A cell-based model system links chromothripsis with hyperploidy

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Abstract

A remarkable observation emerging from recent cancer genome analyses is the identification of chromothripsis as a one-off genomic event, resulting in massive somatic DNA structural rearrangements (SRs). Largely due to lack of suitable model systems, the mechanistic basis of chromothripsis has remained elusive. We developed an integrative method termed "complex alterations after selection and transformation (CAST)," enabling efficient in vitro generation of complex DNA rearrangements including chromothripsis, using cell perturbations coupled with a strong selection barrier followed by massively parallel sequencing. We employed this methodology to characterize catastrophic SR formation processes, their temporal sequence, and their impact on gene expression and cell division. Our in vitro system uncovered a propensity of chromothripsis to occur in cells with damaged telomeres, and in particular in hyperploid cells. Analysis of primary medulloblastoma cancer genomes verified the link between hyperploidy and chromothripsis in vivo. CAST provides the foundation for mechanistic dissection of complex DNA rearrangement processes.

Keywords: chromothripsis; hyperploidy; DNA rearrangements; telomere damage; transformation

Subject Categories: Chromatin, Epigenetics, Genomics & Functional Genomics; DNA Replication, Repair & Recombination; Methods & Resources

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Introduction

During tumorigenesis, a single genetic alteration (or "hit") is generally thought to be insufficient for a cell to develop into cancer. Instead, several gradually acquired mutations or SRs occurring in a stepwise process are required, mediating incremental tumor development (Knudson, 1971; Stratton et al, 2009). However, cancer genomes can evolve in rapid bursts. Recent cancer genomic surveys presented compelling evidence for a process involving massive de novo SR formation in a one-step catastrophic genomic event denoted chromothripsis (chromo for chromosome; thripsis for shattering into pieces) (Stephens et al, 2011; Korbel & Campbell, 2013). Chromothripsis can massively rearrange chromosomal arms or even entire chromosomes, leading to reshuffled genomic regions that frequently harbor clusters of deleted segments (Stephens et al, 2011; Korbel & Campbell, 2013) and occasionally clustered amplifications, in case chromothripsis is followed by double minute chromosome formation (Rausch et al, 2012a). This catastrophic SR process is observed in 2–3% of cancers (Stephens et al, 2011), linked with poor disease outcome (Kloosterman et al, 2014), and has been reported to exhibit increased rates in particular cancer types, including bone cancer, esophageal adenocarcinoma, glioblastoma, and Sonic-hedgehog-subtype medulloblastoma (Stephens et al, 2011; Rausch et al, 2012a; Kloosterman et al, 2014; Nones et al, 2014). Chromothripsis is also observed in the context of congenital disorders (Kloosterman et al, 2011; Liu et al, 2011) and can exhibit a curative effect on genetic disease (McDermott et al, 2015).

Following chromosome shattering mediated by chromothripsis, the resulting fragments are lost or become rejoined into derivative chromosomes, presumably through unfaithful DNA repair (Kloosterman et al, 2011; Stephens et al, 2011; Rausch et al, 2012a). Although cellular catastrophes arising during key stages of the cell cycle are suggested as a potential trigger (Stephens et al, 2011; Korbel & Campbell, 2013), few studies focused on the mechanistic origins and consequences of chromothripsis, presumably due to the lack of suitable experimental model systems. While genomic analysis of primary tumors or cancer cell lines can provide valuable snapshots long after chromothripsis has taken place (Kloosterman et al, 2011; Stephens et al, 2011; Rausch et al, 2012a), their utility for studying the initiating molecular process(es) is more limited.

In this study, we describe the approach CAST (complex alterations after selection and transformation) for studying
chromothripsis and other complex SR formation processes in vitro, a methodology enabling reproducible generation of chromothripsis in a genetically stable cell line. We employ CAST in a proof-of-principle study, provide evidence for association of telomere stability as well as of hyperploidy with chromothripsis, and investigate the functional consequences of this catastrophic DNA rearrangement process.

Results

Development of the CAST approach

The approach CAST for studying complex DNA rearrangement processes in vitro is based on: (i) an untransformed model cell line, (ii) application of genetic or chemical perturbations, (iii) selection of DNA alterations conferring a growth advantage by soft agar colony formation, (iv) screening for extensive copy number alterations using low-pass whole-genome sequencing, and (v) in-depth characterization of DNA structural rearrangements (SRs) by long-range paired-end sequencing (Korbel et al., 2007) (i.e., mate-pair sequencing) (Fig 1A).

