

Supplementary Materials for

A Genome-Wide RNAi Screen Identifies Core Components of the G₂-M DNA Damage Checkpoint

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Figure S1. Caffeine-sensitive G₂-M checkpoint of *Drosophila* S2R+ cells. (A) Fluorescent images of S2R+ cells stained with DAPI (blue) and an antibody against phosphohistone H3 (green). After doxorubicin treatment, the mitotic index (MI) dramatically decreased, and this was suppressed by co-incubation with 5 mM caffeine. **(B)** Quantification of the data in panel A. Average and range of two replicates are shown. The result of Bleocin treatment is also shown.

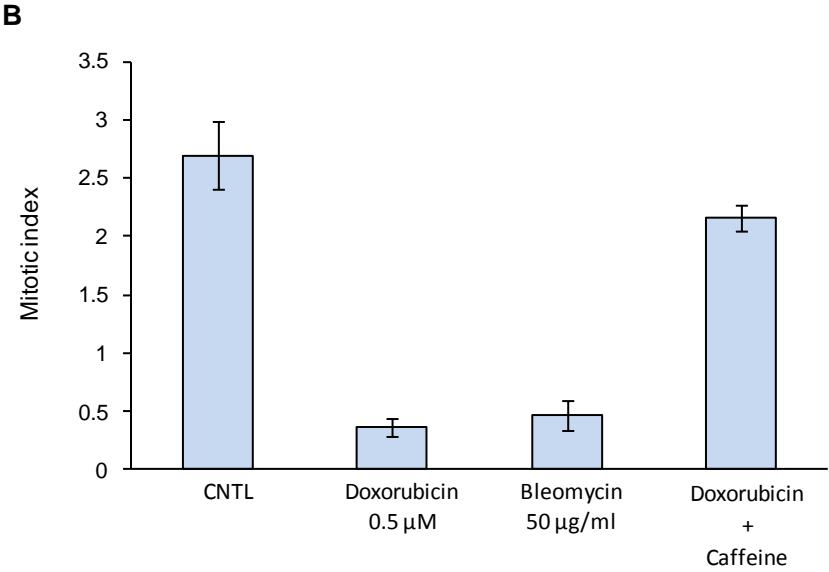
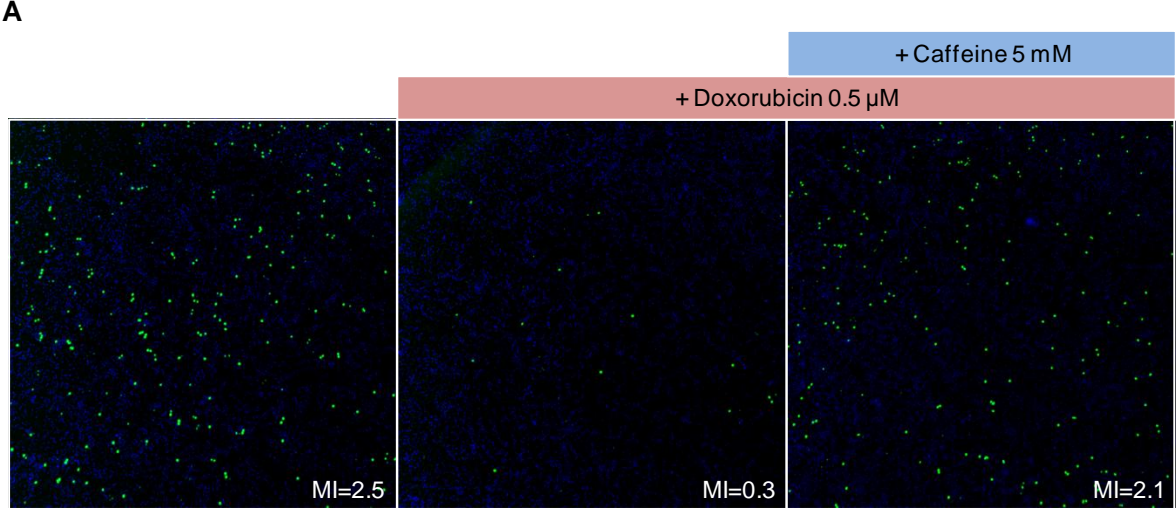
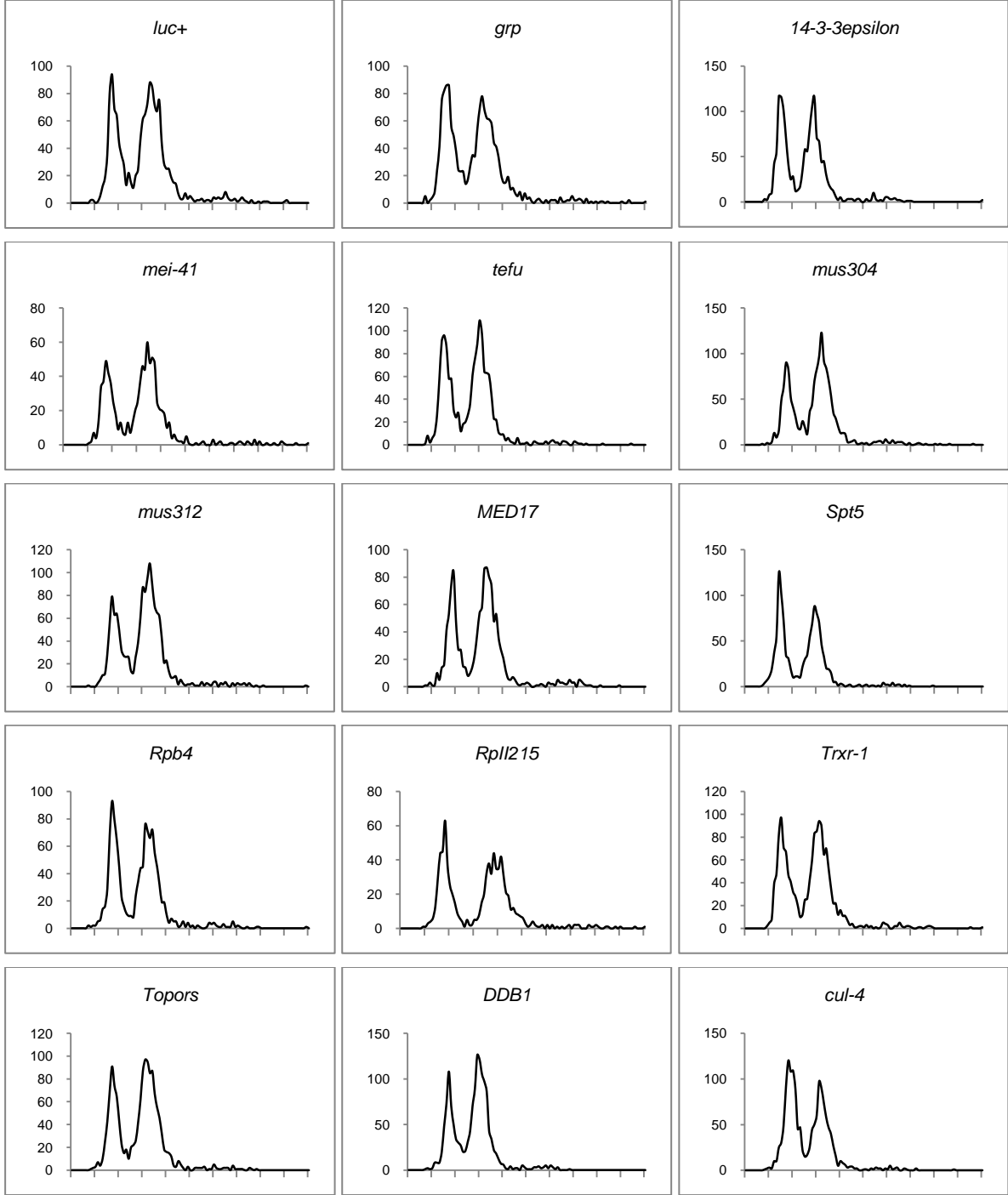
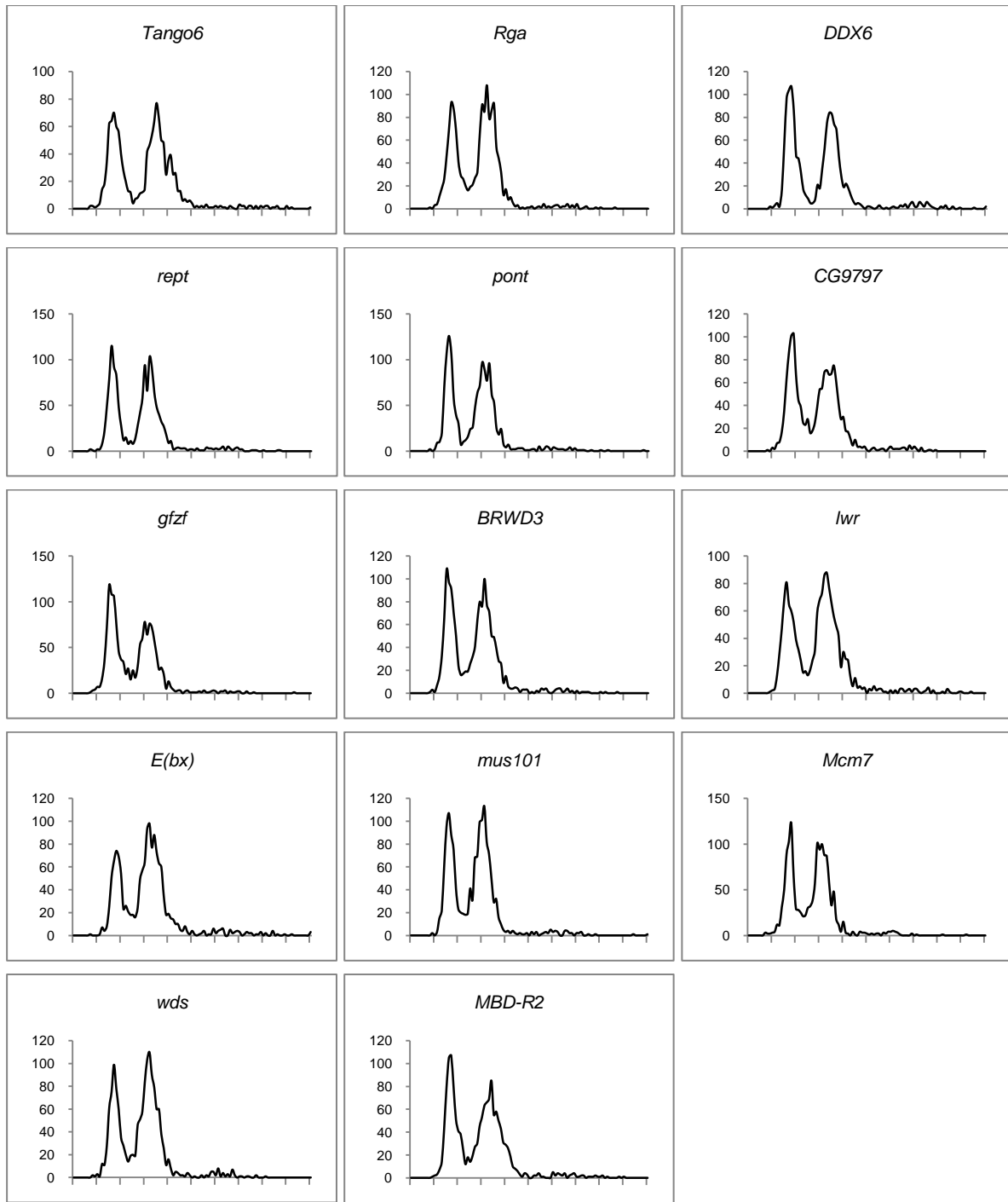


