SAT-122, a potential first-in-class, potent, small-molecule disruptor of RAD51-BRCA2, attenuates RAD51 foci formation and tumor progression in preclinical models

FPN: 35P

Background

The DNA damage repair pathway plays a crucial role in signalling for effective DNA repair and cell cycle progression. DNA double-strand breaks (DSBs) are primarily repaired by homologous recombination. Acting downstream of ATR, ATM and PARP, RAD51 is a central recombinase in HR-mediated DDR pathway that participates in DSB repair via interaction with BRCA2, followed by its nuclear translocation. RAD51:BRCA2 interaction disruptors are first-in-class anticancer agents with therapeutic potential in refractory solid tumors. The sensitivity to RAD51:BRCA2 disruption is high in cells with high Replication Stress, such as oncogene driven tumours, thereby making it selective for cancer cells while sparing healthy cells. Since the mechanism of is distinct from PARP inhibition, SAT-122 action continues to be active in a PARPi resistant setting. SAT-122 has been identified as a candidate for IND enabling studies.

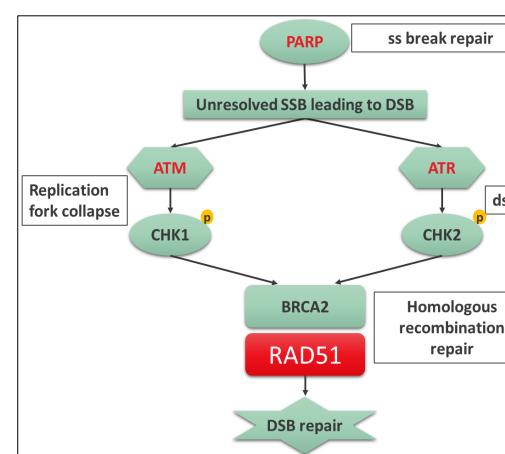
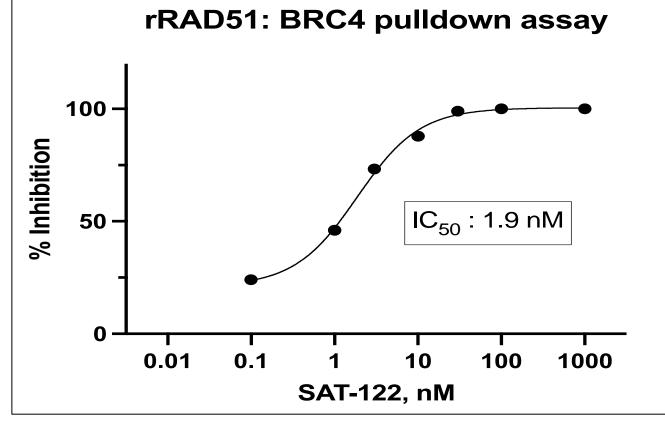
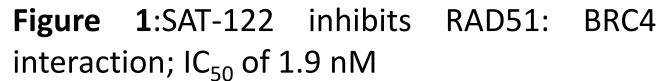


Figure 1. Signalling of Homologous recombination (HR) pathway and RAD51 is a central recombinase in HR pathway

SAT-122 binds to RAD51 and inhibits RAD51:BRCA2 interaction

Biochemical assay was developed using recombinant human RAD51 and biotin labelled BRC4 (domain of BRCA2 having highest affinity for RAD51). Compounds were tested for inhibition of RAD51:BRCA2 interaction





