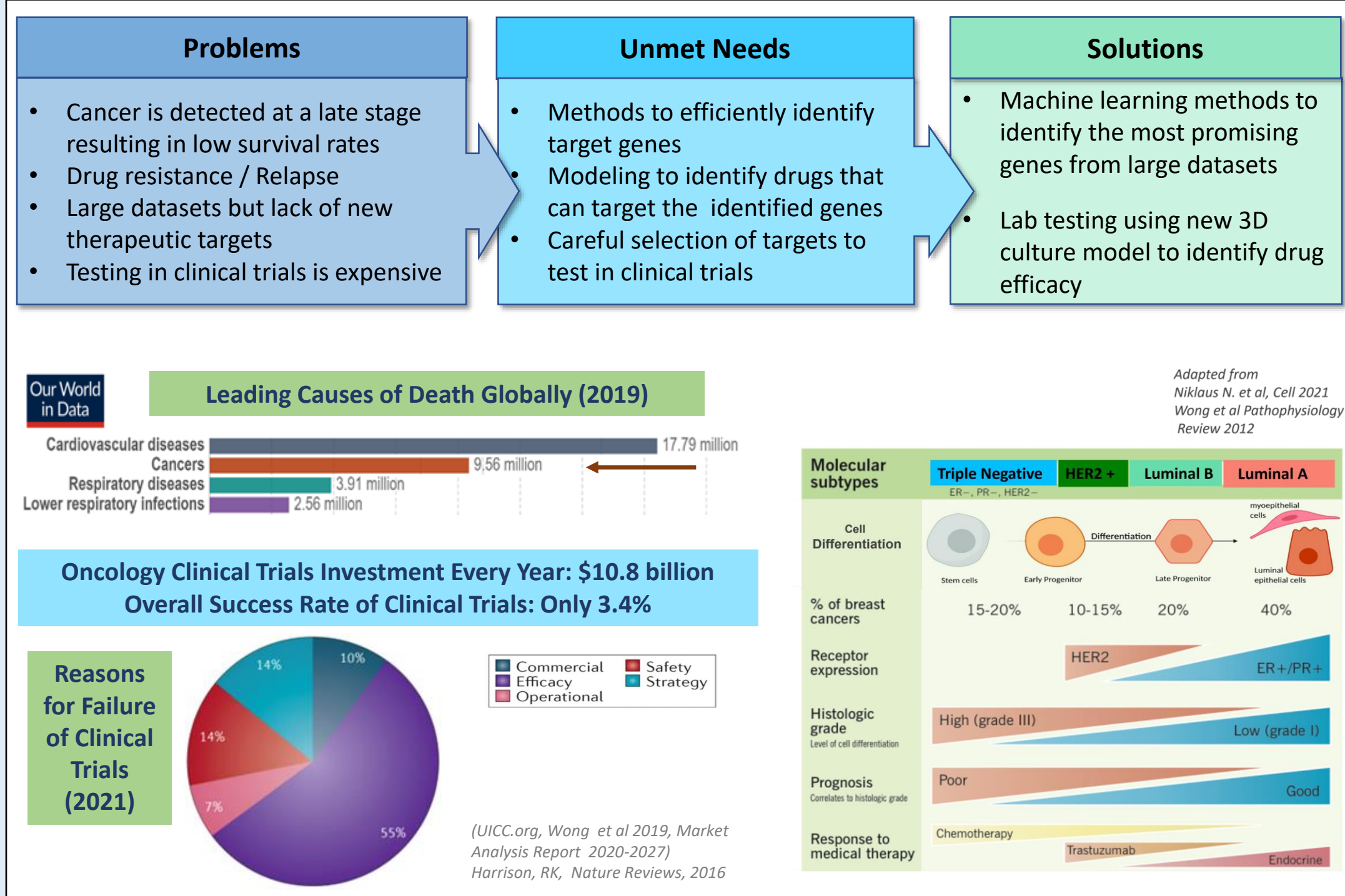
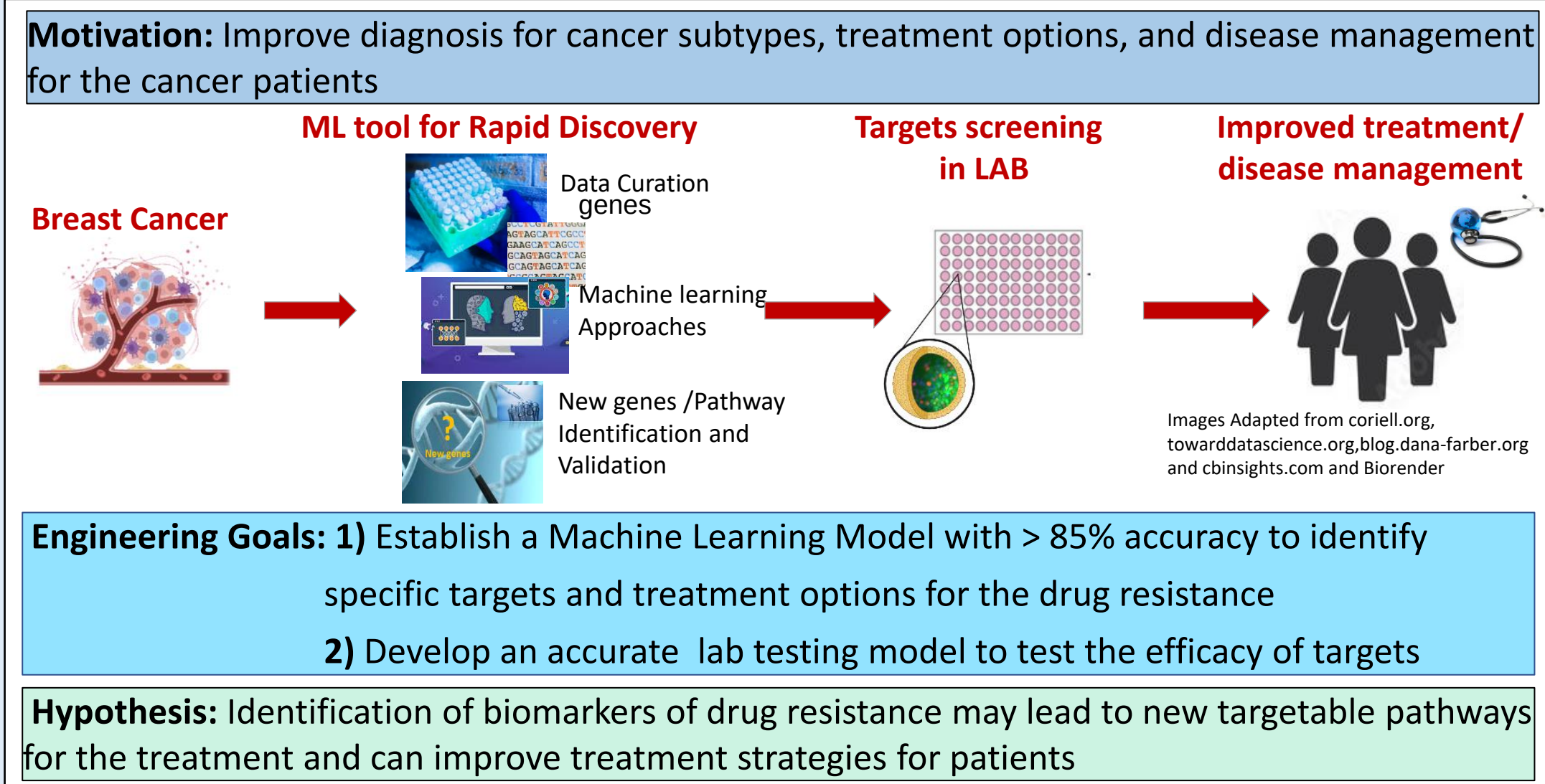


