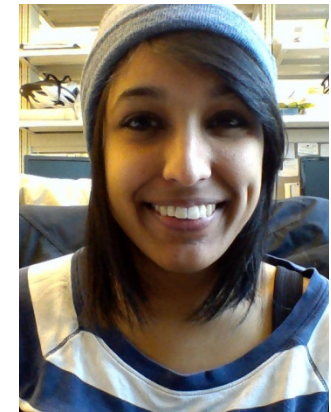


# 20.109 Spring 2014 Mod 2 – Lecture 6

## System Engineering and Protein Foundations



Agi Stachowiak

Shannon Hughes

Aneesh Ramaswamy

Suhani Vora (TA)

Leona Samson (Lectures)

Zachary Nagel (help with development)



## What experimental question will you ask in Module 2?

How efficiently does DNA repair by the Non Homologous End Joining (NHEJ) pathway act on DNA damage with different topologies?



## This raises the following questions

- How does DNA get damaged?
- What is DNA repair?
- Why does DNA repair exist?
- Why do we care about how efficient DNA repair is?
- How does one actually measure DNA repair efficiency?



CANDIDATE  
INTERVIEW

June 16<sup>th</sup> 2009,  
8am!

# Developing Novel Methods to Measure DNA Repair Capacity in Human Populations

*Leona D. Samson*

MIT

Biological Engineering Department

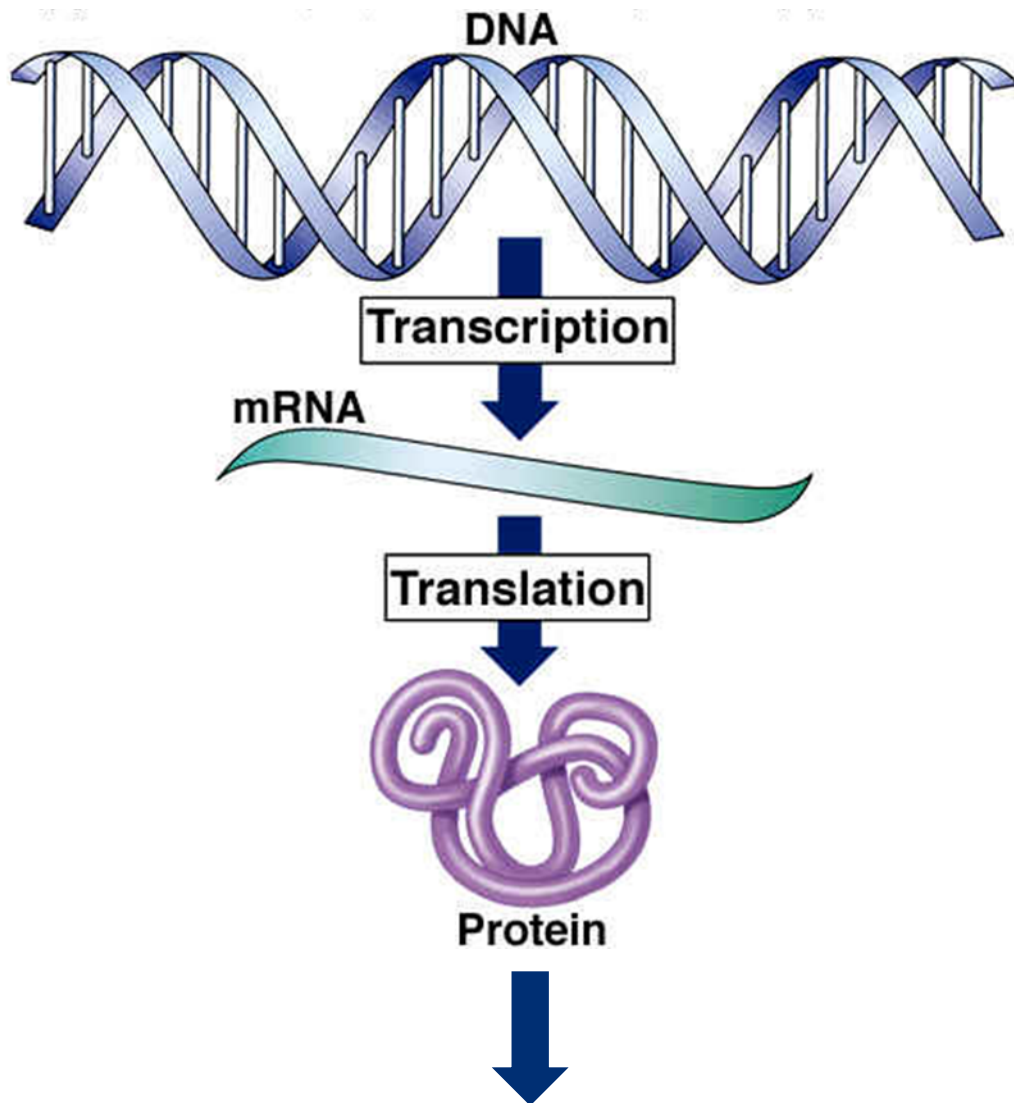
Biology Department

Center for Environmental Health Sciences

Koch Institute for Integrative Cancer Research

Computational and Systems Biology Initiative

Broad Institute (Harvard and MIT)



SNPs – GWAS  
Genome sequencing

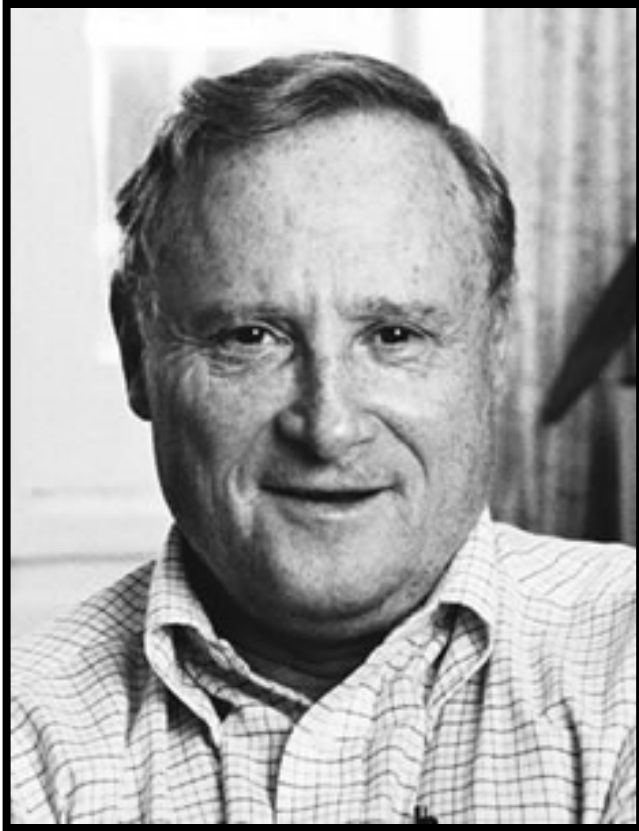
mRNA (miRNA, lncRNA)  
Profiling  
Exome Sequencing

Proteomic Analyses

*In vitro / In vivo*  
**Functional Assays**

**FUNCTION**

# The Proposal was based on the Pioneering work of:



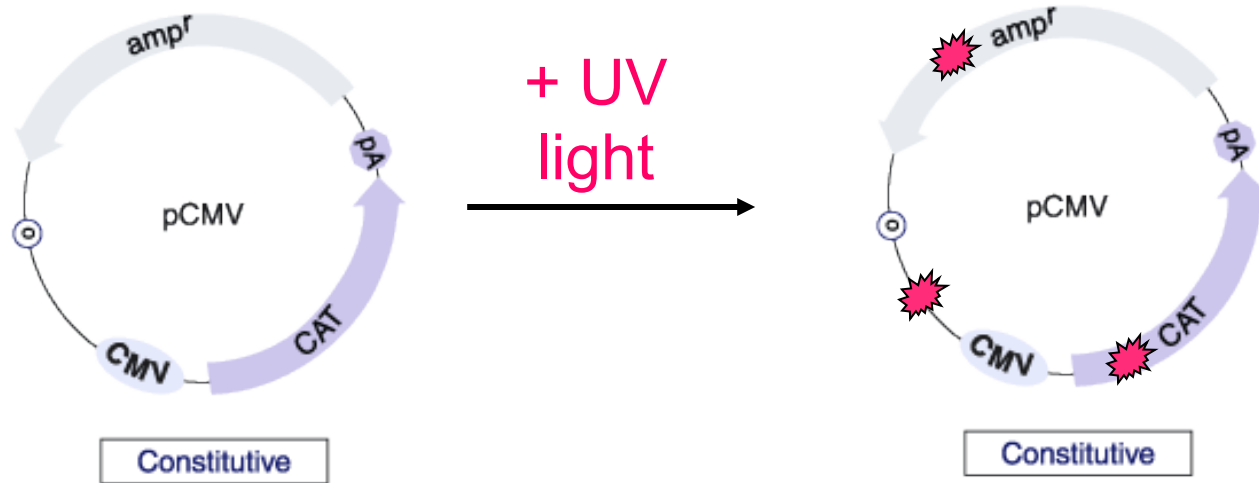
Dr. Lawrence Grossman  
(1924–2006)



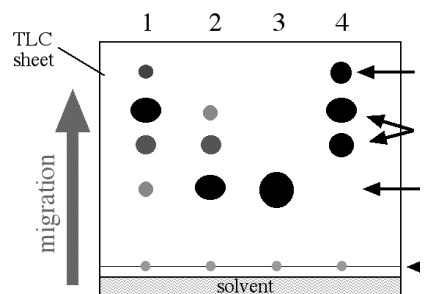
Dr. Qingyi Wei

# Reactivation of UV damaged DNA by Host cell Reactivation (HCR)

Athas & GROSSMAN  
Cancer Res. 1991



Transient transfection peripheral blood lymphocytes



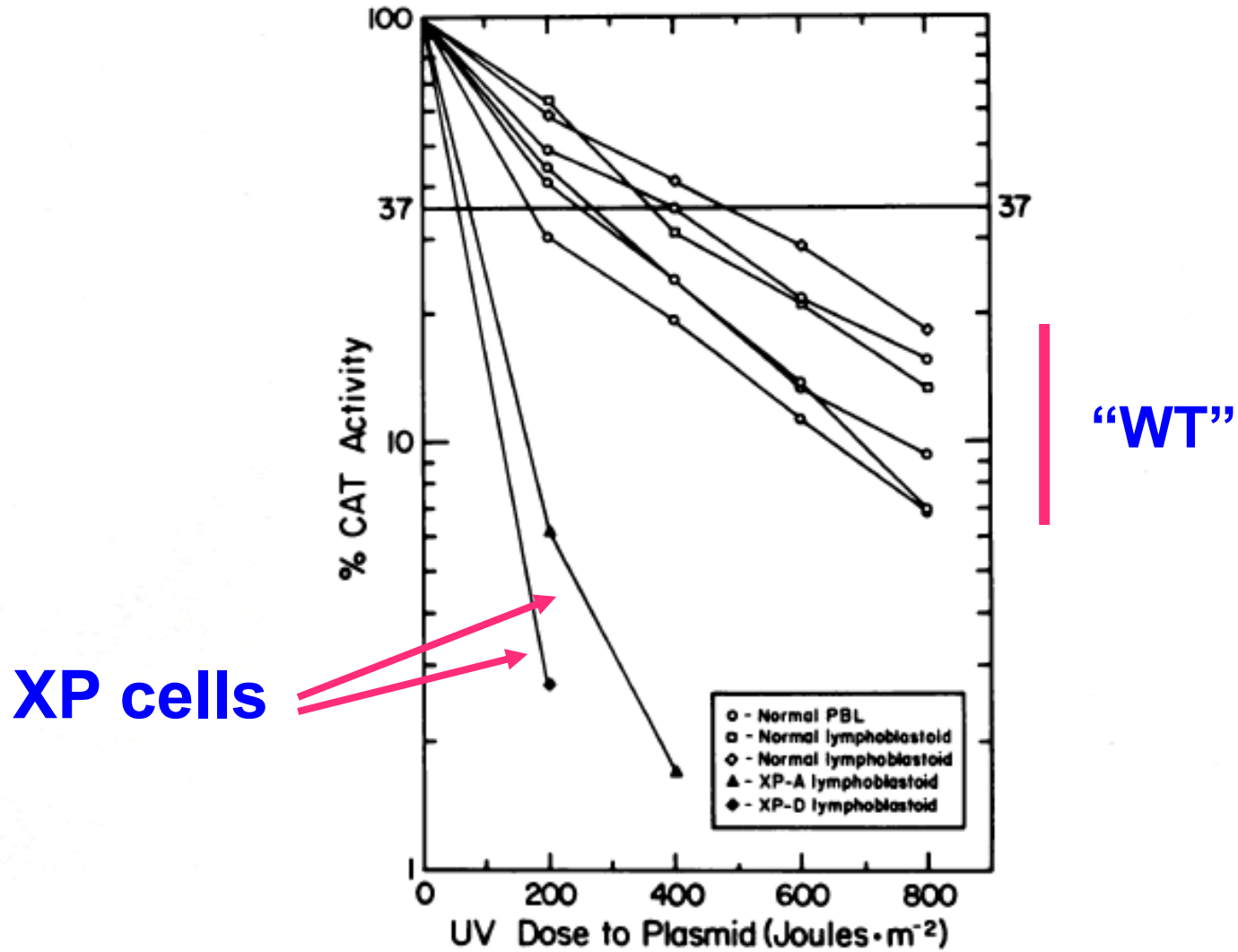
CAT Assay



Time to repair



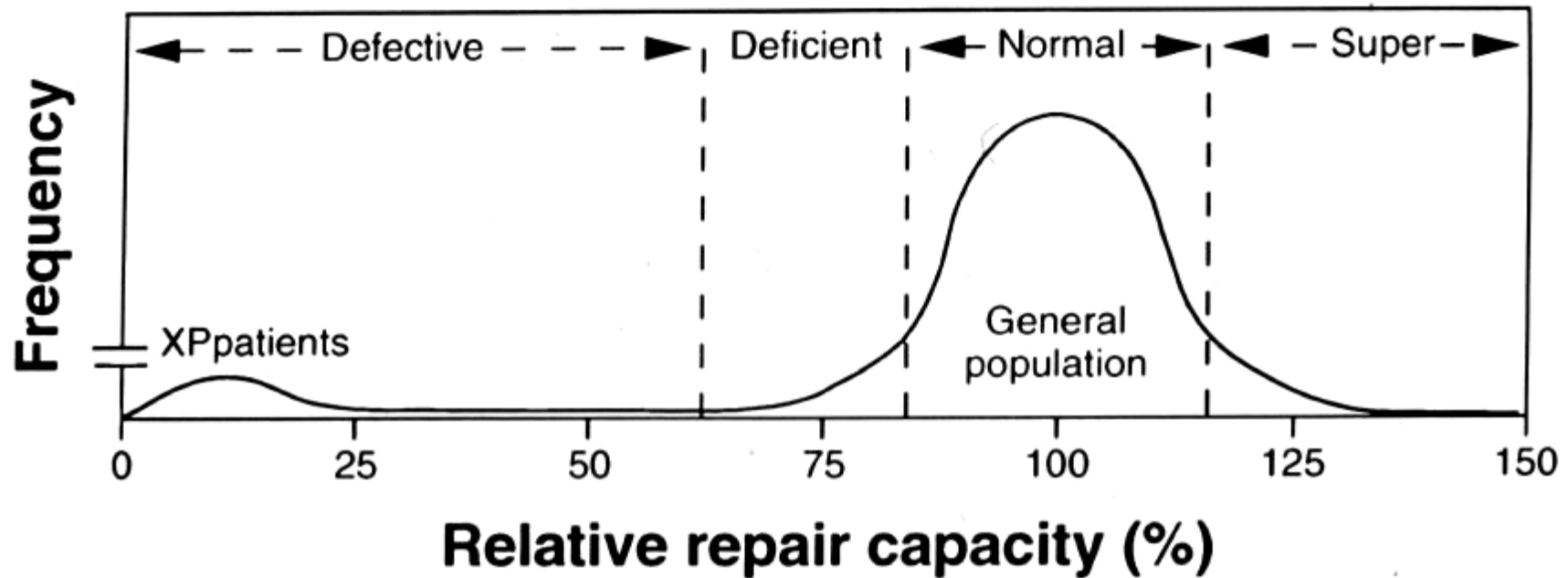
# Fresh Circulating Lymphocyte Plasmid HCR in XP and Normal PBL



Athas & GROSSMAN

[CANCER RESEARCH 51, 5786-5793, November 1, 1991]

## Interindividual Variation in DNA Repair Capacity



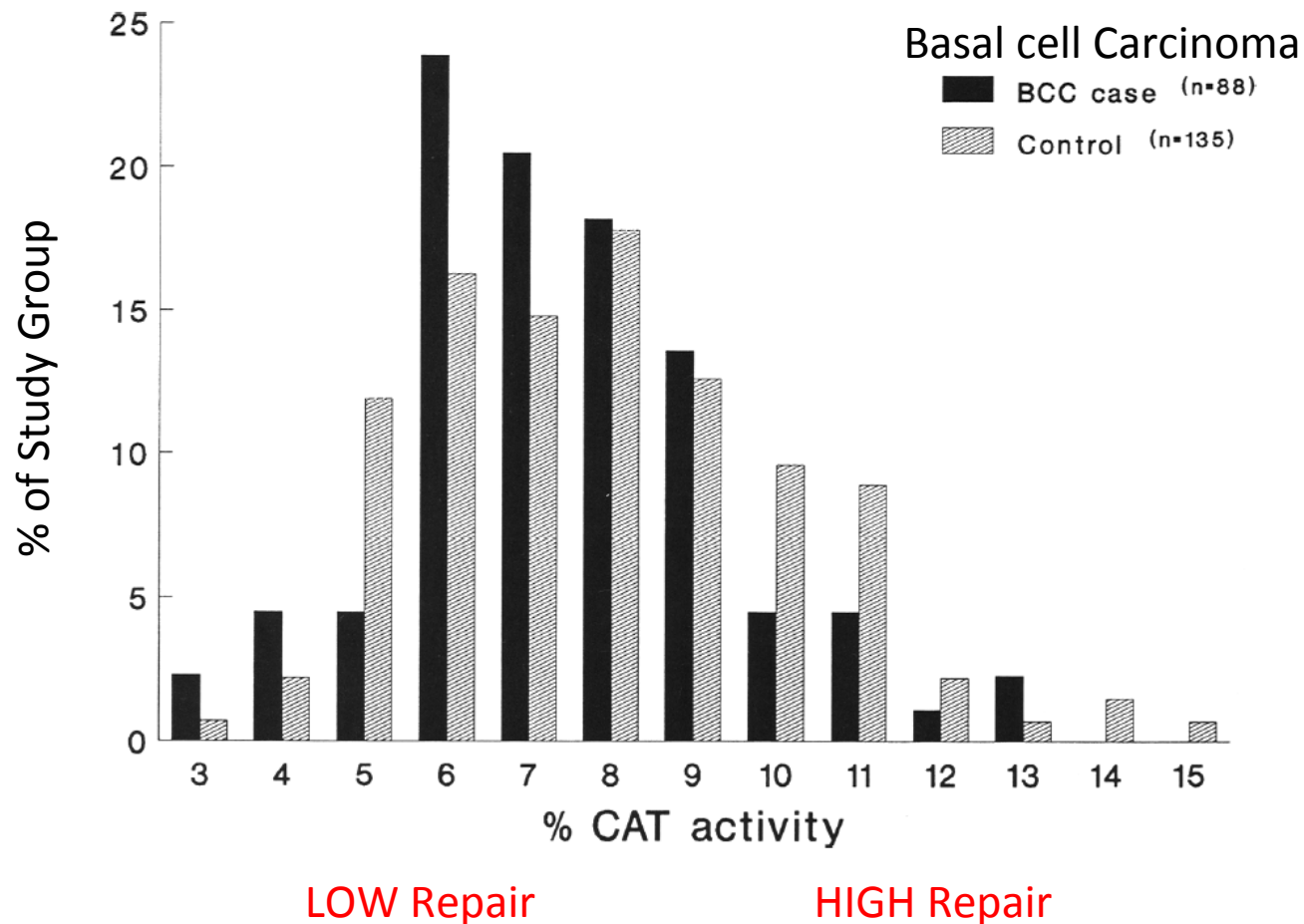
Adapted from **GROSSMAN and Wei (1995)** Clinical Chem 41: 1854-1863

XP frequency =  $\sim 1:250,000$  giving theoretically  $\sim 28,000$  cases worldwide with **2,000-fold increased skin cancer risk**

Even if just 1% of the population is relatively repair deficient, could have tens of millions with several-fold increased risk



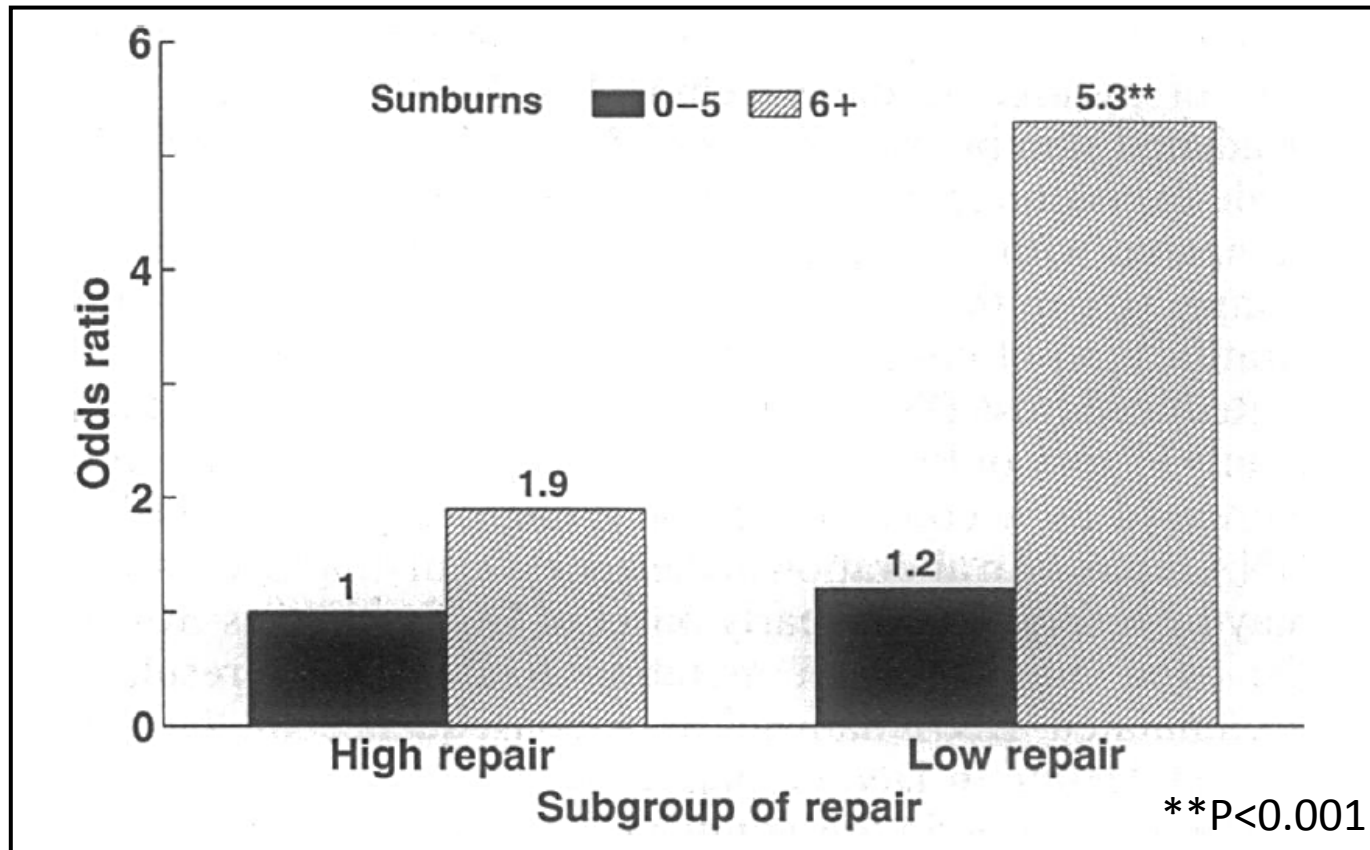
# Case-Control Study monitoring DNA Repair Capacity (DRC) by Host Cell Reactivation (HCR) of plasmids containing DNA damage



[CANCER RESEARCH 54, 437-44(i), January 15, 1994]

**Qingyi Wei**, Genevieve M. Matanoski, Evan R. Farmer, Mohammad A. Hedayati, and **Lawrence GROSSMAN**

# Low NER Repair status combined with excessive sun exposure is very dangerous



**Wei Q**, Matanoski GM, Farmer ER, Hedayati MA, **GROSSMAN L**. Proc Natl Acad Sci U S A. 1993 90:1614-8.

# Virtually all case/control HCR studies have monitored Nucleotide Excision Repair (NER)

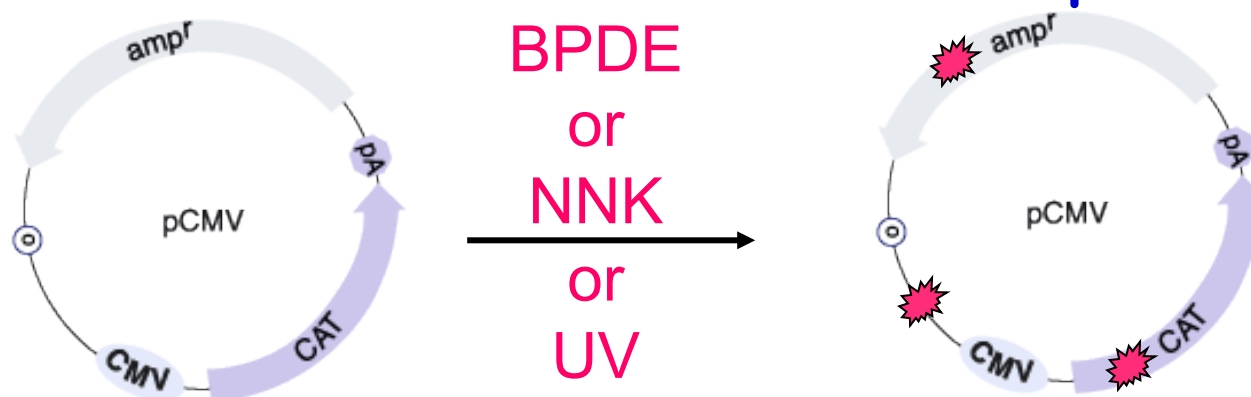


TABLE III – HCR-DRC FOR RISK OF CANCERS

Mutagen	Cancer type	Number Case/control	Risk estimate	Reference
BPDE	Lung	51/56	5.70 (2.10–15.7)	Wei <i>et al.</i> 1996 <sup>25</sup>
	Lung, nonsmall cell	467/488	1.85 (1.42–2.42)	Shen <i>et al.</i> 2003 <sup>58</sup>
	Lung	764/677	1.50 (1.10–3.10)	Spitz <i>et al.</i> 2003 <sup>37</sup>
	SCCHN	55/61	2.20 (1.02–4.77)	Cheng <i>et al.</i> 1998 <sup>61</sup>
	Breast	69/79	3.36 (1.15–9.80)	Shi <i>et al.</i> 2004 <sup>64</sup>
NNK	Lung, adenocarcinoma	48/45	3.21 (1.25–8.21)	Wang <i>et al.</i> 2007 <sup>59</sup>
UV	BCC	146/333	1.62 (1.07–2.45)	Wang <i>et al.</i> 2007 <sup>63</sup>
	SCC	109/333	1.63 (0.95–2.79)	
	CM	312/324	2.02 (1.45–2.82)	Wei <i>et al.</i> 2002 <sup>62</sup>

BPDE, benzo(a)pyrene diol epoxide; UV, ultraviolet; SCCHN, squamous cell carcinoma of head and neck; BCC, basal cell carcinoma; SCC, squamous cell carcinoma; CM, cutaneous melanoma.



CANDIDATE  
INTERVIEW

June 16<sup>th</sup> 2009,  
8am!

