

AACR Special Conference in Cancer Research

EXPANDING AND TRANSLATING CANCER SYNTHETIC VULNERABILITIES

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Targeting genome instability in cancer: Inhibition of Pol θ

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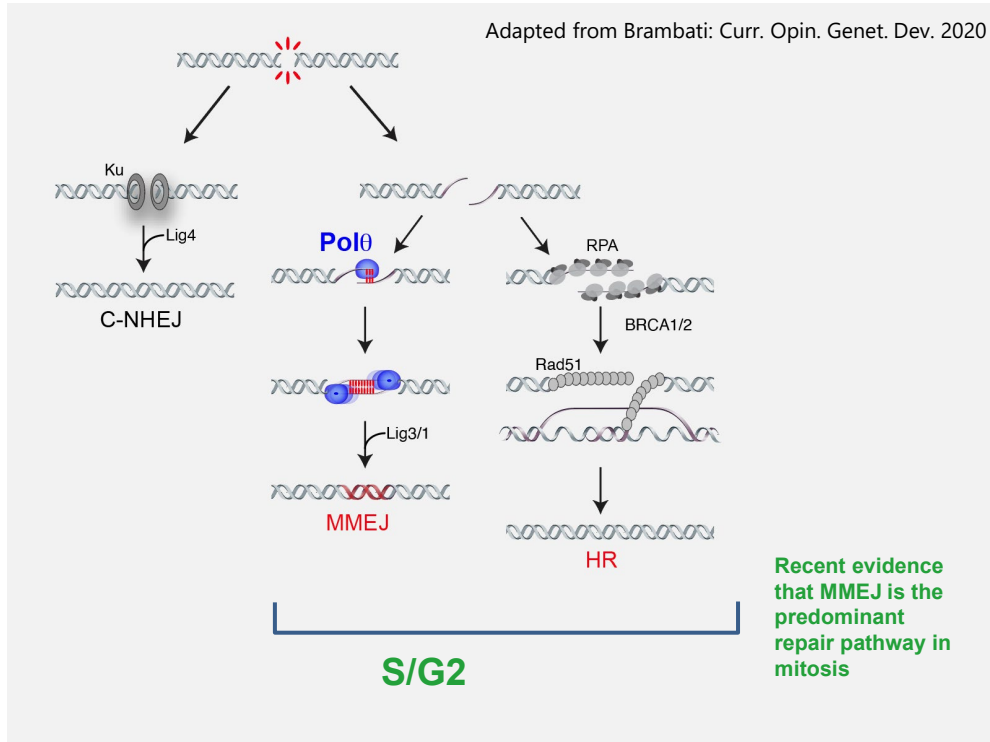
Michael Zinda

I have the following relevant financial relationships to disclose:

Employee of: **Repare Therapeutics**

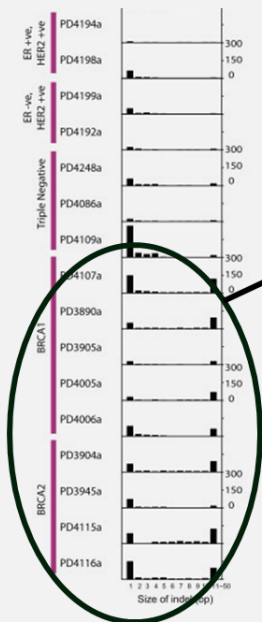
Stockholder in: **Repare Therapeutics**

Polθ Background



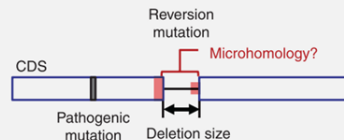
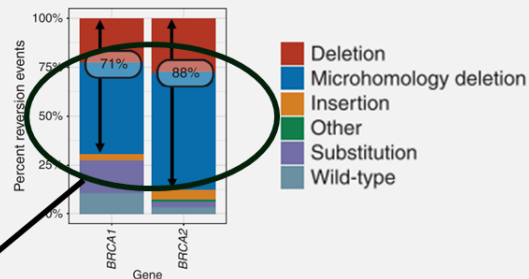
- Unique, multifunctional DNA polymerase with ATP-dependent DNA helicase activity
- Central to microhomology-mediated end joining (MMEJ), a key mechanism of double-strand DNA break repair
- Uniquely active to repair double-strand DNA breaks during mitosis
- Minimally expressed in normal tissue and knockout animals are viable, fertile and exhibit some level of genome instability

MMEJ (Polθ) genomic signatures in BRCA/HRD tumors



MMEJ genomic signatures in HR-deficient tumors at diagnosis

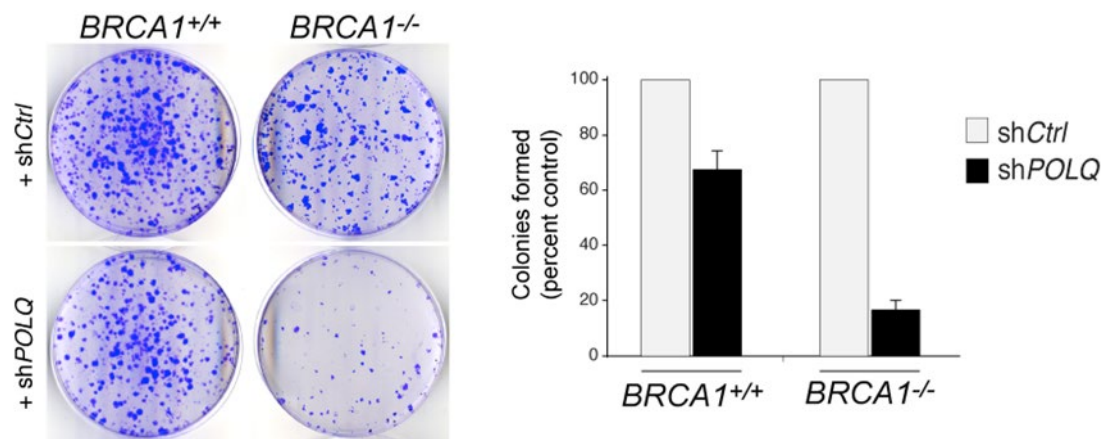
≥50% of BRCA1/2 clinical reversions are generated through MMEJ – highlighting role of Polθ in late-stage cancer