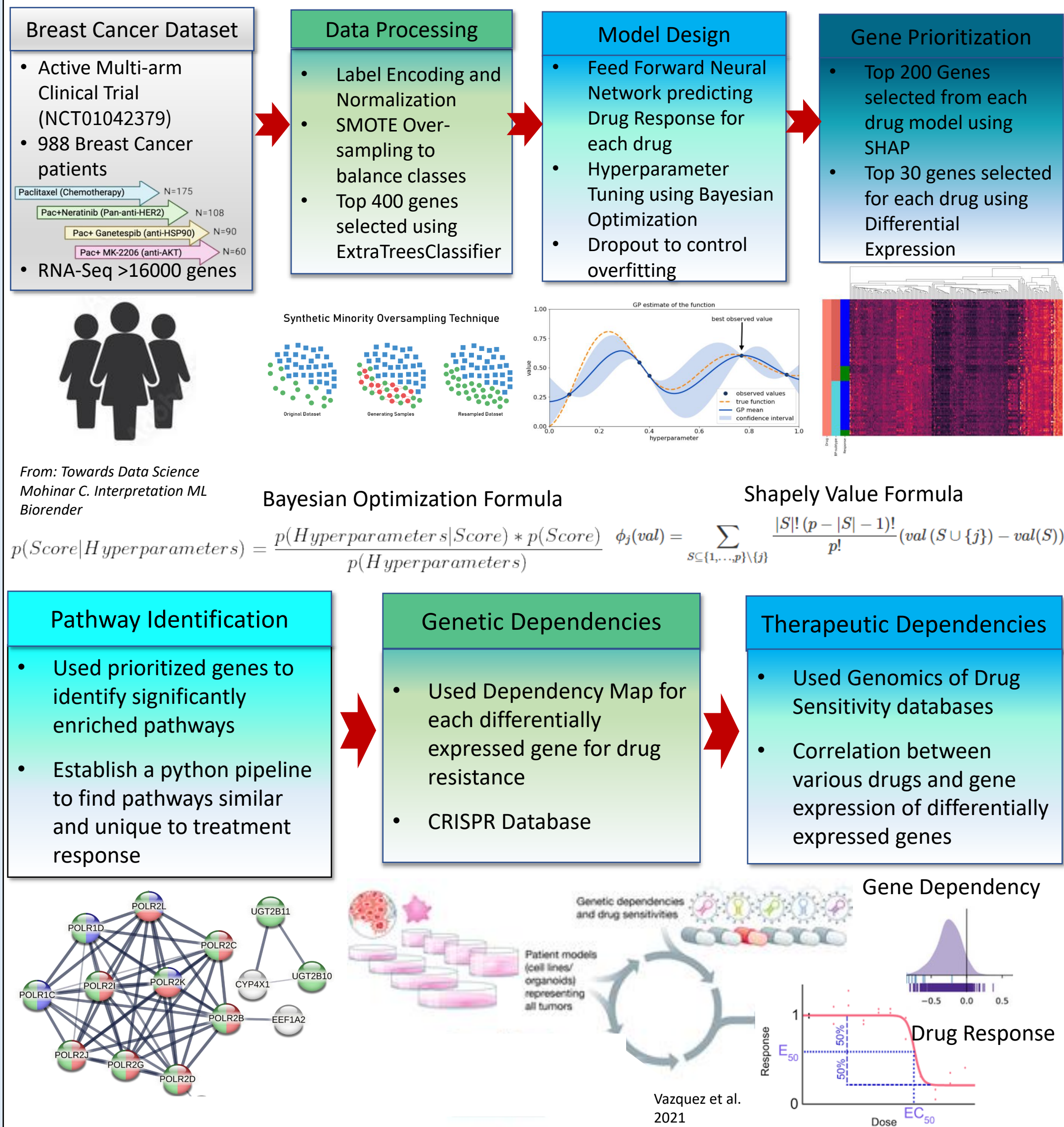
Introduction



Goals and Hypothesis



Methods and Algorithms



Results: Machine Learning

