Supplementary information for manuscript:

Linking species habitat and past paleoclimatic events to evolution of the teleost innate immune system

Monica Hongrø Solbakken[1*], Kjetil Lysne Voje[1], Kjetill Sigurd Jakobsen[1], Sissel Jentoft[1,2]*

Journal: Proceedings of the Royal Society B

Main manuscript: 10.1098/rspb.2016.2810

Contents

Supplementary table 1 Overview of *TLR* copy number and northern and southern latitude boundaries collected from Fishbase.

Latin Name	**TLR 1/6**	**TLR 2**	**TLR 3**	**TLR 4**	**TLR 5**	**TLR 7**	**TLR 8**	**TLR 9**	**TLR 14**	**TLR 21**	**TLR 21_beta**	**TLR 22**	**TLR 23**	**TLR 25**	**TLR 26**	**North.**	**South.**	**Average**
Arctogadus glacilis	0	0	1	0	0	1	3	7	1	2	0	22	1	4	0	87	69	78
Boreogadus saida	0	0	1	0	0	1	1	6	1	1	0	16	1	10	0	87	52	69.5
Trisopterus minutus	0	0	1	0	0	2	1	8	1	2	0	6	3	1	0	66	28	47
Pollachius virens	0	0	1	0	0	3	5	5	1	1	0	15	3	7	0	77	33	55
Melanogrammus aeglefinus	0	0	1	0	0	1	12	5	1	3	0	6	2	4	0	79	35	57
Merlangius merlangus	0	0	1	0	0	2	7	6	1	1	0	11	1	2	0	72	35	53.5
Theragra chalcogramma	0	0	1	0	0	3	7	5	1	1	0	27	1	4	0	68	34	51
Gadiculus argentus	0	0	1	0	0	1	9	10	1	2	0	7	2	5	0	74	24	49
Phycis phycis	1	1	1	0	0	1	1	5	1	2	0	8	2	1	0	45	13	29
Molva molva	1	1	1	0	0	3	1	5	1	2	0	10	3	1	0	75	35	55
Lota lota	1	1	1	0	0	1	1	5	1	2	0	5	3	3	0	78	40	59
Brosme brosme	1	1	1	0	0	1	1	11	1	2	0	9	4	1	0	83	37	60

Merluccius merluccius	1	1	1	0	0	2	1	4	1	2	0	4	5	1	0	76	18	47
Merluccius capensis	1	1	1	0	0	1	4	5	1	2	0	6	4	2	0	-11	-37	-24
Merluccius polli	1	1	1	0	0	1	1	3	1	2	0	5	6	1	0	29	-19	5
Melanonus zugmayeri	1	1	1	0	0	1	1	1	1	1	0	13	6	1	0	60	-49	5.5
Macrourus berglax	1	1	1	0	0	1	2	1	1	1	0	16	3	1	0	82	37	59.5
Malacocephalus occidentalis	1	1	1	0	0	2	1	1	1	1	0	8	2	1	0	43	-37	3
Bathygadus melanobranchus	1	1	1	0	0	1	1	1	1	1	0	2	2	1	0	53	-34	9.5
Muraenolepis marmoratus	1	1	1	0	0	1	3	1	1	1	0	4	5	1	0	-44	-56	-50
Bregmaceros cantori	0	0	1	0	0	1	1	3	1	1	0	0	0	1	0			
Mora moro	1	1	1	0	0	1	1	1	1	1	0	1	1	1	0	64	-51	6.5
Laemonema laureysi	1	1	1	0	0	1	1	4	1	1	0	1	1	1	0	8	-8	0
Polymixia japonica	1	1	1	1	0	1	1	1	1	1	1	2	2	1	0	40	6	23
Percopsis transmontana	1	1	1	0	0	1	1	1	1	1	0	1	0	0	0	44	43	43.5
Typhlichthys subterraneus	1	1	1	0	0	1	1	1	1	1	0	1	0	0	0	39	34	36.5

Zeus faber	1	1	1	0	0	1	1	1	1	1	0	0	0	1	1	75	-49	13
Cyttopsis roseus	1	1	1	0	0	1	1	1	1	1	0	0	0	1	1			
Lamprogrammus exutus	1	1	1	0	1	1	1	1	1	1	1	0	2	0	0	12	-23	-5.5
Brotula barbata	1	1	1	0	1	1	1	1	1	1	1	0	2	1	0	30	-14	8
Carapus acus	1	1	1	0	1	1	1	1	1	1	1	1	1	0	0	42	-15	13.5
Myripristis jacobus	1	1	1	1	1	1	1	1	1	1	0	1	1	0	0	37	-23	7
Holocentrus rufus	1	1	1	1	1	1	1	1	1	1	1	1	3	0	0	33		33
Trachyrincus scabrus	1	1	1	0	0	7	1	1	1	1	0	1	2	1	0	55	-27	14
Chatrabus melanurus	1	1	1	0	1	1	1	1	1	1	0	0	1	1	0	-35		-35
Parasudis fraserbrunneri	1	1	1	0	1	1	1	1	1	1	1	0	1	1	1	21		21
Regalecus glesne	1	1	1	0	0	1	1	1	1	1	0	1	0	0	0	72	-52	10
Lampris guttatus	1	1	1	0	0	1	1	1	1	1	0	1	0	0	0	70	-45	12.5
Guentherus altivela	0	1	1	1	1	1	0	1	1	1	0	1	0	1	1			
Antennarius striatus	1	1	1	0	1	1	1	1	1	1	0	0	1	0	0	43	-50	-3.5

Osmerus eperlanus	1	1	1	0	1	1	1	1	1	1	1	0	0	1	1	70	43	56.5
Perca fluviatilis	1	1	1	0	1	1	1	1	1	1	1	0	17	1	0	74	38	56
Sebastes norvegicus	1	1	1	0	1	1	1	1	1	1	1	1	0	1	0	79	38	58.5
Chaenocephalus aceratus	1	1	1	0	1	1	1	1	1	1	1	3	1	1	0	-53	-65	-59
Borostomias antarcticus	1	1	1	0	1	1	1	1	1	1	1	4	1	1	0	66	-66	0
Benthosema glaciale	0	0	1	0	1	1	1	2	1	0	0	49	8	4	0	81	11	46
Rondeletia loricata	1	1	1	1	1	1	1	1	1	1	0	2	3	1	1	67	-42	12.5
Beryx splendens	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	45	-43	1
Neoniphon sammara	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	30	-30	0
Monocentris japonica	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0			
Acanthochaenus luetkenii	1	1	1	0	1	1	1	1	1	2	0	1	0	0	0	40	-57	-8.5
Stylephorus chordatus	1	0	1	0	0	1	1	2	1	1	0	1	0	1	0	45	-37	4
Spondyliosoma cantharus	1	1	1	0	1	1	1	1	1	1	1	1	2	0	0	63	-20	21.5
Thunnus albacares	1	1	1	0	1	1	1	1	1	1	1	0	7	1	0	52	-45	3.5

Helostoma temminckii	1	1	1	0	1	1	1	1	1	1	1	3	14	1	0	16	-6	5
Anabas testudineus	1	1	1	0	1	1	1	1	1	1	1	2	3	0	0	28	-10	9
Selene dorsalis	1	1	1	0	1	1	1	1	1	1	0	2	0	0	0	39	-28	5.5
Chromis chromis	1	1	1	0	1	1	1	1	1	1	1	2	2	1	0	46	-12	17
Parablennius parvicornis	1	1	1	0	1	1	1	1	1	1	0	1	1	1	0	36	-6	15
Symphodus melops	1	1	1	0	1	1	1	1	1	1	1	1	1	0	0	63	28	45.5
Pseudochromis fuscus	1	1	1	0	0	1	1	1	1	1	1	1	1	1	0	26	-24	1
Myoxocephalus scorpius	1	1	1	0	1	1	1	1	2	1	1	2	4	0	0	80	40	60
Trachyrincus murrayi	1	1	1	0	0	3	1	1	1	1	0	3	2	1	0			
Phycis blennoides	1	1	1	0	0	1	1	7	1	2	0	5	1	1	0	71	20	45.5
Lesueurigobius cf sanzoi	1	1	1	0	1	1	1	1	1	1	0	3	7	2	0	42	-21	10.5
Gadus morhua	0	0	1	0	0	4	8	5	1	1	0	12	1	6	0	83	35	59
Astyanax mexicanus	1	1	1	0	1	1	2	1	1	1	0	0	3	0	1	36	24	30
Danio rerio	1	1	1	3	2	1	2	1	1	1	0	0	0	0	4	33	8	20.5

Gasterosteus aculeatus	1	1	1	0	1	1	1	1	1	2	1	1	0	0	0	71	26	48.5
Oreochromis niloticus	0	1	1	0	1	1	1	1	1	1	0	1	2	1	0	32	10	21
Oryzias latipes	1	1	1	0	1	1	1	1	1	1	0	1	0	1	0	55	10	32.5
Poecilia formosa	1	1	1	0	1	1	1	2	1	1	0	1	3	0	0	27	25	26
Takifugu rubripes	1	1	1	0	1	1	1	1	1	1	0	1	1	0	0	46	21	33.5
Tetraodon nigroviridis	1	1	1	0	1	1	1	1	1	1	0	1	1	0	0			
Xiphophorus maculatus	1	2	1	0	1	1	1	1	1	1	0	2	1	0	0	23	17	20
Salmo salar	2	2	2	0	2	4	4	2	2	2	0	2	2	0	4	72	37	54.5

Supplementary table 2 All query TIR domain sequences used for teleost *TLR* characterization derived from Ensembl.org v83. and GenBank.

Species	Fasta sequence
Danio rerio	>1_DARE_ENSDARP00000139386 KLTRGMDSILLILLEPLPLYLIPSKYYQLKTMMSRRTYLEWPQEGAKQKLFWANLRAALQAELPNTPDREEE
	>14_DARE_ENSDARP00000106955 AIGKTFSDVILVVKEPIDPTSLPSKFCKLKRMLNTKTYLEWPQQPTEQNFFWIQLRSVLGKPNSIRPRTISRHSRLSSARSVSLIEAPQIQDPEGPDEEDHQNSPQPSNKCQLTCIEVA
	>2_DARE_ENSDARP00000110559 IMDEHNDSAVLVLLEPIKKETIPKRFCKLRKIMNSRTYLEWPEDEDKRDEFWSNLRAALQRDEC
	>21_DARE_ENSDARP00000098992 LFQEMQDVLLLVFLEPIPERQLSAYHRMRKVMLKKTYLQWPGSNCSDPNSAKELFWNQLKRALRSSNSGSQDEQKMDDNELRRKEKVCADKEEREYFVNQTPTEDEIYYLMP
	>26a_DARE_ENSDARP00000108970 LQVEHRDILILVFLETIPSRLLSSHHRLARLVKTRTYLDWPQEPEMHEAFWDRLWCKLSSNKAK
	>26b_DARE_ENSDARP00000115820 QLEEQKHRLILIFLQHISPFELSAFHRLAKLVRSRTYLDWPEEEGDREHFWDRL
	>3_DARE_ENSDARP00000014779 VMEDNRDSLILIFLEDVTDYNLNRSLHLRRGMLKPKCVLYWPLHKERIPAFHQKLRSALASTNKVN
	>4_a_DARE_ENSDARP00000110093 FLMERNANIIIIILEDVAERKTKKILGLHKHLKKNTYLKWSRDPLSNMRFWIRLRKAIVATKQ
	>4_b_DARE_ENSDARP00000028819 FLMERNANIIIIILEDVAERKTKKVFGLHKHLKKNTYLKWSRDPLSNMRFWIRLRKAILQK
	>4al_DARE_ENSDARP00000123702 FVVERNANIIIIILEDVAERKTKKVLGLHKHLKKNTYLKWSRDPLSNMRFWIRLRKAIVAT
	>5_a_DARE_ENSDARP00000129438 MLVELKDILVVLVVGNIPQYRLLKYEQLRSFIENRSYLVWPDDGQDLEWFYDQLLHKIIRNTKVKQTNIKEKDKVDENNPEAADVQADTAV
	>5_b_DARE_ENSDARP00000124387 MQAELEDILVVLVVGNIPQYRLLKYKQVRSFIENRSYLVWPDDCQDLEWFYDQLLHKIRKDIKINQTTKEIKREEANFNTNTAV
	>7_DARE_ENSDARP00000105671 LMDERNDVIVLIFLERMPCHSKYLRLRKRLYKKSVLEWPRNPQAQRYFWFSLRSLMATESQYNTLFQETL
	>8_a_DARE_ENSDARP00000133386 LLEENEDVIVLLLLEPVLQYSHFVRLRRRLCARSILEWPHSSSAEAWFWQSLRNAIRVDNQALYSELYSRYFTTK
	>8_b_DARE_ENSDARP00000107821 LLEENEDVIVLLLLEPVLQHSHFVRLRRRLCARSILEWPHSSSAEAWFWQSLRNAIRVDNQALYSELYSRYF
	>9_DARE_ENSDARP00000105677 LLDEKVDVAVLVLLDFLFPKFKYLQMRKRLCKKSVLSWPRNPRVQPLFWNDLRVALVSDNVRAYNKNVTESFF
Gasterosteus aculeatus	>6_GAAC_ENSGACP00000023718 RLAWGTDSVVLVLLEPLPQYLIPSKYYQLKSMMGRHTYLEWPQDRAKHRLFWANLRAALQAELPNAQVTELEE
	>14_GAAC_ENSGACP00000002280 AVGKTFSDVILVVKEPMDPNSLPSKYLKLKKMLRTKTYLEWPQQVNQQAFFWTQLKGVLGKPTATQKRTHSVKS
	>2_GAAC_ENSGACP00000024681 LFDGSAGGEAAILVLLEPLSKEDVPKRFCKLRKLMSSNTYLEWPQREEGRAEFWRRLRCAVGGGEDDPLP
	>21_a_GAAC_ENSGACP00000012342 LFDEHRDVLLLVFLEEISQRQVSSYHRMRKVMLKKTYLQWPGSDCTNPTQAQELFWNKLRRAMRS
	>21_b_GAAC_ENSGACP00000011097 LLYDGSDVLLLVFLEEIPERCLTPYTRLRKIVHKKTYLLWPETPQEQDSFWVRLIDALSVTQMQKVVTHFNSVD

>22_GAAC_ENSGACP00000007196

LFDERKDVLVLVFLEDIPGAELSPYYRMRKLLKRRTYLSWPRAGQHPNLFWEKLRQALGTKDDPGREELVPTLLDRQ

>3_GAAC_ENSGACP00000022288

VIEASRDSVVLVFLQDVHDFKLSRSLFLRRGMLRSCCVLDWPVHKERVPAFHQKLLIALGMTNRLQE

>5_a_GAAC_ENSGACP00000005783

MLEELTNVLIVLVVGKKVAHYQLMRYKAVRAFVQRREYLTWPEDPQDLEWFYERLVSQILKDTKLKKVGEEPDRGPADEDGVQLQAIRAAAV

>7_GAAC_ENSGACP00000005259

LMDEKNDVIVLIFLEKVACNSKYLRLRKRLFKRSVLEWPTNPQAQLYFWFSLRSVLATESHKQYNNLFKETL

>8_GAAC_ENSGACP00000005236

LLDENKDVIVLLMLEPVLQNSHFLRLRKRMCRKSVLEWPKTPAAEPWFWTTLRNVVKVDNQAICNKTYKKYFTVK

>9_GAAC_ENSGACP00000013418

LLDEKVDAAILVLLDEMFPKLKYLELRKRLCRKSVLSWPRNPRAQPLFWNQMRMALSSDNLRSYDNNMSESFI

Takifugu rubripes

>1_6_TARU_ENSTRUP00000025134

HLALGSDSVVLVLLEPVPQYLIPSKYYQLKFMMARHTYLEWPQDRAKQRLFWANLRAALQADLPHLTVTEIEE

>14_TARU_ENSTRUP00000001044

AMGKTFSDVILVVKEPIDPNSLPSKYCKLKKMLSTKTYLEWPQQVNQQAFFWAQLRSVLGRPTAVTRGRQSVRSRISSASISVIGPLVDERNPEMDEDRGTEPNYEVIENSLEVSHQRQIPMVAV

