARQPGPGEHPEFPSCSFQPKPPVFS
Hf\B9      MSISGAISNYFVDSLISHSESEGPSATKFASGQYIVSRQPGVPEHPEFPACNFQPKSPVFG
  
```

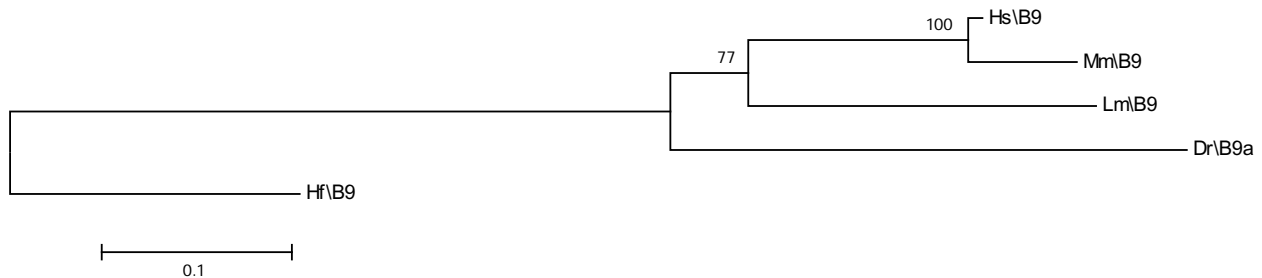
```

Hs\B9      ASWAPLSPHASGSLPSVYHPYIQPQGVPPEAESRYLRTWLEPAPRGEAAPAVK
Mm\B9      ATWAPLSPHASGSLPSVYHPYLQPQGAPAAESRYLRTWLEPAPRAEAPAVK
Lm\B9      ASWTPLNPHSAGTLSSVYHPYIQHQTVPPSDNRYLRTWLEPLPRTDSLSSIK
Dr\B9a     SSWSPFSSHASNGLPAVYHPYIPTQVPVSTDTRYLRTWLDCAPRAEPLPQVK
Hf\B9      TSWAPVYAQPSANVSTLYHPYVQSHPIQP-DSRYLRSWLDPTPRAVSAPSLK
  
```

```

Hs\B9      AEPLLGPGEELLGTPEYSLETSAGREAVSNQRPGYGDNCEGSEDKERPDQ
Mm\B9      AEPLLGPGEELLGTPEYSLETSAGREAVSNQRAGYGDNCEGSEDKERPGQ
Lm\B9      AEPLLGLGEIILGGPEYNLETATGREGSSNQSSYGDNCEGSEDKDRPDQ
Dr\B9a     MEPLLGLGEPPGQHEYYILESSTAREINSGHSAGFEDNCEGSEDKERIKV
Hf\B9      TEVLGGGETLAALQKLHGEYLESETISGKAPCYEDSCEEKGNKETSEQ
  
```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxb9

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>
Hf	Hs	Lm	0.467
Hf	Lm	DrB9a	0.433
Hf	Hs	DrB9a	0.178

Dr – Danio rerio, Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxb13 alignment for relative rate test

```

Hf\B13      LKPRWVDTVMFLYEMEGFVGAGQCRNLMAHSALGAH
Lm\B13      LSPCWVDTVMFVYEMEGMLMGASQCRNLMAHSALGSH
DrB13a      LNPRWADTVMFVYEMEGLVGSGQCRNLMAHSALS GH
Hs\B13      MEPGNYATLDGAKDIEGLLGAGGGRNLV AHSPLTSH
Mm\B13      MEPGNYATLDGAKDIEGLLGAGGGRNLVSHSPLASH

Hf\B13      PSPLVHGSGYSTVDVSGSVEPGKQCTPCPMPQASTAAPLPYGYFGSGYYS CRMGR
Lm\B13      PSTLVHGSGYPTVEMSGSGEVAKQCTPCPVPQSSSTAPLPYGYFGSGYYS CRMGR
DrB13a      PSSLVHGSSYPTVDVSTSAESGKQCTPCPVPQASSTGPIPYGYFGNSYYPCRMGR
Hs\B13      PAALMPAVNYAPLDLPGSAEPPKQCHPCPVPQGTSPAPVPYGYFGGGYYS CRVSR
Mm\B13      PAALMPTVNYAPLDLPGSAEPPKQCHPCPVPQGAS PAVVPYGYFGGGYYS CRVSR

Hf\B13      SSIK PCTQPAPLSYPGDSVPVPTDEY PGRPK EFAFYHGYAGAYQPMP SYLDVSVVQ
Lm\B13      GSLK SCTQPAALS YSAETPVASEDYQARA KEFAFYHGYASPYQP VASYLDVSVVQ
DrB13a      GSLK SCTQPSALS YTAETPVTSEEYPTRAKE FAFYHSYPSPYQSMAS YLDVSVVQ
Hs\B13      SSLK PCAQAATL AYPAETPTAGEEYPSR PTEFAFYPGYPGTYQPMAS YLDVSVVQ
Mm\B13      SSLK PCAQTAAL AYPSETPPAGEEYPSR PTEFAFYPGYPGPYQPMAS YLDVSVVQ

Hf\B13      TISAGEPRHEALLPMEGYQPWPLNGWNSQMCCKEQAQPGHLWKSTLADVA AHQQ
Lm\B13      TISAGEPRHETLLPVDSYQPWAL TGWNSQMYCKDQTQPGHLWKSALADVVA HQ
DrB13a      TLGTGEPRHDSLLPMSYQPWALAGWNSQMYCKDQGQAGHLWKSALADVVA HQ
Hs\B13      TLGPGEPRHDSLLPVDSYQSWALAGWNSQMCCGEQNPPGPFWKAAFASSGQH PP
Mm\B13      TLGPGEPRHDSLLPVDSYQPWALAGWNSQMCCGEQNPPGPFWKAAFAFAPSVQH PP

```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxb13

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0	**
Hf	Lm	Dr13a	0.0771	
Hf	Hs	Dr13a	0.00022	**

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxc4 alignment for relative rate test

```

HsC4      M S S Y L M D S N Y I D P K F P P C E E Y S Q N S Y I P E H S P E Y Y G R T R E S G F Q H H H Q E L Y P R
MmC4      M S S Y L M D S N Y I D P K F P P C E E Y S Q N S Y I P E H S P E Y Y G R T R E S G F Q H H H Q E L Y P R
DrC4a     M S S Y L M D S N Y I D P K F P P C E E Y S Q N S Y I P E H S P E Y Y S R A R D S G Y Q H H H Q E L Y P R
LmC4      M S S Y L M D S N Y I D P K F P P C E E Y S Q N N Y I P E H S P E Y Y S R T R D S G F Q H H H Q E L Y P R
EsharkC4  M S S F L M G S N Y I D P K F P P C E E Y S Q N S Y I P D H S S E Y Y S R P R D S A Y P P Q H Q D L Y Q R
  
```

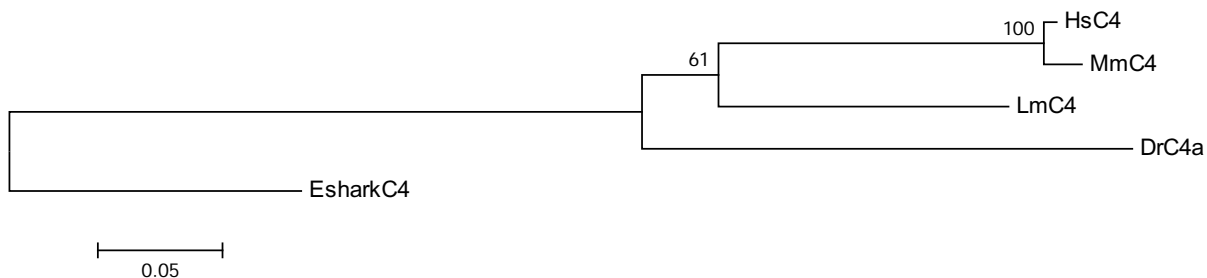
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HsC4      P S Y P E R Q Y S C T S L Q G P G N S R G H G P A Q A G H H H P E K Q S L C E P A P L S G A S A S
MmC4      P S Y P E R Q Y S C T S L Q G P G N S R A H G P A Q A G H H H P E K Q P L C E P A P L S G T S A S
DrC4a     A S Y Q E R Q Y N C A S I P E P D T Q R G H G L P H A G H L L G K G S A S C E P P P L P L S P A T
LmC4      P N Y P E R Q F N C T S I Q G P G N Q R G H G Q P Q A G H H L P E K P L L I E Q P P I S T P S N T
EsharkC4  P N Y P E R Q F A C A T V Q G P G N R A G H E Q H Q V A H Q H I S S P V P Y E P A A L S T S T T T
  
```

```

HsC4      P S P A P P A C S Q P A P D H P S S A A S K Q P I V Y P W M K K I H V S T V N P N Y N G E P
MmC4      P S P A P P A C S Q P A P D H P S S A A S K Q P I V Y P W M K K I H V S T V N P N Y N G E P
DrC4a     P S A A S S A C N Q A T P E H P S S A S A K Q P V V Y P W M K K I H V S T V N S S Y N G E P
LmC4      T S P A P P S C N Q P N T E Q P N N T T S K Q P V V Y P W M K K I H V S T V N P N Y N G E P
EsharkC4  S P P S S A C T Q Q N L E Q Q R T N A K Q P I V Y P W M K K I H V N T V N H S Y T G E I
  
```

NJ tree rooted with elephant shark (Eshark)



