

## **Supplemental Material**

**Supplemental Table I. M-to-G1 expression ratios of analyzed proteins.** The expression of TAP-tagged versions of the indicated proteins in M phase and in G1 were determined by immunoblotting as described in the text. The Pathway, Function and Location of each protein is taken from standard annotations, <http://www.yeastgenome.org/>. n/d, not detectable.

## Supplemental Table 1

ORF	Name	M/G1 ratio	Pathway	Function	Location
YEL061C	CIN8	10	mitotic sister chromatid segregation*	microtubule motor activity	mitochondrion*
YDL028C	MPS1	10	mitotic spindle checkpoint*	protein threonine/tyrosine kinase activity	spindle pole body*
YGL021W	ALK1	10	mitosis	protein serine/threonine kinase activity	nucleus
YHR152W	SPO12	10	regulation of exit from mitosis*	molecular function unknown	nucleus*
YPR119W	CLB2	10	G2/M transition of mitotic cell cycle*	cyclin-dependent protein kinase regulator activity	cytoplasm*
YNL273W	TOF1	10	mitotic sister chromatid cohesion*	molecular function unknown	nuclear chromosome
YNR009W	NRM1	10	biological process unknown	molecular function unknown	cytoplasm*
YPL183C		10	biological process unknown	molecular function unknown	cytoplasm
YMR163C	INP2	10	biological process unknown	molecular function unknown	cytoplasm
YBR138C		10	biological process unknown	molecular function unknown	cytoplasm
YPR106W	ISR1	10	biological process unknown	protein kinase activity	cellular component unknown
YHR061C	GIC1	10	establishment of cell polarity (sensu Fungi)*	small GTPase regulator activity	bud neck*
YER032W	FIR1	10	mRNA polyadenylation	molecular function unknown	bud neck
YDR451C	YHP1	10	negative regulation of transcription from RNA polymerase II promoter*	DNA binding*	nuclear chromosome cellular component
YPL267W	ACM1	10	biological process unknown	molecular function unknown	unknown
YPL242C	IQG1	8	actin filament organization*	cytoskeletal protein binding	bud neck contractile ring
YER111C	SWI4	5	G1/S transition of mitotic cell cycle*	DNA binding*	nucleus
YBR054W	YRO2	5	biological process unknown	molecular function unknown	mitochondrion*
YML064C	TEM1	5	regulation of exit from mitosis	protein binding*	spindle pole body
YLR131C	ACE2	5	G1-specific transcription in mitotic cell cycle	transcriptional activator activity	nucleus*
YMR001C	CDC5	5	protein amino acid phosphorylation*	protein kinase activity*	nucleus*
YMR032W	HOF1	5	cytokinesis*	cytoskeletal protein binding	bud neck contractile ring
YGR108W	CLB1	5	G2/M transition of mitotic cell cycle*	cyclin-dependent protein kinase regulator activity	cytoplasm*
YKL112W	ABF1	5	DNA replication*	DNA binding*	nuclear chromatin

