Supplementary Material & Methods

Antibodies

Rat anti-tubulin antibody (clone YL1/2) and mouse anti-γ-tubulin clone (GTU88) were obtained from Sigma-Aldrich and anti-phospho-histone H3 from Upstate Biotechnology. Rabbit anti-cyclin B (Rb271) and rabbit anti-cyclin A (Rb270) have been described previously[1]. Anti-Mei-S332 antibody[2] was kindly given to us by Terry Orr-Weaver (MIT, USA). Rat anti-pvr antibody[3] was the kind gift of Pernille Rorth. FITC- or Texas red–conjugated goat anti–rat and anti–mouse were obtained from Sigma-Aldrich and Jackson Immuno Research Laboratories. Goat anti-rabbit Alexa-488 antibody (Molecular Probes) was used for FACS analysis. Peroxidase–conjugated goat anti–rabbit or anti–rat antibodies used in Western blotting were from Sigma-Aldrich.

Statistical analysis

Cells were categorised according to phase of mitosis and to centrosome, spindle and DNA morphology and assigned to one of 20 potential mitotic phenotypic abnormalities (see supplementary Tables 3 and 4). Data was then inserted into a datasheet for analysis (supplementary Table 4). Two datasets were obtained for each kinase, from two independent experiments. Seven phenotypic parameters (mitotic index, cytokinetic index, PM ratio, percentage of mitotic defects, percentage of centrosome defects, percentage of spindle defects and percentage of chromosome defects) were normalized and compared across the whole dataset. Normalised results from immunofluorescence countings are given as the Phenotypic Score (PS), which equals $\log_2 (x/\bar{c}_t)$ for all variables (with the exception of chromosomal abnormalities where results are given as

$\log_2(100\text{-}x/100\text{-}\bar{c}_t)$), where x stands for the observed value (relative to total number of cells) and $\bar{c}_t$ for the mean value of the negative controls (relative to total number of cells) performed in the same experiment (same day). Confidence intervals were generated separately for each of the two repeats of experiments using negative control data only. Since there was a significant effect of the day on which the experiment was performed (due mainly to the age of the cells), we had to devise a specific bootstrap procedure for generating confidence intervals by resampling negative controls within days of experiment. The procedure works as follows: we first sample with replacement a batch of experiments t. We then sample with replacement n_t +1control data values, where n_t represents the number of controls in batch t. One control data point is allocated to the numerator; the mean of the remaining n_t data is computed and allocated to the denominator. The base 2 logarithm of this ratio is then computed. The procedure was repeated 2,000 times in order to produce the distribution that allowed us to compute the upper and lower confidence limits. We defined a "mitotic kinase" when PS values for at least one of the mitotic parameters fell out of the 90% CI in two independent experiments. To describe the strength of the phenotype, phenotypic confidence levels were used: at the extreme, arbitrary values -5 and 5 indicate respectively PS values outside the 99%CI at the lower or higher boundary in both experiments; -4 and 4 indicate PS values outside the 95% CI; -3 and 3 indicate PS values outside the 90 %CI; -2 and 2 indicating PS values outside the 85% CI. "Cluster"[4] and "JavaTreeView"[5] were used in clustering the kinases according to their mitotic phenotypes (Fig. 3d).

Supplementary Table 1-List of *Drosophila* protein kinases studied in this work (228) and primers used to synthesize dsRNA. The set of protein kinases was defined based on Morrison *et al.*[6], Manning *et al.*[7] and annotation in FlyBase, based on homologies with protein kinase catalytic sites[7]. All primers led to the synthesis of a single band of dsRNA. Name (as in FlyBase) and CG number are indicated. Two sets of primers are indicated for genes for which different transcripts exist or in cases where we rechecked the phenotype observed. For the majority of these genes, DNA (with T7 polymerase binding site) amplified with these primers is available from http://www.hgmp.mrc.ac.uk/geneservice/reagents/products/descriptions/Dros_RNAi.shtml.

NAME	CG	FORWARD SEQUENCE	REVERSE SEQUENCE
Abl	4032	TAATACGACTCACTATAGGGAGACACGGGCGATAGTCTGGAGCAGAGT	TAATACGACTCACTATAGGGAGACGGAATGGGGCTGGCCTTCGGATTT
Ack	14992	TAATACGACTCACTATAGGGAGATCTACTCGAATTTCAACCAGTCTCT	TAATACGACTCACTATAGGGAGATCATACCAAATACGATTCACCACAC
Akt1	4006	TAATACGACTCACTATAGGGAGATTACATCGGGTCATGCGCTTACGGAACA	TAATACGACTCACTATAGGGAGACACTTTCTTAACGCCGCTGCTATTA
Alk	8250	TAATACGACTCACTATAGGGAGACATCGAGACGGAGATGCTGTGGAAA	TAATACGACTCACTATAGGGAGACGAGGTGAATATGCCATCGAGGAAG
aPKC	10261	GCTTCTAATACGACTCACTATAGGCTCTCCTTCCACAACGAAAT	GCTTCTAATACGACTCACTATAGAACCACAAAAAGTATGCACAAA
aPKC	10261	TAATACGACTCACTATAGGGAGAGCAGCGCAAGCAACAACAACTA	TAATACGACTCACTATAGGGAGAGATGGTAAATGGCTAAACAAAACGCTCAAT
aur	3068	TAATACGACTCACTATAGGGAGAACGTGCGCATATATCTGATCTTGGA	TAATACGACTCACTATAGGGAGAATTAAGGACCAGCAGCTTGGAAATG
aur	3068	TAATACGACTCACTATAGGGAGAACGTGCGCATATATCTGATCTTGGA	TAATACGACTCACTATAGGGAGAATTAAGGACCAGCAGCTTGGAAATG
auxillin	1107	GCTTCTAATACGACTCACTATAGACACACAATTGGTCGCTCAAA	GCTTCTAATACGACTCACTATAGGATTAGGAGCATGTGCCTGTG
BABO	8224	TAATACGACTCACTATAGGGAGAACAATGGAACTTGGACACAGTTGTGG	TAATACGACTCACTATAGGGAGACATCGTAATACGGCAATTGATACTC
BcDNA:GH04978	7028	TAATACGACTCACTATAGGGAGACTCGCAGCAGCTGGTTGTCCACACC	TAATACGACTCACTATAGGGAGACCGCTCTCGTCGCCTGTCTGATTCAAA
BcDNA:GH07910	2829	TAATACGACTCACTATAGGGAGACTGCCAGTCAGCGACAACAAGAAGA	TAATACGACTCACTATAGGGAGATTGTTGCTGCTGTTGCTGCTGGGAT
BcDNA:LD09009	6386	TAATACGACTCACTATAGGGAGACCAACATACTGCTGGGCCTGGAAAA	TAATACGACTCACTATAGGGAGAGCTGCTGGTCTGTGGCTTCATCTTA
BcDNA:LD22679	1344	TAATACGACTCACTATAGGGAGATAAGGCCAAGACTTTCTGCTATCTT	TAATACGACTCACTATAGGGAGAAAATCAGCCATGCACCTTAGTGTTT
BcDNA:LD23371	8878	TAATACGACTCACTATAGGGAGATCGACTTCGGCCTGGCGTCTAAGTT	TAATACGACTCACTATAGGGAGATGTCACACTTGCTGCCATCCACCAC
BcDNA:LD28657	1098	TAATACGACTCACTATAGGGAGACAGCTGGACCACCAAAACATTGTCA	TAATACGACTCACTATAGGGAGATTGATGGCAGTTGACTCGCTGTTAC
BEST:CK01209	9085	TAATACGACTCACTATAGGGAGAACCACCCACACCTCATCTCGCCCACCCACACG	TAATACGACTCACTATAGGGAGACGGCGGCGACAGCGACAGCGAGAGGAAGT
BEST:CK01209	9085	TAATACGACTCACTATAGGGAGAATTGGCGAGTGACCCTGCTGGAC	TAATACGACTCACTATAGGGAGAGGGGGTAACGGGCTCAAAGGGTAG
bsk	5680	TAATACGACTCACTATAGGGAGATTTACACTCAGCAGGAATTATTCAC	TAATACGACTCACTATAGGGAGATCTGGATCAATGACTAGCATTTTAC
bt	1479	TAATACGACTCACTATAGGGAGACGGACCACTTCAAATATCAGATGTG	TAATACGACTCACTATAGGGAGAGGAAACTCGGAATTTGTAGGTTTGG
Btk29A	18355	TAATACGACTCACTATAGGGAGATTGGATCGGGACAGTTTGGTGTTGT	TAATACGACTCACTATAGGGAGATCTTAGAGGAGAAGCGCGTGTAGTT
btl	6714	TAATACGACTCACTATAGGGAGAGTGATATTATTTCGACCGCAACT	TAATACGACTCACTATAGGGAGAAGCAACTTCAGGGATCGACTCTCATTCAGG
BubR1	7838	TAATACGACTCACTATAGGGAGAAAAATCCATCATGCCACGCAGAGTT	TAATACGACTCACTATAGGGAGAGCTCAGAGGTTTCCAATATGGTAGA
BubR1	7838	TAATACGACTCACTATAGGGAGACCAGTAGGCGCAATGTAGGTC	TAATACGACTCACTATAGGGAGATTGCGATGGATAAATGGATGCT
Cad96Ca/HD-14	10239	TAATACGACTCACTATAGGGAGACCAGCTGCCCGGTGTTCAATCCAT	TAATACGACTCACTATAGGGAGACAGAGGCGTCGGCGGCACAAGTA
Caki	13412	TAATACGACTCACTATAGGGAGATCTGTTACCTTCAAGATAGTTCCTT	TAATACGACTCACTATAGGGAGATCGATATCAAGGTGTTCTTAATGTG

