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Filipe Fernandes de Sousa
Dissecting the role of CENP-E in the
maintenance of chromosome alignment

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Dissecting the role of CENP-E in the
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DISSECTING THE ROLE OF CENP-E IN THE MAINTENANCE OF CHROMOSOME ALIGNMENT

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1 **DISSECTING THE ROLE OF CENP-E IN THE MAINTENANCE OF**
2 **CHROMOSOME ALIGNMENT**

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31 **Abstract**

32 The goal of mitosis is to ensure faithful segregation of genomic content into two
33 identical daughter cells. As cells enter mitosis, the DNA becomes condensed into mitotic
34 chromosomes, which must establish stable attachments to the mitotic spindle. Upon
35 establishing proper kinetochore-microtubule attachments, chromosomes can then be
36 guided to the center of the cell. Importantly, efficient chromosome congression is a
37 prerequisite for faithful chromosome segregation, since errors during this process may
38 lead to aneuploidy and chromosomal instability (CIN). One of the key players involved in
39 chromosome congression is CENP-E, a kinesin-like motor protein that is enriched at
40 kinetochores during mitosis, and whose pharmacological inactivation has shown
41 promising results in clinical trials. Despite mounting evidence demonstrating a role for
42 CENP-E in chromosome congression, the importance of CENP-E motor activity once
43 chromosomes are already aligned, is highly controversial. To this purpose, we took
44 advantage of selective small-molecule inhibitors to achieve temporal control over CENP-
45 E inhibition after chromosomes have completed alignment in both CIN and non-CIN
46 human cell lines. We used three CENP-E inhibitors, PF-2771, GSK923295 and
47 Compound A, which act through distinct mechanisms. Using a high-throughput
48 screening assay, we calculated the optimal doses required for partial and total CENP-E
49 inhibition with these three compounds and then performed high-resolution live cell
50 imaging to directly test CENP-E function in the maintenance of chromosome alignment.
51 We show, using three distinct inhibitors, that CENP-E activity is required for the
52 maintenance of chromosome alignment in a condition of prolonged metaphase.
53 Interestingly, the formation of chromosomes at poles occurs more rapidly in GSK923295-
54 treated cells, suggesting that inhibiting CENP-E with this compound may lead to
55 undesired microtubule-associated effects. We find that relative sensitivity to CENP-E
56 inhibitors is proportional for PF-2771 and GSK923295 when comparing CIN and non-
57 CIN cell lines. However, diploid cells are less sensitive to CENP-E inhibition using

58 Compound A, suggesting that this compound may be of higher therapeutic value for the
59 treatment of cancer. Taken together, these results offer insight for our understanding of
60 the therapeutic value of CENP-E inhibitors currently tested in clinical trials.

61

62 **Keywords:** CENP-E; Congression; Chromosome alignment; Mitosis; CIN;

63

64 **Introduction**

65 An effective mitosis ensures the faithful segregation of genomic content into two
66 identical daughter cells. Precisely at the onset of mitosis, characterized by chromosome
67 condensation and nuclear envelope breakdown, dispersed mitotic chromosomes initiate
68 directed movements towards the cell equator. This stochastic motion defines the mitotic
69 stage of prometaphase, whose goal is to promote the initial attachment between
70 chromosomes and kinetochores, essential for chromosome congression (1). One of the
71 key players involved in chromosome congression is CENP- E, a kinesin-like plus -end-
72 directed motor protein (kinesin-7) that associates with the kinetochore fibrous corona
73 and is strongly enriched at kinetochores during prometaphase (2). A role for CENP-E in
74 chromosome congression was established after live-cell imaging of human cells
75 depleted of CENP-E function by antibody microinjection (3-5). While several
76 chromosomes were able to align after perturbation of CENP-E, others remained in close
77 proximity with spindle poles. Subsequently, only peripheral mono-oriented chromosomes
78 were shown to congress in a CENP-E dependent manner by laterally sliding their
79 unattached kinetochores to neighboring mature kinetochore fibers (6, 7). This model
80 predicted that CENP-E guides misaligned chromosomes towards the cell equator.
81 However, some reports have challenged the idea that CENP-E function is restricted to
82 alignment of chromosomes, raising the intriguing possibility that CENP-E function is
83 required to maintain bi-oriented chromosomes at the equator after completing
84 congression (8). Addressing this question has proven to be challenging since most
85 strategies used to impair protein function rely on RNAi or genome editing techniques,
86 which offer no temporal control over protein function. However, the development of small
87 molecule inhibitors has provided a powerful tool that allows precise temporal control over
88 protein function. Indeed, partial CENP-E inhibition using GSK923295 was shown to
89 result in the accumulation of mono-oriented chromosomes and consequently caused a
90 mitotic delay (9). GSK923295 was also used to propose that CENP-E is motor active at

91 the kinetochores of congressed chromosomes, thus facilitating the dynamics of
92 microtubule plus ends and kinetochores (8).

93 To date, the most widely used CENP-E inhibitor is GSK923295, an allosteric
94 small-molecule inhibitor that targets CENP-E motor activity and exhibits potent antitumor
95 activity in several preclinical models of human tumor xenografts (10). The GSK923295
96 inhibitor binding site was mapped to a region similar to that bound by loop-5 inhibitors of
97 the kinesin KSP/Eg5. However, unlike these KSP inhibitors that block release of ADP
98 and destabilize motor-microtubule interaction, GSK923295 inhibited the release of
99 inorganic phosphate resulting in a conformational state with dramatically enhanced
100 affinity for microtubules causing CENP-E to be bound to microtubules in a rigor-like state
101 (10). Similar to GSK923295, a novel CENP-E inhibitor named PF-2771 was generated
102 to study the effects of CENP-E depletion in human basal breast cancer cell lines (11).
103 Importantly, while PF-2771 is noncompetitive with ATP (it acts independently of substrate
104 loading), GSK923295 is uncompetitive with both ATP and microtubules (it requires both
105 substrates to be loaded to perform its function). More recently, a novel small-molecule
106 inhibitor of CENP-E, Compound-A (Cmpd-A) was developed to specifically inhibit CENP-
107 E function independently of its binding to microtubules (12). Unlike GSK923295 and PF-
108 2771, Cmpd-A inhibits the ATPase activity of the CENP-E motor domain, acting as a
109 time-dependent inhibitor with an ATP-competitive-like behavior. Cmpd-A treatment also
110 causes chromosome misalignment and chromosomes at poles, leading to prolonged
111 mitotic arrest, consistent with other reports where CENP-E function was suppressed. By
112 targeting the L5 binding site at 3 different amino acid residues, CENP-E inhibitory activity
113 was increased by fine-tuned chemical modifications (13, 14). Here, we take advantage
114 of the availability of next generation inhibitors as well as state-of-the-art live cell imaging
115 to demonstrate that CENP-E partial inhibition is sufficient to cause misalignment after bi-
116 orientation in a condition of prolonged metaphase. The extent of the misalignment was
117 independent of the inhibitor of choice and was frequently followed by the formation of

118 chromosomes at poles in a dose-dependent manner. We find that GSK923295-treated
119 cells showed a more rapid accumulation of chromosomes at poles, suggesting that
120 microtubule-associated phenotypes induced by GSK923295 treatment may account for
121 these differences. We discuss the implications this may have for normal metaphase
122 durations, and the possible therapeutic advantage of Cmpd-A over GSK923295 and PF-
123 2771.
124

125 **Results**

126 Assessing the sensitivity to chemical inhibitors or pharmacological treatments
127 requires a careful approach to minimize unspecific off-target effects that are
128 concentration dependent (15). In order to establish the optimal doses required for partial
129 and full CENP-E inhibition using each compound, we used an in-house high-throughput
130 screening platform coupled with an automated phenotype imaging analysis (CellProfiler)
131 to quantify mitotic phenotypes in living cells. This automated system of image acquisition,
132 processing and quantification provides a rapid, robust and unbiased phenotypic analysis
133 that can be used with multiple small-molecule inhibitors and cell lines (Fig. 1A and 1B,
134 Supp. Fig. 1A-D). Since peripheral mono-oriented chromosomes rely on CENP-E for
135 efficient congression (7), CENP-E inhibition can reliably be determined by the persisting
136 presence of chromosomes at poles (Supp. Fig. 1C). HeLa, U2OS and RPE1 cells were
137 treated with increasing concentrations of CENP-E inhibitors for 3 hours and their
138 phenotype was assessed every hour (Fig. 1C-E, Supp. Fig. 2A and 2B). We find that
139 CENP-E inhibition using all compounds can generate chromosomes at poles in both
140 diploid (RPE1) and CIN (HeLa and U2OS) cell lines, at comparable concentrations (Fig.
141 1C-E, Supp. Fig. 2A and 2B). We calculated the concentrations for partial inhibition as
142 the lowest concentration required to observe an effect and full inhibition was defined as
143 the lowest concentration required to exert maximal effect in terms of chromosomes at
144 poles (beginning of plateau). Upon reaching the plateau, the percentage of cells with
145 chromosomes at poles was comparable for each compound suggesting that CENP-E
146 can be efficiently inhibited through three distinct mechanisms (Fig. 1F). Nevertheless,
147 this percentage was lower in U2OS and RPE1 cells (Fig. S2A and 2B). Moreover, we
148 found no increase in apoptosis/cell debris within 3 hours of treatment with CENP-E
149 inhibitors (data not shown). Our data suggest that CENP-E inhibition results in the
150 formation of chromosomes at poles, independent of the molecular mechanism used to
151 inhibit CENP-E function.

152 Using the optimal doses that partially and fully inhibit CENP-E function calculated
153 from the high-throughput screen, we used high-resolution live-cell imaging to determine
154 whether CENP-E motor activity is required for the maintenance of chromosome
155 alignment (Fig. 3A). Using the proteasome inhibitor MG-132, HeLa cells were arrested
156 at metaphase with fully aligned chromosomes, then treated with CENP-E inhibitors and
157 imaged every 5 minutes for 3 hours (Fig. 3A). We find that CENP-E inhibition causes
158 general chromosome misalignment accompanied by chromosomes at poles in all cell
159 lines tested, regardless of the inhibitor used (Figs 2B-E; S3). We also observed clear
160 cohesion fatigue that was specific to CIN cells and was exacerbated by treatment with
161 CENP-E inhibitors (Fig S6). Our live cell imaging setup allows us to clearly distinguish
162 between loss of alignment due to cohesion fatigue, where single chromatids start to
163 “peel-off” from the metaphase plate, and a morphology of paired chromatids arranged
164 as chromosomes at poles, consistently observed after CENP-E inhibition (Fig. S7A, C).
165 Nevertheless, we find that the percentage of cells with chromosomes at poles induced
166 by treatment with CENP-E inhibitors is dose-dependent (Fig. 2B-E). This was also
167 observed in RPE1 and U2OS cells (Fig. S3). Concurrently, we also observe a dose-
168 dependent effect on the percentage of cells that remain aligned throughout the
169 experiment, consistent for all cell lines analyzed (Fig. S4). Direct evidence demonstrating
170 that CENP-E inhibitors were actively disrupting CENP-E function, was obtained from
171 neighboring cells that entered mitosis in the presence of CENP-E inhibitors. As expected,
172 these cells presented several chromosomes at poles immediately after nuclear envelope
173 break down and arrested in mitosis with chromosomes at poles (Fig. S5). When we
174 restrict our analysis of the percentage of cells with chromosomes at poles to the first hour
175 of imaging of these artificial metaphases, we notice that there is a stronger phenotype
176 induced by GSK923295 compared with PF-2771 and Cmpd-A, at full inhibition (Fig. 2B-
177 E; S3). At this time-point, events of cohesion fatigue or other epiphenomena related to
178 drug toxicity or metaphase arrest are less likely to take place (16). During the course of
179 the experiment, we also quantified the frequency of terminal events that dictated the

180 exclusion of these cells from the analysis of chromosome alignment from that time point
181 onwards (Fig. S6). Terminal events included cells entering anaphase in the presence of
182 MG-132 without chromosome decondensation (Fig. S7B), cohesion fatigue, mitotic
183 slippage and cells that moved out of the field of view or out of focus. We find that
184 cohesion fatigue was highly prevalent in U2OS cells but rarely observed in other cell
185 types. Importantly, this effect also appeared to be potentiated by the presence of CENP-
186 E inhibitors.

