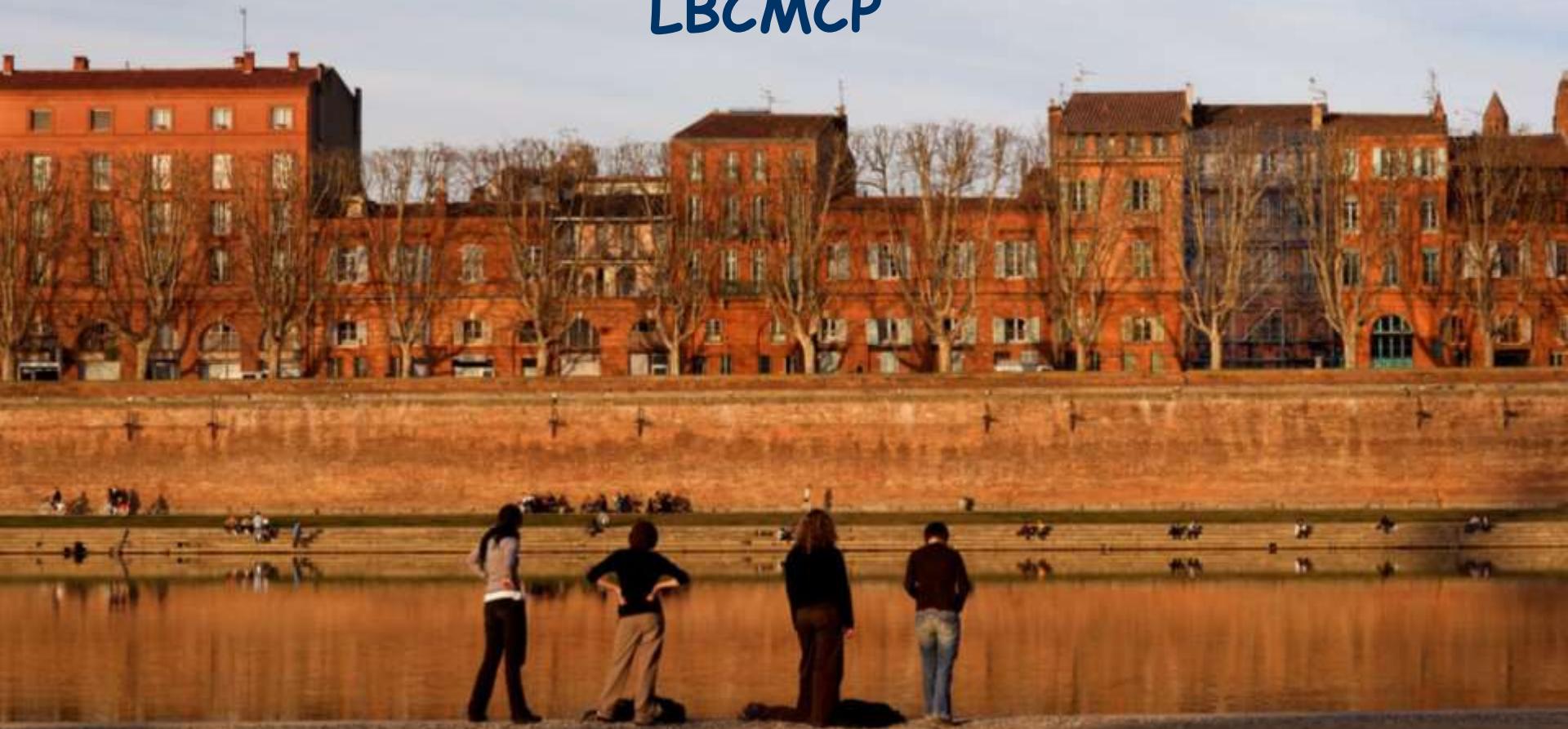
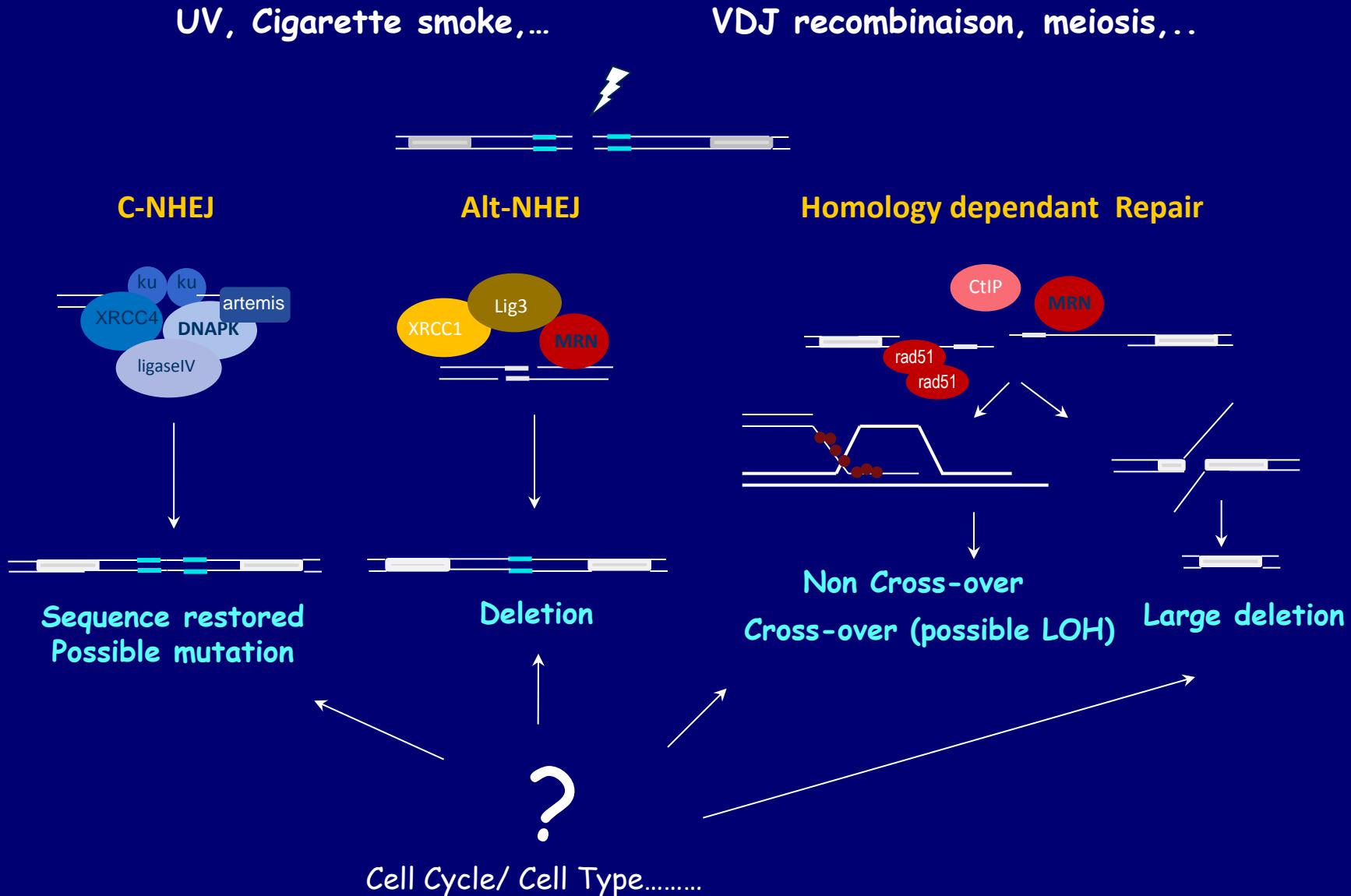