(i) Model cell line: We chose the human hTERT RPE-1 (retinal pigment epithelial) cell line as a model system for characterizing de novo SR formation. This telomerase immortalized cell line exhibits a genomically stable diploid karyotype. Though not tumor derived, RPE-1 cells can be transformed with elevated levels of γ-irradiation leading to gross SR formation detectable by karyotyping. We subjected hTERT RPE-1 (herein termed “RPE-1 wild type”) and previously generated (Riches et al., 2001) RPE-1-transformed cell lines to mate-pair sequencing, which revealed the occurrence of several SRs only in the transformed lines (Appendix Fig S1A–C). We recently described a link between TP53 mutations and chromothripsis, implying that abnormal p53 function may be necessary for the induction, or tolerance, of catastrophic SRs (Rausch et al., 2012a). To establish a model amenable to study chromothripsis, we thus used zinc finger nucleases to generate an RPE-1 derivative deficient in p53. We confirmed p53 loss of function in two independent cell lines, C111 and C29 (Figs 1A and EV1A–C). Interestingly, C29, but not C111, showed an increase in ploidy measured by both DNA content and chromosome counts from metaphase spreads (Figs 1B and C, and EV1D), which may be explained with the previously noted tendency toward tetraploidization upon p53 inactivation (Bunz et al., 2002).

(ii) Cellular perturbations: For a proof of concept of CAST, we employed sublethal doses of the chemical doxorubicin as a source of DNA double-strand breaks mediated through topoisomerase II inhibition in S phase (Fornari et al., 1994).

(iii) Selection barrier: Complex genomic rearrangements resulting from chromothripsis can lead to the simultaneous acquisition of multiple tumor-promoting lesions (Stephens et al., 2011) (e.g., loss of several tumor suppressors). Such lesions promote anchorage-independent cell growth in vitro, a hallmark of transformation and an established in vitro indicator of tumorigenicity (Hahn et al., 1999). We thus reasoned that such a strong selection barrier could be used to selectively enrich for cells harboring catastrophic SRs.

(iv) Screening for extensive copy number switches: To design low-pass whole-genome sequencing experiments, we performed simulations to investigate what level of coverage is required to reliably detect large SRs; and we chose to use pooled, barcoded samples (up to 40 in one sequencing lane) to achieve around 0.05–0.1× genomic sequencing coverage. When assessing low-pass sequenced genomes, we used the circular binary segmentation algorithm on genomic read-depth data to infer copy number switches. We considered copy number switches of ≥500 kb when assessing low-pass whole-genome sequencing (WGS) data.

(v) Characterization of chromothripsis events: Whenever appropriate, cell lines were analyzed in-depth by mate-pair sequencing to high physical coverage (i.e., spanning coverage) in order to enable verification and characterization of chromothripsis events.

Although a small number of isolated (or “simple”) SRs occurred upon p53 loss of function, we verified that in spite of TP53 disruption neither C111 nor C29 showed signs of transformation (Fig EV1E), suggesting their utility for CAST. Upon DNA damage induction, we sorted between 192 and 480 single cells into microtiter plates after 3 days to ensure that the cells go through at least one division following perturbations. We also ensured isolation of single cell-derived clones—by growing single colonies after cell
B

1. RPE-1 TP53 -/- Cells
2. Perturbation
3. Clonal expansion
4. Anchorage-independent growth

TP53 -/- clones

WT C111 C26 C29 C33

DXR -+ -+ -+ -+ -+

anti-P-γ-H2AX
anti-p53
anti-GAPDH

C

Systematic detection of genomic rearrangements

Chromosome 8.

Ascertainment of functional consequences (e.g. gene expression, profiling of cell division)

D

Applications

RPE-1 TP53 -/- Cells

RPE-1 TP53 WT

RPE-1 TP53 -/- C111

RPE-1 TP53 -/- C29

E

BM173 Chr17

BM175 Chr8

BM178 Chr12

BM694 Chr14

BM780 Chr6

BM674 Chr7

BM676 Chr7

Chromosomal coordinates [Megabases]

Log2 ratio of read depth (Sample/Control)

Diploid

Hyperploid

Figure 1.
sorting, and by isolating clones following transformation. Following DNA damage, sorting, and transformation, typically 3–16 clones were recovered per experiment, which were then subjected to low-pass WGS. Consistent with prior reports connecting tetraploidy to genomic instability (Fujiwara et al., 2005), we identified significantly more copy number switches in low-pass WGS data generated for 36 C29 hyperploid transformants compared to 40 C111 diploid transformants (C29 copy number switches, mean and standard deviation: 41.61 ± 17.31; C111 mean and standard deviation: 18.1 ± 10.55; \( P < 2 \times 10^{-5} \); Welch two-sample \( t \)-test). To exclude the possibility that intrinsic differences between C29 and C111 other than the difference in ploidy were responsible for the increase in copy number alterations, we generated another tetraploid cell line directly from the C111 cell line by preventing cytokinesis (dihydroxytocalasin B). Reassuringly, the resulting tetraploid cell line (DCB2) (Appendix Fig S2) amounting to 22 additional transformed clones (Table EV1) exhibited a significantly higher level of copy number alterations as those derived from the diploid cell line C111 (DCB2, copy number switches, mean and standard deviation: 34.39 ± 17.60; \( P < 3 \times 10^{-4} \), when compared to C111 by Welch two-sample \( t \)-test).

