Supplementary Data

Title

Star-PAP controlled Alternative Polyadenylation coupled PA-tail length regulates

protein expression in Hypertrophic heart

Supplementary Figure Legends:

Supplementary Figure 1: UTR sequence of respective *NQO1* PA-site (proximal, distal and middle) and control *SV40* UTR. PA-site, cleavage site, Star-PAP binding motif, and downstream sequence along with various mutations introduced are indicated.

Supplementary Figure 2:(A-D) 3'-RACE assay of Star-PAP target mRNAs with multiple PA-sites (*PTBP2, ANXA7, FOG2, PAK1*). (E) 3'-RACE assay of *NQO1* UTR or control *GAPDH* UTR in the presence of CKI α knockdown after treatment of tBHQ, TCDD or DMSO as indicated. (F) Western blot analysis of NQO1 protein under conditions as in E. Each blot is representative of n=3 independent experiments. (G) 3'-RACE assay of *NQO1* after transfection with various NQO1 mini-gene reporter constructs (proximal, middle, distal and *SV40* driven) in the presence or absence of Star-PAP knockdown and treatment with tBHQ (100 μ M for 4 hour) or TCDD (100 nM for 24 hours). (H-I) Western blot analysis of FLAG NQO1 after transfections of various reporter constructs as indicated as in G.

Supplementary Figure 3: (A) RNA sequence analysis upstream of each PAsites on *NQO1* UTR. Reg RNA2 was used to scan for regulatory sequences and miRNA sites were probed using miRDB. Key sequence element considered that is likely to affect mRNA stability at the UTR (RBS-ribosome binding site, ARE-AU rich element, UTRM-UTR motif (that includes mushashi element, PIWI RNA and more), RES-RNA editing site, RSriboswitches, LS-long stem, RHR-ncRNA hybridisation region) is indicated. (HSS-human splice site, ESE-exon splicing enhance, ESS-exon splicing silencer, ISE-intron splicing enhancer, ISS-intron splicing silencer). Potential miRNA sequences and PIWI motif detected are shown below. (B) Agarose gel analysis of residual RNA templates of short and long A tailed *NQO1* RNA after in vitro translation as in Figure 2M. (C) Western blot analysis of FLAG NQO1 after treatment of reporter *NQO1* distal PA-site specific construct transfected HEK 293 cells with 100 μM cordycepin for various time points as indicated.

Supplementary Figure 4: (A) Analysis of GC and AT composition at *NQO1*, *BIK*, and *GCLC* UTRs upstream of the PA-signal as indicated. (B) Analysis of nucleotide composition (U, G, A and C) downstream of each *NQO1*, *BIK*, *GCLC* and *GAPDH* PA-sites. (C) qRIP analysis of PAP occupancy around the PA-sites within the target mRNA 3'-UTR. The primer sets used for qRIP are illustrated as arrows. The expression of the ORF of target genes was used as internal control (Internal). Error bars represent standard error of the mean of 3 independent experiments with triplicates for each experimental condition. (D-E) Quantification and the in vitro cleavage assay with nuclear extracts after control or siRNA Star-PAP knockdown. Relative intensities (in arbitrary units) for cleaved fragments were expressed as fraction cleavage relative to total intensity of both uncleaved and cleaved fragments. Error bar represents SEM, n=3 independent experiments. Upstream fragment (Cup) and downstream fragment (Cdn) after the cleavage of the template are indicated.

