RASSF1A-LATS1 signalling stabilises replication forks by restricting CDK2-mediated phosphorylation of BRCA2

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Genomic instability is a key hallmark of cancer leading to tumour heterogeneity and therapeutic resistance. BRCA2 has a fundamental role in error-free DNA repair but additionally sustains genome integrity by promoting RAD51 nucleofilament formation at stalled replication forks. CDK2 phosphorylates BRCA2 (pS3291-BRCA2) to limit stabilising contacts with polymerised RAD51, however, how replication stress modulates CDK2 activity and whether loss of pS3291-BRCA2 regulation results in genomic instability of tumours is not known. Here we demonstrate that the hippo pathway kinase LATS1 interacts with CDK2 in response to genotoxic stress to constrain pS3291-BRCA2 and support RAD51 nucleofilaments, thereby maintaining genomic fidelity during replication stalling. We also show that LATS1 forms part of an ATR mediated response to replication stress that requires the tumour suppressor RASSF1A. Importantly, perturbation of the ATR-RASSF1A-LATS1 signalling axis leads to genomic defects associated with loss of BRCA2 function and contributes to genomic instability and 'BRCA-ness' in lung cancers.

Replication stress occurs when the progression of a DNA replication fork is impeded by base lesions, insufficient nucleotides (e.g. hydroxyurea, hypoxia) or oncogene enforced errors and is typified by accumulation of single stranded DNA (ssDNA)[1-5]. Increasing evidence suggests that failure to appropriately protect this ssDNA leads to nucleolytic attack, compromising the integrity of nascent DNA at stalled forks and results in increased chromosomal aberrations in human precancerous lesions[6-9]. Recently, components of the Homologous Recombination (HR) pathway have been identified to have a repair independent function that protects nascent DNA at stalled replication forks[8-11]. BRCA1/2 and FANCD2 tumour suppressors promote the formation of RAD51 nucleofilaments on ssDNA at stalled forks to prevent MRE11 nucleolytic activity and thereby facilitate restart after resolution of replication stress[8-10,12,13]. Failure to efficiently stabilise RAD51 nucleofilaments at stalled forks leads to DNA damage and is purported to be the source of the genomic instability observed in BRCA1/2 mutation carriers and Fanconi Anaemia patients[9].

Formation of a nucleofilament requires initial association of RAD51 monomers with BRC repeats of BRCA2 before polymerisation onto ssDNA. An additional contact of polymerised RAD51 with the C-terminal TR2 domain of BRCA2 stabilises the nucleoprotein filament specifically at replication forks[14,15]. CDK dependent phosphorylation of S3291 within the TR2 domain of BRCA2 decreases binding affinity for polymerised RAD51, resulting in

nucleofilament disruption[16]. Upon genotoxic stress, levels of pS3291-BRCA2 are reported to decrease to ensure that RAD51 filament stabilisation can contribute to fork protection and HR[8,16].

LATS1 is a central Ser/Thr kinase of the hippo (MST) tumour suppressor pathway[17,18] that restricts malignant transformation[19]. We previously reported that activation of MST2 in response to DNA damage requires direct phosphorylation of RASSF1A on S131 by the apical sensor of DNA double strand breaks, ATM. In response to ATM activation, MST2 targets LATS1 which in turn phosphorylates the transcriptional co-activator YAP1 promoting its interaction with p73 and induction of apoptosis[20]. Phosphorylation of Ser131 promotes RASSF1A dimerisation and orientates the associated MST2 monomers to allow stimulation of MST2 kinase activity[20]. The minor allele of a common Single Nucleotide Polymorphism (SNP) (*RASSF1* c.397G>T) results in RASSF1A-A133S, which fails to get phosphorylated by ATM or activate MST2/LATS1[21] and is associated with poor overall survival and early cancer onset in BRCA2-mutation carriers[22-24]. RASSF1A is also a frequent site of epigenetic inactivation in sporadic human malignancies with increasing prognostic significance across multiple tumour types[25-27]. Thus, loss of function via genetic or epigenetic routes can lead to RASSF1A inactivation, loss of hippo pathway signalling and promotes malignant transformation.

LATS1 was identified in a screen for ATM/ATR responsive substrates that are required for genomic stability[28]. In this study we show that in response to fork stalling LATS1 interacts with CDK2, restricting pS3291-BRCA2 and thereby facilitating RAD51 nucleofilament stability. This interaction relies on the ATM and Rad3-related kinase (ATR), the main sensor of replication stress[29] that phosphorylates RASSF1A on Ser131 to activate LATS1. We find that the RASSF1A/LATS1 signalling cascade is required during genotoxic stress to support nascent DNA stability at stalled forks. Moreover, we provide evidence that compromised signalling via genetic or epigenetic events leads to accumulation of chromosomal aberrations and introduction of a 'BRCAness' phenotype in tumours.

Results

LATS1 is necessary for establishment of RAD51 nucelofilaments in response to stress

To gain insight into LATS1 function in response to genotoxic stress we compared the cell cycle profiles of Mouse Embryonic Fibroblasts (MEFs) derived from mice genetically ablated for *Lats1* with their wild type (wt) littermates after exposure in γIR. In line with the findings presented in the genetic screen performed by Matsuoka *et al*[28]., loss of LATS1 through genetic ablation (*Lats1*$^{-/-}$ MEFs) or siRNA mediated silencing, results in enhanced G2/M retention of cells experiencing genotoxic stress (Fig. 1a and Supplementary Fig. 1a). We found that irradiated cells accumulate in G2/M due to elevated levels of γH2AX, a marker of DNA damage and replication fork stalling[12], which persisted in *Lats1*$^{-/-}$ MEFs (Fig. 1b and Supplementary Fig. 1b,d) and LATS1 depleted U2OS cells (Supplementary Fig. 1c,e) but was resolved in control cells. To confirm that high γH2AX levels are indeed due to increased DNA damage, cells were subjected to alkaline single-cell electrophoresis where bright comet tails indicate chromatin unwinding as a result of DNA breaks. As observed for γH2AX, *Lats1*$^{-/-}$ MEFs similarly displayed more DNA breaks (Supplementary Fig. 1f) and re-expression of LATS1 or a kinase dead derivative LATS1-D846A (LATS1-KD) rescued the phenotype, indicating that LATS1 functions to protect against DNA damage independently of kinase activity (Fig. 1b, Supplementary Fig. 1b,d,f). We reasoned that LATS1 either facilitates DNA repair or prevents excessive DNA damage upon genotoxic stress during S phase. Matsuoka *et al.* previously observed that loss of LATS1 leads to increased γH2AX levels and suggested a potential role in HR, the main DNA double strand break repair pathway in S phase cells[28]. To test whether LATS1 facilitates DNA repair via HR, we first assessed recombination competence using the I-SceI assay, where HR activity is required to restore a functional copy of *GFP* and can be scored by FACS. We also monitored RAD51 foci by immunofluorescence as a marker of BRCA2 mediated loading of RAD51 onto resected DNA at break sites which is a prerequisite for HR. Surprisingly, while depletion of LATS1 did not result in significant differences in HR competence (Fig. 1c, Supplementary Fig. 2a), RAD51 foci appeared retarded in response to γIR (Supplementary Fig. 2b). This suggests that elevated γH2AX due to LATS1 ablation is associated with ineffective RAD51 nucleofilament formation. RAD51 catalyses DNA strand exchange to provide a template for HR[30], however, RAD51 also functions in genome protection via a HR independent pathway by forming nucleofilaments that stabilise stalled replication forks[9,10,31].

To determine whether LATS1 contributes to RAD51 foci establishment at stalled forks we depleted nucleotide pools with hydroxyurea (HU) to specifically arrest replication forks. After 6 hours of HU exposure, RAD51 foci were evident in control cells (Fig. 1d) and importantly these were independent of HR associated repair of double strand breaks ($p53BP1^{+ve}$) that occur at later time points (>10hr HU)[32,33]. In response to HU induced stalled forks, wt MEFs form protective RAD51 filaments on nascent ssDNA, however, RAD51 foci fail to establish in *Lats1*$^{-/-}$ MEFs under the same conditions ($RAD51^{+ve}$/$p53BP1^{-ve}$ cells in Fig. 1d). Reconstitution of *Lats1*$^{-/-}$ MEFs with either LATS1 or a LATS1 kinase dead derivative (LATS1-KD) restored RAD51 foci, indicating that LATS1 promotes RAD51 nucleofilaments at stalled replication forks (Fig. 1d). We found that MST2 mediated activation of LATS1 is required to establish RAD51 foci, while the classical substrate YAP is dispensable, correlating with a kinase redundant role for LATS1 and a regulatory output for the hippo pathway independent of YAP (Supplementary Fig. 2c). Interestingly, despite the well described role of LATS1 in the regulation of tissue size, discrepancies between the ablation of *Lats1* in mice and conditional expression of constitutive *Yap1* mutants in murine liver suggests the existence of additional mechanisms through which LATS1 suppresses tumour formation[34-36], most notably the potential kinase independent regulation of CDK[37]. Moreover, LATS1 has been shown to interact with CDK1 in mitosis modulating its kinase activity[37].