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YIL101C	XBP1	5	response to stress	transcription factor activity protein serine/threonine kinase	nucleus
YOL113W	SKM1	5	protein amino acid phosphorylation*	activity	plasma membrane
YCL014W	BUD3	4	cytokinesis*	molecular function unknown	bud neck*
YJR053W	BFA1	4	conjugation with cellular fusion*	GTPase activator activity	spindle pole body
YKL130C	SHE2	3	intracellular mRNA localization	mRNA binding	cytoplasm
YHR023W	MYO1	3	response to osmotic stress* nuclear migration, microtubule- mediated*	microfilament motor activity	bud neck contractile ring
YPL155C	KIP2	3		microtubule motor activity protein serine/threonine kinase	mitochondrion*
YGR092W	DBF2	2	protein amino acid phosphorylation*	activity	bud neck*
YNL088W	TOP2	2	meiotic recombination*	DNA topoisomerase (ATP- hydrolyzing) activity	nucleus*
YGR188C	BUB1	2	protein amino acid phosphorylation* mitotic spindle organization and	protein binding*	nucleus*
YGL216W	KIP3	2	biogenesis in nucleus*	microtubule motor activity	cytoplasmic microtubule*
YPR156C	TPO3	2	polyamine transport	spermine transporter activity	plasma membrane* contractile ring (sensu Saccharomyces)
YJR092W	BUD4	2	bud site selection*	GTP binding	mitochondrion*
YLR190W	MMR1	2	mitochondrion inheritance	molecular function unknown	cytoplasm*
YOR355W	GDS1	2	aerobic respiration	molecular_function unknown	cellular component
YMR102C		2	biological process unknown	molecular function unknown	unknown
YOR233W	KIN4	2	spindle orientation checkpoint mitotic spindle organization and	protein kinase activity structural constituent of	bud neck*
YLR045C	STU2	2	biogenesis in nucleus* establishment of cell polarity (sensu Fungi)*	cytoskeleton*	spindle pole body*
YBL085W	BOI1	2		phospholipid binding	bud neck* cellular component
YBR007C	DSF2	2	biological process unknown	molecular function unknown	unknown
YOR026W	BUB3	1	mitotic spindle checkpoint	molecular function unknown	condensed nuclear chromosome kinetochore
YGR211W	ZPR1	1	regulation of cell cycle	protein binding	cytoplasm*

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YML085C	TUB1	1	mitotic sister chromatid segregation*	structural constituent of cytoskeleton	spindle pole body*
YLR045C	STU2	1	mitotic spindle organization and biogenesis in nucleus*	structural constituent of cytoskeleton*	spindle pole body* cellular component
YML034W	SRC1	1	mitotic sister chromatid segregation	molecular function unknown	unknown
YMR168C	CEP3	1	mitotic spindle checkpoint	DNA bending activity*	condensed nuclear chromosome kinetochore
YMR029C	FAR8	1	cell cycle arrest in response to pheromone	molecular function unknown	cellular component
YHR129C	ARP1	1	mitotic anaphase B	structural constituent of cytoskeleton	unknown
YCL016C	DCC1	1	mitotic sister chromatid cohesion	molecular_function unknown	dynactin complex
YDR517W	GRH1	1	mitotic spindle checkpoint	molecular_function unknown	DNA replication factor
YER016W	BIM1	1	microtubule nucleation*	structural constituent of cytoskeleton	C complex
YOR083W	WHI5	1	G1/S transition of mitotic cell cycle*	transcriptional repressor activity	cytoplasm
YKL052C	ASK1	1	mitotic spindle organization and biogenesis in nucleus*	structural constituent of cytoskeleton	condensed nuclear chromosome kinetochore*
YKR083C	DAD2	1	mitotic spindle assembly (sensu Fungi)	structural constituent of cytoskeleton	condensed nuclear chromosome kinetochore*
YPL174C	NIP100	1	mitotic anaphase B	protein binding*	dynactin complex
YBR133C	HSL7	1	regulation of progression through cell cycle*	protein-arginine N-methyltransferase activity	bud neck
YDL003W	MCD1	1	mitotic sister chromatid cohesion*	molecular_function unknown	nuclear cohesin complex
YOR372C	NDD1	1	G2/M-specific transcription in mitotic cell cycle	transcriptional activator activity	nucleus
YNL078W	NIS1	1	regulation of mitosis	molecular function unknown	nucleus*
YIL122W	POG1	1	G1/S-specific transcription in mitotic cell cycle*	specific RNA polymerase II transcription factor activity	nucleus
YGL008C	PMA1	1	regulation of pH*	hydrogen-exporting ATPase activity, phosphorylative mechanism	plasma membrane*