**Generation of chromothripsis in utero in hyperploid RPE-1 cells**

Notably, we observed individual examples of highly clustered copy number alterations in nine cases, all of which arose in hyperploid lineages (hyperploids: 9/58; diploids: 0/40; \( P < 0.01 \); two-sided Fisher’s exact test; Fig 1D, Dataset EV1), and none of which were observed during control arms of our experiments omitting the selection barrier (Appendix Fig S3). We used mate-pair sequencing for in-depth investigation of 29 hyperploid and 29 diploid transformants exhibiting copy number alterations (Table EV2). Subsequently, we employed recently published criteria (Li et al., 2014) and deductive approaches (Korbel & Campbell, 2013) for evaluating the occurrence and temporal ordering of clustered SRs and to test for chromothripsis events (details on the underlying reasoning (Korbel & Campbell, 2013; Li et al., 2014) are summarized in the Appendix). Applying stringent criteria, we verified the occurrence of chromothripsis in seven hyperploid transformants and additionally confirmed that there is no evidence for chromothripsis events in the diploid transformants. Hence, our analysis indicates an increased rate of chromothripsis events in hyperploids compared to diploids (\( P < 0.05 \); two-sided Fisher’s exact test; Fig 2 and Appendix Figs S4–S9). The tendency of chromothripsis events to occur in hyperploids was further supported by CAST experiments using Zeocin (rather than doxorubicin) as a DNA double-strand break inducing chemical, which revealed 2/12 chromothripsis in C29 hyperploid versus 0/12 chromothripsis in C111 diploid cell line (Fig EV2). For example, chromosome 12 of the RPE-1 cell line BM178, which we derived from doxorubicin treatment of the hyperploid RPE-1 line C29, exhibited the prototypical chromothripsis pattern of oscillating copy numbers (Fig 2A–E, Appendix Fig S4) that numerous studies previously reported in cancer genome surveys (e.g., Kloosterman et al., 2011; Stephens et al., 2011; Rausch et al., 2012a; Korbel & Campbell, 2013; Li et al., 2014; and references therein). Further analyses showed that chromosomes 12 and 22 underwent co-shattering in BM178, with abundant translocation calls connecting both chromosomes (Appendix Fig S4), an outcome of chromothripsis that has also been observed frequently in cancer genomes (Stephens et al., 2011; Korbel & Campbell, 2013).

An additional example of chromothripsis, detected in BM175 which also resulted from doxorubicin treatment of the hyperploid line C29, is shown in Fig 2F–K. Chromosome 8 in this cell line exhibited an amplified region adjacent to a sharp drop in copy number toward the chromosome end. Notably, the boundaries of
Figure 2.

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the amplified region were further demarcated by a fold-back inversion. These genomic patterns indicate the emergence of breakage–fusion–bridge cycles (BFBs) (Campbell et al., 2010), which are thought to underlie a genomic instability process initiated by a double-strand break exposing the end of the affected chromosome (Bunting & Nussenzweig, 2013). During replication, the unstable chromosome ends can fuse by non-homologous end joining, creating a dicentric chromosome that can break during cell division. This characteristically leads to a stepwise increase in copy number toward the chromosome end, followed by a sharp drop (Campbell et al., 2010), as detected in BM175 (Fig 2F–K). In the case of BM175, however, copy number oscillations resulting from chromothripsis overlaid the characteristic genomic patterns of BFBs (Fig 2F–K). On the basis of our analysis, the architectural characteristics of rearrangements on BM175 chromosome 8 indicate that chromothripsis occurred subsequent to initiating BFBs, as when chromothripsis occurs on a previously rearranged chromosome, the resulting segment joins will connect genomic pieces exhibiting different copy number states (see Appendix, inference of chromothripsis events (Li et al., 2014; Rausch et al., 2012a; Stephens et al., 2011)). The extensive translocations to chromosomes 15 and 2 suggest that these chromosomes were most likely co-shattered by chromothripsis, which resulted in highly rearranged derivative chromosomes (Dataset EV1). In addition to BM175, our analysis uncovered other examples of chromothripsis events occurring subsequently to BFB cycles (Appendix Figs S5, S7, and S12). Together with earlier observations on the occasional co-occurrence of BFBs and chromothripsis in acute lymphoblastic leukemia and esophageal adenocarcinoma (Li et al., 2014; Nones et al., 2014), these data suggest that the temporal pattern of BFBs followed by chromothripsis is a more common feature of massively rearranged genomes.

