

(A)

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      1      10      20      30      40      50      60      70      80      90     100
Cons.(zebrafish) GCGGA-CGCAGTGGCGCAGTAGGTAGTGTGTCGCCTCACAGCAAGAAGGTCRCCTGGTTCTGAACCTCGGCTGGGTCAGTTGGTGTTCCTGTGTGGAGTTT
b      atttta·GTGT·A·····G·····CATGA·····T·····TG·····T·GA·····CA·····
e      gatgga·····-·····AA·····G·····A·····-·····G·····-·····
h      aggctt·····G·····(GTCGCGGG)2·····G·····-·····AC·····
M89643 accgca·····-·····T·····G·····G·····
U08874 atgtca··TG-·A·····G·····CATGA·T·····-·····C·A·····A··-C·C·····A··-·····-·····C
L42291 aaagga·····AG·····T·····G·····TG·····T·····-·····CA·····

      110     120     130     140     150     160     170     180     190     200
Cons.      GCATGTTCTCCCTGTGTTKGC GTGGTTTCTCCGGTGCTCCGGTTTCCCCAC-AGTCCAAAGACATGCGGTACAGGTGAATTGGGTAAGCTAAA-TT
b      ·····G·····CA·····G·····T·G·A·····A·····A·····T··
e      ·····C·····-·····G·····-·····
h      ·····CC·T·A·····-·····A·····G·····
M89643 ·····C·T·A·····A·····T···T·····T·····TG·····A··
U08874 ·-·-·····T·····G·T·····-·····A·····G·····C·T·····-··
L42291 ·····CC·CA·····C·····T·····-·····G·····A··

      210     220     230     240     250     260     270     280     290     300
Cons.      GTCCATAGTGTATGA-----GTGTGTGTGGRTGTTTCCAGWGATGGGTTGCGGCTGGAAGGGCATCCGCTGCGTAAAAAACATG
b      ·G·····G·····-----ATAA·····A···G·····T···T·····A···A·····A·····T·····CG··
e      ··TGA·····-----GTGTAAATGA·····AA·····A·····T·····-·····G··
h      ·····-----CTTTGTGTGTGAAT·····A·····A·····C·····A·····-T··
M89643 ··AAAGT·A·GGTGTGCGAATATGGTGTGCGAATAA·····ACGG·····T·····A·····C·T··
U08874 ····T·····T-----G···A·····A
L42291 ····G·····C·····-GTGTGTGTGTGAAT·····A·····A·····-----C·····-T··

      310     320     330     340     350     360     370     380     390     400
Cons.      ---CTGGATAAGTTGGCGGTTTCATTCGCTGTGGCGACCCAGATTAATAAAGGGACTAAGCCGAAAAGAAAATGAATGAATGAATGA
b      ---·····T·····-·····T·····A·····G·····G·····ttttat
e      ---·····A·····G·····T·T·G·····T···T·····TATTggaa
h      ---·····T·····T·····C·····ttcagg
M89643 ---·····T·····A·····A·····A·····A·····T·A·CAATGTAATGAcacaag
U08874 TCC·····AT·····A·····CA·····G·····T·····ATGAATGAATGAATGatgtcat
L42291 -----·····T···GG·····C·····C·····C·····gtacac
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(B)

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      1      10      20      30      40      50      60      70      80      90     100
Cons. (rasbora)  GTGGYTCWGTGGTTAGCACTGTTGCCTCACASCAAGAAGGTCCCTGGTTBGAGCCTCGGCTGGGACAGG---CGTCTCTGT-GTDGAGTTTGCATGTTCT
2      atttt...C..T.....C.....A...G...A.....---A.....C...-T.....
3                      catatatataT...GG.....T.....T.....AGT...T.....G....G.....
4      ccat...T..A.....G.....A...-.....C..T..C....A.....-A.....A..AAT.....-att

      110      120      130      140      150      160      170      180      190     200
Cons.          CCCTGTGTCAGCATGGGTCTACGCTGGGTGCTCTGGTTTCTCCCAACRCCCAARKATAWSCRTSATAGGTTAATTGAAYATTCCAAATTGTCACCCMAA
2          .....-----.....G...-GT...AC·G·C.....T.....C..
3          .....A.....AG...TG·A·G.....C.....AAA

      210      220      230      240      250      260      270      280      290     300
Cons.          CTTGTGGATTGTGWMTCGAATAAGACTTGTGTAT-YGACTGACTGCTTCTYGCCAYRAATATAGCCATAGATGCTGGAGTGGMMTTAAGAAARCAAATAAA
2          ·-----·TC.....AT.....C...CA.....CC.....A.....
3          .....AA.....-C.....T...TG.....AA.....G.....

      310      320      330      340      350      360      370      380      390     400
Cons.          YAAA
2          C...CAAACCCtttaaa
3          T...TAAAAACatagg
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Ogiwara et al. Fig 6B

[illegible]

(D)

