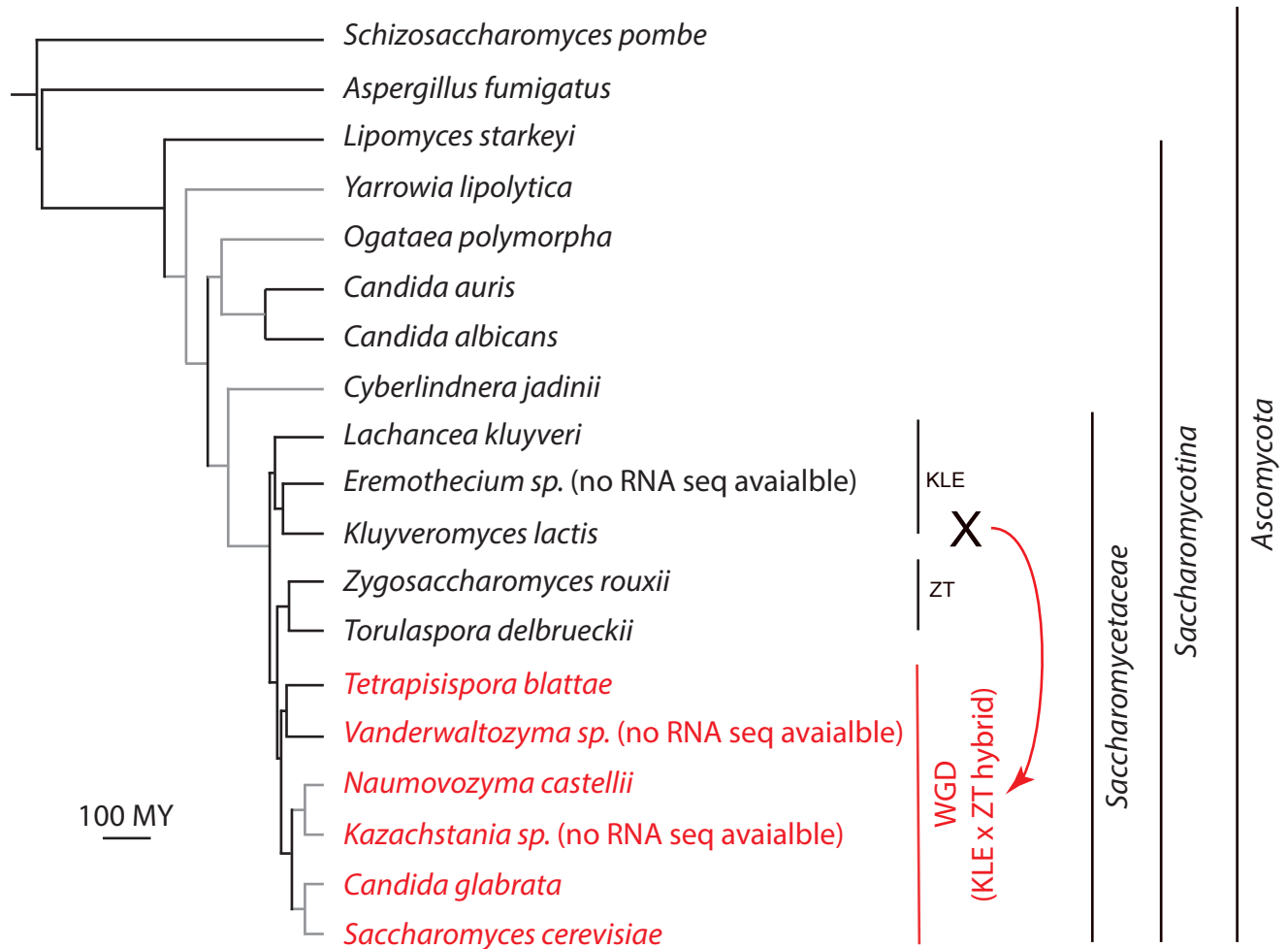


Supplementary Table: Systematic gene names and RNAseq data sets analyzed.

Alternative splicing event	Aspergillus fumigatus	Lpomyces starkei	Yarrowia lipolytica	Ogataea polymorpha	Candida auris	Candida albicans	Cyberindrella jadinii	Lachancea kluyveri	Kluyveromyces fragilis	Torulapora delbrueckii	Zygosaccharomyces rouxi	Tetrapispora blattae chr2olog 1	Tetrapispora blattae chr2olog 2	Naumovozya castellii chr2olog 1	Naumovozya castellii chr2olog 2	Candida glabrata chr2olog 1	Candida glabrata chr2olog 2	Baccharomyces cerevisiae chr2olog 1	Saccharomyces cerevisiae chr2olog 2
SK17/HBS1	AFUA_2G04630	LIPSTDRAFT_140341	YALIOB07557g	OGAPOODRAFT_15909	CJ97_002754	CAALFM_C704260WA	CYBJADRAFT_186489	SAKLOG00594	KLLA0_A07799g	TDELOB02430	ZYRO0A11748g	TBLA_O101600	TBLA0A09240	NCAS_0A03380	NCAS_0G00390	CAGLOK05511g	CAGLOG02255g	SK17	HBS1
YSH1/SYC1	AFUA_1G16800	LIPSTDRAFT_165	YALIOF03817g	OGAPOODRAFT_17082	CJ97_003173	CAALFM_C206230WA	CYBJADRAFT_153538	SAKLOA08096	KLLA0_C04598g	TDELOG03980	ZYROOD14410g	TBLA_0A09750	none	NCAS_0D02950	none	CAGLOF05005g	CAGLOG09779g	YSH1	SYC1
PTC7	AFUA_8G04580	LIPSTDRAFT_72911	YALIOE27533g	OGAPOODRAFT_74966	CJ97_004330	CAALFM_C400340WA	CYBJADRAFT_141740	SAKLOG08580g	KLLA0_D13134g	TDELOE02660	ZYROOD10604g	TBLA_OH01920	TBLA_0A03190	NCAS_0H01710	None	CAGLOJ10692g	None	PTC7	none
SRC1/HEH2	AFUA_8G08530	LIPSTDRAFT_7123	YALIOE11539g	OGAPOODRAFT_93304 OGAPOODRAFT_958067	CJ97_001644	CAALFM_C602930WA	CYBJADRAFT_168209	SAKLOG06116g	KLLA0_B01826g	TDELOA04420	ZYROOD13816g	TBLA_OC01910	TBLA_OE02850	NCAS_0H02840	NCAS_0F01380	CAGLOg07403	CAGLOK06325	SRC1	HEH2
FES1	AFUA_6G04750	LIPSTDRAFT_252835	YALIOF11121g	OGAPOODRAFT_11081	CJ97_002520	CAALFM_C600760WA	CYBJADRAFT_161736	SAKLOB07392g	KLLA0_E11375g	TDELOC04840	ZYROOC15950g	TBLA_OB02500	none	NCAS_0I01190	none	CAGLOK12144	none	FES1	none
NUP100/NUP116	AFUA_4G110707	LIPSTDRAFT_67751	YALIOF28281g	OGAPOODRAFT_15507	CJ97_002114	CAALFM_C306440WA	CYBJADRAFT_166018	SAKLOB11770g	KLLA0_F26697g	TDELOB07030	ZYROOF00660g	TBLA_0A10170	TBLA_OB06810	NCAS_0A08290	NCAS_0H03150	CAGLOF06171	CAGLOL04928	NUP116	NUP100
MDH2/MDH3	AFUA_8G05210	LIPSTDRAFT_3988	YALIOE14190g	OGAPOODRAFT_83598 OGAPOODRAFT_15721 (pseudogene)	CJ97_003540 CJ97_003540	CAALFM_CR00540CA CAALFM_C210480WA	CYBJADRAFT_166114 CYBJADRAFT_170219	SAKLOC12760g SAKLOE04928g	KLLA0_E07525g KLLA0_F17050g	TDELOE00560 TDELOG03230	ZYROOC02684g ZYROOA08470g	TBLA_0A07800 TBLA_OB09220	TBLA_OB0630 none	NCAS_0C04560 NCAS_0A04020	none none	CAGLOE01705g CAGLOL06798g	none none	MDH2 MDH3	none none
GND1/GND2	AFUA_8G08050	LIPSTDRAFT_1792	YALIOB15586p	OGAPOODRAFT_17455	CJ97_001894	CAALFM_C113880CA	CYBJADRAFT_169206	SAKLOH01848g	KLLA0_A09339g	TDELOG00790	ZYROOD07876g	TBLA_OC06670	none	NCAS_0F02030	none	CAGLOM13343g	none	GND1	GND2
PRP5	AFUA_1G10050	LIPSTDRAFT_55276	YALIOC05368g	OGAPOODRAFT_46979	CJ97_002977	CAALFM_C306720WA	CYBJADRAFT_135226	SAKLOA06204g	KLLA0_F10505g	TDELOB04060	ZYROOG14960g	TBLA0D03520	none	NCAS0H01280	none	CAGLOK07029g	none	PRP5	none
MTR2	no clear ortholog	no clear ortholog	YALIOB11132g	OGAPOODRAFT_92810	CJ97_003653	CAALFM_C210640CA	CYBJADRAFT_168117	SAKLOG16214g	KLLA0_B02629g	TDELOE00860	ZYROOB13156g	TBLA0I03130		NCAS0A02660	none	CAGLOD00040g	none	MTR2	none
GCR1	no clear ortholog	no clear ortholog	no clear ortholog	no clear ortholog	no clear ortholog	no clear ortholog	no clear ortholog	SAKLOH10010g	KLLADE23431g	TDELOB03030	ZYROOD03916g	TBLA0B04590	TBLA0H03610	NCAS0C02090	none	CAGLOH05379g	none	GCR1	none
APE2/AAP1	no clear ortholog	no clear ortholog	no clear ortholog	no clear ortholog	no clear ortholog	no clear ortholog	no clear ortholog	SAKLOG10736g	KLLADC11033g	TDELOE03420	ZYROOG16324g	no clear ortholog	no clear ortholog	NCAS0F02430	NCAS0A06570	CAGLOE06226g	CAGLOJ00341g	APE2	AAP1
RNAseq datasets analyzed		SRR9036780 SRR9036793	ERR629124 ERR629125	SRR6289508 SRR6289512 SRR6289518 SRR6289543	SRR6900283 SRR8351131	SRR1654893 SRR1654895 SRR1654896 SRR10419594 SRR10419596	SRR424213 SRR424215 SRR424216	SRR6470147 SRR8690261 SRR8690280	SRR8690273 SRR5132775 SRR5132776	SRR8933807 SRR8933810 SRR8933814 SRR8933818	SRR8621094 SRR8621095 SRR8621096	SRR11352844 SRR11352845		SRR2937545 SRR8690272 SRR8838454		SRR1582640 SRR9020499 SRR9020501		SRR2045244 SRR10842942	

Supplemental figure 1: Expanded species tree that includes full species names, and the position of three genera (*Eremothecium*, *Vanderwaltozyma* and *Kazachstania*) that are mentioned in the main text, but not further analyzed because no RNA sequencing data is available.