Figure 1: Machine Learning Model Accuracy Ranges 77-92%

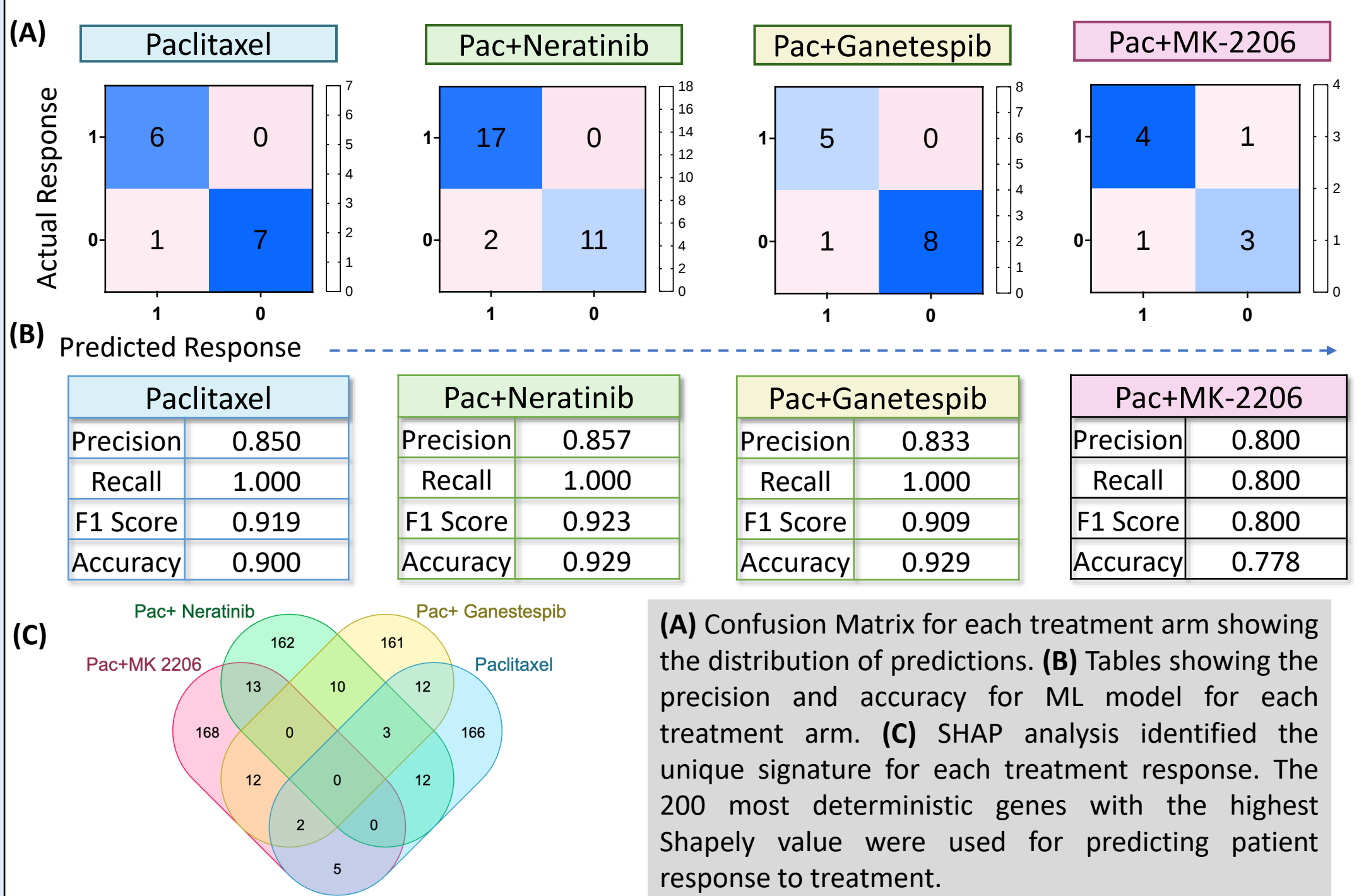
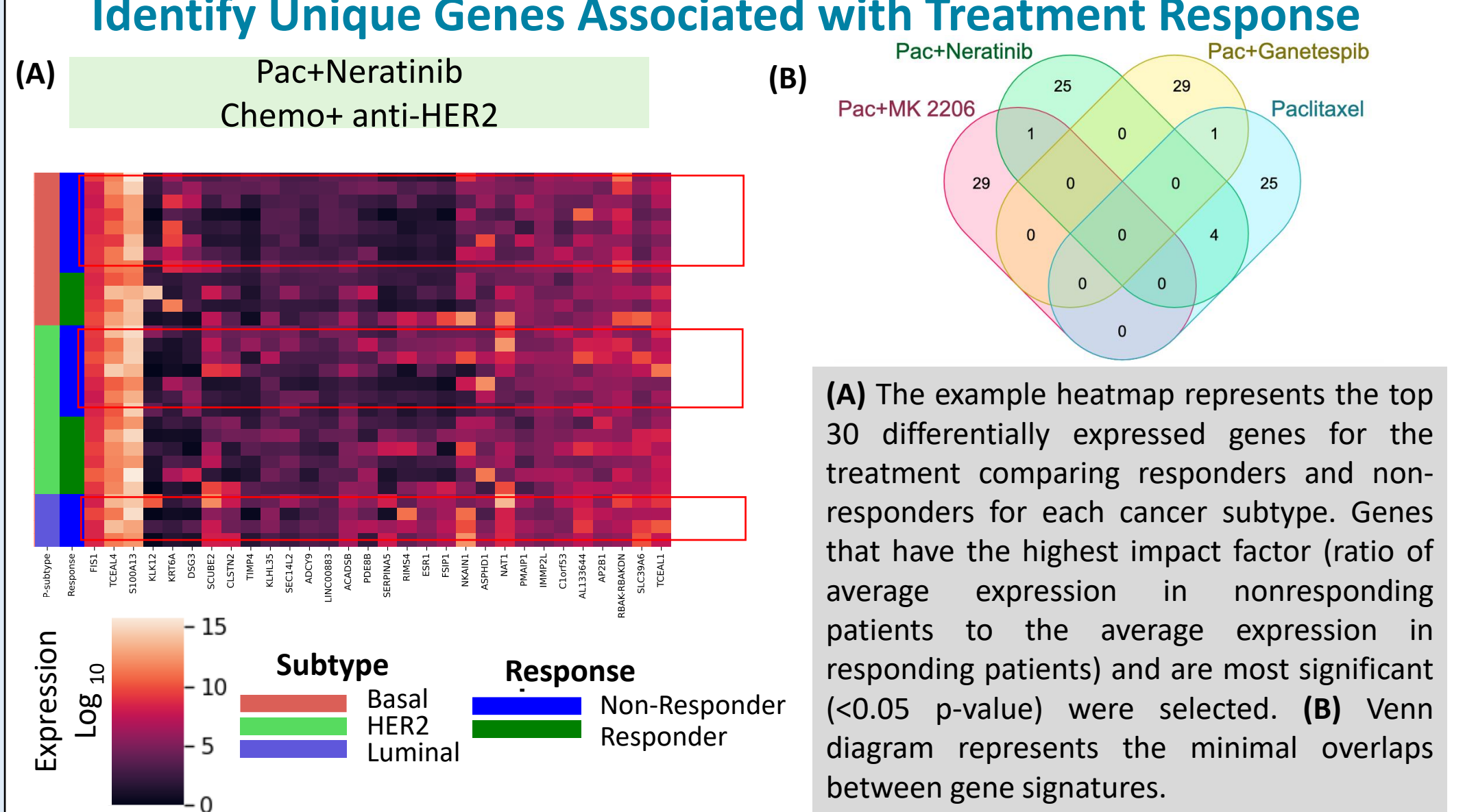


