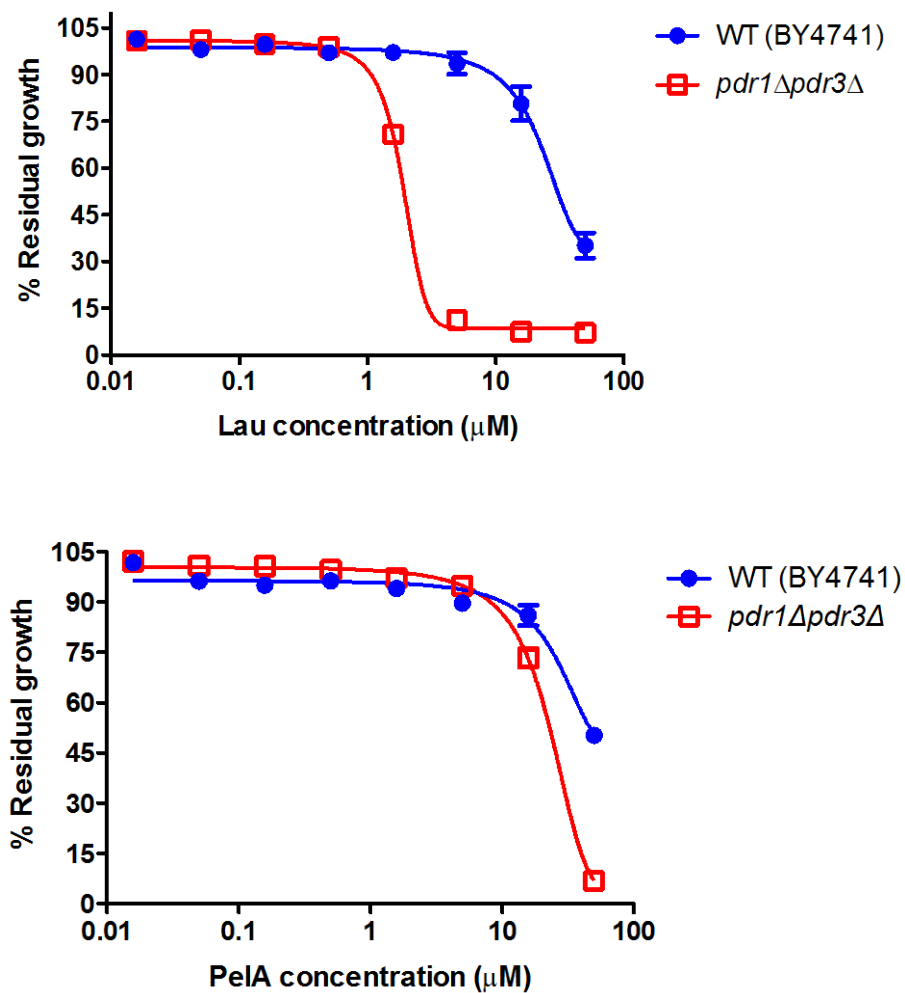
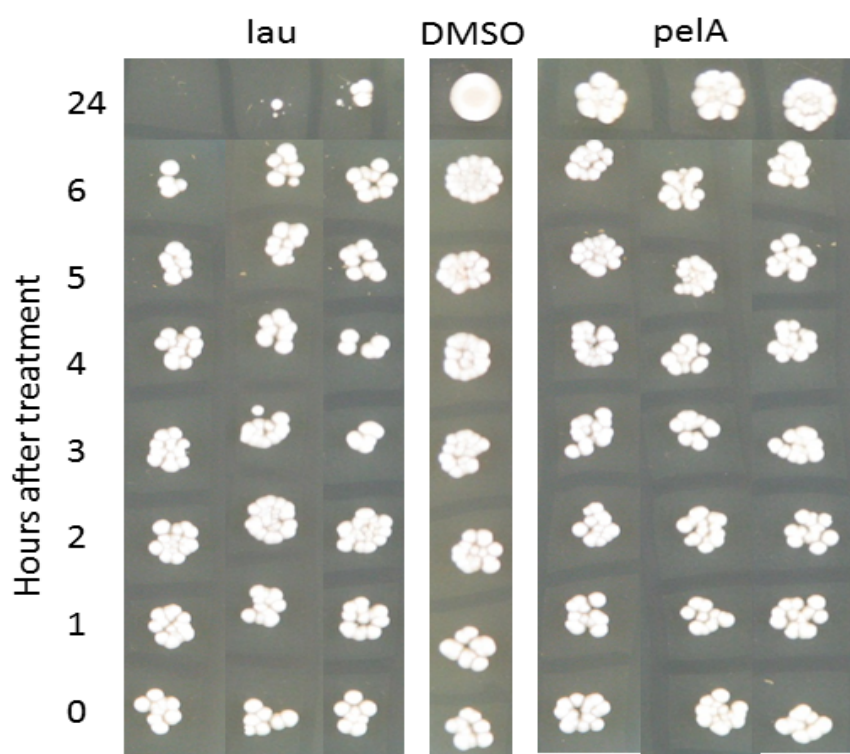


## Supplementary Results

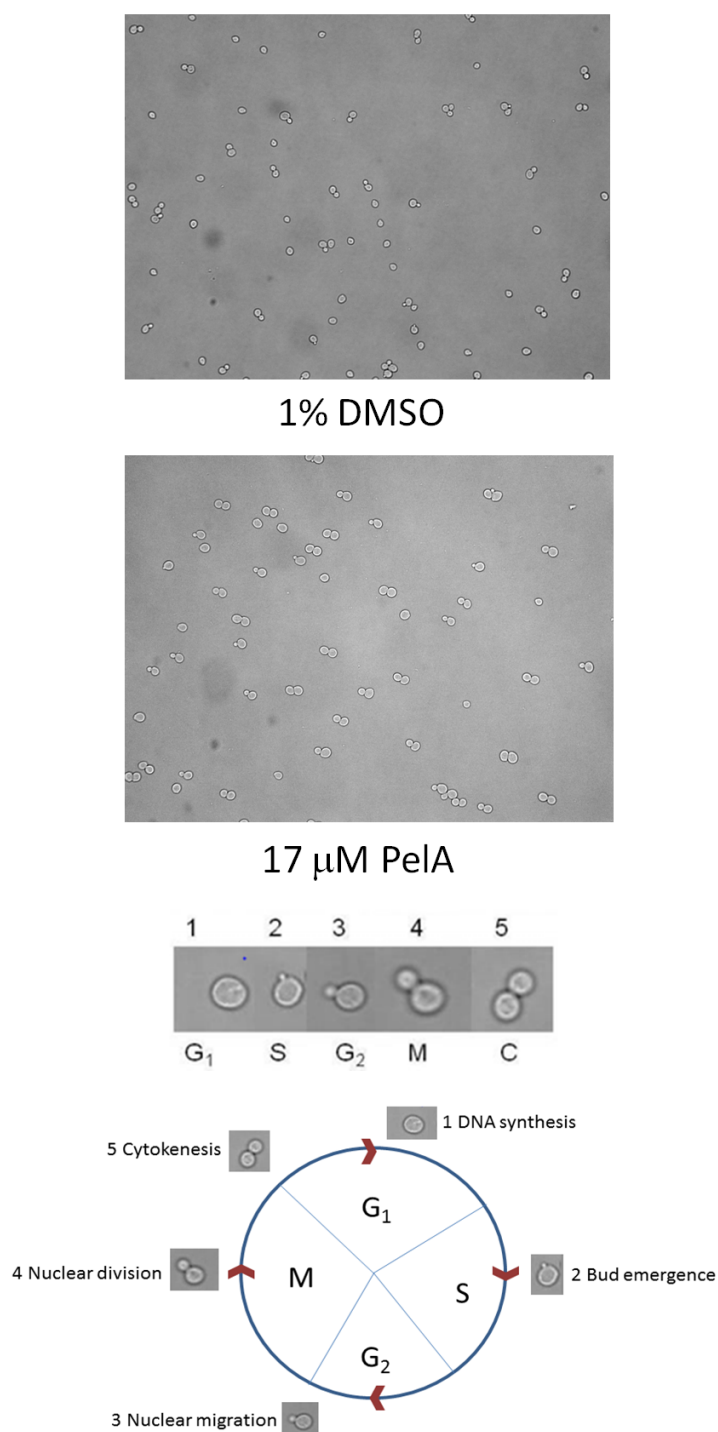


**Fig. S1.** Representative half-log concentration-response curves are for the BY4741 (WT) haploid strain and the *pdr*-deficient strain (*pdr1Δpdr3Δ*) treated with up to 50 μM Lau and PelA in SC medium with 25 mM HEPES for 18 h in technical triplicate.

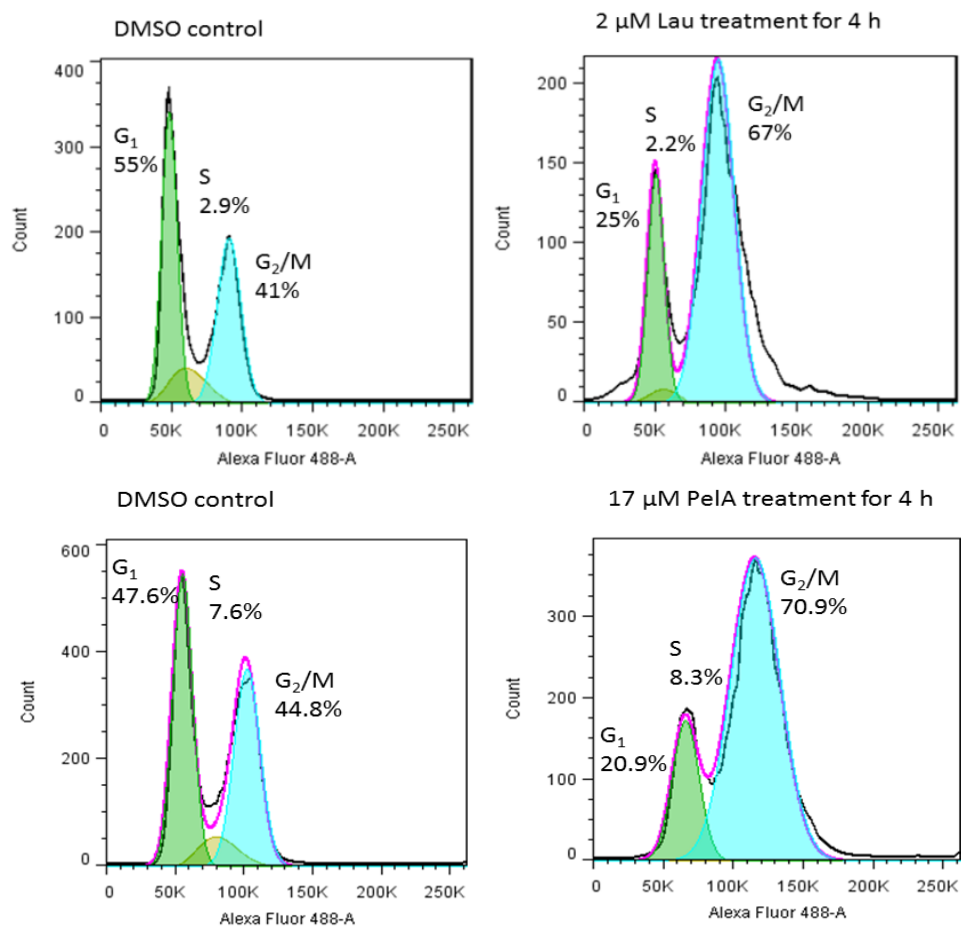


**Fig. S2.** Cytotoxic effects of Lau and PelA.

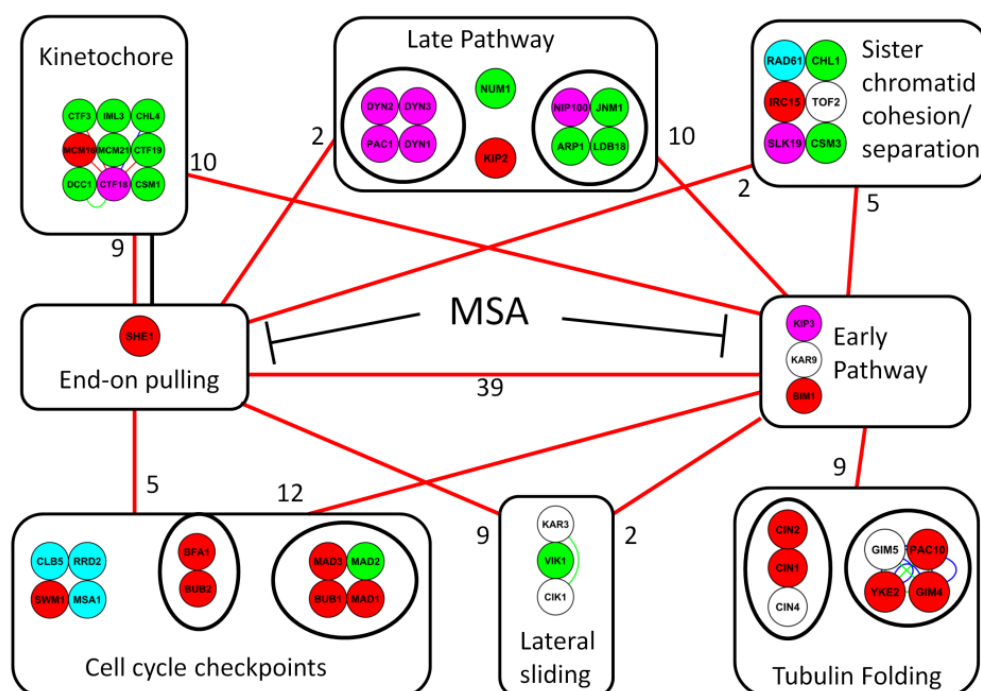
Colony cytotoxicity assays for the *pdr1Δpdr3Δ* strain treated with 10 μM Lau or 30 μM PelA. All experiments were carried out in biological triplicate. Only one of these triplicates is shown for the DMSO control. The image shows growth of 1 μL aliquots of each culture at the time points indicated. The agar plates at the 24-h time point of the whole culture are not shown.



**Fig. S3.** Upper panel: Cell morphologies are shown at each stage of the cell cycle as used to determine the bud index. Lower panel: The *pdr*-deficient strain was treated with 17 μM PelA for 4 h compared to a DMSO (control, upper right). A representative image is shown for 17 μM PelA that was similar to what was seen for treatment with 2 μM Lau for 4 h.



**Fig. S4** Representative flow cytometry results for Lau and PeIA treatments and the DMSO control.



**Fig. S5.** Diagram showing significantly enriched mitosis-related processes from the Lau, PelA, nocodazole (Noc), and benomyl (Ben) profiles. Nodes are coloured according to their specific compound hypersensitivity: Cyan: PelA only; magenta: Lau only; green: PelA/Lau overlap; Red: PelA/Lau overlap with Ben/Noc; White: Ben or Noc only. Negative genetic, synthetic lethal, or growth defect interactions between the genes required for end-on pulling of chromosomes or the early nuclear division pathway and other enriched processes from the Lau and PelA profiles are represented with red lines and the number of interactions between the two groups indicated next to the red lines.

## Supplementary Tables

Table S1. Laulimalide hits. A list of the original (90) and validated (79, in bold) hits for the barcode microarray carried out with the haploid *pdr1Δpdr3ΔxxxΔ* non-essential gene deletion library treated with 2.5 μM Lau (IC<sub>20</sub>). Original hits had a Z score of less than -3, and the validated hits had a % normalised residual growth < 80% of control. The Z-score shown is the average of the UP and DN tags in cases where there was a value < -3 for both. The ratio is an average of the UP and DN tags where there was a value for both. The % normalised residual growth for each individual deletion clone was calculated by the following equation:

$$\% \text{ normalised residual growth} = \frac{\text{Residual growth of validation strain when DMSO 0.3}}{\text{Residual growth of } pdr1\Delta pdr3\Delta his3\Delta \text{ strain when DMSO 0.3}} \times 100$$

SGD ID	Gene name	Z-score	Ratio (Cy5/Cy3)	Normalised residual growth (%)
YCL029C	<b>BIK1</b>	-4.94	0.017	<1
YBR119W	<b>MUD1</b>	-3.13	0.13	<1
YGR188C	<b>BUB1</b>	-3.54	0.057	2
YDR318W	<b>MCM21</b>	-4.82	0.029	3
YCR086W	<b>CSM1</b>	-6.36	0.006	3
YBL031W	<b>SHE1</b>	-2.8	0.148	3
YOR153W	<b>PDR5</b>	-6.73	0.006	4
YMR048W	<b>CSM3</b>	-5.03	0.022	4
YCL016C	<b>DCC1</b>	-5.53	0.013	4
YER016W	<b>BIM1</b>	-4.13	0.043	4
YJL030W	<b>MAD2</b>	-5.74	0.01	4
YDR254W	<b>CHL4</b>	-5.69	0.014	5
YLR200W	<b>YKE2</b>	-3.14	0.08	5
YMR294W	<b>JNM1</b>	-5.04	0.018	6
YMR202W	<b>ERG2</b>	-4.49	0.024	6
YMR078C	<b>CTF18</b>	-3.55	0.064	6
YPL008W	<b>CHL1</b>	-3.5	0.058	7
YMR100W	<b>MUB1</b>	-4.6	0.026	7
YPL174C	<b>NIP100</b>	-5.06	0.021	9
YLR024C	<b>UBR2</b>	-5.27	0.018	10
YPL018W	<b>CTF19</b>	-4.57	0.024	10