Nik-Zainal et al., 2012

Pettitt et al., Cancer Discovery 2020

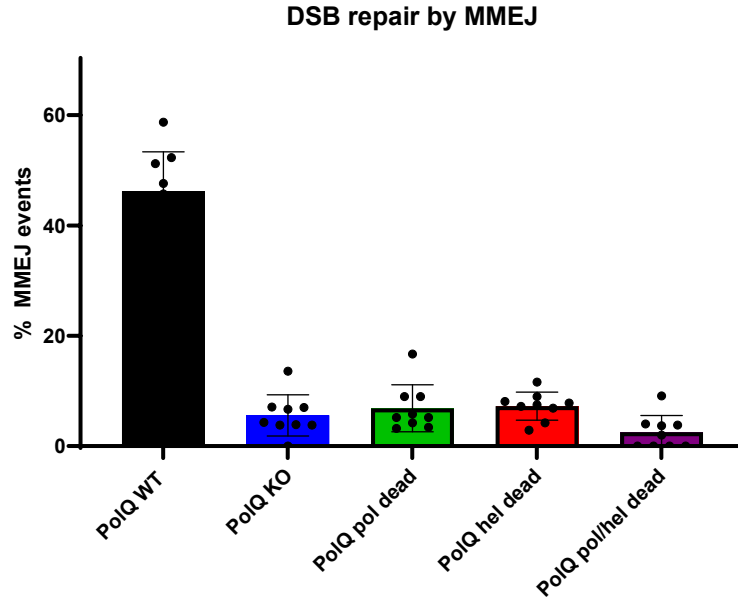
Polθ promotes survival of BRCA deficient cells



PolQ deficiency synthetic with:
ATM (*Shima et al. 2004*)
53BP1 (*Wyatt et al. 2016*)
Ku70/80 (*Wyatt et al. 2016*)

Mateos-Gomez et al. 2015 (HCC1937 cells)
Similar results in FANCD2 model (*Ceccaldi et al. 2015*)

Helicase and polymerase domains are both essential for Pol θ cellular activity



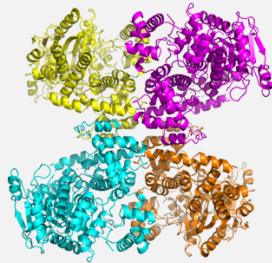
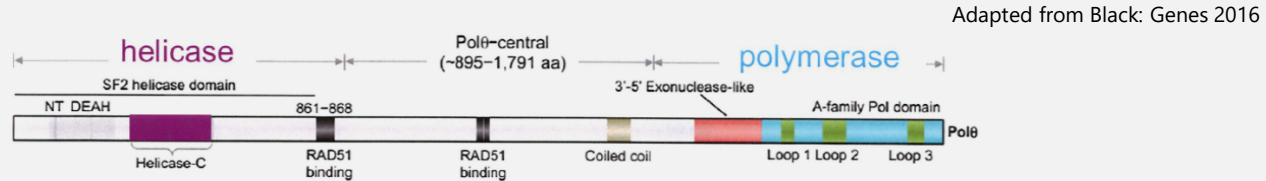
PolQ Polymerase dead: D2540A, E2541A (Yoon et al. 2014)

PolQ Helicase dead: K121M (Ozdemir et al. 2018)

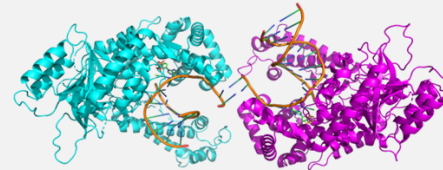
PolQ double-mutant: K121M, D2540A, E2541A

- Knock-in of helicase or polymerase dead mutations equivalently impair MMEJ repair of an engineered DSB

Protein structures enabled discovery of polymerase and helicase inhibitors



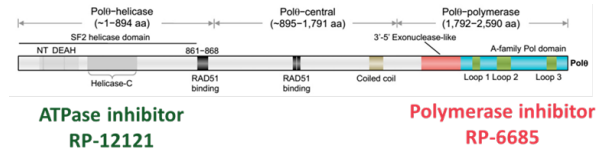
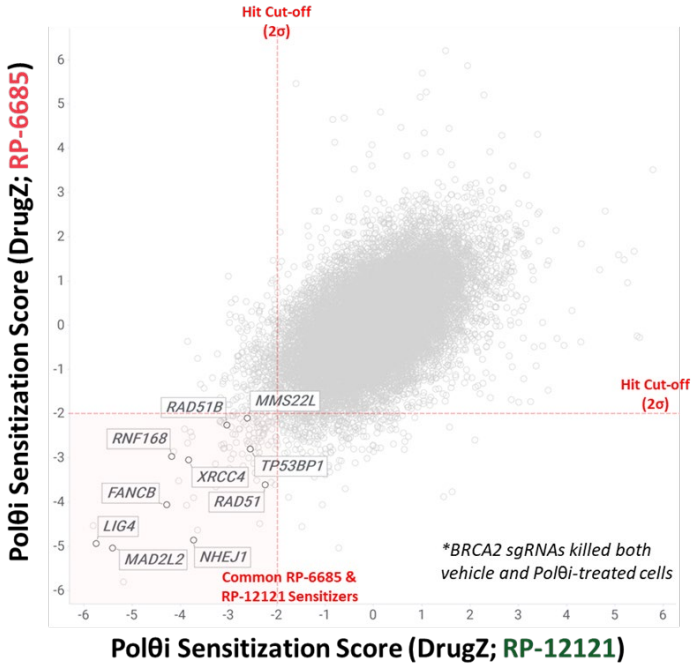
N-Terminal Helicase-Like Domain
Single-Particle Cryo-EM: **2.4 Angstroms**