187 Our live cell imaging assay also allows us to determine how often chromosomes
188 re-align or generate chromosomes at poles, after an initial misalignment event (Fig. S8).
189 Although there is some variability, results suggest that after an initial misalignment event,
190 CENP-E is required for chromosome re-alignment. Indeed, CENP-E disruption often
191 leads to chromosomes at poles in a dose-dependent manner, while this rarely occurs in
192 HeLa and U2OS cells upon DMSO treatment.

193 Next, we analyzed cellular sensitivity to CENP-E inhibitors to understand whether
194 this correlates with the overall effects on chromosome alignment observed using our live
195 cell imaging assay. For that purpose, we used a standard Resazurin Cell Viability assay
196 in which cells were incubated for 72 hours with each CENP-E inhibitor and the IC50s
197 were subsequently calculated (Fig. 3). We find that HeLa cells are the most sensitive to
198 all inhibitors tested and that U2OS cells are generally less sensitive to all compounds
199 when compared to HeLa cells (Fig. 3A-C). Surprisingly, RPE1 cells are 2,1-fold less
200 sensitive to Cmpd-A but are equally sensitive to GSK923295 and PF-2771 treatments
201 suggesting that Cmpd-A has unique properties that potentiate its effect more specifically
202 in CIN cell lines.

203

204 Discussion

205 Microtubule-targeting chemotherapeutics

206 Modern day chemotherapy begun with the discovery of nitrogen mustard's toxic
207 effects on haematopoietic cells and was first administered to lymphoma patients with
208 marked improvements in tumor regression. However, remissions turned out to be brief
209 and incomplete, prompting the discovery and development of other chemotherapeutic
210 agents (17). Chemotherapeutics include alkylators, antimetabolites, platinum agents and
211 natural products. Spindle poisons are plant-derived natural products that target tubulin,
212 the cytoskeletal protein that polymerizes to form microtubules that participate in a
213 plethora of cellular functions. These compounds are broadly defined as anti-mitotics and
214 can be either microtubule destabilizers (i.e. vinca alkaloids, epothilones and eribulin) or
215 stabilizers (i.e. taxanes). Since microtubules are essential for cellular homeostasis, these
216 agents often cause serious side effects such as neurotoxicity and neutropenia and/or
217 may lead to the acquisition of resistance (18-20). CENP-E is a kinesin motor protein
218 expressed predominantly in mitosis (and G2) (5) and its loss of function causes
219 chromosome misalignment and apoptosis due to a prolonged mitotic arrest (21, 22).
220 Although CENP-E requires microtubules to exert its functions, it slowly accumulates in
221 G1, reaching a peak in G2-M phase due to an increased mRNA level, and is ultimately
222 degraded in the end of mitosis (23). Thus far, no specific function was attributed to
223 CENP-E in interphase and therefore, CENP-E inhibition represents a new class of anti-
224 mitotic therapeutics with the potential to reduce microtubule-associated side-effects.

225

226 CENP-E as a molecularly-targeted anti-cancer drug

227 Several preclinical studies have evidenced the efficacy of CENP-E inhibitors with
228 regards to their anti-tumor activity. PF-2771 treatment induced tumor regression in a
229 patient derived basal-like triple negative cancer xenograft tumor model (11). GSK923295

230 showed a dose-dependent antitumor activity against mice bearing xenografts of the
231 Colo205 colon tumor-cell line as well as against a panel of 212 tumor cell lines (10).
232 These promising results led to the first Phase I clinical trials using GSK923295 to treat
233 human subjects with refractory cancer that do not respond to standard therapy. Notably,
234 anemia and fatigue were described as the only adverse events, with a very low
235 occurrence of neutropenia, typically very rare for a bona-fide antimetabolic drug. Despite
236 the promising results, further studies are required to determine the best administration
237 schedules/techniques to reach optimal plasma concentrations that ensure specific
238 CENP-E inhibition (24). More recently, Compound A (Cmpd-A), a novel small-molecule
239 inhibitor of CENP-E was described and shown to exhibit an antiproliferative effect in 14
240 cancer cell lines. Surprisingly, the diploid MRC5 cell line demonstrated reduced
241 sensitivity to CENP-E inhibition, suggesting that CENP-E inhibition using Cmpd-A may
242 target a specific form or domain in CENP-E that is altered in cancer cells. In agreement,
243 the authors found no correlation between CENP-E expression and the anti-proliferative
244 effects of Cmpd-A in the cell lines analyzed (12). In our study we used RPE1 cells as a
245 diploid cell line and found that they are 2,1-fold less sensitive to Compound A but are
246 equally sensitive to GSK923295 and PF-2771. In contrast, chromosomally unstable
247 U2OS and HeLa cells showed a comparable sensitivity between all the inhibitors.
248 However, this effect is not simply explained by the efficiency of mitotic arrest since our
249 live cell imaging experiments show that PF-2771 and GSK923295 treatments were able
250 to induce chromosomes at poles with equal or even higher efficiency in the diploid cell
251 line. These data suggest that either Cmpd-A off-target effects are more evident in CIN
252 cells (CENP-E-independent), the diploid cell line RPE1 has higher drug efflux pump
253 activity and can efficiently pump out specific drug structures, or alternatively, Cmpd-A
254 may target CENP-E isoforms that are more commonly observed in CIN cell lines. These
255 hypotheses could be addressed by performing cell viability assays in the presence of
256 inhibitors of the p-glycoprotein, such as verapamil, and by sequencing CENP-E to
257 address the presence of mutations that may confer resistance.

258 CENP-E as a tethered motor between microtubules and kinetochores

259 Recent models have proposed that CENP-E plays an important role in facilitating
260 the association between kinetochores and dynamic microtubule ends as a tether motor
261 (8). In order to investigate the contribution of CENP-E to link microtubule plus ends to
262 kinetochores on congressed chromosomes the authors used GSK923295 (locks CENP-
263 E in a microtubule-bound, inactive state) at a concentration 4-fold higher than our optimal
264 dose used for full CENP-E inhibition calculated in our titration experiment. Since
265 chromosomes moved towards the pole, the authors concluded that CENP-E continues
266 active at kinetochores of aligned chromosomes, but at these concentrations GSK923295
267 treatment may be indirectly affecting kinetochore-microtubule dynamics. In normal cells,
268 average metaphase durations in HeLa, hTERT-RPE1 and U2OS cell lines are 16, 9 and
269 11 minutes respectively (25). Here we show that in metaphase arrested cells,
270 approximately 30-60 minutes after CENP-E inhibition, misalignment and formation of
271 chromosomes at poles is frequently observed with all compounds tested. However, we
272 show that the formation of chromosomes at poles occurs significantly faster in
273 GSK923295-treated cells, and this appears to be specific to CIN cells. Notably, PF-2771
274 and Compound A act independently of microtubules while GSK923295 provides a gain
275 of function CENP-E phenotype since it causes a rigor like state in a microtubule-bound
276 state. Under these conditions, it is probable that chromosomes are being stripped off the
277 metaphase plate more frequently due to spindle flux. Although we are working with
278 artificial metaphase extensions, our results demonstrate that CENP-E activity is required
279 for the maintenance of chromosome alignment during a prolonged metaphase. However,
280 whether these results reflect CENP-E function in the context of chromosome alignment
281 in normal physiological conditions, remains unknown.

282 Using state-of-art live cell microscopy we were able to follow cells through a
283 continued mitotic arrest induced by proteasome inhibition. It is worth noting that the
284 proteasome inhibitor MG-132 was never washed-out during our experimental setting,

285 which bears important implications for our interpretation of the results. Indeed, recent
286 studies have suggested that a prolonged metaphase arrest may lead to cohesion fatigue,
287 a condition where sister chromatid cohesion is lost but the cell is arrested in mitosis with
288 high levels of Cyclin B1 and separated chromatids (16). Particularly in transformed cells
289 with numerous chromosomes, it may become difficult to distinguish between cohesion
290 fatigue (where individual chromatids are pulled to poles) and whole chromosomes at
291 poles, particularly when looking at static images of cells (i.e., immunofluorescence or
292 time-lapse imaging with low temporal resolution) (26). However, a time-lapse recording
293 with high temporal resolution allows us to follow the dynamics of chromosome and
294 spindle movements, critical for making the distinction between cohesion fatigue and
295 chromosomes at poles (See Figure S7C). Indeed, the striking similarity between the
296 phenotypes of chromosomes and poles and cohesion fatigue incites for a systematic re-
297 evaluation of proteins formerly associated with chromosome alignment using state-of-
298 the-art live cell imaging techniques. Our experimental setup permits us to clearly identify
299 the most dramatic cases of cohesion fatigue on the basis of chromosome morphology,
300 and on the dynamics of chromosome movement and spindle rotation, but the use of a
301 kinetochore marker would provide unequivocal evidence on this subject. Moreover, a
302 proteasome-induced 3-hour mitotic arrest may cause secondary phenotypes that
303 warrant a cautious approach when evaluating the formation of chromosomes at poles,
304 particularly in conditions of prolonged metaphase arrest.

305

306 Under the combined effect of MG-132 and CENP-E inhibition, we find that
307 cohesion fatigue is more prevalent in CIN cells, particularly U2OS, and was rarely
308 observed in RPE1 cells. This suggests that CIN cells may be inherently more susceptible
309 to cohesion fatigue, which is in accordance with results observed using a proteasome
310 inhibitor alone (22). And this rationale further validated the usefulness of Bortezomib
311 (27), a proteasome inhibitor approved for multiple myeloma and refractory mantle cell
312 lymphoma with other new compounds currently at preclinical stage testing (28-30).

313 However, we show that dual inhibition of CENP-E and proteasome activity causes
314 deleterious effects that are exacerbated in CIN cells, thus providing preclinical data in
315 support of a combination therapy regime. Associating CENP-E inhibitors with bortezomib
316 may be another suitable therapeutic strategy in the future, to overcome limitations of
317 individual pharmacokinetics and pharmacodynamics or resistance in drug administration
318 schedules.

