

(A)

	1	10	20	30	40	50	60	70	80	90	100								
Cons. (zebrafish)	GGCGA-CGCAGTGGCGCAGTAGGTAGTGTGCTGCGCTCACAGCAAGAAGGTCRCTGGTCAACCTCGGCTGGTCAGTTGGTGTGTTCTGTGTGGAGTTT																		
b	atttta	GTGT	A	.....	G	.....	CATGA	.....	T	.....	TG	.....	T	GA	.....	CA	.....	.....	
e	gatgga	.....	-	.....	AA	.....	.....	G	.....	A	.....	-	G	.....	.....	.....	.....	.....	
h	aggctt	.....	-G	.....	.....	.....	(GTCGCGGG)2	.....	G	.....	.....	.....	G	.....	.....	AC	.....	.....	
M89643	accgca	.....	-	.....	T	.....	.....	G	.....	G	.....	.....	G	.....	.....	.....	.....	.....	
U08874	atgtca	TG	-A	.....	G	.....	CATGA	T	.....	C	A	.....	A	-C	C	.....	A	-	C
L42291	aaagga	.....	AG	.....	T	.....	.....	G	.....	TG	.....	T	.....	CA	.....	CA	.....	.....	
	110	120	130	140	150	160	170	180	190	200									
Cons.	GCATGTTCTCCCTGTGTTKGCGTGGGTTCCCTCCGGGTGCTCCGGTTCCCCAC	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
b	.....	G	.....	CA	.....	G	.....	.....	T	G	A	.....	.....	A	.....	A	.....	.....	T
e	.....	.....	.....	C	.....	.....	.....	G	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
h	.....	.....	CC	T	A	.....	.....	.....	.....	.....	.....	.....	.....	A	.....	G	.....	.....	.....
M89643	.....	.....	C	T	.....	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	.....	.....	GTGTGTGTTGGRTGTTCCCAGWGATGGTTGGGCTGGAAAGGGCATCCGCTGCGTAAAAAACATG	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
b	.....	G	.....	.....	ATAA	.....	A	G	.....	T	.....	T	.....	A	.....	A	.....	T	CG
e	.....	TGA	.....	.....	GTGTAATGA	.....	AA	.....	A	.....	A	.....	T	.....	.....	G	.....	.....	.....
h	.....	.....	.....	CTTTGTGTGAAT	.....	A	.....	A	.....	.....	C	.....	A	.....	.....	T	.....	.....	.....
M89643	.....	AAAGT	A	GGTGTGCGAATATGGTGTGCGAATAA	.....	ACGG	.....	T	.....	.....	.....	.....	A	.....	C	T	.....	.....	.....
U08874	.....	T	.....	T	.....	.....	.....	.....	.....	.....	G	.....	A	.....	A	.....	A	.....	.....
L42291	.....	G	.....	C	.....	GTGTGTGTGTGAAT	.....	A	.....	A	.....	.....	C	.....	-T	.....	.....	.....	.....
	310	320	330	340	350	360	370	380	390	400									
Cons.	---CTGGATAAGTGGCGGTTCA	TTCCGCTGTGGCGACCC	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
b	.....	.....	T	.....	.....	.....	.....	.....	.....	.....	T	.....	A	.....	G	.....	ttttat	.....	.....
e	.....	.....	.....	A	.....	.....	G	.....	T	T	G	.....	T	.....	.....	TATTggaa	.....	.....	.....
h	.....	.....	.....	.....	T	.....	.....	.....	T	.....	C	.....	T	.....	.....	ttcagg	.....	.....	.....
M89643	.....	.....	T	.....	.....	A	.....	.....	A	.....	A	.....	T	.....	A	CAATGTAATGAcacaag	.....	.....	.....
U08874	TCC	.....	.....	AT	.....	A	.....	CA	.....	.....	G	.....	T	.....	.....	ATGAATGAATGAATGAtgtcat	.....	.....	.....
L42291	.....	.....	.....	.....	T	.....	GG	.....	C	.....	C	.....	C	.....	.....	gtacac	.....	.....	.....

