

The AACR logo features the letters 'AACR' in a bold, black, sans-serif font, with a green 'R' that has a stylized white crossbar. The logo is set against a background of colorful, abstract, crystalline shapes in shades of blue, green, yellow, and red.

American Association
for Cancer Research®

**ANNUAL
MEETING**
2022 *New Orleans*

A green banner with white text, positioned over a collage of images including people, a microscope, and a bar chart. The text reads 'APRIL 8-13, 2022 • #AACR22'.

APRIL 8-13, 2022 • #AACR22

KSQ-4279: A first-in-class USP1 inhibitor for the treatment of cancers with homologous recombination deficiency

Andrew Wylie

KSQ Therapeutics, Cambridge, MA

Disclosure Information

Andrew Wylie

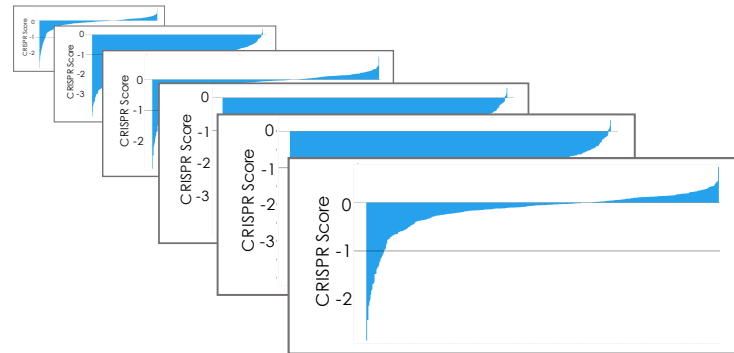
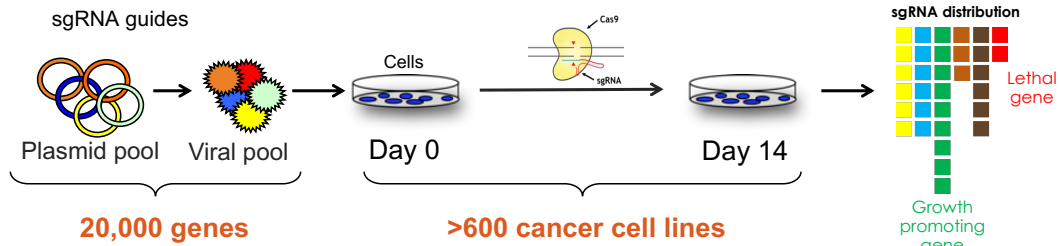
APRIL 8-13 • #AACR22

I have the following relevant financial relationships to disclose:

I am an Employee and Stockholder of KSQ Therapeutics

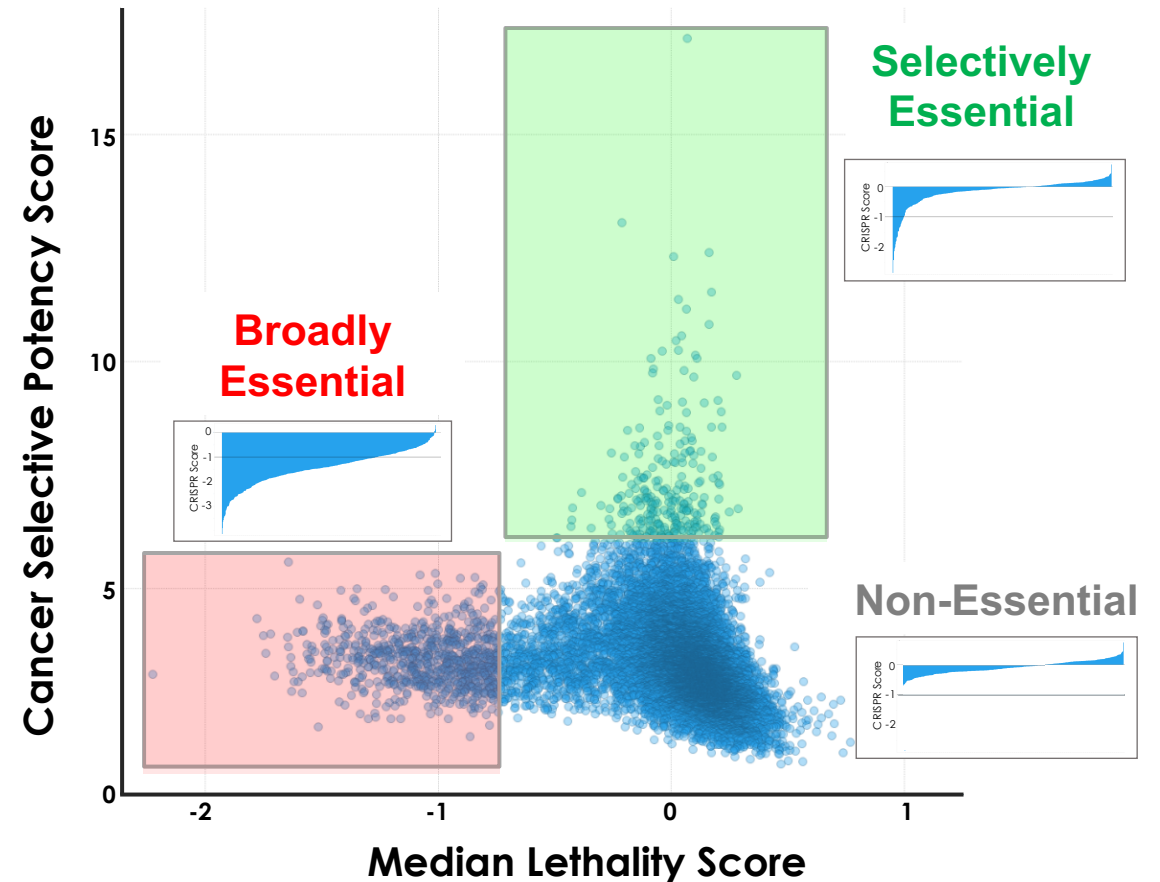
CRISPR screen identifies targets that are selectively essential in cancer cell line subsets

CRISPRomics® database



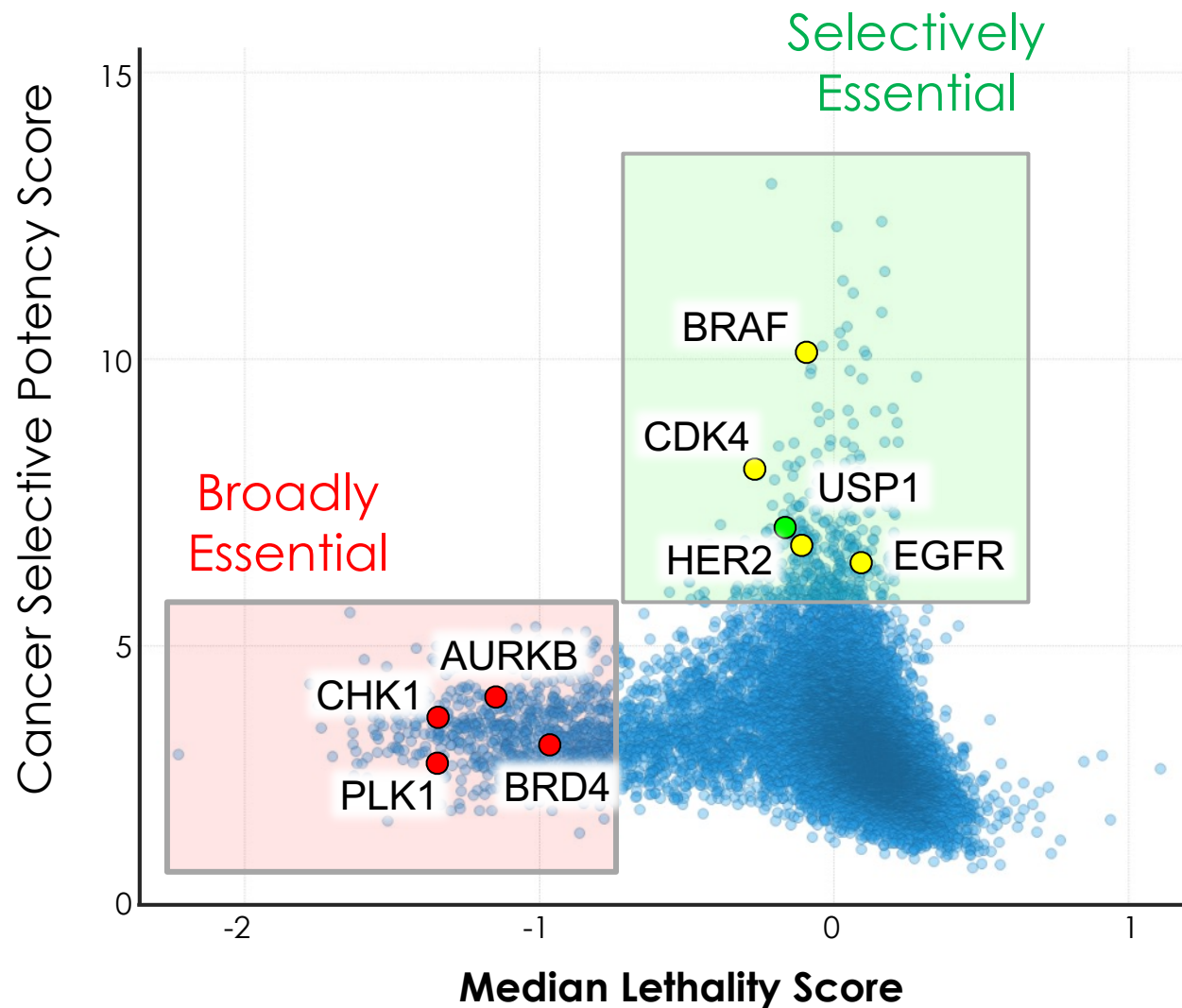
20,000 drop-out profiles

Genome-wide view



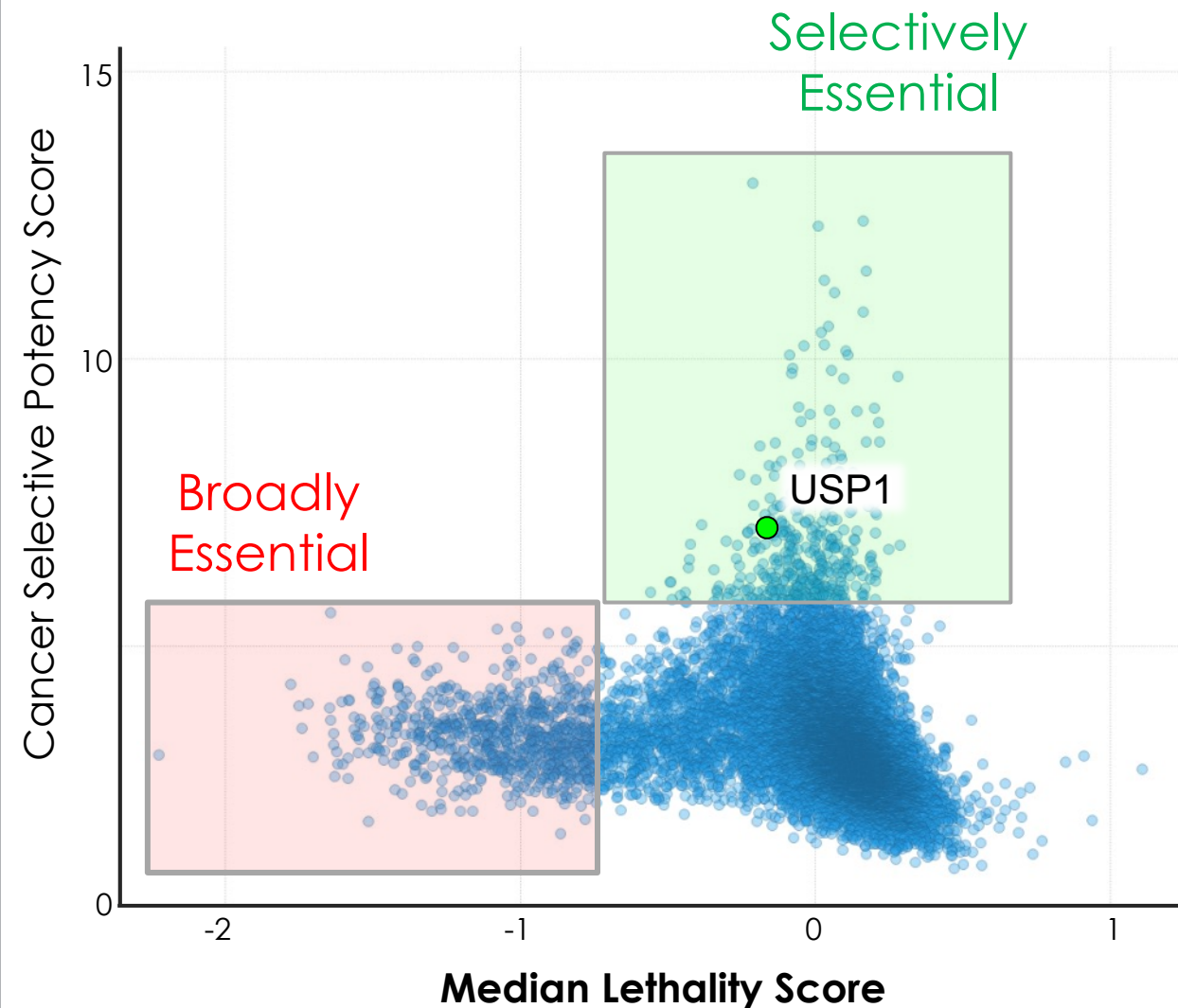
KSQ Knowledgebase: Identification of Cancer-Selective Targets

Database highlights targets with potential for rapid clinical development

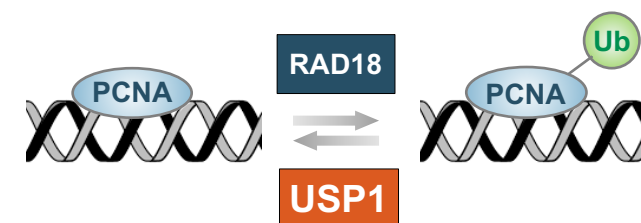


CRISPRomics® Identifies USP1 as a novel, DDR pathway target

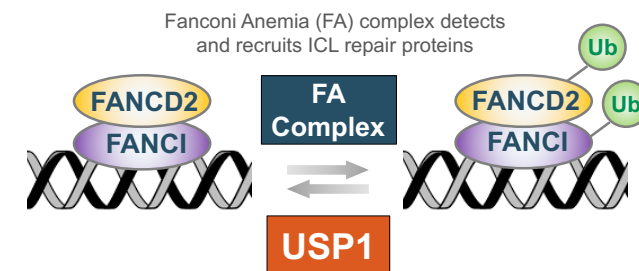
USP1 is a de-ubiquitinase that regulates DNA damage repair pathways



