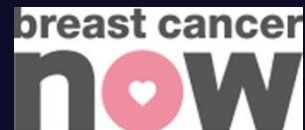




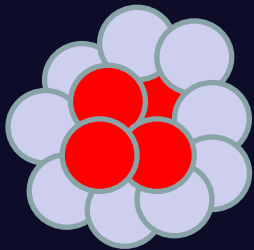
p53 isoforms combinatorics: is it a p53 code?

Jean-Christophe Bourdon, PhD

*Cancer Research Division
Dundee Cancer Centre
University of Dundee*



*p53 defines cell fate outcome
in response to extra and intra-cellular signals*



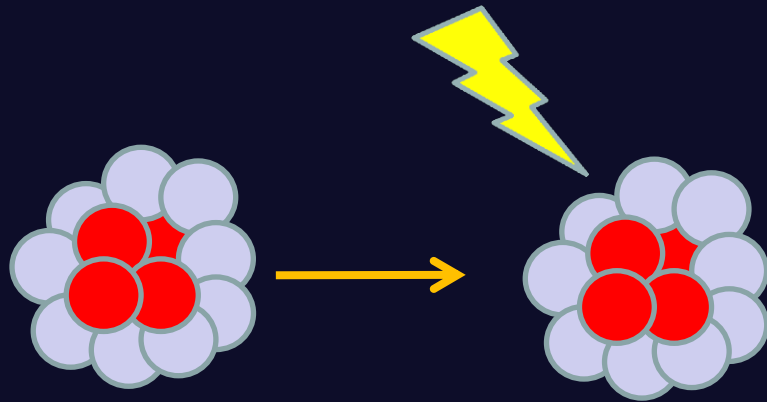
Proliferating breast
cancer cells ●



Stromal breast
cells ●



*p53 defines cell fate outcome
in response to extra and intra-cellular signals*



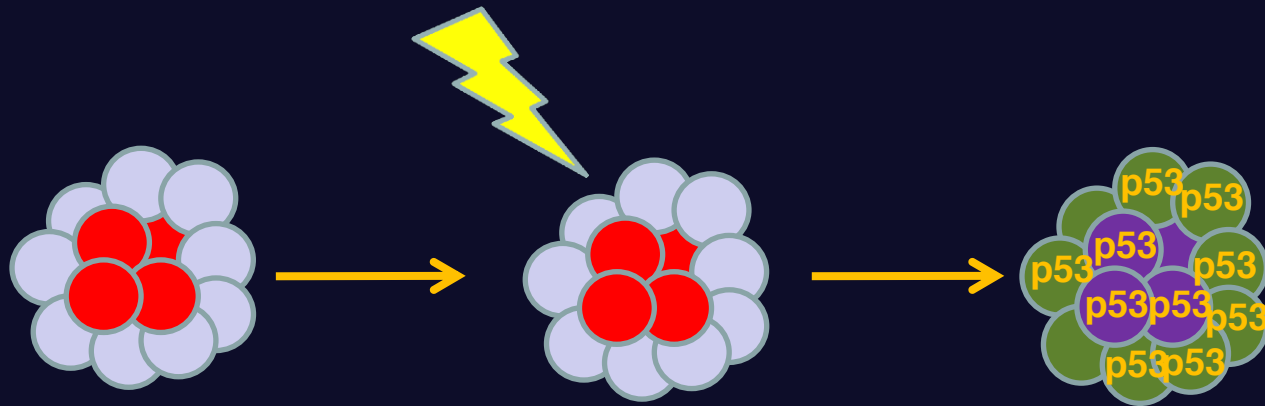
Proliferating breast
cancer cells ●

Stromal breast
cells ●

Endocrine treatment:
inhibition of Estrogen Receptor

Drugs / Ionising radiation:
damage to DNA, cell
membranes and proteins

p53 defines cell fate outcome in response to extra and intra-cellular signals



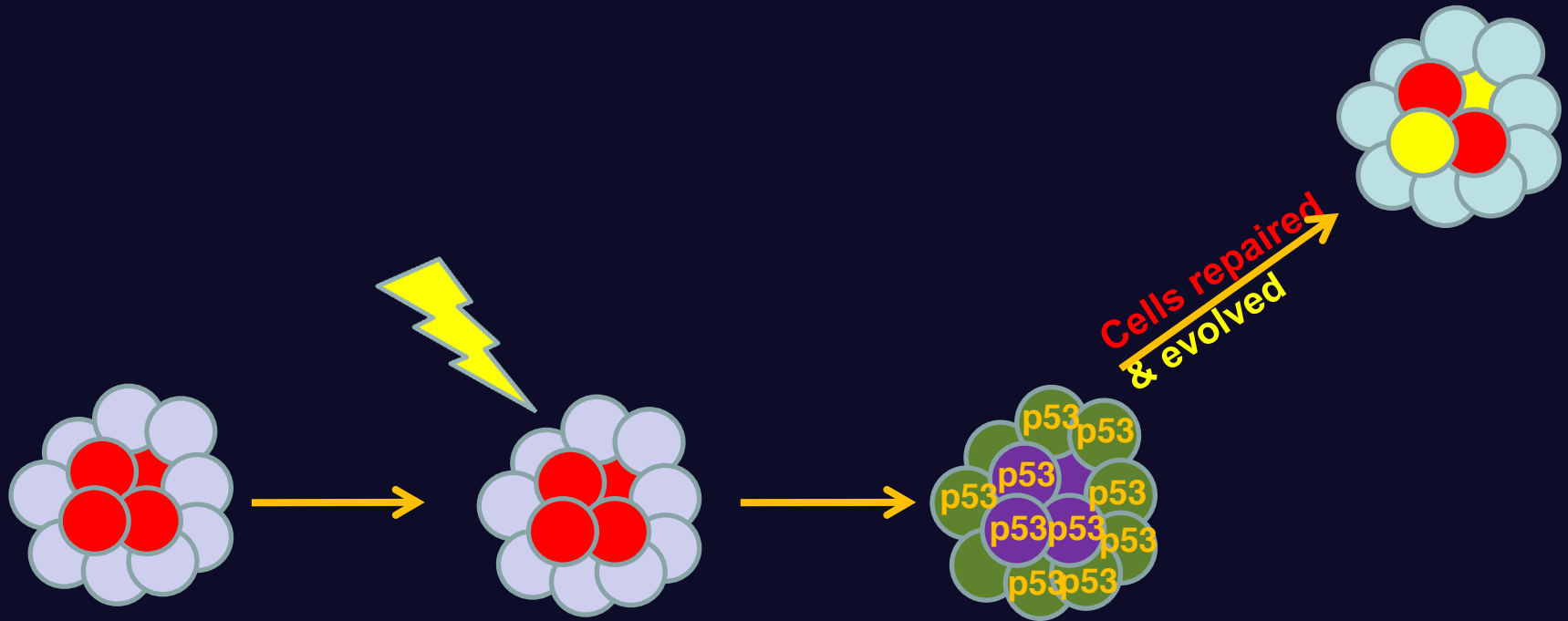
Proliferating breast
cancer cells ●

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Endocrine treatment:
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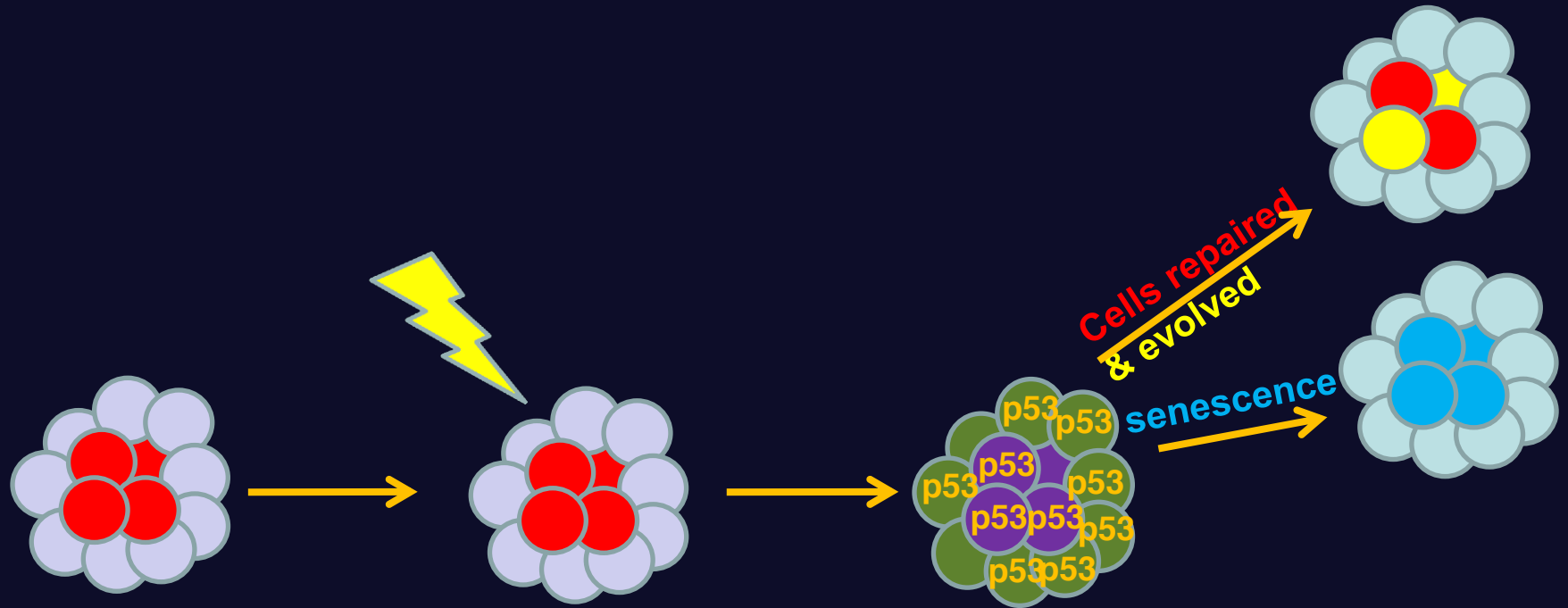
Proliferating breast cancer cells ●

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p53 defines cell fate outcome in response to extra and intra-cellular signals



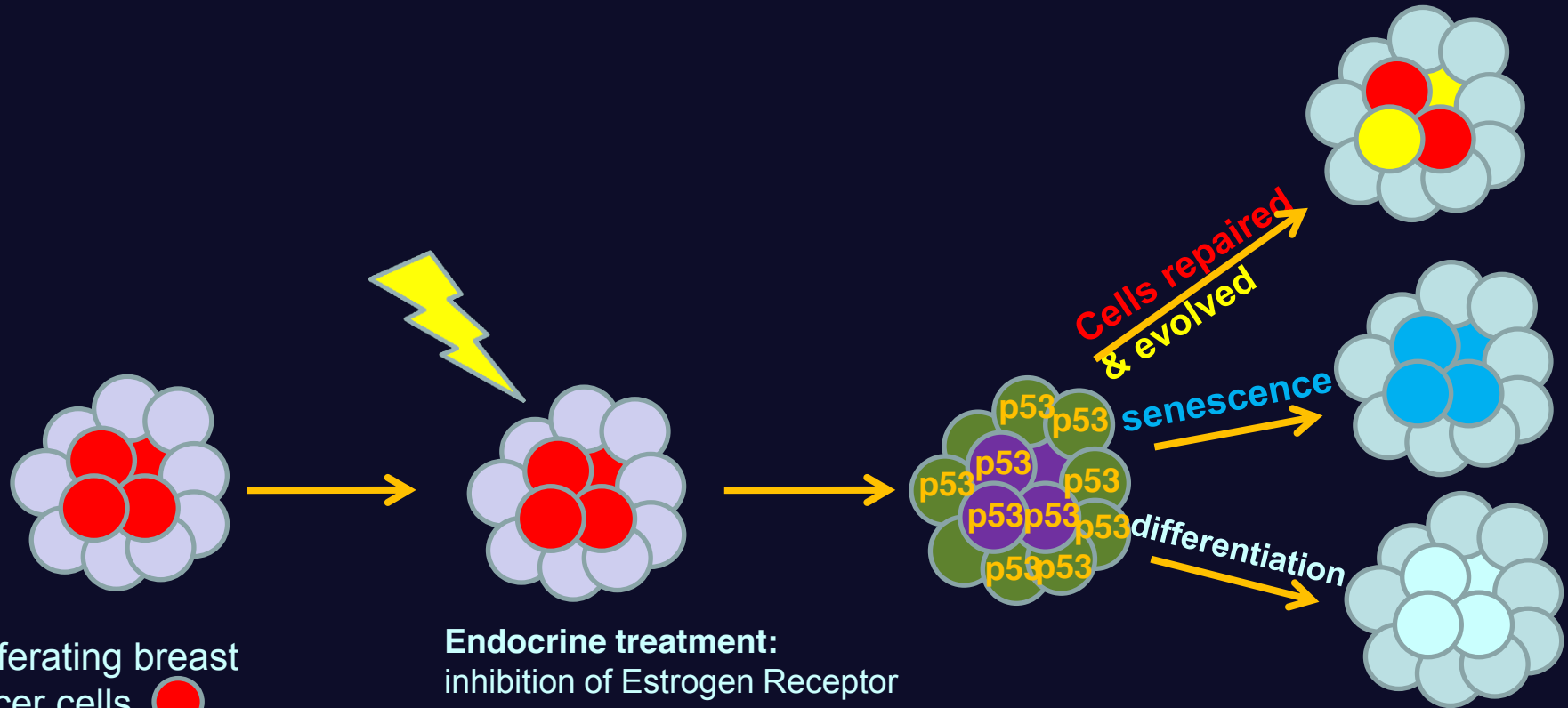
Proliferating breast cancer cells ●

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p53 defines cell fate outcome in response to extra and intra-cellular signals



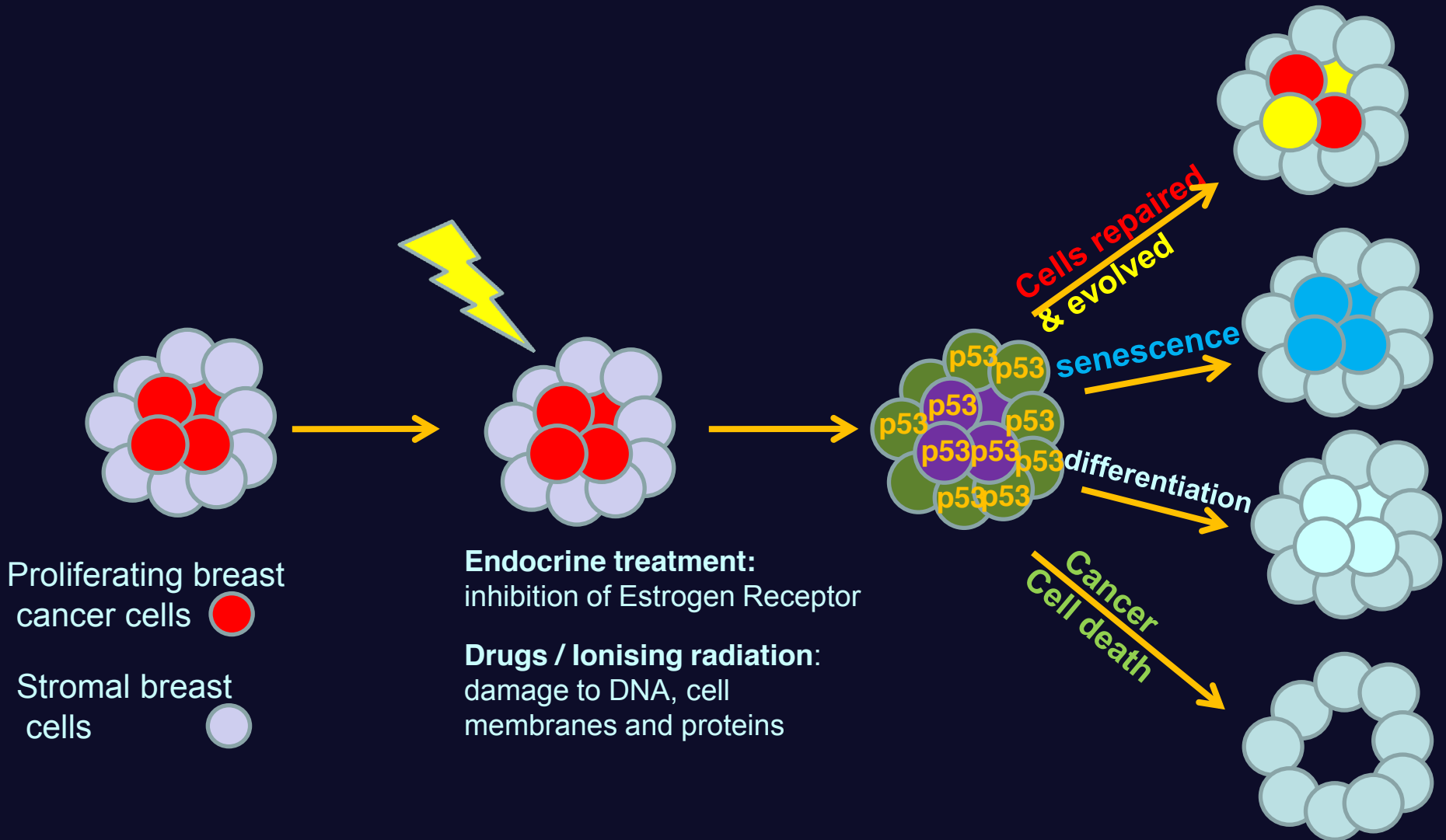
Proliferating breast cancer cells ●

Stromal breast cells ●

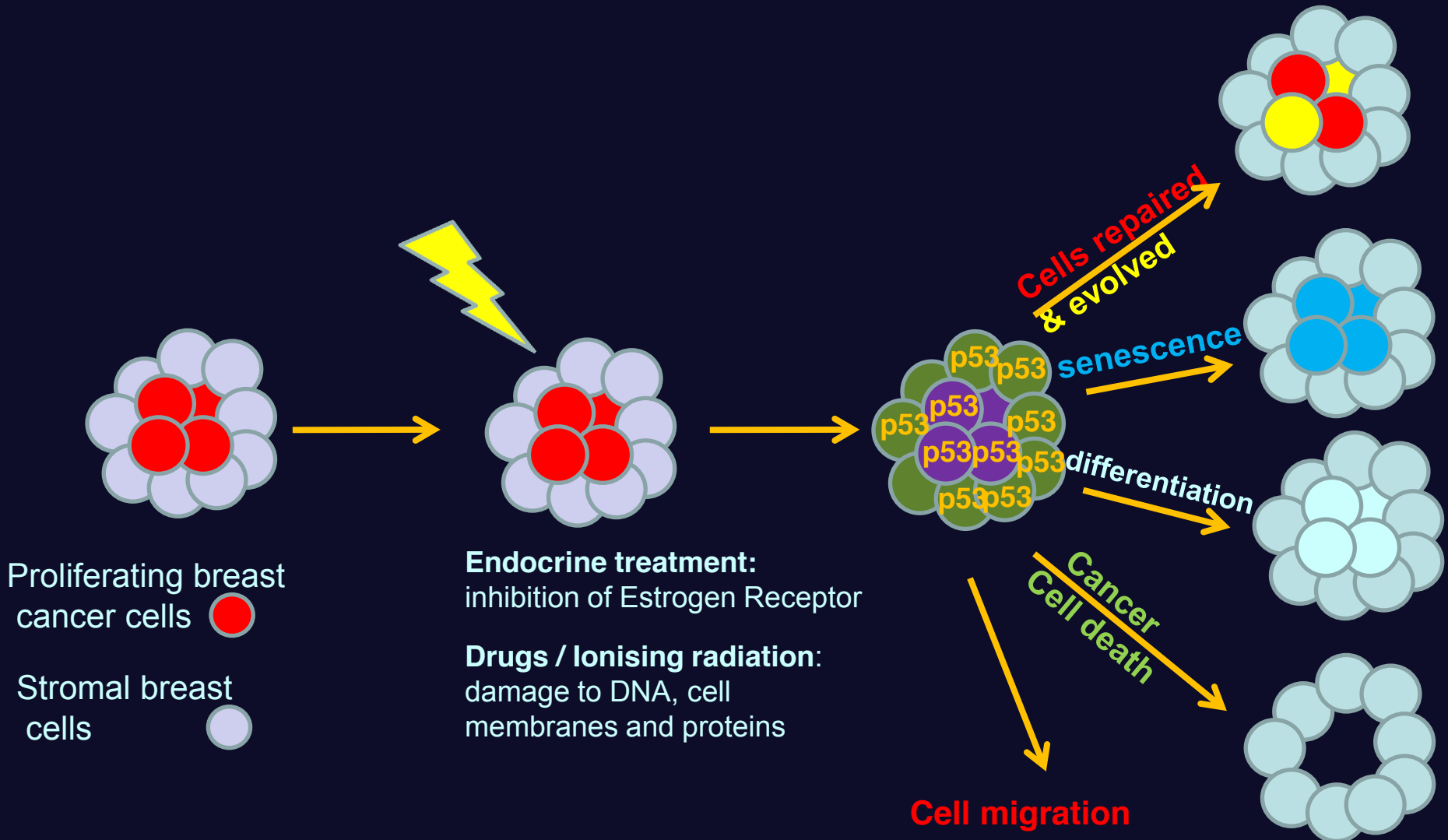
Endocrine treatment:
inhibition of Estrogen Receptor

Drugs / Ionising radiation:
damage to DNA, cell membranes and proteins

p53 defines cell fate outcome in response to extra and intra-cellular signals

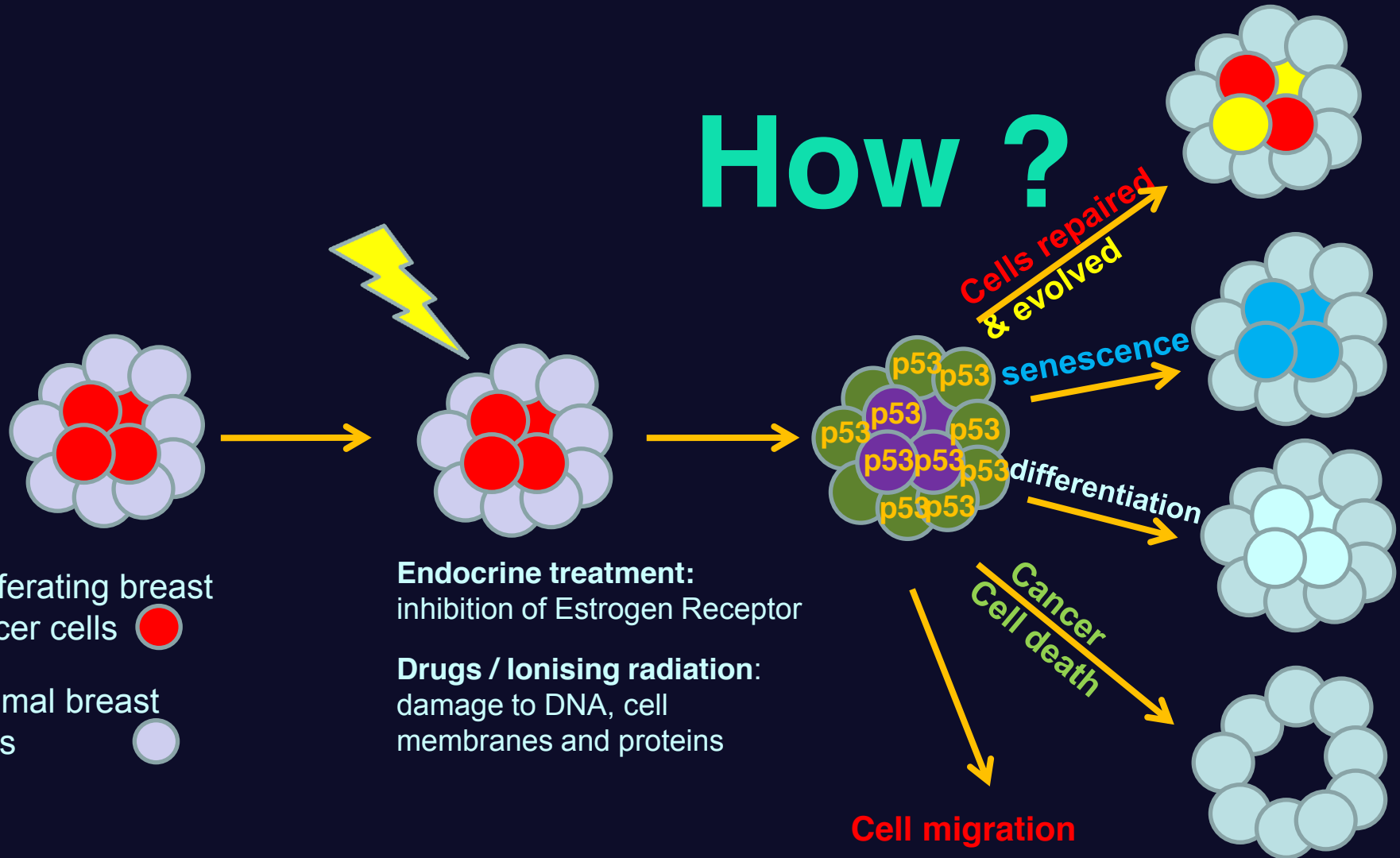


p53 defines cell fate outcome in response to extra and intra-cellular signals



*p53 defines cell fate outcome
in response to extra and intra-cellular signals*

How ?



Proliferating breast cancer cells ●

Stromal breast cells ●

Endocrine treatment:
inhibition of Estrogen Receptor

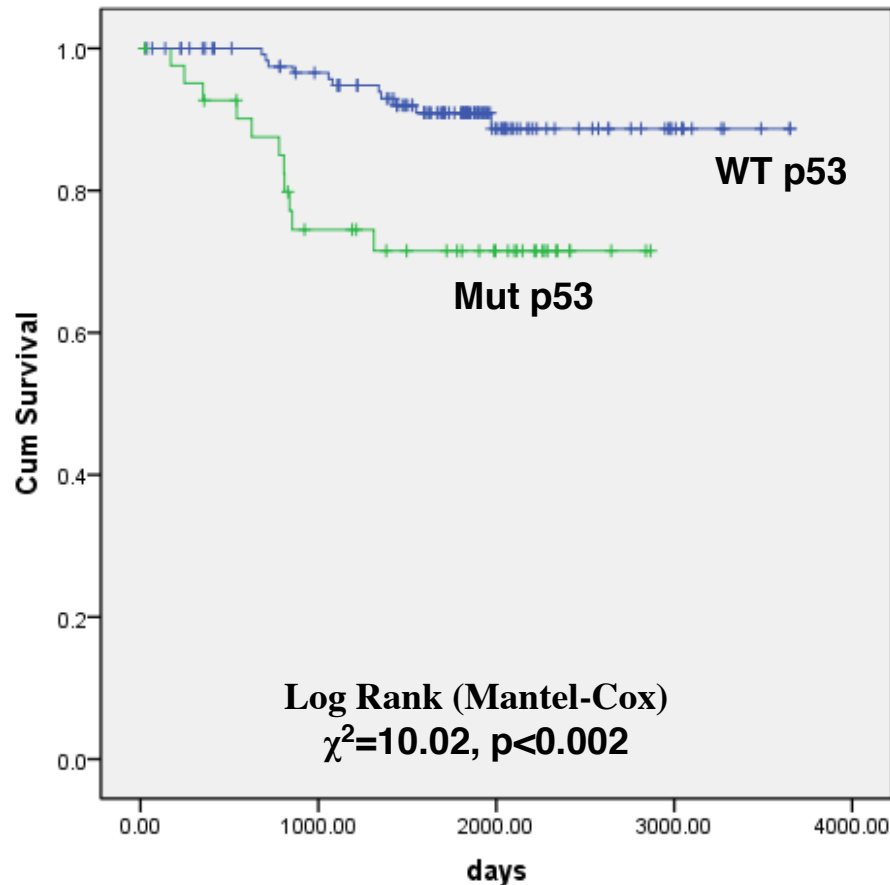
Drugs / Ionising radiation:
damage to DNA, cell membranes and proteins

Cell migration

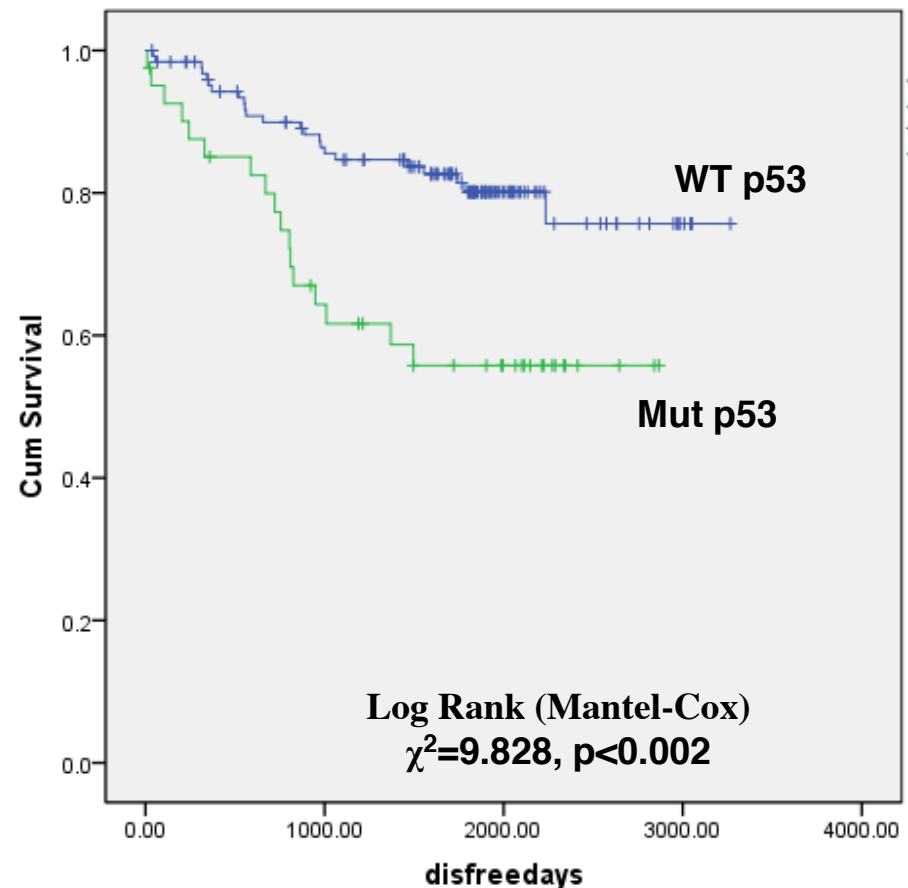
p53 mutation status can be associated with poor prognosis

Kaplan-Meier survival curves

Overall survival



Disease Free survival



Problem:

It is still difficult at the individual level to link p53 mutation status to:

- cancer prognosis
- cancer treatment

=> Other genes are more frequently mutated than p53 and define response to treatment independently of p53

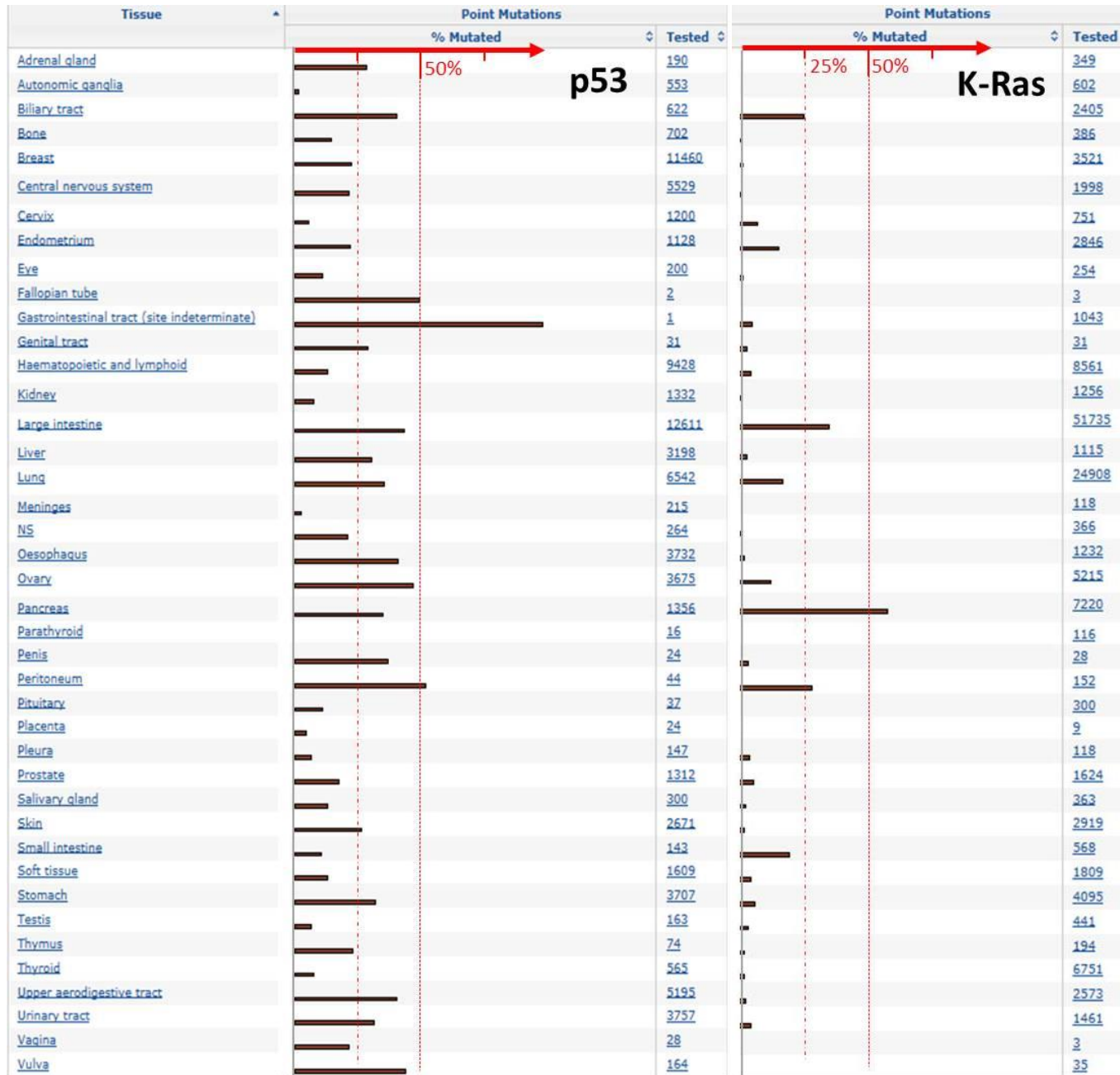
In 2008, creation of The International Cancer Genome Consortium

→ sequence the entire cancer genome of 25000 tumors derived from the 50 most common cancer types

p53 is the most frequently mutated gene in cancers

<http://cancer.sanger.ac.uk/cosmic/analysis>

Cosmic release v68 (02/2014)



Conclusions

- *p53 is **the** unique gene in the entire genome to be highly frequently mutated in all kind of human cancers.*
- *Cancer genome sequencing data are consistent with experimental and genetic data (human and animals),*
- ➔ ***p53 plays a central and fundamental role in human cancers formation, progression and treatment.***

Before the cancer genome sequencing
the question was:

is p53 involved in patients' response to treatment ?

Now the question is:

How is p53 involved in patients' response to treatment ?

Now the question is:

How is p53 involved in patients' response to treatment ?

