

Molecular approaches to assess
repair of chromosome breaks

Molecular assays for DSB repair

1. Imaging of double strand break surrogates


- γ H2AX

2. Imaging of repair factors

- Molecules required for repair (e.g. Rad51)

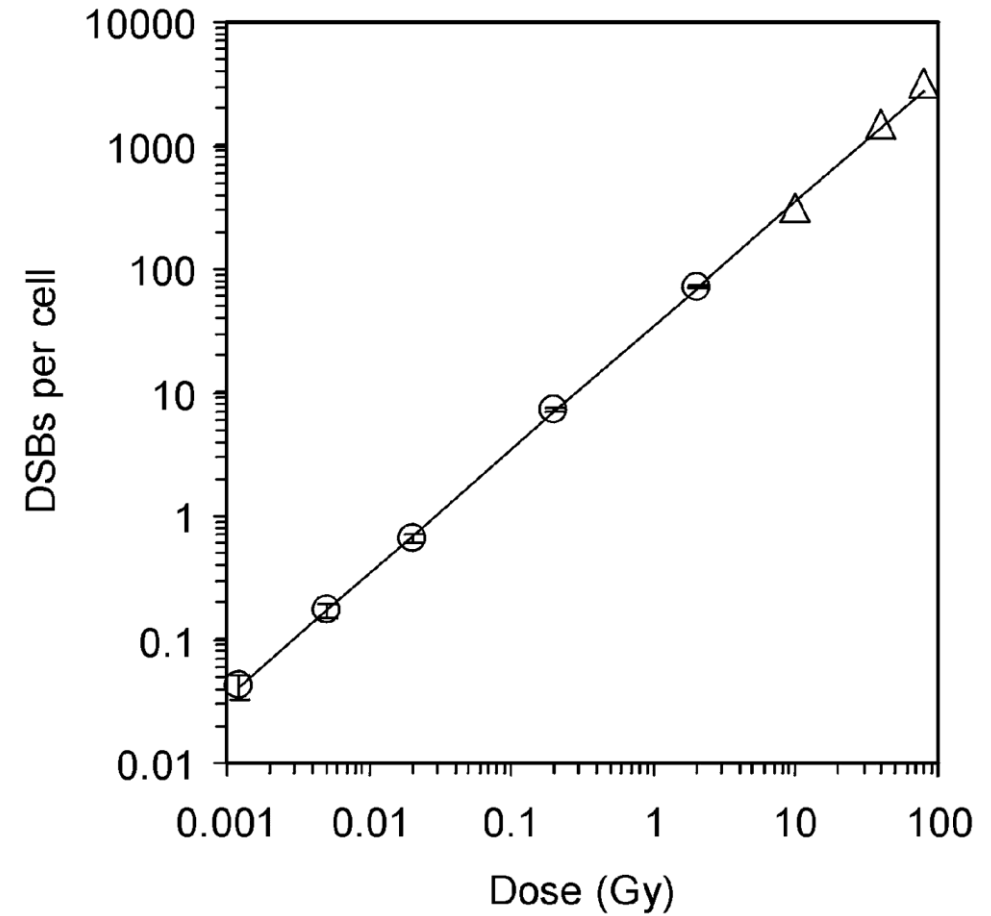
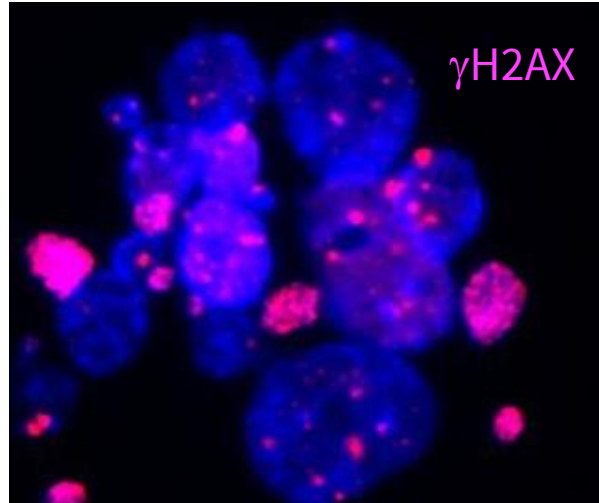
3. Repair

- Pulse field, COMET; detects >100s of DSBs
- typically not suitable for low dose IR
- Repair products
 - Aberrations; cytogenetics, micronuclei
 - Targeted DSBs and reporter assays
 - Sequencing; signatures

- 
- Static picture?
 - not measuring repair unless tracked over time after dose, in living samples

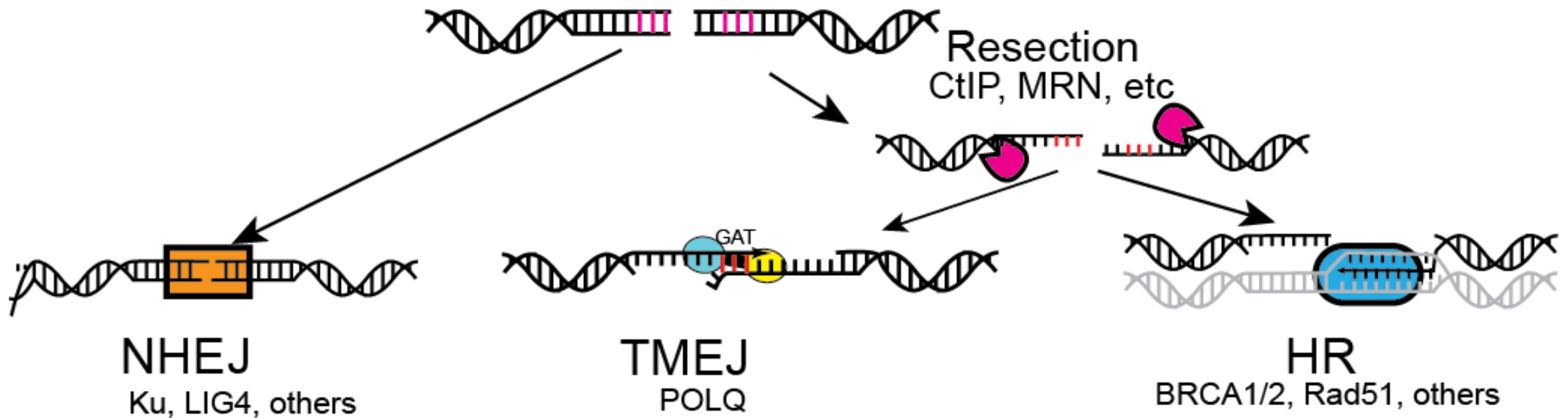
1) DSB surrogates

- γ H2AX
- 53BP1
- TUNEL



Proc Natl Acad Sci U S A. 2003 Apr 29;100(9):5057-62.

