

## Legends for supplementary data

**Supplementary Figure 1.** Alignment of different domains. (A) HD domain. (B) ZLZ domain. The cysteins that could form a zip structure are boxed. (C) START-SAD domain. The point mutations are indicated in the figure.

**Supplementary Figure 2.** (A) Expression of proteins used in binding assay. HD (aa 1-115), HD-ZLZ (aa 1-237), START-SAD (aa 238-725). GbML1 indicates the full-length protein. MBP indicates maltose binding protein. All parts of GbML1 are fused in frame to MBP. The purified MBP or MBP fusion proteins are separated by SDS-PAGE gel and stained by Coomassie Blue. Arrow indicated the cloned protein with correct size. (B) The purified proteins used in point mutation assay. (C) Coomassie Blue staining of a native gel that containing the binding mix with GbML1 full-length protein or HD-ZLZ protein. Arrows indicate the binding mix, which is also detected in figure 2, panel D.

**Supplementary Figure 3.** The property of the sequence in *GbML1* promoter region. The promoter sequence is analyzed using PLACE (<http://www.dna.affrc.go.jp/PLACE/>, Higo et al., 1999).

**Supplementary Figure 4.** Yeast transactivation assay of GbML1, GbMYB25 and GbMYB2. (A) GbML1 is a weak activator while GbMYB25 is a strong activator. BD indicates pDEST32 vector; AD indicates pDEST22 vector. Each BD, BD-GbML1, BD-GbMYB25 and BD-GbMYB2 vector is co-transformed with AD vector into yeast strain AH109. The yeast clones grown on selective plates are presented. (B) C2 part of GbMYB25 confers the strong activation activity. (a) Diagram of the three parts of GbMYB25. MYB indicates the N terminal part of GbMYB25 containing the two MYB repeats (aa: 1-112); C1 indicates the domain predicted with similarity of other MYB proteins (aa: 113-170); C2 is the domain at the C terminus with low similarities to other proteins (aa: 171-309). (b) The yeast clones harboring AD vector and BD-MYB/BD-C1/BD-C2 /BD-GbMYB25 grown on selective plates are presented.

**Supplementary Figure 5.** Alignment of GbMYB25 with GhMYB25. The SNPs are indicated by arrows.

**Supplementary Figure 6.** Alignment of GbMYB2, GaMYB2 and GhMYB2. The SNPs are indicated by arrows.

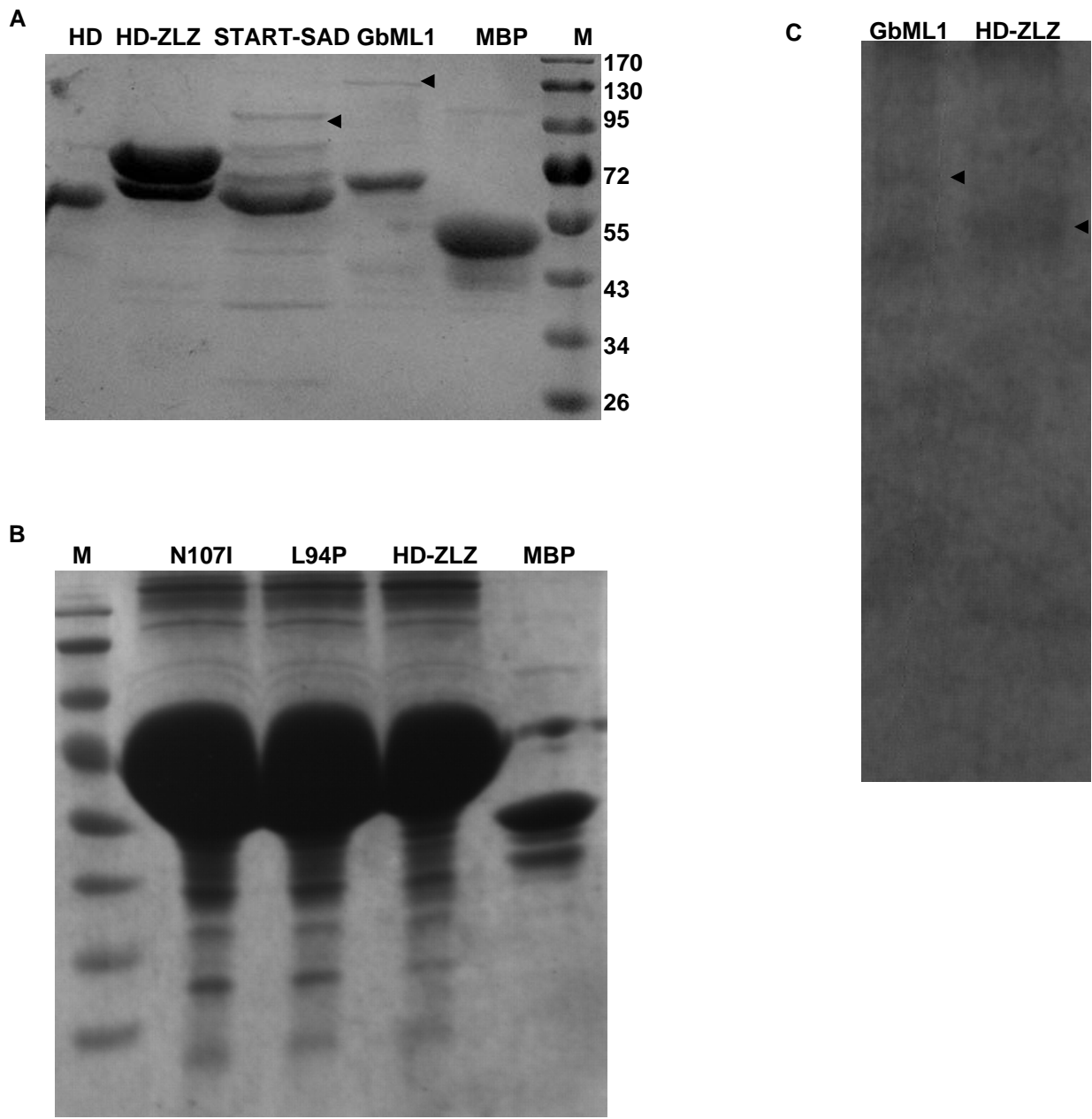
**Supplementary Figure 7.** Alignment that uses to generate the phylogeny tree.

**Supplementary Table S1.** Primers and probes used in this research.

### Reference:

K. Higo, Y. Ugawa, M. Iwamoto and T. Korenaga (1999) Plant cis-acting regulatory DNA elements (PLACE) database. *Nucleic Acids Research* **27**: 297-300





Supplementary figure 2

CTTGACAATTCTCTTCATTTTCCTCACCCCCCTTGGAACTTCAAACCCCTTTCTCTCTCTAGACTTTAACCCCTCTTCTCTCTCAAGGTAGGTCTCTGTCAA  
ACCAGTGACCCCAAACCTTTTAAAAACCACCCTCTTACCTCCTTTCAATTAATCTTTTTCAACAATGTTCAAAAGGGCTTTCTTTTGTTCCTATACGCCCTGTA  
AAAAGTCTCTACTCACGAACTATCTTTTTCTGGACCAGCTTGTATAGCACCCGATCCGTGTTCACTCCATTTGCCATTCTCTTTTCATATATTCGCTTA  
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AGCGGGGCCAAGAATCTAACAAGCAAGAGACTGATATGTGTAGCATGTATTGCTGCTGGTTAGGGTTTTATAGGTCAATGGCTATCTATGTCTCCCAACATG  
AGGTTTCTAGTGACCAACTTACCACTGCATTTAAGACAAGAAAAATAGTTGCCCTAAGCTCTTAGTCCCCTTCTCCAAATAATCCATAAGGTAATTTTCTTTCT  
CCTTTTTCCCAACTTTTGTGCCCCATTTTATTCTCCGAGGTTCTTTCACTTTTCCCATGGGAATAGATTAGGATAAGCTTTTGCATAATCCATCATTTAAT  
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GAGAGATGGTATATGGTTTACAGCTCCATTGTTTATTGCTTTCAAATGTTTTACGATTCCATTGTCATGCACTGGTTTTGACTTTTTAACTTTGACTTACA  
TTTTGTGCTTTTGTACTGTTCTACAGTTTATTTAACCCCTTTTACCCTTTATTTTAGTTTGCTTGACTTGTGTATGTTCTCTCGGCAGAACCCAGAATATCCA  
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TGGTTAG

:MYBATRD22

TAAATGYA

:L1BOXATPDF1

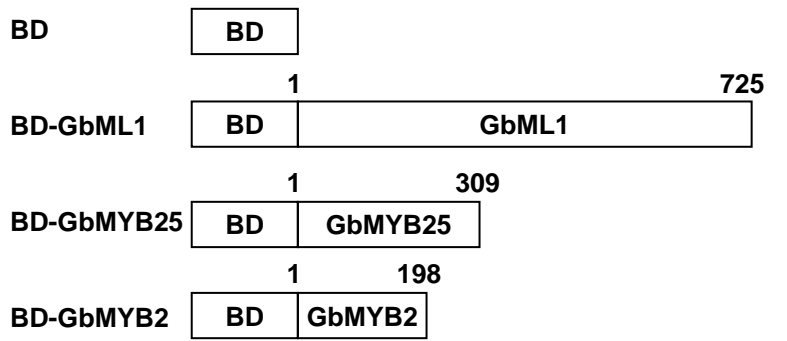
ATG: Translation start codon RACE 5' end nucleotides are italic

Sequence used in EMSA is

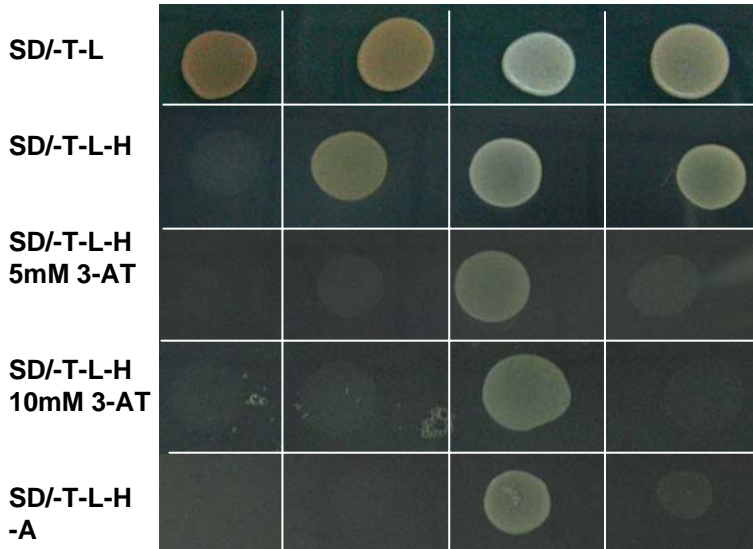
GCATGTATTGCTGCTGGTTAGGGTTTTATAGGTCAATGGCTATCTATGTCTCCCAACATGAGGTTTCTAGTGACCAACTTACCACTGCATTTAAGACAAGAAA  
ATAGTTG