Tajima relative rate test – Hoxc4

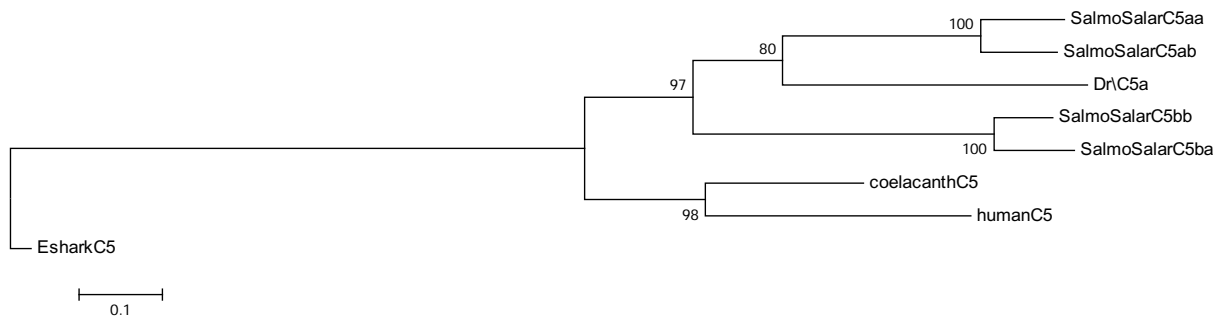
<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>
Eshark	Lm	Hs	0.251
Eshark	Lm	DrC4a	0.257
Eshark	Hs	DrC4a	0.835

Dr – Danio rerio, Eshark – Callorinchus milii, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxc5 alignment for relative rate test

SalmoSalarC5aa	MSSYVASIFKQTHEASSCNMNSLGYGSLSDFDQANYAYNGHFNGTFTSD
SalmoSalarC5ab	MSSYVANIFKQTHEASSFNMSFGYGSLSSLHQDNYAYNGHLNGTFTSD
Dr\C5a	MSSYVGKSFSTQDASSCRMHTFDYGAHSEFHESNYAYEGLLGGSFSSQ
SalmoSalarC5bb	MSSYVASLFKQTHDASTFAVHNHGYGSNPELNVSGYSGYGHHRGSFASR
SalmoSalarC5ba	MSSYVASLFKQTHEASAFALHNHGYGSSPELNVSGYCGFGHHRGSFASP
coelacanthC5	MSSYVASLYKQSQNPAYAMQSYGYGSVSEVHPSRYCYGGLMSITFPSPG
humanC5	MSSYVASFYKQSPNIPAYNMQTCGYGSASEVQASRYCYGGLLSITFPPA
EsharkC5	MNSYSASFCKQDQNGSGCATKGWREGSTLQMCPPRYSYRGLINISLPPAR
SalmoSalarC5aa	ATVSLKREEMNSSLRGNTDTSPPRPQSYSALSSRNSVQCLSDGILSKATE
SalmoSalarC5ab	STASLKREEMETSLRGNTDAPPPRLQSCSAASSRNSVQCLRDGILSKGTG
Dr\C5a	IPTSLRREAINTTDRARSSAAVQRTQSCSALGSRSFVSPLSHGLLSQKAE
SalmoSalarC5bb	SSSSIGMGEMNAALRGNPBDTPRPESSTGDSTQRHLMNSLNLGLYRRKPV
SalmoSalarC5ba	SSSSRGMVEMNSLGHGNPBDTPRPESSTGDASQRRHMNSLNLGLYCRKPE
coelacanthC5	PSSTLNGMDMSSSPRTNPDRSCTVMGSSEHTFSRNDQSSLNLGIYSQKAG
humanC5	PSNSLHGVDMAANPRAHPDRACSAAAPGHAPGRDEAAPLNPGMYSQKAA
EsharkC5	VSHQSAEGAISAIAGNRPFAAMGDSVDGPGSERRQSKATPNPGIYCQTR
SalmoSalarC5aa	MMEVVETPTEESAIVKQVETMQPSKKHQDSQQQPQIFPWTMVKLHMIH
SalmoSalarC5ab	RMEVVENPTEENAIVKQVETMQPSKKHQDSQQQPRIFFPWTMVKLHMSH
Dr\C5a	GMEVMEKPSRTDDIKMETTSASTQRQN-QSQPQIYFPWTMVKLHMSH
SalmoSalarC5bb	TSDLSEMPQTQGEIKVGTLPSTQPQTSEQQPQIYFPWTMVKLHMGH
SalmoSalarC5ba	TSDLFSEMHTQTGEIKVVTLPSTQPQTSEPPQPQIYFPWTMVKLHMGH
coelacanthC5	GIVLEDKPKSTVEIKAEPVQTPQGGQQQSQPQIYFPWTMVKLHMSH
humanC5	RPAL EERAKSSGEIKEEQAQTPAGLSQPPAPPQIYFPWTMVKLHMSH
EsharkC5	GKGVENSQPQIVREPSPETGETHTQRGQTQQQPRIYFPWTMVKVHLSH

NJ tree rooted to elephant shark (Eshark)



Tajima relative rate test – Hoxc5

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>
Eshark	coelacanth	human	0.285
Eshark	coelacanth	DrC5a	0.223
Eshark	human	DrC5a	0.622

Dr – Danio rerio, Eshark – Callorinchus milii

Hoxc6 alignment for relative rate test

```

Lm\C6      MNSYFANPSLSCHLTSGQEVLNVALNSTAYDPVRHFSTYGAAMAQNRIYSSPFYSPQEN
EsharkC6   MNSYFANPSLPCHLASGQEILPSAGLNSAAFDPVRHFSTYGAAVSQGRIYSSPYYSTQEN
Mm\C6      MNSYFTNPSPSLCHLAGGQDVLNVALNSTAYDPVRHFSTYGAAVAQNRIYSTPFYSPQEN
Hs\C6      MNSYFTNPSPSLCHLAGGQDVLNVALNSTAYDPVRHFSTYGAAVAQNRIYSTPFYSPQEN
newt/c6    MNSYFTNPSPSLCHLASGQEVLNVALNSSAYDPVRHFSTYGEAVAQNRIYSSPFYSPQDN
Dr\C6b     MNSYFTNPSPSLCHLNSGQEVLPSVAISSTNYDPVRHFSPYGAAVAQNRIYSNPFYSHQEN
Dr\C6a     MNSYFANPSLSCHLSGGQEVLNPMPLNSTTYDSVRHFSSYGTTVTQNRIYASPFYSPQDN
    
```

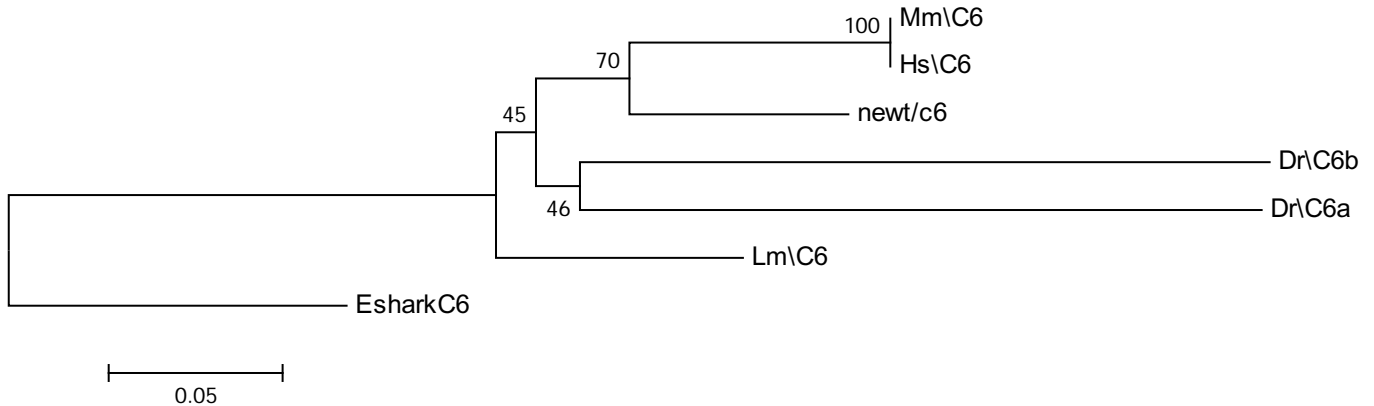
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Lm\C6      VVFGSSRPYDYGSSAFYQEKDMLPSCRQNMINTQTSIAQEFNSDHSRTQEOKST
EsharkC6   VVFGSSGRPFYDGSNAFYQEKDLPASCRQNLGNTDNP IAQDLNGEHIRAQEEKSN
Mm\C6      VVFSSSRPYDYGSNSFYQEKDMLSNCRQNLGNTQTSIAQDFSSSEQGRPQDQKAS
Hs\C6      VVFSSSRPYDYGSNSFYQEKDMLSNCRQNLGNTQTSIAQDFSSSEQGRPQDQKAS
newt/c6    VVFSSGRPYEYGSNAFYQDKDMLSSCRQNMGNTQTSIAQDFSSDQSRVQEOKTS
Dr\C6b     VMFGSSRPYDYGSNMFYQDKDVLPSCRQGFQGTQGS LTQDYASDQGKTVEPKGV
Dr\C6a     VVFGSSRPYEYGSNVFLQDKDVLPSCRQTMGNAQSHVAQEYNLEQARTQDQKAN
    
```

```

Lm\C6      VQIYPWMQRMNSHSHSVGYG
EsharkC6   FPIYPWMQRVNSHSHSVGYG
Mm\C6      IQIYPWMQRMNSHSHSVGYG
Hs\C6      IQIYPWMQRMNSHSHSVGYG
newt/c6    IQIYPWMQRMNSHSHSVGYG
Dr\C6b     VQIYPWMQRMNSHRVGYG
Dr\C6a     IQIYPWMQRMNSHSHSVGYG
    