319

320 **Materials and Methods**

321 Cell lines

322 HeLa, U2OS (kindly provided by M. Barisic) and hTERT-RPE1 cell lines stably
323 expressing H2B-GFP and mCherry- α -Tubulin were used. All cell lines were grown in
324 Dulbecco's Modified Eagle Medium (DMEM) (Gibco, Life Technologies) supplemented
325 with 10% fetal bovine serum (FBS; Gibco Life Technologies) at 37°C in a humidified
326 atmosphere with 5% CO₂.

327 Drugs/compounds used

328 The CENP-E Inhibitors - GSK923295 (Selleckchem), PF-2771 (Medchem Express) and
329 Compound A (Takeda) - and the proteasome inhibitor MG-132 (Calbiochem) were
330 originally dissolved in DMSO (Sigma-Aldrich) and freshly diluted in DMEM medium
331 without phenol red immediately before live cell imaging. Total volume DMSO, either used
332 as control or drug dilution, added to the culture medium never exceeded 1:1000 v/v.

333 Microscopy

334 The titration experiment was performed in the InCell Analyser 2000, equipped with a
335 sCMOS camera, and provided with two laser lines (488 nm and 561 nm). HeLa, U2OS
336 and hTERT-RPE1 (all stably expressing H2B-GFP/mCherry- α -tubulin) cells were kept in
337 a heated chamber (37 °C), with controlled CO₂ conditions. Using a 20x objective (0.45
338 NA), images were collected every hour after CENP-E inhibition, up to 3 hours. Image
339 analysis was performed with CellProfiler software.

340 After determining the optimal dose for inhibiting CENP-E function, live-cell confocal
341 microscopy was performed. HeLa, U2OS and hTERT-RPE1 (all stably expressing H2B-
342 GFP/mCherry- α -tubulin) cells were plated onto 6 well-plates with pre-cut coverslips 24
343 hours prior to the assay. To promote a cell cycle arrest at metaphase, 3 μ M of MG-132
344 prepared in DMEM without phenol red was added to the cells approximately 30 minutes

345 before live cell imaging. After the first frame of imaging (5min), DMSO or the selected
346 concentration of inhibitor was added and cells were followed through time-lapse confocal
347 microscopy. Time-lapse imaging was performed in a heated chamber (37°C) using a
348 100x 1.4 NA Plan-Apochromatic differential interference contrast objective mounted on
349 an inverted microscope (Ti; Nikon) equipped with a CSU-X1 spinning-disk confocal head
350 (Yokogawa Corporation of America) and with two laser lines (488 nm and 561 nm).
351 [MM1] Images were detected with an iXonEM+ EM-CCD camera (Andor Technology).
352 Nine 2µm length z-planes for each channel covering the entire volume of the mitotic
353 spindle were collected every 5 min, for up to 180 minutes. Image and video processing
354 was performed using Image J and Nikon NIS viewer, respectively.

355 CellProfiler pipelines and settings

356 CellProfiler's object identification modules contain a variety of published and tested
357 algorithms for identifying cells based on fluorescence (31). We firstly defined the primary
358 objects as nuclei, through the H2B-GFP signal, and then the secondary objects as cell
359 size and shape, through the Tubulin-mCherry signal. After rendering this segmentation,
360 a gallery of cells was manually classified into four categories for each cell line:
361 interphase, mitotic (excluding chromosomes at poles), chromosomes at poles and
362 apoptosis/cell debris (Fig. S1A-D). This gallery was used as a training set that served
363 the automated classification of the Cell Profiler software.

364

365 IC50 and cell proliferation assay

366 HeLa (1500 cells/well), RPE1 (8000 cells/well) and U2OS (3000 cells/well) cells were
367 seeded on a sterile 96-well plate (TC-Plate 96 well, Cell+, F, Sarstedt) and let adhere for
368 24h. The cells were treated with all CENP-E inhibitors freshly dissolved in DMEM media
369 for 72 hours at the following concentrations: 8 nM, 16 nM, 31 nM, 62.5 nM, 125 nM, 250
370 nM, 500 nM for PF-2771 and Compound A and 4 nM, 8 nM, 16 nM, 31 nM, 62.5 nM, 125
371 nM, 250 nM for GSK923295. The cells were then washed with 1X PBS and incubated

372 with 0,1% Resazurin (Sigma-Aldrich) dissolved in DMEM for 4 hours. The supernatant
373 was transferred to a new 96-well plate and its resorufin fluorescence was measured
374 using a microplate spectrofluorometer (Synergy MX, Biotek) with the following settings -
375 Excitation wavelength: 530 ± 9 nm, Emission wavelength: 590 ± 9 nm.

376

377 **Acknowledgments**

378 We would like to acknowledge AF Maia for his help with the InCell Analyzer 2000 and
379 initial assessment of CellProfiler software.

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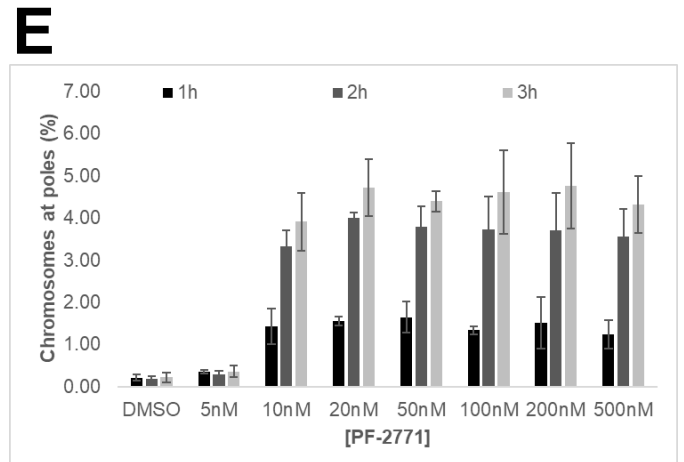
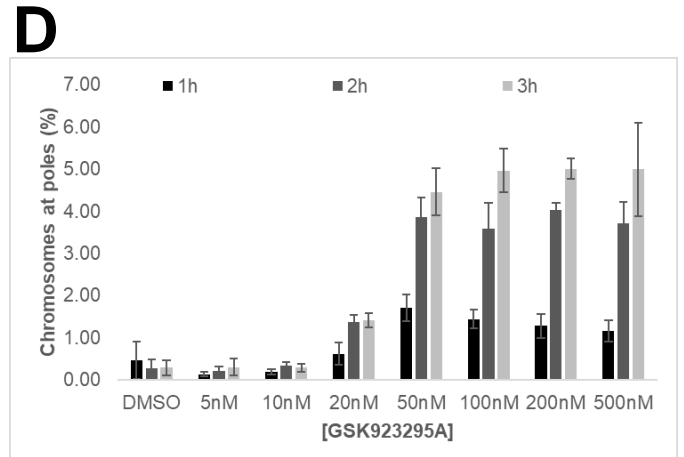
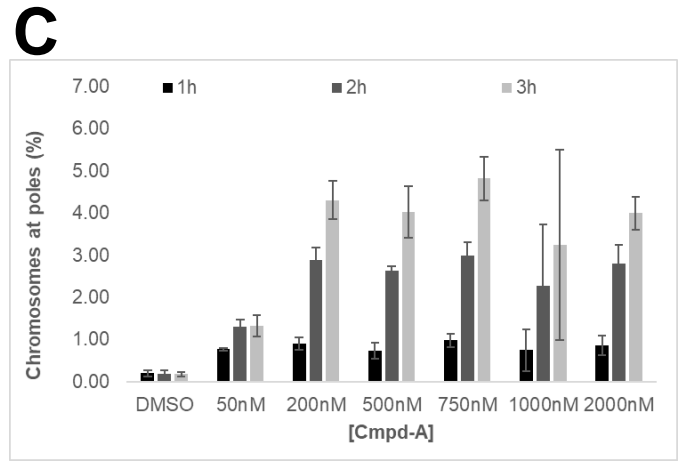
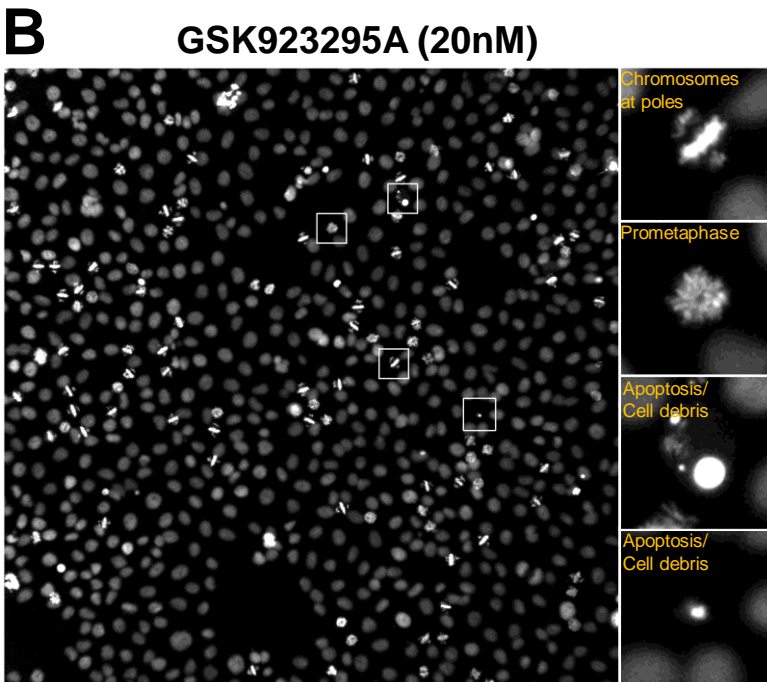
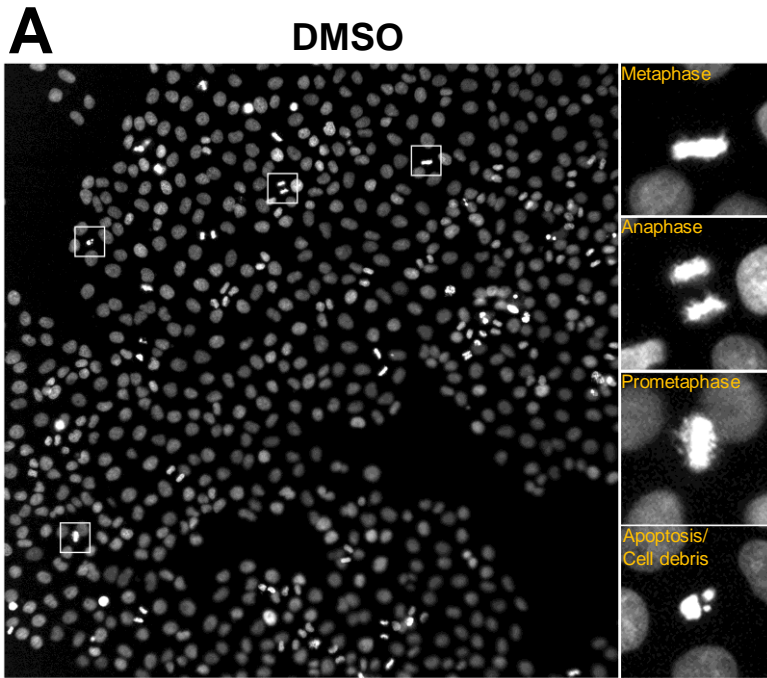
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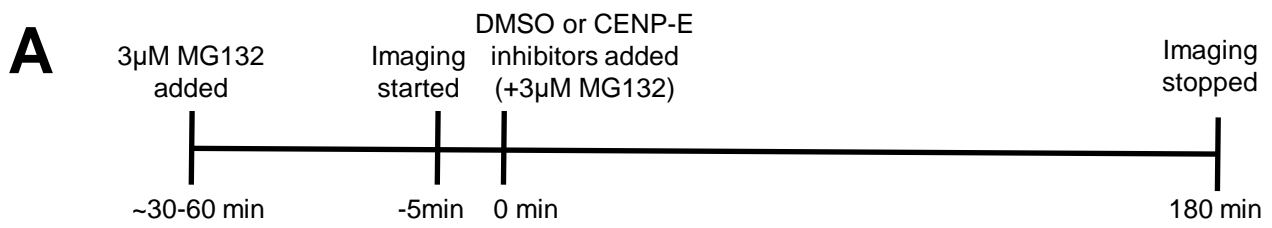
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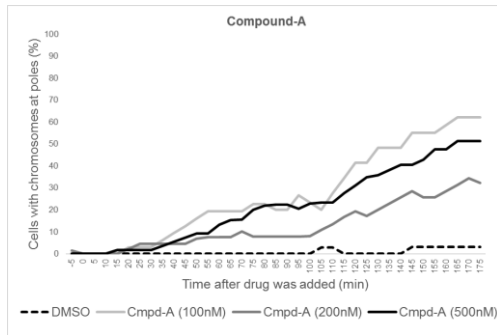
F