YJL197W	<i>UBP12</i>	-4.92	0.022	11
YPR046W	<i>MCM16</i>	-5.52	0.021	12
YDL191W	<i>RPL35A</i>	-3.05	0.095	13
YGR078C	<i>PAC10</i>	-4.69	0.018	14
YPL241C	<i>CIN2</i>	-3.83	0.049	14
YEL003W	<i>GIM4</i>	-4.47	0.03	14
YAR002W	<i>NUP60</i>	-3.42	0.053	14
YJL013C	<i>MAD3</i>	-5.77	0.014	15
YOR269W	<i>PAC1</i>	-4.16	0.042	17
YDR424C	<i>DYN2</i>	-4.27	0.063	17
YER120W	<i>SCS2</i>	-4.1	0.049	19
YBR107C	<i>IML3</i>	-3.27	0.113	19
YCR009C	<i>RVS161</i>	-3.31	0.058	20
YOR061W	<i>CKA2</i>	-3.86	0.043	20
YDR156W	<i>RPA14</i>	-3.87	0.041	21
YNR051C	<i>BRE5</i>	-4.49	0.028	22
YML016C	<i>PPZ1</i>	-3.02	0.112	23
YLR381W	<i>CTF3</i>	-4.62	0.022	23
YMR055C	<i>BUB2</i>	-3.86	0.066	24
YDR260C	<i>SWM1</i>	-3.9	0.06	24
YLL049W	<i>LDB18</i>	-4.84	0.017	25
YOR349W	<i>CINI</i>	-4.05	0.075	25
YDR150W	<i>NUM1</i>	-4.45	0.027	25
YOR082C	<i>YOR082C</i>	-3.79	0.055	26
YKR054C	<i>DYN1</i>	-4.67	0.048	27
YML096W	-	-2.85	0.134	28
YMR031W-A	-	-5.33	0.014	29
YDR360W	-	-2.71	0.229	31
YOR001W	<i>RRP6</i>	-4.81	0.02	32
YPL155C	<i>KIP2</i>	-5.1	0.021	34
YDR333C	-	-1.58	0.867	34
YGL217C	-	-4	0.062	36

YDR149C	-	-4.94	0.016	38
YBR226C	-	-2.88	0.109	40
YJR053W	<i>BFA1</i>	-4.11	0.038	41
YAL004W	-	-3.33	0.1	41
YGL086W	<i>MAD1</i>	-6.15	0.007	42
YPL184C	<i>MRN1</i>	-3.76	0.09	45
YNL142W	<i>MEP2</i>	-2.86	0.114	47
YOL025W	<i>LAG2</i>	-3.85	0.051	48
YOR195W	<i>SLK19</i>	-2.96	0.17	48
YGL096W	<i>TOS8</i>	-3.37	0.08	48
YPL162C	-	-3.26	0.097	49
YGR033C	<i>FMP17</i>	-2.89	0.14	54
YGL139W	-	-2.98	0.129	55
YPL253C	<i>VIK1</i>	-3	0.15	55
YDR466W	<i>PKH3</i>	-3.65	0.06	55
YKR055W	<i>RHO4</i>	-3.55	0.094	56
YBR073W	<i>RDH54</i>	-3.83	0.056	57
YOR140W	<i>SFL1</i>	-3.85	0.053	57
YBR178W	-	-3.96	0.037	58
YNL323W	<i>LEM3</i>	-4.92	0.018	59
YLR194C	-	-2.08	0.707	60
YPR068C	<i>HOS1</i>	-3.39	0.112	64
YNL130C	<i>CPT1</i>	-3.78	0.036	66
YGL216W	<i>KIP3</i>	-3.25	0.071	73
YPL017C	-	-1.98	0.686	76
YMR299C	<i>DYN3</i>	-3.12	0.15	76
YKR053C	<i>YSR3</i>	-2.92	0.146	87
YKR020W	<i>VPS67</i>	-3.22	0.071	87
YAL017W	<i>PSK1</i>	-4.37	0.036	96
YHR129C	<i>ARPI</i>	-3.57	0.049	97
YGR217W	<i>CCHI</i>	-3.12	0.486	103
YMR316C-A	-	-1.74	2.411	110



YMR015C	<i>ERG5</i>	-3.1	0.077	111
YNL136W	<i>EAF7</i>	-3.22	0.074	115
YMR189W	<i>GCV2</i>	-3.16	0.077	131
YKR041W	-	-2.34	0.255	147
YOR231W	<i>MKK1</i>	-1.74	0.74	157

Table S2. Peloruside A hits. A list of the original (77) and validated (65, in bold) hits for the barcode microarray carried out with the haploid *pdr1Δpdr3ΔxxxΔ* non-essential gene deletion library treated with 9 μM PelA (IC<sub>20</sub>).

ORF name	Gene name	Z-scores	Ratio (Cy5/Cy3)	Normalised residual growth (%)
<b>YJL030W</b>	<i>MAD2</i>	-7.2	<b>-6.566</b>	12
<b>YGR188C</b>	<i>BUB1</i>	-5.7	<b>-5.246</b>	13
<b>YGR078C</b>	<i>PAC10</i>	-5.1	<b>-4.652</b>	15
<b>YGR106C</b>	<i>VOA1</i>	-4.5	<b>-4.144</b>	15
<b>YPR046W</b>	<i>MCM16</i>	-4.4	<b>-4.081</b>	16
<b>YER016W</b>	<i>BIM1</i>	-5.6	<b>-5.133</b>	17
<b>YCL016C</b>	<i>DCC1</i>	-5.5	<b>-5.085</b>	17
<b>YPL018W</b>	<i>CTF19</i>	-5.9	<b>-5.415</b>	17
<b>YMR202W</b>	<i>ERG2</i>	-5.4	<b>-4.972</b>	17
<b>YLR381W</b>	<i>CTF3</i>	-6.9	<b>-6.269</b>	17
<b>YHL031C</b>	<i>GOS1</i>	-4.9	<b>-4.523</b>	18
<b>YDR203W</b>	-	-3.7	<b>-3.489</b>	18
<b>YJL029C</b>	<i>VPS53</i>	-3.5	<b>-3.252</b>	19
<b>YDR388W</b>	<i>RVS167</i>	-3.4	<b>-3.225</b>	19
<b>YIL135C</b>	<i>VHS2</i>	-3.2	<b>-3.013</b>	19
<b>YPL017C</b>	<i>IRC15</i>	-4	<b>-3.731</b>	20
<b>YJL013C</b>	<i>MAD3</i>	-7.7	<b>-7.013</b>	20
<b>YAL026C</b>	<i>DRS2</i>	-3.7	<b>-3.437</b>	20
<b>YGL086W</b>	<i>MAD1</i>	-5.5	<b>-5.002</b>	21
<b>YMR031W-A</b>	-	-4.5	<b>-4.119</b>	21
<b>YBR164C</b>	<i>ARL1</i>	-5	<b>-4.537</b>	21
<b>YDR202C</b>	<i>RAV2</i>	-3.3	<b>-3.115</b>	21
<b>YJR033C</b>	<i>RAV1</i>	-4.3	<b>-4.028</b>	22
<b>YDL119C</b>	-	-3.2	<b>-3.04</b>	23
<b>YDR074W</b>	<i>TPS2</i>	-3.3	<b>-3.147</b>	23
<b>YCL029C</b>	<i>BIK1</i>	-6.8	<b>-6.226</b>	24
<b>YJL004C</b>	<i>SYS1</i>	-5.5	<b>-4.967</b>	25
<b>YPL008W</b>	<i>CHL1</i>	-3.7	<b>-3.47</b>	26

YDR014W	<i>RAD61</i>	-3.5	-3.281	27
YOR061W	<i>CKA2</i>	-5.4	-4.921	28
YDR318W	<i>MCM21</i>	-7.7	-7.054	29
YPL253C	<i>VIK1</i>	-5.5	-5.035	30
YBR231C	<i>AOR1</i>	-3.5	-3.219	32
YEL003W	<i>GIM4</i>	-5	-4.602	33
YBR290W	<i>BSD2</i>	-3.1	-2.95	35
YML016C	<i>PPZ1</i>	-3.9	-3.608	35
YDR254W	<i>CHL4</i>	-7.4	-6.692	36
YNL111C	<i>CYB5</i>	-4.2	-3.92	38
YDR435C	<i>PPM1</i>	-4.3	-3.956	40
YCR009C	<i>RVS161</i>	-3.4	-3.155	42
YNL051W	<i>COG5</i>	-4	-3.721	44
YNR051C	<i>BRE5</i>	-3.1	-2.976	45
YML071C	<i>COG8</i>	-4.5	-4.183	46
YOR058C	<i>ASE1</i>	-3	-2.854	47
YOR349W	<i>CINI</i>	-3.5	-3.249	48
YMR048W	<i>CSM3</i>	-4.6	-4.21	49
YER177W	<i>BMH1</i>	-3.8	-3.556	50
YLR024C	<i>UBR2</i>	-4.3	-3.916	50
YDL191W	<i>RPL35A</i>	-4.4	-4.06	53
YKL077W	-	-4.4	-4.026	54
YBR064W	-	-3.5	-3.254	56
YGL094C	<i>PAN2</i>	-3.3	-3.095	59
YGR163W	<i>GTR2</i>	-3.2	-2.992	59
YDR247W	<i>VHS1</i>	-3.5	-3.311	61
YNL296W	-	-3.2	-3.021	62
YCR086W	<i>CSM1</i>	-4.3	-3.923	65
YOR066W	<i>MSA1</i>	-3.4	-3.171	67
YJL053W	<i>PEP8</i>	-4.9	-4.531	68
YJR053W	<i>BFA1</i>	-3.3	-3.097	71
YDR313C	<i>PIB1</i>	-3	-2.863	71

<b>YDR150W</b>	<i>NUM1</i>	<b>-3.4</b>	<b>-3.148</b>	<b>72</b>
<b>YPR120C</b>	<i>CLB5</i>	<b>-3.7</b>	<b>-3.492</b>	<b>73</b>
<b>YLL049W</b>	<i>LDB18</i>	<b>-4.7</b>	<b>-4.304</b>	<b>78</b>
<b>YOR068C</b>	<i>VAM10</i>	<b>-3.2</b>	<b>-2.988</b>	<b>80</b>
<b>YMR294W</b>	<i>JNM1</i>	<b>-4.5</b>	<b>-4.189</b>	<b>80</b>
YDR149C	-	-4.2	-3.903	86
YJL197W	<i>UBP12</i>	-3.4	-3.175	87
YPL152W	<i>RRD2</i>	-4.3	-3.914	89
YPL155C	<i>KIP2</i>	-3.6	-3.335	90
YHL027W	<i>RIM101</i>	-3.4	-3.198	94
YNL130C	<i>CPT1</i>	-3.3	-3.131	95
YJR048W	<i>CYC1</i>	-3	-2.833	102
YHR129C	<i>ARP1</i>	-3.3	-3.117	103
YGL139W	<i>FLC3</i>	-3.1	-2.917	104
YNL323W	<i>LEM3</i>	-6.2	-5.703	110
YMR316C-A	-	-4.2	-3.9	114
YNL041C	<i>COG6</i>	-4.4	-4.123	115

Table S3 GO term enrichment of validated Lau hits using BiNGO.

GO term	corrected p-value	Genes in test set
mitotic cell cycle	2.11E-21	<i>VIK1, SWM1, CTF3, GIM4, MCM16, KIP3, KIP2, LDB18, CTF19, CTF18, IRC15, BFA1, DYN1, SHE1, BUB1, BUB2, BIM1, IML3, DCC1, CSM3, NIP100, CSM1, BIK1, MCM21, MAD1, MAD2, MAD3, YKE2, CHL4, PAC10, SLK19, CHL1</i>
microtubule cytoskeleton	6.68E-21	<i>VIK1, IML3, CTF3, NIP100, PAC1, CIN2, BIK1, KIP3, LDB18, KIP2, MCM21, CTF19, IRC15, BFA1, DYN1, DYN2, SHE1, DYN3, BUB1, BUB2, CHL4, SLK19, JNM1, BIM1</i>
organelle fission	1.86E-20	<i>VIK1, NUM1, SWM1, CTF3, MCM16, KIP2, CTF19, CTF18, BFA1, IRC15, DYN1, SHE1, BUB1, BUB2, BIM1, IML3, DCC1, CSM3, CSM1, BIK1, MCM21, MAD1, MAD2, MAD3, CHL4, SLK19, CHL1</i>
mitosis	1.86E-20	<i>VIK1, SWM1, CTF3, MCM16, KIP2, CTF19, CTF18, BFA1, IRC15, DYN1, SHE1, BUB1, BUB2, BIM1, IML3, DCC1, CSM3, CSM1, BIK1, MCM21, MAD1, MAD2, MAD3, CHL4, SLK19, CHL1</i>
M phase of mitotic cell cycle	1.99E-20	<i>VIK1, SWM1, CTF3, MCM16, KIP2, CTF19, CTF18, BFA1, IRC15, DYN1, SHE1, BUB1, BUB2, BIM1, IML3, DCC1, CSM3, CSM1, BIK1, MCM21, MAD1, MAD2, MAD3, CHL4, SLK19, CHL1</i>
nuclear division	5.18E-20	<i>VIK1, SWM1, CTF3, MCM16, KIP2, CTF19, CTF18, BFA1, IRC15, DYN1, SHE1, BUB1, BUB2, BIM1, IML3, DCC1, CSM3, CSM1, BIK1, MCM21, MAD1, MAD2, MAD3, CHL4, SLK19, CHL1</i>
negative regulation of protein metabolic process	6.84E-20	<i>IML3, NUM1, CTF3, CIN1, NIP100, GIM4, CIN2, BIK1, KIP3, KIP2, CTF19, BFA1, DYN2, BUB1, CHL4, BIM1, LAG2</i>
microtubule-	4.53E-18	<i>VIK1, NUM1, NIP100, PAC1, CIN2, BIK1, KIP3, KIP2,</i>

based process		<i>LDB18, MCM21, CTF19, IRC15, DYN1, DYN2, SHE1, DYN3, BUB1, CHL4, SLK19, JNMI, BIM1</i>
negative regulation of cellular component organization	1.00E-17	<i>CIN1, CTF3, GIM4, CIN2, BIK1, KIP3, KIP2, CTF19, MAD1, MAD2, MAD3, BUB1, BUB2, CHL4, SLK19, CHL1, BIM1</i>
chromosome segregation	1.17E-17	<i>VIK1, IML3, DCC1, CTF3, CSM3, MCM16, CSM1, RDH54, KIP2, MCM21, CTF19, CTF18, IRC15, BFA1, MAD3, DYN1, SHE1, BUB1, BUB2, CHL4, SLK19, CHL1, BIM1</i>
cytoskeletal part	5.55E-17	<i>VIK1, RVSI161, IML3, CTF3, NIP100, PAC1, CIN2, BIK1, KIP3, LDB18, KIP2, MCM21, CTF19, IRC15, BFA1, DYN1, DYN2, SHE1, DYN3, BUB1, BUB2, CHL4, SLK19, JNMI, BIM1</i>
cytoskeleton	2.43E-16	<i>VIK1, RVSI161, IML3, CTF3, NIP100, PAC1, CIN2, BIK1, KIP3, LDB18, KIP2, MCM21, CTF19, IRC15, BFA1, DYN1, DYN2, SHE1, DYN3, BUB1, BUB2, CHL4, SLK19, JNMI, BIM1</i>
M phase	3.66E-16	<i>VIK1, SWM1, CTF3, MCM16, KIP3, KIP2, CTF19, CTF18, BFA1, IRC15, DYN1, SHE1, BUB1, BUB2, BIM1, IML3, DCC1, CSM3, CSM1, RDH54, BIK1, MCM21, MAD1, MAD2, MAD3, CHL4, SLK19, CHL1</i>
sister chromatid segregation	4.29E-15	<i>VIK1, IML3, DCC1, CSM3, CTF3, MCM16, CSM1, RDH54, MCM21, CTF19, CTF18, IRC15, DYN1, BUB1, CHL4, CHL1, BIM1</i>
cell cycle	5.10E-15	<i>VIK1, SWM1, CTF3, GIM4, MCM16, KIP3, KIP2, LDB18, CTF19, CTF18, IRC15, BFA1, DYN1, SHE1, BUB1, BUB2, BIM1, IML3, DCC1, CSM3, NIP100, PAC1, CSM1, RDH54, BIK1, MCM21, MAD1, MAD2, MAD3, YKE2, CHL4, PAC10, SLK19, CHL1</i>
mitotic sister chromatid	4.51E-14	<i>VIK1, IML3, DCC1, CSM3, CTF3, MCM16, CSM1, MCM21, CTF19, CTF18, IRC15, DYN1, BUB1, CHL4,</i>

segregation		<i>CHL1, BIM1</i>
cell cycle phase	5.64E-14	<i>VIK1, SWM1, CTF3, MCM16, KIP3, KIP2, CTF19, CTF18, BFA1, IRC15, DYN1, SHE1, BUB1, BUB2, BIM1, IML3, DCC1, CSM3, CSM1, RDH54, BIK1, MCM21, MAD1, MAD2, MAD3, CHL4, SLK19, CHL1</i>
microtubule	6.88E-14	<i>NIP100, PAC1, CIN2, BIK1, KIP3, KIP2, IRC15, DYN1, SHE1, DYN2, DYN3, SLK19, JNM1, BIM1</i>
mitotic sister chromatid cohesion	1.24E-13	<i>CTF19, VIK1, CTF18, IML3, DCC1, CTF3, CSM3, MCM16, CHL4, CHL1, MCM21, BIM1</i>
cell cycle process	2.19E-13	<i>VIK1, SWM1, CTF3, MCM16, KIP3, KIP2, LDB18, CTF19, CTF18, BFA1, IRC15, DYN1, SHE1, BUB1, BUB2, BIM1, IML3, DCC1, CSM3, NIP100, CSM1, RDH54, BIK1, MCM21, MAD1, MAD2, MAD3, CHL4, SLK19, CHL1</i>
tubulin binding	4.76E-13	<i>NUM1, IRC15, CIN1, NIP100, PAC1, GIM4, YKE2, BIK1, PAC10, BIM1</i>
negative regulation of biological process	6.83E-13	<i>NUM1, CTF3, CIN1, GIM4, CIN2, SCS2, KIP3, KIP2, SFL1, CTF19, BFA1, DYN2, BUB1, BUB2, LAG2, BIM1, IML3, CSM3, NIP100, BIK1, MAD1, MAD2, MAD3, CHL4, SLK19, CHL1</i>
sister chromatid cohesion	3.51E-12	<i>CTF19, VIK1, CTF18, IML3, DCC1, CTF3, CSM3, MCM16, CHL4, CHL1, MCM21, BIM1</i>
microtubule associated complex	1.11E-11	<i>VIK1, DYN1, NIP100, DYN2, DYN3, KIP3, LDB18, KIP2, JNM1</i>
regulation of cellular component organization	1.16E-11	<i>SWM1, CIN1, CTF3, RHO4, GIM4, CIN2, BIK1, KIP3, KIP2, CTF19, MAD1, MAD2, MAD3, BUB1, BUB2, CHL4, SLK19, CHL1, BIM1</i>
microtubule cytoskeleton organization	1.24E-11	<i>NUM1, NIP100, BIK1, KIP3, KIP2, LDB18, MCM21, CTF19, IRC15, DYN1, SHE1, BUB1, CHL4, SLK19, BIM1</i>