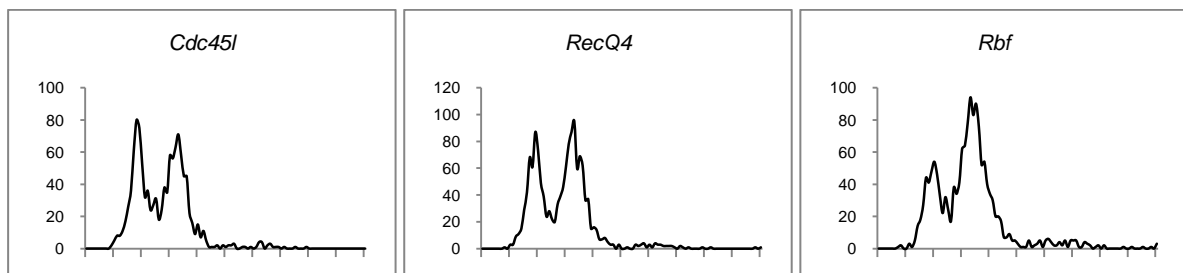
Figure S2. Cell cycle profiles of cells depleted of the candidate genes. The histograms show the cell cycle profile of cells treated with a dsRNA against each of the candidate genes. The X-axis represents DNA content determined by DAPI fluorescence intensities. The Y-axis represents cell counts. The results were grouped according to the change in the cell cycle profile: **(A)** Normal, **(B)** increase in S phase, **(C)** increase in G1, **(D)** increase in G2. The relative proportion of cells in each phase of the cell cycle was visually determined by comparison to the control (*luc+*).