Compound/ Drug	Inhibition mechanism	Inhibitor binding site	Clinical Trials
Cmpd-A	Competitive towards ATP	ATP binding site on CENP-E	Not considered
GSK923295A	Allosteric (induces rigor-like state)	Between helices $\alpha 2$ and $\alpha 3$ on CENP-E motor domain (induces a MT-bound state)	Phase I concluded (2012)
PF-2771	Non-competitive towards ATP	Unknown (decreases CENP-E affinity for ATP)	Not considered

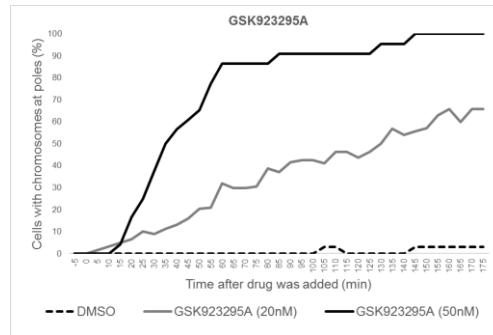
Figure 1 – Titration of CENP-E inhibitors in HeLa cells. Representative images of **(A)** DMSO and **(B)** GSK923295A-treated HeLa cells expressing H2B-GFP after a 3hr treatment. Images acquired using a 20X objective mounted on an IN Cell Analyzer 2000 microscope system. Insets show 5X magnifications of selected regions exemplifying different cellular phenotypes. Images collected were analysed using a custom-made CellProfiler pipeline and the percentage of cells displaying chromosomes at poles (over the total number of cells) is shown for cells treated with **(C)** Cmpd-A, **(D)** GSK923295A and **(E)** PF-2771. Error bars represent SD for quadruplicate experiments. **(F)** Table summarizing chemical properties of CENP-E inhibitors



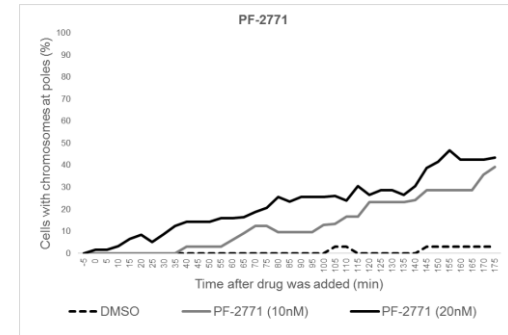
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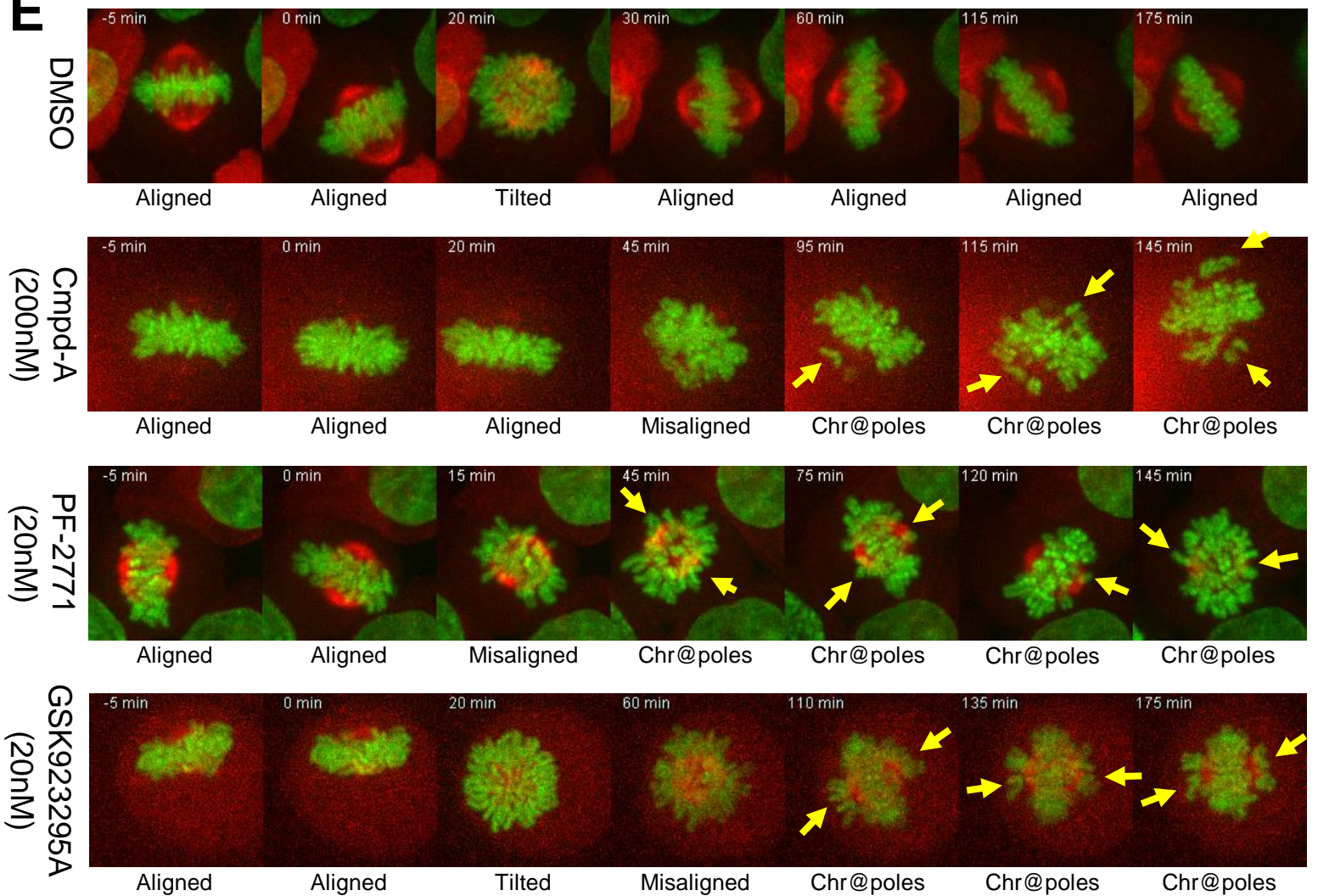


Figure 2 – CENP-E is required for the maintenance of chromosome alignment. (A) Schematic representation of the experimental setup used to assay CENP-E function in the maintenance of chromosome alignment. HeLa cells were treated with MG132 (3 μ M) for ~30min. Cells were selected for imaging on the basis of chromosome alignment and imaging started 5 min before the addition of DMSO or CENP-E inhibitors. MG132 (3 μ M) was maintained in the media containing DMSO or CENP-E inhibitors. Cells were followed through live cell imaging for a further 180min. Quantifications of the percentage of HeLa cells that display chromosomes at poles after treatment with different concentrations of **(B)** Cmpd-A **(C)** GSK923295A or **(D)** PF-2771. **(E)** Selected time-frames of representative cells treated with CENP-E inhibitors demonstrating the progressive misalignment of congressed chromosomes and the subsequent formation of chromosomes at the poles. Please note that while DMSO-treated cells remain mostly aligned throughout the experiment, most of the CENP-E-inhibited cells display misaligned chromosomes that often result in the formation of chromosomes at poles. Yellow arrows indicate chromosomes at poles.

