

# Resource update

Ian Bancroft 9<sup>th</sup> May, 2018

**Oilseed Rape Genetic  
Improvement Network  
(OREGIN) – Phases 4 & 5**

CH0104



**BBSRC Renewable Industrial  
Products from Rapeseed (RIPR)  
Programme**

BB/L002124/1



# OREGIN Phase 4 (extension)

The overall aim is to underpin the genetic improvement of the UK rapeseed crop by:

- Maintaining and expanding interactions between stakeholders and academics
- Provide freely-available physical resources to underpin rapeseed breeding
- Provide freely-available information resources to underpin rapeseed breeding
- Associate trait variation measured in field trials with molecular markers



# 2017/18 OREGIN field trials

<b>OREGIN Phase 4 Annex Table 1. Summary of trait measurements across field trials</b>				
	SOSR UoR	SOSR Elsons	WOSR NIAB	WOSR Elsons
<i>Main function</i>	Rooting, quality, disease	Backup trial	Rooting, NUE, quality, disease	Backup trial
<i>Drill date</i>	3/18	3/18	9/17	9/17
<i>Location</i>	Reading	Scotland	TBA	Harlexton
<i>Fungicide (Treated/Untreated)</i>	T, U	T	T, U	T
<i>N fertiliser (Standard/low)</i>	S	S	S, L	S
<i>Plot size</i>	2 x 12m	12 x3m	12x3m	12 x3m
<i>Number of varieties</i>	100	100	200	200
<i>Rep number</i>	3	3	3	3
<i>Plot number</i>	300	300	600	600
<i>Seed rate</i>	100s/m <sup>2</sup>	100s/m <sup>2</sup>	70s/m <sup>2</sup>	70s/m <sup>2</sup>
<i>Seed number required</i>	5400	5400	7560	7560
Light leaf spot	✓	✓	✓	
Phoma	✓	✓	✓	
Verticillium	✓	✓	✓	
†Rooting			✓	
Seed protein	✓		✓	
Seed oil & fatty acid profile	✓		✓	
Yield at standard N		✓		✓
Yield at low N	✓		✓	
Pest interactions (RRes)			✓	
Pest interactions (JIC)			✓	

†measure on a subset of 100 lines, 2 reps

**Contact: [ian.bancroft@york.ac.uk](mailto:ian.bancroft@york.ac.uk)**

# OREGIN Phase 5

The overall aim is to underpin the genetic improvement of the UK rapeseed crop by:

- Maintaining and expanding interactions between stakeholders and academics
- Provide freely-available physical resources to underpin rapeseed breeding
- Provide freely-available information resources to underpin rapeseed breeding
- **Initiate pre-breeding to assess novel genetic variation in WOSR background**



## OREGIN Phase 5

- Phase 5 project runs 1/3/18 to 31/3/23
- SRUC (Fiona Burnett) brings clubroot pathogen (*Plasmodiophora brassicae*) into core pathogen collection for cost-recovered distribution (alongside *Leptosphaeria maculans*, *L. biglobosa* and *Pyrenopeziza brassicae*); *Verticillium* will also be contributed to pathogen collection by NIAB
- Analysis of heterosis in spring x winter hybrid OSR (Limagrain)
- Field trials reduced to ~30 *B. napus* accessions shown in previous phases to differ for key traits plus ~14 new accessions not previously analysed (2019/20) and early-stage pre-breeding lines (2020/21, 2021/22)
- Sponsorship of UK-BRC meetings and annual Stakeholder Forum, distribution of DFFS lines, trait and molecular data provision all as in previous phases

# OREGIN Phase 5

## Harmonisation across GINs

### 4 Activities specified by Defra:

- **Activity 1 – Stakeholder network**
- **Activity 2 – Genetic tools and resources to address challenges**
- **Activity 3 – Develop and exploit opportunities for further research**
- **Activity 4 – Effective dissemination and knowledge exchange**