LATS1 interacts with CDK2 in response to stress and modulates BRCA2 phosphorylation

Exogenous expression of LATS1 homologs bind and restrict CDK kinase activity[37], but the physiological relevance of an endogenous complex has remained elusive. As CDK activity is reported to destabilise RAD51 nucleofilaments, we considered that LATS1 may exert its effects through modulation of CDK activity. In agreement with previous evidence, we were unable to detect an interaction between CDK1/2 and LATS1 in cycling cells, however, upon exposure of cells to γIR or HU induced replication fork stalling, association of endogenous CDK2 and LATS1 was readily observed in reciprocal immunoprecipitates (Fig. 2a). To map the LATS1/CDK2 interaction we generated LATS1 deletion mutants (Fig. 2b) that indicated that binding occurs in the N-terminus (Fig. 2b, lanes 1, 4) and requires residues 1-200 (Fig. 2b, lanes 2, 3 and 5) which encode an Ubiquitin Associated (UBA) domain that directs distinct biological functions of LATS paralogues[38,39]. In line with defective CDK2 association, the LATS1Δ200 derivative was also incapable of establishing RAD51 foci (Fig. 2c). As previously

reported for wts/cdc2 and LATS1/CDK1 complexes[37], we find that cyclin partners were excluded from the CDK2 fraction that co-immunoprecipitates with LATS1, leading to loss of substrate targeting and kinase activity (Fig. 2d).

CDK2 mediated C-terminal phosphorylation of BRCA2 leads to unstable RAD51 nucleofilaments[16], therefore we reasoned that LATS1 may facilitate RAD51 foci at stalled forks via preventing phosphorylation of S3291-BRCA2. To test this we addressed pS3291-BRCA2 levels after γIR and HU exposure and found a dramatic elevation of pS3291-BRCA2 in the absence of LATS1, while exogenous LATS1 expression restores control levels (Fig. 2e, Supplementary Fig. 3a). Following γIR, pS3291-BRCA2 levels decrease to facilitate fork stability and HR[16], however loss of LATS1 results in maintenance of phosphorylation levels and correlates with lower RAD51 foci and increased damage (Fig. 1b, d, 2e and Supplementary Fig. 2b). In nocodozol arrested cells, where CDK1 is responsible for pS3291-BRCA2[16,40], higher but identical kinetics to cycling cells were observed, in keeping with LATS1 ability to associate with CDK1 (Supplementary Fig. 3a). Furthermore, *in vitro* phosphorylation of a TR2-domain peptide indicates that CDK2 activity was lower in γIR treated *Lats1*$^{+/+}$ compared to *Lats1*$^{-/-}$ MEFs (Supplementary Fig. 3b). Together, these data provide a model where LATS1 binds CDK2, inhibiting BRCA2-TR2 domain phosphorylation and allows RAD51 filament assembly on ssDNA in response to genotoxic stress.

Activation of RASSF1A by ATR is necessary for LATS1 binding to CDK2

In response to DNA damage, RASSF1A activates the hippo cascade via MST2 and LATS1 [20,41]. In H1299 lung cancer cells that lack RASSF1A due to promoter methylation[27], LATS1 is unable to associate with CDK2 in response to either HU or γIR (Fig. 3a lanes 4 and 7), but the interaction was restored upon RASSF1A expression (Fig. 3a, lanes 5 and 8). In response to DNA double strand breaks, ATM targets RASSF1A on S131, but fails to activate the genetic variant RASSF1A-A133S at the same recognition site[21]. In contrast to wt RASSF1A, expression of RASSF1A-A133S could not rescue association with CDK2 (Fig. 3a, lanes 6 and 9). We next addressed the levels of pS3291-BRCA2 in response to stress after RASSF1A depletion and the ability of *Rassf1A* genetically null MEFs (*Rassf1A*$^{-/-}$) to form RAD51 filaments on nascent DNA after exposure to HU. In response to either γIR or HU, pS3291-BRCA2 levels decrease but are maintained in the absence of RASSF1A, indicating a greater level of CDK2 activity (Fig. 3c).

Moreover *Rassf1A*$^{-/-}$ MEFs are unable to form stable Rad51 nucleofilaments in response to HU (Fig. 3b).

Short HU treatments that do not result in double strand breaks lead to ATR rather than ATM activation, which then elicits appropriate cellular responses to both protect stalled DNA forks and promote resolution of breaks or lesions[29]. ATM recognition sites have been shown to be frequently targeted by ATR in response to single strand breaks or replication stress[42,43], prompting us to consider that RASSF1A may be targeted by ATR in response to fork stalling. To this end, U2OS cells were transiently transfected with FLAG-RASSF1A or FLAG-RASSF1A-A133S and exposed to HU in the presence of a specific ATR inhibitor, VE-821. We found that HU treatment elevates phosphorylation of Ser131 (Fig. 3d, lane 5), while addition of VE-821 inhibits HU dependent increase in pS131-RASSF1A, indicating that RASSF1A is an ATR target (Fig. 3d, lane 8). Similar to ATM mediated targeting, the polymorphic variant did not present any detectable levels of phosphorylation in response to ATR activation (Fig. 3d, lanes 6 and 9). Taken together, the above data highlight that ATR activates the RASSF1A-LATS1-CDK2 cascade in response to replication stress.

Disruption of the RASSF1A/LATS1 axis leads to genomic instability

Failure to establish RAD51 nucleofilaments on ssDNA during replication stalling leads to MRE11 nuclease mediated degradation of nascent DNA and subsequent genomic instability[8-11]. To test whether loss of RASSF1A-LATS1 signalling compromises the stability of nascent DNA at stalled forks we employed DNA fiber analysis to monitor track length of replicated DNA via incorporation of halogenated base analogues that can be detected by immunofluorescence. DNA fibers of *Lats1*$^{+/+}$, *Lats1*$^{-/-}$ and *Lats1*$^{-/-}$ cells expressing mycLATS1 did not differ in the length of CldU (nascent DNA) (Supplementary Fig. 4a). However, after 5 hours of HU treatment CIdU tracks appeared shorter in *Lats1*$^{-/-}$ MEFs in comparison to *Lats1*$^{+/+}$ MEFs (6.6 ± 0.14 and 10.09 ± 0.2 μm respectively, *p=0.0001*) and were restored after re-expression of mycLATS1 (10.3 ± 0.6 μm, *p=0.02*) (Fig. 4a and Supplementary Fig. 4c). To establish whether shorter CIdU tracks in the absence of LATS1 is due to the exposure of the nascent DNA to MRE11 nucleolytic activity, the specific MRE11 inhibitor mirin was used during the HU treatment. *Lats1*$^{-/-}$ MEFs that were treated with mirin, present CIdU tracks with a similar length to control MEFs (8.9 ± 0.91 and 9.2 ± 0.8 μm respectively) (Fig. 4b). RASSF1A ablation had identical effects on fork integrity (CIdU length in *Rassf1A*$^{+/+}$ vs *Rassf1A*$^{-/-}$ MEFs of 8.8 ± 0.4

and 5.1 ± 0.3 µm respectively, *p=0.01*), which were efficiently rescued by the re-expression of FLAG-RASSF1A (8.08 ± 0.6 µm) but not the polymorphic mutant (5.3 ± 0.1 µm) (Fig. 4c, Supplementary Fig. 4b, d), indicating that ATR phosphorylation of RASSF1A is necessary to protect nascent DNA at stalled forks. Interestingly, both *Lats1*$^{-/-}$ and *Rassf1A*$^{-/-}$ MEFs show shorter second label IdU tracks (Supplementary Fig. 5a, b) indicating defective replication restart after the HU removal, which is independent of MRE11 nucleolytic activity (Fig. 4b). RAD51 has been proposed to facilitate fork regression and formation of a Holliday junction intermediate or ''chickenfoot'', which offers a more favourable substrate for restart[12,13] and maybe regulated by components that protect fork integrity[44], including RASSF1A and LATS1 .