>2_TARU_ENSTRUP00000007454

LFDGVAGEPAILILLEPLNKDDIPRRFCKLRKLLSSTTYLEWPHGEEKVGEFWKALRTALRGEEEWEE

>21_TARU_ENSTRUP00000009725

LFDEHRDVLLLVLLEPISERQLSSYHRMRKVMLKKTYLQWPGSECTNPPQAQGLFWSQLRRAI

>22_TARU_ENSTRUP00000015072

LFDEQKDVLILIFLEDIPTRQLSPFYRMKKMLKSKTYLSWPRAEGHPEVFWEKLRQALLSKDMLDLKPLARGISHKV

>23_TARU_ENSTRUP00000010624

LFDEQKDVLILLFLEEIPAHQLSPYHRMRKLLKRQTYLSWTQAGRHQAGVFWQNVQRALESGDAPHDQVDPLTGPAEP

>3_TARU_ENSTRUP00000012195

VIEASRDSVVLVFLQDVHDYKLSRTLFLRRGMLRSCCVLYWPVHKERVPAFHQKLLIALGMTNRLQ

>5_a_TARU_ENSTRUP00000011330

MLEELTNILVMVVVGKVAHYQLMRCKAVRVFVQKRQYLTWPEDPQDLDWFYERLVSLLLKDTKEASSESSVPASLASCVF

>7_TARU

LMDEKNDVIVLIFLENIPYNSRYLRLRRRLYRRSVLEWPTNPQARPYFWFSVRSVLATESHKQYNNLFKETL

>8_TARU

LLDENVDVIVLLLLEPVLQHSHFLRLRRRLCGESVVDWPRTAAAEPWFWQNLRNVVRVENQVMYNKNYSKYFTSK

>9_TARU_ENSTRUP00000019170

LLDEKVDTAVLVLLDEMFPKLKYLQLRKRLCRKSVLSWPRNPKAQPLFWNQLRMALSSDNLSFYDNNMSESFI

Tetraodon nigroviridis

>1_6_TENI_ENSTNIP00000017225

HLARSSDSVVLVLLEPVPQYLIPSKYYQLKAMMARHTYLEWPQDKAKQRLFWANLRAALQADLPDLTVS

>2_TENI

LLDGAAQGRTPVLVLLEPLQDGAVPQALLQAAPLLSSTTYLEWPQQEDKVEAF

>21_TENI_ENSTNIP00000011033

LFDEHRDVLLLVFLEAISKKQLSSYHRMRKVMLKKTYLQWPDSECSDPAQAQDLFWSQLRRAIGTSSRIGTEENGAGVLDSEVPEQSENHQSNENCFLLP

>22_TENI_ENSTNIP00000016626

LFDERKDVLILIFLEDIPISQLSPFYRMKKMLKRKTYLSWPRAEGHPLVFWEKLRQALLEKETVQLR

>23_TENI_ENSTNIP00000008068

LFDEQKDVLILLFLEEIPAHQLSPYHRMRKLLKRQTYLSWAQAGRHRAGVFWQNVQRALECGDAPHDRVDPLMGPAQP

>3_TENI_ENSTNIP00000009925

```
VIEASRDSVVLVFLQDVHDHRLSRTLFLRRGMLRSCCVLYWPVHKERVAAFHQKLLIALGMTNRLH
>5_TENI_ENSTNIP00000008738
MLEELTNTLVMLVVGKVAHYQLMRCNAVRAFVQKREYLTWPEDPQDLDWFYQKLISLLLKHTKVKKCAEENPE
PVAQTADRIQLQDI
>7_TENI_ENSTNIP00000016967
LMDEKNDVIVLIFLEKIPSNSKYLRLRRRLYRRSVLEWPTNPQARPYFWFSLRSVLATESHKQYNNLFKETLKGCIT
VPSLLKMCNGIFVFVFLSQ
>8_TENI
LLDENVDVILLLMLEPVLQHSHFLRLRRRLCGESVLDWPRTAAAEPWFWQNLRNLLRVDNQVMYNKNYSKYFT
GK
>9_TENI_ENSTNIP00000018058
LLDEKVDAAVLVLLDETFPKVKYLQLRKRLCRKSVLSWPKNPKAQPLFWNQVRMALSSDNLSFYDNNMSESF
```

Oreochromis niloticus

```
>14_ORNI_ENSONIP00000008442
AMGKTFSDVILVVKEPIDPNSLPSKYCKLKKMLSTKTYLEWPQQVNQQAFFWAQLRSVLGKPTTQERANSVKRR
TLSAGRISVIGPPIEERVPEEDKVTVEKDTEPKKEANKEPLNQIPLVAF
>25_ORNI_ENSONIP00000017788
AISVHRDSLVFILLEPIPTNSLPKKYLRLRSLLRQQTYLEWPKDDRKQQTFWASLKSTLHIADKSVVLKDIAVAISDT
VPLVADQM
>2_ORNI_ENSONIP00000017744
LFEGHATGEAAILILLEPLSKDDVPKRFYKLRKLMSSTTYLEWPQEDEKREEFWRSLRNALRG
>21_ORNI_ENSONIP00000025830
LFDEHRDVLLLVFLEPISERQLSSYHRMRKVMLKKTYLQWPGSDCTNPTQAQELFWNQLRRAIKTGTRLETEECS
ATHESKEAEDFKEERSDENFYLQP
>22_ORNI_ENSONIP00000008192
LFDEQTDVLILVFMEEIPSYLLSPYHRMRKMLKKKTYLSWPRAGEHTELFWEKLCQALETREDPEAKTLLLTVPTM
P
>23_a_ORNI_ENSONIP00000014695
LFDEHKDVLIMVFLEDIPAKQLSPYYQMRSLVKKRSYLSWPQAVQHTGVFWQKIQQALKWKINDCIYQSVKQST
D
>23_b_ORNI_ENSONIP00000014696
LFDEKKDVLILLFLEEIPAQQLSPYYRMRKLVKKRTYLSWPRAGQHPGVFWQNVRRALETGNAPNETTNLLTCSL
PP
>3_ORNI_ENSONIP00000012793
VIEESRDSVILVFLQDVHDHKLFHSLFLRRGMLRPRCILDWPVHKERIAAFHQKLLIALGLTNRLKD
>5_a_ORNI_ENSONIP00000001683
MLEELTNVLIMLVVGKPKVAHYQLMKCNAVRAFVQRKEYLTWPEDPQDMEWFYERLISDILKDSKVKKLKENKP
EPGGPEVQPESHNGINAENIKETSM
>7_ORNI_ENSONIP00000025981
LMDEKNDVIVLIFLEKVPCNSKYLRLRKRLYKRSVLEWPTNPQAQPYFWFSLRSVLATEGHKQYNNLFKETL*REQ
YAGKCSFFSLDCFKCTPLYELLYVNTELFYY
>9_ORNI_ENSONIP00000015639
LLDEKVDVAVLVLMDKMFPKLKYLQLRKRLCRKSVLSWPHHPCAQPLFWNQMRMALSSDNLKFYDNNMSESF
I
```

Oryzias latipes

```
>6_ORLA_ENSORLP00000005545
GLSLGTDGIVLVLLEPLPQYLIPNKYYQLKSMMLRHTYLEWPQDRAKHRLFWANLRAALQADLPNLSVTD
>14_ORLA_ENSORLP00000019663
AMGKTFSDVILVVKEPIDPSSLPSKYCKLKKMLSTKTYLEWPQQPNQQQFFWAQLRSVLGKPTETQDRPHSIRKR
NSEGRISVIGPPVEKNMPKEDMPDADSKDLEFDEGNGIELSNLRQIPIMVL
>25_ORLA_ENSORLP00000015994
SISTQSDSIVFVLLEPIPPDSLPKRFLRLRSLLKQQTYLEWPSDERKQQVFWASLKSLL
>2_ORLA_ENSORLP00000003159
LFDAGGDAAILILLEPMTKDDVPKRFCKLRKLMSSTTYLEWPGEEAQREEFWRSLRNALRGE
>21_ORLA_ENSORLP00000016852
LFDEHRDVLLLVFLEPISERQLSSYHRMRKVMLKKTYLQWPGPDTTNFLQARELFWSQLRRAIRAGNRLETEDEA
QEHYA
>22_ORLA_ENSORLP00000025294
LFDDQKDVLILIFLEEIPLNQLSPYHRMRRLLKRQTYLSWARAQNPQVFWEKLRRALQSGDDLDEGLFLFVAPSM
W
```

```
>3_ORLA_ENSORLP00000010275
VIEASRDSVVLVFLQDVNDYKLSRSLFLRRGMLRPRCILEWPVQRERVPAFHQKLLIAL
>5_a_ORLA_ENSORLP00000020303
MLEELTNILIMLVVEKMAHYQLMKCNAVRAFVRTREYLTWPEDPQDLDWFYEKLSLQILKDTKVKKFALDEHEAGKLARAEPIPDGLEDIGMDDIRVAGV
>7_ORLA
LMDEKNDVIVLIFLEKVSCNSKYLQLRKRLYRRSVLEWPANPQAQQLFWFSLRSVLATESHKQYNNLFKETL
>8_ORLA
LLDENVDVIVLLMLEPVLQHSHFLRLRKRLCGKSVVEWPRTAAAEPWFWQNLKTVIRKDNQGMYNKTYSKYFTNE
>9_ORLA_ENSORLP00000011108
LLDEKMDTAILVLLDETFPKLKYLQLRKRLCRKSVLSWPMNPKAQPLFWNQMRVALALDNLKLYDSNMSESFI
```

Latimeria chalumnae

```
>1_6_a_LACH_ENSLACP00000011409
LFSENSNNLILILLEPIPQYLIPDKYYKLKSLMAKRTYLEWPKDKNKNPLFWANLRAAIKFNLQDVNKKISSCLA
>1_6_b_LACH_ENSLACP00000017183
TFDEKKDSLILLLLEPIPTNSIPDRFCKLRKLMNKNTYLEWPQDEARQTLFWQRLKAVLDL
>14_LACH_ENSLACP00000020140
AIGQGFEDVILVVKETINPNSLPNKFCKLRKMLSTKTYLEWPAEPNRQPFFWMQLKNVLGK
>2_LACH_ENSLACP00000014305
LFEGNDSAILILLEPIRKETIPKRFCKLRRMMNTKTYLEWPQDEGQQHLFWFKLKLAIKD
>21_a_LACH_ENSLACP00000001202
LFQEKKDVLILVFLEDIPKGELSKYHRMRKVMLKKTYISWPQEEDAQDLFWARIRKALKESNSNPEQDNIQLKD
>21_b_LACH_ENSLACP00000002971
LFDEHNDVLILVFLEDIPDHVLSSYYRLRKIVRKKTYLKWPSDQAGQKLFWAKLKDALKSETNAHKRELPSIEA
>3_LACH_ENSLACP00000012956
AIEQSHDSIILVFLEDIPDYKLNHALCLRRGMFKSRCILSWPAQRERVNAFHQKFKVALGSSNREH
>5_LACH_ENSLACP00000017461
YFHDCKDVLIVVVVGRIPQYHLMKYKPIRAFMQSRPYLRWPEELQDVDWFLEKLAYLILKKKTVKRKTNNIRLQRIKTVT
>13_a_LACH_ENSLACP00000007185
LLFDHSDVLILIFLEHIPDYRLSSYYRLCKLVKKTFIQWPEKEEEQELFWMRLKEALRPESVAPEEPKLID
>13_b_LACH_ENSLACP00000014614
LFYNNHDAVILIFLEAIPDYRLSAYQKLRKLVKKQTFISWPEDPNEKQLFWARVRNAIAQKTVNEPNLKLNIAE
>7_a_LACH_ENSLACP00000001158
LIDEKVDVIVLVFLEKALQKSKYLKLRKRLCSSSVLDWPTNPQAQHYFWQCLKNALATDNRMQYSKLFQETL
>7_b_LACH_ENSLACP00000004758
LIDEKLDVIVLVFLEKALQKSKYLKLRKRLCSSSVLDWPTNPQAQRYFWQCLKNALATDNRMQYSKLFQETL
>8_LACH_ENSLACP00000018907
LMDENMDVIVLIVLEPVLQHSQYLRLRRRLCGSSILDWPINPDAERFFWQSLRNVIATDNTVRYNKMYKESIL
>9_LACH_ENSLACP00000020965
LLEEKKDVVILILLDEVLKKSRYLQLRKRLCKKTVLFWPPNPFGQQYFWHKLRTVLDKDNHQYYDKNFSVGFD
```

Lepisosteus oculatus

```
>1_6_a_LEOC_ENSLOCP00000015894
LLSQDSDNIILVLLEPVPQYLIPSKFYKLKAMMAKRTYMEWPQDRNKHKLFWANLRAALQVNLSAGVGTPDTE
>1_6_b_LEOC_ENSLOCP00000021836
VFEERRDSLILLLLEPIPANSIPDRFCKLRKMMNKSTYLEWPPDEACQSMFWKRLKAVLNLEVK
>14_LEOC_ENSLOCP00000009707
AIGKTFQDVILVVKEAIDPDSLPSKYCRLKKMLSTKTYLEWPEETQRRAFFWAQLCSVLGKPTLRV
>25_a_LEOC_ENSLOCP00000020879
ALSIQQDSLVFILLEPIPADSLPRKFLKLRALLRKQTYLEWPKEVRKQTFFWASLKGML
>25_b_LEOC_ENSLOCP00000022014
ALTIHQDSLVFILLEPIPADSLPRRFLKLRTLLRQQTYLEWPKEEKKRQFFWTNLKAMLKTANKHMVMKDVAKDIVDSCPLLKCAE
```

