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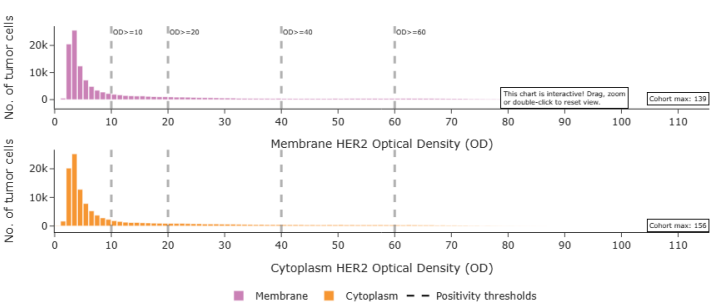
Derisk ADC Development

AI-powered Solutions for Quantitative Continuous Scoring (QCS) and Spatial Proximity Analysis

Antibody drug conjugates (ADCs) hold great promise in oncology, but tumor heterogeneity and the complex mechanism-of-action (MOA) of the drugs and evolving resistance mechanisms present a significant challenge for development. We offer AI-powered spatial proteomic and OD-based quantitative scoring solutions to help you derisk your ADC programs.

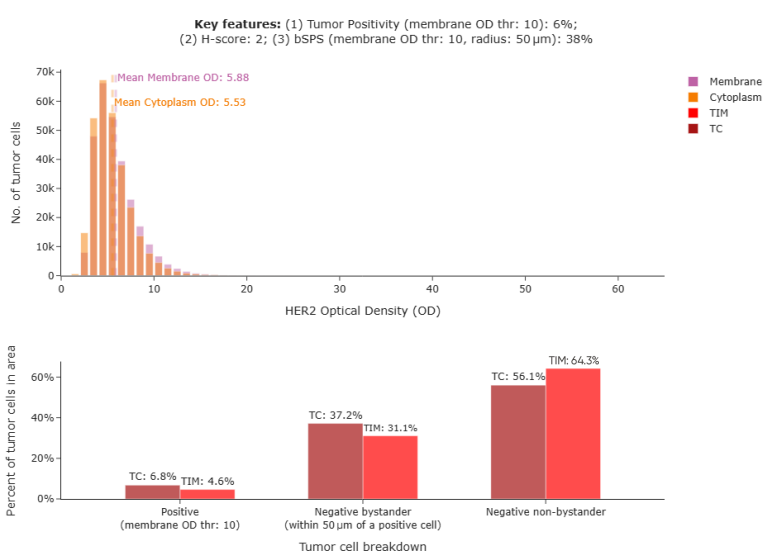
Detect Subcellular Expression: More Granular and Sensitive OD-based Scoring of Immunohistochemistry (IHC) Assays



We've developed a suite of deep learning models to score biomarkers from IHC data that includes defect detection, region segmentation (e.g., tumor, stroma, necrosis), cell type detection, cell segmentation, and OD-based quantitative scoring of target antigen expression to enable more accurate patient stratification.

Figure 1 OD-based Scoring of Membrane and Cytoplasmic Expression (Cross-slide tumor cell sampling)

Model the Bystander Effect: Spatial Biomarker Scoring with Tunable Cut-offs



A recent study from AstraZeneca and Daiichi Sankyo found that Spatial Proximity Scoring (SPS) was able to predict progression-free survival for HER2 negative breast cancer patients enrolled in a Phase I trial for trastuzumab deruxtecan (T-DXd)[1].

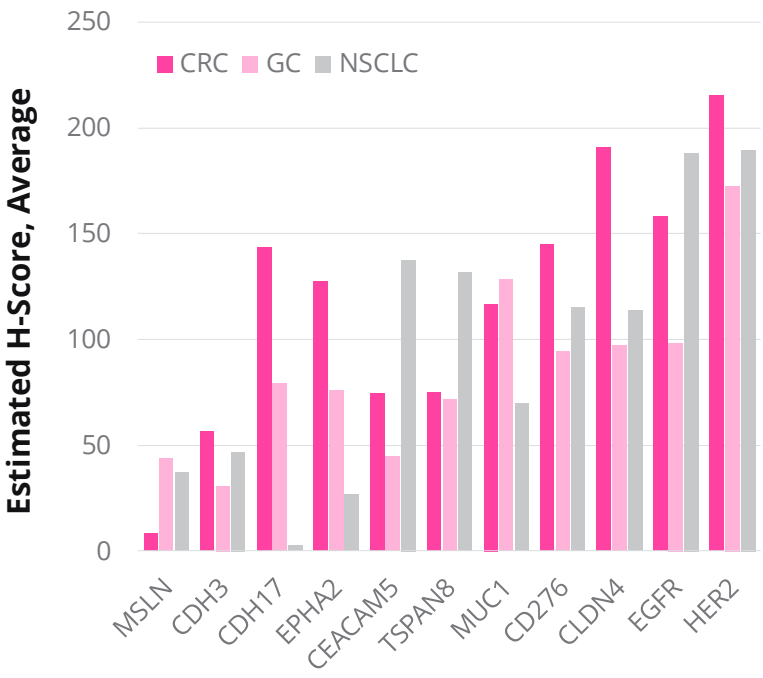
We offer a similar spatial proximity scoring model with tunable parameters:

