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Genetic disruption of aurora B uncovers an essential role for aurora C during early mammalian development

Gonzalo Fernández-Miranda[1,*], Marianna Trakala[1], Javier Martín[2], Beatriz Escobar[1], Alejandra González[1], Norbert B. Ghyselinck[3], Sagrario Ortega[2], Marta Cañamero[4], Ignacio Pérez de Castro[1] and Marcos Malumbres[1,†]

SUMMARY

Mitosis is controlled by multiple kinases that drive cell cycle progression and prevent chromosome mis-segregation. Aurora kinase B interacts with survivin, borealin and incenp to form the chromosomal passenger complex (CPC), which is involved in the regulation of microtubule-kinetochore attachments and cytokinesis. Whereas genetic ablation of survivin, borealin or incenp results in early lethality at the morula stage, we show here that aurora B is dispensable for CPC function during early cell divisions and aurora B-null embryos are normally implanted. This is due to a crucial function of aurora C during these early embryonic cycles. Expression of aurora C decreases during late blastocyst stages resulting in post-implantation defects in aurora B-null embryos. These defects correlate with abundant prometaphase figures and apoptotic cell death of the aurora B-deficient inner cell mass. Conditional deletion of aurora B in somatic cells that do not express aurora C results in chromosomal misalignment and lack of chromosome segregation. Re-expression of wild-type, but not kinase-dead, aurora C rescues this defect, suggesting functional overlap between these two kinases. Finally, aurora B-null cells partially arrest in the presence of nocodazole, suggesting that this kinase is not essential for the spindle assembly checkpoint.

KEY WORDS: Aurora kinase B, Aurora kinase C, Cancer target, Mitosis, Mouse development, Spindle assembly checkpoint

INTRODUCTION

Progression through the cell cycle requires the controlled activation of different families of kinases that regulate diverse cellular processes required for cell division. Early work in *Drosophila* led to the identification of aurora mutants, which carry a loss-of-function mutation in a serine/threonine kinase essential for centrosome separation and the formation of bipolar spindles (Glover et al., 1995). A single aurora protein exists in budding (increase-inploidy 1; Ipl1) or fission (Ark1) yeast, whereas two family members, aurora A and aurora B, are present in worms, flies and frogs. Three different aurora family members, known as aurora A, B and C, exist in mammals (Nigg, 2001). Aurora B and C are close paralogs that probably arose from a cold-blooded vertebrate common ancestor (Brown et al., 2004).

Aurora kinases participate in multiple processes during the mammalian cell cycle (Carmena and Earnshaw, 2003). Aurora A is required for building a bipolar spindle regulating centrosome separation and microtubule dynamics (Barr and Gergely, 2007; Giet et al., 2005). Aurora B belongs to the chromosome passenger complex (CPC) that localizes to the kinetochores from prophase to metaphase and to the central spindle and midbody in cytokinesis (Carmena and Earnshaw, 2003; Ruchaud et al., 2007). Other mammalian CPC proteins include the inner centromere protein incenp, survivin and borealin, which control the targeting, enzymatic activity and stability of aurora B (Ruchaud et al., 2007). The CPC is one of the most upstream regulators of centromere and kinetochore function, being responsible for the recruitment to the kinetochore and centromere of a growing number of proteins, including inner centromeric proteins (Sgo1, Sgo2, MCAK), regulators of the microtubule-kinetochore interaction [such as Ndc80 (HEC1), CENP-E or Plk1 among others] or proteins involved in the spindle assembly checkpoint (SAC; such as Mad2, BubR1 or Mps1) (for a review, see Kelly and Funabiki, 2009). Some of these molecules, including Ndc80, Dam1 and MCAK, are aurora B substrates suggesting a crucial role for the CPC in the destabilization of aberrant microtubule-to-kinetochore attachments and the SAC-dependent delay until these defects are corrected (Nezi and Musacchio, 2009). During cytokinesis, aurora B is localized to the midbody remnant where its local inactivation is crucial for completion of abscission (Guse et al., 2005; Steigemann et al., 2009). Aurora B also participates in mitotic phosphorylation of Ser10 and, probably, Ser 28 in histone H3. These events seem to be necessary for chromosome condensation although the correlation between H3S10 phosphorylation and the condensation of chromosomes is not fully established (Johansen and Johansen, 2006; Nowak and Corces, 2004; Prigent and Dimitrov, 2003). Less is known about aurora C, which can also bind members of the CPC (Li et al., 2004) and its ectopic expression can rescue aurora B loss of function in cultured cells (Sasai et al., 2004; Slattery et al., 2009; Slattery et al., 2008; Yan et al., 2005). Although aurora C is known to have a specific role in spermatogenesis (Dieterich et al., 2007; Kimmins et al., 2007; Tang et al., 2006) and oogenesis (Sharif et al., 2010), its physiological relevance in the regulation of mitosis is not well understood.

In mammals, the CPC seems to be required for early embryonic development and embryos degenerate by E2.5-3.5 in the absence of the CPC components survivin (Uren et al., 2000), incenp (Cutts

[1]Cell Division and Cancer Group, Spanish National Cancer Research Center (CNIO), E-28029, Madrid, Spain. [2]Transgenic Mice Unit, CNIO, 28029 Madrid, Spain. [3]Institut de Genetique et de Biologie Moleculaire et Cellulaire, 67404 Strasbourg, France. [4]Comparative Pathology Unit, CNIO, 28029 Madrid, Spain.

*Present address: Molecular Medicine Program, Institute for Research in Biomedicine (IRB Barcelona), Parc Científic de Barcelona, C/ Baldiri Reixac 10. E-08028 Barcelona, Spain

†Author for correspondence (malumbres@cnio.es)

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et al., 1999) or borealin (Yamanaka et al., 2008). We report here that aurora B-null embryos develop normally during the early cell divisions and die only after implantation, suggesting the presence of normal cell cycles in the early embryonic cell divisions in the absence of aurora B. Interestingly, aurora C is highly expressed during the early cell divisions and it seems to be responsible for CPC function in these pre-implantation embryos. After implantation, aurora B-defective embryos and somatic cells accumulate prometaphase/metaphase figures eventually leading to apoptotic cell death. The cellular defects induced by acute elimination of aurora B in somatic cells can be rescued by re-expressing active aurora C. Finally, we also show that aurora B-null cells can still arrest in the absence of microtubules, suggesting that this protein is not essential for the SAC.

MATERIALS AND METHODS

Aurora B-targeted mice

The conditional targeting construct was assembled by flanking exons 2-6 of the murine *Aurkb locus* with loxP sequences (Fig. 1A). An additional knock-in that expresses the β-galactosidase (*lacZ*) gene was generated (Fig. 1 and see Fig. S1 in the supplementary material) following the FLEx strategy as reported previously (Schnutgen et al., 2003). Tg.pCAG–Flpe (Rodriguez et al., 2000) or Tg.CMV-Cre (Schwenk et al., 1995) transgenic mice were used for ubiquitous expression of Flp or Cre recombinases. All animals were maintained in a mixed 129/Sv (25%) × CD1 (25%) × C57BL/6J (50%) background following the animal care standards of the institution (Ethical Committee ISCIII). Genotyping protocols are available upon request (see also Fig. S1 in the supplementary material). Immunohistochemical examination of the tissues and pathologies analyzed were performed using specific antibodies against aurora B (Abcam), aurora C (Invitrogen), phospho-p53 (Ser15; Cell Signaling), γ-H2AX (Ser139; Millipore), active caspase 3 (R&D Systems), cyclin B1 (Millipore), Sox2 (Millipore) and GATA4 (Santa Cruz Biotechnology). Other routine histological techniques and the quantification of DNA ploidy in sections was performed as described previously (Garcia-Higuera et al., 2008).

Culture and transfection of embryos

Fertilized embryos at E1.5-2.5 were collected by flushing the uteri of pregnant females with M2 medium (Sigma) and cultured in vitro in potassium simplex optimized medium (KSOM; Chemicon International). To generate outgrowths of the inner cell mass, blastocyts were transferred into gelatinized 96-well plates and cultured in embryonic stem (ES) cell medium [DMEM + GlutaMAX, 15% fetal bovine serum (FBS), non-essential amino acids] for several days. Two-cell embryos were incubated with ZM447439 drug (abbreviated as ZM1, Tocris Bioscience) and cultured in vitro for 2 days. For RNA interference in embryos, pronuclei were injected (Leica DMIRE2/ASTP) with pA70 plasmids (a modified Gateway-compatible version of pSuper-Retro plasmid) expressing either shAurB, shAurC or shLuciferase interfering RNAs at a final DNA concentration of 16 ng/μl. In all cases, a H2B-EGFP-expressing plasmid (4ng/μl) was co-injected. The targeted sequences for aurora B and C are the following: shAurB-1, 5′-GTTGGCTGAGAACAAGAGT-3′; shAurB-2, 5′-GAGCCGTTTCATCGTGGCA-3′; shAurB-3, 5′-CAAGAGTC-AGGGCTCCACT-3′; shAurC-1, 5′-GGAAAATCATTTCATCGTG-3′; shAurC-2, 5′-CCAGGAAGCATTTCACCAT-3′; and shAurC-3, 5′-GCTTCTTAGGTACCATCCT-3′. Total RNA was isolated using Trizol (Invitrogen) and gene expression was quantified with the SuperScript III Platinum Assay Kit (Invitrogen), according to the manufacturer's instructions, in a BioRad iCycler Real-Time PCR apparatus. Data analysis was performed using the iQ5 v. 2.0 software (BioRad).

Primary mouse embryo fibroblasts (MEFs)

MEFs were obtained from E14.5 embryos and cultured using routine protocols (Garcia-Higuera et al., 2008). The adenoviruses expressing GFP or the Cre recombinase (Ad5 CMV-Cre) were obtained from The University of Iowa (Iowa City, IA, USA). Infection was carried out for 2 days in cell culture synchronized in G0 by serum deprivation and confluence. DNA content was analyzed by flow cytometry (FACS; Becton-Dickinson). The duration of mitosis was scored by videomicroscopy using Deltavision apparatus. Nocodozole (Sigma) was used at 3.5 μM to completely prevent the formation of microtubules. The mouse aurora C cDNA was amplified by RT-PCR (Superscript II Reverse Transcriptase, Invitrogen) from mouse testis RNA and cloned as GFP- or V5-fusions as described previously (Fernandez-Miranda et al., 2010). The aurora C kinase-dead mutant (K45M) was prepared using the Quick-Change Site Mutagenesis Kit (Invitrogen). The wild-type and kinase-dead (D205A) aurora B cDNAs were described previously (Fernandez-Miranda et al., 2010). For rescue experiments, primary MEFs were first transduced with Cre adenovirus in G0 and 48 hours later they were transfected with GFP-aurora B/C constructs using the Amaxa nucleofection technology (Lonza AG) and seeded in 10% FBS to start a new cell cycle. Mad2 expression was knocked down using specific small interference (si) RNAs from Dharmacon.

