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O, a, b, ab, -
 ca c, a, c
 c a, c ca, T, a
 Ca c, SEEK, ca, a ca c,
 ac, a,
 ca c, a, Ca c, SEEK
 T, a, acc, c DNA a
 b, a, a, a, a,
 (S, a, Ma, a). O, a, c
 ca c, a, a, a, Ca -
 c, SEEK, W, a, a,
 a, a, a, c ca c, a, c, b,
 a, b, a c, W, a -
 (S, a, Ma, a), 626 ca c, a -
 c, Ca c, SEEK T, W, a
 c ca, a, ab, a, ab, ca -

A. ... Proc. Natl. Acad. Sci. U.S.A. ...
 A. ... Nucleic Acids Res. ...
 A. ... Proc. Natl. Acad. Sci. U.S.A. ...
 A. ... Clin. Adv. Hematol. Oncol. ...
 A. ... Expert Rev. Proteomics, ...

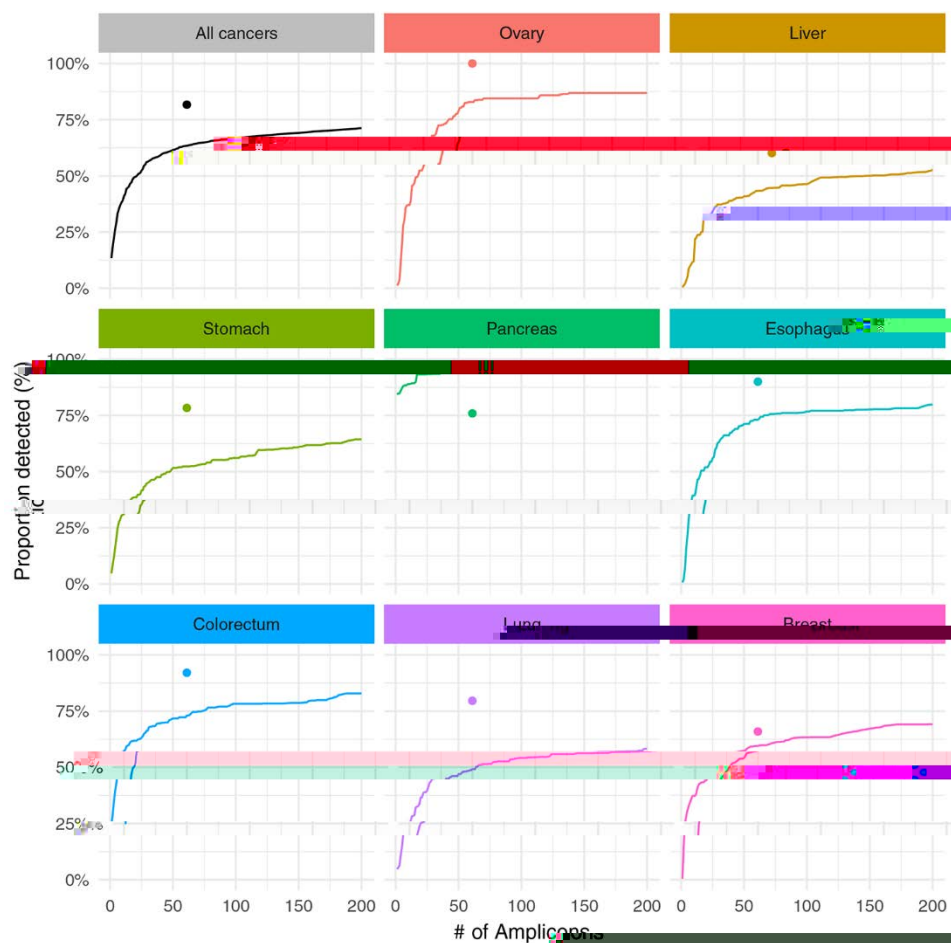


Fig. 1. Development of a PCR-based assay to identify tumor-specific mutations in plasma samples. Colored curves indicate the proportion of cancers of the eight types evaluated in this study that can be detected with an increasing number of short (< 40 bp) amplicons. The sensitivity of detection increases with the number of amplicons but plateaus at ~ 60 amplicons. Colored dots indicate the fraction of cancers detected using the 61-amplicon panel used in 805 cancers evaluated in our study, which averaged 82% (see main text). Publicly available sequencing data were obtained from the Catalog of Somatic Mutations in Cancer (COSMIC) repository.