negative regulation of macromolecule metabolic process	3.85E-11	<i>IML3, NUM1, CINI, CTF3, CSM3, NIP100, GIM4, CIN2, SCS2, BIK1, KIP3, KIP2, SFL1, CTF19, BFA1, DYN2, BUB1, CHL4, CHL1, BIM1, LAG2</i>
nuclear migration	4.50E-11	<i>NUM1, DYN1, PAC1, DYN3, BIK1, KIP3, KIP2, JNM1, BIM1</i>
establishment of nucleus localization	6.66E-11	<i>NUM1, DYN1, PAC1, DYN3, BIK1, KIP3, KIP2, JNM1, BIM1</i>
nucleus localization	6.66E-11	<i>NUM1, DYN1, PAC1, DYN3, BIK1, KIP3, KIP2, JNM1, BIM1</i>
motor activity	9.98E-11	<i>VIK1, DYN1, NIP100, DYN2, SHE1, DYN3, KIP3, KIP2, JNM1</i>
negative regulation of metabolic process	1.36E-10	<i>IML3, NUM1, CINI, CTF3, CSM3, NIP100, GIM4, CIN2, SCS2, BIK1, KIP3, KIP2, SFL1, CTF19, BFA1, DYN2, BUB1, CHL4, CHL1, BIM1, LAG2</i>
kinetochore	1.48E-10	<i>CTF19, MAD1, IML3, CTF3, CSM1, MCM16, BUB1, CHL4, BIK1, SLK19, MCM21, BIM1</i>
spindle	1.70E-10	<i>VIK1, IML3, NIP100, BIK1, KIP2, MCM21, CTF19, BFA1, DYN1, SHE1, BUB2, CHL4, SLK19, BIM1</i>
non-membrane-bounded organelle	3.22E-10	<i>VIK1, RVS161, CTF3, MCM16, CIN2, KIP3, KIP2, LDB18, SFL1, CTF19, CTF18, IRC15, BFA1, DYN1, RPA14, DYN2, SHE1, CKA2, DYN3, BUB1, BUB2, BIM1, IML3, RPL35A, DCC1, CSM3, RRP6, NIP100, PAC1, CSM1, BIK1, MCM21, MAD1, TOS8, CHL4, SLK19, JNM1</i>
intracellular non-membrane-bounded organelle	3.22E-10	<i>VIK1, RVS161, CTF3, MCM16, CIN2, KIP3, KIP2, LDB18, SFL1, CTF19, CTF18, IRC15, BFA1, DYN1, RPA14, DYN2, SHE1, CKA2, DYN3, BUB1, BUB2, BIM1, IML3, RPL35A, DCC1, CSM3, RRP6, NIP100, PAC1, CSM1, BIK1, MCM21, MAD1, TOS8, CHL4, SLK19, JNM1</i>
nuclear migration	3.23E-10	<i>NUM1, DYN1, PAC1, DYN3, BIK1, KIP3, KIP2, BIM1</i>



along microtubule		
microtubule-based transport	5.20E-10	<i>NUM1, DYN1, PAC1, DYN3, BIK1, KIP3, KIP2, BIM1</i>
cytoskeletal protein binding	5.20E-10	<i>NUM1, RVS161, IRC15, CIN1, NIP100, SHE1, PAC1, GIM4, YKE2, BIK1, PAC10, BIM1</i>
establishment of sister chromatid cohesion	6.82E-10	<i>CTF19, IML3, CTF3, CSM3, MCM16, CHL4, MCM21</i>
establishment of mitotic sister chromatid cohesion	6.82E-10	<i>CTF19, IML3, CTF3, CSM3, MCM16, CHL4, MCM21</i>
chromosome, centromeric region	7.87E-10	<i>CTF19, MAD1, IML3, CTF3, CSM1, MCM16, BUB1, CHL4, BIK1, SLK19, MCM21, BIM1</i>
microtubule-based movement	1.74E-09	<i>NUM1, DYN1, PAC1, DYN3, BIK1, KIP3, KIP2, BIM1</i>
protein complex	1.74E-09	<i>VIK1, SWM1, CTF3, GIM4, MCM16, CIN2, KIP3, LDB18, KIP2, CTF19, CTF18, IRC15, DYN1, RPA14, DYN2, SHE1, CKA2, DYN3, TIM21, BUB1, BIM1, IML3, DCC1, CSM3, RRP6, NIP100, PAC1, CSM1, BIK1, MCM21, MAD1, NUP60, MAD2, MAD3, YKE2, CHL4, PAC10, SLK19, JNM1, HOS1</i>
cytoskeleton-dependent intracellular transport	2.47E-09	<i>NUM1, DYN1, PAC1, DYN3, BIK1, KIP3, KIP2, BIM1</i>
organelle organization	3.24E-09	<i>VIK1, RVS161, NUM1, SWM1, CTF3, MCM16, SCS2, KIP3, KIP2, LDB18, CTF19, CTF18, IRC15, BFA1, DYN1, DYN2, SHE1, TIM21, BUB1, BUB2, BIM1, IML3, DCC1, CSM3, RRP6, NIP100, CSM1, RDH54, BIK1, MCM21, MAD1, NUP60, MAD2, MAD3, CHL4, SLK19, CHL1, HOS1</i>

cytoplasmic microtubule	3.86E-09	<i>DYN1, DYN2, PAC1, DYN3, KIP3, KIP2, BIM1</i>
establishment of organelle localization	4.58E-09	<i>NUM1, DYN1, NIP100, PAC1, DYN3, BUB1, BIK1, KIP3, LDB18, KIP2, JNM1, BIM1</i>
cellular component organization	1.46E-08	<i>VIK1, RVS161, NUM1, SWM1, CINI, CTF3, GIM4, MCM16, CIN2, SCS2, YLR194C, KIP3, LDB18, KIP2, CTF19, CTF18, IRC15, BFA1, DYN1, DYN2, SHE1, TIM21, BUB1, BUB2, LEM3, BIM1, IML3, DCC1, CSM3, RRP6, NIP100, CSM1, RDH54, BIK1, MCM21, MAD1, NUP60, MAD2, MAD3, YKE2, CHL4, PAC10, SLK19, CHL1, HOS1</i>
condensed chromosome kinetochore	1.66E-08	<i>CTF19, IML3, CTF3, CSM1, MCM16, BUB1, CHL4, BIK1, SLK19, MCM21</i>
cytoskeleton organization	3.45E-08	<i>RVS161, NUM1, NIP100, BIK1, KIP3, KIP2, LDB18, MCM21, CTF19, IRC15, DYN1, SHE1, BUB1, CHL4, SLK19, BIM1</i>
condensed chromosome, centromeric region	3.63E-08	<i>CTF19, IML3, CTF3, CSM1, MCM16, BUB1, CHL4, BIK1, SLK19, MCM21</i>
condensed nuclear chromosome kinetochore	4.74E-08	<i>CTF19, IML3, CTF3, MCM16, BUB1, CHL4, BIK1, SLK19, MCM21</i>
organelle localization	9.00E-08	<i>NUM1, DYN1, NIP100, PAC1, DYN3, BUB1, BIK1, KIP3, LDB18, KIP2, JNM1, BIM1</i>
regulation of protein metabolic process	1.29E-07	<i>IML3, NUM1, CTF3, CINI, NIP100, GIM4, CIN2, BIK1, KIP3, KIP2, CTF19, BFA1, DYN2, BUB1, CHL4, BIM1, LAG2</i>
condensed nuclear	1.32E-07	<i>CTF19, IML3, CTF3, MCM16, BUB1, CHL4, BIK1, SLK19, MCM21</i>

chromosome, centromeric region		
dynein complex	1.52E-07	<i>DYN1, NIP100, DYN2, DYN3, JNM1</i>
chromosome organization	1.88E-07	<i>VIK1, IML3, DCC1, CTF3, RRP6, CSM3, MCM16, CSM1, RDH54, MCM21, CTF19, CTF18, IRC15, MAD2, DYN1, BUB1, CHL4, CHL1, BIM1, HOS1</i>
meiotic chromosome segregation	2.86E-07	<i>IML3, IRC15, MAD3, CSM3, CSM1, RDH54, CHL4</i>
mitotic cell cycle spindle checkpoint	3.67E-07	<i>MAD1, BFA1, MAD2, MAD3, BUB1, BUB2, BIM1</i>
cell division	4.24E-07	<i>IML3, SWM1, CTF3, PAC1, MCM16, BIK1, KIP2, MCM21, CTF19, MAD1, BFA1, MAD2, MAD3, SHE1, BUB2, CHL4, SLK19, BIM1</i>
spindle checkpoint	5.88E-07	<i>MAD1, BFA1, MAD2, MAD3, BUB1, BUB2, BIM1</i>
spindle pole	6.17E-07	<i>CTF19, VIK1, BFA1, DYN1, NIP100, BUB2, BIK1, SLK19, MCM21, BIM1</i>
microtubule motor activity	1.09E-06	<i>VIK1, DYN1, DYN2, KIP3, KIP2</i>
chromosomal part	1.11E-06	<i>IML3, DCC1, CTF3, CSM3, MCM16, CSM1, BIK1, KIP2, MCM21, CTF19, CTF18, MAD1, TOS8, BUB1, CHL4, SLK19, BIM1</i>
chromosome	1.26E-06	<i>IML3, DCC1, CTF3, CSM3, MCM16, CSM1, BIK1, KIP2, SFL1, MCM21, CTF19, CTF18, MAD1, TOS8, BUB1, CHL4, SLK19, BIM1</i>
meiosis	1.34E-06	<i>IML3, SWM1, CSM3, CTF3, MCM16, CSM1, RDH54, MCM21, CTF19, IRC15, MAD3, CHL4, SLK19</i>
M phase of meiotic cell cycle	1.34E-06	<i>IML3, SWM1, CSM3, CTF3, MCM16, CSM1, RDH54, MCM21, CTF19, IRC15, MAD3, CHL4, SLK19</i>
macromolecular	1.34E-06	<i>VIK1, SWM1, CTF3, GIM4, MCM16, CIN2, KIP3,</i>

complex		<i>LDB18, KIP2, CTF19, CTF18, IRC15, DYN1, RPA14, DYN2, SHE1, CKA2, DYN3, TIM21, BUB1, BIM1, IML3, RPL35A, MUD1, DCC1, CSM3, RRP6, NIP100, PAC1, CSM1, BIK1, MCM21, MAD1, NUP60, MAD2, MAD3, YKE2, CHL4, PAC10, SLK19, JNMI, HOS1</i>
mitotic cell cycle checkpoint	1.93E-06	<i>MAD1, BFA1, MAD2, MAD3, BUB1, BUB2, BIM1</i>
meiotic cell cycle	2.00E-06	<i>IML3, SWM1, CSM3, CTF3, MCM16, CSM1, RDH54, MCM21, CTF19, IRC15, MAD3, CHL4, SLK19</i>
microtubule binding	2.65E-06	<i>IRC15, NIP100, PAC1, BIK1, BIM1</i>
condensed chromosome	5.39E-06	<i>CTF19, IML3, CTF3, CSM1, MCM16, BUB1, CHL4, BIK1, SLK19, MCM21</i>
regulation of mitotic cell cycle	6.04E-06	<i>MAD1, IRC15, BFA1, MAD2, SWM1, MAD3, BUB1, BUB2, BIM1</i>
regulation of mitotic metaphase/anaphase transition	6.88E-06	<i>MAD1, MAD2, SWM1, MAD3, BUB1, BIM1</i>
condensed nuclear chromosome	1.04E-05	<i>CTF19, IML3, CTF3, MCM16, BUB1, CHL4, BIK1, SLK19, MCM21</i>
cell cycle checkpoint	1.10E-05	<i>MAD1, BFA1, MAD2, MAD3, CSM3, BUB1, BUB2, BIM1</i>
microtubule organizing center	1.20E-05	<i>VIK1, BFA1, DYN1, BUB2, BIK1, SLK19, MCM21, BIM1</i>
spindle pole body	1.20E-05	<i>VIK1, BFA1, DYN1, BUB2, BIK1, SLK19, MCM21, BIM1</i>
regulation of mitosis	2.16E-05	<i>MAD1, MAD2, SWM1, MAD3, BUB1, BIM1</i>
regulation of nuclear division	2.16E-05	<i>MAD1, MAD2, SWM1, MAD3, BUB1, BIM1</i>
negative regulation of	4.19E-05	<i>MAD1, MAD2, MAD3, BUB1, BIM1</i>

mitotic metaphase/anaphase transition		
negative regulation of mitosis	4.19E-05	<i>MAD1, MAD2, MAD3, BUB1, BIM1</i>
mitotic cell cycle spindle assembly checkpoint	4.19E-05	<i>MAD1, MAD2, MAD3, BUB1, BIM1</i>
spindle assembly checkpoint	4.19E-05	<i>MAD1, MAD2, MAD3, BUB1, BIM1</i>
negative regulation of nuclear division	4.19E-05	<i>MAD1, MAD2, MAD3, BUB1, BIM1</i>
cellular localization	5.03E-05	<i>RVS161, IML3, NUM1, RRP6, NIP100, PAC1, CSM1, BIK1, KIP3, LDB18, KIP2, CTF19, MAD1, NUP60, IRC15, DYN1, SHE1, DYN3, TIM21, BUB1, CHL4, JNM1, BIM1</i>
establishment of mitotic spindle orientation	5.03E-05	<i>DYN1, NIP100, KIP3, LDB18</i>
establishment of mitotic spindle localization	5.03E-05	<i>DYN1, NIP100, KIP3, LDB18</i>
spindle localization	5.03E-05	<i>DYN1, NIP100, KIP3, LDB18</i>
establishment of spindle localization	5.03E-05	<i>DYN1, NIP100, KIP3, LDB18</i>
establishment of spindle orientation	5.03E-05	<i>DYN1, NIP100, KIP3, LDB18</i>
regulation of	5.03E-05	<i>RVS161, NUM1, SWM1, MUB1, CTF3, CINI, GIM4,</i>

biological process		<i>CIN2, SCS2, KIP3, KIP2, SFL1, CTF19, IRC15, BFA1, DYN2, CKA2, BUB1, BUB2, PKH3, LAG2, BIM1, IML3, CSM3, NIP100, RHO4, BIK1, MAD1, MAD2, TOS8, MAD3, CHL4, SLK19, CHL1, HOS1</i>
cytoplasmic dynein complex	5.77E-05	<i>DYN1, DYN2, DYN3</i>
negative regulation of organelle organization	5.77E-05	<i>MAD1, MAD2, MAD3, BUB1, KIP2, BIM1</i>
organelle part	6.87E-05	<i>VIK1, ERG2, RVSI61, CPT1, SWM1, CTF3, MCM16, CIN2, SCS2, KIP3, LDB18, KIP2, SFL1, CTF19, CTF18, IRC15, BFA1, DYN1, RPA14, DYN2, SHE1, CKA2, DYN3, YPL162C, TIM21, BUB1, BUB2, BIM1, IML3, RPL35A, MUD1, DCC1, RRP6, CSM3, NIP100, PAC1, CSM1, FLC3, BIK1, MCM21, MAD1, NUP60, MAD2, TOS8, MAD3, CHL4, SLK19, JNM1, HOS1</i>
intracellular organelle part	6.87E-05	<i>VIK1, ERG2, RVSI61, CPT1, SWM1, CTF3, MCM16, CIN2, SCS2, KIP3, LDB18, KIP2, SFL1, CTF19, CTF18, IRC15, BFA1, DYN1, RPA14, DYN2, SHE1, CKA2, DYN3, YPL162C, TIM21, BUB1, BUB2, BIM1, IML3, RPL35A, MUD1, DCC1, RRP6, CSM3, NIP100, PAC1, CSM1, FLC3, BIK1, MCM21, MAD1, NUP60, MAD2, TOS8, MAD3, CHL4, SLK19, JNM1, HOS1</i>
biological regulation	6.87E-05	<i>RVSI61, NUM1, SWM1, MUB1, CIN1, CTF3, GIM4, CIN2, SCS2, KIP3, KIP2, SFL1, CTF19, IRC15, BFA1, RPA14, MEP2, DYN2, CKA2, PPZ1, BUB1, BUB2, PKH3, LAG2, BIM1, IML3, CSM3, NIP100, RHO4, BIK1, MAD1, MAD2, TOS8, MAD3, CHL4, SLK19, CHL1, HOS1</i>
regulation of cell cycle	7.52E-05	<i>MAD1, IRC15, BFA1, MAD2, SWM1, MAD3, CSM3, BUB1, BUB2, SLK19, BIM1</i>
nuclear	8.02E-05	<i>CTF19, CTF18, IML3, TOS8, CTF3, CSM3, MCM16,</i>