>2_LEOC_ENSLOCP00000022321

LFDENNDTAILILLEPIPKETIPKRFCKLRKLMNSQTYLEWPEDEALQPIFWHNLKLAIKREEFNLR

>23_LEOC_ENSLOCP00000022417

LFDEQKDVLILVFLEDIPACQLSPYHRMRKLVKKRTYLKWPGHREETRMFWHKLNIALQTRGEADEENPLLSGLDTQD

>3_LEOC_ENSLOCP00000017046

VIEESRDSIVLIFLDDIPDHKLNHCLYIRRGMLNSRCILNWPLQRTRIPAFHQHLKVALGLSNRVH

>5_LEOC_ENSLOCP00000022101

LFTELQDVLIMVVVGGLPQFKLMKCDPIRTFIKSRHCLHWPEDFQDIDWFYEKLAQNILKEEKSKKQTDVLLQNIGVQS

>7_LEOC_ENSLOCP00000012197

LMDEKADVIILIFLEKCLQYSKYLRLRKRLCRSSVLEWPSNPQAQHYFWLCLRNTMATDGHTQYNNPFEETL

>8_a_LEOC_ENSLOCP00000012206

LLDDNTDVIVLVLLEPVLLHSQFFRLRKRLCRKTILEWPKNPRAEKWFWHCLRNIIRVEHQAVYNKLYSCYFINK

>8_b_LEOC_ENSLOCP00000012217

LLDDNTDVIVLVLLEPVLKHSQFFRLRKRLCRKTILEWPTNPHAEKWFWHCLRNIIRVEHQAVYNKLYTSYFTSR

>9_a_LEOC_ENSLOCP00000017493

LLDEKVDVVVLVLLDKVFYKSRYLQMRKILCRKSVLTWPMNPHAHQHFWNSMKTILASDNCKYYDSNVNESFLINNLV

>9_b_LEOC_ENSLOCP00000017758

LLEERADVAVFVLLEKGRRGSRYLQLRRLLCRETVLLWPQNPQAQGYFWHRLRCVLGRDIQASYDRKHCRGVPTPL

Anolis carolinensis

>1_6_ANCA_ENSACAP00000007179

LFSEDVYGLILVLLEPIPTYIIPARYHKLKALMAKRTYLEWPKEKSKHGLFWANLRAAIQTVLPNNEEMEELQG

>1_6b_ANCA_ENSACAP00000019120

LFREDVYGLILVLLEPIPTYIIPARYHKLKALMAKRTYLEWPKEKSKHGLFWANLRAAIQIKLPNNDEMEE

>14_ANCA_ENSACAP00000020761

AVGLGFEDVVLVVKEAVDPQALPRKFCKLRKLLSAKTYLEWPAEPGRQAFFWAQLAAVLGK

>2a_ANCA_ENSACAP00000019306

LFDENNDSAILILLEPIPAETVPRRFCKLRKLMNTKTYLEWPSDEDQKSIFWFNLKTAIKS

>2b_ANCA_ENSACAP00000017757

LFDENNDSAILILLEPIPEETVPRRFCKLRKLMNTKTYLEWPSDEDQKIIFWFNLNIAMKS

>21_ANCA_ENSACAP00000014787

LFDELKDVLVPVFLEEIPERELSAYYRMRKVMLKKTYVTWPPETQAQQLFWAKLRMALAAGTTEEEEDGGRTTH

>23_ANCA_ENSACAP00000018176

IFDQHKDVLILIFLEDIPCEYLSPYHRMRRLIKKKTYLKWPQEEQEIQFFWHKLNMAMKTGEGKEEE

>3_ANCA_ENSACAP00000001660

AIEQSRDSIVLIFRDDIPDYKLNHALCLRRAMFKSCCILEWPVQKDHVNAFYQQLKIALQTSSRIL

>4_ANCA_ENSACAP00000013654

QLLDSKASLVLVVLEGVDNAVVRQKLGLFRYLRRNTYLVWRDRELNRHMFLRQLKSALLEGKTWTEEELKLMLTN

>5_ANCA_ENSACAP00000002366

YFCDLKDVLIMVVAGSLSQYQLMKYQPVRAFLQRDRYLRWPEEDQDVEWFLNALSHQILKEKRTQKKAQKKKVPKKTGTLELKVVTIS

>13_ANCA_ENSACAP00000016366

IYYHGQDPLVVVFMEEISNYRLSPYHRLRKLIKQESYLTWPEEPEAEAVFWTRLREALSPGEQEQEFKPFNIVE

>7_ANCA_ENSACAP00000001544

LMDEKVDVIILIFLEKVLQMSKCLRLRKILCSQSVLEWPTNPRSQCYFWHCLRNSLTANHDTSYSKLFKEMV

Xenopus tropicalis

>6a_XETR_ENSXETP00000057556

LFGKNSNNLILILLDPIPQYSIPNKYNKLRSIMKHRTYLEWPKEKGKHALFWANLREAIHVNLSIKEED

>6b_XETR_ENSXETP00000057561

LYTENNDNLILILLEPIPQYLIPSKYYKLKTLMAQRTYLEWPSEKSKHGLFWANLRAAISIDLTHAESE

>14a_XETR_ENSXETP00000054703

AVGHALEDVILVVKEKVTMEDLPKRFQKLRKLLRTKTYLEWPLEHTRQHFFWIQLRSILGKVSSPVIGQDDLLVDNGAAASWDGPASEAHHEDEI

>14b_XETR_ENSXETP00000038393

AIGHSFEDVILVVKENVTLKDLPKRFHKLRKMLRKKTYLEWPSEPSKQHFFWIQLKNILGSPST

>14c_XETR_ENSXETP00000054700

AIGHAFEDVILVVKEKVTMEDLPKRFQKLRKMMRTKTYLEWPSEQNRQHFFWIQLKSILGKANPP

>14d_XETR_ENSXETP00000054707

AIGHSLEDIILVVKEKVTMEDLPKRFHKLRKMLRTKTYLEWPSEPSKQHFFWIQLKSIL

>2a_XETR_ENSXETP00000003822

LFDENNDSAILILLEPIENETVPKRFCKLRKLMNTKTYLEWPTDEEQQEVFWDNLKTALQS

>2b_XETR_ENSXETP00000003835

LFDENNDSAILILLDPIEKETVPKRFCKLRKLMNTKTYLEWPTDEEQQEVFWDNLKTALQPANAHRP

>21_XETR_ENSXETP00000059090

LFDEMRDVLVLILLDNIPDRELSTYHRMRKLMLKKTYITWPTEPEAQQLFWAKVQEAVSGKRPSEGHQGIKIVK

>23_XETR_ENSXETP00000055333

LFEEHTDVLILLFLEQIPDHHLSPYHQIRKVIKKKTYLIWPQERNATSIFWYRVSQALQTEEREEDEK

>26_XETR_ENSXETP00000061916

LLAEKNDDLILVFLESISGYHLSAYHRLARIVRKKTYIDWPQEENEQAEFWERLRMTVL

>3_XETR_ENSXETP00000012947

AIEQNRDSIILIFLEDIPDYKLYHTIHLRRGMFKSRCILDWPDQMERIKTFYQRLKIALGSTNLVN

>5_XETR_ENSXETP00000032872

YFTELKDVLIMVVVGSLSQYQFMKYQPIRAYVKRAQYLRWPEDIQDVEWFLGRLSYQILKENTVEKKPNQASRKPFNHELQNIETIS

>13_XETR_ENSXETP00000009956

AFSYKEDVLLMVFLEEIPEYRLSAYHKLRKLIKQNTYIDWPEDPRGEEVFWLKLRQALDGGVCEENNIQLCD

>7_XETR_ENSXETP00000011725

LIEEKVDVIILILLEKTLQRSRYLRLRKRLCANSVLYWPSNPNSQSYFWHCLKSAIATENQMGYDKLFKDHT

>8_XETR_ENSXETP00000062585

LMDENMDVIVIVLLEPVLQNSQYLRLRRKICKSSIMEWPKNPNTKSFFWQRMKNVLLTDNCNRYNNFYTDTIAN

>9_XETR_ENSXETP00000013094

LLDEKKDVVALVVLDHKMKMSQYFLTRKRLCPKSFLNWPCNPKAHSHFWHMLRIYIRQDSRRCCGSQLKKYV

Poecilia formosa

>1_6_POFO_ENSPFOP00000020173

RLSQGSDSLVLVLLEPLPQYLIPSKYYQLKSMMKRHTYLEWPQDKAKHRLFWANLRAALQADLPSKLVAETEE

>14_POFO_ENSPFOP00000018414

AMGKTFSDVILVVKEPIDPSSLPSKYCKLKKMLSTKTYLEWPQQVNQQPFFWAQLRSVLGKPTMTREGTNSIRSRNTSERFSVVEERIPEVNKPLEGNKKEIQSEIIHRTEIELQDQRNLEAQ

>2_POFO_ENSPFOP00000000533

LFEAGGDTAILILLEPLSKDDVPKRFCKLRKLMSSTTYLEWPQEEERRPEFWRSLRNALRGDNEQEN

>21_POFO_ENSPFOP00000020442

LFDEHRDVLLLVFLEPISERQLSSYHRMRKVMLKKTYLQWPGPDCTDPSQAQELFWNQLRRAIRAGNRLETEQNDPDEDFARASNETGNYEKLLSDDEDYLQP

>22_POFO_ENSPFOP00000004631

LFDEQKDVLILVFLEDIPTYLLSPFHRMRKLLKKQTYLSWPRAADHPEVFWENLRKALQTGNDPNEEKLQLAVIETY

>23_a_POFO_ENSPFOP00000024685

LFDEKKDVLILLFLEEIPSYHLAPYYRMRKLVKKRTYLSWPQAAQHPGVFWQNVQRALQAGGALTENTDPLTGPAGI

>23_b_POFO_ENSPFOP00000028752

LFDEKKDVLILLFLEDIPPQHLSPYHRMRKLLKKCTYLSWSKAEKHPGVFWQNVRKALQTKDDPPKNPALLTGPTQC

>23_c_POFO_ENSPFOP00000011089

LFDEQKDVLVLLFLENIPAHHLSPYYRMRKLVKKRTYLSWPQAAQHPGVFWQNVQRALQAGGALAENTDLLLGPAGR

>3_POFO_ENSPFOP00000005811

VIEASRDSVVLIFLQDVHDYKLSRSLFLRRGMLHQRCVLNWPAQKERIPAFNQKLLIALGMTNRLQE

>5_POFO_ENSPFOP00000000698

MLEELTNVLVMLVVGKVAHYQLMKCNAVRAFVQRREYLTWPEDPQDLEWFYERLVSLILRDTKVKKFAEDKPETVKPDCQPPAKEKIPLENIRVNNLAGNPLM

>7_POFO_ENSPFOP00000025729

LMDEKNDVIVLIFLEKVSCNSKYLRLRKRLYKRSVLEWPTNPQAQPYFWFSLRSVLATESHKQYSNLFKETL

>8_POFO_ENSPFOP00000027487

LLDENVDVIVLLMLEPVLQHSHFLRLRRRLCEKSVVEWPRTAAAEPWFWQNLRSVVKVDNQIMYSKTYKKFFSSK

>9_POFO_ENSPFOP00000000377

LLDEKVDAAVVVLLDEMFPKLKYLQLRKRLCRKSVLSWPRNPRAQPLFWNQMRMALSSDNLKFYDNNMSESFI

Astyanax mexicanus

>1_6_ASME_ENSAMXP00000026268

RLTRGLDSIILILLEPLPPYLIPSKYHHLKAMMARRTYLEWPQDKTKQRMFWANLRAVLQADLPRSSSLEAGNQE

>14_ASME_ENSAMXP00000019326

AIGKNLRDVILVVKEPIDPKSLPSKYCKLKKMLNTKTYLEWPEQPKQQAFFWAQLRSVMGKPNLLKQNSVIENRRVSKLSRASVIELPEVKPQITAGTEELPERNTENCSLRMPLEQLA

>2_ASME_ENSAMXP00000026287

IVDEHNDSAVLILLEPIAKQTIPKRFCKLRKIMNSKTYLEWPQEEERREEFWSNLQAALKR

>21_ASME_ENSAMXP00000025842

LFHEMQDVLLLVFLESIPERKLSTYHRMRKVMLKKTYLQWPGPDCTDPAKAQGLFWKQLKKALRSSSSTRQEEESMEADVQLGEEKDAPNTEDREYFVNQPHVDEEAYYLMP

>23_a_ASME_ENSAMXP00000025763

LFDEQKDVLILVFLEDIPTQQLSPYHQMRKLVKKKTYLKWPKPGEDTKVFWQKLRLALETKEDLDENALL

>23_b_ASME_ENSAMXP00000026712

LFDEKKDVLILVFLEDIPNSELSPYYRMRRLIKKRTYLKWPKLGKDTQYFWQKLRAALETRGSSDENNSALQSAQ

>23_c_ASME_ENSAMXP00000026713

LFDEKKDVLILVFLENIPAHQLSPYYRMRKLIKKRTYLSWPKPGEDTRVFWEKLRVALETKGTYEEESLLLSGIRRT

>26_ASME_ENSAMXP00000026963

LQVEHRDILILVFLEKIPSKMLSAHHRLARLVKTRTYLAWPQKAELQDEFWERM

>5_ASME_ENSAMXP00000026717

MLEEVQDILLMLLVDQIPQYRLMKYEPIRTYVQTKRYLCWPEDSQDLQWFYNQLQHSILKGTKAKQAKIDAETANNVPEVEAVTVF

>7_ASME_ENSAMXP00000026765

LLDEKNDVIILIFLEKFSSSHSKYLRLRKRLYKRSVLEWPRNPRAQPYFWFCLKSVMAAESQQHYNKLFQETL

>8_a_ASME_ENSAMXP00000026319

LLEEGVDVMVLILLEPVLQHSRILHLRRCLCGNSVLEWPRNPSAQNWFWQSLRNAIKKEKQGMQNKLFKNY

>8_b_ASME_ENSAMXP00000001765

LLEESKDVIVLLMLEPVLQSSHFLRLRQRLCSQSVLEWPRAPAAEPWFWQCLRNAIRVENCDMYSKIYSRYFTSRSSSVRD

>9_ASME_ENSAMXP00000027050

LLDEKVDVAVLVLLDSVFPKVKYLQMRKRLCKKSVLSWPKNPQAQPLFWNDLCVAIASDNVKSYDKKVTESFLSHELL

Gadus morhua

>14_GAMO_ENSGMOP00000004019

AMGKAFSDVILVVMEPIDPHSLPSKYCKLKKMLSTKTYLEWPQQPKHQPFFWAQLKSVLGKPSLTRGRAGSTRSRAASEGRVSMIEPPMEVDQQDHGVNKAELHGEEIETKELFLKPIPIAV