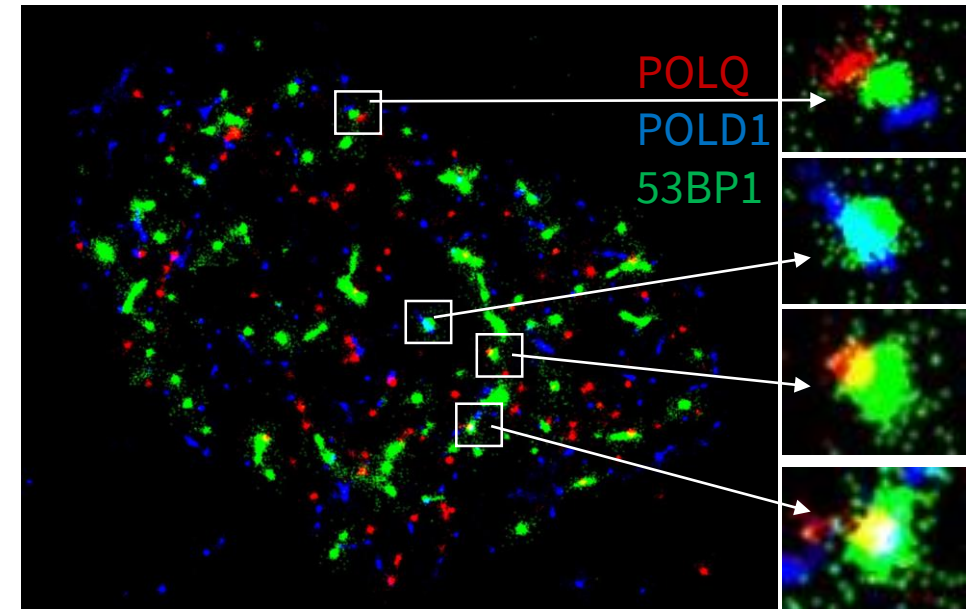
Double strand break repair pathways



Nearly equivalent to...
Microhomology mediated end joining (MMEJ)
Alternative end joining (a-EJ, Alt-NHEJ)

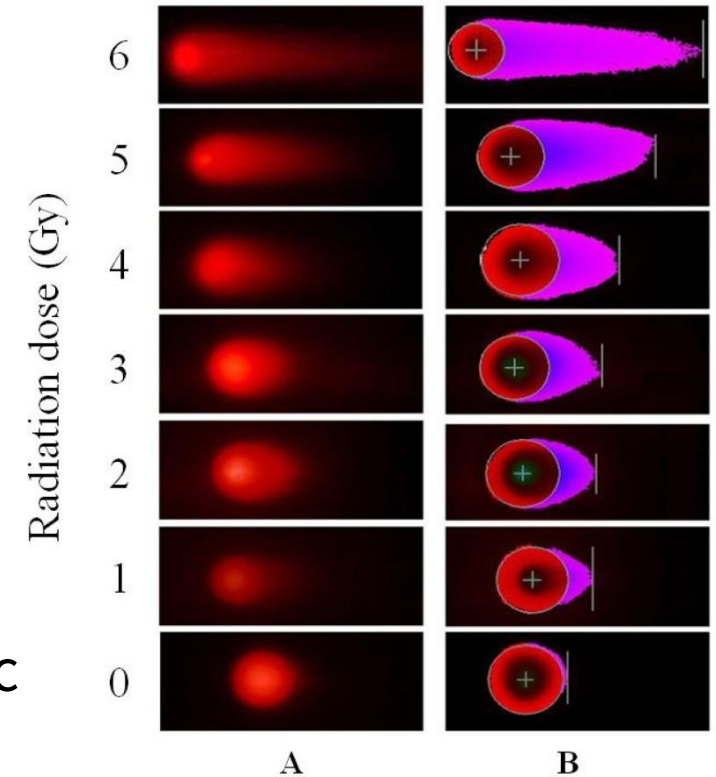
2) Imaging of repair factors

- Immunofluorescence
 - Repair factors aggregate at damage (“colocalize”, form “focus”)
 - Rarely quantitative; repair typically needs only a handful of active molecules
 - Below detection limits
 - Obscured by passive molecules
 - Exception; Rad51, a marker that accurately reflects active HR
- STORM
 - Stochastic Optical Reconstruction Microscopy
 - more sensitive, quantitative
 - better spatial resolution
 - can identify functional associations