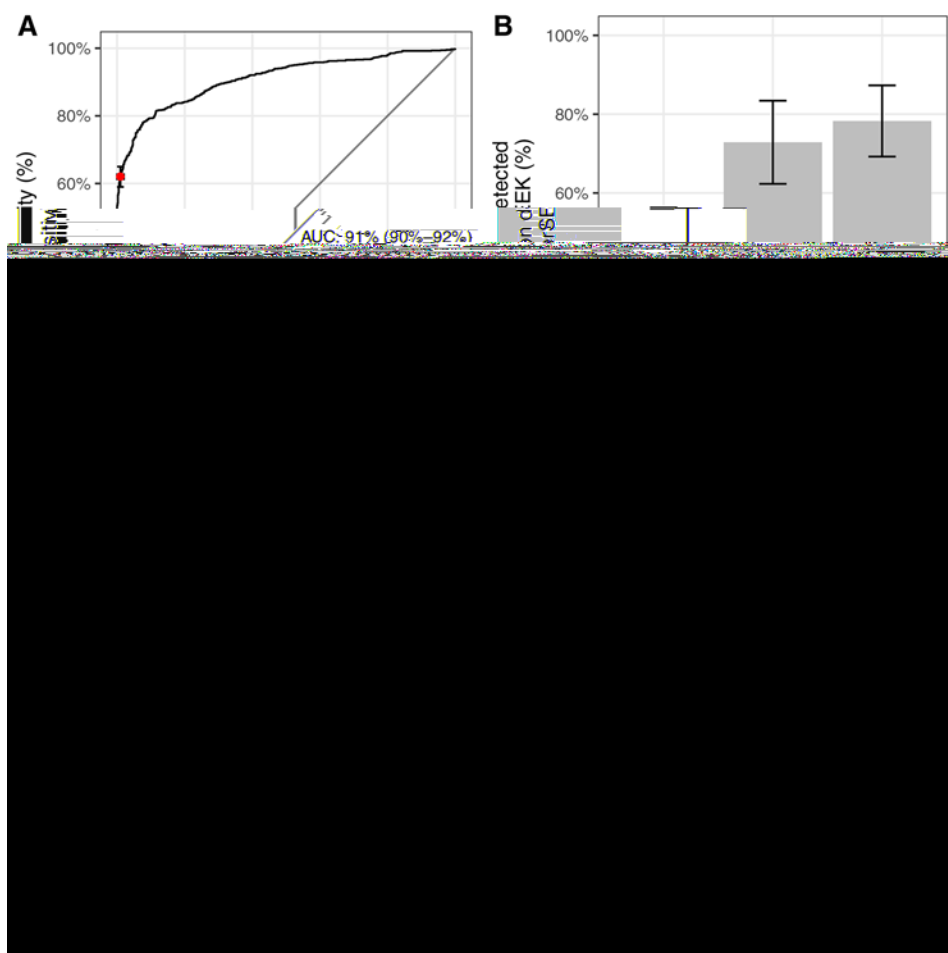


Fig. 2. Performance of CancerSEEK. (A) Receiver operator characteristic (ROC) curve for CancerSEEK. The red point on the curve indicates the test's average performance (62%)

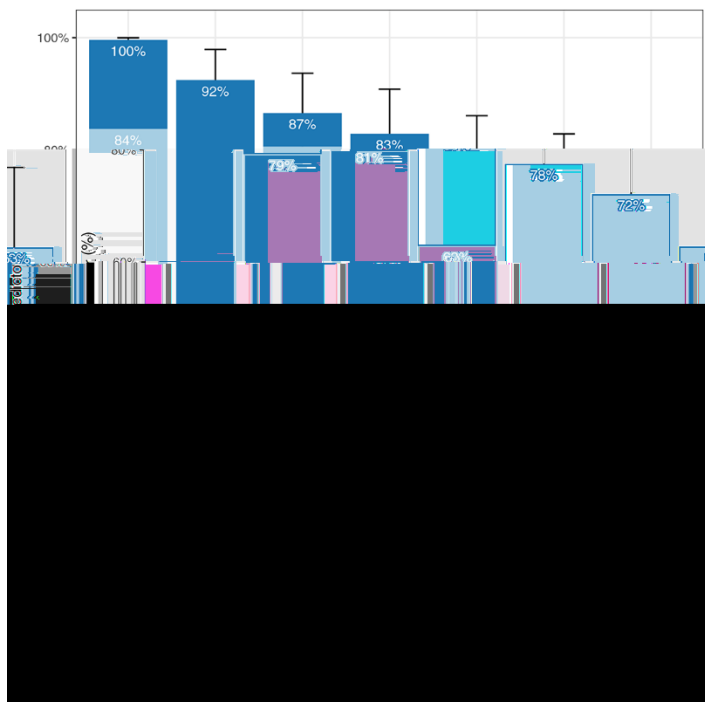


Fig. 3. Identification of cancer type by supervised machine learning for patients classified as positive by CancerSEEK. Percentages correspond to the proportion of patients correctly classified by one of the two most likely types (sum of light and dark blue bars) or the most likely type (light blue bar). Predictions for all patients for all cancer types are provided in table S8. Error bars represent 95% confidence intervals.



Detection and localization of surgically resectable cancers with a multi-analyte blood test

Joshua D. Cohen, Lu Li, Yuxuan Wang, Christopher Thoburn, Bahman Afsari, Ludmila Danilova, Christopher Douville, Ammar A. Javed, Fay Wong, Austin Mattox, Ralph. H. Hruban, Christopher L. Wolfgang, Michael G. Goggins, Marco Dal Molin, Tian-Li Wang, Richard Roden, Alison P. Klein, Janine Ptak, Lisa Dobbyn, Joy Schaefer, Natalie Silliman, Maria Popoli, Joshua T. Vogelstein, James D. Browne, Robert E. Schoen, Randall E. Brand, Jeanne Tie, Peter Gibbs, Hui-Li Wong, Aaron S. Mansfield, Jin Jen, Samir M. Hanash, Massimo Falconi, Peter J. Allen, Shibin Zhou, Chetan Bettegowda, Luis Diaz, Cristian Tomasetti, Kenneth W. Kinzler, Bert Vogelstein, Anne Marie Lennon and Nickolas Papadopoulos

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