>25a_GAMO

AIDAQQDSLVFILLEPIPTNSLPKKFLKLRRLLMQQTYLEWPKDERKQQVFWVNLRSMLQVADHRILKDMALELTQSASLIPDDLVPLLK

>25c_GAMO

ALDAQQDSLVFILLEPISTNSLPKKFLKLRRLLMQQTYLEWPKDERKQQVFWVNLRTMLQVADHRILKDMALELTQSASLIPDDLDPLLK

>25d_GAMO

AIDAQQDSLVFILLEPIPTNSLPKKFLKLRRLLMQQTYLEWPMDERKQQVFWVNLRSMLQVADHRILKDMALELTQSASLIPDDLVPLLK

>25e_GAMO

AIDAQQDSLVFILLEPIPTNSLPKKFLKLRRLLMQQTYLEWPMDERKQQVFWVNLRSMLQMADHRILKDMALELTQSASLIPDDLVPLLK

>25f_GAMO

AIDAQQDSLVFILLEPIPTNSLPKKFLKLRKLLMQQTYLEWPKDERKQQVFWVNLRSMLQVADHRILKDMALELTQSASLIPHDLVPLLK

>21_GAMO_ENSGMOP00000019623

LFDEHRDVLLLVFLEHIPERELSSYHRMRKVMLRKTYLQWPGSECTDPAMAQLLFWKQLRRALRTGSRMEDEDAAGEKKSSGTAEGDQTDSAVNPTAEEIYQ

>22a_GAMO

LFDEQKDVLILVFLEDIPMQQLSPYYRMRRLLKRKTYLSWSRADAHPDLFWEKLRQALDTQEHPMGEHLRLTVEDGPTGERPDQ

>22b_GAMO

LFDEQKDVLILVFLEDIPMQQLSPYYRMRRLLKRKTYLSWSRADAHPDLFWEKLRQALETQEHPMGEHLRLTIEDGPPGERQDQS

>22c_GAMO

LFDEQKDVLILVFLEDIPMQQLSPYYRMRRLLKRKTYLSWSRADAHPDLFWEKLRQALDTQEHPMGEHLRLTVEDGPPGERPDQ

>22d_GAMO

LFDEQKDVLILVFLEDIPMQQLSPYYRMRRLLKRQTYLSWSRADAHPDLFWEKLRQALETREHPMGEHIRLTVVNGPPGERPDH

>22e_GAMO

LFDEQKDVLILVFLEDIPMQQLSPYYRMRRLLKRQTYLSWSRADAHPDLFWEKLRQALDTQEHPMGEHLRLTVEEGPPGERPDQ

>22f_GAMO

LFDEQKDVLILGFLEDIPMQQQLSPYYRMRRLLKRQTYLSWSRADAHPNLFWEKLRQALETQEHPMGEHILLTVEDGPPGERPDQ

>22g_GAMO

LFDEQKDVLILVFLEDIPMQQLSPYYRMRRLLKRQTYLSWSRADAHPNLFWEKLRQALETQEHPMGEHILLTVEDGPPGERPDQ

>22h_GAMO

LFDEQKDVLILVFLEDIPMQQLSPYYRMRRLLKRQTYLSWSRADAHPNLFWEKLRQALETQEHPMGEHILLTVEDGPPGERPDQ

>22j_GAMO

LFDEQKDVLILVFLEDIPMQQLSPYYRMRRLLKRQTYLSWSRADAHPDLFWEMLRQALETREHPMGEHIRLTVVNGPPGERPDH

>22l_GAMO

LFDEQKDVLILVFLEDIPMQQLSPYYRMRWLLKRQTYLSWSRADAHPDLFWEKLQQALDTQEHPMGEHLRLTVVGSPGERPDQ

>23_GAMO

LLDEKKDVLILLFLEELPEKQLSPYYRMRKLVRRSTYLSWPQAARHPGLFWQNVHRALESGDSHDDNTHFLSGPAL

>3_GAMO_ENSGMOP00000000792

VMEERRDAVILVFLQDINDYRLSRSLFLRRGMLQLRCLLNWPVHKERIPAFHEKLHIALGTTNTPKP

>7a_GAMO

LMDEKDDVIVLIFLEKAASNSKYLRLRKRLYRRSVLEWPTNPQAQPYFWFGLRSVLATESNKQYSDMFRETL

>7b_GAMO

LMDEKDDVIVLIFLEKAASNSKYLRLRKRLYRRSVLEWPTNPQAQPYFWFGLRSVLATESNKQYYSDMFRETL

>8a_GAMO

LLDENLDVIVVLMLEPVLQNSHFLRLRRRLCGESVVEWPRTAAAEPWFWQNLRNVVRVDNQTMYTSTYSQYFTCSRERD

>8c_GAMO

LLDENLDVIVVLMLEPVLQNSHFLRLRRRLCGESVVEWPRTAAAEPWFWQNLRNVVRVDNQTMYTSTYSQYFTCSRERD

>8d_GAMO

LLDENLDVIVVLMLEPVLQNSHFLRLRRRLCGESVVEWPRTAAAEAWFWQNLRNVVRLDNQTMYTSTYSQYFTCSRERD

>8e_GAMO

LLDENLDVIVVLMLEPVLQNSHFLRLRRRLCGESVVEWPRTAAAEPWFWQNLRNVVRVDNQTMYTSTYSQYFTCSRERD

>8f_GAMO

LLDENLDVIVVLMLEPVLQNSHFLRLRRRLCGESVLEWPRTAAAEPWFWQNLRNVVRVDNQTMYPSTYSQYFTCSRERD

>8j_GAMO

LLDENLDVIVVLMLEPVLQHSHFLRLRRRLCGESVVEWPRTAAAEPWFWQNLRNVVRVDNQTMYTSTYSQYFT
CSRRERD
>8l_GAMO
LLDENLDVIVVLMLEPVLQNSHFLRLRRRLCGESVVEWPRTVAAEPWFWQNLRNVVRVDNQTMYTSTYSQYFT
CSRERD
>9a_GAMO
LLDEKVDVAVLILLDKMFPKLKYVQLRTRLCKKSVMSWPRNPKAQPLFWNQMRIALSSDNLKLYDKNISESFI
>9b_GAMO
LLDEKVDVAVLILLDKMFPKLKYLQLRTRLCKKSVMSWPRNPQAQPLFWNQMRTALSSDNLKLYDSNISESFI
>9c_GAMO
LLDEKVDVAVVILLDKMFPKLKYLQLRTRLCRKSVMSWPRNPKAQPLFWNQIRTALSSDNLQIYDNNFSEGFI
>9d_GAMO
LLDEKVDVAVLILLDKMFPKLKYLQLRTRLCRKSVMSWPRNPQAQPLFWNQMRTALSSDNLKLYDNNISEGFI
>9e_GAMO
LLDEKVDVAVLILLDKMFPKLKYLQLRTRLCRKSVMSWPRNPQAQPLFWNQMRTALSSDNLKLYDNNISESFI

Xiphophorus maculatus
>1_6_XIMA
RLSQGSDSIVLVLLEPLPQYLIPSKYYQLKSMMNRHTYLEWPQDKAKHRLFWANLRAALQTDLPSKLVSETEE
>14_XIMA_ENSXMAP00000013389
AMGKTFSDVILVLKEPIDPSSLPSKYCKLKKMLSTKTYLEWPQQVNQQPFFWAQLRSVLGKPTMTREGTNSIRSR
NSSE
>2_a_XIMA_ENSXMAP00000008276
LFEAGGDAAILILLEPLSKDNVPKRFCKLRKLMSSTTYLEWPQEEERRPEFWRSLRNALRGDND
>2_b_XIMA_ENSXMAP00000008281
LFEAGGDAAILILLEPLSKDDVPKRFCKLRKLMSSTTYLEWPQEEERRPEFWRSLRNALRGDNEQEN
>22a_XIMA
LFDEQKDVLILVFLEDIPTYLLSPFHRMRQLLKKQTYLSWPRAAGHPEVFWENLRKALQTGNNANEENFLSLTQE
>22b_XIMA
LFDEQKDVLILVFLEDIPTYLLSPFHRMRKLLKKQTYLSWPRAAGHPEVFWENLRKALQTGNDPNEEKLQLTVTET
Y
>23_XIMA
LFDEKKDVLILLFLEEISAHHLSPYYRMRKMLKKRTYLSWSAQHPGVFWQNVQRALQAGDAPENSDMLTGPTG
R
>3_XIMA_ENSXMAP00000018909
VIEASRDSVVLIFLQDVHDYKLSRSLFLRRGMLRPSCVLNWPPQKERIPAFNQKLLIALGMTNRLQE
>5_XIMA_ENSXMAP00000001784
MLEELTNVLVMLVVGKVAHYQLMKCNAVRAFVQRREYLTWPEDPQDLEWFYERLVSLILRDTKVKKFVEDKPEF
VKPDCQPPAKDKIPLENIGVVANSDVGNDVNELTFINVKEEGLYEPTKADSTHSAQVIVTSP
>7_XIMA_ENSXMAP00000004436
LMDEKNDVIVLIFLEKVSCNSKYLRLRKRLYKRSVLEWPTNPQAQPYFWFSLRSVLATESHKQYSSLFKETL
>8_XIMA_ENSXMAP00000004435
LLDENEDVIVLLMLEPVLQHSHFLRLRRRLCEKSVVEWPRTPAAEPWFWQNLRSVVKVDNQIMYSKTYKKFFSSK
>9_XIMA_ENSXMAP00000007651
LLDEKVDAAVVVLLDEMFPKLKYLQLRKRLCRKSVLSWPRNPRAQPLFWNQMRMALSSDNLKFYDNNMSESFI

Petromyzon marinus
>1a_PEMA_ENSPMAP00000011399
LMESRDGALVLVLLEPIPRDSVPSRFCRLRRLMARKTYLEWPVEQSKQALFWANLRATLSCQREQEPQNLEIVV
>1b_PEMA_ENSPMAP00000011400
LMESRDDALVLVLLEPIPRDSVPSRFCRLRRLMGRKTYLEWPAEQGKQVLFWANLRATLGE
>25a_PEMA_ENSPMAP00000011066
VLEQRQDSLVLLLLEPLPRNSVPSKFCRLRKLLNRKTYLEWPAEEGKRSMFWASLRAVLQSDHEPSNPNSNHRSIS
TCNSNPIRNPYV
>25b_PEMA_ENSPMAP00000011211
MVEENQDSLVLLLLEPLPKGSLPSKFCKLRRLLSNKTYLEWPTEERKRAVFWTSLNAVLQSRPPP
>21a_PEMA_ENSPMAP00000011080

LFDEHKDVVIMVFLEDIPDYKLSAYHRMRKIIGDKTYISWPEDAAGKDLFWAKLRAAI

>21b_PEMA_ENSPMAP00000011162

LFNEHKDVLIMVFLETIPSYKLSAYYRMRRIVNNKTYIVWPDDNIGRELFWAKLRTAL

>21c_PEMA_ENSPMAP00000005491

LFSEHRDVLVTLIVEDIADRELSAHHRMHRLLCTKTHVVWPRDEAARPLFWAKLRTALGEPSAAA

>3_PEMA_ENSPMAP00000001776

AIEQNRDDVVLALLEDIPEFELHHKLCLRAAMFPRRCVLRWPQDPTRLPLFLQQLRVALGS

>7_8_9a_PEMA_ENSPMAP00000002547

LLDEKVDMVILVMLERMRSSFTRSRYMRLRQRLSPGSILRWPTNPHAQKIFWQGLRDALAGPSKAATQAAKRRR

>7_8_9b_PEMA_ENSPMAP00000006887

MIDEKKDVMVFVMLERMPSRFLYSRYMRMRKRLCPDSFLQWPPNPHAQHLFWKCLRAEITKSQTEQYWQVYEITV

Gallus gallus

>1_GAGA

LFSENSNSLILILLEPIPSYVIPARYHKLKALMAKRTYLEWPKERSKHALFWANLRAVVNIKLPTSFETDEEQSDVTSTSSITQCLIK

>6_GAGA_ENSGALP00000028126

LFSENSNSLILILLEPIPPYVIPARYHKLKALMAKRTYLEWPKERSKHALFWANLRAAVNIKLPTSFETDEEQSDVTSTSSITQCLIK

>15_GAGA_ENSGALP00000013260

VLDENQDSLIMVVLEDLPPDSVPQKFSKLRKLLKRKTYLKWSPEEHKQKIFWHQLAAVLKTTNEPLVRAENGPNEDVIEME

>16_GAGA_ENSGALP00000043467

LFSENSNSLILILLEPIPPYVIPARYHKLKALMAKRTYLEWPKERSKHALFWANLRAAISINLSVADEQNRTEV

>2a_GAGA

LFDENNDVAILILLEPIQSQAIPKRFCKLRKIMNTKTYLEWPPDEEQQQMFWENLKAALKS

>2b_GAGA

LFDENNDVAILILLEPIQSQAIPKRFCKLRKIMNTKTYLEWPPDEEQQQMFWENLKAALKS

>21_GAGA_ENSGALP00000001118

LLDERRDILVLVLLEDVGDAELSAYHRMRRVLLRRTYLRWPLDPAAQPLFWARLKRALRWGEGGEEEEEEGLGGGTGRPREGDKQM

>3_GAGA_ENSGALP00000021914

AIEQSRDSIILIFLHNIQDYKLNHALCLRRGMFRSCCILNWPVQKERINAFHQQLMMALKSNSK

>4_GAGA_ENSGALP00000011319

QLVEGKAGIIMIILGEVDKTLLRQRLGLSRYLRRNTYLEWKNKEISRHIFWRQLTSVLLEGKKWNHEEIKLM

>5_GAGA_ENSGALP00000015286

YFSDLKEVLIMVVVGSLSQYQLMKHKPIRIFLQRSRYLRWPEDYQDIGWFLDNLSSQILKEKKVQRNVSGIELQTIATVSH

>7_GAGA_ENSGALP00000026726

LLDEKIDVIILIFLEKVLQKSRYVQLRKRLCRSSVLEWPTNPRSQPYFWQRLKNAIAMNNTLSYNKLLQETV

Homo sapiens

>1_HOSA_ENSP00000354932

LFHEGSNSLILILLEPIPQYSIPSSYHKLKSLMARRTYLEWPKEKSKRGLFWANLRAAINIKLTEQAKK

>6_HOSA_ENSP00000480266

LFHEGSNNLILILLEPIPQNSIPNKYHKLKALMTQRTYLQWPKEKSKRGLFWANIRAAFNMKLTLVTENNDVKS

>10_HOSA_ENSP00000478985

LFHENSDHIILILLEPIPFYCIPTRYHKLKALLEKKAYLEWPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLMRTDCL

>2_HOSA_ENSP00000260010

LFDENNDAAILILLEPIEKKAIPQRFCKLRKIMNTKTYLEWPMDEAQREGFWVNLRAAIKS

>3_HOSA_ENSP00000423684

AIEQNLDSIILVFLEEIPDYKLNHALCLRRGMFKSHCILNWPVQKERIGAFRHKLQVALGSKNSVH

>4_HOSA_ENSP00000377997

QFLSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI

>5_HOSA_ENSP00000440643

CLSDLNSALIMVVVGSLSQYQLMKHQSIRGFVQKQQYLRWPEDLQDVGWFLHKLSQQILKKEKEKKKDNNIPLQTVATIS

>7_HOSA_ENSP00000370034

LMDEKVDVIILIFLEKPFQKSKFLQLRKRLCGSSVLEWPTNPQAHPYFWQCLKNALATDNHVAYSQVFKETV

>8_HOSA_ENSP00000312082

LMDENMDVIIFILLEPVLQHSQYLRLRQRICKSSILQWPDNPKAEGLFWQTLRNVVLTENDSRYNNMYVDSIKQY

>9_HOSA_ENSP00000353874

LLEDRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNHHFYNRNFCQGPTAE

Mus musculus

>11_MUMU_ENSMUSP00000068906

LVARPGTTHLLLLFLEPLDRQRLHSYHRLSRWLQKEDYFDLSQGKVEWNSFCEQLKRRLSKAGQERD

>12_MUMU_ENSMUSP00000074381

LLAAPSPPVLLLVFLEPISRHQLPGYHRLARLLRRGDYCLWPEEEERKSGFWTWLRSRLG

>13_MUMU_ENSMUSP00000043101

MFYEHKDVIILIFLEEIPNYKLSSYHRLRKLINKQTFITWPDSVHQQPLFWARIRNALGKETVEKENTHLIVVE

Rattus norvegicus

>11_RANO_ENSRNOP00000051449

LIARPGTTCLLLLFLEPLDRQKLHSYHRLSRWLQKEDYFDLSQGKMEWNTFCEQLKQRLRKARKERED

>12_RANO_ENSRNOP00000062596

LLAAPSPPVLLLVFLEPISRHQLPSYHRLARLLRRGDYCLWPEEEERKGGFWTWLRSRLG

Ictalurus punctatus

>25_ICPU_AEI59680.1

AISVRDDSLVFILLEPIPSDSLPKKFLRLSTMLRQKTYLEWPKDXTKKKVFWSSLRSILQTADKRMVLKEIACDIAENTLLLNAQQ

>26_ICPU_AEI59681.1

LLVENRDVLIVVFLEKISPRQLSAHHRLARVVKKKTYIDWPEEPGRRTAFWDRLWAKLAPEPARTQR

>21_ICPU_AEI59678.1

LFDEMQDVLLLVFLEDIHERQLSAYHRMRKFMLKKTYLQWPGLDCTDPIKAQELFWTQLKRALRSSNSRSQDEEQTLENVQNGPQIDDARVEEREYFMNQGQMDDGPYYLTP

SLOUCH results

BEST ESTIMATES & MODEL FIT – TLR8 phylogeny

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation             11.7482573

Phylogenetic half-life          0.0590000

Phylogenetic correction factor    0.9148817

Stationary variance             4.1000000

PRIMARY OPTIMA

         Estimate Std.error

Theta_global 1.454513 0.2747245

MODEL FIT

          Value

Support   -129.99582

AIC       265.99165

AICc      266.40544

SIC       272.37305

r squared    0.00000

SST        61.78786

SSE        61.78786

> model.fit(ancestor, indata3$time, seq(0.00,0.1, 0.001), seq(1, 10, 0.1), response= indata3$TLR8,
me.response= NULL, fixed.fact=NULL, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL,
random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,  intercept="root",
ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR8 group 0

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation            16.9060288

Phylogenetic half-life         0.0410000

Phylogenetic correction factor    0.9408495

Stationary variance            3.2900000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 5.8583640 1.2414273