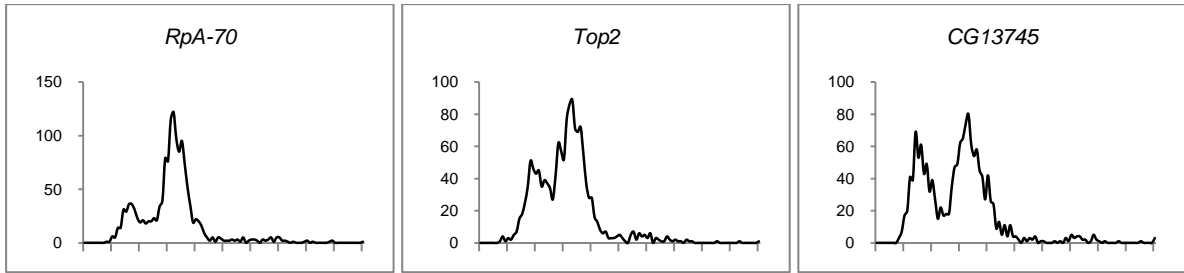
A



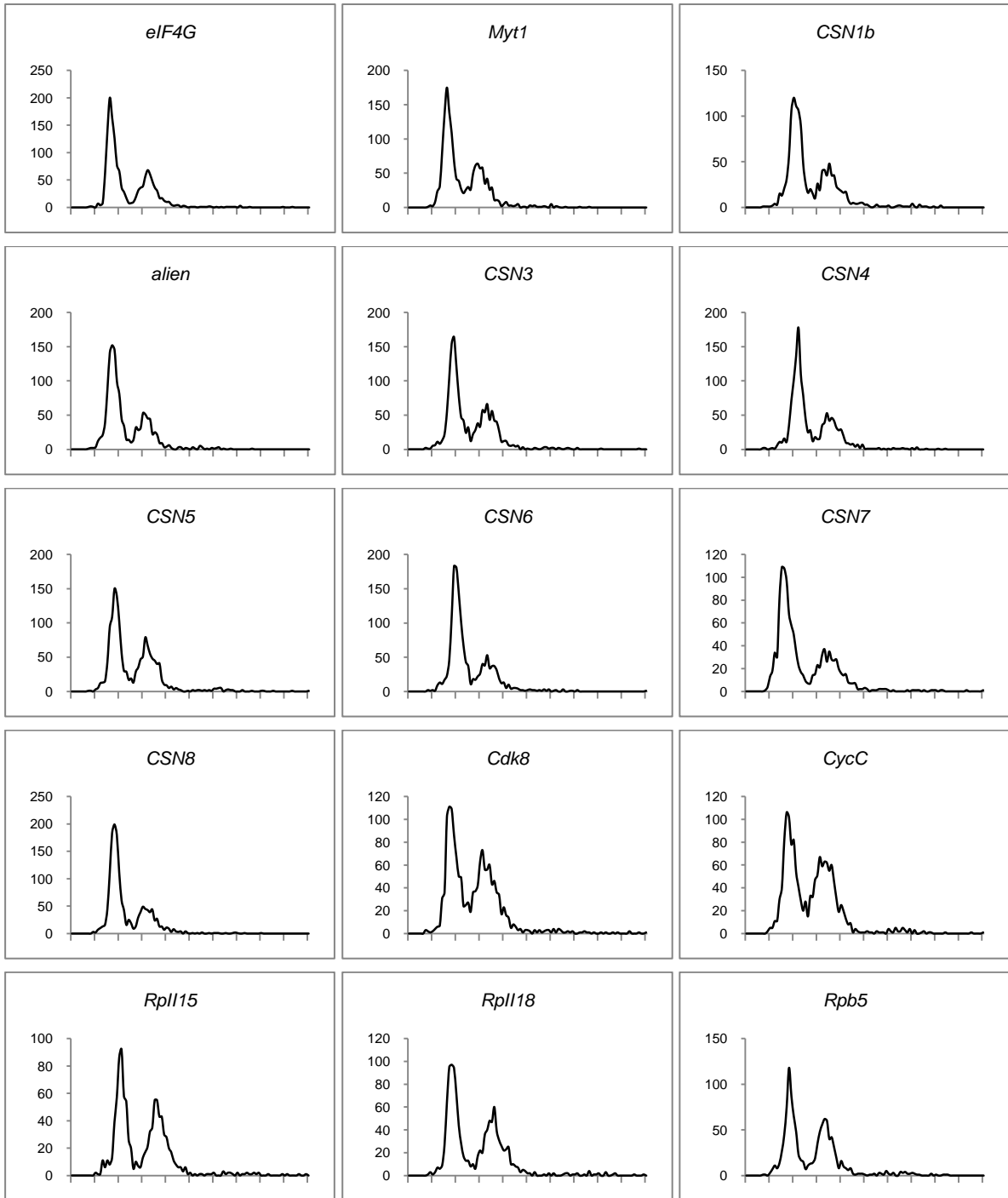


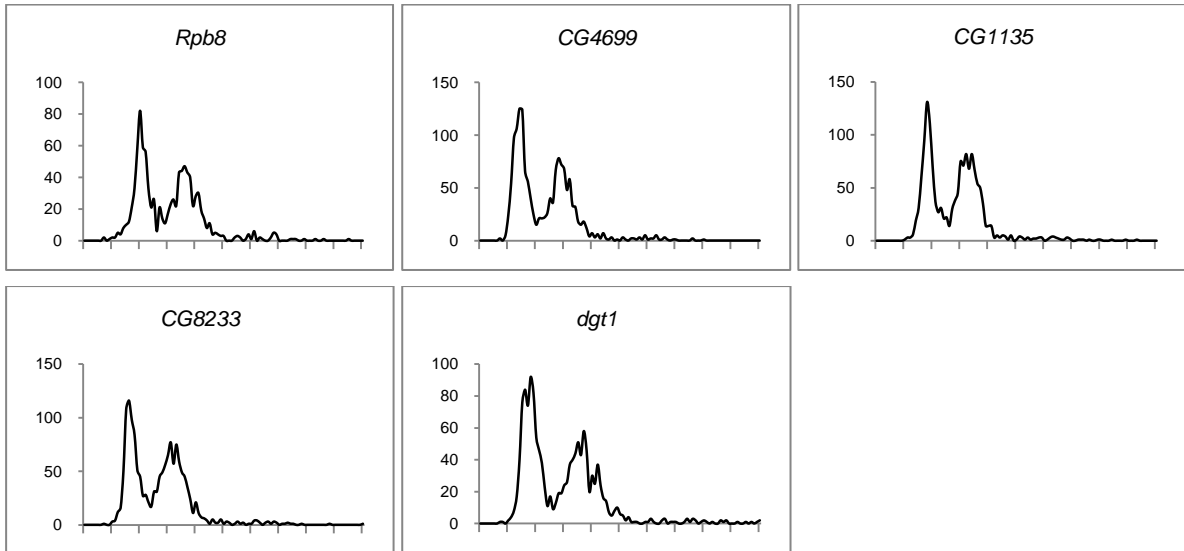
B





C





D

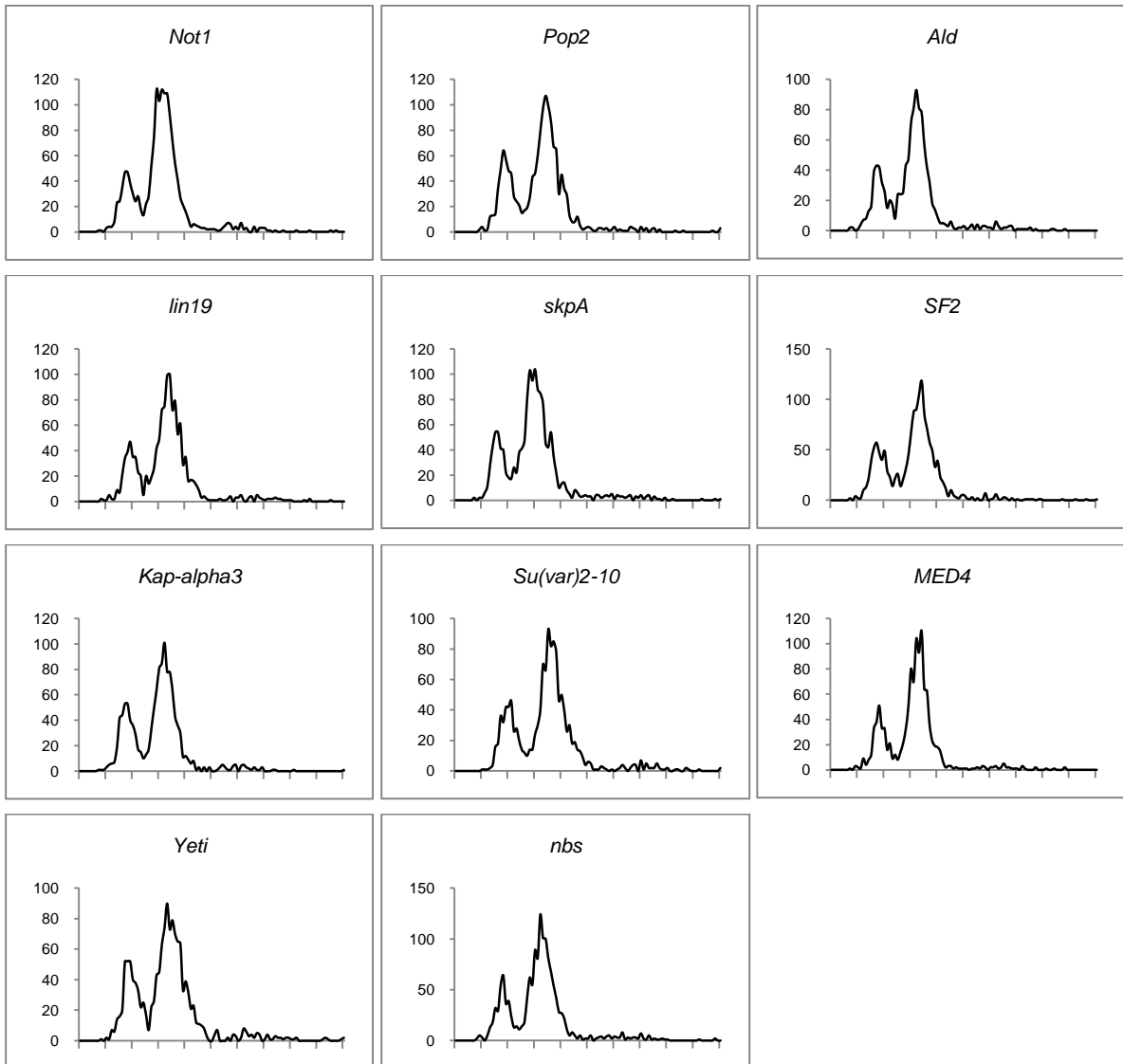


Figure S3. Secondary screen for mitotic exit defects. Relative mitotic index of RNAi-treated cells after an eight-hour incubation with 30 μ M NSC663284. Average and range of two replicates are shown. A dsRNA against Venus (a green fluorescent protein variant) was used as a negative control. The three genes that led to a relative mitotic index of more than 50% were excluded as potential false positives.

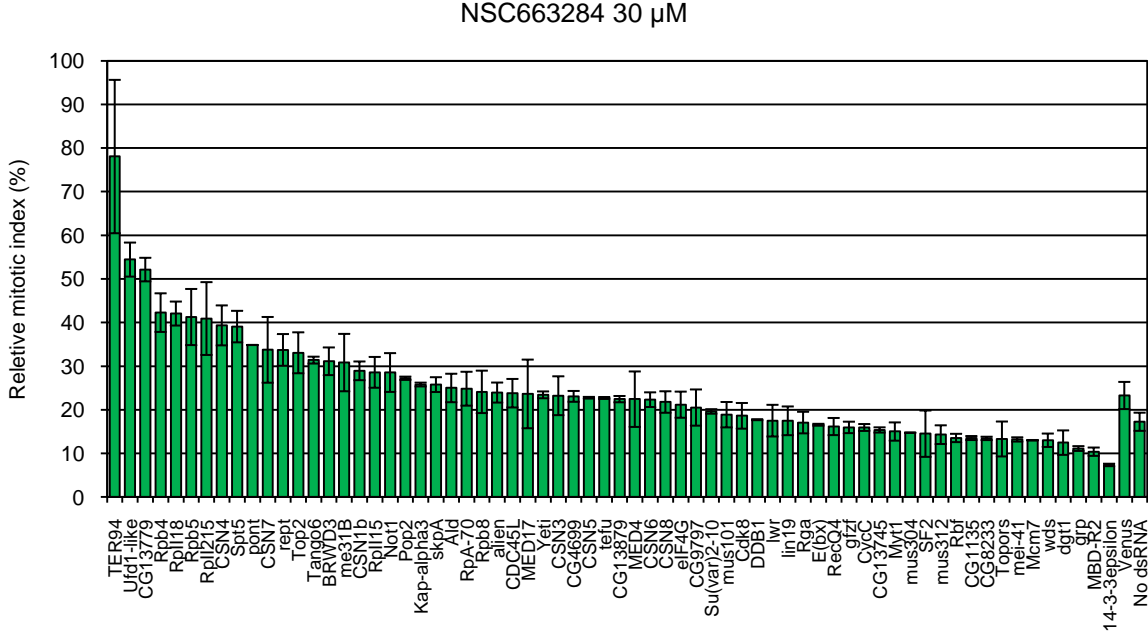
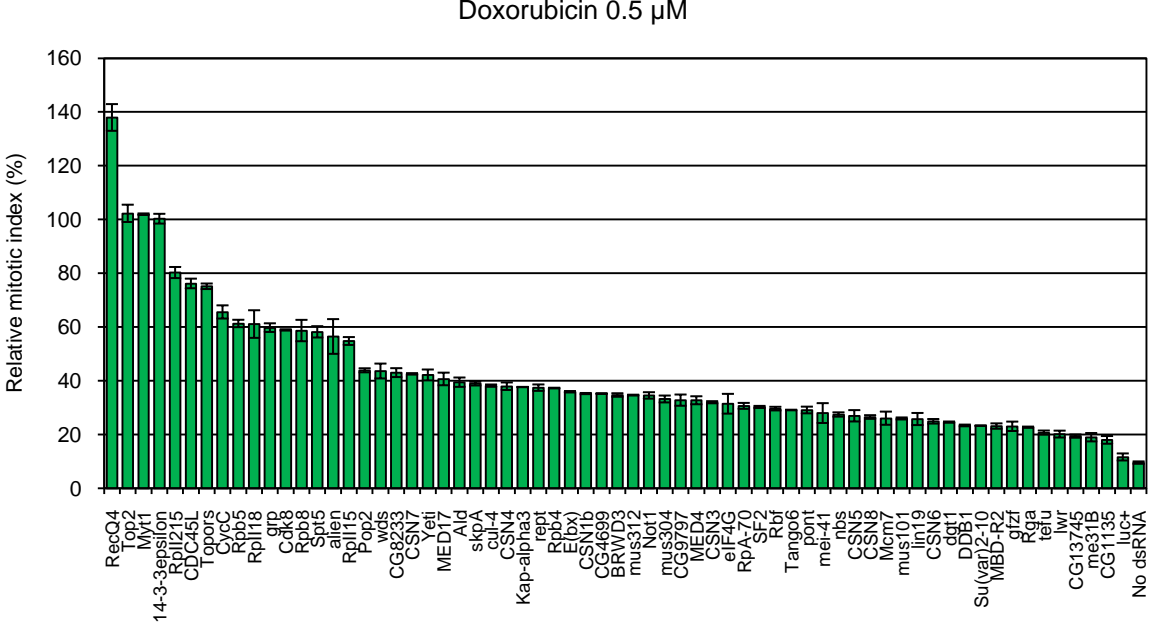
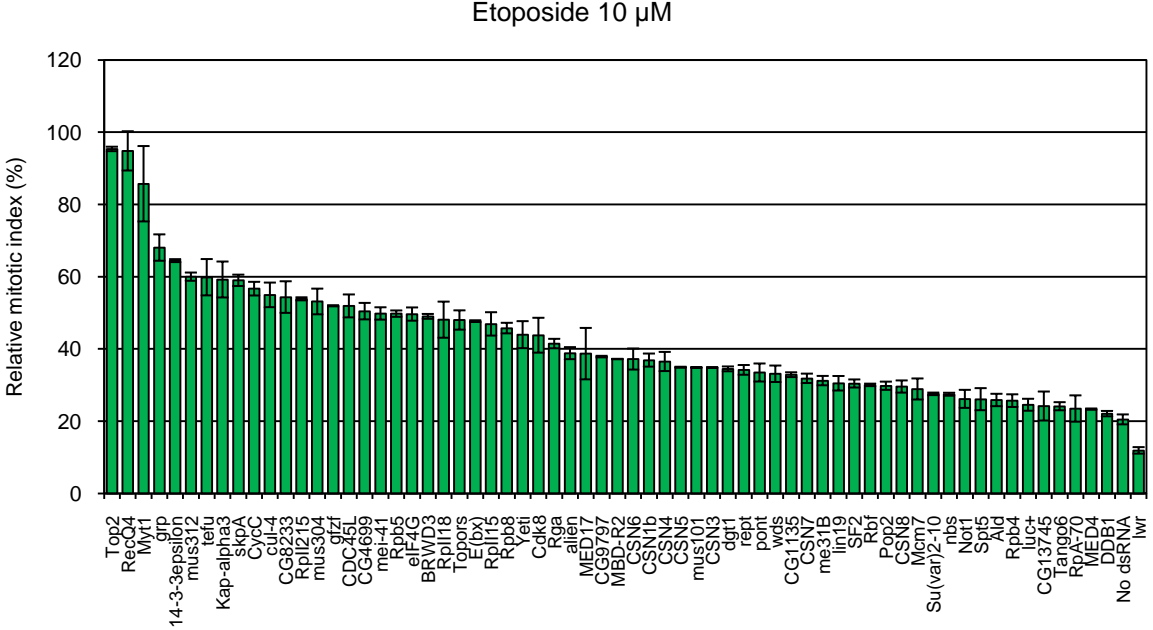