Figure 2: Machine Learning and Differential Expression Analysis Identify Unique Genes Associated with Treatment Response



Harnessing Machine Learning and 3D Spheroid Cultures to Identify Biomarkers for Combating Drug Resistance in Breast Cancer

Results: Computational, and Statistical Analysis

Figure 3: Mechanisms of Drug Resistance in Non-Responder Patients are Distinct for Each Treatment

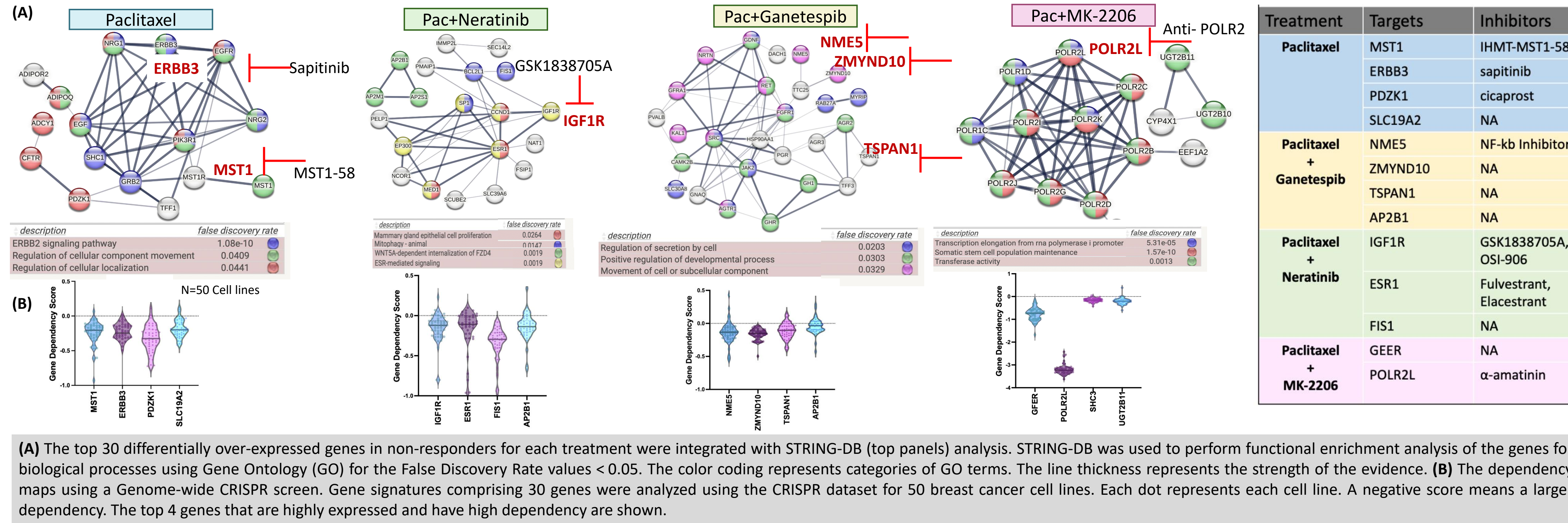
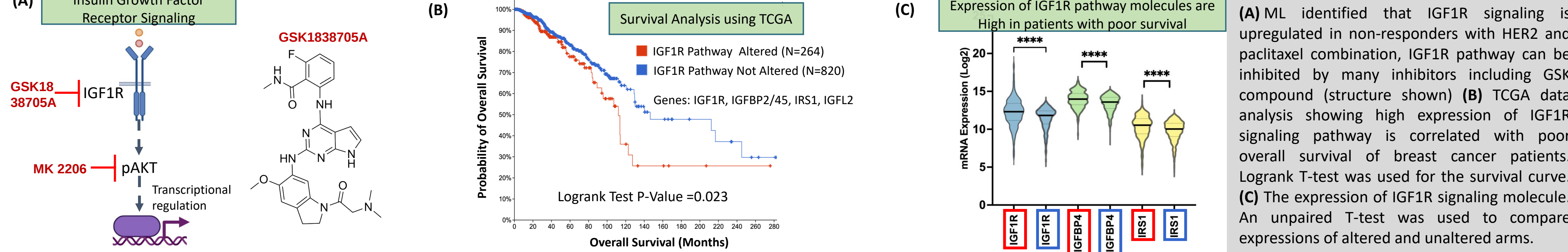


