Hoxa1 tree for relative rate test

```
Mm\A1       MNSFLEYPILGGDSGTCSARAYPSDHGITTFQSCAVSANSCGGDDRFLV
Hs\A1       MNSFLEYPILSGDSGTCSARAYPSDHRITTFQSCAVSANSCGGDDRFLV
Lm\A1       MSSFLDYPIINGDTGTCSSRAYIPDHGITTFQSCAVTTNSCAGDDRFIV
Hf\A1       MNSFLDYSIINGETGTCSSRSYHADQGITTYQSCAVSNNNCNADDRYIV
Dr\A1a      MSTFLDFSSISGSGGSCSVRAFHGDHGLSTFQSCAVRLNSCSGDERFMS

Mm\A1       GRGVQISSPYQTSGNLGISYSHSSCGAQNFSAPYGPYG
Hs\A1       GRGVQIGSPYQTSGNLGVSYSHSSCGSQNFSAPYSPYA
Lm\A1       GRGVHIGPPYQHHNNLGIAYSHPSCGTQSFSTGYNHYS
Hf\A1       SRSVQIGAPYTHPNNLGISYSHPNCGAQSFNTGYSHYS
Dr\A1a      NISSQDVINYQSPGTLSITYSHPSYGTQSFCTGYNHYA

Mm\A1       LNQEADVSGGYPPCAPAVYSGNLSTGYAGTVGSPQYIHHSYGQE
Hs\A1       LNQEADVSGGYPQCAPAVYSGNLSSGYAGAVGSPQYIHHSYGQE
Lm\A1       LNQDIEASGGYSQCAPAVYSGNLSSGFGGTMGPSQCIHHPYGSE
Hf\A1       LNQETDGNGGYPQCAPAVYPGNIASSYGGMVGSGQYPHHPYGQE
Dr\A1a      LNQDVESSVSFPQCGPLVYSGNISSGYSSNVHLHQYGSATYGSD

Mm\A1       QQTLALATYNNSLSPLHASHQEACRSPAETSSPAQTFDWMKVKRNPPKT
Hs\A1       HQSLALATYNNSLSPLHASHQEACRSPAETSSPAQTFDWMKVKRNPPKT
Lm\A1       QQNLSLAGCSNTLSPLLSGHQEDCRSPAEASSQAQTFDWMKVKRNPPKT
Hf\A1       QQGLALAAGCHSLSPVHGSHQEACCSPSETPPPAQTFDWMKVKRNPPKT
Dr\A1a      QANLTFVACSNPLSPLHVPHHDACCSPLDGVPTGQTFDWMKVKRNPPKT
```

NJ tree rooted to horn shark (Hf)

Tajima relative rate test – Hoxa1

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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     MNYEFEREIGFINSQPSLAECLTSFPPVGDTFQSSSIKNSTLSHSTVIPPPFEQTIPSLN
Dr\A2b    MNYEFERETGFINSQPSLAECLTSFPPVGDAFQSSSIKSSTLSHSTLIPPPFEQTIPSLN

Hs\A2     PGSHPRHGPKPSPAGSSPVPAGALPPEYPWMKEKKAAKKTCLSHK
Mm\A2     PGSHPRHGPKSSPAGSSPVPAGALPPEYPWMKEKKAAKKTCLGHK
Lm\A2     PGSHPRHSPKQSPNGSSPLPAAALPPEYPWMKEKKTSKKNCFTQK
Hf\A2     PSSHPRQSPKQSPNGTSPLPAATLPPEYPWMKEKKNSKKNCLSQK
Dr\A2b    PGSHPRHSPKQNPNGSCPLPAASLPPEYPWMKEKKASKKNYFSPQ
```

NJ tree rooted to horn shark (Hf)
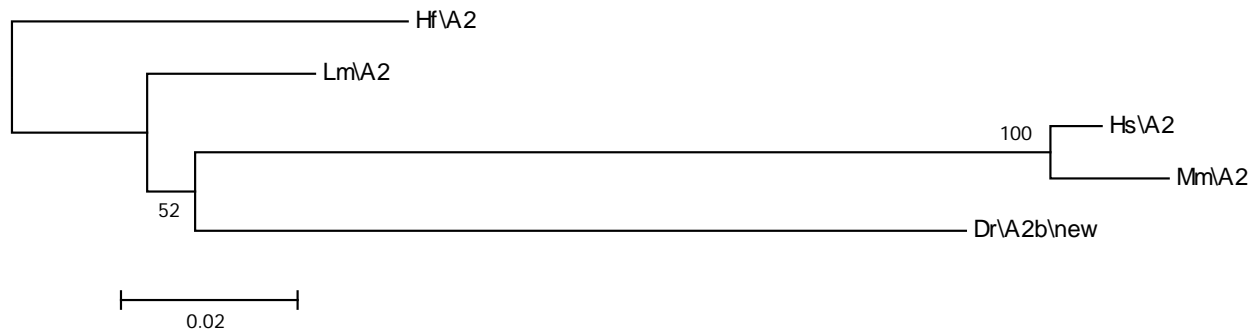
Tajima relative rate test – Hoxa2

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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       MQKATYYDSSAIYGGYPYQAANGFAYNASQQPYYHRPACSLQSPAAG
Hs\A3       MQKATYYDSSAIYGGYPYQAANGFAYNANQQPYYHRPACSLQSPSAG
Dr\A3a      MQKATYCDGSAIYSGLPYQSANGLGYDASQQQYYHRPACSLQSPGSA

Lm\A3       PHHKHNDINESCMRTSNNQPPQPPGISEP
Hf\A3       PHHKPNDINESCMRTSASQPSHHPVIAEP
Mm\A3       GHPKTHELSEACLRTLSGPPSQPPGLGEP
Hs\A3       GHPKAHELSEACLRTLSAPPSQPPSLGEP
Dr\A3a      GLHTSNEMSEVCQQINGTQATVTDTSDNP

Lm\A3       QPTNPVSPSQTSSNNSTPSNSNKNPGITSPTIAKQIFPWMKESRQNSKQKNSSCSS
Hf\A3       PPPPSVSPPQNTSSNSTQSSTSKNPTLTSATISKQIFPWMKESRQNAKQKTSSSSS
Mm\A3       PPPSSVSPPQSANSNPTPASTAKSPLLNSPTVGKQIFPWMKESRQNTKQKTSGSSS
Hs\A3       PPPSSASPPQNASNNPTPANAAKSPLLNSPTVAKQIFPWMKESRQNTKQKTSSSSS
Dr\A3a      TAPSGPSSPSSLNQIPNIDSAAKNPVHVSPSTRKHIFPWMKESRQNTKQKSCSIIS
```

NJ tree rooted to horn shark (Hf)
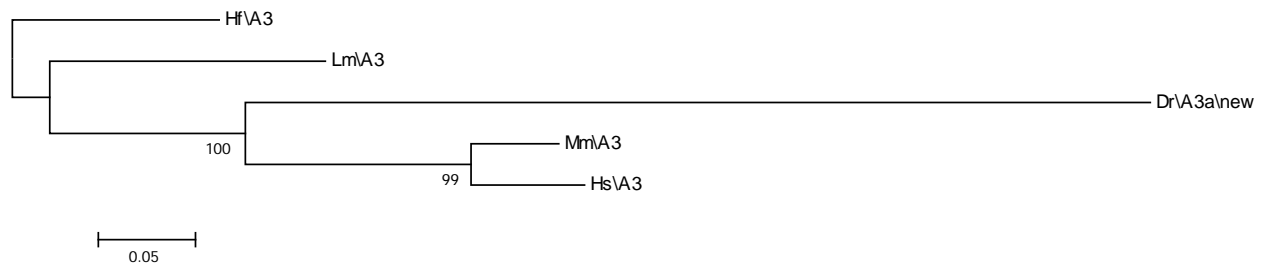
Tajima relative rate test – Hoxa3

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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      MSSYLINSNYIEPSFPPCEEYHQNGKDPGFPHEASYPYQEQSYDYGNSTNDLNDFS
Mm\A4       MSSFLINSNYIEPKFPPFEEFAPHGREPSYPGLYPAPAAACPYACRGASPGRPEQS
Hs\A4       MSSFLINSNYIEPKFPPFEEYAQHSREPAYPALYPAHDTAYPYGYRGASPGRPPQP


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

NJ tree rooted to horn shark (Hf)
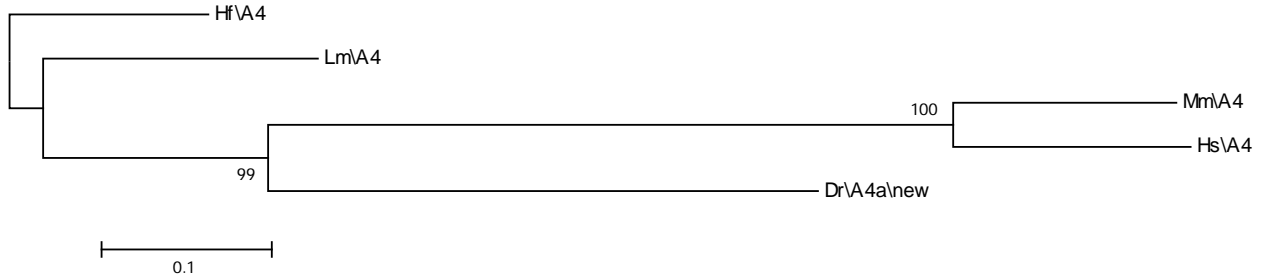
Tajima relative rate test – Hoxa4

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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     GHSSPGHFLSSERTQRYNQPVTEPSSDHLPCSSLANSPVSESHRAL

Lm\A5      KNPIANTTSTNASSSTHIGREGVGTSSGAEDDTPASREQPSSQNPQIYPWMRKLHISH
Hf\A5      KNSIASTTSSNSSSSSHISRDGVGTSPGTEDDTPASSDPPSSQNPQIYPWMRKLHISH
Hs\A5      KNSLSNSGASAAGSTHISSREGVGTASGAEEDAPASSEQASAQSPQIYPWMRKLHISH
Mm\A5      KNSLGNSGASAAGSTHISSREGVGTASAAEEDAPASSEQAGAQSPQIYPWMRKLHISH
Dr\A5a     KISLSSTAGSAKSFGTVLSREGVSVSSSMEEEKPPGSGQTASQNPQIYPWMRKLHISH
```

NJ tree rooted to horn shark (Hf)
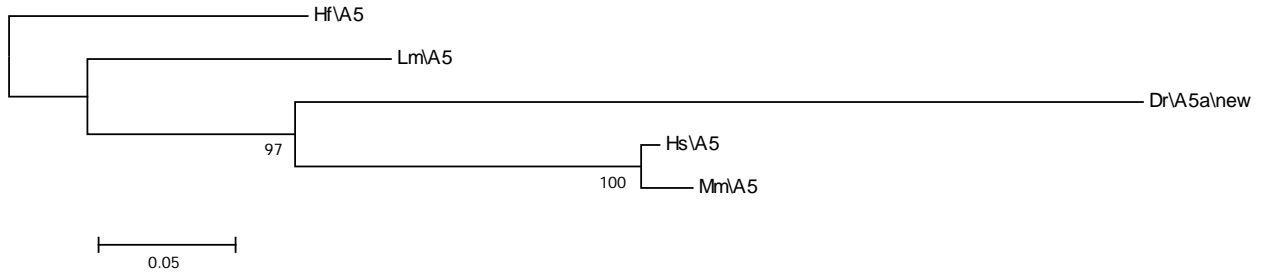
Tajima relative rate test – Hoxa5

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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    MSSYFVNSTFPSNPPSSQDSFLGQIPLYTAGYDALRHFQSYGATTLQ
Mm_A6    MSSYFVNPTFPGSLPSGQDSFLGQLPLYPAGYDALRPFPSYGASSLP
Hs_A6    MSSYFVNPTFPGSLPSGQDSFLGQLPLYQAGYDALRPFPSYGASSLP

Hf_A6    DKSYSSPCYYQQSNSVIACNRASYDYGASCFYPEKDLASVSPSSGK
Lm_A6    DKTYSSSCFYQQSNSVFACNRTPYECGASCLYPEKDTDVSSPSSSK
Mm_A6    DKTYTSPCFYQQSNSVLACNRASYEYGASCFYSDKDLSGASPSNNK
Hs_A6    DKTYTSPCFYQQSNSVLACNRASYEYGASCFYSDKDLSGASPSSGK

Hf_A6    HRAQDDFFSSDQHYKPDCAQNKILSEEGNDRKYSTPIYPWMQRMNSSS
Lm_A6    QRAHGDYLHFDQQHKSECVQNKILNEEVNDRRYTTPIFPWMQRMNSCT
Mm_A6    QRGPGDYLHFEQQYKPDGVQGKALHEEGTDRKYTSPVYPWMQRMNSCA
Hs_A6    QRGPGDYLHFEQQYKPDSGQGKALHDEGADRKYTSPVYPWMQRMNSCA
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NJ tree rooted to horn shark (Hf)
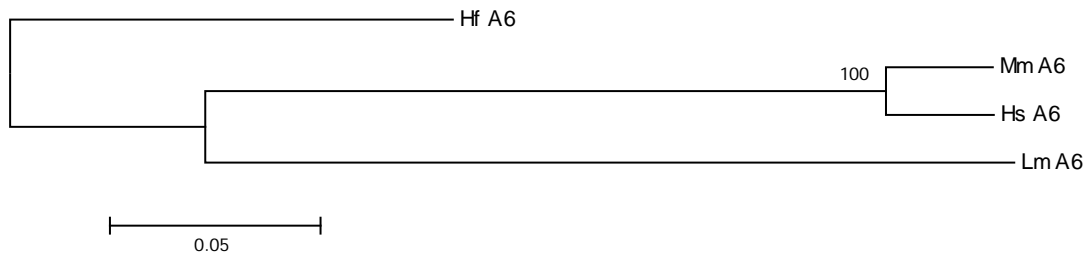
Tajima relative rate test – Hoxa6

Outgroup	Ingroup1	Ingroup2	P-value
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    MSSSYYVNALFPKYTAGTSVFQNASATSCAFATNSQRSSYGAGAS
Lm_A7    MSSSYYVNTFFSKYTTGASLFQNAEPNSCSFATNSQRSSYGPGAG
Mm_A7    MSSSYYVNALFSKYTAGASLFQNAEPTSCSFAPNSQRSGYGPAPA
Hs_A7    MSSSYYVNALFSKYTAGASLFQNAEPTSCSFAPNSQRSGYGAGAG

Hf_A7    AFPAPMAGLYNVNSAIYHGPYNTGYNLNSDSYNLRCSAL
Lm_A7    AFPPSLPGLYNMTSTLYQNPFTSGYNIGSDAYNLHCSSF
Mm_A7    AFASTVPGLYNVNSPLYQSPFASGYGLGADAYNLPCASY
Hs_A7    AFASTVPGLYNVNSPLYQSPFASGYGLGADAYNLPCASY

Hf_A7    DQIPVLCSDLSKQGEKLDQTNVHPQAESNFRIYPWMRNAGPDR
Lm_A7    DQIPVLCNDLTKSNEKSNESSLHPQDENNFRIYPWMRSSGPDK
Mm_A7    DQIPGLCSDLAKGADKADEGVLHGPAEASFRIYPWMRSSGPDR
Hs_A7    DQIPGLCSDLAKGADKTDEGALHGAAEANFRIYPWMRSSGPDR
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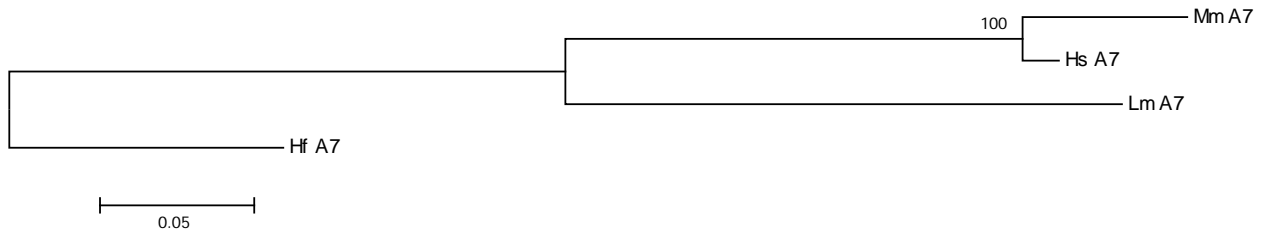
NJ tree rooted to horn shark (Hf)

Tajima relative rate test – Hoxa7

Outgroup	Ingroup1	Ingroup2	P-value
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        MATTGALGYYVDSRYAPGTLGQPPRQLAEHPDFSPCSFQSKATVFGASWNPVGRYMRSW
Mm\A9        MATTGALGYYVDSRYAPGTLGQPPRQLAEHPDFSPCSFQSKAAVFGASWNPVGRYMRSW
Lm\A9        MSTSGTISYFVDSRYNSGALTQPPRQLPDPSDFTPCSFQSKASVFTTSWNPVSRYMRSW
Hf\A9        MSTSGTISYYVDSRYASGSLAQASRQLTEHPDFSPCNFQSKATVFSTSWSPVGRYMRSW
Dr\A9b\new   MSTLGTLSYYADSRFSSGPVVQQQSRLLEYSEQEPYTFQAKSSIFGASWSPVGASVRPW
Dr\A9a\new   MSTSGALTYYVDSRFSSGLGLIQHRPPADLSDLGPCTFPAKQPVYGTSWGHIGDYVQSW

Hs\A9        LEPTPALSFAGLPSSRPYGIKPEPLSARTHTLSLTDYACGSPPVEGAFSE
Mm\A9        LEPTPALSFAGLPSSRPYGIKPEPLSARTHTLSLTDYACGSPPVEGAFSE
Lm\A9        LESMPSLSFSGLPSSRHYGIKPEPLIARAHTLTFSDYGCGSSPVDGILPE
Hf\A9        LDPMPTLSFPGLPSSRHYGIKPEPVASRTHTLALSEYTCGTSPAEVSFSE
Dr\A9b\new   LEPLPALPFTGLSTDTHQDIKLEPLVGSTHTLLVAETDNNTTQTDAVSNG
Dr\A9a\new   LLDSAGLPQTEPPTVNHNHAKSDTNETNPHTILQPVFTNGGCSTEAESSR

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

NJ tree rooted to horn shark (Hf)

Tajima relative rate test – Hoxa9

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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        MSCSDSSAANPFLVDSLVSGRYFPNSSVYLPQASDLPYGLQNCGLFPVL
Dr\A10b\new   MSCSDSPSGNSFLVDSLIHGRYYQNSGVYLQPTSEYSYGLSNCGYFSGL

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

Hs\A10        AFPRPPPDGCSGVPVPGYFRLSQAYGTAKQLGAPFPAQP
Mm\A10        AFPRPPPDGCSGVPVPGYFRLSQAYGTAKQLASPFPAQP
Hf\A10        SFPRLTSESCGGVPVPGYFRLSQAYPTSKQVGAPFVPQS
Lm\A10        SYPRLSTEVCSVIPVPGYFRLSQAYGISKQVGAQFTPPP
Dr\A10b\new   SYSRLTPNSCGCVPVPGYFRLSQTCTTSKQTIPHVVAQR

Hs\A10        PGRFDLPLASGSADAARKEAHASSPAPSESSKASPEKDSL
Mm\A10        PGRFDPPLASGSTEAAGKEAHASSPAPSENSKASPEKDSL
Hf\A10        QIRFGTPSASTPTELGRKEAAASSPVPSESNKNSPEKETK
Lm\A10        QVRFDMSLSSASTETVMKEAHASSPAPSESSKTSPDKEAI
Dr\A10b\new   STRFDSSLSAIAAEASRDELRGSSPEPPDSPEKAVTVTKA
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NJ tree rooted to horn shark (Hf)
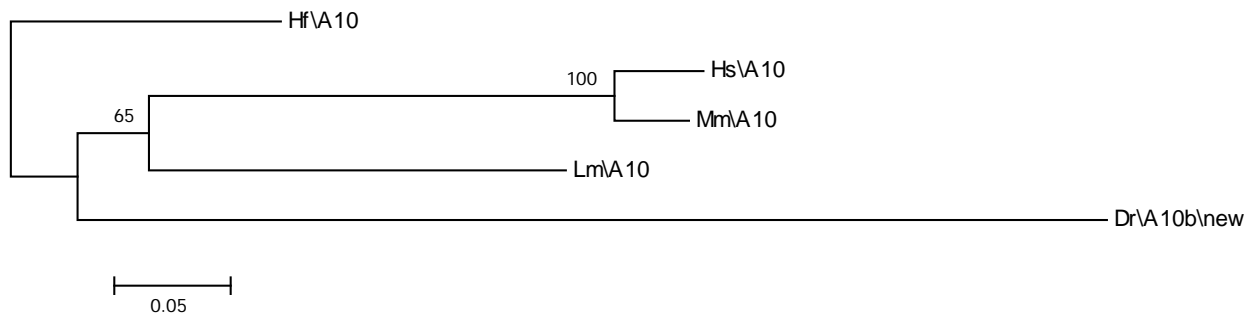
Tajima relative rate test – Hoxa10

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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