### Supplementary Figure 3

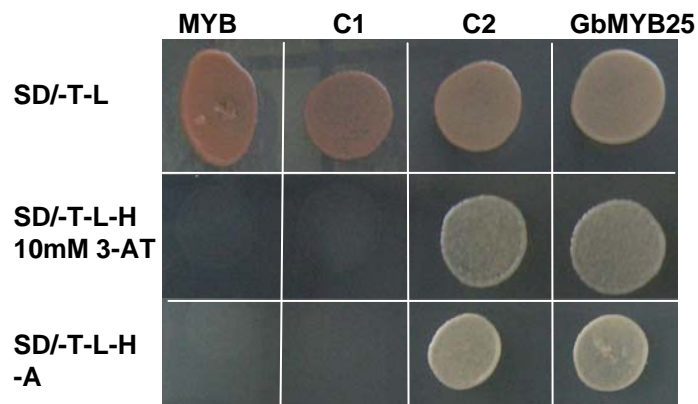
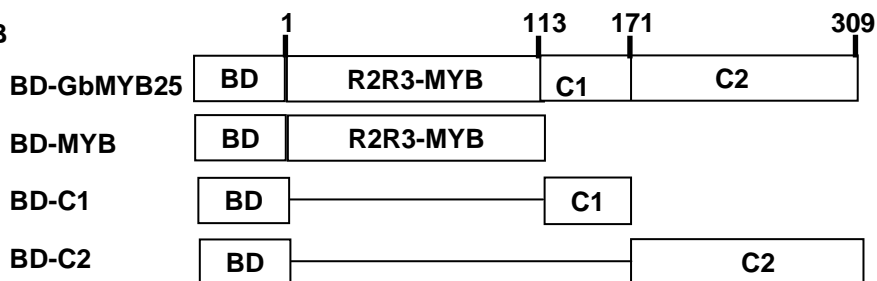
A



BD    BD-GbML1    BD-GbMYB25    BD-GbMYB2



B



Supplementary Figure 4

	10	20	30	40	50	60	70	80
GbMYB25	ATGGGGAGAT	CACCATGTTG	TGAAAAGGTA	GGGTTGAAGA	AAGGTCCATG	GACCCAGAA	GAAGATCAAA	AGCTCTTAGC
GhMYB25	ATGGGGAGAT	CACCATGTTG	TGAAAAGGTA	GGGTTGAAGA	AAGGTCCATG	GACCCAGAA	GAAGATCAAA	AGCTCTTAGC

	90	100	110	120	130	140	150	160
GbMYB25	TTACATTGAA	CAACATGGCC	ATGGAAGCTG	GCGTGCCTTG	CCTTTAAAAG	CTGGGCTTCA	AAGATGTGGA	AAGAGTTGCA
GhMYB25	TTACATTGAA	CAACATGGCC	ATGGAAGCTG	GCGTGCCTTG	CCTTTAAAAG	CTGGGCTTCA	AAGATGTGGA	AAGAGTTGCA

	170	180	190	200	210	220	230	240
GbMYB25	GACTGAGATG	GATTAACTAC	TTGAGACCTG	ATATCAAAAAG	AGGAAAAGTTC	AGTTTACAAG	AAGAACAGAC	CATTATTCAA
GhMYB25	GACTGAGATG	GATTAACTAC	TTGAGACCTG	ATATCAAAAAG	AGGAAAAGTTC	AGTTTACAAG	AAGAACAGAC	CATTATTCAA

	250	260	270	280	290	300	310	320
GbMYB25	CTCCATGCC	TTCTTGAAA	CAGGTGGTCT	GCCATAGCTA	CTCATTGGCC	GAAAAGAACA	GACAAATGAGA	TCAAGAACTA
GhMYB25	CTCCATGCC	TTCTTGAAA	CAGGTGGTCT	GCCATAGCTA	CTCATTGGCC	GAAAAGAACA	GACAAATGAGA	TCAAGAACTA

	330	340	350	360	370	380	390	400
GbMYB25	CTGGAACACA	CATCTAAAAG	AAAAGCTAAC	CAAAAATGGGG	ATCGATCCTG	TCACCCACAA	GCCTAAAACC	GATGCACTCG
GhMYB25	CTGGAACACA	CATCTAAAAG	AAAAGCTAAC	CAAAAATGGGG	ATCGATCCTG	TCACCCACAA	GCCTAAAACC	GATGCACTCG

	410	420	430	440	450	460	470	480
GbMYB25	GTCCACCAC	TGGTAACCCT	AAAGATGCTG	CTAACCTTAG	TCACATGGCT	CAATGGGAGA	GTGCTCGTTT	AGAAGCTGAA
GhMYB25	GTCCACCAC	TGGTAACCCT	AAAGATGCTG	CTAACCTTAG	TCACATGGCT	CAATGGGAGA	GTGCTCGTTT	AGAAGCTGAA

	490	500	510	520	530	540	550	560
GbMYB25	GCTAGACTGG	TTCGTGAGTC	CAAGCTAGTT	CCCTCAAACC	CTCCTCAAAG	CAACCACTTC	ACTGCCGTTG	CGCCTTCGCC
GhMYB25	GCTAGACTGG	TTCGTGAGTC	CAAGCTAGTT	CCCTCAAACC	CTCCTCAAAG	CAACCACTTC	ACTGCCGTTG	CGCCTTCGCC

	570	580	590	600	610	620	630	640
GbMYB25	GACTCCGGCA	ACTAGACCGC	AATGCCTCGA	CGTACTCAA	GCATGGCAA	GTGTCGTCTG	CGGGTTATT	ACTTTCAACA
GhMYB25	GACTCCGGCA	ACTAGACCGC	AATGCCTCGA	CGTACTCAA	GCATGGCAA	GTGTCGTCTG	CGGGTTATT	ACTTTCAACA

	650	660	670	680	690	700	710	720
GbMYB25	TGGACAATAA	CAACTTACAG	TCCCCTACGT	CAACGTTGAA	CTTCATGGAG	AACACCACAA	CATTGCCTAT	GTCATCATCA
GhMYB25	TGGACAATAA	CAACTTACAG	TCCCCTACGT	CAACGTTGAA	CTTCATGGAG	AACACCACAA	CATTGCCTAT	GTCATCATCA

	730	740	750	760	770	780	790	800
GbMYB25	TCGTCTGTTA	ATGGAATGTT	TAAATGAAAAC	TTTGTTGGA	ACTCATCGAT	TAATCCATGT	GAAAAGTGGG	ATATTTTGAA
GhMYB25	TCGTCTGTTA	ATGGAATGTT	TAAATGAAAAC	TTTGTTGGA	ACTCATCGAT	TAATCCATGT	GAAAAGTGGG	ATATTTTGAA

	810	820	830	840	850	860	870	880
GbMYB25	AGTTGAATAT	GGCAGTGATC	AAATTCCAGA	GTTAAAAGGA	AGATTGGATC	ATCCAATGGA	ATTGCATGAA	ATGGACTGTI
GhMYB25	AGTTGAATAT	GGCAGTGATC	AAATTCCAGA	GTTAAAAGGA	AGATTGGATC	ATCCAATGGA	ATTGCATGAA	ATGGACTGTI

	890	900	910	920	930
GbMYB25	CTTCAGAGGG	TACATGGTTT	CAAAGATTGT	TTGGATTTAA	TGGTTTGTGA
GhMYB25	CTTCAGAGGG	TACATGGTTT	CAAAGATTGT	TTGGATTTAA	TGGTTTGTGA

Supplementary Figure 5

	10	20	30	40	50	60	70	80
GaMYB2	ATGGCTCCAA	AGAAGGATGG	AGTGAGCAAA	AGGGTTTTTA	ACAAAGGTTC	TGGACAGCT	GAGGAAGATA	GAAGATTGGC
GbMYB2	ATGGCTCCAA	AGAAGGCTGG	AGTGAGCAAA	AGGGTTTTTA	ACAAAGGTTC	ATGGACAGCT	GAGGAAGATA	GAAGATTGGC
GhMYB2	ATGGCTCCAA	AGAAGGCTGG	AGTGAGCAAA	AGGGTTTTTA	ACAAAGGTTC	ATGGACAGCT	GAGGAAGATA	GAAGATTGGC
	90	100	110	120	130	140	150	160
GaMYB2	TAAATATATT	GAGATTCATG	GGCAAAGAG	ATGGA AAAACA	ATCGCCATTA	AATCAGGTTT	GAATCGATGC	GGCAAGAGTT
GbMYB2	TAAATATATT	GAGATTCATG	GTGCAAAGAG	ATGGA AAAACA	ATCGCCATTA	AATCAGGTTT	GAATCGATGC	GGCAAGAGTT
GhMYB2	TAAATATATT	GAGATTCATG	GTGCAAAGAG	ATGGA AAAACA	ATCGCCATTA	AATCAGGTTT	GAATCGATGC	GGCAAGAGTT
	170	180	190	200	210	220	230	240
GaMYB2	GCAGGTTGAG	ATGGTTGAAC	TACTTGAGAC	CTAACATTAA	GAGAGGCAAC	ATATCAGATG	AAGAAGAGGA	CTTAATTATT
GbMYB2	GCAGGTTGAG	ATGGTTGAAC	TACTTGAGAC	CTAACATTAA	GAGAGGCAAC	ATATCAGATG	AAGAAGAGGA	CTTAATTATT
GhMYB2	GCAGGTTGAG	ATGGTTGAAC	TACTTGAGAC	CTAACATTAA	GAGAGGCAAC	ATATCAGATG	AAGAAGAGGA	CTTAATTATT
	250	260	270	280	290	300	310	320
GaMYB2	AGGCTTCATA	AACTGCTGGG	GAACAGGTGG	TCTTTGATTG	CTGGGAGACT	TCCAGGGCGA	ACAGACAATG	AAATTAAGAA
GbMYB2	AGGCTTCATA	AACTGCTGGG	GAACAGGTGG	TCTTTGATTG	CTGGGAGACT	TCCAGGGCGA	ACAGACAATG	AAATTAAGAA
GhMYB2	AGGCTTCATA	AACTGCTGGG	GAACAGGTGG	TCTTTGATTG	CTGGGAGACT	TCCAGGGCGA	ACAGACAATG	AAATTAAGAA
	330	340	350	360	370	380	390	400
GaMYB2	CTACTGGAAT	TCCCATTTGA	GCAAGAAAAT	AATAAACCAT	GATGTCAGAA	CAGAACA AAC	TTCTCTCTCG	GAACAAATTG
GbMYB2	CTACTGGAAT	TCCCATTTGA	GCAAGAAAAT	AATAAACCAT	GATGTCAGAA	CAGAACA AAC	TTCTCTCTCG	GAACAAATTG
GhMYB2	CTACTGGAAT	TCCCATTTGA	GCAAGAAAAT	AATAAACCAT	GATGTCAGAA	CAGAACA AAC	TTCTCTCTCG	GAACAAATTG
	410	420	430	440	450	460	470	480
GaMYB2	TGCCTCACAA	AGCATGGGAA	ACTGTCCAGA	TGGAAGAAGA	AGAGGTAGTA	AAAGGAAGTG	ATGAAATTGA	AAACTCTGAA
GbMYB2	TGCCTCACAA	AGCATGGGAA	ACTGTCCAGA	TGGAAGAAGA	AGAGGTAGTA	AAAGGAAGTG	ATGAAATTGA	AAACTCTGAA
GhMYB2	TGCCTCACAA	AGCATGGGAA	ACTGTCCAGA	TGGAAGAAGA	AGAGGTAGTA	AAAGGAAGTG	ATGAAATTGA	AAACTCTGAA
	490	500	510	520	530	540	550	560
GaMYB2	TTCAGCATTG	ATGTGGACGA	ATTCTTTGAC	TTCACAACGG	AAGGTTGCTT	TAGTTTGGAT	TGGGTGAATA	AGTTCCTTGA
GbMYB2	TTCAGCATTG	ATGTGGACGA	ATTCTTTGAC	TTCACAACGG	AAGGTTGCTT	TAGTTTGGAT	TGGGTGAATA	AGTTCCTTGA
GhMYB2	TTCAGCATTG	ATGTGGACGA	ATTCTTTGAC	TTCACAACGG	AAGGTTGCTT	TAGTTTGGAT	TGGGTGAATA	AGTTCCTTGA
	570	580	590					
GaMYB2	ACTTGATGAT	CAACAGGATC	CATTAGCAAT	GGTATAA				
GbMYB2	ACTTGATGAT	CAACAGGATC	CATTAGCAAT	GGTATAA				
GhMYB2	ACTTGATGAT	CAACAGGATC	CATTAGCAAT	GGTATAA				