NO      1.5558946 0.4024705

YES    0.9097707 0.3409476

MODEL FIT

           Value

Support   -123.91445

AIC       257.82890

AICc      258.90033

SIC       268.46457

r squared   20.12795

SST        77.60318

SSE        61.98325

> model.fit(ancestor, indata2$time, seq(0.001,0.1, 0.01), seq(3.1, 3.7, 0.01), response= indata2$TLR8,
me.response= NULL, fixed.fact=Group_0, fixed.cov= NULL, me.fixed.cov= NULL,
mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,
intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR8 group 25

```
MODEL PARAMETERS

                          Estimate

Rate of adaptation            16.9060288

Phylogenetic half-life         0.0410000

Phylogenetic correction factor    0.9408495

Stationary variance            3.3500000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN  5.990984 1.2472106

NO      1.442845 0.4835486

YES     1.072728 0.3106295

MODEL FIT

           Value

Support   -124.45568

AIC       258.91137

AICc      259.98279

SIC       269.54704

r squared   18.72125

SST        76.21327

SSE        61.94520

> model.fit(ancestor, indata2$time, seq(0.001,0.1, 0.01), seq(3.3, 3.7, 0.01), response= indata2$TLR8,
me.response= NULL, fixed.fact=Group_25, fixed.cov= NULL, me.fixed.cov= NULL,
mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,
intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR8 group 50

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation            16.9060288

Phylogenetic half-life         0.0410000

Phylogenetic correction factor    0.9408495

Stationary variance            3.3300000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 6.0220382 1.2377241

NO     0.9751567 0.3641890

YES    1.3916402 0.3719837

MODEL FIT

            Value

Support   -124.34093

AIC       258.68187

AICc      259.75330

SIC       269.31754

r squared   19.02160

SST        76.67101

SSE        62.08696
```

```
> model.fit(ancestor, indata2$time, seq(0.001,0.1, 0.01), seq(3.3, 3.7, 0.01), response= indata2$TLR8, me.response= NULL, fixed.fact=Group_50, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR8 group 75

```
MODEL PARAMETERS

                              Estimate

Rate of adaptation             16.9060288

Phylogenetic half-life          0.0410000

Phylogenetic correction factor    0.9408495

Stationary variance             3.3600000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

       Estimates Std.error

UNKNOWN  6.038627 1.2476796

NO      1.141288 0.2862024

YES     1.380672 0.6383280

MODEL FIT

             Value

Support   -124.60759

AIC       259.21519

AICc      260.28662

SIC       269.85086

r squared   18.32199

SST        75.98645

SSE        62.06422
```

```
> model.fit(ancestor, indata2$time, seq(0.001,0.1, 0.01), seq(3.3, 3.7, 0.01), response= indata2$TLR8,
me.response= NULL, fixed.fact=Group_75, fixed.cov= NULL, me.fixed.cov= NULL,
mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,
intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR8 group minus 25

```
MODEL PARAMETERS

                          Estimate

Rate of adaptation             16.9060288

Phylogenetic half-life          0.0410000

Phylogenetic correction factor    0.9408495

Stationary variance             3.3500000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 6.0252608 1.2429907

NO      1.2893210 0.3234544

YES     0.9619736 0.4510656

MODEL FIT

            Value

Support   -124.49214

AIC       258.98427

AICc       260.05570

SIC       269.61995

r squared   18.62558

SST        76.21327

SSE        62.01811
```

```
> model.fit(ancestor, indata2$time, seq(0.001,0.1, 0.01), seq(3.1, 3.7, 0.01), response= indata2$TLR8,
me.response= NULL, fixed.fact=Group_minus_25, fixed.cov= NULL, me.fixed.cov= NULL,
mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,
intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR8 group minus 50

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation            13.5911212

Phylogenetic half-life          0.0510000

Phylogenetic correction factor    0.9264226

Stationary variance             3.4000000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN  5.591644 1.2010945

NO      1.074254 0.2920025

YES     1.199023 0.7783270

MODEL FIT

            Value

Support   -124.62085

AIC       259.24170

AICc      260.31312

SIC       269.87737

r squared   16.34706

SST        74.20444

SSE        62.07419

> model.fit(ancestor, indata2$time, seq(0.001,0.1, 0.01), seq(3.1, 3.7, 0.01), response= indata2$TLR8,
me.response= NULL, fixed.fact=Group_minus_50, fixed.cov= NULL, me.fixed.cov= NULL,
mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,
intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR8 MHCII

```
MODEL PARAMETERS

                        Estimate

Rate of adaptation             16.9060288

Phylogenetic half-life          0.0410000

Phylogenetic correction factor    0.9408495

Stationary variance             3.3200000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN  5.684552 1.2976515

No      1.644295 0.5386467

Yes     1.034836 0.3008714

MODEL FIT

           Value

Support   -124.18068

AIC       258.36135

AICc      259.43278

SIC       268.99703

r squared   19.43909

SST        76.90195

SSE        61.95291
```

```
> model.fit(ancestor, indata3$time, seq(0.001,0.1, 0.01), seq(3.1, 3.7, 0.01),       response=
indata3$TLR8, me.response= NULL, fixed.fact=indata3$MHCII, fixed.cov= NULL, me.fixed.cov= NULL,
mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,
intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR8 group 0 + MHCII

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation            22.3595865

Phylogenetic half-life         0.0310000

Phylogenetic correction factor    0.9552765

Stationary variance            3.1000000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 5.5081865 1.3379683

NoNO    2.7748094 0.6246435

NoYES   0.7863605 0.7210838

YesNO   1.1396624 0.4709201

YesYES  0.9948441 0.3675523

MODEL FIT

            Value

Support   -122.46304

AIC       258.92607

AICc       261.00015

SIC       273.81601

r squared   27.11397

SST        85.15327

SSE        62.06484
```

```
> model.fit(ancestor, indata3$time, seq(0.001,0.1, 0.01), seq(3, 3.6, 0.01),              response= indata3$TLR8, me.response= NULL, fixed.fact=Group_0_MHCII , fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR8 group 25 + MHCII

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation            16.9060288

Phylogenetic half-life          0.0410000

Phylogenetic correction factor    0.9408495

Stationary variance             3.2800000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 5.6499638 1.2905413

NoNO    2.0307791 0.7137641

NoYES   1.2263572 0.7395576

YesNO   0.9711936 0.6443604

YesYES  1.0524881 0.3375849

MODEL FIT

           Value

Support   -123.84106

AIC       261.68211

AICc       263.75618

SIC       276.57205

r squared   20.31684

SST        77.83978

SSE        62.02519
```

```
> model.fit(ancestor, indata3$time, seq(0.001,0.1, 0.01), seq(3, 3.6, 0.01),              response= indata3$TLR8, me.response= NULL, fixed.fact=Group_25_MHCII , fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR8 group 50 + MHCII

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation             16.9060288

Phylogenetic half-life          0.0410000

Phylogenetic correction factor    0.9408495

Stationary variance             3.2100000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 5.8463339 1.2807175

NoNO    0.4190979 0.9921280

NoYES   2.0202578 0.5889784

YesNO   1.0768274 0.3831597

YesYES  0.9711968 0.4654550

MODEL FIT

           Value

Support   -123.11637

AIC       260.23274

AICc       262.30681

SIC       275.12268

r squared   22.15806

SST        79.53722

SSE        61.91331
```

```
> model.fit(ancestor, indata3$time, seq(0.001,0.1, 0.01), seq(3, 3.6, 0.01),               response= indata3$TLR8, me.response= NULL, fixed.fact=Group_50_MHCII , fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR8 group 75 + MHCII

```
MODEL PARAMETERS

                          Estimate

Rate of adaptation             16.9060288

Phylogenetic half-life          0.0410000

Phylogenetic correction factor    0.9408495

Stationary variance             3.3100000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 5.6715824 1.2967512

NoNO    1.5639808 0.6273580

NoYES   1.8182333 0.8824009

YesNO   1.0416566 0.3180857

YesYES  0.9790289 0.9137936

MODEL FIT

            Value

Support   -124.14774

AIC       262.29548

AICc       264.36955

SIC       277.18542

r squared   19.52468

SST        77.13428

SSE        62.07406

> model.fit(ancestor, indata3$time, seq(0.001,0.1, 0.01), seq(3.3, 4.3, 0.01),               response=
indata3$TLR8, me.response= NULL, fixed.fact=Group_75_MHCII , fixed.cov= NULL, me.fixed.cov=
NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,
intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT - TLR8 group minus 50 + MHCII

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation             16.9060288

Phylogenetic half-life          0.0410000

Phylogenetic correction factor    0.9408495

Stationary variance             3.3200000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 5.7152705 1.3068208

NoNO    1.5995507 0.5845279

NoYES   1.8856347 1.3390323

YesNO   1.0424670 0.3184890

YesYES  0.9703738 0.9168541

MODEL FIT

            Value

Support   -124.15854

AIC       262.31708

AICc       264.39115

SIC       277.20702

r squared   19.49666

SST        76.90195

SSE        61.90863
```

```
> model.fit(ancestor, indata3$time, seq(0.001,0.1, 0.01), seq(3, 3.6, 0.01),               response= indata3$TLR8, me.response= NULL, fixed.fact=Group_minus_50_MHCII , fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,  intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR8 group minus 25 + MHCII

```
MODEL PARAMETERS

                          Estimate

Rate of adaptation              16.9060288

Phylogenetic half-life           0.0410000

Phylogenetic correction factor    0.9408495

Stationary variance              3.2600000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 5.4474577 1.3064438

NoNO    2.0547246 0.6663428

NoYES   0.9743304 0.8417862

YesNO   1.0640415 0.3624955

YesYES  0.9768794 0.5240148

MODEL FIT

           Value

Support   -123.64645

AIC       261.29290

AICc       263.36698

SIC       276.18284

r squared   20.81549

SST        78.31732

SSE        62.01519
```

```
> model.fit(ancestor, indata3$time, seq(0.001,0.1, 0.01), seq(3, 3.6, 0.01),              response=
indata3$TLR8, me.response= NULL, fixed.fact=Group_minus_25_MHCII , fixed.cov= NULL,
me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL,
mecov.random.cov=NULL,  intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR9 phylogeny

```
MODEL PARAMETERS

                           Estimate

Rate of adaptation              2.7725887

Phylogenetic half-life          0.2500000

Phylogenetic correction factor    0.6618683

Stationary variance             3.5000000

PRIMARY OPTIMA

          Estimate Std.error

Theta_global 1.410625 0.4140082

MODEL FIT

              Value

Support   -1.187489e+02

AIC       2.434977e+02

AICc       2.439115e+02

SIC       2.498791e+02

r squared -2.289925e-14

SST       6.205816e+01

SSE       6.205816e+01
```

```
> model.fit(ancestor, indata3$time, seq(0.00,0.6, 0.01), seq(1, 10, 0.1), response= indata3$TLR9,
me.response= NULL, fixed.fact=NULL, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL,
random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,  intercept="root",
ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR9 group 0

```
MODEL PARAMETERS

                          Estimate

Rate of adaptation              4.3052620

Phylogenetic half-life          0.1610000

Phylogenetic correction factor    0.7708612

Stationary variance             2.6900000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

        Estimates Std.error

UNKNOWN  4.90548398 0.9785545

NO      1.03000046 0.5615206

YES    -0.02680546 0.4932277

MODEL FIT

            Value

Support   -113.58672

AIC       237.17343

AICc      238.24486

SIC       247.80910

r squared   19.98517

SST        77.39867

SSE        61.93042
```

```
> model.fit(ancestor, indata2$time, seq(0.001,0.24, 0.01), seq(2.4, 3, 0.01), response= indata2$TLR9, me.response= NULL, fixed.fact=Group_0, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR9 group 25

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation             4.3052620

Phylogenetic half-life          0.1610000

Phylogenetic correction factor    0.7708612

Stationary variance             2.7800000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

       Estimates Std.error

UNKNOWN 4.7905910 1.0008819

NO      0.8909195 0.7503926

YES     0.3067360 0.4442190

MODEL FIT

             Value

Support   -114.63289

AIC       239.26577

AICc       240.33720

SIC       249.90144

r squared   17.23875

SST        74.89296

SSE        61.98235
```

```
> model.fit(ancestor, indata2$time, seq(0.001,0.24, 0.01), seq(2.4, 3, 0.01), response= indata2$TLR9,
me.response= NULL, fixed.fact=Group_25, fixed.cov= NULL, me.fixed.cov= NULL,
mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,
intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR9 group 50

```
MODEL PARAMETERS

                    Estimate

Rate of adaptation          4.0534923

Phylogenetic half-life      0.1710000

Phylogenetic correction factor    0.7575823

Stationary variance         2.8200000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

     Estimates Std.error

UNKNOWN 4.7104356 1.0032812

NO     0.2136656 0.5339074

YES    0.5316584 0.5847253

MODEL FIT

          Value

Support   -114.80147

AIC       239.60293

AICc      240.67436

SIC       250.23860

r squared   15.48955

SST       73.48147

SSE       62.09952
```

```
> model.fit(ancestor, indata2$time, seq(0.001,0.2, 0.01), seq(2.4, 3, 0.01), response= indata2$TLR9, me.response= NULL, fixed.fact=Group_50, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR9 group 75

```
MODEL PARAMETERS

                          Estimate

Rate of adaptation             4.3052620

Phylogenetic half-life          0.1610000

Phylogenetic correction factor    0.7708612

Stationary variance             2.7200000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 4.9086983 0.9841078

NO      0.2402895 0.4375494

YES     1.4586448 0.8695819

MODEL FIT

            Value

Support   -113.99901

AIC       237.99802

AICc      239.06945

SIC       248.63369

r squared   18.91388

SST        76.54501

SSE        62.06738

> model.fit(ancestor, indata2$time, seq(0.001,0.28, 0.01), seq(2, 3.4, 0.01), response= indata2$TLR9,
me.response= NULL, fixed.fact=Group_75, fixed.cov= NULL, me.fixed.cov= NULL,
mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,
intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR9 group minus 25

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation             4.0534923

Phylogenetic half-life         0.1710000

Phylogenetic correction factor    0.7575823

Stationary variance            2.7800000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN  4.6624669 0.9972899

NO      0.6239572 0.5167347

YES    -0.1019681 0.6185419

MODEL FIT

           Value

Support   -114.35663

AIC       238.71326

AICc      239.78469

SIC       249.34893

r squared   16.69357

SST        74.53875

SSE        62.09557
```

```
> model.fit(ancestor, indata2$time, seq(0.001,0.24, 0.01), seq(2.4, 3, 0.01), response= indata2$TLR9, me.response= NULL, fixed.fact=Group_minus_25, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR9 group minus 50

```
MODEL PARAMETERS

                          Estimate

Rate of adaptation             4.0534923

Phylogenetic half-life          0.1710000

Phylogenetic correction factor    0.7575823

Stationary variance             2.8000000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

       Estimates Std.error

UNKNOWN  4.7207924 0.9997175

NO      0.4531282 0.4657740

YES    -0.4061054 0.9834336

MODEL FIT

            Value

Support   -114.54596

AIC       239.09192

AICc      240.16335

SIC       249.72760

r squared   16.18313

SST        74.00633

SSE        62.02979

> model.fit(ancestor, indata2$time, seq(0.001,0.24, 0.01), seq(2.4, 3, 0.01), response= indata2$TLR9, me.response= NULL, fixed.fact=Group_minus_50, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR9 + MHC

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation            4.9159375

Phylogenetic half-life        0.1410000

Phylogenetic correction factor    0.7980708

Stationary variance           2.6600000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 4.8358547 1.0086785

No     2.1206591 1.0813497

Yes    0.4504188 0.3750874

MODEL FIT

           Value

Support   -113.96842

AIC       237.93685

AICc      239.00827

SIC       248.57252

r squared   22.41454

SST       80.00114

SSE       62.06925
```

```
> model.fit(ancestor, indata3$time, seq(0.001,0.24, 0.01), seq(2.5, 3, 0.01),     response= indata3$TLR9, me.response= NULL, fixed.fact=indata3$MHCII, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR9 group 0 + MHCII

```
MODEL PARAMETERS

                              Estimate

Rate of adaptation            8.5573726

Phylogenetic half-life        0.0810000

Phylogenetic correction factor    0.8831642

Stationary variance           1.9400000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