Caki	13412	TAATACGACTCACTATAGGGAGACGAGGGAATGCTCTACATGGTCTTC	TAATACGACTCACTATAGGGAGACGTTCGCCGAGATTGATTTCCACTC
CaMKI	1495	TAATACGACTCACTATAGGGAGATGGTTACTGGTGGAGAACTCTTTGA	TAATACGACTCACTATAGGGAGATGCTTGCTTGCAAGTATACCTCTTC
CaMKII	18069	TAATACGACTCACTATAGGGAGAATTACATTGGCGAGCTTTACTTTAC	TAATACGACTCACTATAGGGAGAAACTTACTTTCCCAACTCTTCTT
cdc2	5363	TAATACGACTCACTATAGGGAGAAAATTTCGTTGCTTAAGGAGTTGA	TAATACGACTCACTATAGGGAGAATCGACGGGACAGGAATACC
cdc2c/CDK2	10498	TAATACGACTCACTATAGGGAGAAAGGATTGTTTACGAGGTTATGAC	TAATACGACTCACTATAGGGAGATTGTTGCCGGAAATGACTACG
cdc2rk	1362	TAATACGACTCACTATAGGGAGAAGGATGTCCAGCTTAAAGTCAAACGAT	TAATACGACTCACTATAGGGAGACCCACCACCACCTCACGCAAGCGGACAATA
cdi	6027	TAATACGACTCACTATAGGGAGATCTCTATTACGAAGCAAGCAAAAAGTGATT	TAATACGACTCACTATAGGGAGACCAGATGAAAGGGGAGGCGGCCGATGAGTC
Cdk4	5072	TAATACGACTCACTATAGGGAGACGAACAAGGCAAATAAATCAAGTCAC	TAATACGACTCACTATAGGGAGAGGGGGCAAATCGTCGGAATA
Cdk5	8203	TAATACGACTCACTATAGGGAGACACTGCGACCAGGACCTCAAGAAGT	TAATACGACTCACTATAGGGAGACCACGAGGTGATGGCCGGAAAAGAT
Cdk7	3319	TAATACGACTCACTATAGGGAGATGGTGGACGTTTTCGGTCAACTTTC	TAATACGACTCACTATAGGGAGACAGTTTGCTCAAATGCGGCCATTCA
Cdk8	10572	TAATACGACTCACTATAGGGAGACTTTCCGCAGGACAAGGACTGGGAG	TAATACGACTCACTATAGGGAGATGCTGTTGCTGCTGCTGCTGGTGGT
Cdk9	5179	TAATACGACTCACTATAGGGAGAAGCTGCCAACGTGCTGATTACCAAG	TAATACGACTCACTATAGGGAGATGGGCATGGGATCCGTCCAGAAGAA
CG10177	10177	TAATACGACTCACTATAGGGAGAATGGTGGACTCTTGTAAACGTTGGG	TAATACGACTCACTATAGGGAGAGGATGAAGAGCAAACCAGCAGATTC
CG10522	10522	TAATACGACTCACTATAGGGAGAAGGAGACGGAATTGCGCCAGAAACT	TAATACGACTCACTATAGGGAGAAGCTCTCTCTTGGGTGGCAAACAGT
CG10522	10522	TAATACGACTCACTATAGGGAGACGCCGTTCTGGAAATGCAAGGAGTG	TAATACGACTCACTATAGGGAGAGACGTTTCCAGCACAGGCTTGTGAC
CG10673	10673	TAATACGACTCACTATAGGGAGAAAAGGAGAAGCCTGCCTGATCAAGG	TAATACGACTCACTATAGGGAGACGTGCTCGAAGATATACGGCTGTTC
CG10738	10738	TAATACGACTCACTATAGGGAGAGATTTCAAAACCATCCGCACCAAAC	TAATACGACTCACTATAGGGAGAGGTGACGGATCTTAAACTCTGATAC
CG10951	10951	TAATACGACTCACTATAGGGAGAATACGCAGCGGAAGCAATCGACTTG	TAATACGACTCACTATAGGGAGAAGTTGATGGCACTGGAGATCTGTTC
CG10967	10967	TAATACGACTCACTATAGGGAGAAGCGCAAGAGCAGTGTGAGCAGTGA	TAATACGACTCACTATAGGGAGACGCCAGCACAAAGTTCAGCTTGGAC
CG11221	11221	TAATACGACTCACTATAGGGAGAACGTGGAGCTGCCGCTGATGACCTT	TAATACGACTCACTATAGGGAGAGCTTCACCTTGTGCACCAGCAGACC
CG11228	11228	TAATACGACTCACTATAGGGAGATGGCTACGACTGTGTGGCAGACATA	TAATACGACTCACTATAGGGAGACACCTTGCTCTGCATGCGCTATCAT
CG11228	11228	TAATACGACTCACTATAGGGAGAGGCAACCCAGGAAAACGGAATG	TAATACGACTCACTATAGGGAGAGGAGCAGCTGCCTTGGACA
CG11533	11533	TAATACGACTCACTATAGGGAGAAAATCAATCATGCCAGCCTTCTTC	TAATACGACTCACTATAGGGAGACATCTTGACGGACTCCTTAGCCTTGAC
CG11660	11660	TAATACGACTCACTATAGGGAGATTTCTACGGGCAAAGAGGCTAATGT	TAATACGACTCACTATAGGGAGAAGGAAGTCAAAGGAATGCGGATGAT
CG11859	11859	TAATACGACTCACTATAGGGAGATGGATCAGGCAGATGAGGAGGATGA	TAATACGACTCACTATAGGGAGAAGACGGAGCTATTGTGCTGGTTGTG
CG11870	11870	TAATACGACTCACTATAGGGAGAGGAAATTGTGGAAGGCACACCATAC	TAATACGACTCACTATAGGGAGAAAGCAGGAGAATGGACATCGACTCA
CG12069	12069	TAATACGACTCACTATAGGGAGACACGGTCAACCTGATAGCCTCCTAC	TAATACGACTCACTATAGGGAGACACCAAATGACGCAGAGCTCCACTG
CG12147	12147	TAATACGACTCACTATAGGGAGATCATGAGAAGGACCAGCGACAAGAT	TAATACGACTCACTATAGGGAGACCGAAGTCAATCATGTACACCTGAG
CG1227	1227	TAATACGACTCACTATAGGGAGACAGTCTAATCGACCTTGGGGAAAAC	TAATACGACTCACTATAGGGAGAATAACTCTGGAGCCCGGTAGACAAT
CG14030	14030	TAATACGACTCACTATAGGGAGAAGGAGCATAGCGGACCGTACACAAA	TAATACGACTCACTATAGGGAGAGAGTTATCCAAAGCTGTGGCACTGG
CG14163	14163	TAATACGACTCACTATAGGGAGAAGTGGCAGCGCTGTGGGAATAACG	TAATACGACTCACTATAGGGAGACACCCGATGCTGCACTGATGGACA
CG14217	14217	TAATACGACTCACTATAGGGAGAGCTGCGGCACAGAATCATCACCATA	TAATACGACTCACTATAGGGAGATGACTGCATTGGAGATGGCCTGTTG
CG14305	14305	TAATACGACTCACTATAGGGAGATCACAAGATCGGCGAGGGGTCTTAT	TAATACGACTCACTATAGGGAGAAAGCAGCTGATCCGCAGTATGTCTC
CG15072	15072	TAATACGACTCACTATAGGGAGAGCAGTCAGAGATGCAGGAGCAGGAA	TAATACGACTCACTATAGGGAGAATCGCGCCAGGCATTCCAGCTCAAA
CG17090	17090	TAATACGACTCACTATAGGGAGAGGCTCAAAGCGAATGTGGCTACCAA	TAATACGACTCACTATAGGGAGACCTGGTGATGATGATGTCCATGACTG
CG17309	17309	TAATACGACTCACTATAGGGAGACAGACGACGAACCAGCAGCAACAAC	TAATACGACTCACTATAGGGAGAGGGAAGCATGGTTCATGGCAGTGGT