To determine whether compromised fork integrity in the absence of the RASSF1A/LATS1 axis leads to genomic instability and properties of defective BRCA2 regulation[8], we prepared metaphase spreads from *Lats1*$^{-/-}$ and *Rassf1A*$^{-/-}$ MEFs and checked for typical chromosomal aberrations compared to controls. In line with previous identification of lagging chromosomes in *Rassf1A*$^{-/-}$ mice[45], addition of HU results in increased accumulation of chromosomal aberrations both in the *Lats1* and *Rassf1A* null genetic backgrounds compared to MEFs from littermate controls (aberrations/metaphase: *Lats1*$^{+/+}$ 0.45 vs *Lats1*$^{-/-}$ 4.1 and *Rassf1A*$^{+/+}$ 0.6 vs *Rassf1A*$^{-/-}$ 4.0) indicating that deletion of the RASSF1A/LATS1 axis induces a 'BRCA-ness' phenotype after exposure to stress (Fig. 5a, b and Supplementary Fig. 6a). Similarly, depletion of either LATS1 or RASSF1A from U2OS, increased chromosome aberrations (aberrations/metaphase: control 0.5 vs siLATS1 1.4 or siRASSF1A 1.5, Fig. 5c and Supplementary Fig. 6b) and the number of micronuclei arising from DNA fragments of broken chromosomes (9.6% in siNT versus 18.4% in siLATS1 and 18.2% in siRASSF1A respectively, Supplementary Fig. 6d). Moreover the endemic genomic instability observed in H1299 cells exposed to HU (RASSF1A^{methylated}), was rescued by re-expression of RASSF1A, but not by the polymorphic variant, explaining the predisposition to tumourigenesis of patients that carry this variant (Fig. 5d and Supplementary Fig. 6c)[23]. Moreover, depletion of LATS1 with siRNA ablated the RASSF1A mediated protection of replication stressed H1299 cells, suggesting that RASSF1A contributes to the maintenance of genomic stability via LATS1 (Fig. 5d, Supplementary Fig. 6c).

Methylation of *RASSF1* is a prognostic factor for poor overall survival in lung cancer and decreased therapeutic efficiency to DNA damaging agents in the clinic[46]. To test our

hypothesis that this is due to genomic instability, we used publicly available data from the Cancer Genome Atlas (TCGA) that contains genomic characterization data and sequence analysis of tumour genomes. Using the lung adenocarcinoma cohort, which displays frequent hypermethylation of *RASSF1*, we examined possible correlations between *RASSF1A* promoter methylation status and Copy Number Variation (CNV) of the genome. In this cohort (TCGA Lung adenocarcinoma; April 2014), 188 patients had available data and were separated in two groups based on levels of *RASSF1* promoter methylation (low<0.3 and high>0.3) and further divided in 4 subgroups based on the percentage of the genome that was altered (0-0.1%, 0.1-0.2%, 0.2-0.3% and >0.3%). We found an overall correlation between methylation of the *RASSF1* promoter and the extent of genomic instability (Fig. 6) that is independent of base substitutions (Supplementary Fig. 7); indicative of complex rearrangements that occur after collapsed replication forks observed in Fig. 5. The statistical power is derived from the extremes of the population where relatively stable genomes (<0.1% CNV) have low levels of methylation and unstable genomes (>0.3% CNV) have high methylation of the *RASSF1* promoter ($p=0.0054$), validating that RASSF1A functions to protect genome integrity (Fig. 6).

Thus, our data describes how ATR promotes BRCA2 dependent replication fork stability and identifies a single nucleotide polymorphism in RASSF1A as an allele displaying BRCAness. Moreover, epigenetic loss of RASSF1A in sporadic human malignancies similarly deregulates BRCA2 function, providing a link between the poor prognostic value of RASSF1A loss and BRCA-like phenotypes in common cancers.

Discussion

Previous reports highlighted that depletion of LATS1 leads to genomic instability and tumour predisposition[28,35,37]. We find that LATS1 safeguards genome stability by ensuring stable nucleofilament formation on exposed ssDNA at stalled replication forks (Fig. 7). This is achieved via activation induced conformational changes in LATS1 that stimulate interaction with CDKs as originally suggested by Tao *et al*.[35], and similarly is independent of LATS1 kinase activity. Moreover, in line with identification of LATS1 from screens for regulators of DNA damage[26], the endogenous LATS1-CDK2 interaction occurs in response to replication stress. The core hippo pathway components, RASSF1A and MST1/2 kinase are responsible for activation of LATS1 and are inhibited by growth factor receptor signalling, $KRAS^{WT}$ and RAF1[47-49]. In response to DNA damage, ATM activation results in phosphorylation of RASSF1A on Ser131, activating MST1/2 and LATS1 kinases leading to YAP/p73 proapoptotic complex formation and inhibition of YAP/TEAD mediated malignant transformation[20,41,50]. Failure to activate LATS1 in tumours provides support to $KRAS^{MUT}$ driven oncogenesis through sustained YAP1 transcription[51,52]. However, inefficient activation of LATS1 is likely to have additional effects than solely regulation of YAP1[35-37,39]. In this study we show that MST2 activity is also necessary for the establishment of RAD51 foci at stalled forks but YAP1 is dispensable, providing a new insight into how the core hippo pathway contributes to tumour suppression by maintaining genome integrity.

Schlacher *et al.* proposed that efficient RAD51 nucleofilament formation on nascent DNA of stalled forks is dependent on RAD51 interaction with the TR2 domain of BRCA2 and cannot be restored by re-expression of classical RAD51 binding BRC repeats alone[8,9]. We show that ablation of LATS1 leads to increased pS3291-BRCA2 within the TR2 domain, which prevents RAD51 nucleofilaments during stalling and causes significant shortening in the nascent DNA strands due to MRE11 nucleaolytic activity (Fig. 7). While this is consistent with increased DNA damage, the persistent γH2AX foci after treatment with γIR could also indicate defective DNA repair. Although we did not observe defects in HR, more extensive studies are warranted to determine whether LATS1 plays a role in additional DNA repair pathways. Elevated γH2AX levels may also be attributed to a failure of the fork to restart after resolution of the replication stress. BRCA1/2 and FANCD2 tumour suppressors were originally described as

dispensable for restart[8,9], however, fork recovery is also defective in *Lats1*$^{-/-}$ and *Rassf1A*$^{-/-}$ MEFs which is in line with several studies that indicate a requirement of RAD51 loading for efficient fork restart[12,13]. Moreover FANCD2 was recently reported to interact with BLM and facilitate fork recovery after stress[44]. The proposed role for the nascent DNA and fork regression being required for resolution of stalled fork architecture is controversial but would explain the role for RAD51 in restart.

We show that LATS1-CDK2 interaction and establishment of RAD51 nucleofilaments are RASSF1A dependent. RASSF1A is the most common epigenetically inactivated gene in human tumours. Increasing number of studies have shown that RASSF1A methylation positively correlates with therapeutic resistance and poor survival, indicating the potential utility of RASSF1A as a prognostic/diagnostic marker[25-27,53-55]. The *RASSF1* c.397G>T SNP results in distinct codon usage of Ala instead of Ser at position RASSF1A-133. The minor variant has a sub optimal ATM/ATR activation site and has been reported to act as a dominant allele that correlates with worse prognosis and early cancer onset in BRCA1/2 mutation carriers[21,23,24]. We demonstrate here that ATR activation is necessary for the triggering of the RASSF1A/LATS1 axis and that RASSF1A-Ser133 is unable to stimulate the pathway. Moreover our analysis of lung cancer patients provides a functional insight into how genomic instability and 'BRCAness' arises in sporadic tumours and may be identified by RASSF1A methylation in a wide variety of tumour types.