Figure 4: IGF1R Pathway is Upregulated and Associated with Poor Survival in Breast Cancer Patients



Results: Target Validation using 2D and 3D Culture Models

Figure 5: Experimental Equimolar Treatment Dependency on Identified Pathways using Cancer Cell lines

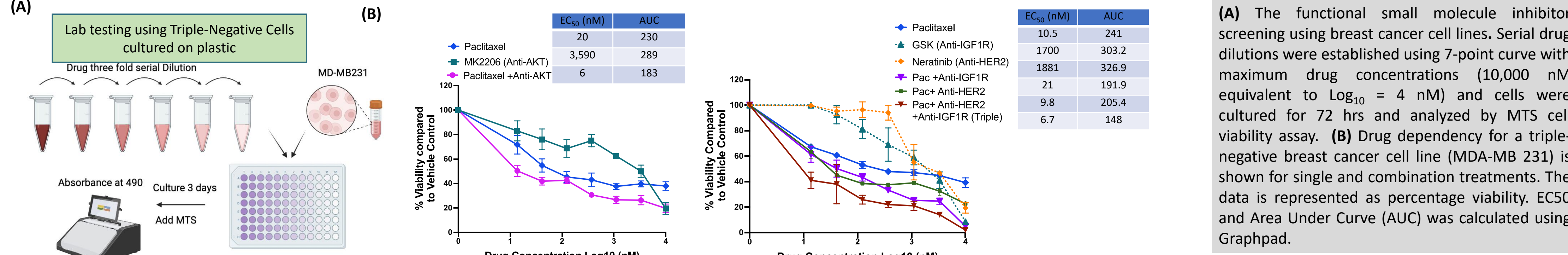


Figure 6: Experimental Synergy Analysis of Triple Drug Combination using Cancer Cell lines

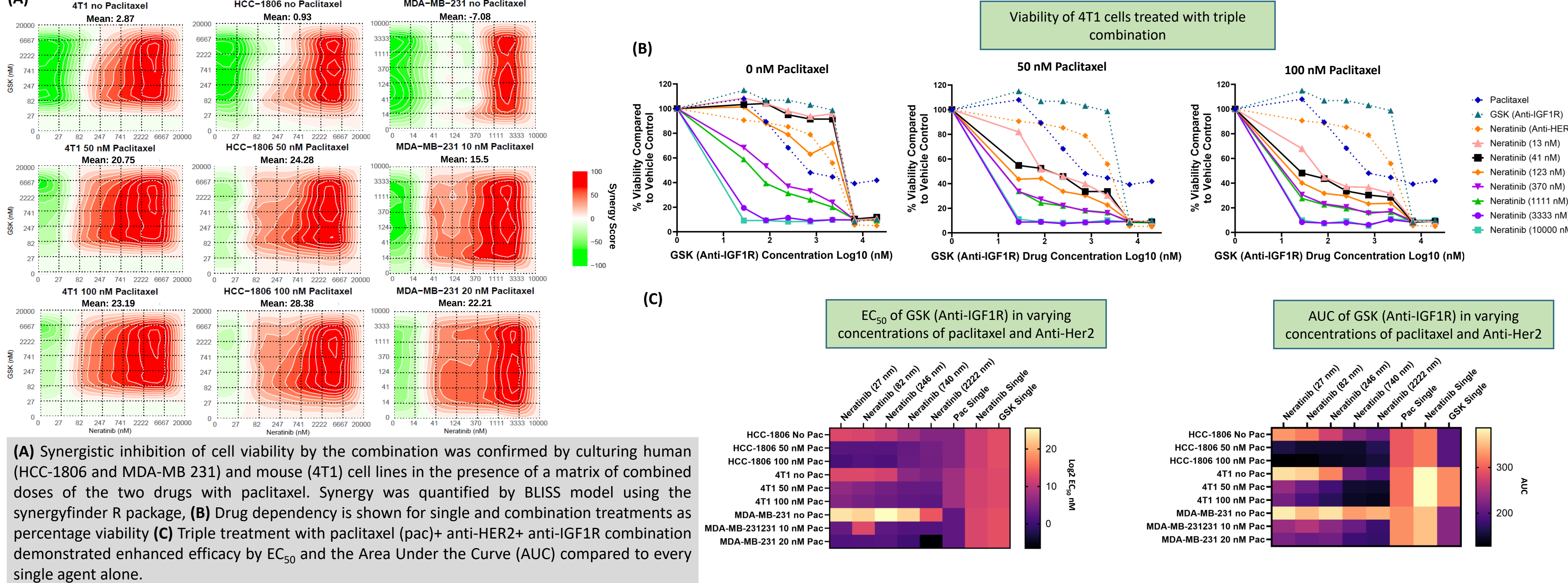


Figure 7: Three-Dimensional (3D) Spheroid Models Identified Effective New Drug Combinations to Overcome Drug Resistance