Immunofluorescence and protein analysis

For immunofluorescence, embryos were fixed with cold methanol or 5% paraformaldehyde (PFA), rinsed with M2 medium, washed in PBS containing 0.1% bovine serum albumin (BSA; Sigma) and incubated with 0.1% Triton X-100 for permeabilization. MEFs were fixed with 4% PFA and permeabilized with 0.15% Triton X-100. Embryos or MEFs were then blocked with 3% BSA and incubated with anti-centromere antibody (ACA; Antibodies Incorporated) or primary antibodies against α-tubulin (Sigma), γ-tubulin (Sigma), aurora B (Abcam or BD Biosciences), BubR1 (a gift from S. S. Taylor, University of Manchester, UK), Mad2 [a gift of E. Salmon (University of North Carolina, USA) or K. Wassmann (CNRS, France)], cyclin B1 (Santa Cruz Biotechnology), incenp (a gift of C. Rodriguez, Hospital Puerta del Mar, Spain) and phospho-histone H3 Ser10 (P-H3; Upstate Biotechnologies). The corresponding secondary antibodies were from Molecular Probes (Invitrogen). Images were obtained using a confocal ultra-spectral microscope (Leica TCS-SP5).

For immunodetection in protein lysates, cells were lysed in RIPA buffer supplemented with protease and phosphatase inhibitory cocktails (Sigma). Proteins were separated on SDS-PAGE, transferred to nitrocellulose membranes (BioRad), and probed using specific antibodies against aurora B (BD Transduction and Abcam), incenp (Abcam), Mad2 (MBL), GFP (Roche) and α-tubulin (Sigma). For immunoprecipitation, total protein lysates were pre-cleared with protein-G-agarose beads (Amersham) and incubated with mouse anti-GFP (Roche). Immunoprecipitates were then washed three times in RIPA buffer and used for immunodetection.

RESULTS

Generation of aurora B mutant mice

To generate an *Aurkb* null allele we first flanked exons 2-6 with loxP sequences using an frt-neo (neomycin-resistant gene)-frt cassette for selection purposes as indicated in Fig. 1A. In addition, we also generated a knock-in allele, *Aurkb*(Z), in which expression of the endogenous *Aurkb* gene is replaced by *lacZ* transcripts encoding β-galactosidase (Fig. 1B,C and see Fig. S1 in the supplementary material). The neomycin-resistant cassettes were removed by crossing with transgenic mice expressing the Flp recombinase (see Materials and methods) resulting in the conditional *Aurkb*(lox) or *Aurkb*(lox^Z) alleles. Germline deletion of exons was achieved by additional crosses with Tg.CMV-Cre transgenic mice to generate the *Aurkb*(–) or *Aurkb*(Z) alleles. These two alleles were null for aurora B expression, as detected by immunofluorescence (see below), and led to similar phenotypes.

Lack of one allele of aurora B did not result in major alterations during the proliferation of cultured cells or during development. *Aurkb*(+/–) embryonic fibroblasts proliferated well in culture and did not display obvious defects during cell cycle progression (see Fig. S2 in the supplementary material). Similarly, *Aurkb*(+/–) mice

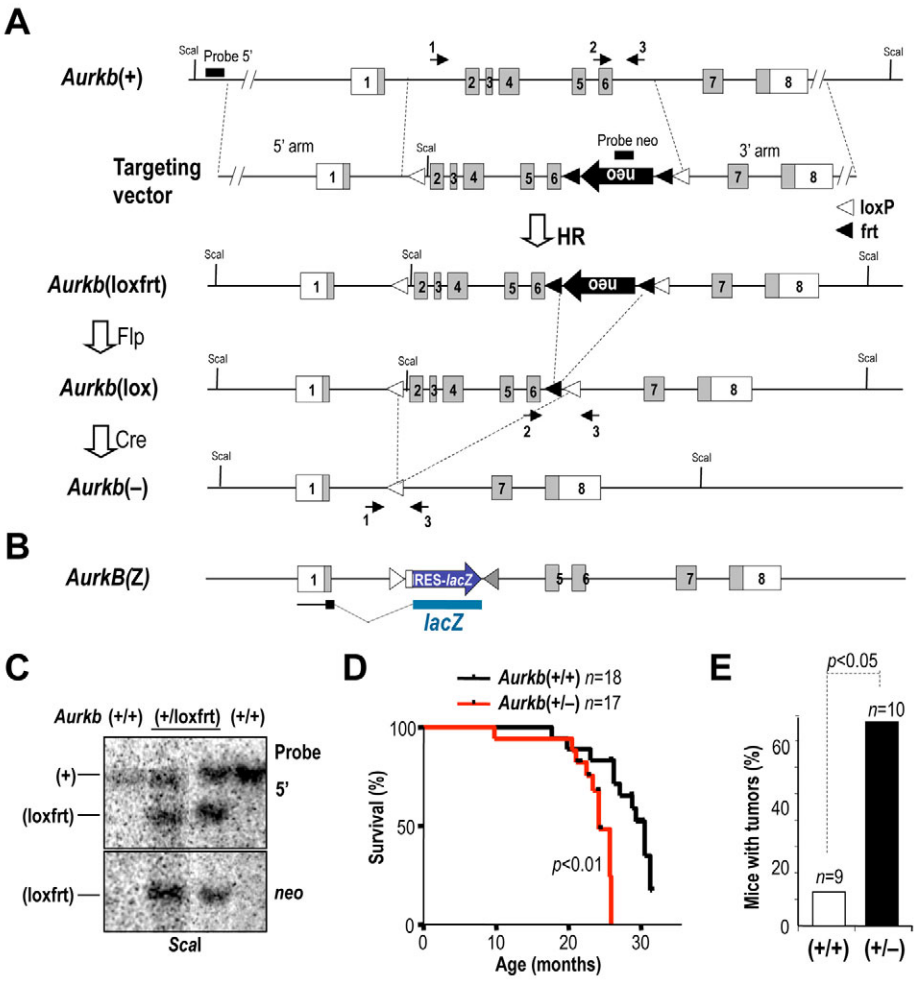

Fig. 1. Characterization of aurora B-deficient mice. (**A**) Schematic of the *Aurkb* alleles used in this study. The mouse *Aurkb* locus encoding aurora B contains eight exons (boxes) containing non-coding (open boxes) or protein-coding (gray boxes) sequences. Wild-type loxP (white triangles) and frt (black triangles) sites are used to flank aurora B exons or the *neo*-resistance cassette (black) in the targeting vector. The neo cassette is eliminated in vivo by crossing *Aurkb*(+/loxfrt) mice with transgenic mice expressing the Flp recombinase. Further excision of exons 2-6 is mediated by expression of the Cre recombinase resulting in the *Aurkb*(–) null allele. The position of oligonucleotides used for genotyping is shown as numbered arrows (see Fig. S1 in the supplementary material). HR, homologous recombination. (**B**) The *Aurkb*(Z) allele contains an IRES-*lacZ* cassette (blue) instead of aurora B exons 2-4. This cassette contains poly-A sequences for termination of transcription but it does not include any promoter sequence. Instead, it is preceded by a spliced acceptor resulting in the expression of β-galactosidase (encoded by the *lacZ* gene) driven by the aurora B regulatory sequences. Wild-type (white triangles) and mutant (gray triangles) loxP sites are flanking this cassette as a consequence of the targeting strategy (see Fig. S1 in the supplementary material for details). (**C**) Southern blot analysis of recombinant embryonic stem (ES) cells showing two *Aurkb*(+/loxfrt) clones that underwent HR. DNA was digested with *Sca*I and hybridized with the probe 5′- (see Fig. 1A) or *neo*-specific sequences. The corresponding analysis for the *Aurkb*(Z) allele is shown as in Fig. S1 in the supplementary material. (**D**) Survival curve of *Aurkb*(+/+) and *Aurkb*(+/–) mice indicating a slight but significant reduction in the life span of these mutant mice. (**E**) This lethality is accompanied by a significant increase in the percentage of tumor-bearing mice in 24-month-old mice. The specific pathologies found in these animals are shown in Fig. S3A in the supplementary material. *n* indicates the number of mice of each genotype analyzed in these assays.

developed normally and were fertile. However, a few *Aurkb*(+/–) males (16.6% incidence) developed oligospermia by 12 months of age (see Fig. S3 in the supplementary material), in agreement with a relevant role of aurora B during spermatogenesis (Kimmins et al., 2007). In addition, *Aurkb*(+/–) mice displayed a shorter life span owing to an increase in spontaneous pathologies (Fig. 1D). In particular, these mutant mice displayed a significant increase in the number of tumors, including pituitary and liver adenocarcinomas or skin papillomas that were not observed in the control group (Fig. 1E and see Fig. S3 in the supplementary material). Lack of one allele of aurora B resulted in a slight, although not significant, protection against 3-MC-induced fibrosarcomas or DMBA+TPA-induced skin tumors (see Fig. S4 in the supplementary material). These results are similar to those obtained with other models with alteration in specific mitotic regulators suggesting that genomic instability caused by these mutations might increase tumor development in old mice but might be protective against rapid, induced tumors due to proliferative defects (Garcia-Higuera et al., 2008; Weaver and Cleveland, 2009).