CG17528	17528	TAATACGACTCACTATAGGGAGATGCGACATCCCCTCAGAGCGTTCCT	TAATACGACTCACTATAGGGAGAATTTGATTCTTAGTGCCTTTCTTGTCG
CG1760	1760	TAATACGACTCACTATAGGGAGACGTCTGTCAAGGCTCTGGTGAAGAA	TAATACGACTCACTATAGGGAGATGATCCAGGCTCAAGTTGTTGGTGG
CG17698	17698	TAATACGACTCACTATAGGGAGACAACATCACCTCTAGATCGAGTTTA	TAATACGACTCACTATAGGGAGATGAATCAGCTAGAAACGGCACATTT
CG1776	1776	TAATACGACTCACTATAGGGAGACCAGAGCCAAAGCACCTACGATGAC	TAATACGACTCACTATAGGGAGAATGCAGCAGGCAATCCTTGGTGGTG
CG18020	18020	TAATACGACTCACTATAGGGAGATGTACGAGGTGATTGCTCAGAATCC	TAATACGACTCACTATAGGGAGAATGGGCTTGTCCTGGAAGTACCACT
CG1951	1951	TAATACGACTCACTATAGGGAGACGGGGTTAAGACACTTAGCTATTTG	TAATACGACTCACTATAGGGAGACTCTGCAGACACAGTTTCTTGATTC
CG1973	1973	TAATACGACTCACTATAGGGAGAGCTGGATCTGTTCATCGCGCACTTG	TAATACGACTCACTATAGGGAGACAAACTGGGATCCTCGGAGACCTTC
CG2049	2049	TAATACGACTCACTATAGGGAGAGTTATACCACAGTTGGGGAAGCTTTAC	TAATACGACTCACTATAGGGAGATTCTTCAGTGCCTTAATAGCGTAGTA
CG2309	2309	TAATACGACTCACTATAGGGAGAAAGAGCTGGACCAAACTGTGGAAAG	TAATACGACTCACTATAGGGAGATCATCATAGATGCGTCTCGAGGAGA
CG2577	2577	TAATACGACTCACTATAGGGAGAGCGCAAGATCGGCTGTGGATCCTTC	TAATACGACTCACTATAGGGAGACCAATGGAGGCGTACCTGGCTGTTC
CG2905	2905	TAATACGACTCACTATAGGGAGAGATAAAGTTCTTGCTACAGTGGAAA	TAATACGACTCACTATAGGGAGAAAAGGTAAAGCATTTGAATCAGGAG
CG3105	3105	TAATACGACTCACTATAGGGAGATGTGACGCTTTACGTTCTGATGTTT	TAATACGACTCACTATAGGGAGATCGCGTAAAGAGTGTCCATTTTGTT
CG3216	3216	TAATACGACTCACTATAGGGAGATCTACCAAATCCTGCCGCGTCCTGT	TAATACGACTCACTATAGGGAGAGGTGGCCGAGGACACATGTATCTTG
CG3277	3277	TAATACGACTCACTATAGGGAGAGATTGTGCTGATTCTCCTGCTGGTGCTA	TAATACGACTCACTATAGGGAGAAAGAACATTGTACGAAGTGCCTAAAAG
CG3608	3608	TAATACGACTCACTATAGGGAGATCGCTTGGGAGGTGGATTTGAAC	TAATACGACTCACTATAGGGAGAGCGTGCGCAGCGTGGACTC
CG4041	4041	TAATACGACTCACTATAGGGAGAGGTCGCTGGCCCTGGTAATGGTGGAG	TAATACGACTCACTATAGGGAGAGCGGCGAGTGGAGCAGGGGAAAGTAGA
CG4224	4224	TAATACGACTCACTATAGGGAGAGGAGGATCGGTTGAAGCTAAGGATA	TAATACGACTCACTATAGGGAGAGAACTGGAGCTGATCTTGCGTTTCA
CG4523	4523	TAATACGACTCACTATAGGGAGAAAACATCAACAGCTCTGTGGACAGT	TAATACGACTCACTATAGGGAGACTGCAGCTCGATTAGCACATTATCA
CG4527	4527	TAATACGACTCACTATAGGGAGAATAATACGGCATCTGGCAGTCATAG	TAATACGACTCACTATAGGGAGATCCTTGGTAAGACCTTGAGCATTTG
CG4549	4549	TAATACGACTCACTATAGGGAGAGGTCACACCAGTCTTTGCGCTCTAC	TAATACGACTCACTATAGGGAGACCATGGCCTGCACTAGATTCTGGGT
CG4588	4588	TAATACGACTCACTATAGGGAGAAAAATGGTTTGGATCTGCTGGAGGA	TAATACGACTCACTATAGGGAGACAATCCGAAGAGCTGCGAAATGTTG
CG4629	4629	TAATACGACTCACTATAGGGAGAGTGCCGATCTGATGCAGTGGGAGAT	TAATACGACTCACTATAGGGAGATAGCTGGCTCAGATCCTCGGTGTTC
CG4839	4839	TAATACGACTCACTATAGGGAGACGGGATGCAAAGGACACTGGAGATG	TAATACGACTCACTATAGGGAGACAACGGCGGTGCTGGCGGTATGTTA
CG4945	4945	TAATACGACTCACTATAGGGAGAGAGCGCAAAGGAGATTAACAGCACCCT	TAATACGACTCACTATAGGGAGATCATCGCCGAAAGAAGGAGCTCTTG
CG5169	5169	TAATACGACTCACTATAGGGAGAAGAAGCTGATGCAGACCACACACTC	TAATACGACTCACTATAGGGAGAGCGCGGCGTTATTTGCATGGAATGA
CG5483	5483	TAATACGACTCACTATAGGGAGATGAACTCTTTCTACAAGACAACCAG	TAATACGACTCACTATAGGGAGAGCAGACTGTTGTATGACATATTCAG
CG5790	5790	TAATACGACTCACTATAGGGAGACGATTTCGGATTGGCTCAAAGGATA	TAATACGACTCACTATAGGGAGAGACCAGAGAGCAAAGAGAGCATTAT
CG6114	6114	TAATACGACTCACTATAGGGAGAGGGTCACAGCTGGCGGCAAAGGGGA	TAATACGACTCACTATAGGGAGACGGAGAGTTGCAGCGCGTGGGACTG
CG6498/MAST	6498	GCTTCTAATACGACTCACTATAGGTGTACGGCACACCCGAGTA	GCTTCTAATACGACTCACTATAGAGACGATCCCGTGGATTCTG
CG6535	6535	TAATACGACTCACTATAGGGAGACAATCTGAAGATGGGCAACCAACAA	TAATACGACTCACTATAGGGAGATCTGATTTAGCTGCTGCTCATCCAA
CG6800	6800	GCTTCTAATACGACTCACTATAGTCCTGACCTAACTGGTCTCTCC	GCTTCTAATACGACTCACTATAGCATATCCACTCCGGTTCCATA
CG7094	7094	TAATACGACTCACTATAGGGAGAACCAGCTGCTAATGCGAATTGAGTG	TAATACGACTCACTATAGGGAGAGCGGAAAAGTATGCGGAATATCTGG
CG7097	7097	TAATACGACTCACTATAGGGAGACACATCAGGCGGCACAGCAGGAACA	TAATACGACTCACTATAGGGAGAAGCTGATGACGCAGAGGACGAGATG
CG7125	7125	GCTTCTAATACGACTCACTATAGCCTCATCTGGACACGTAGAGC	GCTTCTAATACGACTCACTATAGGGAGCTCCTGTCCTGTTCTG
CG7156	7156	TAATACGACTCACTATAGGGAGAAGAGATTCGATGCGGCAGTCATCCA	TAATACGACTCACTATAGGGAGATGACTGAACTCTAGAGCCGCCTCAT
CG7177	7177	TAATACGACTCACTATAGGGAGAGACGAAGATATCGGTATACGAGTGG	TAATACGACTCACTATAGGGAGATGGATAGAGCCAGGCTTGTTTCTGA
CG7236	7236	TAATACGACTCACTATAGGGAGACTGACCAAACAGATCTGCTACCAGA	TAATACGACTCACTATAGGGAGATGTCCAGGCACTTCTTGAGAAAGTC