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Figure legends

Figure 1

LATS1 regulates RAD51 nucleofilament formation in response to replication stress in an HR independent manner. (a) Propidium Iodide profiles at the indicated time points after exposure to 10 Gy γIR of wild type MEFs, and *Lats1*$^{-/-}$ MEFs transfected with mycLATS1 or control plasmid. The percentage of cells in G1, S and G2/M is shown. **(b)** *Lats1*$^{+/+}$, *Lats1*$^{-/-}$ and *Lats1*$^{-/-}$ cells expressing wt hLATS1 (Lats1$^{-/-mycLATS1}$) or a hLATS1 kinase dead derivative LATS1-D846A (*Lats1*$^{-/-LATS1KD}$) were treated with 10 Gy γIR. Total cell extracts were isolated at the

indicated time points after irradiation and analysed for γH2AX expression. Both wtLATS1 and LATS1KD reconstitute the DNA repair kinetics after damage. Representative blots are shown. Error bars represent standard deviation from n=3 independent experiments. **(c)** HR assay of a single DNA break induced by I-SceI endonuclease, using the DR-GFP reporter in U2OS cells treated with the indicated siRNAs. GFP-positive cells indicate HR events after I-SceI expression. Error bars represent standard deviation from n=3 independent experiments **(d)** *Lats1*$^{+/+}$, *Lats1*$^{-/-}$, *Lats1*$^{-/-mycLATS1}$ and *Lats1*$^{-/-mycLATS1KD}$ MEFs were treated with Hydroxyurea (HU) for 4 or 6 hours, fixed and assessed for RAD51 and p53BP1 foci formation. The percentage of RAD51 positive cells without double strand breaks (negative for p53BP1 staining) was quantified and presented. At least 300 cells were scored per conditions in n=3 independent experiments. Error bars represent standard deviation. Statistical significance was determined by a two-tailed, unpaired t-test. * P< 0.05, ** P<0.01, ***P<0.001. Scale bar 10 μm.

Figure 2

LATS1 interacts with CDK2 in response to genotoxic stress modulating its kinase activity towards BRCA2. **(a)** U2OS cells were treated with 4 Gy γIR or 2 mM HU for 4 hours, lysed and total cell extracts were immunoprecipitated with LATS1 or CDK2 antibodies. Total cell lysates and immunoprecipitates were analysed by Western Blot and probed with antibodies against LATS1 and CDK2. **(b)** U20S cells were transiently transfected with full length Myc-LATS1 or LATS1 deletion mutants: Myc-LATS1Δ100, Myc-LATS1Δ200, Myc-ΔC-LATS1 (aa 1-589) or Myc-ΔN-LATS1 (aa 589-1130). 48 hours post transfection cells were treated with HU for 4 hours prior to Myc tag immunoprecipitation. Western blot analysis of total cell extracts and immunoprecipitates is shown. **(c)** *Lats1*$^{+/+}$, *Lats1*$^{-/-}$, *Lats1*$^{-/-mycLATS1}$ and Lats1$^{-/-mycLATS1Δ200}$ MEFs were treated with HU for 6 hours, fixed and stained for RAD51. 200 cells were scored per condition in n=3 independent experiments**.** Error bars represent standard deviation. Statistical significance was determined by a two-tailed, unpaired t-test. * P< 0.05, ** P<0.01, ***P<0.001. Scale bar 10 μm. **(d)** Total cell lysates and LATS1 immunoprecipitates of untreated or treated with γIR U2OS cells probed for the indicated antibodies. **(e)** Upper panel, detection of pS3291-BRCA2 in lysates of HT1080 cells transfected with control siRNA or siRNA against LATS1 and pcDNA3.1 (control) or mycLATS1 constructs. 48 hours post transfection cells were subjected to 4 Gy γIR and total cell extracts were collected over a 300 min time course. Quantitation of pS3291-BRCA2 over a time course presented in Supplementary Fig. 3a, is shown. Lower panel, *Lats1*$^{+/+}$ and *Lats1*$^{-/-}$ MEFs were treated with HU for the indicated times. Total cell extracts were collected and blotted for pS3291-BRCA2. Representative image of n=3 independent experiments is shown. Error bars represent the variation in the densitometry of the representative image.

Figure 3

Tumour suppressor RASSF1A stimulates LATS1/CDK2 interaction in response to ATR activation (a) H1299 cells (methylated *RASSF1 gene* promoter) were transiently transfected with pcDNA3.1, FLAG-RASSF1A (FLAG-R1A) or FLAGR1A-A133S and treated with 2 mM HU for 5 hours or 4 Gy γIR. LATS1 was immunoprecipitated from total cell lysates and co-immunoprecipitation of CDK2 was examined by Western Blot analysis. **(b)** Upper, PCR genotyping of genomic DNA, using a combination of two primer pairs (either RSF-5/RSF-3 or RSF-C/RSF-3), which can distinguish between *Rassf1A*$^{+/+}$ and *Rassf1A*$^{-/-}$ genotypes. Lower, RAD51 foci formation in *Rassf1A*$^{+/+}$ and *Rassf1A*$^{-/-}$ MEFs after exposure to 2 mM HU for the indicated periods. 200 cells were scored in each condition in n=3 independent experiments and bar graph represents quantification. Error bars represent standard deviation. Statistical significance was determined by a two-tailed, unpaired t-test. * P< 0.05, ** P<0.01, ***P<0.001. Scale bar 10 μm. **(c)** Upper, U2OS cells were treated with siRNA against RASSF1A or control siRNA (siNT) and subjected to 4 Gy γIR. Cell extracts were collected at the indicated time points and blotted for pS3291-BRCA2. Lower, *Rassf1A*$^{+/+}$ and Rassf1A$^{-/-}$ MEFs were treated with HU for the indicated times. Total cell extracts were collected and blotted for pS3291-BRCA2 **(d)** U2OS cells were transiently transfected with pcDNA3.1, FLAG-R1A or FLAG-R1A-A133S. Cells were treated with 2 mM HU for 5 hours in the presence or absence of the specific ATR inhibitor VE-821. RASSF1A phosphorylation on Ser131 was assessed in FLAG immunoprecipitates.

Figure 4

Deletion of RASSF1A/LATS1 axis compromises the stability of nascent DNA at stalled forks. **(a)** CIdU tract length distributions analysis from DNA fibres from *Lats1*$^{+/+}$, *Lats1*$^{-/-}$ and *Lats1*$^{-/-}$ ^{mycLATS1} MEFS in the presence of 2 mM HU. Median tract lengths and stand deviations are given in parentheses. Representative pictures for each condition are shown in Supplementary Fig. 4c. Western Blots indicate LATS1 expression. **(b)** CIdU tract length distributions from DNA fibres from *Lats1*$^{+/+}$, *Lats1*$^{-/-}$ and *Lats1*$^{-/-}$ MEFS treated with the MRE11 inhibitor, mirin, after treatment with 2 mM HU and representative pictures for each condition. **(c)** CIdU tract length distributions from DNA fibres from *Rassf1A*$^{+/+}$, *Rassf1A*$^{-/-}$, *Rassf1A*$^{-/-FLAGR1A}$ and *Rassf1A*$^{-/-FLAG-R1A-A133}$ MEFs exposed in 2 mM HU. Representative pictures for each condition are shown in Supplementary Fig. 4d. Western Blots indicate Flag-RASSF1A expression (* indicates non-specific band in MEF lysates). Sketch above delineates experimental design. At least n=100 DNA tracks were scored in each condition. Scale bars 10 μm.

Figure 5

Deletion of RASSF1A/LATS1 axis induces chromosomal aberrations. Number of chromosomal aberrations/metaphase spread of **(a)** *Lats1*$^{+/+}$ and *Lats1*$^{-/-}$ MEFs or **(b)** *Rassf1A*$^{+/+}$ and *Rassf1A*$^{-/-}$ with or without HU prior to colcemid addition. **(c)** U2OS cells were treated with control siRNA or siRNA against LATS1 or RASSF1A and exposed to HU prior to colcemid addition. The number of aberrant chromosomes/metaphase spread and representative metaphase spreads from HU treated cells are displayed. **(d)** H1299 cells were transfected with pcDNA3.1, FLAG-RASSF1A or FLAG-RASSF1A-A133S and exposed to HU prior to colcemid addition. The number of aberrant chromosome/metaphase in each condition and representative pictures from spreads of HU treated cells are shown. n=20 metaphases from MEFS and n=30 metaphases from cancer cells were scored per condition. Aberrant chromosomes in each metaphase are denoted by red asterisk and displayed in higher magnification. Error bars represent standard error of the mean. Statistical significance was determined by a two-tailed, unpaired t-test. P values are given on the figure. Scale bar 10 µm.