# Developing Novel Methods to Measure DNA Repair Capacity in Human Populations

*Leona D. Samson*

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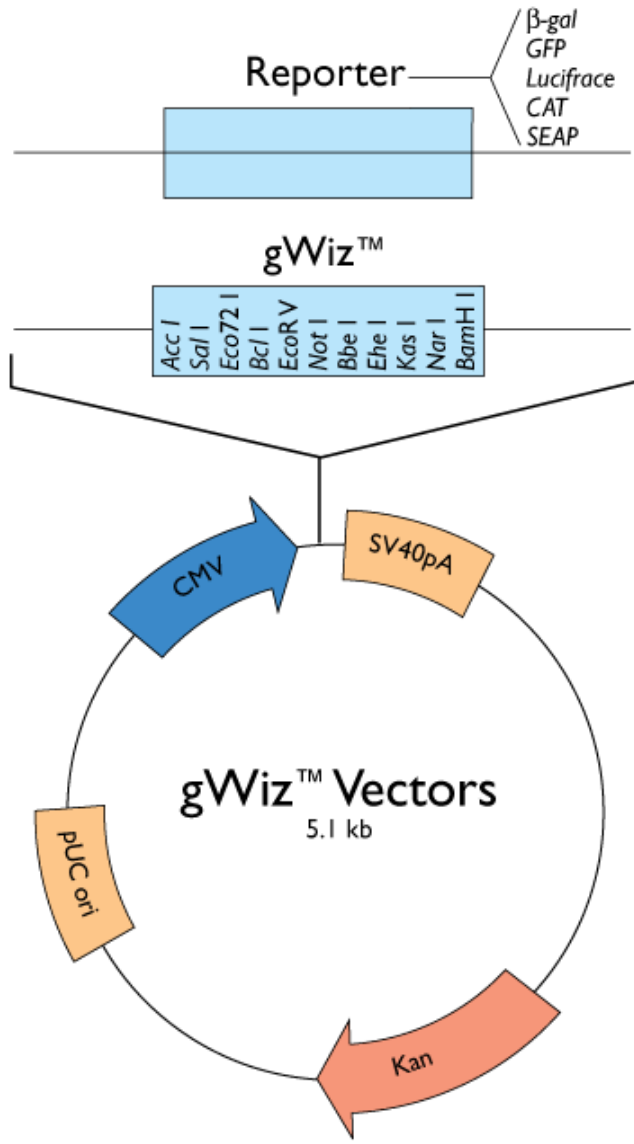
Center for Environmental Health Sciences

Koch Institute for Integrative Cancer Research

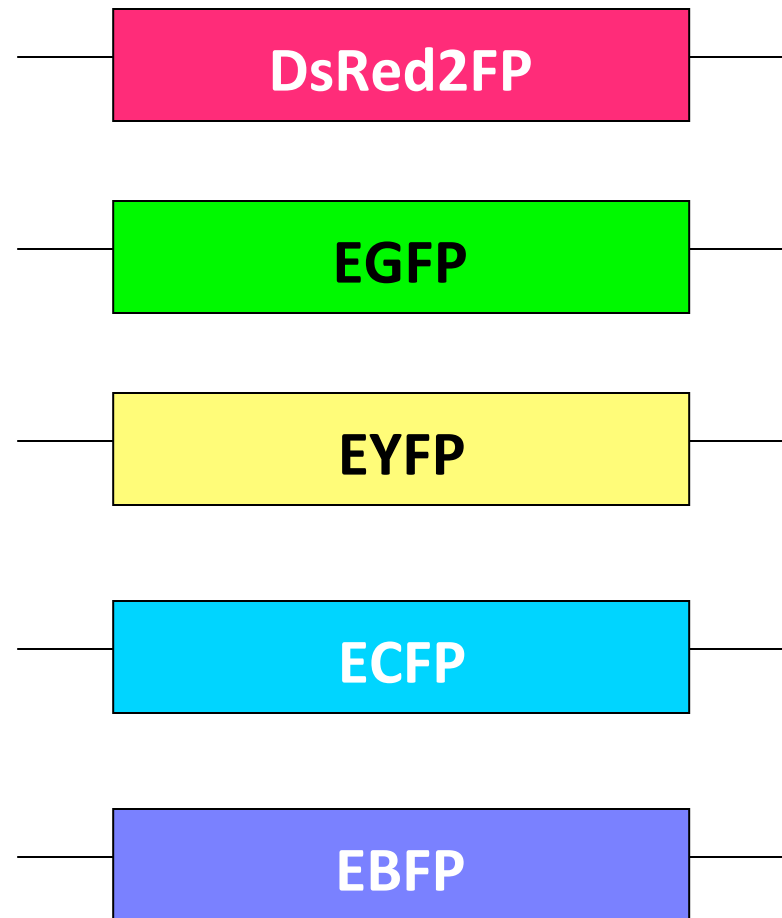
Computational and Systems Biology Initiative

Broad Institute (Harvard and MIT)

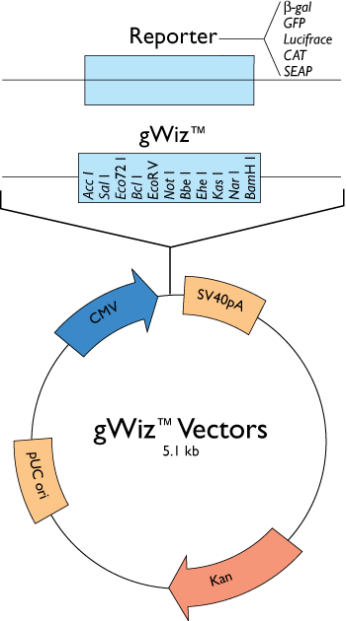
# Reactivation of damaged DNA - multiplexed



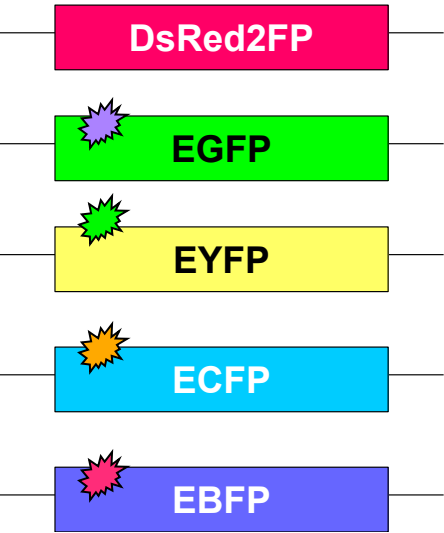
Each Fluorescent Protein gene will harbor a different type of DNA damage



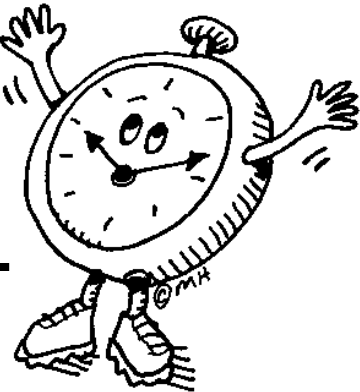
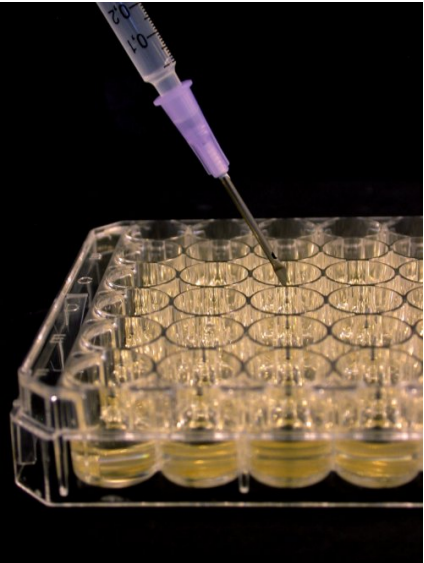
# Reactivation of damaged DNA - multiplexed



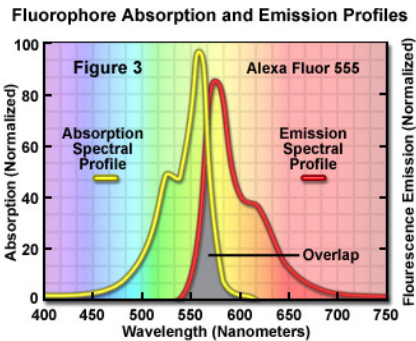
+ different DNA lesions



Transient transfection of mixture

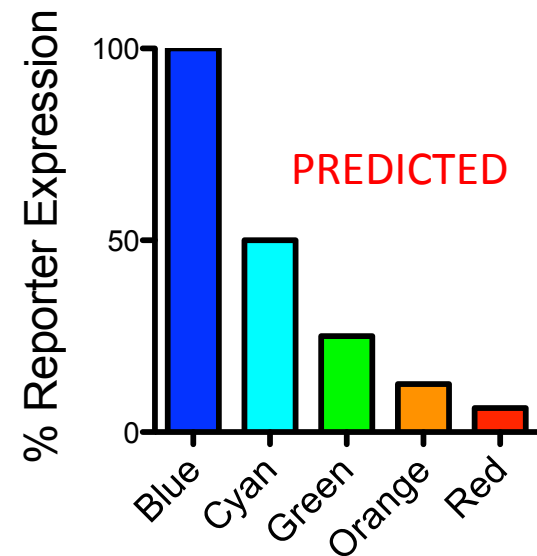
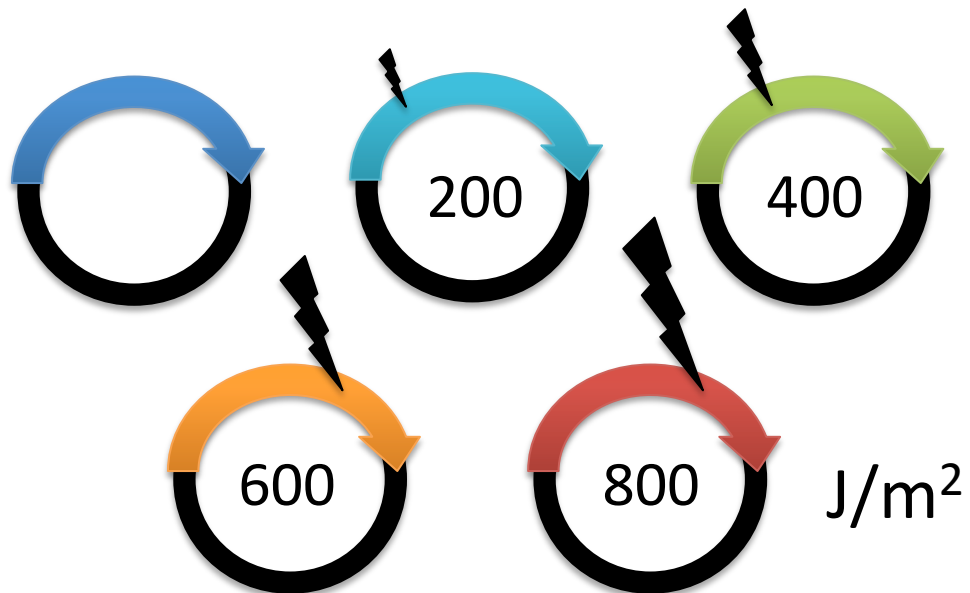
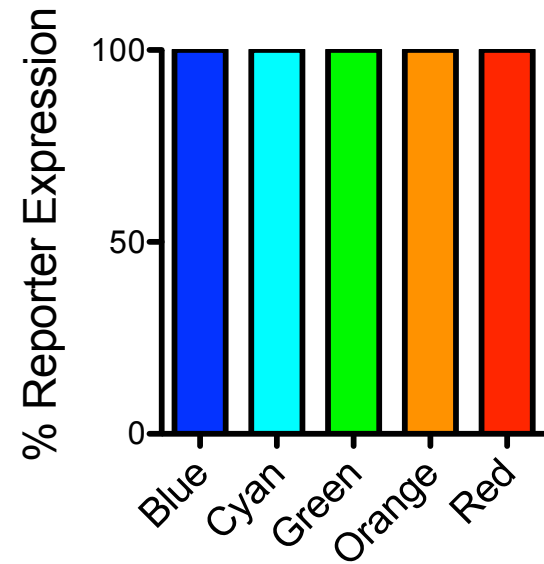
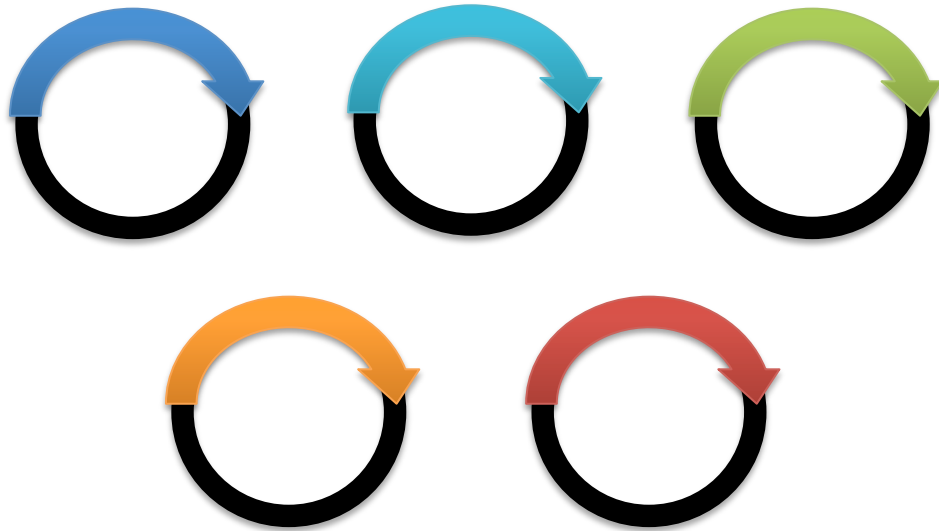


Time to repair

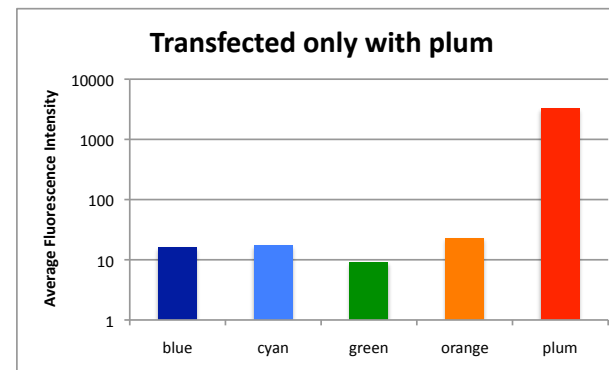
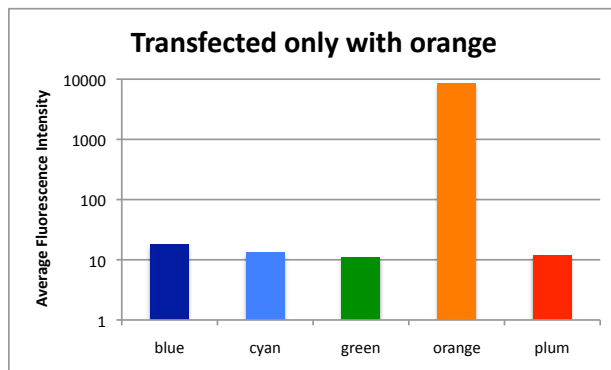
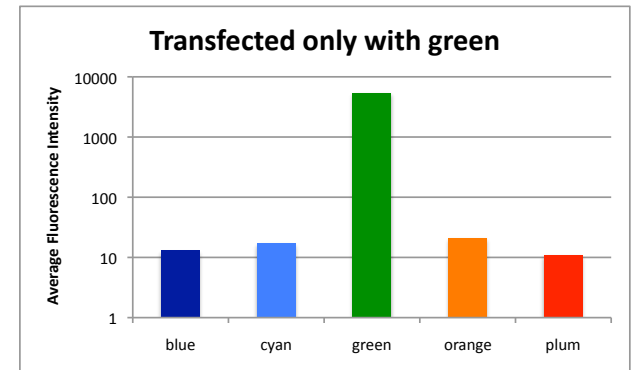
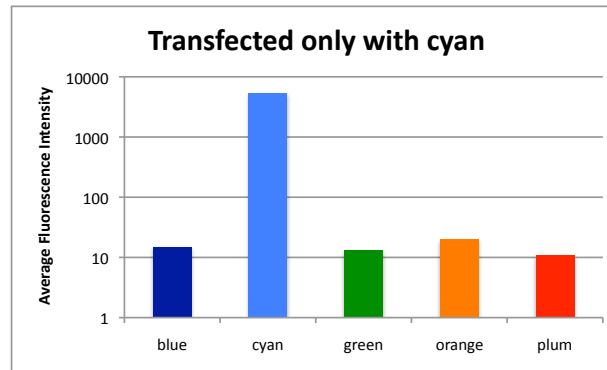
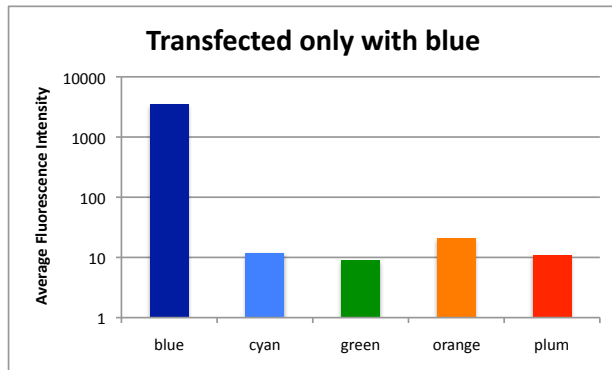


Fluorescence quantitation

Before trying different damages - tried different doses of the same damage (UV)



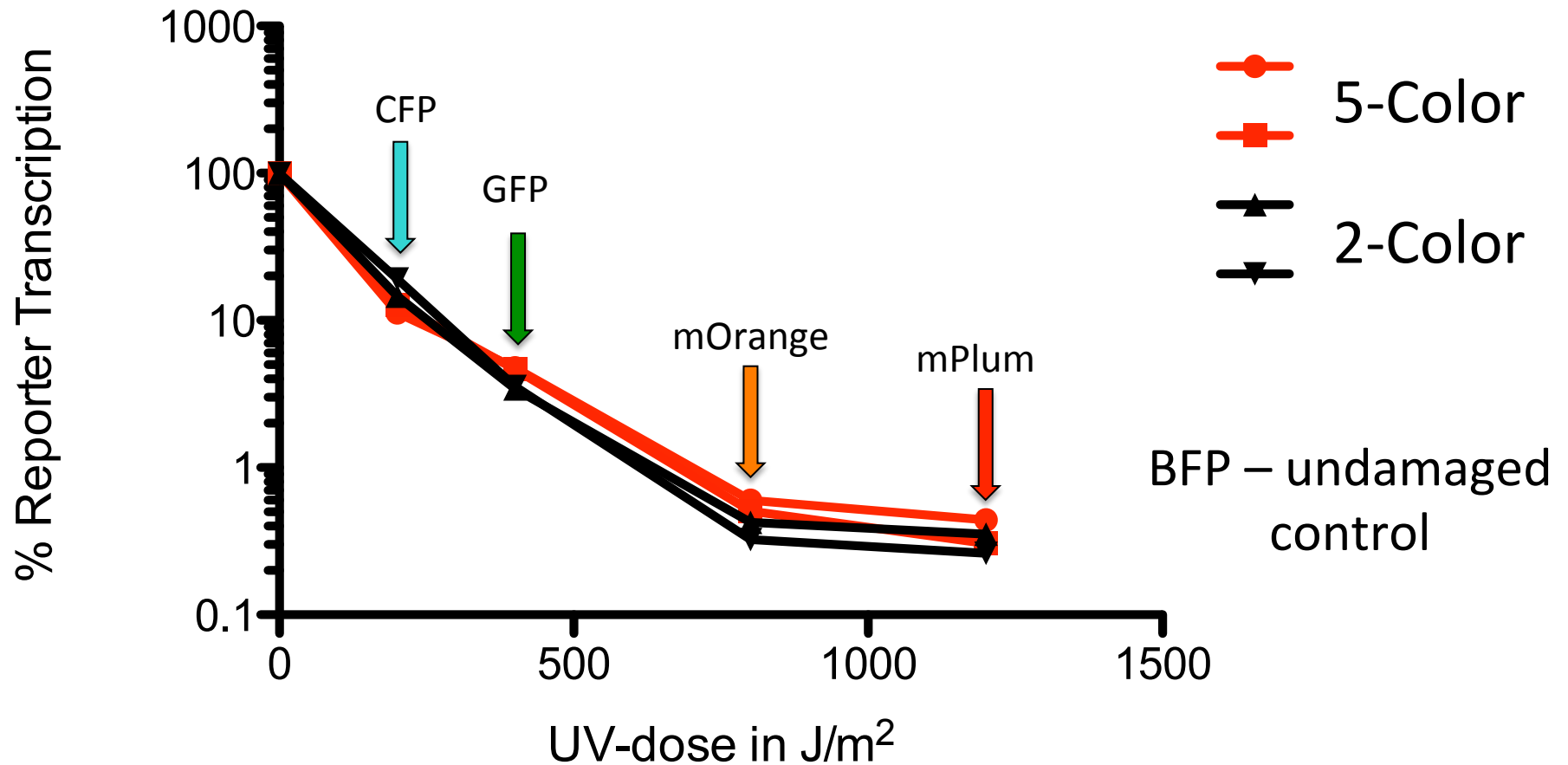
# Sanity Check: Is it even feasible detect 5-colors independently?:



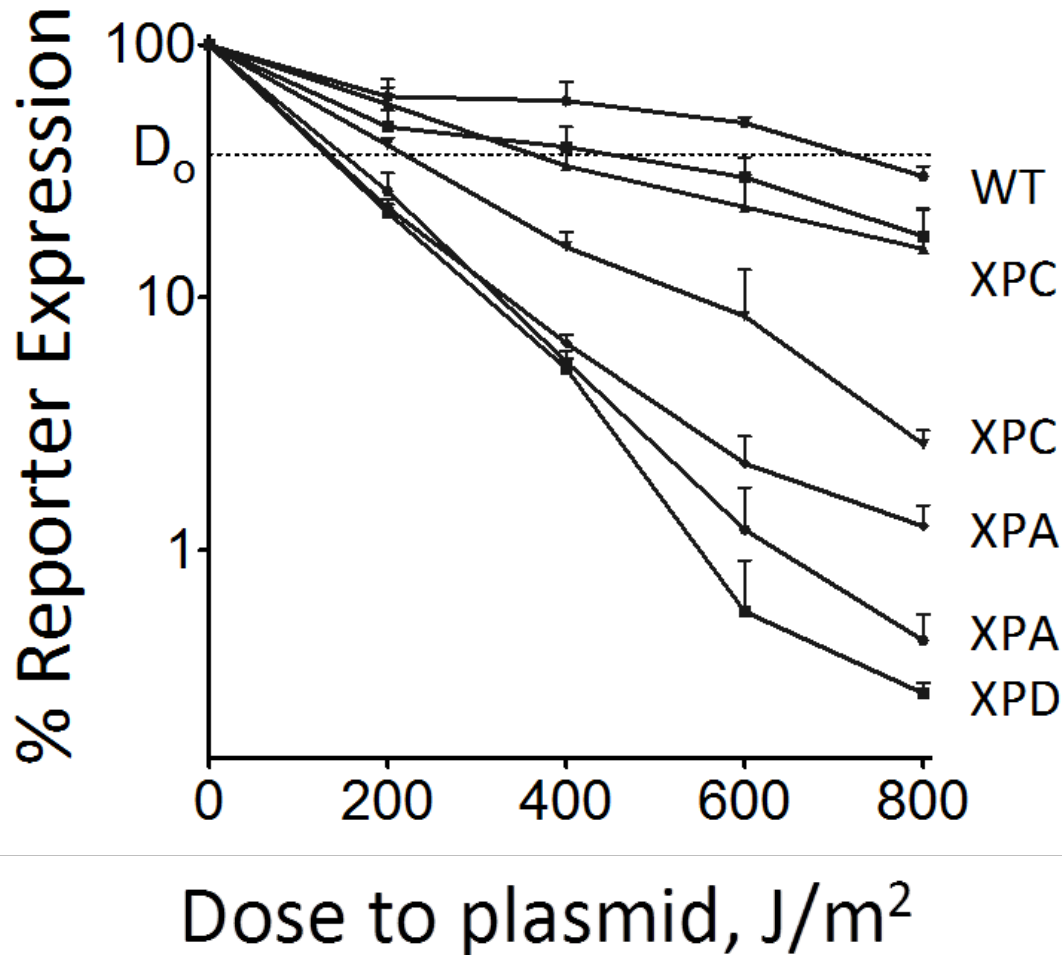


# 2-color versus 5-color HCR of UV-irradiated plasmids

UV HCR: XPA - deficient cell line at 16 hours



# FM-HCR for UV damaged Plasmids (Nucleotide Excision Repair)



**FM-HCR**

**Fluorescence**  
**Multiplexed**

**Host**  
**Cell**  
**Reactivation**

# Development and field-test validation of an assay for DNA repair in circulating human lymphocytes. *Cancer Res.*1991 51:5786-93.

**Athas, Hedayati, Matanoski, Farmer & GROSSMAN**

**Table 2** *Phenotype and plasmid HCR response ( $D_0$  and %CAT<sub>300</sub>) in XP homozygote, and apparent normal lymphoblastoid cell lines*

Cell line	Phenotype	Mean $\pm$ SD	n	95% CI <sup>a</sup>	%CAT <sub>300</sub> <sup>b</sup>
GM0536	Apparent normal	385 $\pm$ 60	3	235–534	59.4
GM0892	Apparent normal	595 $\pm$ 22	4	559–630	57.1
★ GM1953	Apparent normal	717 $\pm$ 78	3	523–91	67.7
GM1989	Apparent normal	594 $\pm$ 76	3	406–783	58.0
★ GM3657	Apparent normal	381 $\pm$ 15	4	357–405	47.0
GM2250	XP-A homozygote	90 $\pm$ 9	3	67–112	3.0
★ GM2344	XP-A homozygote	132 $\pm$ 9	3	110–155	6.4
★ GM2345	XP-A homozygote	90 $\pm$ 9	3	69–111	3.0
★ GM2246	XP-C homozygote	165 $\pm$ 19	4	134–195	22.1
★ GM2249	XP-C homozygote	256 $\pm$ 12	5	241–270	31.2
★ GM2253	XP-D homozygote	75 $\pm$ 5	3	62–88	1.8
GM2485	XP-D homozygote	97 $\pm$ 12	3	67–125	4.5
GM2450	XP-E homozygote	312 $\pm$ 42	5	260–364	

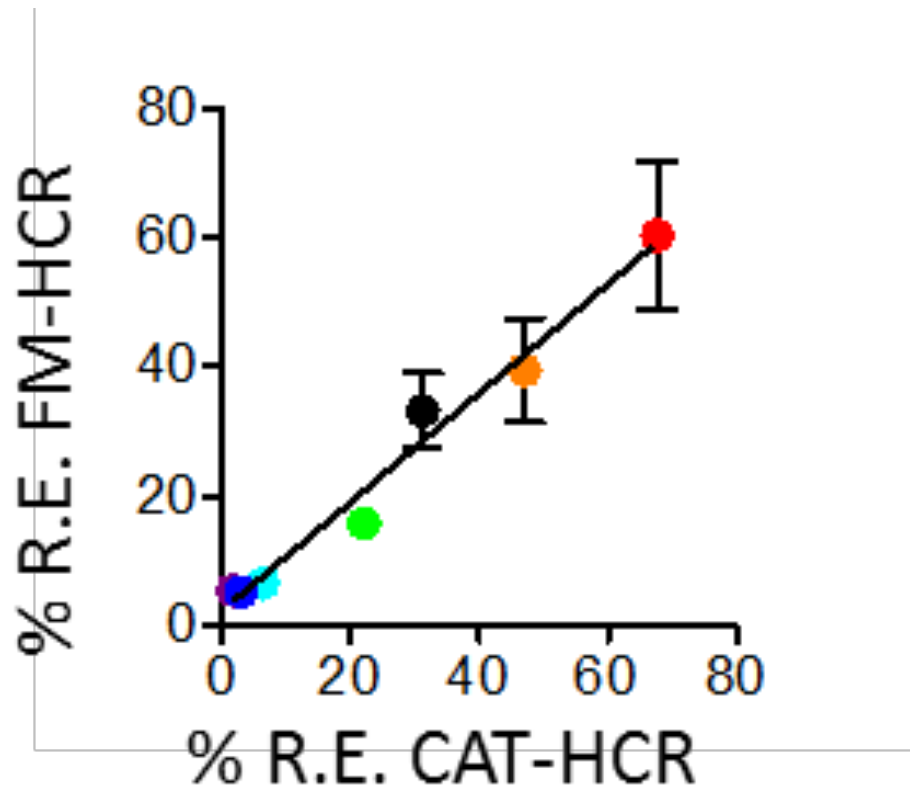
<sup>a</sup> CI, confidence interval.

How does our **FM-HCR** data stack up against  
CAT-HCR, Grossman *et al.*, > 20 years ago?

