**Figure S1. Moe activation controls anaphase relaxation.** (A) The lifetime of individual blebs were plotted according to their expanding (left) or retraction (right) phase, as visualized by time-lapse microscopy, in controls cells or after Slik dsRNA depletion. (B) Rapid time-lapse imaging of a sqh-GFP cell line in control conditions (top) and after Slik depletion. Close-ups correspond to the framed region and show the GFP signal in black. Bars, 10 µm.

**Figure S2. Pp1-87B regulates mitotic Moe activation.** (A) Quantification of P-Moe signal observed in control S2 cells or after depletion of Pp1-87B or Slik in interphase and metaphase ($n = 23$). Horizontal lines are mean values for each condition, a.u., arbitrary unit. (B) The graph plots the percentage of cells showing Moe-GFP signal at the polar cortex at different times after furrow ingression ($n = 40$). (C) Protein extracts from S2 cells treated by the indicated dsRNAs and transiently transfected or not transfected with GFP–Pp1-87B (not targeted by the Pp1-87B 5'UTR or 3'UTR) were analyzed by Western blotting using antibodies against Moe (middle), T559-phosphorylated Moe (P-Moe; top), or GFP (bottom). seq., sequence. (D) Localization of GFP–Pp1-87B in dividing S2 cells undergoing metaphase (top images) or anaphase (bottom images), showing accumulation of Pp1-87 on the metaphase spindle (red) or on chromosomes (red), respectively. Bars, 10 µm.
Figure S3. **The nonphosphorylatable form of Moe is anisotropically distributed during anaphase elongation.** (A) Stable cell line expressing an unphosphorylatable Moe (Moe-TA-GFP) was fixed and labeled for DNA. Anaphase cell displaying significant enrichment of unphosphorylatable Moe at the equator region. (B) The graph plots the pole/equator ratio of Moe-TA-GFP signal for individual anaphase B cells, confirming preferential equatorial distribution. The horizontal line is the mean value of the experiment. Bars, 10 µm.
Control of mitotic shape transformations

Figure S4. PI(4,5)P$_2$ depletion in metaphase triggers Moe redistribution from the cortex to the cytoplasm. (A and B) The graphs plot time course of the decay of cortex-associated GFP signal after rapamycin addition in cells stably expressing GFP-Tubby without RC constructs (A) or with RC constructs (B). (C) Consequences of rapamycin addition on Moe-GFP distribution in RC-expressing cells.

Figure S5. A functional screen for enzymes implicated in phosphoinositide metabolism. The table reports each gene that has been depleted using dsRNA treatment in S2 cells according to their predicted molecular function. Gene names include coding gene (CG) number and synonyms when available as well as respective putative human orthologues. The primary screen was performed on a S2 cell line that stably expresses Tubulin-GFP, and the frequency of cortical deformations is represented with respect of observed cortical dynamics observed in control cells. For each candidate displaying highest perturbations, a second assay was performed using a stable Moe-GFP cell to analyze cortical dynamics, confirming the influence of Skittles, Pten, and CG10260. Accordingly, biochemical dosage of PI(4,5)P$_2$ reveals a significant decrease in intracellular pools of this phosphoinositide (PI) after individual depletion of these three genes. In addition, depletion of mmt and CG3573 further impinge on cell division, leading to a high proportion of bi/multinucleated cells. Colors correspond to phenotype penetrance: yellow, weak; orange, intermediate; red, high. IMP, inositol monophosphate phosphatase; IPP, inositol polyphosphate phosphatase; PI4K, phosphoinositide 4-kinase; WT, wild type.
Video 1. Localization of Moe-GFP and α-Tubulin-mCherry in dividing control S2 cells as shown in Fig. 1 B. Dividing stable cell line expressing Moe-GFP (white, left; green, right) and α-Tubulin-mCherry (red, right). Images were analyzed by time-lapse microscopy using a microscope (DeltaVision) and deconvolved using softWoRx software. Frames (maximum projections) were collected every 1 min. Time compression is 300.