Supplemental figure 2: PTC7 sequences are aligned. For the species with alternative splicing the intron retained sequence is shown and the sequences encoded by the retained intron are highlighted in yellow.

```

AfumPtc7      1 --MILLASSRACSLAC--SSLQPVARD---RSLSFATSTATWSR-HLPDSLFSLSQ--
LstaPtc7      1 -----MPAPT-----RFSLLVAAYPT-ITAALLFAFRRL--
YlipPtc7      1 -----
OpolPtc7      1 --MLIYNTRV-----ASYGP-----GFT
CaurPtc7      1 --MLLSALTK-----RAL-----VGYTS-HHAASECLQTAAFK
CalbPtc7      1 MSMLLTILSK-----KNG-----VSLGS-SF-----
CjadPtc7_retain 1 --MFISSIRR-----SKFIVLVILISLTT-HILLN---TAVV-
LkluPtc7_retain 1 --MFVSAGTRPALRLS-----KRMFLSSLLV-LL-IAMLC-FVAPFVLTQ-Y---
KlacPtc7_retain 1 --MFI--GIRQH-----VPRTVFRSMVPVLFA-FTLYV-LLT-----
ZriuPtc7_retain 1 --MFAKAGLRPIYGSTARGAARRPFLGRQWQGMLWMLVL-ITS---IIVGWSL-----
TdelPtc7_retain 1 --MFVSVGVRASARGPH-----VATNLWHSMFLFVVV-SALVV-VIAGYVLIQGY---
TblaPtc7a     1 --MN----MSI-----MRANSRY---YIFS-ISFVV-LIVTFLFST-----
TblaPtc7b     1 --MFCSSSLRPLRGSITS-----VYK-----ISKISSHSATKLLIKRT---
NcasPtc7_retain 1 --MFAATGLRTTVRQS-----PLLFYSMFTLLAL-ALLIP-ILIPSI-----
CglaPtc7_retain 1 --MY--SAGVRV-----VNPWVLTKSM-LI-ISLIM-LIAGFLLTYTGLYC
ScerPtc7_retain 1 --MFANVGFRTLRVSR-----GPLYGMFIVLFI-GVLIA-KFAGQMLIDSE--T
consensus     1  mf      r                               1  vtl  1  1

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AfumPtc7      51 -RLS-SSY---LPRF---SRRTFHATS-----L
LstaPtc7      29 -QYQ-YPI---LDRIITHQTQARLFQHNTATGLAITTPTNTAAQYTAQISQSATGASG
YlipPtc7      1 -----MFRPTRLPRIQLL-----K
OpolPtc7      17 SR-----LTVSARLGRRCFSNDSY---TFRNFQNGH-----T--IA
CaurPtc7      31 RYFSFSSFSRAPKNSASNPEDTSDNQWSSSESEASFDGSNSSS--SAGAASSTASNYD
CalbPtc7      21 -----I---KTSARSFASSRSYWGYYGKGSARDYSTAAS--P--SATASAA SMNYD
CjadPtc7_retain 32 -----KTKVIRPR-----HFSSSTSSS-----SSSSSSS---
LkluPtc7_retain 42 -L---SDLYK-----YG-KWNHARSFFSS---SSSG-SSS-----S---G
KlacPtc7_retain 32 -----VFDLDYKTLQSFSSS---AGSN--NSNS-----WSSSS--SS
ZriuPtc7_retain 48 -----IH--V-DFAVYQQLRGFFSG---KGSWGWSGT-----SS--TV
TdelPtc7_retain 46 -E---FDLEA--L-SAQLYRGSRRCFSSG---KGDG-YTGGD-----G---S
TblaPtc7a     31 -----V---LKNYF-----ND--WNLKD-----TIKF--TR
TblaPtc7b     37 -----FVNG---SWTTYNKSYSNYNSNNSNSNDGGSSNSN-----YTHH-H--QL
NcasPtc7_retain 39 -E---YNFNR--T-CTQWYPLTKRSFTSA---SGTNGNGHYN-----YSTNQ--SS
CglaPtc7_retain 40 PS---YQIE SGTLYNRVFGNCSRRLFSSG---GKSWYWNGNN-----GSA--TT
ScerPtc7_retain 44 NF---SHIIG--S-CSQIISFSKRTFYSS---AKSG-YQSNN-----SHGDA--YS
consensus     61                               s r fws                               s t

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AfumPtc7      71 FSLDAPRISYRVAASSSPKNRRFHPPTNFHNFQPELHDAIGVVTE-EIDAATRRKRRPDS
LstaPtc7      83 ASMASNNFYTISPSYHAKDRNLVARK-----YSG---S-VAANSKGRATRPAS
YlipPtc7      15 PLFSRRFLSYTIAEAYSAPRPPHQ-----QSKPPAGENRPT
OpolPtc7      48 KHFE TAGHGYLMSLAFEPKDR LKDVNRPD-----DGLISKYRKKVQNTTVYDSPT
CaurPtc7      89 KSSIDRIVNFNVAFAVQPKNR TKS NVF-----TRNTKLT PAELSPS
CalbPtc7      66 -SALTSVSHYNI AVAFQPKDREESNL F-----KKKQ-PSPSLQSPS
CjadPtc7_retain 57 --LHVDSFPFEASVAFQPKEREENRM-----MRRHMKVQRVESPS
LkluPtc7_retain 70 SSSSTLFNYKA AVAYQAKDRNDPVY-----ANIK--VDSPT
KlacPtc7_retain 65 YSASSDAFNYQVAIAYQPKDRNEPIY-----AKLKESLQSP T
ZriuPtc7_retain 80 PQDGSQQFNYKAVVAFQPKDRDDPVY-----KALAGK-FSPT
TdelPtc7_retain 79 NGASSTQFSYKTAVAYQPKDRDDPIY-----KRMKTQLQSAT
TblaPtc7a     51 YSNLEPNFHYVAEAAFAQPKDRSSIY-----QKLANSVDSPT
TblaPtc7b     77 QDTPNNTFSYNTSVAYQPKDREDQIY-----KKLIASKKSPT
NcasPtc7_retain 79 YSTSASPF SYKTAVAYQPKDRDDQIY-----RN LKDSLASPT
CglaPtc7_retain 81 DHTGGNSFVYKTAVAYQPKDREDVIY-----QK LKESLQSLT
ScerPtc7_retain 83 SGSQS GPF TYKTAVAFQPKDRDDL IY-----QK LKDSIRSPT
consensus     121 s s f y avayqpKdRee vy                               lr 1 spt

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AfumPtc7	130	GEDA	FFVSRVGSQDS-----	GAI	FAVADGVGGW	VESKVD	PANF	SHALCL	YMALE	ALSW
LstaPtc7	128	GEDS	FFFSKIRESE-----	ES	VALGVIDGVGGW	NEIGV	DATDF	SHSLAE	AMAE	LTA
YlipPtc7	53	GEDA	FFHVSLSKTDSPDSY	TYSNTAF	GVTDGVGGW	AEMGVN	S	DFSY	YLCH	ESSNLA
OpolPtc7	98	GEDNY	VMAY--ND-----	SK	VLAVGLDGVGGW	SEQG	F	DSSAIS	REL	STHVT
CaurPtc7	130	GEDNL	FVTTQSSD-----	GY	FALGVADGVGGW	AEGYD	S	SAISREL	CH	SMKTIF
CalbPtc7	105	GEDNL	FVSNE-KA-----	GC	IAGVADGVGGW	SEAGYD	S	SAISREL	CAS	LRRQFES
CjadPtc7_retain	96	GEDNY	FIAKA--G-----	SK	LACGVADGVGGW	AELGYD	S	SAISREL	CNS	MKESFTK
LkluPtc7_retain	105	GEDNY	FIGI-NRI-----	D	VYAGVADGVGGW	AEHG	F	DSSAISREL	C	SAMRQFSQT
KlacPtc7_retain	102	GEDS	YFVAP-RSS-----	S	ELYAGVADG	IGGWAN	HGYD	S	TAISREL	CLAMKS
ZriuPtc7_retain	116	GEDNY	FIRS-VNP-----	T	FYAGVADGVGGW	AEHGYD	S	SAISREL	C	SAMSEFALS
TdelPtc7_retain	116	GEDNY	FVTL-NNP-----	G	VYAGVADGVGGW	AEHGYD	S	SAISREL	C	RAMNDFSSL
TblaPtc7a	88	GEDS	YFIAS-NSY-----	N	DIYIGVADGVGGW	AERGYD	S	SAISREL	C	SSMKALCRA
TblaPtc7b	114	GEDNL	FINCSSLN-----	D	EVFAAVADGVGGW	AEGYD	S	SAISREL	C	ENLVFSNSF
NcasPtc7_retain	116	GEDNY	FITSLDNN-----	D	EIFA	AVADGVGGW	AERNYD	S	SAISREL	C
CglaPtc7_retain	118	GEDNY	FIIQA-NAA-----	N	DVYAGVADGVGGW	AEHGYD	S	SAISREL	C	KALKEMAATL
ScerPtc7_retain	120	GEDNY	FVTS-NNV-----	H	DIFAGVADGVGGW	AEHGYD	S	SAISREL	C	KKMDEI
consensus	181	GEDnyfv			diyagVaDGvGGW	ae	hgyd	s	sai	SreLc m l

AfumPtc7	184	DSST-----	DKL	RAKNLL	QSGYD	QLVAD	KS	IRAGG	STASV	GVGLE-DGQ	VEL
LstaPtc7	180	STD	TS	AKRDES	NSIVSK	FSFP	PLVLL	DAGY	NAIR	NSGKV	KAGGSTACV
YlipPtc7	113	AKE	IEKEPA	FAEKP-LAS	LISPKQL	LTNAY	NKIV	REKTV	KAGGSTAC	IGVAGQ-DGQ	VAV
OpolPtc7	147	-----	EDH	LTPLE	ILD	KAYTK	MKQD	GS	VEVGS	TTICF	GVIDAMTNK
CaurPtc7	181	----A-----	SK	QHS	LTPK	SLLCS	AFDE	IAKSP	KVEIG	GT	TACLGII
CalbPtc7	155	----G-----	TE	---	SNPKQL	LSLAF	KEVL	SSPQ	VEIG	GT	TACLGVLTS
CjadPtc7_retain	145	----G-----	DH	---	LSPVQ	LLNHAF	DKIQ	NEDI	V	KVG	GT
LkluPtc7_retain	155	-TN-V-----	W	KENN	F	PKEL	IELG	YKKI	KEEG	S	TVGGTTA
KlacPtc7_retain	153	-----	SKD	IAP	KE	LLQMA	FSSLL	N	EEKVE	VGGTTA	IVAH
ZriuPtc7_retain	166	-----	V	GP	PK	KLIELG	YDKIQ	KE	GT	V	QVGGTTA
TdelPtc7_retain	166	-SN-K-----	K	D	SHA	FP	PK	KLI	EMGYN	KIKND	GIVK
TblaPtc7a	138	-----	Q	T	EL	TPKQL	LSKGY	NKIK	S	DGIVK	VGSTTAN
TblaPtc7b	166	FQLQT-----	T	NA	V	T	KAP	KE	LLD	LAYL	KTKD
NcasPtc7_retain	168	S-----	I	N	K	V	T	TPKQ	VLE	VS	FQKIK
CglaPtc7_retain	169	-----	H	K	P	L	TPKQ	LLD	N	A	YAKIK
ScerPtc7_retain	171	AEN-S-----	S	K	E	T	L	TPK	KI	I	G
consensus	241				lspk	lld	ay	kir	d	vrv	GgtTa

AfumPtc7	230	ANLGDS	GSMLLRLA----	AV	HHYSVP	QTHGF	NT	TPYQL	SIIP	PRM	RAQAS
LstaPtc7	239	ANLGDS	GFFIFRDG----	K	I	H	YMSIP	QTHY	FN	APYQL	AII
YlipPtc7	171	ANLGDS	GFMVFRNG----	K	L	AGG	S	KAQTH	AF	NT	TPYQL
OpolPtc7	191	VNLGDS	WFGVFRKQNSRF	KCV	FESKE	Q	TYS	FN	APYQL	S	VIP
CaurPtc7	227	ANLGDS	WCGVFRDC----	K	L	VEET	Q	F	QTHN	F	NT
CalbPtc7	198	ANLGDS	WCGLFRDS----	K	L	I	NET	T	N	F	QTHN
CjadPtc7_retain	187	ANLGDS	WCGVFRQG----	S	L	I	AE	T	KVQ	THGF	NT
LkluPtc7_retain	203	ANLGDS	WCGVFRES----	K	L	I	F	Q	T	K	F
KlacPtc7_retain	196	SNLGDS	WCGVFRDC----	K	L	T	F	E	T	K	F
ZriuPtc7_retain	208	ANLGDS	WCGVFRND----	Q	L	A	F	Q	T	K	Y
TdelPtc7_retain	214	ANLGDS	WCGVFRDS----	K	L	V	F	Q	T	R	F
TblaPtc7a	181	ANLGDS	WCGVIRDS----	K	I	V	F	Q	T	K	F
TblaPtc7b	216	ANLGDS	WCGVFRDN----	K	L	I	F	Q	T	E	N
NcasPtc7_retain	213	ANLGDS	WCGVFRNE----	T	L	V	F	Q	T	K	L
CglaPtc7_retain	212	TNLGDS	WCAVFRDS----	K	L	V	F	Q	T	E	P
ScerPtc7_retain	220	ANLGDS	WCGVFRDS----	K	L	V	F	Q	T	K	F
consensus	301	aNLGDS	Wcgvfrd		klvf	qtkf	q	tv	g	f	NaPyQLaii

AfumPtc7	286	RDAVVNTNLHMQHGDVLMLATDGVYDNLNNQDILKLITSRMILTGAWTATTDLGIKVSDNL
LstaPtc7	295	S D ANLS T HK L KHGDV V LFCTDGVLDNLLPSDCLRI V NEEMISQGNWIVDRRSGDIQASGE
YlipPtc7	227	AMADQ S F S FTAEPGDVIVLATDGLTDNMSAQDTLKI V NETMLEHGSWIKDDKEGIKS-SGE
OpolPtc7	251	KDADEYE F QLES G DVIMFTTDGLIDNVVIND V ALYLLDDCFA-----ADQ-
CaurPtc7	283	QQSDEYA W Q L K G DLVLFATDGVTDNVVPQ D IE V FLKDKRDK-----KAP-
CalbPtc7	254	EAADEYT W DLKS G DVVMFATDGVTDNVIPQ D IELFLKDHEE-----TNQ-
CjadPtc7_retain	241	DDADEYE F NVVKDDIVIFATDGVIDNI D VKDIELYLKDNE-----KTP-
LkluPtc7_retain	259	SDADEYT F QLAKNDIVVLATDGVTDNIIATED M E I FLKDHAN-----AQD-
KlacPtc7_retain	252	TDADD S Y S FKLQKNDIVVLATDGVTDNIIA V ED M E L FLKDKIES-----SQS-
ZriuPtc7_retain	264	ADADEYT F QLEKGDIVFLATDGVTDNVATED M E L FLKDNQSL-----VGSD-
TdelPtc7_retain	270	SDADEYS F QLAKDDL V VLATDGVTDNISSD D IQLFFRDNEAM-----IEKD-
TblaPtc7a	237	LDADEYS F QLQKEDIVLLATDGLVDNIEPN D IAL F ISNRFAS-----KDN-
TblaPtc7b	272	SDADEYS F QLKPNDIVILATDGVTDNIIATG D IELY L KDNYDNKQ-----LNNKE
NcasPtc7_retain	269	SDADEYT F QLQKNDIVMMATDGVTDNII T DDISLFLKDESAQ-----IQKN-
CglaPtc7_retain	268	SDADEYN F QLSKGDIVILATDGVTDNIIAIED L E L FLRDNNDQ-----LNEN-
ScerPtc7_retain	276	RDADEYS F QLKK D IIILATDGVTDNIIATD D IELFLKDNAAR-----TNDE-
consensus	361	dadeytfql kgDivmlaTDGvtDNi Dielflkd

Supplemental figure 3. Alignment of peroxisomal and cytoplasmic malate dehydrogenase sequences. The C-terminal PTS1 signal is highlighted in yellow.

AfumMdh3	1	-----MVKAAVLGASGGIGQPLSLLLKACPLV-----
AfumMdh2	1	-----MVKAAVLGASGGIGQPLSLLLKACPLV-----
YlipMdh3	1	-----MVKAVVAGAAGGIGQPLSLLKLSPYV-----
YlipMdh2	1	-----MVKAVVAGAAGGIGQPLSLLKLSPYV-----
LstaMdh3	1	-----MVKAVVAGASGGIGQPLSLLKLSPYI-----
LstaMdh2	1	-----MVKAVVAGASGGIGQPLSLLKLSPYI-----
OpolMdh2	1	-----MVKVTVCGAAGGIGQPLSLLMLKMPYI-----
CaurMdh3	1	-----MVKVTVCGAAGGIGQPLSLLKLINARV-----
CaurMdh2	1	-----MVKVTVCGAAGGIGQPLSLLKLINPQV-----
CalbMdh3	1	-----MVKVTVAGAAGGIGQPLSLLKLINPNV-----
CalbMdh2	1	-----MVKVAILGAAGGIGQPLSLLTKLINPNV-----
CjadMdh3	1	-----MTKVTVLGAAGGIGQPLSLLKLSPYV-----
CjadMdh2	1	-----MKVTVCGAAGGIGQPLSLLKLSPYV-----
LkluMdh3	1	-----MVKVTVLGAAGGIGQPLSLLKLSPYI-----
LkluMdh2	1	-----MP-HS---L--TDKQVLKIAVLGAAGGIGQSFMSLLKTLHTLLPPH---S
KlacMdh3	1	-----MVSVTVLGSSGGIGQPLSLLKLDPHV-----
KlacMdh2	1	-----MPAVN---A--QEKEILKISVLGAAGGIGQSLSLLKSNAGFLLPHE---T
ZrouMdh3	1	-----MKVAIVGASGGIGQPLSLLMKLINPLV-----
ZrouMdh2	1	-----MPHSI---N----GDVKIAVLGAAGGIGQSLSLLKTLQTLREL---N
TdelMdh3	1	-----MVKVAVVGASGGIGQPLSLLKLINPYV-----
TdelMdh2	1	-----MPHIV---E--TIPQAIKIAVLGAAGGIGQSLSLLKTLQLR-----S
TblaMdh3	1	-----MKVSVLGACGGIGQPLSLLKKNNEYI-----
TblaMdh2a	1	-----MPVPTNTNANASNQPLTLTVIGAAGGIGQSLSLLKTSNYP-----T
TblaMdh2b	1	MRQTKRAKLDLTSDGNINKDVVDNNQADAVKPVKITIIGAAGGIGQSLSLLKTLQLPNSSAS--KYR
NcasMdh3	1	-----MVKVTVILGASGGVQPLSLLKLINKHI-----
NcasMdh2	1	-----MPHSV---NPALQPNTLKIAILGAAGGIGQSLSLLKTLQLHFPLKTNSTQRD
CglaMdh3	1	-----MVKVAVLGASGGVQPLSLLKLINTMI-----
CglaMdh2	1	-----MPHIT---G--NNEADLVKVSILGAAGGIGQSLSLLVKTLQLVLAGS-----A
ScMDH3	1	-----MVKVAILGASGGVQPLSLLKLSPYV-----
ScMDH2	1	-----MPHSV---TPSIEQDSLKIAILGAAGGIGQSLSLLKAQLQYQLKES--NRS
consensus	1	mvkv vlGaaGGiGQplSl1lKlnp v

AfumMdh3	28	---DELALYDVVN--TPGVAADLSHISVAKVSGYLPKDDG---LKNALTGTDIVVIPAGIPRKPGMTR
AfumMdh2	28	---DELALYDVVN--TPGVAADLSHISVAKVSGYLPKDDG---LKNALTGTDIVVIPAGIPRKPGMTR
YlipMdh3	28	---TELALYDVVN--SPGVAADLSHISTKAKVTGYLPKDDG---LKNALTGANIVVIPAGIPRKPGMTR
YlipMdh2	28	---TELALYDVVN--SPGVAADLSHISTKAKVTGYLPKDDG---LKNALTGANIVVIPAGIPRKPGMTR
LstaMdh3	28	---DELALYDVVN--SPGVAADLSHISTKAKVTGYLPADDG---LKAALTGADVVIPAGIPRKPGMTR
LstaMdh2	28	---DELALYDVVN--SPGVAADLSHISTKAKVTGYLPADDG---LKAALTGADVVIPAGIPRKPGMTR
OpolMdh2	28	---NELSLFDVVN--VPGVGTDLSHIDDTKVSYHLKSDD--NNTGLSQALKGSNFVIPAGVPRKPGMTR
CaurMdh3	28	---SHLSLYDIVN--ARGVAADLSHINTPATVSGHQFANKEDKTALVEALQGSDVVIPAGVPRKPGMTR
CaurMdh2	28	---TELSLFDVVN--VPGVGADLSHINTDAATKAFLPSSKEDKTALAESLKGAIDLVIIPAGVPRKPGMTR
CalbMdh3	28	---DELALFDIVN--AKGVAADLSHINTPAVVTGHQFANKEDKTATEALQGTDLVIPAGVPRKPGMTR
CalbMdh2	28	---DELALFDVVN--VPGVGADLSHINSDSKTQSYLPKDKEDKTALAAALKGSDLVIIPAGVPRKPGMTR
CjadMdh3	28	---DELSLYDIRL--AHGVATDLSHINSSVKVSGFEPKDKNDQQAIAKQALAGTDVVIIPAGVPRKPGMTR
CjadMdh2	27	---THLALYDVVN--APGVGADINHIDTDVVSSHLPQDDG---LQMALTNADLVLIIPAGVPRKPGMTR
LkluMdh3	28	---STLALYDIRL--APGVAQDLSHINTNCSCGYKKE-----EAREALQGAHVVIIPAGVPRKPGMTR
LkluMdh2	43	DKHLHVAMYDINKDAIVGTADLSHIDTPVTLSHHFPASRDDLSALKECLADAALIVIPAGVPRKPGMTR
KlacMdh3	28	---SSLRLYDLKL--SHGNATDLSHIDTNSTSEGFNTA-----EIGQALKGAQLVLIIPAGIPRKPGMSR
KlacMdh2	44	STHIRLSLYDVNKDAIVGTAADLSHIDTPITTTAHYPDDS--NGGIGQCLSNASVVIPAGVPRKPGMSR
ZrouMdh3	27	---TELSLYDIRL--APGVAQDLSHISTNSVCQGFEEKD-----DIARALQGAHVVIIPAGVPRKPGMTR
ZrouMdh2	39	HRHAQLALYDVNADAVRGVAADLSHIDTGVTVTG---YEG---DRIGEALEGTDIVLIIPAGVPRKPGMTR
TdelMdh3	28	---SELALYDVRL--AKGVAQDLSHISTNAECRGYDKE-----EIGQALKGAQVVLIPAGVPRKPGMTR
TdelMdh2	38	TSHVHLALYDVNADGVNGVAVDLSHVDTPTVTVSAHSFQT---NGMMECLAGADLVLIIPAGVPRKPGMTR
TblaMdh3	27	---DELALYDIRL--SQGVATDLSHINTNCRVQGYGKD-----QLSKALEGCDVVVIIVAGIPRKPGMKR
TblaMdh2a	44	TRPVNVNLFVDVNTTGLNGVATDLSHMNTQANVKAC-----HSLQDAVTDADLIVIVAGVPRKPGMTR
TblaMdh2b	69	YGTVHLALYDINKDGVNGVTTDLSHIDTAVHVTSHSGE-----DGLVESLTDSDLIVVTAGVARKPGMTR
NcasMdh3	28	---TELALYDIKP--VEGISKDLSHINTNSECTGFKDS-----EIGEALHGSDIVLIIPAGVPRKPGMSR
NcasMdh2	50	KNHIHLALFDVNEDAINGVADLSHIDTPVVISNHSFK-----TGIEDCLKNCSLVVIPAGMPRKPGMTR
CglaMdh3	28	---SELALYDIKL--AEGVATDLSHINTNADCVGYSTD-----DIGQALKGAAVVVIIPAGVPRKPGITR
CglaMdh2	43	DKNLKLALFDVKNDAVNGVGTDLSHIDTQVEVSMMHNPQEG---DGINSCLKGADIVVIIPAGVPRKPGMTR
ScMDH3	28	---SELALYDIRA--AEGIGKDLSHINTNSSCVGYDKD-----SIENTLSNAQVVLIPAGVPRKPGLTR
ScMDH2	48	VTHIHLALYDVNQEAINGVTADLSHIDTPISVSSHSPA-----GGIENCLHNASIVVIIPAGVPRKPGMTR
consensus	71	elalyDv GvaadlsHi t vsgy p 1 al gadivvipAGvpRkPGmtR

AfumMdh3	89	DDL	F	K	V	N	A	G	I	V	R	D	L	V	T	G	I	A	Q	Y	C	P	K	----	A	F	V	L	I	I	S	N	P	V	N	S	T	V	P	I	A	E	V	L	K	K	Q	-----	G	V	F	D	P	K	R	L	F	G	
AfumMdh2	89	DDL	F	K	V	N	A	G	I	V	R	D	L	V	T	G	I	A	Q	Y	C	P	K	----	A	F	V	L	I	I	S	N	P	V	N	S	T	V	P	I	A	E	V	L	K	K	Q	-----	G	V	F	D	P	K	R	L	F	G	
YlipMdh3	89	DDL	F	K	I	N	A	G	I	V	R	D	L	V	T	G	V	A	Q	Y	A	P	D	----	A	F	V	L	I	I	S	N	P	V	N	S	T	V	P	I	A	E	V	L	K	K	H	-----	N	V	F	N	P	K	K	L	F	G	
YlipMdh2	89	DDL	F	K	I	N	A	G	I	V	R	D	L	V	T	G	V	A	Q	Y	A	P	D	----	A	F	V	L	I	I	S	N	P	V	N	S	T	V	P	I	A	E	V	L	K	K	H	-----	N	V	F	N	P	K	K	L	F	G	
LstaMdh3	89	DDL	F	N	I	N	A	G	I	V	R	D	L	I	T	G	I	A	L	Y	A	P	S	----	A	F	L	I	I	S	N	P	V	N	S	T	V	P	I	A	E	V	L	K	K	H	-----	G	V	F	D	P	K	K	L	F	G		
LstaMdh2	89	DDL	F	N	I	N	A	G	I	V	R	D	L	I	T	G	I	A	L	Y	A	P	S	----	A	F	L	I	I	S	N	P	V	N	S	T	V	P	I	A	E	V	L	K	K	H	-----	G	V	F	D	P	K	K	L	F	G		
OpolMdh2	92	DDL	F	K	I	N	A	G	I	C	S	E	L	A	T	G	I	A	E	T	C	P	D	----	A	T	V	L	V	I	S	N	P	V	N	S	T	V	P	V	F	A	E	V	F	K	K	-----	G	I	F	N	P	R	K	L	F	G	
CaurMdh3	93	A	D	L	F	N	I	N	A	S	I	V	R	D	L	V	A	N	I	G	R	T	C	P	N	----	A	A	I	L	I	S	N	P	V	N	A	T	V	P	I	A	E	V	L	K	K	L	-----	G	V	F	N	P	R	K	L	F	G
CaurMdh2	93	DDL	F	N	I	N	A	S	I	V	K	G	L	A	E	G	I	A	E	N	A	P	K	----	A	F	V	L	I	I	S	N	P	V	N	S	T	V	P	I	A	E	T	L	K	A	K	-----	G	V	F	D	P	A	R	L	F	G	
CalbMdh3	93	A	D	L	F	N	I	N	A	S	I	R	D	L	V	A	N	I	A	R	V	A	P	T	----	A	A	I	L	I	S	N	P	V	N	A	T	V	P	I	A	E	V	L	K	K	L	-----	G	V	F	N	P	R	K	L	F	G	
CalbMdh2	93	DDL	F	N	I	N	A	S	I	V	Q	L	A	E	G	I	A	N	S	P	K	----	A	F	V	L	V	I	S	N	P	V	N	S	T	V	P	I	A	E	T	L	Q	A	K	-----	G	V	D	P	A	R	L	F	G				
CjadMdh3	93	DDL	F	N	I	N	A	G	I	K	S	L	A	S	A	I	A	E	T	A	P	N	----	A	F	V	L	V	I	S	N	P	V	N	S	T	V	P	I	A	E	T	F	K	S	Y	-----	G	V	F	N	P	K	L	F	G			
CjadMdh2	88	DDL	F	A	I	N	A	G	I	V	R	D	L	A	L	A	V	A	T	H	A	P	N	----	A	M	V	L	V	I	S	N	P	V	N	S	T	V	P	I	A	E	V	L	K	A	-----	Q	V	F	N	P	R	L	L	G			
LkluMdh3	87	DDL	F	K	I	N	A	G	I	V	K	L	I	S	Q																																												

AfumMdh3	195	--LDIPADKYDALVNRVQFGGDEVVKA--KDAGSATLSMAYAGFRFAEKVIRASQGGSGI-----
AfumMdh2	195	--LDIPADKYDALVNRVQFGGDEVVKA--KDAGSATLSMAYAGFRFAEKVIRASQGGSGI-----
YlipMdh3	195	--VEIPADKLDDLVKRIQFGGDEVVQA--KDGLSATLSMAQAGFRFAEAVLKGAAAGEKGI-----
YlipMdh2	195	--VEIPADKLDDLVKRIQFGGDEVVQA--KDGLSATLSMAQAGFRFAEAVLKGAAAGEKGI-----
LstaMdh3	195	--VEISGSDRDA LVHRIQFGGDEVVQA--KEGKSATLSMAHAGFRFVDSILKAVAGETGV-----
LstaMdh2	195	--VEISGSDRDA LVHRIQFGGDEVVQA--KEGKSATLSMAHAGFRFVDSILKAVAGETGV-----
OpolMdh2	203	--ALEDEKKIDALVHRVQYGGDEVVQA--KNGAGSATLSMAYAGYKFLHAVLAASTGDTTI-----
CaurMdh3	204	--DKLSPSQYKEFVHRVQFGGDEVVKA--KNGAGSATLSMAYAGYRFAENILDSISGPG-F-----
CaurMdh2	202	--DKLSAEQKKELIHRVQFGGDEVVKA--KDAGSATLSMAYAGYRLAESLLKAAAG-EDV-----
CalbMdh3	200	--GVLSDSDYKNFVHRVQFGGDEVVKA--KNGAGSATLSMAYAGYRFADYVISSLTGATP-----
CalbMdh2	203	--DILSEEQKKELIKRVQFGGDEVVQA--KNGAGSATLSMAYAGYRLAESILAAVNGKTDI-----
CjadMdh3	203	--AKLSTDQKKQLVHRVQFGGDEVVKA--KNGAGSATLSMAYSGYTFAEALLRAVKG ERGV-----
CjadMdh2	197	--QSLNDEQRDALVHRVQYGGDEVVQA--KKGAGSATLSMAYAGFQLAERLMKSAHGDNES-----
LkluMdh3	200	--R--DKHAWERYVKRVQFGGDEVVKA--KDAGSATLSMALAGYFAEKVLKSLHLET-----
LkluMdh2	229	--PLDMEQRKSLIHRVQYGGDEVVKA--KNGAGSATLSMAYAAFKITRKFVDLLGNATS-----
KlacMdh3	200	--R--DSNVYESYVHRVQFGGDEVVKA--KDGSGSATLSMAWAGYTFAKKLLNSLHLNTAG-----
KlacMdh2	228	--NLLDNGMRLKMVHRVQYGGDEVVKA--KNGNGSATLSMAYAGFKIAAKFIDLVGNTDT-----
ZrouMdh3	196	-----KPHYQEFVHRVQFGGDEVVKA--KAGAGSATLSMAFAGYRFADSILKSLAGEQ-----
ZrouMdh2	218	--NRLSQDALEALVQRVQFGGDEVVRA--KNGAGSATLCMAHAAYTVASFIPITGQKRS-----
TdelMdh3	207	-----GAEYGKFVHRVQFGGDEVVKA--KEGAGSATLSMALAGYRFAEQVLRSIHRES-----
TdelMdh2	220	--FPLTKDQLQQLVHRVQYGGDEVVQA--KNGAGSATLSMAHAAFKCAQGFVALLGGEEQEE-----
TblaMdh3	204	--FNNDLEEYKGYIKRIKFGGEEVVKA--KEGSGSATLSMALAGYNFIEIILENIKIARRS-----
TblaMdh2a	211	--AKLSKDQIDSLIHRVQYGGDEVVQA--KNGQGSATLSMAFAAFKVIQLDLPLVLKKIDY-----
TblaMdh2b	260	INTLISEEDVAKLTKRIQFGGDEVVKA--KNGQGSATLAMALAGFRVLEDLTSLLEDEVET-----
NcasMdh3	206	--G---SQHYGEFTHRVQFGGDEVVKA--KNGEGSATLSMALAGYKFTEEILKSI VHEK-S-----
NcasMdh2	234	--KSLDRDQINYLVHRVQYGGDEVVKA--KNGLSATLSMAHAAFKVVNK FVSLLLGNVDQ-----
CglaMdh3	212	--E--KTNKYDEFINRVQYGGDEVVKA--KAKDGSATLSMALAGSKFVNEVLQSVHRRDEHRKRVNRTSD
CglaMdh2	222	--KAVPSEKLGPLVHRVQYGGDEVVKA--KNGAGSATLSMAHAGFQCVVKFAKFLFLGGEKE-----
ScMDH3	206	-----DKQYEHFTHRVQFGGDEVVKA--KQGAGSATLSMAFAGAKFAEEVLR SFHNEK-P-----
ScMDH2	231	--SRLNEDQLKYLIHRVQYGGDEVVKA--KNGKGSATLSMAHAGYKCVVQFVSLLLGNIEQ-----
consensus	281	i d lvhRvqfGGdEvVka KnGaGSATLSMAyagfrfae vlr v g

AfumMdh3	252	-----VEP---TYIYLR-GVTGGE---EIAN-ETG-----VEFFSTLVELGRN-GAEK-AINIL
AfumMdh2	252	-----VEP---TYIYLR-GVTGGE---EIAN-ETG-----VEFFSTLVELGRN-GAEK-AINIL
YlipMdh3	252	-----IEP---AYIYLD-GIDGTS---DIKR-EVG-----VAFFSVPVEFGPE-GAAK-AYNIL
YlipMdh2	252	-----IEP---AYIYLD-GIDGTS---DIKR-EVG-----VAFFSVPVEFGPE-GAAK-AYNIL
LstaMdh3	252	-----VEN---TFVYLS-GIPGGD---AVKSIIPG-----LDFFSVPVELGPS-GAVK-VINVVL
LstaMdh2	252	-----VEN---TFVYLS-GIPGGD---AVKSIIPG-----LDFFSVPVELGPS-GAVK-VINVVL
OpolMdh2	260	-----IES---SYVYLDSDSIPGAK---ETKEIIKG-LYG---GESLDYFAMPVVL SKE-GIKEIKSDIL
CaurMdh3	260	-SSKVPDS---AYVYLPGLRDGAD---LQAKL-ND-----VSFFSVPVHLLNG-EISAFEDPLK
CaurMdh2	258	-----TEC---TFLYLDSSIKGAS---EAKKLVNN-----LDFFSLPVKLSKN-GIAAVEYDVL
CalbMdh3	257	-AGRIPDS---SYIYLPGVSGKE---FSAKYVDG-----VDFFSVPVVL SQG-EIRSFVNPF E
CalbMdh2	260	-----VEC---TFLNLDSSIKGAS---EARKLVKD-----LDFFSLPVQLGKN-GITEVKYDIL
CjadMdh3	260	-----VED---SFVYLDASIPGAS---EVRS-KTG-----VDYLSLPVELGPQ-GAVSVQGGIL
CjadMdh2	254	-A--KYAS---SFIYLD DRIPGAS---YAKE-KLG-----VDYVSLPTVIGAE-GIESIDSSIL
LkluMdh3	253	---TETAP---SFVYLPGITGKE---VQKKLGT-----DVEYFAPVVFYRG-NVVGIDSRCL
LkluMdh2	285	-----LQDT--LYISLKEASGNYIAPGAQELMA-----FINVSYFSIPVTVSTK-GVTHVDSEIL
KlacMdh3	255	--DQHPIP---TFVYLPGLPGKE---LQKKLNT-----SVEFFSAPVKLEKG-IVVAVEHEWV
KlacMdh2	285	-----IDDI--VMYVPLTNRNHQEIAPGSNELRS-----RYINDLLYFSIPLSINRN-GIKKIHYEIL
ZrouMdh3	247	---VSGVP---TFVYLPGINGGSE---VQSKL-G-----GVDFYALPVVFSNG-SVSKVDSSIL
ZrouMdh2	275	-----ISGT--FYVALKDAQGPINSSAKRLG-----SINDLPYFAVPLEITSQ-GVDELDTSVL
TdelMdh3	258	---TDPLP---AFVYLPGLENGSA---AQKKLKD-----TVDYFALPITLVDG-RAAKVDSTVL
TdelMdh2	277	-----YQGT--YYVSLLD RVGQPIGAGAGKLLA-----LVDGCSYFAPVSVTVGGGIRDVDYKVV
TblaMdh3	261	-SQSNVSS---CFVYLN GITNGAE---AQELIRK--YTGL-----KVEYFALPVELMNG-TVKGINLHVL
TblaMdh2a	268	-----VEGA--FYLELQNDILGSVK--LRNLLN-----EPELNYFAAPCKINYT-GTYLIDYSII
TblaMdh2b	319	-----ISDSPGFFLAIRDSNQKPLDITDNDKLTNWL DENFQEKSKNIEFFELPITIDKH-GVKKIDYELL
NcasMdh3	259	--QVATIP---AFVYLPGLVNGKK---VQDKLGK-----DLEYFALPVNLTNG-CVTSVDDKIL
NcasMdh2	291	-----IHGI--CYVSLKDADGSP IAPGAEQLLK-----SIDDCSFFSIPMSISKK-GVTAIDFDII
CglaMdh3	278	RKNVTISS---TYVYLPGLSNGKE---VQEKLKN--LAGIRDASVRCEYFALPVVLEDG-RVTRVDKSIL
CglaMdh2	279	-----FKGT--YYISLKDFNNQPIAKNADALP-----LVNNVPFFALPMTLTLD-GVQSVDSIDI
ScMDH3	258	--ETESLS---AFVYLPGLKNGKK---AQQLVGD-----NSIEYFSLPIVLRNG-SVVSIDTSVL
ScMDH2	288	-----IHGT--YVYVPLKDANNFPIAPGADQLLP-----LVDGADYFAIPLTITTK-GVSYVDYDIV
consensus	351	v yvyl g l veyfsvpv l gi id il

AfumMdh3	296	-QGV----TEQE-KKLL	EACTKGLKGNIEKGIEFVKNTPPKL*-
AfumMdh2	296	-QGV----TEQE-KKLL	EACTKGLKGNIEKGIEFVKNTPPK---
YlipMdh3	296	-PEA---NDYE-KKLL	KVSDGLYGNIAKGEEFIVNPPPAKI*
YlipMdh2	296	-PEA---NDYE-KKLL	KVSDGLYGNIAKGEEFIVNPPPAN*-
LstaMdh3	297	-SQV----SEYE-KGLL	EVAYTGLAANIKKGVDFIVGAPEAKM*
LstaMdh2	297	-SQV----SEYE-KGLL	EVAYTGLAANIKKGVDFIVGAPEAK*-
OpolMdh2	313	-SRV----NNKE-KELL	KICCKTLAGNIAKGASFQ*-----
CaurMdh3	310	-LKV----TSEE-QEFV	KVALKGLSSSIAQGTNFVAGSKI*---
CaurMdh2	305	-EKA----SADE-KKLL	EVAIDQLSKNIEKGVAFATK*-----
CalbMdh3	308	ELTV----TKEE-KKL	VEVALKGLKGSITQGTEFVNASKL*---
CalbMdh2	307	-NQI----SDDE-KKL	LEVAIEQLQKNIEKGVSAKK*-----
CjadMdh3	306	-TQL----DTEE-QRL	FAIAVNTLKKNIKGVAFVNVKVAKL*-
CjadMdh2	302	-DKI----DEHE-EEL	LEVAIDQLKTNIAKGVSTIKGTAA*---
LkluMdh3	302	-DEM----DPEE-RGL	VDTCLKELSTNIDKGKQFVIGGSKL*---
LkluMdh2	337	-NKM----DDYERNT	LLPVCLKNLQGNIIETGLNFVN*-----
KlacMdh3	305	-DKL----NDDE-KKL	IAKCLPILEKNIKKGLAFSKQTKL*---
KlacMdh2	340	-ENL----DSYERDT	LLPICLKTLEGNIIETGLKLV*-----
ZrouMdh3	295	-SSL----SSQE-KKL	VSESVRQLVGNIDKGKKFALGAKL*---
ZrouMdh2	328	-ERM----TKYERER	LLAPCLGKLEGGIRNGLSL*-----
TdelMdh3	307	-DRL----SAQE-HQL	VERAVLELSTSIQKGTGFVVGGSKL*---
TdelMdh2	331	-QAM----SEYERTS	MLPLCFAKLKNGIQAGRDASIV*-----
TblaMdh3	316	-KEILETGSSYT-LG	LLKESVVQVNKDVIKKGQFGLQSKL*---
TblaMdh2a	318	-NGL----NQFEKDV	LLPKAIDELKGNNAQKGERY*-----
TblaMdh2b	383	-LNI----SEYEKKV	LLPPCIDQLIENFDQAKTIEV*-----
NcasMdh3	309	-DHL----SSKE-TQL	VKVAVSELIVNIEKGKKFVLGAAKL*---
NcasMdh2	344	-DRM----DNYERN	EMLPLCLPKLKNSIATGSKFGSQD*-----
CglaMdh3	339	-DSI----SPKE-KEM	VKIAIQELEKNVNGKDFVSGQTKL*---
CglaMdh2	332	-ENM----NIHERK	ELLPICLDQLEKNIAKGLDFSA*-----
ScMDH3	309	-EKL----SPRE-EQL	VNTAVKELRKNIEKGKSFILDS SKL*---
ScMDH2	341	-NRM----NDMER	NQMLPICVSQLKKNIDKGLEFVASRSASS*-
consensus	421	v	t e k l l v i l n i k g f v

Supplemental figure 4: Alignment of Ysh1 and Syc1 sequences.

AfumYsh1	1	MATKRKASALNAAVDDEPVDPSDELA	FYCLGGGNEVGRSCHIIQYKGKTVMLDAGMHPAK
LstaYsh1	1	-----MSAKRQADFEVPDQSDYLE	FVALGGGNEVGRSCHIIINYRGKTVMLDAGVHPAL
YlipYsh1	1	-----MAEK---RESQTDDSDTFS	FVALGGGREVGRSCHVISFKGKTIMLDAGVHPAH
Opolysh1	1	-----MSEELN	FHCLGGGNEVGRSCHIVEYKGKVVMLDAGVHPAF
CaurYsh1	1	-----MAIDNPSEDASENF	KFFGLGGCNEVGRSSHILEYKNKVIMLDSGVHPGL
CalbYsh1	1	-----MNEQNEFSDEENF	KFFGLGGCNEVGRSCHIEYKNKVIMLDSGMHPAL
CjadYsh1	1	-----MDNKIDDTDSF	KFIALLGGSEVGRSCHIIQYKGKTVMLDAGVHPAF
LkluYsh1	1	-----MVQEQTSTNTSF	KFFSLGGSNEVGRSCHILQYKGKTVMLDAGVHPAH
LkSyc1	1	-----	-----
KlacYsh1	1	-----MTQLENEVPDKDHL	RFFSLGGSNEVGRSCHILQYKGKTVMLDAGIHPAH
KlSyc1	1	-----	-----
TdelYsh1	1	-----MDALGKNSL	KFFALGGGNEVGRSCHILQFKGKTIMLDAGVHPAH
TdelSyc1	1	-----	-----
ZrouYsh1	1	-----MMEQPRNNSF	KFFSLGGSNEVGRSSHMLQYKNKTVMLDAGVHPAY
TblaYsh1	1	MDTK-----QSITTTAGSIKPQDF	KFFALGGANEVGRSCHIIQYKGKTVMLDAGIHPAY
TblaSyc1	1	-----	-----
NcasYsh1	1	-----MNEQGNTPF	KFFSLGGSNEVGRSCHILQYKGKTVMLDAGVHPAY
CglaYsh1	1	-----MDVKERSNQF	RFFSLGGGNEVGRSCHIIQFKGKTIMLDAGIHPAY
CglaSyc1	1	-----	-----
Ysh1	1	-----MERTNTTTF	KFFSLGGSNEVGRSCHILQYKGKTVMLDAGIHPAY
Syc1	1	-----	-----
consensus	1		kfy lgg nevgrschiiqykgktvmldagmhp

AfumYsh1	61	EGFSALPFFDEFDLSTVDILLISHFVHDHSSALPYVLS	KTNFKGRVFMTHATKAIYKWLII
LstaYsh1	54	NGLSALPFYDDYDLSTVDILLISHFHLDHAASLPYVMT	HTDFKGRVFMTHPTKAIYRWLL
YlipYsh1	51	SGLASLPFYDEFDLSTIDILLISHFHLDHAASLPYVMQ	KTNFKGRVFMTHPTKGIYRWLL
Opolysh1	41	SGAESLPFYDDFDLSKVDILLISHFHLDHAASLPYVMQ	HTNFKGRVFMTHPTKAIYKWLII
CaurYsh1	50	SGMNSLPFFDEYDLSKVDILLISHFHLDHAASLPYVMQ	QTNFKGRVFMTHATKAIYRWLL
CalbYsh1	49	SGHASFPYFDEYDISKVDILLISHFVHDHSSALPYVMQ	QSNFRGKVFMTHTATKAIYRWLM
CjadYsh1	47	SGIAALPFYDEFDLATVDILLISHFHLDHAASLPYVMQ	HTNFKGRVFMTHPTKAIYRWLL
LkluYsh1	47	QGLASLPFYDEFDLETIDVLLISHFHLDHAASLPYVMQ	RTNFKGRVFMTHPTKAIYRWLL
LkSyc1	1	-----	-----
KlacYsh1	50	QGLASLPFYDEFDLSTIDLLISHFHLDHAASLPYVMQ	RTNFRGRVFMTHPTKAIYRWLL
KlSyc1	1	-----	-----
TdelYsh1	45	QGYSSLPFYDEFDLISKIDVLLISHFVHDHSSALPYVMQ	KTNFKGRVFMTHPTKAIYRWLL
TdelSyc1	1	-----	-----
ZrouYsh1	46	QGYASLPFYDEFDLISKVDILLISHFVHDHSSALPYVMQ	KTNFKGRVFMTHPTKAIYRWLL
TblaYsh1	55	QGLASLPFYDDFDLSTIDVLLISHFHLDHAASLPYVMQ	RTNFRGRVFMTHPTKAIYRWLL
TblaSyc1	1	-----	-----
NcasYsh1	45	QGMASLPFYDEFDLSTIDVLLISHFHLDHAASLPYVMQ	KTNFKGRVFMTHPTKAIYRWLL
CglaYsh1	46	QGMASLPFYDDFDLSIDVLLISHFHLDHAASLPYVMQ	KTNFKGRVFMTHPTKAIYRWLL
CglaSyc1	1	-----	-----
Ysh1	45	QGLASLPFYDEFDLISKVDILLISHFHLDHAASLPYVMQ	RTNFKGRVFMTHPTKAIYRWLL
Syc1	1	-----	-----
consensus	61	g slpfydefdls vdillishfhldhaaslpvymqktnfkgrvfmthptkaiyrwll	

AfumYsh1	121	QDNVRVSN	TASSSDQ-----	RTT	LYTEHDHLS	TLPL	IE	TIDFNT	THTVNS	I	R	I
LstaYsh1	114	SDYVRVSA	ISSN-----	DAST	LYTDADL	NAS	S	FERIE	AIDYHST	T	E	V
YlipYsh1	111	SDFVRVTS	GAES-----	DPD	LYSEADL	TAS	F	NKIET	IDYHST	M	E	V
OpolYsh1	101	NDFVRVTS	IADDNDEN-----	SAN	FLYTDED	LNES	L	DRIET	IDFHST	I	E	V
CaurYsh1	110	SDFVRVTS	MTGGGDEGR	TENNLTNA	AGSAN	LYTDED	L	MTS	SFERIET	IDYHST	I	E
CalbYsh1	109	QDFVRVTS	IGNSRSED-----	GGG	EGSNLYT	DDD	I	MKS	SFDRIET	IDYHST	M	E
CjadYsh1	107	TDFVKVTS	SIGS-----	TNT	LYSDEDL	LES	S	FDKIET	VDYHST	I	E	V
LkluYsh1	107	SDFVKVTN	IGSSS-----	TSK	DDNLYT	DEDLA	E	SFDRIET	IDYHST	M	D	V
LkSyc1	1											
KlacYsh1	110	NDFVKVTS	IGDSPG-Q-----	DSS	NDNLYS	DEDLA	E	SFDRIET	IDYHST	M	E	V
KlSyc1	1											
TdelYsh1	105	RDFVRVTS	IGVSS-----	GGK	DDNLYT	DEDLA	E	SFDRIET	IDFHST	V	D	V
TdelSyc1	1											
ZrouYsh1	106	RDFVRVTS	IGNSA-----	TGK	DENLYT	DEDLA	E	SFDRIET	IDYHST	V	D	V
TblaYsh1	115	RDFVKVTS	IGGDA-----	ENK	DENLYN	DEDLV	E	SFDRIET	IDYHST	I	D	V
TblaSyc1	1											
NcasYsh1	105	RDFVRVTS	IGVNS--T-----	IGN	DDNLYT	DEDLA	E	SFDKIET	VDYHST	V	D	V
CglaYsh1	106	RDFVRVTS	IGSQSS-----	NAE	DDNLYS	NEDLI	E	SFDKIET	IDYHSM	I	D	V
CglaSyc1	1											
Ysh1	105	RDFVRVTS	IGSSSSSM-----	GTK	DEGLFS	DEDLV	D	SFDKIET	VDYHST	V	D	V
Syc1	1											
consensus	121	dfvrvt	sia		lyt	dedl		sfd	riet	id	yhst	mev
												girf

AfumYsh1	169	TPFPAGH	VLGAAMFL	ISIAGL	NILFTG	DYSRE	EDRHL	I	PAEVP	KGIKID	VLIT	EST
LstaYsh1	160	TAYHAGH	VLGAAMYF	IEIGGI	KILFTG	DYSRE	EDRHLN	I	AEVPT	-ERP	DILIT	EST
YlipYsh1	156	TAYHAGH	VLGAAMTY	IEVGGV	KVLFTG	DYSRE	EDRHLN	Q	AEVPP	-MKP	DILIC	EST
OpolYsh1	151	TAYHAGH	VLGAAMF	FVELGGL	KFLFTG	DYSRE	EDRHLSS	A	ELPP	-SRP	DLLIT	EST
CaurYsh1	170	TAYHAGH	VLGACMYF	VEVGGV	KVLFTG	DYSRE	EDRHLK	V	AEVPP	-TRP	DILIT	EST
CalbYsh1	163	TAYHAGH	VLGACMYF	IEIGGL	KVLFTG	DYSRE	ENRHLH	A	AEVPP	-LKP	DILIS	EST
CjadYsh1	151	TAFHAGH	VLGAAMYM	IEISGL	KILFTG	DYSRE	SRHLN	V	AEVPP	-TKP	DILIT	EST
LkluYsh1	156	TAFHAGH	VLGAAMFQ	VEIAGL	RVLFTG	DYSRE	MDRHLN	S	AEIPP	-LPS	DVLV	EST
LkSyc1	1											
KlacYsh1	161	TAFHAGH	VLGAAMFQ	IEIAGV	RVLFTG	DYSRE	VDRHLN	S	AEVPP	-QSS	DVLI	EST
KlSyc1	1											
TdelYsh1	154	TAYHAGH	VLGAAMFQ	IEIAGV	RILFTG	DYSRE	LDRHLN	S	AEVPT	-LPS	DVHI	EST
TdelSyc1	1											
ZrouYsh1	155	TAYHAGH	VLGAAMFQ	IEIAGL	RVLFTG	DYSRE	LDRHLN	S	AEIPP	-FPS	DVLIV	EST
TblaYsh1	164	TAYHAGH	VLGAAMFQ	IEIAGL	RILFTG	DYSRE	LDRHLN	S	AEIPP	-LAS	DILIV	EST
TblaSyc1	1											
NcasYsh1	155	TAFHAGH	VLGAAMFQ	IEIAGL	RVLFTG	DYSRE	MDRHLN	S	AEVPS	-LPS	DVLIV	EST
CglaYsh1	156	TAFHAGH	VLGAAMFQ	IEIAGL	RVLFTG	DYSRE	IDRHLN	S	AEVPP	-LPS	DILIV	EST
CglaSyc1	1											
Ysh1	157	TAFHAGH	VLGAAMFQ	IEIAGL	RVLFTG	DYSRE	VDRHLN	S	AEVPP	-LSS	NVLIV	EST
Syc1	1											
consensus	181	tafhagh	vlgaamf	ieia	gk	ilftg	dysre	drhln	ae	vpp	dvli	estfgta

AfumYsh1	229	TNPRLEREALMKSITGILNRGGRVLLMPVFALGRAQELLLILDEYWETHPEL---	QKIP
LstaYsh1	219	THQPRIEKETRLNLITKTIIVNGGRCLLPVFSLGNAQELLLILDEYWQNH	PDL---DGIP
YlipYsh1	215	THLPRLEREQRLTG LIHSTLDKGGKCLLPVFALGRAQEILLILDEYWEAHPDL---	QEFS
OpolYsh1	210	THVPRVEREAKLTHVIHSTIQQGGRCCLLPVFALGRAQEILLILDEYWQNNPEL---	QNV
CaurYsh1	229	THEPRLEKEARLMKLVHSTILKGGRI LFPVFALGRAQELLLILEEYWSQNKDI---	QIN
CalbYsh1	222	TLEPRIELERKLTTHIHATIAKGGRVLLPVFALGNAQELLLILDEYWSQNE	DL---QNV
CjadYsh1	210	THQPRLEKELRLTNLIHSTLVKGGNVLLPVFALGTAQELLLILDEYWSNHQDL---	ENVR
LkluYsh1	215	THEPRVNREKKLTS LIHSTVSKGGRVLLPVFALGRAQEIMLILDEYWSQHADDLGGGQVP	
LkSyc1	1	-----	
KlacYsh1	220	THEPRQNRERKLTQLIHSTVSKGGRVLLPVFALGRAQEIMLILDEYWQNHKEELGNGQVP	
KlSyc1	1	-----	
TdelYsh1	213	THEPRVNREKLTQLIHSTVSRGGRVLLPVFALGRAQEIMLILDEYWTQHSDELGGGQVP	
TdelSyc1	1	-----	
ZrouYsh1	214	THEPRINRERKLTQLIHSTVTKGGRVLLPVFALGRAQELMLILDEYWSQHA	EELGGGQVP
TblaYsh1	223	THEPRLNREMKLTLQVHSIVSRGGRVLLMPVFALGRAQEIMLILDEYWNNHHEELGGGQVP	
TblaSyc1	1	-----	
NcasYsh1	214	THEPRLNREKNLTQLIHSTVSRGGRVLLPVFALGRAQEIMLILDEYWSQHA	EELGSGQVP
CglaYsh1	215	THEPRLHREKLTQLIHSTVSKGGRVLLMPVFALGRAQELMLILDEYWSQHKEELGSNQIP	
CglaSyc1	1	-----	
Ysh1	216	THEPRLNRERKLTQLIHSTVMRGGRVLLPVFALGRAQEIMLILDEYWSQHADELGGGQVP	
Syc1	1	-----	
consensus	241	th prl re rlt lihstl rggrvllpvfalgraqellllildehyw nh e	nip

AfumYsh1	286	IYYIGNTARRCMVYQTYIGAMNDNIKRLFRQRM	AEAEASGDKSASAGPWDFKFVRS	LR
LstaYsh1	276	VFYASSLARKCLAVYQTYINMMNDSIRKKF-R-	-----	DDRSNPFQFKHIRSLKN
YlipYsh1	272	IYYASALAKKCI	AVYQTYINMMNDSIRRRF-R-	-----DQKTNPFRFKYIKNIKN
OpolYsh1	267	IYYASDLAKKCM	AVYQRYVNMMNDSIRKKF-T-	-----ETNQNPFFHKYIKNITN
CaurYsh1	286	IYYASNLARKCM	AVYQTYTSMNDSIKLNPTG-	-----SSKSNPFDKFYIKS
CalbYsh1	279	VFYASNLAKKCM	AVYETYTGIMNDKIRLSSAS-	-----SEKSNPFDKFYIKS
CjadYsh1	267	VYFASSLAKKCL	TVFQTYVNMMNDSIRKAF-R-	-----DENTNPF
LkluYsh1	275	VFYASNLARRCM	SVFQTYVNMMNDIRKKF-R-	-----DSQTNPFI
LkSyc1	1	-----		
KlacYsh1	280	IFYASNLAKKCM	SVFQTYVNMMNDIRKKFK-	-----DSQTNPFI
KlSyc1	1	-----		
TdelYsh1	273	IYYASNLAKKCM	SVFQTYVNMMNDIRKKF-R-	-----DSQTNPFV
TdelSyc1	1	-----		
ZrouYsh1	274	IYYASNLARKCM	SVFQTYVNMMNDIRRKFR-	-----DSQTNPFV
TblaYsh1	283	IYYASSLAKKCM	SVFQTYVNMMNDIRKKF-R-	-----DSQTNPFI
TblaSyc1	1	-----		
NcasYsh1	274	IYYASNLAKKCM	SVFQTYVNMMNDIRRKFR-	-----DSQTNPFI
CglaYsh1	275	IFYASNLARKCL	SVFQTYVNMMNDSIRKKF-R-	-----DSQTNPFI
CglaSyc1	1	-----		
Ysh1	276	IFYASNLAKKCM	SVFQTYVNMMNDIRKKF-R-	-----DSQTNPFI
Syc1	1	-----		
consensus	301	iiyas larkcm vyqtyinmmnd irrkf		d snpf fk i lrn

AfumYsh1	346	LERFDVGGCVMLASPGMLQGTSTRELLERWAPNERNGVMTGYSVEGTMAKQLLNEPEQ
LstaYsh1	324	LERFDDLGPCVMVASPGMLQNGVSRELLERWAPAKNALILTGYSVDGTLAKQILNEPSE
YlipYsh1	320	LDRFDDMGPCVMVASPGMLQSGVSRSLLELRWAPDPKNTLILTGYSVEGTMAKQIINEPNE
OpolYsh1	315	IEKINDLDSVSLIASPGMLQNGISRKMLEKWSDPDRNSCILTGYSTVEGTMAKILLTEPSE
CaurYsh1	335	VDRVHDIGPCVVVASPGMLQSGVSRQLLERWAPDPKNAVIMTGYSVEGTAKDLLEPTA
CalbYsh1	328	LSKFQDMGPSVVVATPGMLQAGVSRQLEKWPADGKNLVILTGYSVEGTMAKELLKEPTM
CjadYsh1	315	LDRFEDFGPTVVVASPGMLQNGVSRELLEKWAPDSRNSVILTGYSVEGTAKTLITEPDM
LkluYsh1	323	LDEFQDFGPSVMLASPGMLQNGLSRDILLEKWCPEKKNLVLITGYSVEGTMAKFLMLEPDT
LkSyc1	1	-----
KlacYsh1	328	LDEFEDFGPSVMLASPGMLQNGLSRDILLEKWCPEKKNLVLVITGYSVEGTMAKYLLLEPEA
KlSyc1	1	-----
TdelYsh1	321	IDDFQDFGPSVMLASPGMLQSGLSRDVLEKWCPEKKNLVLITGYSVEGTMAKFLMLEPDT
TdelSyc1	1	-----
ZrouYsh1	322	IDEFQDFGPSVMLASPGMLQNGLSREVLERWCPEGKNLVLITGYSVEGTMAKFLMLEPDT
TblaYsh1	331	LDNFEDFGPSVLLASPGMLQSGISRDLLEKWCPEKKNMVLITGYSVEGTMAKYLMVEPDT
TblaSyc1	1	-----
NcasYsh1	322	LEEFQDFGPSVMLASPGMLQSGLSRDVLEKWCPEKKNLVLITGYSIEGTMAKFIIMLEPDT
CglaYsh1	323	LDEFQDFGPSVMLASPGMLQNGLSRDLLERWCPEKKNLVLITGYSVEGTMAKYLLLEPDT
CglaSyc1	1	-----
Ysh1	324	LEDFQDFGPSVMLASPGMLQSGLSRDLLERWCPEKKNLVLITGYSIEGTMAKFIIMLEPDT
Syc1	1	-----
consensus	361	le f d gpsvmlaspgmlq gvsrellerw pe kn vvmtgysvegtmak ll ep

AfumYsh1	466	ILVHGEKHQMMRLKSKLLSLNAD---KAVKVKVYTPANCDEVRI	PFRKDKIAKVVGKLAQ
LstaYsh1	427	ILVHGEQTNMGRLKSALLSKYKDLRQTENEVKVFNPRNSEELRLP	FRGVKVAKVMGSLAA
YlipYsh1	423	ILVHGE LNNMQRLKAALLAKYRGLKNSPREKTIYNPRNCEEVELA	FKGVKVAKTVGKMAE
OpolYsh1	418	ILVHGETNQMGRLKSALLSKYQKFKGTENEIKVYNPRNSSKLSLS	FEGIKVAKVMGQLAT
CaurYsh1	438	ILVHGDSNPMGRLKSALLSKYSSRKGTEDEVKVFNPRNCEEVLIG	FKGVKIAKVVGRLAQ
CalbYsh1	431	ILVHGDSVPMGRLKSALLSKYASRKGTDQEVKVYNPKNCEEELIIG	FKGLKIAKVLGSLAE
CjadYsh1	418	ILVHGESNPMGRLKSALLSKYSKFKGTDQEVKVYNPRNCDELSLK	FKGLTIAKAMGSIVE
LkluYsh1	426	ILVHGESNPMGRLKSALLSNFASLKGTENEVRVFNPRNCVCVDLE	FKGIKIAKAVGNIVD
LkSyc1	1	-----	-----
KlacYsh1	431	ILVHGESNPMGRLKSALLSNFSSLDKTENEVHVFNPRNCVFVDIE	FKDVKVARAVGKIEE
KlSyc1	1	-----	-----
TdelYsh1	424	ILVHGESNPMGRLKSALLSNFASLRGSEQEVHVFNPRNCVDVTFLE	FNGIKIAKAVGNIVD
TdelSyc1	1	-----	-----
ZrouYsh1	425	VLVHGESNPMGRLKSALLSNFASLKGTDQEVHVYNPRNCVEVNLE	FKGIKVAKAVGNIVD
TblaYsh1	434	ILVHGESNPMGRLKSAILSNFTSLKGTENEVHVYNPRNGVEVTFLE	FKGTHIAKAIGSIVD
TblaSyc1	1	-----	-----
NcasYsh1	425	ILVHGESNPMGRLKSAILSNFTALKGTENEVHIFNPRNCVEVELE	FKGIKVAKAIGNIVD
CglaYsh1	426	ILVHGE PNPNGRLKSALLSNYASFKGTEDEVHVHNPRNCYELDIE	CKGVKVAKAVGNIVD
CglaSyc1	1	-----	-----
Ysh1	427	ILVHGEANPMGRLKSALLSNFASLKGTDNEVHVFNPRNCVEVDLE	FQGVKVAKAVGNIVN
Syc1	1	-----	-----
consensus	481	ilvhge npmgrlksalls y kgte evkvynprnc ev i frgvkiak vg l	

AfumYsh1	523	VAP-----	PSDQDDGRL
LstaYsh1	487	KP-----	PMDGQI
YlipYsh1	483	EK-----	PHVGQI
OpolYsh1	478	SL-----	PKEHDT
