

## RADIATION GENOMIC RESEARCH IN THE LABORATORY OF NUCLEAR PROBLEMS

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Fig. 1. Natural and artificial sources of radiation

#### INTRODUCTION

In the modern world, living organisms are increasingly exposed to various sources of radiation. This is facilitated by the use of radiation in medicine, civil and military industries, as well as the presence of a radiation background in nature.

The increased risk of genetic damage to living organisms makes radiobiological research more actual. And the simplest and most suitable object is the fruit fly.



#### **METHODOLOGY**



Irradiation of Drosophila melanogaster males with gamma-rays <sup>60</sup>Co



De novo mutations at the genome level



## Fig. 2. Stages of experiment



**DNA** libraries

#### **METHODOLOGY**

NovaSeq 6000

sequencer

from Illumina

Coverage					
	ezh ezh ezh	6.001 6.001	8.8/2 8.8/21	140 140	8.30° 8.570
ALC: 1014 (144)	PV74	WW FW	PV7 Alley Pribe	PVY Abrev RGV	
MS_0/1010			strend merchanise to be a first		
Variants:		A			
HIV	GCAUTGCGGATGGCATACGACATAGGAGAAAC	T-GAGA GCCAACTGTGATG	A · ATGGGCTTAIGGTT	CATTGAAAATGGAAC-CICGCCAAA	LIGTCAACGGA A
HIT HISEQ 1.	- G CAGTG CGG ATGGC ATAC G A CATAGG A GA A A C - G CAGTG CGG ATGGC ATACG A CATAGG A GA A A C	T - G A G A T C C A A C T G T G A T G T - G A G A T O C C A A C T G T G A T G	A - A T G G G C T T A T G G T T T G G A - A T G G G C T T A T G G T T T G G	Name: G Type: Polymorphism	GTCAACGGA A
*** HISEQ:196	G GCATACGACATAGGAGAAAAC	T-GAGATG CRACTGTGATG	A A TO GO CITA TO GO TO G	Track: Variants: 151417_SND405_8_L008_HKU-2_8	GTCAACGGAGTT-TGGGTTA
117 -HISEQ.1.	- A A G C A G A A G A C G G C A T A C G A G A T A G G A G A A A C	T-GAGATGC Type: Polymorphism	TIGG	Length: 1 [ Interval: 9.304 (8.916)	G TCAACGGA A
HIV	- GCAGTGCGGATGGCATACGACATAGGAGAAAC	T - G A G A T G C Track: Variants: 15141 T - G A G A T G C Length: 1	7_SND405_8_L008_HXU-2_K TGG	Bases: U	GTCAACGGAGTT-TGGGTTA
+rv HISEQ:196_	- GC GGCATACGACATAGGAGAAAAC	T-GAGATG (Interval: 200 (8,853)	TGG	Reference Nudeo tide(s): T	GTCAACGGAGTT-TGGGTTA
H5EQ196_	GCAGTGCGGATGGCATACGACATAGGAGAAAC	T - G A G A T G G Bases: G T - G A G A T G G Change: G ⇒ A	1661	Reference Frequency: 98.1%	GTCAACGGAGTT-TGGGTTA
an	-GAGCAGCAGACGGCATACGACATAGGAGAAAC	T - G A G A T G C Reference Nucleotide	s): G TGG	Variant Nucleotide(s): G	GTCAACGGC A
H5[Q:196.	-GCAGTGCGGATGGCATACGACATAGGAGAAAC	T - G A G A T G G Reference Frequency: T - G A G A T G G Coverage: 32,694	1661	Variant Frequency: 1.1% Variant Raw Frequency: 284	ATCAACGGAGTT-TGGGTTAT
HISEQ 196-	- GCAGTGCGGATGGCATACGACATAGGAGAAAC	T - G A G A T G Variant Nucleotide(s):	A TGGT	Strand-Blas: III.4%	ATCAACG GAGTT-TG GGTTAT