# Chromatin function in DSBs repair

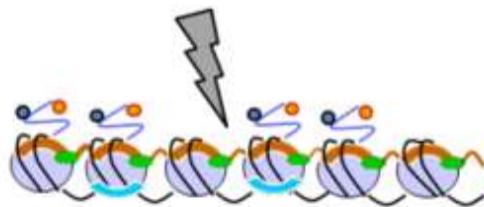
Gaëlle LEGUBE  
LBCMCP



# DSBs repair

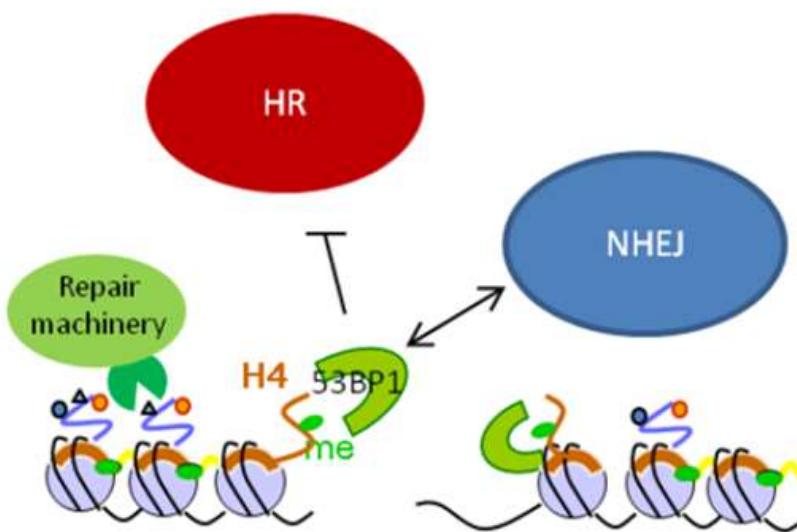


# DSBs repair on chromatin



Influence of **preexisting** chromatin structure on repair

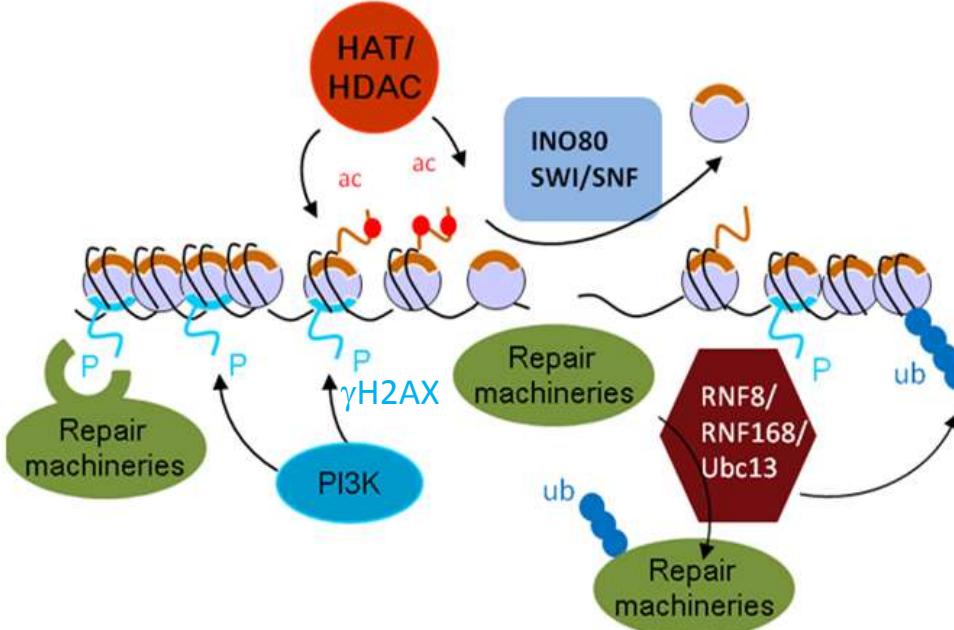
**PRIME**



# DSBs repair on chromatin

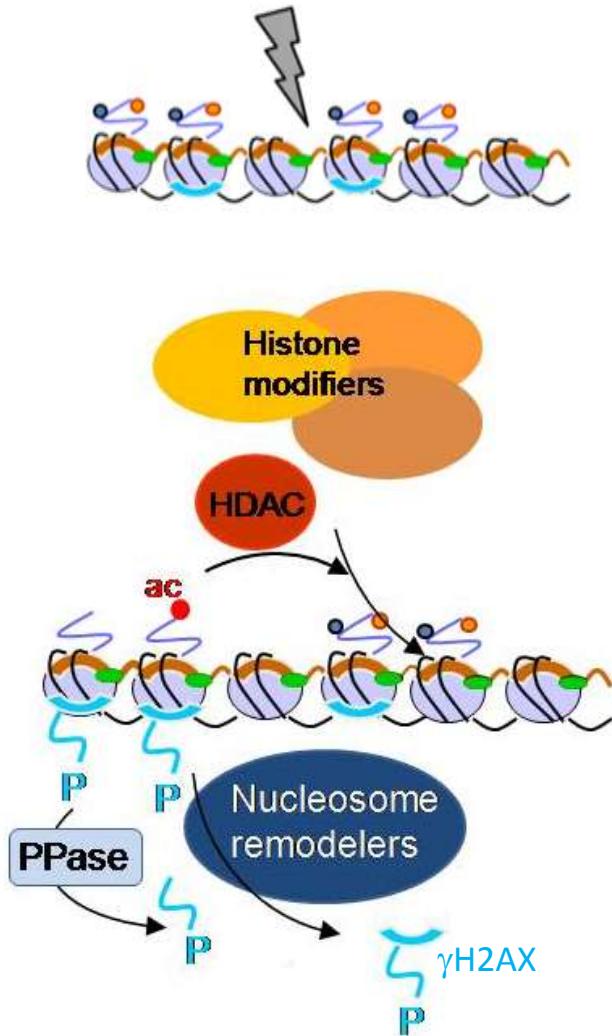
## REPAIR

DSB-induced chromatin changes that helps repair



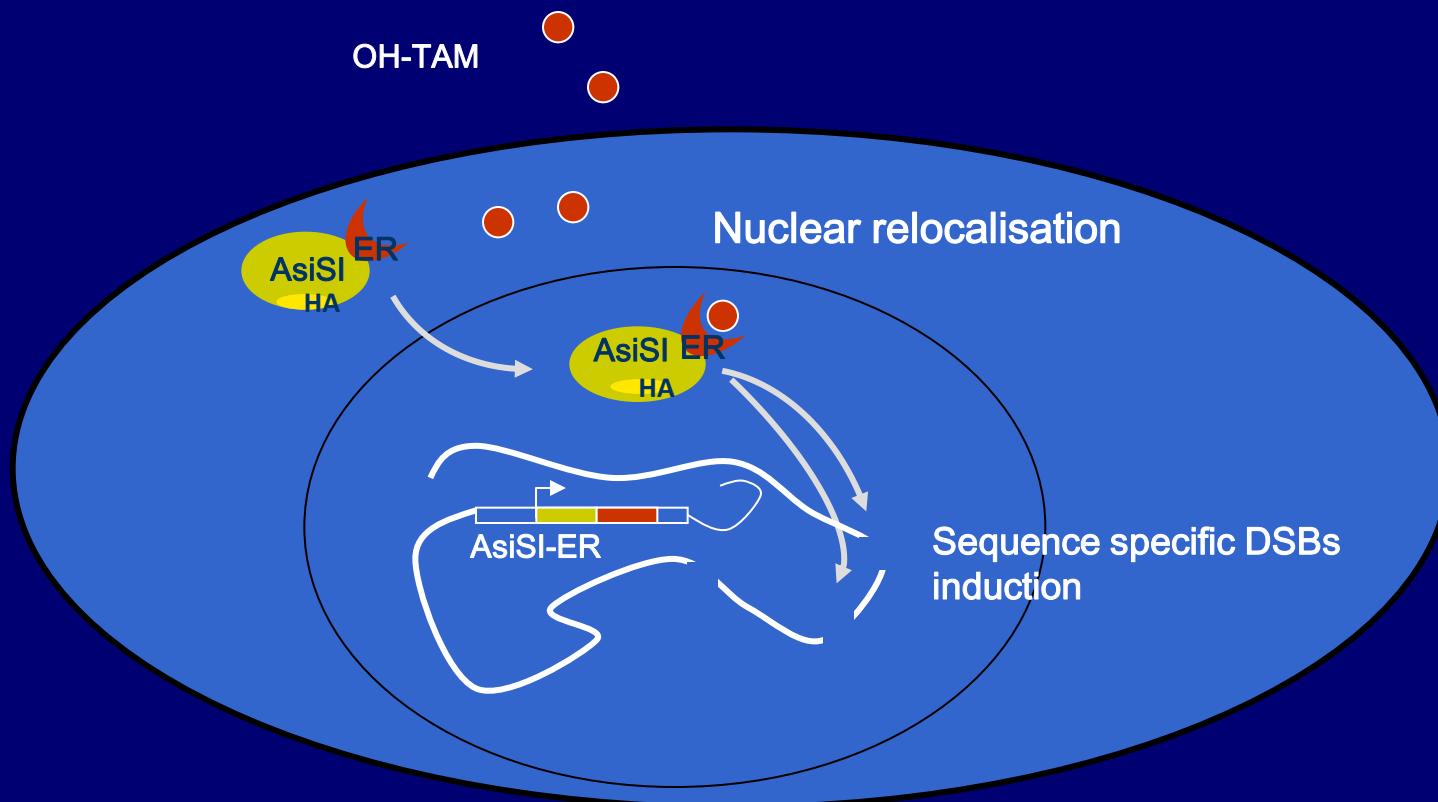
# DSBs repair on chromatin

**RESTORE**



# DIvA, a sequence specific DSB inducible cell line

---



# ChIP-seq to characterize chromatin structure and repair events at AsiSI induced breaks

## Chromatin IP

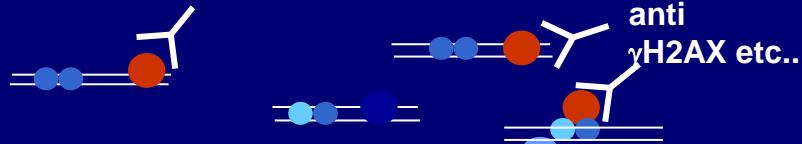
Crosslink



Sonication (~500pb)