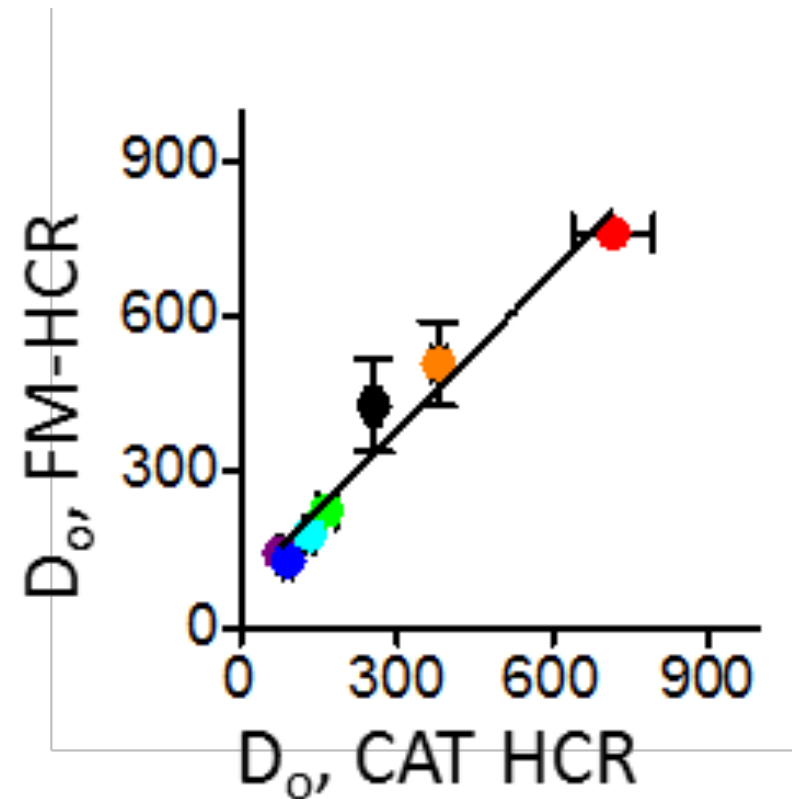
Cancer Research. 1991; **51** (21): 5786-93

# How does our **FM-HCR** data stack up against **CAT-HCR**, Grossman *et al.*, > 20 years ago?

Cancer Research. 1991; 51 (21): 5786-93

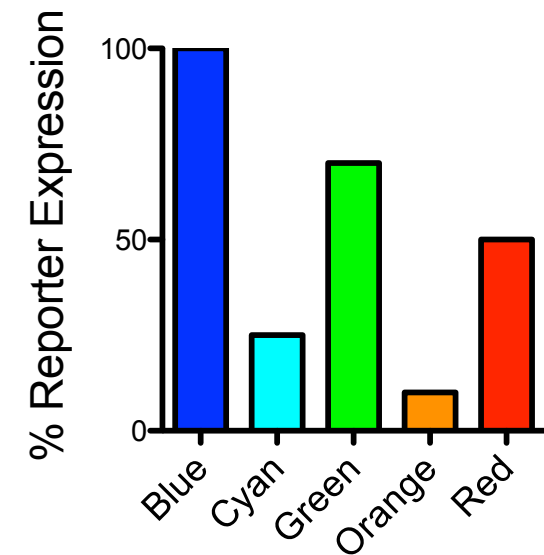
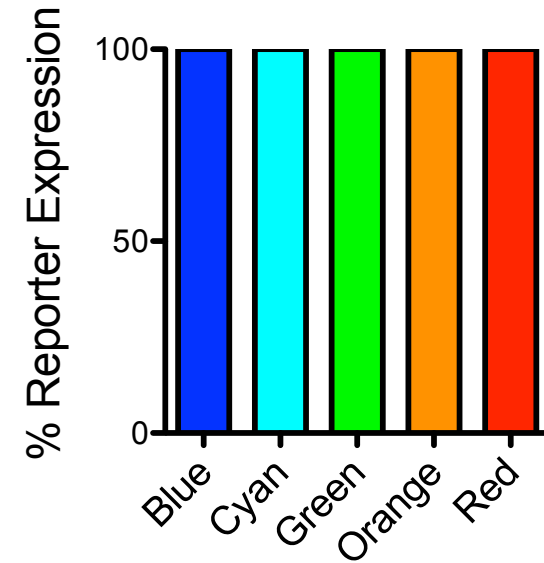
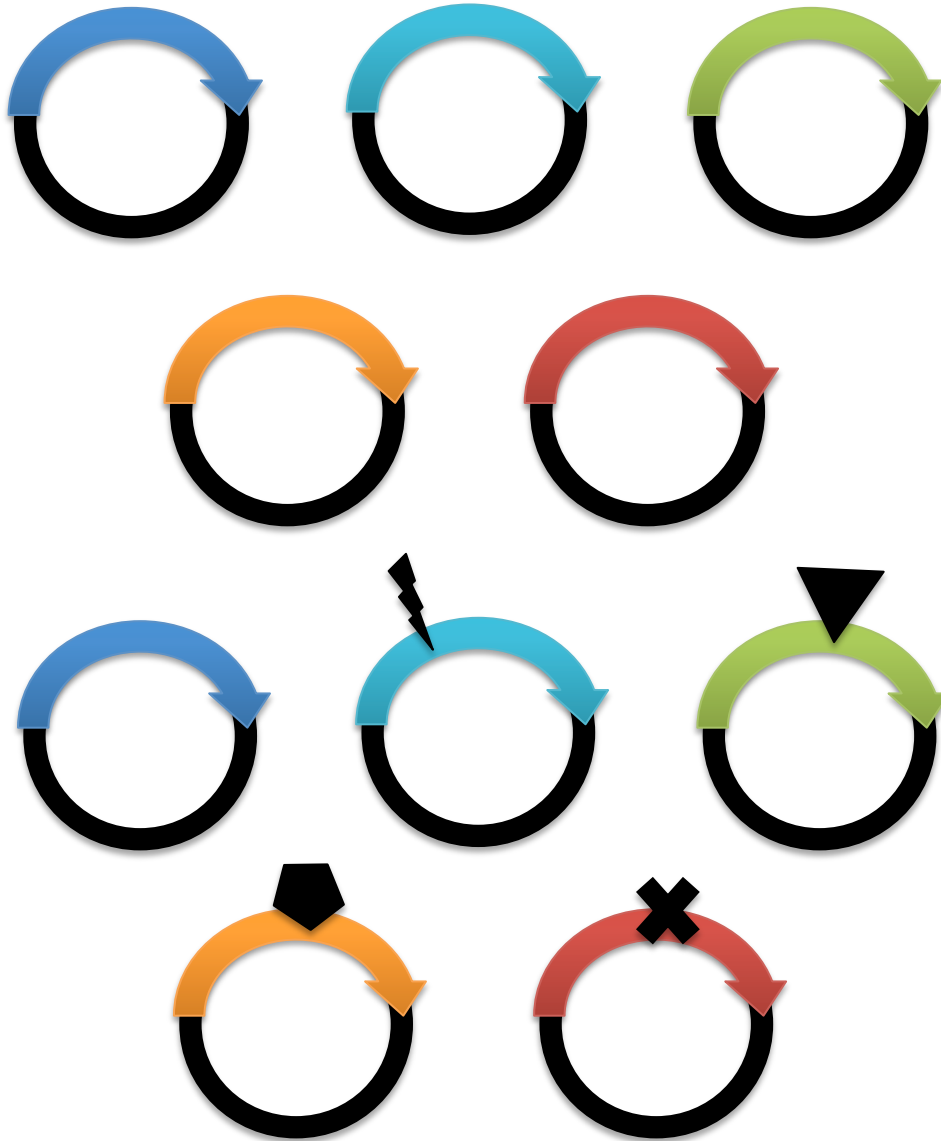


$R^2 = 0.92$ ,  $p = 0.0006$



$R^2 = 0.92$ ,  $p = 0.0001$

# 5 color HCR assay applications



# DNA Repair Strategies

- Direct Reversal

Methyltransferase, Oxidative demethylase

- Excision Repair

Base excision, nucleotide excision, mismatch repair

- Double strand break repair

Homologous recombination, Non-homologous end joining

# DNA Repair Strategies

- Direct Reversal

Methyltransferase, Oxidative demethylase

- Excision Repair

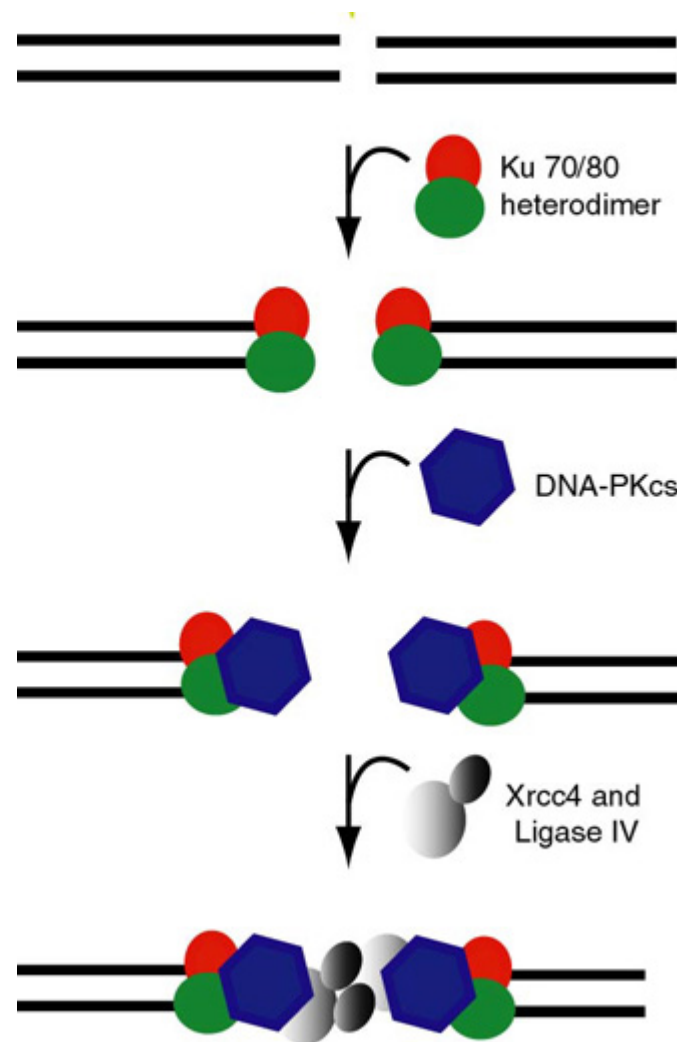
Base excision, nucleotide excision, mismatch repair

- Double strand break repair

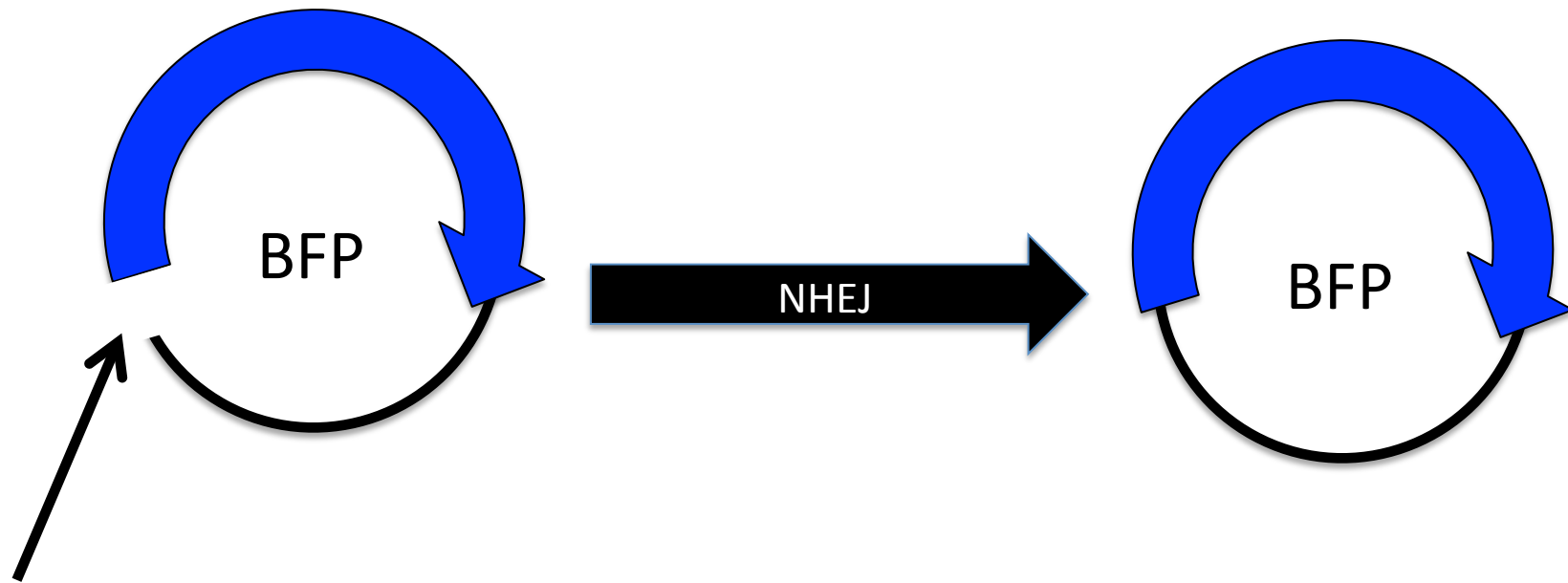
Homologous recombination, Non-homologous end joining



# Non-Homologous End Joining (NHEJ) DNA Double Strand Break Repair

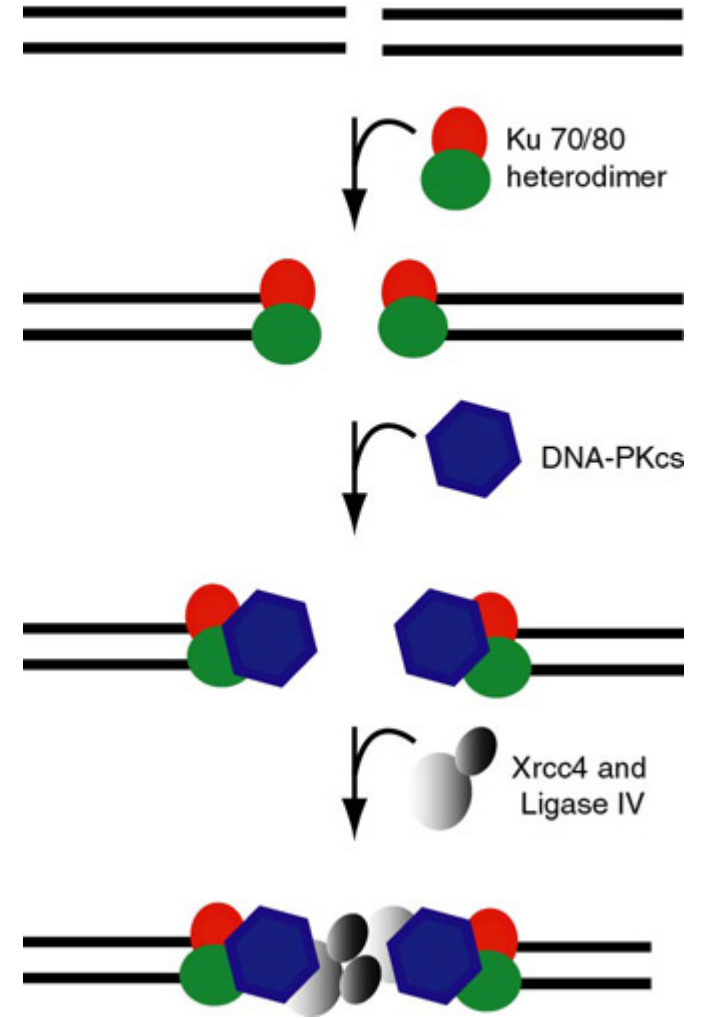
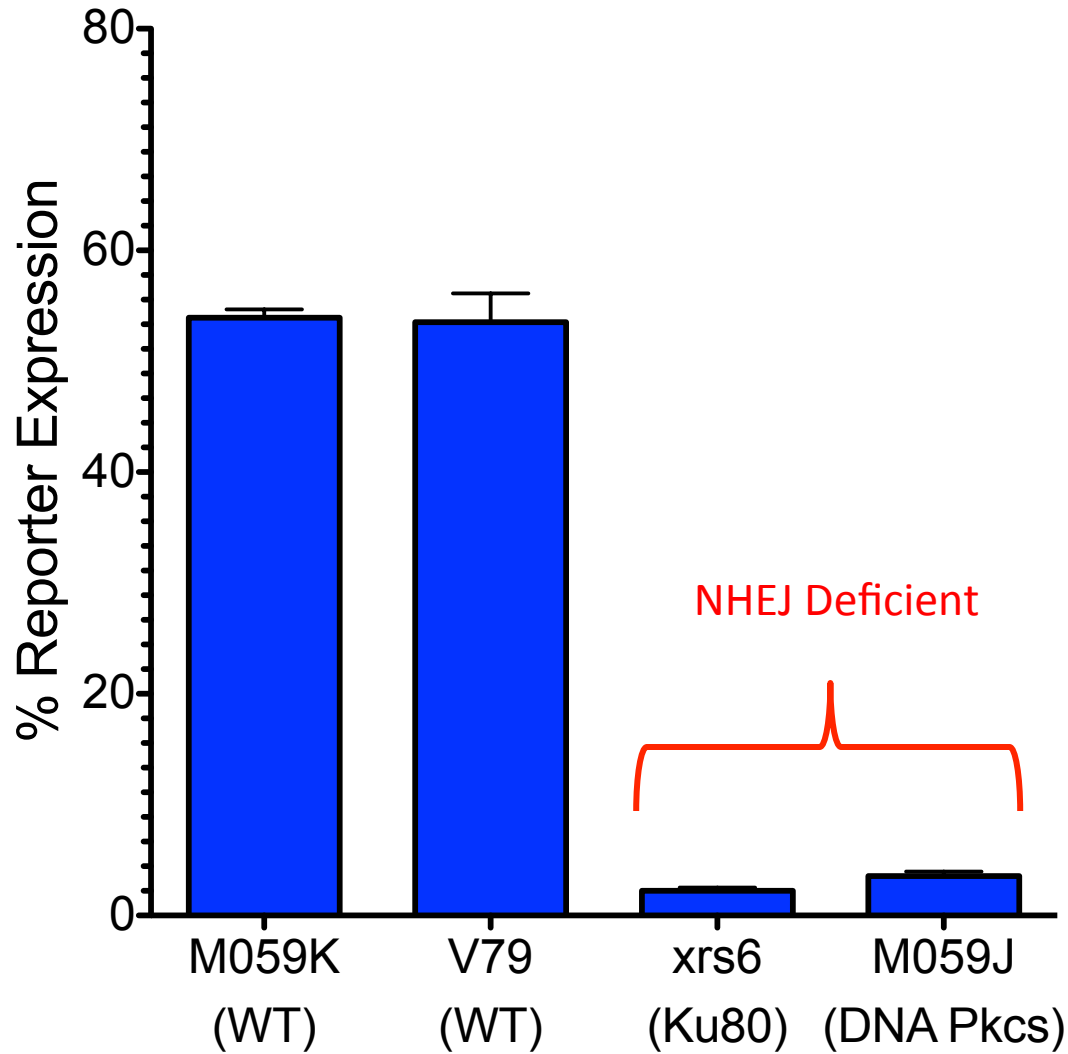


# Non-Homologous End Joining (NHEJ)

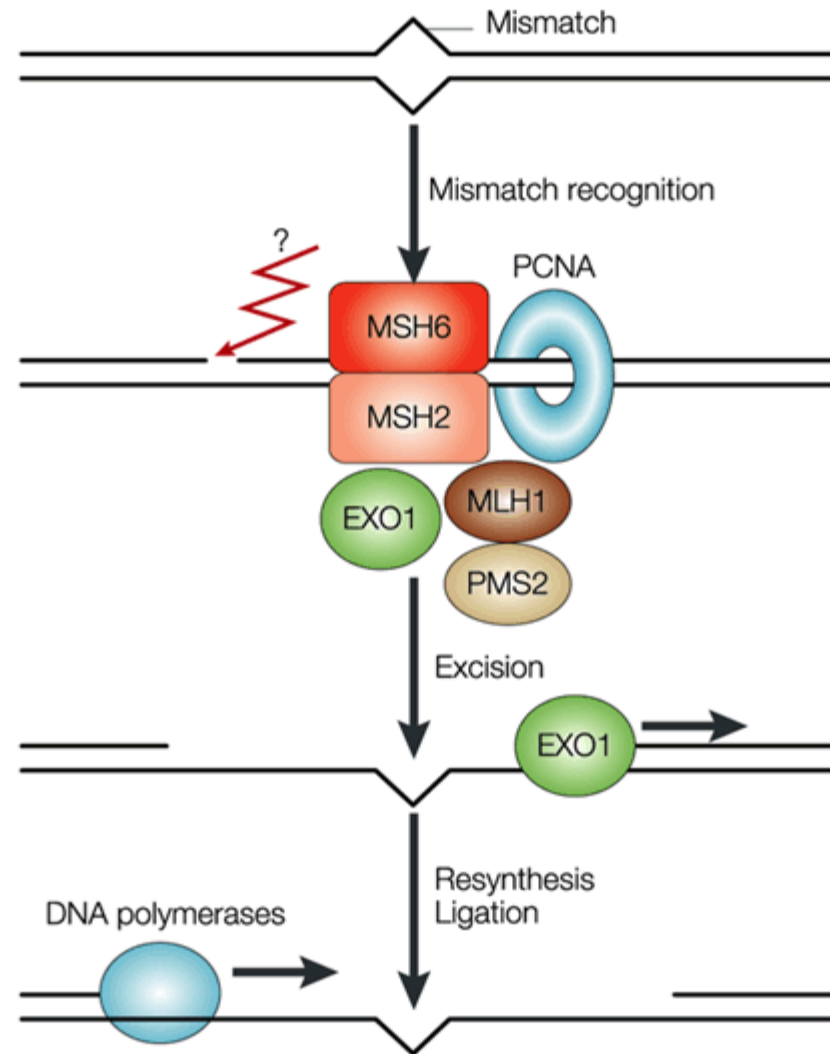


Substrate contains a blunt-end DSB in the 5' UTR

# NHEJ HCR in WT and NHEJ defective cells:

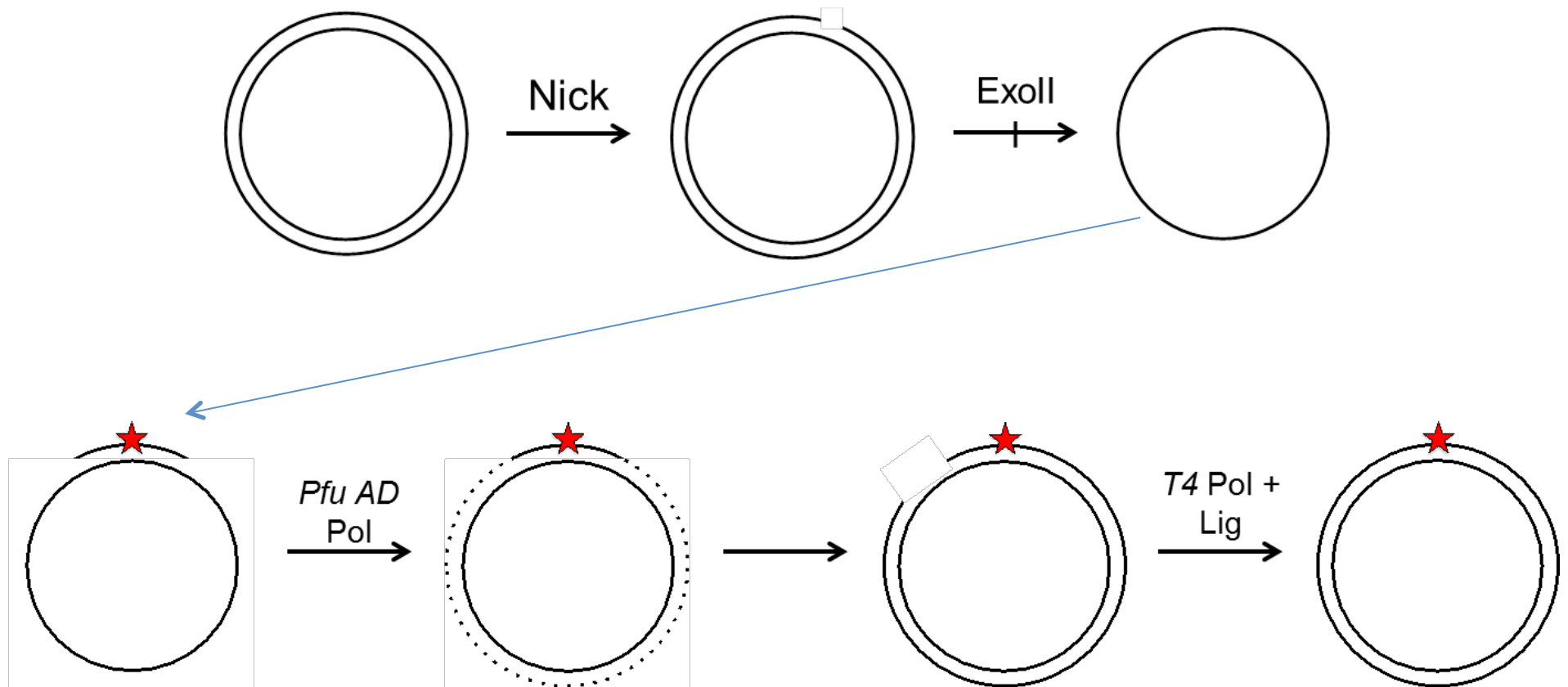


# DNA Mismatch Repair



Nature Reviews | Immunology

# How to build a site-specific reporter? "Primer-Extension"

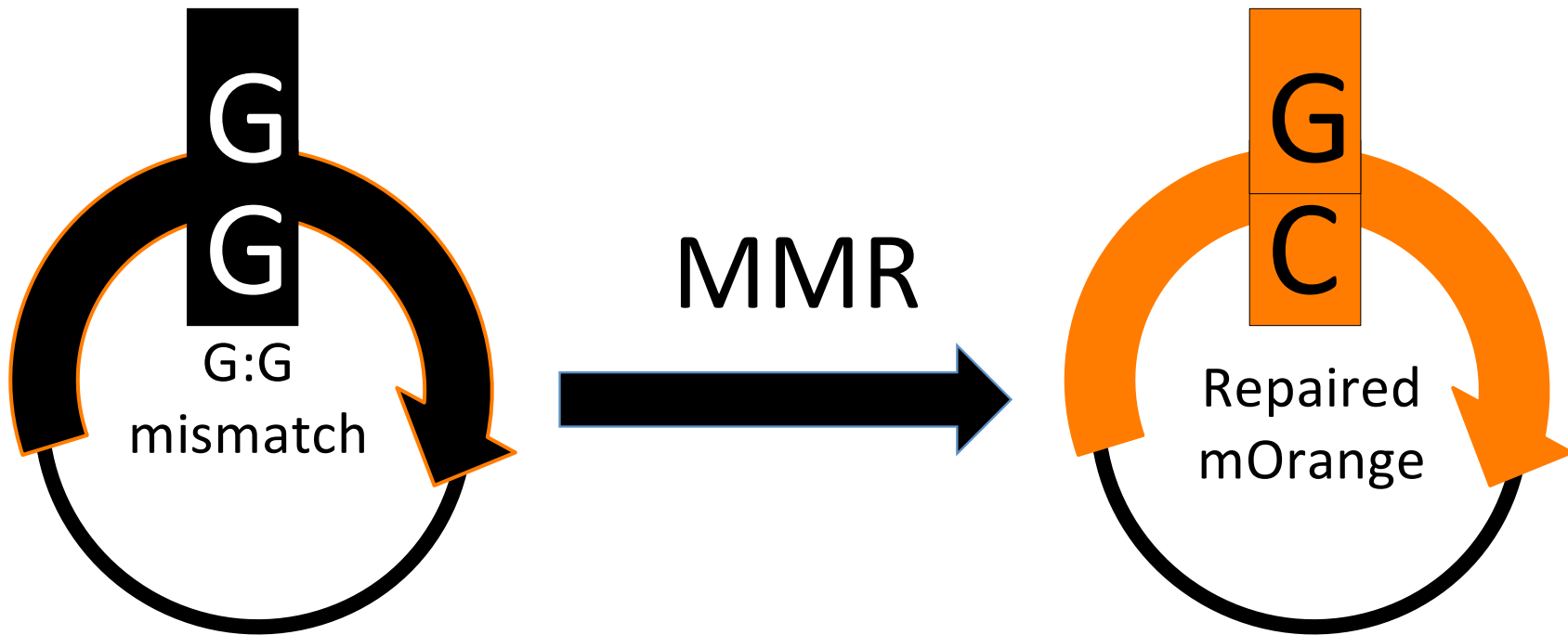


Original protocol from Baerenfaller et al. 2006 *Meth in enzymology*

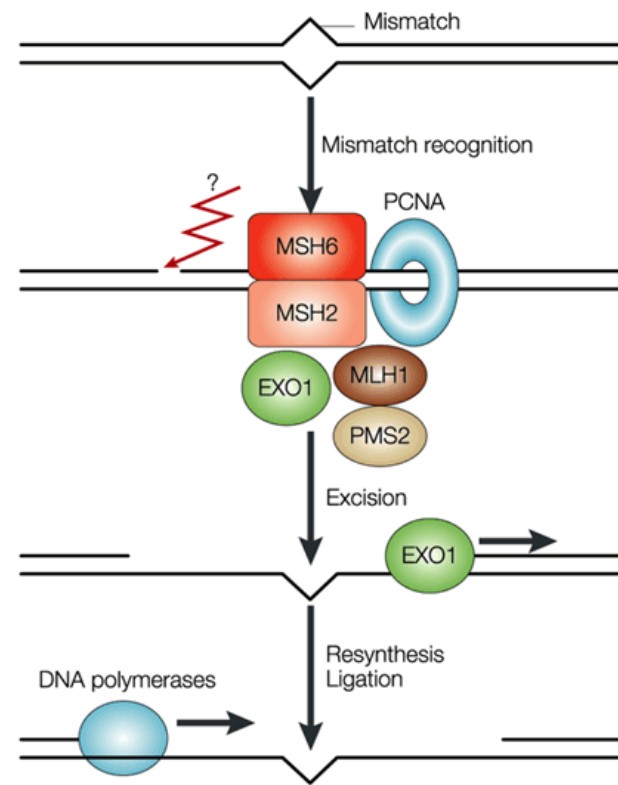
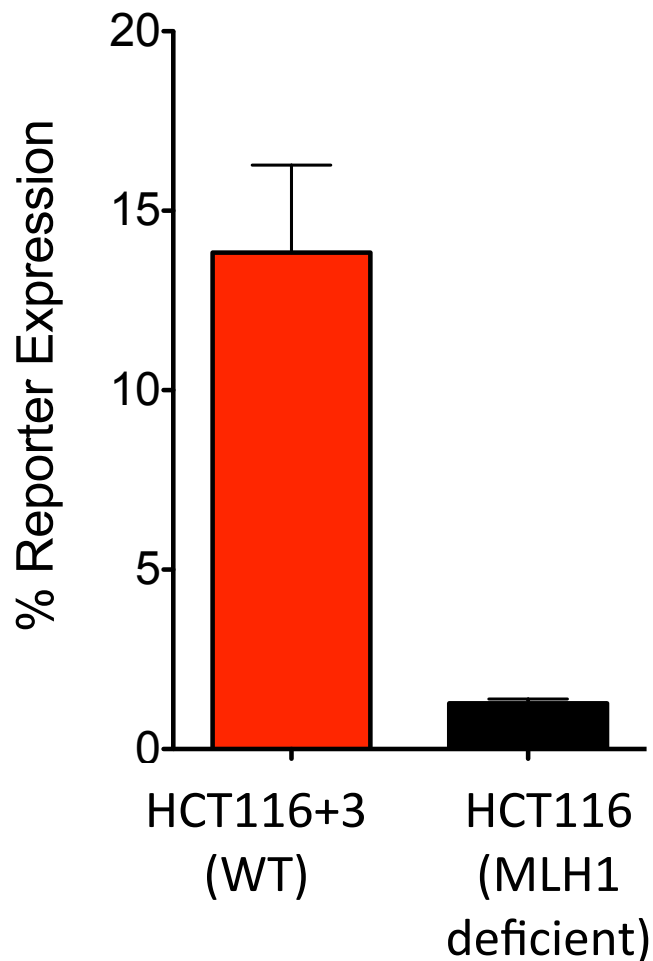
29

