

Supplementary Information

Cdc28–Cln3 phosphorylation of Sla1 regulates actin patch dynamics in different modes of fungal growth

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Figure S1

MSSIIYIGVYK**ALYDYAAQAEEELNIKQNDLLYLLEKSDIDDWWKVKR**VVATGEE
 IVDEPSGLVPSTYIEEAPVIKTATALYDYDKQTEEELSFNENDKFNVFDLNDPDW
 ILVGD**LAK**E**KFGFVPSNYIQ**LDSTAEPAQHQQQQPQQVFQPPPQQQQAIPQQQTQ
 IPINNFPPPP**THKDRTPDFPAPP**AHRDR**SPEHPPPTPEKDYPRMFEQEPR**SLGSR
 YDRQPEGREEEEDEAPPMP**SRPTGS**NIVAPEPVVGRSNTYEQ**ENVEHSEHSYD**
 GEFFT**WYIDEVDGRKKRAIKLSIGQGLVI**IKPNTTNP**KKLRMRSSSSLDN**QWRIK
 DLITFNNEK**KHVFL**E**FKNPAASLE**LHAGSKDVAEAIMAILGDLKGAEAAHGLREV
 AKASKA**SANERNRKIG**RLLYDFEVQGDDELDCKEGDEVYIIDQ**KKSKD**WWMVENI
 ATRRQGVVPSTYIEIIISTSNLDKLT**DGPLRRKSTKSKGRVVETKDKR**SSHRTRE
 ERDRIREKDRAQRDKAPTSQTEQDKSMPNFHRVRTWIDSSGTFK**VEAEFLGC**VEG
 KIH**LHKTNGVKIAVAADKLS**VEDLEYVERVTGTSLEQYKEQVMK**QQA**KRAKSKSK
 SGATAT**PSSTNETKYASSATAA**INDIAPPKPTRPQTTTQVS**NGAPLYDWF**DFFL
 ECGVDIGNCQRYTLNFEREQMDENILEDIS**PSLLRTLGLREGDI**IRVMKYLD**AKF**
 DR**KKTPEAPQ**ONGGLFIDKNGNLK**NNSSSTEISKVSADALP**SPVKTQ**VTSFT**PVN
 ESTQ**NNKIEDDAWAMKPAAR**SEDLLK**PSQPQTPQYT**GALSDLVNIK**PVGTSN**
 ENKAKTEQIPVEPSAPALQ**PMKTSNTAATSSIPPQ**PGV**TPQRTGTLVPVQKTGG**
 LVPVQ**RTGAGLVPVQTGGYLPAQPTGFVPI**TAQ**PTGFIP**IQATGILQ**PQLT**FGIV
 PLQ**TGTSTFNANNKTAPPRPDTAPPPITTFGQQPTFQPAFVPLQ**TGVIT**MPQ**TTF
 GGQ**SQQLPTQITGGAPPQTSFNQ**PALV**PTQRTGGQITGGFVPQSNFGKQITGGFM**
 DTNTLSFGQQITGNAQQQPP**ST**SFGQQITGGLPAT**SFGQQITGGFPQTSFGQQM**
 TGGAPQ**TSFGQHITGGNMPNTSFGQ**PFSQQATSN**PF**PQMANQ**FTQQQQYQQQQPV**
 MNQ**FQQQPQQQQPFYNQFQSQPNLNQMTNMFQNTSIS**SPATFN**QQIPTTTFGQQ**
 PQ**FEGFGSQPLQSQPTGMGFGNAPLQSQPTGKRANLQAATPDNPF**GF

Figure S1. MS mapping of phosphorylation sites on Sla1. Amino acids covered by the mapping are highlighted in bold. CDK consensus sites are shaded in grey and putative Prk1 recognition motifs are underlined. Asterisks (*): phosphorylated Thr or Ser within CDK sites; Black dots (•): phosphorylated Thr within Prk1 recognition motifs; Open circles (o): Other phosphorylated Thr and Ser residues.

Figure S2

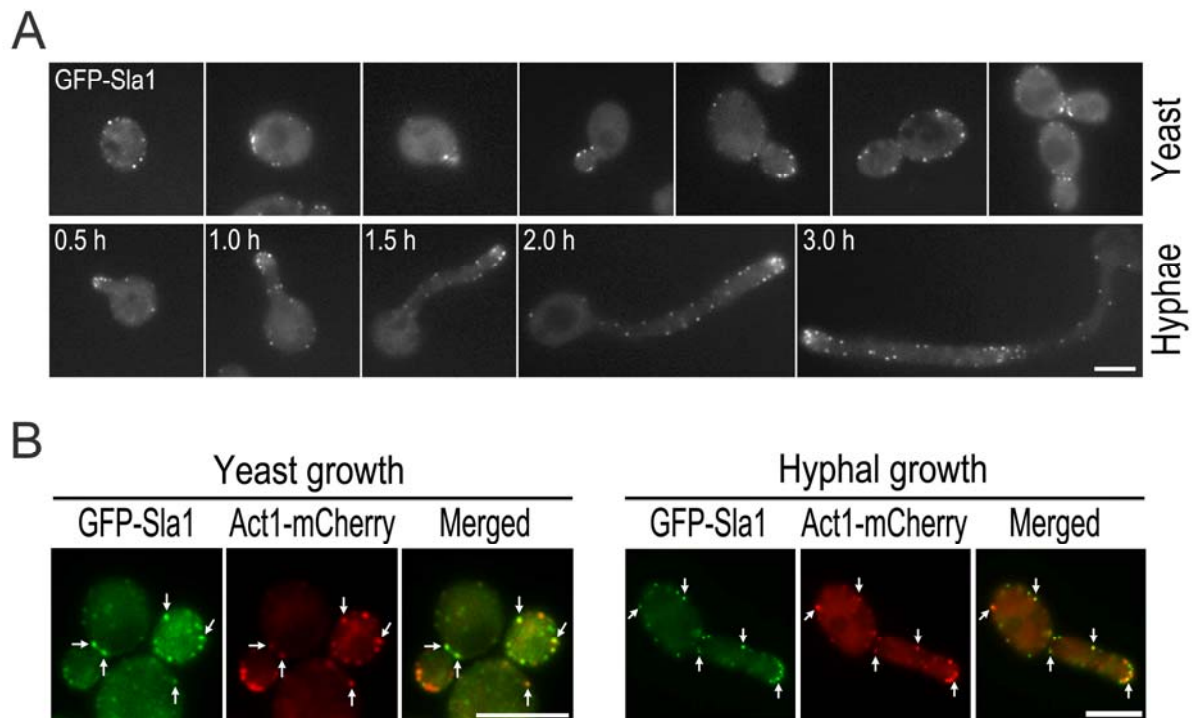


Figure S2. Subcellular localization of Sla1 during yeast and hyphal growth. **(A)** Visualization of GFP-Sla1 in yeast and hyphal cells of GZY707 (*sla1* Δ /*P_{MET3}-GFP-SLA1*). **(B)** Visualization of GFP-Sla1 and Act1-mCherry in yeast and hyphal cells of GZY752 (*sla1* Δ /*P_{MET3}-GFP-SLA1 ACT/ACT1-mCherry*). Cells were either grown in GMM at 30°C, or induced for hyphal formation by incubating with 20% FBS at 37°C for several hours. Samples were taken at the indicated time points and cells were fixed with Stopmix before microscopic visualization. Note that Act1-mCherry is not fully functional in vivo and results in abnormal hyphal morphology.