```

NJ tree rooted to elephant shark (Eshark)



Tajima relative rate test – Hoxc6

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Eshark	Lm	Hs	0.346	
Eshark	Lm	DrC6a	0.006	**
Eshark	Lm	DrC6b	0.004	**
Eshark	Hs	Drc6a	0.061	
Eshark	Hs	Drc6b	0.033	*

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Eshark – Callorhynchus milii, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus, newt – Notophthalmus viridescens

Hoxc8 alignment for relative rate test

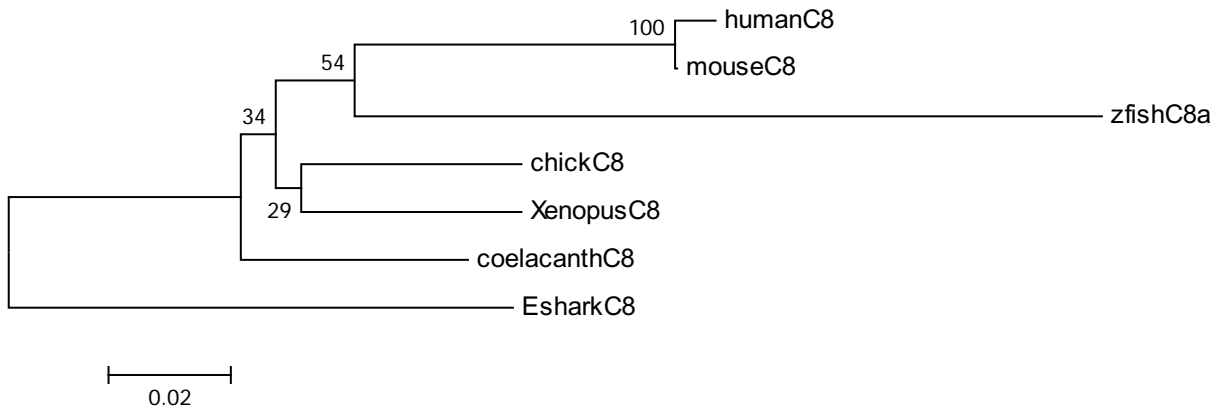
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humanC8      MSSYFVNPLFSKYKAGESLEPAYDCRFPQSVGRSHALVYGP GGSAPGFQHASHVQDF
mouseC8      MSSYFVNPLFSKYKGGESLEPAYDCRFPQSVGRSHALVYGP GGSAPGFQHASHVQDF
chickC8      MSSYFVNPLFSKYKGGESLEPTYDCRFPQSVSRSHALVYGP GTTAPT FQHPSHVQEF
XenopusC8   MSSYFVNPLFSKYKGSSELEPTYDCRFPQSVSRSHALVYGP SATAPGFQHP SHVQEF
coelacanthC8 MSSYFVNPLFSKYKGGESLEPTYDCRFPQSVSRSHALVYGP STTAPS FQHPSHVQDF
EsharkC8    MSSYFVNPLFSKYKTGESLDPTYDCRFPQSVGRSHALVYGP GSGGPGFQHP SHVQEF
zfishC8a    MSSYFVNPLFSKYKGGETLEPTYDCRFPQSVARSH TLVYGHGAAAPGFQHP SHVQDF

humanC8      FHHGTSGISNSGYQQNPCSLSCHGDASKFYGYEALPRQSLYGAQQEASVVQYPDCKSSAN
mouseC8      FHHGTSGISNSGYQQNPCSLSCHGDASKFYGYEALPRQSLYGAQQEASVVQYPDCKSSAN
chickC8      FHHGTSSISNSGYQQNPCALACHGDASKFYGYEALPRQSLYGAQQETT VVQYPDCKSSSN
XenopusC8   FHHGTSSITNSGYQQNPCALTCHGDASKFYGYEALPRQSLYGAQQEASVVQYPDCKSSSN
coelacanthC8 FHHGTSSISSTGYQQNPCALSCHGDASKFYGYEALPRQSLYGAQQEAS MVQYPDCKSSSN
EsharkC8    FHHGTSSLSTSGYQQSPCGLTCHGDASKFYGYEPMPRQSLYGTQQEAS MVQYPDCKSSSG
zfishC8a    FHHGTTGISNPGYQQNPCALACHGDATK FYGYEALPRQPLYGTQQEATLAQYPDCKSSNS

humanC8      TNSSEGQGHNLNQNSSPSLMFPWMRPH
mouseC8      TNSSEGQGHNLNQNSSPSLMFPWMRPH
chickC8      SNSSEGQGHNLNQNSSPSLMFPWMRPH
XenopusC8   TNTSEGQGHNLNQNSSPSLMFPWMRPH
coelacanthC8 SNTGEGQGHNLNQNSSPSLMFPWMRPH
EsharkC8    SNTGEAQGHNLNQNSSPNLMFPWMRPH
zfishC8a    TNPGEGQGHLSQNSSPSLMFPWMRPH
    
```

NJ tree rooted to elephant shark (Eshark)



Tajima relative rate test – Hoxc8

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Eshark	coelacanth	human	0.248	
Eshark	coelacanth	zfishc8a	0.008	**
Eshark	human	zfishc8a	0.071	

Green highlight denotes gene with significantly faster rate of evolution
zfish – Danio rerio, Eshark – Callorhinchus milii

Alignment for Hoxc9 relative rate test

```

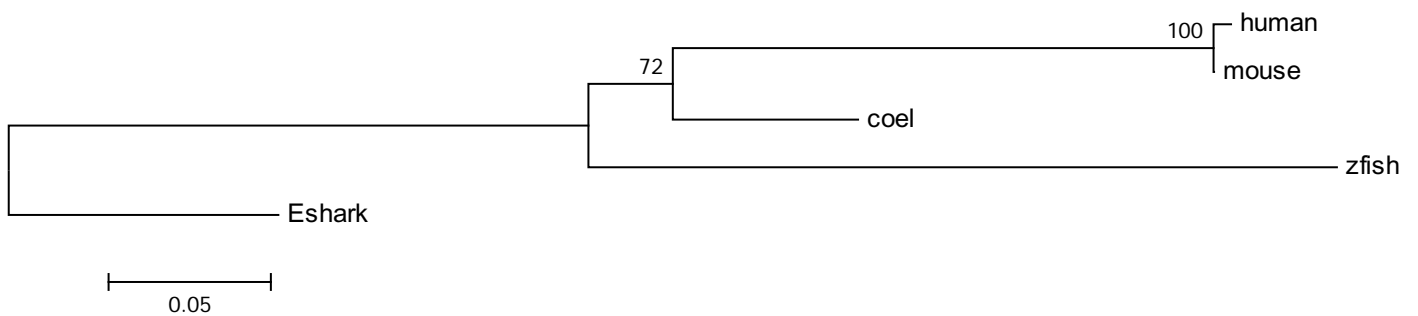
Human-c9      MSATGPISNYVDSLISHDNEDLLASRFPATGAHPAAARPSGLVPDCSDFPSCSFAPKPA
Mouse-c9      MSATGPISNYVDSLISHDNEDLLASRFPATGAHPAAARPSGLVPDCSDFPSCSFAPKPA
Coel-c9       MSTSGPISNYVDSLISHENEEILASRFPATGPHPAASRSSGLVPDCTDFPSCSFAPKPA
Zfish-c9a     MSATGPISNYVDSLINHESDVLASRFATATGPISSSSRPTPLVPECADYPSCSFAPKPP
Eshark-c9     MSTSGALTNYYVDSIINHENEEMFAARFAASGSHPPAPRPAGLVPDCTDFPSCSFTPKPP

Human-c9      VFSTSWAPVPSQSSVVYHPYGPQPHLGADTRYMRTWLEPLSGAVSFPSFPAGGRH
Mouse-c9      VFSTSWAPVPSQSSVVYHPYGPQPHLGADTRYMRTWLEPLSGAVSFPSFPAGGRH
Coel-c9       VFTTSWAPVHSQSSVVYHPYTHQPHIGTDSRYMRSWLEPISGAVSFPGFPTNSRH
Zfish-c9a     VFTTSWAPVHSQSSVVYHPYTHQPHLGTDSRYVRSWLEPIPGTVSFPGYAGNSRH
Eshark-c9     VFTTTWAPAHSQSSVVYHPYSHQPHLGTDTRYMRSWLEPISGVPVPHGFPSTGRH

Human-c9      YALKPDAYPGRRADCEGRSYPDYMYGSPRDRAQTLPSPEADALAGSKHKKEEK
Mouse-c9      YALKPDAYPGRRADCPDGRSYPDYMYGSPRDRAQTLPSPEADALAGSKHKKEEK
Coel-c9       YGLKPDAFPGRRAECTDGRSYPDYMYGSPRERTQNI PSESEIAAASKHKKEEK
Zfish-c9a     YGLKPDTFQDPRADCGNGRTYTDYLYCSAREKQNT PSETESLSSGKHKDDK
Eshark-c9     YGVKPESFPGRRECTDGRSFTDYIYGSSTDKIQSI PSPGSETMVS AKHKDEK

Human-c9      ADLDPSNPVANW
Mouse-c9      ADLDPSNPVANW
Coel-c9       AELDPNPNVANW
Zfish-c9a     AELDPDNPVANW
Eshark-c9     TEIDPSNPAANW
    
```

NJ tree rooted to elephant shark (Eshark)



Tajima relative rate test – Hoxc9

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Eshark	Coelacanth	human	0.004	**
Eshark	Coelacanth	zfish	0.002	**
Eshark	human	zfish	0.631	

Green highlight denotes gene with significantly faster rate of evolution
zfish – *Danio rerio*, Eshark – *Callorhynchus milii*