CaurYsh1	498	AQVELINKALKEETKCPKIEVVEDG-----VSKDKDMVDKNEKEDAKESKTIETDVQ	
CalbYsh1	491	EQLQVLKKIIQDEVSAENSKITELTEEKEEAEIKEDNGETDTTQKPNNESSINVLKTGQV	
CjadYsh1	478	D-----	KDKQV
LkluYsh1	486	EASNILKTEGE----KKVSEIKE-----E---TEEEAAGKLKIDGETV	
LkSyc1	1	-----	-----
KlacYsh1	491	DLDEFITEEDALKNEKRI-----TEIH-----EEDPETEESKTEIVKEENEKI	
KlSyc1	1	-----	-----
TdelYsh1	484	DIRREEEGTEVKEEDKD-NAVEKTSVK-----KEKPDEDVEELPN-GDEQEIV	
TdelSyc1	1	-----	-----
ZrouYsh1	485	EIQKGETTE--VKRESPKVESLDGTE-N-----NGESDQEERELPNGGEEEEIV	
TblaYsh1	494	QIKNKEAEIQKIKDEKLKVEQKEV---K-----YENKDEENITQISKIEEEGIV	
TblaSyc1	1	-----	-----
NcasYsh1	485	EVGKEGLDNLLG-----NKNE-----EKESDDTTEPTIEDKPNSDIV	
CglaYsh1	486	EIKRTEEEVVKPENDAGQ--SKEGI-----EEFTGKTQDVRKDAEGEGAI	
CglaSyc1	1	-----	MSKQNT-
Ysh1	487	EIYKEENVEIKEEIA-AKIEPIK-EENE-----DNLDSQAEKGLVDEEEHKDIV	
Syc1	1	-----	-----
consensus	541		1

AfumYsh1	535	MSGVLVQ--NGFDLSL	MAPDDLREY-AGL	TTTTITCKQHITLS---	SASMDLIRWALEGT
LstaYsh1	495	LSGILVQ--KNFEMS	VMAADDLKEF-SGL	TTSSVIQRQSITV----	EVSAELIKFHLEQM
YlipYsh1	491	ISGVVVQ--KDFNYG	LMGVADLREH-VGL	STSSVLERQTVTV----	NAGVDLVKYHLEQM
OpolYsh1	486	INGVLVQ--KNFDLS	LLKIEDLREF-AGL	TTTVVRQRQSLRC----	TATKSLIKWQLTQM
CaurYsh1	550	ISGVLIS--KDFDMN	IMSLEDLSEF-SQL	STSVVKSNAKLKV----	HANVSLVEWHLEQM
CalbYsh1	551	VSGVLVS--KDFNLN	LLQLQDLHEF-TQL	STSIVKSKMHLKI----	NADISLMVWHLEQM
CjadYsh1	484	LTGVLIA--KDFDLN	LMKVDDVREY-AGL	STTVVKERQTIHV----	DAGRDLIQWHLTQM
LkluYsh1	522	VSGILVSDEKN	FDLNLVSLSDLREH	HTDLSTTVLKERQTIHV----	DCKKELIYWHL CQM
LkSyc1	1	-----	-----	-----	-----M
KlacYsh1	534	VSGILVSDEKN	FDLSLVSLSDLREH	YQQLSTTVLTERQTVHL----	DCKSELVYWHICQM
KlSyc1	1	-----	-----	-----	-----M
TdelYsh1	531	VSGILVSDEKN	FDLNLVSLTDLREH	HTELSTTVLRERQTVHV----	DCKKELIYWHL CQM
TdelSyc1	1	-----	-----	-----	-----M
ZrouYsh1	531	VSGILVSDEKN	FDLNLVSLTDLREH	HNKLSTTVLRERQTVHV----	DCKKELIYWHL CQM
TblaYsh1	540	ISGLLVSNEKN	FNLDLVSLSDLREH	HSELSTTVIKERQSVHV----	DCKKELIYWHL CQM
TblaSyc1	1	-----	-----	-----	-----M
NcasYsh1	522	VSGILVSDEKN	FDLNLVSLSDLREH	HSELSTTVLRERQTVYV----	NCRKELIYWHINQM
CglaYsh1	529	ISSILVSDEKN	FDLNLVSLSDLREH	HPELSTTVIRERQTIQV----	DCKKELIYWHICQM
CglaSyc1	7	--LILRITEK	GVNIDTL-----	-----	IHDVVKPRLMEI
Ysh1	534	VSGILVSDDKN	FELDFLSLSDLREH	HPDLSTTILRERQSVRV----	NCKKELIYWHILQM
Syc1	1	-----	-----MDLPKDKS-----	-----DRTHQRINL	NNSGTDRDNDLYLHIVQT
consensus	601	msgvlv	k fdl lm v dlre	lsttvir rqsi v	dli whl qm

AfumYsh1	589	FGAIEELGSN	ERSKVKEES-----	T-----KAVNGEQEI	KEEPADE-----
LstaYsh1	548	FGTLKDATV	-----	-----	-----
YlipYsh1	544	FGYVEMRE	TENVKIEEMEDDVA	EEEEEDKEVKQEVED	VTMEGEVKDETAEEV
OpolYsh1	539	FGYIQELV	DEDEY-----	V-----	-----
CaurYsh1	603	FGHINVVID	DNQTWECI-----	-----	-----
CalbYsh1	604	FGYINVIND	DDEEWECV-----	-----	-----
CjadYsh1	537	FGYVEVLID	EKDEY-----	E-----	-----
LkluYsh1	578	FGDIEVLLD	DEGVTLLNNLQDK	NPK-----	-----
LkSyc1	2	FGDIEVLLD	DEGVTLLNNLQDK	NPK-----	-----
KlacYsh1	590	FGDVDVYID	EENVSLKNINPEFK	-----	-----
KlSyc1	2	FGDVDVYID	EENVSLKNINPEFK	-----	-----
TdelYsh1	587	FGDIRVVID	EENVTNKLRKRED---	A---D-----	-----GR-----
TdelSyc1	2	FGDIRVVID	EENVTNKLRKRED---	A---D-----	-----GR-----
ZrouYsh1	587	FGDIEVLED	PSNVTNMLKQED---	S---E-----	-----V-----
TblaYsh1	596	FGDVEVIID	EDNVSGIKQEE-----	-----	-----
TblaSyc1	2	FGDVEVIID	EDNVSGIKQEE-----	-----	-----
NcasYsh1	578	FGDIDVLVD	DDNITHSLKPKSEEKT---	D-----	-----VK-----
CglaYsh1	585	FGDVSVLID	DDNVNTKETKL-----	-----	-----
CglaSyc1	34	FESRNTSDL	KDS-----	-----	-----LL
Ysh1	590	FGAEVLQDD	DRVTNQEPKVKEESK	-----	-----
Syc1	36	FGCIETTAT	ENAE-----	-----	-----
consensus	661	Fgdievlv	dee vt		

AfumYsh1	625	-----EIPMEETQTYL VMGC VLIRY-----HSRTREVE LEW EG-NMMNDG-----V
LstaYsh1	557	-----GSG L GYT IMDS VN--V-----FWKPKSIV IEW EG-NMLNDA-----I
YlipYsh1	604	FKQEVEGSDSTS AGTT FV VMNS --VTV-----KHTPTSC TEW VG-SCLNDS-----I
OpolYsh1	554	----- VKVMS AVKITL-----ESKEST ATV EWNS-GMVDDT-----I
CaurYsh1	620	----- IMNMI YITANK--AESDALNV TV EWINDNLMGDS-----L
CalbYsh1	621	----- IMDV VDVFI DR --SKGPGLFI TV EWINDNLMADS-----L
CjadYsh1	552	----- VKVMNE VT VNF -----DNS ICT IEWVS-GVINDT-----I
LkluYsh1	603	-----TSDVKS GELELR VMGDIKVSI-----VRDV ATLE WTQ-GIINDT-----V
LkSyc1	27	-----TSDVKS GELELR VMGDIKVSI-----VRDV ATLE WTQ-GIINDT-----V
KlacYsh1	613	-----TRKIKK GELEIK IMGDVILNI-----VDN VATL QWTQ-NVISDS-----V
KlSyc1	25	-----TRKIKK GELEIK IMGDVILNI-----VDN VATL QWTQ-NVISDS-----V
TdelYsh1	612	-----ISDGKLN GKLV LKV MNDIK LTV-----FDN VATLE WTQ-GLISDT-----V
TdelSyc1	27	-----ISDGKLN GKLV LKV MNDIK LTV-----FDN VATLE WTQ-GLISDT-----V
ZrouYsh1	611	-----SN-GSENK LVLQ IMSDIKLTV-----VDNS ATLE WTQ-GLISDA-----V
TblaYsh1	616	-----PNSEDN GKLV LKL MGDIL LTV-----FEN IATLE WTQ-GLMTDT-----V
TblaSyc1	22	-----PNSEDN GKLV LKL MGDIL LTV-----FEN IATLE WTQ-GLMTDT-----V
NcasYsh1	606	-----PQETTET GKLV L IRIMG DIRLSL-----VDNT AVLE WTQ-GLVSDT-----V
CglaYsh1	606	-----ETSR GMLVLQ IMGAIRLTV-----QHN KAILE WTQ-GLISDT-----I
CglaSyc1	48	YKRTI--EMDEDDNRI LYI GNEVIIDYREYQSSTHSY LLK L KWLQ EIQPSN TPNR LDLFI
Ysh1	615	-----DNLTNT GKLILQ IMGDIKLTI-----VNT LAV VEWTQ-DLMNDT-----V
Syc1	48	-----TKLL MLGD VEVEI-----SASSV SIEW TQKSMISQT-----I
consensus	721	g l lkvmgdi itv iatleWtq gmmsdt v

AfumYsh1	665	ADAV MAVL - LTVESS PASVKQ S AK LKH HHHHSD-----LELP-NPHAHQGPEETFEN
LstaYsh1	591	ADSV LAIL - LSVESS PMSVK ISSK PSHCKA-----NFN RPEK IER
YlipYsh1	649	ADAV LAIL - LTVDN SRASVK MSSK Q CAH SHGHE-----DGHSNSSLDERVLQ
OpolYsh1	585	ADSV LAIL - MSCDSS PASVK ISSK SHSHDHLKQEE-----DVLDEYSREARLAR
CaurYsh1	653	ADSV AIL - LSIDSS PVS VKMTS QHCS HNH IKKEEDTDMVKQEAPKKAHANTDIAS RINR
CalbYsh1	654	ADSV AIL - YSIDSS PASVK LSS Q NHNH GD NHIV KKEDSMEIDRPVEAHAKTDIK SRIER
CjadYsh1	581	ADSV VAIL - MSVDSS PASVK MSSQ CSQHSDN----A-----PVLADASLT TRVKR
LkluYsh1	642	ADSV LAIL - LSIDSS PASVK LSSR SC NHDH HDCG-----DKLHDDV WKIKE
LkSyc1	66	ADSV LAIL - LSIDSS PASVK LSSR SC NHDH HDCG-----DKLHDDV WKIKE
KlacYsh1	652	ADSV MAIL - LSVES APAS IKMSSK SC GHHH GHDD-----HTTK IKN
KlSyc1	64	ADSV MAIL - LSVES APAS IKMSSK SC GHHH GHDD-----HTTK IKN
TdelYsh1	652	ADSV AIL - MSVDSS PASVR MSSR SC EH HHE--EF--S-----DGVMPKDPV WKVKQ
TdelSyc1	67	ADSV AIL - MSVDSS PASVR MSSR SC EH HHE--EF--S-----DGVMPKDPV WKVKQ
ZrouYsh1	649	ADSV VAIL - MSVDS APASVK LTSR SCDN NHNH --QN--V-----EELIQ QDPVWKIKQ
TblaYsh1	655	ADSV AIL - MSVDST PASVK MSSHTC NH GEEH KITEQDK-----AELLQ RDEVWKIKQ
TblaSyc1	61	ADSV AIL - MSVDST PASVK MSSHTC NH GEEH KITEQDK-----AELLQ RDEVWKIKQ
NcasYsh1	646	ADSV AIL - MSVDS APAS IKMSSR SC NHDH DHSNQ---I-----EELNQESDV WKIKQ
CglaYsh1	643	ADSV AIL - MSVDS APSV VKKSSN SC SHG HEHATP-----ILSQPSETD KIKQ
CglaSyc1	106	IECIVS II IANCDSS SIS -----Q-----DTNVVKDENER LRLV
Ysh1	654	ADSV AIL - MNVDS APASVK LSSH SCDD HDH NNVQ---S-----NAQ GKIDE VER VVKQ
Syc1	80	ADSV IMI - IGLCAS DKNV LSE SELK-----ERNHN VWKIQE
consensus	781	adsimail lsvdsspasvkissksc h h d kikn

AfumYsh1	716	LLMMLEA Q FGSNIAP I ERPRI P SGIRANRTTKADPSVSA A VKTKSDAAGETPAESQ E DES
LstaYsh1	630	VLVFLDS Q FGSAVE P ME N P-----
YlipYsh1	695	LSS I LKA Q FGDS I VSE D G-----
OpolYsh1	634	ISKLLSA Q FGDSFKHDA E K-----
CaurYsh1	712	ITSLLKS Q FGDSMT S VS Q -----
CalbYsh1	713	IALLLKA Q FGDSLKE L PE-----
CjadYsh1	626	INL I LEA Q FGDA F TPNE N Q-----
LkluYsh1	687	ISRL F TE Q FGDC F TLL L L D KNE T -----
LkSyc1	111	ISRL F TE Q FGDC F TLL L L D KNE T -----
KlacYsh1	692	ISRV F KE Q FGDT F T L FLNE D S-----
KlSyc1	104	ISRV F KE Q FGDT F T L FLNE D S-----
TdelYsh1	699	IAKL F KE Q FG E T F T L MLAKGDD H K-----
TdelSyc1	114	IAKL F KE Q FG E T F T L MLAKGDD H K-----
ZrouYsh1	696	ISK L F Q E Q FGDS F TLL M NKNGD F K-----
TblaYsh1	707	ISE L F Q E Q FGDS F TLL L L D KEN P -----
TblaSyc1	113	ISE L F Q E Q FGDS F TLL L L D KEN P -----
NcasYsh1	695	VSN L F Q E Q FGDS F TLL L LE K SE S TE-----
CglaYsh1	690	VAEL F K T QFGDS F T L ILNKDDDN D TAE E K-----
CglaSyc1	139	I Q ELMEE Q FGADGY E -----
Ysh1	703	ISRL F KE Q FGDC F T L FLNKDEY A S-----
Syc1	116	LQNL F RE Q FGDS F S I DEGIG K K-----
consensus	841	is lfkeQFGdsftlil k

AfumYsh1	776	TEEIEAAELARLQALGIPYPGIE I K V D K H V AR V WLEN F EV-ECANTV L R D RVR V IER A V
LstaYsh1	649	-----DDGVY I NIDGH I AS V NFR N MD V -ICSYE P L R S R V T H V LD H AV
YlipYsh1	714	-----KS A N I K I DAME A T I S F SD L SV-TGSPP P L V Q R VQ V AD R AI
OpolYsh1	653	-----QC G T I Q I G K NS A K I D S T F EV-TCAS G AL R G R IE G IL N RS L
CaurYsh1	730	-----SEL V IT I G K NE A K V DL N K L AV-EC G SR V L K DR V EN I K R GA
CalbYsh1	731	-----EK A I Q IG K TVAN V DY K R L EV-EC S SK V L K DR V EN V I K R G C
CjadYsh1	645	-----SG A T I K I G K SE A Q V DY V N L TV-TCSS N V L K G R I EN A L N R A T
LkluYsh1	709	-----DHKE D I K GA I T I G K ST A R I N F S N MS V EE C NS N PL K G R IE S LL G I G T
LkSyc1	133	-----DHKE D I K GA I T I G K ST A R I N F S N MS V EE C NS N PL K G R IE S LL G I G T
KlacYsh1	714	-----KE E I K GT I N L G K TT A C I N F SK M V EE C S N S PL K G R IE S LL K I G S
KlSyc1	126	-----KE E I K GT I N L G K TT A C I N F SK M V EE C S N S PL K G R IE S LL K I G S
TdelYsh1	723	-----IED G D I F G V I T I G K NN A R I N F SK M Q IE E C S N S PL K G R VER I LD M GA
TdelSyc1	138	-----IED G D I F G V I T I G K NN A R I N F SK M Q IE E C S N S PL K G R VER I LD M GA
ZrouYsh1	720	-----KNDE D I S GI I T I G K NT A R V N F S Q L K IE E C S N S PL K G R VE Q IL N M G I
TblaYsh1	729	-----STSG D I K G K I S F G KNE S T I N F S Q M K IE E C S N S PL K G R IE S IL N I G A
TblaSyc1	135	-----STSG D I K G K I S F G KNE S T I N F S Q M K IE E C S N S PL K G R IE S IL N I G A
NcasYsh1	719	-----ESED D I F GA V T I G K NN A H I N F SK M K IE E C S N S PL K G R VE S LL R I G A
CglaYsh1	719	-----EDDEF V K L IT I G K NT A S I N F TD M CV EE C S N S PL K G R VE S LL K I G I
CglaSyc1	155	-----QERT K A I V K VG D KT G H V DL V N L K V IE C DS S L L K G R L E G V L R V AE
Ysh1	727	-----NKEET I T G V V T I G K ST A K I D F NN M K I LE C NS N PL K G R VE S LL N I G G
Syc1	138	-----ENV K NS V T I G K SK A T I D F ST M K L ID C NS N PL K G R VE S IL S I G Q
consensus	901	di g itigk arinfs m v ecnsnpLkgRve vl ig

AfumYsh1	835	ETVSSMWGEGHPAARASNGTQG-----NKEVAVSKSNEIEARA-----
LstaYsh1	690	DTILPFDFGKEESDESYESSSSITPIKEERDS-----
YlipYsh1	754	SLVAPLAQKLSAVDLV-EGFKAIENVKDREENGVEVKAEDEEKVKAEKVKEEE
OpolYsh1	693	DLVAPLSRNA-----
CaurYsh1	770	RLAAPLSYQQKMVSA-----
CalbYsh1	771	QLTAPLSQNPZIA-----
CjadYsh1	685	ELVAPLAQRKGLKV-----
LkluYsh1	755	DLVAPLC*-----
LkSyc1	179	DLVAPLC*-----
KlacYsh1	758	DLVAPLC*-----
KlSyc1	170	DLVAPLC*-----
TdelYsh1	769	DLAASLC*-----
TdelSyc1	184	DLAASLC*-----
ZrouYsh1	766	DLVAPLC*-----
TblaYsh1	775	NLAASLC*-----
TblaSyc1	181	NLAASLC*-----
NcasYsh1	765	DLVAPLC*-----
CglaYsh1	765	DMVSSLC*-----
CglaSyc1	199	QLSRPLIGS*-----
Ysh1	773	NLVTPLC*-----
Syc1	182	KLTTPLC*-----
consensus	961	dlvaplc

Supplemental figure 5. In yellow highlighting is the Gle2 binding site in *S. cerevisiae* NUP116 experimentally defined by Bailer et al 1998. A similar sequence is clearly conserved in other genes. Retained introns are highlighted in green.

OGAPODRAFT_1550	1	MFGNSASTTS FGG FGSNNTWNNNN SSPFG TNT-----VNNNT SSPFGS NTN-----
CJI97_002114	1	MF-GR--PNS FGG FSSTAN---NS SSPFG STN-----NTNAS SPFG QNTS--T--
CAALFM_C306440W	1	MFGGG--ASS FGG FGSSTT---TNNS PF GGGAGAG---AATTNTGAS SPFG STNT-----
CYBJADRAFT_168	1	MFG-SSTNTS FGG FGSNTG-----SA FGG GNTATNTGTGFGSTGG SMFGS NTN NNA --
SAKLOB11770g	1	MFGAS---RPT FGN ---T-----G-TAP FG GNNTAA-----P-TNS PF GSAN-----
KLLA0_F26697g	1	MFGAS---RPA FGQ ---T-----S-T SPFG QQTQS-----TTNA FGQ QHSGETT--
TDELOB07030	1	MFGAN---RPA FGG ---A-----S QPF GS-----TS SPFGS QQQQQP--
ZYRO0F00660g	1	MFGSN---RPA FGG ---G-----S QPF GS-----TAS PF AS QP QPQA--
TBLA_0A10170	1	MFGQN---RPA FGN ---N-----Q FGG -----S-SS SPFG M Q N Q Q--
TBLA_0B06810	1	MFSQN---RS FGS ---N-----T-----
NCAS_0A08290	1	MFGSS---RPA FGS ---T-----G SF NSPN-----N-ST SPFG GV PQ QST--
NCAS_0H03150	1	MFGST---RPM FGG ---A-----NT SQPF GGGST-----GS STFG ANN Q Q--
CAGLOF06171	1	MFGQP---RL-F-G---A-----N-S QPF GSTNNT-----G---
CAGLOL04928	1	MFGNT---NSM FGN ---N-----S QTFGA ANTGM-----NSNTNA FGAN -----
NUP116	1	MFGVS---RGA FP S---A-----T-T QPF GS-----TG STFG G Q Q Q Q PV
NUP100	1	MFGNN---RPM FGG ---S-----NLS FGS -----NT SSFG G Q Q S Q P --
consensus	1	MFg s rpgFgg sqpfgt tsspfg n n
OGAPODRAFT_1550	48	-----TNTGGLFGATANTSS SLGT --- FGS NTNTN--APANGTS----SNTGL FGTG
CJI97_002114	41	--SNA FGS SGGGIFGSSNTN-S AFGS -----NNNNNTTTS AFGS NNNPSTGG SAFGSS
CAALFM_C306440W	48	-----NTTGGGIFGSNANSS TFG GSSNA FGASS NTN-TTPAFGGN----TGGGL FGST
CYBJADRAFT_168	52	--T SAFG SGASSGGFGAKPT GST -----
SAKLOB11770g	35	--NT AFGT NT-AN-----N-AAS FGG ---FGATNNATS-----N--NNTGL FGGM
KLLA0_F26697g	37	--NNL FGSSS -AN-----N-AQS FGG ---FGTGGANT-----NPTQTINS PF MS
TDELOB07030	32	--G STFG ---TN-----N-AQS FGG ---FGNAQ NST -----TNANPGGS SLFGMS
ZYRO0F00660g	32	--TT TFGM GVANN-----N-AQS FGG ---FGAANN NTSA -----GTGGPTGS SLFGMS
TBLA_0A10170	32	-QNS SLFG NANSNT-----TSQS FGG ---FGSGGASTS-----G---TS SMFGNS
TBLA_0B06810	14	NNN SLFG NSNNNM-QM-SNAQS FGG ---FT STT NNNN-----TSNS SMFGGN
NCAS_0A08290	35	ASG TF FGMN QQT-----TVQNT FNS ---FG SAA -----TNS PF GAN
NCAS_0H03150	37	-----QSNAS SGFGG ---FGATNNN-----AN SMFGNN
CAGLOF06171	23	-STGA FGNVQ N-----NNVQS FGSG ---FG SNN NASN-----A---PQSGA FGAN
CAGLOL04928	34	--SNA FGTS -----T QTG FGN--NT SNA -----
NUP116	35	ANT SAFGL SQQTN-----TTQAP AFGN ---FGNQ-----TSNS PF MS
NUP100	32	--NS SLFG NSNNNN-STS NAQS FGG---FT SAAG SN-----SNS SLFG --
consensus	61	s fg gqsgfgg fgs n slfg s
OGAPODRAFT_1550	91	SS--FNSSS SPFG QSA-----FGNTAST-----GTMSNGLFGTSNN--T-G
CJI97_002114	92	NTGFGNTGG SVFG STN--NATQNNAS PF GGASNTGG SAFGS -SGGGGIFGNTANKPF-G
CAALFM_C306440W	96	ANGTG---SS PF GQ Q Q Q Q Q Q P QTT SAFGSSN -NSG SVFG SSATGGGLFGSKPATST-F
CYBJADRAFT_168	78	NT----ANT SPFG AAV---NNTSNTTAGFGASSA-FGSNNNTASTGGIFGAKPASSG-F
SAKLOB11770g	72	SN --PTASNG PF QAT-----TATATG-----A
KLLA0_F26697g	76	QQ --QNTTT SPFG GAA-----AGAAAG-NS-----L
TDELOB07030	68	SN --NNSSNS SPFG KTV-----TGGA-----
ZYRO0F00660g	73	TN --NTQNS PF GNST-----GA-----
TBLA_0A10170	70	NN-----ANR PF SATG-----TN-----N
TBLA_0B06810	57	NN-----ASNPM FGN AN-----TNNNTN-----NTSMFGSANNNNNNN
NCAS_0A08290	70	-----S TPFG SAQ-----Q P -----A
NCAS_0H03150	62	N Q --N---R P -----
CAGLOF06171	61	-----TSSLNS PF GSNN-----NAMGT PSN STTSGGGLFGMQNPNTSGM
CAGLOL04928	53	-----FNT-----GANTGL
NUP116	70	GS--TTANG TPFG QSQ-----LTNN-----
NUP100	70	-----
consensus	121	n spfg

OGAPODRAFT_1550	127	SAF	GS	----	TATT	----	SPFG	QQSTAPRFGSTLGATNTQNR	GT	SV	VPFKPLT	EKDP	NT	NG
CJ197_002114	147	SAF	GTP	----	QNN	SI	----	SPFGGGASTSAFGSGAAGGDKVN	GT	AV	KPFT	FP	EKDT	SG
CAALFM_C306440W	151	GGF	GST	----	TAN	AS	----	SPFGA-STTNAFGGGASVDPNVN	GT	AA	KQFT	FP	EKDSA	NM
CYBJADRAFT_168	129	GTT	G	TMFG	QT	ONS	----	SPFGSSA-GSGFGG--LGSAGQN	GT	AI	KPF	QAY	EKDAT	GA
SAKL0B11770g	93	SNPP	SL	FG	AT	-----	-----	ATGGAVGG	GT	AI	KPF	SN	YE	EKDT
KLLA0_F26697g	99	SNPP	SL	FG	GS	QSSG	-----	-----	TATG	VLSSG	PPS	GT	GI	KPF
TDEL0B07030	86	NTS	GS	SL	FG	GNALPS	-----	-----	A-GSS	ITGN	AGS	GT	AI	KPF
ZYRO0F00660g	89	-----	-----	-----	-----	-----	-----	-----	ATT	TGS	NS	GT	AI	KPF
TBLA_0A10170	84	NVGG	SL	FGG	GLTGG	ANITATST	-----	-----	SSNP	MGGL	SGAGS	GT	AI	KPY
TBLA_0B06810	90	NTST	G	MF	GN	NNNS	-----	-----	-----	-----	-----	-----	-----	-----
NCAS_0A08290	82	NAST	SL	FG	NA	NQS	-----	-----	VPAM	TNQL	QNGT	TV	KPF	Q
NCAS_0H03150	67	TST	G	LF	GGG	Q	QQQQ	-----	-----	-----	-----	-----	-----	-----
CAGL0F06171	100	AGGN	SL	FG	MNN	NGNTGTTMMG	-----	-----	GLP	VGM	NAGAGT	GT	AI	KPF
CAGL0L04928	62	NAG	G	LF	GS	QNT	Q	QNT	-----	-----	-----	-----	-----	-----
NUP116	88	NAS	GS	I	FG	MGNNTA	----	L----	-----	SAG	SASV	VPNS	TA	GT
NUP100	70	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
consensus	181	gslfg	n							gtaikpf	f	ekd	tt	

OGAPODRAFT_1550	250	-----
CJI97_002114	271	-----
CAALFM_C306440W	276	-----
CYBJADRAFT_168	249	-----
SAKLOB11770g	222	FGQNQQQQTGGLFG-QNNTATSPFGVNNNN-TFGQNNTANSPFGMNKP---A-ITGGL
KLLAO_F26697g	245	FGQPQQQQTGMFGQQQ---NNSPFGQNTA-----SSSPFGLNKP---A-TSGGL
TDELOB07030	211	FGSLSSSNNTNNTNNTNNSFGSGAFGANTNT-NTGFGNTNNSPFGMNK-----PAAGGL
ZYRO0F00660g	202	FGSVSSGNPSTTG-----TGPFGSTTAAGGNAFGGSGAGPFGSKPA---GTGGL
TBLA_0A10170	209	FGSNSNTGTNQFG---NNAGGFLNNSNTNNSFASSNNNTFGMNNS-----AGSSL
TBLA_0B06810	122	-----SSLFGMNNNN-NNNNNNNNSNPFGMNNNN-----NTTTS
NCAS_0A08290	203	-----NPNTSFGAS-----NTTGL
NCAS_0H03150	103	-----ANTNTGALGNTN-----ANNNASPFGMNKP---S---TGL
CAGLOF06171	214	-----GAQSSPFQK-----PASGGL
CAGLOL04928	145	FGNAN-----STNNAFGSTNNM-----QNNSPFGTNSFGNNTSNTNTGL
NUP116	223	-----GGGFGSGATNSTGLFGSSTNL-----SGNSAFGANPK---A-TSGGL
NUP100	91	FGSLNSSNASNGNT-FGGSSSMGSGFGGNTNNAFNNSNSTNSPFGFNKP---N-TGGTL
consensus	361	fg spfg n ggl

OGAPODRAFT_1550	250	-----NTTSGLFGQS-----NNNTGGNL-----FGA-NK-
CJI97_002114	271	-----SGFGSG-TSAFGSNAGTSAFGQS-----TGAFGQ-NT-
CAALFM_C306440W	276	-----GAANPSGSAFGSAFGSTFGNKPAGTSPFGAA-----S-----
CYBJADRAFT_168	249	-----NNNNTSGGLFGSAN-----ANNTSGGFG-----SAFGANNT-
SAKLOB11770g	275	FGQ-GTAQQPSGGLFGQNNNQQRST--S--GLFGQNNNTSNTNNAFGATNSNVFGTNTQ-
KLLAO_F26697g	289	FGQ-NTTN-----NNSAFGQ--ANNSLFGQQNQQN-----
TDELOB07030	264	FGQ-QPNQGATGGGFGQQN-STFGA--AN-NAFGTTNATG-----
ZYRO0F00660g	251	FGQ-NN-RTASGGLFGQNNNSTFGQ--PQPSAFGSGAGAGTG-----ASAFGS-KP-
TBLA_0A10170	258	FGN-NQNNSTNGGLFGQNNTTTNN---NNMGRFGQQ-----NNAFGTNNA-
TBLA_0B06810	155	FGMNNSNNTSGGLFGMNNNNNNNNNTMGNSMFNKS-----SFGNTTNSFGSNTFG
NCAS_0A08290	218	FGK-TTTGQQGTGMFGQQNNAT-----GNSLFGQQNNNNNT-----
NCAS_0H03150	132	FGQ-NTASAT-----NNN--TGSNMFQQ-----SNAFGTQQN-
CAGLOF06171	230	FGG-NGVGSTSTGLFGSNQSTT-----NTFG-----ANNGSTFGNNAA-
CAGLOL04928	184	FGQ-QN--TSGGGLFGNNQNT-----NAFGGPQNNN-----ANNFTQ---
NUP116	261	FGN-TTNN-----PTNGT--NNTGLFGQQNSNTNG--GLFGQQNSFGANNV-
NUP100	145	FGS-QNNNSAGT-----SSLFGGQSTSTTG---TFGNTGSSFGTGLN-
consensus	421	fgq n n sgglfg nn t lfg fg

OGAPODRAFT_1550	274	-----PATGGLFGSSNNNTSAFGSNNN-SAFG-----SSAA-PFGQTNNSPFGQQQ
CJI97_002114	302	-----N-TGGSFLGQTNNNSPFGQNNNA-GTSA-----FGGG-----
CAALFM_C306440W	308	-----TTGAFGGTNQNQSPFGSNTA-GTFG-----SGASNTFGGGANSTFGKPA
CYBJADRAFT_168	280	-----NTSGGLFGSTNQTSNAFGASNN-TTTG-----GF-GSSFGAAKPSFGGA--
SAKLOB11770g	329	-----QPGLFGQNTTQQQ-----PSGGLFGQT-NQQPQGGGLFGQNNNQ-----Q
KLLAO_F26697g	317	-----PGNAFGQNTGSN-----TFGSTFGQT-NTNNQPGLFGQNNTT-----A
TDELOB07030	299	-----NSGGLFGQNT-----QQGGGLFGNQNNNTFGQNN
ZYRO0F00660g	297	-----AGTGLFGQNTAANQ-----P----FGAN-PAPSTGGGLFGQNSNTGMGG-A
TBLA_0A10170	299	-----SNAGTGLFGQNN-----GQKGNGLFGQNNNSFGNNA
TBLA_0B06810	206	NNTMNNNNNNNTNAFGMNNNN-----NTANSFGMNSNN-----N
NCAS_0A08290	253	-----GGGLFGQKTAN-----P----FGS--NTSSTGTGVFGQNTT-----
NCAS_0H03150	162	-----ANPTNTFGQSKL-----GNTFGSQQAGGATGGLFGQPNTT-----
CAGLOF06171	267	-----SSGGLFGST-NNTNTNTGMFGSASNA-----
CAGLOL04928	219	-----NKPANAFGQPNMTMNAFGNNSTGGLFGST--GTSSSTGGLFGQNASNSFGNNA
NUP116	303	-----SNGGAFGQVNRG-----AFPQQ-QTQQGSGGIFGQSNAN-----
NUP100	183	-----GNGSNIFGAG-----NN-SQSNTTGSFLFGNQSSAFGTNN
consensus	481	gglfgq n fg gglFGqnns g

OGAPODRAFT_1550	318	P-----S-----ATF
CJI97_002114	331	-----S GA FGSTNLNKPSG F -----GT GSA FGQS---
CAALFM_C306440W	351	TGFGSS GGA FGGNT NT --GG-----AG GGL FGSSGNAF
CYBJADRAFT_168	322	---ST GGM FGS NTN QTS A F-----GSG GMN -----
SAKLOB11770g	369	---QPS GGL FGQNA-GTAST FG QPNQ Q --QT GGL FGNK PA -----S GGL FGQQS--
KLLAO_F26697g	355	---ANT GGL FGQ S --NAN NA FGQNN-- NT SG GL FGSK PG -----GTT GGL FGQQA Q --
TDELOB07030	329	---TQ GGL FGQNA- NT NT-TG AF GQNT Q PS GGL FGNK PA -----G GGL FGQNN--
ZYROOF00660g	337	---GSG GGL FGQNN-ATGS V FGQPNQAST GGL FGSK PA -----G GGL FGQPQ N --
TBLA_0A10170	331	---Q QA G GF FGQ S ANN-----Q QA G GI FGQSNMQTSNNSNA AGGL FGNK Q G--
TBLA_0B06810	240	N--N NG G GL FGQNN NN NTNT FG INNTSN NG NS LFG QNN-----
NCAS_0A08290	284	----NN GL FGQ Q N-----N-Q QT ST GL FGQ K P Q -----G----- MFG NN----
NCAS_0H03150	198	----TG GGL FGQ Q NN--NT FG Q Q -----Q QT NS P FGQ P NTN PL ---SSGNS MFG QNTN--
CAGLOF06171	292	----NS GGL FNQ Q N Q TQ Q QSS-----P FG ASS G FGK P PA-----S--S GGL FGQ TGA --
CAGLOL04928	269	S--TTT GGV FGQ NS NP-T NQ FG S -----QNT GL FGSQNN-----
NUP116	336	----AN GGA FGQ Q -----Q GT GA LFG AK PA -----S GGL FGQ SAG --
NUP100	217	----Q Q G S LFGQ Q S Q NT NA FGN Q --N QL GGS S FGSK PV -----G--S S LFGQ S NN--
consensus	541	gglfgqn nn fg n glfg p gglfgq

OGAPODRAFT_1550	323	-----GASSSS PFG QNNNAGT LFG AN NN QTSS PFG Q Q ST TPA FGSNNQTGSG VFG
CJI97_002114	355	-----NNNTSS VFG ANNNQ S V- FG SGN--TGSAFGATNTSNN-----TSS PFG
CAALFM_C306440W	382	GGQSSSG FGA ANSS PFG QAQ-S NA - FG GAN--NNS PFG Q S NT Q Q Q -----S GGL FG
CYBJADRAFT_168	345	-----NS-----NSGG MFG ST NN -NQS PFG TNNNTN-----TS GGL FG
SAKLOB11770g	413	-----GGGS LFG QNTA-----GNST FG
KLLAO_F26697g	401	-----NGPS PFG Q Q NAANST-----P FG
TDELOB07030	374	-----TF-----GSANTGGG LFG QNNNN-----Q Q -S GGL FG
ZYROOF00660g	383	-----N TP FGGGAANTGGG LFG Q NS Q-----PPAGG LFG
TBLA_0A10170	374	-----TS LFG QATST Q SG LFG Q S NTN-----SN Q QSN NLFG
TBLA_0B06810	278	-----NNN-----N-----
NCAS_0A08290	314	-----
NCAS_0H03150	243	-----ANNNS MFG QNNNN-----NN-----
CAGLOF06171	334	-----NP-----FS
CAGLOL04928	300	-----Q Q QSG LFG Q Q NN Q Q-----N Q QNST GLFG
NUP116	367	-----SK-----A FG
NUP100	261	-----TL-----G
consensus	601	lfg n fg

OGAPODRAFT_1550	374	NNNN---QTS A FG NTGT ---NT GN LFGANTTANK P -----T
CJI97_002114	396	GG NT GGFGSS G FGSS NTN ---S GGL FGSNKPATTS-----
CAALFM_C306440W	431	SGTGNAFGS-----N---TG ST FG SN ---NT-----
CYBJADRAFT_168	378	ST NNNA ---G GA FGAS NTG ---T GGL FGSANN TNNA -----
SAKLOB11770g	431	Q NN Q Q Q Q AG LFG Q N ST-AT T -G LFG Q NN Q TQ Q PQ GG LFG Q NN Q Q ---Q--S
KLLAO_F26697g	419	Q V NN--TQAG LFG Q NN TN---T GGL FGQ Q Q P --SNTNST GLFG Q Q S NAA ---S---
TDELOB07030	401	Q NN T NQ -Q S G LFG Q NN TN-Q TS -G LFG Q NN -Q Q Q Q TGG LFG Q NN Q Q -----
ZYROOF00660g	415	Q NN Q PP AGG LFG Q S NT Q -PPAG GGL FGQ S NN--Q PP AGG LFG Q S NNQ P ---S-TG
TBLA_0A10170	407	Q S NN--N Q S GGL FGQ NS GS-Q Q Q S LFGQ P NN---Q Q S GGL FGQ S NNQ Q ---Q-QG
TBLA_0B06810	282	----TSMGS GL L G SK P ----ATNS LFG Q NN NTANN NN NT GM FGQ Q NNNT-----
NCAS_0A08290	314	--TT--Q TP GN MFG M NT NT Q Q Q GSS LFG Q NT VNNQ P Q Q NT GLFG Q NN M N Q-----Q Q NN
NCAS_0H03150	258	----TANTTS MFG NNN-----NS MFG S Q NKAPGTGIGG LFG Q Q A Q NNNNNTNNNTS
CAGLOF06171	338	S-----NNANTA FG Q TA Q Q TP NQ G LFG Q S N Q -----S Q GT GLFG Q S G Q Q Q -----P--Q
CAGLOL04928	325	S NN TS NA MT GGL FGQ K Q S NT NT -----S
NUP116	372	MNTNPTGTT GGL FGQ T N Q Q-Q-S GGL FGQ Q Q N ---SNAG LFG Q NN Q S Q-----N--Q
NUP100	264	NTT---N-----NR NG LFGQ M SS NQ SS NS GLFGQ NS M S -----S--T
consensus	661	n gglfgq ntn s gglfgqnn glfgqn qq

OGAPODRAFT_1550	404	F GGFGS -----S----- GNTSGG -----FG STGN
CJI97_002114	430	--G FGN -----T----- GSPFGQ -----TNNT--
CAALFM_C306440W	452	--G FGA -----G----- GNAFGQ -----QGNT GF
CYBJADRAFT_168	409	---F GA -----TNT--- ASPFASQSKPAFGFGNTTI
SAKL0B11770g	482	GGLFGNNNGAVANAPFGSN ---N QQQNTGLFGNKPAAS - GGLFGNNNNTTGAGF --- GQ
KLLA0_F26697g	464	-----TGGP FGQQNSNSMNQQGGGLFGAKPT -T- GGLFGSNNQS -----
TDEL0B07030	448	GLLGQNNATQ ---ST FGQPQN ---N TNTGLFGNKPA -G- GGLFGQTQNNTGFGA ---NR
ZYRO0F00660g	466	GGLFGQNT --S--SP FGQPNN --QASTGG GLFGNKPA -G- GGLFGQPQNNTFFGG ---GA
TBLA_0A10170	454	RSLFGQTNSNF --SG FGQQ ---TQT QASGGLFGNKST -S- GSLSQSNNQNGFGS ---NM
TBLA_0B06810	323	-----NS IFGQQ ---QQSS GGLFGNKPPQGMGTGLFGQNNT -----
NCAS_0A08290	365	GGHFGQKPQT ---NS FGN ---QN TGGGLFGNKP KPA- GGLFGQNS ---T GF ---GN
NCAS_0H03150	306	TGLFGQQNNT ---SS FGQ ----- QQNNSLFGNKPA --- GGLFGQNNQQATS GF---GA
CAGL0F06171	382	GGLFGQA -----ANGNS LFGSKPQPS -T FGQQTT SAGGF-----
CAGL0L04928	349	TGLFGQQNKPA -----T- GGLFGQSNSTGLFGNSNLGN
NUP116	419	SGLFGQQNS ---SNA FGQP ---N QQGGLFGSKPA --- GGLFGQQQGASTFAS ---GN
NUP100	299	QCVFGQNNNQMQ --I-----NG NNNNSLFGKA -----
consensus	721	glfgq fgq q glfg kp gglfgq q g g

OGAPODRAFT_1550	496	---TNQGGSLFGNKPAA-----NSGGGLFGNNNT---ANTGSGGGFGF
CJI97_002114	499	---ANTSGGLFGSNNNNT-----QTGTGGGLFGS-SN---NQAGSGGLFG
CAALFM_C306440W	548	---PTTGGGLFGSKPAA-----SGLFGGQQS---GQAQQGGGLFG
CYBJADRAFT_168	490	---NANKTTGFG-----TNTGGLFGANN---TT-ATSGGLFG
SAKLOB11770g	619	-QQ--QSGGLFGAKPTGTAGGLFGQN--NGATQQQSGLFGNNNA---TQQQGGGLFG
KLLAO_F26697g	570	NSMANNTGGLFGAKPTGTTGGLFGQS--SQ-QQNTSSGLFGQNN---QNNATGGLFG
TDELOB07030	550	-QQ--QSGGLFGAKPATTTGGLFGNN--Q--TTQTGGGLFGNNQQ---QQQPQSGGLFG
ZYROOF00660g	584	-NQPSTGGGLFGAKPAGGGGLFGQNN--N--QPPAGGGGLFGQSN---NQPPAGGGGLFG
TBLA_0A10170	557	---SQQSNSLFGNKPAGSAGGLFGNN--NN-SSGQPSLFGNNNS-----
TBLA_0B06810	400	-NQQNNSFGGFGNKPSTG--GGLFGNANNNNNTTNTGGGLFGNANNNTNN--MQNSGGLFS
NCAS_0A08290	462	-----SGLFGQKPTT--TGLFGAN--NQQPQPTATGLFGANN---QQQSTG---
NCAS_0H03150	409	-----K--N--PVTSGGGLFGQQQQNNALNPTGTSGGLFG
CAGLOF06171	464	---NTNANSPFGMKSATPAGGLFGNN--QG--QGGGIFNQNN---QQQGNNTGLFG
CAGLOL04928	459	QNQQTSTSLFGNKT-----PASGGGLFGTQNTTNG---TNTLSGGFG
NUP116	515	LQQPQQNNSLFGAKPTGFGNTSLFSN--S--TTNQSNISGNN-----LQQQSGGLFQ
NUP100	386	-NQQQQSTGLFGAKPATTTGSLFGGN--SSTQP---NSLFGTTNVPTSNTQSQQGN---
consensus	901	qs glfg kp a g lfg n n gggflgnnnn q sgglfg

OGAPODRAFT_1550	533	GANNNN--NASSGTLFGNKPASSGTGFGSTNAASGSLFGNKPATTTT-TPSFGTTNNNT-
CJI97_002114	538	SSNQNN--QSSGGGLFGNKPAGQ-----TGGGLFGQSNNTGTT---GFGATQNNNT
CAALFM_C306440W	583	QQNQNN---TSGGLFGNKPPTGPT-----TTNGGGLFGNKPATGGG---LFGGQQQQTQ
CYBJADRAFT_168	521	NANTNT---TASTGFGNKPATTGFGATNTANSGGGLFGNKTTTGFG-APS-----
SAKLOB11770g	670	QNNTAST-NSGSGLFGNKPAGTTA---G---GGGLFGNNTGSN-----
KLLAO_F26697g	623	QNNQQQ--GQSSGSLFGAKPSGTNA---LGATNGGLFGGNTQQQ-----
TDELOB07030	599	QNNQ--Q-QQQPSGLFGAKPATNT-----GGGLFGNSN--NQ-----
ZYROOF00660g	634	NTQNNQP-PAGGGGLFGNKPAGAT-----GGGLFGNANTNTQ-----
TBLA_0A10170	596	-----QQQNGGLFGSRPATQS-----NGLFGNNSNQNS-----
TBLA_0B06810	455	NNNNNLS-----KPMGLN---STLGGGLFGNNTNNNNNTSTMNNN-----
NCAS_0A08290	503	-----GLFGNKPQ-----TGGLFGNNTLNNNQNQTAFNST-----
NCAS_0H03150	440	QNNQQQSSNVGGGLFGNKNPTGTT-----TGGLFGAAPTSSQQQQPGFGAT-----
CAGLOF06171	512	GGQSQQTQSNTAGSLFGKPTGFGS---TAQPNNTSSFGN-----
CAGLOL04928	500	NTQ---ANQASGSLFGSKPPGSAN---TS-GTTGLFGASQQSQQ-----
NUP116	564	NKQ---QPASGGLFGSKPSNTV-----GGGLFGNNQVANQ-----
NUP100	436	-----SLFGATKLTNM-----PFGGNPTANQ-----
consensus	961	q nnn gglfgnkp g gggflFGnq nq

OGAPODRAFT_1550	589	-----NSLFGNKP-----
CJI97_002114	584	-STGFGSKPAGGGGLFGSNN-----
CAALFM_C306440W	631	QQQQPQPSQLGGGLFGAKP-----
CYBJADRAFT_168	567	-----TTTGGGLFGNNTSNNA-----
SAKLOB11770g	707	-----
KLLAO_F26697g	662	-----NTATGGLFGAKPADS-----
TDELOB07030	631	TSL---GQPSGGGLFGSKPAGG-----
ZYROOF00660g	670	PAL---GQPSGGGLFGAKPASAG-----GAP
TBLA_0A10170	624	-----LTNNTGGLFGNKTSSNS-----
TBLA_0B06810	493	-TGNALGQGLGGGLFGNKPNNTSNNNTSLSGAIPGRSASAGLPSLNTLNSFGLNKPAGLN
NCAS_0A08290	533	ANT---NPPNTGGLFGNKPQTG-----
NCAS_0H03150	486	PSIGGLSSTTGGGLFGQNNTNA-----A
CAGLOF06171	548	-----TQSSGGGLFGNKST-----
CAGLOL04928	537	-----TSQPGGGLFGSKPTVGGL-----GAP
NUP116	596	NNP---ASTSGGLFGSKPATG-----
NUP100	457	-----SGSGNSLFGTKPA-----
consensus	1021	ggglfg kp

OGAPODRAFT_1550	597	-----AGT--TS	GGLFGNNNQ-----	SSTS
CJI97_002114	602	-----NN	TSSSGGLFGQNTQ-----	NTNTG
CAALFM_C306440W	650	-----GT	TASSGGLFGGQQ-Q-----	TSNVG
CYBJADRAFT_168	583	----GG-----	ALGGTAQQSGGLFGTNNNS-----	TSNLNTS
SAKLOB11770g	707	NST	TGGLFGNNTA-----SS	NAGGLFGNKAAGG-----TNVGTG
KLLA0_F26697g	677	AST	SGGLFG-----	TKPTGG-----LSSTTG
TDELOB07030	650	ATT	GGLFGNNTN---TT	TNTMCGGLFGNNNATN-----TGNN
ZYROOF00660g	693	STT	GGLFGNTNN-----	ATQPGGGLFGNTNNTS-----Q---GGTG
TBLA_0A10170	640	----AGLLGNNTA-----	ASNAGGLFGNSAANS-----	TTS
TBLA_0B06810	552	NTS	GGSLFANNNSN-----	NNNNNNNNNS-----NINTGATT
NCAS_0A08290	552	---GT	GLFGNTSN-----SS	TNTGGASLFGNNNGTS-----ALGGTG
NCAS_0H03150	509	NTT	STGLFGANNTTANNNQANTVGT	GLFNNNNNNANATTAGNTSFTLGGNNNTAG
CAGLOF06171	561	---G	GGLFGSTNTQ---NT	TSPFG-----SGGT
CAGLOL04928	557	QTT	GTSLFGQNN-----	QSTPGGLFGNKQPTVTGVGSANTTT---PTANTLGTS
NUP116	614	----	SLFGGTNS-----	TAPNASSGGIFGSNNASN-----TAATTNS
NUP100	470	-STT	GSGLFGNNTA-----	STVPSTNGLFGNNANNS-----TSTTN
consensus	1081	st	gglfgn	t s gglfgnnn sstg

OGAPODRAFT_1550	615	GGLFGN-----	KPAT	TGGLFGNNNQSSTS-----	AT	SGGLFGNKP
CJI97_002114	624	GGLFGSSNTGNTTG--	GIGSGTNT	SGGLFGKPTSTFGG-----	QSG	GGLFGSNN
CAALFM_C306440W	671	GGLFG-----	-----G-----	GA-----	AS	TGGLFGAKT
CYBJADRAFT_168	612	GGLFGNKPA-----	APAGGLFGNANN--	T-----	QS	GGLFGNSN
SAKLOB11770g	742	GGLFGNKPPGTAS-----	SAT	TGGLFGAKPTNTFSGT-----	GAT	TGLFGAKT
KLLA0_F26697g	698	GGLFGGKPA GTAP-----	-----	FGATNTNNA	SSI-----	GGGSLFSANK
TDELOB07030	690	GGLFGAKPQGN-----	T	TGGLFGSNQANNN-----	STTG--	GLSGGLFGSKP
ZYROOF00660g	728	GGLFGNKPPAGSTGP-----	TGT	TGGLFGSTNNSLQ	SGASGTGATG--	TAGGGLFGNKP
TBLA_0A10170	667	GGLFGSSQNTQAGSLFDA-KQN	PQ	SGGLFGNNSNTSS-----	-----	TAGGGLFGAKP
TBLA_0B06810	583	TS	LFGKPNNTTAPT--TANSNTGT	TGGLFGSKLGTQPTTT-----	TAT	IGLSGNTN
NCAS_0A08290	586	GGLFN	NLKPPQTS-----	TTSTQGTGLFGNKSN	TTST-----	TNSGGLFGNNA
NCAS_0H03150	569	GGLFGN	RLNSGSM-FNAPSTNTAPK	GGLFNNGTATTST-----	LGQS	STGGLFGNKP
CAGLOF06171	583	QS	LLGAKPAGGLGGLGAQQPAATQ	T	SGLFNKPAT	STSF-----GGTSSLFGNKA
CAGLOL04928	605	TS	LFGNKSS-----	-----TG-----	ST	GSTFGNSL
NUP116	647	T	GLFGNKPPVGAGAS-----	TSAGGLFGNNNNSSLNNS-----	NG	STGLFGSNN
NUP100	505	T	GLFGAKPDSQSKP-----	ALG	GGLFGNSNSNST	IGQNKPVFGGTTQNTGLFGATG
consensus	1141	ggLfgnkp		tgglfg ss s		sgglfgnk

OGAPODRAFT_1550	650	-----AG	TTSGGLFGNNNQSSS-----	
CJI97_002114	671	NTQQ-----	NNATGT	SGGLFGSSVLGGQ-----
CAALFM_C306440W	690	NANA-----	TSNS	TSGGLFGGATTVQQQ-----
CYBJADRAFT_168	646	TQNKPS	LFSSGSSSIASG	SGGLFGGQTQQPQQ-----GSFLSQPQ-
SAKLOB11770g	784	-----	NN	TGGLFGNNLANGT-----INNVSNG
KLLA0_F26697g	733	PAN-----	TGST	GLFGSQNTSGN-----ANT
TDELOB07030	731	ANST-----	N	TLGGGLFGNNSATSN-----GTS
ZYROOF00660g	779	AGAT-----	GTTGGLGGGLFGN	NNNTNNSLGGATQGNTGIAGAGVG
TBLA_0A10170	713	TIG-----	NN	SLPFGNSSTIA-----TSGNS
TBLA_0B06810	632	PLG-----	ASKPF	GLGNNTTTTSTTTT-----SGLSQ-PQT
NCAS_0A08290	630	S-----	VNS	GGLFGGSANKPAT-----GLGG
NCAS_0H03150	620	AGTP-----	GTTT	SGTGLFGAKNTTTTG-L-----GNAGATT
CAGLOF06171	632	GPQ-----	QGS	TGGLFGSNSTSNIG-AGLA-----TSQQ
CAGLOL04928	626	GNNT-----	SATT	STSGGLFGSKSQNNNSSIAFGTQTPSTLAP-STAP
NUP116	690	TSQ-----	ST	NAGGLFQNTSTN-----TSGG
NUP100	557	TNSS-----	AVGS	TGKLFQNNNTLNVGTQNV-----PPVNN
consensus	1201		t	sgglfgnnn gglf

OGAPODRAFT_1550	668	----	FAFGQG-----	QQQQQQQQ-----	QQQPLANLD	PY--	GTNPLFSSV	GANTN-P-	
CJI97_002114	695	----	QQQQQN-----	QTQNQGQQ-----	SLVNIGT	QNPY--	GNNKLFQSI	QGPVQ-S-	
CAALFM_C306440W	714	-----	-----	PQQAQQ-----	ALASINS	QNPY--	GNNPLFQSI	TGTSS-Q-	
CYBJADRAFT_168	687	QAQQQS	SFGQQ-----	QQQSQQQQ	QAGQGYPLV	ATIDS	NPY--	GSSFLEN	GEPGNTG-Q-
SAKLOB11770g	814	-----	G-----	QQQGQQQGQ-----	QQPGQQAN	NPY--	GTNDLFSRVI	-VFN---	
KLLAO_F26697g	763	LQQN-----	-----	QQMQNQ-----	QQAQANS	NPY--	GTDELFSRVI	SIPN---	
TDELOB07030	763	QTGT	QQLGLQGG---	FGQAQQT	QQ-----	QQQQQPAT	NPY--	GTNELFSRIA	-VPS---
ZYROOF00660g	829	QQPA---	GQQPG-----	LPSQQ-----	QSNQNVN	NPY--	GTNELFSRVV	-VPS---	
TBLA_0A10170	741	ANQLNS	-----	STLSLIG-----	SQQHTSV	SDPY--	GTNELFSRIT	-VPS---	
TBLA_0B06810	672	SNAS-	TTGTTTGSAGIG	STWSSG-----	VGVNATTT	-----	IPSSLTNNTL	PVSS---	
NCAS_0A08290	659	NNIN	QNGQS-----	LQTQQQL-----	PPQQGAN	NDPY--	GTDLFSRVV	-VSP---	
NCAS_0H03150	664	AQGGFQLNNNNT	---NN-	NQSQQV-----	GTTPNVL	QNQQ--	VDNKLFSKID	-LPD---	
CAGLOF06171	665	--AN	QQIGNPS----	QNNDQEKL-----	QQQQLLV	TNPY--	GTNELFSKV	QQAAPGSM	
CAGLOL04928	676	AQAPNT	-----	VKTTSLG-----	TGSSINTT	NPTLPLAN	STNSE-Q	KLPN---	
NUP116	719	QSMAS	Q-----	NALQQQQQQ-----	QRLQIQN	NPY--	GTNELFSKAT	-VTN---	
NUP100	599	-----	-----	-----	AVPSLQQA	PV--	TNEQLFSKIS	-IPN---	
consensus	1261		q	qqq qq		qnpy gtn lfsrv	vp		

OGAPODRAFT_1550	708	IVQQPPVPQA---	IPLKQVSKKK-P----	MLTSAYKL	NPKPLF	SPNDLLVTKPGS	IVAA
CJI97_002114	735	SASQAEV-----	PKA--IAVN-PPAKKHVSL	-LAAHKVAP	PLFAPG	KRIAN-----	
CAALFM_C306440W	746	QQQQQQQQQQ	TNNLPQFSLVKSA-API	KKAVTLG	STSQKVT	PLFKVSSL-----	
CYBJADRAFT_168	737	SQATQVH-----	PLAIAKPV	S-TELKQPT	LTLDAYRLAP	KPLFVASSHKNS	PSGS---
SAKLOB11770g	848	SITQPNK-----	P--SATKINAD	VKKKASLT	GAYRLAP	KPLFGHKVSSVSPVSH	PGSI
KLLAO_F26697g	798	SITQPTK-----	P--SATMVSAD	LKKKNSLSA	YKLLPKPLF	DSKKSEPN	SRKVKIHL
TDELOB07030	808	SITQPTK-----	P--SATKVNAD	LKKKASLSS	AYRLAP	KPLFASRSLSVSPVNK	SDKL
ZYROOF00660g	867	SITQPTK-----	P--SATKVNAD	LKKKASLT	GAYRLAP	PRPLFTSKSLSGNAAP	KFDSF
TBLA_0A10170	778	SLVPKPN-----	P--MITKIE-S	LAKNNKLT	SAYKLNPT	PLFSNLKSKS	RTVSSTLTTL
TBLA_0B06810	717	SITQPSK-----	P--STTIMNAS	LKMSRSLT	TAYRSAPKS	LFNSNSLSL	SKSNENSN
NCAS_0A08290	699	SVNNPET-----	P--VVSKTTAE	PKKINLLAM	YKESPRPLF	VPKNM	SKHSNKGNRND
NCAS_0H03150	708	SITKPSV-----	P--TANKIKAD	VKMNGTL	SSAYRSSPKPLF	AAKSAKND	SLLKFNKG