Figure 6

RASSF1A methylation correlates with increased CNV in lung cancer patients. Correlation of RASSF1 promoter methylation (illumina HM450) with genomic Copy Number Variation (CNV) in lung adenocarcinoma dataset from the cancer genome atlas database (TCGA, Provisional). Bar graph representing the percentage of patients in each subgroup based on extent of genome alterations (% of the genome) in cohorts with high (>0.3) or low (<0.3) RASSF1 promoter methylation. A total of 188 patients with Lung Adenocarcinoma were analysed using the Fisher's Extract test. Absolute numbers (n) and *p* values are presented in the table.

Figure 7

Model of RASSF1A/LATS1/CDK2 signalling and the protection of stalled replication forks. (a) In response to fork stalling and ATR activation, RASSF1A triggers LATS1-CDK2 interaction and restricts CDK2 kinase activity towards BRCA2 promoting the establishment of RAD51 filaments. (b) Upon genetic or epigenetic inactivation of RASSF1A, CDK2 remains active resulting in increased levels of pS3291-BRCA2, exposure of nascent DNA to MRE11 nucleolitic activity and genomic instability.

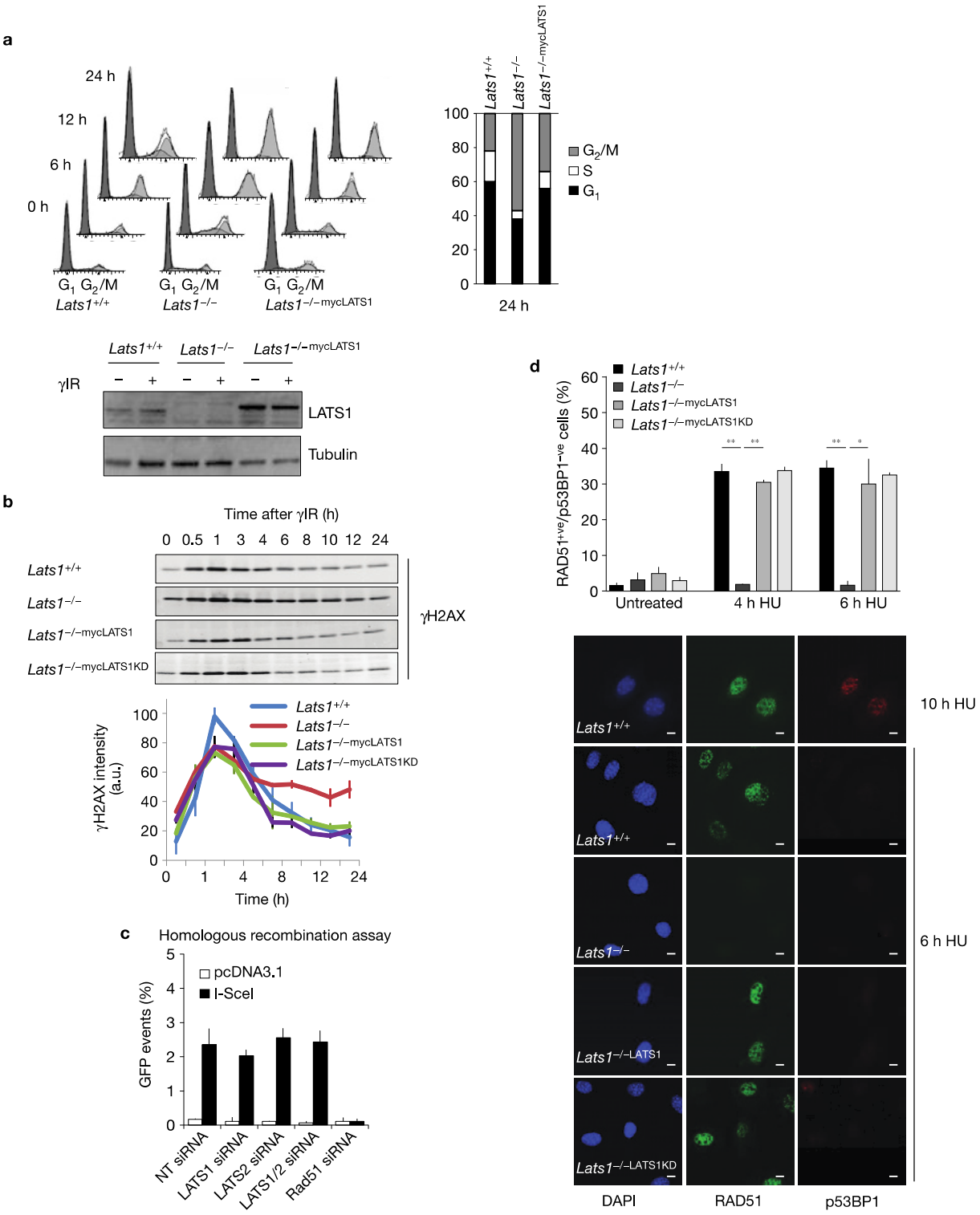
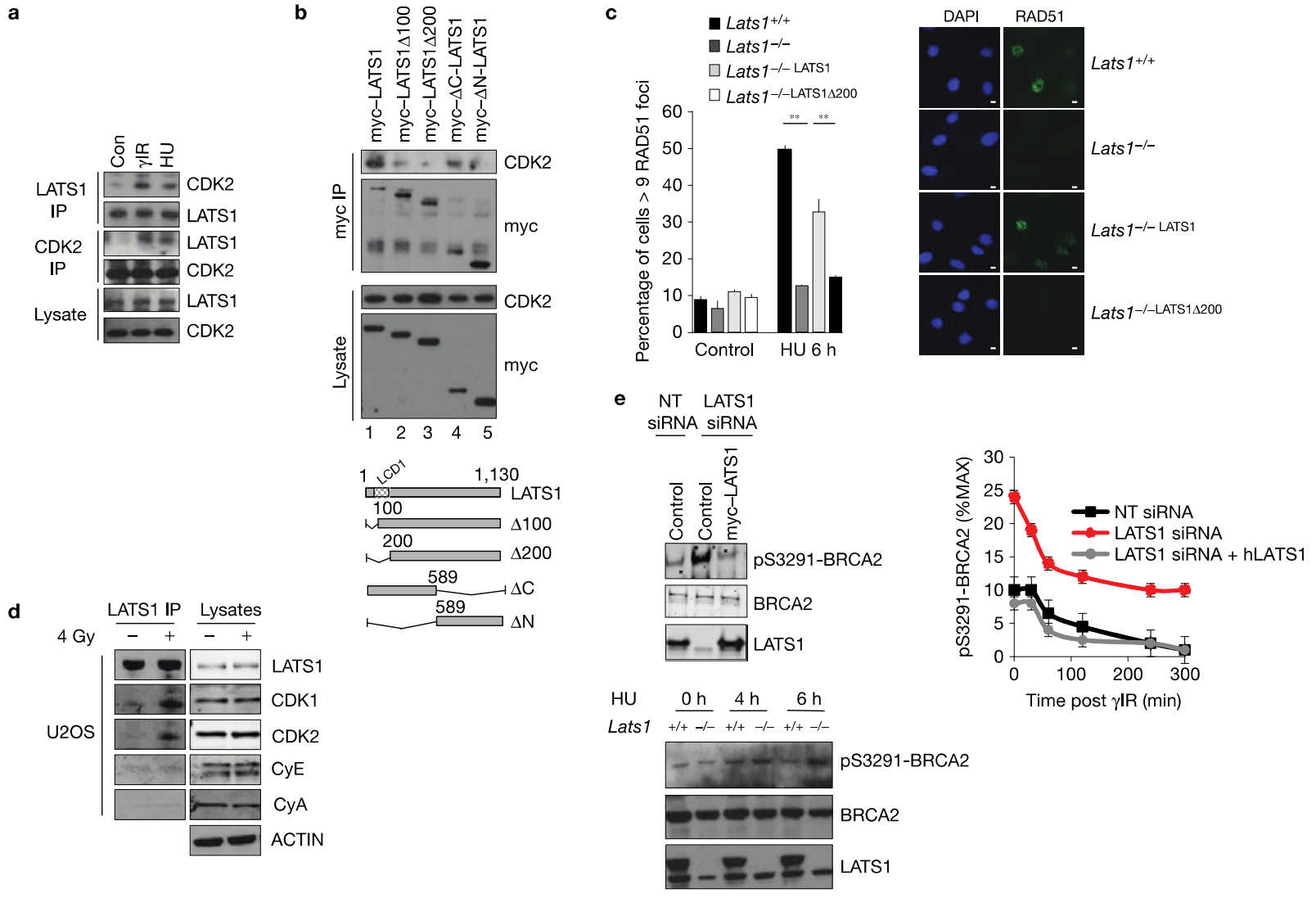

a
24 h
12 h
6 h
0 h
G1 G2/M
Lats1+/+
Lats1−/−
Lats1−/−mycLATS1
100
80
60
40
20
0
G2/M
S
G1
24 h
γIR
LATS1
Tubulin
b
Time after γIR (h)
0 0.5 1 3 4 6 8 10 12 24
Lats1−/−mycLATS1KD
γH2AX
γH2AX intensity (a.u.)
Time (h)
c
Homologous recombination assay
pcDNA3.1
I-SceI
GFP events (%)
NT siRNA
LATS1 siRNA
LATS2 siRNA
LATS1/2 siRNA
Rad51 siRNA
d
Lats1−/−mycLATS1KD
RAD51+ve/p53BP1−ve cells (%)
Untreated
4 h HU
6 h HU
10 h HU
6 h HU
Lats1−/−LATS1
Lats1−/−LATS1KD
DAPI
RAD51
p53BP1