```
Hs\A11        MDFDERGPCSSNMYLPSCTYYVSGPDFSSLPSFLPQTPSSRPMTYSYSSNLPQVQPVREVTFR
Mm\A11        MDFDERGPCSSNMYLPSCTYYVSGPDFSSLPSFLPQTPSSRPMTYSYSSNLPQVQPVREVTFR
Lm\A11        MDFDERVSCSSNMYLPSCTYYVSGPDFSSLPSFLPQTPSSRPMTYSYSSNLPQVQPVREVTFR
Hf\A11        MDFDERVSCGSNLYLPSCTYYVSGPDFSSLPSFLPQTPASRPMTYSYSSNIPQVQPVREVTFR
Dr\A11b\new   MDFDERVPVGSNMYLPGCTYYVSGTDFSSLPPFLPQTPSSCPMTYSYSSSLPQVQSVREVSFR
Dr\A11a\new   MDFDERVSVGSNMYLPSCTYYVPGADFSTLPSFLSQSPSTRPVTYSYASNLPQVQHVREVTFR

Hs\A11        EYAIEPATKWHPRGNLAHCYSAEELVHRDCLGDVLAKSSANVYTPAVSSNFYSTVGRNGVL
Mm\A11        EYAIEPATKWHPRGNLAHCYSAEELVHRDCLGDVLAKSSANVYTPAVSSNFYSTVGRNGVL
Lm\A11        DYAIDTSNKWHPRSNLPHCYSTEEILHRDCLGEIFGKGNANVYGSSTSSNFYNTVGRNGVL
Hf\A11        DYAIDPSNKWHHRGNLPHCYSAEELMHRECLGEMLMKNSASVYSSNASSSFYNPVGRNGVL
Dr\A11b\new   DYAIDTSSKWHSRGNLPHCYATEDMVHRECLGDMLSKNNSVLYNSSHTSNVYGSVGRNGVL
Dr\A11a\new   DYAIDPSTKWPHRGPLAHCYPSEDSVHRECLGEMFPKNNASAYTSNTTSNFYGNVGRNGVL

Hs\A11        PQAFDQFFETAYGTPENASSDYDKSAEKGPATSSSDSSSPESSSGHTEDKAGGS
Mm\A11        PQAFDQFFETAYGTPENASSDYDKNAEKGPATSSSDGSSPESSSGHTEDKAGGS
Lm\A11        PQAFDQFFETAYGTTENHSSDYDKNSDKIPATSRSETSSPESSSGNNEEKSSSS
Hf\A11        PQGFDQFFETAYGSSENQQSEYEKSPDKVPATSSSETSSPESSSGNNEEKGSNS
Dr\A11b\new   PQAFDQFFETAYGNVENQPTEHDRATSKAPAESGSDSSSPEPSSGNNEDKFSGS
Dr\A11a\new   PQAFDQFFDTAYGGSDSVDNDYDKMHSSKQAPAPEQQSSPESSSGNNEEKTSGA
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NJ tree rooted to horn shark (Hf)
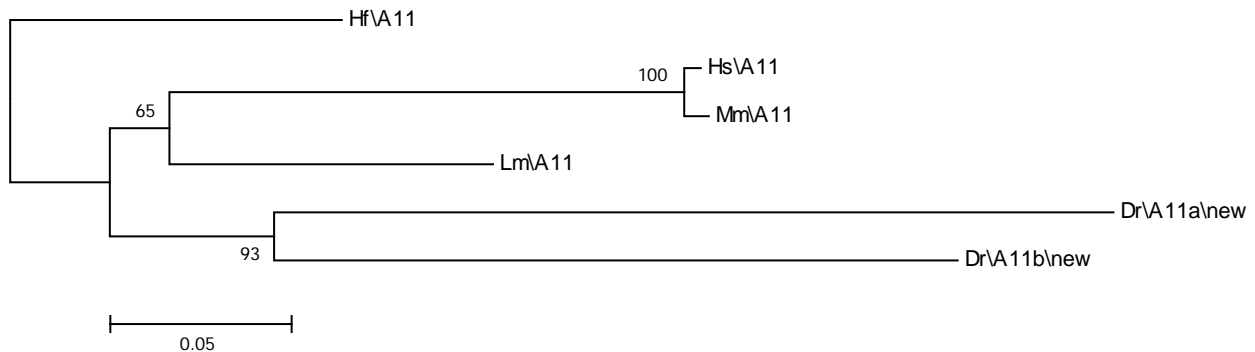
Tajima relative rate test – Hoxa11

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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

```
Hs\A13        MTASVLLHPRWIEPVMFLYDNGDELNKNMEGCRNLMAHPAPLAPKQCSPCSAAAQ
Mm\A13        MTASVLLHPRWIEPVMFLYDNGDELNKNMEGCRNLMAHPAPLAPKQCSPCSAAAQ
Lm\A13        MTASVLLHPRWIDPVMFLYDNGDEVNKNMEGCRNLMAHPASLAPKQCSPCSAAQS
Hf\A13        MTASVILHPRWIDTVMFVYDNSDEINKNMDGCRNLMAHPASLAPKQCSPCPAAQT
Dr\A13b\new   MTASLLLHSRWIDPVMFLYDNGDDMSKNMEGCRNLIAHPSTLAPKQCSPCSAVQN
Dr\A13a\new   MTTSLLLRPRWIDPVMFLYDNGDDTSKNMEGCRNLMSHPASLAPKQCSPCSAVQG

Hs\A13        SSSAALPYGYFGSGYYPCKSCAQKYMDTAAEEFSSRAKEFAFYQGYAGPYQPMPGYLDMP
Mm\A13        SSSAALPYGYFGSGYYPCKSCAQKYMDTAAEEFSSRAKEFAFYQGYAGPYQPVPGYLDMP
Lm\A13        SSSASLPYGYFGSSYYPCKSCAQKYMDTSGEEFTSRAKEFAFYQGYAGPYQPVPSYLDVP
Hf\A13        SSSAALPYGYFGSSYYPCKSCAQKYMDTSGEEFTSRAKEFAFYQGYAGPYQPMPSYLDVP
Dr\A13b\new   TPSASLPYGYFGGSYYPCKSCTQKYMDTSGEEFPSRAKEFAFYQGYSGPYQPVPSYLDVP
Dr\A13a\new   SASASISYGYFGGGYYPCKTCAQKYMDTSGEDYTSRAKEFALYSSYASPYQPVPSYLDVP

Hs\A13        VVPGLGGPGESRHEPLLPMESYQPWALPNGWNGQMYCPKEQAQPPHLWKSTLP
Mm\A13        VVPGLGGPGESRHEPLLPMESYQPWALPNGWNGQMYCPKEQTQPPHLWKSTLP
Lm\A13        VVPTIGGPGEPRHEPLLPMETYQPWAITNGWNGQVYCSKEQAQPNHLWKSTLP
Hf\A13        VVPTISAPGEPRHDTLLPMESYQPWAITNGWNGQVCCSKEQPQATHLWKSSLP
Dr\A13b\new   VVPALSAPSEPRHESLLPVETYQPWAITNGWSSPVYCPKDQTQSSTLWKSSIQ
Dr\A13a\new   VVQAISGPSEPRHESLLPMESYQPWAITTGWNGQVYCTKEQQQTGNVWKSSIP
```

NJ tree rooted to horn shark (Hf)
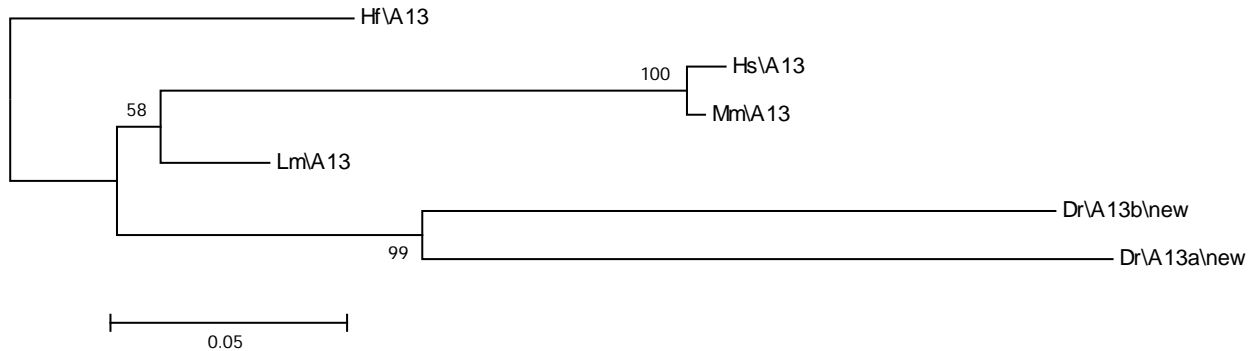
Tajima relative rate test – Hoxa13

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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        MSSFLEYPLCNRGPSAYSFPPCSAPAVDYAGESRYGGGLPSSSSLGVSFPSPASGYAPAACN
Lm\B1        MNSFLEYAICNRGTSAYSFPPCSGTTNDYNGDGRFLGGSAPVSNMGIPYASTGSGYTPQTCN
Hf\B1        MNSFLEYAICNRGTSAYAFAPCAGNVDNCNGDGRFLGGSAHNSSLGNPYASSGNNYTTQTCN
Dr\B1a\gb    MNSFLEYTICNRGTNAYPGPFHTGHASDYNADGRLYGGSNQPTGMGLTYGGTGTSYGTQACA
Dr\B1b\new   MNSYLDYTIYNRGSNTYEYLPSACASTNYIPEGRPVGNTFTSFHLNVDMGKTGSNFCKQTRP


Hs\B1        PSYGQYYPLGQEGDGGYFHPSSYGAQLGGGGAGPGPYYGNEQTASFAPAYD
Mm\B1        PSYGQYYSVGQEGDGSYFHPSSYGAQLGGGGVGSGPYYGTEQTATFASAYD
Lm\B1        PGYGHQYYFGQEPDGMYFQSSGYSNSIGSGVSGPGQYYPHEHQGFLQGTYN
Hf\B1        PGYNHHYFFNQESDGAYFQTSGCTGNIASGVSGPGQYYGQEQQGLAYGIYN
Dr\B1a\gb    NSDYHQYFINPEQDGMYYHSSGFSTSNASGAVPAAPYGQDHQRAYSQGTYD
Dr\B1b\new   PHSDHQHVLTQADDHMRLQSPGFSVVNMGGSVSASHYYGEPEP-HGYGSFK


