Supplemental Methods

Primers used in this study

- RB1 PCR amplification primers:

5‘NNNNGGATCCTTATTTTTGTAACGGGAGTCGGGAGAGGACG-forward

5‘NNGCGGCCGCGTGGCCATAAACAGAACCTGGGAAAG-reverse

- *RB1* Sequencing primers:

RB1-cDNAf1 5‘-GGAAGATGATCTGGTGATTTC

RB1-cDNAf2 5‘-CTGCAGCAGATATGTATCTTTC

RB1-cDNAf3 5‘-GTGCTGAAGGAAGCAACCCTC

RB1-cDNAr1 5‘-CTCCCAATACTCCATCCACAG

RB1-cDNAr2 5‘-GTATCGCTGTGATCCAATTTC

- Rb1 sequencing:

mRb1c-1760f: CCTTGCATGGCTTTCAGATT

mRb1c-2085r: GAAGGCGTGCACAGAGTGTA

nRb1c-1763f : TGCATGGCTTTCAGATTCAC

mRb1c-2111r: GTGCTCTAGCTCTGGGTGGT

mRb1c-996f: GTATCATCTAATGGACTTCCAGAGG

mRb1c-1356r: AGATGTGCCCAACATCCTTT

mRb1c-1006f: ATGGACTTCCAGAGGTTGAAA

mRb1c-1380r: CAGCGTTAGCAAACTTCTCTTT

mRb1 -5´ -f1: TGTAACGGGAGTCGGGTGAG

mRb1 -5´ -r1: TTCTCCCAAGTTAGCCAAGCTC

mRb1 -5´ -f2: TTGTAACGGGAGTCGGGTGA

mRb1 -5´ -r2: TCCATCCACGGATGAAACTT

Rb1 -f1: CCGATCATGTCAGAGAAAGAGCTTG

Rb1 -b1: TCAGGGTTGTTTTTTCGTGGC

Rb1 -f10:GAACGCCACGAAAAAACAACC

Rb1 -b12: GATGATGTGCTCTAGCTCTGGGTG

Rb1 -b13: GAGTCCAGATGATGTGCTCTAGCTC

Rb1 -f19: CATTGAAATCTACCTCCCTTGCC

Rb1 -b29: GCATTCGTGTTCGAGTGGAAGTC

Rb1 -b30 CCTCACTTTTCCTCCTTGTTTGAG

Rb1 -f20: GCTAGAGCACATCATCTGGACTCTG

Rb1 -b31: CTAACATGAGCAGAACCTGGGAAC

Rb1 -b32: GTGGCTTACGAATCACCCACAC

Rb1 -f29: ACTCCTGGCTCATGGTTGTGAC

Rb1 -b35: GCACTTGGGTTGTACTGTACTAGGG

Rb1 -b38: GCAAGTTCAAAAGACCCTGGAAG

Rb1 -f31: CATACCTCAGACCCTCTAAGAACCG

Rb1 -b41: TGGTAAGCCCTTGACCTAAAACC

- Cre genotyping

Cre1 (5’ACCAGCCAGCTATCAACTC 3’)

Cre2 (5’TATACGCGTGCTAGCGAAGATCTCCATCTTCCAGCAG 3’)

- Cre expression assays

Cre-694f	5‘-TCCATATTGGCAGAACGAAA-3‘
Cre-804r	5‘-CAGCTACACCAGAGACGGAA-3‘
Cre-379f	5‘-AACATTTGGGCCAGCTAAAC-3‘
Cre-446r	5‘-AGCATTGCTGTCACTTGGTC-3‘
Cre-642f	5‘-GCCAGGATCAGGGTTAAAGA-3‘
Cre-713r	5‘-TTTCGTTCTGCCAATATGGA-3‘

- R26R genotyping:

R26R forward:	5´AAAGTCGCTCTGAGTTGTTAT-3‘
R26R reverse 1:	5´-GCGAAGAGTTTGTCCTCAACC-3‘
R26R reverse 2:	5´-GGAGCGGGAGAAATGGATATG-3‘

- ARF (p19)

mP19 ARF -f1	TCTCACCTCGCTTGTCACAG
mP19 ARF -r1	CGCTAGCATCGCTAGAAGTG
mP19 ARF -f2	CTCACCTCGCTTGTCACAGT
mP19 ARF -r2	ACGCTAGCATCGCTAGAAGTG

- p53

Trp53_ex.2_f	TGCATCCATACAGTACACAATCTC
Trp53_ex.2_r	TTGTTTCTCTCAGGCAAGGG
Trp53_ex.3+4_f	GCCTGGGATAAGTGAGATTCTG

1	Trp53_ex.3+4_r	AGGCATTGAAAGGTCACACG
2		
3	Trp53_ex.5_f	ACACCTGATCGTTACTCGGC
4	Trp53_ex.5_r	GAATAAGTCAGAAGCCGGGA
5		
6	Trp53_ex.6_f	GTTAGGACTGGCAGCCTCC
7	Trp53_ex.6_r	GACGCACAAACCAAAACAAA
8		
9	Trp53_ex.7_f	GTAGGGAGCGACTTCACCTG
10	Trp53_ex.7_r	GGGACTCGTGGAACAGAAAC
11		
12	Trp53_ex.8_f	TGCTGGTCCTTTTCTTGTCC
13	Trp53_ex.8_r	GAGCAAGAGGTGACTTTGGG
14		
15	Trp53_ex.9_f	TTGAGCTTCACCCCAAAGTC
16	Trp53_ex.9_r	ATGCGAGAGACAGAGGCAAT
17		
18	Trp53_ex.10_f	ACCTTGTCCAGTGCTTCCAT
19	Trp53_ex.10_r	GGAGGGAGGTCTGGGTAGAG
20	Trp53_ex.11_f	GAGGAAAGCCCAAACTGCTA
21	Trp53_ex.11_r	TAAGACAGCAAGGAGAGGGG
22		

- MDM2 primers

mMDM2 g QRT- f1 AGAACTGGCTTCCAGACGAT

mMDM2 g QRT- R1 CCTCAGCACATGGCTCTTTA

mMDM2 g QRT- f2 CTAGCTTCTCCCTGAATGCC

mMDM2 g QRT-R2 TTGCACACGTGAAACATGAC

Statistical analysis: Biological replicates used in these studies are cell lines that were established from different animals. Unless specifically stated all studies were performed with two biological replicates. Data represent mean +/- SD. Statistical analysis was performed using t-test unless stated. ANOVA was sued for anaphase bridges before and after radiation. Statistical significance is indicated by ** P<0.01 or *** P<0.001 in all experiments.

Expression assays: Gene expression assays from Applied Biosystems (CA, USA) were used to quantify human *RB1* mRNA concentration (**Hs01078058_g1)** and mouse *Rb1* mRNA **(Mm00485586_m1).**

Expression assay oligos for junction between exon 18 and 20 of *Rb1*:

Forward primer: GCCTCTCCAGGGTAACCATACT

Reverse primer: TCCGACTAAATACACTCTGTGC

Quencher: CTAGACGGTACAATATCTG