Table S1: Bacterial Strains

Strain name	Description	Genotype	Source or reference
mc^{2}155	Wild type	*ept1*	(1)
Mgm140	Δ*ligD*	mc^{2}155 *ligD*::*ligD*(Δ202–2391)	(2)
Mgm154	Δ*ku*	mc^{2}155 *ku*::*ku*(Δ90–947)	(2)
Mgm177	Δ*recBCD*	mc^{2}155 *recBCD*::*recC*(Δ76–3264) Δ*recB* Δ*recD*	(3)
Mgm199	Δ*recA*	mc^{2}155 *recA*::*recA*(Δ49–1014)	(3)
Mgm1601	Wild type; *lacZ*(I-SceI) with 'no' homology	mc^{2}155 *attB*::pRGM9	This work
Mgm1602	Wild type; *lacZ*(I-SceI) with 'nearby' homology	mc^{2}155 *attB*::pRGM10	This work
Mgm1603	Wild type; *lacZ*(I-SceI) substrate with 'far away' homology	mc^{2}155 *attB*::pRGM9 MSMEG_5848 Ω (1425: *lacZ*-ΔN, MSMEG_5848(706-1425))	This work
Mgm1604	Δ*ku*; *lacZ*(I-SceI) with 'no' homology	Mgm154 *attB*::pRGM9	This work
Mgm1605	Δ*ligD*; *lacZ*(I-SceI) with 'no' homology	Mgm140 *attB*::pRGM9	This work
Mgm1606	Δ*recA*; *lacZ*(I-SceI) with 'no' homology	Mgm199 *attB*::pRGM9	This work
Mgm1607	Δ*ku*; *lacZ*(I-SceI) with 'nearby' homology	Mgm154 *attB*::pRGM10	This work
Mgm1608	Δ*ligD*; *lacZ*(I-SceI) with 'nearby' homology	Mgm140 *attB*::pRGM10	This work
Mgm1609	Δ*recA*; *lacZ*(I-SceI) with 'nearby' homology	Mgm199 *attB*::pRGM10	This work
Mgm1610	Δ*recBCD*; *lacZ*(I-SceI) with 'no' homology	Mgm177 *attB*::pRGM9	This work
Mgm1611	Δ*recBCD*; *lacZ*(I-SceI) with 'nearby' homology	Mgm177 *attB*::pRGM10	This work
Mgm1964	Δ*adnAB*	mc^{2}155 *adnAB*::*adnA*(Δ81–3138)*adnB*(Δ1-3255)	This work
Mgm1965	Δ*adnAB* Δ*recBCD*	Mgm177 *adnAB*::*adnA*(Δ81–3138)*adnB*(Δ1-3255)	This work
Mgm1612	Δ*adnAB*; *lacZ*(I-SceI) with 'no' homology	Mgm1964 *attB*::pRGM9	This work
Mgm1613	Δ*adnAB* Δ*recBCD*; *lacZ*(I-SceI) with 'no' homology	Mgm1965 *attB*::pRGM9	This work
Mgm1614	Δ*adnAB*; *lacZ*(I-SceI) with 'nearby' homology	Mgm1964 *attB*::pRGM10	This work
Mgm1615	Δ*adnAB* Δ*recBCD*; *lacZ*(I-SceI) with 'nearby' homology	Mgm1965 *attB*::pRGM10	This work
Mgm1616	Wild type; pMV306kan	mc^{2}155 *attB*::pMV306kan	This work
Mgm1617	Δ*adnAB*; pMV306kan	Mgm1964 *attB*::pMV306kan	This work
Mgm1618	Δ*adnAB* Δ*recBCD*; pMV306kan	Mgm1965 *attB*::pMV306kan	This work
Mgm1619	Δ*adnAB*; *adnAB*	Mgm1964 *attB*::pRGM23	This work

Table S1: Bacterial Strains

	complemented		
Mgm1620	Δ*adnAB* Δ*recBCD*; *adnAB* complemented	Mgm1965 *attB*::pRGM23	This work

Strain table references

1. Snapper SB, Melton RE, Mustafa S, Kieser T, & Jacobs WR, Jr. (1990) Isolation and characterization of efficient plasmid transformation mutants of *Mycobacterium smegmatis*. Mol Microbiol 4(11):1911-1919.
2. Gong C, et al. (2005) Mechanism of nonhomologous end-joining in mycobacteria: a low-fidelity repair system driven by Ku, ligase D and ligase C. Nat Struct Mol Biol 12(4):304-312.
3. Stephanou NC, et al. (2007) Mycobacterial nonhomologous end joining mediates mutagenic repair of chromosomal double-strand DNA breaks. J Bacteriol 189(14):5237-5246.

Table S2: Plasmids used in the study

Plasmid name	Description	Genotype	Source or reference
pMV206hyg	Mycobacterial extrachromosomal plasmid (vector control)	*hyg oriE oriM*	(1)
pRGM1	*I-SceI* expression plasmid	P_{MOP}*I-SceI hyg oriE oriM*	This work
pRGM9	DSB repair substrate with 'no' homology	*attP* P_{MOP}*lacZ (I-SceI) aph oriE*	This work
pRGM10	DSB repair substrate with 'nearby' homology	*attP* P_{MOP}*lacZ (I-SceI) aph lacZΔN oriE*	This work
pRGM5	Plasmid used to generate the strain with 'far away' *lacZ* homology sequence	*loxP hyg loxP oriE* MSMEG_5848(706-1425) Ω (1425: *lacZ-ΔN*)	This work
pMV306kan	Mycobacterial integrative vector	*attP int aph oriE*	(2)
pRGM23	pMV306kan complemented with full-length *adnAB* operon under its native promoter	*attP int aph oriE adnAB*	This work

Plasmid table references

1. Delogu G, et al. (2004) Expression and purification of recombinant methylated HBHA in *Mycobacterium smegmatis*. FEMS Microbiol Lett 239(1):33-39.
2. Kong D & Kunimoto DY (1995) Secretion of human interleukin 2 by recombinant *Mycobacterium bovis* BCG. Infect Immun 63(3):799-803.