HISEQ:196_	·· GCAGTGCGGATGGCATACGACATAGGAGAAAC	T- GAGATG Variant Raw Frequency	r5'935 TGGT	Strand-Blas > 50% P-value: 2.7 x 10 <sup>11</sup>	ATCAACGGAGTT-TGGGTTAT
H5EQ:196	-G GCATACGACATAGGAGAAAAC	T - G AG A T G C Strand-Blas: 83.2%	TGG1	Strand-Blas > 65% P-value: 7.9 x 1011	GTCAACGGAGTT-TGGGTTAT
HISEQ 196_	- G GCATACGACATAGGAGAAAAC	T-GAGATGG Strand-Bias > 50% P-vi	due: 0.0 TGG1	Average Quality: 30	GTCAACGGAGTT-TGGGTTAI
H\$19.1%-	-G GGCATACGACATAGGAGAAAC	T - G A G A T G C Polymorphism Type S	NP (transition)	GCATTGAAAATGGAAC-CTCGCCAAA	TGTCAACGGAGTT IGGGTTAT
H510.1%	-G GGCATACGACATAGGAGAAAAC	T - G A G A T G Q Average Quality: 37	TGGT	GCATTGAAAATGGAAC · CTCGCCAAA	TGTCAACGGAGTT-TGGGTTAT
W HStolig_	- 6 GG CATACG ACATAG GAGAAAAC - 6 GG CATACG ACATAG GAGAAAAC	T-GAGATGCCAACTGTGATG	A ATGG GCTTATG GTTTGGT	IG CATTGAAAATGGAAC - CTCGCCAAA IG CATTGAAAATGGAAC - CTCGCCAAA	TG TCAACG GAGTI - TG GGTTAT TG TCAACG GAGTT - TG GGTTAT
H5EQ:196_	-GC GCATACGACATAGGAGAAAAC -G GGCATACGACATAGGAGAAAC	T-GAGATGCCAACTGTGATG T-GAGATGCCAACTGTGATG	A - A T G G G C T T A T G G T T T G G T A - A T G G G C T T A T G G T T T G G T	IGCATTGA AAATGG AAC - CTCG CCAAA IG CATTGAAAATGG AAC - CTCG CCAAA	TG TCAACGGAG TT - TG GG TTA TG TCAACG GAGTT - TG GG ITA
H510,196	-G GGCATACGACATAGGAGAAAC GGCATACGACATAGGAGAAAAC	T-GAGATGCCAACTGTGATG T-GAGATGCCAACTGTGATG	A - ATGG GCTTATG GTTTGGT A - ATGG GCTTATG GTTTGGT	G CATTGAAAATGGAAC - CTCGCCAAA G CATTGAAAATGGAAC - CTCGCCAAA	TG TCAACG GAGTT - TG GGTTAT
*** H5EQ-196_	GC GCATACGACATAGGAGAAAAC	T-GAGATGCCAACTGTGATG	A - ATG GGC TTATG GTTTGG 1	GCATTGAAAATGGAAC - CTCGCCAAA	TG TCAACGGAG TT - TG GG TTAT
HISEC 196-	-G GCATACGACATAGGAGAAAAC	- GAGATOCCAACTOTGATO	ATGGGCTTATGGTTTGGT	G CATTGAAAATGGAAC - CTCGCCAAA	TO TCAACO GAOTT - TO GOTTA
HISEQ 196_	- G GGCATACGACATAGGAGAAAC	I-GAGATGCCAACTGTGATG	A - A T G G G C T T A T G G T T T G G T	G CATTGAAAATGGAAC - CTCG CCAAA	TG TCAACG GAGTT - TG GGTTAI
HISEQ1	G CAGTG CGG ATGGC ATACGACATAGG AGAAAC G CAGTG CGG ATGGC ATACGACATAGG AGAAAC	T-GAGATGCCAACTGTGATG	A - ATGG GCTTATGG TTTG GT	ITCATTGAAAATGGAAC CTCGCCAAA	CATCAACGGAGTT-TGGGTTAT
H51Q-196-	-GCAGTGC CGACATAGGAGAAAAC	T- GAGATGCCAACTGTGATG	A - ATG GGCTTATG GTTTGG I	IGCATTGAAAATGGAAC - CTCGCGAAA	TGTCAACGGAGTT-TG
#39 HISEQ:196	-GCAGTGC CGACATAGGAGAAAC	T- GAGATGCCAACTGTGATG	A - ATG GGCTTATG GTTTGG1	GCATTGAAAATGGAAC-CTCGCCAAA	TGTCAACGGAGTT- TG
HSEQ:190.	-GCAGTGC CGACATAGGAGAAAAC	T-GAGATGCCAACTGTGATG	A - A T G G G C T T A T G G T T T G G T	IGCATTG AAAA TG GAAC - C TCG CCAAA IGCATTG AA AA TG GAAC - C TCG CCAAA	TGTCAACGGAGTT-TGGGTTAT
HIV -HISEQ-1	G GGCATACGACATAGGAGAAAC	T- GAGATGCCAACTGTGATG	A - ATG GG CTTATGGTTTG GT	GCATTGAAAATGGAAC - CTCGCCAAA	TOTCAACGGAGTT TEGGTTAT
HISEQ:196-	CAGTG CG GATGG CATACGACATAG GAGAAAC	- GAGATGCCAACTGTGATG	A ATGGGCTTATGGTTTGG	ITCATTGAAAATGGAAC- CTCGCCAAA	CATCAACGGAGTT-TGGGTTAT