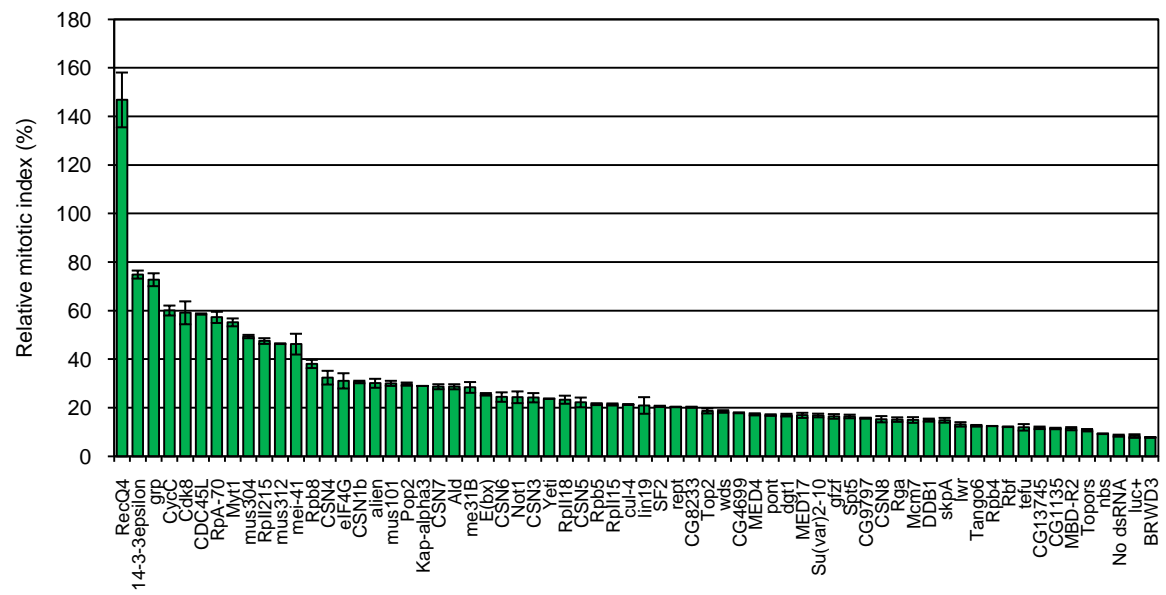
Figure S4. G₂-M checkpoint defect of cells depleted of the candidate genes. The graphs show the relative mitotic index of cells treated with a dsRNA against each of the 64 candidate genes. Average and range of two replicates are shown. The cells were treated with doxorubicin (A), etoposide (B), Bleocin (C), or X-rays (D). In a few cases, the relative mitotic index exceeded 100%. This may be due to compensatory proliferation induced by DNA damage (Pérez-Garijo et al., 2004).

A



B



CBleocin 50 μ g/ μ l**D**

X-ray 150 Gy

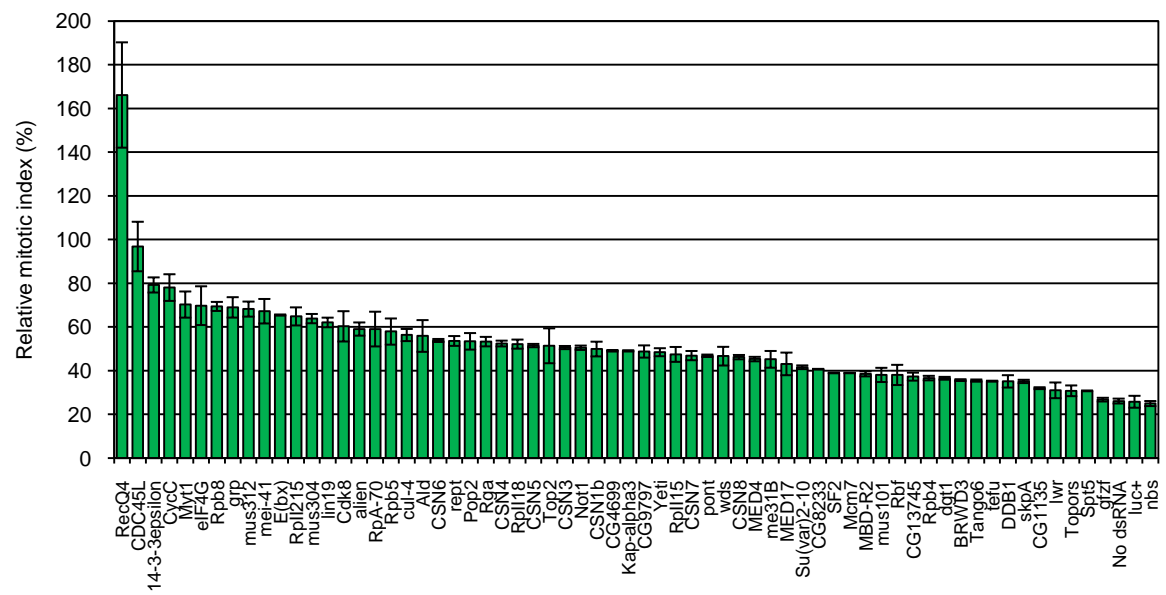


Figure S5. DNA damage-induced phosphorylation of histone H2Av in cells depleted of candidate genes. S2R+ cells were stained with DAPI (blue) and an antibody against phosphohistone H2Av (white). The cells were treated with dsRNAs targeting the indicated genes. **(A)** Before doxorubicin treatment. **(B)** After doxorubicin treatment.

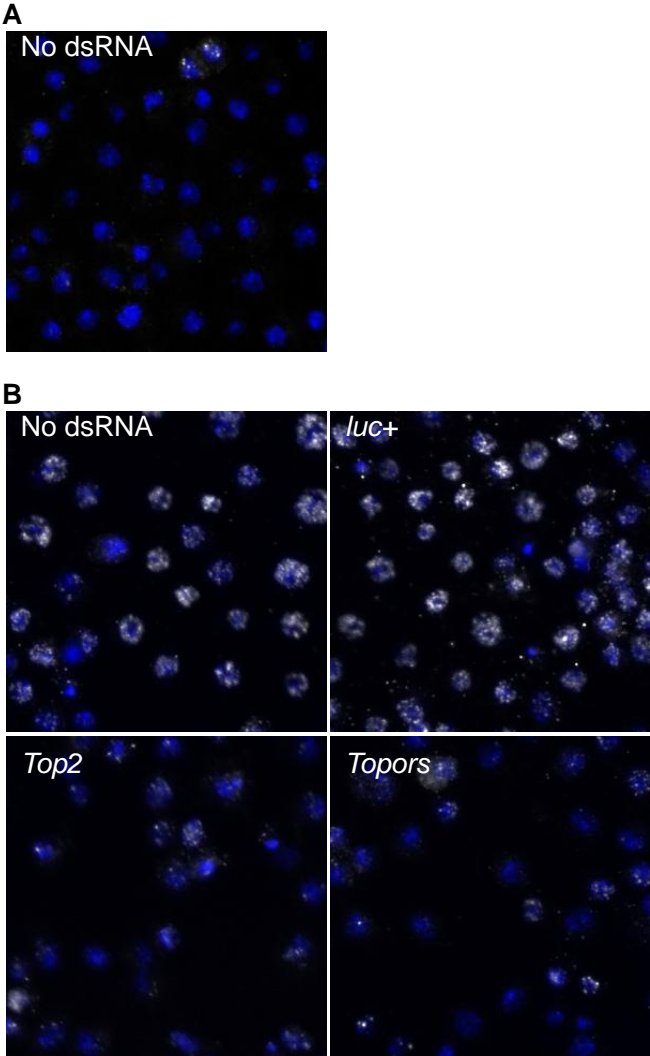
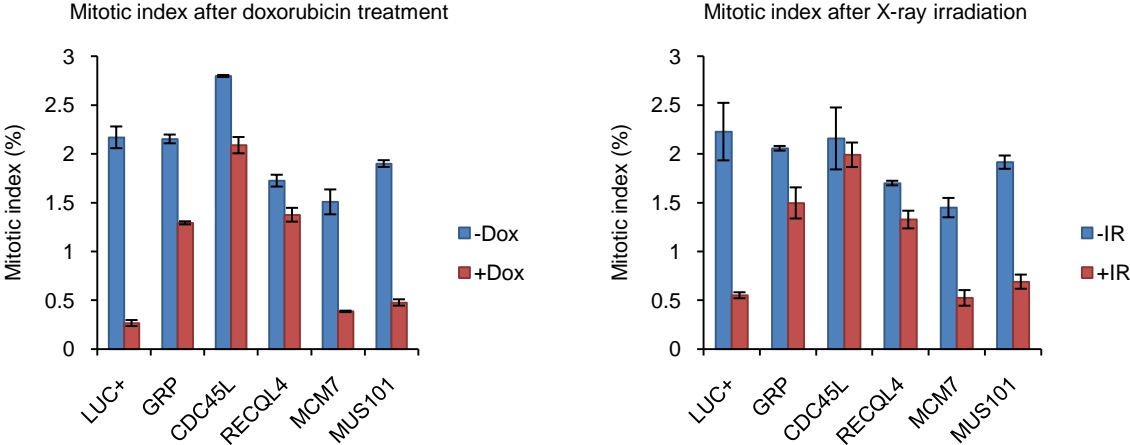


Figure S6. Mitotic index and cell cycle profile of cells depleted of pre-IC proteins. (A) Mitotic index of S2R+ cells treated with a dsRNA for each of the pre-IC genes. The cells were treated with 0.5 μM doxorubicin or 150 Gy of X-rays. Mitotic indices of untreated (blue bars) and treated cells (red bars) are shown. Luciferase (*luc+*) RNAi is shown as a wild-type control. *grp* (known as CHK1 in mammals) RNAi is shown as a positive control of a defective G2/M checkpoint. Knockdown of *mcm7* or *mus101* also produced a decrease in the mitotic index before DNA damage. The relative mitotic indices after DNA damage were *mcm7*, 26.03% (+/-2.45); *mus101*, 25.93% (+/-0.38); *luciferase*, 11.61% (+/-1.31). (B) Cell cycle profiles of the RNAi-treated cells in the absence of DNA damage.