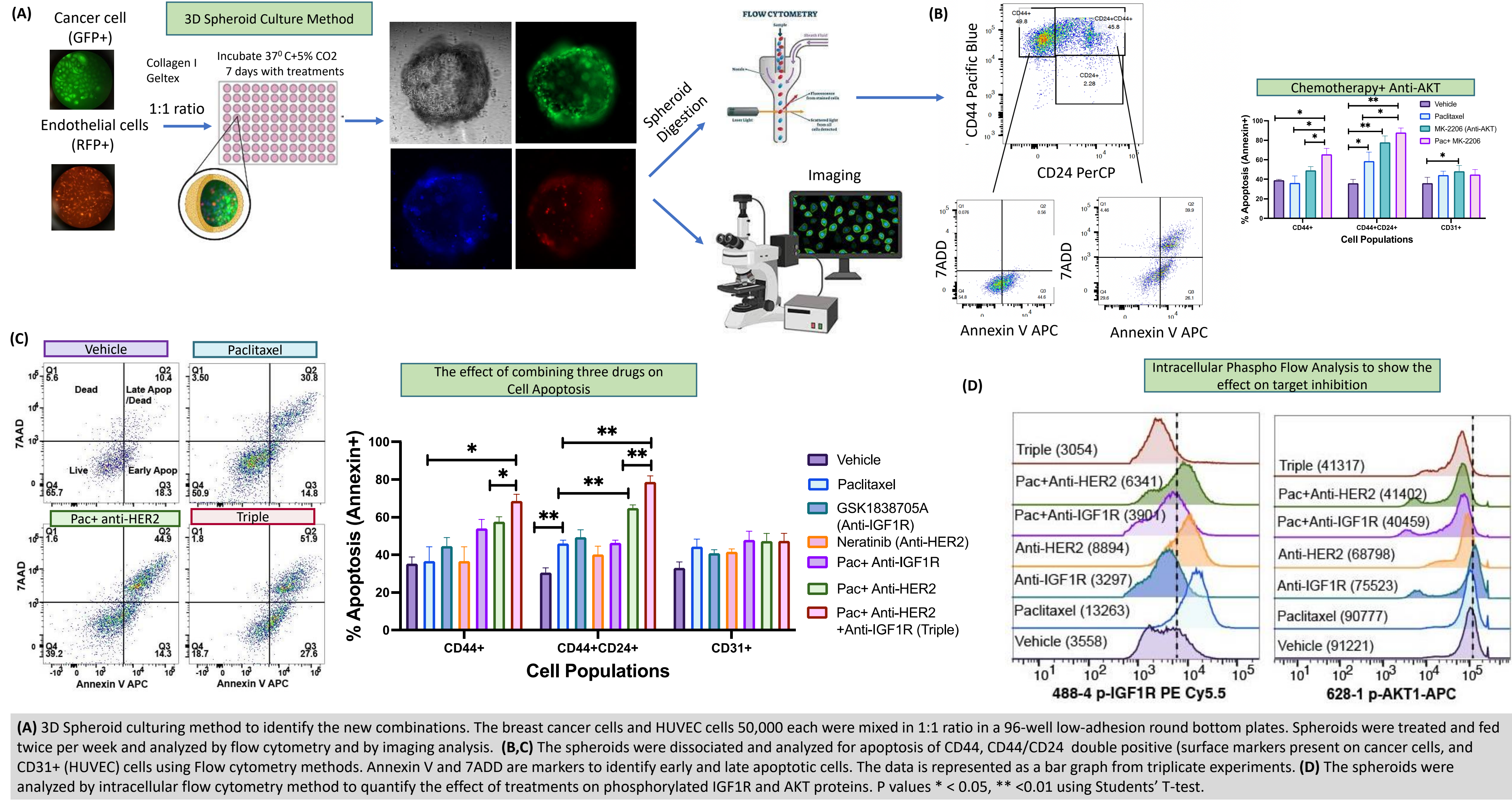


Figure 8: 3D Spheroid Cultured Developed for Inhibitor Screening Identified Effective Drug Combinations