Figure 1

Figure 2


a
Con
γIR
HU
LATS1 IP
CDK2
LATS1
CDK2 IP
LATS1
CDK2
Lysate
LATS1
CDK2
b
myc–LATS1
myc–LATS1Δ100
myc–LATS1Δ200
myc–ΔC-LATS1
myc–ΔN-LATS1
myc IP
CDK2
myc
Lysate
CDK2
myc
1 2 3 4 5
1
LCD1
1,130
LATS1
100
Δ100
200
Δ200
589
ΔC
589
ΔN
c
Lats1+/+
Lats1−/−
Lats1−/− LATS1
Lats1−/−LATS1Δ200
Percentage of cells > 9 RAD51 foci
60
50
40
30
20
10
0
**
**
Control
HU 6 h
DAPI
RAD51
Lats1+/+
Lats1−/−
Lats1−/− LATS1
Lats1−/−LATS1Δ200
d
LATS1 IP
Lysates
4 Gy
–
+
–
+
U2OS
LATS1
CDK1
CDK2
CyE
CyA
ACTIN
e
NT siRNA
LATS1 siRNA
Control
Control
myc–LATS1
pS3291-BRCA2
BRCA2
LATS1
HU
0 h
4 h
6 h
Lats1
+/+
–/–
+/+
–/–
+/+
–/–
pS3291-BRCA2
BRCA2
LATS1
pS3291-BRCA2 (%MAX)
30
25
20
15
10
5
0
0
100
200
300
Time post γIR (min)
NT siRNA
LATS1 siRNA
LATS1 siRNA + hLATS1

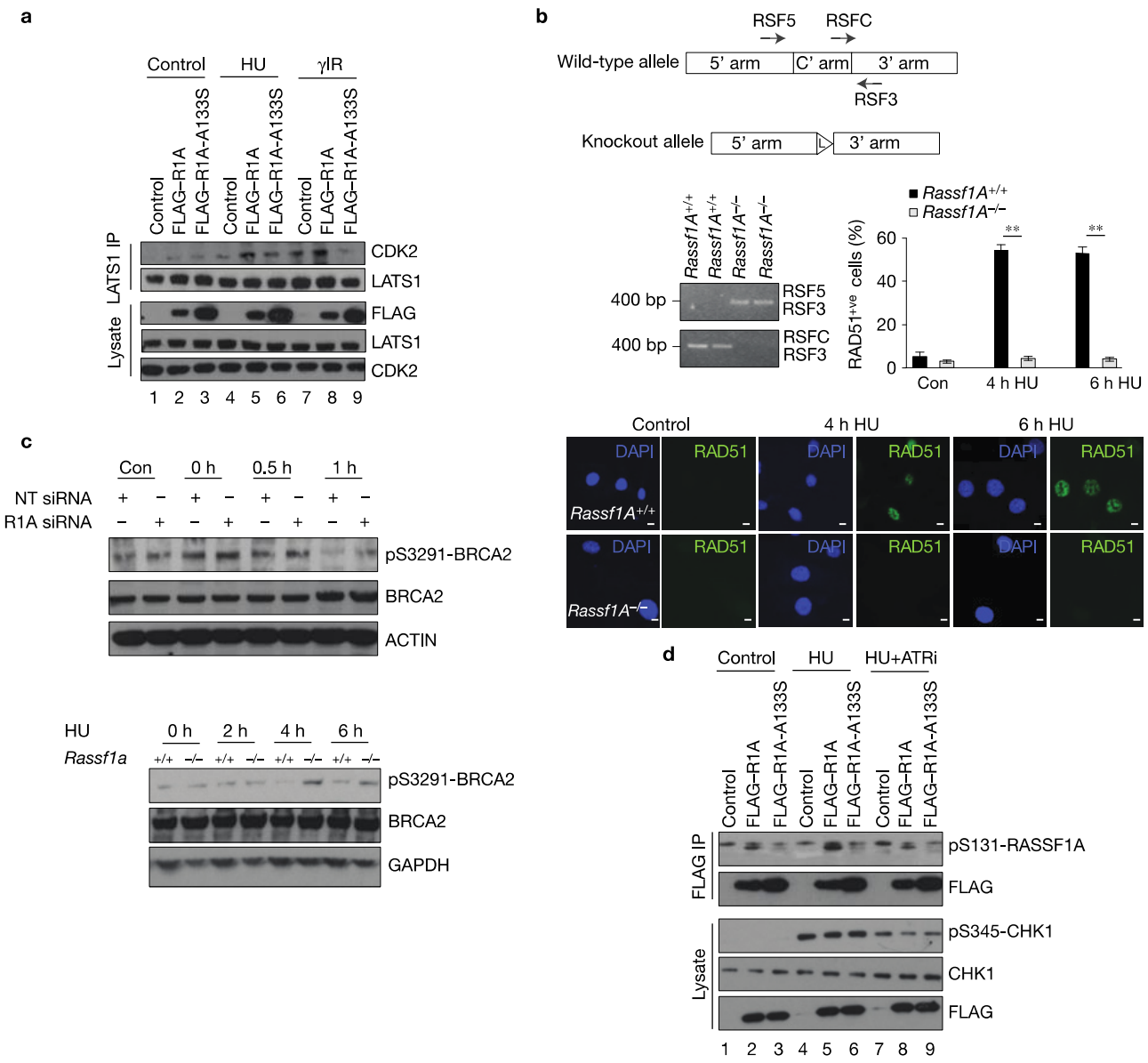

a
Control
HU
γIR
Control
FLAG–R1A
FLAG–R1A-A133S
LATS1 IP
Lysate
CDK2
LATS1
FLAG
LATS1
CDK2
1 2 3 4 5 6 7 8 9
b
RSF5
RSFC
Wild-type allele
5' arm
C' arm
3' arm
RSF3
Knockout allele
5' arm
3' arm
Rassf1A+/+
Rassf1A+/+
Rassf1A−/−
Rassf1A−/−
400 bp
RSF5
RSF3
400 bp
RSFC
RSF3
Rassf1A+/+
Rassf1A−/−
RAD51+ve cells (%)
60
40
20
0
**
**
Con
4 h HU
6 h HU
Control
4 h HU
6 h HU
DAPI
RAD51
Rassf1A+/+
Rassf1A−/−
c
Con
0 h
0.5 h
1 h
NT siRNA
R1A siRNA
pS3291-BRCA2
BRCA2
ACTIN
HU
Rassf1a
0 h
2 h
4 h
6 h
+/+ −/− +/+ −/− +/+ −/− +/+ −/−
pS3291-BRCA2
BRCA2
GAPDH
d
Control
HU
HU+ATRi
Control
FLAG–R1A
FLAG–R1A-A133S
FLAG IP
Lysate
pS131-RASSF1A
FLAG
pS345-CHK1
CHK1
FLAG
1 2 3 4 5 6 7 8 9