       Estimates Std.error

UNKNOWN 5.2355351 0.9269600

NoNO    5.3595659 0.7952621

NoYES   0.6606602 0.7439025

YesNO   0.9759444 0.3906908

YesYES  0.8283597 0.3103422

MODEL FIT

             Value

Support   -106.20238

AIC       226.40476

AICc      228.47883

SIC       241.29470

r squared   53.52633

SST       133.68217

SSE        62.12702
```

```
> model.fit(ancestor, indata3$time,  seq(0.001,0.24, 0.01), seq(1.5, 2.5, 0.01),                response= indata3$TLR9, me.response= NULL, fixed.fact=Group_0_MHCII , fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR9 group 25 + MHCII

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation              5.7284891

Phylogenetic half-life          0.1210000

Phylogenetic correction factor    0.8260016

Stationary variance             2.4100000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 5.2169514 0.9779169

NoNO    3.7279511 1.0997363

NoYES   0.8922586 1.0921411

YesNO   0.2904620 0.6776396

YesYES  0.6353561 0.3476031

MODEL FIT

           Value

Support   -111.52928

AIC       237.05856

AICc      239.13263

SIC       251.94850

r squared   32.69036

SST        92.10708

SSE        61.99694
```

```
> model.fit(ancestor, indata3$time,  seq(0.001,0.24, 0.01), seq(2.2, 3, 0.01),                 response= indata3$TLR9, me.response= NULL, fixed.fact=Group_25_MHCII , fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR9 group 50 + MHCII

```
MODEL PARAMETERS

                              Estimate

Rate of adaptation             5.2911999

Phylogenetic half-life          0.1310000

Phylogenetic correction factor    0.8119587

Stationary variance             2.6000000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

       Estimates Std.error

UNKNOWN 5.0964524 1.0108911

NoNO    1.0000830 1.5794960

NoYES   2.5091732 1.0470249

YesNO   0.5173308 0.4309232

YesYES  0.4629452 0.5190083

MODEL FIT

             Value

Support   -113.51586

AIC       241.03171

AICc       243.10579

SIC       255.92165

r squared   25.71577

SST        83.35805

SSE        61.92189
```

```
> model.fit(ancestor, indata3$time,  seq(0.001,0.24, 0.01), seq(2.2, 3, 0.01),                 response=
indata3$TLR9, me.response= NULL, fixed.fact=Group_50_MHCII , fixed.cov= NULL, me.fixed.cov=
NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,
intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR9 group 75 + MHCII

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation              5.7284891

Phylogenetic half-life           0.1210000

Phylogenetic correction factor    0.8260016

Stationary variance              2.4600000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 5.1795508 0.9855519

NoNO    1.5265383 0.9921389

NoYES   4.2145472 1.3239198

YesNO   0.5368118 0.3411561

YesYES  0.8591806 0.8849256

MODEL FIT

            Value

Support   -112.15606

AIC       238.31212

AICc       240.38620

SIC       253.20206

r squared   31.31560

SST        90.23499

SSE        61.97736
```

```
> model.fit(ancestor, indata3$time,  seq(0.001,0.24, 0.01), seq(2.2, 3, 0.01),                response=
indata3$TLR9, me.response= NULL, fixed.fact=Group_75_MHCII , fixed.cov= NULL, me.fixed.cov=
NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,
intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR9 group minus 25 + MHCII

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation             8.5573726

Phylogenetic half-life         0.0810000

Phylogenetic correction factor    0.8831642

Stationary variance            1.9900000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 5.2313863 0.9393885

NoNO    4.9401744 0.7576044

NoYES   0.3912585 0.8023749

YesNO   0.8823702 0.3001230

YesYES  0.8908535 0.4302339

MODEL FIT

           Value

Support   -106.99338

AIC       227.98675

AICc       230.06083

SIC       242.87669

r squared   52.32525

SST       130.32332

SSE        62.13131
```

```
> model.fit(ancestor, indata3$time,  seq(0.001,0.24, 0.01), seq(1.5, 3.6, 0.01),                 response= indata3$TLR9, me.response= NULL, fixed.fact=Group_minus_25_MHCII , fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,  intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR9 group minus 50 + MHCII

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation              5.2911999

Phylogenetic half-life          0.1310000

Phylogenetic correction factor    0.8119587

Stationary variance             2.4800000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN  4.8799470 0.9823439

NoNO     2.9307760 1.0429763

NoYES   -0.6770935 1.7392722

YesNO    0.5417445 0.3585765

YesYES   0.4117317 0.9292239

MODEL FIT

          Value

Support   -112.04018

AIC       238.08036

AICc      240.15443

SIC       252.97030

r squared   29.16907

SST       87.39151

SSE       61.90021
```

```
> model.fit(ancestor, indata3$time,  seq(0.001,0.24, 0.01), seq(2.2, 2.7, 0.01),                response=
indata3$TLR9, me.response= NULL, fixed.fact=Group_minus_50_MHCII , fixed.cov= NULL,
me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL,
mecov.random.cov=NULL,  intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR22 phylogeny

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation             8.6643398

Phylogenetic half-life         0.0800000

Phylogenetic correction factor    0.8846043

Stationary variance            59.0000000

PRIMARY OPTIMA

           Estimate Std.error

Theta_global 3.740316  1.070306

MODEL FIT

            Value

Support   -211.93005

AIC       429.86009

AICc      430.27389

SIC       436.24150

r squared    0.00000

SST        61.79337

SSE        61.79337

> model.fit(ancestor, indata3$time, seq(0.00,0.5, 0.005), seq(30, 80, 1), response= indata3$TLR22,
me.response= NULL, fixed.fact=NULL, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL,
random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,  intercept="root",
ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR22 group 0

```
MODEL PARAMETERS

                              Estimate

Rate of adaptation             17.3286795

Phylogenetic half-life          0.0400000

Phylogenetic correction factor    0.9422922

Stationary variance            49.4800000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

       Estimates Std.error

UNKNOWN 15.276753  4.837481

NO      5.317817  1.555059

YES     1.698537  1.320510

MODEL FIT

             Value

Support   -207.98755

AIC       425.97510

AICc       427.04653

SIC       436.61077

r squared   13.99005

SST        72.07980

SSE        61.99579
```

```
> model.fit(ancestor, indata2$time, seq(0.01,0.07, 0.01), seq(49.3, 49.6, 0.01),  response= indata2$TLR22, me.response= NULL, fixed.fact=Group_0, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR22 group 25

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation             13.8629436

Phylogenetic half-life          0.0500000

Phylogenetic correction factor    0.9278653

Stationary variance            52.3700000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 15.274336  4.757888

NO      3.363055  1.982522

YES     2.832286  1.248532

MODEL FIT

            Value

Support   -209.393675

AIC       428.787350

AICc      429.858779

SIC       439.423022

r squared    8.857167

SST        68.031163

SSE        62.005530

> model.fit(ancestor, indata2$time, seq(0.01,0.07, 0.01), seq(49.3, 53, 0.01),  response= indata2$TLR22, me.response= NULL, fixed.fact=Group_25, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR22 group 50

```
MODEL PARAMETERS

                          Estimate

Rate of adaptation            17.3286795

Phylogenetic half-life         0.0400000

Phylogenetic correction factor    0.9422922

Stationary variance           49.6500000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 16.059778  4.801144

NO      1.538135  1.404394

YES     4.949255  1.431323

MODEL FIT

            Value

Support   -208.09311

AIC       426.18622

AICc      427.25765

SIC       436.82190

r squared   13.69667

SST        71.83300

SSE        61.99427

> model.fit(ancestor, indata2$time, seq(0.01,0.07, 0.01), seq(49.3, 49.9, 0.01),  response= indata2$TLR22, me.response= NULL, fixed.fact=Group_50, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR22 group 75

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation            17.3286795

Phylogenetic half-life         0.0400000

Phylogenetic correction factor    0.9422922

Stationary variance           43.3500000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 14.896336  4.502874

NO      1.840849  1.025818

YES    10.526348  2.283833

MODEL FIT

           Value

Support   -203.89235

AIC       417.78470

AICc      418.85613

SIC       428.42038

r squared   24.63373

SST        82.27239

SSE        62.00563

> model.fit(ancestor, indata2$time, seq(0.01,0.07, 0.01), seq(43.1, 43.6, 0.01),  response=
indata2$TLR22, me.response= NULL, fixed.fact=Group_75, fixed.cov= NULL, me.fixed.cov= NULL,
mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,
intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR22 group minus 25

```
MODEL PARAMETERS

                          Estimate

Rate of adaptation            13.8629436

Phylogenetic half-life          0.0500000

Phylogenetic correction factor    0.9278653

Stationary variance            51.9400000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

       Estimates Std.error

UNKNOWN 15.152706  4.718837

NO      3.549613  1.308157

YES     1.880127  1.802368

MODEL FIT

              Value

Support   -209.134644

AIC       428.269288

AICc      429.340716

SIC       438.904960

r squared    9.615569

SST       68.594379

SSE       61.998639
```

```
> model.fit(ancestor, indata2$time, seq(0.01,0.07, 0.01), seq(51.8, 52, 0.01),  response= indata2$TLR22, me.response= NULL, fixed.fact=Group_minus_25, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR22 group minus 50

```
MODEL PARAMETERS
                              Estimate
Rate of adaptation            13.8629436
Phylogenetic half-life         0.0500000
Phylogenetic correction factor    0.9278653
Stationary variance           52.1700000
PRIMARY OPTIMA
UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)
       Estimates Std.error
UNKNOWN 15.305218  4.721236
NO      3.189032  1.140366
YES     1.442420  3.043186
MODEL FIT
              Value
Support   -209.275032
AIC       428.550065
AICc      429.621493
SIC       439.185736
r squared    9.205321
SST        68.291969
SSE        62.005474
```

```
> model.fit(ancestor, indata2$time, seq(0.01,0.07, 0.01), seq(52, 52.3, 0.01),  response= indata2$TLR22, me.response= NULL, fixed.fact=Group_minus_50, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR22 + MHCII

```
MODEL PARAMETERS

                              Estimate

Rate of adaptation            23.1049060

Phylogenetic half-life         0.0300000

Phylogenetic correction factor    0.9567191

Stationary variance           49.6700000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

       Estimates Std.error

UNKNOWN 15.449406  5.296066

No      6.339786  1.905175

Yes     2.395662  1.159599

MODEL FIT

             Value

Support   -208.46144

AIC       426.92288

AICc      427.99431

SIC       437.55855

r squared   14.52989

SST        72.54634

SSE        62.00544
```

```
> model.fit(ancestor, indata3$time, seq(0.01,0.07, 0.01), seq(46.8, 50, 0.01),      response= indata3$TLR22, me.response= NULL, fixed.fact=indata3$MHCII, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR22 group 0 + MHCII

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation             23.1049060

Phylogenetic half-life          0.0300000

Phylogenetic correction factor    0.9567191

Stationary variance            47.4500000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 14.370374  5.268514

NoNO     8.044236  2.418499

NoYES    4.010130  2.812764

YesNO    4.281291  1.842147

YesYES   1.248559  1.437704

MODEL FIT

           Value

Support   -207.04178

AIC       428.08356

AICc      430.15763

SIC       442.97350

r squared   18.35575

SST        75.94050

SSE        62.00105
```

```
> model.fit(ancestor, indata3$time, seq(0.01,0.05, 0.01), seq(44, 50, 0.01),                    response=
indata3$TLR22, me.response= NULL, fixed.fact=Group_0_MHCII , fixed.cov= NULL, me.fixed.cov=
NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,
intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR22 group 25 + MHCII

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation             23.1049060

Phylogenetic half-life          0.0300000

Phylogenetic correction factor    0.9567191

Stationary variance            48.6300000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 15.1219338  5.251783

NoNO     7.9505573  2.532362

NoYES    4.5746238  2.642823

YesNO    0.9828537  2.468415

YesYES   2.7853999  1.295901

MODEL FIT

          Value

Support   -207.80551

AIC       429.61103

AICc      431.68510

SIC       444.50097

r squared   16.31934

SST        74.09781

SSE        62.00554

> model.fit(ancestor, indata3$time, seq(0.01,0.05, 0.01), seq(44, 50, 0.01),                 response=
indata3$TLR22, me.response= NULL, fixed.fact=Group_25_MHCII , fixed.cov= NULL, me.fixed.cov=
NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,
intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR22 group 50 + MHCII

```
MODEL PARAMETERS

                              Estimate

Rate of adaptation             23.1049060

Phylogenetic half-life          0.0300000

Phylogenetic correction factor    0.9567191

Stationary variance            48.1500000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

       Estimates Std.error

UNKNOWN 15.633445  5.238683

NoNO     5.158900  3.555368

NoYES    6.712135  2.101357

YesNO    1.129272  1.480123

YesYES   4.255788  1.794038

MODEL FIT

             Value

Support   -207.49638

AIC       428.99275

AICc      431.06683

SIC       443.88269

r squared   17.14967

SST        74.83648

SSE        62.00228
```

```
> model.fit(ancestor, indata3$time, seq(0.01,0.06, 0.01), seq(44, 60, 0.01),                    response= indata3$TLR22, me.response= NULL, fixed.fact=Group_50_MHCII , fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR22 group 75 + MHCII

```
MODEL PARAMETERS

                              Estimate

Rate of adaptation             23.1049060

Phylogenetic half-life          0.0300000

Phylogenetic correction factor    0.9567191

Stationary variance            40.5000000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

       Estimates Std.error

UNKNOWN 15.032341  4.794099

NoNO     5.026109  2.023606

NoYES    9.151258  2.856095

YesNO    1.109897  1.108735

YesYES  13.008162  3.184843

MODEL FIT

             Value

Support   -202.16960

AIC       418.33921

AICc      420.41328

SIC       433.22915

r squared   30.23004

SST        88.97227

SSE        62.07592
```

```
> model.fit(ancestor, indata3$time, seq(0.01,0.06, 0.01), seq(38, 40.5, 0.01),                    response= indata3$TLR22, me.response= NULL, fixed.fact=Group_75_MHCII , fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR22 group minus 25 + MHCII

```
MODEL PARAMETERS

                              Estimate

Rate of adaptation            23.1049060

Phylogenetic half-life         0.0300000

Phylogenetic correction factor    0.9567191

Stationary variance           48.9400000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

       Estimates Std.error

UNKNOWN 14.917277  5.330581

NoNO     7.146068  2.309934

NoYES    4.798604  3.160920

YesNO    2.993395  1.400046

YesYES   1.150329  2.021938

MODEL FIT

             Value

Support   -207.99899

AIC       429.99798

AICc      432.07206

SIC       444.88793

r squared   15.79543

SST        73.62846

SSE        61.99852
```

```
> model.fit(ancestor, indata3$time, seq(0.01,0.05, 0.01), seq(44, 50, 0.01),                    response=
indata3$TLR22, me.response= NULL, fixed.fact=Group_minus_25_MHCII , fixed.cov= NULL,
me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL,
mecov.random.cov=NULL,  intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR22 group minus 50 + MHCII

```
MODEL PARAMETERS

                          Estimate

Rate of adaptation            23.1049060

Phylogenetic half-life         0.0300000

Phylogenetic correction factor    0.9567191

Stationary variance           49.0300000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 14.916259  5.298721