	Mean % NHEJ frequency (SEM; p value vs WT)	Mean % GC frequency (SEM; p value vs WT)	Mean % SSA frequency (SEM; p value vs WT)	Mean % I-SceI inactivation (SEM; p value vs WT)
Strain				
WT	0.0055(0.00029)	0.017 (0.00058)	0.005 (0.0005)	0.017(0.00088)
Δ*ku*	0	0.0287 (0.002; p=0.0039)	0.008(0.0011; p=0.083)	0.0002(0.00002 ; p< 0.0001)
Δ*ligD*	0	0.022 (0.0021; p=0.08)	0.0011 (.00005; p=0.001)	0.0030(0.00058 ; p=0.0002)
Δ*recBCD*	0.00093(0.00006 ; p=0.0001)	0.0457 (0.0012; p<0.0001)	0	0.0033(0.00088 ; p=0.0004)
Δ*adnAB*	0.0037(0.00067; p=0.0651))	0.0091(0.0001; p=0.0002)	0.0018 (0.0003; p=0.004)	0.023(0.0023; p=0.0557)
Δ*recBCD*Δ*adnAB*	0.0067(0.00006; p=0.0170)	0.0078 (0.00003;p<0.0001)	0	0.0268(0.00025 ; p=0.0004)
Δ*recA*	0.0014(0.00008; p=0.0002)	0	0.0005 (0.00007; p=0.0006)	0.0057(0.00033 ; p=0.0003)

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Absolute repair frequencies calculated for all repair outcomes according to the formulas presented in the methods section. Each data cell contains the mean absolute repair frequency for three replicate experiments. In parentheses are the SEM and the p value compared to wild type, calculated by the Student's t-test.

Supplementary Figure Legends

Figure S1 Verification of I-SceI inactivation in surviving I-SceI transformants with unmodified I-SceI cleavage sites

A. I-SceI encoding plasmids were recovered from *M. smegmatis* colonies surviving I-SceI expression that demonstrated repaired I-SceI sites (I-SceI) or unmodified sites (I-SceI*1-5). I-SceI or I-SceI* plasmids were retransformed into *M. smegmatis* Mgm1601 and survival was quantitated. The top panel shows agar plates containing hygromycin-resistant colonies of *M. smegmatis* Mgm1601 transformed with I-SceI or I-SceI* and the bar graph in the bottom panel shows % survival on a logarithmic Y axis for each plasmid.

B. Sequencing of I-SceI* plasmids. The *I-SceI* gene was sequenced using an upstream primer which binds within the MOP promoter region in the I-SceI plasmid. For each plasmid, the mutation present in the DNA sequence and the corresponding protein alteration is listed.

Figure S2 Verification of repair outcomes by PCR

A. Verification of gene conversion (GC). The schematic shows the parental recombination construct with two internally deleted *lacZ* alleles, *lacZ*(I-SceI) and *lacZ*-ΔN, separated by a kanamycin-resistant cassette (green box). The GC outcome that reconstitutes a functional *lacZ* gene with a downstream kanamycin-resistance gene and *lacZ*-Δ*N* copy is also depicted. The positions of primers 1, 2, 3, 4 and 5, used to confirm the DSB repair outcomes after I-SceI cleavage are indicated by black rectangles. PCR products were resolved by agarose gel electrophoresis and visualized by ethidium bromide staining.
The first agarose gel in the bottom panel shows the PCR products obtained using primers 2 and 3. Lane 3 shows amplicons of sizes 850bp and 1350bp obtained from *lacZ*(I-SceI) and *lacZ*-ΔN loci, respectively, of the parental white colony that has not undergone I-SceI cleavage. Lanes 1, 2 and 4 show amplicons from 3 kanamycin-resistant blue colonies that arose after I-SceI cleavage. A single PCR product of the expected size (i.e. 1350 bp) was obtained from both the *lacZ* alleles (*lacZ*-ΔN and *lacZ*). The middle gel shows the PCR products obtained from the first *lacZ* allele exclusively using primers 1 and 2. Lanes 5, 6 and 8 represent amplicons of the expected size 1850bp from three GC outcomes and lane 7 shows the product of size 1350bp obtained from the parental construct. The third gel indicates the results of I-SceI digestion of the gel-purified PCR products attained from *lacZ*(I-SceI) in lanes 1-8. The 1350bp product (lanes 1, 2 and 4) and 1850 bp product (lanes 5, 6 and 8) obtained from the GC outcomes are resistant to I-SceI cleavage as they lack I-SceI sites, whereas the 850bp product (lane 3) and 1350bp product (lane 7) acquired from the parental colony show the expected cleavage pattern of 2 bands of sizes 450/350bp and 850/450bp respectively.

B. Confirmation of single-strand annealing (SSA). The schematic shows the outcome of SSA between the two parental *lacZ* alleles after DSB induction, resulting in the generation of the full-length functional *lacZ* gene with a concomitant loss of the intervening kanamycin-resistance gene. The SSA outcome was confirmed by PCR amplification using primers 4 and 5, which

generate an amplicon of 800bp from either the parental locus or a GC outcome but not from an SSA outcome. The PCR products were analyzed by agarose-gel electrophoresis as shown in the bottom panel. Lanes 1-3, PCR products from 3 independent blue kanamycin-sensitive colonies; lanes 4-6, PCR products from 3 independent blue, kanamycin-resistant colonies.