USP1 regulates key DDR pathways



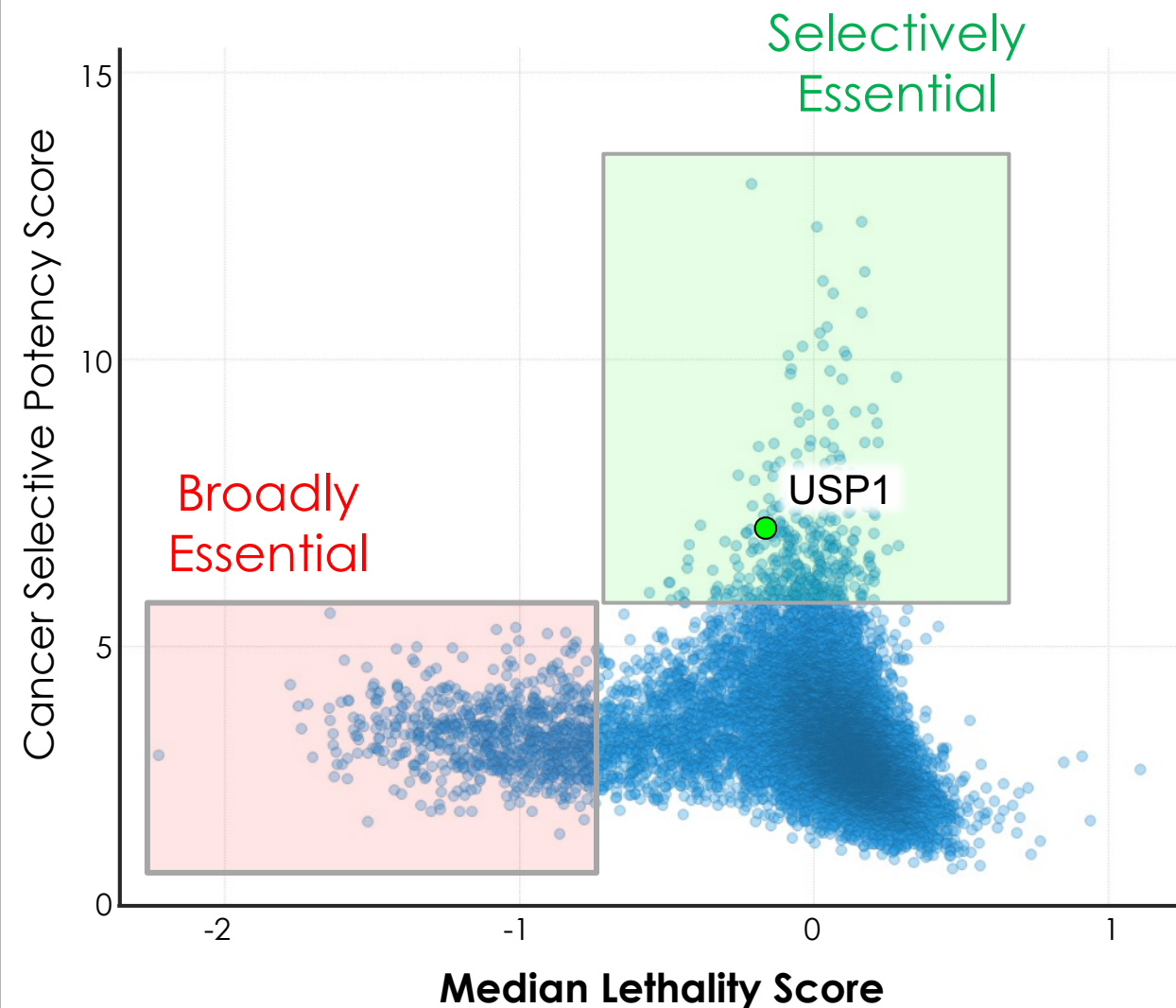
Translesion synthesis



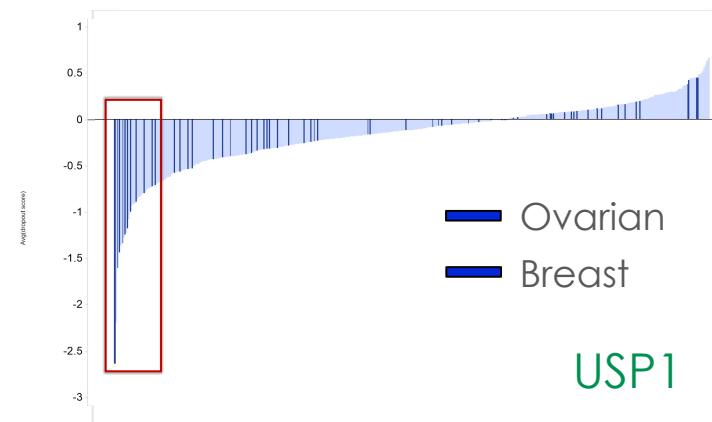
Intra-strand Crosslink Repair

CRISPRomics® Identifies USP1 as a novel, DDR pathway target

Ovarian and Breast cancer lineages are enriched in USP1 sensitive cells



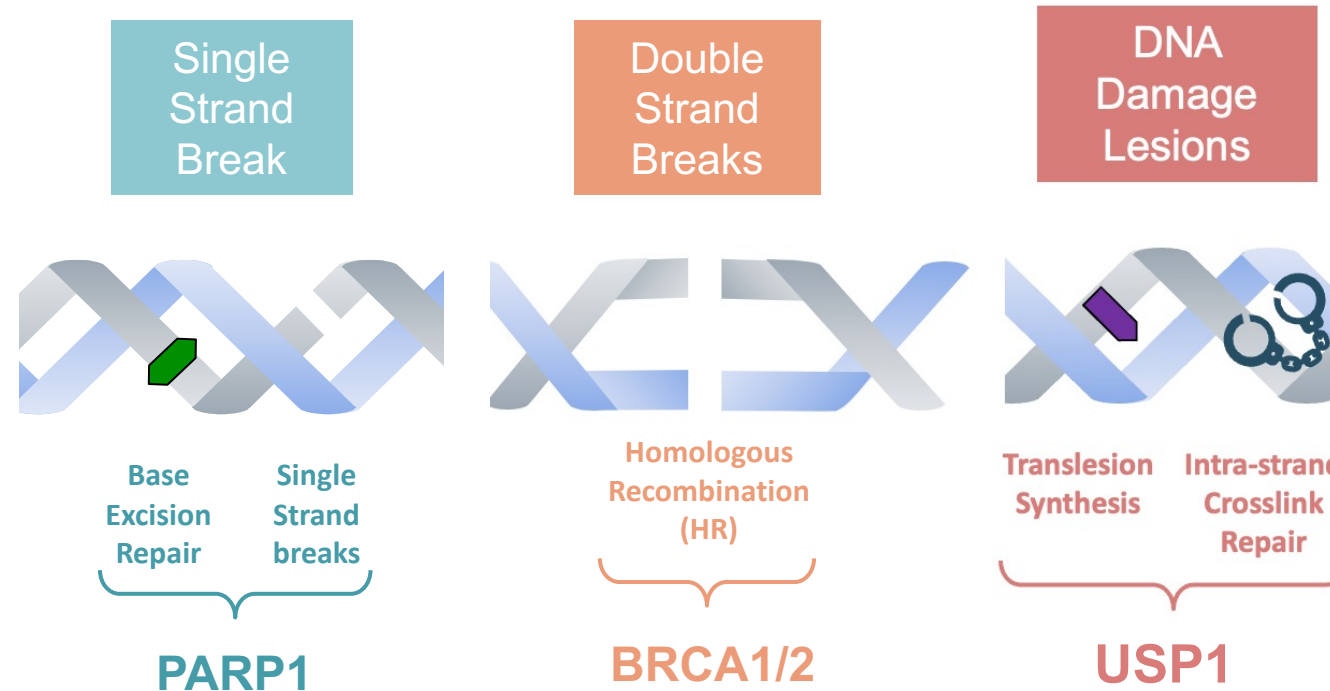
Cell line enrichment profile



- Ovarian/Breast often associated with BRCA1/2^{MUT} and other defects in Homologous Recombination
- 6 of 9 Ovarian/Breast lines with USP1 dependency are HRD+/BRCAmut
- Despite activity of PARP inhibitors, HRD+/ BRCA^{MUT} tumors remain a high unmet clinical need

*HRD+ = homologous recombination deficiency

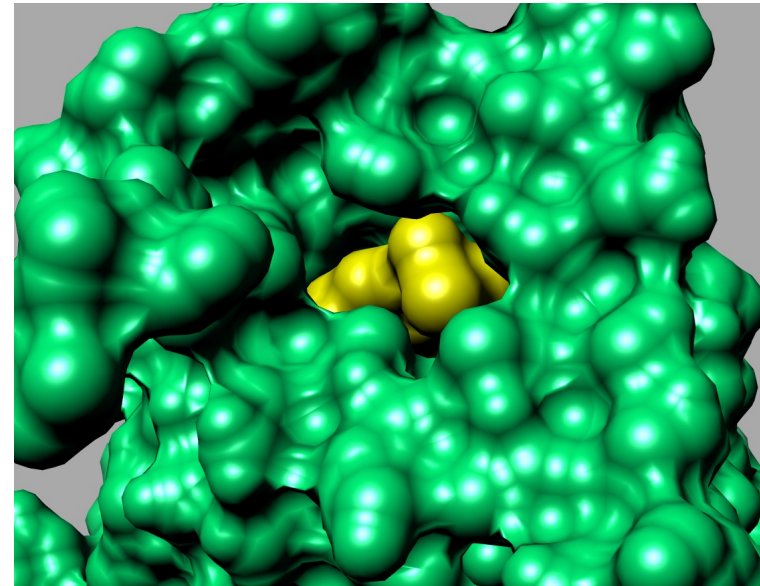
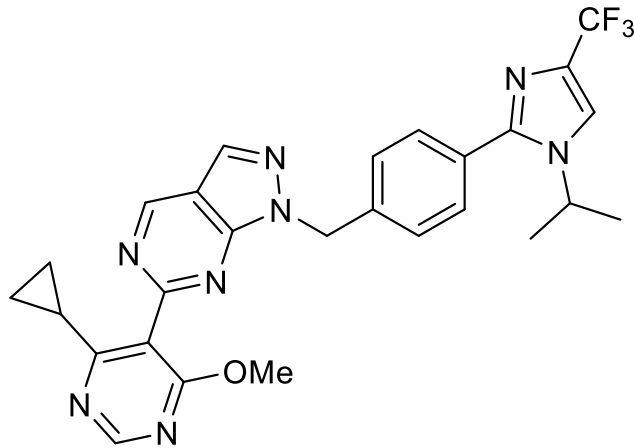
USP1 regulates a distinct set of DNA Damage response pathways from PARP inhibitors



Development of KSQ-4279, a potent, selective USP1 inhibitor

KSQ-4279, a potent, selective USP1 inhibitor

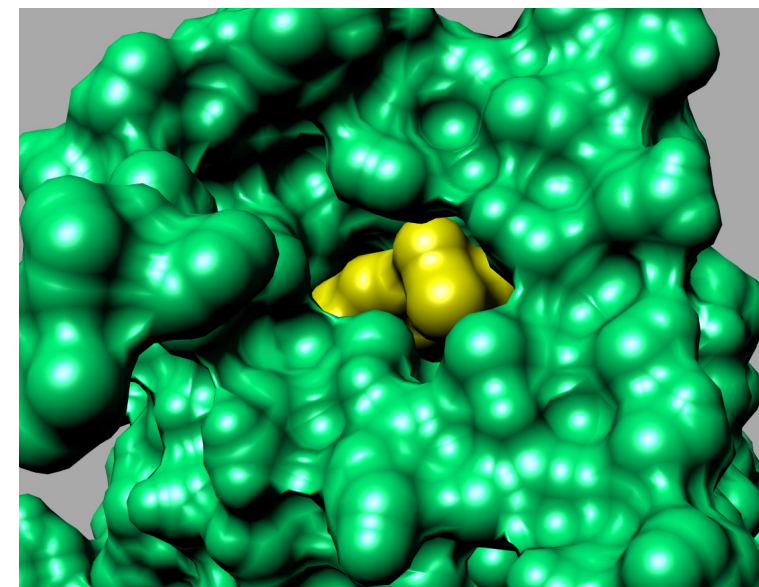
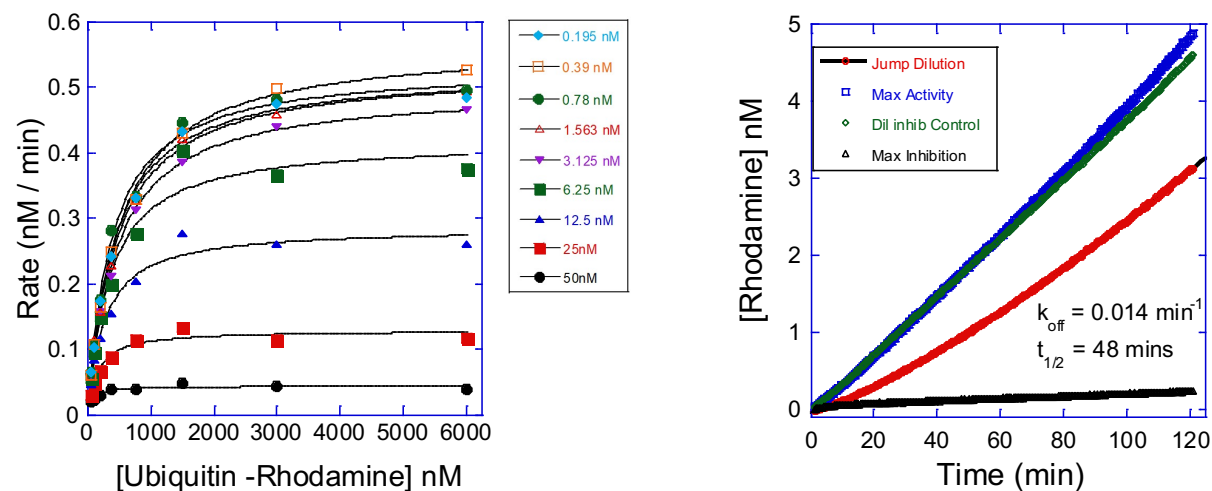
KSQ-4279



- KSQ-4279 is a reversible, allosteric inhibitor of USP1 with a **K_i = 1.2nM**
- Both KSQ-4279-bound and unbound USP1 structures solved revealing an induced fit mechanism