Hs\B1        LLSENTPTARTFDWMKVKRNPPKT
Mm\B1        LLSESTLTPRTFDWMKVKRNPPKT
Lm\B1        ASSPQTSTGQTFEWMKVKRNPPKT
Hf\B1        LSPSSSSSGQTFDWMKVKRNPPKT
Dr\B1a\gb    LSASQPPPGKTFDWMKVKRNPPKT
Dr\B1b\new   YQVSNIKQAPTFDWMKVKRNPPKT
```

NJ tree rooted to horn shark (Hf)
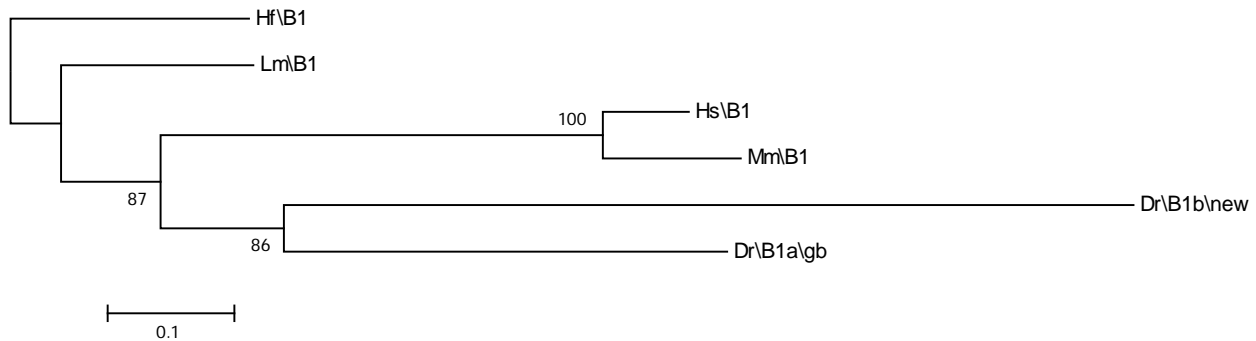
Tajima relative rate test – HoxB1

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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        MNFEFEREIGFINSQPSLAECLTSFPAVLETFQTSSIKESTLIPPPFEQTIPS
Hf\B2        MNFELEREIGFINSQPSLAECLTSFPAVADTFQSSSIKNSTLIPPPFEQTIPS

Dr\B2a\gb    LSPCTGNQARPRSQKRAHEFPWMKEKKSSKAAAASPSQASSGYTTAGLESPT
Hs\B2        LQPGASTLQRPRSQKRAPEFPWMKEKKSAKQSATSPSPAASAVPASGVGSPA
Lm\B2        LNPCSSSQPRPRSQKRAAEFPWMKEKKSSKASSSSSSPASSSVSGSGVGSPT
Hf\B2        LNP-SSNQPQPSREKRAAEFPWMKEKKSSKKNEAPLSLSAPVLGSSQAAESP
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NJ tree rooted to horn shark (Hf)
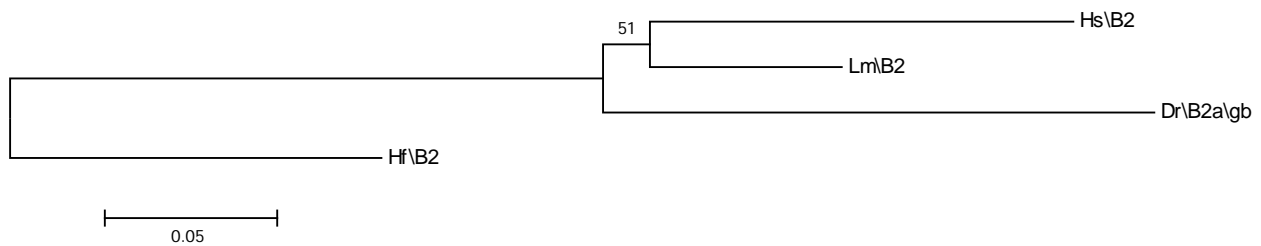
Tajima relative rate test – Hoxb2

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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        MQKTTYYDNSTLFGGYSYQGANGFGYDAPAPAFQNSAHLEGDYQRSACSLQSLGTS
Lm\B3         MQKTTYYDNSTLFGGYSFQGTNGFGYDTPQQPFQASPHIENDYHRSACSLQSLGNN
Hf\B3         MQKTTYYDNCTLFGGYTYQGANGFSYEVAQEPYPPSSHVENDYQRSACSLQPAGTS
Hs\B3         MQKATYYDNAALFGGYSYPGSNGFGFDVPQPPFQAATHLEGDYQRSACSLQSLGNA
Mm\B3         MQKATYYDNAALFGGYSYPGSNGFGYDGPQPPFQAATHLEGDYQRSACSLQSLGNA

Dr\B3a        APHAKTKELNGSCMRPSLPEHHPPPQVSPPQNTVNV
Lm\B3         APHAKSKDLNGSCMRASLPEHHQPPPVSPPQNTTNS
Hf\B3         VPHPKSKDINGSCMRSNLPEHRQPPPVSPPQNSSNS
Hs\B3         APHAKSKELNGSCMRPGLAETLSAPPGSPPPSAPTS
Mm\B3         APHAKSKELNGSCMRPGLAEPLPAPPGSPPPSAPTS

Dr\B3a        SKSSSKSSSMATPTLTKQIFPWMKESRQNTKQKNSSPSA
Lm\B3         SKTATSKSNLSSASITKQIFPWMKESRQNSKQKNSSPST
Hf\B3         SKTLSKSSHTSTPSLTKQIFPWMKESRQNSKQKNNCPST
Hs\B3         SKSGPPKCGPGTSTLTKQIFPWMKESRQTSKLKNNSPGT
Mm\B3         SKSCPPKCGSGSSTLTKQIFPWMKESRQTSKLKNSSPGT
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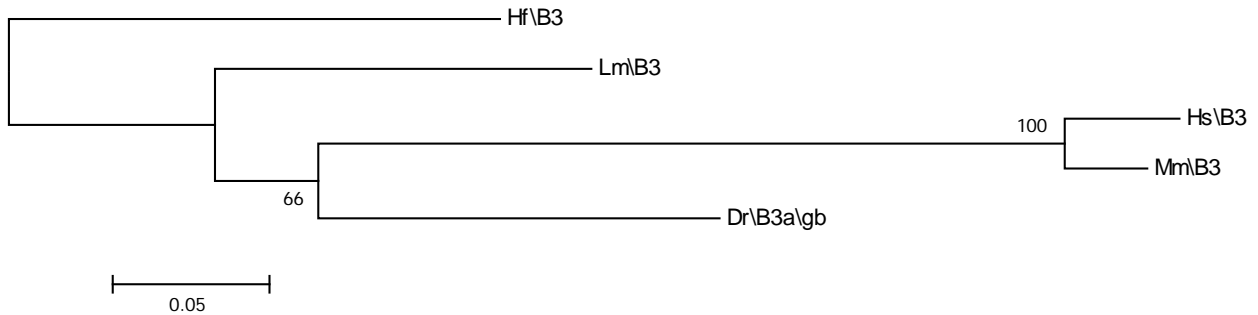
NJ tree rooted to horn shark (Hf)

Tajima relative rate test – Hoxb3

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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        MSSFLINSNYVDPKFPPCEEYSQNNYLPSHSPEYFTRAREPGFQHEAMYPRSAY
Dr\B4a       MSSYLINSNYVDPKFPPCEEYSQSDYLPSHSPDYYSAQRDPSFQHESIYHRSGC
Hs\B4        MSSFLINSNYVDPKFPPCEEYSQSDYLPSHSPGYYAGQRESSFQPEAGFGRAAC
Mm\B4        MSSFLINSNYVDPKFPPCEEYSQSDYLPSHSPGYYAGQRESGFQPEAAFGRAPC

Lm\B4        NEQPFSSCSPRGPVHLQTGLPEQIHHCESVTPSPP
Hf\B4        SEQPYSSCAPRGHVQSQTGLAKHGHQCVSVTPSPP
Dr\B4a       ADPPYSSCSPRGHVLPTTALPEPSHHCDSVTPSPP
Hs\B4        TVQRYAACSPRAPAPPPAGLPEPGQRCEAVSSSPP
Mm\B4        TVQRYAACSPRAPVQPTAGLPEPGQRSEAVSSSPP

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

NJ tree rooted to horn shark (Hf)
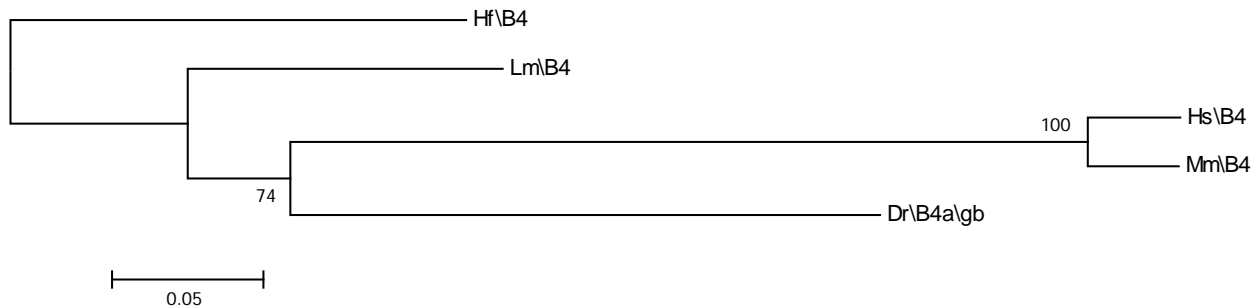
Tajima relative rate test – Hoxb4

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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    MSSYFLNSFSGRYPNGSDYQLLNYGTNGAMNASYRDSTSMHSGSFGYNYNGIDLSVNR
Hs\B5     MSSYFVNSFSGRYPNGPDYQLLNYGSGSSLSGSYRDPAAMHTGSYGYNYNGMDLSVNR
Mm\B5     MSSYFVNSFSGRYPNGPDYQLLNYGSGSSLSGSYRDPAAMHTGSYGYNYNGMDLSVNR
Lm\B5     MSSYFVNSFSGRYPNGPDYQLLNYGTSSSMNGSYRDSSTMHSSSYGYNYNGMDLSINR
Hf\B5     MSSYFVNSFSGRYQNGPDYQLLNYGTSSSENGPYRDSGTMHSGTYGYNYNGMDLSITR

Dr\B5a    TSTGHFGAVGDNSRVFQSPAPETRFRQCSLASPEPLPCSNSESLGPKPS
Dr\B5b    PNNGHFGAVGDNSRAFQNPSQETRYRQCSLSSPDPLSCATSDTLELKPS
Hs\B5     SASSHFGAVGESSRAFPAPAQEPRFRQCSLSSPESLPCTNGDSHGAKPS
Mm\B5     SASSHFGAVGESSRAFPASAKEPRFRQCSLSSPESLPCTNGDSHGAKPS
Lm\B5     SASSHFGAVGENSRGFPSPAQENRFRQCSLSSPESLPCSNSESLGAKPS
Hf\B5     SASSHFGVVNEKSRSYP-PATETRFRQCTLSSPEPLPCSGKDSHGVKPS

Dr\B5a    DQSTTHFTEIDEASASSETEEASHKQETTATSTTSAQAPQIFPWMRKLHISH
Dr\B5b    DQSTTHFADTDETNVSSETEEGAQKQESVATSTTTPQTPQIFPWMRKLHISH
Hs\B5     DQATANFTEIDEASASSEPEEAASRAQPEPMATSTAQTPQIFPWMRKLHISH
Mm\B5     DQATANFTEIDEASASSEPEEAASRAQPEPMATSTAQTPQIFPWMRKLHISH
Lm\B5     EQATTNFTELDETSASSETEEGAPRAQTEPTATSTTQTPQIFPWMRKLHISH
Hf\B5     DPTTSNFTEMDEAGASSDAEEGTPRAQQEPTQATTPQQPQIFPWMRKLHIGH
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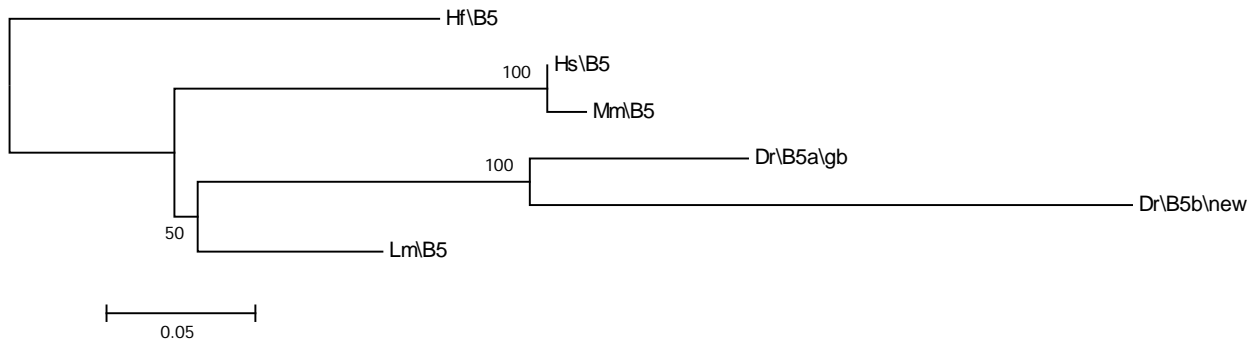
NJ tree rooted to horn shark (Hf)

Tajima relative rate test – Hoxb5

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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       MSSYFVNSTFPVTLASGQESFLGQLPLYSSGYADPLRHYPAPYGPGPGQDKGFATSYY
Mm\B6       MSSYFVNSTFPVTLASGQESFLGQLPLYSSGYADPLRHYPAPYGPGPGQDKGFAASYY
Hf\B6       MSSYFVNSTFPVTLASGQESFLGQIPLYSSGY-DPLRHYPATYGATSMQDKSYPSSYY
Lm\B6       MSSYFVNSTFPVTLPGGQESFLGQIPLYSSGYADPLRHYPGTYGATTVQDKGYPSSYY
Dr\B6a\gb   MSSYFVNSTFPVTLPGGQESFLGQIPLYSSGYTDPLRHYPAAYGGSSVQEKAYPSSFY
Dr\B6b\new  MSSYFVNSTFPVSLPGGQESFLGQIPLYSSGYTDSLRHYPATFGATNVQDKVYTSSYY

Hs\B6       PPAGGGYGRAAPCDYGAPAFYREKESACALSGADEQPPFHPEPRKSDCA
Mm\B6       PPAGGGYGRAAPCDYGAPAFYREKDAACALSGADEPPPFHPEPRKSDCA
Hf\B6       QQANGAYGCRTPCDYGSPSFYREKDPSCGASSLEDPTHFNSEQRKFECA
Lm\B6       QQANGAYSRTAACDFGTAGFYREKDPSCAISTLEDYSQFNQDQRKLDCD
Dr\B6a\gb   QQANGAYSRAGPCDYATASFYREKDPACALASEEHSFVLSQDHRKTDCT
Dr\B6b\new  QQAGGVFGRTSACDYSTPNIYRSADRSCAIGSLEDSLVLTQDQCKTDCT

Hs\B6       QDKSVFGETEEKCSTPVYPWMQRMNSCN
Mm\B6       QDKSVFGETEEKCSTPVYPWMQRMNSCN
Hf\B6       QNRILYGEVDDKSSLPVYPWMQRMNSSS
Lm\B6       QNKSVFGESEEKCSTPVYPWMQRMNSCT
Dr\B6a\gb   TGKSIYPEADEKPSAPVYPWMQRMNSCN
Dr\B6b\new  QGTERYFSTEDKPCTPVYPWMQRMNSCN
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NJ tree rooted to horn shark (Hf)
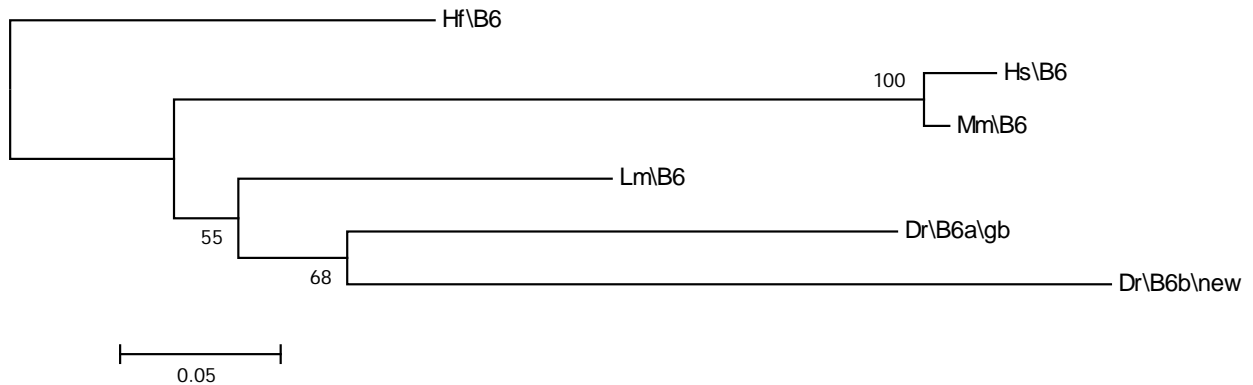
Tajima relative rate test – Hoxb6

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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      MSSLYYANALFSKYQAASSVFPSGVFPEQTSCAFASNSQRSGYGSGSASFAAS
Hf\B7      MSSLYYANALFSKYTAGTSVFPTGVFSEPTSCAFASNSQRSGYGSGSASYAAT
Dr\B7a     MSSLYYANALFSKYQVASSAFSTGVFPEQTSCAFSCSSQRAGYGSASSSSSVS


Hs\B7      MQGLYPGGGGMAGQSAAVYAAGYGLEPSSFNMHCAPFEQNLSPGDSAKAAGA
Mm\B7      VQGLYSGGGAMAGQSAAVYAAGYGLEPSSFNMHCAPFEQNLSPGDAAKAGGA
Lm\B7      MPGLYSNGSSMHPQTPSMYSASYGLEASSFNMHCSPFEQNLSPGDLSKQNCS
Hf\B7      VPGLYSTANSLHHQTPTMYTSPYGLNANSFNMHCSSFDHNISAGESCKQSCS
Dr\B7a     LPSMYTNGTSLSSHTQGMYPTAYELGAVSLNMHSSLFDHNLPAGDLCKASSG


Hs\B7      KEQRDSDLAAENFRIYPWMRSS
Mm\B7      KEQRDSDLAAENFRIYPWMRSS
Lm\B7      KEQRDSEQQNENFRIYPWMRST
Hf\B7      KEQKETDPQSENFRIYPWMKSS
Dr\B7a     KEQRGYHQNNENLRIYPWMRST
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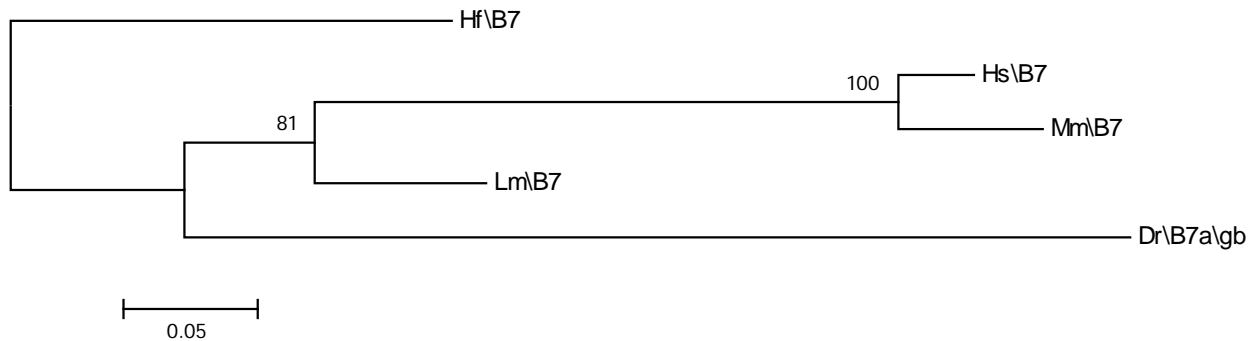
NJ tree rooted to horn shark

Tajima relative rate test – Hoxb7

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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          MSSYFVNSLFSKYKGGETLRPNYYDCGFTQDLGGRPTVVYGPGTGSSFQHPSQIQDFYH
Dr\B8a         MSSYFVNSLFTKYKSGDTLRPNYYECGFAQDLGTRPTVVYGPGTGATFQHAPQIQEFYH
Dr\B8b         MSSYFVNSLFTKFKGGDSLRSNYYDCPYTPDLGGRPSVLYGHNTGSAFQHAAQFPDFYH

Hs\B8          GPSSLSTAPYQQNPCAVACHGDPGNFYGYDPLQRQSLFGAQDPDLVQYADCKLAAA
Mm\B8          GPSSLSTAPYQQNPCAVACHGDPGNFYGYDPLQRQSLFGAQDPDLVQYADCKLAAA
Lm\B8          GTSSLSTSPYQQNPCAVTCHGDPGNFYGYDPLQRQTLFTAQDSDLVQFTDCKLASN
Hf\B8          GAATLSTSAYQQNPCAVTCHGDAGSFYGYDALQRQPIFAAQEAELIQYPDCKSTAN
Dr\B8a         GASTLSAAPYQQSPCAVTCHGEPGNFYGYDALQRQTLFGAQDADLVQYSDCKLATG
Dr\B8b         GTSSFPHASYQQTPCAVAYPGDAGNILGQDGLQKQSFFGAPDSDFTQFGDCNLKVS

Hs\B8          GLGEEAEGSEPSPTQLFPWMRPQ
Mm\B8          GLGEEAEGSEPSPTQLFPWMRPQ
Lm\B8          GVGEEAENSEPSPTQLFPWMRPQ
Hf\B8          SLGEEAENSESSPTQLFPWMRPQ
Dr\B8a         GIGDETDNTEPSPTQLFPWMRPQ
Dr\B8b         GIRDDLESAEPCTAQLFPWMRPQ
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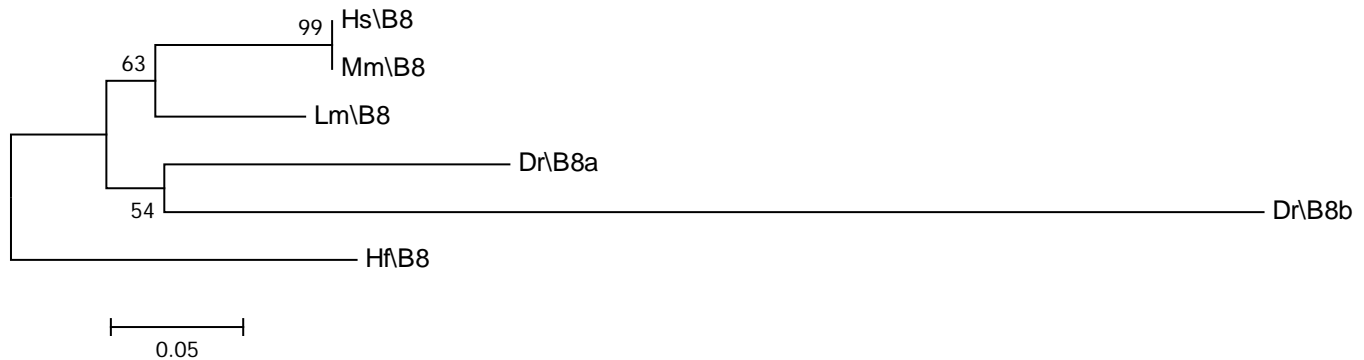
NJ tree rooted to horn shark (Hf)

Tajima relative rate test – Hoxb8

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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      MSISGALSNYYVDSIISHESEEASSAKFSSGQYVSSRQPGHSEHLEFPSCSFQPKPPVFS
Dr\B9a     MSISGTLSNYYVDSIISHEGEDPNASRFSNVQYSSARQPGPGEHPEFPSCSFQPKPPVFS
Hf\B9      MSISGAISNYFVDSLISHESEGSPATKFASGQYIVSRQPGVPEHPEFPACNFQPKSPVFG

Hs\B9      ASWAPLSPHASGSLPSVYHPYIQPQGVPPAESRYLRTWLEPAPRGEAAPAVK
Mm\B9      ATWAPLSPHASGSLPSVYHPYLQPQGAPAAESRYLRTWLEPAPRAEAAPAVK
Lm\B9      ASWTPLNPHSAGTLSSVYHPYIQHQTVPPSDNRYLRTWLEPLPRTDSLSSIK
Dr\B9a     SSWSPFSSHASNGLPAVYHPYIPTQPVPSTDTRYLRTWLDCAPRAEPLPQVK
Hf\B9      TSWAPVYAQPSANVSTLYHPYVQSHPIQP-DSRYLRSWLDPTPRAVSAPSLK

Hs\B9      AEPLLGPGELLGTPEYSLETSAGREAVSNQRPGYGDNCEGSEDKERPDQ
Mm\B9      AEPLLGPGELLGTPEYSLETSAGREAVSNQRAGYGDNCEGSEDKERPGQ
Lm\B9      AEPLLGLGEILGGPEYNLETATGREGSSNQGSSYGDNSEGSEDKDRPDQ
Dr\B9a     MEPLLGLGEPPGQHEYILESSTAREINSGHSAGFEDNCEGSEDKERIKV
Hf\B9      TEVLAGGGETLAALQKLHGEYLESETISGKAPCYEDSCEEKGNKETSEQ
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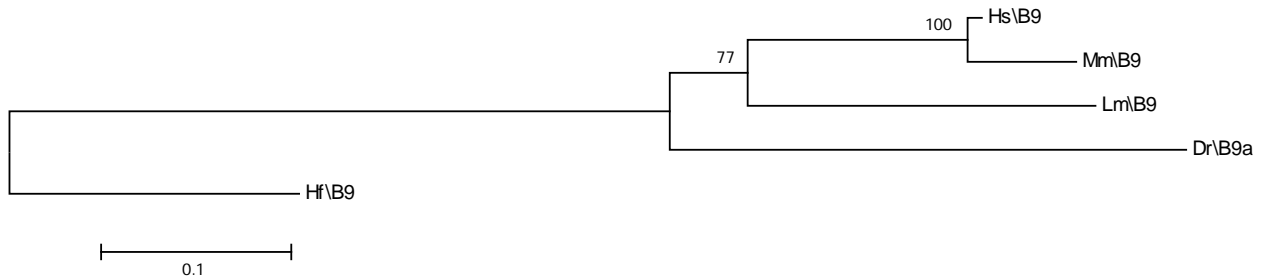
NJ tree rooted to horn shark (Hf)

Tajima relative rate test – Hoxb9

Outgroup	Ingroup1	Ingroup2	P-value
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          LSPCWVDTVMFVYEMEGLMGASQCRNLMAHSALGSH
DrB13a          LNPRWADTVMFVYEMEGLVGSGQCRNLMAHSALSGH
Hs\B13          MEPGNYATLDGAKDIEGLLGAGGGRNLVAHSPLTSH
Mm\B13          MEPGNYATLDGAKDIEGLLGAGGGRNLVSHSPLASH

Hf\B13          PSPLVHGSGYSTVDVSGSVEPGKQCTPCPMPQASTAAPLPYGYFGSGYYSCRMGR
Lm\B13          PSTLVHGSGYPTVEMSGSGEVAKQCTPCPVPQSSSTAPLPYGYFGSGYYSCRMGR
DrB13a          PSSLVHGSSYPTVDVSTSAESGKQCTPCPVPQASSTGPIPYGYFGNSYYPCRMGR
Hs\B13          PAALMPAVNYAPLDLPGSAEPPKQCHPCPVPQGTSPAPVPYGYFGGGYYSCRVSR
Mm\B13          PAALMPTVNYAPLDLPGSAEPPKQCHPCPVPQGASPAPVPYGYFGGGYYSCRVSR

Hf\B13          SSIKPCTQPAPLSYPGDSPVPTDEYPGRPKEFAFYHGYAGAYQPMPSYLDVSVVQ
Lm\B13          GSLKSCTQPAALSYSAETPVASEDYQARAKEFAFYHGYASPYQPVASYLDVSVVQ
DrB13a          GSLKSCTQPSALSYTAETPVTSEEYPTRAKEFAFYHSYPSPYQSMASYLDVSVVQ
Hs\B13          SSLKPCAQAATLAYPAETPTAGEEYPSRPTEFAFYPGYPGTYQPMASYLDVSVVQ
Mm\B13          SSLKPCAQTAALAYPSETPAPGEEYPSRPTEFAFYPGYPGPYQPMASYLDVSVVQ

Hf\B13          TISAGEPRHEALLPMEGYQPWPLNGWNSQMCCKEQAQPGHLWKSTLADVAAHQQ
Lm\B13          TISAGEPRHETLLPVDSYQPWALTGWNSQMYCKDQTQPGHLWKSALADVVAHQQ
DrB13a          TLGTGEPRHDSLLPMDSYQPWALAGWGSQMYCKDQGQAGHLWKSALADVVAHQH
Hs\B13          TLGPGEPRHDSLLPVDSYQSWALAGWNSQMCCGEQNPPGPFWKAAFASSGQHPP
Mm\B13          TLGPGEPRHDSLLPVDSYQPWALAGWNSQMCCGEQNPPGPFWKAAFAPSVQHPP
```