Video 2. Localization of Moe-GFP in dividing control S2 cells as shown in Fig. 2 A. Dividing stable cell line expressing Moe-GFP (black). Images were analyzed by time-lapse microscopy using a microscope (DeltaVision) and deconvolved using softWoRx software. Frames (focal plane) were collected every 7 s. Time compression is 112.5.

Video 3. Localization of Moe-GFP in dividing Slik-depleted S2 cells as shown in Fig. 2 A. Dividing Slik dsRNA-depleted cell stably expressing Moe-GFP (white). Images were analyzed by time-lapse microscopy using a microscope (DeltaVision) and deconvolved using softWoRx software. Frames (maximum projections) were collected every 20 s. Time compression is 100.

Video 4. Localization of Utrophin-GFP and α-Tubulin-mCherry in dividing control S2 cells as shown in Fig. 2 C. Dividing stable cell line expressing Utrophin-GFP (GFP-UtrCH; black, left; green, right) and α-Tubulin-mCherry (red, right). Images were analyzed by time-lapse microscopy using a microscope (DeltaVision) and deconvolved using softWoRx software. Frames (focal planes) were collected every 2.5 s. Time compression is 37.5.

Video 5. Localization of Utrophin-GFP and α-Tubulin-mCherry in dividing Slik-depleted S2 cells as shown in Fig. 2 C. Dividing Slik dsRNA-depleted cell stably expressing Utrophin-GFP (GFP-UtrCH; black, left; green right) and α-Tubulin-mCherry (red, right). Images were analyzed by time-lapse microscopy using a microscope (DeltaVision) and deconvolved using softWoRx software. Frames (focal planes) were collected every 2.5 s. Time compression is 37.5.

Video 6. GFP-Tubby and RC-mRFP in interphase S2 cells as shown in Fig. 4 E. Interphase GFP-Tubby (white, left; green, right) stable cell line transiently expressing the rapamycin constructs (RCs; red, right). Rapamycin was added after 1 min. Images were analyzed by time-lapse microscopy using a microscope (DeltaVision). Frames (focal planes) were collected every 15 s. Time compression is 75.

Video 7. Moe-GFP and RC-mRFP in metaphase S2 cells as shown in Fig. 4 E. Dividing Moe-GFP (white) stable cell line transiently expressing the RCs. Rapamycin was added after 1 min. Images were analyzed by time-lapse microscopy using a microscope (DeltaVision). Frames (focal planes) were collected every 10 s. Time compression is 50.

Video 8. Moe-GFP and RC-mRFP in dividing S2 cells as shown in Fig. 4 F. Dividing Moe-GFP (white) stable cell line transiently expressing the RCs (not depicted) treated with rapamycin. Images were analyzed by time-lapse microscopy using a microscope (DeltaVision) and deconvolved using softWoRx software. Frames (focal planes) were collected every 10 s. Time compression is 90.
Video 9. Moe-GFP and α-Tubulin-mCherry in dividing Skittles-depleted S2 cells as shown in Fig. 6 D. Dividing Skittles dsRNA-depleted cell stably expressing Moe-GFP (white, left; green, right) and α-Tubulin-mCherry (red, right). Images were analyzed by time-lapse microscopy using a microscope (DeltaVision). Frames (focal planes) were collected every 7 min. Time compression is 1,260.

Video 10. Utrophin-GFP and α-Tubulin-mCherry in dividing Skittles-depleted S2 cells as shown in Fig. 2 C. Dividing Skittles dsRNA-depleted cell stably expressing Utrophin-GFP (GFP-UtCH; black, left; green, right) and α-Tubulin-mCherry (red, right). Images were analyzed by time-lapse microscopy using a microscope (DeltaVision). Frames (focal planes) were collected every 7.5 s. Time compression is 37.5.