Hoxc10 alignment for relative rate test

```

Mm\C10      MTCPRNVTPN SYAEPLAAPGGGER YNRNAGMYMQSGSDFNCGMRGCGLAPSLSKRDEGGSPNLA
Hs\C10      MTCPRNVTPN SYAEPLAAPGGGER YSR SAGMYMQSGSDFNCGMRGCGLAPSLSKRDEGSSPSLA
Xenopus\c10 MSCPNNVTPNS FMDSLAGSCRGDNYSTSPGMYLQTGSEFSCGMRNCGI VPSLSKRDDVNNPGLS
Lm\C10      MSFPNNVTANS FMDSVAGTCRGENYSSNTGMYMQPGADFGCGMRNCGI I PLSLSKRDEVNNTNLS
Eshark\C10  MSCPNNVAANT FMDPLAAVCRGENFSSNPGMYMQAGAEFGCGVRNCGLI PALSLSKRDEVNPNLA
Dr\C10a     MSCPNNVAANA FMDSLVGPFRGESYSSNSGMYMQTSAEYGC SMGSFGIVGTLSKRDDLQPSGMH

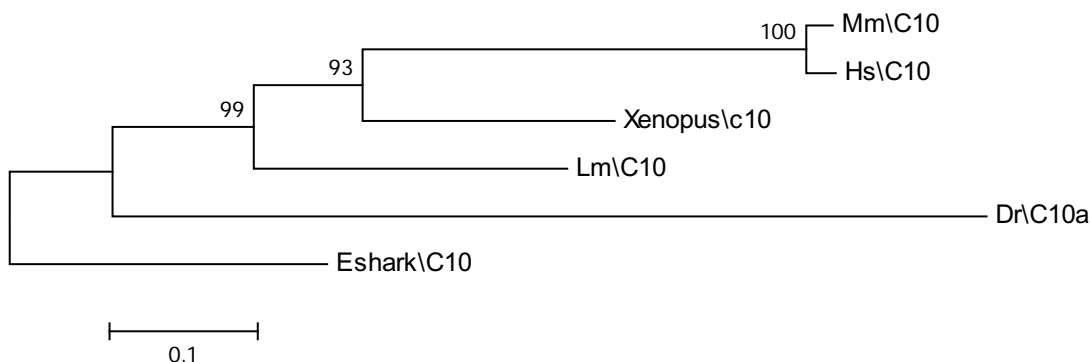
Mm\C10      LNTYPYLSQLDSWGD PKAAYRLEQP VGRPLSSCSYPPSVKEENVCCMYSAEKRAKSGPEAALYSH
Hs\C10      LNTYPYLSQLDSWGD PKAAYRLEQP VGRPLSSCSYPPSVKEENVCCMYSAEKRAKSGPEAALYSH
Xenopus\c10 LNTYPYLSQLDNWCD PKNTYRIEQPVARQLSSCSFPTNVKEENVCCMYNTDKRAKNATEAALYPN
Lm\C10      LNTYPYISQLDSWGD PKNSYRIEQPVARQLPSCSFPTNVKEENVCCMYSSDKGAKGSAESPLYPR
Eshark\C10  LNTYPYLSQLDGWGE HPKSYRIEQPVARTLPSCSFPTTVKEENICCIY GSEKRGKTTGDGALYPG
Dr\C10a     LGSYQYLSQRDTWI AGSKTYRGSQPVAQPLHPCSF PASVKEEAI PCLYQPDIDAKESGEKSTYIR

Mm\C10      PLPESCLGEHEVPVPS YRASPSYKTPHCAGANEF EAPFEQRASLN RTEESPQLGGKVSFPET
Hs\C10      PLPESCLGEHEVPVPS YRASPSYKTPHCAGANEF EAPFEQRASLN RTEESPQLGGKVSFPET
Xenopus\c10 QMPETRPSDHEVPVPS YRATQGYKTPSCHSTGDFETS FENRTSVNRSEEQQQAVGKGGFPEN
Lm\C10      LLSSSCP SDQEVVPVPS YFRVNQGFKN SGCNTTNEFDTSFSSSAS FARANPQQQSVSKEVFSEK
Eshark\C10  LTPETCPTENEVPVPG YFRVSQGYKSPDCSTTAEFDSAFNSAPNLQQIDQQPPTS VTESFIKS
Dr\C10a     LGDN SHPNQSAVSTPDYFRRSQVYASERGHG HGFSGDFNPIPRISPVEASDSCVKSSKARQH

Mm\C10      PSDSQKTEQSLAGPKASP SESEKTADSSPDTSDNEAKEE IKAENTTGNWL
Hs\C10      PSDSQKTEQSLAGPKGSP SESEKAADSSPDTSDNEAKEE IKAENTTGNWL
Xenopus\c10 TTDNQKTEKSLPAPKLPP SEGDKNTDTSTDNSDTEAKEDI KAENAAGNWL
Lm\C10      STDNQKLEDNVSQRIT PVETEKN TDTSTDNSDNEAKEDMKTESATGNWL
Eshark\C10  PKDGGNREDSSRVTP SKETETVTQQDL SSENSDTEFKEETKRENAAGSWL
Dr\C10a     PEDKGTQEDDMDQRQTRKEESVSKTESCTDDSESELKDES KLEKATGNWL

```

NJ tree rooted to elephant shark (Eshark)



Tajima relative rate test – Hoxc10

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Eshark	Lm	Hs	0.015	*
Eshark	Lm	Drc10a	0.0001	*
Eshark	Hs	Drc10a	0.118	

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Eshark – Callorhynchus milii, Lm – Latimeria menadoensis, Hs – Homo sapiens, Mm – Mus musculus

Hoxc11 alignment for relative rate test

```

Hs\C11      VNLGNFCSPSRKERGADFGGERGSCASNLYLPSTYYMPEFSTVSSFLPQAPSRQIS
chick\C11  VNLGNFCSQSRKERSAEFGERAGCASNLYLPSTYYVPEFSTVSSFLPQAPSRQIS
Lm\C11     MNLGNFCSQSRKDRSAEFGDRAGCTSNLYLPSTYYVPEFSSVSSFLPQAPSRQIT
Eshark\C11 MNLGNFCSQTRKERTAEFADRGCANMYLPSTYYVPEFTAMSTFLPQATSrqIT
Dr\C11a    VNLGNFCSQTRKDRTSEFGDRTGCASNIYLPSTYYVPEFSAVSSFLPQGPSRQIT
Dr\C11b    VNIGNFCSQSRKERTSEFGERASCASNLYLPSTYYVPEFSTVSSFLPQAQSRQIT
  
```

```

Hs\C11      YPYSAQVPPVREVSYGLEPSGKWHHRNSYSSCYAADELHMHRECLPPSTVTEI
chick\C11  YPYSTNLSPVREVSYGLEDPSSKWHHRNSYASCYSAEDLMHRECIPPSTMTMTEM
Lm\C11     YPYSTNLPPMREVSYGLEDPSSKWHHRNSYASCYSAEDLMHRECIPPSTMTMTEM
Eshark\C11 YPYSTNLSPVRDVSYGLEDPSSKWHHRNTYTSCYSAEDLMHRDCIPPSTMTTEL
Dr\C11a    YPYSTNLSPVRDVSYGLEDPSSKWHHRNSYASCYSGEDLVHRDCLPPSTMTMTEM
Dr\C11b    YSYSTNFTQVRDLPFELNPSGKWHHRGNYSYAEEDLVHRDCLPPSTMTMTEM
  
```

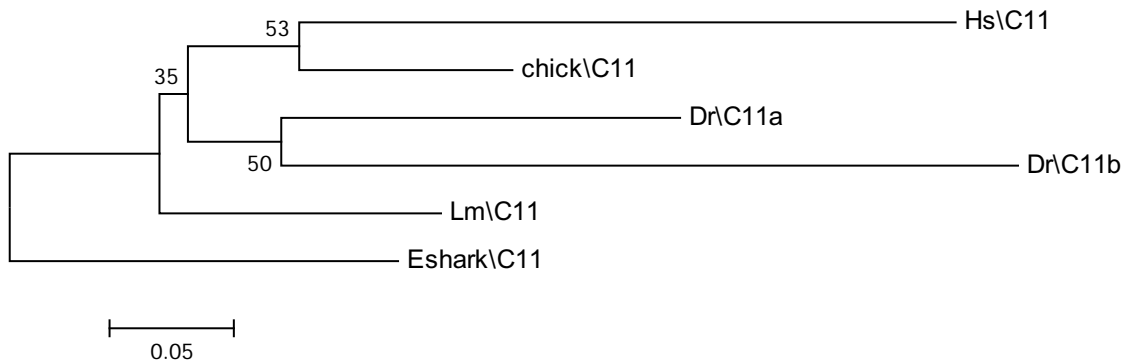
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Hs\C11      LMKNEGSYGHHPHPSAPHPGFYSSVNKNSVLPQAFDRFFDNAYCGDPP
chick\C11  LMKNESAYSHHPSSNHHPGFYGGMNKNTVLPQGFDREFFENAYCANPT
Lm\C11     LMKNESVYNHHPSSNHPSGFYSSMSKNSVLPQGFDREFFENAYCSNQQ
Eshark\C11 LMKNESIYNHHPSSNHSAFYGNVKGSSVLPQGFDREFFETSycASQA
Dr\C11a    LMKNESVYSHHPSSSSGFYTGvGKNNVLPQGFDREFFETAYCSDNQ
Dr\C11b    LMKNENVYNHHPHAIINGGFYSSIGKTNVLPQSFDRFLDCAQsADGG
  
```