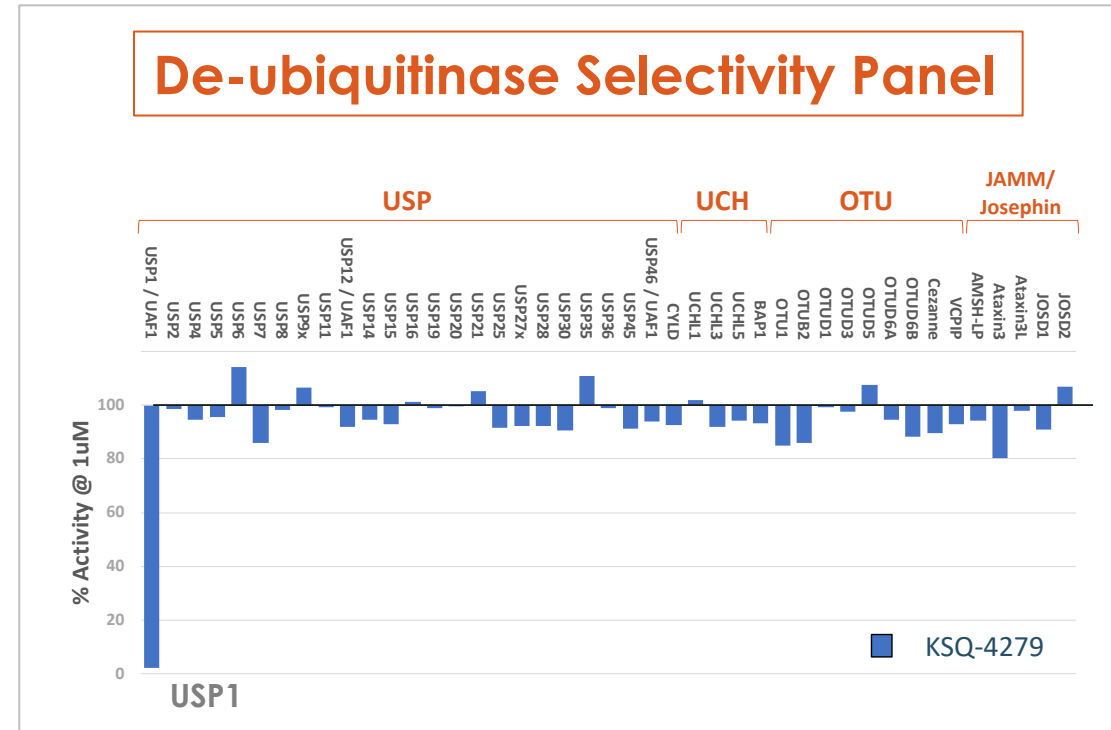
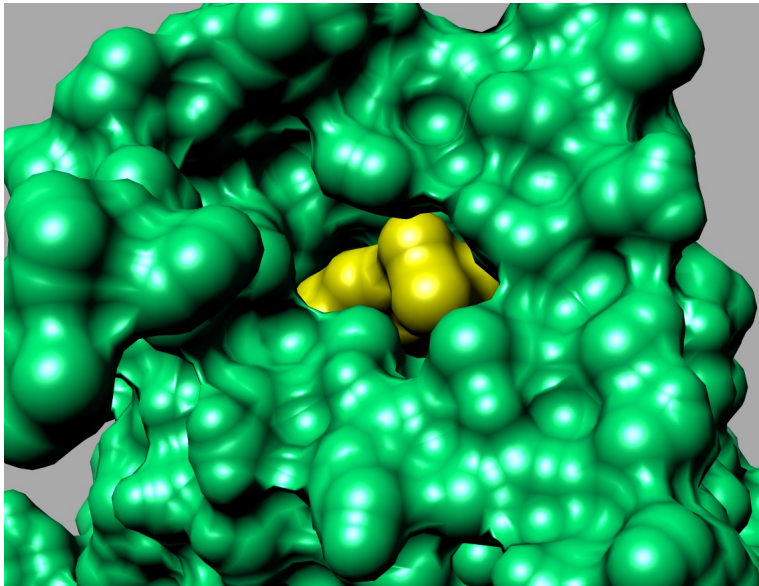
KSQ-4279 is a potent, allosteric inhibitor of USP1 with excellent selectivity

Enzyme kinetics and mode of inhibition



- Both V_{max} and K_m decrease indicating uncompetitive mode of inhibition
- Reversible binding with a slow k_{off} and a $t_{1/2} = 48 \text{ mins}$

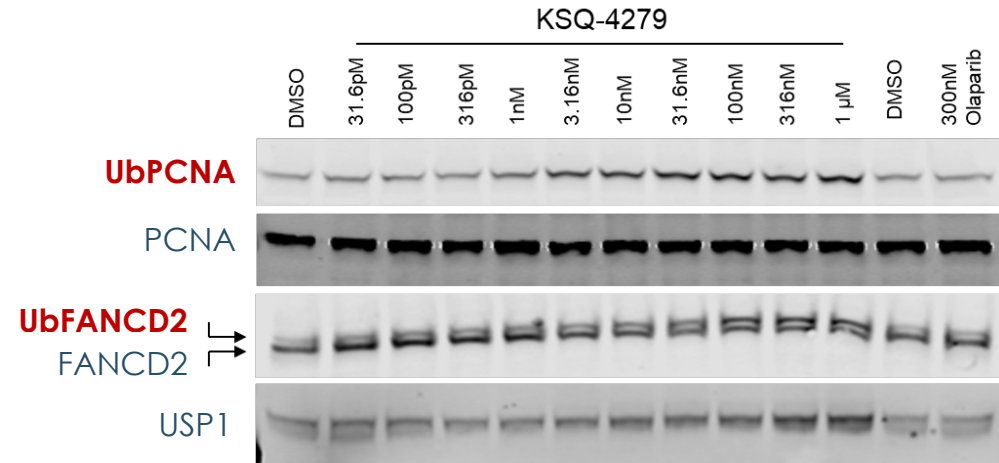
KSQ-4279 is a potent, allosteric inhibitor of USP1 with excellent selectivity



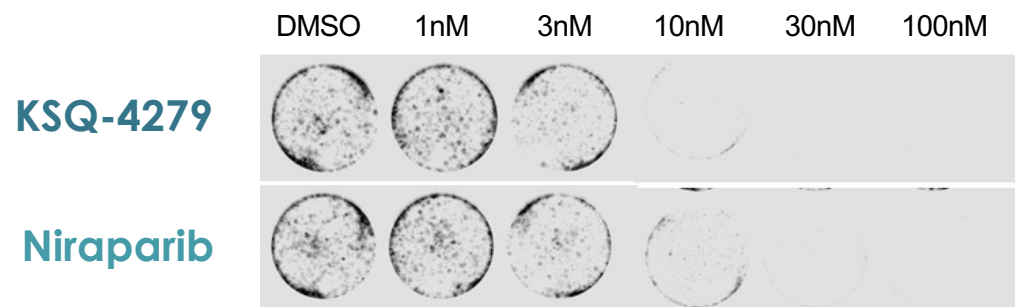
- DUB family profiling indicates KSQ-4279 is a selective inhibitor of USP1

KSQ-4279 leads to accumulation of mono-Ub substrates and anti-proliferative activity correlates with genetic knock-out

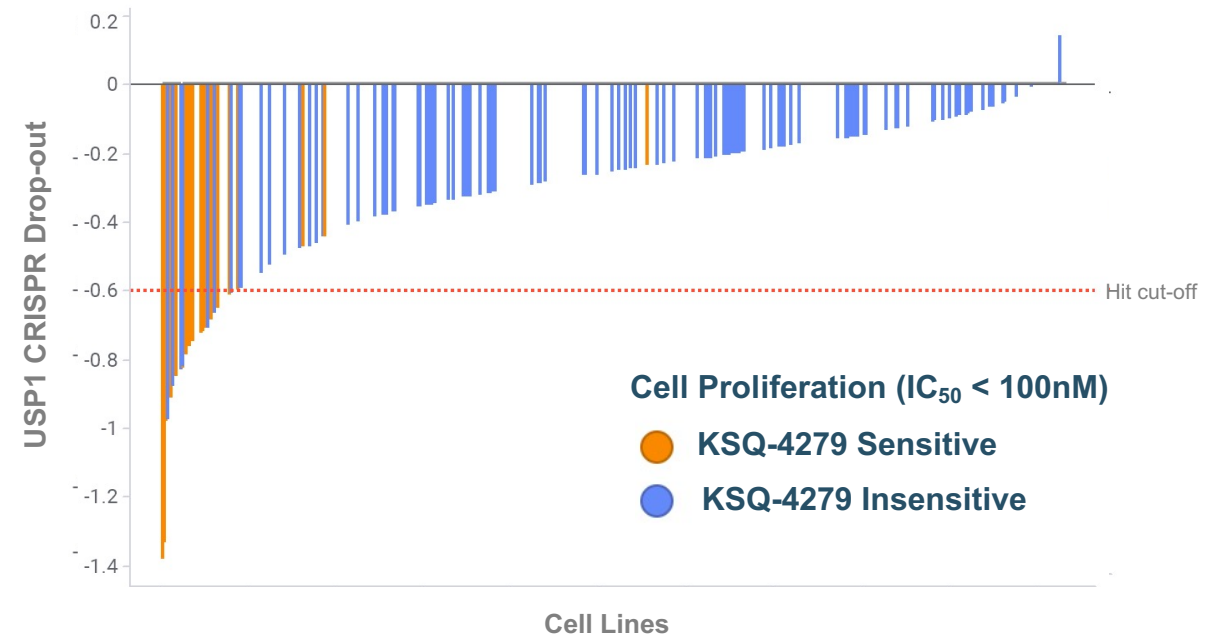
PD changes in MDA-MB-436 (BRCA1^{MT}, p53^{MT})



Colony formation assay in MDA-MB-436 (BRCA1^{MT}, p53^{MT})



Comparison between CRISPR knockout and KSQ-4279 sensitivity

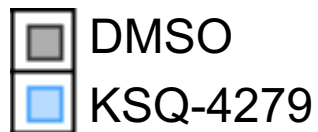
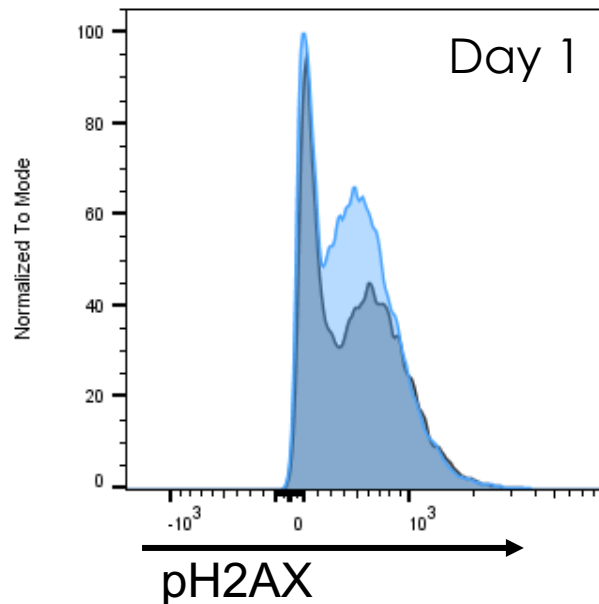


What is the mechanism of action of KSQ-4279?

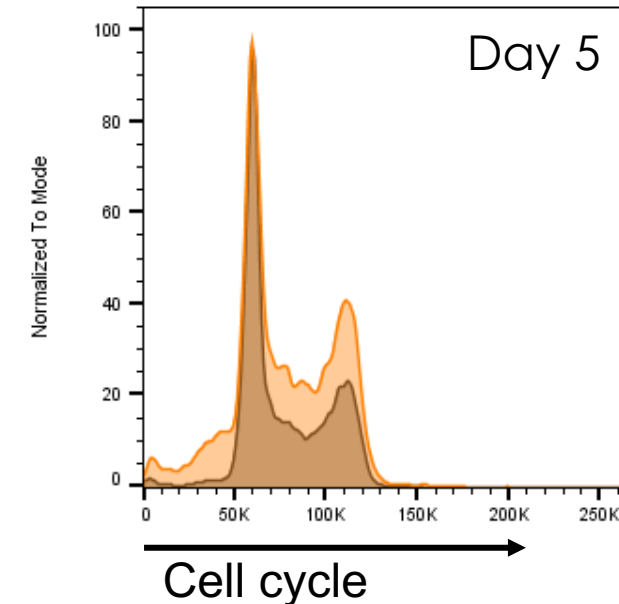
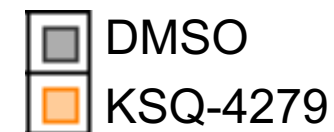
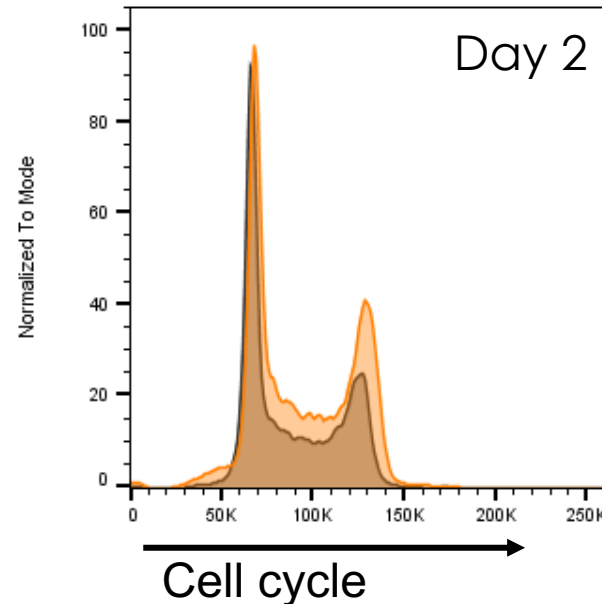
KSQ-4279 Induces DNA Damage and S/G2-Phase Arrest in BRCA1^{MT} Cells

UWB1.289 cells (BRCA1^{MT}, p53^{MT})

pH2AX levels

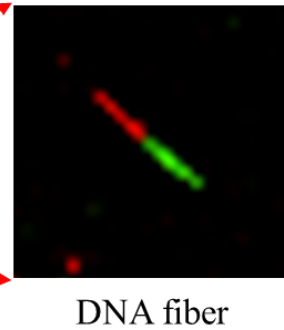
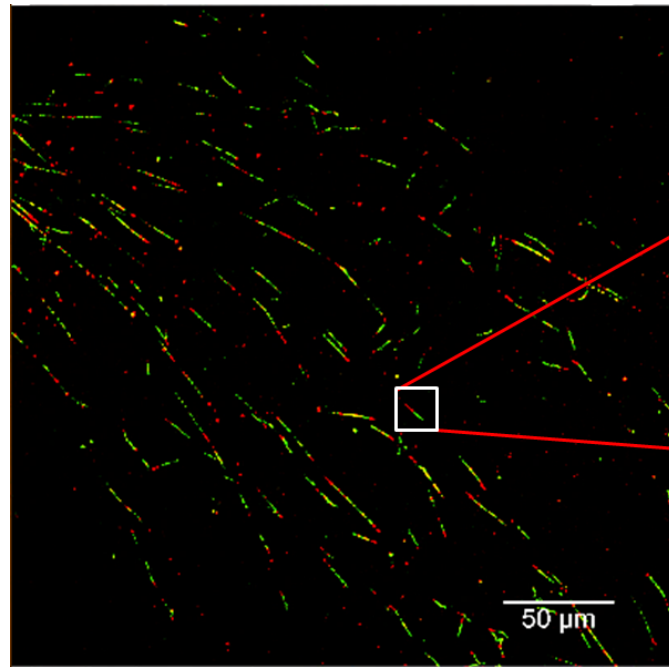
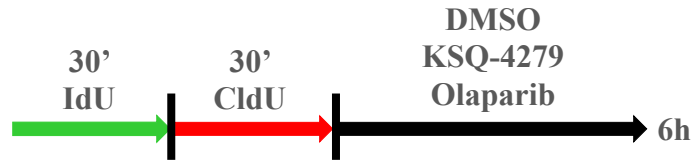