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YMR031C		1	biological process unknown	molecular function unknown	cytoplasm*
YIL106W	MOB1	1	protein amino acid phosphorylation*	kinase regulator activity	bud neck* cellular component
YML034W	SRC1	1	mitotic sister chromatid segregation	molecular function unknown	unknown
YBL023C	MCM2	1	DNA replication initiation*	chromatin binding* protein serine/threonine kinase activity	cytoplasm*
YHR205W	SCH9	1	protein amino acid phosphorylation*	activity	cytoplasm*
YHR215W	PHO12	1	biological process unknown regulation of transcription from RNA polymerase II promoter*	acid phosphatase activity	vacuole (sensu Fungi)
YGL162W	SUT1	1	polymerase II promoter*	transcription factor activity*	nucleus
YJL079C	PRY1	1	biological_process unknown	molecular_function unknown	endoplasmic reticulum*
YDR150W	NUM1	1	nuclear migration (sensu Fungi)*	tubulin binding	bud tip*
YHR135C	YCK1	1	protein amino acid phosphorylation*	casein kinase I activity	endoplasmic reticulum*
YPR019W	CDC54	1	DNA replication initiation*	chromatin binding* protein serine/threonine kinase activity	cytoplasm*
YPR111W	DBF20	1	protein amino acid phosphorylation*	alcohol O-acetyltransferase activity	cytoplasm
YGR177C	ATF2	1	steroid metabolism	activity	cytoplasm*
YJR043C	POL32	1	telomere maintenance* regulation of transcription from RNA polymerase II promoter*	delta DNA polymerase activity*	nucleus*
YGL162W	SUT1	1	polymerase II promoter*	transcription factor activity* structural constituent of cytoskeleton	nucleus
YPL255W	BBP1	1	microtubule nucleation*	protein serine/threonine kinase activity	spindle pole body
YKL048C	ELM1	1	protein amino acid phosphorylation* nuclear migration, microtubule-mediated*	activity	bud neck contractile ring
YDR488C	PAC11	1		microtubule motor activity* protein phosphatase type 2A activity	cytoplasmic microtubule*
YGL190C	CDC55	1	protein biosynthesis*	activity	nucleus*
YPR040W	TIP41	1	signal transduction nucleotide-excision repair, DNA damage recognition*	molecular_function unknown	cytoplasm*
YEL037C	RAD23	1	damage recognition*	damaged DNA binding	repairosome*
YLR114C	EFR4	1	biological_process unknown	molecular_function unknown	cytoplasm
YIR004W	DJP1	1	peroxisome matrix protein import	chaperone binding	cytosol

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YDR505C	PSP1	1	biological_process unknown	molecular_function unknown specific transcriptional repressor activity	cytoplasm*
YKL185W	ASH1	1	pseudohyphal growth*		nucleus*
YHR030C	SLT2	1	cell wall organization and biogenesis* nuclear mRNA splicing, via spliceosome*	MAP kinase activity	cytoplasm*
YLR132C		1		molecular_function unknown	cytoplasm* nuclear telomere cap complex
YDL220C	CDC13	1	telomere maintenance*	single-stranded DNA binding	nucleus
YPL008W	CHL1	1	chromosome segregation*	DNA helicase activity	nuclear origin of replication recognition complex
YBR060C	ORC2	1	DNA replication initiation* osmosensory signaling pathway via two-component system*	DNA replication origin binding	cytoplasm
YLR006C	SSK1	1		enzyme activator activity*	nucleus*
YNL097C	PHO23	1	chromatin modification	histone deacetylase activity	
YDR448W	ADA2	1	histone acetylation*	transcription coactivator activity	SAGA complex*
YGL066W	SGF73	1	histone acetylation	molecular_function unknown	SAGA complex cellular_component
YLR352W		1	biological_process unknown	molecular_function unknown	unknown
YMR259C		1	biological process unknown	molecular function unknown	cytoplasm
YNR031C	SSK2	1	protein amino acid phosphorylation*	MAP kinase kinase kinase activity	cytosol small nucleolar ribo-nucleoprotein complex
YML093W	UTP14	1	processing of 20S pre-rRNA	snoRNA binding	kinetochore*
YPL233W	NSL1	1	chromosome segregation	molecular function unknown	cytoplasm*
YLR182W	SWI6	1	meiosis*	protein binding*	cytoplasm
YBR094W		1	biological process unknown	molecular function unknown	nuclear exosome (RNase complex)
YOR001W	RRP6	1	35S primary transcript processing*	3'-5'-exoribonuclease activity	spindle pole body*
YPR141C	KAR3	1	meiosis*	microtubule motor activity*	nucleus
YMR019W	STB4	1	biological process unknown	DNA binding	kinetochore*
YIR010W	DSN1	1	chromosome segregation	molecular function unknown	

