showed head shape improvements after corrective surgery during clinical evaluation. Linear temporal regression indicates a CSA index decrease of 0.43 ± 0.05 during the first year after surgery. We found no significant correlation between a patient's age at surgery and the patient's CSA index after surgery (Pearson's correlation coefficient 0.17, p = 0.20) or the patient's change in CSA index before and after surgery (Pearson's correlation coefficient 0.22, p = 0.11), suggesting that sagittal craniectomy is equally effective for all patients who are between 85 and 331 days old at the time of surgery. DISCUSSION/SIGNIFICANCE: Our new CSA index is a sex- and age-specific metric of head shape anomalies built upon the observed statistical distributions in the normative pediatric population. Our metric can objectively evaluate pre- and post-surgical head shapes and will allow the investigation of the reported variability in surgical outcomes among patients and procedures.

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Omics based analysis to identify novel markers of TMZ response in Glioblastoma Multiforme

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OBJECTIVES/GOALS: MGMT methylation status is used to predict the response to TMZ. However, a subpopulation of patients lacking MGMT methylation still respond to TMZ. We applied omics approaches and functional studies to a cohort of GBM patients to identify novel markers that may more accurately predict TMZ response. METHODS/STUDY POPULATION: We applied a combination of omics approaches and functional studies to a cohort of GBM patients to search for novel markers that would predict the response to TMZ treatment more accurately than traditional markers. Using a set of 47 primary and secondary GBM tumor samples, we employed comparative transcriptomics, whole exome sequencing, data independent acquisition (DIA) proteomics, and phosphoproteomics to look for DNA mutations and changes in gene expression and/or protein expression that correlated to response or non-response to TMZ. Subsequently, we performed functional studies and analyzed patient treatment data to validate our results. RESULTS/ANTICIPATED RESULTS: This study is in early stage, but we anticipate that our combination of methods may allow us to identify and validate at least one novel biomarker for TMZ response in patient GBM. For example, comparative transcriptomics or phosphoproteomics may identify a previously unrecognized gene or protein over/under-expression in a subset of patients. In this case we will validate findings using western blotting, IHC staining, and through siRNA of target gene/protein on patient derived GBM cells to examine if removal of this marker leads to TMZ sensitivity. We will further confirm prediction of marker correlation through comparison with matched patient treatment data. DISCUSSION/SIGNIFICANCE: The identification of improved biomarkers to predict response to TMZ treatment is a discovery that could rapidly become standard of care for GBM patients. It would ensure that all responders receive TMZ and avoid exposing nonresponders unnecessarily to TMZ and its potential side effects.

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Optimizing the Identification and Prediction of Statin Intolerance to Improve Statin Adherence Using Natural Language Processing and Machine Learning

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OBJECTIVES/GOALS: Aim1: To develop a natural language processing (NLP) algorithm to effectively identify statin associated muscle symptoms (SAMS) in patients'electronic health records (EHRs). Aim2: To develop a machine learning model based on clinical features within EHRs that predict the likelihood of SAMS occurrences. METHODS/STUDY POPULATION: A retrospective cohort of adult patients initiated on statins within the Minnesota Fairview Healthcare System EHRs from 2010 to 2020 will be analyzed. NLP-PIER (Patient Information Extraction for Research) platform will be used to search and identify patients who developed SAMS after statin initiation. Manual annotation of clinical notes will be completed to validate the accuracy of identified SAMS cases. Then, a selection of clinical features within the EHRs will be input as predictors for machine learning algorithms development. Select machine learning classifiers will be deployed to generate models for the prediction of SAMS and the best-performing model will be selected based on model performance. RESULTS/ANTICIPATED RESULTS: The expected outcomes include generation of a fine-tuned NLP algorithm that can rigorously identify SAMS occurrences within EHRs. Further, we anticipate having a practical risk model that accurately predicts patients'risks of developing SAMS when taking statins. DISCUSSION/SIGNIFICANCE: The positive and translational impact of our research will be to equip healthcare providers with such informatics tools to improve statin adherence, ultimately promoting patient optimal health and outcomes by maximizing the tolerance and thus realizing the therapeutic benefits of statins.

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Optimizing Urinary cell mRNA profiling of kidney allograft recipients: Development of a home processing protocol for noninvasive diagnosis of T cell mediated rejection and BK virus nephropathy

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OBJECTIVES/GOALS: Development of a user friendly home kit that enables kidney transplant recipients to process urine at home and post the lysate containing RNA to a Core Laboratory would simplify urinary cell mRNA profiling and facilitate longitudinal monitoring. We report our home processing protocol and investigation of its diagnostic performance characteristics. METHODS/STUDY POPULATION: We developed a home processing protocol (HPP) consisting of urine filtration and lysis of urinary cells, both

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