Figure S3 Influence of a distant homologous sequence on DSB repair.

A. Reporter substrate with homology placed at a distance. The schematic shows the reporter strain wherein the homology donor *lacZ*-ΔN was positioned 1.2Mb away from the kanamycin-resistance cassette (green box) present downstream to the *lacZ*(I-SceI) copy.
B. Table of DSB repair outcomes from cells bearing the construct pictured in (A) after transforming the strain (mgm1603) with the I-SceI plasmid *versus* vector, and selecting for transformants on plates containing hygromycin and X-gal. The % survival and repair outcomes for white and blue colonies from all the three wild-type strains with different reporter substrates (i.e. no homology, nearby homology, and far away homology) are tabulated.

Figure S4 Molecular outcomes of NHEJ in different strains.

The DSB generated after cleavage of the two I-SceI sites is shown at the top of the figure with left and right ends colored blue and red respectively. Molecular outcomes of NHEJ from WT, Δ*recBCD*, Δ *adnAB*, Δ *adnAB*Δ*recBCD* and Δ *recA* backgrounds are listed, from both reporter strains (with and without homology). The number of deleted nucleotides from either end of the break is indicated. Nucleotides added by fill in synthesis of the 5' recessed ends are colored green and microhomology use is underlined.

Figure S5 Complementation of the clastogen sensitivity of the Δ*adnAB* strains by wild type *adnAB*.

The *M. smegmatis adnAB* operon along with 686bp of the 5' untranslated region containing the presumed native promoter was cloned in the mycobacterial integrative vector pMV306kan, to generate pRGM23. Complementation of the *adnAB* deletion phenotype was tested by integrating the kanamycin-resistant pRGM23 at the *attB* site in the chromosome of the *M. smegmatis* strains Δ *adnAB* and Δ *adnAB*Δ*recBCD*, and performing ionizing radiation (A) or hydrogen peroxide (B) killing assays. % survival is graphed on a logarithmic Y axis and the clastogen dose is indicated on the X axis. Each point on the graph represents the mean of biologic duplicates and error bars are SEM. When error bars are not visible, they are within the symbol. *M. smegmatis* strains tested in the assays are indicated next to curves in panel A.

A. Ionizing radiation delivered by a cesium source. Pictures of untreated cells and cells after exposure to 222Gy are shown with the following strain legend: 1=wild type (mc^2155) 2=Δ*adnAB* (mgm1617) 3=Δ*adnAB* + *adnAB* (mgm1619) 4=Δ*adnAB*ΔrecBCD (mgm1618) 5=Δ*adnAB*Δ*recBCD* + *adnAB* (mgm1620).
B. Hydrogen peroxide. Pictures of untreated cells and cells after exposure to 25mM hydrogen peroxide are shown with the same legend as panel A.

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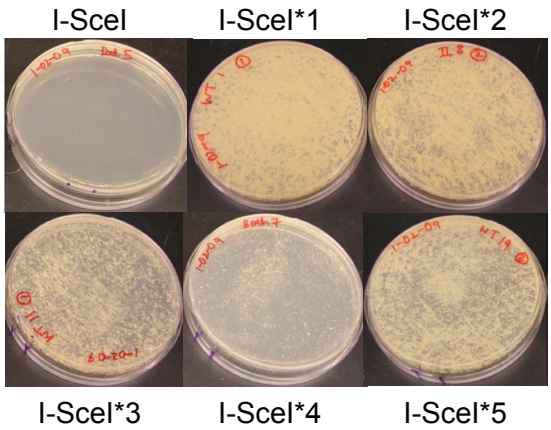
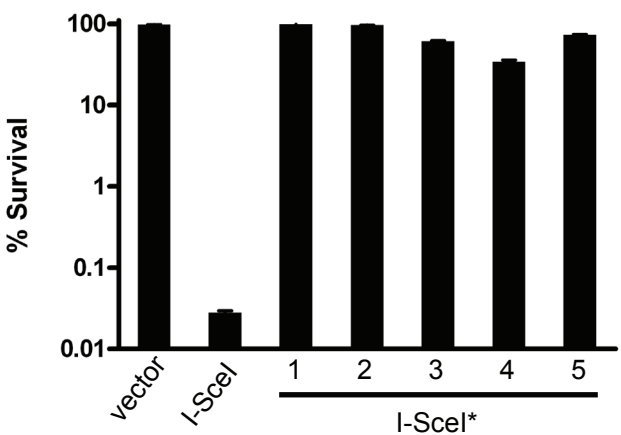
A.