## Supplemental Table 1

					Ada2/Gcn5/Ada3 transcription activator complex
YOR023C	AHC1	1	histone acetylation	histone acetyltransferase activity	cytoplasm*
YLR187W	SKG3	1	biological process unknown	molecular function unknown	cytoplasm*
YBL060W		1	biological process unknown	molecular function unknown	cytoplasm*
YLR335W	NUP2	1	mRNA export from nucleus*	structural molecule activity	mitochondrion*
			microtubule cytoskeleton organization and biogenesis	molecular function unknown	cell wall (sensu Fungi)
YIL123W	SIM1	1	intracellular protein transport*	molecular_function unknown	cytosol
YGR142W	BTN2	1	chromosome segregation*	centromeric DNA binding	nucleus*
YKLO89W	MIF2	1	ubiquitin-dependent protein catabolism*	protein binding*	cytoplasm*
YJL047C	RTT101	1	mRNA catabolism*	mRNA binding*	cytoplasmic mRNA processing body
YOL149W	DCP1	1	chromatin remodeling*	general RNA polymerase II transcription factor activity	SWI/SNF complex*
YBR289W	SNF5	1	negative regulation of transcription from RNA polymerase II promoter*	DNA binding*	nucleus
YML027W	YOX1	0.2	pseudohyphal growth*	signal transducer activity*	intracellular
YDR379W	RGA2	0.2	biological process unknown	molecular function unknown	cytoplasm
YDR266C		0.2	pheromone-dependent signal transduction during conjugation with cellular fusion*	cyclin-dependent protein kinase inhibitor activity	cytoplasm*
YJL157C	FAR1	0.1	negative regulation of exit from mitosis*	protein binding	cytoplasm*
YBR158W	AMN1	n/d	G2/M transition of mitotic cell cycle*	molecular_function unknown	half bridge of spindle pole body
YLL003W	SFI1	n/d	mitotic sister chromatid segregation*	molecular function unknown	nucleus*
YOR073W	SGO1	n/d	biological_process unknown	protein kinase activity	cytoplasm
YPL141C		n/d	DNA replication initiation*	chromatin binding*	cytoplasm*
YBR202W	CDC47	n/d	chromatin silencing at telomere*	DNA binding	nucleus
YOR025W	HST3	n/d	actin cytoskeleton organization and biogenesis*	molecular_function unknown	bud neck*
YPR171W	BSP1	n/d	mitotic sister chromatid segregation*	motor activity	spindle pole body*
YKR054C	DYN1	n/d			

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YOR191W	RIS1	n/d	chromatin assembly or disassembly*	DNA-dependent ATPase activity	nucleus cellular component
YFR039C		n/d	biological process unknown	molecular function unknown	unknown