CG7597	7597	TAATACGACTCACTATAGGGAGAGGCAGAAGGCGCTGAAGGAAATCAT	TAATACGACTCACTATAGGGAGAGGAAGATTGAGCACGCTCTTGTTGG
CG7616	7616	TAATACGACTCACTATAGGGAGAGGCCTGGCTTACGATGGGATAGTAA	TAATACGACTCACTATAGGGAGAGTGCCTAGGTCGCTGATGAATCTCT
CG7643	7643	TAATACGACTCACTATAGGGAGAAAGCCGGATGCAGACTTCATTACCC	TAATACGACTCACTATAGGGAGAACCACCTTCAGGGCGAACTCATTTC
CG7643	7643	TAATACGACTCACTATAGGGAGATAACAAACAGCAACAGCAACATAAC	TAATACGACTCACTATAGGGAGACGTCTTCGAGGTGGAGGGTAA
CG8173	8173	TAATACGACTCACTATAGGGAGACGCACCGGAGGTCATAGACGAAGTG	TAATACGACTCACTATAGGGAGATGGCCGCTGGACGATCCTCGCTGAGA
CG8485	8485	TAATACGACTCACTATAGGGAGAAACAGGAAATTCCACGAATAGAAGG	TAATACGACTCACTATAGGGAGAAGCATTTAGAGCCGGTAACGTGTAT
CG8565	8565	TAATACGACTCACTATAGGGAGACCAGCATGCCGTTCGAAATGAAACA	TAATACGACTCACTATAGGGAGACACCTGCTGGGCAATTTGCTTGATA
CG8655	8655	TAATACGACTCACTATAGGGAGAAAATTGCGCTGGATGCTGGTTTGGG	TAATACGACTCACTATAGGGAGACAGTGGTCTGATCTGGGTACTTGAG
CG8726	8726	TAATACGACTCACTATAGGGAGAACGTGGTCGCTGGGTGGAAGTATGG	TAATACGACTCACTATAGGGAGAATGAAAAATGGCCGGTAAAACGCTGGAACG
CG8767	8767	TAATACGACTCACTATAGGGAGATGCAATTCCTCGAAGATCAAAGTGAA	TAATACGACTCACTATAGGGAGAGGACTATCAAAGTGGAGTGCTAATC
CG8789	8789	TAATACGACTCACTATAGGGAGAAGAACCGAAAGGTGCAGCTGGTGGA	TAATACGACTCACTATAGGGAGACTCTCACGCAATTCAAGAGGAGAGG
CG8866	8866	TAATACGACTCACTATAGGGAGACTCTGGAGCATCGGGGTCATCCTCT	TAATACGACTCACTATAGGGAGAGCCTGCCGTTGACGTTCAGCCAACA
CG9222	9222	TAATACGACTCACTATAGGGAGAATTCTTGAGGAGCATGGCATCATAC	TAATACGACTCACTATAGGGAGAGAAGGTTTTCGAGAGTATCACTTGG
CG9374	9374	TAATACGACTCACTATAGGGAGAGACGCTGGACATGGGTAATATGTTC	TAATACGACTCACTATAGGGAGATTTGATCCAGGGAGAGCAGCAGGTT
CG9374	9374	TAATACGACTCACTATAGGGAGAGTCAAGGCAGCACACCATCATCAT	TAATACGACTCACTATAGGGAGATGCAGCCCGCCGACACAGTA
CG9746	9746	TAATACGACTCACTATAGGGAGAAAACAGAAGATCTGCCACGGGGACA	TAATACGACTCACTATAGGGAGATCCAAGTAATCCTCGGCGCTCTTTC
CG9783	9783	TAATACGACTCACTATAGGGAGAACAACCACTACAAATGCCTCAGTCC	TAATACGACTCACTATAGGGAGATGATGGCGGACTGCGGTTTAGATTG
CG9962	9962	TAATACGACTCACTATAGGGAGAATCTACGAGGCCAAGCACATGGGGT	TAATACGACTCACTATAGGGAGACCGCCGGGACTGCACTTTACAACAA
CkIalpha	2028	TAATACGACTCACTATAGGGAGACGTCACCATGGCAAGGAAAAGAACT	TAATACGACTCACTATAGGGAGAGCGTGGACATCTTCTTTTCGGAGAT
CkIIalpha	17520	TAATACGACTCACTATAGGGAGACAATCAAGACGATTATCAGTTGGTC	TAATACGACTCACTATAGGGAGACCAGTAATTCGGGACCTTTAAAGTA
CkIIalpha	17520	TAATACGACTCACTATAGGGAGAATTAGGCCGTGGAAAGTATT	TAATACGACTCACTATAGGGAGACGAAGCCACACGAACATTAT
dco	2048	TAATACGACTCACTATAGGGAGACGGATAACTTCCTCATGGGTCTTGG	TAATACGACTCACTATAGGGAGAAGGTCCGCCAAACTTAAGCAGGTTC
Ddr	11573	TAATACGACTCACTATAGGGAGACCGGACATTGTGTGCCAGGACTATG	TAATACGACTCACTATAGGGAGACGCACAAATGCAGCTCACCAAATAC
Ddr	9488	TAATACGACTCACTATAGGGAGAACCACCGACACCAAACATACATAC	TAATACGACTCACTATAGGGAGAAATTGCCTTTTCCACACCATAGTT
Ddr	9490	TAATACGACTCACTATAGGGAGAGAATTTCACACTAAGCCATACAAG	TAATACGACTCACTATAGGGAGACTCTCCCAAGCCATCCAG
dnt	17559	TAATACGACTCACTATAGGGAGAGACCGGCGATCAATGTGTCACACAG	TAATACGACTCACTATAGGGAGAACTGGAACTTTCCGTGGCAAGGAGG
Doa	1658	TAATACGACTCACTATAGGGAGAGGCAGCACAAATACCGCTACAGGGA	TAATACGACTCACTATAGGGAGATTGGTCCAGCGGGTATGGCTCATAG
drl	10758	TAATACGACTCACTATAGGGAGACACGAGGAGTACGACGACGATGACT	TAATACGACTCACTATAGGGAGATCAGCTCTTGGAGACGGCGGTTGAA
Drl-2	3915	TAATACGACTCACTATAGGGAGACGGGAATCGAGCACAGCATTGAGTA	TAATACGACTCACTATAGGGAGACTTCGTCCTGTGCTTACACTTCCAC
Drl-2	12463	GCTTCTAATACGACTCACTATAGCCTTGACGAAGAGTCCTATGTG	GCTTCTAATACGACTCACTATAGCCAAGTAATTGGTAAGCTCGAA
Dsor1	15793	TAATACGACTCACTATAGGGAGAGCTGTCCGACGAGGATCTGGAGAAG	TAATACGACTCACTATAGGGAGAAGCTACGGGTGCCCACAAAGGAGTT
EG:22E5.8	4290	TAATACGACTCACTATAGGGAGATCGCTGTTCCATTCAGGCCACCAAG	TAATACGACTCACTATAGGGAGAAGGCACCTGGTCCGATTGGCTGATG
Egfr	10079	TAATACGACTCACTATAGGGAGAGGCCATTAAGGAGCTGCTCAAGTCC	TAATACGACTCACTATAGGGAGACTGGCCAAAGGTCAGCAGTTCCCAA
Eip63E	10579	TAATACGACTCACTATAGGGAGACTACAATTCGGAGGAATACTTGGAC	TAATACGACTCACTATAGGGAGATGACGATGTTGCTGTGTTTCAGTTC
Eph	1511	TAATACGACTCACTATAGGGAGAGGTAACGACATACACTGTGCAGATA	TAATACGACTCACTATAGGGAGACTGAACCAACGGATTGAAGAGTTTG
Fak56D	10023	TAATACGACTCACTATAGGGAGATCATCCACGTGCATATGCCGAACAA	TAATACGACTCACTATAGGGAGAGAAATAATGACGAATGCCCAGACAG