Supplementary Figure 6

10	20	30	40	50	60	70	80
..... .....	..... .....	..... .....	..... .....	..... .....	..... .....	..... .....	..... .....
MNFNGFLDDG	AG----ASKL	LSDAPYNNHF	SFSAVDTMLG	SAAIAP----	---SQSLP--	-FSSGSLSLG	LQTN-----
MNFGSLFDNT	PGGGSTGARL	LSGLSYGNHT	--AATNVLPG	GAMAQAAAAA	SLFSPPLTKS	VYASSGLSLA	LEQPERGTNR
-----	-----	-----	-----	-----	-----	-----	-----
-----	---METKDKKE	KGHMVLNSDN	VFGS----VS	SSPTTTIQNP	NY-FTSFENP	NFPYIFPKEE	YEVMS-----
-----	---MLTMGEGN	---VMTSNN	RFASPPQQPS	SSSPGTIQNP	NFNFIPIFN--	SYSSIIIPKEE	HGMMSSMMMM
-----	-----	-----	-----	-----	-----	---MNGQGDLD	AVGN-----
-----	-----	-----	-----	-----	-----	---MNGDLEVD	MSRG-----
-----	-----	-----	-----	-----	-----	-----	-----
-----	-----	-----	-----	-----	-----	---MFSPN	LFES-PHMFD
-----	-----	-----	-----	-----	-----	---MSFVVGVGG	S-----
-----	-----	-----	-----	-----	-----	---MEFLG---	-----
-----	-----	-----	-----	-----	-----	---MYHPN	MFESHMMFMD
-----	-----	-----	-----	-----	-----	---MYHPN	MFES-HMMFD
-----	---MSMAVDMS	SKQPTKDFFS	SPALSLSLAG	IFRNASSGST	NPEEDELGRR	VVDEEDRTVE	MSSE-----
-----	-----	-----	-----	-----	-----	---MFQPN	MFDSHHHLLD
-----	-----	---MM	I PARHMPP--	MIVRNSAAAY	GS-SSALS--	---LSQPN	LLDSQQ-QLQ
-----	-----	-----	-----	-----	-----	---MFQAN	MFEG-HMMFD
-----	-----	-----	-----	-----	-----	-----	---MASK-----
-----	-----	-----	-----	-----	-----	-----	---MTPK-----
-----	-----	-----	-----	-----	-----	---MFQPA	LFES-HMMFD
-----	---MPAGFI	I PARHVPP--	-LMARHTKAG	YTTSSGLS--	---LAQPN	MAEG---QFD	MSQT-----
-----	---M	TPARRMPP--	VIGRN-GVAY	ESPSAQLP--	---LTQAD	MLDSHHLQQA	LQQQ-----
-----	---MM	I PARHMPS--	MIGRN-GAAY	GS-SSALS--	---LSQPN	LLDNHQFQQA	FQHQQQQHH-
MSFGSLFDGG	SG-----	-----	---GGGG	GGMQFP----	---FTTG	FSSSPALSLG	LDNAG-----
-----	---M	TPARRVPPAA	MIGRN-GFAF	GS-SSALS--	---LSQAD	LLDSHQLQQA	FQQQ-----
-----	---MRLGGVT	VQVPPNGNLG	NLGRSFGELG	GMPAGAMAPP	RQIPPLAMPR	PPPKHYSSPS	LSLGPPTG--
-----	---MRLGGVT	VQVPPNGNLG	NLGRSFGELG	GMPTGAMAPP	RQIPPLAMPR	PPPKHYSSPS	LSLGPPTG--
-----	-----	-----	---MPT	GVFSQP----	RLVPSSIPKN	MFNSPGLSLA	LQQP-----
-----	-----	-----	-----	-----	-----	---MDCGSGGGG	L-----

