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O, a, b, ab, ca, c, ca, T, a, Ca, c, SEEK, ca, a, ca, c, ac, a, c, ca, c, SEEK, T, a, acc, c, DNA, a, b, a, a, a, a, a, a, (S, a, Ma, a). O, a, c, ca, c, a, a, a, Ca, c, SEEK, W, 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, 83% a, (F . 3, ab, S8; $P < 10^{-77}$), b, a, E, ab, ca, c, a, a, a, a, 63% a, (F . 3, ab, S8; $P < 10^{-47}$), b, a, G, a, a, a, c, c, a, a, ca, a, a, a, T, acc, ac, a, a, c, a, c, a, ca, c, (F . 3 a, ab, S10), I, a, a, a, a, a, b, a, ca, c, c, c, T, a, a, a, c, b, c

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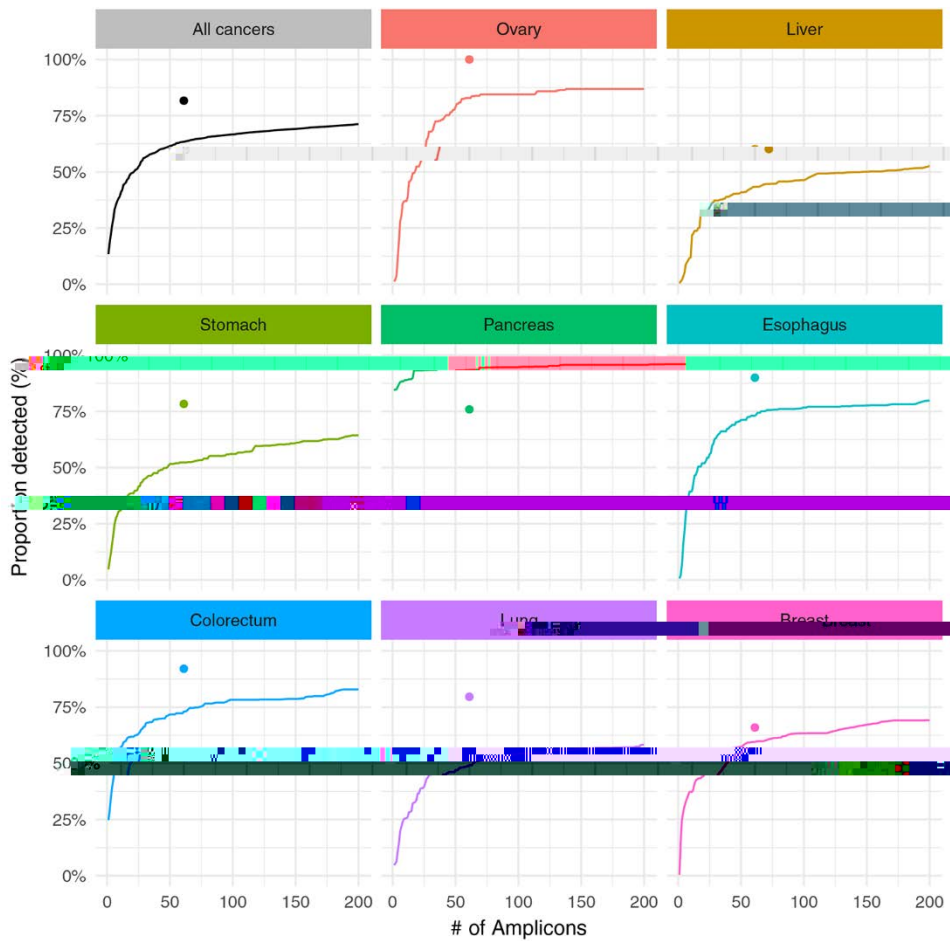


Fig. 1. Detection of a PCR-based assay for 12 cancer types. The assay is based on a panel of 60 amplicons. The detection rate for each cancer type is shown in the bar chart above the plot. The detection rate for each cancer type is shown in the bar chart above the plot. The detection rate for each cancer type is shown in the bar chart above the plot.

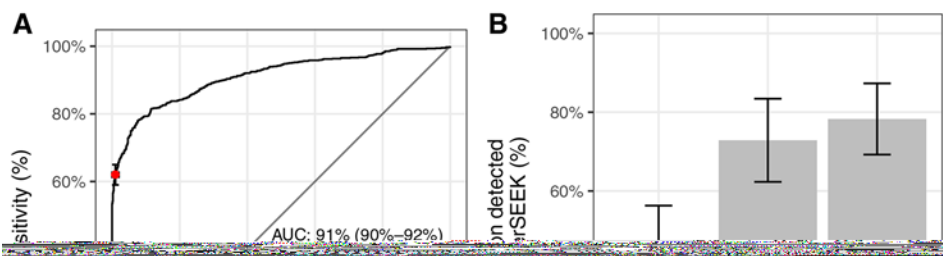


Fig. 2. Performance of Calcium SEEK. (A) Receiver operating characteristic (ROC) curve of Calcium SEEK. The red dot indicates the specificity and sensitivity of the first age group (62%)

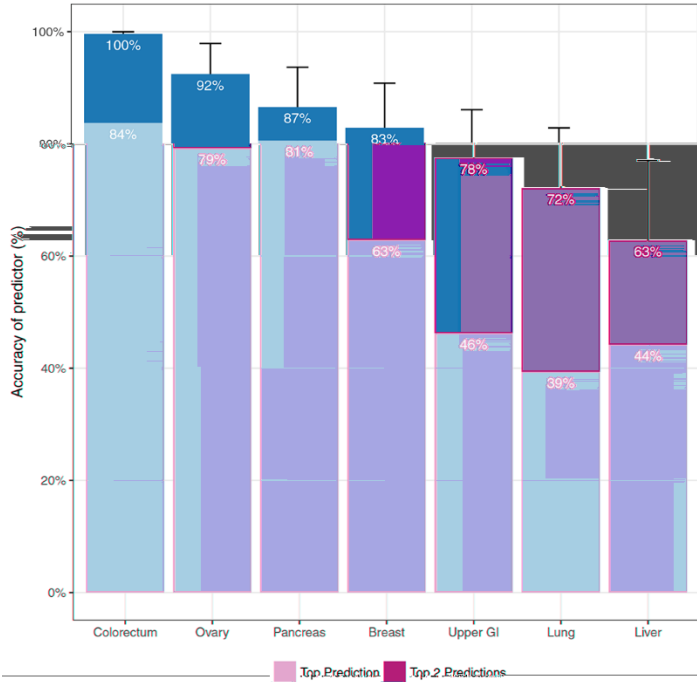


Fig. 3. Identification of cancer subtypes predicted by the leading five genes classified as high by CancerSEEK. Percentages are shown above the bars indicating the total accuracy of the model. The light blue bars represent the top prediction and the purple bars represent the top 2 predictions (highly abundant data). The likelihood of high abundance prediction for all genes for all cancer types are indicated 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, Shilin Zhou, Chetan Bettegowda, Luis Diaz, Cristian Tomasetti, Kenneth W. Kinzler, Bert Vogelstein, Anne Marie Lennon and Nickolas Papadopoulos

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