- Since p53 integrates multiple intracellular and extracellular signals to maintain cell homeostasis
- as all cancer treatments alter cell homeostasis,

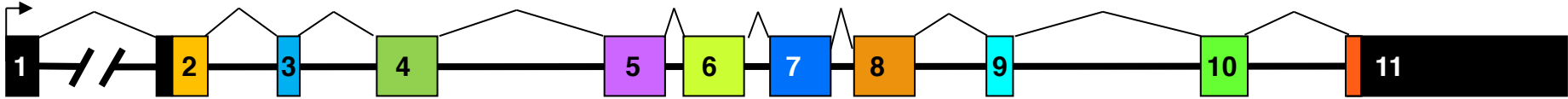
→ **Clinical responses to cancer treatment are, *de facto*, p53-dependent (i.e. for the cancer and normal cells).**

Now the question is:

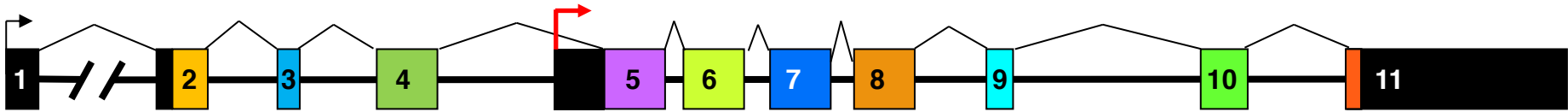
How is p53 involved in patients' response to treatment ?

What did we not understand about p53?

Is p53 “really” the only protein able to regulate gene expression through p53 response elements?

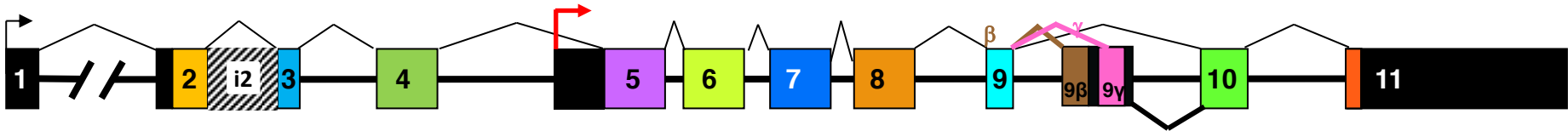


Is p53 “really” the only protein able to regulate gene expression through p53 response elements?



Internal promoter

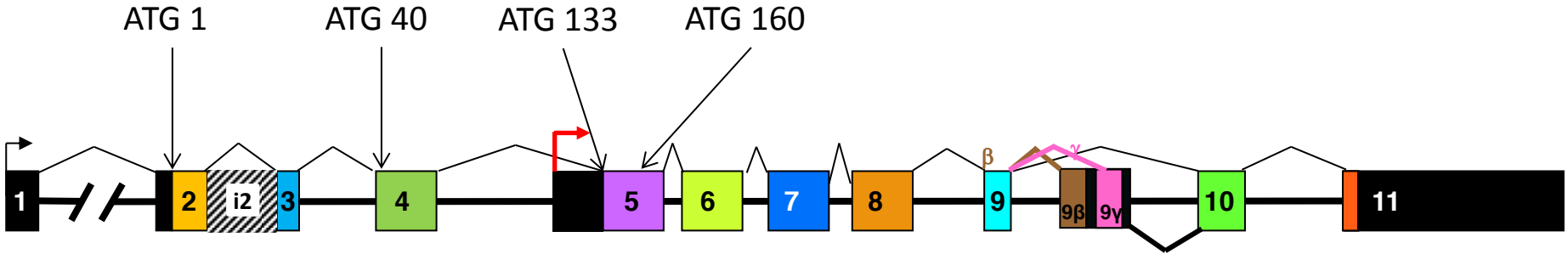
Is p53 “really” the only protein able to regulate gene expression through p53 response elements?



Internal promoter

Alternative splicing

Is p53 “really” the only protein able to regulate gene expression through p53 response elements?

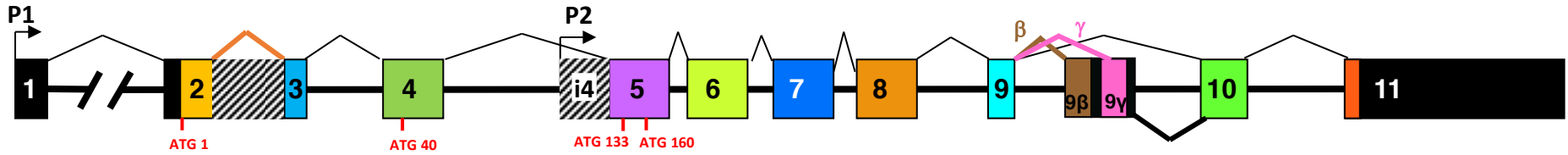


Internal promoter

Alternative splicing

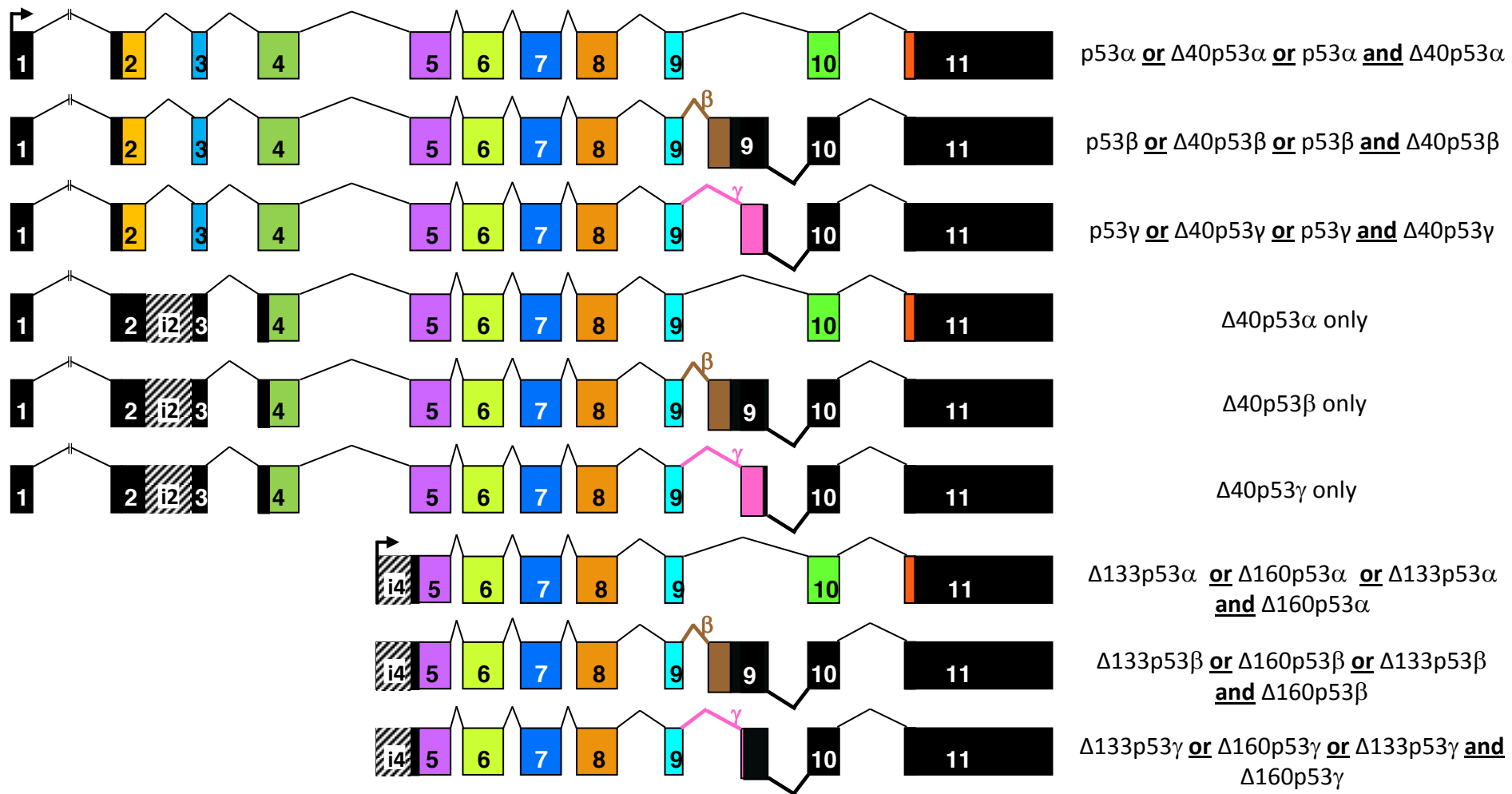
Alternative initiation of the translation

TP53 Gene and p53 mRNAs

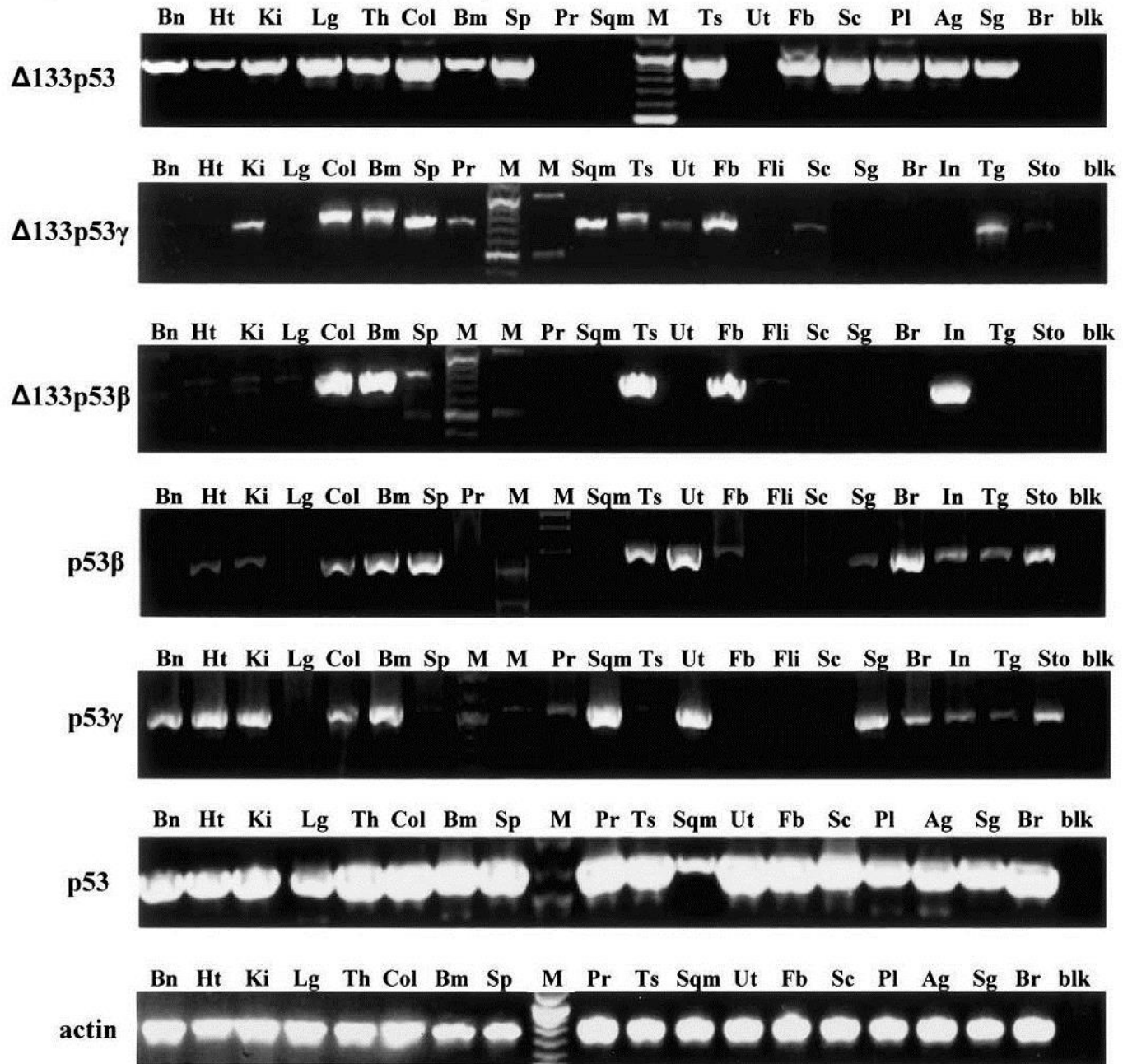


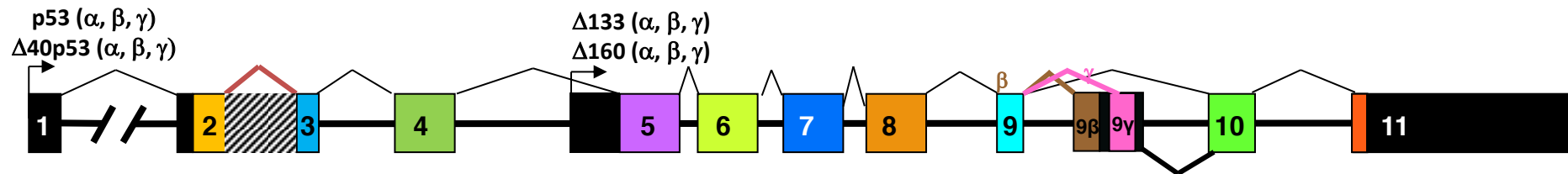
Transcribed mRNA

Translated protein:

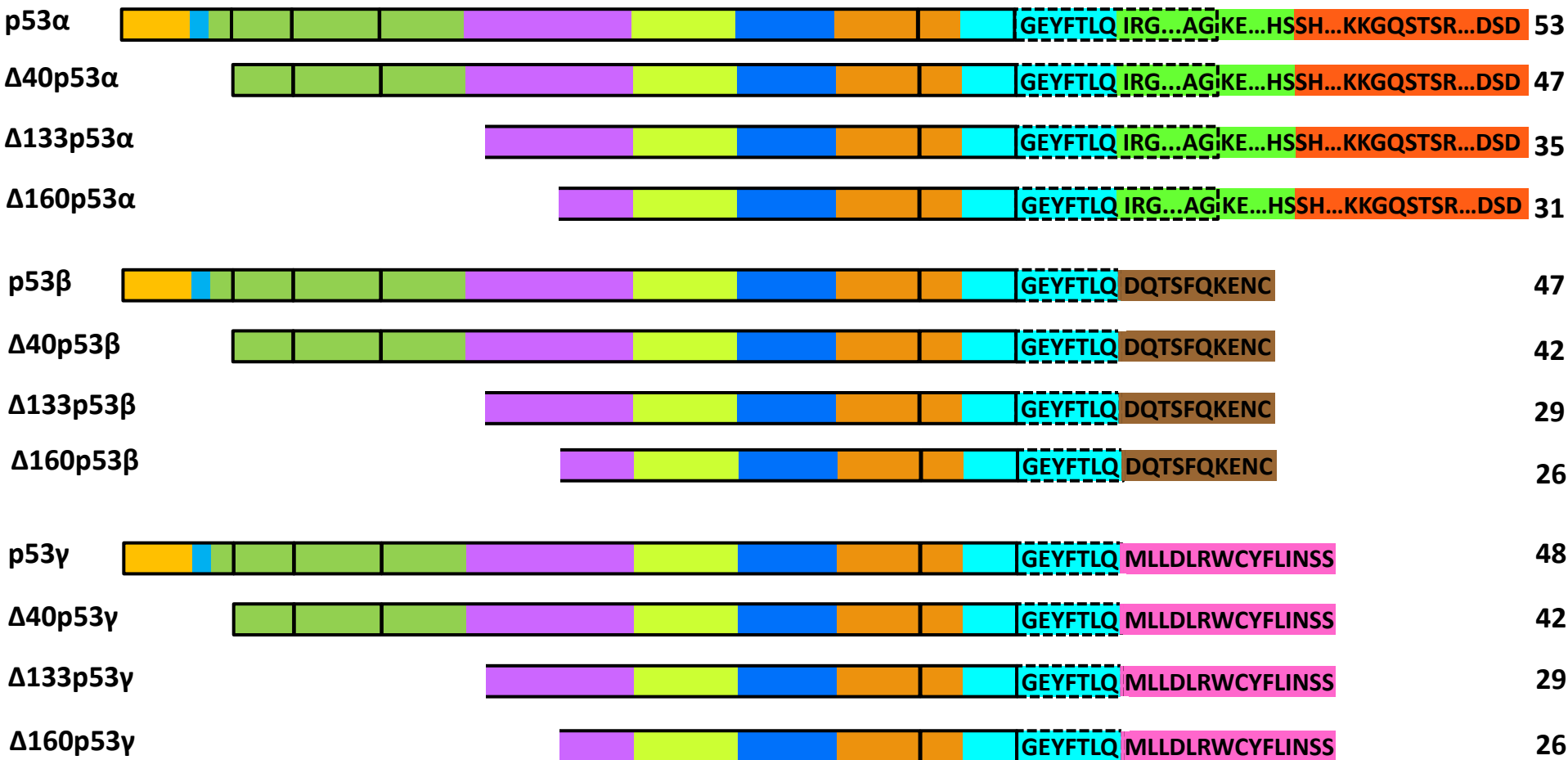


p53 isoforms are expressed in normal human tissues in a tissue dependent manner



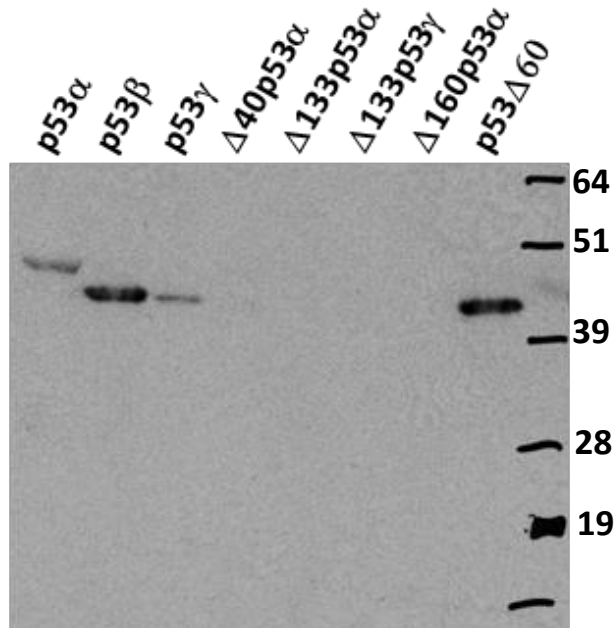


KDa



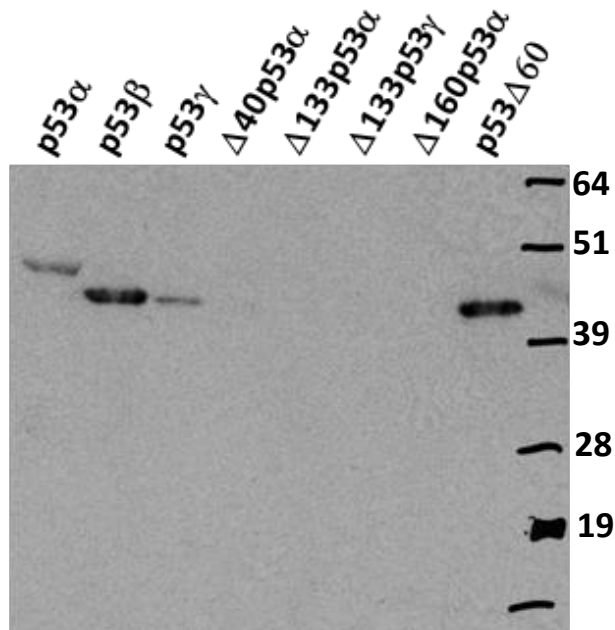
Is p53 expressed as a single protein in human cancers and normal tissues ?

New p53 antibodies detect all p53 protein isoforms

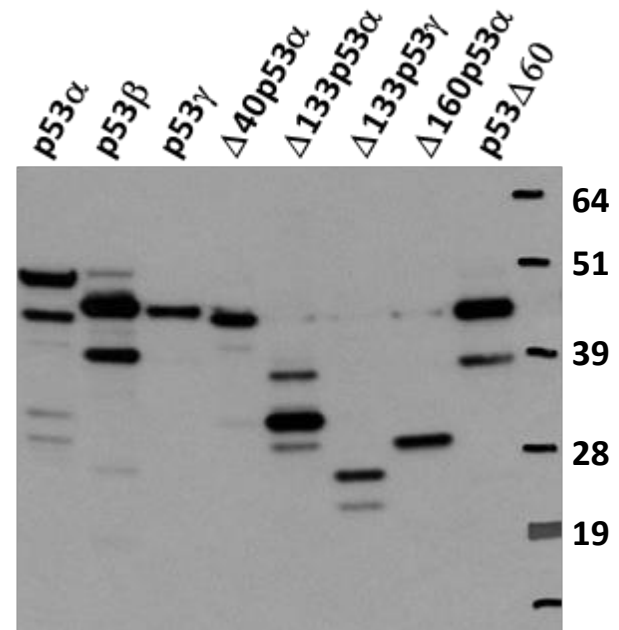


DO-1

New p53 antibodies detect all p53 protein isoforms

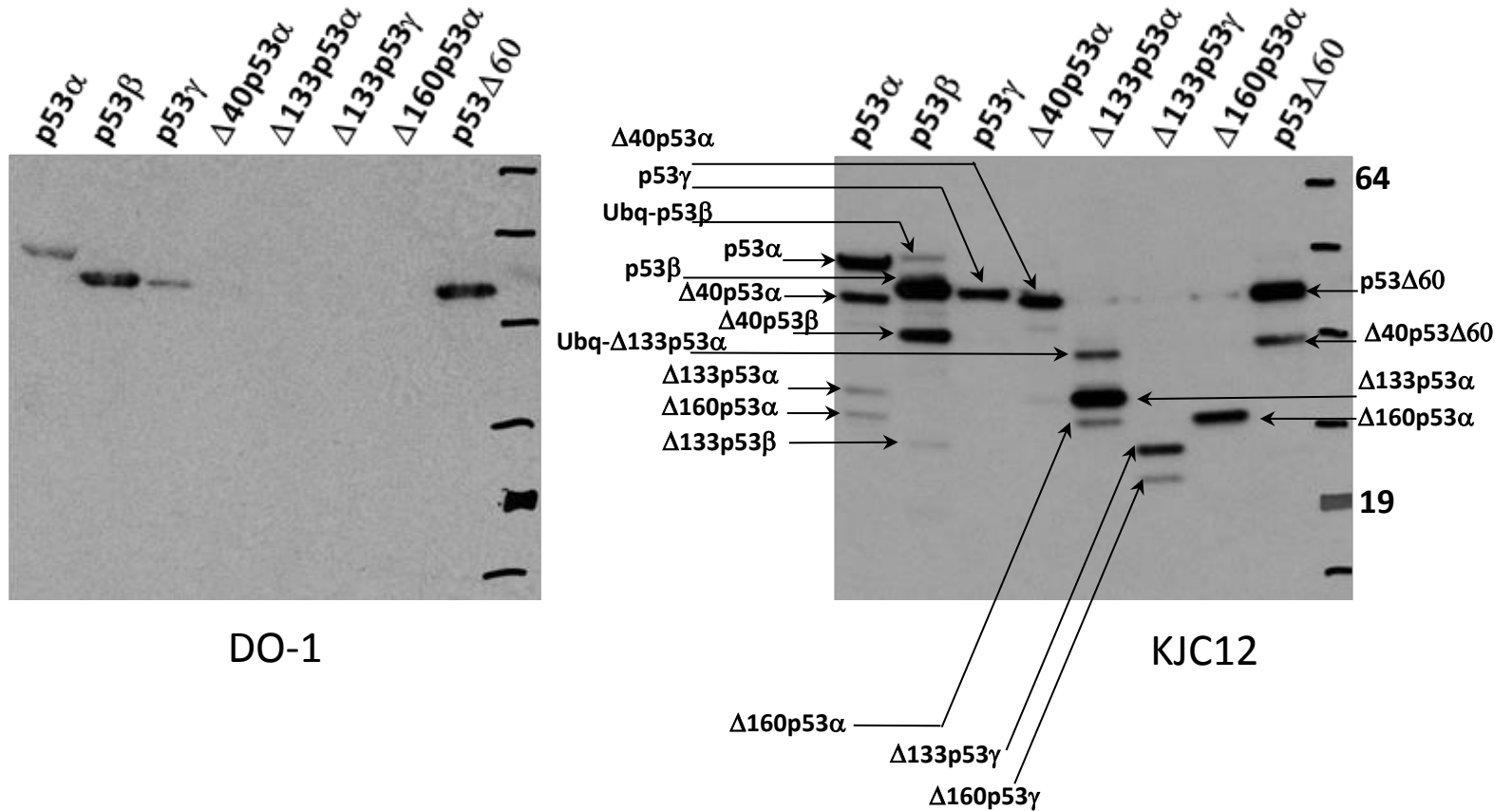


DO-1

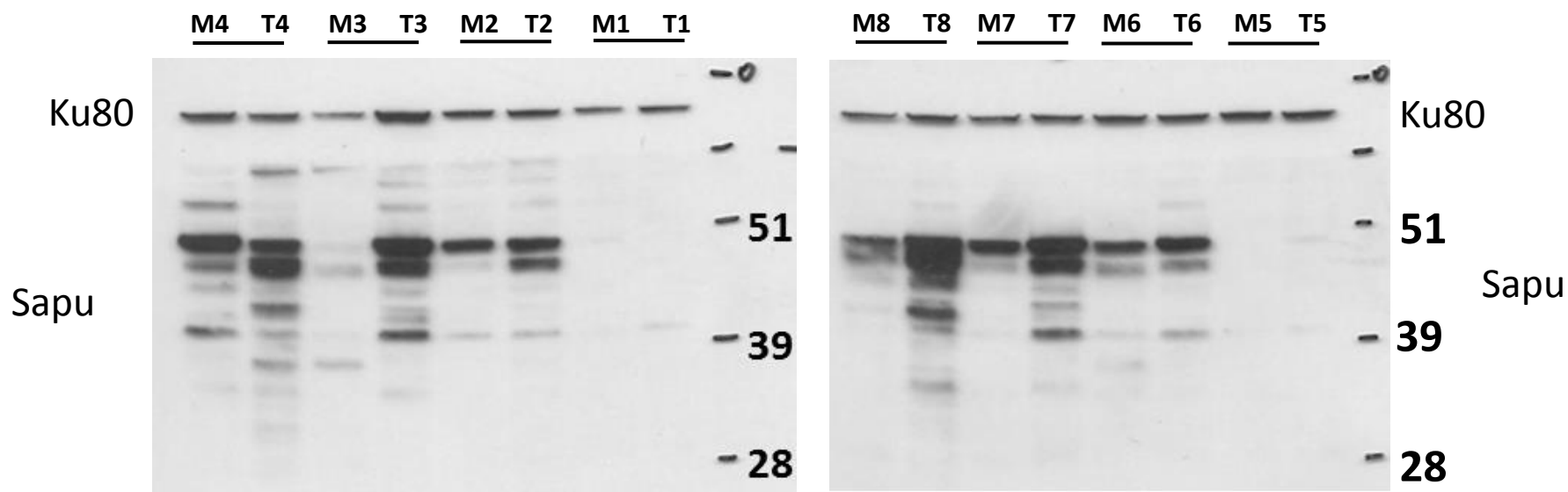


KJC12

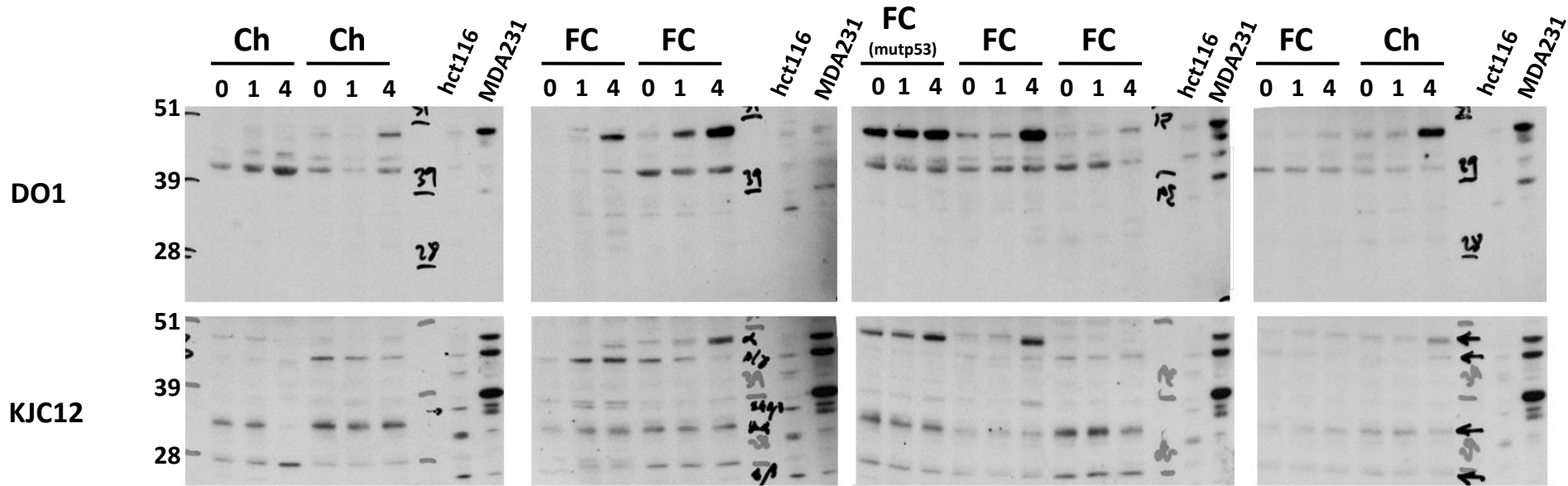
New p53 antibodies detect all p53 protein isoforms



p53 protein isoforms in colon tumours and corresponding liver metastases

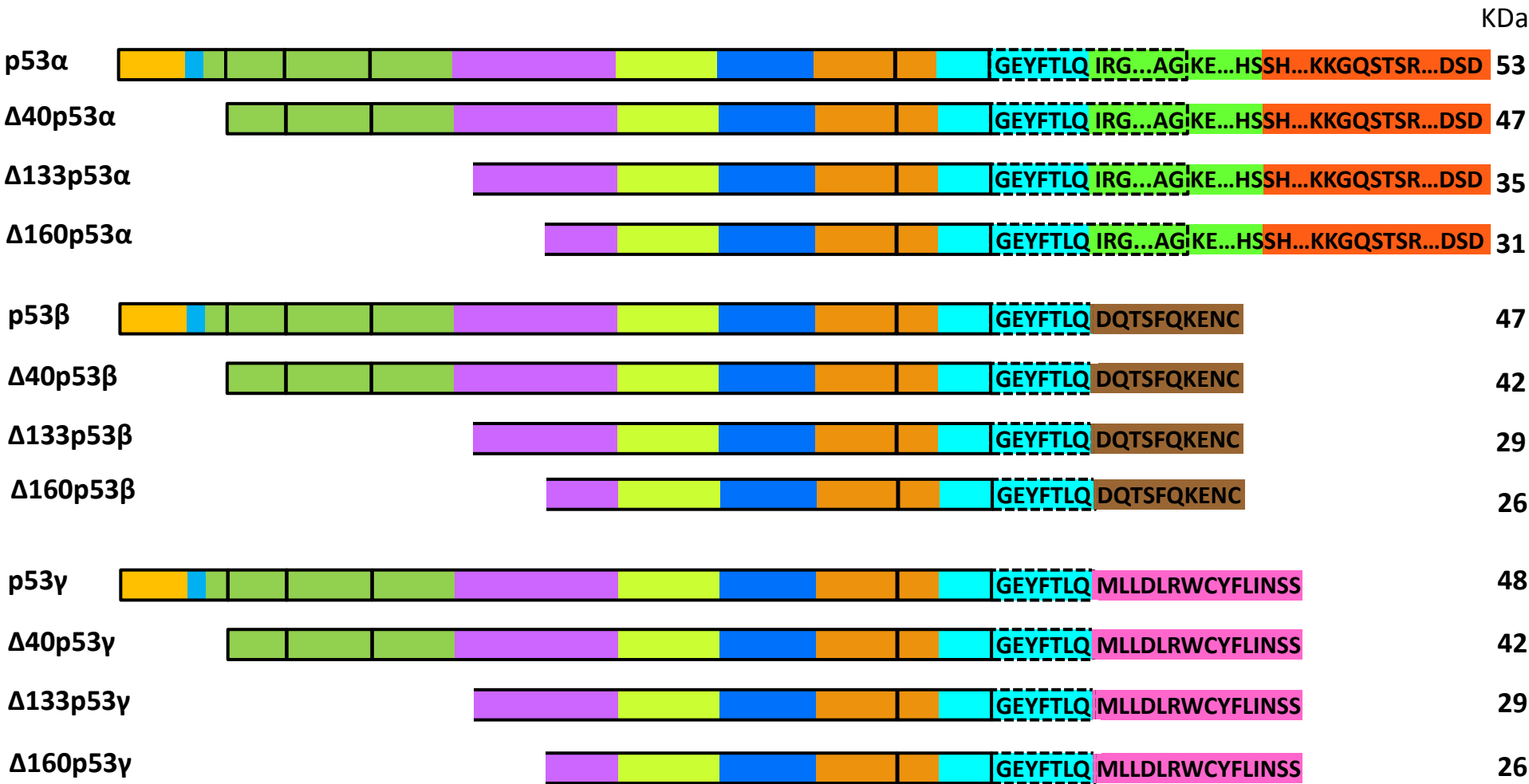
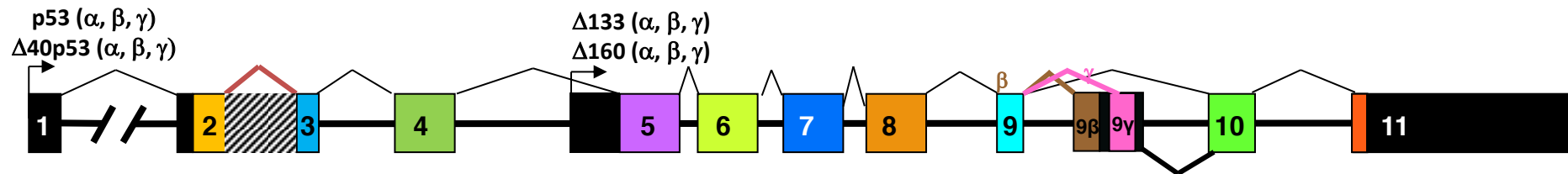