A



B

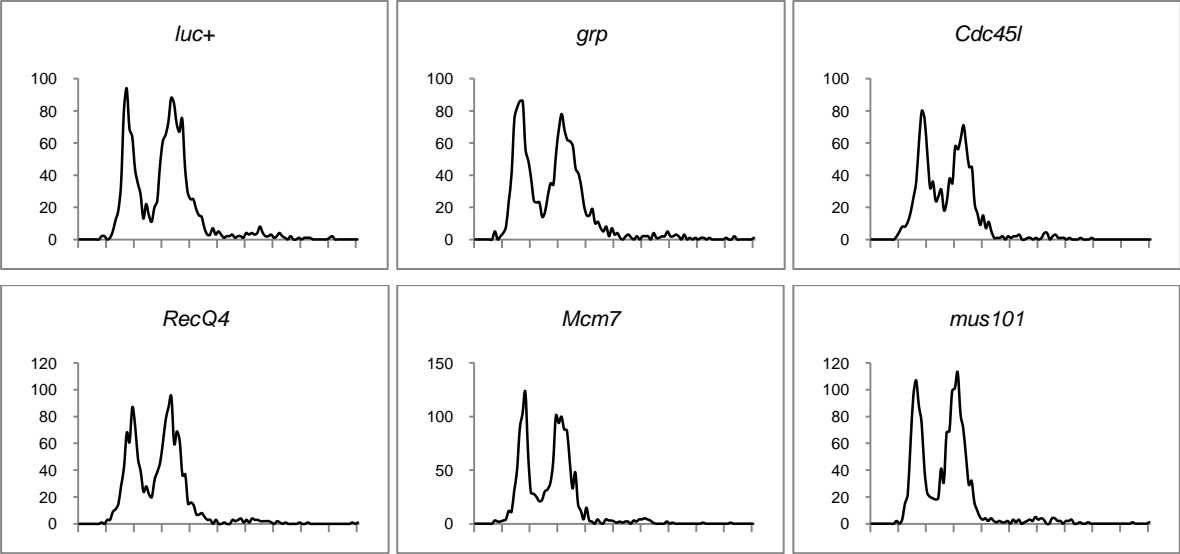


Table S1. Genes required for the G₂-M checkpoint induced by doxorubicin. Listed in the table are the 64 candidate G₂/M checkpoint genes that passed the secondary screen. For each gene, the Flybase (<http://flybase.org/>) gene name, CG number, alternative name, human ortholog, and dsRNA amplicons used are provided. In Fig. 1, the alternative names are used when available.

Gene	CG #	Synonyms	Human ortholog	Amplicon #1	Amplicon #2	Note
<i>mei-41</i>	CG4252	ATR	ATR	DRSC36631		Have a known role in DNA damage checkpoints.
<i>mus304</i>	CG7347	ATRIP	ATRIP	DRSC11372		
<i>tefu</i>	CG6535	ATM	ATM	DRSC16060		
<i>nbs</i>	CG6754	NBS1	NBS1	custom		
<i>grp</i>	CG17161	CHK1	CHK1	DRSC03541		
<i>Myt1</i>	CG32417		MYT1	DRSC30071	DRSC11228	
<i>14-3-3ε</i>	CG31196		14-3-3-EPSILON	DRSC16370		
<i>mus101</i>	CG11156	TOPBP1	TOPBP1	DRSC19388		
<i>CG13745</i>	CG13745	FANCI	FANCI	DRSC06416		
<i>Top2</i>	CG10223		TOP2A	DRSC03459		
<i>pont</i>	CG4003		PONTIN	DRSC17029		REPTIN and PONTIN form a dimer.
<i>rept</i>	CG9750		REPTIN	DRSC11388		
<i>CG4699</i>	CG4699	NSL1	hNSL1	DRSC15625		Components of the Nonspecific Lethal (NSL) complex.
<i>dgt1</i>	CG18041	NSL2	hNSL2	DRSC15301		
<i>CG8233</i>	CG8233	NSL3	hNSL3	DRSC23713	DRSC07116	
<i>CG1135</i>	CG1135	MCRS1	MCRS1	DRSC27788	DRSC08180	
<i>MBD-R2</i>	CG10042		PHF20	DRSC14180		
<i>wds</i>	CG17437	WDR5	WDR5	DRSC18852		
<i>Pop2</i>	CG5684		POP2	DRSC10537		Components of the CCR4-Not complex
<i>Not1</i>	CG34407		NOT1	DRSC06787		
<i>Rga</i>	CG2161	NOT2	NOT2	DRSC12364		
<i>me31B</i>	CG4916	DDX6	DDX6	DRSC03569		
<i>Cdk8</i>	CG10572		CDK8	DRSC11113		Components of the mediator complex
<i>CycC</i>	CG7281		CYCLIN C	DRSC16619		
<i>MED17</i>	CG7957		MED17	DRSC16889		
<i>MED4</i>	CG8609		MED4	DRSC25135		
<i>CSN1b</i>	CG3889		GPS1	DRSC11108		Components of the CO9 signalosome (CSN) complex
<i>alien</i>	CG9556	CSN2	COPS2	DRSC03482		
<i>CSN3</i>	CG18332		COPS3	DRSC25919		
<i>CSN4</i>	CG8725		COPS4	DRSC07350		
<i>CSN5</i>	CG14884		COPS5	DRSC16592		
<i>CSN6</i>	CG6932		COPS6	DRSC16593		
<i>CSN7</i>	CG2038		COPS7A	DRSC06807		
<i>CSN8</i>	CG42522		COPS8	DRSC02257		
<i>DDB1</i>	CG7769		DDB1	DRSC16639	DRSC31603	DDB1 and CUL4 are components of an E3 ubiquitin ligase complex.
<i>cul-4</i>	CG8711	CUL4	CUL4A	DRSC27185		
<i>skpA</i>	CG16983	SKP1	SKP1	DRSC18833		SKP1 and CUL1 are components of the SCF complex.
<i>lin19</i>	CG1877	CUL1	CUL1	DRSC07645		
<i>Rpb4</i>	CG33520		RPB4	DRSC21598		Subunits of the RNA polymerase II complex
<i>Rpb5</i>	CG11979		RPB5	DRSC06100		
<i>Rpb8</i>	CG11246		RPB8	DRSC11642		
<i>Rpl115</i>	CG3284		RPB9	DRSC16832		
<i>Rpl118</i>	CG1163		RPB6	DRSC12366		
<i>Rpl1215</i>	CG1554		RPB1	DRSC20280		
<i>mus312</i>	CG8601		BTBD12	DRSC27742	DRSC11008	
<i>BRWD3</i>	CG31132		BRWD3	DRSC15369	DRSC16032	
<i>E(bx)</i>	CG32346		BPTF	DRSC08583	DRSC08509	
<i>lwr</i>	CG3018	UBC9	UBC9	DRSC27034	custom	
<i>Topors</i>	CG15104		TOPORS	DRSC06531	custom	
<i>Su(var)2-10</i>	CG8068	PIAS	PIAS1	DRSC07721	custom	
<i>RpA-70</i>	CG9633	RPA70	RPA1	DRSC16830	custom	
<i>RecQ4</i>	CG7487	RECQL4	RECQL4	DRSC11265	DRSC27616	
<i>CDC45L</i>	CG3658		CDC45L	DRSC17747	DRSC31324	
<i>Mcm7</i>	CG4978		MCM7	DRSC24311	DRSC11219	
<i>Rbf</i>	CG7413	RB	RB	DRSC18704	custom	
<i>elF4G</i>	CG10811		EIF4G3	DRSC17218	DRSC29786	
<i>Ald</i>	CG6058		ALDOB	DRSC25381	DRSC14109	
<i>gfzf</i>	CG33546		N/A	DRSC12506	DRSC21874	
<i>Tango6</i>	CG18398		TMCO7	DRSC02671	DRSC29389	
<i>Kap-alpha3</i>	CG9423		KPNA3	DRSC16976	DRSC34268	
<i>Spt5</i>	CG7626		SPT5H	DRSC07556	DRSC37651	
<i>SF2</i>	CG6987		SFRS1	DRSC16845	DRSC32604	
<i>CG9797</i>	CG9797		N/A	DRSC16566	custom	
<i>Yeti</i>	CG40218	SWC5	CFDP1	DRSC21138	DRSC37982	

Table S2. Primary hits excluded from further analysis and reasons for exclusion. The following genes identified in the primary screen showed strong phenotypes, but were excluded from further analysis for indicated reasons. Fold change in mitotic index is provided where available.