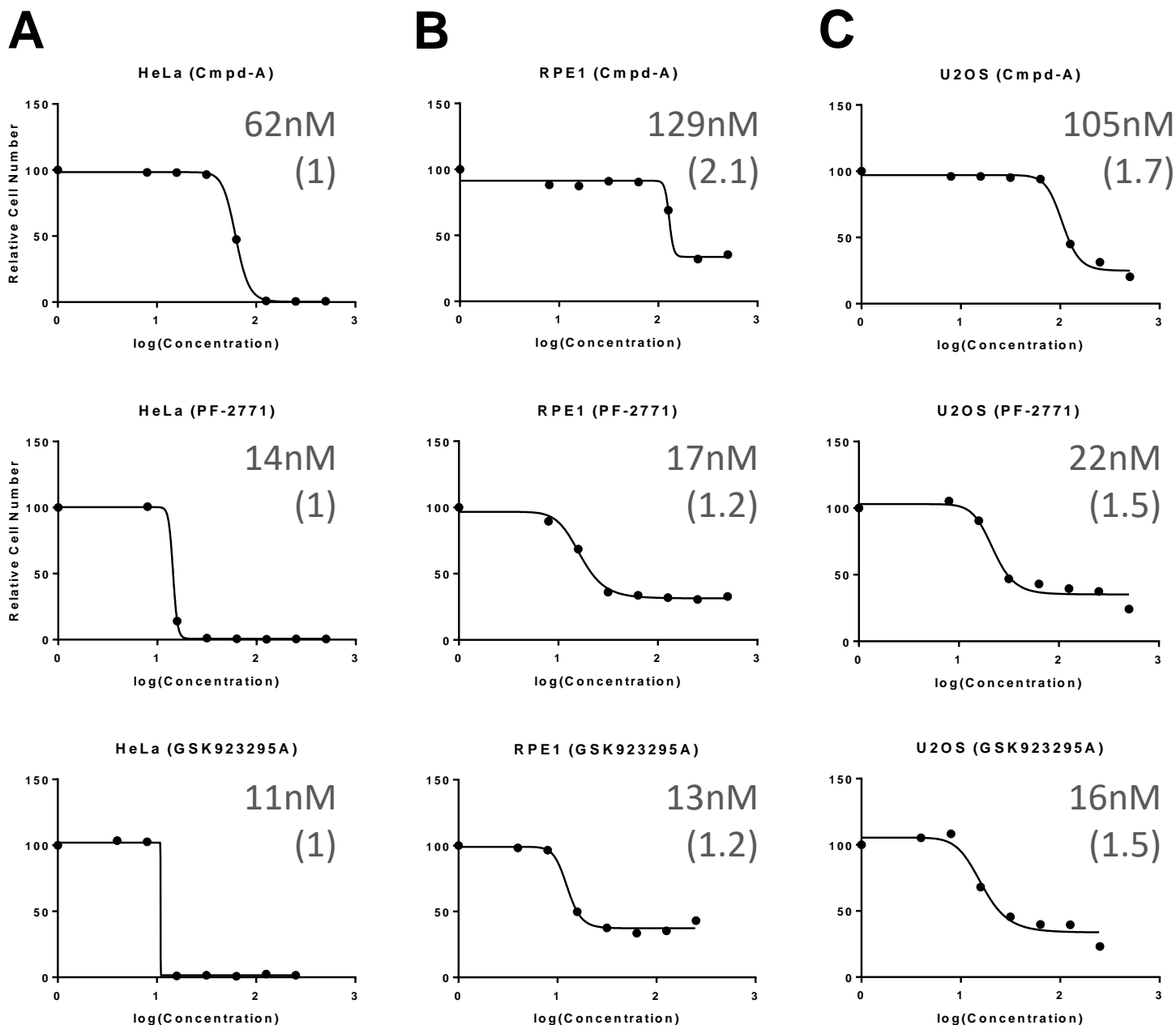
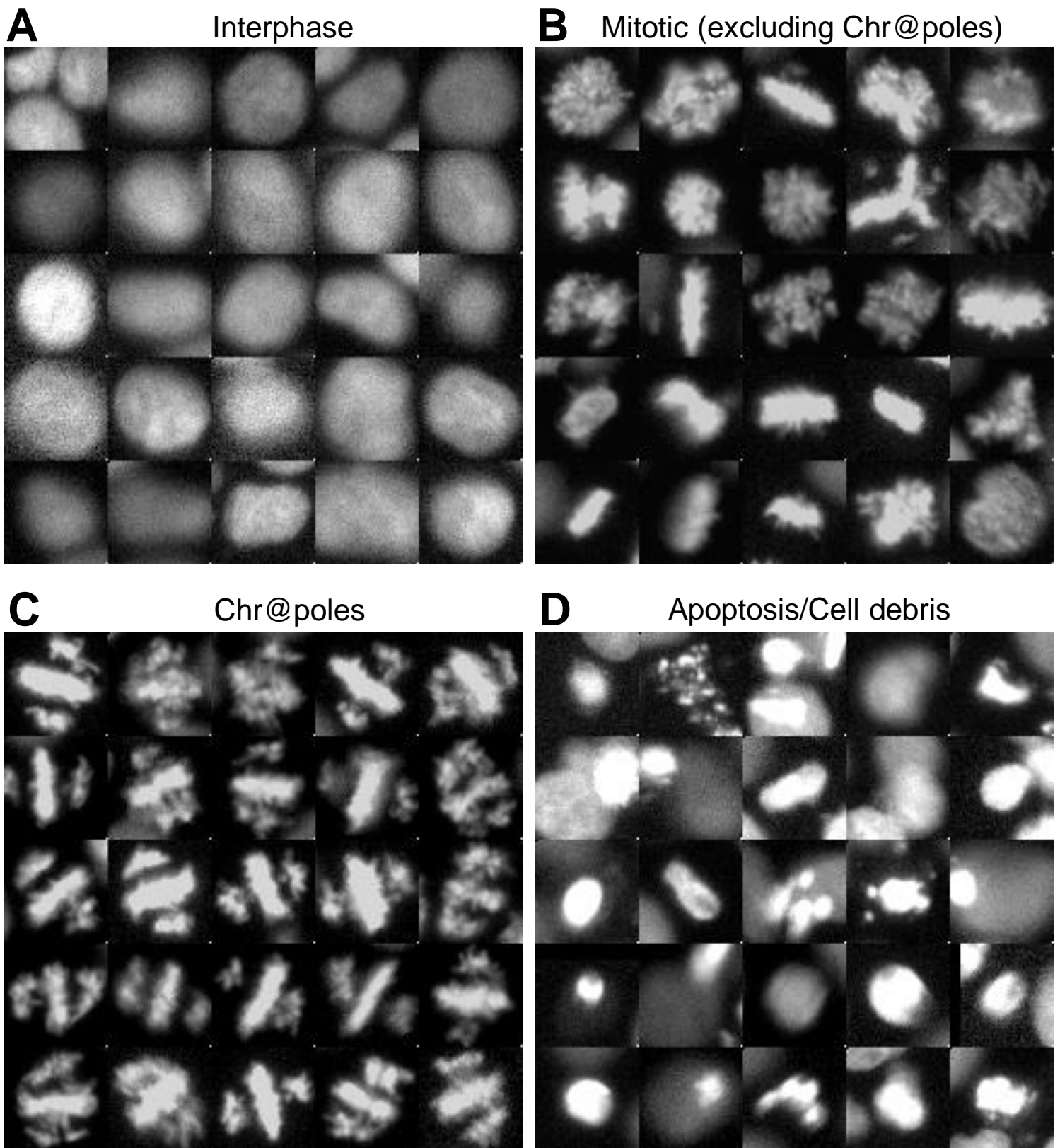
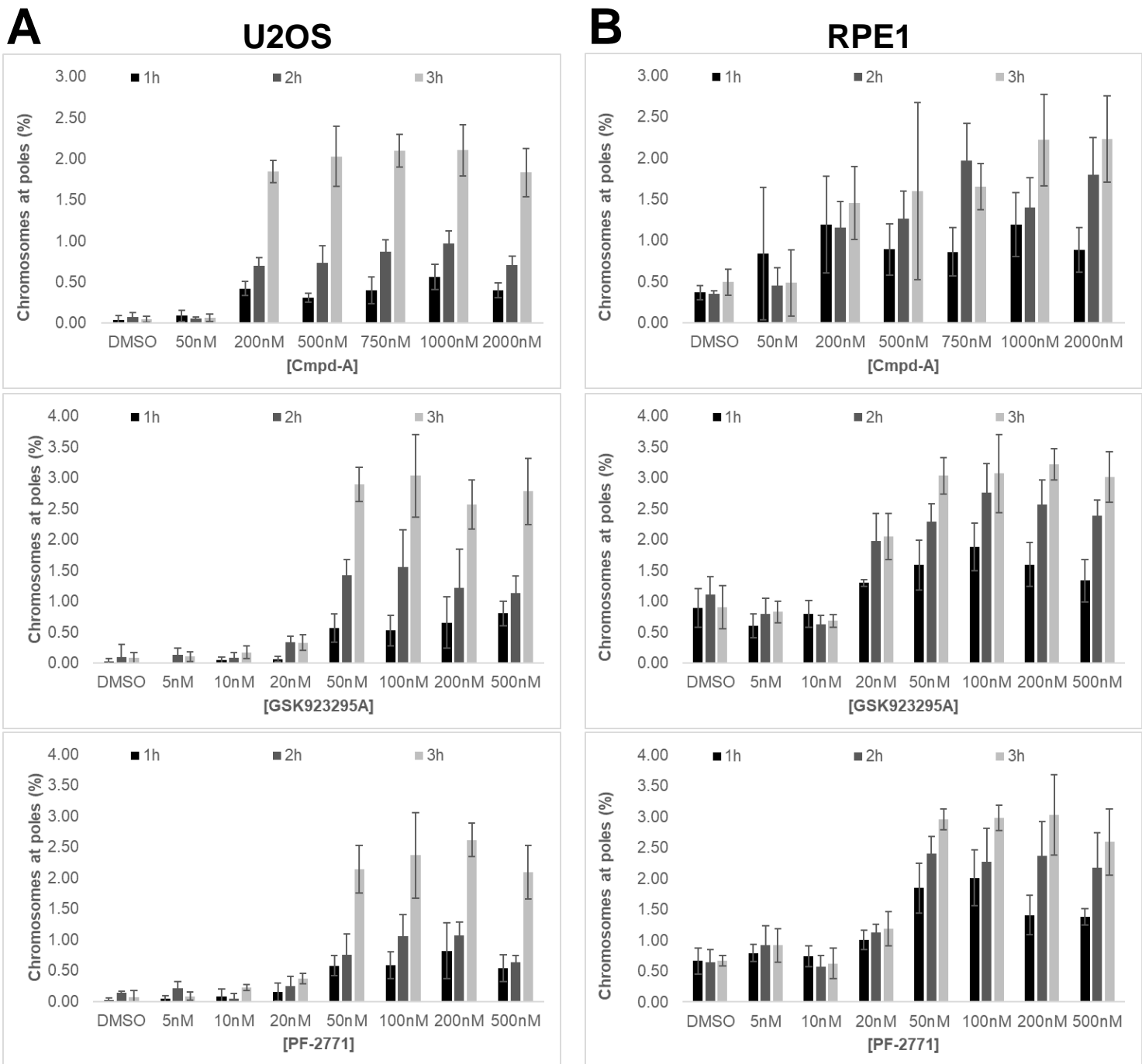