Figure S3

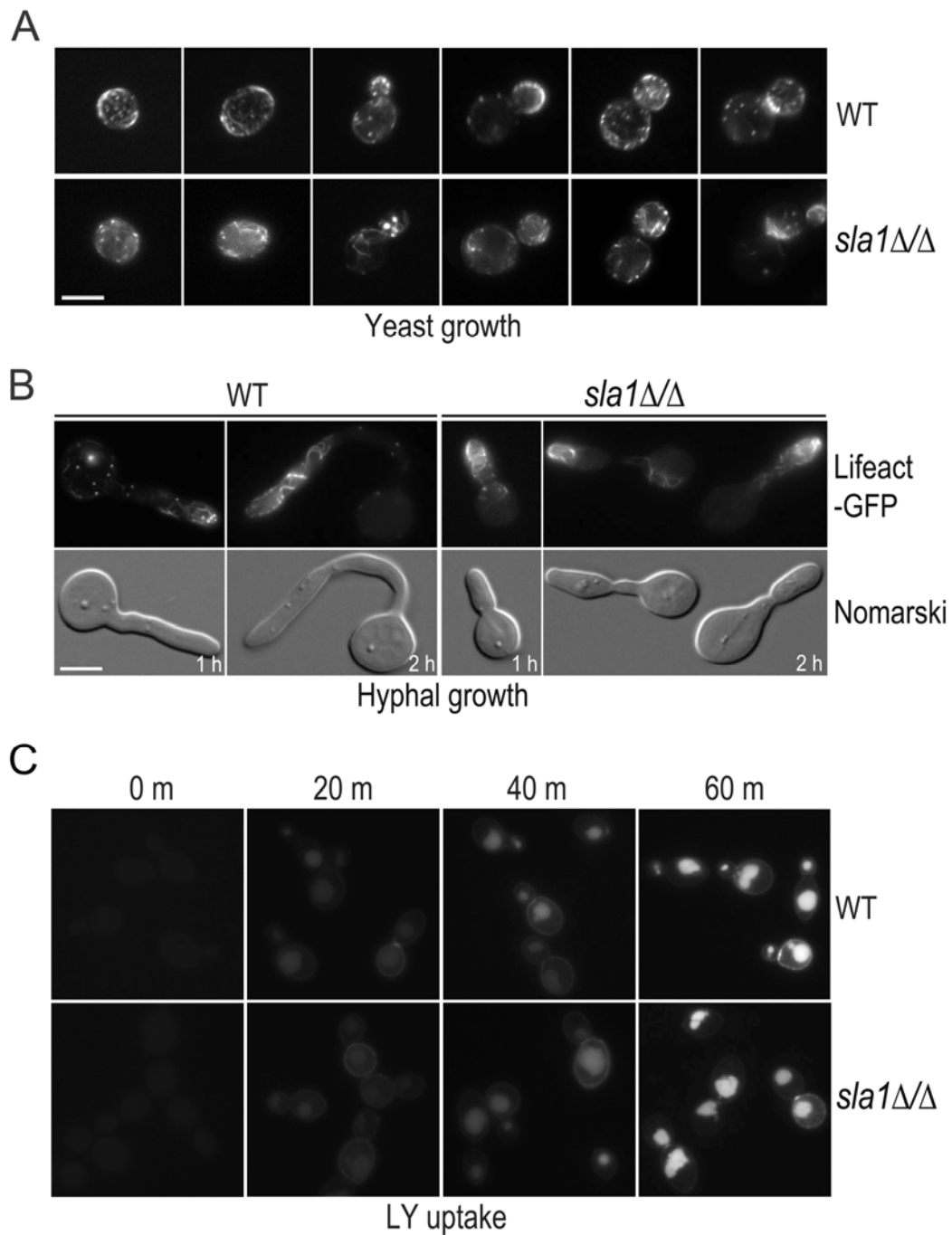


Figure S3. Actin cytoskeleton organization and LY uptake in *sla1Δ/Δ* cells. (**A** and **B**) Direct visualization of actin cytoskeleton in the *sla1Δ/Δ* cells during yeast (A) and hyphal growth (B). WT (GZY730) and *sla1Δ/Δ* (GZY733) cells expressing Lifeact-GFP were either grown in GMM at 30°C or induced for hyphal growth with 20% FBS at 37°C for 1 to 2 h. Cells were fixed with Stopmix for microscopy. (**C**) LY uptake of the *sla1Δ/Δ* cells. WT (BWP17) and *sla1Δ/Δ* (GZY602) cells were grown in GMM at 30°C and incubated with LY for 20, 40, and 60 min, respectively. Cells were washed with PBS and examined for LY uptake.

Figure S4

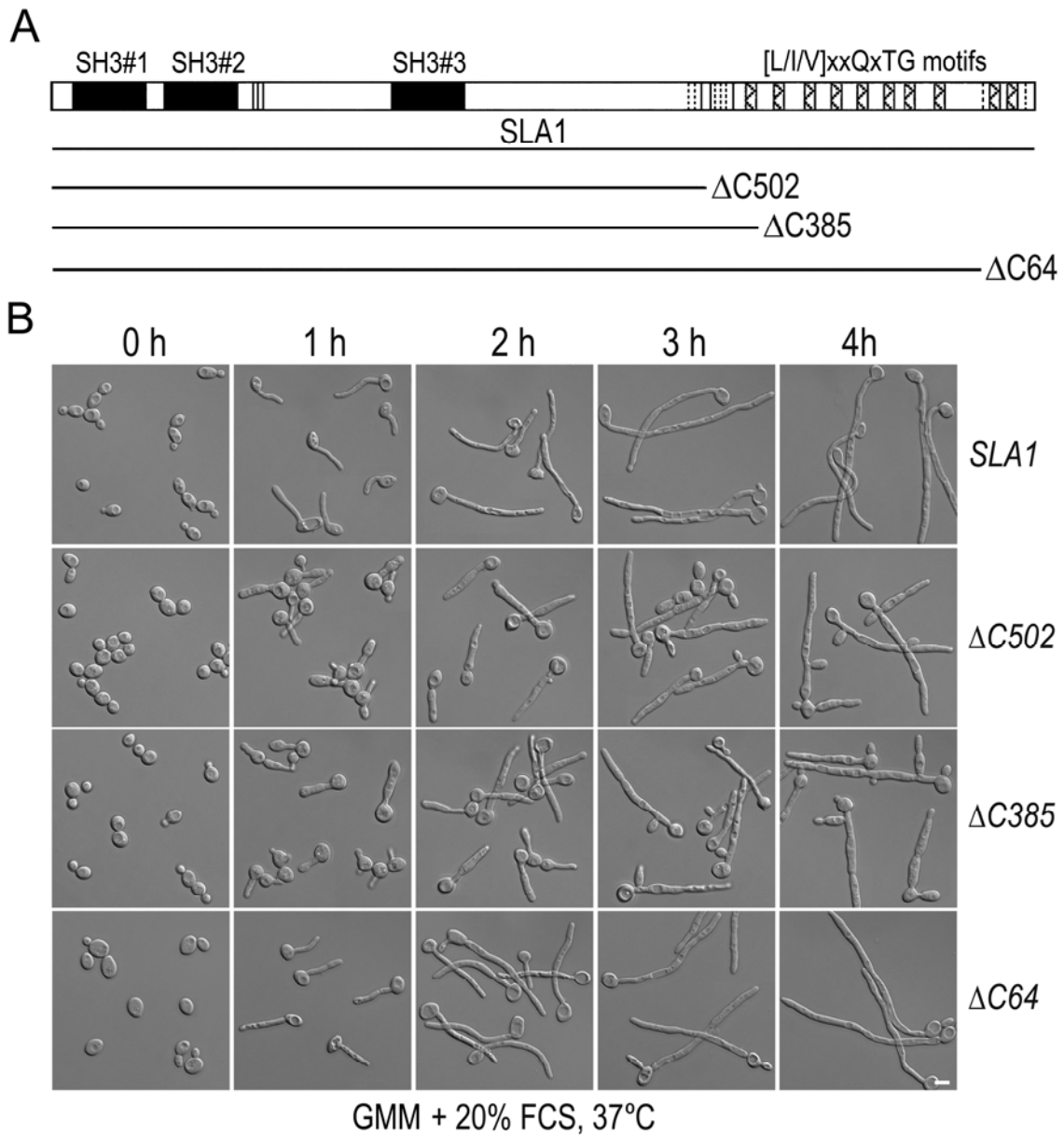


Figure S4. Defective hyphal formation of *sla1* C-terminal truncated mutants. **(A)** Schematic diagram to indicate the regions absent in different *sla1* mutants. **(B)** Hyphal morphology of the *sla1* C-terminal truncated mutants. Cells of *SLA1*-WT (GZY652), *sla1*- $\Delta C502$ (GZY625), *sla1*- $\Delta C385$ (GZY629), and *sla1*- $\Delta C64$ (GZY639) were grown in YPD at 30°C and induced for hyphal growth by incubation with 20% of FBS at 37°C. Samples were taken at 1-h intervals upon hyphal induction for morphological examination.