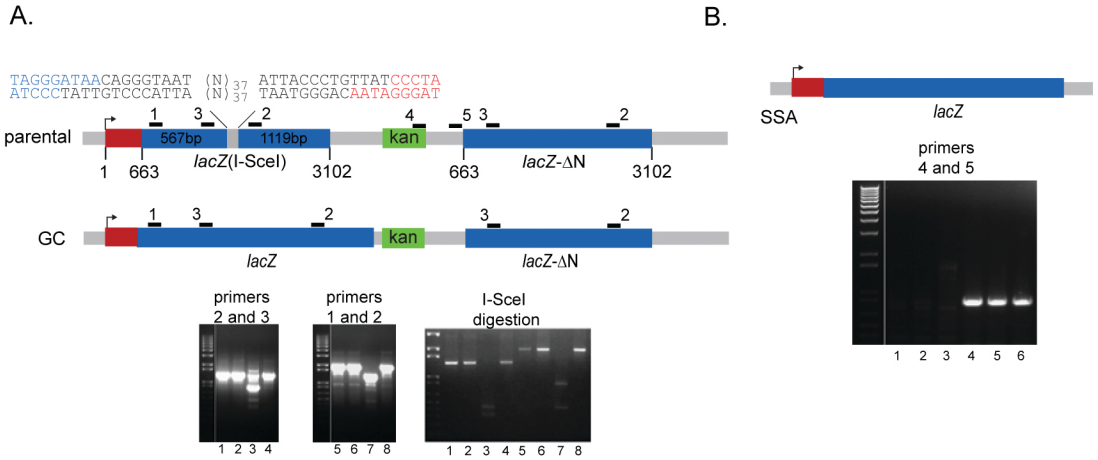




B.

Mutant Plasmid	Gene Mutation /Nucleotide change[a]	Mutation in Protein[b]
I-SceI*-1	Δ100-687	34fsX40
I-SceI*-2	139ins22bp	47fsX51
I-SceI*-3	Δ355-362	119fsX128
I-SceI*-4	446ins27bp	148-149ins9a.a.
I-SceI*-5	Δ75-149	Q24HΔ26-50

a. numbering in relation to the 708bp coding sequence of I-SceI
b, Full length I-SceI endonuclease comprises 235 amino acids
fs, frameshift mutation
X, stop codon
ins, insertion (followed by the number of residues inserted)
a.a., amino acids


A.
TAGGGATAACAGGGTAAT (N)37 ATTACCCTGTTATCCCTA
ATCCCTATTGTCCCATTA (N)37 TAATGGGACAATAGGGAT
parental
1
3
2
4
5
3
2
567bp
1119bp
kan
1
663
lacZ(I-SceI)
3102
663
lacZ-ΔN
3102
GC
1
3
2
3
2
kan
lacZ
lacZ-ΔN
primers
2 and 3
primers
1 and 2
I-SceI
digestion
1 2 3 4
5 6 7 8
1 2 3 4 5 6 7 8
B.
SSA
lacZ
primers
4 and 5
1 2 3 4 5 6

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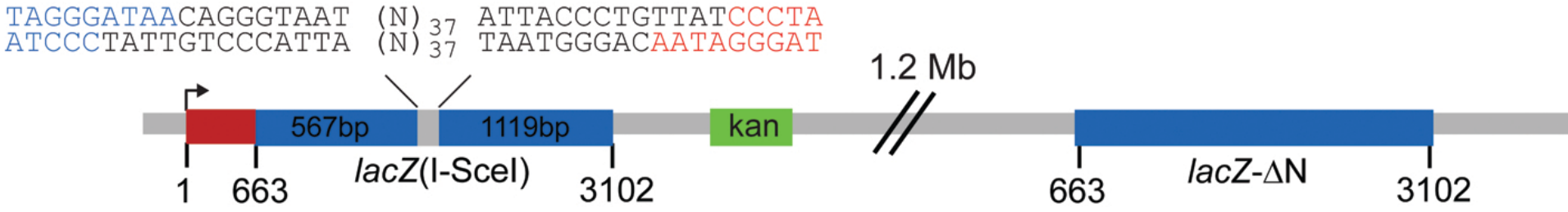
A.



B.

homology location	(%) Survival	% Blue	# White	NHEJ	Loss	# Blue	GC	SSA
-	0.029	0	60	15	45	0	0	0
+(Nearby)	0.044	50	70	16	54	75	60	15
+(Far away)	0.026	44	60	13	47	70	70	0

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```
TACCATGGTAGGGATAA      CCCTAAGCTTATC
ATGGTACCATCCC      AATAGGGATTCGAATAG
```

Wild-type: no homology

1.

```
CCATCCGCTGTGGTA     Δ39/Δ1       TCCCTAAGCTTATC
GGTAGGCGACACC                   ATAGGGATTCGAATAG
```

2.

```
CTGCTGATGAAGCA     Δ93/Δ287     AACGCGACCGCATGG
GACGACTACTTCGT                  TTGCGCTGGCGTACC
```

3.

```
GCAGGATATCCTGCT      Δ103/      TATCCCTAAGCTTAT
CGTCCTATAGGACG                  AATAGGGATTCGAATA
```

4.

```
GATCGCGTCACACT    Δ363/Δ511     GCCGCTGCGCGATCA
CTAGCGCAGTGTGA                  CGGCGACGCGCTAGT
```

5.

```
CCCGAAACTGTGGA    Δ331/Δ1068    AACAGCAACTGATGG
GGGCTTTGACACCT                  TTGTCGTTGACTACC
```

6.

```
TACCATGGTAGGGATA     Δ1/Δ1       TCCCTAAGCTTATC
ATGGTACCATCCCT                  ATAGGGATTCGAATAG
```

7.

```
TACCATGGTAGGGATAA     /Δ2        TCCCTAAGCTTATC
ATGGTACCATCCCTAT                 TAGGGATTCGAATAG
```

8.

```
CATCCGCTGTGGTA     Δ39/Δ435       ATAAGCGTTGGCA
GTAGGCGACA                    CCATTATTCGCAACCGT
```

9.

```
TACCATGGTAGGGAT      Δ2/      TATCCCTAAGCTTATC
ATGGTACCATCCCT                AATAGGGATTCGAATAG
```

10.