NJ tree rooted to horn shark (Hf)

Tajima relative rate test – Hoxb13

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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            MSSYLMDSNYIDPKFPPCEEYSQNSYIPEHSPEYYGRTRESGFQHHHQELYPR
MmC4            MSSYLMDSNYIDPKFPPCEEYSQNSYIPEHSPEYYGRTRESGFQHHHQELYPR
DrC4a           MSSYLMDSNYIDPKFPPCEEYSQNSYIPEHSPEYYSRARDSGYQHHHQELYPR
LmC4            MSSYLMDSNYIDPKFPPCEEYSQNNYIPEHSPEYYSRTRDSGFQHHHQELYPR
EsharkC4        MSSFLMGSNYIDPKFPPCEEYSQNSYIPDHSSEYYSRPRDSAYPPQHQDLYQR

HsC4            PSYPERQYSCTSLQGPGNSRGHGPAQAGHHHPEKQSLCEPAPLSGASAS
MmC4            PSYPERQYSCTSLQGPGNSRAHGPAQAGHHHPEKQPLCEPAPLSGTSAS
DrC4a           ASYQERQYNCASIPEPDTQRGHGLPHAGHLLGKGSASCEPPPLPLSPAT
LmC4            PNYPERQFNCTSIQGPGNQRGHGQPQAGHHLPEKPLLIEQPPISTPSNT
EsharkC4        PNYPERQFACATVQGPGNRAGHEQHQVAHQHISSPVPYEPAALSTSTTT