- Movie 01.** Live cell imaging of Lifeact-GFP in BWP17 (GZY730) yeast cells.
- Movie 02.** Live cell imaging of Lifeact-GFP in *sla1* Δ/Δ (GZY733) yeast cells.
- Movie 03.** Live cell imaging of Lifeact-GFP in BWP17 (GZY730) hyphal cells.
- Movie 04.** Live cell imaging of Lifeact-GFP in *sla1* Δ/Δ (GZY733) hyphal cells.

References

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- Zheng, X., Wang, Y.M., and Wang, Y. (2004). Hgc1, a novel hypha-specific G1 cyclin-related protein regulates *Candida albicans* hyphal morphogenesis. *EMBO J* *23*, 1845-1856.

Table S1. Yeast strains used in this study

Strain	Relevant genotype*
BWP17	<i>ura3::imm434/ura3::imm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG</i> (Wilson et al., 1999)
IS82	<i>ccn1Δ::URA3-FLP/ccn1Δ::ARG4</i> (Sinha et al., 2007)
IS89	<i>cdc28^{F85G}-ARG4/cdc28Δ::HIS1</i> (Sinha et al., 2007)
WYZ12	<i>hgc1Δ::ARG4/hgc1Δ::HIS1</i> (Zheng et al., 2004)
GZY559	<i>CLN3/CLN3-Myc-URA3</i>
GZY584	<i>SLA1/SLA1-HA-ARG4</i>
GZY585	<i>CLN3/CLN3-Myc-URA3 SLA1/SLA1-HA-ARG4</i>
GZY601	<i>SLA1/sla1Δ::FRT</i>
GZY602	<i>sla1Δ::FRT/sla1Δ::ARG4</i>
GZY603	<i>cln3Δ::FRT/P_{MET3}-Myc-CLN3-ARG4</i>
GZY622	<i>cln3Δ::FRT/P_{MET3}-Myc-CLN3-ARG4 SLA1/SLA1-HA-URA3</i>
GZY624	<i>hgc1Δ::ARG4/hgc1Δ::HIS1 SLA1/SLA1-HA-URA3</i>
GZY625	<i>sla1Δ::FRT/sla1Δ::ARG4 sla1-ΔC502-HA-URA3</i>
GZY629	<i>sla1Δ::FRT/sla1Δ::ARG4 sla1-ΔC385-HA-URA3</i>
GZY631	<i>SLA1/P_{GAL1}-HA-SLA1-URA3</i>
GZY639	<i>sla1Δ::FRT/sla1Δ::ARG4 sla1-ΔC64-HA-URA3</i>
GZY641	<i>cdc28^{F85G}-ARG4/cdc28Δ::HIS1 CLN3/CLN3-Myc-URA3</i>
GZY652	<i>sla1Δ::FRT/sla1Δ::ARG4 SLA1-WT-HA-URA3</i>
GZY658	<i>sla1Δ::FRT/sla1Δ::ARG4 sla1-13A-HA-URA3</i>
GZY670	<i>sla1Δ::FRT/sla1Δ::ARG4 sla1-13E-HA-URA3</i>
GZY707	<i>sla1Δ::FRT/P_{MET3}-GFP-SLA1-URA3</i>
GZY718	<i>sla1Δ::FRT/sla1Δ::ARG4 SLA1-WT-HA-URA3 PAN1/PAN1-Myc-HIS1</i>
GZY719	<i>sla1Δ::FRT/sla1Δ::ARG4 sla1-13A-HA-URA3 PAN1/PAN1-Myc-HIS1</i>
GZY720	<i>sla1Δ::FRT/sla1Δ::ARG4 sla1-13E-HA-URA3 PAN1/PAN1-Myc-HIS1</i>
GZY727	<i>sla1Δ::FRT/sla1Δ::ARG4 sla1-23E-HA-URA3</i>
GZY730	<i>TEF1/tef1::P_{TEF1}-LifeAct-GFP-HIS1</i>
GZY733	<i>sla1Δ::URA3-FLP/sla1Δ::ARG TEF1/tef1::P_{TEF1}-Lifeact-GFP-HIS1</i>
GZY739	<i>sla1Δ::FRT/sla1Δ::ARG4 SLA1-WT-HA-URA3 TEF1/tef1:: P_{TEF1}-LifeAct-GFP-HIS1</i>
GZY740	<i>sla1Δ::FRT/sla1Δ::ARG4 sla1-13A-HA-URA3 TEF1/tef1:: P_{TEF1}-LifeAct-GFP-HIS1</i>
GZY741	<i>sla1Δ::FRT/sla1Δ::ARG4 sla1-13E-HA-URA3 TEF1/tef1:: P_{TEF1}-LifeAct-GFP-HIS1</i>

GZY742 *ccn1Δ::FRT/ccn1Δ::ARG4*
GZY744 *ccn1Δ::FRT/ccn1Δ::ARG4 SLA1/SLA1-HA-URA3*
GZY745 *prk1Δ::ARG4/prk1Δ::HIS1 SLA1/sla1Δ::FRT*
GZY746 *MET3/MET3::P_{MET3}-ARN1-GFP-URA3*
GZY747 *sla1Δ::FRT/sla1Δ::ARG4 MET3/MET3::P_{MET3}-ARN1-GFP-URA3*
GZY750 *prk1Δ::ARG4/prk1Δ::HIS1 sla1Δ::FRT/SLA1-HA-URA3*
GZY752 *SLA1/P_{MET3}-GFP-SLA1-HIS1 ACT1/ACT1-mCherry-TADH1-URA3*
GZY761 *sla1Δ::FRT/sla1Δ::ARG4 SLA1-WT-HA-URA3 MET3/MET3::P_{MET3}-ARN1-GFP-HIS1*
GZY762 *sla1Δ::FRT/sla1Δ::ARG4 sla1-13A-HA-URA3 MET3/MET3::P_{MET3}-ARN1-GFP-HIS1*
GZY763 *sla1Δ::FRT/sla1Δ::ARG4 sla1-13E-HA-URA3 MET3/MET3::P_{MET3}-ARN1-GFP-HIS1*

* Strains used in this study are of derivatives of BWP17.