NoNO     6.992132  2.040317

NoYES    2.361683  5.013570

YesNO    2.506920  1.219826

YesYES   1.480402  3.506411

MODEL FIT

           Value

Support   -208.05874

AIC       430.11749

AICc      432.19156

SIC       445.00743

r squared   15.63298

SST        73.49330

SSE        62.00411
```

```
> model.fit(ancestor, indata3$time, seq(0.01,0.05, 0.01), seq(44, 50, 0.01),                    response=
indata3$TLR22, me.response= NULL, fixed.fact=Group_minus_50_MHCII , fixed.cov= NULL,
me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL,
mecov.random.cov=NULL,  intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR25 phylogeny

```
MODEL PARAMETERS
                         Estimate
Rate of adaptation             11.7482573
Phylogenetic half-life          0.0590000
Phylogenetic correction factor    0.9148817
Stationary variance             2.7000000
PRIMARY OPTIMA
          Estimate Std.error
Theta_global 1.021704 0.2229397
MODEL FIT
          Value
Support   -117.4721
AIC       240.9441
AICc       241.3579
SIC       247.3255
r squared    0.0000
SST        62.6399
SSE        62.6399
```

```
> model.fit(ancestor, indata3$time, seq(0.00,0.15, 0.001), seq(1, 10, 0.1), response= indata3$TLR25,
me.response= NULL, fixed.fact=NULL, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL,
random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,  intercept="root",
ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR25 group 0

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation            17.3286795

Phylogenetic half-life         0.0400000

Phylogenetic correction factor    0.9422922

Stationary variance            2.1500000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 4.8602440 1.0083787

NO     1.0701899 0.3241538

YES    0.5886049 0.2752620

MODEL FIT

            Value

Support   -110.74512

AIC      231.49023

AICc      232.56166

SIC      242.12590

r squared   21.83949

SST       79.25891

SSE       61.94917
```

```
> model.fit(ancestor, indata2$time, seq(0.01,0.08, 0.01), seq(1.8, 3, 0.01),   response= indata2$TLR25, me.response= NULL, fixed.fact=Group_0, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR25 group 25

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation            17.3286795

Phylogenetic half-life          0.0400000

Phylogenetic correction factor    0.9422922

Stationary variance             2.1700000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 4.9454882 1.0085298

NO     1.0286538 0.3876642

YES    0.6932093 0.2495884

MODEL FIT

           Value

Support   -111.12050

AIC       232.24099

AICc       233.31242

SIC       242.87666

r squared   20.88742

SST        78.52841

SSE        62.12585

> model.fit(ancestor, indata2$time, seq(0.01,0.08, 0.01), seq(1.8, 3, 0.01),   response= indata2$TLR25,
me.response= NULL, fixed.fact=Group_25, fixed.cov= NULL, me.fixed.cov= NULL,
mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,
intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR25 group 50

```
MODEL PARAMETERS

                          Estimate

Rate of adaptation            17.3286795

Phylogenetic half-life         0.0400000

Phylogenetic correction factor    0.9422922

Stationary variance            2.1400000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 4.9596281 0.9967631

NO     0.5510381 0.2915656

YES    1.0380182 0.2971563

MODEL FIT

           Value

Support   -110.69630

AIC       231.39259

AICc      232.46402

SIC       242.02827

r squared   21.96265

SST        79.62928

SSE        62.14057

> model.fit(ancestor, indata2$time, seq(0.01,0.08, 0.01), seq(1.8, 3, 0.01),   response= indata2$TLR25,
me.response= NULL, fixed.fact=Group_50, fixed.cov= NULL, me.fixed.cov= NULL,
mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,
intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR25 group 75

```
MODEL PARAMETERS

                        Estimate

Rate of adaptation             23.1049060

Phylogenetic half-life          0.0300000

Phylogenetic correction factor    0.9567191

Stationary variance             1.9300000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 5.2370077 1.0103873

NO      0.6168722 0.2122440

YES     2.1608119 0.4634191

MODEL FIT

            Value

Support   -107.77088

AIC       225.54177

AICc      226.61319

SIC       236.17744

r squared   32.25999

SST        91.51601

SSE        61.99296

> model.fit(ancestor, indata2$time, seq(0.01,0.08, 0.01), seq(1.8, 2, 0.01),   response= indata2$TLR25,
me.response= NULL, fixed.fact=Group_75, fixed.cov= NULL, me.fixed.cov= NULL,
mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,
intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR25 group minus 25

```
MODEL PARAMETERS

                          Estimate

Rate of adaptation            17.3286795

Phylogenetic half-life         0.0400000

Phylogenetic correction factor    0.9422922

Stationary variance            2.1800000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 4.9748519 1.0074679

NO      0.8926867 0.2601707

YES     0.5871671 0.3633712

MODEL FIT

            Value

Support   -111.15389

AIC       232.30778

AICc      233.37921

SIC       242.94345

r squared   20.80208

SST        78.16819

SSE        61.90758

> model.fit(ancestor, indata2$time, seq(0.01,0.08, 0.01), seq(1.8, 3, 0.01),   response= indata2$TLR25,
me.response= NULL, fixed.fact=Group_minus_25, fixed.cov= NULL, me.fixed.cov= NULL,
mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,
intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR25 group minus 50

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation            17.3286795

Phylogenetic half-life          0.0400000

Phylogenetic correction factor    0.9422922

Stationary variance             2.1800000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 5.0003525 1.0053592

NO      0.8387468 0.2265925

YES     0.4277453 0.6122499

MODEL FIT

            Value

Support   -111.19170

AIC       232.38339

AICc      233.45482

SIC       243.01907

r squared   20.70535

SST        78.16819

SSE        61.98319
```

```
> model.fit(ancestor, indata2$time, seq(0.01,0.08, 0.01), seq(1.8, 3, 0.01),   response= indata2$TLR25, me.response= NULL, fixed.fact=Group_minus_50, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR25 + MHCII

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation              23.1049060

Phylogenetic half-life           0.0300000

Phylogenetic correction factor    0.9567191

Stationary variance              2.0800000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN  4.990496 1.0837721

No      1.555048 0.3898697

Yes     0.618451 0.2372971

MODEL FIT

           Value

Support   -110.11597

AIC       230.23194

AICc      231.30337

SIC       240.86761

r squared   26.93680

SST        84.91630

SSE        62.04256
```

```
> model.fit(ancestor, indata3$time,  seq(0.01,0.08, 0.01), seq(1.8, 3, 0.01),       response= indata3$TLR25, me.response= NULL, fixed.fact=indata3$MHCII, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR25 group 0 + MHCII

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation             23.1049060

Phylogenetic half-life          0.0300000

Phylogenetic correction factor    0.9567191

Stationary variance             1.9900000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 4.6643980 1.0789381

NoNO    2.0683599 0.4952840

NoYES   0.8537901 0.5760254

YesNO   0.7121886 0.3772530

YesYES  0.5617877 0.2944273

MODEL FIT

           Value

Support   -108.77914

AIC       231.55828

AICc       233.63235

SIC       246.44822

r squared   30.02067

SST        88.75673

SSE        62.11137
```

```
> model.fit(ancestor, indata3$time,  seq(0.01,0.08, 0.01), seq(1.3, 2.8, 0.01),
response= indata3$TLR25, me.response= NULL, fixed.fact=Group_0_MHCII , fixed.cov= NULL,
me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL,
mecov.random.cov=NULL,  intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR25 group 25 + MHCII

```
MODEL PARAMETERS

                              Estimate

Rate of adaptation            23.1049060

Phylogenetic half-life         0.0300000

Phylogenetic correction factor    0.9567191

Stationary variance            2.0300000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

       Estimates Std.error

UNKNOWN 4.9060143 1.0730073

NoNO    1.9682961 0.5173944

NoYES   1.1023082 0.5399630

YesNO   0.4951979 0.5043291

YesYES  0.6525104 0.2647694

MODEL FIT

             Value

Support   -109.37207

AIC       232.74414

AICc      234.81822

SIC       247.63408

r squared   28.66923

SST        87.00783

SSE        62.06336
```

```
> model.fit(ancestor, indata3$time,  seq(0.01,0.08, 0.01), seq(1.3, 2.8, 0.01),
response= indata3$TLR25, me.response= NULL, fixed.fact=Group_25_MHCII , fixed.cov= NULL,
me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL,
mecov.random.cov=NULL,  intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR25 group 50 + MHCII

```
MODEL PARAMETERS

                                  Estimate

Rate of adaptation             23.1049060

Phylogenetic half-life          0.0300000

Phylogenetic correction factor    0.9567191

Stationary variance             2.0600000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

       Estimates Std.error

UNKNOWN 5.0484793 1.0835715

NoNO    1.2000166 0.7353938

NoYES   1.6665774 0.4346457

YesNO   0.4979530 0.3061494

YesYES  0.7953611 0.3710797

MODEL FIT

             Value

Support   -109.76484

AIC       233.52968

AICc       235.60376

SIC       248.41962

r squared   27.75972

SST        85.74073

SSE        61.93935
```

```
> model.fit(ancestor, indata3$time,  seq(0.01,0.08, 0.01), seq(1, 2.5, 0.01),                        response= indata3$TLR25, me.response= NULL, fixed.fact=Group_50_MHCII , fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR25 group 75 + MHCII

```
MODEL PARAMETERS

                         Estimate

Rate of adaptation            23.1049060

Phylogenetic half-life         0.0300000

Phylogenetic correction factor    0.9567191

Stationary variance            1.8500000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 4.8155471 1.0246259

NoNO    1.0017827 0.4324982

NoYES   2.7388718 0.6104231

YesNO   0.5119824 0.2369661

YesYES  1.4982955 0.6806854

MODEL FIT

           Value

Support   -106.45249

AIC       226.90499

AICc       228.97906

SIC       241.79493

r squared   35.08048

SST        95.47346

SSE        61.98091
```

```
> model.fit(ancestor, indata3$time,  seq(0.01,0.08, 0.01), seq(1, 4, 0.01),                          response= indata3$TLR25, me.response= NULL, fixed.fact=Group_75_MHCII , fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL, intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR25 group minus 25 + MHCII

```
MODEL PARAMETERS

                              Estimate

Rate of adaptation            23.1049060

Phylogenetic half-life         0.0300000

Phylogenetic correction factor    0.9567191

Stationary variance            2.0300000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

       Estimates Std.error

UNKNOWN 4.7821822 1.0856518

NoNO    1.8687699 0.4704524

NoYES   0.9558465 0.6437682

YesNO   0.6776808 0.2851401

YesYES  0.4954454 0.4117977

MODEL FIT

             Value

Support   -109.38494

AIC       232.76988

AICc      234.84396

SIC       247.65983

r squared   28.63965

SST        87.00783

SSE        62.08910
```

```
> model.fit(ancestor, indata3$time,  seq(0.01,0.08, 0.01), seq(1.3, 2.8, 0.01),
response= indata3$TLR25, me.response= NULL, fixed.fact=Group_minus_25_MHCII , fixed.cov= NULL,
me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL,
mecov.random.cov=NULL,  intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR25 group minus 50 + MHCII

```
MODEL PARAMETERS

                          Estimate

Rate of adaptation            23.1049060

Phylogenetic half-life         0.0300000

Phylogenetic correction factor    0.9567191

Stationary variance            2.0600000

PRIMARY OPTIMA

UNKNOWN mapped to the root of the tree and includes the coefficent for the ancestral state (Ya)

      Estimates Std.error

UNKNOWN 4.9100324 1.0861097

NoNO    1.6539606 0.4182156

NoYES   0.9515187 1.0276607

YesNO   0.6639259 0.2500348

YesYES  0.2433077 0.7187294

MODEL FIT

            Value

Support   -109.76376

AIC       233.52751

AICc      235.60159

SIC       248.41745

r squared   27.76225

SST        85.74073

SSE        61.93718
```

```
> model.fit(ancestor, indata3$time,  seq(0.01,0.08, 0.01), seq(1.3, 2.8, 0.01),
response= indata3$TLR25, me.response= NULL, fixed.fact=Group_minus_50_MHCII , fixed.cov= NULL,
me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL,
mecov.random.cov=NULL,  intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR9 phylogenetic effect

```
MODEL PARAMETERS

                          Estimate

Rate of adaptation             5.7762265

Phylogenetic half-life         0.1200000

Phylogenetic correction factor    0.6305712

Stationary variance            6.3700000

PRIMARY OPTIMA

          Estimate Std.error

Theta_global 2.324661 0.7098559

MODEL FIT

              Value

Support   -1.183494e+02

AIC       2.426988e+02

AICc      2.430988e+02

SIC       2.491755e+02

r squared -2.221451e-14

SST       6.397104e+01

SSE       6.397104e+01
```

```
model.fit(ancestor, time, seq(0,0.5, 0.01), seq(5, 10, 0.01),  response= TLR9, me.response= NULL, fixed.fact=NULL, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,  intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR9 maximum depth

```
MODEL PARAMETERS

                              Estimate

Rate of adaptation              4.3321699

Phylogenetic half-life          0.1600000

Phylogenetic correction factor    0.5517876

Stationary variance             6.1900000

                    Maxdepth

Predictor theta    7.176028e+02

Predictor variance 2.127460e+07

PRIMARY OPTIMA

Evolutionary regression

         Estimate Std. Error

Intercept  2.55726    0.76584

Maxdepth  -0.00052    0.00020

Optimal regression

        Estimate Std. Error

K         2.40257    0.75533

Maxdepth -0.00093    0.00036

        Bias-corr. regression parameters

K                        2.5572620431

Maxdepth                  -0.0005178823

Decomposition of K assuming Ya = Xa to get the optimal regression intercept Bo

 [1] 2.70278

 (Use this as the intercept when plotting the regression line)

MODEL FIT

Support   -114.709044

AIC       237.418088
```

```
AICc      238.096054

SIC       246.053621

r squared    9.512911

SST        72.640560

SSE        65.730328
```

```
model.fit(ancestor, time, seq(0.05,0.3, 0.01), seq(6.1, 6.3, 0.01),  response= TLR9, me.response=
NULL, fixed.fact=NULL, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov=
Maxdepth, me.random.cov=NULL, mecov.random.cov=NULL,  intercept="root", ultrametric=TRUE,
support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR22 phylogenetic effect

```
MODEL PARAMETERS

                        Estimate

Rate of adaptation          17.3286795

Phylogenetic half-life       0.0400000

Phylogenetic correction factor    0.8526366

Stationary variance         70.6000000

PRIMARY OPTIMA

         Estimate Std.error

Theta_global 4.499373  1.638639

MODEL FIT

          Value

Support   -214.89433

AIC       435.78867

AICc      436.18867

SIC       442.26532

r squared    0.00000

SST        64.02347

SSE        64.02347
```

```
model.fit(ancestor, time, seq(0,0.1, 0.01), seq(60, 100, 0.1),  response= TLR22, me.response= NULL, fixed.fact=NULL, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov= NULL, me.random.cov=NULL, mecov.random.cov=NULL,  intercept="root", ultrametric=TRUE, support=NULL, convergence=NULL)
```

BEST ESTIMATES & MODEL FIT – TLR22 maximum depth

```
MODEL PARAMETERS

                               Estimate

Rate of adaptation             13.8629436

Phylogenetic half-life          0.0500000

Phylogenetic correction factor    0.8200624

Stationary variance            72.1100000

                     Maxdepth

Predictor theta    7.176028e+02

Predictor variance 2.127460e+07

PRIMARY OPTIMA

Evolutionary regression

         Estimate Std. Error

Intercept  2.89181    2.06756

Maxdepth   0.00176    0.00100

Optimal regression

        Estimate Std. Error

K         2.96982    2.04058

Maxdepth  0.00217    0.00122

        Bias-corr. regression parameters

K                          2.891805411

Maxdepth                   0.001762484

Decomposition of K assuming Ya = Xa to get the optimal regression intercept Bo

 [1] 2.689926

 (Use this as the intercept when plotting the regression line)