Modified and optimized by Alex Chaim, Zachary Nagel and Patrizia Mazzucato

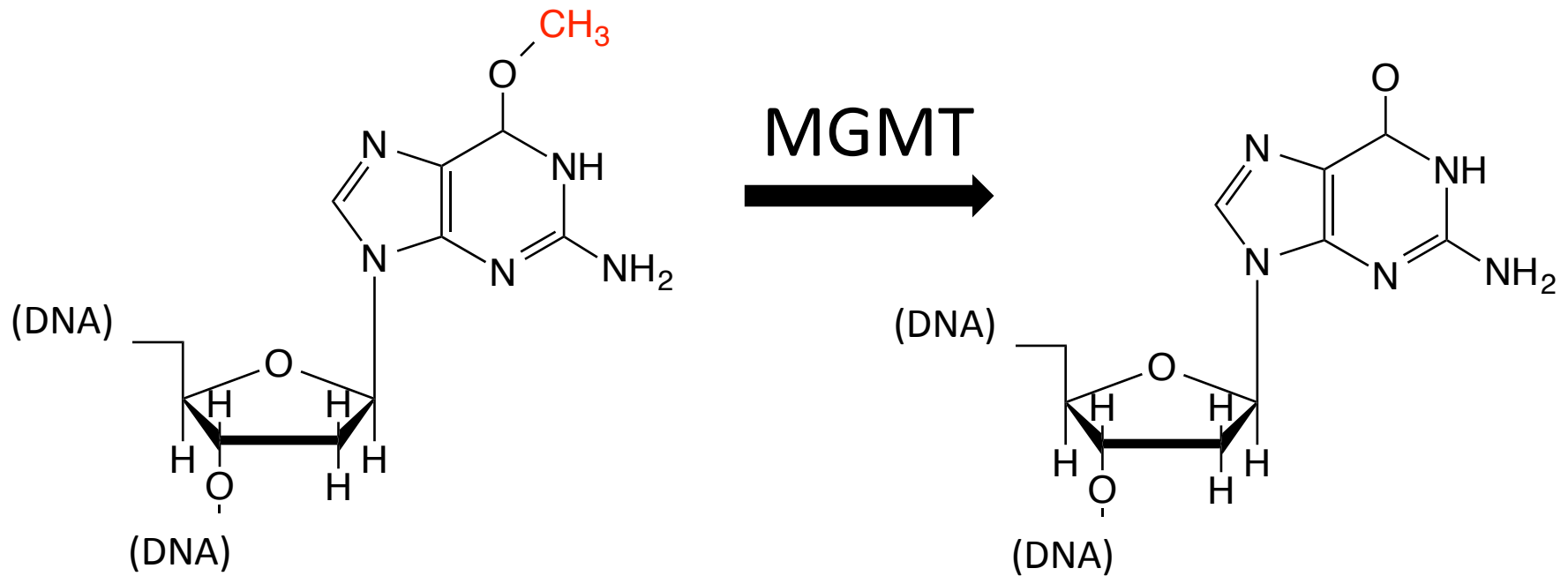
# DNA Mismatch Repair (MMR)



# MMR assay distinguishes between proficient and deficient cell lines:



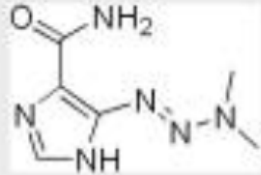
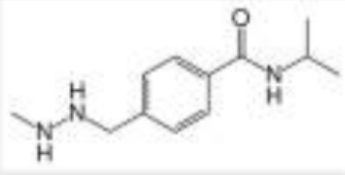
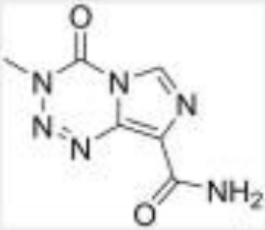
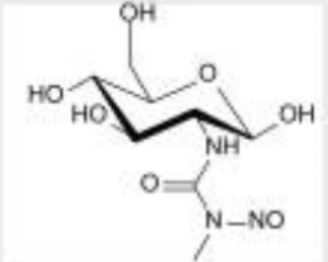
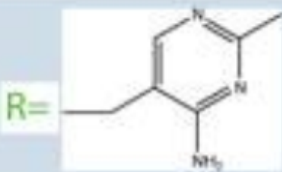

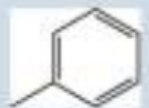
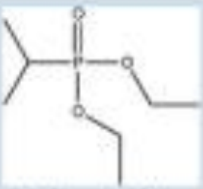
# $O^6$ -Methylguanine DNA Methyltransferase MGMT



Many Cancer Chemotherapy Drugs induce this  
lesion in DNA



# Alkylating agents used in the cancer clinic

<b>a Monofunctional</b>				<b>Lesions<sup>1</sup></b>	
<p><u>Triazene</u></p> <div style="display: flex; justify-content: space-around;"> <div style="text-align: center;">  <p><b>Dacarbazine</b> Metastatic melanoma Hodgkin's lymphoma Sarcoma</p> </div> <div style="text-align: center;">  <p><b>Procarbazine</b> Malignant gliomas Hodgkin's lymphoma</p> </div> <div style="text-align: center;">  <p><b>Temozolomide</b> Malignant gliomas</p> </div> </div>				<p><u>Nitrosourea</u></p> <div style="text-align: center;">  <p><b>Streptozotocin</b> Pancreatic islet cell cancer</p> </div>	<p>7meG 3meA O<sup>6</sup>meG</p>
<p><u>Chloroethylating Nitrosoureas</u></p> <div style="display: flex; justify-content: space-around;"> <div style="text-align: center;">  <p><b>ACNU (Nimustine)</b> Brain tumors Solid tumors</p> </div> <div style="text-align: center;">  <p><b>BCNU (Carmustine)</b> Brain tumors Lymphomas Melanoma</p> </div> <div style="text-align: center;">  <p><b>CCNU (Lomustine)</b> Brain tumors Lymphomas Melanoma</p> </div> <div style="text-align: center;">  <p><b>Fotemustine</b> Metastatic melanoma</p> </div> </div>				<p>7-alkylG O<sup>6</sup>Cl-ethylG N1,O<sup>6</sup>-EG G-C x-link G-G x-link</p>	

# DNA lesions from an RNA polymerase perspective

Block Transcription



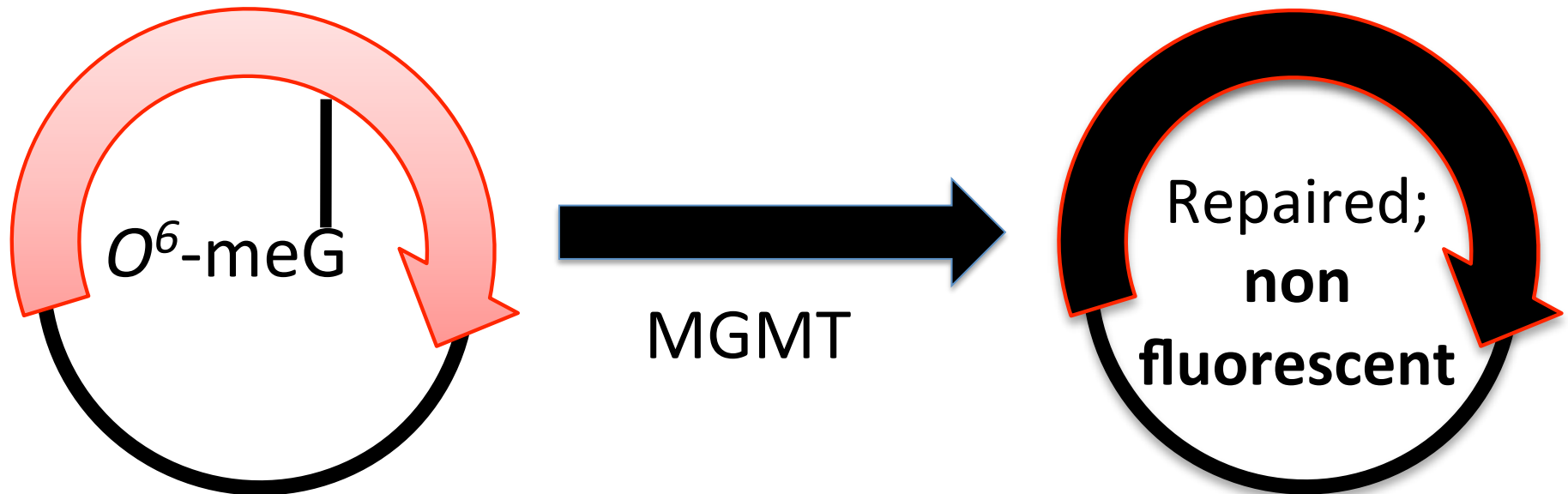
Error-free Bypass



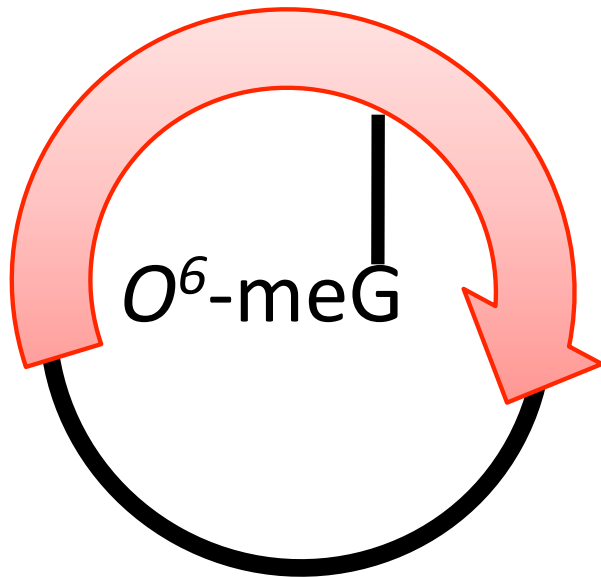
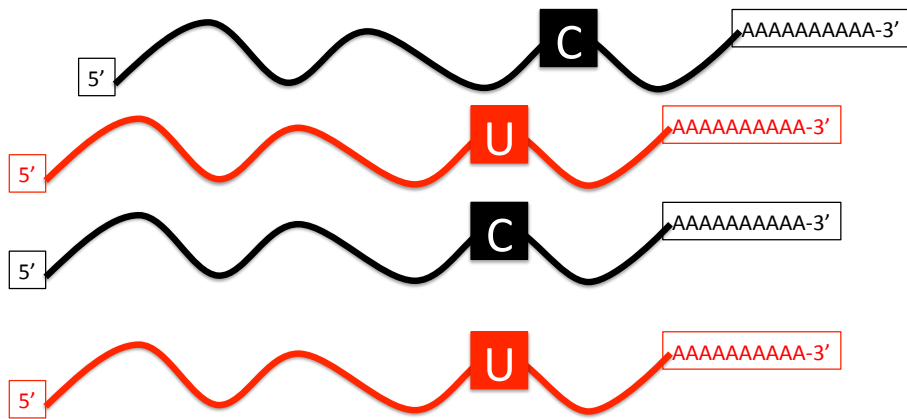
Transcriptional Mutagenesis



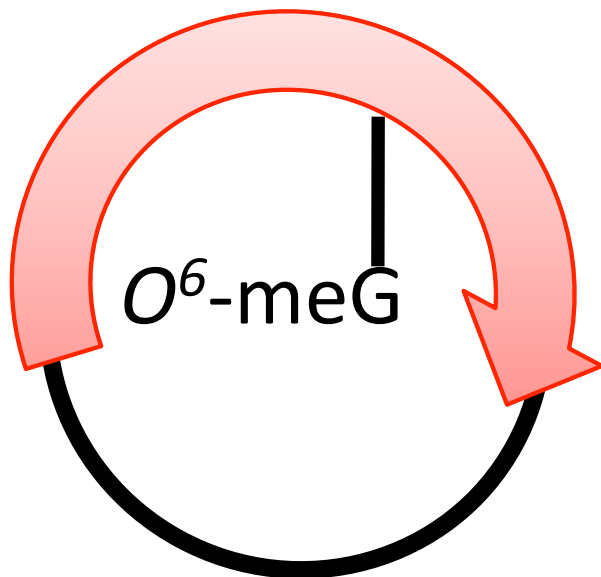
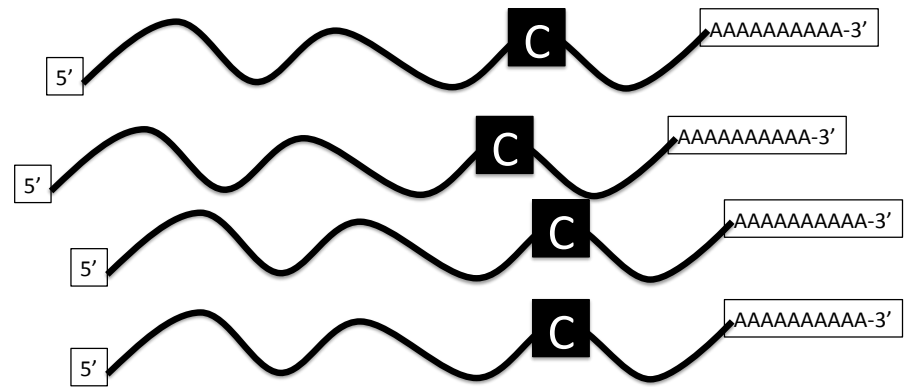
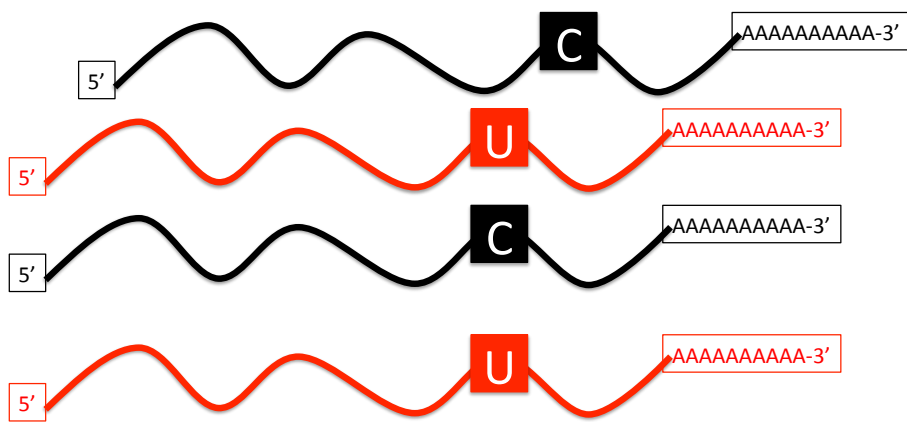
# Direct Reversal of $O^6$ -Methylguanine



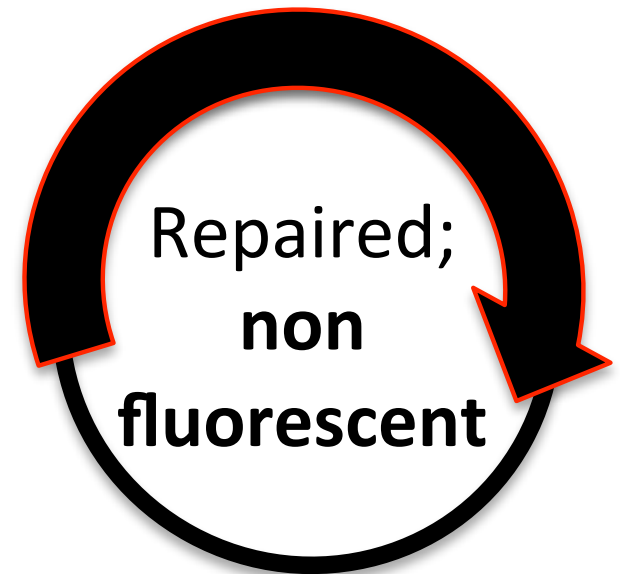
# Direct Reversal of $O^6$ -Methylguanine



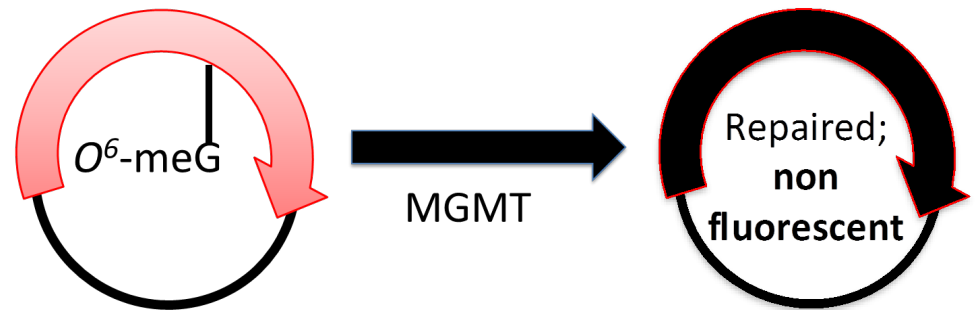
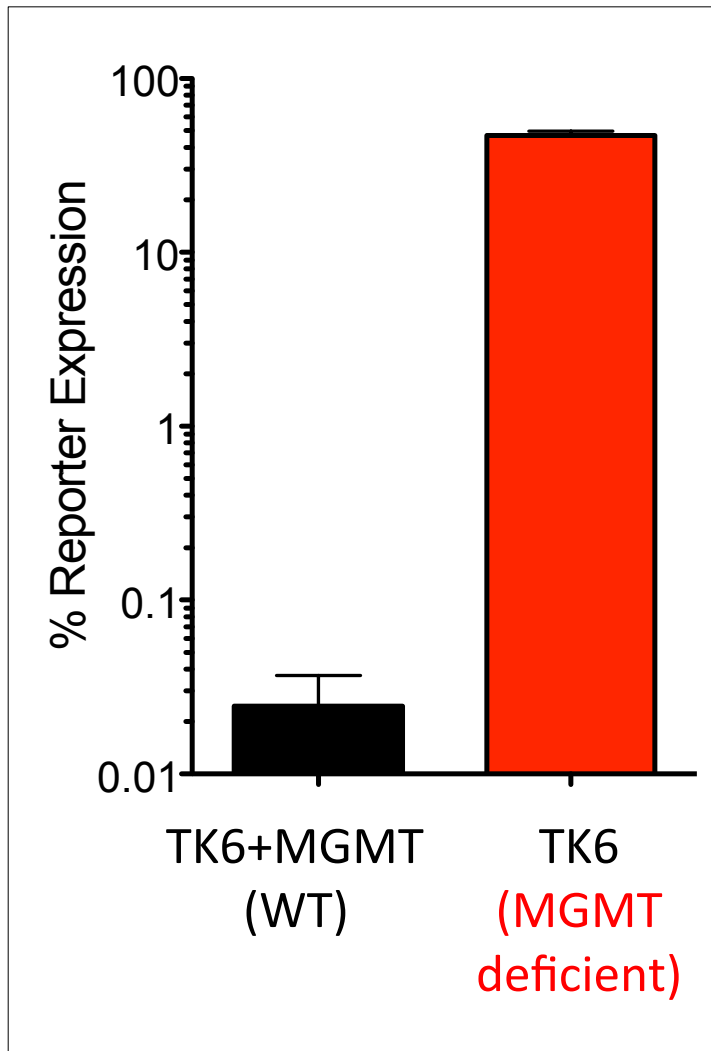
# Direct Reversal of $O^6$ -Methylguanine



Direct Reversal →

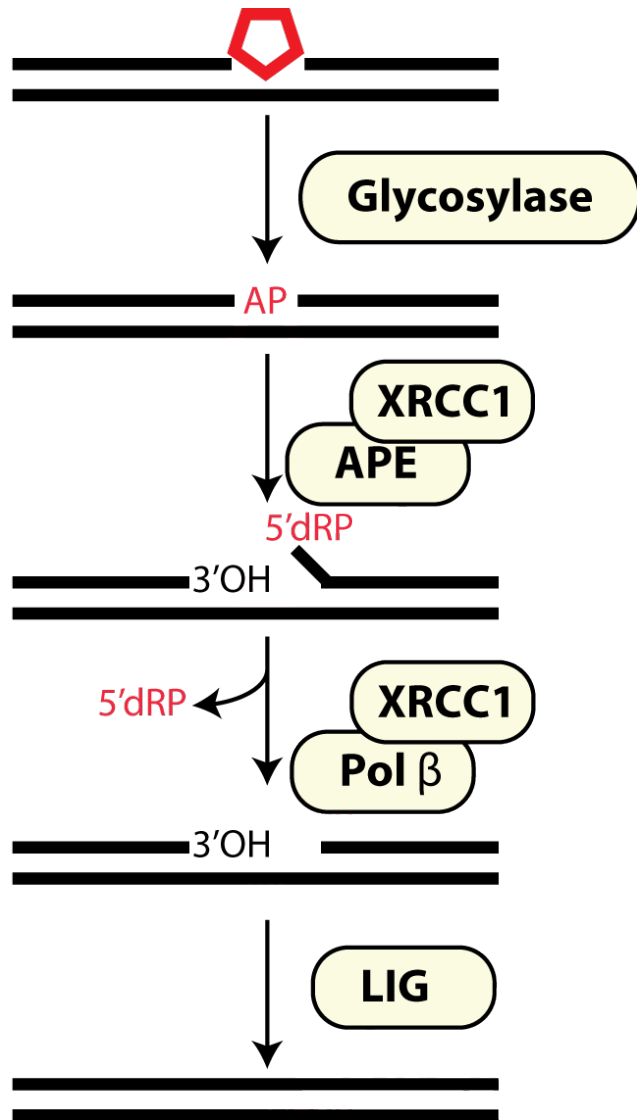


# MGMT deficient cells are distinguished by a high level of reporter expression:



# Base Excision Repair (BER)

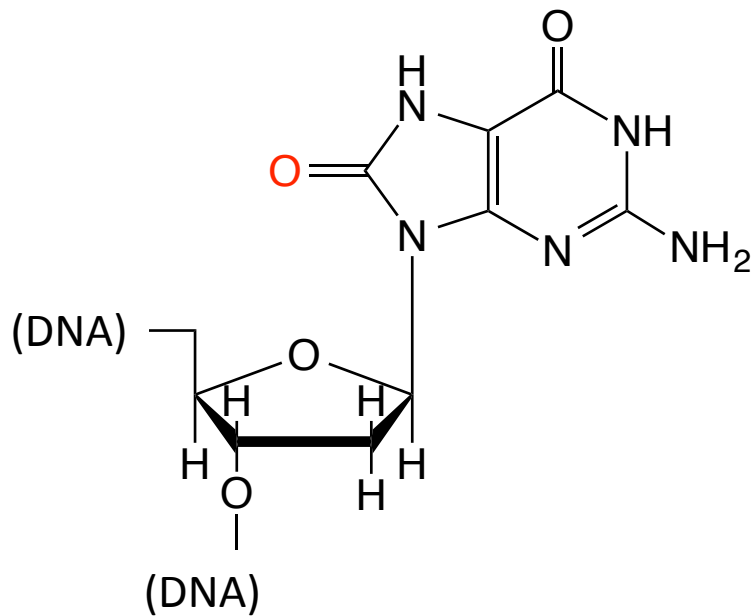
For oxidized, deaminated and alkylated base damage



## DNA Glycosylases

Bifunctional ( $\beta$ elimination)	<b>OGG1</b>	8-oxoguanine DNA glycosylase
	<b>NTHL1</b>	nth endonuclease III-like 1
	<b>NEIL 3</b>	Nei endonuclease VIII-like 3
Monofunctional	<b>UNG</b>	Uracil DNA glycosylase
	<b>SMUG1</b>	Single-strand-selective monofunctional uracil DNA glycosylase 1
	<b>TDG</b>	Thymine DNA glycosylase
	<b>MBD4</b>	Methyl-CpG binding domain protein 4
	<b>AAG</b>	Alkyladenine DNA glycosylase
	<b>MUTYH</b>	mutY homologue
Bifunctional ( $\beta, \delta$ elimination)	<b>NEIL 1</b>	Nei endonuclease VIII-like 1
	<b>NEIL 2</b>	Nei endonuclease VIII-like 2