Cell Cycle Analysis

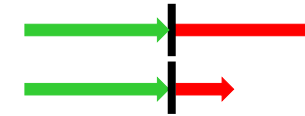


USP1 reported to be required for replication fork protection in BRCA1-deficient tumors

DNA Fiber Fork Protection Assay



Protected Fork
Degraded Fork



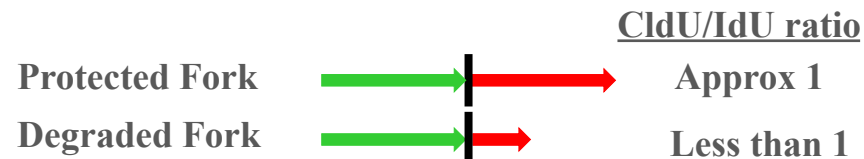
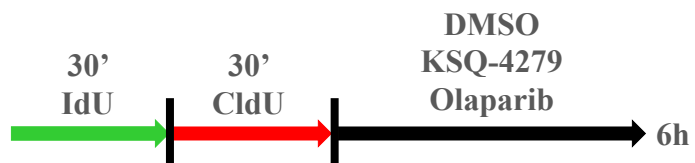
CldU/IdU ratio
Approx 1
Less than 1

USP1 Is Required for Replication Fork Protection in BRCA1-Deficient Tumors

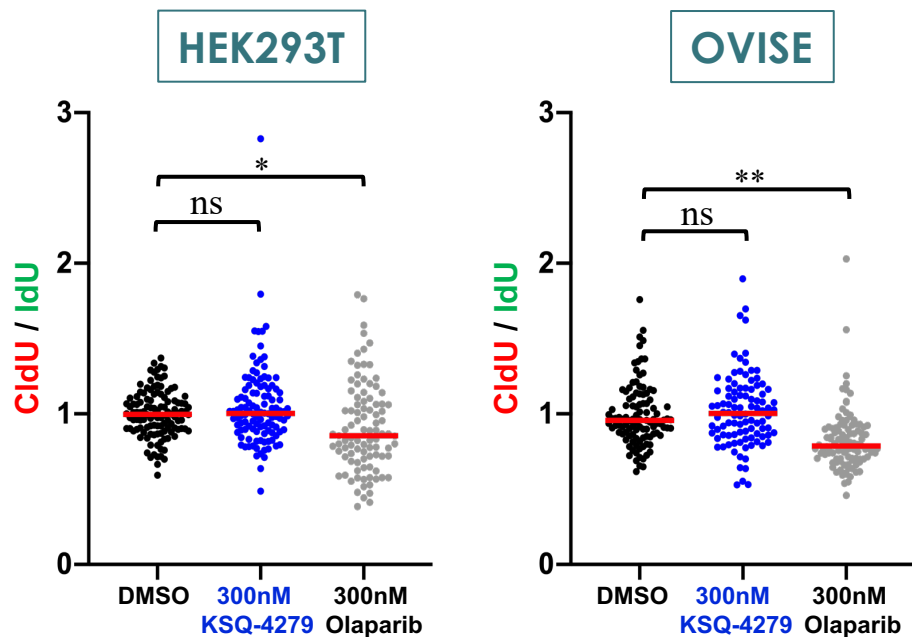
Kah Suan Lim,¹ Heng Li,³ Emma A. Roberts,¹ Emily F. Gaudiano,¹ Connor Clairmont,¹ Larissa Alina Sambel,^{1,2} Karthikeyan Ponninselvan,¹ Jessica C. Liu,¹ Chunyu Yang,^{1,2} David Kozono,¹ Kalindi Parmar,^{1,2} Timur Yusufzai,¹ Ning Zheng,^{3,4} and Alan D. D'Andrea^{1,2,5,*}

Molecular Cell, 72, 925-941 (2018)

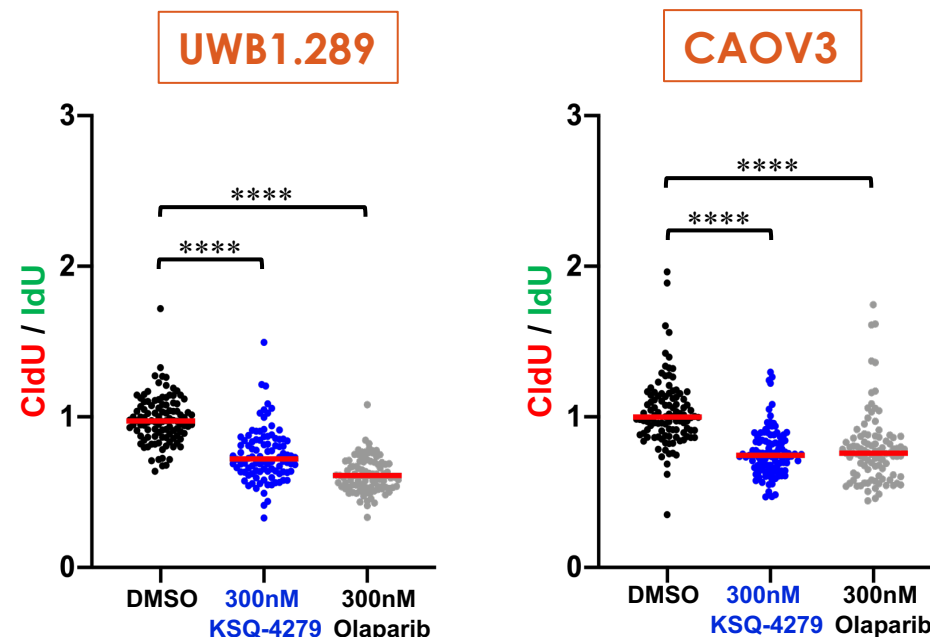
Sensitivity to KSQ-4279 correlates with degradation of the replication fork



Inensitive cell lines

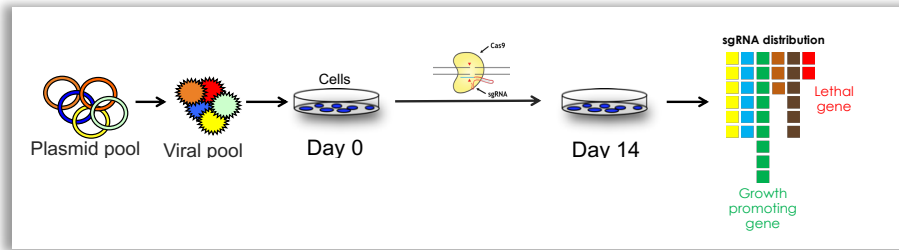


Sensitive cell lines

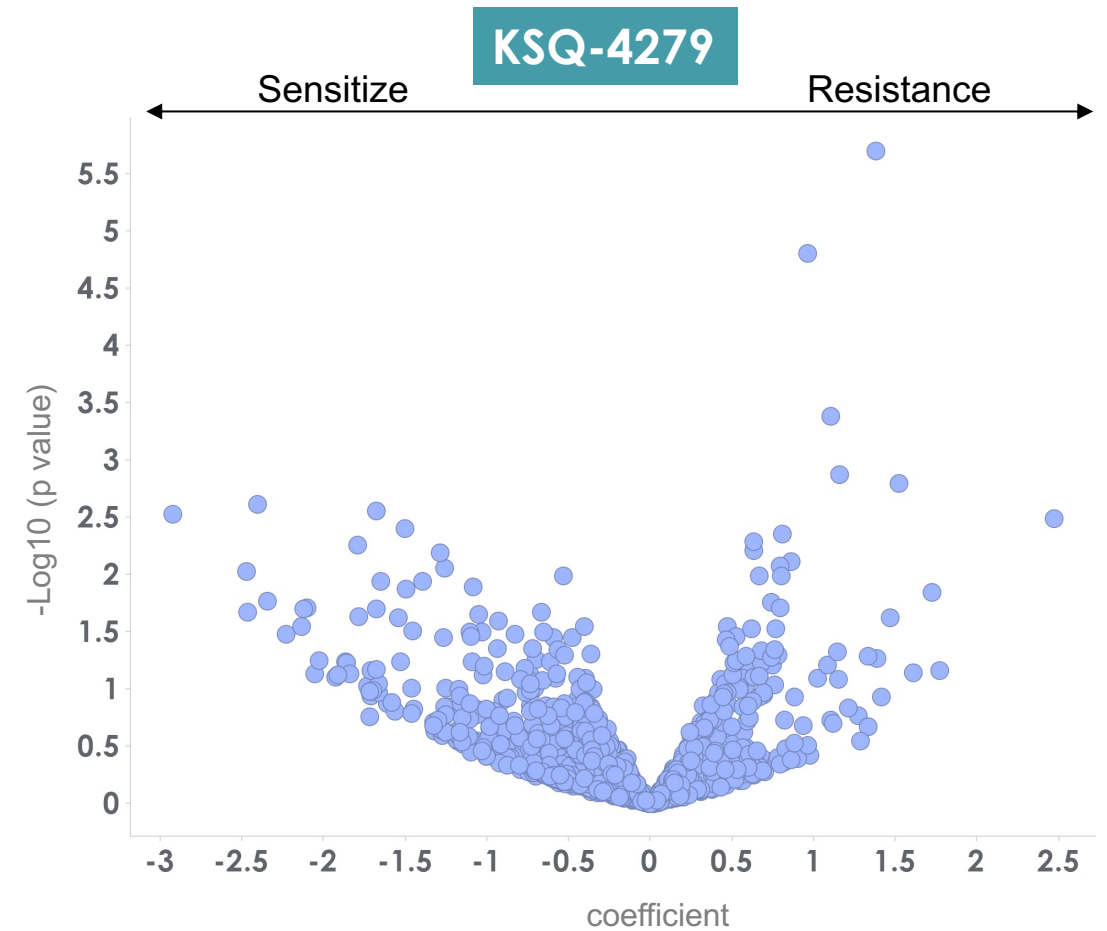
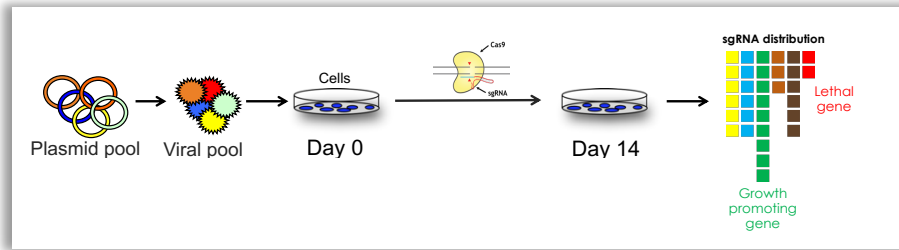


CRISPR screening reveals pathways that influence sensitivity to KSQ-4279

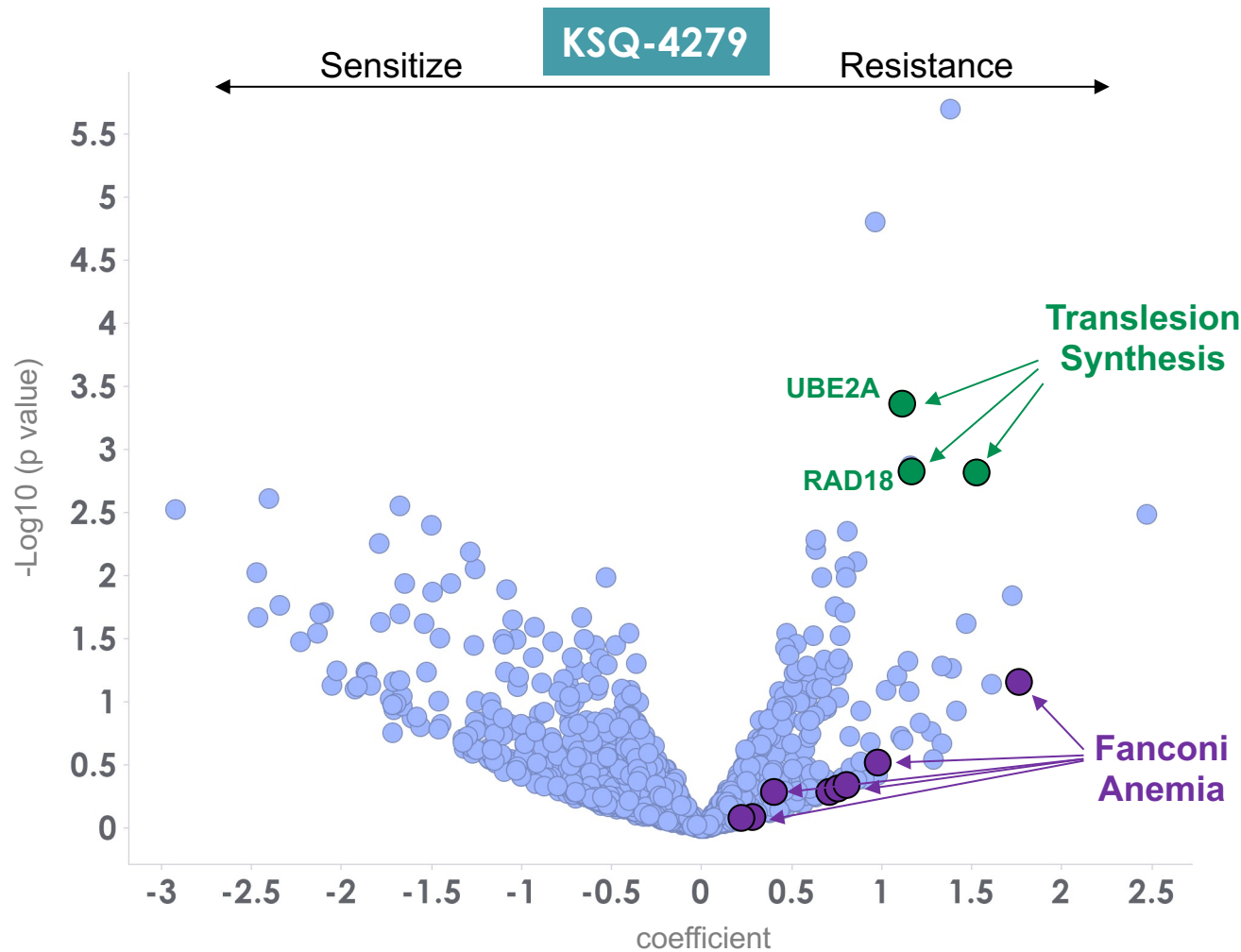
DMSO



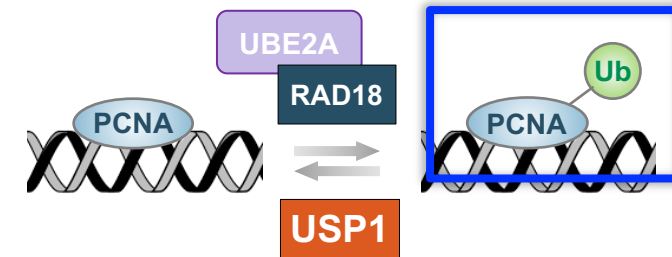
USP1i



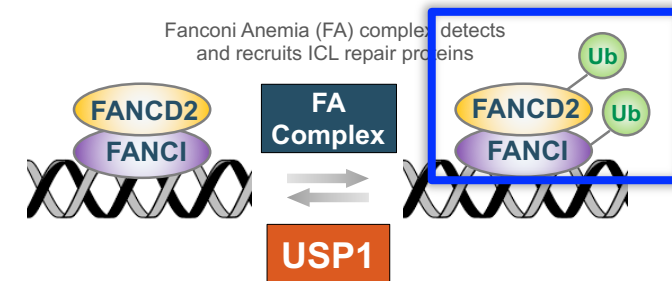
CRISPR screening reveals pathways that influence sensitivity to KSQ-4279