Table S2. Plasmid constructs used in this study

Construct	Description
CIP10U	Yeast integration vector generated by removing the <i>RP10</i> gene from CIP10 (Murad <i>et al.</i> , 2000).
pYGS829	CLN3c-Myc-UTR/CIP10U; DNA fragment encoding Cln3 (268-465 aa) was cloned in frame with a C-terminal 6xMyc epitope (followed by <i>UTR</i> , the 3' untranslated region of <i>CaGAL4</i>) into CIP10U. The plasmid was linearized by <i>BamHI</i> within <i>CLN3</i> for integration to generate <i>CLN3-Myc-URA3</i> .
pYGS837	GST-CLN3; DNA fragment encoding Cln3 (1-465 aa) was cloned into pGEX-4T-1.
pYGS859	SLA1c-HA-UTR/CIP10U; DNA fragment encoding Sla1 (658-1257 aa) was cloned in frame with a C-terminal 2xHA epitope (followed by <i>UTR</i>) into CIP10U. The plasmid was linearized by <i>XcmI</i> within <i>SLA1</i> for integration to generate <i>SLA1-HA-URA3</i> .
pYGS861	CLN3ΔURA3-FLP/pBKS; <i>CLN3</i> promoter region (-556 to -1 bp) and terminator region (1399 to 1773 bp) were cloned to flank the <i>CaURA3</i> flipper in pBKS vector. The knock-out cassette was released by <i>KpnI</i> and <i>SacII</i> for transformation to generate <i>cln3Δ::FRT</i> .
pYGS868	SLA1ΔURA3-FLP/pBKS; <i>SLA1</i> promoter region (-509 to -1 bp) and terminator region (3775 to 4240 bp) were cloned to flank the <i>CaURA3</i> flipper in pBKS vector. The knock-out cassette was released by <i>KpnI</i> and <i>SacII</i> for transformation to generate <i>sla1Δ::URA3-FLP</i> and <i>sla1Δ::FRT</i> .
pYGS870	SLA1ΔARG4/pBKS; <i>CaURA3</i> flipper in pYGS868 was replaced with <i>CaARG4</i> . The knock-out cassette was released by <i>KpnI</i> and <i>SacII</i> for transformation to generate <i>sla1Δ::ARG4</i> .
pYGS877	CLN3ΔARG4-P _{MET3} -Myc/pTEZ; <i>CLN3</i> promoter region (-444 to -1 bp) and coding region (1 to 500 bp) were cloned to flank <i>ARG4-P_{MET3}-Myc</i> (<i>CaARG4</i> followed by 6xMyc epitope under <i>CaMET3</i> promoter control) in pTEZ vector. The knock-in cassette was released by <i>KpnI</i> and <i>SacII</i> for transformation to generate <i>P_{MET3}-Myc-CLN3-ARG4</i> .
pYGS893	SLA1c-HA-UTR/CIP10A; <i>CaURA3</i> in pYGS859 was replaced with <i>CaARG4</i> . The plasmid was linearized by <i>XcmI</i> within <i>SLA1</i> for integration to generate <i>SLA1-HA-ARG4</i> .
pYGS894	SLA1ΔC502-HA-UTR/CIP10U; DNA fragment encoding Sla1 (457-755 aa) was cloned in frame with a C-terminal 2xHA epitope (followed by <i>UTR</i>) into CIP10U. The plasmid was linearized by <i>SaII</i> within <i>SLA1</i> for integration to generate <i>SLA1ΔC502-HA-URA3</i> .
pYGS895	P _{GAL1} -HA-SLA1n/CIP10U; DNA fragment encoding Sla1 (1-304 aa) was cloned in frame with an N-terminal 2xHA epitope (under <i>CaGAL1</i> promoter control) into CIP10U. The plasmid was linearized by <i>BsaBI</i> within <i>SLA1</i> for integration to generate <i>P_{GAL1}-HA-SLA1-URA3</i> .
pYGS896	SLA1ΔC385-HA-UTR/CIP10U; DNA fragment encoding Sla1 (457-872 aa) was cloned in frame with a C-terminal 2xHA epitope (followed by <i>UTR</i>) into CIP10U. The plasmid was linearized by <i>SaII</i> within <i>SLA1</i> for integration to generate <i>SLA1ΔC64-HA-URA3</i> .
pYGS913	SLA1ΔC64-HA-UTR/CIP10U; DNA fragment encoding Sla1 (658-1193 aa) was cloned in frame with a C-terminal 2xHA epitope (followed by <i>UTR</i>) into CIP10U. The plasmid was linearized by <i>XcmI</i> within <i>SLA1</i> for integration to generate <i>SLA1ΔC385-HA-URA3</i> .
pYGS920	Pro-SLA1-WT-HA-UTR/CIP10U; DNA fragment containing <i>SLA1</i> promoter and coding region (-1000 to 3771 bp) was cloned in frame with a C-terminal 2xHA epitope (followed by <i>UTR</i>) into CIP10U. The plasmid was linearized by <i>PmeI</i> (generated by mutagenesis at promoter region -550 bp) for integration to generate <i>SLA1-WT-HA-URA3</i> .