MODEL FIT

              Value

Support   -213.507480
```

```
AIC       435.014959

AICc      435.692926

SIC       443.650492

r squared    4.743322

SST        67.049714

SSE        63.869330
```

```
model.fit(ancestor, time, seq(0.03,0.06, 0.01), seq(72, 73, 0.01),  response= TLR22, me.response=
NULL, fixed.fact=NULL, fixed.cov= NULL, me.fixed.cov= NULL, mecov.fixed.cov=NULL, random.cov=
Maxdepth, me.random.cov=NULL, mecov.random.cov=NULL,  intercept="root", ultrametric=TRUE,
support=NULL, convergence=NULL)
```

Supplementary table 3 Diversifying selection analyses - results from MEME (mixed effects model of evolution)

TLR3 Selection model

*	AC	1	AT
-	*	AC	1
-	-	*	AT
-	-	-	*

MEME results significance level 0.05

Codon	a	ß-	Pr[ß=ß-]	ß+	Pr[ß=ß+]	p-value	q-value
11	0.3127	0.1638	0.7918	5.9282	0.2082	0.0190	1
14	0	0	0.8081	14.4583	0.1919	0.0061	0.7157
23	0.6057	0.3156	0.9597	65.4143	0.0403	0.0393	1
28	0.2113	0	0.7628	1.8349	0.2372	0.0332	1
31	0.5751	0.0995	0.7785	5.3002	0.2215	0.0222	1
40	0.5945	0	0.7064	3.8732	0.2936	0.0403	1
75	0.6945	0.0492	0.7472	8.6920	0.2528	0.0024	0.3717
84	0	0	0.8840	4.2079	0.1160	0.0278	1
97	0.2739	0	0.7741	3.1438	0.2259	0.0461	1
107	0.3551	0.0407	0.8448	9.0952	0.1552	0.0124	0.9796
145	0.1071	0.0489	0.9038	21.9453	0.0962	0.0002	0.1091
162	0.2529	0.1645	0.6936	9.3461	0.3064	0.0270	1
166	0.3948	0	0.8522	45.9382	0.1478	0.0296	1
241	0.8265	0	0.9437	3728.7500	0.0563	0.0193	1
250	0	0	0.8077	2.3165	0.1923	0.0397	1
339	0.8311	0.3103	0.9587	610.8070	0.0413	0.0393	1
394	0	0	0.3060	2.1701	0.6940	0.0023	0.5341
413	0	0	0.7623	8.2909	0.2377	0.0083	0.7863
414	0.2407	0.0924	0.9640	3333.1100	0.0360	0.0176	1

TLR9 1 Selection model

*	AC	1	AT
-	*	AC	CT
-	-	*	AT
-	-	-	*

MEME results significance level 0.05

Codon	a	ß-	Pr[ß=ß-]	ß+	Pr[ß=ß+]	p-value	q-value
4	0	0	0.5120	5.8732	0.4880	0.0095	0.4929
8	0.1018	0	0.3788	1.6997	0.6212	0.0137	0.4764
103	0.1744	0.1744	0.8010	102.6540	0.1990	0	0.0004
127	0.9911	0.5416	0.8643	18.6733	0.1357	0.0443	1
143	0.4189	0	0.9092	10.6899	0.0908	0.0099	0.4398
154	0.1298	0.1298	0	2.0668	1	0.0308	0.8002
172	0.4630	0	0.9787	110.3240	0.0213	0.0223	0.6317
198	0	0	0.9248	29.8538	0.0752	0	0.0004
229	1.6669	0.3283	0.8809	37.5264	0.1191	0.0133	0.5172
230	0.5929	0.1874	0.8734	20.4878	0.1266	0.0011	0.1116
233	1.0481	0.2233	0.8062	12.3231	0.1938	0.0080	0.4991
239	0.7056	0	0.8957	19.4503	0.1043	0.0045	0.3518
311	0.5993	0.5667	0.9270	38.9681	0.0730	0.0168	0.5227

TLR9 2 Selection model

*	AC	1	AT
-	*	AC	1
-	-	*	AT
-	-	-	*

MEME results significance level 0.05

Codon	a	ß-	Pr[ß=ß-]	ß+	Pr[ß=ß+]	p-value	q-value
2	0	0	0.3209	4.6936	0.6791	0.0189	0.4587
17	0.6945	0.2940	0.9768	304.7330	0.0232	0.0012	0.1025
89	1.4672	0	0.9587	25.6757	0.0413	0.0219	0.4636
92	0.0364	0.0364	0.9812	81.0526	0.0188	0.0203	0.4593
96	0.6880	0	0.9607	24.9478	0.0393	0.0010	0.1087
127	0	0	0	1.0409	1	0.0018	0.0994
137	0.3491	0	0.7918	4.5849	0.2082	0.0032	0.1193
149	0.0859	0	0.7482	7.4237	0.2518	0.0263	0.5242
150	0.2284	0.2284	0.9255	21.6380	0.0745	0.0453	0.7314
173	0.7268	0	0.5647	4.3052	0.4353	0.0270	0.5078
177	0.5215	0.0340	0.8707	27.7355	0.1293	0.0144	0.3749
179	1.2577	0.2557	0.9752	189.8810	0.0248	0.0111	0.3418
181	0.2659	0.0664	0.8804	15.5179	0.1196	0.0017	0.1152
198	0	0	0.6072	9.6686	0.3928	0.0024	0.1139
206	0.5019	0	0.8494	5.0683	0.1506	0.0370	0.6279
218	0.2645	0	0.7688	5.8491	0.2312	0.0009	0.1477
242	0.1431	0	0.8267	10.8630	0.1733	0.0005	0.1734
266	0.2078	0.2078	0.8620	10.6094	0.1380	0.0078	0.2635
268	0.6004	0.1383	0.8141	20.7451	0.1859	0.0030	0.1292
270	0.4748	0.0468	0.9506	40057.0000	0.0494	0.0121	0.3411
276	0.5561	0.2925	0.8429	13.0299	0.1571	0.0312	0.5559
320	0.7292	0.7292	0.8764	17.8974	0.1236	0.0488	0.7517

TLR25 1 Selection model

*	AC	1	AC
-	*	AC	1
-	-	*	AC
-	-	-	*

MEME results significance level 0.05

Codon	a	ß-	Pr[ß=ß-]	ß+	Pr[ß=ß+]	p-value	q-value
5	0.3218	0	0.7954	3.4903	0.2046	0.0392	1
57	0.0621	0	0.5173	2.8724	0.4827	0.0489	1

TLR25 2 Selection model

*	AC	1	AT

-	*	AT	AC
-	-	*	AT
-	-	-	*

MEME results significance level 0.05

Codon	a	ß-	Pr[ß=ß-]	ß+	Pr[ß=ß+]	p-value	q-value
36	0	0	0.1088	1.7258	0.8912	0.0112	0.4987
57	0	0	0	1.4135	1	0.0377	1
67	2.1751	0.2475	0.8339	45.4946	0.1661	0.0094	0.6245
79	0	0	0	1.4386	1	0.0057	0.7617

TLR25 3 Selection model

*	AC	1	AT
-	*	AC	CT
-	-	*	AT
-	-	-	*

MEME results significance level 0.05

Codon	a	ß-	Pr[ß=ß-]	ß+	Pr[ß=ß+]	p-value	q-value
96	0.9550	0.4347	0.8928	30.1618	0.1072	0.0175	0.9273
114	0	0	0.7961	6.6317	0.2039	0.0036	0.3848
117	0	0	0.6883	9.3362	0.3117	0.0305	1
193	0	0	0.9450	29.9778	0.0550	0	0.0073
195	0.7467	0.7467	0.9034	51.5451	0.0966	0.0123	0.8694

TLR25 4 Selection model

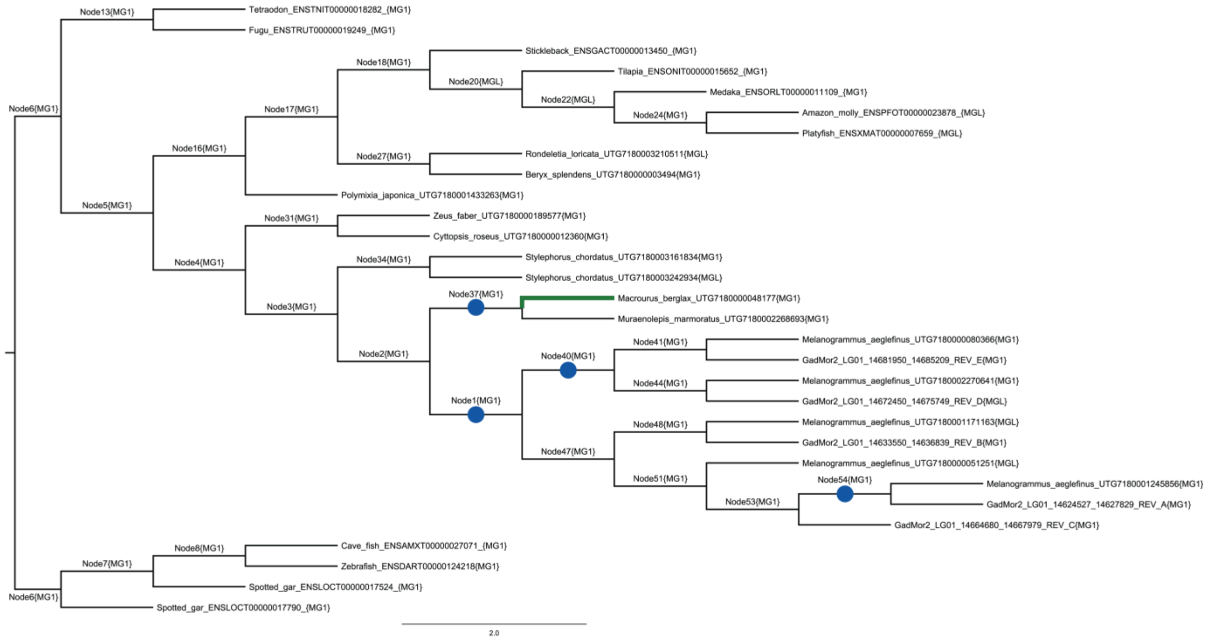
*	AC	1	AC
-	*	AC	1
-	-	*	AC
-	-	-	*

MEME results significance level 0.05

Codon	a	ß-	Pr[ß=ß-]	ß+	Pr[ß=ß+]	p-value	q-value
1	0.2197	0	0.8691	10.1151	0.1309	0.0272	0.9193
10	0.8679	0	0.6632	17.3242	0.3368	0.0065	0.5455
16	0.5304	0.2878	0.8765	18.6946	0.1235	0.0020	0.3359
37	0.2254	0.2254	0.7115	10.9954	0.2885	0.0232	0.9822
62	0.8570	0	0.6552	5.0907	0.3448	0.0305	0.8587
71	0.3064	0	0.9683	120.9230	0.0317	0.0087	0.4929
86	1.5487	0	0.9651	29.8710	0.0349	0.0410	0.9900

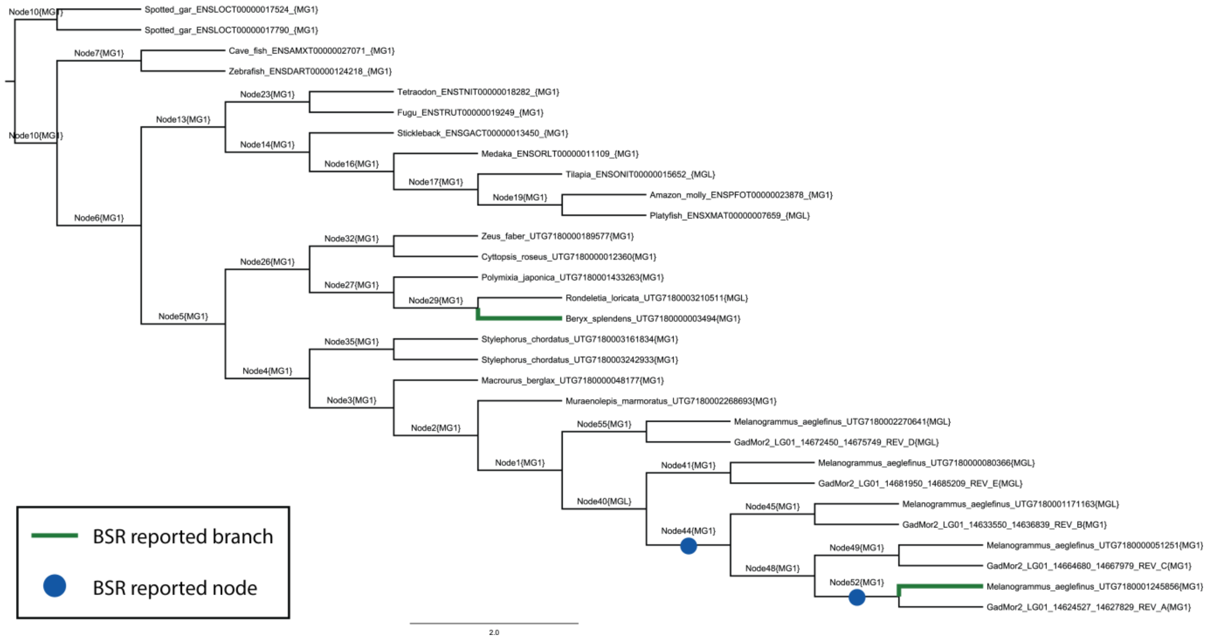
A

TLR9 section 1



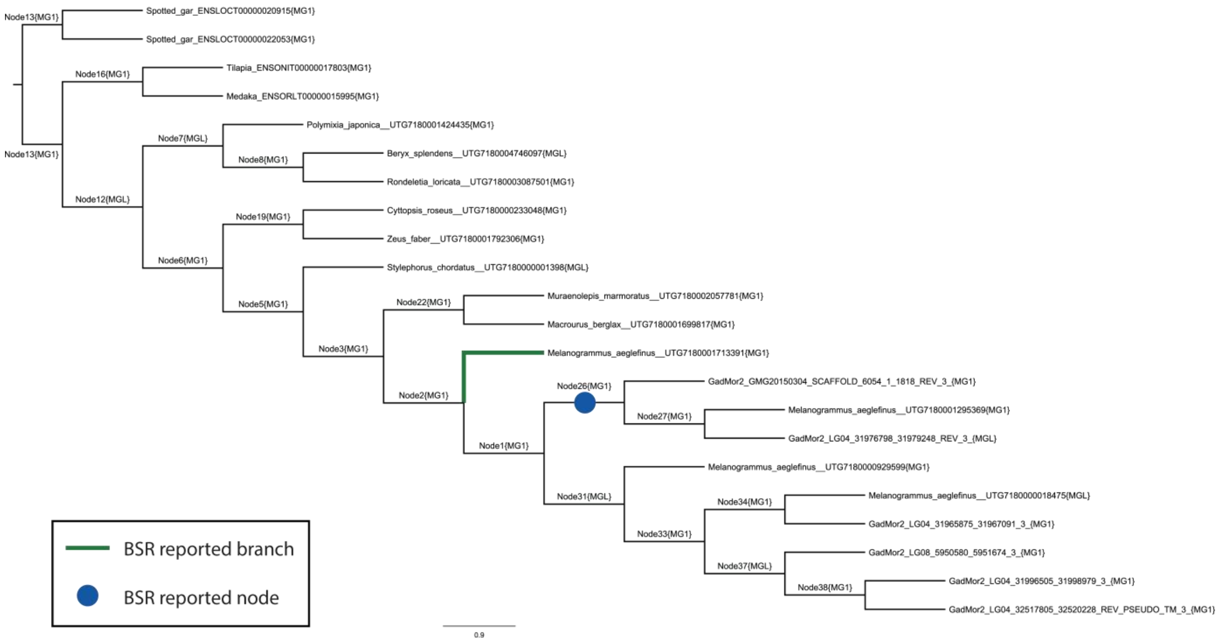
B

TLR9 section 2



Supplementary figure 1 Tree derived from the BSR selection analysis where significantly reported nodes and branches likely to have experience diversifying selection are highlighted. There are two trees representing section 1 (A) and section 2 (B) of the overall TLR9 alignments. The trees were rooted on the sequences from Spotted gar and ordered in FigTree. Colors added in Illustrator.

TLR25 section 3



Supplementary figure 2 Tree derived from the BSR selection analysis where significantly reported nodes and branches likely to have experience diversifying selection are highlighted. The tree represents the BSR analysis performed on section 3 of the overall TLR25 alignment. The tree was rooted on the sequences from Spotted gar and ordered in FigTree. Colors added in Illustrator.