USP1 regulates TLS & FA Pathway

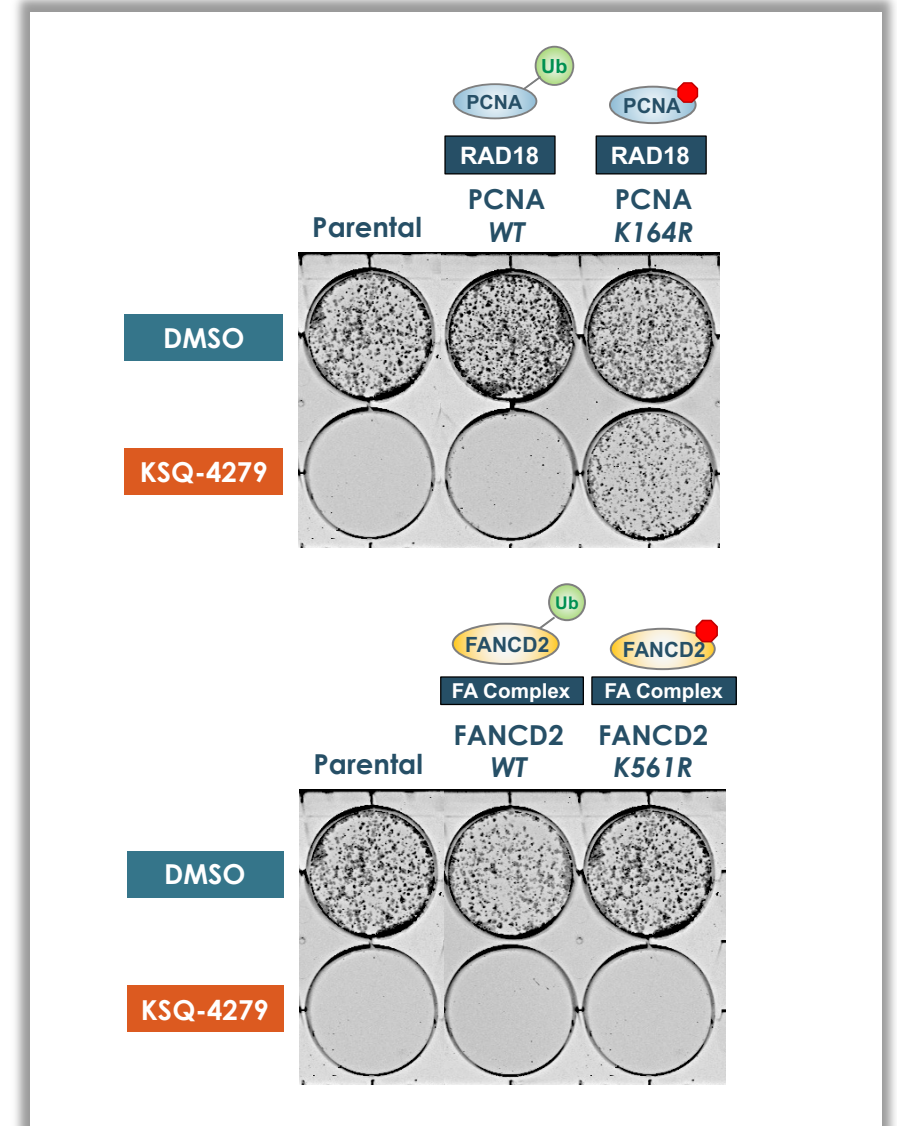
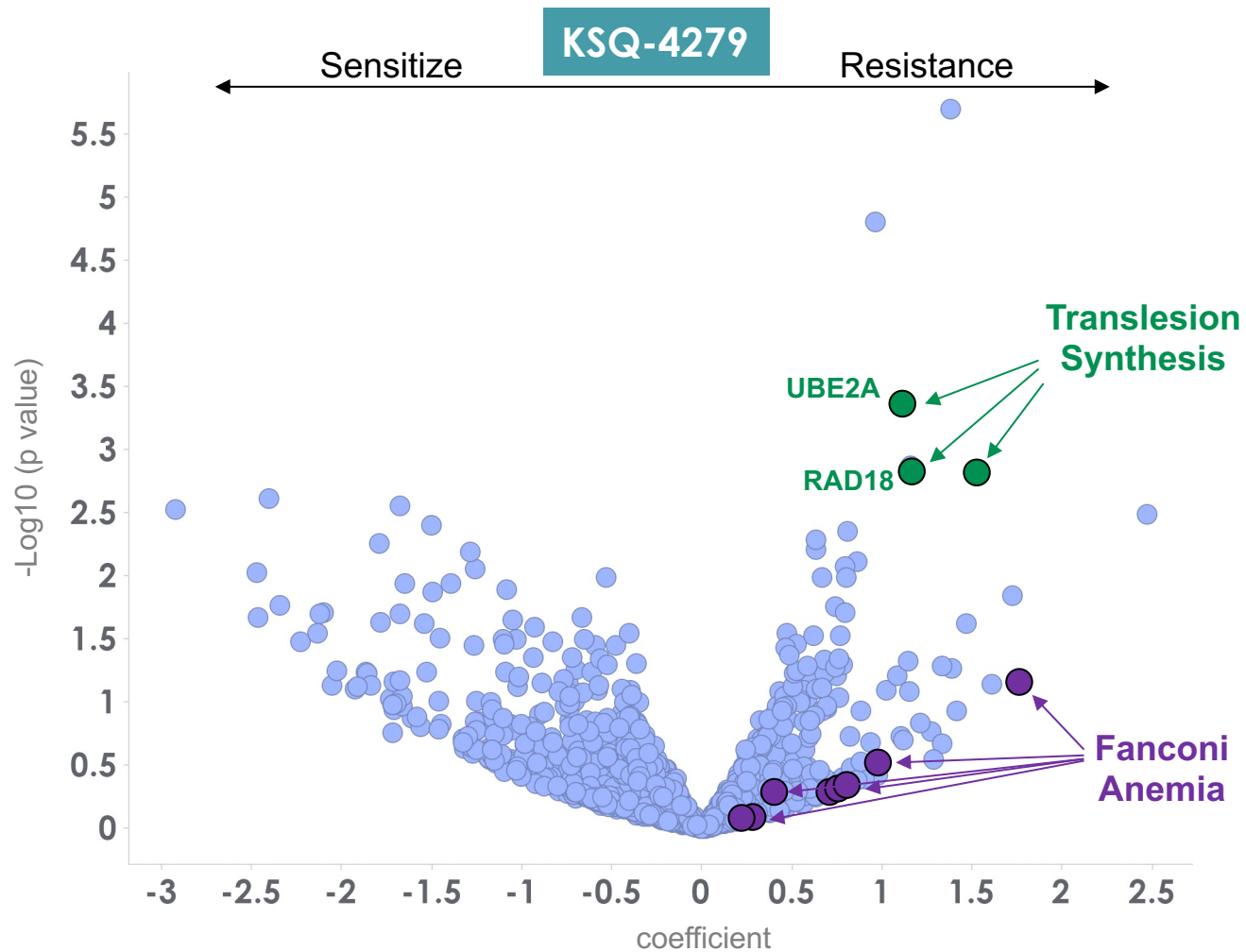


Translesion synthesis

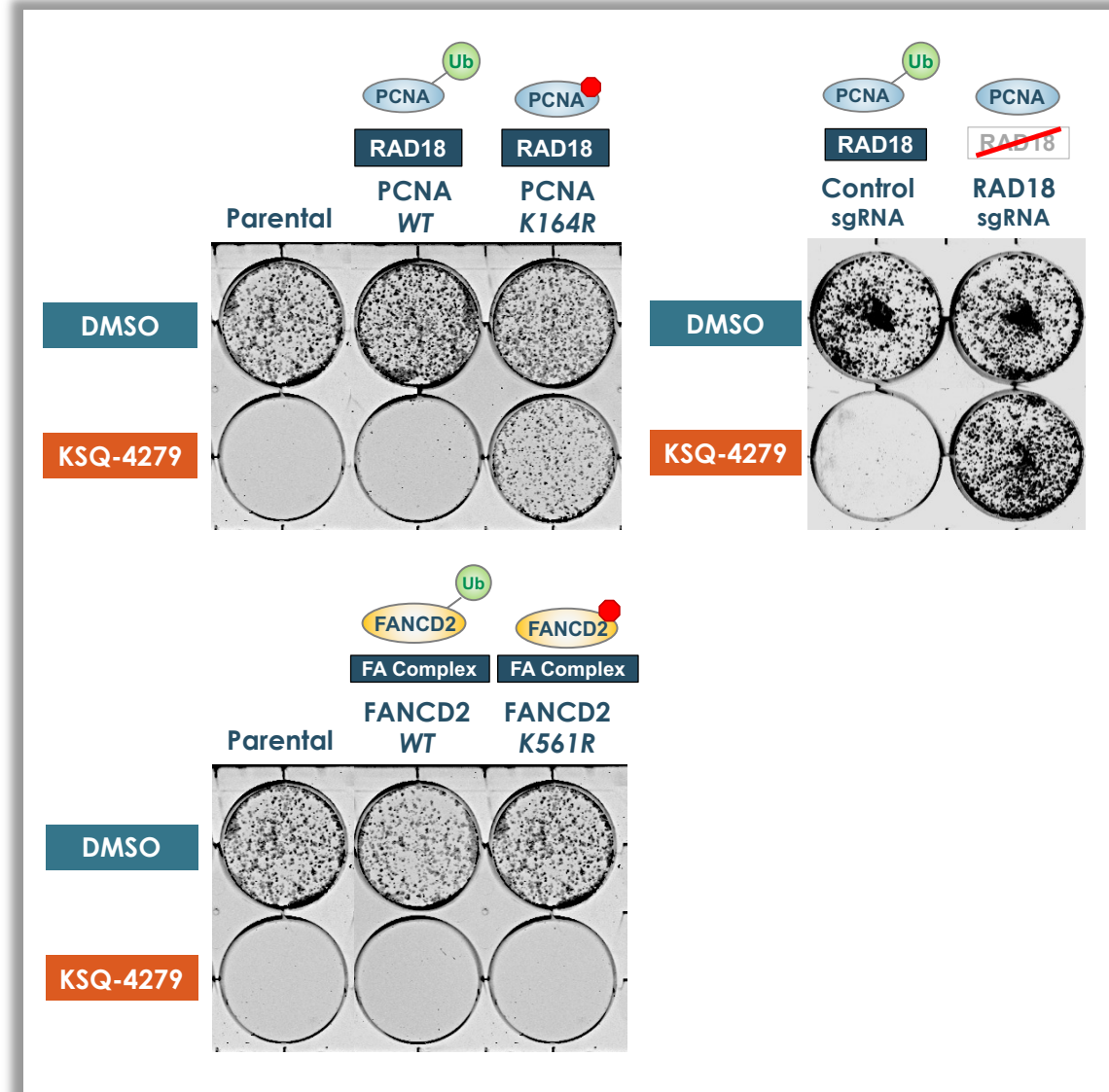
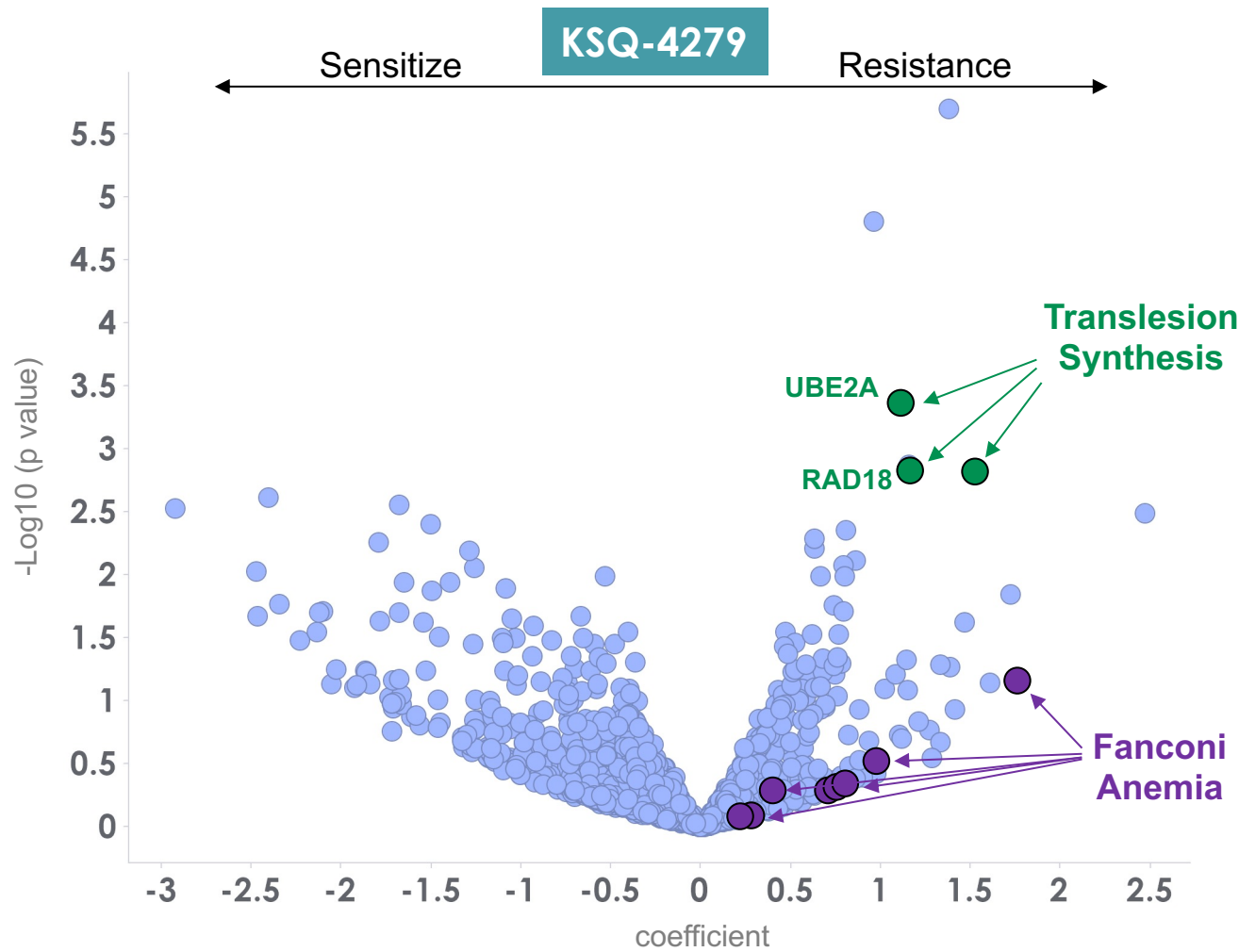