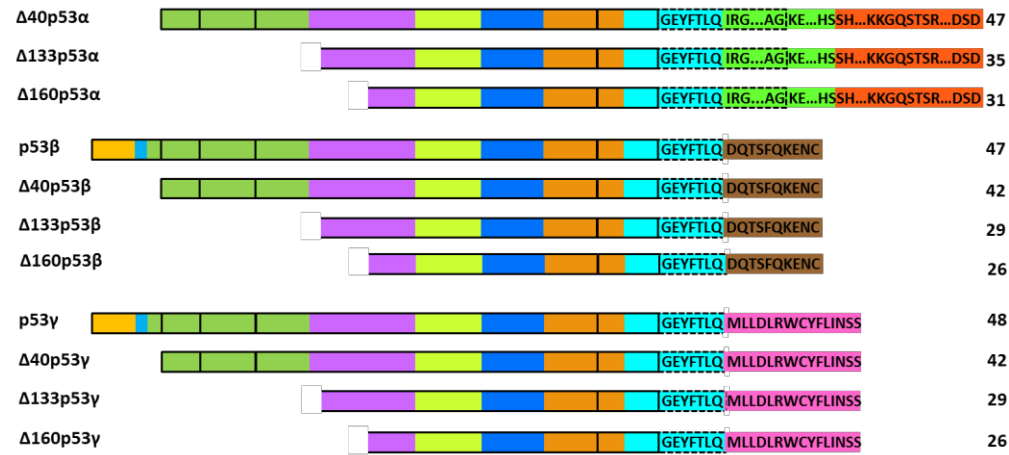
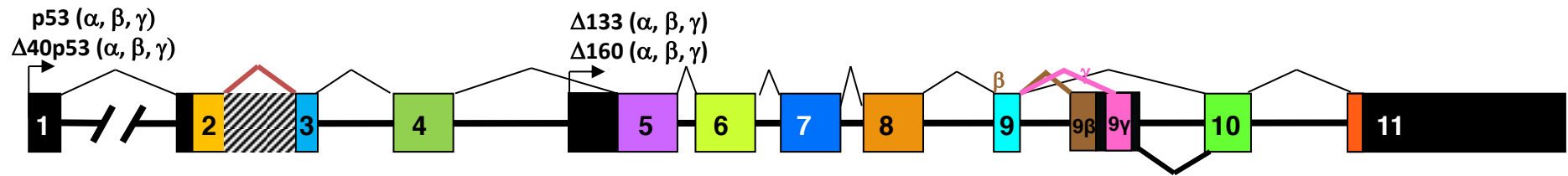
Differential p53 protein isoform expression in CLL patients treated with Chlorambucil (Ch) or 5FU/camptothecin (FC)



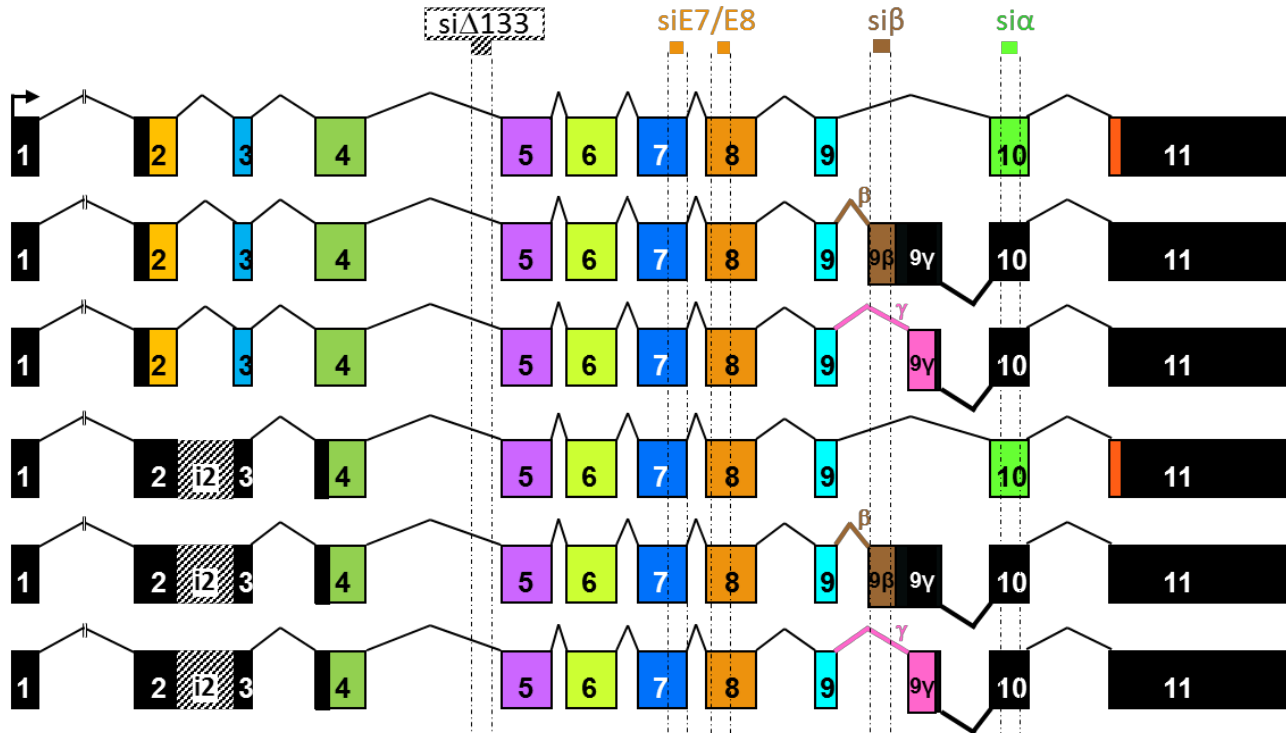
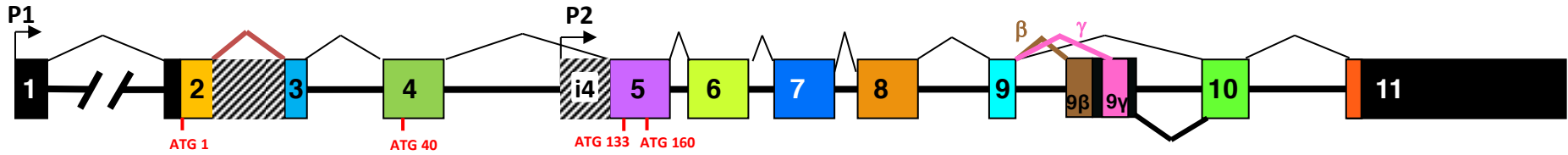
conclusions.

- TP53 gene does not (never) express p53 as a single protein
 - p53 protein isoforms are abundantly expressed
 - Canonical p53 (p53 α) is not systematically the most expressed isoform
- ⇒ p53 is a system of protein expressed in a cell type-dependent manner





Tools- p53 Isoform Specific siRNA's



Translated protein:

p53α or Δ40p53α or p53α and Δ40p53α

p53β or Δ40p53β or p53β and Δ40p53β

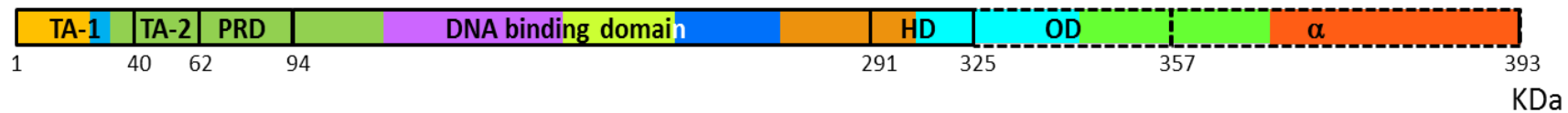
p53γ or Δ40p53γ or p53γ and Δ40p53γ

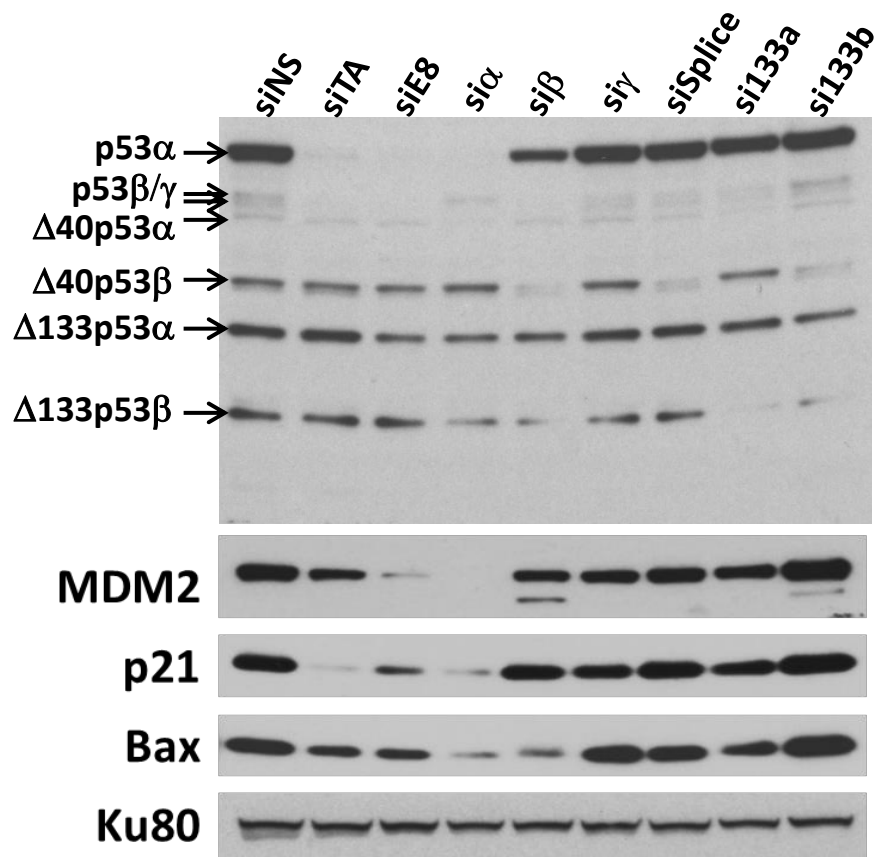
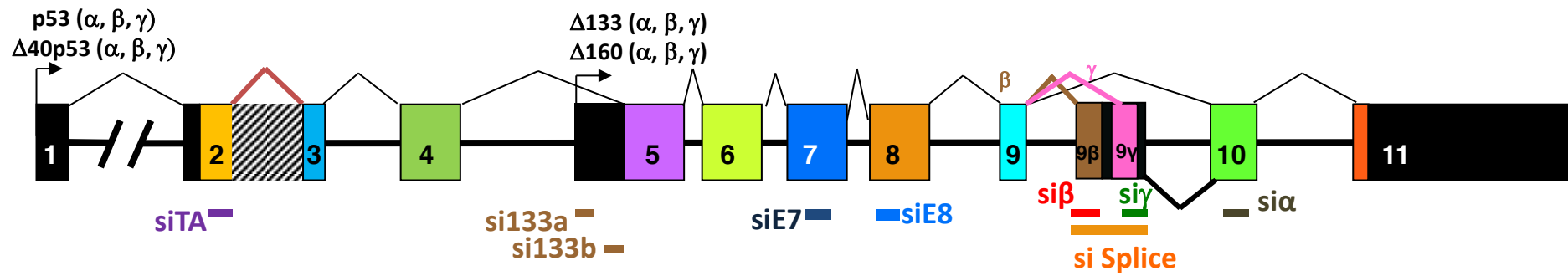
Δ40p53 only

Δ40p53β only

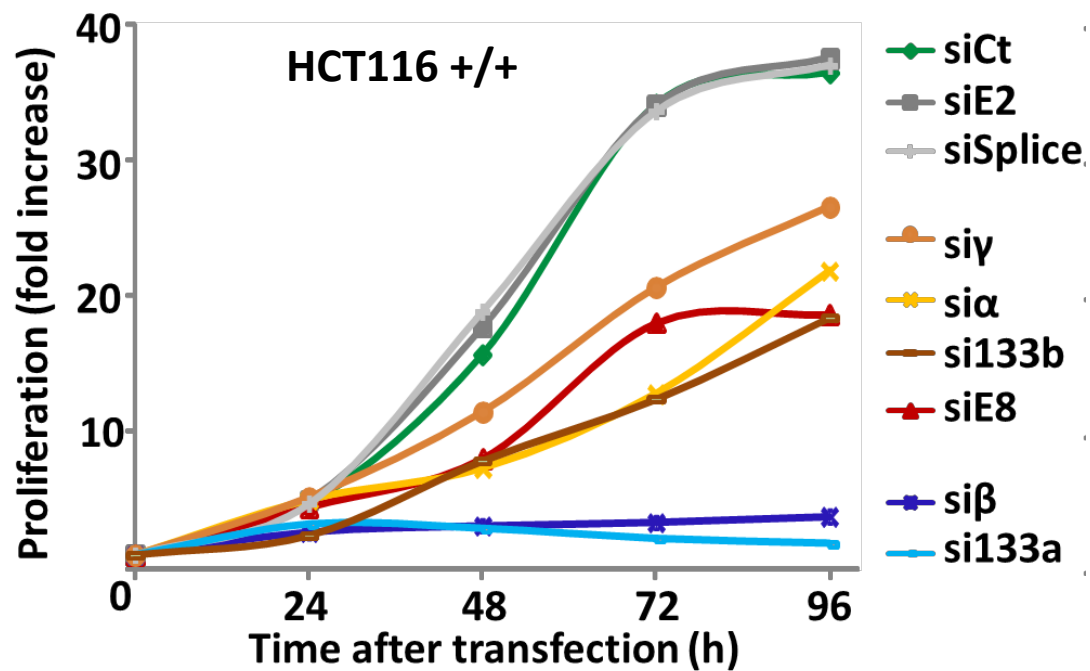
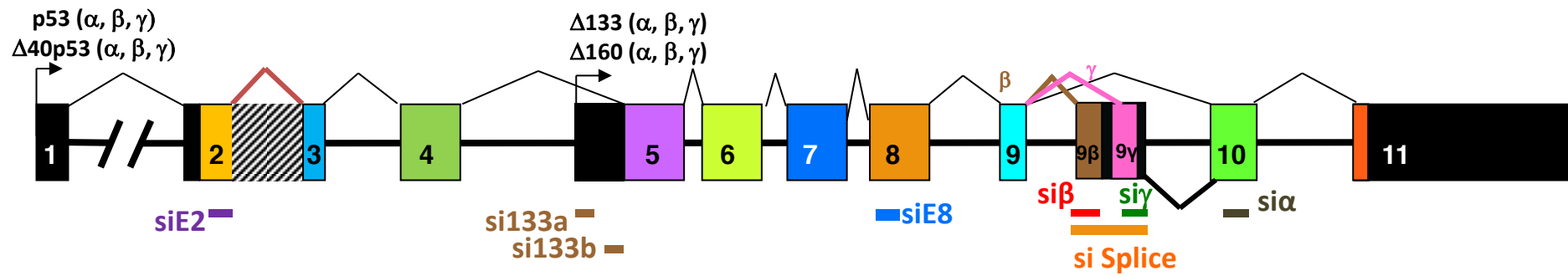
Δ40p53γ only

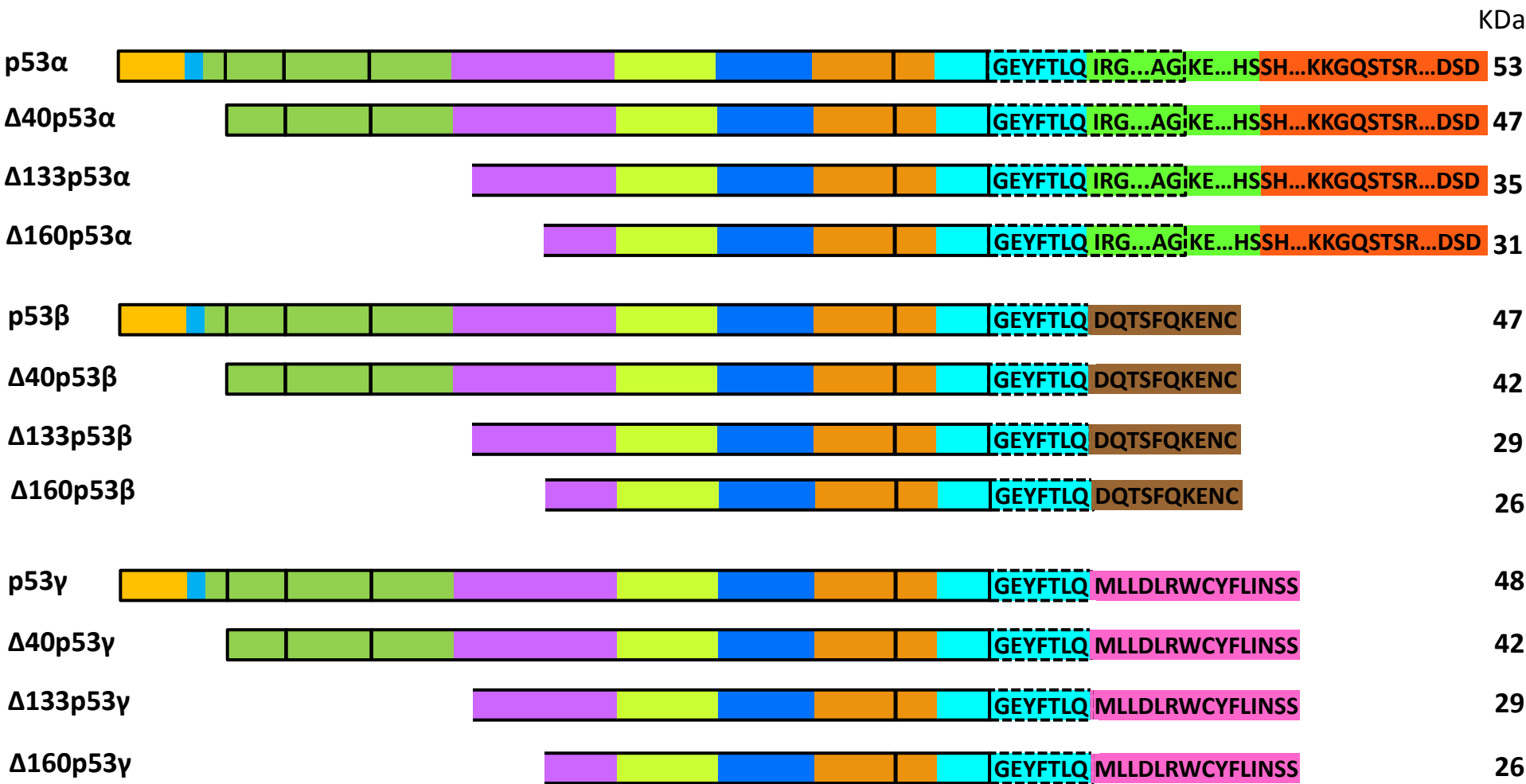
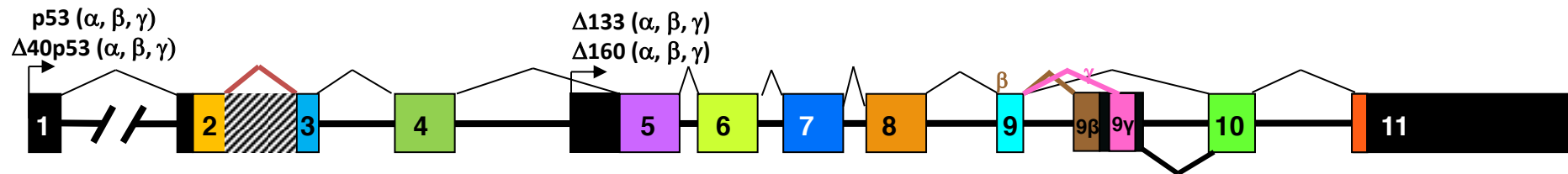
1 2 3
1 2 3 4
1 2 3 4

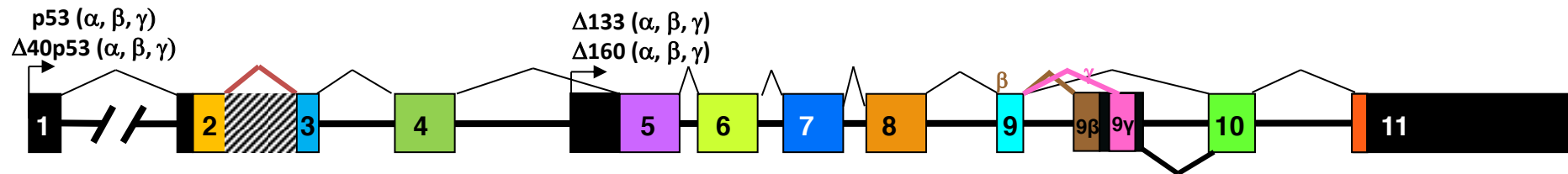




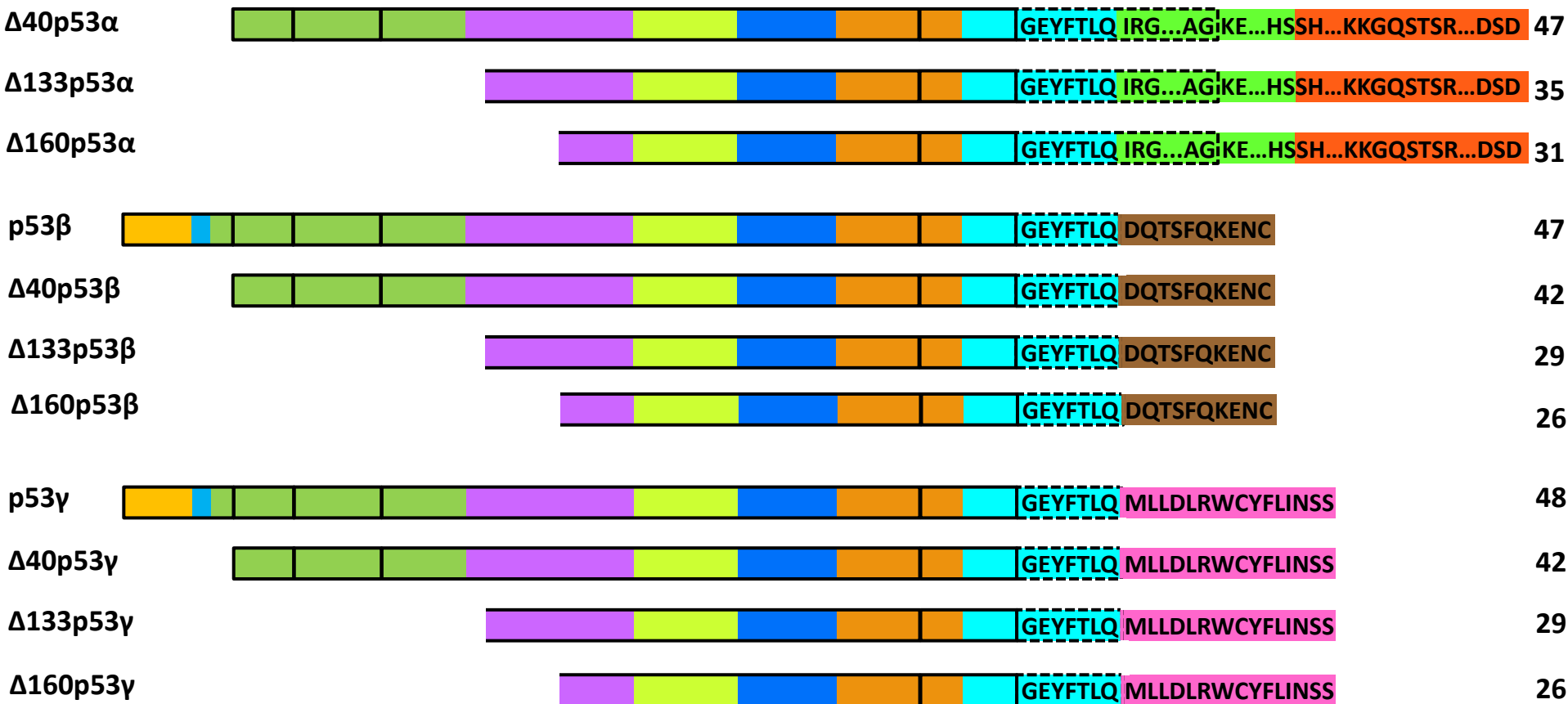
HCT116 +/+

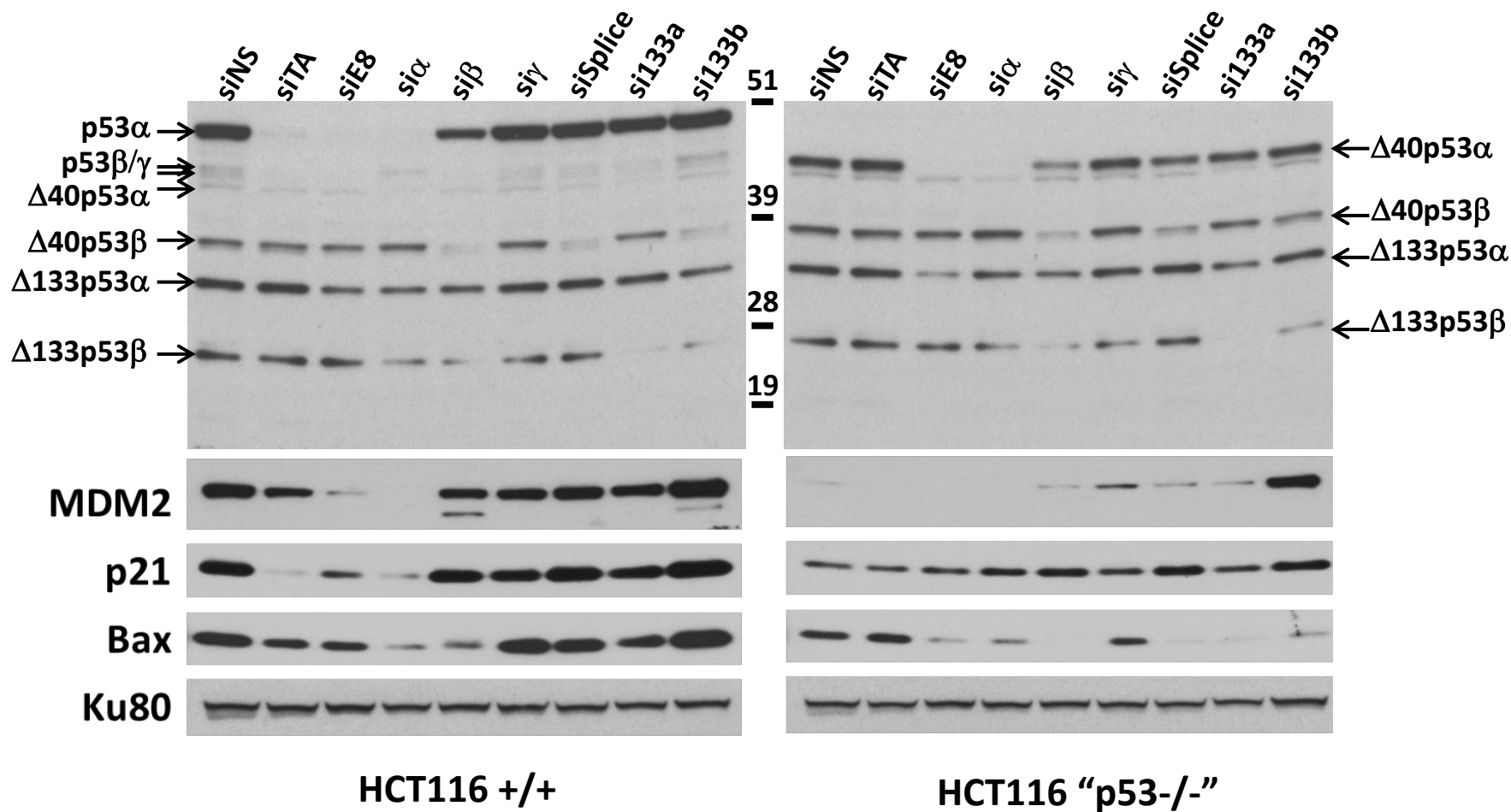
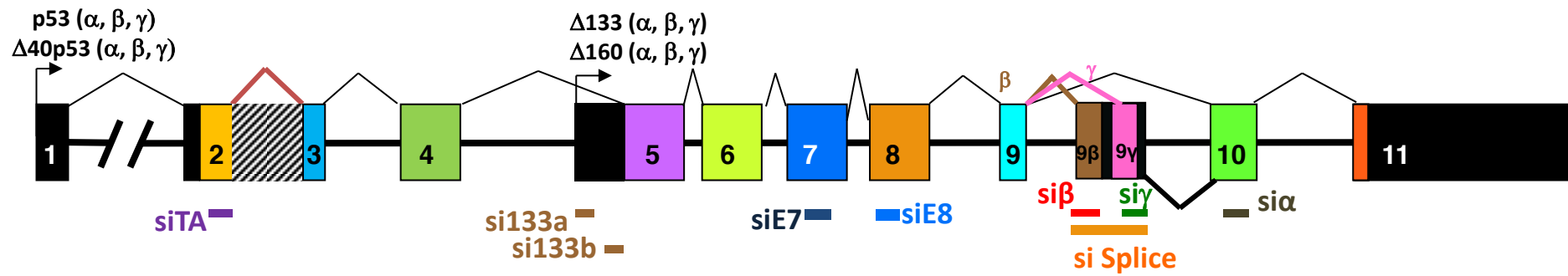


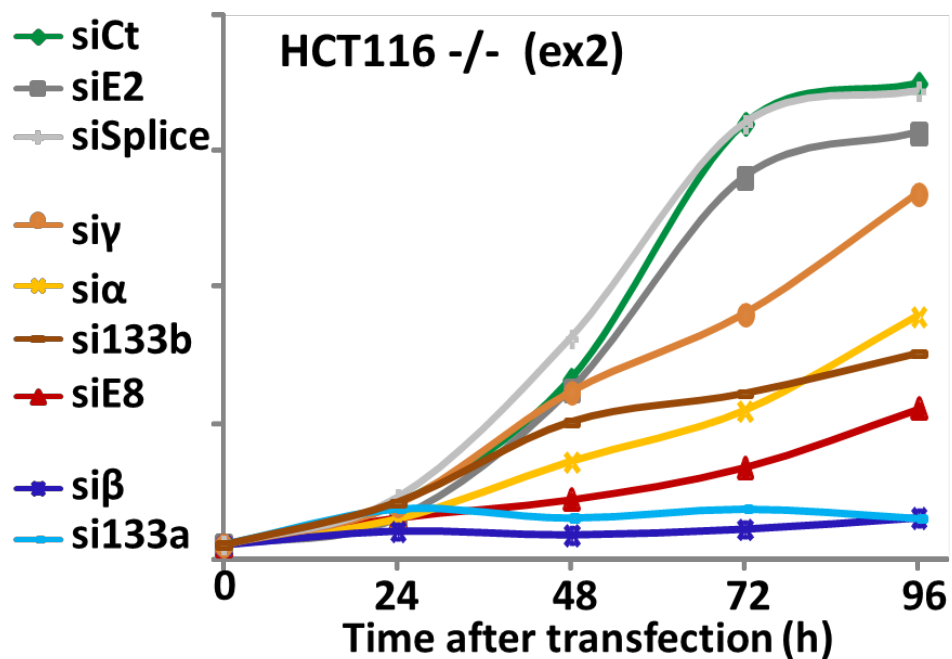
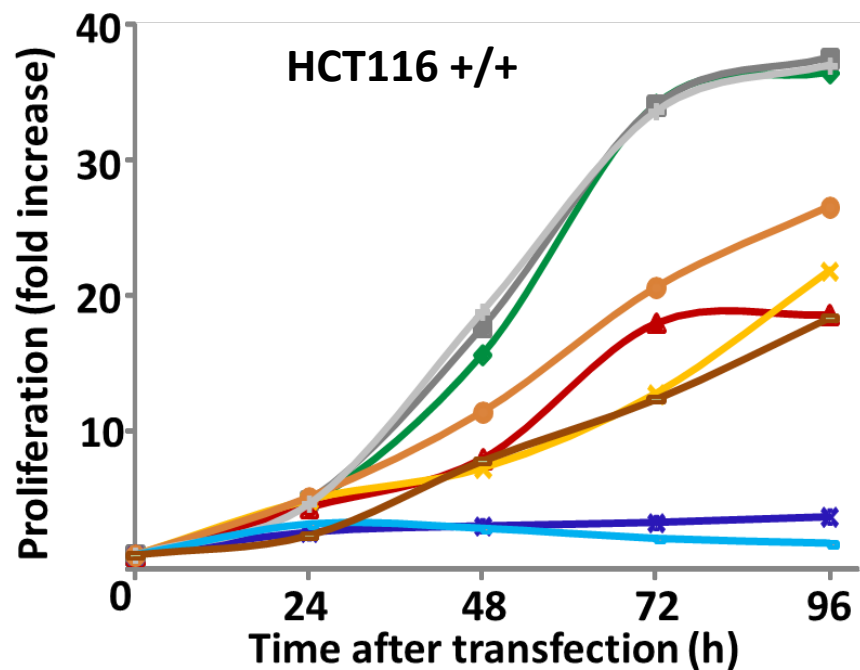
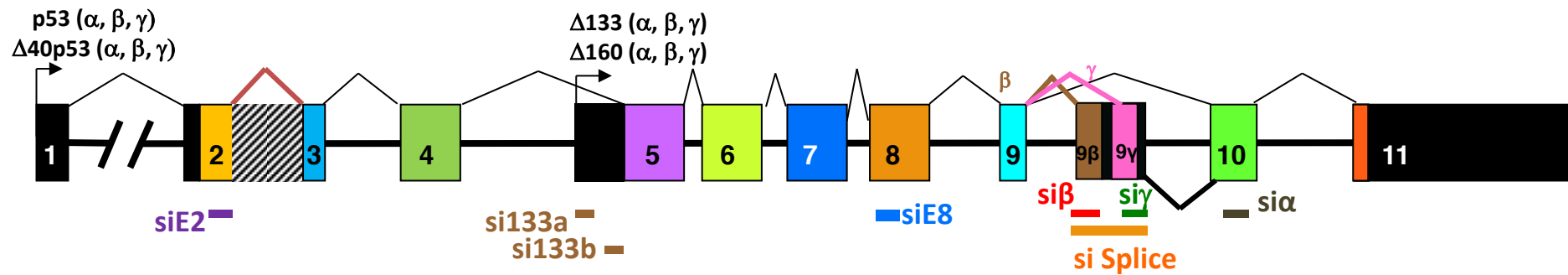