for	10033	TAATACGACTCACTATAGGGAGACGTTCAGCAGAAGTGTGGTCAGGTC	TAATACGACTCACTATAGGGAGACCGTCCGCTGGCAGTTGTACAGGAT
for	10033	TAATACGACTCACTATAGGGAGAGAGGAGCAGAGACAGATACACACAC	TAATACGACTCACTATAGGGAGAAAGGCTTCGGGGATCCTGGTTCAAT
Fps85D	8874	TAATACGACTCACTATAGGGAGACAATAGCAATCACAGTGCCTCACAG	TAATACGACTCACTATAGGGAGAGCACGCAATAGCAGTGATCCTTCAT
Fps85D	8874	TAATACGACTCACTATAGGGAGATACAAGGCCAAACTGAAGTCCACCA	TAATACGACTCACTATAGGGAGACATCAGTATGCCATAGGACCACACA
fray	7693	TAATACGACTCACTATAGGGAGAATTAAGCGCATCAACCTGGAGAAGT	TAATACGACTCACTATAGGGAGACCAAATGTCCGCCTTAAAGTCATAG
fray	7693	TAATACGACTCACTATAGGGAGAACCCGCCAATCTGTCTAGCAATAATGT	TAATACGACTCACTATAGGGAGACTTCCTTCAGTACCGTGGCAATGG
fs(1)h	2252	TAATACGACTCACTATAGGGAGACGGGGCTGACGGACAATTTCTTGAT	TAATACGACTCACTATAGGGAGACTGTTGGTGGTGTTGCTGCTGATGT
fu	6551	TAATACGACTCACTATAGGGAGAGCATATCCTGGACGCAGCTGTTGTG	TAATACGACTCACTATAGGGAGAACTGGCGTACGGTTGGAGCGACTAT
Gcn2	1609	TAATACGACTCACTATAGGGAGAAGAGCGACGAGGTGCTGGAACACAC	TAATACGACTCACTATAGGGAGATCGCGTAATCGGGGCAGTTCACTGG
gek	4012	TAATACGACTCACTATAGGGAGAGCAACAAACACAGGAAAGGCTGAAG	TAATACGACTCACTATAGGGAGAGGATATGAGGTCCGATCTGGTTTGA
gish	6963	GCTTCTAATACGACTCACTATAGGCATATACCATATCGGGAGCAT	GCTTCTAATACGACTCACTATAGCTCGTTTCGTATCACCGATTTT
gish	6963	TAATACGACTCACTATAGGGAGAACTTGTTACTAATCGATTTCCGTTCTCTTTC	TAATACGACTCACTATAGGGAGACGTAGTGCGTTCTGGATCCTCTGTTATTT
Gprk2	17998	GCTTCTAATACGACTCACTATAGAGCTCTCAAACTCCCGGAA C	GCTTCTAATACGACTCACTATAGCAGCGACATCAATCACAAG AA
grp	17161	TAATACGACTCACTATAGGGAGACAGCGACGATGACTTCAATGTCAGA	TAATACGACTCACTATAGGGAGATGGGTCCTTTAAGCACGATATCCTC
GSK3b	31003	TAATACGACTCACTATAGGGAGAAACCACTTCGCAGCAGAGA	TAATACGACTCACTATAGGGAGAATCCCGATGGTGAAGGTGT
gwl	7719	TAATACGACTCACTATAGGGAGAGAAGCTTACTGATTTTGGGTTGAG	TAATACGACTCACTATAGGGAGACGTTTGTAGTGCAGGTATGAGTAA
gwl	7719	TAATACGACTCACTATAGGGAGAGCGATAGCAAGATATCTGGTGTTTC	TAATACGACTCACTATAGGGAGAGCTTAGGTTGTCCACATTCTTCTCA
Gyc32E	6275	TAATACGACTCACTATAGGGAGAGCGTGATTATGCGTCCAACGTGATA	TAATACGACTCACTATAGGGAGACTGTCAGCCAGCATCTGAAGATTGA
Gyc76C	8742	TAATACGACTCACTATAGGGAGAACAGGCCTCGCTTAGCACGCTGAAT	TAATACGACTCACTATAGGGAGAGGAAAGCTGCCTGAATAGCGGAGAG
hep	4353	TAATACGACTCACTATAGGGAGAGAGCTGATGTCCATGTGCTTTGACA	TAATACGACTCACTATAGGGAGACTGATGGTTCTTTGTGAGGCACTTG
hop	1594	TAATACGACTCACTATAGGGAGAAGATTCGCTATCCGGAGCACAAGGA	TAATACGACTCACTATAGGGAGACGTGTGGAAAGACTCGCACATAGAC
htl	7223	TAATACGACTCACTATAGGGAGATCTGCGAGTGGTGCGAAGTCTTCAC	TAATACGACTCACTATAGGGAGACCGCACCAAGCTGGCAATGTCATCA
ial	6620	TAATACGACTCACTATAGGGAGATGTTCAAAGAGGAGCTGCGCAAGGG	TAATACGACTCACTATAGGGAGACTCCATGCGCCGGATCTTGCTGTAG
ik2	2615	TAATACGACTCACTATAGGGAGAGGGCAAACCATATACAAGCTTACTG	TAATACGACTCACTATAGGGAGAAACTAGTCCGATTGGTGAAGAACAC
Ilk	10504	TAATACGACTCACTATAGGGAGAGATAAAAGAGCGCAGCGATGTGAAT	TAATACGACTCACTATAGGGAGAGGCGAATTGCATGCTCCAATAATAG
inaC	6518	TAATACGACTCACTATAGGGAGATCAGTGCGAGGGTAGGTAGAAATGTT	TAATACGACTCACTATAGGGAGAGTCCGCACTCGTCGCAGAATGT
InR	18402	TAATACGACTCACTATAGGGAGAACTCCTGATGGGCAGACTGTAATGG	TAATACGACTCACTATAGGGAGACACTGGGTGACTTGTCAAGTTGGTG
ird5	4201	GCTTCTAATACGACTCACTATAGTCTGCAATGGTGCGATAATTT	GCTTCTAATACGACTCACTATAGCCTTTCTGCCTCTTCGATAGC
ire-1	4583	GCTTCTAATACGACTCACTATAGTCAGGAGAATGTTCAGGTTCC	GCTTCTAATACGACTCACTATAGATATTCCTTGGCCAGCTCAG
JIL1	6297	GCTTCTAATACGACTCACTATAGTCGAGTGTAACGGAAATCGAC	GCTTCTAATACGACTCACTATAGGAATCGGAGTGTGTGTGTGTG
KP78a	6715	TAATACGACTCACTATAGGGAGAATGCCAGGGTGATCTTCCGACAGTT	TAATACGACTCACTATAGGGAGAAAACGGACGCAATCGGTCGGATTCA
KP78b	17216	TAATACGACTCACTATAGGGAGATTGGTGTCTGCTATTGAATACTGTC	TAATACGACTCACTATAGGGAGACGATTTACATCATGCAGATCCATAG
ksr	2899	TAATACGACTCACTATAGGGAGAATGGGCTACCTGCACGCAAGGGAGA	TAATACGACTCACTATAGGGAGAAAAGGTTGACGGGGTGGGAGGGACT
lic	12244	TAATACGACTCACTATAGGGAGAGGACCTTTGACATCGATGCAGATAG	TAATACGACTCACTATAGGGAGAGGCATCAATGGTTTTGGCAATGGAG
LIMK1	1848	GCTTCTAATACGACTCACTATAGCATTGTCGGGGTCAACTACTG	GCTTCTAATACGACTCACTATAGGTCCTTGGGTATCTCGACCAG
Lk6	17342	TAATACGACTCACTATAGGGAGAAAGATGATGAGGATGGAGAGAATGA	TAATACGACTCACTATAGGGAGAGTGTTGTAGTCATAACTGGTGTTTG