Supplementary Figure 5: (A) Phase contrast (PC) and IF imaging of phalloidin stained H9c2 cells after treatment with TCDD at various time points with two different concentrations (10 nM and 100 nM) as indicated along with control isoproterenol (100 μ M for 48 hours)to test induction of hypertrophy. Quantification of cell surface area of the phalloidin stained H9c2 cells are shown B. Average cell surface area was measured for >50 cells per experiment for n>3 independent experiments (p value - 0.001 for DMSO, Isoproterenol, 4 hr TCDD (10 nM), and 0.005 for 88 hours and 72 hours respectively with TCDD 100 nM. Error bar represents SEM. (C-D) Western blot analysis of various hypertrophic markers, and NQO1 after TCDD treatment for different time points as indicated as in A. Each blot is representative of n = 3 independent experiments. (E) Western blot

analysis of Star-PAP, NQO1 and molecular marker SERCA2A from Wistar rat heart at progressive time points of hypertrophic induction (early, mid and late hypertrophy). (F) 3'-RACE assay of *NQO1* APA from control and hypertrophic heart tissue from Wistar rat as in Fig. 4F.Each gel is representative of n=3 independent experiments.

Supplementary Figure 6: Sequence comparison of the *NQO1* 3'-UTR regions of human and rat. Three NQO1 PA-signals (proximal, middle, and distal), along with the Star-PAP binding sites upstream of the distal PA-site in both rat and human are indicated.

List of antibodies:

Rabbit monoclonal anti-FLAG (Sigma), Rabbit monoclonal anti-β-Tubulin (Santacruz), Rabbit polyclonal anti-PIPKIα (Mohan *et. al.* 2015), Rabbit polyclonal anti-Star-PAP (Mohan *et. al.* 2015), Rabbit polyclonal anti-PAPOLA (Bethyl lab), Rabbit polyclonal anti-PAPOLG (Bethyl lab), Mouse monoclonal anti-NQO1 (Novus), Mouse monoclonal anti-SERCA2A (Santa Cruz), Goat polyclonal anti-ANP (Santacruz), Mouse monoclonal anti-GAPDH (Santa Cruz), Rabbit polyclonal anti-RNA Polymerase II (Bethyl lab) and Rabbit polyclonal anti-CKIα (Bethyl lab), and Mouse monoclonal anti-SKA (Santa Cruz) were used for Western blot, IP or RIP experiments.

List of Primers:

qRT-PCR (Human):

 NQ01 FP: 5'-GAACTTCAATCCCATCATTTCCAG-3' RP: 5'-CAGCTTCTTTGTTCAGCCACAAT-3'
FLAG-NQ01 FP: 5'-ATGGATTACAAGGATGACGACG-3' RP: 5'-CCTCCTTCATGGCATAGTTGAA-3'

3. GCLC	FP: 5'-AAGTTCTTGAAACTCTGCAAGAGAAGG-3'
	RP: 5'-GCCTCAACTGTATTGAACTCGGAC-3'
4. GAPDH	FP: 5'-GAAGGTCGGAGTCAACGGATTT-3'
	RP: 5'-GAATTTGCCATGGGTGGAAT-3'

qRT-PCR (Rat):

1. ANP:	FP: 5'- TATACAGTGCGGTGTCCAAC-3'
	RP: 5'-TCTCTGAGACGGGTTGACTT-3'
2. BNP:	FP: 5'-AACAATCCACGATGCAGAAG-3'
	RP: 5'-GTGCCATCTTGGAATTTCG-3'
3. SERCA2A	FP: 5'-TTCGAAGTCTGCCTTCTGTG-3'
	RP: 5'-CTCCAATGGGTGCATAGGTT-3'
4. <i>β-MHC</i>	FP: 5'-ACAAGTTTGGCCACACCAA-3'
	RP: 5'-TGTTCCACTGGATAATCAGCA-3'
5. NQO1	FP: 5'-AAGGCTGGTTTGAGAGAGTG-3'
	RP: 5'- ATTGGCCAGAGAATGACGTT-3'
6. Star-PAP	FP: 5'-AGACCCACAGACTCCAAAGC-3'
	RP: 5'-GTCAGAGCCCAAAGCAGAGT-3'
7. GAPDH	FP: 5'-CCATGTTTGTGATGGGTGTG-3'
	RP: 5'-ACAGTCTTCTGAGTGGCAGTGA-3'
9. <i>α-MHC</i>	FP: 5'- TGCGGGTGAAGAAGAAGA-3'
	RP: 5'- TCTCCTTCAGGTCGTCATTG-3'
2/ DACE (II	man).