KDa







Cell proliferation assay of HCT 116 +/+ and HCT116 p53-/- treated with UV

HCT116 +/+

nosi

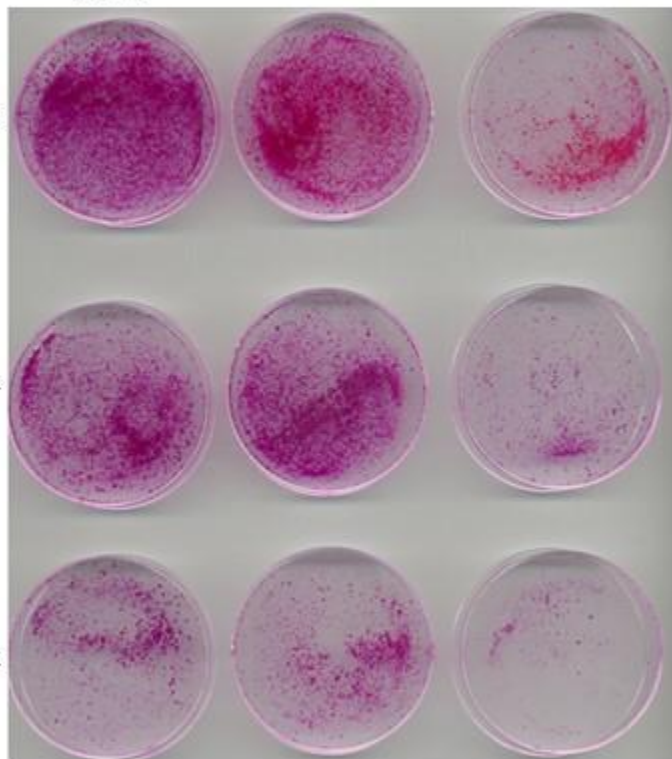
siNS

siE7

0 J/m²

5 J/m²

10 J/m²



HCT116 -/-

nosi

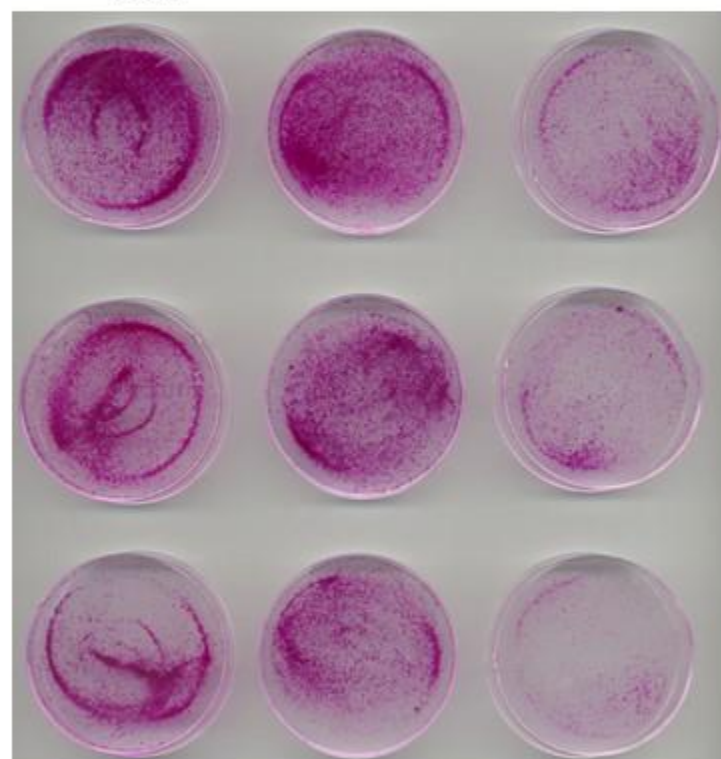
siNS

siE7

0 J/m²

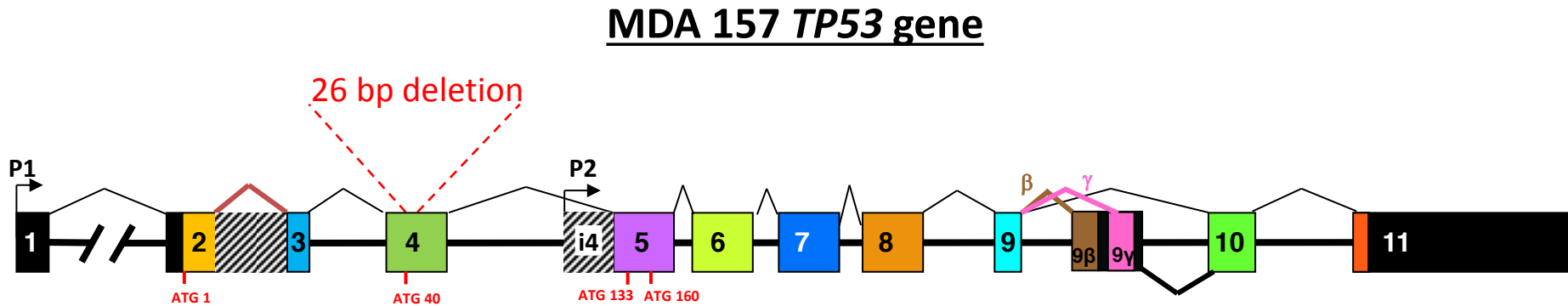
5 J/m²

10 J/m²



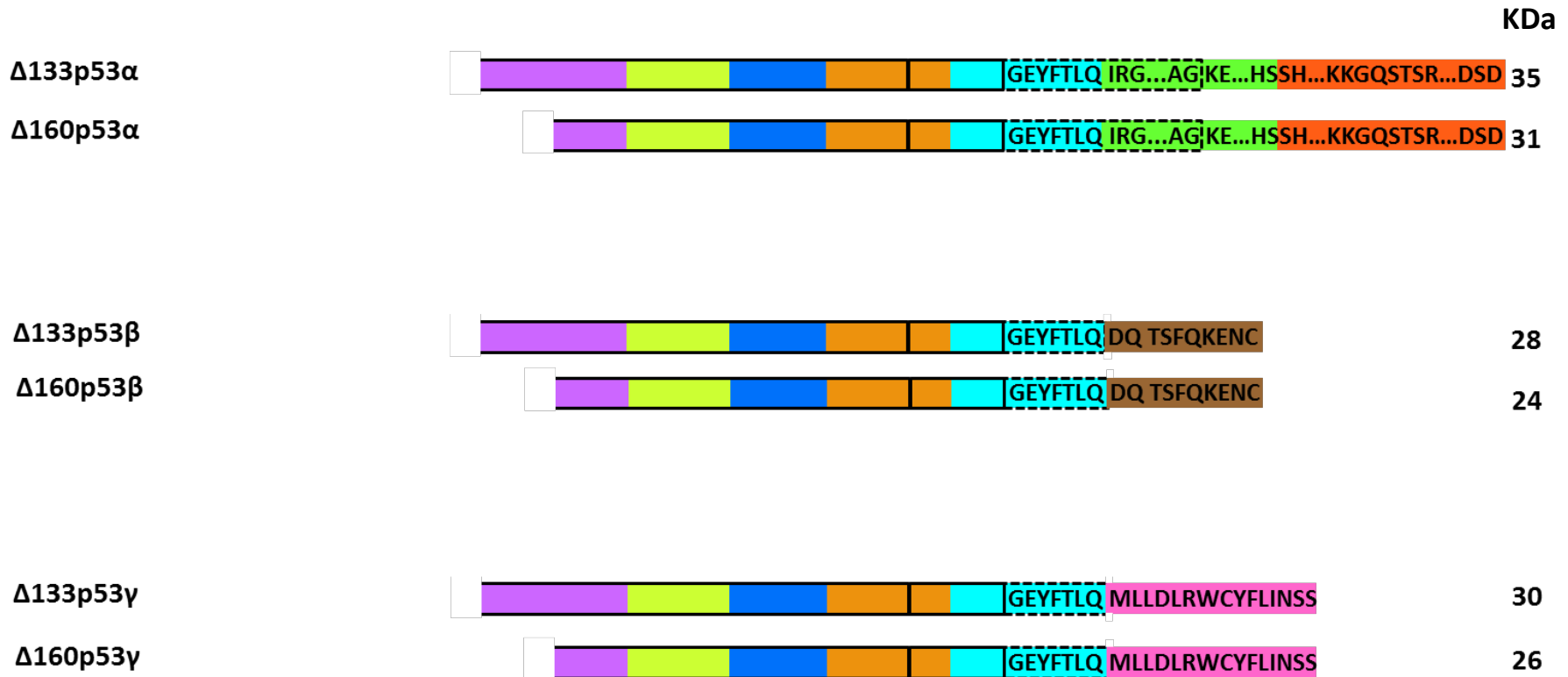
Characterisation of MDA 157

- Widely accepted as p53 “null” due to a 26 base pair deletion in exon 4 preventing expression of full length p53.



- Expression of WT $\Delta 133$ p53 and $\Delta 160$ p53 isoforms should not be affected

Theoretical p53 isoform expression in MDA 157



Characterisation of MDA 157

KJC8

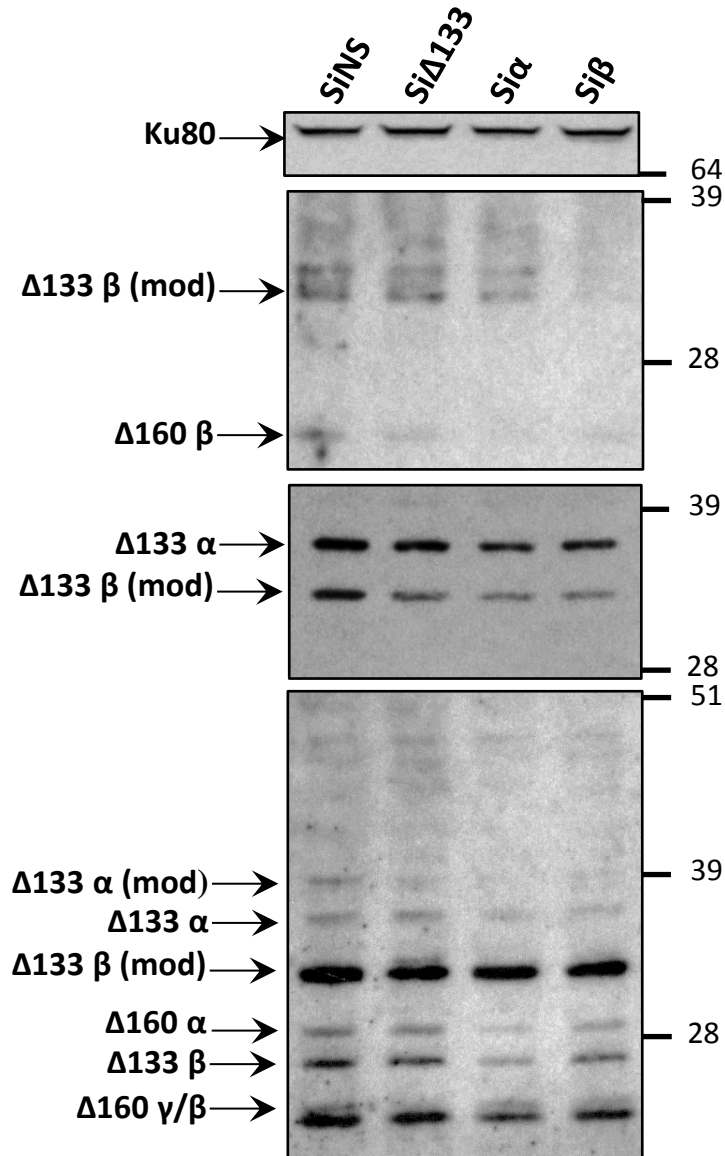
(Detection of β isoforms)

MAP4.9

(Detection of $\Delta 133$ isoforms)

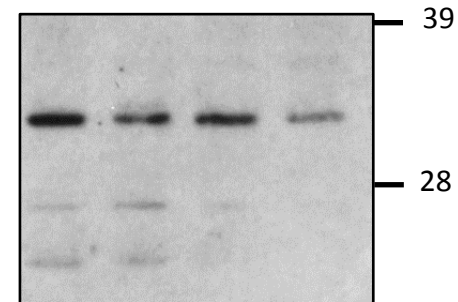
KJC12

(Detection of all isoforms)



Higher Exposure

- MDA 157 express WT $\Delta 133$ p53 and $\Delta 160$ p53 proteins.
- MDA 157 used as a model for $\Delta 133$ p53 and $\Delta 160$ p53 mediated cell response
- **p53 isoform specific siRNAs alter the balance of p53 isoforms**



Lower Exposure

Are p53 isoforms biologically active ?

- Does changing the balance of the endogenous p53 isoforms have a biological impact?
- Determine changes in
 - **Cell proliferation/growth**
 - **Cell differentiation** (morphology)
 - **Cell Death** (CellTox Green)

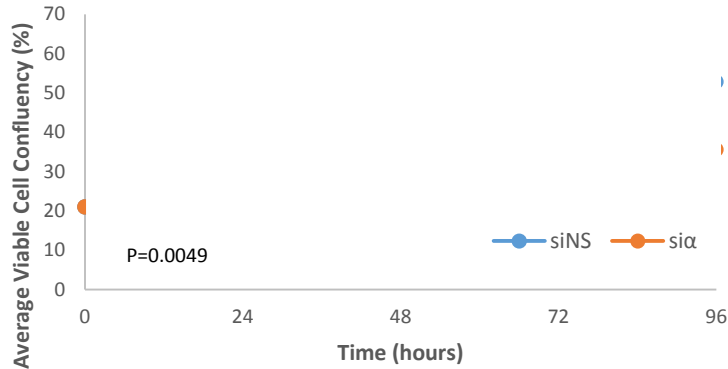
Tools- Live Cell Imaging

- Incucyte Zoom – 10X magnification microscope house inside a standard incubator.
- Images of cells taken every 2 hours for 4 days
- Incucyte Zoom used to observe and quantify changes in cell fate decision in real time.



Depletion of α -p53 isoforms with si α in MDA 157 results in cell differentiation

MDA 157 Cell Growth



- A significant reduction in growth is observed with si α compared to siNS
- si α transfected cells change morphology and emerge as a heterogeneous population
- Si α transfected cells become larger and adopt two distinct phenotypes

MDA 157 siNS

MDA 157 si α

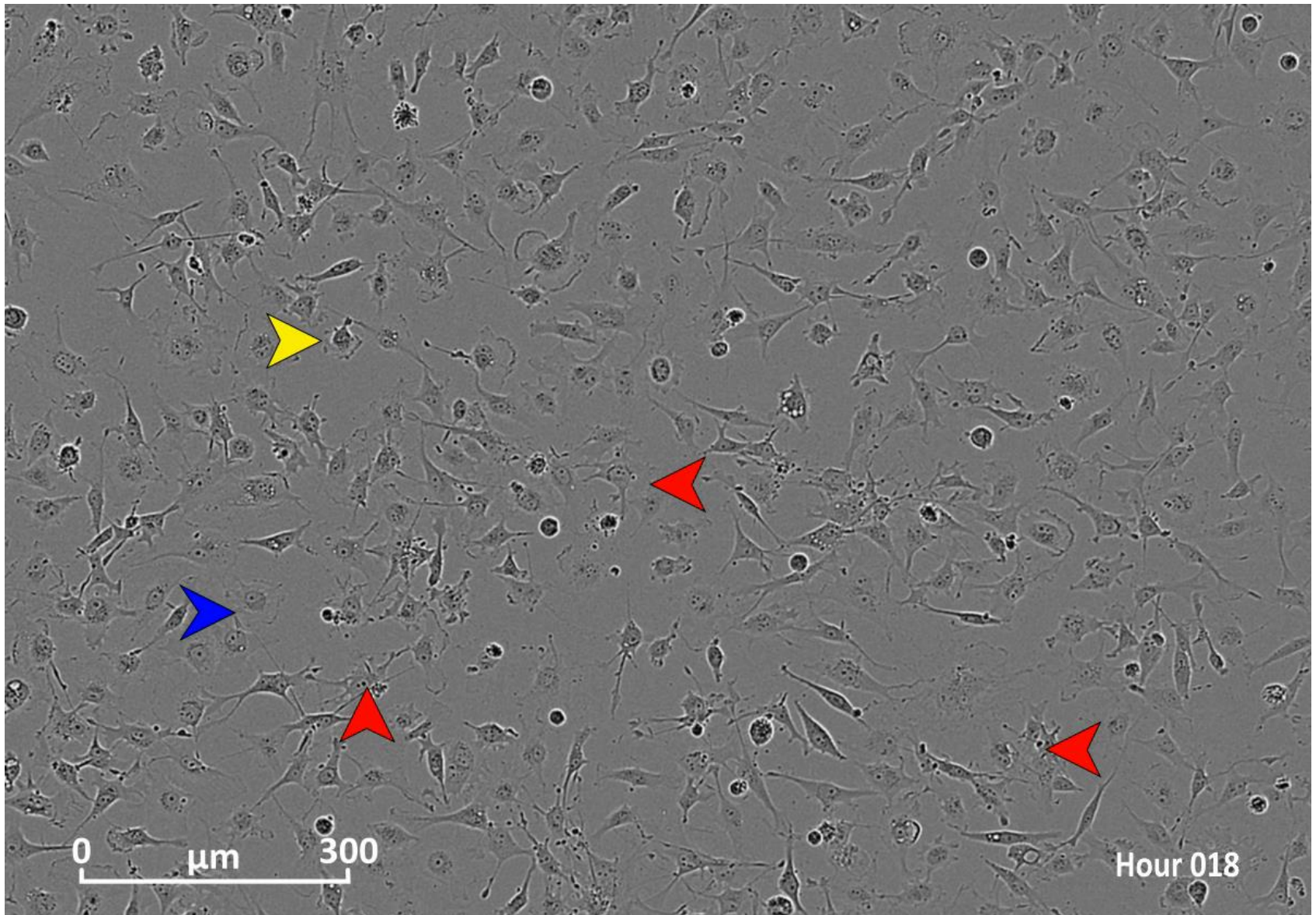
200 μ m

Hour 002

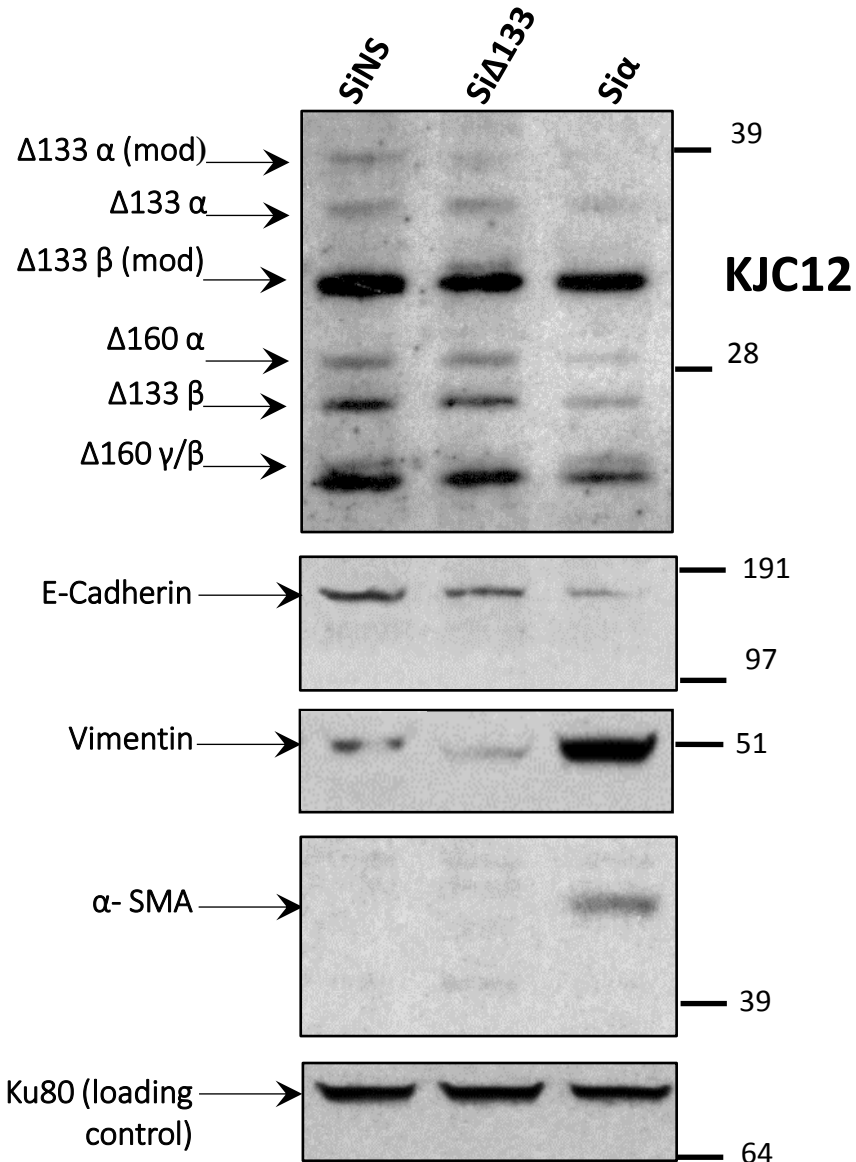
200 μ m

Hour 002

Depletion of α -p53 isoforms with si α in MDA 157 results in cell differentiation



Changes in Markers of EMT and Differentiation with p53 isoform-specific siRNA in MDA 157



- Depletion of different p53 isoform subsets changes expression of EMT and differentiation markers.

⇒ Change of differentiation status



Genome remodelling

McDonald OG et al., 2011;
Genome-scale epigenetic reprogramming during epithelial-to-mesenchymal transition. Nat Struct Mol Biol. 18(8):867-74.

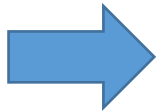
Suva ML et al., 2013;
Epigenetic reprogramming in cancer. Science. 339(6127):1567-70

Summary

- p53 “null” MDA-MB 157 express $\Delta 133p53\alpha$, $\Delta 133p53\beta$, $\Delta 160p53\alpha$ and $\Delta 160p53\beta$ isoforms.
- **Manipulation of p53 isoform expression in the absence of canonical p53 alter cell fate outcome**
- **Cells without canonical p53 but expressing other p53 isoforms have an active p53 pathway-p53 isoforms are biologically active**

Summary

- p53 “null” MDA-MB 157 express $\Delta 133p53\alpha$, $\Delta 133p53\beta$, $\Delta 160p53\alpha$ and $\Delta 160p53\beta$ isoforms.
- **Manipulation of p53 isoform expression in the absence of canonical p53 alter cell fate outcome**
- **Cells without canonical p53 but expressing other p53 isoforms have an active p53 pathway-p53 isoforms are biologically active**



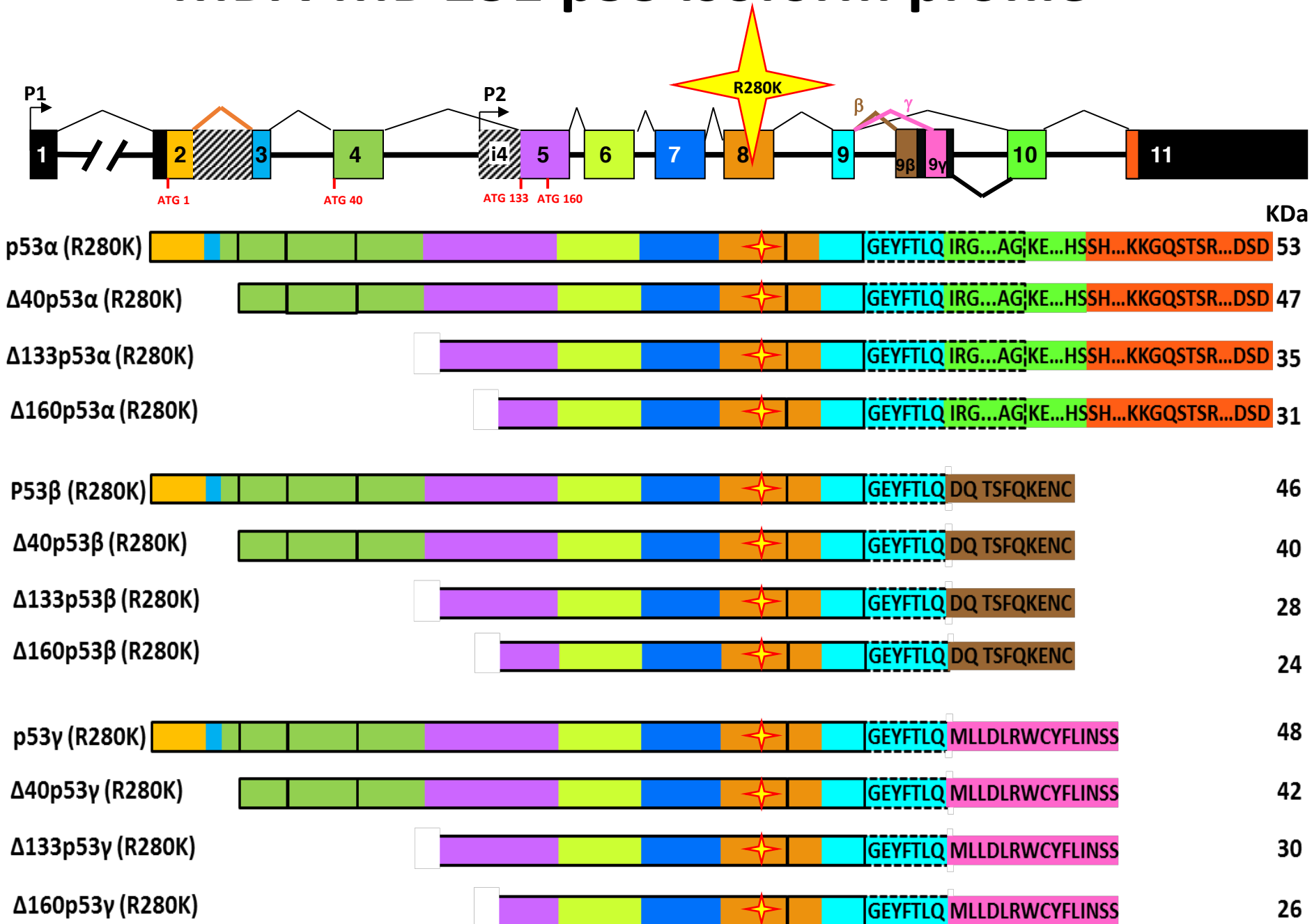
Is this phenomenon particular to the MDA-157 cell line?

Characterisation of MDA 231

(mutation TP53-R280K)

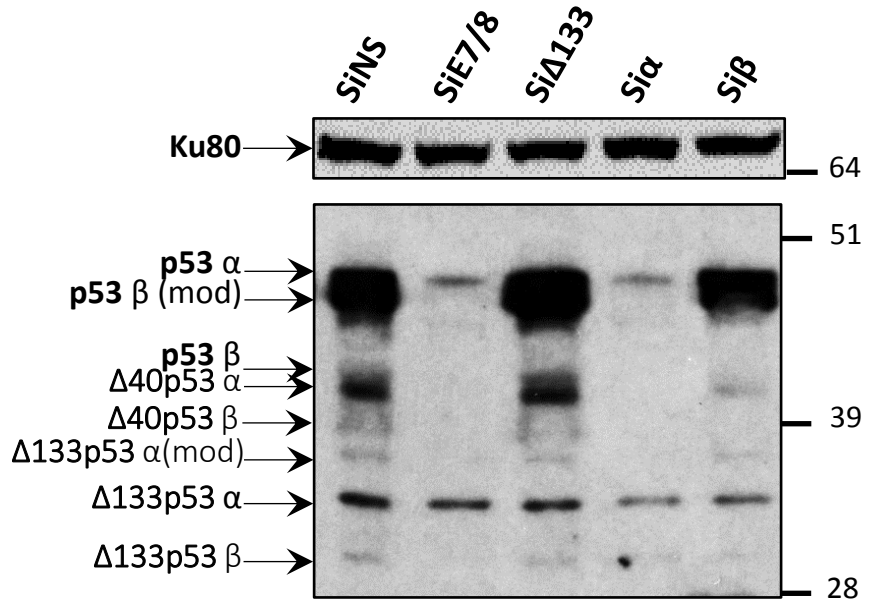
- Can differential expression of mutant p53 isoforms also alter mutant p53-mediated cell fate outcome ?

MDA-MB 231 p53 isoform profile

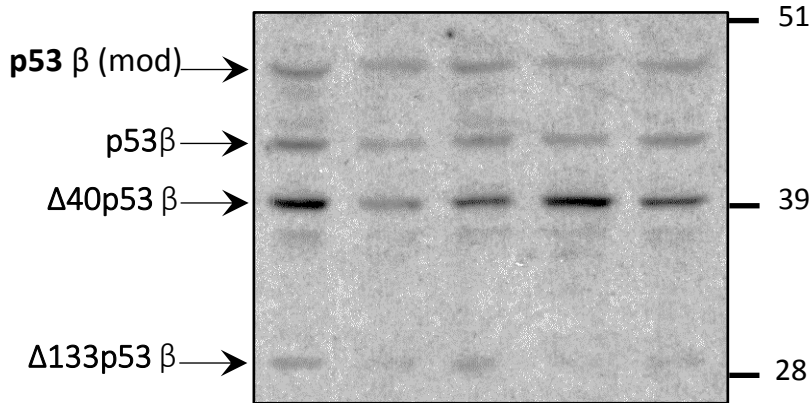


Characterisation of MDA 231

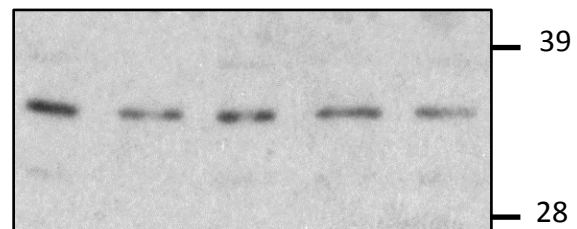
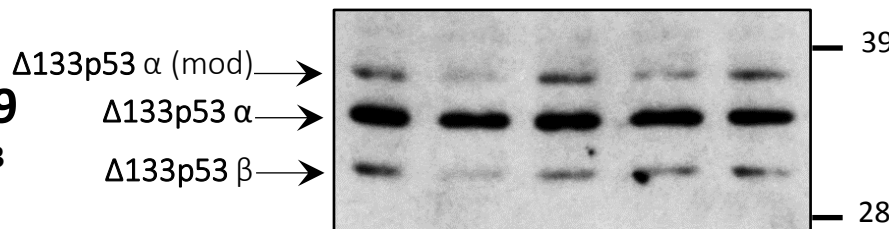
CM1
(most p53 isoforms)



KJC8
(β -p53 isoforms)

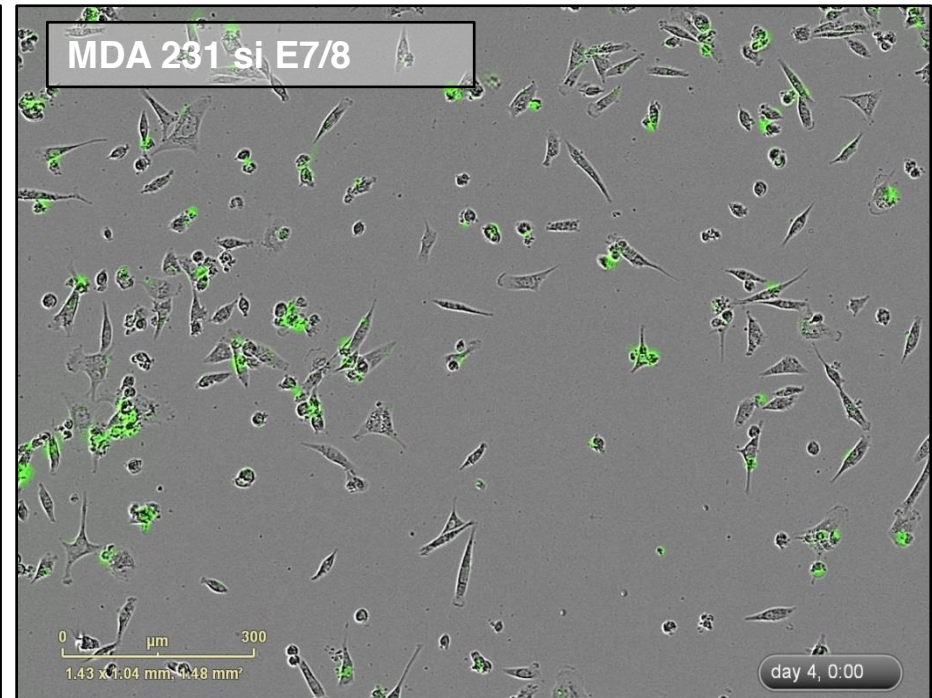
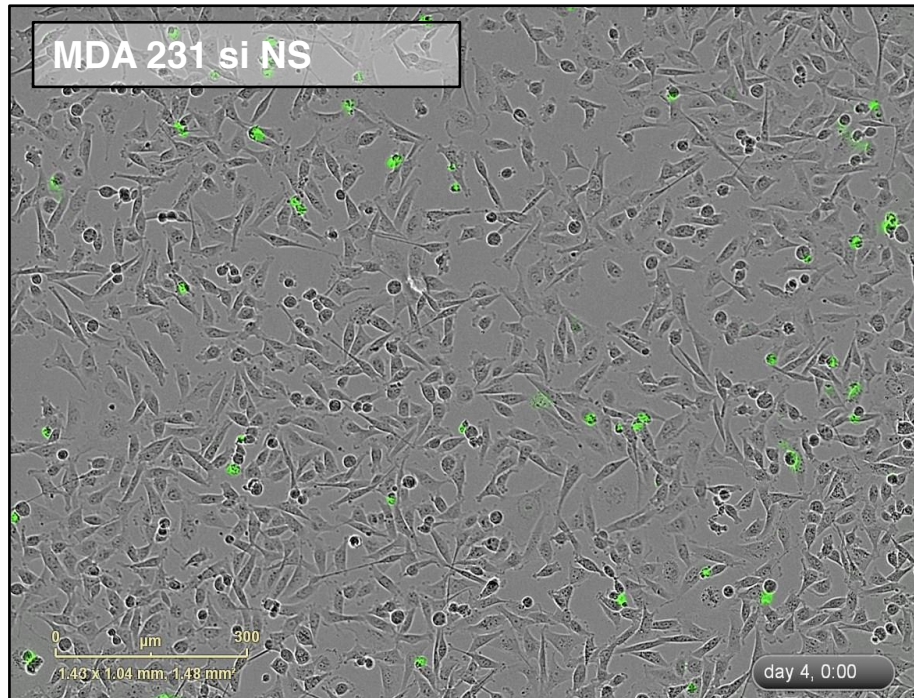
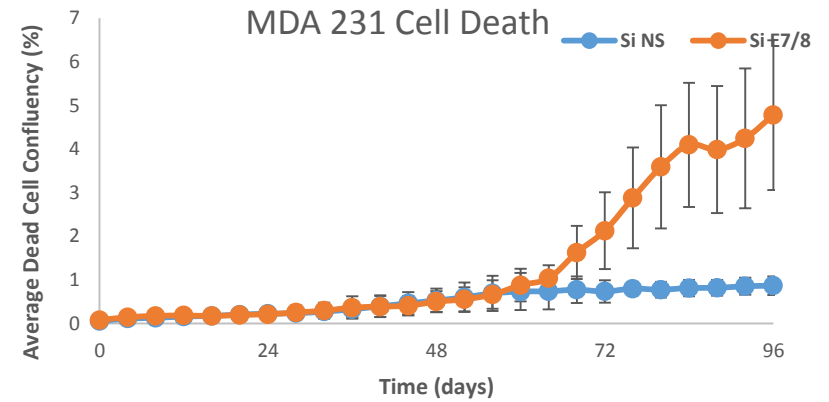
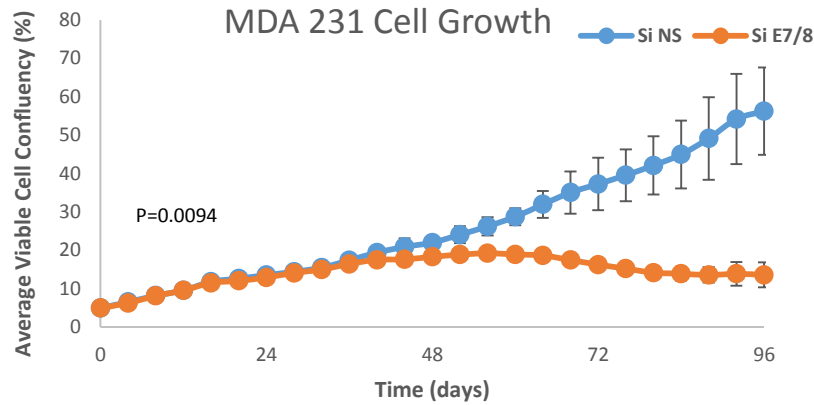


MAP4.9
(Δ133 p53 isoforms)

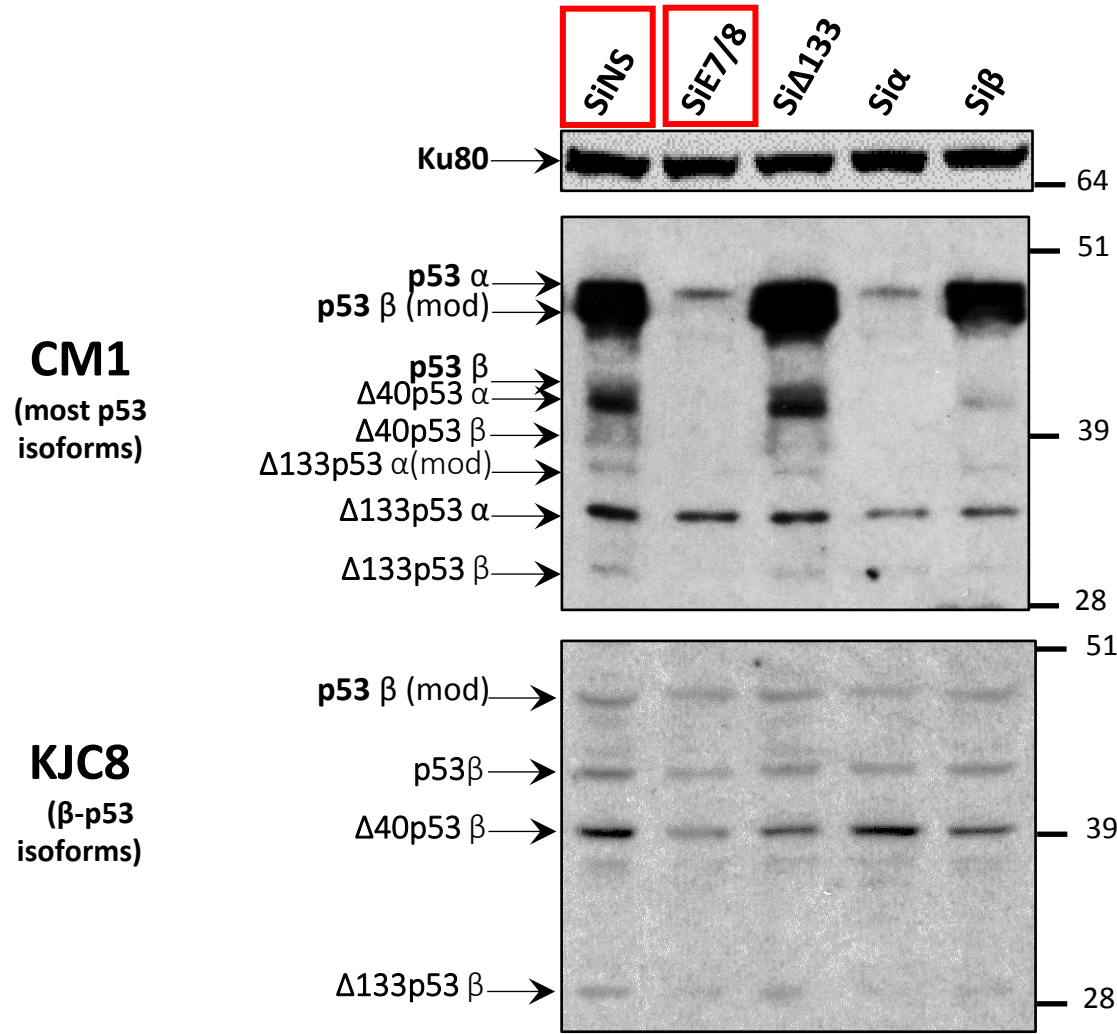


- Show mutant p53 isoform expression at protein level.
- siRNAs differentially in balance mutant p53 isoform expression.