lok	10895	TAATACGACTCACTATAGGGAGACTGCGAACTTACCAATCCAGTTTAT	TAATACGACTCACTATAGGGAGATCGCTAAGTAGTTTGTTGCTGATGA
MAPk-Ak2	3086	TAATACGACTCACTATAGGGAGACCACTGACGGACGACTACGTGACCT	TAATACGACTCACTATAGGGAGAGCAGCGTGTAACTGGTGAATGTCTC
mbt	18582	TAATACGACTCACTATAGGGAGAGCCAGATCCAATTCGCTGCGGAGTT	TAATACGACTCACTATAGGGAGATTGGTGATGGTGCGGATGCGGATGA
mbt	18582	TAATACGACTCACTATAGGGAGACCGGTGCCCATCCCTCCCTGCTCTAT	TAATACGACTCACTATAGGGAGACCCGCTGGAACTGGATGCCCTGGAC
mei-41	4252	TAATACGACTCACTATAGGGAGATTTTGAGAAGCCATTGAAGGAGGAG	TAATACGACTCACTATAGGGAGAGTACCTGGAGACATTCATCGGTTAT
Mekk1	7717	TAATACGACTCACTATAGGGAGATTACCTGCGTGCCAAGTTCG	TAATACGACTCACTATAGGGAGAGCTCTGCTCGCGTCGTAATCGTATG
Mekk1	7717	GCTTCTAATACGACTCACTATAGCATTTTCAGTGTCGAGCCATT	GCTTCTAATACGACTCACTATAGCACCGTAGCATCGTAGTGGTT
Mkk4	9738	TAATACGACTCACTATAGGGAGAACTTCAGACGATCTCGAGGATGAGG	TAATACGACTCACTATAGGGAGACGCATCCTTGGTCTTGGCAATAGAG
mnb	7826	TAATACGACTCACTATAGGGAGAGCACCAACAGCCTGGGCAGCCTGAA	TAATACGACTCACTATAGGGAGATCCGGCGGGCTGAGATGGGAAGAGA
mnb	7826	TAATACGACTCACTATAGGGAGATAGCGGCGGCGTTATGGAT	TAATACGACTCACTATAGGGAGAGCTGGGCACGACGTTTCTTTTT
Mpk2	5475	TAATACGACTCACTATAGGGAGATCAAACATTGCCGTCAACGAGGATT	TAATACGACTCACTATAGGGAGACAAATCCATATCCTCGAAGCTGTGA
msn	16973	TAATACGACTCACTATAGGGAGAGCTCTGCTCGCGTCGTAATCGTATG	TAATACGACTCACTATAGGGAGATGCTACCACCGCTTCCGCTACCACTA
Myt1	10569	GCTTCTAATACGACTCACTATAGCACGACGACAAACACAGACAC	GCTTCTAATACGACTCACTATAGTTGCATGTACAGTCGGTCGTA
Nak	10637	TAATACGACTCACTATAGGGAGACACAGAACACGCAATCAGGGGAAAC	TAATACGACTCACTATAGGGAGAAGATGGGTAACGACCGCTGGTATTG
Nek2	17256	GCTTCTAATACGACTCACTATAGACTACATGAGTCCGGAGTTGGT	GCTTCTAATACGACTCACTATAGTTCACTTCGCAAATCTGGAGTA
ninaC	54125	TAATACGACTCACTATAGGGAGAAGCTACTCGGGCAAGTCCACAAATG	TAATACGACTCACTATAGGGAGACAGCCAAAACTTTGCGAACGGTCTC
nmo	7892	TAATACGACTCACTATAGGGAGAGCCGACCACATCAAGGTGTTCCTGT	TAATACGACTCACTATAGGGAGAAGACGAGCATCTGGCAGAGCAAGTG
Nrk	4007	TAATACGACTCACTATAGGGAGAAGATCTACTAGTCGCTGTTAAGATG	TAATACGACTCACTATAGGGAGAAAGCGAGAACTTGTTGTACAGTATG
otk	8967	TAATACGACTCACTATAGGGAGACAAGCCGACAATTCAGTGGGACAAG	TAATACGACTCACTATAGGGAGACTGCAGGCTGTGTCATCGGATTTCT
p38b	7393	TAATACGACTCACTATAGGGAGAGCGCAAAATGGCCAAATTCTACAAG	TAATACGACTCACTATAGGGAGAAAATCCAGGATGCGAAGCTCACAGT
P38c	FBgn0046322	TAATACGACTCACTATAGGGAGATGAGACTACGAGGCACTGAAAAT	TAATACGACTCACTATAGGGAGAGTCTGCGCACATACGGGATAAAC
Pak	10295	TAATACGACTCACTATAGGGAGATCTTGGAGAAACTGCGCACCATTGT	TAATACGACTCACTATAGGGAGACTACCATCGTTGTGCGTTTGGATTG
Pak3	14895	GCTTCTAATACGACTCACTATAGACCAGTACCGCCCAAG	GCTTCTAATACGACTCACTATAGGTTCCCTTGGGTCATC
Par-1	30132	TAATACGACTCACTATAGGGAGATGGCAGCAACTTTAAGCGACAGAACA	TAATACGACTCACTATAGGGAGAGTGGTGGAGCGACGTGGAATGAT
Par-1	30132	TAATACGACTCACTATAGGGAGACAAGCAGAGCAAGCGCTACGGTGAA	TAATACGACTCACTATAGGGAGATCCTCACGCCGCTTAGACGCTGAAA
PDK	8808	TAATACGACTCACTATAGGGAGAATGTGGTTCGCGATGCTTACGAGAAT	TAATACGACTCACTATAGGGAGAATGATTGCATCTGTTCCGAATCCTT
PEK	2087	TAATACGACTCACTATAGGGAGACACCGCTTGTAGTCACGACTTTCAT	TAATACGACTCACTATAGGGAGAGCATCTGGATGTAGAGGTACACCTT
PhKgamma	1830	TAATACGACTCACTATAGGGAGATCTTCGACTATCTGACCTCTGTGGT	TAATACGACTCACTATAGGGAGACTTGACGGTTATACGTTGCGAAGGA
phl	2845	TAATACGACTCACTATAGGGAGAACTCTGCATGTGGAGGAGATCTTTG	TAATACGACTCACTATAGGGAGAGCATTATCAAACTGCGCTGCACTTC
Pitslre	4268	TAATACGACTCACTATAGGGAGAATGACGATGAGGAAAGCGAGGAGAG	TAATACGACTCACTATAGGGAGACGGGATAATAGTTGGGCAGGGGAAT
Pk17E	7001	TAATACGACTCACTATAGGGAGAACGTCTGGTCTGGTCACACTGCTAC	TAATACGACTCACTATAGGGAGACTGTTGTTGCTGCTGCTGCTGCTCCTGATA
Pk34A	5182	TAATACGACTCACTATAGGGAGAAGCCAGGGCGAAGCAGAAATTATGG	TAATACGACTCACTATAGGGAGATCGGTCATGTTTGTGGCTGGAGAAG
Pk61C	1210	TAATACGACTCACTATAGGGAGACGACCTCAAGCCCGAGAACATCCTG	TAATACGACTCACTATAGGGAGACACCAGGTCCTCGGCGTCCTTATCA
Pk61C	1210	TAATACGACTCACTATAGGGAGACGCGACCTCAAGCCCGAGAACATCC	TAATACGACTCACTATAGGGAGAGCACCAGGTCCTCGGCGTCCTTATC
Pk92B	4720	TAATACGACTCACTATAGGGAGAAGAAGGAGAACCACTTTCCGGACAT	TAATACGACTCACTATAGGGAGACTCCAGAAAGAAGTCCATCCAGAAC
Pka-C1	4379	TAATACGACTCACTATAGGGAGATCGCTGCGCTACCACTTCAAGGACA	TAATACGACTCACTATAGGGAGACAGGTTGCGCAGTAGGTCCTTCAGA