chromosome		<i>BUB1, CHL4, BIK1, SLK19, MCM21, SFL1</i>
nuclear chromosome part	1.28E-04	<i>CTF19, CTF18, IML3, TOS8, CTF3, CSM3, MCM16, BUB1, CHL4, BIK1, SLK19, MCM21</i>
protein complex assembly	1.30E-04	<i>MAD1, NUP60, MAD2, CIN1, DYN2, GIM4, YKE2, CIN2, CHL4, BIK1, PAC10, BIM1</i>
protein complex biogenesis	1.30E-04	<i>MAD1, NUP60, MAD2, CIN1, DYN2, GIM4, YKE2, CIN2, CHL4, BIK1, PAC10, BIM1</i>
COMA complex	1.30E-04	<i>CTF19, IML3, MCM21</i>
dynactin complex	1.30E-04	<i>NIP100, LDB18, JNM1</i>
regulation of cell cycle process	1.67E-04	<i>MAD1, BFA1, MAD2, SWM1, MAD3, BUB1, BUB2, BIM1</i>
negative regulation of cell cycle	1.70E-04	<i>MAD1, MAD2, MAD3, BUB1, BIM1</i>
kinesin complex	2.50E-04	<i>VIK1, KIP3, KIP2</i>
nucleoside-triphosphatase activity	3.04E-04	<i>VIK1, RHO4, NIP100, RDH54, KIP3, KIP2, CTF18, DYN1, SHE1, DYN2, DYN3, PDR5, JNM1, CHL1</i>
meiotic sister chromatid segregation	4.18E-04	<i>IML3, IRC15, RDH54</i>
tubulin complex assembly	4.18E-04	<i>GIM4, YKE2, PAC10</i>
prefoldin complex	4.18E-04	<i>GIM4, YKE2, PAC10</i>
nuclear part	4.87E-04	<i>SWM1, CTF3, MCM16, SCS2, KIP3, SFL1, CTF19, CTF18, RPA14, SHE1, CKA2, BUB1, IML3, MUD1, CSM3, RRP6, CSM1, BIK1, MCM21, MAD1, NUP60, MAD2, TOS8, MAD3, CHL4, SLK19, HOS1</i>
pyrophosphatase activity	4.92E-04	<i>VIK1, RHO4, NIP100, RDH54, KIP3, KIP2, CTF18, DYN1, SHE1, DYN2, DYN3, PDR5, JNM1, CHL1</i>
hydrolase activity, acting on acid anhydrides	4.92E-04	<i>VIK1, RHO4, NIP100, RDH54, KIP3, KIP2, CTF18, DYN1, SHE1, DYN2, DYN3, PDR5, JNM1, CHL1</i>

hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	4.92E-04	<i>VIK1, RHO4, NIP100, RDH54, KIP3, KIP2, CTF18, DYN1, SHE1, DYN2, DYN3, PDR5, JNMI, CHL1</i>
regulation of organelle organization	5.50E-04	<i>MAD1, MAD2, SWM1, MAD3, RHO4, BUB1, KIP2, BIM1</i>
meiosis II	6.30E-04	<i>IML3, IRC15, RDH54</i>
regulation of primary metabolic process	8.47E-04	<i>NUM1, CTF3, CINI, GIM4, CIN2, SCS2, KIP3, KIP2, SFL1, CTF19, BFA1, DYN2, CKA2, BUB1, BUB2, LAG2, BIM1, IML3, CSM3, NIP100, BIK1, TOS8, CHL4, CHL1, HOS1</i>
negative regulation of cell cycle process	1.02E-03	<i>MAD1, MAD2, MAD3, BUB1, BIM1</i>
outer kinetochore of condensed chromosome	1.03E-03	<i>IML3, CHL4</i>
outer kinetochore of condensed nuclear chromosome	1.03E-03	<i>IML3, CHL4</i>
establishment of meiotic sister chromatid cohesion	1.03E-03	<i>IML3, CHL4</i>
signaling	1.17E-03	<i>MAD1, BFA1, MAD2, MAD3, CSM3, RHO4, PPZI, BUB1, BUB2, LEM3, SCS2, PKH3, BIM1</i>
regulation of macromolecule metabolic process	1.19E-03	<i>NUM1, IML3, CINI, CTF3, CSM3, NIP100, GIM4, CIN2, SCS2, BIK1, KIP3, KIP2, SFL1, CTF19, BFA1, TOS8, DYN2, CKA2, BUB1, CHL4, CHL1, HOS1, BIM1, LAG2</i>



mitotic spindle organization	1.48E-03	<i>DYN1, SHE1, BIK1, SLK19, KIP3</i>
spindle organization	1.95E-03	<i>DYN1, SHE1, BIK1, SLK19, KIP3</i>
structural constituent of cytoskeleton	1.95E-03	<i>CTF19, BIK1, SLK19, JNM1, BIM1</i>
regulation of metabolic process	2.26E-03	<i>NUM1, CTF3, CIN1, GIM4, CIN2, SCS2, KIP3, KIP2, SFL1, CTF19, BFA1, DYN2, CKA2, BUB1, BUB2, LAG2, BIM1, IML3, CSM3, NIP100, BIK1, TOS8, CHL4, CHL1, HOS1</i>
attachment of spindle microtubules to chromosome	2.78E-03	<i>CTF19, IRC15, BUB1</i>
microtubule anchoring	2.78E-03	<i>CTF19, IRC15, BUB1</i>
maintenance of sister chromatid cohesion	2.82E-03	<i>IML3, CHL4</i>
maintenance of meiotic sister chromatid cohesion	2.82E-03	<i>IML3, CHL4</i>
localization	3.37E-03	<i>RVS161, NUM1, KIP3, KIP2, LDB18, CTF19, IRC15, DYN1, SHE1, MEP2, DYN3, TIM21, BUB1, LEM3, PDR5, BIM1, IML3, RRP6, NIP100, PAC1, CSM1, FLC3, BIK1, MAD1, NUP60, BRE5, CHL4, JNM1</i>
protein binding	3.37E-03	<i>RVS161, NUM1, CTF3, CIN1, NIP100, GIM4, PAC1, MCM16, BIK1, SCS2, MCM21, CTF19, IRC15, SHE1, YKE2, BUB1, PAC10, BIM1</i>
protein localization to	3.38E-03	<i>IML3, CSM1, CHL4</i>

chromosome		
signal transduction	4.28E-03	<i>MAD1, BFA1, MAD2, MAD3, CSM3, RHO4, BUB1, BUB2, PKH3, BIM1</i>
signal transmission	4.65E-03	<i>MAD1, BFA1, MAD2, MAD3, CSM3, RHO4, BUB1, BUB2, PKH3, BIM1</i>
signaling process	5.22E-03	<i>MAD1, BFA1, MAD2, MAD3, CSM3, RHO4, BUB1, BUB2, PKH3, BIM1</i>
mitotic checkpoint complex	5.22E-03	<i>MAD2, MAD3</i>
microtubule depolymerization	5.22E-03	<i>KIP3, BIM1</i>
protein localization to chromosome, centromeric region	5.22E-03	<i>IML3, CHL4</i>
microtubule polymerization or depolymerization	5.22E-03	<i>KIP3, BIM1</i>
cellular process	5.90E-03	<i>ERG2, RVS161, SWM1, CPT1, UBP12, GIM4, MCM16, KIP3, KIP2, SFL1, RPA14, PPZ1, LEM3, LAG2, BIM1, IML3, RPL35A, CSM3, RRP6, PAC1, CSM1, FLC3, BIK1, UBR2, MCM21, MAD1, MAD2, MAD3, BRE5, CHL4, PAC10, SLK19, CHL1, HOS1, VIK1, NUM1, MUB1, CTF3, CIN1, CIN2, YML096W, YLR194C, SCS2, LDB18, CTF19, CTF18, BFA1, IRC15, DYN1, MEP2, DYN2, SHE1, CKA2, DYN3, TIM21, BUB1, BUB2, PKH3, MUD1, DCC1, NIP100, RHO4, RDH54, NUP60, YKE2, JNM1</i>
mitotic anaphase B	8.28E-03	<i>BIK1, KIP2</i>
post-chaperonin	8.28E-03	<i>CIN1, CIN2</i>

tubulin folding pathway		
negative regulation of microtubule depolymerization	8.28E-03	<i>KIP2, BIM1</i>
regulation of microtubule depolymerization	8.28E-03	<i>KIP2, BIM1</i>
negative regulation of microtubule polymerization or depolymerization	8.28E-03	<i>KIP2, BIM1</i>
negative regulation of cellular process	1.05E-02	<i>MAD1, MAD2, MAD3, CSM3, BUB1, SCS2, KIP2, CHL1, SFL1, LAG2, BIM1</i>
intracellular organelle	1.14E-02	<i>ERG2, RVS161, SWM1, CPT1, UBP12, MCM16, KIP3, KIP2, SFL1, RPA14, PPZ1, LEM3, LAG2, BIM1, IML3, RPL35A, CSM3, RRP6, PAC1, CSM1, FLC3, BIK1, MCM21, MAD1, MAD2, TOS8, MAD3, CHL4, SLK19, CHL1, HOS1, VIK1, NUM1, CTF3, CIN2, SCS2, LDB18, CTF19, CTF18, BFA1, IRC15, DYN1, SHE1, DYN2, YPL162C, DYN3, CKA2, TIM21, BUB1, BUB2, PDR5, MUD1, DCC1, NIP100, RDH54, NUP60, YKE2, JNMI</i>
organelle	1.14E-02	<i>ERG2, RVS161, SWM1, CPT1, UBP12, MCM16, KIP3, KIP2, SFL1, RPA14, PPZ1, LEM3, LAG2, BIM1, IML3, RPL35A, CSM3, RRP6, PAC1, CSM1, FLC3, BIK1, MCM21, MAD1, MAD2, TOS8, MAD3, CHL4, SLK19, CHL1, HOS1, VIK1, NUM1, CTF3, CIN2, SCS2, LDB18, CTF19, CTF18, BFA1, IRC15, DYN1, SHE1, DYN2, YPL162C, DYN3, CKA2, TIM21, BUB1, BUB2, PDR5, MUD1, DCC1, NIP100, RDH54, NUP60, YKE2, JNMI</i>

macromolecular complex assembly	1.17E-02	<i>MAD1, NUP60, MAD2, CINI, DYN2, GIM4, YKE2, CIN2, CHL4, BIK1, PAC10, BIM1</i>
mitotic anaphase	1.17E-02	<i>BIK1, KIP2</i>
attachment of spindle microtubules to kinetochore	1.17E-02	<i>CTF19, IRC15</i>
mitotic cell cycle spindle orientation checkpoint	1.17E-02	<i>BFA1, BUB2</i>
endoplasmic reticulum inheritance	1.17E-02	<i>SHE1, SCS2</i>
mitotic spindle elongation	1.31E-02	<i>DYN1, SHE1, BIK1</i>
spindle elongation	1.31E-02	<i>DYN1, SHE1, BIK1</i>
establishment of localization in cell	1.40E-02	<i>NUM1, NIP100, PAC1, BIK1, KIP3, KIP2, LDB18, MAD1, NUP60, DYN1, SHE1, DYN3, TIM21, BUB1, JNM1, BIM1</i>
mitotic spindle organization in nucleus	1.47E-02	<i>BIK1, SLK19, KIP3</i>
protein depolymerization	1.55E-02	<i>KIP3, BIM1</i>
anaphase	1.55E-02	<i>BIK1, KIP2</i>
Ctf18 RFC-like complex	1.55E-02	<i>CTF18, DCC1</i>
nuclear microtubule	1.55E-02	<i>SHE1, KIP3</i>
actin cytoskeleton	1.73E-02	<i>RVS161, NIP100, SHE1, LDB18, JNM1</i>
meiotic sister	2.01E-02	<i>IML3, CHL4</i>

chromatid cohesion		
spindle midzone	2.01E-02	<i>SLK19, BIM1</i>
cellular protein complex assembly	2.04E-02	<i>NUP60, DYN2, GIM4, YKE2, CHL4, PAC10</i>
intracellular	2.25E-02	<i>ERG2, RVSI61, SWM1, CPT1, UBP12, GIM4, MCM16, KIP3, KIP2, SFL1, RPA14, PPZ1, LEM3, LAG2, BIM1, IML3, RPL35A, CSM3, RRP6, PAC1, CSM1, FLC3, BIK1, UBR2, MCM21, MAD1, MAD2, TOS8, MAD3, BRE5, CHL4, PAC10, SLK19, CHL1, HOS1, VIK1, NUM1, MUB1, CTF3, CIN2, YML096W, SCS2, LDB18, CTF19, CTF18, BFA1, IRC15, DYN1, DYN2, SHE1, CKA2, DYN3, YPL162C, TIM21, BUB1, BUB2, PDR5, MUD1, DCC1, NIP100, RHO4, RDH54, NUP60, MRN1, YKE2, JNMI</i>
negative regulation of protein complex disassembly	3.13E-02	<i>KIP2, BIM1</i>
macromolecular complex subunit organization	3.73E-02	<i>CINI, GIM4, CIN2, BIK1, KIP3, MAD1, MAD2, NUP60, DYN2, YKE2, CHL4, PAC10, BIM1</i>
organelle inheritance	4.08E-02	<i>NUM1, RVSI61, SHE1, SCS2</i>
maintenance of protein location in cell	4.35E-02	<i>CTF19, IRC15, BUB1</i>
nucleus organization	4.47E-02	<i>NUP60, DYN1, DYN2, BIK1</i>
nucleus	4.89E-02	<i>VIK1, SWM1, CTF3, UBP12, MCM16, SCS2, KIP3, SFL1, CTF19, CTF18, RPA14, SHE1, CKA2, PPZ1, BUB1, IML3, MUD1, CSM3, RRP6, PAC1, CSM1,</i>

		<i>RDH54, BIK1, MCM21, MAD1, NUP60, MAD2, TOS8, MAD3, YKE2, CHL4, SLK19, CHL1, HOS1</i>
protein folding	4.89E-02	<i>CIN1, GIM4, YKE2, CIN2, PAC10</i>
establishment or maintenance of cell polarity	4.89E-02	<i>DYN1, NIP100, RHO4, KIP3, LDB18</i>
maintenance of protein location	4.91E-02	<i>CTF19, IRC15, BUB1</i>
structural molecule activity	4.92E-02	<i>CTF19, RPL35A, NUP60, CHL4, SCS2, YLR194C, BIK1, SLK19, JNMI, BIM1</i>

Table S4 GO term enrichment for validated PelA hits using BiNGO.

GO term description	corrected p-value	Genes in test set
mitotic cell cycle	1.44E-18	<i>VIK1, CTF3, GIM4, MCM16, RAD61, LDB18, CTF19, BFA1, IRC15, MSA1, ASE1, BUB1, BIM1, DCC1, CSM3, CSM1, BMH1, CLB5, BIK1, MCM21, MAD1, MAD2, MAD3, CHL4, VHS2, VHS1, PAC10, CHL1</i>
organelle fission	3.28E-14	<i>VIK1, NUM1, DCC1, CTF3, CSM3, MCM16, CSM1, BIK1, RAD61, MCM21, CTF19, MAD1, IRC15, BFA1, MAD2, MAD3, ASE1, BUB1, CHL4, CHL1, BIM1</i>
mitosis	4.33E-14	<i>VIK1, DCC1, CTF3, CSM3, MCM16, CSM1, BIK1, RAD61, MCM21, CTF19, MAD1, IRC15, BFA1, MAD2, MAD3, ASE1, BUB1, CHL4, CHL1, BIM1</i>
M phase of mitotic cell cycle	4.33E-14	<i>VIK1, DCC1, CTF3, CSM3, MCM16, CSM1, BIK1, RAD61, MCM21, CTF19, MAD1, IRC15, BFA1, MAD2, MAD3, ASE1, BUB1, CHL4, CHL1, BIM1</i>
nuclear division	8.11E-14	<i>VIK1, DCC1, CTF3, CSM3, MCM16, CSM1, BIK1, RAD61, MCM21, CTF19, MAD1, IRC15, BFA1, MAD2, MAD3, ASE1, BUB1, CHL4, CHL1, BIM1</i>
negative regulation of protein metabolic process	2.42E-12	<i>CTF19, NUM1, BFA1, CINI, CTF3, ASE1, GIM4, BMH1, BUB1, CHL4, BIK1, BIM1</i>
negative regulation of cellular component organization	2.42E-12	<i>CTF19, MAD1, MAD2, MAD3, CINI, CTF3, ASE1, GIM4, BUB1, CHL4, BIK1, CHL1, BIM1</i>
mitotic sister chromatid cohesion	2.57E-12	<i>CTF19, VIK1, DCC1, CTF3, CSM3, MCM16, CHL4, RAD61, CHL1, MCM21, BIM1</i>
mitotic sister chromatid segregation	5.15E-12	<i>VIK1, DCC1, CSM3, CTF3, MCM16, CSM1, RAD61, MCM21, CTF19, IRC15, BUB1, CHL4, CHL1, BIM1</i>
sister chromatid segregation	8.90E-12	<i>VIK1, DCC1, CSM3, CTF3, MCM16, CSM1, RAD61, MCM21, CTF19, IRC15, BUB1, CHL4, CHL1, BIM1</i>