3'- RACE (Human):

1.	NQO1	5'-AACTTCCAGGCAGGATTCTTA-3'
2.	GAPDH	5'-TTTGGCTACAGCAACAGGGT-3'
3.	ANXA7	5'-TCCGGAATCCCTCTAAGTCT-3'

- 4. PAK1 5'-GGCTCTGTCAAGCTAACTGA-3'
- 5. FOG2 5'-GGCACAGTCTAAATCGAAAC-3'
- 6. *PTBP2* 5'-CCTTGCATTGTAATATTCAGTTT-3'

3'- RACE (Rat):

- 1. NQO1 5'-GTGTACAGCATTGGCCACA-3'
- 2. GAPDH 5'-GTGGACCTCATGGCCTACA-3'

Polysome Profiling (Human):

1. <i>NQO1</i>	FP: 5'-GAACTTCAATCCCATCATTTCCAG-3'
	RP: 5'-CAGCTTCTTTTGTTCAGCCACAAT-3'

2. *FLAG-NQO1*FP: 5'-ATGGATTACAAGGATGACGACG-3'

RP: 5'-CCTCCTTCATGGCATAGTTGAA-3'

3. *GAPDH* FP: 5'-GAAGGTCGGAGTCAACGGATTT-3' RP: 5'-GAATTTGCCATGGGTGGAAT-3'

Polysome Profiling (Rat):

1. NQO1	FP: 5'-AAGGCTGGTTTGAGAGAGTG-3'		
	RP: 5'- ATTGGCCAGAGAATGACGTT-3'		
2. GAPDH	FP: 5'-CCATGTTTGTGATGGGTGTG-3'		
	RP: 5'-ACAGTCTTCTGAGTGGCAGTGA-3'		

In vitro cleavage (Human):

1.	NQO1	Clv FP: 5'-TGCCTTCATCTTCACTGCAA-3'
		Clv RP: 5'-TTGTCAAGCCAGTCACCAAG-3
2.	GCLC	Clv FP: 5'-ATGCCTGGTTTTCGTTTGCA-3'
		Clv RP: 5'-AGCTGTGGAACTCACACACACTCA-3'
3.	GAPDH	Clv FP: 5'-CACACTGAATCTCCCCTCCT-3'

Clv RP: 5'-TTGACACAAGCCCAGCTTC-3'

cRACE and Sequencing:

1.	NQO1-outer	FP	5'-ACTCACTCGGTCATGCTAGT-3'
		RP	5'-GCTCGACCTTTTGGAGGAAA-3'
2.	NQO1-inner	FP	5'-AGGCCGACGTTGGAACACCC-3'
		RP	5'-TATAAAACAACGGAAGTAGA-3'
3.	M13 Sequenc	ing	5' CAGGAAACAGCTATGAC-3'

In vitro translation:

NQ01 FL FP:5'-GGCAAGCTTCGCCACCATGGATTACAAG-3' RP: 5'-CCCGGATCCACTAGTTTTTTTTTTTTG GTACCTTAATTAAGGTA-3' NQ01 TRNC RP: 5'-CCCGGATCCACTAGTTTTTTTTTTTTTT CACCAGTGGTGATGGAAA-3'

siRNA Oligos:

1.	Control scrambled non-targeting	:AGGUAGUGUAAUCGCCUUG
2.	Star-PAP	:GUGUGUUUGUCAGUGGCUU
3.	ΡΙΡΚΙα	: GAAGUUGGAGCACUCUUGG
4.	CKIα	: On target Smart pool (Dharmacon)
5.	ΡΑΡα	: GGAGACUGACUGCGUACUU
6.	ΡΑΡγ	:On target Smart pool (Dharmacon)