90	100	110	120	130	140	150	160
..... .....	..... .....	..... .....	..... .....	..... .....	..... .....	..... .....	..... .....
---GE	MSRNGEIMES	NVSRKSS---	---RGED	VEFSRSEDN-	AEAVSG----	-DDLD---T	SDRPLKKKKR
GEASMRNNNN	VGGGGDTFDG	SVNRRS---	---REEE	HEFSRSGSDN-	VEGISG----	-EDQD---A	ADKPPRKK--R
-----	-YNHEDNNNE	GFLRDDE---	---FDS	PNTKSGSEN-	QEGGS----	---GND-QD	PL-HPNKKKKR
-----	---ENNNNNN	NNGGTDN---	---TN	AGNDSGDQDF	DSGNTSSG--	---NHGEGLGN	NQAPRHHKKK
-----	---KIESG	-SGKST---	---G	SGHDPVENTA	IEQE-----	-----	---PPAAKKKKR
GDG-----	-TVEEMMENG	SAGGSF----	---G	SGSEQAEDPK	FGNESDV---	---NELHDD	EQPPPAAKKKR
-----	-----	-----	---IPKP	GEAEGDEIDM	INDMSG----	---V	NQDQGGRRMR
-----	---DFNPSFFLG	KL-----	---KDDE	FESRSLSDDS	FDAMSGD---	---EDKQ---EQ	RPKKKKRKKTK
-----	-----	-----	---MDN	NGGSSGNEQ	YTSGDAQQ--	-----	---NGKR---T
-----	-----	-----	---MDF	TRDDNSDER	ENDVDANT--	-----	---NNRHEKKKG
-----	-----	-----	---MDS	SHNDSSTD--	EEGIDSN---	-----	---NRRH---
-----	---TSESELM	GKIRDD---	---D	YEIKSVNET-	MDAPS-----	---GDD-QD	PD-QRPKKKKR
-----	---GSGSGGDGG	GSHHHD---	---G	SETDRK---	-----	-----	---KKR
-----	-----	DSQNHD---	---S	SETEKKNK--	-----	-----	---KKKR
-----	---NSENDLG	ITGSHEE---	---D	FETKSGAEVT	MENPL-----	---EEELQD	PNQRPNKKKR
-----	---TSDNDLG	ITGSRED---	---D	FETKSGTEVT	TENPS-----	---GEELQD	PSQRPNKKKR
-----	---NSGP	TRSRSE---	---ED	LEGEDHDDEE	EEEEEDG---	---AAGN	KGTNKRKKKK
-----	---TPESEMG	-KIRDE---	---E	FESKSGTEN-	MDAPS-----	---GDD-QD	PN-QRPKKKKR
---LLDQIP	ATAES---G	DNMGRSGGGR	GSDPLMGGDE	FESKSGSEN-	VDGV-----	---SVDDQD	PNQRPSSKKKR
-----	---SSENDSS	-KLKDD---	---D	YETKSGTET-	MEAQs-----	---GDD-QD	PSEQHPKKKKR
-----	---SSENDLS	-KLKDD---	---D	YETKSGTET-	MEAPS-----	---GDD-QD	PSGQRPKKKKR
-----	---SSENELG	-NLKDDDY--	---D	HETKSGTET-	TEAPS-----	---GDD-QD	PN-QRPKKKKR
-----	---ADSEI	AKIRDE---	---E	FESKSGSDN-	VEGAS-----	---GEDQD	GERRP-RKKR
---YFDQIP	VTTTAAADSG	DNMLHG---	RADAGGLVDE	FESKSGSEN-	VDGAGDG---	---LSGDDQD	PNQRP-RKKR
---LLDQIP	ATAES---G	DNMIRS---R	ASDP-LGGDE	FESKSGSEN-	VDGV-----	---SVDDQD	PNQRP-RKKR
---GGMVGRM	LPVGGAPADG	GMARDA---	---ADAE	NDSRSGSDH-	LDAMSAGAGA	-EDED--DAE	PGNPRKKKKR



```

----LFDQIP TTTVD-DSS DNLIHG---- RSDT--LVDE FESKSCSEN- PDGT-SG--- ---DDGLEED PNQRPNKKKR
----LDGQRE VSQTADNEQQ QKNKEE---- ----- YESRSGSDN- MEGGS----- -----GDED PDNNHPRKKR
----LDGQRE VSQTADNEQQ QKNKEE---- ----- YESRSGSDN- MEGGS----- -----GDED PDNNHPRKKR
---NIDNQGD ETRLGENFEG SIGRRS---- -----REEE HESRSGSDN- MDGSSG---- -DDHPTTAA GDKPPRKR-R
-----G-----ASG SGGDHD---- -----S SDLSRR----- -----KKP

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170	180	190	200	210	220	230	240
.... ....	.... ....	.... ....	.... ....	.... ....	.... ....	.... ....	.... ....
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YHRHTPQQIQ	ELBSMFKECP	HPDEKQRLBL	SKRLCLETRQ	VKFWFQNRRT	QMKTOIERHE	NALLRQENDK	LRAENMSIRE
YHRHTQLQIQ	EMBAFFKECP	HPDDKQRKQL	SRELNLLEPLQ	VKFWFQNKRT	QMKNHHERHE	NSHLRAENEK	LRNDNLRYRE
YHRHTASQIQ	EMBAFFKECP	HPDDKQRYDL	SAQLGLDPVQ	IKFWFQNKRT	QNKNOQERFE	NSBLRNLNNH	LRSENQRLRE
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YHRHTNRQIQ	EMBALFKENP	HPDDKQRKRL	SAELGLKPRO	VKFWFQNRRT	QMKAOQDRNE	NVMLRAENDN	LKSENCHLOA
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CHRHTPQQIQ	RLEAYFKECP	HPDERQRNQL	CRELKLEPQ	IKFWFQNKRT	QSKTQEDRST	NVLLRGENET	LQSDNEAMLQ
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---HSHNQVQ	RLEBAFFHECP	HPDQSQRQL	GNELNLEKPK	IKFWFQNRRT	QARLHNEKAD	NIALRVENMK	LRCVNEAMEK
YHRHTQRQIQ	EMBAFFKECP	HPDDKQRKEL	GRELGLEPLQ	VKFWFQNKRT	QMKAOHERHE	NAILKAENEK	LRAENDRYKE
YHRHTAQQIQ	RLESSEFKECP	HPDEKQRNQL	SRELGLAPRO	IKFWFQNRRT	QIKAOHERAD	NSALKAENDK	LRGENIAIRE
FHRHTPHQIQ	RLEBSTEFECC	HPDEKQRNQL	SRELGLAPRO	IKFWFQNRRT	QIKAOHERAD	NALKAENEK	LRGENIAIRE
YHRHTQRQIQ	ELBSVFKECP	HPDDKQRKEL	SRELSLEPLQ	VKFWFQNKRT	QMKAOHERHE	NQILKSENDK	LRAENNRYKD
YHRHTQRQIQ	ELBSVFKECP	HPDDKQRKEL	SKDLNLEPLQ	VKFWFQNKRT	QMKAOHERHE	NQILKSDMDK	LRAENNRYKE
YHRHTTDQIR	HMBALFKETP	HPDEKQRQQL	SRELGLAPRO	VKFWFQNRRT	QIKAOHERHE	NSLLKAELEK	LRSENKAMRE
YHRHTQHQIQ	EMBAFFKECP	HPDDKQRKEL	SRELGLEPLQ	VKFWFQNKRT	QMKAOHERHE	NSNLRAENEK	LRAENIRYKE
YHRHTQHQIQ	EMBAFFKECP	HPDDKQRKEL	SRELGLEPLQ	VKFWFQNKRT	QMKNOHERHE	NSQLRAENEK	LRAENMRYKE
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YHRHTQRQIQ	EMBAFFQECF	HPDDKQRKEL	SRELGLEPLQ	VKFWFQNKRT	QMKAOHERSE	NSILKAENEK	LRMENNRYKE
YHRHTQRQIQ	EMBAFFKECP	HPDDKQRKEL	SRELGLEPLQ	VKFWFQNKRT	QMKAOHERQE	NSILKAENEK	LRAENNRYKE
YHRHTQHQIQ	EMBMFFKECP	HPDDKQRKEL	SRELGLEPLQ	VKFWFQNKRT	QMKTOHERHE	NTQLRSENEK	LRSENMRYKE
YHRHTQHQIQ	EMBAFFKECP	HPDDKQRKEL	SRELGLEPLQ	VKFWFQNKRT	QMKNOHERHE	NAQLRAENDK	LRAENMRYKE
YHRHTQHQIQ	EMBAFFKECP	HPDDKQRKEL	SRELGLEPLQ	VKFWFQNKRT	QMKNOHERHE	NSQLRSDNEK	LRAENMRYKE
YHRHTPQQIQ	ELBALFKKECP	HPDEKQRDEL	SKRLGLDPRO	VKFWFQNRRT	QMKTOIERHE	NALLRQENDK	LRAENMAIRE
YHRHTQHQIQ	EMBAFFKECP	HPDDKQRKEL	SRELGLEPLQ	VKFWFQNKRT	QMKNOHERHE	NAQLRAENDK	LRAENMRYKE
YHRHTPRQIQ	EMBMFFKECP	HPDDKQRQQL	SRELGLEPLQ	VKFWFQNRRT	QMKAOHERAE	NSMLRAENEK	LRSENLIMRE
YHRHTPRQIQ	EMBMFFKECP	HPDDKQRQQL	SKDLGLEPRO	VKFWFQNRRT	QMKAOHERAE	NSMLRAENEK	VRSENLIMRE
YHRHTPQQIQ	ELBALFKKECP	HPDEKQRLEL	SKRLCLETRQ	VKFWFQNRRT	QMKTOIERHE	NSLLRQENDK	LRAENMSIRD
YHRHTAHQIQ	RLESMFKECP	HPDEKQRLOL	SRELGLAPRO	IKFWFQNRRT	QMKAOHERAD	NSALRAENDK	LRGENIAIRE

250	260	270	280	290	300	310	320
.... ....	.... ....	.... ....	.... ....	.... ....	.... ....	.... ....	.... ....
AMRNP--MCG	NCGGPAVIGE	IS-MEEQHLR	IENSRLKDEL	DRVCAITGKF	LGR-----	-----SNGS-	-----HHIP
AMRNP--ICT	NCGGPAMLGD	VS-LEEHHLR	IENARLKDEL	DRVCNLTGKF	LGH-----	-----HHN--	-----HHY
ALANA--SCP	NCGGPTAIGE	MS-FDEHQLR	IENARLREBI	DRISATAAKY	VGKPLVS---	--NYPLMSP-	-----PPLP
AIHQ--LCP	KCGGQTAIGE	MT-FEEHHLR	ILNARLTBEI	QQLSVTAEKI	SRLTGIP---	VRSHPRVS--	-----PPNP
NFQCL--FCS	TCG-----	-----HNLR	IENARLRQEL	DRLRSIVSMR	NPSPSQ---	-----EITP-	-----
ELRCL--SCE	SCGGFTVLGD	IP-F--NEIH	IENCLRREBI	DRLCCIASRY	TGRPMQ----	--SMPPSQPL	INPSPMLPHH
AMLR--LCN	ICGKATNCGD	TE-YEVQKLM	AENANLEREI	DQFNRSYLSH	PKQ-----	-----	-----RMV
SMRGS--LCI	DCGGAVIPGE	VS-FEQHQLR	IENAKLKEBI	DRICATANRF	IGG-----	-----	-----
ALKSV--LCP	ACGGPFPGRE	ERGHNLQKLR	FENARLKDHR	DRISNFVDQH	KPNEPTV--E	DSLAYVP---	-----SLDR