# Base excision repair of 8-oxo-G



8-oxo-guanine



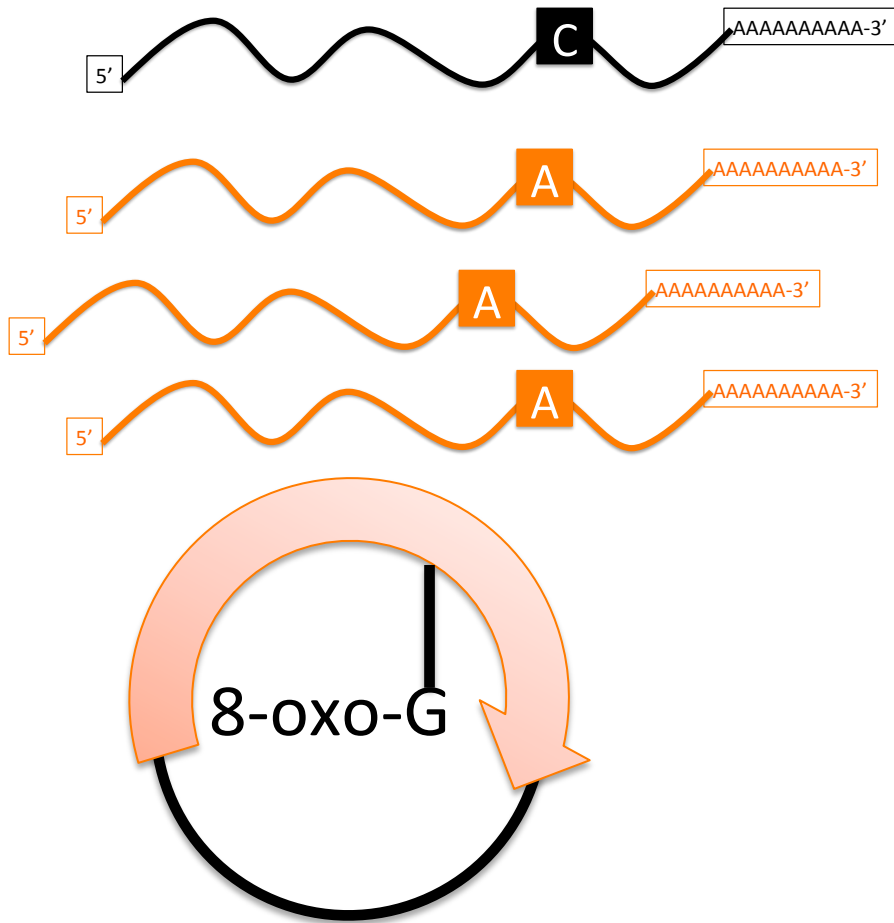
OGG1 DNA Glycosylase



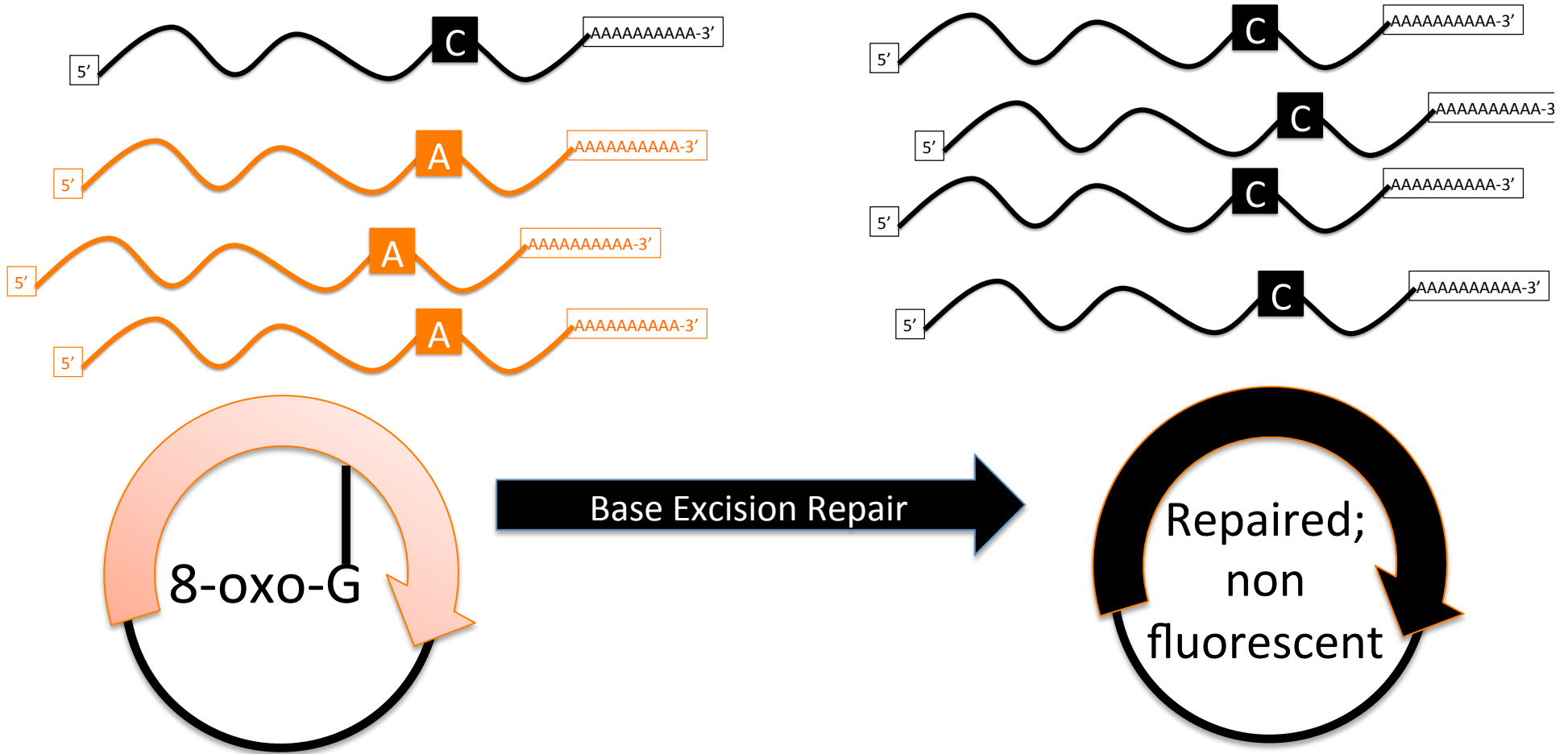
# Base excision repair of 8-oxo-G



# Base excision repair of 8-oxo-G

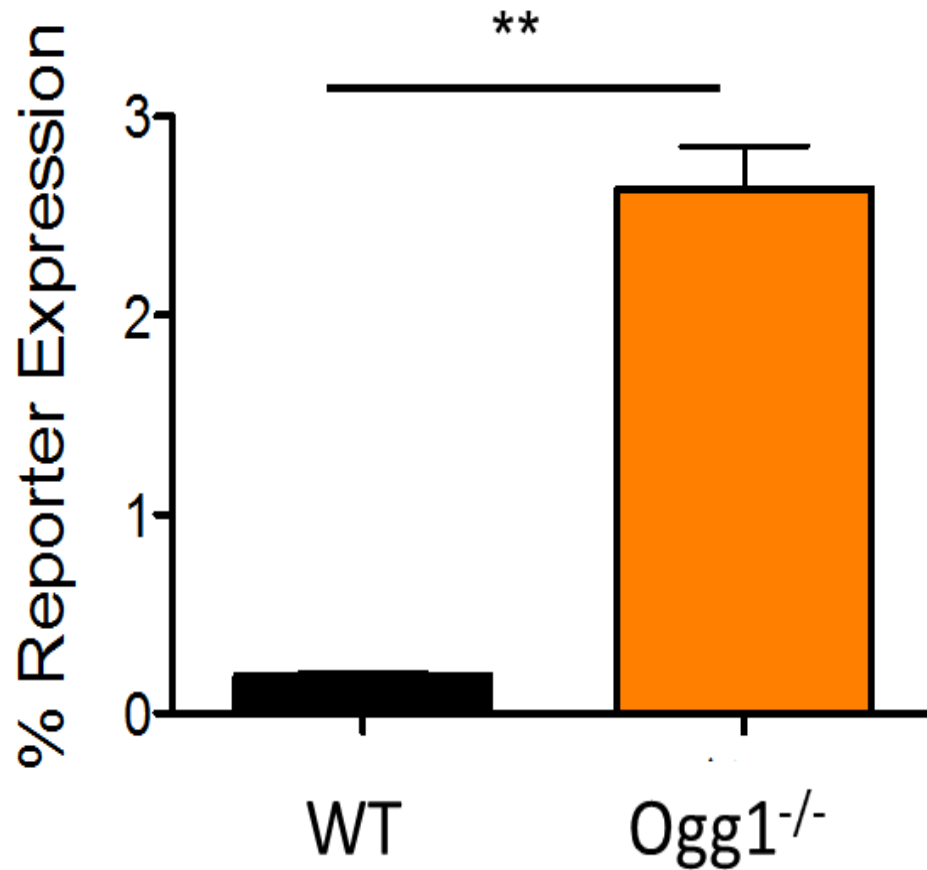


# Base excision repair of 8-oxo-guanine

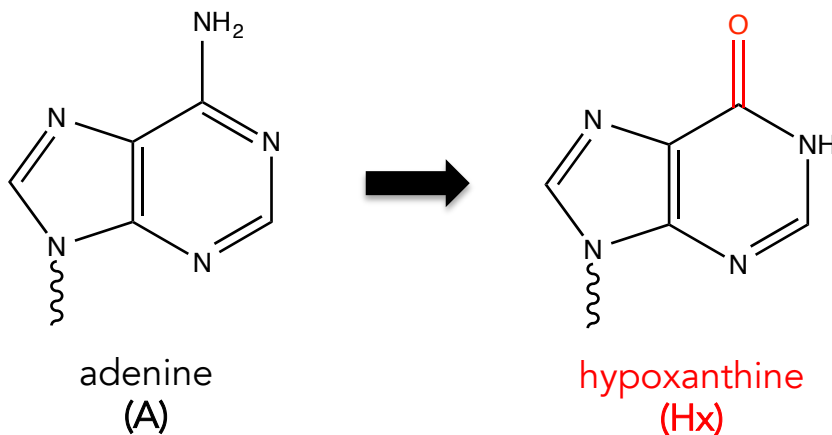


# Measuring BER of 8-oxo-guanine

8-oxoG:C (24h) - MEFs

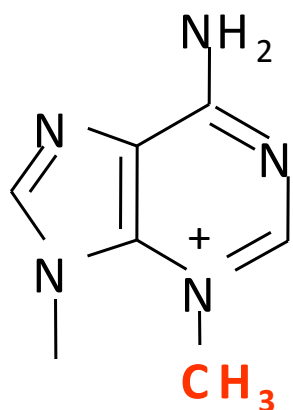


# Base excision repair of Hypoxanthine (Hx)

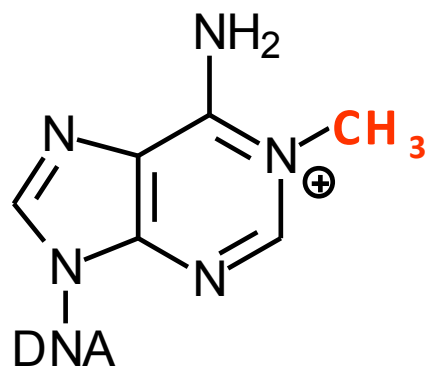


- Found in DNA
  - Product of A deamination
  - Incorporated from the nucleotide pool across C
- Highly mutagenic
  - A→G transitions

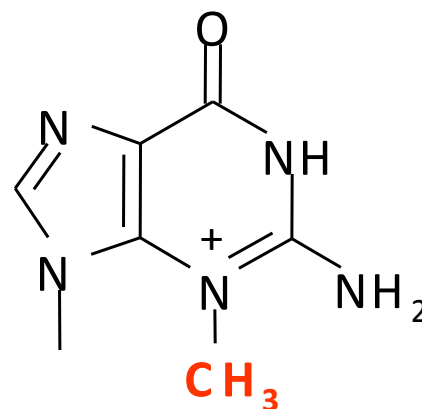
# Human (AAG), and Mouse (Aag) 3MeA DNA Glycosylases Act on Many Lesions



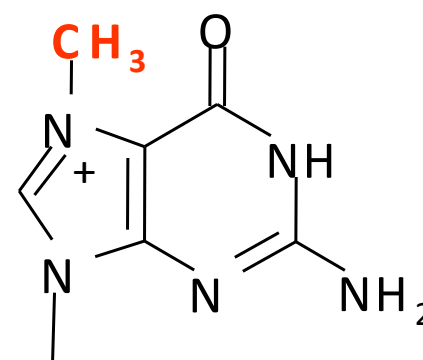
**3meA**



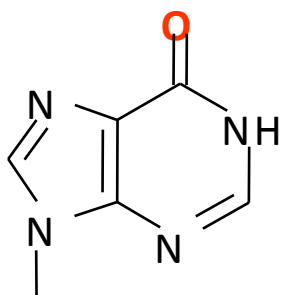
**1meA**



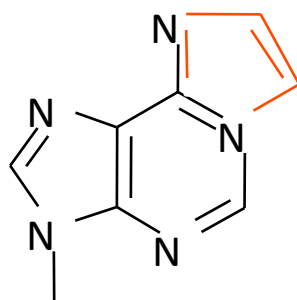
**3meG**



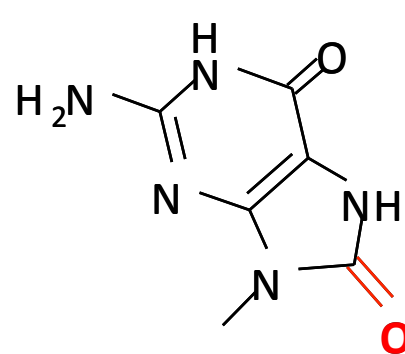
**7meG**



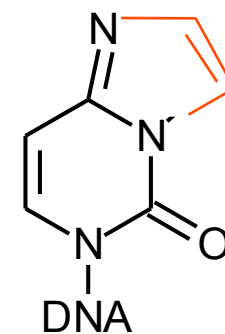
**Hx**



**$\epsilon\text{A}$**

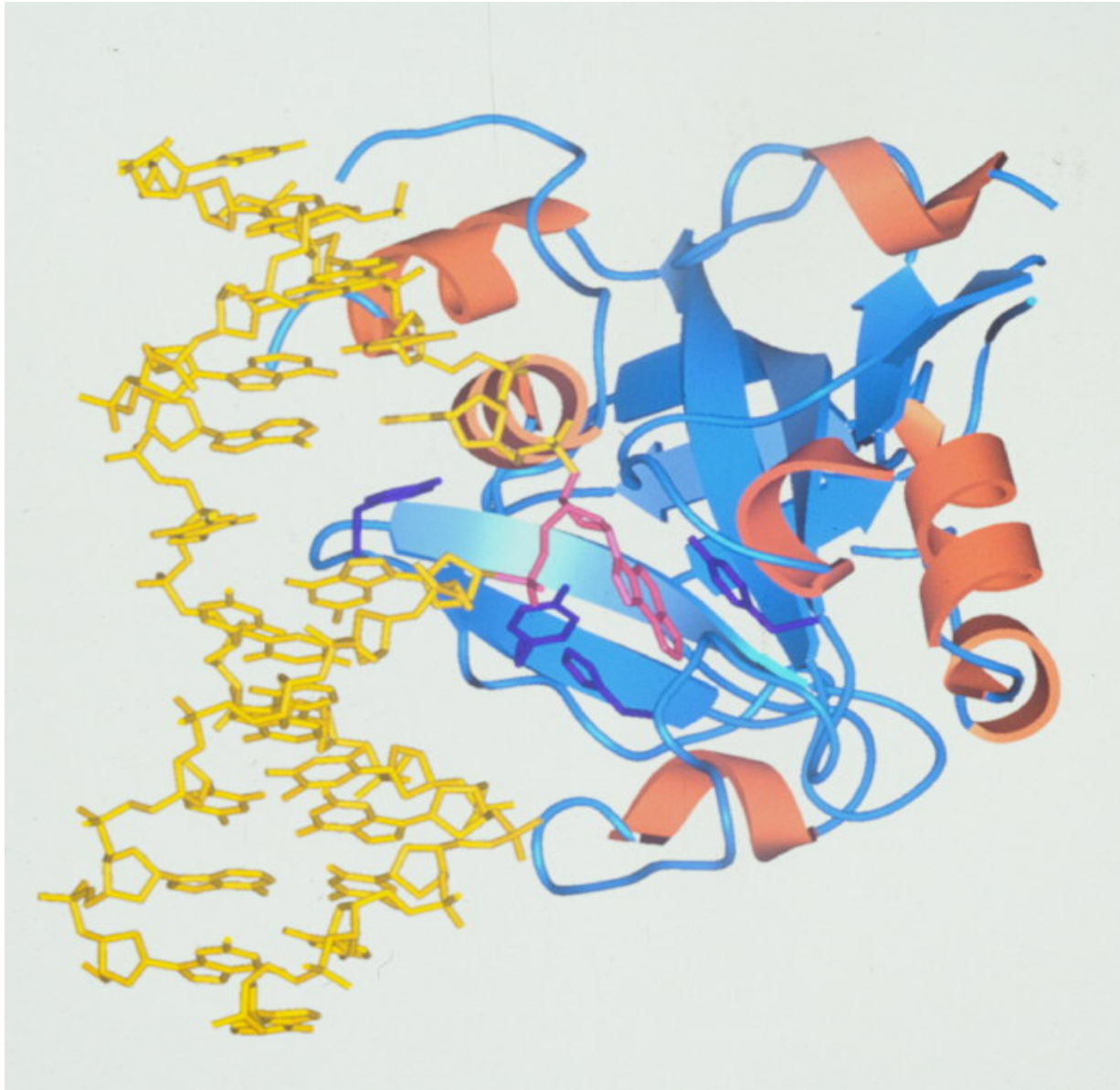


**8-oxoG**



**$\epsilon\text{C}$**

# AAG: Alkyladenine DNA Glycosylase



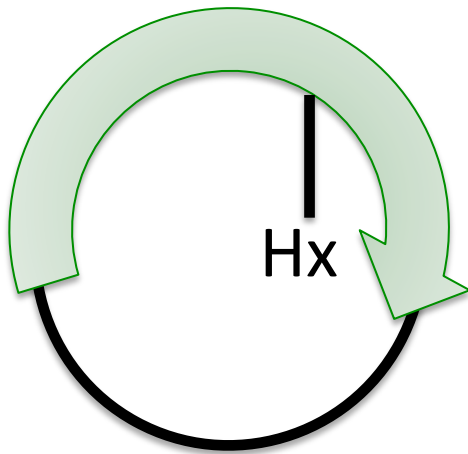
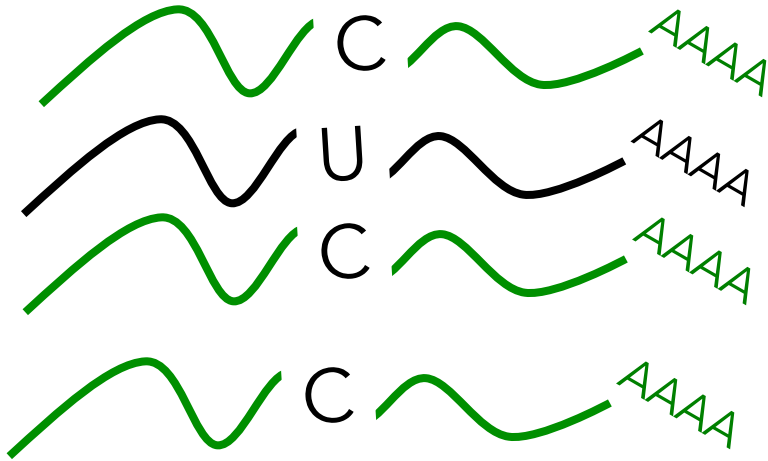
Lau et al. *PNAS*. 2000. **97**:13573-78.

# Base excision repair of Hx

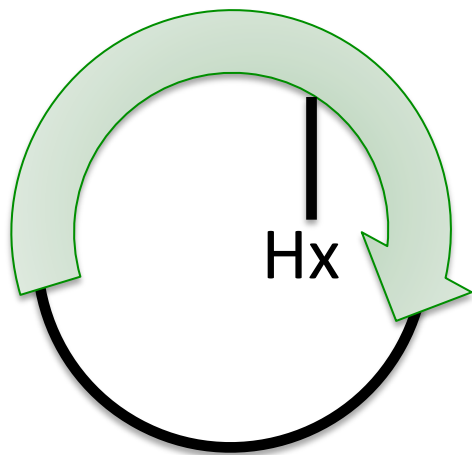
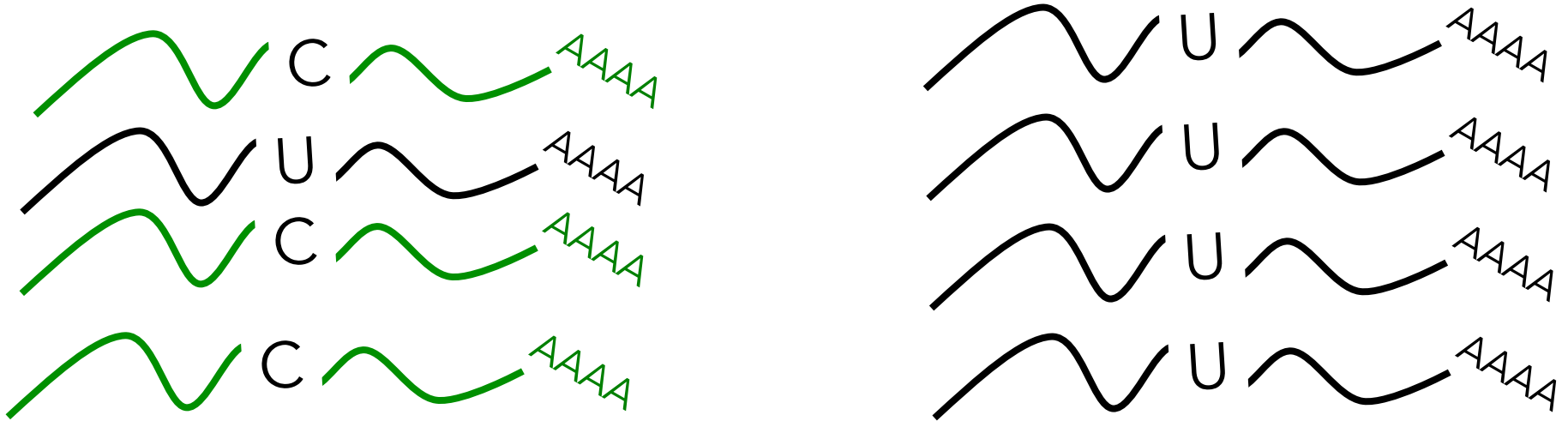




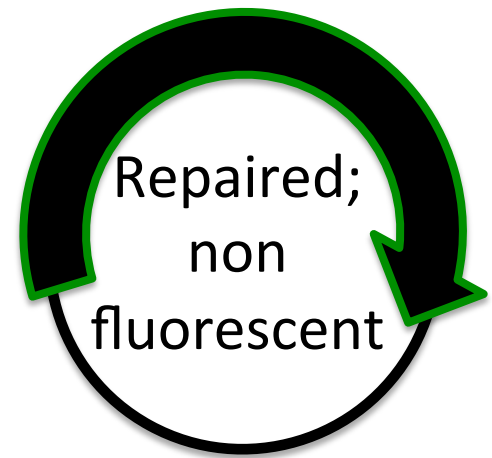
# Base excision repair of Hx



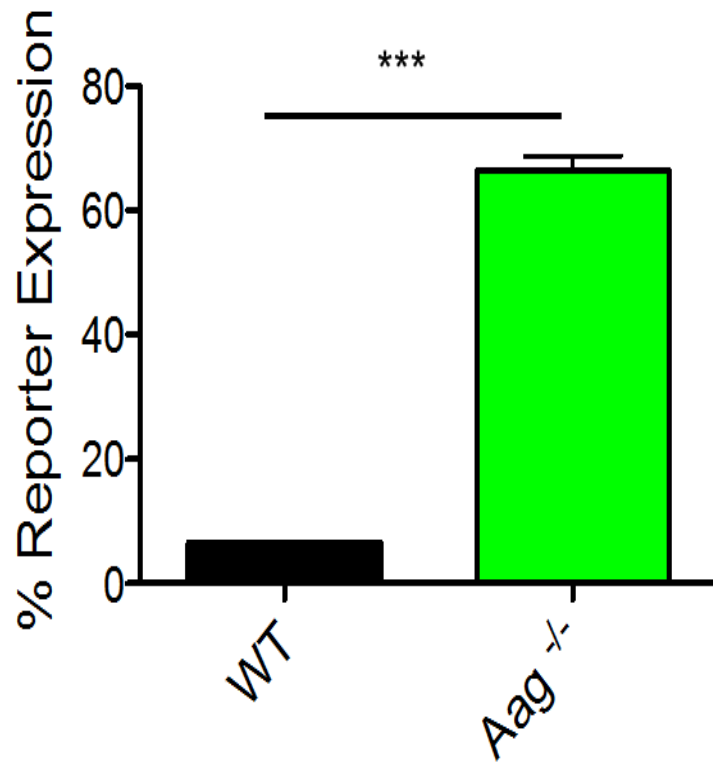
# Base excision repair of Hx



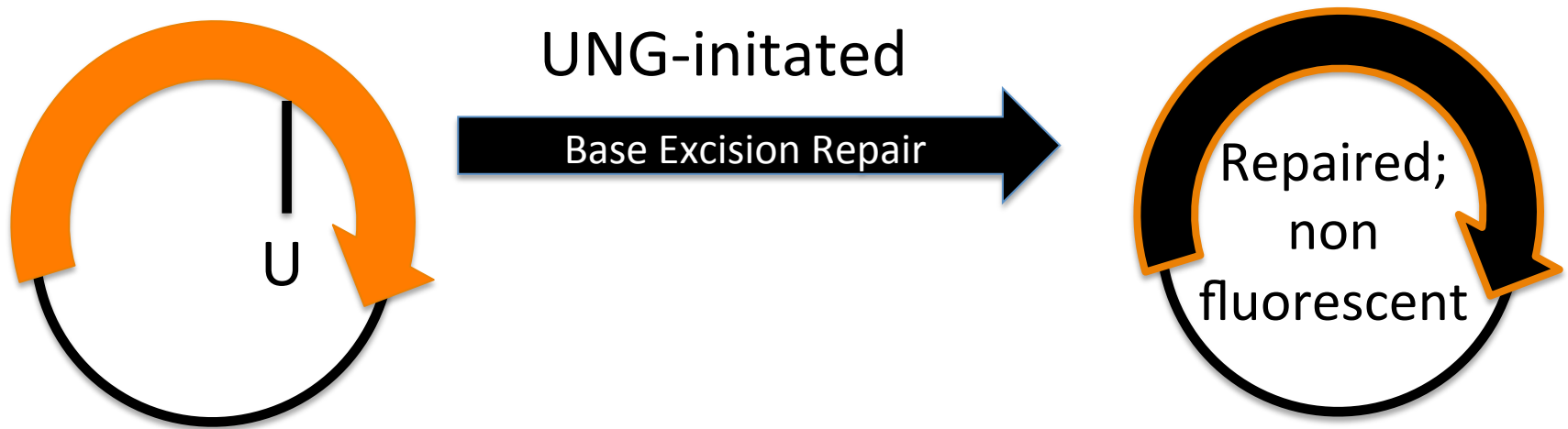
Base Excision Repair



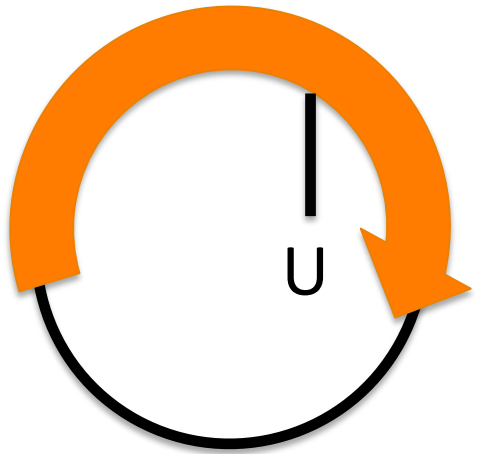
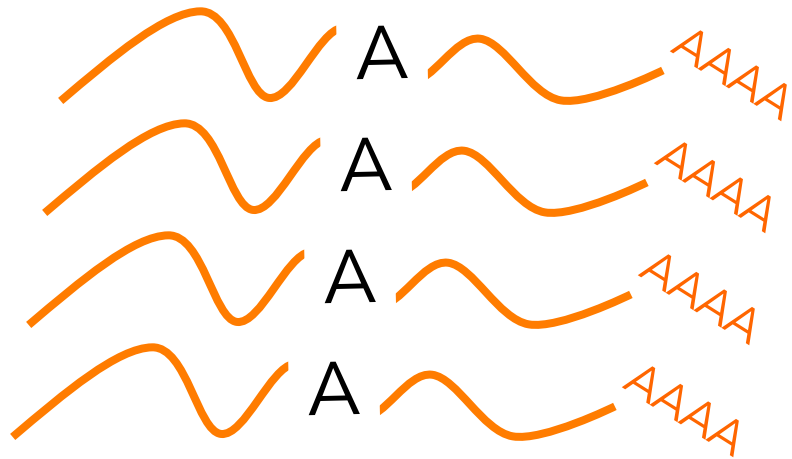
# Measuring BER of Hx



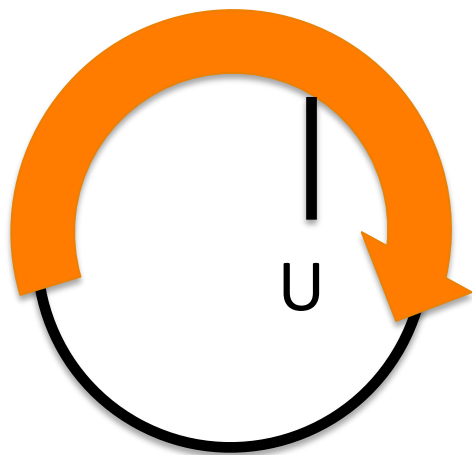
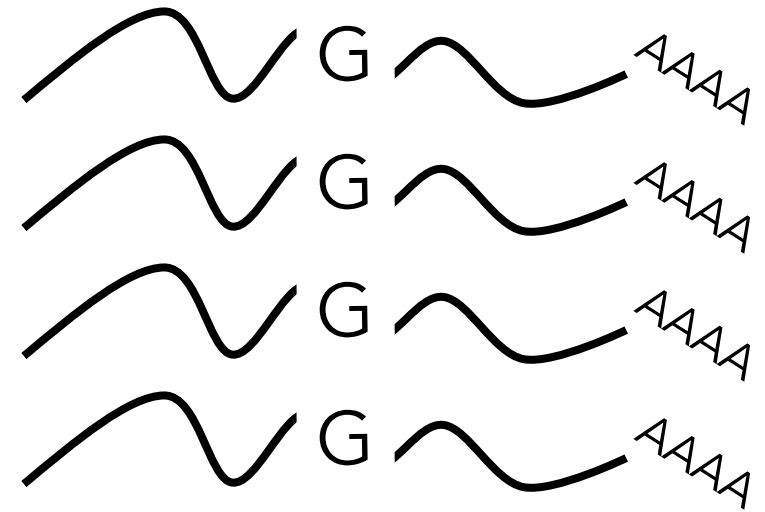
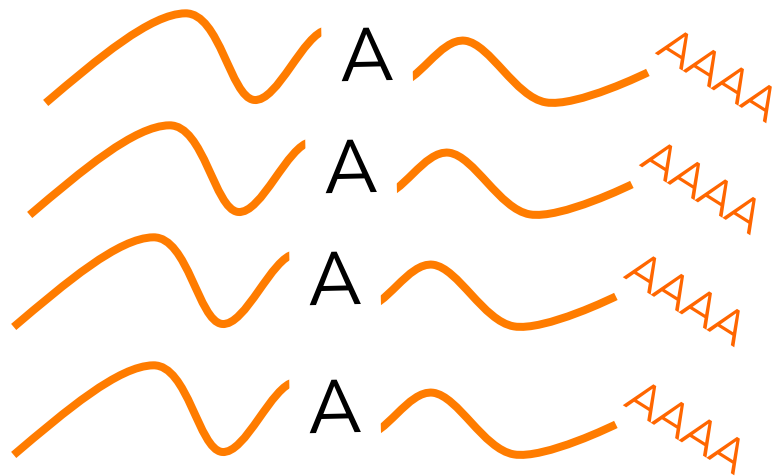
# Base excision repair of Uracil



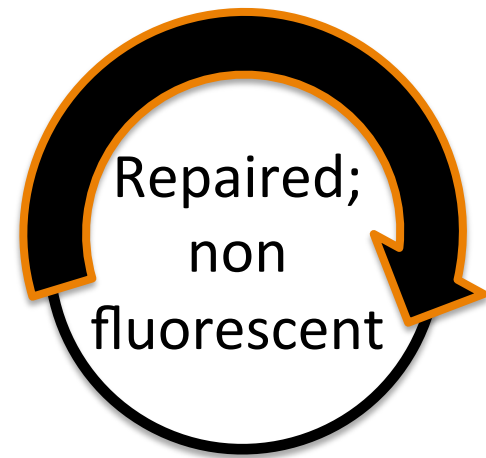
# Base excision repair of Uracil



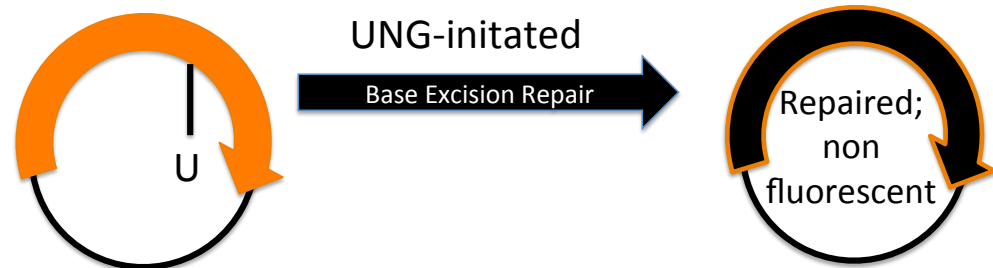
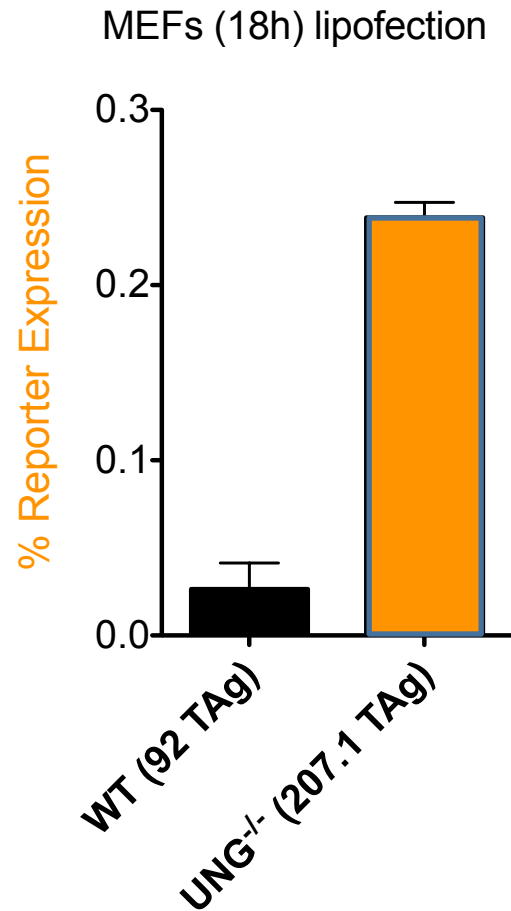
# Base excision repair of Uracil