C-Terminal DNA Polymerase Domain
X-ray Crystallography: **2.0 Angstroms**

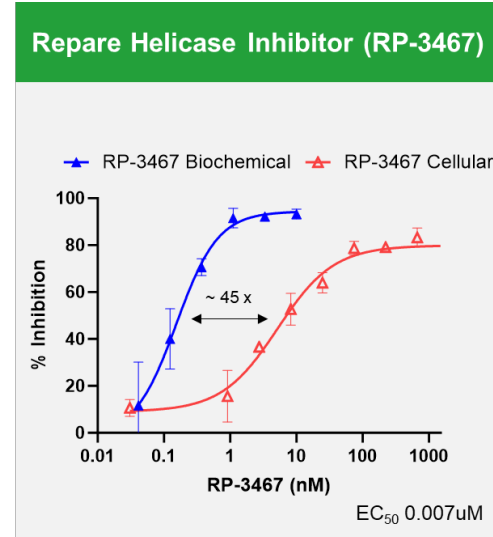
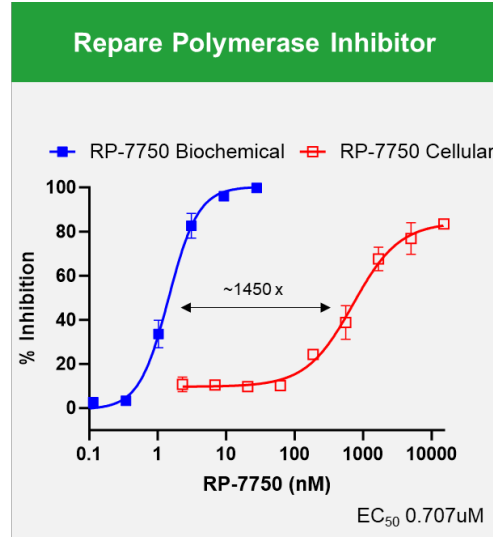
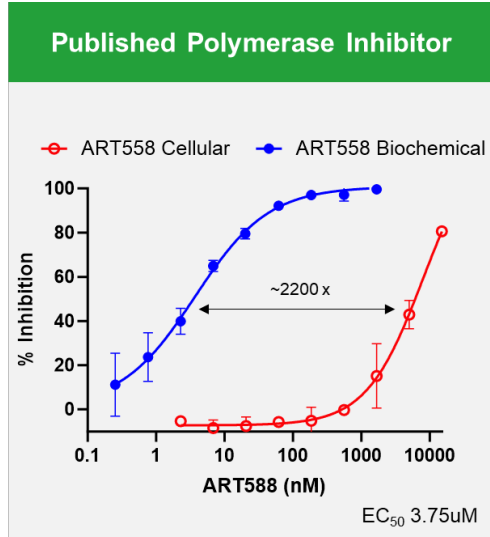
- We generated potent and selective Polθ inhibitors against both the helicase and polymerase (requires co-crystals with DNA) domains

Chemogenomic screens reveal equivalent effects of Helicase and Polymerase inhibitors



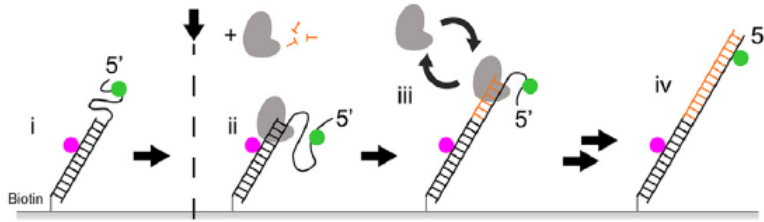
- Polθ polymerase and Helicase inhibitors reveal identical SL interactions in chemogenomic screens – both domains appear to be equivalent

Repare Pol θ helicase inhibitors demonstrate superior cell potency

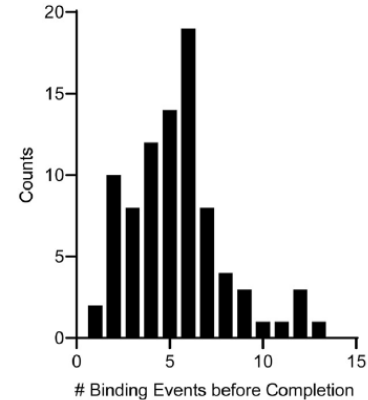


- **Helicase inhibitors demonstrated 100-1000X fold better cellular potency than could be achieved with polymerase-class inhibitors**

Analysis of DNA synthesis in real time at the single-molecule level reveals low processivity



Fijen et al. Mol. Cell 2024



- **Gap-filling DNA synthesis from annealed microhomology involves multiple cycles of Polθ binding and release**
- **Short duration of DNA binding may explain the weak potency of inhibitors acting only on DNA bound Polθ**

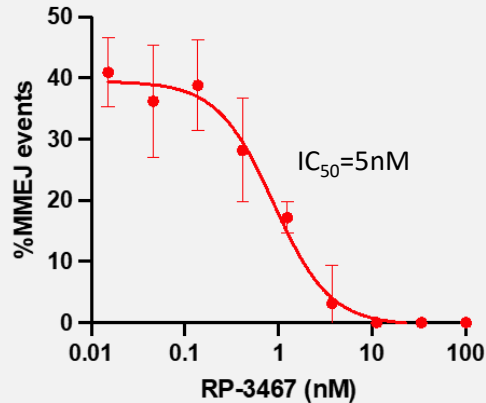
RP-3467: A Highly potent, selective and orally bioavailable Polθ helicase inhibitor

| | Parameter | RP-3467 |
|----------|---|----------|
| In vitro | Polθ ATPase Enzyme IC ₅₀ | <0.25 nM |
| | CETSA cellular target engagement IC ₅₀ | 5 nM |
| | Cell proliferation DLD1 / HCT116 (BRCA2mt) EC ₅₀ | 4 / 7 nM |
| | Off-target ATPase (HELQ, WRN, BLM) IC ₅₀ | > 10 μM |
| | Off-target Polθ polymerase domain IC ₅₀ | > 100 μM |
| ADME | Human Hepatocyte Clearance (μL/min/10 ⁶ cells) | 2.1 |
| | Rat PK (%F, t _{1/2}) | 90%, 13h |
| | Monkey PK (%F, t _{1/2}) | 60%, 3h |

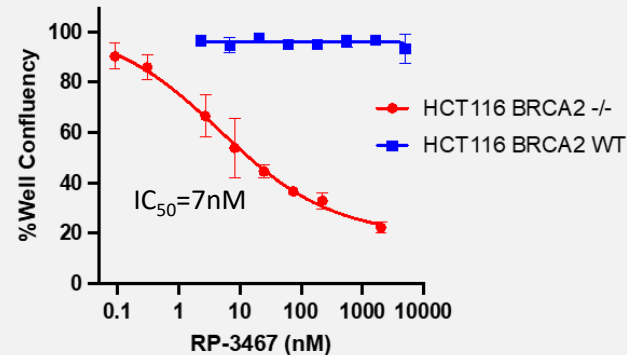
- Clean on PanLabs safety pharmacology screen

