

**Table 2S. Double RNAi experiments**

Protein name	Phenotype	Abnormal spindles $\pm$ s.d. in % ( <i>n</i> )*	$\gamma$ -tubulin localization $\pm$ s.d. % cells ( <i>n</i> ) <sup>†</sup>
D-TACC/Pericentrin	Normal	31 $\pm$ 8.0 (253)	99 $\pm$ 1 (84)
Asp/ $\gamma$ -tubulin 23C	Monopolar/anastral spindles	99 $\pm$ 1.0 (249)	4 $\pm$ 2 (143)
Asp/Centrosomin	Anastral spindles	92 $\pm$ 5.5 (132)	20 $\pm$ 6 (151)
Centrin1/Centrin2	Normal	24 $\pm$ 4.2 (189)	98 $\pm$ 3 (128)
Mps1/Dmob2	Monopolar spindle	36 $\pm$ 7.8 (198)	NA
Dmob2/Dmob1	Normal	24 $\pm$ 7.6 (239)	n.a.
Mps1/Dmob4	Monastral/monastral bipolar	52 $\pm$ 4.0 (155)	n.a.
Dmob4/Dmob3	Monopolar	65 $\pm$ 1.3 (268)	98 $\pm$ 3 (122)
Dgrip84/ $\gamma$ -tubulin 37C	Monopolar spindle	37 $\pm$ 2.6 (145)	27 $\pm$ 10 (127)
Dgrip128/ $\gamma$ -tubulin 37C	Monopolar spindle	70 $\pm$ 4.0 (262)	98 $\pm$ 2 (128)
Dgrip163/ $\gamma$ -tubulin 37C	Monopolar spindle	59 $\pm$ 9.0 (262)	96 $\pm$ 4 (100)
Dgrip91/ $\gamma$ -tubulin 37C	Monopolar spindle	52 $\pm$ 10 (292)	96 $\pm$ 4 (100)
Dgrip75/ $\gamma$ -tubulin 37C	Monopolar spindle	71 $\pm$ 9.0 (279)	98 $\pm$ 2 (172)
Dgrip71/ $\gamma$ -tubulin 37C	Monopolar spindle	57 $\pm$ 12 (255)	98 $\pm$ 2 (111)
Dgrip223/ $\gamma$ -tubulin 37C	Normal	34 $\pm$ 4.0 (239)	99 $\pm$ 2 (113)
Dgrip84/Dgrip128	Monopolar/anastral spindles	94 $\pm$ 2.0 (325)	28 $\pm$ 7 (162)
D-TACC/Minispindles	Multiple spindle defects	66 $\pm$ 16 (287)	98 $\pm$ 2 (125)
Minispindles/ $\gamma$ -tubulin37C	Monopolar spindles	95 $\pm$ 2.0 (208)	5 $\pm$ 4 (160)
Minispindles/Asp	Anastral bipolar spindles	87 $\pm$ 4.0 (129)	95 $\pm$ 4 (111)
Pericentrin-2/3	Normal	24 $\pm$ n.a. (151)	100 $\pm$ n.a. (55)
Pericentrin-1/2/3	Normal	30 $\pm$ n.a. (135)	95 $\pm$ n.a. (66)

For complete gene information, including CG identification numbers and RNAi primer sequences, see supplementary Table S1. Cells were analyzed on day 4 or 5 of RNAi treatment. Averages and s.d. values reflect values of three individual experiments, unless noted otherwise.

\*Calculated by averaging the fold increase in mitotic index for three separate RNAi experiments (mean  $\pm$  s.d.). In each individual experiment, the mitotic index for each sample was divided by the average mitotic index for >15 untreated samples. n.a., too few cells available for analysis.

<sup>†</sup>Percent of cells with localized  $\gamma$ -tubulin, average of three experiments (mean  $\pm$  s.d.). n.a., too few cells available for analysis.