Gene	DRSC amplicon ID	Human ortholog	MI fold change	Reason for exclusion
<i>dup</i>	DRSC07088	CDT1	7.2	
<i>CG3625</i>	DRSC00621	AIG1	3.2	
<i>mask</i>	DRSC16018, DRSC16005, DRSC15370	ANKRD17	2.5	These genes were excluded because of a highly elevated mitotic index (more than two-fold compared to wild type) without DNA damage.
<i>14-3-3ζ</i>	DRSC05028	14-3-3-ZETA	3.1	
<i>CG12420</i>	DRSC14514	N/A	2.3	These genes had an apparent defect in mitotic exit (see Fig. S3).
<i>CG13779</i>	DRSC02282	DSS1		
<i>TER94</i>	DRSC27600	VCP		
<i>CG4673</i>	DRSC15616	NPL4		
<i>Pp1-87B</i>	DRSC16794	PPP1CA		
<i>Pp1-13C</i>	DRSC20269	PPP1CA		Known role in mitosis. These genes encode phosphatases whose knockdown leads to mitotic arrest (Chen et al., 2007).
<i>mts</i>	DRSC03574	PPP2CA	4.8	
<i>Pp2A-29B</i>	DRSC28394	PPP2R1A	5.3	
<i>tws</i>	DRSC27776, DRSC17092	PPP2R2A		
<i>Pp4-19C</i>	DRSC21251	PPP4C		
<i>PpV</i>	DRSC18700	PPP6C		Known role in cytokinesis (Goshima et al., 2007). This dsRNA targets multiple isoforms of Actin.
<i>Act87E, Act5C, Act88F, Act57B, Act79B</i>	DRSC14104	actin		
<i>alphaTub67C</i>	DRSC25162, DRSC11321	α-tubulin		Known role in mitosis. Tubulins play an essential role in spindle assembly (Goshima et al., 2007).
<i>alphaTub84B</i>	DRSC25011, DRSC12622	α-tubulin	8.6	
<i>alphaTub84D</i>	DRSC12623	α-tubulin		
<i>alphaTub85E</i>	DRSC23424, DRSC16899	α-tubulin		
<i>betaTub56D</i>	DRSC23516, DRSC07583	β-tubulin		
<i>betaTub85D</i>	DRSC16910	β-tubulin	5.3	These genes encode components of the CCT chaperone complex, which has an important role in proper folding of actin and tubulin. Thus, they are likely to play an important role in spindle assembly and cytokinesis. They also showed a highly elevated mitotic index without DNA damage.
<i>betaTub97EF</i>	DRSC15666	β-tubulin		
<i>T-cp1</i>	DRSC26661, DRSC16877	CCT1	2.6	
<i>CG7033</i>	DRSC18415	CCT2	3.9	
<i>Cctgamma</i>	DRSC16602	CCT3	3.5	
<i>CG5525</i>	DRSC28909, DRSC02865	CCT4	3.5	
<i>Cct5</i>	DRSC26229, DRSC07357	CCT5	4.6	
<i>Tcp-1zeta</i>	DRSC20095	CCT6	3.3	
<i>Tcp-1eta</i>	DRSC16410	CCT7	3.4	
<i>CG8258</i>	DRSC27213, DRSC07130	CCT8	2.2	
<i>dgt2</i>	DRSC29741, DRSC02548	N/A		Known role in mitosis. These genes encode components of the recently identified Augmin complex, which has an essential role in spindle assembly (Goshima and Kimura, 2010).
<i>dgt3</i>	DRSC04349	N/A		
<i>dgt4</i>	DRSC18659	N/A		
<i>dgt5</i>	DRSC29379, DRSC07280	N/A		
<i>dgt6</i>	DRSC14424	FAM29A		
<i>CG2213</i>	DRSC26406, DRSC08560	N/A	2.0	
<i>CG13879</i>	DRSC28973, DRSC08349	N/A	2.1	
<i>CG13914</i>	DRSC08383	N/A		
<i>Arp11</i>	DRSC19448, DRSC19448	ACTR10		Known role in mitosis. These genes encode Dynactin subunits (Goshima et al., 2007).
<i>Arp87C</i>	DRSC14118	ACTR1A		
<i>Gl</i>	DRSC23441	DCTN1		
<i>Dmn</i>	DRSC07132	DCTN2		
<i>dyn-p25</i>	DRSC03525	DCTN5		
<i>l(2)37Ce</i>	DRSC02609, DRSC22810	DCTN6		Known role in mitosis. These genes encode Dynein subunits (Goshima et al., 2007).
<i>Sdic4, Sdic3, Sdic2, sw, Sdic1</i>	DRSC20696	DYNC112		
<i>Dhc64C</i>	DRSC25497, DRSC08656	DYHC1		
<i>Dlc2</i>	DRSC19824	DYNC1L1		
<i>Grip84</i>	DRSC26202, DRSC20248	TUBGCP2		Known role in mitosis. These genes encode components of the γ-tubulin ring complex (Goshima et al., 2007).
<i>l(1)dd4</i>	DRSC20249	TUBGCP3		
<i>Grip163</i>	DRSC26469, DRSC10538	TUBGCP6		
<i>Grip71</i>	DRSC02042	N/A		Known role in mitosis. These genes encode Kinesin proteins (Goshima et al., 2007).
<i>Klp61F</i>	DRSC28179, DRSC08671, DRSC23255	KIF11		
<i>Klp67A</i>	DRSC26028, DRSC11205	KIF18A	5.4	Known role in mitosis (Goshima et al., 2007).
<i>pav</i>	DRSC08730	KIF23		
<i>dmt</i>	DRSC16932	N/A		
<i>chb</i>	DRSC11469, DRSC39154	CLASP1		
<i>Spindly</i>	DRSC00430	N/A		
<i>polo</i>	DRSC22359	PLK1		
<i>barr</i>	DRSC03488	NCAPH		
<i>Lis-1</i>	DRSC07459	PAFAH1B1		
<i>nudE</i>	DRSC10962	NDEL1		
<i>mars</i>	DRSC06656	DLG7		
<i>SNF1A</i>	DRSC18714	PRKAA2		
<i>SNF4Agamma</i>	DRSC16847	PRKAG2		
<i>endos</i>	DRSC29476, DRSC10658	ARPP-19		

(Continued on next page.)

<i>vin</i>	DRSC23625, DRSC09778	UBCH10	11.0	These genes are components of the anaphase promoting complex (APC), which regulates transition from M to G1. Disruption of APC activity results in accumulation of cells in M phase.
<i>fzy</i>	DRSC03534	CDC20		
<i>shld</i>	DRSC20166	APC1		
<i>mr</i>	DRSC29384	APC2		
<i>Cdc27</i>	DRSC23438, DRSC11112	APC3	13.0	
<i>APC4</i>	DRSC29994, DRSC18360	APC4		
<i>ida</i>	DRSC08163	APC5		
<i>cdc16</i>	DRSC16920	APC6		
<i>cdc23</i>	DRSC02708	APC8		
<i>CG11419</i>	DRSC06071	APC10		
<i>Pomp</i>	DRSC27581, DRSC03201	POMP	2.9	
<i>Pros35</i>	DRSC03401	PSMA1		
<i>Pros25</i>	DRSC28078, DRSC16798	PSMA2		
<i>Prosalpha7</i>	DRSC29365, DRSC07516	PSMA3		
<i>Pros29</i>	DRSC04644	PSMA4		
<i>ProsMA5</i>	DRSC07514	PSMA5		
<i>Prosalpha6</i>	DRSC29087, DRSC07515	PSMA6		
<i>Pros26</i>	DRSC11256	PSMB1		
<i>CG17331</i>	DRSC02603	PSMB2		
<i>Prosbeta3</i>	DRSC16801	PSMB3		
<i>Prosbeta4</i>	DRSC12186	PSMB4		
<i>Prosbeta5</i>	DRSC28939, DRSC07517	PSMB5		
<i>Prosbeta2</i>	DRSC11257	PSMB7		
<i>Rpn1</i>	DRSC11274	RPN1	3.1	These genes are components of the proteasome. Knockdown of these genes result in metaphase arrest presumably due to abrogation of APC activity.
<i>Rpn2</i>	DRSC16839	RPN2	6.3	
<i>Dox-A2</i>	DRSC29446, DRSC03318	RPN3		
<i>Rpn5</i>	DRSC28279, DRSC12367	RPN5		
<i>Rpn6</i>	DRSC07541	RPN6		
<i>Rpn7</i>	DRSC25951, DRSC16841	RPN7		
<i>Mov34</i>	DRSC29897, DRSC04624	RPN8		
<i>Rpn9</i>	DRSC27177, DRSC16840	RPN9		
<i>Pros54</i>	DRSC11876	RPN10		
<i>Rpn11</i>	DRSC03422	RPN11		
<i>Rpn12</i>	DRSC28589, DRSC11275	RPN12		
<i>Rpt1</i>	DRSC07542	RPT1		
<i>Pros26.4</i>	DRSC25012, DRSC16799	RPT2		
<i>Rpt3</i>	DRSC23412, DRSC20283	RPT3		
<i>Rpt4</i>	DRSC18713	RPT4		
<i>Tbp-1</i>	DRSC26269, DRSC16842	RPT5		
<i>r-I</i>	DRSC17042	UMPS		
<i>CG11123</i>	DRSC06040	C14orf21		
<i>CCKLR-17D3</i>	DRSC20015	CCKAR		
<i>CG11425</i>	DRSC28400	PPAP2B		
<i>tlk</i>	DRSC22926	TLK1		
<i>Nxt1</i>	DRSC04630	NXT2		
<i>CG31150</i>	DRSC16524	N/A		
<i>LSm-4</i>	DRSC02845	LOC441016		

These genes were not included in the current analysis for technical reasons.

Table S3. Statistics of the secondary screens. S2R+ cells were treated with indicated DNA damaging agents. Mitotic indices with or without treatment and relative mitotic indices are shown with range of two replicates. The treatment condition is indicated at the top of each table. The data correspond to fig. S4.