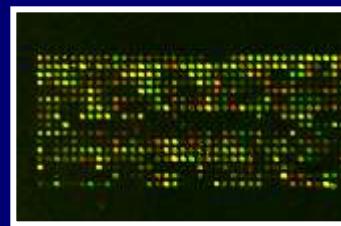


Chromatin IP



Reverse crosslink, DNA purification

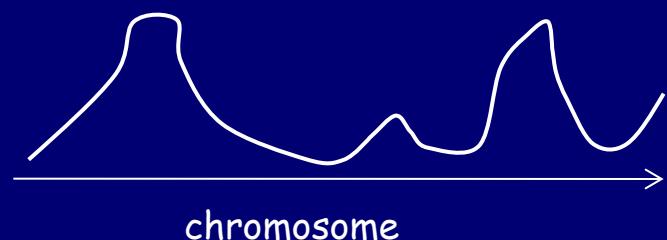
## ChIP-chip



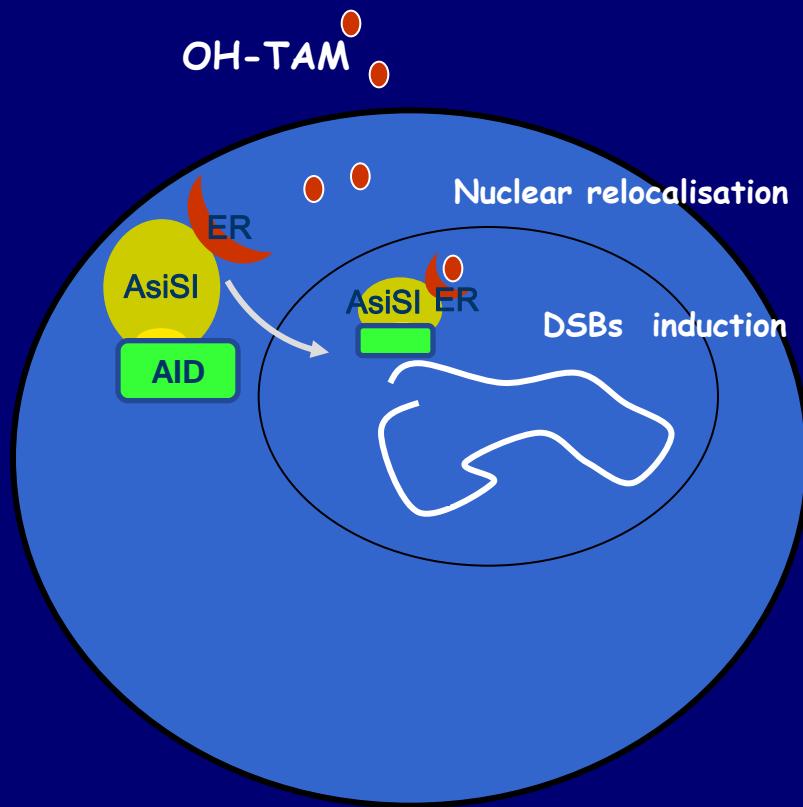
## ChIP-seq



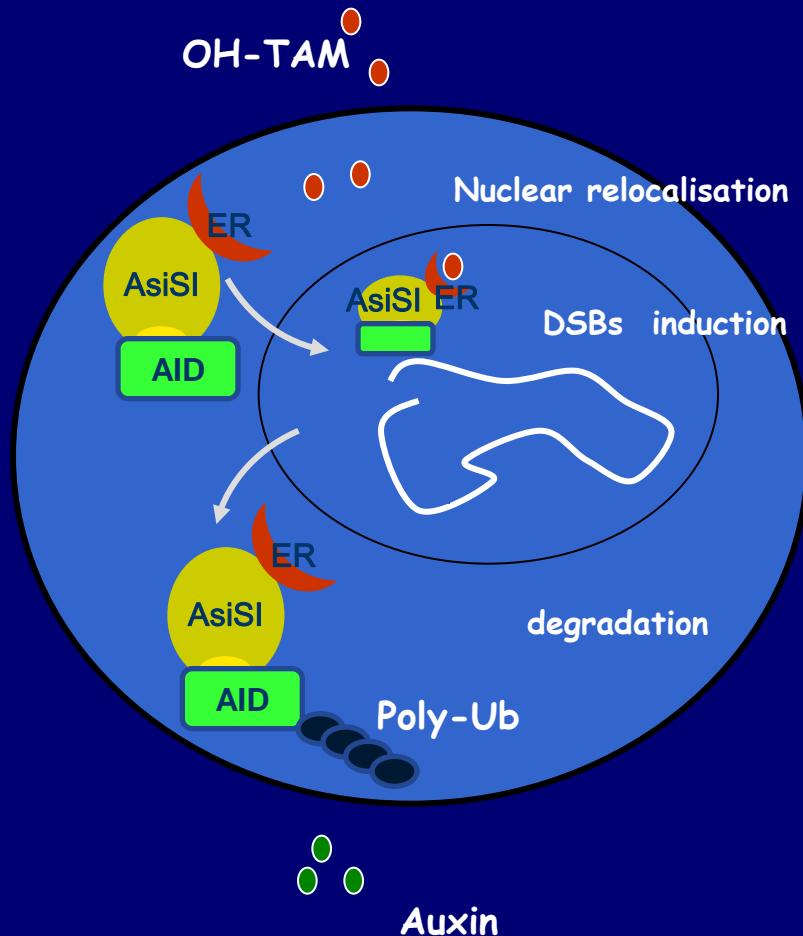
Studying DSB repair on multiples breaks simultaneously, with a high resolution



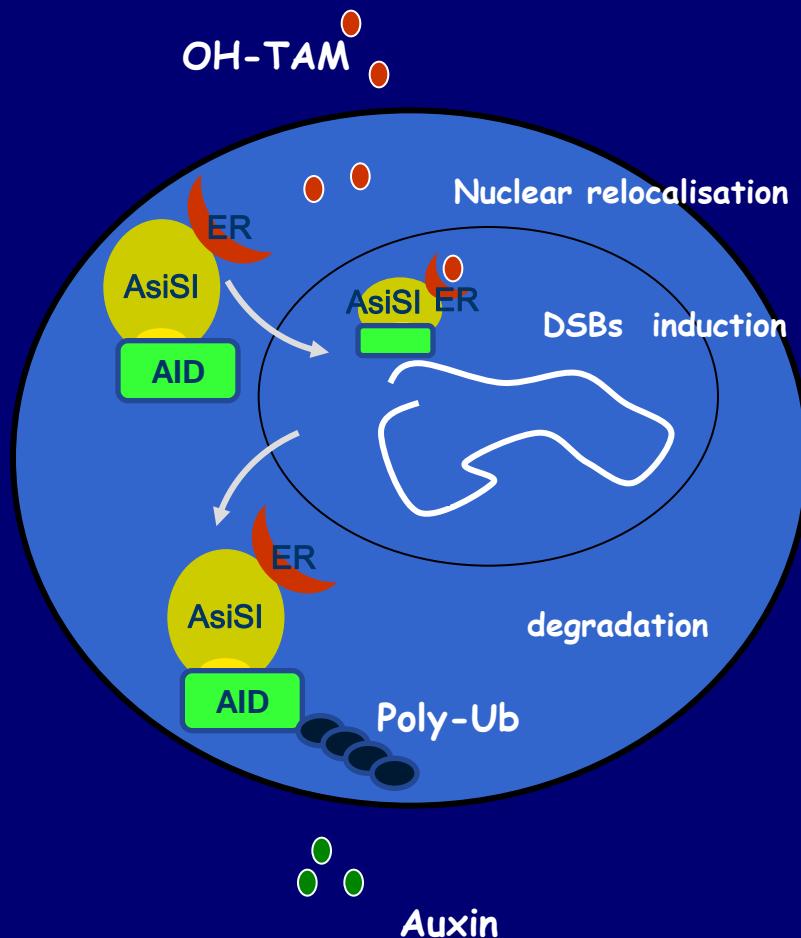
# DIvA, a sequence specific DSB inducible cell line