HsC4            PSPAPPACSQPAPDHPSSAASKQPIVYPWMKKIHVSTVNPNYNGEP
MmC4            PSPAPPACSQPAPDHPSSAASKQPIVYPWMKKIHVSTVNPNYNGEP
DrC4a           PSAASSACNQATPEHPSSASAKQPVVYPWMKKIHVSTVNSSYNGEP
LmC4            TSPAPPSCNQPNTEQPNNTTSKQPVVYPWMKKIHVSTVNPNYNGEP
EsharkC4        SPPSSSACTQQNLEQQQRTNAKQPIVYPWMKKIHVNTVNHSYTGEI
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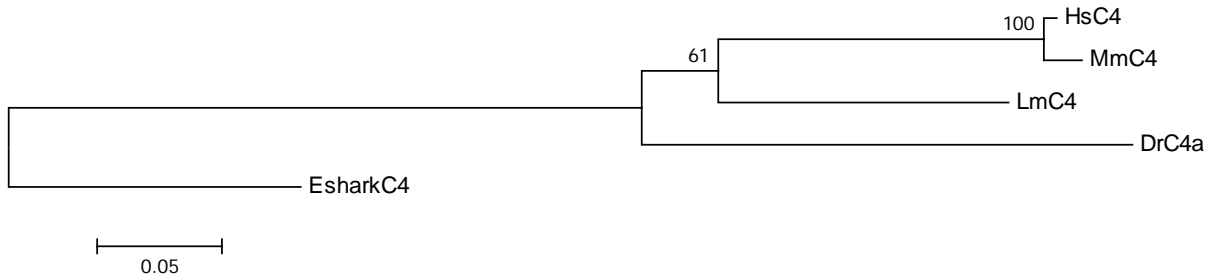
NJ tree rooted with elephant shark (Eshark)

Tajima relative rate test – Hoxc4

Outgroup	Ingroup1	Ingroup2	P-value
Eshark	Lm	Hs	0.251
Eshark	Lm	DrC4a	0.257
Eshark	Hs	DrC4a	0.835

Dr – Danio rerio, Eshark – Callorinchus milli, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus
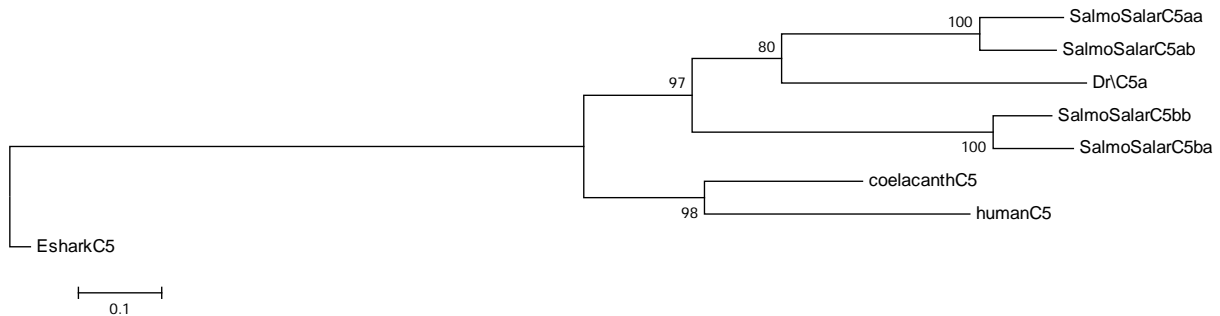
Hoxc5 alignment for relative rate test

```
SalmoSalarC5aa      MSSYVASIFKQTHEASSCNMNSLGYGSLSDFDQANYAYNGHFNGTFTSD
SalmoSalarC5ab      MSSYVANIFKQTHEASSFNMNSFGYGSLSSLHQDNYAYNGHLNGTFTSD
Dr\C5a              MSSYVGKSFSQTQDASSCRMHTFDYGAHSEFHESNYAYEGLLGGSFSSQ
SalmoSalarC5bb      MSSYVASLFKQTHDASTFAVHNHGYGSNPELNVSGYSGYGHHRGSFASR
SalmoSalarC5ba      MSSYVASLFKQTHEASAFALHNHGYGSSPELNVSGYCGFGHHRGSFASP
coelacanthC5        MSSYVASLYKQSQNVPAYAMQSYGYGSVSEVHPSRYCYGGLMSITFPSG
humanC5             MSSYVASFYKQSPNIPAYNMQTCGYGSASEVQASRYCYGGLLSITFPPA
EsharkC5            MNSYSASFCKQDQNGSGCATKGWREGSTLQMCPPRYSYRGLINISLPAR

SalmoSalarC5aa      ATVSLKREEMNSSLRGNTDTSPPRPQSYSALSSRNSVQCLSDGILSKATE
SalmoSalarC5ab      STASLKREEMETSLRGNTDAPPPRLQSCSAASSRNSVQCLRDGILSKGTG
Dr\C5a              IPTSLRREAINTTDRARSSAAVQRTQSCSALGSRSFVSPLSHGLLSQKAE
SalmoSalarC5bb      SSSSIGMGEMNAALRGNPGDTPRPESSTGDSTQRHLMNSLNLGLYRRKPV
SalmoSalarC5ba      SSSSRGMVEMNSGLHGNPGDTPRPESSTGDASQRRHMNSLNLGLYCRKPE
coelacanthC5        PSSTLNGMDMSSSPRTNPDRSCTVMGSSEHTFSRNDQSSLNLGIYSQKAG
humanC5             PSNSLHGVDMAANPRAHPDRACSAAAAPGHAPGRDEAAPLNPGMYSQKAA
EsharkC5            VSHQSAEGAISAIAGNRPFAAMGDSVDGPGSERRQSKATPNPGIYCQTTR

SalmoSalarC5aa      MMEVVETPTEESAIKVETMQPSKKHQDSQQQPQIFPWMTKLHMIH
SalmoSalarC5ab      RMEVVENPTEENAIKVETMQPSKKHQDSQQQPRIFPWMTKLHMSH
Dr\C5a              GMEVMEKPSRTDDIKMETTSASTQRQN-QSQPQIYPWMTKLHMSH
SalmoSalarC5bb      TSDLSEMPTQTGEIKVGTLQPSTQPQTSEQQPQIYPWMTKLHMGH
SalmoSalarC5ba      TSDFSEMHTQTGEIKVVTLQPSTQPQTSEPQPQIYPWMTKLHMGH
coelacanthC5        GIVLEDKPKSTVEIKAEPVQTPQGGQQQSQPQIYPWMTKLHMSH
humanC5             RPALEERAKSSGEIKEEQAQTPAGLSQPPAPPQIYPWMTKLHMSH
EsharkC5            GKGVENSPQIVREPSPETGETHTQRGQTQQQPRIYPWMTKVHLSH
```

NJ tree rooted to elephant shark (Eshark)

Tajima relative rate test – Hoxc5

Outgroup	Ingroup1	Ingroup2	P-value
Eshark	coelacanth	human	0.285
Eshark	coelacanth	DrC5a	0.223
Eshark	human	DrC5a	0.622

Dr – Danio rerio, Eshark – Callorinchus milli

Hoxc6 alignment for relative rate test

```
Lm\C6        MNSYFANPSLSCHLTSGQEVLPNVALNSTAYDPVRHFSTYGAAMAQNRIYSSPFYSPQEN
EsharkC6     MNSYFANPSLPCHLASGQEILPSAGLNSAAFDPVRHFSTYGAAVSQGRIYSSPYYSTQEN
Mm\C6        MNSYFTNPSLSCHLAGGQDVLPNVALNSTAYDPVRHFSTYGAAVAQNRIYSTPFYSPQEN
Hs\C6        MNSYFTNPSLSCHLAGGQDVLPNVALNSTAYDPVRHFSTYGAAVAQNRIYSTPFYSPQEN
newt/c6      MNSYFTNPSLSCHLASGQEVLPNVALNSSAYDPVRHFSTYGEAVAQNRIYSSPFYSPQDN
Dr\C6b       MNSYFTNPSLSCHLNSGQEVLPSVAISSTNYDPVRHFSPYGAAVAQNRIYSNPFYSHQEN
Dr\C6a       MNSYFANPSLSCHLSGGQEVLPNMPLNSTTYDSVRHFSSYGTTVTQNRIYASPFYSPQDN

Lm\C6        VVFGSSRPYDYGSSAFYQEKDMLPSCRQNMINTQTSIAQEFNSDHSRTQEQKST
EsharkC6     VVFGSGRPFDYGSNAFYQEKDLPASCRQNLGNTDNPIAQDLNGEHIRAQEEKSN
Mm\C6        VVFSSSRPYDYGSNSFYQEKDMLSNCRQNLGNTQTSIAQDFSSEQGRPQDQKAS
Hs\C6        VVFSSSRPYDYGSNSFYQEKDMLSNCRQNLGNTQTSIAQDFSSEQGRPQDQKAS
newt/c6      VVFSSGRPYEYGSNAFYQDKDMLSSCRQNMGNTQTSIAQDFSSDQSRVQEQKTS
Dr\C6b       VMFGSSRPYDYGSNMFYQDKDVLPSCRQGFGQTQGSLTQDYASDQGKTVEPKGV
Dr\C6a       VVFGSSRPYEYGSNVFLQDKDVLPSCRQTMGNAQSHVAQEYNLEQARTQDQKAN

Lm\C6        VQIYPWMQRMNSHSVGYG
EsharkC6     FPIYPWMQRVNSHSVGYG
Mm\C6        IQIYPWMQRMNSHSVGYG
Hs\C6        IQIYPWMQRMNSHSVGYG
newt/c6      IQIYPWMQRMNSHSVGYG
Dr\C6b       VQIYPWMQRMNSHRVGYG
Dr\C6a       IQIYPWMQRMNSHSVGYG
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NJ tree rooted to elephant shark (Eshark)
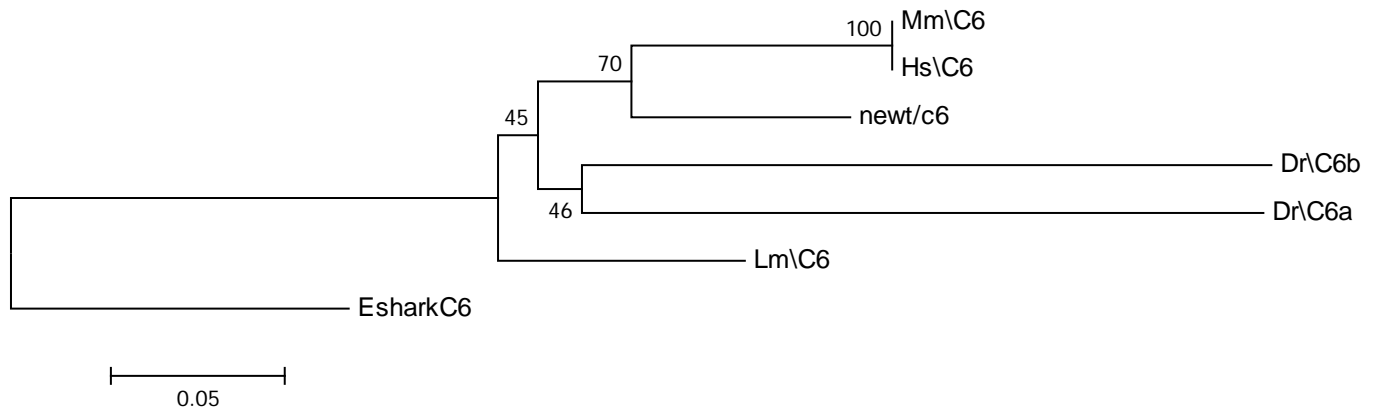
Tajima relative rate test – Hoxc6

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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 – Callorhinchus milii, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus, newt – Notophthalmus viridescens

Hoxc8 alignment for relative rate test

```
humanC8          MSSYFVNPLFSKYKAGESLEPAYYDCRFPQSVGRSHALVYGPGGSAPGFQHASHVQDF
mouseC8          MSSYFVNPLFSKYKGGESLEPAYYDCRFPQSVGRSHALVYGPGGSAPGFQHASHVQDF
chickC8          MSSYFVNPLFSKYKGGESLEPTYYDCRFPQSVSRSHALVYGPGTTAPTFQHPSHVQEF
XenopusC8        MSSYFVNPLFSKYKGSESLEPTYYDCRFPQSVSRSHALVYGPSATAPGFQHPSHVQEF
coelacanthC8     MSSYFVNPLFSKYKGGESLEPTYYDCRFPQSVSRSHALVYGPSTTAPSFQHPSHVQDF
EsharkC8         MSSYFVNPLFSKYKTGESLDPTYYDCRFPQSVGRSHALVYGPGSGGPGFQHPSHVQEF
zfishC8a         MSSYFVNPLFSKYKGGETLEPTYYDCRFPQSVARSHTLVYGHGAAAPGFQHPSHVQDF

humanC8          FHHGTSGISNSGYQQNPCSLSCHGDASKFYGYEALPRQSLYGAQQEASVVQYPDCKSSAN
mouseC8          FHHGTSGISNSGYQQNPCSLSCHGDASKFYGYEALPRQSLYGAQQEASVVQYPDCKSSAN
chickC8          FHHGTSSISNSGYQQNPCALACHGDASKFYGYEALPRQSLYGAQQETTVVQYPDCKSSSN
XenopusC8        FHHGTSSITNSGYQQNPCALTCHGDASKFYGYEALPRQSLYGAQQEASVVQYPDCKSSSN
coelacanthC8     FHHGTSSISSTGYQQNPCALSCHGDASKFYGYEALPRQSLYGAQQEASMVQYPDCKSSSN
EsharkC8         FHHGTSSLSTSGYQQSPCGLTCHGDASKFYGYEPMPRQSLYGTQQEASMVQYPDCKSSSG
zfishC8a         FHHGTTGISNPGYQQNPCALACHGDATKFYGYEALPRQPLYGTQQEATLAQYPDCKSSNS

humanC8          TNSSEGQGHLNQNSSPSLMFPWMRPH
mouseC8          TNSSEGQGHLNQNSSPSLMFPWMRPH
chickC8          SNSSEGQGHLNQNSSPSLMFPWMRPH
XenopusC8        TNTSEGQGHLNQNSSPSLMFPWMRPH
coelacanthC8     SNTGEGQGHLNQNSSPSLMFPWMRPH
EsharkC8         SNTGEAQGHLNQNSSPNLMFPWMRPH
zfishC8a         TNPGEGQGHLSQNSSPSLMFPWMRPH
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NJ tree rooted to elephant shark (Eshark)
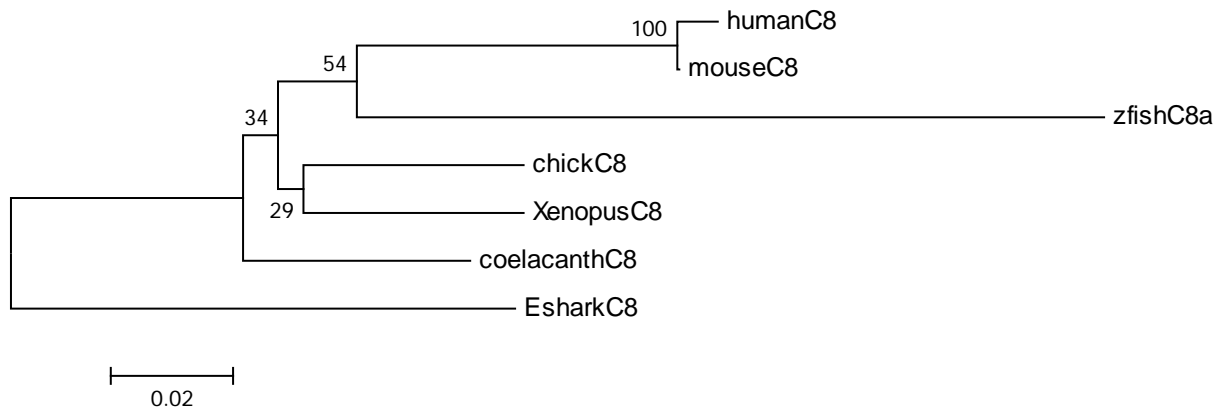
Tajima relative rate test – Hoxc8

