A TP53 wild-type background can confound estimates of gene selection in genetic screens. A Boxplots showing the pooled normalized sgRNA counts per sample (essential and non-essential genes, and non-targeting sgRNAs; 15 day samples are shown). Tested using 1-tailed Mann-Whitney. *** denotes a p

APA citation: Gene editing via CRISPR/Cas9 can lead to cell toxicity and genome instability (2022, August 9) retrieved 5 October 2022 from https://phys.org/news/2022-08-gene-crispr-cas9-cell-toxicity-genome.html

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.