3) Repair

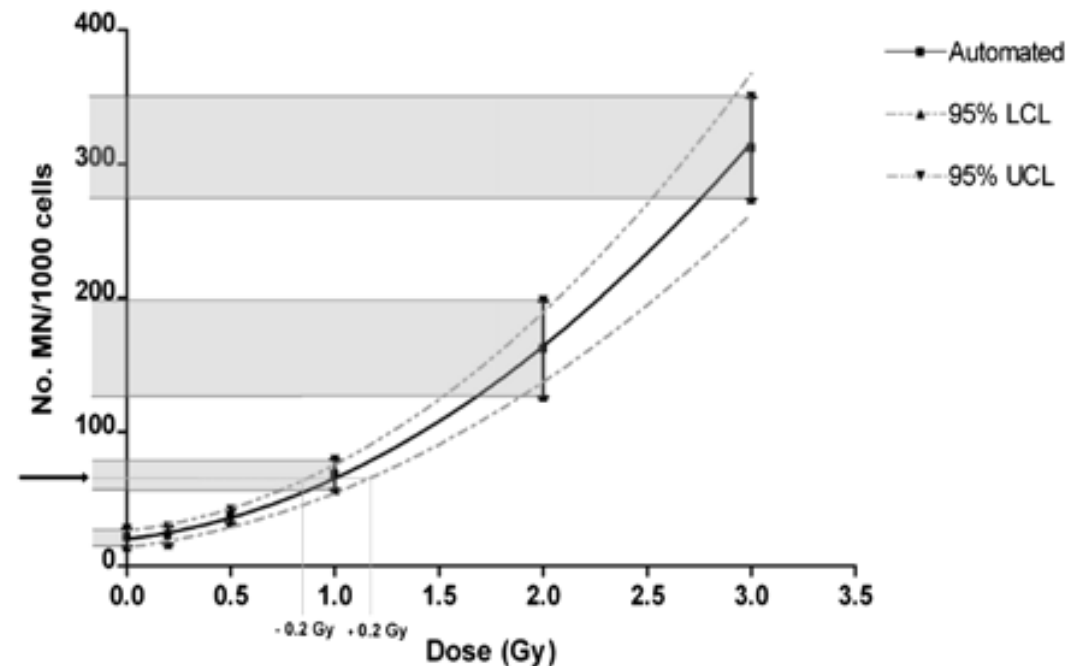
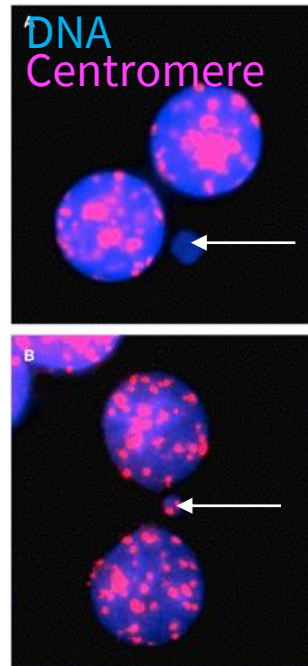
- COMET (and pulse field)
- Embed nucleii in agarose, electrophorese
- Fragmented DNA appears as tail on comet
- Best at 100s of DSBs or more
 - typically not suitable for low dose IR
 - Descriptive; little insight into pathway, consequenc



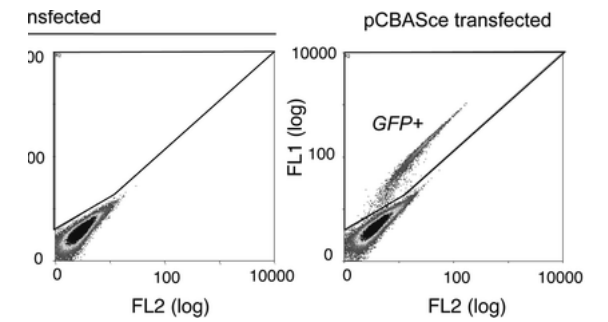
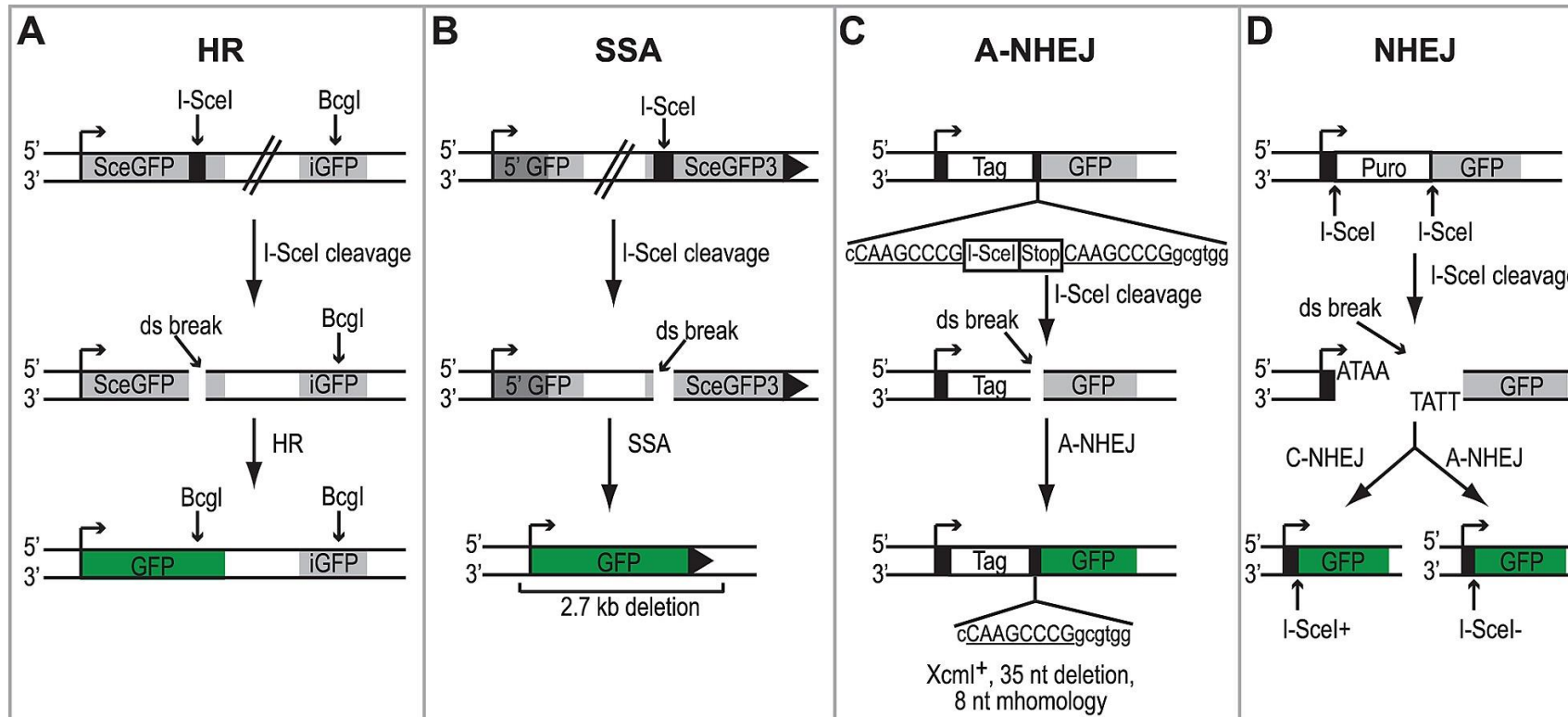
Int J Mol Sci. 2013;14(11):22449-22461.