Genetic ablation of aurora B does not disturb early embryonic divisions

To generate homozygous mutants, we intercrossed *Aurkb*(+/–) or *Aurkb*(+/Z) mice and analyzed their progeny. No homozygous mutant was born and no homozygous embryos were observed at

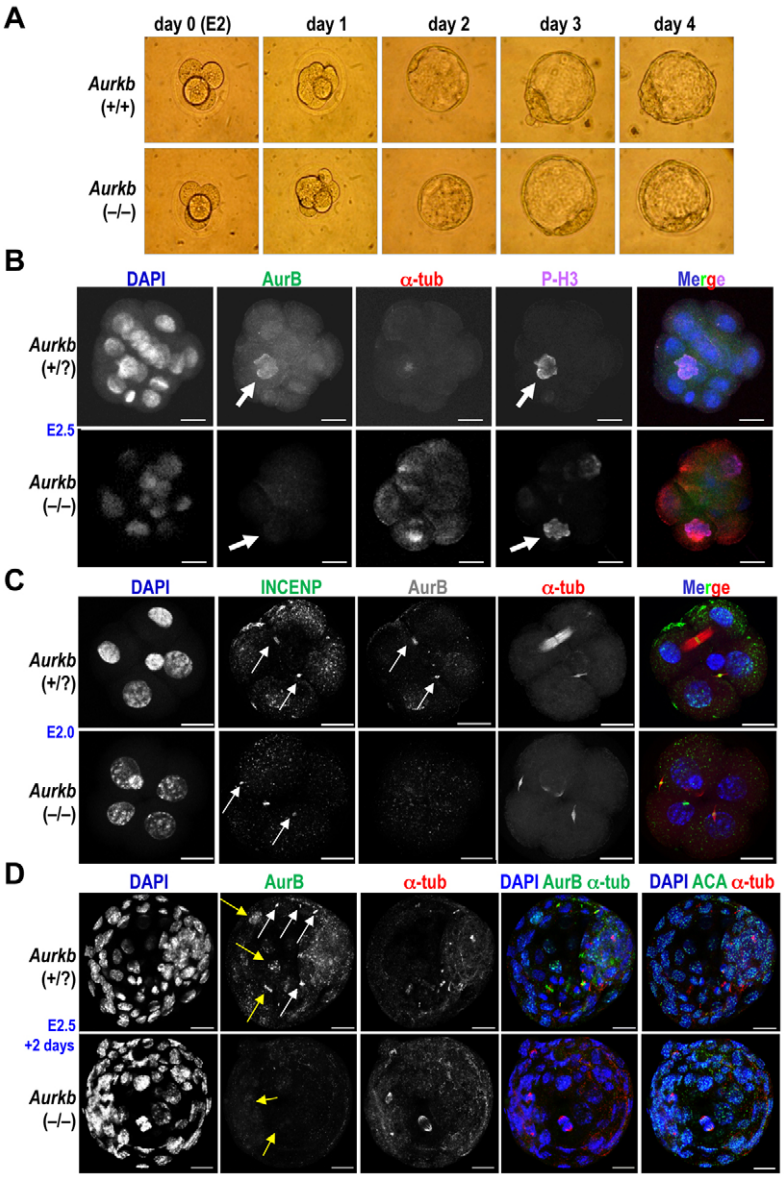

Fig. 2. Normal development of pre-implantation embryos lacking aurora B. (**A**) E2 embryos were isolated from intercrosses between *Aurkb*(+/–) mice, cultured for four additional days and genotyped by PCR. (**B**) Colocalization of aurora B (AurB) with phospho-histone H3 (P-H3) in mitotic cells of E2.5 pre-implantation embryos. In the absence of aurora B, mitotic cells are also present in the same frequency and display normal staining for P-H3. Arrows indicate P-H3-positive cells. (**C**) Incenp is also properly localized (arrows) in early embryos in the presence or absence of aurora B. (**D**) Wild-type and aurora B-null embryos form blastocysts in vitro and display normal mitotic figures (yellow arrows) and cytokinesis bridges (white arrows) despite of the absence of aurora B. The (+/?) genotype indicates either (+/+) or (+/–). α-tubulin (α-tub) staining is shown in red and DAPI (DNA) in blue. ACA, anti-centromeric antigen antibody. Scale bars: 20 μm.

mid gestation, suggesting early embryonic lethality (see Table S1 in the supplementary material). Because genetic ablation of the other CPC components, incenp, borealin or survivin, prevents embryonic cell divisions as early as E2.5 (Cutts et al., 1999; Uren et al., 2000; Yamanaka et al., 2008), we decided to isolate fertilized embryos at E2.0. By this stage, most embryos were at the 4-cell stage (Fig. 2A). After four additional days in culture, wild-type embryos formed normal morulas and blastocysts. Unexpectedly, *Aurkb*(–/–) embryos also formed blastocysts in vitro without any evident sign of decreased size or cellular death. We tested whether this kinase is expressed at these developmental stages and we observed that this protein is detected at the expected cellular structures (centromeres, spindle midzone and cytokinesis bridges) in early *Aurkb*(+/?) [either wild-type or *Aurkb*(+/–)] embryos. Aurora B, however, was not detected in fertilized *Aurkb*(–/–) embryos at the 2-cell stage (see Fig. S5 in the supplementary material) or at later developmental phases (Fig. 2B-D). Thus, the lack of defects in *Aurkb*(–/–) morulas or blastocysts is not a consequence of uncontrolled expression of aurora B or maternal contribution but rather an indication of the dispensability of aurora B during cell division at these stages. Intriguingly, aurora B-null morulas displayed normal phosphorylation of histone H3 (P-H3; Fig. 2B) and the expected localization of CPC components such as incenp, which colocalizes with aurora B in wild-type and aurora B-null mitotic figures (n=12 per genotype; Fig. 2C). After two days in culture, wild-type and *Aurkb*(–/–) blastocysts displayed similar size, cell number and P-H3 staining despite the absence of aurora B in mutant embryos (Fig. 2D and see Fig. S6 in the supplementary material).

Lack of aurora B prevents proper chromosome segregation in the inner cell mass

After a few extra days in culture, wild-type blastocysts hatched from the zona pellucida, attached to the culture dish and generated a normal and proliferative (as indicated by P-H3 staining) inner cell mass (ICM) outgrowth surrounded by trophoblast giant cells (Fig. 3A). Lack of aurora B resulted in a reduced number of trophoblasts with altered nucleus size and morphology (see Fig. S7 in the supplementary material) and deficient ICM outgrowth (Fig. 3A).

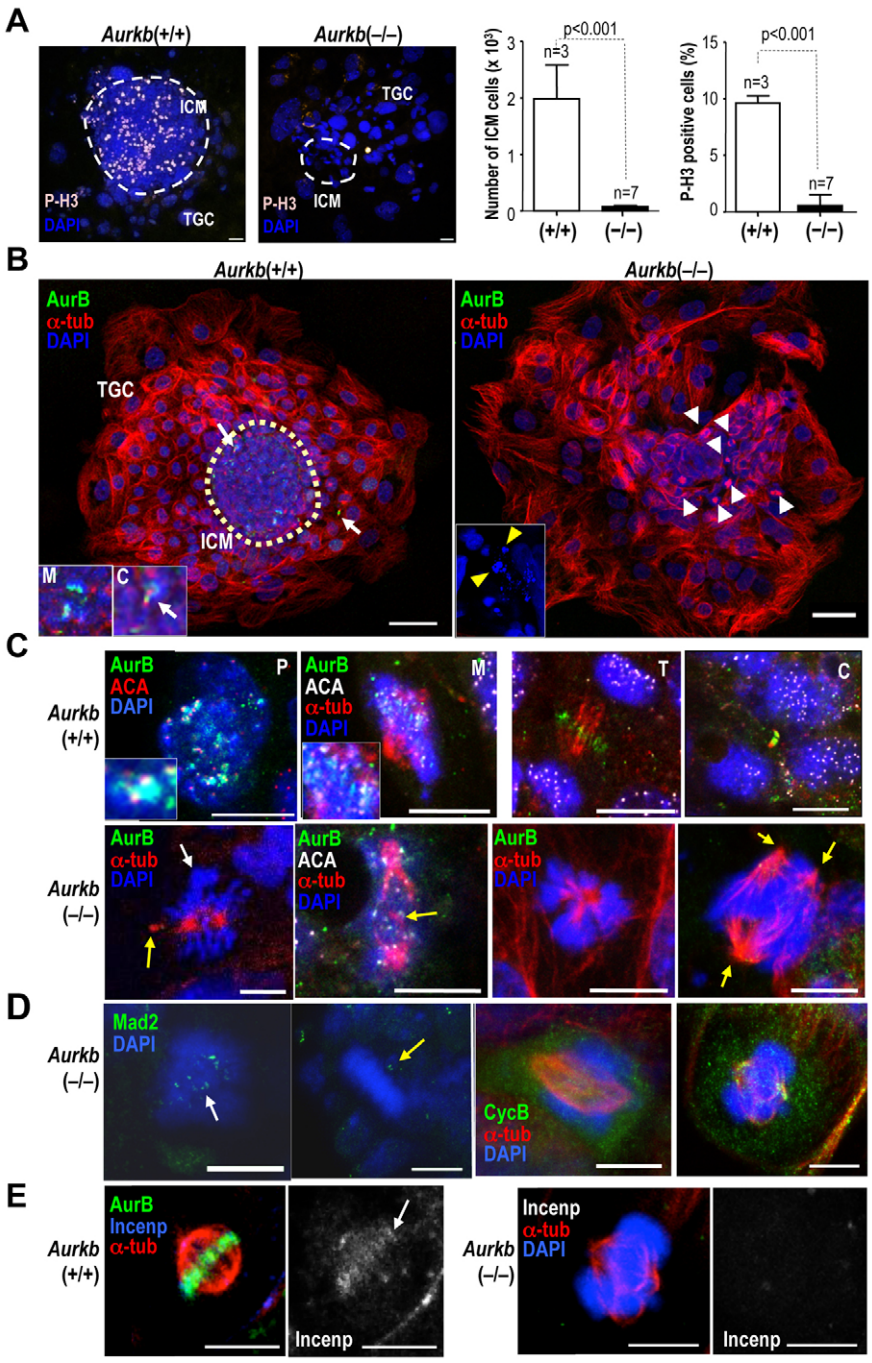

Fig. 3. Lack of aurora B results in mitotic defects in the inner cell mass. (**A**) Genetic ablation of aurora B results in abnormal inner cell mass (ICM; encircled by dashed line) outgrowths in culture. Whereas *Aurkb*(–/–) embryos exhibit abundant trophoblast giant cells (TGC), the ICM outgrowth is dramatically reduced and phospho-histone H3 (P-H3) signal is almost undetectable. Error bars represent s.d. (**B**) Aurora B (green) is present in mitotic and cytokinesis figures in wild-type (arrows and insets) but not in *Aurkb*(–/–) embryos. In the absence of aurora B, abundant mitotic (white arrowheads) and apoptotic (yellow arrowheads) figures are observed in the ICM outgrowth. M, metaphase; C, cytokinesis. Scale bars: 50 μm. (**C**) Mitotic distribution in ICM outgrowths. In wild-type cells, aurora B (green) localizes internal to anti-centromeric antibody (ACA) spots (red or white) during prophase (P) or metaphase (M) owing to its localization to the inner centromere. Aurora B moves to the central spindle during telophase (T) or to the cytokinesis bridge during cytokinesis (C). In *Aurkb*(–/–) embryos, aurora B is not detected and these cells display aberrant bipolar spindles with misaligned chromosomes (white arrow), as well as monopolar or multipolar spindles. Note the presence of multiple poles or isolated α-tubulin spots (yellow arrows). Scale bars: 10 μm. (**D**) *Aurkb*(–/–) cells show the presence of Mad2 (green) at the kinetochores during prometaphase (white arrow) or in misaligned chromosomes in incomplete metaphases (yellow arrow). Cyclin B1 is also present in these mitotic figures showing a diffuse expression in some cases accompanied by enrichment at the poles. Scale bars: 10 μm. (**E**) Although incenp is properly localized at the centromeres (arrow), midbodies or cytokinesis bridges (not shown) in wild-type cells, no incenp signal is observed in aurora B-null cells. Scale bars: 10 μm. For these assays, embryos were isolated at E2.5 and cultured in vitro for five (B-E) or eight (A) additional days.