```

Hs\C11      CSGKGEAKGEPEPPASGLASRAEAGAEAEAEANTNSSGSAHAKEPAKGAAPNAPRTR
chick\C11  CGQKGEKGEAEPEQSHALSSRGETGMDPEDENTTSSASSSNKEGSKSSNSAPRTR
Lm\C11     CVQKSEGKLESESQPSVLSSGGDQEKEPEDENTNSSASSSNKEGSKTSNSSTPRTR
Eshark\C11 CVQKGDRLKLESMAQPSALSSGTDEERTTGDENTISAASSGNRAEGKTSNSSGPRTR
Dr\C11a    CLQKSENKLETSQQPTAVSAAREPEKDPEDehtNSCTSAADGNASKSSHSGTPrTR
Dr\C11b    CLQKGSgKPEsAQVSSVLRSTADGEKELECEtTtSFETSSGNDNQTksGHSTtPRMR
  
```

NJ tree rooted to elephant shark (Eshark)



Tajima relative rate test – Hoxc11

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Eshark	Lm	Hs	0.00001	**
Eshark	Lm	Drc11a	0.071	
Eshark	Lm	Drc11b	0.00002	**
Eshark	Hs	Drc11a	0.004	**
Eshark	Hs	Drc11b	0.884	

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Eshark – Callorhynchus milii, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus, chick – Gallus gallus

Hoxc12 alignment for relative rate test

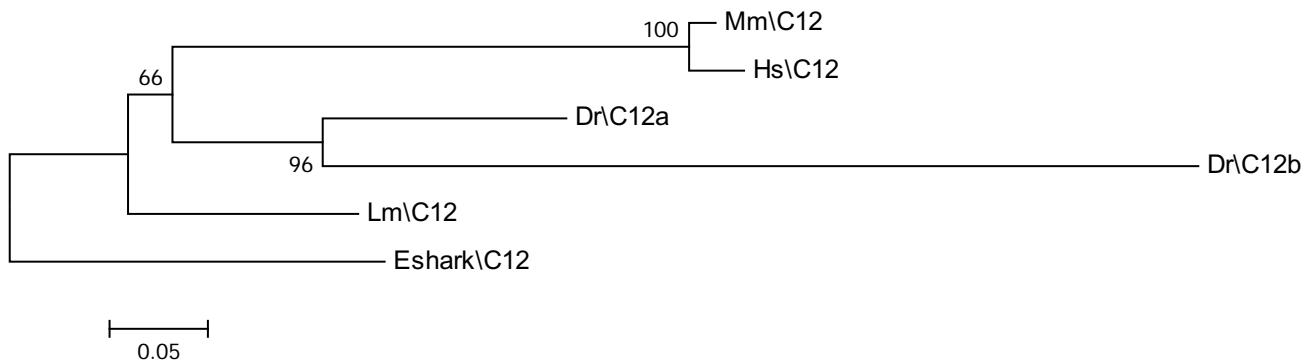
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Mm\C12      MGEHNLLNPGFVGPVLVNIHTGDTFYFPNFRASGAQLPGLPSLSYPRRDNVCSLPWPSAEPCNGYPQ
Hs\C12      MGEHNLLNPGFVGPVLVNIHTGDTFYFPNFRASGAQLPGLPSLSYPRRDNVCSLSWPSAEPCNGYPQ
Lm\C12      MGEHNLLNPGFVGPVLVNIHTGDAFYFPNFRTSGGQLAGLPSLSYPRRDNVCSLPWTSSEPCNGYPQ
Eshark\C12  MGEHNLLNPSFVGPVLVNIHTGDAFYFPNFRTSGGQLAGLSSLSYPRRDNVCSLPWPVSDQCNGYPQ
Dr\C12a     MGEHNLLNPGFVGPVLVNIHTGDRFYFPNFRASGGQLAGLPSLSYPRRDNVCSLPWNPSESCNGYPQ
Dr\C12b     MGEHNLNPGFVGPVLVNIINARDAFYLSNFRASGGQLAGLQTLRLSRRDNVCSLPWNPSEACSGYPQ

Mm\C12      PYLGSVSVLNPPFGRTCELARVEDSKGYREPCAEGGGLKREERGREPGAGPLLQLEPSGPPALGF
Hs\C12      PYLGSVSVLNPPFGRTCELARVEDGKGYREPCAEGGGLKREERGRDPGAGPLLPLEPSGPPALGF
Lm\C12      PYLSNPVSNPSFNACDIARAEENKCYRDACSENSSLKREERARDSSLVPHEPGIPNGMNASF
Eshark\C12  SYLGNTVSNPSFNRTCDIGRVEESKSYRDGGSVVALKREERIRDNSVLPHESAIPNGIGANFS
Dr\C12a     SYFSSPVSINPSFNRSCEITRLEESKCYRDSCDNNSLKREERARDTSVSSHGMHNGMNGSGTFS
Dr\C12b     SHISGPVTLNHTYNQSCDITRQEDNKCFYTSGGGDNNSLISKEGALDNNSSVNGQNNLNGMGGSYS

Mm\C12      KYDYTAGPPHDPSCQSLESDSSSSLLNEGNKSAAGDGSLSVPLNPGGGLSASGAPWYPIHSRSR
Hs\C12      KYDYAAGPPHDPSCQSLESDSSSSLLNEGNKGAAGDGSLSVPLNPGGGLSASGAPWYPIINSRSR
Lm\C12      KYDYSNGEMTQDPSCQSLESDSNSLLNEGSKNSNQSTMSSPISNGNSLSTAGAPWYPMHTRSR
Eshark\C12  KYDYPGSEPHQEHEGACHPLESDSNSPLMNDQEKNCGNNSALASPI THGNSLPAGGTPWFPVHARTR
Dr\C12a     KYDYGTEHLTQDPSCQSLESDSSSSVLNEGGKTSASDQTLVVSQGNHASNIAGGGAPWYPMHTRTR
Dr\C12b     KYDCLTPAPIPNPRLCRSLESVSGCSFINEGAKTSSGIHSLTSPDIQTSVAALNGALWYPMHRQTR
    
```

NJ tree rooted to elephant shark (Eshark)



Tajima relative rate test – Hoxc12

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Eshark	Lm	Hs	0.00006	**
Eshark	Lm	Drc12a	0.007	**
Eshark	Lm	Drc12b	0	**
Eshark	Hs	Drc12a	0.105	
Eshark	Hs	Drc12b	0.005	**

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Eshark – Callorhinchus milii, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxc13 alignment for relative rate test

```

Mm\C13      MDGLGGSCPASHCRDLLPHPVLARPPAPLGAPQGAVYTDIPAPEAARQCPAPPTS
Hs\C13      MDGLGSSCPASHCRDLLPHPVLRPPAPLGAPQGAVYTDIPAPEAARQCPAPPTS
Lm\C13      MEGLSGNCPATHCRDLISHPALGRHSSTIATHQGPVYSDIAAPEAGRQCPAPQTS
Eshark\C13  MEALSGNCSSSHCRDLIHPALGRHSGTLAHHQGPVYSELPAPEAGRQCPAPQTS
Dr\C13a     MEGLSGNCPATHCRELI SHPALGRHSGTIATHQGSVYLDISSPETGRQCPAPQTS
Dr\C13b     MEGLSGNCPASHCRDFISHPALGRHSGSLASHQGTVYPDITTTQDAGRQFPAPQAS
    
```

```

Mm\C13      SSATLGYGYPFGGSYYGCRLSHNVNLQQKAYHPGDKYPEPSGALPGDDLSSRAKEF
Hs\C13      SSATLGYGYPFGGSYYGCRLSHNVNLQQKAYHPGDKYPEPSGALPGDDLSSRAKEF
Lm\C13      SSATLGYGYPFGGTYYGCRLSHNVNLQQKSYHPAEKYAETSSSLPSEELSSRAKEF
Eshark\C13  SSAALGYSYPFGSAYYGCRLPNHNVLQKAYHPSEKYSEAATALPSEELSSRAKEF
Dr\C13a     SSASLSYGYPFGNPNYYGCRLSHNVNLQQKSYHPAEKYAETSSALPTEELSSRAKEF
Dr\C13b     SGTSLGYGYAFGSPYYGCRLSYNVNLQQKSYHPAEKYMETS GALPAEELSSRSKEF
    
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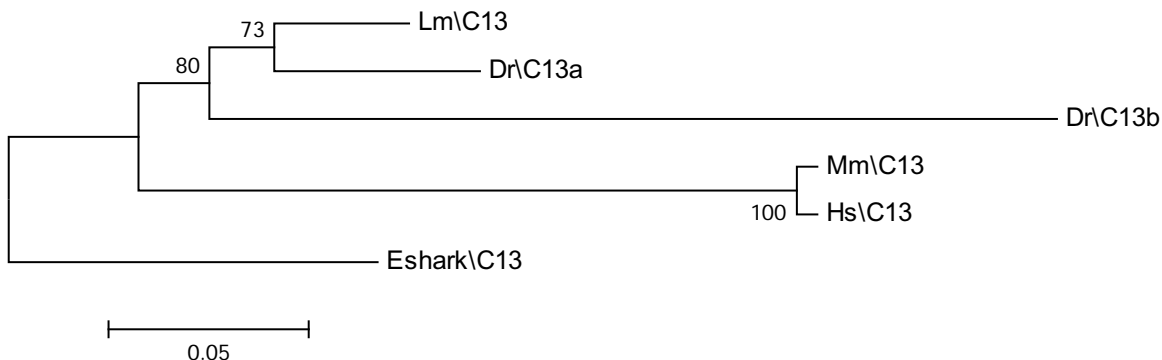
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Mm\C13      AFYPSFASSYQAMPGYLDVSVVPGISGHPEPRHDALIPVEGYQHWALNSGWD
Hs\C13      AFYPSFASSYQAMPGYLDVSVVPGISGHPEPRHDALIPVEGYQHWALNSGWD
Lm\C13      AFYPSFASSYQAVPGYLDVSVVPSISAHPEPRHDALIPMEGYQHWALNSGWD
Eshark\C13  AFYPSFASSYQVPVSYLDVSVVPGIGAHGEPRHDALIPMEGYQHWALNSWD
Dr\C13a     AFYPSFASSYQAVPGYLDMSVVPSISAHPEPRHDALIPMEGYQHWALNSGWD
Dr\C13b     AIYPSFASSYQTVPGYLDVVPVPGISAHPESRHEALFPMDSYQHWALNSGWD
    
```

```

Mm\C13      SQVYCSKEQSQSAHLWKSPPFDVVPLQPEVSSY
Hs\C13      SQVYCSKEQSQSAHLWKSPPFDVVPLQPEVSSY
Lm\C13      GQVYCSKEQTQSTHLWKSPPFDVVPLQPEVNSY
Eshark\C13  GQVYCSKEQTQSSHLWKSPPFDVVPLQPEGSNY
Dr\C13a     GQVYCSKEQTQSSHLWKSPPFDVVPLQPEVSSY
Dr\C13b     EQLYCSKEQTHFNHLWKSQFSDVVPHQAEMNGY
    
```

