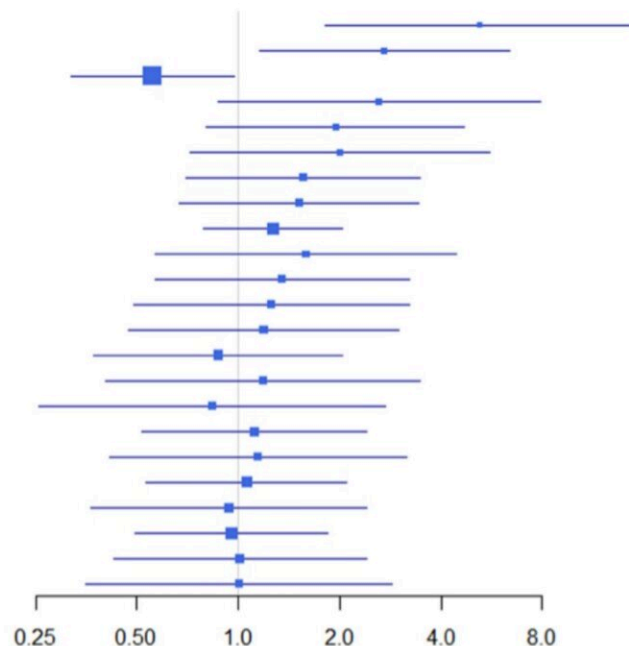


Team studies association between tumor mutations and meningioma recurrence in Grade I/II disease

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Gene	HR (95% CI)	P-Value
ATM	5.227 (1.811 , 15.083)	0.002
CREBBP	2.713 (1.154 , 6.377)	0.022
POLE	0.555 (0.318 , 0.967)	0.038
SETD2	2.614 (0.867 , 7.881)	0.088
ATR	1.946 (0.804 , 4.709)	0.14
RNF43	2.004 (0.721 , 5.572)	0.183
TP53	1.555 (0.698 , 3.465)	0.28
BRCA1	1.519 (0.67 , 3.443)	0.316
NF2	1.268 (0.788 , 2.04)	0.329
TSC2	1.584 (0.567 , 4.423)	0.38
RAD50	1.35 (0.566 , 3.221)	0.499
PTCH1	1.254 (0.487 , 3.226)	0.639
BRCA2	1.189 (0.471 , 3.001)	0.714
NOTCH1	0.871 (0.371 , 2.043)	0.751
CDK12	1.182 (0.403 , 3.464)	0.761
AKT1	0.835 (0.255 , 2.734)	0.766
NOTCH3	1.114 (0.516 , 2.404)	0.784
MET	1.143 (0.414 , 3.159)	0.797
ARID1A	1.057 (0.533 , 2.095)	0.873
NOTCH2	0.937 (0.366 , 2.401)	0.892
NF1	0.955 (0.494 , 1.849)	0.892
PALB2	1.011 (0.426 , 2.398)	0.98
ATRX	1.003 (0.351 , 2.863)	0.996



Adjusted progression-free survival hazard ratios for genes examined. Credit: 2022 Dullea et al.

A new research paper titled "Association between tumor mutations and meningioma recurrence in Grade I/II disease" has been published in *Oncoscience*.

Meningiomas are common intracranial tumors with variable prognoses not entirely captured by commonly used classification schemes. In this new study, researchers from Icahn School of Medicine at Mount Sinai and Sema4 (A Mount Sinai Venture) sought to determine the relationship between meningioma mutations and oncologic outcomes using a targeted next-generation sequencing panel.

The researchers note, "As such, there is a need to further characterize meningioma disease mechanisms in pursuit of better diagnostics and novel targets to improve treatment paradigms."

The team identified 184 grade I and II meningiomas with both more than 90 days of post-surgical follow-up and linked targeted next-generation sequencing. For mutated genes in greater than 5% of the sample, progression-free survival Cox-regression models stratified by gene were computed. The researchers then built a multi-gene model by including all gene predictors with a p-value of less than 0.20. Starting with that model, the researchers performed backward selection to identify the most predictive factors.

ATM (HR = 4.448; 95% CI: 1.517-13.046), CREBBP (HR = 2.727; 95% CI = 1.163-6.396), and POLE (HR = 0.544; HR = 0.311-0.952) were significantly associated with alterations in disease progression after adjusting for clinical and pathologic factors. In the multi-gene model, only POLE remained a significant predictor of [recurrence](#) after adjusting for the same clinical covariates. Backwards selection identified recurrence status, resection extent, and mutations in ATM (HR = 7.333; 95% CI = 2.318-23.195) and POLE (HR = 0.413; 95% CI = 0.229-0.743) as predictive of recurrence.

"Mutations in ATM and CREBBP were associated with accelerated [meningioma](#) recurrence, and mutations in POLE were protective of recurrence. Each mutation has potential implications for treatment. The

effect of these mutations on oncologic outcomes and as potential targets for intervention warrants future study," the researchers conclude.

More information: Jonathan T. Dullea et al, Association between tumor mutations and meningioma recurrence in Grade I/II disease, *Oncoscience* (2022). [DOI: 10.18632/oncoscience.570](https://doi.org/10.18632/oncoscience.570)

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