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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     MSATGPISNYYVDSLISHDNEDLLASRFPATGAHPAAARPSGLVPDCSDFPSCSFAPKPA
Mouse-c9     MSATGPISNYYVDSLISHDNEDLLASRFPATGAHPAAARPSGLVPDCSDFPSCSFAPKPA
Coel-c9      MSTSGPISNYYVDSLISHENEEILASRFPATGPHPAASRSSGLVPDCTDFPSCSFAPKPA
Zfish-c9a    MSATGPISNYYVDSLINHESEDVLASRFTATGPISSSSRPTPLVPECADYPSCSFAPKPP
Eshark-c9    MSTSGALTNYYVDSIINHENEEMFAARFAASGSHPPAPRPAGLVPDCTDFPSCSFTPKPP

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

Human-c9     YALKPDAYPGRRADCPEGRSYPDYMYGSPRDRAQTLPSPEADALAGSKHKEEK
Mouse-c9     YALKPDAYPGRRADCPDGRSYPDYMYGSPRDRAQTLPSPEADALAGSKHKEEK
Coel-c9      YGLKPDAFPGRRAECTDGRSYPDYMYGSPRERTQNIPSPESEAIAASKHKEEK
Zfish-c9a    YGLKPDTFQDPRADCGNGRTYTDYLYCSAREKQQNTPSPETESLSSGKHKDDK
Eshark-c9    YGVKPESFPGRRSECTDGRSFTDYIYGSSTDKIQSIPSPGSETMVSAKHKDEK

Human-c9     ADLDPSNPVANW
Mouse-c9     ADLDPSNPVANW
Coel-c9      AELDPNNPVANW
Zfish-c9a    AELDPDNPVANW
Eshark-c9    TEIDPSNPAANW
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NJ tree rooted to elephant shark (Eshark)
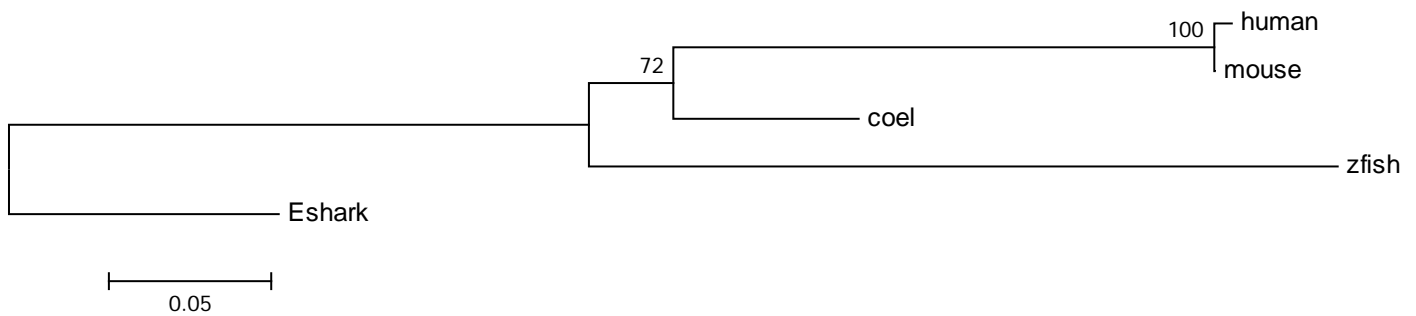
Tajima relative rate test – Hoxc9

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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 – Callorhinchus milii

Hoxc10 alignment for relative rate test

```
Mm\C10          MTCPRNVTPNSYAEPLAAPGGGERYNRNAGMYMQSGSDFNCGMRGCGLAPSLSKRDEGGSPNLA
Hs\C10          MTCPRNVTPNSYAEPLAAPGGGERYSRSAGMYMQSGSDFNCGMRGCGLAPSLSKRDEGSSPSLA
Xenopus\c10     MSCPNNVTPNSFMDSLAGSCRGDNYSTSPGMYLQTGSEFSCGMRNCGIVPSLSKRDDVNNPGLS
Lm\C10          MSFPNNVTANSFMDSVAGTCRGENYSSNTGMYMQPGADFGCGMRNCGIIPSLSKRDEVNNTNLS
Eshark\C10      MSCPNNVAANTFMDPLAAVCRGENFSSNPGMYMQAGAEFGCGVRNCGLIPALSKRDEVNPSNLA
Dr\C10a         MSCPNNVAANAFMDSLVGPFRGESYSSNSGMYMQTSAEYGCSMGSFGIVGTLSKRDDLQPSGMH

Mm\C10          LNTYPYLSQLDSWGDPKAAYRLEQPVGRPLSSCSYPPSVKEENVCCMYSAEKRAKSGPEAALYSH
Hs\C10          LNTYPYLSQLDSWGDPKAAYRLEQPVGRPLSSCSYPPSVKEENVCCMYSAEKRAKSGPEAALYSH
Xenopus\c10     LNTYPYLSQLDNWCDPKNTYRIEQPVARQLSSCSFPTNVKEENVCCMYNTDKRAKNATEAALYPN
Lm\C10          LNTYPYISQLDSWGDPKNSYRIEQPVARQLPSCSFPTNVKEENVCCMYSSDKGAKGSAESPLYPR
Eshark\C10      LTNYPYLSQLDGWGEHPKSYRIEQPVARTLPSCSFPTTVKEENICCIYGSEKRGKTTGDGALYPG
Dr\C10a         LGSYQYLSQRDTWIAGSKTYRGSQPVAQPLHPCSFPASVKEEAIPCLYQPDIDAKESGEKSTYIR

Mm\C10          PLPESCLGEHEVPVPSYYRASPSYKTPHCAGANEFEAPFEQRASLNRTEESPQLGGKVSFPET
Hs\C10          PLPESCLGEHEVPVPSYYRASPSYKTPHCSGANDFEAPFEQRASLNRAEESPQLGGKVSFPET
Xenopus\c10     QMPETRPSDHEVPVPSYYRATQGYKTPSCHSTGDFETSFENRTSVNRSEEQQQAVGKGGFPEN
Lm\C10          LLSSSCPSDQEVPVPSYFRVNQGFKNSGCNTTNEFDTSFSSSASFARANPQGQSVSKEVFSEK
Eshark\C10      LTPETCPTENEVPVPGYFRVSQGYKSPDCSTTAEFDSAFNSAPNLQQIDQQPPTSVTESFIKS
Dr\C10a         LGDNSHPNQSAVSTPDYFRRSQVYASERGHHGDEFGSDFNPIPRISPVEASDSCVKSSKARQH

Mm\C10          PSDSQKTEQSLAGPKASPSESEKTADSSPDTSDNEAKEEIKAENTTGNWL
Hs\C10          PSDSQKTEQSLAGPKGSPSESEKAADSSPDTSDNEAKEEIKAENTTGNWL
Xenopus\c10     TTDNQKTEKSLPAPKLPPSEGDKNTDTSTDNSDTEAKEDIKAENAAGNWL
Lm\C10          STDNQKLEDNVSVQRITPVETEKNTDTSTDNSDNEAKEDMKTESATGNWL
Eshark\C10      PKDGGNREDSSRVTPSKETETVTQQDLSSENSDTEFKEETKRENAAGSWL
Dr\C10a         PEDKGTQEDDMDQRQTRKEESVSKTESCTDDSESELKDESKLEKATGNWL
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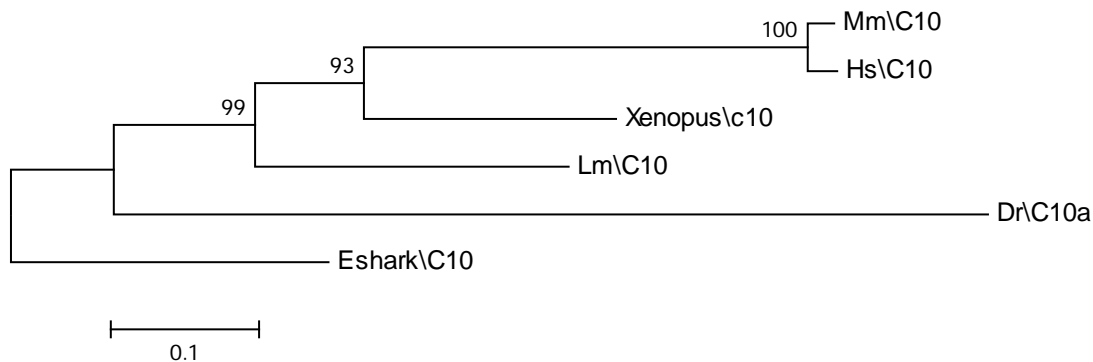
NJ tree rooted to elephant shark (Eshark)

Tajima relative rate test – Hoxc10

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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 – Callorhinchus milii, Lm – Latimeria menadoensis, Hs – Homo sapiens, Mm – Mus musculus

Hoxc11 alignment for relative rate test

```
Hs\C11        VNLGNFCSPSRKERGADFGERGSCASNLYLPSTYYMPEFSTVSSFLPQAPSRQIS
chick\C11     VNLGNFCSQSRKERSAEFGERAGCASNLYLPSTYYVPEFSTVSSFLPQAPSRQIS
Lm\C11        MNLGNFCSQSRKDRSAEFGDRAGCTSNLYLPSTYYVPEFSSVSSFLPQAPSRQIT
Eshark\C11    MNLGNFCSQTRKERTAEFADRGSCGANMYLPSTYYVPEFTAMSTFLPQATSRQIT
Dr\C11a       VNLGNFCSQTRKDRTSEFGDRTGCASNIYLPSTYYVPEFSAVSSFLPQGPSRQIT
Dr\C11b       VNIGNFCSQSRKERTSEFGERASCASNLYLPSTYYVPEFSTVSSFLPQAQSRQIT

Hs\C11        YPYSAQVPPVREVSYGLEPSGKWHHRNSYSSCYAADELMHRECLPPSTVTEI
chick\C11     YPYSTNLSPVREVSYGLDPSSKWHHRSNYASCYSAEDLMHRECIPPSTMTEM
Lm\C11        YPYSTNLPPMREVSYGLDPSSKWHPRSNYASCYSAEDLMHRECIPPSTMTEM
Eshark\C11    YPYSTNLSPVRDVSYGLDPSSKWHHRTNYTSCYSAEDLMHRDCIPPSTMTEL
Dr\C11a       YPYSTNLSPVRDVSYGLDPSSKWHHRSNYASCYSGEDLVHRDCLPPSTMTEM
Dr\C11b       YSYSTNFTQVRDLPFELNPSGKWHHRGNYSSCYAEEDLVHRDCLPPSTMTEM

Hs\C11        LMKNEGSYGHHHPSAPHPGFYSSVNKNSVLPQAFDRFFDNAYCGDPP
chick\C11     LMKNESAYSHHHPSSNHPGFYGGMNKNTVLPQGFDRFFENAYCANPT
Lm\C11        LMKNESVYNHHHPSSNHPSGFYSSMSKNSVLPQGFDRFFENAYCSNQQ
Eshark\C11    LMKNESIYNHHHPSSNHSAFYGNVGKSSVLPQGFDRFFETSYCASQA
Dr\C11a       LMKNESVYSHHHHPNSSSGFYTGVGKNNVLPQGFDRFFETAYCSDNQ
Dr\C11b       LMKNENVYNHHYHPAINGGFYSSIGKTNVLPQSFDRFLDCAQSADGG

Hs\C11        CSGKGEAKGEPEPPASGLASRAEAGAEAEAENTNSSGSAHAKEPAKGAAPNAPRTR
chick\C11     CGQKGEGKGEAEPQSHALSSRGETGMDPEDENTTSSASSSNKEGSKSSNSSAPRTR
Lm\C11        CVQKSEGKLESESQPSVLSSGGDQEKEPEDENTNSSASSSNKEGSKTSNSSTPRTR
Eshark\C11    CVQKGDRKLESMAQPSALSSGTDEERTTGDENTISAASSGNRAEGKTSNSSGPRTR
Dr\C11a       CLQKSENKLETSQQPTAVSAAREPEKDPEDEHTNSCTSAADGNASKSSHSGTPRTR
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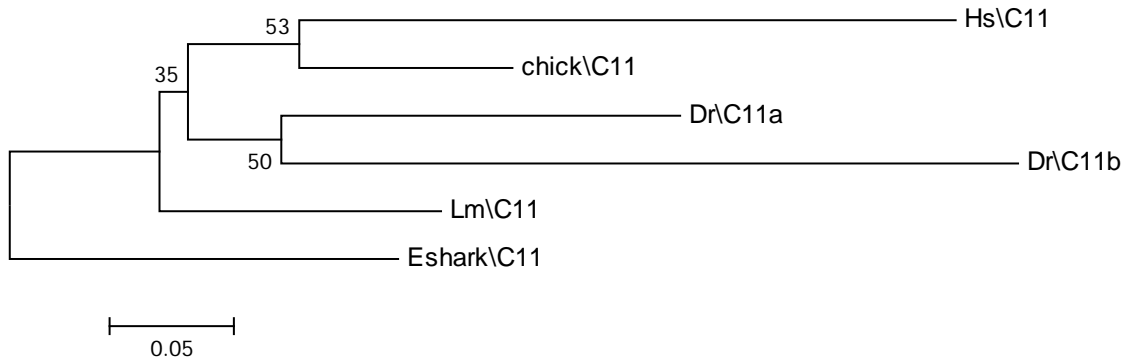
NJ tree rooted to elephant shark (Eshark)

Tajima relative rate test – Hoxc11

Outgroup	**Ingroup1**	**Ingroup2**	**P-value**	**Significance**
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 – Callorhinchus milii, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus, chick – Gallus gallus

Hoxc12 alignment for relative rate test

```
Mm\C12       MGEHNLLNPGFVGPLVNIHTGDTFYFPNFRASGAQLPGLPSLSYPRRDNVCSLPWPSAEPCNGYPQ
Hs\C12       MGEHNLLNPGFVGPLVNIHTGDTFYFPNFRASGAQLPGLPSLSYPRRDNVCSLSWPSAEPCNGYPQ
Lm\C12       MGEHNLLNPGFVGPLVNIHTGDAFYFPNFRTSGGQLAGLPSLSYPRRDNVCSLPWTSSEPCNGYPQ
Eshark\C12   MGEHNLLNPSFVGPLVNIHTGDAFYFPNFRTSGGQLAGLSSLSYPRRDNVCSLPWPVSDQCNGYPQ
Dr\C12a      MGEHNLLNPGFVGPLVNIHTGDRFYFPNFRASGGQLAGLPSLSYPRRDNVCSLPWNPSESCNGYPQ
Dr\C12b      MGEHNLFNPGFVGQLVNINARDAFYLSNFRASGGQLAGLQTLRLSRRDNVCSLPWNPSEACSGYPQ


Mm\C12       PYLGSPVSLNPPFGRTCELARVEDSKGYYREPCAEGGGLKREERGREPGAGPLLQLEPSGPPALGF
Hs\C12       PYLGSPVSLNPPFGRTCELARVEDGKGYYREPCAEGGGLKREERGRDPGAGPLLPLEPSGPPALGF
Lm\C12       PYLSNPVSINPSFNRACDIARAEENKCYYRDACSENSSLKREERARDSSLVPHEPGIPNGMNASFS
Eshark\C12   SYLGNTVSINPSFNRTCDIGRVEESKSYYRDGGSDSVALKREERIRDNSVLPHESAIPNGIGANFS
Dr\C12a      SYFSSPVSINPSFNRSCEITRLEESKCYYRDSCSDNNSLKREERARDTSVSSHGMHNGMGNSGTFS
Dr\C12b      SHISGPVTLNHTYNQSCDITRQEDNKCFYTSGGGDNNSLISKEGALDNSSVSNGQNNLNGMGGSYS


Mm\C12       KYDYTASGPPHDPPSCQSLESDSSSSLLNEGNKSAAGDGSLVSPLNPGGGLSASGAPWYPIHSRSR
Hs\C12       KYDYAAGGPPHDPPSCQSLESDSSSSLLNEGNKGAAGDGSLVSPLNPGGGLSASGAPWYPINSRSR
Lm\C12       KYDYSNGEMTQDPSSCQSLESDSNSSLLNEGSKNSSNQSTMSSPISNGNSLSTAGAPWYPMHTRSR
Eshark\C12   KYDYPGSEPHQEHGACHPLESDSNSPLMNDQEKNCGNNSALASPITHGNSLPAGGTPWFPVHARTR
Dr\C12a      KYDYGTEHLTQDPPSCQSLESDSSSSVLNEGGKTSASDQTLVSQGNHASNIAGGGAPWYPMHTRTR
Dr\C12b      KYDCLTPAPIPNPRLCRSLESVSGCSFINEGAKTSSGIHSLTSPDIQTSVAALNGALWYPMHRQTR
```