3) Repair

- Aberrant repair
 - Micronuclei; fragmented chromosomes
 - Cytogenetic detection of aberrations
 - Like COMET assay, no insight into mechanism



3) Reporter assays

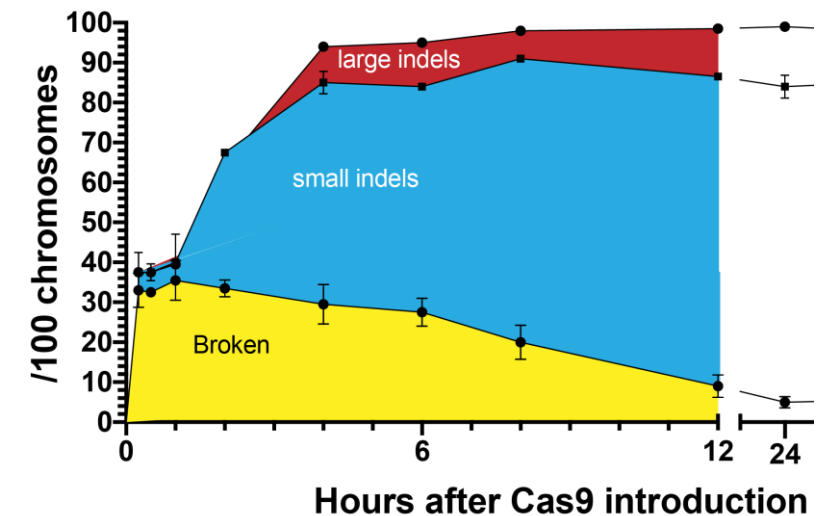
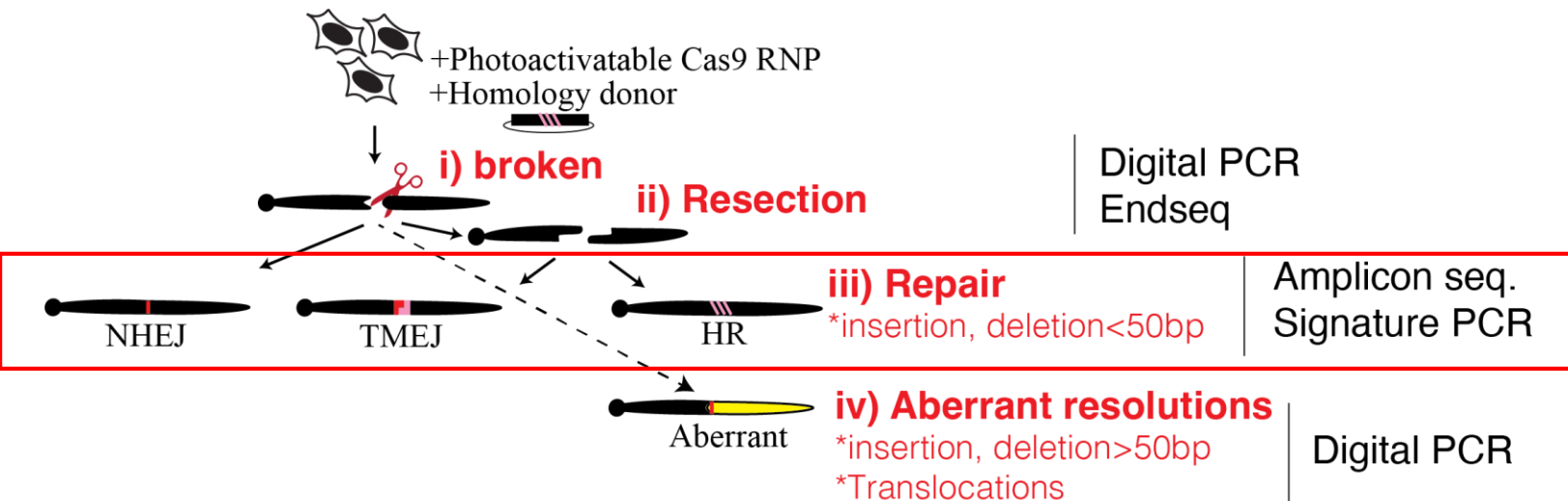


PLoS Pathog. 2012;8(8):e1002862.