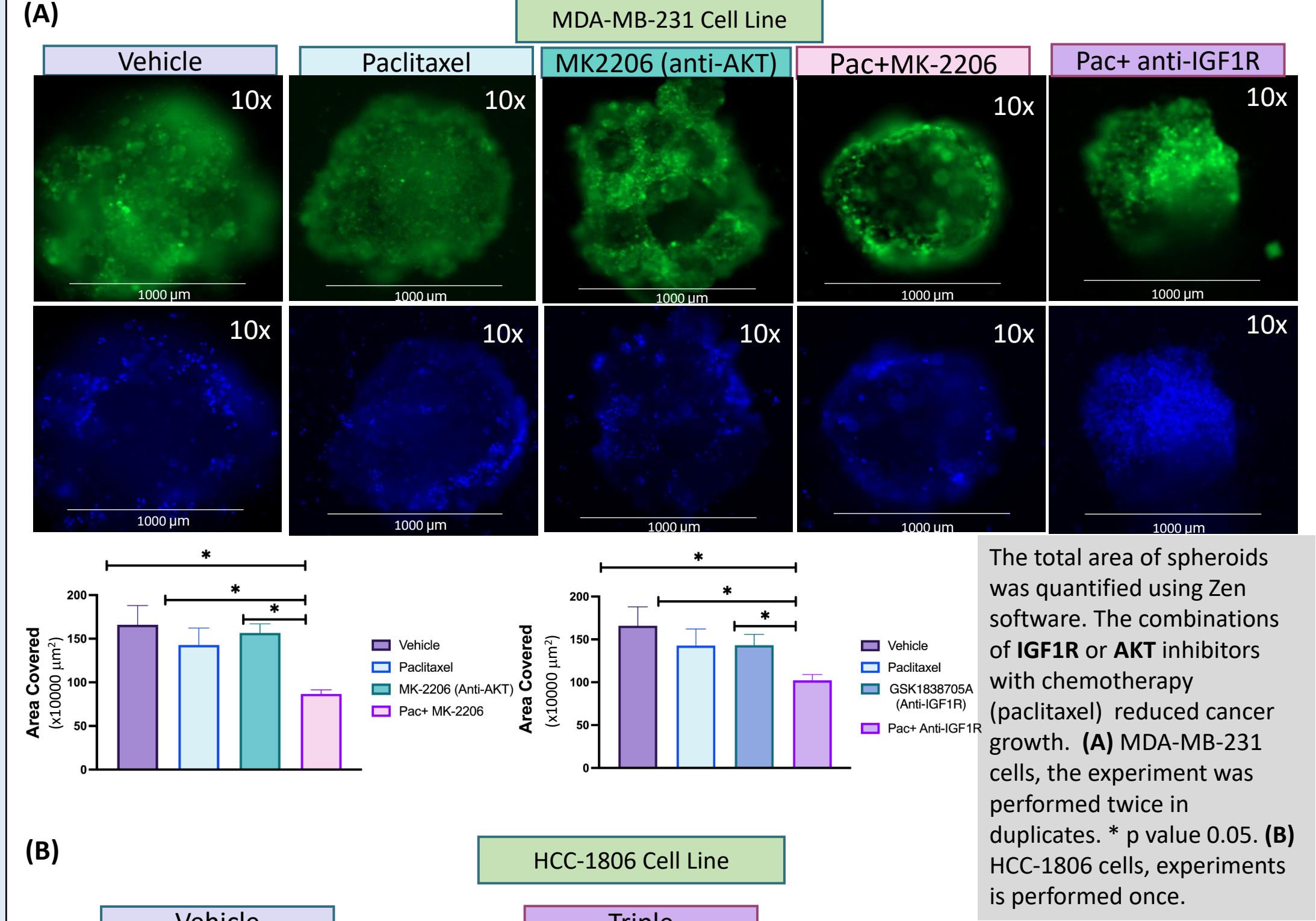
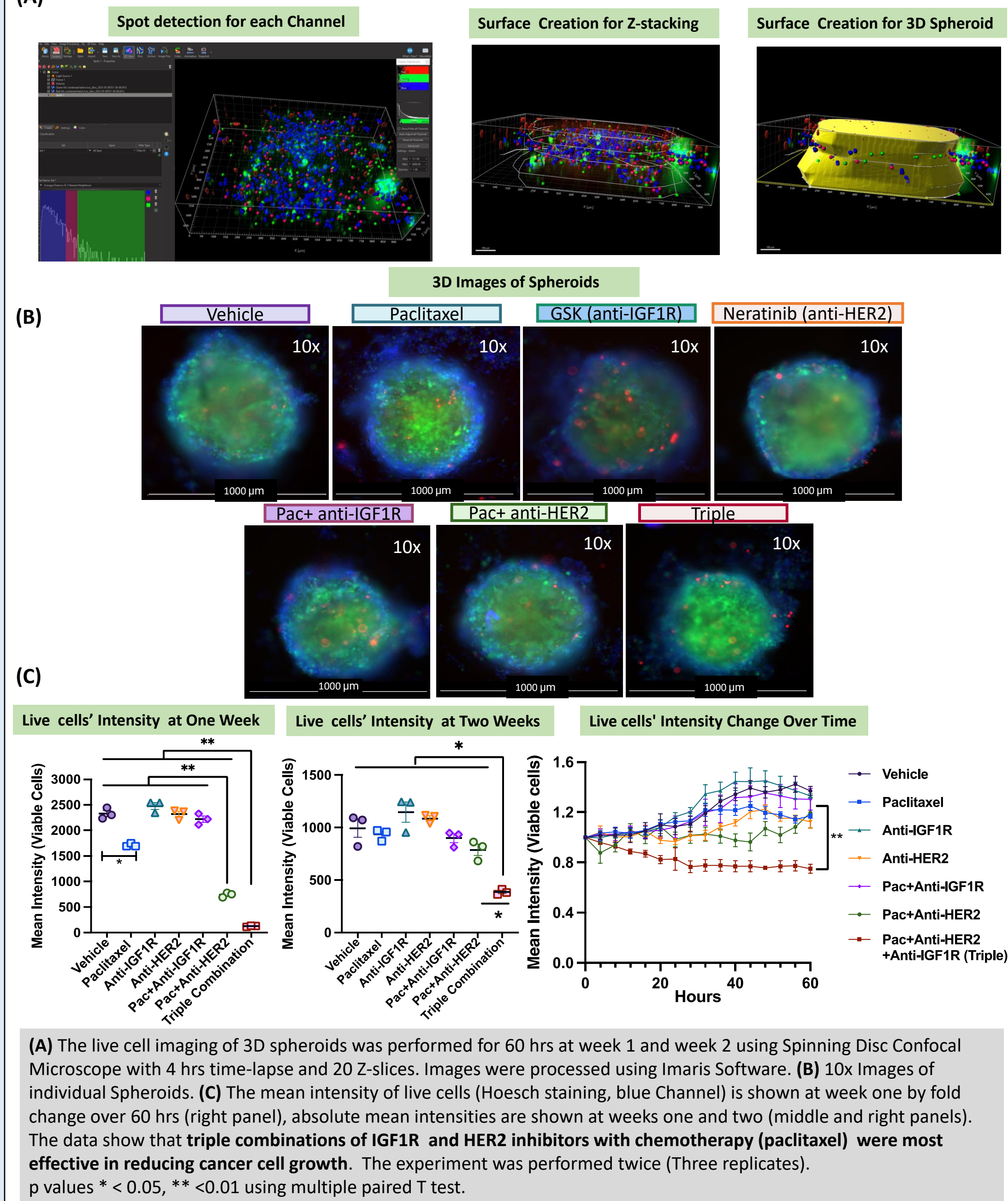
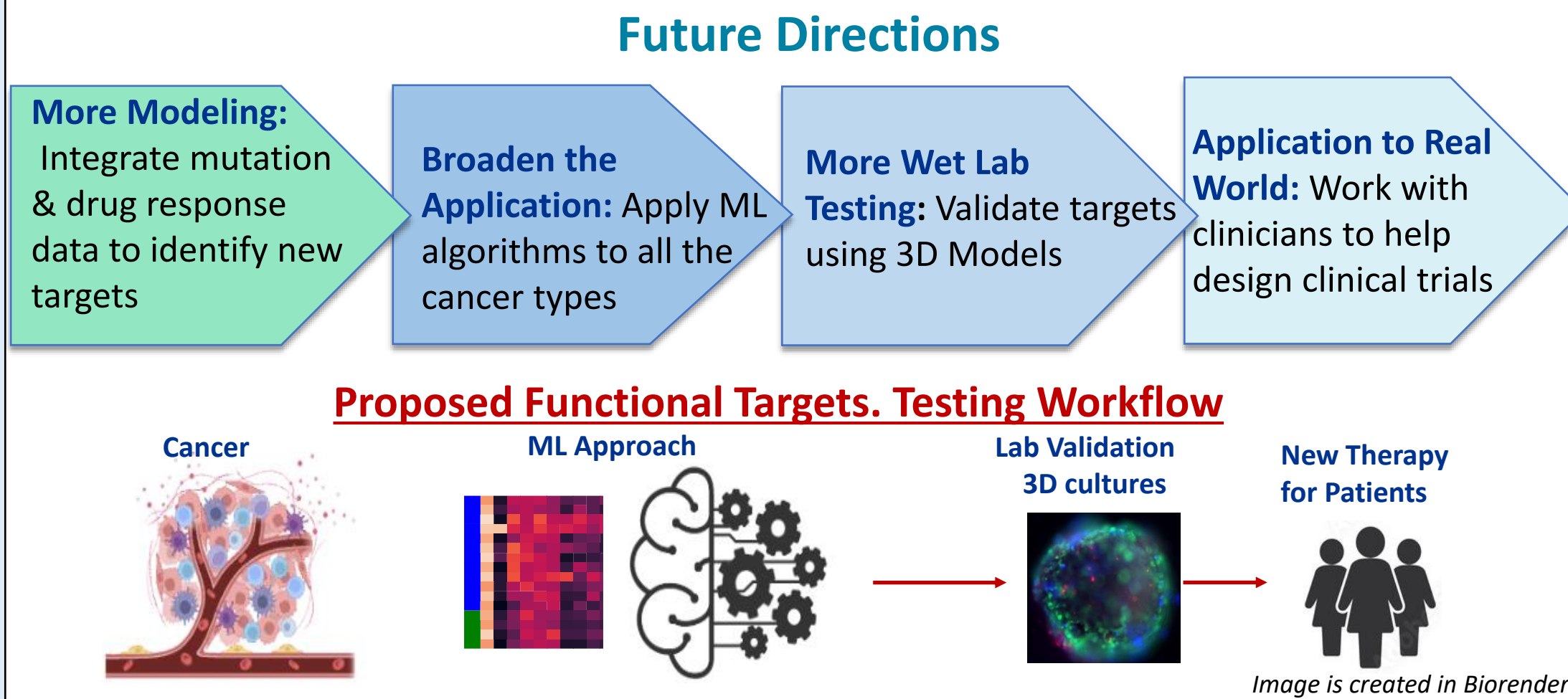