Immunofluorescence of these mutant cells detected numerous ICM cells in prometaphase (PM) or metaphase (M) that were only rarely observed in control cultures (Fig. 3B). Aurora B-deficient cells displayed abnormal spindles with a strong concentration of α-tubulin in the poles and lack of bipolar fibers (Fig. 3C). Multipolar spindles were also frequently observed, suggesting either a defect in organizing bipolar spindles or the presence of polyploid cells. All these mitotic figures displayed misaligned chromosomes (Fig. 3C-E) in the presence of Mad2 (Mad2l1 – Mouse Genome Informatics) and cyclin B1 (Fig. 3D). Finally, incenp is properly located at the metaphase plate and midbodies of wild-type, but not mutant, cells (Fig. 3E), suggesting that aurora B deficiency results in impaired CPC function in ICM outgrowths but not during earlier developmental stages.

Genetic ablation of aurora B results in mitotic aberrations and lethality after implantation

Aurora B-negative embryos could be found at distinct post-implantation stages (15.6% at E6.5, 26% at E7.5 and 16% at E9.5; see Table S1 in the supplementary material; note that embryonic structures were absent in a percentage of deciduas suggesting additional dead embryos after implantation). All these implanted aurora B-deficient embryos displayed small size and a progressive reduction in the number of cells (Fig. 4 and see Fig. S8 in the supplementary material). Histological examination of E6.5 embryos revealed defective structures in aurora B-null embryos accompanied with hemorrhage in the ectoplacental cone and frequent edemas and apoptotic cells (Fig. 4A,B). This atrophy did not seem to be due to a defect in specific cell lineages as Sox2-

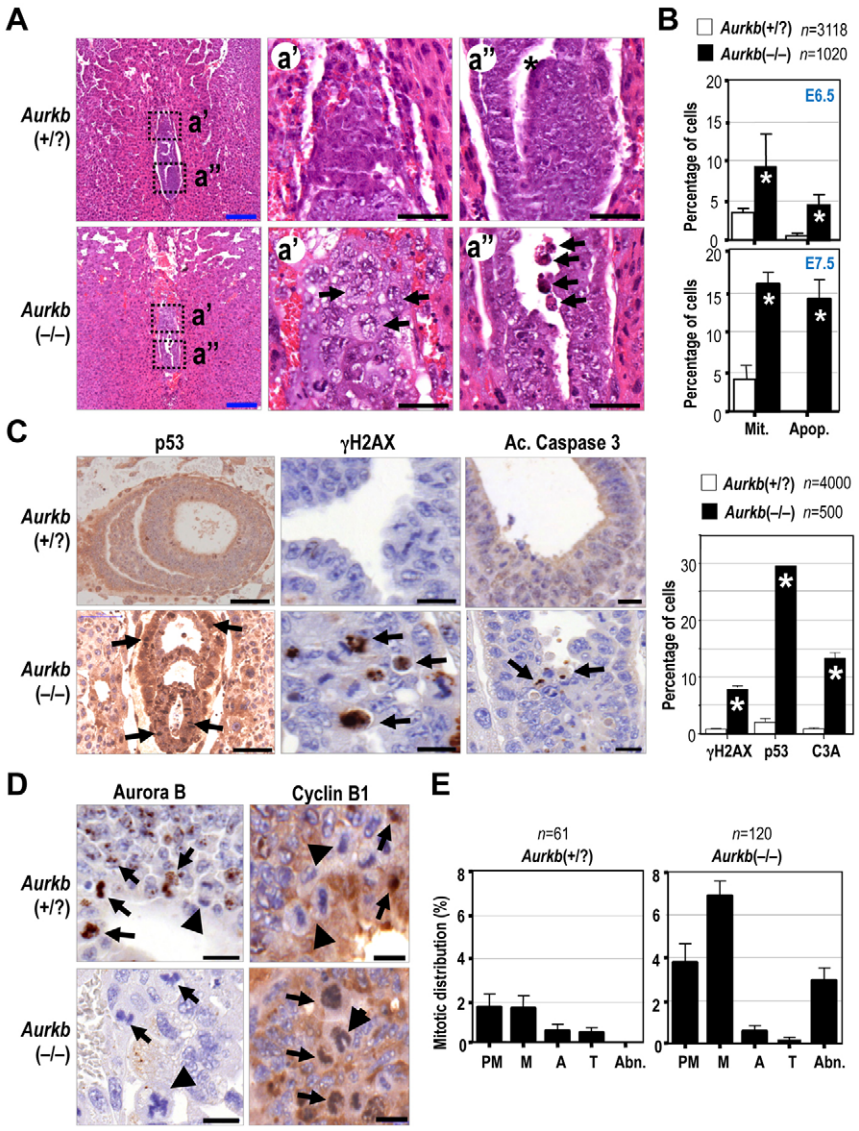

Fig. 4. Post-implantation lethality in aurora B-deficient embryos. (**A**) Abnormal embryonic development of aurora B-null embryos by E6.5. Aberrant ectoplacental cones with degenerative cells and hemorrhage are frequently observed in aurora B-null embryos (A′; arrows). These mutant embryos also display apoptotic cells in the exocoelomic cavity (A″; asterisk). Scale bars: 500 μm (blue) or 100 μm (black). (**B**) Aurora B-null embryos at E6.5-7.5 are accompanied by significant increase in mitotic (Mit.) and apoptotic (Apop.; arrows in A″) figures. (**C**) Increase in the number of cells positive for p53, γH2AX or active caspase 3 (C3A) immunostaining (positive cells are indicated by black arrows) in the absence of aurora B. Scale bars: 100 μm (p53) or 20 μm (γH2AX and C3A). (**D**) Aurora B is readily detectable in mitotic figures (arrows) of *Aurkb*(+/?) but not *Aurkb*(–/–) cells. As a control for specific aurora B staining, an anaphase/telophase cell negative for aurora B chromosomal staining is shown (arrowhead, top left panel). Abnormal mitotic figures are also observed in aurora B-null embryos (arrowhead, bottom left panel). In wild-type cells, cyclin B1 is present in prometaphase figures (arrow) but not in advanced metaphase or anaphase/telophase stages (arrowheads). Normal (arrows) or abnormal (arrowhead) mitotic figures in *Aurkb*(–/–) embryos display a positive staining for cyclin B1. Scale bars: 20 μm. (**E**) Quantification of the distribution of mitotic cells in the different phases of mitosis. Abnormal mitotic figures that are not observed in wild-type embryos mostly correspond to cross-shaped mitosis as shown in D. For all graphs, asterisks indicate $P<0.001$ or $P<0.05$ (mitosis at E6.5), n is the number of cells counted in these embryos and error bars represent s.d.

(epiblast) and Gata4- (primitive endoderm) positive cells were present in both wild-type and mutant embryos (see Fig. S8 in the supplementary material).

Aurora B-null embryos displayed a significant increase in mitotic and apoptotic cells at E6.5-7.5 (Fig. 4B). Many of these cells displayed positive staining for γH2AX (H2afx – Mouse Genome Informatics), p53 (Trp53 – Mouse Genome Informatics) and active caspase 3 (C3A), suggesting DNA damage and activation of the p53 pathway in these cells (Fig. 4C). Interestingly, most of these mitotic figures represented cells in PM and M, including abnormal PM/M figures with misaligned chromosomes (Fig. 4D,E). Most of these mitotic cells displayed a positive signal for cyclin B1, suggesting that anaphase promoting complex (APC/C)-Cdc20 has not been activated. By E9.5, most embryos were degenerated and only displayed either mitotic or apoptotic cells (see Fig. S8 in the supplementary material).

Aurora C is sufficient to drive mitotic progression during early embryonic development

As lack of the other CPC components, incenp, survivin or borealin, results in early lethality by E2.5 (Cutts et al., 1999; Uren et al., 2000; Yamanaka et al., 2008), we wondered whether aurora B could be dispensable owing to the presence of other aurora kinases during early embryonic development. Indeed, aurora C has been shown previously to bind other CPC components when overexpressed in specific cell lines (Sasai et al., 2004; Slattery et al., 2009; Slattery et al., 2008; Yan et al., 2005). As depicted in Fig. 5A,B, aurora C was detected in early embryos (2-cell stage and morulas) and in testis but it was not expressed in late embryos, as examined by RT-PCR or immunostaining in sections. Further analysis of aurora C expression in adult tissues indicated a significant expression in testis (Fig. 5B), as reported previously (Hu et al., 2000; Kimmins et al., 2007; Tang et al., 2006). Similar data indicating expression of aurora C in early embryos, but not in later stages or most somatic tissues, can be obtained from published expression profiles (Hamatani et al., 2004) and public databases (see Fig. S9 in the supplementary material). Aurora C is also expressed in interphasic brain glial cells but we did not detect significant expression of this protein in most of the other tissues analyzed in a human tissue array (see Fig. S9 in the supplementary material).

Next, we treated embryos with a small molecule inhibitor, ZM447439 (frequently abbreviated as ZM1), that is able to efficiently inhibit both aurora B and C kinases [IC_{50} aurora B 50