Gene	Doxorubicin 0.5 μ M					
	MI without treatment (%)		MI after treatment (%)		Relative MI (%)	
	mean	range	mean	range	mean	range
RecQ4	2.98	0.13	4.13	0.05	137.90	4.97
Top2	1.58	0.04	1.62	0.01	102.24	3.21
Myt1	1.82	0.02	1.87	0.04	101.91	0.29
14-3-3epsilon	3.20	0.03	3.29	0.18	100.24	1.82
Rpl1215	0.57	0.00	0.45	0.02	80.22	2.07
CDC45L	2.80	0.01	2.09	0.08	76.16	1.78
Topors	1.87	0.03	1.40	0.01	75.10	1.03
CycC	2.05	0.04	1.37	0.05	65.56	2.45
Rpb5	0.82	0.01	0.51	0.01	61.27	1.37
Rpl118	0.79	0.01	0.51	0.07	61.05	5.13
grp	2.15	0.04	1.29	0.02	59.72	1.61
Cdk8	2.21	0.06	1.33	0.06	58.87	0.23
Rpb8	0.83	0.05	0.49	0.01	58.63	3.97
Spt5	0.82	0.03	0.51	0.07	58.15	2.10
alien	0.71	0.07	0.39	0.02	56.43	6.46
Rpl115	0.77	0.04	0.45	0.06	54.74	1.46
Pop2	1.81	0.01	0.78	0.03	43.84	0.75
wds	2.34	0.18	1.03	0.03	43.58	2.76
CG8233	1.72	0.02	0.72	0.04	42.99	1.65
CSN7	0.72	0.02	0.30	0.02	42.52	0.27
Yeti	1.67	0.02	0.68	0.05	42.12	2.03
MED17	1.10	0.06	0.45	0.00	40.63	2.34
Ald	1.29	0.05	0.51	0.01	39.42	1.74
skpA	1.71	0.04	0.69	0.06	38.89	0.69
cul-4	1.20	0.10	0.49	0.07	38.14	0.43
CSN4	0.67	0.03	0.25	0.00	37.93	1.40
Kap-alpha3	0.96	0.02	0.37	0.02	37.64	0.04
rept	1.45	0.02	0.55	0.02	37.39	1.20
Rpb4	1.08	0.04	0.42	0.03	37.24	0.12
E(bx)	2.41	0.02	0.88	0.03	35.86	0.27
CSN1b	0.73	0.02	0.26	0.01	35.20	0.21
CG4699	1.80	0.07	0.66	0.05	35.19	0.07
BRWD3	1.79	0.01	0.61	0.02	34.66	0.65
mus312	1.76	0.03	0.62	0.01	34.62	0.15
Not1	1.80	0.03	0.63	0.03	34.50	1.19
mus304	2.21	0.02	0.75	0.04	33.18	1.28
CG9797	2.53	0.04	0.89	0.13	32.74	2.09
MED4	1.60	0.02	0.55	0.06	32.70	1.49
CSN3	0.87	0.01	0.28	0.00	31.96	0.40
eIF4G	1.42	0.09	0.46	0.04	31.40	3.68
RpA-70	1.28	0.00	0.41	0.03	30.61	1.11
SF2	2.31	0.06	0.72	0.05	30.22	0.39
Rbf	3.04	0.15	0.96	0.13	29.59	0.68
Tango6	1.16	0.01	0.34	0.01	29.10	0.09
pont	1.38	0.02	0.43	0.05	29.08	1.25
mei-41	2.25	0.17	0.66	0.07	27.94	3.69
nbs	2.27	0.20	0.70	0.15	27.41	0.80
CSN5	1.07	0.06	0.28	0.01	26.92	2.11
CSN8	0.92	0.00	0.24	0.01	26.47	0.69
Mcm7	1.51	0.13	0.39	0.01	26.03	2.45
mus101	1.90	0.03	0.48	0.03	25.93	0.38
lin19	1.15	0.09	0.29	0.01	25.72	2.25
CSN6	0.93	0.04	0.23	0.00	24.87	0.85
dgt1	2.02	0.01	0.50	0.00	24.59	0.21
DDB1	1.28	0.03	0.31	0.02	23.33	0.31
Su(var)2-10	1.86	0.01	0.43	0.00	23.25	0.01
MBD-R2	2.12	0.01	0.47	0.04	23.10	1.00
gzf	1.93	0.12	0.45	0.01	23.01	1.75
Rga	2.04	0.09	0.49	0.05	22.69	0.21
tefu	1.97	0.07	0.41	0.00	20.66	0.77
lwr	1.84	0.01	0.39	0.04	20.12	1.27
CG13745	2.17	0.03	0.43	0.02	19.36	0.60
me31B	1.68	0.08	0.33	0.02	18.95	1.56
CG1135	2.20	0.02	0.43	0.07	17.96	1.43
luc+	2.17	0.11	0.27	0.03	11.61	1.31
No dsRNA	2.05	0.06	0.20	0.02	9.51	0.44

Etoposide 10 μ M							
Gene	MI without treatment (%)		MI after treatment (%)		Relative MI (%)		
	mean	range	mean	range	mean	range	
RecQ4	1.27	0.02	1.15	0.10	94.79	5.43	
Top2	1.92	0.01	1.85	0.04	95.33	0.62	
Myt1	1.55	0.14	1.27	0.09	85.70	10.43	
14-3-3epsilon	2.65	0.00	1.70	0.02	64.42	0.41	
Rpl1215	1.30	0.01	0.71	0.02	53.84	0.42	
CDC45L	1.65	0.03	0.82	0.07	51.88	3.17	
Topors	1.55	0.01	0.70	0.09	47.98	2.67	
CycC	1.19	0.04	0.68	0.01	56.66	1.89	
Rpb5	1.13	0.01	0.56	0.01	49.74	0.88	
Rpl118	1.09	0.07	0.50	0.04	48.07	5.00	
grp	2.44	0.06	1.61	0.09	68.03	3.65	
Cdk8	1.33	0.12	0.56	0.03	43.77	4.83	
Rpb8	1.09	0.10	0.53	0.06	45.74	1.46	
Spt5	1.15	0.01	0.33	0.06	26.07	3.05	
alien	0.91	0.02	0.34	0.02	38.81	1.67	
Rpl115	1.13	0.05	0.54	0.03	46.90	3.23	
Pop2	2.03	0.04	0.61	0.02	29.79	1.14	
wds	2.03	0.01	0.63	0.09	33.10	2.28	
CG8233	1.43	0.11	0.77	0.00	54.33	4.38	
CSN7	0.89	0.02	0.30	0.03	31.84	1.30	
Yeti	1.27	0.05	0.53	0.05	43.93	3.74	
MED17	1.18	0.13	0.41	0.07	38.67	7.11	
Ald	1.29	0.00	0.36	0.04	25.85	1.71	
skpA	1.66	0.05	0.98	0.00	58.96	1.57	
cul-4	1.47	0.03	0.77	0.07	54.94	3.40	
CSN4	1.02	0.00	0.40	0.05	36.50	2.65	
Kap-alpha3	1.15	0.05	0.65	0.06	59.19	4.98	
rept	1.76	0.02	0.62	0.03	34.17	1.35	
Rpb4	0.93	0.09	0.23	0.01	25.66	1.76	
E(bx)	2.91	0.01	1.37	0.03	47.67	0.24	
CSN1b	0.91	0.04	0.33	0.00	36.89	1.81	
CG4699	1.76	0.02	0.91	0.06	50.43	2.28	
BRWD3	1.87	0.07	0.94	0.04	48.98	0.67	
mus312	1.56	0.04	0.93	0.01	59.98	1.14	
Not1	2.32	0.09	0.64	0.07	26.16	2.49	
mus304	2.45	0.11	1.33	0.06	53.11	3.55	
CG9797	2.66	0.05	0.98	0.05	37.85	0.21	
MED4	1.49	0.03	0.34	0.02	23.33	0.16	
CSN3	1.06	0.01	0.37	0.00	34.83	0.11	
eIF4G	1.85	0.09	0.91	0.02	49.62	1.83	
RpA-70	1.28	0.09	0.32	0.05	23.49	3.64	
SF2	1.76	0.05	0.54	0.01	30.41	1.12	
Rbf	2.61	0.00	0.78	0.02	30.02	0.34	
Tango6	1.25	0.04	0.30	0.01	24.12	1.12	
pont	1.58	0.13	0.53	0.01	33.45	2.50	
mei-41	2.51	0.00	1.21	0.09	49.79	1.71	
nbs	2.11	0.04	0.58	0.00	27.44	0.41	
CSN5	1.24	0.02	0.43	0.01	34.93	0.12	
CSN8	1.01	0.01	0.31	0.03	29.57	1.69	
Mcm7	1.31	0.07	0.36	0.04	28.89	2.91	
mus101	1.44	0.03	0.51	0.02	34.84	0.05	
lin19	1.10	0.16	0.36	0.05	30.47	2.01	
CSN6	0.91	0.04	0.35	0.02	37.18	2.91	
dgt1	1.52	0.01	0.54	0.03	34.45	0.67	
DDB1	1.22	0.02	0.27	0.01	22.07	0.74	
Su(var)2-10	1.63	0.01	0.44	0.01	27.54	0.35	
MBD-R2	1.62	0.03	0.61	0.02	37.18	0.06	
gfzf	1.63	0.02	0.84	0.02	51.91	0.16	
Rga	2.27	0.02	0.92	0.05	41.46	1.31	
tefu	2.28	0.09	1.30	0.12	59.83	5.03	
lwr	1.74	0.10	0.20	0.01	11.90	0.90	
CG13745	1.66	0.08	0.44	0.09	24.17	4.01	
me31B	1.35	0.04	0.42	0.01	31.21	1.30	
CG1135	1.61	0.01	0.52	0.01	32.84	0.67	
luc+	1.82	0.09	0.40	0.10	24.52	1.65	
No dsRNA	1.50	0.04	0.31	0.03	20.48	1.38	