- Radius from negative cell
- Number of positive neighbors for affected cells
- Positive cells (all positive, high intensity)

[1]Kapil, Ansh et al. Scientific reports vol. 14, 1 12129. 27 May. 2024

Figure 2 An example of a HER2 sample with weak staining, very low average OD, with patchy positive cells that may potentially cause a notable bystander effect

An AI-powered Spatial Inference Platform: Extract ADC and Bispecific Insights from Multiplex Immunofluorescence (mIF) Data



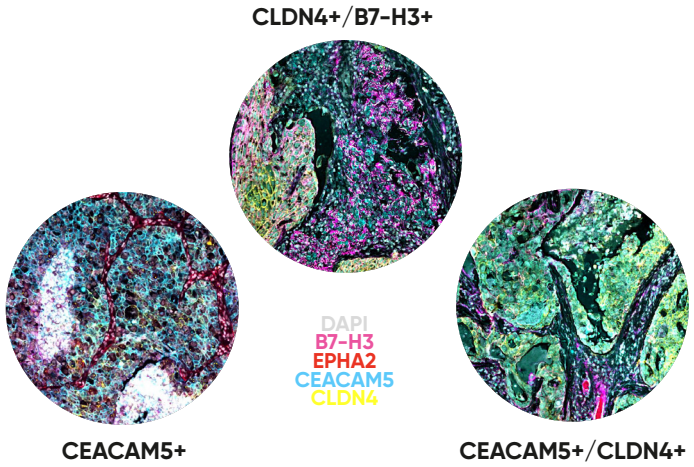
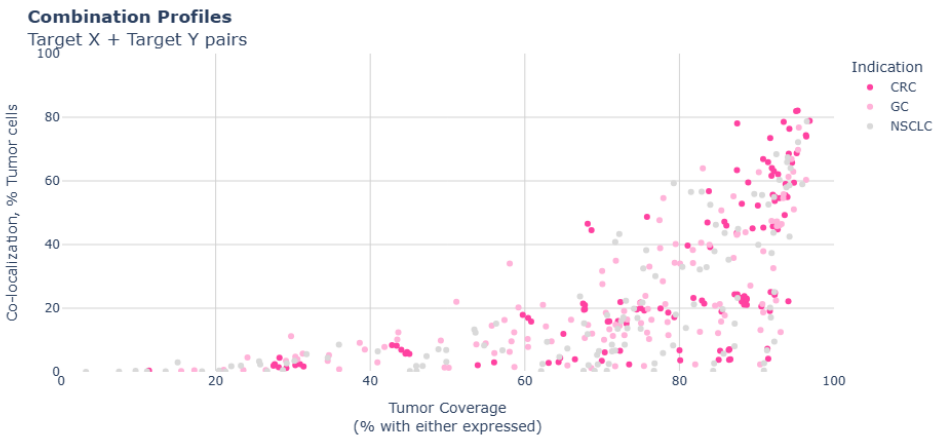


Figure 3 Representive data from a 30-plex mIF panel targeting tumor antigens, immune cells, and signaling cascades run on 217 samples across lung, gastric, colorectal cancers and in normal tissue.

AI powered results provide insights into which targets are commonly expressed across different tissue samples tested. Standard pathological measurements estimated from mIF expression can include H-scores, percent positivity and other pathologically relevant benchmarks based on target expression.

Credentialing Multi-specifics and Combinations



Tumors can be evaluated for the relative expression of multiple candidates, but co-localization helps identify targets for multispecific development. Candidates that are consistently colocalized and tumor specific may be ideal for development across indications.

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