### 4 Challenge areas to be addressed:

- **Resource efficiency**
- **Sustainability**
- **Resilience**
- **Quality traits**

# OREGIN Phase 5

## Harmonisation across GINs

### 4 Activities specified by Defra:

- Activity 1 – Stakeholder network
- Activity 2 – Genetic tools and resources to address challenges
- Activity 3 – Develop and exploit opportunities for further research
- Activity 4 – Effective dissemination and knowledge exchange

### 4 Challenge areas to be addressed:

- Resource efficiency
  - Sustainability
  - Resilience
  - Quality traits
- 
- The diagram shows four challenge areas on the left, each connected by a line to one or more specific sub-areas on the right:
- Resource efficiency is connected to Fertilizer use efficiency.
  - Sustainability is connected to Fertilizer use efficiency and Pest and pathogen resistance.
  - Resilience is connected to Pest and pathogen resistance and Establishment/early vigour.
  - Quality traits is connected to Establishment/early vigour and Seed composition.

# OREGIN Phase 5

## Harmonisation across GINs

### 4 Activities specified by Defra:

- Activity 1 – Stakeholder network
- Activity 2 – Genetic tools and resources to address challenges
- Activity 3 – Develop and exploit opportunities for further research
- Activity 4 – Effective dissemination and knowledge exchange

### 4 Challenge areas to be addressed:

- Resource efficiency — Fertilizer use efficiency **Low stakeholder priority**
- Sustainability —
- Resilience — Pest and pathogen resistance **Highest stakeholder priority**
- Quality traits — Establishment/early vigour **Lower stakeholder priority**  
Seed composition **Not a stakeholder priority**

# OREGIN Phase 5

## Harmonisation across GINs

### 4 Activities specified by Defra:

- **If you have novel *B. napus* germplasm for pre-breeding evaluation, please contact: [ian.bancroft@york.ac.uk](mailto:ian.bancroft@york.ac.uk)**
- Activity 1 – Develop and exploit opportunities for further research
- Activity 2 – Genetic tools and resources to address challenges
- Activity 3 – Develop and exploit opportunities for further research
- Activity 4 – Effective dissemination and knowledge exchange

### 4 Challenge areas to be addressed:

- Resource efficiency — Fertilizer use efficiency **Low stakeholder priority**
- Sustainability — Pest and pathogen resistance **Highest stakeholder priority**
- Resilience — Establishment/early vigour **Lower stakeholder priority**
- Quality traits — Seed composition **Not a stakeholder priority**

# Data management

**Brassica information portal**  
**bip.earlham.ac.uk**

**Brassica Information Portal**

The Brassica Information Portal is a web repository for population and trait scoring information related to the Brassica breeding community. It provides information about quantitative trait loci and links curated Brassica phenotype experimental data with genotype information stored in external data sources. Advanced data submission capabilities and APIs enable users to store and publish their own study results in our Portal.

Learn more

Search for:  SEARCH

Examples: [plantpop\\_2013\\_0103](#)

- Browse database**  
Browse and query more than 200 thousand trait scores and look for related QTLs in a variety of Brassica subspecies. [BROWSE DATA](#)
- Submit new data**  
Submit your experimental Brassica population data along with scored traits and identified genetic mappings to be published in the Portal. [SUBMIT DATA](#)
- API Documentation**  
Learn how to integrate your own software with our Portal in order to automatically retrieve and submit large quantities of data. [API DOCUMENTATION](#)

Latest user submissions

Submission	Submitted on	DETAILS
Plant scoring trait: Flowering Time QTL Analysis in Brassica napus (BNCORB - Traits scored: flowering time)	Submitted on March 24, 2018 09:49	<a href="#">DETAILS</a>
Plant scoring trait: Ripeness (Brassica napus) (RPR - Traits scored: L271 Na2   B11   P3)	Submitted on February 19, 2018 16:16	<a href="#">DETAILS</a>
Plant scoring trait: Ripeness (Brassica napus) (RPR - Traits scored: L271 Na2   B11   P3)	Submitted on February 19, 2018 16:09	<a href="#">DETAILS</a>
Plant scoring trait: Ripeness (Brassica napus) (RPR - Traits scored: L271 B11   P3   11 Mg)	Submitted on February 19, 2018 16:02	<a href="#">DETAILS</a>
Plant population: 420157-16 (Brassica napus)	Submitted on	<a href="#">DETAILS</a>