Poly A Distal UTR		
-120Star-PAP binding region		
CACUGGUGGUUUUUGCUCUCGACAGUAUCCACAAUAGCUGACGGCUGGGUGUUUCAGUUUGĂAA <u>ĂUA</u>		
(USE)60 Binding motif		
<u>UUUUGUUGCCUUCAUCUUCACUGCAA</u> UUUUGUGUAAAUUUCUCAAAGAUCUGAAUUAAAUA <u>AAUAAA</u>		
CSSub optimal DSE PAS		
AUUCAUUUCUACAGACCCACACUCAUUGGUAUCAGUGAAGCUAAUGAUAGUGGAAUCUAGUGGGAGG		
Poly A Distal Mutation		
-120Star-PAP non-binding region		
CACUGGUGGUUUUUGCUCUCGACAGUAUCCACAAUAGCUGACGGCUGGGUGUUUCAGUUUGAAAAUA		
(USE)		
UUUUGUUGCCUUCAUCUUCACUGCAAUUUUGUGUAAAUUUCUCAAAGAUCUGAAUUAAAUA <u>AAUAAA</u>		
CSDSE with CstF binding region AUUCAUUUCUACAGACCCAC <mark>A</mark> CUCAUUGGUAUCAGUGAA <u>UUUUUU</u> GAUAGUGGAAUCUAGUGGGAGG		
Poly A Proximal UTR		
-120 Equivalent USE (Star-PAP non-binding)		
UAGAAAAUGAGAUUCCTTAGCCUGGAUUUCCUUCUAACAUGUUAUCAAAUCUGGGUAUCUUUCCAGG		
60 PAS		
CUUCCCUGACUUGCUUUAGUUUUUAAGAUUUGUGUUUUUCUUUUUCCACAAGG <u>AAUAAA</u> UGAGAGGG		
CSDSE with CstF binding region AAUCGACUGUAUUCGUGCAUUUUUGGAUCAUUUUUAACUGAUUCUUAUGAUUACUAUCAUGGCAUAU		
Poly A Proximal Mutation		
-120 Equivalent USE (Star-PAP hinding)		
UAGAAAAUGAGAUUCCTTAGCCUGGAUUUCCUUCUAACAUGUUAUCAAAUAUUUUUAUCUUUCCAGG		
Binding motif PAS		
CUUCCCUGACUUGCUUUAGUUUUUAAGAUUUGUGUUUUUCUUUUUCCACAAGGAAUAAAUGAGAGGG		
CSSub optimal DSE		
AAUCGACUGUAUUCGUGCAUUUUUGGAUCAUUUUUAACUGAUUCUUAUGAUUACUAUCAUGGCAUAU		
Poly A Middle UTR		
-120Equivalent USE		
AUUACAAAGCAGUUACUAAUAUGCCUAGCACAAGUACCACUCUUGGUCAGCUUUUGUUGUUGCACAA		
(Star-PAP non-binding)		
GUACCACUCUUGGUCAGCUUUUGUUGUUUAUAUAUACAGUACACAGAUACCUUGAAAGGAAGAGCUAAU		
CSDSE with CstF binding region		
Poly A SV40 UTR PAS		
AAUGAAUGCAAUUGUUGUUGUUAACUUGUUUAUUGCAGCUUAUAAUGGUUACAAAUAAAGCAAAUAG		
DSE with CstF binding region		
CAUCACAAAUUUCACAAAUAAAGCĂ <u>UUŬUUU</u>		







	Proximal	Middle	Distal	С
miRNA binding sites	1	6	4	Tim
AU rich elements	0	0	0	1111
piwi interacting RNA	0	5	0	α·F
₽)	M	D	β -Tu
a-miR-6833-5p (98) h	sa-miR-5197-3	p (97) hsa-miR-0	3833-5p (98)	A-ta
h	sa-miR-18b-3p	(97) hsa-miR-	1237-3p (94)	
h	sa-miR-1237-3	p (94) hsa-miR-4	4659b-5p (81)	
h	sa-miR-3613-3	p (84) hsa-miR-0	605-3p (82)	

hsa-miR-2114-5p (82) hsa-miR-3908 (81)

hsa-m

Cordycepin treatment ïme(hr) 0 8 10 12 4 6 24 2 ι·FLAG Tubulin -tail 36 12 nd 70 _