NJ tree rooted to elephant shark (Eshark)



Tajima relative rate test – Hoxc13

Eshark	Lm	Hs	0.005	**
Eshark	Lm	Drc13a	0.248	
Eshark	Lm	Drc13b	0.00006	**
Eshark	Hs	Drc13a	0.039	*
Eshark	Hs	Drc13b	0.258	

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Eshark – Callorhynchus milii, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxd1 alignment for relative rate test

```

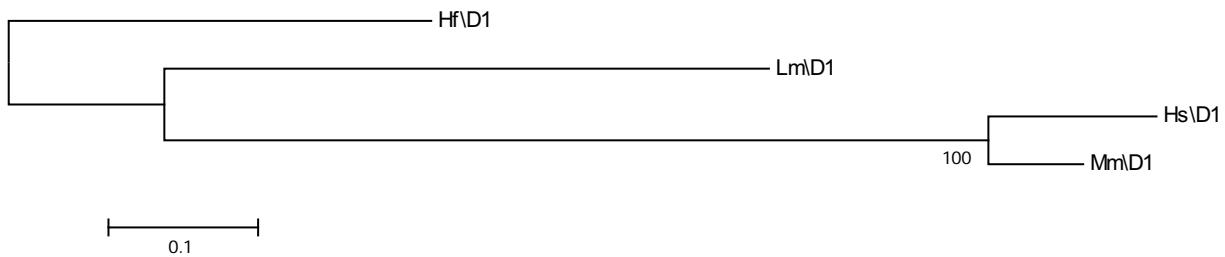
Lm\D1      MNTFIEYISSGEILAFSSKFYADHRPASLQLYSGENHCVGSLPIG
Hf\D1      MNSYLEYIPSAIDILTFSPKFCSNSPPVSLQQCSGEGRYAASEPGG
Hs\D1      MSSYLEYVSCSSVLSLAPKFCS DARPVALQPAFGDGAFVSCCLPLA
Mm\D1      MSSYLEYVSCAAVLAFAPKFCCADARPVALQPAFGDGAFVSCCLPLA

Lm\D1      LHSPTHHYLHHQAPGSLEAFYEYNSPESNFIAQGSSD
Hf\D1      NPSPSHHHLHQSVPAALELSYDSSPSDINLLPQSNLD
Hs\D1      AARPSARPSVPPAQCTLEGAYEPGAADYGFLGSGPAD
Mm\D1      TARPTAQSPVPQAPCTLEGAYERGAAEYGFLGSGPAD

Lm\D1      FPLGANHELDNNEGHAQYANVYSGNESFSFNQRQSDYNTFEDHCRRHDTEQYDFY
Hf\D1      FPYAANQELDDTGGLIPYNTVYSGSASFPLTRQHEYNSEQEYQTYGKEFPNFY
Hs\D1      FPGVLGRAADDGGSHVHYATVFSGGGSFLLSGQVDYAGEPGPPACLKASADGH
Mm\D1      FPGALGRAADEGGAHVHYATVFSGGGSFLLSGQVDFAGEPGPPACLKEPADGH

Lm\D1      PENHQNPSQGTGSYSSPPSTAQATANTFDWMKVKNPP
Hf\D1      PGHYQSPSTSQGGYQSPAAQKITANTFEWMKVKNPP
Hs\D1      PGAFQTASPAPGTYPSPASGLPAAFSTFEWMKVKNAS
Mm\D1      GPPFQTVSPAPGACPSPTSSLPAAHSTFEWMKVKNAP
    
```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxd1

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0.033	*

Green highlight denotes gene with significantly faster rate of evolution
Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxd3 alignment for relative rate test

```

Hf\D3      MQKATYYDNSGIFGGYSYQKTNAYSYSSSHQAYPPTSSENDYQSSTCPIQTSSV
Lm\D3      MQKTAYYDNSGLFGGYPYTKSDAYGYNSTHQPYQSATETDYPSSACSIQTSTI
Dr\D3      MQKATYYDNAGLFGGYSYPKSDSYTYGPTHQGFSSSSIENDYQSPICPIQTTSV
Hs\D3      MQKAAYYENPGLFGGYGYSKTDYGYSTPHQPYPSSLDTDYPGSACSIQSSAL
Mm\D3      MQKAAYYENPGLFGGYGYSKADTYGYSTPHQPYPNSLSDYDYPSSACSIQSSAL
    
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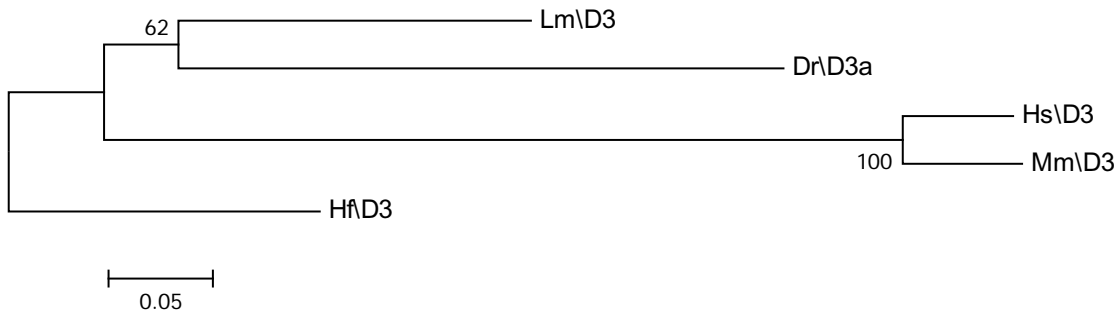
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Hf\D3      RAPNHKPTDINGNCMRTSGSQGSAQPPSINEPQQPPPLPSSPNASNTSTQK
Lm\D3      RPPHHKSSDINGTCMRTSGSQGTCQPPSISEQQPAPSLPSSPNANSIATQK
Dr\D3      RPATHKNGDINGSCMRPSASQGNSQPESISEQQQAAPLASSPSPSTNSTQK
Hs\D3      RPAHKGAELNGSCMRPQGGGGGSQPPGLNSEQQPPQPPPPPTLPPSSPTN
Mm\D3      RPAHKGAELNGSCMRPQGGGGGNQPPGLNSEQQPPQPPPPPTLPPSSPTN
    
```

```

Hf\D3      RTKSI PNSSSPAATLTKQIFPWMKESRQNAKQKNNCTVA
Lm\D3      KNKPVSNSSTPTATISKQIFPWMKESRQNAKQKNNCTAT
Dr\D3      KKSPSSNGSTATPVISKQIFPWMKETRQNAKQKTNCPAA
Hs\D3      AKKPKGGPNSSSATISKQIFPWMKESRQNSKQKNSCATA
Mm\D3      AKKTKGGLSSSSSTISKQIFPWMKESRQNSKQKNSCATS
    
```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxd3

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0.007	**
Hf	Lm	Dr	0.182	
Hf	Hs	Dr	0.166	

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxd4 alignment for relative rate test

```

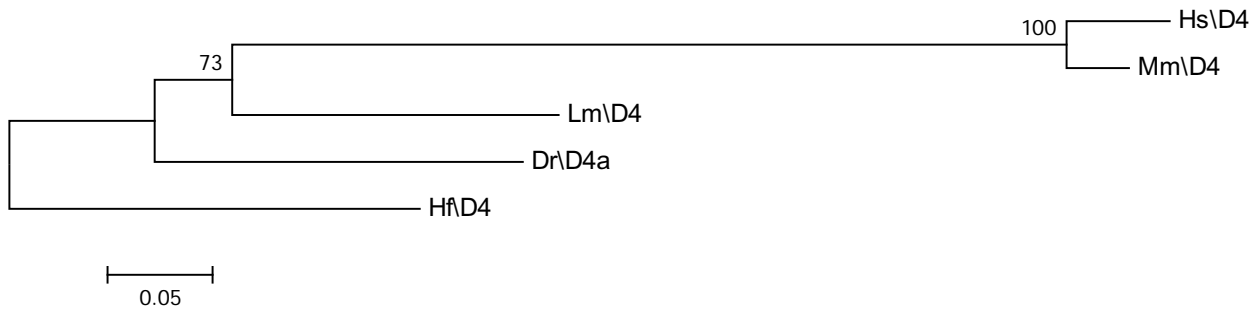
Lm\D4      MSSYMVNSKYVDPKFPPCEEYSQNNYIAEQSTDYYS
Dr\D4a     MSSYMVNSKYVDPKFPPCEEYSQNSYIPEQSPGYYS
Hf\D4      MSSYLMNTKYVDPKFPPCEEYSQNNYIPDHCSEYYSQ
Hs\D4      MSSYMVNSKYVDPKFPPCEEYLQGGYLGEQGADYYGG
Mm\D4      MSSYMVNSKYVDPKFPPCEEYLQGGYLGEQGADYYGS

Lm\D4      SEDTDFQLQGIFFRSNYSEQTYGCGNVQDSTEQPRGHVQEQQSGPQSHFPVQQEHCSP
Dr\D4a     SQDTEFQHPGIYSRSNYSEQPYSCSTVQGSSVQPRGHVQDQASTPSFFPAQTEQCPA
Hf\D4      SQDSDFQHGGIYPRSNYSQSYNCSNARGSPVQQRGHVQAQPAPQNHLTGQGEVAP
Hs\D4      AQQADFQPPGLYPRPDFGEEQPFGGSGPGGSALPARGHGQEPGGPGGHYAAPGEPCPA
Mm\D4      AQQADFQPSGLYPRPDFGEEQPFGGSGPGGSALPARGHGQEPGGPGSHYGAPGEPCPA

Lm\D4      PIPTSRSCNQQQNKNSGTVSKQPAIVYPWMKKVHVNS
Dr\D4a     QISGSRTCGQQQNKQTONGIPTKQPAVVYPWMKKVHVTT
Hf\D4      QVSI GRPCSQQHNKNQNGTATKQPAVVYPWMKKI HVNT
Hs\D4      PLPGARAYSQSDPQPPSGTALKQPAVVYPWMKKVHVNS
Mm\D4      PLPGARACSQTGPQPPPGTALKQPAVVYPWMKKVHVNS