```
ACGCAGGTCGCCAG    Δ429/Δ146   GCGCTGGATGGTAAG
TGCGTCCAGCGGTC                CGCGACCTACCATTC
```

11.

```
AGCATCATCCTCTG    Δ149/Δ431     GGTAATAAGCGTT
TCGTAGTAGGA                   GACCCATTATTCGCAA
```

12.

```
TACCATGGTAGGGAT      Δ2/      TATCCCTAAGCTTATC
ATGGTACCATCCCT                AATAGGGATTCGAATAG
```

13.

```
TCCTGTTATCCCTA    Δ15/Δ288    ACGCGACCGCATGGT
AGGACAATAGGGAT                TGCGCTGGCGTACCA
```

14.

```
ATTTCAGCCGCGCT    Δ521/Δ81    TCGAAAGACTGGGCC
TAAAGTCGGCGCGA                AGCTTTCTGACCCGG
```

15.

```
GGCACCGCGCCTTT    Δ414/Δ3      TCCCTAAGCTTATC
CCGTGGCGCGGAAA                 AGGGATTCGAATAG
```

Wild-type: with homology (nearby)

1.

```
CAGACGATGGTGCA    Δ114/Δ6     CTAAGCTTATCGATG
GTCTGCTACCACGT                GATTCGAATAGCTAC
```

2.

GATCGCGTCACACT Δ363/Δ511 GCCGCTGCGCGATCA
CTAGCGCAGTGTGA CGGCGACGCGCTAGT

3.

CTGCTGATGAAGCA Δ93/Δ287 AACGCGACCGCATGG
GACGACTACTTCGT TTGCGCTGGCGTACC

4.

ACAACTTTAACGCC Δ77/Δ1143 TCCATATGGGGATTG
TGTTGAAATTGCGG AGGTATACCCCTAAC

5.

CCCGAAACTGTGGA Δ331/C/Δ1144 **C**CCATATGGGGATTG
GGGCTTTGACACCT **G**GGTATACCCCTAAC C insertion

6.

CTGCTGATGAAGCA Δ93/Δ1183 AGTATCGGCGGAATT
GACGACTACTTCGT TCATAGCCGCCTTAA

7.

GCTGATTGAAGCAGA Δ258/ TTATCCCTAAGCTTA
CGACTAACTTCGTCT AATAGGGATTCGAAT

8.

CGATGGTGCAGGATA Δ109/Δ631 CGAAGCAGCGTTGTT
GCTACCACGTCCTAT GCTTCGTCGCAACAA

9.

CAGGTCGCCAGCGGC Δ425/Δ1037 GACTTCCAGTTC
GTCCAGCGGTC CCGCTGAAGGTCAAG

10.

ACGTCGAAAACCCG Δ341/Δ1018 CCCACACCAGTGGCG
TGCAGCTTTTGGGC GGGTGTGGTCACCGC

11.

CCCGAAACTGTGGA Δ331/Δ366 TCCCCGCCGCGTCCC
GGGCTTTGACACCT AGGGGCGGCGCAGGG

12.

ACTTTAACGCCGTG Δ74/Δ998 ACGCGCGAATTGAAT
TGAAATTGCGGCAC TGCGCGCTTAACTTA

13.

GAGCAGACGATGGT Δ117/Δ513 CGCTGCGCGATCAGT
CTCGTCTGCTACCA GCGACGCGCTAGTCA

14.

ATTTCAGCCGCGCT Δ521/Δ81 TCGAAAGACTGGGCC
TAAAGTCGGCGCGA AGCTTTCTGACCCGG

15.

CGGCACCGCGCCTTT Δ414/Δ3 TCCCTAAGCTTATC
GCCGTGGCGCGGAAA AGGGATTCGAATAG

16.

CGCCGACGGCACGCT Δ270/Δ367 CCCCGCCGCGTC
GCGGCTGCCG TGCGAGGGGCGGCGCAG

Δ*adnAB*Δ*recBCD*: no homology

1.

TATCCTGTTATCCC Δ17/Δ1208 CCGGTCGCCTACCAT
ATAGGACAATAGGG GGCCAGCGGATGGTA

2.

TCCATGTTGCCACT Δ548/Δ543 TGGATAACGACATTG
AGGTACAACGGTGA ACCTATTGCTGTAAC

3.

GTGATGGTGCTGCG Δ666/Δ428 CTGGGTAATAAGCGT
CACTACCACGACGC GACCCATTATTCGCA

4.

GTGATGGTGCTGCG Δ666/Δ428 CTGGGTAATAAGCGT
CACTACCACGACGC GACCGATTATTCGCA

5.

ACACCGCCGACGGC Δ275/Δ270 TACGCGTAGTGCAAC
TGTGGCGGCTGCCG ATGCGCATCACGTTG

6.

CCGAACCATCCGCT Δ45/Δ302 TCAGAAGCCGGGCAC
GGCTTGGTAGGCGA AGTCTTCGGCCCGTG

7.

ATGGTCTGCTGCT Δ207/Δ326 TGGCAGCAGTGGCGT
TACCAGACGACGA ACCGTCGTCACCGCA

8.

GAGCAGACGATGGT Δ117/Δ1128 TGAATATCGACGGTT
CTCGTCTGCTACCA ACTTATAGCTGCCAA

9.

GGCGTTAACCGTCA Δ165/Δ798 GCGATACACCGC
CCGCAATTGGCAGT CGCTATGTGGCG

10.

TCTGCTGCTGCTGAA Δ199/Δ716 AACCTTATTTAT
AGACGACGACGAC TTTTGGAATAAATA

11.

CGAACCATCCGCTG Δ44/Δ512 CCGCTGCGCGATCAG
GCTTGGTAGGCGAC GGCGACGCGCTAGTC

12.

GGCAGGGTGAAACG Δ440/Δ689 ACCGCTCACGCGTG
CCGTCCCACTT TGCTGGCGAGTGCGCAC

Δ*adnAB*: no homology

1.

TCGATGAGCGTGGT Δ386/Δ1209 CGGTCGCCTACCATT
AGCTACTCGCACCA GCCAGCGGATGGTAA

2.

AACCCGAAACTGTG Δ333/ Δ1169 TCCTGGAGCCCGTCA
TTGGGCTTTGACAC AGGACCTCGGGCAGT

3.

CATGGTAGGGATAA /Δ997 GACGCGCGAATTGAA
GTACCATCCCTATT CTGCGCGCTTAACTT

4.

CGAACCATCCGCTG Δ44/ Δ1033 CGGCGACTTCCAGTT
GCTTGGTAGGCGAC GCCGCTGAAGGTCAA

5.

TATCCTGTTATCCCTA Δ24/ AGCTTATCGA
ATAGGAC AATAGGGATTCGAATAGCT

6.

TATCCTGTTATCCCTA Δ24/ AGCTTATCGA
ATAGGAC AATAGGGATTCGAATAGCT

7.