Ogiwara et al. Fig 6A

**(B)**

1 10 20 30 40 50 60 70 80 90 100  
Cons. (rasbora) GTGGYTCWGTGGTTAGCACTGTTGCCTCACASCAAGAAGGTCCCTGGTTBGAGCCTCGGCTGGGACAGG---CGTCTCTGT-GTDGAGTTGCATGTTCT  
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. CCCTGTGTCAGCATGGGTCTACGCTGGGTGCTCTGGTTCCCTCCACCRCCCAARKATAWSCRTSATAGGTTAATTGAAYATTCCAAATTGTCACCCMAA  
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-YGACTGACTGCTCTYGCCAYRAATATAGCCATAGATGCTGGAGTGGMMTTAAGAACCAAATAAA  
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...CAAACCCttaaa  
3 T...TTAAAAACatagg

Ogiwara et al. Fig 6B

(C)

1 10 20 30 40 50 60 70 80 90 100  
Cons. (lamprey) GTGHDATGGGTGGYCCAGKKGTAAHACTTGHGCCTCGCAGDAAGAAGGCGCTGGGTCGATTCCAAHTCGGVYGCCTTCTGYRTGRAGTTGTAYG  
3 tgatgtat...CAT.....CG...TG...GT...C.....T.....T.....TG...C...ACA.....CG...G...C...T...  
4 tttggat...AAT...C...T...T...A...AA...G.....T...A...GCT...T...CA...TAC...T...  
1 ggtgtcA...G...TG...A...GT...GT...CT...C...T...G...A...ATG...T...GAT...AT...A...CT...CG...TG...A...  
6 ctgaactca...CAT...T...GCG...GAGTTT...A...TCC  
2 taaccctgac...T...AA...T...A...TG...G...G...C...  
110 120 130 140 150 160 170 180 190 200  
Cons. TTCTCCCCCTGTTCTGCGTGGGTTCCCTCCGGTTCTCCGGTTCCCTCCCATAGCTAAA-----TTGGSMAAACATYC  
3 ...A...G...T...G...T...T...A...A...A...A...-----GGTCTTGG...GC...GGT...A...  
4 ...A...T...T...C...C...TAA...A...A...CAAAAAGTACAATGT...AAGTGGT...A...GA...T...T...  
1 ...TA...C...G...G...A...T...A...G...GAATGCACCGTGTGC...CGGGAAATGGA...AA...CG...T...T...  
6 C...G...C...A...T...A...A...T...G...T...C...C...TACCAACCACATACAATGTTCCCTGCTG...CT...C...  
2 ...C...A...TA...A...T...G...T...C...C...TATAAGTACAATGA...AATTGCTT...CC...CC...  
210 220 230 240 250 260 270 280 290 300  
Cons. CAATGCTGAAACHTG-ASCTG-CAAAACTGTTMAATTGGGATKACACA-CAGC-AGCA  
3 ...AC...T...C...C...A...AA...T...ACAtggctcccgatttgaaaacttggcaa  
4 ...GA...T...G...A...A...G...CAGCATCAatacttggcagcacccatttcagaag  
1 ...A-T...CG...C...G...GTC...CGG...G...G...G...G...GCAGCGAGCAGCAAggtggtcgcctc  
6 ...G...T...G...GC...T...C...G...TTA...GA...C...G...T...A...T...caaaacaccctctcataaacaacagtttc  
2 ...aatcgcaggaccc

Ogiwara et al. Fig 6C

**(D)**

1 10 20 30 40 50 60 70 80 90 100  
Cons. (lungfish) CASTGRTGAMATGGGTAGCATTGTCRCCCTCACAGCGAGAAGTTCTCCGGTTCAATTCTCGGCT-GGGTGCTTCTGTGCAGAGTTGCATGT  
1 ggttaacaca.....TG.....T.....A.....TG.....T.....-.....G.....  
6 gcatttt.....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 ggcattggttt.....A..G.....C.....C..C.....  
110 120 130 140 150 160 170 180 190 200  
Cons. CCTCCCTGCATTCGCTGGGTTYCTCCRGGTGCTCCAGTTCCCTCCACACTCCAAAGACATGCWGTAGGTGGACTCTAAATTGCCCATAGG  
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. --TGTGHTGTGTGAGTGAAGAAGTGGGATCAGTAATAGGGAGGGTGTATTGTGGCTGGGTGTTCAHGGTCTCT-GGATCATTGCCAGTAGATTCC  
1 --..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 .....CCTATGAACCTATGtcaaggtt  
6 .....G.....tacattgctgtaaggct  
4 .....TCTATGAACCTATGctggactga