Figure 3

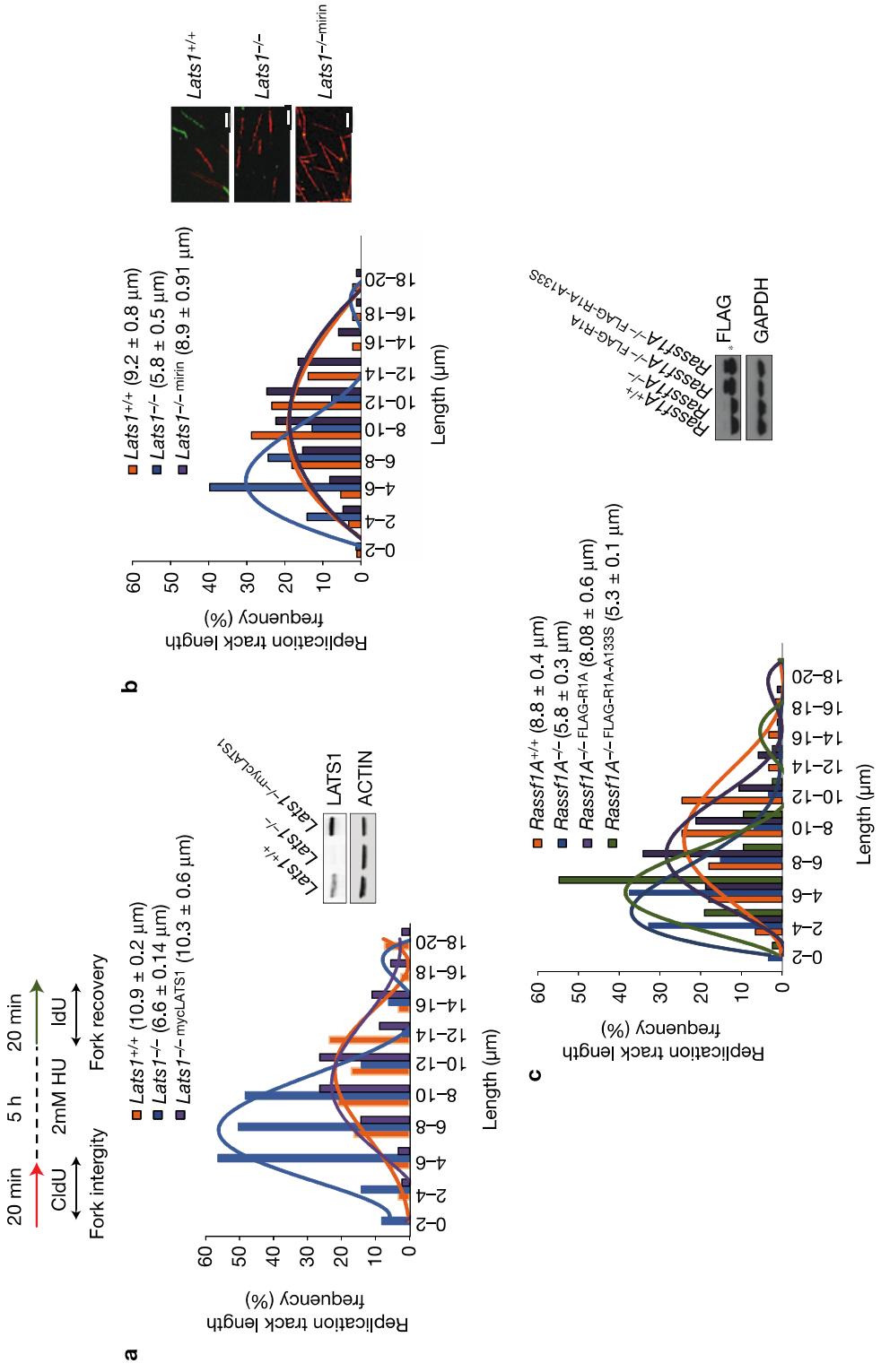

20 min
5 h
20 min
CldU
2mM HU
IdU
Fork intergity
Fork recovery
a
Lats1+/+ (10.9 ± 0.2 µm)
Lats1−/− (6.6 ± 0.14 µm)
Lats1−/− mycLATS1 (10.3 ± 0.6 µm)
Replication track length frequency (%)
Length (µm)
0–2
2–4
4–6
6–8
8–10
10–12
12–14
14–16
16–18
18–20
Lats1+/+
Lats1−/−
Lats1−/−mycLATS1
LATS1
ACTIN
b
Lats1+/+ (9.2 ± 0.8 µm)
Lats1−/− (5.8 ± 0.5 µm)
Lats1−/− mirin (8.9 ± 0.91 µm)
Replication track length frequency (%)
Length (µm)
Lats1+/+
Lats1−/−
Lats1−/−mirin
c
Rassf1A+/+ (8.8 ± 0.4 µm)
Rassf1A−/− (5.8 ± 0.3 µm)
Rassf1A−/− FLAG-R1A (8.08 ± 0.6 µm)
Rassf1A−/− FLAG-R1A-A133S (5.3 ± 0.1 µm)
Replication track length frequency (%)
Length (µm)
Rassf1A+/+
Rassf1A−/−
Rassf1A−/− FLAG-R1A
Rassf1A−/− FLAG-R1A-A133S
FLAG
GAPDH

Figure 4

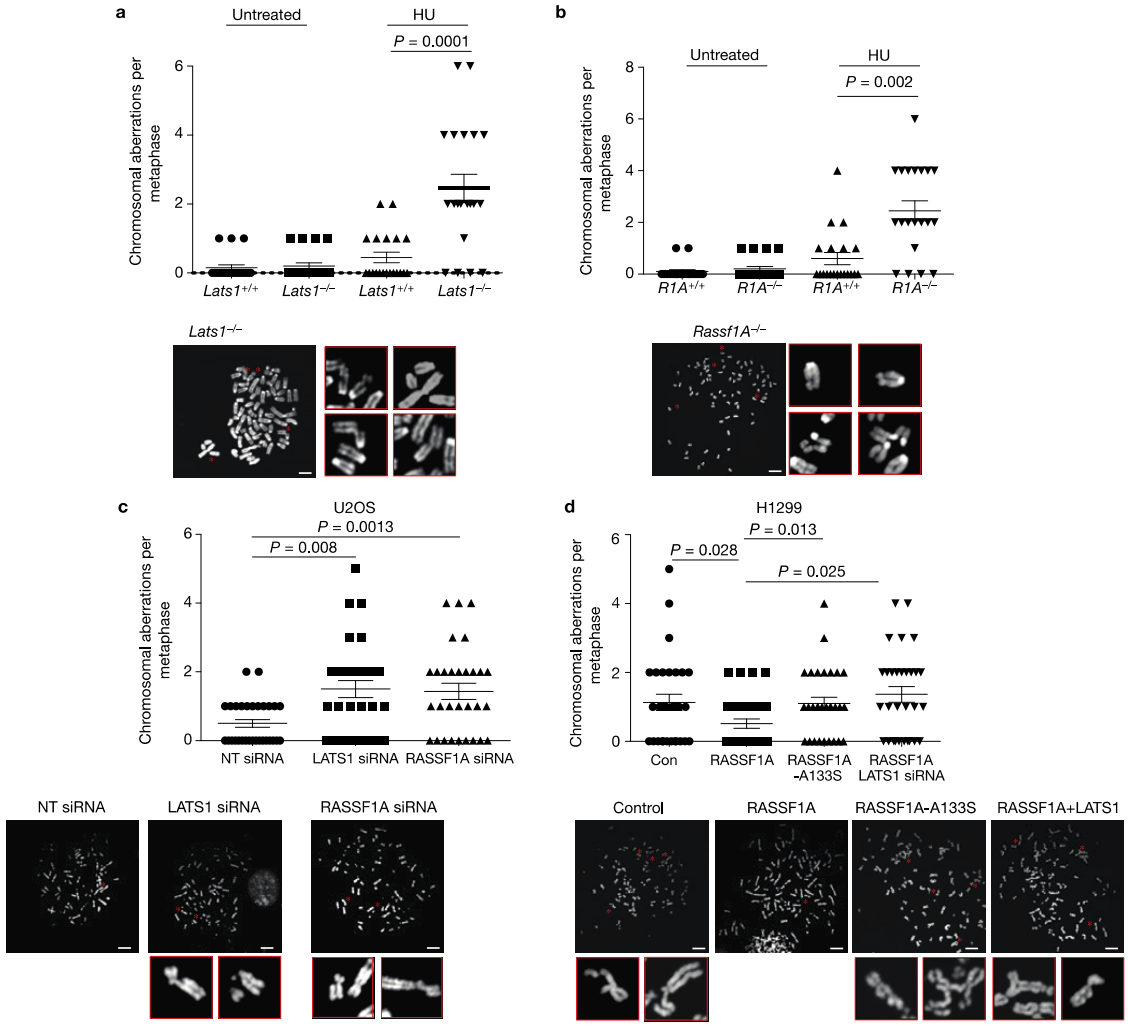

a
Untreated
HU
P = 0.0001
Chromosomal aberrations per metaphase
Lats1+/+
Lats1−/−
Lats1+/+
Lats1−/−
Lats1−/−
b
Untreated
HU
P = 0.002
Chromosomal aberrations per metaphase
R1A+/+
R1A−/−
R1A+/+
R1A−/−
Rassf1A−/−
c
U2OS
P = 0.0013
P = 0.008
Chromosomal aberrations per metaphase
NT siRNA
LATS1 siRNA
RASSF1A siRNA
NT siRNA
LATS1 siRNA
RASSF1A siRNA
d
H1299
P = 0.013
P = 0.028
P = 0.025
Chromosomal aberrations per metaphase
Con
RASSF1A
RASSF1A -A133S
RASSF1A LATS1 siRNA
Control
RASSF1A
RASSF1A-A133S
RASSF1A+LATS1