Evidence for a link between telomere attrition and chromothripsis

BFB cycles can be triggered through losses of telomeric ends of chromosomes (Bunting & Nussenzweig, 2013). In order to test whether telomeric end loss can give rise to chromothripsis using our CAST system, we depleted cells of the shelterin complex protein TRF2 (de Lange, 2005) and further challenged the siRNA-treated cells with chemicals used to help overcome mitotic checkpoint barriers in TRF2-depleted cells (i.e., reversine and hesperadine (Santaguida et al., 2010)). Notably, we identified two chromothripsis events (Figs 3 and EV3) of which one additionally exhibited the genomic alteration patterns of a BFB cycle (Fig 3). To our knowledge, these data provide, for the first time, experimental evidence that telomere attrition can mediate chromothripsis. Hence, our data add to and significantly extend prior observations based on cancer genome analysis that BFBs, which are thought to frequently arise as a consequence of telomere shortage, occasionally occur in conjunction with chromothripsis events (see Li et al., 2014; Nones et al., 2014; as well as our genomic data in Fig 2F–K and Appendix Figs S5, S7, and S12). Furthermore, following TRF2 depletion, the RPE-1 cells notably became hyperploid and stayed in hyperploid condition (data not shown), in support of the association of hyperploidy with chromothripsis that we observed for doxorubicin-treated RPE-1 cells.

Link between hyperploidy and chromothripsis in medulloblastoma

To determine whether hyperploidy is also linked to chromothripsis in vivo, we performed an analysis of WGS data from pediatric medulloblastoma tumor specimens (Jones et al., 2012; Rausch et al., 2012a; Kool et al., 2014), since chromothripsis is common and a presumed early event in medulloblastoma tumorigenesis (Rausch et al., 2012a). Chromothripsis and tetraploidy have been reported to occur in medulloblastoma (Jones et al., 2012; Rausch et al., 2012a), but a statistical association between chromothripsis and hyperploidy has to date not been established. We focused on the Sonic-hedgehog pathway-driven medulloblastoma subtype (SHH-MB), a subtype in which chromothripsis is associated with inactivating germ line TP53 mutations (Rausch et al., 2012a), and which hence exhibits genetic similarity to our TP53-deficient model cell line. We reanalyzed cancer genomes from 44 previously published SHH-MBs (Jones et al., 2012; Rausch et al., 2012a; Kool et al., 2014) and additionally generated 30× coverage tumor and matched blood WGS data for a recently diagnosed SHH-MB patient with a germline mutation in TP53 (MB243). Our analyses demonstrate that chromothripsis indeed occurs significantly more often in hyperploid compared to diploid SHH-MBs (hyperploids: 5/11; diploids: 2/34; P < 0.01; one-tailed Fisher’s exact test; Table EV3). An exemplary chromothripsis event for MB34, showing excessive oscillating copy number alterations, is shown in Fig 4A–C and Appendix Figs S10 and S11. Similar to our cell-based model system, we also observed chromothripsis events preceded by BFB cycles in these data from tumors in vivo, for instance on chromosome 15 in MB243 (Fig 4D–F and Appendix Fig S11). Notably, based on our analyses of SRs, copy number states, and haplotype-based profiling of allelic imbalances, patterns of somatic alteration in SHH-MB are consistent with hyperploidization preceding chromothripsis, implicating hyperploidization as a “risk factor” for chromothripsis in vivo (Fig EV4).