CAGLOF06171	710	QVSQIQ-----	V--SATKIDAD	NKKKSDLI	SAYKHTPKPLF	FAAALSGKGL	VAEKTNE
CAGLOL04928	715	SLTQPVK-----	I--PPSTMKA	ASKKDS	SLTSAYRLAP	PRALFMSSDD	KTTSTLRSHSA
NUP116	759	TVSYPIQ-----	P--SATKIKADE	RKKASLT	NAYKMI	PKTLFTAKLKT	NNSVMDKAQI
NUP100	622	SITNPVK-----	A--TTSKVNAD	MKRNSLT	SAYRLAP	KPLFAPSSNGDA	KFKQWKGT
consensus	1321	svtqp h	p	satkv advkkk	sltsayrl	pkpLF	

OGAPODRAFT_1550	759	SSPSTAGSSA-SGKSATQ	TLIEDSKDSVNGSKSEKFL	SPT-----	TDDAILS--	SYIFA	
CJI97_002114	776	STPK-----	KESVVTVDTVRNGRNK	DLFDAD-----	VDAAIMS--	SEIFA	
CAALFM_C306440W	794	PTKT-----	STELVKEDTVKNKKT	DDLFSAA-----	TDQAIS--	SDIFR	
CYBJADRAFT_168	785	--PKTT-----	NANALATSTKSPVN	LLGSA-----	TDEALLG--	DFILS	
SAKLOB11770g	899	VVSSGKSRVSSVASISP-	ESAGNELVSTSN	GSAAAF	SNE-----	SDEVILSNS	LLFN
KLLAO_F26697g	849	KLSKPKEE-----	DSSTAL-TRKPM	DSSIFTAS-----	TDEAILT	TGELLFN	
TDELOB07030	859	LITDSR---AASAGSVV-	DSANKDLTSSTSR-AAV	FSP-----	TDEAILSADK	LLFN	
ZYROOF00660g	918	SGSSTR---SSSASSSP-	DSIGKELVPTSTG-STL	FSP-----	TDEAILSADK	LLFN	
TBLA_0A10170	828	GSSTNNTH---QPKSLP-	DTN--ATVTSGS	LLGDVKNN-----	SNDAILS	SVSNMFGN	
TBLA_0B06810	768	SLT-----	SIETSP-----	TVETKTITLEN-----	DNNKP	ILFQ	
NCAS_0A08290	750	EIEKTKMDI	ISS-----	DRTTK---DRNLK	TIDLTPD-----	VEDSLFALLES	IFH
NCAS_0H03150	759	SSTQSTSSSLSSANS----	S-----	SSNVSLISF	TNTNEAMKLLK	SEKSTTPS	LLFN
CAGLOF06171	761	IKNDL-----	-----	DKETSTRIM	NNE-----	IDANFQQIG	SKLFE
CAGLOL04928	766	SK-----	-----	DSKNST-----	EITHLPLE-----	NITNTSRSL	GDQLLFFN
NUP116	810	KVDP-----	KLSISI--DKKNNQIAI	----	SNQQEEN-----	LDESILKASE	LLFN
NUP100	673	LERSDRGS---S-----	-----	TSNSITD-----	PESSYLNSND	LLFD	
consensus	1381		es	s	tddails	llfn	

OGAPODRAFT_1550	810	PS-RNVTKLIIDKTKQEDEFEGLKASNLVTPRQITMKA-----SMSSL-----
CJI97_002114	814	PK-TNYRKLVLNGTKNNSNGL-LTYTDTMTRTHQVSFTVDNEK-----E-----
CAALFM_C306440W	832	PK-ESFKSLVLDKSKASNA-L-LTE-SSSGPTKQVTFVLDKSE-----SKLSAS-----
CYBJADRAFT_168	820	NS-TKTQKTLFNATA-----TPKKAISNSTNDEE-----PENKPVL-----
SAKLOB11770g	951	PDKKSFKNLIINRKKMEESEEDG-----EAKRITFN-TDIE-----DDDKQANGTAKN
KLLAO_F26697g	891	PDKKSFKNLIINRQKMEEDDTSS-----GELKFIIFN-TDDG-----PQKKME-----
TDELOB07030	907	PDRKSFKNLIINRKKMEEEDSANK-QLHSEPRRITFT-SSAA-----EGEKGVTGLANG
ZYROOF00660g	966	PDKKSFKNLIINKRKAGEGPAEDDG-----EVKKITLQ-SDSN-----GDSNSVN--KSL
TBLA_0A10170	875	NKMQDFKTLINRREKAQALENRISSTDEDPSTRLTFKVSSKKECKDSDQEK-----
TBLA_0B06810	797	PDKENVKALLMKNKIDAEVQEQQEQE---QEQQEQQLSDSKSMEQNNNKSEEFITSN---
NCAS_0A08290	793	GDYESYKTFIERKRSTQLEQQKPKA-QLSSNVNRPSTL-NK-----
NCAS_0H03150	807	PDKKSFKHLVLNKKKSPPKVQESSG---KEDVKKISFTTPKAAGSSESSGDNQLSNGATI
CAGLOF06171	792	PDSLMFKQLLKSNGHRNKDLKS-----KEKLFIANVADSN-LNEADKDKAKNEIAKL
CAGLOL04928	798	PDKKSFSLSLIKNKKVPEKIAN-----EYKRITFEAKNKNQGV-----ES
NUP116	850	PDKRSFKNLIINRRLMIASEEKNNNG-SQNN---DMNFK-SKSE-----EQETILG-KPKM
NUP100	703	PDRRYLKHLLVIKNNKLNLVINHND--DEASKVKLVTF-TESA-----SKDDQASSSIAA
consensus	1441	pdkrsfk liinkkk kritf e

OGAPODRAFT_1550	853	-----TPKPY-----MSPSK-----TVLE--N-----
CJI97_002114	856	-----NIE--N-----
CAALFM_C306440W	878	-----TPEPL-----DKDEK-----SKLE--L-----
CYBJADRAFT_168	854	-----RLEE-----RK-----SPA-----T-----
SAKLOB11770g	998	TTISPTKDTPVSFDDKVQE--TPTT--KDPRK-----ANGL-FSQKELSSSTPVSKI
KLLAO_F26697g	933	-----QKENNDIFSKIQE--TPVS--KHPDL-----SPER-E-----T--
TDELOB07030	960	-----GESHLFDQVHE--SPTV--SKDIK-----NKAR-TN--NISSSSPS--
ZYROOF00660g	1013	-----NESTTFGGVLD--SPTV--GKDFS-----AKDF-GMNRDILSVSPA--
TBLA_0A10170	927	-----SSTESSIFDQPQF--TPTISSSKNKIID---DEKKAHYE-EMDKSKSRTSSN--
TBLA_0B06810	850	-----SIDATMNSIQL--V----TKEPKSIGTIDSSENEKDCSNMDDV-----
NCAS_0A08290	832	-----ASSTNVGQSHTGLVETEPKTTEVT-----NKDQ-DMAIAI---IPSD
NCAS_0H03150	864	SVEQQ-PKGVDDHFDLTL-----TKPK-----L-DNNESF---STPVSM
CAGLOF06171	844	-----NASQVVATTLA-----SS-----VRET-EKQEKI---ET--
CAGLOL04928	840	ELESPRNDTPSPYVNTSGR--IS-----TPSK-----AMA--AM--EF-----
NUP116	899	DEKETANGGERMVLSSKNDGEDSAT--KHHSR-----NMDE-ENKENV-----AD-
NUP100	755	SKLTEKAHSPQTDLKDHD-----ES-----TPDP-----QSKSP---
consensus	1501	

OGAPODRAFT_1550	868	-GNSQEPPAEISSTPKSV-SES-TSTNEEWPEGYWISPSLEELQKMSATQLKSVPDFKVG
CJI97_002114	860	-----G-----DSK-PKA-IEHEDVDDGGYTLPSLSELKKKPLGELRAVKDFTVG
CAALFM_C306440W	893	-QGEQQ-----KQQ-QGQ-DQDSVDVDEGYWMSPSLQELKKKSLLELKSIPKFKIG
CYBJADRAFT_168	865	-----RASEVSETKNIKPTRE-EDISFVDEDDGYWMSPSLDELENMSLLELRKVSGLFVVG
SAKLOB11770g	1044	LTGTTVK-NDISIAEKVKPRGIGDDISFTDDGYMTPSLETLSMTLLQLRKVSGLTIG
KLLAO_F26697g	961	---SIII-DTDKKRKVFHKSCLVEDDISFTENGYYISPSFETLESLLTMDARKVENLVIG
TDELOB07030	994	LQ-PQE--VQPKEANQSKPRGIGDDISFTDDGYIISPSLDTLASKTLPQLRKVSGLVIG
ZYROOF00660g	1049	RNQSSDL-EESASDKNIKTRGIGEDISFTDNGYYISPSFESLSTKSLPQLRKLSGLLVIG
TBLA_0A10170	973	-----DFTQTNIMKKASIDDEDDITWLDNGYSISPSLETLSMSILQLRKVSGLTVS
TBLA_0B06810	888	-----SSVTSATDDELPHGLNTDDISFE-DDYYISPSFTTLNSLPFVQLRNVKNLIIG
NCAS_0A08290	870	-----DKNISIPVTNSLGHKDDFYSYVGDKYYISPSLDTLTSMSYLQLLKVKGVLIVG
NCAS_0H03150	899	KATSIEPLQSENTTAFMDKKPLKNDISFLDNGYYISPSLETLESTSLDLRHKVKNLVVG
CAGLOF06171	869	-----DICNENAISESKLDGIDDLFVDENYYISPSLDTLATLSKYEIQKVENLVVG
CAGLOL04928	872	NTTSVNKSSAIDSNNTKKEQLSDVNDISFTDHGYIIPSLDTLNGMPLVELRSVNGLVVG
NUP116	941	---LQKQ-EYSEDDKAVFADVAEKDASFINENYYISPSLDTLSSYLQLRKVPHLVVG
NUP100	785	-NGSTSIPMIENEKISSKVPGLLSNDVTFKNNYYISPSIETLGNKSLIELRKINNLVIG
consensus	1561	k i ddisf degYyisPSletL smsllqlrkv lvvg

OGAPODRAFT_1550	925	RTGYGKIEFLKPVDLTSILL--QKI-PEIIVFDKQSCIYIPDLN-TRPPVGEGFNIPATV
CJI97_002114	904	RKHYGKVKFLEPVDLA-FNLDEIC-GNLITFGPKNVVIYPEDD-EKPKEGEGFNIPAQV
CAALFM_C306440W	941	RKHYGELEFLEPVDLTSIVNLDDIA-GNLVTFSNKTCVVYPDD--NPKPKGEGNLNIPARI
CYBJADRAFT_168	918	RRGFGKIEFLKVDLTTQGSLASIP-GGVIVFLRQSCVVYPQDLMIAPGKGEGNLNIPAKI
SAKLOB11770g	1103	HRDYGKIEFLEPVDLN-ISLPALC-GQLVVFQPKTCVYANST-NKPEKGEGNLNVRARI
KLLAO_F26697g	1017	HDDYGKIEFLKPVDLN-SLPLSLC-GKLVIFENRCCTV-SYIG-DKPEKGQGLNLPAKI
TDELOB07030	1051	HKDYGKIEFLEPVDLN-SLPLSLC-GKLVIFENRCCTV-SYIG-DKPEKGQGLNLPAKI
ZYROOF00660g	1108	HKNYGKIEFLEPVDLN-SLPLSLC-GKLVIFENRCCTV-SYIG-DKPEKGQGLNLPAKI
TBLA_0A10170	1025	HPPYGKIEFQAPVDLST-VPIIPLC-GDIISLTNDSFLI-ENEE-GDGNALNGMNVAAKI
TBLA_0B06810	940	HKKYGHIEFLQNVDLN-VPLKLLAHGQLVAFYPKSCSIYANSR-SKPAKGEGLNVKCR
NCAS_0A08290	922	HEDYGKIEFLEPVDLN-ISLTSIC-GDIIRFSSRTCLVGGSD-ATLSQCKGIDVAAKI
NCAS_0H03150	959	RKDVGKVEFLKPVDLN-VALNSIC-EGIIAFEPESFVAFGNYS-NPQIGEGNLNVSARV
CAGLOF06171	921	NKQYGKIEFLDPVDLSD-IPLGSIC-DDLVVFQPMVLLYNNST-NVPEKGKGLNVRARI
CAGLOL04928	932	HKDYGKVEFLEPVDLN-VPLNSIC-DKLIHFEPKTCILYPNSP-IPKPKGEGMNVPAKI
NUP116	997	HKSYGKIEFLEPVDLN-IPLTSLG-GVITTFEPKTCIIYANLP-NRPKRGEGLNVARI
NUP100	844	HRNYGKVEFLEPVDLN-TPLD TLC-GDLVTFGPKSCSIYENCS-IPKPKGEGNLNRCRV
consensus	1621	hk yGkieFlepVDLsn lpl slc g li f pksciiy n rp kgeGlnv ari

OGAPODRAFT_1550	981	SLEGCFPLSKDTKKPITDPHHAVVKKHIRRLQMI PNTEFVGYSISG TWQFKLEHV*---
CJI97_002114	961	TLEG CYPINKKTKLSILDPKDEIVKKHIEKLKALPDMTFKDYEP TGNWTFTEHV*---
CAALFM_C306440W	998	TLEG CYPINKADKLPILDPKSEIVKRHIENLKTIP EMKFISYDPTNGHWT FEVQEMD*--
CYBJADRAFT_168	977	TLEG CFP LARDTRKPIKDVSHALYKKHLQRLQNP GTFKFSYDSKGTGTWTF SV EYTV A*-
SAKLOB11770g	1160	STSG CYPINKSNREP IKDPNHPILKRHVEKMKAI PGVKFESYDPQSGTWVFTVDHTVA*-
KLLAO_F26697g	1073	TLVGCYPKDKSSGKPIKDPHTPLKKHIENLKS MKEAQFESYDPETG SWCFVTEEPVV*-
TDELOB07030	1108	SLYKCYPSDKATREPIKDATHQLVKKHIEKMKRQKQAKFESYDPVTG CWTFFVQH PAH*-
ZYROOF00660g	1165	SCYKCYPADKATRAPIKDANHLVKRHIIEKLKLPNTKFDSYDPVTG CYRFVVEHPITS*
TBLA_0A10170	1081	TRYNCFP IRKENKEYIKDP SHPLMQRHIERLKS MPGVTFESFDP TGMVYFSSPNIVSVF
TBLA_0B06810	998	TLYDCYPTNIATGQPV LDSKHPSVALHVNKLKKYSECFESYNPMDGIL TLMIDHP ILED
NCAS_0A08290	979	TCYRCYPKDRSTRKIVNNPDHQIVKRHIEKLKRLDGRKYENYNPLTGEYTF SVQH AVSG*
NCAS_0H03150	1016	TLYHCYATDKATRKPIKDFNHP LVKRFTANLKKRENSFFENYNPSSGEYTFILDQITA*-
CAGLOF06171	978	SCYNCYPLDKSTRKPIKDPNHRIMERYSEKLKIPHTHFESYDPASGT YCFTVDHALI*-
CAGLOL04928	989	TCFDCFPINKSTRPILDANSTLLKKHIDKLKVP GTKFVSYEEKTGKYVFTVDEPIL*-
NUP116	1054	TCFNCYPVDKSTRKPIKDPNHLVKRHIIEKLKLPNSKFESYDADSGTYVFI VNHAAEQT
NUP100	901	TLYSCFPIDKETRKPIKNITHPL LKRSIAKLKENPVYKFESYDPVTGTYSYTI DH PVL T*
consensus	1681	tly Cypldk trkpikdp h lvkrhieklkrip kfesydp tG ytftveh v

OGAPODRAFT_1550	--
CJI97_002114	--
CAALFM_C306440W	--
CYBJADRAFT_168	--
SAKLOB11770g	--
KLLAO_F26697g	--
TDELOB07030	--
ZYROOF00660g	1224 --
TBLA_0A10170	1141 L*
TBLA_0B06810	1058 *-
NCAS_0A08290	1038 --
NCAS_0H03150	--
CAGLOF06171	--
CAGLOL04928	--
NUP116	1114 *-
NUP100	960 --
consensus	1741

Supplemental figure 6: Alignment of GND sequences. Alternative exons are highlighted in yellow. Predicted PTS2 is in bold.

AfumGndProx	1	-----MSTQA VARLAGINVGAPAR ----- PLPS ADFGGLIGLAVMGQNLIILNVADHGFTVCAYNRT
AtumGndDist	1	-----MSTQAV-----ADFGGLIGLAVMGQNLIILNVADHGFTVCAYNRT
LstaGndProx	1	-----MSEP VARLAGLAGGFTRN ----- SYPS GDIGLIGLAVMGQNLIILNAADHGFTVVAFNRT
LstaDist	1	-----MSEPV-----GDIGLIGLAVMGQNLIILNAADHGFTVVAFNRT
YlipGndIncl	1	-----MTDTSNI KLRLNQVMSQVKVK -----P VAD I AL IGLIGLAVMGQNLIILNMADHG YE VVAYNRT
YlipGndSkip	1	-----MTDTSNIK-----P VAD I AL IGLIGLAVMGQNLIILNMADHG YE VVAYNRT
OpolGnd	1	-----MSEA Q GDIGLIGLAVMGQNLIILNAADHGFTVVAFNRT
CaurGndProx	1	MSTP TFLSRLIMGAQERLSIVRRHL ----- TNHSS GDIGLIGLAVMGQNLIILNAADHGFTVVAFNRT
CaurGndDist	1	MSTPT-----GDIGLIGLAVMGQNLIILNAADHGFTVVAFNRT
CalbGndProx	1	MSSAP KMKKNFNALSRLSILSKQLSF ---- NNTNSSIAR GDIGLIGLAVMGQNLIILNMADHGFTVVAFNRT
CalbGndDist	1	MSSAPK-----GDIGLIGLAVMGQNLIILNMADHGFTVVAFNRT
CjadGndProx	1	-----MSEP KQRLHQFAHTLPNSDPPTYTNSNASPR GDIGLIGLAVMGQNLIILNAADHGFTVVAFNRT
CjadGndDist	1	-----MSEPK-----GDIGLIGLAVMGQNLIILNAADHGFTVVAFNRT
LkluGnd	1	-----MSQ P TGDIGLIGLAVMGQNLIILNAADHGFTVVAFNRT
KlacGnd	1	-----MSE P AGDIGLIGLAVMGQNLIILNAADHGFTVVAFNRT
TdelGnd	1	-----MAA V ADFGGLIGLAVMGQNLIILNVADHGFTVVAFNRT
ZrouGnd	1	-----MS AD FG LV GLAVMGQNLIILNVADHG FS AVVYNT
TblaGnd	1	-----MS AD FG L IGLAVMGQNLIILNAADHGFTVCAYNRT
NcasGnd	1	-----MS AD FG L IGLAVMGQNLIILNAADHGFTVCAYNRT
CglaGnd	1	-----MS AD FG L IGLAVMGQNLIILNIADHG Y TVVAYN RS
ScerGnd1	1	-----MS AD FG L IGLAVMGQNLIILNAADHGFTVCAYNRT
ScerGnd2	1	-----MSK AV GD LG LVGLAVMGQNLIILNAADHGFTVVAFNRT
consensus	1	gDigLiGLAVMGQNLIILNaaDHGftvvayNRT

AfumGndProx	56	TSKVDRFLANEAKGKSI V GAHS V EEFC AK LKRPRRIMLLVMAGKPVD D FI ES LLPHLEEGDIIIDGGNSH
AtumGndDist	39	TSKVDRFLANEAKGKSI V GAHS V EEFC AK LKRPRRIMLLVMAGKPVD D FI ES LLPHLEEGDIIIDGGNSH
LstaGndProx	55	VSKVDHFLANEAKGKS V GAHS I AEL CA LK K PRR V IL LV KAGKAVD D FI DL LLPHMEPGDIIIDGGNSY
LstaDist	38	VSKVDHFLANEAKGKS V GAHS I AEL CA LK K PRR V IL LV KAGKAVD D FI DL LLPHMEPGDIIIDGGNSY
YlipGndIncl	56	TSKVDHFLANEAKGKSI I GAHS I KE L CA LL KRPRR I IL LV KAGA AVD SFI EQ LLPY LD KGDIIDGGNSH
YlipGndSkip	43	TSKVDHFLANEAKGKSI I GAHS I KE L CA LL KRPRR I IL LV KAGA AVD SFI EQ LLPY LD KGDIIDGGNSH
OpolGnd	38	VSKVDHFLANEAKGKSI I GAHS V EEL CA LK K PRR V IL LV KAGDAVD N FI Q LLPHMEKGDIIDGGNSH
CaurGndProx	52	VSKVDDFLN NE AKGKSI I GAHS I EEL CA N L KRPRR I IL LV KAGK PVD AFI EQ LLPHLEKGDIIDGGNSH
CaurGndDist	38	VSKVDDFLN NE AKGKSI I GAHS I EEL CA N L KRPRR I IL LV KAGK PVD AFI EQ LLPHLEKGDIIDGGNSH
CalbGndProx	68	TAKVDRFL NE AKGKSI I GAHS I KE L VD Q LKRPRRIMLLVKAGAPV DE FI NQ LLPY LE EGDIIIDGGNSH
CalbGndDist	39	TAKVDRFL NE AKGKSI I GAHS I KE L VD Q LKRPRRIMLLVKAGAPV DE FI NQ LLPY LE EGDIIIDGGNSH
CjadGndProx	64	VSKVDHFI NE AKGKSI I GARS I QELVD N LKRPRR I IL LV KAGA AVD AFI EQ LLPY LE KGDIIDGGNSH
CjadGndDist	38	VSKVDHFI NE AKGKSI I GARS I QELVD N LKRPRR I IL LV KAGA AVD AFI EQ LLPY LE KGDIIDGGNSH
LkluGnd	38	VSKVDHFL NE AKGKSI I GAHS V KE L ID N LKRPRR I IL LV KAGA AVD AFI EQ LLPY LD KGDIIDGGNSH
KlacGnd	38	VSKVDHFLANEAKGKSI I GAHS V EEL CR N L KRPRR I IL LV KAGDAVD AFI Q Q LLPFLEKGDIIDGGNSH
TdelGnd	37	TSKVDHFL NE AKGKSI V GAHS L EEL V SK L K K PRKIMLLVKAGK PVD Y L IND LV PL LD KGDIIDGGNSH
ZrouGnd	35	TS RV DEFLANEAKGKNI Q GAHS I KE F VD K LKRPR K LM LL VKAGK PVD Y L IGD LL PY LE EGDIIIDGGNSH
TblaGnd	35	TSKVDAFLANEAKGKSI V GAH S LQEL V SK L KRPR V M LL VKAGAVD TT ID SL VPFLEKGDIIDGGNSH
NcasGnd	35	VSK VE HFLANEAKGKSI V GAT S ID D FLSK L KRPR K V ML LVKAGAPVD AL INEL V PRLEKGDIIDGGNSH
CglaGnd	35	VDKVH Q FLD NE AKGKSI I GA S IE D LVAK L KRPR K IM ML VKAGAPVD GL IA Q LVPHLEKGDIIDGGNSH
ScerGnd1	35	QSKVDHFLANEAKGKSI I GAT S IE D FI V SK L KRPR K V ML LVKAGAPVD AL IN Q IVPLLEKGDIIDGGNSH
ScerGnd2	38	QSKVDRFLANEAKGKSI I GAT S IE D LVAK L KRPR K IM LL IKAGAPVD TL IKEL V PH LD KGDIIDGGNSH
consensus	71	vskVdhFlaNEAKGKsiiGAhSieelvakLKrPRrimlLvKAGapVD fIeqllP lekGDIIDGGNSh

AfumGndProx	126	FPDSNRRTKYLKEKGIRFVGSGVSGGEEGARYGPSLMPGGNEEAWPFIKDIFQSI	AAKSDGEACCDWVG
AtumGndDist	109	FPDSNRRTKYLKEKGIRFVGSGVSGGEEGARYGPSLMPGGNEEAWPFIKDIFQSI	AAKSDGEACCDWVG
LstaGndProx	125	FPDSNRRCKELAAKGFLFVGSGVSGGEEGARYGPSLMPGGNEAAWPYIKNIFQDI	AAKSDGEPCCDWVG
LstaDist	108	FPDSNRRCKELAAKGFLFVGSGVSGGEEGARYGPSLMPGGNEAAWPYIKNIFQDI	AAKSDGEPCCDWVG
YlipGndIncl	126	FPDSNRRYEELNEKGILFVGSGVSGGEEGARYGPSLMPGGNKEAWPHIKKIFQDISA	KADGEPCCDWVG
YlipGndSkip	113	FPDSNRRYEELNEKGILFVGSGVSGGEEGARYGPSLMPGGNKEAWPHIKKIFQDISA	KADGEPCCDWVG
OpolGnd	108	FPDTNRRYAELKEKGIYFVGSGVSGGEEGARYGPSLMPGGAPEAWPHIKKIFQSI	AAKSDGEPCCDWVG
CaurGndProx	122	FPDTNRRFEELKQQGILFVGSGVSGGEEGARYGPSLMPGGHPDAWPHIKDIFQSI	AAKSDGEPCCDWVG
CaurGndDist	108	FPDTNRRFEELKQQGILFVGSGVSGGEEGARYGPSLMPGGHPDAWPHIKDIFQSI	AAKSDGEPCCDWVG
CalbGndProx	138	FPDSNRRYEELAKKGILFVGSGVSGGEEGARTGPSLMPGGNEKAWPHIKDIFQDVA	AAKSDGEPCCDWVG
CalbGndDist	109	FPDSNRRYEELAKKGILFVGSGVSGGEEGARTGPSLMPGGNEKAWPHIKDIFQDVA	AAKSDGEPCCDWVG
CjadGndProx	134	FPDSNRRYEELKKGKIRFVGSGVSGGEEGARYGPSLMPGGDAEAWPYIKKIFQSI	SAKSDGEPCCDWVG
CjadGndDist	108	FPDSNRRYEELKKGKIRFVGSGVSGGEEGARYGPSLMPGGDAEAWPYIKKIFQSI	SAKSDGEPCCDWVG
LkluGnd	108	FPDSNRRYEELKKGKIRFVGSGVSGGEEGARYGPSLMPGGDAEAWPYIKKIFQSI	SAKSDGEPCCDWVG
KlacGnd	108	FPDSNRRYDELKEKGIYFVGSGVSGGEEGARYGPSLMPGGAEAWPHIKDIFQSI	SAKSDGEPCCDWVG
TdelGnd	107	FPDSNRRFEELKKGKILFVGSGVSGGEDGARYGPSLMPGGAEAWPHIKPIFQAI	SAKSDGEPCCDWVG
ZRouGnd	105	FPDTNRRYEELKQKGIHFVGSGVSGGEDGARWGPSLMPGGDEAWPAIKSIFQSV	SAKSDGEPCCDWVG
OpolGnd	105	FPDSNRRYEALKEKGIHFVGSGVSGGEEGARNGPSLMPGGAEAWPYIKDIFQSI	SAKSDGEPCCDWVG
NcasGnd	105	FPDTNRRYEELKQKGIHFVGSGVSGGEDGARYGPSLMPGGAEAWPHIKDIFQSI	SAKSDGEPCCDWVG
CglaGnd	105	FPDSNRRYEELKAKGILFVGSGVSGGEDGARYGPSLMPGGAEAWPHIKKIFQSI	SAKSDGEPCCDWVG
ScerGnd1	105	FPDSNRRYEELKKKGILFVGSGVSGGEEGARYGPSLMPGGSEAWPHIKNIFQSI	SAKSDGEPCCDWVG
ScerGnd2	108	FPDTNRRYEELTKQGILFVGSGVSGGEDGARFGPSLMPGGSAEAWPHIKNIFQSI	AAKSDGEPCCDWVG
consensus	141	FPDSNRRyeeLk kGILFVGSGVSGGEEGARYGPSLMPGG eeAWPhIKdIFQsisAKsdGepCCdWVG	

AfumGndProx	196	EGAGHFVKMVHNGIEYGDMLICEAYDIMKRGLGMPVNEIADVFAKWNKGVLDSFLIEITRDVLYFND-N	
AtumGndDist	179	EGAGHFVKMVHNGIEYGDMLICEAYDIMKRGLGMPVNEIADVFAKWNKGVLDSFLIEITRDVLYFND-N	
LstaGndProx	195	EGAGHFVKMVHNGIEYGDMLICEAYDILKRAGAGFTDKEIGDVFTQWNKGVLDSFLIEITRDILYFND-D	
LstaDist	178	EGAGHFVKMVHNGIEYGDMLICEAYDILKRAGAGFTDKEIGDVFTQWNKGVLDSFLIEITRDILYFND-D	
YlipGndIncl	196	AGAGHFVKMVHNGIEYGDMLICEAYDLMKRAGAGFTNEEIGDVFAKWNNGILDSFLIEITRDIFKYDD-G	
YlipGndSkip	183	AGAGHFVKMVHNGIEYGDMLICEAYDLMKRAGAGFTNEEIGDVFAKWNNGILDSFLIEITRDIFKYDD-G	
OpolGnd	178	AGAGHYVKMVHNGIEYGDMLICEAYDLMKRVGGSFSDKEISDVFAKWNKGVLDSFLIEITRDILAYND-T	
CaurGndProx	192	GGAGHYVKMVHNGIEYGDMLICEAYDLLKRVGKFTDKEIGDVFAKWNKGVLDSFLIEITRDIMYFNDPT	
CaurGndDist	178	GGAGHYVKMVHNGIEYGDMLICEAYDLLKRVGKFTDKEIGDVFAKWNKGVLDSFLIEITRDIMYFNDPT	
CalbGndProx	208	AGAGHYVKMVHNGIEYGDMLICEAYDLMKRVGKFEDKEIGDVFAWNGVLDSFLIEITRDILYFNDPT	
CalbGndDist	179	AGAGHYVKMVHNGIEYGDMLICEAYDLMKRVGKFEDKEIGDVFAWNGVLDSFLIEITRDILYFNDPT	
CjadGndProx	204	AGAGHYVKMVHNGIEYGDMLISEAYYIMKTVGGLTDKEIGDVFAQWNKGVLDSFLIEITRDILYFND-T	
CjadGndDist	178	AGAGHYVKMVHNGIEYGDMLISEAYYIMKTVGGLTDKEIGDVFAQWNKGVLDSFLIEITRDILYFND-T	
LkluGnd	178	AGAGHYVKMVHNGIEYGDMLITEAYDIMKRVGGFDTKEIGEVFTKWNKGVLDSFLIEITRDILLYDD-V	
KlacGnd	178	AGSGHYVKMVHNGIEYGDMLITEAYDIMKRIGGFDTKEIGEVFSQWNKGVLDSFLVEITRDILLYDD-V	
TdelGnd	177	AGAGHYVKMVHNGIEYGDMLICEVYDILKRVGGFEDKEISEVFAKWNKGVLDSFLIEITRDILKKN-D-T	
ZRouGnd	175	AGAGHFVKMVHNGIEYGDMLICEVYDILKRVGKFEDKEIGEIFEKWNKGVLDSFLIEITTDILKKN-D-K	
TblaGnd	175	AGAGHFVKMVHNGIEYGDMLICEAYDIMKRVGGFDTNKEIADVFAWNGVLDSFLIEITRDILKFD-D-V	
NcasGnd	175	AGAGHYVKMVHNGIEYGDMLICEAYDIMKRVGHFTDKEIGDVFFETWNGVLDSFLIEITRDILKFN-D-V	
CglaGnd	175	AGSGHYVKMVHNGIEYGDMLICEAYDIMKRIGGFDTKEISEVFGKWDGVLDSFLVEITTNILKKN-D-V	
ScerGnd1	175	AGAGHYVKMVHNGIEYGDMLICEAYDIMKRLGGFTDKEISDVFAKWNKGVLDSFLVEITRDILKFD-D-V	
ScerGnd2	178	AGSGHYVKMVHNGIEYGDMLICEAYDIMKRIGRFTDKEISEVFDKWNKGVLDSFLIEITRDILKFD-D-V	
consensus	211	aGaGHyVKMVHNGIEYGDMLicEaYdimKrvvggftdkElgdvFakWnkGvLDSfLiEITrdil fnD	

AfumGndProx	265	DGTPLVEKILDKAGQKGTGKWTAINALDLGMPVTLIGEAVFARCLSAIKDERIRASSLLDGPTPQ---FT
AtumGndDist	248	DGTPLVEKILDKAGQKGTGKWTAINALDLGMPVTLIGEAVFARCLSAIKDERIRASSLLDGPTPQ---FT
LstaGndProx	264	DGTPLVEKILDTAGQKGTGKWTAINALDLGMPVTLIGEAVFARTLSAIKPERVRASKILTGPVPA---FK
LstaDist	247	DGTPLVEKILDTAGQKGTGKWTAINALDLGMPVTLIGEAVFARTLSAIKPERVRASKILTGPVPA---FK
YlipGndIncl	265	SGTPLVEKISDTAGQKGTGKWTAINALDLGMPVTLIGEAVFARCLSALKQERVRASKVLDGPEPV--KFT
YlipGndSkip	252	SGTPLVEKISDTAGQKGTGKWTAINALDLGMPVTLIGEAVFARCLSALKQERVRASKVLDGPEPV--KFT
OpolGnd	247	DGTPLVEKILDSAGQKGTGKWTAINALDLGMPVTLIGEAVFARCLSALKERGRASTLLAGPSSA--PKI
CaurGndProx	262	DGKPLVEKILDTAGQKGTGKWTAVNALDLGMPVTLIGEAVFARCLSALKDERTRAANVLKGPIVEGESPI
CaurGndDist	248	DGKPLVEKILDTAGQKGTGKWTAVNALDLGMPVTLIGEAVFARCLSALKDERTRAANVLKGPIVEGESPI
CalbGndProx	278	DGKPLVEKILDTAGQKGTGKWTAVNALDLGIPVTLIGEAVFSRCLSAMKAERVEASKALKGPQVTGESPI
CalbGndDist	249	DGKPLVEKILDTAGQKGTGKWTAVNALDLGIPVTLIGEAVFSRCLSAMKAERVEASKALKGPQVTGESPI
CjadGndProx	273	DGTPLVEKILDQAGQKGTGKWTAMNALDLGIPLTLVGEAVFARCLSAVKGERVKASSILPGQIPK-DAV
CjadGndDist	247	DGTPLVEKILDQAGQKGTGKWTAMNALDLGIPLTLVGEAVFARCLSAVKGERVKASSILPGQIPK-DAV
LkluGnd	247	DGTPLVEKILDSAGQKGTGKWTAINALDLGMPVTLIGEAVFARCLSSLKDERIRASKVLPGPTIAK-DVV
KlacGnd	247	DGTPLVEKILDSAGQKGTGKWTAINALDLGMPVTLIGEAVFARCLSSLKDERVRASKLLPGQIPK-DAV
TdelGnd	246	DGVPLVEKILDTAGQKGTGKWTAINALDLGQPVTLIGEAVFSRCLSALKERGRASKVLPGPEIPK-NAI
ZRouGnd	244	DGVPLVEKILDTAGQKGTGKWTAVNALDLGQPVTLIGEAVFSRCLSALKPERTRASKILPGPEIPD-GVV
TblaGnd	244	DGKPLVEKILDSAGQKGTGKWTAMNALDLGMPVTLIGEAVFARCLSSLKSERTRASKVLPGPTVPK-DAV
NcasGnd	244	DGKPLVEKIMDTAGQKGTGKWTAINALDLGIPVTLIGEAVFSRCLSALKSERIRASKTLLGPEVPK-DLI
CglaGnd	244	DGKPLVEKIMDSAGQKGTGKWTAINALDLGMPVSLIGEAVFARCLSALKCERVKASKTLPGPEIPK-DLI
ScerGnd1	244	DGKPLVEKIMDTAGQKGTGKWTAINALDLGMPVTLIGEAVFARCLSALKNERIRASKVLPGPEVPK-DAV
ScerGnd2	247	DGKPLVEKIMDTAGQKGTGKWTAINALDLGMPVTLIGEAVFARCLSAIKDERKRASKLLAGPTVPK-DAI
consensus	281	dGtPlVEKiLDtAGQKGTGKWTaiNALDLGmPvtLiGEAVFaRcLSaLK ERirAskLl GP v i

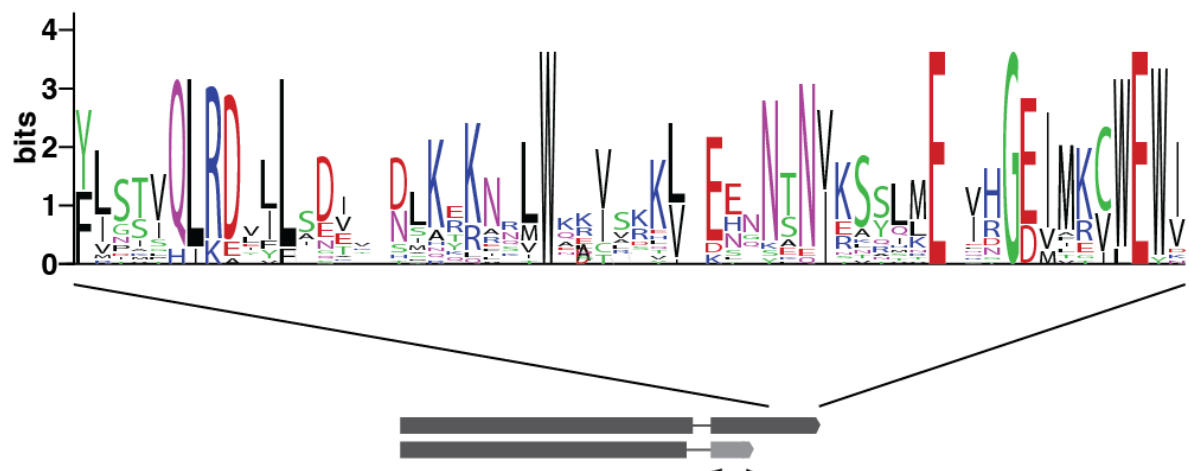
AfumGndProx	332	GDKQAFIDDDLEQALYASKIISYAQGFMLIQEAAREYGWKLNKPSIALMWRGGCIIRSVFLKDITNAYRNN
AtumGndDist	315	GDKQAFIDDDLEQALYASKIISYAQGFMLIQEAAREYGWKLNKPSIALMWRGGCIIRSVFLKDITNAYRNN
LstaGndProx	331	GDKKELVDQLEQALYASKIISYAQGFMLIREAGREYGTWTLNNPAIALMWRGGCIIRSVFLADITRAYRQK
LstaDist	314	GDKKELVDQLEQALYASKIISYAQGFMLIREAGREYGTWTLNNPAIALMWRGGCIIRSVFLADITRAYRQK
YlipGndIncl	333	GDKKEFVDQLEQALYASKIISYAQGFMLIREAAKTYGWE LNNA GIALMWRGGCIIRSVFLADITKAYRQD
YlipGndSkip	320	GDKKEFVDQLEQALYASKIISYAQGFMLIREAAKTYGWE LNNA GIALMWRGGCIIRSVFLADITKAYRQD
OpolGnd	315	TDKQAFIDDDLEQALYASKIISYAQGFMLIREAAKEYNWKLNFP SIALMWRGGCIIRSVFLAEITAAYREN
CaurGndProx	332	TDKEKFVDDLEQALYASKIISYAQGFMLIREAAKEYNWKLN NPAIALMWRGGCIIRSVFLGEITSAYREH
CaurGndDist	318	TDKEKFVDDLEQALYASKIISYAQGFMLIREAAKEYNWKLN NPAIALMWRGGCIIRSVFLGEITSAYREH
CalbGndProx	348	TDKKQFIDDDLEQALYASKIISYTQGFMLMNQAAKDYGWKLNNAGIALMWRGGCIIRSVFLAEITAAYRKK
CalbGndDist	319	TDKKQFIDDDLEQALYASKIISYTQGFMLMNQAAKDYGWKLNNAGIALMWRGGCIIRSVFLAEITAAYRKK
CjadGndProx	342	KDKKEFIDNLEQALYASKIISYAQGFMLIREAAKEYNWD LNFPAIALMWRGGCIIRSVFLGEITKAFKED
CjadGndDist	316	KDKKEFIDNLEQALYASKIISYAQGFMLIREAAKEYNWD LNFPAIALMWRGGCIIRSVFLGEITKAFKED
LkluGnd	316	KDRQQFVDDLEQALYASKIISYAQGFMLIREAGKTYGWKLNNPAIALMWRGGCIIRSVFLAEITKAYREN
KlacGnd	316	KERQQFVDDLEQALYASKIISYAQGFMLIREAGKTYGWKLNNPAIALMWRGGCIIRSVFLGEITKAYREN
TdelGnd	315	TDKKQFVDDLEQALYAAKIIISYAQGFMLIREAGKTYGWKLNNPAIALMWRGGCIIRSAFLGEITKAYRQN
ZRouGnd	313	KDKKQFVDDLEQALYASKIISYAQGFMLIREAGKEYGWKLNNPAIALMWRGGCIIRSAFLGEITKAYRQD
TblaGnd	313	KNKQEFIDDDLEQALYASKIISYTQGFMLIREAGKNYGWKLNNPSIALMWRGGCIIRSVFLGEITKAYRQN
NcasGnd	313	KDKKQFVDDLEQALYASKIMSYAQGFMLIREAGKTYGWKLNNPAIALMWRGGCIIRSVFLGEITKAYRED
CglaGnd	313	KDRQQFIDDDLEQALYASKIISYAQGFMLIREAAKTYGWKLNNPAIALMWRGGCIIRSVFLGEITKAYREN
ScerGnd1	313	KDREQFVDDLEQALYASKIISYAQGFMLIREAAATYGWKLNNPAIALMWRGGCIIRSVFLGQITKAYREE
ScerGnd2	316	HDREQFVYDLEQALYASKIISYAQGFMLIREAARSYGWKLNNPAIALMWRGGCIIRSVFLAEITKAYRDD
consensus	351	dkk fvddLEQALYAsKiISyAQGFMLireAakeYgWkLNnpaIALMWRGGCIIRSVFLgeITkAYre

AfumGndProx	402	PDLENLLFDDFFKAAIQKAQQGWRNVVSKGALWGIPTPAFSTALSFYDGYRTRDLPANLLQAQRDYFGAH
AtumGndDist	385	PDLENLLFDDFFKAAIQKAQQGWRNVVSKGALWGIPTPAFSTALSFYDGYRTRDLPANLLQAQRDYFGAH
LstaGndProx	401	PDLENLLFDEFFHTAIDKAQPSWRQTVANAALWGIPTPAFSTALSFYDGYRSERLPANLLQAQRDYFGAH
LstaDist	384	PDLENLLFDEFFHTAIDKAQPSWRQTVANAALWGIPTPAFSTALSFYDGYRSERLPANLLQAQRDYFGAH
YlipGndIncl	403	PNLENLLFNDDFFKNAISKANPSWRATVAKAVTWGVPTPAFASALAFYDGYRSKLPANLLQAQRDYFGAH
YlipGndSkip	390	PNLENLLFNDDFFKNAISKANPSWRATVAKAVTWGVPTPAFASALAFYDGYRSKLPANLLQAQRDYFGAH
OpolGnd	385	PDLENLLFHFFFNKAAIKAKAQAGWRKTLGVAIEAGIPTPAFSTALSFYDGYRSKQLPANLLQAQRDYFGAH
CaurGndProx	402	PDLENLLFHFFQDAVTAKAQKGWRSTIAKAVEYGVVPVPAFSTALSFYDGYRSSKLPANLLQAQRDYFGAH
CaurGndDist	388	PDLENLLFHFFQDAVTAKAQKGWRSTIAKAVEYGVVPVPAFSTALSFYDGYRSSKLPANLLQAQRDYFGAH
CalbGndProx	418	PDLENLLLYPFFNDAITKAQSGWRASVKGAIQYGIPTPAFSTALAFYDGLRSERLPANLLQAQRDYFGAH
CalbGndDist	389	PDLENLLLYPFFNDAITKAQSGWRASVKGAIQYGIPTPAFSTALAFYDGLRSERLPANLLQAQRDYFGAH
CjadGndProx	412	PQLENLLFNKFFTDAVTKAQAGWRKTVSLTAEYGIAPAFTTALSFYDGYRTAYLPANLLQAQRDYFGAH
CjadGndDist	386	PQLENLLFNKFFTDAVTKAQAGWRKTVSLTAEYGIAPAFTTALSFYDGYRTAYLPANLLQAQRDYFGAH
LkluGnd	386	PELENLLFNKFFTEAITKAQQGWRRTIGLAATWGIPTPAFSTALGFYDGYRSERLPANLLQAQRDYFGAH
KlacGnd	386	PELENLLFNKFFADAVEKAQSGWRKTIGLAVSYGIPTPAFSTALSFYDGYRSERLPANLLQAQRDYFGAH
TdelGnd	385	PELENLLFHSFFSDAVSKAQSGWRKTAALATQYGIPTPAISTALAFYDGYRCERLPANLLQAQRDYFGAH
ZRouGnd	383	PDLENLLFHDFFTQAVTKAQGGWRRILGISTTYGVPTPALATALAFYDGYRSARLPANLLQAQRDYFGAH
TblaGnd	383	PELENLLFNKFFGDAVTAKAQSGWRKTVLGGATYGIPTPAFSTALAFYDGYRSERLPANLLQAQRDYFGAH
NcasGnd	383	PELENLLFNKFFSDAVTKAQGTWRKSIALATTYGIPTPAFSTALAFYDGYRSERLPANLLQAQRDYFGAH
CglaGnd	383	PDLENLLFHKKFFKDAVTAKAQGGWRRSLALAAATYGIPTPAFATALSFYDGYRSERLPANLLQAQRDYFGAH
ScerGnd1	383	PDLENLLFNKFFADAVTKAQSGWRKSIALATTYGIPTPAFSTALSFYDGYRSERLPANLLQAQRDYFGAH
ScerGnd2	386	PDLENLLFNEFFASAVTKAQSGWRRTIALAATYGIPTPAFSTALAFYDGYRSERLPANLLQAQRDYFGAH
consensus	421	PdLENLLf FF dAvtKAq gWRktvava yGiPtPAfstALsFYDGYRserLPANLLQAQRDYFGAH

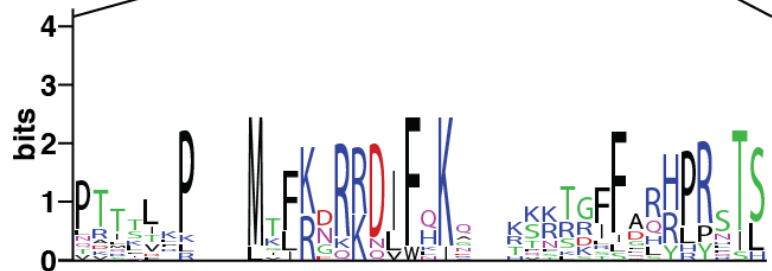
AfumGndProx	472	TFRVKPECANENYPEGKDIHVNWGTGRGGDVSASTYVV*
AtumGndDist	455	TFRVKPECANENYPEGKDIHVNWGTGRGGDVSASTYVV*
LstaGndProx	471	TFHILPEFSSEKYPKDDTVHVNWGTGRGGNVSASTYLA*
LstaDist	454	TFHILPEFSSEKYPKDDTVHVNWGTGRGGNVSASTYLA*
YlipGndIncl	473	TYQLLDG-----DGKW IHTNWTGRGGEVSSSTYDA*
YlipGndSkip	460	TYQLLDG-----DGKW IHTNWTGRGGEVSSSTYDA*
OpolGnd	455	TFKILPEYATEDRKVGDIYIHINWTGKGGNVSASTYNA*
CaurGndProx	472	TFQVLPGEENDFLKKDQWVHVNWGTGRGGNISASTYDA*
CaurGndDist	458	TFQVLPGEENDFLKKDQWVHVNWGTGRGGNISASTYDA*
CalbGndProx	488	TFKVLPGQENELKKKDEWIHINWTGRGGDVSSTTYDA*
CalbGndDist	459	TFKVLPGQENELKKKDEWIHINWTGRGGDVSSTTYDA*
CjadGndProx	482	TFKVVPEKANDNLKVGEAIIHINWTGHGGNVSAATTYDA*
CjadGndDist	456	TFKVVPEKANDNLKVGEAIIHINWTGHGGNVSAATTYDA*
LkluGnd	456	TFKVLPECADDHLPAGQDIHINWTGKGGNVSASTYQA*
KlacGnd	456	TFRVLPEAASBNLPADQNIHINWTGKGGNVSAASYQA*
TdelGnd	455	CFKVLPEFASATFPEGKDIHVNWGTGHGGNISASSYDA*
ZRouGnd	453	TFQVLPECANADFPAGQDIHFNWGTGHGGNISSSSYQA*
TblaGnd	453	TFKILPEAASBSLPEGKNIHINWTGHGGNVSASTYDA*
NcasGnd	453	TFRVLPECASDNLPLDKDIHINWTGHGGNVSSSTYQA*
CglaGnd	453	TFRVLPECASDSLPGKDKDIHINWTGHGGNVSSTTYDA*
ScerGnd1	453	TFRVLPECASDNLVPDKDIHINWTGHGGNVSSSTYQA*
ScerGnd2	456	TFRILPECASAHLPVDKDIHINWTGHGGNISSTYQA*
consensus	491	tfrvlpe a e lp diHiNWTGrGGnvSastYda

Supplemental figure 7. Alignment of Src1/Heh2 sequence. **A:** The alternative exon of *SCR1/HEH2* orthologs is translated in two different reading frames. Sequence logos depict the most conserved regions in each reading frame. **B:** alignment of the constitutive exons. **C:** Alignment of the alternative exon in the full-length frame. **D:** Alignment of the alternative exon in the truncated frame.

A.
Conservation in full length reading frame:



Conservation in truncated reading frame:



B.

AfumSrc1	1	-----MADGLDYLSPDFDLNLTLPRLRSILVSHDV
LstaSrc1	1	-----MDDLSEYPNFDQKLRVPPELRRVLLMHDV
YlipSrc1	1	-----MDSYEYLTEGFDPKSLRIADLRRIFAHHDI
OpolSrc1a	1	MQRRGAGLRDRVSIGDCFSFKAFSVTIAPIPQRQALTPFDLNSLRVIDLKKILHKRGV
OpolSrc1b	1	-----MDSVEYLDPDFDPHKVTVPRLRSILVDRKI
CaurSrc1	1	-----MEKDYLSDNFDPSRIKVAQLRSILRENDI
CalbSrc1	1	-----MDHLKEDFDPTTFTAAQLRKVLNLHEI
CjadSrc1	1	-----MDPEVYLQPDFDPAHKMADLRNILLQNDV
LkluSrc1	1	-----MDSYLLGEGFDPKTLKVAQLRRILVEHGV
KlacSrc1	1	-----MSKEEDSSAADSSFNDSILKDDFDLSLTKIAQLKTVLTSNEI
TdelSrc1	1	-----MDTKYLEPGFDPSSLKVAQLRRILTEGV
ZrouSrc1	1	-----MDEYLPGFDPSSLKVAQLRRILTENNV
TblaSrc1a	1	-----MDSLLEYLEDGFDPSSLTVKQIKRILDEHKV
TblaSrc1b	1	-----MYTKHLEPGFNTKLKLAQLKQILRENGV
NcasSrc1a	1	-----MNNEYEYLPNFKFKSLTVSQLRRILVENNV
NcasSrc1b	1	-----MEKKYLESGLDLKKLRVPPELKKILAENNV
CglaSrc1a	1	-----MVTNILLPGFKPESLTVAKLRRVLTEHGV
CglaSrc1b	1	-----MSENQIGIDLSKLTAAQLRFVLAENKV
Src1	1	-----MNSDLEYLEDGFDPNSMKVATLRRILVENNV
Heh2	1	-----MDHRNLDPKTLKVSQLRRLVLENDV
consensus		dyl pgfdp tlkvaqlrril en v

AfumSrc1 32 SYPASAKKAQLIRILEEEVLPAQAKLLRERERVKR-TSAG-----ITDMPSRATSVASD-
 LstaSrc1 31 PFPSSAKKAALVELFKQHITPNSANLLAAKEGSGG-AVPD-----IVDASITS-----
 YlipSrc1 31 EYNVSGKKAEMTSVFRNEISPRAAELYAREIATPG--GEG-----IVDAGAPKIKSKKEG
 OpolSrc1a 61 SIPRSARKADLIELLKAQTRAVEKEKTQEQTQSE----G-----
 OpolSrc1b 31 DYPSSAKKAELIQLYEEYIRPNAAKWLEEYKNSIE-KSVN-----IEEANTPSKR--S-A
 CaurSrc1 30 EYPGAKKKELVEIFTKNIDSIKSKGLPIEPSPTPNSDE-----IEVIDSEPEEKPA-S
 CalbSrc1 28 QYDSSAPKSSLIEIFNKEIAPNSKKLLSEYNAKVE-NMND-----DDFINASDFDKPS-E
 CjadSrc1 31 AYPSSARKQHLDLNFNEHIRPLAEQKLKELNSVVA-AGDG-----IEIEKKDNA-RS-G
 LkluSrc1 30 DIQLNSKKAELVKAFNRNIKPRREELLKKKTKLP-SSEG-----IVKVKKKSKKRA-K
 KlacSrc1 43 GFKAHDKKASLVKLVEDNLGSIKRNLEKD-GGLSP-LVIP-----SVKVTKKKRESKK-R
 TdelSrc1 30 EFQPQAKKNTLLGLFNEHVKPKIPKLRRYENLLP-SDKG-----IVTVGTVNKKKKK-K
 ZrouSrc1 29 EFPSSHKKAMLVRLFEENVGPRLPKLRKKHAKALS-NING-----KGVRTRSAAKTKS-R
 TblaSrc1a 31 FYPKTNKKQTLNTYKIEFQPLVPLLRAEYNSRLD-QLQKEKIEQDLRMATDSKDYDS-N
 TblaSrc1b 30 KYPEKAKKSQIMKLYETEITPKLPKLRTHEQNRRK-KEADLKNQQQLKHD--NNKSFPQ--
 NcasSrc1 32 PYHSRSKKSELMQLFKDAIVQIPSLREKYLNVDS-NTAD-----IIRIPKRRKKSFA-L
 NcasSrc1b 30 NFPSRAKKHVLIKLFNSKIKAAPRILRSKEGVVKQ-STKT-----KDSNR-S
 CglaSrc1a 30 EYPANAKKAELAKLFKKHIKPKIPEMRKKEKGVRA-SSDG-----ISRITSKKKTME-I
 CglaSrc1b 28 SFPSKAKKADLLRLCNKL-----
 Src1 32 DFPNARKNALVGLFDEKVKPQIPQLRKMYLNVRP-SDEG-----IVKMDRPPSSPSI-A
 Heh2 26 AFPANARKPVLVKLFEKVRQRLQSSPEA-SKVRT-SIQK-----VVKSGAKNAD---R
 consensus yp akK li lfe i p l v g iv m

AfumSrc1 85 -----YDQGREYVD-----
 LstaSrc1 78 -----
 YlipSrc1 84 KEKKEKK---EDKEKTTRA---PAK-----RRVTSRN-----KTPELQ-APD
 OpolSrc1a 97 -----SEDET-----EISS-----
 OpolSrc1b 82 -KSSRYSTPDKGSRKSL-----SPAP-----D-
 CaurSrc1 84 KEATPT-----KNTRKPRKVS KAK-
 CalbSrc1 81 KSTTSEK---AS---A-----LFVSDTESDGENEKIDVSKTRNKTCKVTKPK-
 CjadSrc1 83 RSKTPAAKPESDSDSEG-----VEVIGGPEKISATKTTRTAATRKSPR-
 LkluSrc1 83 SEEAD-----GSR-SK-----GS-----ARVASTS-----SAFSETESID
 KlacSrc1 95 KSTTP-----ESLEKS-----LTKA-----KA-----
 TdelSrc1 83 KNKLE-----SNP--S-----GS-----ENYEAD-----INASKSDTLD
 ZrouSrc1 82 DSSDD-----SSK-KS-----RK-----RRVSS-----VS
 TblaSrc1a 89 ISDTDVNEPRTGSNIEAVDTNTKEQDTNIEEKD TDVQLKEESFSELSN--KNSKQSSALD
 TblaSrc1b 86 ---TP---KHST-DKS-----F-----YNLITAS-----K---YTML-
 NcasSrc1a 85 EETIE-----GNESS-----GN-----NNVIGKK-----KA---TPM-
 NcasSrc1b 75 RSSSPIKRRTKEINSR-----E-----DGAT---EK---KTKNHKDIVE
 CglaSrc1a 83 RKAQA-----K-----QKVVPPEP-----KESSESASD-
 CglaSrc1b 46 -----
 Src1 85 SPRRS---RRARREKS-----A-----SPMA-----KQFKKNRILD
 Heh2 75 KKTLK---S-KKLESS-----S-----SES-----KTV-
 consensus s k

AfumSrc1 94 -----RESMPP
 LstaSrc1 78 -----SLPA
 YlipSrc1 119 EIQVRRS-----PRRSP-----SKQDISLDLDEVLASPK
 OpolSrc1a 106 -----GAEDERK-----TGDTRSSPP
 OpolSrc1b 103 -----
 CaurSrc1 103 -----EN---GEETNNL-----KHESDSS---
 CalbSrc1 122 -----LRASSGNQKSTSRSSSRKSPESD TESKDD
 CjadSrc1 126 --RVAQSD-----TAKRPTRIASGDL-KD-----IPKLEA--ESPE-
 LkluSrc1 112 GLKVLKKE-----
 KlacSrc1 112 ----IKKS-----
 TdelSrc1 110 -PSAHLKE-----
 ZrouSrc1 101 -----
 TblaSrc1a 147 DIILDSYASSDIDQDLSEKEEIQDGDSEIIGGNALEE-----INMDDDEVEIKDM
 TblaSrc1b 108 -----GDNPVRTNRSP-----SPSRDNLGL-----NTPL
 NcasSrc1a 110 -----
 NcasSrc1b 109 SVKL-----VNIEDDTT-----
 CglaSrc1a 105 -----SE-----SDTESS--
 CglaSrc1b 46 -----
 Src1 113 DVSNDDDDDDDDDDND-----KKDDPLIVPSGTD TDE-----VDDEEDDVITS--
 Heh2 94 -----
 consensus 181

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AfumSrc1 100 --PPTPSTVSTATGT-----RRGRSRMSTRASTADIEEN-----
LstaSrc1 82 SEFPKSARKSTARKS-----TAVRSRTPGRSGRK---TT-----
YlipSrc1 148 KK-----KASLDSPK-----KKVGR-----PRK--IKEPSP-----EPE
OpolSrc1a 122 KHKPTTSHVPSSK-----
OpolSrc1b 103 -----QTVPQKRGS-----
CaurSrc1 119 -----VASDVS-----
CalbSrc1 154 EAKPASRSSRLSSR-----GNRSKPLNS--LFDLDDS-VLNLRKPSKNSKSKSRTT
CjadSrc1 157 -----PRVRER-----S--RSREQPR--LRDRSP-----RRVA
LkluSrc1 120 -----SSPFTDVNDF---QKSVLPKKRRGKHE--EEDDE-----ETPR
KlacSrc1 116 -----TIKEEENEA---KDGERPVSKKRKKR--TKDED-----GQRS
TdelSrc1 117 -----STPFSDVNEF---QQSSGFNRKARKRK--VTEES-----NVKD
ZrouSrc1 101 -----GDDN-----EGH-----NKNE-----NNED
TblaSrc1a 199 EIE--TRSFDDNRESKDIQQDQNSQVSKDDID--MQDD-----MEV--DNDDIHEEIE
TblaSrc1b 132 D---TKNSSDIRHAHNIN-----
NcasSrc1a 110 -----DIAFSSDSNS---A-----LS
NcasSrc1b 121 -----HLKRRKKPENE-----VDQSRKKRKKR--LRDLRE-NKLTID-----
CglaSrc1a 113 -----SSTASDSSSA---SSSSSS-----SSSS
CglaSrc1b 46 -----
Src1 157 -----SSNKSDTNDF---QQNSDTRKKRKDPD--SDDWSESNSKENKI--DNKHL-NLLS
Heh2 94 -----KDEN-----VETNKRKRE-----QIS
consensus sd d

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AfumSrc1 132 -----NVPST--PSIVTK---KKVPKSEN-----KH-----AR
LstaSrc1 113 -----LVADTPQPEIKS-----EN-----EK-----
YlipSrc1 175 SEEE-EEAEEIIEQVKTTTRKLELDDIPV-----IAAPKQQRQPSGY
OpolSrc1a 135 -----IPPKVTK--PL--AKIPKPKR-----VLNLP-----
OpolSrc1b 112 -----EEATPKRKKLHRKKRSTEENGVSDDAES-
CaurSrc1 125 -VSDNEKITDNTPDVTDQNSDIKSLPSSSTK-----KKSKKRKSSAFEDDEHSK
CalbSrc1 203 LKLKTKKTAESTPEVTETSDTEKEKVEEPV-----KKE-----TGKESTPENT
CjadSrc1 181 SGSD-SKRHVA-----SNSEKSPTKIKEDTE-----KIEKTRVSPFKVDPKLES
LkluSrc1 153 -----AK-----K--THAKKPK--E-----EKLPTLNSP-----
KlacSrc1 147 DT-----EDTKPV--KKTRKTKK---K-----VKSEEIGSP-----
TdelSrc1 150 ADGD-LEMDMK-----V--EETDKRR--R-----KIGEGDHTP-----
ZrouSrc1 116 DEGD-VNMDEAKPSSSRGSTI--KNKNKKRK--R-----IGDQSNTPT-----
TblaSrc1a 246 EDS-EDMDDIQEEVQEKQDDKQDKPNT-K---A-----NVEKQVNSN-----
TblaSrc1b 147 S---NALGDPKPKVRSLSREIRKAANKGTS---Y---KDCNKKKRDESV-----
NcasSrc1a 123 SESD-SEF---TKQIRRGAEV---TPKSKK--R-----KIEKQTGTP-----
NcasSrc1b 154 -----VKDRDILSPIKVEESS--
CglaSrc1a 133 SNSS-SSYEMEQQDDTVETENE--FQTARSKR-----KA--EQEVE-----
CglaSrc1b 46 -----
Src1 204 SDS-IEQDYQ-----K--AKKRKTS-SD--L-----NQEHGNGSA-----
Heh2 110 TDNE-AKMQIQ-----E--EKSPKKKR--K-----KRSSKA-----
consensus e k kr sp

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AfumSrc1 155 AFDRELHDDGPVT-----PVARDMV-----T
LstaSrc1 129 -----
YlipSrc1 215 AVDDDEVV-----EMDEQEVAEL-----IAPIVD-----QS
OpolSrc1a 158 -----QT-----KTAPPAKGK-RLK--SLV
OpolSrc1b 141 -----TVSRIEEE-AKS
CaurSrc1 172 APQRGNIFQVDVSDSDTVI-----F-S-----PKPKKLPSSPK
CalbSrc1 246 NFSKENVFQSPPGSSTKKRKHQDAEEEDD-S-----TLVKKIKPSQRT
CjadSrc1 224 SFSDHNVFQSPIPSSPDFKKVIPKKRVKSTESPEKEVSCKNPRVLKKTAFSSSPAP-QRS
LkluSrc1 173 -----ITEKVR-S-KRT
KlacSrc1 173 -----IAKKIT--TKS
TdelSrc1 179 -----ITDKVA--RKT
ZrouSrc1 154 -----IEKVA--KKS
TblaSrc1a 285 -----ERDKK-
TblaSrc1b 187 -----
NcasSrc1a 156 -----ILDRVS--SKS
NcasSrc1b 170 -----EGT
CglaSrc1a 168 -----ELKVE-----
CglaSrc1b 46 -----
Src1 233 -----ILGKLS--VKT
Heh2 136 -----NKP
consensus i dkv kt

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AfumSrc1 176 PRKST-----
 LstaSrc1 129 -----
 YlipSrc1 241 PKKSPKKNKRRLSQPVVDPERSD-----NEDA-----
 OpolSrc1a 174 GQSV**PQKRSL**-----EDSNDDAD-----
 OpolSrc1b 151 --SKSIKSP**LSLEKFE**SESPVEEGD-----
 CaurSrc1 206 PESP---**KLKVRNTPDERNRSQSK**---RSSLSF-----SE-----IAKS
 CalbSrc1 289 AEEN---**RSLF**---DDDNDSDVEF---LEEFMR-----TE-----KKKS
 CjadSrc1 283 **PEKSPLKSLTISKFE**DENDSFSEKFKGSEALQFD-----
 LkluSrc1 183 **PTKSPH-RSLVIDKF**ESSSESSASLAG-SRSPMSKENFLVFEQEKDVKDKLPI--QDED
 KlacSrc1 182 **PIKSPH-RSLIDKF**ESSDDASDET**GKDDSF**INFSIKK-----TAKPKKS-----
 TdelSrc1 188 **TKKSPH-RSLTIDKF**ESSSSSDSSFNES-SILNVS-----RRDQSGHL-S--MEVA