Table S3. List of GST-Cln3 affinity purified proteins identified by MS

Protein ID	Matched Peptides (Bold)										
URA2	1	MAQLSVPIPT	PMESTGDVLM	TLETQDGIAL	QGYSFGAAPK	AAGEVVFQTD	MVGPESITD	PSYEGQILVI	TYPLVGNVYV	PDRELLDEDY	EPALPKYFES
	101	NKIHIAGLV	AHYTEEYSHW	LAKSSSLGKWL	QEQQIPAIYG	VDTRSLTKRL	REKSTLGLRL	AIQNSDYKSE	EIISQSKSNP	QNKWKFVFPV	EFDDPNVKNL
	201	VAKVSTDKPI	LITTPKNTNEN	IKLGMKNGKI	RLLAVDVGMK	YQIRSCFVRK	GEVLLVVPWD	YDFTFTEYDG	LFISNMGPCD	AVMMDKTVERL	QKILKEGKTP
	301	VFGICLGHQL	LARATGASTL	KLKFGNRGHN	IPCTSTISGR	CYITSONHG Y	AVDTATLSNG	WKELFVNAND	GSNNEGIYHS	KPFFSVQFHP	ESTPGPRDTE
	401	FLFDVFIKSV	VDNFQSGGVY	KQVEFPGGKL	AENRAAHPKV	DVKKVLVLGS	GGLSIGQAGE	FDYSGSQAIK	ALKEEGEYTV	LINPNIAITQI	TSKGLADKVV
	501	FLPVTPEFVR	KVIKHERPDG	IYCTFGGQTA	LSVGIALKDE	FEGLGVKVLG	TQIDTVITTE	DRELFASAMA	EINEKCARSE	ACNTVKEADV	AANAIGYPLI
	601	VRAAYALGGL	GSGFADNEEE	LVALCNKAKA	TSPQVLVERS	MKGWKEVEYE	VVRDAFDNCI	TVCNMENFDP	LGIHTGDSIV	VAPSQTLSDS	DYNMLRRTAV
	701	NVIRHLGVV	ECNIQYALNP	FSKEYCILEV	NARLSRSSAL	ASKATGYPLA	YTAAKLGLNI	PLNEIKNSVT	KSTSACFPEV	LDYCVVKIPR	WDLKCFTRVS
	801	ALLSSSMKSV	PMSMAIGRTF	EEAIQKAIRS	TDYHNLGFNK	TAAALMSIDID	QELQTPSDQR	LFAIANALSD	GYSVDKVKFL	TNIDKWFNLK	LDGLIKFNGK
	901	IASYGAKEDV	GEMSLRQAKQ	LGFEEDRQIAK	FLGSNEVAIR	RLRKDAGIIP	FVKQIDTVAA	EFPFAFTNYLY	VYNNADSSDV	KPDDNGVIVL	GSGVVRIGSS
	1001	VEFDWCVA	IRTLRENNVK	TVMINYNPET	VSTDYDEADR	LYFEPINLER	VLDIYDLQES	SGVIISMGGQ	TSNNIALPLY	RQNVKILGTS	PEMIDSAENR
	1101	YKFSRMLDRI	GVDQPAWKE	TSIDEAEDFA	EKVGYPVLVR	PSYVLSGAM	NTVYSKDDLA	SYLGGQAVDVS	PDYVPIVTKY	TENAKEIEMD	AVAKDGKMM
	1201	HVVSHEVENA	GVHSGDATLI	VPPQDLDPET	VRRIVEATAK	IGKALDITGP	YNIQPIAKDN	DIKVICENVR	ASRSPFPVSK	VVGVDLIEMA	TKAMLDLPIV
	1301	PYPGERLPED	YCAVKVPEFS	FSRLAGADPV	LGVEMASTGE	VATFGKNKYE	AYLKSLLISTG	FKLPKKNILF	SIGSFKEQEK	LLPSIAKLHE	LGKIFPATAG
	1401	TADFLIKEHGI	PVHYLEVLSK	DEDQKSEYNL	SQHLANNLID	LYVNLPSANR	FRRPASYMSK	GYESRRMAVD	YAVPLVTNVK	NAKLLVEAIA	RNISLEVSNR
	1501	DAFDNHSHTAI	LPGLINITSF	ATSFDDFEQT	TKESLAAGFT	FNAPLPHQTA	GASVTDYRSL	IDAIDAVGAS	AYTDSVSIAS	ASETNSQSVS	DAADNAGSLD
	1601	LPFNTFSGAT	VNSALTAQFSS	WPNNPKPIITD	AKTDTLDSVLT	LLASLYNRSI	HLTGVSCKED	LDLTKMAKEK	LTQVTCDAV	HLVFTSKDEL	DPYLPNKSFL
	1701	QYLYWENLKD	VDCFSIGVLP	YLIAKASGTE	IAPGMGKIEA	VPDLLTAVKA	GKLTIGDIVS	KPHDNPAKIF	NLKPQDAQV	LDLDFEATVE	PVYPEFSKLR
	1801	LRGAVERVNSF	HNETVVLDSG	VLSQIALGKN	EVVPRSRFGS	TAGIPESPLR	GKRVVSPFSSD	MRRPRLAPET	PEPQPAIFEK	LVGSDVSOPI	AGSLGEIAAL
	1901	SDYIRHNSVP	LRNNIISVKD	ITRSDLLHSLF	TVAQEMRLAV	TRHGVDLQLQ	GNRVLATMFYE	PSTRITSTSPD	AAMRQVIFXK	VADVHGSSSV	KSKLGTQDIT
	2001	RTLSCYSDAI	VLRHPSSESA	DIAAKYSPVP	IINAGNGTKE	HPTQALLDLF	TIREELGTVN	GITVTTFMGDL	XYGRPVHSLC	HLLRHYQVRV	QLVAPKELQI
	2101	PAEIRQLQID	NNMLIAESE	LTKELILARS	VLVYCTRVQEE	RFADKEQYQR	LKDTYIVDNK	ILSNAKQHM	VMHPLRPTNE	IREEVPDPQR	AAYFRQMRHG
2201	LFIRMALLAM	VIGVDF									
FAS1	1	MSTHRPFLQT	HGSIEHTLLV	PNDLFFNYSQ	LKDFEIKTLP	EPTGEGAGDD	EPSSPAELYG	KFIGFISNAQ	FPQIVELSLK	DFESRFLDNN	NDNIHSAFAV
	101	LLDDETYPTT	IAKVKENIVK	NYKAVKNSIN	KVESNLLYHC	KHDAKVAIFV	GGQNTDDYF	EELRELYTLY	QGLIEBLLVS	IAEKLNLQHP	SFDKIYQGL
	201	NILSLWKHPE	TPDQDYLLS	VPVSCFVICV	IQLCHYITTC	KVGLLTPGFE	RNSLKWSTGH	SQGLVTAVTI	AASDSDSFL	KNSLTAVSLL	LFIGSRCLST
	301	YPRTSLPPTM	QSDLSLNGEG	RPSPLMSVRD	LSIKQVEKFI	BQTNLSHVRK	KHIAISLING	ARNLVLGGP	ESLYGPNLNL	RNQGAPMLGD	QSRVFPSEK
	401	LKCSNRPLPI	FAPFHSLLLA	DATLLELDV	KEHGLSPEGL	KIPVYDTPDG	SDQALKKEPI	IDRVVVLITE	LPVHWEAATN	HKATMLIDFG	PGGVSGLGLV
	501	THRNEKGTGA	RILLAGLTD	NPIDDEYGFK	HEIFQTSADK	AIKWAPDMLK	ELRPLTVKNS	EKGIYVTKFE	QOLLRAPLIM	VAGMPTPTVN	TDIVSASLNA
	601	GHIELLAGGG	YFSPVMTRTA	IDDIVSRIRK	GYGLGINLIY	VNPFMLQWGI	PLIKDLREKK	YPIQSLTIGA	GVPSIEVATE	YIEDLGLTHL	GLKPGSVDAI
	701	SQVIAIAKHA	PTFPVILQWT	GGRGGGHSF	EDFHQPIIQM	YSKIRCSNI	VLVAGSGFGS	DEBTTYPLSG	YNWSEKFNYP	KPFDGVLFGS	RVMTSKBSHT
	801	LSAAKKLIVE	KQCVDPQWE	QTYKPKAGGI	ITVRSMEGEP	IHKIATRGMV	FVLELDDTIF	NLPKNKLLDA	LNKRKHDIK	MPNDGFQKPV	FGKANVGVCD
	901	LQEMTYKEVA	NRLVELMYVK	KSHRWIDVSL	RNMVGDPLRR	VEERFTSSAG	TVSLQLQNFQ	LNPEPQFAD	FFVFKPQAGK	QLISEEDCDY	FLMALARPGQ
	1001	KVPFPVPLVD	RFEPFFPKKD	SLWQSEDLSE	VVDEVDVCTR	LLHGVFVASQY	KTVDEPIGD	ILNSIHGHIH	ARLILKEEYAG	DESKIPVVEY	FGGKIPASVS
	1101	ATSVNVTDGN	QVVEYIDSEL	PNKQEWLDDL	AGTELNLWQA	FISTDRIVQG	SKHVSNPJHD	ILTPAKHSKV	TIDKTKTKLT	AFENIKGDLL	PVVEIELVKE
	1201	NTIQLSLIEH	RTADANFVAL	PFLYKYNPAD	GFAPILEIME	DRNERIKEFY	WKLWFGSSVP	YNSNDINVEKA	ILGDEITISS	QTISEFTHAI	GAKDCAFVDR
	1301	PGKATLAPMD	FAIVIGWKAI	IKAIFFPKSVD	GDLLKLVHLS	NGYKMITGAA	PLKKGVDVST	KAEIKAVLNQ	PSGKLVBEVG	TIYREGKPEV	EVTSQFLYRG
	1401	EYNDYCNLTFQ	FKTETPVQVA	FKSAKDLAVL	RSKENFHEK	DVQFDVLTRG	CESTYKFKSA	NVYSSIKTGT	QVLELLEPTK	VIYQGSVDVE	ACTSYGNVPT
	1501	DYLSRNGKTI	EESVIFENAI	PLSSGEEELS	KAPGTNEPYA	IVSGDYNPIH	VSRVFAAYAK	LPGTITHGMY	SSASIRALVE	EWAANNVAAR	VRAFKCDVFG
	1601	MVLPNDTLTQ	TMEHVGMING	RKLIKVETRN	VEDELPLVIG	EAEIEPTTTF	YVFTGQSSQE	QMGMELELYNS	SEVARVEWDK	ADRHVFNMYG	FSDILDIQNN
	1701	PNELTILHFG	KAGRAIRDNY	IGMMFFETIGE	DGALKSEKIF	KDIDETTTYSY	TVFSPPTGLS	ATQFTQPALT	LMEKAYVEDI	KSRGLPLPSDI	MPAGHSIYBN