Intra-strand Crosslink Repair

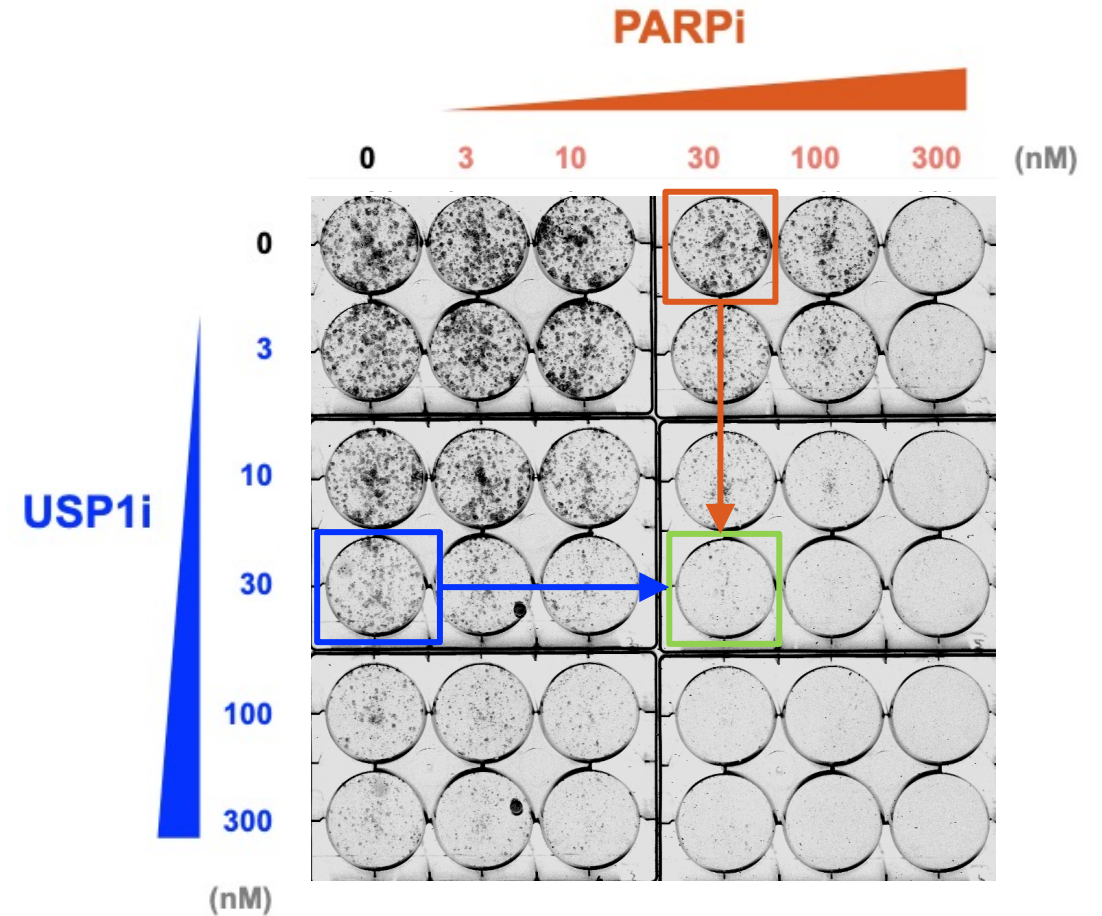
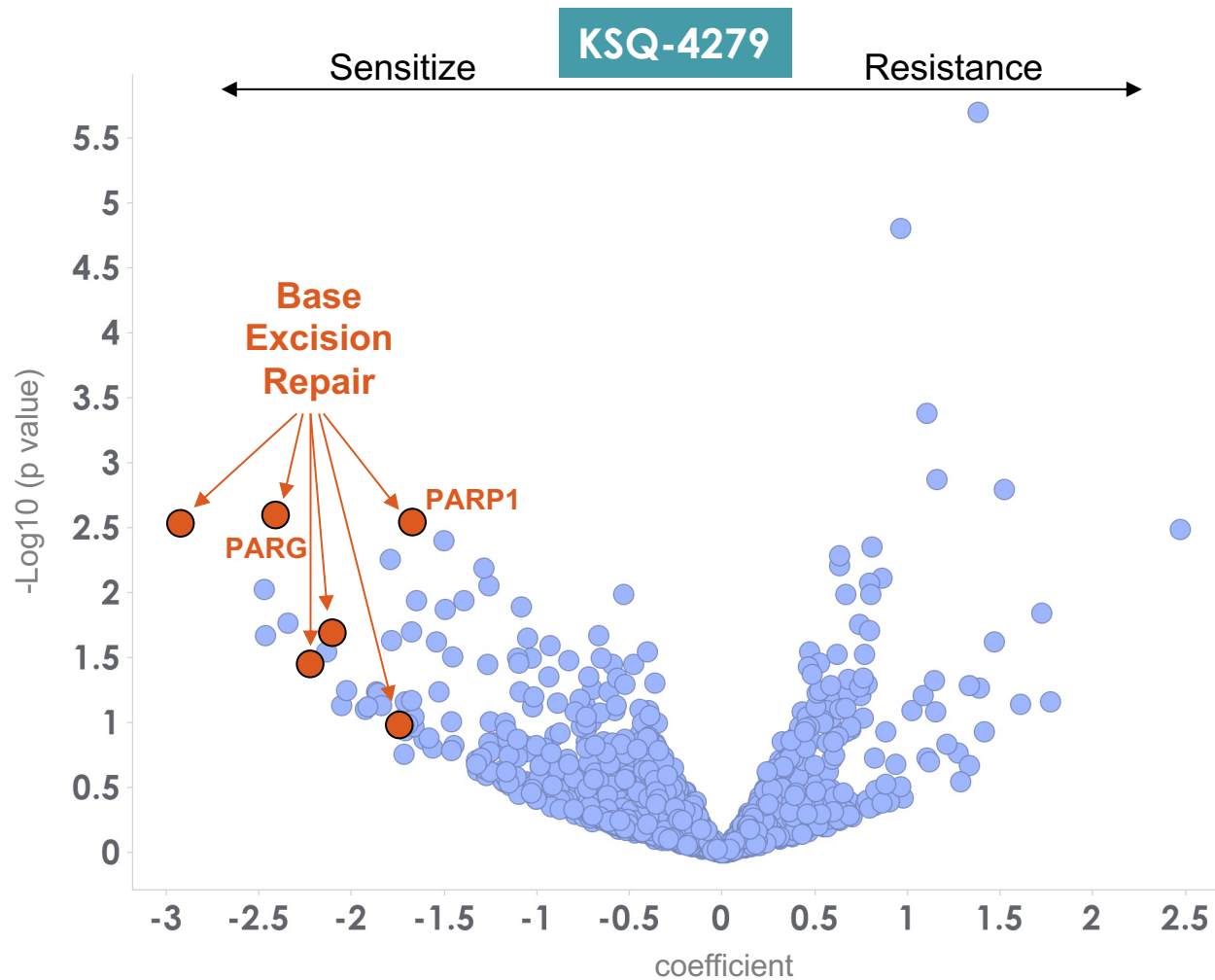
CRISPR screening reveals pathways that influence sensitivity to KSQ-4279