1	GGAAGAAACGCCTGGAGAATATTTGGGATGAGACACCACTGTATTTTGCTCCAAGCAGCC	Hsapiens	TGACCTCAGGTGATCC
1	GGAAGAAGCGTCTGGAGACTGTCTGGGAGGAGGAGTCACCACTCTACTTTGCTCCAAGCAGCT	Rnorvegicus	
61	TCTTTGACCTAAACTTCCAGGCAGGATTCTTAATGAAAAAAGAGGTACAGGATGAGGAGA	Hsapiens	GCTGGGATTACAG
61	TGTTTGACCTAAACTTCCAGGCAGGATTCTTACTGAAAAAAGAGGTTCAAGAGGAGCAGA	Rnorvegicus	CCAAAATGAAAACCAG * * * * ***
121	AAAACAAGAAATTTGGCCTTTCTGTGGGCCATCACTTGGGCAAGTCCATCCCAACTGACA	Hsapiens	TTTGCAGAGATAAACC
121	AAAAGAACAAGTTTGGCCTTTCTGTGGGCCATCATTTGGGCAAGTCCATTCCAGCCGACA	Rnorvegicus	TTGTGAAATCAATGAC
181	ACCAGATCAAAGCTAGAAAATGAGATTCCTTAGCCTGGATTTCCTTCTAACATGTTATCA	Hsapiens	ATTCAAGAAAGGAA
181	ACCAGATCAAAGCTAGAAAATAAGGTTTTCCATACCATGTAGTAGACCCAGG	Rnorvegicus	GAGCTGGGGACCGAAC
241	AATCTGGGTATCTTTCCAGGCTTCCCTGACTTGCTTTAGTTTTTAAGATTTGTGTTTTTC	Hsapiens	ACTTTATTTCTGATCT
231	TTTCTTTTTCCCCAGTTTGCCTGCCTTGCTTTCAGTTTTCGCCTTTGT * ** ** * ** ***** *************	Rnorvegicus	AATCCCCAACCCCTCC * * * * *
301	TTTTTCCACAAGGAATAAATGAGAGGGAATCGACTGTATTCGTGCATTTTTGGATCATTT	Hsapiens	ATGACTTACTATGGGA
282	TCCACAAGGATAGGAAAAGGAGGAGGAGGGCTCGCCTCATGCGTTTTTGGATAGTTC	Rnorvegicus	GGGAA
361	TTAACTGATTCTTATGATTACTATCATGGCATATAAC-CAAAATCCGACTGGGCTCAAGA	Hsapiens	GTTTTATCAACTTTGG
335	TGCCACGGCTGTGACAGCAAAATGAACGAGGTCAGGATTAGGGGCCTCAGGTGGCCTGGGA Proximal **	Rnorvegicus	GGTTTATGAATATGTG * **** ** *
420	GGCCACTTAGGGAAAGATGTAGAAAGATGCTAGAAAAATGTTCTTTAAAGGCATCTACAC	Hsapiens	
395	TATGAATCAGGGAGAGGTGTAGCCGCGAGGGGGAAAATACTCTTCTAGGTCTTTTGTAC * * ****** ** ***** ** ***** ** ***** ****	Rnorvegicus	AGAGCTGGAGTTACAA
480	AATTTAATTCCTCTTTTTAGGGCTAAAGTTTTAGGGTACAGTTTGGCTAGGTATCATTCA	Hsapiens	ATTATATAATTCAAGG