	1801	SALSSLANVW	PESLVDVVF	YRGMTMQAVV	PRDELGRSNY	GMVAVNPSSV	SATFDDSSALR	FVVDEVANKT	KWLELVVNYN	VENQYQVAAG	DLRALDTLTN
	1901	VLNVLKLNKI	DIVKLQEQMS	IEKVKEHLYE	IVDEVAAKSL	AKQPIDDLER	GFAVIPLKGI	SVPFHSSYLM	SGVKPFPORFL	CKKIKPKSSVK	PQDLIGKIYIP
	2001	NLTAKPFELT	KEYQSVYDL	TKSEKIKSIL	DNWEQYE						
	KEM1	1	MNSILHTCTH	SNDNTITRSL	DDQMYAAIFN	YIEHLFQIIK	PQKTFYMAID	GVAPRAKMNQ	QRARRFRATY	EAEINLKKAI	ENGEIPEKED
101		TFEMANTLNN	LKYFIHKKIT	EDSSWANIEI	ILSGHEVPGE	GEHRIMEYIR	SIRSQDDYNP	NLRHCYGLD	ADLIMLGLVT	HDPHFALLRE	EVTFGPQRKV
201		GPKDLHQKQF	YLLHLALLRE	YLSLEFQIEI	NQNLNFEYDFD	RILDDPILIM	YVIGNDFLPN	LPDLFINKGA	PFLILAAAFKQ	TLLESDDGYIN	ENKGINLVLV
301		NIYIKILSKF	ELENFEKHEV	DVEWPNKLLD	DISISGEKRR	QRIGKLLILK	EQKLLVGFIK	PWLMEWASQP	INELLNLDQO	GKLPDLHLNK	DVEKNLEFPI
401		KEFAIEAGFL	IHSQSNNDTY	EAKLDIDGIS	PTSESEEBHE	RITLBRKTIK	QYQSANLIES	EBVLNETKEV	YSEKFSQWKN	DYVQPKLHFS	IDTEBEGGDL
501		IEMTKHYEIG	LQWVLYYYIR	GCPSWNWYIR	YHYAPRISDI	SLGLEELLNE	KTDLKFELSH	PFKPFQOLMA	VLVARSKMLN	PYVTRPLMSD	EKSPINFPY
601		HEVDIDMNGK	TASNEAVVLL	DFVDEKLEIE	ALKPIESKLT	PEEKQRNSYV	HAIKFHLNQP	IDHVFSSPLP	GFPHDLHEDQ	CYEBEFKLPK	IENLKI GFIK
701		GAKTGKDLA	GFPTLSTIFP	TSELALNEVK	IFNFPSSRES	MILNVEDVWS	DLTVAQFAQS	FVNLKLVYSKW	VFLRECRVVK	YVSEENKFP	IKTNTGLKKV
801		VTNELSVEDK	KSFRSEVSNL	KVTWDKFKGV	KLGEINALVY	VKPVNHLIRN	KHGAIVKTYV	KDVEVYPLQL	PKLEIRNNDKQ	RYLTRPPLPI	DOQFPIDLSQV
901		VFLGDMAYGS	PAKIVGYNED	KTKLGVKIFK	IQSTAEPNIG	KKRILTBEKNE	IKVYPSFEVA	KTLRLNPLLL	SKLITSQFMVQ	SDSSGKGVNIG	LELKFPESKRQ
1001		KVLGYTRKSS	NGKFWFESPL	AINLINTYKT	GFAPLFXKLL	NNVSGSNFTK	IVYSSISLEEL	KEIRSWLKEV	KSELIPVMSLE	SESFKTFSYQ	ATEQVMSNRYL
1101		SMNQIPIPTK	DIKGVPREAI	LNANESYQLL	SQDRFELGDR	IIVYQDFGKV	SILSKGTVAS	ILTVGSKTSL	GVIPDQPLLS	NNMNGKLNLS	NRGLIIDSSL
1201		VLNLTNCFQV	YHSHASKNRK	KLTDDEKIAK	LKAIIEAKNQ	KQQQKVEQKQ	QKGANELLSL	LLKXKSDMNST	TTNSTDGDC	KLTKTEKDYD	IKTEKDYD
1301		NNGNEDERVD	PNAIKQIYGH	IYSNVMNQGN	VRPPPPPTG	PGHQPPFPY	MP1PPGAPM	HPGIYIPVVG	NPLPPSFYQQ	YPPNGQVFN	SQPPPPPPPP
1401	PSQQQQPVA	ESTSDEKSKN	DNKHVNWGRG	RGGRGRGRGY	RGRGRGRGRG	GNKSSHQNQ	PKDKVKQES				
SLA1	1	MSSIIYGVYK	ALYDYAAQAE	EELNIKQNDL	LYLLEKSDID	DWVKVKKRVV	ATGEEIVDEP	SGLVPSTYIE	EAPVIKTATA	LYDYDKQTEE	ELSPNENDKF
	101	NVFDLNDPDW	ILVGDLAKEK	FGFVPSNIYQ	LDSTAEPAQH	QQQQQQQVQF	PPPQQQAIP	QQQTQIPINN	FPFPPHTKDR	TPDFPAPPAP	RDRSPEHPPP
	201	TPEKDYPRMF	EQEPRSLGSR	YDRQPEGREE	EDEEAAPPMP	SRPTGNSNIVA	PEPVVGRSNT	YEQBEENVEHS	EHSYDGEFFT	WYIDEVDGRK	KRAIKLSIGQ
	301	GLVVIKPNNT	NPKKLRMRSS	SSLDNQWRIK	DLITFNNEKK	HVFLFKPNPA	ASLELHAGSK	DVAEAIMAIL	GDLKGAEAAR	GLREVAKASK	ASANERNRNI
	401	GRLLYDFEVO	GDELDCKEKG	DEVYIIDQKK	SKDWMVVENI	ATRRQGVNPS	TYIEIISTSN	LDKLTGDLPL	RKSTKSKGRV	VETKDKRSSH	HRTREERDRI
	501	REKDKRAQRK	APTSQTEQDK	SMPNPHRVRT	WIDSSGTFVK	EAEFLGCVBG	KIHLHKTNGV	KIAVAADKLS	VEDLEVERVY	TGTSLELYQKE	QVMAQQAKRA
	601	KSKSKSGATA	TPSSSTNETKY	ASSATAAIND	IAPPKPTRPQ	TTTQVSNNGA	LVYDFWDFPL	ECQVDIGNCQ	RYTLNFEREQ	MDENILEDIS	PSLLRRTLGLR
	701	EGDIIRVMKY	LDAKFDKRKT	PEAPQQNGGL	FIDKNGNLKN	NSSSTIEISKV	SADALPSPVK	TQVTSFTPVN	VEATQNNKIE	DDAWAMKPA	RSSDELKPS
	801	POPQTPQYTG	ALSDLVNIKP	VGTSNENKAK	TEQIPVEPSA	PALQPKMKTN	TAATSSIPPP	GGVTPQRTG	TLVPEVQKGG	LVPVQRTGAG	LVPVQRTGGL
	901	PAQPTGFVPI	TAQPTGFIP	QATGILQPLQ	TFGIVPLQTG	TSTFNANNKT	APPRPDATAP	PITTFGQOFT	FQPAFVPLQT	GVITMPQTF	GGQSQQLPTQ
	1001	ITGGAPQTS	FNQPALVPTQ	RTGGQITGGF	VQSNFNGKQI	TGGFMDTNTL	SFGQQTIGNA	QQQPPSTSF	QQQITGGLPA	TSFGQOITGG	FPQTSFGQQM
	1101	TGGAPQTSFG	KHITGGMNPN	TSFGQPFSSQ	ATSNPPQMA	NQFTQQQQQY	QQQVPMNQFQ	QQPQQQQQPF	YNPQSQPNL	NQMTNMFQNT	SISSPATFNQ
1201	QIPTTTFGQQ	PQFEGFGSQP	LQSQPTGMGF	GNAPLQSQPT	GKRANLQAAT	FDNPPFGF					
TIF46	1	MSDNTTSNQS	STGDSKSTPG	AVPSSTDGSS	SAPIGNSVNS	VDQTSVSTDK	QHGNNQVQPS	SGAYSQGNYN	ANYQYGGYNN	NYNNNYNNNN	NNPNYYHKN
	101	QYNKNYTGNG	SGGSGGRQNN	YNNANQNNQN	QRNNKMKQY	NQKMMHHHHH	NOQQPQQOYV	NYPYNTAAAA	ASQMYGYMNP	GYPQYVGLPL	QYGGIPATPG
	201	QYYPQVAVSP	VVPTVQFQOI	STPPTPKIRL	TKDKGKPVLD	DEKRRKTASS	TPVASFQPAR	ATTVSSSEKDK	TPSSSATPAT	ENKPAIGASIA	EEFKKTRIRER
	301	AAAAAASAAK	GKETKEETKE	ETTATETKKE	TEETPIAKES	SSTVDQPSVV	PQESHKDIV	ETPKPEVETV	STKNDLELPA	DETKELVSSA	EETNDTAVEK
	401	PKVEEKPEVE	NDKVESQIEL	QSPSVEGDSE	SIVENEDBEE	STISEKGEPO	TETETETETQ	TEPEPESEPT	PTANAPEFTI	SQFLERLKIA	TPIDDILATK
	501	YPETIQGVDS	SKQISGKKYR	YDPQLIQFR	VDISYTTDPT	FKAHLESLDI	HPNAMKRSQS	TRDASSRGLL	PNKPTGGLPA	RFNPGGGKGG	GQFDGGGRQS
	601	RSGSRKGGGR	GASSRDKSTR	KGTPSKRGRG	GGDRSEMRER	GGAGAAGAGG	AGGENDGNQO	GDGKPVVEVK	PLEKSNARKE	PKSRMQAKRE	TKVABDGTIL
	701	LEPEDIKTKT	KSLLNKLTL	MFTAISDEII	ALTNSQKHEK	DAATIKQIIS	LTPAKACDEP	HWSEMYAKLC	AKMCTSVNSD	ITDESITLTKD	GTHASGVGLA
	801	RRLLNATCQK	EYEGKWTDKL	FTNPDGSSLE	PEMMSDEYYA	MAAAAKRRGL	LVKFIGHLYN	LNMLNDHVIV	VCLMDQTKNT	VDESDDSLNE	LTLQLQITVGP
	901	KLDSNERTRT	MLKIVFDYIE	KVLEGVKLT	RKFLMLDLQ	DLREAKVWSL	KGDAGKPTIE	EIHRDABIKK	MEBERAKNEK	KRKHQQLGGG	VGGGSDSRSN
	1001	SSRGGSNWNN	NNNNNNNNNN	NQSSNGPFMK	KSPSPMTQRV	GSSRSPTST	FQNSDLQRTD	SKRSEPSQSN	IFAALEGGDD	DEDE	