ALNNV--VCP	PCGGRGPGRE	DQLRHLQKLR	AQNAYLKDEY	ERVSNYLKQY	GGHSMHN---	VEATPYLHGP	SNHASTSKNR
ALETV--LCP	PCGG--PHGKE	EQLCNLQKLR	TKNVILKTEY	ERLSSYLTKH	GGYSIPS---	VDALPDLHGP	STYGSTSNNR
ALSNA--TCP	SCGGPAALGE	MS-FDEQHLR	IENARLREBI	DRISGTAAKY	VGKPLS---	--SLPHLS--	-----SHLH
ALKHA--ICP	NCGGFPVSED	PY-FDEQKLR	IENAHLEBEI	ERMSTASKY	MGRPLS----	--QLS----	-----TLHPMH
AIKHA--ICP	SCGDSPVNED	SY-FDEQKLR	IENAO LRDEL	ERVSSTAAFE	LGRPLS----	--HLPP----	-----LLNPMH
ALSNA--TCP	NCGGPAALGE	MS-FDEQHLR	IENARLREBI	DRISATAAKY	VGKPLMANS-	--SSFPQLSSS	-----HHIP
ALSNA--TCP	NCGGPAALGE	MS-FDEQHLR	IENARLREBI	DRISATAAKY	VGKPLG----	--SSFAPLA--	-----IHAP
SFSKANSSCP	NCGGFP----	-----DDLH	IENSKLKAEI	DKLRAALGRT	PYPLQAS---	-----CSDDQ-	-----EHR
ALSNA--TCP	HCGGPASIGE	MS-FDEQHLR	IENARLRDEI	DRISGTAAKY	VGKPLV----	--SYPHLS--	-----THTS
ALSSA--SCP	NCGGPAALGE	MS-FDEHHLR	VENARLREBI	DRISATAAKY	VGKPLMVSFP	VLSSPPLAGAR	-----P----
ALRNA--SCP	NCGGPAALGE	MS-FDEQHLR	IENVRLREBI	DRISGTAAKY	VGKPLS----	--SLSNLS--	-----PHLP

ALSSA--SCP	NCGGPAALGE	MS-FDEQHLLR	TENARLRREI	DRISGTAAKY	VGKPLS----	--SLSNLS--	-----HHL
ALSNA--SCP	NCGGPATLGE	IS-FDEQHLLR	TENARLRREI	DRLSGTAAKY	IGKPLS----	--SLSHLS--	-----SHLP
ALNNA--SCP	NCGGPAALGE	MS-FDEQQLR	MENARLRREI	DRISGTAAKY	VGKPLS----	-FGPSPLS--	-----SIP
ALSSA--SCP	NCGGPAALGE	MS-FDEHHLR	VENARLRDEI	DRISGTAAKH	VGKPPIVSFS	VLSSPLAVAA	-----A
ALSSA--SCP	NCGGPAALGE	MS-FDEHHLR	TENARLRREI	DRISATAAKY	VGKP-MVFPF	VLSNPMAAAA	-----SR--
AMRSP--MCP	SCGSPAMLGE	VS-LEEQHLC	TENARLKDEL	NRVYALATKF	LKMPVLSG	PMLQPNLS--	-----LPMP
ALGTA--SCP	SCGGAALGE	MS-FDEHHLR	TENARLRDEI	DRISGTAAKH	VGKP-MVSFP	VLSSPLAAAA	-----AAAA
ALKNP--QCP	HCGGPATVGE	MT-FDEQQLR	TENVRLKEEL	DRVSALAACY	LGRPIT----	--PMAPLA--	-----LP
ALKNP--QCP	HCGGPATVGE	MT-FDEQQLR	TENVRLKEEL	DRVSALAACY	LGRPIT----	--PMAPLA--	-----LP
AMRNP--ICT	NCGGPAIIGD	MS-LEEQLLR	TENARLKDEL	DRVCALACKF	LGR-----	----PITG--	-----PPLP
ALKNV--ICP	SCGGPANED	SY-FDDQKMR	MENAQLKEEL	DRVSSIAAKY	IGRPLS----	--QLP-----	-----PVQPVH

330	340	350	360	370	380	390	400
.... ....	.... ....	.... ....	.... ....	.... ....	.... ....	.... ....	.... ....
DSALVLDGVG	GSGGC---N	VGGGFTLSSP	LLPQASPRFE	ISNGTGSGLV	ATVNRQQPVS	VSDFDQRSRY	LDLALAAAMDE
NSSLFLAVGT	N-----N	NGGHFAFPP-	-----	-DFGGGGGCL	PPQ-QQSTV	INGIDQKSVL	DELALTAMDE
PRPLFLAMGN	-----	--IGGEAYGN	-----	-----NPN	DLLKS---IT	APTESDKPVI	IDLVAAMEE
PPNFEFGMGS	KGN---V	GNHSRETTGP	-----	-----	-----	-ADANTKPII	MELAFGAMEE
-----	-----	-----	-----	-----	-----	ETNKNNDNM	LIABEEKPID
QPSLELDMSV	YAGN--FPEQ	SCTDMMMLP-	-----P	QDTACFFPDQ	TANNNNNNNM	LLADEEKVIA	MELAVSCVQE
STSEQAP---	-----S	SSS-----	-----	---NPGINAT	PVLDFSGGTR	TSEK-ETSIF	LNLAITALRE
SISLEQP---	-----S	NG-----	-----	---GIGSQHL	PIG-----H	CVSGGTSIMF	MELAMEAMDE
-ISYGINNGN	MYEPSSSYGP	PN-----	-----	-----	---FQIQPR	PLAETDMSLL	SELTAASAVEE
PALYGTSSNR	LPEPSSIFRG	PYTRGN---	-----	-MNTTAPPQP	RKPLEMQNFQ	PLSQLEKIAM	LEBAEKAVSE
PASYGSSSNH	LPQSSLLRR	PFTREL----	-----	-INTTLP---	-KPVLLQHFQ	QLSQLEKNRM	FELAKNAVAE
SRSVLDGASN	FGN-----Q	SGFVGMEDRS	-----	-----G	DLLRS---VS	GPTEADKPMI	VELAVAAMEE
ISPLDLSMTS	LTGCGPFGHG	PSLDFDLLP-	-----G	SSMAVGPNN-	--NLQSQPNL	AISDMDKPII	TGIALTAMEE
VSPLLEL----	-----FHTG	PSLDFDLLP-	-----G	SCSSMSVPP-	--SLPSQPNL	VLSEMDKSLM	TNIAVTAMEE
SRSLDLEVGN	FGNNN--NSH	TGFVGMFSG	-----	-----S	DILRS---VS	IPSEADKPMI	VELAVAAMEE
SRSLDLEVGN	FGN---Q	TGFVGEYGT	-----	-----G	DILRS---VS	IPSETDKPII	VELAVNAAMEE
LGSLDFYTG-	-----	-----	-----	-----	-----	-VFALEKSR	DELAVRATLE
SRSLDLGVGN	FGA-----Q	SGIVGDMYGG	-----	-----G	DLLRS---VS	LPTEADKPMI	VELAVAAMEE
-SPLDIGGGV	GG---AAA	YGAV-DMFGG	-----	-----GVAV	DLLRGAVPQS	---DADKPMI	VELAVTAMEE
SRSLDLGVSN	FGA-----Q	SGFVGMFPGA	-----	-----T	DLLRS---VT	GPTEADKSMI	VELAVAAMEE
SRSLDLGVSN	YGA-----H	SGFVGMFPGA	-----	-----T	ALLGA---VT	GPTEADKPMI	VELAVAAMEE
SRSLDLGVSN	FGT-----Q	SGYVGEYGA	-----	-----T	DFLRS---IT	GPTEAEKPMI	VELAVAAMEE
RSNLDLAVGS	YG-----VQ	PNIGDIYGS	-----	-----SSG	EIGNR---SLV	GPTEAEKPMV	VELAVAAMEE
RSPLDLAG--	-----A	YGVVTPGLDM	-----	---FGG-AG	DLLRG--VHP	--LDADKPMI	VELAVAAMDE
-APLDLP---	-----VAP	YGVPGDMFGG	-----	-----GGAG	ELLRG--VQS	---EVDKPMI	VELAVAAMEE
SSSLELAVGG	LRGLG---S	IPSLDEFAG-	-----G	VSSPLGTVIT	PARATGSAPP	PMVGVDRSML	DELALISAMDE
RSPLDLAG--	-----A	YGVQSAAGL	G-----A	DH-LFGAGAG	DLLRS--VSA	GQLDADKPMI	VELAVAAMDE
SSSLLDQVGG	GSSFSGMHPA	PGNLDVVAGP	-----	-----SVA	DVATR---PG	GLTEAEKPMV	VELAVTAMEE
SSSLLDQVGG	GSSFSGMHP	PGNLDLVAGP	-----	-----SVA	DVATR---PG	GLTEAEKPMV	VELAVTAMEE
NSSLLELGVGT	NG-----T	FGTMTATT-	-----	-TLPLGHDAL	PTM-VVPSNR	PATTLDRSMF	DELALAAAMDE
ISSLDLFRMAS	FDGYG-VGAG	PSLDDLPLP-	-----G	SSSSMP----	--NLPPQP-V	VISIDIKSLM	SDIAANAMEE

410	420	430	440	450	460	470	480
.... ....	.... ....	.... ....	.... ....	.... ....	.... ....	.... ....	.... ....
LVKMAQTRFP	LWVRSSDS--	----GFEVLN	QEYDTSFSE	CV--GPKQDG	FVSEASKEAG	TVIIN-SLAL	VELTMDSERW
LVKLAQSEEP	LWVKSLDG--	----ERDELN	QDEYMRTEF-	----STKPTG	LATEASRTSG	MVIIN-SLAL	VELTMDSNRW
LMRVQVDEP	LWK-----	----SLVLD	EEYARTFPR	G--IGPRPAG	YRSEASRESA	VVIMN-HVNI	VELTMDVNQW
LLVMAQVAEP	LWVG--GFNG	----TSLALN	LDEYEKTEFT	G--LGPRIGG	FRTEASRETA	LVAMC-PTGI	VELMLQENLW
IAKMCDINEP	LWNNKRLD--	---NESVCLN	EEYKMKFLW	PLMNDDDR--	FRREASRANA	VIMIN-CITL	VKAFLDADKW
LTKMCDTEEP	LWLKKSDDKI	G--GEILCLN	EEYMRLEPW	PMENQNNKGD	FLREASKANA	VVIMN-SITL	VDAFLNADKW
LITLGEVDCP	FWMIDPIVRS	----KGVSKI	YEKYRSSENN	----VTKPPG	QIVEASRAKG	LVPMT-CVTL	VELTMDTGKW
LLKLALELETS	LWSSKSEK-	-----	---GSMNHFP-	-----	----GSRETG	LVLIN-SLAL	VELTMDTNNK
LKRLFLAEQ	FVVKSCIDET	-----YVID	TESYERFSHA	VKH---FSST	TAHVESSKAV	TVVHVEAINL	IQMFLDPEKW
VLSLIQMDDT	MWKKSSIDDR	-----LVID	PGLYEKYFTK	-----TNT	NGRPESSKDV	VVVQMDAGNL	IDIFLTAEKW
VMSLIQMEHS	MWIKSTIDGR	-----AID	PGNYKRYFTK	NSHLKRSAL	QSHHSSMEV	VVVQMDARNL	VDMFLNTEKW
LIRMAQSGEP	LWV---PGDN	----STDVLN	EDEYLRTFPR	G--IGPKPLG	LRSEASRESA	VVIMN-HVNL	VELTMDVNQW
LLRLLQTNEP	LWTR-TDGCR	-----DILN	LGSYENVFPR	SSNRG-KNQN	FRVEASRSSG	IVFMN-AMAL	VDMFMDCVKW
LLRLLQTNEP	LWIK-TDGCR	-----DVLN	LENYENMETR	SSTS GGKKN	LGMEASRSSG	VVFTN-AITL	VDMLMNSVKL



LVRMAQTGDP	LWV---SSDN	----SVEILN	EEEYERTEPR	G--IGPKPIG	LRSEASREST	VVIMN-HINL	IEILMDVNQW
LVRMAQTGDP	LWL---STDN	----SVEILN	EEEYERTEPR	G--IGPKPLG	LRSEASRQSA	VVIMN-HINL	VEILMDVNQW