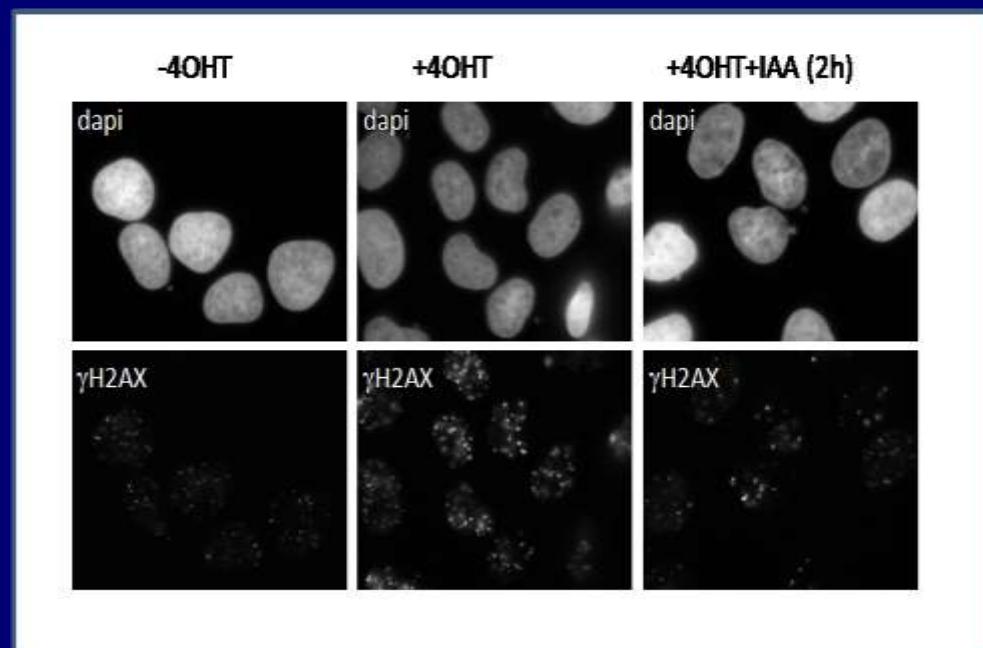
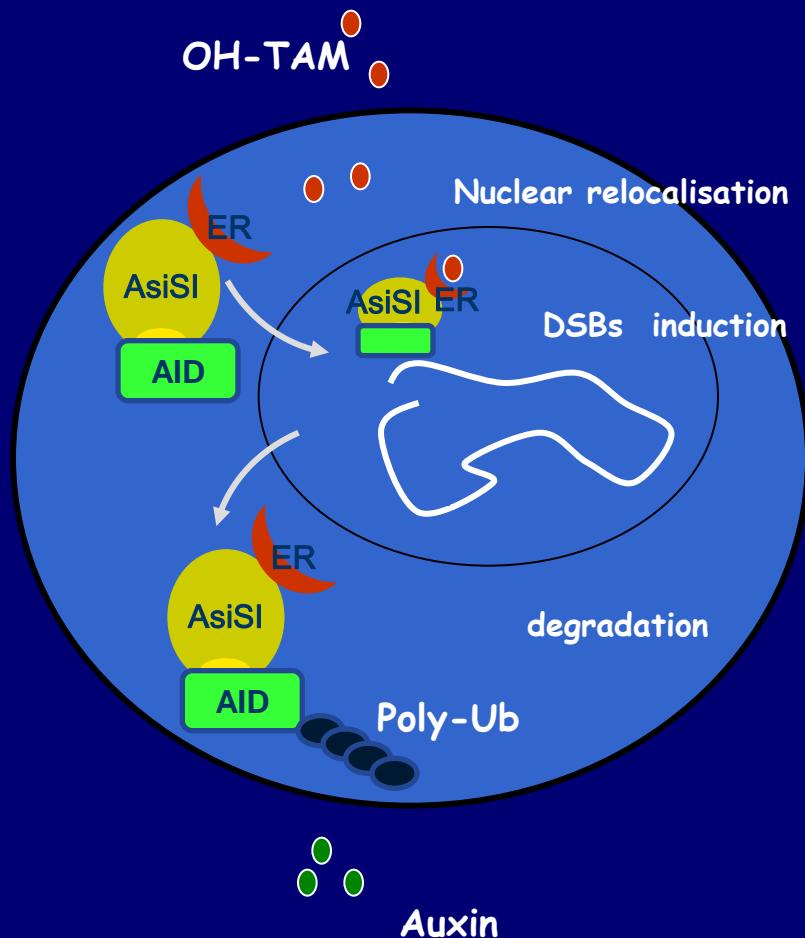
# DIvA, a sequence specific DSB inducible cell line



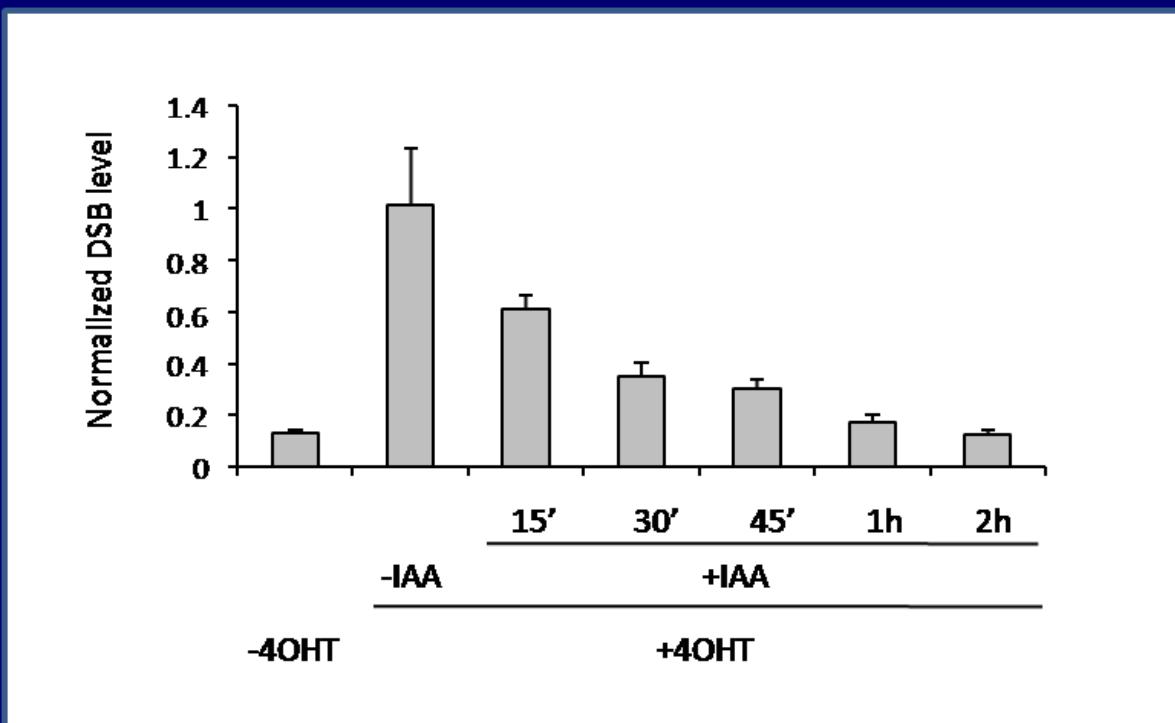
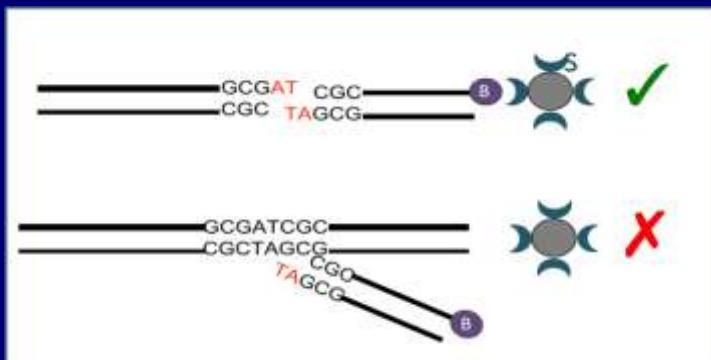
# DIvA, a sequence specific DSB inducible cell line



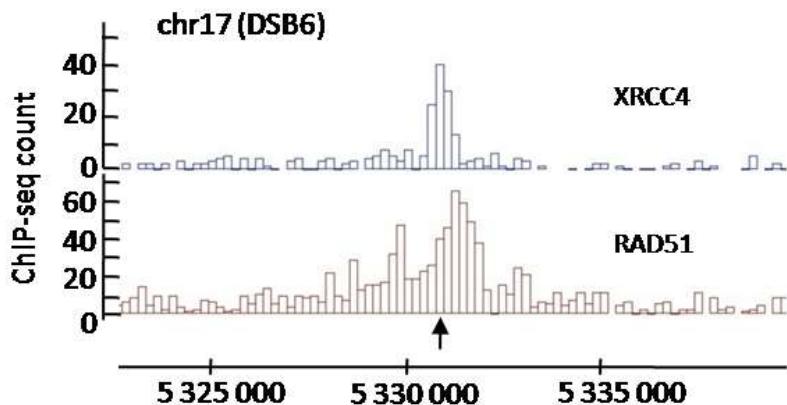
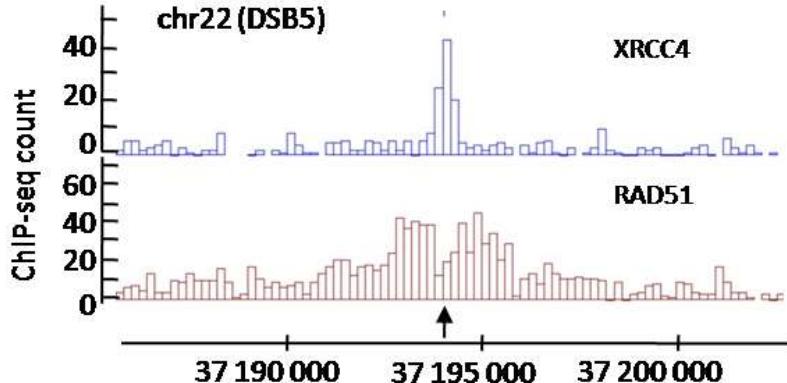
# DIVA, a sequence specific DSB inducible cell line