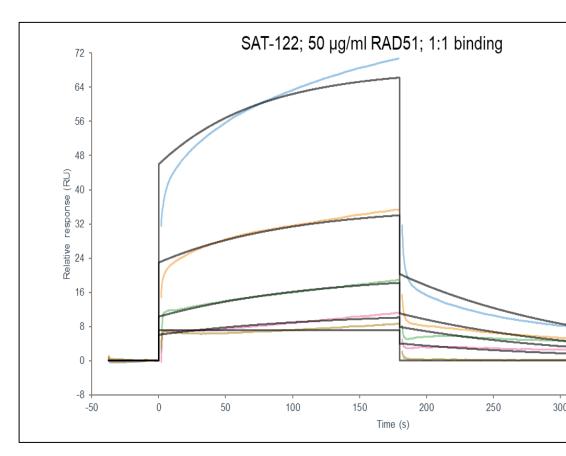
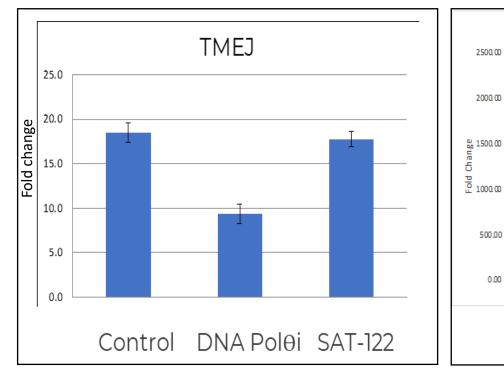


Figure 2: Binding of SAT-122 to RAD51 was measured using Surface Plasmon Resonance

Specificity within DDR pathways and Selectivity over kinases



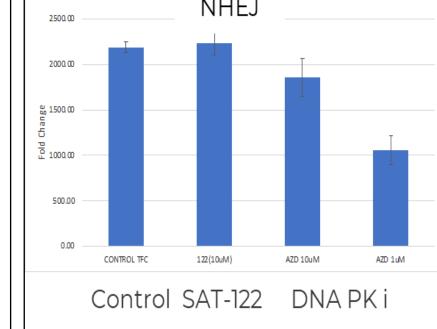


Figure 3: SAT-122 does not inhibit TMEJ and NHEJ pathways and is specific to the RAD51 pathway