LQRMATSGEP	MWLRSVETGR	-----EILN	YDEYLKBEFQ	AQ-ASSFPGR	KTIEASRDAG	IVFMD-AHKL	AQSFMDVGGW
LIRMAQAGEP	LWI--PTSDN	----STEILS	EDEYLRTEPR	G--IGPKPLG	LKSEASRETA	VVIMN-HISL	VEILMDVNQW
LVRMAQLDEP	LWN-APGLDG	----SAETLN	EEEYAHMFPG	G--IGPKQYG	FKSEASRDSS	VVIMT-HANL	VEILMDVNQY
LMRIAQAGEP	LWI---QGEN	----NTEMLN	EEEYLRTEPR	G--IGPKPLG	MRSEASRESA	VVIMN-HVNL	VEILMDANQW
LMRMAQAGEP	LWI---QGEN	----NTEMLN	EEEYLRTEPR	G--IGPRPLG	MRSEASRESA	VVIMS-HVNL	VEILMDANQW
LMRMAQAGDP	LWV---PGEN	S---TTEVLN	EEEYLRTEPR	G--IGPRPLG	LRSEASRESA	VVIMN-HVNL	VEILMDVNQW
LVRMAQLGEP	LWT--SHPED	----STDILN	EDEYLRTEPR	G--IGPRPYG	LKAEASRETA	VVIMN-AINL	VETLMDVNQW
LVQMAQLDEP	LWS---SSSEP	----AAALLD	EEEYARTEPR	G--IGPKQYG	LKSEASRHGA	VVIMT-HSNL	VEILMDVNQF
LVRMAQLDEP	LWSVAPPLDA	TAA-AMETLS	EEEYARTEPR	G--IGPKQYG	LRSEASRDSA	VVIMT-HANL	VEILMDANQY
LVKLAQVDEP	LWLPSLSGSP	----DKKILN	EEEYAHSEPR	SV-GAVKPVG	YVSEASRESG	LVIIIDNSLH	VEILMDVRRW
LLRMAPDAL	LWGGGASAGA	----QQQ-LD	EEEYVRETPA	G--IGPRQYG	LRSEASRDSA	VVIMT-CDSL	IEILMDANRE
LVRMAQTEEP	LWVNMGEVVK	-----EQLN	YEEYMRQEP	G--IGCPPPG	LKTEATRETA	LVMMN-GVNL	VETLMDATQW
LVRMAQAEPP	LWLSM-DSGK	-----AQLN	YDEYMRQEP	G--IGMRPSG	LKBEATRETA	LVMMN-GVNL	VETLMDATQW
LVRMAQTDEP	LWIKNIEG--	----GREMLN	HDEYLRTEPR	CI--GLKPNG	FVTEASRETG	VVIIN-SLAL	VETLMDSNRW
LLRLLQTNPE	LWIKSTNDGK	-----DALN	LESYERTEPR	PNNTHFKSPN	IRVEASRDSG	VVIMN-GLAL	VDMFMDSNKW

490	500	510	520	530	540	550	560
.... ....	.... ....	.... ....	.... ....	.... ....	.... ....	.... ....	.... ....
AEMFPMVSR	TSTTEIISG	-MGG-RNGAL	HLMHAELQVL	SPLVPVQVS	FLRYCKQ-HA	EGVWAVVDVS	IDSIR-----
TEMFPCNVAR	ATITDVISGG	-MAGTINGAL	QLMNAELOVL	SPLVPVRNVN	FLRYCKQ-HA	EGVWAVVDVS	IDPVR-----
STIFAGMVS	AMTLAVLSTG	-VAGNYNGAL	QVMSAEFQVP	SPLVPTRYEY	FARYCKQ-QG	DGSWAVVDIS	LDSLQPN---
STMFAGVGR	ARTHEQIMAD	-AAGNFNGNL	QIMSAYQVL	SPLVPTREYS	FVRYCKQ-QG	EGLWAVVDIS	IDHLLPN---
SEMFFPIVSS	AKTAQIISG	-ASG-PSGTL	LLMFAELQVV	SPLVPTRYEAY	FLRYVEQNAE	EGKWMVVDFF	IDRIKPF---A
SEMFCISIVAR	AKTVQIISG	-VSG-ASGSL	LL-----VL	SPLVPTRYEAY	FLRYVEQNAE	TGNWAVVDFF	IDSFHDQMQP
VNVFAPIVPV	ASTHKVLSG	-SGGTKSGSL	QQIQAEFQVI	SPLVPKRKVT	FLRYCKE-IR	QGLWVVDVT	PTQNP-----
AEMFECIVAV	ASTLEVISNG	-SDGSRNGSI	LLMQAEFQVM	SPLVPIKQKK	FLRYCKQ-HG	DGLWAVVDVS	YDINR-----
KELFPTIVNK	ANTIHVLSG	LPIRGNCNVL	QVMWEQLHIL	SPLVPAREFM	VVRCCQE-IE	KGIWVIADVS	HRAN-----
ARLEPTIVNE	AKTIHVLDL	VDHRGKT-FS	RVVYEQLHIL	SPLVPAREFM	ILRTCCQ-IE	DNVWMIADVS	CHLPNIE---
ARLEPTIVTE	AKTIHVLDL	MDHPRQT-FS	RVVYEQLHIL	SPLVLPREFI	ILRTCCQ-MK	EDLWVIADVS	CYLQNV----
SSVFCGIVSR	AMTLEALSTG	-VAGNYNGAL	QVMTAEFQVP	SPLVPTRYEY	FVRYCKQ-HI	DGTWAVVDVS	LDNLRPN---
TELEPSIIAA	SKTLAVISSG	-MGGTHEGAL	HLLYEEMVVL	SPLVATREFC	ELRYCQ-TE	QGSWIVVNVS	YD-----LP
TELEPSIVAS	SKTLAVISSG	-LRGNHGDAL	HLMIEELOVL	SPLVATREFC	VLRYCQ-IE	HGTWAVVNVS	YE-----FP
SSVFCGIVSR	AMTLEVLSTG	-VAGNYNGAL	QVMTAEFQVP	SPLVPTRYEY	FVRYCKQ-HS	DGTWAVVDVS	LDSLSPS---
SCVFSGIVSR	AMTLEVLSTG	-VAGNYNGAL	QVMTAEFQVP	SPLVPTRYEY	FVRYCKQ-HS	DGSWAVVDVS	LDSLSPS---
KETBACLISK	AATVDVIRQG	EGPSRIDGAI	QLMFGELQVL	TPVVPTRYEY	FVRSRQ-LS	PEKWAVVDVS	VSVEDSN---
SSVFSGIVSR	AMTLEVLSTG	-VAGNYNGAL	QVMTAEFQVP	SPLVPTRYEY	FVRYCKH-HP	DGTWAVVDVS	LDNLRSG---
ATVFSIVSR	AMTLEVLSTG	-VAGNYNGAL	QVMSVEFQVP	SPLVPTRYEY	FVRYCKQ-NA	DGSWAVVDVS	LDSLSPS---
STIFCGIVSR	AMTLEVLSTG	-VAGNYNGAL	QVMTAEFQVP	SPLVPTRYEY	FVRYCKQ-HT	DGTWAVVDVS	LDSLSPS---
STIFCGIVSR	AMTLEVLSTG	-VAGNYNGAL	QVMTAEFQVP	SPLVPTRYEY	FVRYCKQ-HT	DGTWAVVDVS	LDSLSPS---
STVFCGIVSR	AMTLEILSTG	-VAGNYNGAL	QVMTAEFQVP	SPLVPTRYEY	FVRYCKQ-HV	DGTWAVVDVS	LDNLRPN---
SSMFBGIVSR	PHTVDVFSG	-VAGNYNGAL	QVMHAEFQVP	SPLVPTRYEY	FVRYCKQ-HS	DSIWAVVDVS	LDSLSPS---
ATVFSIVSR	ASTHEVLSTG	-VAGNYNGAL	QVMSMEFQVP	SPLVPTRYEY	FVRYCKN-NS	DGTWAVVDVS	LDSLSPS---
AAVFSNIVSR	AMTLEVLSTG	-VAGNYNGAL	QVMSVEFQVP	SPLVPTRYEY	FVRYCKQ-NA	DGTWAVVDVS	LDSLSPS---
SDMFSMIAK	ATVLEEVTSG	-IAGSRNGAL	LLMKAELOVL	SPLVPTREVT	FLRYCKQ-LA	EGAWAVVDVS	IDGLVRDHNS
AAVFSIVSR	ASTHEVLSTG	-VAGSYNGAL	QVMSMEFQVP	SPLVPTRYEY	FVRYCKN-NP	DGTWAVVDVS	LDSLSPS---
MDMFCIVSR	ALTVDVLATG	-VTGNRNGAL	QLMYAELQVL	SPLVPTRYEY	FLRYCKQ-HA	EGVWAVVDVS	VDSLSDN---
MDMFCMVS	ALTVDVLATG	-VTGNRNGAL	QLMYAELQVL	SPLVPTRYEY	FLRYCKQ-HA	EGVWAVVDVS	VDSLSDN---
AEMFHCMIAR	TSTTDVISNG	-MGGTRNGAL	QLMNAELOVL	SPLVPTRYEVS	FLRYCKQ-HA	EGVWAVVDVS	VDTIK-----
LELEPTIVSI	AKTIEVISPG	-MLGTHRSL	QLMYEELQVL	SPLVPTRYEY	TLRYCQ-IE	QGLWAVVNVS	YD-----LP

570	580	590	600	610	620	630	640
.... ....	.... ....	.... ....	.... ....	.... ....	.... ....	.... ....	.... ....
--EGSS--SS	CRRLPSCGLV	QDMANGYSKV	TWIEHTEYDE	--NHTRLYR	PLLRGGLAFG	AHRWMAALQR	QCECLTILMS
--ENSGGAPV	IRRLPSCGVV	QDVSNYSKV	TWVEHAEYDE	--NQIHQLYR	PLLRSGLGFG	QRWLATLQR	QCECLAILIS
-----PPAR	CRRRASGCLI	QELPNYSKV	TWVEHVEVDD	--RGVHLYK	HMVSTGHAFG	AKRWVAILDR	QCECLASVMA
-----INLK	CRRRPSGCLI	QEMHSGYSKV	TWVEHVEVDD	--AGSYIFE	KLICTGQAFG	ANRWVGTLLR	QCECLISSILS
SAT---TTDQ	YRRKPSGCI	QAMRNGYSQV	TWVEHVEVEE	K-HVQDEVVR	EFVESGVAFG	AERWLSVLKR	QCECLASLMA
MNT---ITHE	YRRKPSGCI	QDMPNYSQV	KWVEHVEVDE	K-HVH-ETFA	EYVKSMAFG	ANRWLDVLR	QCECLASLMA
---TLLPYGC	SKRRLPSGLI	DDLNSYSQV	TWIEQAEYNE	--SHIHQLYQ	PLTGYGIGLG	AKRWLATLQR	HCECLSTLSS
GNENLKSYYG	SKMFPSCGCI	QDIGNGCSKV	TWIEHSEYEE	--SHTHSLYQ	PLSSSVGLG	ATKWLATLQR	QCESFTMLLS

---	FDGNAA	CYKRPSGCLI	QALPDAHSKV	MWIEHVEVDH	-KLDTHKLYR	DLLSGSGYGY	AKRWVITLER	MCERMALSS-
---	FDLSFPI	CTKRPSGVLI	CALPHGFSKV	TWIEHVVVND	NRVRPEKLYR	DLLYGFGYGY	ARRWVITLER	TCERLIFSTS
---	FESTAPI	CTKRPSGVLI	QALPHGRSKV	TWIEHVEVTD	-KVVPHQLYR	DLLYGFGYGY	ARRWTATLQR	MCERLSLYS-
-----	PMSK	CRRRPSGCLI	QELPNGYSKV	IWVEHVEVDD	--RAVHNIYR	PVVNSGLAFG	AKRWVATLDR	QCEERLASSMA
QFV---	SHSQ	SYRFPSGCLI	QDMPNGYSKV	TWVEHIEETEE	K-ELVHELTYR	EIIHRGIAFG	ADRWVITLQR	MCERFASLSV
QFI---	SQSR	SYRFPSGCLI	QDMSNGYSKV	TWVEHGEFEE	Q-EPITHEMFK	DIVHKGLAFG	AERWIATLQR	MCERFTNLLE
-----	PITR	SRRRPSGCLI	QELQNGYSKV	TWVEHIEVDD	--RSVHNYMK	PLVNTGLAFG	AKRWVATLDR	QCEERLASSMA
---	T--PILR	TRRRPSGCLI	QELPNGYSKV	TWIEHMEVDD	--RSVHNYMK	PLVQSGAFG	AKRWVATLER	QCEERLASSMA
-TEKEASLLK	CRKLPSPGCLI	EDTSNGHSKV	TWVEHLDVSA	--STVQPLFR	SLVNTGLAFG	ARHWVATLQL	HCERLVFFMA	
-----	PITR	NRRRPSGCLI	QELPNGYSKV	IWVEHVEVDD	--RAVHNIYR	PLVNSGLAFG	AKRWVATLDR	QCEERLASAMA
-----	SVLK	CRRRPSGCLI	QEMPNGYSKV	TWVEHVEVDD	--RSVHNIYK	LLVNSGLAFG	PPRWVGTLDP	QCEELPSVMP