Figure 9: Live Cell Image Analysis of 3D Spheroids Identified Effective Triple Drug Combinations Validated ML-based Findings



Take Aways and Future Directions

- Take Aways and Conclusions**
- Accomplished Engineering Goal:** My machine learning (ML) approach can predict treatment response with up to 92% accuracy
 - AHA Moment:** Identifying unique gene signatures for each treatment for breast cancer patients
 - Favorite Moment:** Seeing 3D models working and validating new targets in both 2D culture /3D spheroids
 - Significant Finding:** Identified pathways and targets that can serve as biomarkers for treatments for personalized therapy including IGF1R, ESR1, ERBB3, MS1T1, and POLR2L



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- I have been engaged in cancer research for the past 4 years, learning both computational and wet lab sides. My goal is to help make this world cancer free. I am motivated to share my research with scientific communities and recently published in *Sensors* and as a preprint in bioRxiv (ISEF-2022), presented at AACR 2022 and ASMBM 2023
- Sensors, Jan 2023**
Simulating the Effect of Gut Microbiome on Cancer Cell Growth Using a Microfluidic Device
Rashmi Mittal, Gaurav Gupta and Vaishnavi Vikaswasi Kulkarni
- Computational Pipeline to Identify Gene signatures that Define Cancer Subtypes**
Rashmi Mittal, Gaurav Gupta, and Vaishnavi Vikaswasi Kulkarni
doi: https://doi.org/10.1101/2023.11.29.518458
- Natural mining and experimental approaches to identify combinations of data derived after bacterial infections**
AACR 2022, Cancer Research 83 (7, Supplement), 5908-5908
ASMBM 2023 Journal of Biological Chemistry 299 (3), 524
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