(E)

1 10 20 30 40 50 60 70 80 90 100  
Cons. (fugu) GGCGGCACGGTGGTGTGGTTAGCACTGTCCTCACAGCAAGAAGGCCCTGGGTTGATCCCCGGTTGGG--AC-TGA-----GGCTG  
18567+595 tatgaa.....G.....T.....A.....T.....  
22111+140 ccggtagagtaaaataa.....T.....N.....A.....  
6442+8 .....T.....C.....  
Cons. (medaka) GGCTGCACGGTGGTGCAGTGGTAGCGCTTGCCTCACAGCAAGAAGGCCCGGTTCAAGTCCGGCTGGGGACMTGAAA--CAGAACATCAGYGGG  
AB021490 aaagtctG.....C.....A.....AA.....T.....  
D64033 ctctatcattct.....A.....T.....C.....A.....A.....C.....C.....AC.....  
110 120 130 140 150 160 170  
Cons. (fugu) GGGACTTTCTGTGGAGTGTGCATGTTCTCCCTGTGCCTGCGTGGGTCTCTCCGGGTACTCCGGCTTCCT-----CCAC  
18567+595 .....T.....C.....  
22111+140 .....N.....N.....N.....N.....NN.....  
6442+8 .....N.....N.....N.....N.....  
Cons. (medaka) GGACCTTTCTGTGGAGTTGCATGTTCTCCCTGTGCCTGCGTGGGTCTCTCCGGGTCTCCGGCTTCCT-----CCAC  
AB021490 .....C.....A.....  
D64033 .....T.....G.....A.....T.....AGCTTCCTAGTTCTAGCTTCCT.....  
180 190 200 210 220 230 240 250 260 270  
Cons. (fugu) AGTCCAAAGACATGCATGATTGGGATTAGGCTAATTGGAAACTC-TAAATTGCCCTAGGTGTGAGTGTGAGAGAGAATGGTTGTTGTCTATA-TGTG  
18567+595 .....AA.....  
22111+140 N.....N.....A.....C.....C.....N.....C.....N.....N.....A.....A.....N.....A.....AG.....A.....G.....NT.....NN.....  
6442+8 .....N.....T.....A.....G.....  
Cons. (medaka) YGTCCAAAACATGCTTYATAGG-----TTAATTGGAAACTC-TAAATTGCCATAGGTGTGAGTGTGAGAG-GAATGGGTGTTGTCTATA-TGTG  
AB021490 CA.....C.....C.....A.....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) TTAGCCCTCGATTGACTGGCGTCCAGTCAGGTGTACCC--TGCCTCCGCCATT-GT-GCTGGGATAGGCTCAGTCCCCCGCGACCCTCAGTGG  
18567+595 .....T.....N.....  
22111+140 ..N.....A.....C.....N.....N.....N.....N.....N.....N.....T.....  
6442+8 .....M.....A.....A.....A.....A.....C.....  
Cons. (medaka) TT---CCTWCACAGACTGGGACCTGTCCAGGGTGTCCCC--TGCCTTCG-CCACAAGTGGCTGGGATAGGCTCAGCAGCCCCGTGACCCRAAGGG  
AB021490 .CTAA.....T.....A.....T.....T.....CC.....G.....G.....  
D64033 .....A.....G.....GC.....A.....  
380 390 400 410 420  
Cons. (fugu) GGAACAAGCGGTAGAAAGTGAG  
18567+595 .....A.....tgaataatttggaaagt  
22111+140 C.....A.....TGAGTGAGTGAGtcaa  
6442+8 .....A.....TGAGggatttcatgt  
Cons. (medaka) ATAAAACRG--AAGAAA-TGAA  
AB021490 .....G.....TT.....TGAgctctggcaac  
D64033 .....A.....TTAatctattctcacc