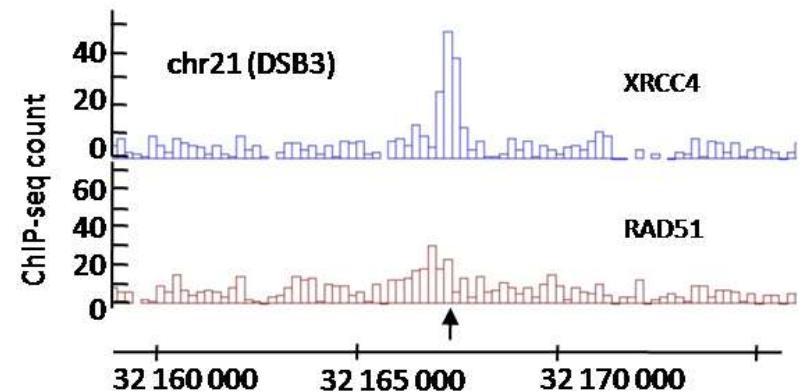
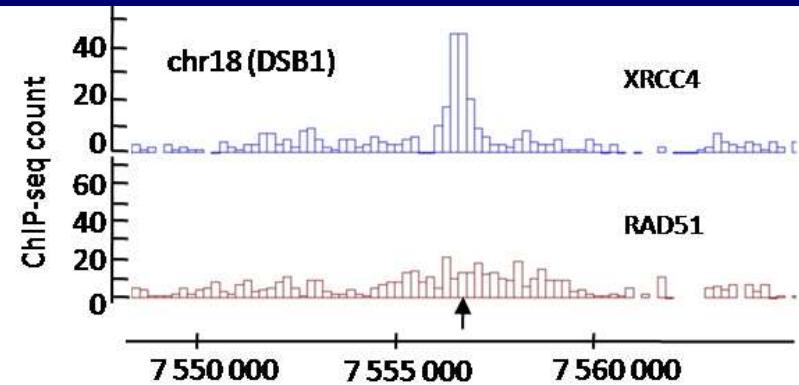
# A protocol to measure repair kinetics at AsiSI induced breaks