cell cycle phase	1.47E-11	<i>VIK1, DCC1, CTF3, CSM3, MCM16, CSM1, CLB5, BIK1, RAD61, MCM21, CTF19, MAD1, IRC15, BFA1, MAD2, MSA1, MAD3, ASE1, BUB1, CHL4, VHS2, VHS1, CHL1, BIM1</i>
cell cycle	2.00E-11	<i>VIK1, CTF3, GIM4, MCM16, RAD61, LDB18, CTF19, BFA1, IRC15, MSA1, ASE1, BUB1, BIM1, DCC1, CSM3, CSM1, BMH1, CLB5, BIK1, MCM21, MAD1, MAD2, MAD3, CHL4, VHS2, VHS1, PAC10, CHL1</i>
cell cycle process	2.52E-11	<i>VIK1, CTF3, MCM16, RAD61, LDB18, CTF19, BFA1, IRC15, MSA1, ASE1, BUB1, BIM1, DCC1, CSM3, CSM1, BMH1, CLB5, BIK1, MCM21, MAD1, MAD2, MAD3, CHL4, VHS2, VHS1, CHL1</i>
sister chromatid cohesion	3.58E-11	<i>CTF19, VIK1, DCC1, CTF3, CSM3, MCM16, CHL4, RAD61, CHL1, MCM21, BIM1</i>
M phase	1.56E-10	<i>VIK1, DCC1, CTF3, CSM3, MCM16, CSM1, CLB5, BIK1, RAD61, MCM21, CTF19, MAD1, IRC15, BFA1, MAD2, MAD3, ASE1, BUB1, CHL4, CHL1, BIM1</i>
chromosome segregation	1.63E-10	<i>VIK1, DCC1, CSM3, CTF3, MCM16, CSM1, RAD61, MCM21, CTF19, IRC15, BFA1, MAD3, BUB1, CHL4, CHL1, BIM1</i>
tubulin binding	8.36E-10	<i>NUM1, IRC15, CINI, ASE1, GIM4, BIK1, PAC10, BIM1</i>
regulation of cellular component organization	2.13E-09	<i>CINI, CTF3, GIM4, CLB5, BIK1, CTF19, MAD1, MAD2, MAD3, RAV1, ASE1, RAV2, BUB1, CHL4, CHL1, BIM1</i>
microtubule-based process	4.39E-09	<i>VIK1, NUM1, CLB5, BIK1, LDB18, MCM21, CTF19, IRC15, ASE1, BUB1, CHL4, JNM1, BIM1</i>
microtubule cytoskeleton	1.26E-08	<i>VIK1, CTF3, BIK1, LDB18, MCM21, CTF19, BFA1, IRC15, ASE1, BUB1, CHL4, JNM1, BIM1</i>
kinetochore	2.34E-08	<i>CTF19, MAD1, CTF3, CSM1, MCM16, BUB1, CHL4, BIK1, MCM21, BIM1</i>
establishment of sister chromatid cohesion	4.53E-08	<i>CTF19, CTF3, CSM3, MCM16, CHL4, MCM21</i>



establishment of mitotic sister chromatid cohesion	4.53E-08	<i>CTF19, CTF3, CSM3, MCM16, CHL4, MCM21</i>
cytoskeletal protein binding	6.56E-08	<i>NUM1, RVS161, IRC15, CIN1, ASE1, GIM4, RVS167, BIK1, PAC10, BIM1</i>
chromosome, centromeric region	9.40E-08	<i>CTF19, MAD1, CTF3, CSM1, MCM16, BUB1, CHL4, BIK1, MCM21, BIM1</i>
cytoskeletal part	1.18E-07	<i>VIK1, RVS161, CTF3, BIK1, LDB18, MCM21, CTF19, BFA1, IRC15, ASE1, RVS167, BUB1, CHL4, JNM1, BIM1</i>
microtubule cytoskeleton organization	1.34E-07	<i>CTF19, NUM1, IRC15, ASE1, BUB1, CHL4, CLB5, BIK1, LDB18, MCM21, BIM1</i>
cytoskeleton	2.60E-07	<i>VIK1, RVS161, CTF3, BIK1, LDB18, MCM21, CTF19, BFA1, IRC15, ASE1, RVS167, BUB1, CHL4, JNM1, BIM1</i>
negative regulation of biological process	4.18E-07	<i>NUM1, CIN1, CSM3, CTF3, GIM4, BMH1, BIK1, SWC5, CTF19, MAD1, BFA1, MAD2, MAD3, ASE1, BUB1, CHL4, CHL1, BIM1</i>
protein complex	7.07E-07	<i>VIK1, CTF3, GIM4, MCM16, VPS53, LDB18, CTF19, IRC15, RAV1, PEP8, RAV2, ASE1, CKA2, BUB1, GTR2, BIM1, PAN2, DCC1, CSM3, CSM1, BIK1, MCM21, SWC5, MAD1, COG5, MAD2, MAD3, COG8, GOS1, CHL4, PAC10, TPS2, JNM1</i>
negative regulation of macromolecule metabolic process	1.18E-06	<i>NUM1, CSM3, CTF3, CIN1, GIM4, BMH1, BIK1, SWC5, CTF19, BFA1, ASE1, BUB1, CHL4, CHL1, BIM1</i>
cellular localization	1.66E-06	<i>SYS1, NUM1, RVS161, ARL1, CSM1, VPS53, BIK1, LDB18, CTF19, BSD2, MAD1, COG5, IRC15, DRS2, PEP8, RAV1, COG8, ASE1, GOS1, RVS167, BUB1, CHL4, JNM1, BIM1</i>
condensed chromosome	2.58E-06	<i>CTF19, CTF3, CSM1, MCM16, BUB1, CHL4, BIK1, MCM21</i>

kinetochore		
negative regulation of metabolic process	2.86E-06	<i>NUM1, CSM3, CTF3, CINI, GIM4, BMH1, BIK1, SWC5, CTF19, BFA1, ASE1, BUB1, CHL4, CHL1, BIM1</i>
regulation of mitotic cell cycle	3.43E-06	<i>MAD1, IRC15, BFA1, MAD2, MAD3, ASE1, BUB1, CLB5, BIM1</i>
cytoskeleton organization	4.01E-06	<i>RVS161, NUM1, CLB5, BIK1, LDB18, MCM21, CTF19, IRC15, ASE1, RVS167, BUB1, CHL4, BIM1</i>
condensed chromosome, centromeric region	4.37E-06	<i>CTF19, CTF3, CSM1, MCM16, BUB1, CHL4, BIK1, MCM21</i>
organelle organization	5.97E-06	<i>VIK1, RVS161, NUM1, CTF3, MCM16, RAD61, LDB18, CTF19, BFA1, IRC15, DRS2, ASE1, BUB1, BIM1, SYS1, DCC1, CSM3, CSM1, CLB5, BIK1, MCM21, SWC5, MAD1, MAD2, MAD3, GOS1, RVS167, CHL4, VAM10, CHL1</i>
mitotic cell cycle spindle checkpoint	6.49E-06	<i>MAD1, BFA1, MAD2, MAD3, BUB1, BIM1</i>
cell cycle checkpoint	6.49E-06	<i>MAD1, BFA1, MAD2, MAD3, CSM3, BMH1, BUB1, BIM1</i>
condensed nuclear chromosome kinetochore	8.63E-06	<i>CTF19, CTF3, MCM16, BUB1, CHL4, BIK1, MCM21</i>
spindle checkpoint	9.28E-06	<i>MAD1, BFA1, MAD2, MAD3, BUB1, BIM1</i>
cellular component organization	1.76E-05	<i>VIK1, RVS161, NUM1, CTF3, CINI, GIM4, MCM16, RAD61, LDB18, CTF19, IRC15, BFA1, DRS2, ASE1, BUB1, GTR2, BIM1, SYS1, PPM1, DCC1, CSM3, CSM1, CLB5, BIK1, MCM21, SWC5, MAD1, MAD2, MAD3, GOS1, RVS167, CHL4, VOA1, VAM10, PAC10, CHL1</i>
condensed nuclear chromosome, centromeric region	1.81E-05	<i>CTF19, CTF3, MCM16, BUB1, CHL4, BIK1, MCM21</i>

chromosome organization	2.40E-05	<i>VIK1, DCC1, CSM3, CTF3, MCM16, CSM1, RAD61, MCM21, SWC5, CTF19, IRC15, MAD2, BUB1, CHL4, CHL1, BIM1</i>
mitotic cell cycle checkpoint	2.56E-05	<i>MAD1, BFA1, MAD2, MAD3, BUB1, BIM1</i>
negative regulation of mitotic metaphase/anaphase transition	3.19E-05	<i>MAD1, MAD2, MAD3, BUB1, BIM1</i>
negative regulation of mitosis	3.19E-05	<i>MAD1, MAD2, MAD3, BUB1, BIM1</i>
mitotic cell cycle spindle assembly checkpoint	3.19E-05	<i>MAD1, MAD2, MAD3, BUB1, BIM1</i>
spindle assembly checkpoint	3.19E-05	<i>MAD1, MAD2, MAD3, BUB1, BIM1</i>
negative regulation of nuclear division	3.19E-05	<i>MAD1, MAD2, MAD3, BUB1, BIM1</i>
regulation of cell cycle	3.19E-05	<i>MAD1, IRC15, BFA1, MAD2, MAD3, CSM3, ASE1, BMH1, BUB1, CLB5, BIM1</i>
localization	3.70E-05	<i>RVS161, NUM1, VPS53, PIB1, LDB18, CTF19, BSD2, IRC15, DRS2, RAV1, PEP8, RAV2, ASE1, BUB1, GTR2, BIM1, SYS1, ARL1, CSM1, BIK1, YDL119C, CYB5, MAD1, COG5, COG8, GOS1, RVS167, CHL4, BRE5, JNM1</i>
chromosomal part	3.70E-05	<i>DCC1, CSM3, CTF3, MCM16, CSM1, BIK1, MCM21, SWC5, CTF19, MAD1, BUB1, CHL4, GTR2, BIM1</i>
negative regulation of organelle organization	4.01E-05	<i>MAD1, MAD2, MAD3, ASE1, BUB1, BIM1</i>
establishment of nucleus localization	4.58E-05	<i>NUM1, ASE1, BIK1, JNM1, BIM1</i>
nucleus localization	4.58E-05	<i>NUM1, ASE1, BIK1, JNM1, BIM1</i>

microtubule binding	8.91E-05	<i>IRC15, ASE1, BIK1, BIM1</i>
regulation of cell cycle process	9.61E-05	<i>MAD1, BFA1, MAD2, MAD3, ASE1, BUB1, CLB5, BIM1</i>
meiotic chromosome segregation	9.61E-05	<i>IRC15, MAD3, CSM3, CSM1, CHL4</i>
regulation of mitotic metaphase/anaphase transition	9.61E-05	<i>MAD1, MAD2, MAD3, BUB1, BIM1</i>
spindle	1.06E-04	<i>CTF19, VIK1, BFA1, ASE1, CHL4, BIK1, MCM21, BIM1</i>
negative regulation of cell cycle	1.33E-04	<i>MAD1, MAD2, MAD3, BUB1, BIM1</i>
chromosome	1.42E-04	<i>DCC1, CSM3, CTF3, MCM16, CSM1, BIK1, MCM21, SWC5, CTF19, MAD1, BUB1, CHL4, GTR2, BIM1</i>
condensed chromosome	1.63E-04	<i>CTF19, CTF3, CSM1, MCM16, BUB1, CHL4, BIK1, MCM21</i>
regulation of protein metabolic process	1.79E-04	<i>CTF19, NUM1, BFA1, CIN1, CTF3, ASE1, GIM4, BMH1, BUB1, CHL4, BIK1, BIM1</i>
protein localization	1.95E-04	<i>SYS1, ARL1, CSM1, VPS53, PIB1, CTF19, BSD2, COG5, IRC15, DRS2, PEP8, RAV1, COG8, RAV2, GOS1, BUB1, GTR2, CHL4</i>
macromolecular complex	2.04E-04	<i>VIK1, CTF3, GIM4, MCM16, VPS53, LDB18, CTF19, IRC15, RAV1, PEP8, RAV2, ASE1, CKA2, BUB1, GTR2, BIM1, PAN2, RPL35A, DCC1, CSM3, CSM1, BIK1, MCM21, SWC5, MAD1, COG5, MAD2, MAD3, COG8, GOS1, CHL4, PAC10, TPS2, JNM1</i>
regulation of mitosis	2.27E-04	<i>MAD1, MAD2, MAD3, BUB1, BIM1</i>
regulation of nuclear division	2.27E-04	<i>MAD1, MAD2, MAD3, BUB1, BIM1</i>
protein binding	2.32E-04	<i>RVS161, NUM1, CIN1, CTF3, GIM4, MCM16, BMH1, VPS53, BIK1, MCM21, CTF19, BSD2, IRC15, ASE1, GOS1, RVS167, BUB1, PAC10, BIM1</i>
protein complex	2.34E-04	<i>PPM1, MAD1, MAD2, CIN1, ASE1, GIM4, CHL4, BIK1,</i>

assembly		<i>PAC10, VOA1, BIM1</i>
protein complex biogenesis	2.34E-04	<i>PPM1, MAD1, MAD2, CIN1, ASE1, GIM4, CHL4, BIK1, PAC10, VOA1, BIM1</i>
cell division	2.75E-04	<i>CTF3, MCM16, CLB5, BIK1, MCM21, CTF19, MAD1, BFA1, MAD2, MAD3, ASE1, CHL4, BIM1</i>
establishment of organelle localization	3.00E-04	<i>NUM1, ASE1, BUB1, BIK1, LDB18, JNM1, BIM1</i>
condensed nuclear chromosome	3.67E-04	<i>CTF19, CTF3, MCM16, BUB1, CHL4, BIK1, MCM21</i>
establishment of localization in cell	4.35E-04	<i>SYS1, ARL1, NUM1, VPS53, BIK1, LDB18, BSD2, MAD1, COG5, DRS2, PEP8, RAV1, COG8, ASE1, GOS1, BUB1, JNM1, BIM1</i>
non-membrane- bounded organelle	4.35E-04	<i>VIK1, RVS161, RPL35A, DCC1, CTF3, CSM3, MCM16, CSM1, BIK1, LDB18, MCM21, SWC5, CTF19, MAD1, IRC15, BFA1, ASE1, CKA2, RVS167, BUB1, GTR2, CHL4, JNM1, BIM1</i>
intracellular non- membrane-bounded organelle	4.35E-04	<i>VIK1, RVS161, RPL35A, DCC1, CTF3, CSM3, MCM16, CSM1, BIK1, LDB18, MCM21, SWC5, CTF19, MAD1, IRC15, BFA1, ASE1, CKA2, RVS167, BUB1, GTR2, CHL4, JNM1, BIM1</i>
organelle part	6.44E-04	<i>ERG2, VIK1, RVS161, CTF3, MCM16, VPS53, LDB18, PIB1, CTF19, BSD2, IRC15, BFA1, DRS2, RAV1, RAV2, ASE1, CKA2, BUB1, GTR2, BIM1, SYS1, ARL1, RPL35A, DCC1, CSM3, CSM1, YDL119C, BIK1, CYB5, MCM21, SWC5, MAD1, COG5, MAD2, MAD3, COG8, GOS1, RVS167, CHL4, VOA1, VAM10, JNM1</i>
intracellular organelle part	6.44E-04	<i>ERG2, VIK1, RVS161, CTF3, MCM16, VPS53, LDB18, PIB1, CTF19, BSD2, IRC15, BFA1, DRS2, RAV1, RAV2, ASE1, CKA2, BUB1, GTR2, BIM1, SYS1, ARL1, RPL35A, DCC1, CSM3, CSM1, YDL119C, BIK1, CYB5, MCM21, SWC5, MAD1, COG5, MAD2, MAD3, COG8, GOS1, RVS167, CHL4, VOA1, VAM10, JNM1</i>

establishment of localization	6.86E-04	<i>RVS161, NUM1, VPS53, PIB1, LDB18, BSD2, DRS2, RAV1, PEP8, RAV2, ASE1, BUB1, GTR2, BIM1, SYS1, ARL1, BIK1, YDL119C, CYB5, MAD1, COG5, COG8, GOS1, RVS167, BRE5, JNM1</i>
negative regulation of cell cycle process	6.86E-04	<i>MAD1, MAD2, MAD3, BUB1, BIM1</i>
meiosis	6.86E-04	<i>CTF19, IRC15, MAD3, CTF3, CSM3, CSM1, MCM16, CHL4, MCM21</i>
M phase of meiotic cell cycle	6.86E-04	<i>CTF19, IRC15, MAD3, CTF3, CSM3, CSM1, MCM16, CHL4, MCM21</i>
nuclear migration	6.91E-04	<i>NUM1, BIK1, JNM1, BIM1</i>
cytoskeleton-dependent intracellular transport	8.14E-04	<i>NUM1, ASE1, BIK1, BIM1</i>
meiotic cell cycle	8.87E-04	<i>CTF19, IRC15, MAD3, CTF3, CSM3, CSM1, MCM16, CHL4, MCM21</i>
nuclear chromosome part	1.04E-03	<i>CTF19, CTF3, CSM3, MCM16, BUB1, GTR2, CHL4, BIK1, MCM21, SWC5</i>
macromolecule localization	1.23E-03	<i>SYS1, ARL1, CSM1, VPS53, PIB1, CTF19, BSD2, COG5, IRC15, DRS2, PEP8, RAV1, COG8, RAV2, GOS1, BUB1, GTR2, CHL4</i>
organelle localization	1.33E-03	<i>NUM1, ASE1, BUB1, BIK1, LDB18, JNM1, BIM1</i>
cellular process	1.78E-03	<i>ERG2, RVS161, GIM4, MCM16, VPS53, RAD61, PIB1, BSD2, PEP8, RAV1, ASE1, RAV2, PPZ1, BIM1, PAN2, ARL1, RPL35A, CSM3, CSM1, CLB5, BIK1, UBR2, MCM21, MAD1, MAD2, MAD3, CHL4, BRE5, VHS2, VHS1, VAM10, PAC10, CHL1, VIK1, NUM1, CTF3, CINI, LDB18, CTF19, BFA1, IRC15, DRS2, MSA1, CKA2, BUB1, GTR2, SYS1, PPM1, DCC1, BMH1, YDL119C, CYB5, SWC5, COG5, COG8, GOS1, RVS167, TPS2, JNM1</i>

regulation of organelle organization	1.79E-03	<i>MAD1, MAD2, MAD3, ASE1, BUB1, CLB5, BIM1</i>
spindle pole	1.98E-03	<i>CTF19, VIK1, BFA1, BIK1, MCM21, BIM1</i>
attachment of spindle microtubules to chromosome	2.29E-03	<i>CTF19, IRC15, BUB1</i>
microtubule anchoring	2.29E-03	<i>CTF19, IRC15, BUB1</i>
microtubule	2.44E-03	<i>IRC15, ASE1, BIK1, JNM1, BIM1</i>
nuclear chromosome	2.49E-03	<i>CTF19, CTF3, CSM3, MCM16, BUB1, GTR2, CHL4, BIK1, MCM21, SWC5</i>
regulation of biological process	2.52E-03	<i>RVS161, NUM1, CTF3, CIN1, GIM4, CTF19, BFA1, IRC15, MSA1, RAV1, RAV2, ASE1, CKA2, BUB1, GTR2, BIM1, ARL1, CSM3, BMH1, CLB5, BIK1, SWC5, MAD1, MAD2, MAD3, RVS167, CHL4, CHL1</i>
RAVE complex	2.59E-03	<i>RAV1, RAV2</i>
maintenance of protein location in cell	3.56E-03	<i>CTF19, IRC15, PEP8, BUB1</i>
maintenance of protein location	4.35E-03	<i>CTF19, IRC15, PEP8, BUB1</i>
macromolecular complex assembly	4.47E-03	<i>PPM1, MAD1, MAD2, DRS2, CIN1, ASE1, GIM4, CHL4, BIK1, PAC10, VOA1, BIM1</i>
maintenance of location in cell	4.72E-03	<i>CTF19, IRC15, PEP8, BUB1</i>
mitotic checkpoint complex	4.86E-03	<i>MAD2, MAD3</i>
spindle assembly	4.86E-03	<i>ASE1, CLB5</i>
microtubule organizing center	4.87E-03	<i>VIK1, BFA1, BIK1, MCM21, BIM1</i>
spindle pole body	4.87E-03	<i>VIK1, BFA1, BIK1, MCM21, BIM1</i>
signaling	5.08E-03	<i>MAD1, ARL1, BFA1, MAD2, MAD3, CSM3, PEP8,</i>

