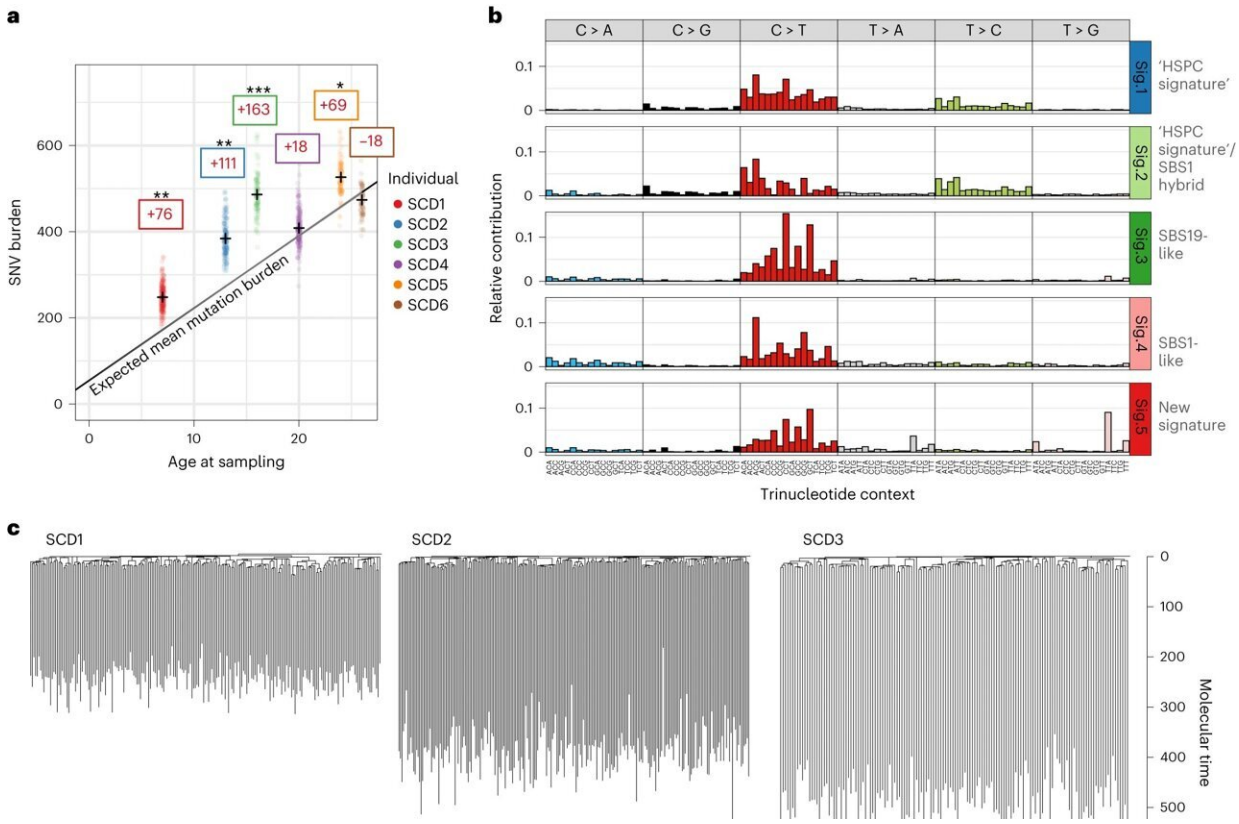
Medical Xpress

New research advances understanding of cancer risk in gene therapies

November 16 2023



Landscape of somatic mutations in SCD. **a**, Dot-plot showing the number of mutations per HSPC for each patient plotted against the patient age at the time of sampling. SNV mutation burdens of individual HSPC colonies from before GT, with correction for coverage, are displayed per patient. Mean mutation burdens per individual are indicated by a cross. The black line indicates the expected mean mutation burden by age from a previous study looking at hematopoietically healthy individuals[28]. The average total number of mutations per HSPC above (+)/below (−) the expected value is indicated in the colored

boxes. The mutation burdens for each patient were individually tested against the reference mutation set using a linear mixed-effects model with 'age' and 'patient/reference status' as fixed effects, and 'individual' as a random effect, to see if the 'patient/reference status' term was significant (*P

Citation: New research advances understanding of cancer risk in gene therapies (2023, November 16) retrieved 8 May 2024 from https://medicalxpress.com/news/2023-11-advances-cancer-gene-therapies.html

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