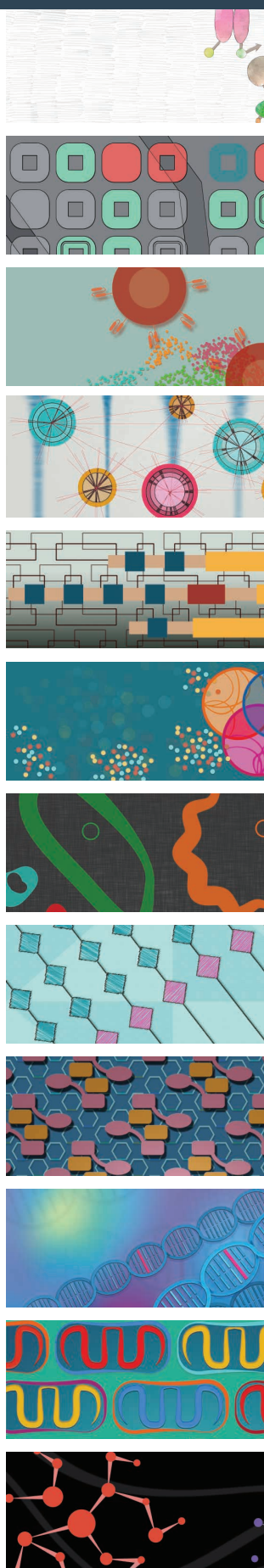
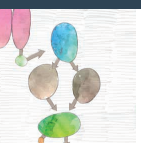
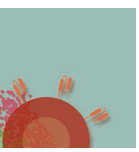
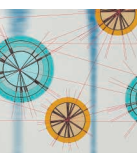
CANCER DISCOVERY

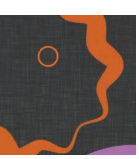
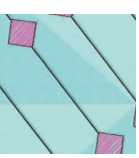
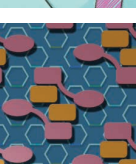
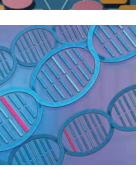
CONTENTS

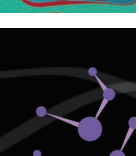
SEPTEMBER 2021 ■ VOLUME 11 ■ NUMBER 9







Précis: A bulk and single-cell atlas of premanufacture T-cells was generated from 71 patients on trial treated with anti-CD19 CAR T-cell therapy, and integrative analysis identified key molecular factors associated with clinical CAR T-cell persistence.

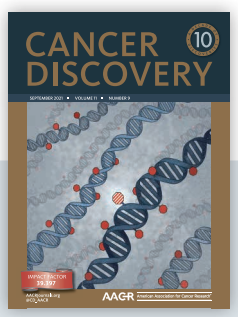
See commentary, p. 2129

CANCER DISCOVERY

CONTENTS

AC icon indicates AuthorChoice

For more information please visit http://www.aacrjournals.org



ON THE COVER Focal increases in cytosine methylation at gene promoters are widespread in human cancers and thought to contribute to silencing of tumor suppressor genes, but tools are lacking to distinguish methylation events that are oncogenic drivers from those that are merely passengers. Pan and colleagues developed MethSig, a statistical inference framework that accounts for variations in the stochastic hypermethylation rate across the genome and between patients, analogous to approaches used to identify driver mutations. Application of MethSig to bisulfite sequencing data or DNA methylation array data identified specific promoter hypermethylation events as potential drivers among a large number of candidate methylation changes, several of which were confirmed to enhance cancer cell fitness, and identified methylation events associated with poor clinical outcome and relapse. Cover artwork by SciStories. For more information, see the article by Pan and colleagues on page 2266.

doi: 10.1158/2159-8290.CD-11-9-CVR