		<i>PPZ1, BMH1, BUB1, BIM1</i>
biological regulation	5.09E-03	<i>RVS161, NUM1, CTF3, CIN1, GIM4, CTF19, BFA1, IRC15, MSA1, RAV1, PEP8, RAV2, ASE1, CKA2, PPZ1, BUB1, GTR2, BIM1, ARL1, CSM3, BMH1, CLB5, BIK1, SWC5, MAD1, MAD2, MAD3, RVS167, CHL4, CHL1</i>
intracellular part	5.09E-03	<i>ERG2, RVS161, GIM4, MCM16, VPS53, RAD61, PIB1, BSD2, PEP8, RAV1, ASE1, RAV2, PPZ1, BIM1, PAN2, ARL1, RPL35A, CSM3, CSM1, CLB5, BIK1, UBR2, MCM21, MAD1, MAD2, MAD3, YKL077W, CHL4, BRE5, VHS2, VOA1, VHS1, VAM10, PAC10, CHL1, VIK1, NUM1, CTF3, LDB18, CTF19, BFA1, IRC15, DRS2, MSA1, CKA2, BUB1, GTR2, SYS1, DCC1, BMH1, YDL119C, CYB5, SWC5, COG5, COG8, GOS1, RVS167, TPS2, JNM1</i>
intracellular transport	5.09E-03	<i>SYS1, ARL1, NUM1, VPS53, BIK1, BSD2, MAD1, COG5, DRS2, PEP8, RAV1, COG8, ASE1, GOS1, BIM1</i>
G1/S transition of mitotic cell cycle	5.27E-03	<i>MSA1, CLB5, VHS2, VHS1</i>
nuclear migration along microtubule	6.21E-03	<i>NUM1, BIK1, BIM1</i>
intracellular organelle	6.21E-03	<i>ERG2, RVS161, MCM16, VPS53, RAD61, PIB1, BSD2, PEP8, RAV1, ASE1, RAV2, PPZ1, BIM1, ARL1, RPL35A, CSM3, CSM1, CLB5, BIK1, MCM21, MAD1, MAD2, MAD3, YKL077W, CHL4, VOA1, VAM10, CHL1, VIK1, NUM1, CTF3, LDB18, CTF19, BFA1, IRC15, DRS2, MSA1, CKA2, BUB1, GTR2, SYS1, DCC1, BMH1, YDL119C, CYB5, SWC5, COG5, COG8, GOS1, RVS167, TPS2, JNM1</i>
organelle	6.21E-03	<i>ERG2, RVS161, MCM16, VPS53, RAD61, PIB1, BSD2, PEP8, RAV1, ASE1, RAV2, PPZ1, BIM1, ARL1, RPL35A, CSM3, CSM1, CLB5, BIK1, MCM21, MAD1, MAD2, MAD3, YKL077W, CHL4, VOA1, VAM10, CHL1, VIK1, NUM1, CTF3, LDB18, CTF19, BFA1,</i>



		<i>IRC15, DRS2, MSA1, CKA2, BUB1, GTR2, SYS1, DCC1, BMH1, YDL119C, CYB5, SWC5, COG5, COG8, GOS1, RVS167, TPS2, JNM1</i>
vesicle-mediated transport	6.38E-03	<i>SYS1, ARL1, RVS161, COG5, DRS2, RAV1, PEP8, COG8, GOS1, RVS167, VPS53</i>
intracellular	6.42E-03	<i>ERG2, RVS161, GIM4, MCM16, VPS53, RAD61, PIB1, BSD2, PEP8, RAV1, ASE1, RAV2, PPZ1, BIM1, PAN2, ARL1, RPL35A, CSM3, CSM1, CLB5, BIK1, UBR2, MCM21, MAD1, MAD2, MAD3, YKL077W, CHL4, BRE5, VHS2, VOA1, VHS1, VAM10, PAC10, CHL1, VIK1, NUM1, CTF3, LDB18, CTF19, BFA1, IRC15, DRS2, MSA1, CKA2, BUB1, GTR2, SYS1, DCC1, BMH1, YDL119C, CYB5, SWC5, COG5, COG8, GOS1, RVS167, TPS2, JNM1</i>
maintenance of location	6.56E-03	<i>CTF19, IRC15, PEP8, BUB1</i>
signal transduction	6.56E-03	<i>MAD1, ARL1, BFA1, MAD2, MAD3, CSM3, BMH1, BUB1, BIM1</i>
microtubule-based transport	6.63E-03	<i>NUM1, BIK1, BIM1</i>
microtubule associated complex	6.63E-03	<i>VIK1, LDB18, JNM1</i>
mitotic anaphase B	6.63E-03	<i>ASE1, BIK1</i>
negative regulation of microtubule depolymerization	6.63E-03	<i>ASE1, BIM1</i>
COMA complex	6.63E-03	<i>CTF19, MCM21</i>
regulation of microtubule depolymerization	6.63E-03	<i>ASE1, BIM1</i>
negative regulation of microtubule polymerization or	6.63E-03	<i>ASE1, BIM1</i>

depolymerization		
dynactin complex	6.63E-03	<i>LDB18, JNM1</i>
signal transmission	6.63E-03	<i>MAD1, ARL1, BFA1, MAD2, MAD3, CSM3, BMH1, BUB1, BIM1</i>
signaling process	7.52E-03	<i>MAD1, ARL1, BFA1, MAD2, MAD3, CSM3, BMH1, BUB1, BIM1</i>
mitotic anaphase	9.49E-03	<i>ASE1, BIK1</i>
attachment of spindle microtubules to kinetochore	9.49E-03	<i>CTF19, IRC15</i>
Golgi to plasma membrane protein transport	9.49E-03	<i>SYS1, ARL1</i>
microtubule-based movement	9.49E-03	<i>NUM1, BIK1, BIM1</i>
structural constituent of cytoskeleton	1.01E-02	<i>CTF19, BIK1, JNM1, BIM1</i>
macromolecular complex subunit organization	1.22E-02	<i>PPM1, CINI, GIM4, BIK1, SWC5, MAD1, MAD2, DRS2, ASE1, CHL4, VOA1, PAC10, BIM1</i>
negative regulation of cellular process	1.22E-02	<i>MAD1, MAD2, MAD3, CSM3, ASE1, BMH1, BUB1, CHL1, SWC5, BIM1</i>
tubulin complex assembly	1.26E-02	<i>GIM4, PAC10</i>
prefoldin complex	1.26E-02	<i>GIM4, PAC10</i>
anaphase	1.26E-02	<i>ASE1, BIK1</i>
transport	1.28E-02	<i>SYS1, NUM1, RVS161, ARL1, VPS53, YDL119C, BIK1, CYB5, BSD2, MAD1, COG5, DRS2, PEP8, RAV1, COG8, ASE1, RAV2, GOS1, RVS167, GTR2, BRE5, BIM1</i>
regulation of microtubule cytoskeleton	1.28E-02	<i>ASE1, CLB5, BIM1</i>

organization		
regulation of microtubule-based process	1.28E-02	<i>ASE1, CLB5, BIM1</i>
establishment of protein localization	1.32E-02	<i>SYS1, ARL1, BSD2, COG5, DRS2, RAV1, PEP8, COG8, RAV2, GOS1, GTR2, VPS53, PIB1</i>
Golgi vesicle transport	1.32E-02	<i>SYS1, ARL1, COG5, DRS2, COG8, GOS1, VPS53</i>
Golgi apparatus part	1.48E-02	<i>SYS1, ARL1, COG5, DRS2, COG8, GOS1, VPS53</i>
spindle midzone	1.58E-02	<i>ASE1, BIM1</i>
Golgi transport complex	1.58E-02	<i>COG5, COG8</i>
regulation of macromolecule metabolic process	1.58E-02	<i>NUM1, CSM3, CTF3, CINI, GIM4, BMH1, CLB5, BIK1, SWC5, CTF19, BFA1, MSA1, ASE1, CKA2, BUB1, GTR2, CHL4, CHL1, BIM1</i>
protein transport	1.96E-02	<i>SYS1, ARL1, BSD2, COG5, DRS2, RAV1, PEP8, COG8, RAV2, GOS1, GTR2, VPS53</i>
cellular component assembly	2.08E-02	<i>PPM1, CINI, GIM4, CLB5, BIK1, MAD1, MAD2, DRS2, ASE1, CHL4, VOA1, PAC10, BIM1</i>
endosome transport	2.20E-02	<i>SYS1, RAV1, PEP8, VPS53</i>
negative regulation of protein complex disassembly	2.43E-02	<i>ASE1, BIM1</i>
regulation of primary metabolic process	2.45E-02	<i>NUM1, CSM3, CTF3, CINI, GIM4, BMH1, CLB5, BIK1, SWC5, CTF19, BFA1, MSA1, ASE1, CKA2, BUB1, GTR2, CHL4, CHL1, BIM1</i>
cellular monovalent inorganic cation homeostasis	3.02E-02	<i>RAV1, RAV2, PPZI</i>
post-Golgi vesicle-mediated transport	3.58E-02	<i>SYS1, ARL1, DRS2, VPS53</i>
vacuolar membrane	3.59E-02	<i>BSD2, RAV1, GTR2, VAM10, VOA1, PIB1</i>
monovalent	3.99E-02	<i>RAV1, RAV2, PPZI</i>

inorganic cation homeostasis		
endosome membrane	4.21E-02	<i>RAV2, GTR2, VPS53, PIB1</i>
vacuolar part	4.28E-02	<i>BSD2, RAV1, GTR2, VAM10, VOA1, PIB1</i>
negative regulation of cytoskeleton organization	4.52E-02	<i>ASE1, BIM1</i>
protein localization to chromosome	4.52E-02	<i>CSM1, CHL4</i>
endomembrane system	4.62E-02	<i>SYS1, ERG2, MAD1, COG5, MAD2, RAV1, PEP8, COG8, GOS1, CSM1, VOA1, CYB5</i>
regulation of metabolic process	4.72E-02	<i>NUM1, CSM3, CTF3, CIN1, GIM4, BMH1, CLB5, BIK1, SWC5, CTF19, BFA1, MSA1, ASE1, CKA2, BUB1, GTR2, CHL4, CHL1, BIM1</i>
vacuole	4.72E-02	<i>BSD2, RAV1, YKL077W, GTR2, VAM10, VOA1, PIB1</i>
cellular protein complex assembly	4.91E-02	<i>PPM1, ASE1, GIM4, CHL4, PAC10</i>
endosome	4.91E-02	<i>PEP8, RAV2, GTR2, VPS53, PIB1</i>
Golgi apparatus	4.94E-02	<i>SYS1, ARL1, COG5, DRS2, COG8, GOS1, VPS53</i>
actin cortical patch localization	4.94E-02	<i>RVS161, RVS167</i>
regulation of microtubule polymerization or depolymerization	4.94E-02	<i>ASE1, BIM1</i>

Table S5 GO term enrichment of common hits between the Lau and PelA microarray results using BiNGO.

GO term description	corrected p-value	Genes in test set
sister chromatid cohesion	1.42E-11	<i>CTF19, VIK1, IML3, CSM3, DCC1, CTF3, CHL4, CHL1, MCM21</i>
chromosome segregation	1.01E-08	<i>CTF19, VIK1, IML3, CSM3, DCC1, CTF3, CSM1, CHL4, CHL1, MCM21</i>
kinetochore	2.82E-06	<i>CTF19, IML3, CTF3, CSM1, CHL4, MCM21</i>
COMA complex	9.58E-06	<i>CTF19, IML3, MCM21</i>
dynactin complex	9.58E-06	<i>ARP1, LDB18, JNM1</i>
dynein complex	3.18E-03	<i>ARP1, JNM1</i>
mitotic sister chromatid cohesion	2.17E-12	<i>CTF19, VIK1, IML3, CSM3, DCC1, CTF3, CHL4, CHL1, MCM21</i>
mitotic sister chromatid segregation	5.09E-11	<i>CTF19, VIK1, IML3, CSM3, DCC1, CTF3, CSM1, CHL4, CHL1, MCM21</i>
sister chromatid segregation	6.09E-11	<i>CTF19, VIK1, IML3, CSM3, DCC1, CTF3, CSM1, CHL4, CHL1, MCM21</i>
organelle fission	1.96E-10	<i>CTF19, VIK1, IML3, NUM1, MAD2, CSM3, DCC1, CTF3, CSM1, CHL4, CHL1, MCM21</i>
establishment of sister chromatid cohesion	2.17E-10	<i>CTF19, IML3, CSM3, CTF3, CHL4, MCM21</i>
establishment of mitotic sister chromatid cohesion	2.17E-10	<i>CTF19, IML3, CSM3, CTF3, CHL4, MCM21</i>
mitotic cell cycle	5.72E-10	<i>VIK1, IML3, CTF3, DCC1, CSM3, CSM1, ARP1, LDB18, MCM21, CTF19, MAD2, CHL4, CHL1</i>
mitosis	1.01E-09	<i>CTF19, VIK1, IML3, MAD2, CSM3, DCC1, CTF3, CSM1, CHL4, CHL1, MCM21</i>
M phase of mitotic cell cycle	1.03E-09	<i>CTF19, VIK1, IML3, MAD2, CSM3, DCC1, CTF3, CSM1, CHL4, CHL1, MCM21</i>
nuclear division	1.49E-09	<i>CTF19, VIK1, IML3, MAD2, CSM3, DCC1, CTF3, CSM1, CHL4, CHL1, MCM21</i>

microtubule cytoskeleton	2.76E-08	<i>CTF19, VIK1, IML3, CTF3, CHL4, ARP1, LDB18, JNMI, MCM21</i>
cytoskeletal part	1.89E-07	<i>CTF19, VIK1, IML3, RVS161, CTF3, CHL4, ARP1, LDB18, JNMI, MCM21</i>
cell cycle process	2.92E-07	<i>VIK1, IML3, CTF3, DCC1, CSM3, CSM1, ARP1, LDB18, MCM21, CTF19, MAD2, CHL4, CHL1</i>
cytoskeleton	2.92E-07	<i>CTF19, VIK1, IML3, RVS161, CTF3, CHL4, ARP1, LDB18, JNMI, MCM21</i>
microtubule-based process	2.92E-07	<i>CTF19, VIK1, NUM1, CHL4, ARP1, LDB18, JNMI, MCM21</i>
M phase	4.13E-07	<i>CTF19, VIK1, IML3, MAD2, CSM3, DCC1, CTF3, CSM1, CHL4, CHL1, MCM21</i>
negative regulation of protein metabolic process	5.96E-07	<i>CTF19, IML3, NUM1, CTF3, CHL4, ARP1</i>
cell cycle	1.61E-06	<i>VIK1, IML3, CTF3, DCC1, CSM3, CSM1, ARP1, LDB18, MCM21, CTF19, MAD2, CHL4, CHL1</i>
condensed chromosome kinetochore	1.88E-06	<i>CTF19, IML3, CTF3, CSM1, CHL4, MCM21</i>
chromosome organization	2.39E-06	<i>CTF19, VIK1, IML3, MAD2, CSM3, DCC1, CTF3, CSM1, CHL4, CHL1, MCM21</i>
cell cycle phase	2.59E-06	<i>CTF19, VIK1, IML3, MAD2, CSM3, DCC1, CTF3, CSM1, CHL4, CHL1, MCM21</i>
condensed chromosome, centromeric region	2.68E-06	<i>CTF19, IML3, CTF3, CSM1, CHL4, MCM21</i>
chromosome, centromeric region	6.88E-06	<i>CTF19, IML3, CTF3, CSM1, CHL4, MCM21</i>
microtubule associated complex	1.46E-05	<i>VIK1, ARP1, LDB18, JNMI</i>
condensed nuclear chromosome kinetochore	1.63E-05	<i>CTF19, IML3, CTF3, CHL4, MCM21</i>