Figure 5

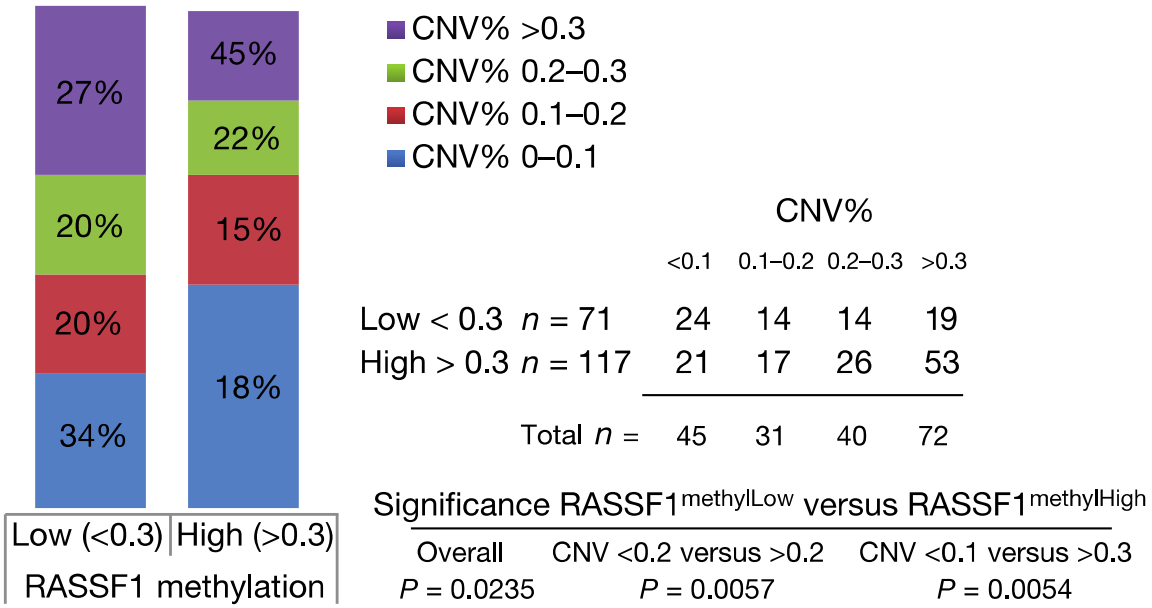

27%
20%
20%
34%
45%
22%
15%
18%
Low (<0.3)
High (>0.3)
RASSF1 methylation
CNV% >0.3
CNV% 0.2–0.3
CNV% 0.1–0.2
CNV% 0–0.1
CNV%
<0.1 0.1–0.2 0.2–0.3 >0.3
Low < 0.3 n = 71 24 14 14 19
High > 0.3 n = 117 21 17 26 53
Total n = 45 31 40 72
Significance RASSF1methylLow versus RASSF1methylHigh
Overall
P = 0.0235
CNV <0.2 versus >0.2
P = 0.0057
CNV <0.1 versus >0.3
P = 0.0054

Figure 6

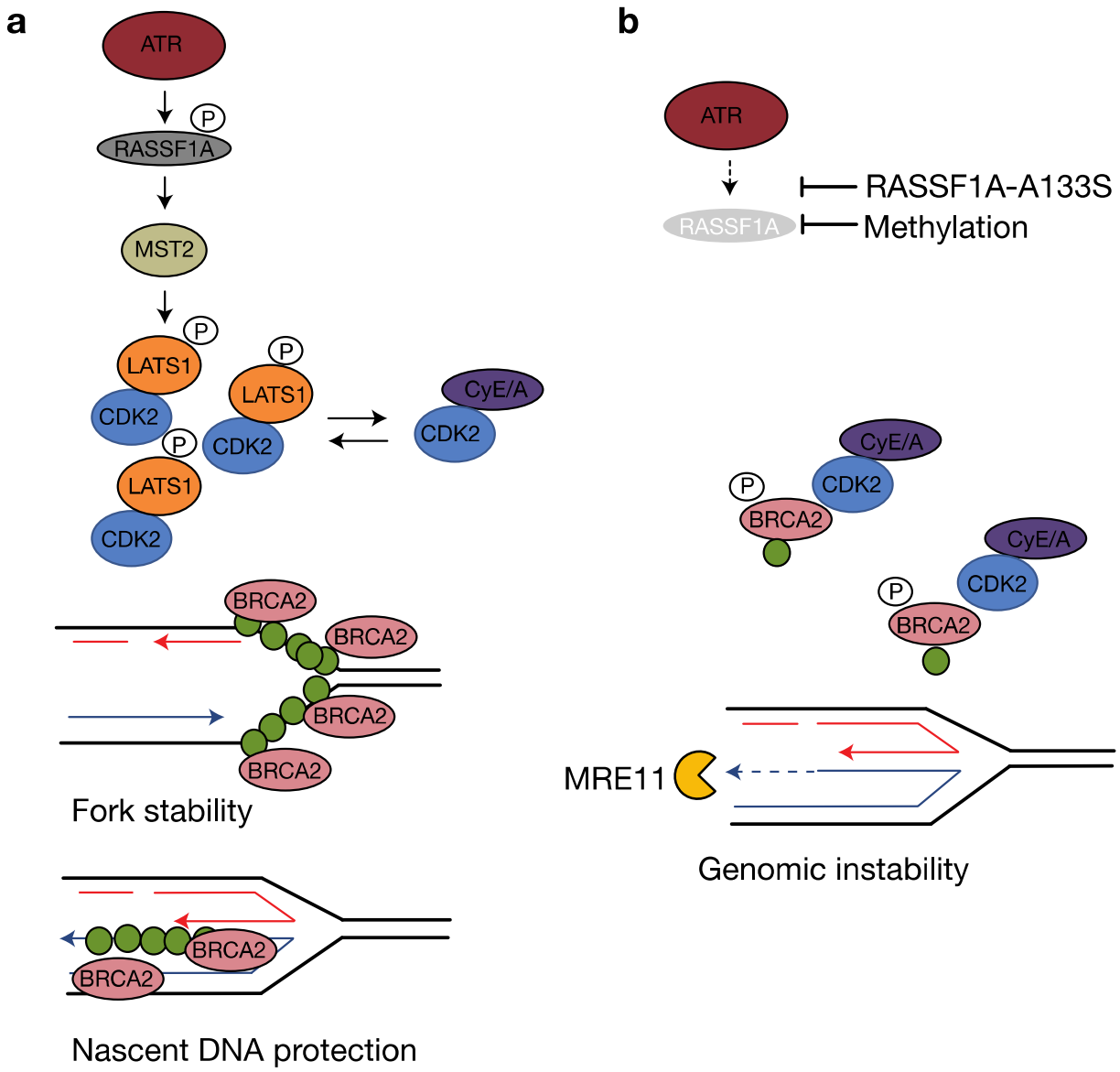

a
ATR
P
RASSF1A
MST2
P
LATS1
CDK2
P
CDK2
LATS1
LATS1
CDK2
CyE/A
CDK2
BRCA2
BRCA2
BRCA2
BRCA2
Fork stability
BRCA2
BRCA2
Nascent DNA protection
b
ATR
RASSF1A-A133S
RASSF1A
Methylation
CyE/A
CDK2
P
BRCA2
CyE/A
CDK2
P
BRCA2
MRE11
Genomic instability

Figure 7