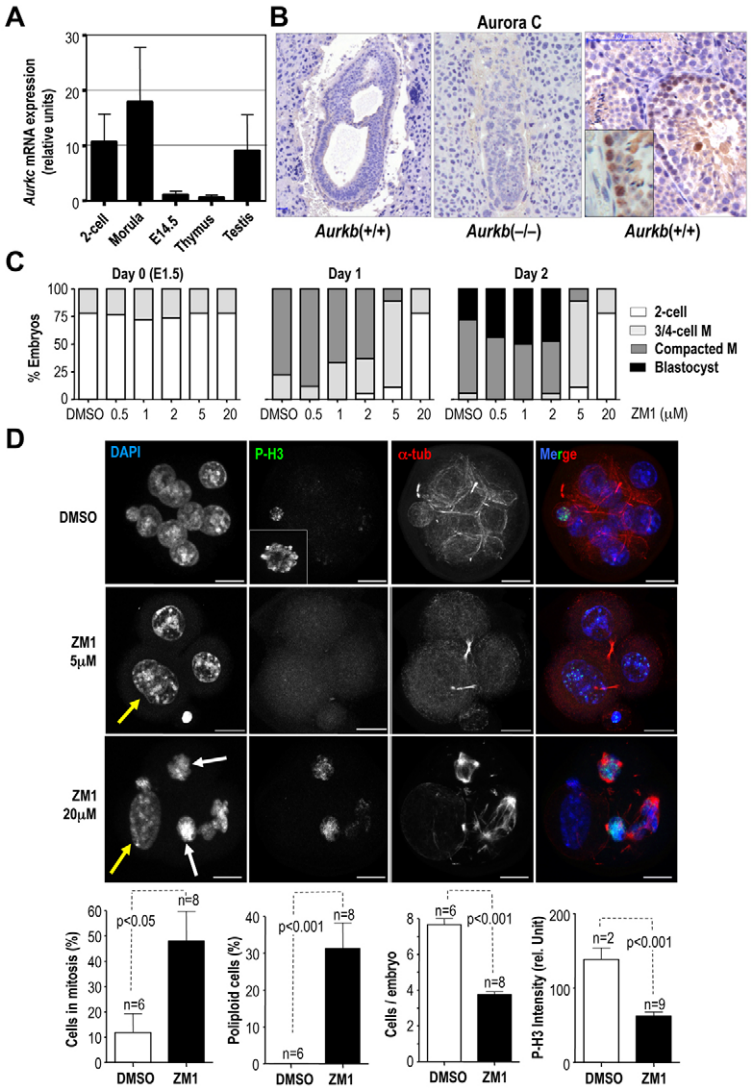

Fig. 5. Aurora C is expressed in early zygotes and cell division is sensitive to aurora B/C small molecule inhibitors during early cell divisions. (**A**) Expression of aurora C at the 2-cell stage, morula, mid-gestation (E14.5) or adult mouse tissues as measured by real-time RT-PCR. mRNA levels were normalized relative to the expression of GADPH. (**B**) Detection of aurora C by immunohistochemistry in paraffin sections (E7.5) from wild-type (left) or aurora B-deficient (middle) post-implantation embryos indicating lack of expression at this stage. Aurora C is not detected in most adult tissues (see Fig. S9 in the supplementary material) but it is highly expressed in germ cells of the testis (right-hand panel). Inset shows a detail of aurora C-positive germ cells. (**C**) Sensitivity of embryos at the 2-cell stage (*n*=20 per group) to different doses of ZM1, a small-molecule inhibitor of aurora B and aurora C (see also Fig. S10 in the supplementary material). (**D**) Immunofluorescence analysis at day 1 indicates a significant accumulation of cells in mitosis (white arrows) or in cytokinesis, generation of polyploid cells (yellow arrows) with a subsequent reduction in the number of cells per embryo in ZM1-treated cells. Phosphorylation of histone H3 (P-H3) is significantly reduced in these ZM1-treated mitotic cells although some signal is still detected. Scale bars: 20 μm. *n* indicates the number of embryos scored in the different assays. For all graphs, error bars represent s.d.

nM; IC_{50} aurora C 250 nM (Girdler et al., 2006)]. Wild-type E1.5 (2-cell) embryos were treated with different ZM1 doses (0.5, 1, 2, 5, 20 and 100 μm) or carrier and analyzed 24 and 48 hours later. As represented in Fig. 5C and Fig. S10 in the supplementary material, ZM1 treatment from 5 to 20 μM resulted in a severe arrest at the 2 to 4-cell stage in nearly all of treated embryos. Importantly, treatment with ZM1 resulted in a phenotype similar to that observed in aurora B-deficient embryos by E7.5, including aberrant prometaphase figures with misaligned chromosomes and tetraploid cells (Fig. 5D). To explore further the possibility that aurora C is responsible for supporting cell division during the morula and early blastocyst stage, we microinjected three short hairpin interfering RNAs (shRNAs) specific for aurora B or aurora C kinases, along with a reporter plasmid that expresses the green fluorescent protein (GFP) fused to histone H2B (Fig. 6A). One day after microinjection, most embryos were at the 2-cell stage and expressed the fusion protein GFP-H2B in the nucleus of these embryonic cells (Fig. 6B). After three days in culture, most embryos injected with a shRNA against luciferase or Aurora B progressed normally forming morulas with 4-8 cells. However, most embryos injected with aurora C shRNAs or a combination of aurora B and aurora C shRNAs were arrested at the 2-cell stage (Fig. 6B). These embryos displayed a high number of mitotic figures, mostly PM or M by day 3 (Fig. 6C) as previously described in the aurora B-deficient inner cell mass. These abnormal divisions frequently resulted in chromosomal bridges and giant nuclei, suggesting a defect in cytokinesis (Fig. 6D) resulting in an arrest at the 2-4 cell stage (Fig. 6D). Taken together, these results suggest that aurora C, but not aurora B, has a crucial role in driving proper cell division during early embryonic development.

Aurora B is required for chromosome congression but it is not essential for the spindle assembly checkpoint

We took advantage of the conditional *Aurkb*(lox) allele to analyze the cellular effects of the acute deletion of aurora B in cultured cells that do not express aurora C. Primary *Aurkb*(lox/lox) MEFs were isolated from E14.5 embryos and cultured in complete medium. Aurora C was not expressed in these mid-gestation embryos or in immortal fibroblasts derived from them (Fig. 5A and see Fig. S9 in the supplementary material). Confluent MEFs were infected with adenoviruses expressing either GFP (AdGFP) or the Cre recombinase (AdCre) in the presence of low serum (0.1% FBS) and seeded in 10% FBS at low confluency 48 hours later (t=0) to allow cells to enter into a new cell cycle (Fig. 7A). Expression of Cre, but not GFP, resulted in an almost complete deletion of exons

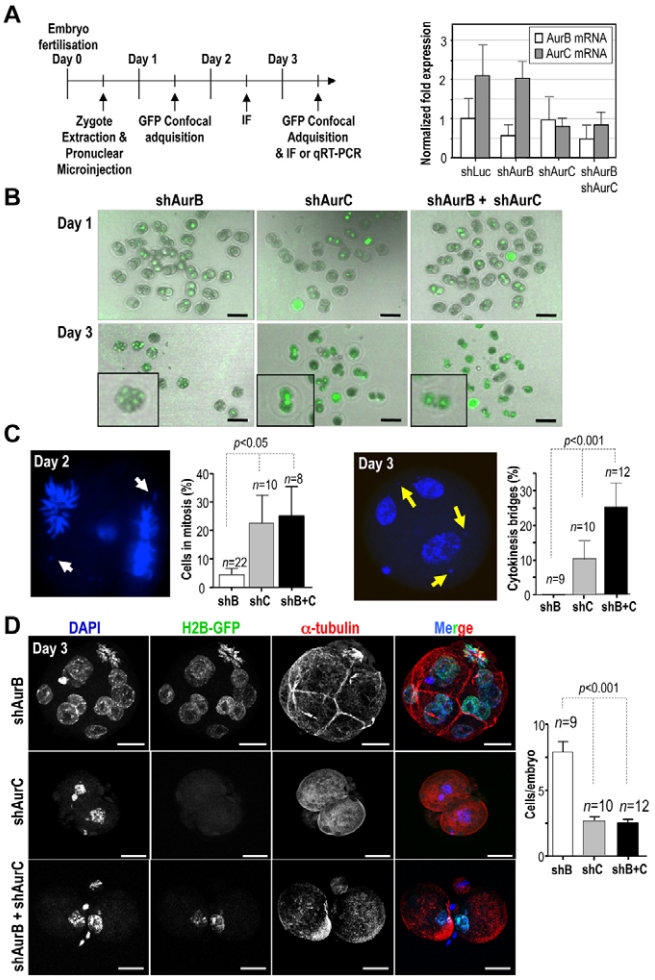

Fig. 6. Knock down of aurora C but not aurora B results in cell cycle arrest in early embryonic development. (**A**) Schematic of the protocol followed for knocking down aurora B and/or aurora C in zygotes. Embryos were isolated at E0.5 and microinjected with vectors expressing short hairpin interfering RNAs (shRNAs) against luciferase (shLuc) and aurora B (shAurB) and/or aurora C (shAurC), as well as a plasmid expressing H2B-GFP. qRT-PCR analysis shows a clear downregulation of aurora C in these assays and a more modest reduction of aurora B. However, it is important to note that aurora B mRNA levels are close to background levels at this stage and close to the limits of mRNA detection in these assays. (**B**) Microscopy images (combined bright field and green fluorescence) of embryos treated with these shRNAs indicating an arrest at the 2- to 4-cell stage in embryos treated with shAurC, shAurB-shAurC, but not shAurB or embryos treated with shRNAs against luciferase (not shown). Scale bars: 20 μm. Insets show representative embryos. (**C**) Knock down of aurora C (shC) or aurora B+aurora C (shB+C) results in a significant increase in mitotic cells in most cases showing misaligned chromosomes (white arrows). By day 3, most treated embryos display polyploid cells as well as cytokinesis bridges or micronuclei (yellow arrows). (**D**) Immunofluorescence analysis of these zygotes by day 3 shows mitotic aberrations and apoptotic figures after microinjection of shAurC or shAurB+AurC. These embryos arrest at the 2- or 4-cell stage whereas shAurB or shLuc embryos show an average of eight cells per embryo. Scale bars: 10 μm. For all graphs, error bars represent s.d.

2-6 [*Aurkb*(Δ) allele; Fig. 7B]. Aurora B-deficient cells underwent mitosis and accumulated as 4N or >4N DNA content cells after expression of the Cre recombinase (Fig. 7C). Examination of these cultures by immunofluorescence 48 hours after serum stimulation indicated an efficient elimination of aurora B at the protein level in Cre-infected cells (Fig. 7D). As cells are infected with Cre in G0 and are maintained in G0 for two additional days before entering into G1, this protocol ensures the degradation of residual aurora B proteins, possibly by APC/C-Cdh1 complexes. The residual *Aurkb*(lox) allele seen in Fig. 7B therefore indicates residual cells in which Cre was not active and Aurora B was still present (as identified by immunofluorescence; not shown) rather than residual aurora B protein in *Aurkb*(Δ/Δ) cells. Lack of aurora B was accompanied by a massive accumulation of abnormalities, including multiple nuclei, micronuclei and apoptotic figures, as well as lack of cytokinesis (Fig. 7D-F). About 25% of aurora B-deficient cells displayed an accumulation of α-tubulin asters that were either connected to chromosomes in multipolar cells or not connected to chromosomes (‘multiaster’ phenotype; Fig. 7G, arrowheads). The multiple microtubule organizing centers (MTOCs) might also explain monopolar spindles as these figures frequently contain multiple γ-tubulin spots grouped around the single pole (see Fig. S11 in the supplementary material).