Depletion of all mutant p53 isoforms with si E7/8 in MDA 231 induces cell death



Depletion of all mutant p53 isoforms induces cell death in MDA-MB 231



- siE7/8 transfection results in depletion of all p53 isoforms- including canonical p53
- Biologically depletion of all p53 isoforms results in cell death

Depletion of mutant α -p53 isoforms with si α in MDA 231 changes cell morphology and growth rate

MDA 231 Cell Growth



- A significant reduction in growth is observed with si α compared to siNS
- si α transfected cells change morphology.

MDA-MB 231 si NS

MDA-MB 231 si α

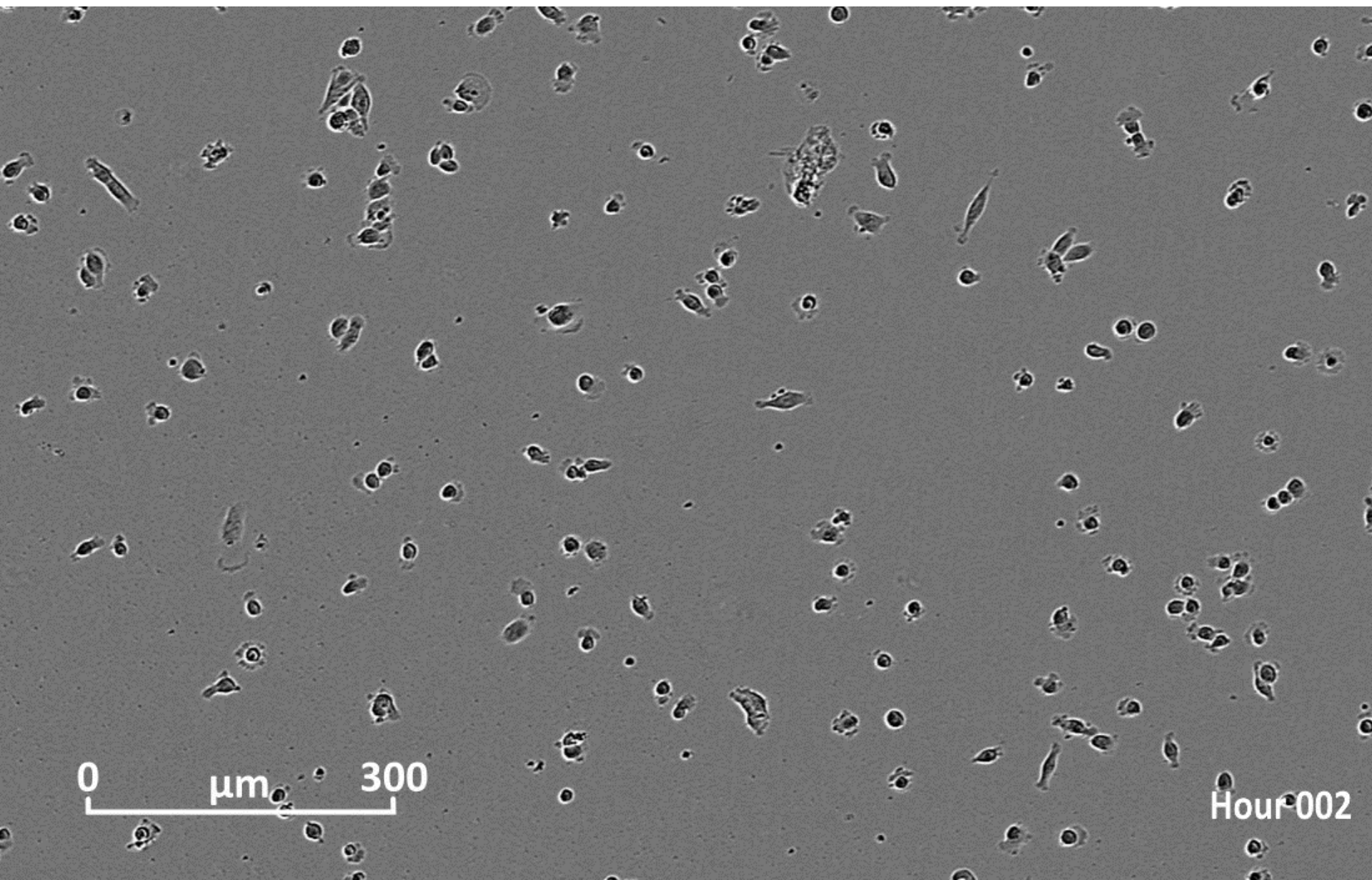
200 μ m

Hour 002

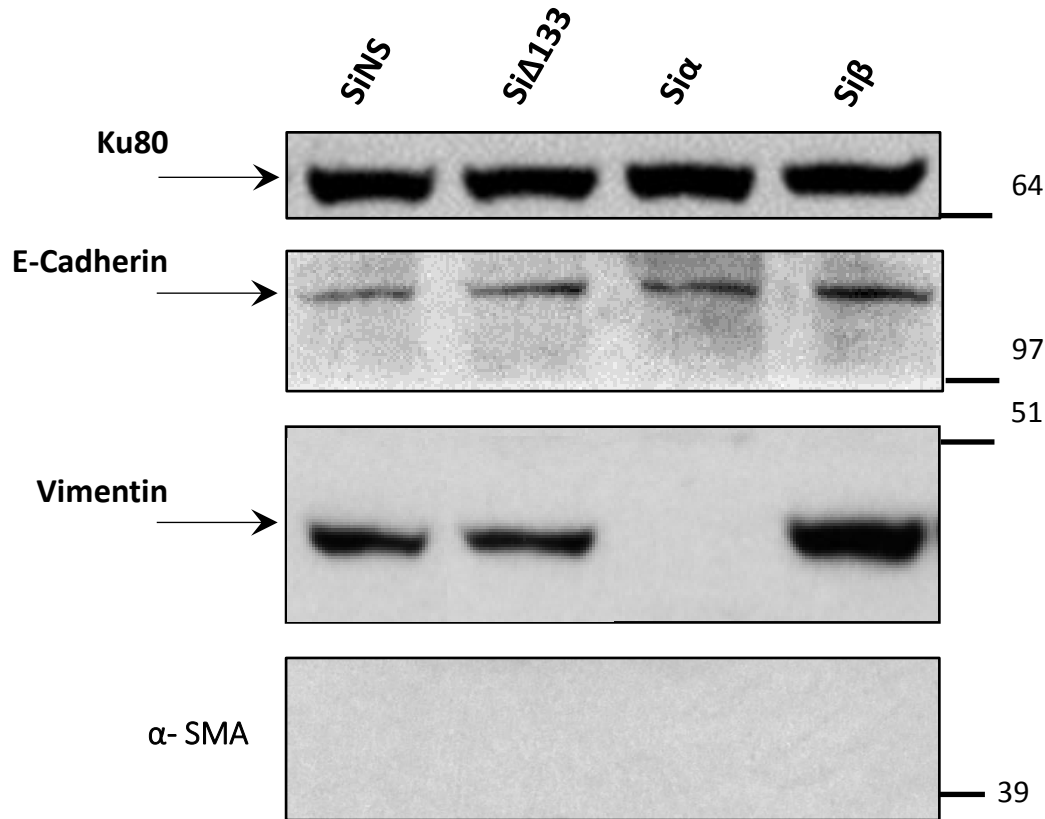
200 μ m

Hour 002

Depletion of mutant α -p53 isoforms with si α in MDA 231 changes cell morphology and growth rate



Manipulation of p53 isoforms changes expression of EMT markers in MDA 231



- Depletion of different mutant p53 isoform subsets changes expression of EMT markers.
- Change of differentiation status
 - ⇒ Genome remodelling (Cellular plasticity)

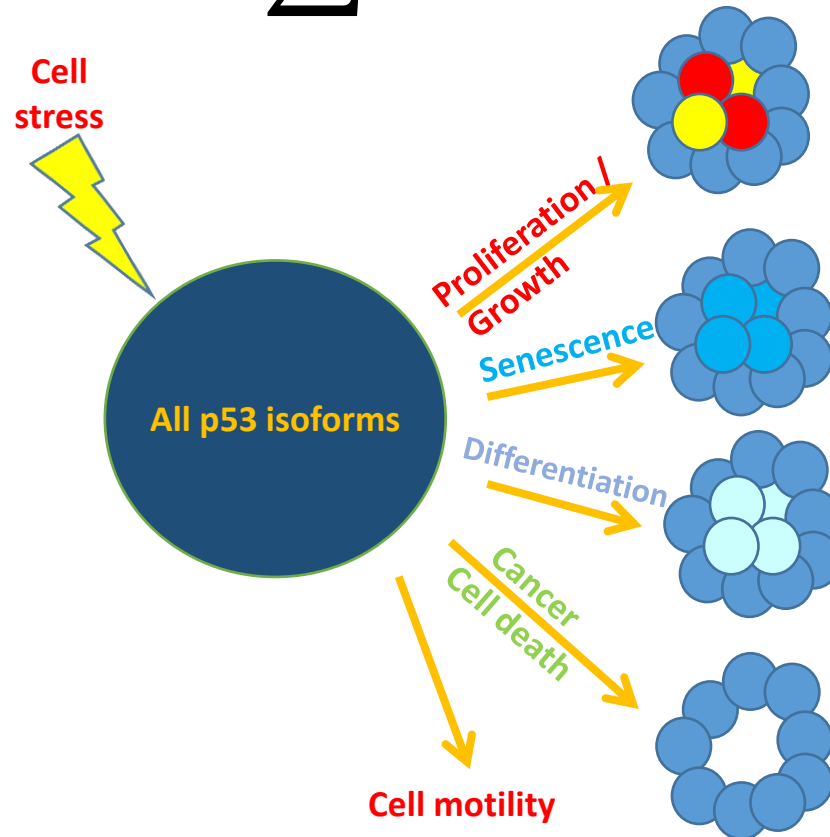
Conclusions

- The p53 pathway is still active in absence of canonical p53 (MDA 157 cell results).
- Biological activity attributed to *TP53* is not exclusively carried out by canonical p53 - p53 isoforms work in combination to elicit p53-mediated cell fate response.
- Manipulating p53 isoform expression (WT or mutant) changes cell fate through global genome remodelling.

p53 Isoform Model

$TP53$ gene activity = p53 α **X**

$TP53$ gene activity = \sum All p53 isoforms present

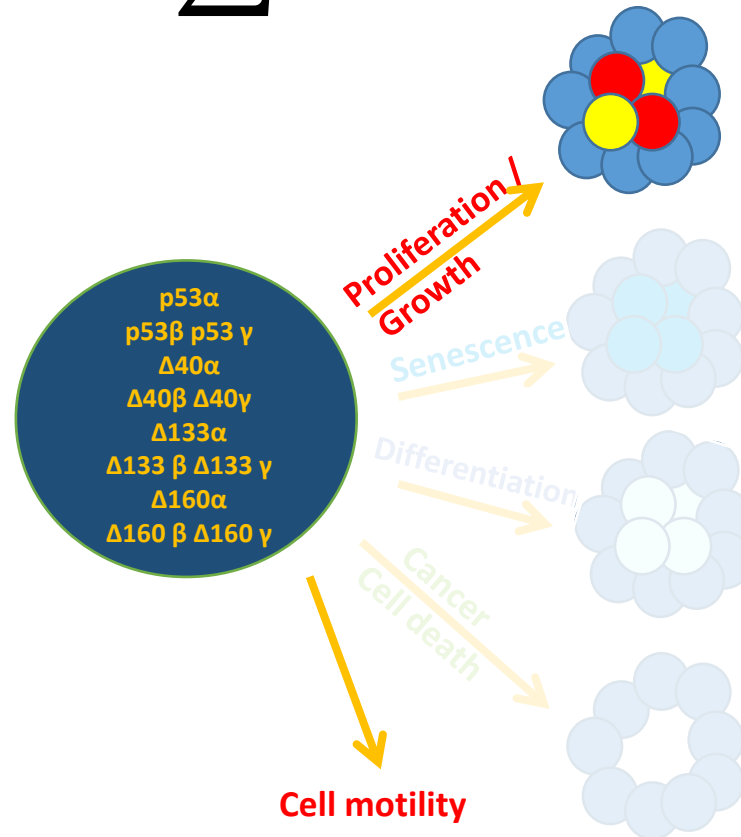


P53 Isoform Model

$TP53$ gene activity = p53 α **X**

$TP53$ gene activity = \sum All p53 isoforms present

MDA 231

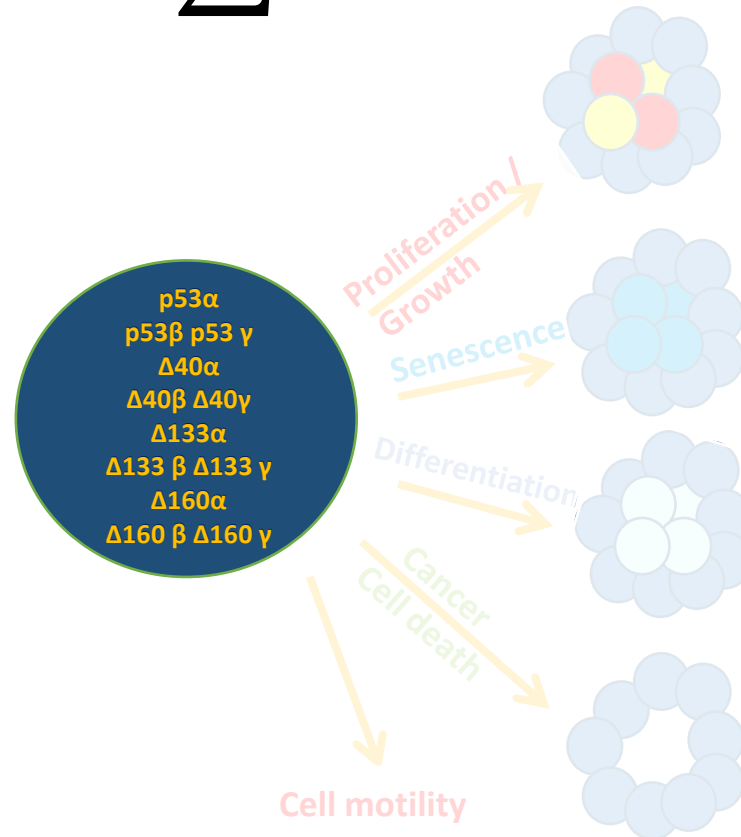


P53 Isoform Model

TP53 gene activity = p53 α **X**

TP53 gene activity = \sum All p53 isoforms present

Si E7/8 transfection
in MDA 231

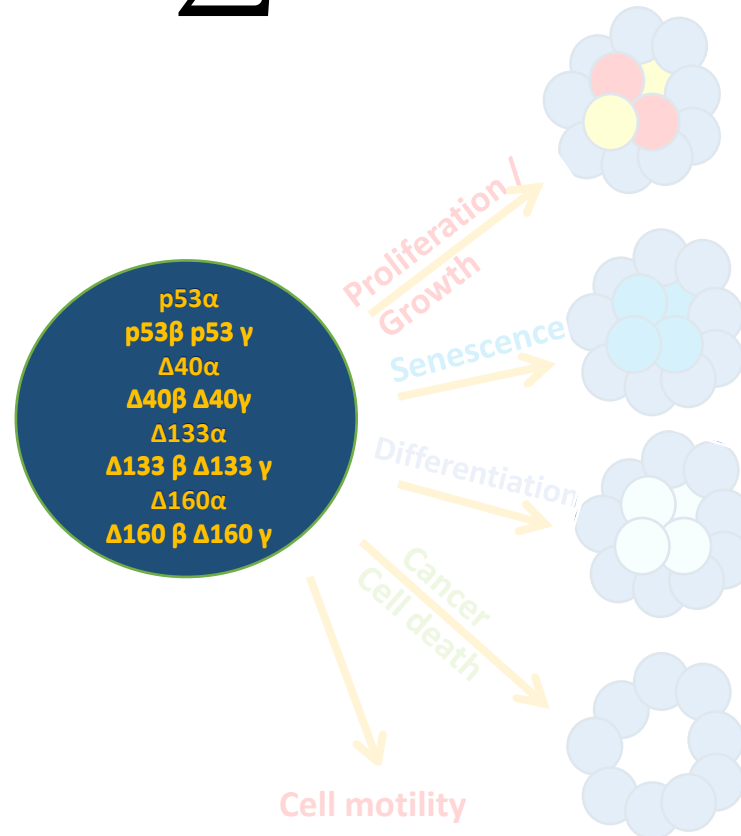


P53 Isoform Model

$TP53$ gene activity = p53 α **X**

$TP53$ gene activity = \sum All p53 isoforms present

Six transfection
in MDA 231



Parameters that influence p53 activity

- Intracellular components:

- Cancer type (tissue and driver oncogene)
- Composition in p53 isoforms
- TP53 mutation status

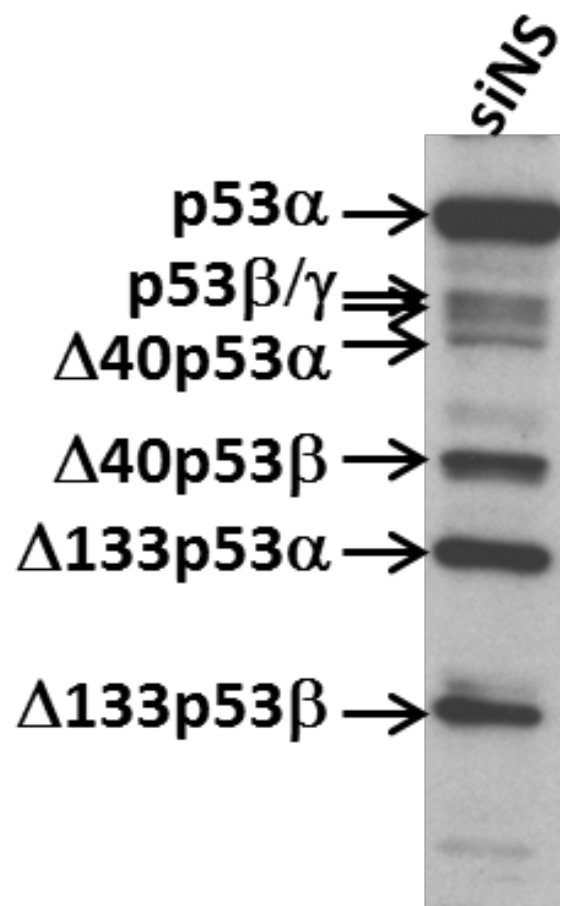
- Extracellular components

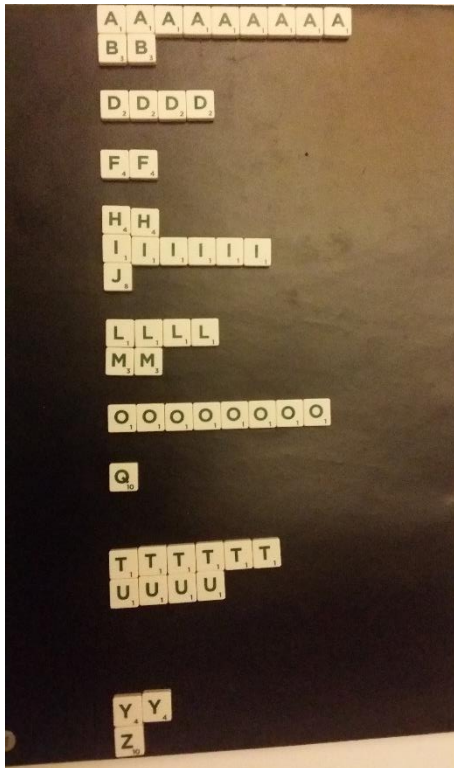
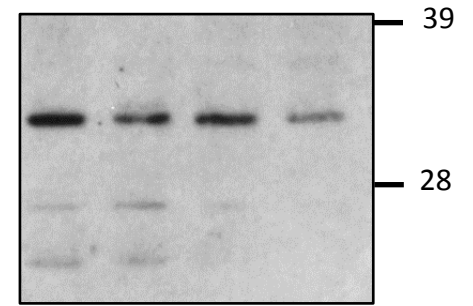
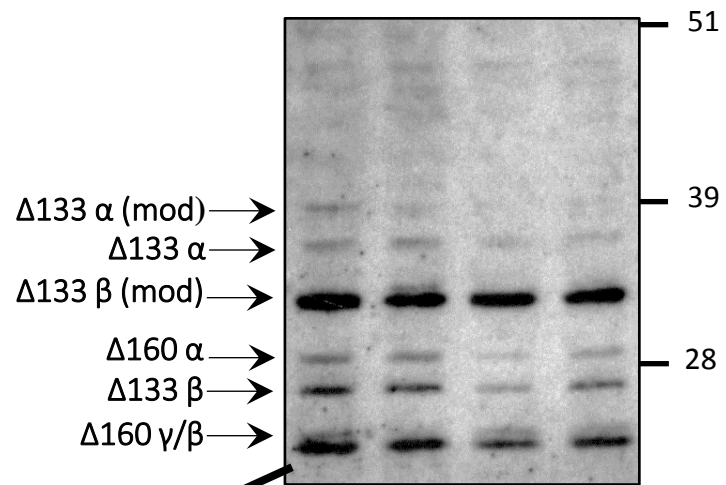
- Nutrient and extracellular signals
- Type, intensity and duration of the treatment

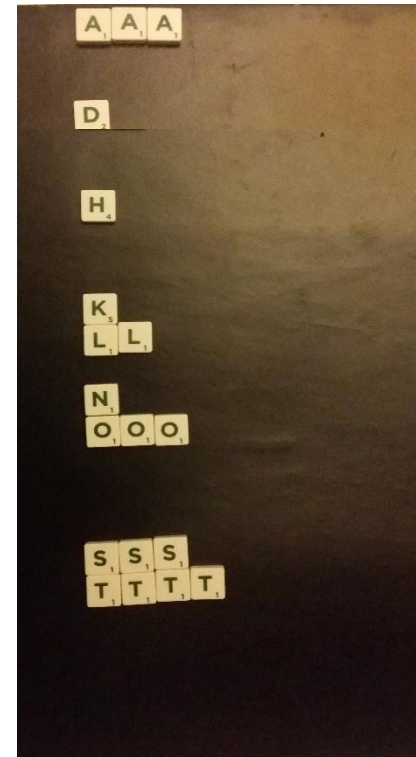
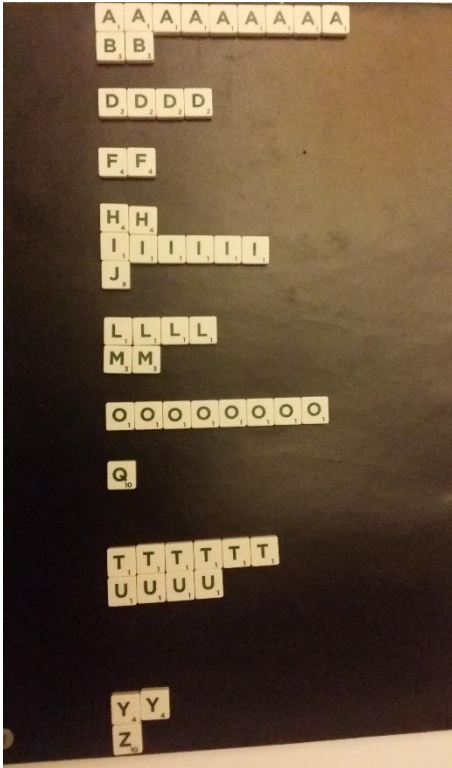
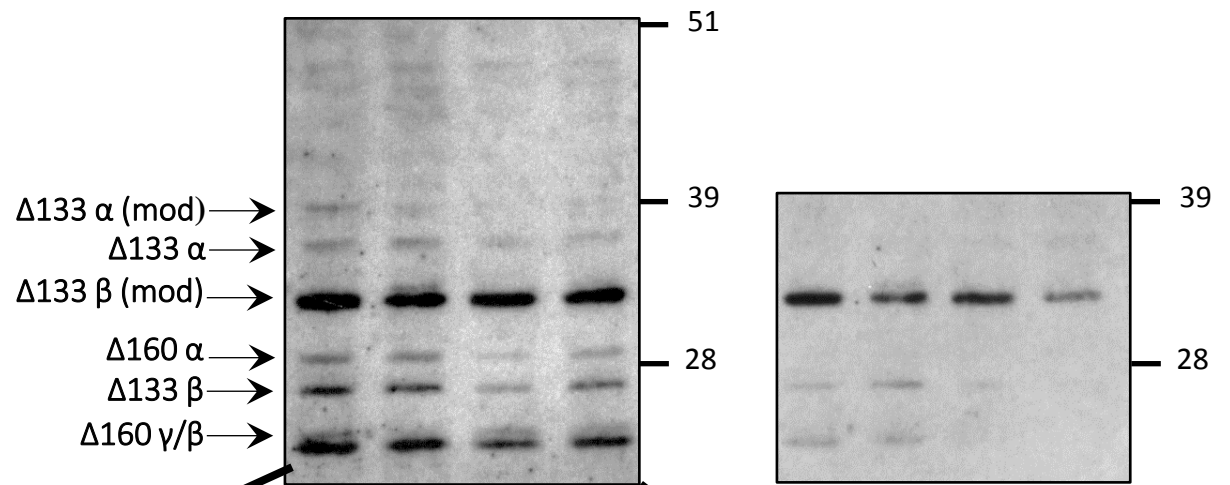


If none of the p53 isoforms is absolutely required to trigger a p53 mediated response, what is the underlying mechanism?





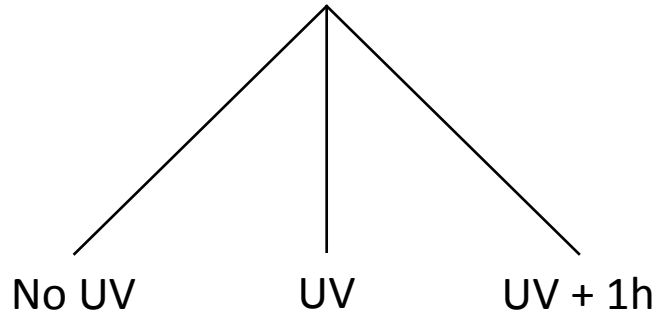




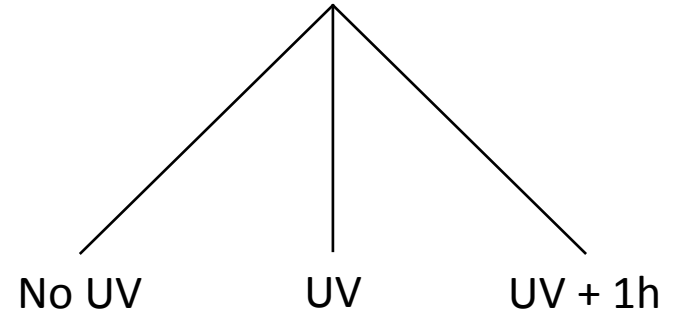
HCT116 +/+
(All isoforms)

HCT116 -/-
(No TAp53 α , β , γ)

HCT116 +/+
(All isoforms)

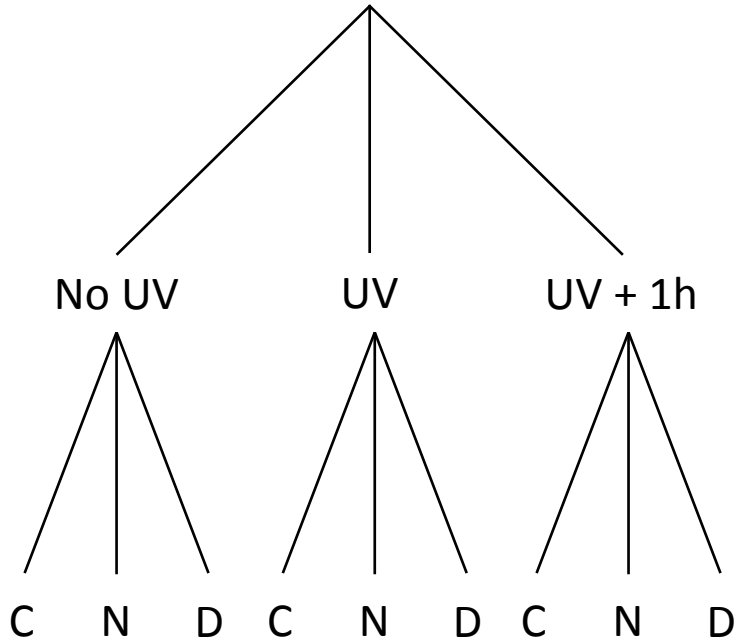


HCT116 -/-
(No TAp53 α , β , γ)



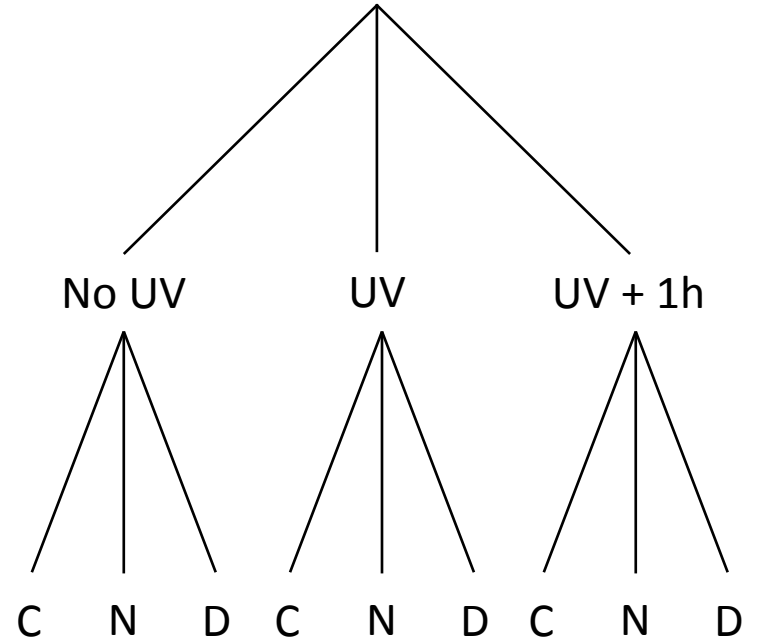
UV treatment
(20 Joules)

HCT116 +/+
(All isoforms)



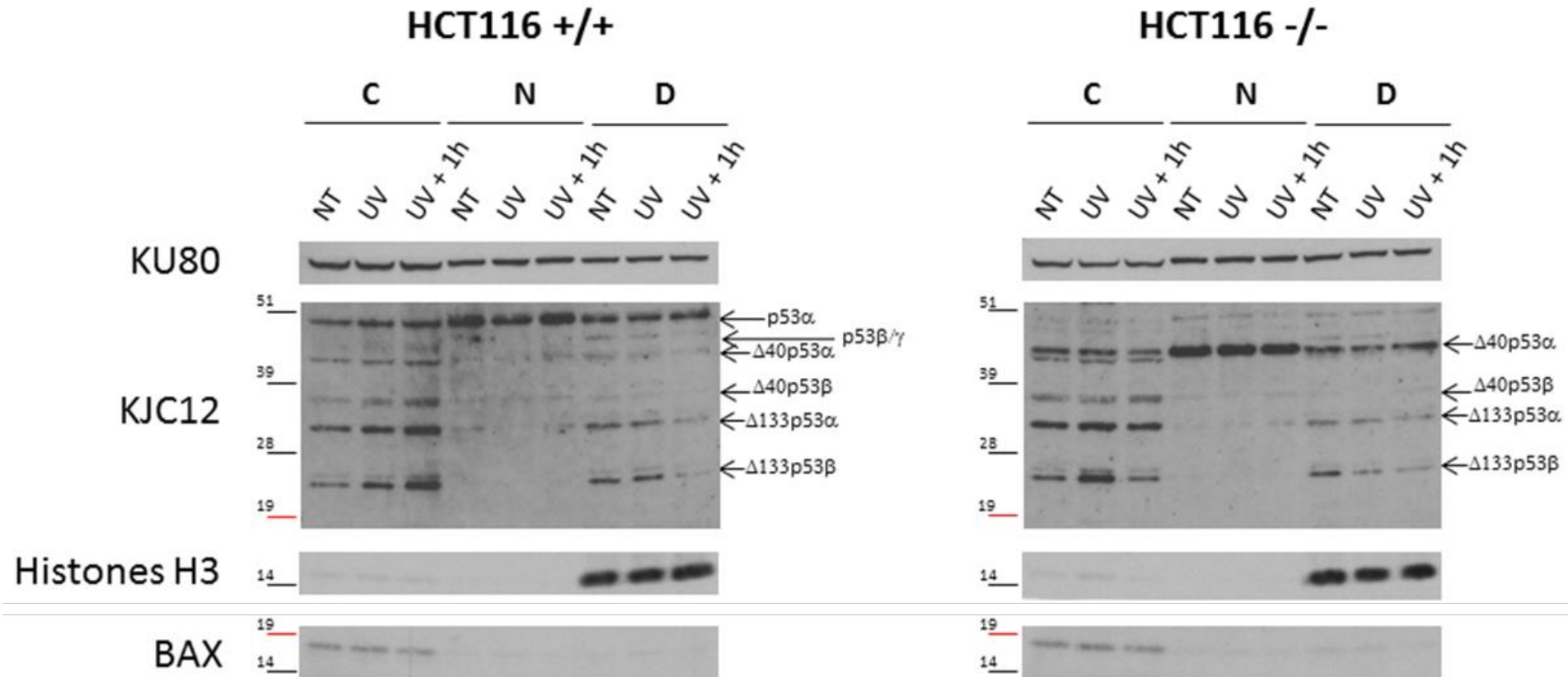
UV treatment
(20 Joules)