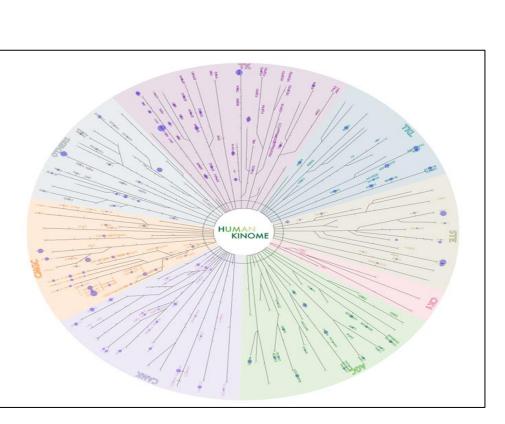
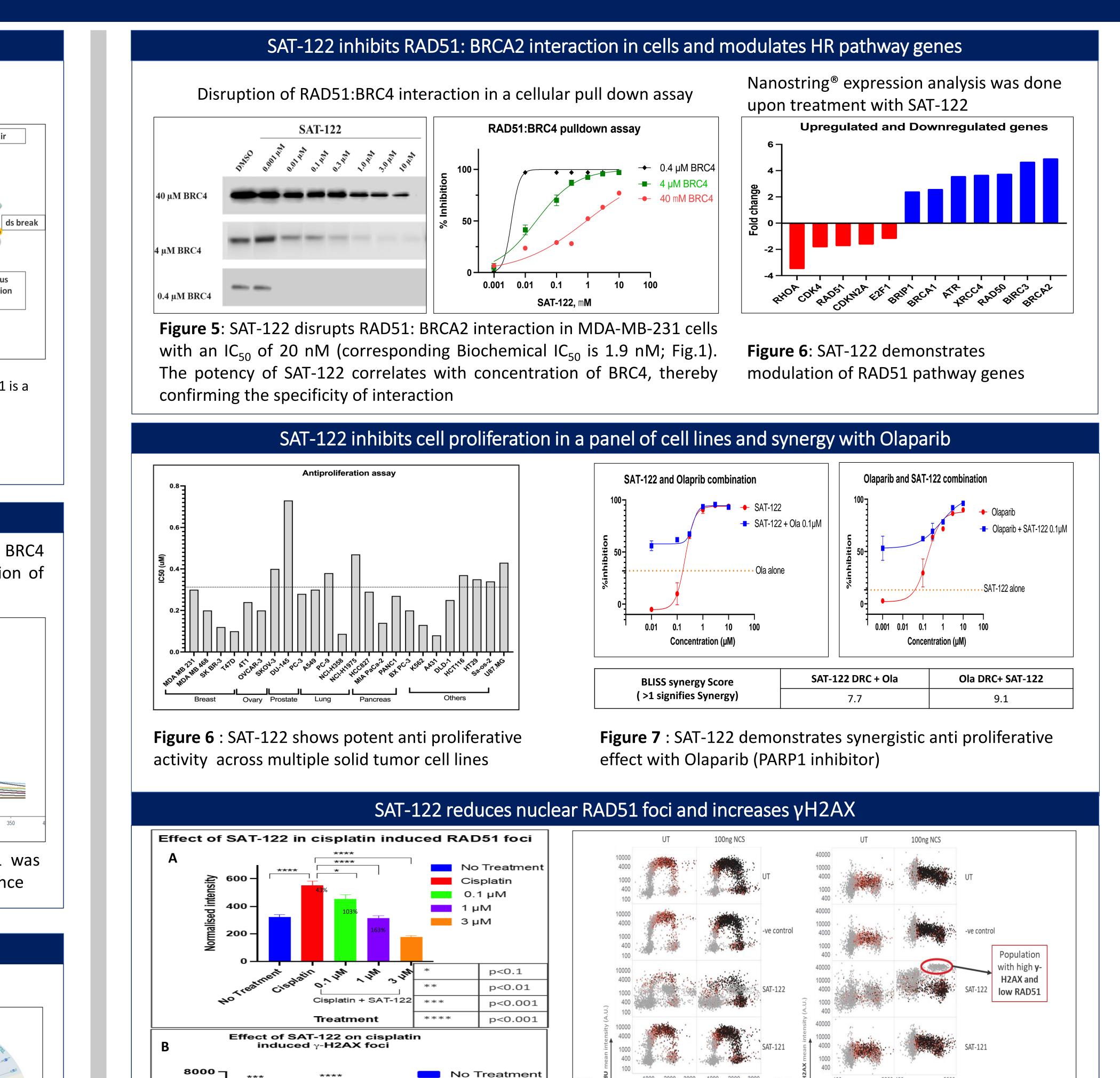