Aurora B is essential for the error correction mechanism required for full chromosome alignment in metaphase. During this function, aurora B can generate unattached kinetochores thus resulting in unsatisfied SAC and mitotic arrest. It is, however, currently controversial to what extent aurora B might directly regulate the SAC independent of the error-correction mechanism. We therefore tested mitotic arrest in the presence of 3.5 μM of nocodazole, a condition under which microtubules are not formed. In wild-type MEFs, the duration of mitosis (DOM) was 435±135 minutes in the presence of nocodazole, as detected by videomicroscopy. In the absence of aurora B, the average DOM was 251±43.5 minutes, indicating a clear arrest when comparing with cells treated with DMSO (52±15 minutes) (Fig. 8A). This nocodazole-induced arrest is, however, smaller than that induced in wild-type cells, suggesting certain impairment in building a robust SAC response. The arrest can be partially overcome by Mad2 downregulation, suggesting an SAC-dependent delay both in wild-type and aurora B-deficient cells (Fig. 8A,B). Aurora B-null cells displayed a partial defective localization of BubR1 (Bub1b – Mouse Genome Informatics) to unattached kinetochores in the presence of nocodazole whereas Mad2 was properly localized (Fig. 8C), in agreement with the data in early embryos (Fig. 3). The genetic disruption of aurora B therefore supports the hypothesis that aurora B is not completely essential for the SAC, although it might directly participate in the recruitment of BubR1 to unattached kinetochores.

Aurora C can compensate for the lack of aurora B in somatic cells

We next tested whether the abnormalities caused by the absence of aurora B could be rescued by the expression of aurora C. *Aurkb*(lox/lox) cells were first infected with AdCre to generate *Aurkb*(Δ/Δ) cells (day 2 in Fig. 7A) and these cells were then transfected (day 4 in Fig. 7A) with GFP-fusion constructs expressing wild-type aurora B or aurora C or a kinase-dead form of these proteins. As represented in Fig. 9, the elimination of aurora B resulted in an aberrant mitotic distribution with almost inexistent anaphase or telophase figures (Fig. 9A). The expression of exogenous wild-type, but not kinase-dead, aurora B rescued the defects, and *Aurkb*(Δ/Δ);GFP-AurB^{WT} cultures displayed a normal ratio of cells in anaphase, telophase or cytokinesis (Fig. 9B-D). The exogenous GFP-tagged protein was properly located at cytokinesis

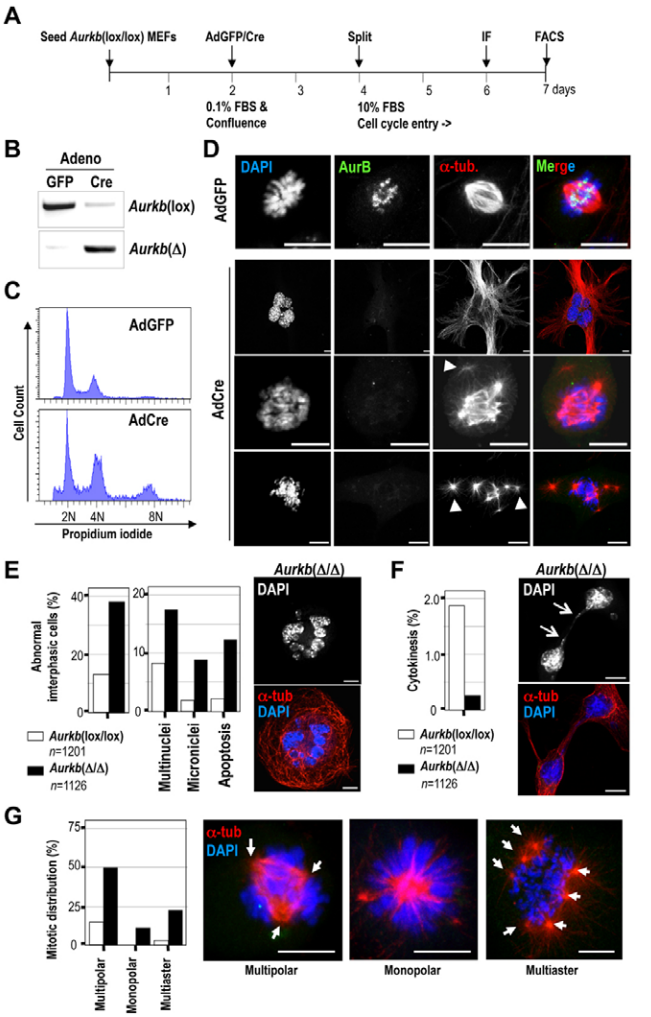

Fig. 7. Cellular phenotypes following acute deletion of aurora B in mouse embryo fibroblasts (MEFs). (**A**) Schematic of the protocol followed for acute ablation of aurora B in G0-arrested cells. *Aurkb*(lox/lox) cells are arrested in low serum and confluence and transduced with AdGFP or AdCre vectors. Forty-eight hours later, cells are split into new medium supplemented with 10% fetal bovine serum to induce entry into the cell cycle. Samples are taken at 48 hours for immunofluorescence (IF) or at 72 hours for fluorescence-activated cell sorting (FACS) analysis. (**B**) Representative PCR showing the generation of the *Aurkb*(Δ) null allele 48 hours after Cre expression. The *Aurkb*(lox) allele is genotyped using oligonucleotides 2 and 3 (see. Fig. 1), whereas primers 1 and 3 are used to genotype the *Aurkb*(Δ) null allele. (**C**) Infection with AdCre in primary MEFs results in an accumulation of 4N and >4N cells 72 hours after the exit from quiescence as detected by propidium iodide staining and flow cytometry. (**D**) Examination of these cultures by immunofluorescence at 48 hours indicates efficient depletion of aurora B (green in merge) in AdCre-infected cells. These mutant cells display aberrant morphologies as identified by staining with α-tubulin antibodies (red in merge) and DAPI (DNA) staining (blue in merge). (**E**) *Aurkb*(Δ/Δ) primary MEFs display an accumulation of abnormal interphase cells, including cells with several nuclei or micronuclei (see image) and apoptotic cells. (**F**) In addition, there is a dramatic reduction in cytokinesis figures suggesting a defect in the later stages of cell division. The remaining cytokinesis figures in *Aurkb*(Δ/Δ) cells are usually abnormal with long chromosomal bridges (arrows). *n* indicates the number of cells counted for each genotype. (**G**) Ablation of aurora B results in multiple spindle poles that might cluster forming monopolar spindles. Some of the multiple α-tubulin spots might display a robust nucleation of microtubules (multiaster phenotype; arrows). Scale bars: 10 μm.

bridges in these cells (Fig. 9C). Interestingly, expression of wild-type, but not kinase-dead, aurora C resulted in a similar phenotypic rescue (Fig. 9B-D) and aurora C was able to interact with incenp in these cells (Fig. 9E).

DISCUSSION

Mammalian aurora B and C are two closely related paralogs that probably evolved from a duplication event involving the ancestral aurora B/C found in cold-blood vertebrates (Brown et al., 2004). Aurora B is widely expressed in dividing cells. Aurora C, however, displays a very restricted expression pattern with a clear abundance during spermatogenesis and oocyte fertilization (Fig. 5 and see Fig. S7 in the supplementary material). Aurora C deficiency results in viable mice with subfertility defects, such as heterogeneous chromatin condensation, loose acrosomes and blunted sperm heads (Kimmins et al., 2007). Interestingly, aurora C displays frameshift mutations in infertile patients with abnormal spermatozoa characterized by large heads and increased chromosomal content (Dieterich et al., 2007), suggesting a crucial role in mammalian spermatogenesis. Additional loss-of-function studies of aurora C in oocytes suggest specific roles for this protein in meiosis (Sharif et al., 2010; Yang et al., 2010). However, its relevance in CPC function and mitosis in vivo has not been elucidated given the reduced endogenous expression levels in cultured cell lines.

The fact that aurora B-null embryos survive up to post-implantation stages is certainly surprising given the earlier lethality of incenp, survivin or borealin-deficient embryos (Cutts et al., 1999; Uren et al., 2000; Yamanaka et al., 2008) and the crucial roles of the CPC in cell division. During pre-implantation, incenp is properly located in the absence of aurora B and the phenotypes expected from perturbed CPC function are not observed. However, these embryos are sensitive to aurora B/C inhibitors such as ZM1. Aurora C expression is higher than that of aurora B during these early stages (Fig. 6) and the interference of aurora C results in cell division defects in early zygotes [our data and Lykke-Andersen et al. (Lykke-Andersen et al., 2008)]. The fact that aurora C-null embryos develop normally (Kimmins et al., 2007) might be explained by the presence of maternal aurora C in these embryos. Indeed, the aurora B/C ancestor was recently described to be an essential maternal-effect gene in zebrafish (Yabe et al., 2009). In addition, the mouse genome contains several aurora C loci originally considered to be pseudogenes but that might express functional proteins (Yang et al., 2010) thus making difficult to evaluate a loss-of-function aurora C mutant in this organism. Lack of aurora A results in lethality at the morula/blastocyst stage due to defective formation of a mitotic bipolar spindle, thus confirming the functional differences between aurora A and aurora B/C in vivo (Ang et al., 2008; Cowley et al., 2009; Sasai et al., 2008). Together, these results suggest that aurora C is the major CPC kinase during these early cell divisions in vivo.

Conditional ablation of aurora B in primary MEFs reveals a crucial role for this kinase in chromosome congression, as previously described (Ditchfield et al., 2003; Hauf et al., 2003; Vader et al., 2007). These mitotic defects can be rescued by expressing wild-type, but not kinase-dead, aurora C. Indeed, aurora C interacts with incenp and seems to act as a CPC component when exogenously expressed (our results) (Sasai et al., 2004; Slattery et al., 2009; Slattery et al., 2008; Yan et al., 2005). These data, along the relevance of aurora C during meiosis (Dieterich et al., 2007; Sharif et al., 2010; Yang et al., 2010) and in the early cell divisions (this work) indicate that aurora C has crucial roles in vivo, at least in germ cells and during early embryo development.

