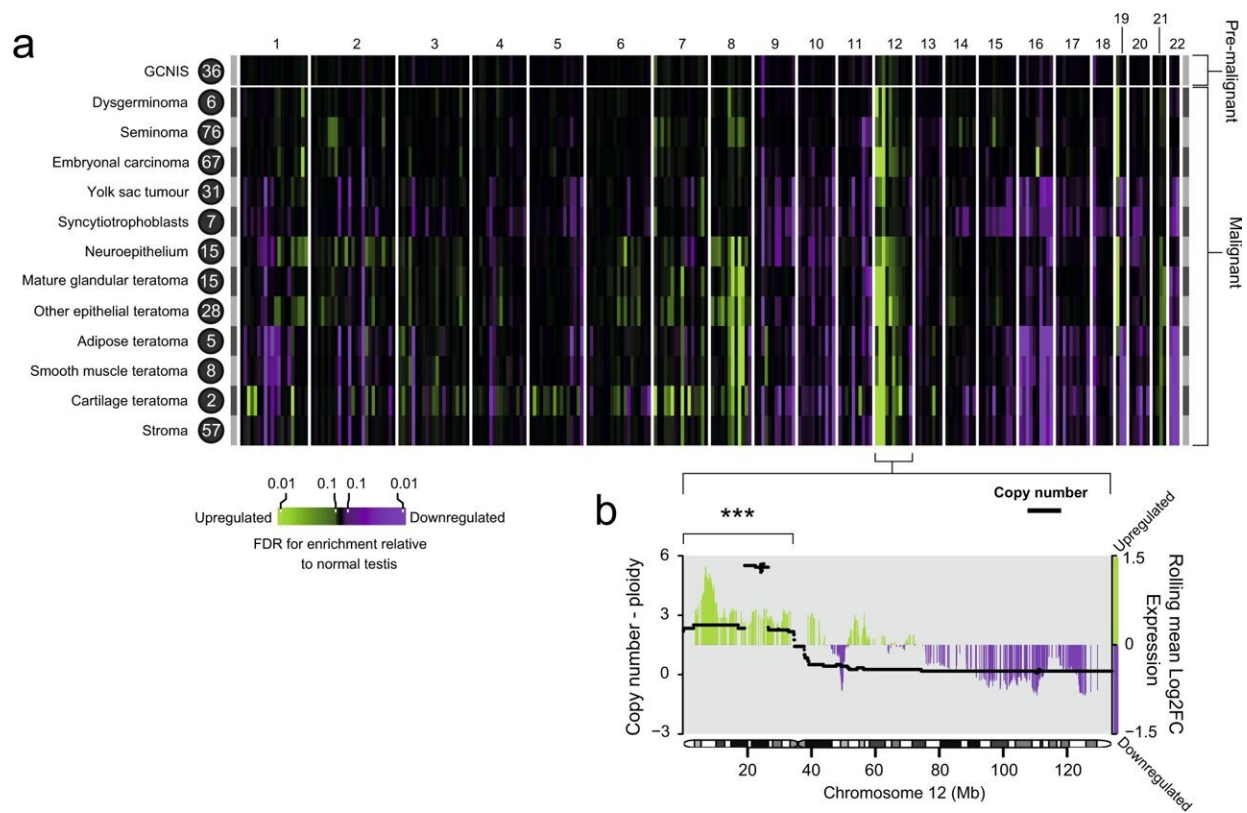


Origins of germ cell tumors suggest possible opportunities for future treatment

August 11 2022



The relationship between GCT genome and transcriptome. a Heatmap showing gene enrichment per GCT tissue relative to healthy seminiferous tubules, binned by cytoband. Colors correspond to significance of enrichment according to the adjusted p-value (false discovery rate correction). The number next to each histology is the number of eligible microbiopsies that informs the analysis (Supplementary Data 16). b Combined plot of the chromosome 12 copy number changes across all invasive tumors and the rolling average log₂ fold-change in gene expression compared with healthy seminiferous tubules. The window size

for the rolling average is 50 genes. The average log₂ fold-change in expression across 12p was significantly higher than across comparable numbers of genes found across regions with near baseline ploidy (one-sided permutation test, p

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