SSA1	<p>1 MSKAVGIDLG TTYSCVAHFA NDRVEIAND QGNRTTSPFV APTDTERLIG DAANKQAAMN PANTVFDADR LIGRKFDDHE VQGDIKHPPF KVVDKASKPM 101 IQVEYKGETK TFSPEEISSM ILGKMKETAE GFLGTTVKDA VVTVPAYFND SQRQATKDAG TIAGLNVMRI INEPTAAATA YGLDCKSEAE KNVLIFDLGG 201 GTFDVYLLSI EDGIFEVKAT AGDTHLGGED FNRLNVNFFI QBFKRKNKRD ISTNQALRR LRTACERAKR TLSSSAQTSI EIDSLYEGID FYTSTRARF 301 EELCADLFRS TLEFVDKVLS DAKIDKSKVD EIVLVGGSTR IPKVQKLVSD YFNKGEPNRS INPDEAVAYG AAVQAALSG DTSSTKQDLL LLDVAPLSLG 401 IETAGGIMTK LIPRNSTIPT KKSETFSTYA DNQPGVLQV FEGERAQTKD NLLGKGFELS GIPPAPRGVP QIEVTFPIDA NGILNVSALE KGTGKTQKIT 501 ITNDKGRLSK EIEKMWSEA EKFKEEDEKE ASRVQAKNQL ESYAYSJKNT LGEEQFKSKL DASEIEEVTK AADETIAWLW SNQTATQEEF ADQKQKLESEK 601 ANBIMTKAYQ AGATPSGAAG AAPGFPFGA APEPSNDGPT VEEVD</p>
SSB1	<p>1 MADGVFQGA I GIDLGTYS VVATYDSAVEI IANEQGNRVT PSFVAPTSEE RLIIGDAAKNQ AALNPKNTVF DAKRLIGRAF DDESVDKDIK SWPFKVVESN 101 GQPLIEVEYL DETKTFSPQE ISSMVLTKMK EIAEAKIGKK VEKAVVTVPA YFNDAQRQAT KDAGAIAGLN VLRIINEPTA AAAYAGLGG KSEKERHVLI 201 FDLGGGTFDV SLLNITGGVF TVKATAGDTH LGGQDFDTNL LEHFKEFKQK KTGNDISGDA RALRRLRTAC ERAKRSLSSG TQTTVEIDSL FDGEDFSANI 301 TRARFEDINS ALFKSSTLEPV EQVLKDAKIS KSGQDEVVLV GGSTRIPKVQ KLLSDFFDGK QLEKSINPDE AVAYGAAVQG AILTQGSTND DTKDLLLDDV 401 IPLSLGVAMQ GNVFAPVVR NTVPTIKRR TTTVADHQT TVQFFVYQGE RVNCTENTLL GEFDLKNIPP MQAGEPVEA IFEVDANGIL KVTAVEKSTG 501 RSANITISNS IGRISTEIEI KMISDAEKFK SSDDAFAKRH EQQKLEAVV ASVESTVTDV VLSAKLKSA KDKIEAALS D ALQTLIEIES SADDYRKAEL 601 ALKRAVTKGM ATR</p>
TEF1	<p>1 MGKEKTHVNV VVIGHVDSGK STTGHLIYK CGGIDKRTIE KFEKEAAELG KGSFKYAWVL DKLKAERERG ITIDIALWKF ETPKYHVTVI DAPGHRDFIK 101 NMITGTSQAD CAILLIAGGT GEFEGAGISKD GQTRHALLA YTLGVKQLIV AVNKMDSVKW DKNRFEEIHK ETSNFVKVGV YNPKVTFPVF ISGWNGDNMI 201 EPSTNCVPYK GWEKETKSGK VTGKTLLEAI DAIEPPTRPT DKPLRLPLQD VYKIGIGTV PVGRVETGII KAGMVTFFAP AGVTEVKS EMHHEQLAEG 301 VPGDNVGFNV KNVSVKEIRR GNVCGDSKND PPKGDSFNA QVIVLHNPQ ISAGYSVPLD CHTAHIACKF DTLVEKIDRR TGKLEENPK FVKSGDAIV 401 KMVPTKPMCV EAFTDYPPGL RFAVRDMRQT VAVGVKSVE KSDKAGKVTK AAQKAACK</p>
TEF2	<p>1 MGKEKTHVNV VVIGHVDSGK STTGHLIYK CGGIDKRTIE KFEKEAAELG KGSFKYAWVL DKLKAERERG ITIDIALWKF ETPKYHVTVI DAPGHRDFIK 101 NMITGTSQAD CAILLIAGGT GEFEGAGISKD GQTRHALLA YTLGVKQLIV AVNKMDSVKW DKNRFEEIHK ETSNFVKVGV YNPKVTFPVF ISGWNGDNMI 201 EASTNCVPYK GWEKETKSGK VTGKTLLEAI DAIEPPTRPT DKPLRLPLQD VYKIGIGTV PVGRVETGII KAGMVTFFAP AGVTEVKS EMHHEQLAEG 301 VPGDNVGFNV KNVSVKEIRR GNVCGDSKND PPKGDSFNA QVIVLHNPQ ISAGYSVPLD CHTAHIACKF DTLVEKIDRR TGKLEENPK FVKSGDAIV 401 KMVPTKPMCV EAFTDYPPGL RFAVRDMRQT VAVGVKSVE KSDKAGKVTK AAQKAACK</p>
ORF 19.7085	<p>1 MFSPPFYNGDY SYDQPIDFES LFDLLHQHQP YYKENTRPRV IKKLETEDEF QIQIYKPYGN YNNYEVNVVK SNPPIVNVVI SSVQDNFKTV LFPNVNYIDI 101 DNINWQWYK QNVLVLNIPK RIHYVHSNVQ DILNCLLGCN DADASSALKA PNQOPYAKPQ TKKDVQAKTS PKKKEEFKVK KKEIANNNNN NLASRDANLK 201 DSIEEHNLI EQAANALKQA TENSCKQVKQ DLNGKANALS AGAQAAEAHK HKEALEKTKQ ELEAQRKAAH DKIVKAQQEL EBIARKEAEA VKLHEAAKQK 301 ELBEEKRQVE AEQQKAKEKE DLEQKEYDQF VKQQQEBLQK FFGFNLGPAI PTKDGANAFY TAAKQAKKQK PKVAPKPKQL QTQPVKQAKD EESIPSEPE 401 TEEPESKSH NSNENLHKHP SLEEEVEDES VMFRFRFGH</p>
ENO1	<p>1 MSYATKI HAR VYVDSRGNPT VEVDFTDQK LFRSIVPSGA STGVHEALEL RDGDKSKWLG KGVLKAVANV NDIIPALIK AKIDVVDQAK IDEFLLSLDG 101 TPNKSKLGN ALLGVSLAAA NAAAAAQGIP LYKHIANISN AKKGKPVLPV PFGVNLGGS HAGGALAFQE FMIAPTGVST FSEALRIGSE VYHNLKSLTK 201 FAPTKTWRWR NVKVNHNKR YATASALAS AVTSLVLAR GHRVEQVKELP LVVSNFESV KTKDVAVAL KAVGAHKDVV KVIKSKLRA GKGKLRGRFF 301 ABDDNDVAWH PFERVGDQIK IVGDDLTVTN PIRIKTAIEK KANALLLVK NQIGTLTBSI QAANDSYAAG WGVVMVSHRS ETEDDTIADL SVGLRSQGIK 401 TGAPARSERL AKLNQILRIE EELGSEAIYA GKDFQKASQL</p>