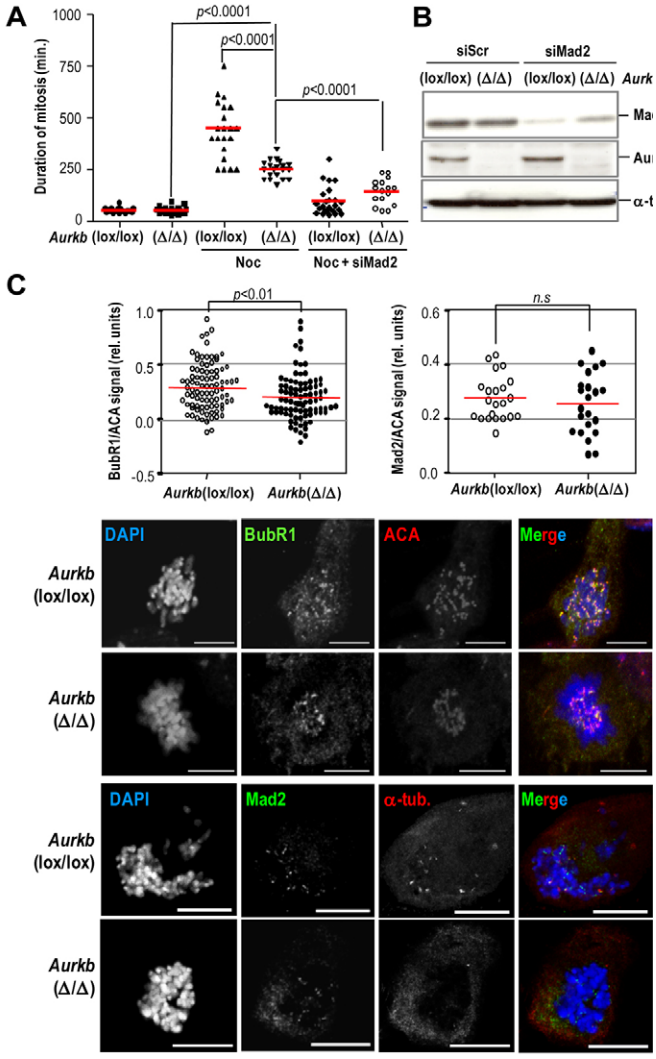

Fig. 8. Genetic ablation of aurora B does not prevent mitotic arrest in the presence of nocodazole. (**A**) Duration of mitosis (in minutes) in primary *Aurkb*(lox/lox) or *Aurkb*(Δ/Δ) mouse embryo fibroblasts (MEFs) in the absence or in the presence of 3.5 μM nocodazole (Noc). Knock down of Mad2 expression by small interfering RNA (siRNA) was performed to inactivate the spindle assembly checkpoint (SAC) upon nocodozale treatment. (**B**) Mad2 protein levels are partially diminished in *Aurkb*(lox/lox) and *Aurkb*(Δ/Δ) cells, as shown by immunoblotting. (**C**) Localization of BubR1 and Mad2 to kinetochores in the presence of nocodazole. The ratio between BubR1 (*n*=88 per genotype) or Mad2 (*n*=22) and anti-centromere antibody (ACA; centromere) signals is shown. Representative images of BubR1 or Mad2 signals (green) in nocodazole-treated *Aurkb*(lox/lox) and *Aurkb*(Δ/Δ) cells. ACA is shown in red and DNA (DAPI) in blue. The α-tubulin signal (red) indicates lack of microtubules in cells treated with 3.5 μM nocodazole. Scale bars: 10 μm.

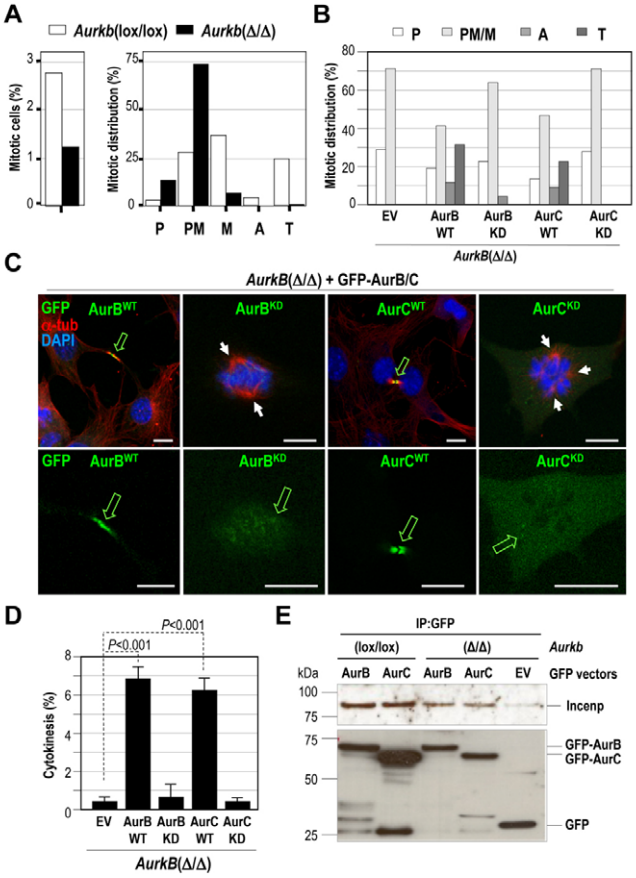

Fig. 9. Functional rescue of aurora B-null cells by aurora C. (**A**) Mitotic distribution in control *Aurkb*(lox/lox) (*n*=1234 cells) or *Aurkb*(Δ/Δ) (*n*=1141) primary mouse embryo fibroblasts (MEFs; 48 hours after the expression of Cre). The percentage of mitotic cells (versus the total number of cells in the culture) and the percentage of mitotic cells in prophase (P), prometaphase (PM), metaphase (M), anaphase (A) and telophase (T) are represented. (**B**) *Aurkb*(Δ/Δ) cells were transfected 2 days after AdCre (day 4 in Fig. 7A) with plasmids expressing GFP (empty vector, EV); or GFP-fusion proteins containing wild-type aurora B ($AurB^{WT}$), aurora C ($AurC^{WT}$), or kinase-dead mutant forms of these proteins ($AurB^{KD}$ and $AurC^{KD}$). (**C**) Representative images of *Aurkb*(Δ/Δ) cultures in the presence of the empty vector (GFP; left) or the different GFP-aurora B or aurora C fusion proteins. Both GFP-$AurB^{WT}$- and GFP-$AurC^{WT}$-expressing cells reach cytokinesis with proper localization of the exogenous GFP-AurB/C fusion protein to cytokinesis bridges (green arrows). However, most mitotic cells expressing the kinase-dead (KD) mutants display prometaphase figures typical of aurora B-null cells with multipolar spindles (white arrows). Scale bars: 10 μm. (**D**) Percentage of cytokinesis figures in the indicated cultures. *n*=250 cells were scored for each of the different cultures in B and C. Error bars represent s.d. (**E**) Interaction between GFP-tagged aurora B and aurora C with incenp in *Aurkb*(lox/lox) and *Aurkb*(Δ/Δ) MEFs. GFP-Aurora proteins were immunoprecipitated 48 hours after transfection using anti-GFP antibodies and immunoblotted with antibodies against incenp or GFP. Both aurora B and aurora C form conjugates with incenp.

Loss-of-function studies of mammalian aurora B have typically used RNA interference or small-molecule chemical inhibitors (Ditchfield et al., 2003; Hauf et al., 2003; Ruchaud et al., 2007). These studies have the caveat that the elimination of this protein might be incomplete and residual kinase activity might support certain activities. For instance, aurora B-null cells do not reach anaphase, suggesting that previous anaphase figures or abnormal cytokinesis observed upon RNA interference are likely to be due to partial inhibition. Although we cannot discard a minimum trace of aurora B kinase activity in *Aurkb*(Δ/Δ) cells, genetic disruption of aurora B in G0 results in the strongest defects reported so far in the mitosis that follows. Yet, aurora B-null cells display a significant arrest in nocodazole, suggesting that this kinase is not essential for the SAC. As aurora B-deficient cells display

inefficient localization of BubR1 (Fig. 8) (Ditchfield et al., 2003; Hauf et al., 2003), this kinase might partially contribute, possibly as a separate arm (Morrow et al., 2005), to the SAC response by recruiting BubR1 to unattached kinetochores.

Aurora kinases have recently received much attention owing to their possible involvement in tumor development and their potential therapeutic value (Keen and Taylor, 2004; Lens et al., 2010; Perez de Castro et al., 2008). Whereas initial efforts were focused on aurora A, recent data suggest that aurora B is a relevant cancer target (Girdler et al., 2006; Girdler et al., 2008). In addition, the ability of aurora C to drive CPC function suggests the relevance of this protein in specific cell types. Intriguingly, whereas no point mutations have been reported for aurora B, four mis-sense changes in aurora C (G18E, G53A, E114Q and H210Q) have been found in lung adenocarcinomas (Davies et al., 2005; Forbes et al., 2008). Some of these changes affect the P-loop or activation segment of the kinase domain, a conserved and key functional region known to harbor activating somatic mutations in other kinases in cancer (Davies et al., 2005). Understanding the specific requirements for aurora B/C in different cell types might, therefore, provide useful information for future therapeutic efforts.

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Competing interests statement
The authors declare no competing financial interests.

