Cancer-specific AI identifies multi-modal biomarkers of therapeutic response for 1,951 drugs including TNG348, a highly selective USP1 inhibitor.

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Abstract #

Summary

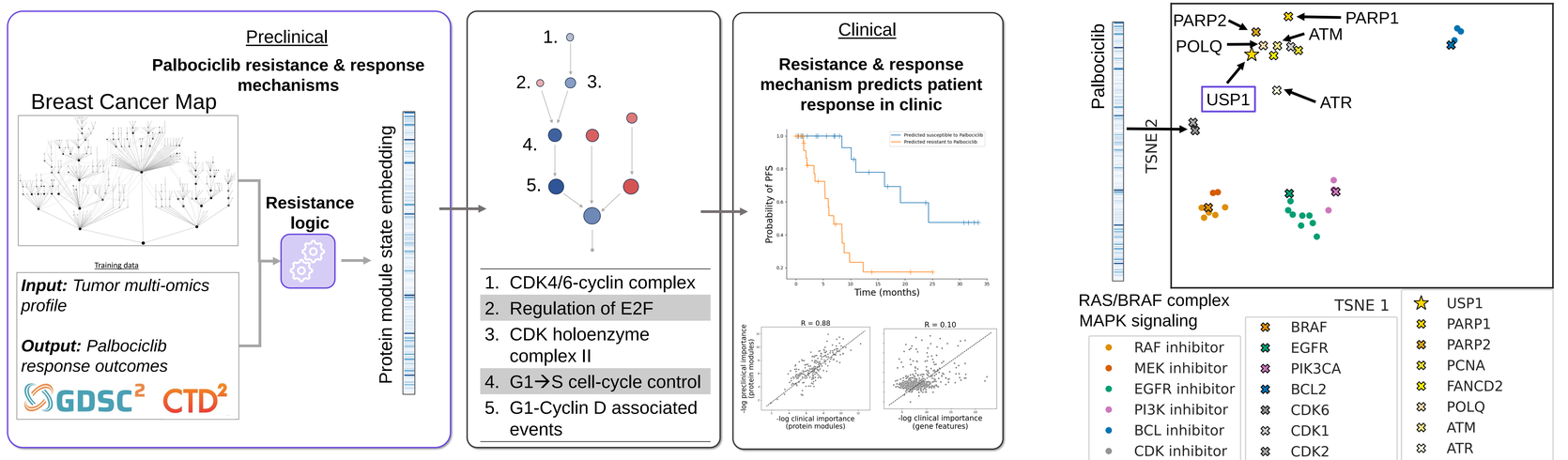
Background: Comprehensively **u**nderstanding a drug's mechanisms of response is critical to identify biomarkers predictive of efficacy, prevent resistance, and design rational combinations.

Methods: Serinus Bio has developed an AI platform that systematically learns mechanisms of response & resistance for a drug of interest by leveraging disease-specific maps of cellular architecture.

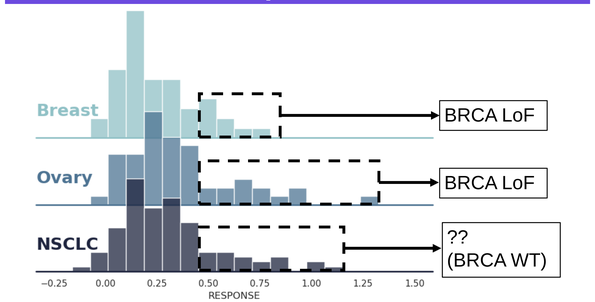
Results: Learned mechanisms for ~20K drugs & targets capture key functional relationships. Applying the platform to TNG348, a highly selective USP1 inhibitor, we identified & validated cellular mechanisms explaining >50% of variation in drug response across lung cancer cell lines & PDX models. Response mapping enabled the development of a predictive biomarker logic and potential rational combinations.

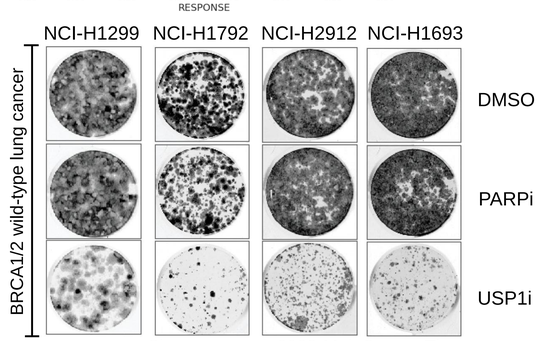
Conclusions: The Serinus Bio platform is an integrated computational-experimental approach to map drug response mechanisms & design strategies to maximize therapeutic potential.