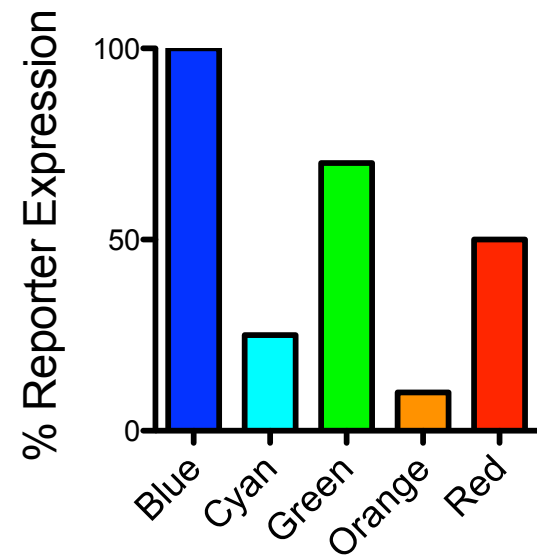
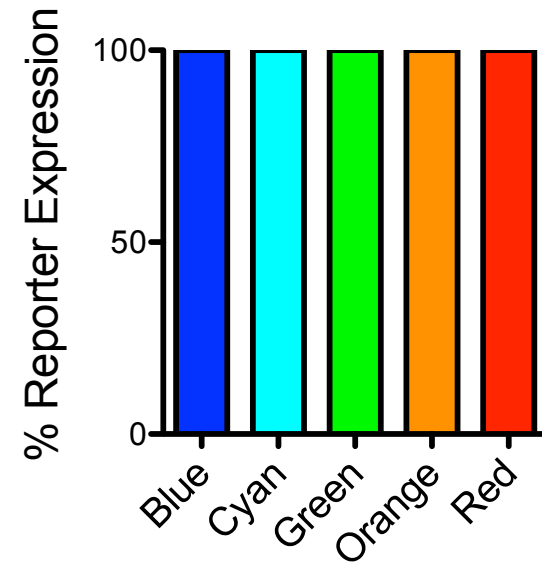
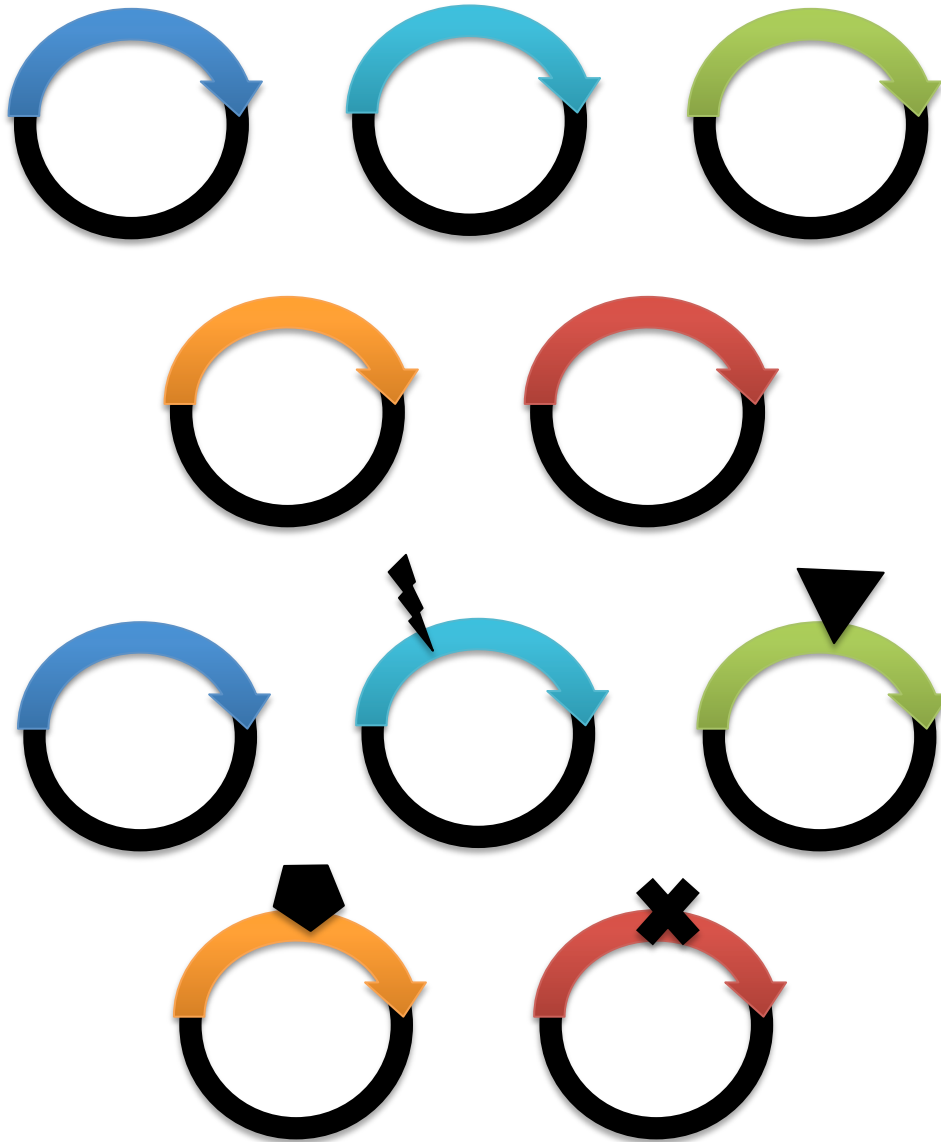
Base Excision Repair



# Measuring BER of Uracil

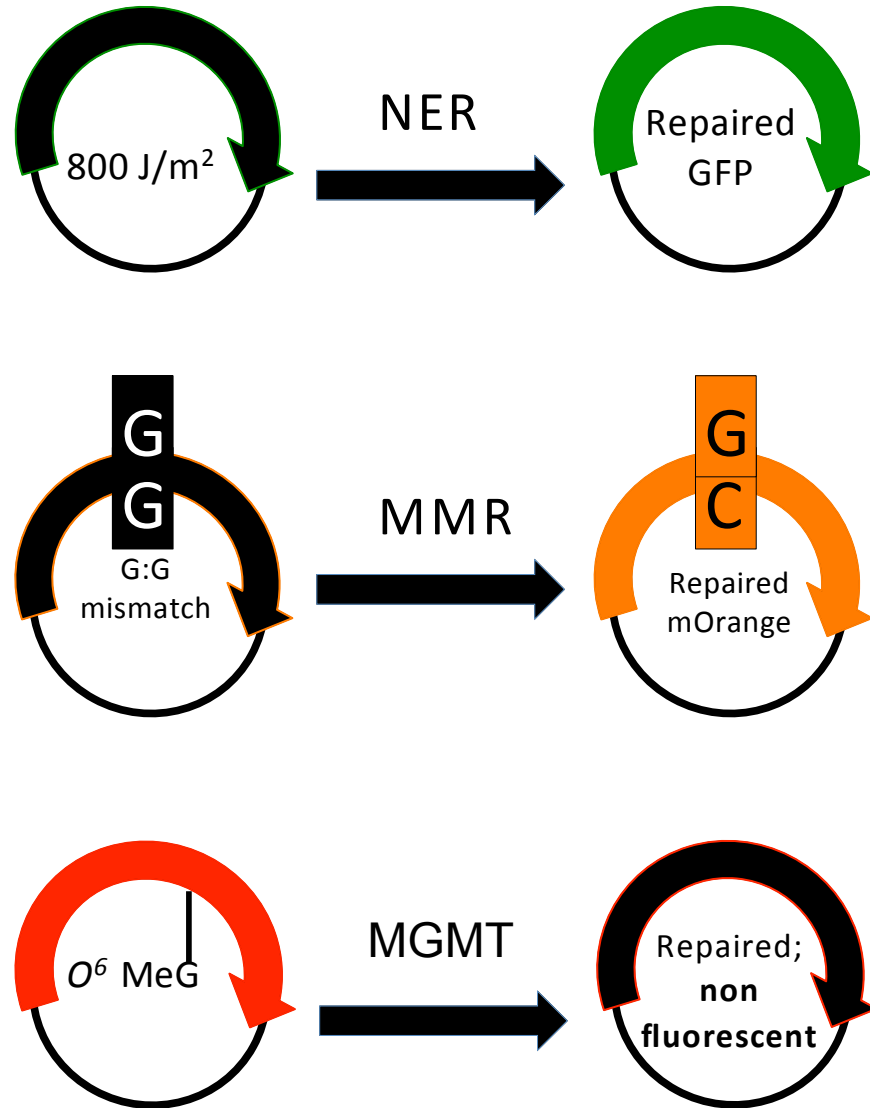


# 5 color HCR assay applications

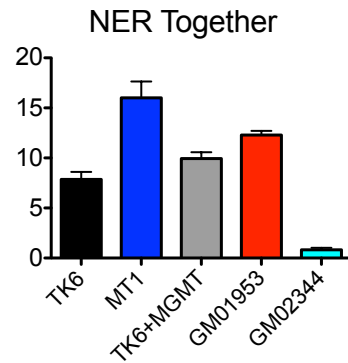
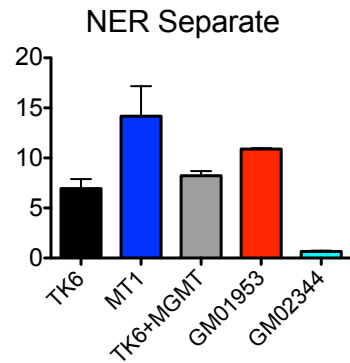




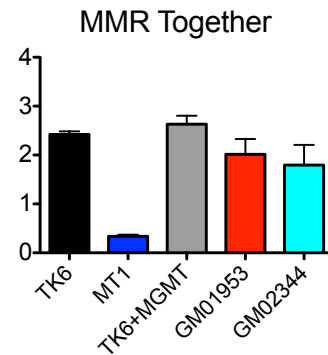
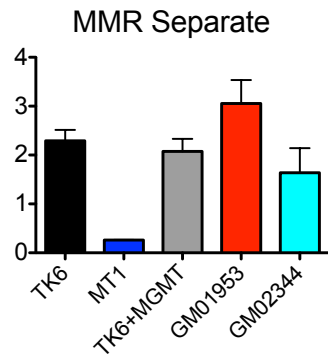
# Started by Measuring DRC in 3 pathways



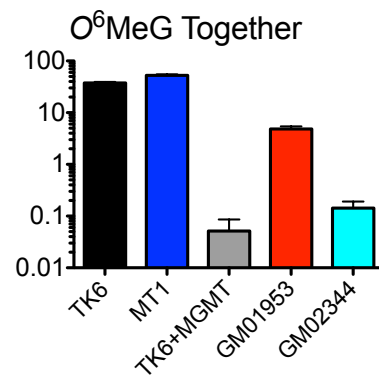
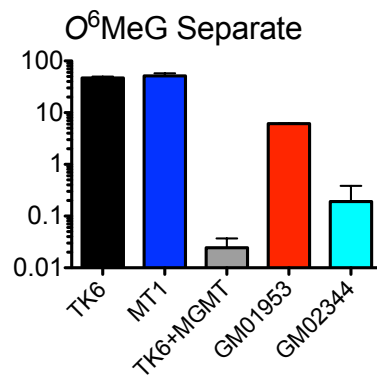
# Started by Measuring DRC in 3 pathways in 5 different cell lines



GM02344  
NER-deficient (XPA)

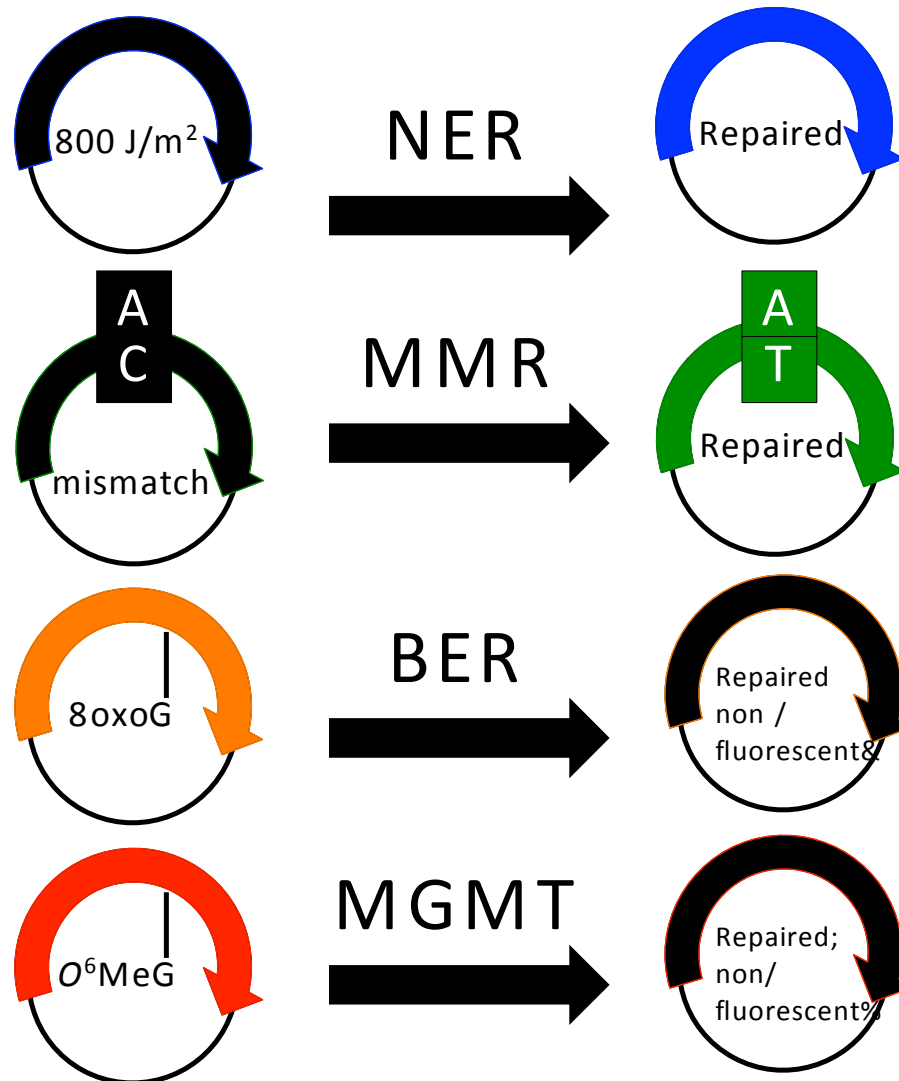


MT1  
MMR-deficient (MSH6 null)

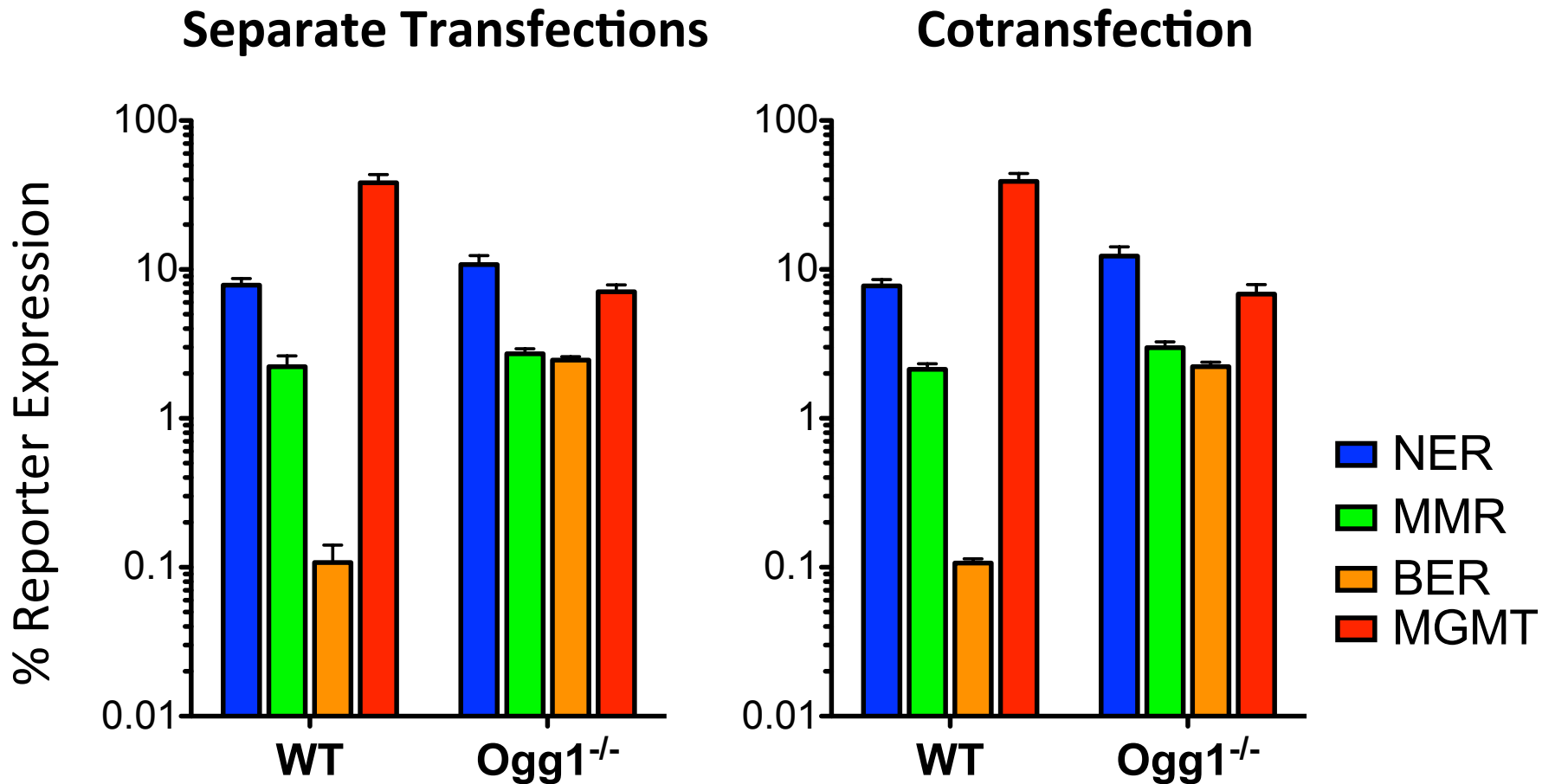


TK6+MGMT  
Overexpressing MGMT  
(TK6 and GM1953 "WT")

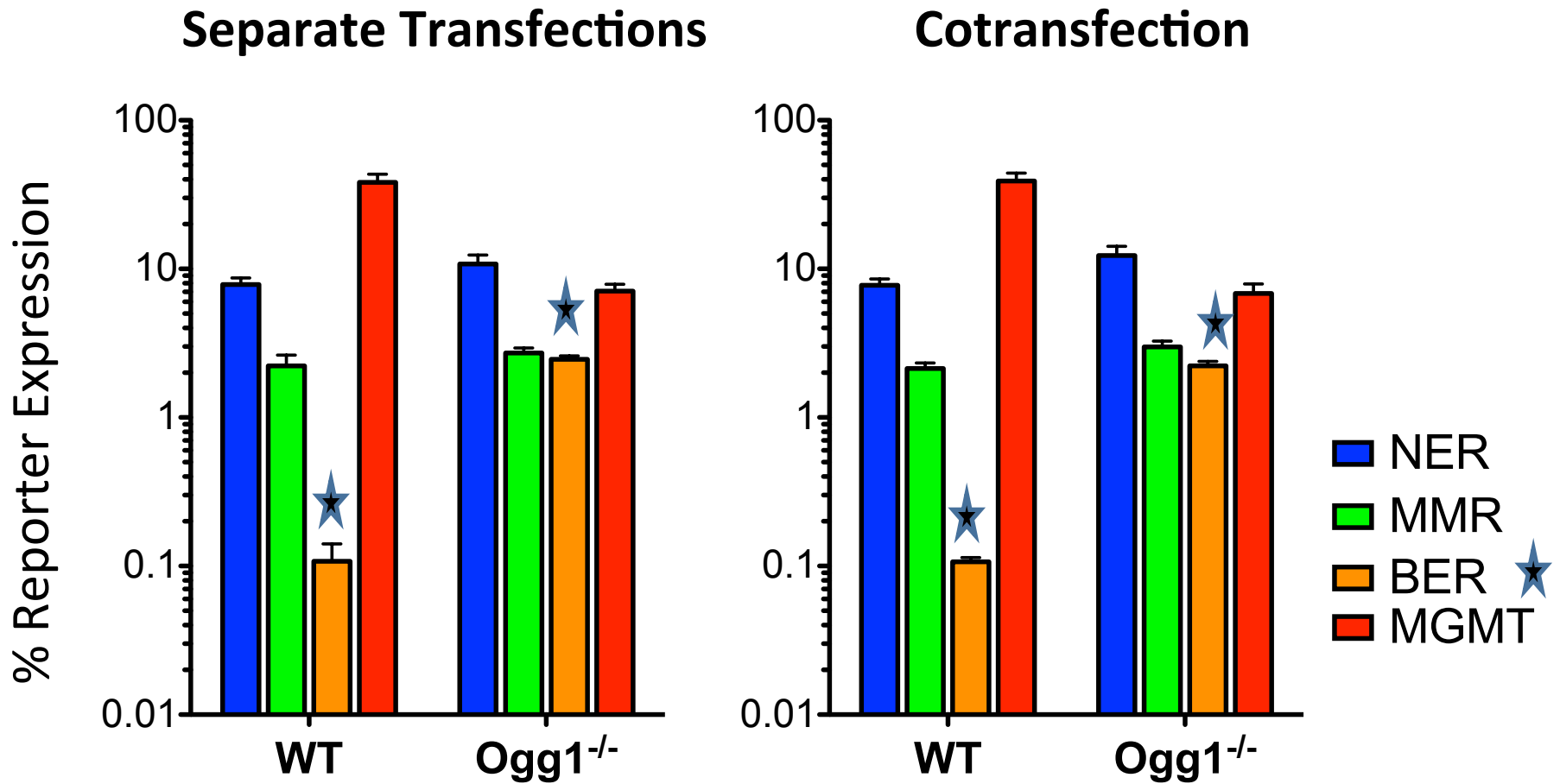
# Then Measured DRC in 4 pathways in a single assay:



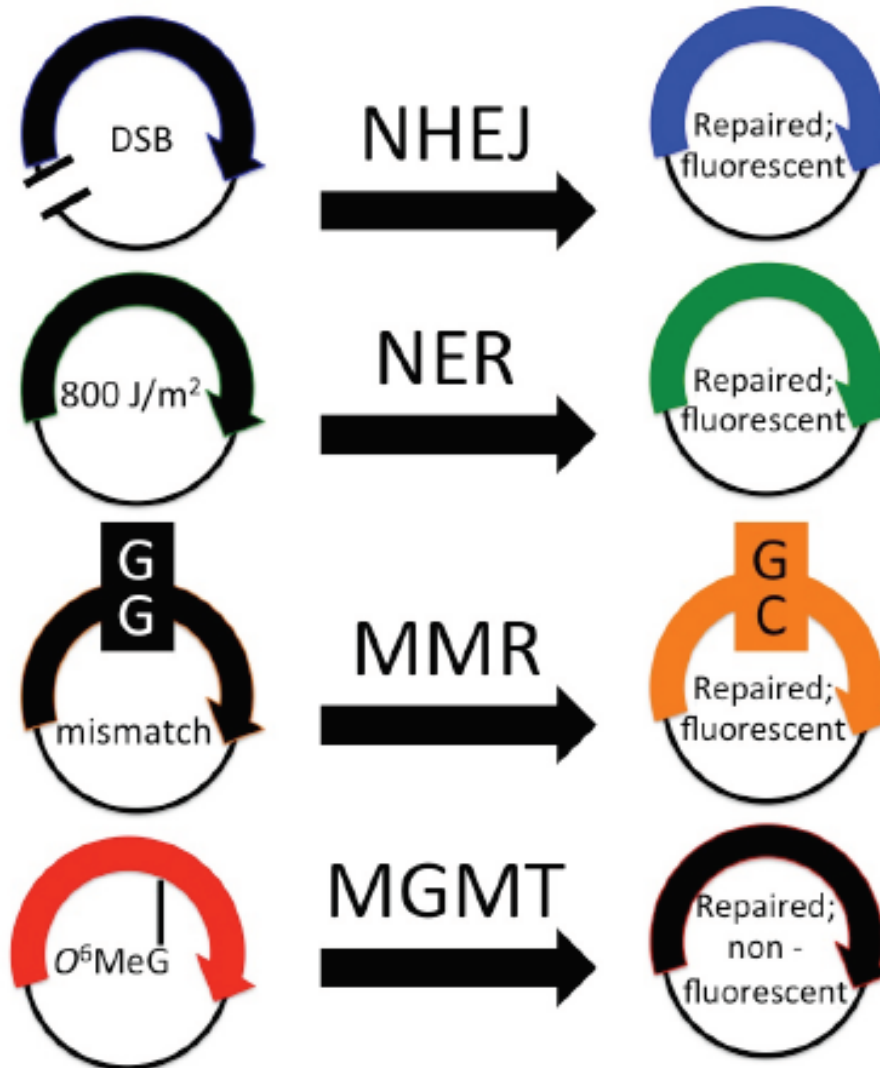
# Then Measured DRC in 4 pathways in a single assay (1 of 2):