Inhibits DNA repair and is synthetic lethal with BRCA2 loss

Inhibition of DNA Repair

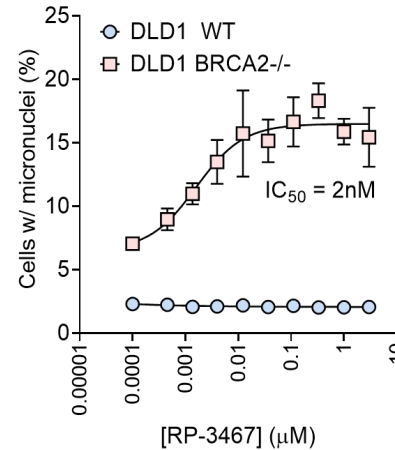
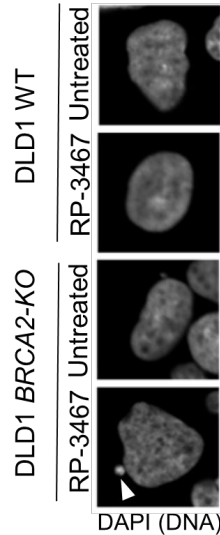


Cell Proliferation HCT116 Isogenic



- Demonstrates potent *in vitro* cellular target engagement and activity
- Huge synthetic lethal window – no effect on BRCA2 WT cells

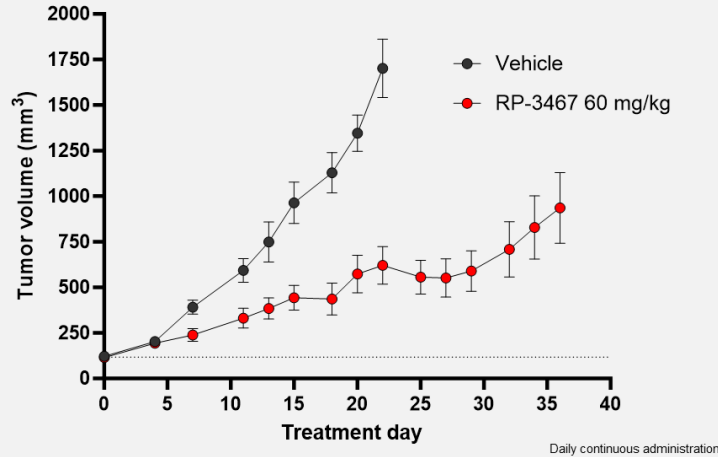
RP-3467 induces micronuclei in BRCA2-/- cells



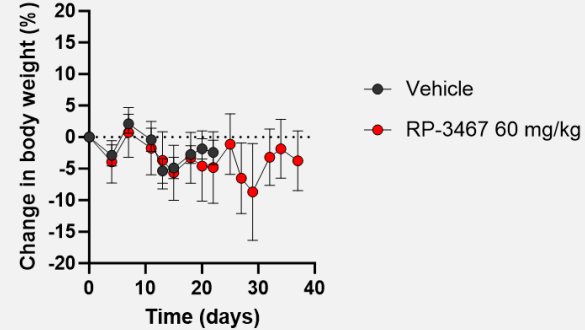
- **Pol θ inhibition induces micronuclei formation in HRD cells**
- **Micronuclei formation are a biomarker for Pol θ inhibition**

Monotherapy activity against BRCA2 $-/-$ tumors

HCT116 BRCA2 $-/-$ tumors

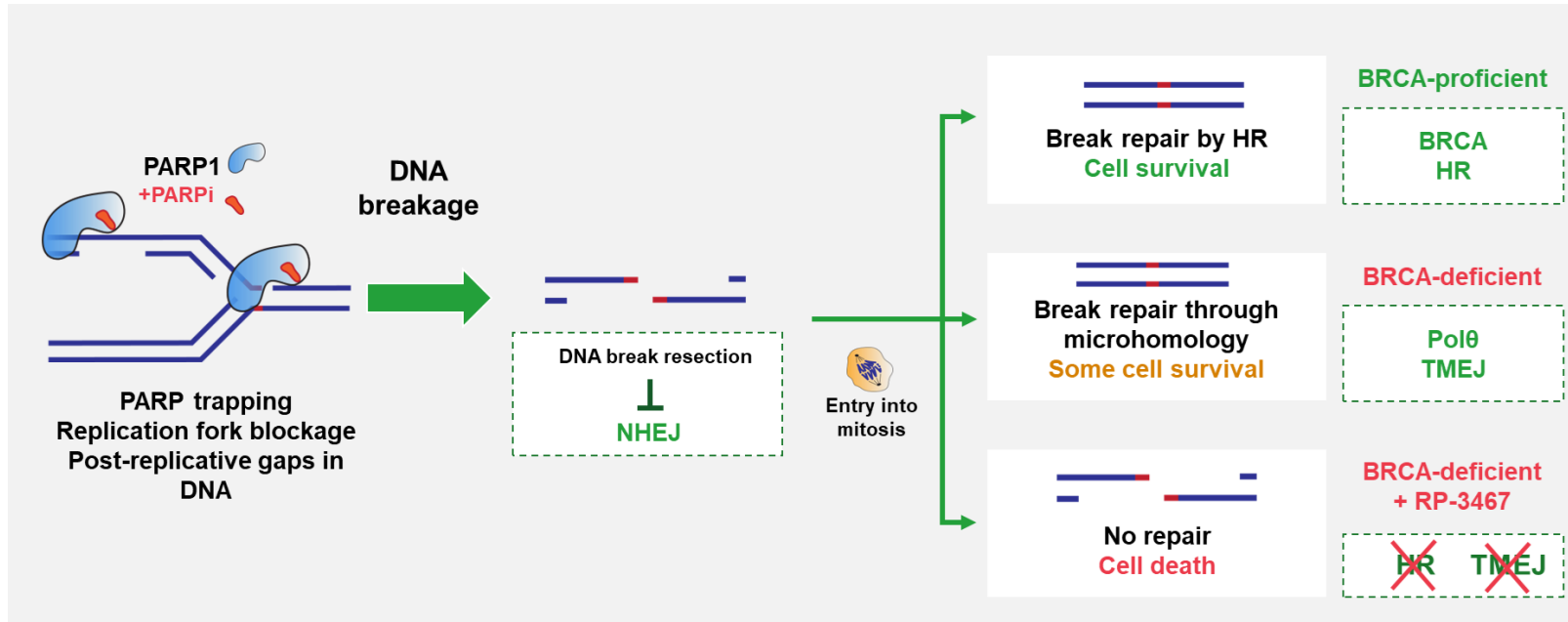


Body Weight



- Monotherapy tumor growth suppression at a well-tolerated dose of RP-3467

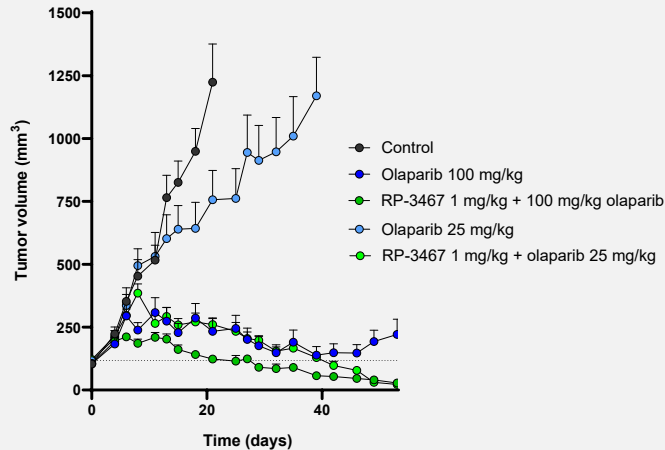
Rationale for synergy between Polθi and PARPi



