18050 - Methylation-Based Predictor of Meningioma Recurrence

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Technology description

DNA-methylation-based predictor discovered in peripheral blood samples may result in increased remission of meningioma patients

In the United States, meningioma accounts for 37% of primary brain tumors. An estimated 31,990 people will be diagnosed with meningioma in 2019. The greatest clinical challenge faced in meningioma is the inability to predict recurrence for individual patients, limiting the ability to select patients who would benefit from adjuvant radiation therapy to prevent recurrence and resulting in poorer overall outcomes.

The University Health Network Drs. Zadeh, Aldape, Nassiri, and Maimaitijiang have developed a potentially disruptive innovation in meningioma treatment. Their lab has developed a DNA-methylation-based predictor of meningioma recurrence in individual patients, which can be used to guide decision making regarding adjuvant treatment, resulting in better outcomes for patients with this condition.

Tests to date have demonstrated that the methlyome-based predictor was independently associated with RFS in each of the two validation sets, after adjusting for tumor grade and extent of resection. Using a 5-year RFS metric, the methylome-based predictor performed favourably compared to a grade-based predictor in both validation cohorts. Functional annotation of the included probes implicated the homeobox gene family. A nomogram constructed using the validated methylome-predictor with WHO grade and EOR demonstrated greater predictive performance than a nomogram using clinical factors alone and resulted in two different risk groups with distinct recurrence patterns.

Application area

Peripheral blood marker for recurrent meningioma

Institution

University Health Network

联系我们

叶先生

电 话：021-65679356
手 机：13414935137
邮 箱：yeyingsheng@zf-ym.com