 ZrouSrc1 163 **PSKSPR-KSLVIEKF**ESSESASDSASDSASLS-----
 TblaSrc1a 291 ----TSSD**QLTFTKLNKKPRAC**LT---R**SKIG**-----CDRTKPCDN---NCTKKNK
 TblaSrc1b 187 -----LEEDDL**DLKLS**-----
 NcasSrc1a 165 **PSKTPN-KSRTIETFD**LSSSSPSPVALKDSSL-----YRNV--SSTQPPLRTPTK
 NcasSrc1b 173 **PQIPSN**-----NDTDIA-----VKDETED-----L
 ChlaSrc1a 174 -----
 CglaSrc1b 46 -----
 Src1 242 **PIKNTNRKPVSM**DNFNDSLTSSTGE--NDPFVP-----NIRHNP-
 Heh2 139 PESP**PQSKSD**-----GKATSADLT---SELE--TVE---ELHKKDSSDDKP-----
 consensus p ksp rsl l e s

AfumSrc1 181 -----TRK**L**RNSEIAPSIEPE-----PHTVYVK-
 LstaSrc1 129 -----PKVA-----DETVKGE-
 YlipSrc1 268 -----RPKKKK**LSKEEKEAKALRKEKKRKEKEAL**-AR-----KVFSFE
 OpolSrc1a 192 -----AT**VHKEYSKILKKQ**TNHKRV-----FSSS
 OpolSrc1b 174 -----I-----SDILAR---LVSPKKEEPKNQIV-EMEMENTFEAV
 CaurSrc1 239 S-YQ**DV**KNN---LNI-----TPSK--SAG**IP**KKETVPRKQPF-----VKE
 CalbSrc1 319 SKVLKSGNS---QTL-----AP**SS**-S-----TKKEPK-----
 CjadSrc1 318 ----TSNEK-----S**IEVTN**-----DTSAN-----NSYIA-
 LkluSrc1 239 SAYH**DFS**FK--RKTMSPD**LSKLKVS**PAFA**QLMKVTNQNQ**STPA--K--KTSSEPSFDNL
 KlacSrc1 226 ---EFPEANSILSDIPNE**QSLK**TRAEFPSVTDSSLN**PST**-----
 TdelSrc1 234 SPKN**DFS**YG--KRTLAPD**LTKLV**SPAFEE**ELK**MAYKES-SVP-----VLARS
 ZrouSrc1 194 ----SFSNKK-EENSPTD**L**SH**LKVS**DAFAAQWKKALNNDEGA**EF**--V--KGEKPNVFPAD
 TblaSrc1a 335 CIYP**DVP**STANSSNKPKD**LEKLHP**NADLQNA**VKNTEQADN**HMNK--RD-ANTVENPKESV
 TblaSrc1b 198 ----ANSSNDTFNRPP**LKKLKT**ENTKSTKYTSQV**SIEAELGTAALDLNR**NIEVSFSK-
 NcasSrc1a 213 AA**EFDFS**QK--RRTLSPD**LDKLV**SAFA**QQLKKA**VKENEK**SK**--V-----PSFASM
 NcasSrc1b 193 VGRPEVP-----SN**LNLIS**SEFAHT**LQSALS**SEEPPI**SFAV**-----PEGTLISL
 CglaSrc1a 179 PVHL**DFS**YKKQKGNELDH**LKLSIKV**SDKMA**SLINNAISDMEKEK**D--K--EN-KDVS--M
 CglaSrc1b 46 -----
 Src1 279 ---K**ELGTAN**-GTGHST**PLSKLV**SASFAD**KLPQKEVP**STI-----
 Heh2 177 -----RVKELPKPE**LPNLV**SN**EF**LA**QLNKELASA**ATENY--D--HSIK-----
 consensus d l lkvs l

AfumSrc1 204 -----SEPKEDSVFTDDNPFQSGSSPA----
 LstaSrc1 140 -----IKVEEGSSFSENPFQTPRTRT----
 YlipSrc1 305 DAETA-ESKLL-GEDEEVADFEYKKVDTPLKVKEEDSADSPFTSQNVFQSGGTPDKKRR
 OpolSrc1a 216 APTTPNNSTIV--SPKKETDVK-----VESTPKID-----
 OpolSrc1b 206 E-----
 CaurSrc1 273 --E--VTRPILDPVPDSTTDVSRDE-----TNDSSKKLGDSFK
 CalbSrc1 342 -----KKEILLFSPGSASKVKPKSLTKKVTPKKSG-----EKLVP**SAATNDK**SF
 CjadSrc1 339 -----SANVG-----D-----NLESDDVFHVSSD
 LkluSrc1 293 PSFSA-----TG-KGKEEGAE-----
 KlacSrc1 262 -----SESTPIK-----
 TdelSrc1 279 DSQ-----SG-QDKEYASG-----
 ZrouSrc1 245 V-----E--GDVTFGSPLRIST-----
 TblaSrc1a 392 SSIYEKTTEIY--SKSSPAEISNTTQTTT-----PIKTTKLSIKK**VS**I---
 TblaSrc1b 252 -----NSNYIVPEEKGETN**FSL**-----SDTQFS-----
 NcasSrc1a 262 KADSDSDSEIY--SIFNEQDFDSIKTRRKALLGSDSD-SDSEY**EKA**KRMVSGSVSNTDTK
 NcasSrc1b 237 NEN-----NENTHIHKHVS**NQRENFEKE**-TLSDSSVVAISSL
 CglaSrc1a 231 -----HDG-NDSEPSSSSNLISDQ**GAPKESD**
 CglaSrc1b 46 -----
 Src1 316 -----
 Heh2 217 -----STDLS--
 consensus

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AfumSrc1 226 -----SRSISRD-----VKRKT
LstaSrc1 162 -----SPKGSRKTS-----LTSVKREG
YlipSrc1 363 RKSEVAENSAR-KVRKAEEDDDFNASLDQTFA-----SV
OpolSrc1a 244 ----QKNSNK-----DEHGTPF-----KEDN
OpolSrc1b 207 -----NVQV
CaurSrc1 307 DD--FE-----DDAKNFDTALSCLKGDVSHSKET-----DGGRKDEEI
CalbSrc1 387 KS--IE-----DETKDFDAELKKIQNKKNQ-----PQVNPDL
CjadSrc1 358 DD--KQNNNT-----VVRDTDYATPQ-----
LkluSrc1 308 -----QEQQEQEQ-----EEEEEEEEKQSSREA
KlacSrc1 269 -----KKVEDSKPAKTLQKV-----EQESVKKEL
TdelSrc1 292 -----P-----ADVSLEK
ZrouSrc1 260 -----PELPTQK-H---VDETEE--RVKKLEK
TblaSrc1a 435 ----PQTNST-----TETSTISNAQPITNPQ-----
TblaSrc1b 275 -----KESS
NcasSrc1a 319 KS--SHKNSKNNSNTSFENMPSEFKSETSMSQKDIPSGTPQEIIITILESSDEEEKNVKENI
NcasSrc1b 273 Q---EKN---NPP---KKIDNFDLSLTEMADITEHSSTPA-----AA
CglaSrc1a 256 AQ--PH-----TSGTDMYNAFIKEDTPSDTAPEVEEQ---TTQVKNEIN
CglaSrc1b 46 -----IDESDAEEV-----
Src1 316 -----LVPEVEQQE-----PSQSERT
Heh2 223 -----IRIETE-----
consensus e

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AfumSrc1 238 -----
LstaSrc1 180 -----
YlipSrc1 396 PE--AFSGLGGAAQIPSLSPPAFFSH--QQQPTT---A-----
OpolSrc1a 261 ----QEGTEII-----
OpolSrc1b 211 PS-----
CaurSrc1 343 ---AKLLGVDVE-----
CalbSrc1 417 ---AKLLGITIQ-----
CjadSrc1 377 -----SGNASRISIASSIQGTPSR-----
LkluSrc1 332 ---T-----ESSESYEASG-----KN--
KlacSrc1 293 PEVPA-----TELPTLREVKK-----
TdelSrc1 300 ---N-----ES-----
ZrouSrc1 281 ---E-----A-----
TblaSrc1a 457 --LSA----MEQTASIQPNSLKLPNAIDIQIPKNLSDNNISKRPDDSQSDHSLKENSS
TblaSrc1b 279 PSVRISLNSSLNEISLKPKNLIKT-----KDNTN-----
NcasSrc1a 377 PTLVN-----AQKPIIPTPHLPTKNGAYQTKE-----KTNT
NcasSrc1b 305 P--VLHEGFGEFSNYPSYSTN-----
CglaSrc1a 294 S---STEDFGNE-----
CglaSrc1b 55 -----SQRIGAAIAKERVVDHETKLRLRQKK-----MKE---
Src1 332 PSLFSSSEGSGSESEAPLLPEITT-----
Heh2 229 -----EPVGPST-----
consensus

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AfumSrc1 238 -----SSRLSTASPAFSHGLRPRK-----SETPYDL
LstaSrc1 180 -----APKFSITPPVAK---PTI-----IASPK--
YlipSrc1 428 -----TSQTPSS---STQFSPPHSTNSRINRF-----
OpolSrc1a 269 -----HTKKEASRS-PPPADTQ-----
OpolSrc1b 213 -----FLDEMLAGPDR-----ILDNE-SGD-----DERTI
CaurSrc1 352 -----GVKVK-----P---KGR-RVI-----TPR--
CalbSrc1 426 -----GFEP-----VVTPSKTKDILKDL-----TPAKD
CjadSrc1 396 -----TPK-----IPYSKAQSSLRENLTSWF-----K---KTPKAE
LkluSrc1 345 -----EDPTEKSQSVGAISN--ESNEQGLLS-----ETEVEGE
KlacSrc1 309 -----LQEQVNQSIIT-----ETGE
TdelSrc1 303 -----SISVTPVRSEPASEEEVVLS-----EATVSK
ZrouSrc1 283 -----QPQVNKESP-----KLNVE-
TblaSrc1a 510 LNNSTKKRKIDK---STSLIEEK-LSTKSPKPNENSIVMENF-----DMDV-----
TblaSrc1b 310 -----NNFKHLSPLQSIILDTSTNRGSIDYMTECTPKNN
NcasSrc1a 409 L-----QDKINGQEGASEPLVEEMVQDQIRPAQPVTEDELISEH-----DAMIQEDEITS
NcasSrc1b 324 -----IKPVKEEQE---F-----HSKGY
CglaSrc1a 303 -----AQPLDNSNDISLT-----SKTTVQNPFAD
CglaSrc1b 83 -----SAKANS--EPAESLPAEKVSVQKSPNKKSVAGKKHSRTESEDESDKNKKKRAK
Src1 355 -----PGP---HQPM-----GN
Heh2 236 -----GAETRNESEVME-----
consensus li

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AfumSrc1	264	--D-----GD	IS	SRTP-----	-----	TRSPVGS	PV-----
LstaSrc1	200	-----	AV	SSPT-----	-----	GESDFGT	PV-----
YlipSrc1	454	-----	MF	SSPE-----	-----	RDDENVN-----	VVSSTPPLPVA-
OpolSrc1a	285	-HD-----	QSF	VVPTL-----	-----	LSST	PMVFD--
OpolSrc1b	237	ASA-----	TK	MTQRELL-----	-----	-----	-----
CaurSrc1	367	--R-----	PI	VISER-RL-----	-----	-----	-----
CalbSrc1	450	EST-----	PVT	KVEKQOI---T-NNS-----	-----	ASKTET	PKKL---
CjadSrc1	424	END-----	TTE	GVTEGVT---E-G---VTEGA-----	-----	T--E-----	-----
LkluSrc1	375	EPD-----	ET	IASSEA-----	-----	E-DDEE-----	PIEISELEQQIDTPK----
KlacSrc1	324	ESD-----	TT	ITKAETFA---K-D-----E-----	-----	ESEEEV	PKSAT--
TdelSrc1	329	EE-----	V	APRE-----	-----	SSTDELEQ-----	K-----
ZrouSrc1	297	-----	KK	REL-----	-----	E-VNER-----	PAEKQEPEVKLEED-----
TblaSrc1a	553	-SD-----	SS	MSS-NSFI---Y-GNDVNVTTLEEN----	-----	KIG-SDPK-MILT	PKKLCSPL
TblaSrc1b	344	SPENVDLFNEI	I	NSAHSIAEDTYETDKENFNKNS-----	-----	KKQLSMKLLD	TYI
NcasSrc1a	459	EQD-----	DIF	EEDFAIS---E-KNDI-VNEEEEEARASKDIGGETVETILEL	-----	P	LLAAKN
NcasSrc1b	339	TSD-----	IK	FVSNANEN---Y-----	-----	NLST	PGCN---
CglaSrc1a	327	TSN-----	SS	IQEIN-----	-----	ISRPQVDNSF	-----
CglaSrc1b	135	STD-----	DN	IKIKNNQS-----	-----	AAVN-----	STSALATPVKAAE-
Src1	364	TSN-----	NV	VEMID-----	-----	-----	-----
Heh2	248	-----	NIN	L-----	-----	E-----	-----
consensus			i	e			p

AfumSrc1	281	-----	FP	REEVEMDGKE-----	-----	-----	-----
LstaSrc1	215	-----	KF	SSELFPLDPQEY-----	-----	-----	-----
YlipSrc1	479	---SS-----	SQ	NRQSFMPGLDELNLSSKFA-----	-----	-----	-----
OpolSrc1a	304	-----	SP	RKP-----	-----	IPSLDV-SDFAAQLEKLSGPTKPIALDGSEQK-----	-----
OpolSrc1b	249	-----	-----	-----	-----	TNVDSSD-----	-----
CaurSrc1	377	-----	AS	NRGSLLE-----	-----	DL-----	-----
CalbSrc1	477	---NTSNEKPKKKSTKIQTARKRPSNVSTPSTKGKSTK-----	-----	-----	-----	KISPLVT	-----
CjadSrc1	446	-----	SV	AVKEDPEQLEDEHEDED-----	-----	-----	-----
LkluSrc1	406	-----	-----	-----	-----	-----	-----
KlacSrc1	351	-----	-----	-----	-----	-----	-----
TdelSrc1	345	-----	-----	-----	-----	-----	-----
ZrouSrc1	322	-----	-----	-----	-----	-----	-----
TblaSrc1a	595	AKNSNLKKLSPFKK--RL--APDLANLNVSPEFANQLVTAIEENNDYLSNQ---	-----	-----	-----	IQPN-T	-----
TblaSrc1b	391	ANSKN---AIFLKK-TN-----	-----	-----	-----	FLYQLLKGFCK-----	I-----
NcasSrc1a	508	PNEVILES-SHIK-----	-----	-----	-----	NTVGKN---VSPTETFQSRGHVELKTN-R	-----
NcasSrc1b	361	-----	DN	VV-----	-----	AEEILPD-T	-----
CglaSrc1a	347	SNTINSDN-----	-----	-----	-----	VFIGKL---KSENSFLFDDHEE-----	-----
CglaSrc1b	165	-----	SS	SPSRN--KLESKPDI-----	-----	PVTRGAM-----	HDEIK---
Src1_prox	374	-----	TD	SSNLVSDDEVLVPT-R	-----	-----	-----
Heh2	253	-----	-----	-----	-----	-----	-----
consensus							

AfumSrc1	293	-----	DE	SELSAGEEFTPEEQLALE-----	-----	-----	-----
LstaSrc1	229	----PE-----	AE	SGSLESEEEYEVETPEVLE-----	-----	-----	-----
YlipSrc1	503	-----	EEL	RKQKEEELN-----	-----	-----	-----
OpolSrc1a	340	-TSSKPE-----	SP	DST--NDEEVLTLQLQHEID-----	-----	-----	-----
OpolSrc1b	256	-----	TE	VE--EAE--VKIQESEVR-----	-----	E-----	-----
CaurSrc1	388	EKDVPVPVPSDIP	IE	-----	-----	KETIS--EDDQLSKPENEQVTTLSSNVKEDEMINSKNLQTLDR	-----
CalbSrc1	519	KSALTPKPRLISLG-----	-----	-----	-----	SQKYESDDES--DEEDVS-----	-----
CjadSrc1	465	-----	E--AS	IDVLQSLQNEIE-----	-----	-----	S-----
LkluSrc1	406	IST--PE---	LP--TK--HD	ID--AMEERLKEEEKIR-----	-----	-----	-----
KlacSrc1	351	-----	EE--Q	SEN--LLEDENEVD-----	-----	-----	-----
TdelSrc1	345	NYT--PE---	LI--TE--Q	DVQ--ESDDRVKHMQEVID-----	-----	-----	-----
ZrouSrc1	322	IKL--QE---	I---EE--P	DVE--EDEE-EKEEEEEST-----	-----	-----	-----
TblaSrc1a	647	INAINPKTQTI	I	ISNGLSESS--EDDQLSKPENEQVTTLSSNVKEDEMINSKNLQTLDR	-----	-----	-----
TblaSrc1b	417	-----	IS	YHFTANIKT-YSESLINHMRKIIIT-----	-----	-----	L-----
NcasSrc1a	545	ASA--SE--QA--NI--PSSS--SDEELL---	-----	-----	-----	EIE-----	-----
NcasSrc1b	373	EET-----	KE	ISKSLPSIESEDTIKEDSNTFLS-----	-----	SS-----	-----
CglaSrc1a	374	-----	VA--EE--PE	VK--TIQ-----	-----	IEVE-----	-----
CglaSrc1b	192	-----	KE	SSAKGKKKLQEIENLVTSQ---	-----	TPKKL--SEQVQKISQ	-----
Src1	392	IET--PQ---	LP--TE--K	DVE--KEARVQELQEEN-----	-----	-----	-----
Heh2	253	-----	VQ--PE	VK--EAKHEELTKISETFD-----	-----	-----	-----
consensus			i	e	ee	l	eel

AfumSrc1 313 -----KQQA**E**-----LM-----YP-----TAP-
 LstaSrc1 251 -----RHAE**E**-----LV-----GYD-----NA--
 YlipSrc1 515 ---D-DDDEEE**E**VDVKSKGKETTSITK-----TKTKNKP-
 OpolSrc1a 365 VTQE**Q**I**E**EKSKQ-----
 OpolSrc1b 273 VV-EID**G**E**Q**Q**T**E-----AAEP-----ETIKETV
 CaurSrc1 416 -----D**I**E-----DE-----
 CalbSrc1 549 -----E**I**R-----KP-----
 CjadSrc1 481 VYESVV**N**ETNEA-----VKQVNDLFK-----DEDVD
 LkluSrc1 433 ---E-GDE**K**PER-----AVGPENKNKP-
 KlacSrc1 366 ---G-GDE**G**ERT--I---VKDPTS**I**IE-----AA---KNKTDE-
 TdelSrc1 372 ---D-IN**E**KA**Q**E-----TPRR-
 ZrouSrc1 347 ---H-A**E**E**K**P**V**E-----Q-----ITP-
 TblaSrc1a 705 IYEDY**I**DD**E**S**N**STQ**F**---TKEPTEA-----SKIDDFN
 TblaSrc1b 444 IY----F**I**SK**T**-----F**I**F**I**IE**C**I**Y**L----LFFLALY**G**-I---YKLGFI
 NcasSrc1a 568 ---E-F**E**E**Q**K**T**E-----TKRPKSNMSDKIPRVKN--NSNLKV**T**AL**P**NA**Q**KKHENKTEPT
 NcasSrc1b 403 --E**S**---Q**V**TR**E**TS**Y**---MRHL**T**RS**I**I**Q**SLSCVKLPKKKS**I**HFFHCK-----
 CglaSrc1a 390 ---S-V**D**DEAS**E**SDL---VKES-----TE--
 CglaSrc1b 228 KAEEVV**E**I**K**E**D**-----I**K**EEL-----C-----PTKDEF-
 Src1 419 ---E-Q**L**E**H**ENG-----SEFD
 Heh2 273 ---N-Q**D**EEDTS-----RLSSK-----KN-----IRSPKGRTRHF
 consensus de e

AfumSrc1 325 -----RI--RR**R**AA**Q**STANKA**A**P**W**IL**I**FSLL**C**FG**G**W**W**R
 LstaSrc1 263 -----ATFVFPFKIFT**A**W**I**IVL-LGL**S**YLM**W**W**R**
 YlipSrc1 545 -----VVFKA-KKPS---VLSKID**F**K**A**VF**N**LL**K**L**V**TIGAL**I**-SGL**V**IAG**G**W**Y**R
 OpolSrc1a 377 -----ALKSIGAPP-----PSNLVYRL**V**TAW**L**L**T**-LS**L**MYA**F**T**S**Y**R**
 OpolSrc1b 295 V-----VVD**S**KPVQKR**R**Y**K**Y**A**LL**L**L**P**IL**S**SL**F**F**Y**R
 CaurSrc1 421 ----ADGPKDV**M**PEK**K**SR**S**H**S**-----KKS**K**W**T**TS**L**Y-I**G**L**V**W**S**I-LAF**A**M**F**G**Y**W**Y**R
 CalbSrc1 554 ----VTATKDVDSAGT**S**T**K**PF**A**-----LPFS**I**RR**F**LL**S**-M**F**L**V**W**F**V-CS**G**GL**F**GL**W**Y**R**
 CjadSrc1 507 VEG-----AD**E**TTVEV**K**SK**L**---SL**S**IP**W**RC**I**F**N**FL**Q**K-LV**V**F**I**ML**C**V-LV**V**GG**L**W**Y**R
 LkluSrc1 451 -----K**T**A---HI**K**AF**V**H**C**VGR**F**L**F**K-V**S**T**F**V**L**IVL-P**I**L**F**GL**W**Y**R**
 KlacSrc1 392 -----I**P**TQ**E**T**N**ISS---I**I**RKGLISTGR**F**LL**K**-V**I**S**F**LL**L**IL-L**P**IL**F**AL**W**Y**R**
 TdelSrc1 384 -----T**Y**S---KV**S**SF**F**K**S**LATT**L**Q**A**-LS**I**FF**L**V**M**T-P**I**I**Y**GL**W**Y**R**
 ZrouSrc1 359 -----V**P**C---FWK**R**S**F**K**F**I**G**K**A**I**Y**N-LS**I**FS**F**IV**F**-P**I**L**Y**GL**W**Y**R**
 TblaSrc1a 734 VHNDK**L**T**E**-SD**I**K**N**K**Q**SD-----TR**K**L**I**L**F**L-K-L**V**AL**L**LL**L**PM**I**LC**F**C**I**Y**R**
 TblaSrc1b 476 LYLAVL-----SLMS**I**HNY**R**I**H**K**K**LRCFFIN-TAKV**S**S**I**-L**L**P**I**L**F**L**I**W**Y**R
 NcasSrc1a 616 IQDES**L**TK-K**E**TFH**V**K**F**GRSD---F**I**NG**L**F**R**K**C**Y**W**IL**K**K-L**L**T**L**T**V**L**T**F-L**F**FG**F**W**Y**R
 NcasSrc1b 442 ICGLL**T**IK**E**Q**V**KTINRLR**S**S**F**NAR**F**FK**L**T**N**F**L**I**P**L**L**N-V**I**W**F**LM**F**AV-P**V**V**F**AL**W**Y**R**
 CglaSrc1a 407 -----E**I**M**N**PP**P**K**K**S---F**V**CKAL**L**LL**K**L**L**L-IVAGAL**I**AI-I**N**LAV**W**Y**R**
 CglaSrc1b 252 -----V**K**HKE**E**EP**S**---K**L**FAVLDE**I**MI**Y**---L**F**K**F**L**V**IVL-P**I**L**F**FL**W**Y**R**
 Src1 431 VK**Q**-----G**S**G**K**VGN**R**H---K**F**K**R**AL**K**F**L**SK**S**LLAL**F**L**F**C**I**F**I**V**I**-P**L**L**F**GL**W**Y**R**
 Heh2 299 I**A**-----N**K**TKRGID---IM**K**PFIA**H**L**F**I**W**L**W**N-GAI**F**LS**I**IC-P**I**L**F**GL**W**Y**R**
 consensus r v l v wilill lifglwyr

AfumSrc1 358 KE**K**IE**I**G**Y**CGIGKPT**W**SLA**E**TRVP-----E**W**A-RVLE**P**Q**C**E**P**CP**H**A**F**CYPN
 LstaSrc1 290 NE**K**FK**V**G**Y**CE**V**EGLGR**Y**IP**E**LPD**H**-----S**F**R-KLLE**P**D**C**T**P**CP**H**AV**C**FAN
 YlipSrc1 589 KE**K**FA**V**G**Y**CGTGEHA**Q**ALSK**Y**DE-----F**I**E**F**W-KEVL**P**P**C**T**P**CP**E**NA**E**CYRG
 OpolSrc1a 412 **E****Q**R**I**RV**G**FC**G**SE**V**YSPL**F**E---YDR--IA**H**PM**I**SH**L**DK**I**ES**I**FTL**S**CV**P**CP**E**H**G**Q**C**F**Y**P
 OpolSrc1b 325 **S**MA**V**D**V**GC**R**GE**I**RS**V**RS**W**MP**T**EN**Q**FLA**Q**FASKAD**A**FL-E**Q**I**K**P**Q**C**I**CP**E**HA**I**C**R**YD
 CaurSrc1 468 **E****Q**T**F**L**I**G**Y**CG**H**E**I**DK**P**T**I**PKGS**D**TS----ALL**N**VFGD**Y**L**D**NN**F**K**P**T**C**V**P**CP**Q**HA**R**C**F**PH
 CalbSrc1 601 **E****Q**K**Y**AV**G**YCG**Q**E**I**D**Q**PT**F**IN**Y**--DN----E**Y**L**N**KL**G**Q**L**L**D**T**N**F**K**PE**C**I**N**CP**L**HAR**C**YAN
 CjadSrc1 555 **E****Q**R**I**L**I**G**Y**CG**S**E**I**D**V**PT**F**P---Y**T**E---N-I**H**L**Q**Q**L**D**D**FL-Q**D**Y**K**P**Q**CL**K**CP**E**HA**I**CL**P**K
 LkluSrc1 487 **E****Q**RV**L**V**G**YCG**H**E**I**N**L**PT**F**---Q**N**PD-N-L-Q**V**D**G**VE**S**FL-E**Q**Y**K**P**Q**CL**P**CP**E**NA**I**C**Y**P**Y**
 KlacSrc1 435 **E****Q**R**I**AV**G**FC**A**SE**V**D**I**PT**L**---GREY--SN-P**Y**INE**F**EN**Q**L-ER**F**K**P**H**C**I**P**CP**S**DA**I**C**Y**P**Y**
 TdelSrc1 420 **E****Q**RV**L**V**G**YCG**H**E**I**ESS**P**S---LD**F**E---S-P**V**LA**E**FGD**L**L-E**A**Q**K**PR**C**L**P**CP**D**HA**I**C**Y**P**Y**
 ZrouSrc1 395 **E**SR**I**SV**G**YCG**Q**ELPP**P**SL---PE**Q**-----L-G**T**-----LP**F**-SL**P**K**P**N**C**L**P**CP**D**NA**L**C**Y**PR
 TblaSrc1a 780 **D**Q**K**MY**V**G**Y**CD**N**Q**L**PI**K**SVSE**Y**L**P**DN**V**N**T**L-P**V**SK**I**D**N**WL-ED**H**K**P**EC**I**CP**C**P**N**NA**I**C**Y**PM
 TblaSrc1b 523 **E****Q**K**L**AT**G**YCG**Y**SLSP**P**SI**I**HS---K**S**N**V**FS**Q**M**I**FK**F**DA**W**L**K**Q**K**FS**P**SC**V**SP**K**NA**L**Y**T**FN
 NcasSrc1a 669 **E****Q**K**F**Q**V**G**Y**CG**T**ELRK**P**MH---LP**N**GL**K**F**Q**-Q**L**M**Q**L**D**ELL**Q**-EN**F**RP**Q**CV**P**CP**D**NA**I**C**Y**P**Y**
 NcasSrc1b 500 **E**EQ**I**A**I**G**Y**C**N**TRYEL**N**NTGT**T**SE----H**H**EL**W**N**I**L**G**TY**L**-EAT**K**PK**C**I**P**CP**E**HA**S**C**Y**AN
 CglaSrc1a 451 **E**Q**S**IM**V**G**Y**CG**Q**EREGR**S**E---Y**F**E**K**LN-L-P**Y**RDE**V**ES**F**L-EP**Y**K**P**EC**Q**EC**P**E**H**GL**C**YPN
 CglaSrc1b 291 **E****Q**K**I**RV**G**FC**G**HE**L**PVAK**F**AP**Y**AN---SN-K**V**WAS**V**DK**T**L-ER**F**L**P**K**K**CL**C**PE**H**AI**C**K**T**HY
 Src1 477 **E**Q**R**LL**I**G**Y**CG**H**EVPS**H**RV---SG**N**S---F-E**F**I**Q**KL**D**N**L**L-Q**D**Y**R**PK**C**I**P**CP**F**NG**A**I**C**TY**Y**
 Heh2 342 **E****Q**R**I**Q**V**G**Y**CG**H**E**K**PL**K**SL---A**I**SA---F-P**Q**TER**V**DS**V**L-Q**A**Y**R**P**N**C**L**EC**P**E**H**IG**C**SS**F**
 consensus eqki vGyCg ev sl i d wl fkp CvpCPehaicyyp

AfumSrc1 404 FEAS**C**EN**D**FILKPHPL**S**LG--**G**L**I**P**L**PPT**C**EP**D**SE**K**ARR**V**KAV**T**D**K**A**I**EE**L**R**D**RA**K**FE**C**
 LstaSrc1 336 FRA**E****C**EP**D**YV**V**ASI**W**SLG--**G**IM**F**FAP**K**CV**P**DE**K**LQ**R**ARI**L**ME**E**S**L**Q**L**LR**E**Y**A**D**V**Q**C**
 YlipSrc1 636 FE**L**EC**H**EG**F**VA**E**AH**P**LS**F**N--**G**F**L**P**L**PP**K**CV**Y**D**T**R----**I**VS**V**AQ**Q**V**L**D**Y**L**R**L**Q**NS**Y**AE**C**
 OpolSrc1a 467 S**R**LY**C**DR**D**Y**T**I**H**K**P**L**K**SL**F**--**G**L**I**PT**Y**Q**T**CV**L**DS**V**K**V**K**I**DK**M**V**K**VAT**D**L**N**R**R**NA**E**Y**K**C
 OpolSrc1b 384 SK**L**E**C**KSG**Y**T**V**SR**P**W**Q**SL**L**--**G**L**I**PR**M**EQ**C**V**Y**DEN**R**LE**K**I**K**LM**T**EF**T**LD**I**L**R**R**K**NG**K**E--
 CaurSrc1 523 **L**K**L**AC**Y**ED**F**VE**Y**K**P**W**Y**D**Y**W**P**A**F**D**P**KAK**K**C**I**P**D**TK**K**AE**K**VEL**M**IE**E**AL**D**L**L**RA**R**NA**N**I**Q**C
 CalbSrc1 654 **L**E**I**GC**F**ED**F**ME**Y**K**P**W**F**DF**I**----**V**PG**H**KK**C**I**P**D**T**KK**A**E**K**LE**I**MI**D**VA**L**D**L**RS**K**NA**I**Q**C**
 CjadSrc1 607 **L**T**I**K**C**KED**Y**I**V**N**Q**PW**Y**K**F**Y--**N**VF**P**FP**D**Y**C**V**K**D**H**E**K**EN**A**I**S**EV**V**AK**S**LD**L**LR**T**RNA**V**K**C**
 LkluSrc1 540 **M**R**I**K**C**K**P**D**Y**A**I**TP**S**KL**S**LY--**G**L**F**PV**S**D**Y**CV**K**DS**K**KE**K**LI**S**EV**V**K**S**LE**L**LR**T**K**N**SR**I**K**C**
 KlacSrc1 488 **L**E**I**K**C**K**P**GY**I**VE**S**PL**S**LH--**G**L**I**P**V**HAK**C**V**K**DS**R**K**Q**KL**V**Q**E**V**V**K**T**LE**L**LR**T**K**N**AQ**E**SC
 TdelSrc1 472 **M**K**M**KCG**P**E**Y**TL**Q**PN**R**W**S**LH--**G**L**I**PL**S**DA**C**V**K**DS**R**RE**K**LI**G**EV**V**K**S**LE**F**LR**T**K**N**AQ**H**SC
 ZrouSrc1 441 **M**Q**L**K**C**R**P**E**Y**AL**K**R**N**P**F**SL**Y**--**G**LL**P**LS**D**SC**V**K**D**S**E**RE**K**LI**G**EV**V**D**K**SL**Q**FL**V**K**N**AR**V**AC
 TblaSrc1a 838 **M**Q**M**K**C**K**P**D**H**I**I**R**K**NI**F**N**L**F--**G**SL**P**LP**D**SC**V**R**D**N**K**RE**K**IV**N**E**I**V**K**S**L**E**F**LA**K**NS**A**V**S**C
 TblaSrc1b 580 **M**NAN**C**QSG**F**E**F**TY**S**F**F**NY--**G**L**I**PM**R**R**H**CE**K**M**K**LD**T**K**L**N**K**IL**T**N**I**MA**I**L**T**K**N**TE**A**I**Y**
 NcasSrc1l 724 **L**K**L**K**C**K**P**K**Y**RL**V**K**P**LL**G**LN--**G**LL**P**LS**D**SC**V**R**D**D**Q**RE**Q**LV**S**E**A**V**R**K**S**LD**F**LR**S**K**N**AQ**I**SC
 NcasSrc1b 554 **M**Q**L**IC**D**NN**Y**ERT**T**NY**L**SL**F**--**K**L**I**PL**A**DS**C**HE**A**SA--**E**RV**L**E**I**AN**H**LT**D**V**L**R**K**Q**N**ARI**Q**C
 CglaSrc1a 505 **L**E**L**R**C**K**P**GY**R**L**Q**NS**L**Y**S**LN--**G**L**I**P**I**GA**S**CE**K**D**D**ER**M**IS**E**IV**A**KA**L**EL**R**IK**N**AQ**V**EC
 CglaSrc1b 345 **L**Q**M**S**C**KDG**Y**VL**R**K**S**W**N**LE--**S**LL**P**LAD**K**C**I**TK**R**KA**A**N**K**KT-**P**LL**F**AL**D**LL**R**TQ**N**ANT**H**C
 Src1 529 **L**K**L**K**C**K**P**D**Y**K**L**AP**S**RL**D**FL--**E**II**P**AQ**G**K**C**V**K**DD**K**K**Q**Q**L**V**S**EV**V**E**K**S**L**E**F**LA**K**NAQ**I**SC
 Heh2 394 **M**N**V**EC**P**GY**E**PK**S**ILE**T**Y--**G**I**I**PF**P**K**Y**CA**K**DES**K**E**K**EV**D**EL**V**W**K**V**N**E**Y**L**K**K**N**AQ**H**EC
 consensus 1 lkChpdy l wsl gliPl Cvksdrk rlv evv kslellr kna v c

AfumSrc1 462 **G**ER**L**ED**G**KE**V**T**S**PE**M**SE**A**D----**L**K**Q**AIA**Q**KRR**R**GM**S**D**T**EF**D**EL**W**K**G**AL**G**-**E**IV**A**K**D**EV**V**T**K**TK**Q**
 LstaSrc1 394 **G**R**G**---**G**K**Q**ND**P**T**V**AV**D**----**L**RA**K**L**F**SM**K**SP**S**LP**D**NA**F**Q**E**L**W**E**Q**AF**K**-**D**L**V**E**Q**EE**V**Y
 YlipSrc1 690 **G**SP--**E**SEA---**T**G**F**D**V**Q**V**K**T**E**F**T**Y**DE**L**Y**D**Y**G**R**K**N**V**-**H**AF**D**D**K**V**W**A**Q**AM**K**-**A**V**G**E**Q**ED**I**I
 OpolSrc1a 525 **G**R**G**--**E**D**H**E---**V**G**M**A**I**PH---**L**Q**N**Y**I**IE**T**F--**D**L**K**DD**D**FD**Y**L**W**E**K**T**F**A-**V**L**K**Q**R**PE**L**V
 OpolSrc1b 440 -----**M**T**L**EE----**L**H**N**FL**K**AT**K**SAD**M**VE**D**FE**E**Y**W**LR**F**VE**Q**IS**K**E**P**E**I**K
 CaurSrc1 583 **G**ST**S**VD**N**FE---**A**GI**E**S**R**E---**L**HD**L**LL**L**AK**A**PY**I**TE**E**FE**E**L**W**K**R**SV**V**-**E**LE**K**E**P**E**I**TV
 CalbSrc1 710 **Q**QNP**D**-EE---**S**GI**K**LN**D**---**L**HD**L**LL**S**M**K**AP**Y**IT**I**DE**F**E**E**L**W**DR**S**VI-**E**LE**K**E**P**D**I**VR
 CjadSrc1 665 **G**D**G**--**D**D**L**E---**V**GI**S**DD**E**---**L**Y**E**FF**Y**NS**K**K**P**S**I**S**D**E**E**FD**N**I**W**SK**V**LE-**D**LE**K**E**P**E**I**IV**R**
 LkluSrc1 598 **G**ES-D**N**DFE---**S**G**I**TE**E**E---**L**H**Q**IF**Y**ES**R**AP**W**IN**D**E**E**FD**L**W**V**Q**V**VE-**D**L**K**NE**P**E**I**IV
 KlacSrc1 546 **G**ED-ED**D**Y**K**---**S**G**I**S**N**AE---**L**Y**E**IF**Y**ES**K**K**P**W**IN**D**E**E**F**D**L**W**Q**Q**V**EV-**D**L**K**E**P**E**I**IV
 TdelSrc1 530 **G**E**G**-K**D**DL**K**---**S**G**M**TE**E**E---**L**Y**Q**IF**Y**ES**R**AP**W**IN**D**E**E**FD**E**L**W**AQ**A**VA-**D**L**I**Q**E**PE**I**TW
 ZrouSrc1 499 **G**E**C**-S**D**DI**K**---**C**G**I**LE**D**E---**L**Y**Q**IF**Y**ES**K**AP**W**IN**D**E**E**FD**E**L**W**IQ**A**VA-**D**L**K**E**P**E**I**TW
 TblaSrc1a 896 **G**E**G**-T**D**DL**K**---**S**G**V**SS**Q**D---**L**Y**N**IF**N**E**A**RP**W**ID**S**N**F**E**I**WS**Q**V**V**K-**H**L**K**D**Q**K**D**IL**W**
 TblaSrc1b 638 **F**LN-----**S**N**Y**VT**F**SK**D**D---**L**Y**E**FL**L**GR--**Y**F**N**D**G**K**E**V**D**I**Y**F**E**T**V**V**K**-**S**L**K**NN**P**D**I**V**W**
 NcasSrc1a 782 **G**D**G**-N**D**DI**K**---**S**GL**N**ENE---**L**F**Q**IF**N**E**A**RA**A**W**I**S**D**E**E**FN**E**I**W**D**Q**V**S**-**N**L**K**NE**P**E**I**IV
 NcasSrc1b 610 **G**K**G**-AN**D**L**K**---**S**GL**S**E**K**H---**I**FN**L**LS-**L**W**Y**T**W**V**H**E**E**N**F**DD**L**W**L**N**V**Q**S**-**E**L**K**K**K**P**D**IS**F**
 CglaSrc1a 563 **G**ES-S**D**DI**E**---**S**G**I**TE**E**I---**V**Y**Q**IF**E**ES**K**K**D**W**I**SE**E**Q**F**N**E**L**W**SS**V**IK-**Q**LE**K**E**P**E**I**TM
 CglaSrc1b 402 **G**ST**L**P**D**NY**Q**---**A**G**M**LE**K**D---**L**FN**N**V**Y**E**Y**RD**M**MT**K**ES**F**E**K**E**W**AV**L**SN-**S**L**K**RL**P**E**I**Y**Y**
 Src1 587 **G**D**G**-K**D**DI**E**---**S**G**M**TE**D**A---**L**Y**Q**IF**N**E**A**RP**W**IR**D**DE**F**ED**L**W**I**Q**V**IK-**D**L**T**E**P**E**I**IL**W**
 Heh2 452 **G**E**G**-EN**L**FE---**S**G**E**T**E**TK---**L**Y**D**IF**S**HS**R**PS**W**ES**Q**RE**F**N**D**HW**K**N**V**LE-**I**L**K**K**K**D**D**II**W**
 consensus ge dd sgmse d lyqif e r pwi deefdelw qvv el epeivw

C.

AfumSrc1_dist	522	-----PSDVLV-----	-----
LstaSrc1	446	RVDVGESERLG-----	-----
YlipSrc1_prox	743	IGSIRISESQRA-----	-----T
OpolSrc1a	573	IG-----	-----
CaurSrc1_prox	636	-KRSAHNLRAP--GD-D-----	-----AD---TVG
CalbSrc1_prox	763	--QKRQTNVAT--GE-F-----	-----TFDFDNTET
CjadSrc1_prox	717	--IIESSSPQS--TE-----	-----ENISSD-EAEET
LkluSrc1_dist	650	-RQLQPSTTEF--STDTD-----	-----NSTETNDIQKQKG
KlacSrc1_dist	598	-RQLPTRSGNNTISGDSNDIDTSNWD-----	-----VEIERPEG
TdelSrc1_ret	582	-RQVSNIFFE-----SNSISRALFTNDFNQYVQLSNGKFEVDPSPSDDAETDGLQRAEG	
TdelSrc1_dist	582	-RQL-----SNGKFEVDPSPSDDAETDGLQRAEG	
ZrouSrc1_ret	551	-RQVSTTDFLK--N--F-EVFTRIFDTNIVESWQSSEGEYRIHGDSQNQTETDDISRKER	
ZrouSrc1_dist	551	-RQ-----SSEGEYRIHGDSQNQTETDDISRKER	
TblaSrc1a_dist	948	-RQLSANEISQKS-----	-----YKNKHQANGFQKQKG
TblaSrc1b	686	-KEVEDLSGSKYDKH-----	-----NNV-----
NcasSrc1a_ret	834	-RQVSNTEFLI--AK--A-YDDQHFTNNIITCSLQSS-DSISRNAANVNFGSNDFFQKQKG	
NcasSrc1b	661	-SVVPVEN-----	-----
CglaSrc1a_dist	615	-RQLPANRHRQIKP-----	-----RYKSKTNDNQKQKE
CglaSrc1b	455	-KTFVSKNVAG-----	-----
Src1_dist	639	-RQLSPTDNNI--GGNS-----	-----NNI IKTNDVPRQKR
Heh2	504	-WLPLDFETNGK-----RE-----	-----
consensus		k	

AfumSrc1_dist	528	-----LSSTSI---ARLPLTC---AFRRHIRLSLLAY-----R	
LstaSrc1	457	-----STSP-----SEFPFTC---MIKTELGA FVSANRSKFVGT	
YlipSrc1_prox	756	RLVEGE---PEVYEDVVVAQETYKSISDAYFTLRCKCDKFVRGWLAQNQFYILGLVIA	
OpolSrc1a	575	-----ENFIRSNLS---KLSIKC---RLIRMFMDV FVRLKWHLLAL	
CaurSrc1_prox	654	E-----EEKQDTVFRSTSLS---HISLMC---HLSNHMVDLLVSYI PHFMVV	
CalbSrc1_prox	784	E-----IKDKYKILRSTSLS---NISLKC---QIRNSVMGSVTEHKYKLLGI	
CjadSrc1_prox	740	VI-----PQGPSKVLFRSNSSL---KLSISC---KFKKEVYERFEENKYYVTGV	
LkluSrc1_dist	678	HFQ-----Y-PEDKEAGLFRSTSCK---YIGLKC---KFEREVYQTYKRFRVVIWSG	
KlacSrc1_dist	631	H-----FQETEFQGGYFRSTSCK---YIGLKC---QFERQVHTTWKRYQRIILTV	
TdelSrc1_ret	635	HLS-----QANGYEKNRVFRSTSCK---YIGLRC---RFEREISNTYHRFSHF IWTV	
TdelSrc1_dist	610	HLS-----QANGYEKNRVFRSTSCK---YIGLRC---RFEREISNTYHRFSHF IWTV	
ZrouSrc1_ret	605	HFP-----KA--GNQTGIFRSTSCK---YIGLRC---KFENEIYRTCYRNRKLI IPL	
ZrouSrc1_dist	579	HFP-----KA--GNQTGIFRSTSCK---YIGLRC---KFENEIYRTCYRNRKLI IPL	
TblaSrc1a_dist	975	CIS-----QEPGSPENTVIRSISCK---YIGIKC---RFEREV FQYIKYRVLVIWTS	
TblaSrc1b	703	T-----ISAVEEVFYSTKTN---FPGFNY---LFKNKL---APFLMLILS	
NcasSrc1a_ret	887	HIP-----KGDQQKEGGYFRSTSCK---YISLRC---KFEGEIHQNYQRYRYLIWVV	
NcasSrc1b	668	-----STNSTLWLRSNSRR---YINLKC---FFQP--TENIMKQSR YIFVL	
CglaSrc1a_dist	643	SIPER-----RERENFILRSSCK---YISLGC---HFENELHQTIMKYRKIL I LIV	
CglaSrc1b	465	-----NIENIQLFRLSLKQ---NVS YFCGIFKLLKEF---PIEKNVLFVA	
Src1_dist	667	HLPEK-----FISKTRNFRSTSCK---YIGMKC---RFEREIYQTYKKFQRP I WLM	
Heh2	516	-----KSKSNNTNYIYRSTSCK---WVTLQC---HLEGDIQEYITKYGGS L FIT	
consensus		vfrs sk l l c k i v	

AfumSrc1_dist	555	LPLSILIIIMVLGLVYTRAKILAR-RSDLARVPELVATTLDRLATQAAL--H-ARGEAREP	
LstaSrc1	488	LLIALATLFLYRLSSSYSE-----RKAKVQDLVRQSM S I LSEQQTRSDS-DHSNTPR	
YlipSrc1_prox	812	ASAAIVG-----KEWYNQRKREQQH VSELVNQVNEMMTQAREHDADSTGLKQPR	
OpolSrc1a	611	VLFA SLIKYI---SVKFTQYRNRKIL---VNDLTTKTIEKLRKQAE LY---RLGQSPQP	
CaurSrc1_prox	695	LLVVMTFVI---RAKHREARLQ AHR---VETLYNEVLSKLRKQARNA---RDSENVPA	
CalbSrc1_prox	825	VLA FII IKI I---QYKYRQYQLYSVK---IDILYEEVLKKLKTQSNMT---KENPEVNP	
CjadSrc1_prox	783	LASLVIFTTL---YLWYSQYQQRQSK---IREVSAVIISKLRKQQRDA-INDTTGLTNR	
LkluSrc1_dist	723	SVILLMVQAI---KYKLQRYFEEQKK---VETLTEQV I KKLKRTANE-----TVGNKPK	
KlacSrc1_dist	675	VSLLVIVQLL---KRYISKKLQERER---IEKISQQV I KRLQQAII-----LQKQPR	
TdelSrc1_ret	681	ITISILIKLI---SYKIRNYKQREA---VDHISKKV I IRLKATKKQ---Q--QGAN	
TdelSrc1_dist	656	ITISILIKLI---SYKIRNYKQREA---VDHISKKV I IRLKATKKQ---Q--QGAN	
ZrouSrc1_ret	649	ILGALLGKFL---LSINRKLSQEKAK---VDKLTRKV VDR LKSTKRS-----EE-SETP	
ZrouSrc1_dist	623	ILGALLGKFL---LSINRKLSQEKAK---VDKLTRKV VDR LKSTKRS-----EE-SETP	
TblaSrc1a_dist	1021	SILV I I G K I L---HLKVKWTIQEQNR---INDIATDI I AS LKKKKMEQ-L---HPNTPP	
TblaSrc1b	740	PLLY I I I T I F L I T L V S Y - K T Y L T R K K --- V Q H I V Q R V I D L K S A K R --- S D N S L D	
NcasSrc1a_ret	933	VSILVLVKIL---ERKL RNY YETKV K --- I I N L T R K V I N E L K Q V K K --- N G R S P K	
NcasSrc1b	706	LLLI F I I Y G L --- W N Y V H G I F E R R H G D A A N I E Q L F V T T L R L L Q D A K K --- E K D M P	
CglaSrc1a_dist	688	LGFI I S I A V I --- R Y K I R T Y F E Q K K --- I A N Y T N E V I E L L K D K K A --- T D K G D A	
CglaSrc1b	504	L T I F S C T V T L --- E I I L Q K L W K C Q N R E N A F V E K S T E K A L E K L R E A S --- R D P E V K	
Src1_dist	712	F L L I V I S K V I --- E I K L K N Y Y R K K A R --- I E E L V T Q T M E K L K F Q K I K S - M --- S D P K E N A	
Heh2	559	L G V L F L I K K I --- Q S T L D N Y V Q G E Q I --- I E K L V K E A I D K L K D V K K --- N K G E E P	
consensus		1 i l v v l l l	

AfumSrc1_dist	611	YIPIGQLRDDVLRSEL-HGKRREELWRRVRNVV--EGNANIRAAVREGRGDVARVWEWI
LstaSrc1	540	YVIMSQLKDNLLFDTY-DAAERRRVWGSVQKLV--EANTNVRSRQME-VHGEIMRIWEWI
YlipSrc1_prox	862	FLPVPQLRDELVDTA-TSKRKASLWKKVADTV--EQNANVESQTKE-VRGEVTRVWEWV
OpolSrc1a	661	YIGKIQLRDYYLIDASLSPKQKAKVWNEVSRHV--ETNSNVKTYMME-VRGEMFKVWEWI
CaurSrc1_prox	745	YIGSIHLRDLILSNEK-NSARKMRTWEAVSRKV--SRNTNVKAYQLE-YRGDIMKVWEWI
CalbSrc1_prox	875	YIGASQLRDLILSNED-NLHQIRITMWKDVSVKV--EHNNSNISSQIVE-NNGEIMKVWEYI
CjadSrc1_prox	835	YLSTIQLRDELLAQVR--SKEKFNIWASILSQV--EKNSNVRSSSKE-IHGDIVRVLEWI
LkluSrc1_dist	771	FLSTVQLRDVLLSDIV-DLKFKNHLWNKVAKKL-EHNNTNVKSSLME-VHGEIMKCWEWI
KlacSrc1_dist	721	YMSSVQLRDLILNDMN-DLNEKNRLWALTTKKL-D-GNTNVKSTLME-IHGEIMKCWEWI
TdelSrc1_ret	727	FLSTVQLRDVLLADIT-DLKRKNSMWQRVVRKL-ENNNTNVKSSLME-IHGEIMKCWEWV
TdelSrc1_dist	702	FLSTVQLRDVLLADIT-DLKRKNSMWQRVVRKL-ENNNTNVKSSLME-IHGEIMKCWEWV
ZrouSrc1_ret	696	FLSTVQLRDVLLSDVV-DLKYKNRLWQKCSKKL-EHNNTNIKSSLME-IHGEIMKCWEWI
ZrouSrc1_dist	670	FLSTVQLRDVLLSDVV-DLKYKNRLWQKCSKKL-EHNNTNIKSSLME-IHGEIMKCWEWI
TblaSrc1a_dist	1070	YLSSVQLRDVYLLSDVN-NIQKKNIWKRISDKV-EYCNTNINSSLNE-VHGEIMKCWEWV
TblaSrc1b	788	YRNTTQIKELIFEEEK-DMKTLRNLWKLIRLEL--SNYLEVTNYIKE-QDGEIIECWEWD
NcasSrc1a_ret	979	YLSSIQLRDIFLIEVV-NLKEKNQLWKQIERKL-ENNNSNIKSSLLE-VHGDIMKCWEWI
NcasSrc1b	755	FVNTLQIKDQIFKDIK-DMRTLRLNLWKKVSAKL-EEDKKQIKVYHLE-VDGEIMECWEWI
CglaSrc1a_dist	734	FISSVHLRDYILDGKG-STKTKNKLWEEILKKL--NQNTNIKSSLME-VHGDMMKCLEWV
CglaSrc1b	553	FLDTVQLREFFLSETT-NLKKKNQLWDKISSKL--LENENVEKRQME-LYGEVLGIWEWN
Src1_dist	762	YLSIVQLRDIFLSDIV-DLKYKNQLWSEVVKYL-EHNNSNIKSNLTE-IRGEIMKCWEWI
Heh2	605	FLTTVQLRATLLSDIP-NIKEQNNLWQTKKEIMKEQSENIELYLLE-ENGEIMTCWEWK
consensus		yi qlrd l r lw v n ni e gdmv wewi
AfumSrc1_dist	668	GGIGGVHGNALLESSAIRRESNRQLSYSSPSSEGNRPPGDQQQLTPRSPGELRRWDEGRPVY*
LstaSrc1	596	GI*-----
YlipSrc1_prox	918	GNLN*-----
OpolSrc1a	718	ATI*-----
CaurSrc1_prox	801	SHLD*-----
CalbSrc1_prox	931	GI*-----
CjadSrc1_prox	890	GE*-----
LkluSrc1_dist	828	GPLEDETTN*-----
KlacSrc1_dist	777	GVLPEFENESDEGSTKNKNENDQKSQE*-----
TdelSrc1_ret	784	GPVESEPNNEEEREHGRQ-QE-----*
TdelSrc1_dist	759	GPVESEPNNEEEREHGRQ-QE-----*
ZrouSrc1_ret	753	GPLEDVRDDKDT--GNQ-TH-----*
ZrouSrc1_dist	727	GPLEDVRDDKDT--GNQ-TH-----*
TblaSrc1a_dist	1127	GPSNDNSIPNNDNESNDGNNNT-----*
TblaSrc1b	844	SNERY*-----
NcasSrc1a_ret	1036	GPLDDNISDKH*-----
NcasSrc1b	812	DPISDNDFNTI*-----
CglaSrc1a_dist	790	GPTDVKRRIKPD--GINENQ*-----
CglaSrc1b	609	D*-----
Src1_dist	819	GPMELNEPKDSAENKI*-----
Heh2	663	E*-----
consensus		

D.

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AfumSrc1_prox 522 DH-----NAITDP---M-----SLFSHLPQSHGSPSHAP
YlipSrc1_dist 743 VRSDQFV-----SVNP-----KEQRDWLKENRKSTTRTSWLHRRTSQSPTPTSL
Opo1Src1b     482 VDFTTSSISIENKIPTQFLTRTPG-----ARRTKKSKFFQRYPPPTSTFGGFSA
CaurSrc1_dist 636 RLSDLLI-TFV-PQVTMLTLL-----ARKKSSRTRFFDQRPYHTSH*-----
CalbSrc1_dist 763 RDKQML--QPANLHLTTLK-----RKSKTNTKFFDQRHYLTLV*-----
CjadSrc1_dist 717 -YELSN--LAVPSLPKRTFPP---MKLK-RRQLFHKGPQRSFSDRILH*-----
LkluSrc1_prox 650 SYSPVQ -LSFQQTPTQLKP---MTFNRRDIFNIQKT-KKRDFFARHPRSTSGSSVNSK
KlacSrc1_prox 598 SYQQDQETILFQETPTLIHPTGTLKLKDRDIFKQN--SSRGIFDLRLRSTSV*-----
TdelSrc1_prox 582 SYQTVN--LKSLIAPVTLRP---MVFKGRKDIFHQTDTKRTGFFARHPRSTASGVDLK
ZrouSrc1_prox 551 SHQKVS--IEFTETPRTKLRP---MIFGRKDIFQKQ--TRLGFFARHPRSTLA*-----
TblaSrc1a_prox 948 SYPPMR---YPKNHTRTSIKP---MGFKNKDVFHKNQGHQKTRLFAQYPRNISALNVDLK
NcasSrc1a_spli 834 SPLTV---SLGMPPTSILDP---MTFNRRDIFQKVTNRKNKGIFARHPRSTSVSDVNLK
CglaSrc1a_prox 615 SYQPID--IENRLSQDIKVKP---MTIKDRKNLFQKGEN-VKTSFFGHHPRSI*-----
Src1_prox     639 SYHPLT--TTLAEIPTSLKP---MTFRDRDIFQKNSS-PRRGIFGRRPRNTLE*-----
consensus      sy l i p ttlrp m k rrdlf kn ks ffahrprsts

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AfumSrc1_prox 549 SAATSDSLSLHIDSLFQF*-----
YlipSrc1_dist 786 SDASATSLFEDGWLKISSIFSGF*
Opo1Src1b     531 YGN*-----
CaurSrc1_dist -----
CalbSrc1_dist -----
CjadSrc1_dist -----
LkluSrc1_prox 704 ERSIRPINDSEL*-----
KlacSrc1_prox EK*-----
TdelSrc1_prox -----
ZrouSrc1_prox -----
TblaSrc1a_prox1003 EKYFKNTSNIDL*-----
NcasSrc1a_spli 888 EKSIKIINGIDI*-----
CglaSrc1a_prox -----
Src1_prox     -----

