

Guilt Gene Diana M Raab Plain

doi: 10.1007/978-1-4939-7231-9 2 - link.springer - such as gene knockdown, overexpression, or editing are often not suitable for analyzing an extensive pool of ncRNA candidates. However, it is possible to perform genome-wide investigations **clinical research contents vol 13, no 4** - gene expression profiling reveals potential biomarkers of human hepatocellular carcinoma. hu-liang jia, qing-hai ye, lun-xiu qin, anuradha budhu, marshonna forgues, **multiple knockout mouse models reveal lincRNAs are ...** - lines via RNA-seq. (c) guilt-by-association (GBA) analysis for 17/18 lincRNA candidates. individual tiles represent significant (p