CRISPR screening reveals pathways that influence sensitivity to KSQ-4279

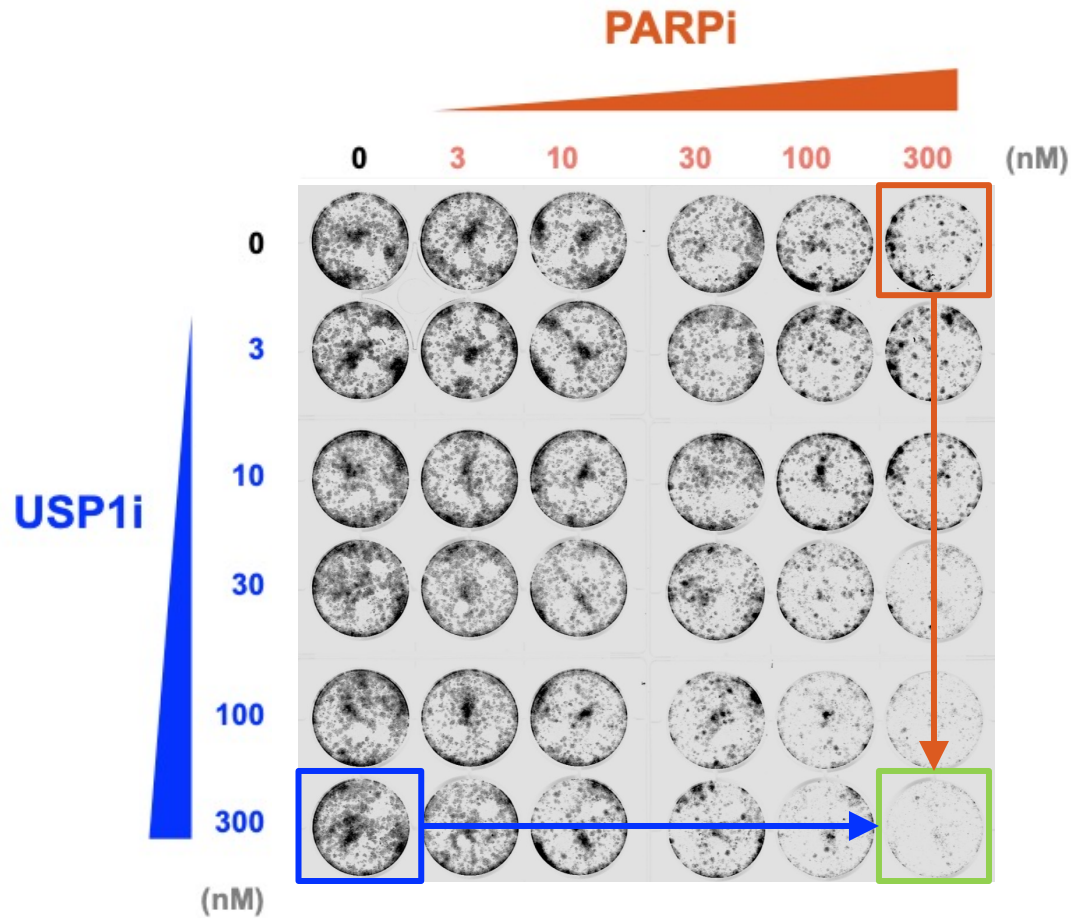


CRISPR screening reveals pathways that influence sensitivity to KSQ-4279

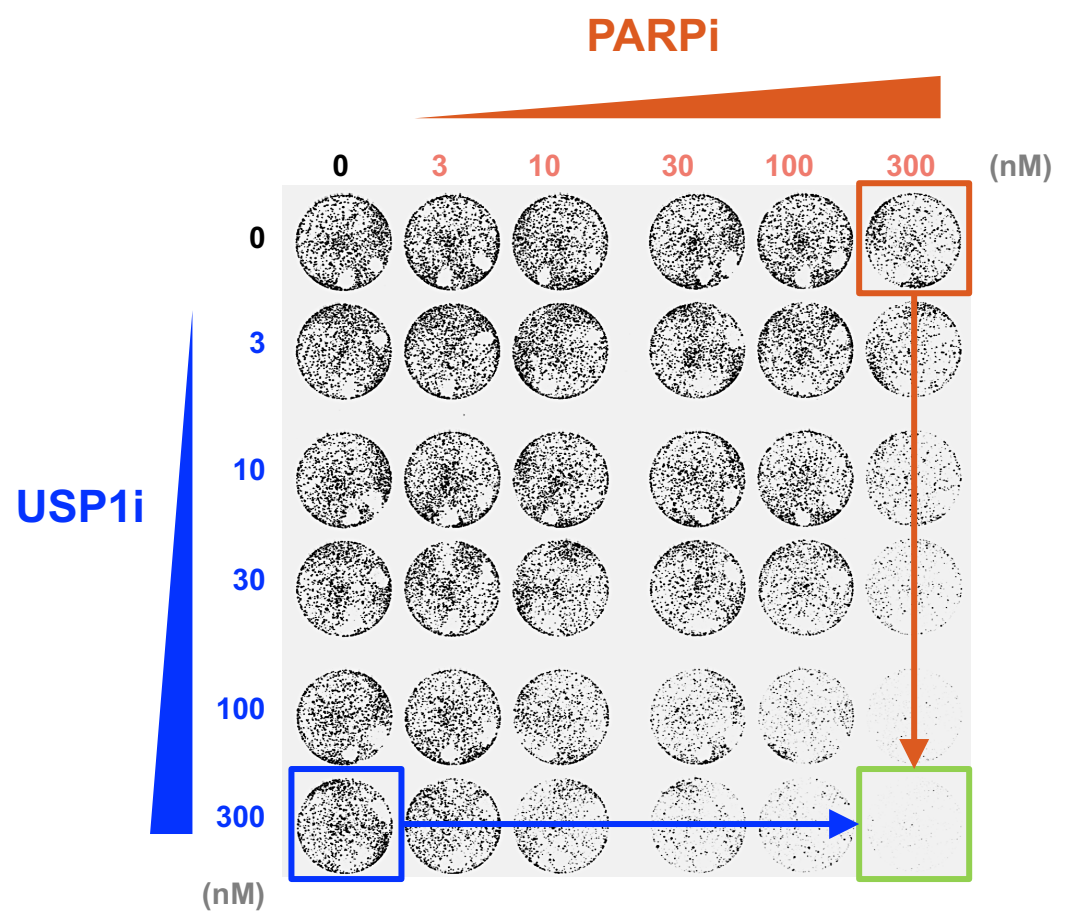


UWB1.289 – TP53^{MUT}, BRCA1^{MUT}
 Ovarian Cancer

USP1i and PARPi have synergistic activity across different lineages

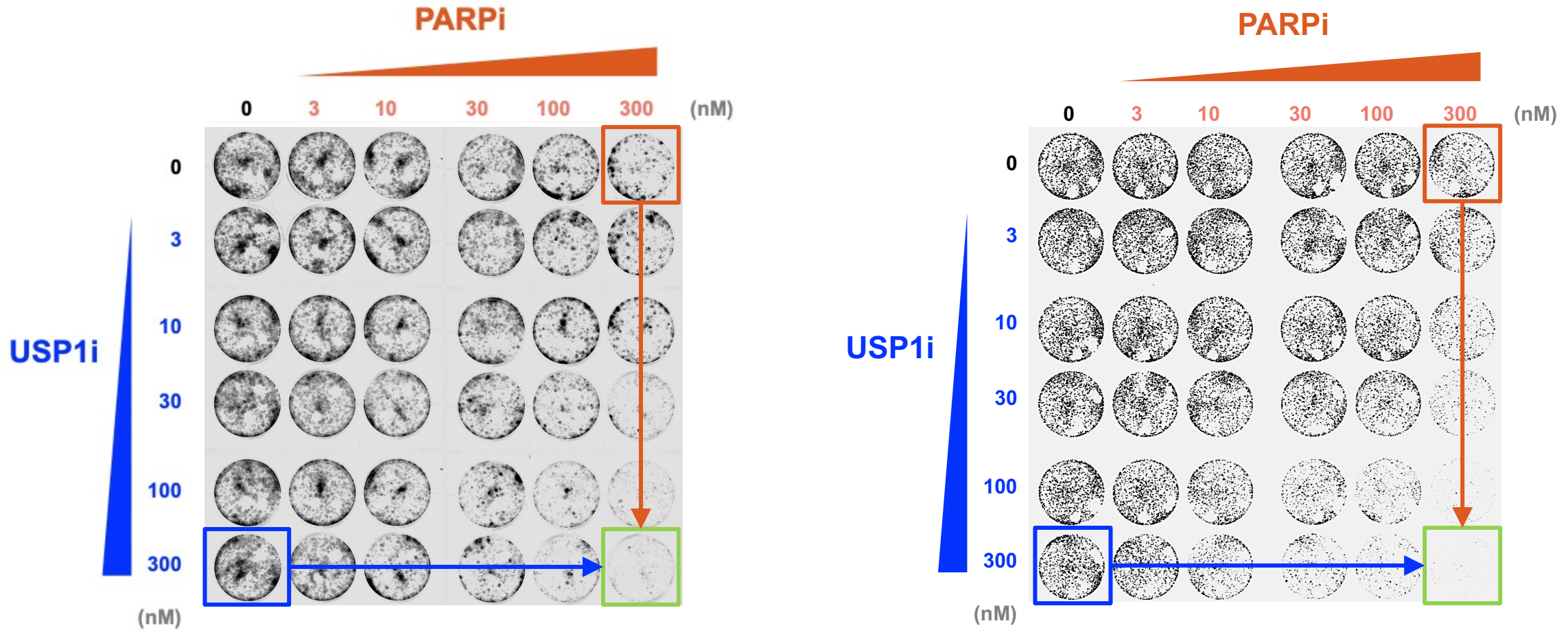


SUM149PT – TP53^{MUT}, BRCA1^{MUT}
Triple-Negative Breast Cancer



NCI-H520 – TP53^{MUT}, ATM^{MUT}
Lung squamous cell carcinoma

USP1i and PARPi have synergistic activity across different lineages

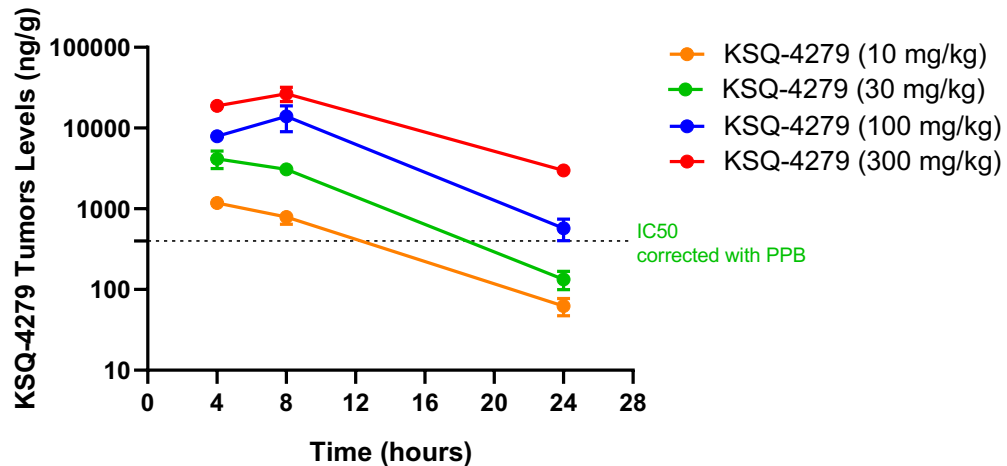


- Of ~160 cell lines evaluated using USP1i + PARPi combination, strong synergy observed in ~10-15% lines

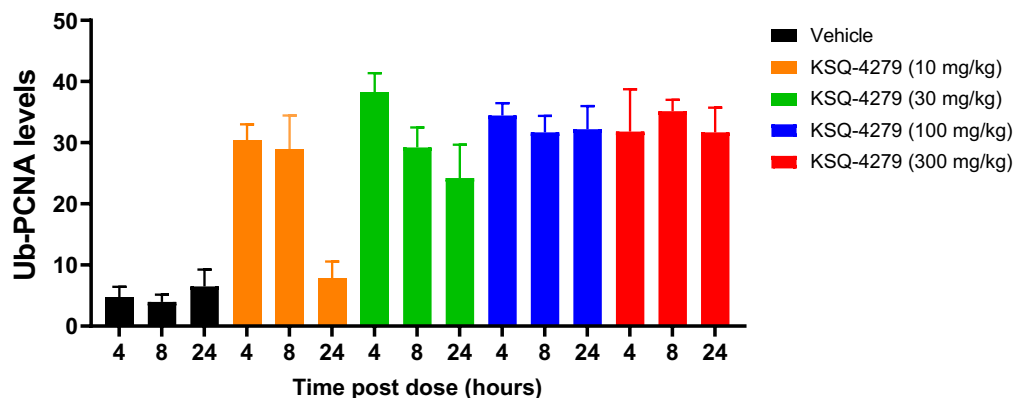
What is the in vivo activity of KSQ-4279 as a single agent and in combination?

KSQ-4279 dose dependent efficacy correlates with induction of Ub-PCNA in Ovarian PDX model

KSQ-4279 Tumor Exposure

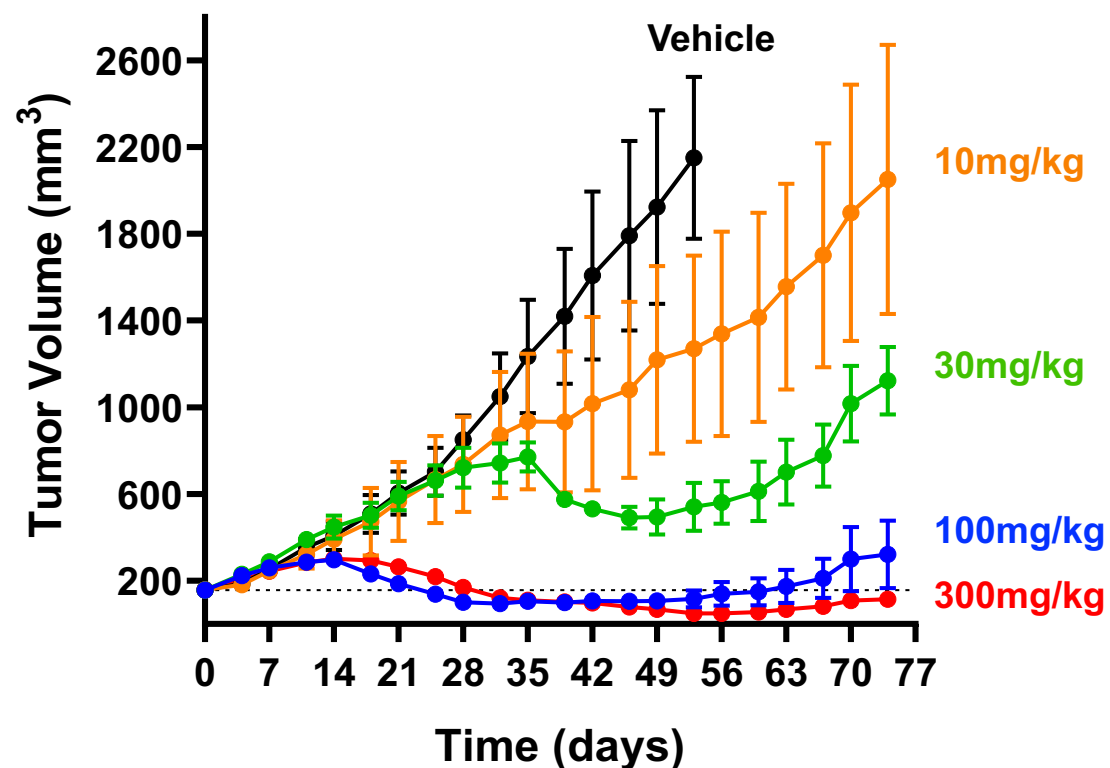


Ub-PCNA levels in Tumor



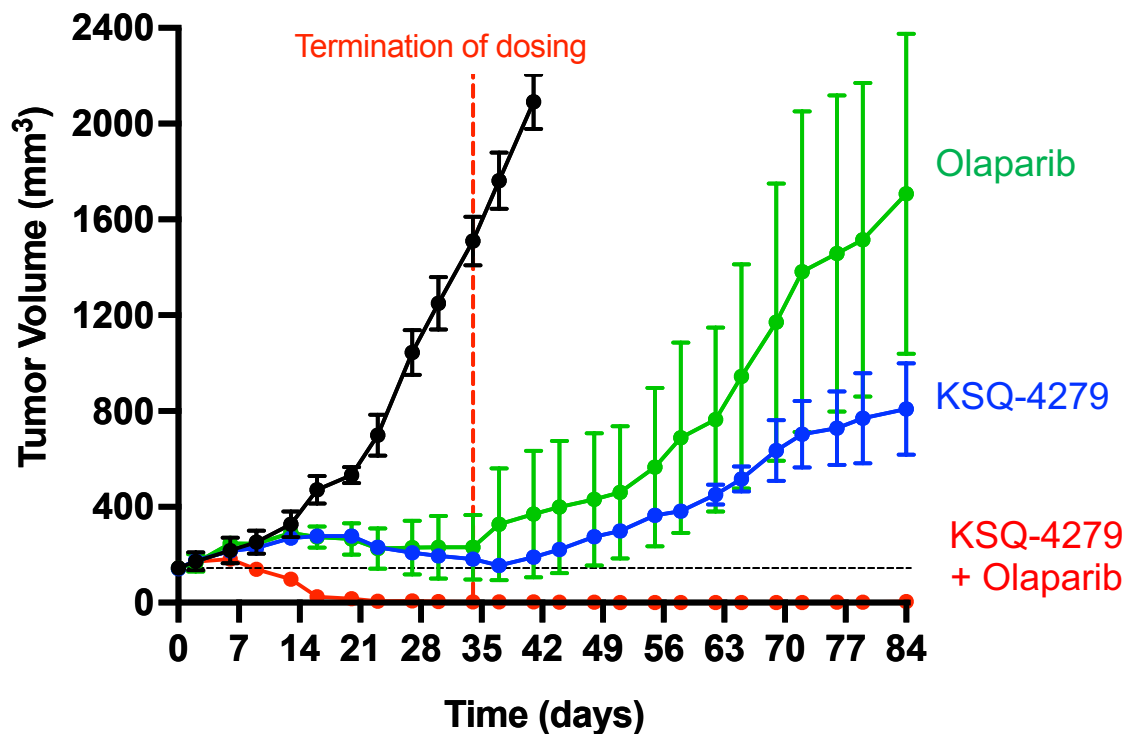
KSQ-4279 PDX Tumor Efficacy

Ovarian PDX *BRCA1^{MT} and p53^{MT}*

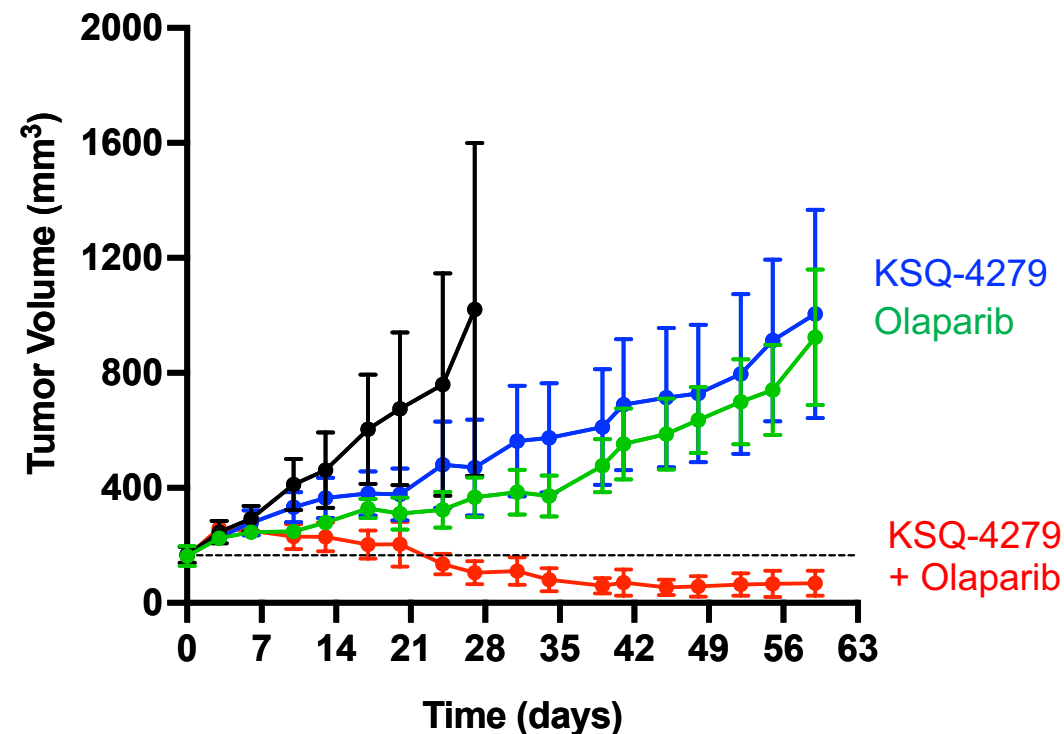


KSQ-4279 in combination with Olaparib leads to durable tumor regression in Ovarian PDX's

