

patterns between patient tumor RNA-seq and clinical outcomes and map these associations on to higher-resolution data like spatial and single-cell transcriptomics. We apply DEGAS to prostate and pancreatic cancer spatial transcriptomics samples, as well as one normal sample of prostate tissue. We used the TCGA prostate cancer cohort to with the accompanying survival information and publicly accessible prostate cancer ST data from 10X Genomics to predict survival associations in the ST slides derived from the TCGA patients. Based on these survival associations, we identify higher risk subsections of ST slides which can be further studied. RESULTS/ANTICIPATED RESULTS: We were able to validate our method by comparing it to Scissor and were able to show that the number of high-risk regions in prostate cancer slides increased with the stage of disease. Furthermore, we identify transcriptomic signatures enriched for ontology terms associated with growth regulation and apoptosis, inflammation, immune signaling, and autophagy in histologically normal prostate tissues and adjacent normal pancreatic cancer tissues that were identified as high-risk by DEGAS. The regions highlighted by DEGAS could reflect transcriptional precursors to intraepithelial neoplasia—a well-recognized premalignant morphological change in glandular epithelium. DISCUSSION/SIGNIFICANCE: Identifying biomarkers of tissue stress that precede morphologic diagnosis of high-grade pre-malignant lesions by a pathologist may help triage patients at high risk for future development of cancer, or aid in better understanding whether histologically normal pre-malignant tissues at tumor margins contribute to recurrence.

270

### Development of a Predictive Nomogram for Circumferential Resection Margin in Rectal Cancer Surgery

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OBJECTIVES/GOALS: A negative circumferential resection margin (CRM) after surgical resection of rectal cancer decreases local recurrence and increases overall survival. While MRI is used to predict this risk, there is no predictive model that incorporates clinical factors to predict the risk of CRM positivity. METHODS/STUDY POPULATION: Utilizing the National Cancer Database from 2010-2014, we performed a retrospective study evaluating factors predictive for positive CRM after surgical resection of rectal cancer. The primary outcome was positive CRM (tumor  $\leq$  1 mm from the surgical margin). Our population included patients with clinical stage I-III rectal cancer who underwent total mesorectal excision. For the primary outcome, multivariable logistic models were used to estimate the probability of a positive CRM. Model performance was evaluated by using the area under the receiver operating characteristic curve (AUC). Model calibration was assessed by examining the calibration plot. Bootstrapping method (300-iteration) was used to internally validate and estimate optimism-adjusted measures of discrimination and overall model fit. RESULTS/ANTICIPATED RESULTS: There were 28,790 patients included. 2,245 (7.8%) had positive CRM. Older age, race, larger tumor size, higher tumor grade, mucinous and signet tumor histology, APR, open operative approach, facility location, higher T stage, lymphovascular invasion, lack of neoadjuvant chemotherapy/radiation, and perineural invasion were all significantly associated with positive CRM (p

positive CRM and associated poor clinical outcomes is possible to be used in conjunction with MRI. Positive CRM is associated with specific patient demographics, tumor characteristics, and operative approach. These factors can be used to predict CRM positivity in the preoperative period and plan accordingly.

271

### Diagnosis and Detection of Thrombosis in PCOS

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OBJECTIVES/GOALS: Identify and stratify clinical presentations of thrombotic pathology in PCOS patients. This will be accomplished by 1) evaluating clinical assays for the detection of hypofibrinolysis, and 2) analyzing clinical symptomology of thrombosis in PCOS via Symptom-Disease Pair Analysis of Diagnostic Error (SPADE). METHODS/STUDY POPULATION: Preliminary study populations include n=3 for each of the following groups PCOS with thrombotic complications, PCOS without thrombotic complications, healthy controls, and healthy control samples treated ex vivo with PAI-1. Coagulation assays include ACL coagulation panel, antiphospholipid antibody assays, viscoelastic testing with TEG and Quantra devices, and global fibrinolytic capacity. Coagulation assays will be performed on three samples taken at 4-week intervals. The SPADE techniques will be used to evaluate symptomology of thrombosis in the study period and patient electronic medical history. Molecular testing will be performed for pro-thrombotic polymorphisms (PAI-1 and Apo E) and mutations (Factor V Leiden and Prothrombin). RESULTS/ANTICIPATED RESULTS: We anticipate PCOS and ex vivo PAI-1 samples to show signs of hypofibrinolysis on TEG and Quantra devices outside of reference ranges and with statistical significance. We also anticipate seeing a statistical significance with ACL coagulation panels, however, these results are expected to still be within the reference ranges, as seen in previous studies. We believe the SPADE method will identify clinical presentations of hypofibrinolysis in PCOS patients coinciding with patterns in laboratory tests that were misdiagnosed due to being within reference ranges. We hope to stratify clinical presentations predictive of thrombosis in PCOS patients with standard clinical assays and with increased precision using viscoelastic assays. DISCUSSION/SIGNIFICANCE: The incidence rate of thrombosis is 40x higher in PCOS compared to healthy populations. However, the mechanisms of thrombosis in PCOS are unknown and are undetectable with current clinical assays. We hypothesize that chronic cellular stress in PCOS disrupts the regulation of interconnected immune pathways, causing hypofibrinolysis.

272

### Differential expression of two Plasmodium falciparum variant surface antigen families in Malian children with cerebral malaria compared to mild malaria\*

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OBJECTIVES/GOALS: Recent in vitro evidence suggests that diverse parasite protein families called RIFINs and STEVORs are displayed