-----	LLSK	CRRRPSGCLI	QELPNGYSKV	VWVEHIEVDD	--RSVQNIYR	PLVNSGLAFG	AKRWVGTLDR	QCEERLASSMA
-----	LMSK	CRRRPSGCLI	QELPNGYSKV	VWVEHIEVDD	--RSVHNIYR	PLVNSGLAFG	AKRWVGTLDR	QCEERLASSMA
-----	PIAR	SRRRLSGCVI	QDLPNGYSKV	TWIEHIEVDD	--RSVHSLYR	PLVNSGLAFG	AKRWVAILDR	QCEERLASSMA
---	SS-SVIR	CRRRPSGCLI	QEMPNSYSKV	TWVEHVEADD	--RAVHHIYR	QLVNSGMAFG	AKRWIATLQR	QCEERLASVLA
-----	PVQK	CRRRPSGCLI	QEMPNGYSKV	TWVEHVEVDD	--SSVHNIYK	PLVNSGLAFG	AKRWVGTLDR	QCEERLASAMA
-----	PVLK	CRRRPSGCLI	QEMPNGYSKV	TWVEHVEVDD	--RSVHNIYK	LLVNSGLAFG	ARRWVGTLDR	QCEERLASVMA
GTASNAGNIR	CRRLPSPGCVI	QDTPNGYCKV	TWVEYTEYDE	--ASVHQLYR	PLVNSGLAFG	ARRWLAMLQR	QCECLAILMS	
-----	PVIK	CRRRPSGCLI	QEMPNGYSKV	TWVEHVEVDD	--RSVHNIYR	PLVNSGLAFG	AKRWVGTLDR	QCEERLASAMA
---	PPPSLMR	CRRRPSGVLI	QDTPNGYAKV	TCVEHMEYDD	--RAVHRMYR	DLVNTGMAFG	AQRWLATLQR	QCEERLASLLA
---	PPPSLMR	CRRRPSGVLI	QDTPNGYAKV	TCVEHMEYDD	--RAVHRMYR	ELVNTGMAFG	AQRWLATLQR	QCEERLASLLA
--ESTT-FVT	CRRLPSPGCVI	QDMPNGYSKV	IWAHAHAYDE	--SQVHQLYR	PLVNSGLAFG	AQRWVAALQR	QCECLAILMS	
QFA---	SQCR	SHRLPSPGCLI	QDMPNGYSKV	TWLERVEIED	K-TPHRLYR	DLVHSGSAFG	ARRWLTTLQR	MCEWFACLRY

650	660	670	680	690	700	710	720
.... ....	.... ....	.... ....	.... ....	.... ....	.... ....	.... ....	.... ....
STVSTSTNPS	PINCN--GRK	SMLKLAQRMT	DNFCGGVCAS	SLOKWSKLN-	-VGNVDEdVR	IMTRKSVNPP	GEPPGIILNA
SSVTSHDN-T	SITPG--GRK	SMLKLAQRMT	FNFCSGLSAP	SVHNSKILT-	-VGNVDEdVR	VMTRKSVDDP	GEPPGIVLSA
TNISSGEVGV	ITNQE--GRR	SMLKLAERMV	ISFCAGVSAS	TAHTWTILS-	--GTGAEDVR	VMTRKSVDDP	GRPPGIVLSA
TDFQSVDSGD	HITLTNHGKM	SMLKIAERIA	RTFFAGMTNA	TGS--TIFS-	--GVEGEDIR	VMTRKSVNDP	GKPPGVIICA
TNIT--DLG-	VIPSVE-ARK	NLMKLSQRMV	KTFCFLNINS	HGQ-----	--APTQDVTK	IVSRKVCG--	----GLVPCA
RNIT--DLG-	VISSAE-ARR	NIMRLSQRLV	KTFCVNI STA	YGQSWTALS-	--ETTKDITVR	ITTRKMCE-P	GOPTGVVLC A
TNLTEISP--	GLSAK--GAT	EIVKLAQRMT	LNYYRGITSP	SVDKWQKIQ-	-VENVAQNMS	FMTRKVNNEP	GELTGIVLSA
S-----EDHT	GLSHA--GTK	SILKLAQRMK	LNFYSGITAS	CIHKWEKIL-	-AENVGDTR	ILTRKSLI--	--PSGIVLSA
IQTLPSPDRS	EVITTGEARR	SVMKLGEMV	KNFNEMITMS	GKIDFPQQS-	-----KNGVR	VSIRMN-IEA	GOPPGIVVSA
VPALPNNDNP	GVVQTI GRN	SVMHLGERML	KNFAWMKMV	NKLDLFPQSE	---TNNSGIR	IGVRIN-NEA	GOPPGLIVCA
MTDFPPTDYP	GVVKTIEGRR	SVMSLGERML	KNFAWIMKMS	DKLDLPQSG	---ANNSGVR	ISVRTN-TEA	GOPPLIVCA
TNIPAGDL CV	ITSPE--GRK	SMLKLAERMV	TSFCTGVGAS	TAHAWTILS-	--ATGSDDVR	AMTRKSMDDP	GRPPGIVLSA
PASSRDLGG	VILSPE-GKR	SMMRLAQRMI	SNYCLSVRS	NNTRSTVVS-	--ELNEVGIR	VTAKS----	PEPNGTVLCA
PATSSIDLGG	VIPSPE-GKR	SIMRLAHRMV	SNFCLSVGTS	NNTRSTVVS-	--GLDEFGIR	VTSHKSR---	HEPNGMVLCA
SNIPACDL SV	ITSPE--GRK	SMLKLAERMV	MSFCTGVGAS	TAHAWTILS-	--TTGSDDVR	VMTRKSMDDP	GRPPGIVLSA
SNIPG-DLSV	ITSPE--GRK	SMLKLAERMV	MSFCSGV GAS	TAHAWTILS-	--TTGSDDVR	VMTRKSMDDP	GRPPGIVLSA
TNVPTKDSLG	VITLA--GRK	SVLKMAQRMT	QSFYRALI AS	SYHQWTKIT-	--TKTGQDMR	VSRKNLHDP	GEPTGIVVCA
SNIPAGDVGV	ITSPE--GRK	SMLKLAERMV	MSFCAGV GAS	TTHITWTILS-	--GSGADDVR	VMTRKSMDDP	GRPPGIVLSA
STIPTSDMGV	ITSTE--GRK	SMLKLAERMV	MSFCGGVTAS	AAHQWTILS-	--GSGAEDVR	VMTRKSVDDP	GRPPGIVLNA
INIPSGDL CV	ITTAE--GRK	SMLKLAERMV	MSFCTGVGAS	TAHAWTILS-	--ATGSDDVR	VMTRKSMDDP	GRPPGIVLSA
INIPTGDL CV	ITTPE--GRK	SILKLAERMV	MSFCTGVGAS	TAHTWTILS-	--ATGSDDVR	VMTRKSMDDP	GRPPGIVLSA
INIPAGDL CV	ITSPE--GRK	SMLKLAERMV	MSFCSGV GAS	TAHAWTILS-	--ATGSDDVR	VMTRKSMDDP	GRPPGIVLCA
INIPAGDLGV	IPSPE--GRK	SILKLAERMV	TSFCAGVSAS	TAHTWTILS-	--GSGAEDVR	VMTRKSIDDP	GRPPGIILSA
SNIPNGDLGV	ITSVE--GRK	SMLKLAERMV	ASFCGGVTAS	VAHQWTILS-	--GSGAEDVR	VMTRKSVDDP	GRPPGIVLNA
SNIPTSDIGV	ITSSE--GRK	SMLKLAERMV	VSFCCGVTAS	VAHQWTILS-	--GSGAEDVR	VMTRKSVDDP	GRPPGIVLNA
PDTVSANDSS	VITQE--GKR	SMLKLAARRMT	ENFCAGVSAS	SAREWSKLDG	AAGSIGEDVR	VMTRKSVDEP	GEPPGVVLSA
SNIPNGDLGV	ITSIE--GRK	SMLKLAERMV	ASFCGGVTAS	AAHQWTILS-	--GSGAEDVR	VMTRKSVDDP	GRPPGIVLNA
SNIASRDLGG	VPSAS--GRR	SMLKLAQRMT	NNFCAGVSAS	TVHTWTILS-	--GSGDDDVR	VMTRKSVNDP	GEPPGIVLSA
SNIASRDLGG	VPSAS--GRR	SMLKLAQRMT	NNFCAGVSAS	TVHTWTILS-	--GSGDDDVR	VMTRKSVNDP	GEPPGIVLSA
STVPTRDH-T	AITAS--GRR	SMLKLAQRMT	DNFCAGVCAS	TVHKWNKLN-	-AGNVDEdVR	VMTRKSIDDP	GEPPGIVLSA
SSTSTRDLGG	VIPSPE-GRR	SMMKLAQRMT	NNFCTSVGTS	NSHRSTILS-	--GSNEVGVR	VTVHKSSD-P	GOPNGIVLSA

730	740	750	760	770	780	790	800
.... ....	.... ....	.... ....	.... ....	.... ....	.... ....	.... ....	.... ....
ATSVWMPVSE	RRLFDLGN E	RLRSEWDILS	NGGPMKEMAH	IAGHPRSN S	VSLLRASA-I	NAN-----	---QSSMLIL
ATSVWLPAP	QRLYDFLRNE	RMRCEWDILS	NGGPMQEMAH	ITKQDQCG--	VSLLRASNA-M	NAN-----	---QSSMLIL



ATSEWLPVPP	KRVDFDLRDE	NSRNEWIDLS	NGGVQVEMAH	IANGRDITGNC	VSLLRVNS-A	NSS	-----	---QSNMLIL
ATSEWLPAPP	NTVDFDLREA	THRHNWDVLC	NGEMMHKIAE	ITNGIDKRCNC	ASLLRHG---	HTS	-----	---KSKMMIV
VSVTLPLPYSH	QVDFDLRDN	QRLSQLEILF	MGSSFQEVAAH	IANGSHLGNS	ISLLRINVES	NSS	-----	---HNVELML
VSTTLPFSH	HQVDFDLRQ	HHQSLELVLF	NGNSPHEVAH	IANGSHPGNC	ISLLRINVAS	NSW	-----	---HNVELML
STSVWLPVNO	HTLFAFLSHL	SFRHEWDILT	NDTTMBETIR	IQKAKRHGNI	ISLLKIVN--	-----	-----	---NGMLVL
ATSLWLPVTQ	QRLFEFLCDG	KCRNQWDILS	NGASMENTLL	VPKGOQEGSC	VSLLRAG-N	DQN	-----	---ESSMLIL
SSSLAIPLTP	LQVFAFLQNL	DTRQOWDILS	YGTVVFETAR	IVTGSSETNC	VTLRVHPTH	EENNDKMVVQ	-----	---DCKDDMLML
GSSLSLPLPP	VQVYDFLKNL	EVRHQWDVLC	HGNPATEAAR	FVTGSNPRNT	VSELEPSIRD	I	-----	---NTKLMIL
GSSLSLPLPP	LQVYDFLRNL	EVRHQWDVHC	QGNPTEAAR	FVTGPDQKNN	VTELQSSVG	-----	-----	---EYKLMIL
ATSEWLPVPP	KRVDFDLRDE	NSRSEWDILS	NGGLVQVEMAH	IANGRDPGNC	VSLLRVNS-A	NSS	-----	---QSNMLIL
ATTFWLPNSP	QNVFNFLKDE	RTRPQWDVLS	NGNAVQEVAAH	ISNGSHPGNC	ISVLRGSNAT	HS	-----	---NNMLIL
ATSEWLPISP	QNVFNFLKDE	RTRPQWDVLS	NGNSVQEVAAH	ITNGSNPGNC	ISVLRGFNAS	SSQ	-----	---NNMLIL
ATSEWLPVAP	KRVDFDLRDE	NSRSEWDILS	NGGLVQVEMAH	IANGRDPGNS	VSLLRVNS-G	NSG	-----	---QSNMLIL
ATSEWLPVAP	KRVDFDLRDE	NSRKEWDILS	NGGMVQVEMAH	IANGHEPGNC	VSLLRVNS-G	NSS	-----	---QSNMLIL
SSSLWLPVSP	ALLFDFLDE	ARRHEWDALS	NGAHVQSIAN	LSKGODRGNS	VAIQTVKS--	--R	-----	---EKSIVWL
ATSEWLPVPP	KRVDFDLRDE	NSRSEWDILS	NGGLVQVEMAH	IANGRDPGNC	VSLLRVNS-A	NSS	-----	---QSNMLIL
ATSEWLPVPP	KRVDFDLRDE	SSRSEWDILS	NGGVVQVEMAH	IANGRDHGNC	VSLLRVNS-T	NSN	-----	---QSNMLIL
ATSEWLPVQS	KRMDFDLRDE	NHRSEWDILS	NGGEVQVEMAH	IANGRDPGNC	VSLLRVNS-A	NSS	-----	---QSNMLIL
ATSEWLPVPS	KKVDFDLRDE	NHRSEWDILS	NGGQVQVEMAH	IANGRDPGNC	VSLLRVNS-T	NSS	-----	---QSNMLIL
ATSEWLPVPP	KRVDFDLRDE	NHRSEWDILS	NGGQVQVEMAH	IANGRDPGNC	VSLLRVIS-A	NSS	-----	---QSNMLIL