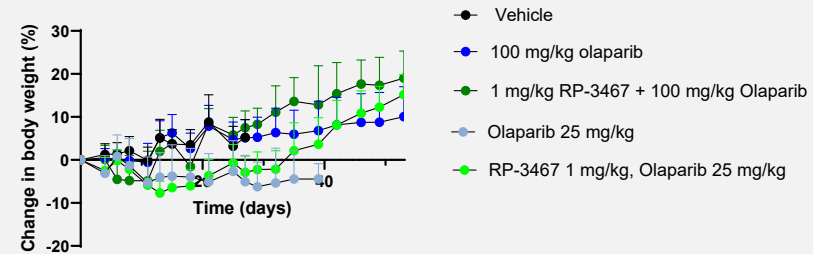
- **PARPi + Polθi combination synergizes to kill homologous recombination deficient tumor cells**

RP-3467 drives complete regressions in combo with full-dose olaparib

Efficacy HCT116 BRCA2 -/-



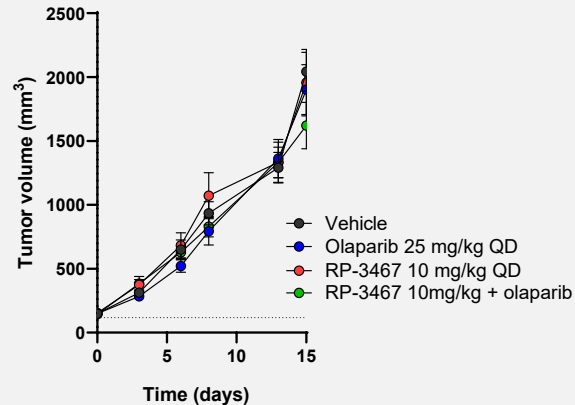
Body Weight



- Complete regressions with high and low dose Olaparib suggest that RP-3467 will allow PARPi dose reductions

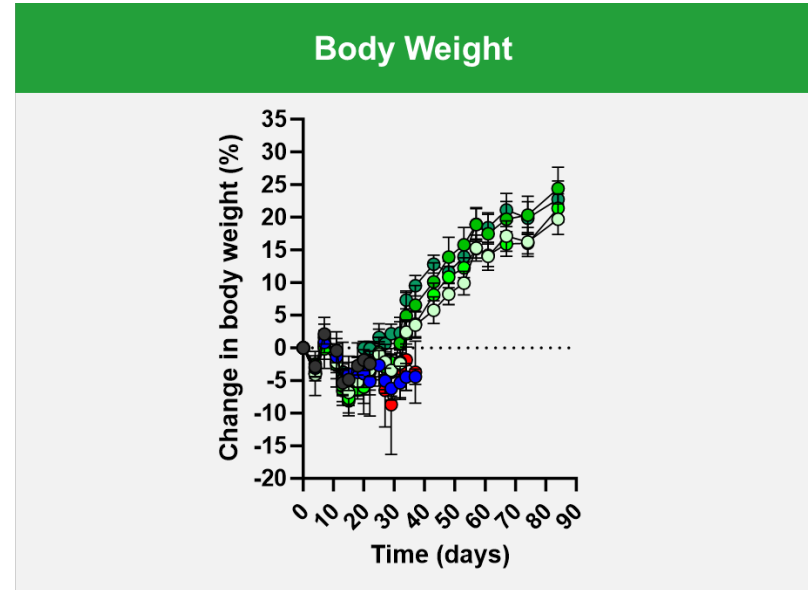
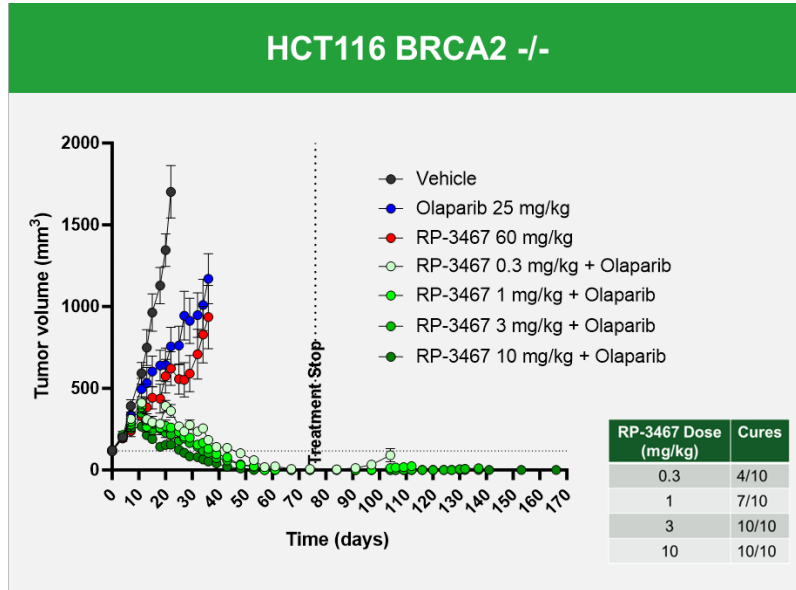
RP-3467 does not potentiate PARPi in BRCA WT cells