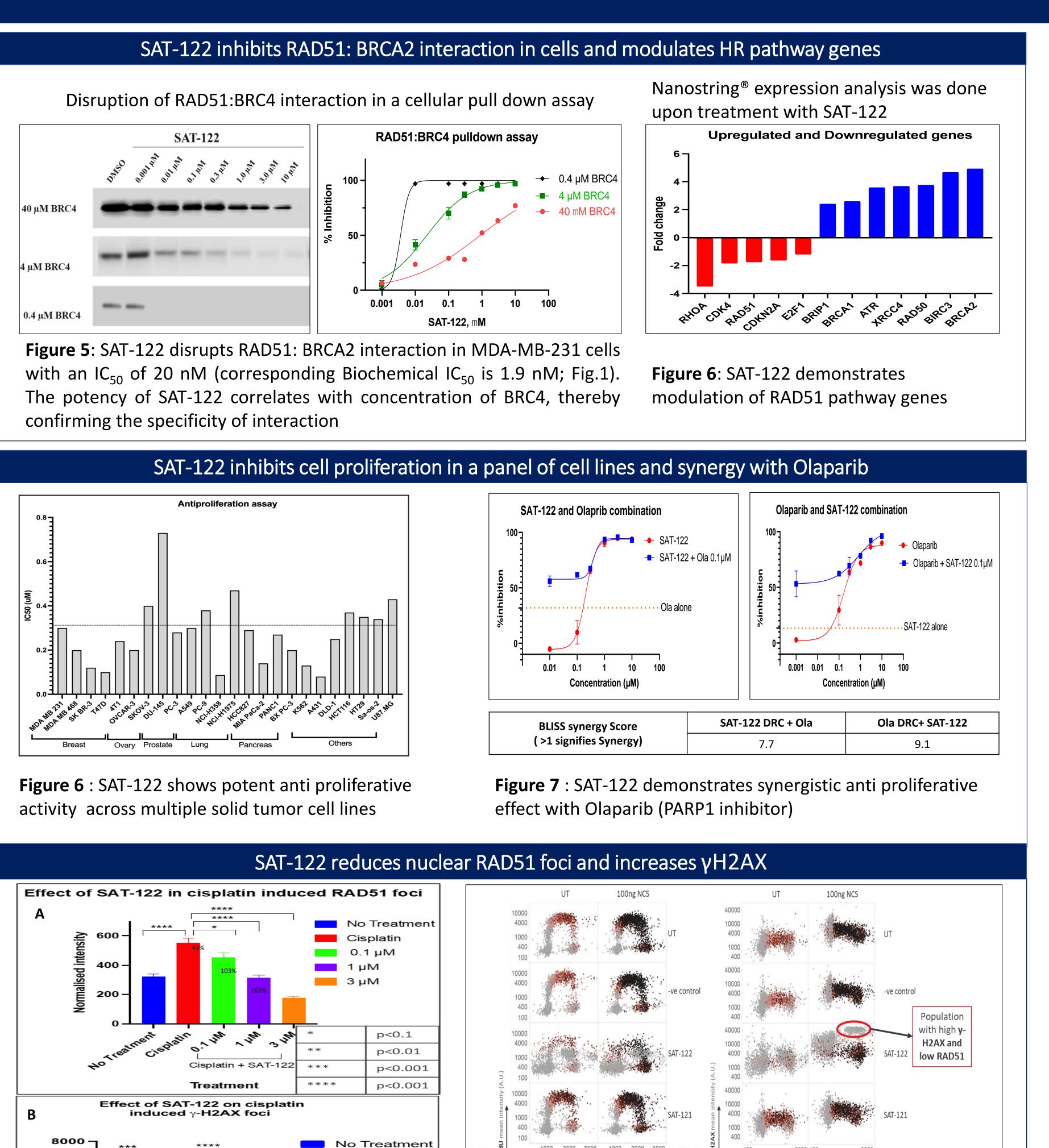
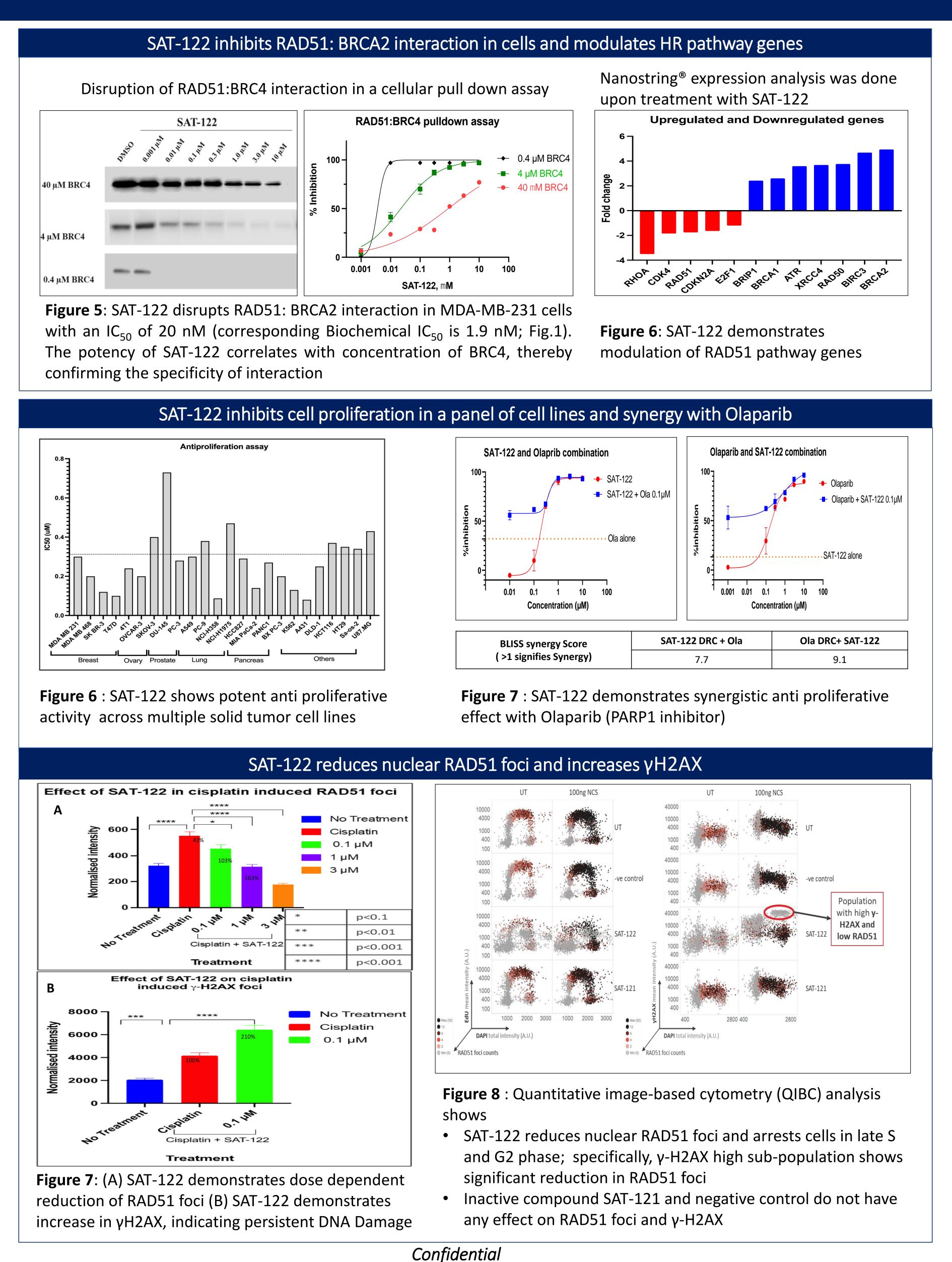