# ChIP-seq XRCC4/RAD51

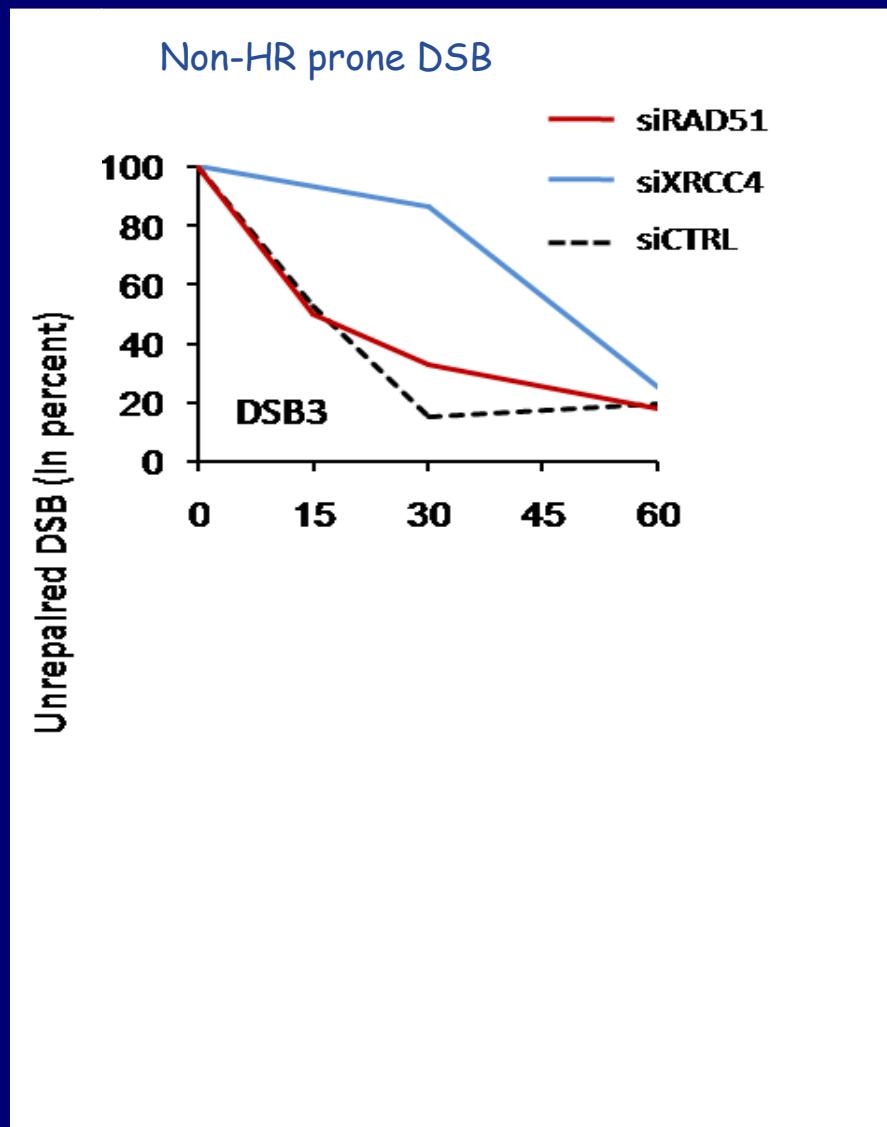


HR-prone

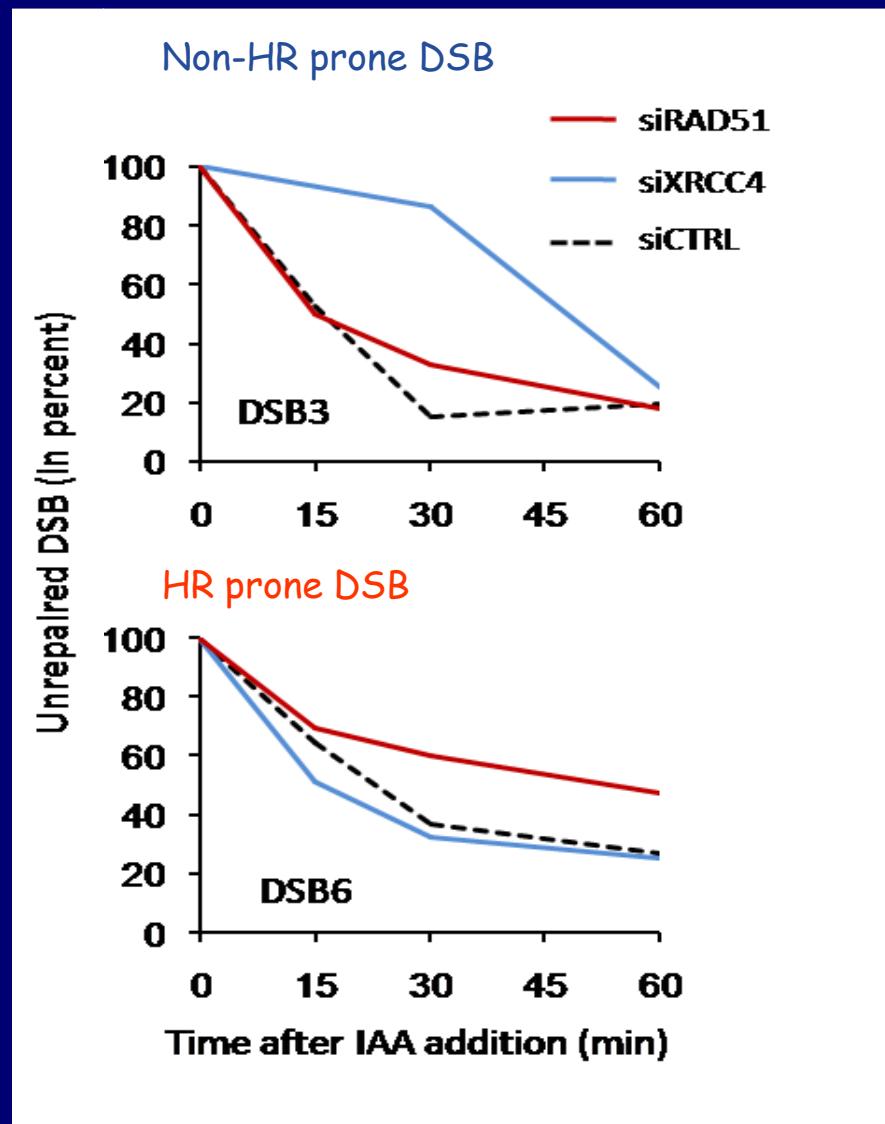


Non HR-prone

# HR-prone sites rely on RAD51 for repair

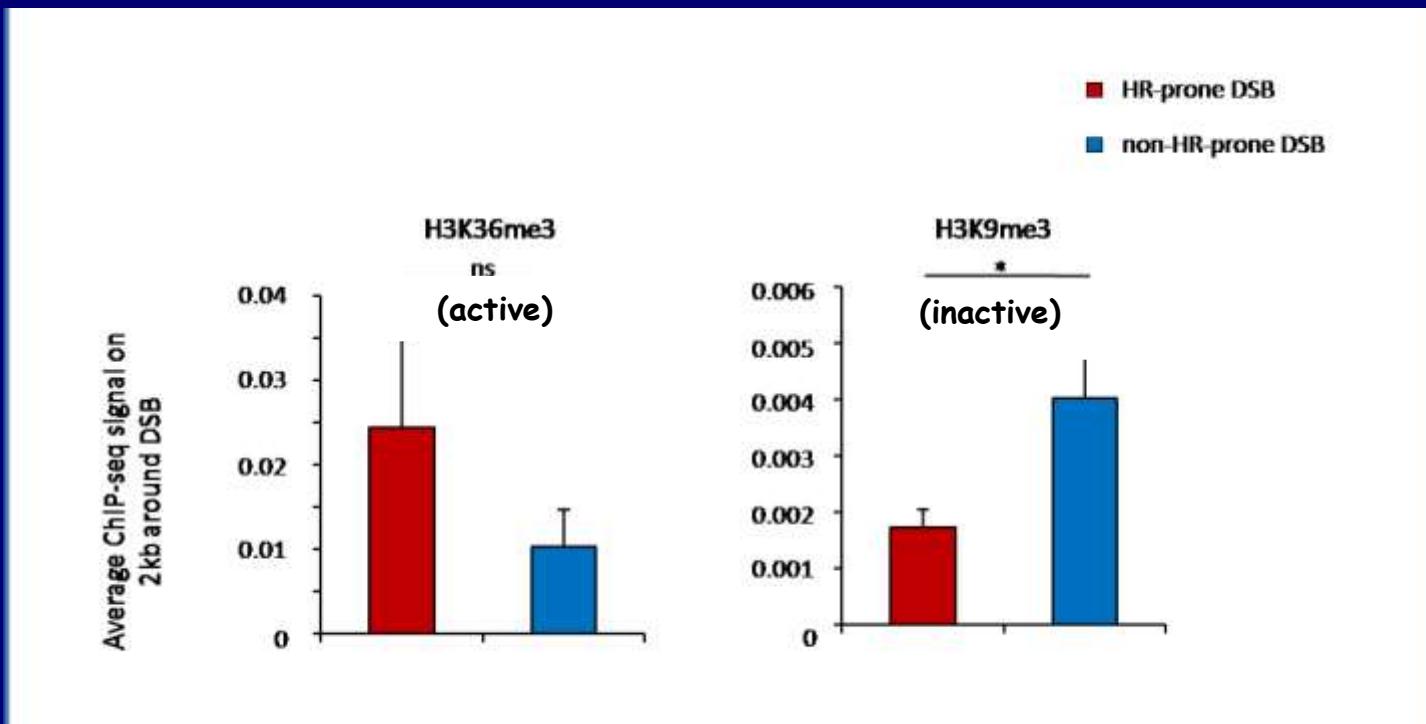


# HR-prone sites rely on RAD51 for repair

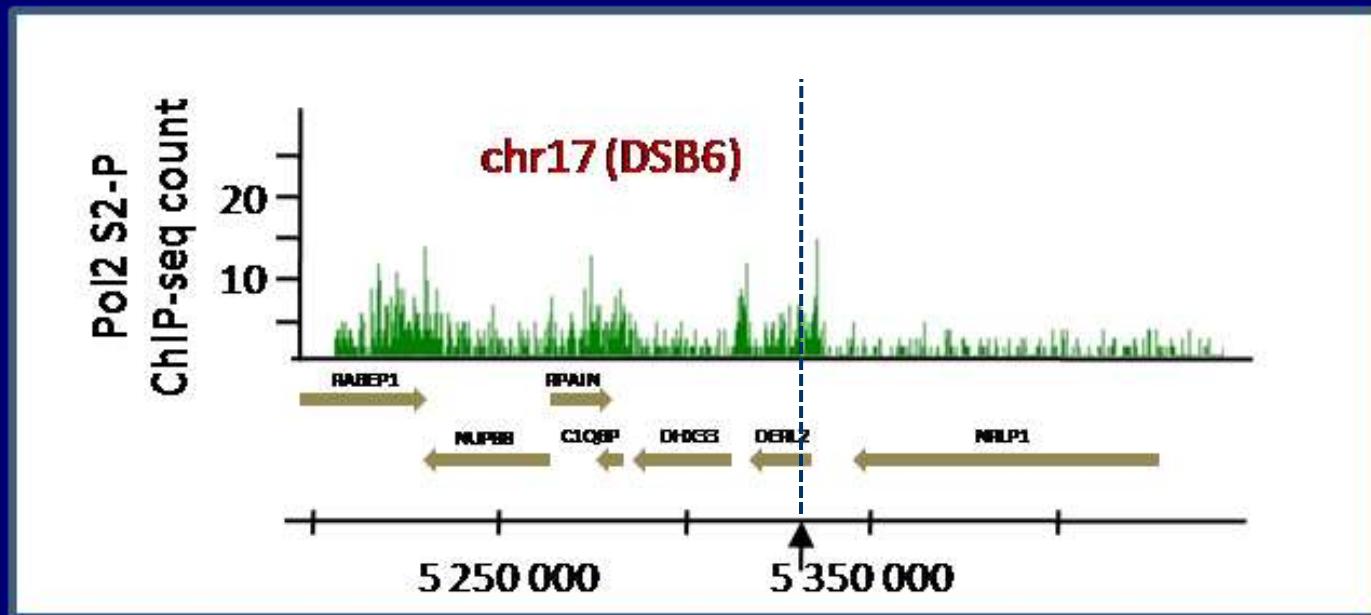


# HR-prone sites are enriched in active marks.

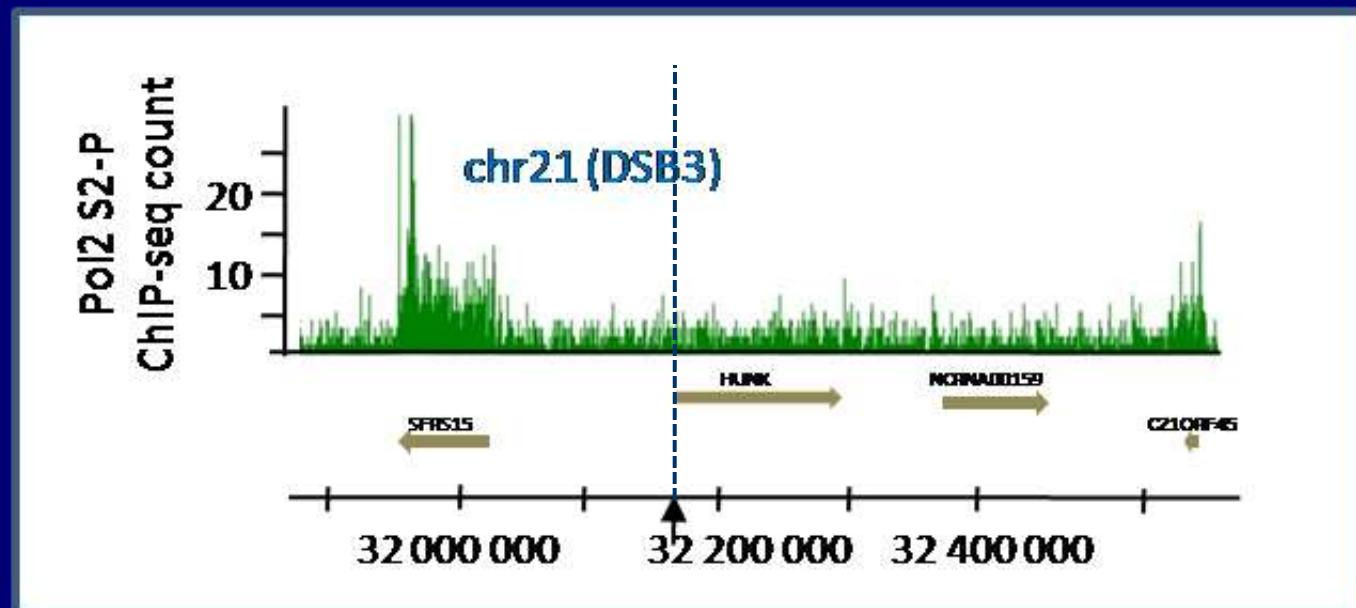
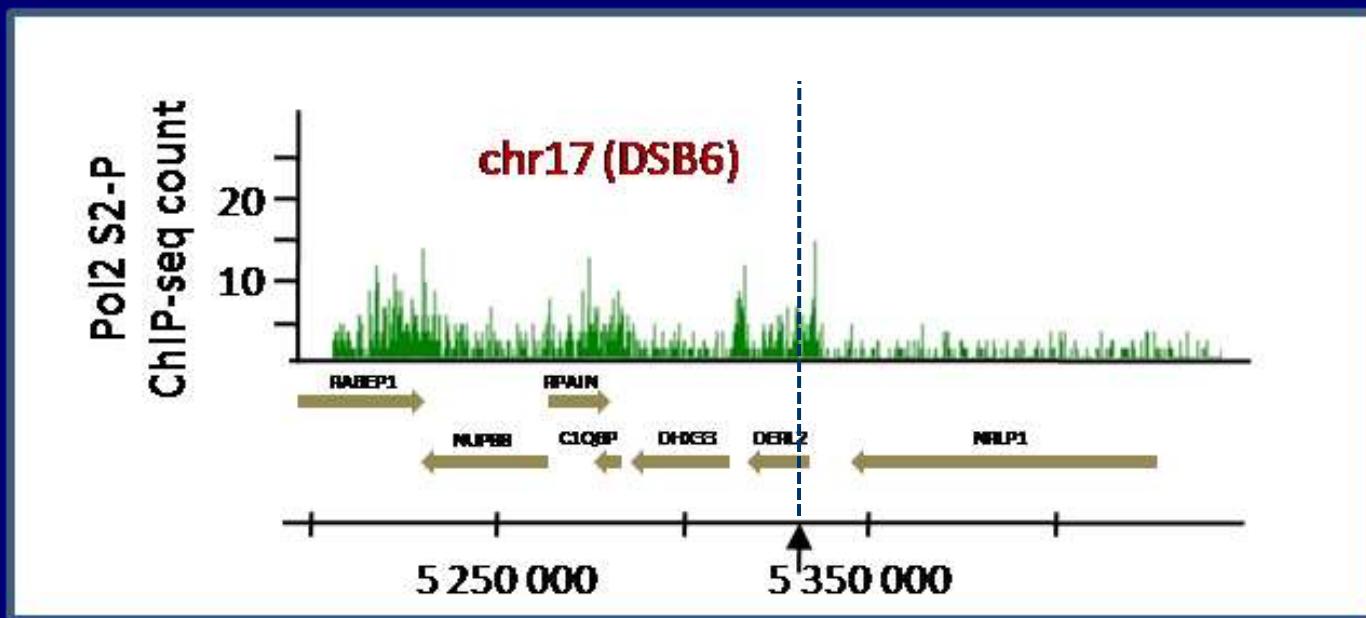
ENCODE Epigenome project