IND HISECCI.	G A TG G CATACGACATAGG AGAAAC G CAGTG CGG A TG G CATACGACATAG G AGAAAC	T - GAGATGCCAACTGTGATG T - GAGATGCCAACTGTGATG	A - A T G G G C T T A T G G T T T G G T A - A T G G G C T T A T G G T T T G G T	ITCATTGAAAATGGAAC - CTCGCCAAA ITCATTGAAAATGGAAC - CTCGCCAAA	CATCAACGGAGTT-TGGGTTAT
HISEQ 1	GCAGTGCGGATGGCATACGACATAGGAGAAAC	T-GAGATGCCAACTGTGATG	A - ATGGGCTTATGGTTTGGI	TCATTGAAAATGGAAC- CTCGCCAAA	CATCAACGGAGTT- TGGGTTAT
HISEQ 196_	-GCAGTGC CGACATAGGAGAAAC	I-GAGAIGCCAACIGIGAIG	A - A TO GOCTTATO GITTOGI	IG CATTG AAAATG GAAC - C TCG CG AAA I G CATTG AAAATG GAAC - C TCG CG AAA	TGTCAACGGAGTT-TG
H5EQ:196	-GCAGTGC CGACATAGGAGAAAC	T-GAGATGCCAACTGTGATG	A - ATG GGCTTATG GTTTGG I	GCATTGAA AATGGAAC - CTCGCGAAA	TG TCAACG GAG TT-TG
400	G GCATACGACATAGGAGAAAC	I-GAGATGCCAACTGTGATG	A-ATGGGCTTATGGTTTGGT	IGCATTGAAAATGGAAC-CTCGCCAAA	TGTCAACGGAGTT- TGGGTTA
H5EQ:1%	GCAGIGCGGAIGGCAI AGAAAC	T-GAGATGCCAACTGTGATG	A - ATGGGCTTATGGTTTGGT	GCATIGAAAATGGAAC-CTCGCCAAA	IGICAACGGAGIT-TGGGTTA
HISEQ.196_	GCAGTGCGGATGGCAT AGAAAC	T-GAGATGCCAACTGTGATG	A - ATGGGCTTATGGTTTGGI	IG CATTGAAAATGGAAC - CTCGCCAAA	TGICAACGGAGTT-TGGGTTA
HISEQ 196	GCAGTGCGGATGGCATACGACATAGGAGAAAC	T- GAGATGCCAACTGTGATG	A-AIGGGCTTAIGGITTGG	I CATTGAAAATGGAAC-CTCGCCAAA	CATCAACGGAGTT-TGGGTTA
HISEQ:196	GCAGTGCGGATGGCAT AGAAAC	T- GAGATGCCAACTGTGATG	A - ATGGGCTTATGGTTTGG	IGCATTGAAAATGGAAC CTCGCCAAA	TGTCAACGGAGTT-TGGGTTA
HISEQ 196.	- GCAGTGC GACATAGGAGAAAC	T GAGATGCCAACTGTGATG	A - A T G G G C T T A T G G T T T G G T	IG CATTGAAAATGGAAC - CTCGCCAAA IG CATTGAAAATGGAAC - CTCGCGAAA	TGTCAACGGAGTT-TGGGTTA
ATT HISEQ 196	-GCAGTGCGGATGGCAT AGAAAC	T- GAGATGCCAACTGTGATG	A-ATGGGCTTATGGTTTGG	IGCATTGAAAATGGAAC- CTCGCCAAA	TGTCAACGGAGTT- TGGGTTA





Fig. 4. The number and type of changes for each sample

Fig. 5. Localization and distribution of the changes over the genome

FOR

The methods chosen in the experiment, correctly selected protocols and highquality execution made it possible to successfully conduct a pilot experiment.

To a first approximation, we can say that

1. Radiation increases the occurrence of small deletions by 3.5 times. 2. Such types of changes as large deletions, inversions, duplications and translocations are characteristic of radiation mutagenesis.

1. Continued bioinformatics analysis of minor DNA substitutions, indels).

2. An increase in the sample of the control and gamma-induced groups to obtain not only a qualitative picture, but also quantitative dependences.

3. Conducting experiments with neutrons and carbon ions to reveal the role of various types of radiation in mutagenesis at the genome level.

### **CONCLUSIONS and PERSPECTIVES**

- changes (base



# THANK YOU FOR YOUR ATTENTION!