```

Supplemental figure 8. Alignment of nuclear and cytoplasmic Fes1 sequences. The C-terminal NLS signal is highlighted in yellow.

AfumFes1	1	MDPNMNNLLKWSIENSTSA	QAGNSNGTGP	APASRSNLNPEMLSALFGG	-----PSDADLMKAAMEALHS
LstaFes1	1	----MEKLLKWSIENSQEADT	-----DPDSQRQKAPN	PEVLAQLFGQ	-----PEDAQLMRAAMHTILD
YlipFes1	1	----MDKLLAWSVKQQEGT	-----NEPP	PDPKLLAQLFGA	-----PDDAQLMVQAMVITQ
OpolFes1Nuc	1	----MEKLLQWSIANQSDDE	-----LRAKTPAPDP	PELLAQLFGQ	-----AVDEPTQMKQNMVITS
OpolFes1cyt	1	----MEKLLQWSIANQSDDE	-----LRAKTPAPDP	PELLAQLFGQ	-----AVDEPTQMKQNMVITS
CaurFes1	1	----MEKLLQWSIASQSGDKE	-----TMDKIGKPDPEML	SKLFGN	----GPDEPTLMKQSI
CalbFes1	1	----MEKLLHWTIAQQSGDKA	-----ALEKIGEPDQKALN	QLFGG	-----PDEATLMKESI
CjadFes1Nuc	1	----MDKILLNWSLAQQ--DPE	-----TAGKVPAPDSKLLAKL	FGA	-----ADDPQLMKEAIAV
CjadFes1Cyt	1	----MDKILLNWSLAQQ--DPE	-----TAGKVPAPDSKLLAKL	FGA	-----ADDPQLMKEAIAV
LkluFes1nuc	1	----MEKLLHWSIANANGDKE	-----AIEKAGQDPDKLLQQL	FGS	----GPDEPALMKQAIL
LkluFes1Cyt	1	----MEKLLHWSIANANGDKE	-----AIEKAGQDPDKLLQQL	FGS	----GPDEPALMKQAIL
KlacFes1Nuc	1	----MEKLLHWSIANAQGDDE	-----AKARAGQDPDKLLEQL	FGG	----GPDEPTLMKHAMAVISN
KlacFes1Cyt	1	----MEKLLHWSIANAQGDDE	-----AKARAGQDPDKLLEQL	FGG	----GPDEPTLMKHAMAVISN
ZrouFes1Nuc	1	----MEKLLHWSIANSQGDQQ	-----TKERVGGQDPDKLLEQL	FGT	----GPDEPTLMKQSM
ZrouFes1Cyt	1	----MEKLLHWSIANSQGDQQ	-----TKERVGGQDPDKLLEQL	FGT	----GPDEPTLMKQSM
TdelFes1Nuc	1	----MEKLLHWSIVNAQEDKE	-----AIAKVGGQDPDKLLQQL	FGG	----GPDDPTLMREAMAVVRN
TdelFes1Cyt	1	----MEKLLHWSIVNAQEDKE	-----AIAKVGGQDPDKLLQQL	FGG	----GPDDPTLMREAMAVVRN
TBlaFes1	1	----MEKLLHWSIVNAQGDKE	-----EIAKAGAPDPRLLLEQL	FGKGN	--QVDDPTLMKEALLVAKN
NcasFes1Nuc	1	----MEKLLHWSIANAQGDKE	-----AIAKAGQDPDRLQLL	FGGAGSS	GPDDPTLMKEQMEVIMN
NCasFes1Cyt	1	----MEKLLHWSIANAQGDKE	-----AIAKAGQDPDRLQLL	FGGAGSS	GPDDPTLMKEQMEVIMN
CglaFes1Nuc	1	----MEKLLHWSIANAQGDKE	-----AIEKAGAPDKLLEQL	FGG	----GPDDPTLMKEAMAVIMN
CglaFes1Cyt	1	----MEKLLHWSIANAQGDKE	-----AIEKAGAPDKLLEQL	FGG	----GPDDPTLMKEAMAVIMN
ScerFes1Nuc	1	----MEKLLQWSIANSQGDKE	-----AMARAGQDPDKLLQQL	FGG	----GPDDPTLMKESMAVIMN
ScerFes1Cyt	1	----MEKLLQWSIANSQGDKE	-----AMARAGQDPDKLLQQL	FGG	----GPDDPTLMKESMAVIMN
consensus	1	MekllhWsian qgdke	amak gqpdpklL	qLFGg	gpddptlMkeamavi n

AfumFes1	66	DEV	DLENKMI	AFDNFEQLIES	IDNANNLE	PLGLWTPL	VELLKHE--	EAEM	RMAAWC	IGTAVQNN	NEKAQD			
LstaFes1	55	PNID	ETKET	AFDNLEML	VENLDNANN	LES	LDLWAPL	IEQLANP--	SPVL	LRKMACW	VIGTAVQNN	PKSQA		
YlipFes1	49	PDN	KLEDKE	VAFDNFEM	LVENLDNAN	MMKN	LKLWEPL	LLAQLLSSP--	HPSL	QKLA	AWVVA	TATQNN	PKSQE	
OpolFes1Nuc	54	PEID	LENKL	VAFDNFEM	LLENLDNANN	IENLKL	WDPLL	QLLSSP--	EPKL	QALACS	IGTATQNN	PKSQH		
OpolFes1cyt	54	PEID	LENKL	VAFDNFEM	LLENLDNANN	IENLKL	WDPLL	QLLSSP--	EPKL	QALACS	IGTATQNN	PKSQH		
CaurFes1	54	PEAT	DEAKET	ALNFEM	LVENLDNANN	IENLKL	WPSVIAQL	LSSS--	NLNL	SVLAAS	IIGVATQNN	PNSQK		
CalbFes1	53	TDV	SLEDKE	IALNFEM	LLENLDNANN	IGNLKL	WNPLIDIL	LAKEDTP	VELK	VLICGI	IGTAVQNN	PKSQE		
CjadFes1Nuc	51	EEAE	LETKL	TALNFEM	LLENLDNANN	IENLKL	WDAIIDLL	SLEK--	ELEL	QQLACS	IVGTAVQNN	DKSQA		
CjadFes1Cyt	51	EEAE	LETKL	TALNFEM	LLENLDNANN	IENLKL	WDAIIDLL	SLEK--	ELEL	QQLACS	IVGTAVQNN	DKSQA		
LkluFes1nuc	54	PEAE	LENKL	IAFDNFEM	LLENLDNANN	IENLKL	WEPLISV	LKSN--	EEEL	RAFALS	VIGTAVQNN	TKSQE		
LkluFes1Cyt	54	PEAE	LENKL	IAFDNFEM	LLENLDNANN	IENLKL	WEPLISV	LKSN--	EEEL	RAFALS	VIGTAVQNN	TKSQE		
KlacFes1Nuc	54	PEAT	LENKL	VAFDNFEM	LLENLDNANN	IENLKL	WEPLITV	LDDP--	EPEL	RAFALS	VTGTAVQNN	DQSQN		
KlacFes1Cyt	54	PEAT	LENKL	VAFDNFEM	LLENLDNANN	IENLKL	WEPLITV	LDDP--	EPEL	RAFALS	VTGTAVQNN	DQSQN		
ZrouFes1Nuc	54	PEAD	LENKL	TAFDNFEM	LMDNANN	IENLKL	WNPLL	QLLESP--	ETDL	RTYALS	CVGTASQNN	VKTQD		
ZrouFes1Cyt	54	PEAD	LENKL	TAFDNFEM	LMDNANN	IENLKL	WNPLL	QLLESP--	ETDL	RTYALS	CVGTASQNN	VKTQD		
TdelFes1Nuc	55	QEAE	LENRL	VAMDNFEM	LLENLDNANN	IENLKL	WTPLLET	LSDS--	EEDL	RAAALS	VIGTAAQNN	NEPTQN		
TdelFes1Cyt	55	QEAE	LENRL	VAMDNFEM	LLENLDNANN	IENLKL	WTPLLET	LSDS--	EEDL	RAAALS	VIGTAAQNN	NEPTQN		
TBlaFes1	56	KVATA	ENRI	IALNFEM	LLENLDNANN	IENLKL	WEPLINLL	VVEE--	NLEI	VALVCS	IIGTAVQNN	VDSQT		
NcasFes1Nuc	58	PDVEL	DIKL	VAIDNFEM	LLENLDNANN	IENLKL	WDPI	LKILEFE--	EDEL	VSQALS	IIGTSVQNN	TNSQD		
NCasFes1Cyt	58	PDVEL	DIKL	VAIDNFEM	LLENLDNANN	IENLKL	WDPI	LKILEFE--	EDEL	VSQALS	IIGTSVQNN	TNSQD		
CglaFes1Nuc	55	PEAD	LENKL	IAYDNFEM	LLENLDNANN	IENLKL	WEPLILK	TLEDN--	EADL	RASGLS	VIGTAVQNN	TD		
CglaFes1Cyt	55	PEAD	LENKL	IAYDNFEM	LLENLDNANN	IENLKL	WEPLILK	TLEDN--	EADL	RASGLS	VIGTAVQNN	TD		
ScerFes1Nuc	55	PEVD	LET	TKLVAF	DNFEM	LLENLDNANN	IENLKL	WEPLLDV	L	VQTK--	DEEL	RAAALS	IIGTAVQNN	LD
ScerFes1Cyt	55	PEVD	LET	TKLVAF	DNFEM	LLENLDNANN	IENLKL	WEPLLDV	L	VQTK--	DEEL	RAAALS	IIGTAVQNN	LD
consensus	71	peadlenkli	AfdNFemLi	EnLDNANN	ienlkl	Wepll	lL		e	elra	alsvigtavQNN	ksQ		

AfumFes1	134	KLIVFN----	VLPTLVAMSTSD-PAPAA	ARKKAVYAISSGVRNYQPAMDEFVKHLPEGYTS-----
LstaFes1	123	ALLMYPK---	AVPNLLRIASD-PSKE	ARLKAMYSLSAIRNHASGYDSFKNAEGWQVLMSTIRQESQDK
YlipFes1	117	ALVE--QGDAGIKKLV	DLTSHD--DPEVVVKS	LFALASAIRNCDDAYKLFESADGLKKVVGHLKP-D---
OpolFes1Nuc	122	NFLQYAEGENGMAKLV	ELASDK--SPE	TNLKAIYALANIVRHNKEGVESFEKHNGWDIAPILNSDK---
OpolFes1cyt	122	NFLQYAEGENGMAKLV	ELASDK--SPE	TNLKAIYALANIVRHNKEGVESFEKHNGWDIAPILNSDK---
CaurFes1	122	AFLEKEN---	GLEILINLVKADSTPRE	LALKALFALSFCVRNYPEATERFTNLGGWEALH--LQGS---
CalbFes1	123	DFNETE---	GLSELIELAQDD-KKF	ELQSKALFAISSFIRNFQPGYAKFEKLQGLKLIN---FDN---
CjadFes1Nuc	120	DFTKYPQ---	GVPSLIA	LAHKK---ESRLKSLYALSSLIRNNTKAYESFDEHKGWELIGPILSDDE---
CjadFes1Cyt	120	DFTKYPQ---	GVPSLIA	LAHKK---ESRLKSLYALSSLIRNNTKAYESFDEHKGWELIGPILSDDE---
LkluFes1nuc	122	NFLKYED---	GLPGVIEI	AGNAKEVPAVRTKAFYALSNLIRHNSDVYEFVSLGGLEIISPVLGDET---
LkluFes1Cyt	122	NFLKYED---	GLPGVIEI	AGNAKEVPAVRTKAFYALSNLIRHNSDVYEFVSLGGLEIISPVLGDET---
KlacFes1Nuc	122	NFAKYDG---	ALAKVIKLASGRAEDA	QVRTKAFYTLNLIIRHNKLIYDQFNQNLGLQIAPVLKIDAN---
KlacFes1Cyt	122	NFAKYDG---	ALAKVIKLASGRAEDA	QVRTKAFYTLNLIIRHNKLIYDQFNQNLGLQIAPVLKIDAN---
ZrouFes1Nuc	122	DFLKYDG---	GLRKVIELASDINEP	NEVRTKALYALSNLIRNHSKSSFAFCELRGLEVIPPIVHDTK---
ZrouFes1Cyt	122	DFLKYDG---	GLRKVIELASDINEP	NEVRTKALYALSNLIRNHSKSSFAFCELRGLEVIPPIVHDTK---
TdelFes1Nuc	123	AFSKQEE---	GLMKIIQLANDTKEPLN	VRLKAFYALSNLIKNTVLTATEFLKSHGLDIAPVLSDPSPS---
TdelFes1Cyt	123	AFSKQEE---	GLMKIIQLANDTKEPLN	VRLKAFYALSNLIKNTVLTATEFLKSHGLDIAPVLSDPSPS---
TBlaFes1	124	NFTKYEN---	GKTLIELANTT-SNID	VKIKALYALSNLIRNNEKASAKFEKLNGLDVISPILKDKT---
NcasFes1Nuc	126	KFLKHEN---	GLNKVIQLANDKSQS	FEVRTKALYALSNLVRNHEHMAKFRLENGLDIPPIILNDPK---
NCasFes1Cyt	126	KFLKHEN---	GLNKVIQLANDKSQS	FEVRTKALYALSNLVRNHEHMAKFRLENGLDIPPIILNDPK---
CglaFes1Nuc	123	NFLKYEG---	GLKILIAIAKSSEEPS	DVRKAFYALSNLIRNHIEAGKKFQALGGLDVFPVALNDPK---
CglaFes1Cyt	123	NFLKYEG---	GLKILIAIAKSSEEPS	DVRKAFYALSNLIRNHIEAGKKFQALGGLDVFPVALNDPK---
ScerFes1Nuc	124	NFMKYDN---	GLRSLIEIASDKTKPL	DVRTKAFYALSNLIRNHKDISSEKFFKLNGLDCIAPVLSDNNT---
ScerFes1Cyt	124	NFMKYDN---	GLRSLIEIASDKTKPL	DVRTKAFYALSNLIRNHKDISSEKFFKLNGLDCIAPVLSDNNT---
consensus	141	flkye	gl li la	evrlKavyalsnlirn a d F l gldvi pil d

AfumFes1	189	-----	GEKIDAADMEAI	DALLDK-----LRAHP---SEVSA-----
LstaFes1	189	FDEQTKNVPDSQRHWY	ESDEDIRRSIFLLAGIL	STPEF-DDKIEILRSLSAVPSLLELLHVEDSYSAIE
YlipFes1	179	-----	ATAQVKS	KTGLVLTGILESE---TDLMKPEEKRVQFDILVKELETDDHIPSLE
OpolFes1Nuc	187	-----	SSEKLKLRLALSLLNA	ALSTS-ID SARLEKLQDDQVVKSLLGLIKVDGHI
OpolFes1cyt	187	-----	SSEKLKLRLALSLLNA	ALSTS-ID SARLEKLQDDQVVKSLLGLIKVDGHI
CaurFes1	184	-----	EDHKL	LLRKLSTLSALLSTG-LDEKKLDHFKNRFDNLISTFD-SQNVGCID
CalbFes1	181	-----	KNNKYQLRILSLISSI	LSNG-LDSSLKAQFKEAKLPHYLASVNLNEDSNTSLVD
CjadFes1Nuc	180	-----	TDNKT	KLRSLSLLSSILSSG-KQEDVWDHIRQYDIVIKLASLISKENDISLVD
CjadFes1Cyt	180	-----	TDNKT	KLRSLSLLSSILSSG-KQEDVWDHIRQYDIVIKLASLISKENDISLVD
LkluFes1nuc	186	-----	SNDKL	KMRVLALLAAVLTAVEFNASFVEVLRKDGIESTLDFLVPDGGLYIID
LkluFes1Cyt	186	-----	SNDKL	KMRVLALLAAVLTAVEFNASFVEVLRKDGIESTLDFLVPDGGLYIID
KlacFes1Nuc	186	-----	ASEKL	KLRLAMALLSTVLTADMNADFFALLRAYNIIETTLEFLHPECNLYIID
KlacFes1Cyt	186	-----	ASEKL	KLRLAMALLSTVLTADMNADFFALLRAYNIIETTLEFLHPECNLYIID
ZrouFes1Nuc	186	-----	ANNKL	KMRALSLSAFLTSSTINEGLMDLLRKEGIVESTIDCLNMPFDVYIAD
ZrouFes1Cyt	186	-----	ANNKL	KMRALSLSAFLTSSTINEGLMDLLRKEGIVESTIDCLNMPFDVYIAD
TdelFes1Nuc	187	-----	SKPKL	KTRAVSLLNAFLSSVEVTEGLISTLREDGVVEAAICCLRS
TdelFes1Cyt	187	-----	SKPKL	KTRAVSLLNAFLSSVEVTEGLISTLREDGVVEAAICCLRS
TBlaFes1	187	-----	VKPKIK	LRTINLLSAYMSTININEEFVTALRKDNIIISTIERLQEDTDLNLIID
NcasFes1Nuc	190	-----	AKTKL	KMRALALLTAFLTSTEISESLISDMRKDGTIEATIDCLNSETDLNLIID
NCasFes1Cyt	190	-----	AKTKL	KMRALALLTAFLTSTEISESLISDMRKDGTIEATIDCLNSETDLNLIID
CglaFes1Nuc	187	-----	ATPKL	KMRALSALS
CglaFes1Cyt	187	-----	ATPKL	KMRALSALS
ScerFes1Nuc	188	-----	AKPKL	KMRALALLTAYLSSVKIDENIISVLRKDGVIESTIECLSDSNLNIID
ScerFes1Cyt	188	-----	AKPKL	KMRALALLTAYLSSVKIDENIISVLRKDGVIESTIECLSDSNLNIID
consensus	211		klklramsllta lss	i e lie lrkdgvves ie l e i lid


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AfumFes1      -----
LstaFes1      258 KIVQILLVIAKSQAGFTREEKEGIRRGLSRAKKDG--LLDLDETQNEELTAEWRLLQEELNSDKRE
YlipFes1      229 RSLHVLVLLNQKGFPFTEPEEQVKKAAKRVGE---KLDEEDVKYNEDLKYYVNNL-----
OpolFes1Nuc   239 SATSIVTTLMSHKYSFDDEKKLVQAVEQLE-KMKDQISHEDLQILKTYSKVDYLRSIKKSG--
OpolFes1cyt   239 SATSIVTTLMSHKYSFDDEKKLVQAVEQLE-KMKDQISHEDLQILKSVS-----
CaurFes1      235 KALNIISQLQSLQYKFTSDEIKRLVSQLESVS-HLKDKFNEEDYHTATIIASQ-----
CalbFes1      233 KSLNIVSQLNQLNYESLEEKYEINRGIQVVE-GLSEKLNIDDLNNAKQATSS-----
CjadFes1Nuc   232 KAINIIVELIRAGFKFTSDRKVITEKVGFIETELMDVNLDDVQILRSFYKLELIRKSHSK--
CjadFes1Cyt   232 KAINIIVELIRAGFKFTSDRKVITEKVGFIETELMDVNLDDVQILRQVTL-----
LkluFes1nuc   239 RVLNFLSQLISFGFKFNKQEMSKLRQGYENIE-SLKDRLNEDDYQTVSTFHKMQFIKRIRSR---
LkluFes1Cyt   239 RVLNFLSQLISFGFKFNKQEMSKLRQGYENIE-SLKDRLNEDDYQTVRQVL*-----
KlacFes1Nuc   239 RVLNFFSQLINVGFEFSATELEKLVGVKNIE-PVEAQLNEDDYKTVHTFNHGLGHKRAKY----
KlacFes1Cyt   239 RVLNFFSQLINVGFEFSATELEKLVGVKNIE-PVEAQLNEDDYKTVQYVSK*-----
ZrouFes1Nuc   239 RVLNILAQMVTANVQFTDGEKQKLQAGMQSIE-PEQDRLNEDDLQTVNTYYSVTFFKKRHKQQQ---
ZrouFes1Cyt   239 RVLNILAQMVTANVQFTDGEKQKLQAGMQSIE-PEQDRLNEDDLQTVKYVL*-----
TdelFes1Nuc   240 RVLNFLSRLITAGIKFTEEEVSELSLGMKNIE-GLKEKLNEDDFSTVNTFYKMQYIKRIRK----
TdelFes1Cyt   240 RVLNFLSRLITAGIKFTEEEVSELSLGMKNIE-GLKEKLNEDDFSTVKYVL*-----
TBlaFes1      240 RILNFLSQLYASKIKLDAEKATLEKGFNSIQ-HLQDSLNEEDFASTKSFL*-----
NcasFes1Nuc   243 RVLNLLAQLISAGIKFNQVEMEKLKTGFQKVE-PLKDRLNEDDYLTVKTFCKMQFIKMRMSK---
NCasFes1Cyt   243 RVLNLLAQLISAGIKFNQVEMEKLKTGFQKVE-PLKDRLNEDDYLTVKYVL*-----
CglaFes1Nuc   239 RVLSVLSHLISSGIKFNDSELEMLQKEFEKID-SLKDRLNEDDYLAVKTYTTLFIKKSRRH----
CglaFes1Cyt   239 RVLSVLSHLISSGIKFNDSELEMLQKEFEKID-SLKDRLNEDDYLAVKYVFSKK*-----
ScerFes1Nuc   241 RVLSFSLSHLISSGIKFNEQELHKLNEGYKHIE-PLKDRLNEDDYLAVENTFCKMEFIKKVRRGK---
ScerFes1Cyt   241 RVLSFSLSHLISSGIKFNEQELHKLNEGYKHIE-PLKDRLNEDDYLAVKYVL*-----
consensus     281 rvlnils lis g kftd ei 1 gl ie lkdklneddy tvk

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Supplemental Figure 9. Alignment of GCR1 orthologs from Saccharomycetacea. Many of these genes have an alternate transcription and translation initiation sites within the intron. Yellow highlighting indicates the sequence that is encoded within the intron.