Measure efficiency of pathway specific “signature” repair product

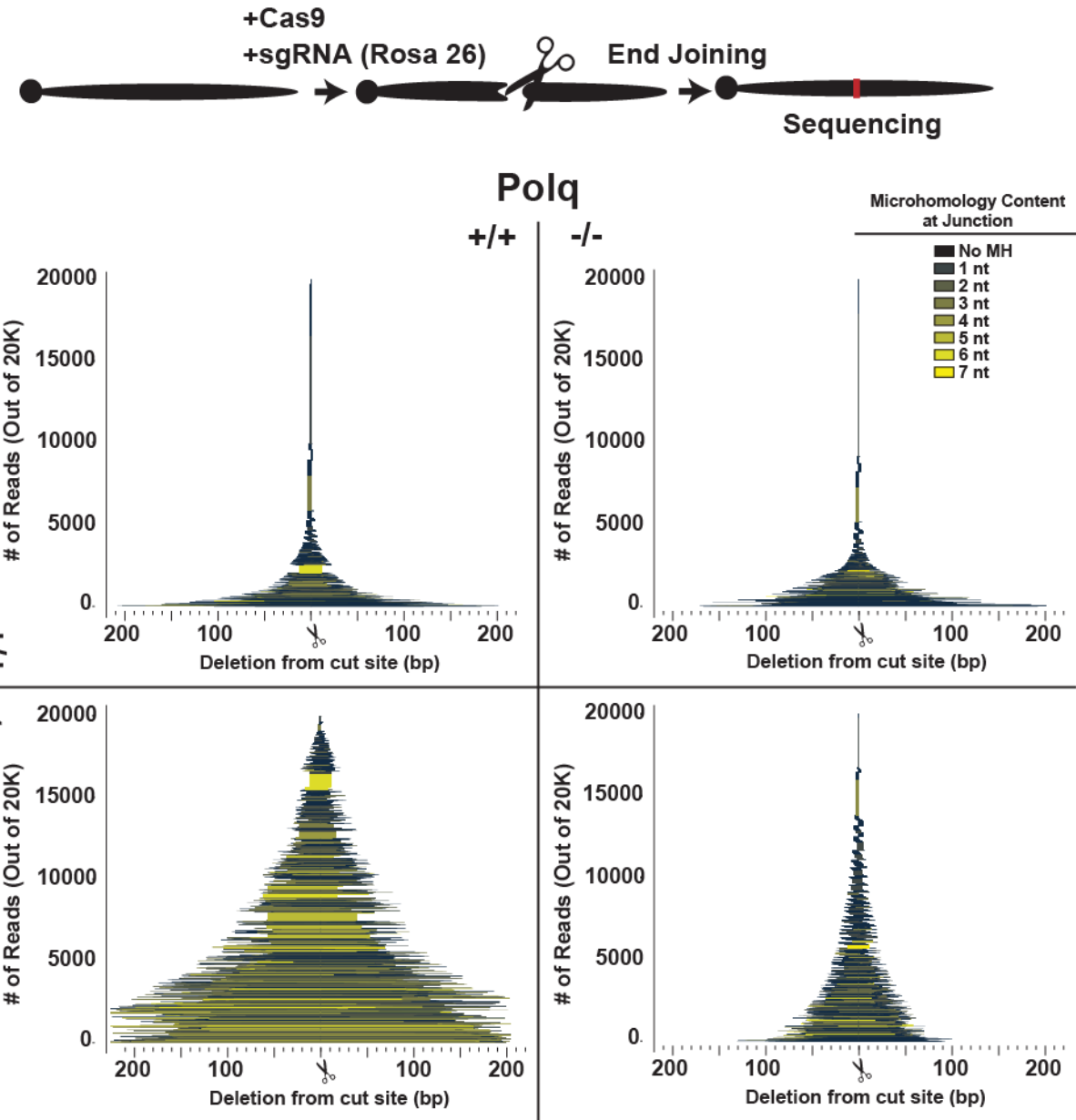
3) Sequencing repair products

- Targeted, induced chromosome break
- Track ALL intermediates, products, over time
 - Combination of digital PCR, amplicon sequencing
 - Insertions and deletions (indels) <50bp=accurate repair
 - Deletions >50 bp, translocations=aberrant

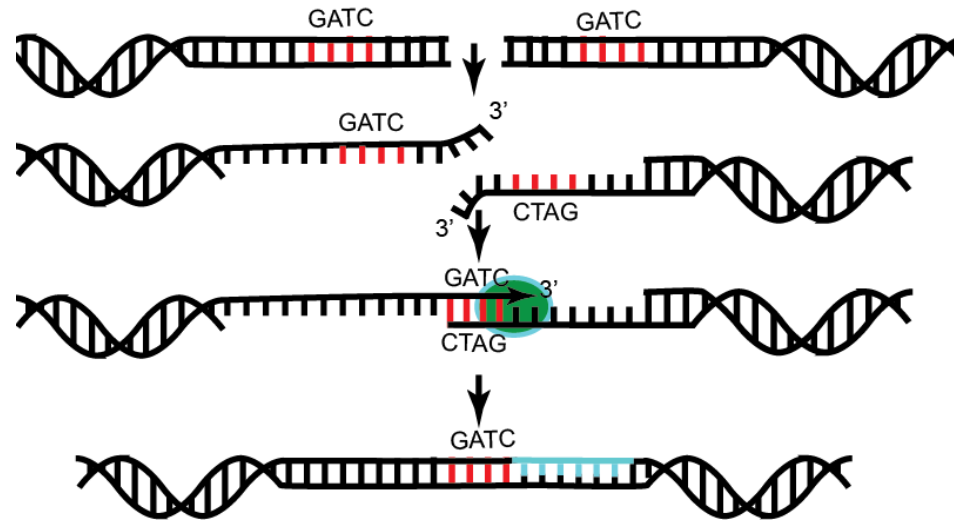
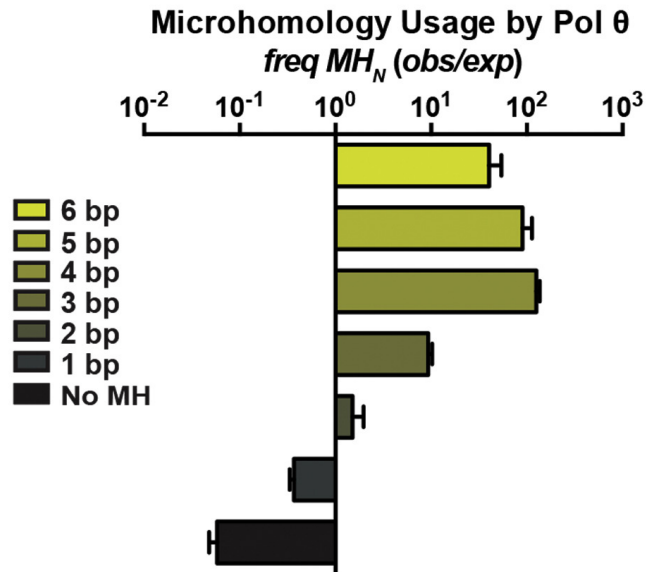