NJ tree rooted to elephant shark (Eshark)
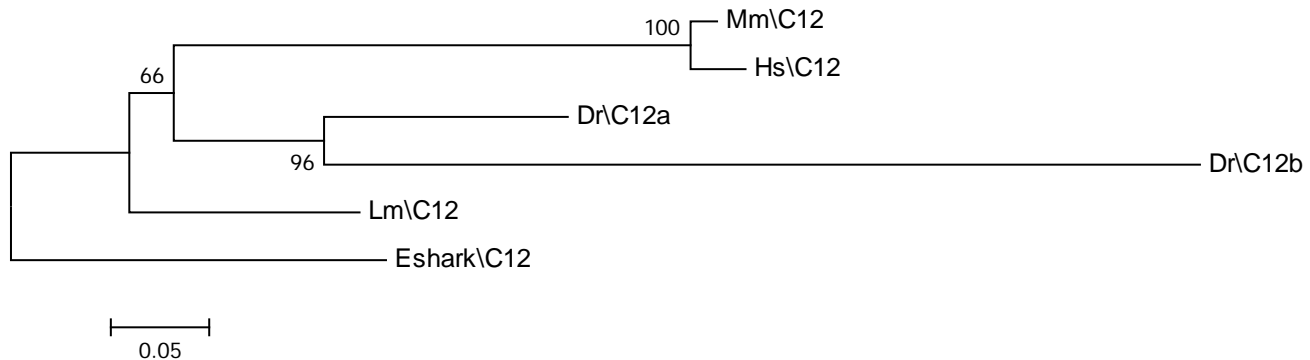
Tajima relative rate test – Hoxc12

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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         MDGLGSSCPASHCRDLLPHPVLGRPPAPLGAPQGAVYTDIPAPEAARQCPAPPTS
Lm\C13         MEGLSGNCPATHCRDLISHPALGRHSSTIATHQGPVYSDIAAPEAGRQCPAPQTS
Eshark\C13     MEALSGNCSSSHCRDLIPHPALGRHSGTLAHHQGPVYSELPAPEAGRQCPAPQTS
Dr\C13a        MEGLSGNCPATHCRELISHPALGRHSGTIATHQGSVYLDISSPETGRQCPAPQTS
Dr\C13b        MEGLSGNCPASHCRDFISHPALGRHSGSLASHQGTVYPDITTQDAGRQFPAPQAS

Mm\C13         SSATLGYGYPFGGSYYGCRLSHNVNLQQKAYHPGDKYPEPSGALPGDDLSSRAKEF
Hs\C13         SSATLGYGYPFGGSYYGCRLSHNVNLQQKAYHPGDKYPEPSGALPGDDLSSRAKEF
Lm\C13         SSATLGYGYPFGGTYYGCRLSHNVNLQQKSYHPAEKYAETSSSLPSEELSSRAKEF
Eshark\C13     SSAALGYSYPFGSAYYGCRLPHNVNLPQKAYHPSEKYSEAATALPSEELSSRAKEF
Dr\C13a        SSASLSYGYPFGNPYYGCRLSHNVNLQQKSYHPAEKYAETSSALPTEELSSRAKEF
Dr\C13b        SGTSLGYGYAFGSPYYGCRLSYNVNLQQKSYHPAEKYMETSGALPAEELSSRSKEF

Mm\C13         AFYPSFASSYQAMPGYLDVSVVPGISGHPEPRHDALIPVEGYQHWALSNGWD
Hs\C13         AFYPSFASSYQAMPGYLDVSVVPGISGHPEPRHDALIPVEGYQHWALSNGWD
Lm\C13         AFYPSFASSYQAVPGYLDVSVVPSISAHPEPRHDALIPMEGYQHWALSNGWD
Eshark\C13     AFYPSFASSYQPVPSYLDVSVVPGIGAHGEPRHDALIPMEGYQHWALSNSWD
Dr\C13a        AFYPSFASSYQAVPGYLDMSVVPSISAHPEPRHDALIPMEGYQHWALSNGWD
Dr\C13b        AIYPSFASSYQTVPGYLDVPVVPGISAHPESRHEALFPMDSYQHWALSNGWD

Mm\C13         SQVYCSKEQSQSAHLWKSPFPDVVPLQPEVSSY
Hs\C13         SQVYCSKEQSQSAHLWKSPFPDVVPLQPEVSSY
Lm\C13         GQVYCSKEQTQSTHLWKSPFPDVVPLQPEVNSY
Eshark\C13     GQVYCSKEQTQSSHLWKSPFPDVVPLQPEGSNY
Dr\C13a        GQVYCSKEQTQSSHLWKSPFPDVVPLQPEVSSY
Dr\C13b        EQLYCSKEQTHFNHLWKSQFSDVVPHQAEMNGY
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NJ tree rooted to elephant shark (Eshark)
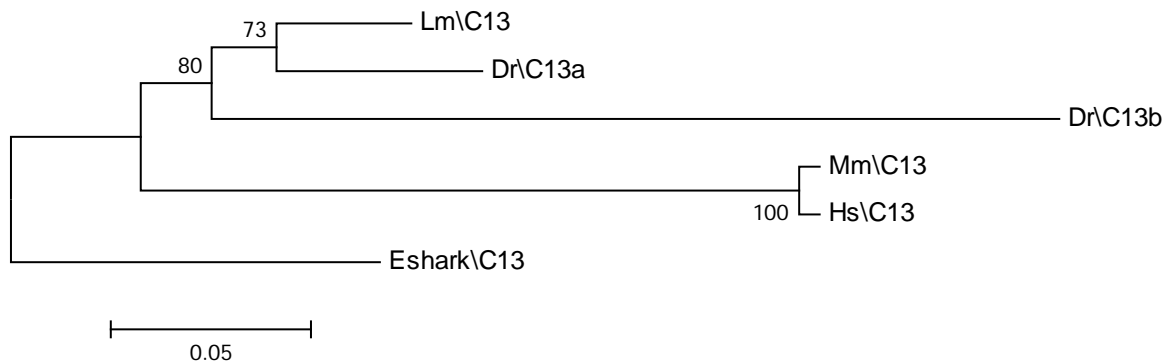
Tajima relative rate test – Hoxc13

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 – Callorhinchus milii, Hs – Homo sapiens, Lm – Latimeria menadoensis, Mm – Mus musculus

Hoxd1 alignment for relative rate test

```
Lm\D1            MNTFIEYISSGEILAFSSKFYADHRPASLQLYSGENHCVGSLPIG
Hf\D1            MNSYLEYIPSADILTFSPKFCSNSPPVSLQQCSGEGRYAASEPGG
Hs\D1            MSSYLEYVSCSSVLSLAPKFCSDARPVALQPAFGDGAFVSCLPLA
Mm\D1            MSSYLEYVSCAAVLAFAPKFCADARPVALQPAFGDGAFVSCLPLA

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

Lm\D1            FPLGANHELDNNEGHAQYANVYSGNESFSFNRQSDYNTFEDHCRRHDTEQYDFY
Hf\D1            FPYAANQELDDTGGLIPYNTVYSGSASFPLTRQHEYNSEQEQYQTYGKEFPNFY
Hs\D1            FPGVLGRAADDGGSHVHYATVFSGGGSFLLSGQVDYAGEPGPFPACLKASADGH
Mm\D1            FPGALGRAADEGGAHVHYATVFSGGGSFLLSGQVDFAGEPGPFPACLKEPADGH

Lm\D1            PENHQNPSQGTGSYSSPPSTAQATANTFDWMKVKRNPP
Hf\D1            PGHYQSPSTSQGGYQSPAAQKITTANTFEWMKVKRNPP
Hs\D1            PGAFQTASPAPGTYPSPASGLPAAFSTFEWMKVKRNAS
Mm\D1            PGPFQTVSPAPGACPSPTSSLPAAHSTFEWMKVKRNAP
```

NJ tree rooted to horn shark (Hf)
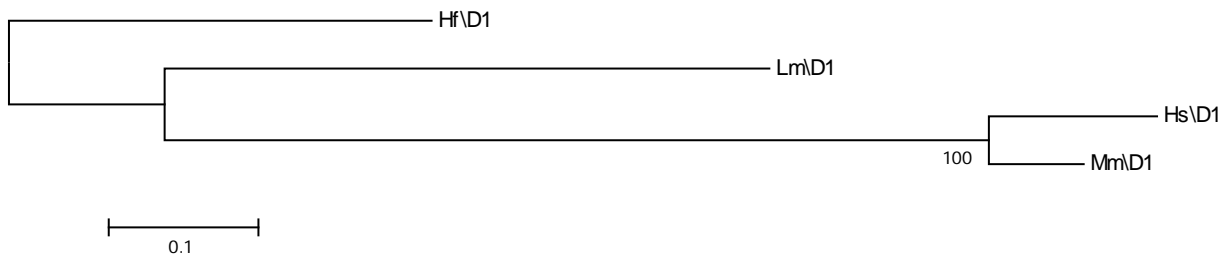
Tajima relative rate test – Hoxd1

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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        MQKATYYDNSGIFGGYSYQKTNAYSYSSSHQAYPPTSVENDYQSSTCPIQTSSV
Lm\D3        MQKTAYYDNSGLFGGYPYTKSDAYGYNSTHQPYSQSATETDYPSSACSIQTSTI
Dr\D3        MQKATYYDNAGLFGGYSYPKSDSYTYGPTHQGFSSSSIENDYQSPICPIQTTSV
Hs\D3        MQKAAYYENPGLFGGYGYSKTDTYGYSTPHQPYPPSSLDTDYPGSACSIQSSAL
Mm\D3        MQKAAYYENPGLFGGYGYSKADTYGYSTPHQPYPPNSLDSDYPSSACSIQSSAL

Hf\D3        RAPNHKPTDINGNCMRTSGSQGSAQPPSINEPQQPPPLPSSPNASNTSTQK
Lm\D3        RPPHHKSSDINGTCMRTSGSQGTCQPPSISEQQPAPSLPSSPNANSIATQK
Dr\D3        RPATHKNGDINGSCMRPSASQGNSQPESISEQQQAAPLASSPSPSTNSTQK
Hs\D3        RAPAHKGAELNGSCMRPQGGGGGSQPPGLNSEQQPPQPPPPPTLPPSSPTN
Mm\D3        RAPAHKGAELNGSCMRPQGGGGGNQPPGLNEQQPPQPPPPPPTLPPSSPTN

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

NJ tree rooted to horn shark (Hf)
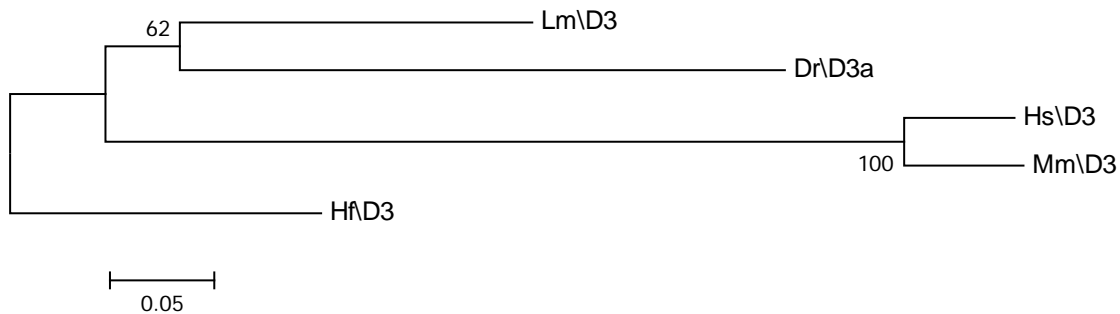
Tajima relative rate test – Hoxd3

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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        MSSYMVNSKYVDPKFPPCEEYSQNNYIAEQSTDYYSP
Dr\D4a       MSSYMVNSKYVDPKFPPCEEYSQNSYIPEQSPGYYSP
Hf\D4        MSSYLMNTKYVDPKFPPCEEYSQNNYIPDHCSEYYSQ
Hs\D4        MSSYMVNSKYVDPKFPPCEEYLQGGYLGEQGADYYGG
Mm\D4        MSSYMVNSKYVDPKFPPCEEYLQGGYLGEQGADYYGS

Lm\D4        SEDTDFQLQGIFPRSNYSEQTYGCGNVQDSTEQPRGHVQEQSGPQSHFPVQQEHCSP
Dr\D4a       SQDTDFQHPGIYSRSNYSEQPYSCSTVQGSSVQPRGHVQDQASTPSPFPAQTEQCPA
Hf\D4        SQDSDFQHQGIYPRSNYSGQSYNCSNARGSPVQQRGHVQAQPAPQNHLTGQGEPVAP
Hs\D4        AQGADFQPPGLYPRPDFGEQPFGSGPGPGSALPARGHGQEPGGPGGHYAAPGEPCPA
Mm\D4        AQGADFQPSGLYPRPDFGEQPFGGGPGPGSALPARGHGQEPSGPGSHYGAPGEPCPA

Lm\D4        PIPTSRSCNQQQNKNQSGTVSKQPAIVYPWMKKVHVNS
Dr\D4a       QISGSRTCGQQQNKTQNGIPTKQPAVVYPWMKKVHVTT
Hf\D4        QVSIGRPCSQQHNKNQNGTATKQPAVVYPWMKKIHVNT
Hs\D4        PLPGARAYSQSDPQPPSGTALKQPAVVYPWMKKVHVNS
Mm\D4        PLPGARACSQTGPQPPPGTALKQPAVVYPWMKKVHVNS
```

NJ tree rooted to horn shark (Hf)

Tajima relative rate test – Hoxd4

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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
NJ tree rooted to horn shark (Hf)

```
HfD8  MSSYFVNPFYSKYKPGEALSPTYYDCRFPQDVTSRHAVVYSSGASFQHPAQQDFY
LmD8  MSSYFVNPFYSKYKSGEAINTNYYDCQFSQDLNNRHSVIYSNGTSFQHPTQQELC
MmD8  MSSYFVNPLYSKYKAGEAINPTYYDCHFAPEVSGRHALQYNSAAGFPHAHPQDYF
HsD8  MSSYFVNPLYSKYKAGEAINPTYYDCHFAPEVGGRHALQYNSAAGFPHAPPQEYF

HfD8  AVVYSSGASFQHPAQQDFYHHGTSALPNTGFQQNPGITCHGDPSKFYGYDNLQR
LmD8  SVIYSNGTSFQHPTQQELCHQGASVCSNMGYQQNHGITCRGEPSKFYGYDNLQR
MmD8  ALQYNSAAGFPHAHPQDYFHAGSPTAAYQAAPPPPGIACHGEPAKFYGYDNLQR
HsD8  ALQYNSAAGFPHAPPQEYFHPGSPAAAYQAAPPPPGIACHGEPAKFYGYDNLQR