KlacGcr1	1	-----MDKDNLNINL-----
LkluGcr1	1	-----
ZrouGcr1unsp	1	--MNLD-----PFD-----
ZrouGcr1spli	1	-----
TdelGcr1unsp	1	--MINLS-----LPN-----
TdelGcr1spli	1	-----
TblaGcr1aunsp	1	-----MLRSGPNNSNK---
TblaGcr1aspli	1	-----
TblaGcr1b	1	-----MDLYQTATNNT-----
NcasGcr1unsp	1	MNFFNQ-----FPQTDPTILN
NcasGcr1spli	1	-----
CglaGcr1unsp	1	MNFLGLSPITKGDTTNVSKTNKADEESVSNLNRGMSAPSLSTSIFAMPRTIPTTNNDKQK
CglaGcr1spli	1	-----
Gcr1unspliced	1	MNFLT-----QAMSETFQGTNNRIK-
Gcr1spli	1	-----
consensus	1	-----

KlacGcr1	11	QDWL---ND-----PMLAAQLNRAQSSTPTIF
LkluGcr1	1	-----MNR-----
ZrouGcr1unsp	8	RN-RISSSNRNASSPSSSSSQAIFLP-----LNNISNANDDLVHVLNSQDQQ-----
ZrouGcr1spli	1	-----MDQQ-----
TdelGcr1unsp	9	QGANLATLTAPSNPPTS---SYFSSHP-----NNINNNISNQLHFFLTQKDQQ-----
TdelGcr1spli	1	-----MDQQ-----
TblaGcr1aunsp	12	NNA-----NKPARKGF-Y-IPDSPGSSTISGNSTPKITELNTNIIQFFLQKQDQQQSLYY
TblaGcr1aspli	1	-----MQSLYY
TblaGcr1b	12	-----NEKTPPGI-----SSSLKSTVENQLRHYLKQDKL-----
NcasGcr1unsp	17	QNTRGYTRGRAATAPFSYSPSPS-----SLSPYKRNVTNKLQHLLSQQEQQ-----
NcasGcr1spli	1	-----MEQQ-----
CglaGcr1unsp	61	QNNWVISEN--QTNPA---QETIDARKFNEDATSPKQVDITNNKLKSLLLKQEEH-----
CglaGcr1spli	1	-----MEEH-----
Gcr1unspliced	21	RN-----VR---TQSVPTSYNNG--KESYGPNTNQLNALLSQLEQQ-----
Gcr1spli	1	-----MQ-----
consensus	61	1 1 dqg

KlacGcr1	35	NGMDDTANGSSVVQ-----QKSDPTKTQLQSVDNASASELSNFLMNSRLNLGTLMKFV
LkluGcr1	4	---SPTKQSSASNSPNVMHNPTSPKSS--CQAVTSNDLPLMLSASQIKIISIMTYI
ZrouGcr1unsp	55	-----ARISSTNISSNFYELITQYI
ZrouGcr1spli	5	-----ARISSTNISSNFYELITQYI
TdelGcr1unsp	54	-----ARISNTNISSNFHLISQYI
TdelGcr1spli	5	-----ARISNTNISSNFHLISQYI
TblaGcr1aunsp	65	DNNNFFNNGGSNINNDSSLTNSNPNPNTT--TSNFININHNNSNISTNFFTITKYI
TblaGcr1aspli	7	DNNNFFNNGGSNINNDSSLTNSNPNPNTT--TSNFININHNNSNISTNFFTITKYI
TblaGcr1b	42	-----ASNFNSPALVSGFSTIVQFL
NcasGcr1unsp	64	-----TKVNSSTNTSNFYTITQYI
NcasGcr1spli	5	-----TKVNSSTNTSNFYTITQYI
CglaGcr1unsp	111	-----SNINSADTTTNFYAISQYI
CglaGcr1spli	5	-----SNINSADTTTNFYAISQYI
Gcr1unspliced	58	-----TSVDSTSTSSNFYSIAQYI
Gcr1spli	3	-----TSVDSTSTSSNFYSIAQYI
consensus	121	rl ssnsssnfytitqyi

KlacGcr1	88	CIE F FKCNK-DELAN LRL LDLTQDST F Q T LT L RNM--QTE--NSH Y K F FNTINRDKSIT
LkluGcr1	57	LNKFY N VDNSTIQ S SLKLIDLIVDQTY P ESLT L RKL--NDSL S NRQ Y YFNTISR N KDIT
ZrouGcr1unsp	74	LQAYFKV S F-TE L RS L KLVDLIVDQTY A ESLT L RKL--NEGAS V RS Y EYFNTV P RQ E DIT
ZrouGcr1spli	24	LQAYFKV S F-TE L RS L KLVDLIVDQTY A ESLT L RKL--NEGAS V RS Y EYFNTV P RQ E DIT
TdelGcr1unsp	73	LQ I Y Y KVDF-SGL S SLKLIVDLIVDQTY P DSIT L RKL--NENT S IK P Y E YFNTISR D EDIS
TdelGcr1spli	24	LQ I Y Y KVDF-SGL S SLKLIVDLIVDQTY P DSIT L RKL--NENT S IK P Y E YFNTISR D EDIS
TblaGcr1aunsp	122	LQ S YFKVSN-NDL P PL L RLVDLIVDQ I YPDSL T L R KL--NENAS M RP Y HYNTVSRDENIS
TblaGcr1aspli	64	LQ S YFKVSN-NDL P PL L RLVDLIVDQ I YPDSL T L R KL--NENAS M RP Y HYNTVSRDENIS
TblaGcr1b	62	LQ Y YCNVDL-IDV A S I KLIDMYTTNKNAN M LIVRKTQ L TQSTGLV K A E Y Y QELQ R DE D IT
NcasGcr1unsp	83	LQTYFKVDL-NSL S SLKLIDLIVDQTY P DSL T L R KL--HEG S SVQ P Y E YFNTVSRDS D IS
NcasGcr1spli	24	LQTYFKVDL-NSL S SLKLIDLIVDQTY P DSL T L R KL--HEG S SVQ P Y E YFNTVSRDS D IS
CglaGcr1unsp	130	LQ S YFKANS-SD L AS L KLVDLIVDQTY Q DSL T L R KL--NETT A MQ P Y Y FNTVSRNP D IS
CglaGcr1spli	24	LQ S YFKANS-SD L AS L KLVDLIVDQTY Q DSL T L R KL--NETT A MQ P Y Y FNTVSRNP D IS
Gcr1unspliced	77	LQ S YFKVNV-DSL N SLKLVDLIVDQTY P DSL T L R KL--NEG A TGQ P Y D FNTVSRD A DIS
Gcr1spli	22	LQ S YFKVNV-DSL N SLKLVDLIVDQTY P DSL T L R KL--NEG A TGQ P Y D FNTVSRD A DIS
consensus	181	lqsyfkv el sklklvDlivdqtypdsltlRkl ne sv pyeyfntvsRd dIS

KlacGcr1	143	SCP V FA I AL Y SFIT W KQT-- A IS W KN F M N L P L I FDSKD I M-----LQGN N QLRL P
LkluGcr1	115	RC P IFC I G I Y S IF K WGGNRG N AIR F DN F TE V PL V GDISRSGTPTNE Y TPSVSE I PHYST N
ZrouGcr1unsp	131	RC P IFALAT Y FVIRWS H PN-PP I SVEN F DR I PL L DPT I T W NKG-FQ-E---L---N H T
ZrouGcr1spli	81	RC P IFALAT Y FVIRWS H PN-PP I SVEN F DR I PL L DPT I T W NKG-FQ-E---L---N H T
TdelGcr1unsp	130	RC P IFAL I YFVIRWS H PN-PP I T I EN F DN I PL L DP N F I SIN N TGAN-G---V N SAAN S L
TdelGcr1spli	81	RC P IFAL I YFVIRWS H PN-PP I T I EN F DN I PL L DP N F I SIN N TGAN-G---V N SAAN S L
TblaGcr1aunsp	179	RC P IFSLAV Y FLIRWS H PN-PP I T E NY M N I PL L DV S FL S LNQ N V D Y-K---GPVPLK T P
TblaGcr1aspli	121	RC P IFSLAV Y FLIRWS H PN-PP I T E NY M N I PL L DV S FL S LNQ N V D Y-K---GPVPLK T P
TblaGcr1b	121	QCP V FAL T MF M FL V W H NP K -IP I T A Q N FES F PL L DP S S I NN I F N PLK S HI Y STPEN L T D
NcasGcr1unsp	140	K C PLFAL I Y F IIRWS H PN-PP I S I Y N SS I PL L DP E Y I SLDSN P LL Y G---EN P DL S NI
NcasGcr1spli	81	K C PLFAL I Y F IIRWS H PN-PP I S I Y N SS I PL L DP E Y I SLDSN P LL Y G---EN P DL S NI
CglaGcr1unsp	187	RC P IFALAV Y FVIRWS H PN-PP I T I NN Y HL I SL L DS N FID P NA K LV N -N---EN P DHQ Q L
CglaGcr1spli	81	RC P IFALAV Y FVIRWS H PN-PP I T I NN Y HL I SL L DS N FID P NA K LV N -N---EN P DHQ Q L
Gcr1unspliced	134	K C PIFAL T IFFVIRWS H PN-PP I S I EN F TT V PL L DS N F I SLNS N P L L-Y---IQ N Q N P N S
Gcr1spli	79	K C PIFAL T IFFVIRWS H PN-PP I S I EN F TT V PL L DS N F I SLNS N P L L-Y---IQ N Q N P N S
consensus	241	rCPiFalalyfvirWshpn ppIisieNf ipLld fisin n

KlacGcr1	192	VYTS N MI-R-----ST V T P KK E ML S F V FP W LPAL E RD Y LN H DR S NY I L F S I VEL F Y F LAK
LkluGcr1	175	SHGN K IL-R-----SS L EP N EL I EV L FP W LN L LE D FQ N KD R T N Y N L H SL F EL F H F LG K
ZrouGcr1unsp	181	KEGY K VS R S-----V S FE P AN E L A D I IF P W L PS L RQ D ME I MD R S N Y K L H S F LE L FE F MA R
ZrouGcr1spli	131	KEGY K VS R S-----V S FE P AN E L A D I IF P W L PS L RQ D ME I MD R S N Y K L H S F LE L FE F MA R
TdelGcr1unsp	185	MNTQ K VS R S-----Q L F N PS Q EL I N L IF P W L SP L KQ D ML F ID R T N Y K L N S F VEL F EF F AI
TdelGcr1spli	136	MNTQ K VS R S-----Q L F N PS Q EL I N L IF P W L SP L KQ D ML F ID R T N Y K L N S F VEL F EF F AI
TblaGcr1aunsp	234	TSSE K IS R A-----NN F DP P KE L I Y LL F PW L PT L KQ E I Q LL E RS N Y R L Y SL E LF E FF I AK
TblaGcr1aspli	176	TSSE K IS R A-----NN F DP P KE L I Y LL F PW L PT L KQ E I Q LL E RS N Y R L Y SL E LF E FF I AK
TblaGcr1b	180	QNDF L IN K KL R FD N NG N FD K VL S N M V F PW L PK L RS D M K Y Y H R T N F K L Y S F C N L F E F FG R
NcasGcr1unsp	196	NSNV K I A RS-----E S FE P S R EL I D I V F PW L P Y L R Q E ML L V D R T NY K L H SL C EL F EF F MG R
NcasGcr1spli	137	NSNV K I A RS-----E S FE P S R EL I D I V F PW L P Y L R Q E ML L V D R T NY K L H SL C EL F EF F MG R
CglaGcr1unsp	242	SQNT K IL R S-----E I F H PS P DM I EL V FP W LP A L K Q D ML L ID R T N Y K L F SL C EL F EF F MG K
CglaGcr1spli	136	SQNT K IL R S-----E I F H PS P DM I EL V FP W LP A L K Q D ML L ID R T N Y K L F SL C EL F EF F MG K
Gcr1unspliced	189	NSSV K VS R S-----Q T FE P S K EL I D I V F PW L S Y L K Q D ML L ID R T N Y K L Y SL C EL F EF F MG R
Gcr1spli	134	NSSV K VS R S-----Q T FE P S K EL I D I V F PW L S Y L K Q D ML L ID R T N Y K L Y SL C EL F EF F MG R
consensus	301	kisrs tfepskelielvFPWLp LkqdmllmdRtNykLfS1 eLFeFmgk

KlacGcr1	246	IVLQDFAF	LQCTG-Q	LPHLQELIKSEL	SWQFLESDD	WNLFKDEMQR	QID-----
LkluGcr1	229	VVVQDLAY	LSCT-G	ILPHLQSI	IMEHIPKLY	Q-CIFFKTF	KKDLQKEIDG-----
ZrouGcr1unsp	236	TIVQDLKYL	QLNSGL	LLPNIVTF	VAKFIPDLF	Q-HPKFQK	AKPVFNERGG-----
ZrouGcr1spli	186	TIVQDLKYL	QLNSGL	LLPNIVTF	VAKFIPDLF	Q-HPKFQK	AKPVFNERGG-----
TdelGcr1unsp	240	TIIQDLRYL	LHTHPN	LLPNIVS	FVAKFIPDL	FK-NEHFK	ARMVGENIYGNN-----
TdelGcr1spli	191	TIIQDLRYL	LHTHPN	LLPNIVS	FVAKFIPDL	FK-NEHFK	ARMVGENIYGNN-----
TblaGcr1aunsp	289	SLIQDLKYL	TKNPSL	LLPNIVTF	VAKFVPDLF	Q-HELFV	VNDKSTSKNISN-EPILNNSTRY
TblaGcr1aspli	231	SLIQDLKYL	TKNPSL	LLPNIVTF	VAKFVPDLF	Q-HELFV	VNDKSTSKNISN-EPILNNSTRY
TblaGcr1b	240	VFIQDCTYL	SRSPNI	YGNLLHY	VSFFPQFENI	----LH	SKSINDTHAG-----
NcasGcr1unsp	251	IVIQDLRYL	NHHAL	LLPNILS	FIANFIPDL	FQ-NHQF	KAIDQFGTTNITTNDVLTSSM--
NcasGcr1spli	192	IVIQDLRYL	NHHAL	LLPNILS	FIANFIPDL	FQ-NHQF	KAIDQFGTTNITTNDVLTSSM--
CglaGcr1unsp	297	VIIQDLRYL	SQHSM	LLPKIVE	FISKFIPEL	FE-NEQF	KSSSEDEFMMERQGS----DF--
CglaGcr1spli	191	VIIQDLRYL	SQHSM	LLPKIVE	FISKFIPEL	FE-NEQF	KSSSEDEFMMERQGS----DF--
Gcr1unspliced	244	VAIQDLRYL	SQHPL	LLPNIVT	FISKFIPEL	FQ-NEEF	KGIGSIKNS-----
Gcr1spliced	189	VAIQDLRYL	SQHPL	LLPNIVT	FISKFIPEL	FQ-NEEF	KGIGSIKNS-----
consensus	361	iviQDlryLs	h	llpnivsf	iakfipdlf	q ne fk	q

KlacGcr1	294	-----
LkluGcr1	277	-----
ZrouGcr1unsp	284	-----
ZrouGcr1spli	234	-----
TdelGcr1unsp	289	-----
TdelGcr1spli	240	-----
TblaGcr1aunsp	347	NSGPNNNNIDTPNVNYSNNQNLNNGNTNYLWSNYNNNIMNSNESSNNTDNNRNNNFNSM
TblaGcr1aspli	289	NSGPNNNNIDTPNVNYSNNQNLNNGNTNYLWSNYNNNIMNSNESSNNTDNNRNNNFNSM
TblaGcr1b	285	---SNTKNV-----CSSNNFK--
NcasGcr1unsp	308	-----RINDNR--
NcasGcr1spli	249	-----RINDNR--
CglaGcr1unsp	350	-----QPNSYD--
CglaGcr1spli	244	-----QPNSYD--
Gcr1unspliced	289	-----NN--
Gcr1spliced	234	-----NN--
consensus	421	

KlacGcr1	294	-----
LkluGcr1	277	-----
ZrouGcr1unsp	284	-----
ZrouGcr1spli	234	-----
TdelGcr1unsp	289	-----
TdelGcr1spli	240	-----
TblaGcr1aunsp	407	YNNITSSVNNEQFNKFNGMYSSVSSNGQSLINPMPFSSNGISSQNSSVNFTSNVSKINSV
TblaGcr1aspli	349	YNNITSSVNNEQFNKFNGMYSSVSSNGQSLINPMPFSSNGISSQNSSVNFTSNVSKINSV
TblaGcr1b	298	-----DEL-----
NcasGcr1unsp	314	-----SFMNGINNE
NcasGcr1spli	255	-----SFMNGINNE
CglaGcr1unsp	356	-----TNLQISRE
CglaGcr1spli	250	-----TNLQISRE
Gcr1unspliced	291	-----NALNNV--T
Gcr1spliced	236	-----NALNNV--T
consensus	481	v i

KlacGcr1	294	--NELLQMDCFN S VC G K I ED R FT K LS K DL V TEND K LS N EL R TM K S Q MA S MTAV V N Q IF H T
LkluGcr1	277	---DSVQSDWCN I LM D K I EE S F I EV S KK F TV E NT R L T Q E V K DL K LE L SD I K Q L V S Q IL Q S
ZrouGcr1unsp	284	-----DDE D SH F L Q LS K R L TT E NV R LA Q Q I T Q L K T D LS N V Q Y M CD Q IL K L
ZrouGcr1spli	234	-----DDE D SH F L Q LS K R L TT E NV R LA Q Q I T Q L K T D LS N V Q Y M CD Q IL K L
TdelGcr1unsp	289	-----DSETNN V LN N ND T R F LE L SR R LT T EN I RL S Q Q IT N L K SE L SS V Q S MC D Q I L Q L
TdelGcr1spli	240	-----DSETNN V LN N ND T R F LE L SR R LT T EN I RL S Q Q IT N L K SE L SS V Q S MC D Q I L Q L
TblaGcr1aunsp	467	GTEDISTDKYKEALPR M L D SH Y MS I SK R L T T E NV R LS Q Q V T Q L R SD L SV N SM C R Q LL E L
TblaGcr1aspli	409	GTEDISTDKYKEALPR M L D SH Y MS I SK R L T T E NV R LS Q Q V T Q L R SD L SV N SM C R Q LL E L
TblaGcr1b	301	-----SENK----K I L D K Q ----IQDTL E R N I F LGRA V DD M Q N DLS A M K MS C N T M I D L
NcasGcr1unsp	323	N--NNIPISNDYK I PQ E I ES R F L EL S K K L T V E NV R LS Q Q V T Q L K SE L SS I T A MC D Q I L H G
NcasGcr1spli	264	N--NNIPISNDYK I PQ E I ES R F L EL S K K L T V E NV R LS Q Q V T Q L K SE L SS I T A MC D Q I L H G
CglaGcr1unsp	365	GTQNGYINN--SVLE K MI S Q F VS L SK K L T T E N I RL S Q E IT Q L K SD L SV T SM C N Q IL Q L
CglaGcr1spli	259	GTQNGYINN--SVLE K MI S Q F VS L SK K L T T E N I RL S Q E IT Q L K SD L SV T SM C N Q IL Q L
Gcr1unspliced	298	GIETQFLNPSTEE V S Q K V DS Y FM E LS K K L TT E N I RL S Q E IT Q L K AD M NS V GN V C N Q I LL L
Gcr1spliced	243	GIETQFLNPSTEE V S Q K V DS Y FM E LS K K L TT E N I RL S Q E IT Q L K AD M NS V GN V C N Q I LL L
consensus	541	v idsrfi lskkltteNvrLsqgitqlksdlssv mc qil l

KlacGcr1	352	QR Q LL S YQ I HN P ANN I --T S TM-----
LkluGcr1	334	QR Q M L SG S ST S -----T S TM-----
ZrouGcr1unsp	329	QQ Q QLVN N DR N Y R -----
ZrouGcr1spli	279	QQ Q QLVN N DR N Y R -----
TdelGcr1unsp	342	QR Q LL S GS S Q S TSG S D-----
TdelGcr1spli	293	QR Q LL S GS S Q S TSG S D-----
TblaGcr1aunsp	527	Q K K L L T N V NN F NNNN N HINN N YNN N IG I Q P TNN A NNIN I ND S ID N SN L D Q LL G GN S N A Y N
TblaGcr1aspli	469	Q K K L L T N V NN F NNNN N HINN N YNN N IG I Q P TNN A NNIN I ND S ID N SN L D Q LL G GN S N A Y N
TblaGcr1b	346	Q L K V L N N L Q S E Q ED N RL Q N-----
NcasGcr1unsp	381	QQ E L I L Q NN T ST S -R-----
NcasGcr1spli	322	QQ E L I L Q NN T ST S -R-----
CglaGcr1unsp	423	QR K I A NG E N Q TR D R-----
CglaGcr1spli	317	QR K I A NG E N Q TR D R-----
Gcr1unspliced	358	QR Q LL S GN Q AIG S K-----
Gcr1spliced	303	QR Q LL S GN Q AIG S K-----
consensus	601	Qrqlls nq

KlacGcr1	372	-----ANF N S Q AM N ST N V T NN N NN N V N S N T M I N
LkluGcr1	345	-----NNAS N G I L I L D K N S I SS N LL N N
ZrouGcr1unsp	342	-----Q N N--NNNN G V I V I D K NS V NS I W N N
ZrouGcr1spli	292	-----Q N N--NNNN G V I V I D K NS V NS I W N N
TdelGcr1unsp	358	-----VN N S Q --V T D K N G L I L D K N SL N LS M LS N
TdelGcr1spli	309	-----VN N S Q --V T D K N G L I L D K N SL N LS M LS N
TblaGcr1aunsp	587	NNNN N AN P K N ND N Q Q AM Y S Q NY P AAT D AS N ST G F N S--K N G N NN I I L D K NS I N M ET L S Q
TblaGcr1aspli	529	NNNN N AN P K N ND N Q Q AM Y S Q NY P AAT D AS N ST G F N S--K N G N NN I I L D K NS I N M ET L S Q
TblaGcr1b	365	-----N K NN S LS N ST V TS
NcasGcr1unsp	396	-----SD N TR--V P E K DR I M I T N VDD Q AE--S I N K
NcasGcr1spli	337	-----SD N TR--V P E K DR I M I T N VDD Q AE--S I N K
CglaGcr1unsp	437	-----SM G NS--V N G E GN I I L D K NA L NS Q L I N Q
CglaGcr1spli	331	-----SM G NS--V N G E GN I I L D K NA L NS Q L I N Q
Gcr1unspliced	372	-----SE N IV--S S TGGG I L I L D K N S I NS N VLS N
Gcr1spliced	317	-----SE N IV--S S TGGG I L I L D K N S I NS N VLS N
consensus	661	t q n n iiildknsvns lm n

KlacGcr1	401	T---SNNTMIPTSNTN-----
LkluGcr1	367	LVNGEEQPHSL-----
ZrouGcr1unsp	367	LAQNTAAVSASGGNNSTS--N-----
ZrouGcr1spli	317	LAQNTAAVSASGGNNSTS--N-----
TdelGcr1unsp	385	LVHTIEESQKQQQQQQQQ--QQQQQQQPQIQQL-QQLQLQLRQQQ-----QQL
TdelGcr1spli	336	LVHTIEESQKQQQQQQQQ--QQQQQQQPQIQQL-QQLQLQLRQQQ-----QQL
TblaGcr1aunsp	645	LFSYMNQNSSKTSNTNQLGQEYQQFQQPNVQASQQLPFQLSQQLQSVLSTQYSNQQQM
TblaGcr1aspli	587	LFSYMNQNSSKTSNTNQLGQEYQQFQQPNVQASQQLPFQLSQQLQSVLSTQYSNQQQM
TblaGcr1b	378	-----ENIRK-----P-----
NcasGcr1unsp	422	ILGSLTNPESNPM-----DIP-----LH-----
NcasGcr1spli	363	ILGSLTNPESNPM-----DIP-----LH-----
CglaGcr1unsp	464	LVHSADDTSQQ-----
CglaGcr1spli	358	LVHSADDTSQQ-----
Gcr1unspliced	399	LVQSIDPNHSPNGQAQT--HQRG-----
Gcr1spliced	344	LVQSIDPNHSPNGQAQT--HQRG-----
consensus	721	lv ti

KlacGcr1	414	-----PNI---AYSVNYS
LkluGcr1	378	-----API
ZrouGcr1unsp	386	-----NEEP-----QES-----S
ZrouGcr1spli	336	-----NEEP-----QES-----S
TdelGcr1unsp	430	QQQQ-----QLQQQQQP-----QQFQQADTPFT-A---P---T
TdelGcr1spli	381	QQQQ-----QLQQQQQP-----QQFQQADTPFT-A---P---T
TblaGcr1aunsp	705	QHQLQAQTQQNASQNFISSGNRSQSVNNPPETMIQQHQESNIQEQLQRGRSYPMQAS
TblaGcr1aspli	647	QHQLQAQTQQNASQNFISSGNRSQSVNNPPETMIQQHQESNIQEQLQRGRSYPMQAS
TblaGcr1b	384	-----QESSSLTI---PSQTYPSKLN
NcasGcr1unsp	440	-----PS-----SAVPSPSISA---S---E
NcasGcr1spli	381	-----PS-----SAVPSPSISA---S---E
CglaGcr1unsp	475	-----KGLESSL-A---P---I
CglaGcr1spli	369	-----KGLESSL-A---P---I
Gcr1unspliced	422	-----KGQSH-----AQVQSTNSPAL-A---P---I
Gcr1spliced	367	-----KGQSH-----AQVQSTNSPAL-A---P---I
consensus	781	tp i a p

KlacGcr1	424	KMMNDKR-----HIY--
LkluGcr1	381	NMFPSLSSS-----
ZrouGcr1unsp	394	NL-----
ZrouGcr1spli	344	NL-----
TdelGcr1unsp	457	NMFPSLS-----NP-----
TdelGcr1spli	408	NMFPSLS-----NP-----
TblaGcr1aunsp	765	TQFKEIQSMHQENFTNTQQTSSSTNNISTISANEDKQTLQQPSIPPQ---QARATHIVND
TblaGcr1aspli	707	TQFKEIQSMHQENFTNTQQTSSSTNNISTISANEDKQTLQQPSIPPQ---QARATHIVND
TblaGcr1b	402	R--TDIQ-----ATS-----LTRSSIESQKPKTPPSIDMSGSKSVHI---
NcasGcr1unsp	454	QVLPSSN-----
NcasGcr1spli	395	QVLPSSN-----
CglaGcr1unsp	486	GTFNLSLQ-----SK-----
CglaGcr1spli	380	GTFNLSLQ-----SK-----
Gcr1unspliced	441	NMFPSLS-----NS-----
Gcr1spliced	386	NMFPSLS-----NS-----
consensus	841	nmf sl

KlacGcr1	434	---NQ P -M N SIKR-----MKLDGKD-----MSNFDSS-S-----
LkluGcr1	390	-----AVQDT Q -----
ZrouGcr1unsp	396	---A P MLAS-----F- P -----LVNPEVNR-- K -----
ZrouGcr1spli	346	---A P MLAS-----F- P -----LVNPEVNR-- K -----
TdelGcr1unsp	466	---I P S M L T S-----Q V P Q QLTSAQSQDSTL-- K -----
TdelGcr1spli	417	---I P S M L T S-----Q V P Q QLTSAQSQDSTL-- K -----
TblaGcr1aunsp	821	EIV L S P I M N SVELHKSSSNSNQL P SQH--LLQHQDT Q GT K QNLGQQSYAYSTADTRVISQ
TblaGcr1aspli	763	EIV L S P I M N SVELHKSSSNSNQL P SQH--LLQHQDT Q GT K QNLGQQSYAYSTADTRVISQ
TblaGcr1b	437	---L P P I INKT-----
NcasGcr1unsp	461	---MG-M K S-----SY P SPLIHQQRHSPL Q -- K -----
NcasGcr1spli	402	---MG-M K S-----SY P SPLIHQQRHSPL Q -- K -----
CglaGcr1unsp	495	---L Q N-----SEA Q -- K -----
CglaGcr1spli	389	---L Q N-----SEA Q -- K -----
Gcr1unspliced	450	---I Q P M L G T-----LAP Q P-----QDIV Q -- K -----
Gcr1spli	395	---I Q P M L G T-----LAP Q P-----QDIV Q -- K -----
consensus	901	i p m m s p q k

KlacGcr1	458	---R R L S Q P Q P S ----- P L-----
LkluGcr1	396	--- K R K -L P L P N----- Q P F S ----- P -----
ZrouGcr1unsp	413	--- R K L -- P ---PP----- Q P G L S P F L----- P S P G ---
ZrouGcr1spli	363	--- R K L -- P ---PP----- Q P G L S P F L----- P S P G ---
TdelGcr1unsp	490	--- R K L -- P L T S A P----- A S G L G P F S ----- P S P G ---
TdelGcr1spli	441	--- R K L -- P L T S A P----- A S G L G P F S ----- P S P G ---
TblaGcr1aunsp	879	D Q Q Q N L-IST P H H S S Q V S S I H S T P S Q P G I Q T T I T Q P T-DS Q P A R R P Y R I P T T I P S T G N G I
TblaGcr1aspli	821	D Q Q Q N L-IST P H H S S Q V S S I H S T P S Q P G I Q T T I T Q P T-DS Q P A R R P Y R I P T T I P S T G N G I
TblaGcr1b	445	-----P-----TAP K N K T D N P S I Q F -----L S P G L S V
NcasGcr1unsp	483	---R R F -- P S L P I P T-----TK V K S P F S ----- P T P A ---
NcasGcr1spli	424	---R R F -- P S L P I P T-----TK V K S P F S ----- P T P A ---
CglaGcr1unsp	503	--- R K L -- P F P S H Q A A T S N I -----V N V P M N N A N G A S P Y S ----- P S I N ---
CglaGcr1spli	397	--- R K L -- P F P S H Q A A T S N I -----V N V P M N N A N G A S P Y S ----- P S I N ---
Gcr1unspliced	468	--- R K L -- P L P G S I A S -----A A T G S P F S ----- P S -----
Gcr1spli	413	--- R K L -- P L P G S I A S -----A A T G S P F S ----- P S -----
consensus	961	r k l p p g s p f s p s g

KlacGcr1	470	----- Q I G S P ----- L E A L L S K P I S P K I T V S M L N N ----
LkluGcr1	410	----- Q L I D S P F K - K F K -----
ZrouGcr1unsp	431	---P V --L P T V A E S P Y T K R L R I -- D D K R T P S Q S A L D L L S K T A S S P R F P S L P N N ----
ZrouGcr1spli	381	---P V --L P T V A E S P Y T K R L R I -- D D K R T P S Q S A L D L L S K T A S S P R F P S L P N N ----
TdelGcr1unsp	512	---P A T V G P T N P D S P F K R F R Y -- D D K P T P S Q T A L D S L L S K S I G S P K Y S N L Q N Q G A I P N
TdelGcr1spli	463	---P A T V G P T N P D S P F K R F R Y -- D D K P T P S Q T A L D S L L S K S I G S P K Y S N L Q N Q G A I P N
TblaGcr1aunsp	937	L L L S P I N E D D R N L G P S P K R I R L -- D D K Q T T S Q T A L N A L L K K S N D N M M P T N K N V I P --L N
TblaGcr1aspli	879	L L L S P I N E D D R N L G P S P K R I R L -- D D K Q T T S Q T A L N A L L K K S N D N M M P T N K N V I P --L N
TblaGcr1b	467	T V -----S S S H S F K A -----N A L Q S L T N -----
NcasGcr1unsp	505	-----T S D S P F A K R Q K A N V D K L T P S Q T A L E A L L P N A L S S D F N N D K -L N K I T E Q
NcasGcr1spli	446	-----T S D S P F A K R Q K A N V D K L T P S Q T A L E A L L P N A L S S D F N N D K -L N K I T E Q
CglaGcr1unsp	538	---M----- Q P D S P Y N K R Y R L -- E D K S T P S Q N A L D S L L S K S V A S P R V G S S V N G S N I M
CglaGcr1spli	432	---M----- Q P D S P Y N K R Y R L -- E D K S T P S Q N A L D S L L S K S V A S P R V G S S V N G S N I M
Gcr1unspliced	489	---P-----V G E S P Y S K R F K L -- D D K P T P S Q T A L D S L L T K S I S S P R L P L S T L A N T A V T
Gcr1spli	434	---P-----V G E S P Y S K R F K L -- D D K P T P S Q T A L D S L L T K S I S S P R L P L S T L A N T A V T
consensus	1021	p dspf krfri ddk tpsqtaid llsksi spk ln

KlacGcr1	496	-SV-----ASPPPN-PMAMSPL-PYISEP
LkluGcr1	422	-----DESKSHTA----
ZrouGcr1unsp	478	HVAKMPSR-----YSSPTAFAMTGSPS-----
ZrouGcr1spli	428	HVAKMPSR-----YSSPTAFAMTGSPS-----
TdelGcr1unsp	566	NAARLSSR-----FATPPTFPVPESPS-----
TdelGcr1spli	517	NAARLSSR-----FATPPTFPVPESPS-----
TblaGcr1aunsp	993	NNE ^R NSITVDNQPGNMLGNQTSNVSNASHENDDDLAFPGMSPSQTVFFDNHGLTPQIDSV
TblaGcr1aspli	935	NNE ^R NSITVDNQPGNMLGNQTSNVSNASHENDDDLAFPGMSPSQTVFFDNHGLTPQIDSV
TblaGcr1b	485	-----DINIGNYKLNTNIT--
NcasGcr1unsp	553	VES ^K SQAI IQRRPELVQTKS-----MSTPASPLASLPGSTKPVNFVIGRED-----
NcasGcr1spli	494	VES ^K SQAI IQRRPELVQTKS-----MSTPASPLASLPGSTKPVNFVIGRED-----
CglaGcr1unsp	586	DSP ^R SRNRN-----NSIDKKFFMTGQYN-----
CglaGcr1spli	480	DSP ^R SRNRN-----NSIDKKFFMTGQYN-----
Gcr1unspliced	537	ESF ^R SPQQ-----FQHSPDFVVGSSS-----
Gcr1spliced	482	ESF ^R SPQQ-----FQHSPDFVVGSSS-----
consensus	1081	r s f m gs

KlacGcr1	551	-----VR-----S-----NAQTTS
LkluGcr1	457	---LT-----TGA-TP-T-----
ZrouGcr1unsp	577	EPNEEA-----EEDASEEDGR-----DDE-----ND---
ZrouGcr1spli	527	EPNEEA-----EEDASEEDGR-----DDE-----ND---
TdelGcr1unsp	654	-----DSANQ T GN-----KD---
TdelGcr1spli	605	-----DSANQ T GN-----KD---
TblaGcr1aunsp	1173	ANSNLNTKGNQDITIETNAEINDTNATSAKENKGNSSP-SNAAITVPNNSESSKSNVTS
TblaGcr1aspli	1115	ANSNLNTKGNQDITIETNAEINDTNATSAKENKGNSSP-SNAAITVPNNSESSKSNVTS
TblaGcr1b	565	-----FISGNNDSTQSITAP-----
NcasGcr1unsp	680	QPSSLD-----EVSPK T ---AD-V---VT D T D-----KNKATQK
NcasGcr1spli	621	QPSSLD-----EVSPK T ---AD-V---VT D T D-----KNKATQK
CglaGcr1unsp	695	SNQLPK-----PQLASRAS-----T---IV D P D-----L-----
CglaGcr1spli	589	SNQLPK-----PQLASRAS-----T---IV D P D-----L-----
Gcr1unspliced	606	VDREKP-----PESSKSEPNDNSP-E---SK D P E-----KNGK---
Gcr1spli	551	VDREKP-----PESSKSEPNDNSP-E---SK D P E-----KNGK---
consensus	1261	tg de

KlacGcr1	560	KINSL-----GS-----
LkluGcr1	465	-----
ZrouGcr1unsp	598	-----DSKALSPKSSEAR P R
ZrouGcr1spli	548	-----DSKALSPKSSEAR P R
TdelGcr1unsp	664	-----DQGSLSNDDK-----
TdelGcr1spli	615	-----DQGSLSNDDK-----
TblaGcr1aunsp	1232	NSNSMTSSSNISETPNTVITPNTQDDSSNEQTGSNTSVAADTNETTSNKKLNTKDK P V T I
TblaGcr1aspli	1174	NSNSMTSSSNISETPNTVITPNTQDDSSNEQTGSNTSVAADTNETTSNKKLNTKDK P V T I
TblaGcr1b	582	-----RPS I P I
NcasGcr1unsp	708	KINTFSSKSNAS-----STMKWGDSNT-----THSP I KLAPL K S I P L
NcasGcr1spli	649	KINTFSSKSNAS-----STMKWGDSNT-----THSP I KLAPL K S I P L
CglaGcr1unsp	716	-----SVEVM H T I P A
CglaGcr1spli	610	-----SVEVM H T I P A
Gcr1unspliced	635	-----NSNPLGTDAD K P V P I
Gcr1spli	580	-----NSNPLGTDAD K P V P I
consensus	1321	l k vp

KlacGcr1	567	-----NEKDELRNGN
LkluGcr1	465	-----Q-----LSSQSATPVAST-----
ZrouGcr1unsp	613	-----PVS-----SQQ--VPS-----S--NPDN-----
ZrouGcr1spli	563	-----PVS-----SQQ--VPS-----S--NPDN-----
TdelGcr1unsp	674	-----S-----S--SPRS-----
TdelGcr1spli	625	-----S-----S--SPRS-----
TblaGcr1aunsp	1292	VTPITTSSIYS-----ESSEKFGTAAEYSAAPVESSSNSNITLI S NYRSLPILPSG-
TblaGcr1aspli	1234	VTPITTSSIYS-----ESSEKFGTAAEYSAAPVESSSNSNITLI S NYRSLPILPSG-
TblaGcr1b	588	-----P-----NSFS P SS-----N
NcasGcr1unsp	745	ITKSTNLPKLHKMNHTVQPQLYANLGTFLNKVST--KSKRTPPLNL-G--N P EDNLKSGE
NcasGcr1spli	686	ITKSTNLPKLHKMNHTVQPQLYANLGTFLNKVST--KSKRTPPLNL-G--N P EDNLKSGE
CglaGcr1unsp	726	-----PGHSNLQ-----HTLEKGY--EGK-----S--SRDDIEKN--
CglaGcr1spli	620	-----PGHSNLQ-----HTLEKGY--EGK-----S--SRDDIEKN--
Gcr1unspliced	650	-----SNIHNSTE-----AANSSGT--VTK-----T--APSF P QSS--
Gcr1spli	595	-----SNIHNSTE-----AANSSGT--VTK-----T--APSF P QSS--
consensus	1381	s p

KlacGcr1	577	DSENEPKVMTRNNSKGKRTGNPNMDIKYKLSRDNKT	IWDLYNEWYHGLNGKLSIKELIEK
LkluGcr1	478	-----RTAKRTSTSSSTGGPNEAIKYKLSRDNKT	IWDLYTEWYLGLP GKPSIKSLIEK
ZrouGcr1unsp	627	--T--SSGPNNQNRPMELGPNRH	IKYKLSRDNKT IWDLYTEWYIGLNGQSSIKSLIET
ZrouGcr1spli	577	--T--SSGPNNQNRPMELGPNRH	IKYKLSRDNKT IWDLYTEWYIGLNGQSSIKSLIET
TdelGcr1unsp	680	--E--RDSNSKKNPQNGEKIGPNKH	IKYKLSRDNKT VWDLYTEWYIGLNGKPSIKNLIDD
TdelGcr1spli	631	--E--RDSNSKKNPQNGEKIGPNKH	IKYKLSRDNKT VWDLYTEWYIGLNGKPSIKNLIDD
TblaGcr1aunsp	1343	-----MDTWSGYQNTKLDSTGTDNSK	IKYKLSRDNKT VWDLYTEWYIGLNGNLP IVE LIKS
TblaGcr1aspli	1285	-----MDTWSGYQNTKLDSTGTDNSK	IKYKLSRDNKT VWDLYTEWYIGLNGNLP IVE LIKS
TblaGcr1b	597	-----NISTTTNNDI-NPPEKDNTY	LKNSFAATIWDVYRDWYIGSSGTL SIKEQLIN
NcasGcr1unsp	800	DRG--EYKETKESVASNKNGPNEN	IKYKLSRENKTIWDLYA EWFIGLNGNPSIKK LIEK
NcasGcr1spli	741	DRG--EYKETKESVASNKNGPNEN	IKYKLSRENKTIWDLYA EWFIGLNGNPSIKK LIEK
CglaGcr1unsp	752	-KK--METQKRKKGDGASKPEHLPP	LKYKLSRDNKT IWDLYAEWYIGLNGQPSIRK LIED
CglaGcr1spli	646	-KK--METQKRKKGDGASKPEHLPP	LKYKLSRDNKT IWDLYAEWYIGLNGQPSIRK LIED
Gcr1unspliced	677	-SK--FEII---NKKDTKAGPNEAIKYKLSRENKTIWDLYA EWYIGLNGKSSIKK LIEN	
Gcr1spli	622	-SK--FEII---NKKDTKAGPNEAIKYKLSRENKTIWDLYA EWYIGLNGKSSIKK LIEN	
consensus	1441	d r k gpn ikYklsrdnktIWDLY eWyIGlnGq sIk lie	

KlacGcr1	637	YGYRRWKVTEDSHFFPTRRIIDYIETETDRSINLKRFLNLSPLLKDRDAVRKHIVKDLE	
LkluGcr1	531	FGWRRWKVSDDSHFFPTRRIIDYIERECKRGLRLGRFS----	LEQDREBIKKIIVAQDLE
ZrouGcr1unsp	683	YGLRRWKVSDDSHFFPTRRIIMDYIEMECDRGIKLGRFTN---	PDQPREDIRKIIIVGDLE
ZrouGcr1spli	633	YGLRRWKVSDDSHFFPTRRIIMDYIEMECDRGIKLGRFTN---	PDQPREDIRKIIIVGDLE
TdelGcr1unsp	736	YGWRRWKVSEDSHFFPTRRIIMDYIENECDRGIKLGRFTN---	PDQPREIRKVLVGDLE
TdelGcr1spli	687	YGWRRWKVSEDSHFFPTRRIIMDYIENECDRGIKLGRFTN---	PDQPREIRKVLVGDLE
TblaGcr1aunsp	1398	YGFRKWKVSQDSHFFPTRRIIDYIESECDRDINLGRFRD---	LSKPREDFRKIIVGDLE
TblaGcr1aspli	1340	YGFRKWKVSQDSHFFPTRRIIDYIESECDRDINLGRFRD---	LSKPREDFRKIIVGDLE
TblaGcr1b	649	NNFNINLVKKNVFNFAEAKSLLMKYVEMECSNSISNGRFS	D---SNKTRDEIRKIIIVRDVD
NcasGcr1unsp	858	FGWRRWKVSEDSHFFPTRRIIMDYIENECDRGIKLGRFK---	PDQSREIRKIIIVSDLE
NcasGcr1spli	799	FGWRRWKVSEDSHFFPTRRIIMDYIENECDRGIKLGRFK---	PDQSREIRKIIIVSDLE
CglaGcr1unsp	809	YGYRRWKVSDDSHFFPTRRVIDYIETECDRGIKLGRFTN---	PNQPREDIRKIIIVGDLE
CglaGcr1spli	703	YGYRRWKVSDDSHFFPTRRVIDYIETECDRGIKLGRFTN---	PNQPREDIRKIIIVGDLE
Gcr1unspliced	730	YGWRRWKVSEDSHFFPTRRIIMDYIETECDRGIKLGRFTN---	PQQPREDIRKIIVGDLE
Gcr1spli	675	YGWRRWKVSEDSHFFPTRRIIMDYIETECDRGIKLGRFTN---	PQQPREDIRKIIVGDLE
consensus	1501	ygyrrwkVsedshfFptrriimdYiE EcdrGiklgRftn p qpRedirKiivgDle	

KlacGcr1	697	TFREENGLTLNSLSLYFRNYTRWGKEICIDYDNFKDWSLVTMNEEEKVKYCKRKTLSKEN	
LkluGcr1	587	KFRMSNGLTLNSLSLYFRNLTRNKEICMYDNFQDWSLLLINDDDKNKYCKRQQTNAV*-	
ZrouGcr1unsp	740	KFRINNGTLTLNSLSMYFKNLTRNKEICIFENFKNWSVRAMTEEEKNKYCKRQHTKETL*	
ZrouGcr1spli	690	KFRINNGTLTLNSLSMYFKNLTRNKEICIFENFKNWSVRAMTEEEKNKYCKRQHTKETL*	
TdelGcr1unsp	793	KFRINSGTLTLNSISVYFKNLTKENKEICIFSDFDNWTVRSMTEEEKVKYCKRQHMKENG*	
TdelGcr1spli	744	KFRINSGTLTLNSISVYFKNLTKENKEICIFSDFDNWTVRSMTEEEKVKYCKRQHMKENG*	
TblaGcr1aunsp	1455	KFRINNSLTTLNSLSMYFRNLKANKEICIFENSTSWPVRKIGDAEKAQYCKRQPTSQNSH	
TblaGcr1aspli	1397	KFRINNSLTTLNSLSMYFRNLKANKEICIFENSTSWPVRKIGDAEKAQYCKRQPTSQNSH	
TblaGcr1b	706	SFMNLTNGMTLETLILHLNSTRQN--TSIYKDLKTWEVNTLNDN*-----	
NcasGcr1unsp	914	KFRINNGTLTLNSLSLYFRNLTKNKEIGIFENFKTWSVRYMTEDEKVKYCKRQHISTSSS	
NcasGcr1spli	855	KFRINNGTLTLNSLSLYFRNLTKNKEIGIFENFKTWSVRYMTEDEKVKYCKRQHISTSSS	
CglaGcr1unsp	866	RFRINNALTTLNSLSVYFRKLKENNEICIFENFNWQVRAMTEEEKIRYCKRQHGPADRN	
CglaGcr1spli	760	RFRINNALTTLNSLSVYFRKLKENNEICIFENFNWQVRAMTEEEKIRYCKRQHGPADRN	
Gcr1unspliced	787	KFRINNGTLTLNSLSLYFRNLTKNKEICIFENFKNWNVRSMTEEEKLKYCKRRHNTPS*-	
Gcr1spli	732	KFRINNGTLTLNSLSLYFRNLTKNKEICIFENFKNWNVRSMTEEEKLKYCKRRHNTPS*-	
consensus	1561	kFrinnnglTLnslslyfrnltnkeicifenfknWsvr mteeeekvkyckrqh	

KlacGcr1	757	RDDNYSQDDNE*-----
LkluGcr1		-----
ZrouGcr1unsp	799	-----
ZrouGcr1spli	749	-----
TdelGcr1unsp	852	-----
TdelGcr1spli	803	-----
TblaGcr1aunsp	1515	DSTD*-----
TblaGcr1aspli	1457	DSTD*-----
TblaGcr1b		-----
NcasGcr1unsp	974	SSHAASRSSEAQQSTKQLIELSATLLNLKKEITETNSEKDKKKKNKKKKKSASTEPNSQK
NcasGcr1spli	915	SSHAASRSSEAQQSTKQLIELSATLLNLKKEITETNSEKDKKKKNKKKKKSASTEPNSQK
CglaGcr1unsp	926	VTTTNESHSSVTDSQRPNMIAKQTFNNPIENPTTTSIERE-----SSSSSEKNSSP
CglaGcr1spli	820	VTTTNESHSSVTDSQRPNMIAKQTFNNPIENPTTTSIERE-----SSSSSEKNSSP
Gcr1unspliced		-----
Gcr1spli		-----
consensus	1621	

KlacGcr1		-----
LkluGcr1		-----
ZrouGcr1unsp		-----
ZrouGcr1spli		-----
TdelGcr1unsp		-----
TdelGcr1spli		-----
TblaGcr1aunsp		-----
TblaGcr1aspli		-----
TblaGcr1b		-----
NcasGcr1unsp	1034	KSEDSVETGTEKQHETVVGDEKKKD---ETIDVEAEKKDDIIEKSSIKVLTSAPPSDKSR
NcasGcr1spli	975	KSEDSVETGTEKQHETVVGDEKKKD---ETIDVEAEKKDDIIEKSSIKVLTSAPPSDKSR
CglaGcr1unsp	977	RQED-AEVGNTLPKNADADDDRNNEHNDNVTNNEFNDKDETA*-----
CglaGcr1spli	871	RQED-AEVGNTLPKNADADDDRNNEHNDNVTNNEFNDKDETA*-----
Gcr1unspliced		-----
Gcr1spli		-----
consensus	1681	

KlacGcr1		-----
LkluGcr1		-----
ZrouGcr1unsp		-----
ZrouGcr1spli		-----
TdelGcr1unsp		-----
TdelGcr1spli		-----
TblaGcr1aunsp		-----
TblaGcr1aspli		-----
TblaGcr1b		-----
NcasGcr1unsp	1091	EKIYPITTTSTNVTTTNASPDKTTPRSSNDLSIDIEPETANVLSKGGTPTVT*
NcasGcr1spli	1032	EKIYPITTTSTNVTTTNASPDKTTPRSSNDLSIDIEPETANVLSKGGTPTVT*
CglaGcr1unsp		-----
CglaGcr1spli		-----
Gcr1unspliced		-----
Gcr1spli		-----
consensus	1741	

Supplemental figure 10: Ape2 and Aap1 orthologs from the Saccharomycetaceae are aligned. Many of these genes have an alternate transcription and translation initiation sites within the intron. Yellow highlighting indicates the sequence that is encoded within the intron.