**OREGIN information**  
**oregin.info**

University of Hertfordshire UH

**OREGIN**  
 Oilseed Rape Genetic Information Network

defra

Home > Oregin

About OREGIN  
 Information  
 Stakeholders  
 Linkage map  
 Trait data  
 Pathogen Collection  
 Contact OREGIN

**Contact OREGIN**  
 Get in touch with the OREGIN project and see how we can help you.

3/3

**Project outline**  
 See an outline of the OREGIN project to date...  
 Read more about project outline

**Trait data**  
 View and download our trait data table...  
 Read more about trait data

**Contact OREGIN**  
 Contact the team at the OREGIN project...  
 Read more about contact oregin

Top of page

**Rapid data access**  
**yorkknowledgebase.info**

Yorkknowledgebase.info

York Oilseed Rape Knowledgebase

Bancroft group, University of York

Menu

Links to related information resources

[Brassica.info](#) [CropStore](#) [OREGIN new website](#) [OREGIN old website](#)  
[Brassica Information Portal](#)

SRA accession codes

SRA project code	Description
<a href="#">PRJEB2588</a> and <a href="#">PRJEB5294</a>	Leaf mRNAseq from TNDH mapping population
<a href="#">PRJNA309367</a>	RIPR: Brassica napus transcriptome
<a href="#">PRJNA309368</a>	RIPR: Brassicaceae transcriptome

# RIPR

The overall aim is to underpin the economically sustainable exploitation of industrial co-products from oilseed rape whilst improving the environmental sustainability of the crop by underpinning improvement of nutrient use efficiency.