Functional consequences of chromothripsis in RPE-1 cells

Our method, in conjunction with the availability of isogenic cell lines prior to and subsequent to chromothripsis, will not only enable probing for chromothripsis initiating genetic factors, but also facilitate studies of the consequences of catastrophic SRs under controlled experimental conditions. To exemplify this, we performed transcriptome sequencing (mRNA-Seq) of BM175 and BM178 as well as of their parental cell lines and compared gene expression levels in pre- and post-chromothripsis stages. We observed appreciable expression changes in genomic regions affected by chromothripsis at a false discovery rate (FDR) of 10%. For instance, in BM178, a number of significantly downregulated genes were observed on the chromosome arm rearranged by chromothripsis, including two tumor suppressors (the RASSF3 and RASSF9 members of the RAS-associated family of tumor suppressors (Volodko et al., 2014); Fig 5A). Additional members of this tumor suppressor family (RASSF4/S) residing on different chromosomes were likewise downregulated (Fig EV5A), potentially due to coordinated regulation of these interacting partners (Behrends et al., 2010) subsequent to the rearrangement. For BM175, we observed downregulated downregulation of BUBR1 and CASC5 residing on
chromosome 15, which was the most significantly affected chromosome in terms of expression deregulation, with 14% of the expressed genes showing significant deregulation (chi-squared outlier test, \( P = 0.0048 \)). As a result of chromothripsis, both genes were brought into a new genomic context (Fig EV5B–D). The products of both genes are involved in faithful kinetochore–microtubule attachments (Foley & Kapoor, 2013), and their downregulation was previously reported to result in reduced mitotic timing (Kittler et al., 2007). Further supporting our gene expression measurements, high-resolution live cell imaging showed significantly decreased mitotic timing in BM175 relative to its parental line, presumably due to reduced expression of BUBR1 and CASC5 (\( P < 9.4e-14 \); Welch two-sample \( t \)-test; Fig 5B and C). Taken together, these analyses exemplify investigation of the consequences of chromothripsis as an additional use case of CAST.

**Discussion**

CAST makes one of the most striking outcomes of cancer genome analyses identified to date—the discovery of chromothripsis as a one-off catastrophic rearrangement process (Stephens et al., 2011)—amenable to laboratory studies, enabling investigations of causes and consequences of chromothripsis. CAST utilizes initially untransformed cell lines together with a strong selection barrier that can be overcome following genetic and chemical perturbations. Our experimental data based on CAST do not only demonstrate the reproducible generation of chromothripsis events, but also implicate hyperploidy and telomere attrition as predisposing factors for chromothripsis. Along with the link between TP53 germ line mutations and chromothripsis that we previously reported for medulloblastoma (Rausch et al., 2012a), and links between constitutional Robertsonian translocations and chromothripsis in acute lymphoblastic leukemia (Li et al., 2014), our *in vitro* findings reinforce the notion that rather than occurring in isolation chromothripsis is prone to arise in cellular contexts which facilitate genomic instability—such as in the context of hyperploidy, which may mediate instability by “buffering” against haploinsufficiency or by causing an increased rate of mitotic failures promoting SR formation. Indeed, hyperploidy is frequently observed in human cancers (Davoli & de Lange, 2011), can increase resistance to chemotherapy and radiotherapy (Castedo et al., 2006), and has previously been suggested as a source of genetic instability (Storchova & Kuffer, 2008; Davoli & de Lange, 2011), albeit not in the context of
chromothripsis. Interestingly, an important feature of external granular layer (EGL) cells, the cells of origin of SHH-MB, is their capacity to actively proliferate in a tissue where most other cell types do not divide (Schuller et al., 2008; Westra et al., 2008). Potentially relevant to the observations reported here, a previous study using cultured EGL progenitors identified aneuploidy in 15% of cells, with hyperploidy being the most commonly observed form (Westra et al., 2011; Li et al., 2015). Although we failed to detect micronuclei in our cell lines after chromothripsis occurred (Appendix Fig S12), this does not formally exclude a potential initiating role of micronuclei in chromothripsis in our system. Micronuclei can mediate chromothripsis events (Zhang et al., 2010), and telomere attrition can mediate the formation of dicentric chromosomes through micronuclei formation can mediate chromothripsis events (Zhang et al., 2015). Although we failed to detect micronuclei in our cell lines after chromothripsis occurred (Appendix Fig S12), this does not formally exclude a potential initiating role of micronuclei in chromothripsis in our RPE-1 cell system. Micronuclei can form as a consequence of chromosomes lagging at anaphase (Crasta et al., 2012), dicentric chromosomes are prone to be lagging at anaphase (Pampalona et al., 2010), and telomere attrition can mediate the formation of dicentric chromosomes (van Steensel et al., 1998). Hence, it is conceivable that micronuclei arose in our cells treated with TFR2 siRNA, presumably when double-strand breaks occurred following telomere attrition.

By comparison, and complementary to the approach by Zhang et al., CAST can be used to investigate the potential lethality of massive SRs resulting from chromothripsis, the ability of cells to benefit from these, and additional consequences of chromothripsis. By enabling research on these aspects for the first time, CAST provides a powerful tool for investigating natural triggers and consequences of chromothripsis, a catastrophic SR process that is likely

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**Figure 4. Evidence for hyperploidy being a risk factor for chromothripsis in SHH-type medulloblastoma.**

A Oscillating copy number states and SRs on chromosome 14 in MB34 (based on WGS data), resulting from chromothripsis. SRs are color-coded: red, deletion type (T-T); blue, head-to-head (H-H) type; purple, tail-to-tail (T-T) type; gray, inter-chromosomal.