HCT116 -/-
(No TAp53 α , β , γ)

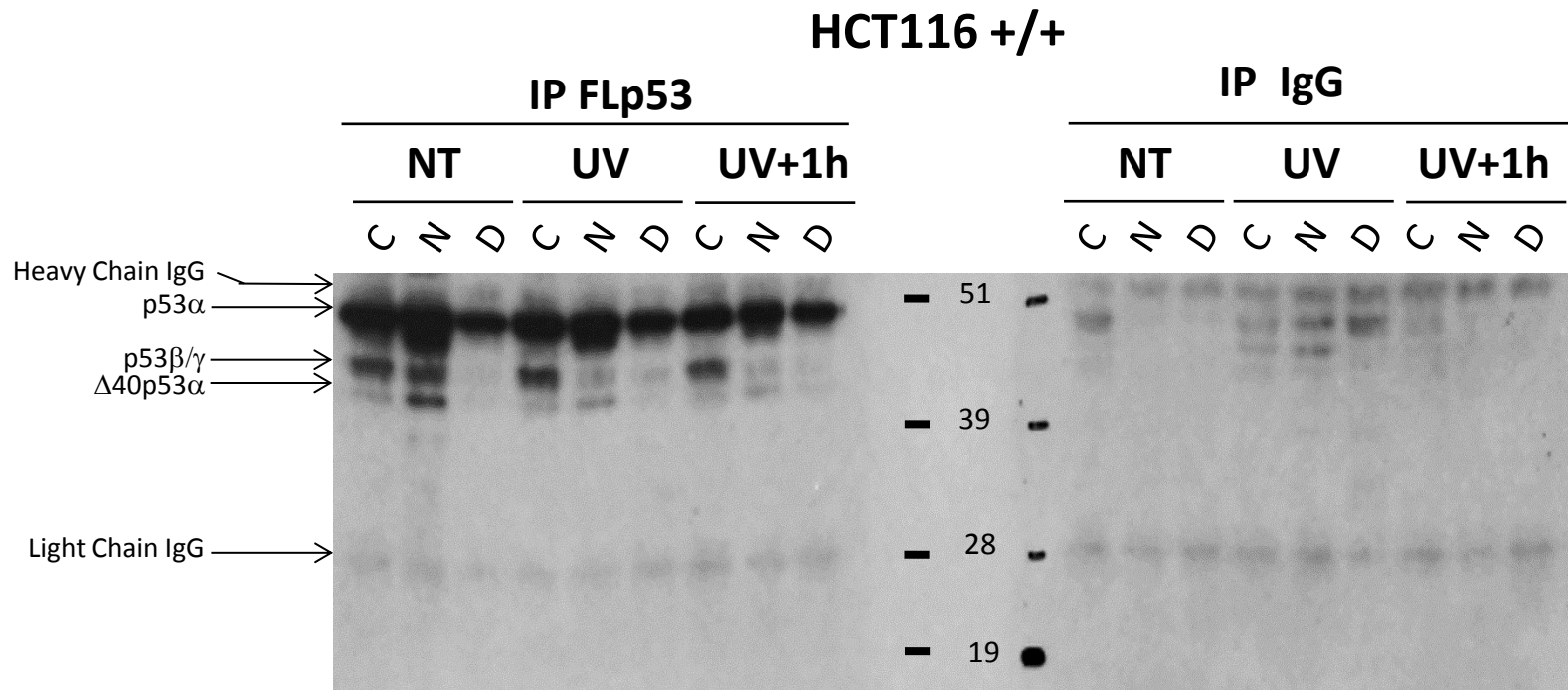


C = Cytoplasm
N = Nucleoplasm
D = DNA

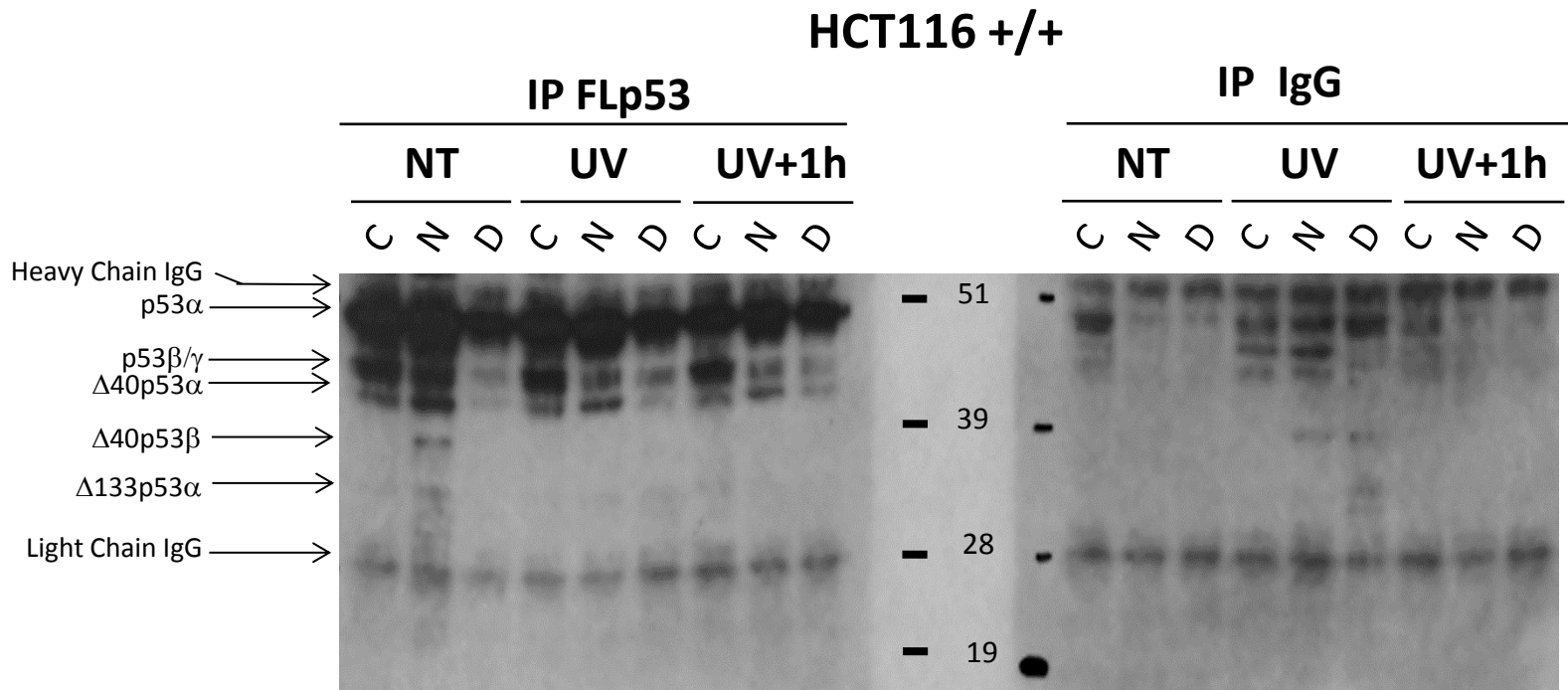
How do p53 isoforms behave in respond to stress?



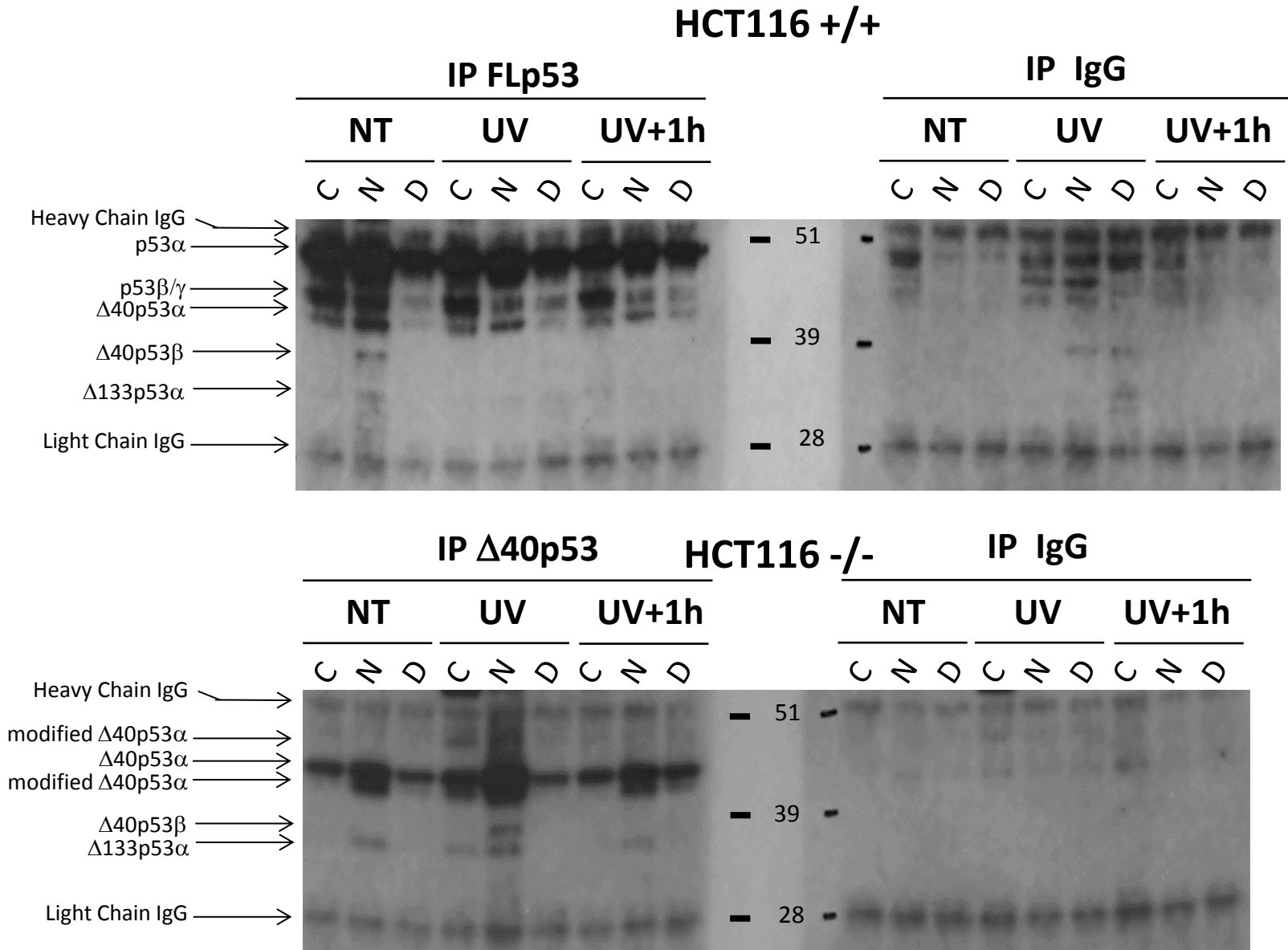
Do p53 isoforms act alone or in combination?



Do p53 isoforms act alone or in combination?



Do p53 isoforms act alone or in combination?



→ Endogenous p53 isoforms oligomerise together in HCT116 +/+ and HCT116 -/- cells

→ Endogenous p53 isoforms oligomerise together in HCT116 +/+ and HCT116 -/- cells

→ Composition and localisation of the oligomers dynamically change in response to UV stress



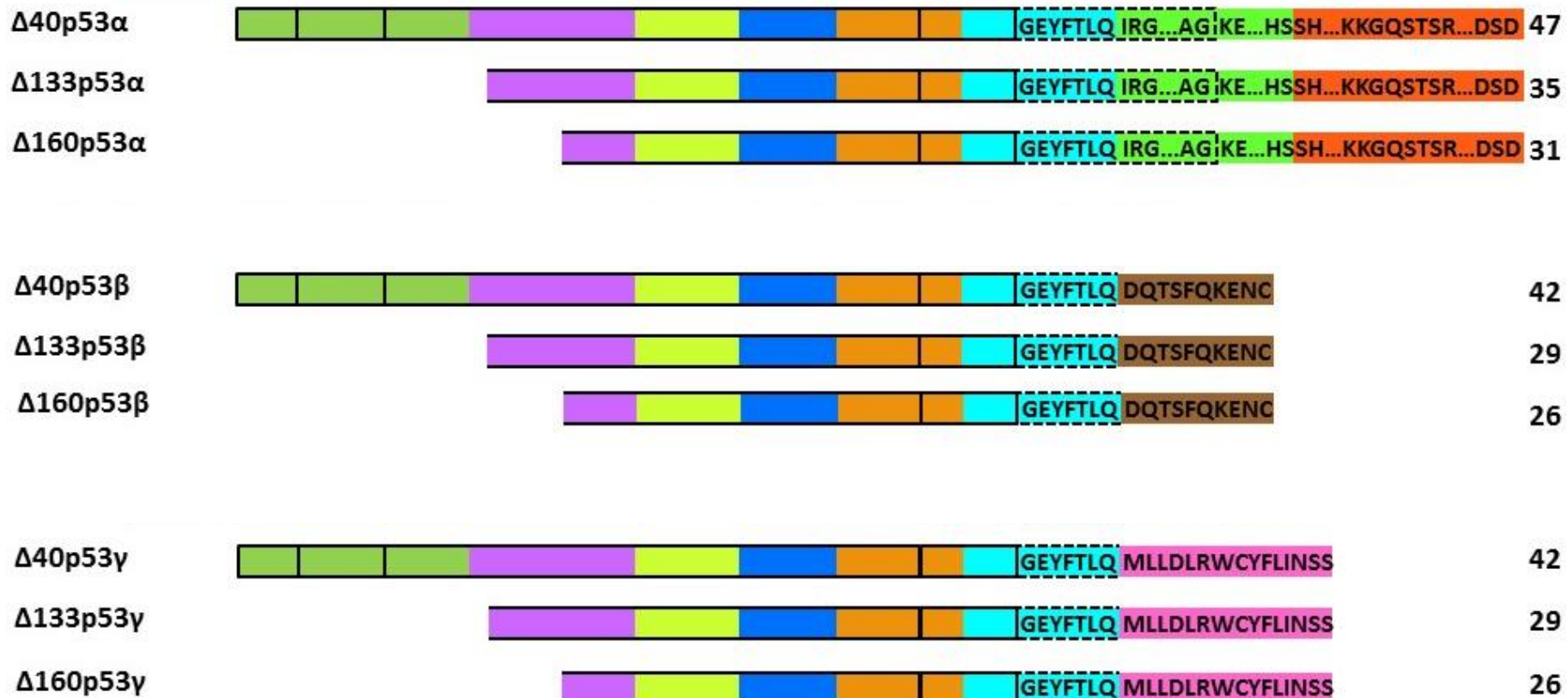
Are these oligomers transcriptionally active?



Are these oligomers transcriptionally active?

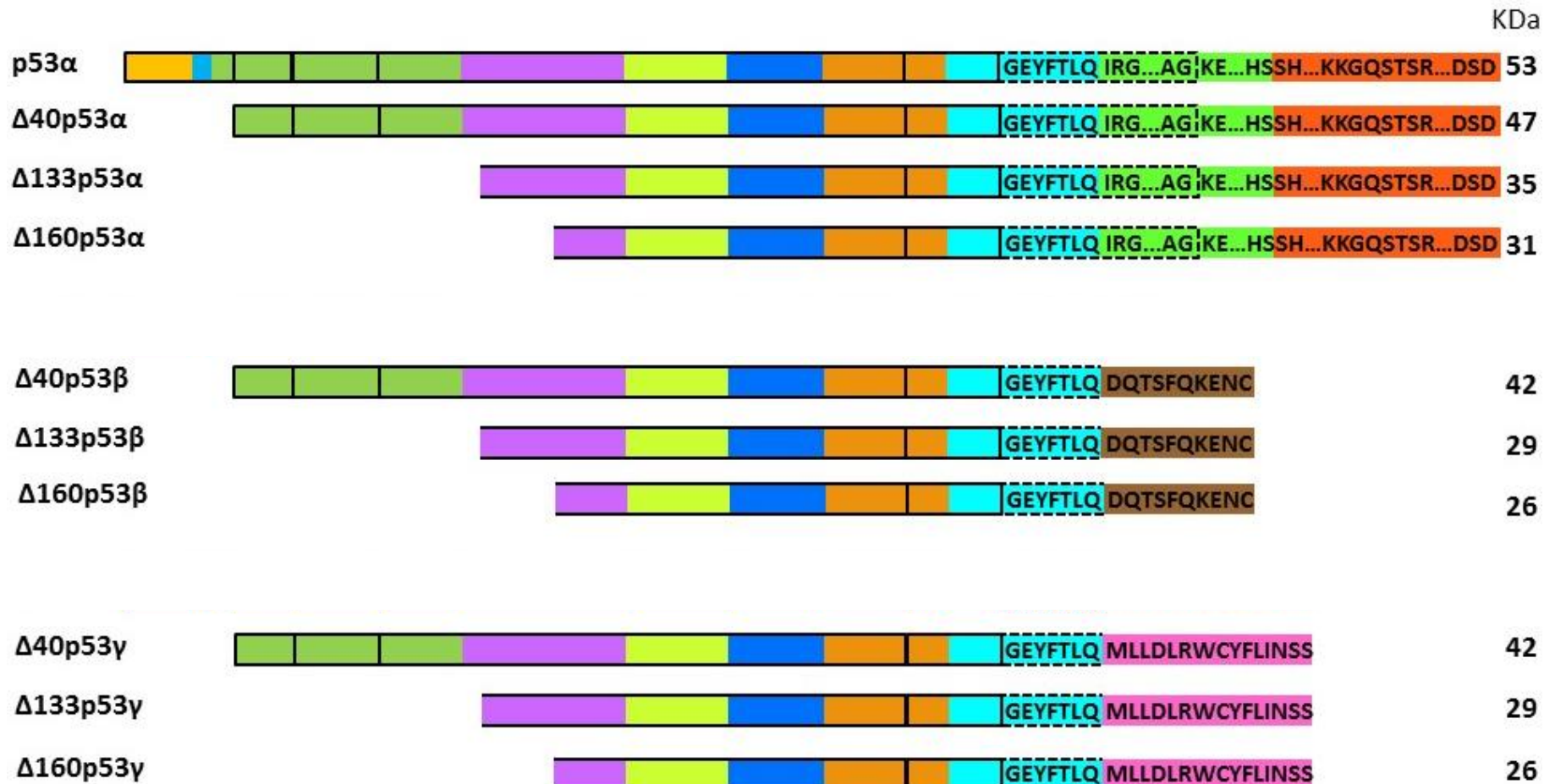
HCT116 -/- cell

KDa



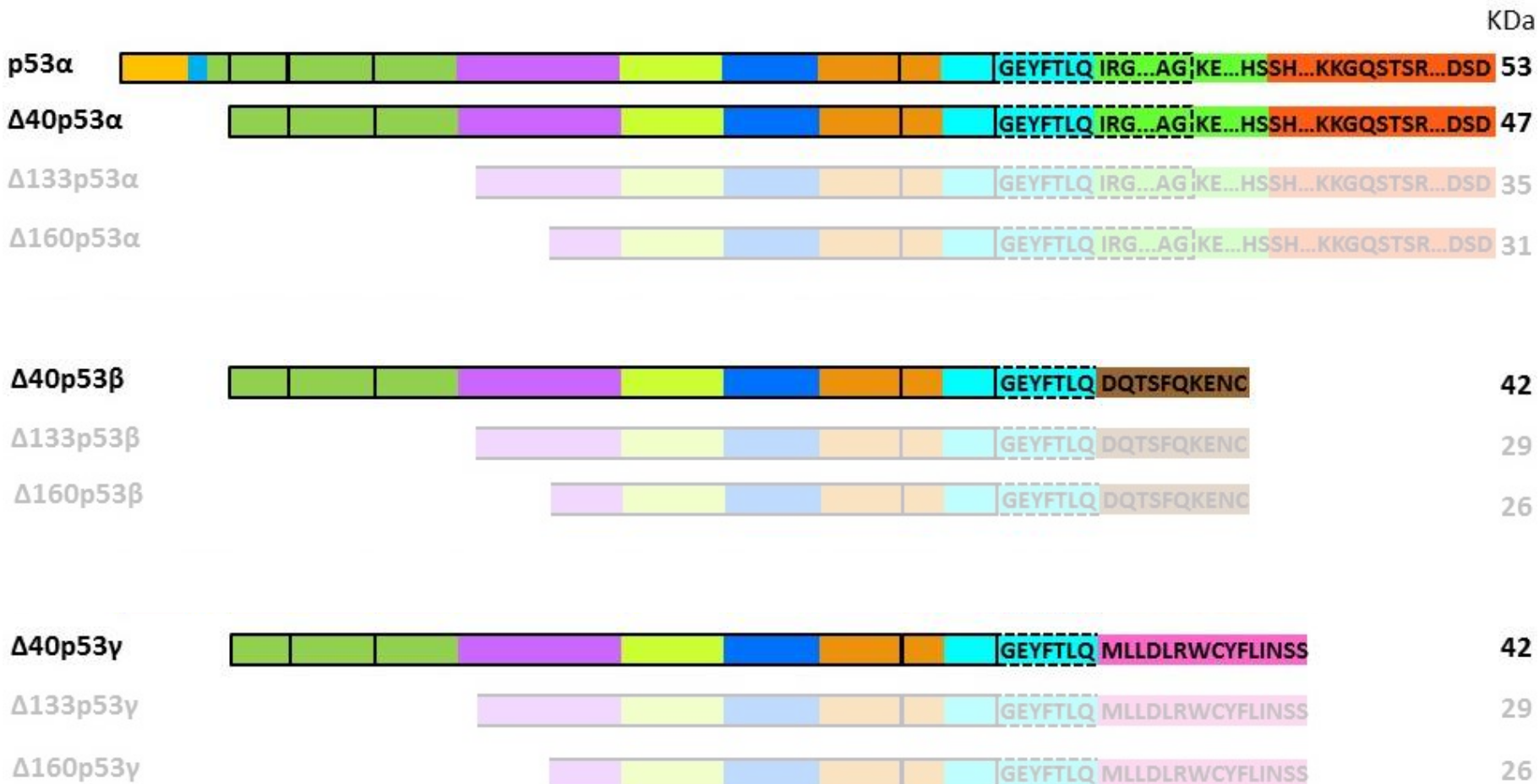
Are these oligomers transcriptionally active?

« p53 α rescued » HCT116 -/- cell



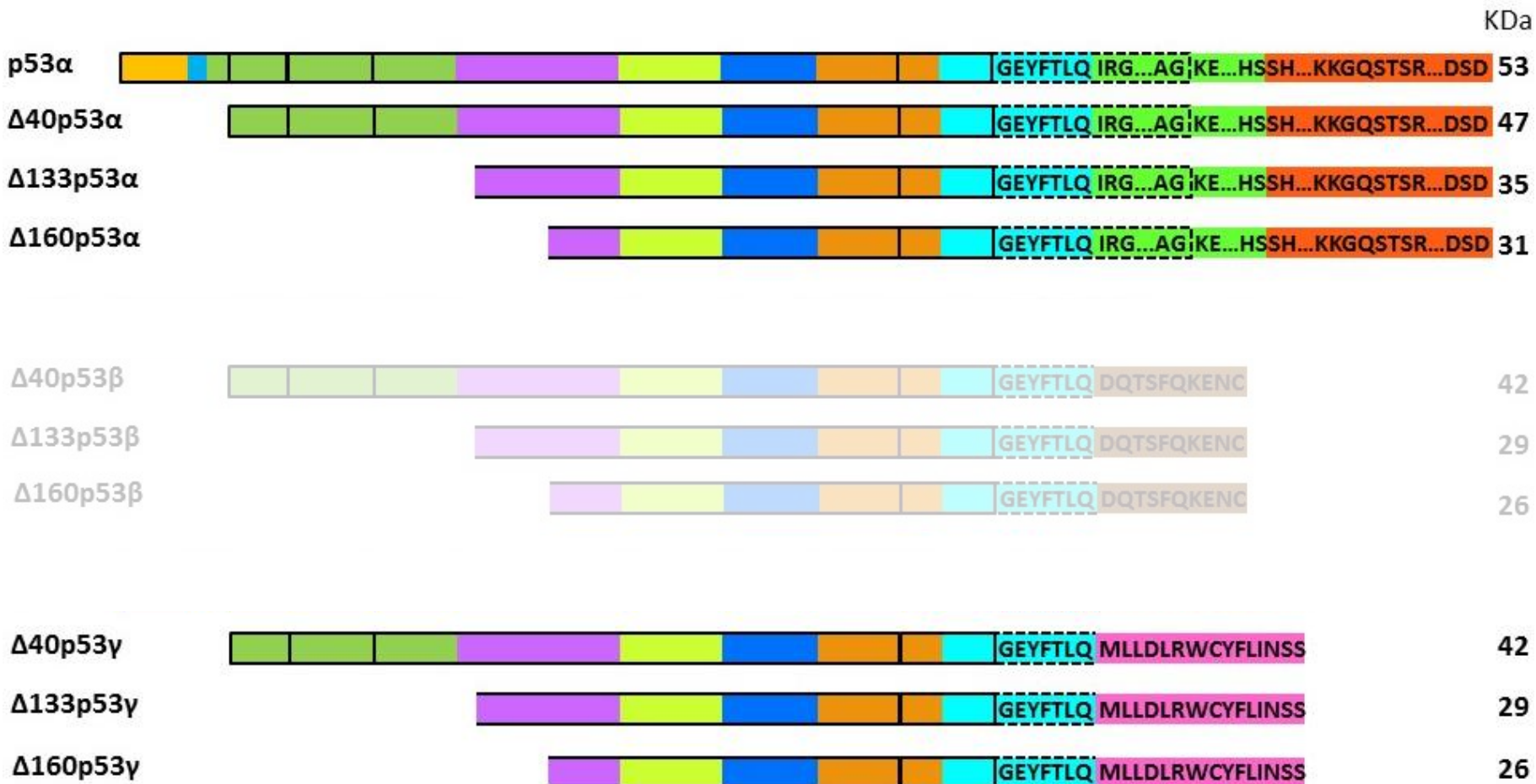
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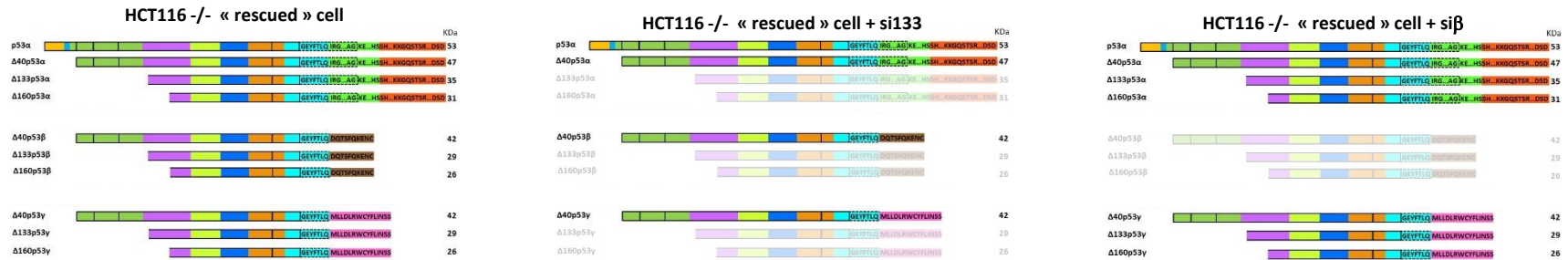


Are these oligomers transcriptionally active?

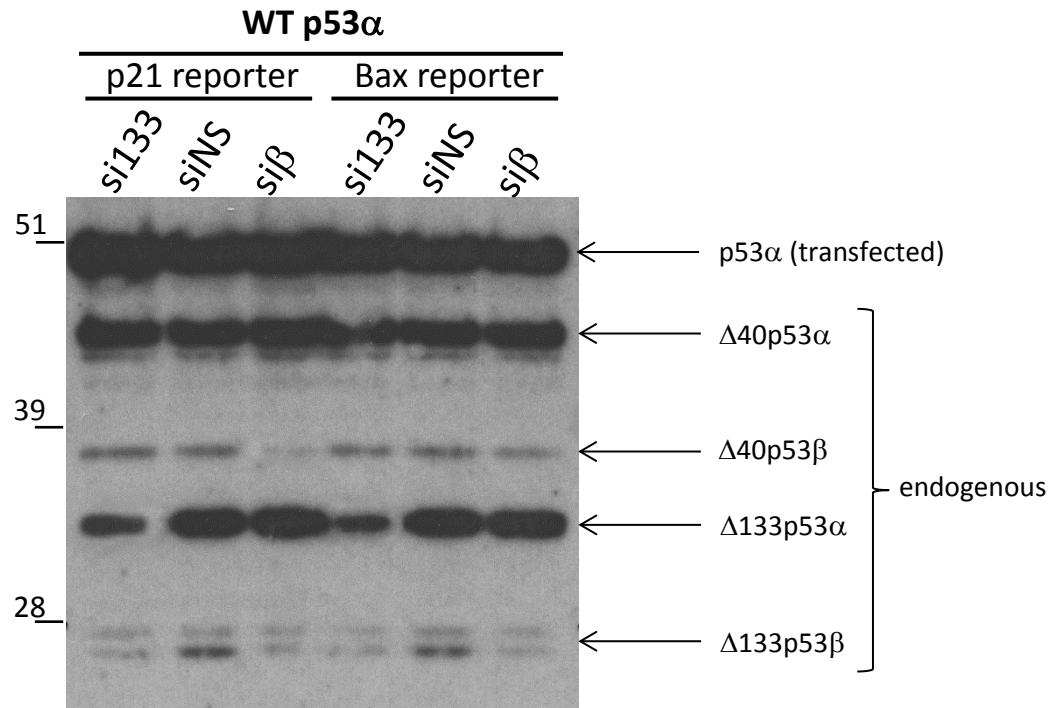
« p53 α rescued » HCT116 -/- cell



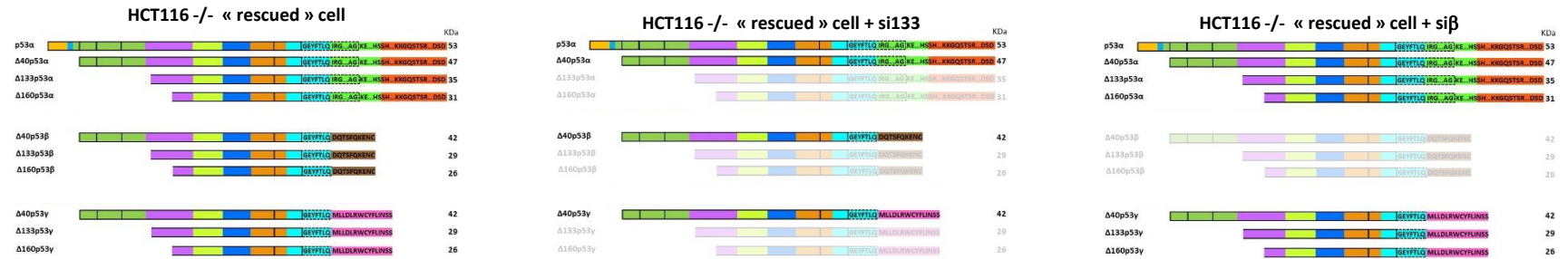
Are these oligomers transcriptionally active?



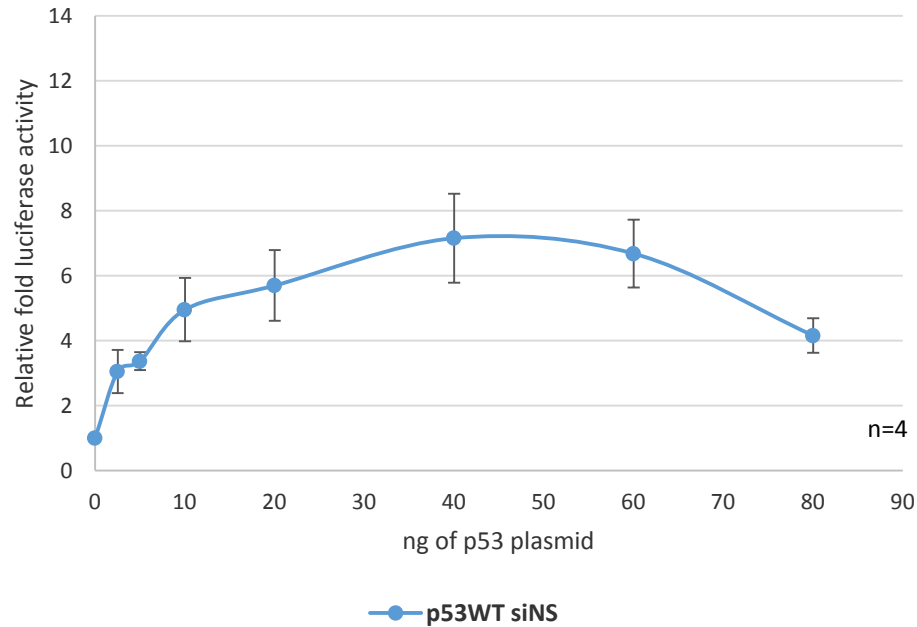
HCT116 $-/-$ cells depleted of $\Delta 133$ or β isoforms and co-transfected with WT p53 α and p21 or Bax reporter



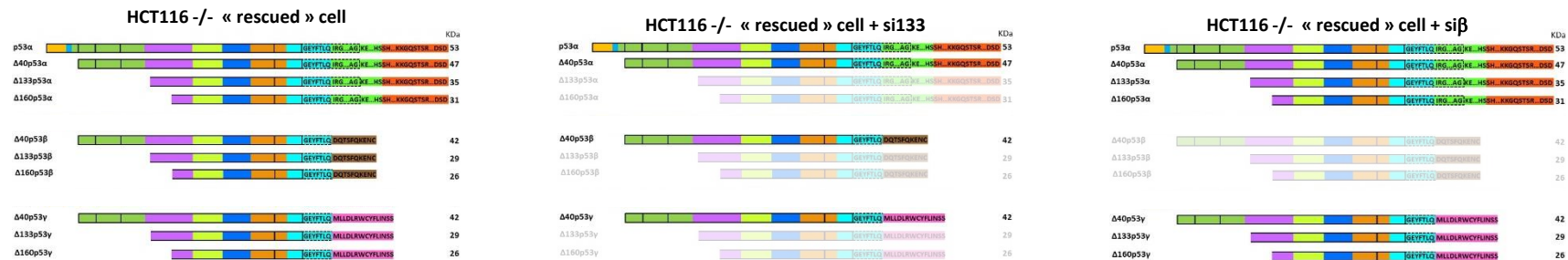
Are these oligomers transcriptionally active?