Ovarian PDX #1 *BRCA1^{MT}, p53^{MT}*



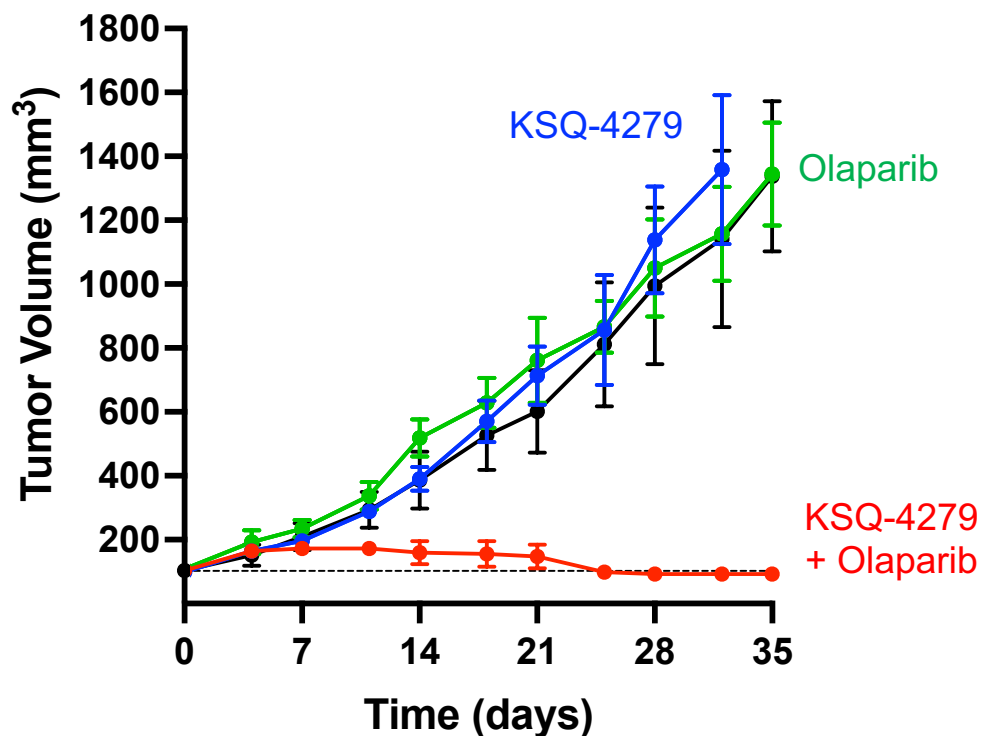
Ovarian PDX #2 *BRCA1^{MT}, p53^{MT}*



KSQ-4279 in combination with Olaparib leads to durable tumor control in Olaparib-resistant TNBC PDX models

TNBC PDX #1

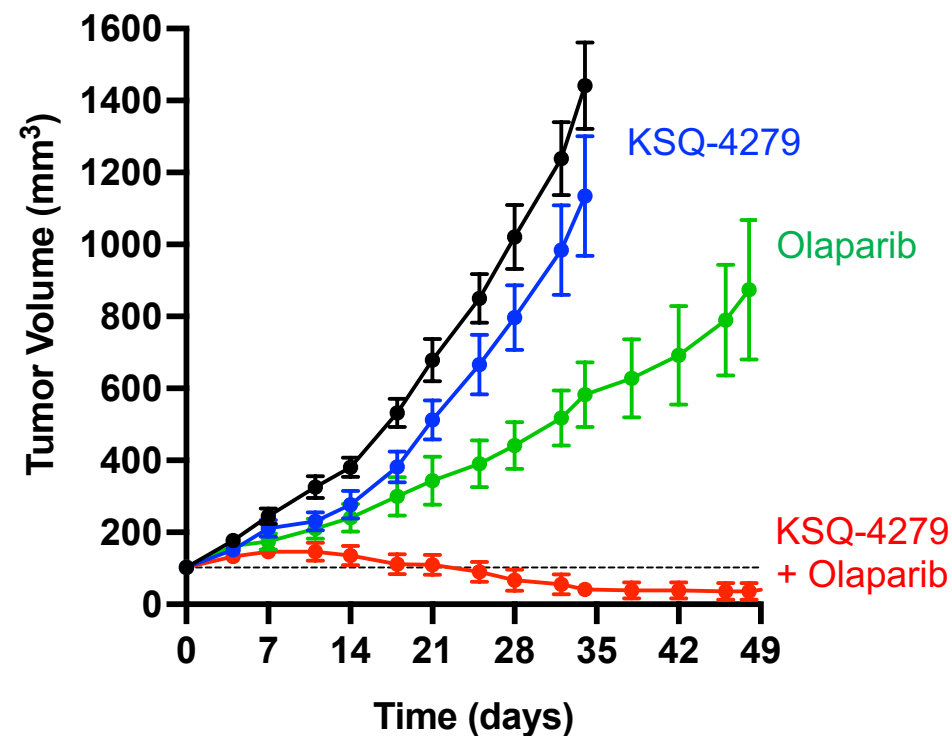
BRCA1^{MT}, p53^{MT}



- Vehicle (qd, po)
- KSQ-4279 (100 mg/kg, qd, po)
- Olaparib (100mg/kg, qd, po)
- KSQ-4279 (100mg/kg) + Olaparib (100mg/kg)

TNBC PDX #2

BRCA1^{MT}, p53^{MT}



- Vehicle (qd, po)
- KSQ-4279 (100mg/kg, qd, po)
- Olaparib (50mg/kg, qd, po)
- KSQ-4279 (100mg/kg) + Olaparib (50mg/kg)

KSQ-4279 – A First-in-Class USP1 Inhibitor for the Treatment of cancers with homologous recombination deficiency



- **KSQ CRISPRomics[®] platform identified USP1 as an attractive cancer target**
 - USP1 regulates DNA damage repair pathways distinct from PARP inhibitors
- **KSQ-4279 is a potent, selective, allosteric inhibitor of USP1**
- **Efficacy observed both as a single agent and in combination with PARPi across multiple BRCA/HRD xenograft models**
- **CRISPRomics[®] resistance screens indicate that KSQ-4279 has a complimentary resistance profile to PARP inhibitors**
- **KSQ-4279 Phase I trial ongoing**

Acknowledgements

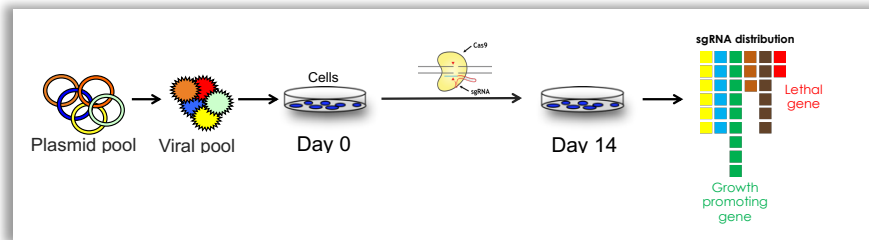


Are Distinct Resistance Profiles Associated With USP1 vs PARP Inhibitors?

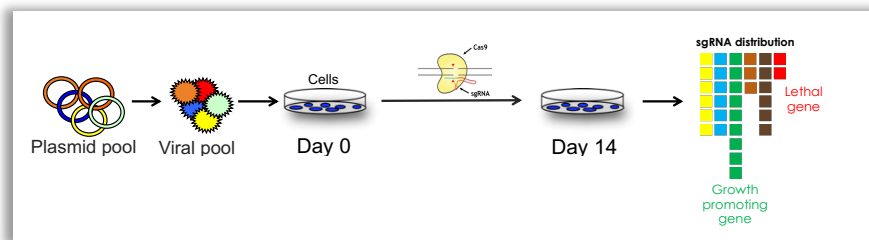
CRISPR screens used to investigate primary mechanisms of resistance to USP1i and PARPi

Treatment

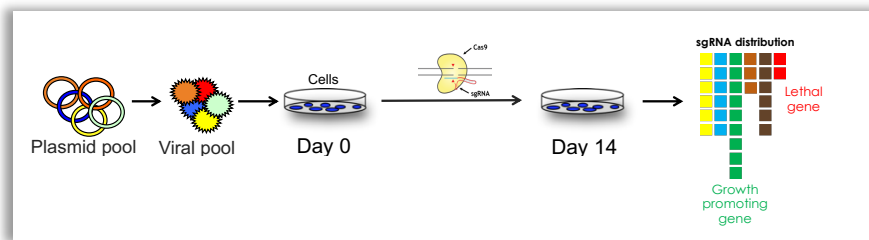
DMSO



USP1i



PARPi



CRISPRomics plot for Gene X

Guide enrichment

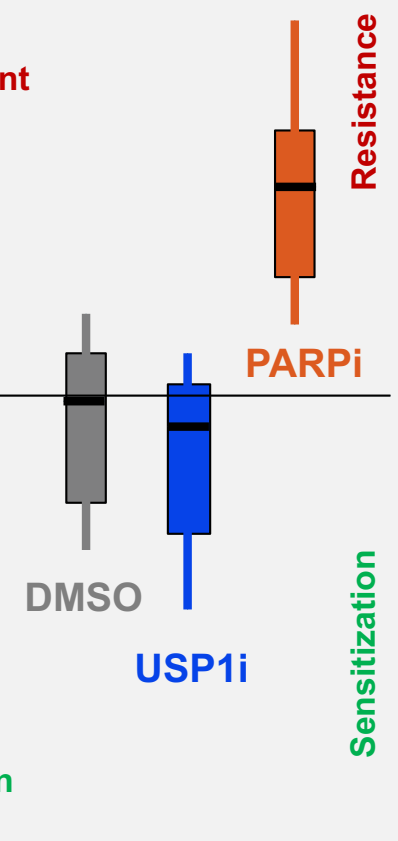


Z-score

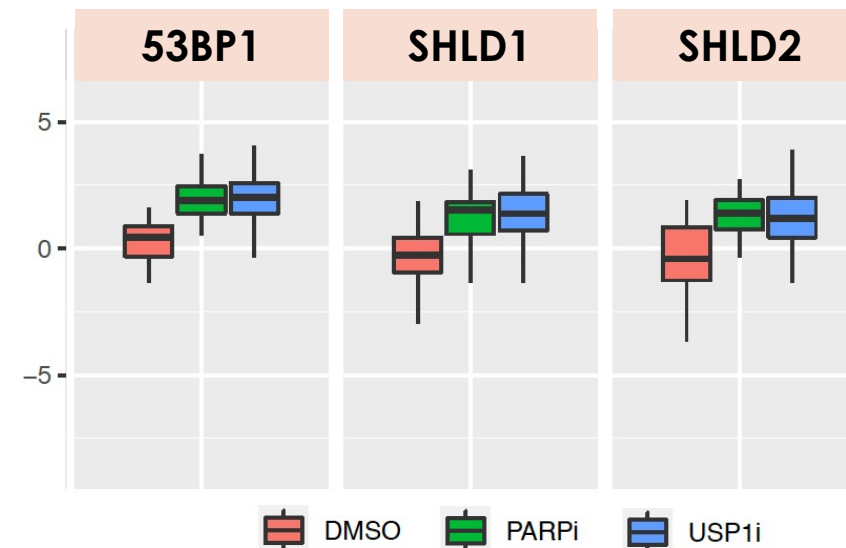
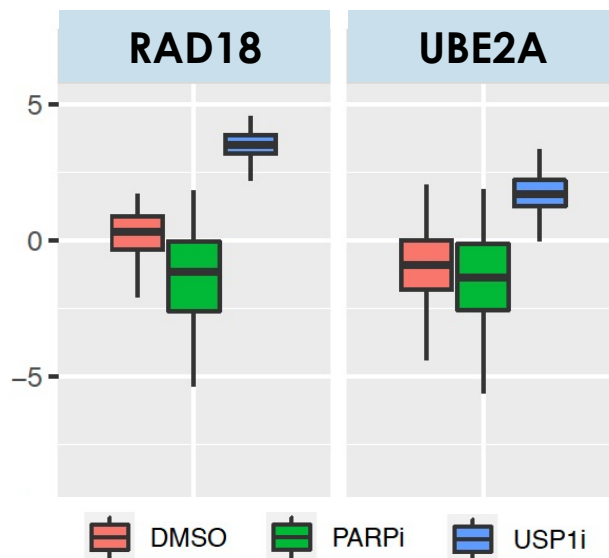
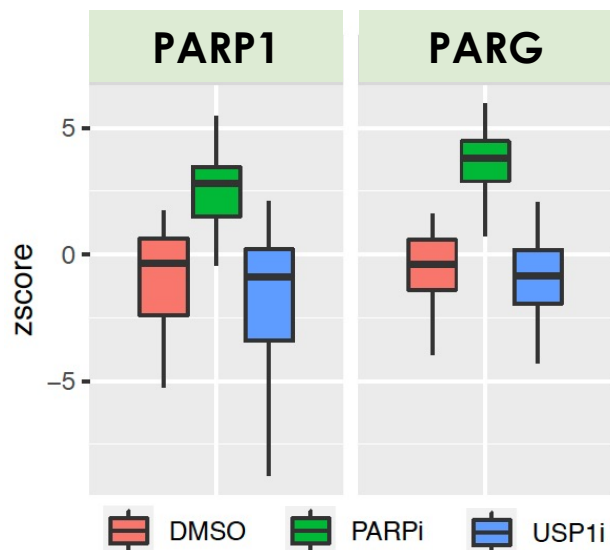
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Guide depletion



CRISPR screening highlights different mechanisms of resistance to USP1i and PARPi

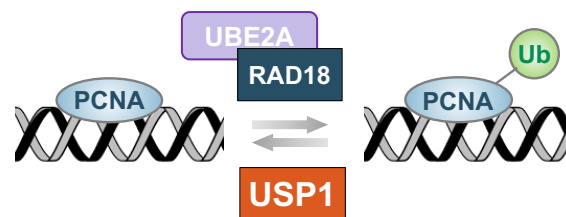


Selective Loss of PARG Restores PARYlation and Counteracts PARP Inhibitor-Mediated Synthetic Lethality

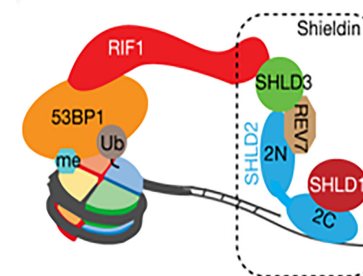
Genome-wide and high-density CRISPR-Cas9 screens identify point mutations in *PARP1* causing PARP inhibitor resistance

Ewa Gogola,¹ Roel de Bruijn, Bram van den Donk, J. Ogi, Miguel Andujar, and Sven Rott

Stephen J. Pettitt^{1,2}, Dragomir B. Krastev^{1,2}, Inger Brandsma^{1,2}, Amy Dréan^{1,2}, Feifei Song^{1,2}, Radoslav Aleksandrov³, Maria I. Harrell⁴, Malini Menon^{1,2}, Rachel Brough^{1,2}, James Campbell^{1,2}, Jessica Frankum^{1,2}, Michael Ranes⁵, Helen N. Pemberton^{1,2}, Rumana Rafiq^{1,2}, Kerry Fenwick⁶, Amanda Swain⁶, Sebastian Guettler⁵, Jung-Min Lee⁷, Elizabeth M. Swisher⁸, Stoyno Stoyanov³, Kosuke Yusa⁸, Alan Ashworth⁹ & Christopher J. Lord^{1,2}



Translesion synthesis



Non-Homology End Joining (NHEJ)