```
CATGGTAGGGATAA  INSERT/1169   TCCTGGAGCCCGTCA
GTACCATCCCTATT                AGGACCTCGGGCAGT
INSERTED SEQUENCE: CAGGGT
```

8.

```
TACCATGGTAGGGATA     Δ1/Δ1     TCCCTAAGCTTATCG
ATGGTACCATCCCT               ATAGGGATTCGAATAGC
```

9.

```
CCCGAAACTGTGGAGC    Δ329/Δ169     AAGCGGTGAAGT
GGGCTTTGACACCT                  CGTTCGCCACTTCA
```

10.

```
ATCGCGTCACACT     Δ363/Δ1209    CGGTCGCCTACCA
TAGCGCAGTGTGA                   GCCAGCGGATGGT
```

Δ*adnAB*: with homology

1.

```
ATCGATGAGCGTGG    Δ387/Δ224    CCTGAACTACCGCA
TAGCTACTCGCACC                 GGACTTGATGGCGT
```

2.

```
GAGCAGACGATGGT    Δ117/Δ224    CCTGAACTACCGCA
CTCGTCTGCTACCA                 GGACTTGATGGCGT
```

3.

```
TACCATGGTAGGGATAA     /Δ2       TCCCTAAGCTTATC
ATGGTACCATCCCTAT                TAGGGATTCGAATAG
```

4.

```
TATCCTGTTATCCCTA   Δ24/            AGCTTATCGA
ATAGGAC                  AATAGGGATTCGAATAGCT
```

5.

```
CCTGCTGATGAAGC      Δ94/Δ2      ATCCCTAAGCTTATC
GGACGACTACTTCG                  TAGGGATTCGAATAG
```

6.

```
CCATCCGCTGTGGT     Δ40/Δ814     GGCGCGGATTGGCCT
GGTAGGCGACACCA                  CCGCGCCTAACCGGA
```

7.

```
CATGGTAGGGATAA    INSERT/1169   TCCTGGAGCCCGTCA
GTACCATCCCTATT                  AGGACCTCGGGCAGT
INSERTED SEQUENCE: CAGGGT
```

8.

```
TCCTGTTATCCCTA     Δ15/Δ288     ACGCGACCGCATGGT
AGGACAATAGGGAT                  TGCGCTGGCGTACCA
```

9.

```
ATGGTCTGCTGCTG    Δ206/Δ317     ATCAGCGCCTGGCAG
TACCAGACGACGAC                  TAGTCGCGGACCGTC
```

10.

```
GCAGACGATGGTGC    Δ115/Δ507      TGACGCCGCTGCGC
CGTCTGCTACC                   ACGACTGCGGCGACGCG
```

Δ*adnAB*Δ*recBCD*: with homology

1.