HCT116 WT



- Lack of effect in HR competent cells supports safety in normal tissues

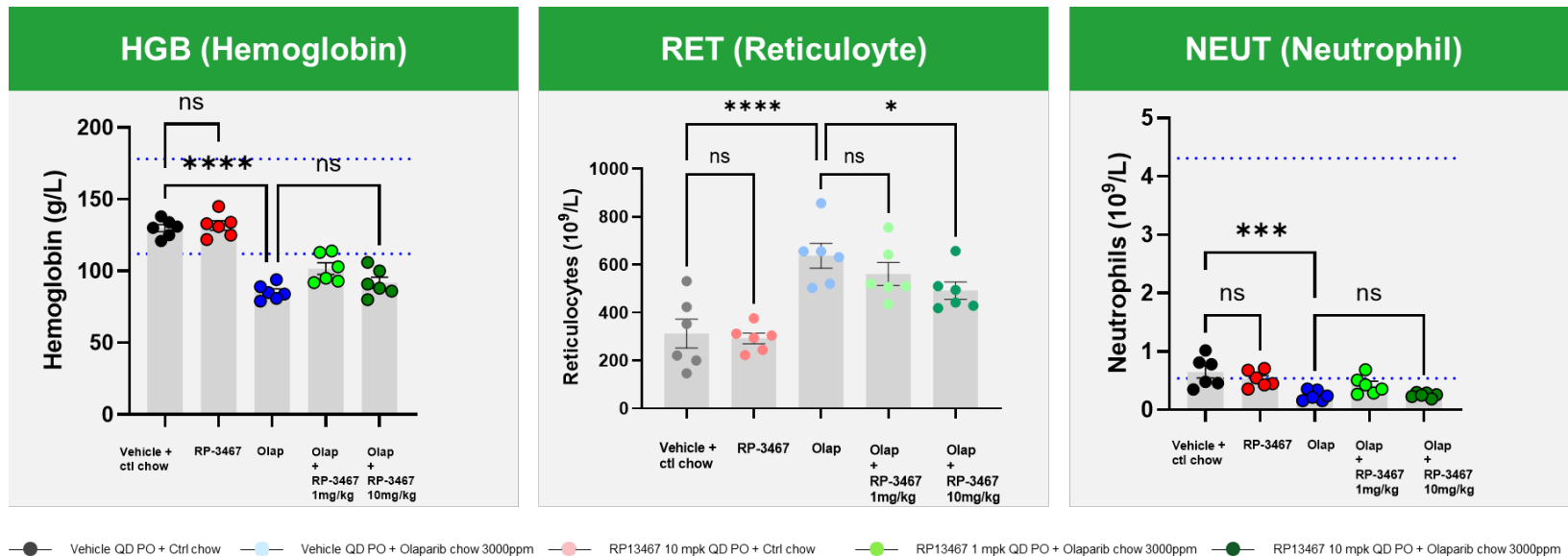
Profound, durable synergy with PARP1/2 inhibition



- Deep/durable complete regressions across a wide dose range and extremely well tolerated

No added hematological toxicity in combination over PARP1/2i alone

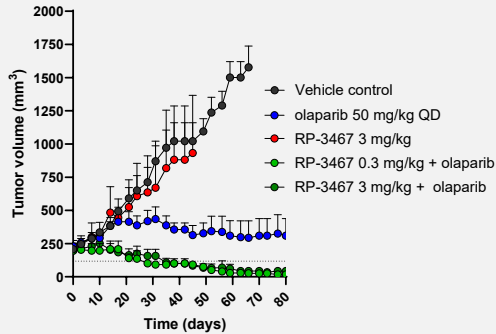
5 weeks co-administration of human clinical PK equivalent dose of olaparib with RP-3467 up to 10mg/kg in CD1 mice



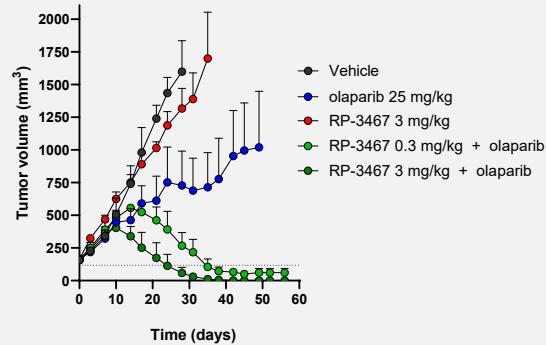
- Extremely well tolerated combination at relevant olaparib doses

Synergy with PARPi combinations across BRCA2 null PDX models

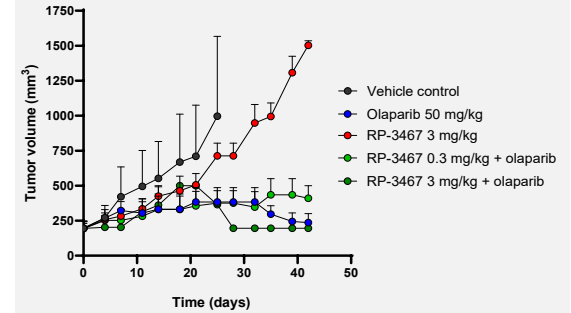
Breast ER+



Breast TNBC

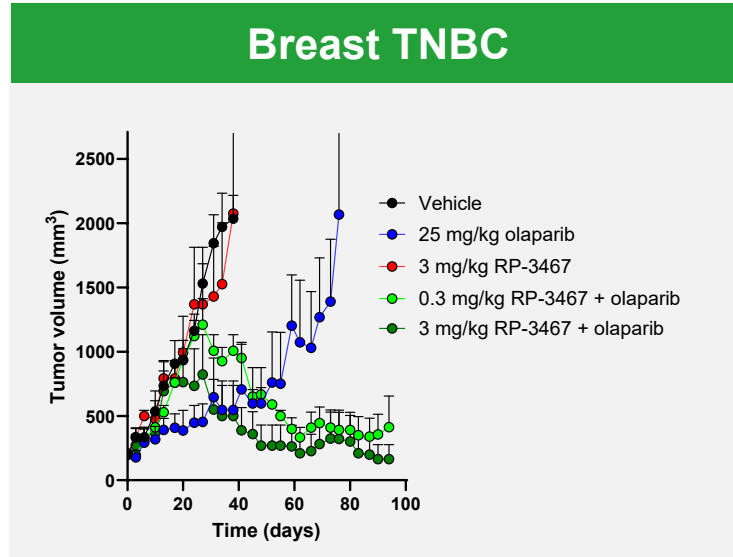


Breast ER+



- Complete/partial regression in BRCA2 null PDX models

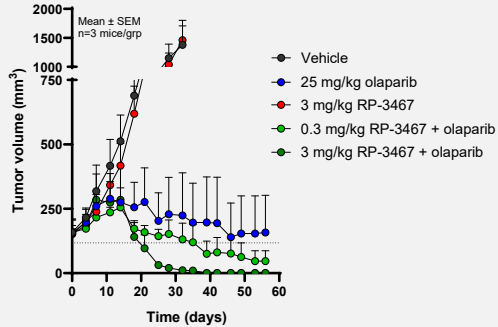
Synergy with PARP1i combinations in a PALB2 null PDX model