non-membrane-bounded organelle	1.63E-05	<i>VIK1, RVS161, RPL35A, IML3, CTF3, DCC1, CSM3, CSM1, ARP1, LDB18, MCM21, CTF19, CKA2, CHL4, JNM1</i>
intracellular non-membrane-bounded organelle	1.63E-05	<i>VIK1, RVS161, RPL35A, IML3, CTF3, DCC1, CSM3, CSM1, ARP1, LDB18, MCM21, CTF19, CKA2, CHL4, JNM1</i>
condensed nuclear chromosome, centromeric region	2.73E-05	<i>CTF19, IML3, CTF3, CHL4, MCM21</i>
microtubule cytoskeleton organization	3.33E-05	<i>CTF19, NUM1, CHL4, ARP1, LDB18, MCM21</i>
condensed chromosome	4.72E-05	<i>CTF19, IML3, CTF3, CSM1, CHL4, MCM21</i>
meiotic chromosome segregation	4.88E-05	<i>IML3, CSM3, CSM1, CHL4</i>
negative regulation of cellular component organization	5.21E-05	<i>CTF19, MAD2, CTF3, CHL4, CHL1</i>
M phase of meiotic cell cycle	5.32E-05	<i>CTF19, IML3, CSM3, CTF3, CSM1, CHL4, MCM21</i>
meiosis	5.32E-05	<i>CTF19, IML3, CSM3, CTF3, CSM1, CHL4, MCM21</i>
meiotic cell cycle	6.65E-05	<i>CTF19, IML3, CSM3, CTF3, CSM1, CHL4, MCM21</i>
negative regulation of macromolecule metabolic process	7.06E-05	<i>CTF19, IML3, NUM1, CSM3, CTF3, CHL4, ARP1, CHL1</i>
organelle organization	7.48E-05	<i>VIK1, NUM1, RVS161, IML3, CTF3, DCC1, CSM3, CSM1, ARP1, LDB18, MCM21, CTF19, MAD2, CHL4, CHL1</i>
negative regulation of biological process	8.48E-05	<i>CTF19, IML3, NUM1, MAD2, CSM3, CTF3, CHL4, ARP1, CHL1</i>
negative regulation of metabolic process	1.13E-04	<i>CTF19, IML3, NUM1, CSM3, CTF3, CHL4, ARP1, CHL1</i>
cytoskeleton	1.58E-04	<i>CTF19, RVS161, NUM1, CHL4, ARP1, LDB18,</i>

organization		<i>MCM21</i>
establishment of meiotic sister chromatid cohesion	1.58E-04	<i>IML3, CHL4</i>
outer kinetochore of condensed chromosome	1.58E-04	<i>IML3, CHL4</i>
outer kinetochore of condensed nuclear chromosome	1.58E-04	<i>IML3, CHL4</i>
protein localization to chromosome	1.95E-04	<i>IML3, CSM1, CHL4</i>
chromosomal part	1.98E-04	<i>CTF19, IML3, CSM3, DCC1, CTF3, CSM1, CHL4, MCM21</i>
condensed nuclear chromosome	2.39E-04	<i>CTF19, IML3, CTF3, CHL4, MCM21</i>
spindle	4.22E-04	<i>CTF19, VIK1, IML3, CHL4, MCM21</i>
maintenance of sister chromatid cohesion	4.22E-04	<i>IML3, CHL4</i>
maintenance of meiotic sister chromatid cohesion	4.22E-04	<i>IML3, CHL4</i>
chromosome	4.59E-04	<i>CTF19, IML3, CSM3, DCC1, CTF3, CSM1, CHL4, MCM21</i>
nuclear migration	7.97E-04	<i>NUM1, ARP1, JNM1</i>
protein localization to chromosome, centromeric region	7.97E-04	<i>IML3, CHL4</i>
protein complex	8.62E-04	<i>VIK1, IML3, CTF3, DCC1, CSM3, CSM1, ARP1, LDB18, MCM21, CTF19, MAD2, CKA2, CHL4, JNM1</i>
establishment of nucleus localization	8.62E-04	<i>NUM1, ARP1, JNM1</i>
nucleus localization	8.62E-04	<i>NUM1, ARP1, JNM1</i>



motor activity	9.61E-04	<i>VIK1, ARP1, JNM1</i>
nuclear chromosome part	2.06E-03	<i>CTF19, IML3, CSM3, CTF3, CHL4, MCM21</i>
actin cytoskeleton	2.60E-03	<i>RVS161, ARP1, LDB18, JNM1</i>
establishment of organelle localization	2.92E-03	<i>NUM1, ARP1, LDB18, JNM1</i>
meiotic sister chromatid cohesion	3.18E-03	<i>IML3, CHL4</i>
organelle part	3.25E-03	<i>ERG2, VIK1, RVS161, RPL35A, IML3, CPT1, CTF3, DCC1, CSM3, CSM1, FLC3, ARP1, LDB18, MCM21, CTF19, MAD2, CKA2, CHL4, JNM1</i>
intracellular organelle part	3.25E-03	<i>ERG2, VIK1, RVS161, RPL35A, IML3, CPT1, CTF3, DCC1, CSM3, CSM1, FLC3, ARP1, LDB18, MCM21, CTF19, MAD2, CKA2, CHL4, JNM1</i>
nuclear chromosome	3.49E-03	<i>CTF19, IML3, CSM3, CTF3, CHL4, MCM21</i>
regulation of protein metabolic process	4.02E-03	<i>CTF19, IML3, NUM1, CTF3, CHL4, ARP1</i>
cellular component organization	4.68E-03	<i>VIK1, NUM1, RVS161, IML3, CTF3, DCC1, CSM3, CSM1, ARP1, LDB18, MCM21, CTF19, MAD2, CHL4, CHL1</i>
intracellular organelle	5.23E-03	<i>ERG2, VIK1, IML3, NUM1, RVS161, RPL35A, CPT1, CSM3, DCC1, CTF3, UBP12, CSM1, FLC3, ARP1, LDB18, MCM21, CTF19, MAD2, CKA2, PPZ1, CHL4, JNM1, CHL1</i>
organelle	5.23E-03	<i>ERG2, VIK1, IML3, NUM1, RVS161, RPL35A, CPT1, CSM3, DCC1, CTF3, UBP12, CSM1, FLC3, ARP1, LDB18, MCM21, CTF19, MAD2, CKA2, PPZ1, CHL4, JNM1, CHL1</i>
establishment of mitotic spindle orientation	5.24E-03	<i>ARP1, LDB18</i>
establishment of mitotic spindle localization	5.24E-03	<i>ARP1, LDB18</i>
spindle localization	5.24E-03	<i>ARP1, LDB18</i>

establishment of spindle localization	5.24E-03	<i>ARPI, LDB18</i>
establishment of spindle orientation	5.24E-03	<i>ARPI, LDB18</i>
macromolecular complex	5.24E-03	<i>VIK1, RPL35A, IML3, CTF3, DCC1, CSM3, CSM1, ARPI, LDB18, MCM21, CTF19, MAD2, CKA2, CHL4, JNM1</i>
regulation of cellular component organization	5.65E-03	<i>CTF19, MAD2, CTF3, CHL4, CHL1</i>
structural constituent of cytoskeleton	6.14E-03	<i>CTF19, ARPI, JNM1</i>
organelle localization	6.16E-03	<i>NUM1, ARPI, LDB18, JNM1</i>
cellular localization	8.65E-03	<i>CTF19, IML3, RVS161, NUM1, CSM1, CHL4, ARPI, LDB18, JNM1</i>
cell division	1.02E-02	<i>CTF19, IML3, MAD2, CTF3, CHL4, MCM21</i>
C-8 sterol isomerase activity	2.39E-02	<i>ERG2</i>
chromosome decondensation	2.39E-02	<i>MAD2</i>
negative regulation of DNA metabolic process	2.69E-02	<i>CSM3, CHL1</i>
spindle pole	2.71E-02	<i>CTF19, VIK1, MCM21</i>
cellular process	3.00E-02	<i>ERG2, VIK1, IML3, NUM1, RVS161, RPL35A, CPT1, CSM3, DCC1, CTF3, UBP12, CSM1, FLC3, UBR2, ARPI, LDB18, MCM21, CTF19, MAD2, CKA2, PPZ1, CHL4, JNM1, CHL1</i>
diacylglycerol cholinephosphotransferase activity	4.45E-02	<i>CPT1</i>
CDP-choline pathway	4.45E-02	<i>CPT1</i>
replication fork arrest	4.45E-02	<i>CSM3</i>

Table S6 GO term enrichment of common hits between Lau and PelA microarray results and literature benomyl and nocodazole hypersensitive gene deletions reported in Parsons et al., 2006.

GO term description	corrected p-value	Genes in test set
negative regulation of cellular component organization	7.46E-11	<i>MAD1, MAD3, CIN1, GIM4, BUB1, BIK1, KIP2, BIM1</i>
mitotic cell cycle	1.34E-10	<i>MAD1, IRC15, BFA1, MAD3, GIM4, MCM16, BUB1, BIK1, PAC10, KIP2, BIM1</i>
tubulin binding	2.97E-10	<i>IRC15, CIN1, GIM4, BIK1, PAC10, BIM1</i>
negative regulation of protein metabolic process	3.23E-10	<i>BFA1, CIN1, GIM4, BUB1, BIK1, KIP2, BIM1</i>
mitosis	1.30E-09	<i>MAD1, IRC15, BFA1, MAD3, MCM16, BUB1, BIK1, KIP2, BIM1</i>
M phase of mitotic cell cycle	1.30E-09	<i>MAD1, IRC15, BFA1, MAD3, MCM16, BUB1, BIK1, KIP2, BIM1</i>
nuclear division	1.65E-09	<i>MAD1, IRC15, BFA1, MAD3, MCM16, BUB1, BIK1, KIP2, BIM1</i>
organelle fission	2.29E-09	<i>MAD1, IRC15, BFA1, MAD3, MCM16, BUB1, BIK1, KIP2, BIM1</i>
cell cycle	7.21E-08	<i>MAD1, IRC15, BFA1, MAD3, GIM4, MCM16, BUB1, BIK1, PAC10, KIP2, BIM1</i>
regulation of cellular component organization	8.25E-08	<i>MAD1, MAD3, CIN1, GIM4, BUB1, BIK1, KIP2, BIM1</i>
mitotic cell cycle spindle checkpoint	8.78E-08	<i>MAD1, BFA1, MAD3, BUB1, BIM1</i>
spindle checkpoint	1.15E-07	<i>MAD1, BFA1, MAD3, BUB1, BIM1</i>
M phase	1.47E-07	<i>MAD1, IRC15, BFA1, MAD3, MCM16, BUB1, BIK1, KIP2, BIM1</i>
cytoskeletal protein binding	1.49E-07	<i>IRC15, CIN1, GIM4, BIK1, PAC10, BIM1</i>
mitotic cell cycle	2.34E-07	<i>MAD1, BFA1, MAD3, BUB1, BIM1</i>

checkpoint		
regulation of mitotic cell cycle	3.34E-07	<i>MAD1, IRC15, BFA1, MAD3, BUB1, BIM1</i>
negative regulation of biological process	3.34E-07	<i>MAD1, BFA1, MAD3, CIN1, GIM4, BUB1, BIK1, KIP2, BIM1</i>
negative regulation of organelle organization	3.34E-07	<i>MAD1, MAD3, BUB1, KIP2, BIM1</i>
chromosome segregation	4.64E-07	<i>IRC15, BFA1, MAD3, MCM16, BUB1, KIP2, BIM1</i>
cell cycle phase	5.59E-07	<i>MAD1, IRC15, BFA1, MAD3, MCM16, BUB1, BIK1, KIP2, BIM1</i>
mitotic cell cycle spindle assembly checkpoint	1.49E-06	<i>MAD1, MAD3, BUB1, BIM1</i>
negative regulation of mitotic metaphase/anaphase transition	1.49E-06	<i>MAD1, MAD3, BUB1, BIM1</i>
negative regulation of mitosis	1.49E-06	<i>MAD1, MAD3, BUB1, BIM1</i>
spindle assembly checkpoint	1.49E-06	<i>MAD1, MAD3, BUB1, BIM1</i>
negative regulation of nuclear division	1.49E-06	<i>MAD1, MAD3, BUB1, BIM1</i>
microtubule cytoskeleton	2.57E-06	<i>IRC15, BFA1, BUB1, BIK1, KIP2, BIM1</i>
kinetochore	2.57E-06	<i>MAD1, MCM16, BUB1, BIK1, BIM1</i>
cell cycle process	2.83E-06	<i>MAD1, IRC15, BFA1, MAD3, MCM16, BUB1, BIK1, KIP2, BIM1</i>
cell cycle checkpoint	3.00E-06	<i>MAD1, BFA1, MAD3, BUB1, BIM1</i>
regulation of mitotic metaphase/anaphase transition	3.44E-06	<i>MAD1, MAD3, BUB1, BIM1</i>
negative regulation of cell cycle	4.44E-06	<i>MAD1, MAD3, BUB1, BIM1</i>
chromosome,	4.74E-06	<i>MAD1, MCM16, BUB1, BIK1, BIM1</i>

centromeric region		
regulation of mitosis	6.82E-06	<i>MAD1, MAD3, BUB1, BIM1</i>
regulation of nuclear division	6.82E-06	<i>MAD1, MAD3, BUB1, BIM1</i>
negative regulation of macromolecule metabolic process	7.66E-06	<i>BFA1, CIN1, GIM4, BUB1, BIK1, KIP2, BIM1</i>
regulation of protein metabolic process	8.02E-06	<i>BFA1, CIN1, GIM4, BUB1, BIK1, KIP2, BIM1</i>
cellular component organization	8.52E-06	<i>MAD1, IRC15, BFA1, MAD3, CIN1, GIM4, MCM16, BUB1, LEM3, BIK1, PAC10, KIP2, BIM1</i>
negative regulation of metabolic process	1.16E-05	<i>BFA1, CIN1, GIM4, BUB1, BIK1, KIP2, BIM1</i>
regulation of cell cycle	1.53E-05	<i>MAD1, IRC15, BFA1, MAD3, BUB1, BIM1</i>
regulation of cell cycle process	1.63E-05	<i>MAD1, BFA1, MAD3, BUB1, BIM1</i>
negative regulation of cell cycle process	1.63E-05	<i>MAD1, MAD3, BUB1, BIM1</i>
microtubule cytoskeleton organization	1.71E-05	<i>IRC15, BUB1, BIK1, KIP2, BIM1</i>
microtubule binding	1.92E-05	<i>IRC15, BIK1, BIM1</i>
cell division	2.75E-05	<i>MAD1, BFA1, MAD3, MCM16, BIK1, KIP2, BIM1</i>
microtubule-based process	3.21E-05	<i>IRC15, BUB1, BIK1, KIP2, BIM1</i>
regulation of organelle organization	3.41E-05	<i>MAD1, MAD3, BUB1, KIP2, BIM1</i>
cytoskeletal part	3.87E-05	<i>IRC15, BFA1, BUB1, BIK1, KIP2, BIM1</i>
microtubule	4.59E-05	<i>IRC15, BIK1, KIP2, BIM1</i>
protein complex assembly	4.89E-05	<i>MAD1, CIN1, GIM4, BIK1, PAC10, BIM1</i>
protein complex biogenesis	4.89E-05	<i>MAD1, CIN1, GIM4, BIK1, PAC10, BIM1</i>
cytoskeleton	5.15E-05	<i>IRC15, BFA1, BUB1, BIK1, KIP2, BIM1</i>

nuclear migration along microtubule	5.35E-05	<i>BIK1, KIP2, BIM1</i>
microtubule-based transport	6.16E-05	<i>BIK1, KIP2, BIM1</i>
nuclear migration	9.19E-05	<i>BIK1, KIP2, BIM1</i>
microtubule-based movement	9.19E-05	<i>BIK1, KIP2, BIM1</i>
cytoskeleton-dependent intracellular transport	9.95E-05	<i>BIK1, KIP2, BIM1</i>
establishment of nucleus localization	9.95E-05	<i>BIK1, KIP2, BIM1</i>
nucleus localization	9.95E-05	<i>BIK1, KIP2, BIM1</i>
mitotic sister chromatid segregation	1.76E-04	<i>IRC15, MCM16, BUB1, BIM1</i>
protein binding	1.91E-04	<i>IRC15, CIN1, GIM4, MCM16, BUB1, BIK1, PAC10, BIM1</i>
establishment of organelle localization	1.95E-04	<i>BUB1, BIK1, KIP2, BIM1</i>
sister chromatid segregation	2.00E-04	<i>IRC15, MCM16, BUB1, BIM1</i>
chromosomal part	2.14E-04	<i>MAD1, MCM16, BUB1, BIK1, KIP2, BIM1</i>
mitotic anaphase B	2.25E-04	<i>BIK1, KIP2</i>
regulation of microtubule depolymerization	2.25E-04	<i>KIP2, BIM1</i>
negative regulation of microtubule polymerization or depolymerization	2.25E-04	<i>KIP2, BIM1</i>
negative regulation of microtubule depolymerization	2.25E-04	<i>KIP2, BIM1</i>
spindle	3.21E-04	<i>BFA1, BIK1, KIP2, BIM1</i>
signaling	3.23E-04	<i>MAD1, BFA1, MAD3, BUB1, LEM3, BIM1</i>