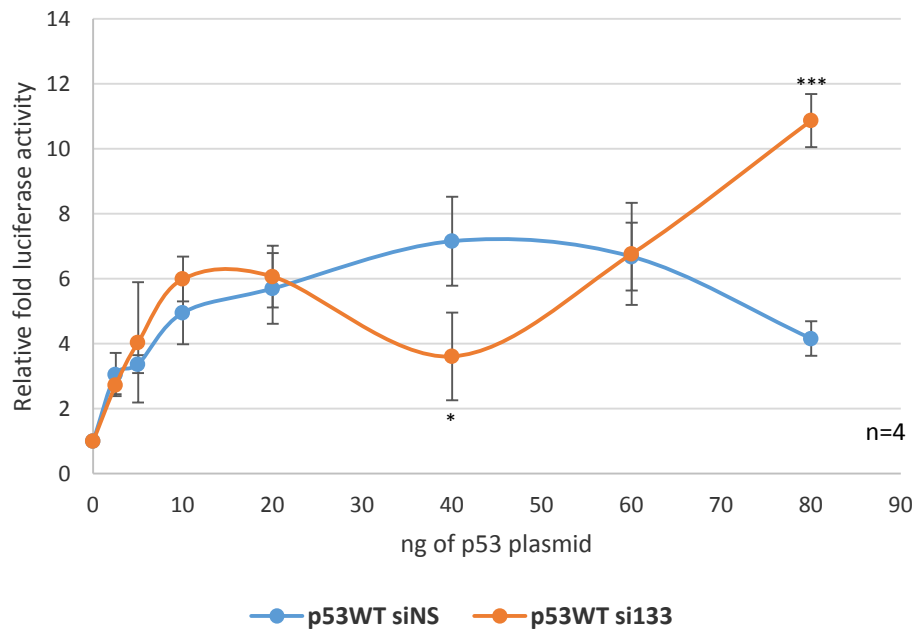
p53α activity on p21 promoter



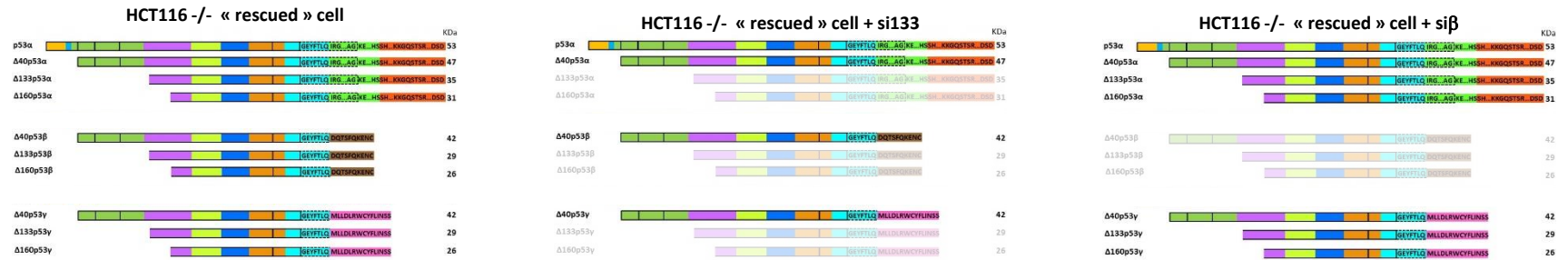
Are these oligomers transcriptionally active?



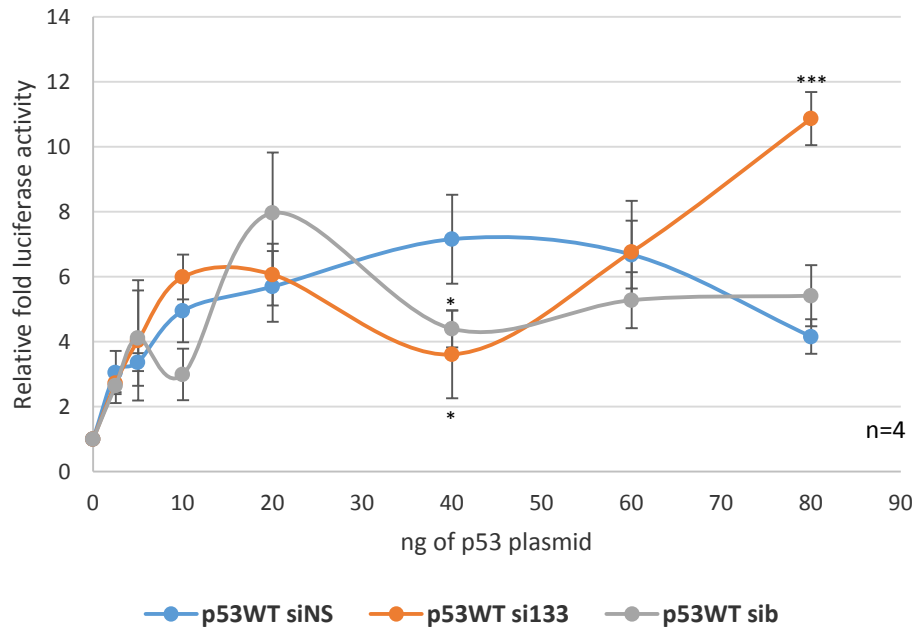
p53α activity on p21 promoter



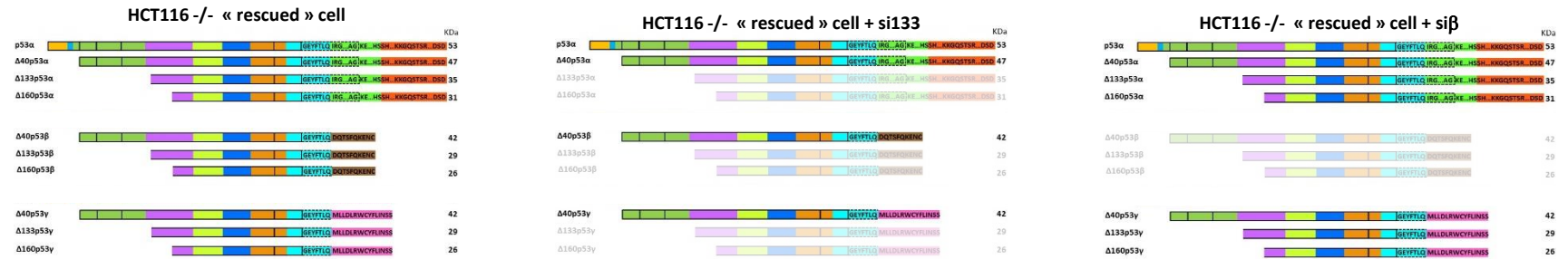
Are these oligomers transcriptionally active?



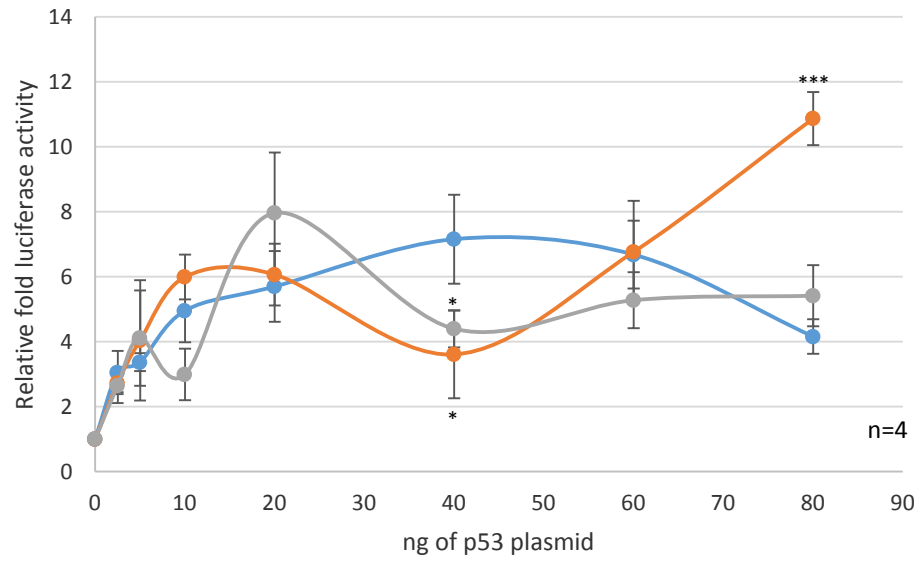
p53α activity on p21 promoter



Are these oligomers transcriptionally active?

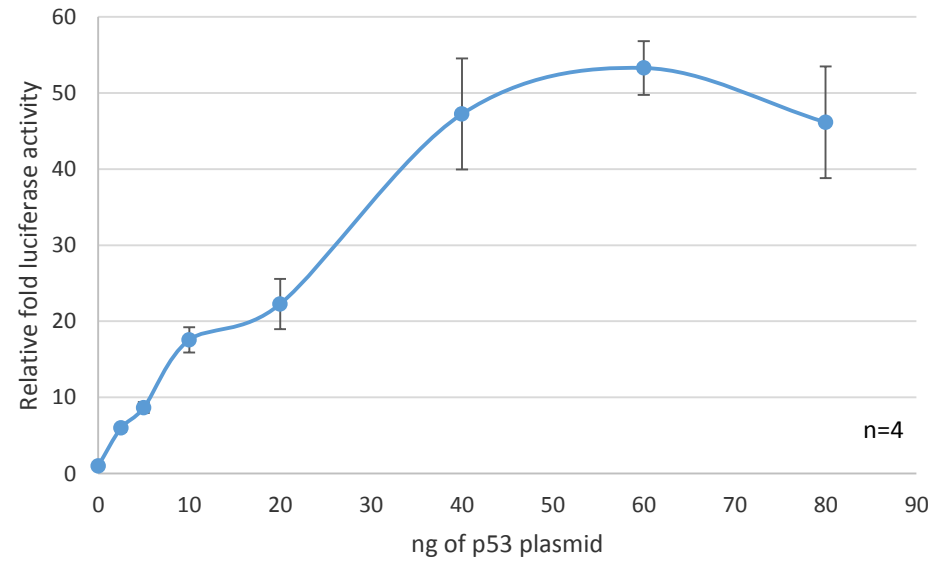


p53α activity on p21 promoter



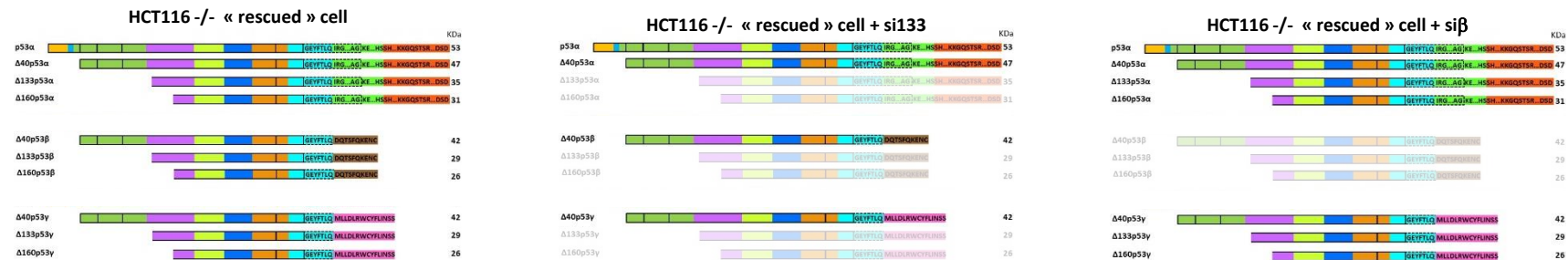
—●— p53WT siNS —●— p53WT si133 —●— p53WT sib

p53α activity on Bax promoter

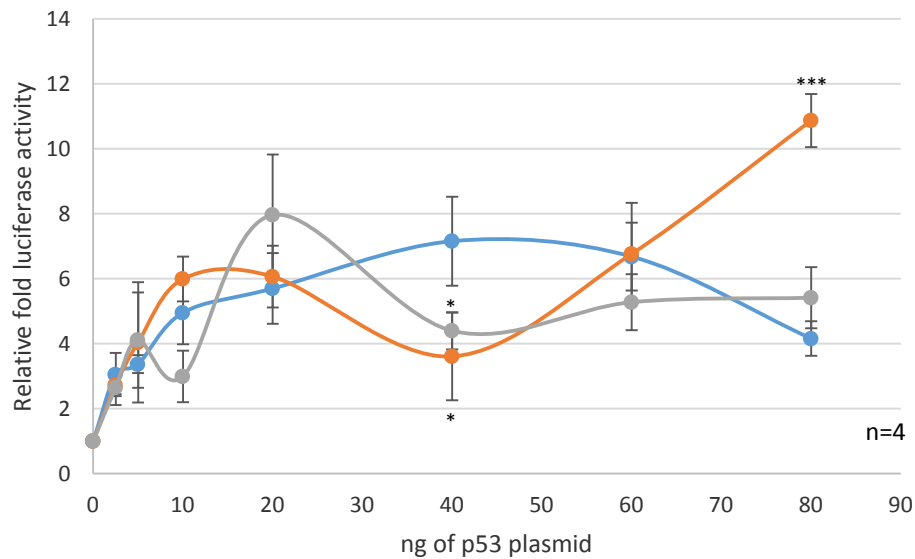


—●— p53WT siNS

Are these oligomers transcriptionally active?

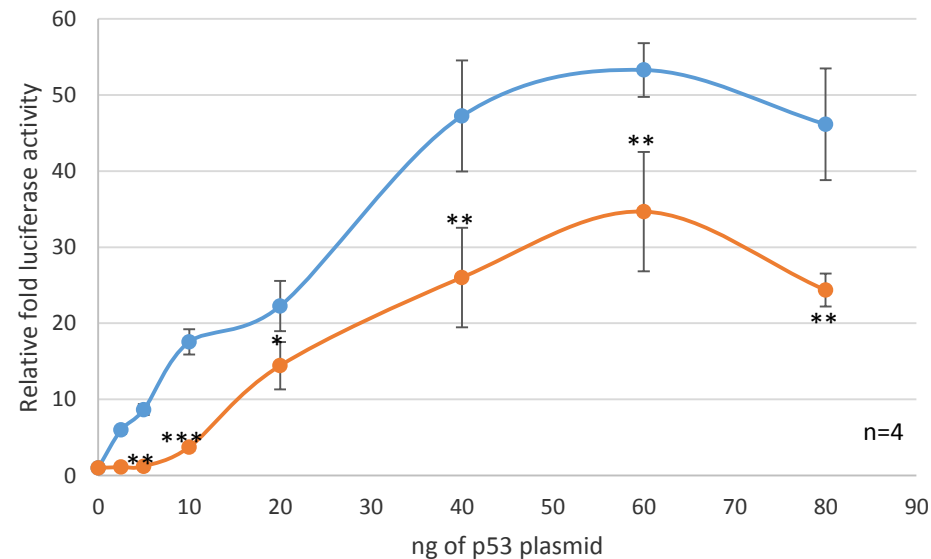


p53α activity on p21 promoter



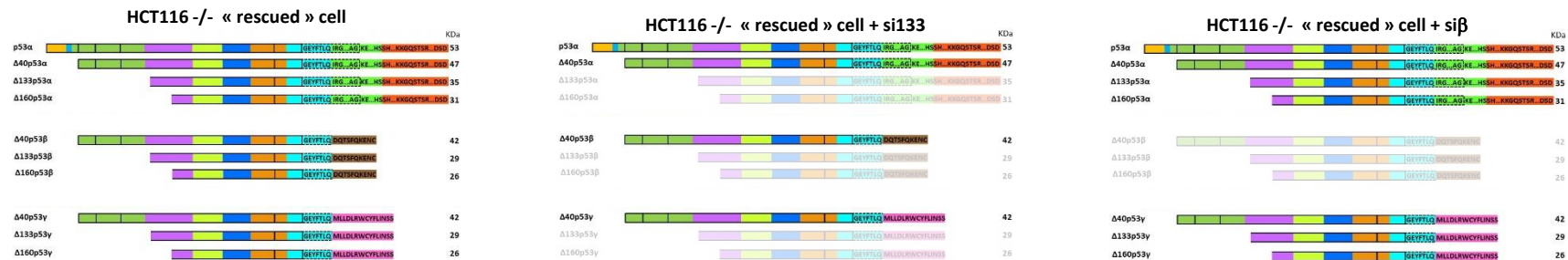
—●— p53WT siNS —●— p53WT si133 —●— p53WT sib

p53α activity on Bax promoter

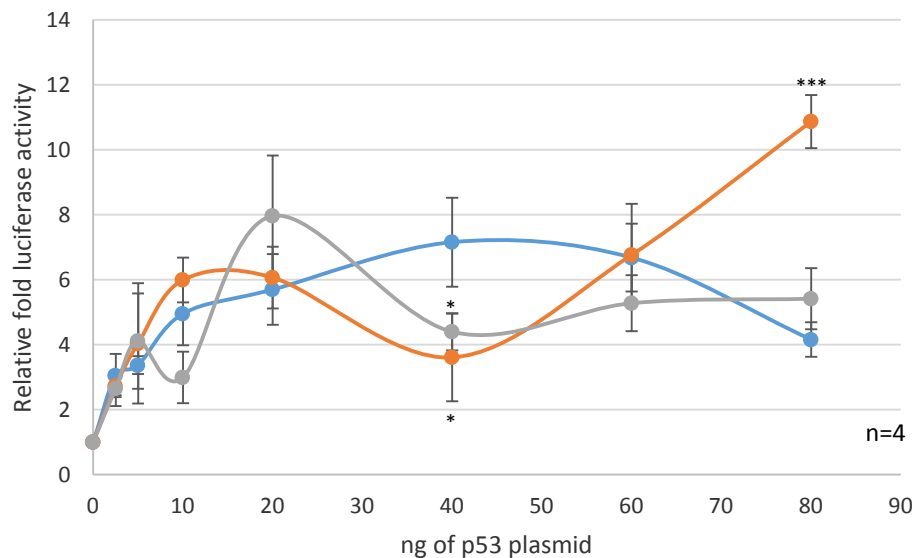


—●— p53WT siNS —●— p53WT si133

Are these oligomers transcriptionally active?

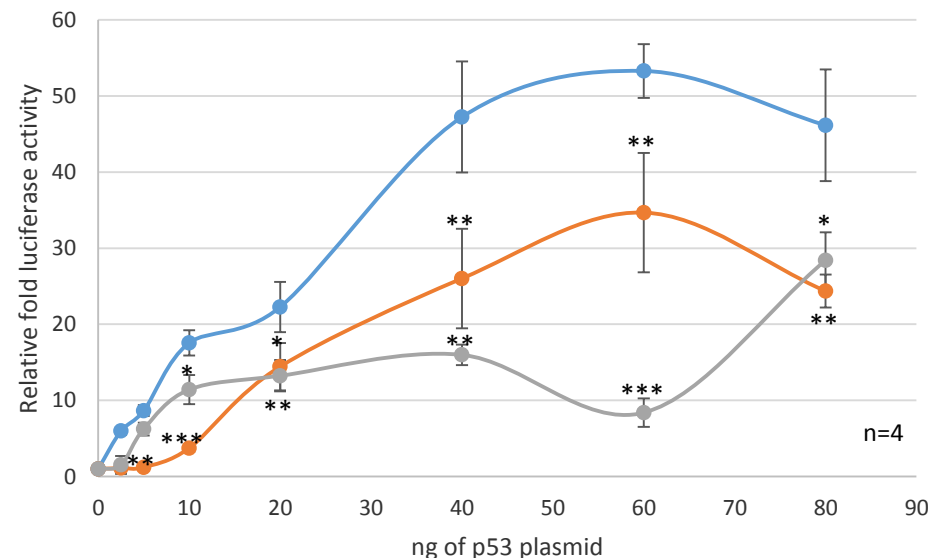


p53α activity on p21 promoter



—●— p53WT siNS —●— p53WT si133 —●— p53WT sib

p53α activity on Bax promoter



—●— p53WT siNS —●— p53WT si133 —●— p53WT sib

→ Cell content of p53 protein isoforms affects the transcriptional activity of p53 α in a promoter dependent manner

Is the oligomerisation of p53 isoforms regulated by post-translational modifications?

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SHL**KSKK**GQSTSRH**KK**LMF**K**TEGPDSD
367 393

Is the oligomerisation of p53 isoforms regulated by post-translational modifications?

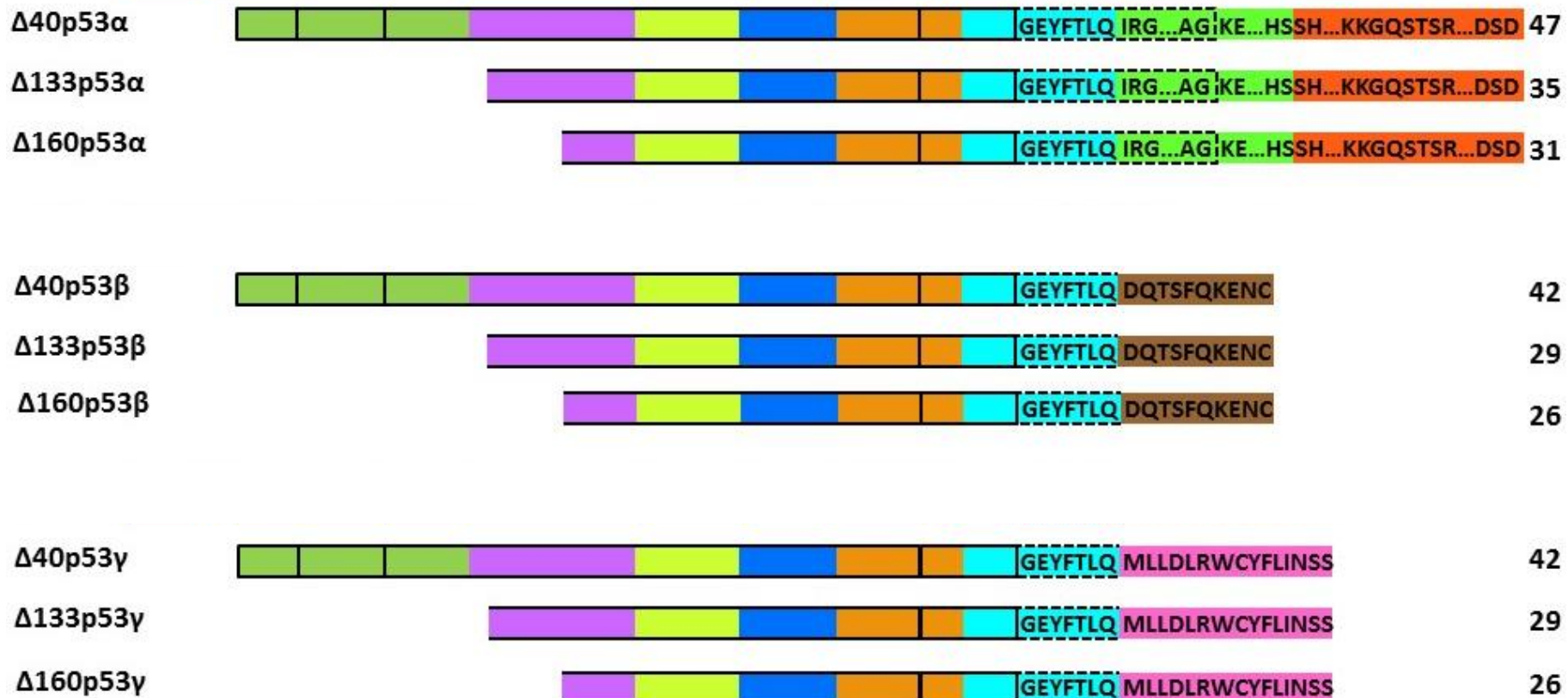
SHL**KSKK**GQSTSRH**KK**LMF**K**TEGPDS
367 393

6 c-terminal lysines of p53 α known to be **post-translationally modified** and to **modulate the oligomerisation and regulatory domains**

Are these oligomers transcriptionally active?

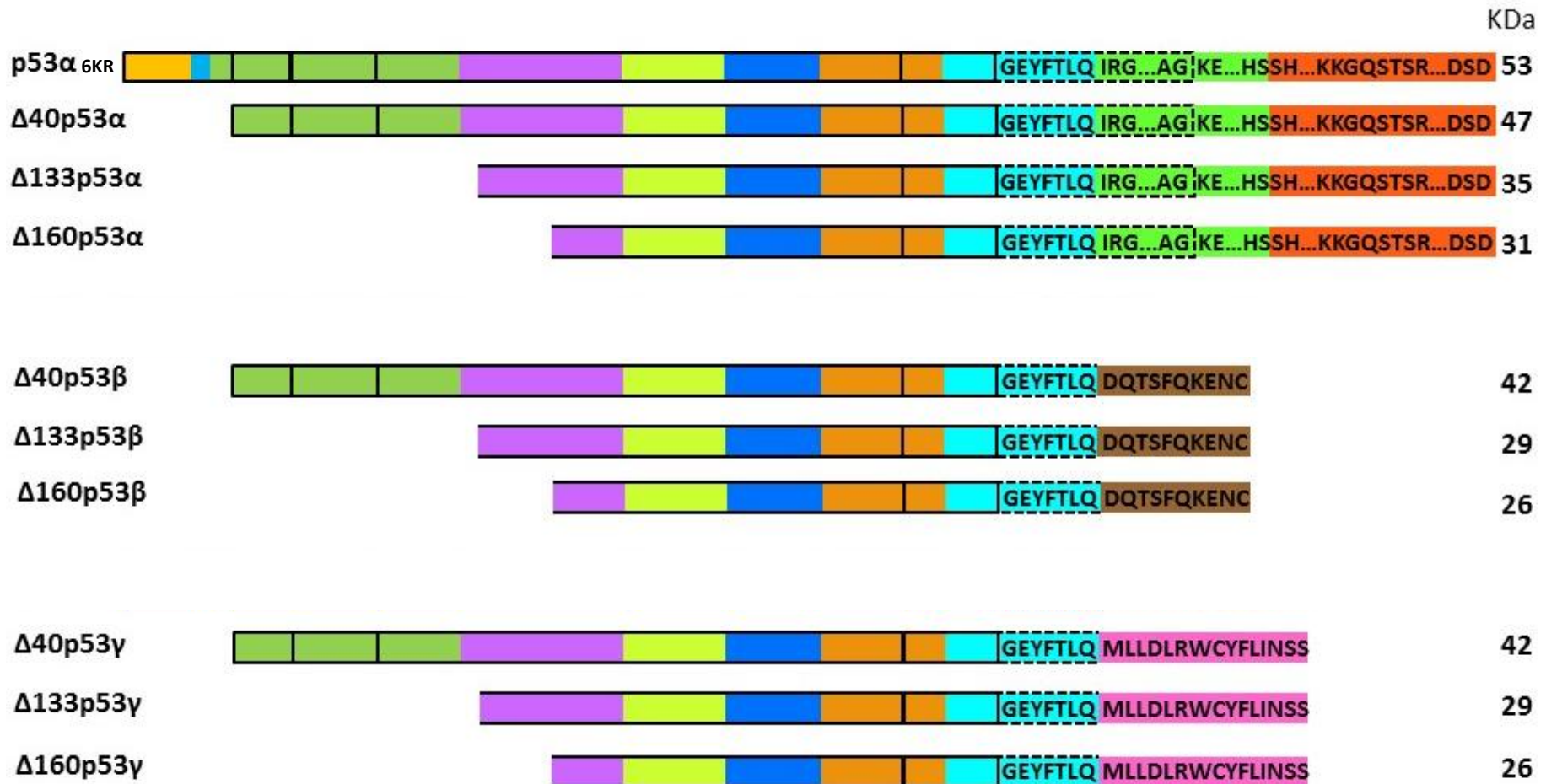
HCT116 -/- cell

KDa



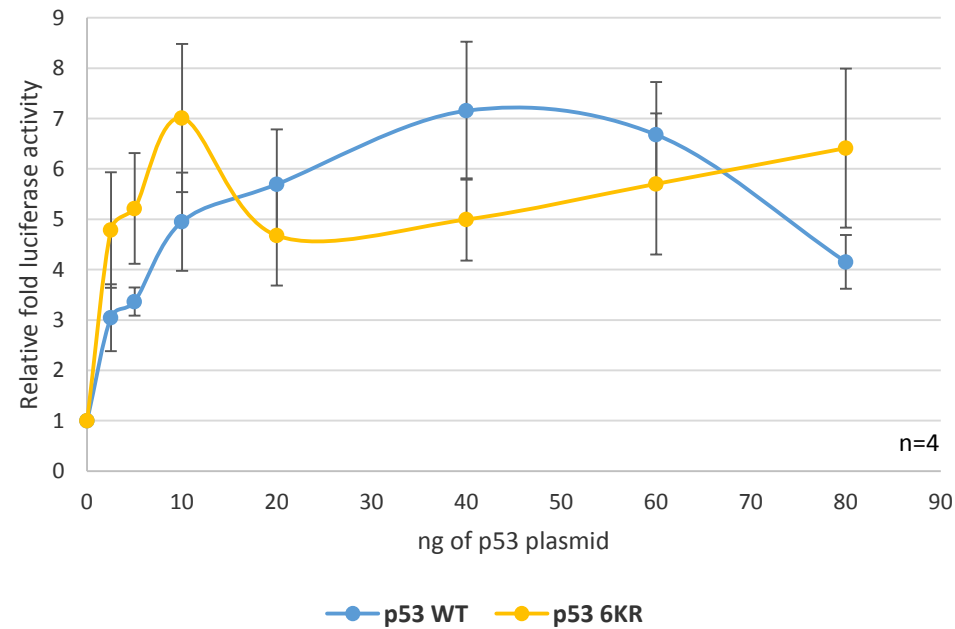
Are these oligomers transcriptionally active?

« p53 α 6KR rescued » HCT116 -/- cell



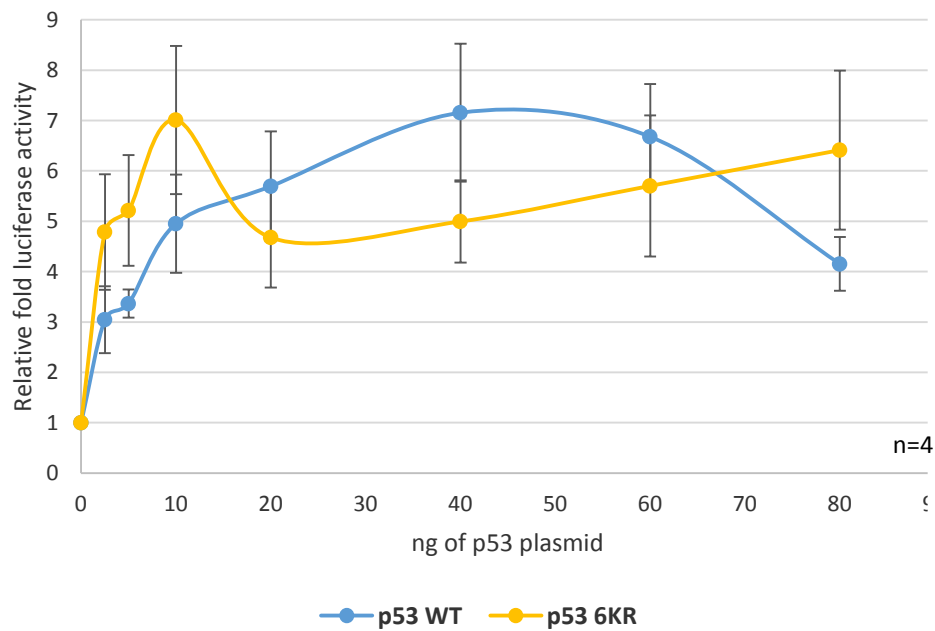
Is the oligomerisation of p53 isoforms regulated by post-translational modifications?

Activity of p53 α WT / 6KR on p21 promoter

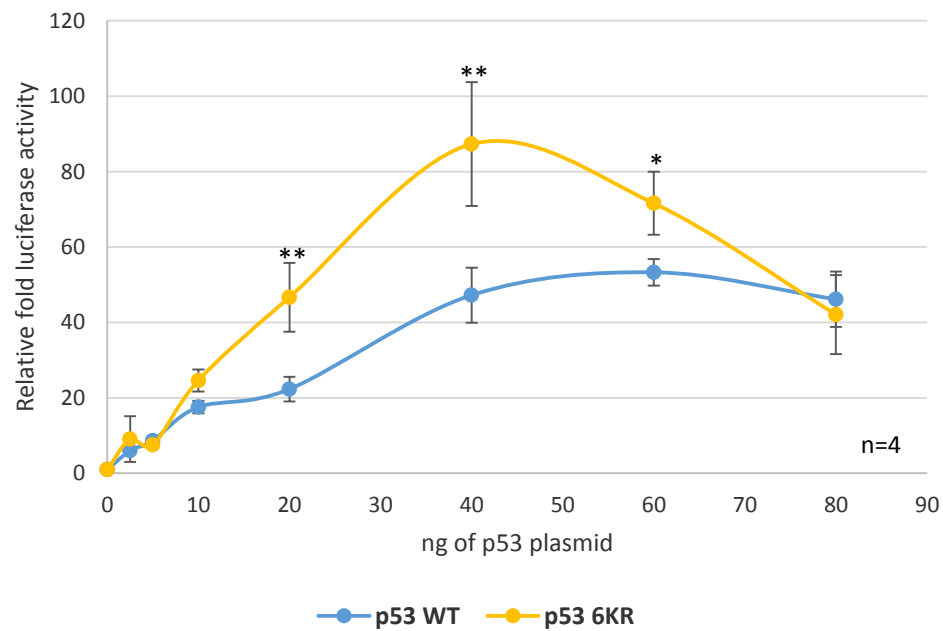


Is the oligomerisation of p53 isoforms regulated by post-translational modifications?