B Copy number jump distribution for chromosome 14 in MB34, with diagonal points indicating chromothripsis occurred on a previously unrearranged chromosome.

C Distribution of copy number segment switches for chromosome 14 in MB34.

D Oscillating copy number states and SRs on chromosome 15 in MB243 (based on WGS data), resulting from chromothripsis and BFBs.

E Copy number jump distribution for chromosome 15 in MB243, with off-diagonal points indicating chromothripsis occurred on a previously rearranged chromosome.

F Distribution of copy number segment switches for chromosome 15 in MB243.
to be initiated by more than one cellular pathway. In this context, the flexibility of our approach along with its capacity to reproducibly generate chromothripsis events will facilitate further studies on chromothripsis, by enabling the testing of specific hypotheses on pathways and mechanisms that may give rise to catastrophic SRs, including involvement of errors in mitosis, transcription, and DNA replication (Jones & Jallepalli, 2012).

**Materials and Methods**

**Cell lines and treatments**

RPE-1 cells were purchased from ATCC and checked for mycoplasma contamination. The cells were cultured in DMEM-F12 medium supplemented with 10% fetal bovine serum and antibiotics (Life Technologies). \( TP53^{−/−} \) cell lines were generated by pre-designed zinc finger nucleases (Sigma) that target the second exon of the \( TP53 \) gene. After electroporation of the cells with the nucleases (Neon Transfection system, Life Technologies), cells were incubated for 48 h, single sorted, and grown to single colonies in the absence of any selection marker. Loss of p53 was assayed by immunoblotting after doxorubicin treatment. For functionality assays, 1.5 \( \mu M \) doxorubicin was applied for 1 h.

In the context of the CAST approach, cells were perturbed with sublethal concentrations of doxorubicin (0.15 \( \mu M \)) and Zeocin (50 \( \mu g/ml \)) for 12 h or hesperadine (100 nM) and reversine (5 \( \mu M \)) after 48 h of TRF2 siRNA (Ambion), released into fresh media, and incubated for 3 days before they were sorted for single cells in 96-well plates.

To generate tetraploid cells from the C111 clone, 2 \( \mu M \) dihydrocytochalasin B (DCB, Sigma), a chemical compound preventing remodeling of the actin cytoskeleton, was applied. After 20 h of DCB treatment, cells were single sorted and grown to colonies. Tetraploidy was assessed by flow cytometry for DNA content using Hoechst (33342, Life Technologies).

RPE-1 WT, C111, C29, and BM175-H2B-mCherry cells were generated by retroviral transduction of the pQCXIP-H2B-mCherry plasmid. Cells positive for mCherry were then sorted in bulk.

**Immunoblotting**

Cells were seeded on 6-well plates to reach 70–80% confluence. Prior to cell extraction, cells were either treated with 1.5 \( \mu M \) doxorubicin
Cells were cultured on 10-cm-diameter plates up to a confluence of 90% and then were either treated with 1.5 μM doxorubicin for 1 h or left untreated. Treated and untreated cells were seeded on 6-well plates (40–50% confluency) and were stained for senescence-associated β-galactosidase activity after 24, 48, and 72 h using the Senescence-βGal Staining Kit (Cell Signaling Technology) following the manufacturer’s instructions. All the experiments were repeated three times, and one of the representative results is shown.

**Transformation assays**

After sorting, single cells were grown into colonies, before subjecting them to soft agar consisting of 0.5% bottom layer agar and 0.35% top layer agarose to assay for in vitro transformation. As an alternative, 96-well soft agar assays were purchased from CellBio-labs and used according to manufacturer’s instructions. The transformed colonies (observed after 30 days with our in-house protocol or after 10-15 days with the commercial kit) were recovered from 96-well plates, and recultured on 6-well plates. Single colonies were isolated and grown for further analysis.

**DNA libraries and sequencing**

Genomic DNA was extracted from the cells using the DNA Blood Mini Kit (Qiagen). In the context of CAST, library preparation was performed with a Beckman Biomek FX automated liquid handling system, with 500 ng starting material using SPrIworks HT chemistry (Beckman Coulter). For low-coverage sequencing, samples were prepared with custom 6 base pair barcodes to enable pooling. Library quantification and quality control were performed using a Fragment Analyzer (Advanced Analytics Technologies, Ames, USA). WGS was pursued on an Illumina HiSeq 2500 platform (Illumina, San Diego, USA), using 50 base pair single reads for low-pass sequencing.