# Then Measured DRC in 4 pathways in a single assay (1 of 2):

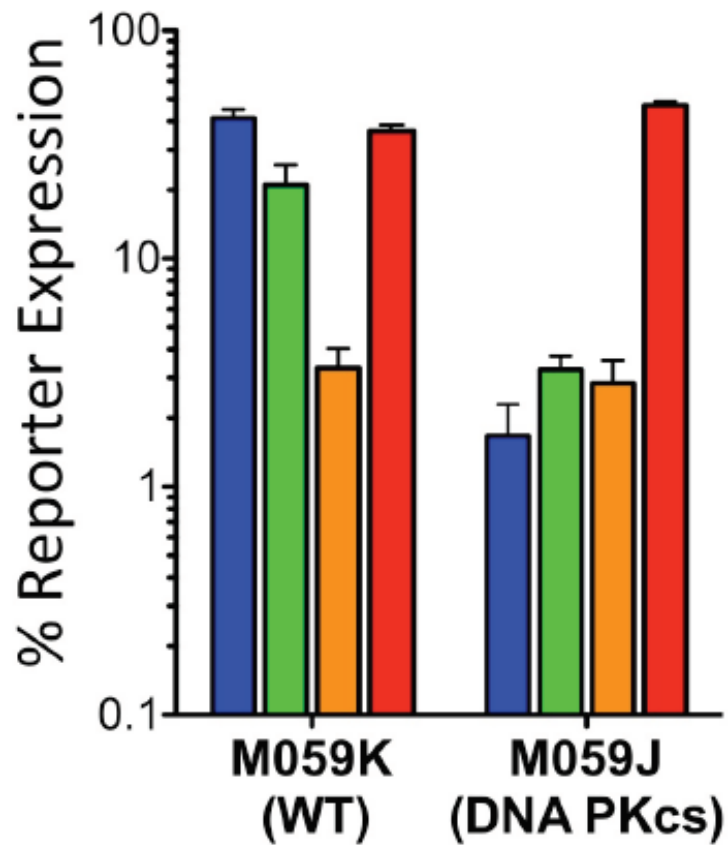


# Then Measured DRC in 4 pathways in a single assay (2 of 2):

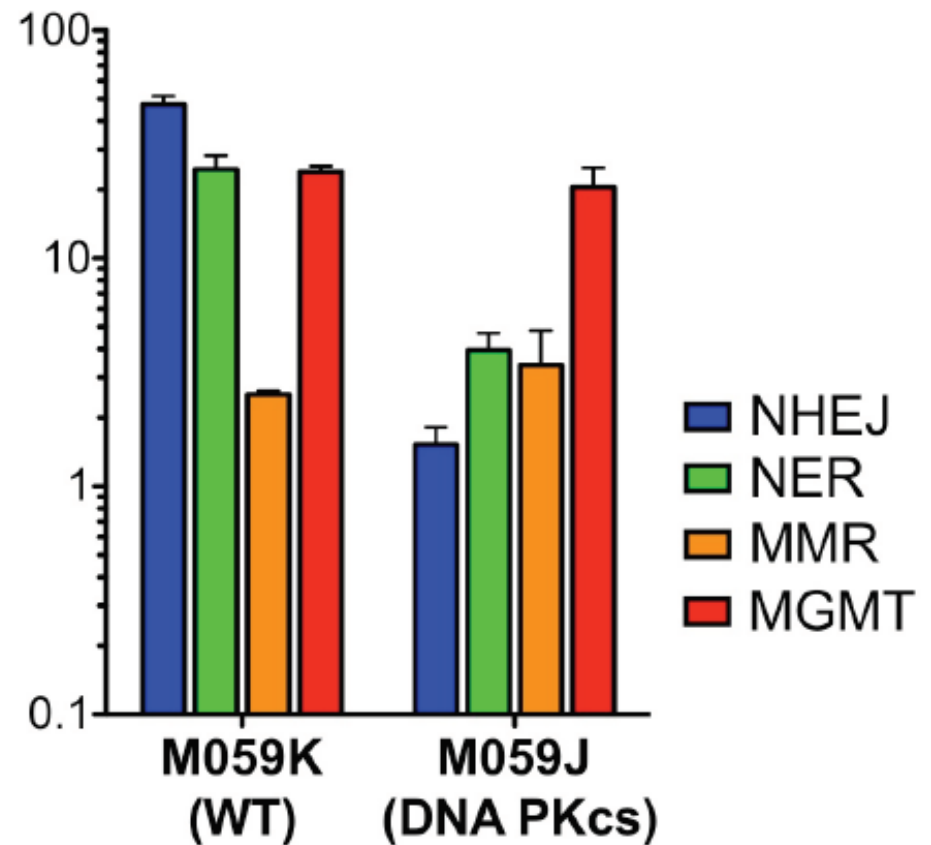


# Then Measured DRC in 4 pathways in a single assay (2 of 2):

## b Separate

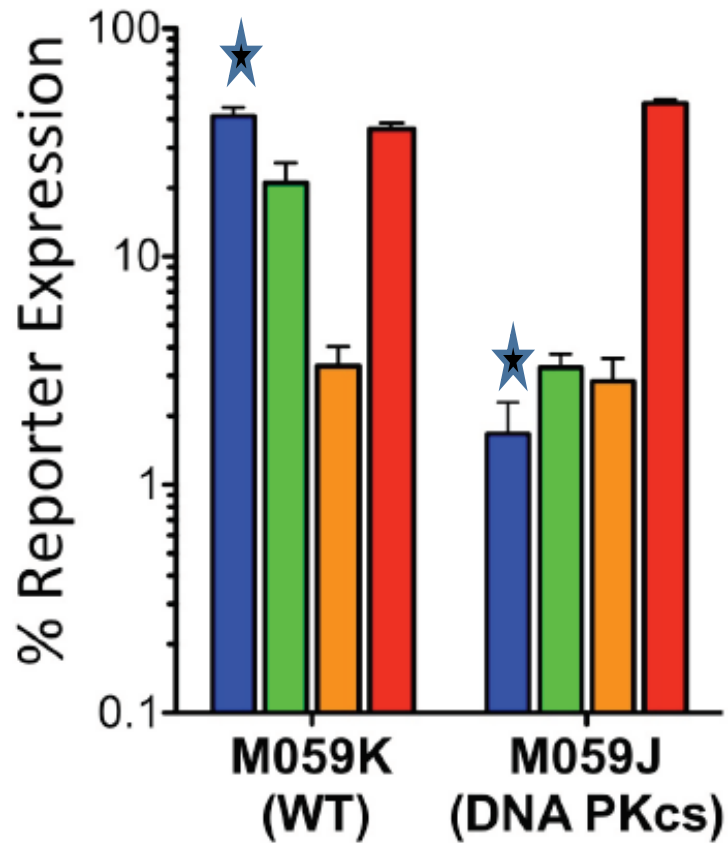


## c Together

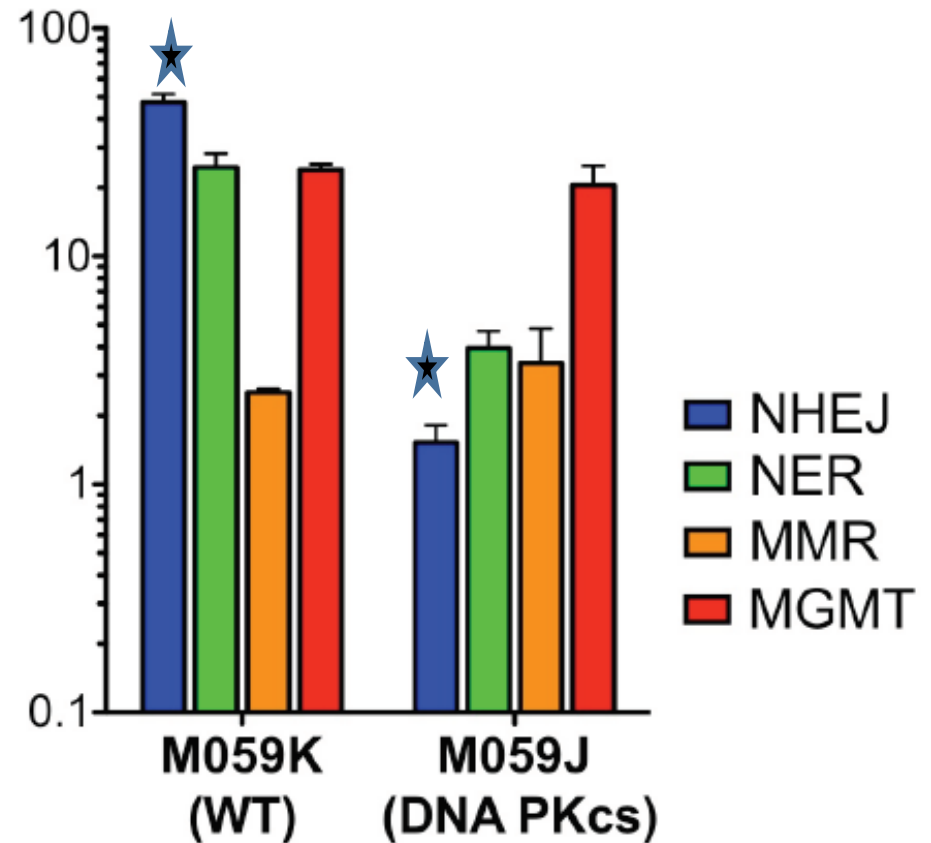


# Then Measured DRC in 4 pathways in a single assay (2 of 2):

## b Separate

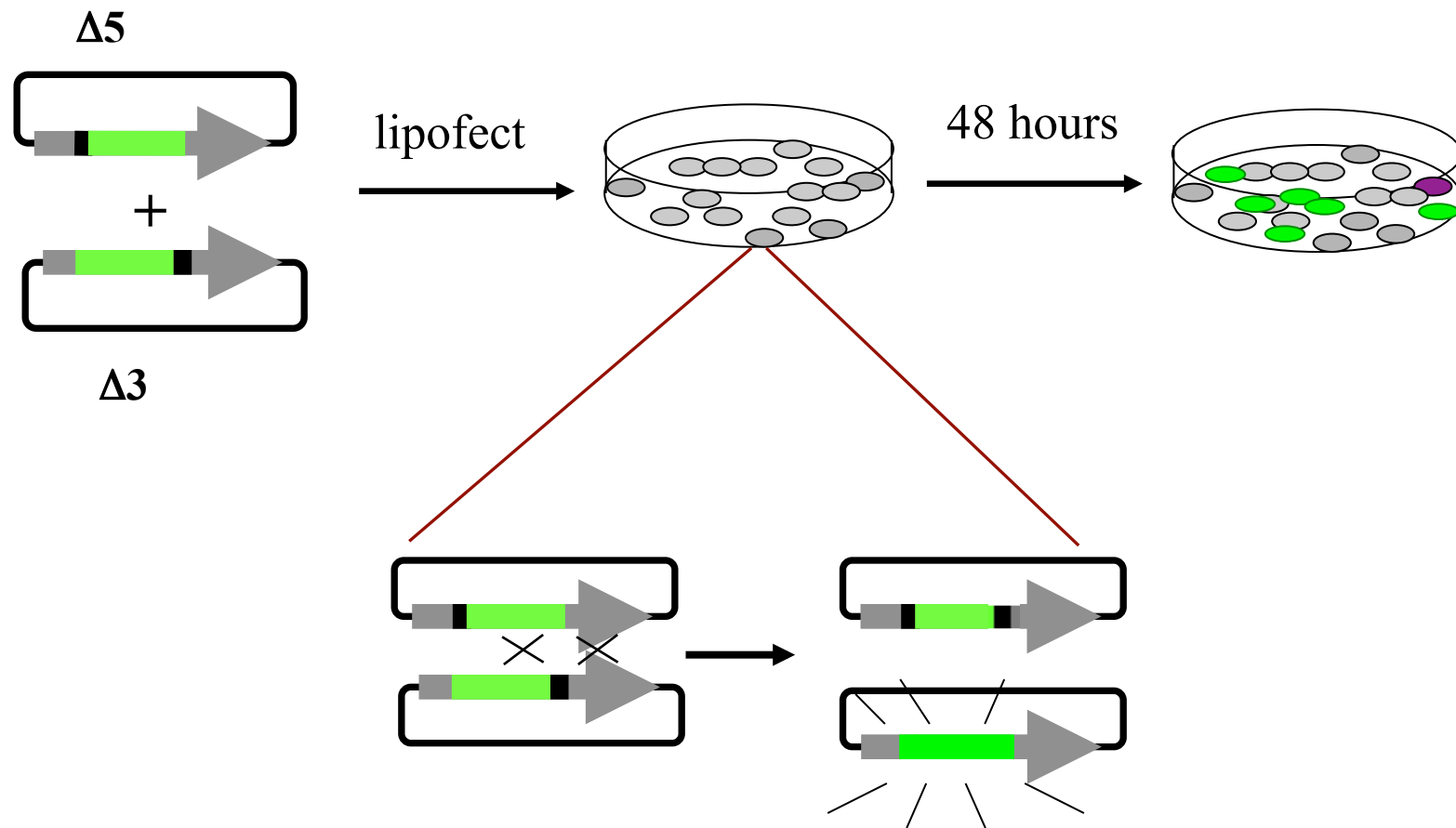


## c Together

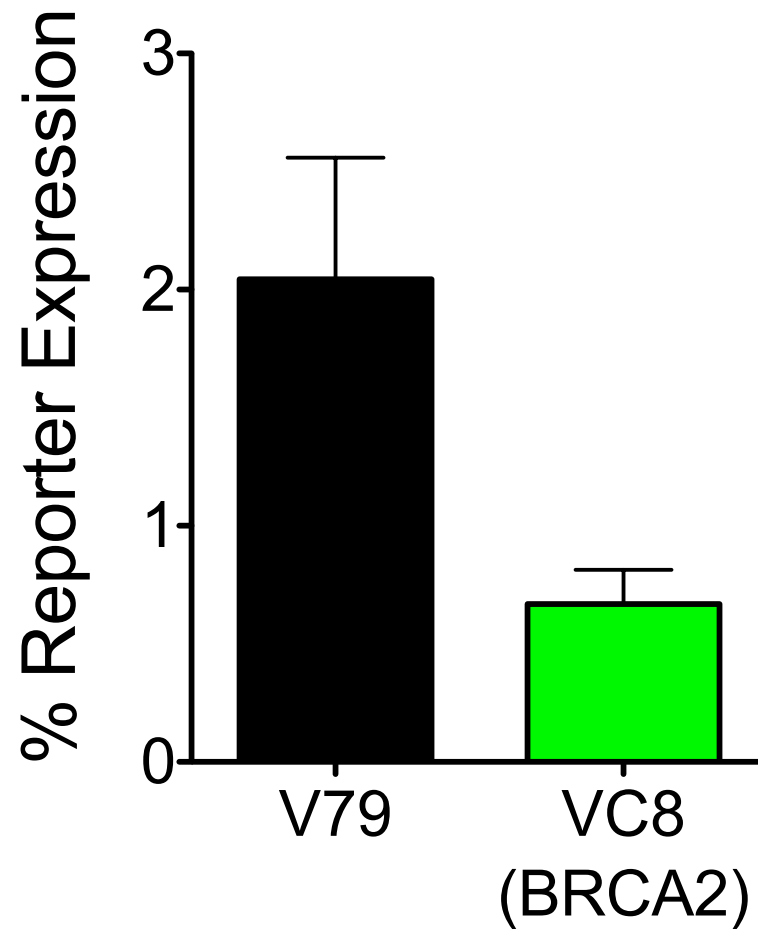




# A Plasmid-Based Assay for Homologous Recombination in Mammalian Cells



# A Plasmid-Based Assay for Homologous Recombination in Mammalian Cells



# Virtually all case/control HCR studies have monitored Nucleotide Excision Repair (NER)

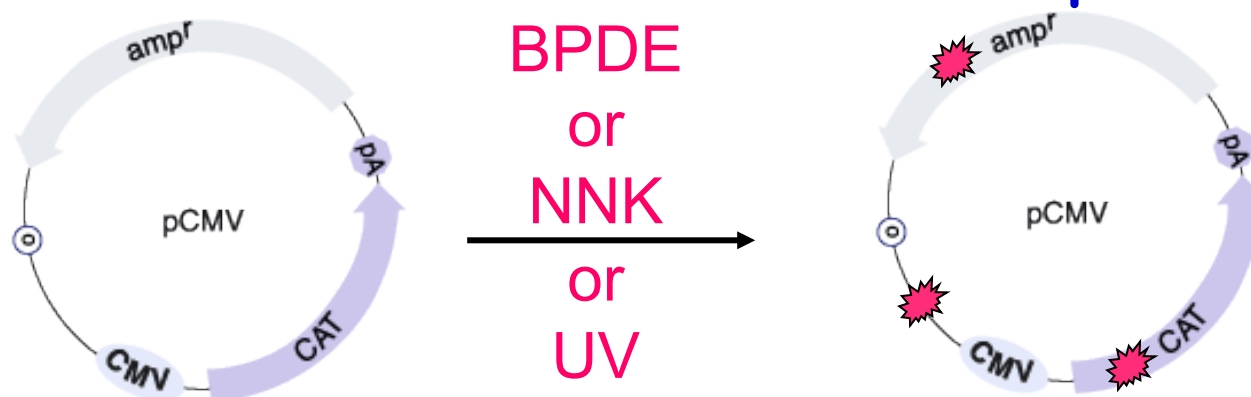
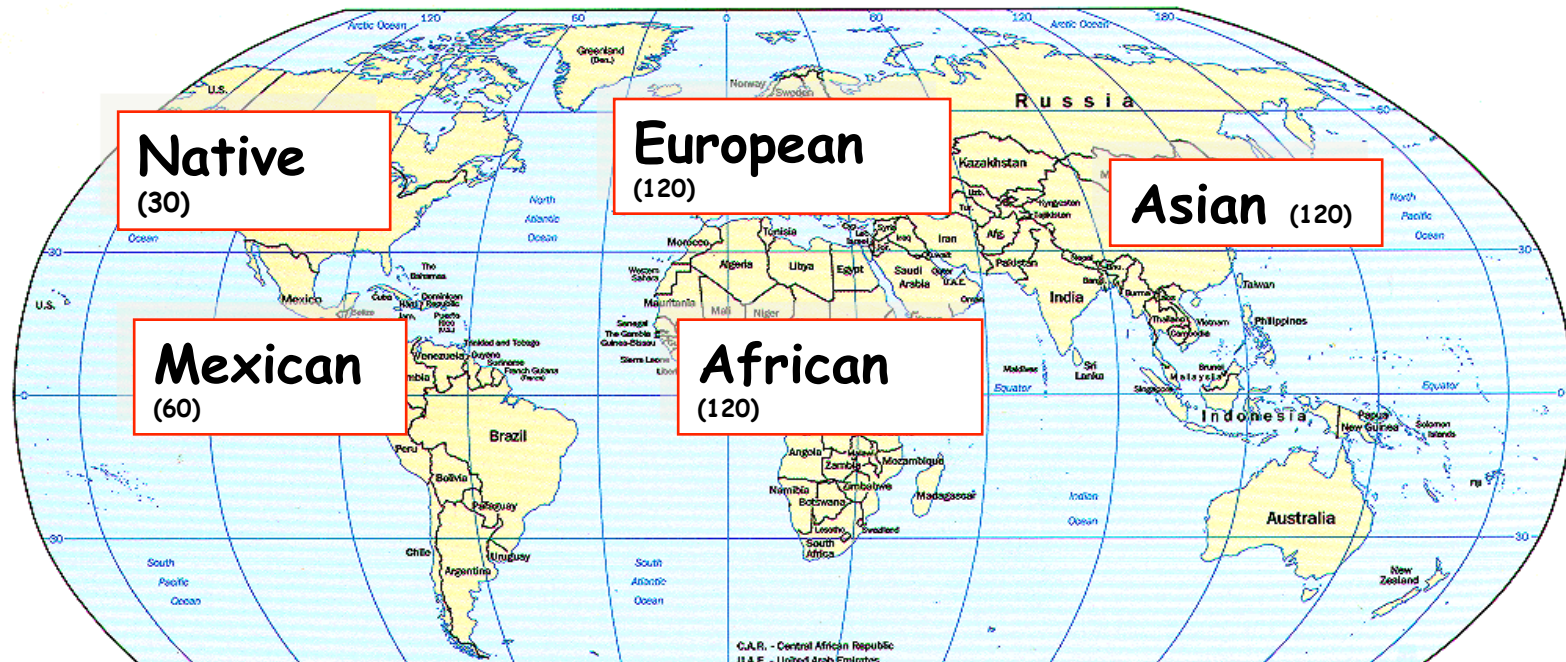


TABLE III – HCR-DRC FOR RISK OF CANCERS

Mutagen	Cancer type	Number Case/control	Risk estimate	Reference
BPDE	Lung	51/56	5.70 (2.10–15.7)	Wei <i>et al.</i> 1996 <sup>25</sup>
	Lung, nonsmall cell	467/488	1.85 (1.42–2.42)	Shen <i>et al.</i> 2003 <sup>58</sup>
	Lung	764/677	1.50 (1.10–3.10)	Spitz <i>et al.</i> 2003 <sup>37</sup>
	SCCHN	55/61	2.20 (1.02–4.77)	Cheng <i>et al.</i> 1998 <sup>61</sup>
	Breast	69/79	3.36 (1.15–9.80)	Shi <i>et al.</i> 2004 <sup>64</sup>
NNK	Lung, adenocarcinoma	48/45	3.21 (1.25–8.21)	Wang <i>et al.</i> 2007 <sup>59</sup>
UV	BCC	146/333	1.62 (1.07–2.45)	Wang <i>et al.</i> 2007 <sup>63</sup>
	SCC	109/333	1.63 (0.95–2.79)	
	CM	312/324	2.02 (1.45–2.82)	Wei <i>et al.</i> 2002 <sup>62</sup>

BPDE, benzo(a)pyrene diol epoxide; UV, ultraviolet; SCCHN, squamous cell carcinoma of head and neck; BCC, basal cell carcinoma; SCC, squamous cell carcinoma; CM, cutaneous melanoma.

