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- **Title of the Presentation:**
Learning the Language of Cancer Response from Histopathology Images
- **Executive Summary / Investment Rational**
Pangea Biomed's ENLIGHT-DP treats the H&E pathology slide as a biological text — one that encodes, at the pixel level, information about the underlying transcriptomic state of a tumor. The platform reads this text in two steps: a deep-learning layer infers genome-wide gene expression directly from slide images, and ENLIGHT — our existing pan-cancer response prediction engine — translates those inferred expression patterns into treatment-specific response predictions, without ever training on clinical response data.
This two-step architecture reflects a broader principle: biological representation learning is most powerful when it separates the problem of encoding biological state from the problem of interpreting it. By grounding the image-to-expression inference in a large, well-characterized transcriptomic space, ENLIGHT-DP generalizes across cancer types and treatments in a way that end-to-end response-prediction models cannot.
ENLIGHT-DP has now been validated across over 1,000 cases, with an average odds ratio of 4.1 in validations over 14 independent cohorts – competitive with NGS-based approaches that require full sequencing. It outperforms PD-L1 and TMB in predicting response to immunotherapy and survival stratification across lung, head & neck, breast, and other cancers, and has shown prospective signal in a Sheba Medical Center trial. An NCI-sponsored interventional trial (SYNTHESIS-Breast) is actively recruiting.
- **Business strategy**
Pangea is advancing ENLIGHT-DP toward clinical deployment through collaborations with leading academic medical centers – including Cedars-Sinai in the US and IGR in Europe – generating the real-world validation evidence needed for regulatory-grade diagnostic tests. Pangea is currently raising funding to bring its first ENLIGHT-DP tests to market.
- **Core Technology**
ENLIGHT-DP is built on two modular layers. The first is a deep-learning framework trained to infer genome-wide gene expression from standard H&E slides – learning a biological representation without any treatment-response supervision. The second is ENLIGHT, a pan-cancer platform that predicts treatment response from expression patterns using network-based models of synthetic lethality and tumor-immune interaction. The combination converts a routinely collected pathology image into a multi-treatment response prediction, requiring no genomic sequencing and no matched response training data.