Mate-pair DNA library preparation was performed using the Nextera Mate Pair Sample Preparation Kit (Illumina). In brief, 4 μg of high molecular weight genomic DNA was fragmented by the tagnmentation reaction in 400 μl, followed by strand displacement. Samples were size-selected to 4–5 kb following the Gel-Plus path of the protocol. A total of 300–550 ng of size-selected DNA was circularized in 300 μl for 16 h at 30°C. After an exonuclease digestion step to get rid of remaining linear DNA, fragmentation to 300–700 bp with a Covaris S2 instrument (LGC Genomics), and binding to streptavidin beads, the libraries were completed via End Repair, A-Tailing, and Illumina TrueSeq adapter ligation. The final sequencing library was obtained after PCR for 1 min at 98°C, followed by five cycles of 30 s at 98°C, 30 s at 60°C, 1 min at 72°C, and a final elongation step of 5 min at 72°C. Sequencing was carried out with Illumina HiSeq2000 (2 × 101 bp reads), MiSeq (2 × 75 bp reads), or NextSeq (2 × 150 bp reads) instrument using v3 or v4 chemistry to reach an average spanning coverage of 20–30× for the mate-pair libraries and an average sequencing coverage of 20–30× for deep WGS libraries. After sequencing, the reads were aligned to the hg19 build of the human reference genome using the Illumina-provided alignment software ELAND (version 2) for all RPE-1-derived sequencing data, and using BWA for the cancer genomic data.

**Analysis of DNA sequencing data**

Deletions, tandem duplications, inversion, inter-chromosomal SRs, and combinations thereof (complex SRs) were inferred using DELLY...
v0.0.11 (Rausch et al., 2012b). For inference of SRs in cell lines, we considered all DELLY-inferred SRs as “somatic” that were not present in 8-fold coverage WGS-sequenced genomes from 1,106 healthy individuals sampled by the 1,000 Genomes Project (1000GP, phase 2/3) (Genomes Project et al., 2012)—that is, specimens obtained from normal individuals with ancestry from diverse human populations (Genomes Project C et al., 2012). SRs in primary tumor samples were inferred by comparing tumor with paired normal samples from the same patient and additionally through subtracting calls corresponding to SRs detected in the 1000GP. SRs were considered as identical if their start and end coordinates differed by less than 5.0 kb (approximate insert size of a long-range paired-end library) and if their reciprocal overlap was larger than 50%. Variants that were present in the control samples were either true germ line variants or represented artifacts caused by misalignment of reads (e.g., due to inaccuracies in the hg19 human reference genome assembly). To consider a variant prediction as high confident, we further required at least four supporting read pairs with a minimum median mapping quality of 20 for each event to exclude false-positive predictions caused by random mapping of low-quality DNA reads. Tetraploidy in medulloblastoma samples was inferred by clustering tumor B-allele frequency (BAF) assignments together with WGS coverage ratios (tumor versus normal) for all inferred heterozygous SNP sites.

### Haplotype-based profiling of allelic imbalances

We profiled haplotype-specific allelic imbalances and copy numbers in samples with WGS data (> 25-fold sequence coverage). We inferred germ line SNPs using the variant caller freebayes (Garrison, 2012) (v0.9.15 and v0.9.20; default parameters, -i -X –u; https://github.com/ekg/freebayes) and only retained high quality bi-allelic SNPs (QUAL > 20) that overlapped SNPs from the 1000 Genomes Project (2014 release). Heterozygous sites were statistically phased using SHAPEIT2 (Delaneau et al., 2013) (v2; parameters: -window 10 Mb, -ststates 5008, -no-mcmc, overlap between chunks: 1 Mb) with a haplotype reference panel based on the 1000GP October 2014 release. Phased heterozygous SNPs were genotyped in tumor genomes (or clones with SRs) using freebayes (default parameters, -l @). We excluded rare variants (MAF < 1%, Ensembl 75) and variants that were covered by less than four reads from further analysis to minimize errors in phase estimation and quantification of allelic imbalance. We segmented phased allelic ratios with the CBS analysis to minimize errors in phase estimation and quantification of variants that were covered by less than four reads from further analysis.

### PCR validations

Primers were constructed with our in-house primer design pipeline, based on primer3 software (http://bioapps.primer3 www.cgl), and purchased from Sigma. PCR experiments were performed as follows: 10 ng of genomic DNA was used with the SequaPrep Long PCR Kit (Invitrogen) in 20 µl volumes applying the following PCR conditions in a MJ Mini thermocycler (BioRad): 94°C for 3 min, followed by 10 cycles of 94°C for 10 s, 62°C for 30 s and 68°C for 6 min and 25 cycles of 94°C for 10 s, 60°C for 30 s, and 68°C for 7 min, followed by a final cycle of 72°C for 10 min. PCR products were analyzed on a 1% agarose gel stained with SYBR Safe Dye (Invitrogen).