**Supplementary Table II.** *S. cerevisiae* strains used in this study.

<b>Strain</b>	<b>Relevant Genotype</b>	<b>Source</b>
YJB14 (W303a)	<i>MATa ade2-1 trp1-1 leu2-3,112 his3-11,15 ura3-1 bar1::URA3</i>	(Burton and Solomon, 2000)
YJB115	<i>MATa cdc23-1 bar1::URA3</i>	(Burton and Solomon, 2000)
YJB200	<i>MATa cdc15-2</i>	(Burton and Solomon, 2000)
DOY734	<i>MATa cdc15-2 cdh1Δ::natMX4</i>	This study
YJB368	<i>MATa cdc28-13::TRP1 cdh1Δ::LEU2</i>	(Burton and Solomon, 2000)
YJB910	<i>MATa pep4-3 leu2-3,112 his3-1,15 ura3-1 CDC16-TAP::CDC16 APC4-HA::APC4</i>	(Ostapenko <i>et al.</i> , 2008)
PJ69-4a	<i>MATa LYS2::GAL1-HIS3 GAL2-ADE2 met2::GAL7-lacZ</i>	(James <i>et al.</i> , 1996)
A6808	<i>MATa URA3::MET-CDC20</i>	(D'Aquino <i>et al.</i> , 2005)
CDC28-as1	<i>MATa cdc28-as</i>	(Bishop <i>et al.</i> , 2000)
DOY1006	YJB14 [ <i>GAL-NRMI-TAP-YCplac22</i> ]	This study
DOY1070	YJB14 [ <i>GAL-YHP1-TAP-YCplac22</i> ]	This study
DOY1007	YJB14 [ <i>GAL-nrm1-mdb-TAP-YCplac22</i> ]	This study
DOY1098	YJB14 [ <i>GAL-yhp1-mkb/mdb-TAP-YCplac22</i> ]	This study
DOY1277	YJB14 [ <i>GAL-nrm1-4TA-TAP-YCplac22</i> ]	This study
DOY1355	YJB14 [ <i>GAL-nrm1-4TD-TAP-YCplac22</i> ]	This study
DOY1056	YJB14 [ <i>nrm1Δ::natMX4</i> ]	This study
DOY1103	YJB14 [ <i>yhp1Δ::natMX4</i> ]	This study
DOY1057	YJB14 [ <i>nrm1Δ URA3:NRMIp-NRMI-TAP</i> ]	This study

DOY1058	YJB14 [ <i>nrm1</i> Δ:: <i>natMX4 URA3:NRM1p-nrm1-mdb</i> -TAP]	This study
DOY1157	YJB14 [ <i>yhp1</i> Δ:: <i>natMX4 URA3:YHP1p-YHP1</i> -TAP]	This study
DOY1158	YJB14 [ <i>yhp1</i> Δ:: <i>natMX4 URA3:YHP1p-yhp1-mkb/mdb</i> -TAP]	This study
DOY1036	YJB14 [ <i>HIS3:NRM1</i> -TAP <i>URA:GALL-cdh1-m11</i> ]	This study
DOY1065	YJB14 [ <i>HIS3:YHP1</i> -TAP <i>URA:GALL-cdh1-m11</i> ]	This study
DOY1030	YJB115 [ <i>GAL-NRM1</i> -TAP-YCplac22]	This study
DOY1073	YJB368 [ <i>GAL-YHP1</i> -TAP-YCplac22]	This study
DOY1090	YJB200 [ <i>HIS3:YHP1</i> -TAP]	This study
DOY1091	DOY734 [ <i>HIS3:YHP1</i> -TAP]	This study
DOY1124	A6808 [ <i>LEU2:YHP1p-YHP1</i> -TAP]	This study
DOY1125	A6808 [ <i>LEU2:YHP1p-yhp1-mkb/mdb</i> -TAP]	This study
DOY1137	A6808 [ <i>LEU2:NRM1p-NRM1</i> -TAP]	This study
DOY1148	A6808 [ <i>LEU2:NRM1p-nrm1-mdb</i> -TAP]	This study
DOY1021	CDC28-as1 [ <i>GAL-NRM1</i> -TAP-YCplac22]	This study
DOY1153	CDC28-as1 [ <i>GAL-nrm1-mdb</i> -TAP-YCplac22]	This study
DOY1236	PJ69-4a [ <i>CDH1-ΔN200</i> -pAS1 <i>YHP1</i> -pACT]	This study
DOY1240	PJ69-4a [ <i>CDH1-ΔN200</i> -pAS1 <i>yhp1-mkb/mdb</i> -pACT]	This study