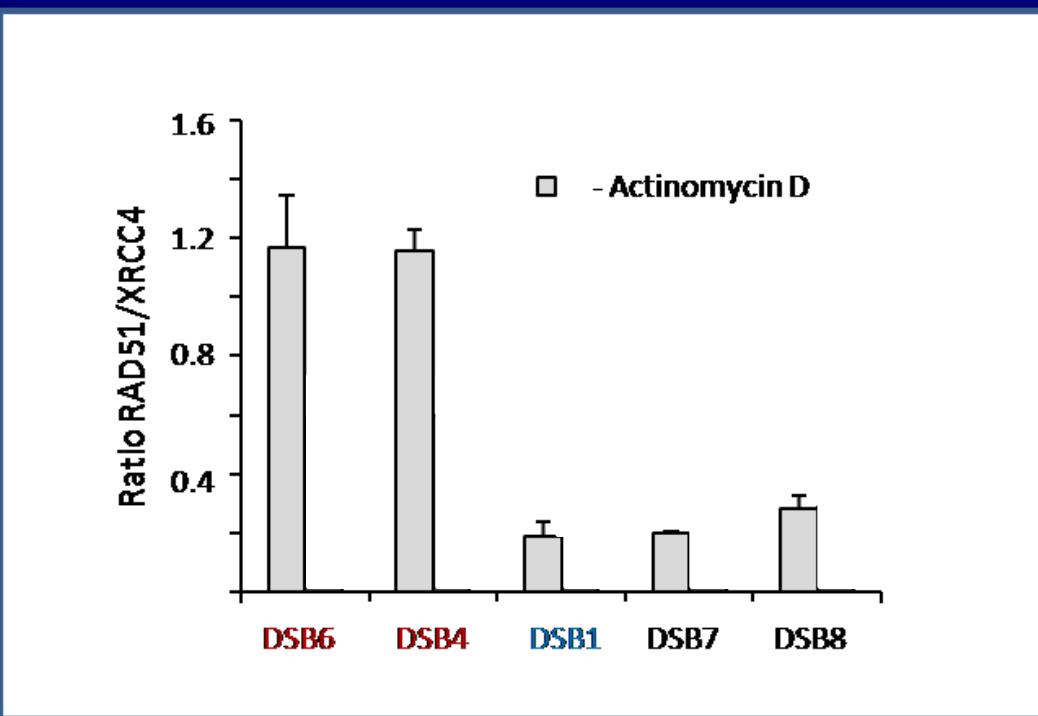
# HR-prone sites lie in transcribed units



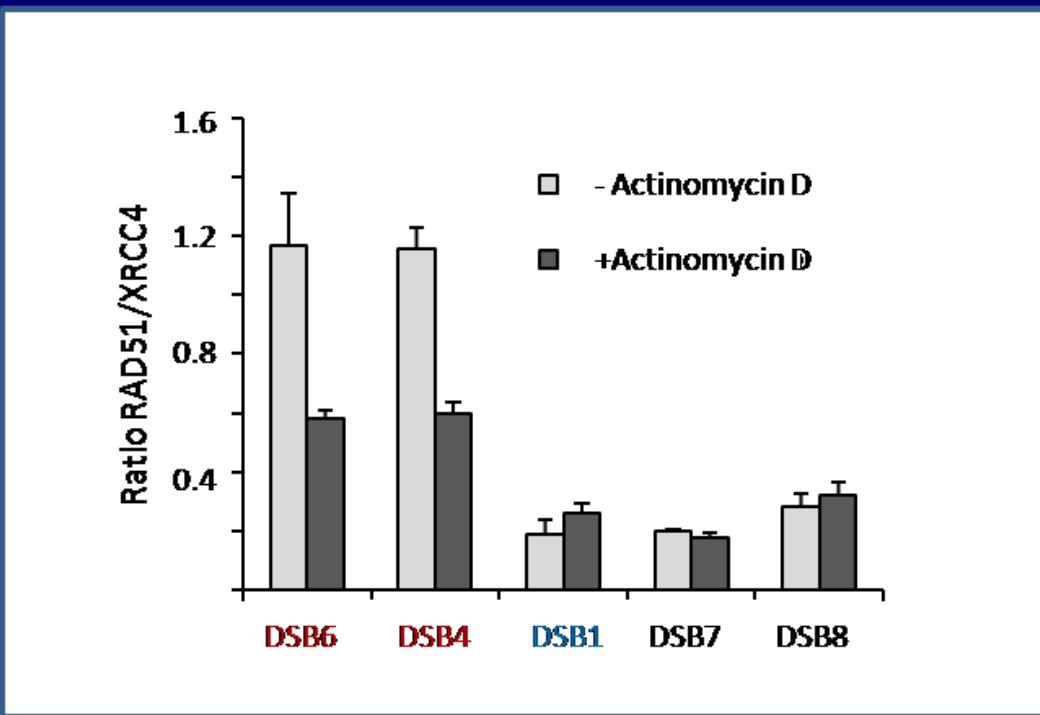
# HR-prone sites lies in transcribed units