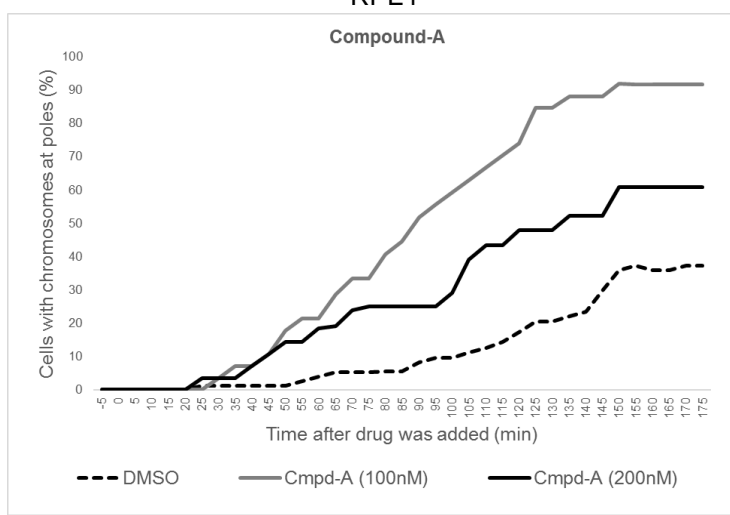
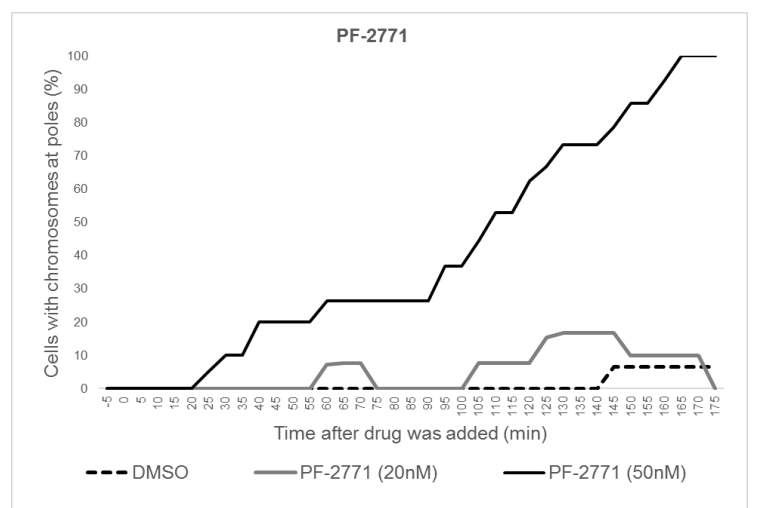
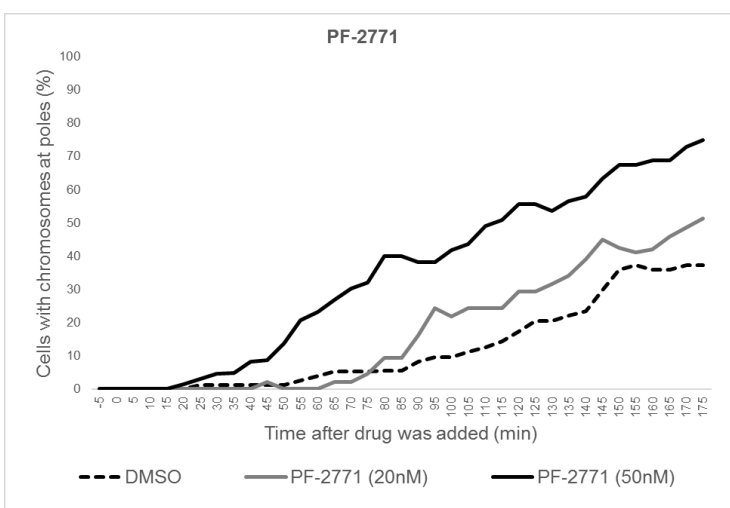
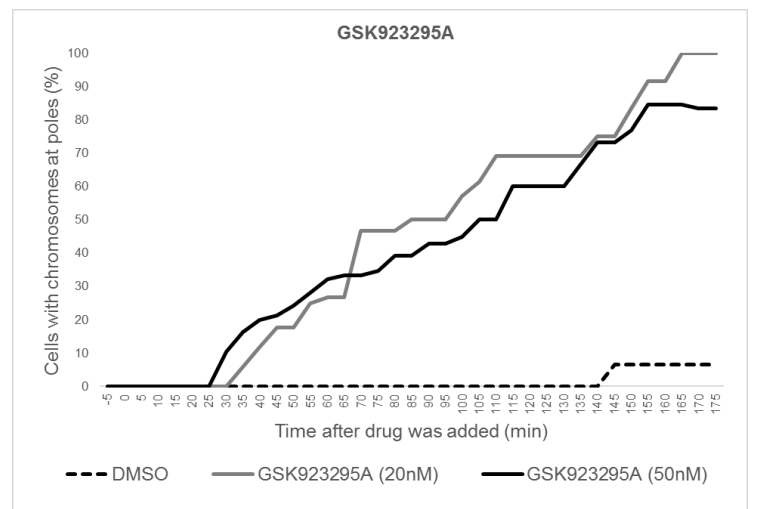
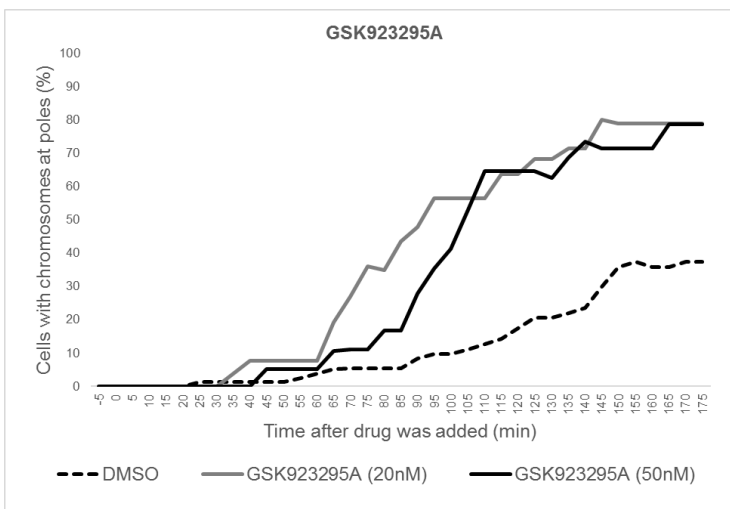
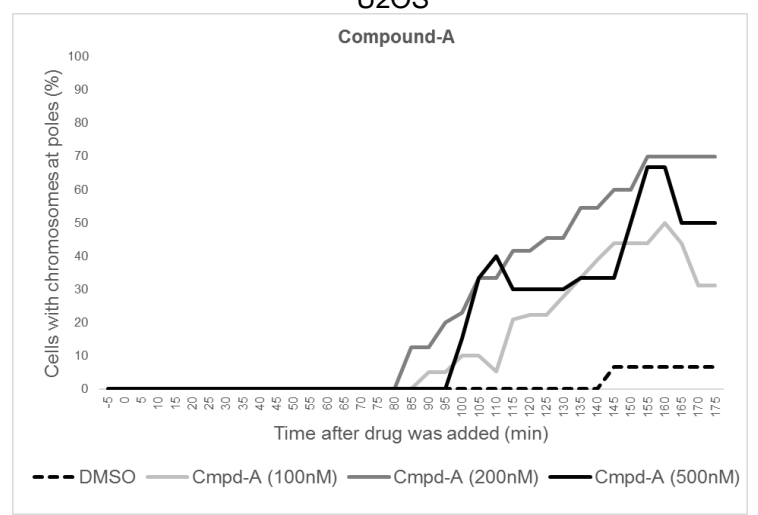
Figure 3 – Diploid cells are less sensitive to Cmpd-A-mediated cell death . (A) HeLa, **(B)** RPE1 and **(C)** U2OS cells were treated with varying concentrations of Cmpd-A (top row), GSK923295A (middle row) or PF-2771 (bottom row) and the relative cell number was calculated 5 days after addition of the drugs. Relative cell number was calculated using a custom-generated Resazurin Cell Viability assay. Calculated (represented in nM) and relative (represented below as -fold of HeLa cells) IC₅₀ values are shown in gray in the top right corner of each graph.



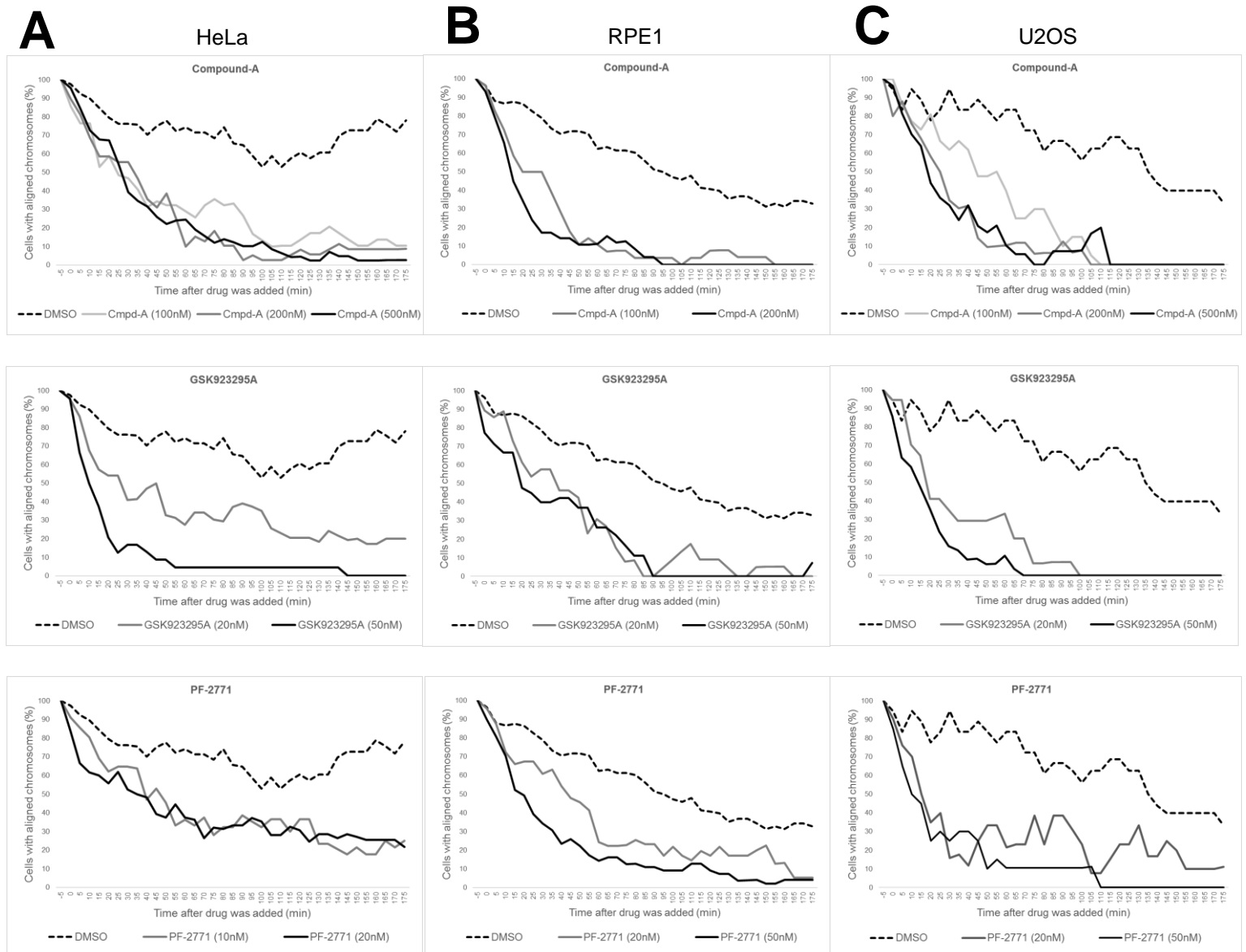
Supplementary Figure 1 – CellProfiler2.2.0 image training gallery used for quantifying cellular state. Panels show randomized images used to train CellProfiler Analyst software using the following cellular classes: **(A)** Interphase, **(B)** Mitotic (mitotic cells without chromosomes at poles), **(C)** Mitotic cells with chromosomes at poles or **(D)** Apoptotic/Cell debris.