# Coriell Lymphoblastoid Cell line collection derived from ethnically diverse HEALTHY humans

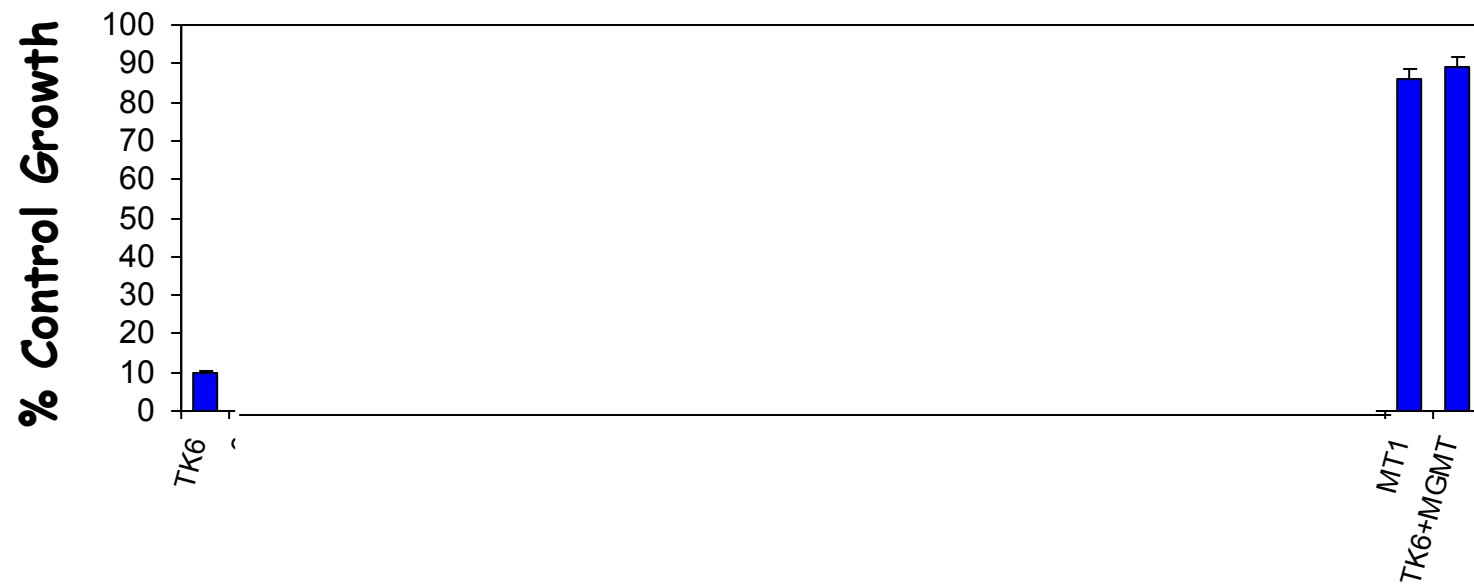


**450 healthy unrelated US residents with ancestry from around the globe**

Nested subsets: 90, 44, **24**, 8

Ethical reasons: no medical, phenotypic, or ethnic information is provided

# Extensive Range of Sensitivity in Cells Exposed to Alkylation Damage - **Control** Cell Lines



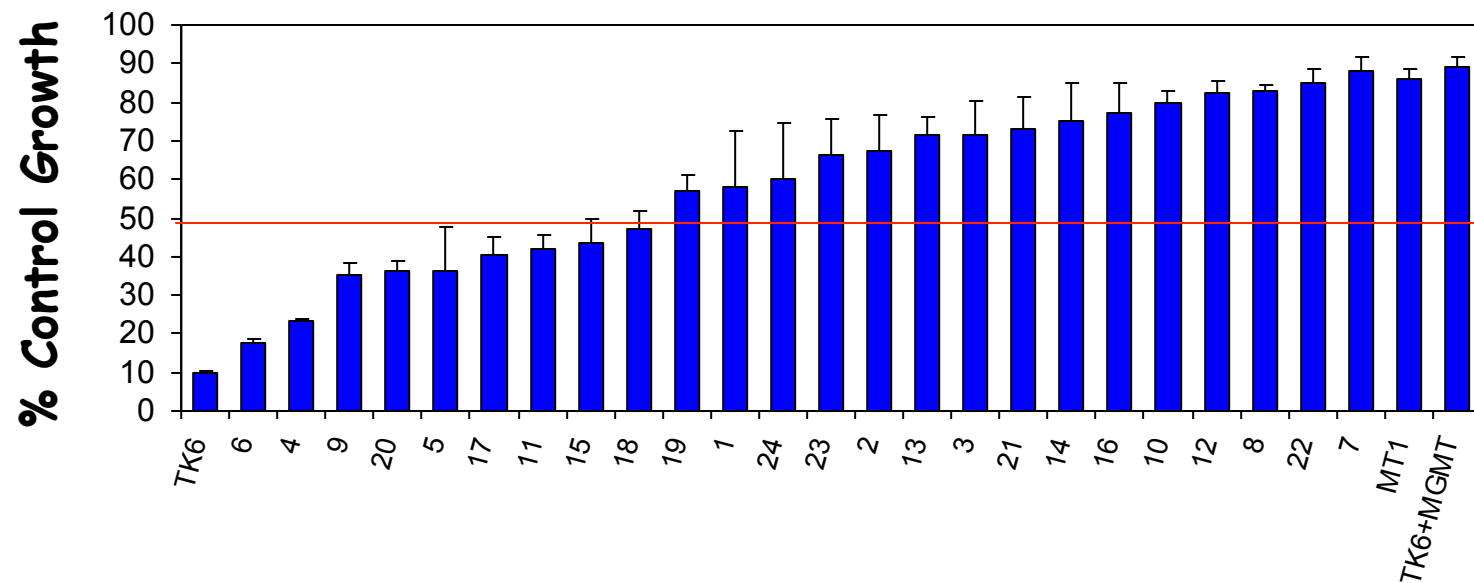
**Sensitive**

To MNNG

**Resistant**

To MNNG

# Extensive Range of Sensitivity in Cells Exposed to Alkylation Damage - **Coriell** Cell Lines



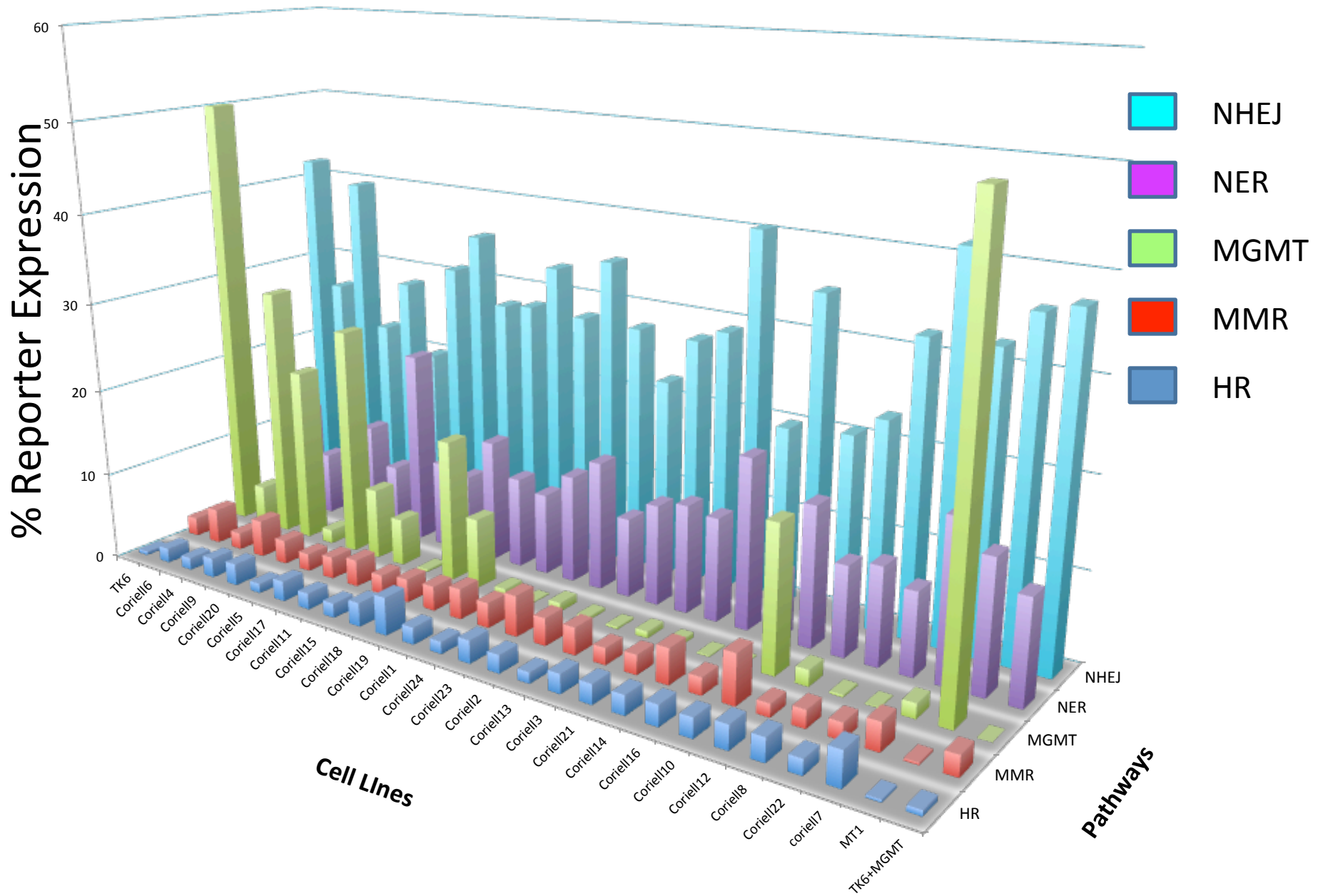
**Sensitive**

To MNNG

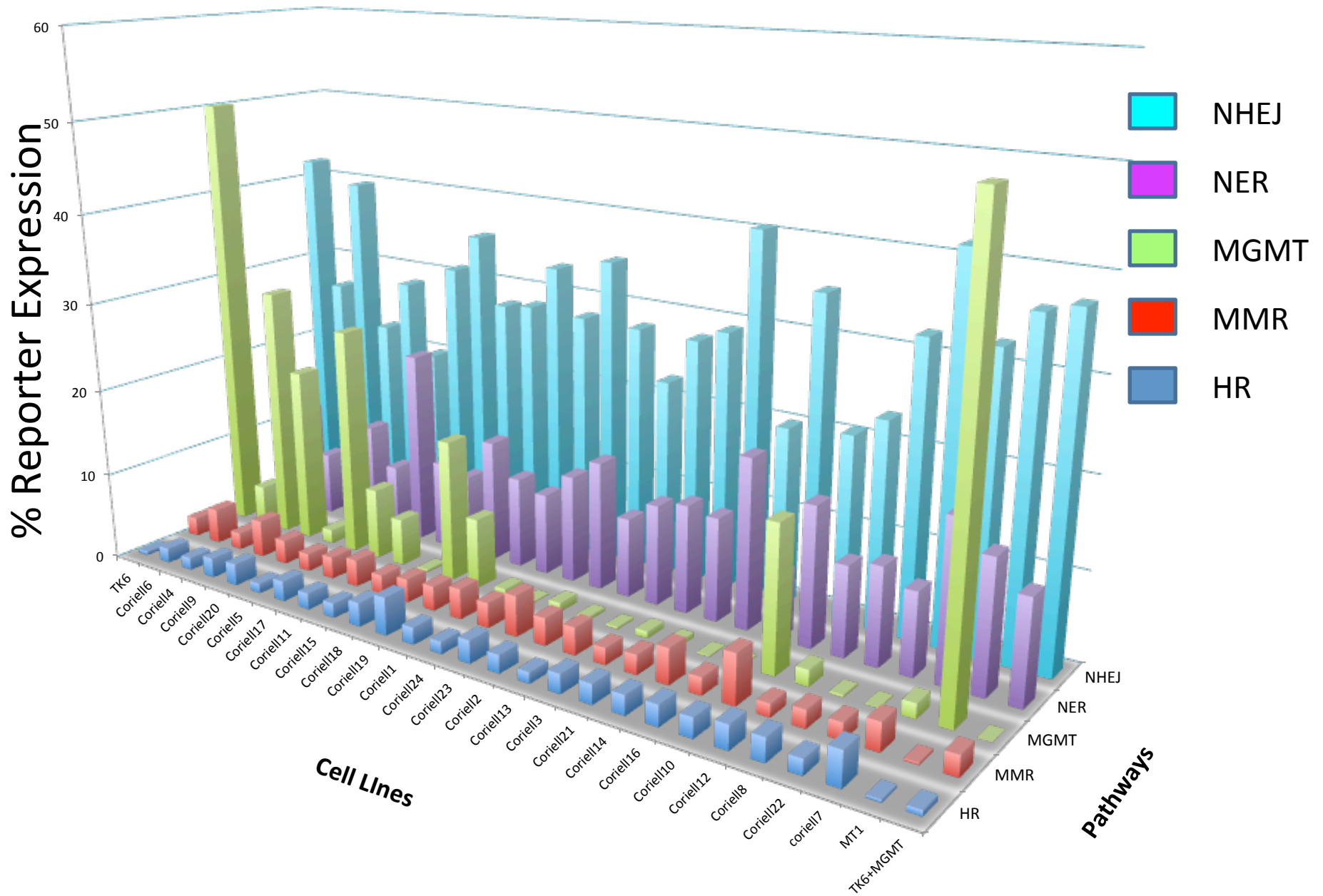
**Resistant**

To MNNG

# DRC vs. MNNG sensitivity



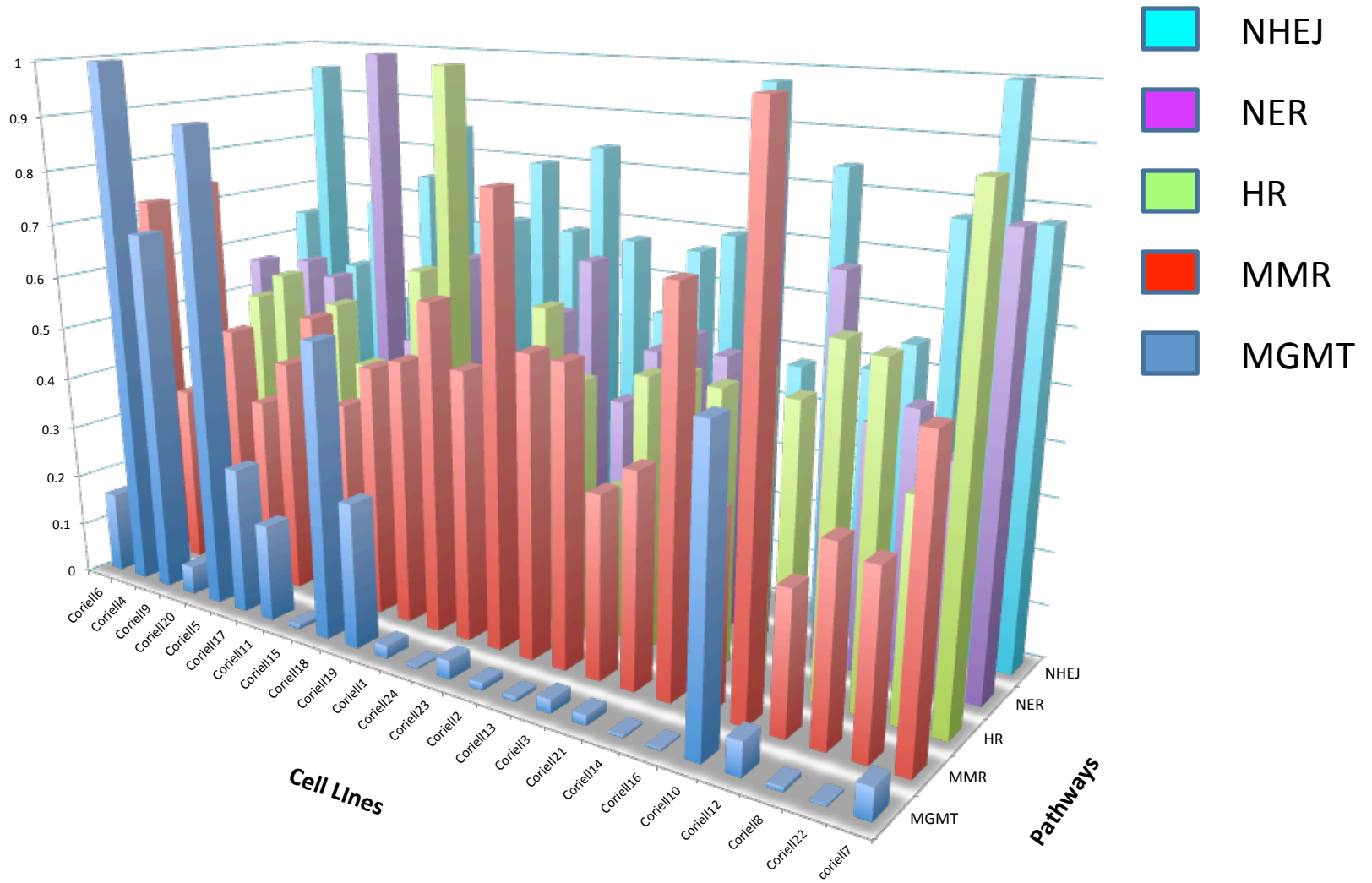
# DRC vs. MNNG sensitivity



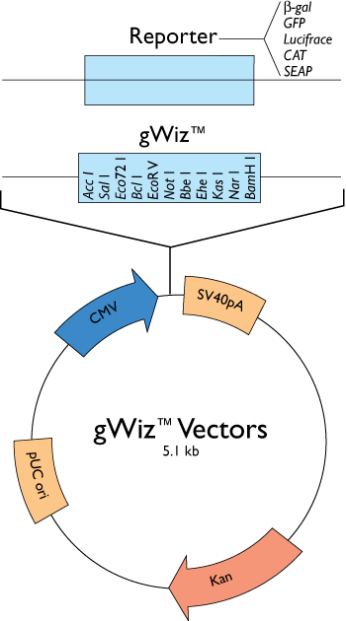


# DRC vs. MNNG sensitivity

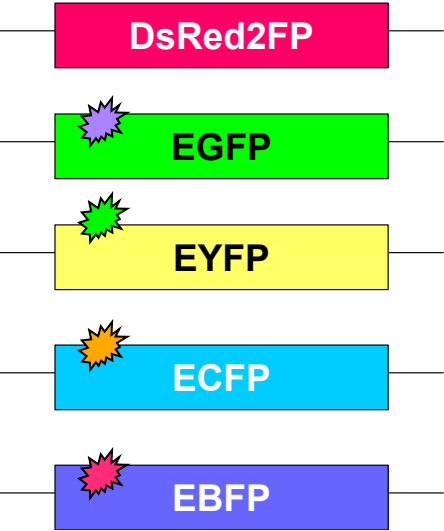
% Reporter Expression



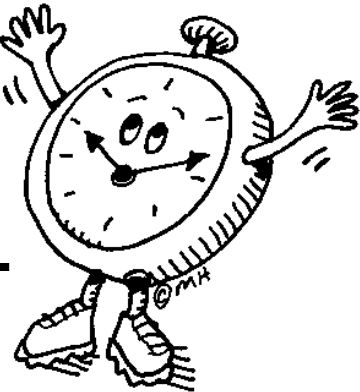
# Reactivation of damaged DNA - multiplexed



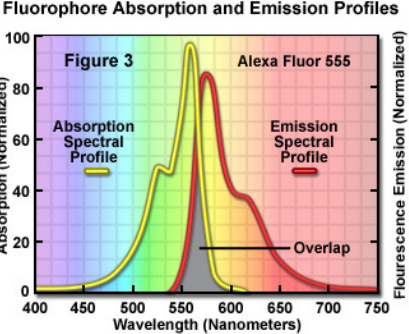
+ different DNA lesions



Transient transfection of mixture

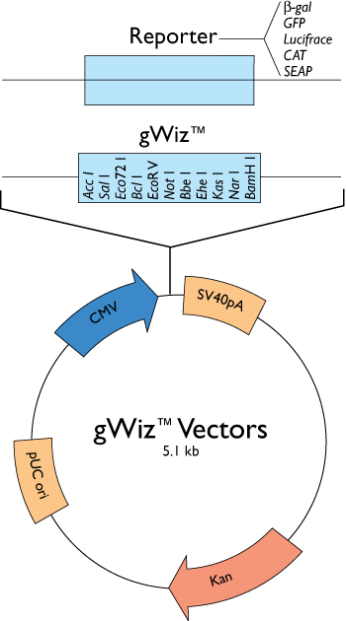


Time to repair

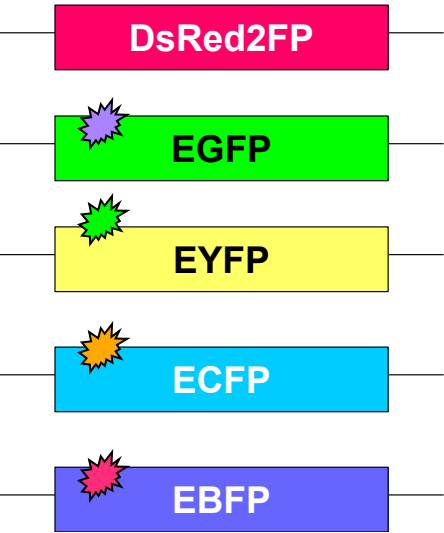


Fluorescence quantitation

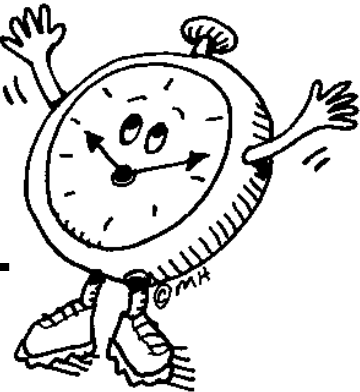
# Reactivation of damaged DNA - multiplexed



+ different DNA lesions



Transient transfection of mixture



Time to repair



Next Gen Sequencing

# DNA Repair Strategies

- Direct Reversal

Methyltransferase, Oxidative demethylase

- Excision Repair

Base excision, nucleotide excision, mismatch repair

- Double strand break repair

Homologous recombination, Non-homologous end joining

# The Pioneer Team



Dr. Zachary Nagel



Carrie  
Thompson



Dr. Anwaar  
Ahmad



Isaac (Alex)  
Chaim



Patrizia  
Mazzucato



Siobhan  
McRee

Thanks to the NIH Director's Pioneer Award & the NIEHS!!!

# DNA lesions from an RNA polymerase perspective

Block Transcription



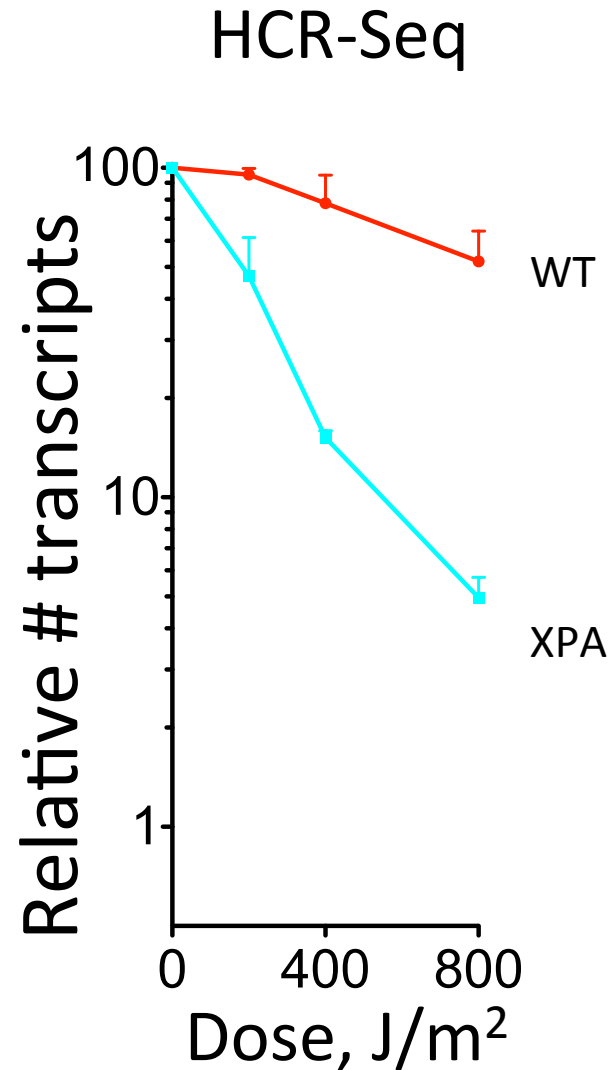
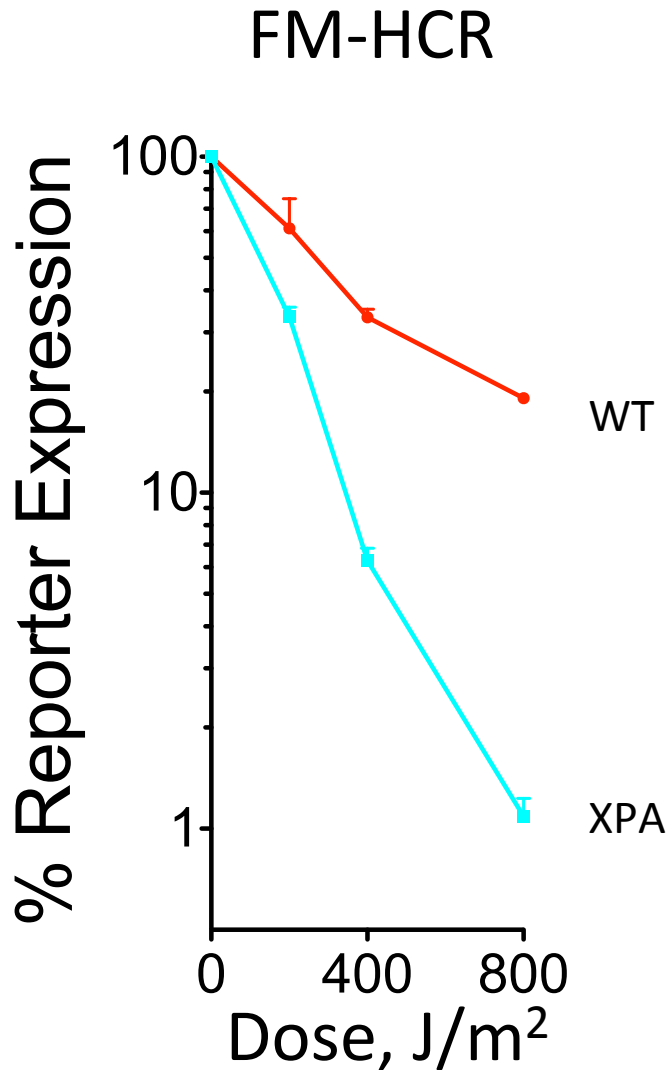
Transcriptional Mutagenesis



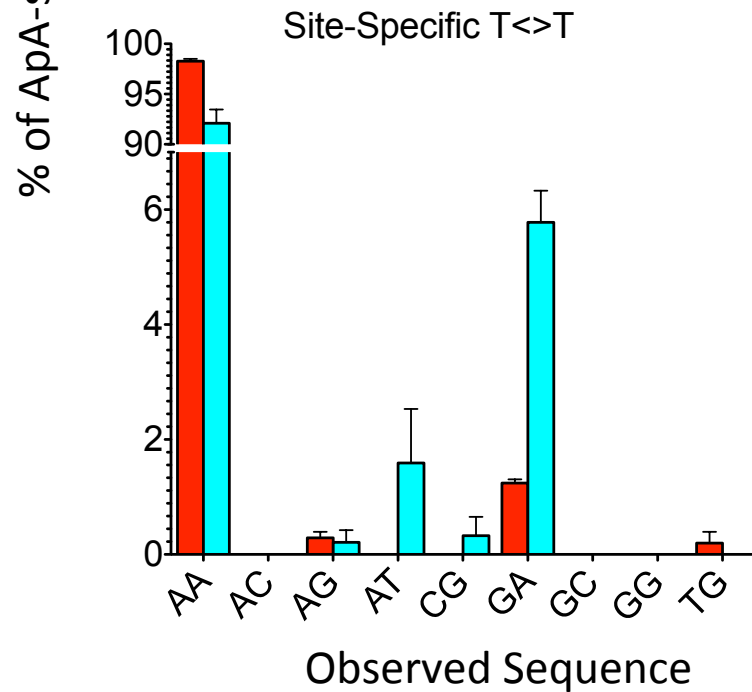
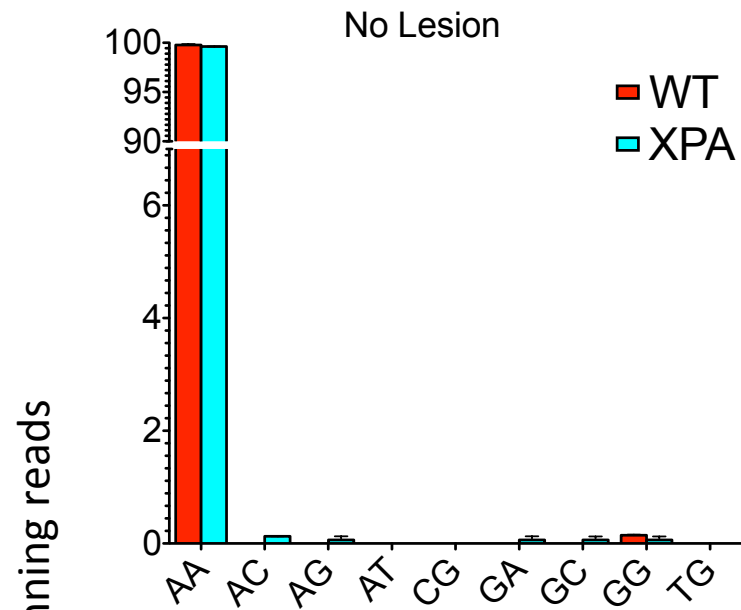
Error-free Bypass



# Dose-dependent reporter protein and reporter transcript expression from irradiated plasmids:

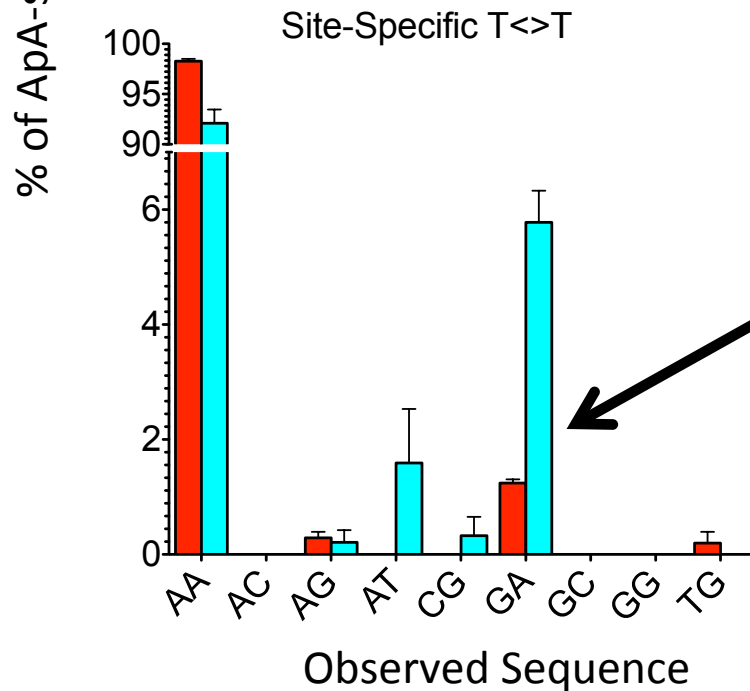
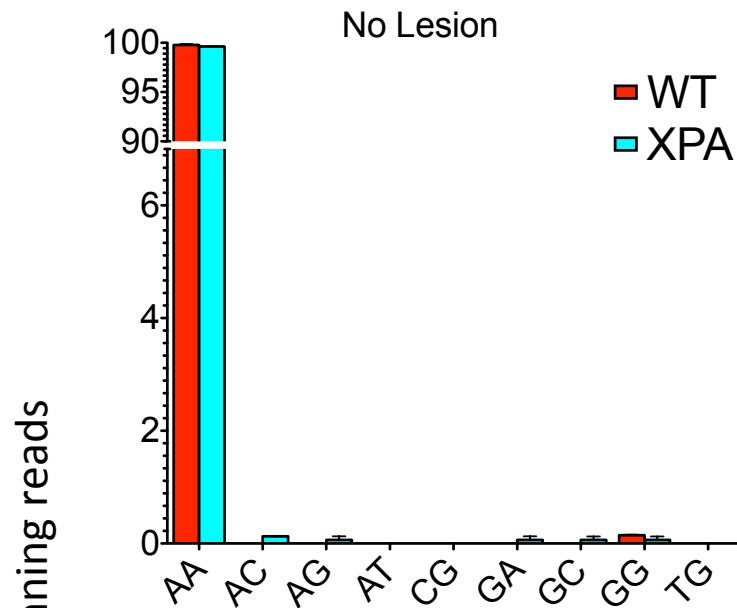
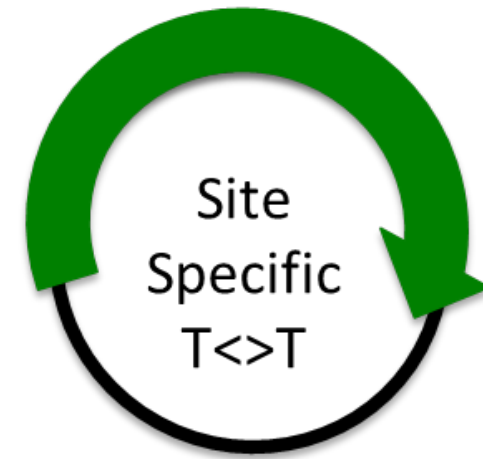


Transcriptional errors are induced by a site-specific thymine dimer



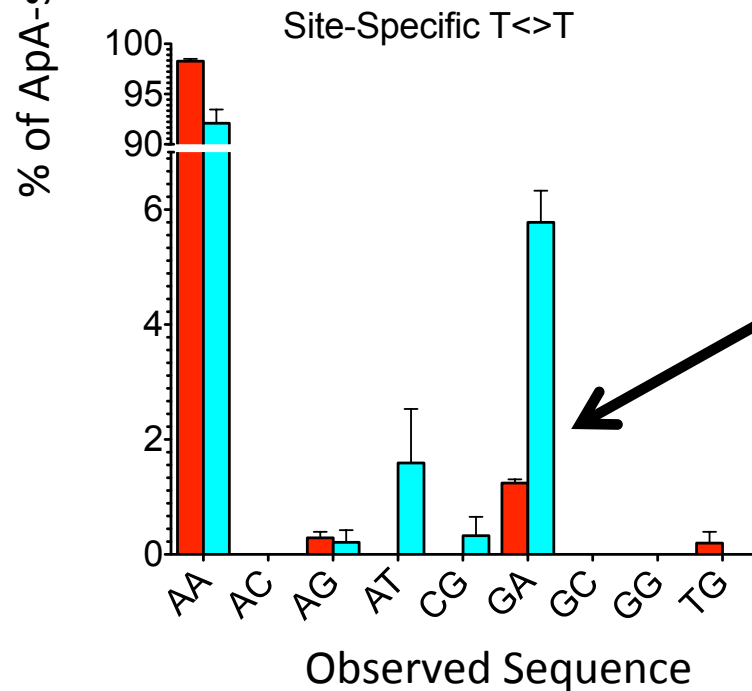
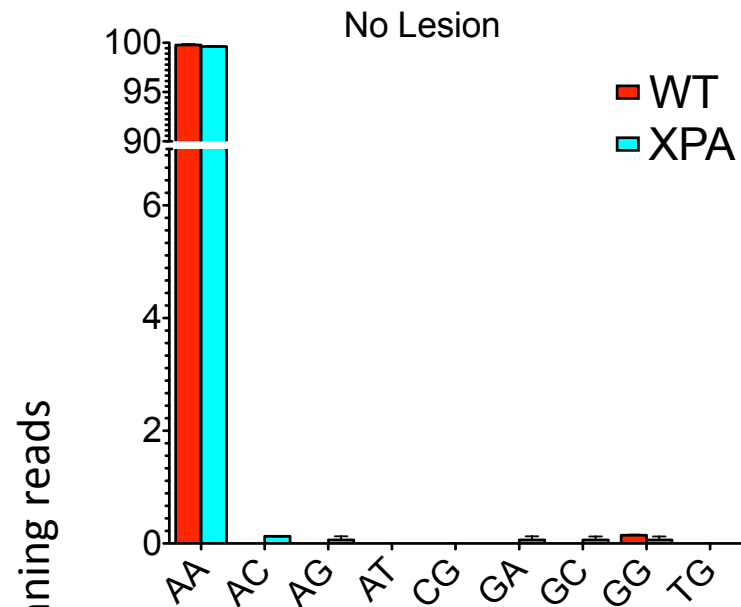
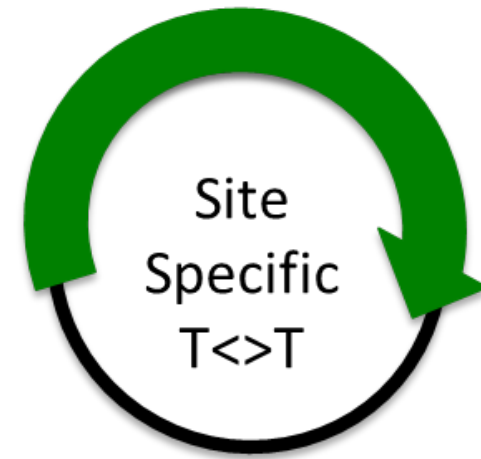


Transcriptional errors are induced by a site-specific thymine dimer



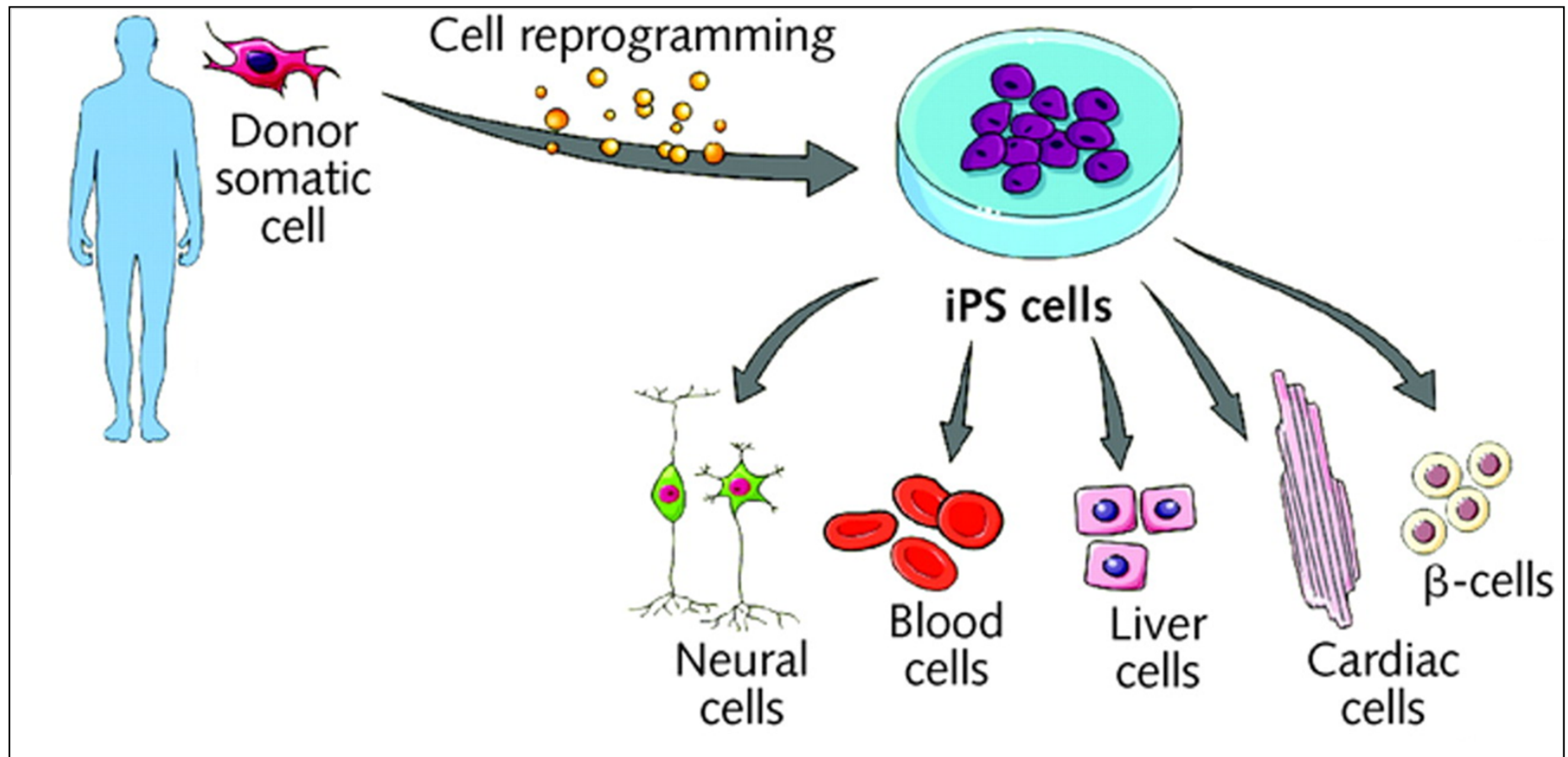
AA → GA was the most frequently observed sequence change

Transcriptional errors are induced by a site-specific thymine dimer



Transcriptional errors are more frequent in the NER-deficient XPA cells

Ultimately want to measure DRC for every major DNA repair activity in many different cell types - ideally derived from each individual



Modified from Power C , Rasko J E Ann Intern Med 2011;155:114-121