mitotic anaphase	3.23E-04	<i>BIK1, KIP2</i>
cytoskeleton organization	3.89E-04	<i>IRC15, BUB1, BIK1, KIP2, BIM1</i>
chromosome	3.89E-04	<i>MAD1, MCM16, BUB1, BIK1, KIP2, BIM1</i>
protein complex	3.91E-04	<i>MAD1, IRC15, MAD3, GIM4, MCM16, BUB1, BIK1, PAC10, KIP2, BIM1</i>
prefoldin complex	4.16E-04	<i>GIM4, PAC10</i>
tubulin complex assembly	4.16E-04	<i>GIM4, PAC10</i>
anaphase	4.16E-04	<i>BIK1, KIP2</i>
organelle localization	4.32E-04	<i>BUB1, BIK1, KIP2, BIM1</i>
macromolecular complex assembly	6.10E-04	<i>MAD1, CINI, GIM4, BIK1, PAC10, BIM1</i>
condensed nuclear chromosome kinetochore	6.43E-04	<i>MCM16, BUB1, BIK1</i>
signal transduction	7.17E-04	<i>MAD1, BFA1, MAD3, BUB1, BIM1</i>
signal transmission	7.47E-04	<i>MAD1, BFA1, MAD3, BUB1, BIM1</i>
signaling process	8.07E-04	<i>MAD1, BFA1, MAD3, BUB1, BIM1</i>
negative regulation of protein complex disassembly	8.14E-04	<i>KIP2, BIM1</i>
condensed nuclear chromosome, centromeric region	8.54E-04	<i>MCM16, BUB1, BIK1</i>
condensed chromosome kinetochore	1.09E-03	<i>MCM16, BUB1, BIK1</i>
regulation of biological process	1.21E-03	<i>MAD1, IRC15, BFA1, MAD3, CINI, GIM4, BUB1, BIK1, KIP2, BIM1</i>
organelle organization	1.31E-03	<i>MAD1, IRC15, BFA1, MAD3, MCM16, BUB1, BIK1, KIP2, BIM1</i>
attachment of spindle microtubules to chromosome	1.31E-03	<i>IRC15, BUB1</i>
microtubule anchoring	1.31E-03	<i>IRC15, BUB1</i>

condensed chromosome, centromeric region	1.31E-03	<i>MCM16, BUB1, BIK1</i>
negative regulation of cytoskeleton organization	1.49E-03	<i>KIP2, BIM1</i>
microtubule organizing center	1.58E-03	<i>BFA1, BIK1, BIM1</i>
spindle pole body	1.58E-03	<i>BFA1, BIK1, BIM1</i>
regulation of microtubule polymerization or depolymerization	1.67E-03	<i>KIP2, BIM1</i>
regulation of protein complex disassembly	1.86E-03	<i>KIP2, BIM1</i>
cytoplasmic microtubule	1.86E-03	<i>KIP2, BIM1</i>
macromolecular complex subunit organization	2.24E-03	<i>MAD1, CINI, GIM4, BIK1, PAC10, BIM1</i>
negative regulation of cellular process	2.29E-03	<i>MAD1, MAD3, BUB1, KIP2, BIM1</i>
spindle pole	2.86E-03	<i>BFA1, BIK1, BIM1</i>
non-membrane-bounded organelle	2.86E-03	<i>MAD1, IRC15, BFA1, MCM16, BUB1, BIK1, KIP2, BIM1</i>
intracellular non-membrane-bounded organelle	2.86E-03	<i>MAD1, IRC15, BFA1, MCM16, BUB1, BIK1, KIP2, BIM1</i>
cellular component assembly	3.12E-03	<i>MAD1, CINI, GIM4, BIK1, PAC10, BIM1</i>
condensed nuclear chromosome	3.28E-03	<i>MCM16, BUB1, BIK1</i>
microtubule nucleation	3.28E-03	<i>IRC15, BIM1</i>
biological regulation	3.63E-03	<i>MAD1, IRC15, BFA1, MAD3, CINI, GIM4, BUB1, BIK1, KIP2, BIM1</i>
macromolecular complex	4.27E-03	<i>MAD1, IRC15, MAD3, GIM4, MCM16, BUB1, BIK1, PAC10, KIP2, BIM1</i>
regulation of microtubule	4.42E-03	<i>KIP2, BIM1</i>



cytoskeleton organization		
regulation of microtubule-based process	4.42E-03	<i>KIP2, BIM1</i>
meiotic chromosome segregation	5.08E-03	<i>IRC15, MAD3</i>
condensed chromosome	5.25E-03	<i>MCM16, BUB1, BIK1</i>
protein folding	5.34E-03	<i>CIN1, GIM4, PAC10</i>
distributive segregation	6.41E-03	<i>MAD3</i>
attachment of spindle microtubules to kinetochore involved in mitotic sister chromatid segregation	6.41E-03	<i>IRC15</i>
maintenance of protein location in cell	8.02E-03	<i>IRC15, BUB1</i>
mitotic sister chromatid cohesion	8.39E-03	<i>MCM16, BIM1</i>
maintenance of protein location	8.77E-03	<i>IRC15, BUB1</i>
maintenance of location in cell	9.16E-03	<i>IRC15, BUB1</i>
regulation of macromolecule metabolic process	9.21E-03	<i>BFA1, CIN1, GIM4, BUB1, BIK1, KIP2, BIM1</i>
cellular localization	1.10E-02	<i>MAD1, IRC15, BUB1, BIK1, KIP2, BIM1</i>
maintenance of location	1.13E-02	<i>IRC15, BUB1</i>
regulation of primary metabolic process	1.14E-02	<i>BFA1, CIN1, GIM4, BUB1, BIK1, KIP2, BIM1</i>
localization	1.14E-02	<i>MAD1, IRC15, BUB1, BRE5, LEM3, BIK1, KIP2, BIM1</i>
regulation of cytoskeleton organization	1.15E-02	<i>KIP2, BIM1</i>

dihydrolipoyl dehydrogenase activity	1.15E-02	<i>IRC15</i>
positive regulation of mitotic cell cycle	1.15E-02	<i>IRC15</i>
beta-tubulin binding	1.15E-02	<i>CINI</i>
sister chromatid cohesion	1.27E-02	<i>MCM16, BIM1</i>
structural constituent of cytoskeleton	1.42E-02	<i>BIK1, BIM1</i>
regulation of metabolic process	1.56E-02	<i>BFA1, CINI, GIM4, BUB1, BIK1, KIP2, BIM1</i>
ribophagy	1.67E-02	<i>BRE5</i>
meiosis	1.75E-02	<i>IRC15, MAD3, MCM16</i>
M phase of meiotic cell cycle	1.75E-02	<i>IRC15, MAD3, MCM16</i>
meiotic cell cycle	1.93E-02	<i>IRC15, MAD3, MCM16</i>
mitotic checkpoint complex	2.12E-02	<i>MAD3</i>
microtubule polymerization or depolymerization	2.12E-02	<i>BIM1</i>
microtubule depolymerization	2.12E-02	<i>BIM1</i>
cellular component biogenesis	2.31E-02	<i>MAD1, CINI, GIM4, BIK1, PAC10, BIM1</i>
chromosome organization	2.52E-02	<i>IRC15, MCM16, BUB1, BIM1</i>
post-chaperonin tubulin folding pathway	2.59E-02	<i>CINI</i>
establishment of localization in cell	2.69E-02	<i>MAD1, BUB1, BIK1, KIP2, BIM1</i>
establishment of localization	2.92E-02	<i>MAD1, BUB1, BRE5, LEM3, BIK1, KIP2, BIM1</i>
mitotic cell cycle spindle	3.00E-02	<i>BFA1</i>

orientation checkpoint		
kinesin complex	3.00E-02	<i>KIP2</i>
attachment of spindle microtubules to kinetochore	3.00E-02	<i>IRC15</i>
unfolded protein binding	3.28E-02	<i>GIM4, PAC10</i>
nuclear chromosome part	3.29E-02	<i>MCM16, BUB1, BIK1</i>
mitotic metaphase plate congression	3.29E-02	<i>BUB1</i>
meiotic sister chromatid segregation	3.29E-02	<i>IRC15</i>
positive regulation of cell cycle	3.29E-02	<i>IRC15</i>
sister chromatid biorientation	3.29E-02	<i>BUB1</i>
protein depolymerization	3.29E-02	<i>BIM1</i>
metaphase plate congression	3.29E-02	<i>BUB1</i>
establishment of chromosome localization	3.29E-02	<i>BUB1</i>
meiosis II	3.66E-02	<i>IRC15</i>
nuclear migration involved in conjugation with cellular fusion	3.66E-02	<i>BIK1</i>
spindle midzone	3.66E-02	<i>BIM1</i>
phospholipid translocation	3.66E-02	<i>LEM3</i>
lipid translocation	4.06E-02	<i>LEM3</i>
protein localization to kinetochore	4.06E-02	<i>BUB1</i>
nuclear chromosome	4.20E-02	<i>MCM16, BUB1, BIK1</i>
regulation of cellular process	4.43E-02	<i>MAD1, IRC15, BFA1, MAD3, BUB1, KIP2, BIM1</i>

microtubule motor activity	4.80E-02	<i>KIP2</i>
chromosome localization	4.80E-02	<i>BUB1</i>
oxidoreductase activity, acting on sulfur group of donors, NAD or NADP as acceptor	4.80E-02	<i>IRC15</i>

## Supplementary Discussion

### MSA and MDA hypersensitive gene deletions

The profiles of both Lau and PelA showed enrichment for genes in the tubulin complex assembly process (Tables S3, S4 and S6), including the prefoldin complex (Gim4p, Yke2p and Pac10p) that is required for  $\alpha$ - and  $\gamma$ -tubulin folding<sup>1</sup> and Cin1p and Cin2p that are specifically required for efficient  $\beta$ -tubulin folding.<sup>2, 3</sup> Deletion of these genes would reduce the amount of functional tubulin in the cell and sensitise the cell to sub-inhibitory concentrations of an MSA or MDA, presumably because there is a lower concentration of the drug target.

A number of checkpoints exist in the yeast cell cycle that ensure an even distribution of chromatin to both mother and daughter cell. The deletion of genes required for the spindle assembly check point (*MAD1*, *MAD2*, *MAD3* and *BUB1*),<sup>4</sup> the anaphase-promoting complex (*SWMI*),<sup>5</sup> and the Bfa1p-Bub2 mitotic exit checkpoint (*BFA1* and *BUB2*)<sup>6</sup> cause hypersensitivity to both MSA and MDA (Fig. 4 and Table S6). This is genetic evidence that perturbing microtubule function in any manner causes spindle-kinetochore attachment defects, thereby activating the spindle assembly checkpoint. In support of this, deletion of *MCM16*, a component of the kinetochore itself,<sup>7</sup> *SHE1*, a Dam1 complex-associated protein,<sup>8</sup> and *IRC15*, a gene involved in chromosome segregation,<sup>9</sup> cause hypersensitivity to both MSA and MDA, though the deletion of a selection of other kinetochore components cause hypersensitivity to MSA exclusively. It makes intuitive sense that MSA should inhibit the transition from metaphase into anaphase by preventing microtubule depolymerisation-dependent chromosome separation. However, these results also suggest anaphase progression is reliant on microtubule dynamics and not only depolymerisation.

### Supplementary Methods

#### *Saccharomyces cerevisiae* media

Yeast strains were stored at -80°C in yeast peptone dextrose (YPD) containing 15% glycerol. Yeast were streaked onto 10 cm 2% agar (Invitrogen) plates containing YPD (1% yeast extract (DIFCO, Detroit, MI, USA), 2% bacto-peptone (DIFCO), and 2% glucose). Synthetic complete medium (SC) consisted of 0.17% bacto-yeast nitrogen base (DIFCO, Detroit, MI, USA), 0.1% monosodium glutamate, 0.2% amino acid mixture (3 g adenine, 0.2 g para-aminobenzoic acid, 10 g leucine, and 2 g each of uracil, inositol, alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine,

lysine, methionine, phenylalanine, proline, serine, threonine, tyrosine, tryptophan, and valine), and 2% glucose. Synthetic defined medium minus uracil (SD-ura) consisted of SC medium without uracil in the amino acid mix. The above media were supplemented with 200 µg/mL G418 (Geneticin, Gibco, Invitrogen) and/or 100 µg/mL Nat (nourseothricin, Werner BioAgents) where applicable. After streaking, the plates were incubated at 30°C for 48 h (when on YPD agar) or 72 h (when on SC or SD-ura agar), and the plates were then stored at 4°C for later single colony counting.

### Concentration-response curves

Half-logarithmic concentration-response curves were created for the BY4741 (WT) and *pdr1Δpdr3Δ* knockout strains to determine if Lau and PelA were substrates for the yeast pleiotropic drug efflux pumps and to find the optimum concentrations to use for cytotoxicity assays, bud index assays, and flow cytometry. A single colony of each was inoculated in triplicate into 2 mL of SC medium and grown overnight in a Glascol<sup>®</sup> rotator (Total Lab Systems, New Zealand) set at 40 rpm. The concentration of each culture was estimated by haemocytometer and the cells diluted to 5 x 10<sup>5</sup> cells/mL in 10 mL of SC medium. A 99 µL aliquot of the diluted cells of each replicate was pipetted into each of eight wells of a 96-well plate (Jet BioFil, Elgin, IL, USA) for each drug concentration. Drug (1 µL) was then added to give the appropriate final concentration: 100, 30, 10, 3, 1, 0.3, 0.1, and 0 µM in 1% DMSO. Each plate had three wells of 100 µL SC medium without cells for the medium blank. The plate was incubated at 30°C for 18 h and read at 590 nm on a multiwell plate reader (Versamax, Molecular Devices, Sunnyvale, CA, USA). The percent residual growth was calculated from the following equation:

$$\% \text{ residual growth} = \left[ \frac{\text{Mean}_{\text{exp abs}} - \text{Mean}_{\text{medium blank}}}{\text{Mean}_{\text{DMSO abs}} - \text{Mean}_{\text{medium blank}}} \right] \times 100$$

### Cytotoxicity assay

To test for cytotoxicity of the compounds, overnight cultures of *pdr1Δpdr3Δ* (n=3 biological replicates) were set up in liquid culture at 2 x 10<sup>4</sup> cells/mL. A 50 µL aliquot of cells was pipetted into each of two 1.5 mL microcentrifuge tubes. One tube was treated with 1% DMSO (diluent control) and one with a concentration of MSA that inhibited growth by 100%. This was carried out separately for Lau (10 µM) and PelA (30 µM). The tubes were incubated at 30°C in a Glascol<sup>®</sup> rotator, and 1 µL of cells from each culture was pipetted onto a YPD plate without MSA at 0, 1, 2, 3, 4, 5, 6 and 24 h after incubation with the MSAs.

Between the 0-6 h time points, the YPD plate was left at room temperature, then after the 6-h time point, the YPD plate was incubated for 2 days at 30°C. For the 24-h time point, 1 µL of cells was pipetted onto a separate YPD plate and treated similarly to the shorter MSA exposures without compound and incubated for 2 days at 30°C.

### **Bud index assay**

A bud index assay was carried out for Lau and PelA using the efflux pump deficient strain to determine how these MSA affect the yeast cell cycle. A mid-log culture ( $1 \times 10^7$  cells/mL) of cells grown in SC medium was treated with 2 µM Lau or 17 µM PelA, or the equivalent volume of 1% DMSO. These concentrations of MSA inhibited cell growth by about 50%. The cells were incubated for a further 4 h at 30°C and then counted and categorised according to their bud index (Fig. 2). High power (60x oil immersion objective) microscope images were taken using a light microscope with bright-field and phase-contrast optics (Model AX70, Olympus NZ Pty Ltd, Auckland, NZ). A histogram of the percentage of cells in each phase of the cell cycle was plotted using Prism software (Graphpad Prism, v6.0, San Diego, CA, USA).

### **Flow Cytometry**

Flow cytometry was used to determine if Lau and PelA blocked normal progression through the cell cycle. The amount of DNA present in different phases of the cell cycle was quantified for treated and untreated cells. Cells (*pdr1Δpdr3Δ*) were treated with 2 µM Lau or 17 µM PelA, or the equivalent volume of 1% DMSO, using the same method as in the bud index assay. The flow cytometry protocol was carried out as previously described.<sup>10</sup> Flowjo software (Tree Star, Inc., Ashland, OR, USA) was used to calculate the area under each cell cycle peak to obtain a cell count. The cell count was converted into a percentage and adjusted for the area excluded due to gating. Histograms of the averaged data were drawn using Prism 6.0.

### Supplementary References

1. S. Geissler, K. Siegers and E. Schiebel, *EMBO J.*, 1998, **17**, 952–966.
2. M. A. Hoyt, J. P. Macke, B. T. Roberts and J. R. Geiser, *Genetics*, 1997, **146**, 849-857.
3. G. Tian, Y. Huang, H. Rommelaere, J. Vandekerckhove, C. Ampe and N. J. Cowan, *Cell*, 1996, **86**, 287-296.
4. I. M. Cheeseman, D. G. Drubin and G. Barnes, *J. Cell Biol.*, 2002, **157**, 199-203.
5. M. C. Hall, M. P. Torres, G. K. Schroeder and C. H. Borchers, *J. Biol. Chem.*, 2003, **278**, 16698-16705.
6. Y. Wang, F. Hu and S. J. Elledge, *Curr. Biol.*, 2000, **10**, 1379-1382.
7. V. Measday, D. W. Hailey, I. Pot, S. A. Givan, K. M. Hyland, G. Cagney, S. Fields, T. N. Davis and P. Hieter, *Genes Dev.*, 2002, **16**, 101-113.
8. J. Wong, Y. Nakajima, S. Westermann, C. Shang, J.-s. Kang, C. Goodner, P. Houshmand, S. Fields, C. S. M. Chan, D. Drubin, G. Barnes and T. Hazbun, *Mol. Biol. Cell*, 2007, **18**, 3800-3809.
9. B. E. Keyes and D. J. Burke, *Curr. Biol.*, 2009, **19**, 472-478.
10. S. B. Haase and S. I. Reed, *Cell Cycle*, 2002, **1**, 117-121.