LkluApe2spliced	1	-----MLARCLTRNITSRGFATSSLPKSATLLLQQQPYHFLTVQR	
LkluApe2unsplic	1	-----	
KlacApe2spliced	1	-----	
KlacApe2unsplic	1	-----	
ZrouApe2spliced	1	-----MLFGTV-----SRRFLSSIGSRYVPRM---GKYQVGLSSL	
ZrouApe2unsplic	1	-----	
TdelApe2spliced	1	MSM-----FTKTLGRLSPRVALS-----RSMFAVVYG---QYQAVVSWT	
TdelApe2unsplic	1	-----	
NcasApe2spliced	1	--MYSRASFLGRARGISLALKTNNCLANSVRIRRISSSIYTAG-----QYVIQP-RQ	
NcasApe2unsplic	1	-----	
NcasAap1	1	-----	
CglaApe2spliced	1	-----MFPKLSL---KTVASSFARLPATSFL-----	
CglaApe2unsplic	1	-----	
CglaAap1	1	-----	
Ape2_dist	1	MPIVRWLLLKSAVRGSSSLIGKAHPCLRSIAAHPRYLSNVYSPPAGVSR---SLRINVMWK	
Ape2_prox	1	MPIVRWLLLKSAVRGSSSLIGKAHPCLRSIAAHPRYLSNVYSPPAGVSR---SLRINVMWK	
Ape2unspliced	1	-----	
Aap1	1	-----	
consensus	1		
LkluApe2spliced	41	R--V-----PQKNLLSN-YGAVFKRRLFSGAVTPCAKCEKLKDQLA---NKNETPDR	
LkluApe2unsplic	1	-----MSSETPDR	
KlacApe2spliced	1	MFGHVPKILNGIRG---AWARPMAASRSLFTHTKFHCNKCERTKNHL-----LSQPDR	
KlacApe2unsplic	1	-----MSSQPDR	
ZrouApe2spliced	33	R-AIKPAALNGTTKASMGPIVSTTIAKRSFFRESCHKCQKATQR-----ADV SASR	
ZrouApe2unsplic	1	-----MSSADV SASR	
TdelApe2spliced	37	R-----PASRPFFKESCHKCQKMAES-----HTVSATTKR	
TdelApe2unsplic	1	-----MSSVSATTKR	
NcasApe2spliced	50	REPVKP-----TNIGACHNSLLAFSRRSLFTETLHSCAKCQRTSDMLTK---TATVNR	
NcasApe2unsplic	1	-----MTSATVNR	
NcasAap1	1	-----MTSQPIDR	
CglaApe2spliced	24	--KV-----TKAPIATSIVNGRSFFTDTKYKCGKCERQKEISK---TISENR	
CglaApe2unsplic	1	-----MNSENR	
CglaAap1	1	-----MDR	
Ape2_dist	58	QSKLTP-----P-----RFVKIMNRRPLFTTETSHACAKCQKTSQLL-----NKTPNR	
Ape2_prox	58	QSKLTP-----P-----RFVKIMNRRPLFTTETSHACAKCQKTSQLLKTTMTSNKTPNR	
Ape2unspliced	1	-----MTSKTPNR	
Aap1	1	-----MSR	
consensus	61		s t R
LkluApe2spliced	87	DILPVNVSPVHYDLTIEPNFETFKFDGTVEIDLKVNDATVPTVKLNTLDIDIHSAID-D	
LkluApe2unsplic	9	DILPVNVSPVHYDLTIEPNFETFKFDGTVEIDLKVNDATVPTVKLNTLDIDIHSAID-D	
KlacApe2spliced	51	IILPQNVSPVHYDLTIEPNFETFKFDGTVEIDLKVNDKESDFVELNTFELDIHEAKIN-D	
KlacApe2unsplic	8	IILPQNVSPVHYDLTIEPNFETFKFDGTVEIDLKVNDKESDFVELNTFELDIHEAKIN-D	
ZrouApe2spliced	83	EVLPTNVTPVHYDLVLEPDFQTFKFGGHLKLDLQVNDPKVDSIWLNSLDIDLHSAALTDG	
ZrouApe2unsplic	11	EVLPTNVTPVHYDLVLEPDFQTFKFGGHLKLDLQVNDPKVDSIWLNSLDIDLHSAALTDG	
TdelApe2spliced	67	EVLPTNVTPVHYDLKVEPDFETFKYNGTVKIDLQVNDPKVNNVQLNTIDIDIHSAKIG-S	
TdelApe2unsplic	11	EVLPTNVTPVHYDLKVEPDFETFKYNGTVKIDLQVNDPKVNNVQLNTIDIDIHSAKIG-S	
NcasApe2spliced	100	EVLPTNVTPVHYDLQIEPDFKDFKFDGLAKIDLKINDENTDFIKLNTLEIDIHSAKID-D	
NcasApe2unsplic	9	EVLPTNVTPVHYDLQIEPDFKDFKFDGLAKIDLKINDENTDFIKLNTLEIDIHSAKID-D	
NcasAap1	9	EVLPTNVTPVHYDLSFEPDFKNFTFEGSANIKLRINDPTIDVLTNTLEIKYHEVKIE-E	
CglaApe2spliced	66	EVLPTNVTPVHYDLSLEPNFETFKFHGLEEINLKVNDKTDNVITLNSIEIDIHSAKID-D	
CglaApe2unsplic	7	EVLPTNVTPVHYDLSLEPNFETFKFHGLEEINLKVNDKTDNVITLNSIEIDIHSAKID-D	
CglaAap1	4	EILPSNVTPVHYDLVLEPSFETFKFDGSVTIDLQVNDSTVDSISLNTLEIDIKAVTLDGS	
Ape2_dist	100	EILPDNVVPLHYDLTVEPDFKTFKFEGSVKIELKINNPAIDTVTLNTVDTDIHSAKIG-D	
Ape2_prox	106	EILPDNVVPLHYDLTVEPDFKTFKFEGSVKIELKINNPAIDTVTLNTVDTDIHSAKIG-D	
Ape2unspliced	9	EILPDNVVPLHYDLTVEPDFKTFKFEGSVKIELKINNPAIDTVTLNTVDTDIHSAKIG-D	
Aap1	4	EVLPTNVTPVHYDLTIEPNFRAFTFEGSLKIDLQINDHSINSVQINYLEIDFHSARIE-G	
consensus	121	evLPtNVtPlHYdltiEPdFetFkfdGtvkidLkvNd vdtv lNtldidihsa ki d	

LklApe2spliced	146	VTATEITFDKDEQTTTFLFPEGTL---KDE-VTLAIKFTGVLNDNMAGFYRAKYTDKKTG
LklApe2unspliced	68	VTATEITFDKDEQTTTFLFPEGTL---KDE-VTLAIKFTGVLNDNMAGFYRAKYTDKKTG
KlacApe2spliced	110	VKSLETVTDEENQTSRFKFPAGTLKD-SDN-VTIDIKFTGILNDTMAGFYRAKYIDNATG
KlacApe2unspliced	67	VKSLETVTDEENQTSRFKFPAGTLKD-SDN-VTIDIKFTGILNDTMAGFYRAKYIDNATG
ZrouApe2spliced	143	TKATEVKHNDNQVTEFKFPAGTIAKNGEK-VTLEISFTGELNDYMAGFYRAKYEDKLTG
ZrouApe2unspliced	71	TKATEVKHNDNQVTEFKFPAGTIAKNGEK-VTLEISFTGELNDYMAGFYRAKYEDKLTG
TdelApe2spliced	126	YEAKDVSYDKDSQVSTFTFDDKVLSA-DKK-VTLEIDFTGTLNDNMAGFYRAKYEDKATG
TdelApe2unspliced	70	YEAKDVSYDKDSQVSTFTFDDKVLSA-DKK-VTLEIDFTGTLNDNMAGFYRAKYEDKATG
NcasApe2spliced	160	IKPSSIEYNKEDQISEFYFPKGTMAKLAGS-ATLEIKFTGILNDQMAGFYRAKYVDKLTG
NcasApe2unspliced	69	IKPSSIEYNKEDQISEFYFPKGTMAKLAGS-ATLEIKFTGILNDQMAGFYRAKYVDKLTG
NcasAap1	68	TPASDINVDDKAQTVQFIFPKGTIAQQGTEEFILQTKFTGILNDQMAGFYRAKYTDKSTG
CglaApe2spliced	125	VEPKQTKFDHDKQTVFVFPEGTAK-SND-PTLKLDFGTGILNDNMAGFYRAKYQDKKTG
CglaApe2unspliced	66	VEPKQTKFDHDKQTVFVFPEGTAK-SND-PTLKLDFGTGILNDNMAGFYRAKYQDKKTG
CglaAap1	64	ITPSEIKVDEAAQVTEFVFEKGTLSEKK--SVKLEIKFIGILNDQMAGFYRAKYEDKQTG
Ape2_dist	159	VTSEIIISEEQVTTFAFPKGTMSFKN-AFLDIKFTGILNDNMAGFYRAKYEDKLTG
Ape2_prox	165	VTSEIIISEEQVTTFAFPKGTMSFKN-AFLDIKFTGILNDNMAGFYRAKYEDKLTG
Ape2unspliced	68	VTSEIIISEEQVTTFAFPKGTMSFKN-AFLDIKFTGILNDNMAGFYRAKYEDKLTG
Aap1	63	VNAIEVNKNENQKATLVFPNGTFENLGPS-AKLEIIFSGILNDQMAGFYRAKYTDKVTG
consensus	181	v tei d d Qvt f Fp gtl vtldikFtGiLNDnMAGFYRAKY Dk TG

LklApe2spliced	202	KTKYMATTQMEPTDARRAFPCFDEPNLKATFAINLISDPSLTHLSNMDVKSESVVD-GKK
LklApe2unspliced	124	KTKYMATTQMEPTDARRAFPCFDEPNLKATFAINLISDPSLTHLSNMDVKSESVVD-GKK
KlacApe2spliced	168	ETKYMATTQMEPTDARRAFPCFDEPNLKASFEITLVSDPKLTHLSNMDVKKEEIFD-GKK
KlacApe2unspliced	125	ETKYMATTQMEPTDARRAFPCFDEPNLKASFEITLVSDPKLTHLSNMDVKKEEIFD-GKK
ZrouApe2spliced	202	ETKYMATTQMEATDARRAFPCYDEPNRKATFDITLVSEPHLTHLSNMDVKKESVED-GKK
ZrouApe2unspliced	130	ETKYMATTQMEATDARRAFPCYDEPNRKATFDITLVSEPHLTHLSNMDVKKESVED-GKK
TdelApe2spliced	184	KTKYMATTQMEPTDARRAFPCFDEPNLKATFDISLVSDKSLTHLSNMDVKSEENLDGNKK
TdelApe2unspliced	128	KTKYMATTQMEPTDARRAFPCFDEPNLKATFDISLVSDKSLTHLSNMDVKSEENLDGNKK
NcasApe2spliced	219	ETKYMATTQMEPTDARRAFPCFDEPSLKATYAITLISDPTLTHLSNMDVKSENVVD-GKK
NcasApe2unspliced	128	ETKYMATTQMEPTDARRAFPCFDEPSLKATYAITLISDPTLTHLSNMDVKSENVVD-GKK
NcasAap1	128	EVKYMATTQFEATDARRAFPSFDEPKLKSTFDITLISPELTNLSNMDVKTEEIIIN-GKK
CglaApe2spliced	183	ETKYMATTQMEPTDARRAFPCFDEPNLKATFGITLISDPSLTHLSNMDVKNETISE-SKK
CglaApe2unspliced	124	ETKYMATTQMEPTDARRAFPCFDEPNLKATFGITLISDPSLTHLSNMDVKNETISE-SKK
CglaAap1	122	ETKYMATTQMEATDARRAFPCFDEPNLKSTFDVTLISDKHLTQLSNMDVKSETIEG-EKK
Ape2_dist	218	ETKYMATTQMEPTDARRAFPCFDEPNLKASFAITLVSDPSLTHLSNMDVKNEYVKD-GKK
Ape2_prox	224	ETKYMATTQMEPTDARRAFPCFDEPNLKASFAITLVSDPSLTHLSNMDVKNEYVKD-GKK
Ape2unspliced	127	ETKYMATTQMEPTDARRAFPCFDEPNLKASFAITLVSDPSLTHLSNMDVKNEYVKD-GKK
Aap1	122	ETKYMATTQMEATDARRAFPCFDEPNLKATFAVTLVSEFLTHLSNMDVVRNETIKE-GKK
consensus	241	etKYMATTQmEpTDARRAFPCfDEPNlKatfaitLvSdpsLThLSNMDVKE v d gKK

LklApe2spliced	261	LTAFNTPPKMSTYLVAFIVAEELNYVENKDFRIPVRVYATPGDEHQGFADLTAKTLAFF
LklApe2unspliced	183	LTAFNTPPKMSTYLVAFIVAEELNYVENKDFRIPVRVYATPGDEHQGFADLTAKTLAFF
KlacApe2spliced	227	FTYFNTPPKMSTYLVAFIVAELEYVECKDFRIPVRVYATPGSEHLGQYAANLTAKTLSFF
KlacApe2unspliced	184	FTYFNTPPKMSTYLVAFIVAELEYVECKDFRIPVRVYATPGSEHLGQYAANLTAKTLSFF
ZrouApe2spliced	261	VTSFNTPPKMSTYLVAFIVAEELKYVENNDFRIPVRCYATPGYEHGQFAADLTAKTLAFF
ZrouApe2unspliced	189	VTSFNTPPKMSTYLVAFIVAEELKYVENNDFRIPVRCYATPGYEHGQFAADLTAKTLAFF
TdelApe2spliced	244	LTKFNTPPKMSTYLVAFIVAEELKYVENKDFRIPVRVYATPGNEKHGQYAADLTAKTLAFF
TdelApe2unspliced	188	LTKFNTPPKMSTYLVAFIVAEELKYVENKDFRIPVRVYATPGNEKHGQYAADLTAKTLAFF
NcasApe2spliced	278	VTSFNTPPKMSTYLVAFIVADLKYVECKDFRIPVRVYATPGNEKDQGFADLTAKTLNFF
NcasApe2unspliced	187	VTSFNTPPKMSTYLVAFIVADLKYVECKDFRIPVRVYATPGNEKDQGFADLTAKTLNFF
NcasAap1	187	ITKFNTPPLMSTYLVAYIVADLRYVESNEFRLPVRRIYSTPGDEHLGKFAADLSARTLTFF
CglaApe2spliced	242	VTTFNTPPKMSTYLVAFIVAEELNYVENKEFRIPVRVYATPGDEHLGQYAADLTAKTLAFF
CglaApe2unspliced	183	VTTFNTPPKMSTYLVAFIVAEELNYVENKEFRIPVRVYATPGDEHLGQYAADLTAKTLAFF
CglaAap1	181	ITKFNTPPKMSTYLIAFIVAEELKYVESKEFRIPVRIYSTPGDEHLGEFAASLTARTLKFF
Ape2_dist	277	VTLFNTPPKMSTYLVAFIVAEELKYVESKNFRIPVRVYATPGNEKHGQFAADLTAKTLAFF
Ape2_prox	283	VTLFNTPPKMSTYLVAFIVAEELKYVESKNFRIPVRVYATPGNEKHGQFAADLTAKTLAFF
Ape2unspliced	186	VTLFNTPPKMSTYLVAFIVAEELKYVESKNFRIPVRVYATPGNEKHGQFAADLTAKTLAFF
Aap1	181	YTFNTPPKMSTYLVAFIVADLRYVESNNFRIPVRVYSTPGDEKFGQFAANLAARTLRFF
consensus	301	vT FNTPPkMSTYLvAfIVAEELkYVE kdFRiPVRvYaTPG EhhGqfAAdLtAkTLaFF

LklApe2spliced	321	EKA	FGIKYPLPKMDNVAVHEFSAGAMENWGLVTYRVVDLLLDRENSTLERVQ	RVAEV	VQ
LklApe2unsplic	243	EKA	FGIKYPLPKMDNVAVHEFSAGAMENWGLVTYRVVDLLLDRENSTLERVQ	RVAEV	VQ
KlacApe2spliced	287	EKA	FGIEYPLPKMDSVAVHEFSAGAMENWGLVTYRVVDLLLDKKNASLERIK	RVAEV	VQ
KlacApe2unsplic	244	EKA	FGIEYPLPKMDSVAVHEFSAGAMENWGLVTYRVVDLLLDKKNASLERIK	RVAEV	VQ
ZrouApe2spliced	321	EKT	FNIKYPLPKMDNVAVHEFAAGAMENWGLVTYRVVDVLLDKENSTLDRIQ	RVAEV	IQ
ZrouApe2unsplic	249	EKT	FNIKYPLPKMDNVAVHEFAAGAMENWGLVTYRVVDVLLDKENSTLDRIQ	RVAEV	IQ
TdelApe2spliced	304	EKS	FGIKYPLPKMDNVAVHEFSAGAMENWGLVTYRVVDLLLDENSTLDRIQ	RVAEV	VQ
TdelApe2unsplic	248	EKS	FGIKYPLPKMDNVAVHEFSAGAMENWGLVTYRVVDLLLDENSTLDRIQ	RVAEV	VQ
NcasApe2spliced	338	EKT	FGIQYPLPKMDNVAVHEFSAGAMENWGLVTYRVVDVLLDKENSTLDRIE	RVAEV	VQ
NcasApe2unsplic	247	EKT	FGIQYPLPKMDNVAVHEFSAGAMENWGLVTYRVVDVLLDKENSTLDRIE	RVAEV	VQ
NcasAap1	247	EKT	FGIEYPLPKMDMVAVHEFSAGAMENWGLVTYRVADLLLDKENSTLDRIQ	RVAEV	IQ
CglaApe2spliced	302	EKT	FGIKYPLPKMDNVAVHEFSAGAMENWGLVTYRVVDLLLDENSSLDRIQ	RVAEV	VQ
CglaApe2unsplic	243	EKT	FGIKYPLPKMDNVAVHEFSAGAMENWGLVTYRVVDLLLDENSSLDRIQ	RVAEV	VQ
CglaAap1	241	EST	FDIEYPLPKMDMVAVHEFSAGAMENWGLVTYRVVDLLLDKENSTLDRIQ	RVAEV	IQ
Ape2_dist	337	EKT	FGIQYPLPKMDNVAVHEFSAGAMENWGLVTYRVVDLLLDKDNSTLDRIQ	RVAEV	VQ
Ape2_prox	343	EKT	FGIQYPLPKMDNVAVHEFSAGAMENWGLVTYRVVDLLLDKDNSTLDRIQ	RVAEV	VQ
Ape2unspliced	246	EKT	FGIQYPLPKMDNVAVHEFSAGAMENWGLVTYRVVDLLLDKDNSTLDRIQ	RVAEV	VQ
Aap1	241	EDT	FNIEYPLPKMDMVAVHEFSAGAMENWGLVTYRVIDLDDIENSSLDRIQ	RVAEV	IQ
consensus	361	EktFgI	YPLPKMDnVAVHEFSA	GAMENWGLVTYRVvDlLLDkeNstLdRiq	RVAEVvQH

LklApe2spliced	381	ELAHQWFGN	LVTMDWWEGLWLNEG	FATWMSWYSCNEFE	PEWKVWEQYVSDTLQHALALDA
LklApe2unsplic	303	ELAHQWFGN	LVTMDWWEGLWLNEG	FATWMSWYSCNEFE	PEWKVWEQYVSDTLQHALALDA
KlacApe2spliced	347	ELAHQWFGN	LVTMDWWEGLWLNEG	FATWMSWYACNQFQ	PEWKVWEQYVADDLQ
KlacApe2unsplic	304	ELAHQWFGN	LVTMDWWEGLWLNEG	FATWMSWYACNQFQ	PEWKVWEQYVADDLQ
ZrouApe2spliced	381	ELAHQWFGN	LVTMDWWEGLWLNEG	FATWMSWYSCNEFE	PEWKVWEQYVADTLQNALALDS
ZrouApe2unsplic	309	ELAHQWFGN	LVTMDWWEGLWLNEG	FATWMSWYSCNEFE	PEWKVWEQYVADTLQNALALDS
TdelApe2spliced	364	ELAHQWFGN	LVTMDWWEGLWLNEG	FATWMSWYSCNAFQ	PEWKVWEQYVDTLQHALALDS
TdelApe2unsplic	308	ELAHQWFGN	LVTMDWWEGLWLNEG	FATWMSWYSCNAFQ	PEWKVWEQYVDTLQHALALDS
NcasApe2spliced	398	ELAHQWFGN	LVTMDWWEGLWLNEG	FATWMSWYSCNKFEP	EWNVWQEQYVDTLQHALALDS
NcasApe2unsplic	307	ELAHQWFGN	LVTMDWWEGLWLNEG	FATWMSWYSCNKFEP	EWNVWQEQYVDTLQHALALDS
NcasAap1	307	ELAHQWFGN	LVTMEWWEGLWLNEG	FATWMSWYACNDFQ	PDWKVWEQYVSDNLQ
CglaApe2spliced	362	ELAHQWFGN	LVTMDWWEGLWLNEG	FATWMSWYSCNEFQ	PSWNVWQYVDTLQHALSLDA
CglaApe2unsplic	303	ELAHQWFGN	LVTMDWWEGLWLNEG	FATWMSWYSCNEFQ	PSWNVWQYVDTLQHALSLDA
CglaAap1	301	ELAHQWFGN	LVTMDWWEGLWLNEG	FATWMSWYSCNEFQ	PQWNVWQYVADSLQ
Ape2_dist	397	ELAHQWFGN	LVTMDWWEGLWLNEG	FATWMSWYSCNEFQ	PEWKVWEQYVDTLQHALSLDS
Ape2_prox	403	ELAHQWFGN	LVTMDWWEGLWLNEG	FATWMSWYSCNEFQ	PEWKVWEQYVDTLQHALSLDS
Ape2unspliced	306	ELAHQWFGN	LVTMDWWEGLWLNEG	FATWMSWYSCNEFQ	PEWKVWEQYVDTLQHALSLDS
Aap1	301	ELAHQWFGN	LVTMDWWEGLWLNEG	FATWMSWYSCNKFQ	PEWKVWEQYVDTNLQ
consensus	421	ELAHQWFGN	LVTMDWWEGLWLNEG	FATWMSWYsCNeFqPeWkVWeqYVtDtLqHaLaLDS	

LklApe2spliced	441	LRSSHPIEVPV	KRADEINQIFDAISYSKGS	SLLRMI	SKWLGEDVFIKGV	SQYLNKFEYGN
LklApe2unsplic	363	LRSSHPIEVPV	KRADEINQIFDAISYSKGS	SLLRMI	SKWLGEDVFIKGV	SQYLNKFEYGN
KlacApe2spliced	407	LRSSHPIEVPV	KRADEINQIFDHI	SYAKGS	SLLRMI	SQWLGEDVFIKGV
KlacApe2unsplic	364	LRSSHPIEVPV	KRADEINQIFDHI	SYAKGS	SLLRMI	SQWLGEDVFIKGV
ZrouApe2spliced	441	LRSSHPIEVPV	KRADEINQIFDAISYSKGS	SVLRMV	SKWLGEDVFIQGV	SKYLQKFKFSN
ZrouApe2unsplic	369	LRSSHPIEVPV	KRADEINQIFDAISYSKGS	SVLRMV	SKWLGEDVFIQGV	SKYLQKFKFSN
TdelApe2spliced	424	LRSSHPIEVPV	KRADEINQIFDAISYSKGA	SLLRMI	SKWLGEDVFIKGV	SQYLSKFKYGN
TdelApe2unsplic	368	LRSSHPIEVPV	KRADEINQIFDAISYSKGA	SLLRMI	SKWLGEDVFIKGV	SQYLSKFKYGN
NcasApe2spliced	458	LRSSHPVEVPV	KKADEINQIFDAISYSKGA	SLLRMI	SKWLGEDVFIKGV	SQYLTkFKYGN
NcasApe2unsplic	367	LRSSHPVEVPV	KKADEINQIFDAISYSKGA	SLLRMI	SKWLGEDVFIKGV	SQYLTkFKYGN
NcasAap1	367	LRSSHPIEVPV	KNADEINQIFDAISYSKGS	SLLRMI	SKWLGEDVFIKGV	SAYLkFKYGN
CglaApe2spliced	422	LRSSHPIEVPV	KRADEINQIFDAISYSKGA	SLLRMI	SKWLGEDVFIKGV	SNYLNNFKYGN
CglaApe2unsplic	363	LRSSHPIEVPV	KRADEINQIFDAISYSKGA	SLLRMI	SKWLGEDVFIKGV	SNYLNNFKYGN
CglaAap1	361	LRSSHPIEVPV	KNADEINQIFDAISYSKGS	SLLRMI	SKWLGEDFI	KGVAEYLNKFKYGN
Ape2_dist	457	LRSSHPIEVPV	KKADEINQIFDAISYSKGA	SLLRMI	SKWLGEETFI	KGV
Ape2_prox	463	LRSSHPIEVPV	KKADEINQIFDAISYSKGA	SLLRMI	SKWLGEETFI	KGV
Ape2unspliced	366	LRSSHPIEVPV	KKADEINQIFDAISYSKGA	SLLRMI	SKWLGEETFI	KGV
Aap1	361	LRSSHPIEVPV	NNADEINQIFDAISYSKGS	SLLRMI	SKWLGEETFI	KGV
consensus	481	LRSSHPiEVPVkrADEINQIFDaISYsKG	SLLRMiSkWLGE	dvFikGVsqYLnkFkygN		

LklApe2spliced	501	AKTEDLWDALSSASGKDVRKVMNVWTKQVGFPVSVKEDG-GKITFTQNRYLTTGDVKPD
LklApe2unsplic	423	AKTEDLWDALSSASGKDVRKVMNVWTKQVGFPVSVKEDG-GKITFTQNRYLTTGDVKPD
KlacApe2spliced	467	AKTEDLWDALSEASGKDVRNVMDIWTKKVGFPVSVTEDGH-KITFKQNRYLNTADVKE
KlacApe2unsplic	424	AKTEDLWDALSEASGKDVRNVMDIWTKKVGFPVSVTEDGH-KITFKQNRYLNTADVKE
ZrouApe2spliced	501	ARTGDLWDSLSSEASGKDVRKVMNDIWTGKVGPVISVKEDGK-KITFTQNRYLSTGDLKPE
ZrouApe2unsplic	429	ARTGDLWDSLSSEASGKDVRKVMNDIWTGKVGPVISVKEDGK-KITFTQNRYLSTGDLKPE
TdelApe2spliced	484	AKTEDLWESLSQASGKDVVKVMDIWTKKVGFPVISVKEEGN-KVTFTQNRYLSTGDKKE
TdelApe2unsplic	428	AKTEDLWESLSQASGKDVVKVMDIWTKKVGFPVISVKEEGN-KVTFTQNRYLSTGDKKE
NcasApe2spliced	518	AKTEDLWEALSASGKDVSAVMNIWTKKVGPVITVKEDGN-KITLTQNRYLSTGDKAE
NcasApe2unsplic	427	AKTEDLWEALSASGKDVSAVMNIWTKKVGPVITVKEDGN-KITLTQNRYLSTGDKAE
NcasAap1	427	AKTEDLWDALSAASGKDVPMVMNIWTKKVGPVITVKEDGN-NITFTQNRYLSTGDKKE
CglaApe2spliced	482	AKTDDLWDALAKASGKDVRGMNIWTKKVGPVISIEENGSEIQFTQNRYLTTGDVKPE
CglaApe2unsplic	423	AKTDDLWDALAKASGKDVRGMNIWTKKVGPVISIEENGSEIQFTQNRYLTTGDVKPE
CglaAap1	421	AKTEDLWDSLSSEASGKDVTKVMNIWTKQIGYPIVTVNEEGE-KISFTQHRFLSTGDKPE
Ape2_dist	517	AKTEDLWDALADASGKDVRSMNIWTKKVGPVISVSEDGNGKITFRQNRYLSTADVKE
Ape2_prox	523	AKTEDLWDALADASGKDVRSMNIWTKKVGPVISVSEDGNGKITFRQNRYLSTADVKE
Ape2unspliced	426	AKTEDLWDALADASGKDVRSMNIWTKKVGPVISVSEDGNGKITFRQNRYLSTADVKE
Aap1	421	AKTGDLWDALADASGKDVCSVMNIWTKRVGFPVLSVKEHKN-KITLTQHRYLSTGDKKE
consensus	541	AkTeDLWdaLseASGKDVR VMniWtkkvGfPvisvkEdgn kitftQnRyLsTgDvKpe

LklApe2spliced	560	EDNTLYPVFLALKTKDGVDSSSLVLDERSKTVELKDSEFFKVNAEQAGIFITSYSDERWDK
LklApe2unsplic	482	EDNTLYPVFLALKTKDGVDSSSLVLDERSKTVELKDSEFFKVNAEQAGIFITSYSDERWDK
KlacApe2spliced	526	EDKTLYPVFLSLKTN SGVDHSLTLDERELTVTVEDVDFIKTNANQAGIYVTSYSDRWTT
KlacApe2unsplic	483	EDKTLYPVFLSLKTN SGVDHSLTLDERELTVTVEDVDFIKTNANQAGIYVTSYSDRWTT
ZrouApe2spliced	560	EDETLYPVFLTLATNQVDSSSLVLDQRSKSIELQDP SFFKTNSAQSGIYITSYSDERWAK
ZrouApe2unsplic	488	EDETLYPVFLTLATNQVDSSSLVLDQRSKSIELQDP SFFKTNSAQSGIYITSYSDERWAK
TdelApe2spliced	543	EDETLYPVFLALATKDGVDNSLVLNERAKTVELKDP SFFKANGAQAGIYITSYSDERWAK
TdelApe2unsplic	487	EDETLYPVFLALATKDGVDNSLVLNERAKTVELKDP SFFKANGAQAGIYITSYSDERWAK
NcasApe2spliced	577	EDETLYPVFLAIKSKDGVDNSLTLNEKTKTVELKDSEFFKLNSEQSGIYITSYTDERWAK
NcasApe2unsplic	486	EDETLYPVFLAIKSKDGVDNSLTLNEKTKTVELKDSEFFKLNSEQSGIYITSYTDERWAK
NcasAap1	486	EDKTLYPVFLALKTSNGVDSTNINLERTKTIELADAKFFKVNADQAGAYITSYSDERWTK
CglaApe2spliced	541	EDETLYPVFLALKTKSGVDNSLVLSESKAVTIDDS SFYKVNTDQSGIFITAYPEDRWEK
CglaApe2unsplic	482	EDETLYPVFLALKTKSGVDNSLVLSESKAVTIDDS SFYKVNTDQSGIFITAYPEDRWEK
CglaAap1	480	EDETLYPVFLAIKTKDGIDNNINLDEREKTIELKDNEFFKINGNAGVYVTCYSDERWAK
Ape2_dist	577	EDKTLYPVFLALKTKNGVDSSVVLSESKTIELEDPTFFKVNSEQSGIYITSYTDERWAK
Ape2_prox	583	EDKTLYPVFLALKTKNGVDSSVVLSESKTIELEDPTFFKVNSEQSGIYITSYTDERWAK
Ape2unspliced	486	EDKTLYPVFLALKTKNGVDSSVVLSESKTIELEDPTFFKVNSEQSGIYITSYTDERWAK
Aap1	480	EDTTIYPILLALKDSTGIDNTLVLNEKSATFELKNEEFFKINGDQSGIFITSYSDERWAK
consensus	601	EDeTlYPvfLalktk GvD slvL ersktvel d sFfKvN eQsGiyiTsYsdeRWak

LklApe2spliced	620	LGQQADKLSVEDRTGLVADAKALSASGYTSTTNFLKLISKWN-NESSFVWVEQIVNSLFS
LklApe2unsplic	542	LGQQADKLSVEDRTGLVADAKALSASGYTSTTNFLKLISKWN-NESSFVWVEQIVNSLFS
KlacApe2spliced	586	LSKQSDLLTVEDRTGLVADCKTSLSGYTSTKNFLQLISQWK-NEDSFVWVEQMINSLS
KlacApe2unsplic	543	LSKQSDLLTVEDRTGLVADCKTSLSGYTSTKNFLQLISQWK-NEDSFVWVEQMINSLS
ZrouApe2spliced	620	FGQQANLLSVEDRVGLVADSKALSASGYTSTKNFLNLVSQWD-KEQSFVWVEQILASLSS
ZrouApe2unsplic	548	FGQQANLLSVEDRVGLVADSKALSASGYTSTKNFLNLVSQWD-KEQSFVWVEQILASLSS
TdelApe2spliced	603	LGGQADKLTVEDRTGLVADVKTLSASGYTSTTNFLKLVSQWE-NEKSFVWVEQIINSISS
TdelApe2unsplic	547	LGGQADKLTVEDRTGLVADVKTLSASGYTSTTNFLKLVSQWE-NEKSFVWVEQIINSISS
NcasApe2spliced	637	FGKQSELLSVEDRIGLVADAKSLASSGYTSTTNFLNLVANWN-KEESFVWLEQIILNSIGS
NcasApe2unsplic	546	FGKQSELLSVEDRIGLVADAKSLASSGYTSTTNFLNLVANWN-KEESFVWLEQIILNSIGS
NcasAap1	546	FSEQANLLSVEDRTGLVADVKNLSASGYTSTVNFLNLIAKWRQNEQSFVWVRQIINSISS
CglaApe2spliced	601	FGKQSDLLSVEDRTGLVADAKALSSGYINTTSFFKLISNWK-DEKSFVWVDQIIISLAS
CglaApe2unsplic	542	FGKQSDLLSVEDRTGLVADAKALSSGYINTTSFFKLISNWK-DEKSFVWVDQIIISLAS
CglaAap1	540	LSKQAEFLSVEDRTGLVADVKSALSSGYTSTTNFLNLISNWS-NEESFVWVTQMINSISA
Ape2_dist	637	LGQQADLLSVEDRVGLVADVKTLSASGYTSTTNFLNLVSQWN-NEKSFVWVDQIINSISS
Ape2_prox	643	LGQQADLLSVEDRVGLVADVKTLSASGYTSTTNFLNLVSQWN-NEKSFVWVDQIINSISS
Ape2unspliced	546	LGQQADLLSVEDRVGLVADVKTLSASGYTSTTNFLNLVSQWN-NEKSFVWVDQIINSISS
Aap1	540	LSKQANLLSVEDRVGLVADAKALSASGYTSTTNFLNLISNWK-NEDSFVWVEQIINSLSA
consensus	661	lg QadlLsVEDRtGLVAD KtLsaSGYtsttnFlnLisqW nE SFVWveQiInSlss

LklApe2spliced	679	LKTTWMEFEPEEVNDALNEFTKELVADKAHSMGWEFNSSDSFATQRLKVMFGAACAADT
LklApe2unspliced	601	LKTTWMEFEPEEVNDALNEFTKELVADKAHSMGWEFNSSDSFATQRLKVMFGAACAADT
KlacApe2spliced	645	LKAAWAFEPKETLEALDEFTRQLVSEKTHSLGWEFSENESYASQRLKVMFSSSAAAKDP
KlacApe2unspliced	602	LKAAWAFEPKETLEALDEFTRQLVSEKTHSLGWEFSENESYASQRLKVMFSSSAAAKDP
ZrouApe2spliced	679	LKAAWTFEPQETKEALNNFTRKLVSKAHNLGWEFSSSDSFATQRLKVAMFGAAAGARDT
ZrouApe2unspliced	607	LKAAWTFEPQETKEALNNFTRKLVSKAHNLGWEFSSSDSFATQRLKVAMFGAAAGARDT
TdelApe2spliced	662	LKSTWIFEPQEVKDALDTFTRKLVSRAHSLGWDFSGSDSFAEQRLKVTMFGAAAARDE
TdelApe2unspliced	606	LKSTWIFEPQEVKDALDTFTRKLVSRAHSLGWDFSGSDSFAEQRLKVTMFGAAAARDE
NcasApe2spliced	696	LKATWAFEPPEEVRDALNTFTRGLVSKRAHELGYQFSNDSFATQRMKVLFGAACSSRD
NcasApe2unspliced	605	LKATWAFEPPEEVRDALNTFTRGLVSKRAHELGYQFSNDSFATQRMKVLFGAACSSRD
NcasAap1	606	LEGAWIFEDDEVKDALTGFIHNLVSDKVHELGWDFSSSEDSYSVQRLKVF LF GAACSSKDV
CglaApe2spliced	660	LKAAWLFESPEVKDALEAFSRNLVADKAKTLGWEFKESDSFATQRLKVLF GAACAARDE
CglaApe2unspliced	601	LKAAWLFESPEVKDALEAFSRNLVADKAKTLGWEFKESDSFATQRLKVLF GAACAARDE
CglaAap1	599	LESAWVFEDES IKTGLKNYVTKLSIEKAHKLGWEFSSNEDSYSTQKLKVL LFDVACSNDD
Ape2_dist	696	MKSTWLFEPKETQDALDNFTKQLISGMTHHLGWEFKSSDSFSTQRLKVTMFGAACAARDA
Ape2_prox	702	MKSTWLFEPKETQDALDNFTKQLISGMTHHLGWEFKSSDSFSTQRLKVTMFGAACAARDA
Ape2unspliced	605	MKSTWLFEPKETQDALDNFTKQLISGMTHHLGWEFKSSDSFSTQRLKVTMFGAACAARDA
Aap1	599	LKSTWVFEPEDI LNALDKFTLDLVLNKLSELGWNIGEDDSFAIQRLKVT LFSAACTSGNE
consensus	721	lk tWmFEp evkdaLd ftr Lvs kah lGwefs sdSfatQrlKV mFGaacaard

LklApe2spliced	739	RTETAALMFKEYIAGDKKAIPALIKPIVFNAVGRNGGVENYEKIYQIYLNPTSTDEKLA
LklApe2unspliced	661	RTETAALMFKEYIAGDKKAIPALIKPIVFNAVGRNGGVENYEKIYQIYLNPTSTDEKLA
KlacApe2spliced	705	VVVKAALKMFKEYTSGDSNAIPPLIKSSSVFGTVARDGNAKNYEKLF AIYKNPSSSDEKLS
KlacApe2unspliced	662	VVVKAALKMFKEYTSGDSNAIPPLIKSSSVFGTVARDGNAKNYEKLF AIYKNPSSSDEKLS
ZrouApe2spliced	739	EVEKSALDMFTKYAAGDKHAIPALIKPIVFSAAARAGGV DNYEKILHIYKNPTSTDEKLA
ZrouApe2unspliced	667	EVEKSALDMFTKYAAGDKHAIPALIKPIVFSAAARAGGV DNYEKILHIYKNPTSTDEKLA
TdelApe2spliced	722	KVEKAALMFDDKYIAGDKKAIPALIKPTVFNTVARAGGLENYEKIFNIYNNPISNDEKLA
TdelApe2unspliced	666	KVEKAALMFDDKYIAGDKKAIPALIKPTVFNTVARAGGLENYEKIFNIYNNPISNDEKLA
NcasApe2spliced	756	IVEKAALDMFAKYVEGDKKAIPALIKPIVFNAVARAGKPEDYERLFNIYKNP INNDEKLA
NcasApe2unspliced	665	IVEKAALDMFAKYVEGDKKAIPALIKPIVFNAVARAGKPEDYERLFNIYKNP INNDEKLA
NcasAap1	666	KVESAAKMFDEYMKGNKEAIPALIKPDVFS TVATMGGK DNYEKIFNIFKNPISNDEKMA
CglaApe2spliced	720	VVEKAALDMFEKYVSGDKKAIPALIKPSVFN AVARKGGK DNYEKIFNIYKNPVSTDEKLA
CglaApe2unspliced	661	VVEKAALDMFEKYVSGDKKAIPALIKPSVFN AVARKGGK DNYEKIFNIYKNPVSTDEKLA
CglaAap1	659	KAQSAALDMFNKYISGDKKAIPALIKPSVFN TVASKGGEESYQKLYNIYKNPMATDEKLA
Ape2_dist	756	DVEKAALKMFTDYCSGNKEAIPALIKPIVFNTVARV GGAENYEKVYKIYLDPI SNDEKLA
Ape2_prox	762	DVEKAALKMFTDYCSGNKEAIPALIKPIVFNTVARV GGAENYEKVYKIYLDPI SNDEKLA
Ape2unspliced	665	DVEKAALKMFTDYCSGNKEAIPALIKPIVFNTVARV GGAENYEKVYKIYLDPI SNDEKLA
Aap1	659	KMQSI AVEMFE EYANGNKQAI PALFKAVVFN TVARLGGENYEKIFNIYQNPVSSEKII
consensus	781	vekaAleMFekYi GdckAIPaLiKpiVFntvar Gg enYekifnIyknPistdEKla

LklApe2spliced	799	ALRTLGRFSDPALIERTLGYL LDG SVLTQDIYIPMQGLRTHKEGVNALWTWLQNNWDEIV
LklApe2unspliced	721	ALRTLGRFSDPALIERTLGYL LDG SVLTQDIYIPMQGLRTHKEGVNALWTWLQNNWDEIV
KlacApe2spliced	765	ALRCLGRFEDPALMKRTLGYLFDGTVLNQDIYIPMGMRGHKEGIKTLWAWTKENWDALH
KlacApe2unspliced	722	ALRCLGRFEDPALMKRTLGYLFDGTVLNQDIYIPMGMRGHKEGIKTLWAWTKENWDALH
ZrouApe2spliced	799	ALRTLGRFEDAKLLERTLGYLTDGTVLNQDIYIPMQGMRT HKQGIETLWSWLQTNWEDIS
ZrouApe2unspliced	727	ALRTLGRFEDAKLLERTLGYLTDGTVLNQDIYIPMQGMRT HKQGIETLWSWLQTNWEDIS
TdelApe2spliced	782	ALRTLGRFTDAKLLDRTL SYLFDGTVLNQDIYIPMQGMRAHKEGIEALWSWVQTNWDEVV
TdelApe2unspliced	726	ALRTLGRFTDAKLLDRTL SYLFDGTVLNQDIYIPMQGMRAHKEGIEALWSWVQTNWDEVV
NcasApe2spliced	816	ALRTLGRFKDSKLLERTLSYLLDGTVLNQDIYIPMQGMRSHKEGIEALWGWLQKNWDEVVS
NcasApe2unspliced	725	ALRTLGRFKDSKLLERTLSYLLDGTVLNQDIYIPMQGMRSHKEGIEALWGWLQKNWDEVVS
NcasAap1	726	ALKTLGLFKPEL IQRTLGYLLDGTILNQDFYTPMVGLRNHKEGIETMWKWLQKNWEDIV
CglaApe2spliced	780	ALRTLGRFKEDALLDRTLGYLFDGTVLNQDIYIPMQGMRAHKEGVTALWKWLQENWDEIA
CglaApe2unspliced	721	ALRTLGRFKEDALLDRTLGYLFDGTVLNQDIYIPMQGMRAHKEGVTALWKWLQENWDEIA
CglaAap1	719	ALRALGKFKE DKLITKTL SYLLDGTVLSQDFYIPMQGLRTHKEGILAMW EFLKQNWTEII
Ape2_dist	816	ALRSLGRFKEPKLLERTLGYLFDGTVLNQDIYIPMQGMRAHQEGVEALWNWVKKNWDELIV
Ape2_prox	822	ALRSLGRFKEPKLLERTLGYLFDGTVLNQDIYIPMQGMRAHQEGVEALWNWVKKNWDELIV
Ape2unspliced	725	ALRSLGRFKEPKLLERTLGYLFDGTVLNQDIYIPMQGMRAHQEGVEALWNWVKKNWDELIV
Aap1	719	ALRALGRFEDKELLERTLSYLLDGTVLNQDFYIPMQGIRVHKKGIERLWAWMQEHWDEIA
consensus	841	ALrtLGrFkd kLlerTLgYLFdGtvLnQDiYiPMqGmRgHkeGiealW wlq nWdeiv

LkluApe2spliced	859	DRLPAELSMLGSVVTITTSGFASLEAIKEIKQFFSTRSTKGFDQSLAQSLDTITSKAQWV
LkluApe2unsplic	781	DRLPAELSMLGSVVTITTSGFASLEAIKEIKQFFSTRSTKGFDQSLAQSLDTITSKAQWV
KlacApe2spliced	825	KKFPPSLTMLGSILTVATSGFTSRQAIDEIEDFFKDKSTKGFDQSLAQTLDTITSKANWV
KlacApe2unsplic	782	KKFPPSLTMLGSILTVATSGFTSRQAIDEIEDFFKDKSTKGFDQSLAQTLDTITSKANWV
ZrouApe2spliced	859	KRLPPGMSMLGSVVIISTSAFTSLEVIDQIKKFFSDKSTKGFDQSLAQSLDTIVSKAKWV
ZrouApe2unsplic	787	KRLPPGMSMLGSVVIISTSAFTSLEVIDQIKKFFSDKSTKGFDQSLAQSLDTIVSKAKWV
TdelApe2spliced	842	RRLPPGLSMLGSVVVIGTSGFTSFEAISDIKKFFDKSTKGFDQSLAQSLDTITSKAQWV
TdelApe2unsplic	786	RRLPPGLSMLGSVVVIGTSGFTSFEAISDIKKFFDKSTKGFDQSLAQSLDTITSKAQWV
NcasApe2spliced	876	KRLPPGLSMLGSVVVICTSGFTSFKSIDEIKKFFNTKSTKGFDQSLAQSLDTITSKAQWL
NcasApe2unsplic	825	KRLPPGLSMLGSVVVICTSGFTSFKSIDEIKKFFNTKSTKGFDQSLAQSLDTITSKAQWL
NcasAap1	786	KRIQPGSPVLGHILTVGITGFTSM EAYKNI EKFFSDKDTKGYDQSLARVLDTVKSQAQWV
CglaApe2spliced	840	RRLPPGLSMLGSVVAISTSGFSSLEAVDEIKTFFNTKSTKGFDQSLAQSLDTITSKAQWV
CglaApe2unsplic	781	RRLPPGLSMLGSVVAISTSGFSSLEAVDEIKTFFNTKSTKGFDQSLAQSLDTITSKAQWV
CglaAap1	779	KKLQPGSPVLGGVLT VSVSSLASVEKID DVKQFFSDKPTKGFDQTLAQALDTATSKSKWV
Ape2_dist	876	KRLPPGLSMLGSVVT LGTSGFTSMQKIDEIKKFFATKSTKGFDQSLAQSLDTITSKAQWV
Ape2_prox	882	KRLPPGLSMLGSVVT LGTSGFTSMQKIDEIKKFFATKSTKGFDQSLAQSLDTITSKAQWV
Ape2unspliced	785	KRLPPGLSMLGSVVT LGTSGFTSMQKIDEIKKFFATKSTKGFDQSLAQSLDTITSKAQWV
Aap1	779	KRLQPGSPVLGGVLT LGLTNFTSFEALEKISAFYSRKVTKGFDQTLAQALDTIRSKAQWV
consensus	901	krppglsmLGsvvtiatsgftSleaideikkFf tksTKGfDQsLAqsLDTitSKaqWv

LkluApe2spliced	919	NRDREVVSQY LKDN GYYKN*
LkluApe2unsplic	841	NRDREVVSQY LKDN GYYKN*
KlacApe2spliced	885	DRDREVVKF LKEH NYK*--
KlacApe2unsplic	842	DRDREVVKF LKEH NYK*--
ZrouApe2spliced	919	NRDREVVKDY LKEH GYF*--
ZrouApe2unsplic	847	NRDREVVKDY LKEH GYF*--
TdelApe2spliced	902	NRDRDVVNKY LKNNG FYK*--
TdelApe2unsplic	846	NRDRDVVNKY LKNNG FYK*--
NcasApe2spliced	936	NRDRDLVKDY LKKN GYSK*--
NcasApe2unsplic	845	NRDRDLVKDY LKKN GYSK*--
NcasAap1	846	ARDRAVVRKY LQE CK*----
CglaApe2spliced	900	DRDRESISKY LSDNG YM*--
CglaApe2unsplic	841	DRDRESISKY LSDNG YM*--
CglaAap1	839	ARDGEVVRKY LEDNG YFIN*
Ape2_dist	936	NRDRDVVNKY LKENG YY*--
Ape2_prox	942	NRDRDVVNKY LKENG YY*--
Ape2unspliced	845	NRDRDVVNKY LKENG YY*--
Aap1	839	SRDREIVATY LREHEY DQ*--
consensus	961	nRDrevv kyLkengyy