455	ACTATAAGCTTTTTTCTTCGGGCTAGCCCTGGCTAAATGGCATCCA	Rnorvegicus	TACATTCAGTTTAAGG
540	ACTCTCCAATGTTCTATTAATCACCTCTCTGTAGTTTATGGCAGAAGGGAATTG	Hsapiens	AGATGAGAAATGATGA
501	ATCCTCCACCCACTTGTTGCTATTAGTTACCTCTCTGTGGTTTAGGGCAGGAGGGAATTG	Rnorvegicus	ATTTTATGTA-GACAA
594	CTCAGAGAAGGAAAAGACTGAATCTACCTGCCCTAAGGGACTTAACTTGTTTGGTAGTTA	Hsapiens	TACTTGCCAAGAAAAT
561	CTCAAACAATGGCTGAGCA	Rnorvegicus	GAGCCACCATGTGGTT
654	GCCATCTAATGCTTGTTTATGATATTTCTTGCTTTCAATTACAAAGCAGTTACTAATATG	Hsapiens	ACTGGCACTGGTGGTT
596	GTTAGCTAAAGCCTGTTTATGATCCATCCTGGTTTCAATTACTGTGCAGTGACTGAC	Rnorvegicus	TCTGGAAGAGC-AGTC
714	CCTAGCACAAGTACCACTCTTGGTCAGCTTTTGTTGTTTATATACAGTACACAGATACCT	Hsapiens	<u>GTTTCAGTTTGAA</u>
656	CCTCGGGGGATTGCTCTCCAGCTCTTCTGCCTTGTACATAGCACACCCAGGTCCTG Middle	Rnorvegicus	CTTATTATCTACAGTA
774	TGAAAGGAAGAGCT <mark>AATAAA</mark> TCTCTTTCTTTGCTGCAGTCATCTACTTTTTTTTAATTAA	Hsapiens	CTCAAAGATCTGA
714	GGAAATGAATACAAAAAACAGGTCTCCGCCTCATTCTTGCTATTCTTTCT	Rnorvegicus	CTAATGAATAGTCTTA Star-PAP binding
834		Hsapiens	
110	IGIGIGIGIGGAAAAAAAAAAAAAAAAAGIGGAAAAAAAA	Knorvegicus	
889	TGTGATCTCGGCTCACTGCAACCTCTGCCTCCCAGGTTCCAGCAATTCTCCTGC-CT	Hsapiens	CAAACTGCAGCTGGAA
822	TTTGAGCCCTTCAATACTTAACAACAGCCCCCTCCTGAGCTGGCGCGATGACTCAGCAGC	Rnorvegicus	ACGCGTGAGTGTGGCA
945	CAGCCTCCCTAGTAGCTGGGATGACAGGCGCCTGCCATCATGCCTGACTAATTTTTGTAT	Hsapiens	
882	TAAGAGCCCTTGTGGCTCTAGCAGGAAACCCACCTAAAGGCTAACTGCTGTTCCTAA	Rnorvegicus	TTACAGGCATTTGTAA
1005	TTTTAGTAGAGACGGCGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCC	Hsapiens	GAATTCAAAGGAAAGA
939	CTCCAGTTCTAAAGAACCCAGCGCCCTCTCCTGGTTTCTTCAGGCACTGCATGCA	Rnorvegicus	GAACAGCAAGGGCTTT