The Serinus Bio Platform learns clinically relevant response & resistance mechanisms across drugs & targets



NSCLC cell lines are selectively dependent on USP1 without a predictive biomarker





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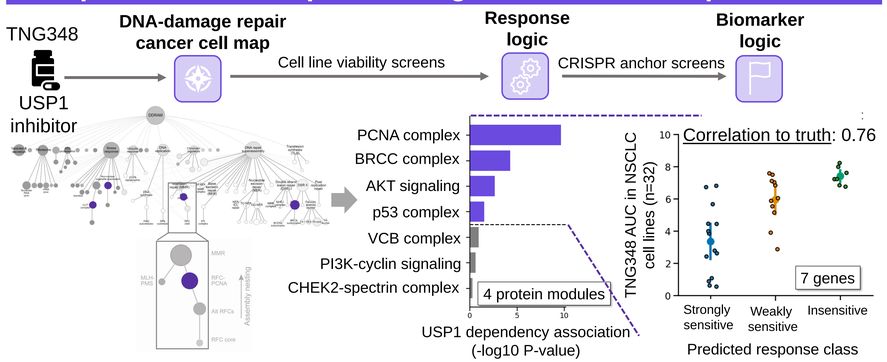
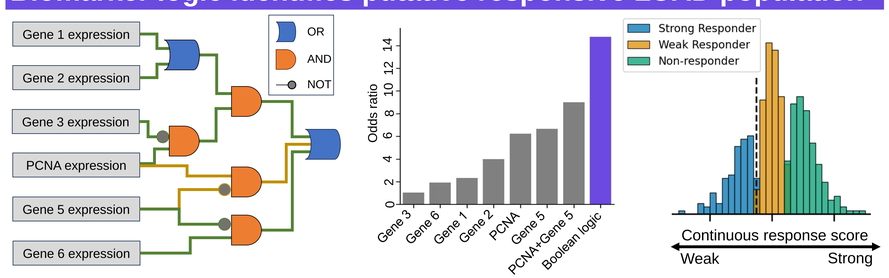
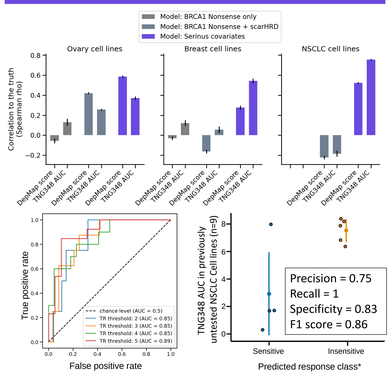
DDR protein modules predict lung cancer USP1i response



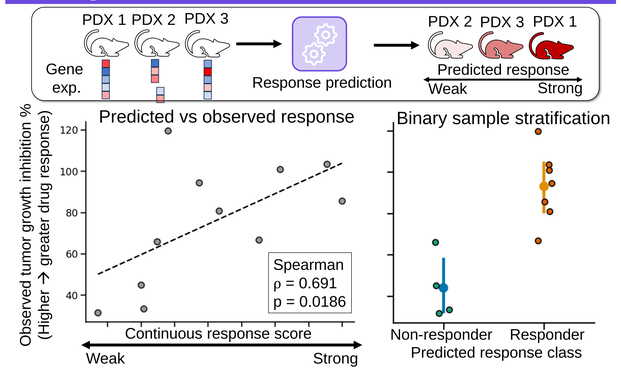
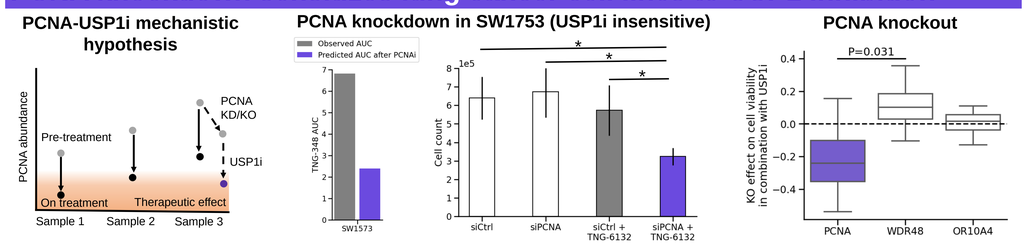
Biomarker logic identifies putative responsive LUAD population



Biomarkers generalize to untested cell lines



Biomarker model predicts USP1i response in lung cancer PDX models



PCNA knockdown sensitizes lung cancer cell lines to USP1 inhibition