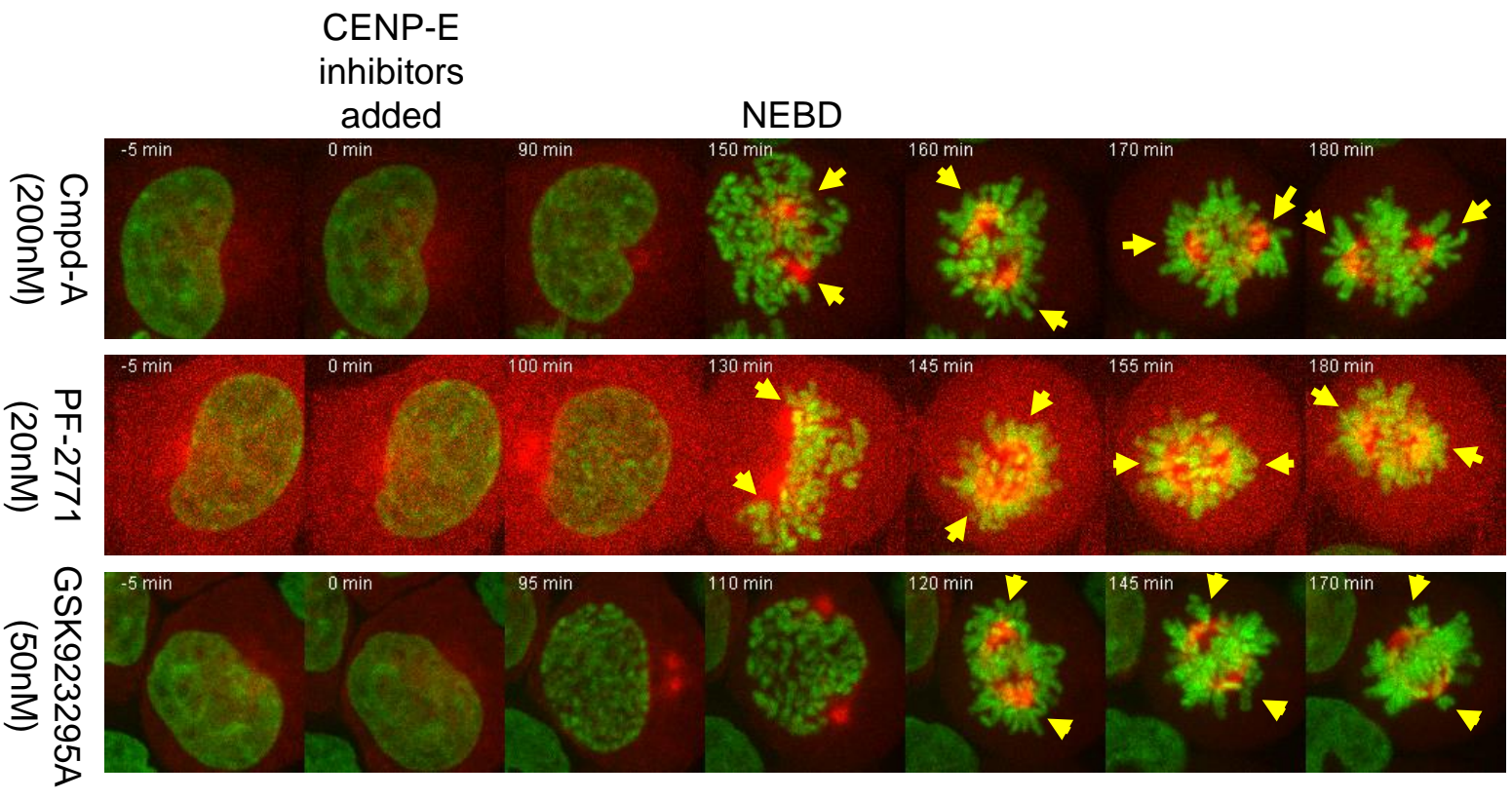
Supplementary Figure 2 – Titration of CENP-E inhibitors in U2OS and RPE1 cells. CellProfiler analysis of the percentage of cells displaying chromosomes at poles (over the total number of cells) is shown for cells treated with **(A)** U2OS and **(B)** RPE1 cells. Error bars represent SD for quadruplicate experiments.

A**B**

Supplementary Figure 3 – Inhibiting CENP-E function during metaphase causes chromosomes at poles in RPE1 and U2OS cells. Quantification of the percentage of cells with chromosomes at poles for **(A)** RPE1 or **(B)** U2OS cells treated with Cmpd-A (top row), GSK923295A (middle row) or PF2771 (bottom row). Results were obtained from the analysis of live cell imaging. Please note that cells undergoing any of the terminal events were removed from the analysis from that time point onwards.



Supplementary Figure 4 – Inhibiting CENP-E function during metaphase induces chromosome misalignment. Quantification of the percentage of cells that remain aligned during imaging for (A) HeLa, (B) RPE1 or (C) U2OS cells treated with Cmpd-A (top row), GSK923295A (middle row) or PF2771 (bottom row). Results were obtained from the analysis of live cell imaging. Please note that cells undergoing any of the terminal events were removed from the analysis from that time point onwards.



Supplementary Figure 5 – Addition of CENP-E inhibitors prior to NEBD induces chromosomes at poles. Selected time frames of representative HeLa cells treated with (A) Cmpd-A (200nM) (B) PF-2771 (20nM) or (C) GSK923295A (20nM) for at least 100min before NEBD. Yellow arrows indicate chromosomes at poles.

A	HeLa			
	Anaphase	Out of focus	Cohesion Fatigue	Mitotic slippage
DMSO	10.3	0.0	12.8	0.0
Cmpd-A (100nM)	16.7	0.0	3.3	0.0
Cmpd-A (200nM)	23.3	0.0	9.3	0.0
Cmpd-A (500nM)	38.7	0.0	12.9	0.0
GSK923295A (20nM)	49.2	0.0	1.6	0.0
GSK923295A (50nM)	8.7	0.0	0.0	4.3
PF-2771 (10nM)	36.6	0.0	7.3	2.4
PF-2771 (20nM)	21.6	0.0	7.8	0.0
PF-2771 (50nM)	Not imaged	Not imaged	Not imaged	Not imaged

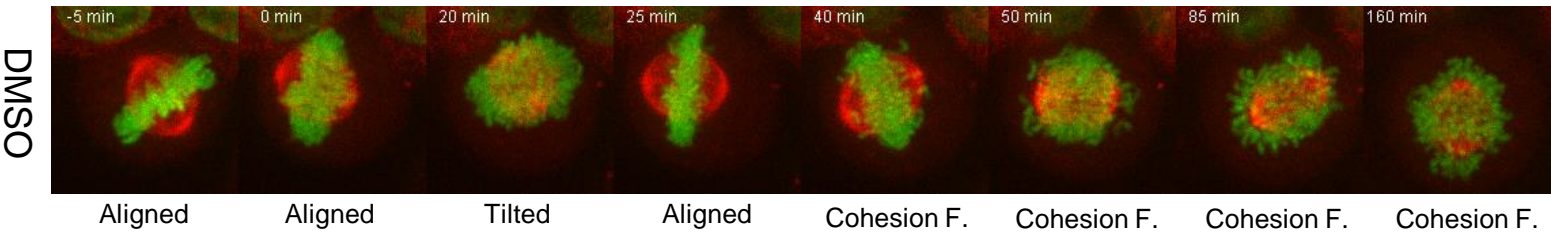
B	RPE1			
	Anaphase	Out of focus	Cohesion Fatigue	Mitotic slippage
DMSO	2.5	13.6	4.9	0.0
Cmpd-A (100nM)	0.0	10.7	3.6	0.0
Cmpd-A (200nM)	3.7	3.7	7.4	0.0
Cmpd-A (500nM)	Not imaged	Not imaged	Not imaged	Not imaged
GSK923295A (20nM)	8.0	28.0	0.0	0.0
GSK923295A (50nM)	11.8	29.4	0.0	0.0
PF-2771 (10nM)	Not imaged	Not imaged	Not imaged	Not imaged
PF-2771 (20nM)	4.3	17.4	0.0	0.0
PF-2771 (50nM)	32.4	11.3	8.5	0.0

C	U2OS			
	Anaphase	Out of focus	Cohesion Fatigue	Mitotic slippage
DMSO	0.0	0.0	11.8	0.0
Cmpd-A (100nM)	0.0	4.5	22.7	0.0
Cmpd-A (200nM)	0.0	0.0	75.0	0.0
Cmpd-A (500nM)	3.8	0.0	76.9	0.0
GSK923295A (20nM)	0.0	0.0	35.3	0.0
GSK923295A (50nM)	0.0	0.0	77.8	0.0
PF-2771 (10nM)	Not imaged	Not imaged	Not imaged	Not imaged
PF-2771 (20nM)	21.1	0.0	36.8	0.0
PF-2771 (50nM)	0.0	0.0	35.3	0.0

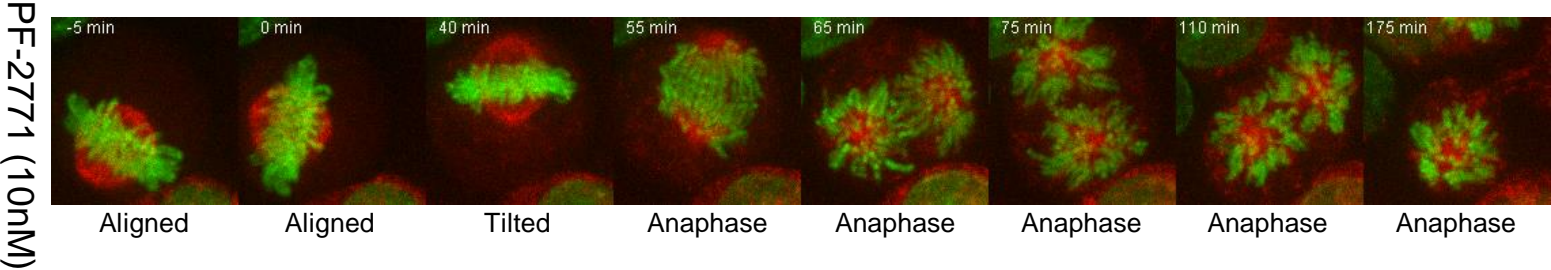
Supplementary Figure 6 – Terminal events that occurred during time-lapse imaging. Tables indicate the percentage of cells that undergo any of the terminal events shown for **(A)** HeLa, **(B)** RPE1 and **(C)** U2OS cells. Please note that each terminal event happened only once in each cell and those cells were excluded from the analysis of chromosome alignment from that point onwards.