HfD8  QQIFTTQQEADLVQYPDCKSSSSIGEENQNSSPTQMFPWMRPQApg
LmD8  QLSFTTQREADLVEYPDCKSSNGIVEEQETSSPSQMFPWMRSQAtg
MmD8  QPIFTTQQEAELVQYPDCKSSSGIGEDNQSSSPSQMFPWMRPQApg
HsD8  QPIFTTQQEAELVQYPDCKSSSGIGEDNQSSSPSQMFPWMRPQApg
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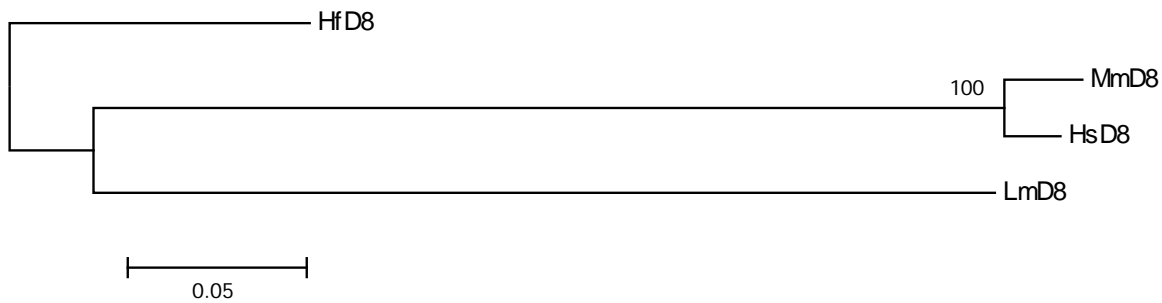

Tajima relative rate test – Hoxd8

Outgroup	Ingroup1	Ingroup2	P-value
Hf	Hs	Lm	0.746

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

Hoxd9 alignment for relative rate test

```
Lm\D9        MSTSGTLSNYYVDSLIGLEPEEIYGARFAQGTHCTTSRPSSVADDLTSCSFAP
Hf\D9        MSTGGTIHNYYVDSLIGQETEDLYAARYAQGSHSTASRPSGVADDFSSCSFTS
Dr\D9\new    MSTSSALSSYYVDTIMGHEAEDVYGARYIQGSHTAPARPSGVVEDFSSCSFAP
Hs\D9        MSSSGTLSNYYVDSLIGHEGDEVFAARFGPPGPGAQGRPAGVADEFASCSFAP
Mm\D9        MSSSGTLSNYYVDSLIGHEGDEVFAARFGPPGPGTQGRPAGVADEFASCSFAP

Lm\D9        KSALFSTSWSSIHPQTSAAMTGIYHPYMHQTHLADNRYVHSWIDPISSSVSFPSFH
Hf\D9        KSTAFSNPWSPVHPQSSAAVAGIYHPYMHQSHLADTRYVRSWLEPLSSSVSFPGFH
Dr\D9\new    KSAVFPASWSSVHQPSTAAVSGIYHPYVHQTHLSDNRYVRSWIEPVANHISLTGFH
Hs\D9        RSAVFSASWSAVQPPAAAAMSGLYHPYVPPPPLAPGRYVRSWMEPLPGPSPGPSGP
Mm\D9        KSSVFSASWSAVQPPAAATMSGLYHPYVSPPPLAPGRYVRSWMEPLPGPVPSPGGP

Lm\D9        HNGRHYGIKPETLTSKRTECSSSEVQALSLTEYTSNTFSETRDKPSSDNCSGDH
Hf\D9        PNGRHYGIKPETLSSKRTECSSYELQTLSLPEFTCGSYPECREKLPKELTSSET
Dr\D9\new    SNSRHSGTKTESLPPKRTESAAFETETPSVPEFSLNAVSESAYKATEERVGSDN
Hs\D9        ANGRHYGIKPETSSSKRTECSVAESQGSSGPEFSCNSFLQEKAAGSSEPCSDHP
Mm\D9        ANGRHYGIKPETSSSKRTECSAAESQGSGGPEFPCNSFLRDKAAGSSEPCSDHP

Lm\D9        SMNSELKEEKPKQLDPDNPAAIWL
Hf\D9        TSNSEHKEEKQQQLDPNHPAINWI
Dr\D9\new    SSHGEPKDEKQQQLDPSNPAANWI
Hs\D9        IPGCSLKEEEQQQLDPNNPAANWI
Mm\D9        SPGCSLKEEEPQQLDPNNPAANWI
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NJ tree rooted to horn shark (Hf)
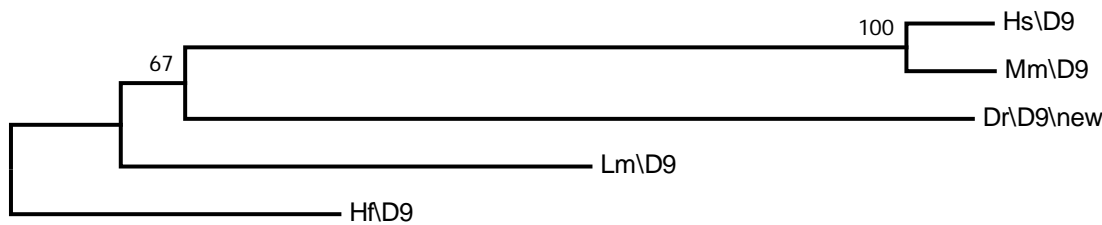
Outgroup	Ingroup1	Ingroup2	P-value	Significance
Hf	Hs	Lm	0.003	**
Hf	Lm	Dr	0.017	*
Hf	Hs	Dr	0.26	

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        MSCPNSSPATNSFLVDSLISACRGDFYSTSSMYMPSSTDMGTYGMQTCGLLPTMTKR
Lm\D10        MSFPNSSSATNTFLVDSLISACRSDLYSNGSMYMPSNTDMGNYGMQTCGLLPTLAKR
Dr\D10a       MSFPNSSPAANTFLVDSLIGACRTDFYSSSNMYMPATAEMGNYGMQTCGLLPALGKR

Hs\D10        EVNHQNMGMNVHYIPQVDSWTDPNRSCRIEQPVTQVPTCSFTTNIKEESNCCMYSD
Mm\D10        EVNHQNMGMNVHYIPQVDSWTDPNRSCRIEQPVTQVPTCSFTANIKEESNCCMYSD
Hf\D10        EVNHQNMSISVHYLSQVDGWADPSRPCRIEQPVTQMPTCSFPASVKEESTCCMYSD
Lm\D10        ELNHQNMGMNAHHFSQVDSWADPTRSCRIDQSISQTPTCSFNNNIKEETNCCMFSD
Dr\D10a       EVNHQNMDMTVHYIPQTDTWADPSRSCRLEQPLNQMSTCTFSQSIKEETNCCMYSD

Hs\D10        KRNKLISAEVPSYQRLVPESCPVENPEVPVPGYFRLSQTYATGKTQEYNNSPEGSSTVML
Mm\D10        KRNKLISAEVPSYQRLVPESCPVENPEVPVPGYFRLSQTYATGKTQEYNNSPEGSSTVML
Hf\D10        KRAKLNPTAIPAYPRLVSENCSIENPEIPIPGYFRLCQAYPLEKSLDYNYAGEISSNVMP
Lm\D10        KRGNINSSEIPCYHRFVPESRSSDNPEIPVPGYFRLSQTYATAKTQEYSNAEENSSNTMM
Dr\D10a       KRAKVSSSEIPAYSSLIPESCSVDSPEIPVPGYFRLSQTYATAKNPDYDNETMSPNTTLM

Hs\D10        QLNRGAAKPQLSAQLQMEKKMNEPQEPTKVSQVESPEAKGGLPERSCLAEVSVS
Mm\D10        QLNRAAAKPELSAQLQMEKKMNESQEPTKVSQVESPEAKGGLPERSCLAEVSVS
Hf\D10        QSNGLISKLQVSSQPPMERKINEKQESTKGIYVESPEPKPRLLEVSATAEGAAT
Lm\D10        QLNRMNSKPHIPPEPQLEKKISENQETQNISPVESPELTSALQDRNRSTNVSAS
Dr\D10a       QLNRATPKAQSTPFVEVEKKLAHDRDTRSSSPAQSPEPKVSTLEKNCSTEASVS

Hs\D10        SPEVQEKESK
Mm\D10        SPEVQEKESK
Hf\D10        SSELSDNETK
Lm\D10        SPEIKEKEGK
Dr\D10a       SPELPHREGK
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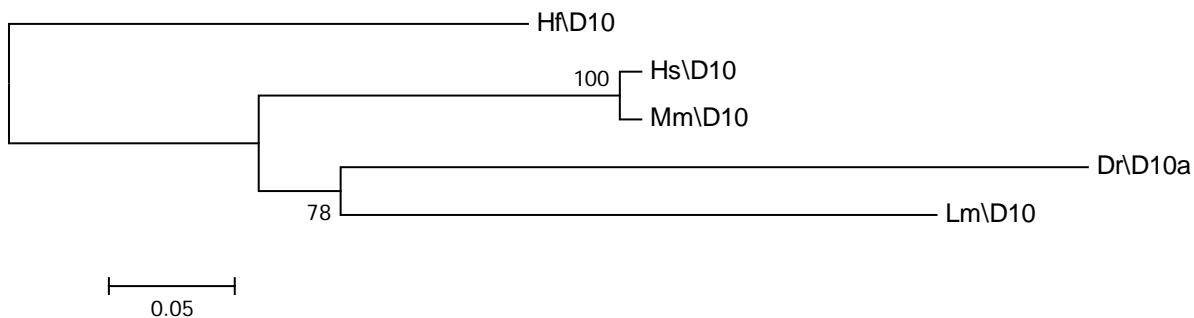
NJ tree rooted to horn shark (Hf)

Tajima relative rate test – Hoxd10

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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     MYLPYYVSRSDFPSVSSFLPQTTSCQMTFPYSSNLAQVQPRRDVSFRDYGLEHTKWQYR
Hf\D11     MYLPYYVSAPDFSSVSTFLPPTTSCQMTFPYSSNLAQVQPVRELSFRDYGLEHTKWHYR
Dr\D11a    MYLPYYVSTPDFSSVSSFLPQTTSCQVNFPYSSNIAQVQPVREVTFRDYGLDHSKWHYR
Hs\D11     MYLPYYVAPSDFASKPSFLSQPSSCQMTFPYSSNLAHVQPVREVAFRDYGLERAKWPYR
Mm\D11     MYLPYYVAPSDFASKPSFLSQPSSCQMTFPYSSNLAHVQPVREVAFRDYGLERAKWPYR

Lm\D11     EEVVHRDLVQQATRTDMLFKNDSVYGHHGSSNTPGNMYATVGRNGILPQGFD
Hf\D11     EEIMHRDYIQPPTRTGMLFKNDTVYSQRGSSNPSCNFYTTVGRNGILPQGFD
Dr\D11a    EEIMHRDLLQSTNRAEMIFKNDSMYSHHAGTNSSCSFFTNVGRNGVLPQGFD
Hs\D11     EAAMQRELLPPAGRPDVLFKAEPVCAAHGPAGAASNFYSAVGRNGILPQGFD
Mm\D11     EAAMQRDLLPPAGRPDVLFKAEPVCGAHGPAAAASNFYSAVGRNGILPQGFD

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

Lm\D11     NSTDLPSDKVVAEKHSNS
Hf\D11     KSTVESSGTSATEKNSLS
Dr\D11a    TVEEESSVSTCDEKNSGS
Hs\D11     GSGEGPPGEAGAESSSAV
Mm\D11     GGGEGPPGEAGAESGGTV
```

NJ tree rooted to horn shark (Hf)
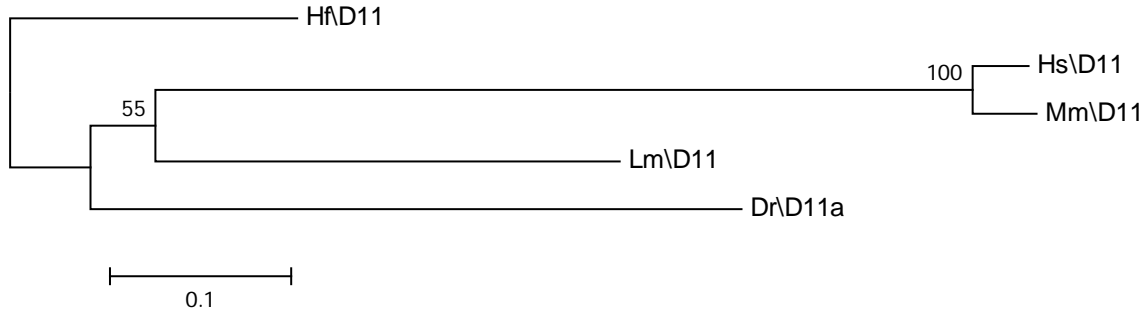
Tajima relative rate test – Hoxd11

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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       MCEHNLLSSGYVAPLLNFHSPDSLYLQNLRGNGVHLSGLPQMSYSRRSLPWSSNS
Hs\D12        MCERSLYRAGYVGSLLNLQSPDSFYFSNLRPNGGQLAALPPISYPRGALPWATPA
Mm\D12        MCERSLYRAGYVGSLLNLQSPDSFYFSNLRANGSQLAALPPISYPRSALPWATPA

Lm\D12        CASPPQSRAFSGYSQAYLTSSVPINISSSNNNKESLDEKYYFQDTNSKSDERYR
Hf\D12        CASPPQSRAFSGYSQSYLSNSVSISINRHVSDKAAAGEKYYFQDSSRKVEERCR
Dr\D12a       CTAPAQSRAYSGYSQPFFSNSAAVSASLNTHKKGSLEERYYFQDVSHKSEEPGR
Hs\D12        SCAPAQATAFGGFSQPYLAGSGPLGLQPPTAKDGPEEQKFYAPEAAAGPEERGR
Mm\D12        SCTPAQASAFGGFSQPYLTGSGPIGLQSPGAKDGPEDQKFYTPDAPTASEERSR

Lm\D12        EHQSFVTDNTAKYDYSNMERVLNSCTSAVSEGVKQPV
Hf\D12        HNQSYPSDNPAKYEYPNVETELNSNSPTVNDGIKQSV
Dr\D12a       PNAAYASESSASNGLSNLERELSCVEQPESDASKQSV
Hs\D12        TRPSFAPEKAAKYDYAGVGRQGAPCAPGFKDDTKGPL
Mm\D12        TRPPFAPEKGTKYDYAGVGRQGAPCASSFKEDTKGPL
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NJ tree rooted to horn shark (Hf)
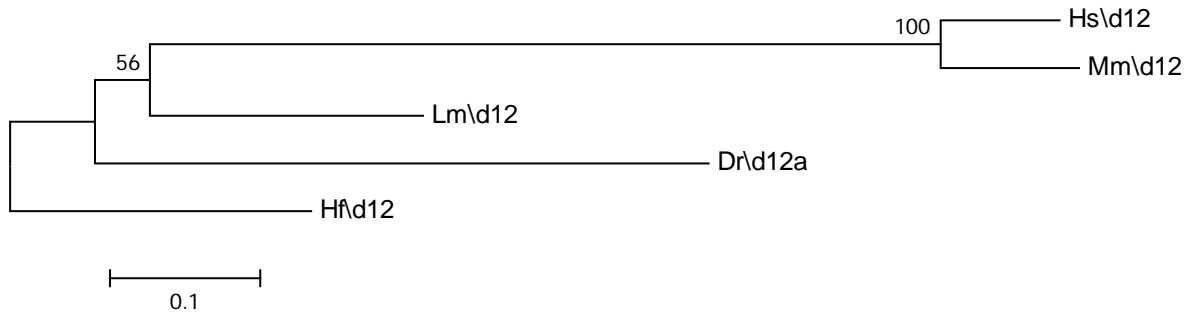
Tajima relative rate test – Hoxd12

Outgroup	Ingroup1	Ingroup2	P-value	Significance
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