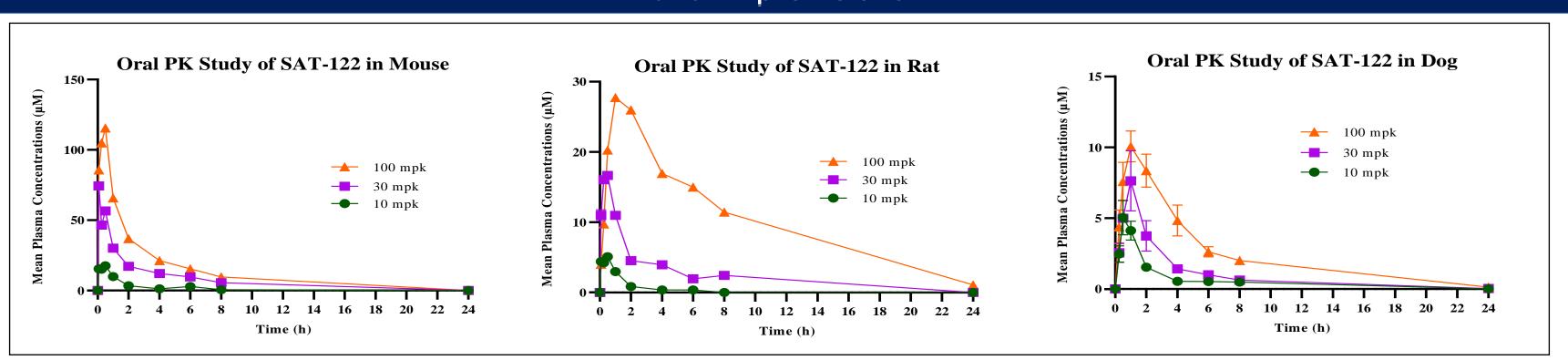
Figure 4 : SAT-122 does not have any activity at 1μ M against a 345 kinase panel (Reaction biology)