CENP-E
inhibitors
added

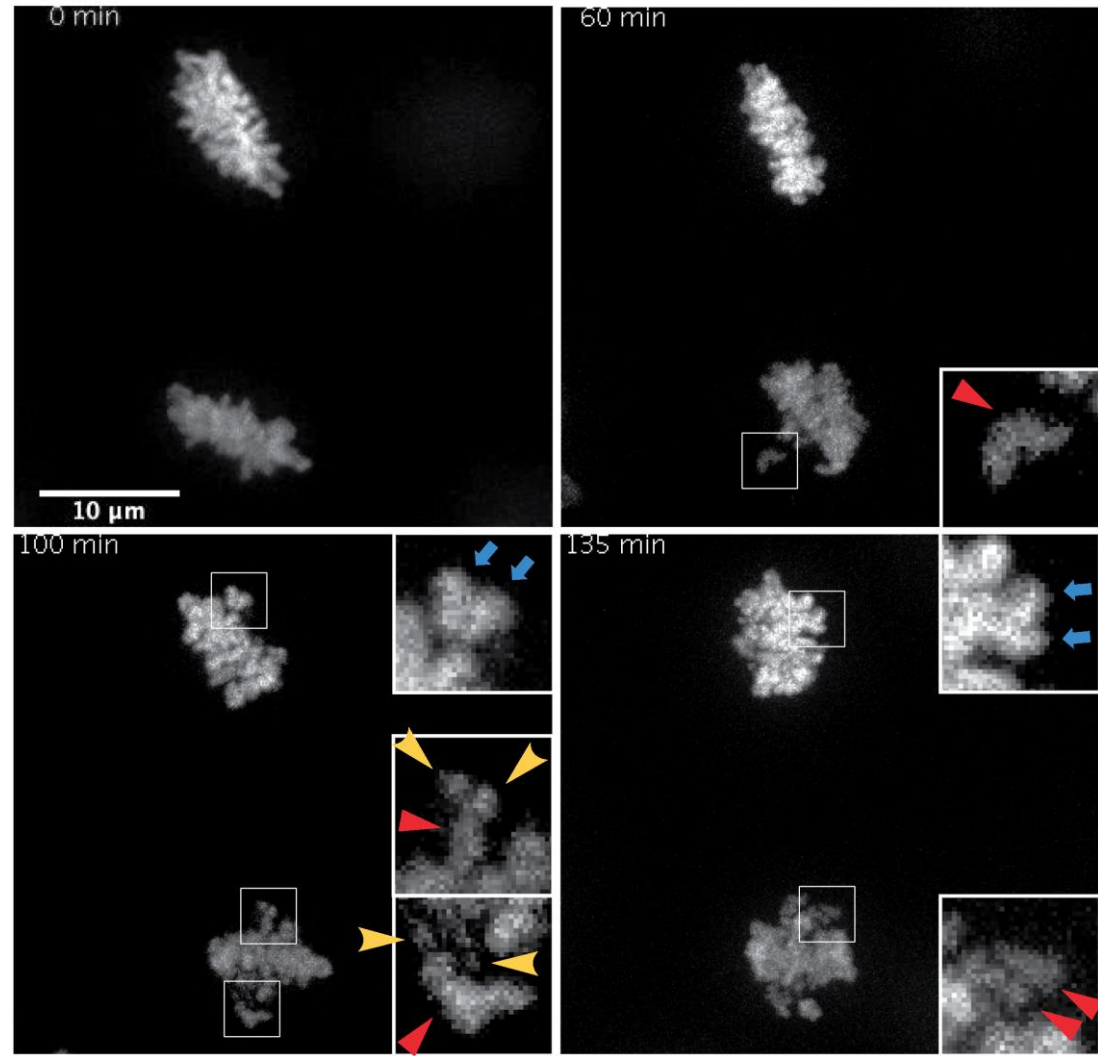
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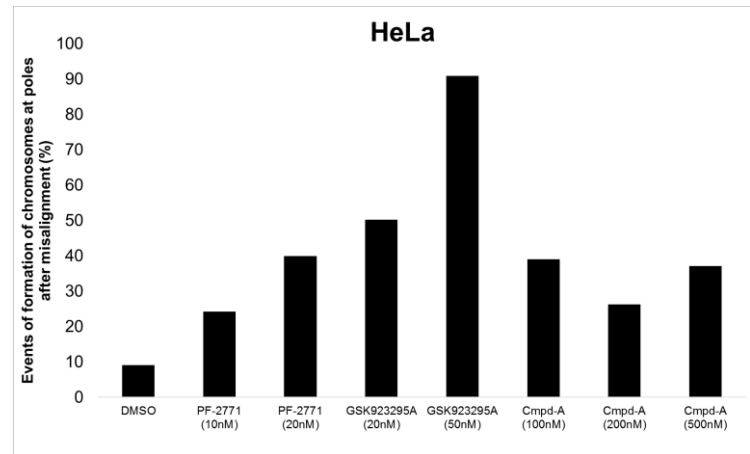
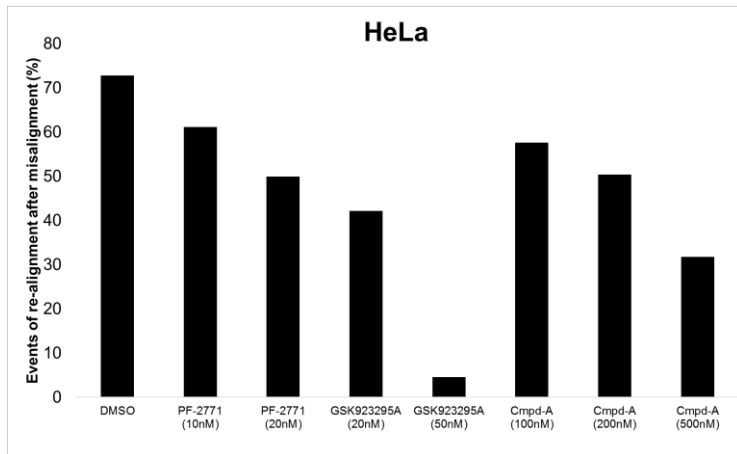
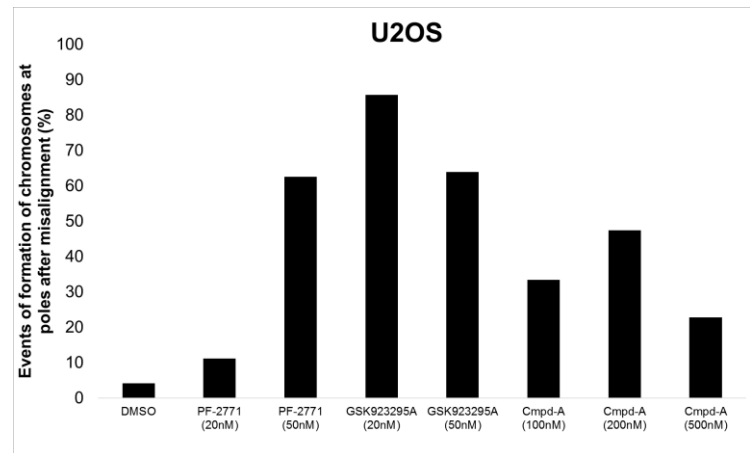
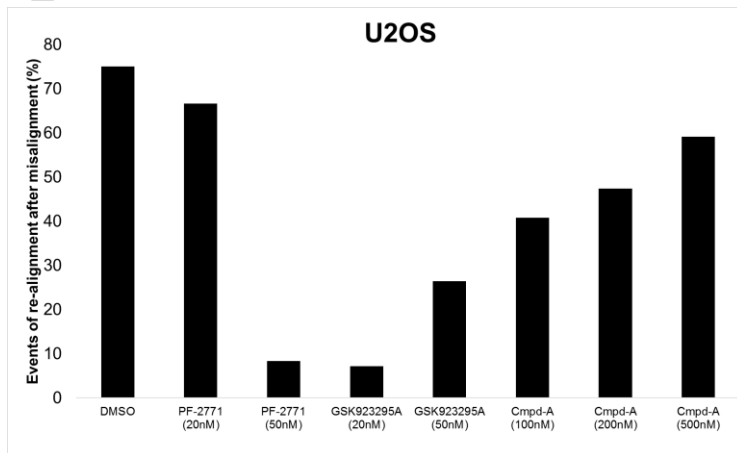
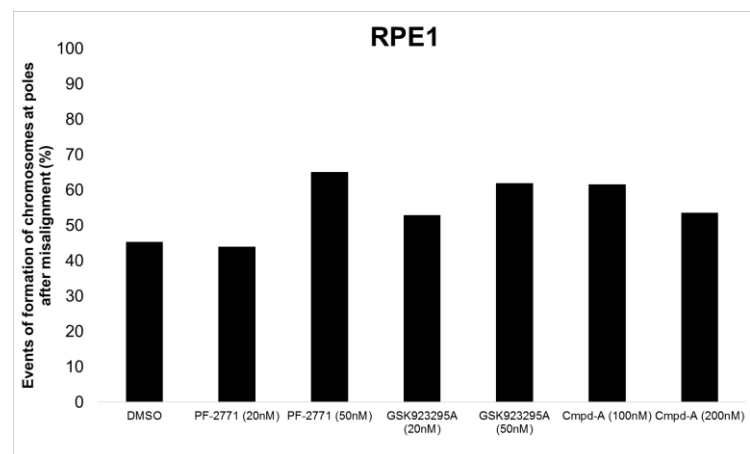
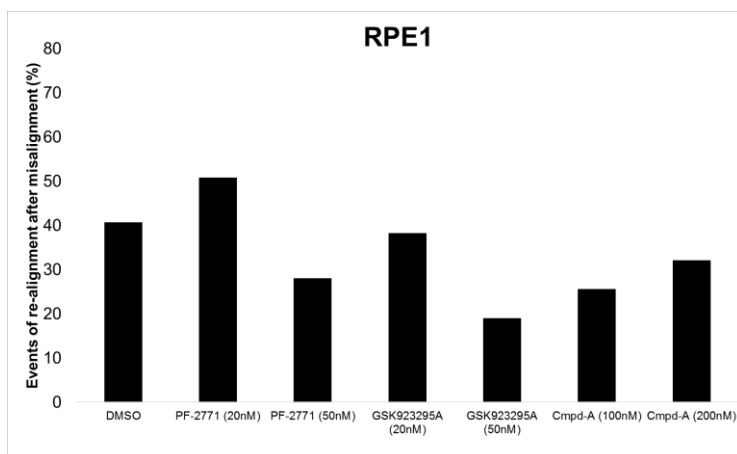


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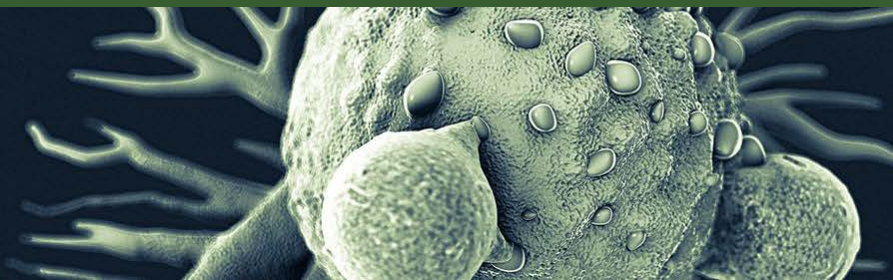


Supplementary Figure 7 – Treatment with CENP-E inhibitors induces mitotic exit through cohesion fatigue and anaphase.

Selected time frames of representative HeLa cells treated with **(A)** DMSO or **(B)** PF-2771 (10nM) showing representative examples of cohesion fatigue and anaphase, respectively. **(C)** Selected time-frames of maximum intensity projections of U2OS cells treated with Cmpd-A (100nM). Insets represent 3X magnifications of selected regions. Red arrowheads indicate single chromatids; yellow arrowheads indicate chromosome fragments (consistent with cohesion fatigue) and blue arrows indicate paired sister chromatids organized as chromosomes.

A**B****C**

Supplementary Figure 8 – CENP-E is required for chromosome re-alignment. Percentage of alignment events after misalignment (left graph) and percentage of cells that generate chromosomes at poles after misalignment (right graph) for **(A)** HeLa, **(B)** U2OS or **(C)** RPE1 cells.



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Abstract:

Syrjala KL, Abrams JR, Storer B, Heiman JR. Prospective risk factors for five-year sexuality late effects in men and women after haematopoietic cell transplantation. *Bone Marrow Transplant* 2006; **37**(Suppl 1): S4 (abstract 107).

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