LYS12	<p>1 MLAARSSIRR CFSTSTTLK SLKIGLIPGD GIGREVIPAG KAVLENLPAK HDLQFQFVNL DAGFELFKKT GTALPDQETVD VLKKECDGAL FGAVSPTTK 101 VAGYSSPIVA LRKLLGLYAN VRPVKSVGIK GRPVDMIVR ENTEDLYIEM ERYVKKEDGT KVAEAIKRIT ETASTRIAKM AYEIALQREA VRKGTSGKQL 201 HEKSPVTVTH KSNVLSQSDG LFRQTCRAVY DANANEYGGI EYKQIVDSM VYRMFPREPI FQVVAVNLPI GDILLSGAAA LVGSLGVVPS ANVGDNPAIG 301 EPCHGSAPDI EGKGISNPVA TIRSTALMLE FMGYPEAAAT IYQAVDANLA EDKIKTPDLG GNSTTQEVID DIIRRF</p>
RPL4B	<p>1 MSSRPQSVI SVKGEQSSQ LPLPAVFAAP VRPDLVHSVF VRVKNKRQA YAVAENAGHQ TSAESWGTGR AVARIPRVGG GQTHRSQQA FGNMCRGGRM 101 FAPTKTWRWR NVKVNHNKR YATASALAS AVTSLVLAR GHRVEQVKELP LVVSNFESV KTKDVAVAL KAVGAHKDVV KVIKSKLRA GKGKLRGRFF 201 TORRGPVLYV AQDNGIVKAL RNVPVETAS VKHLGLLQLA PQAHLGRFII WTQAFESLD SVYGSSTKS IKSQYTLPSN IISNTDVTDL INSAEVQAVV 301 RPAGEKTKK SHVLKKNPLK NKQVLLRLNP YAKAYAAEKV GSAKVEQAKV KPSKQGFQAEV LKN</p>
TDH3	<p>1 MAIKIGINGF GRIGRLVLRV ALGRKIDIEV AVNDPFIAPD YAAVMFKYDS THGRYKGEVT ASGDDLVIDG HKIKVQPER PANIPWKGSG VDYVIESTGV 101 FTKLEGAQKH LDAGAKKVI I TAPSADAMPF VVGVDNDKYT PDLKII SNAS CTNCLAPLA KVVNDTPEGIE EGLMTVHSI TATQKTVDGP SHKDWGRGRT 201 ASGNIIPSST GAAKAVGKVI PELNGKLTGM SLRVPPTDVS VVDLTVRLKK AASYEIAQA IKKASEGPKL GVLGYTEDAV VSTDFLGSY SSIPEKAGI 301 LLSPTFKVLI SWYDNEYGYS TRVVDLLEHV AKASA</p>
NOP1	<p>1 MAFGAPRGRG GPARGGRGGF GGGRRGGGA RGGRRGGARG GSRGGARGGA RGGARGGARG GRGGARGGAR GGAQVVEIEP RHAGVFIARG KEDLLVTRNI 101 APGESVYGEK RISVEEPAKE EGAAPTKIEY RVWNPPRSKL AAGIMGGIDE LGTAPGKVL YLGAASGTSV SHVADVUGE GLYVAVFESH RPRELIGMA 201 KKRPNVPII DDARHPQYR MLIGMVDFCV ADVAQPDQAR IIALNSHLFL KDGLLVISI KANCIDSTVD AETVFAREVQ KLREERIKPL EQLTLEPYER 301 DCIVVGRYM RSGKK</p>
NPL3	<p>1 MGDPEVETKQ LFRVPLRNDV TREEVQDHS RAAPVVEVRL MEGYAVTFPE NEDDAQALE LLNDAEFNGE KLQIEFAKER REDTRGKYRL LITNLAEFTA 101 WQDIKDFVRE KTDSPQSYVK VFTNFDNGET TCSMQFQSR E DLDRAIPLLD KAVFRDITIG ABEEDTSPYIP PPPRGRGGFR GRGRGGFDRG FRGGRGGYDR 201 YDRGFRGGGR GGFDRGFRDG GFRGGRGGYD RGGFRGGRG FDRGGFRGGR GFRGGRGGY DRGGYDRDNF NDRGGSYDRE RSPTRF</p>
RPL8B	<p>1 MAPKGGKVP APLATKSAS SESKNLPEFS TPKNFIGIQS IQPKRNLRSF LVWPEYVRLQ RQKILSLRL KVPSIAQFS QTLDKNTAAQ AFKLLNKYRP 101 ETSAEKKERL TKEAAAIAEG KTAKDVSPPK VVVYKGLNHV VSLLEKNKAK LVLIANDVDP IELVFLPAL CKKMGVPIAI VKGKARLGLT VHKKTSAVAA 201 LTEVNSADEA ESKLISTIN ANYIEKYEEN RKHWGGGIMG SKANDKIACK AKAAAAAVST SN</p>
RPS7	<p>1 MSSKILSEN TELELKVQA FVDLESQADL KAELRPLQFK SIKEIDVNGG KVALAVFVPP PSLQAYRKVQ TRLTRELEKK FPDRHVFLA ERRILPKPAR 101 KARKQQRPR SRTLTAVHKD ILEDLVFPEE IIGKRVLYL GGNKIQKVLK DSKDSTAVDY KLDSFQQLYS KLTGKQVVEF IPGESH</p>
ORF 19.8442	<p>1 MSWFGFFDPP FDDFFGRPRK YATEVPPNPN PRKIAQGDNG KQQQVSRYGA GAGPHRALA RRDFFDDEFV KNFSSGGYFV GFDDNVKITE ESDKYVVSVD 101 QENLSPDEVN VDFDKQENEL IITVTQETEK DGTKKSSTFH SNLKFKEPVN FDDISAEIGE QGVQVTLPKV HADHEKIVNI PISKAAAK</p>
RPL16A	<p>1 MSQVAPKWYQ SEDVPAPKQT RKTARPOKLR ASLVPGTVLI LLAGRFRGKR VVYLKNELDN TLLVSGPFKV NGVPLRRVNA RYVIATSTKV NVSGVDVSKF 101 NVEYFAREKS SKSKKSEAEF FNESQPKKEI KAERVADQKS VDAALLSEIK KTPLLKQYLA ASFSLKNGDR PHLLKF</p>
RPL11	<p>1 MSQVAPKWYQ SEDVPAPKQT RKTARPOKLR ASLVPGTVLI LLAGRFRGKR VVYLKNELDN TLLVSGPFKV NGVPLRRVNA RYVIATSTKV NVSGVDVSKF 101 NVEYFAREKS SKSKKSEAEF FNESQPKKEI KAERVADQKS VDAALLSEIK KTPLLKQYLA ASFSLKNGDR PHLLKF</p>