Gene	Bleocin 50 µg/µl					
	MI without treatment (%)		MI after treatment (%)		Relative MI (%)	
	mean	range	mean	range	mean	range
RecQ4	2.98	0.13	4.22	0.30	146.83	11.28
Top2	1.58	0.04	0.30	0.02	18.74	1.04
Myt1	1.82	0.02	0.99	0.03	55.21	1.63
14-3-3epsilon	3.20	0.03	2.36	0.06	74.89	1.65
Rpl1215	0.57	0.00	0.28	0.02	47.52	1.17
CDC45L	2.80	0.01	1.65	0.03	58.63	0.25
Topors	1.87	0.03	0.21	0.01	10.79	0.49
CycC	2.05	0.04	1.25	0.03	60.08	2.04
Rpb5	0.82	0.01	0.17	0.01	21.52	0.38
Rpl118	0.79	0.01	0.19	0.02	23.35	1.67
grp	2.15	0.04	1.59	0.05	72.77	2.65
Cdk8	2.21	0.06	1.23	0.14	59.14	4.71
Rpb8	0.83	0.05	0.31	0.01	38.09	1.70
Spt5	0.82	0.03	0.15	0.02	16.45	0.75
alien	0.71	0.07	0.22	0.01	30.12	1.84
Rpl115	0.77	0.04	0.17	0.01	21.39	0.43
Pop2	1.81	0.01	0.55	0.02	29.78	0.65
wds	2.34	0.18	0.45	0.04	18.50	0.52
CG8233	1.72	0.02	0.35	0.00	20.24	0.23
CSN7	0.72	0.02	0.19	0.03	28.70	1.03
Yeti	1.67	0.02	0.40	0.01	23.74	0.07
MED17	1.10	0.06	0.18	0.00	16.90	1.05
Ald	1.29	0.05	0.37	0.00	28.68	1.05
skpA	1.71	0.04	0.24	0.02	14.88	1.00
cul-4	1.20	0.10	0.28	0.05	21.36	0.17
CSN4	0.67	0.03	0.23	0.02	32.43	2.83
Kap-alpha3	0.96	0.02	0.29	0.01	29.02	0.02
rept	1.45	0.02	0.29	0.00	20.33	0.07
Rpb4	1.08	0.04	0.14	0.01	12.51	0.04
E(bx)	2.41	0.02	0.64	0.04	25.58	0.52
CSN1b	0.73	0.02	0.22	0.00	30.64	0.52
CG4699	1.80	0.07	0.34	0.03	17.95	0.17
BRWD3	1.79	0.01	0.14	0.01	7.82	0.14
mus312	1.76	0.03	0.83	0.03	46.40	0.13
Not1	1.80	0.03	0.47	0.07	24.36	2.42
mus304	2.21	0.02	1.09	0.01	49.37	0.69
CG9797	2.53	0.04	0.40	0.00	15.74	0.21
MED4	1.60	0.02	0.27	0.01	17.31	0.43
CSN3	0.87	0.01	0.19	0.03	24.17	1.91
eIF4G	1.42	0.09	0.45	0.03	31.11	3.14
RpA-70	1.28	0.00	0.76	0.06	57.27	2.31
SF2	2.31	0.06	0.48	0.01	20.61	0.27
Rbf	3.04	0.15	0.39	0.04	12.16	0.06
Tango6	1.16	0.01	0.15	0.01	12.61	0.34
pont	1.38	0.02	0.24	0.02	17.02	0.32
mei-41	2.25	0.17	1.05	0.03	46.24	4.28
nbs	2.27	0.20	0.23	0.04	9.31	0.11
CSN5	1.07	0.06	0.23	0.02	22.24	2.01
CSN8	0.92	0.00	0.15	0.02	15.32	1.29
Mcm7	1.51	0.13	0.23	0.00	14.99	1.18
mus101	1.90	0.03	0.58	0.02	30.08	1.05
lin19	1.15	0.09	0.22	0.04	20.98	3.41
CSN6	0.93	0.04	0.22	0.02	24.44	1.95
dgt1	2.02	0.01	0.33	0.03	17.01	0.55
DDB1	1.28	0.03	0.20	0.02	14.95	0.62
Su(var)2-10	1.86	0.01	0.30	0.03	16.86	0.76
MBD-R2	2.12	0.01	0.23	0.02	11.41	0.65
gfzf	1.93	0.12	0.32	0.00	16.46	0.96
Rga	2.04	0.09	0.30	0.01	15.17	0.92
tefu	1.97	0.07	0.25	0.04	11.98	1.33
lwr	1.84	0.01	0.26	0.03	13.19	0.92
CG13745	2.17	0.03	0.26	0.02	11.78	0.52
me31B	1.68	0.08	0.49	0.03	28.41	2.22
CG1135	2.20	0.02	0.26	0.02	11.50	0.30
luc+	2.17	0.11	0.19	0.01	8.38	0.74
No dsRNA	2.05	0.06	0.18	0.01	8.54	0.42

X-ray 150 Gy							
Gene	MI without treatment (%)		MI after treatment (%)		Relative MI (%)		
	mean	range	mean	range	mean	range	
RecQ4	2.15	0.37	3.40	0.19	166.15	24.10	
Top2	1.59	0.29	0.77	0.05	51.38	7.99	
Myt1	1.85	0.14	1.28	0.03	70.26	5.99	
14-3-3epsilon	3.20	0.19	2.49	0.08	79.23	3.46	
Rpl1215	1.07	0.05	0.62	0.16	64.83	4.13	
CDC45L	2.16	0.32	1.99	0.13	96.81	11.33	
Topors	1.94	0.21	0.57	0.04	30.78	2.45	
CycC	2.25	0.22	1.71	0.07	78.02	6.11	
Rpb5	1.06	0.04	0.57	0.09	57.90	6.00	
Rpl118	1.18	0.12	0.57	0.08	52.15	2.08	
grp	2.06	0.02	1.50	0.16	68.96	4.67	
Cdk8	2.35	0.27	1.40	0.00	60.28	6.93	
Rpb8	1.20	0.09	0.75	0.17	69.40	2.07	
Spt5	1.35	0.04	0.40	0.03	30.75	0.17	
alien	0.81	0.06	0.46	0.02	59.04	3.02	
Rpl115	1.17	0.03	0.50	0.11	47.44	3.41	
Pop2	1.94	0.20	1.00	0.06	53.42	3.79	
wds	2.49	0.10	1.10	0.12	46.64	4.27	
CG8233	1.94	0.11	0.74	0.10	40.66	0.16	
CSN7	0.89	0.02	0.41	0.02	46.89	2.11	
Yeti	1.49	0.14	0.68	0.08	48.45	1.83	
MED17	1.35	0.06	0.54	0.09	43.10	5.18	
Ald	1.37	0.17	0.76	0.01	55.87	7.27	
skpA	2.02	0.08	0.69	0.03	35.07	0.76	
cul-4	1.29	0.11	0.69	0.05	56.31	2.78	
CSN4	0.73	0.07	0.36	0.05	52.42	1.33	
Kap-alpha3	1.12	0.05	0.52	0.04	49.05	0.28	
rept	1.79	0.20	0.89	0.13	53.60	2.25	
Rpb4	1.05	0.04	0.38	0.01	36.60	1.03	
E(bx)	3.21	0.05	2.06	0.08	65.45	0.26	
CSN1b	0.79	0.08	0.38	0.02	49.90	3.37	
CG4699	2.20	0.08	1.03	0.09	49.11	0.35	
BRWD3	1.72	0.12	0.56	0.10	35.67	0.41	
mus312	1.88	0.19	1.21	0.13	68.18	3.44	
Not1	1.74	0.12	0.83	0.09	50.49	0.99	
mus304	2.36	0.15	1.46	0.09	63.83	2.12	
CG9797	2.44	0.35	1.08	0.20	48.77	2.80	
MED4	1.60	0.16	0.67	0.11	45.31	1.03	
CSN3	0.95	0.03	0.47	0.02	50.58	0.72	
eIF4G	1.67	0.26	1.11	0.07	69.74	8.87	
RpA-70	1.07	0.12	0.64	0.03	59.04	7.95	
SF2	2.35	0.12	0.87	0.09	38.96	0.16	
Rbf	2.61	0.31	0.98	0.00	38.05	4.62	
Tango6	1.42	0.12	0.46	0.10	35.47	0.50	
pont	1.81	0.13	0.79	0.10	46.81	0.55	
mei-41	1.94	0.12	1.32	0.05	67.21	5.60	
nbs	2.12	0.24	0.49	0.07	24.95	1.15	
CSN5	1.06	0.04	0.52	0.06	51.49	0.76	
CSN8	0.85	0.05	0.36	0.07	46.19	1.00	
Mcm7	1.45	0.10	0.52	0.08	38.91	0.09	
mus101	1.91	0.07	0.69	0.07	38.05	3.25	
lin19	1.40	0.07	0.79	0.15	62.07	2.19	
CSN6	0.85	0.06	0.43	0.05	53.82	0.68	
dgt1	2.44	0.08	0.85	0.09	36.52	0.64	
DDB1	0.96	0.12	0.32	0.03	35.10	2.82	
Su(var)2-10	1.74	0.09	0.70	0.05	41.56	0.85	
MBD-R2	2.69	0.07	0.98	0.12	38.53	1.15	
gfzf	2.15	0.06	0.54	0.07	26.74	0.85	
Rga	2.22	0.19	1.13	0.11	53.29	2.17	
tefu	2.18	0.15	0.71	0.11	35.19	0.21	
lwr	1.72	0.21	0.52	0.01	31.00	3.60	
CG13745	2.06	0.08	0.76	0.01	37.26	1.83	
me31B	1.98	0.24	0.86	0.06	45.18	3.83	
CG1135	2.55	0.08	0.78	0.07	31.99	0.43	
luc+	2.23	0.29	0.55	0.03	25.77	2.73	
No dsRNA	2.12	0.18	0.52	0.05	26.10	1.12	

Table S4. Sequences of primers used for synthesizing dsRNA templates. The following primers were used to PCR-amplify DNA templates for in vitro transcription of dsRNAs.

luc+-F:	TAATACGACTCACTATAGGGAGCCTTCAGGATTACAAGATTCAAAG
luc+-R:	TAATACGACTCACTATAGGGATCAGAGACTTCAGGCGGTCAACG
Venus-F:	TAATACGACTCACTATAGGGATGGTGAGCAAGGCGGAGG
Venus-R:	TAATACGACTCACTATAGGGGAAGTTGGCCTTGATGCCG
Su(var)2-10-F:	TAATACGACTCACTATAGGGTGACTGAGGATGCTGACTGC
Su(var)2-10-R:	TAATACGACTCACTATAGGGCTGTTTGACGTTGATGTGGG
lwr-F:	TAATACGACTCACTATAGGGTCACCATCAAGCAAATCCTG
lwr-R:	TAATACGACTCACTATAGGGAGAATAATCGGCACCTGCAC
CG9797-F:	TAATACGACTCACTATAGGGACGATTTTCATTTTCGGATTGC
CG9797-R:	TAATACGACTCACTATAGGGAATATCCTCGCCCATGACAG
Trxr-1-F:	TAATACGACTCACTATAGGGCGCGTCTATGGACTGCACTA
Trxr-1-R:	TAATACGACTCACTATAGGGAGTTCCACTGGTGTCTGTTCC
Rbf-F:	TAATACGACTCACTATAGGGCGATCTCATCAACCCCAAAT
Rbf-R:	TAATACGACTCACTATAGGGTGCTTCACGTTGTTAGTGCC
Topors-F:	TAATACGACTCACTATAGGGCGGGAAAAGGACATCTCGTA
Topors-R:	TAATACGACTCACTATAGGGAACGAACTTAATGGAGCCGA
RPA70-F:	TAATACGACTCACTATAGGGCAATGGAGGTGGTGACAGTG
RPA70-R:	TAATACGACTCACTATAGGGGCGCAGCTTAAAGATGTGTG
nbs-F:	TAATACGACTCACTATAGGGACACCCTGCATATCGAGGAC
nbs-R:	TAATACGACTCACTATAGGGGAAGAGACGGGTACGCTCAG
mus81-F:	TAATACGACTCACTATAGGGAAAAATGCCACCACCAAG
mus81-R:	TAATACGACTCACTATAGGGGCTGCTTCTCCTGAACCTTG

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