Pka-C2	12066	TAATACGACTCACTATAGGGAGACAACGGAAGTTTCGGCACTGTGATG	TAATACGACTCACTATAGGGAGACCACCAGTCCACCGATTTGTTGTAG
PKA-C3	6117	TAATACGACTCACTATAGGGAGAGCCCGCTTCTGCACGCCTTTGTCATC	TAATACGACTCACTATAGGGAGAACTCGTCGTCGTCCTCCTCGTCATCGGTTTC
Pkc53E	6622	TAATACGACTCACTATAGGGAGATGGACCGTTTGTTCTTTGTAATGGA	TAATACGACTCACTATAGGGAGAGCTTATTTGGCTGCTTAGTTAGGAA
Pkc53E	6622	TAATACGACTCACTATAGGGAGACACCTTTCCTGGTCCAATTACACTC	TAATACGACTCACTATAGGGAGACTTTGCTCAGGCTCTTTGGATAGGA
Pkc98E	1954	TAATACGACTCACTATAGGGAGACGAAGCAGATGGCCGAGATACTCAG	TAATACGACTCACTATAGGGAGAAACGCAGTCAGGAAGGGATGGTTGG
PKCdelta	10524	TAATACGACTCACTATAGGGAGAAGCCCGAGAAGCCCGTGACT	TAATACGACTCACTATAGGGAGATGCGTTCGATGAGCGTGGAG
Pkg21D	3324	TAATACGACTCACTATAGGGAGACAGACGTTCTGGAGCTGGAGTTCTA	TAATACGACTCACTATAGGGAGAGGCAAAGATATCCACGCGATCCTGA
pll	5974	TAATACGACTCACTATAGGGAGAACGTTAGCGAGGATCTGCACAAGTA	TAATACGACTCACTATAGGGAGAGCTTACCACCTTTGATGCTGTATCC
png	11420	GCTTCTAATACGACTCACTATAGGGAACTGGGTGACTCTAAGCTG	GCTTCTAATACGACTCACTATAGACTCGAGTCCCACTACCATGTC
Polo	12306	TAATACGACTCACTATAGGGAGAGGAGTTCGAATGCCGCTACTACATT	TAATACGACTCACTATAGGGAGATCAGACAAGAGCTGGGCAAGAACAT
Polo	12306	TAATACGACTCACTATAGGGAGACGTTCTCCGCTTTGTGCTTGGTTTTCGTG	TAATACGACTCACTATAGGGAGACGCTTGTAGGTTTTCCGCTGGTTGATGTCG
PR2	3969	TAATACGACTCACTATAGGGAGAACGAGAACATGCCGACAGTGGGTAA	TAATACGACTCACTATAGGGAGAGTTTCGGCAACGGACTTCCTGTTCA
put	7904	TAATACGACTCACTATAGGGAGAACGAGGCTGAGATAACAAACTCATC	TAATACGACTCACTATAGGGAGACTGGAATATCATGGCCAAACCAAAG
Pvr	8222	TAATACGACTCACTATAGGGAGATACAACGTTCAGGAATATGCCAATC	TAATACGACTCACTATAGGGAGAGTATATGCGTTCCACACTCAACTTT
Pvr	8222	TAATACGACTCACTATAGGGAGACCCTGCAAGAGCGCCATTATCCTG	TAATACGACTCACTATAGGGAGACTCTGTGTCCGGCATGGCTGGTTTA
Ret	14396	TAATACGACTCACTATAGGGAGATGACTACCGCTCACCAAACTCAAGT	TAATACGACTCACTATAGGGAGAGGGTCCATTATCATTGCGATCCAGT
Ret	14396	TAATACGACTCACTATAGGGAGAAGTTGCGAACTGAAGGTCAAGTCTC	TAATACGACTCACTATAGGGAGACATTCGAAACCGGCCACATTTAGGA
rl	12559	TAATACGACTCACTATAGGGAGAGGCTGCCAAAAGACTGATGTA	TAATACGACTCACTATAGGGAGAGGAAGGAGAACCGCAAGATA
rok	9774	GCTTCTAATACGACTCACTATAGTGCGTCAACACAACTA	GCTTCTAATACGACTCACTATAGTTGTTCGCGACACATA
Ror	4926	TAATACGACTCACTATAGGGAGACTTTGCCCAGCTTGTGTTTCAGTTCA	TAATACGACTCACTATAGGGAGAGGCAATCCTCCACACCCACCATCC
S6k	10539	TAATACGACTCACTATAGGGAGAAAAGGTGGTTATGGCAAAGTATTTC	TAATACGACTCACTATAGGGAGAAAAATTTCAGGTGCCATGTACTCAA
S6kII	17596	TAATACGACTCACTATAGGGAGAATTTTGCCGCTGATTGGTGGAGTTT	TAATACGACTCACTATAGGGAGACAGCAGGAATAGGAGCTATACTATG
SAK	7186	TAATACGACTCACTATAGGGAGACGCTATATGAACCACATCGCCAGAC	TAATACGACTCACTATAGGGAGAAACATAAAGGGATGGCAGAGAACAG
SAK	7186	TAATACGACTCACTATAGGGAGAATACGGGAGGAATTTAAGCAAGTC	TAATACGACTCACTATAGGGAGATTATAACGCGTCGGAAGCAGTCT
SAX	1891	TAATACGACTCACTATAGGGAGACGCGATGCCGATGGTCAGGTGCAGGAG	TAATACGACTCACTATAGGGAGACCTCGTCCAATGCACTCGATCAGGG
sev	18085	TAATACGACTCACTATAGGGAGATGCAGAGTTTATTGGCGAACTGGAC	TAATACGACTCACTATAGGGAGAAAGCTTCCAGCATGCAGACGGATTA
sgg	2621	TAATACGACTCACTATAGGGAGAATGCCAAGCCGAAGAACCGACTTTT	TAATACGACTCACTATAGGGAGACATCATCCACATCCTCTTGCACATC
shark	18247	TAATACGACTCACTATAGGGAGACAGTAGCTCAATGTTCAACACTCTG	TAATACGACTCACTATAGGGAGAATGAAGATAGCTGGCCATCTCACTT
Slob	6772	TAATACGACTCACTATAGGGAGAACCACCAGTGCCCGAAAAGAAAGTG	TAATACGACTCACTATAGGGAGAACCGAGGCATCTGTGACAAGAAACC
slpr	2272	GCTTCTAATACGACTCACTATAGCTCACCGTCCATTGCTTCTAC	GCTTCTAATACGACTCACTATAGGCACAACTGGGACTTTAGCAT
slpr	2272	TAATACGACTCACTATAGGGAGATTAAAAAGCGAAGGAAGCAAAGAGAAAACAACAAA	TAATACGACTCACTATAGGGAGATCCACCAGCCCACATCGCCAGACACC
smi35A	4551	TAATACGACTCACTATAGGGAGACCTGCAGCGTTGCTTGGAGTGGGAT	TAATACGACTCACTATAGGGAGATTTCCTGGTGGCCGCTGACGAGACA
SNF1A	3051	TAATACGACTCACTATAGGGAGATGTGAAGCACGGCAAGCTGCAGGAG	TAATACGACTCACTATAGGGAGAGTAGGCCGGGAGGTCCTTTTGGAAC
Src42A	7873	TAATACGACTCACTATAGGGAGAAGAACCGTGGTACTTCCGCAAAATC	TAATACGACTCACTATAGGGAGACATGATCTGGGCTTCCGCTAAGAAA
Src64B	7524	TAATACGACTCACTATAGGGAGAAGGAGTACATGTCCAAGGGCAGTCT	TAATACGACTCACTATAGGGAGAGCACTGGAGCAGCAGCTGATAAATG
SRPK	8174	TAATACGACTCACTATAGGGAGATCGAATTCAACGCTGCCAACACCTC	TAATACGACTCACTATAGGGAGAGGGCGTAAGGAACGAAGCGAATGAC

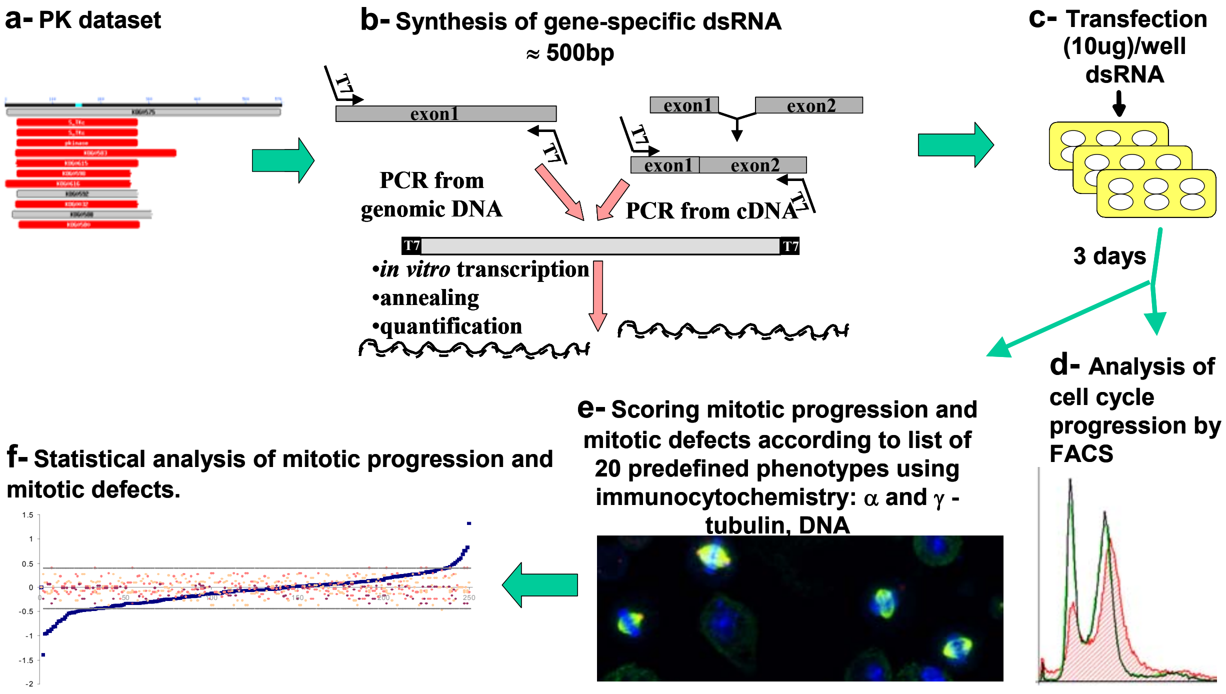
Strn-Mlck	8304	TAATACGACTCACTATAGGGAGATTCAGTGGTTTAAGGACAGCATTGA	TAATACGACTCACTATAGGGAGACAGGAAGCATGAAATCTTAACCTTG
Taf250	17603	TAATACGACTCACTATAGGGAGAGCGGTTCGGGCCTGCACAGATTTGGTAT	TAATACGACTCACTATAGGGAGATTTGCTGGGCCTTTTTGCTTGATGCTC
Tak1	1388	TAATACGACTCACTATAGGGAGACGACGTGGAGGCGAATGGCTTTGAT	TAATACGACTCACTATAGGGAGACTGCTTCTGTTCGCGCTCGGTTCGGTCCAT
Takl2	4803	GCTTCTAATACGACTCACTATAGCAGCCGAAAGCAGTAATTCAT	GCTTCTAATACGACTCACTATAGTTGCCTTCATTAATAGCCATGT
Tie	7525	TAATACGACTCACTATAGGGAGATTGGTGGGGCAGAGAAAGAGGAG	TAATACGACTCACTATAGGGAGAGTCGCCGGCGGTCGCATTCAACTG
tkv	14026	TAATACGACTCACTATAGGGAGAGAACCATTGCCAAGCAGATTCAGAT	TAATACGACTCACTATAGGGAGATGAATGACATCCAGTTCCGAGTTGT
tor	1389	TAATACGACTCACTATAGGGAGACGGTTTGACGTTGGACAAGGTTCAT	TAATACGACTCACTATAGGGAGACATCTGGTTGCTAAAACGAGTGGAG
TOR	5092	TAATACGACTCACTATAGGGAGAGGCGCACTCGAATGCTTTGAAAAGG	TAATACGACTCACTATAGGGAGAGCTGACTTGGAAGCGACTGTTAGAG
trbl	5408	TAATACGACTCACTATAGGGAGACAAGCTCATCCAACAGCGTTATCTG	TAATACGACTCACTATAGGGAGAAAGTAGAACCGCTTGAGCTTGAGGT
trc	8637	TAATACGACTCACTATAGGGAGAAGAACTACTACAGCAACCTGGTGAC	TAATACGACTCACTATAGGGAGAGCCGTCTCACTGATATAGAACTGTG
trc	8637	TAATACGACTCACTATAGGGAGAATGAGCAGCAGAACGCAGGAC	TAATACGACTCACTATAGGGAGATCGCTTCAGCCGGAGATACT
twf	3172	TAATACGACTCACTATAGGGAGATCGGATCAGCATACATCACAGAGGA	TAATACGACTCACTATAGGGAGAGAGAAAAGGAGCCTTACAGCTTGAG
wee	4488	TAATACGACTCACTATAGGGAGAGATAGAGGGCCTACGCTATATTCAT	TAATACGACTCACTATAGGGAGAATATAGACTGCGAAGTGGGCCTCTT
wee	4488	TAATACGACTCACTATAGGGAGAGCATCGGGTACGGCCACATTATTA	TAATACGACTCACTATAGGGAGACGCCGCCTTCTTTGCCTATCTTAC
wit	10776	TAATACGACTCACTATAGGGAGACAGATACCTCTAGCTGCCTTGGAAC	TAATACGACTCACTATAGGGAGACGGAGGTTTATCGAGGCGAGGATTA
wts	12072	TAATACGACTCACTATAGGGAGAAACAGCAACTGCAGGCCTTGAGGGT	TAATACGACTCACTATAGGGAGAATACGTGCGCTGGCGATACGACTTG