```
ACAACTTTAACGCC     Δ77/Δ366     TCCCCGCCGCGTCCC
TGTTGAAATTGCGG                  AGGGGCGGCGCAGGG
```

2.

GACAGTCGTTTGCC Δ732/Δ245 AGCGCCGGGCAACTC
CTGTCAGCAAACGG TCGCGGCCCGTTGAG

3.

TGCGTGACTACCTA Δ473/Δ48 ACTGCCAGGCATCAA
ACGCACTGATGGAT TGACGGTCCGTAGTT

4.

TATCCTGTTATCCCTA Δ24/ AGCTTATCGA
ATAGGAC AATAGGGATTCGAATAGCT

5.

CGCTGTGGTACACGC Δ34/Δ148 GCTGGATGGTAAGCC
GCGACACCATGTG CGCGACCTACCATTCGG

6.

TGAAGCAGAAGCCT Δ253/Δ366 TCCCCGCCGCGTCCC
ACTTCGTCTTCGGA AGGGGCGGCGCAGGG

7.

GATCGCGTCACACT Δ363/Δ1142 TCCATATGGGGATTG
CTAGCGCAGTGTGA AGGTATACCCCTAAC

8.

TTGACCTGAGCGCAT Δ709/Δ2 CCCTAAGCTTATCGA
AACTGGACTCGCG TAGGGATTCGAATAGCT

9.

GTTATCTGGAAGAT Δ638/Δ1 TATCCCTAAGCTTAT
CAATAGACCTTCTA ATAGGGATTCGAATA

10.

CGTTAACTCGGCGTT Δ788/ ATCCCTAAGCTTATC
GCAATTGAGCCGC AATAGGGATTCGAATAG

11.

TTCCATGTTGCCAC Δ549/Δ430 GGGTAATAAGCGTTG
AAGGTACAACGGTG CCCATTATTCGCAAC

12.

TGACCTGAGCGCAT Δ709/Δ338 CGTCTGGCGGAAAAC
ACTGGACTCGCGTA GCAGACCGCCTTTTG

Δ*recBCD*: no homology

1.

GGTTACGGCCAGGA Δ744/Δ463 AGGCTTTCTTTCACA
CCAATGCCGGTCCT TCCGAAAGAAAGTGT

2.

AATGGTCTGCTGCT Δ207/Δ182 CCTCTGGATGTCGCT
TTACCAGACGACGA GGAGACCTACAGCGA

3.

TATCCTGTTATCCCTA Δ24/ AGCTTATCGA
ATAGGAC AATAGGGATTCGAATAGCT

4.

CGAAACTGTGGAGC Δ329/Δ126 AGCTCCTGCACT
GCTTTGACACCTCG TCGAGGACGTGA

5.

CCGAACCATCCGCT Δ45/Δ132 TGCACTGGATGGTGG
GGCTTGGTAGGCGA ACGTGACCTACCACC

6.

TGAAGCAGAAGCC Δ254/Δ276 TAGTGCAACCGAACG
ACTTCGTCTTCGG ATCACGTTGGCTTGC

7.

TACCATGGTAGGGATAA /Δ2 TCCCTAAGCTTATC
ATGGTACCATCCCTAT TAGGGATTCGAATAG

8.

GGTGCAGGATATCC Δ106/Δ290 GCGACCGCATGGTCA
CCACGTCCTATAGG CGCTGGCGTACCAGT

9.

CGAAACTGTGGAGCG Δ328/Δ122 GTGGAGCTCCTGCAC
GCTTTGACACCT CGCCACCTCGAGGACGTG

10.

TTTAACGCCGTGCG Δ72/Δ124 GGAGCTCCTGCACTG
AAATTGCGGCACGC CCTCGAGGACGTGAC

11.

CCGAACCATCCGCT Δ45/Δ366 TCCCCGCCGCGTCCC
GGCTTGGTAGGCGA AGGGGCGGCGCAGGG

Δ*recBCD*: with homology

1.

GAGCATCATCCTCT Δ150/Δ255 AACTCTGGCTCACAG
CTCGTAGTAGGAGA TTGAGACCGAGTGTC

2.

GGCACGCTGATT Δ264/ ATCCCTAAGCTTATC
CCGTGCGACT AATAGGGATTCGAATAG

3.

CCCGAATCTCTATC Δ307/Δ366 TCCCCGCCGCGTCCC
GGGCTTAGAGATAG AGGGGCGGCGCAGGG

4.

AGCGGCACCGCGCCTT Δ417/ ATCCCTAAGCTTATC
TCGCCGTGGCGCGG AATAGGGATTCGAATAG

5.

TACCATGGTAGGGAT Δ2/ TATCCCTAAGCTTATC
ATGGTACCATCCCT AATAGGGATTCGAATAG

6.

GGTCTGCTGCTGCT Δ204/Δ171 GCGGTGAAGTGCCTC
CCAGACGACGACGA CGCCACTTCACGGAG

7.

ATCCCGAATCTCTA Δ309/Δ1183 AGTATCGGCGGAAT
TAGGGCTTAGAGAT TCATAGCCGCCTTA

8.

GACGCGAATTATTTTT Δ808/ ATCCCTAAGCTTATC
CTGCGCTTAATAAA AATAGGGATTCGAATAG

9.

AACAACTTTAACGCCG Δ74/Δ1033 GCGACTTCCAGTTCA
TTGTTGAAATTGCG GCCGCTGAAGGTCAAGT

10.

ACCCGAAACTGTGG Δ332/Δ289 CGCGACCGCATGGTC
TGGGCTTTGACACC GCGCTGGCGTACCAG

11.

GGCACCGCGCCTTT Δ414/Δ108 CCATCATGGCCGCGG
CCGTGGCGCGGAAA GGTAGTACCGGCGCC

12.

GAGCAGACGATGGT Δ117/Δ513 CGCTGCGCGATCAGT
CTCGTCTGCTACCA GCGACGCGCTAGTCA

Δ*recA*: no homology

1.

AACTTTAACGCCGT Δ75/Δ4 CCCTAAGCTTATC
TTGAAATTGCGGCA GGGATTCGAATAG

2.

ATGTGCGGCGAGTT Δ486/Δ881 CCGCAAGAAAACTA
TACACGCCGCTCAA GGCGTTCTTTTGAT

3.

CCATGGTAGGGATAA /Δ4 CCCTAAGCTTATC
AGTACCATCCCTATT GGGATTCGAATAG

4.

TACCATGGTAGGGATA Δ1/Δ1 TCCCTAAGCTTATC
ATGGTACCATCCCT ATAGGGATTCGAATAG

5.

GCTGTTCGCATTAT Δ59/ CCCTAAGCTTATC
CGACAAGCGT AATAGGGATTCGAATAG

6.

TACCATGGTAGGGATA Δ1/Δ1 TCCCTAAGCTTATC
ATGGTACCATCCCT ATAGGGATTCGAATAG

7.

GAGCAGACGATGGT Δ117/Δ97 TTCGTTTTATGCC
CTCGTCTGCTACCA AAGCAAAATACGG

8.

CCGAACCATCCGCT Δ45/Δ245 AGCGCCGGGCAACT
GGGTTGGTAGGCGA TCGCGGCCCGTTGA

9.

ATCCTGTTATCCCT Δ16/Δ92 GGCCTTTCGTTTT
TAGGACAATAGGGA CCGGAAAGCAAAA

10.

TACCATGGTAGGG Δ4/ TTATCCCTAAGCTTATC
ATGGTACCATCCC AATAGGGATTCGAATAG

11.

TGTCGGTTTCCGCG Δ235/Δ561 TAAGTGAAGCGA
ACAGCCAAAGG CGCATTCACTTCGCT

12.

TTTATGGCAGGGTG Δ445/Δ326 TGGCAGCAGTGGCGT
AAATACCGTCCCAC ACCGTCGTCACCGCA

13.

CCATCCGCTGTGGTA Δ39/Δ1 TCCCTAAGCTTATC
GGTAGGCGACACC ATAGGGATTCGAATAG

Δ*recA*: with homology

1.