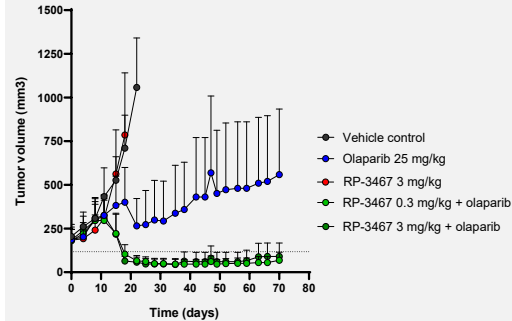
- Partial regression in a PALB2 null PDX models

Synergy with PARPi combinations across BRCA1 null PDX models

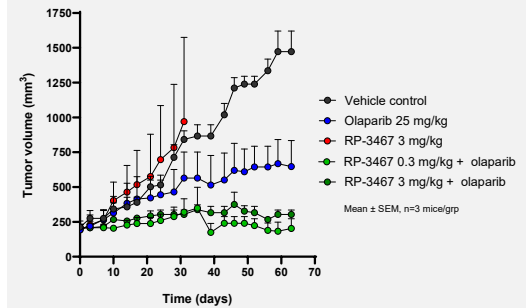
Breast TNBC



Breast TNBC

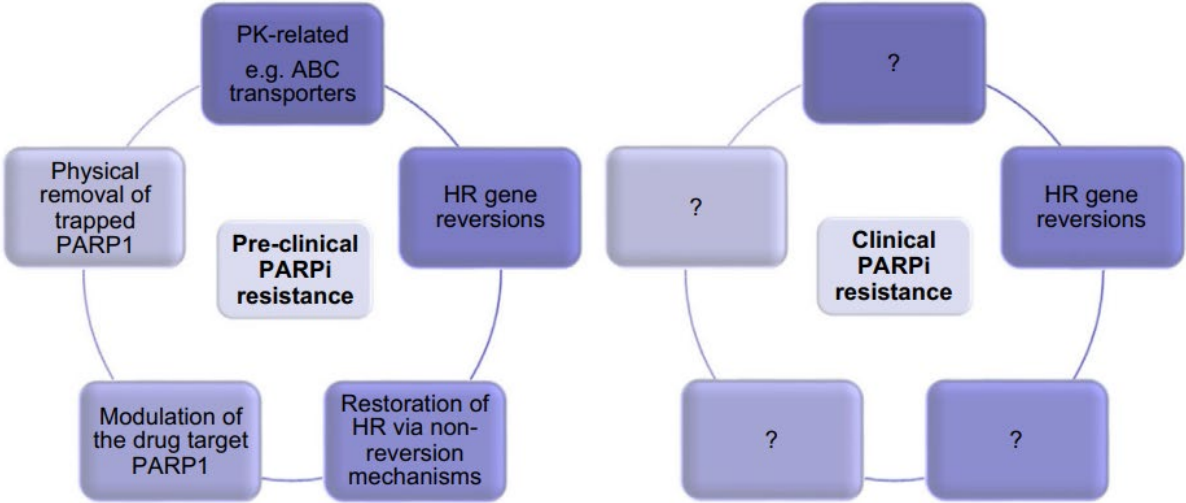


Breast TNBC



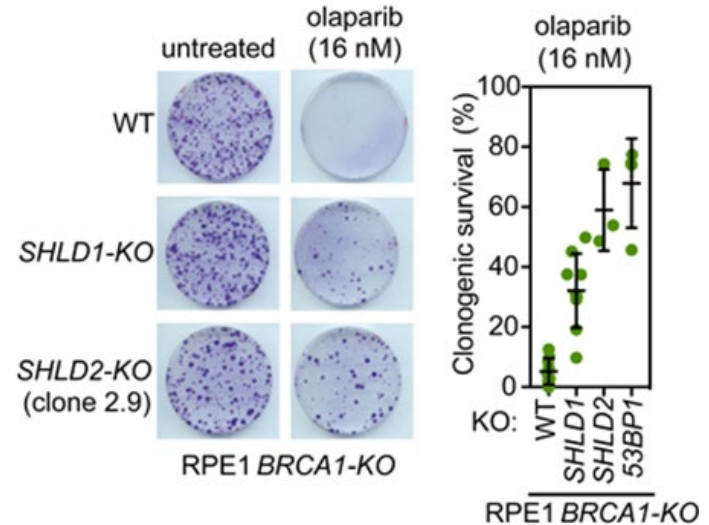
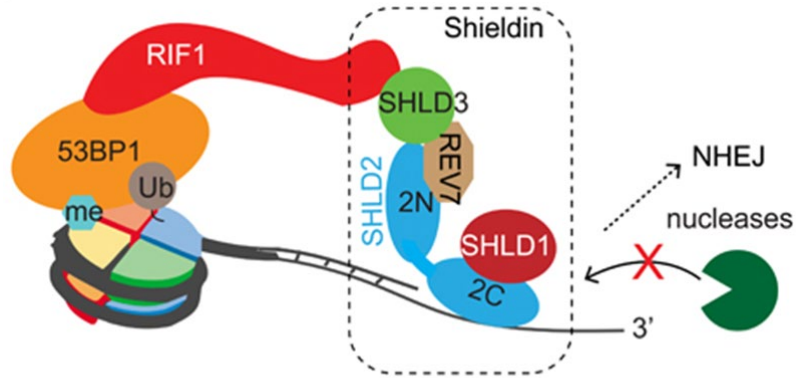
- Complete/partial regression in BRCA1 null PDX models