Supplementary Table 2- List of *Drosophila* protein kinase regulators studied in this work and primers used to synthesize dsRNA. All primers led to the synthesis of a single band of dsRNA. Name and CG number are indicated.

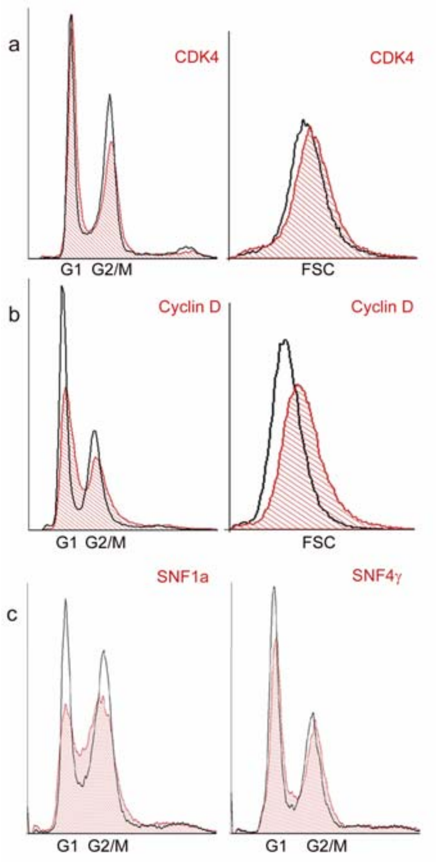
NAME	CG	FORWARD SEQUENCE	REVERSE SEQUENCE
CkIIbeta	15224	TAATACGACTCACTATAGGGAGATGGGTCACCTGGTTCTGTGGACTTC	TAATACGACTCACTATAGGGAGAGACGCTTGGGACGATATTCGGGATG
SNF4Agamma	17299	TAATACGACTCACTATAGGGAGACGCCGCCGAGAAAACCTACAAC	TAATACGACTCACTATAGGGAGACCGGCGCCGTCTCCTCTTC
PVF1	7103	TAATACGACTCACTATAGGGAGATGTCCTCTAACGCCATTGAAAACT	TAATACGACTCACTATAGGGAGAGTGGCGGCGGCGTAGAAGAACC
PVF2	13780	TAATACGACTCACTATAGGGAGATATCGCGATCGGAGTGCTAAT	TAATACGACTCACTATAGGGAGAGACCGCTCGATCCTCAAAGTA
PVF3	13782	TAATACGACTCACTATAGGGAGATGAGACTGCGGCTTGCCTTGATTTTCCTA	TAATACGACTCACTATAGGGAGATGAGACGCCGGTTTCGATGGTGTGC
CyclinE	3938	TAATACGACTCACTATAGGGAGACGTGCCATTCTCTTGGACTGGTTGA	TAATACGACTCACTATAGGGAGACTGCCAGCACCGAGTAGGAATAGTT
CyclinD	9096	TAATACGACTCACTATAGGGAGATGAGAGTGCGGCGATCCATAGAAT	TAATACGACTCACTATAGGGAGACTCCAGACACCGATCCGAATACAA

Supplementary Table 3- Codes used for quantitation of mitotic phenotypes.

Description of phenotype	Defect code
Centrosomal defects	
Centrosome number zero	CN0
Single centrosome	CN1
Centrosome number high (3-5)	CNH
Centrosome number very high (>5)	CNVH
Centrosome Position Defects	CPD
Spindle Defects	
Monopolar	SMO
Tripolar	STR
Multipolar	SMP
Multipolar Cytokinesis	MC
Abnormal	AS
Branched	SBR
Splayed pole	SSP
No astral microtubules	NAS
Central Spindle defects	CSD
Chromosome defects	
Chromosome condensation defect	CRCD
Chromosome number high	CRNH
Lagging chromatids	CRLC
Chromosome alignment defect	CRAD
Chromosome segregation defects	CRSD
Uneven DNA	UD



Supplementary Figure 1- Screening protocol. a) A protein kinase (PK) data set of 228 protein kinases was defined based on Morrison et al (2000), Manning et al (2002) and FlyBase (Supplemental Table 1). **b)** PCR primers specific for each PK were designed with a T7 RNA polymerase overhang (Supplementary Table 1). PCR fragments were generated (average 500bp) from either *Drosophila* genomic DNA or cDNA. These templates were transcribed to generate dsRNA. **c)** *Drosophila* S2 cells were transfected as previously described[8,9]. *GFP* and *polo* dsRNAs were used as negative and positive controls. After 72 hours cells were harvested, fixed and stained for FACS analysis (DNA content (FL2; propidium iodide) and cell size (Forward Light Scatter)) **(d)** and immunocytochemistry **(e-f)** Mitotic defects were quantitated blindly by fluorescence microscopy and statistically analysed. 1000-3000 cells were scored per slide (comprising at least 60 mitotic cells). Cells were categorised according to phase of mitosis and to centrosome, spindle and DNA morphology (we defined 20 potential mitotic phenotypic abnormalities, coded to facilitate computer analysis of the data; see Supplementary Tables 3 and 4). We considered how to counter artifacts that might arise in such a survey. To avoid scoring background cell cycle defects in the S2 line[10] we were conservative in the definition of phenotypes and only considered as positives those kinases that consistently showed a FACS phenotype in 3-6 independent experiments or a quantitative mitotic phenotype in 2 independent experiments. The second possible artifact is lack of specificity and effectiveness of the technique. In *Drosophila* cells RNAi does not seem to present the same problems regarding specificity and effectiveness that mammalian systems do[11]. However, as a check on specificity, we have used different primer pairs to produce dsRNA for a quarter of the kinases that showed a cell cycle phenotype and were able to replicate our results. Additionally, in the case of CDK4, SNF1a, CKIIα and Pvr kinases, we also carried out RNAi with positive regulators of their activity and found similar phenotypes (see main text). It is also our experience that RNAi is usually highly effective in cultured *Drosophila* cells and this was confirmed by our ability to identify the majority of known cell cycle kinases. We also considered whether some kinases might be not expressed in S2 cells leading us to miss cell cycle functions. However, there is very little redundancy of kinases in the *Drosophila* genome and we would expect the majority of cell cycle kinases to be expressed in these cells.



Supplementary Figure 2-RNAi of regulators gives similar phenotypes to depletion of the kinases. The examples each show a control FACS profile in black (cells transfected with dsRNA for *GFP*) and sample profile in red. a) and b) Depletion of CDK4 gives rise to an increase in the percentage of cells in G1 relative to G2, with a small but consistent increase in cell size. An increase in cell size was also observed after depletion of cyclin D, a regulator of CDK4 activity. c) Depletion of both SNF1a and its regulatory partner SNF4γ gives rise to a consistent increase in the population of cells with S phase DNA content.

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