- **Phytosterols and waxes**



- **Tocopherols**



- **Functional polysaccharides**



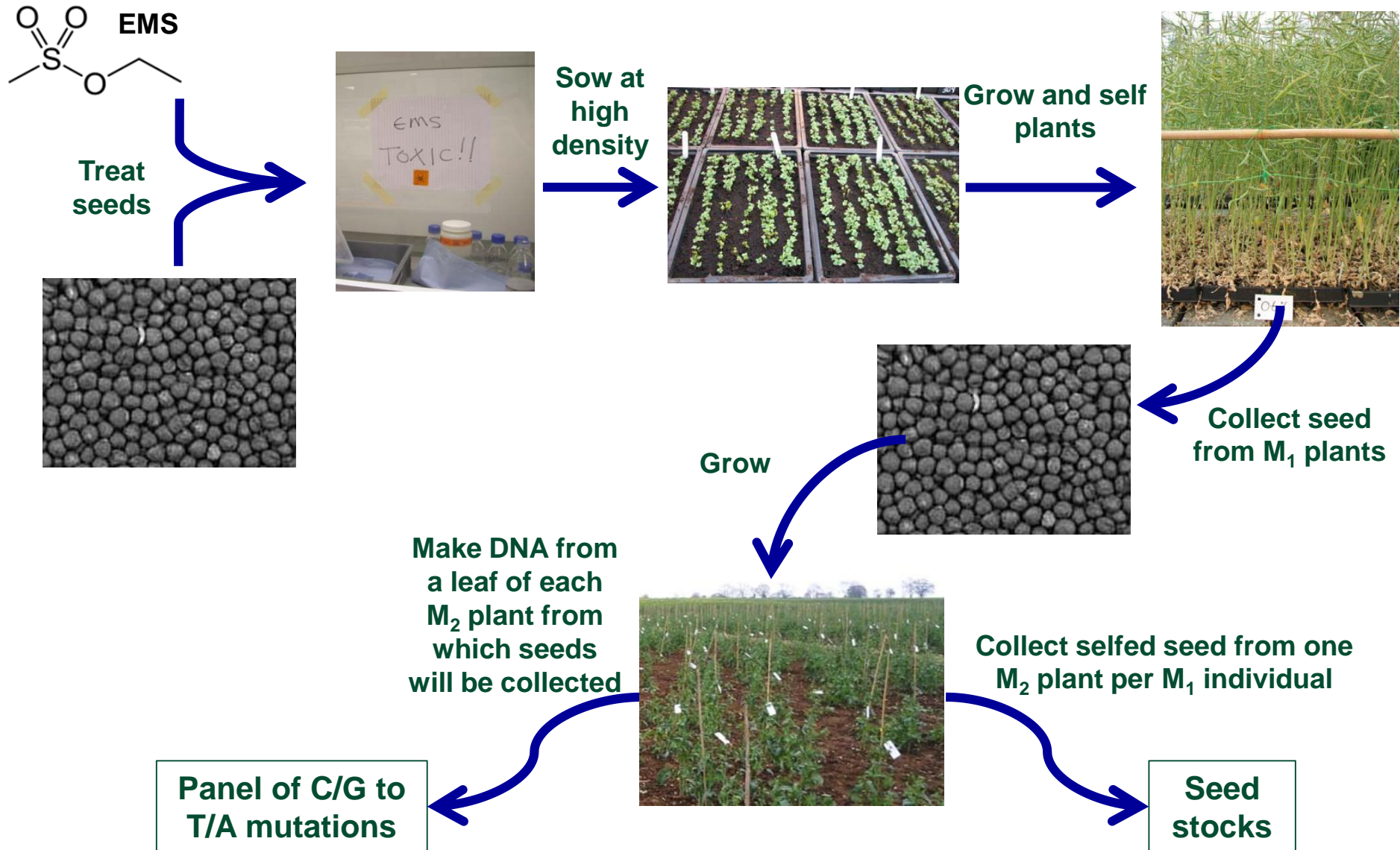
- **Nitrogen use efficiency**



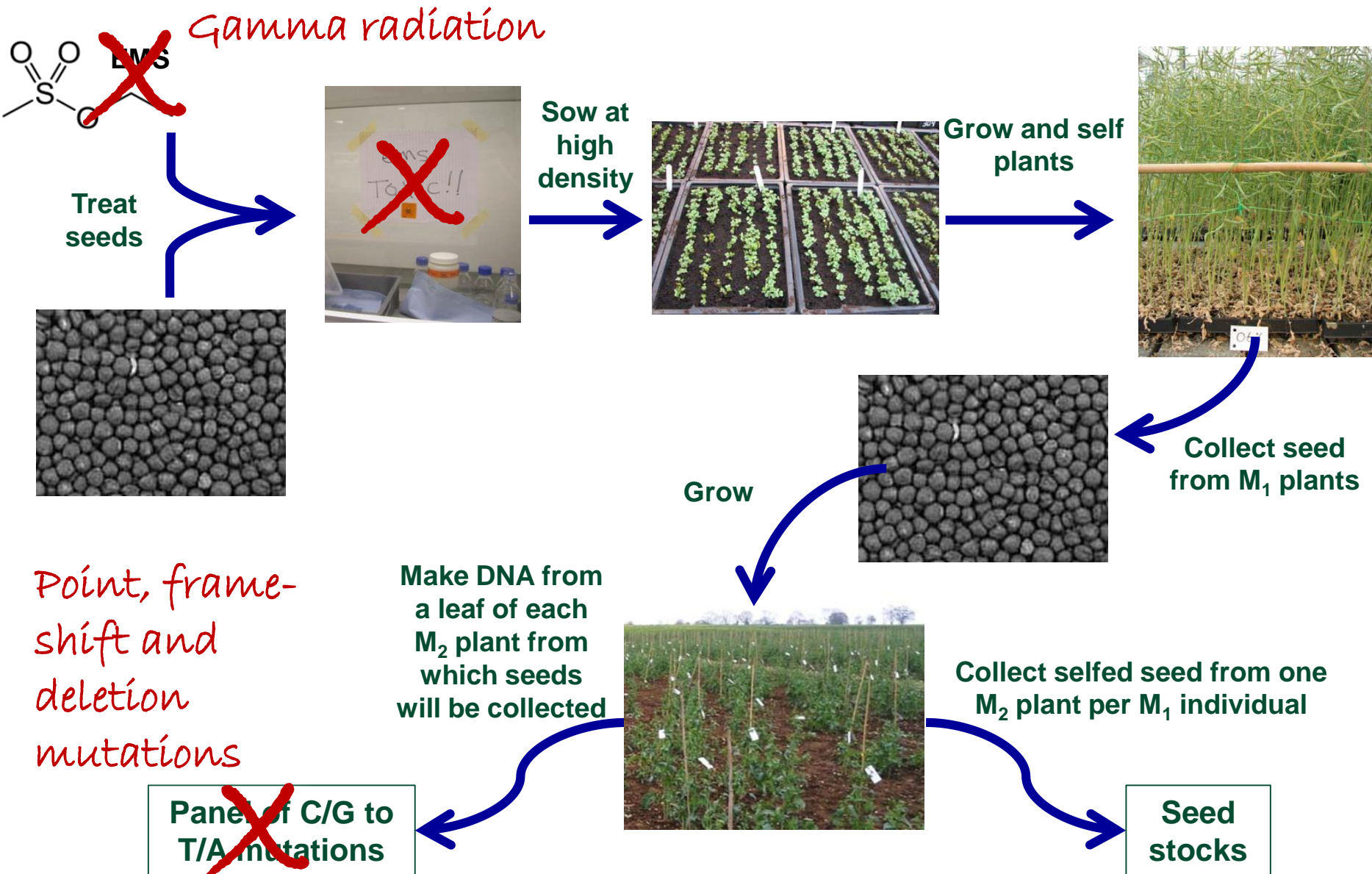
- **Micronutrient use efficiency**



# Genomics-led predictive mutation breeding (TILLING)



# Genomics-led predictive mutation breeding (radiation)



# RIPR-York genome re-sequenced radiation mutagenesis panel

Background genotype: Maplus (OP, high erucic, low glucosinolates, winter oilseed rape)

~800 M<sub>2</sub> lines produced, mostly gamma radiation, produced as part of RIPR

Genome re-sequencing (~12x) and variant scoring under way:

- 16 individual untreated Maplus plants
- 404 M<sub>2</sub> lines genome re-sequenced at BGI
- 188 M<sub>2</sub> lines genome re-sequencing in progress