# Transcription inhibition orients repair toward a RAD51 independant pathway

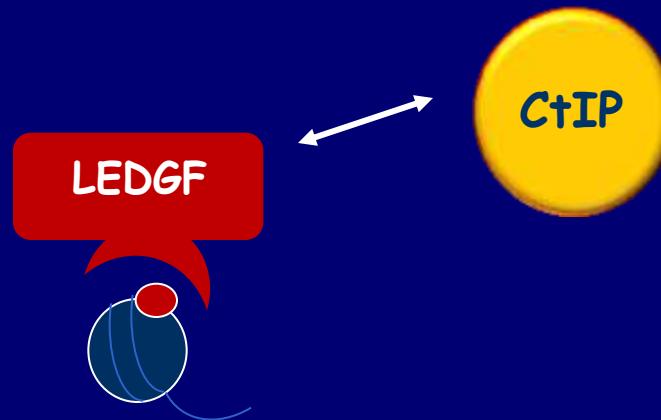


# Transcription inhibition orients repair toward a RAD51 independant pathway

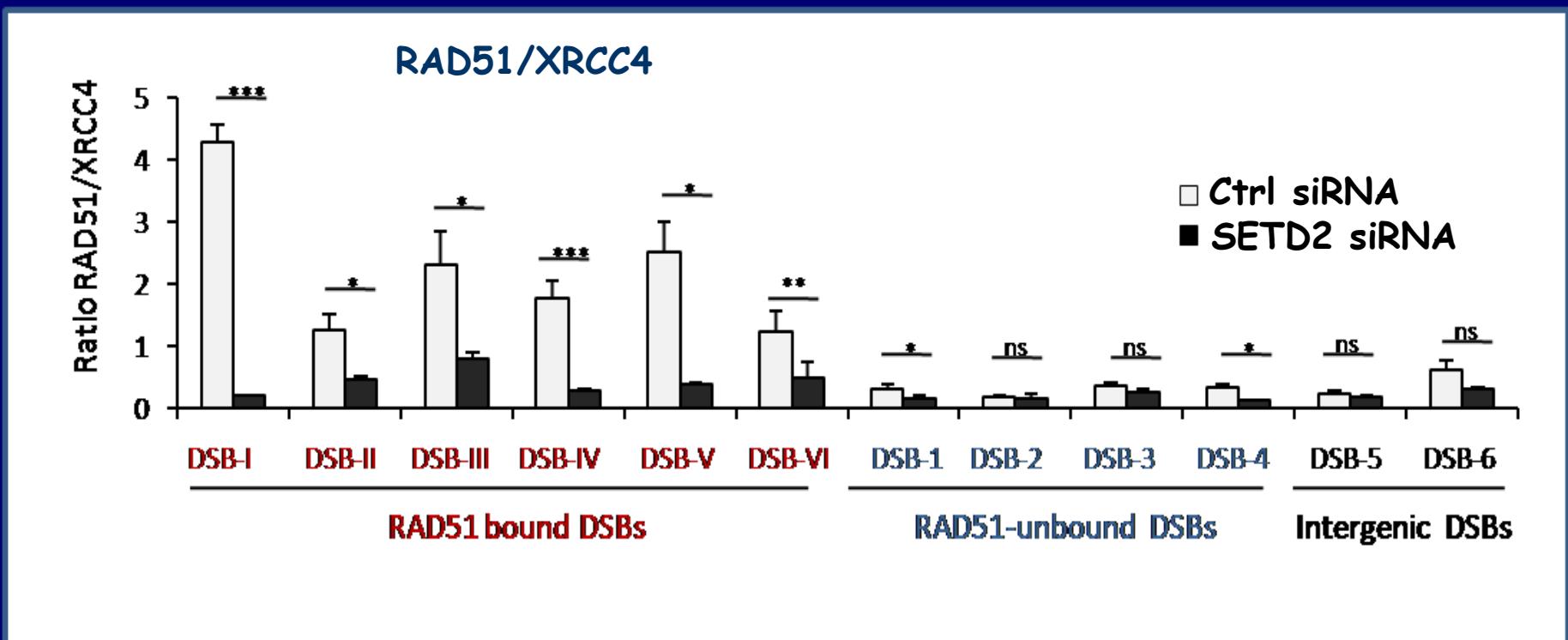


# LEDGF (p75) promotes DNA-end resection and homologous recombination

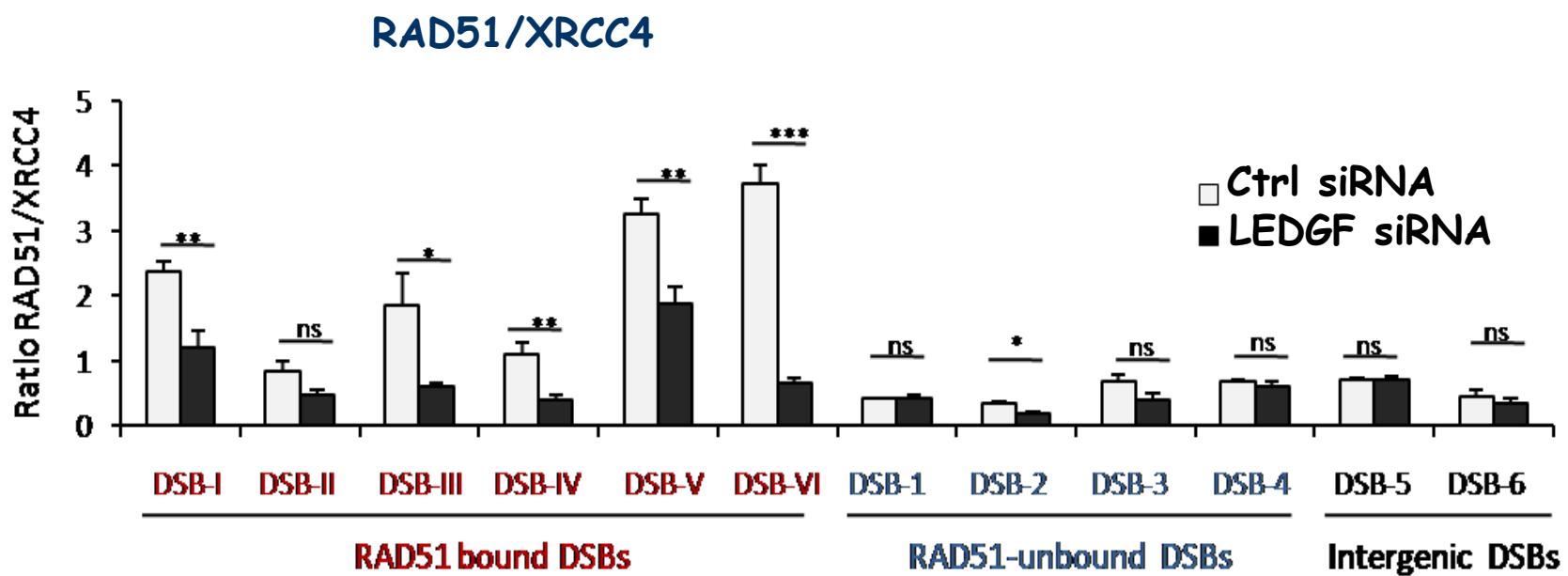
Mads Daugaard<sup>1-3</sup>, Annika Baude<sup>1,2</sup>, Kasper Fugger<sup>4</sup>, Lou Klitgaard Povlsen<sup>1,2,8</sup>, Halfdan Beck<sup>4</sup>,  
Claus Storgaard Sørensen<sup>4</sup>, Nikolaj H T Petersen<sup>1,2</sup>, Poul H B Sorensen<sup>3</sup>, Claudia Lukas<sup>2,5</sup>, Jiri Bartek<sup>2,6,7</sup>,  
Jiri Lukas<sup>2,5</sup>, Mikkel Rohde<sup>1,2</sup> & Marja Jäättelä<sup>1,2</sup>



# H3K36me3 is required for channeling HR at active genes

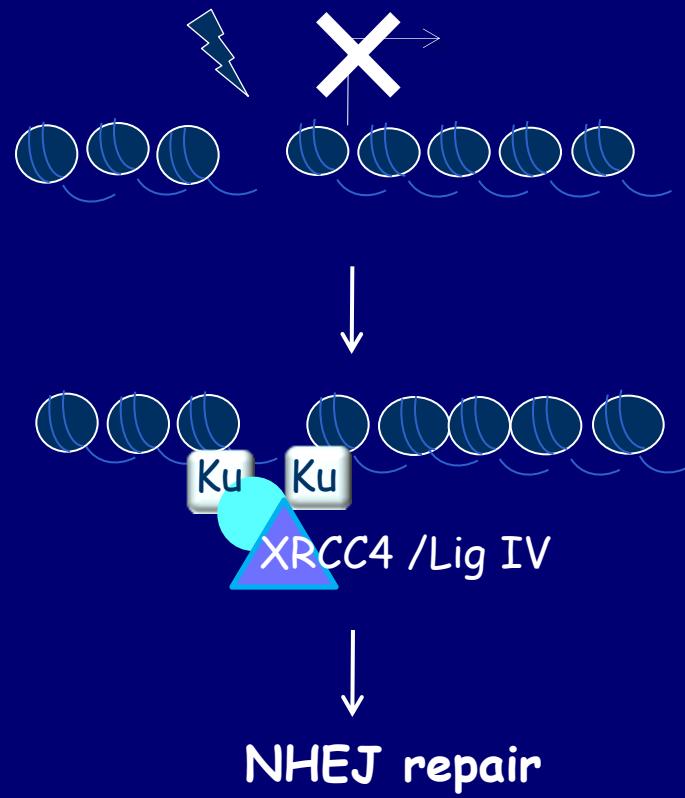
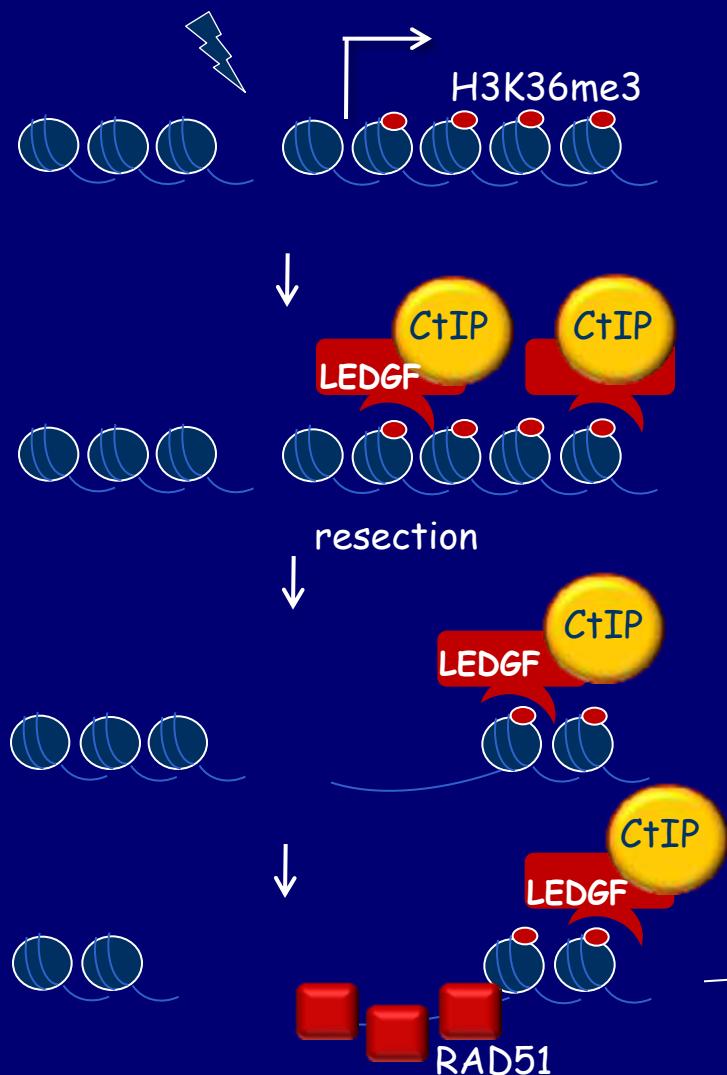


# The H3K36me3- interacting factor LEDGF is required for channeling HR at active genes



## Transcribed locus

## Untranscribed locus (inactive gene or intergenic)



# Acknowledgments



Fondation RITC  
Recherche Innovation  
Thérapeutique Cancérologie



## Lab members

Bea Bugler (CR1)

Emmanuelle Guillou (Post Doc)  
Thomas Clouaire (Post Doc)

François Aymard (PhD)  
Jonathan Choudjaye (PhD)

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EMBL Genomic Core  
Vladimir Benes,  
Tomi Ivacevic



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Tanya Paull, Auxin US  
Sagar Sengupta, New Dehli India  
Jason Iacovoni, Toulouse  
Erwan Watrin, Rennes  
Emmanuelle Fabre, Pasteur/ Kerstin Bystricky (LBME)