Mechanisms of resistance to PARPi



J. S. Baxter et al. Molecular Oncology (2022)

53BP1/Shieldin Loss: A potential mechanism of PARPi resistance

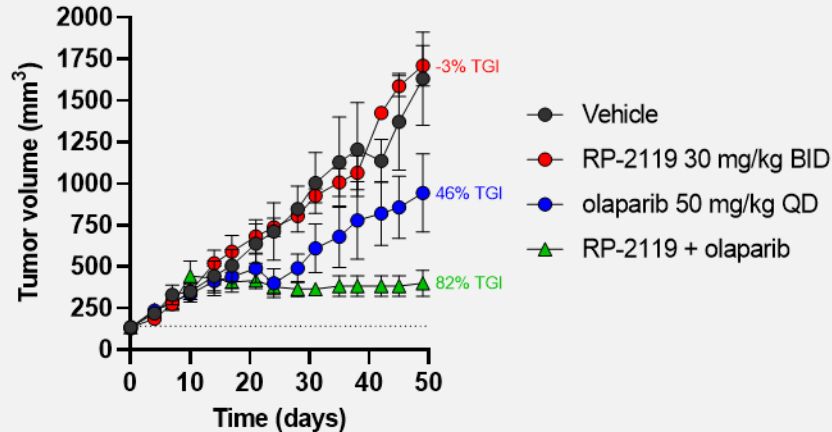


Noordermeer et al. (2018) Nature

- Loss of components of the 53BP1 pathway results in PARPi resistance

Polθi is active in PARPi resistant PDX model

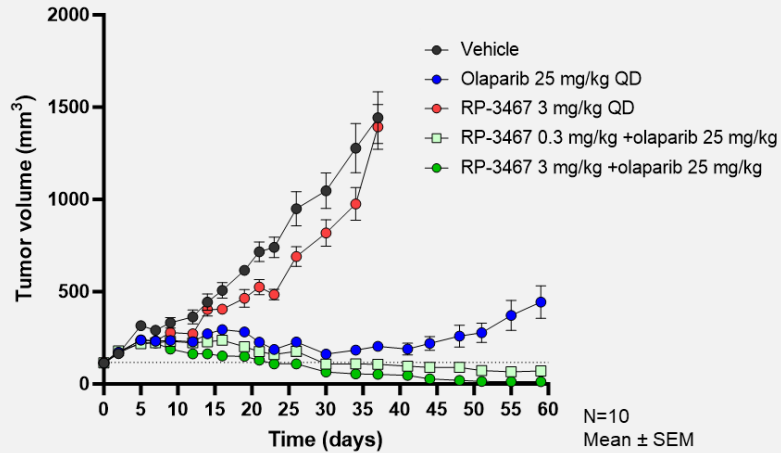
Breast TNBC (BRCA1mt, SHLD2 LOF)



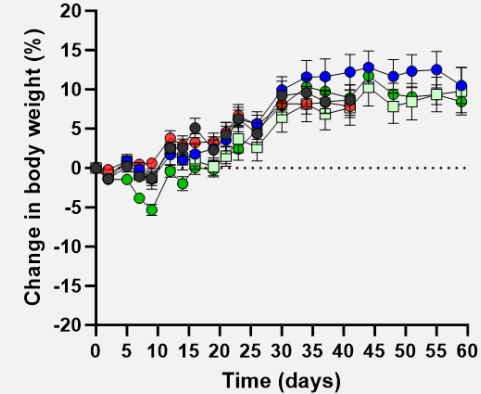
- PARPi + Polθi synergize in tumors with alterations of the Shieldin complex (a mechanism of PARPi resistance)

Durable synergy with PARPi inhibition in a BRCA1 null CDX

MDA-MB-436



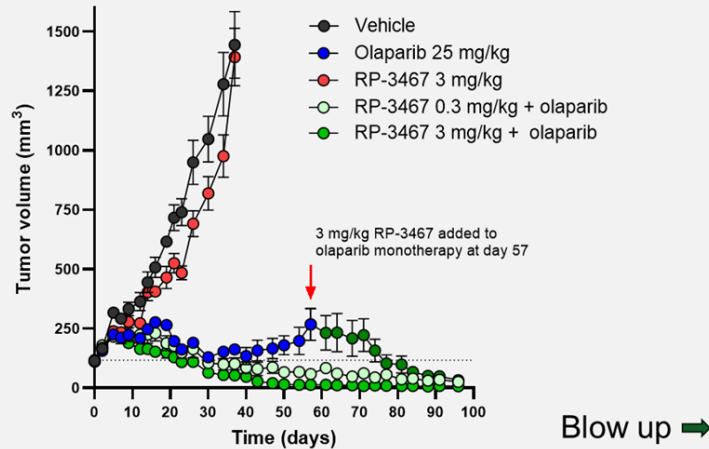
Body Weight



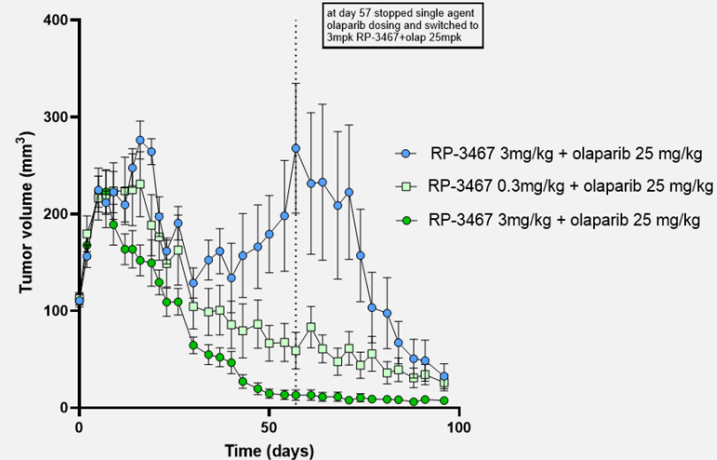
- **RP-3467 and olaparib co-treatment results in tumor regressions in a BRCA1 deficient model**

Tumors regrowing on Olaparib are sensitive to RP-3467 + PARPi combo

RP-3467- causes regression in MDA-MB-436 BRCA1 deficient tumors



Combination with RP-3467 provides regression in tumors that escape olaparib single agent treatment



- Tumors that escape single-agent therapy can be successfully retreated with the combination

- **Phase 1 clinical trial initiation expected in 2H 2024**
- **Primary Goal: PK, safety and recommended Phase 2 dose**

Synthetic lethal opportunity – homologous recombination deficient (HRD) genetic alterations

Exciting combination opportunity – Polθ inhibition is extremely well tolerated preclinically, with no expected overlapping toxicities

PARPi combinations – Upfront in HRD driven prostate, ovarian, breast and pancreatic cancer, innate/acquired PARPi resistance

Radioligand Therapy (RLT) – Potential for *unselected* RLT combinations and external beam irradiation

Chemotherapy/ADCs – Combinations with dsDNA break inducing chemo therapies (e.g. first line ovarian (CarboTaxol), ADC therapies with topoisomerase payloads)

Acknowledgements

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