3) Repair

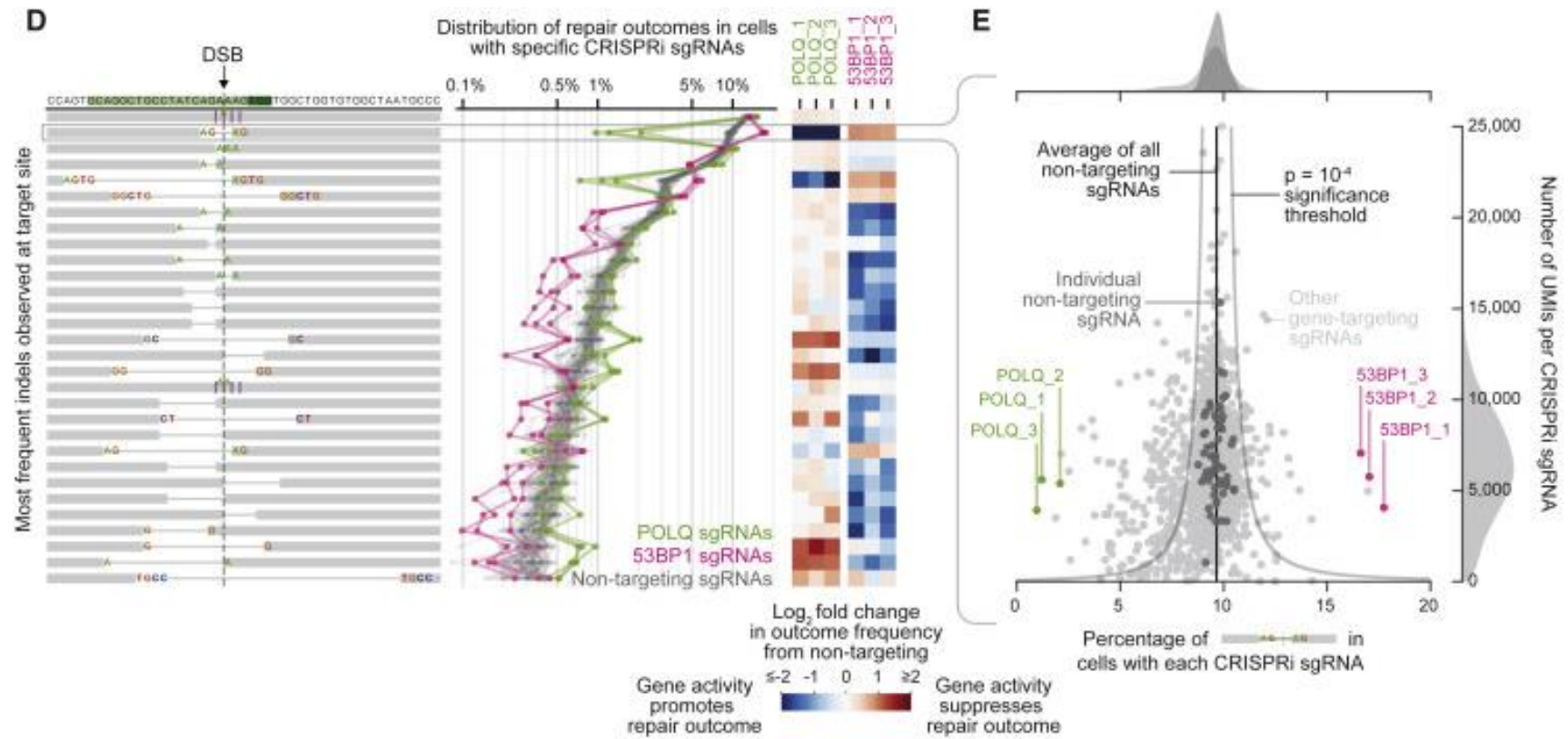
- “Repairseq”
- Ku (NHEJ) required for
 - short (<5bp) insertion and deletion
 - Little role for microhomology
- POLQ required for deletions at microhomologies (yellow)



TMEJ and microhomologies



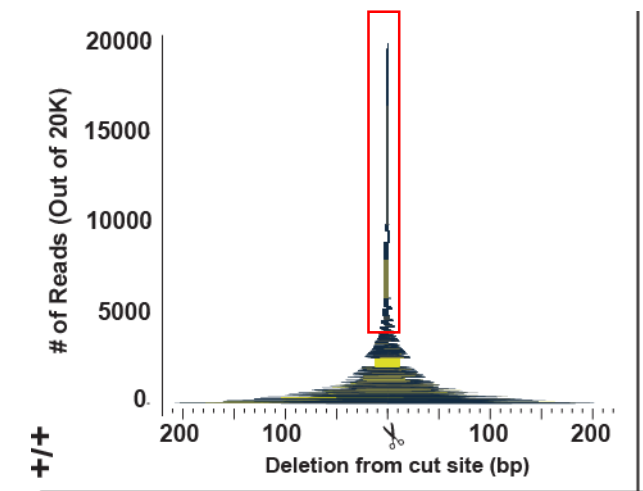
3) Repairseq



Cell. 2021 Oct 28;184(22):5653-5669.e25. 2021 Oct 20.

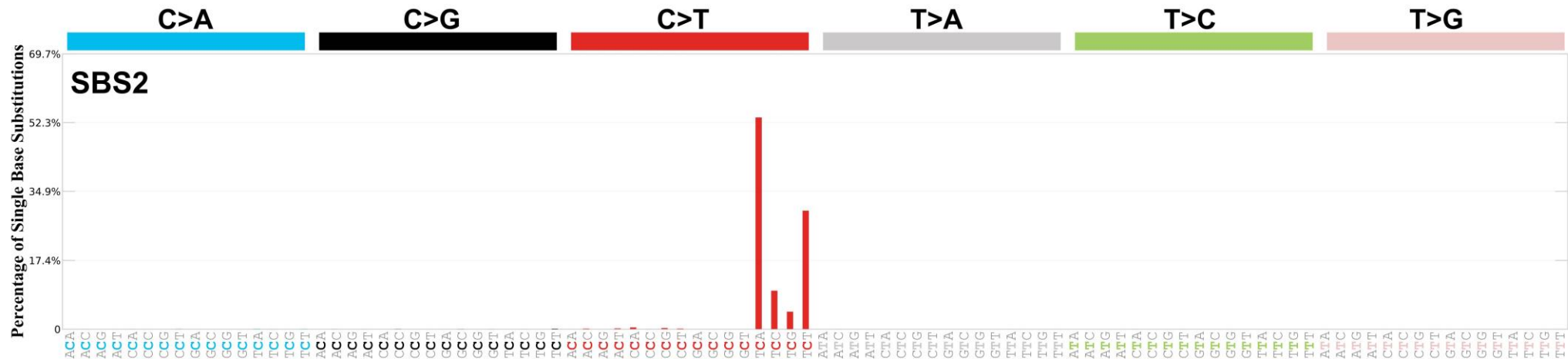
3) Repair signatures

- Whole genome sequencing
 - Statistics driven "clustering" of somatic mutation types, according to e.g. sequence context, tumor type
 - Accurate repair is "invisible"
- DSB repair: focus on insertion and deletions ("indels")
 - most, but not all, of NHEJ...even TMEJ=small indels; 0-5 bp, but...
 - This is quickly buried underneath more frequent replication associated errors
 - For anything short of very high dose
 - longer insertion and deletions...