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References

Ang, X. L., Seeburg, D. P., Sheng, M. and Harper, J. W. (2008). Regulation of postsynaptic RapGAP SPAR by polo-like kinase 2 and the SCFÎ²-TRCP ubiquitin ligase in hippocampal neurons. *J. Biol. Chem.* **283**, 29424-29432.
Barr, A. R. and Gergely, F. (2007). Aurora-A: the maker and breaker of spindle poles. *J. Cell Sci.* **120**, 2987-2996.
Brown, J. R., Koretke, K. K., Birkeland, M. L., Sanseau, P. and Patrick, D. R. (2004). Evolutionary relationships of Aurora kinases: implications for model organism studies and the development of anti-cancer drugs. *BMC Evol. Biol.* **4**, 39.
Carmena, M. and Earnshaw, W. C. (2003). The cellular geography of aurora kinases. *Nat. Rev. Mol. Cell Biol.* **4**, 842-854.
Cowley, D. O., Rivera-Perez, J. A., Schliekelman, M., He, Y. J., Oliver, T. G., Lu, L., O'Quinn, R., Salmon, E. D., Magnuson, T. and Van Dyke, T. (2009). Aurora-A kinase is essential for bipolar spindle formation and early development. *Mol. Cell. Biol.* **29**, 1059-1071.
Cutts, S. M., Fowler, K. J., Kile, B. T., Hii, L. L., O'Dowd, R. A., Hudson, D. F., Saffery, R., Kalitsis, P., Earle, E. and Choo, K. H. (1999). Defective chromosome segregation, microtubule bundling and nuclear bridging in inner centromere protein gene (Incenp)-disrupted mice. *Hum. Mol. Genet.* **8**, 1145-1155.
Davies, H., Hunter, C., Smith, R., Stephens, P., Greenman, C., Bignell, G., Teague, J., Butler, A., Edkins, S., Stevens, C. et al. (2005). Somatic mutations of the protein kinase gene family in human lung cancer. *Cancer Res.* **65**, 7591-7595.
Dieterich, K., Soto Rifo, R., Faure, A. K., Hennebicq, S., Ben Amar, B., Zahi, M., Perrin, J., Martinez, D., Sele, B., Jouk, P. S. et al. (2007). Homozygous mutation of AURKC yields large-headed polyploid spermatozoa and causes male infertility. *Nat. Genet.* **39**, 661-665.
Ditchfield, C., Johnson, V. L., Tighe, A., Ellston, R., Haworth, C., Johnson, T., Mortlock, A., Keen, N. and Taylor, S. S. (2003). Aurora B couples chromosome alignment with anaphase by targeting BubR1, Mad2, and Cenp-E to kinetochores. *J. Cell Biol.* **161**, 267-280.
Fernandez-Miranda, G., Pérez de Castro, I., Carmena, M., Aguirre-Portolés, C., Ruchaud, S., Fant, X., Montoya, G., Earnshaw, W. C. and Malumbres, M. (2010). SUMOylation modulates the function of Aurora-B kinase. *J. Cell Sci.* **123**, 2823-2833.
Forbes, S. A., Bhamra, G., Bamford, S., Dawson, E., Kok, C., Clements, J., Menzies, A., Teague, J. W., Futreal, P. A. and Stratton, M. R. (2008). The Catalogue of Somatic Mutations in Cancer (COSMIC). *Curr. Protoc. Hum. Genet.* **Chapter 10**, Unit 10.11.
Garcia-Higuera, I., Manchado, E., Dubus, P., Canamero, M., Mendez, J., Moreno, S. and Malumbres, M. (2008). Genomic stability and tumour suppression by the APC/C cofactor Cdh1. *Nat. Cell Biol.* **10**, 802-811.
Giet, R., Petretti, C. and Prigent, C. (2005). Aurora kinases, aneuploidy and cancer, a coincidence or a real link? *Trends Cell Biol.* **15**, 241-250.
Girdler, F., Gascoigne, K. E., Eyers, P. A., Hartmuth, S., Crafter, C., Foote, K. M., Keen, N. J. and Taylor, S. S. (2006). Validating Aurora B as an anti-cancer drug target. *J. Cell Sci.* **119**, 3664-3675.
Girdler, F., Sessa, F., Patercoli, S., Villa, F., Musacchio, A. and Taylor, S. (2008). Molecular basis of drug resistance in aurora kinases. *Chem. Biol.* **15**, 552-562.
Glover, D. M., Leibowitz, M. H., McLean, D. A. and Parry, H. (1995). Mutations in aurora prevent centrosome separation leading to the formation of monopolar spindles. *Cell* **81**, 95-105.
Guse, A., Mishima, M. and Glotzer, M. (2005). Phosphorylation of ZEN-4/MKLP1 by aurora B regulates completion of cytokinesis. *Curr. Biol.* **15**, 778-786.
Hamatani, T., Carter, M. G., Sharov, A. A. and Ko, M. S. (2004). Dynamics of global gene expression changes during mouse preimplantation development. *Dev. Cell* **6**, 117-131.
Hauf, S., Cole, R. W., LaTerra, S., Zimmer, C., Schnapp, G., Walter, R., Heckel, A., van Meel, J., Rieder, C. L. and Peters, J. M. (2003). The small molecule Hesperadin reveals a role for Aurora B in correcting kinetochore-microtubule attachment and in maintaining the spindle assembly checkpoint. *J. Cell Biol.* **161**, 281-294.
Hu, H. M., Chuang, C. K., Lee, M. J., Tseng, T. C. and Tang, T. K. (2000). Genomic organization, expression, and chromosome localization of a third aurora-related kinase gene, Aie1. *DNA Cell Biol.* **19**, 679-688.
Johansen, K. M. and Johansen, J. (2006). Regulation of chromatin structure by histone H3S10 phosphorylation. *Chromosome Res.* **14**, 393-404.
Keen, N. and Taylor, S. (2004). Aurora-kinase inhibitors as anticancer agents. *Nat. Rev. Cancer* **4**, 927-936.
Kelly, A. E. and Funabiki, H. (2009). Correcting aberrant kinetochore microtubule attachments: an Aurora B-centric view. *Curr. Opin. Cell Biol.* **21**, 51-58.
Kimmins, S., Crosio, C., Kotaja, N., Hirayama, J., Monaco, L., Hoog, C., van Duin, M., Gossen, J. A. and Sassone-Corsi, P. (2007). Differential functions of the Aurora-B and Aurora-C kinases in mammalian spermatogenesis. *Mol. Endocrinol.* **21**, 726-739.
Lens, S. M., Voest, E. E. and Medema, R. H. (2010). Shared and separate functions of polo-like kinases and aurora kinases in cancer. *Nat. Rev. Cancer* **10**, 825-841.
Li, X., Sakashita, G., Matsuzaki, H., Sugimoto, K., Kimura, K., Hanaoka, F., Taniguchi, H., Furukawa, K. and Urano, T. (2004). Direct association with inner centromere protein (INCENP) activates the novel chromosomal passenger protein, Aurora-C. *J. Biol. Chem.* **279**, 47201-47211.
Lykke-Andersen, K., Gilchrist, M. J., Grabarek, J. B., Das, P., Miska, E. and Zernicka-Goetz, M. (2008). Maternal Argonaute 2 is essential for early mouse development at the maternal-zygotic transition. *Mol. Biol. Cell* **19**, 4383-4392.
Morrow, C. J., Tighe, A., Johnson, V. L., Scott, M. I., Ditchfield, C. and Taylor, S. S. (2005). Bub1 and aurora B cooperate to maintain BubR1-mediated inhibition of APC/CCdc20. *J. Cell Sci.* **118**, 3639-3652.
Nezi, L. and Musacchio, A. (2009). Sister chromatid tension and the spindle assembly checkpoint. *Curr. Opin. Cell Biol.* **21**, 785-795.
Nigg, E. A. (2001). Mitotic kinases as regulators of cell division and its checkpoints. *Nat. Rev. Mol. Cell Biol.* **2**, 21-32.
Nowak, S. J. and Corces, V. G. (2004). Phosphorylation of histone H3: a balancing act between chromosome condensation and transcriptional activation. *Trends Genet.* **20**, 214-220.
Perez de Castro, I., de Carcer, G., Montoya, G. and Malumbres, M. (2008). Emerging cancer therapeutic opportunities by inhibiting mitotic kinases. *Curr. Opin. Pharmacol.* **8**, 375-383.
Prigent, C. and Dimitrov, S. (2003). Phosphorylation of serine 10 in histone H3, what for? *J. Cell Sci.* **116**, 3677-3685.
Rodriguez, C. I., Buchholz, F., Galloway, J., Sequerra, R., Kasper, J., Ayala, R., Stewart, A. F. and Dymecki, S. M. (2000). High-efficiency deleter mice show that FLPe is an alternative to Cre-loxP. *Nat. Genet.* **25**, 139-140.

Ruchaud, S., Carmena, M. and Earnshaw, W. C. (2007). Chromosomal passengers: conducting cell division. *Nat. Rev. Mol. Cell Biol.* **8**, 798-812.
Sasai, K., Katayama, H., Stenoien, D. L., Fujii, S., Honda, R., Kimura, M., Okano, Y., Tatsuka, M., Suzuki, F., Nigg, E. A. et al. (2004). Aurora-C kinase is a novel chromosomal passenger protein that can complement Aurora-B kinase function in mitotic cells. *Cell Motil. Cytoskeleton* **59**, 249-263.
Sasai, K., Parant, J. M., Brandt, M. E., Carter, J., Adams, H. P., Stass, S. A., Killary, A. M., Katayama, H. and Sen, S. (2008). Targeted disruption of Aurora A causes abnormal mitotic spindle assembly, chromosome misalignment and embryonic lethality. *Oncogene* **27**, 4122-4127.
Schnutgen, F., Doerflinger, N., Calleja, C., Wendling, O., Chambon, P. and Ghyselinck, N. B. (2003). A directional strategy for monitoring Cre-mediated recombination at the cellular level in the mouse. *Nat. Biotechnol.* **21**, 562-565.
Schwenk, F., Baron, U. and Rajewsky, K. (1995). A cre-transgenic mouse strain for the ubiquitous deletion of loxP-flanked gene segments including deletion in germ cells. *Nucleic Acids Res.* **23**, 5080-5081.
Sharif, B., Na, J., Lykke-Hartmann, K., McLaughlin, S. H., Laue, E., Glover, D. M. and Zernicka-Goetz, M. (2010). The chromosome passenger complex is required for fidelity of chromosome transmission and cytokinesis in meiosis of mouse oocytes. *J. Cell Sci.* **123**, 4292-4300.
Slattery, S. D., Moore, R. V., Brinkley, B. R. and Hall, R. M. (2008). Aurora-C and Aurora-B share phosphorylation and regulation of CENP-A and Borealin during mitosis. *Cell Cycle* **7**, 787-795.
Slattery, S. D., Mancini, M. A., Brinkley, B. R. and Hall, R. M. (2009). Aurora-C kinase supports mitotic progression in the absence of Aurora-B. *Cell Cycle* **8**, 2984-2994.
Steigemann, P., Wurzenberger, C., Schmitz, M. H., Held, M., Guizetti, J., Maar, S. and Gerlich, D. W. (2009). Aurora B-mediated abscission checkpoint protects against tetraploidization. *Cell* **136**, 473-484.
Tang, C. J., Lin, C. Y. and Tang, T. K. (2006). Dynamic localization and functional implications of Aurora-C kinase during male mouse meiosis. *Dev. Biol.* **290**, 398-410.
Uren, A. G., Wong, L., Pakusch, M., Fowler, K. J., Burrows, F. J., Vaux, D. L. and Choo, K. H. (2000). Survivin and the inner centromere protein INCENP show similar cell-cycle localization and gene knockout phenotype. *Curr. Biol.* **10**, 1319-1328.
Vader, G., Cruijsen, C. W., van Harn, T., Vromans, M. J., Medema, R. H. and Lens, S. M. (2007). The chromosomal passenger complex controls spindle checkpoint function independent from its role in correcting microtubule kinetochore interactions. *Mol. Biol. Cell* **18**, 4553-4564.
Weaver, B. A. and Cleveland, D. W. (2009). The role of aneuploidy in promoting and suppressing tumors. *J. Cell Biol.* **185**, 935-937.
Yabe, T., Ge, X., Lindeman, R., Nair, S., Runke, G., Mullins, M. C. and Pelegri, F. (2009). The maternal-effect gene cellular island encodes aurora B kinase and is essential for furrow formation in the early zebrafish embryo. *PLoS Genet.* **5**, e1000518.
Yamanaka, Y., Heike, T., Kumada, T., Shibata, M., Takaoka, Y., Kitano, A., Shiraishi, K., Kato, T., Nagato, M., Okawa, K. et al. (2008). Loss of Borealin/DasraB leads to defective cell proliferation, p53 accumulation and early embryonic lethality. *Mech. Dev.* **125**, 441-450.
Yan, X., Cao, L., Li, Q., Wu, Y., Zhang, H., Saiyin, H., Liu, X., Zhang, X., Shi, Q. and Yu, L. (2005). Aurora C is directly associated with Survivin and required for cytokinesis. *Genes Cells* **10**, 617-626.
Yang, K. T., Li, S. K., Chang, C. C., Tang, C. J., Lin, Y. N., Lee, S. C. and Tang, T. K. (2010). Aurora-C kinase deficiency causes cytokinesis failure in Meiosis I and production of large polyploid oocytes in mouse. *Mol. Biol. Cell* **21**, 2371-2383.