### RNA libraries and sequencing

Total RNA was extracted from cells using the RNeasy mini kit (Qiagen). RNA quality control was performed using the 2100 Bioanalyzer platform (Agilent). A total of 500 ng total RNA was used as a starting material for the RNA sequencing libraries, which were prepared using the TruSeq strand-unspecific protocol with Ribo-Zero Gold (Illumina) and sequenced on the Illumina HiSeq 2000 platform with 2 × 51 cycles according to the manufacturer’s instructions. In order to minimize batch effects, samples were processed on a Beckman Biomek FX robot following the manufacturers’ instructions.

### RNA sequencing analyses

RNAseq reads were aligned to the reference built by bowtie based on Ensembl v. 62 exons, build GRCh37.p3. Gene-specific read counts were obtained with the Genomic Alignments package in R, using a strand-unspecific model together with the Ensembl transcript database. Differential expression was assessed with the R package DESeq.

### Statistical testing

For the analysis of non-random distributed samples, permutation testing was applied. The labels of the two groups switched, and the mean difference was computed 10,000 times and then compared to the observed difference. For the analysis of breakpoint clustering, a KS test was applied testing for statistically significant deviation from the null hypothesis of no breakpoint clustering. For the analysis of random distribution of SR types, multinomial testing against the null hypothesis “equal distribution of joins” was applied using the R package “EMT.”

### Fluorescence in situ hybridization

Cells were cultured in 225-cm flasks (Sigma Aldrich, CLS431082) up to a confluence of 95% and then treated with 100 ng/ml of colcemid (Sigma Aldrich, D1925) for 6 h. Cells were collected by mitotic shake-off and transferred to a freshly prepared hypotonic solution (KC1 0.55% (Merck-Milipore) and Na-citrate (Merck-Milipore) 1% mixed 1:1) following centrifugation. Cells were swollen in hypotonic solution and subsequently fixed by methanol-acetic acid mixture (3:1, Merck-Milipore). Fixed cells were dropped on glass slides prewarmed with steam, which were previously treated with methanol (Merck-Milipore). The slides were then dried, and the confluence and the quality of the spreads were checked under a microscope. For chromosome counts, cells were probed with PNA centromere probe coupled to Cy3 dye (Panagene) according to manufacturers’ instructions. DNA was stained with 0.2 g/ml Hoechst 33342 (Life Technologies).
Microscopy

Imaging on most indirect immunofluorescence samples was performed at 25°C on a DeltaVision RT system (Applied Precision) with an Olympus IX71 microscope. This system was equipped with FITC, TRITC, and Cy5 filters (Chroma Technology), a plan-Apo 100× NA 1.4 and 60× NA 1.4 oil immersion objective (Olympus), a CoolSNAP HQ camera (Photometrics), a temperature controller (Precision Control), and Softworx software (Applied Precision).

Live cell imaging

Cells were seeded into chambered cover glasses (LabTEK: Thermo Fisher Scientific), and the lids of the chambers were sealed with baysilone paste (Neolab). Approximately 30 min before imaging, culture medium was exchanged to prewarmed CO2-independent medium without phenol red, containing 20% FCS, 2 mM glutamine, and 100 mg/ml penicillin-streptomycin. Live cell microscopy was performed in 37°C microscope incubators (EMBL GP106) on a Zeiss 780 confocal microscope with a 63× PlanApochromat oil objective (NA 1.4, Carl Zeiss) and in-house temperature controller, controlled by the Zen 2010 Software. Six z stacks with 2.00-μm intervals were used for each position. Images were acquired with 5-min time resolution. When applicable, automated quantitative analysis of cells was pursued to monitor mitotic progression in single cells. To this end, nuclei were detected in the H2B-mCherry channel and classified as previously described (Held et al, 2010; Walter et al, 2010) with an overall accuracy of > 90.0%. Cells were tracked with a constrained-nearest-neighbor tracking procedure, and mitotic onset was detected as interphase–prophase or interphase–prometaphase transition. To reduce the effect of classification errors on phase length measurements, classification results were corrected using hidden Markov models (Held et al, 2010).

Data deposition

Cell-line-based sequencing data (DNA and RNA based) are deposited at ENA, accession PRJEB8037, and patient sequencing data at EGA, accession EGAS00001000215.

Expanded View for this article is available online: http://msb.embopress.org

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