Protein depleted	Western blot	Effect on CLIP- 190 localization	Other phenotype observed
CLIP-190	Control CLIP-190 RNAi RNAi CLIP-190 Tubulin 6 Days RNAi	CLIP-signal disappears	-
EB1	Tubulin  EB1 6 Days RNAi	Removes CLIP-190 From interphase MT-plus-ends	EB1 signal decreases; Small and unastral mitotic spindles
Rod	-	Removes CLIP-190 from unattched kinetochores	Low mitotic index (MI; 1.6%, compared to 2.4% in control) Failure to arrest in colchicine (3.9% MI, compared to 22.1% in control)
Dhc	-	Removes CLIP-190 from unattched kinetochores	High MI (7.2%, compared to 2.4% in control); Inefficient arrest in colchicine (12.9% MI, compared to 22.1% in control)
Dic	Control Dic RNAi RNAi  Dic  Tubulin  5 Days RNAi	Removes CLIP-190 from unattched kinetochores	High MI (8.1%, compared to 4.6% in control); Inefficient arrest in colchicine (15% MI, compared to 27% in control)
p150-Glued	Control p150-Glued RNAi RNAi p150-Glued Tubulin 5 Days RNAi	Removes CLIP-190 from unattched kinetochores	High MI (7.5%, compared to 4.6% in control); Inefficient arrest in colchicine (11% MI, compared to 27% in control)
Lis1	-	Removes CLIP-190 from unattched kinetochores	High MI (11.7%, compared to 2.4% in control); Inefficient arrest in colchicine (19.5% MI, compared to 22.8% in control)
Mad1	-	-	Low MI (0.4%, compared to 3.1% in control); Failure to arrest in colchicine (1.7% MI, compared to 16.3% in control)
BubR1	-	BubR1 signal disappears	Low MI (0.3%, compared to 3.2% in control); Failure to arrest in colchicine (0.5% MI, compared to 22.1% in control)
CENP-meta	-	-	Chromosome misalignment; Low MI (2%, compared to 3.5% in control); Inefficient arrest in colchicine (11.5% MI, compared to 15.4% in control)
NudE	-	-	High MI (5.8%, compared to 3.1% in control); Inefficient arrest in colchicine (15.8% MI, compared to 20% in control)
NudC	-	-	Cells quite sick Low MI (0.8%, compared to 3.1% in control); Failure to arrest in colchicine (6.7% MI, compared to 20% in control)
NudC-like	-	-	-

All counts for mitotic index (MI) were done for at least 1000 cells per sample.