3) Repair signatures

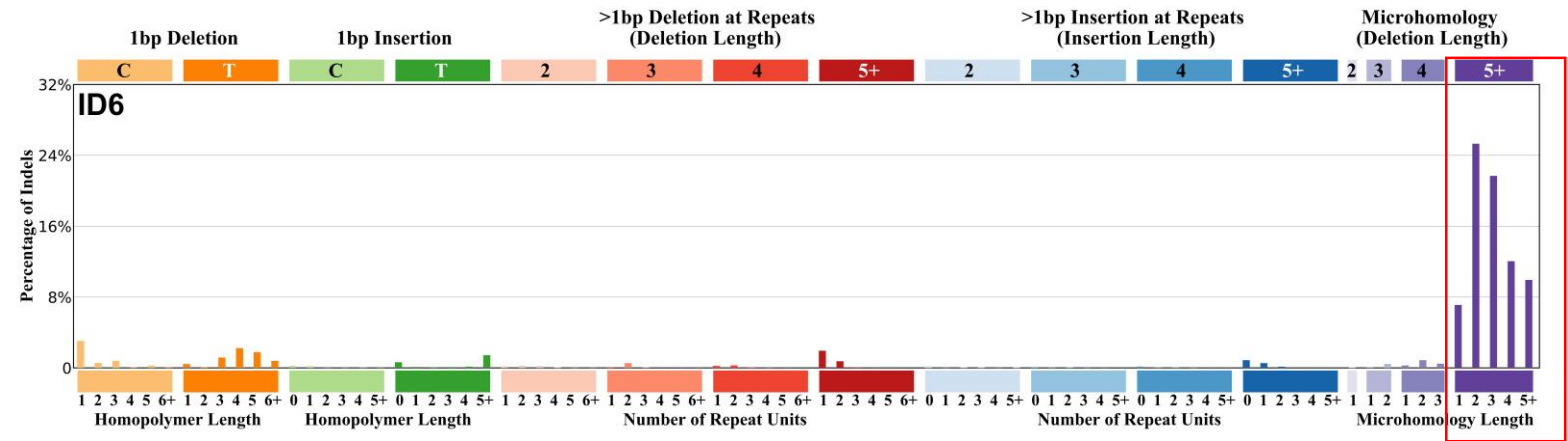
- Whole genome sequencing
 - Statistics driven "clustering" of somatic mutation types, according to e.g. sequence context, tumor type
 - Accurate repair is "invisible"



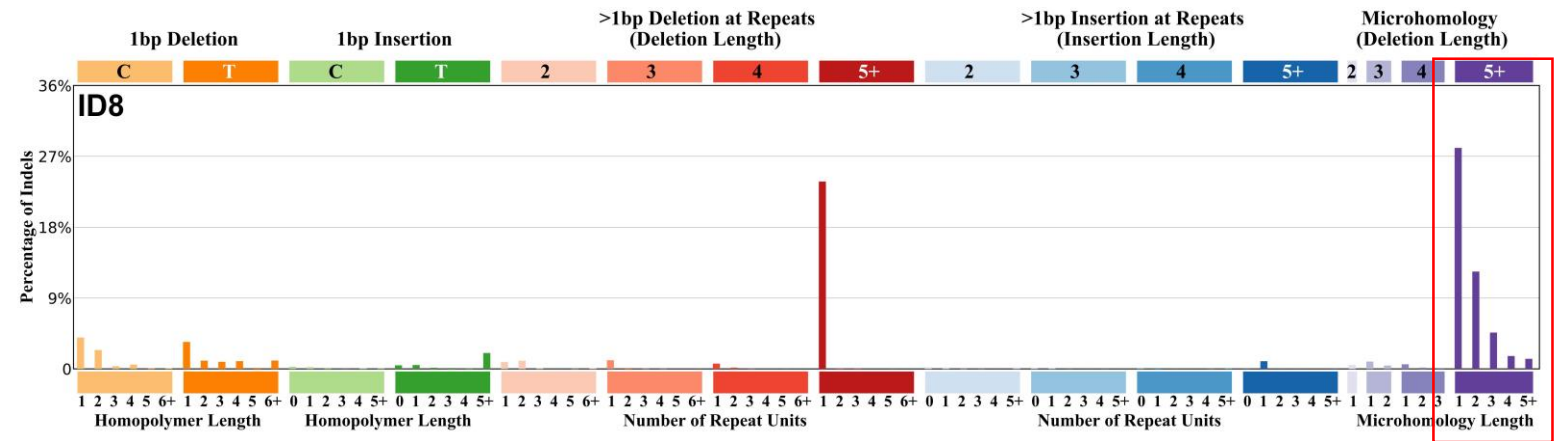
Nature. 2020 Feb;578(7793):94-101.

3) DSB Repair signatures

- Repair by TMEJ (mostly)



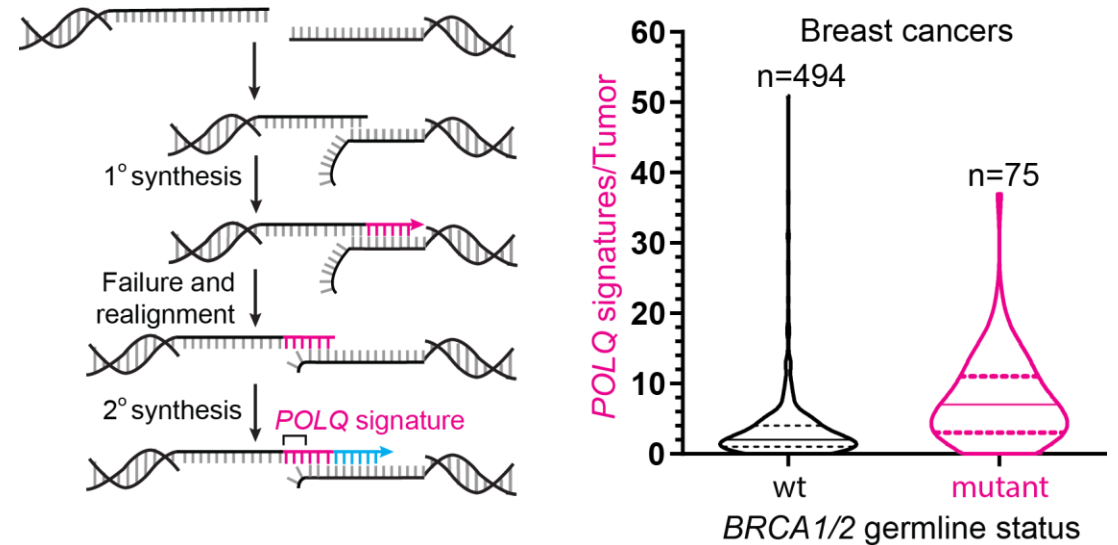
- Repair by NHEJ (mostly)



Nature. 2020 Feb;578(7793):94-101.