```
ATCCCGAATCTCTA      Δ307/     TTATCCCTAAGCTTATC
TAGGGCTTAGAGAT                AATAGGGATTCGAATAG
```

2.

```
GTGCAGGATATCCT   Δ105/Δ1183   AGTATCGGCGGAATT
CACGTCCTATAGGA                TCATAGCCGCCTTAA
```

3.

```
GAACAACTTTAACG    Δ79/Δ268    AGTACGCGTAGTGCA
CTTGTTGAAATTGC                TCATGCGCATCACGT
```

4.

```
ATCGATGAGCGTGG      Δ387/     TTATCCCTAAGCTTATC
TAGCTACTCGCACC                AATAGGGATTCGAATAG
```

5.

```
TACCATGGTAGGGATAA     /Δ2       TCCCTAAGCTTATC
ATGGTACCATCCCTAT                TAGGGATTCGAATAG
```

6.

```
AACTGTGGAGCGCC   Δ326/Δ370    CGCCGCGTCCCACGC
TTGACACCTCGC                 GGGCGGCGCAGGGTGCG
```

7.

```
TACCATGGTAGGGAT      Δ2/      TATCCCTAAGCTTATC
ATGGTACCATCCCT                AATAGGGATTCGAATAG
```

8.

```
TACCATGGTAGGG        Δ4/      TTATCCCTAAGCTTATC
ATGGTACCATCCC                 AATAGGGATTCGAATAG
```

9.

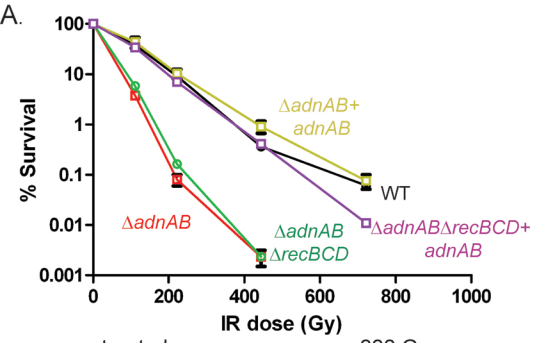
CGGTGATGGTGCTG △668/△470 CTTTCACAGATGTGG
GCCACTACCACGAC GAAAGTGTCTACACC

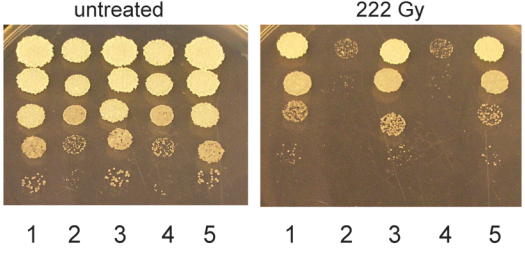
10.

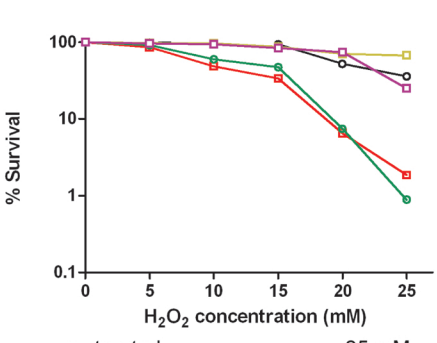
CAGACGATGGTGCA Δ114/Δ6 CTAAGCTTATCGATG
GTCTGCTACCACGT GATTCGAATAGCTAC

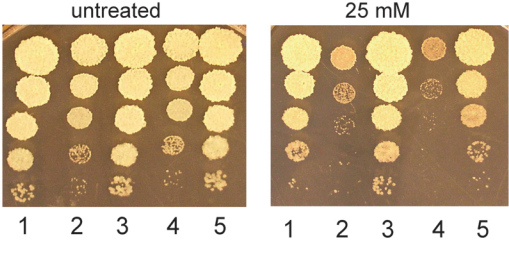
11.

TACCATGGTAGGGATA Δ1/Δ1 TCCCTAAGCTTATC
ATGGTACCATCCCT ATAGGGATTCGAATAG


A.
100
10
1
0.1
0.01
0.001
% Survival
0
200
400
600
800
1000
IR dose (Gy)
ΔadnAB+
adnAB
WT
ΔadnAB
ΔadnAB
ΔrecBCD
ΔadnABΔrecBCD+
adnAB


untreated
222 Gy
1 2 3 4 5
1 2 3 4 5


B.
100
10
1
0.1
% Survival
0
5
10
15
20
25
H2O2 concentration (mM)


untreated
25 mM
1 2 3 4 5
1 2 3 4 5