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SAT-122 shows desirable ADME properties (good solubility across pH, metabolically stable across species, no inhibition observed with 7 CYP isoforms) with no hERG liability. SAT-122 is dose proportional with exposures well above IC_{90} concentrations.

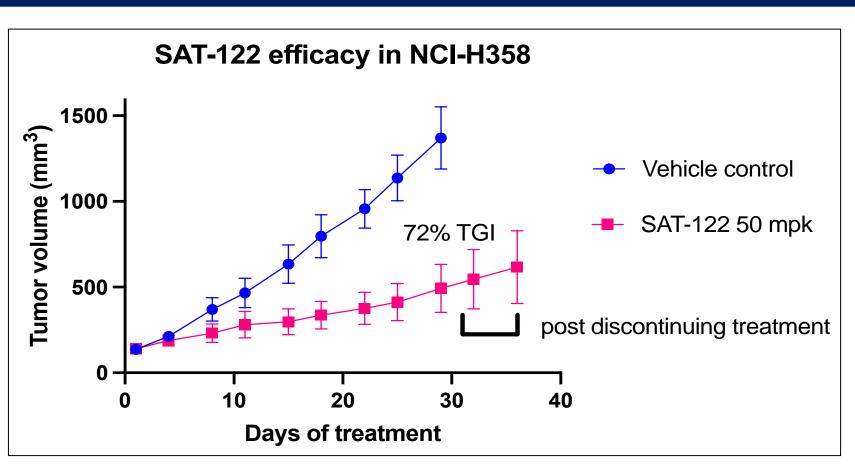
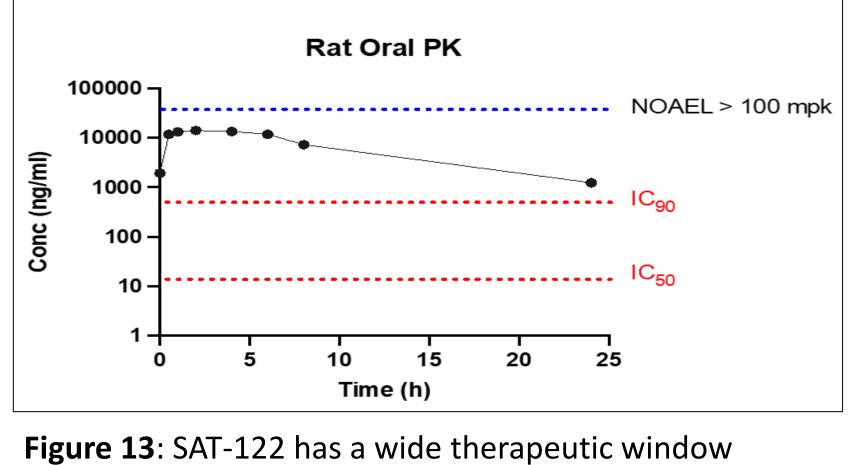


Figure 10: SAT-122 demonstrated 72% TGI in Nci-H358 xenograft model



- potentially sparing non-targeted cells
- genes, in line with the mechanism of action





ADME and PK profile of SAT-122

Figure 9: SAT-122 PK profile across species

Efficacy and tolerability of SAT-122

SAT-122 efficacy MDA-MB-231 Vehicle control َ 1000 ع ---- SAT-122 25 mpk 53% TGI <u>§</u> 500 · 20 Days of treatment



- SAT-122 demonstrated efficacy in multiple xenograft models. Single agent efficacy is superior to other reported DDR pathway inhibitors.
- 14-day repeat dose toxicity study in rats showed no clinical signs or significant body weight changes and no change in clinical parameters in both the genders
- SAT-122 has a wide therapeutic window (NOAEL $>100 mpk and LD_{50} > 1000 mpk$

Summary

SAT-122 is a first in class, potent inhibitor of RAD51: BRCA2 interaction with an IC₅₀ of 1.9 nM

SAT-122 demonstrates potent anti proliferative activity across panel of cell lines

Direct PD demonstrated by a reduction of nuclear RAD51 foci; additionally, single cell analysis by QIBC shows cells with persistent DNA damage have minimal nuclear RAD51 foci.

SAT-122 has desirable ADME properties and dose proportional PK across species

SAT-122 inhibits only the RAD51 mediated HR pathway (and not the other DDR pathways i.e. NHEJ and TMEJ) –

NanoString gene expression profile upon treatment with SAT-122 shows significant modulation of RAD51 pathway

SAT-122 demonstrates efficacy in multiple xenograft models with no effect on body weight/clinical signs

14-day toxicity studies show no adverse events and no drug accumulation

Synergy with Olaparib, and retention of activity in Olaparib resistant cells opens a clinical path in HRD cancers

SAT-122 can be a treatment option for patients bearing RAS/EGFR mutant tumors characterized by high replication

stress, both as a single agent and in combinations with SOC.