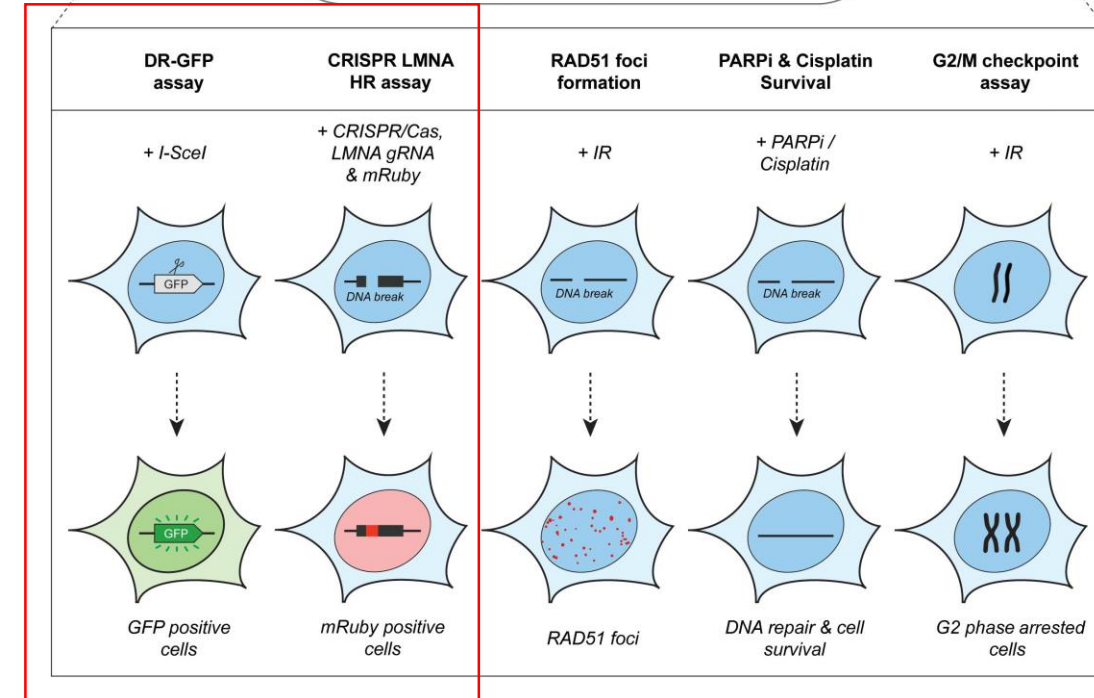
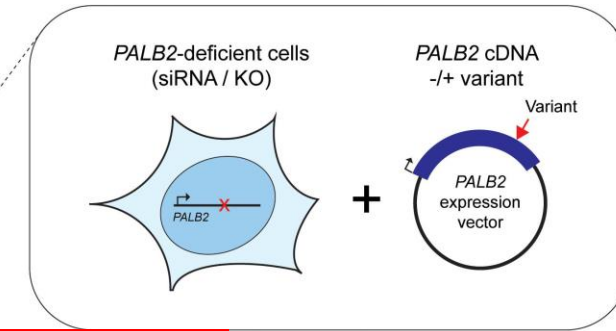
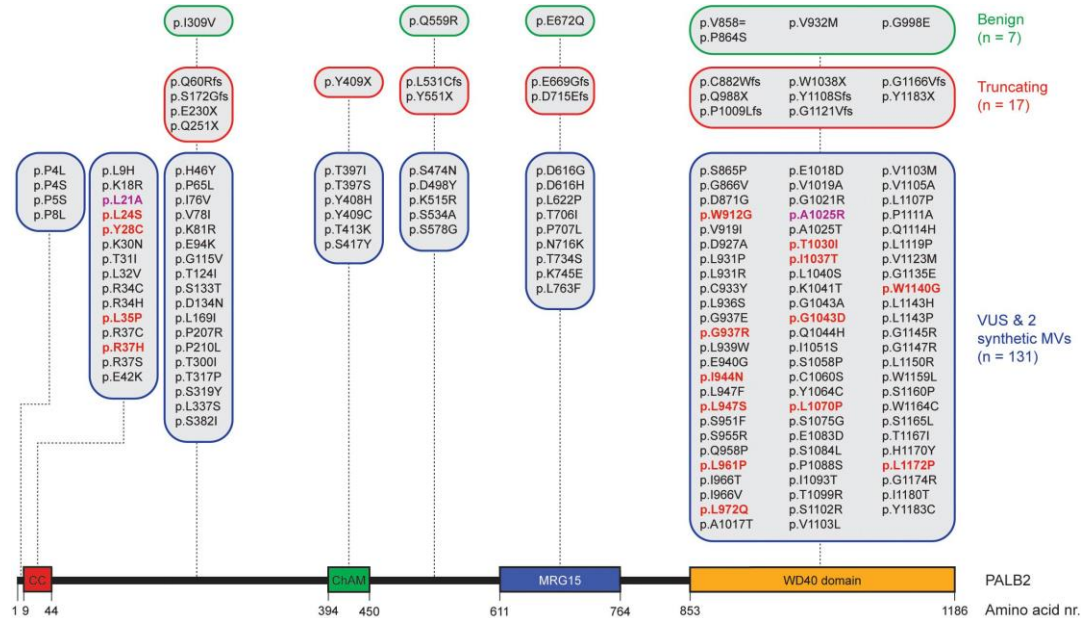
More exotic indels

- TMEJ
 - Templed insertions
 - <15 bp repeat of nearby sequence (within 30 bp)
 - Interrupted repeat, NOT tandem
- NHEJ
 - short (10-50 bp) tandem repeat



Templed insertions in BRCA mutant cancer

3) Functional assays to predict effects of variants of uncertain significance



4) Future directions

- Need more robust, quantitative, and sensitive methods to image damage, repair factors
- Signature detection
 - Currently stats only- blind to aetiology
- Employ newly integrated functional assays and genetic models (like Repairseq) to
 - Provide aetiology for signatures
 - Evaluate factors (environmental, genetic) that impact repair efficiency
 - Including effects of variants of uncertain significance on DSB repair genes