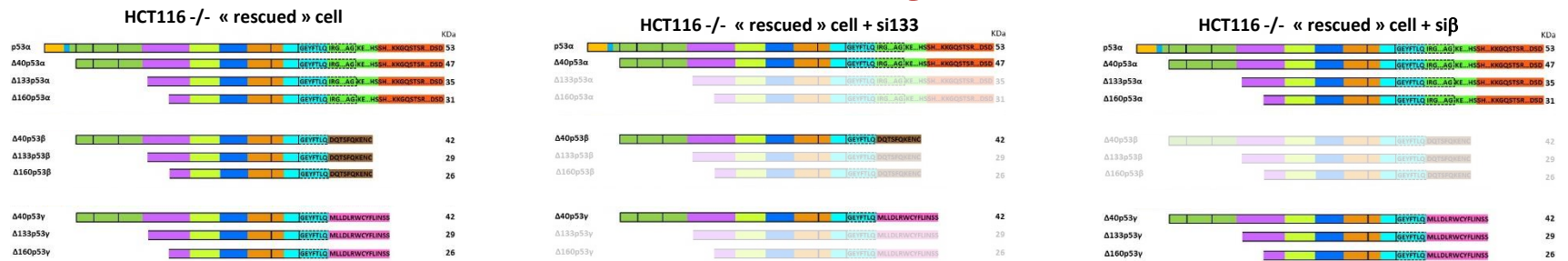
Activity of p53 α WT / 6KR on p21 promoter



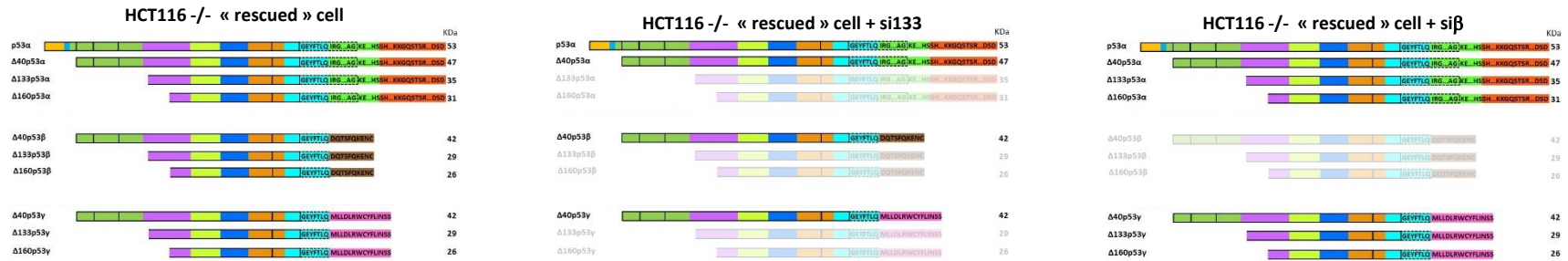
Activity of p53 α WT / 6KR on Bax promoter



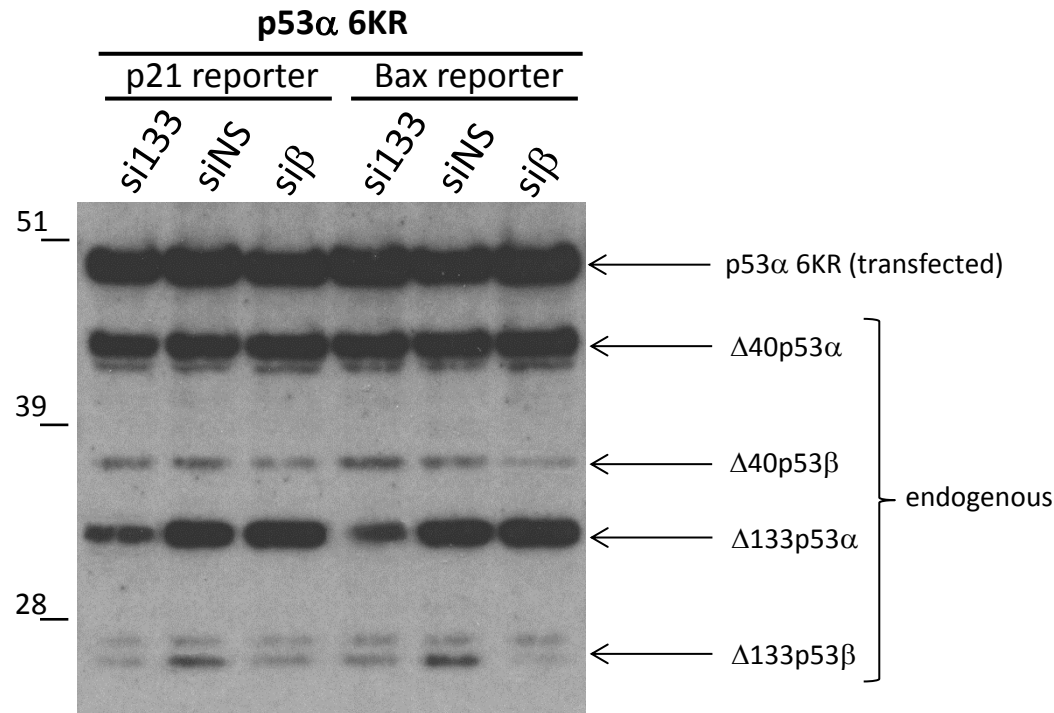
Is the oligomerisation of p53 isoforms regulated by post-translational modifications?



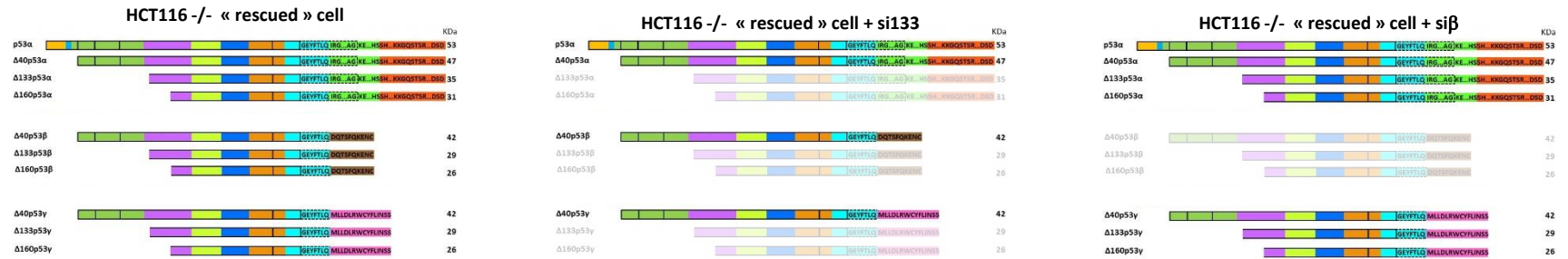
Is the oligomerisation of p53 isoforms regulated by post-translational modifications?



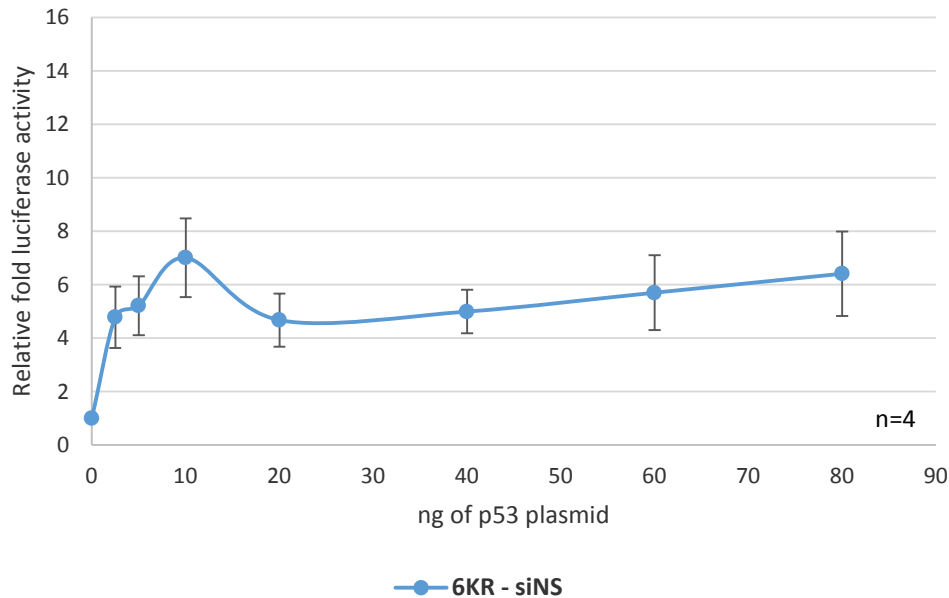
HCT116 -/- cells depleted of Δ133 or β isoforms and co-transfected with p53α 6KR and p21 or Bax reporter



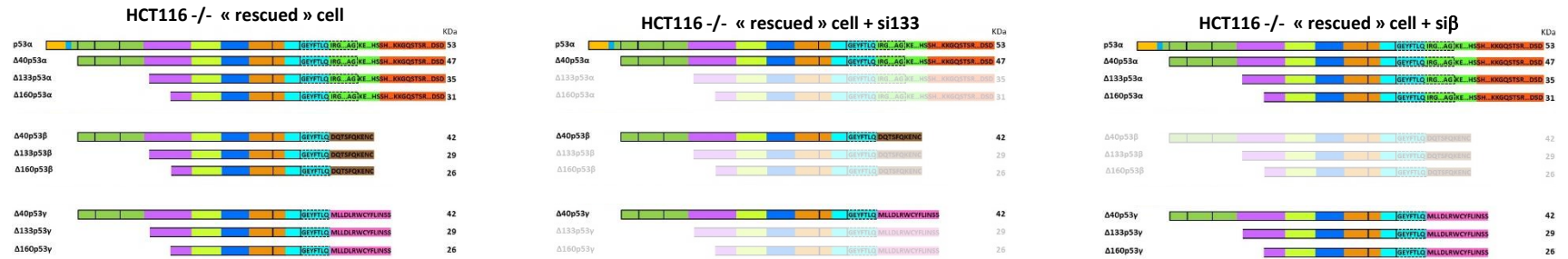
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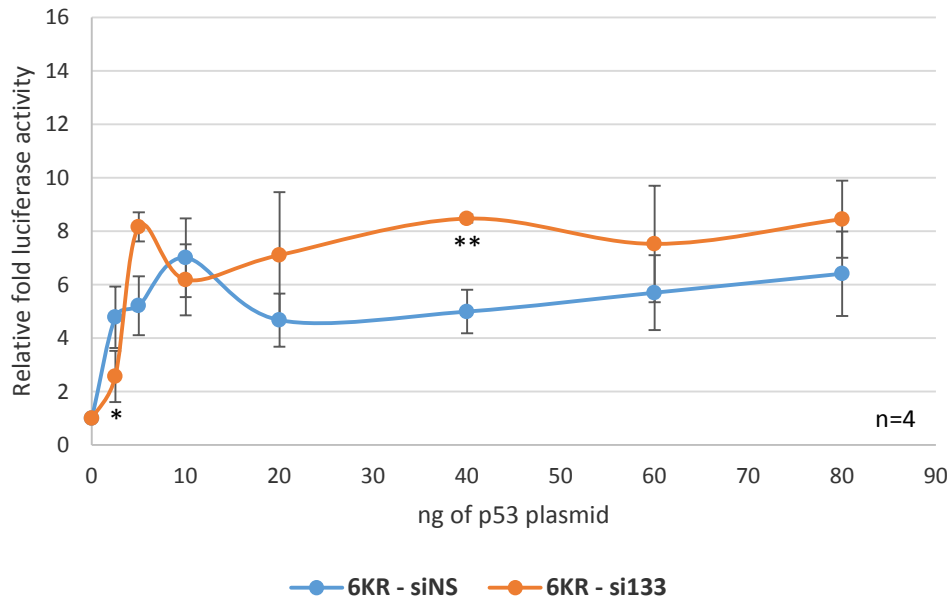
p53α-6KR activity on p21 promoter



Is the oligomerisation of p53 isoforms regulated by post-translational modifications?



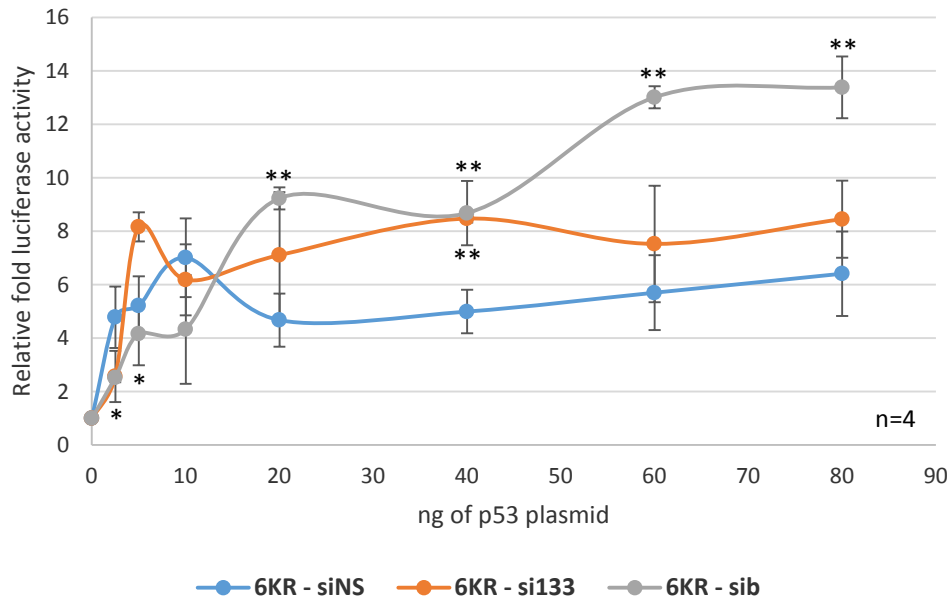
p53α-6KR activity on p21 promoter



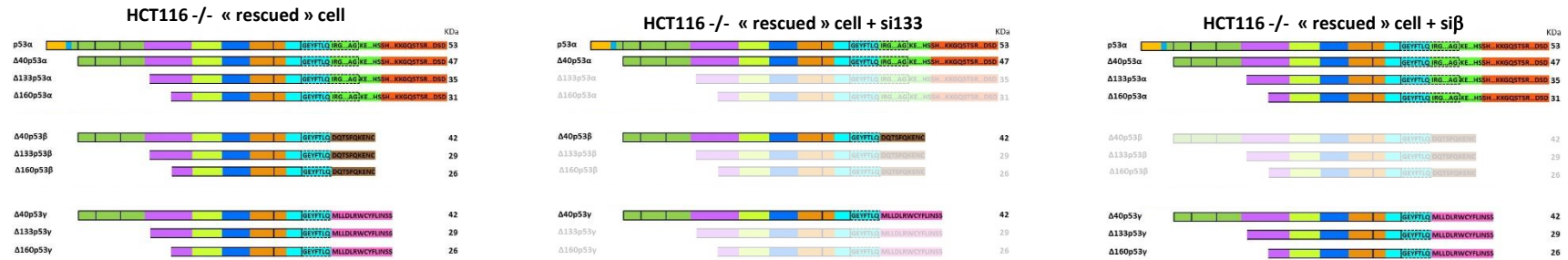
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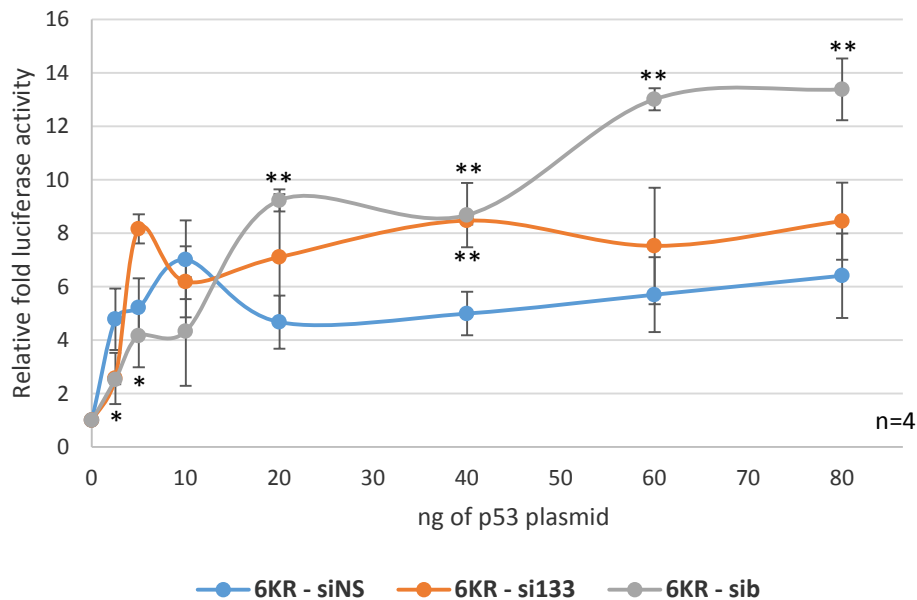
p53α-6KR activity on p21 promoter



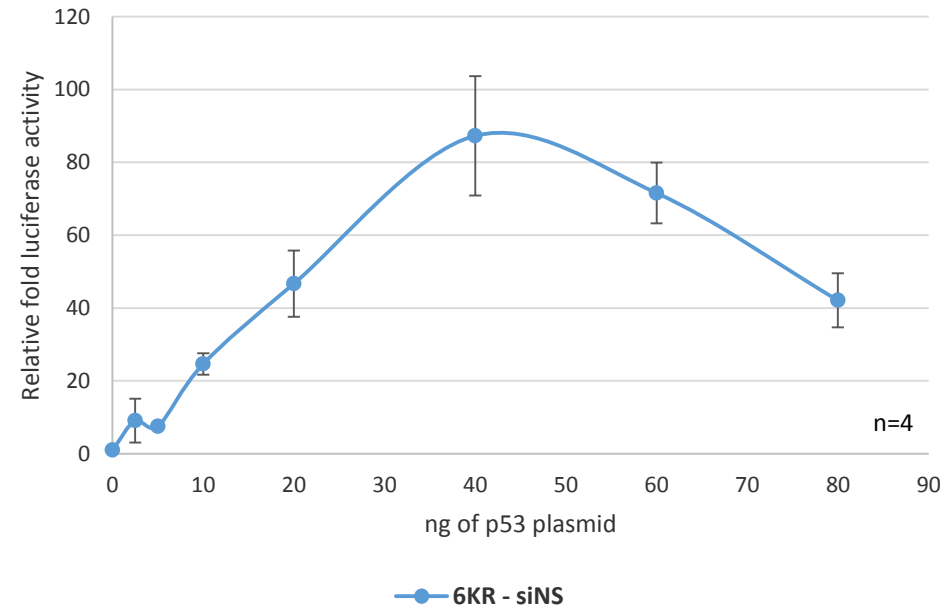
Is the oligomerisation of p53 isoforms regulated by post-translational modifications?



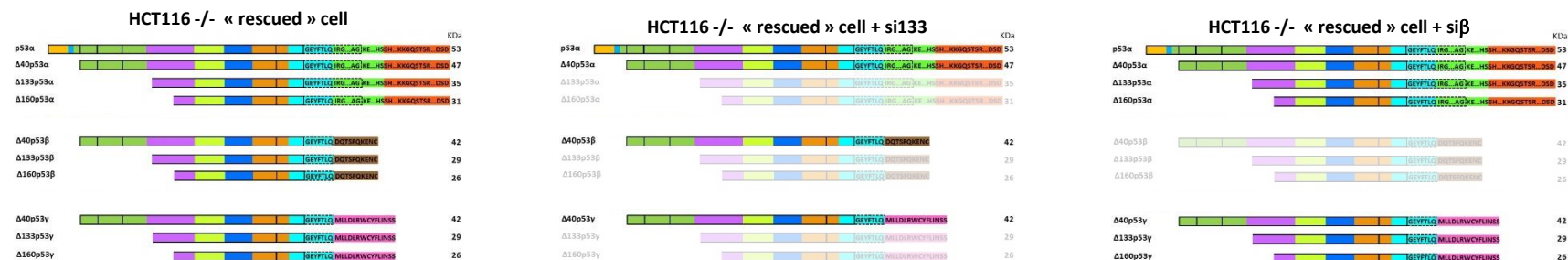
p53α-6KR activity on p21 promoter



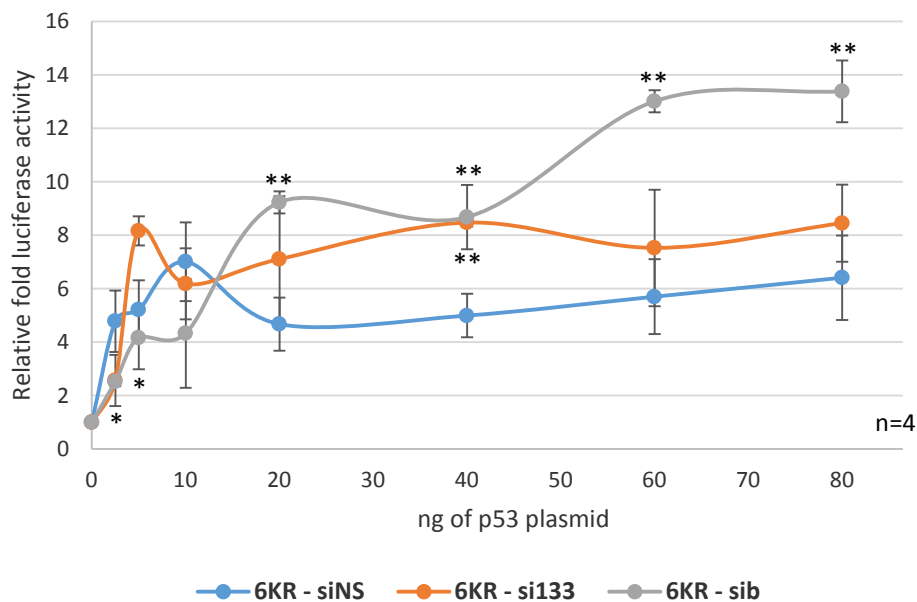
p53α-6KR activity on Bax promoter



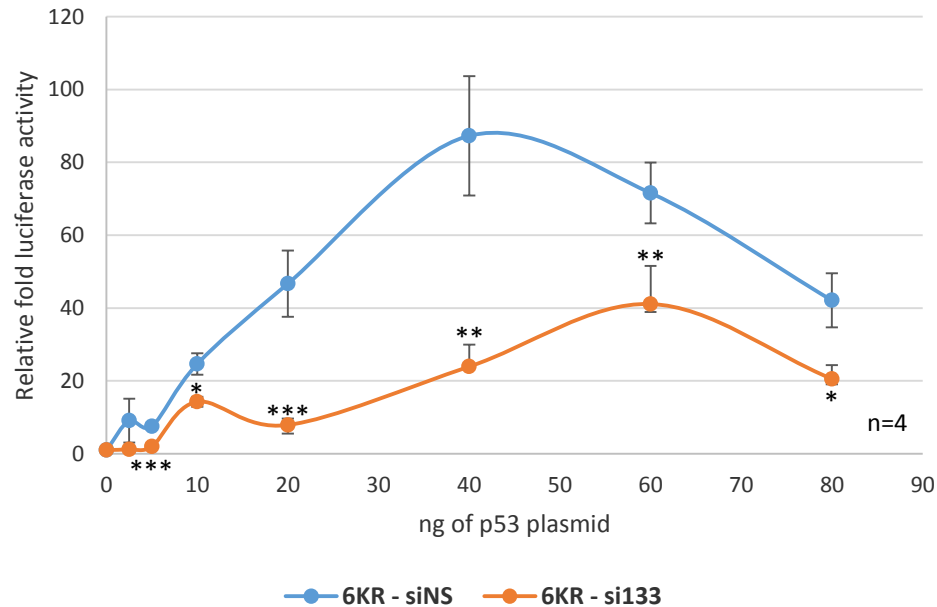
Is the oligomerisation of p53 isoforms regulated by post-translational modifications?



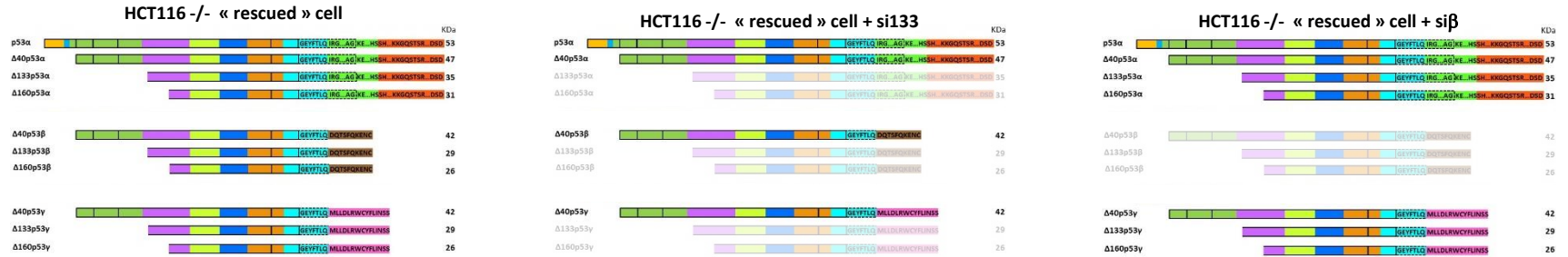
p53α-6KR activity on p21 promoter



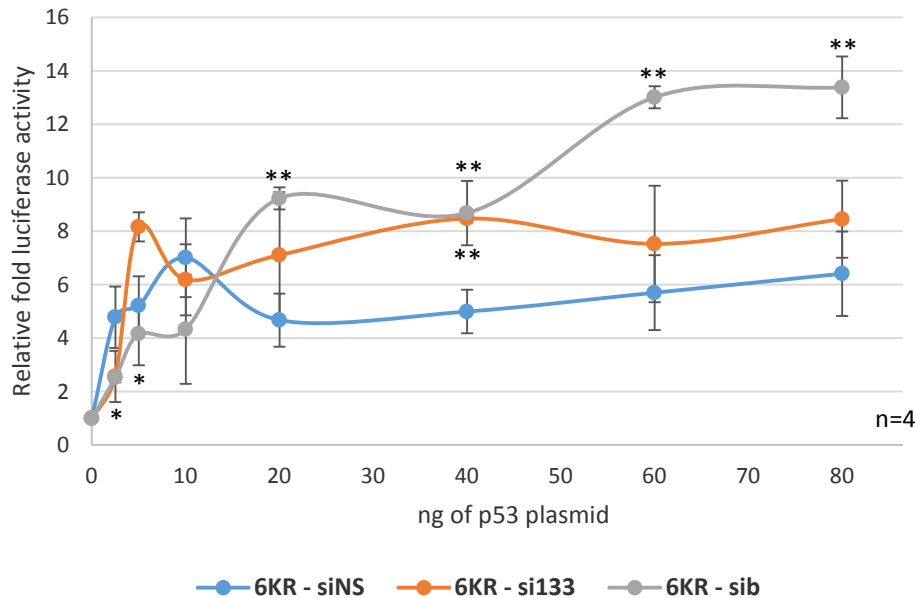
p53α-6KR activity on Bax promoter



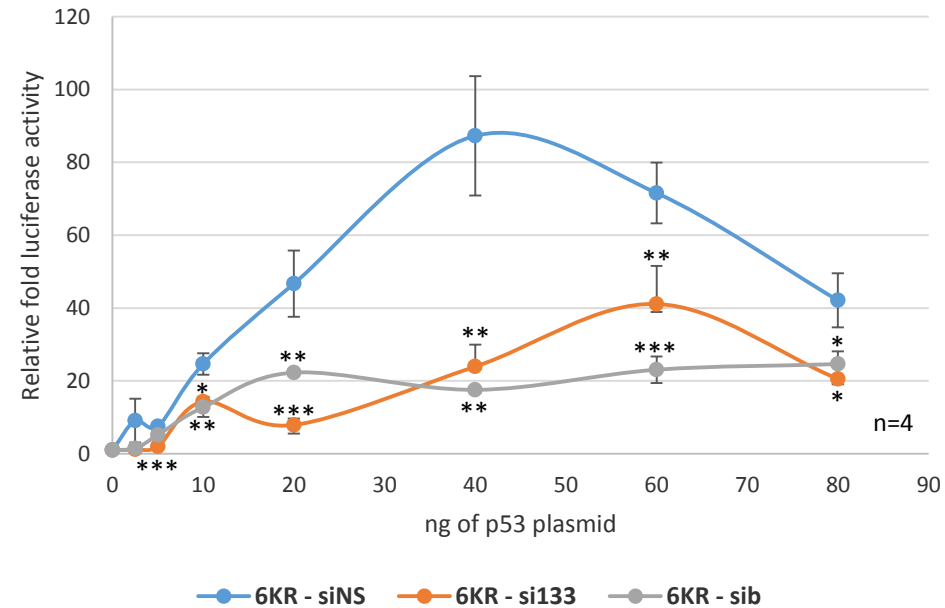
Is the oligomerisation of p53 isoforms regulated by post-translational modifications?



p53α-6KR activity on p21 promoter



p53α-6KR activity on Bax promoter



Take home messages...

Take home messages...

→ p53 isoforms oligomerise together

Take home messages...

- p53 isoforms oligomerise together
- Composition and localisation of the oligomers depend on stress

Take home messages...

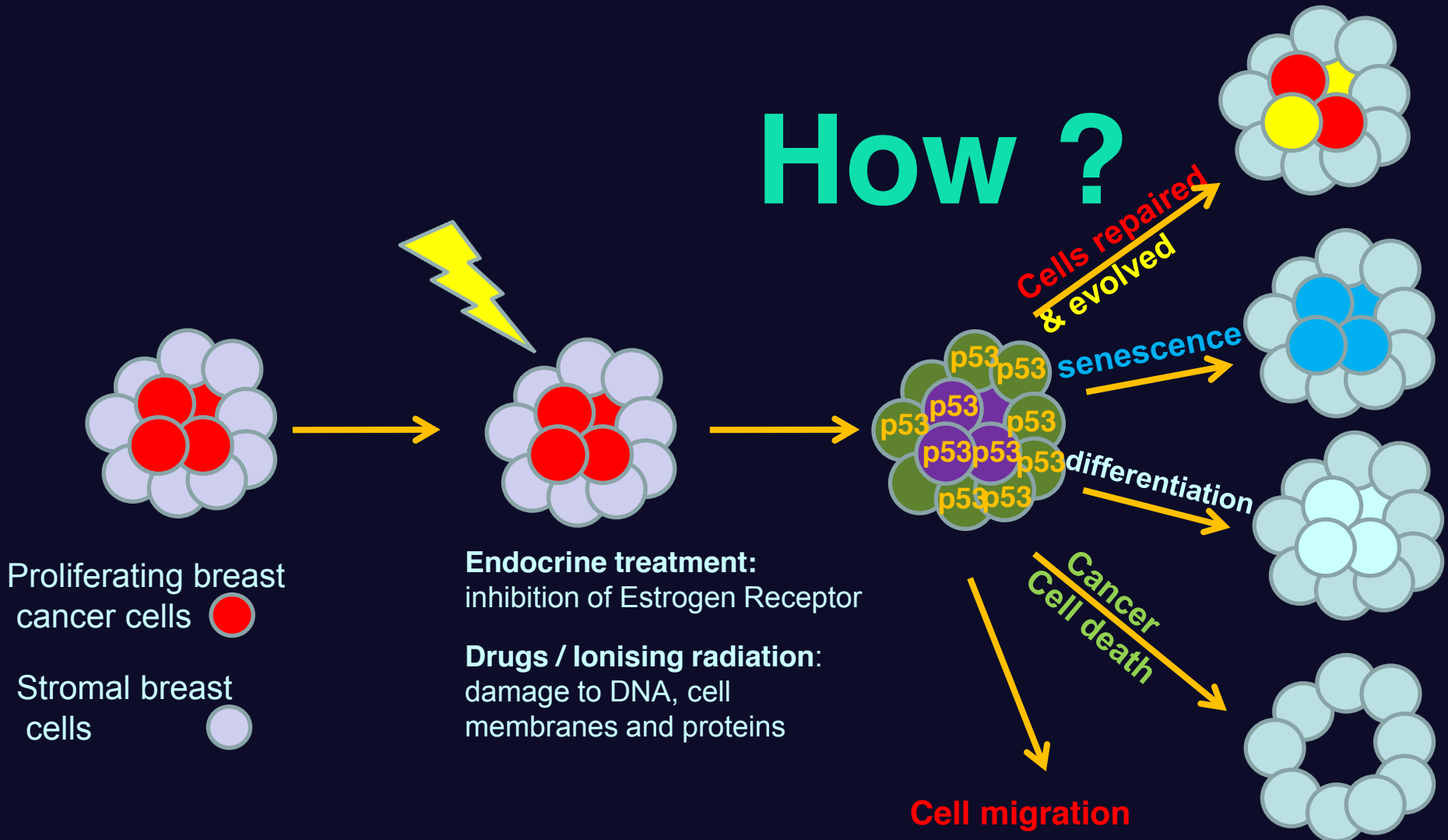
- **p53 isoforms oligomerise together**
- **Composition and localisation of the oligomers depend on stress**
- **Oligomers are regulated by post-translational modifications**

Take home messages...

- **p53 isoforms oligomerise together**
- **Composition and localisation of the oligomers depend on stress**
- **Oligomers are regulated by post-translational modifications**
- **The oligomers regulate target gene expression in a promoter dependant manner**

p53 isoforms influence the decision of cell fate outcome whether TP53 gene is wild-type or mutant.

How ?



Parameters that influence p53 activity

- Intracellular components:

- Cancer type (tissue and driver oncogene)
- Composition in p53 isoforms
- TP53 mutation status

- Extracellular components

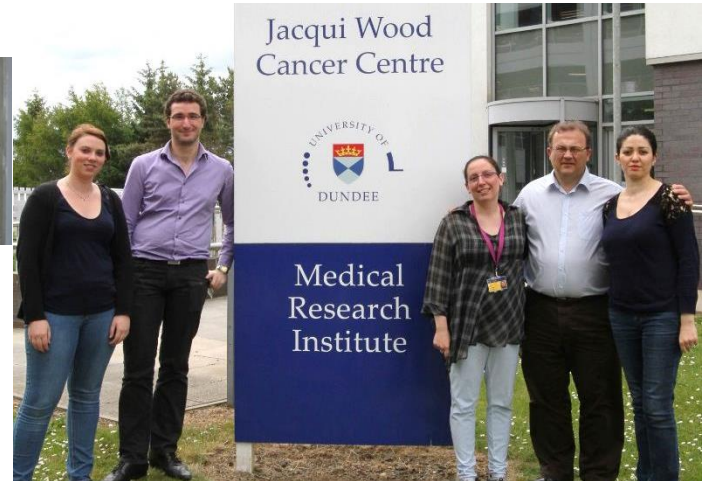
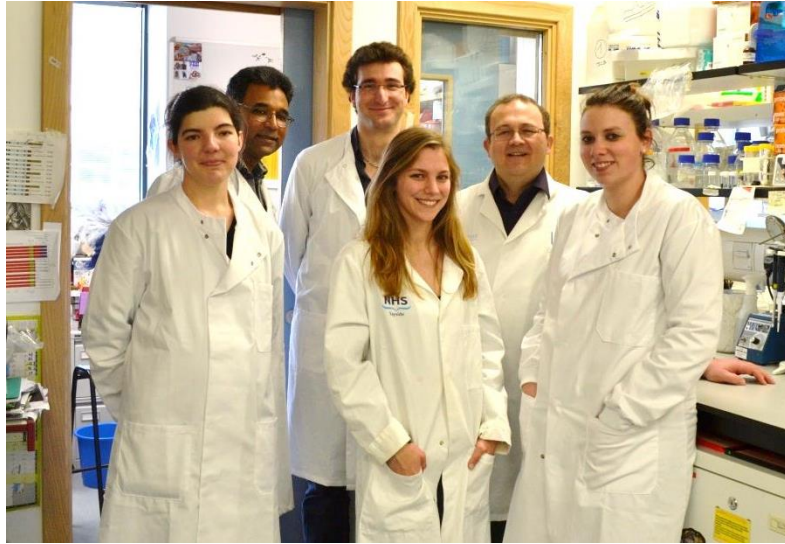
- Nutrient and extracellular signals
- Type, intensity and duration of the treatment

Take home messages...

- p53/p63/p73 isoforms oligomerise together
- The oligomers composition and location depend on stress
 - ***Is there a p53 code?***
- Oligomers are regulated by post-translational modifications
 - The oligomers regulate target genes expression in a promoter dependant manner



Acknowledgements



Former team members:

Kenneth FERNANDES

Marie KHOURY

Sylvanie SURGET

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