TGACCTCAGGTGATCCGCCTACCTCAGCCTCCCAAAGT	1093
TGCACAGACATAACACGCGAGCCGAAAAAATGGGTAGACACATACAAATAAAT	1058
GCTGGGATTACAGGCGTGATCCACCACACCTGGCCCTTGCAATCTTCTACTTTAAGG	1150
CÇAAAATGAAAACÇAGTAGCCTŢĊŢĄĊÇAAĄĊGTCŢĢGĄĄGGŢŢTŢŢĊŢĠŢĄGTA	1113
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TTTGCAGAGATAAACCAATAAATCCACACCGTACATCTGCAATATGA	119/
	11/3
ATTCAAGAAAGGAAATAGTACCTTCAA-TACTTAAAAATAGTCTTCCACAAAAAAT	1252
GAGCTGGGGACCGAAACCCAAGGGCCTTGCACTTCCTAGGCAAGCGCTCTACCACTGAGCTA	1233
ACTTTATTTCTGATCTATACAAATTTTCAGAAGGTTATTTTCTTTATCATTGCTAAACTG	1312
AATCCCCAACCCCTCCTTTCTTATTTTAAAGAT-CTGTTTTGTTT	1292
ATGACTTACTATGGGATGGGGTCCAGTCCCATGACCTTGGGGTACAATTGTAAACCTAGA	1372
GGGAAGGGTGTGCGCGCGCGCGCGTG-CGCGCGCACGCGTGCCTGAG	1336
GTTTTATCAACTTTGGTG-AACAGTTTTGGCATAATAGTCAATTTCTACTTC	1423
GGTTTATGAATATGTGTGTACAAGTGCTCACAGACTCCTGAAGAAGGCCTTCCAGGCCCCC	1396
TGGAAGTCATCTCATTCCACTGTTGGT	1450
AGAGCTGGAGTTACAAGTGGCTGCTCTTAGCTATGAAACCATCTCCCCAGCCCTGATGAT ** ** ** * ** ** ** ** ** ** ** ** ** *	1456
аттататааттсаабдадаататдатаааасастдссстсттдтдддаддаадаад	1510
FACATTCAGTTTAAGGAAATATGCAGATATCATGTAGGTCTTTTTTTT	1516
AGATGAGAAATGATGAAAAGGTTGCCT-GAAAAATGGGAGACAGCCTCT	1558
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TACTTGCCAAGAAAATGAAGGGATTGGACCGAGCTGGAAAACCTCCTTTACCAGATGCTG	1618
GAGCCACCATGTGGTTGCTGGGATTTGAACTCAGGACCTC	1615
ACTGGCACTGGTGGTTTTTGCTCTCGACAGTATCCACA <u>ATAGCTGACGGCTGGG</u>	1673
TCTGGAAGAGC-AGTCAGTGCTCTTAACCACTGAGCCATCTCTCTAGCCCTCATATAGGT	1674
GTTTCAGTTTGAAAATATTTTGTTGCCTTCATCTTCACTGCAA	1730
CTTATTATCTACAGTAAATAATTTT <u>AAGACTGTGTGTGTGTTGGTG</u>	1721
CTCAAAGATCTGAATTAAATAAATAAAATTCATTTCTACAGACCCACACTCATTGGT	1787
<u>_IAAIGAAIAGICIIACGAAIGIGAAGCIAGCAICCIACIGII</u> GAACIACAIICIGCGII ** * * * * * * * * * * * * * * * * *	1781
ATCAGTGAAGCTAATGATAGTGGAATCTAGTGGGAGGCAGATCAGAGGATTCAATCA	1844
LLLAAIIIIUGUAIAA <mark>AAIIA</mark> GIGIIAIIIAGUIGIGIGIGL ** * * **** **** * Distal	1824
CAAACTGCAGCTGGAAGCCCCTTGGTGACTGGCTTGACAACTCACCCAGCAGGGCTGCTT	1904
ACGCGTGAGTGTGGCATGCCTGTAGAGACTAGAAGGCAGAGTCACATCTCCTGGCTGG	1884
CCTACTAAATGGTA-ATAGAACAACCTATTCAGTCCTCTCAGG	1946
IIALAGGLAIIIGIAAGLUUIGIGAGIGUILAGAAIIGAACIULAUIGGICCTCTGCTA ** * ** * * * * * * * * * * * * * * *	1944
GAATTCAAAGGAAAGAGAGTGGTATAGAAATC	1978
GAACAGCAAGGGCTTTTAAATGTTGGGCCACCTC *** **** * ** * * *	1978