ATSLWLPVPP	KKVDFDLRDE	NSRNEWIDLS	NGGLVQVVDH	IANGQDPGNC	VSLLRVNT-V	NSN	-----	---QSNMLIL
ATSEWLPVPP	AAVDFDLRDE	TSRSEWDILS	NGGAVQVEMAH	IANGRDHGNS	VSLLRVNS-A	NSN	-----	---QSNMLIL
ATSEWLPVPP	KRVDFDLRDE	SSRSEWDILS	NGGIVQVEMAH	IANGRDQGNC	VSLLRVNS-S	NSN	-----	---QSNMLIL
PTSVWLPVAP	EKLNFNLRDE	QLRAEWDILS	NGGPMQVEMAH	IAKGQEHGNS	VSLLRASA-M	SAN	-----	---QSSMLIL
ATSEWLPVPP	KRVDFDLRDE	TSRSEWDILS	NGGAVQVEMAH	IANGRDHGNC	VSLLRVNS-A	NSN	-----	---QSNMLIL
ATSMWLPVSP	ARVFQFLRDE	RLRSEWDILS	NGGMVQVEMAH	IAKGQDPGNS	VSLLRVNA-M	NSS	-----	---QSNMLIL
ATSMWLPVSP	ARVFQFLRDE	RLRSEWDILS	NGGIVQVEMAH	IAKGQDPGNS	VSLLRVNA-M	NSN	-----	---QSNMLIL
ATSVWLPVSP	QRLFDFLRNE	RLRSEWDILS	NGGPMQVEMAH	IAKGQDHGNC	VSLLRASA-M	NAN	-----	---QSSMLIL
ATTFWLPVSP	QNVFNFLKDE	RTRPQWDVLS	NGNAVQEVAAH	IANGSHPGNC	ISVLRAFNTS	HN	-----	---NMLIL

810	820	830	840	850	860	870	880		
QETSIDAA-G	AVVVYAPVDI	PAMQAVMNGG	-DSAYVALLP	SGFAILPNGQ	AGTQRCAAE	RN	-----	---SIGNGG	
QETCIDAS-G	ALVVYAPVDI	PAMHVMNGG	-DSSYVALLP	SGFALPDGG	IDGG	-----	-----	---GSGDGD	
QESCTDPT-A	SEVIYAPVDI	VAMNIVLNGG	-DPDYVALLP	SGFALPDGN	ANS GAP	----	-----	-----	
QETSTDPT-A	SEVLYAPVDM	TSMDITLHGG	GDPDEVVILP	SGFAIFPDGT	GKPGGKE	----	-----	-----	
QETCTDNS-G	SLLVYSTVDP	VAVQLAMNGE	-DPSEIPLLP	VGFSSVVPNP	SDGVEGSSVS	SP	-----	-----	
QESCTDNS-G	SLIVYSTVDV	DSIQQAMNGE	-DSSNIPLLP	LGFSIVVPNP	PEGISVNSHS	PP	-----	-----	
QETWINDAS-G	AMVVYAPVET	NSIELVKRGE	-NSDSVKELP	SGFSIVPDGV	N	-----	-----	---GSYH	
QETWINDVS-G	ALVVYAPVDI	PSMNTVMSGG	-DSAYVALLP	SGFSILPDGS	SSSS	-----	---D	---DTDGG	
QDCYMDAL-G	GMIVYAPVDM	ATMHFAVSGE	VDPESHIPILP	SGFVITSSDGR	RSTVEDGG	--	-----	-----	
QDSFKDAL-G	GMVAYAPVDI	NTACAALS GD	IDPTTIPILP	SGFMISRDR	PSEGEAEGGS	Y	-----	-----	
QDGFIDAL-G	GMVVYAPMNL	NTAYSALSQ	VDPSTIPILP	SGFITSRDHS	PSSSEVDGGS	M	-----	-----	
QESCTDAK-G	SYVVYAPVDI	VAMNIVLSGG	-DPDYVALLP	SGFALPDGP	GVNNGG	----	-----	---ILEI	
QESSTDSS-G	AFVVYSPVDL	AALNIAMS GE	-DPSYIPLLS	SGFITSPDGN	GSNSEQGGAS	TSS	-----	-----	---G
QESCTDSSSA	ALVIYTPVDL	PALNIAMSQ	-DTSYIPLLP	SGFAISPDP	---	SSKGG	----	-----	-----
QESCTDAS-G	SYVIYAPVDI	IAMNVVLSGG	-DPDYVALLP	SGFALPDGS	ARGGGSANA	SAGAGVEGGE	GNNLEVVTIT	-----	---
QESCTDAS-G	SYVIYAPVDI	VAMNVVLSGG	-DPDYVALLP	SGFALPDGS	VGGD	----	-----	---Q	---HQEMVSTSS
QDSSTNSY-E	SVVVYAPVDI	NTTQLVLGH	-DPSNIQILP	SGFSIIPDGV	ESRPLVITST	QD	-----	-----	---
QESCTDPT-G	SYVIYAPVDI	VAMNVVLSGG	-DPDYVALLP	SGFALPDGA	VLHGG	----	-----	-----	---ILDV
QESCTDAS-G	SYVIYAPVDV	VAMNVVLN GG	-DPDYVALLP	SGFALPDGP	AGSNMQDGD	----	-----	-----	---GV
QESCTDST-G	SYVIYAPVDI	SAMNIVLSGG	-DPDYVALLP	SGFALPDGP	GYGSAG	----	-----	-----	---ILDV
QESCTDST-G	SYVIYAPVDI	SAMNIVLSGG	-DPDYVALLP	SGFALPDGP	GYGPAG	----	-----	-----	---ILDV
QESCTDST-G	SYVIYAPVDI	AAMNIVLSGG	-DPDYVALLP	SGFALPDGP	GFSPGI	----	-----	-----	---ILDV
QESCTDAS-G	SEVIYAPVDI	VAMNVVLSGG	-DPDYVALLP	SGFALPDSP	KCMAVTNSG	----	-----	-----	---INDL
QESCTDAS-G	SYVVYAPVDI	VAMNVVLN GG	-DPDYVALLP	SGFALPDGP	S-GNAQA AVG	E	-----	-----	---NGS
QESCTDAS-G	SYVIYAPVDV	VAMNVVLN GG	-DPDYVALLP	SGFALPDGP	AHDGGDGDGG	----	-----	-----	---VGV
QETCTDAS-G	SMVVYAPVDI	PAMQLVMNGG	-DSTYVALLP	SGFALPDGP	-----	-----	-----	-----	---SSVGA
QESCTDAS-G	SYVVYAPVDV	VAMNVVLN GG	-DPDYVALLP	SGFALPDGP	PPAGAAPSHG	E	-----	-----	---GL
QESCTDVS-G	SLVIYAPVDI	PAMNVLQGG	-DPAYVALLP	SGFALPDGP	GGDRGALGNE	QG	-----	-----	---GQLTEI
QESCTDVS-G	SLVIYAPVDI	PAMNVLQGG	-DPAYVALLP	SGFALPDGP	GGERGS LGVD	QG	-----	-----	---SGLTES
QETCIDAA-G	SLVVYAPVDI	PAMHVMNGG	-DSAYVALLP	SGFAIVPDGP	RSHGPI SNHG	VN	-----	-----	---GNTGG

QESCIDSS-G SLVVCYCPVDL PAINVAMSGE -DPSYIPLLE SGFTITPDGH LEQGDGASTS SST-----G

890	900	910	920	930	940	950	
.....	.....	.....	.....	.....	.....	.....	..
CMEEG-SLL	TVAFQILVN	--SLPTAKLT	VESVETVNNL	ISCTVQRIKA	ALHCDST---	~~~~~	HDG1
QRPVGGGSL	TVAFQILVN	--NLPTAKLT	VESVETVNNL	ISCTVQRIKA	ALQCES----	-----	ANL2
GGD--GGSL	TVAFQILVD	--SVPTAKLS	LGSVATVNNL	IACVVERIKA	SMSCETA---	-----	HDG2
-----GGSL	TISFQMLVE	--SGPEARLS	VSSVATTENL	IRTTVRRIKD	LFPCQTA---	-----	HDG3
-----S	CLLTVAIQVL	GS--NVTTE	RLDLSTVSVI	NHRICATVNR	ITSALVN---	-----DVG N-	HDG4
-----SCLL	TVGIQVLAS	--NVPTAKPN	LSTVTTINNH	LCATVNOITS	ALSNTITPVI	ASSADVSNQE V-	HDG5
RGNTGGGCLL	TFGLQILVG	--INPTAALI	OQTVKSVETL	MAHTIVKIKS	ALDLQT----	-----	FWA
VNQESKGCCLL	TVGFQILVN	--SLPTAKLN	VESVETVNNL	IACVVERIKA	ALRIPA---	-----	HDG7
-----TLL	TVAFQILVSG	K-ANRSREVN	EKSVDTVSAL	ISSTIQRIKQ	LLNCPEC---	-----	HDG8
-----TLL	TVAFQILVSG	P-SYSPDTNL	EVSATTVNTL	ISSTVQRIKA	MLKCE-----	-----	HDG9
-----TLL	TFAFQIEVTG	P-SYYTDLNL	KDSATTVNTL	VSSAVQRIKA	MLNCE-----	-----	HDG10
GS--GGSL	TVAFQILVD	--SVPTAKLS	LGSVATVNSL	IKCTVERIKA	AVKCENNA---	-----	GbML1
RA-SASGSL	TVGFQIMVS	--NLPTAKLN	MESVETVNNL	IGTTVHQIKT	ALSGPTASTT	A-----	HDG11
-----GSL	TVGFQIMVS	--GLQPAKLN	MESMETVNNL	INTTVHQIKT	TLNCPSTA---	-----	HDG12
GSC--GGSL	TVAFQILVD	--SVPTAKLS	LGSVATVNSL	IKCTVERIKA	ALACDGA---	-----	ATML1
GSC--GGSL	TVAFQILVD	--SVPTAKLS	LGSVATVNSL	IKCTVERIKA	AVSCDVGGGA	-----	PDF2
DRNSQGGSL	TFALQTLIN	--PSPAACKLN	MESVESVTNL	VSVTLHNIKR	SLQIEDC---	-----	GL2
GS--GGSL	TVAFQILVD	--SAPTAKLS	LGSVATVNSL	IKCTVERIKA	AVSCENT---	-----	VvHD1
GS--GGSL	TVAFQILVD	--SVPTAKLS	LGSVATVNSL	IACVVERIKA	AVSGES-NPQ	Q-----	SbHD1
GS--GGSL	TVAFQILVD	--SVPTAKLS	LGSVATVNSL	IKCTVERIKA	AVMCDNA---	-----	PtHD1
GS--GGSL	TVAFQILVD	--SVPSVKLS	LGSVATVNSL	IKCTVERIKA	AVMCDNP---	-----	PtHD2
GS--GGALV	TVAFQILVD	--SIPTAKLS	LGSVATVNNL	IKCTVERIKA	AVTCETA---	-----	RcHD1
GT--GGSL	TVAFQILVD	--SVPTAKLS	LGSVATVNSL	ISCTVDRIKA	AVMRENP---	-----	PaHD1
GSG--GGSL	TVAFQILVD	--SVPTAKLS	LGSVATVNSL	IACVVERIKA	AVCRDS-NPQ	-----	ROC1
GS--GGSL	TVAFQILVD	--SVPTAKLS	LGSVATVNSL	IACVVERIKA	AVSGES-NPQ	-----	ROC2
EHKTG-SLL	TVAFQILVN	--SQPTAKLT	VESVETVNNL	IFCTIKKIKT	ALQCD-----	-----	ZmOCL1
DAGG-GGSL	TVAFQILVD	--SVPTGKLS	LGSVATVNSL	IACVVERIKA	AVCAEAGNPQ	-----	ZmOCL5
GRG--TGSL	TVAFQILVS	--SIPSARLS	LESVATVNNL	ISCTVQRIKS	ALLVEDA---	-----	PhHDZ41
SRG--TGSL	TVAFQILVS	--SIPSARLS	LESVATVNNL	ISCTVQRIKS	ALLVEDA---	-----	PhHDZ43
GSSSVGGSP	TVAFQILVN	--SSPTAKLT	VESVETVNNL	ISCTVQRIKA	ALQCES----	-----	GhHOX1
HGRSSGGSL	TVAFQILVS	--SLPSAKLN	LDSVTIVNNL	IANTVQRIKA	ALNCPSS---	-----	GhHOX3

Supplementary Figure 7