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      1      10      20      30      40      50      60      70      80      90     100
Cons. (lungfish)  CASTGRTGAMATGGGTAGCATTTGTCRCCTCACAGCGAGAAGTTCTCCGGTTCAATTCTCGGCT-GGGTGCTTTCTGTGCAGAGTTTGCATGT
1                ggттаacaca·····TG·····T·····A·····TG·····T·····-·····G·····
6                gcatttatt·····G·····T·····-·····G·····-·····A·····
5      tgctatGGTG·G·G·AG·T·····A·····A·····C·····-·····G·····CA·····TG·····
4      taatatGGGAGACA·C·A·C·····A·····-·····T·····-·····A·····-·····C·····
2                                ggcatgggttt·····A·····G·····C·····C·····
      110      120      130      140      150      160      170      180      190     200
Cons.      CCTCCCTGCATTTGCGTGGGTTTCTCCRGGTGCTCCAGTTTCTCCACACTCCAAAGACATGCWGTAGGTGGATTGGACACTCTAAATTGCCCATAGG
1          ·····TG·CA·····T·TG·····G·····A·····CA·····A·····T·····T·····
6          ·····-CA·····T·····C·C·A·····-·····G·C·····-·····T·····-CA·····C·····-
5          G·····-CT·T·····-·····T·····A·····CA·C·····gggctgtgca
4          ·····C·T·····T·····TG·····G·····-·····T·····-·····TG·····G·····
2          ·T·····ATG·····A·····C·T·A·····AA·····TT·T·T·····AC·····T·····A·G·····C·····aggatacc
      210      220      230      240      250      260      270      280      290     300
Cons.      --TGTGHGTGTGTGAGTGAAAAAGTGGGATCAGTAATAGGGAGGGTGTATTTGTGGCTGGGTGTTCAHGGTCCTCT-GGATCATTTGCCCAGTAGATTCC
1          --·····A·····A·····A·····A·····A·····A·CA·····-·····
6          TC···ACA·····T··GG··T····TG····C··A····A·····C·A·····C·····A·C···
4          TG·C·T·····A·····-·····T·····-·····
      310      320
Cons.      TATGAA
1          ·····CCTATGAACCTATGtcaagttgt
6          ·····G·····tacattgctgtaaggctct
4          ·····TCTATGAACCTATGctggactga
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(E)

	1	10	20	30	40	50	60	70	80	90	100
Cons. (fugu)	GGCGGCACGGTGGTGTGGTGGTTAGCACTGTTGCCTCACAGCAAGAAGGCCCTGGGTTTCGATCCCCGGTTGGG--AC-TGA-----GGCTG										
18567+595	tatgaa.....G.....T.....A---T-----										
22111+140	ccggtagagtaaattaa...T.....N.....A.....										
6442+8T.....C-----T..										
Cons. (medaka)	GGCTGCACGGTGGTGCAGTGGTTAGCGCTCTTGCCTCACAGCAAGAAGGCCCCCGGTTCAAGTCCCGGCTGGGGGACMTGAAA--CAGAACATCAGYGGG										
AB021490	aaagtctG.....C.....A.....AA.....T..										
D64033	ctctatcattct...A.....T.....C.....A.....A.....C.....AC..										
	110	120	130	140	150	160	170				
Cons. (fugu)	GGGACTTTCTGTGTGGAGTGTGCATGTTCTCCCTGTGCCTGCGTGGGTTCCTCTCCGGGTACTCCGGCTTCCT-----CCCAC										
18567+595T.....C.....										
22111+140	...N.....N.....N.....N.....NN.....										
6442+8N.....N.....N.....										
Cons. (medaka)	GGACCTTTCTGTGTGGAGTTGCATGTTCTCCCTGTGCCTGCGTGGGTTCCTCTCCGGGTCTCCGGCTTCCT-----CCCAC										
AB021490C.....A.....										
D64033T.....G.....A.....T.....AGCTTCCTAGTTTCTAGCTTCCT.....										
	180	190	200	210	220	230	240	250	260	270	
Cons. (fugu)	AGTCCAAAGACATGCATGATTGGGGATTAGGCTAATTGGAAACTC-TAAATTGCCCGTAGGTGTGAGTGTGAGAGAGAATGGTTGTTTGTCTATA-TGTG										
18567+595AA.....										
22111+140	N.....N...A.....C...C.N.N.....C.....N.....N...A...A...N.A.AG.A.G.....NT.NN..										
6442+8N.....N.....T.....G.....G.....										
Cons. (medaka)	YGTCCAAAACATGCTTATAGG-----TTAATTGGAAACTC-TAAATTGWCCATAGGTGTGAGTGTGAGAG-GAATGGGTGTTTGTGTATA-TGTG										
AB021490	CA.....C.....C.....A.....C.G...T.....G...G...A...GAGGACAT										
D64033	T.....G.....T.....C.....C.....T.....A.....A.....AT.....A.....										
	280	290	300	310	320	330	340	350	360	370	
Cons. (fugu)	TTAGCCCTGCGATTGACTGGCGTCCAGTCCAGGGTGTACCC--TGCCTCCGCCCAT-T-GT-GCTGGGATAGGCCTCCAGTCCCCCGCGACCCCTCAGTGA										
18567+595T.....N.....										
22111+140	.N.....A...C.N.....N.....N.N.....N.....T.....										
6442+8M...A...A.....A.....C.....										
Cons. (medaka)	TT---CCTWCGACAGACTGGCGACCTGTCCAGGGTGTCCCC--TGCCTTCG-CCACAAGTGGCTGGGATAGGCTCCAGCAGCCCCGTGACCCCRAAAGGG										
AB021490	CTAA...T.A...A.....T...T.....CC.....G.....G.....										
D64033A.....G.....GC.....A.....										
	380	390	400	410	420						
Cons. (fugu)	GGAACAAGCGGTAGAAAAGTGAG										
18567+595A.....tgaataatttgaagt										
22111+140	C.....A.....TGAGTGAAGTGAAtcaa										
6442+8A.....TGAGggtatttcatgt										
Cons. (medaka)	ATAAAACRG--AAGAAA-TGAA										
AB021490G.TT.....TGAgctctctgggcaac										
D64033A.....A.....TTAatctatttctcacc										