80 lines in collaboration  
with OCRI-CAAS Wuhan

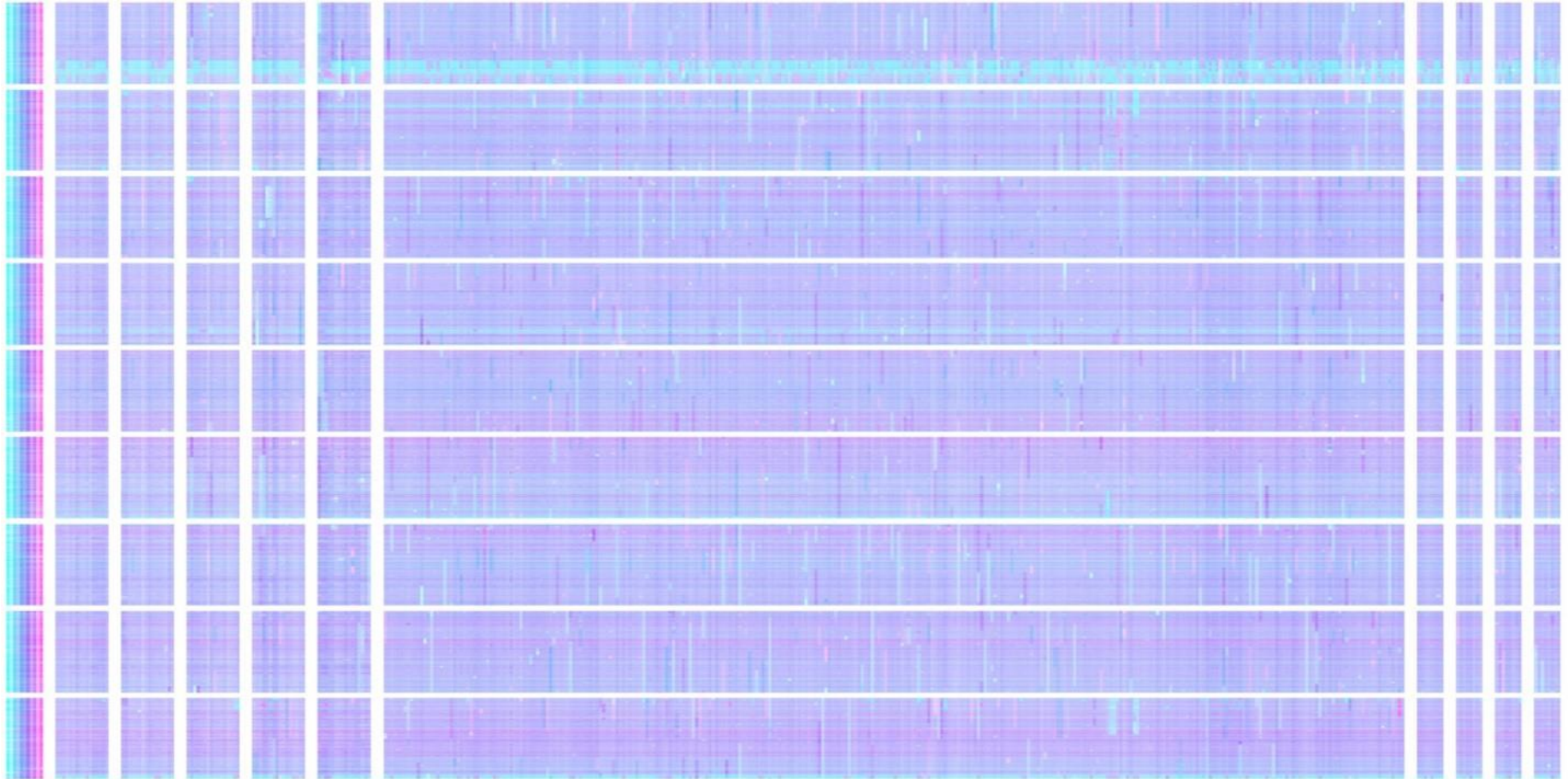
Pilot study based on transcriptome resequencing indicated at optimum dosage:

- Broad spectrum of point mutations induced
- ~150,000 point mutations detectable per line
- Frame-shift InDels induced in ~1% of genes per line
- ~4 large-scale deletions or duplications induced per line
- Siblings can inherit a duplication in one line corresponding to a deletion in another

# RIPR-York genome re-sequenced radiation mutagenesis panel

Analysis of first 404 genome re-sequenced lines and 16 Maplus individuals indicate:

- High rate of sequence and genome structural variants segregating in the background
- Many chromosome-scale structural variants generated
- Multiple candidate deletion and frame-shift InDels detected for most genes



# Acknowledgements



**Helen  
Riordan**

**Aoife  
Sweeney**

**Dorota  
Radkiewicz**

**Julia  
Crawford**

**Lenka  
Havlickova**

**Ian  
Bancroft**

**Natalia  
Stawniak**

**Jamie  
Huckstep**

**Alison  
Fellgett**

**Harjeevan  
Kaur**

**Lihong  
Cheng**

**Varanya  
Kittipol**

**Roxana  
Teodor**

**Zhesi  
He**

**Veronika  
Yankova**