```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxd4

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0.001	**
Hf	Lm	Dr	0.683	
Hf	Hs	Dr	0.001	**

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxd8 alignment for relative rate test

HfD8 MSSYFVNPFYSKYKPGEALSPTYDRCRFPQDVTSRHAVVYSSGASFQHPAQQDFY
 LmD8 MSSYFVNPFYSKYKSGEAINNTNYDCQFSQDLNRRHSVIYSSNGTSFQHPTQQELC
 MmD8 MSSYFVNPLYSKYKAGEAINPTYYDCHFAPEVSGRHALQYNSAAGFPHAHPPQDYF
 HsD8 MSSYFVNPLYSKYKAGEAINPTYYDCHFAPEVGGRRHALQYNSAAGFPHAPPQEYF

HfD8 AVVYSSGASFQHPAQQDFYHHGTSALPNTGFQQNPGITCHGDPSKIFYGYDNLQR
 LmD8 SVIYSSNGTSFQHPTQQELCHQGASVCSNMGYQQNHGITCRGEPKIFYGYDNLQR
 MmD8 ALQYNSAAGFPHAHPPQDYFHAGSPTAAYQAAPPPPGIACHGEPKIFYGYDNLQR
 HsD8 ALQYNSAAGFPHAPPQEYFHPGSPAAAYQAAPPPPGIACHGEPKIFYGYDNLQR

HfD8 QQIFTTQQEADLVQYPDCKSSSSIGEEQNSSPTQMFPWMPQApG
 LmD8 QLSFTTQREADLVEYPDCKSSNGIVEEQETSSPSQMFPWMRSQAtG
 MmD8 QPIFTTQQEAEALVQYPDCKSSSSGIGEDNQSSSPSQMFPWMPQApG
 HsD8 QPIFTTQQEAEALVQYPDCKSSSSGIGEDNQSSSPSQMFPWMPQApG

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxd8

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>
Hf	Hs	Lm	0.746

Hf – horn shark, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxd9 alignment for relative rate test

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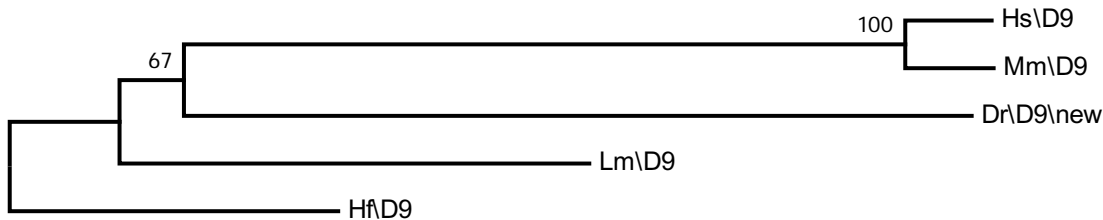
Lm\D9      MSTSGTLSNYYVDSLIGLEPEEIIYGARFAQGTHCTTSRPSSVADDLTSCSFAP
Hf\D9      MSTGGTIHNYVDSLIGQETEDLYAARYAQGSHSTASRPSGVADDFSSCSFTS
Dr\D9\new  MSTSSALSSYYVDTIMGHEAEDVYGARYIQGSHTAPARPSGVVEDFSSCSFAP
Hs\D9      MSSSGTLSNYYVDSLIGHEGDEVFAARFGPPGPGAQGRPAGVADEFASC SFAP
Mm\D9      MSSSGTLSNYYVDSLIGHEGDEVFAARFGPPGPGTQGRPAGVADEFASC SFAP

Lm\D9      KSALFSTSWSSIHPQ TSAAMTGIYHPYMHQTHLADNRYVH SWIDPISSSVSFPSFH
Hf\D9      KSTAFSNPWSPVHPQSSAAVAGIYHPYMHQSHLADTRYVRSWLEPLSSSVSFPGFH
Dr\D9\new  KSAVFPASWSSVHQ PSTAAVSGIYHPYVHQTHLSDNRYVRSWIEPVANHISLTGFH
Hs\D9      RSAVFSASWSAVQPPAAAAMSGLYHPYVPPPPLAPGRYVRSWMEPLPGSPGSPGP
Mm\D9      KSSVFSASWSAVQPPAAATMSGLYHPYVSPPLAPGRYVRSWMEPLPGVPSPGGP

Lm\D9      HNGRHYGIKPETLT SKRTECSSSEVQALS LTEYTSNTFSETRDKPSSDNCSDGH
Hf\D9      PNGRHYGIKPETLSSKRTECSSYELQ TLSLPEFTCGSYPECREKLPKELTSSSET
Dr\D9\new  SNSRHS GTKTESLPPKRTE SAAFETETPSVPEFSLNAVSESAYKATEERVGSDN
Hs\D9      ANGRHYGIKPETSSSKRTECSVAESQ GSSGPEFSCNSFLQEKAAGSSEPCSDHP
Mm\D9      ANGRHYGIKPETSSSKRTECSAAESQ GSGGPEFPCNSFLRDKAAGSSEPCSDHP

Lm\D9      SMNSELKEEKPKQLDPDNPAAIWL
Hf\D9      TSNSEHKEEKQQQLDPNHPAINWI
Dr\D9\new  SSHGEPKDEKQQQLDPSNPAANWI
Hs\D9      IPGCSLKEEEEQQQLDPNNPAANWI
Mm\D9      SPGCSLKEE EEPQQQLDPNNPAANWI
    
```

NJ tree rooted to horn shark (Hf)



<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0.003	**
Hf	Lm	Dr	0.017	*
Hf	Hs	Dr	0.26	

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxd10 alignment for relative rate test

```

Hs\D10      MSFPNSSPAANTFLVDSLISACRSDFYSSSSMYMPPSADMGTYGMQTCGLLPSLAKR
Mm\D10      MSFPNSSPAANTFLVDSLISACRSDFYSSSSMYMPPSADMGTYGMQTCGLLPSLAKR
Hf\D10      MSCPNSSPATNSFLVDSLISACRDFYSTSSMYMPPSSTDMGTYGMQTCGLLPTMTR
Lm\D10      MSFPNSSSATNTFLVDSLISACRSDFYSSNGSMYMPSTDMGNYGMQTCGLLPTLAKR
Dr\D10a     MSFPNSSPAANTFLVDSLIGACRTDFYSSSNMYMPATAEMGNYGMQTCGLLPAIGKR

Hs\D10      EVNHQNMGMNVHYIPQVDSWTDPNRSCRIEQPVTQVPTCSFTTNIKEESNCCMYSD
Mm\D10      EVNHQNMGMNVHYIPQVDSWTDPNRSCRIEQPVTQVPTCSFTANIKEESNCCMYSD
Hf\D10      EVNHQNMMSISVHYLSQVDGWADPSRPCRIEQPVTQMPTCSFPASVKEESTCCMYSD
Lm\D10      ELNHQNMGMNAHHFSQVDSWADPTRSCRIDQSIISQTPTCSEFNNNIKEETNCCMFSD
Dr\D10a     EVNHQNDMDTVHYIPQTDTWADPSRSCRLEQPLNQMSTCTFSQSIKEETNCCMYSD

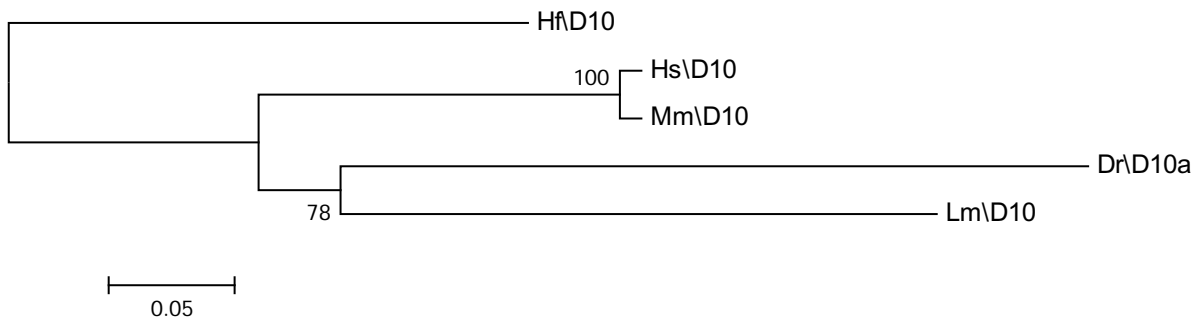
Hs\D10      KRNKLI SAEVPSYQRLVPESCPVENPEVPVPGYFRLSQTYATGKTQEYNNSPEGSSTVML
Mm\D10      KRNKLI SAEVPSYQRLVPESCPVENPEVPVPGYFRLSQTYATGKTQEYNNSPEGSSTVML
Hf\D10      KRAKLNPTAIPAYPRLVSENC SIENPEIPIPGYFRLCQAYPLEKSLDYN YAGEISSNVMP
Lm\D10      KRGNINSSEIPCYHRFVPESSDNPEIPVPGYFRLSQTYATAKTQEYSNAEENSNTMM
Dr\D10a     KRAKVSSEIPAYSSLIPESCSVDSPEIPVPGYFRLSQTYATAKNPDYDNETMSPNTTLM

Hs\D10      QLN RGA AKPQLSAQLQMEKKMNEPQEPTKVSQVESPEAKGGLPERSCLA EVSVS
Mm\D10      QLN RAA AKPELSAQLQMEKKMNESQEPTKVSQVESPEAKGGLPERSCLA EVSVS
Hf\D10      QSNGLISKLQVSSQPPMERKINEKQESTKGIYVESPEPKPRLLEVSATAEGAAT
Lm\D10      QLN RMNSKPHIPPEPQLEKKI SENQETQNI SPVESPELTSALQDRNRSTNV SAS
Dr\D10a     QLN RATPKAQSTPFVEVEKKLAHDRDRSSSPAQSPEPKVSTLEKNCSTEASVS

Hs\D10      SPEVQEKESK
Mm\D10      SPEVQEKESK
Hf\D10      SSELSDNETK
Lm\D10      SPEIKEKEGK
Dr\D10a     SPELPHREGK

```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxd10

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Lm	Hs	0.017	*
Hf	Lm	Dr	0.354	
Hf	Hs	Dr	0	**

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxd11 alignment for relative rate test

```

Lm\D11      MYLPYYVSRSDFPSVSSFLPQTTSCQMTFPYSSNLAQVQPRRDVSEFRDYGLEHTKWQYR
Hf\D11      MYLPYYVSAPDFSSVSTFLPPTTSCQMTFPYSSNLAQVQPVRELSFRDYGLEHTKWHYR
Dr\D11a     MYLPYYVSTPDFSSVSSFLPQTTSCQVNFYSSNIAQVQPVREVTFRDYGLDHSKWHYR
Hs\D11      MYLPYYVAPSDFAASKPSFLSQPSSCQMTFPYSSNLAHVQPVREVAFRDYGLEERAKWPYR
Mm\D11      MYLPYYVAPSDFAASKPSFLSQPSSCQMTFPYSSNLAHVQPVREVAFRDYGLEERAKWPYR

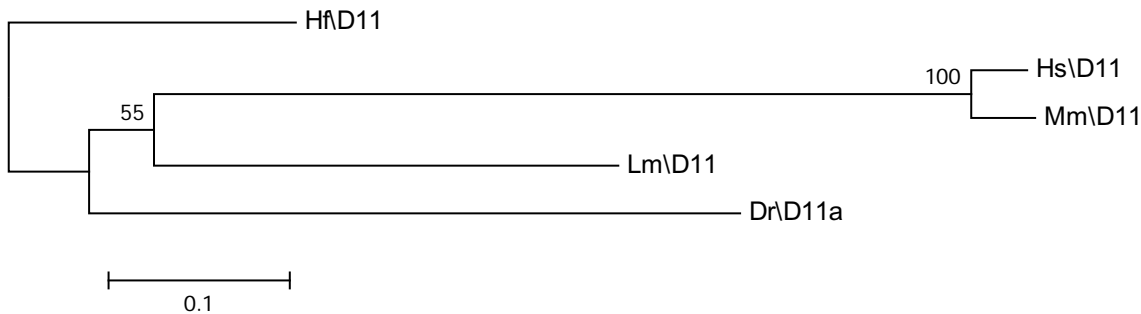
Lm\D11      EEVVRDLVQQATRTRDMLFKNDVSYGHHGSSNTPGNMYATVGRNGILPQGFD
Hf\D11      EEIMHRDYIQPPTRTGMLFKNDTVYSQRGSSNPSCNFYTTVGRNGILPQGFD
Dr\D11a     EEIMHRDLLQSTNRAEMIFKNDVSMYSHHAGTNSSCSFFTNVGRNGVLPQGFD
Hs\D11      EAAMQRELLPPAGRDPVLFKAEPVCAAHGPAGAASNFYSAVGRNGILPQGFD
Mm\D11      EAAMQRDLLPPAGRDPVLFKAEPVCGAHGPAASNFYSAVGRNGILPQGFD

Lm\D11      QFFDTEIESHEQSSKTHMTEKTLFKCQNNASCIKLSSDRKANE
Hf\D11      QFFETAYGISDSSNYEQLTEKSVSTCQSITASEKVSSGQEATE
Dr\D11a     QFFETANSEKPNPEQSKQKPDTSVPGDAACNPSTDSAEQTPTD
Hs\D11      QFYEAAPGPQPEGAADKGDPRGTGAGGGGGSPCTKATPGSEAAE
Mm\D11      QFYEAAPGPQPEGAADKGDPKPGAGGGGGSPCAKATPGPEAAE

Lm\D11      NSTDLPSDKVVAEKHSNS
Hf\D11      KSTVESSGTSATEKNLSL
Dr\D11a     TVEEESVSTCDEKNSGS
Hs\D11      GSGEGPPGEAGAESSAV
Mm\D11      GSGEGPPGEAGAESGGTV

```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxd11

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0	**
Hf	Lm	Dr	0.149	
Hf	Hs	Dr	0.022	*

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxd12 alignment for relative rate test

```

Lm\D12      MCERNLLNSGYVSSLLNFHSPDSFYFPSLRGNGTQLAGLPQISYPRRSLPWTSSS
Hf\D12      MCEHNLLNSGYVGSLLNFTSPEPFYFANLRPNGTQLATLPALSYTRRSLPWTSSP
Dr\D12a     MCEHNLLSSGYVAPLLNFHSPDSLQNLQNLRGNGVHLSGLPQMSYSRRSLPWSSNS
Hs\D12      MCERSLYRAGYVGSLLNLQSPDSFYFNSNLRPNNGQLAALPPIISYPRGALPWATPA
Mm\D12      MCERSLYRAGYVGSLLNLQSPDSFYFNSNLRANGSQLAALPPIISYPRSALPWATPA
    
```

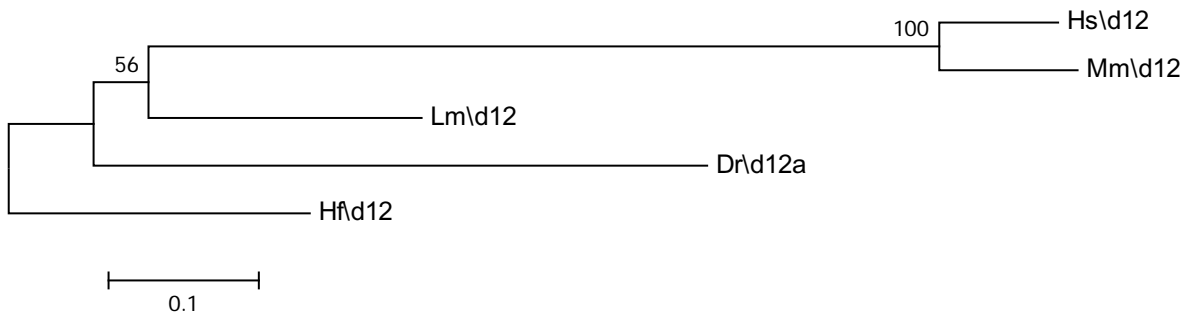
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Lm\D12      CASPPQSRAFSGYSQAYLTSSVPINISSNNNKESSLDEKYYFQDTNSKSDERYR
Hf\D12      CASPPQSRAFSGYSQSYLSNSVSVSINRHVSDKAAAGEKYYFQDSSRKVEERCR
Dr\D12a     CTAPAQSRAYSQYSPFFSNSAAVSASLNTHKKGSLEERYFQDVSHKSEEPGR
Hs\D12      SCAPAQATAFGGFSQPYLAGSGPLGLQPPTAKDGPPEEQKFYAPEAAAAGPEERGR
Mm\D12      SCTPAQASAFGGFSQPYLTGSGPIGLQSPGAKDGPEDQKFYTPDAPTASEERSR
    
```

```

Lm\D12      EHQS FVT DNTAKYDYSNMERVLNSCTSAVSEGVKQPV
Hf\D12      HNSQYPSDNP AKYEY PNVETELNSNSPTVNDGIKQSV
Dr\D12a     PNAAYASESSASNGLSNLERELSCVEQPESDASKQSV
Hs\D12      TRPSFAPEKAAKYDYAGVGRQGAPCAPGFKDDTKGPL
Mm\D12      TRPPFAPEKGTKYDYAGVGRQGAPCASSFKEDTKGPL
    
```

NJ tree rooted to horn shark (Hf)



Tajima relative rate test – Hoxd12

<u>Outgroup</u>	<u>Ingroup1</u>	<u>Ingroup2</u>	<u>P-value</u>	<u>Significance</u>
Hf	Hs	Lm	0	**
Hf	Lm	Dr	0.007	**
Hf	Hs	Dr	0.027	*

Green highlight denotes gene with significantly faster rate of evolution

Dr – Danio rerio, Hf – Heterodontus francisci, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus